Barley infected by powdery mildew

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Host transcriptome and proteome changes and the integration of both data sets

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1. Abbreviations 1

2. Abstract 4

3. Zusammenfassung 6

4. Introduction 8

4.1. *Hordeum vulgare* as worldwide important crop and model system 8

4.2. Plant interactions with other organisms 9

4.3. Pathology and the plant immune system 10

4.3.1. Host- and nonhost resistance 10

4.3.2. Plant resistance and defence mechanisms 11

4.3.3. Pathogen recognition by the in plant innate immune systems 13

4.3.4. Induced resistance 17

4.4. Powdery mildew 18

4.4.1. Regulation events during the interaction, classification and life cycle 18

4.4.2. Response of barley to powdery mildew 20

4.4.2.1. Papilla-based resistance 20

4.4.2.2. Hypersensitive resistance 21

4.4.2.3. Susceptibility-related genes 22

4.4.2.4. Secondary metabolism 23

4.4.2.5. Hormones 23

4.4.2.6. Protein turnover 24

4.4.2.7. Sugar metabolism 24

4.5. Transcriptome analysis 25

4.6. Proteome analysis 26

4.7. Integration 28

4.8. Aims of the study 29

5. Material and Methods 31

5.1. Plant and fungal material 31

5.1.1. Growth of germinated barley seedlings ... 31
5.1.2. Maintenance of powdery mildew ... 31
5.1.3. Inoculation of experimental plants ... 31
5.1.4. Collecting of biological material ... 32
5.1.5. Further processing of the samples ... 32
5.1.6. Measurement of chlorophyll concentration in the samples ... 32
5.2. Transcriptome Analysis ... 33
5.2.1. Extraction of RNA ... 33
5.2.2. Concentration and quality of RNA ... 33
5.2.3. Isolation of mRNA from total RNA ... 34
5.2.4. cDNA synthesis ... 34
5.2.5. Radioactive labelling of cDNA with ^{33}P ... 35
5.2.6. The PGRC2-13k-cDNA-macroarray ... 35
5.2.7. Spotting and pattern of the macroarray membranes ... 35
5.2.8. Hybridization of the macroarray with ^{33}P-labelled cDNAs ... 37
5.2.9. Scanning of macroarrays ... 37
5.2.10. Processing of signals and data evaluation ... 37
5.3. Proteome Analysis ... 39
5.3.1. Extraction of proteins ... 39
5.3.2. Dialysis, ultrafiltration and protein concentration ... 39
5.3.3. Labelling of proteins for DIGE ... 40
5.3.4. Pipetting scheme for DIGE gels ... 40
5.3.5. 2-D gels ... 41
5.3.6. Protein separation for DIGE gels ... 41
5.3.7. Visualization of proteins and image acquisition ... 42
5.3.8. Preparative gel ... 42
5.3.9. Coomassie staining ... 43

5.3.10. Image analysis of 2-D spot pattern 43

5.3.11. Spot picking and mass spectrometry 44

5.3.11.1. Analysis of peptide masses with MALDI-TOF-MS 44

5.3.11.2. *De novo* sequencing of peptides by tandem MS/MS 44

5.3.12. Identification of proteins of both mass spectrometry techniques 45

5.4. Integration of the transcriptome and proteome analyses 46

6. Results 47

6.1. General 47

6.1.1. Yield of samples 47

6.1.2. Chlorophyll concentrations in epidermal samples 47

6.2. Transcriptome analysis 48

6.2.1. RNA concentration and hybridization 48

6.2.2. Quality control of technical replication 49

6.2.3. Principle component analysis of all samples 49

6.2.4. Statistically significant regulation events 50

6.2.5. Plant derived, pathogen-regulated transcripts 51

6.2.6. Regulation events at discrete time points 52

6.2.7. Classification of genes into hierarchical functional categories 53

6.2.8. Classification of regulated transcripts of the PGRC2-13k-cDNA-macroarray 54

6.2.9. Distribution of regulated transcripts across categories 54

6.2.10. Investigation of over- and underrepresentation of regulation in functional classification 55

6.2.11. More detailed view of biological clusters in BINs and Sub-BINs 58

6.2.12. Localization of transcript regulation events 59

6.3. Proteome analysis 64

6.3.1. Quality control of technical replication 66

6.3.2. PCA/HCL of all samples 67

6.3.3. Statistical analysis 68

6.3.4. Picking and identification of proteins ... 69

6.3.5. Functional classification of identified proteins ... 74

6.3.6. Clustering of regulated protein spots ... 75

6.4. Comparative matching of transcriptome and proteome analyses ... 76

6.4.1. Detailed analysis of sections ... 79

6.4.1.1. Section I: FDR of q<0.05 both at transcript and at protein level ... 79

6.4.1.2. Section II: FDR of q<0.05 only at transcript level ... 80

6.4.1.3. Section III: FDR of q<0.05 only at protein level ... 80

6.4.1.4. Section IV: FDR of q<0.05 neither at protein nor at transcript level ... 81

7. Discussion ... 82

7.1. The interaction of *Bgh* with barley is restricted to the epidermis ... 82

7.2. Large scale transcriptome analysis ... 83

7.2.1. Identification of barley candidate genes involved in the interaction with *Bgh* ... 85

7.2.2. Functional classification of the genes ... 85

7.2.3. Pathogen-regulated genes were preferentially expressed in the epidermis ... 89

7.2.4. Summary of the transcriptome analysis ... 90

7.3. Proteome analysis ... 91

7.3.1. Barley candidate proteins involved in the interaction with *Bgh* ... 92

7.3.2. Classification of proteins into functional categories ... 94

7.3.3. Proteins whose transcripts are not spotted ... 96

7.3.3.1. Upregulated proteins ... 96

7.3.3.2. Downregulated proteins ... 99

7.3.4. Proteins whose transcripts are below detection threshold ... 99

7.3.5. Summary of the proteome ... 100

7.4. Comparative matching of transcriptome and proteome analyses ... 100

7.4.1. Parallel trends in upregulation ... 102

7.4.1.1. TCA cycle ... 103

7.4.1.2. Amino acid metabolism 104
7.4.1.3. Stress-related 105
7.4.1.4. Transcription regulation 107
7.4.2. Upregulated at transcript, downregulated at protein level 107
7.4.3. Parallel trends in downregulation 109
7.4.3.1. Stress-related 110
7.4.3.2. Cell wall conversion 111
7.4.3.3. Protein degradation 111
7.4.4. Downregulated at transcript, upregulated at proteome level 112
7.4.4.1. Metabolism 113
7.4.4.2. Nucleo-cytoplasmatic transport 114
7.4.5. Summary of the comparative matching 117
8. Outlook 119
8.1. More detailed analyses 119
8.2. Functional experiments 120
9. Literature 121
10. Appendix 135
11. Curriculum vitae 213
12. Presentations and posters 214
12.1. Presentations 214
12.2. Posters 214
13. Acknowledgements 216
14. Declaration 218
15. Personal Informations 219

1. Abbreviations

µ	micro
^{0}C	celsius
2-D	two-dimensional
2-ME	2-mercaptoethanol
A.thaliana	*Arabidopsis thaliana*
ABA	abscisic acid
acc.	according
AcN	acetonitrile
AdoMetDC	S-adenosylmethionine decarboxylase
AdoMetSyn	S-adenosylmethionine synthetase
AM	arbuscular mycorrhiza
aqua dest.	destilled water
ATP	adenosine triphosphate
avr	avirulent
B. graminis	*Blumeria graminis*
BAC	bacterial artifical chromosome
Bgh	*Blumeria graminis* f.sp. *hordei*
Bgt	*Blumeria graminis* f.sp. *tritici*
BIC	barley chemically induced
BIR	biological induced resistance
BLAST	basic local alignment search tool
c(m)	centi(meter)
CC	CC-domain-containing
cCBB	colloidal coomassie brilliant blue
c-di-GMP	cyclic dimeric GMP
cDNA	complementary DNA
CHAPS	3-[(3-cholamidopropyl)dimethylammonio]-1-propanesulfonate
chl.	chlorophyll
CHO metabolism	carbohydrate metabolism
CHS	chalcone synthase
CIR	chemical induced resistance
cont	control sample
CTP	cytosine triphosphate
cys	cystein
d	day(s)
Da	dalton
DAMP	damage-associated molecular patterns
DEPC	diethylpyrocarbonate
DHAP	dihydroxyacetone phosphate
DIGE	differential in-gel electrophoresis
DMF	dimethylformamid
DTT	dithiothreitol
dTTP	deoxy-thymidine-triphosphate
e.g.	for example
E/M	epidermis-to-mesophyll
EDTA	ethylenediaminetetraacetic acid
EST	expressed sequence tag
ETI	effector-triggered immunity
EtOH	ethanol
ETS	effector-triggered susceptibility

f.sp.	forma speciales
FA	fatty acids
FAD	flavin adenine dinucleotide
FDR	false discovery rate
g	gram(s)
x g	gravity
GAP	GTPase activating protein
GAP-DH	glycerine-aldehyde-3-phosphate-dehydrogenase
Gb	gigabases
G-dyes 100, 200 and 300	flourescent dyes for protein labelling
GER	germin
GLP	germin-like proteins
GPX	glutathione peroxidase
GST	glutathione S-transferase
GTP	guanosine triphosphate
h.a.i.	hours after inoculation
h/hrs	hour/hours
H_2O	water
H_2O_2	hydrogen peroxide
HarvEST	EST database-viewing software
HCL	hierarchical clustering
HCl	hydrogen chloride
HR	hyper-sensitive response
HSP	heat shock protein
HvBI-1	barley BAX inhibitor 1
IEF	isoelectric focusing
Inf	infected sample
IPB	Leibniz-Institute for Plant Biochemistry
IPG	immobilized pH gradient
IPK	Leibniz-Institute for Plant Genetics and Crop Plant Research
IR	induced resistance
ISR	induced systemic resistance
JA	jasmonic acid
KCl	potassium chloride
l	liter
LAR	localized acquired resistance
LC-ESI-Q-TOF	liquid chromatography electrospray-ionisation quadrupole time-of-flight
LRR-LK	leucine-rich repeat receptor-like kinases
m	milli
M	molar
M. grisea	*Magnaporthe grisea*
MALDI-TOF	matrix-assisted laser desorption/ionization time-of-flight
MAMP	microbe-associated molecular patterns
MAPK	mitogen-activated protein kinase
max.	maximum
ME	mercaptoethanol
Met	methionine
Mg^{2+}	magnesium
min	minute(s)
mRNA	messenger RNA
MS	mass spectrometry
MS/MS	tandem mass spectrometry
MΩ	milliohm
n	nano
n.e.	not estimated

NaCl	natrium chloride
NADP(H)	nicotinamide adenine dinucleotide phosphate
NADP-ME	NADP malic enzyme
nanoLC-ESI-Q-TOF	nano-liquid-chromatography-electrospray-ionization-quadrupol-time-of-flight
NBS-LRR	nucleotide-binding site leucine-rich repeat
NCBI	National Center for Biotechnology Information
NiC	nucleoporin-interacting protein
NPC	nucleoporin complex
NPP	diphosphonucleotide pyrophosphatase
NTP	nucleoside triphosphate
p	pico
P. indica	*Piriformospora indica*
PAGE	polyacrylamide gel electrophoresis
PAL	phenylalanine ammonia-lyase
PAMP	pathogen-associated molecular patterns
PCA	principle component analysis
PCR	polymerase chain reaction
PDC	pyruvate decarboxylase
PGRC	plant genetic resources center
PR	pathogenesis-related
PRR	PAMP recognition receptors
PTI	PAMP-triggered immunity
R. secalis	*Rhynchosporium secalis*
R-gene	resistance gene
RNA	ribonucleic acid
RNAi	RNA interference
RNAse	ribonuclease
ROS	reactive oxygen species
RT	reverse transcriptase
RuBisCO	ribulose-1,5-bisphosphate carboxylase oxygenase
SA	salicylic acid
S-ACP-DES	stearoyl-acyl-carrier protein desaturase
SAM	S-adenosyl methionine
SAR	systemic acquired resistance
SCF	Skp1, Cullin, F-box
SDH	sorbitol dehydrogenase
SDS	sodium dodecyl sulphate
sek	seconds
SOD	superoxide dismutase activity
SuperBIN	functional annotation of genes
TBE	tris/borate/EDTA
TCA cycle	tricarboxylic acid cycle
TEMED	tetramethylethylenediamine
TFA	trifluoroacetic acid
TIGR	The Institute of Genomics Research
TIGS	transient induced gene silencing
TPS	trehalose-6-phosphate synthase
Tris	tris(hydroxymethyl)aminomethane
TTP	thymidine triphosphate
U	unit
UBA	ubiquitin-associated
UbL	ubiquitin-like
v/v	volume to volume ratio
w/v	weight by volume ratio

2. Abstract

As a major cereal, barley plays an important role in agriculture across the world. Powdery mildew caused by the obligate biotrophic fungus *Blumeria graminis* f.sp. *hordei* (*Bgh*) is a widespread disease affecting barley, causing harvesting losses of up to 30%. Therefore combating this fungal infection is important to improve the yield of this crop. *Bgh* invades exclusively epidermal cells and thus the interaction affects predominantly this tissue. In order to survive, the plant has to recognize *Bgh* infection and to develop sufficient defence mechanisms, whereas the aim of the fungus is to suppress them and to ensure a continuous nutrient acquisition from invaded epidermal cells, thus establishing biotrophism. Pathogen-induced stress has been found to be associated with the changes in the expression of many host genes, which is reflected by changes in transcriptome and proteome. In order to recognize critical time points for gene-expression changes, the infection process has to be examined over a certain period of time.

The aim of the present study was to describe and integrate changes in host transcriptome and proteome during a susceptible interaction of barley with *Bgh*. This should provide a better understanding of mechanisms of susceptibility and might reveal – besides gene expression changes – additional levels of regulation such as protein stability or post-translational modification.

The present study investigated epidermal tissue from barley infected with *Bgh* in five time points from 12 to 120 hours after inoculation (h.a.i.) and compared this data to non-inoculated controls. The tissue samples were divided for transcriptome as well as proteome analyses. The data sets were analysed first independently and subsequently matched to each other.

Transcriptome and proteome analysis was done by using a PGRC-13k-cDNA macroarray and 2-D PAGE/mass spectrometry, respectively. In the transcriptome around 1 500 significantly regulated genes were identified, whereas in the proteome 325 significantly regulated protein spots were detected. Out of these, 86 protein spots were picked based on their abundance and regulation level and could be identified via mass spectrometry. In addition 77 protein spots were picked and analysed, which were not significantly regulated. In the comparative transcriptome/proteome matching 90 regulated transcript-protein pairs fell into the following distinct groups: regulated at transcriptome level only, at proteome level only

or at both levels. Major findings for the transcriptome are the overrepresentation of regulated transcripts involved in secondary metabolism and stress response.

Comparative matching of both datasets showed parallel and non-parallel regulations revealing different response kinetics or post-transcriptional/-translational regulatory mechanisms. For instance a peroxidase 10 and a GTPase interacting protein could be identified as upregulated at transcript, but downregulated at protein level. Furthermore the functional importance of nucleo-cytoplasmatic transport was suggested by a nucleoporin-interacting component and a dnaK-type molecular chaperone heat shock protein 70 and a probably nucleic acid-binding KH domain protein being downregulated at transcript, but upregulated at protein level.

I conclude that extending time course studies of the interaction of barley with *Bgh* to late time points is important to develop hypotheses about mechanisms of susceptibility allowing obligate biotrophs to grow massively without killing host tissues. Furthermore the comparative matching of transcriptome and proteome data will further the understanding of post-transcriptional/-translational modifications driven by fungal effectors in order to suppress plant defence and maximize the supply of nutrients. Results of this and follow-up studies could help to limit the damage to crop plants by fungal infection through a better understanding of the interaction at the biochemical level.

3. Zusammenfassung

Gerste als eine der Hauptgetreidearten spielt weltweit eine große Rolle in der Landwirtschaft. Der obligat biotrophe Pilz *Blumeria graminis* f.sp. *hordei* (*Bgh*) ist der Auslöser des weit verbreiteten Gerstenmehltaus und hat bis zu 30% Ernteausfall zur Folge. Die Bekämpfung dieses Pilzbefalls ist wichtig, um den Ernteertrag zu steigern. *Bgh* dringt ausschließlich in die Epidermiszellen ein, weshalb die Auswirkungen der Interaktion vornehmlich in dieser Schicht des Blattes zu erwarten sind. Um zu überleben, muss die Pflanze den Befall durch *Bgh* erkennen und daraufhin ausreichende Abwehrmechanismen entwickeln. Für den Pilz hingegen ist die Unterdrückung der pflanzlichen Abwehr wichtig, und gleichzeitig die Gewährleistung fortlaufender Aufnahme von Nährstoffen über die infizierten Epidermiszellen. Nach pathogen-induziertem Stress wurden Expressionsänderungen vieler Pflanzengene gefunden, welche sich sowohl in Änderungen im Transkriptom als auch im Proteom niederschlagen. Um die kritischen Zeitpunkte im Infektionsverlauf erkennen zu können, müssen die Effekte über den gesamten Zeitraum untersucht werden.

Das Ziel der vorliegenden Arbeit ist die Beschreibung und die Verknüpfung von Regulierungen des pflanzlichen Transkriptoms und Proteoms in der Interaktion zwischen *Bgh* und einer anfälligen Gerstensorte. Dies soll zu einem besseren Verständnis der Mechanismen der Anfälligkeit führen und könnte, neben Genexpressionsänderungen, zusätzliche Steuerungsebenen wie Proteinstabilität oder post-translationelle Modifikationen aufzeigen.

Die vorliegende Arbeit untersucht Epidermisproben von Gerstekeimlingen, in einem Zeitraum von 12 bis 120 Stunden nach Inokulation mit *Bgh*, und vergleicht sie mit Epidermisproben nichtinfizierter Kontrollpflanzen gleichen Alters. Die Proben wurden für die Transkriptom- und Proteomuntersuchungen aufgeteilt. Zuerst wurden die resultierenden zwei Datensätze einzeln analysiert, anschließend miteinander verknüpft und verglichen.

Die Untersuchung des Transkriptoms wurde mit dem PGRC-13k-cDNA macroarray, die des Proteoms mit 2-D PAGE und darauf folgender Massenspektrometrie durchgeführt. Etwa 1 500 Gene und 325 Proteine waren signifikant reguliert. Für die Gesamtanalyse wurden 86 dieser 325, sowie zusätzliche 77 nicht signifikant regulierte Proteinspots ausgestochen und per Massenspektrometrie identifiziert. In der vergleichenden Analyse der Transkript- und Proteomdaten wurden 90 Transkript-Proteinpaare gefunden, die in folgende Gruppen kategorisiert werden konnten: reguliert auf Transcript-, auf Protein- oder auf beiden Ebenen.

Bei der Transkriptomuntersuchung stellte sich als Hauptbefund die Überrepräsentation regulierter Gene des Sekundärmetabolismus sowie der Stressantwort dar.

Die vergleichende Analyse beider Datensätze zeigte parallele als auch nichtparallele Regulierungen, welche unterschiedliche Kinetiken sowie Regulationsmechanismen auf post-transkriptioneller und post-translationeller Ebene aufzeigen. Als Beispiel wurde bei einer Peroxidase 10 und einem GTPase-beeinflussenden Protein eine Steigerung der Transkriptsynthese, aber eine Verminderung der Proteinsynthese gefunden. Des Weiteren deutete sich der Nukleo-zytoplasmatische Transport als wichtiges Regulationsmittel an, da die Transkriptsynthese sowohl einer Nucleoporin-beeinflussenden Komponente, eines molekularen Chaperons (Hitzeschockprotein 70) des dnaK-Typs, als auch eines potentiellen nukleinsäurebindenden Proteins mit einer KH-Domäne unterdrückt, wobei die Proteinsynthese dieser genannten gesteigert war.

Ich möchte hiermit zusammenfassen, dass Untersuchungen über mehrere Zeitpunkte bis in die späten Stadien der Interaktion von Gerste und *Bgh* wichtig sind. Damit lassen sich Hypothesen der Mechanismen entwickeln, die es dem obligat biotrophen Pilz ermöglichen, sich auf einer anfälligen Gerstensorte zu entwickeln und zu gedeihen, ohne jedoch seine Wirtspflanze zu töten. Des Weiteren wird die Gegenüberstellung von vergleichbaren Transkript- und Proteindaten das Verständnis von post-transkriptionellen und -translationellen Modifikationen erweitern, welche durch Effektoren des Pilzes ausgelöst werden, um die Abwehr der Pflanze zu unterdrücken und die Nährstoffzufuhr zu gewährleisten. Die Ergebnisse dieser und darauf aufbauender Studien können dazu führen, die Interaktionen zwischen Pflanze und Pilz auf biochemischer Ebene besser zu verstehen und dadurch den Schaden durch Ernteausfälle bei Kulturpflanzen zu vermindern.

4. Introduction

4.1. *Hordeum vulgare* as worldwide important crop and model system

Barley (*Hordeum vulgare*) is probably the first crop plant that has been used for cultivation purposes by man for 12 000 years (Schiemann, 1948). Originally coming from the Near East and the Eastern Balkans and now spread over the world, in the beginning barley was used to feed humans and animals. The importance of barley as a cereal lies in its nutritional value, its high mineral content and its ability to grow also on poor soils. The main producers of barley worldwide in 2007 were the Russian Federation (16 million tons), Spain (12 million tons), Canada (11 million tons) and Germany (10 million tons). Barley is the second most cultivated cereal in Germany after wheat (21 millions tons) (http://faostat.fao.org/site/339/default.aspx). Nowadays, however, barley is used primarily for malting and animal feeding rather than for human's basic food (Bothmer, 2003).

In the face of the increasing world population and combined with an increased demand for high-quality food, a significant improvement in the agricultural production both qualitatively and quantitatively is necessary. The area available for agricultural use will decrease through erosion, oversalting, pollution with chemicals and flooding in some regions, together with the spread of urbanization to house the growing population. (Bruinsma, 2003). The supply of the market with the above mentioned cereals in adequate amounts and for reasonable prices makes it necessary to avoid loss in productivity of crops by abiotic (e.g. drought, salt) or biotic factors (insects, plant diseases).

The genome of barley is diploid with 2 n = 14 chromosomes and with a size of approximately 5.4 Gb. Within the scientific community barley is used as a model plant for *Triticeae* such as wheat and rye because of its diploidy, which stands in contrast to the hexaploidy of wheat (Graner and Altschmied, 2001). Therefore genetic and genomic studies can be carried out more easily in barley.

One of the major problems in cereals is the spread of phytopathogenic organisms with new types of virulence, which may cause severe agronomic losses due to reduced harvest quantity or quality. Agriculture will have to become further intensified in order to face these challenges, although the ensuing monocultures will be vulnerable to the spreading effect of

virulent pathogens, resulting in potentially aggravated losses (Bruinsma, 2003). Therefore, a deeper knowledge of the genes and proteins as well as the underlying signalling cascades in plant-pathogen interaction will help to achieve a new quality of pathogen control and sustainable plant protection. This ultimately will lead to stabilizing the yield of these important crops.

4.2. Plant interactions with other organisms

Plants are sessile organisms and besides abiotic stress are also affected by biotic stress, which is caused by many different parasites: microbes, fungi or herbivores. Plant pathogens employ diverse strategies in order to live on their host. Some enter their host plant via gas or water pores or gain access via wounds. Nematodes and aphids feed by inserting a stylet directly into a plant cell, and fungi can directly enter plant cells, extend their hyphae across the surface, or grow through the cells. Fungi can also invaginate the host cell membrane with their feeding structures (haustoria). The haustorial plasma membranes, the extracellular matrix and the host plasma membranes form an intimate interface, which determines the outcome of the interaction. On the other hand there are also symbiotic fungi such as arbuscular mycorrhiza (AM) which interact with the plant. They help the plant by enhancing the uptake of minerals out of the soil through their hyphae in exchange for carbohydrates (Marschner, 1994, Pfeffer et al., 1999, Bago et al., 2003). This enhances the productivity of the plants, resulting in better growth, a higher seed yield and increased phosphorus content (Powell, 1981, Azcon-Aguilar et al., 1996, Al-Karaki et al., 2004, Li et al., 2006). Furthermore AMs enhance the plant's salt and drought tolerance (Feng et al., 2002). Additionally a mycorrhization helps to overcome phytopathogenic bacteria, fungi and insects in the roots but also in the leaves through the induction of local and systemic resistance (Cordier et al., 1998, Pozo et al., 2002, Liu et al., 2007a). The increase in salt tolerance of barley roots after infection by the endophyte *Piriformospora indica* is based among other things on the increase in the concentration of antioxidants and on an enhanced activity of antioxidative enzymes (Waller et al., 2005, Baltruschat et al., 2008). The dispersal of the necrotrophic and hemibiotrophic pathogens *Fusarium culmorum, Fusarium graminearum* and *Cochliobolus sativus* is obstructed by colonization in barley roots (Waller et al., 2005, Deshmukh and Kogel, 2007, Schafer et al., 2007). Systemic resistance was observed in barley and wheat leaves against the biotrophic pathogens *Blumeria graminis* f.sp. *hordei* (*Bgh*) and *Blumeria graminis* f.sp*. tritici* (*Bgt*), respectively (Waller et al., 2005, Serfling et al., 2007).

Because of the positive and negative effects of these interactions on plants, a system of differentiation between self and non-self and between pathogenic and beneficial organisms

would be beneficial so as to be able to react to an infection in a suitable way. There is a hypothesis that defence-related features are suppressed by *Glomus intraradices* during early stages of colonization and therefore connected with the successful establishment of AM symbiosis (Guenoune et al., 2001). As one example, plant lectins are said to join the direct root symbiosis and plant defence (De Hoff et al., 2009). Also the specificity of calcium response with regard to signature, amplitude, duration, frequency and location is shown to be important for *Arabidopsis thaliana* (*A.th.*) when recognizing pathogenic or beneficial plant microbes (Vadassery and Oelmuller, 2009).

4.3. Pathology and the plant immune system

If a pathogen infects the host successfully, the interaction is called compatible, the host is referred to as susceptible and the pathogen virulent (Schlösser, 1997). The tolerance against pathogens (particularly viruses) is a special case when the pathogen is proliferating in susceptible plants, but the plant does not show severe disease symptoms (Agrios, 1997). When the penetration or the proliferation of a microorganism is successfully prevented, the ensuing interaction is incompatible, the host is resistant and the pathogen is avirulent. Most pathogens are successfully repelled by this mechanism (Thordal-Christensen, 2003). One can differentiate the following types of resistance: (a) nonhost resistance, (b) race-specific, qualitative host resistance and (c) race-unspecific, quantitative basal host resistance.

4.3.1. Host- and nonhost resistance

One of the oldest traits of a plant is its ability to resist pathogens, and nonhost resistance is the most widely distributed resistance against many microorganisms (Thordal-Christensen, 2003). The term “nonhost resistance” describes the durable resistance observed when all genotypes of a plant species exhibit resistance to all members of a given pathogen species (Heath, 2000, Thordal-Christensen, 2003). Plants show nonhost resistance against most potential pathogens because they do not fulfill the physiological needs of the pathogen (Thordal-Christensen, 2003), and the preformed and induced general chemical, enzymatic and structural defence mechanisms of the plant are effective. During the co-evolution of plants and compatible phytopathogens, nonhost resistance is permanently broken by the pathogen, leading to a basal compatibility. In this case plants in their turn have evolved new resistance mechanisms that are called host resistance. One can hereby differentiate between race or cultivar unspecific (quantitative) and race or cultivar specific (qualitative) resistance, however a sharp border cannot be drawn always between them (Poland et

al., 2009). The term “quantitative resistance” means that it is active against all races of a pathogen and describes a basal effect, whereby infection of the pathogen is often stopped in its early stages and losses are minimized (Thordal-Christensen, 2003). Due to its polygenic inheritance this type of resistance is relatively robust although it does not offer complete protection (Parlevliet, 2002, Thordal-Christensen, 2003). The race-specific qualitative resistance, on the other hand, is monogenic based on a specific interaction between a resistance gene (R-gene) of the host and a corresponding avirulent (avr) gene of the pathogen. Harold Flor proposed that every pathogenic effector protein is recognized by resistance proteins of the plant and named this model ‘gene-to-gene-hypothesis’ (Flor, 1955). It was confirmed almost 40 years afterwards by cloning the first pair of R–avr proteins from tomato and tobacco (Martin et al., 1994). The rice Pi-Ta resistance protein, an NBS-LRR protein, and the secreted avr protein avr Pi-Ta, from the rice blast fungus *Magnaporthe grisea* are a first example from cereals (Jia et al., 2000). The resistance-gene product is often an NBS-LRR protein that interacts directly or indirectly with the Avr product (specific effector) and initiates the defence response. Especially the hypersensitive reaction is typical for the qualitative, R-protein-mediated resistance (Eichmann and Huckelhoven, 2008). Strong resistance can also be based on the enzymatic detoxification of fungal toxins (Johal and Briggs, 1992) or the modulation of the defence response to enhance penetration resistance as in the case of Mlo in barley (Buschges et al., 1997), which is a prototype for a monogenic, race non-specific resistance in barley. However because of its specificity, R-gene-mediated qualitative resistance sometimes only lasts a few years in the field until a new species of the pathogen develops. A recent example is the new race Ug99 of the wheat stem rust *Puccinia graminis* f.sp. *tritici*, which has overcome prevailing R-genes (Stokstad, 2007a, Stokstad, 2007b). Finally, the defence strategies and biochemical changes that occur in host- and nonhost resistance can partly overlap (Somssich and Hahlbrock, 1998, Thordal-Christensen, 2003).

4.3.2. Plant resistance and defence mechanisms

In general the plant’s defence is based on preformed barriers and induced responses. A compatible host-parasite-interaction can be disabled, if the pathogen cannot recognize the host because of the absence of structural or physiological clues (Thordal-Christensen, 2003). In other cases resistance or defence mechanisms are formed constitutively or induced after infection.

Preformed defence mechanisms are the first line of defence (Thordal-Christensen, 2003), they can be mechanical and structural barriers (cuticle, plant cell walls, trichomes) or biochemical and enzymatic compounds like toxic secondary metabolites [Terpenes (e.g.

saponins), phenols (e.g. cumarines), nitrogenic compounds (e.g. alkaloids, cyanogenic glycosides)] and antimicrobial proteins (e.g. defensins, chitinases, glucanases, enzyme inhibitors) plus detoxifying enzymes (Papadopoulou et al., 1999, Heath, 2000, Taiz, 2000). If a pathogen overcomes these preformed barriers, the next hurdle is the induced plant defence. These again are either structural, enzymatic or chemical (Thordal-Christensen, 2003). Transcription of some genes leading to defence-related proteins can be found shortly after pathogen attack. These defence-related proteins consist of 17 families and belong to the PR-(pathogenesis-related) proteins, which are overviewed in (van Loon et al., 2006) and are massively induced both locally around infection sites and systemically. In these families we can find as members: lytical enzymes such as beta-glucanases (PR-2) and chitinases (PR-3, PR-7, PR-8 and PR-11), lignin-forming peroxidases (PR-9), ribosome inhibiting proteins, PR-10, defensins (PR-12), thionines (PR-13); LTPs (lipid transfer proteins, PR-14), oxalate-oxidases (PR-15, PR-16) and further proteins with unknown functions. Transiently silenced PR-1 expression showed that PR-1b is one of the factors that limits penetration of the leaves by *Bgh* (Schultheiss et al., 2003). Early recognition of a pathogen is necessary for the plant to be able to quickly leading to a fast activation of defence-response genes (von Ropenack et al., 1998, Thordal-Christensen, 2003). Preformed as well as induced defence responses can prevent penetration (penetration resistance) or the further development of the pathogen.

Resistance against penetration may be attained in at least three different ways: (a) a local thickening of the cell wall (papillae forming), (b) the inhibition of pathogenic enzymes which degrade the plant's cell-wall or (c) the secretion of anti-microbial substances that kill the entering pathogen (Huckelhoven, 2005). Reinforcement of the cell wall takes place in incompatible as well as in compatible interactions, although in compatible interactions it usually occurs rather late during the course of host colonisation by the pathogen. The accumulation of compounds such as lignin, suberin, thionines, HRGP (hydroxyproline-rich glycoproteins) and polysaccharides such as cellulose, callose and pectins at penetration sites are required for the thickening of the cell walls and the formation of papilla (Brisson et al., 1994, von Ropenack et al., 1998). Many of these compounds form complex polymers and can crosslink (Brisson et al., 1994) catalyzed by hydrogen peroxide (H_2O_2). The presence of H_2O_2 in cell wall deposition is a biochemical marker showing that barley cells have been penetrated by *Bgh* (Huckelhoven et al., 1999, Hückelhoven et al., 2000, Trujillo et al., 2004). The speed of the formation and the resulting strength of the cross-linking determine whether the papillae can stop a pathogen (von Ropenack et al., 1998, Assaad et al., 2004).

The hyper-sensitive response (HR) of the infected cells or the surrounding tissue is a ubiquitous feature, which stops further distribution of the pathogen after it has penetrated the

plant (post-penetration resistance)(Kombrink and Schmelzer, 2001). The HR accompanies many but not all incompatible interactions and is considered one of the important mechanisms leading to resistance. It was shown that during the HR, the accumulation of reactive oxygen species (ROS), cytotoxic or cell-death promoting proteins and phytoalexins leads to a rapid collapse of tissue, and therefore biotrophic and hemi-biotrophic pathogens lack their food resource (Greenberg and Yao, 2004). The HR's role in defending against necrotrophic pathogens that obtain their energy from dead cells is not yet fully revealed. Possibly toxic compounds of the vacuole that are secreted due to the death of the cell contribute to the defence (Hammond-Kosack and Jones, 1996). On the other hand, cell death might be beneficial for necrotrophic pathogens (Kumar et al., 2001). The most important aspect for a successful defence in many interactions is choosing the right time point for the onset of HR (Huckelhoven, 2007). The transient accumulation of ROS, the "oxidative burst" is a relatively early response to pathogens and elicitors (Thordal-Christensen et al., 1997a). Inducing an oxidative burst at the plasma membrane is a part of the HR and produces active oxygen species such as superoxide that is rapidly dismutated to hydrogen peroxide (Wojtaszek, 1997, Vranova et al., 2002). ROS can be produced extracellularly by NADPH-oxidases, peroxidases, aminoxidases, super-oxide dismutases and oxalate-oxidases (Huckelhoven, 2007). Besides their importance in HR and the cross-linking of cell wall components, ROS have a direct toxic effect on pathogens and a role as signalling molecules (Jabs et al., 1997, Torres et al., 2002). However, ROS can also have antagonistic effects in the cell death reaction (Torres et al., 2005). During a successful infection of barley leaves by *Bgh* one can find an accumulation of superoxide radical anions in the mesophyllic cells underlying the attacked epidermal cells and later in the attacked epidermal cells around the developing haustoria (Thordal-Christensen et al., 1997b, Vanacker et al., 2000). It seems that ROS itself is not alone sufficient, but that synergy with other signalling molecules like nitric oxygen is necessary (Huckelhoven, 2007). In addition local HR is often associated with the onset of systemic acquired resistance (SAR, see chapter 4.3.4) in distal plant tissues.

4.3.3. Pathogen recognition by the in plant innate immune systems

With induced defence mechanisms the plant must be able to differentiate between "self" and "non-self" and also between pathogenic and beneficial organisms and to react in a suitable way. Unlike mammals, plants lack mobile defender cells or a somatic adaptive immune system. Animal and plant innate immune systems use a set of similar receptors to recognize pathogens. These receptors are located on the cell surface, contain a protein kinase domain (Song et al., 1995) and are called pathogen-associated molecular patterns (PAMP)-recognition receptors (PRRs). When receptor-like kinase proteins detect the presence of a

pathogen they activate defence genes, triggering ion channel gating, oxidative burst, cellular redox changes and protein kinase cascades. These are all responses that either directly activate cellular changes or changes in gene expression and thereby boost plant defence responses.

The plant innate immune system uses a two-layer recognition system (Jones and Dangl, 2006). Whereas the first layer detects certain conserved epitopes that are widely spread in many classes of microorganisms, the second one reacts directly or indirectly to specific pathogen effectors.

The first layer consists of the detection PAMPs or microbe-associated molecular patterns (MAMPs), which are conserved, secreted molecules (Nurnberger et al., 2004) by PRRs (Jones and Dangl, 2006). PRRs activate PAMP-triggered immunity (PTI) and prevent further colonization of the host (Jones and Dangl, 2006, de Wit, 2007). PTI is the first inducible layer of plant defence and often underlies the nonhost and quantitative host resistance (Schweizer, 2007). Examples of bacterial MAMPs are lipopolysaccharides from gram-negative bacteria, peptidoglycanes from gram-positive bacteria or bacterial flagellin (Underhill and Ozinsky, 2002, Chamaillard et al., 2003, Smith et al., 2003). Major fungal PAMPs for which PRRs are identified are endopolygalacturonases, xylanases, beta-glucan and cell wall components like fungal chitin or elicitin (Schweizer et al., 2000, Poinssot et al., 2003, Nürnberger and Lipka, 2005, Gaulin et al., 2006). The known receptors from *Arabidopsis thaliana* for the bacterial MAMPs flagellin (flg22) and the elongation factor Ef-TU, Flagellin-sensing 2 and Ef-TU receptor group into the class of leucine-rich repeat receptor-like kinases (LRR-LK). PRRs of fungal PAMPs are known amongst others in tomato, namely LeEIX1 and -2 (Ron and Avni, 2004) and the CEBIP in rice plants (Kaku et al., 2006). CEBIP is a transmembrane chitin oligosaccharide elicitor binding protein, whereas LeEIX1 and -2 code LRR-containing glycoproteins are situated on the cell surface. The signal transduction cascades of PAMP/MAMP-recognition are not yet known in detail. Subordinate mitogen-activated protein kinases (MAPK)-cascades play a role in the case of flg22. Besides recognizing PAMPs and MAMPs, plants have also acquired mechanisms to detect degradation of self-molecules, which are termed damage-associated molecular patterns (DAMPs). They often result from the hydrolytic degradation of cell wall components through secreted fungal enzymes during host invasion (Matzinger, 2007). An example of recognized DAMPs that emanate from damaged cell walls in *Arabidopsis thaliana* are oligo-alpha-galacturonides (Denoux et al., 2008). In addition plant hormones have a function in the signalling cascades, such as salicylic acid (SA), jasmonic acid (JA) and nitric oxide (Nürnberger and Lipka, 2005).

The second layer of the plant immune system is based on the recognition of a pathogenic avirulence product (effector) by a corresponding plant R-gene product. The majority of R-gene products are encoded as nucleotide-binding site leucine-rich repeat (NBS-LRR) proteins with a characteristic nucleotide binding domain and a C-terminal, LRR-domain. This large family of hundreds of diverse genes can be divided into Toll/interleukin-1 receptor-domain-containing (TIR-NBS-LRR) and coiled-coil-domain-containing (CC-NBS-LRR) subfamilies (McHale et al., 2006). The presence of an effector inside or outside the cells or the alteration that the effector has caused to a host protein may be detected by a corresponding R-gene product, which leads to race-specific effector-triggered immunity (ETI). R-gene products control a broad set of defence reactions that often rapidly and strongly stop or retard further growth and spread of the pathogen. Harold Flor's "gene-to-gene hypothesis" could be demonstrated by the description of these effector-R-protein interactions (Jia et al., 2000).

The co-evolution of the pathogens to overcome or suppress detection by the plant and the corresponding co-evolution of the host to avoid this is summarized in the zig-zag-model (Figure 1) (Jones and Dangl, 2006). In the first phase the presence of the PAMPs inside or outside the cells or the alteration that the effector has caused to a host protein are detected by PRRs, which leads to a PAMP-mediated immunity. Pathogens that suppress the PAMP-mediated immunity or manipulate the key components of resistance by effectors can colonize the plant (second phase). Pathogen virulence is often enhanced by these effectors suppressing basal host defence, named effector-triggered susceptibility (ETS). Bacterial effectors from *P. syringae* can repress callose deposits and the expression of host genes that are essential for papillae to form (Hauck et al., 2003, DebRoy et al., 2004, Torres et al., 2005). In the third phase effectors are recognized by plant R-genes, which leads to a race-specific effector-triggered immunity (ETI). The presence of R-genes puts pressure on the pathogen to evolve mutated or additional effectors to creep over the ETI, followed by the establishment of new NBS-LRRs from the plants, recognizing the mutated effectors (Jones and Dangl, 2006). A co-evolution of R-genes and pathogenic effectors is ongoing, affected by population dynamic processes and the fitness costs for the plant and the pathogen through expression of certain R-genes and effectors.

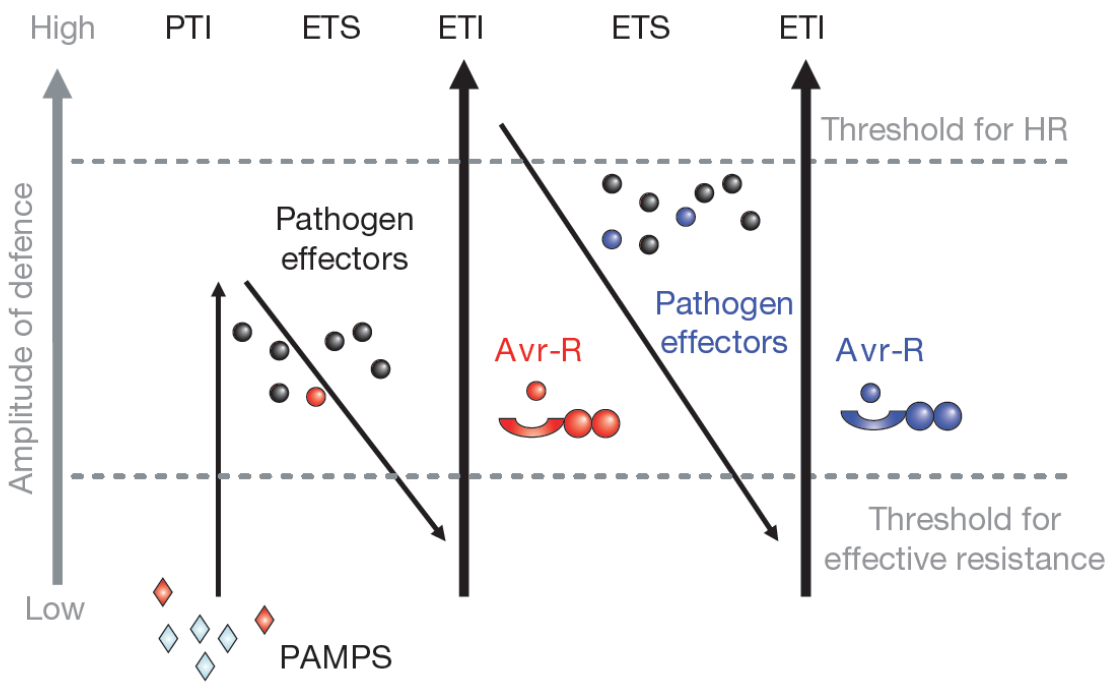


Figure 1: Jones and Dangl's zig-zag-model according to (Jones and Dangl, 2006): PAMPs and effectors co-evolve with the recognition abilities of the plant; PAMPs are recognized by the plant by using PRRs, resulting in PTI. Effectors increase the susceptibility of the plant's ETS. R-proteins recognize the effectors and specific resistance is established: ETI. New effectors develop, resulting in ETS, whereupon new resistance proteins recognize them (ETI).

Race-specific resistance sometimes only lasts a few years until a new race of a pathogen develops. As direct interaction of avr-proteins and R-proteins could not be detected in many systems (Dangl and Jones, 2001), the guard-hypothesis (Van der Biezen and Jones, 1998, Dangl and Jones, 2001) and the derived decoy-model (van der Hoorn and Kamoun, 2008) were proposed. In both cases it is assumed that the R-protein does not recognize the effector (avr-protein) alone, but the interaction of the target partner with the effector.

In the guard model the R-protein monitors a target protein that is essential for the virulence of the pathogen. With this model a single R-protein can recognize multiple unrelated effectors that interact with the same target in the plant (Houterman et al., 2009). This indirect interaction between R-protein and effector has been reported in many non-fungal pathogenic interactions, evidently suggesting that a majority of interactions agrees with the guard model (Jones and Dangl, 2006). The advantage of this model for the plant lies in the difficulty for the pathogen to overcome the resistance mechanism by solely mutating this effector (Jones and Dangl, 2006, de Wit, 2007). In the decoy-model the R-protein monitors an imitation of a target protein that is important for the virulence. This imitated protein interacts with the Avr-protein, but has no influence on the fitness of the non-attacked host. Based on this, the sort of conflicting selection pressure upon a target protein that is essential for both the pathogen virulence and plant growth and development as it appears in the guard model is avoided.

This conflicting selection pressure arises from R-gene polymorphisms in a population; some individuals have this certain R-gene, others do not have it. Without the R-gene the selection will develop a reduced binding affinity of the target gene to the effector. In the presence of a R-gene it will be selected in the direction of an increased binding affinity (van der Hoorn and Kamoun, 2008).

Defence mechanisms induced through recognition of virulent or avirulent pathogens are not limited locally, but the information can also induce preventive defence in distant areas of the plant.

4.3.4. Induced resistance

Plants can show enhanced resistance against further infections if infected by a virulent or avirulent pathogen. This phenomenon is termed biological induced resistance (BIR). The enhanced defensive state that can last several months is also called priming (Conrath et al., 2002). If the induced resistance is not restricted to the location of the first infection (LAR, localized acquired resistance) it is SAR (Ross, 1961, van Loon et al., 1998). This mechanism was first described in the system tobacco-tobacco mosaic virus (Chester, 1933), but BIR can also be caused by non-pathogenic mycorrhizal rhizobia. This is induced systemic resistance (ISR) (van Loon et al., 1998), in contrast to SAR.

SAR is accompanied by the accumulation of salicylic acid and the expression of PR-proteins in several studied dicotyledonous plants (Van Loon and Van Strien, 1999). The SA-accumulation is crucial for the occurrence of resistance in transgenic NahG plants, in which a salicylic acid hydroxylase degrades SA and neither a priming effect nor SAR can be observed (Gaffney et al., 1993). An intact cuticle in distal tissues seems to be essential for the induction of SAR in plants (Xia et al., 2009). In contrast, ISR is usually independent of SA but needs components of the jasmonate- and ethylene signalling cascades (Pozo et al., 2004) where no induction of PR-genes is observed (Pieterse et al., 1996, Press et al., 1997, Pieterse et al., 1998).

Beside these forms of BIR there is also chemical induced resistance (CIR) (Ryals et al., 1996, Beßer et al., 2000), which is brought about by exogenous SA or through its functional analogues 2,6-dichloroisonicotinic acid and benzol (1,2,3) thiadiazole-7-carbothioic acid S-methyl ester. This mechanism is active in dicotyledonous as well as in monocotyledonous plants. In barley chemically induced-genes are expressed after treatment with the above mentioned resistance inducers and serve as markers for the CIR (Beßer et al., 2000). At least in *Arabidopsis thaliana* (*A.thaliana*), all these forms of induced resistance (BIR, CIR,

ISR, SAR) depend on the expression of NPR1/NIM1 (nonexpressor of pathogenesis-related genes 1/noninducible immunity 1), resulting in a key role in the development of the resistance (Cao et al., 1994, Delaney et al., 1995, Shah and Klessig, 1996). The NPR1-protein shows homology to the animal signal transduction factor I kappa B proteins (Ryals et al., 1997) and acts as a transcription co-activator on genes involved in the development of the resistance. This suggests that the SAR signalling pathway in plants represents an ancient and ubiquitous defence mechanism in higher organisms.

4.4. Powdery mildew

4.4.1. Regulation events during the interaction, classification and life cycle

Powdery mildew is caused by a large group of obligate biotrophic ascomycete fungi from the order of the Erysiphales. This order contains only one family, the Erysiphaceae (Huckelhoven, 2005, Huckelhoven, 2007) and can be divided into five tribes by sequence analysis of nuclear DNA (Mori et al., 2000), namely the Erysipheae, Golovinomycetinae, Cystotheceae, Phyllactinieae and Blumerieae as well as further subtribes and more than ten genera (Braun, 2002). Members of the order Erysiphales in general have developed very specific and specialized mechanisms to avoid the resistance of their host and to acquire the nutrient they need without causing too much damage. Most species of powdery mildew are very host-specific, infecting only a narrow range of host plants, or sometimes only one particular host species. It is therefore assumed that the relationship between powdery mildew and their hosts represents close co-evolution. The Erysiphales are therefore, and because of their agronomic relevance, a good model system for the investigation of the evolutionary relationships between pathogenic fungi and their host plants (Mori et al., 2000).

One member of the Erysiphales, *Blumeria graminis* (*B. graminis*), infects cereals. *Bgh* is a widely spread fungal pathogen in a humid or semi-arid environment. It is strictly host-specific to barley and can cause a yield loss of up to 30 % through reducing the number of grains per spike (Huckelhoven, 2005). Multiple races of this fungus exist and new ones continue to emerge as a result of genetic recombination. Other factors that favour powdery mildew development are: presence of susceptible cultivars, dense plantings, high nitrogen fertilization and finally a combination of cold and humid weather.

Haploid conidiae of *Bgh* are spread by the wind. When growing on the plant, *Bgh* infects only epidermal cells of the organs above ground (Huckelhoven, 2005, Zhang et al., 2005). As an obligate biotrophic ectoparasite, it extracts its nutrients from living cells through specialized

hyphae that penetrate the epidermal cells of the host and produce absorbing organs in the epidermis called haustoria (Green et al., 2002, Glawe, 2008). A conidium germinates after contact with the leaf surface within two hours and develops a primary germ tube. This is necessary, as it can recognize the host and take up water (Carver and Ingerson, 1987, Pryce-Jones, 1999). The secondary germ tube (appressorial germ tube) develops within four to eight hours, swells and differentiates into an appressorium. The development of the appressorium is independent of whether a compatible or an incompatible interaction is present. With the help of a penetration peg it penetrates the cuticle and cell wall through mechanical force and enzymatic processes (cellulases, cutinases). The penetration can be stopped by the plant through development of papillae. Free cutin monomers that are produced by fungal degradation of plant cuticles can be detected by the plant and act as biochemical signals, inducing a transient alcalinization response, as in the case of chitin (Schweizer et al., 1996). After successful penetration, the fungus develops a haustorium inside the epidermal cell, which is surrounded by the invaginated plant plasma membrane, thus keeping the plant epidermal cell intact.

After the successful establishment of the haustorium, secondary hyphae are developed, which form secondary appressoriae to establish further haustoria and allow the fungus to spread over the leaf. Pathogens need access to nutrients from their host for reproduction and *Bgt* changes solute transport in its host wheat (Sutton et al., 2007), whereby glucose, not sucrose is transferred from the leaf to the pathogen (Sutton et al., 1999). Sugar efflux is essential for inter-cellular exchange of carbon and energy in multicellular organisms. Nutrient efflux mechanisms of the host such as sugar efflux transporters are highjacked by pathogens to redirect nutrient flux for their development. Thereby effectors of virulent strains are interacting with promoters and inducing the expression of several transporters and of invertases to alter the sugar efflux (Fotopoulos et al., 2003, Chen et al., 2010b). Several sugar glucose uptake transporters were identified, and RNAi silencing was used to reveal which effectors need which transporters, in an attempt to find new strategies for combating fungal infections (Chen et al., 2010b). In addition to the redirection of the carbon flux, the fungus actively prevents the death of the host, resulting in the so-called ‘green island effect’ (Huckelhoven, 2005) whereas in contrast, necrotrophic pathogens thrive on dead host cells (Friesen et al., 2008) and even provoke programmed cell death of their host (Hoefle et al., 2009). Under optimal conditions the infection cycle of *Bgh* is completed within five to six days through the formation of upright standing spore-chains, containing the next generation of conidiae to spread the disease.

At the end of the growing season sexual reproduction of the fungus occurs by the formation of brownish cleistothecia with up to 25 asci, each comprising eight haploid ascospores after

the meiosis. The liberation of the ascospores takes place in the next spring season when the cleistothecia swell and break open (Agrios, 1997).

4.4.2. Response of barley to powdery mildew

The interaction between barley and *Bgh* has been well characterized genetically and physiologically. A physiological specialization in this pathosystem was first observed in 1930 by Mains and Dietz (Mains and Dietz, 1930) and research since then has shown that the host-pathogen interaction is also consistent with Flor's gene-for-gene concept (Zhang et al., 2005).

4.4.2.1. Papilla-based resistance

The basal resistance of barley to *Bgh* in forming papillae is a quantitatively inherited trait that is based on non-hypersensitive mechanisms of defence. Complex regulatory mechanisms have evolved to control defensive responses. Whether the defence is effective or not is determined by the regulation of particular genes by the plant. In the case of susceptible interactions, *Bgh* can successfully invade some epidermal cells, whereas others resist the fungal penetration by means of papilla-based basal resistance. This papilla-based resistance is accompanied by changes in the cell walls and the formation of papillae at attack sites. Both spatial and temporal gene expression modulate the positive as well as the negative control of defence (Rushton and Somssich, 1998). In the past few years, plant microarray data have been collected showing that in both compatible and incompatible plant-pathogen interactions, hundreds of genes are up- and downregulated. In many cases, differences in susceptibility and resistance are associated with differences in the timing and magnitude of these changes rather than with the expression of different sets of genes (Tao et al., 2003).

In the barley-*Bgh* interaction, susceptibility or resistance is determined by the proportion of epidermal cells that respond either in a susceptible or resistant manner to the initial fungal attack. These mixed cellular responses have made it difficult to determine which of the events seen in whole bulk analysis are related to resistance and which to susceptibility. Single cell transcript profiling has shown that many genes are shared between resistant and infected cells in a susceptible barley cultivar (Gjetting et al., 2007). However, in that paper it was shown that transcript regulation does not differ in the direction (up- or downregulation) in both cell types, but rather in the amplitude.

The cell wall thickening of the plant is mediated through the regulation of oxalate oxidase-like proteins and germin-like proteins (GLPs), whose influence in plant defence is likely to be related to the generation of active oxygen species. Overexpression of germins (GERs) and

GLPs leads to enhanced penetration resistance (Schweizer et al., 1999). “They are targeted to the cell wall and apoplast, and while their functions are largely unknown, some members related to the barley HvGER4 subfamily exhibit superoxide dismutase activity” (Manosalva et al., 2009), which is involved in the reinforcement of the cell wall (Wei et al., 1998). HvGER4 accumulates at 3 hours after inoculation (h.a.i.), reaches a maximum at 15 to 24 h.a.i. and stays that high until 96 h.a.i. (Wei et al., 1998). Overexpression of a germin-like protein subfamily 4 (GLP4) enhances resistance against *B. graminis* in wheat and barley, whereas transient silencing by iRNA reduces this resistance (Christensen et al., 2004, Zimmermann et al., 2006). Additionally overexpression of a peroxidase enhances penetration resistance through reactive oxygen species generation in wheat (Schweizer, 2008). Transient RNAi-mediated silencing of HvRBOHA (barley respiratory burst oxidase homologue A) has shown an increased basal penetration resistance to *Bgh* (Trujillo et al., 2006).

Possibly processes of primary and secondary metabolism are also involved in the penetration resistance against *Bgh*. Genes that code for enzymes downstream the shikimate-pathways, such as HvCS (barley chorismate synthase), HvASa2 (barley anthranilate synthase alpha subunit 2), and HvCM1 (barley chorismate mutase 1), are involved in the production of aromatic amino acids. Transient silencing of these genes on the single-cell level increases resistance in the susceptible barley genotype. The overexpression of these genes leads to an enhanced susceptibility in resistant barley with Mlo background, resulting in penetration and the formation of haustoria and secondary hyphae (Hu et al., 2009).

4.4.2.2. Hypersensitive resistance

At least 85 dominant or semi-dominant barley mildew genes have been characterized, including Mlk genes and 28 highly homologous genes which map to the Mla locus on chromosome 1H (Jensen et al., 1980, Jorgensen, 1994). Several Mla genes are cloned, and they all code for (CC-NBS-LRR)-type R proteins. They recognize isolate-specific *Bgh* effectors (Halterman et al., 2001, Halterman and Wise, 2004). Avirulence genes avrk1 and avra10 are cloned from *Bgh* and recognized by barley R-genes Mlk 1 and Mla10, mediating defence response. Both these genes belong to a large multigene family of more than 30 paralogues in *Bgh*, whereas homologues can be found in formae speciales that infect other grass species. In the nucleus, Mla10 showed an Avr10-dependent physical association where two WRKY transcription factors (HvWRKY1 and HvWRKY2) bring about fungal effector-induced gene expression through binding to W-box elements (Shen et al., 2007). This suggests that these transcription factors serve as immediate downstream targets for the activated receptor. The WRKY1 gene is activated rapidly and locally around fungal infection

sites, and as a transcription factor it regulates gene expression via binding to promoter elements, e.g. those of PR-10 (Eulgem et al., 1999). To mediate resistance, the Mla6 protein requires the zinc-binding protein RAR1 (Shirasu et al., 1999), and a subunit of the SCF (Skp1, Cullin, F-box) ubiquitin ligase complex, SGT1, whereas Mla1 does not require this (Zhou et al., 2001, Azevedo et al., 2002).

4.4.2.3. Susceptibility-related genes

In a small number of cases, plant genes have been found that are effective against an entire pathogen species, like the barley Mlo against *Bgh* or the wheat Lr34 against leaf rust (*Puccinia triticina*). The Mlo-powdery mildew interaction is a well-studied example for R-gene mediated resistance, and Mlo is the most prominent susceptibility gene in barley, which is also investigated with respect to an interaction with other pathogens (Jansen et al., 2007, Reinstadler et al., 2010, Zellerhoff et al., 2010). Mlo has a seven-transmembrane domain, and lack of Mlo confers broad spectrum resistance to *Bgh* by firstly attenuating the hydrogen oxide burst restricted to the cell wall at possible invasion of epidermal cells and secondly by suppressing this burst and cell death in the mesophyll. This results in an unsuccessful epidermal cell penetration by the fungus. At the sites of unsuccessful penetration the cell wall is remodelled and reinforced by oxidative cross-linking, although other molecular events may also be involved. Depending on the mutation in the mlo gene the penetration resistance is complete or partial (Piffanelli et al., 2002). Mlo as a negative regulator of penetration resistance by preventing cell death plays a role not only in the resistance to the penetration and development of biotrophic *B. graminis*, but also in responses to other biotic and abiotic stresses. As a disadvantage mlo mutants show spontaneous cell death in the absence of *Bgh* which is suggested to be a part of a quickened leaf senescence.

In barley the conserved cell death regulator protein BAX inhibitor (HvBI-1) inhibits BAX-induced cell death and suppresses defence response and resistance to powdery mildew. Overexpression of barley HvBI-1 decreases cell-wall-associated H_2O_2 formation, as well as breaking down the mlo-mediated penetration resistance (Huckelhoven et al., 2003, Babaeizad et al., 2009). This is associated with a reduced HR response. In contrast young barley seedlings are more susceptible to the necrotrophic fungus *Fusarium graminearum*, which besides the loss in yield results in mycotoxine contamination.

Recently new susceptible factors have been found in barley, such as blufensin1 (BLN1), a small peptide belonging to a new family of proteins, which enhances the susceptibility against powdery mildew in a compatible interaction, indicating that BLN1 can act in a S-gene like manner (Meng et al., 2009).

4.4.2.4. Secondary metabolism

An accumulation of phenolic compounds can be seen in the papillae formed during the primary infection (Mayama and Shishiyama, 1978). Inhibition of phenylalanine ammonia-lyase (PAL), the key enzyme for phenylpropanoid synthesis, suppresses chemically induced resistance in wheat against *B. graminis* (Stadnik and Buchenauer, 2000). PAL is an important enzyme, which leads to several secondary metabolites involved in cell wall thickening and to the production of phytoalexins, and therefore it plays a role in defence. Besides PAL, transcripts of other enzymes of secondary metabolism such as caffeic acid O-methyltransferase, ferulic acid hydroxylase, caffeoyl-CoA O-methyltransferase, and cinnamyl alcohol dehydrogenase accumulate, particularly in the epidermis. These genes are involved in the lignin biosynthesis by biosynthesis of the phenylpropane subunits. Transient gene silencing in the epidermis via RNAi leads to a higher penetration efficiency of wheat to *Bgt* and also to the inappropriate pathogen *Bgh* (Bhuiyan et al., 2009). Co-silencing leads to greater penetration of *Bgt* or *Bgh* than when the genes were silenced separately. Fluorescence emission spectra analyses revealed that gene silencing hindered the host's autofluorescence response where the fungus has contact. These results illustrate that "monolignol biosynthesis is critically important for host defence against both appropriate and inappropriate pathogen invasion in wheat" (Bhuiyan et al., 2009).

The accumulation of enzymes involved in secondary metabolism (such as PAL, chalcone synthase (CHS) flavonoid and caffeic acid O-methyltransferases and allene oxide cyclase) is activated in susceptible and resistant lines of barley upon infection with powdery mildew, whereas in resistant lines the accumulation of these enzymes is even higher.

4.4.2.5. Hormones

The first evidence that JA induces alterations of gene expression was found in 1987 (Weidhase et al., 1987). An endogenous rise in JA can be seen in the plant's responses both to abiotic and to biotic stresses (Wasternack and Hause, 2002). Allene oxide cyclase converts an allene oxide formed by an allene oxide synthase and is a jasmonic acid biosynthetic enzyme. The presence of mRNAs of allene oxide cyclase correlate with that of other biosynthetic enzymes (like lipoxygenases, allene oxide synthases) and with PR1b (Maucher et al., 2004). Exogenous methyl jasmonate induces systemic protection against *Bgh* in barley seedlings by changing the polyamine metabolism. "These changes are accompanied by increased activity on the parts of soluble ornithine decarboxylase […], soluble and particulate arginine decarboxylase […], and S-adenosylmethionine decarboxylase (AdoMetDC)" (Walters et al., 2002). This finding supports the role of JA in the stress response of barley but defence responses in plants against biotrophic pathogens

seem to be more dependent on SA (Métraux et al., 2002). On the other hand, some results suggest that neither SA nor JA have a role in the signalling of *Bgh*-infected barley leaves (Schweizer et al., 1993, Huckelhoven et al., 1999). So the role of hormones in plant response is contradictory.

4.4.2.6. Protein turnover

A rapid adaptation to the infection by powdery mildew can be achieved by enhancing protein turnover. The depletion of cellular ubiquitin levels by transient induced gene silencing (TIGS) enhances the susceptibility of barley (Dong et al., 2006). In *Arabidopsis thaliana*, the KEG (KEEP ON GOING) gene, a ubiquitin ligase protein, is overexpressed in edr1 mutants, which show higher resistance to powdery mildew. Transgenic overexpression of the KEG induces massive cell death. Genes coding for an aspartate protease and a cysteine protease are upregulated upon infection of *Bgh* in barley (Hückelhoven et al., 2001). These results suggest that the proteasomal and other protein-degradation pathways play a role in the basal host resistance of barley.

4.4.2.7. Sugar metabolism

When the pathogen enters the epidermal cell layer, haustoria are formed. Haustoria gain access to the intracellular soluble molecules through the extrahaustorial membrane, redirecting the metabolism of the cells to export nutrients into the haustoria (Green et al., 2002, Panstruga, 2003). The biotrophic fungus induces alterations in source-sink relationships in infected leaves to let infected areas act as sinks and lower their energy production as well as enhancing energy consumption. “During a susceptible interaction, photosynthesis was progressibely reduced both in cells directly below fungal colonies and in adjacent cells when compared with non-inoculated“ leaves (Swarbrick et al., 2006). The lower rate of photosynthesis was accompanied with a downregulation of photosynthetic gene expression of ribulose-bisphoshate carboxylase ribulose-1,5-bisphosphate carboxylase oxygenase (RuBisCO) and chlorophyll a/b binding protein. An increase of invertase activity was also shown, resulting in an increase in the accumulation of hexoses. The accumulation of hexoses may have a direct role in feeding the fungus and reducing the export of sucrose from the infected leaf. These results are also consistent with another role of invertase in the generation of hexoses, namely providing an extra energy supply for defence reactions and/or inducing defence responding gene expression (Fotopoulos et al., 2003, Swarbrick et al., 2006). The accumulation of hexoses is also accompanied by the upregulation of PR-1. Carbohydrate accumulation in intact barley leaves was demonstrated to induce senescence and nitrogen remobilization through enhanced accumulation of several proteolysis enzymes, such as aminopeptidases, Clp proteases, the proteasome system, carboxypeptidase, thiol

proteases, aspartic protease and serine carboxypeptidase (Parrott et al., 2005). These results suggest a redirection of energy for defence and feeding the fungus.

4.5. Transcriptome analysis

The purpose of studying gene expression by means of large-scale transcriptome analysis is to address biological issues which are fundamentally important for living cells. The levels of gene expression are dependent on the cell type, its stage of development and the way it is influenced by environmental factors. Transcriptional activity needs to be well-coordinated in order to ensure the proper function of cells and tissues.

Upon defence reactions the transcriptome is highly regulated overall. Analysis of the transcriptome at several time points after inoculation gives a good insight into the kinetics of responses. Through developments in array technology (miniaturisation and automation of array production) it has become possible to produce arrays with several thousand transcripts on a few square centimetres. A macroarray consists of a set of DNA sequences - often called probes - which are immobilized on a solid surface such as a nylon membrane. A sample contains a complex mixture of nucleic acid sequences often referred to as targets, which can bind to the probes on the array. This binding happens due to the fact that complementary nucleic acid sequences hybridize to each other. With the use of macroarrays many thousands of transcripts in one single sample can be investigated in parallel. Therefore this method can be used to study many processes occurring within the course of the infection.

The most obvious question to which researchers are hoping to find the answer using array-based experiments is the following: which particular sets of genes are differently transcribed in different conditions, tissues, developmental stages or time points. A very simple approach is to calculate the ratio of each gene in the infected compared to the control sample. The drawback of this method is that the fold-change does not reveal anything about the statistical reliability. In addition, those transcripts with the highest fold-change are not necessarily those with the most biological relevance. Therefore statistics which rank the transcripts like the t-test are most common (Cui and Churchill, 2003, Hatfield et al., 2003, Smyth, 2004). After that the researcher has to decide a critical value above which the gene expression is considered to be significant.

Tools such as MapMan (Usadel et al., 2005) classify the genes according to their functional category and can assist in getting an overview of the transcriptional changes. Recent data has become available from single cell assays taken from susceptible and resistant cells of

one plant. Additionally *Bgh* transcription profiles have been the subject of analysis during the asexual development cycle, including the profiles of ungerminated and germinated conidiae, the epidermis containing haustorium and the epiphytic mycelium (Both et al., 2005, Bindschedler et al., 2009). RNA amplification steps, however, can also introduce amplification bias. As well as the complicated protocols for isolating single cells and extracting, RNA or DNA amplification could introduce additional amplification bias. However, data about the transcription levels of single cells would vastly increase the possibilities to learn more about cell functions and regulation.

There are nevertheless some drawbacks in macroarray analysis. First, homologue mRNAs with a high similarity in the hybridized sequence can cause cross-hybridization on the array. Secondly, if the transcript level of a certain gene is too low and therefore its signal close to the background level, it will not be included in the analysis. Thirdly, only mRNAs that are spotted on the membrane can be investigated, and new gene transcripts will not be investigated. Although examination of the transcriptome can help to identify candidate genes involved in the interaction, their function has to be confirmed experimentally by over-expression, gene disruption or silencing in planta. Also post-transcriptional processing of mRNA and protein levels cannot be identified by transcript profiling; hence, interpretation of the data could potentially lead to false conclusions.

4.6. Proteome analysis

As mentioned above, transcriptome analysis by itself cannot answer all possible questions regarding the regulation of proteins under certain environmental conditions. For a deeper comprehension it is essential to understand the changes in complex biological systems at the post-transcriptional level, since transcript levels do not always reflect protein levels and protein activities. This issue is further complicated by evidence of RNAs acting directly or indirectly with mRNA molecules to influence the accumulation, and thus indirectly the activities of proteins (Selbach et al., 2008). In general it is agreed that the biological activity of proteins depends on post-translational modifications and protein-protein interactions. It is therefore necessary to include the proteome aspect to any integrated analysis which attempts to study gene function, protein expression and localisation.

Proteome analysis is a tool for investigating those regulation events that are not revealed by transcript changes. The first proteome analyses were done in the 1970´s (Klose, 1975, O'Farrell, 1975) by using two-dimensional (2-D) gels to resolve the different proteins in the crude extract by isoelectric point and mass. The principle of 2-D gel electrophoresis is based

on separation of the proteins in the first dimension according to their charge using isoelectric focusing (IEF) and in the second dimension according to their size using sodium dodecyl sulphate (SDS)-PAGE. But it was not until the 1990's that technological progress in the separation of proteins by 2-D gel electrophoresis and the development of mass spectrometric techniques like MALDI-TOF-MS (Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry) or LC-ESI-Q-TOF-MS/MS (liquid chromatography electrospray-ionisation quadrupole time-of-flight tandem mass spectrometry) allowed rapid and sensitive analyses of peptides and proteins. Comprehensive expressed sequence tag (EST)-databases for barley have made this plant accessible for proteome analysis. Today proteome studies include phosphorylation and glycosylation patterns as well as investigations of protein-protein interactions and "'differential display' proteomics for the comparison of protein levels" (Pandey and Mann, 2000). It is now also possible to distinguish between highly homologues proteins even if they differ only in one amino acid position, and therefore to anticipate the roles of individual isoforms of proteins in plants (Schlesier et al., 2004).

With the introduction of the differential in-gel electrophoresis (DIGE) (Unlu et al., 1997), up to three extracts labelled with different fluorescent dyes which have different absorption and emission wave lengths attached to the proteins in an extract can be loaded onto gels and detected in parallel. The reliability of the outcome of the experiments is increased by reducing gel-to-gel variances and by including an internal standard sample. Due to the high sensitivity of the detection method less material is needed, which makes it particularly suitable for limited tissue resources. First introduced in the area of medicine, nowadays this staining technique for 2-D gel analysis is used more and more in plant science, too.

Nevertheless, 2-D gel electrophoresis has some limitations. With a macroarray one can analyse several thousands of transcripts at once, but even high resolution 2-D gels can resolve only about 1 000 spots, and these represent only the highly abundant proteins in a crude mixture. Furthermore, only proteins that are not extremely acidic or basic can be resolved by 2-D gel electrophoresis using conventional pH gradients ranging from 3 to 10. For the analysis of proteins belonging to extremely acidic or basic groups, other methods have been established, like the separation of peptides based on liquid chromatography. Using 2-D gels, the application of prefractionation techniques and narrow-range pH gradients improves the resolution considerably.

Studies of barley grain and root proteomes in response to salinity have been performed in different genotypes (Witzel et al., 2009a, Witzel et al., 2009b). Also plasma membrane of germinating barley embryos (Hynek et al., 2009), or the proteome changes in leaf tonoplasts of barley exposed to cadmium have been examined (Schneider et al., 2009). Recently

several studies of *Bgh* ´s proteome of ungerminated spores, epiphytic sporulation hyphae, haustoria inside the epidermal cells at different stages and conidiospores with up to several hundreds of identified proteins have been published (Bindschedler et al., 2009, Godfrey et al., 2009, Noir et al., 2009). Some of the relevant findings are as follows: in haustoria proteins with the function in stress response and carbohydrate, monosaccharide and vitamin metabolism were overrepresented in comparison to conidiae and hyphae. Some haustorial proteins with a predicted N-terminal signal peptide were found in infected tissue. whereas "the global functional distribution of proteins in conidia and the sporulating hyphae was very similar" (Bindschedler et al., 2009).

Despite the fact that the influence of some stress factors in barley are being studied, an investigation of the proteome changes in the epidermis of a susceptible barley genotype upon an interaction with *Bgh* over the growing period has been missing until now.

The epidermis is the only infected cell layer of barley in an interaction with powdery mildew; therefore in this study we are only addressing the regulation of proteins in the epidermis. This restriction to epidermal samples not only reduces the complexity of the sample and therefore increases the visibility of changes, but in the case of leaf proteomes there is a further advantage: it is estimated that RuBisCO accounts for up to over half of the total leaf protein content, which means that it conceals many other underlying proteins (Ellis, 1979, McCabe et al., 2001). Thus studying the epidermal proteome which is largely free of RuBisCO, it will be possible to investigate these proteins that would be concealed in the study of the proteome of the whole leaf.

4.7. Integration

Relevant information for effective candidate genes can be achieved by the integration of genome, transcriptome, proteome and metabolome profiling experiments. This data integration provides additional information about cellular functions, assisting with the interpretation of the results and arriving at meaningful conclusions. It is of advantage to carry out different types of investigation to arrive at more reliable conclusions upon data integration. At best, samples analysed with different methods should come from the same tissue sample. For example, transcriptome and proteome profiles of different rapeseed microspore-derived embryo cultures were evaluated (Joosen et al., 2007). However the same batch of cultures was not used here, only the time points of the investigation were the same. This approach could be problematical, because technical variation might interfere with the integration of the data. Proteome and metabolome of tobacco cell suspension cultures

have been investigated directly (Lippmann et al., 2009), and a virtual method of comparison of metabolome and proteome data of grapevine was initiated (Grimplet et al., 2009). Recently, a study has compared the transcript, protein and metabolome profiles of maize lines (Barros et al., 2010).

Nevertheless studies directly comparing results of several –omics platforms are rare. So far no large scale comparative study has dealt with the susceptible interaction of a plant with a biotrophic fungus at transcriptome and proteome level using identical tissue samples.

There are also some drawbacks of integrating transcriptome and proteome data. Small proteins that are encoded by low abundant transcripts could often not be found. Instead, there was a significant molecular mass bias for the detection of high molecular weight proteins, which corresponded to low abundant transcripts. With more abundant mRNA it was possible to also detect small proteins (Baginsky et al., 2005). Another limitation of transcriptome and proteome integration is the fact that a majority of array data cannot be easily linked with the relatively small number of identified proteins on 2-D gels.

4.8. Aims of the study

This study investigates changes of transcript and protein levels in susceptible barley epidermis infected by the biotrophic fungus *Bgh*. Connected with this study, but carried out independently, analysis of barley infected by the necrotrophic fungus *Rhynchosporium secalis* (*R.secalis)* is ongoing. The contrasting pathogenic life styles of both fungi may have a different impact on gene expression and protein patterns of the infected host tissue. Both pathogens are restricted in their growth to the epidermal layer of the host. Therefore both studies are focussing on cellular reaction patterns in the epidermis of infected versus control samples at five time points, from 12 to 120 h.a.i. As seen in Figure 2, the entire lifecycle of the infection, from the germination to the end of the reproductive stage, is covered.

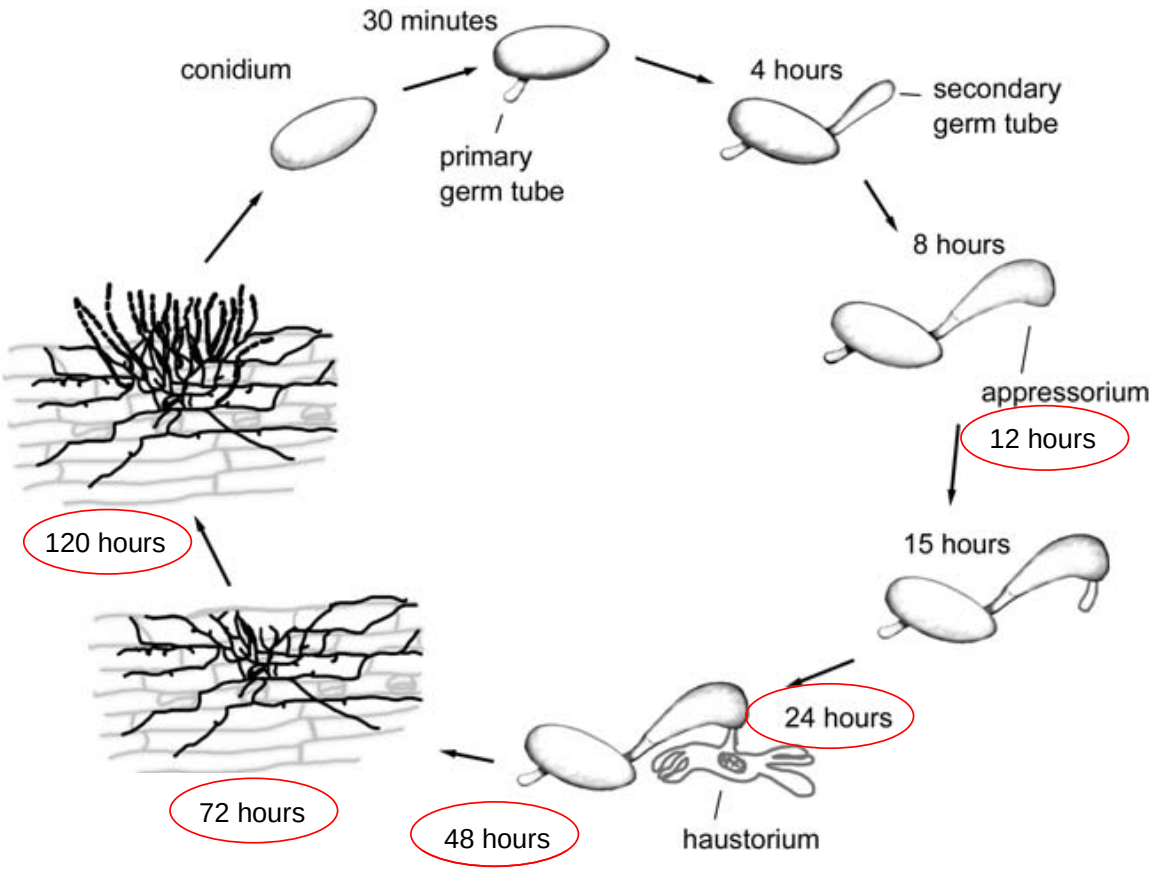


Figure 2: Lifecycle of *Bgh*. In red the chosen time points for this experiment are marked (Figure adapted from M Both, 2005).

Patterns of mRNA transcripts have been investigated using a cDNA macroarray that was produced in-house. This macroarray includes many ESTs of barley epidermis infected by powdery mildew and is therefore especially well-suited for the approach. The study of the proteome pattern has been done on 24 cm 2-D DIGE gels, and differentially accumulated protein spots have been picked and identified by mass spectrometry. The goal of the work is to compare both sets of data systematically and to gain insight into the kinetics of induced changes. The correlation of transcripts and proteins may unravel new key players of defence or susceptibility, and could identify transcriptional and translational effects on the plant during the initiation and establishment of a susceptible interaction. This comparison may lead to the identification of candidate host genes, which can be functionally addressed by means of single cell RNAi or virus-induced gene silencing (Douchkov et al., 2005).

By comparing the data presented in this study and those from the work on barley infected with *R.secalis* a comprehensive comparative analysis of the contrasting response of barley cells to infection by these two different pathogens could subsequently be made. The overall aim of this research project is to acquire a better and more thorough understanding of the mechanisms of host susceptibility to an obligate biotrophic pathogen in a system of reduced biological complexity such as the epidermis.

5. Material and Methods

5.1. Plant and fungal material

5.1.1. Growth of germinated barley seedlings

In this study the spring barley (*Hordeum vulgare* ssp. *vulgare*), cultivar “Ingrid” was used. Plastic pots of ten cm in diameter were filled with soil. Ten grams (approximately 100 - 150 grains) pre-soaked barley grains were put in them, covered with one cm soil and watered. The seedlings were cultivated for seven days in a climate chamber (Siemens; Simatic OP7) at a day night rhythm of 16h - 8h with a temperature of 20 ^{o}C and at a relative humidity of 60 %. The pots stood in trays filled with one cm of water. These seven-day-old seedlings were used for all inoculation experiments. The pots were randomly positioned in the growth chamber in each of the three biological replicates, so that effects of the location in the growth chamber could be avoided.

5.1.2. Maintenance of powdery mildew

Powdery mildew (*Bgh*) is an obligate biotrophic fungus. For this reason the production of conidia is only possible on living plants. Conidia of *Bgh* were produced in large amounts on the susceptible barley cultivar “Golden Promise”. Seven days after inoculation conidia of *Bgh* (isolate CH 4.8) were transferred to the next batch of seven-day barley seedlings by shaking the infected plants over them.

5.1.3. Inoculation of experimental plants

Twelve pots, each with 100 - 150 seven-day-old “Ingrid” seedlings (see chapter 5.1.1) were inoculated with *Bgh* by shaking infected plants over them as described in chapter 5.1.2. These and further 12 pots of non-incubated plants were left to grow in a climate chamber. The inoculated plants were covered with a self-made “tent” consisting of plastic foil attached to a frame to prevent the inoculum being transferred to the control plants. Three biological replicates were carried out at an interval of two months. At each harvest (biological replicate) the arrangement of the pots in the growing chamber was altered. The growing conditions remained those mentioned in chapter 5.1.1.

5.1.4. Collecting of biological material

Epidermis peels were collected from the inoculated plants at the following time points: 12 , 24 , 48 , 72 and 120 h.a.i. Epidermis from non-inoculated control plants grown in parallel was stripped at the same time points.

The adaxial side of the first leaf was slit carefully with a scalpel. The abaxial epidermis was peeled from the leaf and immediately frozen in liquid nitrogen. At 120 h.a.i. and 168 h.a.i. leaf samples were collected in addition.

5.1.5. Further processing of the samples

The collected samples were homogenized to powder under liquid nitrogen in a cooled mortar. 100 - 200 mg of each ground sample was separated for transcriptome analysis. The remainder of the samples was used for proteome analysis.

5.1.6. Measurement of chlorophyll concentration in the samples

The concentrations of the chlorophylls in the epidermis samples were analysed according to Lichtenthaler (1987) to check potential contamination with mesophyll cells.

The chlorophyll content of epidermis samples was measured through the absorbance of the sample in acetone at 645 and 662 nm. For this approximately 10 mg of ground sample were dissolved in acetone (100 µl/1 mg) by shaking. After incubation for 5 min the solution was centrifuged (5 min, 18 000 g) and the supernatant was transferred to a new tube. The absorption of the extracts was measured at 645 nm (A_{645}) and 662 nm (A_{662}). Before each measurement the instrument was calibrated with acetone. At every stage attention was paid not to expose the extracts to sunlight in order to avoid degradation of the chlorophylls.

The concentrations of the chlorophylls (chl.) a and b and the sum of them were calculated according to the formulas in (Lichtenthaler, 1987):

chl. a: $(11.24 \times A_{662})-(2.04 \times A_{645})$

chl. b: $(20.13 \times A_{645})-(4.19 \times A_{662})$

chl a+b: $(7.05 \times A_{662})-(18.09 \times A_{645})$

The results of the epidermis samples were related to the mean chlorophyll content of two reference samples of infected and not-infected leaves that were taken at 24 h.a.i.

5.2. Transcriptome Analysis

5.2.1. Extraction of RNA

Due to the low concentration of RNA in the epidermis, various commercially available extraction kits and other methods were tested to compare the resulting yield and quality of RNA. According to the results of these testings the well-established guanidinium thiocyanate-phenol-chloroform method, modified according to (Chomczynski and Sacchi, 1987) was chosen because of its reliable yield and quality.

100 - 200 mg ground epidermis and leaf sample material were thawed in 800 µl solution D (4 M guanidinium thiocyanate; 25 mM Na-citrate pH 7.0; 0.5 % sarcosyl; 0.1 M ß-mercaptoethanol)+ beta-mercaptoethanol (2-ME) in a bath of 60 ^{o}C-warm water and dissolved through pipetting up and down and vortexing. 80 µl 2 M Na-Acetate (pH 4.0), 800 µl waterlogged phenol and 160 µl $CHCl_3$ (24:1 IAA) were added under vortexing. The solution was incubated for 15 min on ice.

Insoluble particles were pelleted by centrifugation (20 min, 10 000 g, 4 ^{o}C). In a new 2 ml-tube the RNA was sedimented from the supernatant by adding 80 µl ice-cold isopropanol and incubating at -20 ^{o}C over night. After centrifugation (15 min, 15 000 g, 4 ^{o}C) the RNA remained in the interphase. The upper aqueous layer was discarded and the rest precipitated with ice-cold isopropanol. The precipitate was washed twice with 75 % EtOH and briefly dried (max. 10 min). The pellet was resolved in 30 µl Diethylpyrocarbonate (DEPC)-treated H_2O (65 ^{o}C, 10 min) and stored at -20 ^{o}C.

5.2.2. Concentration and quality of RNA

The RNA concentration was measured with NanoDrop 3300 (Thermo Scientific, Wilmington, USA). This apparatus requires 1 µl of a sample and detects also small concentrations. The quality can be checked by comparing the absorptions of the sample at different wavelengths. The ratio 260 nm/280 nm should be 1.8 - 2.0. A lower ratio indicates contamination of the RNA.

The quality of the RNA was further analysed on an agarose gel (1.7 % low melting agarose, 50 ml 1x Tris/Borate/EDTA (TBE)-buffer, 10 mg/ml ethidiumbromide). 1 µg of solved RNA was denatured at 70 ^{o}C for 10 min. After adding 2 µl loading buffer (2.5 % Ficoll-Bromophenol blue) the mixture was run on the gel for 45 min at 100 V. A high quality-RNA shows two major bands of ribosomal RNA (28S-rRNA and 18S-rRNA).

5.2.3. Isolation of mRNA from total RNA

The mRNA was isolated with magnetic polystyrol-bead solution (Dynabead mRNA Purification Kit; Dynal, Oslo, Norway). The 3'-poly A^+-end of the mRNA hybridizes with oligo-$(dT)_{25}$ which is bound covalently to the Polystyrol-beads. By pulling the Dynabeads magnetically to the tube wall, the mRNA is separated and purified from DNA, tRNA, rRNA, proteins, sugars and other unwanted compounds in the sample. 100 µl of resuspended Propanol suspension were washed twice with 50 µl of the dynal binding buffer and solved in DEPC-treated water. Twenty and 37 µl RNA solution of epidermal samples and leaf samples, respectively, were adjusted to 50 µl with DEPC-treated water and incubated at 65 ^{0}C to dissolve secondary structures, after which they were incubated on ice for 5 min. The RNA solution was added to the propanol suspension. The mixture was inverted for 5 min to bind the mRNA to the oligo-$(dT)_{25}$ nucleotides of the propanol. The Dynabeads with the bound mRNA were washed twice with 100 µl dynal washing buffer and with 250 µl dynal RT-buffer (250 mM Tris-HCl, 250 mM KCl, 50 mM $MgCl_2$, adjusted to pH 8.3, autoclaved, add RNA secureTM Reagent, 10' 60 °C) and stored on ice. All steps were performed according to the manual. The resulting concentration was measured at 260 nm with the NanoDrop reader.

5.2.4. cDNA synthesis

The enzyme reverse transcriptase, a modified MMLV-RT (*Moloney murine leukemie virus* reverse transcriptase) originating from a retrovirus was used to synthesize cDNA. This is a RNA-depending DNA-polymerase and the SuperScriptTM II featuring no intrinsic RNase activity allows the production of long reverse transcripts.

Dynabeads with bound mRNA were suspended in 50 µl RT-mix (10 µl 5 x RT-buffer, 10 µl 100 mM DTT, 2.5 µl 10 mM dNTP, 1.3 µl RNAse Inhibitor, 34.8 µl H_2O) and incubated at 42 ^{o}C for 2 min. By adding 1 µl RT (200 U/µl; Superscript II; GibcoBRL; Invitrogen, Carlsbad, California) the reverse transcription was started. The mixture was incubated at 42 ^{o}C for 60 min and mixed every 15 min. The RT-mix was removed from the mRNA::cDNA-heteroduplices bound to Dynabeads. The beads were washed twice with 250 µl 1x RT-buffer, eluted in 50 µl elution-buffer (Na-EDTA 2 mM, add NaOH pH 8.0) and incubated at 95 ^{o}C for 2 min to melt the mRNA::cDNA heteroduplices. The mRNA in the supernatant was removed. This step was repeated once, and the Dynabeads with the attached cDNA were washed twice with 250 µl distilled water.

5.2.5. Radioactive labelling of cDNA with ^{33}P

Hexameres (Hexanucleotidemix, Roche, Penzberg) of random sequences were used as primers for the DNA-Polymerase to label the cDNA radioactively ("random priming") during the synthesis of the second DNA-strand. An exonuclease-free Klenow-fragment (Amersham Biosciences) was used as DNA-polymerase for incorporating radioactive [α-^{33}P]dCTP (Hartmann Analytic GmbH, Braunschweig, Germany). cDNA probes were produced by second-strand ^{33}P labelling, as described in Sreenivasulu et a., (2002).

Dynabeads with the attached cDNA were washed with 250 µl H_2O. Dynabeads were resuspended in 19 µl destilled water (aqua dest.) and 6 µl dNTP-Mix (0.5 mM dATP, 0.5 mM dGTP, 0.5 mM dTTP; Fermentas, St. Leon-Rot, Germany), boiled at 95 °C for 2 min to dissolve secondary structures and chilled on ice for 5 min. 4 µl Hexanucleotidemix-Mix (Roche, Basel, Suisse), 5 µl [α-^{33}P]dCTP and 2 µl Klenow fragment (10 U/µl, Amersham Biosciences) were added. Second strand synthesis was done by incubation for at least 1 h at 37 °C. After separating, the radioactivity of the Dynabeads and the supernatant was measured to determine the incorporation ratio of the radioactive compound. The Dynabeads were twice resuspended in 50 µl elution buffer, incubated at 95 °C for 3 min, and the collected supernatant was filtered through a moistened anapore column. The radioactivity of both the flow-through and the remaining Dynabeads was measured by a Geiger-Müller counter (Amersham Biosciences Europe GmbH, Freiburg, Germany).

5.2.6. The PGRC2-13k-cDNA-macroarray

For the transcriptome analysis mRNA were hybridized to the PGRC2-13k-cDNA-macroarray (description in the "Flarex"-database on http://pgrc-35.ipk-gatersleben.de/portal/page/portal/PG_BICGH/P_BICGH/P_BICGH_RESOURCES/P_BICGH_IRES_FLAREX).

This array consists of ESTs from different barley cultivars and tissues. From the 13 050 spotted clones represented on the array, 2 993 (23%) derive from epidermal tissue, and 2 450 (19%) from the epidermis of seven day old plants sampled 6 and 24 h.a.i. inoculated with *Bgh* or *Bgt*. All relevant cDNA libraries can be found in the list on http://pgrc.ipk-gatersleben.de/cr-est/liball.php.

5.2.7. Spotting and pattern of the macroarray membranes

Biodyne B Membrane (0.45 µm, Pall GmbH, Dreieich, Germany) was used to fixate cDNAs. The surface of this membrane has a high density of quaternary ammonium groups. This

results in a positive charged surface over a wide pH range. This positive charge enables a high bonding of negatively charged molecules, such as nucleic acids.

Equal volumes each of PCR-amplified cDNA fragment, 1 M NaOH and 5 M NaCl were mixed and then spotted onto the Biodyne nylon membranes, in duplicate using five transfers to each spot with solid pins of 0.2 mm diameter on a BioGrid robot (Biorobotics, Cambridge, UK). After spotting, the arrays were washed with 0.4 M NaOH, 1.5 M NaCl, neutralized with 0.5 M Tris-HCl, pH 7.5, 1.5 M NaCl, UV treated (120 mJ, Stratalinker, Stratagene, La Jolla, USA) to crosslink the DNA, washed with 2x SSC (0.3 M NaCl and 0.03 M sodium citrate) and dried for 30 min at 80 °C. Thereafter the arrays were stored at room temperature until further use. 13 050 cDNAs representing unigenes of EST-libraries of leaves and other tissues of barley were distributed over two membranes (A+B). Each membrane was divided into 384 subarrays, each consisting of 36 spots in a 6 x 6 pattern (Figure 3). Due to double spotting, each subarray consists of 17 cDNA-clones and 1 blank. Each spot possessed a “spotting”-number, e.g. A-13-L:5a means Membrane A, Subarray 13-L, cDNA clone 5, first double spot (a). The same gene also had a technical replicate on position A-13-L:5b.

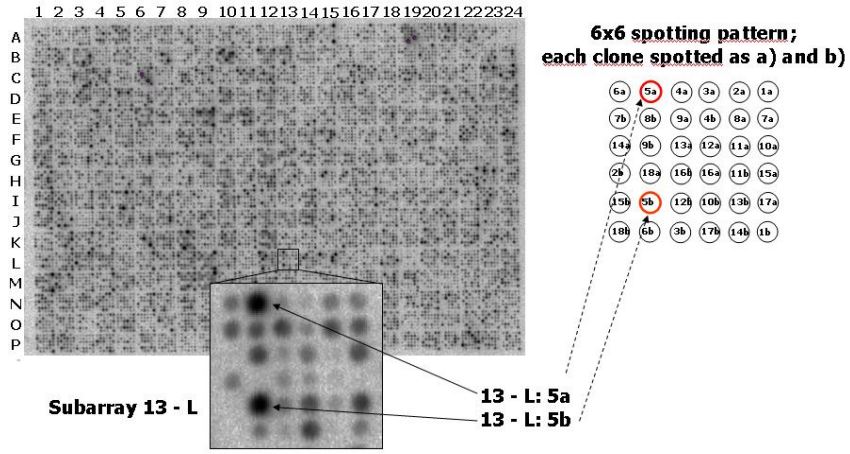


Figure 3: Arrangement of the cDNA-clones on one array. An array consists of two membranes, each divided in 384 subarrays. In the zoomed picture a subarray consisting of 17 double-spotted EST-clones and a blank doublespot

The list of spotted EST-clones can be found on http://pgrc.ipk-gatersleben.de/cr-est/liball.php. The probes of the array consisted of ESTs from different tissues of barley like leaf, root, but also inflorescences and others, and sometimes the samples have undergone some stress treatment. 18 % (2450 probes) have their origin in the library of epidermis infected by powdery mildew.

5.2.8. Hybridization of the macroarray with ^{33}P-labelled cDNAs

The membranes were washed prior to the hybridization by shaking in boiled 0.1 x SSC, 0.1 % (w/v) SDS for 15 min at RT and subsequent denaturation in 0.4 M NaOH, 0.1 % (w/v) SDS followed by neutralisation in 0.2 M Tris HCl, pH 7.4 for 2 x 15 min and 15 min washing in 0.1 x SSC, 0.1 % (w/v) SDS. The membranes were allowed to dry at room temperature.

The membranes were placed in hybridization bottles with the spotted side facing inwards and prewarmed to 65 ^{o}C. Ten ml pre-warmed (65 ^{o}C) pre-hybridization solution (10 % (w/v) dextrane sulphate, 0.8 % (w/v) SDS, 1 M NaCl) and 100 µl denatured (95 ^{o}C, 3 min; 4 ^{o}C, 5 min) salmon sperm were pipetted in to saturate unspecific binding sites. After 4 h the pre-hybridization buffer was replaced. The ^{33}P-labelled cDNA-probe and 100 µl salmon sperm were denatured for 3 min at 95 ^{o}C, chilled on ice for 5 min and added to the bottle. 20 µg mRNA was used for epidermis samples and 37 µg mRNA for leaf samples respectively. After 22 – 24 h the membranes were washed twice with 25 ml 0.1 x SSC + 0.1 % (w/v) SDS for 20 min.

5.2.9. Scanning of macroarrays

The hybridized membranes were wrapped in plastic wrap avoiding air bubbles. The membranes were exposed to clean phosphoimager screens (FUJI MS) for 4 - 12 days.

The phosphoimager screens were scanned in the phosphoimager FLA 3000 reader (Raytest, Straubenhart, Germany) with 65,536 grey scales at 100 µm pixel size, 16 bit, IP reading. Up to 300 pixels should show saturated signal intensities to assure maximum range of spot intensities.

5.2.10. Processing of signals and data evaluation

Spot detection and calculation of signal intensities were carried out using the AIDA image analyser v4.08 (Raytest, Straubenhardt, Germany), and signal intensities were quantile normalized after local background subtraction by applying a statistical procedure coded by Marc Strickert (former member Pattern Recognition Group (PRG), IPK Gatersleben). The samples were then normalized for each time point separately. The following R-script was used (Table 1).

