Plant-virus interactions : role of virus- and host-derived small non-coding RNAs during infection and disease

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Abbreviations

Viruses acronyms	*Full name*	***Genus***
BCMV	*Bean common mosaic virus*	***Potyvirus***
BCTV	*Beet curly top virus*	***Curtovirus***
BMV	*Brome mosaic virus*	***Bromovirus***
CalCuV	*Cabbage leaf curl virus*	***Begomovirus***
CaMV	*Cauliflower mosic virus*	***Caulimovirus***
CMV	*Cucumber mosaic virus*	***Cucumovirus***
CymRDV	*Cymbidium ringspot virus*	***Potexvirus***
CymRSV	*Cymbidium ringspot tombusvirus*	***Tombusvirus***
LMV	*Lettuce mosaic virus*	***Potyvirus***
ORMV	*Oilseed rape mosaic virus*	***Potyvirus***
PepGMV	*Pepper golden mosaic virus*	***Begomovirus***
PVX	*Potato virus X*	***Potexvirus***
PVY	*Potato virus Y*	***Potyvirus***
SMV	*Soybean mosaic virus*	***Potyvirus***
TBRV	*Tomato black ring virus*	***Nepovirus***
TEV	*Tobacco etch virus*	***Potyvirus***
TMV	*Tobacco mosaic virus*	***Tobamovirus***
ToMV	*Tomato mosaic virus*	***Tobamovirus***
ToRSV	*Tomato ringSpot Virus*	***Nepovirus***
TRV	*Tobacco rattle virus*	***Tobravirus***
TSV	*Tobacco streak Virus*	***Ilarvirus***
TuMV	*Turnip mosaic virus*	***Potyvirus***
TuYV	*Turnip yellows virus*	***Polerovirus***
TVMV	*Tobacco vein mottling virus*	***Potyvirus***

Word abbreviations	
(β-ME)	β-mercaptoethanol
ABA	Abscisic acid
ADF3	Actin depolymerization factor 3
AGO	ARGONAUTE
AtSuc:GFP	*Arabidopsis thaliana* sucrose symporter promoter driving expression of GFP
BAK1	BRASSINOSTEROID INSENSITIVE 1-ASSOCIATED KINASE 1
BG	β-(1.3)-Glucanase
BiFC	Biomolecular fluorescence complementation
BLOS2	Biogenesis of lysosome-related organelles complex 1 subunit 2
Ca^{2+}	Calcium
CalS	Callose synthase
casiRNA	*cis*-acting small interfering RNA

CB60G	Calmodulin-binding protein 60G
CDPK	Calcium-dependent protein kinase
CFDA	Carboxyfluorescein diacetate
ChIP	Chromatin immuno-precipitation
CI	Cylindrical inclusion protein
CIP	Calf intestinal phosphatase
ConTR01	Conditional TuMV resistance 01
COPI	Coat protein complex I
CP	Coat protein
Ct	Cycle threshold
DAMP	Damage-associated molecular pattern
DCL	Dicer-like
DE	Differential expression
DEAD-box	DExD/H-Box RNA helicase
DI	Defective interfering
DM	Mock-treated *B. napus* cv. Drakkar
dsRBD	dsRNA-binding domain
dsvRNA	double-stranded viral RNA
DT	Virus-treated *B. napus* cv. Drakkar
DTX47	DETOXIFICATION 47
DUB	Deubiquitinylation protein
DUF283	Domain of unknown function 283
eEF1A	Eukaryotic elongation factor 1A
EF2	Elongation factor 2
eIF	Eukaryotic initiation factor
eIFiso4E	Eukaryotic-Initiation factor isoform 4E
EIN5	ETHYLENE-INSENSITIVE 5
ER	Endoplasmic reticulum
ERES	ER exit site
ERF RAP 2	Ethylene-responsive transcription factor RELATED TO APETALA 2
ETI	Effector-triggered immunity
FC	Fold change
FLS2	FLAGELLIN SENSING 2
GFP	Green fluorescent protein
GO	Gene ontology
hc-siRNA	Heterochromatic small interfering RNA
HcPro	Helper component proteinase
HD-ZIPIII	Class-III homeodomain-leucine zipper
HEN1	HUA ENHANCER 1
HMW	High molecular weight RNA
HR	Hypersensitive resistance
hsRNA	Host-derived siRNA
JA	Jasmonic acid
L8z2	*A. thaliana* line 8z2

LCD	La-motif-containing domain
LMW	Low molecular weight
LRD	Leucine-rich domain
LRR	Leucine-rich repeat
MAMP	Microbe-associated molecular pattern
MAP	Microtubule-associated protein
MAPK	Mitogen-activated protein kinase
met-tRNA	Methionine-tRNA
miRNA	microRNA
MP	Movement protein
mRNAseq	mRNA sequencing
MT	Microtubule
MTA	Material transfer agreement
MTase	Methyltransferase domain
NAC60	NAC domain-containing protein 60
NB	Nucleotide binding
NB-LRR	Nucleotide-binding leucine-rich repeat
NGS	Next-generation sequencing
NIMIN-2	NIM1-INTERACTING 2
OAS	Origin of assembly
P3N-PIPO	Trans-frame N-terminus fused P3-PIPO
PABP	Poly(A)-binding protein
PAGE	Polyacrylamide gel electrophoresis
PAMP	Pathogen-associated molecular pattern
PARE	Parallel analysis of RNA ends
PAREseq	mRNA degradome profiling using PARE sequencing
PAZ	Piwi/Argonaute/Zwille
PD	Plasmodesmata
PDCB	PLASMODESMATA CALLOSE BINDING
PDLP	PLASMODESMATA-LOCATED PROTEIN
phasiRNA	Phased small interfering RNA
PIPO	Pretty interesting potyviral ORF
PM	Plasma membrane
POL IV	RNA polymerase VI
PP2A2	PHLOEM PROTEIN 2-LIKE A2
PPR	Pentatricopeptide repeat
pri-miRNA	Primary microRNA precursor
PRR	Pattern recognition receptor
PTGS	Post-transcriptional gene silencing
PTI	Pattern-triggered immunity
PVIP	VPg-interacting protein
QTL	Quantitative trait loci
RACE	Rapid amplification of cDNA ends
rasiRNA	Repeat-associated small interfering RNA

RdDM	RNA-directed DNA methylation
RDRP, RDR	RNA-dependent RNA polymerase
REn	Replication enhancer
retr01	Resistance 01
RIN	RNA integrity number
RIN4	RPM1-INTERACTING PROTEIN 4
RISC	RNA-induced silencing complex
RLK	Receptor-like kinase
RLP	Receptor-like protein
RNAi	RNA-interference
ROS	Reactive oxygen species
rpm	Reads per million
SA	Salicylic acid
SAM	Shoot apical meristem
SAR	Systemic acquired resistance
SCL	SCARECROW-LIKE
SDS	Sodium dodecyl dulphate
SEL	Size exclusion limit
SERK1	SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE 1
SGS3	SUPPRESSOR OF GENE SILENCING 3
siRNA	Small interfering RNA
SNARE	Soluble N-ethyl-maleimide-sensitive-factor attachment protein receptor
SNP	Single nucleotide polymorphism
SPL	SQUAMOSA PROMOTER-BINDING-LIKE
SR	Serine/arginine-rich
sRNA	Small RNA
sRNAseq	Small RNA sequencing
ssRNA	Single-stranded RNA
ST	Symptom Type
TAO1	TARGET OF AVRB OPERATION 1
TAP	Tobacco acid pyrophosphatase
tasiRNA	trans-acting small interfering RNA
TEMED	N,N,N',N'- tetramethyl-1-,2-diaminométhane
TF	Transcription factor
TGS	Transcriptional gene silencing
TM	Mock-treated *B. napus* cv. Tanto
TOE2	TARGET OF EAT 2
TOM	TOBAMOVIRUS MULTIPLICATION
TrAP	Transcription activator protein
tRNA	Transfer RNA
TT	Virus-treated *B. napus* cv. Tanto
TuMV-GFP	GFP-tagged TuMV
UGPase	UDP-GLUCOSE PYROPHOSPHORYLASE
UTR	Untranslated region

VIGS	Virus-induced gene silencing
VPg	Genome-linked viral protein
VRC	Viral replication complex
vRNA	Viral RNA
vsiRNA	Virus-derived small interfering RNA
VSR	Viral suppressor of RNA silencing
XRN4	EXORIBONUCLEASE 4
Y2H	Yeast two-hybrid

General introduction

Virus infection in plants depends on the ability of viruses to replicate and spread their genomes from cell to cell and systemically through plasmodesmata (PD) and the connected phloem. Viruses encode only a limited set of proteins and depend on molecular mechanisms provided by their hosts for propagation. Numerous studies have illuminated cellular membrane- and cytoskeleton-associated mechanisms as well as specific host factors involved in virus replication and movement. However, our knowledge about gene regulatory processes that orchestrate virus infection remains limited. Viruses may employ mechanisms to manipulate host gene expression to ensure that defenses are minimized and resources required for viral replication are maximized, whereas the cell may counteract through opposite mechanisms that maximize defenses and minimize the resources for the virus. This battle between the virus and its host is best illustrated by a gene regulatory process known as post-transcriptional gene silencing (PTGS, also known as 'RNA silencing' or 'RNA interference' [RNAi]). During infection, PTGS functions as an important antiviral defense response that controls viral accumulation by targeting the viral RNA for cleavage or translational repression. Viruses, in turn, have evolved specific effector proteins (Viral Suppressor of RNA silencing, VSR) that interfere with the RNA silencing pathway at specific steps and thereby enhance their propagation. As the antiviral RNA silencing pathway shares components with other transcriptional and post-transcriptional RNA silencing pathways playing a role in the regulation of gene expression, viruses may apply their VSRs also for the modulation of host gene expression. In addition, while cellular alterations are most commonly orchestrated by virus-encoded proteins, viruses may manipulate their hosts also by using their virus genome-encoded small RNAs as RNA effectors. This strategy is best illustrated by DNA viruses belonging to the Herpesviridae family, which were found to encode between 1 and 14 miRNAs (Cox and Sullivan 2014). While some of these miRNAs engage in the regulation of viral gene expression during the viral replication cycle, other miRNAs act as mimics for endogenous cellular miRNAs and modulate the levels of host gene transcripts, thereby creating an environment more amenable to replication and/or latency (Gottwein et al. 2007; Kincaid et al. 2012). A similar strategy has also been evolved by certain plant pathogenic fungi. Similar to the DNA viruses in mammals, these fungi use small RNAs derived from their own genome to hijack the host RNA silencing pathway to target the expression of host defense genes and thereby enhance host susceptibility (Suffert et al. 2011; Weiberg et al. 2013). Based on these examples, it can be expected that also plant viruses have evolved such RNA effectors. Although most plant viruses are RNA viruses that replicate in the cytoplasm and, therefore, do not encode miRNAs (Aguado and tenOever 2018),

the virus-derived small interfering RNAs (vsiRNAs) that are produced during antiviral silencing may have the potential to target host genes. In addition, given the sheer amount of small RNAs produced by RNA silencing pathways in plants, it may also be conceivable that plants themselves encode small RNAs with homology to viruses that infect them and that are part of the arms arsenal available to plants to control their viruses. Certain reported cases in *Arabidopsis* literature, illustrate that vsiRNAs and VSRs have the potential to interfere with host processes required for normal host cellular function and development (Kasschau et al. 2003; Qi et al. 2009; Jay et al. 2011; Hu et al. 2011; Avina-Padilla et al. 2015). Therefore, it appears likely that such mechanisms may be involved in the triggering of virus-induced diseases in cultivated plants, which cause losses worth of 20-60 billion US$ worth in yield annually (Randles and Ogle 1997; Sastry and Zitter 2014).