The normalization steps in brief:

The maximum and minimum value for each spot over each time point was computed and the average of the minima was subtracted. The values were log-transformed to fit between 0 and 1. Quantile normalization was used for technical and biological replicates simultaneously and after that over all experiments. The mean of the experiments were substracted, divided by the standard deviation and exponentially transformed. The average value of the technical replicates was annotated with the probe-set names.

Table 1: R-script for quantile normalization of the macroarray data sets

```
require(affy)
dat <- as.matrix(read.table('raw-bg.dat', head=T))
spt <-
as.matrix(read.table('spotting_13kHvPGRC_A_070112.txt',sep="\t",head=T))
nm <- colnames(dat)
hpis <- c('12','24','48','72','120')
for(hpi in hpis) {
 sidx <- grep(hpi,colnames(dat))
 u <- dat[,sidx]
 r <- apply(u,2,range)
 rm <- apply(r,1,mean)
 u <- t(t(u) - r[1,]) # subtract min + 10
 u <- t(t(u) / (r[2,] - r[1,])) # range: [0 1]
 u <- u  * (rm[2] - rm[1]) + 0.5
 u <- normalize.quantiles(u)
 dat[,sidx] <- u
dat <- cbind(dat[grep("a$",spt[,1]),],dat[grep("b$",spt[,1]),])
dt <- t(apply(dat, 1, function(x) .5*( x[1:(length(x)/2)] +
x[(1+length(x)/2):length(x)] )))
colnames(dat) <-
paste(colnames(dat),rep(c("1","2"),each=ncol(dat)/2),sep=".")
dat <- dat[,c(matrix(1:ncol(dat),2,byrow=T))]
dat <- cbind(gsub(".$","",spt[idx,1]),spt[idx,5],dat)
colnames(dat)[1:2] <- c("Locus","ID")
write.table(dat,'qnA.dat',quote=F,col.names=T,row.names=F,sep="\t")
dat <- cbind(gsub(".$","",spt[idx,1]),spt[idx,5],dt)
colnames(dat)[1:2] <- c("Locus","ID")
write.table(dat,'qnA-mn.dat',quote=F,col.names=T,row.names=F,sep="\t")
```

Transcripts were scored as “present” for which the signal intensity on the corresponding sub-array reached at least 2.5-fold compared with negative control of the same subarray in at least three hybridizations, as measured with the software ”Arrayvision“.

For further analysis only ‘present transcripts’ were taken. Analyses of significant transcript regulation was done with EDGE v.1.1.291 (Storey et al., 2005, Leek et al., 2006) in a pairwise static match approach. Only transcripts with a false discovery rate (FDR) of less than 5 % were assumed to be significantly regulated. In order to find robustly regulated transcripts, data for each time point and treatment were averaged and a 2-fold regulation

threshold was applied. Clustering analyses of transcript regulation were done using the “Multi experiment viewer” (MeV) v.4.3.01 (Dana-Farber Cancer Institute, Boston, MA, USA).

5.3. Proteome Analysis

5.3.1. Extraction of proteins

The same finely ground epidermis and leaf samples were used as for the analysis of the transcriptome (see chapter 5.1.5). TCA/Acetone precipitation was used acc. to (Schlesier and Mock, 2006) to extract the proteins from the samples with the following steps: Approximately 1g frozen sample was mixed and dissolved in a 10-fold volume of 10 % TCA/0.07 % 2-ME/Acetone-solution. The suspension was shock-frozen to 2 ml-Eppendorf tubes in liquid nitrogen (30 s) to break the cell walls, and proteins were precipitated at -20 ^{o}C for 45 min to 2 h. The reaction was inverted after 5, 10 and 15 min. Proteins were sedimented by centrifugation (Mikro 22R, Hettich, Tuttlingen, Germany; 15 min, 4 °C, 36 000 x g). The pellet was washed twice with 1.5 ml ice-chilled acetone + 0.07 % 2-ME and disrupted in an ultra sonic bath for 5 min. The suspension was shock-frozen in liquid nitrogen, incubated for 30 min at -20 ^{o}C and pelleted (36 000 x g, 4 ^{o}C). The pellet was dried in a vacuum centrifuge (Concentrator 5301, Eppendorf, Hamburg, Germany) until the acetone was evaporated and subsequently weighed and was resolved in 50 µl DIGE-rehydration-buffer (8 M urea, 2 % CHAPS) per mg protein-pellet, vortexed and homogenized in an ultra sonic bath (5 min). After incubation at 37 ^{o}C for 1 h, insoluble material was pelleted (36 000 x g, 15 min). Remaining solid residues were removed from the supernatant by centrifugation through a Sartorius 0.2 µm C4 microzentrifuge filter cellulose acetate (Sartorius, Freiburg, Germany, 10 min, 12 000 x g, RT). The flow-through was stored at -20 ^{o}C.

5.3.2. Dialysis, ultrafiltration and protein concentration

The extract (see chapter 5.3.1) was dialysed against the 40-fold volume of the rehydration buffer to remove substances which interfere with IEF such as salts or sugars. The Ettan Mini Dialysis Kit (1 kDa cut off, GE Healthcare, Freiburg) was used acc. to the manual. The samples were concentrated to half of the volume through centrifugation (14 000 x g, 20 ^{o}C) against a semipermeable membrane with a cut-off of 3 kDa (Vivaspin 500, 3 kDa, Sartorius, Freiburg) according to the manual. The 2-D Quant Kit (GE Healthcare, München, Germany)

was used following the manufacturer's instructions to determine the protein concentration of the samples.

5.3.3. Labelling of proteins for DIGE

The 2-D DIGE minimal labelling technique was used to carry out the experiment. Fluorescent dyes were provided from NH DyeAGNOSTICS GmbH, Halle (http://www.dyeagnostics.com/). The absorption and emission wave length of these dyes (G-Dye100, 200 and 300, respectively) were tested to be similar to that provided by Amersham Biosciences (Cy2, Cy3 and Cy5, respectively). The Cy-like dyes attach covalently with their NHS-ester reactive group to the ε-amino group of lysine of proteins via an amide linkage. 50 µg each of two protein samples and 50 µg of an internal standard were labelled with a different dye and loaded simultaneously on one gel. The internal standard was an equal mix of all ten epidermis protein samples of one biological harvest (five of the control and five of the infected plants) and labelled with G-Dye100. On a technical replicate gel the labelling of control and infected sample were swapped (see Figure 4). 50 µg protein sample was labelled with 160 pmol dye, resolved in dimethylformamid (DMF). Incubation time was 30 min in the dark. 1 µl 10 mM Lysine (Sigma) was used to stop the labelling reaction. After 10min incubation time the three samples were combined, diluted to 450 µl with rehydration buffer, and 1 mM DTT and 0,5 % IPG buffer was added.

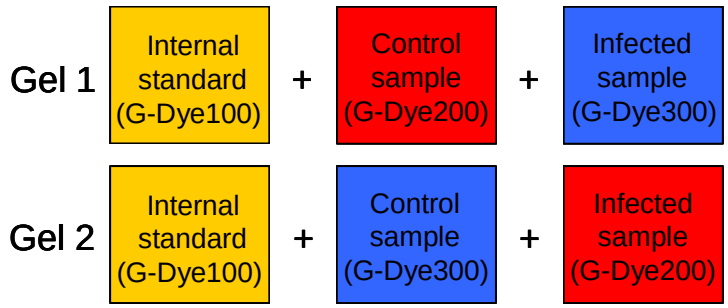


Figure 4: Labelling scheme of technical replicate gels (dye swap)

5.3.4. Pipetting scheme for DIGE gels

Control and infected samples of one time point of one harvest were labelled together with G-Dye200 and G-Dye300 respectively. For each experiment two gels (gel A and gel B) were run with a dye-swap of G-Dye200 and G-Dye300. The IEF of one harvest was done simultaneously, the focused strips were stored at -20 ^{o}C until needed, and the second dimension followed by an analysis of the differences was carried out for each comparison individually.

As an example the labelling scheme for epidermal samples of the 1st harvest is shown in Table 2.

Table 2: Labelling scheme for the technical replicate gels (A) and (B). Internal standard labelled with G-Dye100, control and infected

	G-Dye100	G-Dye200	G-Dye300
12 h-gelA	Internal standard	Control	Infected
12 h-gelB	Internal standard	Infected	Control
24 h-gelA	Internal standard	Control	Infected
24 h-gelB	Internal standard	Infected	Control
48 h-gelA	Internal standard	Control	Infected
48 h-gelB	Internal standard	Infected	Control
72 h-gelA	Internal standard	Control	Infected
72 h-gelB	Internal standard	Infected	Control
120 h-gelA	Internal standard	Control	Infected
120 h-gelB	Internal standard	Infected	Control

5.3.5. 2-D gels

SDS-polyacrylamide gels consisted of two layers, an 11.25 % separation gel and a 1.5 cm-layer of a 6 % collecting gel on top of that. The separation gel solution was poured into the glass slides up to 1.5 cm from the upper edge and layered with n-butanol to get an even surface. After polymerization of the lower layer and removing the n-butanol, 1 cm collecting gel was poured on top and also layered with n-butanol. For the DIGE gels non-fluorescent glass plates were used.

5.3.6. Protein separation for DIGE gels

IEF and subsequent SDS-PAGE were carried out as described in Schlesier and Mock (Schlesier and Mock, 2006). Proteins were separated on rehydrated immobilized pH gradient (IPG) strips of 24 cm length and a pH gradient of 3 - 11. After rehydration small snippets of wetted Whatman-papers were attached between the electrodes of the tray and the end of the IPG strips, absorbing ions and other charged small compounds. These snippets were removed 1 h after running under voltage. The IEF was performed on an IPGphor II unit (Amersham/GE Healthcare): 14 h rehydration without current, 2 h gradient to 150 V, 2 h gradient to 300 V, 2 h gradient to 1 000 V, 3 h gradient to 3 000 V, 3 h gradient to 6 000 V, 10 h at 6 000 V and 2 h at 250 V), resulting in approximately 81.5 kVh. Strips not

immediately applied to the 2nd dimension were stored at -20 °C. To prepare the strips for the 2nd dimension, they were equilibrated with 10 ml buffer A (50 mM Tris/HCl, pH 8.8, 6 M urea, 30 % v/v glycerine, 2 % w/v SDS, 20 mM DTT, 0.01 % bromophenol blue) and additionally in 10 ml buffer B (50 mM Tris/HCl, pH 8.8, 6 M urea, 30 % v/v glycerine, 2 % w/v SDS, 135 mM iodoacetamide, 0.01 % bromophenol blue) for 15 min each. The strips were placed on a SDS polyacrylamide gel and covered with 0.5 % agarose. Separation of the second dimension was performed using a DaltSix apparatus (GE Healthcare), starting with 30 V for 1 h followed by 90 V for 18 h at 20 °C.

5.3.7. Visualization of proteins and image acquisition

Image acquisition was accomplished on a Fuji-FLA-5100 scanner (FujiFilm, Tokyo, Japan) with the Image Reader FLA-5000 v1.0 software while the DIGE gels remained inside the glass slides. Scanning parameters were: resolution 100 µm, 16 bit picture. For the dyes different excitation wavelengths, detected emission wavelengths and power levels were used.

G-Dye100: excitation: 473 nm, emission: 510-550 nm, power: 700 Volt

G-Dye200: excitation: 532 nm, emission: 550-590 nm, power: 650 Volt

G-Dye300: excitation: 635 nm, emission: >665 nm, power: 650 Volt

For the automated spot picking (Proteineer SP, Bruker Daltonics, Bremen, Germany), holes were picked in each of the four corners of the gel before scanning as fixed coordinates.

After scanning of the fluorescence the gels were immediately picked and stained with colloidal coomassie in order to fix the protein spots in the gel and prevent their diffusing.

5.3.8. Preparative gel

For the preparative gels 450 µg and 600 µg respectively of protein taken from a mixture of samples (Table 3) were separated on two 2-D gels and stained with colloidal Coomassie. Subsequent picking of interesting candidate spots was done by automated picking and by hand.

Table 3: Pipetting scheme for the two preparative gels; Control and Infected samples were mixed to reach a distribution over time points and treatments.

Probe	450 µg preparative gel	600 µg preparative gel
EC 48h, 1.Kin		72 µl (100 µg)
EC 72h, 1.Kin	40 µl (75 µg)	53 µl (100 µg)
EC 24h, 3.Kin		56 µl (100 µg)
EC 72h, 3.Kin	32 µl (75 µg)	
E*Bgh* 48h, 1.Kin	42 µl (75 µg)	56 µl (100 µg)
E*Bgh* 72h, 1.Kin	59 µl (150 µg)	39 µl (100 µg)
E*Bgh* 24h, 3.Kin		75 µl (100 µg)
E*Bgh* 72h, 3.Kin	32 µl (75 µg)	
	= 150 µg C + 300 µg *Bgh*	= 300 µg C + 300 µg *Bgh*

5.3.9. Coomassie staining

SDS-gels were incubated for 10min in water and 10 min in 5 % phosphoric acid under shaking conditions before staining using GelCodeBlue Stain Reagent (Pierce Thermo Scientific, Pittsburgh, USA) following the manufacturer's instructions. Image acquisition was performed using a UMAX Power Look III Scanner (Umax Systems, Willich, Germany) with the MagicScan software v4.5 from Umax.

5.3.10. Image analysis of 2-D spot pattern

First one of the gels was defined as a reference gel, then all the other gels were aligned to that using the program TT900 S2S (Nonlinear Dynamics, Newcastle upon Tyne, United Kingdom). For the 2-D image analysis the Progenesis SameSpots v2.0.27 software from the same company was applied for comparative image analysis with the setup for multiplexed images. During spot detection, exclusion of spots has to be handled stringently to avoid analysing artefacts such as dust particles or clouds of proteins rather than the individual proteins. The protein spots have to be focussed at one point and have to show a certain intensity. The background subtraction method used was "Progenesis background", the normalization method was total spot volume multiplied by total area and spots were filtered by area and volume (area>800, volume>1 700). Statistical analysis was carried out using EDGE v.1.1.291 (Storey et al., 2005, Leek et al., 2006) in the same manner as for the transcriptome analysis. Thereby the internal standard corrected values of control and

infected samples were used. Clustering analyses was done with Multi experiment viewer MeV v.4.3.01 (MeV, Dana-Farber Cancer Institute, Boston, MA, USA).

5.3.11. Spot picking and mass spectrometry

Excision of protein spots from the gels was performed by automated spotpicking as well as manually. The coordinates of G-Dye100 were used for the picking of DIGE gels. After washing with 200 µl 50 % acetonitrile (AcN) + 10 mM ammonium bicarbonate for 30 min, the gel pieces were dried. A volume of 7.5 µl trypsin solution (Sequencing grade Modified Trypsin V511, Promega, Madison , USA, 1 ng/µl in 5 mM ammonium bicarbonate including 5 % acetonitrile) was added to each sample for the digestion of proteins at Arg or Lys residues at 37 ^{o}C for 5 h. Digestion reaction was stopped by adding 1 µl 1 % TFA. Proteins were identified using mass spectrometry.

5.3.11.1. Analysis of peptide masses with MALDI-TOF-MS

For the analysis of the peptide masses by the MALDI-TOF-MS, a volume of 1 µl digest was mixed with 2 µl of the matrix solution (5 mg α-cyano-4-hydroxycinnamic-acid in 80 % v/v acetonitrile and 0.1 % w/v TFA). The resulting mix was then concentrated by Millipore ZipTip Pipette Tips (Millipore, Billerica, USA) to half of the volume in accordance with the user manual. 1 µl of this mixture was placed onto the matrix-assisted laser desorption/ionization target (Bruker Daltonics, Bremen, Germany). Peptide mass finger print data was purchased on a REFLEX III MALDI-TOF (Bruker Daltonics), operating in reflector mode. Spectra were calibrated using external or internal calibration and subsequent internal mass correction under the application of the flexAnalysis 2.4 software (Bruker Daltonics). Peptide masses from keratin and trypsin were excluded from the database search. Protein identification was performed with the Mascot search engine (Matrix science, London, UK) (Perkins et al., 1999). The parameters for searching were: monoisotopic mass accuracy 100 - 200 ppm and one missed cleavage; permitted variable modifications were oxidation (methionine), propionamide (cysteine) and carbamidomethyl (cysteine).

5.3.11.2. *De novo* sequencing of peptides by tandem MS/MS

Proteins that could not been identified clearly in this way were subjected to Nano-Liquid-nanoLC-ESI-Q-TOF MS/MS and the *de novo* sequencing (Amme et al., 2006, Kaczmarczyk, 2008). For the nanoLC-ESI-Q-TOF MS/MS and the *de novo* sequencing, 2 µl of the digest were submitted to nanoscale reversed phase liquid chromatography analysis on a nanoAcquity ultra performance liquid chromatography system (Waters Corporation, Milford, MA, USA). The mobile phase flow from the binary pump was used to preconcentrate and

desalt the digest samples on a 20 mm x 180 µm Symmetry 5 mm C18 precolumn (Waters Corporation) for 3 min at 4 µl/min with an aqueous 0.1 % formic acid solution. The peptides were subsequently eluted onto a 100 mm x 75 µm analytical 1.7 µm BEH C18 column (Waters Corporation) and separated at 0.6 µl/min with an increasing AcN gradient from 5 % to 40 % B in 30 min. Mobile phase A consisted of 0.1 % formic acid in water and mobile phase B of 0.1 % formic acid in AcN. The nanoscale LC effluent from the analytical column was directed to the NanoLockSpray source of a Q/TOF Premier hybrid orthogonal accelerated Time-of-Flight mass spectrometer (Waters Corporation, MS Technologies Centre, Manchester, UK). The mass spectrometer operated in a positive ion mode with a source temperature of 80 °C and a cone gas flow of 30 l/h. A voltage of approximately 2 kV was applied to the nano flow sample tip. The mass spectra were acquired with the TOF mass analyzer in V-mode of operation and spectra were integrated over intervalsof one second. Mass spectrometry and tandem mass spectrometry data were acquired in a continuum mode using MassLynx 4.1 software (Waters Corporation, Technologies Centre). The instrument was calibrated with a multi-point calibration using selected fragment ions of the collision induced dissociation of Glu-Fibrinopeptide B (Sigma-Aldrich Chemie GmbH, Taufkirchen, Germany). Automatic data directed analysis was employed for tandem mass spectrometry analysis on doubly and triply charged precursor ions. The product ion tandem mass spectrometry spectra were collected from m/z 50 to m/z 1600. Lock mass correction of the precursor and the product ions was conducted with 150 pmol/µl Glu-Fibrinopeptide B in 0.1 % formic acid in AcN/water (1:1, v/v) respectively, and introduced via the reference sprayer of the NanoLockSpray interface. ProteinLynx Global*SERVER* v2.3 software was used as a software platform for data processing, deconvolution and *de novo* sequence annotation of the spectra and various database search types. A 10 ppm peptide, 0.1 Da fragment tolerance, one missed cleavage, and variable oxidation (methionine) and propionamide (cysteine) were used as search parameters. The *de novo* sequencing of peptides was done by Dr. Andrea Matros.

5.3.12. Identification of proteins of both mass spectrometry techniques

The peptide mass spectrometry spectra searches were conducted using the HarvEST:Barley database v.1.68 (http://harvest.ucr.edu/). This database consists of consensus sequences based on ESTs, whole cDNAs and genomic sequences and is downloadable from http://harvest.ucr.edu/.

The database used contains best basic local alignment search tool X (BLASTX) hits from UniProt, rice and Arabidopsis. Assembly 35 was used and the numbering always begins with

35_. The unigene numbers are different for each assembly and do not correspond to unigene numbers in any other assembly or database.

5.4. Integration of the transcriptome and proteome analyses

The integration of transcriptome and proteome analyses was effected by linking the datasets. First it was checked whether ESTs contributing to a certain HarvEST:Barley-ID were present on the array (direct linking, Figure 5a). Secondly, if a direct link could not be found, two other alternatives were used: i) the HarvEST:Barley contig was blasted against the HarvEST:Barley database to find homologs or isoforms with at least 95 % sequence identity to which a contributing EST is on the array. ii) two of the three databases (BLASTX UniProt, BLASTX Rice, BLASTX Arabidopsis) share the same best hit between the initial and alternative HarvEST:Barley-IDs (alternative linking, Figure 5b and c). If several ESTs present on the array were matching a specific protein spot, the one with the best FDR (q-value) was used for the final linking.

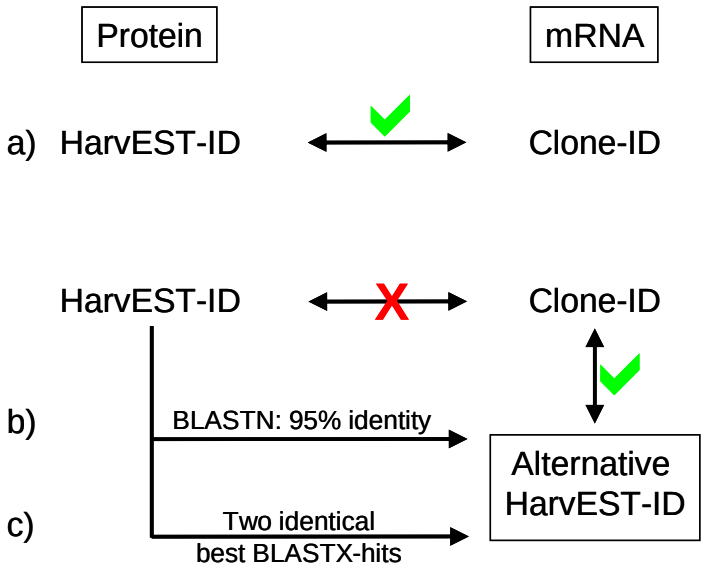


Figure 5: Strategies for linking of protein and transcript. a) direct linking: a clone which is a part of the HarvEST:Barley consensus sequence is spotted on the array. b) and c): indirect linking: a clone of an alternative HarvEST:Barley consensus sequence, which is found to be highly similar by BLASTN search or shows two identical best BLASTX hits to the original one is present on the array.

6. Results

6.1. General

The plant epidermis has a crucial role in the defence mechanisms of host and nonhost interactions against a broad range of fungal diseases including powdery mildew caused by *Bgh*. The epidermal transcriptome and proteome of infected barley leaves were analysed at several time points during the infection process in relation to that of control leaves, in order to be able not only to analyse both data sets among themselves, but also to integrate them. Both approaches used split samples of identical biological material. This should also allow addressing post-translational and post-transcriptional changes following fungal attack.

6.1.1. Yield of samples

Under favourable conditions the fungus can complete an asexual replication cycle in five days. The time points to study the effect of *Bgh* on the barley epidermis were chosen at 12, 24, 48, 72 and 120 h.a.i., covering the entire lifecycle of the infection (see Figure 2). Epidermal peels of non-infected (control) and infected (*Bgh*) barley seedlings were collected in three individual harvests. Particularly at later time points the yield of infected epidermis samples was reduced probably because of tissue maceration by the fungus. It was therefore not possible to analyse later time points by epidermal peels, because the epidermis of the *Bgh*-infected leaves could not be peeled off after 120 h.a.i. Additionally leaf samples were collected at 120 and 162 h.a.i.

The resulting amounts of collected material were between 0.6 g and 2.5 g for the epidermis samples and 3.5 g to 6.5 g for the leaf samples.

6.1.2. Chlorophyll concentrations in epidermal samples

Chlorophylls are mainly present in the chloroplasts of the mesophyll cells, although chloroplasts are also present in the stomatal cells of the epidermis. We used the chlorophyll (chl) content as an indication for mesophyll contamination of the epidermal peels. The threshold was set to a ratio of 10 % $chl_{epidermis}/chl_{leaf}$ The chlorophyll content of the epidermis samples ranged from 3 % to 8 % of that of the leaf samples and did not show strong

variations between different time points or ways of treatment (see Table 16 in the appendix). This reflects a sufficient purity of the epidermal samples.

6.2. Transcriptome analysis

The key question of the transcriptome analysis was to identify genes, which are regulated in barley epidermis upon the infection process with *Bgh* in at least one of the time points. The question whether the regulated genes in the epidermis are only expressed in epidermis or rather uniformly distributed will also be addressed.

A cDNA macroarray enabled us to study the levels of approximately 13 000 transcripts simultaneously, providing a comprehensive overview of the gene activities in a given tissue.

6.2.1. RNA concentration and hybridization

RNA was extracted by the guanidinium thiocyanate-phenol-chloroform method (modified acc. Chomczynsky et al., 1987) from 100 mg-200 mg of freshly ground samples. The achieved RNA concentration ranged from 0.5 ng/µl to 3.2 ng/µl. The 260 nm/280 nm ratio was above 1.8 and clear bands showed up in an RNA-gel (1.7 % low melting agarose, 50 ml 1x TBE-buffer, 10 mg/ml ethidiumbromide), thus demonstrating the good quality of the extracted sample.

The hybridized membranes were exposed 6 to 10 d to phosphoimager screens and subsequently scanned. The hybridization was successful except for one sample (infected sample at 48 h.a.i. of the 2nd harvest). This hybridization gave a picture with low intensity dots. A second labelling of the cDNA was not successful and a new reverse transcription with the rest of the material did not give any better signal. Subsequent analysis on a RNA gel of this sample showed that the mRNA was degraded. Although the mRNA amounts extracted from epidermis material were rather low compared to those from leaf material, only 20 µg RNA extracted from the epidermis (about half of the recommended amount) was sufficient for the reverse transcription and to obtain good hybridization results. This may be because the overwhelming amount of mRNAs of the photosynthesis complex in the leaves is smaller in the epidermis, so that the interesting non-photosynthetic transcripts are more prominent in the epidermal sample.

6.2.2. Quality control of technical replication

The quality of the hybridization and normalization was checked by means of a correlation analysis of both technical replicates of all features within the arrays. The samples were quantile normalized for each time point separately because the aim was to compare the control and the infected samples at that moment in the development and to arrive at a ratio of regulation in transcripts upon infection. The quantile method aims to make the distribution of probe intensities for each array in a set of arrays comparable (Bolstad et al., 2003). Correlation coefficients ranged from r = 0.9811 to r = 0.9959. A typical example is shown in Figure 6. This shows that the quality of the steps until hybridization as well as the used normalization method was appropriate. Therefore in the next steps mean values of both replicates could be used.

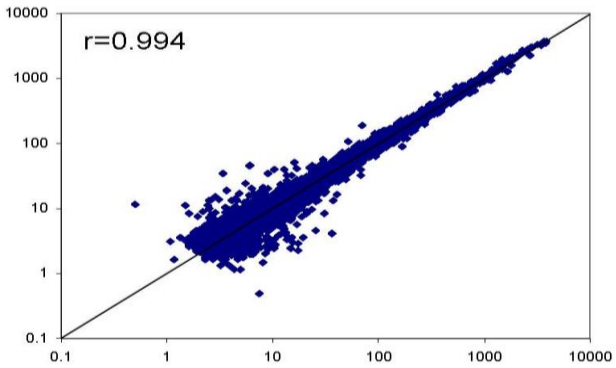


Figure 6: Example of the correlation of technical replicates of one sample. The coordinates on the x-axis represent s the value for one, the value of the y-axis for the other technical replicate within a macroarray. Axes have $\log_{10}$-scaling.

6.2.3. Principle component analysis of all samples

^{33}P-labelled cDNA probes of the mRNA samples were hybridized to the array. Of the spotted 13 050 features, 8 528 were included in further analyses, because their signal in 3 out of 30 hybridizations was at least 2.5-fold higher than the background. This criterion is based on the accepted fact that the signals of weakly present transcripts are more susceptible to artefacts (Sreenivasulu et al., 2002). These 8 528 features will now be referred to as “present transcripts”.

The present transcripts were clustered in a Principle Component Analysis (PCA) and by means of hierarchical clustering (HCL, Pearson correlation). PCA shows clustering of the biological replicates according to the treatment and the time points. At the first time point (12 h.a.i.), one sample of infected epidermal tissue clustered into the control population (Figure 7, box). Because the infection process was less developed and probably did not yet

cause strong changes, a methodological mistake could be excluded. The above mentioned infected sample at 48 h.a.i. in the 2nd harvest that gave weak hybridization signals due to partially degraded mRNA (see chapter 6.2.1) clustered outside the experiment (Figure 7, circle). This sample was excluded from the following analyses.

The PCA furthermore show that the samples of each time point cluster along the x-axis and the samples also cluster along the y-axis depending on the treatment. This indicates, that the data are useful, because the effect of biological and technical variations are lower than developmental and treatment effects. The correlation of the biological replicates is shown in Table 18 in the appendix.

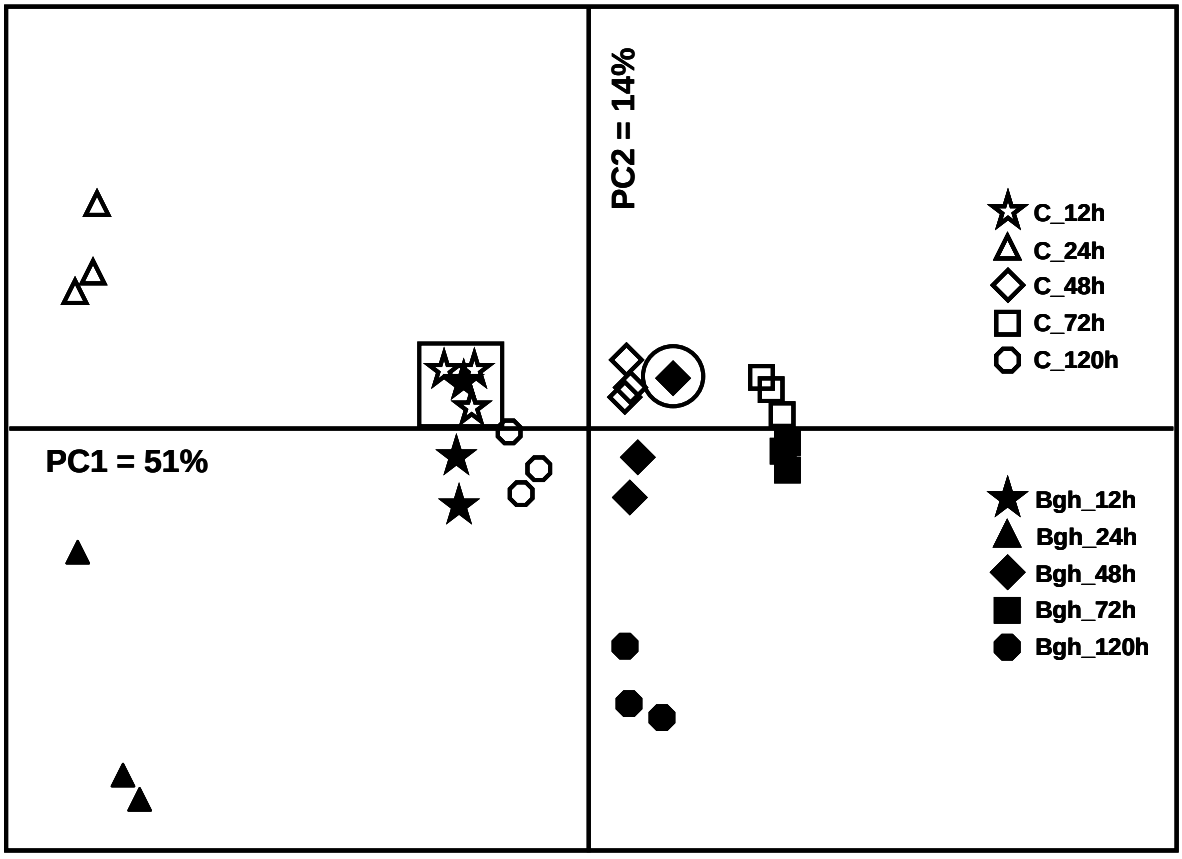


Figure 7: Principle component analysis of biological replicate samples. Control samples: open symbols; *Bgh*-inoculated samples: filled symbols; description of symbols on the right; Box: control samples and one *Bgh* sample at 12 h.a.i. Circle: infected sample, 48 h.a.i., 2nd harvest.

6.2.4. Statistically significant regulation events

Statistically relevant changes in the transcriptome were analysed first via a pairwise t-test. The normalized and $\log_2$-transformed intensities of the treated epidermal samples were tested against their corresponding control samples.

Of the significantly regulated spotted features (PCR products) for regulated transcripts a total of 3 002 were regulated with an FDR of $q<0.05$. In order to find robustly regulated transcripts that react to the pathogen in a way that can be reproduced, gene expression data for each time point and treatment were averaged and a 2-fold regulation level was used to determine transcripts that are highly regulated in at least one time point. Using the above mentioned criteria 1 815 candidate spotted features were selected and subjected to further analyses. These spotted features correspond to 1 798 unigenes because around 1 % of the features were spotted as duplicates from independent PCR reactions at different positions on the array for control purposes.

6.2.5. Plant derived, pathogen-regulated transcripts

The spotted features on the array originate from several EST libraries. As some of these libraries derive from infected plant material, fungal transcripts are included. In order to exclude these fungal transcripts from the analysis it is necessary to identify the corresponding transcripts. For this aim two different database search algorithms were used. The ESTs were firstly blasted against the contigs of Affimetrix Barley1 chip (Sreenivasulu et al., 2008) via stringent BLASTN and secondly against the nonredundant NCBI-database via BLASTX. These spotted features for regulated transcripts can be either fungal transcripts or interesting plant transcripts. It was decided to exclude spotted features for regulated transcripts which showed no plant-derived identifiers with $e<1^{-10}$ in one of the database searches in order to ensure that only plant mRNAs were analysed. However, it has to be considered that in this cluster of eliminated transcripts probably interesting plant transcripts might also be included, since they have no plant hit because they are unknown so far. With this prerequisite 337 (19%) of the original 1 815 features were therefore excluded from the analysis. 15 of these features were linked to a SuperBIN with defined biological annotation, 120 to the SuperBIN “not assigned” and 202 were not linked to any SuperBIN. These agree prevailingly with the list of assumed fungal genes in other publications and personal conversation in our working group (Zierold, Gay). Furthermore 73 % of the excluded features show an upregulation, which is a hint that these transcripts belong to the fungal load on the epidermis.

With this, 1 478 spotted features were identified as definitely plant-derived regulated transcripts. The list of these 1 478 EST-clones is shown in the appendix (see Table 19). The process of selection of relevant regulated transcripts is shown in Figure 8.

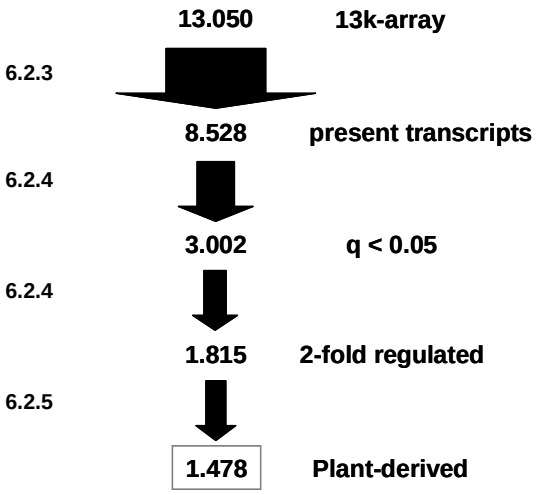


Figure 8: Selection process for relevant regulated transcripts. Numbers on the left: chapter explaining the steps; numbers in the middle: transcripts identified in each step; on the right name of the step.

6.2.6. Regulation events at discrete time points

In this analysis the number of >2-fold regulated transcripts was compared for each time point separately. As can be seen in Table 4, no plant transcripts were downregulated at 12 h.a.i. The number of regulations increased at 24 h.a.i. At 48 h.a.i. the number of changes decreased, in particular the downregulation events. At 72 h.a.i. the number of regulation events once more increased. Also up- and downregulated transcripts were equally distributed at this time point. At 120 h.a.i., regulation events in both directions were further enhanced, especially the downregulateed transcripts.

Table 4: Numbers of spotted features, at least 2-fold up- or downregulated. Numbers according to their occurrence at each time point separately.

Time point	upregulated	downregulated
12 h.a.i.	122	0
24 h.a.i.	294	327
48 h.a.i.	160	86
72 h.a.i.	228	182
120 h.a.i.	425	623

6.2.7. Classification of genes into hierarchical functional categories

The MapMan visualization software was originally developed for the ATH1 array to display *A. thaliana* gene expression experiments (Thimm et al., 2004, Usadel et al., 2005). This software can be used as a web-based or stand-alone application (http://gabi.rzpd.de/projects/MapMan/). The principle of the MapMan ontology is to characterize gene expression in a cell-biological context through a hierarchical ‘‘BIN’’-based structure (SuperBINs, BINs, subBINs down to individual proteins). The Super-BINS 1-34 describe functional classifications, whereas transcripts in the Super-BIN 35 (“not assigned”) are not further categorized. An example of the organization of biological functions in the MapMan binning system is shown in Figure 9. The colour coding linked to the SuperBINs shown in Figure 9 is used in this order in all subsequent pie charts.

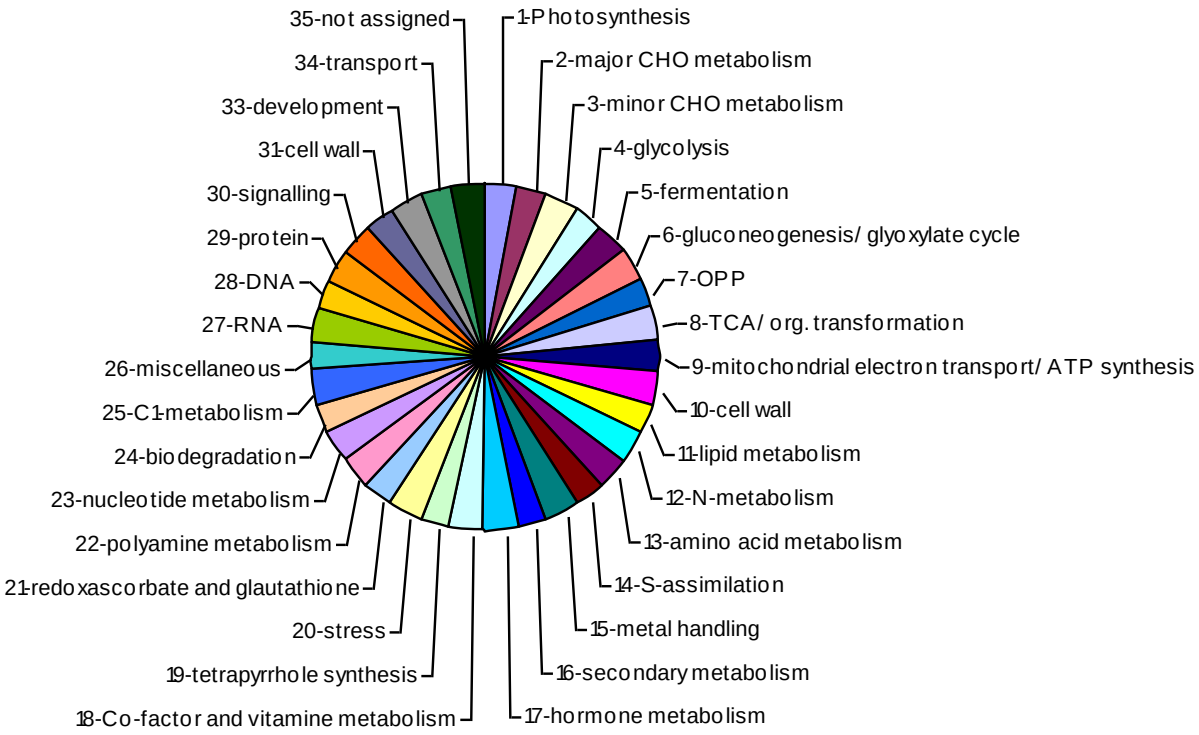


Figure 9: Scheme of the organization of the MapMan SuperBINs and colour coding used in the diagrams in this study. The SuperBINs 1 to 34 are classified with biological functions (“OPP: “oxidative pyrophosphate”, “TCA”: “triglyceride citric acid”), the SuperBIN 35 (“not assigned”) is not annotated with a certain biological function.

Each SuperBIN comprises items of similar biological function and can be further split into subBINs of the same function and the BIN-Code reflects this structure. Thus SuperBIN 20 (stress) can be subdivided into 20.1 (stress.biotic) and 20.2 (stress.abiotic). The name of the SuperBIN and its numerical code shows the relationship between itself and its BINs and subBINs, which is particularly important for SuperBINs with a large number of BINs, like “signalling” (30), which has eleven BINs. The MapMan visualization enables the user to

display genomic datasets in pictorial diagrams of metabolic pathways or other processes, and to visualize the responses of gene expression in a biological context.

The adaptation of MapMan to barley by mapping the Affymetrix Barley1 GeneChip probe identifiers into the MapMan functional categorization was done recently by Sreenivasulu et al. (2008). Through this the software platform was extended to allow it to be applied to barley, but not yet for the macroarray used in this study.

6.2.8. Classification of regulated transcripts of the PGRC2-13k-cDNA-macroarray

By comparing EST-clones of the PGRC2-13k-cDNA-macroarray to the contigs of the Affimetrix Barley1 chip by stringent BLASTN (carried out by Dr. Matthias Lange, Bioinformatics and Information Technology Department, IPK Gatersleben), it was possible to classify the results of this study into the hierarchical functional categories of the MapMan binning system.

With this method, 10 724 of the 13 050 spotted features (82%) could be matched to the Affymetrix Barley1 probes and therefore to the MapMan hierarchy. When the MapMan binning system was applied to the 1 478 plant-derived spotted features for regulated transcripts, 1 048 were categorized into the SuperBINs 1-34 and therefore into biological functions, whereas 344 were put into the SuperBIN 35 (“not assigned”). The remaining 86 transcripts on the array were present on the 13k-array, but were not linkable to any contigs on the Affimetrix Barley1 chip and therefore were not present on the MapMan binning system (see Table 5).

Table 5: Classification of regulated transcripts into MapMan binning system by linking the 13k-array with the binning system (done by M. Lange, IPK)

Classification	Number of features
linked, classified	1 048
linked, not assigned	344
not linked	86

6.2.9. Distribution of regulated transcripts across categories

Among the present features a high percentage could be located in the SuperBIN “protein” and “RNA” (26% and 14%, respectively, Figure 10A), whereas the percentage of spotted features that showed statistically relevant changes of at least 2-fold at at least one time point

in these SuperBINs were lower (16 % and 12 %, respectively, Figure 10B). The proportion of the members of the SuperBIN “transport” did not differ in present and regulated spotted features. In contrast, the proportion of the SuperBINs “stress” and “misc” in the present spotted features was only 4 % and 6 %, compared to 6 % and 10 % in the regulated ones, respectively. This suggests that these biological functions are important in the interaction between *Bgh* and the barley epidermis.

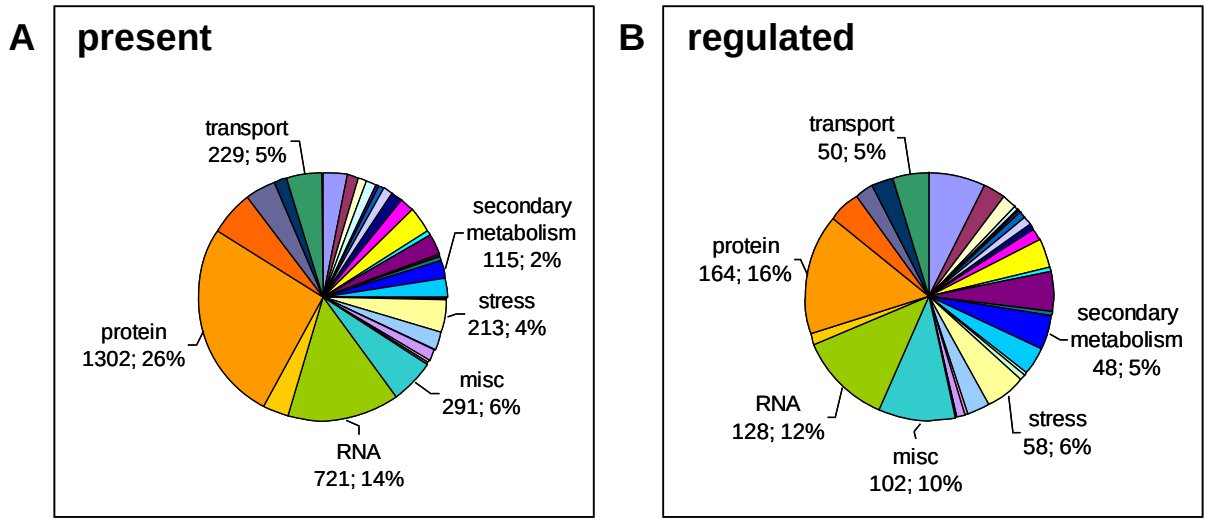


Figure 10: Percentage of A) present and B) regulated transcripts into functional classes. . The number of spotted features and the overall percentage of the specific SuperBINs are shown. The colour coding and organization of the SuperBINs are according to Figure 9.

6.2.10. Investigation of over- and underrepresentation of regulation in functional classification

In order to find out whether transcripts belonging to specific functional groups of genes were preferentially regulated in response to *Bgh*-attack, it is necessary first to check if up- or downregulation was over- or under-represented in a certain SuperBIN, irrespective of the absolute number. For this purpose the Chi-square test was applied. For these testings the number of transcripts with an increase or decrease in regulation of at least 2-fold in *Bgh* samples in relation to control samples was counted.

Figure 11 exemplarily shows the graphical depiction of the Chi-square results. The first (black) column means that the percentage of 2-fold regulated genes in this SuperBIN is 4-fold higher than the overall percentage of regulated genes among all present genes. The chi-square testing calculated this case as statistically relevant with $p<0.005$ (adapted from Figure 12, upregulated genes of the SuperBIN “secondary metabolism” at 12 h.a.i.). The second (grey) column shows that the percentage of 2-fold regulated genes in this case is 2.8-fold lower than the percentage of all present genes with a $p<0.05$ (as can be seen in the downregulated genes of SuperBIN “protein” at 72 h.a.i., Figure 12).

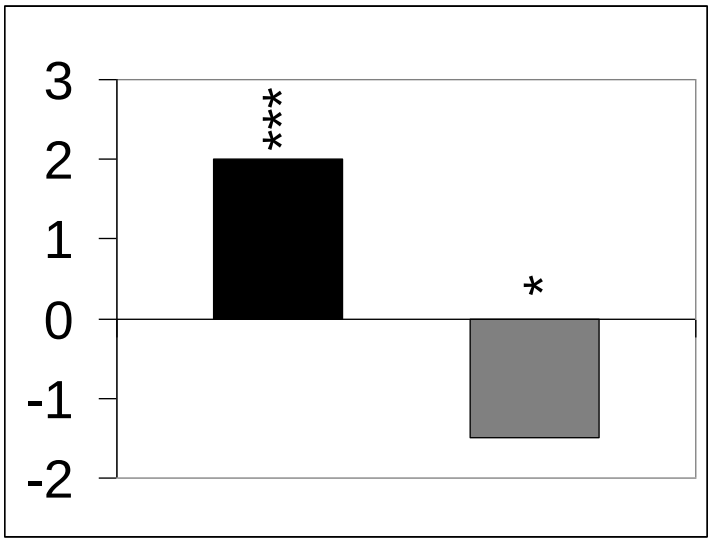


Figure 11: Example of chi-square testing of over- or underrepresentation of functional groups among regulated transcripts. Black column: overrepresentation (positive amplitude on y-axis) of the regulated genes is 4-fold (after log_2-transformation: 2) and statistically significant with $p<0.005$ (***). Grey column: underrepresentation (negative amplitude on y-axis) of the regulated genes is 2.8-fold (after log_2-transformation: 1.5) and statistically significant with $p<0.05$ (*).

Only the level of SuperBINs was taken into account when analysing the samples, because the unigene numbers per BIN would have been too low for statistical analysis. Analysis on the basis of the SuperBINs was carried out for each time point and for up- and downregulated transcripts separately if at least three transcripts were regulated.

Figure 12 demonstrates that several functional groups were significantly over- or under-represented among the groups of pathogen-regulated transcripts. For example the SuperBINs that were significantly over-represented in the upregulated transcripts at all time points within the infection process were the following:”stress”, “secondary metabolism” and “miscellaneous (misc)”. Breaking down the SuperBIN “miscellaneous” into specific BINs revealed that more than 75 % contains unigenes belonging to pathogenesis- or stress-related multigene families. Therefore, the SuperBIN “miscellaneous” represents the basal defence response of barley. On the other hand the SuperBIN ”protein” was significantly under-represented in the upregulated transcripts at all time points and also under-represented in the downregulated transcripts at the time points 24 h.a.i., 48 h.a.i. and 72 h.a.i.

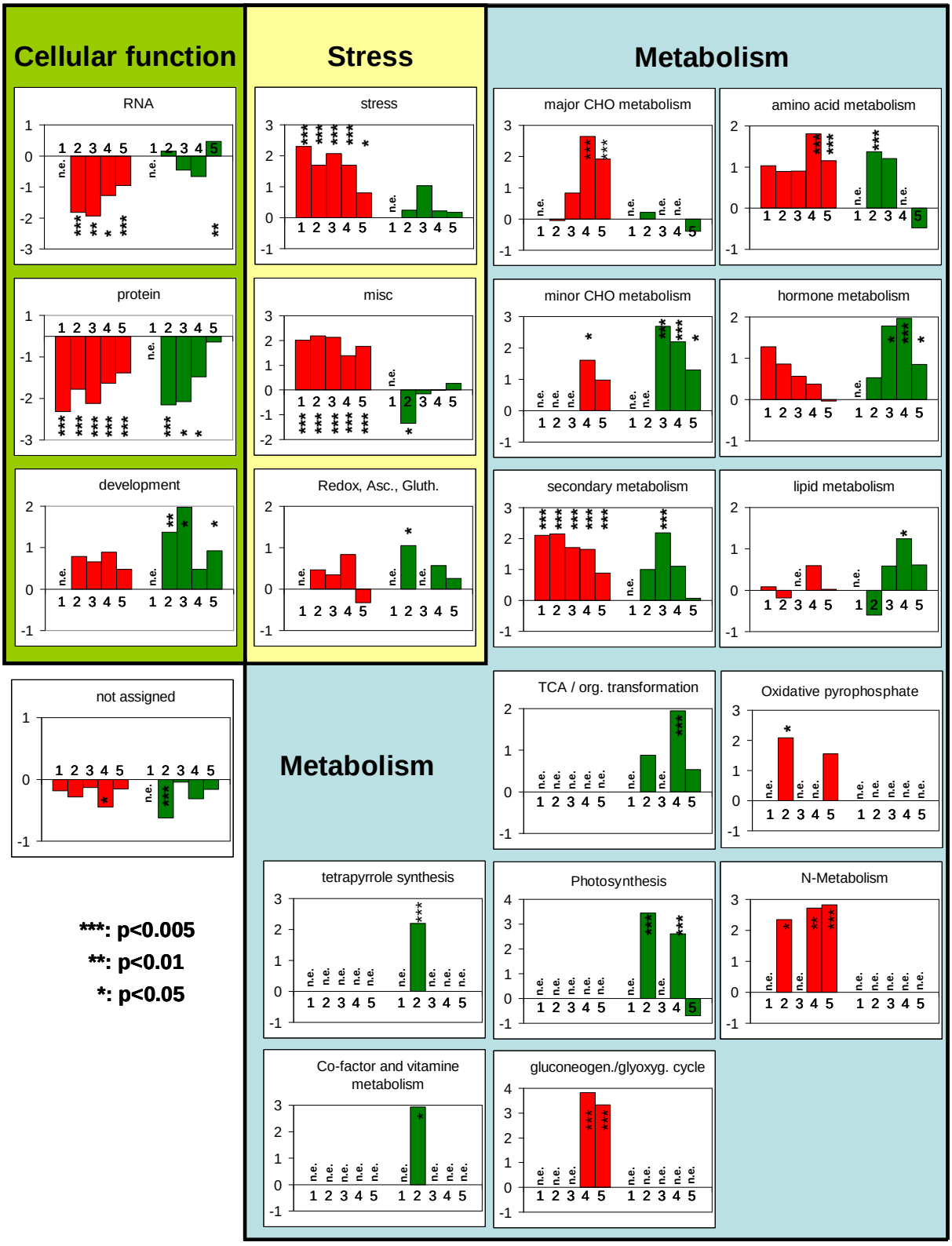


Figure 12: Over- or under-representation of up- or downregulated transcripts for each SuperBIN, separated for each time point. Red columns: upregulated transcripts, green columns: downregulated transcripts; Numbers on the x-axis represent the time points: 1: 12 h.a.i.; 2: 24 h.a.i.; 3: 48 h.a.i.; 4: 72 .a.i.; 5: 120 .a.i.. Numbers on the y-axis shows the overrepresentation (positive values) and underrepresentation (negative values). The values of over- or under-representation are shown after log_2-transformation. Statistical significance level (Chi-square testing) is shown with asterisks. *: p<0.05; **: p<0.01; ***: p<0.005 SuperBINs containing less than three transcripts for a specific time point are not estimated (n.e.).

6.2.11. More detailed view of biological clusters in BINs and Sub-BINs

So far we have restricted our view to the regulation and representation of transcripts, clustered into the SuperBINs. However within a SuperBIN, subgroups may react differently. In order to make these effects visible one can use the MapMan-based program PAGEMAN. This program orders the transcripts into their SuperBINs, BINs and sub-BINs in a hierarchical system (e.g. SuperBIN “stress”, BIN “stress.abiotic”, SubBin “stress.abiotic.heat”). Figure 13A shows the ratios of regulation for the Sub-BINs, BINs and SuperBINs at all five time points. The advantage of this visualization method is an immediate overview of regulated biological processes; it structures the information of the array experiment in detail. However, this table does not show how many individual genes are involved in each category. As an example, in the interaction of the biotic fungus *Bgh* with barley, the transcripts classified into the BIN “stress.biotic” were upregulated (red), the transcripts for the Sub-BINs “stress.abiotic.heat” and” stress.abiotic.salt/drought“ were downregulated (green) (Figure 13C, 1). In the second example “protein degradation” (Figure 13C, 2) we can see a strong upregulation for the Sub-BIN “subtilases” (red) in the degradation of proteins, but a downregulation for “ubiquitin” (green). The full picture can be seen in the appendix (Figure 42).

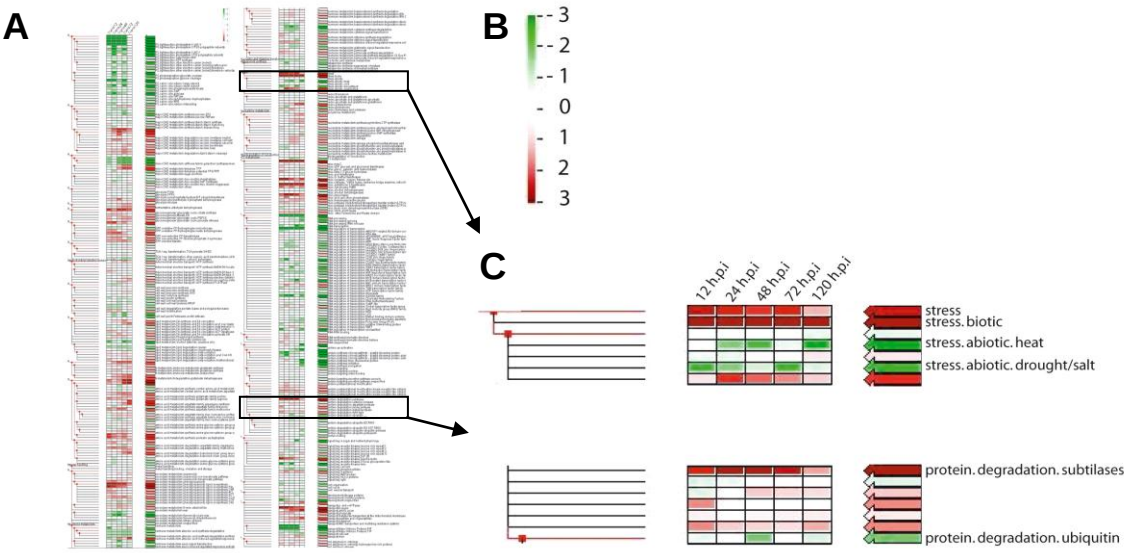


Figure 13: Visualisation of regulation by PageMan. A) all 1478 spotted features for regulated transcripts. B) color coding for ratios after log_2-transformation for down- (green) to upregulation (red). The extent of the change is given by the intensity of the color. C) detailed view of two classifications: SuperBIN “stress” and the BIN “protein.degradation”; from left to right: Dendrogram: Hierarchical clustering of SuperBIN to Sub-bin; five coloured boxes: regulation for each time point of genes involved in this hierarchical cluster; coloured arrow: mean regulation value of the five time points.

6.2.12. Localization of transcript regulation events

From a histological point of view the growth of *Bgh* is limited to the epidermis of barley. Therefore it can be assumed that crucial pathogen-induced changes for defence or fungal support mostly occur in the epidermis or that certain pathogenesis-related genes are exclusively expressed in the epidermis. For this reason regulation events were evaluated primarily in epidermal tissues. To determine the degree of epidermis specificity of a given transcript, non-inoculated samples of the epidermis as well as of the remaining leaves harvested at 120 h.a.i. were hybridized onto the array. Because a whole leaf of barley consists only to about 24 % of epidermis (Zierold, 2005), and the relative amount of mRNA in the epidermis is about 4-fold lower (own experiments), the macroarray expression data of mRNA of remaining leaf tissues after peeling (still containing the adaxial epidermis) were assumed to be mostly mesophyllic and from now on will be referred to as “mesophyll” sample. A transcript was assumed to be present in a certain tissue if the intensity-to-background-ratio was higher than 2.5 in two of three biological replicates.

Under these criteria, a total of 8 184 features or 8 109 transcripts were detected, 3 987 features were exclusively present in the epidermis, 120 transcripts exclusively in the remaining leaf and 4 077 features were present in both tissues. To determine if the spotted features were of plant origin, the same criteria as described in chapter 1.2.5 were applied. 7 353 features of the 8 184 present ones are definitely plant-derived. The other remaining 831 features are either fungal-derived or yet unknown relative plant transcripts.

From the 1 478 plant derived features, that were pathogen-regulated in the epidermis (chapter 6.2.5), 124 (8 %) were not present in the control samples of leaf or epidermis, and the location of preferred accumulation could therefore only be determined for 1 354 of them.

For each present feature the ratio of the normalized signal intensities of epidermis sample to that of the leaf sample was calculated and $\log_2$-transformed to produce the E/M value (E/M; epidermis-to-mesophyll-ratio). For example, an E/M ratio of 1 means the expression of a gene is enriched by 2-fold in the epidermis, whereas with an E/M ratio of - 1 the expression of a gene is enriched by 2-fold in the mesophyll. To test this prediction, the E/M values of uniformly distributed candidate genes with known transcript localization were analysed. “Chlorophyll-binding proteins” and “RuBisCO” were postulated as mesophyll-enriched transcripts. “Ubiquitin-conjugating enzymes”, “cytoplasmatic GAP-DH” (Glycerine-aldehyde-3-phosphate-dehydrogenase) and “Actin” stand for ectopically expressed transcripts. The mean value of 96 ectopically expressed ESTs after $\log_2$-transformation show an E/M = 0.39, the mean E/M ratio of 88 mesophyll-enriched ESTs is -0.70 and the mean value of nine assumingly epidermis-enriched expressed “oxalate-oxidase or germin-like” genes is 1.94.

Figure 14 shows the distribution E/M values after log_2-transformation of the 7 353 plant-derived present transcripts.

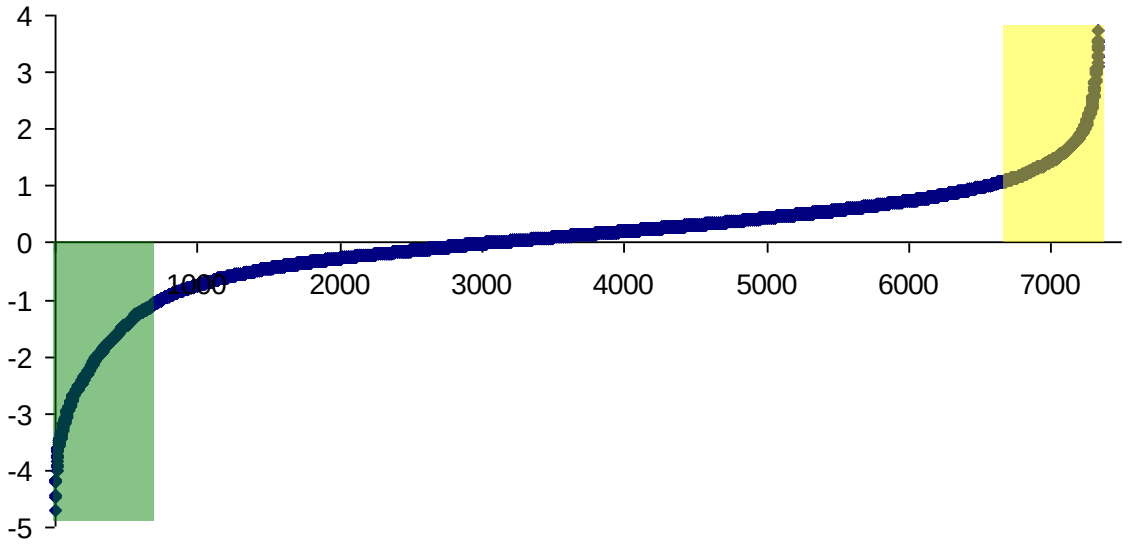


Figure 14: Distribution of present transcripts with their corresponding E/M (epidermis-to-mesophyll) value. Transcripts (x-axis) are ordered according to their E/M signal ratio after log_2-transformation (y-axis). Green area: transcripts with an E/M value of <-1 (mesophyll-enriched). Yellow area: transcripts with an E/M value of >1 (epidermis-enriched). On the left side the transcripts with mesophyll-enriched expression (green), on the right side with epidermis-enriched expression (yellow) are located. The E/M-value of most transcripts lies in the range between -1 and 1 (uniformly distributed expression).

It can be seen that the proportion of tissue-specific accumulation was equal in the regulated plant transcripts and in the present ones (Table 6).

Table 6: Numbers and percentage of tissue-enriched expressed transcripts in present and regulated plant transcripts.

	all	mesophyll-enriched	epidermis-enriched
Present transcripts	7 353	743 (10 %)	802 (11 %)
regulated transcripts	1 354	260 (19 %)	265 (20 %)

The next step was to differentiate between present and regulated plant transcripts and then to assign the proportion of mesophyll- or epidermis-enriched expressed features for the MapMan SuperBINs. All plant-derived transcripts were classified with the MapMan categories into genes with known (SuperBINs 1-34) or unknown (SuperBIN 35: “not assigned”) functional categories, besides those that could not be linked to this classification scheme (“not linked”). Figure 15 shows the proportion of present and regulated transcripts from the analysis of regulation in epidermis samples upon infection from chapter 6.2.5 (Figure 8), split up into mesophyll-enriched, uniformly distributed and epidermis-enriched expression. The proportions did not differ much between present and regulated transcripts, except in the epidermis-enriched regulated ones, which have a higher proportion of transcripts that are functionally classified.

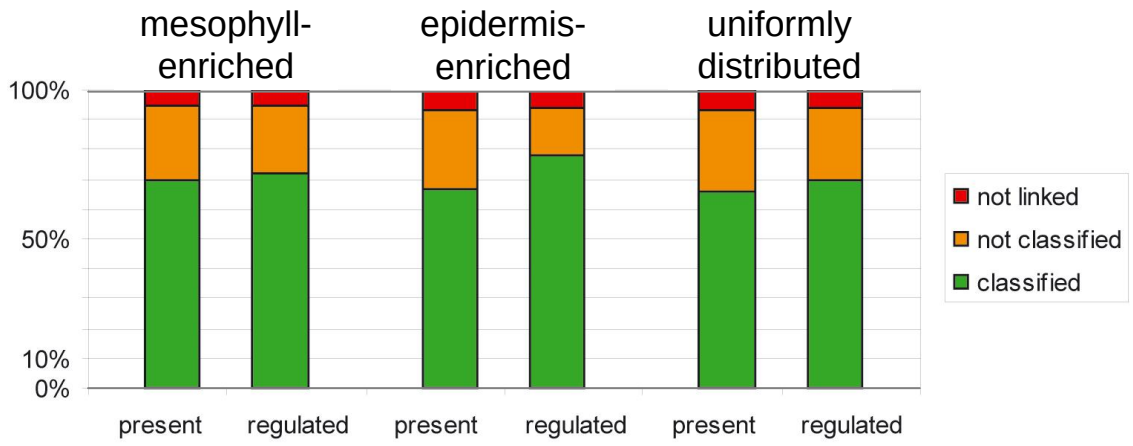


Figure 15: Distribution of present and regulated transcripts of treated epidermis samples, splitted into mesophyll-enriched (E/M<-1), epidermis-enriched (E/M>1) and uniformly distributed (-1<E/M<1) expressed transcripts.

Figure 16 shows a more detailed view of the percentage of transcripts falling into different SuperBINs. Of all present transcripts in the different functional categories (Figure 16A), 26 % were clustered into the SuperBIN “protein”. The inspection of the mesophyll-enriched transcripts (Figure 16B) separated by biological function revealed that the percentage of the SuperBINs “photosynthesis (PS)” (21 %) and “amino acid metabolism” (8 %) were elevated. The epidermis-enriched transcripts (Figure 16C) had a higher percentage in the SuperBINs “miscellaneous” (11 %), “stress” (7 %) and “minor CHO” (3 %).

Mesophyll-enriched regulated transcripts (Figure 16E) had a higher proportion of the SuperBINs “PS” (photosynthesis) (34 %) and “amino acid metabolism” (12 %) in contrast to mesophyll-enriched, present transcripts (Figure 16B), whereas the number of transcripts in “protein” was lowered (7 %). The proportion of regulated transcripts that were preferentially accumulated in the epidermis (Figure 16F) was elevated in the SuperBINs “secondary metabolism” (6 %) and “misc” (15 %), whereas “protein” was lowered (14 %). In general it is interesting, that epidermis-enriched transcripts contained fewer SuperBINs than mesophyll-enriched or uniformly distributed transcripts, underlining the specialization in biological functions of this tissue.

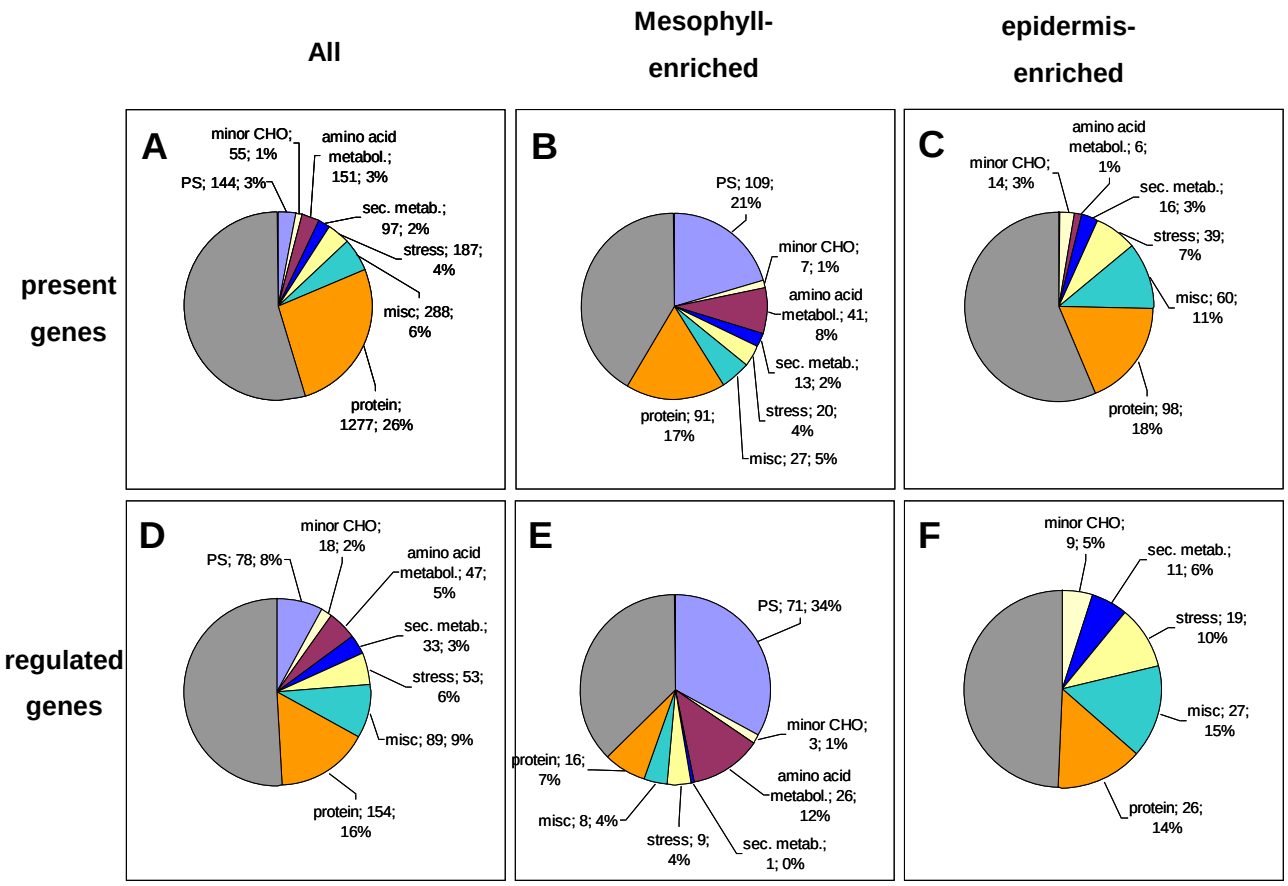


Figure 16: Distribution of transcripts over the SuperBINs. A) all present transcripts; B) mesophyll specific present transcripts; C) epidermis-enriched present transcripts; D) all regulated transcripts; E) mesophyll-enriched regulated transcripts; F) epidermis-enriched regulated transcripts. Colour coding acc. to Figure 9.

In Table 20 of the appendix the mean E/M values for the SuperBINs are summarized. Figure 17 shows a comparison of the mean E/M value between present (grey) and regulated (yellow) transcripts. The E/M value of regulated transcripts was increased in the SuperBINs “not assigned”, “protein”, “RNA”, “miscellaneous”, “stress”, “secondary metabolism” and “minor CHO”, whereas it was decreased for regulated transcripts in the SuperBINs “amino acid metabolism”, “photosynthesis” and “TCA”.

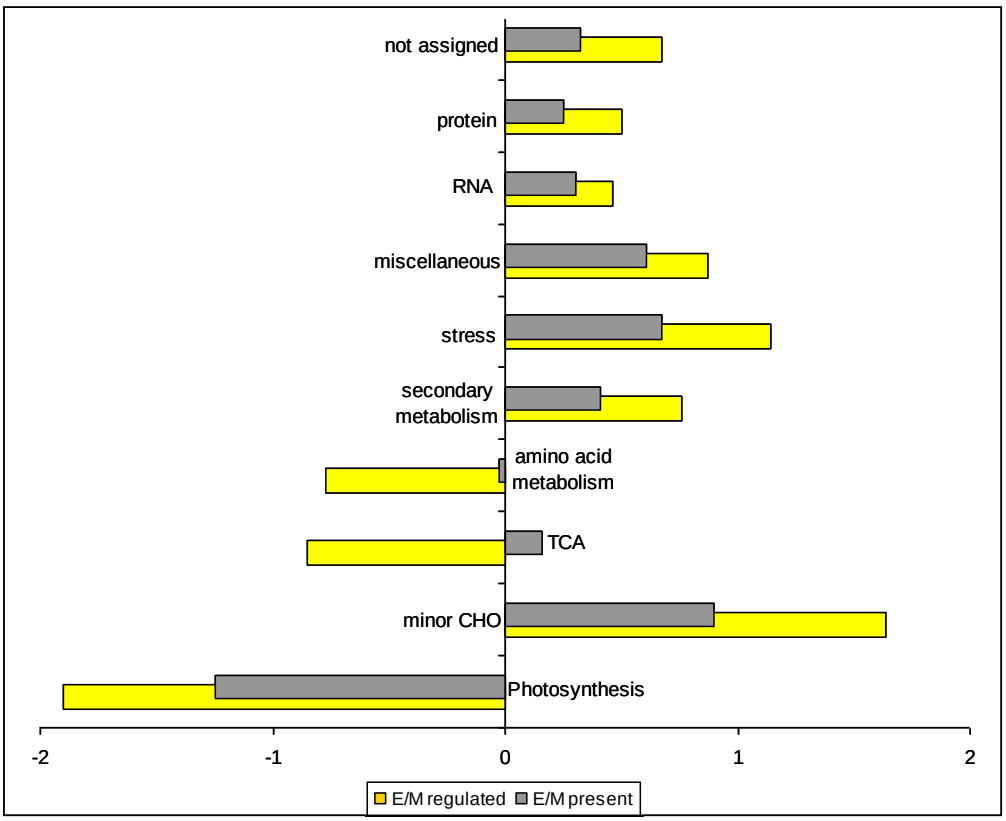


Figure 17: The mean E/M value of transcripts in specific SuperBINs. The grey columns show the value of present transcripts, the yellow columns values of regulated transcripts. E/M-values are log_2-transformed. Negative and positive values indicate mesophyll-enriched and epidermis-enriched expression of transcripts, respectively.

To test if the regulated mesophyll- or epidermis-enriched transcripts were under- or over-represented in a certain SuperBIN, Fischer's exact test was carried out. This made it possible to estimate the number of mesophyll- or epidermis-enriched transcripts which were significantly over- or under-represented in a certain SuperBIN.

Figure 18 shows those SuperBINs in which a significant under- or overrepresentation of tissue-enriched pathogen-regulated transcripts of at least $p<0.05$ was evident. The SuperBINs "not assigned", "protein" and "RNA" showed an underrepresentation in mesophyll-enriched transcripts. An overrepresentation of epidermis-enriched transcripts could be seen in "not assigned" and "minor CHO", whereas an underrepresentation of epidermis-enriched transcripts could not be found. No transcripts were epidermis-enriched in the SuperBINs "PS", "amino acid metabolism" and TCA" ("not estimated"), whereas in these SuperBINs the mesophyll-enriched accumulated transcripts were overrepresented. Additionally the SuperBINs "secondary metabolism", "miscellaneous" and "stress" are shown because of their relevance of regulation in the epidermis, although they only showed a statistical significance of $p<0.1$. The epidermis-enriched transcripts of the SuperBINs were overrepresented, whereas the mesophyll-enriched transcripts were underrepresented in the SuperBIN "secondary metabolism".

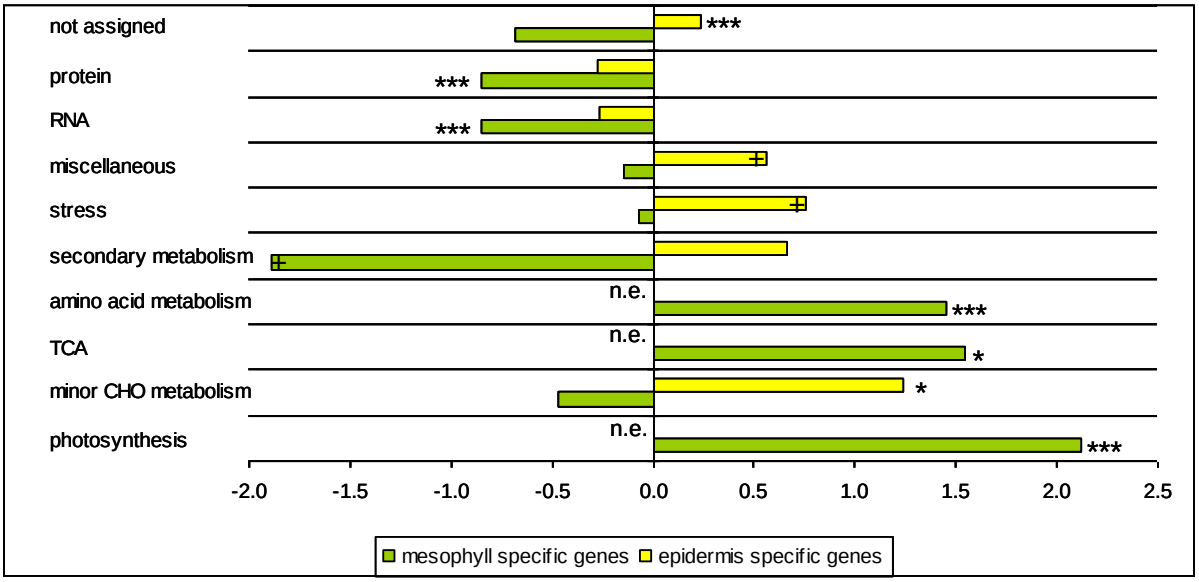


Figure 18: Over- or underrepresentation of regulated transcripts in epidermis or mesophyll belonging to specific SuperBINs. Overrepresentation is indicated by positive and negative values, respectively (log_2-transformed). Yellow bars: epidermis-enriched transcripts; Green bars: mesophyll-enriched transcripts. +: p<0.1; *: p<0.05; **: p<0.01; ***: p<0.005 for representation through Fischer's exact test. SuperBINs containing less than three transcripts for a specific hybridization are not estimated (n.e.).

6.3. Proteome analysis

Epidermal samples of non-infected and infected barley seedlings were extracted using the TCA method. After that the samples were dialysed to dilute non-proteineous substances. The protein concentration of epidermis samples was approximately one-fifth of the protein concentration of leaf samples according to trial experiments. Trial work showed, however, that a large sample volume, reaching a certain amount of proteins, regularly caused problems in the IEF, which was prevented by concentrating the samples. Because of the reduced epidermis stability of infected barley seedlings at later time points, only 37 µg of pure proteins could be extracted at 120 h.a.i. of the first harvest. With this small amount of protein sample it is not possible to do an analysis on 2-D gels, therefore neither control nor infected sample of this could be included.

With the 2-D DIGE minimal labelling, the samples and the internal standard can be separated and compared on one gel simultaneously, avoiding gel-to-gel-variances. The internal standard permits a better normalization between different gels. Another advantage is the higher sensitivity of this method, therefore a smaller amount of protein sample is needed (150 µg sample for two gels including internal standard vs. 450 µg per gel, stained with colloidal Coomassie). Because of these advantages, the reliability of the results are much ore reliable than those coming from other methods like silver or Coomassie staining

(see chapter 6.3.1). The dye-swap of control and infected samples on the technical replicate gels avoids having a false calculated effect because of a potentially favoured labelling behaviour of one dye with a certain protein, and it also provides a higher statistical relevance.

Spot detection of all DIGE gels together was performed in one analysis with the software "Phoretix Same Spot" (Nonlinear Dynamics). This analysis detected 716 protein spots (see Figure 19), calculating and normalizing the values against those of the internal standard.

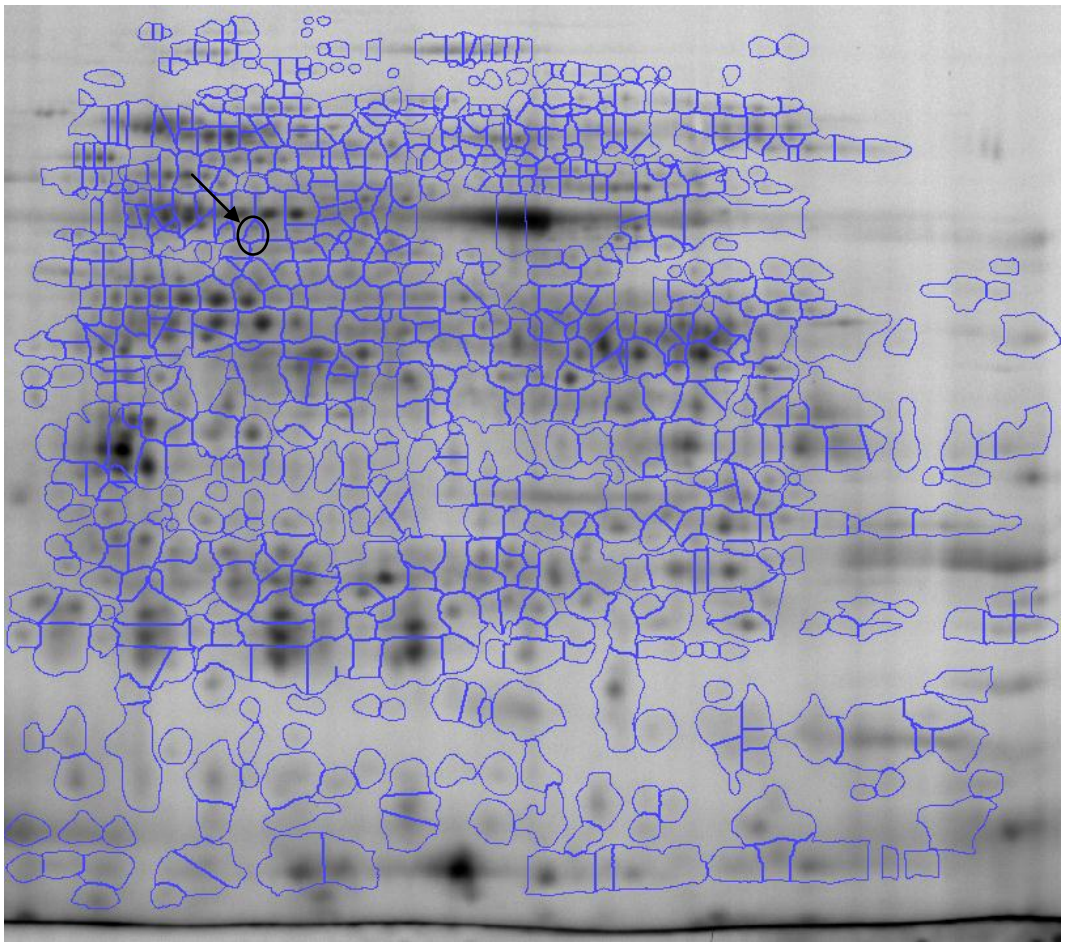


Figure 19: Spot detection of epidermal sample. Picture of the G-Dye100 channel of the virtual reference gel of the mean of all epidermis samples on 24cm-gels, pH 3-11; blue outline: area of the spots; circle: Spot 9

Figure 20A shows in an exemplary manner the values for spot 9 at all five time points for the internal standard, the control and the infected samples. From this it can be seen how the protein pattern of the control samples remained the same whereas the spot became more strongly expressed during the infection process. Figure 20B shows the values of spot 9 in control and infected samples averaged over all technical replications and harvests after normalization with the internal standards.

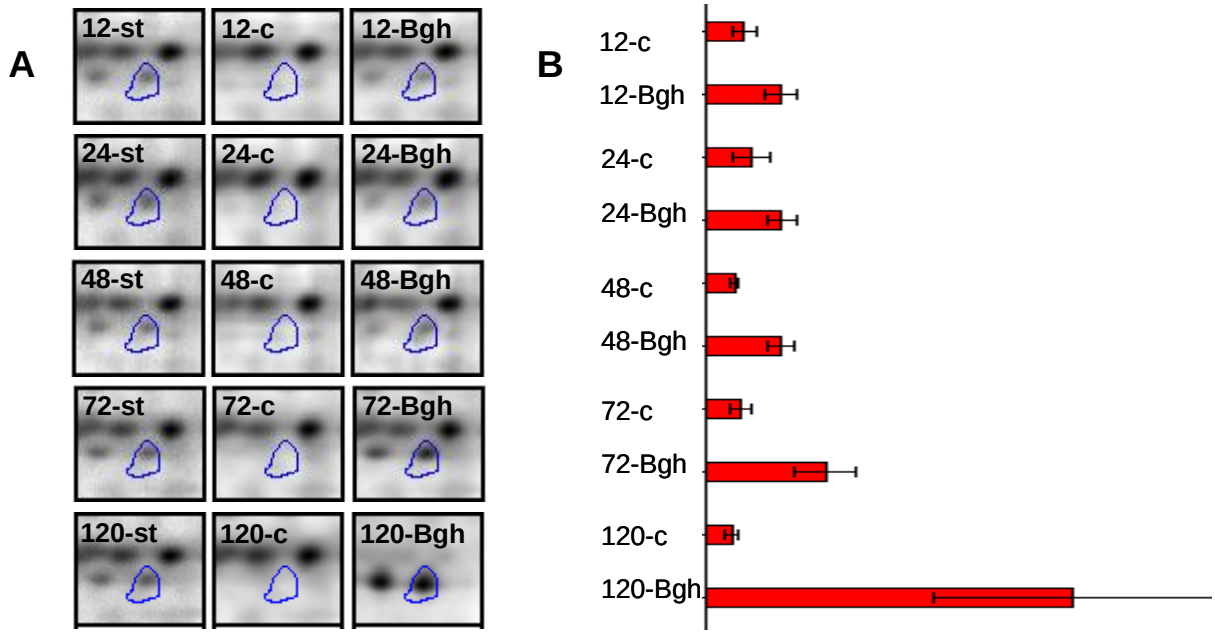


Figure 20: Exemplary expression of spot 9. A: enlarged 2-D gel section of the three G-Dye-labelled samples of each time point; blue outline: spot 9. B: spot quantities as normalized volumes of the average of all technical and biological replicates of spot 9 under integration of the internal standard. Numbers means h.a.i.; st = internal standard, c = control sample, *Bgh* = infected sample

6.3.1. Quality control of technical replication

Figure 21 shows the picture of the hierarchical clustering of all G-Dye-pictures. All the internal standards clustered together.

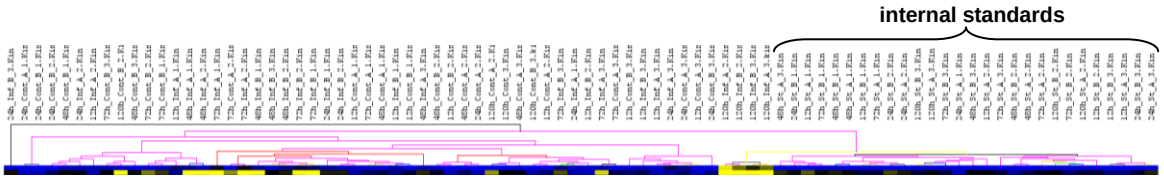


Figure 21: Hierarchical clustering of the samples, technical replicates and biological replicates. The internal standards all cluster together as shown here.

After normalization and integration of the internal standard into each sample, the quality of the focussing and normalization of the DIGE gels was checked using correlation analysis of the technical replicates. The mean correlation of the 28 samples was 0.79, ranging from 0.60 to 0.93 (Table 21 in the appendix). An example is shown in Figure 22.

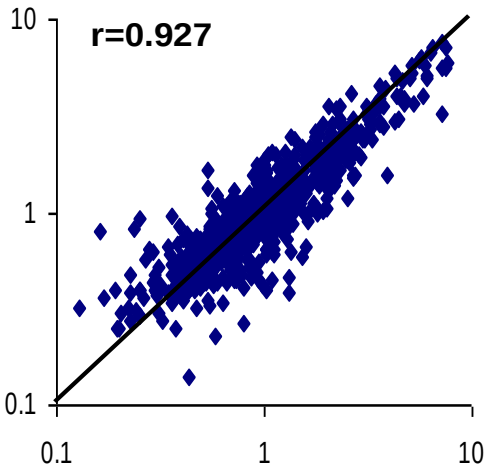


Figure 22: Example of the correlation of technical replicates of one sample (infected sample, 120 h.a.i., 2nd harvest). The coordinates on the x-axis represent s the value for one, the y-axis the value for the other technical replicate gel picture. Axes are on log_{10}-scaling.

6.3.2. PCA/HCL of all samples

Mean values of the two technical replicates of each sample were used for the following analysis of the correlation of biological replicates on the overall proteome. The samples were first log_2-transformed and clustered by PCA and HCL. These clustering methods demonstrated that the treatment had the largest influence (control samples cluster in the negative field, whereas the infected samples clustered in the positive field of the x-axis), explaining 62% of the variation. A trend over the y-axis could be seen relating to the time points. It can be seen in Figure 23 that the biological replicates clustered together. The control samples separated less according to their time points, whereas the infected samples splitted more due to the different time points after inoculation. The correlation of the biological replicates is shown in Table 22 in the appendix.

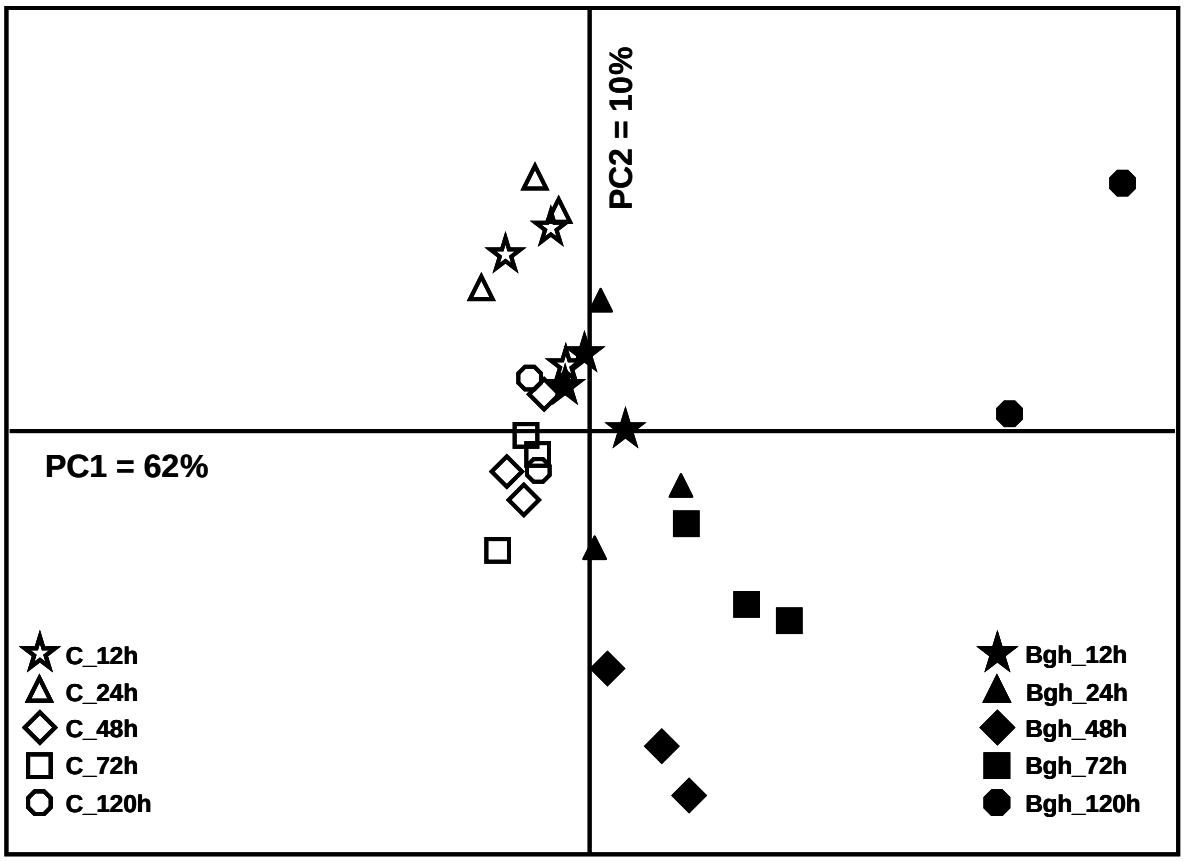


Figure 23: Principle component analysis of biological replicate gels of control (blank symbols) and infected samples (filled symbols) after normalization. C: control samples, *Bgh*: infected samles. Description of the symbols in the corners at the bottom. Biological replicates sample together, the time points ordered on the y-axis (PC2), treatment explains the variation on the x-axis (PC1).

6.3.3. Statistical analysis

Statistical analysis of the 716 proteins was made similar to the procedure done for the transcripts (pairwise t-test) using EDGE. In order to eliminate false-positives, the normalized and $\log_2$-transformed intensities of the treated epidermal samples were tested against their corresponding control samples in a pairwise manner similar to the test for the transcriptome. The sample *Bgh* 120 h.a.i. 1st harvest as well as the corresponding control sample was not included in this testing because of missing data (see chapter 6.3). 325 of the 716 detected protein spots were regulated at an FDR of $q<0.05$.

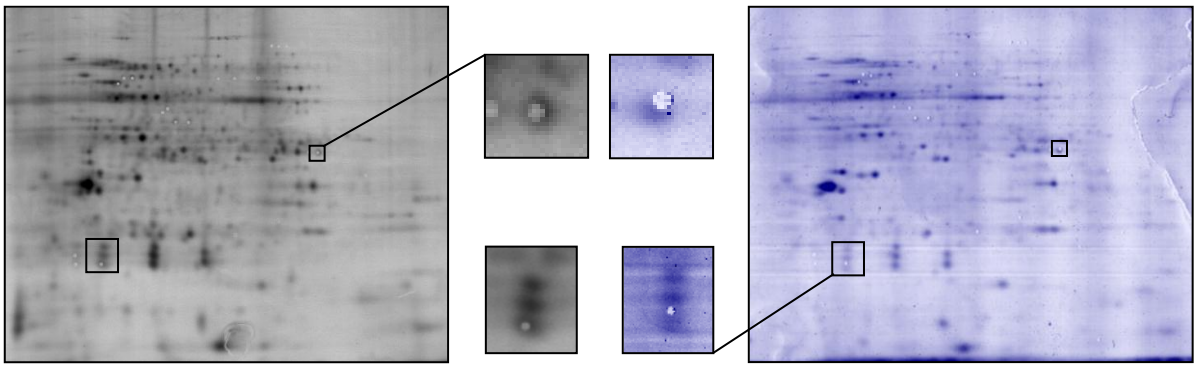
From these last mentioned 325 protein spots the number which was >1.8-fold up or downregulated was compared for each time point separately. As can be seen in Table 7, the number of upregulated genes increased steadily during the infection process. On the other hand, no plant proteins were downregulated at 12 h.a.i., only one at 24 h.a.i. and at 48 h.a.i. there were eleven. At 72 h.a.i. there was no protein spot downregulated, whereas at 120 h.a.i. there were 27.

Table 7: Numbers of proteins, at least 1.8-fold up- or downregulated. Numbers according to their occurrence at each time point separately.

Time point	upregulated	downregulated
12 h.a.i.	5	0
24 h.a.i.	20	1
48 h.a.i.	32	11
72 h.a.i.	44	0
120 h.a.i.	122	27

6.3.4. Picking and identification of proteins

The initial idea was to pick and identify interesting spots out of DIGE gels. With this minimal labelling 1 – 5 % of the protein is labelled. This low amount of the overall protein has a higher molecular mass and is the only amount that is detected by the fluorescent reader. If one picks the proteins based on the DIGE-coordinates in the gel, the mass of the protein (unlabelled) is moved further in the SDS-PAGE. This effect is more pronounced in the lower molecular mass range of the gels (Figure 24). Picking on the basis of the colloidal Coomassie labelled spot was often not possible due to a low protein concentration in the gel and therefore low visual intensity of the Coomassie labelling. Another problem connected with this method is the identification of a low concentrated spot through mass spectrometry. Initial trial experiments showed an identification rate of only 10 % of the picked spots (data not shown).



Picking points on the basis of G-Dye100-labelled proteins pattern in a gel

Resulting picking points on the basis of Coomassie-labelled protein pattern of the same

Figure 24: Different coordinates of unlabelled proteins and G-Dye-labelled proteins. A) G-Dye100-picture, B) the same gel, labelled with colloidal Coomassie; in between two exemplary spots and the resulting difference in coordinates

Because of these drawbacks two preparative gels with a higher concentration of proteins had to be provided for the purposes of the identification. 450 µg sample were assembled with a

mixture of the remaining samples over all time points and harvests, and control and infected samples in equal amounts. Another gel was compiled with 600 µg protein of the remaining stocks. The fact that the individual probes originated from different time points and harvests meant that the whole sample represents average protein content over both time points and treatment. The preparative gels were warped to the DIGE gels so that any spots collected from the preparative gel could be connected to the values of the DIGE gel analysis. However, some spots from the preparative gel could not be matched to the DIGE analysis due to weak or lacking intensity on the DIGE gels. 179 candidate protein spots based on size, regulation and reliability of the warping were collected out of the preparative gel with an automatic spot picker (see Figure 25) and used for the mass spectrometry-based identification.

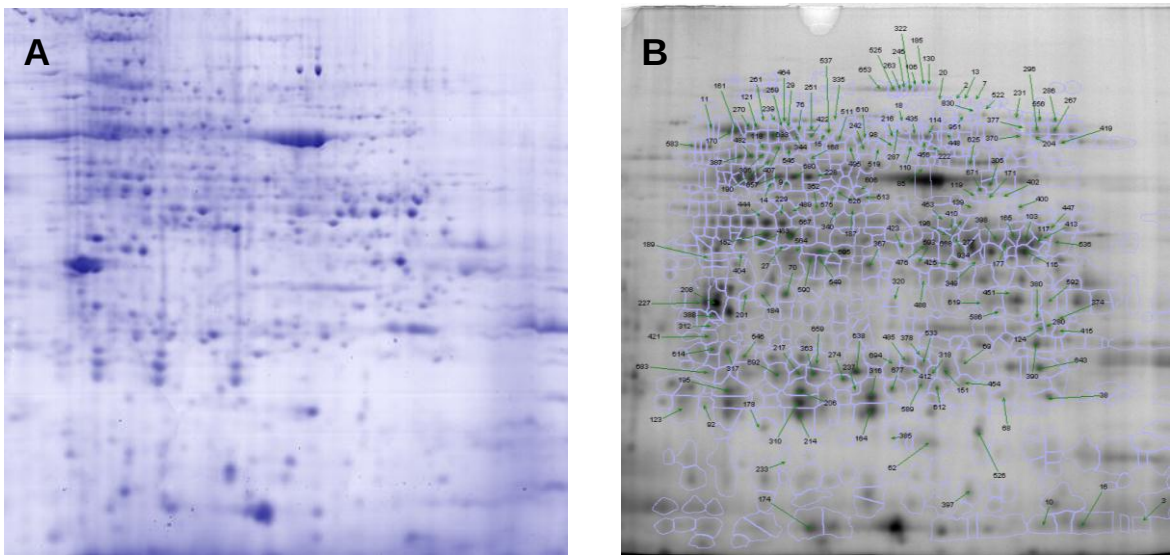


Figure 25: A: preparative gel; B: Identified protein spots on the corresponding DIGE reference gel

After tryptic digestion, the proteins were analysed by MALDI-TOF-MS, on the basis of peptide mass fingerprinting, and LC-ESI-Q-TOF MS/MS. Examples for the above mentioned methods are shown in Figure 26 and Figure 27. For the identification of the proteins a homology-based database search of amino acid sequences was used. All spot pictures of the identified protein spots are shown in Table 25 in the appendix.

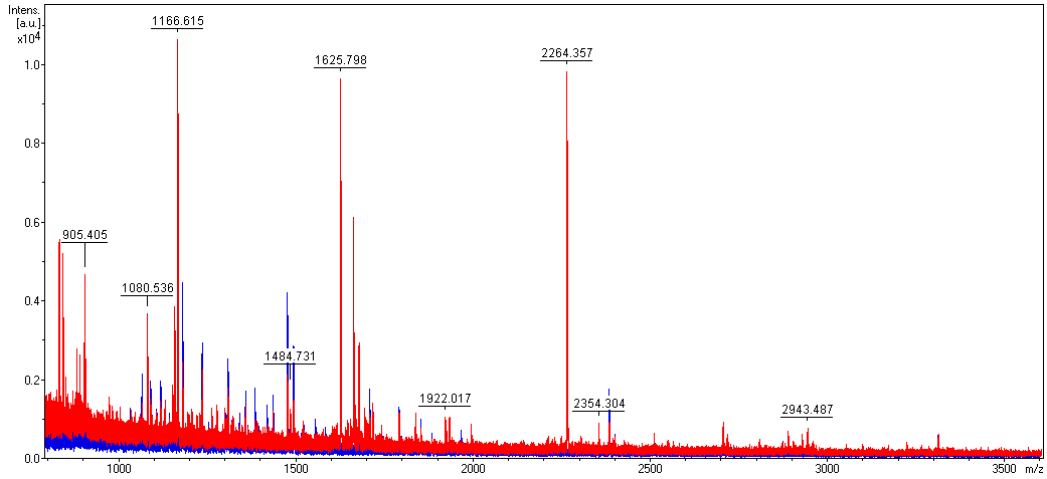


Figure 26: Example of a MALDI-TOF-MS peptide mass spectrum. On the x-axis the m / z-ratio of the measured peptides, and on the y-axis their measured intensities are shown. The numbers show some of the peptide masses used for the identification in the HarvEST:Barley database.

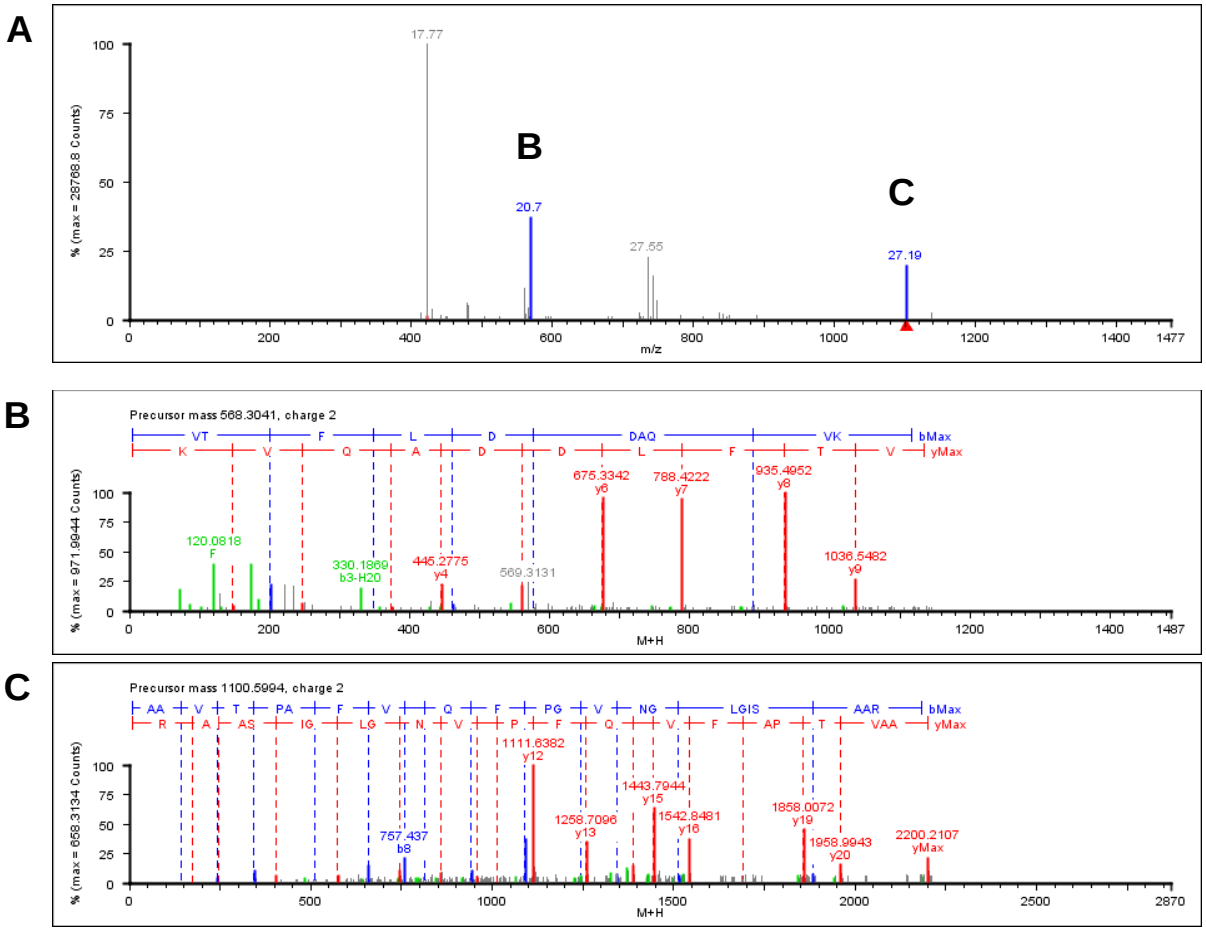


Figure 27: Example of a peptide mass spectrum and the peptide sequences acquired by LC-ESI-Q-TOF MS/MS. In diagram A the measured peptide masses analog to Figure 26 are shown. The corresponding amino acid sequence of the peptides B and C are shown in the corresponding diagrams B and C.

162 protein spots were successfully identified as plant proteins and led to 128 HarvEST:Barley-IDs, 102 proteins were identified uniquely and the rest could be assigned to

a total of 26 proteins. Additionally one protein led to two identifiers, one plant and one fungal, presumably because the fungal protein was adjacent to the plant one in the gel. Therefore this spot had to be disregarded in further analysis. The list of the identified proteins is attached in the appendix (Table 23 and Table 24).

The most abundant proteins were isoforms of HvGER2a (35_14824 and 35_48123) identified in 6 spots, covering a range of 20-25 kDa and from pH 4.5-6.5 based on their location on the 2-D map (Figure 28).

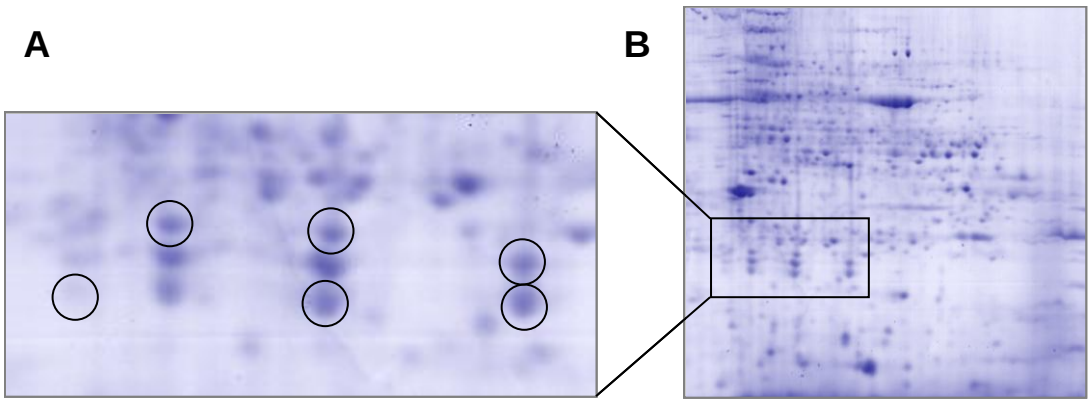


Figure 28: Six spots identified as HvGER2a. Picture A shows the zoomed picture and the position of the six spots. Picture B shows the whole preparative gel with the relative postion of picture A.

Most proteins that were found at different locations on the gel represent pI-shifts or a combination of mass and pI-shifts.

86 identified protein spots were statistically relevant with a FDR of $q<0.05$, 76 were not significant with a FDR of $q>0.05$. Some proteins were identified in more than one spot, and these spots were not uniformly significant or not significant. Protein spots of 65 HarvEST:Barley-IDs were found to be only significant, whereas 49 were only not significant. Of 14 IDs at least one spot was significant and at least one spot was not significant. The numbers are shown in Figure 29.

6.3

6.3.3

6.3.4

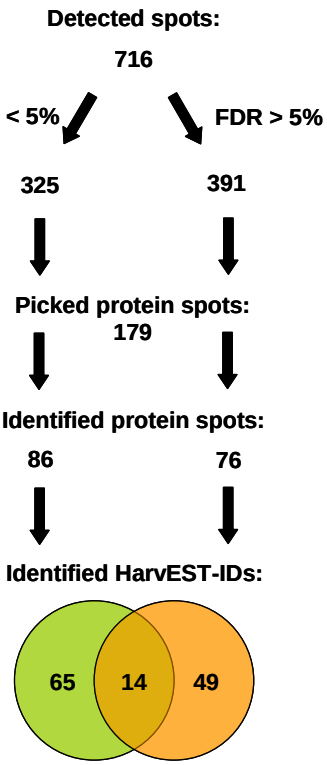


Figure 29: Process of detection and identification of protein spots: The numbers on the left indicate the chapters explaining the stages. The picture shows the numbers of protein spots and protein IDs, respectively, at the different stages. Green circle: IDs found to be only significant, orange circle: IDs found to be not significant; overlapping part: IDs, for which significant and not significant spots are found.

The K-means clustering of the regulation ratios of all 162 identified protein spots revealed five clusters (see Figure 30):

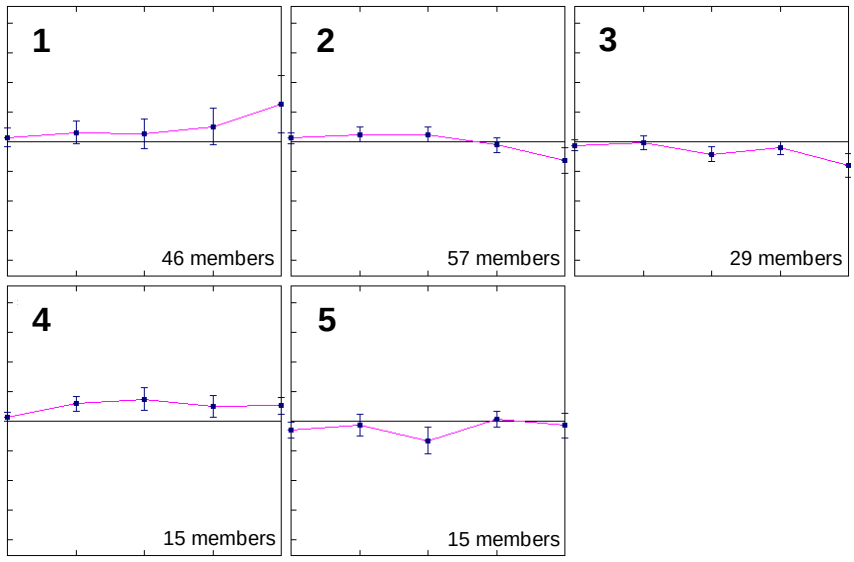


Figure 30: K-means clustering of log_2-transformed regulation values of the five time points of all identified protein spots: Cluster1: Strong increasing upregulation; Cluster2: low regulation values; Cluster3: Downregulation, the most at 120 h.a.i.; Cluster4: Upregulation, the most at 48 h.a.i.; Cluster5: Downregulation, the most at 48 h.a.i. In each cluster are the values from left to right:: 12, 24, 48, 72 and 120 h.a.i.

6.3.5. Functional classification of identified proteins

All identified HarvEST:Barley-IDs of the proteins were matched to MapMan-contigs and the protein spots were grouped into their functional classes.

In Figure 31 the distribution of members in the classified SuperBINs are shown. It can be seen that the proportions of all proteins and regulated ones in certain SuperBINs mostly did not change. However proteins involved in the “TCA” were higher represented (15 % to 10 %) and proteins categorized in “glycolysis” were lower represented (5 % to 11 %) in the regulated group. The highest proportions of proteins in the regulated SuperBINs were grouped into defence (“stress” (17 %) and “miscellaneous” (7 %)), as well as involved in energy production ("tricarboxylic acid (TCA) cycle” (15 %) and “glycolysis” (5 %)).

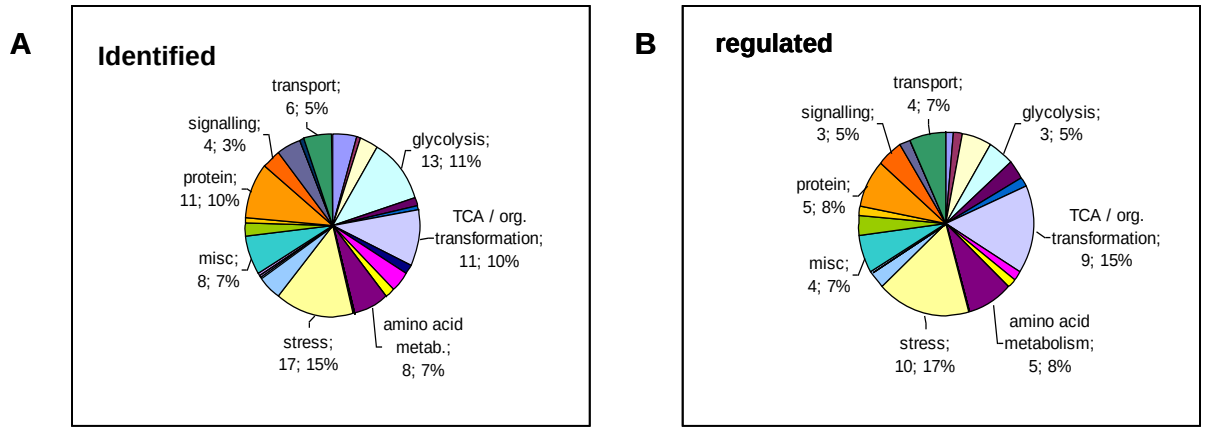


Figure 31: Distribution of proteins into the SuperBINs. A: distribution for all identified proteins, B: distribution of significantly regulated proteins

Table 8 shows the numbers of protein spots in the different categories according to the SuperBINs for all identified spots and for the statistically regulated ($q<0.05$) spots. The distribution into classes with or without biological classification or the ones that could not be linked did not significantly differ between all identified protein spots and the statistically significant regulated ones.

Table 8: Classification of all and regulated proteins according to the MapMan binning. Absolute numbers and percentage are shown.

	All identified spots	Statistically regulated
Classified	116 (70 %)	57 (68 %)
Not classified	19 (12 %)	11(12 %)
not linked	32 (18 %)	19 (20 %)

6.3.6. Clustering of regulated protein spots

In order to see which proteins show a homogenous regulation upon infection over the time period, K-means clustering was performed, identifying the following four classes (Figure 32A):

1) strong increasing upregulation over all time points

2) early downregulation

3) late downregulation

4) increasing upregulation over all time points

Cluster 1 has six members, mostly stress-related and shows a strong similarity in regulation. The majority of the 22 spots of the cluster 2 are classified as related to stress, amino acid metabolism, glycolysis and protein. Cluster 3 has 10 members of stress-related, minor CHO metabolism and signalling pathway. In the largest Cluster 4 with 48 members, many different biological effects are involved, such as TCA, stress-related, amino acid metabolism, transport and others. The clusters and their regulation levels can also be seen in the hierarchical cluster (Figure 32B). In this dendrogram also it can also be seen that the almost all profiles showed a trend in the same direction, rather than transient translation profiles.

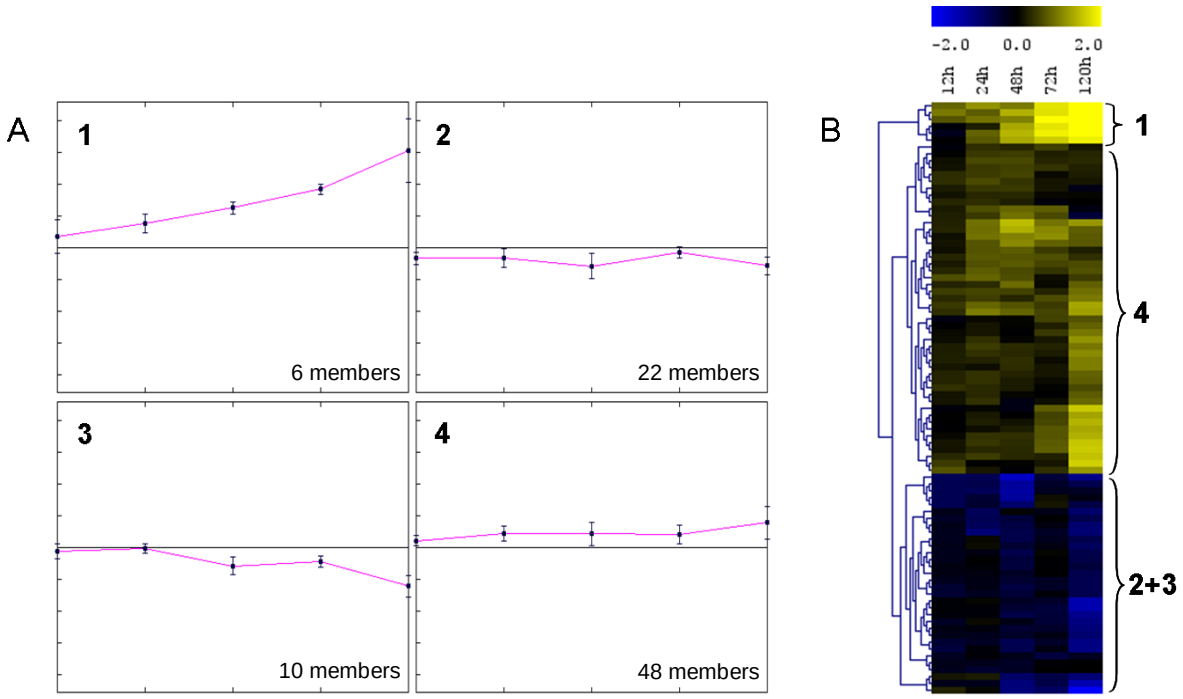


Figure 32: Clustering of identified regulated protein spots. A: K-means clustering of log_2-transformed regulation values of the five time points in four clusters. From left to right: 12, 24, 48, 72 and 120 h.a.i.; B) hierarchical clustering of log_2-transformed regulation ratios. colour coding: blue: ratios down to -2 (downregulation); yellow: ratios up to 2 (upregulation). Numbers added on the right correspond to the clusters in A.

The ratios of the proteins with the highest upregulation levels rise steadily within the course of the infection. In contrast, the most extreme regulation levels of the downregulated proteins are not only lower in the amplitudes, they also show a regulation peak at 48 h.a.i., that drops at 72 h.a.i., followed by a rise at 120 h.a.i.

6.4. Comparative matching of transcriptome and proteome analyses

The identification of the proteins was carried out by sequence comparison (BLASTP) to ESTs from the HarvEST:Barley database. The next step was to look for EST-clones (spotted features) present on the cDNA macroarray, which correspond to the BLAST-identified unigenes from the HarvEST:Barley database. If more than one spotted feature linked to a HarvEST:Barley-ID, the one with the best q-value in the transcriptome analysis was used. Out of 163 protein spots (129 unique IDs), 126 spots (91 unique IDs) could be linked to clones present on the array. 36 protein spots did not match to an EST-clone, 28 of them were not present on the array, whereas for 8 spots at least one clone was spotted on the array, but transcripts were not present. The successful transcript-protein links were categorized in four sections according to their false discovery rate of regulation, as reflected by q-values.

Section I) FDR of $q<0.05$ in both transcript and protein

Section II) $q<0.05$ only in transcript

Section III) $q<0.05$ only in protein

Section IV) $q<0.05$ neither in transcript nor in protein

The complete list of the successful transcript-protein links is attached (see Table 27 in the appendix) Of these, the first three sections are the most interesting ones, the section IV consists of 36 links with no regulation in one of the analyses. The numbers in the sections are shown in Table 9.

Table 9: Numbers of transcript-protein links in the different sections of the epidermal transcriptome and/or proteome

Section I	Regulated in both –omes	34
Section II	Regulated in transcriptome	27
Section III	Regulated in proteome	29
Section IV	Not regulated	36
No section	Not linked	36

Ninety links of the sections I-III were classified according to their biological functions. Figure 33 shows the distribution across functional categories. One fourth of all linked protein-transcript pairs are categorized as stress-related ("stress" (16 %) and "misc" (9 %)), a high proportion can also be seen in energy-source-related categories ("TCA" (11 %), glycolysis (4 %), photosynthesis "PS" (7 %)), "amino acid metabolism" (9 %) and "protein" (8 %).

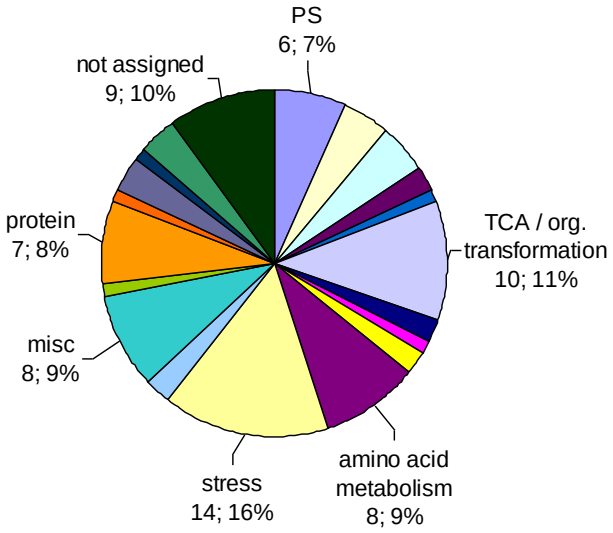


Figure 33: Distribution of 90 linked protein-transcript pairs with a significant regulation at transcript and/or protein level according to functional categories with a proportion of at least 5 % are shown. Colour coding acc. to Figure 9.

The next step was to investigate the distribution of links to a functional SuperBIN in each of the sections separately. In the following pie charts in Figure 34 the distribution of SuperBINs that have more than three members are shown for each of the four sections.

Thirty-four transcript-protein matches met the stringent criteria of $q<0.05$ in transcriptome and proteome (section 1). Figure 34A shows the proportional distribution in the functional categories. The SuperBINs "stress" and miscellaneous" represent 31 % of all links, followed by a large proportion of "amino acid metabolism" (11 %) and "minor CHO" (9 %).

In the 27 matches that are only regulated at transcriptome level, photosynthetic genes are highly abundant (19 %), together with genes involved in “stress” (15 %) and “amino acid metabolism” (11 %) (see Figure 34B).

In the 29 matches that are only regulated at the protein level, a relatively high proportion of the SuperBINs “TCA” (24 %), “protein” (14 %) and “stress” (14 %) were found (see Figure 34C). Compared to the two classes before, the distribution to stress-related IDs is not very high.

In the 36 matches with regulation neither at transcript nor at protein level, quite a high proportion belongs to the SuperBIN “glycolysis” (28 %), followed by “protein” (14 %), “redox” (11 %) and “mitochondrial electron transport” (8 %) (see Figure 34D).

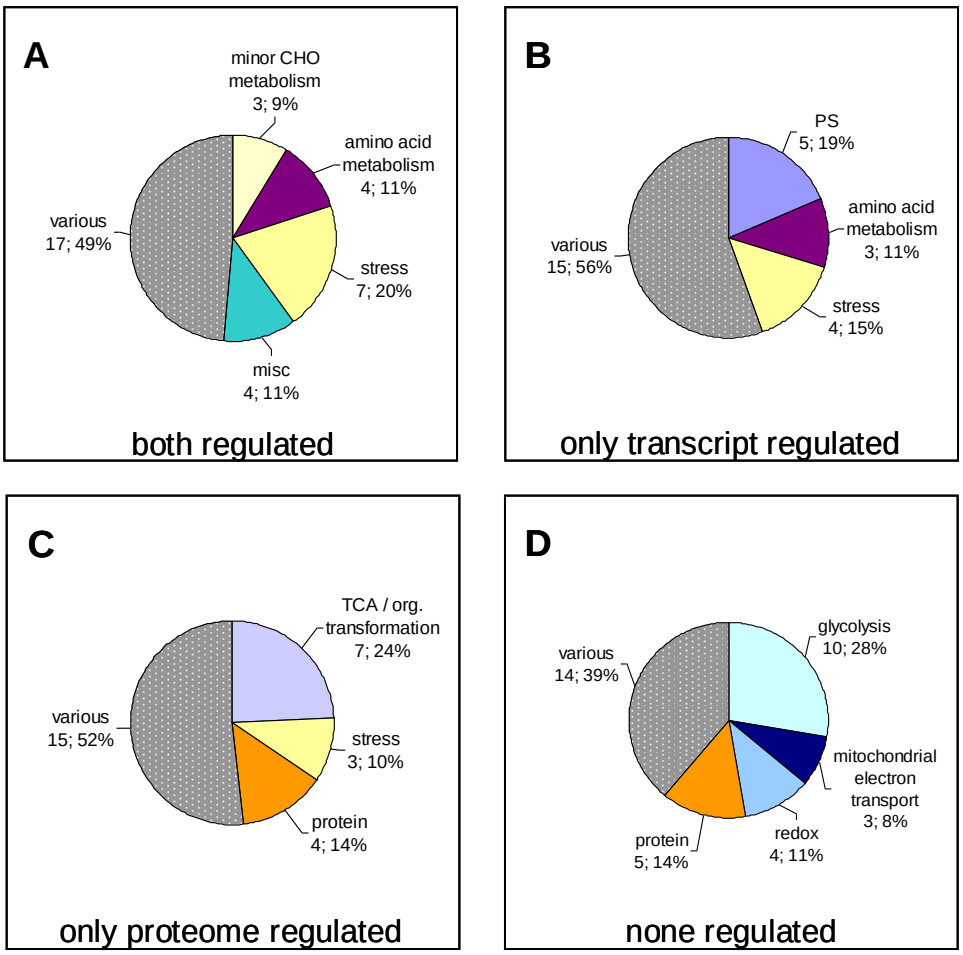


Figure 34: Distribution of the links over functional categories ordered according to their significance in statistics. Sections of links with regulations on 1) both transcript and protein level; 2) only on the transcript level; 3) only on the protein level; 4) in none of the levels are shown. Only SuperBINs with at least 3 matches are shown, the others are grouped into “various”. The first number under the BIN name signifies the number of links involved and their contribution to the whole as a percentage.

6.4.1. Detailed analysis of sections

6.4.1.1. Section I: FDR of q<0.05 both at transcript and at protein level

Comparison of the regulation over time shows mostly a positive correlation between transcriptome and proteome (Figure 35) with some exceptions. Besides this, in section I are the events with the greatest amplitude of down- or upregulation. Based on the K-means clustering, Figure 35A1 shows twelve links that are downregulated both in transcriptome and proteome. Five links are related to stress, four of which are related to abiotic stress. In Figure 35A2, six transcripts are initially strongly upregulated in transcriptome, compared with a linear increase of upregulation in proteome, and they all are stress-related. In the cluster shown in Figure 35A3 there is no conspicuous allocation to particular biological functions as well as in that of Figure 35A4. The five links in Figure 35A3 show a downregulation in transcriptome, but an upregulation in proteome. The eleven links in Figure 35A4 show a maximum upregulation at 120 h.a.i. in the transcriptome, whereas the upregulation in the proteome remains steady and lower.

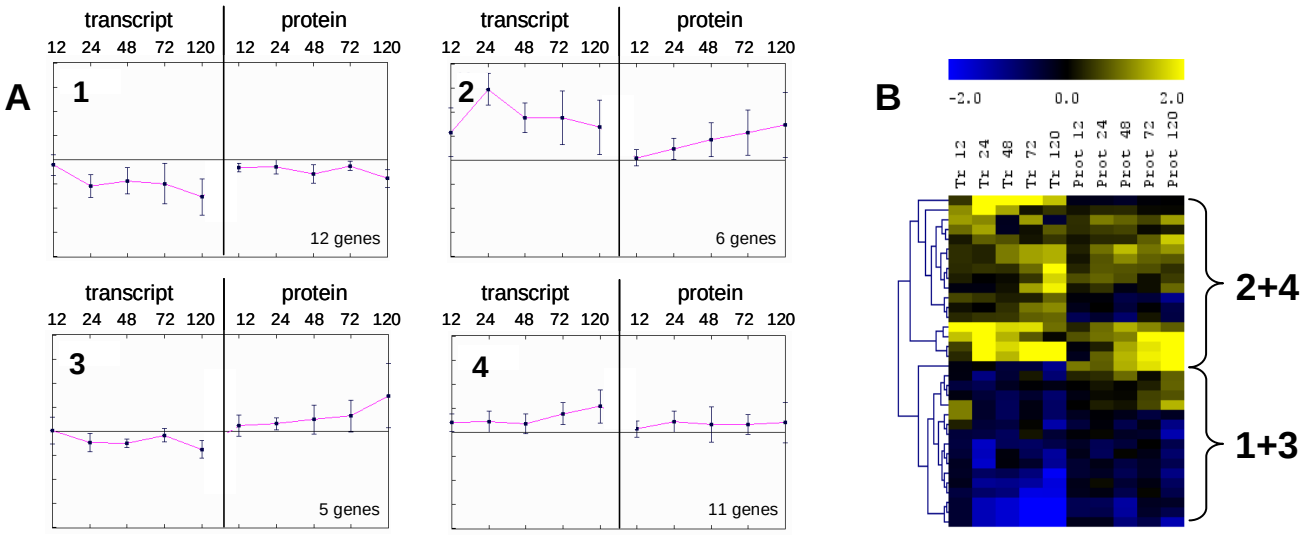


Figure 35: Clustering of links showing a statistical relevant regulation of at least q<0.05 at transcript and protein level. A) K-means clustering of the links into 4 clusters. The ratios of regulation after log_2-transformation are shown for the transcript and the protein levels at the five time points (12, 24, 48, 72 and 120 h.a.i.). Upregulation or downregulation is shown by positive and negative values on the y-axis, respectively. B) Hierarchical clustering of signal ratios (*Bgh*/control) of transcripts (left) and proteins (right). The scale of the colour coding ranges from -2.0 (blue) to +2.0 (yellow). The numbers on the right correspond to K-means clusters (A).

6.4.1.2. Section II: FDR of q<0.05 only at transcript level

In general the 27 links that are only regulated at transcriptome level are downregulated. As an exception there are two links that are upregulated in transcriptome, a **peroxidase 10** and a **Glyceraldehyde-3-phosphate dehydrogenase, cytosolic**. This exceptional behaviour can be seen in K-means and hierarchical clustering (Figure 36A2, B2). The other three clusters of the K-means analysis (1, 3, 4) cannot be resolved so clearly by hierarchical clustering.

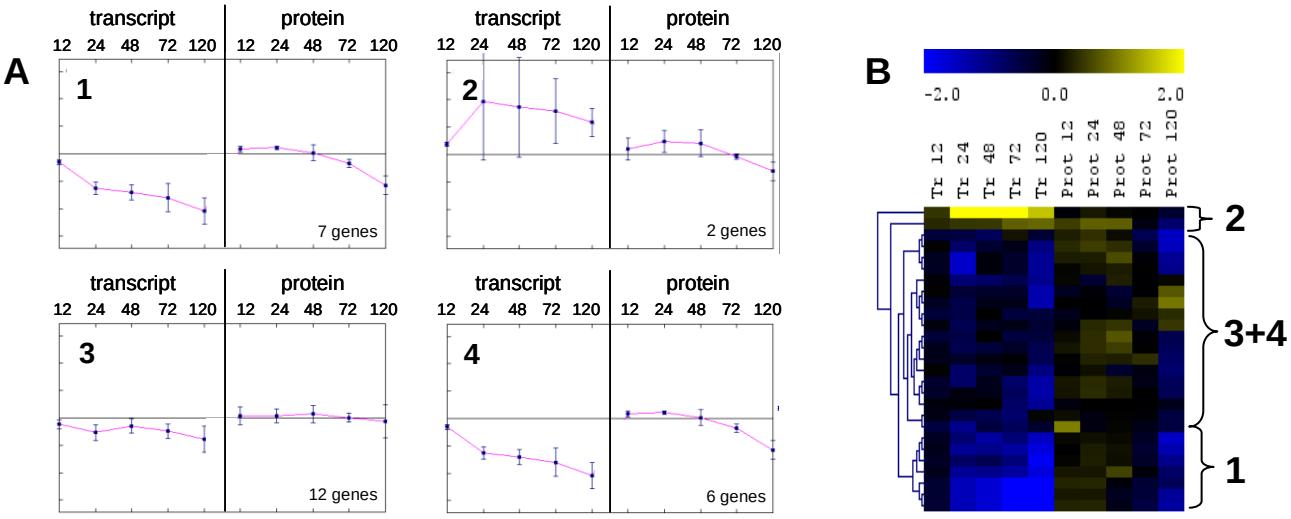


Figure 36: Clustering of links with a statistical relevant regulation of at least q<0.05 at transcript level. A) K-means clustering into 4 clusters is shown. y-axis: ratios of regulation; x-axis, left side: transcript levels at five time points; x-axis, right side: correlating protein levels at five time points. Positive y-axis: upregulation; negative y-axis: downregulation B) Hierarchical clustering of all ratios of transcripts (left) and proteins (right). Colour coding: scale from - 2.0 (blue) to + 2.0 (yellow). Numbers correspond to K-means clusters.

6.4.1.3. Section III: FDR of q<0.05 only at protein level

Levels of changes of these 29 links are not very high. Both up- and downregulation occurs. Figure 37A shows a high standard deviation of values in each of the clusters. Cluster 1 in Figure 37A shows a downregulation and clusters 2, 3 and 4 show a upregulation of the proteins. Also the hierarchical clustering (Figure 37B) reveals a high variability of regulation trends among and between linked pairs.

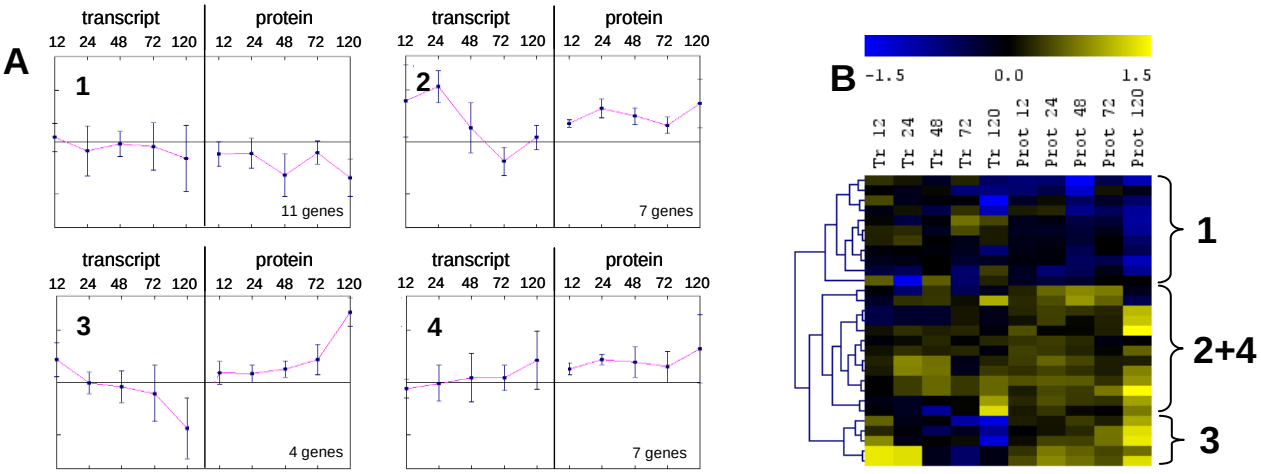


Figure 37: Clustering of links showing a statistical relevant regulation of q<0.05 at protein level. In A) K-means clustering into 4 clusters is shown. y-axis: ratios of regulation; x-axis, left side: transcript levels at five time points; x-axis, right side: correlating protein levels at five time points. Positive y-axis: upregulation; negative y-axis: downregulation B) Hierarchical clustering of all ratios of transcripts (left) and proteins (right). Colour coding: scale from -1.5 (blue) to +1.5 (yellow). Numbers correspond to K-means clusters.

6.4.1.4. Section IV: FDR of q<0.05 neither at protein nor at transcript level

36 links were identified that show an FDR higher than 5 % in both –omes (see Figure 38). This means they are not regulated in a statistically significant manner and members of this section are not relevant in the context of the interaction, but are shown to complete the results. Levels of regulation are quite low, thus only a few links show a regulation of more than 2-fold at any one time point. Hierarchical clustering does also not show a distinctive pattern.

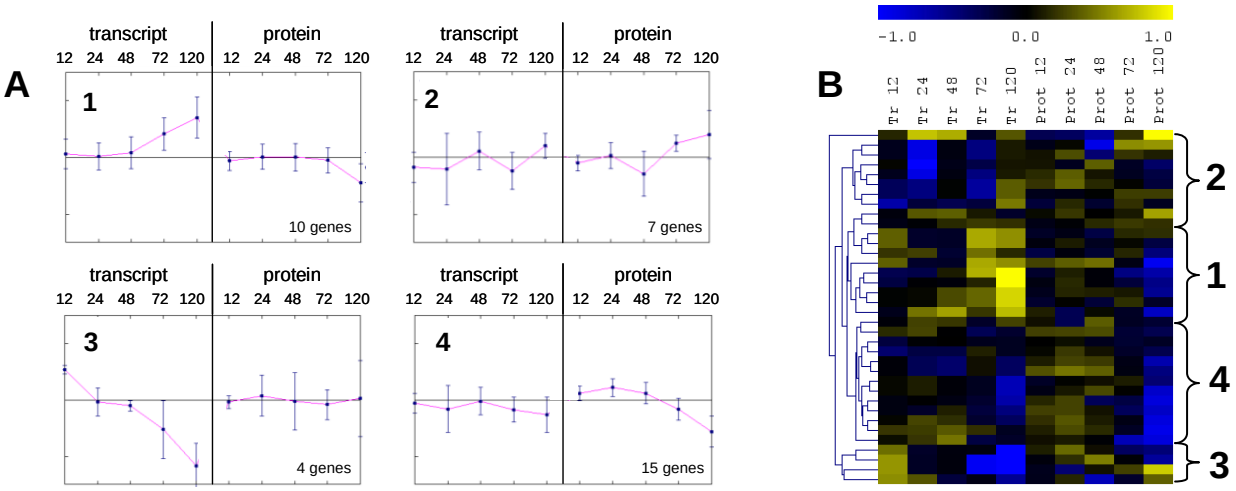


Figure 38: Hierarchical Clustering of links showing no statistical relevant regulation of q<0.05 at transcript or at protein level. ratios of transcripts (left) and proteins (right) at five time points. In A) K-means clustering into 4 clusters is shown. y-axis: ratios of regulation; x-axis, left side: transcript levels at five time points; x-axis, right side: correlating protein levels at five time points. Positive y-axis: upregulation; negative y-axis: downregulation B) Hierarchical clustering of all ratios of transcripts (left) and proteins (right). Colour coding: scale from -1.0 (blue) to +1.0 (yellow). Numbers correspond to K-means clusters.

7. Discussion

The basis of this PhD project was the investigation of transcriptome and proteome changes in the epidermis of the susceptible barley cultivar “Ingrid” infected by the barley powdery mildew pathogen *Bgh* and the integration of both datasets. For this purpose a time-course study from 12 to 120 h.a.i. was performed to cover the whole infection process of *Bgh*.

The study can be grouped in three work packages:

1) transcriptome analysis using the PGRC2-13k-cDNA-macroarray

2) proteome analysis on 2-D DIGE gels

3) integration of transcriptome and proteome data.

Barley seedlings were also inoculated in parallel with *R. secalis* in the same growth chamber, and epidermal peels were collected together with my material at the same time points. The group of Dr. Knogge at the Leibniz-Institute for Plant Biochemistry (IPB), Halle is still investigating this material and their upcoming results will be compared with the results presented here.

7.1. The interaction of *Bgh* with barley is restricted to the epidermis

The barley leaf epidermis is a highly differentiated, non-photoautotrophic tissue. According to theoretical considerations, only 5 % of the mRNA and proteins of the whole leaf derive from the epidermis, the remainder coming from the more densely packed mesophyll cells. Due to the fact, that the direct interaction of barley and Bgh is restricted to the leaf epidermis in all developmental stages, investigations in the epidermis bear the promise of enhanced sensitivity due to its reduced complexity, which however requires removal of remaining leaf tissue by peeling.

However due to the method used for epidermis peeling, it was inevitable that some mesophyll cells were attached to the epidermis. Stomatal guard cells of the epidermis contain chlorophyll (Zierold, 2005) and also epidermal non-green leucoplasts may emit red autofluorescence usually attributed to chlorophyll in chloroplasts (Suh et al., 2005) and may be therefore wrongly counted as chlorophyll-containing cells. However, the small amounts of

chlorophyll detected in the epidermis peels (3 – 8 %, on average 4 % chlorophyll content compared to that in total leaf), indicated that contamination by non-epidermal tissues was small and probably negligible.

Initially the intention was to use only epidermal samples, but at 120 h.a.i. the seedlings were heavily infected, apparently resulting in epidermal cell-wall maceration and subsequently low amounts of peeled epidermal sample. It was not clear whether enough epidermal material for both transcript and proteome analysis could be sampled. To obtain results also for the late time point, whole leaves were sampled at 120 h.a.i. additionally to the epidermal tissue. Although there was finally enough epidermal material for analysis at 120 h.a.i., the additional whole-leaf samples made it possible to investigate whether transcripts were preferentially accumulating in mesophyll or in epidermis tissue. A problem to bear in mind is that even in susceptible plants a certain percentage of epidermal cells prevent infection by forming papilla as described in the introduction (chapter 4.4.2). This mixed cellular response makes it difficult to determine which of the events seen at tissue level are related to cellular resistance or susceptibility. Whether the defence is effective or not may be determined by how particular transcripts of the plant are regulated, and (Gjetting et al., 2007) demonstrated that transcript regulation differs quantitatively in susceptible and resistant epidermal cells of a susceptible barley cultivar. Therefore regulated transcripts in epidermal extracts, when compared to regulated transcripts in single cells, exhibited a high degree of correspondence, although, as in the recent work, a transcriptional change cannot a priori be attributed to resistance or susceptibility at cellular level.

In order to maximize the comparability of the results of transcriptome and proteome analysis, individual samples were split into two parts for the two analyses. Therefore they are exactly identical in content, which is the best possible basis for valid comparisons.

7.2. Large scale transcriptome analysis

To investigate the mRNA levels of genes in the epidermis, we used the PGRC2-13k-cDNA-macroarray that contains 13 050 spotted features. According to ‘The Institute of Genomics Research’ database (TIGR; http://www.tigr.org/tdb/tgi/plant.shtml), the barley genome is estimated to contain approximately 32 000 genes based on assemblies of about 450 000 barley ESTs, which are probably not all present in the epidermis. Thus the 13 050 probe sets on the PGRC2-13k-cDNA-macroarray do not cover the whole transcriptome. The reasons for using this macroarray instead of a commercial microarray (such as the Barley1 from Affimetrix Co.) were the following:

1) In-house produced Macroarrays are a cost-efficient resource, especially as the large scale transcriptome analysis with the PGRC2-13k-cDNA-macroarray is a well-established procedure in our working group.

2) 2 450 of the spotted 13 050 clones (representing 19 %) are derived from epidermal tissue, which makes the macroarray well suited for the investigation of mRNA regulation in epidermal tissue.

3) The results of the present study can be easily compared with further work done using related or identical macroarrays at the IPK Gatersleben (Sreenivasulu et al., 2002, Pleines, 2008, Schweizer, 2008) and by the collaborating partner W. Knogge at the IPB, Halle.

Cross-hybridization of *Bgh* homologues to barley genes is highly unlikely because of evolutionary distance, whereas cross-hybridization of closely paralogous barley genes is possible and could not be prevented. It should be noted that the 13k-PGRC2-cDNA-macroarray does contain transcripts of *Bgh* because it is enriched in cDNAs of *Bgh*-attacked barley epidermis.

Overall the macroarray experiments produced useful data to analyse the interaction of barley epidermis with *Bgh*, because

1) Using the selection criteria defined in chapter 5.2.10 a total of 1 478 regulated plant transcripts were found.

2) Within this selection many known pathogen-induced genes could be found (e.g. chitinase, protease inhibitors, PR1-genes, GLPs, GERs)

3) Known epidermis and mesophyll-specifically accumulated genes could be assigned with the expected E/M value. For example, almost all the present and all the regulated transcripts that were assigned to the SuperBIN “Photosynthesis” were specifically accumulated in the mesophyll.

4) cDNA-fragments of the same unigenes derived from amplifications of different EST-clones showed similar hybridization results.

5) *Bgh*-derived transcripts were associated with high E/M values.

7.2.1. Identification of barley candidate genes involved in the interaction with *Bgh*

In order to estimate the influence of the developmental stages and the reactions of the plant to the infection in the three biological replicates, all present transcripts (whether regulated or not) from the biological samples were clustered by means of a Principle Component Analysis (chapter 6.2.3, Figure 7). In general it can be seen that the control and infected samples of the same time point cluster on the PC1 axis. This is also due to the fact that control and infected samples of each time point were normalized for that time point. The PCA show that increasing leaf age had the largest influence, explaining 50 % of the variation (PC1), whereas the influence of the treatment accounted for only 14 % of the changes (PC2). One could potentially reduce the influence of the developmental changes in relation to the changes driven by the infection, if more adult plants were used for the infection. Methodically; however, the peeling of epidermis samples in later developmental stages proved to be very difficult.

The 24 h.a.i. samples clustered at the greatest distance from the rest of the samples on the time axis (PC1), but also differed the most on the treatment axis (PC2). This might be related to the fact that at this time point haustoria are formed and thus the fungus causes a major impact on the plant's transcriptome. This proposition is in agreement with further studies (Zierold, 2005). The 120 h.a.i. samples also differed markedly on the treatment axis which might correlate with the high number of infected epidermal cells.

7.2.2. Functional classification of the genes

As Uetz and Finley wrote, "a system-level understanding of any biological process requires a map of the relationships among the various molecules involved. […] These maps can be used to study how genes work together to form molecular machines and regulatory pathways. They also provide a framework for constructing predictive models of how information and energy flows through biological networks" (Uetz and Finley, 2005). To be able to integrate candidate regulated genes (plant genes, FDR<5 %, >2-fold change in transcript levels) into functional categories, the binning system established for the Affimetrix Barley1 chip was adapted to the EST clones spotted on the PGRC2-13k-cDNA-macroarray. Among the regulated 1 478 transcripts were many which show sequence homology to genes in the SuperBIN "not assigned" and can therefore not be discussed further here. This finding is in line with the effect previously described by (Sreenivasulu et al., 2008) when using the Affimetrix array in barley-gene expression experiments.

Also 10 % of the ESTs of the PGRC2-13k-cDNA-macroarray could not be annotated to the MapMan binning system as they are not represented on the Affimetrix array. These genes have to wait for further characterizations in the future.

To learn about the importance of functional groups of genes during the interaction, a Chi-square testing was carried out. In this testing the fraction of regulated transcripts in each SuperBIN containing at least three members is related to the fraction of present plant transcripts in the same SuperBIN. This was done separately for the upregulated and for the downregulated transcripts and shows whether in a specific SuperBIN there is an over- or underrepresentation of up- or downregulated transcripts. However, this method does not take into account the quantitative change in transcript levels.

If we have a look at the 1 478 regulated transcripts in each of the time points studied, no plant gene was repressed at 12 h.a.i., which represents the time when *Bgh* forms an appressorium and attempts penetration. This observation also correlates with the findings in (Zierold, 2005). The upregulated functional categories at that time point were overrepresented in the SuperBINs “stress”, as well as “miscellaneous” and “secondary metabolism”. Upregulation of genes of “secondary metabolisms” was involved in phenylpropanoid metabolism and lignin biosynthesis such as PAL or cinnamate 4-hydroxylase. In the SuperBIN “stress” and “miscellaneous”, genes involved in biotic and abiotic stresses such as “Mlo3”, “chitinase”, “HV1LRR1”, “disease resistance response protein-like”, “BAX inhibitor 1”, “oxalate oxidase-like protein or germin-like protein”, “GLP-4”, “glucanases”, “oxidases”, “glutathione S-transferases”, “cytochrome P450” genes, “peroxidases”, “phosphatases” and “protease inhibitors” could all be found. Additionally stress-related genes in the SuperBIN “not assigned” were found, such as “HSP70”, “caffeic acid O-methyltransferase”, “pathogenesis-related protein 10”, “pathogen-induced protein WIR1”, “putative wall-associated”, “polyubiquitin”, “multidrug resistance associated protein MRP2”, “PDR-like ABC transporter” and “leucine rich repeat containing protein kinase”. Interesting to mention here is that the highest amplitude of transcript regulation shows up for “pathogenesis-related protein”, “HSP 70”, “cytochrome P450 monooxygenase” and “oxalate oxidase-like protein or germin-like protein” and “putative 4-coumarate-CoA ligase”. These well-known markers of PTI were also verified by proteome analysis (see chapter 6.3) and seem to be the key primary tools of the plant to counteract fungal infection. This leads to the conclusion that the barley plant tries to prevent the pathogen from entering the plant epidermal cells via different systems such as reinforcement of the cell wall by lignification as well as papilla formation. At the same early time point upregulated genes of the SuperBIN “protein” were underrepresented, which suggests that at this time point protein synthesis and

turnover is less important for the primary response. Alternatively, members of the SuperBIN "protein" might be regulated predominantly at post-transcriptional level.

The total number of regulation events increased at 24 h.a.i., when a fully functional haustorium is formed. The trend seen at 12 h.a.i. considerably changed at 24 h.a.i. with a high number of upregulated transcripts but even more repressed transcripts. This is in correlation with the findings in Zierold's dissertation (Zierold, 2005). As seen in Table 4, many transcripts were downregulated, most of them involved in "photosynthesis", "cofactors and tetrapyrrole synthesis". These cofactor-genes are involved in thiamine synthesis, which is required to form adenosine triphosphate (ATP), used by the plant as energy equivalent. As Terry and Smith explained, "regulation of the tetrapyrrole pathway in plants is particularly crucial, since it is required for efficient photosynthesis, protection from the harmful phototoxicity of the pathway intermediates, [synthesis of Häm in POX or CytP450] and because of the proposed role played by some of the intermediates in signalling" (Terry and Smith, 2009). However, because epidermis contains almost no chlorophyll, the genes mentioned above can also be shadows of the changes in the mesophyll, due to some inevitable though minor contamination by mesophyll cells, or this might reflect the changes in the chloroplast-containing stomata cells. The downregulated transcripts in the SuperBIN "amino acid metabolism" were also overrepresented. Similar to 12 h.a.i., upregulated transcripts were overrepresented in the SuperBINs "secondary metabolism", "stress" and "miscellaneous" at 24 h.a.i. The fact that downregulated transcripts were underrepresented in the SuperBIN "miscellaneous" suggests that stress-related mechanisms are highly upregulated. Emerging effector target categories at that time point were genes of "N-metabolism", such as "glutamate ammonia ligase" and "glutamate dehydrogenase". As described in the introduction (see chapter 4.4.1) a good nitrogen fertilization of the plants favours *Bgh* infection. Besides that, it is likely that the plant uses the higher turnover in nitrogen for the production of toxic nitrogenic compounds (e.g. alkaloids, cyanogenic glycosides) or changes in energy metabolism, in which these genes are also involved. At the energy level upregulated transcripts of the SuperBIN "oxidative pyrophosphate" such as phosphogluconate dehydrogenase and non-reductive pyrophosphatases were overrepresented. These findings together suggest that the plant instead of using its energy for developing processes consumes it in defence and feeding of the fungus.

At 48 h.a.i., a time when elongating secondary hyphae grow on the surface of the leaf, fewer transcripts were regulated. In particular the proportion of downregulated ones was reduced. Nevertheless upregulated transcripts involved in developmental processes and secondary metabolism were overrepresented. Upregulated transcripts involved in sucrose degradation such as invertases, hexokinases, glucosidases, amylases (in the SuperBIN "major CHO")

were overrepresented. Additionally downregulated transcripts involved in galactose synthesis (SuperBIN “minor CHO metabolism”) were overrepresented. As described in Fotopoulos (2003), “the pathogen acts as an additional sink, competing with host[’s] sinks” (Fotopoulos et. al., 2003). The “infection [by powdery mildew] results in enhanced Glc [(glucose)] uptake in infected [A.thaliana] tissue, an increase in the expression of the host monosaccharide transporter gene,” and the accumulation and activity of host cell wall invertases (Fotopoulos et al., 2003). The storage forms of glucose may be degraded/not synthesized, because the energy equivalents of the glucose are required, either for the defense reaction of the plant or connected with the uptake of glucose by the fungus (Bago et al., 2003, Swarbrick et al., 2006). Glucose and stress appear independently to regulate the source and sink ratio and defence mechanisms in cultured *Chenopodium rubrum* cells (Ehness and Roitsch, 1997), which makes it difficult to determine what is the cause and what is the effect.

Downregulated transcripts involved in hormone metabolism were overrepresented from 48 h.a.i. onwards. This can mean that the plant’s natural alarm system is downregulated and that the regulation of defence and development and therefore energy flow is out of control. Also hormonal control of the affected plant tissue no longer took place, perhaps due to the wide-ranging changes in the plant’s metabolism and development.

At 72 h.a.i. the first conidia basal cells are formed and the number of regulation events once more increased. It has to be kept in mind that in the course of the fungal infection the amount of affected epidermal cells increases. This means that the ratio (infected to control) of a certain transcript will be higher in later samples, even though the ratio in the individual affected cell may remain constant. For this reason, the detection of even small changes in transcript will become more and more likely. Up- and downregulated transcripts were equally distributed at this time point. As in the previous time points, the catabolism of sugar storage compounds was upregulated and the synthesis of these was downregulated. Interestingly transcripts for “trehalose-6-phosphate phosphatase”, which produces trehalose, were upregulated. In contrast a “trehalose-6-phosphate synthase” which is reducing trehalose levels is downregulated. That is in agreement with the general view, that trehalose is involved in developmental processes of the plant, in stress, signalling and in plant-pathogen interactions (Wang et al., 2005). Upregulated transcripts at the SuperBIN “Gluconeogenesis/glyoxylate cycle” were overrepresented, indicating increased demand of pyruvate for respiration in the TCA-cycle, which corresponds with the findings that the respiration and hexose content of *Bgh*-infected leaves is induced (Swarbrick 2006). Downregulated transcripts of the SuperBIN ”minor CHO” were overrepresented, such as an “extracellular invertase”, a “cell-wall invertase”, a “WSI76 (waterstress-induced)”, a “beta-fructofuranosidase”, “ribulokinase” and “myo-inositol 1-phosphate synthase”. The

upregulated transcripts of “amino acid metabolism” were overrepresented at 72 h.a.i. A study showed that the obligate pathogenic *Bgh* appears to have all the amino acid biosynthetic pathways of non-parasitic living fungi (Giles et al., 2003), which might indicate that the plant itself needs a higher amino acid turn-over at this stage of the infection.

At 120 h.a.i., when the fungal life cycle is completed by massive sporulation, the numbers of regulation events in upregulation and downregulation were further enhanced and reached the highest level of the study, especially the number of downregulated transcripts. Nevertheless at this time point no new regulation pathways seem to be involved. Instead, a linear intensification of the changes observed at 72 h.a.i. appeared to be occurring.

7.2.3. Pathogen-regulated genes were preferentially expressed in the epidermis

This part of the study evaluated whether the transcripts of a certain biological function (SuperBIN) were preferentially present in the mesophyll, in the epidermis or uniformly distributed. Due to the restriction of direct fungal contact to the epidermis, crucial pathogen-induced changes should be occurring preferably in this tissue. To address this question, the ratio of transcript signals in peeled epidermis and in the remaining leaf of non-infected seedlings at 120 h.a.i. was calculated. This allowed one to assess whether the transcripts that were regulated in the epidermis showed preferential accumulation in the epidermis or in the mesophyll. A statistical analysis of over- or underrepresentation of regulated transcripts belonging to a certain SuperBIN in either epidermis or mesophyll was carried out by a Chi-square testing.

In this testing the fraction of regulated transcripts in each SuperBIN containing at least three members is related to the fraction of present regulated plant transcripts in the same SuperBIN. This was done separately for the epidermis-enriched and for the mesophyll-enriched transcripts and shows whether in a specific SuperBIN there is an over- or an underrepresentation of epidermis- or mesophyll-enriched regulated transcripts. However, this method does not take into account either the quantitative change or the direction (up- or downregulation) in expression levels.

The transcripts belonging to “amino acid metabolism”, “photosynthesis” and “TCA” were preferentially accumulated in the mesophyll. So it is not unexpected that regulated transcripts of those categories were also overrepresented there. However, this might also be a result of contamination of the epidermal samples with mesophyll cells. The significant overrepresentation of epidermis-enriched, regulated transcripts occurred in the SuperBIN “minor CHO metabolism”, such as trehalose-6-phosphate phosphatase, beta-

fructofuranosidase, aldose reductase and WSI76 protein. This might reflect the altered energy use required by the plant's defence reactions and/or enforced feeding of the fungus. The other group of overrepresented epidermis-enriched regulated transcripts were to be found in the SuperBIN "not assigned". Since some of these transcripts are connected with pathogen defence, there is a need for further studies of these genes. If one lowers the statistical significance level to $p<0.1$, the epidermis-enriched regulated transcripts of the SuperBINs "stress" and "miscellaneous" were overrepresented. Although not statistically significant, this result indicates the specific importance of the epidermal layer for defence reactions and the importance of the transcriptome analysis in this tissue.

7.2.4. Summary of the transcriptome analysis

In general it can be stated that at all time points upregulated transcripts of the stress-related SuperBINs "stress" and "miscellaneous" were overrepresented, as expected. Also, at all time points upregulated "secondary metabolism" transcripts were overrepresented, especially apparent in the sub-BIN "lignin biosynthesis". Downregulated ones in this Super-BIN belonged to "flavonoids", "waxes", "simple phenols" and "phenylpropanoids", such as methyl transferases. It is also evident that the regulation of genes of the SuperBINs "protein" and "RNA" was underrepresented, which does not indicate that these SuperBINs do not play an important role in plant's defence. Rather it is an indication that most of the relevant transcription and protein turn-over mechanisms were regulated post-transcriptionally and/or post-translationally. Genes of degradation of starch, which produce glucose, were upregulated, and those for the synthesis of sucrose were downregulated. This finding goes along with the overrepresentation of upregulated transcripts in the "glyoxylate cycle" and of downregulated transcripts in "photosynthesis" and suggests the shift of the leaves away from photosynthetic carbon assimilation towards stress-related pathways and respiration. The overrepresentation of downregulated genes in the SuperBIN "photosynthesis" could be explained by minor contamination of epidermal peels with mesophyll cells and by chlorophyll-containing epidermal guard cells.

Downregulated transcripts did not occur at 12 h.a.i., whereas their number was higher than the upregulated ones at 24 h.a.i. and 120 h.a.i. I should stress the importance of looking at several time points of the interaction, because there were SuperBINs that show over- or underrepresentation in regulation at some stages only. For example, if one is interested in changes of the hormone metabolism, the late time points are more relevant to examine. Here the hormone metabolism was suppressed, in particular auxin and ethylene signal transduction and response factor genes.

7.3. Proteome analysis

The proteome analysis is a suitable method to study the current metabolic status of a given plant tissue. The proteome has a continuous turn-over, and not all genetically encoded proteins are present at all time points, their levels and activities being strongly dependent on other factors. In order to cover the maximum mass range of proteins, the 2-D PAGE was used alongside gene transcription. The other main advantage of using 2-D PAGE is the considerable amount of proteins that can be analysed at any one time. 2-D PAGE is particularly good for looking at proteins within the mass range of 10 - 200 kDa and pI of 3 - 11. Proteins of a particular pI and mass, can be focused on by using pH isoelectric focusing strips and the right percentage of acrylamide used in the 2^{nd} dimension PAGE gel, respectively. However, 2-D PAGE is a process that has a low throughput of samples and is a time-consuming process (3-4 days per run). It involves many manual steps and requires a high level of laboratory skill to obtain good results. For this study the advantages outweighed the possible drawbacks because of the well-established methodical suitability for investigating the proteome at large scale.

Several methods are available to visualize the protein spots on the gel such as Coomassie, silver or fluorescent staining. In the case of Coomassie or silver staining, proteins are separated by isoelectric focussing and gel electrophoresis, and the proteins in the gels are stained afterwards before scanning. In contrast with this, in the 2-D DIGE technique protein samples are prelabelled with three fluorescent dyes (G-Dye100, G-Dye200 and G-Dye300) prior to isoelectric focussing and gel electrophoresis and are scanned immediately after focussing. Because of the availability of the three fluorescent dyes, it is possible to analyse several samples on the same gel. This prevents artefacts due to experimental gel-to-gel variation that can often be observed when samples are run on different gels separately. This allows for the discovery of minor protein-expression changes between comparative diagnostic groups on the same 2-D gel, which might have been masked by differences between gels. Because of the availability of the three dyes, one can analyse two samples in parallel and can also add an internal standard, still on the identical gel. The internal standard has the following advantages:

(1) Improved accuracy of spot volume quantification: all spots are present in the internal standard, hence the effect of gross changes in expression between samples is minimized.

(2) Ability to link numerous gels in a large experimental design: the image of the internal standard should be identical in each gel, thus allowing meaningful statistical analyses.

(3) Discrimination between biological and gel-to-gel variation: changes in a certain spot volume between different gels can be set off against changes in the respective spot volume in the internal standard.

The Cy-like G-Dyes are attached to 2-5 % of the lysine residues of a certain protein. However, this means that the DIGE-labelling technique is not applicable to those proteins without lysine residues. Therefore the DIGE-image of 2-D gels also differs marginally from the Coomassie staining.

The 2-D DIGE technique is very sensitive, and only 75 µg of protein is needed for each sample, compared to 300 to 1 000 µg of protein required for one Coomassie-stained gel. This was very useful here as it overcomes the problem of limited epidermal material being available. The fact that fewer gels and less protein amount per gel are needed has led to the establishment of the DIGE-technique as a method for separation of epidermal proteins on 24 cm-gels for the present work. Nevertheless, the limited epidermal material that was available, especially for the infected samples at the late time point, forced us to restrict the experiment at the 120 h.a.i. time point to only two biological replicates (see chapter 6.3).

Because of (3), it is no longer necessary to use technical replicates, and samples are usually separated only once (http://www.appliedbiomics.com/tech_2DDIGE_vs_2DGel.html) (Winkel, 2009). Nevertheless preparing a second replicate gel with a Dye-swap design gave more reliability in the data set. After normalizing the spot volumes and integration of the internal standard, the correlation of the technical replicates of the 716 analysed protein spots was more accurate compared to that of Coomassie-labelled 2-D gels.

7.3.1. Barley candidate proteins involved in the interaction with *Bgh*

The spot detection software already calculates the internal standard into the samples labelled with G-Dye200 and G-Dye300. The implemented normalization method is different from the one used for the transcriptome analysis, which was based on the time points. Because of the difference in normalization the PCA image of the biological samples looks less characteristic than the image of the PCA of the transcripts. Here, the clustering of the biological samples especially for the control samples is more mixed between the time points. This explains why the time points only count for 10 % of the variation, whereas the treatment counts for 62 % of the variation, which contrasts with the findings in the transcriptome analysis. Interestingly the infected epidermal samples cluster better between the time points, especially after 24 h.a.i. So the time points seem to be very crucial for the changes at

proteome level upon infection, whereas in control plants the biological or technical diversification is more important for the level of the plants' proteins.

For the statistical analysis, as in the transcriptome analysis the "time course" was not integrated into the analysis of the proteome, because with this setting the testing showed no statistically relevant changes due to the lack of one biological sample-pair at 120 h.a.i. After using the static match approach as in the transcriptome, almost half of the analysed protein spots showed a statistical significant FDR<5 %. This is a high proportion compared to the regulated transcripts and demonstrates the reliability for this task of the used method.

Initially the proteins of the spots should have been identified out of the DIGE gels. Many protein spots picked out of DIGE gels were digested by trypsin and it was attempted to analyse them via MALDI-TOF-MS and LC-Q-TOF-ESI MS/MS. These attempts to identify the spots out of DIGE gels resulted in low signal intensities corresponding to the low quantity of the protein, and the low number of peptides were insufficient for unambiguous protein identification by peptide mass fingerprinting, leading to identification of only 10 % of the protein spots. This is because of the following reasons:

(1) The labelled proteins have a higher molecular weight (around 500 Da) than the unlabelled ones, causing the labelled and the unlabelled proteins to migrate to different positions within the SDS-PAGE gel. This effect is more pronounced the lower the molecular mass of the proteins. The labelled fraction of a protein is only a minority of the proteins volume (2 - 5 %), so if the G-Dye-labelled protein amount is picked, the majority of the total amount of each protein will not be picked.

(2) Manual picking on the basis of the Coomassie picture of the DIGE gels was limited due to the low concentration of the proteins in the gel and therefore their low visibility.

In general it is possible to excise proteins from the gel, subject them to in-gel proteolysis and analyse them by mass spectrometry, provided that sufficient sample is present on the gel (>300 µg of total protein). Thus the analysis was done on 2-D DIGE gels, but for the picking a preparative gel was needed. Therefore samples of all treatment, biological replicates and time points are mixed (such as the internal standard) and loaded with four times the amount of epidermis protein in comparison to the DIGE gels. The image of the preparative gel was matched with that of the analytical gels and the spots could easily be excised and the majority of the spots was clearly identified. The advantage of this method was also that the spots cover all time points coming both from control and infected samples. It is important not to identify a spot as originating from barley in a pure plant control sample, when it is getting

bigger in the course of the infection, as it may also be technically overlaid by a fungal protein. This happened with one protein spot, which led to two identifiers, one fungal (35_40992: **Hypothetical protein - *Gibberella zeae* (*Fusarium graminearum***) and one plant protein (35_15462: **Proteasome subunit alpha type 6 - *Oryza sativa***). So the assumption is that in this spot on the gel the barley protein and the *Bgh* protein appeared at the same place coincidentally.

Another spot which was very interesting due to the regulation value was identified as **Isocitrate dehydrogenase subunit 1, mitochondrial** (35_40248) from *Magnaporthe grisea* (*M. grisea*). Sequence comparison by BLASTX revealed no plant protein in the list of the first 100 hits. Since the plant was not infected by *Magnaporthe grisea*, the protein is clearly derived from *Bgh*, which leads to the conclusion that *Bgh* proteins can be found separately and distinct from proteins of plant origin.

Furthermore the identification of the same protein in several spots occured, e.g. **HvGER2a**. As already published (Berna and Bernier, 1997), GLPs have many family members and can differ in their glycolysation pattern during pathogen attack and are therefore visible at several coordinates in a 2-D gel. Because phosphorylation or other modifications cannot be analysed within the workflow of this thesis, further work has to be done regarding these spots. It might also be that these spots are isoforms, but with significant hits to only one identifier.

7.3.2. Classification of proteins into functional categories

The proteins were connected to ESTs of the PGRC2-13k-array and the MapMan binning system. The majority of the proteins could be linked (see chapter 6.4) but some not, because either the ESTs are spotted but are not present or the corresponding ESTs are not spotted on the array.

It was not applicable to analyse the overrepresentation or the underrepresentation of proteins in the SuperBINs by means of a Chi-square testing as was done for the transcripts (see chapter 6.2.10) because of the small number of proteins in the different functional classifications. However, looking at the absolute numbers of identified and regulated proteins, one can deduce that proteins of the TCA-metabolism were more regulated and proteins of glycolysis were less regulated. The other SuperBINs showed no great difference. This is due to the fact that the choice of spots to be picked was based on already visible changes in the pattern and the whole proteome was not examined.

Table 10 shows the list of the significantly regulated proteins that were maximally up- or downregulated in absolute values after $\log_2$-transformation. Here it has to be mentioned that

the maximal detected upregulation occurred at 120 h.a.i., whereas the maximal downregulation for some proteins was already found at 48 h.a.i. The upregulation of the proteins was mainly increasing over the time points, and therefore these might be proteins which are co-opted by *Bgh*, or the upregulation might reflect increasing defence mechanisms of the plant. The downregulated proteins might mirror the suppression of defence mechanisms by the fungus. Interestingly this seems to mirror the different stages of fungal infection, as the time point 48 h.a.i. is the one, where the fungus develops and enters further epidermal cells, when SAR and cell death inhibition is needed.

Table 10: List of proteins with the highest down- and upregulation, respectively: First column shows the HarvEST:Barley-ID and the second the function of the proteins. In the next five columns the regulation levels of infected/control are shown after log_2-transformation, with the highest number highlighted in bold. The highest value and the corresponding time point is summarized in the next column, followed by the significance of the regulation (q-value).

HarvEST-ID	Putative function	12h	24h	48h	72h	120h	maximum	q-value
35_2434	Retrotransposon encoded protein (unknown)	0.8	1.2	1.0	1.8	**4.6**	**4.6 (120h)**	0.0004
35_4982	Nucleoporin interacting component	1.0	0.7	1.4	1.8	**3.8**	**3.8 (120h)**	0.0006
35_16041	Peroxidase 50	0.7	0.9	1.0	2.1	**3.1**	**3.1 (120h)**	0.0010
35_704	Pathogenesis-related protein PRB1-2	-0.2	0.8	1.4	1.9	**2.5**	**2.5 (120h)**	0.0016
35_702	Pathogenesis-related protein PRB1-2	-0.1	0.2	1.3	1.8	**2.4**	**2.4 (120h)**	0.0027
35_4712	GATA transcription factor 25	0.0	0.7	1.3	1.6	**1.9**	**1.9 (120h)**	0.0032
35_1124	Citrate synthase	0.2	0.3	0.3	0.7	**1.6**	**1.6 (120h)**	0.0119
35_16117	Fumarase	0.2	0.4	0.4	0.7	**1.6**	**1.6 (120h)**	0.0098
35_728	Glutathione peroxidase	0.3	0.5	0.3	0.3	**1.5**	**1.5 (120h)**	0.0114
35_15429	Succinate dehydrogenase, mitochondrial	0.5	0.0	0.0	0.2	**1.6**	**1.6 (120h)**	0.0420
35_14981	Salt stress root protein RS1	-0.4	-0.3	-0.6	-0.3	**-1.0**	**-1.0 (120h)**	0.0074
35_1022	ATP synthase delta' chain,	-0.1	-0.1	-0.6	-0.5	**-1.1**	**-1.1 (120h)**	0.0198
35_15495	Stress-induced protein sti1	-0.7	-0.4	**-1.2**	0.1	-0.2	**-1.2 (48h)**	0.0231
35_14824	HvGER2a	-0.6	-0.6	**-1.2**	-0.3	-0.6	**-1.2 (48h)**	0.0040
35_14824	HvGER2a	-0.6	-0.7	**-1.3**	-0.3	-0.3	**-1.3 (48h)**	0.0082
35_15726	UBA/TS-N domain containing protein	-0.1	0.1	-0.3	-0.3	**-1.4**	**-1.4 (120h)**	0.0376
35_19417	Trehalose-6-phosphate synthase	0.0	-0.1	-0.4	-0.5	**-1.4**	**-1.4 (120h)**	0.0256
35_48123	HvGER2a	-0.2	-0.2	-1.0	-0.6	**-1.4**	**-1.4 (120h)**	0.0136
35_25207	UBA/TS-N domain containing protein	-0.7	-0.6	**-1.5**	-0.5	-1.1	**-1.5 (48h)**	0.0046
35_5689	Hydrolase, alpha/beta fold family domain containing protein	0.3	0.1	-1.0	-0.8	**-2.0**	**-2.0 (120h)**	0.0376

In general this study focuses on the integration of transcript and protein data. However, for some proteins no transcript data could be acquired. This might be because the correlated transcript is not spotted on the array (discussed in chapter 7.3.3) or the level of transcription is not sufficient for the detection threshold above background (discussed in chapter 7.3.4). The proteins which allow full integration with transcript data are discussed in chapter 7.4.

7.3.3. Proteins whose transcripts are not spotted

7.3.3.1. Upregulated proteins

Among those proteins whose corresponding ESTs are not spotted, the protein with the highest upregulation at the early stages of all analysed proteins was identified as **retrotransposon** encoded protein of unknown function (35_2434). In wheat, about 90 % of the genome consists of repetitive sequences and 68 % of transposable elements (Li et al., 2004). Retrotransposons can amplify themselves in the genome. Hereby the retrotransposons copy themselves to RNA and via a self-encoded reverse transcriptase back to DNA, which can then integrate itself at another place in the genome. Transposition and survival of retrotransposons within the host genome are possibly regulated both by retrotransposon and by host-encoded factors. Under normal conditions the retrotransposon genes are methylated and are not transcribed. Under certain stress conditions they can be activated and there are specific enzymes only for the demethylation of transposon genes. By comparing the DNA sequence with other known sequences by BLAST at NCBI, the consensus sequence 35_2434 showed the highest similarity to retrotransposons of the *copia*-type. Also in the *Triticeae* Repeat Sequence Database (TREP, http://wheat.pw.usda.gov/ITMI/Repeats) the consensus sequence showed the highest similarity to *copia*-like retrotransposons. The sequence of this type of retrotransposon consists of a group-specific antigene (*gag*) and a polyprotein (*pol*) which are together flanked by long terminal repeats (Figure 39). The *pol* contains a protease-, an integrase-, an RT- and an RNAseH region.

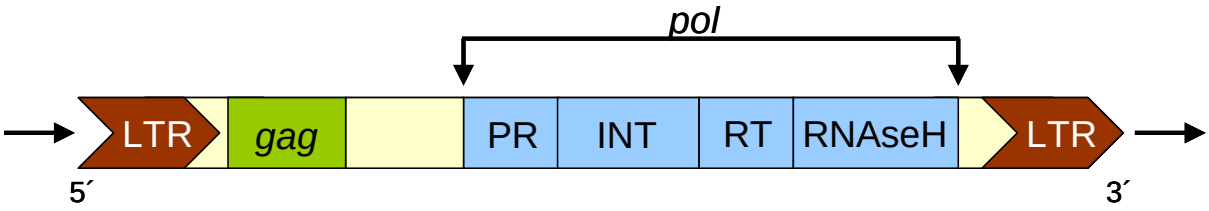


Figure 39: Schematic representation of the general structure of *copia*-like retrotransposons. LTR: long terminal repeats; *gag* gene encodes a capsid-like protein; *pol* gene contains: PR: protease; INT: integrase; RT: reverse transcriptase.

Although retrotransposons were formerly thought to be only junk in the genome, nowadays it is discussed to what extent retrotransposons are involved in the ability of plants to react on environmental changes by integration into coding or regulatory regions, thereby affecting gene expression. It is postulated that the promoters of retrotransposons mimic those of stress-related genes and it is shown that they are activated by pathogen elicitors or hormones (Grandbastien, 1998, Beguiristain et al., 2001). However, retrotransposons are also able to transduce host genes (Elrouby, 2005). When loading the 140 amino acids (aa) of

the transcribed consensus sequence of 35_2434 into the “SBASE” protein domain prediction database (http://hydra.icgeb.trieste.it/sbase), for the first 68 amino acids a “glycoside hydrolase family 19” domain was found (Figure 40, 1). Members of this family are comprised of enzymes with chitinase activity only. Chitinases catalyses the hydrolysis of chitin and functions in the defence against fungi by destroying their chitin-containing cell wall. However, it has to be said that comparing the 68 amino acids of the glycoside hydrolase domain by BLAST, no chitinase hit can be found. Another domain (Figure 40, 2) (aa 78-116) was described as an “EAL“, but only with a low score. As described in Schmidt et al. (2005), “the EAL-domain […] is a ubiquitous signal transduction domain in bacteria” involved in the hydrolysis of the signaling molecule cyclic dimeric GMP (c-di-GMP) into GMP, but these domains can exist in active as well an inactive forms (Schmidt et al., 2005). Furthermore c-di-GMP regulates cellulose synthesis in Acetobacter xylinum (Ross et al., 1987, Ross et al., 1990) as well as pathogenesis (Tamayo et al., 2007). The involvement in cellulose synthesis is interesting in the context, that the second best identifier of the protein spot in the TIGR database (not shown), but which is below threshold, was a cellulose synthase.

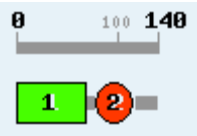


Figure 40: Domain prediction results for the amino acid sequence of 35_2434. The first domain (1, aa 1-68) is annotated as a “glycoside hydrolase family 19”; the second (2, aa 78-116) as an “EAL” domain.

The outcome of the identification is confusing, as retrotransposons are not known to be translated into proteins. Therefore a possible assumption could be that this HarvEST:Barley-ID is a chimeric one. In summary for this protein spot the regulation pattern is highly interesting but the function of the protein is uncertain.

When using clustering of all proteins in the analysis (see chapter 6.3.6), the accumulation of the retrotransposon encoding protein clustered together with the second highly upregulated protein **GATA transcription factor 25** (35_4712) whose transcript was also not spotted. The GATA transcription factor accumulation increased over the time, beginning with a 60% increase at 24 h.a.i. As “GATA” as a target domain is pretty unspecific, this induction can be explained as an unspecific enhancement of the transcription, but specificity of the transcription factor cannot be excluded. Interestingly, NtMyb2 as a regulator of the tobacco retrotransposon Tto1 is induced by various stresses such as elicitor treatment. The promoter of NtMyb2 possesses a GATA-type binding domain, suggesting, that also the retrotransposon protein in this study could be regulated by the found GATA transcription factor.

Furthermore three other protein spots that could be linked to ESTs, clustered together with the retrotransposon protein and the GATA transcription factor at protein level, namely two spots of a **Pathogenesis-related protein PRB1-2** (35_702 and 35_704) and a **nucleoporin interacting component** (35_4982). Therefore they will be discussed together with their transcript data (Comparative matching: chapter 7.4.1 and 7.4.4, respectively).

Other upregulated proteins whose corresponding ESTs are not spotted are seen below, many of them involved in transcription control or protein modification control:

- AAA-type ATPase family protein (35_4446)
- basic helix-loop-helix domain containing protein (35_38367)
- F-box domain containing protein (35_10955)
- two protein spots of Subtilisin-like serine proteinase (35_18209)
- TBC domain containing protein (35_2726)
- aminoacylase (35_1864)
- ABA responsive element binding factor 3 (35_4140)
- protein-L-isoaspartate O-methyltransferase (35_11352)
- high-affinity potassium transporter (35_15780)
- unknown protein (35_9359)

Among these interesting candidates the **L-isoaspartate O-methyltransferase** should especially be mentioned since it is a repair enzyme which methylates abnormal L-isoaspartate residues that are spontaneously degraded as a result of aging (Thapar and Clarke, 2000). There are at least two protein isoforms that are translated via alternative splicing. In Arabidopsis at least one of this isoforms is found to be constitutively expressed in leaves and can be increased by various stresses. In our context this presumably happens in response to increasing endogenous abscisic acid (Xu et al., 2004). This leads to the conclusion that barley induces the repair mechanisms after infection.

The **F-box-domain-containing protein** was upregulated the highest at 24-72 h.a.i., F-box domains have been recognized as a protein-protein interaction motif. The F-box domain is found in adaptor proteins of the E3 ubiquitin ligase SCF complex and thus plays a role in selective protein degradation by the ubiquitin-proteasome pathway (Craig and Tyers, 1999, del Pozo and Estelle, 2000). F-box proteins are also represented in gene networks broadly regulated by gene silencing via RNA interference through microRNA (Jones-Rhoades et al.,

2006). This suggests the importance of poat-transcriptional effects in the biotrophic interaction.

7.3.3.2. Downregulated proteins

Proteins that were downregulated are according to the MapMan binning system involved in the regulation of transcription, signalling and protein modification as a highly regulated **hydrolase, alpha/beta fold family domain containing protein** (35_5689), a **trehalose-6-phosphate synthase** (35_19417), a **protein NB-ARC domain containing protein** (35_28067), a **dirigent-like protein** (35_3542), a **putative subtilisin homologue** (35_17049) and an **expressed protein** with unknown function (35_19575).

Among these candidates the **trehalose-6-phosphate synthase** (TPS) should be discussed further because of the high regulation level (see chapter 7.3.2, Table 10) and its biological functionality. TPS is the first enzyme in trehalose biosynthesis, TPSs are widely distributed in nature, whereas in plants they are rather low abundant. Trehalose is a sugar that has an osmoprotective effect in bacteria, invertebrates, fungi and plants. Transgenic tomato plants attain enhanced drought resistance by overexpression of bacterial TPS (Yeo et al., 2000). This is discussed as being due to the osmotic response from the production of ROS during osmotic stress (Barra et al., 2003). In plants trehalose and TPS play an essential role in various stages of development (Gomez et al., 2010), as well as in the regulation of carbon metabolism, regulation of starch storage (Chary et al., 2008) and photosynthesis. In addition, it has a role in the regulation of abscisic acid and stress signalling (Avonce et al., 2004). However, in fungi, trehalose is an important carbon storage compound and TPS quickly converts hexoses into the precursor of trehalose. New investigations showed that trehalose-6-phosphate at least in certain cells is involved in signalling or cell wall metabolism, possibly coupled to ethylene action (Thiel et al., 2008). Because of the findings that trehalose is an important storage compound in the fungus and on the other hand that overexpression of the TPS1 protein enhances abiotic as well as biotic stresses, the downregulation of TPS expression in our study can be due either to the plant's attempt to limit trehalose supply for the fungus or to *Bgh* itself downregulating the expression to suppress defence reactions of the plant.

7.3.4. Proteins whose transcripts are below detection threshold

Four upregulated proteins were linked to array clones with undetectable transcript signal. They were identified as a **protein tRNA methyltransferase** (35_4628, HT01O14), a **glycerol-3-phosphate acyltransferase** (35_2185, HM04G18), a **proteasome activator**

subunit 4-like (35_16401, HO05G02) and a **Glucose-1-phosphate adenyltransferase** (35_2078, HO03H23). These proteins are involved either in the protein synthesis, lipid metabolism, protein degradation or turnover of starch. The interesting question is, why they were identified in the proteome, when the mRNA-level was so low that they are not present in the transcriptome. This might be due to low protein turnover. Due to the technical limitations of the transcript analysis these candidates were not further discussed in this study.

7.3.5. Summary of the proteome

The protein analysis was based on 2-D DIGE analytical gels and corresponding preparative gels in order to identify regulated proteins. Among many proteins the highest upregulation values were found at 120 h.a.i. Most of these proteins correlated with transcript data and are therefore discussed in the next chapter. Within the upregulated group not linked to the 13k-PGRC-macroarray, the most strongly regulated candidates were a retrotransposon encoded protein of unknown function and a GATA transcription factor. Among the ten most stongly downregulated proteins, maximal downregulation occurred at 48 h.a.i., which suggests that this time point is critical for the maintenance of susceptibility and the suppression of the plant's defence reponses by the fungus and thus should be included in further investigations. Functionally interesting is a trehalose-6-phosphate synthase as it was highly downregulated.

7.4. Comparative matching of transcriptome and proteome analyses

With the progress of genomic initiatives to sequence genomes and profile gene expression in the context of plant-pathogen interaction, proteome profiling is increasingly needed for a better understanding of plant defence mechanisms against pathogen stress.

A major objective of this study was to reveal a possible additional level of complexity in the response of barley to *Bgh* attack. Results from two types of analysis (transcriptome and proteome) of epidermis samples were described in the previous chapters. For an accurate comparison of the results it is essential that the plant material for both analyses was identical.

The combined transcriptomic and proteomic approaches made it possible to find out whether transcripts and the corresponding proteins are regulated in a parallel or an anti-parallel manner. The interest of this analysis lies in the answer to the question, whether a change in

a transcript is mirrored in the encoded protein, and how the kinetics of such changes compare to each other. This was achieved by integrating transcriptome and proteome data.

Parallel trends could be seen where the transcript and also the protein was upregulated (probably with a delay in time) and anti-parallel trends could be seen if the transcript was regulated, but the protein not (or vice versa) or when the transcript was regulated in the other direction from the corresponding protein.

Statistical analysis of quantitative changes of linked transcript-protein pairs resulted in a categorization in four sections (see Table 11 or chapter 6.4.1) and the transcript-protein pairs were classified according to their regulation at transcript and protein levels by four clusters in each section.

Table 11: Categorization of transcript-protein pairs into sections according to their statistical significance.

	Protein significant	Protein non-significant
Transcript significant	Section I	Section II
Transcript non-significant	Section III	Section IV

However, trends of regulation could be observed in clusters across the sections, of which the most interesting are described as follows: Pairs of section I, cluster 2 and 4 and of section III, cluster 2 showed a parallel upregulation (25 pairs, see Table 12), whereas pairs in section I, cluster 1 and section II, cluster 1 and 4 showed a parallel downregulation (24 pairs, see Table 14). Pairs in section I, cluster 3 and section III, cluster 3 showed a downregulation at transcript and an upregulation at protein level (9 pairs, see Table 15).

Deviations from parallel changes in both “-omes” are likely to reflect post-transcriptional or post-translational regulation events. It has to be kept in mind that section I consists of transcript-protein pairs with statistical significance in both –omes, and section II and III contain data with a statistical significance in only one –ome. In spite of this restriction members of section II and III could support the findings of the regulation pattern in section I when looking at individual biological functions beyond statistical calculation which is determined only by a pure mathematical threshold.

7.4.1. Parallel trends in upregulation

The first pairs to be discussed are those which are upregulated in a parallel manner in both transcript and protein, and these will be discussed in groups according to their biological function (see Table 12). Hereby it is noticable that a relatively high proportion of pairs in this group were concerned with stress and energy. Most of the members showed statistical significance in both transcript and protein data, the exception being the majority of those categorized in the MapMan SuperBIN "TCA cycle“ which were only significant in their protein data.

Table 12: List of parallel upregulated transcript-protein pairs. These are categorized into section I, cluster 2 and 4 and section III, cluster 2 according to chapter 6.4.1. The pairs are listed according to their biological function. Values which are not significantly regulated at transcript level are shown in *italic*.

HarvEST-ID	Putative function	Binning	RNA	Protein	Section	Cluster
35_702	PRB1-2 precursor]	stress	2.9 (72 h)	2.4 (120 h)	I	2
35_704	PRB1-2 precursor	stress	2.8 (120 h)	2.5 (120 h)	I	2
35_50935	HvGER4	stress	4 (24 h)	1.4 (48 h)	I	2
35_16041	peroxidase 50 [Oryza sativa (japonica cultivar-group)]	miscellaneous	2.3 (24 h)	3.1 (120 h)	I	2
35_14091	glutathione transferase F5 [Triticum aestivum]	miscellaneous	2.9 (24 h)	0.3 (48 h)	I	2
35_1124	citrate synthase [Oryza sativa]	TCA / org. transform.	0.8 (24 h)	1.6 (120 h)	I	4
35_16233	NAD-dependent isocitrate dehydrogenase [Oryza sativa (japonica cultivar-group)]	TCA / org. transform.	*0.8* *(24 h)*	0.6 (24 h)	III	2
35_15429	succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]	TCA / org. transform.	*0.5* *(120h)*	1.6 (120 h)	III	2
35_16117	fumarase; fumarate hydratase [Arabidopsis thaliana]	TCA / org. transform.	*0.6* *(48h)*	0.9 (120 h)	III	2
35_16117	fumarase; fumarate hydratase [Arabidopsis thaliana]	TCA / org. transform.	*1.6* *(48h)*	1.6 (120 h)	III	2
35_960	NADP malic enzyme [Oryza sativa (japonica cultivar-group)]	TCA / org. transform.	*1.4* *(24h)*	1.3 (120 h)	III	2
35_960	NADP malic enzyme [Oryza sativa (japonica cultivar-group)]	TCA / org. transform.	*2.4* *(24h)*	0.7 (24 h)	III	2
35_802	cytosolic 6-phosphogluconate dehydrogenase [Zea mays]	OPP	1.3 (24 h)	0.5 (48 h)	I	4
35_368	S-adenosylmethionine synthetase 1_HORVU	amino acid metabolism	1.4 (120 h)	1.5 (48 h)	I	4
35_366	AdoMet synthase 1 [Hordeum vulgare subsp. vulgare]	protein	1.4 (120 h)	1.1 (48 h)	I	4
35_16286	Chaperonin CPN60-2, (HSP60-2)	not assigned	*0.8* *(24h)*	0.8 (120 h)	III	2
35_14470	HSP70	not assigned	1.2 (12 h)	1.3 (120 h)	I	4
35_15997	phosphoglycerate mutase-like protein	not assigned	2 (120 h)	0.7 (24 h)	I	4
35_3277	mitochondrial chaperonin-60 [Oryza sativa (japonica cultivar-group)]	not assigned	1.7 (120 h)	0.8 (24 h)	I	4
35_23963	PHD finger protein-related [Arabidopsis thaliana]	not assigned	1.9 (120 h)	0.8 (120 h)	I	4

7.4.1.1. TCA cycle

Enzymes of the TCA cycle were upregulated at the early time points as well as at the late stages. The TCA cycle provides energy equivalents via cellular respiration in the matrix of the mitochondrion. In total 7 protein spots are upregulated at transcript and protein level. The enhanced expression of enzymes of the TCA cycle are shown in other biotrophic plant-fungal interactions (Fauteux et al., 2006, Doehlemann et al., 2008, Wildermuth, 2010). A citrate synthase, which catalyses the first and pace-making step in this cycle by condensing oxaloacetate and acetyl-CoA to citrate, was upregulated significantly in both –omes. The other six spots referring to four unique identifiers were only significant at protein level, but the transcript data support the trend at transcript level as well.

Of the proteins involved in the TCA-cycle, I intend to go into more detail on the **NADP malic enzyme** (NADP-ME), because of its high upregulation in transcript and also its proven relevance in stress response. In this study this protein was found to be upregulated in two spots in the early stages and stays upregulated during whole infection process, suggesting the importance of this enzyme over the entire infection process. The NADP-ME catalyzes the oxidative decarboxylation of L-malate to produce pyruvate, NADPH and CO_2. Supporting functions such as providing NADPH for assimilatory process (e.g. lipid biosynthesis) or the biosynthesis of specific defence compounds (e.g. phytoalexins, lignins, osmolytically active compounds) are important under stress or when acting as cofactor for antioxidative enzymes (Drincovich et al., 2001). Various authors suggested a relationship between the non-photosynthetic isoform of NADP-ME and plant defence response, such as fungal elicitors, water and salt stress (Maurino et al., 2001, Synkova and Valcke, 2001, Sun et al., 2003, Chi et al., 2004). The induction of NADP-ME is shown in rice under environmental stresses, and overexpression in *A.thaliana* confers salt and osmotic stress tolerance (Liu et al., 2007b). Transcript as well as protein accumulation were induced by the potato virus Y in *Nicotiana tabacum* (Doubnerova et al., 2009). In *Egeria densa* the induction of NADP-ME under UV-B radiation is correlated with an increase in the activity of several enzymes involved in the antioxidant metabolism, such as SOD, ascorbate peroxidase, and peroxidase (Casati et al., 2002), as can also be seen in the defence response of barley to *Bgh*.

The enzymes of the TCA cycle were regulated in various plants under different stresses, which results from their central importance in supplying usable energy for metabolic and stress-related pathways. The early upregulation is possibly connected with the energy needed for assimilatory defence mechanisms, whereas the late upregulation presumably is a result of the damage to the chloroplast system in the mesophyll and the switch of the infected leaf to a “sink organism” due to the feeding of the fungus. On the other hand many other

biosynthetic reactions involved both in energy production and biosynthesis, such as gluconeogenesis, fatty acid biosynthesis or amino acid biosynthesis use the intermediates of the TCA cycle as substrates. The removal of these intermediates necessitates anaplerotic reactions to replenish these intermediates. Upregulation of TCA cycle enzymes ensures the continued function of this cycle and also the provision of substrate to other reactions.