This thesis project was aimed to address the role of host- and virus-encoded small RNAs in plant:virus interactions during virus spread in infected tissues and in determining host disease. The thesis is organized in three different chapters:

Chapter I introduces the viruses *Oilseed rape mosaic virus* (ORMV) and *Turnip mosaic virus* (TuMV) that were used as pathogens in the present thesis, describes cellular mechanisms involved their cell-to-cell movement and presents a review article (Pitzalis and Heinlein 2017) describing viral movement mechanisms and the potential role of endoplasmic reticulum:plasma membrane (ER:PM) contact sites and associated proteins during infection.

Chapter II describes the results of a project applying Next Generation Sequencing (NGS) approaches to the analysis of virus infection and which led to important new insights into the functions of host- and virus derived-small RNAs in regulating their specific RNA targets during the spread of infection in leaves. This work was applied to local sites of infection caused by an economically important virus (TuMV) within the leaves of rapeseed (*Brassica napus,* 'Canola'), an economically important oilseed crop species. Thus, the obtained results suggest important new gene targets for crop breeding.

Finally, work described in **Chapter III** revealed the genetic and functional basis of disease symptoms and symptoms recovery observed in Arabidopsis plants infected with ORMV. Symptoms recovery relates to the ability of plants to recover from an established viral disease. Understanding this phenomenon is a key to important mechanisms that support plant health and the survival of plants in natural environments full of viruses. The results of this study were published in the journal *Nature Plants* (Kørner et al. 2018) and led to the important discovery that recovery does not require the silencing inhibition of the virus but is associated with the achievement of a tolerant state in which the virus and the host can coexist without disease. The work led to the identification of RNA silencing

pathway genes and of a mechanism by which plants use these RNA silencing pathway genes for the robust production of secondary small interfering RNAs (siRNAs) as well as intercellular communication and systemic regulation to use these siRNAs to downregulate the virus-encoded VSR in physiological sink tissues and thereby achieve the tolerant state in newly emerging leaves (Kørner et al. 2018).

Together, the results described in these three chapters of the thesis provide novel insights into the regulatory mechanisms involved in the interaction of viruses with their hosts and which have the potential to indicate novel strategies for crop protection.

Chapter I: Virus infection and mechanisms involved in disease

1. Introduction

Viruses use different mechanisms for plant-to-plant transmission (Hosford 1967; Hull 2009) and for their propagation within the infected plants (Verchot-Lubicz et al. 2010; Niehl and Heinlein 2011; Agbeci et al. 2013; Laliberte and Zheng 2014; Liou et al. 2015; Schoelz et al. 2016; Pitzalis and Heinlein 2017). As plants are sessile, viruses usually depend on fungi, nematodes, protists, or insects as vectors for transmission. Moreover, several viruses, for example the tobamoviruses (e.g. *Tobacco mosaic virus*, TMV), are mechanically transmitted by wind, water, soil, seeds, as well as by humans through virus-infected plant handling and processing (Hull 2009).

Work described in this thesis involved experimentation with TMV and ORMV as well as with TuMV, a potyvirus. Whereas TMV and ORMV are mechanically transmitted, TuMV is transmitted by several aphid species. Once a virus has been transmitted and entered a host cell, it is uncoated and translated to produce proteins required for replication, cell-to-cell movement, viral counter-defense (e.g. a Viral Suppressor of RNA silencing, VSR), virion assembly and transmission.

1.1. Plasmodesmata

Viruses cause systemic plant infection by cell to cell movement through PD and long-distance movement via the phloem (Deom et al. 1987; Wolf et al. 1989; Heinlein 2002; Lucas et al. 2006; Guenoune-Gelbart et al. 2008; Benitez-Alfonso et al. 2010; Sager and Lee 2014; Heinlein 2015). The PD are symplastic channels in the cell walls through which adjacent plant cells communicate. They are about 50 nm in diameter and provide a direct passageway for the intercellular transport of diffusible factors (e.g. metabolites, certain hormones, ions), and macromolecules (Lucas and Wolf 1993; Kragler et al. 1998; Cantrill et al. 1999; Heinlein 2002; Heinlein and Epel 2004; Kragler 2013). The PD provide both cytoplasmic as well as membrane continuity between adjacent cells. The plasma membrane (PM) delimits the PD channel against the surrounding cell wall and a thin tubule of the endoplasmic reticulum (ER) (the “desmotubule”) extends through the center of the channel (Ding et al. 1992)(see Figure 1). The cytoplasmic space (also referred as the “cytoplasmic sleeve”) between the PM and the desmotubule is thought to represent the major pathway for intercellular molecular trafficking. The size of this space determines the size exclusion limit (SEL) of PD, thus the maximal size of molecules that can be transported though this channel. The PD SEL is under tight

control and dynamically regulated to control PD permeability. Thus, in allowing multicellularity, the PD also act as important gatekeepers permitting or restricting the cell-to-cell trafficking of informational macromolecules in response to intrinsic and extrinsic signals, thereby playing a crucial role during plant development and immunity against pathogen attack (Lee and Lu 2011; Lee 2014; Sager and Lee 2014; Tilsner et al. 2016; Brunkard and Zambryski 2017; Cheval and Faulkner 2018; Sager and Lee 2018).

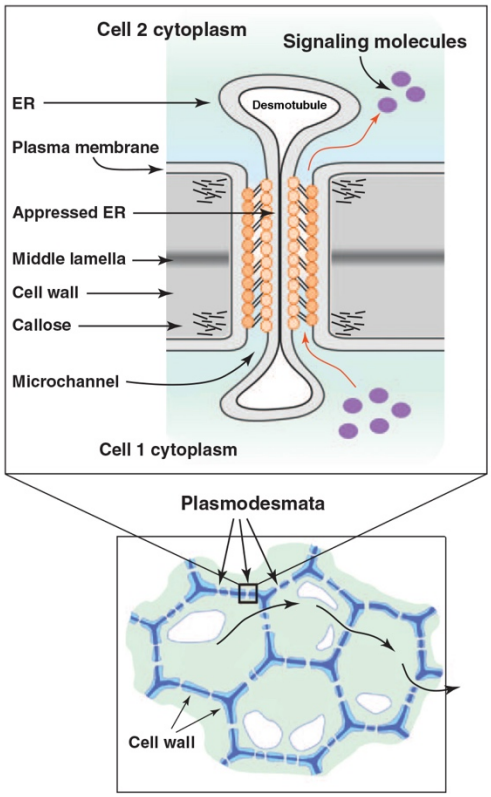

Figure 1: Schematic illustration of plasmodesmata (PD)
Ultrastructure and cell-to-cell trafficking of diffusible signalling molecules (modified from Lee et al. 2011). The SEL of PD is regulated primarily by the degree of callose deposition in the cell wall near the PD neck regions. In addition, the SEL may also be regulated by proteins that tether the ER to the plasma membrane (orange-yellow spheres and short rods) and may regulate the size of the cytoplasmic sleeve between these membranes.

The mechanism regulating PD SEL is not clearly resolved today, but appears to involve alterations in Calcium (Ca^{2+}) levels, the redox state within the cell, and phytohormones. The major mechanism by which the SEL is increased or decreased involves the deposition and degradation of callose in the cell walls around the neck regions of PD (Olesen and Robards 1990; Iglesias and Meins 2000; Bucher et al. 2001; Radford and White 2001). The deposition of callose by callose-synthase (CalS) reduces PD SEL by moving the PM closer to the desmotubule (Olesen and Robards 1990; Simpson et al. 2009;

Gui et al. 2014; Grison et al. 2015), whereas the degradation of callose deposits by β-(1.3)-Glucanase (BGs) increases the PD SEL by increasing the size of the cytoplasmic sleeve (Iglesias and Meins 2000; Bucher et al. 2001; Radford and White 2001; Levy et al. 2007). Upstream to callose synthesis, Ca^{2+}, has been found to regulate intercellular communication by closure of PD in staminal hairs of *Setcreasea purpurea* (Tucker 1990). During PD closure, Ca^{2+} may function as a putative regulator of CalS (Andrawis et al. 1993). Callose deposition at PD is also induced by the accumulation of reactive oxygen species (ROS), which are known to take part in regulating development and pathogen responses (Bolwell et al. 2002; Pitzschke et al. 2006; Torres 2010). ROS accumulation increases callose deposition at PD (Benitez-Alfonso and Jackson 2009; Benitez-Alfonso et al. 2010) and influences the abundance of Ca^{2+} (Bolwell et al. 2002; Foreman et al. 2003). It seems that a ROS-Ca^{2+} activation system is able to trigger callose deposition at PD but the underlying mechanism is still unknown (Benitez-Alfonso et al. 2011; De Storme and Geelen 2014; Tilsner et al. 2016). PD are associated with numerous proteins implicated in regulating PD permeability such as different receptor kinases involved in the sensing of pathogens and developmental signals, the PD-Located Protein (PDLP) family of proteins, and callose-binding proteins (PDCBs). Moreover, the desmotubule may be associated with Ca^{2+}-sensitive proteins that tether the desmotubule to the PM and control the size of the cytoplasmic sleeve by varying tether length in response to Ca^{2+} (Tilsner et al. 2016; Sager and Lee 2018).

1.2. TMV and ORMV infection

ORMV, also known as *Youcai mosaic virus* or *Chinese rape mosaic virus* (Aguilar et al. 1996), is an Arabidopsis-infecting tobamovirus. Compared to TMV, the 3' Untranslated Region (UTR) of ORMV is longer than in TMV and differences exist between the viruses in the overlap of movement protein (MP) and coat protein (CP) open reading frames (ORFs). *Tobamoviruses* have been classified into different subgroups according the sequence location of their origin of virion assembly (OAS) (Fukuda et al. 1981; Gibbs 1986). The OAS is the viral RNA region used to target and initiate particle assembly by forming aggregates of CP in the form of discs leading to the formation of virions. ORMV and TMV differ in the host range in which they cause disease. Whereas ORMV efficiently infects and causes symptoms in *Cruciferae* plants such as *Arabidopsis*, TMV and the highly homologous *Tomato mosaic virus* (ToMV) efficiently infect and cause symptoms in *Solanacea* plants such as tobacco, tomato and pepper (Melcher 2003; Cai et al. 2009). TMV and ORMV have a positive-sense ssRNA genome of about 6300 nt in length. The viral RNA is capped at the 5' end and forms a tRNA-like structure at the

3’ end (see Figure 2). The TMV and ORMV genomes contain three major ORFs. The first ORF encodes two subunits of the replicase (126k/183k for TMV; 125k/182k for ORMV), whereby the larger subunit is produced by translational read-though of an amber-stop codon. The shorter protein contains 5’ methyltransferase and helicase domains, whereas the longer protein in addition contains an RNA-dependent RNA polymerase (RDR) domain (Beier et al. 1984).

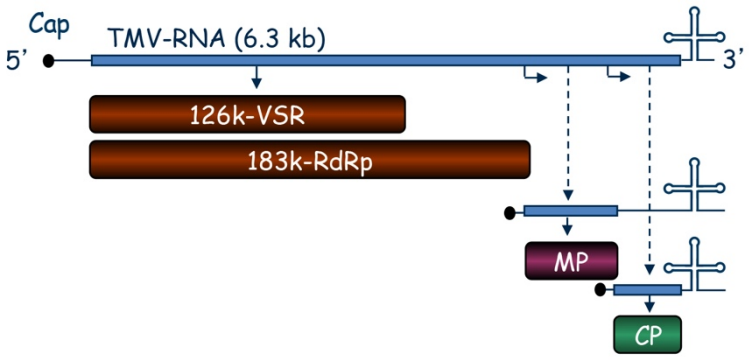

Figure 2: The RNA genome of TMV and encoded proteins
The RNA genome of TMV is caped at its 5’ end and forms a tRNA-like structure at the 3’ end. The RNA encodes four proteins, the large 183 kDa (183k-RdRp) and small 126 kDa (126k-VSR) subunits of the replicase, the 30 kDa movement protein (MP), and the 17.5 kDa coat protein (CP). The large 183 kDa replicase subunit is produced by read-through of an amber stop codon that terminates the translation of the short subunit. The two replicase subunits interact *in vivo*. Whereas the large subunit contains an RNA-dependent RNA polymerase domain and is sufficient for replication of viral RNA, the small subunit has Viral Suppressor of RNA silencing (VSR) activity and increases viral replication efficiency.

The small replicase subunit has VSR activity and suppresses antiviral RNA silencing by sequestration of small RNA duplexes, thereby interfering with small RNA loading into the RNA-induced silencing complex (RISC) (Kubota et al. 2003; Ding et al. 2004; Csorba et al. 2007; Vogler et al. 2007). The replicase subunits are translated from the viral RNA that enters the cell whereas the MP and CP encoded by the two remaining ORFs are translated during viral replication from sub-genomic RNAs. The 30 kDa MP is required for the cell-to-cell spread of the virus and was the first protein known to facilitate virus movement (Deom et al. 1987; Holt and Beachy 1991). Studies on this prototype MP revealed that this protein targets PD and triggers an increase in the PD SEL (Wolf et al. 1989). This activity has been correlated with a reduction in callose-deposition in the PD neck regions (Ueki et al. 2010) and may involve a direct or indirect interaction of MP with a callose-degrading BG (Zavaliev et al. 2013). The MP interacts with ER membranes and microtubules (MTs) (Heinlein et al. 1995; Heinlein et al. 1998; Reichel and Beachy 1998; Ashby et al. 2006; Ferralli et al. 2006; Fujiki et al. 2006; Peiro et al. 2014) and plays fundamental roles in the anchoring of viral replication complexes (VRCs) at distinct, MT-associated, cortical ER sites (Boyko et al. 2000a,b; Niehl et al. 2013b; Peña

and Heinlein 2013; Heinlein 2015). According to current models, which are also described in the attached review by Pitzalis and Heinlein (2017), infection starts when the mechanically transmitted virion is uncoated and the free viral RNA (vRNA) binds to the ER via it's 5'CAP (Christensen et al. 2009). Subsequently, the replicase, which is translated from the vRNA, binds to the 5'UTR for replication (Kawamura-Nagaya et al. 2014). The MP, which then also becomes translated, anchors the ER-associated VRCs to MT. The MT-associated ER sites (also called "cMERs") are proposed to be equivalent to cortical sites of MT-associated, stable ER proposed to function as hubs for membrane trafficking and exchange/delivery of membrane cargo (Niehl et al. 2013b; Peña and Heinlein 2013; Heinlein 2015), through which the VRCs may recruit membranes and host factors. For example, the host proteins TOBAMOVIRUS MULTIPLICATION (TOM) 1, 2a and 3 are involved in the formation of VRCs (Ishibashi et al. 2010). Detachment of the VRCs allows their trafficking along the ER, which is continuous through PD (Ding et al. 1992) and provides a direct route for cell-to-cell movement. MP-containing VRC particle movements along the ER occur in a stop-and-go fashion and are guided by MT (Boyko et al. 2007; Niehl et al. 2013b; Peña and Heinlein 2013; Niehl et al. 2014; Heinlein 2015). The ER membrane is tightly associated with actin filaments and numerous studies demonstrated the role of myosin motor proteins in ER motility and the transport of organelle and membrane cargo along the ER-actin network (Boevink et al. 1998; Avisar et al. 2008; Peremyslov et al. 2008; Prokhnevsky et al. 2008; Sparkes et al. 2008; Sparkes et al. 2009; Ueda et al. 2010; Griffing et al. 2017). Consistently, it was shown that the intra-and intercellular movement of the MP-containing particles along the ER as well as the intercellular spread of TMV infection depend on actin and specific class VIII and class XI myosins (Wright et al. 2007; Sambade et al. 2008; Harries et al. 2009; Hofmann et al. 2009; Amari et al. 2014). Thus, VRC movement occurs along the ER while MTs initially anchor VRCs at specific ER sites and guide their movements along the ER-actin network (Niehl et al. 2013b; Peña and Heinlein 2013; Heinlein 2015; Pitzalis and Heinlein 2017). However, not all of the early VRCs are mobile. Instead most of them remain stationary and grow over time to become viral factories.

During these later stages of infection also the 17.5 kDa CP is produced and encapsidates replicated vRNA. The rod-shaped TMV particle contains 2130 CP subunits (Dunigan et al. 1988) and provides stable protection of the viral genome until the virus is mechanically transmitted to a new host. The CP is dispensable for viral cell-to-cell movement but plays a yet unknown role in the long distance spread of infection via the vascular phloem (Saito et al. 1990; Holt and Beachy 1991; Hilf and Dawson 1993).

The MP of ORMV associates with MT-associated ER sites like the MP of TMV and is proposed to support ORMV movement by mechanisms similar to the model described for TMV above. However, unlike the MP of TMV, the MP of ORMV is expressed at a lower level and does not accumulate in viral factories and along MTs to a level seen with the MP of TMV (Niehl et al. 2014). The observation that the MP of TMV accumulates in viral factories and along MT before it is degraded during late stages of infection was a motivation for studies showing that the MP is a MT-associated protein (MAP) able to bind directly to the MT surface (Ashby et al. 2006) and for addressing the mechanism of MP turnover. During infection, the MP becomes polyubiquitylated and degraded by the 26S proteasome (Reichel and Beachy 2000). Interestingly, the MP fraction that accumulates along MTs during late infection is not ubiquitinylated (Ashby et al. 2006). Consistently, it was shown that the degradation of MP depends on CELL DIVISION CYCLE 48 (CDC48), a triple A (AAA) ATPase (these ATPases are machines that use ATP hydrolysis to exert force on macromolecules for unfolding and translocation) that interacts with MP and extracts the protein from the ER (Niehl et al. 2012). CDC48 substrates are de-ubiquitinylated before extraction from the ER and become re-ubiquitinylated before degradation by the proteasome (Ernst et al. 2011; Tsai and Weissman 2011). This suggest the hypothesis, that ubiquitinylated MP is de-ubiquitinylated and then extracted from MT-associated ER-localized virus factories by CDC48. Once present in high amounts in the cytoplasm, the MP aligns along MT according to its intrinsic MAP activity before it is re-ubiquitinylated and degraded by the proteasome (Niehl et al. 2012; Niehl et al. 2013a). More recent studies indicate that the MP is also a target of deubiquitinylation (DUB) enzymes (Niehl et al. unpublished), which is consistent with this model.

1.3. TuMV infection

TuMV belongs to the Potyvirus family, the second largest plant virus family after *Geminiviridae* (Ivanov et al. 2014), and is among the most damaging plant viruses worldwide (Tomlinson 1987; Nguyen et al. 2013; Yasaka et al. 2015). Potyviruses give rise to different types of symptoms such as yellow mosaic patterning, leaf tip necrosis, or the formation of black necrotic ring spots, and can cause growth inhibition and strong seed losses (Tomlinson et al. 1970 ; Hull 2014; Kenyon et al. 2014). TuMV infects a wide range of 318 species in 156 genera of 43 families. Among the hosts are wild and cultivated *Brassica* species, in which it causes different types of symptoms, seed losses, and even plant death (Tomlinson et al. 1970; Walsh and Tomlinson 1985; Tomlinson 1987; Edwardson and Christie 1991; Moreno and Fereres 2012).

The filamentous viral particles of potyviruses contain a positive-sense, single-stranded (ss)RNA genome of 10 kb. Following transmission and entry of the filamentous virions into the host cell by the stylet of aphids, the vRNA is uncoated and translated into a single polyprotein (Carrington et al. 1989; Nicolas and Laliberté 1992), which is then processed into eleven proteins by virus-encoded proteolytic cleavage. The vRNA carries a genome-linked viral protein (VPg) at its 5' end and is 3' poly-adenylated. Processing of the virus-encoded polyprotein leads to the production of the Protease P1, the Helper Component Proteinase (HcPro), the Protease P3, the two 6 kDa proteins 6K1 and 6K2, a cylindrical inclusion CI protein, the VPg, the cysteine protease NIa-Pro, the nuclear inclusion b (NIb; RDR), the CP, and the P3-"Pretty Interesting Potyviral ORF" Protein (P3-PIPO), which is produced as a trans-frame fusion to the amino terminus of P3 (P3N-PIPO) (Vijayapalani et al. 2012). Seven of the nine polyprotein cleavages are processed by NIa-Pro, whereas the two remaining cleavages occur by cis-cleavage by the P1 and HcPro proteases at their own C-terminal end (Carrington et al. 1989; Verchot et al. 1992). The vRNA is used for both translation and replication but the exact process of replication in potyviruses is still unclear. P3, VPg, Nla-Pro, Nlb, 6K2, Hc-Pro, vRNA and double-stranded viral RNA (dsvRNA) are present in VRCs (Schaad et al. 1997; Li et al. 1997; Haldeman-Cahill et al. 1998; Fellers et al. 1998; Thivierge et al. 2008; Cui et al. 2010; Wei et al. 2010a; Ala-Poikela et al. 2011). Translation and replication are closely linked and occur in association with the ER membrane (Martin et al. 1995; Schaad et al. 1997). During infection the ER produces organelle-like vesicles that function as compartments for potyviral replication (Wei et al. 2010a). Each vesicle originates from a single translated genome into which viral proteins are also translated (Cotton et al. 2009). The replication protein 6K2 is found also in larger, perinuclear compartments derived from the ER (Schaad et al. 1997). These structures are functionally linked to the production of 6K2 vesicles and their trafficking to the cortical ER via transvacuolar strands (Grangeon et al. 2012). The 6K2 protein was shown to colocalize with the ER exit site (ERES) proteins Sar1, Sec23, and Sec24. Disruption of the two major coating machineries involved in ER-Golgi trafficking, the coat protein complex I (COPI) and COPII, led to reduced accumulation of 6K2 at ERES, smaller sizes of infection foci on leaves, and reduced TEV-GFP fluorescence, thus supporting the importance of ER-Golgi trafficking for efficient infection (Wei and Wang 2008). After accumulation at ERES and transport via the COPI/II Golgi early secretory pathway, the VRC-containing vesicles are transported along actin microfilaments to chloroplasts using a myosin XI-K and XI-2-dependent mechanism (Wei et al. 2010a; Agbeci et al. 2013). The presence of these vesicles at chloroplasts is indicated by the observation of 6K2 protein aggregates and the formation of membrane