7.4.1.2. Amino acid metabolism

As overexpression of genes involved in the production of amino acids leads to enhanced susceptibility in resistant barley (Hu et al., 2009), and amino acids are the only uptake source of nitrogen for the fungus (Spanu et al., 2010), the significant upregulation both at transcript and at protein level of two protein spots for a putative **S-adenosylmethionine synthetase** (AdoMetSyn) is interesting. AdoMetSyn is induced by many stresses, such as the early response to *Bgt* in wheat. Interestingly, “this induction was specific to the epidermis and linked to host cell wall apposition formation, suggesting that the pathways for the generating of methyl units are transcriptionally activated for the host defence response” (Bhuiyan et al., 2007). AdoMetSyn plays an important role in the production of S-adenosyl methionine (SAM) which is the precursor for the biosynthesis of several compounds involved in defence responses, namely phenylpropanoids, cell wall components and polyamines (Roje et al., 2006). The polyamines are known to interact with ribonucleic acids and can stabilize supercoiled or folded DNA. They are also involved in nucleic acid and protein biosynthesis. SAM is the substrate for the speed-limiting step in the synthesis of polyamines such as spermidin, which may have a hormone-like effect on the plant (Schröder and Schröder, 1995). Applying tri-substituted spermidines from pollen of *Quercus alba* before or after inoculation of powdery mildew to barley seedlings reduced the fungal infection significantly and also affected AdoMetDC activity (Walters et al., 2001). AdoMetDC is the key enzyme in polyamine synthesis and is regulated in response to polyamine levels as well as in response to methyl jasmonate in barley leaves (Walters et al., 2002, Hanfrey et al., 2003). The upregulation of AdoMetDC is discussed as revealing possible routes of methyl transfer towards polyamine, lignin and ethylene biosynthesis (Bhuiyan et al., 2007). AdoMetDC was not a subject of my study, but it might be interesting to find out whether the upregulation of AdoMetSyn is connected to a regulation of AdoMetDC with the production of polyamines, or whether the upregulation of AdoMetSyn is connected with the other above-mentioned pathways. However, as *Bgh* has a lack of genes to assimilate inorganic nitrogen, its only feasible nitrogen source is host-derived amino acids (Spanu et al., 2010). The protein level for AdoMetSyn first rised for both identified spots, followed by a rise in transcript level, which could be an indication for post-transcriptional effects. It would be an interesting task for

further studies to investigate whether the fungus is directly upregulating AdoMetSyn accumulation or if the plant is reacting to the lack of amino acids taken up by the fungus.

7.4.1.3. Stress-related

Stress-related genes were highly and significantly upregulated at both transcript and protein level. Because of their relevance and known pathogen-related effect as well as their high regulation levels it is necessary to look at some of them in more detail, in particular the HvGER4, a peroxidase 51 and two PR-proteins.

The highest transcript upregulation already at 12 h.a.i. could be seen for one pair, identified as **HvGER4**. The transcript level reached a really high upregulation of up to 16-fold. The upregulation on the protein level followed with a delay, and upregulation remained in later stages. Several studies have shown that fungal infection leads to an increased accumulation of germin-like proteins in barley and wheat (Dumas et al., 1995, Zhang et al., 1995, Hurkman and Tanaka, 1996). These proteins belong to multigene families and are shown not only to be induced by fungal attack, but also by external H_2O_2 and might cooperate for the fine tuning of basal resistance against *Bgh* (Zimmermann et al., 2006). Superoxide dismutase activity (SOD) is associated with this GLP subfamily, thus being a potentially important source of H_2O_2, which accumulates at the sites of the attempted penetration as well as at contact points between epidermal cells undergoing an HR and the subjacent mesophyll cells (Thordal-Christensen et al., 1997a). Transient overexpression of HvGER4 protects barley epidermal cells from attack by *Bgh*. Induced accumulation raises the resistance, whereas TIGS induces hypersusceptibility (Zimmermann et al., 2006). The data in this study underlines the importance of that gene product in early defence, such as HR or the reinforcement of the cell wall texture by cross-linking events in host and nonhost resistance and also in the later stages of the interaction as shown by analysis of the infection over 120 h.a.i.

As GLPs are induced by an elevated hydrogen peroxide concentration (Zimmermann et al., 2006), many peroxidases are linked to quantitative trait loci of resistance to *Bgh* in barley. The **peroxidase 50** presented here showed the highest upregulation of all pairs on the protein level. It was shown that the barley *HvPrx7* peroxidase mRNA accumulates in response to *Bgh* infection in barley leaves (Zhou et al., 1998). One of the roles of peroxidases in basal plant defence is the reinforcement of cell wall physical barriers and lignification (Vance et al., 1980, Bowles, 1990), and overexpression enhances penetration resistance through reactive oxygen species generation in wheat (Schweizer, 2008). This protein is very interesting because of the high amplitude of its regulation in transcript and protein, and because at transcript level it had an upregulation at early time points, whereas at

protein level the upregulation rised steadily over the time course. This suggests that the translation is either very efficient or it is even post-transcriptionally or -translationally enhanced. The question that arises about this particular protein is whether the upregulation at late time points also occurs in resistant interactions or if it is specific only for the susceptible interaction, indicating that the plant is trying to prolong the defence reaction of the enzyme.

Two of the spots with this high upregulation were referred to **PRB1-2 precursor** proteins. PR-proteins are said to be key players in the early defence reactions via forming penetration resistance, and silencing of PR-1b facilitates the *Bgh´*s penetration (Schultheiss et al., 2003). A more than 2-fold upregulation was shown at transcript level, whereas this level appeared at protein level from 48 h.a.i. onwards. Interestingly the transcript regulations of both protein spots showed a lower level at 48 h.a.i. than at 24 h.a.i. and 72 h.a.i., which was not mirrored at protein level. This could be a hint that this PR-protein not only has an effect on the early penetration resistance, but also on later time points. It is not clear whether the plant does not manage to express the protein early enough or whether the fungus is able to suppress the expression of the protein post-transcriptionally. It might well be the case that this delay in protein expression is a weak point of the plant's defence, enabling the fungus to penetrate into the epidermis. However, these PR-proteins may also play an important role in the later phase of the infection. Overexpression or silencing of these proteins in the later phase could tell us more about their roles.

A **glutathione S-transferase** (GST) was upregulated the highest at 120 h.a.i. at transcript level, but only slightly regulated at protein level, which was significantly so in both –omes. Enzymes of this family catalyze a variety of reactions, such as detoxification of lipophilic endogenous compounds as well as xenobiotics via the conjugation with glutathione. Transgenic plants overproducing polyamines induce glutathione transferases and have an enhanced tolerance toward salt stress (Baltruschat et al., 2008). GSTs of wheat are induced by pathogen attack (Mauch and Dudler, 1993), and early H_2O_2 accumulation in mesophyll cells during the HR in barley-powdery mildew interaction leads to induction of glutathione (Vanacker et al., 2000), suggesting that glutathione controls oxygen (Noctor and Foyer, 1998). The high upregulation of this enzyme at transcript level which was not mirrored at protein level may be a hint that this defence reaction is suppressed at protein level by *Bgh*.

7.4.1.4. Transcription regulation

Finally, it has to be pointed out that another protein was upregulated at both levels: a **PHD-finger protein-related** was upregulated at late stages at transcript level and at protein level. Despite the fact that this protein is not assigned into a biological function in the MapMan binning system, PHD-fingers are found in transcriptional regulators and chromatin-modifying proteins, which would characterize it as a member of the SuperBIN "RNA". PHD-finger-proteins have been reported to tri-methylate histones or bind to already tri-methylated histones (Ndamukong et al., 2010) and therefore are called *epigenetic readers*. Overexpression of PHD-type transcription regulators improves salt-tolerance in soy bean and PHD-type transcription regulators are involved in water-deficit stress in rice (Wei et al., 2009, Ray et. al, 2010). Thus, this protein may link the stress to late occurring changes in gene transcription. Overexpression of this protein might further enhance the stress tolerance by diminishing the oxidative stress effect.

7.4.2. Upregulated at transcript, downregulated at protein level

In Table 12 a number of transcript-protein pairs could be functionally categorized showing upregulation at transcript as well as at protein level. However, few pairs showed upregulation at transcript and downregulation at protein level (see Table 13).

Table 13 : List of parallel pairs, upregulated at transcript and downregulated at protein level. Values which are not significantly regulated only at transcript level are shown in *italic*.

HarvEST-ID	Putative function	Binning	RNA	Protein	Section	Cluster
35_4322	GTPase activating protein [Oryza sativa (japonica cultivar-group)]	not assigned	*0.7 (120h)*	-0.9 (120 h)	III	1
35_13856	peroxidase 10 [Triticum monococcum]	miscellaneous	3.4 (24 h)	-0.3 (48 h)	I	2
35_49	GAPDH	glycolysis	0.8 (120 h)	-0.8 (48 h)	I	4
35_1714	dihydrolipoamide dehydrogenase precursor [Oryza sativa (japonica cultivar-group)]	TCA / org. transform.	1.1 (120 h)	-0.6 (120 h)	I	4
35_1022	ATP synthase delta' chain, mitochondrial precursor [Oryza sativa (japonica cultivar-group)]	mitochondrial electron transport / ATP synthesis	0.8 (120 h)	-1.1 (120 h)	I	4

Among the few candidates in Table 13 the transcript-protein pair of **Peroxidase 10** is mandatory to mention, because it showed one of the highest upregulations at transcript level (>10-fold at 24 h.a.i.) of all transcript-protein pairs but was associated with downregulation at protein level, significantly regulated at both -omes. Although literature research did not reveal the function of this particular protein, it can be speculated that *Bgh* actively suppressed the translation or enhanced the protein degradation e.g. to overcome ROS, resulting in the fact that, despite the measured upregulation on mRNA levels, the net amount of protein was decreasing.

A **GTPase activating protein** (GAP) was non-significantly upregulated at transcript, but significantly downregulated at protein level. This protein is of special interest due to its functional involvement in the nucleo-cytoplasmic transport. The members of the GAP family are regulatory proteins in the cytoplasm, which can bind to activated G proteins such as Ran, and stimulate their GTPase activity. Ran-GTP is localized in the nucleus, whereas Ran-GDP in the cytoplasm. To mediate a transport into the nucleus, Ran has to be in the Ran-GDP-state. GAP is suggested to be involved in mildew infection in barley (Wheeler et al., 2003). The GAP found in this study may interact with Ran, meaning to enhance nuclear import. The downregulation at protein level occurring here may show an interference of the fungus, which hinders the import of certain defence response mediating proteins.

The regulation differences at transcript versus protein level of the pairs discussed here might be explained by a constitutive mRNA levels without translation, in a kind of “stand-by modus”, not yet prepared to be expressed as protein in order to be able to quickly react to external triggers. These proteins demonstrate the existence of post-translational modification, as their changes at transcript level differ.

7.4.3. Parallel trends in downregulation

Transcript-protein pairs that were downregulated in both –omes were categorized in Section I, cluster 1 and in section II, cluster 2 and 4 (see Table 14). Here, members of stress-related proteins were represented to a high degree.

Table 14: List of parallel downregulated transcript-protein pairs. These are categorized into section I, cluster 1 and section II, cluster 2 and 4 according to chapter 6.4.1. The pairs are listed according to their biological function. Values which are not significantly regulated at protein level are shown in *italic*.

HarvEST-ID	Putative function	Binning	RNA	Protein	Section	Cluster
35_13900	RuBisCO activase isoform 1 [Hordeum vulgare subsp. vulgare]	photosystem	-1.5 (24 h)	-0.8 (120 h)	I	1
35_360	chaperonin 60 beta precursor	photosystem	-1.4 (120 h)	*0.9 (120 h)*	II	4
35_1092	xylose isomerase [Hordeum vulgare subsp. vulgare	minor CHO metabolism	-1.3 (120 h)	-1.0 (120 h)	I	1
35_15726	alpha-galactosidase [Hordeum vulgare subsp. vulgare]	minor CHO metabolism	-0.7 (48 h)	-1.4 (120 h)	I	1
35_784	pyruvate decarboxylase [Oryza sativa (japonica cultivar-group)]	fermentation	-0.8 (120 h)	-0.5 (72 h)	I	1
35_36841	cytoplasmic malate dehydrogenase [Zea mays]	TCA / org. transform.	-1.2 (120 h)	*-0.2 (120 h)*	II	4
35_259	glycine decarboxylase P subunit [x Tritordeum sp.]	amino acid metabolism	-1.6 (24 h)	-0.6 (120 h)	I	1
35_429	Aminomethyltransferase	amino acid metabolism	-1.5 (24 h)	-0.7 (24 h)	I	1
35_14602	alanine aminotransferase [Oryza sativa (indica cultivar-group)]	amino acid metabolism	-1.1 (120 h)	*-0.4 (24h)*	II	4
35_14981	plasma membrane polypeptide -like [Oryza sativa (japonica cultivar-group)] Salt-stress root protein RS1	stress	-1.9 (120 h)	-1.0 (120 h)	I	1
35_14981	plasma membrane polypeptide -like [Oryza sativa (japonica cultivar-group)] Salt-stress root protein RS1	stress	-1.9 (120 h)	*-1.1 (120 h)*	II	1
35_14824	HvGER2a	stress	-2.5 (120 h)	-1.2 (48 h)	I	1
35_14824	HvGER2a	stress	-2.5 (120 h)	-1.3 (48 h)	I	1
35_48123	HvGER2a	stress	-2.5 (120 h)	-1.4 (120 h)	I	1
35_14824	HvGER2a	stress	-2.5 (120 h)	*-1.2 (120 h)*	II	1
35_14824	HvGER2a	stress	-2.5 (120 h)	*-1.3 (120 h)*	II	1
35_14824	HvGER2a	stress	-2.5 (120 h)	*-0.7 (120 h)*	II	1
35_40361	peroxidase 6 [Triticum monococcum]	miscellaneous	-1.8 (72 h)	-0.6 (48 h)	I	1
35_14630	Endo-beta-1,3-1,4 glucanase II	miscellaneous	-1.5 (120 h)	*-1.6 (120 h)*	II	1
35_14174	Actin, putative, expressed	cell	-0.6 (24 h)	*-0.6 (120 h)*	II	4
35_14477	eukaryotic translation initiation factor 5A1 [Triticum aestivum]	protein	-1.4 (120 h)	*0.7 (120 h)*	II	4
35_25207	UBA/TS-N domain containing protein	protein	*-0.6 (120h)*	-1.5 (48h)	III	1
35_17334	66 kDa stress protein [Oryza sativa (japonica cultivar-group)]	development	-0.6 (24 h)	*-0.3 (72h)*	II	4
35_14519	diphosphonucleotide phosphatase [Oryza sativa (japonica cultivar-group)]	not assigned	-1.7 (120 h)	-0.7 (120 h)	I	1
35_14519	diphosphonucleotide phosphatase [Oryza sativa (japonica cultivar-group)]	not assigned	-1.7 (120 h)	*-1.4 (120 h)*	II	1
35_14519	diphosphonucleotide phosphatase [Oryza sativa (japonica cultivar-group)]	not assigned	-1.7 (120 h)	*-0.8 (120 h)*	II	1

7.4.3.1. Stress-related

Stress-related transcript-protein pairs in this category were downregulated and therefore might not be active in the defence response of barley or might be actively supressed by *Bgh*. Because of its high regulation and appearance in several protein spots, **HvGER2a** has to be further discussed. It was identified in six protein spots and showed a high level of downregulation at transcript as well as at protein level with increasing downregulation over the infection process. Three of the protein spots were significantly regulated, the other three showed the same trend. Two of the protein spots are in the list of the ten most downregulated pairs in the early stages, which is consistent with the results of (Zimmermann et al., 2006), and four of them in the later stages. HvGER2a, formerly known as HvGLP1 may serve as marker for oxidative stress in cereals after heat and H_2O_2 treatment as well as pathogen infection (Vallelian-Bindschedler et al., 1998). According to Zimmermann, only two HvGER2 unigenes are present in barley, and the sequence identity of GLPs in barley and wheat ranges from 31 %-99.5 % (Carter et al., 1998). The change in only one amino acid residue was found to affect the electrophoretic mobility in SDS-PAGE (de Jong et al., 1978) and the protein spots in the current analysis differed by approximately 0.5 pH units and also by the mass. In principle, these differences in the SDS-PAGE-coordinates of these protein spots can be due to different isoforms, to alternative splicing or to post-translational modifications, as GLP sequences have at least one site for glycolysation and differ in the glycolysation pattern (Berna and Bernier, 1997). The downregulation of these protein spots indicates an important involvement of HvGER2a for the early stages, but also might show the involvement of isoforms or different modifications of this protein in the later stages.

In this study, also a co-chaperone Sti1 (stress-induced protein 1) was found to be downregulated both at transcript and at protein level, but only significantly at protein level. This protein, even though it is in section II, cluster 1 and therefore not in the focus of the discussion, is interesting in the context of PAMP recognition and transport of PRRs. The SGT1-RAR1-HSP90 chaperone complexes are found to be required for nucleo-cytoplasmic shuttling for Mla and RX1 (Takahashi et al., 2003, Stewart, 2006), as both Mla and RX1 do not contain nuclear localisation signals (Shen et al., 2007, Tameling et al., 2010). Chen et al. investigated the chitin receptor OsCERk1 in rice. They found, that it “interacts with the Hop/Sti1-HSP90 chaperone complex in the endoplasmic reticulum” (Chen et al., 2010a) and facilitates the recognition of PAMPS. “Hop/Sti1 was required for chitin-triggered immunity and resistance to rice blast fungus”, suggesting that “the Hop/Sti1-Hsp90 chaperone complex plays an important and likely conserved role in the maturation and transport of PRRs and may function to link PRRs and Rac/Rop GTPases” (Chen et al., 2010a), and would therefore be important for plant innate immunity The downregulation of this protein and thus the

insufficient recognition of Bgh may be a reason for the susceptibility of the barley used in this study to pathogens, a susceptibility caused by insufficient activation of defense response.

7.4.3.2. Cell wall conversion

Besides stress-related proteins, interestingly three other transcript-protein pairs were significantly and highly downregulated at transcript and protein levels, the most at the late stages. These are connected with cell wall metabolism and should be discussed together, a **xylose isomerase,** an **alpha-galactosidase** and an **Endo-beta-1,3-1,4 glucanase II**. The xylose isomerase catalyses the chemical reaction D-xylulose and D-xylose, whereby xylose is a precursor to hemicellulose. Alpha-galactosidase belongs to the glycosyl hydrolase family and plays a role in the modification of cell wall polysaccharides. The downregulation seen in this study contrasts to the findings of Alexandra Molitor in her PhD thesis, where she was able to see an upregulation of this gene when the plant interacts with *Bgh* (Molitor, 2009). However these contrasting results might only be due to the different barley lines used (Molitor: Golden promise and Pallas; the present study: Ingrid). According to (Chrost et al., 2007) this protein might fulfil an important role in the leaf development of barley and arabidopsis through its function in loosening and expanding the cell wall. The highest downregulation at transcript level of the three is shown by an **Endo-beta-1,3-1,4 glucanase II**. This enzyme is involved in the cell elongation by degrading 1,3-1,4 glucanes as cellulose or chitin. The downregulation at protein level is also quite high, but not significant.

In addition to the above mentioned proteins involved in cell wall metabolism, a **Diphosphonucleotide pyrophosphatase** (NPP) was downregulated at transcript and at protein level and was identified in three protein spots; one of them was significantly regulated at protein level, the other two supporting the same trend. The barley NPPs belong to a large group of structurally related and functionally divergent nucleotide hydrolases which occur in membrane systems, accumulate in vacuoles, or are secreted from the cell (Nanjo et al., 2006). Plant NPPs may respond to the physiological needs of the cell by diverting carbon flux from starch and cell wall polysaccharide biosynthesis to other metabolic pathways (Baroja-Fernandez et al., 2001). The downregulation of this protein in this study also can be seen in context of the generally changed carbon flux in the plant as well as the changes in cell wall metabolism.

7.4.3.3. Protein degradation

Another interesting transcript-protein pair showing the highest downregulation value at protein level at 48 h.a.i. is an ubiquitin-associated **UBA/TS-N domain containing protein**. “The family of proteins containing ubiquitin-like (UbL) and ubiquitin-associated (UBA)

domains takes part in proteasomal degradation" (Su and Lau, 2009) and therefore is involved in post-translational modification. UbL–UBA domain containing proteins regulate the proper turnover of proteins through linking substrates determinated for degradation with subunits of the proteasome (Su and Lau, 2009). The fact that the transcript-protein pair in this study was not significantly regulated at transcript, but showed the highest regulation level at protein level points to the fact that the fungus is suppressing this strong defence mechanism of the plant on a post-transcriptional level.

7.4.4. Downregulated at transcript, upregulated at proteome level

Besides the many members of transcript-protein pairs that showed regulation in a parallel manner, some pairs showed regulation in opposite directions (see Table 15). Pairs which were downregulated at transcript level, but upregulated at protein level mostly appear in section I, cluster 3 and section III, cluster 3. This regulation pattern indicates post-transcriptional or post-translational regulation. The members of this group spread over diverse biological functions.

Table 15: List of opposite regulated transcript-protein pairs. These are categorized into section I, cluster 3 and section III, cluster 3 according to chapter 6.4.1. The pairs are listed according to their biological function. Values which are not significantly regulated at transcript level are shown in *italic*.

Function	Binning	RNA	Protein	Section	Cluster
sorbitol dehydrogenase [Oryza sativa (japonica cultivar-group)]	minor CHO metabolism	-0.6 (24 h)	0.8 (120 h)	I	3
pyruvate decarboxylase [Oryza sativa (japonica cultivar-group)]	fermentation	-0.8 (120 h)	1.4 (120 h)	I	3
lsuccinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]	TCA / org. transform.	*0.3 (24 h)*	0.6 (120 h)	III	3
stearoyl-acyl-carrier protein desaturase [Oryza sativa (japonica cultivar-group)]	lipid metabolism	-0.8 (120 h)	0.7 (120 h)	I	3
aspartate aminotransferase [Oryza sativa (japonica cultivar-group)]	amino acid metabolism	*-0.9 (120 h)*	1.3 (120 h)	III	3
dnaK-type molecular chaperone hsp70 [Oryza sativa (japonica cultivar-group)]	stress	*-1.3 (120 h)*	1.4 (120 h)	III	3
actin [Elaeis oleifera]	cell	*-1.3 (120 h)*	1.0 (120 h)	III	3
KH domain protein [Oryza sativa (japonica cultivar-group)]	RNA	-1.0 (24 h)	0.9 (48 h)	I	3
nucleoporin interacting component family protein [Arabidopsis thaliana]	protein	-1.1 (120 h)	3.8 (120 h)	I	3

7.4.4.1. Metabolism

Two proteins were involved in energy supply mechanisms, a **sorbitol dehydrogenase** (SDH) and a **pyruvate decarboxylase** (PDC). Sorbitol like sucrose is translocated into sink tissues such as apples, peach, prunes and pears and transformed to fructose by SDH. In water-stressed apple trees it is known that the biosynthesis of sorbitol is prioritized over starch because of its osmotic influence to adjust sink-source relations (Naschitz et al., 2010). Nevertheless, sorbitol is not a research issue in barley so far. The downregulation of SDH at transcript level could be explained by the plant's attempt to hinder the conversion of sorbitol into hexoses that can be taken up by *Bgh*. The fungus might post-transcriptionally enhance the expression of this enzyme because of its continuing need for nutrients or to enhance the sink capacity of infected cells. This hypothesis could be supported by the fact, that the downregulation at transcript level is occurring firstly, whereas the upregulation at protein level is following, suggesting that the fungus is reacting on the plant's transcript downregulation.

The enzyme **pyruvate decarboxylase** (PDC) decarboxylates pyruvic acid to acetaldehyde and CO_2 and is categorized into the SuperBIN "fermentation". Recently there has been growing evidence that fermentation processes are important in biotic interactions for enhancing metabolic capacity (Pathuri et al., 2011). Fermentation as well as glycolysis and respiration is upregulated at penetration sites of powdery mildew in *A.thaliana*, and the regulation of another fermentation enzyme, namely alcohol dehydrogenase 1 is connected with successful penetration of *Bgh* in barley (Pathuri et al., 2011). It is possible that fermentation is more likely to happen because the pathogen acquires nutrients (Chandran et al., 2010, Wildermuth, 2010). PDC is discussed as being involved in hypoxia, and these metabolic changes may help the cell to generate ATP anaerobically for survival, preventing cell death (Drew, 1997, Licausi et al., 2010). More interesting in this context is the fact that PDC was not found in the proteome of *Bgh* (Godfrey et al., 2009). As fermentation and its enzymes play an important role for a successful infection and *Bgh* is not expressing PDC itself, it is likely that it depends on the enhanced expression of that enzyme by the plant.

Applying the above observed functional dependencies to the study, the downregulation at transcript level may point to the plant's effort to block the fermentation pathway, whereas the fungus post-transcriptionally enhances PDC expression to maintain nutrients and prevent cell death. But it has to be mentioned here that another protein spot identified as PDC was downregulated at transcript and at protein level, both significantly (see Table 14), suggesting that the pathogen is only modifying one of the isoforms. The hypothesis that the fungus is enhancing fermentation cannot be supported by results from other fermentation enzymes,

because they were not evident in the examined protein spots and acetaldehyde is an intermediate involved in many pathways.

More rewarding to discuss is the regulation pattern of the **stearoyl-acyl-carrier protein desaturase** (S-ACP-DES), that was significantly downregulated at transcript level and upregulated at protein level. This enzyme reduces ACP-bound saturated fatty acids (FA) into monounsaturated FAs such as oleic acid (18:1), which is one of the major monounsaturated FA of membrane glycerolipids and is required to build up waxes for the cuticle. An intact cuticle is shown to be required to the induction of SAR, and mutants in ACP (acp4) are impaired not only in the cuticular wax and cutin formation, but also in the recognition of SAR signalling (Xia et al., 2009). The production of the antifungal polyketides is also linked to the metabolism of fatty acids through ACP. Changes in the amount of oleic acid alter the JA- and SA-mediated defence response, which are cross-talking to each other in an antagonistic manner. This is why FA-derived signalling has started to emerge as one of the important defence pathways (Kachroo et al., 2001, Weber, 2002, Singh et al., 2011).

The protein investigated in this study shows a high homology to the *A.thaliana* SSI2 (suppressor of SA insensitivity 2). Besides SA, the S-ACP-DES-defective mutant ssi2 accumulates high levels of stearic acid (18:0) and low level of oleic acid (18:1). The low level of oleic acids enhances the expression of multiple PR-genes, cell death and resistance to multiple pathogens like bacteria and oomycetes in Arabidopsis, rice and soybean, which can be restored by the restoration of oleic acid level in the mutant (Kachroo et al., 2004, Kachroo et al., 2007, Kachroo et al., 2008, Jiang et al., 2009). This shows that SSI2 is important as a negative regulator of defence responses through the induction of SA-responsive genes, including several WRKY factors (Jiang et al., 2009, Gao et al., 2011). Therefore, the downregulation of the S-ACP-DES level found in this study might help the plant's defence reaction through a subsequent rise of PR-proteins and of cell death. The fungus, potentially co-opting this susceptibility protein through post-transcriptional stabilization might thus reduce host plant defence.

7.4.4.2. Nucleo-cytoplasmatic transport

Also to be discussed is the highly relevant **nucleoporin-interacting component protein** (NiC). The nucleoporin complex (NPC) is a macromolecular assembly of protein subcomplexes formed of multiple copies of around 30 proteins (Cronshaw et al., 2002). The NPC consists of two coaxial ring-like structures on the nuclear and cytoplasmic sides and the central core. NPCs mediate bidirectional molecular trafficking of fully folded proteins, RNA, large ribonucleoprotein particle complexes and small molecules between the nucleoplasm and the cytoplasm which is an energy-consuming process mediated by RanGTP (Xu and

Meier, 2008, Meier and Brkljacic, 2009) (see Figure 41). The nucleoporin-interacting protein investigated in this study is homologous to the Nup93 protein in human and yeast. According to immunolocalization studies Nup93 as well as Nip96 are found symmetrically situated on both sides deep in the NPC core, as part of the central spoke-ring complex (Rout et al., 2000, Krull et al., 2004). Nup93 is not vital for the formation of the NPC, but is important for the long-term maintenance and stability (Krull et al., 2004). Nuclear import of proteins is an essential step in regulating gene expression and its importance for defence response has recently been becoming evident, as discussed in the following paragraph.

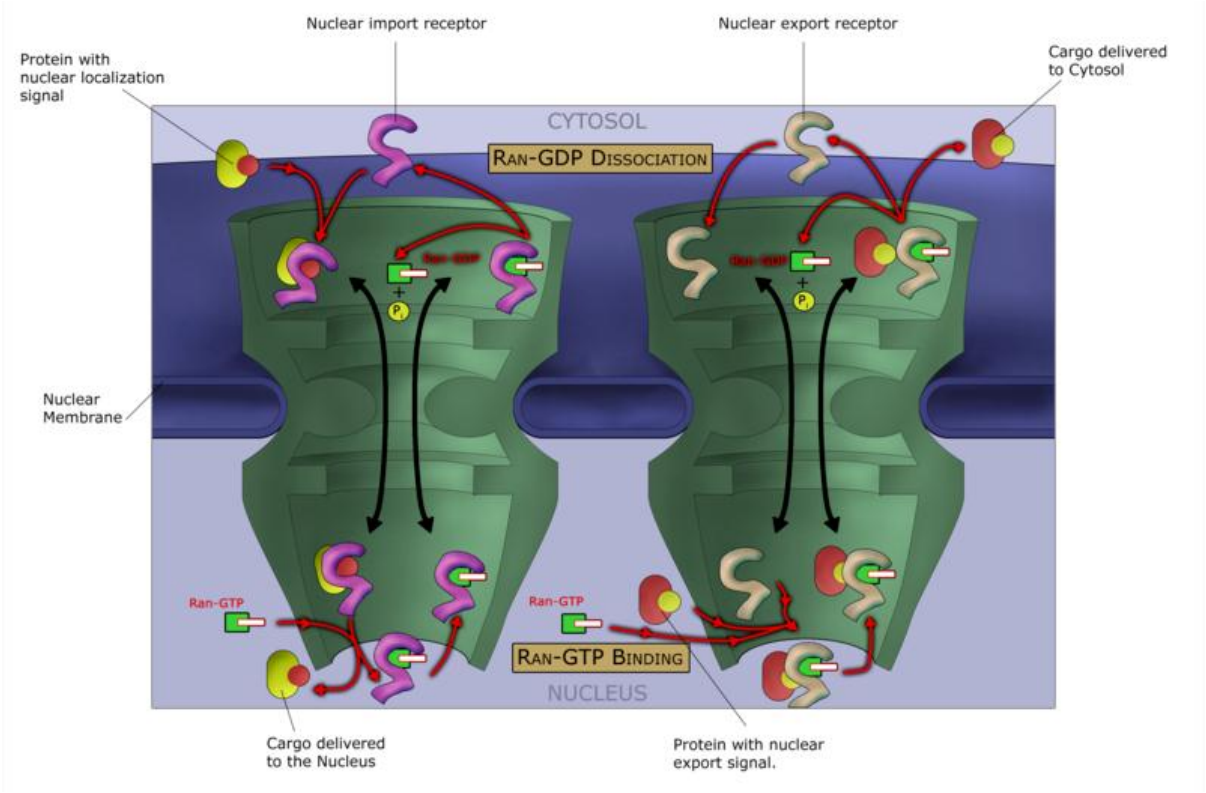


Figure 41: The nucleoporin complex and its regulation. The nucleoporin complex lies in the nuclear membrane, translocation of cargo is regulated and mediated by receptors, activated by nuclear transport proteins. On the left side the mechanism for import, on the right side for the export is shown. Picture is taken from http://commons.wikimedia.org/wiki/File:Cicle_de_la_Ran-GTP.PNG.

The recognition of effectors by R-proteins and their ensuing activation by conformational changes take place in the cytoplasm, but the R-proteins target host transcription in the nucleus. Therefore dynamic import into the nucleus is important for initiating defence (Tameling et al., 2010), and nucleo-cytoplasmic distribution of R-proteins as well as their effectors are important for plant defence (Burch-Smith et al., 2007, Shen et al., 2007). As an example for a resistant barley-*Bgh* interaction mediated by Mla, the localization of Mla into the nucleus is required for the proper function of ETI (Shen et al., 2007). There, the Mla interacts with the transcription factors HvWRKY1and HvWRKY2 and suppresses their repressor activity on expression of defence (Shen et al., 2007). Transcriptional

reprogramming of the plant cell mediated by antagonizing members of plant-specific WRKY transcription factors arrests pathogen growth during innate immune response (Eulgem and Somssich, 2007). The diffusion of molecules over 60kD into the nucleus is not possible (Gasiorowski and Dean, 2003). Because of their mass, R-proteins can only enter the nucleus via NPC-mediated transport. The anti-parallel regulation of NiC (Nup93-analogue) in this study has two possible explanations. Either the fungus silenced the transcription of the mRNA to suppress the expression of NiC and the plant neutralised this suppression by post-translational modifications. This would be the case, if defence-enhancing mechanisms were "switched on". This is feasible, as it is known that R-proteins are transported via NPCs into the nucleus (Tameling et al., 2010), regulating transcription factors directly there (Burch-Smith et al., 2007, Shen et al., 2007). The other possibility is that the plant downregulated the transcription of the NiC-mRNA and the fungus is co-opting and stabilizing protein expression post-transcriptionally, in order to stimulate the import of defence-suppressing plant or fungal proteins, which is also possible due to the deep impact of the infection on regulation changes of the plant. Whichever explanation is the correct one and whichever cargos are transported, the GATA transcription factor mentioned in chapter 7.3.3 might be targeted in the nucleus, since it is similarly regulated as the NiC at protein level. A KH domain protein, discussed in the next paragraph might also be targeted due to the same regulation pattern. To answer the question about the transported proteins and the subsequent effects, mutants in NiC would have to be investigated in order to find out if these plants are more susceptible or more resistant to *Bgh*. Additionally, immunolocalization studies could find out which proteins are transported and which transcription factors are targeted by these transported proteins.

A potential nucleus-localized protein is a **KH domain protein** showing the same regulation pattern as the NiC at transcript and at protein level. The KH domains are present in a wide variety of nucleic-acid-binding proteins and specific targets cannot be suggested so far. Amino acid sequence on subcellular localization signals using LOCtree (Nair and Rost, 2005) at www.predictprotein.org predicts nuclear localization of the protein with a high reliability (6 out of 10). Also LOCkey used at the same homepage mentioned above predicts this protein to be localized in the nucleus by 90%. The similar regulation pattern and nuclear localisation signals in the sequnce may give a hint, that the KH domain protein is targeted by proteins transported via a NiC-containing NPC.

Another interesting protein with an anti-parallel regulation is the **dnaK-type molecular chaperone HSP70**. HSP70s are members of a ubiquitous protein family that is highly conserved across all domains of life (Gupta and Golding, 1993). The expression of HSP70 family members is regulated by developmental and environmental stimuli (Lin et al., 2001).

Cytoplasmic proteins that are transported through the NPC show conformational changes before being translocated. In *Arabidopsis*, 14 out of 18 members of HSP70 belong to the dnaK-type ones and they are said to have roles in the transport of proteins across membranes into organelles, the folding of newly translated proteins, and the rescue of misfolded proteins (Lin et al., 2001, Aoki et al., 2002, Mayer and Bukau, 2005). However, it is not possible to distinguish among dnaK-type paralogs due to their high similarity in amino acid sequence. Because of the similar regulation pattern, it could be discussed that the dnaK-type molecular chaperone HSP70 found in this study may be involved in the re-folding step before the NPC-mediated transport as well as in the transport itself. Besides upregulation by heat stress, certain HSP70s are upregulated in barley-*Bgh* and barley-*Piriformospora indica* interaction (Hartl and Hayer-Hartl, 2002, Mayer and Bukau, 2005, Molitor, 2009). As the family of HSP70s is complex, more specific studies would need to be done for that special dnaK-type chaperone. For example, at 12 h.a.i., the transcript level was upregulated, then rapidly declining during the infection process (a pattern observed only in very few proteins) in contrast to the protein level, which gradually rised during the course of the infection. The biological reference of this complex partly anti-parallel mode of transcriptome and protein regulation is currently not clear.

7.4.5. Summary of the comparative matching

If post-transcriptional and post-translational modulations occur in an organism, they can only be detected by comparing the changes of transcript levels together with those at protein levels. Through this comparison parallel and anti-parallel regulations are identified within transcript-protein pairs.

In the detected parallel upregulated transcript-protein pairs, many known stress-related genes were found with high amplitudes of regulation. Many enzymes within this group were involved in the TCA cycle. Regarding the transcript-protein pairs which were parallel downregulated, known stress-related proteins and enzymes for cell-wall conversion were detected.

Due to the different time points analysed in this study it is evident that for some parallel regulated transcript-protein pairs the change in protein preceded a change in transcript, leading to the hypothesis that a basal level of “resting”, non-translated transcript might be present allowing faster response of the cell to infection.

Transcript-protein pairs that were regulated in an anti-parallel manner were most likely involved in post-translational modification. Members of these categories were found to be involved in a range of biological functions.

Pairs that were upregulated at transcript and downregulated at protein level are few. Two of them are a peroxidase 10 and a GAP. This might reflect one way in which the fungus suppresses the plant's defence at the protein level. The transcript-proteins pairs that were downregulated at transcript level and upregulated at protein level are likely to be post-transcriptionally or post-translationally modulated by the fungus co-opting susceptibility proteins. This is conceivable in the case of PDC and S-ACP-DES, as the upregulation is likely to be involved in acquiring nutrients and suppressing cell death and PDC is not present in the fungus. In the case of NiC, one possible scenario is that an upregulation is contraproductive for the fungal development, as R-protein transport into the nucleus triggers defence responses by activating transcription factors. In this case, the fungus would have silenced the gene while the plant stabilized the protein. Another possible interpretation is that the fungus is highjacking the nucleo-cytoplasmic transport mechanism to insert into nucleus regulation factors of its own or of the plant that are beneficial to itself. In this way it could manipulate the plant's defence directly in the nucleus. To achieve this, components of the nuclear pore complex are stabilized despite downregulation of corresponding transcripts by the plant. Possible targets in the nucleus might be transcriptional factors such as the KH domain protein or the GATA transcription factor. Unfortunately no transcriptional data were available for the latter. It is worth mentioning that a dnaK-type molecular chaperone HSP70, which is probably necessary for nucleo-cytoplasmic transport, was also regulated significantly at protein level in the same way as the KH domain protein and the NiC. Thus a range of proteins involved in nucleo-cytoplasmic transport appeared to be regulated in a similar way.

As protein modifications induced by the fungus are likely triggers for susceptibility, it is important not to investigate changes only at the transcriptome, but additionally at the proteome level in order to obtain a more complete picture of *Bgh*-induced modifications, which is the most innovative aspect of this approach. Furthermore, to investigate transient regulations the measurement of different time points is mandatory. A significant advancement in this field of study was the discovery of anti-parallel trends which were only revealed through the combination of the data of both –omes.

8. Outlook

This study having investigated the correlation of transcript and protein regulation at different time points during *Bgh* infection, the next step would be to deduce experiments to deeper understand the functions or targets of the respective proteins.

8.1. More detailed analyses

- Investigation of modification for those proteins that appear in more than one spot such as HvGER2a.

- Profiling of additional time points to validate or to find transient effects, e.g. for the dnaK-type molecular chaperone HSP70.

- Generate transcript data by RT-PCR of interesting proteins that are not represented on the array, such as the GATA transcription factor, in order to find out if the transcript is also regulated in a parallel or anti-parallel manner.

- Confirmation of the transcript data for interesting candidates of the array studies by real time-PCR.

- Full-length sequencing of interesting candidates in order to describe potential protein modification sites (phosphorylations; difference between NiC and other NUPs).

- Analysis of dissected epidermal cells infected by *Bgh* that are absolutely free of mesophyll cells to exclude contamination effects.

- Injection of fungal extracts into the plant e.g. into the phloem to dilute epidermis-specific recognition-followed effects vs. unspecific effects in order to dilute epidermis-specific from non-tissue-specific effects.

- Application of fungal elicitors (PAMPs) in order to dilute elicitor-triggered plant effects from effects caused by nutrient stresses caused by the fungus' nutrient uptake.

8.2. Functional experiments

- Elucidation of the specific targets and the functionality of pairs which are regulated in an anti-parallel manner (e.g. GAD, KH-domain containing protein, dnaK-type molecular chaperone HSP70).

- Further investigation of the functionality of dnaK-type molecular chaperone HSP70, especially due to transient transcription.

- Finding the cargo and the functionality of the NiC in immunoassays or by tagged client proteins.

- TIGS for certain interesting genes e.g. the NiC.

- Investigation of differences in transcript and protein regulation pattern compared with *Rhynchosporium secalis* in order to dilute regulations to pathogens of different life styles.

- In general for the pairs responsible for the highest regulation events: search of publicly available TILLING (Targeting Induced Local Lesions in Genomes) mutants, establish transient or stable gene silencing and overexpression studies in order to find out if altered expression leads to enhanced or diminished susceptibility. This could answer the question whether such changes are connected with the plant's susceptibility or basal incomplete resistance to the fungus.

9. Literature

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10. Appendix

Table 16: Chlorophyll content of epidermis samples: The chlorophyll content (chl. content) of the epidermis samples were calculated acc. to (Lichtenthaler, 1987). “Econt” are the non-infected, “E*Bgh*” the infected epidermis samples. “I”, “II” and “III” stands for 1st, 2nd and 3rd harvest. The relative chlorophyll content (rel. chl. content) was calculated by comparing the measurements by the average content of control and infected leaf samples 24 h.a.i. (Lcont 24h and L*Bgh* 24h, respectively).

Sample	645nm	662nm	chl. content	rel. chl. content
ECont I 12h	0.014	0.027	0.44	3%
ECont II 12h	0.028	0.044	0.82	5%
ECont III 12h	0.019	0.028	0.54	4%
ECont I 24h	0.026	0.063	0.91	6%
ECont II 24h	0.02	0.037	0.62	4%
ECont III 24h	0.025	0.045	0.77	5%
ECont I 48h	0.015	0.026	0.45	3%
ECont II 48h	0.022	0.037	0.66	4%
ECont III 48h	0.023	0.038	0.68	5%
ECont I 72h	0.021	0.037	0.64	4%
ECont II 72h	0.018	0.035	0.57	4%
ECont III 72h	0.015	0.031	0.49	3%
ECont I 120h	0.019	0.033	0.58	4%
ECont II 120h	0.022	0.037	0.66	4%
ECont III 120h	0.013	0.028	0.43	3%
E*Bgh* I 12h	0.018	0.033	0.56	4%
E*Bgh* II 12h	0.011	0.027	0.39	3%
E*Bgh* III 12h	0.016	0.029	0.49	3%
E*Bgh* I 24h	0.015	0.022	0.43	3%
E*Bgh* II 24h	0.026	0.036	0.72	5%
E*Bgh* III 24h	0.017	0.034	0.55	4%
E*Bgh* I 48h	0.015	0.029	0.48	3%
E*Bgh* II 48h	0.014	0.032	0.48	3%
E*Bgh* III 48h	0.014	0.033	0.49	3%
E*Bgh* I 72h	0.022	0.042	0.69	5%
E*Bgh* II 72h	0.02	0.036	0.62	4%
E*Bgh* III 72h	0.016	0.033	0.52	3%
E*Bgh* I 120h	0.02	0.044	0.67	4%
E*Bgh* II 120h	0.018	0.029	0.53	4%
E*Bgh* III 120h	0.012	0.024	0.39	3%
Average epidermis	0.02	0.03	0.58	4%
Lcont 24h	0.441	1.155	16.12	107%
L*Bgh* 24h	0.383	0.993	13.93	93%
Average leaf	0.41	1.07	15.02	100%

Table 17: Exposure time and signal intensities of A-Membranes of the PGRC2-13k-cDNA-macroarray. Control: non-infected samples; Infected: samples infected with *Bgh*. 1, 2, 3 are the number of the biological replicates (harvests). The upper row shows the time points after inoculation.

	12h	24h	48h	72h	120h
Exposure time	7d	10d	6d	10d	8d
Control 1	3323.9	4107.1	1978.2	1365.5	3955.3
Control 2	2336.5	3966.4	1649.5	164.6	4108.4
Control 3	3408.9	4071.3	3764.3	560.2	4049.4
Infected 1	2799.7	3921.5	3676.3	850.8	3823.0
Infected 2	3196.2	2583.2	204.3	206.7	2068.2
Infected 3	2117.8	3974.5	1477.5	434.7	3968.9

Table 18: Correlation of biological replicates of the PGRC-13k-cDNA-macroarray. Control: non-infected samples; Infected: samples infected with *Bgh*. 1, 2, 3 are the number of the biological replicates (harvests). The upper row shows the time points after inoculation.

	12h	24h	48h	72h	120h
Control 1-2	0.951	0.938	0.955	0.776	0.884
Control 3-1	0.967	0.929	0.930	0.895	0.900
Control 2-3	0.940	0.974	0.952	0.852	0.948
Infected 1-2	0.884	0.965	----	0.924	0.928
Infected 3-1	0.932	0.914	0.912	0.948	0.736
Infected 2-3	0.909	0.916	----	0.910	0.760

Table 19: Significantly regulated transcripts, sorted by their biological classification: Regulation (Infected/control) is shown after log_2-transformation for the epidermal samples at the five time points, followed by the false discovery rate level (q-value). The next column shows the putative function and the biological category (Binning). The E/M-value shows if the particular transcript is enriched in the epidermis (E/M>1), in the mesophyll (E/M<-1) or uniformly distributed or could not be defined (#NV). The text in the columns "putative function" and "binning" is cut to limit the use of more pages.

Clone-ID	12h.a.i.	24h.a.i.	48h.a.i.	72h.a.i.	120h.a.i	q-value	Putative function	Binning	E/M
HO19N07	-0.20	**-2.06**	-1.21	-1.22	-0.78	0.012	chlorophyll a/b binding protein	1.01.01.01 PS.lightreaction.photosyste	-0.94
HO01D09	-0.13	**-2.33**	-0.75	-1.25	-0.71	0.014	Chlorophyll a-b binding protein 3C, chloroplast precursor (LHCII type I CAB-	1.01.01.01_PS.lightreaction.photosyste	-1.05
GCA003J	-0.03	**-2.03**	-0.45	-0.33	-0.66	0.028	Unknown (protein for IMAGE:5194336) [Homo sapiens]	1.01.01.01_PS.lightreaction.photosyste	-0.94
HP11K05	-0.27	**-1.36**	-0.33	-0.92	0.04	0.025	light-harvesting complex IIa protein;	1.01.01.01 PS.lightreaction.photosyste	-2.26
HO12D09	-0.49	**-1.68**	-0.20	-0.98	0.04	0.019	light-harvesting complex IIa protein;	1.01.01.01_PS.lightreaction.photosyste	-1.78
HB21N18	-0.36	**-1.97**	-0.69	-1.21	-0.88	0.012	chlorophyll a/b binding protein [Oryza sativa (japonica cultivar-group)]	1.01.01.01 PS.lightreaction.photosyste	-1.85
HO05I21	-0.55	**-2.08**	-0.40	-1.02	-0.20	0.017	chlorophyll a/b binding protein 2	1.01.01.01_PS.lightreaction.photosyste	-1.94
HE01E12	-0.14	**-2.00**	-0.76	-1.10	-0.63	0.013	chlorophyll a/b binding protein 2	1.01.01.01_PS.lightreaction.photosyste	-1.95
HP02O06	-0.27	**-2.70**	-0.66	-1.32	-0.62	0.023	chlorophyll a/b-binding protein WCAB precursor [Triticum aestivum]	1.01.01.01 PS.lightreaction.photosyste	-1.82
HP01F10	0.37	**-1.24**	-0.72	-0.29	-0.87	0.037	chlorophyll a/b binding protein	1.01.01.01_PS.lightreaction.photosyste	0.01
HP01G12	-0.20	**-2.07**	0.04	-0.63	-0.46	0.043	chlorophyll a/b-binding protein WCAB precursor [Triticum aestivum]	1.01.01.01_PS.lightreaction.photosyste	-1.07
GCA003B	-0.28	**-2.90**	-0.50	-1.08	-0.81	0.027	chlorophyll a/b-binding protein WCAB precursor [Triticum aestivum]	1.01.01.01_PS.lightreaction.photosyste	-1.46
HP01O18	-0.27	**-1.86**	-0.48	-0.15	-0.54	0.032	chlorophyll a/b binding protein precursor [Zea mays] Chlorophyll a-b binding	1.01.01.01_PS.lightreaction.photosyste	-1.78
HY06K22	0.03	-0.81	-0.38	-0.20	**-1.02**	0.023	Precursor of CP29, core chlorophyll a/b binding (CAB) protein of	1.01.01.01_PS.lightreaction.photosyste	#NV
HO28H16	-0.29	**-2.31**	-0.48	-1.01	-0.31	0.029	chlorophyll a/b-binding protein WCAB precursor [Triticum aestivum]	1.01.01.01_PS.lightreaction.photosyste	-1.81
HE01N10	-0.38	**-1.98**	-0.63	-1.02	-0.70	0.020	chlorophyll a/b binding protein	1.01.01.01 PS.lightreaction.photosyste	-2.00
HA10D16	-0.54	**-1.26**	-0.10	-0.82	0.15	0.039	chlorophyll a/b-binding protein WCAB precursor [Triticum aestivum]	1.01.01.01_PS.lightreaction.photosyste	-1.71
HA04F09	-0.48	**-1.41**	-0.34	-0.77	-0.87	0.012	chlorophyll a/b binding protein	1.01.01.01 PS.lightreaction.photosyste	-0.87
HY02B02	-0.39	-1.15	-0.63	**-1.20**	-0.69	0.012	Unknown (protein for IMAGE:5194336) [Homo sapiens]	1.01.01.01_PS.lightreaction.photosyste	-0.82
HE01L05	-0.43	**-2.00**	-0.62	-1.15	-0.79	0.014	Unknown (protein for IMAGE:5194336) [Homo sapiens]	1.01.01.01_PS.lightreaction.photosyste	-1.92
GCA004C	-0.21	**-2.34**	-0.71	-1.06	-0.11	0.037	Unknown (protein for IMAGE:5194336) [Homo sapiens]	1.01.01.01 PS.lightreaction.photosyste	-1.24
HG01I24	-0.50	**-1.71**	-0.59	-1.26	-0.74	0.015	chlorophyll a/b-binding protein WCAB precursor [Triticum aestivum]	1.01.01.01_PS.lightreaction.photosyste	-1.46
HA14H03	-0.58	**-1.76**	-0.66	-1.07	-0.49	0.016	LHCII type I protein [Hordeum vulgare subsp. vulgare]	1.01.01.01_PS.lightreaction.photosyste	-1.70
HE01A14	-0.12	-1.04	-0.45	**-1.16**	0.53	0.036	putative photosystem II 10K protein [Oryza sativa (japonica cultivar-group)]	1.01.01.02_PS.lightreaction.photosyste	-2.56
GCA004B	-0.08	**-1.36**	-0.37	-1.06	0.42	0.033	putative photosystem II 10K protein [Oryza sativa (japonica cultivar-group)]	1.01.01.02_PS.lightreaction.photosyste	-2.32
HDP07F0	-0.23	**-1.51**	-0.56	-0.72	-0.85	0.012	unknown protein [Arabidopsis thaliana] unknown protein [Arabidopsis	1.01.01.02_PS.lightreaction.photosyste	-2.71
HZ51K03	-0.05	**-1.14**	-0.28	-0.54	0.15	0.047	putative photosystem II protein reaction center W [Oryza sativa (japonica	1.01.01.02_PS.lightreaction.photosyste	-2.00
HO13J20	-0.27	**-1.15**	0.01	-0.52	-0.12	0.038	putative 33kDa oxygen evolvingprotein of photosystem II [Oryza sativa	1.01.01.02 PS.lightreaction.photosyste	-2.19
HO25L12	-0.27	**-1.33**	0.01	-0.46	-0.17	0.031	putative 33kDa oxygen evolvingprotein of photosystem II [Oryza sativa	1.01.01.02_PS.lightreaction.photosyste	-2.20
HY05D21	-0.20	**-1.71**	-0.11	-0.53	-0.10	0.045	putative 33kDa oxygen evolvingprotein of photosystem II [Oryza sativa	1.01.01.02_PS.lightreaction.photosyste	-2.86
GBN005P	-0.29	**-1.19**	-0.28	-0.10	-0.99	0.019	paf93 [Hordeum vulgare subsp. vulgare]	1.01.01.02 PS.lightreaction.photosyste	-2.74
HO02J19	-0.08	**-1.08**	-0.79	-0.51	0.22	0.026	chlorophyll a/b binding protein precursor [Hordeum vulgare]	1.01.02.01_PS.lightreaction.photosyste	-1.54
HM02D24	-0.44	**-1.63**	-0.39	-0.63	0.22	0.032	chlorophyll a/b binding protein precursor [Hordeum vulgare]	1.01.02.01 PS.lightreaction.photosyste	-2.72
HM11H23	-0.34	**-1.68**	-0.38	-0.93	-0.98	0.011	LHCI-680, photosystem I antenna protein [Hordeum vulgare subsp. vulgare]	1.01.02.01_PS.lightreaction.photosyste	-2.63
HK03H10	-0.41	**-1.73**	-0.03	-1.41	-0.78	0.013	LHCI-680, photosystem I antenna protein [Hordeum vulgare subsp. vulgare]	1.01.02.01_PS.lightreaction.photosyste	-3.29
HZ48I22	-0.07	**-1.99**	-0.27	-0.71	-0.77	0.020	LHCI-680, photosystem I antenna protein [Hordeum vulgare subsp. vulgare]	1.01.02.01_PS.lightreaction.photosyste	-3.15
HY04K14	-0.29	**-1.33**	-0.59	-0.70	-0.66	0.011	PREDICTED OJ1524_D08.28	1.01.02.01_PS.lightreaction.photosyste	-2.64
HM01O24	-0.23	**-1.45**	-0.26	-0.96	-0.64	0.022	Unknown (protein for IMAGE:5194336) [Homo sapiens]	1.01.02.02 PS.lightreaction.photosyste	-1.12
HA05K09	-0.28	**-2.43**	-0.51	-0.98	0.07	0.029	OJ991214_12.3 [Oryza sativa (japonica cultivar-group)] OJ991214_12.3	1.01.02.02_PS.lightreaction.photosyste	-3.76

HY09K19	-0.57	**-2.43**	-0.36	-0.95	-0.05	0.026	OJ991214 12.3 [Oryza sativa (japonica cultivar-group)] OJ991214 12.3	1.01.02.02 PS.lightreaction.photosyste	-4.15
HP08H05	-0.18	**-1.12**	0.02	-0.67	-0.71	0.017	photosystem I polypeptide PSI-G precursor [Hordeum vulgare] photosystem	1.01.02.02_PS.lightreaction.photosyste	-1.94
HO07N12	-0.03	**-1.22**	-0.43	-0.42	-0.63	0.025	putative Rieske Fe-S precursor protein [Triticum aestivum] Cytochrome b6-f	1.01.03_PS.lightreaction.cytochrome	-2.90
HK05G04	-0.58	**-1.12**	-0.01	-0.67	-0.42	0.021	putative Rieske Fe-S precursor protein [Triticum aestivum] Cytochrome b6-f	1.01.03 PS.lightreaction.cytochrome	-3.24
HM02O10	-0.18	**-1.24**	-0.16	-0.50	0.15	0.039	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	1.01.03_PS.lightreaction.cytochrome	-2.90
HY10N24	-0.21	**-1.13**	-0.49	-0.45	-0.43	0.021	putative ATP synthase gamma chain 1, chloroplast (H(+)-transporting two-	1.01.04 PS.lightreaction.ATP synthase	-2.61
HA30I17	-0.42	-0.84	-0.73	-0.96	**-1.15**	0.013	plastocyanin precursor - barley	1.01.05.01_PS.lightreaction.other	-1.32
HZ39G18	-0.01	**-1.28**	-0.47	-1.02	-0.11	0.026	ferredoxin [Triticum aestivum] Ferredoxin, chloroplast precursor	1.01.05.02_PS.lightreaction.other	-2.66
GBN006G	-0.15	**-1.10**	-0.05	-0.36	-0.35	0.031	2Fe-2S iron-sulfur cluster protein-like [Oryza sativa (japonica cultivar-group)]	1.01.05.02_PS.lightreaction.other	-1.97
HO12K19	-0.18	**-1.23**	-0.26	-0.88	-0.11	0.025	ferredoxin-NADP(H) oxidoreductase [Triticum aestivum]	1.01.05.03_PS.lightreaction.other	-2.78
HG01J16	-0.53	**-2.20**	-0.59	-1.33	-0.58	0.017	glycolate oxidase [Oryza sativa]	1.02.02 PS.photorespiration.glycolate	-2.23
HO37J09	-0.31	**-1.68**	-0.08	-1.07	-0.79	0.014	glycolate oxidase [Oryza sativa]	1.02.02_PS.photorespiration.glycolate	-1.73
HK03J04	0.21	**-1.25**	-0.48	-0.53	-0.48	0.032	putative glycolate oxidase [Oryza sativa (japonica cultivar-group)]	1.02.02 PS.photorespiration.glycolate	-3.20
HM03F02	-0.33	**-1.87**	-0.29	-0.90	0.32	0.033	putative glycine decarboxylase subunit [Triticum aestivum]	1.02.04_PS.photorespiration.glycine	-3.40
HY06J04	-0.56	-0.70	-0.69	**-1.06**	-0.85	0.009	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	1.03.01_PS.calvin cyle.rubisco large	-0.13
HY01G14	0.11	-0.16	-0.28	-0.75	**-1.23**	0.037	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	1.03.01 PS.calvin cyle.rubisco large	-0.01
GBN002E	-0.54	**-2.25**	-0.63	-0.81	-0.33	0.017	O-methyltransferase [Oryza sativa (japonica cultivar-group)]	1.03.02_PS.calvin cyle.rubisco small	-3.53
HO22I16	-0.19	**-1.13**	-0.44	-0.57	-0.48	0.026	putative rubisco small subunit [Triticum turgidum subsp. durum]	1.03.02_PS.calvin cyle.rubisco small	-2.06
HO04E03	-0.36	**-1.18**	-0.68	-0.75	-0.43	0.021	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit [Triticum	1.03.02_PS.calvin cyle.rubisco small	-1.91
HO05I23	-0.45	**-1.51**	0.09	-0.84	-0.55	0.019	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit [Triticum	1.03.02_PS.calvin cyle.rubisco small	-1.90
HY07K23	0.00	-0.66	-0.08	**-1.31**	-0.62	0.022	hypothetical protein [Secale cereale]	1.03.02_PS.calvin cyle.rubisco small	-1.98
HO05F14	0.09	**-1.09**	-0.65	-0.41	-0.07	0.031	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit [Triticum	1.03.02_PS.calvin cyle.rubisco small	-1.60
HO03F06	-0.45	**-1.20**	0.08	-0.70	-0.61	0.018	putative tetratricopeptide repeat (TPR)-containing protein [Oryza sativa	1.03.02 PS.calvin cyle.rubisco small	-2.05
HO05H18	-0.64	**-1.41**	-0.11	-0.59	-0.39	0.022	phosphoglycerate kinase [Triticum aestivum] unnamed protein product	1.03.03_PS.calvin	-2.88
HA12L17	-0.26	**-1.81**	0.04	-0.78	-0.54	0.022	phosphoglycerate kinase [Triticum aestivum] unnamed protein product	1.03.03 PS.calvin	-2.96
HY02K08	-0.33	**-1.39**	-0.46	-0.70	-0.31	0.017	corresponds to a region of the predicted gene.~similar to glyceraldehyde-3-	1.03.04_PS.calvin cyle.GAP	-2.67
HO05A22	0.07	-1.07	0.04	**-1.09**	0.13	0.040	G3PA_TOBAC Glyceraldehyde-3-phosphate dehydrogenase A, chloroplast	1.03.04_PS.calvin cyle.GAP	-2.08
HO01D01	-0.19	-1.05	-0.12	-0.59	**-1.55**	0.017	Putative inositol 1,3,4-trisphosphate 5/6-kinase [Oryza sativa (japonica	1.03.04 PS.calvin cyle.GAP	-1.42
HE01B07	-0.49	**-1.08**	-0.49	-0.72	-0.37	0.016	Fructose-bisphosphate aldolase class-I [Oryza sativa (japonica cultivar-	1.03.06_PS.calvin cyle.aldolase	-2.19
HO28H23	-0.34	**-1.64**	-0.47	-0.86	-0.74	0.013	Fructose-bisphosphate aldolase class-I [Oryza sativa (japonica cultivar-	1.03.06_PS.calvin cyle.aldolase	-2.76
GBN006G	-0.31	**-1.65**	-0.71	-0.60	-0.82	0.015	hypothetical protein [Arabidopsis thaliana] seven in absentia (SINA) family	1.03.06_PS.calvin cyle.aldolase	-3.34
HK04F06	-0.14	**-1.24**	-0.42	-0.19	0.07	0.049	fructose-bisphosphatase [Triticum aestivum] unnamed protein product	1.03.07_PS.calvin cyle.FBPase	-3.07
HO14L20	-0.16	**-1.55**	-0.15	-0.56	-0.36	0.023	sedoheptulose-1,7-bisphosphatase [Triticum aestivum] sedoheptulose-	1.03.09_PS.calvin cyle.seduheptulose	-2.64
HO02I17	-0.23	**-1.07**	-0.16	-0.32	-0.30	0.037	putative ribulose-5-phosphate-3-epimerase [Arabidopsis thaliana] putative	1.03.11_PS.calvin cyle.RPE	-2.43
HE01P01	-0.44	**-1.48**	-0.10	-0.67	-1.22	0.015	ribulose 1,5-bisphosphate carboxylase activase isoform 1 [Hordeum vulgare	1.03.13 PS.calvin cyle.rubisco	-2.10
HK03L13	-0.39	**-1.42**	-0.48	-0.77	-0.59	0.017	ribulose-bisphosphate carboxylase activase (EC 6.3.4.-) A long form	1.03.13_PS.calvin cyle.rubisco	-2.75
HO15I09	-0.10	**-1.48**	0.14	-0.70	-1.14	0.024	ribulose 1,5-bisphosphate carboxylase activase isoform 1 [Hordeum vulgare	1.03.13_PS.calvin cyle.rubisco	-2.25
HO03B18	-0.30	**-1.14**	-0.41	-0.80	-0.95	0.015	RUBISCO ACTIVASE :::ribulose 1,5-bisphosphate carboxylase activase	1.03.13 PS.calvin cyle.rubisco	-2.38
HO05A23	0.05	**-1.41**	-0.38	-0.68	-1.11	0.018	ribulose 1,5-bisphosphate carboxylase activase isoform 1 [Hordeum vulgare	1.03.13_PS.calvin cyle.rubisco	-2.12
HO05N10	0.02	**-1.32**	-0.35	-0.58	-1.19	0.018	ribulose 1,5-bisphosphate carboxylase activase isoform 1 [Hordeum vulgare	1.03.13 PS.calvin cyle.rubisco	-2.35
HD02D21	-0.50	-0.94	-0.61	**-1.14**	-0.84	0.008	sucrose-phosphate synthase [Triticum aestivum]	2.1.1.01_major CHO	-0.75
HO16J07	-0.25	-0.76	-0.28	-1.11	**-2.74**	0.015	sucrose-phosphate synthase 7 [Triticum aestivum]	2.1.1.01_major CHO	2.50
HO18K04	-0.24	**-1.62**	-0.79	-0.96	-0.32	0.015	fructose-1,6-bisphosphatase [Porteresia coarctata]	2.1.1.03_major CHO	-2.62
HM01N22	-0.01	-0.14	-0.28	-0.74	**-1.30**	0.024	fructose-1,6-bisphosphatase [Pisum sativum]	2.1.1.03_major CHO	-0.14
HU01I17	0.10	0.89	0.60	0.30	**1.29**	0.020	putative fructose-1,6-bisphosphatase [Oryza sativa (japonica cultivar-group)]	2.1.1.03 major CHO	1.83

HO18H23	-0.13	-1.05	-0.69	-0.40	**-1.73**	0.018	OSJNBa0053K19.19 [Oryza sativa (japonica cultivar-group)]	2.1.2.02 major CHO	-0.27
HV02L24	0.55	0.21	-0.25	-0.05	**1.45**	0.048	1,4-alpha-D-glucan 6-alpha-D-(1,4-alpha-D-glucanotransferase	2.1.2.03_major CHO	0.65
HA03P16	-0.40	**-1.66**	-0.19	-0.18	-0.08	0.033	85kDa isoamylase [Hordeum vulgare subsp. vulgare]	2.1.2.04_major CHO	-2.99
HM02P23	0.59	**1.06**	0.92	0.22	-0.03	0.030	invertase, putative [Oryza sativa (japonica cultivar-group)]	2.2.1.03.01 major CHO	-0.27
HO38O19	-0.40	**-1.30**	-0.01	-0.70	-0.85	0.018	OSJNBa0042I15.24 [Oryza sativa (japonica cultivar-group)]	2.2.1.03.01_major CHO	-2.30
HW02D08	-0.03	1.79	**1.89**	1.03	1.26	0.010	apoplastic invertase [Oryza sativa subsp. indica]	2.2.1.03.02 major CHO	-0.95
HW09G14	0.99	**1.25**	0.65	0.27	0.35	0.015	cell wall invertase [Saccharum hybrid cultivar]	2.2.1.03.02_major CHO	0.22
HW07B12	0.30	-0.14	0.05	-0.77	**-1.15**	0.039	vacuolar invertase [Triticum aestivum]	2.2.1.03.03_major CHO	2.27
HW02F11	-0.24	0.23	0.31	1.22	**4.06**	0.024	sucrose-sucrose-1-fructosyltransferase [Hordeum vulgare subsp. vulgare]	2.2.1.03.03_major CHO	-0.70
HW08M06	0.60	0.82	0.49	1.23	**3.29**	0.012	putative hexokinase 1 [Oryza sativa (japonica cultivar-group)]	2.2.1.04_major CHO	-0.83
HY10G10	-0.07	0.30	0.78	**1.64**	1.19	0.015	sucrose synthase [Hordeum vulgare subsp. vulgare] sucrose synthase (EC	2.2.1.05 major CHO	0.03
HY07L04	-0.10	0.22	0.40	**1.24**	0.99	0.026	sucrose synthase [Hordeum vulgare subsp. vulgare] sucrose synthase (EC	2.2.1.05_major CHO	0.67
HT01D06	-0.13	0.02	0.62	1.13	**1.29**	0.023	sucrose synthase [Hordeum vulgare subsp. vulgare] sucrose synthase (EC	2.2.1.05 major CHO	-0.13
HT01D06	0.00	0.24	1.17	0.71	**1.48**	0.023	sucrose synthase [Hordeum vulgare subsp. vulgare] sucrose synthase (EC	2.2.1.05_major CHO	-0.13
HY09O14	0.00	0.24	0.41	1.30	**1.40**	0.017	sucrose synthase [Hordeum vulgare] sucrose synthase (EC 2.4.1.13) -	2.2.1.05_major CHO	0.34
HO37G20	0.03	0.36	0.84	1.50	**1.66**	0.013	sucrose synthase [Hordeum vulgare subsp. vulgare] sucrose synthase (EC	2.2.1.05 major CHO	0.18
HY05O13	0.10	0.40	0.80	**1.41**	1.29	0.012	sucrose synthase [Hordeum vulgare] sucrose synthase (EC 2.4.1.13) -	2.2.1.05_major CHO	-0.14
HY07F09	-0.10	0.35	0.76	**1.94**	1.27	0.015	sucrose synthase [Hordeum vulgare] sucrose synthase (EC 2.4.1.13) -	2.2.1.05_major CHO	-0.05
HU03P12	-0.20	0.36	0.84	1.28	**1.28**	0.019	sucrose synthase [Bambusa oldhamii]	2.2.1.05_major CHO	0.12
HO05C07	0.33	0.45	1.12	1.49	**1.60**	0.009	sucrose synthase [Hordeum vulgare] sucrose synthase (EC 2.4.1.13) -	2.2.1.05_major CHO	0.12
HO15E10	-0.06	0.21	0.89	1.08	**1.47**	0.027	sucrose synthase [Hordeum vulgare] sucrose synthase (EC 2.4.1.13) -	2.2.1.05_major CHO	0.14
HY08B17	-0.01	0.21	0.36	0.30	**2.26**	0.039	putative high pI alpha-glucosidase [Oryza sativa (japonica cultivar-group)]	2.2.2.01_major CHO	0.06
HV13K13	-0.07	0.69	0.57	**1.16**	1.03	0.015	alpha-amylase	2.2.2.01 major CHO	-0.15
HY02A06	**1.32**	0.99	0.24	1.07	-0.20	0.020	high pI alpha-glucosidase [Hordeum vulgare]	2.2.2.01_major CHO	-0.07
HE01C20	-0.30	-0.77	-1.07	-0.87	**-1.65**	0.013	WSI76 protein induced by water stress [Oryza sativa (japonica cultivar-	3.1.1.01 minor CHO	3.32
HO01D06	-0.56	-0.68	-0.87	-1.20	**-2.17**	0.010	WSI76 protein induced by water stress [Oryza sativa (japonica cultivar-	3.1.1.01_minor CHO	3.11
HE01K13	-0.08	-0.88	-0.86	-1.18	**-2.18**	0.012	WSI76 protein induced by water stress [Oryza sativa (japonica cultivar-	3.1.1.01_minor CHO	2.73
HO05H07	-0.32	-0.78	-0.89	-1.27	**-1.76**	0.010	WSI76 protein induced by water stress [Oryza sativa (japonica cultivar-	3.1.1.01 minor CHO	2.35
HO11I05	-0.19	-0.71	-1.19	-1.34	**-1.99**	0.011	WSI76 protein induced by water stress [Oryza sativa (japonica cultivar-	3.1.1.01_minor CHO	3.18
HI04D20	-0.04	1.11	1.18	2.20	**3.54**	0.010	putative trehalose-6-phosphate phosphatase [Oryza sativa (japonica	3.2.2_minor CHO	#NV
HW06C09	-0.66	-0.31	0.67	2.60	**2.82**	0.034	trehalose-6-phosphate phosphatase [Oryza sativa (japonica cultivar-group)]	3.2.2_minor CHO	1.02
HP01D04	-0.17	**-2.07**	-0.26	-0.22	-0.31	0.039	putative trehalose-6-phosphate synthase [Oryza sativa (japonica cultivar-	3.2.3_minor CHO	-3.68
HO25G20	0.07	-0.28	-0.02	-0.49	**-1.03**	0.043	putative ribulokinase [Oryza sativa (japonica cultivar-group)]	3.3_minor CHO metabolism.sugar	-0.58
HA03L22	-0.04	-0.29	-0.15	-0.81	**-1.32**	0.019	putative ribulokinase [Oryza sativa (japonica cultivar-group)]	3.3_minor CHO metabolism.sugar	0.00
HO19I23	0.04	-0.70	-0.65	-0.50	**-1.08**	0.020	P0683B11.14 [Oryza sativa (japonica cultivar-group)]	3.4.01 minor CHO metabolism.myo-	1.44
HY08E09	-0.09	**-1.79**	-0.58	-0.11	-0.21	0.033	myo-inositol 1-phosphate synthase; INO1 [Hordeum vulgare] inositol-3-	3.4.03_minor CHO metabolism.myo-	-2.79
HM04H23	0.16	0.58	0.16	0.24	**1.39**	0.030	putative myo-inositol oxygenase [Oryza sativa (japonica cultivar-group)]	3.4.04_minor CHO metabolism.myo-	-0.69
HW08M04	0.20	0.83	-0.01	0.00	**1.63**	0.026	putative myo-inositol oxygenase [Oryza sativa (japonica cultivar-group)]	3.4.04 minor CHO metabolism.myo-	-1.44
HA02E14	-0.39	-0.55	-1.03	-0.96	**-1.68**	0.010	putative aldose reductase [Oryza sativa (japonica cultivar-group)] putative	3.5_minor CHO metabolism.others	1.40
HO10F17	-0.25	-0.64	-0.46	-1.17	**-2.17**	0.012	OSJNBa0041A02.19 [Oryza sativa (japonica cultivar-group)]	3.5 minor CHO metabolism.others	0.97
HW07H17	0.09	0.84	0.39	**1.01**	0.80	0.017	extracellular invertase; beta-fructofuranosidase [Triticum monococcum]	3.5_minor CHO metabolism.others	-0.61
HW08G11	1.37	**3.35**	1.86	2.30	3.06	0.002	OSJNBa0036B21.19 [Oryza sativa (japonica cultivar-group)]	3.5_minor CHO metabolism.others	0.43
HW01H17	-0.33	-0.83	-1.21	-1.19	**-2.07**	0.010	putative beta-fructofuranosidase [Oryza sativa (japonica cultivar-group)]	3.5_minor CHO metabolism.others	1.22
HU04B24	-0.10	-0.89	-0.30	-0.75	**-1.57**	0.013	phosphoglucomutase [Triticum aestivum]	4.02_glycolysis.PGM	-1.39
HY05I13	0.12	-1.00	-0.65	-0.58	**-1.18**	0.015	phosphoglucomutase [Triticum aestivum]	4.02 glycolysis.PGM	-1.20

HB28K22	-0.08	-0.54	-0.31	-0.55	**-1.16**	0.018	putative diphosphate-fructose-6-phosphate 1-phosphotransferase [Oryza	4.04 glycolysis.PPFK	0.16
HA08M22	-0.13	**-1.19**	-0.44	-0.26	0.02	0.041	putative diphosphate-fructose-6-phosphate 1-phosphotransferase alpha	4.05_glycolysis.pyrophosphate-	-1.30
HT08F19	0.20	0.64	1.13	0.60	**1.14**	0.015	G3PC_HORVU Glyceraldehyde-3-phosphate dehydrogenase, cytosolic	4.09_glycolysis.glyceraldehyde 3-	0.11
HZ48K22	0.47	1.01	1.07	0.45	**1.18**	0.012	G3PC HORVU Glyceraldehyde-3-phosphate dehydrogenase, cytosolic	4.09 glycolysis.glyceraldehyde 3-	-0.11
HX02G03	-0.18	0.23	1.00	1.85	**3.24**	0.018	aldehyde dehydrogenase [Oryza sativa] aldehyde dehydrogenase [Oryza	5.10_fermentation.aldehyde	-0.75
HY06I22	-0.38	0.75	0.87	2.31	**3.65**	0.015	aldehyde dehydrogenase [Oryza sativa] aldehyde dehydrogenase [Oryza	5.10 fermentation.aldehyde	-0.83
HW09E06	0.23	1.16	0.76	0.60	**1.29**	0.010	putative Citrate synthase, glyoxysomal precursor (GCS) [Oryza sativa	6.01_gluconeogenese/ glyoxylate	-0.10
HK04F13	0.86	**1.52**	0.99	0.92	-0.05	0.012	glyoxysomal malate dehydrogenase [Triticum aestivum]	6.03_gluconeogenesis.Malate DH	0.69
HU13M03	1.04	0.20	1.07	2.29	**3.95**	0.008	phosphoenolpyruvate carboxykinase [Zoysia japonica]	6.04_gluconeogenese/ glyoxylate	-1.76
HO15F17	0.86	0.27	0.66	1.42	**2.04**	0.013	pyruvate orthophosphate dikinase [Triticum aestivum]	6.05_gluconeogenese/ glyoxylate	-0.93
HW09E07	1.26	-0.21	0.82	2.27	**3.37**	0.012	putative Citrate synthase, glyoxysomal precursor (GCS) [Oryza sativa	6.01 gluconeogenese/ glyoxylate	-1.76
HM03K01	-0.63	**-1.42**	-0.85	-0.61	-1.05	0.007	putative 6-phosphogluconolactonase [Oryza sativa (japonica cultivar-group)]	7.1.02_OPP.oxidative PP.6-	-1.58
HR01P23	0.36	1.08	-0.10	0.15	**1.43**	0.033	putative dehydrogenase [Oryza sativa (japonica cultivar-group)] putative D-	7.1.03 OPP.oxidative PP.6-	0.39
HO10A18	0.85	**1.30**	-0.25	0.13	0.72	0.025	putative cytosolic 6-phosphogluconate dehydrogenase [Zea mays]	7.1.03_OPP.oxidative PP.6-	0.26
HZ01L17	0.70	**1.44**	0.98	1.07	1.35	0.006	putative transaldolase [Oryza sativa (japonica cultivar-group)]	7.2.02_OPP.non-reductive	1.29
GBN007J	1.03	**3.06**	2.57	0.49	-2.36	0.044	PncB [Mycoplasma gallisepticum R] PncB [Mycoplasma gallisepticum R]	7.2.03 OPP.non-reductive PP.ribulose-	2.53
HD03I05	0.26	0.69	0.54	1.00	**1.04**	0.009	ferredoxin precursor [Triticum aestivum]	7.3_OPP.electron transfer	0.02
HV02A19	-0.17	0.43	0.27	0.92	**1.39**	0.030	0	7.3_OPP.electron transfer	0.97
HO20L22	-0.43	**-1.25**	-0.89	-0.28	-0.17	0.025	putative dihydrolipoamide dehydrogenase precursor [Oryza sativa (japonica	8.1.01.03_TCA / org.	-1.84
HW09M08	0.14	0.00	0.38	0.93	**1.09**	0.034	putative dihydrolipoamide dehydrogenase precursor [Oryza sativa (japonica	8.1.01.03_TCA / org.	-1.01
HO03F18	0.20	0.74	0.77	1.59	**2.84**	0.016	endosomal cargo receptor (Erp3), putative [Aspergillus fumigatus Af293]	8.1.06_TCA / org.	#NV
HY05N23	-0.10	-0.08	0.01	-0.81	**-1.17**	0.031	cytoplasmic malate dehydrogenase [Zea mays] Malate dehydrogenase,	8.2.09_TCA / org. transformation.other	-0.57
HV01J10	-0.12	0.00	0.08	-0.67	**-1.30**	0.033	putative cytosolic malate dehydrogenase [Arabidopsis thaliana] putative	8.2.09 TCA / org. transformation.other	-0.06
GCN004D	-0.14	-1.15	-0.72	-1.47	**-1.65**	0.010	carbonic anhydrase probable carbonate dehydratase (EC 4.2.1.1) - barley	8.3_TCA / org. transformation.carbonic	-1.39
HO36J03	-0.40	-1.32	-0.54	-1.39	**-2.04**	0.007	carbonic anhydrase probable carbonate dehydratase (EC 4.2.1.1) - barley	8.3 TCA / org. transformation.carbonic	-0.38
HO28I13	0.00	-1.14	-0.67	-1.33	**-1.97**	0.010	carbonic anhydrase probable carbonate dehydratase (EC 4.2.1.1) - barley	8.3_TCA / org. transformation.carbonic	-1.05
HO38I13	0.03	-1.00	-0.28	-1.13	**-1.71**	0.013	carbonic anhydrase probable carbonate dehydratase (EC 4.2.1.1) - barley	8.3_TCA / org. transformation.carbonic	-0.93
HO02J18	-0.26	-0.93	-0.72	-1.31	**-1.93**	0.007	putative GTP-binding protein [Oryza sativa (japonica cultivar-group)] putative	8.3 TCA / org. transformation.carbonic	-0.57
HG01D09	-0.16	-1.00	-0.27	-1.28	**-1.82**	0.010	carbonic anhydrase probable carbonate dehydratase (EC 4.2.1.1) - barley	8.3_TCA / org. transformation.carbonic	-1.17
GCA001O	-0.19	-0.96	-0.66	**-1.50**	-1.48	0.010	carbonic anhydrase probable carbonate dehydratase (EC 4.2.1.1) - barley	8.3_TCA / org. transformation.carbonic	-1.35
HA08N03	0.13	0.32	0.05	0.49	**1.48**	0.037	putative NADH dehydrogenase 10.5K chain [Arabidopsis thaliana] putative	9.1.2_mitochondrial electron transport /	-0.66
GNW002J	0.13	-0.19	-0.22	-0.49	**-1.02**	0.031	0	9.1.2_mitochondrial electron transport /	0.71
HA01C20	-0.47	0.06	-0.09	-0.22	**-1.04**	0.032	putative fiber protein Fb14 [Oryza sativa (japonica cultivar-group)] putative	9.1.2_mitochondrial electron transport /	0.67
HW02K06	0.94	**1.02**	0.30	-0.02	0.38	0.030	putative NADH dehydrogenase [Oryza sativa (japonica cultivar-group)]	9.2.2_mitochondrial electron transport /	0.10
HY02I14	-0.07	-0.28	-0.55	-0.12	**-1.38**	0.028	putative NADH dehydrogenase [Oryza sativa (japonica cultivar-group)]	9.2.3 mitochondrial electron transport /	0.71
HW02E11	-0.37	0.20	0.39	1.01	**1.44**	0.046	0	9.3_mitochondrial electron transport /	-0.87
HT02P01	-0.18	0.06	0.27	0.75	**2.85**	0.033	mitochondrial uncoupling protein 2 [Saccharum officinarum]	9.8_mitochondrial electron transport /	-0.68
HV01P08	-0.03	0.33	0.64	0.41	**1.20**	0.048	putative mitochondrial F0 ATP synthase D chain [Oryza sativa (japonica	9.9 mitochondrial electron transport /	-1.07
HY02A11	-0.02	0.49	0.59	**1.19**	0.51	0.035	F1-ATPase [Triticum aestivum]	9.9_mitochondrial electron transport /	-0.38
HO06B15	-0.20	-0.65	-0.22	-0.20	**-1.10**	0.028	UDP-D-glucose epimerase 1 [Hordeum vulgare]	10.1.02 cell wall.precursor	0.72
GPN002C	-0.01	0.57	0.43	0.98	**1.70**	0.020	putative phase-variable hemagglutinin [Mycoplasma synoviae 53] putative	10.1.04_cell wall.precursor	-0.32
HY03B24	-0.08	-0.13	-0.53	0.10	**-1.41**	0.039	putative UDP-glucose dehydrogenase [Sorghum bicolor]	10.1.04_cell wall.precursor	0.90
HK03F21	-0.13	**-1.21**	-0.67	-0.07	0.05	0.039	putative inner membrane protein [Salmonella typhimurium LT2] putative	10.2_cell wall.cellulose synthesis	#NV
HV03F17	-0.28	-0.52	-0.12	-0.36	**-1.27**	0.016	putative phytochelatin synthetase, 3'-partial [Oryza sativa (japonica cultivar-	10.2_cell wall.cellulose synthesis	-0.17
HW03P07	-0.01	0.60	0.76	0.65	**1.20**	0.037	putative cellulose synthase-5 [Oryza sativa (japonica cultivar-group)]	10.2 cell wall.cellulose synthesis	1.94

HE01I09	-0.39	**-1.20**	-0.34	-0.68	-0.38	0.013	putative cellulose synthase-5 [Oryza sativa (japonica cultivar-group)]	10.2 cell wall.cellulose synthesis	#NV
HO15K20	0.29	0.75	0.27	0.95	**1.88**	0.015	putative cellulose synthase-like protein OsCslE1 [Oryza sativa (japonica	10.2_cell wall.cellulose synthesis	#NV
HDP30O1	-0.57	-0.47	-0.77	-1.04	**-1.38**	0.010	putative glycosyl transferase [Oryza sativa (japonica cultivar-group)]	10.4_cell wall.pectin synthesis	#NV
HI01N18	-0.19	-0.65	-0.77	-0.49	**-1.52**	0.013	expressed protein [Oryza sativa (japonica cultivar-group)]	10.5.4 cell wall.cell wall proteins.HRGP	0.66
HW09B11	-0.42	-0.30	-0.27	-0.07	**-1.00**	0.037	putative polygalacturonase [Oryza sativa (japonica cultivar-group)] putative	10.6.3_cell wall.degradation.pectate	1.09
HF02C24	-0.30	**-2.16**	-1.17	-0.59	-0.51	0.012	polygalacturonase PG1-like [Oryza sativa (japonica cultivar-group)]	10.6.3 cell wall.degradation.pectate	#NV
HO34H21	**1.51**	1.29	1.48	0.01	1.50	0.014	expansin EXPA7 [Triticum aestivum]	10.7_cell wall.modification	-1.21
HO03A02	-0.50	-0.91	0.20	-1.13	**-1.88**	0.011	putative pectinacetylesterase precursor [Oryza sativa (japonica cultivar-	10.8.02_cell	1.60
HT12D18	0.01	**-1.53**	-1.23	-1.12	0.48	0.026	P0028G04.28 [Oryza sativa (japonica cultivar-group)] putative	10.8.02_cell	-1.20
HW05K10	0.16	**1.28**	0.80	1.05	0.50	0.014	OSJNBa0006M15.17 [Oryza sativa (japonica cultivar-group)]	11.1_lipid metabolism.FA synthesis and	0.56
HD02K23	0.43	-0.08	0.19	0.80	**2.14**	0.028	OSJNBa0018M05.15 [Oryza sativa (japonica cultivar-group)]	11.1.08 lipid metabolism.FA synthesis	-0.38
GBN004E	0.57	0.06	0.01	0.61	**2.27**	0.029	unnamed protein product [Tetraodon nigroviridis]	11.1.08_lipid metabolism.FA synthesis	-0.60
HU01C23	-0.22	0.26	0.08	1.15	**2.14**	0.026	AMP-binding protein [Arabidopsis thaliana]	11.1.08 lipid metabolism.FA synthesis	-0.69
GBN004M	-0.41	-0.65	-0.68	-0.48	**-1.46**	0.010	hypothetical protein MAP3321c [Mycobacterium avium subsp.	11.1.10_lipid metabolism.FA synthesis	1.95
HO09B16	-0.45	-0.84	-0.68	-1.63	**-2.51**	0.012	Putative fiddlehead-like protein [Oryza sativa (japonica cultivar-group)]	11.1.10_lipid metabolism.FA synthesis	2.84
GNW001	-0.29	-0.56	-0.27	-0.01	**-1.20**	0.022	S17928 acyl carrier protein 3 precursor, chloroplast - barley Acyl carrier	11.1.12 lipid metabolism.FA synthesis	-1.07
HD03L06	-0.31	-0.34	-0.16	-0.37	**-1.22**	0.020	S17928 acyl carrier protein 3 precursor, chloroplast - barley Acyl carrier	11.1.12_lipid metabolism.FA synthesis	-0.37
HO07A15	1.08	**1.33**	0.33	0.91	-0.35	0.028	OSJNBb0089B03.6 [Oryza sativa (japonica cultivar-group)]	11.1.15_lipid metabolism.FA synthesis	-0.35
HU02E16	0.66	1.23	0.39	**1.34**	-0.35	0.035	STAD_ORYSA Acyl-[acyl-carrier-protein] desaturase, chloroplast precursor	11.1.15_lipid metabolism.FA synthesis	-0.28
HW02K22	-0.47	0.75	1.55	0.65	**1.56**	0.020	putative dihydrolipoamide acetyltransferase [Oryza sativa (japonica cultivar-	11.1.31_lipid metabolism.FA synthesis	0.26
HX02O13	0.19	**1.34**	0.69	1.05	0.69	0.017	OSJNBa0043L09.15 [Oryza sativa (japonica cultivar-group)]	11.3_lipid metabolism.Phospholipid	0.21
HY09E20	0.29	**1.26**	0.79	1.12	0.92	0.013	OSJNBa0043L09.15 [Oryza sativa (japonica cultivar-group)]	11.3_lipid metabolism.Phospholipid	-0.26
HY10L11	0.03	0.90	0.53	**1.25**	0.64	0.018	OSJNBa0043L09.15 [Oryza sativa (japonica cultivar-group)]	11.3 lipid metabolism.Phospholipid	0.17
GCA002J	0.45	0.57	0.09	0.23	**1.01**	0.034	type 1 non-specific lipid transfer protein precursor [Triticum aestivum]	11.6_lipid metabolism.lipid transfer	0.49
HT01P02	-0.18	-1.15	-1.44	-1.45	**-2.86**	0.011	lipid transfer protein-like [Oryza sativa (japonica cultivar-group)]	11.6 lipid metabolism.lipid transfer	2.45
GBN006C	1.11	**2.49**	0.71	0.38	2.05	0.011	unnamed protein product [Homo sapiens]	11.6_lipid metabolism.lipid transfer	#NV
HO02D05	-0.22	-0.53	-1.26	-1.05	**-1.40**	0.023	hypothetical protein [Oryza sativa (japonica cultivar-group)] hypothetical	11.6_lipid metabolism.lipid transfer	3.75
HO02B06	-0.48	-0.79	0.00	-0.77	**-1.46**	0.023	lipid transfer protein 7a2b [Hordeum vulgare subsp. vulgare]	11.6 lipid metabolism.lipid transfer	3.54
HO02B02	0.22	-0.32	-0.92	-2.02	**-3.05**	0.020	CW18=non-specific lipid transfer protein [barley, cv. Bomi, leaves, Peptide,	11.6_lipid metabolism.lipid transfer	2.26
HK03J16	-0.09	-0.73	-0.96	-1.77	**-2.82**	0.014	CW18=non-specific lipid transfer protein [barley, cv. Bomi, leaves, Peptide,	11.6_lipid metabolism.lipid transfer	1.70
HO38E21	0.05	-0.25	-0.56	-2.03	**-3.12**	0.021	CW18=non-specific lipid transfer protein [barley, cv. Bomi, leaves, Peptide,	11.6_lipid metabolism.lipid transfer	1.67
HO37H04	0.08	-0.53	-0.56	-2.00	**-3.08**	0.017	CW18=non-specific lipid transfer protein [barley, cv. Bomi, leaves, Peptide,	11.6_lipid metabolism.lipid transfer	1.71
HO06H03	-0.15	-0.20	-0.58	-0.34	**-1.40**	0.026	'putative 1,4-benzoquinone reductase' [Oryza sativa (japonica cultivar-	11.8_lipid metabolism.'exotics'	1.87
HR01N04	-0.32	-0.13	-0.19	-0.71	**-1.32**	0.021	putative quinone oxidoreductase [Cicer arietinum]	11.8_lipid metabolism.'exotics'	1.68
HO03J05	-0.27	**-1.35**	-0.17	-0.73	-0.76	0.013	Putative Squalene monooxygenase [Oryza sativa (japonica cultivar-group)]	11.8 lipid metabolism.'exotics'	-0.81
HI04G06	-0.53	-0.39	-0.28	-0.80	**-1.38**	0.013	putative lecithin diacylglycerol cholesterol acyltransferase [Oryza sativa	11.8_lipid metabolism.'exotics'	0.56
GCN002B	-0.21	-0.97	-0.70	-0.99	**-2.12**	0.010	predicted protein [Gibberella zeae PH-1] predicted protein [Gibberella zeae	11.8_lipid metabolism.'exotics'	1.24
HU04A21	-0.06	-1.00	-0.60	-1.22	**-2.07**	0.010	squalene synthase [Oryza sativa (japonica cultivar-group)] squalene	11.8 lipid metabolism.'exotics'	0.72
HO10J20	-0.91	-1.36	-1.33	-1.44	**-1.86**	0.002	putative lipase [Oryza sativa (japonica cultivar-group)]	11.9.2_lipid metabolism.lipid	-1.54
HO04A23	-0.26	-0.49	-0.32	-0.64	**-1.39**	0.012	PLDA1_MAIZE Phospholipase D alpha 1 (PLD alpha 1) (Choline	11.9.3 lipid metabolism.lipid	-0.04
HW08B08	-0.18	-0.32	-0.81	**-1.52**	-1.24	0.012	PLDA1_MAIZE Phospholipase D alpha 1 (PLD alpha 1) (Choline	11.9.3_lipid metabolism.lipid	0.98
HS01I13	-0.28	-0.55	0.05	-0.48	**-1.01**	0.022	biostress-resistance-related protein [Triticum aestivum]	11.9.3_lipid metabolism.lipid	-0.54
HS01I13	-0.02	-0.90	-0.28	-0.07	**-1.44**	0.022	biostress-resistance-related protein [Triticum aestivum]	11.9.3_lipid metabolism.lipid	-0.54
HO09B23	-0.38	-0.81	-0.39	-0.73	**-1.58**	0.014	hypothetical protein [Oryza sativa (japonica cultivar-group)] hypothetical	11.9.4_lipid metabolism.lipid	-2.88
HO31N02	0.52	0.75	0.62	0.94	**1.16**	0.008	putative acyl-CoA oxidase [Oryza sativa (japonica cultivar-group)] putative	11.9.4.02 lipid metabolism.lipid	-0.09

HW01A21	0.77	0.57	0.34	1.04	**1.14**	0.010	putative acyl-CoA oxidase [Hordeum vulgare subsp. vulgare]	11.9.4.02 lipid metabolism.lipid	-0.53
HO08A16	0.11	-0.10	-0.05	0.78	**1.48**	0.049	putative 3-ketoacyl-CoA thiolase; acetyl-CoA acyltransferase [Oryza sativa	11.9.4.05_lipid metabolism.lipid	0.09
HO02I04	1.44	0.69	0.23	1.02	**1.88**	0.013	putative glyoxysomal fatty acid beta-oxidation multifunctional protein [Oryza	11.9.4.09_lipid metabolism.lipid	#NV
HO01H01	-0.46	**-2.38**	-0.62	-0.57	0.18	0.025	cAMP-dependent protein kinase A catalytic subunit [Blumeria graminis f. sp.	11.9.4.13 lipid metabolism.lipid	#NV
HD01J18	-0.06	0.41	0.29	0.88	**2.05**	0.021	NADH-dependent glutamate synthase [Oryza sativa (japonica cultivar-	12.2.01_N-metabolism.ammonia	0.80
GBN009K	0.43	**1.48**	1.24	0.30	1.36	0.010	ste6 [Schizosaccharomyces pombe]	12.2.02 N-metabolism.ammonia	-2.55
HY02F09	0.13	-0.53	0.02	-0.14	**-1.18**	0.037	hypothetical protein [Oryza sativa (japonica cultivar-	12.2.99_N-metabolism.ammonia	-0.10
HY07D14	-0.08	1.02	0.74	1.88	**3.54**	0.012	OSJNBb0038F03.5 [Oryza sativa (japonica cultivar-group)]	12.3.01_N-metabolism.N-	0.21
HA07A13	-0.15	1.16	1.11	1.47	**3.43**	0.013	OSJNBb0038F03.5 [Oryza sativa (japonica cultivar-group)]	12.3.01_N-metabolism.N-	0.17
HC14N16	-0.43	0.62	0.29	1.13	**1.60**	0.024	glutamate dehydrogenase [Oryza sativa (japonica cultivar-group)]	12.3.01_N-metabolism.N-	1.45
HW07J24	-0.15	0.90	0.77	0.97	**1.96**	0.017	T03294 glutamate dehydrogenase (EC 1.4.1.2) - maize Glutamate	12.3.01 N-metabolism.N-	0.45
HY09C24	-0.16	**-1.04**	-0.49	-0.73	-0.98	0.010	putative glutamate decarboxylase [Hordeum vulgare]	13.1.1.1_amino acid	-1.39
HA23J10	-0.29	-0.65	**-1.04**	-0.61	-0.98	0.013	putative glutamate decarboxylase [Hordeum vulgare]	13.1.1.1 amino acid	0.36
HF02G08	0.18	0.95	0.27	0.60	**1.88**	0.018	GAD1 [Hordeum vulgare]	13.1.1.1_amino acid	#NV
GCN001M	0.07	-0.60	-0.74	-0.38	**-1.25**	0.029	aspartate transaminase precursor, mitochondrial [Oryza sativa (japonica	13.1.1.2_amino acid	0.16
HW03O12	-0.26	0.10	0.63	1.21	**1.79**	0.029	delta-1-pyrroline-5-carboxylate dehydrogenase [Hordeum vulgare] putative	13.1.2.2 amino acid	-0.71
HU01K16	0.19	0.30	0.13	0.46	**1.32**	0.032	delta-1-pyrroline-5-carboxylate dehydrogenase [Hordeum vulgare] putative	13.1.2.2_amino acid	-0.29
HT01P21	1.00	**1.25**	0.71	0.45	0.24	0.012	argininosuccinate lyase [Arabidopsis thaliana]	13.1.2.3_amino acid	0.19
HW08J17	0.62	0.73	0.82	1.13	**1.54**	0.007	putative acetylornithine aminotransferase [Oryza sativa (japonica cultivar-	13.1.2.3_amino acid	-1.20
HW08M03	0.12	-0.24	0.36	0.72	**3.73**	0.030	asparragine synthetase [Zea mays] asparagine synthase (glutamine-	13.1.3.1_amino acid	-0.52
HD02J11	-0.07	0.09	0.62	1.83	**3.81**	0.020	glutamine-dependent asparagine synthetase [Triticum aestivum]	13.1.3.1_amino acid	-2.60
HD04L01	-0.15	**-1.49**	-0.41	-0.61	0.29	0.043	putative threonine synthase [Oryza sativa (japonica cultivar-group)] putative	13.1.3.2_amino acid	#NV
HW03P14	0.36	0.28	0.98	1.28	**1.38**	0.012	putative AdoMet synthase 1 [Hordeum vulgare subsp. vulgare]	13.1.3.4 amino acid	0.04
HB22A20	-0.13	0.85	0.98	1.08	**1.50**	0.013	expressed protein [Oryza sativa (japonica cultivar-group)]	13.1.3.4_amino acid	-0.20
HO04P10	1.78	**2.90**	1.59	1.52	-0.07	0.010	hypothetical protein AN4207.2 [Aspergillus nidulans FGSC A4] hypothetical	13.1.3.4 amino acid	0.71
HY09B08	1.28	**2.45**	1.46	1.43	-0.23	0.012	methionine synthase 2 enzyme [Hordeum vulgare subsp. vulgare]	13.1.3.4_amino acid	0.46
HI04J17	1.63	**2.99**	1.78	1.57	-0.27	0.012	methionine synthase 2 enzyme [Hordeum vulgare subsp. vulgare]	13.1.3.4_amino acid	0.48
HB10K20	-0.31	1.09	0.89	0.83	**1.83**	0.016	putative aspartate kinase [Oryza sativa (japonica cultivar-group)]	13.1.3.6.1.1 amino acid	-0.09
GNW001	-0.39	**-1.41**	-1.18	-0.04	-0.03	0.031	0	13.1.3.6.2_amino acid	-2.93
GNW002B	-0.44	**-1.20**	-0.70	-0.86	-0.67	0.007	0	13.1.3.6.2_amino acid	-1.17
GCW001L	-0.53	**-1.07**	-0.80	0.03	-0.51	0.015	0	13.1.3.6.2_amino acid	-1.38
HF01L22	-0.24	**-2.13**	-1.34	-0.60	-1.23	0.012	phosphoethanolamine methyltransferase [Triticum aestivum]	13.1.3.6.2_amino acid	-3.18
HI01M18	-0.39	**-2.17**	-0.95	-0.82	-1.02	0.011	phosphoethanolamine methyltransferase [Triticum aestivum]	13.1.3.6.2_amino acid	-3.18
HO09G03	-0.34	**-2.11**	-0.74	-0.88	-1.04	0.012	phosphoethanolamine methyltransferase [Triticum aestivum]	13.1.3.6.2_amino acid	-2.92
HB27P08	-0.07	**-1.76**	-1.14	-1.41	-0.80	0.010	phosphoethanolamine methyltransferase [Triticum aestivum]	13.1.3.6.2 amino acid	-3.17
HV01P14	-0.19	0.18	-0.11	0.48	**2.32**	0.043	putative phosphoethanolamine methyltransferase [Oryza sativa (japonica	13.1.3.6.2_amino acid	-1.11
HY08O05	0.19	0.45	0.22	0.69	**1.32**	0.026	Putative phosphoserine aminotransferase [Oryza sativa (japonica cultivar-	13.1.5.1_amino acid	-0.11
HO15O08	-0.45	**-1.09**	-0.49	-0.70	-0.93	0.011	putative glycine hydroxymethyltransferase [Oryza sativa (japonica cultivar-	13.1.5.2 amino acid	-2.18
HP01C18	-0.33	**-1.20**	-0.16	-0.25	-1.19	0.021	putative glycine hydroxymethyltransferase [Oryza sativa (japonica cultivar-	13.1.5.2_amino acid	-2.93
GCN001F	0.20	0.72	0.81	**1.20**	1.07	0.013	OSJNBa0019G23.9 [Oryza sativa (japonica cultivar-group)]	13.1.5.3.01 amino acid	-1.98
HW07D08	0.19	0.48	1.13	**1.51**	0.94	0.014	OSJNBa0019G23.9 [Oryza sativa (japonica cultivar-group)]	13.1.5.3.01_amino acid	-2.33
HD03L05	0.64	1.10	0.37	**1.23**	0.88	0.008	putative tryptophan synthase beta-subunit [Oryza sativa (japonica cultivar-	13.1.6.5_amino acid	-0.95
HO02G11	0.71	0.98	0.59	**1.25**	1.22	0.006	Putative phosphoribosylanthranilate transferase [Oryza sativa (japonica	13.1.6.5_amino acid	-1.83
HY08M03	**1.25**	1.16	0.71	0.38	0.38	0.014	putative indole-3-glycerol phosp	13.1.6.5_amino acid	-0.85
HO05F01	-0.13	-0.13	-0.61	**-1.24**	-0.96	0.023	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Hordeum	13.2.3.1 amino acid	-0.12