invaginations at the chloroplast envelope (Cotton et al. 2009; Wei et al. 2010a). Experiments involving the down-regulation of Syp71, a component of the Soluble N-ethyl-maleimide-sensitive-factor Attachment protein REceptor (SNARE) complex involved in vesicle-membrane fusion, indicated that the fusion of the VRC-containing vesicles with the chloroplast membrane is essential for successful viral infection (Wei et al. 2013). Thus, potyvirus replication occurs within chloroplasts as well as on the ER. While the formation of the ER-derived vesicles and their trafficking to chloroplast is not absolutely essential for virus replication, the formation and trafficking of the vesicles is nevertheless necessary for virus cell-to-cell movement. Yeast two-hybrid and co-immunoprecipitation experiments coupled to deletion mapping and site-specific mutagenesis indicated that the formation of the mobile ER-derived vesicles require the N-terminal soluble domain of 6K2, which interacts with Sec24a, a COPII coatomer component. Mutations in the 6K2 N-terminus that interfere with vesicle formation still allowed virus replication but abolished virus cell-to-cell movement. Moreover, TuMV systemic movement was delayed in an Arabidopsis mutant defective in Sec24a (Jiang et al. 2015). Thus, the motile ER-derived 6K2 vesicles contribute to the distribution and propagation of viral replication centers in the infected cell and are essential for transporting the infectious viral RNA into the neighboring cells (see Figure 3). Consistent with their role in virus movement, the 6K2 vesicles are also transported to PD and can move cell-to-cell (Grangeon et al. 2013). However, the mechanism of movement through the PD is still unclear. Unlike most other viruses, potyviruses do not encode a designed MP. Instead many viral proteins have been reported to have MP-related functions. HcPro and the CP can increase the SEL of PD (Rojas et al. 1997). In addition, CP and the cylindrical inclusion (CI) protein are required for virus intercellular movement (Dolja et al. 1994; Dolja et al. 1995; Carrington and Whitham 1998). CI was shown to associate with PD and to produce conspicuous conical structures that extend through PD (Rodriguez-Cerezo et al. 1997; Roberts et al. 1998). CI targets PD through interaction with P3N-PIPO (Wei et al. 2010b), which itself is targeted to the PM through an interaction with the host protein PCaP1 (Vijayapalani et al. 2012). However, how the 6K2-associated vesicles that contain the viral RNA interact with these potyvirus-induced movement structures for movement through PD is still not known. Nevertheless, a recent study demonstrated that the intercellular movement of 6K2 vesicles depends on the interaction of 6K2 with CI. Thus, CI structures at PD may act as a docking point for 6K2 vesicles destined for intercellular transport (Movahed et al. 2017).

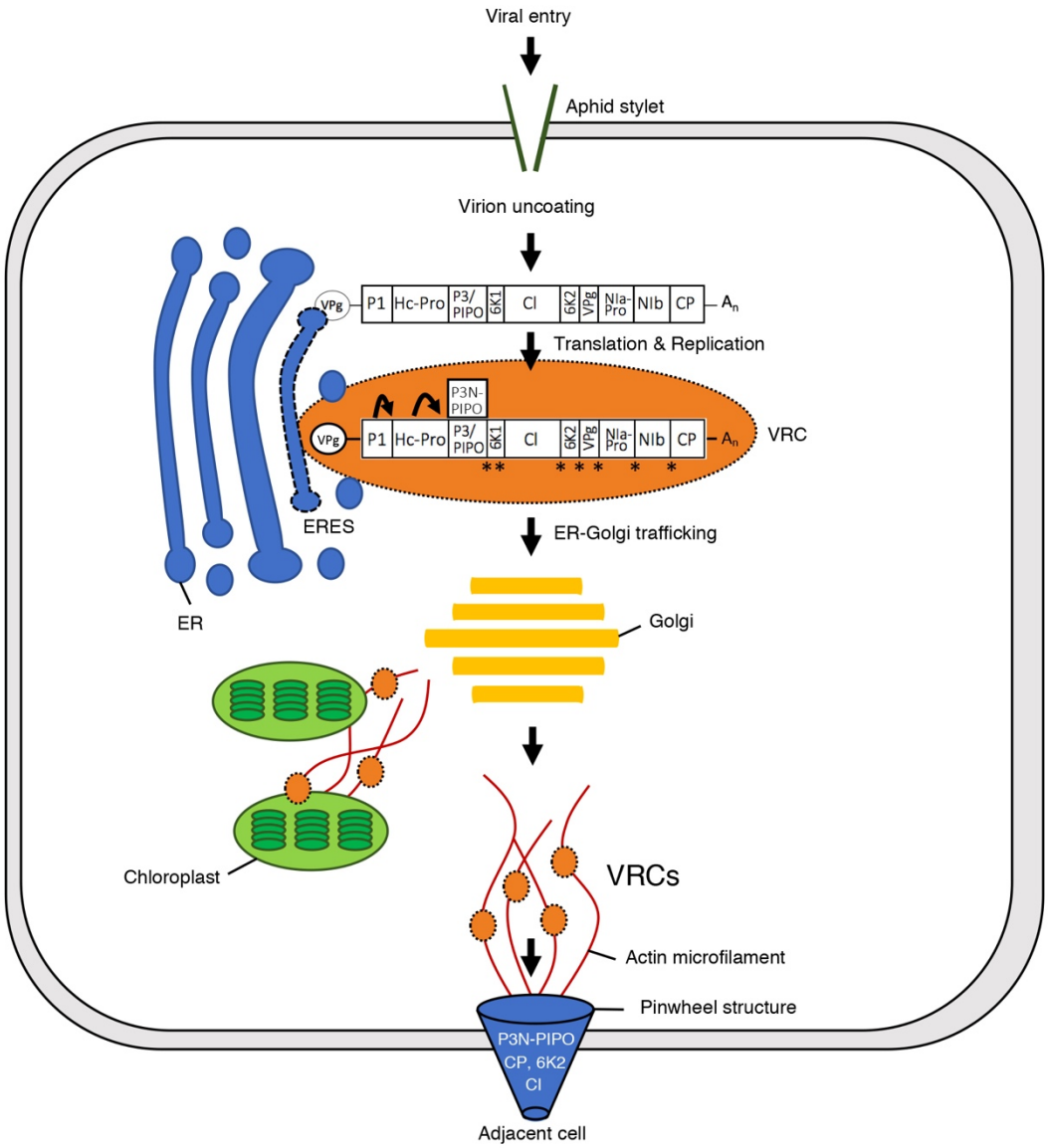

Figure 3: Potyvirus infection
The filamentous particle is uncoated, and the viral RNA is translated and replicated. Viral replication and production of viral replication complexes (VRCs) take place close to the ER at ER-exit sites (ERES). VRC-containing vesicles move along actin microfilaments to chloroplasts and also to pinwheel structures formed at PD for cell-to-cell movement.

Although viruses are generally believed to move their genomes over long-distances into other leaves via the phloem, GFP-tagged 6K2 vesicles were observed in xylem vessels as well as in phloem sieve elements of infected plants (Wan et al. 2015). The authors suggest that the 6K2 vesicles may enter into immature xylem vessels and replicate in the cytoplasm and then move upward in the plant before programmed cell death occurs and the xylem becomes a hollow vessel. It would be interesting to see by which mechanism the vesicles can enter and exit the xylem. It has been observed that membrane-impermeant fluorophores such as carboxyfluorescein-diacetate (CFDA) and also much larger Texas Red-labeled dextran (10 kD) molecules unload from xylem via the xylem

vessel-xylem parenchyma pit membranes, potentially by endocytosis (Botha et al. 2008). Such pathway may also be used by TuMV, since 6K2 was observed in xylem parenchyma cells. Several other cases where virus particles or components were found in xylem have been reported previously (Andrianifahanana et al. 1997; Opalka et al. 1998; French and Elder 1999; Ding et al. 2001; Verchot et al. 2001; Moreno et al. 2004; Betti et al. 2012; Manabayeva et al. 2013). Thus, several systems are available that may ultimately challenge the stronghold model that systemic virus movement occurs strictly via the phloem.

The attached review article by Pitzalis and Heinlein (2017) provides an overview about the major pathways used by plant viruses for their cell-to-cell movement. As described in detail above, TMV exemplifies a pathway that targets PD and spreads into adjacent cells by movement of mobile VRCs along the ER-actin network. Since this network is continuous through PD into adjacent cells, this type of movement may not require a specific docking mechanism at PD but certainly depends on a MP or other proteins with MP-related functions able to modify the gating function of PD in order to allow VRC movement through the channel. This pathway of virus movement is in contrast to the pathway used by viruses that move cell-to-cell in the form of whole virion particles. To allow whole virion movement, some of these viruses were shown to cause strong structural alterations in PD structure by replacing the centrally located desmotubule by a tubule-like structure assembled by viral MP. Tubule assembly by these “tubule-forming” viruses and their intercellular movement depend on members of the PDLP family that act as docking point for tubule-forming MPs at PD (Amari et al. 2011). To allow virion movement through the tubule, the tubule-guided movement mechanism usually depends on an interaction between MP and CP. The tubule-guided movement mechanism also depends on the secretory pathway which is required for targeting PDLP to PD. As described above, potyviruses use a special mechanism for movement that neither fits to the tubule-guided mechanism, nor to the non-tubule-guided mechanism used by TMV.
The review article by Pitzalis and Heinlein (2017) continues to further discuss the roles of the ER-Golgi secretory pathway in virus infection and then focusses on the roles of myosin motor proteins, particularly on class VIII myosins. These plant-specific motor proteins were shown to be essential for efficient TMV movement and function in the targeting of the MP to PD (Amari et al. 2014). Myosin VIII proteins also have been localized to PD (Reichelt et al. 1999; Baluska et al. 2001; Golomb et al. 2008; Haraguchi et al. 2014). The potential function of myosin VIII is discussed together with the potential roles of the synaptotagmin SYT1/SYTA. This protein is a target of MP (Lewis and

Lazarowitz 2010; Uchiyama et al. 2014; Levy et al. 2015) and is supposed to act as a tether protein that links the ER to the PM at ER-PM contact sites. Both class VIII myosin and SYT1/SYTA are discussed as potential components of ER-PM contact sites within PD and at the cortical ER sites at which viruses like TMV set up their replication complexes. The PD is proposed to contain ER-PM contact sites because of the very close apposition of ER and PM along the length of the PD channel (Tilsner et al. 2016). Although the SEL of PD is regulated by deposition and removal of callose in the PD neck regions, the SEL may also be regulated by myosin VIII and synaptotagmin as ER-embedded proteins that may tether the ER to the PM and determine the size of the cytoplasmic sleeve by regulating their tether length. Hypothetical models are presented to explain how MP could modify the PD SEL through interaction with these tether proteins. The two mechanisms are not mutually exclusive and may instead complement each other in regulating PD. Whereas tether contraction may allow rapid and short-term PD regulation to control trafficking of individual molecules (e.g. virus) between individual cells or groups of cells, the enzymatic changes in callose levels in the cell walls surrounding the PD may allow the plant to change PD conductivity over the longer term and thus to respond more persistently to developmental or environmental cues. The observation that the MP of TMV increases the SEL of PD only transiently during infection (Oparka et al. 1997) and also the reported molecular interaction of MP with SYT1 (Lewis and Lazarowitz 2010; Uchiyama et al. 2014; Levy et al. 2015; Ishikawa et al. 2018; Yuan et al. 2018) support the model that MP alters PD SEL through manipulating SYT1 tether length in PD. The regulation of PD SEL by membrane tethering proteins is in agreement with the ability of PD to regulate their SEL in response to Ca^{2+} (Tucker and Boss 1996) as Ca^{2+} concentration influences tether length as shown for mammalian Syt-1 (Fernandez-Busnadiego et al. 2015). Thus, MP may change the SEL of PD through direct interactions with the tether proteins or rather indirectly by causing changes in the local concentration of Ca^{2+} within the channel.

The article then continues to discuss the possibility that ER-PM contact sites may represent the primary target of viral MP. This idea comes from the fact that ER-PM contact sites are associated with ER-actin and MT, thus cellular components that also coincide at the cortical MT-associated ER sites at which TMV forms mobile VRCs with the help of MP. It is proposed that the MP may target (i) SYT1 localized at MT-associated ER sites to establish mobile VRCs and (ii) SYT1 localized at PD to modify SYT1 tether length to allow the mobile VRCs to move through PD. However, this model is highly speculative and must be addressed by further experimentation before conclusions can be

drawn. Nevertheless, a recent publication supports this model by showing that SYTA binds to the N-terminal region of MP and stabilizes the interaction of MP with PD (Yuan et al. 2018).

PITZALIS AND HEINLEIN 2017. THE ROLES OF MEMBRANES AND ASSOCIATED CYTOSKELETON IN PLANT VIRUS REPLICATION AND CELL-TO-CELL MOVEMENT. J EXP BOT 69, 117-132.

Chapter II: RNA silencing and role of small RNAs

1. Introduction

Virulence comes from the Latin "*virulentus*" and associates "*vīrus*" (poisonous liquid) and "*ulentus*" (full of). It defines the capacity of a pathogen to accumulate in the host. To do so, the host must provide the cellular mechanisms and the host factors the pathogen requires for propagation. The lack of any such factors reduces the ability of the pathogen to be virulent and is at the basis of host recessive resistance. In addition, the pathogen must have evolved the capacity to efficiently interact with these host mechanisms and host factors. Moreover, to propagate efficiently, the pathogen should be able to overcome the host defense mechanisms. To protect themselves against invading pathogens, hosts have evolved the ability to recognize conserved molecules associated with the presence of pathogens (e.g. with pathogen-recognition receptors) and to raise different defense layers such as Pattern-Triggered Immunity (PTI) and the expression of defense-related genes, or RNA silencing. To break these barriers, pathogens have evolved effector proteins that interfere with these defense pathways by various mechanisms. In some hosts this has led to the evolution of resistance genes triggering Effector Triggered Immunity (ETI), which finally often initiate a hypersensitive response upon recognition of the pathogen effector, or of its activity, leading to the death of the infected cell. In these hosts, the pathogen has lost its virulence and is "avirulent", and the gene of the pathogen that encodes the effector, which is recognized by the protein encoded by the host resistance gene, is referred to as the "avirulence gene" ("Gene-for-gene" resistance).

In comparison to bacteria and fungi, viruses encode only a limited number of proteins (see Chapter I). Most of them associate with host mechanisms for replication as well as for intercellular and systemic spread of their infectious genomes, whereas other specific proteins act as effectors to suppress host defense. Only since recently, it is known that plant viruses can trigger PTI (Kørner et al. 2013; Niehl et al. 2016; Nicaise and Candresse 2017) and only few effectors of some viruses able to suppress PTI have been identified so far (Gouveia et al. 2017; Nicaise and Candresse 2017; Kong et al. 2018).

However, the major defense response controlling the accumulation of viruses in infected plant cells is RNA silencing, which relies on the production of small 21-24 nt long siRNAs and microRNAs (miRNAs) that associate with an ARGONAUTE (AGO) protein-containing RNA-induced Silencing Complex (RISC) to target viral and host RNAs for cleavage or translational repression in a target sequence-specific manner (Bologna and Voinnet 2014). Viruses encode effector proteins that

suppress RNA silencing (VSR) (Csorba et al. 2015) and Arabidopsis mutants affected in DICER-Like (DCL) and other RNA silencing pathway genes showed enhanced susceptibility (Mourrain et al. 2000; Morel et al. 2002; Bouché et al. 2006; Deleris et al. 2006), thus indicating the importance of RNA silencing in antiviral defense and plant-virus co-evolution (Pumplin and Voinnet 2013). However, the role of RNA silencing in plant:virus interactions may be more complex as it targets both the virus and its host. For example, it is conceivable that similar to certain mammalian DNA viruses (Herpesviridae) (Hook et al. 2014) and plant-pathogenic fungi (Weiberg et al. 2013), also plant viruses may have evolved the ability to hijack the host RNA silencing pathway with their own small RNAs in order to modulate host gene expression.

To further explore the function of small RNAs (sRNAs) during plant:virus interactions, we have used next-generation RNA profiling technologies and specific gene analysis to address the function of sRNAs accumulating during early TuMV infection in leaves of oilseed rape (*Brassica napus*). As described in the attached draft manuscript by Pitzalis et al., this work led to the identification of a whole network of host- and virus-derived sRNAs correlated with specific host mRNA and viral RNA cleavage events during infection. The observations indicate that viruses and their hosts exchange multiple sRNA signals for mutual control and regulation.

The attached draft manuscript (Pitzalis et al.) and also Chapter III mention numerous components of different RNA silencing pathways, which are briefly explained in the following paragraphs.

2. RNA silencing pathways and their components

RNA silencing relies on pathways that involve the production of 21-24 nt long sRNAs from double-stranded sRNA precursor molecules by DICER enzymes [DICER-Like (DCL), in plants]. Upon cleavage of dsRNA into 21-24 nt sRNA duplexes, one strand of a given duplex associates with an AGO family protein within RISC and guides this complex for sequence-specific, AGO-mediated, slicing or translational repression of the corresponding target transcript (Hammond et al. 2000; Zamore et al. 2000). The endogenous dsRNA molecules that function as substrates for DCL enzymes can originate from transcripts of dedicated miRNA (MIR) genes able to fold into hairpin structures, or can represent long dsRNA molecules produced by transcription of inverted repeat loci, the alignment of overlapping transcripts produced from opposite strands of DNA, or the activity of viral or endogenous RDR that convert single stranded (ss) RNA molecules into dsRNA molecules. Unlike the miRNAs that are encoded by MIR genes, the sRNAs that are derived from DCL processing of long

dsRNA precursors are referred to as siRNAs. The RISC-mediated cleavage of viral RNA or of mRNA transcripts of transgenes can be amplified by RDR enzymes by conversion of the RNA cleavage fragments into new dsRNA, thereby providing new dsRNA template for the production of "secondary sRNAs" that again target the same transcript or viral RNA. This process involves "transitivity", which describes the fact that the secondary siRNAs involved in secondary silencing are different from the siRNA that caused the initial cleavage event and map to the target transcript to sites adjacent to the original siRNA (Dalmay et al. 2000; Himber et al. 2003). An interesting and important feature of siRNAs and of some miRNAs is their intercellular and systemic mobility through PD (Vatén et al. 2011) and phloem by which they coordinate abiotic and biotic stress responses across the plants (Buhtz et al. 2008; Molnar et al. 2010; Brosnan and Voinnet 2011; Melnyk et al. 2011; Zhang et al. 2014; Borges and Martienssen 2015; Lewsey et al. 2016). The systemic mobility of siRNAs and the systemic silencing of their targets is supported by the increased level of target-specific siRNAs produced by RDR-dependent secondary siRNA production (Himber et al. 2003). The *A. thaliana* genome encodes four DCLs (DCL1 to DCL4), ten AGOs (AGO1 to AGO10) and six RDRs (RDR1 to RDR6) (Vazquez 2006) that function in different RNA silencing pathways.

2.1. Role and function of DCL proteins

DICER proteins are ribonucleases that belong to the RNAse III (also called RNAse C) family. Initially found in *Escherichia coli* (Chen et al. 1990), they were later found to be present and conserved also among flies, plants, fungi and mammals (Bernstein et al. 2001). The DCL proteins in Arabidopsis were originally identified as SIN1/SUS1/CAF and were then re-named because of their similarity to DICER proteins in *Drosophila* and *Coenorhabditis* (Schauer et al. 2002). For example, the *A. thaliana* DCL1 was shown to share with DICER1 proteins of *S. pombe*, *C. elegans*, *D. melanogaster*, *Mouse* or *Human* species the DExD/H-Box RNA helicase (DEAD-box) and helicase-C domains both used for unwinding secondary RNA structures (Tanner and Linder 2001), a Domain of Unknown Function 283 (DUF283), which may help for targeting helper proteins (Qin et al. 2010), a PIWI/ARGONAUTE/ZWILLE (PAZ) domain used as a binding module able to recognize the 3' end of sRNAs (Song et al. 2003), two catalytic RNAse III domains, and one or two dsRNA-binding domain (dsRBD) important for sRNA binding and miRNA accumulation (Schauer et al. 2002; Margis et al. 2006; Chapman and Carrington 2007; Bologna and Voinnet 2014) (see DCLs, Figure 4).

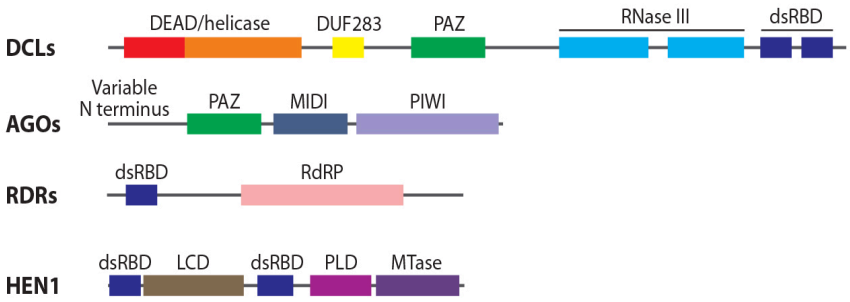

Figure 4: Conserved domain organization of RNA silencing pathway proteins
(modified from Bologna and Voinnet 2014).