HO08M02	0.74	**2.15**	0.91	0.99	0.31	0.013	S-adenosyl-L-homocysteine hydrolase [Hordeum vulgare subsp. vulgare]	13.2.3.4 amino acid	0.66
HV01B17	0.78	**1.80**	1.03	0.96	0.38	0.011	S-adenosyl-L-homocysteine hydrolase [Hordeum vulgare subsp. vulgare]	13.2.3.4_amino acid	0.05
HY02L18	0.40	**1.24**	0.58	0.50	-0.11	0.036	wheat adenosylhomocysteinase-like protein [Oryza sativa (japonica cultivar-	13.2.3.4_amino acid	0.38
HY04N10	0.19	0.72	0.41	1.33	**4.41**	0.016	putative gamma-lyase [Oryza sativa (japonica cultivar-group)] putative	13.2.3.4 amino acid	#NV
HF16H22	0.05	0.22	0.48	0.96	**2.59**	0.021	3-methylcrotonyl-CoA carboxylase, biotin-carrier domain	13.2.4.4_amino acid	-1.69
HT01K19	-0.10	0.01	0.70	1.08	**3.02**	0.029	putative isovaleryl-CoA dehydrogenase [Oryza sativa (japonica cultivar-	13.2.4.4 amino acid	-1.17
HW07O22	-0.19	0.26	0.41	1.62	**2.99**	0.021	putative isovaleryl-CoA dehydrogenase [Oryza sativa (japonica cultivar-	13.2.4.4_amino acid	-1.52
HO14K14	-0.05	-0.92	-0.79	-0.59	**-1.12**	0.013	alanine aminotransferase [Oryza sativa (indica cultivar-group)]	13.2.4.5_amino acid	-2.32
HY04C19	-0.32	**-1.44**	-0.44	-0.20	-1.09	0.021	putative alanine aminotransferase [Oryza sativa (japonica cultivar-group)]	13.2.4.5_amino acid	-3.34
HY10G24	0.51	0.18	0.85	0.99	**1.10**	0.018	alanine aminotransferase [Hordeum vulgare subsp. vulgare] alanine	13.2.4.5_amino acid	-0.73
HO10C24	-0.02	**-1.35**	-0.44	-0.62	-0.72	0.015	putative hydroxypyruvate reductase [Oryza sativa (japonica cultivar-group)]	13.2.5.1 amino acid	-2.39
HO13N23	-0.08	**-1.22**	-0.62	-0.59	0.14	0.029	putative hydroxypyruvate reductase [Oryza sativa (japonica cultivar-group)]	13.2.5.1_amino acid	-2.74
HY06H18	-0.26	**-1.58**	-0.08	-0.34	-1.17	0.019	glycine decarboxylase P subunit [x Tritordeum sp.]	13.2.5.2 amino acid	-2.36
HO01G10	0.15	-1.07	-0.29	-0.89	**-1.22**	0.019	glycine decarboxylase P subunit [x Tritordeum sp.]	13.2.5.2_amino acid	-2.48
HV04H08	-0.50	**-1.54**	-0.70	-0.76	-0.58	0.010	OSJNBa0053K19.11 [Oryza sativa (japonica cultivar-group)]	13.2.5.2_amino acid	-2.92
GCN004C	1.35	**2.78**	1.77	1.12	1.30	0.004	putative phosphoglycerate dehydrogenase [Oryza sativa (japonica cultivar-	13.2.5.2 amino acid	-0.10
HY08L09	-0.40	**-1.03**	-0.86	-0.73	0.01	0.012	metallothioneine type2 [Hordeum vulgare subsp. vulgare]	15_metal handling	-0.96
HA04K22	-0.28	1.09	1.49	3.58	**4.37**	0.007	ferritin [Triticum aestivum]	15.2_metal handling.binding, chelation	-1.09
HO01M02	-0.18	-0.48	0.13	-0.51	**-2.25**	0.024	farnesylated protein 3 [Hordeum vulgare subsp. vulgare]	15.2_metal handling.binding, chelation	2.71
HO09P21	-0.38	0.01	-0.36	-0.43	**-1.82**	0.024	farnesylated protein 3 [Hordeum vulgare subsp. vulgare]	15.2_metal handling.binding, chelation	2.36
HO29H20	-0.12	-0.71	-0.84	-0.81	**-2.58**	0.014	farnesylated protein 2 [Hordeum vulgare subsp. vulgare]	15.2_metal handling.binding, chelation	2.66
HO13M12	-0.15	-0.41	-0.55	-0.41	**-1.39**	0.018	farnesylated protein 2 [Hordeum vulgare subsp. vulgare]	15.2_metal handling.binding, chelation	1.35
HO01P17	0.27	0.87	0.81	0.82	**1.29**	0.013	putative calmodulin-binding protein phosphatase [Oryza sativa (japonica	16.1.1 secondary	#NV
HY07P24	-0.27	**-1.09**	-0.27	-0.80	-0.17	0.017	geranylgeranyl hydrogenase [Triticum aestivum]	16.1.1_secondary	-1.25
HI02M15	-0.43	**-1.10**	-0.05	-0.67	-0.30	0.017	putative farnesyl-pyrophosphate synthetase [Oryza sativa (japonica cultivar-	16.1.2 secondary	#NV
HO38H14	-0.08	0.70	0.98	1.01	**2.00**	0.014	Isolation and Characterization of a cDNA Encoding 3-Hydroxy-3-	16.1.2_secondary	-0.37
GBN004P	-0.13	-0.92	-0.21	-0.05	**-1.32**	0.031	0	16.2_secondary	1.24
HO34C07	-0.43	-0.73	-0.44	-1.15	**-2.81**	0.013	putative cinnamoyl CoA reductase [Oryza sativa (japonica cultivar-group)]	16.2 secondary	0.35
HW01K17	-0.90	-1.62	-1.94	-1.81	**-3.25**	0.009	O-methyltransferase [Secale cereale]	16.2_secondary	2.24
HW04A17	-0.40	-0.88	-0.67	-0.52	**-1.69**	0.013	O-methyltransferase [Oryza sativa (japonica cultivar-group)]	16.2_secondary	1.43
HK06E02	-0.59	**-1.88**	-0.95	-0.28	-0.36	0.017	O-methyltransferase [Oryza sativa (japonica cultivar-group)]	16.2_secondary	#NV
GBN002N	**2.56**	2.08	0.63	0.54	1.61	0.011	agmatine coumaroyltransferase [Hordeum vulgare]	16.2_secondary	#NV
GBN003D	-0.50	-0.12	0.01	-1.51	**-2.49**	0.019	flavonoid 7-O-methyltransferase-like [Oryza sativa (japonica cultivar-group)]	16.2_secondary	0.88
HO17I21	0.69	0.61	0.98	1.99	**3.69**	0.010	putative elicitor inducible gene product EIG-I24 [Oryza sativa (japonica	16.2_secondary	#NV
HO15O04	**1.38**	0.83	-0.02	0.21	0.40	0.024	phenylalanine ammonia-lyase [Triticum aestivum] Phenylalanine ammonia-	16.2.1.01 secondary	#NV
HO02F16	**2.12**	1.20	0.90	0.79	0.30	0.010	phenylalanine ammonia-lyase	16.2.1.01_secondary	0.38
HO13H24	**1.87**	1.32	0.89	0.52	-0.21	0.020	phenylalanine ammonia-lyase	16.2.1.01_secondary	#NV
HM02L09	**1.45**	1.35	0.23	0.11	-0.05	0.033	phenylalanine ammonia-lyase [Hordeum vulgare subsp. vulgare]	16.2.1.01 secondary	0.06
HO04F05	**1.32**	1.13	0.56	0.43	0.02	0.022	phenylalanine ammonia-lyase [Hordeum vulgare subsp. vulgare]	16.2.1.01_secondary	1.09
HO14A06	0.14	1.83	**2.03**	1.78	0.71	0.011	phenylalanine ammonia-lyase [Hordeum vulgare subsp. vulgare]	16.2.1.01 secondary	0.69
HR01H18	0.07	0.61	1.21	3.02	**3.66**	0.010	putative phenylalanine ammonia-lyase [Bambusa ventricosa]	16.2.1.01_secondary	1.62
HW03O11	0.33	2.19	2.25	**2.50**	0.99	0.007	phenylalanine ammonia-lyase [Hordeum vulgare subsp. vulgare]	16.2.1.01_secondary	0.53
HZ50B24	**1.20**	0.62	0.36	0.06	0.33	0.034	cinnamate 4-hydroxylase [Citrus x paradisi]	16.2.1.02_secondary	#NV
HO04L04	**2.80**	2.55	0.68	0.80	1.10	0.009	putative 4-coumarate-CoA ligase [Oryza sativa (japonica cultivar-group)]	16.2.1.03_secondary	#NV
HA11A22	0.54	**1.28**	0.25	0.13	0.95	0.033	OSJNBa0029H02.14 [Oryza sativa (japonica cultivar-group)]	16.2.1.04 secondary	0.81

HO09L02	0.73	**1.49**	0.65	0.63	0.11	0.031	0	16.2.1.06 secondary	1.31
HW02G20	-0.03	**1.03**	0.74	0.97	0.89	0.013	metallothioneine type1 [Hordeum vulgare subsp. vulgare]	16.2.1.06_secondary	0.02
GNW001E	0.15	1.03	1.40	**1.46**	1.09	0.010	novel protein similar to human non-muscle myosin, heavy polypeptide 10	16.2.1.06_secondary	0.09
HO14P24	-0.17	**1.57**	1.46	1.16	0.19	0.019	metallothioneine type1 [Hordeum vulgare subsp. vulgare]	16.2.1.06 secondary	1.40
HZ38G08	0.03	**1.08**	0.89	1.07	-0.03	0.021	metallothioneine type1 [Hordeum vulgare subsp. vulgare]	16.2.1.06_secondary	1.33
HY03D14	0.07	0.53	0.05	0.80	**1.79**	0.033	putative caffeoyl CoA O-methyltransferase [Triticum aestivum]	16.2.1.06 secondary	-0.44
GBN001K	0.21	1.14	0.81	0.38	**1.82**	0.016	carboxyl-terminal peptidase-like [Oryza sativa (japonica cultivar-group)]	16.2.1.07_secondary	#NV
HM01F04	-0.41	-0.97	-1.19	-0.77	**-1.77**	0.010	cinnamyl alcohol dehydrogenase 1a [Festuca arundinacea]	16.2.1.10_secondary	0.53
GPN003M	0.17	**1.52**	1.28	0.20	-0.05	0.034	hypothetical protein FG09897.1 [Gibberella zeae PH-1] hypothetical protein	16.4.1_secondary metabolism.N	-0.24
HD03C17	0.05	**1.20**	0.92	0.26	-0.05	0.043	ABC transporter permease protein-like protein [Oryza sativa (japonica	16.4.1_secondary metabolism.N	-0.25
HW03B14	0.30	-0.12	0.40	1.20	**1.94**	0.023	putative CPRD2 [Oryza sativa (japonica cultivar-group)]	16.4.1 secondary metabolism.N	1.15
HP01M24	-0.23	-0.86	-0.49	**-1.04**	-0.87	0.017	putative very-long-chain fatty acid condensing enzyme CUT1 [Oryza sativa	16.7_secondary metabolism.wax	0.69
HA04C02	-0.59	-0.77	**-1.47**	-0.87	-1.23	0.010	very-long-chain fatty acid condensing enzyme CUT1 [Arabidopsis thaliana]	16.7 secondary metabolism.wax	1.69
HO08B14	-0.09	**-1.88**	-0.28	-0.32	-0.46	0.031	P0434B04.11 [Oryza sativa (japonica cultivar-group)]	16.7_secondary metabolism.wax	-2.29
HW03O04	0.33	**1.14**	0.64	0.26	0.94	0.041	b-keto acyl reductase [Hordeum vulgare]	16.7_secondary metabolism.wax	1.77
HZ50P18	-0.41	0.15	-0.38	-0.56	**-1.48**	0.024	putative chalcone synthase [Oryza sativa (japonica cultivar-group)]	16.8.2 secondary	1.34
HO06G02	0.03	**-2.28**	-1.40	-0.50	-0.77	0.013	unknown protein [Arabidopsis thaliana] unknown protein [Arabidopsis	16.8.2_secondary	#NV
HO33F20	-0.42	-1.46	**-1.82**	-1.13	0.24	0.018	chalcone synthase [Hordeum vulgare] naringenin-chalcone synthase (EC	16.8.2_secondary	#NV
HO04K22	-0.34	**-2.17**	-1.10	-0.73	-0.33	0.013	chalcone synthase [Secale cereale] Chalcone synthase 1 (Naringenin-	16.8.2_secondary	#NV
HO06N01	0.42	2.39	1.88	1.43	**2.57**	0.004	0	16.8.3_secondary	0.00
HO15F23	0.48	2.25	1.50	1.20	**2.43**	0.004	Putative flavanone 3-hydroxylase [Oryza sativa (japonica cultivar-group)]	16.8.3_secondary	0.56
HY09O15	-0.39	**-1.19**	-0.49	-0.89	-0.09	0.014	OSJNBb0015D13.10 [Oryza sativa (japonica cultivar-group)]	16.8.3_secondary	-0.74
HE01H04	-0.94	**-2.12**	-0.78	-0.74	-0.38	0.015	laccase LAC5-4 [Lolium perenne]	16.10 secondary metabolism.simple	#NV
HZ50J03	-0.02	-0.81	-0.41	**-1.32**	-1.25	0.014	T04478 probable carbonate dehydratase (EC 4.2.1.1) - barley	16.99_secondary	-0.60
HW05O06	-0.39	-0.58	-0.28	-0.34	**-1.08**	0.014	putative amidotransferase [Oryza sativa (japonica cultivar-group)] putative	16.99 secondary	-0.63
HG01C09	-0.57	-1.51	-1.04	-1.73	**-2.77**	0.010	9-cis-epoxycarotenoid dioxygenase 1 [Oryza sativa (japonica cultivar-group)]	17.1.1.1.10_hormone	-1.13
HW08D06	-0.09	0.12	0.76	2.15	**3.70**	0.017	OSJNBa0038O10.18 [Oryza sativa (japonica cultivar-group)]	17.1.3_hormone metabolism.abscisic	0.32
HW07E11	-0.52	-0.13	0.07	-1.11	**-1.30**	0.025	22 kDa drought-inducible protein [Saccharum hybrid cultivar] drought	17.1.3 hormone metabolism.abscisic	2.56
HT01C17	-0.34	0.22	0.48	0.50	**1.88**	0.042	protein kinase HvPKABA1 [Hordeum vulgare subsp. vulgare] protein kinase	17.1.3_hormone metabolism.abscisic	#NV
HT02M13	-0.30	0.67	0.40	0.11	**2.15**	0.047	At5g13200 [Arabidopsis thaliana] ABA-responsive protein-like [Arabidopsis	17.1.3_hormone metabolism.abscisic	1.42
HO02G17	0.14	-0.58	-0.40	-0.52	**-1.89**	0.027	0	17.2.2_hormone	-0.18
HO09E07	0.08	-0.49	-0.60	-0.34	**-1.39**	0.019	auxin response factor 2 [Oryza sativa]	17.2.2_hormone	0.41
HY03M18	-0.05	-0.36	-0.41	-0.29	**-1.29**	0.034	auxin response factor 2 [Oryza sativa]	17.2.2_hormone	0.28
GBN003E	-0.29	-0.55	-0.40	-0.92	**-1.66**	0.012	unnamed protein product [Homo sapiens]	17.2.3_hormone	1.53
HO08E10	0.74	**1.00**	0.35	0.25	0.30	0.018	auxin-repressed protein-like protein ARP1 [Manihot esculenta]	17.2.3 hormone	1.35
HS01N22	-0.20	-0.06	-1.14	-1.12	**-1.30**	0.014	Auxin-responsive protein IAA1:: unknown protein [Oryza sativa (japonica	17.2.3_hormone	1.84
HW01J23	-0.01	0.01	-0.61	-1.26	**-1.76**	0.022	Auxin-responsive protein IAA15:: unknown protein [Oryza sativa (japonica	17.2.3_hormone	1.48
GPN001F	-0.64	**-1.84**	-0.65	-0.08	-1.03	0.013	aux/IAA protein [Populus tremula x Populus tremuloides]	17.2.3 hormone	-0.86
HW05N03	0.64	1.27	0.96	2.07	**2.88**	0.006	putative indole-3-acetic acid-regulated protein [Oryza sativa (japonica	17.2.3_hormone	-0.50
HO10E15	-0.01	-0.86	-0.85	-1.73	**-2.82**	0.013	IAA8 auxin regulated transcriptional repressor:: unknown protein [Oryza	17.2.3 hormone	0.96
HM02O06	-0.23	**-1.48**	-0.81	-0.15	0.46	0.041	putative auxin-induced protein [Oryza sativa (japonica cultivar-group)]	17.2.3_hormone	#NV
HDP28O0	0.31	**1.10**	1.03	0.52	0.49	0.031	OSJNBa0020J04.7 [Oryza sativa (japonica cultivar-group)]	17.3.1.1.1_hormone	0.48
HW01E16	-0.07	0.68	0.02	0.25	**1.85**	0.043	brassinosteroid biosynthesis-like protein [Zea mays]	17.3.1.2.08_hormone	-0.41
HO02N08	-0.30	**-1.37**	-0.20	-1.23	-0.76	0.012	Putative Squalene monooxygenase [Oryza sativa (japonica cultivar-group)]	17.3.1.2.99_hormone	0.00
HO14P22	-0.48	**-1.60**	-0.16	-0.95	-0.82	0.010	Putative Squalene monooxygenase [Oryza sativa (japonica cultivar-group)]	17.3.1.2.99 lipid metabolism.'exotics'	0.25

HP06J13	-0.16	**-1.81**	-1.68	-1.69	-0.66	0.009	putative cytokinin oxidase [Oryza sativa (japonica cultivar-group)]	17.4.1 hormone	#NV
HS17I05	-0.28	**-1.23**	-1.18	-0.71	-0.42	0.013	putative P450 [Oryza sativa (japonica cultivar-group)]	17.4.2_hormone	-0.82
HO08P21	0.15	0.62	-0.19	0.78	**1.66**	0.026	putative ethylene-forming enzyme [Oryza sativa (japonica cultivar-group)]	17.5.1_hormone	#NV
HW05I22	1.03	**1.92**	0.78	0.60	0.24	0.017	iron/ascorbate-dependent oxidoreductase [Hordeum vulgare]	17.5.1 hormone	0.37
HO05P22	0.11	-0.65	-0.71	-1.24	**-2.01**	0.017	putative RuBisCO subunit binding-protein beta subunit, chloroplast	17.5.1_hormone	1.28
HH05C14	-0.08	-1.04	-0.92	-1.45	**-2.09**	0.016	ACC oxidase [Musa acuminata] 1-aminocyclopropane-1-carboxylate oxidase	17.5.1 hormone	0.90
HO29J24	-0.04	-0.76	-0.97	-1.37	**-2.95**	0.018	1-aminocyclopropane-1-carboxylate oxidase [Phyllostachys edulis]	17.5.1_hormone	1.30
HM03B15	0.08	-0.16	-0.96	-0.20	**-1.22**	0.029	EIN3-like protein 1 [Oryza sativa (japonica cultivar-group)]	17.5.2_hormone	1.95
HW01F08	-0.25	0.01	-0.02	**-1.31**	-1.04	0.018	EIN3-like protein 1 [Oryza sativa (japonica cultivar-group)]	17.5.2_hormone	0.58
HO06P13	2.30	**3.68**	1.81	1.52	0.34	0.008	iron/ascorbate-dependent oxidoreductase [Hordeum vulgare]	17.5.3_hormone	0.65
HO12L20	1.59	**1.99**	0.92	0.75	0.30	0.012	Similar to Prunus armeniaca ethylene-forming-enzyme-like dioxygenase.	17.5.3 hormone	0.74
HW04K06	1.98	**3.71**	1.48	1.59	0.33	0.007	ethylene-forming-enzyme-like dioxygenase-like protein [Oryza sativa	17.5.3_hormone	0.59
GBN001H	1.50	**3.42**	2.26	1.07	0.45	0.010	ethylene-forming-enzyme-like dioxygenase-like protein [Oryza sativa	17.5.3 hormone	0.20
HZ60L03	-0.42	-0.25	-1.05	-1.12	**-1.29**	0.010	nuclear transcription factor SLN1 [Hordeum vulgare]	17.6.2_hormone	0.81
HO02M08	-0.50	-0.49	-0.43	-0.78	**-1.24**	0.012	nuclear transcription factor SLN1 [Hordeum vulgare]	17.6.2_hormone	0.62
HS01E18	0.69	**1.43**	0.47	0.13	-0.14	0.035	LOX1 HORVU Lipoxygenase 1 lipoxygenase 1 lipoxygenase	17.7.1 hormone	0.54
HB21O08	-0.45	-0.15	-0.84	-0.47	**-1.97**	0.017	oxo-phytodienoic acid reductase [Oryza sativa (japonica cultivar-group)] 12-	17.7.1_hormone	0.99
HB21O08	-0.45	-0.15	-0.84	-0.47	**-1.97**	0.017	oxo-phytodienoic acid reductase [Oryza sativa (japonica cultivar-group)] 12-	17.7.1_hormone	0.99
HW04I04	0.39	0.22	0.49	0.30	**1.20**	0.037	12-oxo-phytodienoic acid reductase [Zea mays]	17.7.1.5_hormone	-1.11
GCW004P	-0.10	-0.06	-0.32	-0.13	**-1.48**	0.039	putative LRR-containing F-box protein [Oryza sativa (japonica cultivar-	17.7.3_hormone	1.55
HO03C19	-0.61	-1.32	-0.94	-1.25	**-1.47**	0.003	thiamine biosynthetic enzyme [Oryza sativa (japonica cultivar-group)]	18_Co-factor and vitamine metabolism	-1.79
HY09L03	-0.44	**-1.10**	-1.06	-0.91	-0.76	0.005	putative thiamine biosynthesis protein [Oryza sativa (japonica cultivar-	18_Co-factor and vitamine metabolism	-1.40
HV04H14	-0.38	**-1.25**	-1.06	-1.10	-0.65	0.005	putative thiamine biosynthesis protein [Oryza sativa (japonica cultivar-	18 Co-factor and vitamine metabolism	-1.75
HY02F14	0.17	-0.38	-0.21	-0.17	**-1.10**	0.041	magnesium chelatase subunit I precursor [Zea mays] magnesium chelatase	19.1_tetrapyrrole synthesis.magnesium	0.44
HA15B22	-0.29	**-1.09**	0.31	-0.29	-0.50	0.037	Mg-chelatase subunit XANTHA-F [Hordeum vulgare subsp. vulgare]	19.10 tetrapyrrole	-1.93
HA12H05	-0.04	**-1.62**	0.09	-0.35	-0.55	0.027	Mg-chelatase subunit XANTHA-F [Hordeum vulgare subsp. vulgare]	19.10_tetrapyrrole	-1.62
HO01L15	-0.16	**-1.36**	-0.11	-0.35	-0.78	0.025	Mg-chelatase subunit XANTHA-F [Hordeum vulgare subsp. vulgare]	19.10_tetrapyrrole	-1.75
HDP10M0	-0.27	-0.77	-0.17	-0.80	**-1.45**	0.013	chlorophyll synthase [Avena sativa]	19.15 tetrapyrrole synthesis.chlorophyll	-0.80
GBN003H	-0.56	**-1.67**	-0.22	-0.36	-0.47	0.018	putative chlorophyll synthase [Oryza sativa (japonica cultivar-group)]	19.16_tetrapyrrole synthesis.chlorophyll	-2.83
HG01L05	-0.34	**-1.44**	-0.58	-0.76	-0.32	0.018	putative stress enhanced protein [Oryza sativa (japonica cultivar-group)]	20_stress	-2.64
HW09H19	-0.18	**-1.53**	-1.27	-0.75	-1.20	0.013	disease resistance protein (CC-NBS-LRR class), putative [Arabidopsis	20.1_stress.biotic	0.24
HO18E19	-0.37	-0.43	-0.61	-0.67	**-2.03**	0.013	pollen signalling protein with adenylyl cyclase activity [Zea mays]	20.1_stress.biotic	1.57
HO09F07	1.02	**1.28**	0.39	0.68	0.34	0.013	Mlo3 [Hordeum vulgare subsp. vulgare]	20.1_stress.biotic	#NV
HO14K07	1.37	1.46	0.56	1.57	**3.88**	0.006	chitinase [Hordeum vulgare subsp. vulgare]	20.1_stress.biotic	-2.07
HW04D09	-0.30	0.03	1.99	2.17	**2.39**	0.015	chitinase (EC 3.2.1.14) III C10701 - rice [Oryza sativa (japonica cultivar-	20.1 stress.biotic	0.73
HK03P07	1.04	2.94	2.03	1.59	**3.41**	0.004	0	20.1_stress.biotic	1.01
HO12M23	0.83	0.90	0.60	0.53	**2.07**	0.017	putative class IV chitinase (CHIV) [Oryza sativa (japonica cultivar-group)]	20.1_stress.biotic	1.02
HO03B03	**1.77**	1.41	0.58	0.28	0.72	0.014	HV1LRR1 [Hordeum vulgare]	20.1 stress.biotic	-0.26
HV02N06	1.05	1.39	2.49	2.70	**3.84**	0.003	disease resistance response protein-like [Oryza sativa (japonica cultivar-	20.1_stress.biotic	0.11
GCA001P	0.36	2.24	1.26	2.87	**3.01**	0.004	PR-1a pathogenesis related protein (Hv-1a) [Hordeum vulgare subsp.	20.1 stress.biotic	-2.85
GCA001O	0.30	2.06	1.40	**3.45**	2.91	0.004	PR-1a pathogenesis related protein (Hv-1a) [Hordeum vulgare subsp.	20.1_stress.biotic	-2.46
HD01N05	0.66	2.33	**2.45**	2.19	1.78	0.004	type-1 pathogenesis-related protein [Hordeum vulgare]	20.1_stress.biotic	1.47
HO16H10	0.52	2.68	1.71	**2.87**	2.51	0.004	PR-1a pathogenesis related protein (Hv-1a) [Hordeum vulgare subsp.	20.1_stress.biotic	-2.03
HO08E12	0.77	1.88	1.38	2.23	**2.92**	0.004	PR-1a pathogenesis related protein (Hv-1a) [Hordeum vulgare subsp.	20.1_stress.biotic	-2.06
HO04D12	0.01	-0.56	-0.51	-1.99	**-3.17**	0.017	Cf2/Cf5 disease resistance protein homolog [Hordeum vulgare]	20.1 stress.biotic	2.16

GBN006D	-0.02	-0.62	0.01	-0.30	**-1.32**	0.038	putative vacuolar defense protein [Triticum aestivum]	20.1 stress.biotic	2.10
HY05J20	**1.30**	0.81	0.73	0.09	0.83	0.012	BAX inhibitor 1 [Hordeum vulgare subsp. vulgare]	20.1_stress.biotic	-0.24
HT01E04	1.56	**2.64**	0.73	1.29	1.78	0.004	secretory protein [Triticum aestivum]	20.1_stress.biotic	-0.82
HV04B05	0.75	1.61	0.75	0.60	**1.76**	0.011	thaumatin-like protein TLP2 [Hordeum vulgare] pathogenesis-related protein	20.1 stress.biotic	-3.12
HW03O22	1.10	**2.52**	0.78	1.14	0.53	0.010	unknown	20.1_stress.biotic	-0.59
HP01C14	**1.61**	1.57	0.73	1.47	1.59	0.004	hypothetical protein [Hordeum vulgare]	20.1 stress.biotic	-0.53
HW03J02	1.22	**2.41**	0.79	0.79	0.10	0.014	hypothetical protein [Hordeum vulgare]	20.1_stress.biotic	-0.36
HU04J24	-0.03	-0.59	-0.45	-0.45	**-1.99**	0.017	unknown protein [Arabidopsis thaliana]	20.2.1_stress.abiotic.heat	0.70
HW02C07	0.22	-0.27	0.02	-0.53	**-1.98**	0.034	cytosolic heat shock protein 90 [Hordeum vulgare]	20.2.1_stress.abiotic.heat	-0.07
HP09E02	0.08	**-1.47**	-0.48	-0.86	-0.27	0.027	unknown protein [Oryza sativa (japonica cultivar-group)] PREDICTED	20.2.1_stress.abiotic.heat	-3.16
HY04B04	0.01	-0.66	-0.49	0.25	**-1.05**	0.042	DNAJ heat shock N-terminal domain-containing protein-like [Oryza sativa	20.2.1 stress.abiotic.heat	-0.21
HO07F04	-0.30	**-1.29**	-0.87	-0.48	-0.82	0.015	heat shock protein 17.9 [Pennisetum glaucum]	20.2.1_stress.abiotic.heat	0.15
HY03K23	-0.08	-0.75	-0.45	-0.31	**-1.18**	0.020	heat shock protein 17.9 [Pennisetum glaucum]	20.2.1 stress.abiotic.heat	0.21
HF01J12	-0.51	-0.83	-0.49	-0.02	**-1.22**	0.016	heat shock protein 70 [Cucumis sativus]	20.2.1_stress.abiotic.heat	-0.56
HU03K19	-0.04	-1.04	-0.55	0.34	**-1.24**	0.047	Psst70 (stress 70 protein) [Pisum sativum] Stromal 70 kDa heat shock-	20.2.1_stress.abiotic.heat	-0.86
HK05M06	-0.25	-0.65	-0.41	-0.18	**-1.40**	0.020	putative DnaJ-like protein MsJ1 [Oryza sativa (japonica cultivar-group)]	20.2.1 stress.abiotic.heat	0.29
HC11C04	-0.26	-0.36	-0.02	-0.18	**-1.24**	0.026	DnaJ-like protein [Oryza sativa]	20.2.1_stress.abiotic.heat	0.96
HO14F02	-0.18	-0.53	-0.85	-0.04	**-1.31**	0.025	DnaJ-like protein [Oryza sativa]	20.2.1_stress.abiotic.heat	1.35
HH01D07	-0.28	-1.00	**-1.14**	-1.08	-0.56	0.013	heat-shock protein [Secale cereale]	20.2.1_stress.abiotic.heat	-0.26
HX03B07	-0.29	-0.24	0.01	-0.42	**-2.07**	0.023	DnaJ protein, putative [Oryza sativa (japonica cultivar-group)]	20.2.1_stress.abiotic.heat	1.27
HY06F15	-0.11	-0.15	-0.48	-0.25	**-1.65**	0.026	DnaJ homolog [Salix gilgiana]	20.2.1_stress.abiotic.heat	0.64
HX05N22	0.52	**1.35**	0.37	0.85	-0.03	0.018	heat shock protein 70 [Triticum aestivum]	20.2.1_stress.abiotic.heat	0.04
HO05L11	-0.57	**-1.33**	-0.22	-0.59	0.34	0.030	plasma membrane protein [Triticum aestivum] salt-stress induced	20.2.2 stress.abiotic.cold	#NV
GNW001	-0.48	**-1.38**	-0.35	-0.99	-0.20	0.012	plasma membrane protein [Triticum aestivum] salt-stress induced	20.2.2_stress.abiotic.cold	-0.22
HU11A04	-0.01	0.02	0.58	0.56	**1.52**	0.035	0	20.2.2 stress.abiotic.cold	0.42
HO10B22	-0.62	-1.11	-0.55	-1.58	**-2.26**	0.005	putative ERD4 protein [Oryza sativa (japonica cultivar-group)] putative ERD4	20.2.3_stress.abiotic.drought/salt	1.43
HO05L13	2.52	**3.45**	1.38	1.31	0.05	0.012	oxalate oxidase-like protein or germin-like protein [Hordeum vulgare subsp.	20.2.99_stress.abiotic.unspecified	2.68
HA02I01	-0.24	0.59	1.01	1.72	**2.45**	0.013	fiber protein Fb19 [Gossypium barbadense]	20.2.99 stress.abiotic.unspecified	-0.24
GCN002I2	2.07	**4.02**	3.32	1.76	3.13	0.002	germin E [Hordeum vulgare]	20.2.99_stress.abiotic.unspecified	#NV
HD01A05	1.43	**2.79**	2.35	0.55	1.84	0.006	oxalate oxidase [Triticum aestivum]	20.2.99_stress.abiotic.unspecified	#NV
HK04J17	0.29	1.93	0.83	0.83	**3.56**	0.010	germin F [Hordeum vulgare]	20.2.99_stress.abiotic.unspecified	0.51
HC09O22	0.95	3.20	1.37	2.36	**4.47**	0.003	germin F [Hordeum vulgare]	20.2.99_stress.abiotic.unspecified	#NV
GCN003H	-0.13	**1.55**	1.18	0.68	1.49	0.029	putative type-1 pathogenesis-related protein [Oryza sativa (japonica cultivar-	20.2.99_stress.abiotic.unspecified	3.26
GBN004L	0.32	2.48	1.45	2.67	**2.84**	0.004	pathogenisis-related protein 1.1 [Triticum aestivum]	20.2.99_stress.abiotic.unspecified	-2.39
HK03B24	-0.39	-1.44	-1.65	-2.05	**-2.52**	0.009	adenosine diphosphate glucose pyrophosphatase [Hordeum vulgare subsp.	20.2.99 stress.abiotic.unspecified	1.41
HO09G05	-0.69	-1.15	-1.41	-2.10	**-3.72**	0.009	adenosine diphosphate glucose pyrophosphatase [Triticum aestivum]	20.2.99_stress.abiotic.unspecified	2.88
HO28N08	-0.25	-1.05	-1.29	-2.34	**-3.83**	0.013	adenosine diphosphate glucose pyrophosphatase [Hordeum vulgare subsp.	20.2.99_stress.abiotic.unspecified	3.27
HW05P01	-0.30	-0.75	-0.64	-0.96	**-1.93**	0.009	unnamed protein product [Oryza sativa (japonica cultivar-group)] plasma	20.2.99 stress.abiotic.unspecified	1.67
HO01P11	3.01	**4.04**	1.70	1.77	0.89	0.005	oxalate oxidase-like protein or germin-like protein [Hordeum vulgare subsp.	20.2.99_stress.abiotic.unspecified	2.70
HO01J20	2.84	**3.57**	1.66	1.39	0.36	0.009	oxalate oxidase-like protein or germin-like protein [Hordeum vulgare subsp.	20.2.99 stress.abiotic.unspecified	2.36
HO09I08	2.59	**3.40**	1.03	1.11	-0.09	0.012	germin-like protein 4 [Triticum monococcum]	20.2.99_stress.abiotic.unspecified	3.01
HO03H18	3.04	**3.89**	1.98	1.69	0.74	0.005	oxalate oxidase-like protein or germin-like protein [Hordeum vulgare subsp.	20.2.99_stress.abiotic.unspecified	2.07
HY10M20	-0.33	-0.82	-0.66	-0.42	**-1.18**	0.010	OSJNBa0089N06.15 [Oryza sativa (japonica cultivar-group)]	21.01_redox.thioredoxin	1.23
HO12M13	-0.03	0.23	-0.41	-0.58	**-1.20**	0.044	thioredoxin h-like protein [Hordeum vulgare subsp. vulgare]	21.01_redox.thioredoxin	0.64
HY02D14	0.22	-0.25	-0.54	-0.42	**-1.38**	0.028	thioredoxin h-like protein [Hordeum vulgare subsp. vulgare]	21.01 redox.thioredoxin	0.19

HZ39K18	0.03	**-1.23**	-0.38	-0.46	-0.29	0.035	thioredoxin M [Triticum aestivum] thioredoxin M precursor [Triticum turgidum	21.01 redox.thioredoxin	-3.57
HG01O09	-0.14	**-1.20**	-0.10	-0.38	-0.31	0.047	thioredoxin M [Triticum aestivum] thioredoxin M precursor [Triticum turgidum	21.01_redox.thioredoxin	-3.42
HD01B16	0.59	**1.28**	1.10	-0.11	0.64	0.017	putative disulfide-isomerase precursor [Oryza sativa] putative disulfide-	21.01_redox.thioredoxin	-0.26
HX02E11	1.09	**1.12**	0.24	0.21	-0.31	0.046	disulfide isomerase	21.01 redox.thioredoxin	0.44
HU01O15	**1.21**	1.11	0.25	0.85	-0.53	0.033	disulfide isomerase	21.01_redox.thioredoxin	0.11
HY05E24	-0.17	0.14	-0.32	**-1.18**	-0.39	0.041	OSJNBa0084A10.16 [Oryza sativa (japonica cultivar-group)]	21.01 redox.thioredoxin	0.59
HO23O13	0.09	-0.46	-0.61	**-1.25**	-0.28	0.033	OSJNBb0039L24.15 [Oryza sativa (japonica cultivar-group)]	21.02_redox.ascorbate and glutathione	-1.03
HW05M08	0.00	0.15	-0.17	-0.55	**-1.39**	0.042	putative cytochrome B5 [Oryza sativa (japonica cultivar-group)] putative	21.02_redox.ascorbate and glutathione	0.44
HG01H12	-0.31	**-1.03**	0.10	-0.72	-0.45	0.021	peroxisome type ascorbate peroxidase [Hordeum vulgare subsp. vulgare]	21.02_redox.ascorbate and glutathione	-2.20
HS01D17	-0.16	0.34	0.36	**1.90**	1.52	0.017	putative steroid membrane binding protein [Oryza sativa (japonica cultivar-	21.02_redox.ascorbate and glutathione	0.24
HV02I19	0.56	**1.70**	0.79	1.03	0.84	0.010	ascorbate peroxidase [Hordeum vulgare subsp. vulgare]	21.02 redox.ascorbate and glutathione	-0.70
HO11B02	0.28	**-1.44**	-0.36	-0.46	-1.06	0.022	thylakoid L-ascorbate peroxidase [Triticum aestivum] thylakoid ascorbate	21.02_redox.ascorbate and glutathione	-2.55
HO07L19	-0.14	-0.94	-0.22	-0.84	**-1.00**	0.013	putative glutathione peroxidase [Oryza sativa (japonica cultivar-group)]	21.02 redox.ascorbate and glutathione	-1.98
HW02N05	0.52	**1.26**	0.75	0.23	0.33	0.016	monodehydroascorbate reductase [Oryza sativa (japonica cultivar-group)]	21.2.1_redox.ascorbate and	0.34
HZ40N18	-0.17	**-1.22**	-0.62	-0.27	-0.37	0.026	OSJNBa0041A02.10 [Oryza sativa (japonica cultivar-group)]	21.2.1_redox.ascorbate and	#NV
HO23F13	0.01	-0.28	0.19	-1.14	**-1.79**	0.024	putative phospholipid hydroperoxide glutathione peroxidase [Oryza sativa	21.2.2 redox.ascorbate and	0.72
HY10A14	-0.05	-0.13	-0.08	-1.21	**-1.40**	0.024	putative phospholipid hydroperoxide glutathione peroxidase [Oryza sativa	21.2.2_redox.ascorbate and	0.54
HW04P13	-0.03	-0.41	-0.24	-0.30	**-1.60**	0.023	putative phospholipid hydroperoxide glutathione peroxidase [Oryza sativa	21.2.2_redox.ascorbate and	0.91
HS03J20	-0.07	-0.07	-0.09	1.13	**2.88**	0.032	glutaredoxin protein family-like [Oryza sativa (japonica cultivar-group)]	21.04_redox.glutaredoxins	0.19
HA04P20	0.27	1.98	2.27	2.45	**3.19**	0.004	glutaredoxin [Triticum aestivum]	21.04_redox.glutaredoxins	-0.90
HK03C04	-0.48	**-1.03**	-0.29	-0.05	-0.45	0.027	thioredoxin peroxidase [Secale cereale]	21.05_redox.periredoxins	-1.51
GBN004J	-0.09	**-1.29**	0.03	-0.47	-0.32	0.033	thioredoxin peroxidase [Secale cereale]	21.05_redox.periredoxins	-1.49
HD04B10	-0.18	**-1.52**	-0.17	-0.19	-1.20	0.017	peroxiredoxin [Hordeum vulgare subsp. vulgare] HvB15C [Hordeum vulgare	21.05 redox.periredoxins	-0.98
HG01C08	-0.18	**-1.23**	-0.26	-0.66	-1.05	0.015	CATA1_WHEAT Catalase 1 catalase [Triticum aestivum]	21.06_redox.dismutases and catalases	-2.57
HY01K15	0.09	0.42	0.48	0.95	**1.04**	0.016	CATA1_HORVU Catalase isozyme 1 catalase	21.06 redox.dismutases and catalases	0.19
HU04N05	-0.02	0.26	0.36	**1.22**	0.83	0.035	CATA1_HORVU Catalase isozyme 1 catalase	21.06_redox.dismutases and catalases	0.61
HY03C01	-0.31	0.34	0.38	**1.22**	1.02	0.031	catalase [Triticum aestivum] Catalase	21.06_redox.dismutases and catalases	0.92
HO05O21	0.61	1.83	1.63	**1.91**	0.90	0.007	catalase [Secale cereale]	21.06 redox.dismutases and catalases	-2.30
HO10H12	0.93	**1.19**	0.86	0.07	0.17	0.026	putative cytochrome b5 reductase [Oryza sativa (japonica cultivar-group)]	21.06_redox.dismutases and catalases	0.11
HM14D14	-0.25	**-1.23**	-0.24	-0.41	-0.65	0.013	flavin containing polyamine oxidase [Hordeum vulgare subsp. vulgare]	22_polyamine metabolism	#NV
HW07A08	0.12	0.44	0.83	1.69	**3.02**	0.015	putative CTP synthase [Oryza sativa (japonica cultivar-group)]	23.1.1.10_nucleotide	0.53
HW07B23	0.58	-0.09	-0.10	0.59	**1.85**	0.037	putative amidophosphoribosyltransferase [Oryza sativa (japonica cultivar-	23.1.2.1_nucleotide	-0.96
HD07K22	-0.37	-0.42	-0.52	-0.70	**-1.04**	0.012	putative inosine monophosphate dehydrogenase [Oryza sativa (japonica	23.1.2.30_nucleotide	-0.23
HU02M23	-0.11	-0.80	-0.59	0.01	**-1.87**	0.020	putative GMP synthetase [Oryza sativa (japonica cultivar-group)] putative	23.1.2.31_nucleotide	0.01
HF25H14	-0.41	-0.51	-0.19	-0.55	**-1.08**	0.015	diphosphonucleotide phosphatase 1 [Zea mays]	23.2 nucleotide	-0.56
HR01E18	0.19	1.03	0.66	0.52	**1.36**	0.016	putative inosine-uridine nucleoside N-ribohydrolase [Oryza sativa (japonica	23.2_nucleotide	#NV
GCN003C	0.01	0.18	0.58	0.68	**1.49**	0.023	putative dihydropyrimidine dehydrogenase [Oryza sativa (japonica cultivar-	23.2_nucleotide	-1.25
HF08H24	-0.10	-0.43	0.21	1.05	**2.34**	0.042	putative uricase [Oryza sativa (japonica cultivar-group)] putative uricase	23.2 nucleotide	#NV
HM04K17	-0.13	0.62	**1.27**	1.24	0.21	0.023	adenine phosphoribosyltransferase [Triticum aestivum]	23.3.1.1_nucleotide	0.36
HY09I18	-0.45	**-1.76**	-0.04	-0.67	-0.06	0.033	putative adenylate k	23.4.1 nucleotide	-3.33
HI01P16	-0.31	**-1.19**	-0.50	-0.47	-1.04	0.013	inorganic pyrophosphatase [Oryza sativa (japonica cultivar-group)]	23.4.99_nucleotide	-1.67
HS01H12	-0.02	0.42	0.21	0.36	**1.65**	0.034	inorganic pyrophosphatase [Hordeum vulgare subsp. vulgare]	23.4.99_nucleotide	0.05
HA05O22	-0.27	0.56	0.53	0.74	**1.38**	0.026	putative ribonucleotide reductase [Oryza sativa (japonica cultivar-group)]	23.5_nucleotide	#NV
HB01P05	-0.34	**-1.29**	-0.32	-0.22	-0.62	0.017	putative heat shock protein [Oryza sativa (japonica cultivar-group)] putative	24_Biodegradation of Xenobiotics	-1.66
HW02B01	**1.06**	1.00	0.28	0.17	0.85	0.027	putative glyoxalase II [Oryza sativa (japonica cultivar-group)]	24 Biodegradation of Xenobiotics	0.65

HO09M09	0.26	-0.41	-1.01	-0.92	**-1.64**	0.016	OSJNBa0086B14.2 [Oryza sativa (japonica cultivar-group)]	25 C1-metabolism	0.89
HY02N05	0.18	-0.53	-0.66	-0.46	**-1.47**	0.023	GAD1 [Hordeum vulgare]	26_misc	-0.85
HY02N05	0.53	-0.76	-0.65	-0.81	**-1.48**	0.023	GAD1 [Hordeum vulgare]	26_misc	-0.85
HW05G03	0.72	**1.44**	0.84	-0.40	0.98	0.029	OSJNBa0036B21.10 [Oryza sativa (japonica cultivar-group)]	26.01 misc.misc2	0.07
HU01O19	-0.14	-0.55	-0.41	0.16	**-1.59**	0.029	'putative endo-1,3;1,4-beta-D-glucanase' [Oryza sativa (japonica cultivar-	26.01_misc.misc2	0.45
HU01O19	-0.39	-0.61	-0.37	-0.02	**-1.39**	0.029	'putative endo-1,3;1,4-beta-D-glucanase' [Oryza sativa (japonica cultivar-	26.01 misc.misc2	0.45
HO10O15	0.41	1.01	0.63	0.74	**1.25**	0.015	putative 2-nitropropane dioxygenase [Arabidopsis thaliana] putative 2-	26.01_misc.misc2	-0.29
HK03H20	0.20	0.19	0.20	1.04	**1.38**	0.028	putative glucosyltransferase [Oryza sativa (japonica cultivar-group)]	26.02_misc.UDP glucosyl and	-0.83
HO19H23	0.60	0.41	0.12	-0.16	**1.05**	0.040	hypothetical protein [Oryza sativa (japonica cultivar-group)] hypothetical	26.2_misc.UDP glucosyl and glucoronyl	0.98
HB09F20	0.39	0.19	-0.04	0.69	**1.33**	0.031	beta-glucosidase isozyme 2 precursor [Oryza sativa (japonica cultivar-	26.03_misc.gluco-, galacto- and	-0.82
HA14A09	-0.67	-0.15	-0.50	-0.88	**-2.28**	0.013	putative beta-glucosidase [Oryza sativa (japonica cultivar-group)] putative	26.03 misc.gluco-, galacto- and	1.37
HO38B03	-0.22	-0.77	-0.60	-0.59	**-2.30**	0.013	beta-glucosidase (with alternative splicing) [Oryza sativa (japonica cultivar-	26.03_misc.gluco-, galacto- and	1.05
HM03J01	-0.27	-0.55	-0.70	-0.74	**-2.20**	0.013	beta-glucosidase (with alternative splicing) [Oryza sativa (japonica cultivar-	26.03 misc.gluco-, galacto- and	0.97
HB01N04	0.35	1.16	0.02	0.75	**2.02**	0.012	beta-glucosidase [Musa acuminata]	26.03_misc.gluco-, galacto- and	0.47
HM01J08	0.13	0.95	0.72	0.73	**2.11**	0.012	beta-glucosidase [Musa acuminata]	26.03_misc.gluco-, galacto- and	0.43
HT01E20	0.41	1.50	1.54	0.44	**2.57**	0.010	beta-glucosidase [Musa acuminata]	26.03 misc.gluco-, galacto- and	0.04
HK04O19	-0.35	-0.97	-0.31	-0.02	**-1.39**	0.017	OSJNBa0004N05.21 [Oryza sativa (japonica cultivar-group)]	26.03_misc.gluco-, galacto- and	0.35
HK04O19	-0.69	-0.67	-0.54	-0.45	**-1.09**	0.017	OSJNBa0004N05.21 [Oryza sativa (japonica cultivar-group)]	26.03_misc.gluco-, galacto- and	0.35
HY01L20	1.25	**2.34**	0.49	0.00	0.62	0.020	putative beta-1,3-glucanase [Oryza sativa (japonica cultivar-group)] putative	26.04_misc.beta 1,3 glucan hydrolases	#NV
HO09H21	0.99	-0.34	0.94	0.29	**1.08**	0.042	stress responsive protein [Triticum aestivum]	26.04_misc.beta 1,3 glucan hydrolases	-3.74
HW05K08	0.70	0.67	0.03	0.48	**1.26**	0.038	putative beta-1,3-glucanase precursor [Oryza sativa (japonica cultivar-	26.04_misc.beta 1,3 glucan hydrolases	0.23
HV01J14	-0.38	-0.30	-0.72	-1.99	**-2.00**	0.026	beta glucanase:ISOTYPE=II	26.04_misc.beta 1,3 glucan hydrolases	2.27
HV01J14	-0.27	-0.87	-1.26	-0.92	**-1.49**	0.026	beta glucanase:ISOTYPE=II	26.04 misc.beta 1,3 glucan hydrolases	2.27
HV04D23	-0.23	-0.51	-0.84	-1.76	**-1.96**	0.020	beta glucanase:ISOTYPE=II	26.04_misc.beta 1,3 glucan hydrolases	1.88
HU04K16	0.63	0.01	0.82	0.87	**2.62**	0.023	putative elicitor inducible beta-1,3-glucanase NtEIG-E76 [Oryza sativa	26.04 misc.beta 1,3 glucan hydrolases	0.48
HU04K16	0.33	-0.10	0.81	0.65	**2.55**	0.023	putative elicitor inducible beta-1,3-glucanase NtEIG-E76 [Oryza sativa	26.04_misc.beta 1,3 glucan hydrolases	0.48
HB28L10	-0.25	0.88	0.12	0.92	**1.40**	0.027	Glucan endo-1,3-beta-glucosidase precursor ((1->3)-beta-glucan	26.04_misc.beta 1,3 glucan hydrolases	1.16
HO02G05	-0.16	**1.33**	0.74	0.76	0.46	0.050	putative beta-1,3-glucanase [Oryza sativa (japonica cultivar-group)] putative	26.04 misc.beta 1,3 glucan hydrolases	2.35
HU04I02	0.17	-0.86	-0.65	-0.64	**-1.12**	0.022	beta-1,3-glucanase-like protein [Oryza sativa (japonica cultivar-group)]	26.04_misc.beta 1,3 glucan hydrolases	#NV
HU03F15	-0.01	-0.13	-0.95	-1.32	**-1.55**	0.016	lichenase [Hordeum vulgare subsp. vulgare] (1-3,1-4)-beta-D-glucanase	26.04_misc.beta 1,3 glucan hydrolases	1.95
HX01M12	-0.04	0.17	-0.24	-0.43	**-2.03**	0.037	acetyltransferase 1-like [Oryza sativa (japonica cultivar-group)]	26.05_misc.acyl transferases	0.76
HO07C04	0.08	-0.21	-0.14	-0.29	**-1.01**	0.044	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	26.06_misc.O- methyl transferases	-0.06
HY01G08	1.06	1.26	0.62	1.31	**1.54**	0.004	putative Blue copper protein precursor [Oryza sativa (japonica cultivar-	26.07_misc.oxidases - copper, flavone	0.17
HH02O14	0.28	2.04	1.24	1.73	**2.44**	0.007	putative NADPH:quinone oxidoreductase [Oryza sativa (japonica cultivar-	26.07_misc.oxidases - copper, flavone	-0.38
HO11C07	1.67	**2.57**	0.18	0.09	1.92	0.011	putative blue copper binding protein [Oryza sativa (japonica cultivar-group)]	26.07 misc.oxidases - copper, flavone	#NV
HO04H13	-0.32	**-1.21**	-0.14	-0.48	-0.03	0.031	blue copper binding protein [Hordeum vulgare subsp. vulgare]	26.07_misc.oxidases - copper, flavone	-2.28
HO04J12	1.87	**2.56**	0.86	0.01	-0.18	0.025	serine/threonine protein phosphatase PP2A-1 catalytic subunit [Oryza sativa	26.07_misc.oxidases - copper, flavone	3.46
HW07J04	1.41	**2.23**	0.45	0.22	1.53	0.012	blue copper-binding protein [Oryza sativa (japonica cultivar-group)]	26.07 misc.oxidases - copper, flavone	#NV
HU02L08	0.17	0.42	0.40	-0.04	**1.55**	0.036	OSJNBa0022H21.18 [Oryza sativa (japonica cultivar-group)]	26.07_misc.oxidases - copper, flavone	-1.16
HO03P06	-0.27	-0.47	-0.33	-0.93	**-1.35**	0.010	Cation/multidrug efflux pump [Nostoc punctiforme PCC 73102]	26.09 misc.glutathione S transferases	-0.08
HD03F05	0.61	1.35	1.26	1.31	**2.37**	0.006	glutathione transferase F2 [Triticum aestivum]	26.09_misc.glutathione S transferases	0.41
HO10H15	1.40	**2.68**	1.99	1.67	1.06	0.003	unknown protein [Oryza sativa (japonica cultivar-group)]	26.09_misc.glutathione S transferases	1.77
HW05H18	0.53	0.85	0.31	0.57	**1.51**	0.015	putative glutathione S-transferase [Oryza sativa (japonica cultivar-group)]	26.09_misc.glutathione S transferases	0.31
HU01G03	-0.21	1.30	0.06	0.52	**2.99**	0.022	glutathione-S-transferase [Hordeum vulgare]	26.09_misc.glutathione S transferases	#NV
HZ61C04	0.09	-0.64	-0.10	0.75	**2.41**	0.047	glutathione-S-transferase [Hordeum vulgare]	26.09 misc.glutathione S transferases	-3.59

HW07M12	1.12	**2.87**	1.31	0.17	0.42	0.022	glutathione transferase F5 [Triticum aestivum]	26.09 misc.glutathione S transferases	0.21
HO12P05	0.68	**1.95**	0.93	0.88	1.42	0.008	glutathione transferase [Triticum aestivum] probable glutathione transferase	26.09_misc.glutathione S transferases	-0.90
HW08N18	0.74	**1.44**	0.65	1.20	1.06	0.009	glutathione transferase [Triticum aestivum] probable glutathione transferase	26.09_misc.glutathione S transferases	-0.65
HS01J15	1.30	1.50	0.76	0.88	**1.58**	0.004	glutathione transferase [Triticum aestivum] probable glutathione transferase	26.09 misc.glutathione S transferases	-1.16
HT01D11	0.54	**1.09**	0.27	0.29	0.51	0.024	glutathione transferase [Triticum aestivum] probable glutathione transferase	26.09_misc.glutathione S transferases	-0.26
HV02L23	-0.38	-0.92	-0.65	-0.58	**-2.03**	0.010	putative glutathione S-transferase [Oryza sativa (japonica cultivar-group)]	26.09 misc.glutathione S transferases	1.08
HD02A06	1.13	2.09	1.60	1.97	**3.67**	0.003	putative glutathione S-transferase [Oryza sativa]	26.09_misc.glutathione S transferases	-1.02
HW02N04	-0.03	-0.15	-0.26	**-1.48**	-0.55	0.024	glutathione S-transferase [Anopheles gambiae] ENSANGP00000018719	26.09_misc.glutathione S transferases	0.24
HU03D01	-0.05	-0.01	0.87	1.44	**3.05**	0.018	glutathione S-transferase GST 34 [Zea mays]	26.09_misc.glutathione S transferases	-0.71
HW04H20	0.39	1.44	1.86	2.87	**3.20**	0.004	glutathione transferase F4 [Triticum aestivum]	26.09_misc.glutathione S transferases	0.01
GBN004E	0.44	1.17	1.14	0.46	**1.43**	0.013	Putative glutathione S-transferase [Oryza sativa (japonica cultivar-group)]	26.09 misc.glutathione S transferases	-0.91
HO05O18	0.56	1.14	1.01	0.59	**1.20**	0.015	Putative glutathione S-transferase [Oryza sativa (japonica cultivar-group)]	26.09_misc.glutathione S transferases	-0.84
GNW001I	0.91	**1.11**	0.47	0.19	0.51	0.018	0	26.09 misc.glutathione S transferases	0.63
HW08P09	0.84	**1.03**	0.38	0.70	0.22	0.018	putative glutathione transferase [Oryza sativa (japonica cultivar-group)]	26.09_misc.glutathione S transferases	0.84
GPN002K	**1.95**	1.87	0.97	-0.21	1.32	0.013	hypothetical protein FG04588.1 [Gibberella zeae PH-1] hypothetical protein	26.10_misc.cytochrome P450	#NV
HDP35A1	-0.14	**-1.15**	-0.01	-0.52	-0.53	0.021	putative cytochrome P450 [Oryza sativa (japonica cultivar-group)] putative	26.10 misc.cytochrome P450	-0.89
HD02G17	3.23	**4.24**	1.70	1.92	1.71	0.002	putative cytochrome P450 monooxygenase [Oryza sativa (japonica cultivar-	26.10_misc.cytochrome P450	1.17
HO19C11	0.29	0.47	0.36	1.21	**2.69**	0.014	unnamed protein product [Oryza sativa (japonica cultivar-group)] sterol C-22	26.10_misc.cytochrome P450	1.27
HY03M06	-0.28	-0.83	-0.29	-0.55	**-1.13**	0.015	alcohol dehydrogenase class III [Oryza sativa (japonica cultivar-group)]	26.11_misc.alcohol dehydrogenases	-0.20
HK03F23	-0.15	-1.03	-1.00	-0.63	**-2.28**	0.015	putative alcohol dehydrogenase [Oryza sativa (japonica cultivar-group)]	26.11.01_misc.alcohol dehydrogenases	1.80
GBN002E	0.26	**1.17**	0.60	0.96	-0.20	0.024	OSJNBa0064M23.14 [Oryza sativa (japonica cultivar-group)]	26.11.01_misc.alcohol dehydrogenases	-0.86
HO13D15	1.97	**3.85**	1.25	1.46	3.40	0.003	putative peroxidase [Oryza sativa (japonica cultivar-group)] TPA: class III	26.12_misc.peroxidases	#NV
HO36H17	0.76	3.26	2.76	**3.51**	2.24	0.002	peroxidase [Hordeum vulgare]	26.12 misc.peroxidases	1.49
HK03G01	0.46	2.84	2.30	**2.94**	2.28	0.003	peroxidase [Hordeum vulgare]	26.12_misc.peroxidases	1.89
HD01A02	0.42	**3.33**	3.19	2.46	2.09	0.003	peroxidase [Hordeum vulgare]	26.12 misc.peroxidases	1.69
HD01A02	0.50	2.96	2.49	**3.16**	2.29	0.003	peroxidase [Hordeum vulgare]	26.12_misc.peroxidases	1.69
HU02O23	0.20	**1.13**	0.45	0.76	0.97	0.040	putative peroxidase [Oryza sativa (japonica cultivar-group)] PREDICTED	26.12_misc.peroxidases	1.60
HW07H16	0.42	**3.45**	3.02	2.43	1.54	0.004	peroxidase 10 [Triticum monococcum]	26.12 misc.peroxidases	#NV
HW07H16	0.25	**3.25**	2.80	2.64	1.53	0.004	peroxidase 10 [Triticum monococcum]	26.12_misc.peroxidases	#NV
HW03O08	0.21	**1.65**	1.08	0.84	1.16	0.013	peroxidase 9 [Triticum monococcum]	26.12_misc.peroxidases	2.00
HW03O08	0.32	**1.66**	1.06	0.91	1.27	0.013	peroxidase 9 [Triticum monococcum]	26.12_misc.peroxidases	2.00
HW02B05	1.33	**3.03**	1.96	1.33	1.21	0.007	peroxidase [Triticum aestivum]	26.12_misc.peroxidases	-2.49
HV02E13	0.27	**1.54**	0.86	0.93	0.53	0.017	peroxidase 2 [Triticum monococcum]	26.12_misc.peroxidases	-0.54
HV02L18	0.62	**1.39**	0.85	0.59	1.06	0.017	peroxidase 8 [Triticum monococcum]	26.12_misc.peroxidases	2.51
HW03P04	0.55	**1.72**	1.09	0.68	0.96	0.013	peroxidase 8 [Triticum monococcum]	26.12 misc.peroxidases	2.25
HW03P04	0.55	**1.47**	0.82	0.88	1.04	0.013	peroxidase 8 [Triticum monococcum]	26.12_misc.peroxidases	2.25
HD04F12	0.10	0.18	0.75	0.78	**1.20**	0.021	TPA: class III peroxidase 135 precursor [Oryza sativa (japonica cultivar-	26.12_misc.peroxidases	0.58
HO02P03	2.53	4.22	1.54	2.65	**4.57**	0.001	cytochrome c oxidase subunit Vb precursor [Oryza sativa (japonica cultivar-	26.12 misc.peroxidases	#NV
HW09H06	1.35	**2.67**	1.06	0.76	2.29	0.009	putative peroxidase [Oryza sativa (japonica cultivar-group)] TPA: class III	26.12_misc.peroxidases	1.00
HW09H06	1.01	**2.72**	0.74	0.69	2.25	0.009	putative peroxidase [Oryza sativa (japonica cultivar-group)] TPA: class III	26.12 misc.peroxidases	1.00
HE01C14	-0.50	-0.82	-0.96	**-1.80**	-1.78	0.007	peroxidase 6 [Triticum monococcum]	26.12_misc.peroxidases	0.41
HP01I20	-0.22	-1.53	-1.51	-2.02	**-3.14**	0.012	peroxidase 6 [Triticum monococcum]	26.12_misc.peroxidases	0.28
HA14O10	-0.32	-0.57	-0.25	-0.07	**-1.23**	0.019	putative peroxidase [Oryza sativa (japonica cultivar-group)] putative	26.12_misc.peroxidases	-0.83
HO37C01	-0.32	-0.24	0.07	-0.67	**-2.98**	0.046	CAA303712.1 protein [Oryza sativa]	26.12_misc.peroxidases	2.51
HY07C24	-0.22	**-1.27**	-0.52	-1.16	-0.53	0.016	OSJNBa0039K24.14 [Oryza sativa (japonica cultivar-group)]	26.12 misc.peroxidases	-2.08

HO06A23	-0.16	0.87	0.00	0.80	**1.84**	0.023	nucleotide pyrophosphatase/phosphodiesterase [Hordeum vulgare]	26.13 misc.acid and other	0.44
HO09E14	0.76	**1.86**	0.40	-0.05	0.46	0.027	0	26.13_misc.acid and other	#NV
HO04L24	0.40	**1.02**	-0.44	0.31	0.64	0.035	putative secretory acid phosphatase precursor [Oryza sativa (japonica	26.13_misc.acid and other	0.38
HDP24J2	-0.52	0.74	1.27	2.05	**2.71**	0.014	OSJNBb0108J11.20 [Oryza sativa (japonica cultivar-group)]	26.16 misc.myrosinases-lectin-jacalin	-0.41
HF01I19	1.55	**2.04**	1.24	0.82	1.69	0.004	lysine decarboxylase-like protein [Oryza sativa (japonica cultivar-group)]	26.21_misc.protease inhibitor/seed	#NV
HW04J01	1.08	**1.99**	0.53	0.22	0.14	0.017	nonspecific lipid transfer protein [Hordeum vulgare]	26.21 misc.protease inhibitor/seed	#NV
HH01B07	-0.22	-0.53	-0.31	0.19	**-1.36**	0.035	J Chain J, Trypsin:bbi Complex Chain I, Trypsin:bbi Complex	26.21.1_misc.protease inhibitor/seed	0.20
HO16H23	-0.32	-0.83	-0.40	-0.12	**-1.20**	0.014	OSJNBa0081C01.18 [Oryza sativa (japonica cultivar-group)]	26.22_misc.short chain	-0.18
HG01L11	-0.41	-0.75	-0.30	-0.76	**-1.25**	0.009	Lipid, fatty-acid and isoprenoid metabolism::OSJNBa0081C01.18 [Oryza	26.22_misc.short chain	-0.70
HW03B03	0.17	0.90	0.59	0.20	**1.12**	0.037	unnamed protein product [Oryza sativa (japonica cultivar-group)]	26.28_misc.GDSL-motif lipase	1.56
HW07N03	0.11	0.29	0.14	1.12	**1.88**	0.027	lipase-like protein [Oryza sativa (japonica cultivar-group)] lipase-like protein	26.28 misc.GDSL-motif lipase	0.40
HT01I09	0.99	1.47	1.22	1.50	**1.93**	0.004	Ferredoxin III, chloroplast precursor (Fd III) Fd III [Zea mays] ferredoxin	26.30_misc. other Ferredoxins and	-0.17
GCN003L	0.69	**1.02**	0.47	-0.13	0.55	0.032	putative RNA methyltransferases [Oryza sativa] putative RNA	27.1 RNA.processing	-0.46
HS08E10	-0.10	0.49	0.51	0.32	**1.09**	0.036	Putative FH protein interacting protein FIP1 [Oryza sativa (japonica cultivar-	27.1_RNA.processing	0.49
HY08P19	0.10	1.08	1.13	1.05	**2.04**	0.013	putative cleavage stimulation factor subunit 1 [Hordeum vulgare subsp.	27.1_RNA.processing	0.25
HO03A09	-0.11	-0.15	-0.43	-0.20	**-1.02**	0.031	putative pre-mRNA splicing factor [Oryza sativa (japonica cultivar-group)]	27.1 RNA.processing	0.91
HT01I20	0.14	-0.23	0.08	-0.39	**-1.16**	0.038	poly(A)-binding protein [Triticum aestivum]	27.1_RNA.processing	0.48
HY10G15	-0.17	-0.10	-0.31	-0.70	**-1.22**	0.021	poly(A)-binding protein [Triticum aestivum]	27.1_RNA.processing	0.30
HV01N19	-0.05	-0.13	-0.06	-0.10	**-1.03**	0.047	poly(A)-binding protein [Triticum aestivum]	27.1_RNA.processing	0.46
HA03I08	-0.03	-0.40	-0.20	-0.36	**-1.50**	0.023	putative pre-mRNA splicing factor SF2 [Oryza sativa (japonica cultivar-	27.1_RNA.processing	0.01
GBN002K	-0.33	**-1.40**	-0.87	-0.17	-0.26	0.017	triose phosphate translocator [Triticum aestivum]	27.1_RNA.processing	-1.43
HO09J01	-0.53	**-1.16**	-0.95	-1.07	-0.11	0.013	putative snRNP splicing factor -related [Oryza sativa (japonica cultivar-	27.1_RNA.processing	#NV
HS01I19	0.33	-0.31	-0.37	-0.20	**-1.96**	0.041	putative U4/U6-associated RNA splicing factor [Oryza sativa (japonica	27.1 RNA.processing	0.41
HI04L05	0.02	-0.29	-1.04	-0.95	**-1.65**	0.022	putative U5 snRNP-specific 40 kDa protein [Oryza sativa (japonica cultivar-	27.1_RNA.processing	1.66
HD03I16	-0.02	-0.39	-0.22	-0.08	**-1.20**	0.040	EST AU056133(S20320) corresponds to a region of the predicted	27.1 RNA.processing	0.73
HK04H02	-0.11	-0.65	-0.38	-0.79	**-1.39**	0.012	trans-sialidase, putative [Trypanosoma cruzi] trans-sialidase, putative	27.1.1_RNA.processing.splicing	-0.40
HF01M07	-0.19	-0.36	-0.61	-0.21	**-1.56**	0.017	putative splicing factor-like protein [Oryza sativa (japonica cultivar-group)]	27.1.1_RNA.processing.splicing	1.00
HY08D08	0.21	-0.15	-0.59	-0.19	**-1.48**	0.045	putative splicing factor [Oryza sativa (japonica cultivar-group)] putative	27.1.1 RNA.processing.splicing	0.54
HW04F22	-0.25	-0.24	-0.25	-0.82	**-1.57**	0.018	hypothetical protein [Oryza sativa (japonica cultivar-group)] hypothetical	27.1.1_RNA.processing.splicing	0.72
HR01F20	0.05	-0.32	-0.33	-0.11	**-1.04**	0.049	putative pre-mRNA splicing factor RNA helicase [Arabidopsis thaliana]	27.1.2_RNA.processing.RNA helicase	0.74
HT01M03	0.00	0.06	-0.11	-0.99	**-1.13**	0.036	putative membrane protein [Mycobacterium marinum]	27.2_RNA.transcription	0.65
HO08O22	-0.83	-0.46	-0.53	-1.27	**-1.53**	0.008	hypothetical protein [Oryza sativa (japonica cultivar-group)] hypothetical	27.2_RNA.transcription	0.98
HX06A22	-0.80	-1.07	-0.88	-0.93	**-2.23**	0.007	putative RNA polymerase transcriptional regulation mediator [Oryza sativa	27.2_RNA.transcription	0.71
HK06K04	-0.53	**-1.14**	-0.63	0.03	-0.95	0.016	putative aspartic proteinase nepenthesin I [Oryza sativa (japonica cultivar-	27.3_RNA.regulation of transcription	1.08
HM04L02	-0.75	-0.38	-0.43	-0.84	**-1.44**	0.011	OSJNBb0058J09.5 [Oryza sativa (japonica cultivar-group)]	27.3 RNA.regulation of transcription	0.30
HY02A24	-0.14	-0.16	-0.20	-0.05	**-1.02**	0.035	0	27.3_RNA.regulation of transcription	0.23
HM11G04	-0.24	-0.54	0.08	-0.48	**-1.29**	0.022	putative RNA-binding protein [Arabidopsis thaliana] putative RNA-binding	27.3_RNA.regulation of transcription	-1.70
HY10O24	-0.15	**-1.21**	-0.23	-0.31	-0.98	0.018	g5bf protein [Arabidopsis thaliana]	27.3 RNA.regulation of transcription	-2.55
HO06A09	-0.35	-0.49	-0.70	0.15	**-1.38**	0.029	Putative RNA-binding protein [Oryza sativa (japonica cultivar-group)]	27.3_RNA.regulation of transcription	0.77
HW08L08	-0.47	-0.61	-0.10	-0.39	**-1.27**	0.016	Putative RNA-binding protein [Oryza sativa (japonica cultivar-group)]	27.3 RNA.regulation of transcription	0.36
HU04C14	-0.13	**-1.01**	-0.42	0.20	-0.89	0.032	putative KH domain protein [Oryza sativa (japonica cultivar-group)] putative	27.3_RNA.regulation of transcription	0.15
HW08A05	0.18	0.03	0.84	1.58	**3.62**	0.018	RNA-binding like protein [Oryza sativa (japonica cultivar-group)]	27.3_RNA.regulation of transcription	-0.07
HM07P14	-0.78	**-1.27**	-0.22	-0.31	-0.13	0.016	transcription factor viviparous 1-like [Oryza sativa (japonica cultivar-group)]	27.3.01_RNA.regulation of	-0.59
HA07E03	0.00	-0.59	-0.57	-0.51	**-1.32**	0.019	probable zinc finger protein - alfalfa (fragment) [Oryza sativa (japonica	27.3.02_RNA.regulation of	0.05
GCW002L	0.29	0.58	0.35	0.23	**1.10**	0.030	putative myb protein [Oryza sativa (japonica cultivar-group)] putative myb	27.3.03 RNA.regulation of	#NV

HH02D09	0.02	0.65	0.72	0.90	**4.18**	0.017	AP2 transcriptional activator DRF1.3 [Hordeum vulgare] dehydration-	27.3.03 RNA.regulation of	#NV
HO19M04	-0.01	-0.41	-0.68	-0.71	**-1.64**	0.015	APETALA2 protein homolog HAP2 [Hyacinthus orientalis]	27.3.03_RNA.regulation of	1.81
HM01D04	-0.22	**-2.17**	-0.89	-0.34	-0.07	0.035	putative bHLH protein [Oryza sativa (japonica cultivar-group)] hypothetical	27.3.06_RNA.regulation of	-3.14
HDP20C0	0.18	-0.82	-0.33	-1.25	**-1.52**	0.016	unknown protein [Oryza sativa (japonica cultivar-group)]	27.3.07 RNA.regulation of	-0.24
HO09O18	0.18	-0.77	-0.31	-0.70	**-1.34**	0.019	unknown protein [Oryza sativa (japonica cultivar-group)]	27.3.07_RNA.regulation of	0.34
HO02J01	0.00	-1.25	**-1.26**	-0.81	0.19	0.017	OJ990528 30.8 [Oryza sativa (japonica cultivar-group)] OJ990528 30.8	27.3.07 RNA.regulation of	-0.53
HO13O23	-0.16	**-1.02**	-0.46	-0.22	0.06	0.029	putative zinc-finger protein [Oryza sativa (japonica cultivar-group)]	27.3.07_RNA.regulation of	#NV
HO29B24	-0.55	-0.90	-0.71	-0.04	**-1.43**	0.013	dof zinc finger protein [Hordeum vulgare subsp. vulgare]	27.3.08_RNA.regulation of	0.88
HA09H06	0.21	-0.31	-0.18	-0.11	**-1.80**	0.039	unknown protein [Oryza sativa (japonica cultivar-group)]	27.3.09_RNA.regulation of	0.13
HV11C20	-0.15	0.46	0.79	2.08	**2.60**	0.013	Putative GATA-1 zinc finger protein [Oryza sativa]	27.3.09_RNA.regulation of	-0.32
HA04E17	0.04	0.44	0.74	0.18	**1.03**	0.027	putative yabby protein [Oryza sativa (japonica cultivar-group)] unknown	27.3.10 RNA.regulation of	0.14
HA08M24	-0.18	-0.55	-0.15	-0.81	**-1.38**	0.013	putative zinc finger protein [Oryza sativa (japonica cultivar-group)] Zinc	27.3.11_RNA.regulation of	0.03
HT01J17	-0.69	**-1.78**	-0.15	0.41	-0.95	0.025	pregnancy-associated glycoprotein-4 [Capra hircus]	27.3.12 RNA.regulation of	0.69
HP01L16	-0.25	**-2.14**	-0.36	-0.72	-0.45	0.031	putative finger transcription factor [Oryza sativa (japonica cultivar-group)]	27.3.12_RNA.regulation of	-1.47
HF15E04	-0.47	-0.79	-0.09	-0.92	**-1.43**	0.010	CCAAT-box transcription factor complex WHAP4 [Triticum aestivum]	27.3.14_RNA.regulation of	0.78
HY07B17	-0.06	-0.84	-0.83	0.12	**-1.14**	0.023	chitin-inducible gibberellin-responsive protein [Oryza sativa (japonica	27.3.21 RNA.regulation of	0.98
HT04L13	-0.42	**-1.30**	-0.46	0.18	-1.17	0.020	benzothiadiazole-induced homeodomain protein 1; BTH-induced	27.3.22_RNA.regulation of	0.60
HT03O14	-0.27	-0.55	0.19	-0.75	**-1.05**	0.017	homeodomain transcription factor [Zea mays]	27.3.22_RNA.regulation of	0.47
HP06J12	-0.13	-0.48	-0.76	-0.57	**-1.17**	0.013	homeodomain protein JUBEL1 [Hordeum vulgare]	27.3.22_RNA.regulation of	1.52
HO09J14	-0.58	-0.19	-0.69	-0.65	**-1.19**	0.017	TRAP dicarboxylate transporter, DctM subunit [Polaromonas sp. JS666]	27.3.22_RNA.regulation of	1.60
HDP03K0	-0.25	-1.52	-0.99	-1.53	**-3.04**	0.009	Putative heat shock protein [Oryza sativa (japonica cultivar-group)] heat	27.3.23_RNA.regulation of	-1.20
HDP04H0	-0.17	-0.64	-0.15	-0.41	**-1.07**	0.018	MADS box protein VRT-2 [Triticum aestivum]	27.3.24_RNA.regulation of	-0.28
HT02F22	0.00	1.00	0.40	1.96	**2.63**	0.011	thaumatin-like protein TLP8 [Hordeum vulgare]	27.3.25 RNA.regulation of	-2.35
HDP01K0	-0.15	-0.48	0.00	-0.48	**-1.34**	0.020	putative response regulator 9 [Oryza sativa (japonica cultivar-group)]	27.3.25_RNA.regulation of	-0.70
HO10C18	-0.01	-0.29	-0.02	-0.65	**-1.22**	0.026	putative response regulator 9 [Oryza sativa (japonica cultivar-group)]	27.3.25 RNA.regulation of	-0.47
HO12O01	-0.67	-0.20	-1.12	-0.37	**-1.52**	0.016	putative MYB transcription factor [Oryza sativa (japonica cultivar-group)]	27.3.25_RNA.regulation of	0.96
HS01P04	0.20	0.22	0.04	**-1.12**	-1.11	0.042	putative transcriptional adaptor [Oryza sativa (japonica cultivar-group)]	27.3.26_RNA.regulation of	1.24
HO03F19	-0.20	-1.39	-0.39	-0.65	**-1.72**	0.016	von Willebrand factor type A domain containing protein [Oryza sativa	27.3.26 RNA.regulation of	1.15
HO01M09	-0.10	-1.26	-1.18	-1.01	**-1.85**	0.014	putative LHY protein [Oryza sativa (japonica cultivar-group)] putative LHY	27.3.26_RNA.regulation of	1.38
HZ52A02	-0.59	**-1.09**	-0.70	-0.55	0.25	0.018	putative MCB2 protein [Oryza sativa (japonica cultivar-group)]	27.3.26_RNA.regulation of	-0.58
HB17L11	0.08	-0.99	-0.76	-1.39	**-2.32**	0.013	myb family transcription factor-like [Oryza sativa (japonica cultivar-group)]	27.3.26_RNA.regulation of	-0.12
HO03E02	-0.13	-1.03	-0.56	-1.34	**-2.10**	0.013	axoneme-associated protein [Giardia lamblia ATCC 50803]	27.3.26_RNA.regulation of	-0.54
HZ58M22	0.28	0.75	0.44	1.08	**1.50**	0.019	Putative NAM (no apical meristem) protein [Oryza sativa (japonica cultivar-	27.3.27_RNA.regulation of	0.80
HI07N05	-0.01	0.31	0.42	1.13	**1.85**	0.019	NAC domain transcription factor [Triticum aestivum]	27.3.27_RNA.regulation of	1.21
HS01J09	-0.30	0.08	0.05	0.96	**1.87**	0.037	NAC domain transcription factor [Triticum aestivum]	27.3.27 RNA.regulation of	1.05
HO13D12	0.21	0.25	0.22	0.64	**1.81**	0.023	ankyrin-like protein [Oryza sativa (japonica cultivar-group)]	27.3.27_RNA.regulation of	1.56
HK06O09	-0.69	-0.34	-0.25	-0.83	**-2.22**	0.015	putative NAC domain protein NAC1 [Oryza sativa (japonica cultivar-group)]	27.3.27_RNA.regulation of	0.74
HU01C17	-0.08	-0.23	-0.09	-0.05	**-1.32**	0.044	ternary complex factor MIP1-like [Oryza rufipogon] ternary complex factor	27.3.27 RNA.regulation of	0.42
HO10D06	-0.20	**2.05**	1.38	0.11	0.85	0.036	TPA: WRKY transcription factor 45 [Oryza sativa (indica cultivar-group)]	27.3.32_RNA.regulation of	0.73
HO10M04	0.02	**2.89**	1.62	0.25	1.21	0.016	0	27.3.32 RNA.regulation of	0.53
HE01K23	0.22	0.60	-0.21	0.24	**1.84**	0.031	OSJNBb0015N08.8 [Oryza sativa (japonica cultivar-group)] TPA: WRKY	27.3.32_RNA.regulation of	0.98
HT01I23	-0.63	-0.74	-0.50	-0.84	**-1.38**	0.010	putative tubby related protein [Oryza sativa (japonica cultivar-group)]	27.3.33_RNA.regulation of	1.06
HA07M06	-0.57	**-1.10**	-0.75	-0.16	0.20	0.026	zinc finger-like [Oryza sativa (japonica cultivar-group)] PREDICTED	27.3.35_RNA.regulation of	#NV
HO03G11	-0.31	-0.71	-1.06	-0.80	**-1.55**	0.009	blz-1 protein [Hordeum vulgare subsp. vulgare]	27.3.35_RNA.regulation of	1.35
HY07G12	1.09	**1.57**	0.64	0.65	1.14	0.010	bZIP transcription factor-like [Oryza sativa (japonica cultivar-group)]	27.3.35 RNA.regulation of	0.15

HS03H09	1.15	**1.37**	0.29	0.30	1.27	0.013	bZIP transcription factor-like [Oryza sativa (japonica cultivar-group)]	27.3.35 RNA.regulation of	0.60
HX01H11	-0.40	-0.96	-0.07	-0.83	**-2.03**	0.010	putative zwille protein [Oryza sativa (japonica cultivar-group)] unnamed	27.3.36_RNA.regulation of	-0.12
HDP22L1	-0.47	-1.03	-0.41	-0.69	**-2.06**	0.013	IAA1 protein [Triticum aestivum]	27.3.40_RNA.regulation of	-0.14
HO04I20	-0.18	-1.30	-0.70	-0.76	**-2.07**	0.010	IAA1 protein [Triticum aestivum]	27.3.40 RNA.regulation of	-1.13
HO04H02	-0.39	-1.08	-1.23	-0.59	**-1.63**	0.009	IAA1 protein [Triticum aestivum]	27.3.40_RNA.regulation of	0.42
HW06I24	-0.09	-1.25	-0.67	-0.47	**-2.19**	0.016	IAA1 protein [Triticum aestivum]	27.3.40 RNA.regulation of	0.01
HY08I12	-0.22	**-1.21**	-0.27	-0.04	-0.69	0.045	unnamed protein product [Oryza sativa (japonica cultivar-group)]	27.3.40_RNA.regulation of	-0.76
HI01L04	-0.36	**-1.03**	-0.25	0.13	-0.77	0.023	putative aux/IAA protein [Oryza sativa (japonica cultivar-group)] putative	27.3.40_RNA.regulation of	-0.51
HA12H15	-0.32	-0.91	-0.21	-0.26	**-1.61**	0.018	putative auxin-regulated protein [Oryza sativa (japonica cultivar-group)]	27.3.40_RNA.regulation of	-0.81
HK06L22	-0.22	-1.13	-0.34	-0.04	**-1.18**	0.019	hypothetical protein PC000860.02.0 [Plasmodium chabaudi] conserved	27.3.40_RNA.regulation of	0.02
HX13M06	-0.09	-0.27	0.14	-0.15	**-1.50**	0.042	chromatin-remodeling factor CHD3 [Oryza sativa]	27.3.44 RNA.regulation of	0.10
HU02M16	-0.13	-0.70	-0.23	-0.03	**-1.18**	0.030	putative DNA methyltransferase DMT106 [Oryza sativa (japonica cultivar-	27.3.46_RNA.regulation of	-0.43
GBN007J	-0.24	**-1.33**	-0.71	-0.60	-0.69	0.012	hypothetical protein [Oryza sativa] Protein of unknown function, DUF573,	27.3.49 RNA.regulation of	0.31
HW09N04	0.51	**2.16**	0.60	0.61	2.14	0.011	putative global transcription factor group E [Oryza sativa (japonica cultivar-	27.3.52_RNA.regulation of	0.50
HA08A06	-0.41	-0.34	-0.70	-0.74	**-1.27**	0.013	unnamed protein product [Tetraodon nigroviridis]	27.3.53_RNA.regulation of	0.11
HA01B07	-0.22	-0.03	0.22	-0.60	**-1.05**	0.037	putative histone deacetylase [Oryza sativa (japonica cultivar-group)] putative	27.3.55 RNA.regulation of	0.67
HA11M22	-0.25	-0.52	-0.07	-0.26	**-1.02**	0.017	putative LEUNIG [Oryza sativa (japonica cultivar-group)] putative LEUNIG	27.3.58_RNA.regulation of	#NV
HO15D24	-0.22	-0.29	-0.65	-0.53	**-1.08**	0.015	putative methyl-binding domain protein MBD106 [Zea mays]	27.3.59_RNA.regulation of	1.09
HY08D12	0.00	-0.61	-0.29	-0.52	**-1.16**	0.023	putative methyl-binding domain protein MBD105 [Zea mays]	27.3.59_RNA.regulation of	0.06
HO31O03	-0.41	-1.06	-0.65	-0.94	**-2.15**	0.010	putative high mobility group protein [Triticum aestivum]	27.3.62_RNA.regulation of	0.81
HY01N10	-0.41	-1.10	-0.71	-0.20	**-1.18**	0.014	putative high mobility group protein [Triticum aestivum]	27.3.62_RNA.regulation of	0.35
HX04D24	-0.08	-0.02	-0.38	-0.36	**-1.28**	0.031	0	27.3.62_RNA.regulation of	1.02
HO26A03	-0.09	-0.83	-0.81	-1.21	**-2.60**	0.013	putative phosphatidylinositol/phosphatidylcholine transfer protein [Oryza	27.3.65 RNA.regulation of	1.01
HW08M08	-0.41	-0.44	0.04	-0.28	**-1.03**	0.017	OSJNBa0035I04.11 [Oryza sativa (japonica cultivar-group)]	27.3.67_RNA.regulation of	0.74
HU03G14	-0.26	-0.22	-0.20	-0.26	**-1.05**	0.026	remorin-like protein [Oryza sativa (japonica cultivar-group)] remorin-like	27.3.67 RNA.regulation of	0.71
HDP33G1	-0.32	-0.61	-0.42	-0.13	**-1.47**	0.017	putative transcription elongation factor, 5'-partial [Oryza sativa (japonica	27.3.67_RNA.regulation of	0.44
HP01C04	-0.03	0.77	1.03	0.90	**1.24**	0.012	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	27.3.71_RNA.regulation of	0.61
GCN003P	0.63	**1.01**	0.47	0.03	0.50	0.028	remorin protein-like [Oryza sativa (japonica cultivar-group)] remorin protein-	27.3.99 RNA.regulation of	1.42
HS04F20	-0.20	-0.58	-0.23	-0.39	**-1.36**	0.016	putative pollen-specific LIM domain protein [Oryza sativa (japonica cultivar-	27.3.99_RNA.regulation of	0.21
HH01F01	0.44	0.74	0.64	0.30	**1.42**	0.022	PG1 [Hordeum vulgare]	27.3.99_RNA.regulation of	0.15
HY04A08	-0.36	-0.92	-0.60	-1.23	**-1.41**	0.009	putative multiple stress-responsive zinc-finger protein [Oryza sativa	27.3.99_RNA.regulation of	0.60
HM05B17	-0.06	0.09	-0.05	-0.57	**-1.40**	0.042	putative wound inductive gene [Oryza sativa (japonica cultivar-group)]	27.3.99_RNA.regulation of	0.37
HA11H01	-0.36	**-1.63**	-0.26	-0.64	-1.03	0.013	cp31BHv [Hordeum vulgare subsp. vulgare]	27.3.99_RNA.regulation of	-2.10
HY08P02	-0.24	**-1.35**	-0.23	-0.64	-0.45	0.016	cp31BHv [Hordeum vulgare subsp. vulgare]	27.3.99_RNA.regulation of	-2.25
HO03N24	-0.67	-0.45	-0.55	-0.87	**-2.55**	0.013	putative DHHC-type zinc finger domain-containing protein [Oryza sativa	27.3.99 RNA.regulation of	3.01
HY06I01	-0.20	-0.37	0.02	-0.45	**-1.20**	0.016	putative RNA Binding Protein [Oryza sativa (japonica cultivar-group)]	27.3.99_RNA.regulation of	0.12
HO38K23	-0.66	-1.65	-0.39	-0.53	**-1.86**	0.010	OSJNBb0039L24.13 [Oryza sativa (japonica cultivar-group)]	27.3.99_RNA.regulation of	0.52
HT01O11	-0.34	**-1.17**	-0.38	-0.61	0.30	0.034	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	27.3.99 RNA.regulation of	-1.09
HA09M17	-0.38	-0.49	0.09	-0.53	**-1.68**	0.016	LIM transcription factor homolog [Zea mays]	27.3.99_RNA.regulation of	0.34
HA07J05	-0.45	-0.66	0.05	-0.36	**-1.28**	0.016	Emr1 [Triticum aestivum]	27.3.99 RNA.regulation of	-0.29
HW04J19	0.10	0.19	0.54	0.93	**2.22**	0.017	zinc finger transcription factor ZFP30 [Oryza sativa (japonica cultivar-group)]	27.3.99_RNA.regulation of	-1.24
HO09O22	-0.47	-0.51	-0.22	-0.35	**-1.57**	0.016	putative DHHC-type zinc finger domain-containing protein [Oryza sativa	27.3.99_RNA.regulation of	0.50
HA01B12	-0.19	0.26	-0.35	-0.55	**-1.72**	0.034	OSJNBa0084K01.4 [Oryza sativa (japonica cultivar-group)]	27.3.99_RNA.regulation of	0.54
HX03O05	-0.29	-0.42	-0.10	-0.55	**-1.18**	0.015		27.3.99_RNA.regulation of	0.00
HY09B21	0.16	-0.55	-0.08	**-1.18**	-0.81	0.036	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Bromus	27.4 RNA.RNA binding	-0.87