Whereas DCL1 is predominantly involved in the processing of 21-24 nt miRNAs from miRNA precursors transcribed from MIR genes (Reinhart et al. 2002), DCL2 and DCL4 target long dsRNA molecules and produce 22 and 21 nt long siRNAs, respectively. They play a major role in antiviral silencing in *Arabidopsis* (Akbergenov et al. 2006; Blevins et al. 2006; Deleris et al. 2006) by cleaving viral dsRNA, which is produced by the viral RDR (replicase) during viral replication, into viral siRNAs (vsiRNAs). DCL1 and DCL4 [and an additional DCL5 in rice (previously called DCL3b)] are involved together in the biogenesis of 21-24 nt trans-acting small interfering RNAs (tasiRNAs) and phased small interfering RNAs (phasiRNAs), derived from long dsRNAs produced by RDR6 and/or RDR1 from transcripts encoded by TAS and PHAS loci (Peragine et al. 2004; Vazquez et al. 2004; Song et al. 2012). DCL2 functions as a surrogate for DCL4 function in producing vsiRNAs (Gasciolli et al. 2005) and was shown also to stimulate transitive secondary siRNA production together with RDR6 (Parent et al. 2015). DCL3 has a central function in transcriptional gene silencing (TGS) by processing 24 nt long siRNAs from dsRNA molecules generated by RDR2 from RNAs transcribed by RNA polymerase VI (POL IV) from intergenic or repetitive regions, transposons, and other loci undergoing RNA-dependent DNA methylation (RdDM) (Xie et al. 2004; Henderson et al. 2006; Pontes et al. 2006; Matzke et al. 2009; Blevins et al. 2015).

2.2. Role and function of AGO proteins

The AGO proteins are highly conserved among organisms (Carmell et al. 2002) and represent the main RNA silencing effectors by acting as the “slicers” of the RISC complex (Fang and Qi 2016). AGOs are RNAse H-like enzymes containing a variable N-terminal domain and a conserved RNA-binding PAZ (for PIWI, AGO, and Zwille), MID (middle) domain able to recognize the 5’nucleotide of sRNAs, and PIWI domains able to correctly position the RNAs relative to their target and to perform double

stranded-RNA-guided hydrolysis of ssRNA (Song et al. 2004; Wang et al. 2009; Wei et al. 2012) (see AGOs, Figure 4). The number of AGO proteins ranges from 1 AGO in *S. pombe* to 27 AGOs in *C. elegans*. The different AGO proteins share similarities but not all share slicing activity functions. For example, most miRNAs and their associated AGOs in animals function in translational repression rather than cleavage because of limited complementarity with the target RNA in the sRNA seed region (nucleotide 2 to 7) (Lewis et al. 2003; Lewis et al. 2005; Bhattacharyya et al. 2006; Mallory and Vaucheret 2010). The functions of the 10 AGO proteins in Arabidopsis have been reviewed in detail (Bologna and Voinnet 2014; Zhang et al. 2015). Although translational repression is also observed in plants and involves miRNA- and siRNA-guided AGO1 and AGO10 (Brodersen et al. 2008), slicing appears to be the dominant activity of AGO proteins in plants (Song et al. 2004) and has been experimentally demonstrated for *Arabidopsis* AGO1, AGO2, AGO7, and AGO10 (mediating PTGS) and AGO4 (mediating TGS) (Zhu et al. 2011; Carbonell et al. 2012; Manavella et al. 2012). miRNAs are loaded into AGO1, AGO2, AGO7 and AGO10 to guide mRNA target cleavage during stress responses, plant development, and antibacterial immunity (Baumberger and Baulcombe 2005; Montgomery et al. 2008). AGO1 also acts as an effector for tasiRNA production and function (see paragraph 3.2), and also mediates antiviral silencing upon loading with 21 and 22 nt vsiRNAs produced by DCL4 and DCL2, respectively (Pumplin and Voinnet 2013). AGO1 is associated with endomembranes and its homeostasis is controlled by miR168-AGO1 dependent slicing and miR168-AGO10-dependent translational repression of its mRNA. Moreover, the P0 VSR of poleroviruses targets AGO1 for ubiquitinylation and subsequent degradation by autophagy (Derrien et al. 2012).

AGO10, the closest AGO1 homolog in *Arabidopsis* specifically binds miRNA members of the MIR165/166 family to regulate shoot apical meristem development (Zhu et al. 2011). Current models suggest that AGO10 may compete with AGO1 for miR165/166 to protect the target RNAs (encoding class-III HomeoDomain-leucine ZIPper [HD-ZIPIII] transcription factors) for expression in the meristems (Zhang and Zhang 2012; Bologna and Voinnet 2014). AGO10 also associates with miR168 to mediate the translational repression of AGO1 mRNA (Mallory et al. 2009) and was shown to act in antiviral defense against TuMV in inflorescence tissues (Garcia-Ruiz et al. 2015).

AGO2 displays additive and overlapping functions with AGO1. Like AGO1, also AGO2 functions in antiviral defense and loads vsiRNAs to trigger cleavage of the vRNA (Takeda et al. 2008; Mallory and Vaucheret 2010; Bologna and Voinnet 2014). Similar to regulation of AGO1 by miR168, AGO2 is regulated by miR403 in an AGO1-dependent manner (Allen et al. 2005). Thus, AGO2 can act as a

surrogate AGO to AGO1, when AGO1 itself is not available, for example when targeted by polerovirus P0.

AGO7 is almost exclusively associated with miR390 to initiate the biogenesis of tasiRNAs from the TAS3 gene (Montgomery et al. 2008) but also plays a role in antiviral defense in leaves (Garcia-Ruiz et al. 2015).

AGO4, AGO6 and AGO9 were shown to bind DCL3-dependent 24 nt heterochromatic small interfering RNAs (hcRNAs) and to act in RdDM (Zheng et al. 2007; Gao et al. 2010; Havecker et al. 2010; Blevins et al. 2015). Whereas AGO6 and AGO9 load hcRNAs derived from transposable elements (Olmedo-Monfil et al. 2010; McCue et al. 2015), AGO9 incorporates hcRNAs to control female gamete formation (Olmedo-Monfil et al. 2010). AGO5 was shown to associate with phasiRNAs, may induce megagametogenesis (Mi et al. 2008; Tucker et al. 2012; Komiya et al. 2014; Zhang et al. 2015) and to trigger antiviral defense against systemic PVX infection in Arabidopsis (Brosseau and Moffett 2015). The exact function(s) of AGO3 and AGO8 have not yet been determined.

AGO proteins generally act as platforms to bind proteins containing Gly-Trp (GW) dipeptides. These "GW proteins" often act as essential cofactors in various RNA silencing reactions (El-Shami et al. 2007; Till et al. 2007; Poulsen et al. 2013).

2.3. Role and function of RDR proteins

RDR proteins are RNA-dependent RNA polymerases that produce dsRNAs from single-stranded RNA templates. They are found in RNA viruses, plants, fungi, protists and *C. elegans* but are absent in *Drosophila* and mammals. They are characterized by the presence of a catalytic psi-β-barrel DxDGD (DFDGD in Arabidopsis) motif at the C-terminus, which is highly conserved among the identified eukaryotic and viral RDRs (Makeyev and Bamford 2002; Wassenegger and Krczal 2006) (see RDRs, Figure 4). As already mentioned, these proteins have a key role in producing long dsRNA substrates for the sequential processing of secondary siRNAs by DCL2 and DCL4. By linkage with specific siRNA-processing DCLs, the different RDRs are functionally diversified into different RNA silencing pathways. Loss of RDR1, RDR2, or RDR6 results in enhanced susceptibility to RNA and DNA viruses, thus confirming their important role in antiviral defense (Pumplin and Voinnet 2013). One of the major roles of RDR1 and RDR6 is to produce dsRNA to amplify vsiRNAs production by DCL2 and DCL4 for antiviral silencing (Donaire et al. 2008; Wang et al. 2010). RDR6 is the most studied RDR. In addition to its major role in antiviral defense (Himber et al. 2003; Schwach 2005; Vazquez 2006),

RDR6 is also the major RDR involved in the production of tasi- and phasiRNAs (Vazquez 2006) and has important functions during plant development, for example in the regulation of self-incompatibility (Tantikanjana et al. 2009), juvenile-to-adult phase change (Peragine et al. 2004), or leaf and pistil development (Peragine et al. 2004; Willmann et al. 2011).

RDR2 has a prominent role in TGS by conversion of capped or non-capped ssRNAs transcribed by POLIV from heterochromatic regions into dsRNAs for sequential processing by DCL3 into 24 nt long hcRNAs and loading into AGO4-RISC. RDR2 plays a central role in RNA-mediated DNA methylation, histone modification, and telomeric heterochromatic formation and its maintenance (Vrbsky et al. 2010; Blevins et al. 2015). RDR2 has also been shown to be involved in nucleolar dominance (silencing of one parental set of ribosomal RNA genes) (Autran et al. 2011). RDR2 and RDR6 are both involved in female gamete formation with the presence of multiple abnormalities in female gametophytes in *rdr2* and *rdr6* mutants (Olmedo-Monfil et al. 2010) as well as in transgene silencing. The exact functions of RDR3 and RDR5 have not been shown until now and remain to be demonstrated.

2.4. Role and function of HEN1 proteins

HUA ENHANCER 1 (HEN1) is a RNA methyltransferase (fully named S-adenosyl-L-methionine-dependent RNA methyltransferase) that ligates a methyl group (CH_3) onto the 2'-OH of each strand of all DCL-derived products (Li et al. 2005; Yu et al. 2005; Yang et al. 2006). HEN1-mediated methylation causes the stabilization of sRNAs by preventing their uridinylation degradation signaling (Yu et al. 2005; Kim et al. 2010). HEN1 has five domains. Four of them directly interact with sRNA substrates, namely the two dsRNA binding domains (dsRBD1 located at the N-terminus and dsRBD2 located in the center), the La-motif-containing domain (LCD), which specifically recognizes the 3'-OH group (Bologna and Voinnet 2014), and the methyltransferase domain (MTase) (Yu et al. 2005). The fifth domain is the PPIase-like domain (PLD), which does not interact with sRNA substrates (Huang et al. 2009). This domain has been proposed to function as a protein-protein interaction domain (Ying et al. 2009; Vasudevan et al. 2015) (see HEN1, Figure 4). It has been speculated that the methylation mechanism is initiated by the targeting of the 18-24 nt siRNA duplex by dsRBD1 and dsRBD2, which places one of the terminal ends of the duplex close to the MTase domain and the other end close to the LCD domain for protection (Ying et al. 2009). The MTase then methylates the 3'terminus in a Mg^{2+}-dependent mechanism.

3. Roles and pathways of RNA silencing

DCL proteins that process miRNAs and siRNAs from RNA precursor molecules and AGO-RISC complexes that use these miRNAs and siRNAs for RNA cleavage or translational repression constitute the core components of many known RNA silencing pathways. The different pathways are distinguished by the specific types and origins of sRNA, their specific processing by specific DCL proteins, their specific association with specific AGO proteins, and their specific role. Generally, RNA silencing pathways act at either the transcriptional or post-transcriptional levels. TGS acts in the nucleus and uses DCL3-dependent 24 nt siRNAs referred to as repeat-associated siRNAs (rasiRNAs) or heterchromatic siRNA (hcRNAs). The hcRNAs are processed from dsRNA precursors generated by RDR2 from RNA POL IV transcripts of heterochromatic regions and associate with AGO4 to guide RNA-dependent DNA methylation (RdDM) and histone modification leading to the epigenetic modification of transposons and endogenous repeat loci (Matzke et al. 2009) (Figure 5a). PTGS pathways, in contrast, use either miRNAs derived from MIR genes or siRNAs processed from different long dsRNA precursors (e.g. viral dsRNA, extended hairpin mRNAs encoded by inverted repeat loci, dsRNAs produced by RDR using viral RNA or single-stranded RNAs derived from TAS or PHAS loci as template) to regulate the abundance of mRNAs (or viral RNAs) and proteins by mRNA cleavage or translational repression.