HY10N11	-0.14	0.12	0.06	**1.19**	0.75	0.042	OsGRP2 [O	27.4 RNA.RNA binding	0.06
GCW003B	0.10	-0.20	-0.24	-0.53	**-1.05**	0.041	nucleolar RNA-binding Nop10p-like protein [Oryza sativa (japonica cultivar-	27.4_RNA.RNA binding	0.26
HA12B08	-0.22	0.07	-0.07	-0.43	**-1.37**	0.035	nucleolar RNA-binding Nop10p-like protein [Oryza sativa (japonica cultivar-	27.4_RNA.RNA binding	0.57
HM08J21	-0.35	**-1.09**	-0.32	-0.48	-0.89	0.018	cp31AHv protein [Hordeum vulgare subsp. vulgare]	27.4 RNA.RNA binding	-1.80
GCA001H	-0.18	**-1.17**	0.07	-0.71	-0.48	0.020	cp31AHv protein [Hordeum vulgare subsp. vulgare]	27.4_RNA.RNA binding	-2.51
HO02H09	1.82	0.70	0.56	1.51	**2.88**	0.010	unknown protein [Oryza sativa (japonica cultivar-group)]	28.1 DNA.synthesis/chromatin	#NV
HA04M04	-0.25	-0.10	-0.14	-0.85	**-1.06**	0.019	putative RNA helicase [Oryza sativa (japonica cultivar-group)] putative RNA	28.1_DNA.synthesis/chromatin	-0.08
HA11I06	-0.22	-0.10	-0.39	-0.29	**-1.03**	0.032	protein H2B-8 [Triticum aestivum]	28.1.3_DNA.synthesis/chromatin	0.73
HA04F14	-0.14	0.13	-0.81	-0.27	**-1.28**	0.031	HSWT2B histone H2B.2 - wheat Histone H2B.2	28.1.3_DNA.synthesis/chromatin	1.13
HDP33I06	1.20	**1.95**	1.22	1.50	1.42	0.004	unnamed protein product [Tetraodon nigroviridis]	28.1.3_DNA.synthesis/chromatin	-3.46
GCA001K	0.72	1.59	0.97	1.00	**1.61**	0.004	unnamed protein product [Tetraodon nigroviridis]	28.1.3 DNA.synthesis/chromatin	-3.46
HS04E16	-0.31	-0.26	-0.37	-0.60	**-1.02**	0.019	histone 3 [Picea abies] histone H3 [Oryza sativa (japonica cultivar-group)]	28.1.3_DNA.synthesis/chromatin	1.33
GNW004B	-0.19	0.55	0.70	0.20	**1.55**	0.029	CI2D [Hordeum vulgare]	28.1.3 DNA.synthesis/chromatin	0.46
HI14A17	-0.29	0.13	-0.48	-0.26	**-1.29**	0.040	histone 3 [Picea abies] histone H3 [Oryza sativa (japonica cultivar-group)]	28.1.3_DNA.synthesis/chromatin	1.42
GNW004	-0.24	0.02	-0.48	**-1.20**	-0.68	0.031	histone H3 [Tortula ruralis]	28.1.3_DNA.synthesis/chromatin	1.30
HO10A20	1.54	**2.26**	1.43	0.71	0.06	0.013	putative peroxidase [Oryza sativa (japonica cultivar-group)] TPA: class III	28.99 DNA.unspecified	0.70
HV02D11	-0.06	-0.82	0.06	-0.18	**-1.19**	0.026	OSJNBb0020O11.15 [Oryza sativa (japonica cultivar-group)]	28.99_DNA.unspecified	0.12
HDP23F0	0.05	-0.67	0.05	**-1.02**	-0.75	0.023	metal-dependent hydrolase-like protein [Oryza sativa (japonica cultivar-	28.99_DNA.unspecified	-1.48
HZ39P17	0.19	-0.09	-0.27	-0.50	**-1.15**	0.035	chromatin-remodeling factor CHD3 [Oryza sativa]	28.99_DNA.unspecified	0.39
HB16J18	0.17	-0.14	-0.31	-0.38	**-1.36**	0.033	chromatin-remodeling factor CHD3 [Oryza sativa]	28.99_DNA.unspecified	0.35
HZ45H15	-0.25	-0.49	-0.18	-0.63	**-1.55**	0.016	putative glycyl-tRNA synthetase [Oryza sativa (japonica cultivar-group)]	29.1_protein.aa activation	-0.49
HY08M21	-0.07	-0.37	-0.20	-0.06	**-1.40**	0.038	putative glycyl-tRNA synthetase [Oryza sativa (japonica cultivar-group)]	29.1_protein.aa activation	-0.49
HD01N22	-0.12	0.34	0.00	0.27	**1.73**	0.044	putative phenylalanyl-tRNA synthetase beta chain (PheRS) [Oryza sativa	29.1 protein.aa activation	0.41
HZ53A14	-0.07	0.17	-0.12	-0.46	**-1.56**	0.036	putative Arginyl-tRNA synthetase [Oryza sativa (japonica cultivar-group)]	29.1_protein.aa activation	0.16
HX03M04	-0.08	-0.65	-0.14	-0.80	**-1.12**	0.018	putative aminoacyl-t-RNA synthetase [Oryza sativa (japonica cultivar-group)]	29.1 protein.aa activation	0.33
HO13P14	-0.09	**-1.39**	-0.24	-0.19	0.01	0.049	ribosomal protein L17-like protein [Oryza sativa (japonica cultivar-group)]	29.2.1.1_protein.synthesis.chloroplast/	#NV
HO15O23	-0.08	-0.54	-0.35	-0.94	**-1.54**	0.018	ribosomal protein L16 [Triticum aestivum] Chloroplast 50S ribosomal protein	29.2.1.1_protein.synthesis.chloroplast/	#NV
GCN001E	-0.41	-0.88	-0.14	-0.34	**-1.11**	0.016	hypothetical protein DDB0204912 [Dictyostelium discoideum] hypothetical	29.2.1.1 protein.synthesis.chloroplast/	-1.19
HG01G06	-0.34	**-1.40**	-0.22	-0.26	-0.36	0.022	putative plastid ribosomal protein CL9 [Triticum aestivum]	29.2.1.1_protein.synthesis.chloroplast/	-2.54
HY08L03	-0.41	**-1.38**	-0.46	-0.69	0.21	0.031	plastid-specific ribosomal protein 6 precursor [Spinacia oleracea]	29.2.1.1_protein.synthesis.chloroplast/	-1.90
HDP02I23	-0.28	-0.16	-0.25	-0.36	**-1.09**	0.023	putative plastid ribosomal protein L19 precursor [Oryza sativa (japonica	29.2.1.99_protein.synthesis.chloroplast/	-0.33
HM02H12	-0.40	**-1.29**	-0.60	-0.66	-0.88	0.007	putative ribosomal protein [Oryza sativa (japonica cultivar-group)] putative	29.2.1.99_protein.synthesis.chloroplast/	-1.41
HY02L10	-0.31	-0.94	-0.98	-0.30	**-1.36**	0.012	putative ribosomal protein L5 [Oryza sativa (japonica cultivar-group)] 60S	29.2.2_protein.synthesis.misc	-0.35
HY02H15	0.15	0.07	-0.21	-1.05	**-1.66**	0.033	LIM transcription factor homolog [Zea mays]	29.2.2_protein.synthesis.misc	-0.09
HA01O17	-0.03	-0.05	-0.16	-0.31	**-1.17**	0.043	ribosomal protein L6 [Triticum aestivum]	29.2.2 protein.synthesis.misc	0.42
HU02N07	-0.10	0.39	0.19	-1.07	**-1.35**	0.049	putative ribosomal protein S27 [Hordeum vulgare subsp. vulgare] putative	29.2.2_protein.synthesis.misc	0.79
HH04D07	-0.02	-0.07	-0.13	-0.35	**-2.19**	0.037	ribosomal protein s6 RPS6-2 [Oryza sativa (japonica cultivar-group)]	29.2.2_protein.synthesis.misc	0.51
HY03N20	-0.11	0.32	-0.22	-0.73	**-1.73**	0.034	putative 60S ribosomal protein L38 [Oryza sativa (japonica cultivar-group)]	29.2.2 protein.synthesis.misc	0.46
HY03N20	-0.06	0.31	-0.37	-0.61	**-1.61**	0.034	putative 60S ribosomal protein L38 [Oryza sativa (japonica cultivar-group)]	29.2.2_protein.synthesis.misc	0.46
HO18M01	-0.17	0.16	-0.08	-0.22	**-1.81**	0.041	ribosomal protein S7 [Triticum aestivum]	29.2.2 protein.synthesis.misc	-0.08
HY02G15	0.01	0.13	-0.09	-0.64	**-1.54**	0.036	ribosomal protein S7 [Triticum aestivum]	29.2.2_protein.synthesis.misc	0.07
HH02I10	0.10	0.58	0.17	0.48	**1.01**	0.023	putative ribosomal protein L32 [Oryza sativa (japonica cultivar-group)]	29.2.2_protein.synthesis.misc	0.47
HW05M07	-0.17	0.19	-0.08	-0.38	**-1.39**	0.044	putative ribosomal protein [Oryza sativa (japonica cultivar-group)] putative	29.2.2_protein.synthesis.misc	0.12
HZ01I09	-0.16	0.22	0.08	-0.74	**-1.39**	0.040	PREDICTED: similar to KIAA0050 [Pan troglodytes]	29.2.2_protein.synthesis.misc	1.03
HW03H10	0.08	0.71	0.21	0.62	**1.47**	0.022	ribosomal protein L11 [Triticum aestivum]	29.2.2 protein.synthesis.misc	0.08

GPN001K	-0.25	**1.19**	0.67	0.48	0.42	0.026	putative ribosomal protein S29 [Oryza sativa (japonica cultivar-group)]	29.2.2 protein.synthesis.misc	#NV
HZ61M20	0.03	0.04	-0.18	-0.33	**-2.24**	0.047	putative 60s Ribosomal protein L25 [Oryza sativa (indica cultivar-group)]	29.2.2_protein.synthesis.misc	0.78
HY04G14	-0.04	-0.21	-0.25	-0.09	**-1.99**	0.033	OSJNBa0029H02.21 [Oryza sativa (japonica cultivar-group)]	29.2.2_protein.synthesis.misc	0.15
HY10C21	0.06	-0.39	-0.18	-0.06	**-1.51**	0.040	60S ribosomal protein L7A [Oryza sativa (japonica cultivar-group)]	29.2.2 protein.synthesis.misc	-0.08
HD08F02	0.07	0.34	0.38	0.68	**1.25**	0.022	60S ribosomal protein L44 [Phalaenopsis hybrid cultivar]	29.2.2_protein.synthesis.misc	-0.34
HW08I06	-0.12	0.20	0.32	0.94	**1.25**	0.033	putative ribosomal protein L35A [Oryza sativa (japonica cultivar-group)]	29.2.2 protein.synthesis.misc	0.20
HH01A03	0.02	-0.02	-0.13	-1.05	**-1.19**	0.025	ribosomal protein L35A [Zea mays]	29.2.2_protein.synthesis.misc	0.61
HT01J07	0.18	-0.27	-0.22	-0.64	**-1.32**	0.037	cytoplasmatic ribosomal protein S13 [Triticum aestivum]	29.2.2_protein.synthesis.misc	0.29
HY02C07	**1.58**	1.28	0.07	0.84	-0.09	0.017	A99480 hypothetical protein SSO2991 [imported] - Sulfolobus solfataricus	29.2.2_protein.synthesis.misc	-0.07
HS01I23	-0.58	**-1.64**	-0.93	-1.02	-0.89	0.012	OJ000126_13.9 [Oryza sativa (japonica cultivar-group)] OJ000126_13.9	29.2.2_protein.synthesis.misc	0.87
HA11N18	-0.45	-0.07	0.01	-0.53	**-1.47**	0.026	putative TGF(transfoming growth factor) beta inducible nuclear protein	29.2.2 protein.synthesis.misc	-0.18
HA06D05	-0.03	-0.34	-0.18	-0.20	**-1.61**	0.027	putative ZEITLUPE [Oryza sativa (japonica cultivar-group)]	29.2.2_protein.synthesis.misc	0.60
GCA006N	-0.10	**1.51**	0.53	1.08	0.95	0.017	wali6 wali6 gene	29.2.2 protein.synthesis.misc	2.48
HW05J18	0.05	0.14	-0.29	-1.16	**-1.17**	0.032	ribosomal protein L2 [Lycopersicon esculentum] ribosomal protein L8,	29.2.2_protein.synthesis.misc	0.68
GBN002G	-0.38	-0.09	-0.25	0.23	**-1.48**	0.038	60S ribosomal protein L30-like protein [Oryza sativa (japonica cultivar-	29.2.2_protein.synthesis.misc	-0.02
HW01B06	0.13	-0.42	-0.44	0.03	**-1.21**	0.047	60S ribosomal protein L30-like protein [Oryza sativa (japonica cultivar-	29.2.2 protein.synthesis.misc	0.03
HO33E23	-0.25	-0.03	-0.20	-0.55	**-1.28**	0.029	OSJNBa0084K01.7 [Oryza sativa (japonica cultivar-group)]	29.2.2_protein.synthesis.misc	-0.82
HA02N04	-0.09	-0.15	-0.37	-0.06	**-1.40**	0.032	ribosomal protein L36 [Triticum aestivum]	29.2.2_protein.synthesis.misc	-0.24
HH01C09	0.13	-0.35	**-1.14**	-0.79	-0.22	0.032	putative anthranilate phosphoribosyltransferase [Oryza sativa (japonica	29.2.2_protein.synthesis.misc	-0.52
HW05G16	0.03	-0.42	-0.36	-0.34	**-1.36**	0.026	eukaryotic translation initiation factor 5A1 [Triticum aestivum]	29.2.3_protein.synthesis.initiation	0.20
HU01M07	-0.12	-0.30	-0.12	-0.96	**-1.36**	0.014	eukaryotic initiation factor 4A [Oryza sativa (japonica cultivar-group)]	29.2.3_protein.synthesis.initiation	0.26
GNW004	-0.09	0.14	-0.09	-0.47	**-1.71**	0.046	protein synthesis elongation factor-1 alpha [Hordeum vulgare subsp.	29.2.3_protein.synthesis.initiation	0.33
HV01F10	-0.08	-0.36	-0.03	0.00	**-1.67**	0.033	EF1A1_HORVU Elongation factor 1-alpha (EF-1-alpha)	29.2.3 protein.synthesis.initiation	0.49
HO06G24	-0.02	0.21	-0.16	-0.59	**-1.60**	0.046	elongation factor 1-alpha [Hordeum vulgare subsp. vulgare] Elongation	29.2.3_protein.synthesis.initiation	0.83
HX02M17	-0.20	-0.16	-0.08	-0.05	**-1.07**	0.042	cap-binding protein CBP20 [Oryza sativa (japonica cultivar-group)]	29.2.3 protein.synthesis.initiation	0.40
HY10O17	0.18	0.09	-0.44	-0.16	**-1.60**	0.050	EF1A1_HORVU Elongation factor 1-alpha (EF-1-alpha)	29.2.3_protein.synthesis.initiation	1.11
HA08E24	-0.28	-0.36	-0.11	0.12	**-1.41**	0.028	protein synthesis elongation factor-1 alpha [Hordeum vulgare subsp.	29.2.3_protein.synthesis.initiation	0.99
HW01C16	-0.27	**-1.11**	-0.30	-0.34	-0.53	0.019	translation initiation factor 5A [Oryza sativa (japonica cultivar-group)]	29.2.3 protein.synthesis.initiation	-0.68
HH04I05	-0.50	-0.64	-0.48	**-1.50**	-1.05	0.016	low temperature-responsive RNA-binding protein	29.2.3_protein.synthesis.initiation	1.77
HS04J20	-0.21	-0.31	-0.36	-0.19	**-1.12**	0.022	putative MYB29 protein [Oryza sativa (japonica cultivar-group)] putative	29.2.4_protein.synthesis.elongation	1.11
HY09J03	-0.04	-0.04	-0.32	0.00	**-1.48**	0.043	putative elongation factor 1-gamma [Oryza sativa (japonica cultivar-group)]	29.2.4_protein.synthesis.elongation	0.20
HV03F11	-0.02	0.36	1.34	2.68	**4.01**	0.010	xylanase inhibitor [Hordeum vulgare]	29.2.4_protein.synthesis.elongation	0.42
HY05B23	-0.18	-0.23	0.03	-0.19	**-2.27**	0.034	putative elongation factor 1 beta [Hordeum vulgare subsp. vulgare]	29.2.4_protein.synthesis.elongation	0.51
HO34D10	-0.15	-0.11	-0.14	-0.54	**-1.95**	0.025	elongation factor 1 beta' [Triticum aestivum] translation elongation factor	29.2.4_protein.synthesis.elongation	0.07
HW05H20	-0.11	-0.46	-0.41	**-1.17**	-0.72	0.013	translation initiation factor [Triticum aestivum]	29.2.4 protein.synthesis.elongation	-0.59
HO03H09	-0.01	-0.38	-0.87	-0.49	**-1.38**	0.016	OSJNBa0091D06.15 [Oryza sativa (japonica cultivar-group)]	29.2.4_protein.synthesis.elongation	1.15
HA03M20	-0.12	0.03	-0.47	-0.47	**-1.09**	0.029	unknown protein [Arabidopsis thaliana] unknown protein [Arabidopsis	29.3.1_protein.targeting.nucleus	1.11
HE01F18	-0.09	**-1.11**	-0.90	-0.63	-0.66	0.012	putaive mitochondrial inner membrane protein [Oryza sativa (japonica	29.3.2 protein.targeting.mitochondria	-1.15
HE01B19	-0.12	**-1.01**	-0.95	-0.87	-0.17	0.015	amino acid selective channel protein [Hordeum vulgare subsp. vulgare]	29.3.2_protein.targeting.mitochondria	-2.30
HX02F10	-0.25	0.01	0.15	-0.35	**-1.22**	0.044	small zinc finger-like protein [Oryza sativa] Mitochondrial import inner	29.3.2 protein.targeting.mitochondria	0.02
HS01A06	0.73	**1.63**	0.85	0.41	-0.06	0.017	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	29.3.2_protein.targeting.mitochondria	0.32
HV02H04	0.91	0.34	-0.15	0.20	**1.59**	0.029	putative vacuolar targeting receptor [Oryza sativa (japonica cultivar-group)]	29.3.4.3_protein.targeting.secretory	1.07
HA28B06	-0.46	-1.03	-0.42	-0.67	**-1.87**	0.010	asparaginyl endopeptidase [Oryza sativa (japonica cultivar-group)] putative	29.3.4.3_protein.targeting.secretory	0.74
GCW001A	-0.37	-1.13	-0.38	-0.63	**-1.40**	0.011	legumain-like protease [Zea mays]	29.3.4.3_protein.targeting.secretory	1.70
HT02G12	-0.85	-1.17	-0.65	-1.07	**-1.53**	0.004	C13 endopeptidase NP1 precursor [Zea mays]	29.3.4.3 protein.targeting.secretory	1.39

HI01O08	-0.10	-0.58	-0.33	-0.30	**-1.62**	0.019	putative ADP-ribosylation factor [Oryza sativa (japonica cultivar-group)]	29.3.4.99 protein.targeting.secretory	-0.09
HZ64A18	-0.19	-0.40	-0.28	-0.08	**-1.77**	0.029	putative ADP-ribosylation factor [Oryza sativa (japonica cultivar-group)]	29.3.4.99_protein.targeting.secretory	1.21
HY09D08	0.04	-0.52	-0.19	-0.23	**-1.71**	0.030	putative ADP-ribosylation factor [Oryza sativa (japonica cultivar-group)]	29.3.4.99_protein.targeting.secretory	-0.36
HK04F03	-0.30	-0.73	-0.19	-0.75	**-1.14**	0.010	signal recognition particle 54 kDa subunit [Hordeum vulgare] Signal	29.3.4.99 protein.targeting.secretory	-0.28
HY10O21	-0.20	-0.36	-0.47	-0.32	**-1.05**	0.026	putative signal recognition particle 72KD protein [Oryza sativa (japonica	29.3.4.99_protein.targeting.secretory	1.00
GNW001B	-0.21	0.04	0.11	**-1.14**	-0.24	0.042	putative signal recognition particle receptor beta subunit (SR-beta) [Oryza	29.3.4.99 protein.targeting.secretory	0.10
HW02H19	0.08	0.94	1.28	1.43	**1.65**	0.009	putative signal recognition particle receptor [Oryza sativa (japonica cultivar-	29.3.4.99_protein.targeting.secretory	0.32
GCA004F	1.37	**1.77**	0.55	0.07	0.66	0.016	P0697C12.13 [Oryza sativa (japonica cultivar-group)]	29.3.4.99_protein.targeting.secretory	0.19
HW06P02	0.02	0.49	0.13	0.57	**1.23**	0.029	putative ADP-ribosylation factor [Oryza sativa (japonica cultivar-group)]	29.3.4.99_protein.targeting.secretory	-0.80
HW08L06	0.34	-0.29	-0.27	0.71	**1.78**	0.039	putative protein phosphatase type-2C [Oryza sativa (japonica cultivar-	29.4_protein.postranslational	-0.83
HO02D22	-0.42	-0.41	-0.75	-1.15	**-2.50**	0.014	OSJNBa0058G03.4 [Oryza sativa (japonica cultivar-group)]	29.4 protein.postranslational	0.37
HK06G09	-0.32	-0.28	-0.51	-1.15	**-2.03**	0.015	putative protein kinase [Oryza sativa (japonica cultivar-group)] putative	29.4_protein.postranslational	0.07
HA11P14	-0.23	-0.54	-0.59	-0.23	**-1.13**	0.017	F20B17.6 [Arabidopsis thaliana]	29.4 protein.postranslational	1.65
HO07O13	0.06	-0.10	-0.23	-0.31	**-1.11**	0.049	putative CRK1 protein(cdc2-related kinase 1) [Oryza sativa (japonica	29.4_protein.postranslational	1.59
HW03G06	0.33	**1.29**	0.76	0.78	1.12	0.014	putative tyrosine phosphatase [Arabidopsis thaliana] tyrosine phosphatase-	29.4_protein.postranslational	2.05
GBN003O	0.17	-0.47	0.04	-0.64	**-1.42**	0.046	SRPK4 [Oryza sativa] SRPK4 [Oryza sativa]	29.4 protein.postranslational	1.23
HDP14F2	-0.31	0.78	0.86	0.66	**1.84**	0.017	OSJNBa0084K11.9 [Oryza sativa (japonica cultivar-group)]	29.4_protein.postranslational	#NV
HY06C05	-0.03	-0.16	-0.01	-0.16	**-1.48**	0.050	unnamed protein product [Oryza sativa (japonica cultivar-group)] putative	29.4_protein.postranslational	0.34
HY03N07	0.13	0.03	-0.02	-0.89	**-1.44**	0.039	unnamed protein product [Oryza sativa (japonica cultivar-group)] putative	29.4_protein.postranslational	0.77
HH01O06	-0.17	-0.11	-0.38	-0.53	**-2.06**	0.022	putative proteinase inhibitor [Hordeum vulgare subsp. vulgare]	29.4_protein.postranslational	0.22
GBN008H	-0.67	0.36	-0.36	-0.33	**-1.12**	0.040	B1060H01.30 [Oryza sativa (japonica cultivar-group)] unknown protein	29.4_protein.postranslational	0.32
HX04M22	-0.08	-0.19	-0.42	-0.80	**-1.11**	0.016	unnamed protein product [Oryza sativa (japonica cultivar-group)] putative	29.4_protein.postranslational	0.41
HT02O18	-0.15	-0.32	-0.17	-0.14	**-1.38**	0.035	putative protein kinase ADK1 [Oryza sativa (japonica cultivar-group)]	29.4 protein.postranslational	0.70
HX01D11	-0.14	0.13	0.06	-0.74	**-1.05**	0.042	serine/threonine protein phosphatase PP2A-5 catalytic subunit [Oryza sativa	29.4_protein.postranslational	-0.41
HK05N12	0.49	**1.21**	0.14	0.55	0.92	0.013	At5g20635 [Arabidopsis thaliana] putative protein [Arabidopsis thaliana]	29.4 protein.postranslational	-1.29
GNW001	-0.19	-0.67	-0.94	-0.48	**-1.41**	0.016	putative casein kinase I [Oryza sativa (japonica cultivar-group)] casein	29.4_protein.postranslational	2.05
HW03M18	-0.03	1.19	0.62	0.67	**1.44**	0.015	putative protein phosphatase 2C [Oryza sativa (japonica cultivar-group)]	29.4_protein.postranslational	-0.41
HF16L24	0.08	-0.28	-0.23	-0.60	**-1.12**	0.035	serine/threonine protein phosphatase PP2A-2 catalytic subunit [Oryza sativa	29.4 protein.postranslational	-0.55
HI05E01	-0.04	0.04	-0.16	**-1.05**	-1.00	0.031	putative calmodulin [Oryza sativa (japonica cultivar-group)] PREDICTED	29.4_protein.postranslational	0.78
HO05M11	-0.56	**-1.63**	-1.30	-1.04	-1.45	0.004	CIPK-like protein [Oryza sativa (japonica cultivar-group)] CIPK-like protein 1	29.4_protein.postranslational	2.27
HO03B22	0.09	1.06	0.75	1.96	**3.86**	0.011	casein protein kinase 2 alpha subunit [Lolium perenne]	29.4_protein.postranslational	#NV
HM01J20	-0.14	0.88	1.00	-0.05	**1.11**	0.032	putative Phosphatidylinositol N-acetylglucosaminyltransferase [Oryza sativa	29.4_protein.postranslational	0.61
HO10P19	-0.17	-0.75	-0.29	-0.41	**-1.68**	0.015	putative wpk4 protein kinase [Oryza sativa (japonica cultivar-group)] putative	29.4_protein.postranslational	0.52
HY07O11	0.25	-0.42	-0.12	-0.33	**-1.03**	0.047	putative wpk4 protein kinase [Oryza sativa (japonica cultivar-group)]	29.4_protein.postranslational	1.09
HA04I07	-0.29	-0.80	-0.47	-0.42	**-1.81**	0.014	putative wpk4 protein kinase [Oryza sativa (japonica cultivar-group)] putative	29.4 protein.postranslational	1.46
HY04E03	-0.23	-0.67	-0.45	-0.40	**-1.18**	0.016	expressed protein [Oryza sativa (japonica cultivar-group)]	29.4_protein.postranslational	0.39
HW04N20	0.02	-0.20	-0.47	-0.18	**-1.07**	0.033	putative protein kinase [Oryza sativa (japonica cultivar-group)]	29.4_protein.postranslational	0.06
HO11N24	0.68	**1.88**	0.88	0.71	1.02	0.012	OSJNBa0088H09.6 [Oryza sativa (japonica cultivar-group)]	29.4.1.52 protein.postranslational	#NV
HO09A14	1.59	**3.14**	1.17	1.76	1.72	0.003	Putative serine/threonine protein kinase [Oryza sativa (japonica cultivar-	29.4.1.57_protein.postranslational	1.47
HO08D21	-0.40	-0.48	-0.61	-0.60	**-1.02**	0.009	putative PTI1-like kinase [Zea mays]	29.4.1.58 protein.postranslational	0.33
HB01N12	-0.05	-0.87	0.18	-0.06	**-1.27**	0.040	replication protein A 70kDa [Oryza sativa (japonica cultivar-group)]	29.5_protein.degradation	-1.43
HD01J13	0.42	1.11	0.88	-0.16	**1.31**	0.021	nucellin-like aspartic protease [Zea mays]	29.5_protein.degradation	-0.95
HO09L21	-0.14	0.65	0.42	0.33	**1.21**	0.033	nucellin-like aspartic protease [Oryza sativa (japonica cultivar-group)]	29.5_protein.degradation	#NV
HD03N01	-0.28	-0.48	-0.12	-0.10	**-1.23**	0.029	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	29.5_protein.degradation	-0.02
HM02I21	-0.01	1.47	**2.18**	2.02	1.37	0.010	subtilisin-like serine protease AIR3-like protein [Oryza sativa (japonica	29.5.01 protein.degradation.subtilases	#NV

HM02I21	-0.24	1.26	1.81	**2.18**	1.06	0.010	subtilisin-like serine protease AIR3-like protein [Oryza sativa (japonica	29.5.01 protein.degradation.subtilases	#NV
HO14K19	0.86	**1.89**	0.90	1.05	0.46	0.018	putative subtilisin-like serine proteinase [Oryza sativa (japonica cultivar-	29.5.01_protein.degradation.subtilases	1.60
HO10M21	1.95	**3.35**	2.96	1.66	1.32	0.004	putative subtilisin-like serine proteinase [Oryza sativa (japonica cultivar-	29.5.01_protein.degradation.subtilases	1.57
HW06J24	1.82	**2.78**	2.23	1.06	1.02	0.006	putative subtilisin-like serine proteinase [Oryza sativa (japonica cultivar-	29.5.01 protein.degradation.subtilases	0.89
GBN007O	0.11	-0.10	0.71	0.99	**1.05**	0.041	cysteine proteinase Mir3 [Zea mays]	29.5.03_protein.degradation.cysteine	-1.26
HW04F17	-0.36	0.35	0.75	**1.11**	0.66	0.035	cysteine proteinase Mir3 [Zea mays]	29.5.03 protein.degradation.cysteine	-0.17
HK04C12	-0.75	**-2.72**	-1.77	-1.14	0.15	0.016	putative thiol protease [Hordeum vulgare subsp. vulgare]	29.5.03_protein.degradation.cysteine	-1.16
HK04I21	-0.16	**-2.48**	-1.51	-0.81	-0.63	0.014	putative thiol protease [Hordeum vulgare subsp. vulgare]	29.5.03_protein.degradation.cysteine	0.21
HP01O19	-0.49	**-3.07**	-1.27	-0.91	0.01	0.025	putative thiol protease [Hordeum vulgare subsp. vulgare]	29.5.03_protein.degradation.cysteine	-1.01
HY10O06	-0.34	0.20	0.87	0.93	**1.46**	0.033	aspartic proteinase [Hordeum vulgare subsp. vulgare] Phytepsin precursor	29.5.04_protein.degradation.aspartate	0.33
HY10O06	-0.56	0.05	0.65	1.07	**1.44**	0.033	aspartic proteinase [Hordeum vulgare subsp. vulgare] Phytepsin precursor	29.5.04 protein.degradation.aspartate	0.33
HP11G05	0.11	0.04	-0.50	-1.08	**-1.09**	0.046	serine carboxylase II-3 [Hordeum vulgare subsp. vulgare] CP-MII.3=serine	29.5.05_protein.degradation.serine	0.16
HW08A02	0.78	-0.39	0.15	1.01	**1.84**	0.048	ATP-dependent Clp protease ATP-binding subunit precursor [Oryza sativa	29.5.05 protein.degradation.serine	-2.92
HY05C20	**1.50**	0.98	0.12	0.88	-0.48	0.038	ATP-dependent protease [Oryza sativa (japonica cultivar-group)]	29.5.05_protein.degradation.serine	0.14
HY06E11	-0.09	-0.18	-0.19	-0.48	**-1.09**	0.024	serine carboxypeptidase II-1 [Hordeum vulgare subsp. vulgare] CP-	29.5.05_protein.degradation.serine	0.54
HDP24H1	0.18	0.13	0.39	0.56	**1.19**	0.034	putative zinc protease PQQL [Oryza sativa (japonica cultivar-group)]	29.5.07 protein.degradation.metalloprot	-0.20
HY04D22	0.33	0.93	0.62	0.64	**1.41**	0.013	putative AAA-type ATPase [Oryza sativa (japonica cultivar-group)] putative	29.5.09_protein.degradation.AAA type	-0.03
HP01M22	0.36	-0.04	0.32	0.68	**1.42**	0.027	hypothetical protein [Oryza sativa (japonica cultivar-group)] hypothetical	29.5.09_protein.degradation.AAA type	0.79
HY04H05	-0.12	-0.85	-0.70	-0.83	**-1.21**	0.015	putative transaldolase ToTAL2 [Oryza sativa (japonica cultivar-group)]	29.5.09_protein.degradation.AAA type	0.02
HS03I12	0.55	2.29	1.37	0.89	**2.34**	0.005	ATPase 2 [Hordeum vulgare subsp. vulgare]	29.5.09_protein.degradation.AAA type	#NV
HW07F14	0.29	0.66	0.35	0.48	**1.00**	0.022	putative N-ethylmaleimide sensitive fusion protein [Oryza sativa (japonica	29.5.09_protein.degradation.AAA type	0.15
HM03L01	-0.19	-0.10	-0.29	-0.17	**-1.39**	0.027	polyubiquitin 2 [Oryza sativa (japonica cultivar-group)] polyubiquitin 2 [Oryza	29.5.11_protein.degradation.ubiquitin	0.03
HW04A19	-0.36	0.20	0.13	1.65	**2.43**	0.027	polyubiquitin 2 [Oryza sativa (japonica cultivar-group)] polyubiquitin 2 [Oryza	29.5.11 protein.degradation.ubiquitin	0.85
HO05P05	-0.29	-0.38	0.28	-0.38	**-1.38**	0.031	putative ubiquitin conjugating enzyme [Oryza sativa (japonica cultivar-	29.5.11_protein.degradation.ubiquitin	0.20
HD03P22	0.26	-0.61	-0.35	-0.62	**-1.31**	0.022	putative ubiquitin conjugating enzyme [Oryza sativa (japonica cultivar-	29.5.11 protein.degradation.ubiquitin	-0.37
HW06O23	-0.48	-0.73	-0.63	-0.78	**-1.41**	0.008	ubiquitin-conjugating enzyme OsUBC5a [Oryza sativa (japonica cultivar-	29.5.11.03_protein.degradation.ubiquiti	0.28
HY05M15	0.12	-0.05	-0.48	-0.44	**-1.11**	0.043	ubiquitin conjugating enzyme [Oryza sativa (japonica cultivar-group)]	29.5.11.03_protein.degradation.ubiquiti	0.22
HH01J04	0.21	0.12	-0.36	-0.24	**-1.48**	0.048	ubiquitin-conjugating enzyme protein E2 [Zea mays]	29.5.11.03 protein.degradation.ubiquiti	0.37
HD04N16	-0.10	0.14	-0.17	-0.75	**-1.29**	0.031	putative ubiquitin-conjugating enzyme family protein [Oryza sativa (japonica	29.5.11.03_protein.degradation.ubiquiti	0.87
HW06E08	-0.07	-0.24	0.31	1.11	**2.68**	0.045	putative acetohydroxyacid isomeroreductase [Oryza sativa (japonica	29.5.11.03_protein.degradation.ubiquiti	0.50
HDP18O1	-0.44	0.14	-0.40	-0.66	**-1.53**	0.020	putative ubiquitin-conjugating enzyme [Oryza sativa (japonica cultivar-	29.5.11.03_protein.degradation.ubiquiti	1.11
HW06P20	-0.02	-0.05	-0.46	-1.01	**-1.17**	0.021	ubiquitin conjugating enzyme [Oryza sativa (japonica cultivar-group)]	29.5.11.03_protein.degradation.ubiquiti	0.36
HW08I19	0.51	0.09	0.50	0.79	**1.68**	0.015	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	29.5.11.04.02_protein.degradation.ubiq	0.32
HO15D13	0.07	-0.45	-0.10	-0.75	**-1.23**	0.022	PREDICTED P0680A05.13 gene product [Oryza sativa (japonica cultivar-	29.5.11.04.02_protein.degradation.ubiq	0.80
HW04M23	-0.56	-0.96	-0.79	-0.39	**-1.52**	0.015	putative PGPD14 protein (pollen germination related protein) [Oryza sativa	29.5.11.04.02 protein.degradation.ubiq	1.57
HI02J10	-0.32	**-1.15**	-0.74	-0.17	0.34	0.040	putative hydroxyproline-rich glycoprotein [Oryza sativa (japonica cultivar-	29.5.11.04.02_protein.degradation.ubiq	-1.15
HS01N13	0.05	1.25	0.85	0.59	**1.25**	0.015	copine III-like [Oryza sativa (japonica cultivar-group)] copine III-like [Oryza	29.5.11.04.02_protein.degradation.ubiq	1.08
HT01G08	0.64	0.68	-0.84	0.38	**2.06**	0.050	0	29.5.11.04.02 protein.degradation.ubiq	1.84
GCN003F	-0.19	**-1.08**	-0.36	-0.24	-0.11	0.031	H+-transporting ATP synthase chain 9-like protein [Oryza sativa (japonica	29.5.11.04.02_protein.degradation.ubiq	-2.54
HW07L17	-0.25	**-1.13**	-0.80	-0.46	-0.75	0.009	unnamed protein product [Oryza sativa (japonica cultivar-group)] unknown	29.5.11.04.03.02 protein.degradation.u	-1.29
HW02J08	0.46	0.74	0.05	0.40	**1.79**	0.020	kelch repeat-containing F-box-like [Oryza sativa (japonica cultivar-group)]	29.5.11.04.03.02_protein.degradation.u	-1.04
HW07A04	-0.01	0.20	0.52	1.75	**2.17**	0.020	kelch repeat-containing F-box-like [Oryza sativa (japonica cultivar-group)]	29.5.11.04.03.02_protein.degradation.u	0.47
HT01M14	-0.09	0.11	0.26	1.57	**2.28**	0.025	kelch repeat-containing F-box-like [Oryza sativa (japonica cultivar-group)]	29.5.11.04.03.02_protein.degradation.u	0.08
HF02M16	-0.44	-0.53	-0.83	-0.57	**-1.09**	0.009	hypothetical protein [Oryza sativa (japonica cultivar-group)] hypothetical	29.5.11.04.03.02_protein.degradation.u	0.29
HF03K09	-0.39	-0.55	-0.08	-0.68	**-1.43**	0.013	Putative ubiquitin-specific protease 3 [Oryza sativa (japonica cultivar-group)]	29.5.11.05 protein.degradation.ubiquiti	0.36

HI01J10	-0.21	-0.42	-0.24	-0.01	**-1.77**	0.029	putative ubiquitin-specific protease 23 [Oryza sativa (japonica cultivar-	29.5.11.05 protein.degradation.ubiquiti	0.62
HH01O12	-0.24	-0.08	-0.21	-0.19	**-1.14**	0.028	PSA5_ORYSA Proteasome subunit alpha type 5 (20S proteasome alpha	29.5.11.20_protein.degradation.ubiquiti	1.09
HV01B09	-0.05	-0.55	-0.39	0.01	**-2.20**	0.044	heat shock protein cognate 70 [Oryza sativa (japonica cultivar-group)] heat	29.6_protein.folding	0.86
HW08J03	-0.07	-0.04	-0.31	-0.15	**-2.29**	0.036	beta-glucosidase [Oryza sativa (japonica cultivar-group)]	29.6 protein.folding	0.95
GCN001D	-0.14	0.23	0.28	**-1.41**	-0.69	0.049	hypothetical protein FG04322.1 [Gibberella zeae PH-1] hypothetical protein	30.1_signalling.in sugar and nutrient	1.40
HO04E10	-0.49	-0.23	-0.56	-1.31	**-2.03**	0.015	pyruvate dehydrogenase kinase 1 [Oryza sativa (japonica cultivar-group)]	30.1 signalling.in sugar and nutrient	0.73
HO15M04	-0.58	-0.26	-0.23	-0.64	**-1.72**	0.023	pyruvate dehydrogenase kinase 1 [Oryza sativa (japonica cultivar-group)]	30.1_signalling.in sugar and nutrient	1.54
HO06C07	0.08	-0.08	-0.47	-0.41	**-1.25**	0.043	BP-5 protein [Oryza sativa]	30.11_signalling.light	1.37
HW05D16	0.81	0.14	-0.11	0.42	**2.15**	0.022	putative protein kinase [Oryza sativa (japonica cultivar-group)] putative	30.2.11_signalling.receptor	-0.28
HM03L11	-0.77	**-1.03**	-0.95	0.09	0.02	0.027	hypothetical protein [Oryza sativa (japonica cultivar-group)]	30.2.17_signalling.receptor	1.27
HO10E22	2.13	**2.50**	1.62	0.61	0.04	0.013	putative receptor-type protein kinase LRK1 [Oryza sativa (japonica cultivar-	30.2.19 signalling.receptor	0.85
GBN003E	**1.29**	1.24	0.52	0.75	0.02	0.017	putative receptor protein kinase-like protein [Oryza sativa (japonica cultivar-	30.2.19_signalling.receptor	1.57
HO05A19	**1.19**	1.16	0.73	0.42	-0.09	0.032	putative receptor protein kinase-like protein [Oryza sativa (japonica cultivar-	30.2.19 signalling.receptor	1.14
HW07J23	0.80	0.64	0.68	0.47	**1.69**	0.014	putative wall-associated protein kinase [Oryza sativa (japonica cultivar-	30.2.19_signalling.receptor	-0.41
HO14K22	0.71	**1.54**	0.80	0.15	-0.34	0.041	somatic embryogenesis protein kinase 1 [Oryza sativa (japonica cultivar-	30.2.2_signalling.receptor	0.68
HO23E13	-0.02	-0.92	-0.38	-0.60	**-1.77**	0.015	putative S-receptor kinase KIK1 precursor [Oryza sativa (japonica cultivar-	30.2.24 signalling.receptor kinases.S-	-0.09
HF19O04	-0.27	**-1.29**	-0.42	-0.11	0.07	0.031	leucine-rich repeat transmembrane protein kinase 1 [Zea mays]	30.2.5_signalling.receptor	0.31
HU02N02	-0.01	-0.93	-0.72	-0.82	**-1.19**	0.015	TMK [Oryza sativa (indica cultivar-group)]	30.2.9_signalling.receptor	0.90
HA05F15	-0.58	-0.38	-1.25	-0.38	**-1.46**	0.013	putative leucine-rich receptor-like protein kinase [Oryza sativa (japonica	30.2.99_signalling.receptor	1.15
GBN003M	-0.74	**-1.26**	-0.66	-0.70	-0.41	0.007	predicted protein [Neurospora crassa] predicted protein [Neurospora crassa]	30.2.99_signalling.receptor	#NV
HI05D09	0.05	-0.48	**-1.08**	-0.36	-0.45	0.026	receptor-like protein kinase-like protein [Oryza sativa (japonica cultivar-	30.2.99_signalling.receptor	-0.53
HY09L05	-0.61	-1.10	-0.80	-0.42	**-1.11**	0.008	putative calcineurin B subunit [Oryza sativa (japonica cultivar-group)]	30.3_signalling.calcium	-0.47
HW07M16	-0.33	-0.25	-0.43	-1.28	**-2.21**	0.012	unknown protein [Oryza sativa (japonica cultivar-group)]	30.3 signalling.calcium	1.42
HA05C13	-0.12	-0.19	-0.99	-0.56	**-1.31**	0.016	O-GlcNAc-transferase-like protein [Castanea sativa]	30.3_signalling.calcium	1.12
HA06N06	0.01	**-1.57**	-0.38	-0.83	-1.06	0.019	Fructose-bisphosphate aldolase class-I [Oryza sativa (japonica cultivar-	30.3 signalling.calcium	-2.97
HO14L11	-0.31	-0.94	-0.64	**-1.16**	-0.53	0.011	OSJNBa0058G03.4 [Oryza sativa (japonica cultivar-group)]	30.3_signalling.calcium	#NV
HH02M23	0.21	**1.07**	0.55	-0.08	0.60	0.034	putative receptor-mediated endocytosis 1 isoform I [Oryza sativa (japonica	30.3_signalling.calcium	-0.22
HO13H20	0.32	**1.04**	0.94	0.72	-0.14	0.025	putative calmodulin [Oryza sativa (japonica cultivar-group)] putative	30.3 signalling.calcium	0.82
HF01P22	**1.32**	0.97	0.07	-0.23	0.24	0.037	OSJNBb0012E08.10 [Oryza sativa (japonica cultivar-group)]	30.3_signalling.calcium	0.58
HW08P01	0.60	-0.29	0.15	0.71	**1.86**	0.044	unknown [Pasteurella multocida subsp. multocida str. Pm70] hypothetical	30.3_signalling.calcium	-2.63
HZ01D16	0.83	**2.14**	1.25	0.81	0.99	0.010	calmodulin-like protein [Arabidopsis thaliana] At3g10190 [Arabidopsis	30.3_signalling.calcium	0.74
HO05J14	0.06	-0.98	**-1.15**	-0.67	0.10	0.027	OSJNBb0020J19.9 [Oryza sativa (japonica cultivar-group)]	30.4_signalling.phosphinositides	0.03
HW08C16	0.28	-0.65	-0.17	-0.04	**-1.29**	0.049	FYVE finger-containing phosphoinositide kinase-like [Oryza sativa (japonica	30.4_signalling.phosphinositides	0.76
HU01M09	-0.63	**-1.31**	-1.11	-0.33	-1.08	0.007	phosphatidylinositol 3- and 4-kinase family-like [Oryza sativa (japonica	30.4_signalling.phosphinositides	0.15
HY03P07	-0.31	-1.13	-0.83	**-1.62**	-1.49	0.005	phosphatidylinositol 3- and 4-kinase family-like [Oryza sativa (japonica	30.4 signalling.phosphinositides	0.85
HX02N10	-0.09	-0.55	-0.36	-0.29	**-1.52**	0.019	phosphatidylinositol 4-phosphate 5-kinase [Oryza sativa (japonica cultivar-	30.4_signalling.phosphinositides	1.25
HO05F22	0.54	2.29	2.44	4.99	**5.64**	0.001	OSJNBb0067G11.10 [Oryza sativa (japonica cultivar-group)]	30.5_signalling.G-proteins	#NV
HO01H24	0.13	1.01	0.80	1.12	**1.28**	0.010	calreticulin	30.5 signalling.G-proteins	0.76
HY01C23	0.13	0.65	0.38	0.53	**1.09**	0.018	unknow protein [Oryza sativa (japonica cultivar-group)]	30.5_signalling.G-proteins	0.35
GCW003	-0.02	0.51	0.64	0.57	**1.34**	0.027	G3PC_HORVU Glyceraldehyde-3-phosphate dehydrogenase, cytosolic	30.5 signalling.G-proteins	-0.03
HS04L15	0.40	0.89	0.24	0.13	**1.45**	0.026	RAB11A [Lotus corniculatus var. japonicus] Ras-related protein Rab11A	30.5_signalling.G-proteins	0.71
HS01M05	-0.29	-0.70	-0.70	-0.37	**-1.19**	0.013	RAB7_PENCL Ras-related protein Rab7 (Possible apospory-associated	30.5_signalling.G-proteins	1.08
HO09K23	0.08	0.12	-0.32	-0.39	**-1.11**	0.043	extra-large G-protein-like [Arabidopsis thaliana] extra-large G-protein-like	30.5_signalling.G-proteins	0.48
HO02N12	0.35	0.21	0.81	2.35	**3.50**	0.013	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	30.6_signalling.MAP kinases	#NV
HF01I15	-0.36	-0.14	-0.09	-0.68	**-1.42**	0.019	putative mitogen-activated protein kinase, msrmk3 [Oryza sativa (japonica	30.6 signalling.MAP kinases	-0.09

HZ40G20	0.25	-0.56	-0.68	-0.67	**-1.39**	0.020	putative Mitogen-activated protein kinase [Oryza sativa (japonica cultivar-	30.6 signalling.MAP kinases	1.27
HA07M02	0.01	**-1.51**	-0.89	-0.37	-1.09	0.013	14-3-3 protein homologue [Hordeum vulgare subsp. vulgare] pir||S18911 14-	30.7_signalling.14-3-3 proteins	#NV
HZ01A17	0.15	0.64	0.46	0.32	**1.01**	0.027	14-3-3 protein [Hordeum vulgare]	30.7_signalling.14-3-3 proteins	0.23
HH01K04	-0.35	-0.67	-0.63	-0.69	**-1.11**	0.007	HMG-I/Y protein HMGa [Triticum aestivum]	31.1 cell.organisation	0.07
HA11G05	-0.32	-0.77	-0.53	-0.61	**-1.30**	0.010	putative microtubule-associated protein [Oryza sativa (japonica cultivar-	31.1_cell.organisation	0.85
HW01J16	-0.27	-0.58	-0.54	-0.50	**-1.27**	0.012	alpha1-tubulin [Zea mays] Tubulin alpha-1 chain (Alpha-1 tubulin)	31.1 cell.organisation	-0.68
HH02K14	0.93	0.54	-0.13	-0.19	**1.11**	0.040	OSJNBb0079B02.14 [Oryza sativa (japonica cultivar-group)]	31.1_cell.organisation	-0.05
HK05I13	-0.46	**-1.17**	-0.47	-0.21	-1.13	0.016	putative microtubule-associated protein MAP65-1a [Oryza sativa (japonica	31.1_cell.organisation	0.18
HW02O21	-0.25	0.60	0.70	0.47	**1.25**	0.039	putative annexin P35 [Oryza sativa (japonica cultivar-group)] putative	31.1_cell.organisation	0.48
HA08M15	0.24	**1.39**	0.99	0.12	-0.26	0.049	putative annexin [Oryza sativa (japonica cultivar-group)]	31.1_cell.organisation	-0.23
HO12A18	0.05	0.02	0.18	-0.53	**-1.39**	0.041	putative actin-depolymerizing factor [Oryza sativa (japonica cultivar-group)]	31.1 cell.organisation	1.01
HY01O15	-0.36	0.03	-0.26	-0.17	**-1.26**	0.037	putative actin-depolymerizing factor [Oryza sativa (japonica cultivar-group)]	31.1_cell.organisation	0.82
GCA004N	-0.19	-1.23	-0.24	**-1.59**	0.48	0.045	putative actin [Oryza sativa (japonica cultivar-group)]	31.1 cell.organisation	-2.92
HW09A18	-0.01	-0.05	0.14	0.87	**1.75**	0.035	putative actin depolymerizing factor 5 [Arabidopsis thaliana] putative actin	31.1_cell.organisation	-1.55
HO10N13	-0.03	-0.15	-0.10	-0.26	**-1.32**	0.034	putative NLI-interacting factor [Oryza sativa (japonica cultivar-group)]	31.1_cell.organisation	0.67
HH01N11	-0.16	-0.21	-0.09	**-1.38**	-1.28	0.018	probable cytochrome P450 monooxygenase - maize (fragment)	31.1 cell.organisation	-0.22
HW09A09	-0.10	**-1.35**	-0.72	-0.53	0.45	0.035	putative annexin [Oryza sativa (japonica cultivar-group)] PREDICTED	31.1_cell.organisation	-1.01
HA12B19	-0.65	-0.66	-0.46	-0.19	**-1.02**	0.013	putative kinesin [Oryza sativa (japonica cultivar-group)]	31.1_cell.organisation	0.34
HO01P10	-0.12	0.56	0.89	2.81	**3.05**	0.013	Peptidase M24A, methionine aminopeptidase, subfamily 1 [Bacillus	31.1_cell.organisation	#NV
HI15D17	-0.38	-0.20	-0.81	-0.39	**-1.70**	0.018	alpha-tubulin 3 [Hordeum vulgare subsp. vulgare] Tubulin alpha-3 chain	31.1_cell.organisation	0.00
HA16O02	0.10	-0.22	-0.12	-0.41	**-1.12**	0.029	p34cdc2 [Triticum aestivum]	31.3_cell.cycle	0.04
HX03N24	-0.15	-0.03	-0.38	-0.23	**-1.09**	0.043	PREG-like protein [Oryza sativa]	31.3_cell.cycle	0.21
GCN001J	-0.31	-0.23	-0.19	-0.03	**-1.19**	0.037	OSJNBa0059D20.11 [Oryza sativa (japonica cultivar-group)]	31.3 cell.cycle	-0.49
HA09N10	-0.30	-0.23	0.01	-0.06	**-1.02**	0.035	cyclophilin [Oryza sativa (japonica cultivar-group)] cyclophilin [Oryza sativa	31.3_cell.cycle	-0.25
GCW002	-0.10	-0.19	-0.81	0.05	**-1.71**	0.030	putative oxysterol binding protein [Oryza sativa (japonica cultivar-group)]	31.4 cell. vesicle transport	0.15
HZ01H24	-0.41	-0.34	-0.19	-0.53	**-1.27**	0.018	putative syntaxin of plants 52 [Oryza sativa (japonica cultivar-group)]	31.4_cell. vesicle transport	1.14
HY08E19	0.25	0.35	0.84	0.38	**1.17**	0.019	putative vesicle transport v-SNARE protein [Oryza sativa (japonica cultivar-	31.4_cell. vesicle transport	-0.19
HA09O01	-0.08	-0.56	-0.28	-0.41	**-1.70**	0.018	PREDICTED P0039H02.103 gene product [Oryza sativa (japonica cultivar-	31.4 cell. vesicle transport	0.41
HO03B06	-0.05	**-1.65**	-0.09	-0.41	-0.54	0.028	putative syntaxin of plants 31 [Oryza sativa (japonica cultivar-group)]	31.4_cell. vesicle transport	-3.16
HT01H23	-0.07	-0.94	**-1.00**	-0.45	-0.77	0.013	storage protein embryo globulin barley embryo globulin 1	33.1_development.storage proteins	0.60
HB09K20	-0.35	0.11	0.31	-0.80	**-1.14**	0.030	HOG3_HORVU Gamma-hordein 3	33.1_development.storage proteins	0.45
HW02I20	0.32	0.17	0.27	0.50	**1.66**	0.022	patatin-like protein [Sorghum bicolor]	33.1_development.storage proteins	-0.28
HB01E05	-0.34	-0.14	-0.57	-1.67	**-2.19**	0.012	putative gamma-gliadin [Triticum aestivum]	33.1_development.storage proteins	0.68
HB09G12	0.06	0.31	-0.15	-0.01	**2.12**	0.050	B hordein precursor [Hordeum vulgare subsp. vulgare]	33.1_development.storage proteins	-0.47
HB09A12	0.07	-0.06	-0.09	-0.88	**-1.76**	0.026	B hordein precursor [Hordeum vulgare subsp. vulgare]	33.1 development.storage proteins	-0.07
HY02O05	0.78	**1.08**	0.24	0.11	0.38	0.027	hordoindoline-a [Hordeum vulgare subsp. vulgare] hordoindoline-a	33.50_development.inhibitor proteins	0.04
HO09B17	0.66	**1.24**	0.59	-0.14	0.04	0.046	senescence-associated protein-like protein [Oryza sativa (japonica cultivar-	33.99_development.unspecified	1.80
HO18C10	0.36	1.89	1.04	1.36	**2.29**	0.009	putative late embryogenesis abundant protein [Oryza sativa (japonica	33.99 development.unspecified	0.45
HH02G10	-0.17	0.49	0.29	0.26	**1.26**	0.043	putative late embryogenesis abundant protein [Oryza sativa (japonica	33.99_development.unspecified	0.44
HY08A20	0.48	1.46	0.88	1.36	**1.78**	0.009	putative late embryogenesis abundant protein [Oryza sativa (japonica	33.99 development.unspecified	-0.09
HA15G18	0.90	**2.10**	1.36	1.08	1.86	0.005	putative B12D protein [Oryza sativa (japonica cultivar-group)] putative B12D	33.99_development.unspecified	0.74
HW06H01	1.94	2.92	1.19	1.16	**3.12**	0.002	putative B12D protein [Oryza sativa (japonica cultivar-group)] putative B12D	33.99_development.unspecified	0.00
HU04H13	-0.32	0.22	0.47	**1.06**	0.96	0.040	putative calcium binding protein [Oryza sativa (japonica cultivar-group)]	33.99_development.unspecified	-0.22
HY04P02	-0.29	-1.49	-1.07	**-1.87**	-1.33	0.009	B12Dg1 [Hordeum vulgare subsp. vulgare] HvB12D [Hordeum vulgare	33.99_development.unspecified	-0.37
HO20G13	-0.59	-1.36	-0.94	-0.89	**-1.57**	0.004	B12Dg1 [Hordeum vulgare subsp. vulgare] HvB12D [Hordeum vulgare	33.99 development.unspecified	0.86

HM02L06	-0.61	-1.63	-1.16	**-1.87**	-1.77	0.004	putative NEC1 [Oryza sativa (japonica cultivar-group)] PREDICTED	33.99 development.unspecified	0.79
HW08N14	-0.39	-0.50	-0.81	-0.70	**-2.29**	0.014	putative senescence-associated protein [Oryza sativa (japonica cultivar-	33.99_development.unspecified	0.92
HO12E12	-0.69	-0.11	-0.10	-0.46	**-1.06**	0.015	MADS-box protein 1-2 [Hordeum vulgare subsp. vulgare]	33.99_development.unspecified	0.88
HO10B05	0.02	-0.24	-0.19	-0.31	**-1.47**	0.034	MADS-box protein 1-2 [Hordeum vulgare subsp. vulgare]	33.99 development.unspecified	1.44
HS01E17	-0.24	**-1.28**	-0.85	-0.20	-1.20	0.013	OSJNBb0022F16.7 [Oryza sativa (japonica cultivar-group)]	33.99_development.unspecified	1.04
HC11E02	-0.36	**-1.52**	-0.51	-0.15	0.14	0.027	putative nodulin-like protein 5NG4 [Oryza sativa (japonica cultivar-group)]	33.99 development.unspecified	-1.51
GBN008D	-0.06	**-1.17**	-0.24	-0.43	-0.56	0.027	OSA15 protein [Oryza sativa (japonica cultivar-group)]	33.99_development.unspecified	-1.72
HO25K05	-0.36	**-1.25**	-0.07	-0.40	-0.88	0.019	OSA15 protein [Oryza sativa (japonica cultivar-group)]	33.99_development.unspecified	-1.69
HO08P10	0.13	**-1.07**	0.00	-0.54	-0.32	0.035	OSA15 protein [Oryza sativa (japonica cultivar-group)]	33.99_development.unspecified	#NV
HK04O09	-0.49	-1.19	-0.59	-0.49	**-1.21**	0.009	0	33.99_development.unspecified	-0.09
HY05M02	-0.77	-1.47	-1.24	-0.04	**-2.30**	0.010	methionine synthase [Hordeum vulgare subsp. vulgare]	33.99 development.unspecified	0.22
HM02H04	-0.32	-0.99	-0.32	-0.95	**-1.81**	0.010	putative 24 kDa seed maturation protein [Oryza sativa (japonica cultivar-	33.99_development.unspecified	0.06
HO10E13	0.27	-0.04	-0.24	-0.64	**-1.08**	0.038	Vacuolar ATP synthase subunit B isoform 1 (V-ATPase B subunit 1)	34.1 transport.p- and v-ATPases	1.33
GBN002P	0.21	0.65	0.54	0.38	**1.19**	0.025	sorbitol transporter [Malus x domestica]	34.2_transporter.sugars	0.22
HF02F19	0.30	**1.21**	0.42	0.33	0.72	0.020	putative monosaccharide transporter [Oryza sativa (japonica cultivar-group)]	34.2_transporter.sugars	1.48
HO15G24	1.65	**2.25**	1.04	0.53	1.14	0.010	putative monosaccharide transport protein MST1 [Oryza sativa (japonica	34.2 transporter.sugars	2.02
HW05O02	1.83	**2.03**	1.27	0.44	0.83	0.011	putative glucose transport protein STP1 [Oryza sativa (japonica cultivar-	34.2_transporter.sugars	1.91
HO02I03	1.24	**1.44**	0.50	0.79	0.17	0.013	putative sorbitol transporter [Oryza sativa (japonica cultivar-group)]	34.2_transporter.sugars	1.02
HW08L23	1.43	**2.45**	1.12	0.88	1.54	0.007	hypothetical protein, conserved [Leishmania major]	34.2_transporter.sugars	-0.11
HO12F18	0.76	1.39	0.26	0.90	**2.16**	0.008	monosaccharide transporter 4 [Oryza sativa (japonica cultivar-group)]	34.2_transporter.sugars	0.68
HM01B10	0.02	-0.03	0.93	1.12	**1.84**	0.023	putative amino acid or GABA permease [Oryza sativa (japonica cultivar-	34.3_transport.amino acids	-0.25
HW07E12	0.64	**2.00**	1.14	0.68	1.91	0.010	putative amino acid transporter [Oryza sativa (japonica cultivar-group)]	34.3_transport.amino acids	#NV
HF12I14	-0.20	0.50	0.26	0.74	**2.20**	0.023	putative cationic amino acid transporter [Oryza sativa (japonica cultivar-	34.3 transport.amino acids	-0.10
HO15C20	-0.39	0.24	0.41	0.76	**2.23**	0.033	putative cationic amino acid transporter [Oryza sativa (japonica cultivar-	34.3_transport.amino acids	-0.49
HDP02K0	-0.25	0.09	0.42	0.61	**2.11**	0.044	putative peptide transporter protein [Oryza sativa (japonica cultivar-group)]	34.3 transport.amino acids	0.03
HO09B08	-0.05	0.41	0.38	0.53	**1.63**	0.023	putative amino acid permease [Oryza sativa (japonica cultivar-group)]	34.3_transport.amino acids	-0.79
HM01E09	0.91	**2.12**	1.86	0.74	0.98	0.013	phosphate transporter 6 [Hordeum vulgare subsp. vulgare]	34.7_transport.phosphate	0.89
HZ01P22	0.86	**1.02**	0.42	0.34	-0.29	0.033	mitochondrial carrier protein-like protein [Oryza sativa (japonica cultivar-	34.9 transport.metabolite transporters	0.56
HW02F20	-0.04	0.31	0.11	1.02	**1.14**	0.026	Graves disease mitochondrial solute carrier protein-like [Oryza sativa	34.9_transport.metabolite transporters	0.22
HZ52D05	-0.33	-0.55	-0.21	-0.53	**-1.68**	0.016	putative peroxisomal Ca-dependent solute carrier [Oryza sativa (japonica	34.9_transport.metabolite transporters	-0.92
HW04F15	-0.16	-0.83	-0.59	-0.70	**-1.26**	0.012	putative peroxisomal Ca-dependent solute carrier [Oryza sativa (japonica	34.9_transport.metabolite transporters	-0.88
HO10G15	0.24	0.22	0.19	0.80	**1.55**	0.024	plastidic 2-oxoglutarate/malate transporter [Zea mays]	34.9_transport.metabolite transporters	-1.14
HG01L19	0.51	0.64	1.12	1.08	**2.79**	0.013	putative peptide transport protein [Oryza sativa (japonica cultivar-group)]	34.13_transport.peptides and	-1.75
HD03D23	1.22	0.97	0.32	0.58	**1.27**	0.013	putative peptide transporter protein [Hordeum vulgare subsp. vulgare]	34.13_transport.peptides and	#NV
HB29E24	0.93	**2.75**	2.47	1.95	2.63	0.002	putative potassium transporter [Oryza sativa (japonica cultivar-group)]	34.15 transport.potassium	0.30
HO11F02	-0.21	-0.01	0.10	2.87	**3.41**	0.019	putative potasium transporter [Oryza sativa (japonica cultivar-group)]	34.15_transport.potassium	1.60
HO05N23	-0.34	-0.49	-0.13	-0.99	**-1.41**	0.014	outward-rectifying potassium channel [Hordeum vulgare subsp. vulgare]	34.15_transport.potassium	1.12
HK03F06	0.45	**-1.02**	-0.27	-0.42	-0.88	0.037	0	34.15 transport.potassium	1.14
HDP28E0	0.66	**1.10**	0.30	0.08	0.30	0.033	OSJNBa0040D17.13 [Oryza sativa (japonica cultivar-group)]	34.16_transport.ABC transporters and	0.61
HO26B20	-0.35	-0.75	-0.23	-0.81	**-1.59**	0.010	putative ABC transporter [Oryza sativa (japonica cultivar-group)] putative	34.16 transport.ABC transporters and	-0.49
HO14N24	0.34	1.56	0.97	1.08	**2.07**	0.009	putative ABC transporter [Oryza sativa (japonica cultivar-group)] putative	34.16_transport.ABC transporters and	0.67
HO38F06	-0.31	-0.32	-0.10	-0.76	**-1.55**	0.015	ABC transporter family protein:: At5g06530/F15M7_6 [Arabidopsis thaliana]	34.16_transport.ABC transporters and	2.06
HW08K21	0.17	0.02	0.34	0.82	**1.26**	0.024	putative multidrug-resistance associated protein [Oryza sativa (japonica	34.16_transport.ABC transporters and	-0.27
HM01E18	-0.29	-0.80	-0.62	-0.67	**-2.30**	0.013	ABC transporter family protein::OSJNBa0074L08.3 [Oryza sativa (japonica	34.16_transport.ABC transporters and	2.02
HU02M04	-0.13	-1.02	-0.80	-0.32	**-1.95**	0.017	OSJNBa0074L08.3 [Oryza sativa (japonica cultivar-group)]	34.16 transport.ABC transporters and	1.60

HY01K18	-0.10	-0.95	-0.12	-0.12	**-1.66**	0.026	major facilitator superfamily antiporter [Oryza sativa (japonica cultivar-	34.16 transport.ABC transporters and	-0.40
HM03H07	0.79	**1.11**	0.57	0.40	0.07	0.021	putative MRP-like ABC transporter [Oryza sativa (japonica cultivar-group)]	34.16_transport.ABC transporters and	0.11
HH02B24	-0.50	-1.05	-0.92	-0.98	**-1.26**	0.013	putative plasma membrane intrinsic protein [Populus tremula x Populus	34.19.1_transport.Major Intrinsic	1.54
GPN002H	0.10	-0.53	-0.26	-0.27	**-1.28**	0.028	NADH dehydrogenase subunit 5 [Cucumaria miniata] NADH dehydrogenase	34.19.1 transport.Major Intrinsic	1.44
HM11F17	-0.39	-0.42	-0.22	-0.77	**-1.24**	0.014	plasma membrane intrinsic protein 1 [Triticum aestivum]	34.19.1_transport.Major Intrinsic	1.29
HD13C24	-0.52	**-1.22**	-0.89	-0.74	-0.91	0.013	PIP aquaporin isoform [Hordeum vulgare]	34.19.1 transport.Major Intrinsic	0.82
HW05A12	-0.53	**-1.34**	-0.73	-0.40	-0.55	0.011	HvPIP1;3 [Hordeum vulgare subsp. vulgare]	34.19.1_transport.Major Intrinsic	-0.74
HW06D12	-0.72	**-1.18**	-0.52	-0.76	-0.63	0.013	aquaporin PIP1 [Triticum aestivum]	34.19.1_transport.Major Intrinsic	0.38
HY08B10	-0.27	**-1.31**	-0.97	-0.73	-1.17	0.016	HvPIP1;5 [Hordeum vulgare subsp. vulgare]	34.19.1_transport.Major Intrinsic	1.03
HW04J15	-0.76	**-1.63**	-1.06	-0.76	-0.67	0.008	PIP aquaporin [Hordeum vulgare]	34.19.1_transport.Major Intrinsic	0.66
GCW004K	-0.48	-1.50	-1.08	**-1.55**	-0.41	0.010	0	34.19.2 transport.Major Intrinsic	1.33
GNW001	-0.47	-0.70	-0.69	-1.24	**-2.68**	0.010	putative Ca2+/H+-exchanging protein [Oryza sativa (japonica cultivar-	34.21_transport.calcium	2.06
HO15I03	0.34	**1.08**	0.36	0.21	0.71	0.029	secretory carrier membrane protein [Oryza sativa (japonica cultivar-group)]	34.99 transport.misc	0.18
HY10E05	0.23	0.80	0.41	**1.40**	1.19	0.013	putative ripening regulated protein DDTFR18 [Oryza sativa (japonica	34.99_transport.misc	0.17
HX09I06	1.00	**1.32**	0.14	0.89	0.55	0.014	putative metal-binding protein [Oryza sativa (japonica cultivar-group)]	34.99_transport.misc	0.71
HO06J04	0.54	0.48	0.01	0.77	**1.27**	0.016	putative plastidic ATP/ADP-transporter [Oryza sativa (japonica cultivar-	34.99 transport.misc	0.39
HO04P24	-0.81	**-1.46**	-0.42	-0.40	-0.16	0.016	putative permease 1 [Oryza sativa (japonica cultivar-group)] PREDICTED	34.99_transport.misc	-0.92
HY02O18	-0.37	**-1.33**	-0.22	-0.69	-0.61	0.016	putative membrane protein [Oryza sativa (japonica cultivar-group)]	35.1_not assigned.no ontology	-2.66
HO25L06	0.13	**-1.38**	-0.40	-0.41	-0.25	0.032	unknown protein [Oryza sativa (japonica cultivar-group)]	35.1_not assigned.no ontology	-2.58
HDP37A1	-0.27	**-1.57**	-0.45	-0.44	0.33	0.032	unknown protein [Arabidopsis thaliana] forkhead-associated domain-	35.1_not assigned.no ontology	-2.45
HDP09A1	0.12	**-1.14**	0.09	-0.79	-0.73	0.024	putative chloroplast inner envelope protein [Oryza sativa (japonica cultivar-	35.1_not assigned.no ontology	-2.45
HDP16E0	-0.46	**-1.00**	-0.41	-0.28	-0.64	0.012	GCN5-related N-acetyltransferase (GNAT) family-like protein [Oryza sativa	35.1_not assigned.no ontology	-2.00
HU04O04	0.35	-0.01	1.13	1.42	**3.30**	0.016	putative MtN19 [Oryza sativa (japonica cultivar-group)] putative MtN19	35.1 not assigned.no ontology	-1.87
HX02L03	-0.28	**-1.01**	-0.28	-0.50	-0.64	0.012	cell division inhibitor-like [Oryza sativa (japonica cultivar-group)]	35.1_not assigned.no ontology	-1.79
HP08C09	-0.33	**-1.38**	-0.20	-0.65	-0.68	0.015	unknown protein [Oryza sativa (japonica cultivar-group)]	35.1 not assigned.no ontology	-1.77
HY01G17	0.31	0.08	0.38	0.65	**2.11**	0.027	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.1_not assigned.no ontology	-1.56
HU05D10	-0.17	**-1.11**	-0.51	-0.47	-0.57	0.017	unknown protein [Arabidopsis thaliana] unknown protein [Arabidopsis	35.1_not assigned.no ontology	-1.49
HO08G22	0.30	0.33	-0.28	0.67	**1.31**	0.030	Putative cell death suppressor protein [Oryza sativa] Putative cell death	35.1 not assigned.no ontology	-1.33
HW03I08	0.91	0.59	0.27	1.25	**1.46**	0.009	ammonium transporter [Triticum aestivum]	35.1_not assigned.no ontology	-1.13
HDP31B2	-0.28	**-1.09**	-0.06	-1.07	-0.18	0.017	[Arabidopsis thaliana] X95263 Periodic tryptophan protein 2 gene (PWP2)	35.1_not assigned.no ontology	-1.10
HR01H11	0.65	1.40	1.08	1.16	**3.14**	0.008	putative membrane protein [Oryza sativa (japonica cultivar-group)] putative	35.1_not assigned.no ontology	-1.02
HY05K07	0.16	0.31	-0.07	0.46	**1.57**	0.038	unknown protein [Oryza sativa (japonica cultivar-group)] unknow protein	35.1_not assigned.no ontology	-0.83
HD01J07	0.13	0.00	0.18	0.64	**1.30**	0.038	hydrolase-like [Oryza sativa (japonica cultivar-group)]	35.1_not assigned.no ontology	-0.82
HI05G11	-0.32	-0.59	-0.35	-0.91	**-1.49**	0.010	light-inducible protein ATLS1 [Arabidopsis thaliana] light-inducible protein	35.1_not assigned.no ontology	-0.82
HT01O20	0.34	0.41	0.37	0.85	**2.02**	0.017	OSJNBa0068L06.8 [Oryza sativa (japonica cultivar-group)]	35.1 not assigned.no ontology	-0.64
HW03J13	-0.38	-0.89	-0.59	-0.48	**-1.27**	0.009	light-inducible protein ATLS1 [Arabidopsis thaliana] light-inducible protein	35.1_not assigned.no ontology	-0.59
HV01J19	-0.33	-0.68	-0.09	**-1.40**	-0.82	0.011	light-inducible protein ATLS1 [Arabidopsis thaliana] light-inducible protein	35.1_not assigned.no ontology	-0.56
HDP11G0	-0.21	-0.22	-0.14	-0.40	**-1.23**	0.025	unknown protein [Oryza sativa (japonica cultivar-group)]	35.1 not assigned.no ontology	-0.54
GCN003D	0.27	-0.05	0.33	0.60	**1.90**	0.033	putative NADPH-dependent reductase [Oryza sativa (japonica cultivar-	35.1_not assigned.no ontology	-0.48
HV03P11	0.04	0.65	0.75	0.77	**1.14**	0.020	putative 1-acylglycerol-3-phosphate acyltransferase [Oryza sativa (japonica	35.1 not assigned.no ontology	-0.39
HD11L07	0.06	-0.34	-0.22	-0.57	**-1.11**	0.026	unknown proein [Oryza sativa (japonica cultivar-group)] unknown protein	35.1_not assigned.no ontology	-0.29
HO01D13	0.85	**1.04**	0.62	0.31	0.19	0.019	putative pirin-like protein [Oryza sativa (japonica cultivar-group)] putative	35.1_not assigned.no ontology	-0.18
HO02A01	1.82	**2.96**	2.31	1.93	1.68	0.002	putative phospholipase [Arabidopsis thaliana] putative phospholipase	35.1_not assigned.no ontology	-0.08
HS01A12	-0.16	**-1.21**	-0.82	-0.63	-0.94	0.015	putative signal transduction protein [Oryza sativa] putative signal	35.1_not assigned.no ontology	-0.05
HV08D16	0.48	-0.23	0.07	0.40	**1.87**	0.050	P0529H11.19 [Oryza sativa (japonica cultivar-group)] SOUL heme-binding	35.1 not assigned.no ontology	-0.04

HO11F15	-0.17	0.20	0.22	0.45	**1.52**	0.047	putative Xaa-Pro dipeptidase [Oryza sativa (japonica cultivar-group)]	35.1 not assigned.no ontology	-0.02
HO03B15	-0.35	-0.50	-0.30	-0.77	**-1.15**	0.009	putative zinc finger protein [Oryza sativa (japonica cultivar-group)]	35.1_not assigned.no ontology	0.00
HW03H04	0.13	0.52	0.35	0.00	**1.03**	0.031	putative LN1 protein [Oryza sativa] putative LN1 protein [Oryza sativa]	35.1_not assigned.no ontology	0.02
HW06P03	0.43	-0.04	0.02	0.80	**1.82**	0.026	P0529H11.19 [Oryza sativa (japonica cultivar-group)] SOUL heme-binding	35.1 not assigned.no ontology	0.06
HO14N08	-0.22	**-1.07**	-0.22	-0.31	-0.72	0.015	hydrolase-like protein [Oryza sativa (japonica cultivar-group)]	35.1_not assigned.no ontology	0.14
HA02O01	**1.25**	1.08	-0.24	1.22	-0.40	0.042	HSP70	35.1 not assigned.no ontology	0.17
HA10H01	-0.20	-0.29	-0.23	-0.21	**-1.06**	0.030	TCTP_HORVU Translationally controlled tumor protein homolog (TCTP)	35.1_not assigned.no ontology	0.17
HK04F01	-0.11	-1.37	**-1.62**	-0.14	-0.42	0.023	putative chloroplast inner envelope protein [Oryza sativa (japonica cultivar-	35.1_not assigned.no ontology	0.22
HF25D04	0.03	0.03	-0.58	-0.37	**-1.18**	0.038	putative S-formylglutathione hydrolase [Oryza sativa (japonica cultivar-	35.1_not assigned.no ontology	0.24
HH02C14	1.91	**2.90**	1.12	1.18	-0.45	0.015	uridylyl transferase-like [Oryza sativa (japonica cultivar-group)] uridylyl	35.1_not assigned.no ontology	0.48
HX11I09	-0.22	-0.39	-0.01	-0.59	**-1.05**	0.019	putative F8K7.10 protein [Oryza sativa (japonica cultivar-group)]	35.1 not assigned.no ontology	0.50
HY05D23	0.33	-0.40	-0.61	-0.15	**-1.62**	0.047	ripening-related protein-like [Oryza sativa (japonica cultivar-group)] ripening-	35.1_not assigned.no ontology	0.57
HA04D14	-0.60	-0.52	-0.41	-0.48	**-1.52**	0.010	putative PIR7A protein [Oryza sativa (japonica cultivar-group)] PREDICTED	35.1 not assigned.no ontology	0.61
HU01A06	1.04	1.25	0.83	0.48	**2.30**	0.009	putative PrMC3 [Oryza sativa (japonica cultivar-group)] putative PrMC3	35.1_not assigned.no ontology	0.65
HW02L20	0.35	0.32	-0.18	0.49	**1.01**	0.035	extra-large G-protein-like [Oryza sativa (japonica cultivar-group)] extra-large	35.1_not assigned.no ontology	0.65
HZ43P13	0.08	-0.12	0.04	0.88	**1.65**	0.035	endonuclease [Hordeum vulgare subsp. vulgare]	35.1 not assigned.no ontology	0.70
HD03K09	-0.41	-1.13	-1.38	**-1.53**	-1.39	0.004	unknown protein [Oryza sativa (japonica cultivar-group)]	35.1_not assigned.no ontology	0.72
HW05M19	-0.29	-0.29	0.68	0.80	**2.29**	0.041	putative oxidase-like [Oryza sativa (japonica cultivar-group)] putative	35.1_not assigned.no ontology	0.74
HK03I07	-0.30	-0.36	-0.55	-0.01	**-1.51**	0.026	putative protein [Arabidopsis thaliana] putative protein [Arabidopsis thaliana]	35.1_not assigned.no ontology	0.77
HO16P15	-0.24	0.29	1.02	1.88	**1.93**	0.017	nuclease I [Hordeum vulgare]	35.1_not assigned.no ontology	0.79
HF04K19	-0.20	-0.81	-0.63	-1.06	**-1.70**	0.008	unknown protein [Oryza sativa (japonica cultivar-group)]	35.1_not assigned.no ontology	0.83
HO31E08	0.12	-0.56	-0.14	-0.50	**-1.59**	0.026	putative 37kDa chloroplast inner envelope membrane polypeptide precursor	35.1_not assigned.no ontology	0.87
HR01A14	-0.19	0.13	-0.62	-0.09	**-1.11**	0.047	putative NADPH:quinone oxidoreductase [Oryza sativa (japonica cultivar-	35.1 not assigned.no ontology	0.99
GCN002C	-0.04	-0.73	-0.76	-0.72	**-2.09**	0.013	0	35.1_not assigned.no ontology	1.09
GCW004F	-0.44	-0.44	-0.39	-0.56	**-1.26**	0.015	0	35.1 not assigned.no ontology	1.20
HO06I12	-0.23	-0.73	-0.44	-0.03	**-1.30**	0.018	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.1_not assigned.no ontology	1.36
HV04K10	-0.24	**1.31**	0.66	0.67	0.04	0.046	putative beta-glucan binding protein [Oryza sativa (japonica cultivar-group)]	35.1_not assigned.no ontology	1.52
GBN003I1	3.92	**5.21**	2.15	2.08	4.14	0.000	0	35.1 not assigned.no ontology	1.60
GNW001J	-0.27	0.29	0.13	-0.90	**-1.20**	0.038	0	35.1_not assigned.no ontology	1.72
HO26F08	-0.28	-0.74	-0.75	**-1.08**	-0.99	0.013	putative polyketide synthase [Oryza sativa (japonica cultivar-group)] putative	35.1_not assigned.no ontology	2.08
HM01A22	-0.22	-1.11	-0.77	-0.50	**-1.36**	0.013	hypothetical protein [Oryza sativa (indica cultivar-group)]	35.1_not assigned.no ontology	2.32
HV04K17	-0.05	1.27	2.29	3.82	**5.30**	0.005	putative oxidase-like [Oryza sativa (japonica cultivar-group)] putative	35.1_not assigned.no ontology	#NV
HH01B09	-0.57	-0.86	-0.53	**-2.04**	-0.68	0.009	mitochondrial F1 ATP synthase beta subunit [Arabidopsis thaliana]	35.1.5_not assigned.no	-0.60
HY05D19	-0.08	-0.43	-0.28	-0.46	**-1.54**	0.029	MADS box transcription factor [Triticum aestivum]	35.1.5_not assigned.no	0.18
HO31B15	0.44	0.45	0.27	0.66	**3.40**	0.023	putative octicosapeptide/Phox/Bem1p (PB1) domain-/tetratricopeptide	35.1.5 not assigned.no	0.37
GBN005N	-0.14	-0.28	-0.37	-0.66	**-1.07**	0.015	0	35.1.5_not assigned.no	1.21
GCN004P	-0.16	-0.49	0.01	-0.35	**-1.21**	0.018	unknown protein [Arabidopsis thaliana]	35.1.19_not assigned.no ontology.C2	0.69
HO03F10	-0.08	0.68	0.53	1.51	**2.96**	0.015	hypothetical protein [Neurospora crassa] hypothetical protein [Neurospora	35.1.19 not assigned.no ontology.C2	0.99
HO07N23	-0.27	-0.55	-0.71	-0.61	**-1.33**	0.010	unknown protein; 15069-22101 [Arabidopsis thaliana] C2 domain-containing	35.1.19_not assigned.no ontology.C2	1.17
HO10O06	0.43	0.23	-0.15	0.52	**1.25**	0.032	PREDICTED: similar to CG4330-PA, partial [Strongylocentrotus purpuratus]	35.1.19 not assigned.no ontology.C2	1.18
HDP34P0	-0.12	-0.16	-0.29	-0.44	**-1.26**	0.026	zinc finger and C2 domain protein-like [Oryza sativa (japonica cultivar-	35.1.19_not assigned.no ontology.C2	1.21
HH02F11	-0.33	-0.19	-0.38	**-1.19**	-0.48	0.022	putative p23 co-chaperone [Oryza sativa (japonica cultivar-group)]	35.1.40_not assigned.no	-0.43
HO06H23	-0.28	-0.93	-1.04	-0.47	**-1.67**	0.018	actin binding protein [Arabidopsis thaliana] unnamed protein product	35.1.41_not assigned.no	0.41
HV03N06	-0.33	-0.82	-0.21	-0.83	**-1.29**	0.013	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.1.41_not assigned.no	1.82
HP01B14	-0.03	**-2.46**	-0.27	-0.61	-0.13	0.032	SR-rich pre-mRNA splicing activator [Oryza sativa (japonica cultivar-group)]	35.2 not assigned.unknown	-3.75

HV07N02	-0.13	**-1.53**	-0.30	-0.44	-0.30	0.027	Unknown protein [Oryza sativa (japonica cultivar-group)] Unknown protein	35.2 not assigned.unknown	-3.18
HD08N06	-0.13	**-1.52**	-0.77	-0.97	0.06	0.018	metallothionein-like protein type 3 [Hordeum vulgare subsp. vulgare]	35.2_not assigned.unknown	-3.18
HV03C20	-0.14	-1.02	-0.74	**-1.03**	-0.63	0.012	metallothionein-like protein type 3 [Hordeum vulgare subsp. vulgare]	35.2_not assigned.unknown	-2.96
GCN004H	-0.38	**-1.41**	0.03	-0.72	-0.08	0.020	ptp-2 [Cryptophlebia leucotreta granulovirus] ptp-2 [Cryptophlebia leucotreta	35.2 not assigned.unknown	-2.78
HDP34I16	-0.09	**-1.32**	-0.15	-0.07	-0.45	0.037	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2_not assigned.unknown	-2.62
GCN004M	-0.13	**-1.33**	-0.46	-0.13	-0.36	0.031	0	35.2 not assigned.unknown	-2.51
HG01D06	-0.62	**-1.45**	-0.32	-0.61	-0.24	0.016	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2_not assigned.unknown	-2.48
GCN003O	-0.06	**-1.40**	0.03	-0.37	-0.25	0.038	hypothetical protein FG00046.1 [Gibberella zeae PH-1] hypothetical protein	35.2_not assigned.unknown	-2.36
HG01L20	-0.17	**-1.34**	-0.44	-0.97	-0.38	0.014	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2_not assigned.unknown	-2.30
HP05N14	-0.35	**-1.03**	-0.55	-0.93	0.11	0.030	unknown protein [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	-2.25
HB02J10	-0.31	**-1.20**	-0.55	-0.37	-0.91	0.017	At3g55760 [Arabidopsis thaliana] expressed protein [Arabidopsis thaliana]	35.2 not assigned.unknown	-2.02
HP09N21	-0.19	**-1.26**	-0.59	-0.58	-0.34	0.018	cold acclimation induced protein 2-1 [Triticum aestivum]	35.2_not assigned.unknown	-1.95
HO01M12	-0.41	**-1.15**	-0.34	-0.20	0.29	0.047	hypothetical protein [Oryza sativa (japonica cultivar-group)] hypothetical	35.2 not assigned.unknown	-1.91
HV02G20	0.15	0.92	0.52	0.12	**1.63**	0.016	pathogenesis-related protein [Hordeum vulgare]	35.2_not assigned.unknown	-1.73
HP01C15	-0.38	**-1.17**	-0.83	-0.52	-0.08	0.018	expressed protein [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	-1.70
HD02I06	-0.25	-0.92	-0.25	-0.25	**-1.03**	0.020	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2 not assigned.unknown	-1.52
HDP10P1	-0.63	-1.01	0.40	-0.23	**-2.34**	0.034	putative potyviral helper component protease-interacting protein 2 [Oryza	35.2_not assigned.unknown	-1.40
HI04N19	0.02	-0.83	-0.35	-0.70	**-1.50**	0.016	OSJNBa0035M09.9 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	-1.24
HO09M20	0.78	**1.92**	1.40	0.09	-0.23	0.026	T06988 pathogen-induced protein WIR1A - wheat WIR1A PROTEIN WIR1A	35.2_not assigned.unknown	-1.22
GBN009C	-0.11	0.14	0.59	0.69	**1.54**	0.023	Similar to Avr9/Cf-9 rapidly elicited protein 65::::::::contains ESTs	35.2_not assigned.unknown	-1.18
HA03J11	-0.12	0.69	0.58	0.55	**1.73**	0.019	OSJNBa0080E14.9 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	-1.15
HF15O17	-0.14	-0.44	0.04	-0.54	**-1.14**	0.034	hypothetical protein [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	-1.03
HG01H16	-0.16	-0.79	-0.79	-1.35	**-1.99**	0.009	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2 not assigned.unknown	-0.95
GCN004J	-0.39	-0.64	-0.28	-0.13	**-1.67**	0.019	putative B2 protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2_not assigned.unknown	-0.94
HW01C02	0.83	**1.64**	0.83	0.32	-0.21	0.023	methionine synthase 1 enzyme [Hordeum vulgare subsp. vulgare]	35.2 not assigned.unknown	-0.88
HO12B09	-0.45	0.65	0.81	0.95	**2.46**	0.020	ES2A [Hordeum vulgare]	35.2_not assigned.unknown	-0.84
HW05B04	0.43	0.92	1.11	0.84	**2.79**	0.012	hypothetical protein [Oryza sativa (japonica cultivar-group)] hypothetical	35.2_not assigned.unknown	-0.78
HA20K19	-0.03	0.19	0.38	0.53	**1.25**	0.035	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2 not assigned.unknown	-0.76
HD07M22	1.40	1.84	1.44	3.27	**3.90**	0.002	putative protease inhibitor [Hordeum vulgare]	35.2_not assigned.unknown	-0.74
HW02N13	0.03	0.25	-0.01	0.39	**1.04**	0.044	unknown protein [Arabidopsis thaliana] unknown protein [Arabidopsis	35.2_not assigned.unknown	-0.72
HG01D18	-0.04	-0.58	-0.25	-0.56	**-1.00**	0.016	methyltransferase-like [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	-0.70
HY08K16	0.15	-0.22	0.27	0.46	**2.65**	0.049	unknown protein [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	-0.69
HV04A08	-0.06	-0.65	-0.27	-0.09	**-1.37**	0.026	putative RNA-binding protein [Avena sativa]	35.2_not assigned.unknown	-0.63
HZ41F14	0.03	-0.23	-0.25	-0.84	**-1.25**	0.022	unknown protein [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	-0.58
HI01P23	-0.30	-0.54	-0.19	0.30	**-1.19**	0.042	putative nucleolin [Oryza sativa (japonica cultivar-group)] putative nucleolin	35.2 not assigned.unknown	-0.57
HG01P09	-0.95	-2.13	-1.51	-1.44	**-2.32**	0.004	OSJNBb0088C09.11 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	-0.57
HD03J08	-0.21	-0.88	-0.68	-0.59	**-1.22**	0.010	OSJNBa0020J04.13 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	-0.56
HO14F24	0.95	1.67	0.85	3.11	**4.14**	0.003	putative protease inhibitor [Hordeum vulgare]	35.2 not assigned.unknown	-0.51
HDP01A0	-0.21	-0.82	-0.53	-0.59	**-1.43**	0.010	name [Oryza sativa (japonica cultivar-group)] name [Oryza sativa (japonica	35.2_not assigned.unknown	-0.50
HM02F05	-0.34	0.76	1.45	1.72	**2.49**	0.014	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2 not assigned.unknown	-0.47
HK04D03	-0.58	-0.86	-0.39	-0.83	**-1.77**	0.013	actin binding protein [Arabidopsis thaliana] unnamed protein product	35.2_not assigned.unknown	-0.46
HV08M01	-0.28	**-1.01**	-0.03	-0.55	-0.80	0.017	centromere protein-like [Oryza sativa (japonica cultivar-group)] centromere	35.2_not assigned.unknown	-0.37
HB01L18	0.12	0.58	0.30	0.11	**1.37**	0.038	unknown protein [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	-0.35
HM01J06	-0.15	-0.52	-0.09	-0.17	**-1.01**	0.048	auxin response factor 2 [Oryza sativa]	35.2_not assigned.unknown	-0.34
HI14D02	-0.30	-0.47	-0.53	-0.34	**-1.08**	0.017	OSJNBa0084K01.16 [Oryza sativa (japonica cultivar-group)] unknown	35.2 not assigned.unknown	-0.33

HI02I15	-0.26	-1.19	-0.47	-0.87	**-1.22**	0.009	expressed protein [Arabidopsis thaliana] F8K4.12 [Arabidopsis thaliana]	35.2 not assigned.unknown	-0.32
HK01M10	-0.33	-0.62	-0.49	-0.26	**-1.07**	0.014	At2g43970/F6E13.10 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	-0.31
HA11H06	-0.04	-0.48	-0.17	-0.01	**-1.03**	0.033	histone deacetylase 2 isoform b [Zea mays] Histone deacetylase 2b (HD2b)	35.2_not assigned.unknown	-0.30
HW02A10	-0.34	-0.52	-0.40	-0.21	**-1.00**	0.022	unknown protein [Oryza sativa (japonica cultivar-group)] PREDICTED	35.2 not assigned.unknown	-0.28
HW08A14	-0.10	0.37	0.43	0.65	**1.89**	0.029	P0456F08.26 [Oryza sativa (japonica cultivar-group)] unknown protein	35.2_not assigned.unknown	-0.27
HD06P17	-0.32	-0.20	-0.48	-0.84	**-1.05**	0.013	OSJNBa0032F06.22 [Oryza sativa (japonica cultivar-group)]	35.2 not assigned.unknown	-0.25
HF01D11	-0.31	-0.51	**-1.25**	-0.79	-0.69	0.015	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2_not assigned.unknown	-0.24
HD01L18	0.42	0.01	-0.23	0.26	**1.73**	0.036	unknown protein [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	-0.24
HI12F07	-0.54	-0.46	-0.46	-0.54	**-1.56**	0.010	rac GTPase activating protein 1 [Oryza sativa (japonica cultivar-group)] rac	35.2_not assigned.unknown	-0.23
HM02F02	-0.23	0.61	0.84	**1.50**	0.86	0.019	OSJNBa0004N05.23 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	-0.21
HO31B05	0.08	-0.51	-0.11	-0.48	**-1.09**	0.029	NB-ARC domain, putative [Oryza sativa (japonica cultivar-group)]	35.2 not assigned.unknown	-0.20
HY09I16	-0.12	-0.36	-0.17	-1.04	**-1.08**	0.020	hypothetical protein [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	-0.18
HT01H06	-0.11	-0.04	0.04	-1.05	**-1.35**	0.026	OSJNBb0079B02.16 [Oryza sativa (japonica cultivar-group)]	35.2 not assigned.unknown	-0.18
HY06M04	-0.56	-0.94	-0.27	**-1.17**	-1.07	0.007	0	35.2_not assigned.unknown	-0.17
HU01G06	-0.29	-0.47	-0.27	-0.34	**-1.24**	0.015	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2_not assigned.unknown	-0.17
HF17K02	-0.05	0.37	0.35	0.46	**1.48**	0.048	unknown protein [Oryza sativa (japonica cultivar-group)]	35.2 not assigned.unknown	-0.16
HB04I15	0.32	0.50	0.11	0.16	**1.35**	0.029	OSJNBa0043A12.39 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	-0.16
HM01G05	0.01	0.17	0.27	0.29	**2.39**	0.041	ubiquitin-activating enzyme E1-like [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	-0.12
HG01D20	0.15	-0.21	-0.17	-0.79	**-1.50**	0.022	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2_not assigned.unknown	-0.11
HY04M06	-0.46	-0.50	-0.57	**-1.49**	-1.13	0.009	unknown protein [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	-0.07
HW08E20	0.99	0.95	1.12	3.69	**4.70**	0.004	putative proteinase inhibitor-related protein [Triticum aestivum]	35.2_not assigned.unknown	-0.07
HO03C22	0.63	**1.12**	0.55	0.86	-0.02	0.017	'putative glucan 1,3-beta-glucosidase' [Oryza sativa (japonica cultivar-	35.2_not assigned.unknown	-0.06
HW04D04	0.19	-0.48	-0.07	-0.33	**-1.25**	0.037	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2 not assigned.unknown	-0.04
HT01J12	0.76	0.71	0.51	-0.05	**1.04**	0.024	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2_not assigned.unknown	-0.03
HA02H20	-0.20	-0.40	-0.07	-0.31	**-1.41**	0.026	unknown protein [Oryza sativa (japonica cultivar-group)]	35.2 not assigned.unknown	-0.01
GCW001A	0.30	**1.76**	1.08	0.46	0.57	0.016	OSJNBb0015G09.12 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	0.02
HW04O05	0.62	0.29	0.62	1.79	**1.82**	0.011	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2_not assigned.unknown	0.02
HA12L05	-0.29	-0.54	-0.30	-0.62	**-1.99**	0.015	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2 not assigned.unknown	0.02
HT07C17	-0.35	-0.57	-0.63	-0.60	**-1.28**	0.010	unknown protein [Oryza sativa (japonica cultivar-group)] expressed protein	35.2_not assigned.unknown	0.04
HF01C06	0.48	0.36	-0.14	0.25	**1.90**	0.038	0	35.2_not assigned.unknown	0.05
HDP05O1	-0.53	**-1.00**	-0.59	-0.78	-0.47	0.013	unknown protein [Arabidopsis thaliana] unknown protein [Arabidopsis	35.2_not assigned.unknown	0.06
GBN003O	-0.11	-0.88	-0.75	-0.56	**-1.08**	0.010	DNA polymerase [Uncultured T7-like podovirus]	35.2_not assigned.unknown	0.06
GPN004G	-0.04	-0.23	-0.50	-0.46	**-1.14**	0.019	putative protein kinase ADK1 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	0.07
GCN001K	-0.43	-0.32	-0.16	**-1.39**	-0.93	0.012	hypothetical protein FG09845.1 [Gibberella zeae PH-1] hypothetical protein	35.2_not assigned.unknown	0.07
HW05E16	0.09	-0.41	-0.40	-0.21	**-1.12**	0.038	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2 not assigned.unknown	0.08
HW03G16	-0.28	-0.63	-0.49	-1.64	**-2.11**	0.009	'unknown protein, contains ACT domain, PF01842' [Oryza sativa (japonica	35.2_not assigned.unknown	0.09
HD02G23	-0.13	0.17	0.69	0.33	**1.69**	0.049	P-type ATPase [Hordeum vulgare]	35.2_not assigned.unknown	0.09
HW09I19	-0.27	-0.80	-0.53	-0.78	**-1.68**	0.012	unknown [Oryza sativa (japonica cultivar-group)]	35.2 not assigned.unknown	0.10
HO06D17	-0.46	**-1.42**	-0.72	-0.40	-1.42	0.010	P0638D12.11 [Oryza sativa (japonica cultivar-group)] cold induced protein-	35.2_not assigned.unknown	0.10
HW04O06	-0.08	-0.18	-0.25	-0.26	**-1.52**	0.033	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2 not assigned.unknown	0.10
HT08G20	-0.34	**-1.05**	-0.18	-0.56	-0.32	0.013	aspartic proteinase nepenthesin II -like [Oryza sativa (japonica cultivar-	35.2_not assigned.unknown	0.11
HV01N12	-0.06	-0.48	-0.31	-0.17	**-1.32**	0.022	tonneau 1 [Oryza sativa]	35.2_not assigned.unknown	0.13
HF01O19	-0.17	-0.59	0.08	-0.91	**-1.24**	0.014	27K protein [Triticum aestivum]	35.2_not assigned.unknown	0.15
HF02B09	-0.35	-0.28	0.05	-0.20	**-1.07**	0.034	putative singal peptidase [Oryza sativa (indica cultivar-group)]	35.2_not assigned.unknown	0.15
HS04I02	0.01	-0.44	-0.46	-0.37	**-1.28**	0.020	putative makorin RING finger protein [Oryza sativa (japonica cultivar-group)]	35.2 not assigned.unknown	0.15