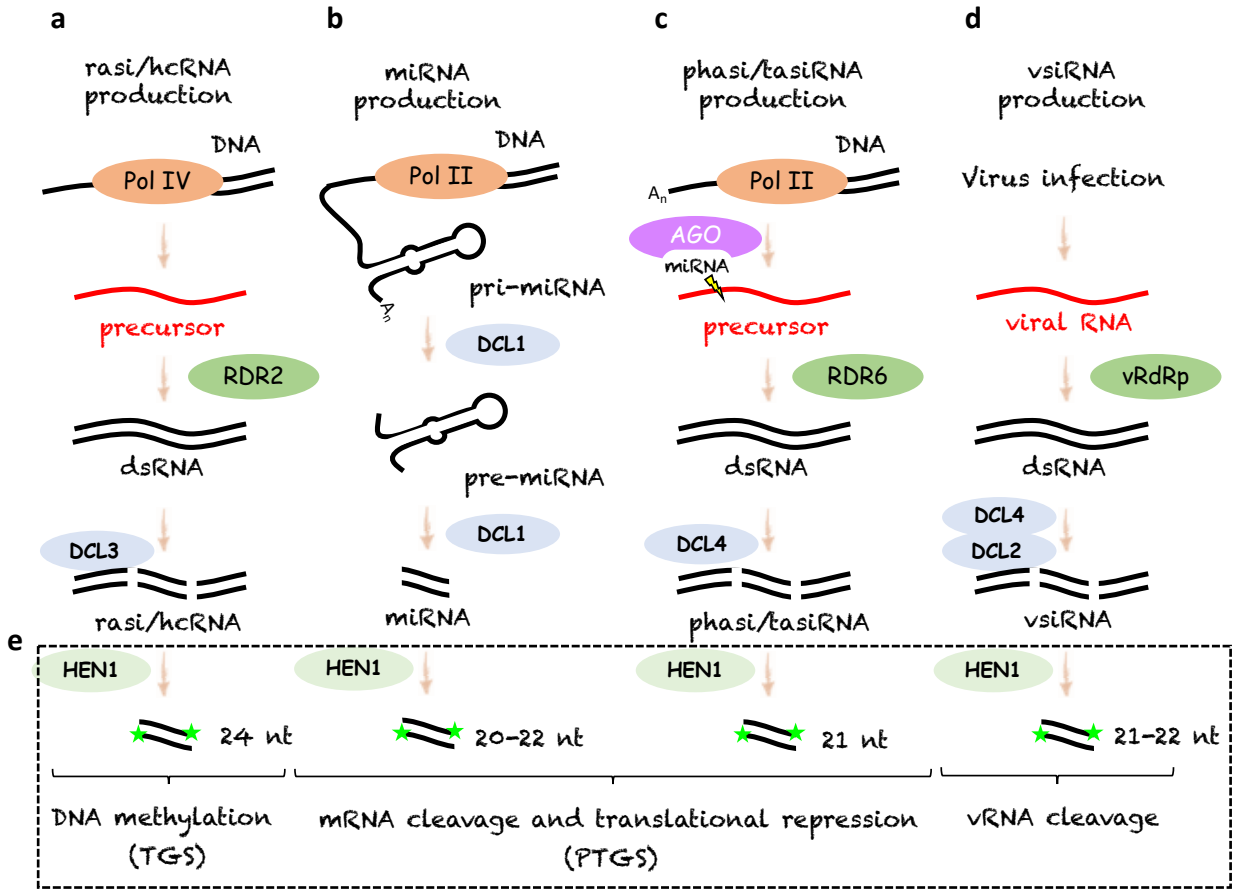

Figure 5: Biogenesis of sRNAs and RNA silencing pathways
a. PolIV transcripts derived from transposable elements and repeats are converted to dsRNA by RDR2 and then cleaved by DCL3 into rasi/hcRNAs. **b.** After transcription of pri-miRNA from a MIR gene by RNA polymerase II (Pol II) the double-stranded foldback structure is cleaved by DCL1 into a 20-22 nt long miRNA duplex. **c.** PhasiRNAs (which include tasiRNAs) are transcribed from coding genes or non-coding genes (e.g. TAS genes in Arabidopsis) by Pol II and converted into dsRNA by the RDR6 protein. The dsRNA is then processed by DCL4 into phased 21 nt siRNAs. **d.** Viral RNA replication by the viral RNA dependent RNA polymerase (vRdRp) leads to the formation of double-stranded RNA (dsRNA) which is cleaved by DCL2 and DCL4 into 21-22 nt long siRNA duplexes. **e.** rasi/hcRNA, miRNA, phasi/tasiRNA, and vsiRNA are methylated by HEN1 and loaded into the AGO-RISC complex for DNA methylation and chromatin formation/maintenance (TGS) or direct cleavage or translational repression of target RNA (PTGS).

3.1. miRNA biogenesis and function

miRNAs are 20-22 nt long sRNAs derived from non-coding MIR genes (Figure 5b). Transcription of the MIR gene by RNA polymerase II (Pol II) leads to production of capped, single-stranded and polyadenylated primary miRNA (pri-miRNA) that folds into a hairpin-like structure. Initial cleavage by DCL1 leads to a shorter stem-loop structure called precursor miRNA (pre-miRNA), which is again cleaved by DCL1 to produce the mature miRNA duplex (Reinhart et al. 2002; Kurihara and Watanabe 2004; Qi et al. 2005; Park et al. 2005). Following methylation by HEN1 at both 3'-ends the duplex is exported from the nucleus into the cytoplasm dependent on an exportin-5 homolog called HASTY. In the cytoplasm, one strand of the duplex is loaded into a RISC complex containing either AGO1,

AGO2, AGO7 or AGO10 to guide the complex to its mRNA target for sequence-specific cleavage. Published miRNA sequences and associated annotations are deposited in the miRbase database (http://www.mirbase.org; Kozomara and Griffiths-Jones 2014).

3.2. phasiRNA biogenesis and function

phasiRNAs are generated from a long dsRNA precursor at intervals of 21-26 nt (Figure 5c). As exemplified by the category of Arabidopsis *trans*-acting siRNAs (tasiRNAs), phasiRNAs are derived from an mRNA converted to dsRNA by RDR6 and processed by DCL4 (Vazquez et al. 2004). The origin of referring to some phasiRNAs as tasiRNAs stems from their ability to act like miRNAs in homology-dependent manner, directing AGO1-dependent cleavage of mRNAs from genes other than that of their source mRNA (Fei et al. 2013). The term phased indicates that the phasiRNAs are produced in a head-to-tail arrangement, starting precisely at a specific nucleotide. This specific nucleotide is usually determined by cleavage of the transcript by a 22 nt-long miRNA or siRNA (e.g. tasiR2140; Chen et al. 2007), which is followed by dsRNA formation and DCL4 cleavage. Due to the phasing of the siRNAs, the phasiRNA-producing PHAS loci can be identified with the help of computational algorithms. Such algorithms can be used in genome-wide scanning and allow identifying PHAS loci according to a p-value or phasing score as a threshold or cutoff. In Arabidopsis, this approach led to the original identification of tasiRNAs as well as to the identification of new phasiRNA-producing loci. Importantly, many of these these phasiRNA-producing loci actually represent coding genes [many of which encode Nucleotide-Binding, Leucine-Rich Repeat (NB-LRR) proteins, PENTATRICOPEPTIDE REPEAT (PPR) proteins, or MYB transcription factors (Howell et al. 2007; Zhai et al. 2011; Xia et al. 2012; Zhu et al. 2012)], thus showing that phased, secondary siRNAs can be generated from protein-coding transcript and not only from non-coding genes, such as TAS genes. It is important to note that phasiRNAs are defined just as being phased whereas tasiRNAs are defined as being phased and shown to be trans-acting (Zhai et al. 2011). Although phasiRNAs were shown to act in *trans* (tasi-RNAs), they may also act in *cis* (called casiRNAs) and be part of a self-regulatory network (Zhai et al. 2011), in which phased siRNAs target homologous regions in both the transcript of origin and in transcripts of homologous genes, enabling the plant to maintain the homeostasis of transcripts encoded by the whole gene family. Such autoregulatory network plays an important role in controlling the expression of hundreds of homologous of NB-LRR genes present in *Medicago* (Young et al. 2011; Zhai et al. 2011) or potato (Wang et al. 2011; Xu et al. 2011a; Zhai et al. 2011; Lozano et al. 2012; Shivaprasad et al. 2012).

Interestingly, certain coding genes in *Arabidopsis* were shown to produce phasiRNAs only upon viral infection and to play a role in defense against infection by *Cucumber mosaic virus* (CMV) and TuMV (Cao et al. 2014a). These virus-activated siRNAs (vasiRNAs) were processed from dsRNA generated by RDR1 rather than RDR6 and associated with AGO2 for target cleavage.

3.3. Virus-derived siRNAs (vsiRNAs)

Replication of RNA viruses leads to the production of viral dsRNA as a replication intermediate. This dsRNA is recognized by the host and triggers RNA silencing as an antiviral defense response in which the viral dsRNA is processed by DCL4 and DCL2 into 21-22 nt long vsiRNAs (Blevins et al. 2006; Deleris et al. 2006). Although the cleavage of the viral replication intermediate already interferes with efficient viral replication, vsiRNAs are methylated by HEN1 and incorporated into AGO1, AGO2, and AGO10 (Pumplin and Voinnet 2013; Garcia-Ruiz et al. 2015) for further RISC-mediated cleavage of viral RNA (Voinnet 2005; Pantaleo et al. 2007). RDR6, but also RDR1 and RDR2 support antiviral RNA silencing through the production of secondary vsiRNAs (Donaire et al. 2008; Vaistij and Jones 2009). To counter-act antiviral RNA silencing, viruses evolved specialized proteins known as suppressor of RNA silencing (VSR). The VSRs of different viruses have evolved independently and inhibit distinct steps of the silencing pathway (Table 1; Csorba et al. 2015).