HO10C14	0.88	**2.05**	0.91	-0.23	-0.15	0.029	B1146B04.13 [Oryza sativa (japonica cultivar-group)]	35.2 not assigned.unknown	0.16
HW02N20	-0.13	0.66	0.55	1.42	**1.65**	0.014	hypothetical protein, conserved [Trypanosoma cruzi] hypothetical protein,	35.2_not assigned.unknown	0.16
HO11O01	**2.74**	2.44	1.08	2.58	2.33	0.002	P0451D05.3 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	0.16
HD02L02	1.81	**2.08**	0.61	0.24	-0.19	0.024	hypothetical protein [Oryza sativa (japonica cultivar-group)]	35.2 not assigned.unknown	0.18
HH02O17	-0.22	0.21	0.35	0.52	**1.73**	0.040	putative histone deacetylase HD2 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	0.20
HW09N11	0.07	-0.47	-0.26	-0.20	**-1.00**	0.028	Leucine Rich Repeat, putative [Oryza sativa (japonica cultivar-group)]	35.2 not assigned.unknown	0.20
HX02I09	-0.39	-0.34	-0.29	-0.34	**-1.38**	0.017	hypothetical protein [Oryza sativa (japonica cultivar-group)] hypothetical	35.2_not assigned.unknown	0.22
HW08H11	0.20	0.72	0.37	0.63	**1.29**	0.017	Ribosomal protein L2 [Oryza sativa (japonica cultivar-group)] ribosomal	35.2_not assigned.unknown	0.22
GNW001	-0.32	0.48	0.19	0.50	**1.96**	0.048	suppressor-like protein [Oryza sativa (japonica cultivar-group)] suppressor-	35.2_not assigned.unknown	0.22
HO14D18	1.31	**4.62**	-0.20	0.88	0.79	0.016	MutT/nudix protein-like [Oryza sativa (japonica cultivar-group)] MutT/nudix	35.2_not assigned.unknown	0.25
HO05K06	-0.17	-0.31	-0.16	-0.22	**-1.02**	0.032	CAA30376.1 protein [Oryza sativa]	35.2 not assigned.unknown	0.26
HO01C17	1.82	**2.65**	2.15	1.30	0.93	0.007	Mlo3 [Hordeum vulgare subsp. vulgare]	35.2_not assigned.unknown	0.27
HY08E03	1.69	**2.44**	1.06	0.55	-0.66	0.026	caffeic acid O-methyltransferase [Triticum aestivum]	35.2 not assigned.unknown	0.28
HO05D08	-0.58	-1.15	-0.88	**-1.21**	-0.85	0.005	lipase-like [Oryza sativa (japonica cultivar-group)] lipase-like [Oryza sativa	35.2_not assigned.unknown	0.28
HF14F21	-0.27	-0.16	-0.09	-0.01	**-1.01**	0.046	BRI1-KD interacting protein 132 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	0.28
HS01F18	-0.20	-0.80	-0.34	-0.54	**-1.13**	0.012	putative ABI3-interacting protein 2 [Oryza sativa (japonica cultivar-group)]	35.2 not assigned.unknown	0.29
HG01B11	-0.22	-1.17	-1.09	-1.25	**-1.73**	0.008	putative diphosphonucleotide phosphatase [Oryza sativa (japonica cultivar-	35.2_not assigned.unknown	0.29
HW02L17	-0.25	-0.64	-0.19	-0.16	**-1.03**	0.029	P0501G01.11 [Oryza sativa (japonica cultivar-group)] unknown protein	35.2_not assigned.unknown	0.30
HW05H10	0.38	**2.03**	1.11	1.14	0.64	0.010	PDI-like protein [Zea mays]	35.2_not assigned.unknown	0.33
HO16K18	0.22	0.67	0.56	0.93	**1.39**	0.010	OSJNBa0043A12.39 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	0.35
HA08A15	-0.08	-0.23	0.13	-0.16	**-1.04**	0.048	3-beta-glucuronosyltransferase [Hordeum vulgare]	35.2_not assigned.unknown	0.35
HO06G10	1.37	**2.66**	1.16	0.52	-0.49	0.022	caffeic acid O-methyltransferase [Triticum aestivum]	35.2_not assigned.unknown	0.36
HY07B11	-0.34	-0.28	-0.44	-0.53	**-1.22**	0.014	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2 not assigned.unknown	0.36
HW06B06	0.12	0.06	0.12	1.20	**1.78**	0.040	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2_not assigned.unknown	0.37
GCN002G	-0.02	0.17	-0.51	-0.28	**-1.38**	0.039	hypothetical protein FG08622.1 [Gibberella zeae PH-1] hypothetical protein	35.2 not assigned.unknown	0.38
HD11L09	0.19	-0.30	0.18	-0.67	**-1.19**	0.037	putative polypyrimidine tract-binding protein [Oryza sativa] putative	35.2_not assigned.unknown	0.38
HW06F18	-0.51	-1.50	-1.17	-1.18	**-1.74**	0.006	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2_not assigned.unknown	0.39
HDP38A0	0.36	**1.62**	1.08	1.29	0.38	0.010	OSJNBa0084K11.10 [Oryza sativa (japonica cultivar-group)]	35.2 not assigned.unknown	0.39
HG01K14	-0.15	-0.75	-0.43	-0.82	**-1.81**	0.013	putative 37kDa chloroplast inner envelope membrane polypeptide precursor	35.2_not assigned.unknown	0.40
HA01J11	-0.01	-0.23	-0.07	-0.19	**-1.33**	0.033	growth-regulating factor 1-like protein [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	0.42
HV02K04	0.10	-0.87	-0.23	0.00	**-1.09**	0.039	unknown protein [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	0.43
HO09J17	2.05	**3.23**	1.29	0.82	2.44	0.006	putative 33 kDa secretory protein [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	0.43
HK04H12	-0.56	**-1.19**	-0.87	-0.20	-0.14	0.017	OSJNBa0086B14.2 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	0.43
HK04E01	-0.89	**-1.46**	-1.09	-0.65	-0.84	0.008	pore-forming toxin-like protein Hfr-2 [Triticum aestivum]	35.2_not assigned.unknown	0.45
HY04H14	-0.09	-0.12	-0.15	-0.40	**-1.86**	0.032	hypothetical protein [Oryza sativa (japonica cultivar-group)] hypothetical	35.2 not assigned.unknown	0.45
HY05P19	0.05	-0.41	-0.46	0.35	**-1.60**	0.044	respiratory burst oxidase protein B [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	0.45
HO08M14	-0.37	0.02	0.00	-0.11	**-1.20**	0.041	OSJNBa0043A12.25 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	0.46
GCA001C	3.35	**4.17**	1.54	1.06	1.82	0.003	pathogenesis-related protein 10 [Hordeum vulgare]	35.2 not assigned.unknown	0.47
HV01D21	-0.78	**-1.25**	-0.98	-1.20	-1.24	0.004	pore-forming toxin-like protein Hfr-2 [Triticum aestivum]	35.2_not assigned.unknown	0.47
HO04C10	-0.25	-0.10	-0.10	-0.76	**-1.39**	0.017	'unknown protein, contains ubiquitin carboxyl-terminal hydrolase' [Oryza	35.2 not assigned.unknown	0.47
HU03M22	-0.18	0.00	-0.11	-0.25	**-1.11**	0.050	putative aminotransferase [Oryza sativa (japonica cultivar-group)] putative	35.2_not assigned.unknown	0.49
HDP18E0	-0.11	-0.44	-0.17	-0.11	**-1.03**	0.032	hypothetical protein SB20O07.12 [Sorghum bicolor]	35.2_not assigned.unknown	0.49
HV01H13	-0.04	-0.88	-0.96	-0.31	**-1.07**	0.019	phosphosulfolactate synthase-related protein [Oryza sativa (japonica	35.2_not assigned.unknown	0.50
HY10N22	-0.10	-0.97	-0.44	-0.56	**-1.21**	0.013	putative ABI3-interacting protein 2 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	0.52
HZ42H05	0.24	-0.02	0.09	0.43	**1.68**	0.043	mitochondrial chaperonin-60 [Oryza sativa (japonica cultivar-group)]	35.2 not assigned.unknown	0.53

HR01M18	-0.47	-0.52	-0.94	**-1.24**	-0.59	0.010	isoleucyl-tRNA synthetase [Deinococcus radiodurans] isoleucyl-tRNA	35.2 not assigned.unknown	0.53
HA12D17	-0.50	**-1.49**	-1.13	-0.57	-0.84	0.010	NPH3 family protein [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	0.54
GBN008A	-0.12	-0.12	-0.17	-0.88	**-1.03**	0.016	unknown [Schistosoma japonicum]	35.2_not assigned.unknown	0.54
HO15N23	0.00	-0.35	-0.55	-0.47	**-1.20**	0.027	putative protein [Arabidopsis thaliana] expressed protein [Arabidopsis	35.2 not assigned.unknown	0.54
HF06I08	-0.38	0.01	-0.31	-0.70	**-1.04**	0.019	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2_not assigned.unknown	0.55
HM08I23	-0.30	-0.38	0.11	0.20	**-1.01**	0.048	proline-rich protein [Zea mays]	35.2 not assigned.unknown	0.56
GBN003O	-0.42	-0.48	0.03	-0.46	**-1.14**	0.018	unnamed protein product [Tetraodon nigroviridis]	35.2_not assigned.unknown	0.56
HD03E20	-0.18	0.38	0.75	**1.55**	1.00	0.029	subtilisin-chymotrypsin inhibitor 2 [Hordeum vulgare subsp. vulgare] putative	35.2_not assigned.unknown	0.56
HO08F24	0.61	**1.27**	-0.12	0.81	-0.11	0.034	'putative glucan 1,3-beta-glucosidase' [Oryza sativa (japonica cultivar-	35.2_not assigned.unknown	0.56
HO29L12	-0.33	-0.27	-0.01	-0.60	**-1.09**	0.020	expressed protein [Oryza sativa (japonica cultivar-group)] expressed protein	35.2_not assigned.unknown	0.57
HA10I09	0.04	-0.33	0.08	-0.46	**-1.10**	0.035	unknown protein [Oryza sativa (japonica cultivar-group)]	35.2 not assigned.unknown	0.57
HI01L02	0.36	0.92	0.47	1.02	**1.52**	0.009	Similar to Avr9/Cf-9 rapidly elicited protein 65::::::::contains ESTs	35.2_not assigned.unknown	0.59
GNW002	0.17	0.68	0.22	1.02	**1.16**	0.019	BRICK1 [Zea mays]	35.2 not assigned.unknown	0.59
HO14M19	0.25	-0.08	-0.22	-1.03	**-1.11**	0.037	OSJNBa0094O15.3 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	0.60
HV02A23	0.24	0.06	-0.25	0.49	**1.10**	0.046	hypothetical protein [Oryza sativa (japonica cultivar-group)] hypothetical	35.2_not assigned.unknown	0.61
HW06F04	-0.26	0.23	0.48	1.16	**2.72**	0.026	putative GAJ protein [Oryza sativa (japonica cultivar-group)] putative MND1	35.2 not assigned.unknown	0.62
HW09A06	-0.05	0.02	0.50	0.63	**1.21**	0.047	ESTs AU064537(E31904),AU082147(E31904) correspond to a region of the	35.2_not assigned.unknown	0.63
HO10B06	0.35	0.32	0.22	0.82	**1.45**	0.022	OSJNBa0060P14.12 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	0.63
HT01C16	-0.23	0.03	-0.25	-0.37	**-1.10**	0.029	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2_not assigned.unknown	0.65
HY06M01	0.27	-0.34	-0.39	**-1.12**	-0.81	0.033	unnamed protein product [Oryza sativa (japonica cultivar-group)] unknown	35.2_not assigned.unknown	0.67
HO09K14	1.51	**2.96**	1.73	0.02	-0.69	0.023	T06989 pathogen-induced protein WIR1 - wheat WIR1B PROTEIN WIR1	35.2_not assigned.unknown	0.67
HY06P19	-0.26	-0.47	-0.27	-1.04	**-2.50**	0.014	putative B2 protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2_not assigned.unknown	0.70
HW02G12	-0.11	0.53	0.00	0.22	**1.56**	0.048	OSJNBa0083I11.13 [Oryza sativa (japonica cultivar-group)]	35.2 not assigned.unknown	0.72
HW08C24	0.59	1.21	1.01	0.36	**1.22**	0.017	Stromal cell-derived factor 2-like protein [Oryza sativa (japonica cultivar-	35.2_not assigned.unknown	0.72
HO14G15	-0.28	-0.08	-0.29	-0.63	**-1.25**	0.023	putative 4-methyl-5(B-hydroxyethyl)-thiazol monophosphate biosynthesis	35.2 not assigned.unknown	0.72
HW09K19	-0.02	-0.38	-0.69	-0.15	**-1.06**	0.023	expressed protein [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	0.73
HY02I16	-0.08	-0.09	-0.14	-0.60	**-1.30**	0.031	zinc finger (CCCH-type) protein-like [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	0.74
HO06C19	2.75	**3.83**	0.97	0.56	2.10	0.004	pathogenesis-related protein 10 [Hordeum vulgare]	35.2 not assigned.unknown	0.74
HW06G08	-0.47	-0.18	1.36	2.64	**2.76**	0.024	subtilisin-chymotrypsin inhibitor 2 [Hordeum vulgare subsp. vulgare] putative	35.2_not assigned.unknown	0.76
HC14D22	0.36	1.02	0.79	3.88	**5.37**	0.005	putative proteinase inhibitor-related protein [Triticum aestivum]	35.2_not assigned.unknown	0.77
GCA001J	2.02	**3.03**	1.70	0.24	-0.68	0.018	T06988 pathogen-induced protein WIR1A - wheat WIR1A PROTEIN WIR1A	35.2_not assigned.unknown	0.77
HO08J14	0.01	0.43	0.23	0.46	**1.07**	0.043	hypothetical protein [Oryza sativa (japonica cultivar-group)] hypothetical	35.2_not assigned.unknown	0.78
HZ38A10	-0.20	1.13	1.42	1.16	**1.62**	0.011	hypothetical protein [Arabidopsis thaliana] At5g16060 [Arabidopsis thaliana]	35.2_not assigned.unknown	0.79
GBN005K	1.70	**2.98**	2.47	0.94	2.01	0.003	0	35.2_not assigned.unknown	0.81
HO15J23	-0.57	-0.31	**-1.04**	-0.42	0.03	0.020	AT5g40470/K21I16 20 [Arabidopsis thaliana] unnamed protein product	35.2 not assigned.unknown	0.83
HO02D04	-0.31	-0.02	-0.20	-0.91	**-1.16**	0.018	P0519D04.18 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	0.85
HU04P10	-0.21	-0.52	-0.68	-0.13	**-1.06**	0.021	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2_not assigned.unknown	0.85
HR01J10	0.09	0.60	1.28	2.04	**3.49**	0.010	NAR2.3 [Hordeum vulgare subsp. vulgare]	35.2 not assigned.unknown	0.86
HW06P06	-0.48	0.17	0.34	2.08	**2.59**	0.027	unknown protein [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	0.87
HO16L18	-0.19	-0.70	-0.30	-0.44	**-1.03**	0.013	OSJNBa0027G07.27 [Oryza sativa (japonica cultivar-group)]	35.2 not assigned.unknown	0.87
HW04K16	-0.02	-0.16	-0.10	-0.52	**-1.15**	0.043	hexokinase [Triticum aestivum]	35.2_not assigned.unknown	0.87
HO26N18	0.27	-0.30	-0.59	**-1.01**	-0.99	0.033	unnamed protein product [Oryza sativa (japonica cultivar-group)] unknown	35.2_not assigned.unknown	0.88
HS01P05	0.46	**1.11**	0.44	0.13	0.44	0.021	Erwinia induced protein 2 [Oryza sativa (japonica cultivar-group)] Erwinia	35.2_not assigned.unknown	0.88
HX03K11	-0.25	-0.55	-0.69	-0.37	**-1.18**	0.011	putative ABI3-interacting protein 2 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	0.89
HA10I11	0.01	-0.38	-0.44	-0.51	**-1.00**	0.019	unknown protein [Arabidopsis thaliana] unknown protein [Arabidopsis	35.2 not assigned.unknown	0.89

HW09K18	0.30	0.44	0.86	0.22	**1.99**	0.030	0	35.2 not assigned.unknown	0.89
HF16I21	-0.29	-0.68	-0.30	-0.76	**-1.12**	0.021	putative epimerase/dehydratase [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	0.89
HY05N14	-0.67	**-1.67**	-1.21	-1.46	-1.19	0.010	P0410E03.24 [Oryza sativa (japonica cultivar-group)] unknown protein	35.2_not assigned.unknown	0.91
HO01A24	0.68	**1.21**	0.42	0.52	-0.03	0.022	kinase interacting protein 1 -like [Oryza sativa (japonica cultivar-group)]	35.2 not assigned.unknown	0.94
HY04B11	0.13	**1.36**	0.64	-0.24	0.41	0.047	Erwinia induced protein 2 [Oryza sativa (japonica cultivar-group)] Erwinia	35.2_not assigned.unknown	0.95
GCA003G	0.62	0.56	-0.06	0.23	**2.13**	0.023	unknown protein [Oryza sativa (japonica cultivar-group)] PREDICTED	35.2 not assigned.unknown	0.96
HI05L08	0.56	0.79	-0.20	0.08	**1.58**	0.040	unknown protein [Oryza sativa (japonica cultivar-group)] PREDICTED	35.2_not assigned.unknown	0.96
HO07N18	-0.08	-0.02	-0.08	-0.70	**-1.23**	0.033	unknown protein [Arabidopsis thaliana] unknown protein [Arabidopsis	35.2_not assigned.unknown	0.97
HO10M08	-0.22	-0.28	0.01	-0.25	**-1.60**	0.025	expressed protein [Oryza sativa (japonica cultivar-group)] expressed protein	35.2_not assigned.unknown	0.98
GBN002J	-0.01	1.52	0.78	0.44	**1.76**	0.016	envelope glycoprotein [Human immunodeficiency virus 1]	35.2_not assigned.unknown	0.99
HA09H23	-0.38	-0.73	-0.66	-0.65	**-1.20**	0.010	putative syntaxin [Oryza sativa (japonica cultivar-group)] putative syntaxin	35.2 not assigned.unknown	0.99
HY10B14	-0.06	-0.04	-0.16	-0.95	**-1.29**	0.021	hypothetical protein [Arabidopsis thaliana] hypothetical protein [Arabidopsis	35.2_not assigned.unknown	1.00
HY01D21	-0.30	0.28	0.13	**-1.19**	-0.78	0.040	putative dentritic cell 2 protein<DC2 protein [Oryza sativa (japonica cultivar-	35.2 not assigned.unknown	1.00
HA02O15	0.59	**2.18**	1.33	0.74	0.81	0.011	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2_not assigned.unknown	1.00
HO30B02	-0.23	0.79	0.74	**1.62**	0.75	0.022	subtilisin-chymotrypsin inhibitor 2 [Hordeum vulgare subsp. vulgare] putative	35.2_not assigned.unknown	1.02
HO11C14	-0.03	0.02	-0.14	-0.79	**-1.48**	0.026	expressed protein [Oryza sativa (japonica cultivar-group)]	35.2 not assigned.unknown	1.02
HY07B21	-0.14	-0.52	-0.53	-1.00	**-1.59**	0.016	putative transformer serine/arginine-rich ribonucleoprotein [Oryza sativa	35.2_not assigned.unknown	1.03
HB12B19	-0.21	0.28	-0.19	-0.58	**-1.27**	0.033	BRI1-KD interacting protein 130 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	1.04
HO07P12	-0.01	-0.11	-0.13	-0.42	**-1.20**	0.037	unknown protein [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	1.05
HO06N09	0.17	0.12	-0.09	-1.11	**-1.64**	0.038	putative protein C prepropeptide [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	1.06
HV09B20	0.37	0.70	0.29	0.23	**1.63**	0.027	unknown protein [Oryza sativa (japonica cultivar-group)] PREDICTED	35.2_not assigned.unknown	1.07
HD01A18	-0.46	-0.88	-0.68	-1.13	**-1.70**	0.006	putative microtubule-associated protein MAP65-1a [Oryza sativa (japonica	35.2_not assigned.unknown	1.09
HO10E06	-0.28	-0.63	-0.32	-1.52	**-2.27**	0.012	putative copia polyprotein [Sorghum bicolor]	35.2 not assigned.unknown	1.12
HW08I23	-0.01	1.37	0.94	0.63	**1.80**	0.013	GRAB2 protein [Triticum sp.]	35.2_not assigned.unknown	1.13
HT01H16	0.12	-0.30	-0.46	**-1.00**	-0.81	0.035	unnamed protein product [Oryza sativa (japonica cultivar-group)] unknown	35.2 not assigned.unknown	1.14
HO38J06	-0.52	-0.83	-0.65	-1.17	**-1.23**	0.006	OSJNBb0038F03.8 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	1.14
HDP16M1	-0.01	-0.16	-0.68	-0.88	**-1.10**	0.017	AT3g12300/F28J15_117 [Arabidopsis thaliana] AT3g12300/F28J15_117	35.2_not assigned.unknown	1.14
HO01M07	0.98	**1.32**	0.39	0.40	-0.28	0.031	kinase interacting protein 1 -like [Oryza sativa (japonica cultivar-group)]	35.2 not assigned.unknown	1.16
HS03K03	-0.31	**-1.46**	-0.30	0.02	-0.70	0.020	P0460C04.20 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	1.17
HP01P03	-0.63	-1.39	-1.32	-1.30	**-2.22**	0.004	ankyrin repeat-like protein [Oryza sativa (japonica cultivar-group)] ankyrin	35.2_not assigned.unknown	1.20
HO06C23	-0.33	0.59	1.41	**3.17**	2.44	0.013	subtilisin-chymotrypsin inhibitor 2 [Hordeum vulgare subsp. vulgare] putative	35.2_not assigned.unknown	1.21
HM02I16	0.07	**1.28**	0.27	0.01	0.36	0.044	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2_not assigned.unknown	1.22
HO07L10	-0.40	0.00	-0.52	-0.77	**-1.76**	0.017	putative RNA polymerase sigma factor [Oryza sativa (japonica cultivar-	35.2_not assigned.unknown	1.23
HX03P09	0.14	0.07	-0.28	-0.36	**-1.16**	0.050	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2_not assigned.unknown	1.26
HW03P05	0.47	1.16	0.66	0.52	**1.21**	0.015	unknown protein [Oryza sativa (japonica cultivar-group)]	35.2 not assigned.unknown	1.33
HV02P22	-0.08	**1.11**	1.03	0.34	0.70	0.022	subitilisin-chymotrypsin inhibitor [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	1.33
HR01K13	0.04	1.99	2.55	**3.67**	3.66	0.004	putative dermal glycoprotein precursor [Oryza sativa (japonica cultivar-	35.2_not assigned.unknown	1.34
HA12E18	-0.12	-0.13	-0.66	-0.28	**-1.23**	0.024	putative disease resistance protein [Oryza sativa (japonica cultivar-group)]	35.2 not assigned.unknown	1.40
HO01F03	-0.18	-0.95	-0.80	-0.75	**-1.24**	0.009	OSJNBa0089N06.15 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	1.43
HY10E13	-0.26	-0.62	-0.49	-0.93	**-1.09**	0.012	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2 not assigned.unknown	1.47
HB03G04	-0.55	-0.30	-0.20	-0.57	**-1.05**	0.012	OSJNBa0014K14.6 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	1.47
HO05E17	-0.46	0.25	-0.67	-0.66	**-1.44**	0.022	putative B2 protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2_not assigned.unknown	1.51
HO09K09	-0.06	**1.50**	0.52	0.28	1.41	0.042	unknown [Glycine max]	35.2_not assigned.unknown	1.52
HZ51F23	-0.51	-1.00	**-1.03**	-1.03	0.20	0.013	OSJNBa0074L08.21 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	1.62
HO30D21	-0.18	-0.95	-1.10	-1.12	**-2.60**	0.010	transcription factor BHLH9-like protein [Oryza sativa (japonica cultivar-	35.2 not assigned.unknown	1.68

HO01D04	-0.18	0.00	-0.83	-0.95	**-1.53**	0.016	Putative anion transporter [Oryza sativa] Putative anion transporter [Oryza	35.2 not assigned.unknown	1.70
HS06P15	0.10	-0.55	-1.04	-0.69	**-1.30**	0.018	ethylene responsive protein [Oryza sativa]	35.2_not assigned.unknown	1.70
HZ58F11	-0.16	-1.11	**-1.68**	-1.10	-0.82	0.009	1303209A translation inhibitor II	35.2_not assigned.unknown	1.72
HX04M21	0.15	0.06	-0.30	-0.68	**-1.43**	0.031	cticosapeptide/Phox/Bem1p (PB1) domain-containing protein-like [Oryza	35.2 not assigned.unknown	1.75
HW05A03	1.03	**2.06**	1.22	-0.10	0.93	0.017	hypothetical protein [Oryza sativa (japonica cultivar-group)] hypothetical	35.2_not assigned.unknown	1.79
HP01E21	-0.17	1.20	**1.60**	1.46	0.91	0.012	subitilisin-chymotrypsin inhibitor [Oryza sativa (japonica cultivar-group)]	35.2 not assigned.unknown	1.79
HW09C05	-0.01	-0.06	-0.43	-0.88	**-1.04**	0.036	OSJNBa0043A12.4 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	1.81
HO12E01	-0.40	-0.01	**-1.14**	-0.82	-0.11	0.042	OSJNBa0042I15.6 [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	1.83
HK04F21	-0.68	-1.20	-1.16	-1.53	**-1.85**	0.014	hypothetical protein [Oryza sativa (japonica cultivar-group)] hypothetical	35.2_not assigned.unknown	1.92
HD01M10	-0.52	0.56	0.66	1.27	**1.37**	0.025	subitilisin-chymotrypsin inhibitor [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	2.02
HO13F22	-0.24	-0.51	-0.44	-0.35	**-1.87**	0.021	PREDICTED: similar to Hypothetical protein CBG15579, partial [Bos taurus]	35.2 not assigned.unknown	2.19
HO07P16	-0.70	-1.21	-0.42	-0.28	**-1.77**	0.011	abscisic stress ripening protein-like protein [Musa acuminata]	35.2_not assigned.unknown	2.31
HV04B15	-0.59	-0.05	-0.68	-1.11	**-1.93**	0.016	Putative anion transporter [Oryza sativa] Putative anion transporter [Oryza	35.2 not assigned.unknown	2.56
HO04L10	-0.16	-0.79	-1.08	-0.64	**-1.15**	0.020	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2_not assigned.unknown	2.79
HO38M07	1.06	**2.65**	0.97	0.19	-0.27	0.026	blue copper binding protein [Hordeum vulgare subsp. vulgare]	35.2_not assigned.unknown	2.83
HO03D05	-0.28	-1.08	-0.35	-0.52	**-2.22**	0.013	Putative Phytosulfokines precursor [Oryza sativa (japonica cultivar-group)]	35.2 not assigned.unknown	3.04
HO05J06	-0.25	-0.91	-0.72	-0.31	**-1.45**	0.017	gi|38349106|gb|AAR18074.1| LIM homeobox 8 [Homo sapiens]	35.2_not assigned.unknown	3.06
HK05I15	-0.16	-1.24	-0.44	-0.72	**-2.90**	0.023	putative 5'-3' exoribonuclease [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	3.06
HO13E04	-0.55	-1.02	-0.67	-0.74	**-2.30**	0.010	Putative Phytosulfokines precursor [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	3.55
HO14O16	-0.54	-0.64	-1.41	-0.41	**-1.45**	0.017	embryo-specific protein [Oryza sativa]	35.2_not assigned.unknown	3.58
HM01H15	0.49	**1.03**	0.18	0.09	0.14	0.048	Putative protein with similarity to putative prostate cancer tumor suppressor	35.2_not assigned.unknown	#NV
HO06J02	-0.83	-1.48	-1.84	**-1.94**	-0.86	0.003	pore-forming toxin-like protein Hfr-2 [Triticum aestivum]	35.2_not assigned.unknown	#NV
HV02G19	0.36	0.17	1.38	1.67	**3.83**	0.014	putative GLE1L protein [Oryza sativa (japonica cultivar-group)] putative	35.2 not assigned.unknown	#NV
HR01O15	0.40	2.22	1.63	2.46	**5.33**	0.005	expressed protein [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	#NV
HO17O23	0.37	0.75	1.16	2.32	**3.42**	0.009	NBS-LRR disease resistance protein homologue [Hordeum vulgare]	35.2 not assigned.unknown	#NV
HA29H05	-0.18	**-1.40**	-1.15	-0.53	-0.37	0.013	PREDICTED OJ1218_D07.16 gene product [Oryza sativa (japonica cultivar-	35.2_not assigned.unknown	#NV
HG01A24	1.22	**1.25**	0.03	0.20	1.17	0.017	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2_not assigned.unknown	#NV
HK03A08	0.89	2.30	1.36	0.82	**3.02**	0.006	unknown protein [Arabidopsis thaliana] unknown protein [Arabidopsis	35.2 not assigned.unknown	#NV
GBN003M	0.02	0.83	0.38	0.40	**1.93**	0.018	putative human tumor susceptibility gene-like protein [Oryza sativa (japonica	35.2_not assigned.unknown	#NV
HD13K04	0.37	0.11	1.41	0.33	**3.27**	0.020	JI23_HORVU 23 kDa jasmonate-induced protein	35.2_not assigned.unknown	#NV
HDP26H0	0.13	0.32	0.28	-0.15	**1.08**	0.049	P0698A10.25 [Oryza sativa (japonica cultivar-group)] membrane protein	35.2_not assigned.unknown	#NV
HD06O20	0.11	0.18	0.09	0.52	**1.28**	0.031	unknown protein [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	#NV
HP11P08	-0.46	**-1.05**	-0.51	-0.41	-0.23	0.015	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	35.2_not assigned.unknown	#NV
HP11L18	-0.34	**-1.64**	-1.18	-0.58	-0.04	0.014	putative proton-dependent oligopeptide transport [Oryza sativa (japonica	35.2_not assigned.unknown	#NV
HO15P04	1.81	**2.64**	1.49	0.30	-0.31	0.018	P0483G10.26 [Oryza sativa (japonica cultivar-group)] putative bundle sheath	35.2 not assigned.unknown	#NV
HB01P22	1.63	**2.51**	1.02	1.45	1.65	0.003	Transport, integral membrane::: hypothetical protein AT1G12600	35.2_not assigned.unknown	#NV
HY04F23	0.57	0.47	0.27	0.14	**3.16**	0.022	putative leucine-rich protein [Oryza sativa (japonica cultivar-g	35.2_not assigned.unknown	#NV
HO01F23	-0.51	**-1.71**	-0.70	-0.36	0.27	0.024	TPA: class III peroxidase 70 precursor [Oryza sativa (japonica cultivar-	35.2 not assigned.unknown	#NV
HZ01B13	-0.13	0.08	-0.32	0.90	**4.32**	0.033	putative nuclear protein [Hordeum vulgare subsp. vulgare]	35.2_not assigned.unknown	#NV
HX01J18	-0.21	**-1.55**	-1.43	-0.60	0.22	0.021	defensin [Triticum aestivum]	35.2 not assigned.unknown	#NV
HO09F01	-0.30	**-1.36**	-0.73	-0.95	-0.68	0.009	putative chloroplast nucleoid DNA-binding protein cnd41 [Oryza sativa	35.2_not assigned.unknown	#NV
HO01K17	0.68	1.08	0.69	0.69	**1.19**	0.012	putative non-LTR retroelement reverse transcriptase [Zea mays]	35.2_not assigned.unknown	#NV
HO01F16	0.62	1.47	2.07	4.02	**5.05**	0.003	kinesin motor protein (kin2), putative [Arabidopsis thaliana]	35.2_not assigned.unknown	#NV
HO02B20	1.50	2.00	2.07	3.98	**6.28**	0.001	putative wall-associated kinase [Oryza sativa (japonica cultivar-group)]	35.2_not assigned.unknown	#NV
HO14C15	0.65	1.57	0.89	0.78	**2.40**	0.009	hypothetical protein [Oryza sativa (japonica cultivar-group)]	35.2 not assigned.unknown	#NV

HO06M03	-0.06	-0.62	-0.67	-0.94	**-2.09**	0.013	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	#NV	3.02
HO15P11	0.22	-0.14	0.38	-1.51	**-2.98**	0.046	putative receptor-like protein kinase 1 [Oryza sativa (japonica cultivar-	#NV	2.58
HO18F04	-0.30	-0.76	-0.66	-1.13	**-1.20**	0.013	myb-like protein [Arabidopsis thaliana] MYB transcription factor [Arabidopsis	#NV	2.36
HO15D14	-0.40	-0.54	-0.68	-1.01	**-1.33**	0.010	unknown protein [Oryza sativa (japonica cultivar-group)] unknown protein	#NV	2.28
HO01I10	0.93	**2.25**	1.33	0.48	1.03	0.011	histidine amino acid transporter [Oryza sativa (indica cultivar-group)]	#NV	2.05
HK03K16	-0.12	-0.93	-0.90	-1.57	**-2.62**	0.012	lipid transfer protein-like, PREDICTED P0417F02.20 gene product [Oryza	#NV	1.85
HY04M16	-0.38	-1.12	-0.95	**-1.61**	-0.80	0.010	gamma-TIP-like protein [Hordeum vulgare subsp. vulgare]	#NV	1.57
HO10M17	-0.34	-1.15	-0.81	**-1.48**	0.20	0.016	unnamed protein product [Oryza sativa (japonica cultivar-group)]	#NV	1.55
HO10M01	0.77	**1.14**	0.42	0.17	-0.38	0.046	receptor serine/threonine kinase PR5K-like [Oryza sativa (japonica cultivar-	#NV	1.52
HO03P07	-0.25	-0.33	-0.19	-1.04	**-2.45**	0.016	hypothetical protein FG01177.1 [Gibberella zeae PH-1] hypothetical protein	#NV	1.52
HO08B09	1.13	**2.62**	1.71	0.51	-1.29	0.026	leucine rich repeat containing protein kinase [Oryza sativa]	#NV	1.50
HO12J07	1.31	**2.78**	1.44	0.44	-1.01	0.027	leucine rich repeat containing protein kinase [Oryza sativa]	#NV	1.45
HO07K18	0.83	0.87	0.38	0.39	**1.53**	0.015	putative chloroplast nucleoid DNA binding protein [Oryza sativa (japonica	#NV	1.16
HO04C18	0.00	-0.59	-0.14	0.01	**-1.13**	0.030	putative calcium-dependent protein kinase [Oryza sativa (japonica cultivar-	#NV	1.03
HO06E03	0.01	-0.59	-0.97	-0.50	**-1.69**	0.018	putative late elongated hypocoty [Oryza sativa (japonica cultivar-group)]	#NV	0.87
HT02G10	-0.61	-0.84	-0.29	-0.70	**-1.14**	0.010	Putative RNA-binding protein [Oryza sativa (japonica cultivar-group)]	#NV	0.76
HO04G13	-0.16	-0.65	-0.23	-0.42	**-1.93**	0.018	putative protein serine /threonine kinase [Sorghum bicolor]	#NV	0.70
GCN001B	0.79	0.85	0.42	0.16	**1.72**	0.016	putative minichromosome maintenance (MCM) protein [Arabidopsis thaliana]	#NV	0.65
HV03E13	-0.01	0.02	0.32	1.75	**2.41**	0.025	12-oxo-phytodienoic acid reductase [Zea mays]	#NV	0.64
HY02B19	0.09	-0.10	-0.40	-0.27	**-2.01**	0.037	heat shock protein cognate 70 [Oryza sativa (japonica cultivar-group)] heat	#NV	0.64
HO22J02	-0.05	-0.42	-0.56	-0.47	**-1.07**	0.018	putative HSF-type DNA-binding protein [Oryza sativa (japonica cultivar-	#NV	0.61
HI04P06	1.00	**1.53**	0.37	0.58	1.03	0.010	unknown protein [Arabidopsis thaliana] unknown protein [Arabidopsis	#NV	0.56
HO11A08	1.23	0.79	1.22	**1.29**	0.74	0.009	putative PDR-like ABC transporter [Oryza sativa (japonica cultivar-group)]	#NV	0.53
HW02O08	0.94	**1.17**	0.58	0.13	-0.03	0.030	kinase interacting protein 1 -like [Oryza sativa (japonica cultivar-group)]	#NV	0.52
HH01G13	-0.09	0.11	0.03	-0.37	**-1.32**	0.049	putative ABI3-interacting protein 2; CnAIP2 [Oryza sativa (japonica cultivar-	#NV	0.47
GNW004	0.57	**1.48**	0.32	-0.23	0.91	0.023	TMV response-related protein-like [Oryza sativa (japonica cultivar-group)]	#NV	0.42
HI01L12	-0.12	-0.13	0.14	1.27	**1.91**	0.035	unknown protein [Arabidopsis thaliana] PHD finger protein-related	#NV	0.42
HS01I08	-0.19	-0.31	-0.76	-0.55	**-1.52**	0.015	respiratory burst oxidase homolog [Solanum tuberosum]	#NV	0.39
HI04I01	0.03	-0.02	-0.20	-0.66	**-1.25**	0.031	putative ear1 protein [Oryza sativa (japonica cultivar-group)]	#NV	0.39
HY01G10	-0.20	0.37	0.57	**1.67**	1.43	0.017	cell-wall invertase 7 [Oryza sativa (japonica cultivar-group)] Beta-	#NV	0.37
HY02N01	-0.32	-0.51	-0.45	-1.00	**-1.20**	0.012	Ran binding protein-1 [Lycopersicon esculentum]	#NV	0.36
HY02N21	0.07	-0.41	-0.65	0.18	**-1.12**	0.035	ribosomal protein L13a [Triticum aestivum]	#NV	0.36
HD03B06	0.64	**1.03**	0.27	0.28	0.86	0.017	LEM3-like [Oryza sativa (japonica cultivar-group)]	#NV	0.33
HI04K14	0.28	0.46	0.06	0.65	**1.07**	0.037	hypothetical protein [Oryza sativa (japonica cultivar-group)]	#NV	0.30
HO07F02	1.01	**1.38**	0.41	-0.05	0.85	0.028	putative acetyl transferase [Oryza sativa (japonica cultivar-group)] 10-	#NV	0.24
HS01N21	0.07	-0.05	-0.32	-0.17	**-1.30**	0.049	ribosomal protein L3 [Triticum aestivum] ribosomal protein L3 [Triticum	#NV	0.21
HW02H13	-0.22	-0.56	0.11	-0.50	**-1.06**	0.020	putative cellulose synthase catalytic subunit [Hordeum vulgare]	#NV	0.21
HO05A24	-0.46	-0.61	-0.16	-0.05	**-1.37**	0.018	putative sodium transporter [Oryza sativa (japonica cultivar-group)] putative	#NV	0.15
HO10M20	0.12	0.59	0.33	0.44	**1.31**	0.027	fimbrin/plastin-like [Triticum aestivum]	#NV	0.14
HO11B11	-0.33	-0.11	-0.77	-0.98	**-1.57**	0.013	ACT domain-containing protein [Arabidopsis thaliana], expressed protein	#NV	0.12
HO08N04	-0.23	-0.74	-1.29	**-1.32**	-1.25	0.007	PREDICTED OSJNBa0034J04.14 gene product [Oryza sativa (japonica	#NV	0.05
HV02C01	-0.04	-0.49	-0.40	-0.49	**-1.07**	0.018	putative DHHC-type zinc finger domain-containing protein [Oryza sativa	#NV	0.02
HO11B09	1.07	**1.98**	1.43	1.12	0.45	0.010	multidrug resistance associated protein MRP2 [Triticum aestivum]	#NV	-0.03
HD03F03	-0.35	0.36	0.77	0.44	**1.67**	0.034	putative signal recognition particle receptor [Oryza sativa (japonica cultivar-	#NV	-0.08
HY02H04	**1.29**	1.14	0.28	0.78	-0.29	0.023	OSJNBa0043L09.29 [Oryza sativa (japonica cultivar-group)]	#NV	-0.15

HO01L08	0.02	0.19	1.20	2.43	**5.24**	0.013	putative protein kinase [Oryza sativa (japonica cultivar-group)]	#NV	-0.18
HY09A16	-0.04	0.56	0.53	0.60	**1.74**	0.020	putative flavonol glucosyltransferase [Oryza sativa (japonica cultivar-group)]	#NV	-0.20
HU04M15	-0.21	-0.05	0.88	0.58	**1.55**	0.043	C Chain C, Crystal Structure Of Prophytepsin, A Zymogen Of A Barley	#NV	-0.22
HY08P17	-0.18	-0.02	-0.02	0.44	**2.66**	0.050	putative nucleoid DNA-binding protein cnd41, chloroplast [Oryza sativa	#NV	-0.35
HD03P06	0.53	**1.58**	0.64	0.35	-0.29	0.036	methionine synthase [Hordeum vulgare subsp. vulgare]	#NV	-0.41
HU03B19	0.24	1.38	1.27	1.30	**2.13**	0.008	iron transport protein 2 [Oryza sativa], [Oryza sativa (japonica cultivar-	#NV	-0.49
HT02K05	0.15	-0.23	0.77	0.35	**2.82**	0.040	unknown protein [Oryza sativa (japonica cultivar-group)]	#NV	-0.54
HY03E06	-0.46	-0.23	0.02	1.06	**3.24**	0.049	lysine ketoglutarate reductase/saccharopine dehydrogenase [Zea mays]	#NV	-0.61
GCW004E	0.49	1.70	1.86	2.47	**2.80**	0.004	glutaredoxin [Triticum aestivum]	#NV	-0.72
HM03F14	-0.27	-0.59	-0.18	-0.20	**-1.37**	0.019	chaperonin [Secale cereale] RuBisCO subunit binding-protein beta subunit,	#NV	-0.77
HO04J10	1.34	**1.87**	1.21	0.45	1.36	0.008	glutathione transferase [Triticum aestivum] probable glutathione transferase	#NV	-0.89
HS01G09	0.03	0.05	0.76	0.50	**1.00**	0.038	ESTs AU031435(E61570),AU078245(E61570) correspond to a region of the	#NV	-0.90
HK05A13	0.90	0.77	0.40	**1.08**	1.05	0.010	Glutamine synthetase leaf isozyme, chloroplast precursor (Glutamate--	#NV	-1.16
HG01O22	-0.02	**-2.39**	-1.13	-1.25	-0.72	0.016	putative SecA [Oryza sativa (japonica cultivar-group)]	#NV	-1.21
HU03C23	-0.30	**-1.05**	-0.09	-0.29	0.07	0.036	zinc finger protein-like [Oryza sativa (japonica cultivar-group)] zinc finger	#NV	-1.21
HW02D01	0.46	0.26	0.20	0.08	**1.73**	0.040	subtilisin-like protease [Oryza sativa (japonica cultivar-group)] subtilisin-like	#NV	-1.32
HP01M16	-0.10	-0.79	-0.38	-0.37	**-1.09**	0.017	NdhC [Hordeum vulgare]	#NV	-1.46
HH01C22	0.79	0.83	0.25	**1.19**	0.98	0.010	putative anthranilate N-benzoyltransferase [Oryza sativa (japonica cultivar-	#NV	-1.85
HC14E01	-0.13	0.14	0.61	1.49	**3.58**	0.021	glutamine-dependent asparagine synthetase 1 [Hordeum vulgare subsp.	#NV	-1.94
HA06H07	-0.18	**-1.23**	-0.03	-0.69	-0.46	0.019	unknown [Arabidopsis thaliana]	#NV	-2.06
HE01E04	-0.06	**-1.13**	-0.36	-0.67	-0.44	0.018	hypothetical protein [Oryza sativa] hypothetical protein [Oryza sativa]	#NV	-2.31
HS01N11	0.43	1.38	1.17	**2.17**	0.87	0.011	catalase [Secale cereale]	#NV	-2.41
HH04O19	0.67	1.89	1.88	**1.92**	0.90	0.008	catalase [Secale cereale]	#NV	-2.48
HU02E18	0.97	1.65	**2.27**	1.75	1.04	0.005	catalase 2 [Hordeum vulgare]	#NV	-2.64
GCN003C	-0.39	**-1.52**	-0.11	-0.24	-0.80	0.027	OSJNBb0017I01.21 [Oryza sativa (japonica cultivar-group)]	#NV	-3.78
HO23A20	-0.10	**-1.60**	-0.16	-1.08	-0.42	0.027	unnamed protein product [Hordeum vulgare] Glutamine synthetase leaf	#NV	-3.92
HY09O01	-0.18	**-1.73**	-0.16	-0.36	-0.63	0.031	phosphoribulokinase; ribulose-5-phosphate kinase [Triticum aestivum]	#NV	-3.95
HO14N21	3.10	4.62	5.82	**7.05**	7.05	0.000	heat shock protein 70-1 [Nicotiana tabacum]	#NV	#NV
HO07E03	1.97	1.85	1.69	3.12	**5.39**	0.002	putative polyubiquitin [Arabidopsis thaliana]	#NV	#NV
HO06E17	2.24	2.41	1.23	1.04	**2.63**	0.003	PDR-like ABC transporter [Oryza sativa (japonica cultivar-group)]	#NV	#NV
HY01L11	0.23	-0.11	0.24	0.66	**3.89**	0.029	sucrose-sucrose-1-fructosyltransferase [Hordeum vulgare subsp. vulgare]	#NV	#NV
HD03I12	0.02	-0.66	-0.87	**-1.05**	0.26	0.029	putative transposase [Zea mays]	#NV	#NV
HO10A02	1.69	**2.65**	-0.22	-0.01	0.15	0.031	hypothetical protein [Oryza sativa (japonica cultivar-group)] hypothetical	#NV	#NV
HO07A10	0.81	**1.98**	0.32	0.00	-0.28	0.046	origin recognition complex subunit 2 [Oryza sativa (japonica cultivar-group)]	#NV	#NV
HO08B23	1.20	1.97	1.36	1.72	**5.97**	0.004	putative senescence-associated protein [Pisum sativum]	#NV	#NV
HK03E09	-0.12	**-1.06**	-0.24	-0.21	-0.37	0.026	P0506B12.13 [Oryza sativa (japonica cultivar-group)]	#NV	#NV
HA02G22	0.27	0.82	0.16	0.13	**2.59**	0.030	unknown [Arabidopsis thaliana]	#NV	#NV
HO13C10	0.07	0.17	0.48	1.12	**2.87**	0.019	putative AP2-related transcription factor [Oryza sativa]	#NV	#NV
HX03K07	-0.01	0.32	0.37	0.64	**1.59**	0.041	hypothetical protein [Oryza sativa (japonica cultivar-group)] hypothetical	#NV	#NV
HO08G13	0.06	**-1.20**	-0.25	-0.59	-0.26	0.034	GI homologue 1 [Lemna paucicostata]	#NV	#NV
HO03E08	0.06	0.57	0.41	1.20	**3.83**	0.019	Ascorbate peroxidase::OSJNBb0072N21.3 [Oryza sativa (japonica cultivar-	#NV	#NV
GCN002E	0.83	**1.74**	1.26	0.47	0.53	0.013	putative GTPase-activating protein :::: P0672D08.28 [Oryza sativa (japonica	#NV	#NV
HO05L23	0.39	0.85	0.54	2.20	**3.58**	0.011	hydroxyproline-rich glycoprotein-like [Oryza sativa (japonica cultivar-group)]	#NV	#NV
HO01H02	0.67	1.06	1.18	2.59	**4.33**	0.007	putative fatty acyl coA reductase [Oryza sativa (japonica cultivar-group)]	#NV	#NV

Figure 42: PageMAN: Expressions of regulated genes in all SuperBINs, BINs und sub-BINs. The ratio of regulation is averaged over all genes per hierarchical section and shown for all of the five time points upon infection. Upregulation is shown in red, downregulation in green; the values are in a log_2-transformed scale from 3 to -3 (8-fold up- or downregulated in infected vs. control samples).


mitochondrial electron transport / ATP synthesis
mitochondrial electron transport / ATP synthesis.NADH-DH.localis
mitochondrial electron transport / ATP synthesis.NADH-DH.type II.
mitochondrial electron transport / ATP synthesis.NADH-DH.type II.
mitochondrial electron transport / ATP synthesis.electron transfer f
mitochondrial electron transport / ATP synthesis.uncoupling prote
mitochondrial electron transport / ATP synthesis.F1-ATPase
cell wall.precursor synthesis
cell wall.precursor synthesis.UGE
cell wall.precursor synthesis.UGD
cell wall.cellulose synthesis
cell wall.pectin synthesis
cell wall.cell wall proteins
cell wall.cell wall proteins.HRGP
cell wall.degradation.pectate lyases and polygalacturonases
cell wall.modification
cell wall.pectin*esterases.acetyl esterase
lipid metabolism.FA synthesis and FA elongation
lipid metabolism.FA synthesis and FA elongation.acyl coa ligase
lipid metabolism.FA synthesis and FA elongation.beta ketoacyl Cc
lipid metabolism.FA synthesis and FA elongation.ACP protein
lipid metabolism.FA synthesis and FA elongation.ACP desaturase
lipid metabolism.FA synthesis and FA elongation.pyruvate DH
lipid metabolism.Phospholipid synthesis
lipid metabolism.lipid transfer proteins etc
lipid metabolism.'exotics' (steroids, squalene etc)
lipid metabolism.lipid degradation.lipases
lipid metabolism.lipid degradation.lysophospholipases
lipid metabolism.lipid degradation.beta-oxidation
lipid metabolism.lipid degradation.beta-oxidation.acyl CoA DH
lipid metabolism.lipid degradation.beta-oxidation
lipid metabolism.lipid degradation.beta-oxidation.mutifunctional
N-metabolism.ammonia metabolism.glutamate synthase
N-metabolism.ammonia metabolism.glutamine synthase
N-metabolism.ammonia metabolism.unspecified
N-metabolism.N-degradation.glutamate dehydrogenase
amino acid metabolism.synthesis.central amino acid metabolism.
amino acid metabolism.central amino acid metabolism.aspartate
amino acid metabolism.synthesis.glutamate family.proline
amino acid metabolism.synthesis.glutamate family.arginine
amino acid metabolism.aspartate family.asparagine.synthesis
amino acid metabolism.synthesis.aspartate family.threonine
amino acid metabolism.synthesis.aspartate family.methionine
amino acid metabolism.aspartate family.misc.homoserine.synthes
amino acid metabolism.synthesis.aspartate family.misc.homoserin
amino acid metabolism.aspartate family.misc.homocysteine.synth
amino acid metabolism.synthesis.serine-glycine-cysteine group.se
amino acid metabolism.synthesis.serine-glycine-cysteine group.gl
amino acid metabolism.synthesis.serine-glycine-cysteine group.cy
amino acid metabolism.synthesis.aromatic aa.tryptophan
amino acid metabolism.degradation.aspartate family.asparagine
amino acid metabolism.degradation.aspartate family.methionine
amino acid metabolism.degradation.branched-chain group.leucir
amino acid metabolism.degradation.branched chain group.isoleu
amino acid metabolism.degradation.serine-glycine-cysteine group
amino acid metabolism.degradation.serine-glycine-cysteine group
metal handling
metal handling.binding, chelation and storage
secondary metabolism.isoprenoids
secondary metabolism.isoprenoids.non-mevalonate pathway
secondary metabolism.isoprenoids.mevalonate pathway
secondary metabolism.phenylpropanoids
secondary metabolism.phenylpropanoids.lignin biosynthesis
secondary metabolism.phenylpropanoids.lignin biosynthesis.PAL
secondary metabolism.phenylpropanoids.lignin biosynthesis.C4H
secondary metabolism.phenylpropanoids.lignin biosynthesis.4CL
secondary metabolism.phenylpropanoids.lignin biosynthesis.HCT
secondary metabolism.phenylpropanoids.lignin biosynthesis.CCoA
secondary metabolism.phenylpropanoids.lignin biosynthesis.CCR1
secondary metabolism.phenylpropanoids.lignin biosynthesis.CAD
secondary metabolism.N misc.alkaloid-like
secondary metabolism.wax
secondary metabolism.flavonoids.chalcones
secondary metabolism.flavonoids.dihydroflavonols
secondary metabolism.simple phenols
secondary metabolism.unspecified
metal handling
hormone metabolism


Co-factor and vitamine metabolism
tetrapyrrole synthesis
stress
polyamine metabolism
Biodegradation of Xenobiotics
C1-metabolism
hormone metabolism.
hormone metabolism.abscisic acid.synthesis-degradation
hormone metabolism.abscisic acid.synthesis-degradation.synthesi
hormone metabolism.abscisic acid.induced-regulated-responsive-
hormone metabolism.auxin.signal transduction
hormone metabolism.auxin.induced-regulated-responsive-activate
hormone metabolism.brassinosteroid.synthesis-degradation
hormone metabolism.brassinosteroid.synthesis-degradation.BRs
hormone metabolism.brassinosteroid.synthesis-degradation.BRs.DE
hormone metabolism.brassinosteroid.synthesis-degradation.sterols.
hormone metabolism.brassinosteroid.synthesis-degradation.sterols.
hormone metabolism.cytokinin.synthesis-degradation
hormone metabolism.cytokinin.signal transduction
hormone metabolism.ethylene.synthesis-degradation
hormone metabolism.ethylene.signal transduction
hormone metabolism.ethylene.induced-regulated-responsive-activ
hormone metabolism.gibberelin.signal transduction
hormone metabolism.jasmonate
hormone metabolism.jasmonate.synthesis-degradation
hormone metabolism.jasmonate.synthesis-degradation.12-Oxo-PD
hormone metabolism.jasmonate.induced-regulated-responsive-ac
Co-factor and vitamine metabolism
tetrapyrrole synthesis
tetrapyrrole synthesis.magnesium chelatase
tetrapyrrole synthesis.chlorophyll synthase
tetrapyrrole synthesis.chlorophyll synthase
stress
stress.biotic
stress.abiotic
stress.abiotic.heat
stress.abiotic.cold
stress.abiotic.drought/salt
stress.abiotic.unspecified
redox.thioredoxin
redox.ascorbate and glutathione
redox.ascorbate and glutathione.ascorbate
redox.ascorbate and glutathione.glutathione
redox.glutaredoxins
redox.peniredoxins
redox.dismutases and catalases
polyamine metabolism
nucleotide metabolism.synthesis.pyrimidine.CTP synthetase
nucleotide metabolism.synthesis.purine.amidophosphoribosyltrans
nucleotide metabolism.synthesis.purine.IMP dehydrogenase
nucleotide metabolism.synthesis.purine.GMP synthetase
nucleotide metabolism.degradation
nucleotide metabolism.salvage
nucleotide metabolism.salvage.phosphoribosyltransferases.aprt
nucleotide metabolism.phosphotransfer and pyrophosphatases
nucleotide metabolism.phosphotransfer and pyrophosphatases.ad
nucleotide metabolism.phosphotransfer and pyrophosphatases.mis
nucleotide metabolism.deoxynucleotide metabolism
Biodegradation of Xenobiotics
C1-metabolism
misc.misc2
misc.UDP glucosyl and glucoronyl transferases
misc.gluco-, galacto- and mannosidases
misc.beta 1,3 glucan hydrolases
misc.acyl transferases
misc.O- methyl transferases
misc.oxidases - copper, flavone etc.
misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline
misc.glutathione S transferases
misc.cytochrome P450
misc.alcohol dehydrogenases
misc.alcohol dehydrogenases
misc.peroxidases
misc.acid and other phosphatases
misc.myrosinases-lectin-jacalin
misc.protease inhibitor/seed storage/lipid transfer protein (LTP) far
misc.protease inhibitor/seed storage/lipid transfer protein (LTP) far
misc.short chain dehydrogenase/reductase (SDR)
misc.GDSL-motif lipase
misc. other Ferredoxins and Rieske domain
RNA.processing
RNA.processing.splicing
RNA.processing.RNA helicase
RNA.transcription
RNA.regulation of transcription
RNA.regulation of transcription.ABI3/VP1-related B3-domain-cont
RNA.regulation of transcription.Alfin-like
RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene
RNA.regulation of transcription.ARF, Auxin Response Factor famil
RNA.regulation of transcription.ARR
RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix famil
RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zir
RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family
RNA.regulation of transcription.C2C2(Zn) GATA transcription factc
RNA.regulation of transcription.C2C2(Zn) YABBY family
RNA.regulation of transcription.C2H2 zinc finger family
RNA.regulation of transcription.C3H zinc finger family
RNA.regulation of transcription.CCAAT box binding factor family,
RNA.regulation of transcription.EIN3-like(EIL) transcription factor f
RNA.regulation of transcription.GRAS transcription factor family


RNA.regulation of transcription.HB,Homeobox transcription factor
RNA.regulation of transcription.HSF,Heat-shock transcription facto
RNA.regulation of transcription.MADS box transcription factor fam
RNA.regulation of transcription.MYB domain transcription factor fa
RNA.regulation of transcription.MYB-related transcription factor fa
RNA.regulation of transcription.NAC domain transcription factor fa
RNA.regulation of transcription.WRKY domain transcription factor
RNA.regulation of transcription.TUB transcription factor family
RNA.regulation of transcription.bZIP transcription factor family
RNA.regulation of transcription.Argonaute
RNA.regulation of transcription.Aux/IAA family
RNA.regulation of transcription.Chromatin Remodeling Factors
RNA.regulation of transcription.DNA methyltransferases
RNA.regulation of transcription.GeBP like
RNA.regulation of transcription.Global transcription factor group
RNA.regulation of transcription.High mobility group (HMG) family
RNA.regulation of transcription.HDA
RNA.regulation of transcription.LUG
RNA.regulation of transcription.Methyl binding domain proteins
RNA.regulation of transcription.Nucleosome/chromatin assembly f
RNA.regulation of transcription.Polycomb Group (PcG)
RNA.regulation of transcription.putative DNA-binding protein
RNA.regulation of transcription.SNF7
RNA.regulation of transcription.unclassified
RNA.RNA binding
DNA.synthesis/chromatin structure
DNA.synthesis/chromatin structure.histone
DNA.unspecified
protein.aa activation
protein.synthesis.chloroplast/mito - plastid ribosomal protein
protein.synthesis.chloroplast/mito - plastid ribosomal protein.plasti
protein.synthesis.chloroplast/mito - plastid ribosomal protein.unkno
protein.synthesis.misc ribososomal protein
protein.synthesis.initiation
protein.synthesis.elongation
protein.targeting
protein.targeting.nucleus
protein.targeting.mitochondria
protein.targeting.secretory pathway.vacuole
protein.targeting.secretory pathway.unspecified
protein.postranslational modification
protein.postranslational modification.kinase.receptor like cytoplas
protein.postranslational modification.kinase.receptor like cytoplas
protein.postranslational modification.kinase.receptor like cytoplas
protein.degradation
protein.degradation.subtilases
protein.degradation.cysteine protease
protein.degradation.aspartate protease
protein.degradation.serine protease
protein.degradation.metalloprotease
protein.degradation.AAA type
protein.degradation.ubiquitin
protein.degradation.ubiquitin.E2
protein.degradation.ubiquitin.E3.RING
protein.degradation.ubiquitin.E3.SCF.FBOX
protein.degradation.ubiquitin.ubiquitin protease
protein.degradation.ubiquitin.proteasom
protein.folding
signalling.in sugar and nutrient physiology
signalling.receptor kinases.leucine rich repeat II
signalling.receptor kinases.leucine rich repeat V
signalling.receptor kinases.leucine rich repeat IX
signalling.receptor kinases.leucine rich repeat XI
signalling.receptor kinases.DUF 26
signalling.receptor kinases.legume-lectin
signalling.receptor kinases.S-locus glycoprotein like
signalling.receptor kinases.misc
signalling.calcium
signalling.phosphinositides
signalling.G-proteins
signalling.MAP kinases
signalling.14-3-3 proteins
signalling.light
cell.organisation
cell.cycle
cell. vesicle transport
development.storage proteins
development.inhibitor proteins
development.unspecified
transport.p- and v-ATPases
transporter.sugars
transport.amino acids
transport.phosphate
transport.metabolite transporters at the mitochondrial membrane
transport.peptides and oligopeptides
transport.potassium
transport.ABC transporters and multidrug resistance systems
transport.Major Intrinsic Proteins.PIP
transport.Major Intrinsic Proteins.TIP
transport.calcium
transport.misc
not assigned.no ontology
not assigned.no ontology.hydroxyproline rich proteins
not assigned.unknown

Table 20: Tissue-specific expression of regulated and present genes, separate into SuperBIN. E/M: epidermis-to-mesophyll ratio, mean for all (regulated/present) genes; Epidermal: number of genes with E/M>=1; Mesophyll: number of genes with E/M<=-1 in a certain SuperBIN. “Present” and “regulated” according to if present or regulated in response to *Bgh* in the epidermal samples.

Super-BIN	Biological classification	E/M present	E/M regulated	Epidermal present	Epidermal regulated	Mesophyllic present	Mecophyllic regulated
No. 1	Photosynthesis	-1.25	-1,90	1	0	107	71
No. 2	Major CHO	0.13	0,38	4	3	13	3
No. 3	Minor CHO	0.90	1,64	14	9	7	3
No. 4	Glycolysis	0.01	-0,47	3	0	4	3
No. 5	Fermentation	0,5	-0,79	2	0	0	0
No. 6	Gluconeogenesis	-0,18	-0,31	2	0	0	1
No. 7	OPP	0,40	1,00	6	2	5	1
No. 8	TCA/org. transformation	0,16	-0,85	7	0	8	6
No. 9	mitochondrial electron transport / ATP synthesis	0,13	0,00	2	0	2	1
No. 10	cell wall	0,38	0,73	9	3	6	2
No. 11	lipid metabolism	0,64	1,26	31	12	12	3
No. 12	N-metabolism	-0,06	0,40	2	1	5	1
No. 13	amino acid metabolism	-0,03	-0,77	6	0	41	26
No. 14	S-assimilation	-0,84	---	3	0	0	0
No. 15	metal handling	0,83	1,84	6	4	2	1
No. 16	secondary metabolism	0,41	0,76	16	12	13	2
No. 17	hormone metabolism	0,46	0,85	19	10	14	2
No. 18	Co-factor and vit. Metab.	-0,99	-1,64	6	0	0	3
No. 19	tetrapyrrole synthesis	-0,72	-1,02	10	0	0	4
No. 20	Stress	0,67	1,14	38	19	20	9
No. 21	redox	0,01	-0,07	3	1	20	10
No. 22	polyamine metabolism	0,06	---	1	0	1	0
No. 23	nucleotide metabolism	0,19	-0,39	4	0	8	3
No. 24	Biodegradation of Xenobiotics	0,09	-0,09	1	0	1	1
No. 25	C1-metabolism	0,18	0,89	1	0	1	0
No. 26	miscellaneous	0,61	0,87	59	26	27	8
No. 27	RNA	0,30	0,46	59	18	37	14
No. 28	DNA	0,49	0,49	25	4	7	3
No. 29	Protein	0,25	0,50	98	27	91	16
No. 30	signalling	0,55	0,71	55	13	10	2
No. 31	cell	0,31	0,09	15	2	11	4
No. 33	development	0,52	0,40	12	3	12	3
No. 34	transport	0,44	0,80	39	17	14	2
No. 35	Not assigned	0,32	0,67	205	66	184	37
„No bin“	Not linked	0,44	0,55	53	13	37	15
„Un-known“	Not of plant origin	0,52	0,82	141	62	65	20

Table 21: Correlation of technical replicates sample separated on DIGE gels with dye-swap. Control: non-infected samples; Infected: samples infected with *Bgh*. 1, 2, 3 are the number of the biological replicates (harvests). The upper row shows the time points after inoculation.

	12h	24h	48h	72h	120h
Control 1	0.775	0.840	0.888	0.783	----
Control 2	0.716	0.826	0.790	0.839	0.858
Control 3	0.761	0.784	0.660	0.794	0.603
Infected 1	0.818	0.750	0.886	0.826	----
Infected 2	0.648	0.794	0.796	0.833	0.927
Infected 3	0.729	0.728	0.840	0.752	0.894

Table 22: Correlation of biological replicates of the DIGE gel. Control: non-infected samples; Infected: samples infected with *Bgh*. 1, 2, 3 are the number of the biological replicates (harvests). The upper row shows the time points after inoculation.

	12h	24h	48h	72h	120h
Control 1-2	0.748	0.601	0.408	0.787	----
Control 3-1	0.736	0.570	0.574	0.740	----
Control 2-3	0.672	0.639	0.725	0.828	0.748
Infected 1-2	0.636	0.670	0.816	0.819	----
Infected 3-1	0.711	0.577	0.767	0.633	----
Infected 2-3	0.670	0.598	0.725	0.786	0.803

Table 23: Proteins of barley epidermis identified via MALDI-TOF-MS using the HarvEST:Barley database v.1.74 (http://harvest.ucr.edu/). Spot numbers based on the numbering in the analysis of DIGE gels, resulting HarvEST:Barley-ID, numbers of peptides leading to the identification and the score for the identification. Mass and pI calculated using the “Compute pI/Mw tool“ (http://www.expasy.org/tools/pi_tool.html).

Spot	**HarvEST-ID**	**Score**	**Peptides**	**Mw (kDa)**	**p*I***
2	35_2434	78	8	15.8	4.87
9	35_4982	84	8	96.5	7.71
16	35_4712	83	6	33.1	7.19
62	35_17794	70	8	52.1	6.40
69	35_15462	126	10	27.6	6.64
70	35_5689	70	7	32.1	4.95
92	35_25207	68	5	61.6	5.02
98	35_15429	67	9	68.9	7.07
103	35_99	100	10	36.5	6.67
106	35_259	74	10	111.4	6.48
110	35_38367	69	5	17.6	4.38
114	35_14519	177	18	69.9	5.87
116	35_49	131	13	36.9	7.15
117	35_15726	223	21	45.8	8.09
118	35_15021	122	13	60.6	5.29
119	35_2185	73	7	55.7	9.36
124	35_14630	36	4	32.8	9.00
139	35_1124	72	6	52.2	7.71
151	35_50935	62	7	24.7	6.02
161	35_453	85	10	71.4	5.03
162	35_13900	117	11	47.5	5.92
165	35_14654	85	9	39.3	7.71
168	35_784	96	10	62.7	6.16
170	35_16286	75	12	21.6	6.30
171	35_16117	96	10	53	7.98
177	35_15726	210	19	45.8	8.09

184	35_19417	79	10	51.6	6.04
185	35_14519	118	12	69.9	5.87
187	35_368	92	9	42.8	5.49
190	35_4628	78	7	51.2	4.90
196	35_15143	78	9	47.8	8.35
204	35_28067	84	11	97	6.20
216	35_15495	123	12	64.9	6.03
226	35_14444	186	22	48.2	5.71
229	35_14174	93	10	41.7	5.16
231	35_10955	76	7	48.9	7.22
233	35_23963	97	8	76.2	9.22
237	35_19575	68	5	25.2	9.89
239	35_14172	115	14	41.7	5.06
242	35_960	77	9	64.6	6.99
251	35_11352	90	6	24.7	4.90
259	35_15178	88	10	68.5	4.96
261	35_14172	66	5	41.7	5.06
263	35_12756	76	6	99.5	5.60
267	35_15245	83	9	67.4	7.96
270	35_14470	115	11	73.4	5.09
274	35_861	107	8	23.3	5.88
277	35_49	132	11	36.9	7.15
280	35_15968	73	7	30.1	7.27
286	35_18209	112	9	78.7	6.29
287	35_1092	68	6	53.6	5.31
305	35_1200	81	10	53.9	7.51
306	35_3277	113	10	61.3	5.42
317	35_14510	82	9	27.1	5.01
320	35_21531	82	9	45.9	7.59
322	35_5591	68	8	69	7.79
335	35_25069	69	8	74.3	5.09
340	35_366	134	15	43.3	5.94
344	35_15178	81	19	68.5	4.96
349	35_14099	78	9	38.9	7.39
367	35_1354	109	12	35.6	6.69
374	35_19141	70	6	28.8	7.76
380	35_4322	79	7	62.3	5.25
387	35_360	95	13	63.8	6.21
390	35_5860	79	12	90.9	5.76
398	35_99	101	10	36.5	6.67
400	35_16401	70	5	191.4	6.56
402	35_16117	119	13	53	7.98
404	35_41618	81	6	21.6	6.30
407	35_15021	114	12	60.6	5.29
410	35_16233	82	7	40.5	7.64
413	35_693	87	11	139.4	5.66
419	35_1530	71	8	58.8	5.09
421	35_15997	70	7	30.5	5.69
422	35_4446	75	8	77	6.37
423	35_48714	77	6	45.3	7.07
435	35_14519	195	19	69.9	5.87
444	35_14172	122	17	41.7	5.06
447	35_429	159	15	44.4	8.55
448	35_784	71	7	62.7	6.16
451	35_14632	170	15	26.6	7.42

453	35_15785	90	9	39.3	6.43
456	35_17334	92	8	66.3	6.91
463	35_16425	86	9	38	9.97
464	35_14174	105	11	41.7	5.16
476	35_14099	101	10	38.9	7.39
482	35_16286	77	9	21.6	6.30
485	35_4140	94	12	35.6	6.54
489	35_976	148	14	50.4	6.19
495	35_960	128	14	64.6	6.99
511	35_1801	139	17	82	5.59
519	35_15429	77	9	68.9	7.07
522	35_2078	79	7	55.4	7.43
525	35_15073	182	23	107.6	6.93
526	35_9359	70	8	25	9.41
533	35_2726	77	9	47.6	7.67
536	35_14100	95	10	38.4	7.46
537	35_2125	72	9	80.5	5.95
545	35_15021	142	15	60.6	5.29
546	35_8676	66	6	48.9	8.87
549	35_14539	72	9	58.5	6.65
556	35_18209	93	10	78.7	6.29
564	35_15567	85	9	46.1	5.87
575	35_1864	148	13	49.8	5.88
586	35_22900	75	5	27.8	7.63
589	35_17129	82	12	53	8.95
590	35_13769	83	9	42	6.39
593	35_13856	125	10	31.4	4.93
606	35_802	113	12	53.6	7.49
610	35_1801	135	17	82	5.59
612	35_1190	33	3	25	7.04
619	35_14632	149	15	26.6	7.42
625	35_1714	117	13	53.4	7.85
626	35_9734	98	8	77.5	8.97
633	35_15178	104	13	68.5	4.96
638	35_14635	97	8	27.3	8.84
653	35_15073	72	9	107.6	6.93
657	35_14444	138	15	48.2	5.71
659	35_14505	91	9	27	5.15
668	35_15785	96	9	39.3	6.43
671	35_14602	177	16	53.7	8.02
677	35_14091	85	8	23.4	5.78
680	35_14451	211	24	48.2	5.71
683	35_22985	74	6	39.2	8.80
694	35_32881	95	6	n/a	n/a
830	35_15780	78	11	87.8	7.43
934	35_12150	83	9	71.6	8.78
976	35_47029	93	6	79.3	6.08

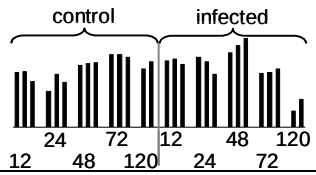
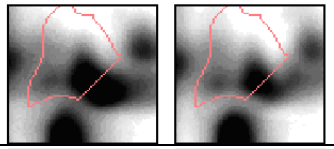
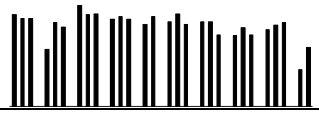
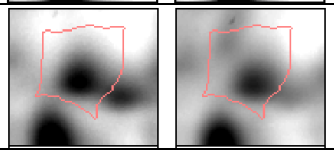
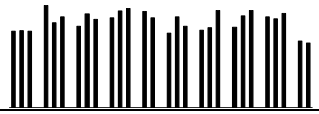
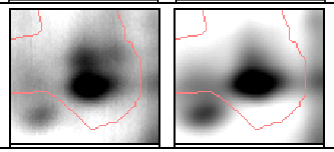
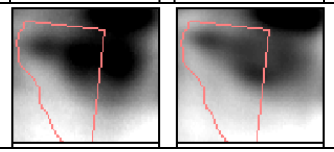
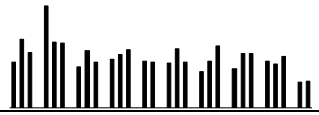
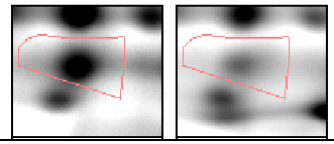
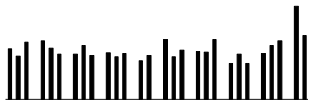
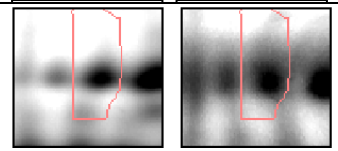
Table 24: Proteins of barley epidermis identified via LC-based mass spectrometry using the HarvEST:Barley database v.1.74 (http://harvest.ucr.edu/). Spot numbers based on the numbering in the analysis of DIGE gels, resulting HarvEST:Barley-ID, peptide sequence(s) and modification and the score for the identification. Mass and pI were calculated using the "Compute pI/Mw tool" (http://www.expasy.org/tools/pi_tool.html).

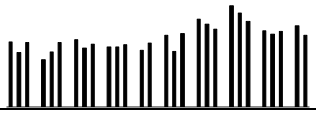
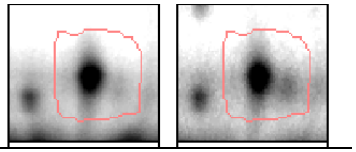
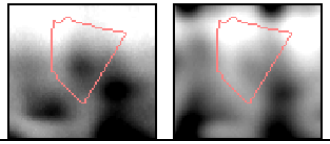
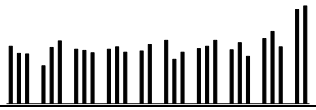
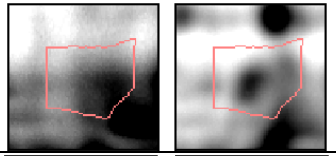
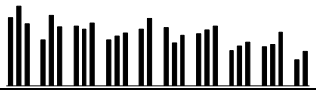
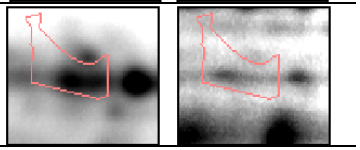
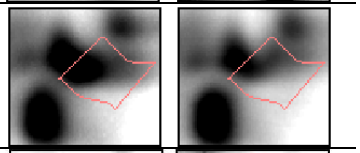
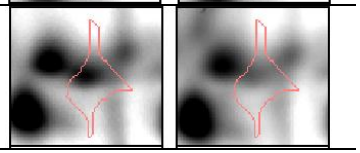
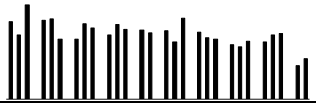
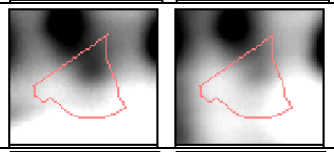
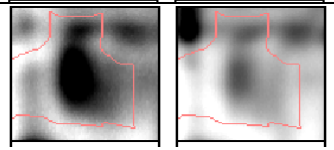
Spot	HarvEST-ID	Peptides	Score	Mw (kDa)	p*I*
3	35_704	G)GVFITCNYEPR(G) Carbamidomethyl C (6)	10.838	17.6	9.00
10	35_702	(A)LQAYAQSYANQR(A) (A)ASTSIGCAR(A) Carbamidomethyl C (7)	9.941	17.7	9.08
27	35_16041	(A)LDGLSSTASSVAGK(C)	10.838	35.8	6.11
69	35_15462	(C)LYQVEYAFK(G) (G)SAGVTSIGVR(C) (C)YTGLLATGLTADAR(C) (A)EQEAINFLEK(T) (A)ATEIEVGVVR(C)	10.838	27.6	6.64
98	35_15429	(T)STNTILATGGYGR(G)	8.647	68.9	7.07
103	35_99	(C)IGINGFGR(C) (A)VALQSDDVELVAVNDPFITTEYMTYMFK(C) Oxidation M (23), Oxidation M (26) (A)TLLFGEKPVTVFGVR(T) (A)NPEEIPWGEAGADYVVESTGVFTDK(G) (G)VIISAPSK(C) (T)DAPMFVVGVNEDK(G) (T)DAPMFVVGVNEDK(G) Oxidation M (4) (A)AASFNIIPSSTGAAK(A) (G)VLPELNGK(A) (G)VPTVDVSVVDLTVR(A) (G)AASYDDIKK(C) (T)GIMGYVEEDLVSTDFVGDSR(C) (T)GIMGYVEEDLVSTDFVGDSR(C) Oxidation M (3) (C)AGIALNDHFVK(T)	10.792	36.5	6.67
117	35_15726	(C)ETADALINTGLAK(C) (G)YVNIDDCWAELNR(C) Carbamidomethyl C (7) (G)ALADYVHGK(A) (G)LGIYSDAGTQTCSNK(C) Carbamidomethyl C (12) (G)TFASWGIDYLK(T) (C)YDNCNDAGR(G) Carbamidomethyl C (4) (T)TTGDIADNWGSMTSR(A) Oxidation M (12) (G)APLLIGCDVR(A) Carbamidomethyl C (7) (C)TIISNQEVIAVNQDR(A) (A)AVVLWNR(T)	10.838	45.8	8.09
123	35_14824	(G)AAVTPAFVGQFPGVNGLGISAAR(C) (G)VTFLDDAQVK(C)	10.838	21.8	5.68
124	35_14630	(C)SNIQAYPK(A)	10.271	32.8	9.00
139	35_1124	(T)SVMEETGSNITTDQLK(A) Oxidation M (3)	10.838	52.2	7.71
164	35_14824	(G)AAVTPAFVGQFPGVNGLGISAAR(C) (G)VTFLDDAQVK(C)	10.838	21.8	5.68
174	35_3542	(G)DDIGAAVR(G) (A)ELSVVGGTGQFR(T) (C)MATGYVLWK(C) Oxidation M (1)	10.838	17.5	5.49
178	35_728	(C)DVDLSTYK(C) (C)AEYPIFDK(T) (T)VDVNGDNVAPVYK(G) (G)GSLFGDNIK(C) (T)YAPTTSPLSIEK(G)	10.838	25.7	8.99
195	35_14824	(G)AAVTPAFVGQFPGVNGLGISAAR(C) (G)VTFLDDAQVK(C) (G)VTFLDDAQVKK(T)	10.838	21.8	5.68

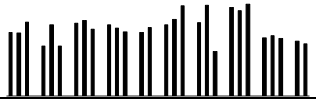
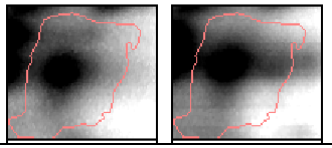
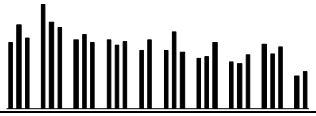
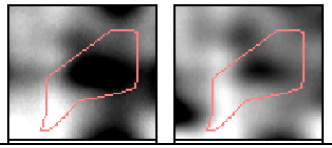
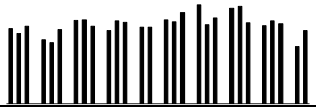
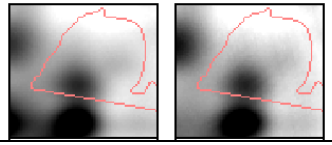
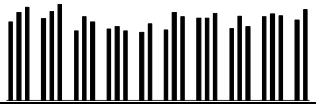
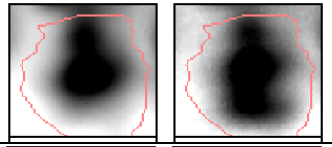
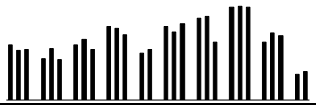
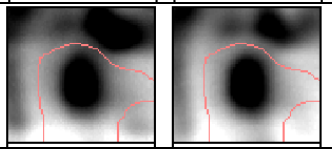
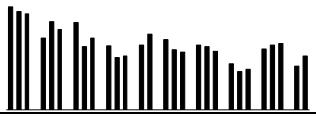
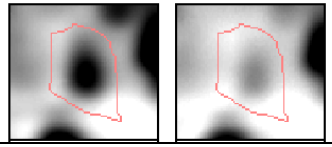
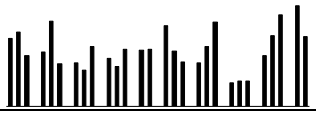
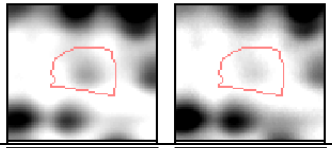
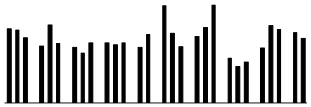
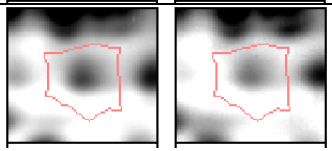
206	35_14824	(G)AAVTPAFVGQFPGVNGLGISAAR(C) (G)VTFLDDAQVK(C)	10.838	21.8	5.68
208	35_14981	(C)KAAAAEFLK(A) (A)AAAAEFLK(A) (C)VVETIEASPPEIK(A) (A)FLDEMAK(C) Oxidation M (5) (G)SGTTPLSPAIVFILDK(C) (T)VAPFVPAPK(T) (T)VAPFVPAPKEEPK(A) (A)EEPKAEPEAAAAAPAEETTTR(C) (C)AEPEAAAAAPAEETTTR(C) (C)EVAVEEEK(T) (C)EVAVEEEKK(G) (T)KEEAEPSAAPAEAAAPAEVAAPAEVVEEK(A) (T)EEAEPSAAPAEAAAPAEVAAPAEVVEEK(A)	10.800	21.8	4.92
214	35_48123	(T)VTFLDDAQVK(T) (T)VTFLDDAQVKK(T)	10.837	21.8	6.50
217	35_14505	(A)SLLGESSEFVGEK(T) (A)VAYALAQGLK(G) (C)VIACVGETLEQR(G) Carbamidomethyl C (4) (G)EAGSTMEVVAEQTK(T) Oxidation M (6) (C)VATPAQAQEVHANLR(T) (T)TNVSPEVAESTR(C)	10.838	27.0	5.15
227	35_14981	(C)VVETIEASPPEIK(A) (C)AEPEAAAAAPAEETTTR(C) (C)EVAVEEEK(T)	10.838	21.8	4.92
245	35_259	(C)ITCADANAIAEEAR(T)Carbamidomethyl C (3)(G)FCDALISIR(T)Carbamidomethyl C (2)	10.838	111.4	6.48
274	35_861	C)AAVGHPDTLGDCPFSQR(T) Carbamidomethyl C (12) (C)VLLTLEEK(C) (C)VPVFNGGDGK(G) (C)WIADSDVITQVIEEK(G) (G)YPTPSLVTPPEYASVGSK(G) (A)ENLIAGWAPK(A)	10.377	23.3	5.88
296	35_259	(A)GVDTVVLGVEK(A) (G)LTVEDPVTVEYITR(T) (A)ALLEVVESGGK(C) (G)QLEEDEIDEYVAEIETEK(A)	10.838	111.4	6.48
310	35_1022	(T)LTVNFVLPYK(C) (C)GLAEFTAK(T) (A)LGSASTDLK(A) (A)LGSASTDLKK(G)	10.814	21.2	5.72
312	35_14382	(T)YEEMVEFMEK(G) Oxidation M (4) Oxidation M (8) (G)TADVGELTVEER(C) (T)GNEAYVASIK(A) (T)LLDSHLVPSATAAESK(A) (G)EAAENTLVAYK(G)	10.838	29.4	4.83
316	35_14824	(G)AAVTPAFVGQFPGVNGLGISAAR(C) (G)VTFLDDAQVK(C) (G)VTFLDDAQVKK(T)	10.838	21.8	5.68
318	35_739	(A)NVLAVYEAR(G)	10.838	23.4	5.96
363	35_43946	(T)VLLTLEEK(A) (T)VPVFNGGDGK(G) (C)WIADSDVITQVIEEK(A) (C)YPTPSLVTPPEYASVGSK(T)	10.831	23.4	5.88
377	35_17049	(C)TPEFLGLDR(T)	10.800	78.5	6.19
378	35_3176	(A)TTIFSPEGR(C) (G)AAAVGANSQAAQSMLK(G) Oxidation M (14) (C)EEAVALALK(G) (A)TMDSTSLTADK(T) Oxidation M (2)	10.838	27.0	6.44
385	35_14477	(T)VVEVSTSK(C) (T)LPTDDVLLGQIK(C)	10.838	17.4	5.70
397	35_15925	(A)AAENVYIK(C)	10.838	12.9	9.56
402	35_16117	(T)SLQNFDIGGER(T) (G)VNMEYGLDPTIGK(C)	10.838	53.0	7.98

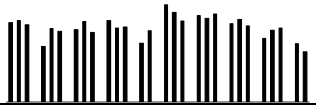
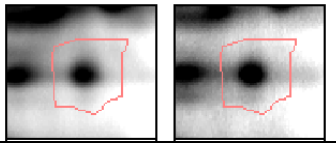
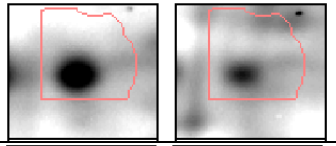
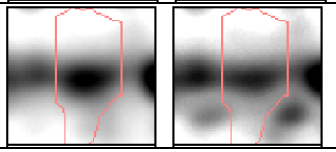
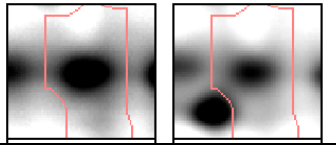
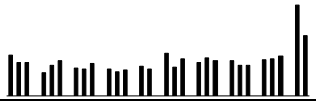
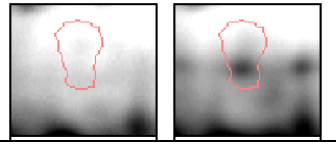
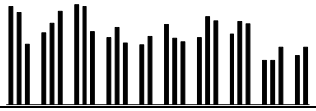
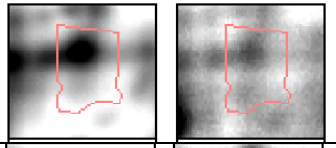
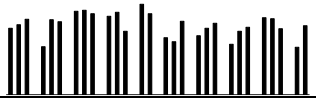
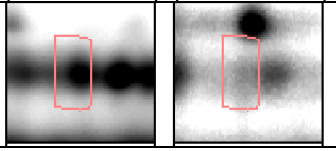
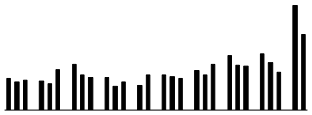
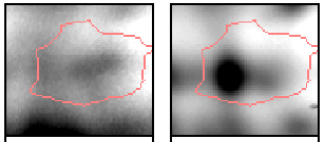
		Oxidation M (3)			
412	35_41150	(C)NPMDANADDFFK(C) Oxidation M (3) (T)AAALDKPR(T)	10.812	24.7	6.02
415	35_15350	(C)FSFDPSTK(C) (G)LASSYPNFK(C) (G)DLGYTSQMVYK(A) Oxidation M (8)	10.838	27.1	7.72
454	35_15770	(T)AFFDATGGLWR(A) (A)AGIVPVSYR(C)	10.185	21.6	6.30
488	35_13856	(T)IVGDLVAETFR(A) (A)DVGVAPALIR(G) (C)YYFDLIVR(T) (A)SDQALIDHPDTR(G) (A)QNCAVPNR(C)	10.838	31.4	4.93
567	35_38507	(C)ENAPAIIFIDEVDAIATAR(C)	8.900	45.8	5.42
592	35_40361	(A)TAFPNVDSVR(T) (T)GYEVIDEIK(G) (T)GYEVIDEIKK(A)	10.838	42.7	8.51
612	35_1190	(C)ALEQLDAAVGK(G) (A)YAGEEYEK©	10.838	25.0	7.04
614	35_14510	(G)TGGPFGTMK(C) Oxidation M (8) (T)EGLLQLPTDK(C) (C)VLLTDPAFRPLVDK(T)	10.838	27.1	5.01
643	35_14148	(C)LDPGQSWQLNMPAGTAGAR(T) Oxidation M (11) (T)TGCTFDR(G) Carbamidomethyl C (3) (T)VSGEQPATLAEYTLGQGGNR(G) (C)CPDAYSYAK(G) Carbamidomethyl C (1)	10.838	24.9	6.04
692	35_14505	(A)SLLGESSEFVGEK(T) (A)VAYALAQGLK(G) (C)VIACVGETLEQR(G) Carbamidomethyl C (4) (G)EAGSTMEVVAEQTK(T) Oxidation M (6) (C)VATPAQAQEVHANLR(T) (T)TNVSPEVAESTR(C)	10.838	27.0	5.15
695	35_14420	(G)MELVDAAFPLLK(C) (G)MELVDAAFPLLK(C) Oxidation M (1) (T)SQASALEAHAAPNCK(A) Carbamidomethyl C (14) (G)VLVVANPANTNALILK(T) (A)EFAPSIPEK(C) (G)ALGQISER(C) (G)LNVQVSDVK(G) (A)LSSALSAASSACDHIR(G) Carbamidomethyl C (12) (T)MDATAQELSEEK(T) (T)MDATAQELSEEK(T) Oxidation M (1)	10.800	35.7	6.78
951	35_524	(A)AGPTGLAADTR(C) (C)TLTNVGAAGTYK(C)	10.838	80.0	5.88
971	35_15109	(A)GVDTVVLGVEK(A) (G)LTVEDPVTVEYITR(T) (A)ALLEVVESGGK(C) (G)QLEEDEIDEYVAEIETEK(A)	10.838	27.3	6.93

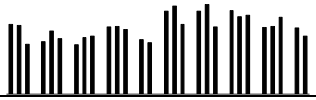
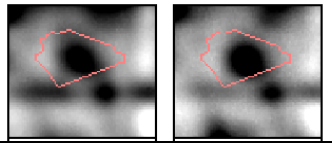
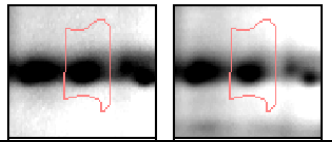
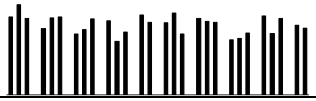
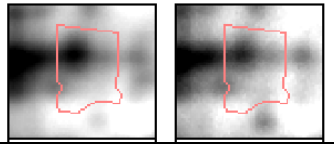
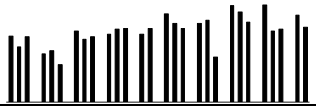
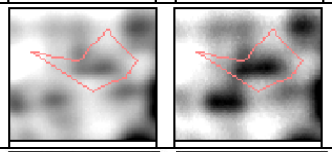
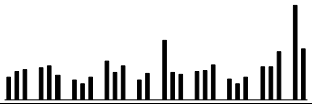
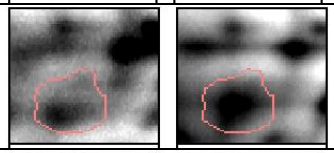
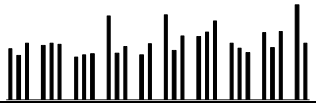
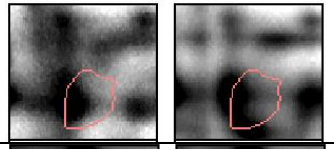
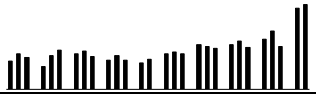
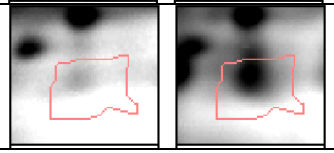
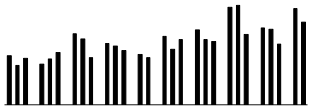
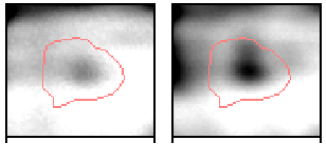
Table 25: List of all identified protein spots, arranged according to their biological function. First the spotnumber in the analysis, than the function and the biological function. The spot intensities are shown for all biological replicates in the study, ordered by their time after inoculation and whether from control or infected samples (see shown at the first spot). The regulation value is shown for the time point with the maximum after log_2-transformation, regulation of 1.8-fold is bolt. The spots pictures are from analytical DIGE gel, of the time point at which the highest regulation was shown.

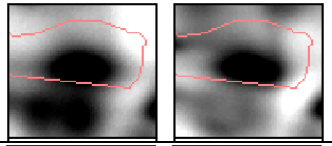
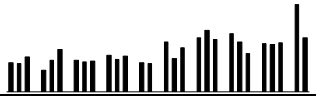
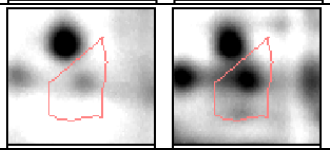
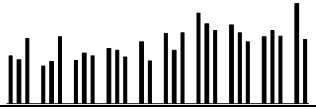
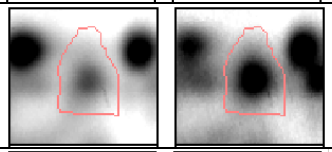
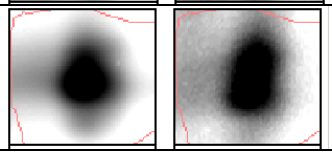
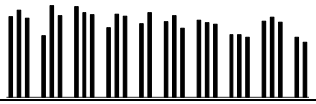
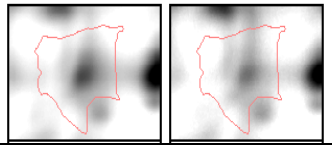
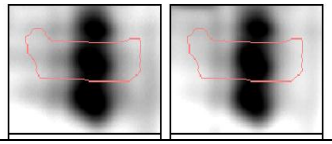
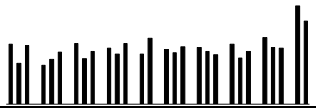
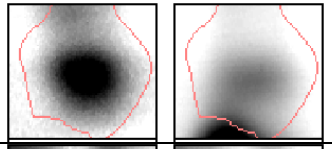
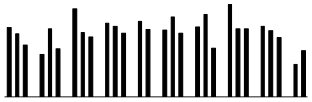
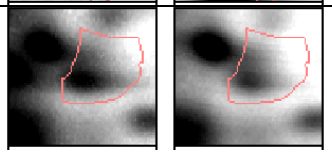
Spot	HarvEST-ID	Putative function	Functional group	Spot intensities	Regulation Infected / control	q-value	Spot picture
103	35_99	glyceraldehyde-3-phosphate dehydrogenase	PS.lightreaction.photosystem II.LHC-II		**-1.49 (120h)**	0.3396	
398	35_99	glyceraldehyde-3-phosphate dehydrogenase	PS.lightreaction.photosystem II.LHC-II		**-0.85 (120h)**	0.0597	
638	35_14635	Oxygen-evolving enhancer protein 2, chloroplastic	PS.lightreaction.photosystem II.PSII polypeptide subunits		-0.51 (120h)	0.1235	
590	35_13769	fructose-bisphospate aldolase isozyme	PS.calvin cyle.aldolase		-0.5 (120h)	0.0513	
162	35_13900	Ribulose bisphosphate carboxylase/oxygenase activase A, chloroplastic	PS.calvin cyle.rubisco interacting		-0.84 (120h)	0.0312	
387	35_360	T-complex protein	PS.calvin cyle.rubisco interacting		**0.93 (120h)**	0.1465	

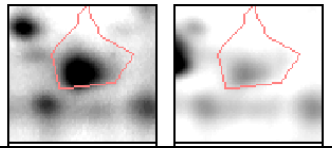
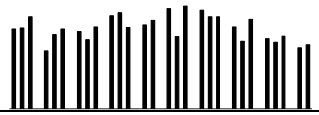
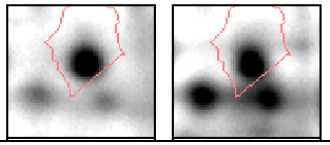
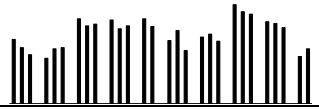
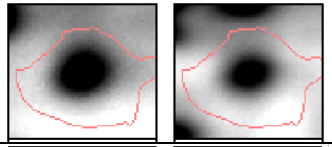
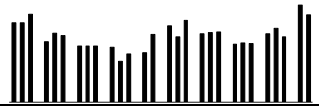
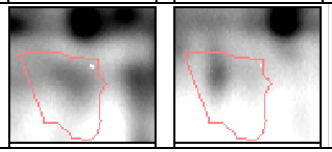
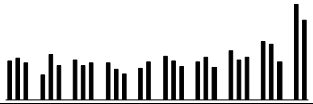
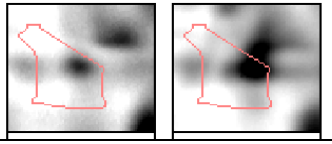
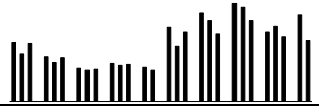
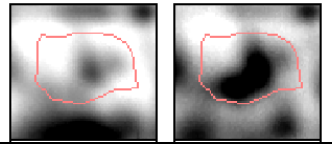
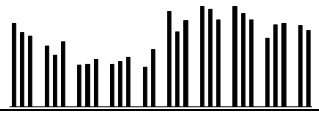
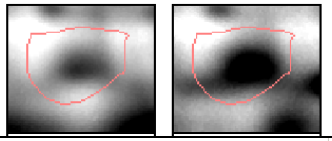
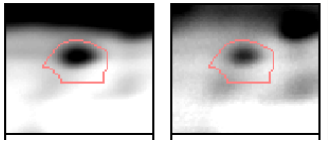
522	35_2078	Glucose-1-phosphate adenylyltransferase	major CHO metabolism.synthesis.starch.AGPase		0.58 (24h)	0.0083	
668	35_15785	Sorbitol dehydrogenase	minor CHO metabolism.sugar alcohols		-0.45 (120h)	0.1934	
453	35_15785	Sorbitol dehydrogenase	minor CHO metabolism.sugar alcohols		0.78 (120h)	0.0365	
287	35_1092	Xylose isomerase	minor CHO metabolism.others		**-1.04 (120h)**	0.0156	
117	35_15726	Alpha-galactosidase	minor CHO metabolism.galactose.alpha-galactosidases		**-1.53 (120h)**	0.1487	
177	35_15726	Alpha-galactosidase	minor CHO metabolism.galactose.alpha-galactosidases		**-1.37 (120h)**	0.0376	
349	35_14099	Fructose-bisphosphate aldolase cytoplasmic isozyme	glycolysis.aldolase		**-0.86 (120h)**	0.0163	
476	35_14099	Fructose-bisphosphate aldolase cytoplasmic isozyme	glycolysis.aldolase		-0.47 (120h)	0.0547	

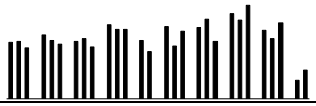
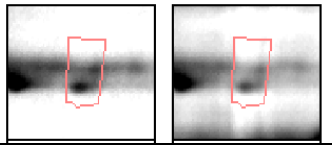
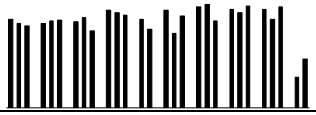
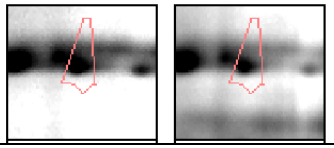
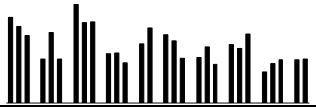
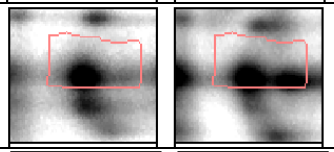
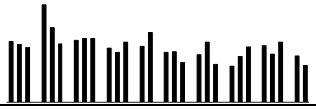
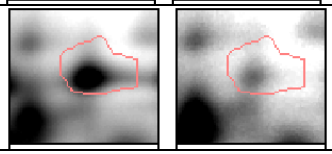
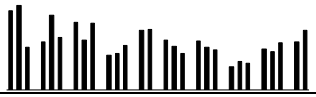
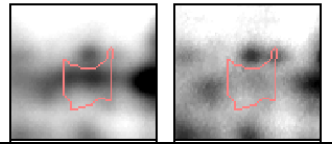
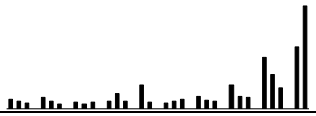
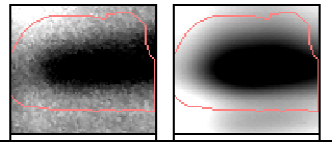
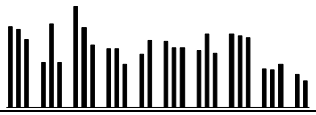
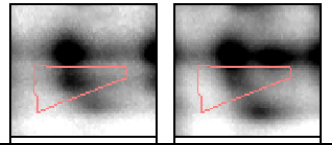
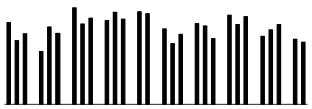
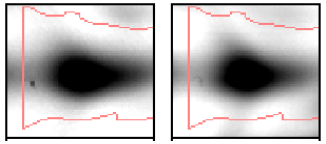
536	35_14100	Fructose-bisphosphate aldolase cytoplasmic isozyme	glycolysis.aldolase		-0.31 (120h)	0.1723	
217	35_14505	Triosephosphate isomerase, cytosolic	glycolysis.TPI		**-0.87 (120h)**	0.0098	
659	35_14505	Triosephosphate isomerase, cytosolic	glycolysis.TPI		0.41 (24h)	0.0642	
692	35_14505	Triosephosphate isomerase, cytosolic	glycolysis.TPI		0.25 (72h)	0.1710	
116	35_49	glyceraldehyde-3-phosphate dehydrogenase	glycolysis.glyceraldehyde 3-phosphate dehydrogenase		**-0.85 (120h)**	0.0594	
277	35_49	glyceraldehyde-3-phosphate dehydrogenase	glycolysis.glyceraldehyde 3-phosphate dehydrogenase		-0.83 (48h)	0.0145	
118	35_15021	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	glycolysis.phosphoglycerate mutase		**-0.91 (48h)**	0.3285	
407	35_15021	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	glycolysis.phosphoglycerate mutase		-0.44 (48h)	0.2635	

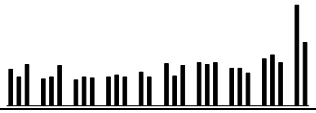
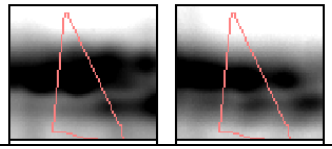
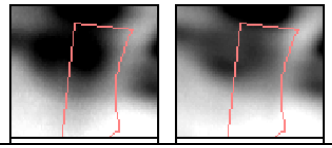
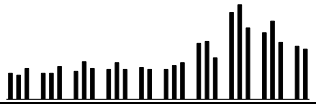
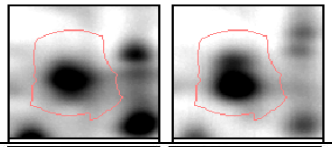
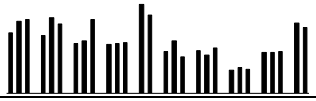
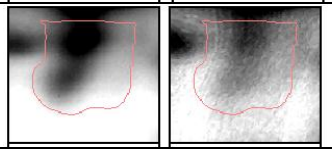
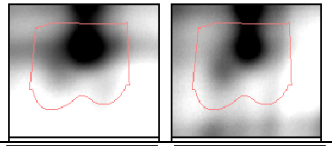
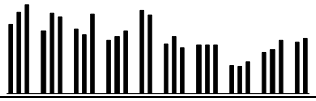
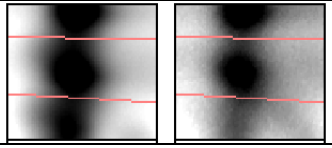
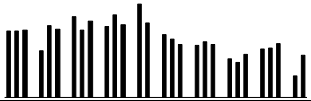
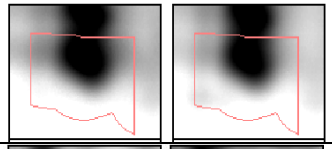
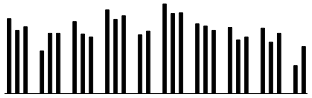
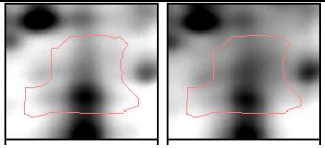
545	35_15021	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	glycolysis.phosphoglycerate mutase		0.37 (24h)	0.1892	
226	35_14444	Enolase 2	glycolysis.enolase		**-0.94 (120h)**	0.1988	
657	35_14444	Enolase 2	glycolysis.enolase		-0.27 (48h)	0.1934	
680	35_14451	Enolase 2	glycolysis.enolase		-0.26 (120h)	0.2047	
168	35_784	Pyruvate decarboxylase	fermentation.PDC		**1.43 (120h)**	0.0222	
448	35_784	Pyruvate decarboxylase	fermentation.PDC		-0.5 (72h)	0.0236	
625	35_1714	Dihydrolipoyl dehydrogenase	TCA / org. transformation.TCA.pyruvate DH.E3		-0.56 (120h)	0.0338	
139	35_1124	Citrate synthase	TCA / org. transformation.TCA.CS		**1.6 (120h)**	0.0119	

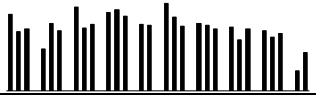
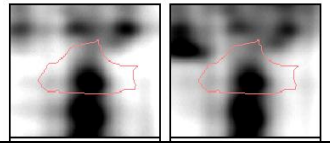
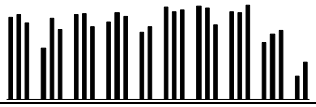
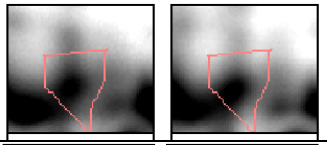
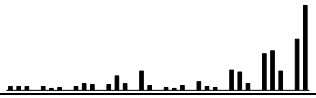
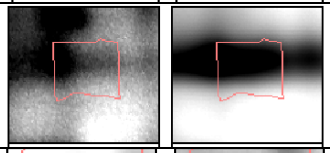
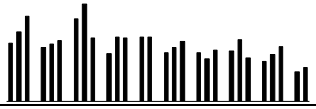
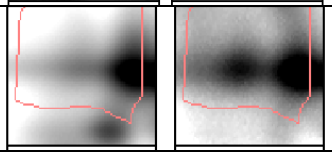
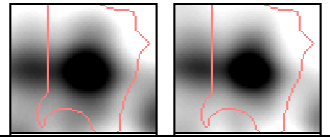
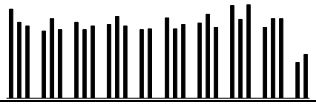
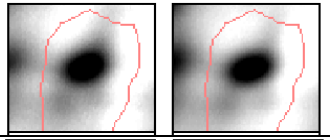
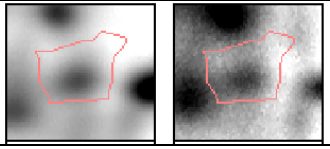
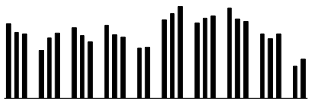
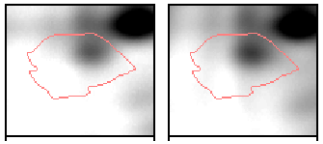
606	35_802	6-phosphogluconate dehydrogenase	OPP.oxidative PP.6-phosphogluconate dehydrogenase		0.54 (48h)	0.0087	
525	35_15073	Putative aconitate hydratase, cytoplasmic	TCA / org. transformation.TCA.aconitase		-0.57 (120h)	0.2627	
653	35_15073	Putative aconitate hydratase, cytoplasmic	TCA / org. transformation.TCA.aconitase		-0.22 (48h)	0.1451	
410	35_16233	IDH1 (isocitrate dehydrogenase 1)	TCA / org. transformation.TCA.IDH		0.6 (24h)	0.0095	
98	35_15429	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	TCA / org. transformation.TCA.succinate dehydrogenase		**1.65 (120h)**	0.0420	
519	35_15429	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	TCA / org. transformation.TCA.succinate dehydrogenase		0.58 (120h)	0.0236	
171	35_16117	Fumarate hydratase 1, mitochondrial	TCA / org. transformation.TCA.fumarase		**1.56 (120h)**	0.0098	
402	35_16117	Fumarate hydratase 1, mitochondrial	TCA / org. transformation.TCA.fumarase		**0.88 (120h)**	0.0027	

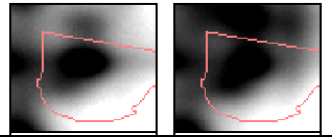
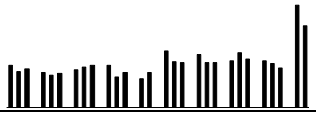
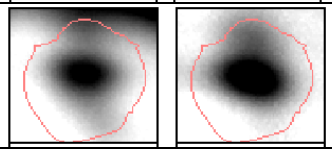
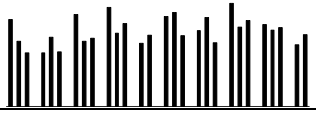
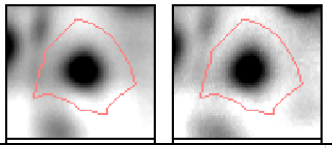
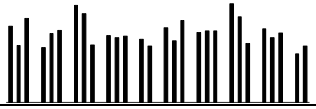
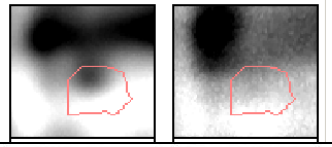
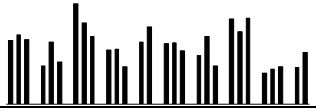
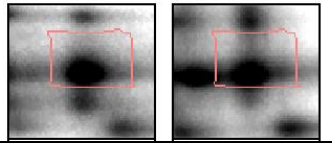
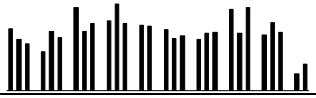
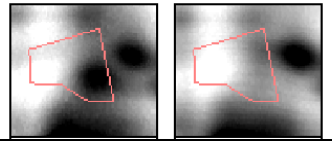
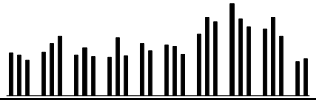
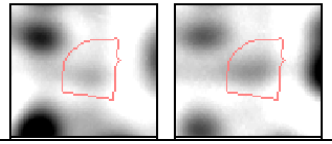
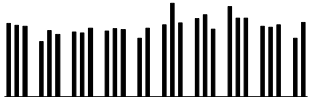
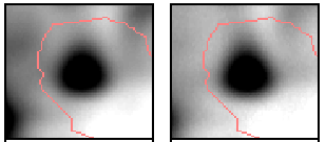
695	35_36841	cytoplasmic malate dehydrogenase	TCA / org. transformation.other organic acid transformaitons.cyt MDH		-0.19 (120h)	0.1329	
242	35_960	NADP-dependent malic enzyme	TCA / org. transformation.other organic acid transformations.malic		**1.32 (120h)**	0.0038	
495	35_960	NADP-dependent malic enzyme	TCA / org. transformation.other organic acid transformations.malic		0.73 (24h)	0.0047	
451	35_14632	Vacuolar ATP synthase subunit E	mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear		**-0.86 (120h)**	0.1162	
619	35_14632	Vacuolar ATP synthase subunit E	mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear		-0.48 (48h)	0.0303	
310	35_1022	putative ATP synthase delta' chain, mitochondrial precursor	mitochondrial electron transport / ATP synthesis.F1-ATPase		**-1.1 (120h)**	0.0198	
397	35_15925	expressed protein	mitochondrial electron transport / ATP synthesis.F1-ATPase		0.64 (120h)	0.0520	
415	35_15350	Mitochondrial ATP synthase	mitochondrial electron transport / ATP synthesis.F1-ATPase		**-0.86 (120h)**	0.3138	

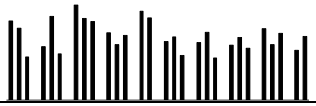
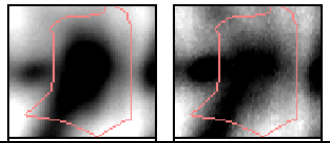
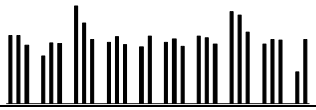
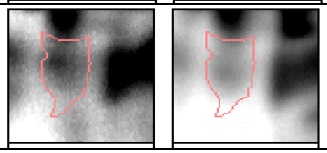
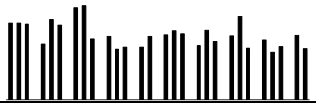
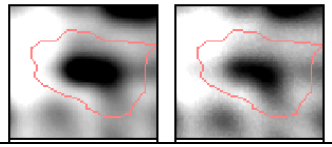
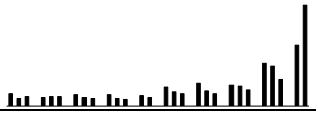
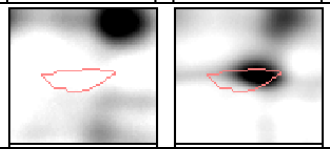
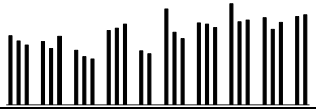
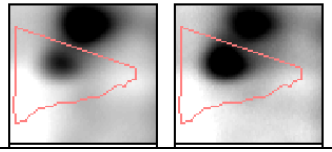
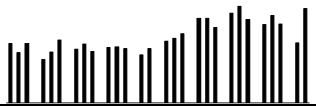
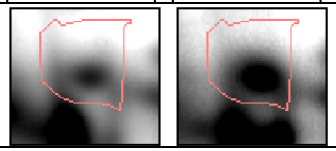
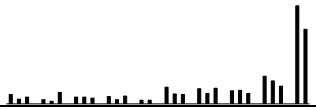
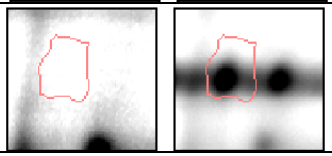
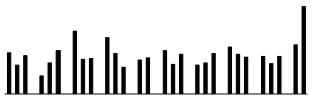
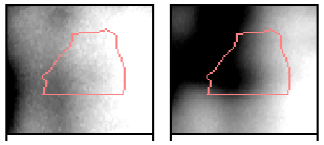
511	35_1801	Alpha-L-arabinofuranosidase/beta-D-xylosidase isoenzyme ARA-I	cell wall.degradation.mannan-xylose-arabinose-fucose		-0.59 (120h)	0.0221	
610	35_1801	Alpha-L-arabinofuranosidase/beta-D-xylosidase isoenzyme ARA-I	cell wall.degradation.mannan-xylose-arabinose-fucose		-0.47 (120h)	0.3189	
454	35_15770	NADPH-dependent FMN reductase domain containing protein	lipid metabolism.'exotics' (steroids, squalene etc)		-0.67 (120h)	0.2220	
423	35_48714	acyl-desaturase, chloroplast precursor	lipid metabolism.FA synthesis and FA elongation.ACP desaturase		0.66 (120h)	0.0477	
196	35_15143	Aspartate aminotransferase	amino acid metabolism.synthesis.central amino acid metabolism.aspartate		**1.32 (120h)**	0.0222	
187	35_368	S-adenosylmethionine synthetase 1	amino acid metabolism.synthesis.aspartate family.methionine		**1.5 (48h)**	0.0021	
340	35_366	S-adenosylmethionine synthetase 1	amino acid metabolism.synthesis.aspartate family.methionine		**1.09 (48h)**	0.0032	
671	35_14602	Alanine aminotransferase	amino acid metabolism.degradation.branched chain group.isoleucine		-0.4 (24h)	0.3189	

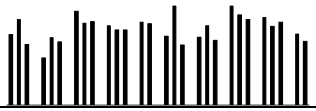
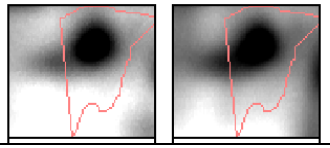
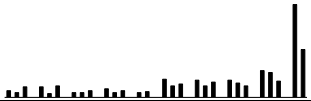
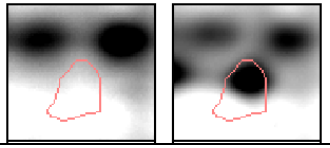
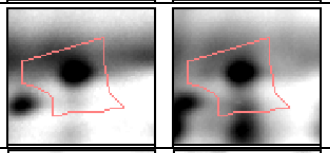
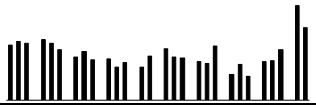
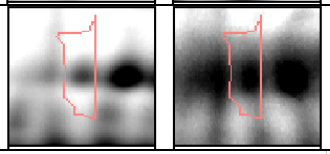
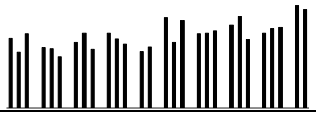
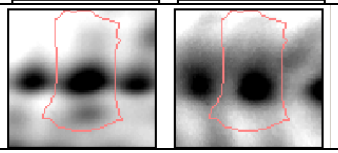
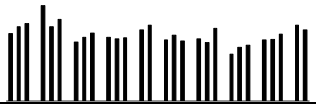
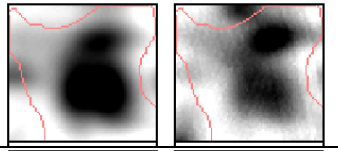
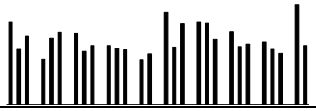
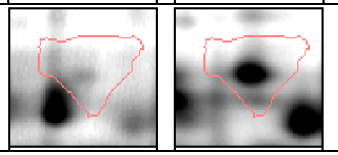
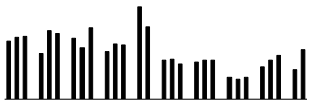
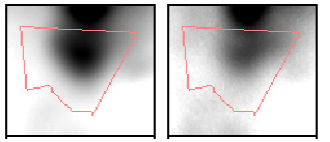
106	35_259	glycine dehydrogenase	amino acid metabolism.degradation.serine -glycine-cysteine group.glycine		**-1.16 (120h)**	0.2562	
245	35_259	glycine dehydrogenase	amino acid metabolism.degradation.serine -glycine-cysteine group.glycine		**-1.07 (120h)**	0.2704	
296	35_259	glycine dehydrogenase	amino acid metabolism.degradation.serine -glycine-cysteine group.glycine		-0.62 (120h)	0.0099	
447	35_429	aminomethyltransferase	amino acid metabolism.degradation.serine -glycine-cysteine group.glycine		-0.66 (24h)	0.0141	
216	35_15495	Putative stress-induced protein sti1	stress		**-1.22 (48h)**	0.0231	
10	35_702	Pathogenesis-related protein PRB1-2	stress.biotic		**2.4 (120h)**	0.0027	
204	35_28067	protein NB-ARC domain containing protein	stress.biotic		**-1.01 (120h)**	0.0393	
643	35_14148	Thaumatin-like protein TLP5	stress.abiotic		-0.53 (120h)	0.1046	

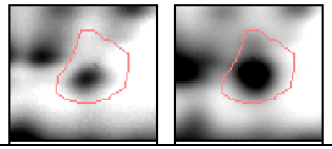
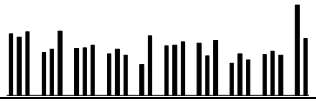
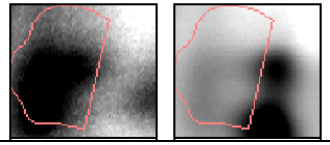
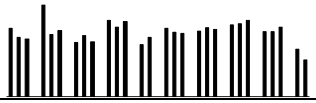
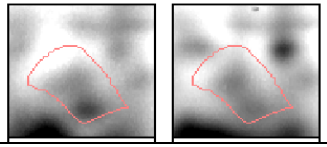
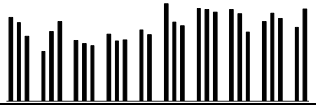
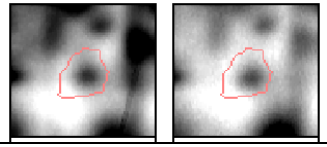
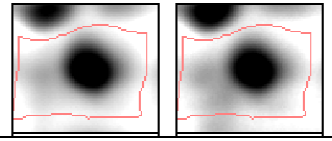
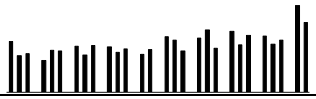
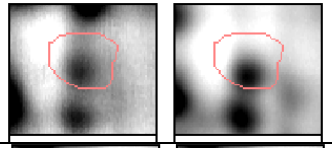
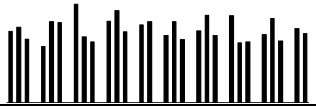
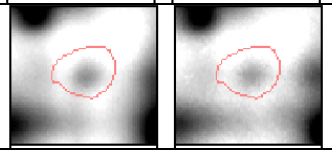
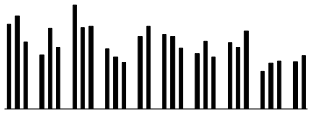
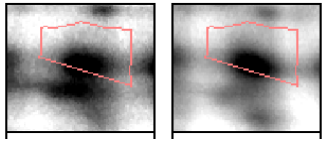
161	35_453	dnaK-type molecular chaperone HSP70	stress.abiotic.heat		**1.39 (120h)**	0.0099	
549	35_14539	Dehydrin 5	stress.abiotic.unspecified		-0.66 (120h)	0.0502	
151	35_50935	HvGER4	stress.abiotic.unspecified		**1.39 (48h)**	0.0022	
123	35_14824	HvGER2a	stress.abiotic.unspecified		**-1.26 (48h)**	0.0082	
164	35_14824	HvGER2a	stress.abiotic.unspecified		**-1.27 (120h)**	0.1148	
195	35_14824	HvGER2a	stress.abiotic.unspecified		**-1.22 (48h)**	0.0040	
214	35_48123	HvGER2a	stress.abiotic.unspecified		**-1.39 (120h)**	0.0136	
316	35_14824	HvGER2a	stress.abiotic.unspecified		-0.69 (120h)	0.2282	

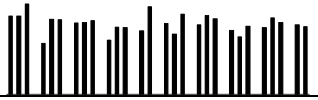
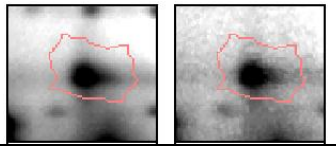
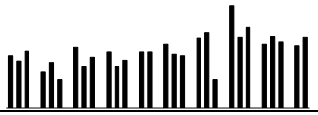
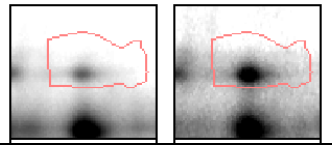
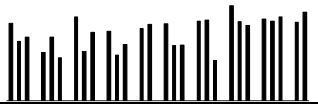
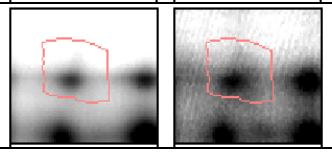
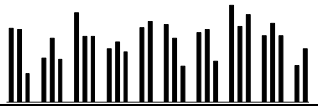
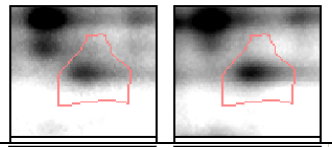
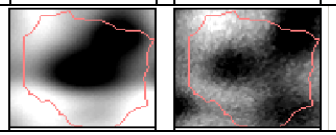
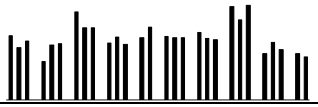
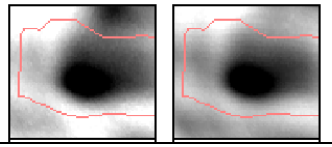
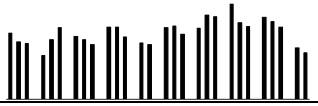
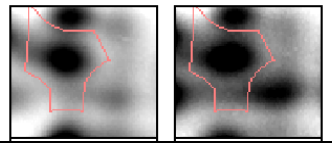
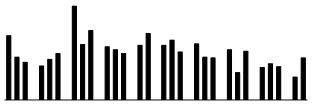
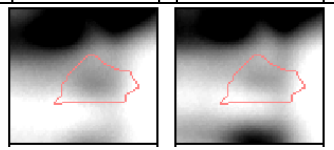
206	35_14824	HvGER2a	stress.abiotic.unspecified		**-1.2 (120h)**	0.0795	
165	35_14654	NAD dependent epimerase/dehydratase family domain containing protein	stress.abiotic.unspecified		**-1.21 (120h)**	0.1999	
3	35_704	Pathogenesis-related protein PRB1-2	stress.abiotic.unspecified		**2.48 (120h)**	0.0016	
227	35_14981	Salt stress root protein RS1	stress.abiotic.unspecified		**-1.02 (120h)**	0.0074	
208	35_14981	Salt stress root protein RS1	stress.abiotic.unspecified		**-1.09 (120h)**	0.1601	
317	35_14510	Ascorbate peroxidase	redox.ascorbate and glutathione		-0.79 (120h)	0.2569	
614	35_14510	Ascorbate peroxidase	redox.ascorbate and glutathione		-0.44 (120h)	0.1901	
274	35_861	Dehydroascorbate reductase	redox.ascorbate and glutathione.ascorbate		-0.5 (120h)	0.0775	

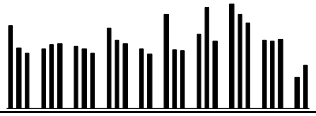
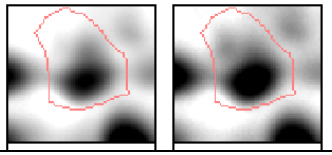
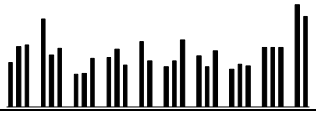
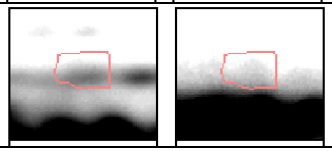
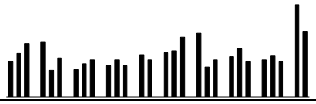
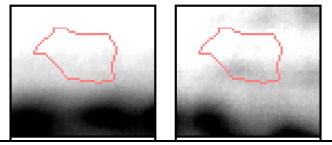
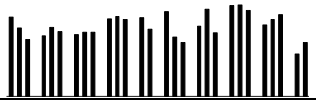
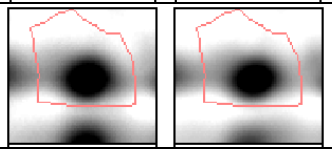
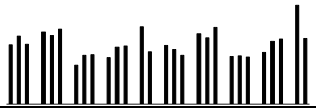
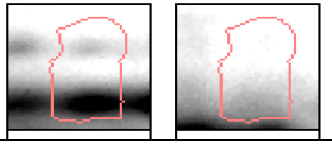
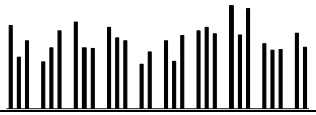
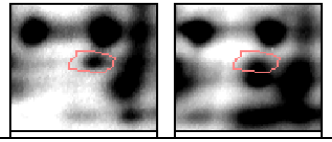
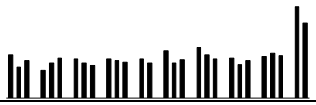
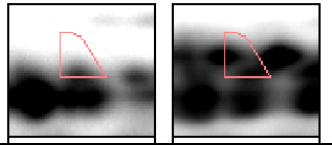
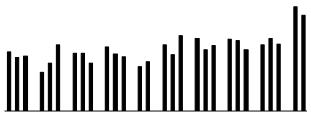
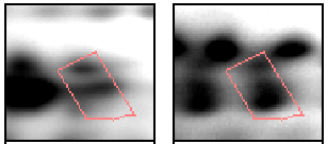
363	35_43946	dehydroascorbate reductase	redox.ascorbate and glutathione.ascorbate		-0.69 (120h)	0.3088	
178	35_728	GPX12Hv, glutathione peroxidase-like protein	redox.ascorbate and glutathione.glutathione		**1.54 (120h)**	0.0114	
612	35_1190	Superoxide dismutase [Mn], mitochondrial	redox.dismutases and catalases		0.36 (24h)	0.0354	
586	35_22900	adenylate kinase	nucleotide metabolism.phosphotransfer and pyrophosphatases.uridylate kinase		-0.19 (120h)	0.2896	
267	35_15245	periplasmic beta-glucosidase precursor	misc.gluco-, galacto- and mannosidases		-0.67 (120h)	0.0523	
124	35_14630	Lichenase-2 (Fragment)	misc.beta 1,3 glucan hydrolases		**-1.57 (120h)**	0.1004	
318	35_739	glutathione S-transferase	misc.glutathione S transferases		**0.9 (48h)**	0.0189	
677	35_14091	Glutathione transferase F5	misc.glutathione S transferases		0.33 (48h)	0.0218	

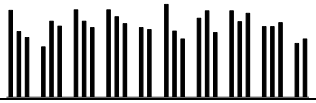
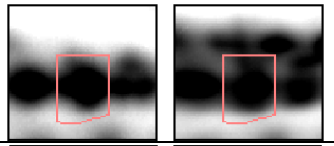
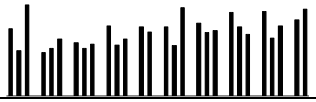
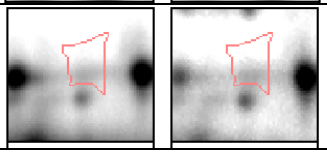
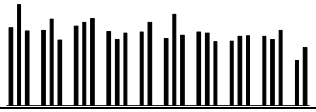
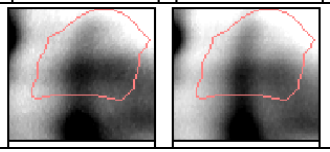
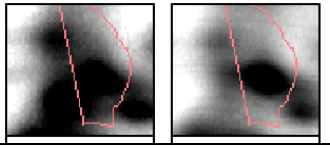
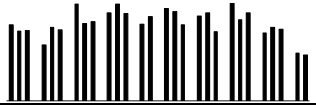
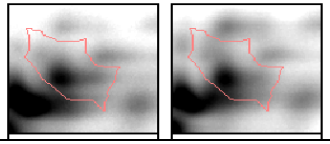
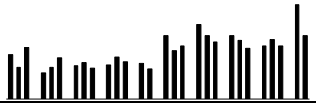
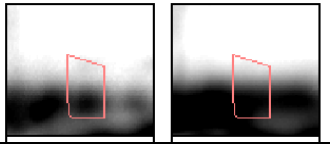
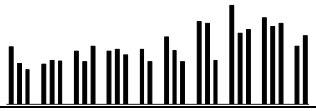
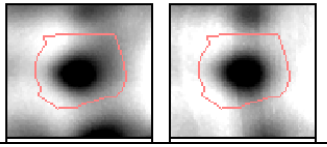
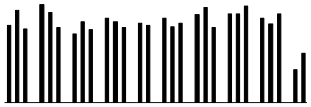
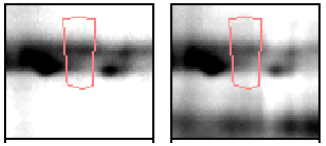
592	35_40361	Peroxidase 6	misc.peroxidases		-0.59 (48h)	0.0260	
488	35_13856	Peroxidase 10 (Fragment)	misc.peroxidases		-0.37 (120h)	0.2839	
593	35_13856	Peroxidase 10 (Fragment)	misc.peroxidases		-0.31 (48h)	0.0312	
27	35_16041	Peroxidase 51	misc.peroxidases		**3.08 (120h)**	0.0010	
463	35_16425	KH domain containing protein	RNA.regulation of transcription		**0.85 (48h)**	0.0093	
485	35_4140	ABA responsive element binding factor 3	RNA.regulation of transcription.bZIP transcription factor family		0.72 (48h)	0.0032	
2	35_2434	Retrotransposon encoded protein (unknown)	RNA.regulation of transcription.unclassified		**4.56 (120h)**	0.0004	
320	35_21531	E3 ubiquitin ligase	RNA.regulation of transcription.unclassified		**0.95 (120h)**	0.1284	

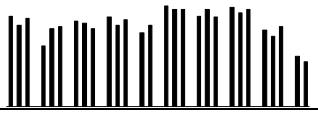
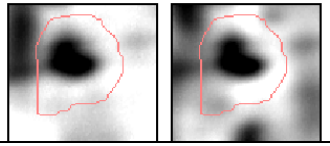
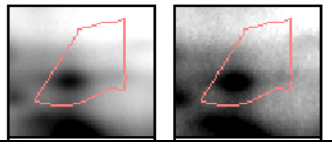
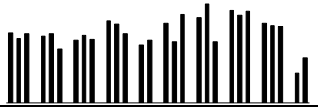
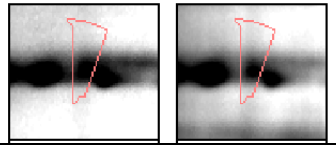
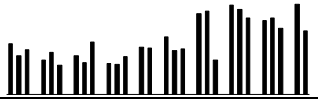
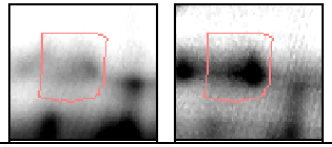
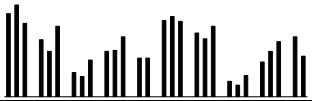
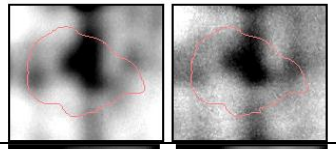
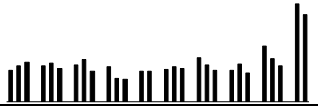
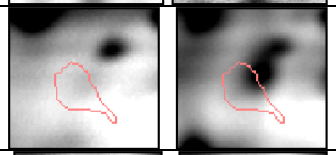
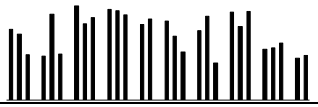
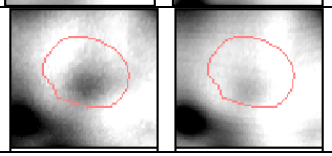
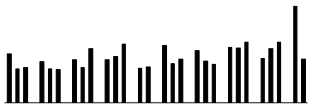
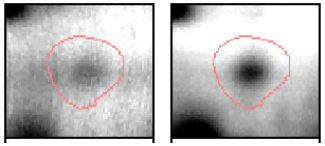
589	35_17129	SEC14 cytosolic factor family protein	DNA.unspecified		-0.29 (120h)	0.1461	
9	35_4982	Nucleoporin interacting component	protein.targeting.nucleus		**3.82 (120h)**	0.0006	
305	35_1200	Mitochondrial processing peptidase alpha-chain	protein.targeting.mitochondria		-0.77 (120h)	0.0983	
170	35_16286	Chaperonin CPN60-1, mitochondrial	protein.postranslational modification		**1.12 (120h)**	0.2442	
482	35_16286	Chaperonin CPN60-1, mitochondrial	protein.postranslational modification		0.78 (120h)	0.0083	
564	35_15567	vacuolar-processing enzyme precursor	protein.degradation		-0.38 (24h)	0.0256	
537	35_2125	Putative Subtilisin homologue	protein.degradation.subtilases		0.73 (120h)	0.0477	
92	35_25207	UBA/TS-N domain containing protein	protein.degradation.ubiquitin		**-1.54 (48h)**	0.0046	

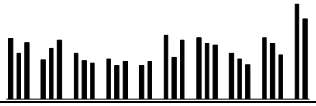
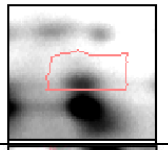
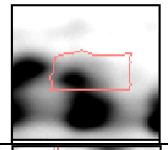
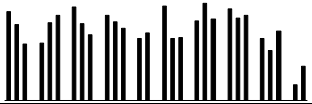
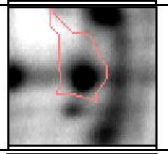
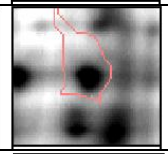
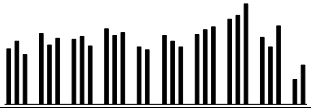
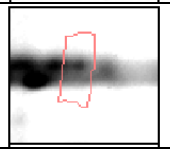
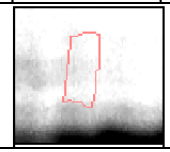
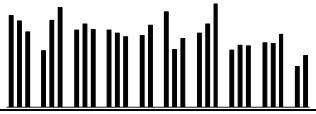
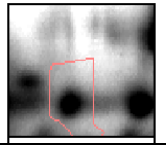
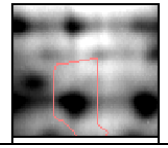
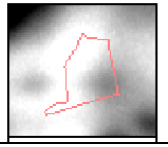
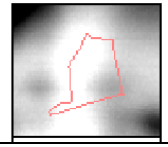
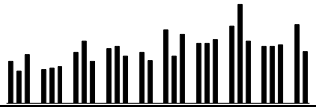
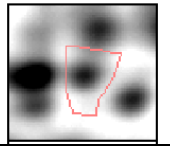
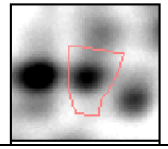
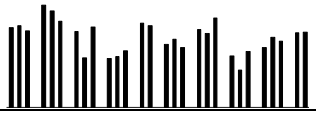
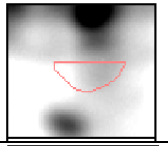
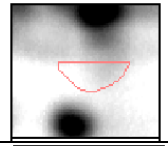
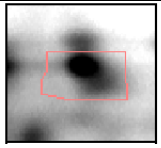
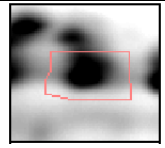
190	35_4628	tRNA methyltransferase	protein.synthesis.initiation		**0.97 (120h)**	0.0041	
385	35_14477	Translation initiation factor 5A	protein.synthesis.initiation		0.7 (120h)	0.2756	
489	35_976	Translational elongation factor Tu	protein.synthesis.initiation		-0.41 (120h)	0.3054	
575	35_1864	Putative aminoacylase	protein.degradation.ubiquitin.E2		0.52 (48h)	0.0089	
567	35_38507	putative 26S proteasome regulatory particle triple-A ATPase subunit3	protein.degradation.ubiquitin.proteasom		0.36 (48h)	0.2820	
378	35_3176	Proteasome subunit alpha type-4-1	protein.degradation.ubiquitin.proteasom		**0.95 (120h)**	0.0093	
971	35_15109	Proteasome subunit alpha type-7-A	protein.degradation.ubiquitin.proteasom		-0.19 (72h)	0.1245	
377	35_17049	Putative Subtilisin homologue	protein.degradation.subtilases		-0.62 (120h)	0.0137	

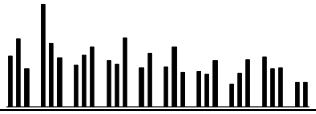
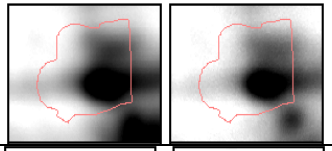
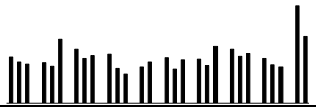
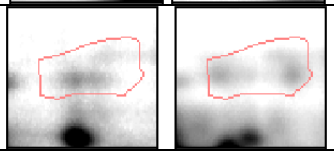
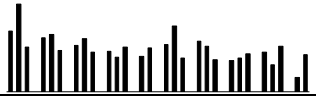
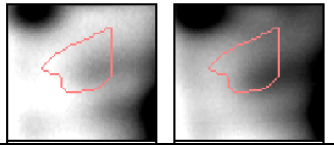
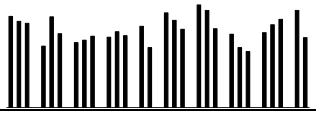
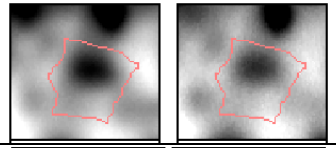
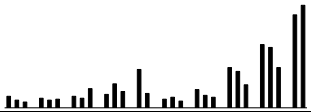
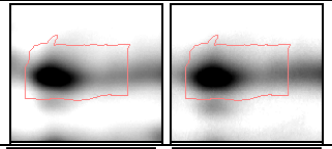
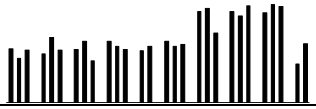
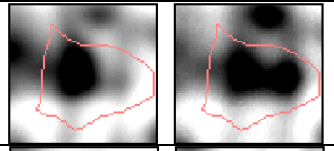
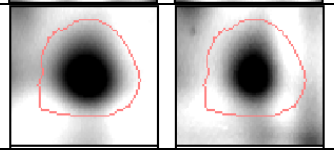
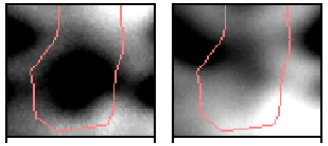
951	35_524	Putative Subtilisin homologue	protein.degradation.subtilases		-0.22 (12h)	0.2772	
286	35_18209	Subtilisin-like serine proteinase	protein.degradation.subtilases		0.73 (48h)	0.0098	
556	35_18209	Subtilisin-like serine proteinase	protein.degradation.subtilases		0.51 (72h)	0.0266	
419	35_1530	Putative TCP-1/cpn60 chaperonin family protein	protein.folding		-0.79 (120h)	0.1781	
184	35_19417	trehalose-6-phosphate synthase	signalling.receptor kinases.S-locus glycoprotein like		**-1.36 (120h)**	0.0256	
390	35_5860	S-locus-like receptor protein kinase	signalling.receptor kinases.S-locus glycoprotein like		-0.6 (120h)	0.2975	
533	35_2726	TBC domain containing protein	signalling.G-proteins		0.46 (48h)	0.0204	
312	35_14382	14-3-3-like protein A	signalling.14-3-3 proteins		**-0.9 (120h)**	0.0466	

229	35_14174	actin	cell.organisation		0.68 (48h)	0.1274	
239	35_14172	actin	cell.organisation		0.8 (120h)	0.1901	
261	35_14172	actin	cell.organisation		**0.99 (120h)**	0.0198	
444	35_14172	actin	cell.organisation		-0.6 (120h)	0.2669	
464	35_14174	actin	cell.organisation		0.35 (120h)	0.2073	
456	35_17334	WD domain, G-beta repeat domain containing protein	development.unspecified		0.44 (120h)	0.0923	
259	35_15178	Vacuolar ATP synthase catalytic subunit A (Fragment)	transport.p- and v-ATPases		**1.17 (120h)**	0.0261	
344	35_15178	Vacuolar ATP synthase catalytic subunit A (Fragment)	transport.p- and v-ATPases		**1.1 (120h)**	0.0135	

633	35_15178	Vacuolar ATP synthase catalytic subunit A (Fragment)	transport.p- and v-ATPases		-0.3 (120h)	0.3306	
830	35_15780	Putative high-affinity potassium transporter	transport.potassium		0.49 (48h)	0.0109	
546	35_8676	Lysine and histidine specific transporter	transport.amino acids		-0.61 (120h)	0.0231	
280	35_15968	bacterial transferase hexapeptide domain containing protein	not assigned.no ontology		**-0.91 (120h)**	0.3043	
413	35_693	PIR protein	not assigned.no ontology		-0.79 (120h)	0.2627	
270	35_14470	protein DnaK family protein	not assigned.no ontology		**1.26 (120h)**	0.0027	
421	35_15997	protein phosphoglycerate mutase	not assigned.no ontology		0.7 (24h)	0.0046	
322	35_5591	hydroxyproline-rich glycoprotein family protein	not assigned.no ontology.hydroxyproline rich proteins		**-0.92 (120h)**	0.2548	

367	35_1354	stress responsive protein	not assigned.no ontology.hydroxyproline rich proteins		-0.7 (120h)	0.2887	
976	35_47029	Bzip-like transcription factor-like protein	not assigned.unknown		0.13 (24h)	0.3197	
263	35_12756	DUF869 domain containing protein	not assigned.unknown		-0.7 (120h)	0.1440	
231	35_10955	F-box domain containing protein	not assigned.unknown		**1.13 (72h)**	0.0043	
62	35_17794	Fe-S metabolism associated domain containing protein	not assigned.unknown		-0.72 (48h)	0.1440	
119	35_2185	glycerol-3-phosphate acyltransferase	not assigned.unknown		**1.59 (120h)**	0.0404	
374	35_19141	leucine rich repeat containing protein	not assigned.unknown		**-0.86 (120h)**	0.0613	
400	35_16401	Proteasome activator subunit 4-like	not assigned.unknown		**0.99 (120h)**	0.0189	

251	35_11352	protein-L-isoaspartate O-methyltransferase	not assigned.unknown		**1.3 (120h)**	0.0289		
114	35_14519	Putative diphosphonucleotide phosphatase	not assigned.unknown		**-1.38 (120h)**	0.1164		
185	35_14519	Putative diphosphonucleotide phosphatase	not assigned.unknown		-0.8 (120h)	0.2362		
435	35_14519	Putative diphosphonucleotide phosphatase	not assigned.unknown		-0.74 (120h)	0.0337		
380	35_4322	Putative GTPase activating protein	not assigned.unknown		**-0.94 (120h)**	0.0177		
306	35_3277	T-complex protein	not assigned.unknown		0.8 (24h)	0.0036		
404	35_41618	Xet3 protein	not assigned.unknown		-0.51 (48h)	0.0571		
422	35_4446	AAA-type ATPase family protein	n.a.		**0.94 (120h)**	0.0297		

174	35_3542	dirigent-like protein	n.a.		**-0.92 (24h)**	0.0122	
335	35_25069	DnaK family protein	n.a.		**1.09 (120h)**	0.081	
237	35_19575	expressed protein	n.a.		-0.63 (120h)	0.0165	
626	35_9734	expressed protein	n.a.		0.3 (24h)	0.0912	
16	35_4712	GATA transcription factor 25	n.a.		**1.89 (120h)**	0.0032	
412	35_41150	COP1 [Oryza sativa subsp. indica]	n.a.		0.81 (48h)	0.0109	
70	35_5689	hydrolase, alpha/beta fold family domain containing protein	n.a.		**-1.99 (120h)**	0.0376	
694	35_32881	No hit	n.a.		-0.12 (120h)	0.1828	

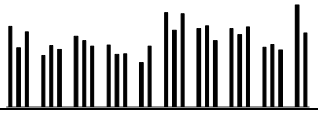
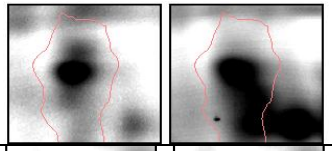
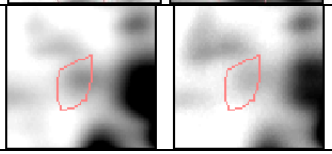
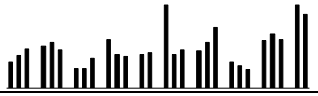
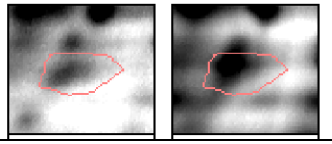
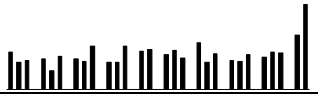
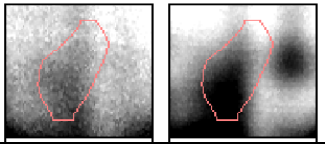
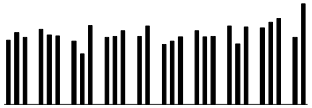
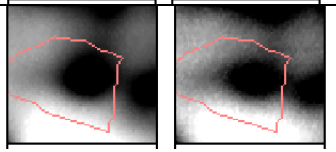
526	35_9359	No hit	n.a.		0.74 (120h)	0.0148	
934	35_12150	AAA-type ATPase family protein	n.a.		-0.34 (12h)	0.3189	
110	35_38367	basic helix-loop-helix domain containing protein	n.a.		**1.2 (120h)**	0.0302	
233	35_23963	protein binding protein	n.a.		0.82 (120h)	0.0421	
683	35_22985	sulfotransferase domain containing protein	n.a.		0.23 (72h)	0.0795	

Table 26 shows the identified proteins. The protein spots are ordered firstly according to their regulation pattern (clusters) (see Figure 30 in chapter 6.3.4) and secondly according to the biological functions they are categorized according to MapMan binning system. First row shows the number in the DIGE analysis. Secondly the code and name of the HarvEST:Barley-ID is shown, followed by the described function, the MapMan-Binning and the annotation of the binning (Biological classification), the highest regulation event and its time point, the false discovery rate (q-value) and the cluster the protein spot belongs to. If the HarvEST:Barley-ID has no naming, "n.a." is written, as well as if the HarvEST:Barley-ID is not connected to a contig and therefore the binning of MapMan can not be used. The p-value shows the statistical propability of false discovery rate. As threshold for the proteome analysis q<0.05 was used. The bold regulation values indicate regulation is more than 1.8-fold.

Spot-Nr.	HarvEST-ID	Putative Function	Binning	Biological function	Regulation Infected/control	q-value	Cluster
387	35_360	T-complex protein	1.03.13	PS.calvin cyle.rubisco interacting	**0.93 (120h)**	0.147	1
453	35_15785	Sorbitol dehydrogenase	3.3	minor CHO metabolism.sugar alcohols	0.78 (120h)	0.036	1
692	35_14505	Triosephosphate isomerase, cytosolic	4.08	glycolysis.TPI	0.25 (72h)	0.171	1
168	35_784	Pyruvate decarboxylase	5.02	fermentation.PDC	**1.43 (120h)**	0.022	1
139	35_1124	Citrate synthase	8.1.02	TCA / org. transformation.TCA.CS	**1.6 (120h)**	0.012	1
98	35_15429	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	8.1.07	TCA / org. transformation.TCA.succinate dehydrogenase	**1.65 (120h)**	0.042	1
519	35_15429	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	8.1.07	TCA / org. transformation.TCA.succinate dehydrogenase	0.58 (120h)	0.024	1
171	35_16117	Fumarate hydratase 1, mitochondrial	8.1.08	TCA / org. transformation.TCA.fumarase	**1.56 (120h)**	0.010	1
402	35_16117	Fumarate hydratase 1, mitochondrial	8.1.08	TCA / org. transformation.TCA.fumarase	**0.88 (120h)**	0.003	1
242	35_960	NADP-dependent malic enzyme	8.2.10	TCA / org. transformation.other organic acid transformations.malic	**1.32 (120h)**	0.004	1
397	35_15925	expressed protein	9.9	mitochondrial electron transport / ATP synthesis.F1-ATPase	0.64 (120h)	0.052	1
423	35_48714	acyl-desaturase, chloroplast precursor	11.1.15	lipid metabolism.FA synthesis and FA elongation.ACP desaturase	0.66 (120h)	0.048	1
196	35_15143	Aspartate aminotransferase	13.1.1.2	amino acid metabolism.synthesis.central amino acid metabolism.aspartate	**1.32 (120h)**	0.022	1
671	35_14602	Alanine aminotransferase	13.2.4.5	amino acid metabolism.degradation.branched chain group.isoleucine	-0.4 (24h)	0.319	1
10	35_702	Pathogenesis-related protein PRB1-2	20.1	stress.biotic	**2.4 (120h)**	0.003	1
161	35_453	dnaK-type molecular chaperone HSP70	20.2.1	stress.abiotic.heat	**1.39 (120h)**	0.010	1
3	35_704	Pathogenesis-related protein PRB1-2	20.2.99	stress.abiotic.unspecified	**2.48 (120h)**	0.002	1
178	35_728	GPX12Hv, glutathione peroxidase-like protein	21.2.2	redox.ascorbate and glutathione.glutathione	**1.54 (120h)**	0.011	1
27	35_16041	Peroxidase 51	26.12	misc.peroxidases	**3.08 (120h)**	0.001	1
593	35_13856	Peroxidase 10 (Fragment)	26.12	misc.peroxidases	-0.31 (48h)	0.031	1
2	35_2434	Retrotransposon encoded protein (unknown)	27.3.99	RNA.regulation of transcription.unclassified	**4.56 (120h)**	0.000	1
320	35_21531	E3 ubiquitin ligase	27.3.99	RNA.regulation of transcription.unclassified	**0.95 (120h)**	0.128	1
190	35_4628	tRNA methyltransferase	29.2.3	protein.synthesis.initiation	**0.97 (120h)**	0.004	1
385	35_14477	Translation initiation factor 5A	29.2.3	protein.synthesis.initiation	0.7 (120h)	0.276	1

9	35_4982	Nucleoporin interacting component	29.3.1	protein.targeting.nucleus	**3.82 (120h)**	0.001	1
170	35_16286	Chaperonin CPN60-1, mitochondrial	29.4	protein.postranslational modification	**1.12 (120h)**	0.244	1
482	35_16286	Chaperonin CPN60-1, mitochondrial	29.4	protein.postranslational modification	0.78 (120h)	0.008	1
564	35_15567	vacuolar-processing enzyme precursor	29.5	protein.degradation	-0.38 (24h)	0.026	1
537	35_2125	Putative Subtilisin homologue	29.5.01	protein.degradation.subtilases	0.73 (120h)	0.048	1
378	35_3176	Proteasome subunit alpha type-4-1	29.5.11.20	protein.degradation.ubiquitin.proteasom	**0.95 (120h)**	0.009	1
239	35_14172	actin	31.1	cell.organisation	0.8 (120h)	0.190	1
261	35_14172	actin	31.1	cell.organisation	**0.99 (120h)**	0.020	1
464	35_14174	actin	31.1	cell.organisation	0.35 (120h)	0.207	1
259	35_15178	Vacuolar ATP synthase catalytic subunit A (Fragment)	34.1	transport.p- and v-ATPases	**1.17 (120h)**	0.026	1
344	35_15178	Vacuolar ATP synthase catalytic subunit A (Fragment)	34.1	transport.p- and v-ATPases	**1.1 (120h)**	0.013	1
270	35_14470	DnaK family protein	35.1	not assigned.no ontology	**1.26 (120h)**	0.003	1
119	35_2185	glycerol-3-phosphate acyltransferase	35.2	not assigned.unknown	**1.59 (120h)**	0.040	1
251	35_11352	protein-L-isoaspartate O-methyltransferase	35.2	not assigned.unknown	**1.3 (120h)**	0.029	1
400	35_16401	Proteasome activator subunit 4-like	35.2	not assigned.unknown	**0.99 (120h)**	0.019	1
16	35_4712	GATA transcription factor 25	n.a.	n.a.	**1.89 (120h)**	0.003	1
110	35_38367	protein basic helix-loop-helix domain containing protein	n.a.	n.a.	**1.2 (120h)**	0.030	1
233	35_23963	protein binding protein	n.a.	n.a.	0.82 (120h)	0.042	1
335	35_25069	DnaK family protein	n.a.	n.a.	**1.09 (120h)**	0.081	1
422	35_4446	AAA-type ATPase family protein	n.a.	n.a.	**0.94 (120h)**	0.030	1
526	35_9359	nichts	n.a.	n.a.	0.74 (120h)	0.015	1
934	35_12150	protein AAA-type ATPase family protein	n.a.	n.a.	-0.34 (12h)	0.319	1
668	35_15785	Sorbitol dehydrogenase	3.3	minor CHO metabolism.sugar alcohols	-0.45 (120h)	0.193	2
536	35_14100	Fructose-bisphosphate aldolase cytoplasmic isozyme	4.07	glycolysis.aldolase	-0.31 (120h)	0.172	2
659	35_14505	Triosephosphate isomerase, cytosolic	4.08	glycolysis.TPI	0.41 (24h)	0.064	2
116	35_49	glyceraldehyde-3-phosphate dehydrogenase	4.09	glycolysis.glyceraldehyde 3-phosphate dehydrogenase	**-0.85 (120h)**	0.059	2
545	35_15021	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	4.11	glycolysis.phosphoglycerate mutase	0.37 (24h)	0.189	2
226	35_14444	Enolase 2	4.12	glycolysis.enolase	**-0.94 (120h)**	0.199	2
448	35_784	Pyruvate decarboxylase	5.02	fermentation.PDC	-0.5 (72h)	0.024	2
415	35_15350	Mitochondrial ATP synthase	9.9	mitochondrial electron transport / ATP synthesis.F1-ATPase	**-0.86 (120h)**	0.314	2
454	35_15770	NADPH-dependent FMN reductase domain containing protein	11.8	lipid metabolism.'exotics' (steroids, squalene etc)	-0.67 (120h)	0.222	2
204	35_28067	protein NB-ARC domain containing protein	20.1	stress.biotic	**-1.01 (120h)**	0.039	2
643	35_14148	Thaumatin-like protein TLP5	20.2	stress.abiotic	-0.53 (120h)	0.105	2

317	35_14510	Ascorbate peroxidase	21.02	redox.ascorbate and glutathione	-0.79 (120h)	0.257	2
614	35_14510	Ascorbate peroxidase	21.02	redox.ascorbate and glutathione	-0.44 (120h)	0.190	2
612	35_1190	Superoxide dismutase [Mn], mitochondrial	21.06	redox.dismutases and catalases	0.36 (24h)	0.035	2
267	35_15245	periplasmic beta-glucosidase precursor	26.03	misc.gluco-, galacto- and mannosidases	-0.67 (120h)	0.052	2
124	35_14630	Lichenase-2 (Fragment)	26.04	misc.beta 1,3 glucan hydrolases	**-1.57 (120h)**	0.100	2
318	35_739	glutathione S-transferase	26.09	misc.glutathione S transferases	**0.9 (48h)**	0.019	2
677	35_14091	Glutathione transferase F5	26.09	misc.glutathione S transferases	0.33 (48h)	0.022	2
488	35_13856	Peroxidase 10 (Fragment)	26.12	misc.peroxidases	-0.37 (120h)	0.284	2
419	35_1530	Putative TCP-1/cpn60 chaperonin family protein	29.6	protein.folding	-0.79 (120h)	0.178	2
533	35_2726	TBC domain containing protein	30.5	signalling.G-proteins	0.46 (48h)	0.020	2
229	35_14174	actin	31.1	cell.organisation	0.68 (48h)	0.127	2
444	35_14172	actin	31.1	cell.organisation	-0.6 (120h)	0.267	2
633	35_15178	Vacuolar ATP synthase catalytic subunit A (Fragment)	34.1	transport.p- and v-ATPases	-0.3 (120h)	0.331	2
280	35_15968	bacterial transferase hexapeptide domain containing protein	35.1	not assigned.no ontology	**-0.91 (120h)**	0.304	2
413	35_693	PIR protein	35.1	not assigned.no ontology	-0.79 (120h)	0.263	2
114	35_14519	Putative diphosphonucleotide phosphatase	35.2	not assigned.unknown	**-1.38 (120h)**	0.116	2
185	35_14519	Putative diphosphonucleotide phosphatase	35.2	not assigned.unknown	-0.8 (120h)	0.236	2
263	35_12756	DUF869 domain containing protein	35.2	not assigned.unknown	-0.7 (120h)	0.144	2
306	35_3277	T-complex protein	35.2	not assigned.unknown	0.8 (24h)	0.004	2
374	35_19141	leucine rich repeat containing protein	35.2	not assigned.unknown	**-0.86 (120h)**	0.061	2
103	35_99	glyceraldehyde-3-phosphate dehydrogenase	1.01.01.01	PS.lightreaction.photosystem II.LHC-II	**-1.49 (120h)**	0.340	2
638	35_14635	Oxygen-evolving enhancer protein 2, chloroplastic	1.01.01.02	PS.lightreaction.photosystem II.PSII polypeptide subunits	-0.51 (120h)	0.123	2
590	35_13769	fructose-bisphospate aldolase isozyme	1.03.06	PS.calvin cyle.aldolase	-0.5 (120h)	0.051	2
162	35_13900	Ribulose bisphosphate carboxylase/oxygenase activase A, chloroplastic	1.03.13	PS.calvin cyle.rubisco interacting	-0.84 (120h)	0.031	2
117	35_15726	Alpha-galactosidase	3.8.2	minor CHO metabolism.galactose.alpha-galactosidases	**-1.53 (120h)**	0.149	2
606	35_802	6-phosphogluconate dehydrogenase	7.1.03	OPP.oxidative PP.6-phosphogluconate dehydrogenase	0.54 (48h)	0.009	2
525	35_15073	Putative aconitate hydratase, cytoplasmic	8.1.03	TCA / org. transformation.TCA.aconitase	-0.57 (120h)	0.263	2
410	35_16233	IDH1 (isocitrate dehydrogenase 1)	8.1.04	TCA / org. transformation.TCA.IDH	0.6 (24h)	0.009	2
695	35_36841	cytoplasmic malate dehydrogenase	8.2.09	TCA / org. transformation.other organic acid transformaitons.cyt MDH	-0.19 (120h)	0.133	2
610	35_1801	Alpha-L-arabinofuranosidase/beta-D-xylosidase isoenzyme ARA-I	10.6.2	cell wall.degradation.mannan-xylose-arabinose-fucose	-0.47 (120h)	0.319	2
106	35_259	glycine dehydrogenase	13.2.5.2	amino acid metabolism.degradation.serine-glycine-cysteine group.glycine	**-1.16 (120h)**	0.256	2

245	35_259	glycine dehydrogenase	13.2.5.2	amino acid metabolism.degradation.serine-glycine-cysteine group.glycine	**-1.07 (120h)**	0.270	2
164	35_14824	HvGER2a	20.2.99	stress.abiotic.unspecified	**-1.27 (120h)**	0.115	2
165	35_14654	NAD dependent epimerase/dehydratase family domain containing protein	20.2.99	stress.abiotic.unspecified	**-1.21 (120h)**	0.200	2
208	35_14981	Salt stress root protein RS1	20.2.99	stress.abiotic.unspecified	**-1.09 (120h)**	0.160	2
316	35_14824	HvGER2a	20.2.99	stress.abiotic.unspecified	-0.69 (120h)	0.228	2
549	35_14539	Dehydrin 5	20.2.99	stress.abiotic.unspecified	-0.66 (120h)	0.050	2
274	35_861	Dehydroascorbate reductase	21.2.1	redox.ascorbate and glutathione.ascorbate	-0.5 (120h)	0.078	2
363	35_43946	dehydroascorbate reductase	21.2.1	redox.ascorbate and glutathione.ascorbate	-0.69 (120h)	0.309	2
489	35_976	Translational elongation factor Tu	29.2.3	protein.synthesis.initiation	-0.41 (120h)	0.305	2
305	35_1200	Mitochondrial processing peptidase alpha-chain	29.3.2	protein.targeting.mitochondria	-0.77 (120h)	0.098	2
567	35_38507	putative 26S proteasome regulatory particle triple-A ATPase subunit3	29.5.11.20	protein.degradation.ubiquitin.proteasom	0.36 (48h)	0.282	2
390	35_5860	S-locus-like receptor protein kinase	30.2.24	signalling.receptor kinases.S-locus glycoprotein like	-0.6 (120h)	0.297	2
322	35_5591	hydroxyproline-rich glycoprotein family protein	35.1.41	not assigned.no ontology.hydroxyproline rich proteins	**-0.92 (120h)**	0.255	2
367	35_1354	stress responsive protein	35.1.41	not assigned.no ontology.hydroxyproline rich proteins	-0.7 (120h)	0.289	2
412	35_41150	germin-like protein (Germin-like 12) (Germin-like 8)	n.a.	n.a.	0.81 (48h)	0.011	2
694	35_32881	n.a.	n.a.	n.a.	-0.12 (120h)	0.183	2
398	35_99	glyceraldehyde-3-phosphate dehydrogenase	1.01.01.01	PS.lightreaction.photosystem II.LHC-II	**-0.85 (120h)**	0.060	3
287	35_1092	Xylose isomerase	3.5	minor CHO metabolism.others	**-1.04 (120h)**	0.016	3
177	35_15726	Alpha-galactosidase	3.8.2	minor CHO metabolism.galactose.alpha-galactosidases	**-1.37 (120h)**	0.038	3
349	35_14099	Fructose-bisphosphate aldolase cytoplasmic isozyme	4.07	glycolysis.aldolase	**-0.86 (120h)**	0.016	3
476	35_14099	Fructose-bisphosphate aldolase cytoplasmic isozyme	4.07	glycolysis.aldolase	-0.47 (120h)	0.055	3
217	35_14505	Triosephosphate isomerase, cytosolic	4.08	glycolysis.TPI	**-0.87 (120h)**	0.010	3
680	35_14451	Enolase 2	4.12	glycolysis.enolase	-0.26 (120h)	0.205	3
625	35_1714	Dihydrolipoyl dehydrogenase	8.1.01.03	TCA / org. transformation.TCA.pyruvate DH.E3	-0.56 (120h)	0.034	3
451	35_14632	Vacuolar ATP synthase subunit E	9.1.2	mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear	**-0.86 (120h)**	0.116	3
619	35_14632	Vacuolar ATP synthase subunit E	9.1.2	mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear	-0.48 (48h)	0.030	3
310	35_1022	putative ATP synthase delta' chain, mitochondrial precursor	9.9	mitochondrial electron transport / ATP synthesis.F1-ATPase	**-1.1 (120h)**	0.020	3
511	35_1801	Alpha-L-arabinofuranosidase/beta-D-xylosidase isoenzyme ARA-I	10.6.2	cell wall.degradation.mannan-xylose-arabinose-fucose	-0.59 (120h)	0.022	3
296	35_259	glycine dehydrogenase	13.2.5.2	amino acid metabolism.degradation.serine-glycine-cysteine group.glycine	-0.62 (120h)	0.010	3
206	35_14824	HvGER2a	20.2.99	stress.abiotic.unspecified	**-1.2 (120h)**	0.079	3
214	35_48123	HvGER2a	20.2.99	stress.abiotic.unspecified	**-1.39 (120h)**	0.014	3

227	35_14981	Salt stress root protein RS1	20.2.99	stress.abiotic.unspecified	**-1.02 (120h)**	0.007	3
586	35_22900	adenylate kinase	23.4.3	nucleotide metabolism.phosphotransfer and pyrophosphatases.uridylate kinase	-0.19 (120h)	0.290	3
592	35_40361	peroxidase 6	26.12	misc.peroxidases	-0.59 (48h)	0.026	3
589	35_17129	SEC14 cytosolic factor family protein	28.99	DNA.unspecified	-0.29 (120h)	0.146	3
377	35_17049	Putative Subtilisin homologue	29.5.01	protein.degradation.subtilases	-0.62 (120h)	0.014	3
971	35_15109	Proteasome subunit alpha type-7-A	29.5.11.20	protein.degradation.ubiquitin.proteasom	-0.19 (72h)	0.124	3
184	35_19417	trehalose-6-phosphate synthase	30.2.24	signalling.receptor kinases.S-locus glycoprotein like	**-1.36 (120h)**	0.026	3
312	35_14382	14-3-3-like protein A	30.7	signalling.14-3-3 proteins	**-0.9 (120h)**	0.047	3
546	35_8676	Lysine and histidine specific transporter	34.3	transport.amino acids	-0.61 (120h)	0.023	3
380	35_4322	Putative GTPase activating protein	35.2	not assigned.unknown	**-0.94 (120h)**	0.018	3
435	35_14519	Putative diphosphonucleotide phosphatase	35.2	not assigned.unknown	-0.74 (120h)	0.034	3
70	35_5689	hydrolase, alpha/beta fold family domain containing protein	n.a.	n.a.	**-1.99 (120h)**	0.038	3
174	35_3542	dirigent-like protein	n.a.	n.a.	**-0.92 (24h)**	0.012	3
237	35_19575	expressed protein	n.a.	n.a.	-0.63 (120h)	0.016	3
522	35_2078	Glucose-1-phosphate adenylyltransferase	2.1.2.01	major CHO metabolism.synthesis.starch.AGPase	0.58 (24h)	0.008	4
495	35_960	NADP-dependent malic enzyme	8.2.10	TCA / org. transformation.other organic acid transformations.malic	0.73 (24h)	0.005	4
187	35_368	S-adenosylmethionine synthetase 1	13.1.3.4	amino acid metabolism.synthesis.aspartate family.methionine	**1.5 (48h)**	0.002	4
340	35_366	S-adenosylmethionine synthetase 1	13.1.3.4	amino acid metabolism.synthesis.aspartate family.methionine	**1.09 (48h)**	0.003	4
151	35_50935	HvGER4	20.2.99	stress.abiotic.unspecified	**1.39 (48h)**	0.002	4
463	35_16425	KH domain containing protein	27.3	RNA.regulation of transcription	**0.85 (48h)**	0.009	4
485	35_4140	ABA responsive element binding factor 3	27.3.35	RNA.regulation of transcription.bZIP transcription factor family	0.72 (48h)	0.003	4
286	35_18209	Subtilisin-like serine proteinase	29.5.01	protein.degradation.subtilases	0.73 (48h)	0.010	4
556	35_18209	Subtilisin-like serine proteinase	29.5.01	protein.degradation.subtilases	0.51 (72h)	0.027	4
575	35_1864	Putative aminoacylase	29.5.11.03	protein.degradation.ubiquitin.E2	0.52 (48h)	0.009	4
456	35_17334	WD domain, G-beta repeat domain containing protein	33.99	development.unspecified	0.44 (120h)	0.092	4
830	35_15780	Putative high-affinity potassium transporter	34.15	transport.potassium	0.49 (48h)	0.011	4
421	35_15997	protein phosphoglycerate mutase	35.1	not assigned.no ontology	0.7 (24h)	0.005	4
231	35_10955	F-box domain containing protein	35.2	not assigned.unknown	**1.13 (72h)**	0.004	4
683	35_22985	sulfotransferase domain containing protein	n.a.	n.a.	0.23 (72h)	0.079	4
277	35_49	glyceraldehyde-3-phosphate dehydrogenase	4.09	glycolysis.glyceraldehyde 3-phosphate dehydrogenase	-0.83 (48h)	0.015	5
118	35_15021	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	4.11	glycolysis.phosphoglycerate mutase	**-0.91 (48h)**	0.329	5
407	35_15021	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	4.11	glycolysis.phosphoglycerate mutase	-0.44 (48h)	0.263	5
657	35_14444	Enolase 2	4.12	glycolysis.enolase	-0.27 (48h)	0.193	5

653	35_15073	Putative aconitate hydratase, cytoplasmic	8.1.03	TCA / org. transformation.TCA.aconitase	-0.22 (48h)	0.145	5
447	35_429	aminomethyltransferase	13.2.5.2	amino acid metabolism.degradation.serine-glycine-cysteine group.glycine	-0.66 (24h)	0.014	5
216	35_15495	Putative stress-induced protein sti1	20	stress	**-1.22 (48h)**	0.023	5
123	35_14824	HvGER2a	20.2.99	stress.abiotic.unspecified	**-1.26 (48h)**	0.008	5
195	35_14824	HvGER2a	20.2.99	stress.abiotic.unspecified	**-1.22 (48h)**	0.004	5
92	35_25207	UBA/TS-N domain containing protein	29.05.11	protein.degradation.ubiquitin	**-1.54 (48h)**	0.005	5
951	35_524	Putative Subtilisin homologue	29.5.01	protein.degradation.subtilases	-0.22 (12h)	0.277	5
62	35_17794	Fe-S metabolism associated domain containing protein	35.2	not assigned.unknown	-0.72 (48h)	0.144	5
404	35_41618	Xet3 protein	35.2	not assigned.unknown	-0.51 (48h)	0.057	5
976	35_47029	Bzip-like transcription factor-like protein	35.2	not assigned.unknown	0.13 (24h)	0.320	5
626	35_9734	expressed protein	n.a.	n.a.	0.3 (24h)	0.091	5

Table 27: Transcript-protein links of the 4 categories according to chapter 6.4. They are ordered firstly according to their statistical significance (sections), secondly according o their regulation pattern (cluster) and third according to their biological function. I) regulated at transcript and protein level; II) regulated at transcript level; III) regulated at protein level; IV) regulated nor at transcript nor at protein level; First Row: HarvEST:Barley-ID; second row: Function of the ID; third row: Biological classification through MapMan binning; fourth row to seventh row: highest regulation level (log_2-transformed) and the corresponding time point in RNA and protein level, respectively; eighth row: cluster the protein spot belongs to according to Figure 35 to Figure 38 in chapter 6.4.1. n.s.: not significant, therefore no value for the regulation level.

Regulated both at transcript and at protein level (section I)

HarvEST-ID	Putative function	Biological function	mRNA		Protein		Cluster
35_13900	ribulose 1,5-bisphosphate carboxylase activase isoform 1 [Hordeum vulgare subsp. vulgare]	photosystem	-1,5	(24 h)	-0,8	(120 h)	1
35_1092	xylose isomerase [Hordeum vulgare subsp. vulgare] xylose isomerase	minor CHO metabolism	-1,3	(120 h)	-1,0	(120 h)	1
35_15726	alpha-galactosidase [Hordeum vulgare subsp. vulgare]	minor CHO metabolism	-0,7	(48 h)	-1,4	(120 h)	1
35_784	pyruvate decarboxylase [Oryza sativa (japonica cultivar-group)]	fermentation	-0,8	(120 h)	-0,5	(72 h)	1
35_259	glycine decarboxylase P subunit [x Tritordeum sp.]	amino acid metabolism	-1,6	(24 h)	-0,6	(120 h)	1
35_429	Aminomethyltransferase	amino acid metabolism	-1,5	(24 h)	-0,7	(24 h)	1
35_14824	HvGER2a	stress	-2,5	(120 h)	-1,2	(48 h)	1
35_14981	plasma membrane polypeptide -like [Oryza sativa (japonica cultivar-group)] Salt-stress root protein RS1	stress	-1,9	(120 h)	-1,0	(120 h)	1
35_14824	HvGER2a	stress	-2,5	(120 h)	-1,3	(48 h)	1
35_48123	HvGER2a	stress	-2,5	(120 h)	-1,4	(120 h)	1
35_40361	peroxidase 6 [Triticum monococcum]	miscellaneous	-1,8	(72 h)	-0,6	(48 h)	1
35_14519	diphosphonucleotide phosphatase [Oryza sativa (japonica cultivar-group)]	not assigned	-1,7	(120 h)	-0,7	(120 h)	1
35_702	PR-1a pathogenesis related protein (Hv-1a) [Hordeum vulgare subsp. vulgare]	stress	2,9	(72 h)	2,4	(120 h)	2
35_704	pathogenisis-related protein 1.1 [Triticum aestivum]	stress	2,8	(120 h)	2,5	(120 h)	2
35_50935	HvGER4	stress	4,0	(24 h)	1,4	(48 h)	2
35_16041	peroxidase [Oryza sativa (japonica cultivar-group)] TPA: class III peroxidase 50 precursor	miscellaneous	2,3	(24 h)	3,1	(120 h)	2
35_14091	glutathione transferase F5 [Triticum aestivum]	miscellaneous	2,9	(24 h)	0,3	(48 h)	2
35_13856	peroxidase 10 [Triticum monococcum]	miscellaneous	3,4	(24 h)	-0,3	(48 h)	2
35_15785	sorbitol dehydrogenase [Oryza sativa (japonica cultivar-group)]	minor CHO metabolism	-0,6	(24 h)	0,8	(120 h)	3
35_784	pyruvate decarboxylase [Oryza sativa (japonica cultivar-group)]	fermentation	-0,8	(120 h)	1,4	(120 h)	3
35_48714	stearoyl-acyl-carrier protein desaturase [Oryza sativa (japonica cultivar-group)]	lipid metabolism	-0,8	(120 h)	0,7	(120 h)	3
35_16425	KH domain protein [Oryza sativa (japonica cultivar-group)]	RNA	-1,0	(24 h)	0,9	(48 h)	3
35_4982	Protein At2g41620 nucleoporin interacting component family protein [Arabidopsis thaliana]	protein	-1,1	(120 h)	3,8	(120 h)	3
35_49	GAPDH	glycolysis	0,8	(120 h)	-0,8	(48 h)	4
35_802	cytosolic 6-phosphogluconate dehydrogenase [Zea mays]	OPP	1,3	(24 h)	0,5	(48 h)	4
35_1714	dihydrolipoamide dehydrogenase precursor [Oryza sativa (japonica cultivar-group)]	TCA / org. transform.	1,1	(120 h)	-0,6	(120 h)	4
35_1124	citrate synthase [Oryza sativa]	TCA / org. transform.	0,8	(24 h)	1,6	(120 h)	4

35_1022	ATP synthase delta' chain, mitochondrial precursor [Oryza sativa (japonica cultivar-group)]	mitochondrial electron transport / ATP synthesis	0,8	(120 h)	-1,1	(120 h)	4
35_368	S-adenosylmethionine synthetase 1 n=21 Tax=Magnoliophyta RepID=METK1_HORVU	amino acid metabolism	1,4	(120 h)	1,5	(48 h)	4
35_366	AdoMet synthase 1 [Hordeum vulgare subsp. vulgare]	amino acid metabolism	1,4	(120 h)	1,1	(48 h)	4
35_14470	HSP70	not assigned	1,2	(12 h)	1,3	(120 h)	4
35_15997	phosphoglycerate mutase-like protein:::OSJNBa0068L06.8 [Oryza sativa (japonica cultivar-group)] OSJNBa0068L06.8 [Oryza sativa (japonica cultivar-group)]	not assigned	2,0	(120 h)	0,7	(24 h)	4
35_3277	mitochondrial chaperonin-60 [Oryza sativa (japonica cultivar-group)]	not assigned	1,7	(120 h)	0,8	(24 h)	4
35_23963	PHD finger protein-related [Arabidopsis thaliana]		1,9	(120 h)	0,8	(120 h)	4

Regulated at transcript level (section II)

HarvEST-ID	function	SuperBIN	mRNA		Protein		Cluster
35_14824	HvGER2a	stress	-2,5	(120 h)	n.s.		1
35_14824	HvGER2a	stress	-2,5	(120 h)	n.s.		1
35_14981	plasma membrane polypeptide -like [Oryza sativa (japonica cultivar-group)] Salt-stress root protein RS1	stress	-1,9	(120 h)	n.s.		1
35_14824	HvGER2a	stress	-2,5	(120 h)	n.s.		1
35_14630	Endo-beta-1,3-1,4 glucanase II; Lichenase	miscellaneous	-1,5	(120 h)	n.s.		1
35_14519	diphosphonucleotide phosphatase [Oryza sativa (japonica cultivar-group)]	not assigned	-1,7	(120 h)	n.s.		1
35_14519	diphosphonucleotide phosphatase [Oryza sativa (japonica cultivar-group)]	not assigned	-1,7	(120 h)	n.s.		1
35_49	GAPDH	glycolysis	0,8	(120 h)	n.s.		2
35_13856	peroxidase 10 [Triticum monococcum]	miscellaneous	3,4	(24 h)	n.s.		2
35_99	Precursor of CP29, core chlorophyll a/b binding (CAB) protein of photosystem II (PSII) [Hordeum vulgare subsp. vulgare] chlorophyll a/b-binding protein	photosystem	-1,0	(120 h)	n.s.		3
35_99	Glyceraldehyde 3-phosphate dehydrogenase	photosystem	-1,0	(120 h)	n.s.		3
35_14635	23kDa oxygen evolving protein of photosystem II [Triticum aestivum] photosystem II oxygen-evolving complex protein 2 precursor	photosystem	-0,8	(72 h)	n.s.		3
35_13769	Fructose-bisphosphate aldolase class-I [Oryza sativa (japonica cultivar-group)]	photosystem	-1,1	(24 h)	n.s.		3
35_15726	alpha-galactosidase [Hordeum vulgare subsp. vulgare]	minor CHO metabolism	-0,7	(48 h)	n.s.		3
35_15770	1,4-benzoquinone reductase	lipid metabolism	-1,3	(120 h)	n.s.		3
35_259	glycine decarboxylase P subunit [x Tritordeum sp.]	amino acid metabolism	-1,6	(24 h)	n.s.		3
35_259	glycine decarboxylase P subunit [x Tritordeum sp.]	amino acid metabolism	-1,6	(24 h)	n.s.		3
35_1530	TCP-1/cpn60 chaperonin family protein [Oryza sativa (japonica cultivar-group)]	protein	-0,7	(120 h)	n.s.		3
35_14174	protein actin, putative, expressed	cell	-0,6	(24 h)	n.s.		3
35_1354	stress responsive protein	not assigned	-1,3	(120 h)	n.s.		3
35_12756	DUF869 domain containing protein	not assigned	-0,6	(120 h)	n.s.		3
35_360	chaperonin 60 beta precursor	photosystem	-1,4	(120 h)	n.s.		4
35_36841	cytoplasmic malate dehydrogenase [Zea mays] Malate dehydrogenase	TCA / org. transform.	-1,2	(120 h)	n.s.		4

35_14602	alanine aminotransferase [Oryza sativa (indica cultivar-group)]	amino acid metabolism	-1,1	(120 h)	n.s.	4
35_14477	eukaryotic translation initiation factor 5A1 [Triticum aestivum]	protein	-1,4	(120 h)	n.s.	4
35_14174	protein actin, putative, expressed	cell	-0,6	(24 h)	n.s.	4
35_17334	66 kDa stress protein [Oryza sativa (japonica cultivar-group)]	development	-0,6	(24 h)	n.s.	4

Regulated at protein level (section III)

HarvEST-ID	function	SuperBIN	mRNA		Protein		Cluster
35_14099	fructose-bisphosphate aldolase [Oryza sativa (japonica cultivar-group)]	glycolysis	n.s.		-0,9	(120 h)	1
35_14505	Triosephosphate isomerase, cytosolic (TIM) [Hordeum vulgare]	glycolysis	n.s.		-0,9	(120 h)	1
35_14632	YLP [Hordeum vulgare]	mitochondrial electron transport / ATP synthesis	n.s.		-0,5	(48 h)	1
35_1801	alpha-L-arabinofuranosidase/beta-D-xylosidase isoenzyme ARA-I [Hordeum vulgare]	cell wall	n.s.		-0,6	(120 h)	1
35_15495	stress-induced protein sti1 [Oryza sativa (japonica cultivar-group)]	stress	n.s.		-1,2	(48 h)	1
35_728	GPX12Hv, glutathione peroxidase-like protein [Hordeum vulgare subsp. vulgare]	redox	n.s.		-1,1	(120 h)	1
35_15567	C13 endopeptidase NP1 precursor [Hordeum vulgare]	protein	n.s.		-0,4	(24 h)	1
35_25207	UBA/TS-N domain containing protein	protein	n.s.		-1,5	(48 h)	1
35_14382	14-3-3 protein homologue [Hordeum vulgare subsp. vulgare] 14-3-3 protein homolog - barley	signalling	n.s.		-0,9	(120 h)	1
35_8676	amino acid transporter-like protein 2 [Arabidopsis thaliana] lysine and histidine specific transporter, [Arabidopsis thaliana]	transport	n.s.		-0,6	(120 h)	1
35_4322	GTPase activating protein [Oryza sativa (japonica cultivar-group)]	not assigned	n.s.		-0,9	(120 h)	1
35_16233	NAD-dependent isocitrate dehydrogenase [Oryza sativa (japonica cultivar-group)]	TCA / org. transform.	n.s.		0,6	(24 h)	2
35_15429	succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]	TCA / org. transform.	n.s.		1,6	(120 h)	2
35_16117	fumarase; fumarate hydratase [Arabidopsis thaliana]	TCA / org. transform.	n.s.		0,9	(120 h)	2
35_16117	fumarase; fumarate hydratase [Arabidopsis thaliana]	TCA / org. transform.	n.s.		1,6	(120 h)	2
35_960	NADP malic enzyme [Oryza sativa (japonica cultivar-group)]	TCA / org. transform.	n.s.		1,3	(120 h)	2
35_960	NADP malic enzyme [Oryza sativa (japonica cultivar-group)]	TCA / org. transform.	n.s.		0,7	(24 h)	2
35_16286	Chaperonin CPN60-2, mitochondrial precursor (HSP60-2)	protein	n.s.		0,8	(120 h)	2
35_15429	succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]	TCA / org. transform.	n.s.		0,6	(120 h)	3
35_15143	aspartate aminotransferase [Oryza sativa (japonica cultivar-group)]	amino acid metabolism	n.s.		1,3	(120 h)	3
35_453	dnaK-type molecular chaperone HSP70	stress	n.s.		1,4	(120 h)	3
35_14172	actin [Elaeis oleifera]	cell	n.s.		1,0	(120 h)	3
35_1190	manganese superoxide dismutase [Triticum aestivum]	redox	n.s.		0,4	(24 h)	4
35_739	glutathione s-transferase [Arabidopsis thaliana]	miscellaneous	n.s.		0,9	(48 h)	4
35_2125	subtilisin-like proteinase [Oryza sativa (japonica cultivar-group)]	protein	n.s.		0,7	(120 h)	4
35_3176	alpha 3 subunit of 20S proteasome [Oryza sativa (japonica cultivar-group)]	protein	n.s.		1,0	(120 h)	4
35_41150	COP1 [Oryza sativa subsp. indica]	protein	n.s.		0,8	(48 h)	4

35_15178	vacuolar proton-ATPase [Hordeum vulgare subsp. vulgare]	transport	n.s.	1,1	(120 h)	4
35_15178	vacuolar proton-ATPase [Hordeum vulgare subsp. vulgare]	transport	n.s.	1,2	(120 h)	4

Regulated neither at transcript nor at protein level (section IV)

HarvEST-ID	function	SuperBIN	mRNA	Protein	Cluster
35_14099	fructose-bisphosphate aldolase [Oryza sativa (japonica cultivar-group)]	glycolysis	n.s.	n.s.	1
35_14444	enolase [Oryza sativa (japonica cultivar-group)]	glycolysis	n.s.	n.s.	1
35_14444	enolase [Oryza sativa (japonica cultivar-group)]	glycolysis	n.s.	n.s.	1
35_14451	enolase [Oryza sativa (japonica cultivar-group)]	glycolysis	n.s.	n.s.	1
35_15073	Aconitate hydratase [Oryza sativa (japonica cultivar-group)]	TCA / org. transform.	n.s.	n.s.	1
35_15073	Aconitate hydratase [Oryza sativa (japonica cultivar-group)]	TCA / org. transform.	n.s.	n.s.	1
35_14148	thaumatin-like protein TLP5 [Hordeum vulgare]	stress	n.s.	n.s.	1
35_15245	Endo-beta-1,3-1,4 glucanase II; Lichenase	miscellaneous	n.s.	n.s.	1
35_1200	mitochondrial processing peptidase alpha-chain precursor [Dactylis glomerata]	protein	n.s.	n.s.	1
35_38507	26S proteasome regulatory particle triple-A ATPase subunit3 [Oryza sativa (japonica cultivar-group)]	protein	n.s.	n.s.	1
35_14505	Triosephosphate isomerase, cytosolic (TIM) [Hordeum vulgare]	glycolysis	n.s.	n.s.	2
35_15021	'2,3-bisphosphoglycerate-independent phosphoglycerate mutase' [Oryza sativa (japonica cultivar-group)]	glycolysis	n.s.	n.s.	2
35_15021	'2,3-bisphosphoglycerate-independent phosphoglycerate mutase' [Oryza sativa (japonica cultivar-group)]	glycolysis	n.s.	n.s.	2
35_15925	F1F0-ATPase inhibitor protein [Oryza sativa (japonica cultivar-group)]	mitochondrial electron transport / ATP synthesis	n.s.	n.s.	2
35_16286	Chaperonin CPN60-2, mitochondrial precursor (HSP60-2)	protein	n.s.	n.s.	2
35_524	gypsy type transposon, [Oryza sativa (japonica cultivar-group)]	protein	n.s.	n.s.	2
35_22985	flavonol 4'-sulfotransferase [Oryza sativa (japonica cultivar-group)]		n.s.	n.s.	2
35_1801	alpha-L-arabinofuranosidase/beta-D-xylosidase isoenzyme ARA-I [Hordeum vulgare]	cell wall	n.s.	n.s.	3
35_14172	actin [Elaeis oleifera]	cell	n.s.	n.s.	3
35_14172	actin [Elaeis oleifera]	cell	n.s.	n.s.	3
35_17794	quinolinate synthetase A-related:::unknown protein [Arabidopsis thaliana]	not assigned	n.s.	n.s.	3
35_14100	fructose-bisphosphate aldolase [Oryza sativa (japonica cultivar-group)]	glycolysis	n.s.	n.s.	4
35_14505	Triosephosphate isomerase, cytosolic (TIM) [Hordeum vulgare]	glycolysis	n.s.	n.s.	4
35_15021	'2,3-bisphosphoglycerate-independent phosphoglycerate mutase' [Oryza sativa (japonica cultivar-group)]	glycolysis	n.s.	n.s.	4
35_14632	YLP [Hordeum vulgare]	mitochondrial electron transport / ATP synthesis	n.s.	n.s.	4
35_15350	mitochondrial ATP synthase precursor [Triticum aestivum]	mitochondrial electron transport / ATP synthesis	n.s.	n.s.	4
35_14510	ascorbate peroxidase [Hordeum vulgare]	redox	n.s.	n.s.	4
35_14510	ascorbate peroxidase [Hordeum vulgare]	redox	n.s.	n.s.	4
35_861	dehydroascorbate reductase [Triticum aestivum]	redox	n.s.	n.s.	4

35_43946	dehydroascorbate reductase [Triticum aestivum]	redox	n.s.	n.s.	4
35_976	translational elongation factor Tu [Oryza sativa (japonica cultivar-group)]	protein	n.s.	n.s.	4
35_15109	proteasome alpha subunit [Oryza sativa (japonica cultivar-group)]	protein	n.s.	n.s.	4
35_15178	vacuolar proton-ATPase [Hordeum vulgare subsp. vulgare]	transport	n.s.	n.s.	4
35_693	ARP2/3 regulatory protein subunit PIRP::PIROGI [Arabidopsis thaliana]	not assigned	n.s.	n.s.	4
35_15968	transcription factor APFI [Oryza sativa (japonica cultivar-group)]	not assigned	n.s.	n.s.	4
35_19141	leucine-rich repeat family protein [Arabidopsis thaliana]	not assigned	n.s.	n.s.	4

11. Curriculum vitae

Name:	Ernst Michael Metzner
Date of birth:	02.12.1978
Place of birth:	Dettelbach
Nationality:	German

Work experience and postgraduate studies

12/2005-05/2011	PhD Student in the Applied Biochemistry Group and the Transcriptome Analysis Group, Leibniz Institute of Plant Genetics and Crop Plant Research Gatersleben
02/2005-10/2005	Scientific expert, RSG Bad Kissingen

Education

11/1998-08/2004	Diploma study of Biology at the Julius-Maximilians-Universität Würzburg
12/2003-08/2004	Diploma thesis: „Mykorrhiza-induzierte Kalium-Kanäle und Kalium-Transporter in Medicago truncatula“ at the institute of molecular plant physiology and biophysics (Julius-Maximilians-Universität Würzburg)
10/2002-12/2002	Practical experience at the Instituto de Investigationes Farmaco Bioquímicas in La Paz, Bolivia
1995-1997	Celtis-Gymnasium Schweinfurt
1987-1995	Gymnasium Franken-Landschulheim Schloss Gaibach

12. Presentations and posters

12.1. Presentations

Metzner, E. (2006): "Transcriptome and proteome dynamics of pathogen-attacked barley epidermis". 2nd ISC IPK student conference Gatersleben, 29th May-1st June.

Metzner, E., Leitner, A. (2008): ”Proteome and transcriptome dynamics in pathogen-attacked barley epidermis”. Network meeting, IAMO, Halle/S., 28th March.

Metzner, E. (2008): "Transcriptome and Proteome changes of barley to reveal potential important biological functions in the interaction with *Bgh*“. Summer school “On the Evolution of Plant Pathogen Interactions: from Principles to Practice”, Wageningen, Netherlands, 17th-19th June.

Metzner, E. (2008): "Transcriptome and proteome analysis of barley infected by powdery mildew“. 4th Plant Science Student Conference, Gatersleben, 2nd July.

Metzner, E. (2008): "Proteome and transcriptome dynamics of barley epidermis infected by Powdery mildew“. Tritigen, Albena, Bulgaria, 22nd-24th September.

Metzner, E. (2009): "Proteome and transcriptome dynamics of barley epidermis infected by powdery mildew“. 5th Plant Science Student Conference, Leibniz Instutitute of Plant Biochemistry, Halle/S, 24th June.

12.2. Posters

Kaspar, S., Metzner, E., Matros, A., Klukas, C., Schreiber, F., Schweizer, P. & Mock, H.-P. (2007): "Proteome analysis of barley epidermal tissue“. IPK Institut’s day, Gatersleben, 22nd-23rd October.

Metzner, E., Mock, H.-P. & Schweizer, P. (2007): "Transcriptome and proteome dynamics of pathogen-attacked barley epidermis“. 3rd Plant Science Student Conference PSSC, Leibniz Instutitute of Plant Biochemistry, Halle/S, 05th-08th June

Metzner, E., Mock, H.-P. & Schweizer, P. (2008): "Changes in barley epidermal tissue within infection process with *Blumeria graminis*". PlantGEM, Albena, Bulgaria, 20th-22nd September.

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14. Declaration

Hereby, I declare that all the work presented in this dissertation is my own, carried out solely with the help of the literature and the aids cited. I do apply for a "Doktorgrade" the first time.

Ich erkläre hiermit, dass ich mich mit der vorliegenden wissenschaftlichen Arbeit erstmals um die Erlangung des Doktorgrades bewerbe. Ich erkläre, die Arbeit selbstständig verfasst und keine anderen als die angegebenen Quellen und Hilfsmittel benutzt und die den benutzten Werken wörtlich oder inhaltlich entnommenen Stellen als solche kenntlich gemacht habe.

Halle, Mai 2011

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