Table 1: Examples of identified VSRs and their activity

Viruses	VSR function	Inhibited RNA silencing pathway step
P14 (PoLV), NS3 (RSV)	dsRNA binding	Inibition of vRNA cleavage and vsiRNA production
CaMV leader	Decoy RNA	
P38 (TCV), P1 (RYMV)	Blocking DCL activity	
CaMV P6	Inbition of DCL co-factor	
P19 (TBSV), Hc-Pro (TuMV), 126k (TMV)	Sequestration of ds-siRNA duplex	Inhibition of vsiRNA activity
RNAse 3 (SPVD)	Direct ds-siRNA cleavage	
Hc-Pro (TuMV)	HEN1 ds-siRNA binding	
P6 RYSV), Hc-Pro (TuMV)	RDR6 inhibition	Inhibition of secondary siRNAs processivity
P2 (RSV), VPg (PVA)	RDR6 co-factor inactivation	
P25 (PVX), P0 (BWYV)	AGO degradation	Inactivation of RISC complex activity (vRNA or host mRNA PTGS and TGS inhibition)
P38 (TCV), P1 (SPMMV)	AGO inactivation	

The VSRs of several viruses, including the tombusvirus P19, the potyvirus HcPro, and the tobamoviral p122/p125/p126 proteins sequester siRNA duplexes after DCL processing and inhibit their HEN1 methylation of siRNAs and their incorporation into RISC. Some VSRs act earlier in the pathway, such as the sobemovirus P1 or the carmovirus P38 that inhibit the processing of siRNAs by DCL4, or act downstream in the pathway, such as the polerovirus P0 that targets AGO1 for degradation.

Several plant pathogenic fungi were shown to hijack the host RNA silencing pathway with their own siRNAs to manipulate the expression of defense-related genes, in a process referred to "cross-kingdom RNAi" (Weiberg et al. 2015). Given that viruses replicate within cells, it seems likely that they have evolved similar strategies to target host genes with their own vsiRNAs. Indeed, the cloning of host-derived sequences into the replicating virus genome is used as a strategy to silence plant genes in a process call virus-induced gene silencing (VIGS). There is indeed evidence that natural viruses encode vsiRNAs that can act *in trans.* Early studies demonstrated that vsiRNAs of *Cymbidium ringspot virus* (CymRDV) target subviral satellite RNA (Pantaleo and Burgyan 2008). Moreover, vsiRNAs produced by TMV-Cg were shown to cleave two Arabidopsis mRNA targets (Qi et al. 2009) and vsiRNAs from the Y-satellite of *Cucumber mosaic virus* (CMV) cleaved a *Nicotiana benthamiana* chlorophyll synthesis gene (Shimura et al. 2011; Smith et al. 2011). More recent approaches utilizing genome-wide studies to correlate vsiRNAs and host RNA degradome data using CleaveLand software (Addo-Quaye et al. 2009) revealed numerous potential mRNAs that are targeted by viruses in *Vitis vinifera* (Miozzi et al. 2013). However, while improved degradome analysis software became available (e.g. PAREsnip, Folkes et al. 2012; sPARTA, Kakrana et al. 2014) and an increasing number of studies aim to identify novel miRNAs and their targets in various species (e.g. Baksa et al. 2015; Cao et al. 2014b; Wang et al. 2016), the further analysis of the sRNA network utilized by both viruses and their hosts to control viral accumulation and gene expression in the infected cell is lagging behind. Knowing more about this network will greatly increase our understanding of plant:virus interactions.

4. Draft manuscript: "Virus- and host-derived small RNAs coordinate infection in oilseed rape" by Pitzalis *et al*.

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Introduction

Viruses are among the parasites that induce the most severe damages on cultivated plants, estimated to cause up to US $30 billion worth of damage worldwide to agriculture and forestry industries (Randles and Ogle 1997; Sastry and Zitter 2014). In view of the major economic problem caused by viruses, breeders usually rely on the development of resistant cultivars. However, this strategy often turns out not to be durable since virus evolution favors the emergence of adapted virus populations able to overcome such resistance (Garcia-Arenal and McDonald 2003). Although the incidence of plant virus diseases can be controlled to some extent by controlling the viral insect vectors, the repeated application of insecticides poses a threat to our environment. The development and application of innovative and sustainable approaches for protecting cultivated plants against their pathogenic viruses depends on the identification of gene targets that are part of the fundamental molecular mechanisms that determine virus:host compatibility and disease. Viruses utilize host mechanisms to support their replication and movement and, at the same time, trigger host defense responses. Numerous previous studies have demonstrated that viral infection in susceptible hosts is associated with the altered expression of genes and the activation of defense responses such Pattern-Triggered-Immunity (PTI) (Kørner et al. 2013) and RNA silencing (Ding and Voinnet 2007). Both defense responses are triggered by the recognition of double -stranded RNA (dsRNA) produced during viral replication. However, whereas PTI involves BAK1 (Kørner et al. 2013) and the recognition of dsRNAs by an unknown pathogen-recognition receptor together with SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE 1 (SERK1) as a potential co-receptor (Niehl et al. 2016), RNA silencing relies on the recognition of dsRNA by DICER-LIKE (DCL) proteins. Moreover, PTI involves the activation of transcriptional signaling cascades and confers broad-spectrum pathogen resistance (Dodds and Rathjen 2010; Jones and Dangl 2006; Spoel and Dong 2012), whereas RNA silencing relies on the production of small 21-24 nt long small interfering RNAs (siRNAs) and microRNAs (miRNAs) that associate with an ARGONAUTE (AGO) protein-containing RNA-induced silencing complex (RISC) to target viral and host RNAs for cleavage or translational repression in a target sequence-specific manner (Bologna and Voinnet 2014). RNA silencing plays a central role in plant-virus interactions as it targets both the virus and its host. Viruses encode effector proteins that suppress RNA silencing (VSR) (Csorba et al. 2015) and Arabidopsis mutants affected in DCL and other RNA silencing pathway genes showed enhanced susceptibility (Bouché et al. 2006; Deleris et al. 2006; Morel et al. 2002; Mourrain et al. 2000), thus indicating the importance of RNA silencing in antiviral defense and plant-virus co-evolution (Pumplin and Voinnet 2013). However, the role of

RNA silencing in plant:virus interactions may be more complex. For example, it is conceivable that similar to certain mammalian DNA viruses (Herpesviridae) (Hook et al. 2014) and plant-pathogenic fungi (Weiberg et al. 2013), also plant viruses may have evolved the ability to hijack the host RNA silencing pathway with their own small RNAs in order to modulate host gene expression.

To further explore the function of sRNAs during plant:virus interactions, we here used next-generation RNA profiling technologies and specific gene analysis to address the function of sRNAs accumulating during early *Turnip mosaic virus* (TuMV) infection in leaves of oilseed rape (*Brassica napus*). sRNA:RNA target pairs correlated with specific host mRNA and viral RNA cleavage events during infection were identified. Moreover, our analysis revealed the targeting of specific host genes by virus-encoded siRNAs. The results also suggest the existence of specific host genes that function as virus-induced hubs for secondary siRNA synthesis and the regulation of downstream secondary gene target networks. We also show that the virus itself is targeted for RISC-mediated cleavage by sRNAs encoded by the host. This finding indicates that the network of sRNA-mediated interactions between the virus and its host includes the activity of plant-encoded sRNAs with homology to viral genomes and that are part of the arms arsenal available to plants to control their viruses. Collectively, the observations indicate that viruses and their hosts cells form tightly organized niches in which both sides exchange multiple sRNA signals for mutual control and regulation. *B. napus* is a global economically important crop grown for its oil-rich seeds and vulnerable to a number of widespread viruses including TuMV. By focusing the analysis on dissected local sites of infection in leaves, we identified regulatory hubs and sRNA target genes that control plant-virus interactions during the onset of virus infection before disease symptoms arise. The identified genes and mechanisms are potential targets for crop breeding aiming to interfere with the onset of infection already during early stages.

Results

The rapeseed cultivars Drakkar and Tanto differ in susceptibility to TuMV-GFP

The analysis involved two different commercial *B. napus* cultivars, Tanto and Drakkar, which showed strong differences in their susceptibility for GFP-tagged TuMV (TuMV-GFP) (Fig. 1). Both cultivars develop green fluorescent infection foci visible under UV light in the inoculated leaves. However, although the foci in the two cultivars develop and further grow similarly in size, the foci in Drakkar leaves are homogenously green fluorescent (Fig. 1a), whereas the foci in the Tanto leaves occur as

fluorescent halos (Fig. 1b). This halo-like phenotype of infection sites were previously reported for GFP-tagged viruses with compromised VSR activity (Garcia-Ruiz et al. 2015; Kubota et al. 2003; Vogler et al. 2007) indicating that the virus is silenced or otherwise inhibited shortly after infection of new cells. Consistent with a stronger antiviral response in Tanto, infection foci in Tanto leaves contain slightly less viral RNA as compared to the foci in Drakkar leaves (Fig. 1e). The difference between the two cultivars in TuMV susceptibility is also expressed at the level of systemic infection. Whereas Drakkar plants show extensive green fluorescent areas in the local and systemic tissues two to three weeks after inoculation (Fig. 1c), the upper leaves in Tanto plants show only few dispersed fluorescent spots (Fig. 1d).

Profiling of TuMV-GFP induced gene expression within local infection foci in Drakkar and Tanto leaves

Local green fluorescent infection foci in leaves and similar leaf samples of mock-treated plants were excised for transcriptome profiling using RNAseq. The analysis was performed for three independent replicate infection experiments, thus involving three independent RNA samples each for mock-treated Drakkar (DM), mock-treated Tanto (TM), virus-treated Drakkar (DT), and virus-treated Tanto (TT). To determine the profiles of sRNAs and their activity in mRNA target cleavage, exactly the same 12 RNA samples were also used for sRNA and mRNA degradome profiling (sRNAseq and PAREseq). The RNAseq analysis of the 12 samples gave 35 to 72 million clean paired reads per sample (Table S1). To allow appropriate mapping of the reads the Drakkar and Tanto DNA genomes were re-sequenced with 15 x coverage (Table S2) and reconstructed by alignment of the respective genomic sequencing data to the Darmor-bzh reference genome (Chalhoub et al. 2014) and by inferring the cultivar-specific high confidence single nucleotide polymorphisms (SNPs) (about 1.5 SNPs per kilobase; Table S2; Fig. S1) into the reference sequence. Using the reconstructed Drakkar- and Tanto-specific DNA genome data, around 80 % of the quality-filtered mRNAseq reads could be mapped with a maximum of one mismatch (Table S1).

Differential mRNA expression analysis revealed numerous transcripts that are significantly either up or down-regulated in virus-infected cells as compared to cells of mock-treated samples in both cultivars or in a cultivar-specific manner (Fig. 1f). The 24 genes that were most strongly regulated at transcript levels in both cultivars (fold change [$\log_2$] $\geq$ +4/-4; $p<0.05$; Fig. S2) may provide an important signature profile for early virus infection in rapeseed. These include a transcript predicted to encode CALMODULIN-BINDING PROTEIN 60G (CB60G), a master immune regulator that

promotes the expression of key genes involved in salicylic acid (SA) biosynthesis and in regulating pathogen-associated molecular pattern (PAMP)-triggered immunity (PTI), effector-triggered immunity (ETI) and systemic acquired resistance (SAR) (Sun et al. 2015). Genes that are expressed in a cultivar-specific manner or which show stronger regulation in one cultivar than in the other are candidates involved in determining the difference in virus susceptibility between the two cultivars (Table S3 – S7). Consistent with resistance, transcripts highly abundant specifically in Tanto encode proteins playing a role in defense, such as DETOXIFICATION 47 (DTX47**)**/EDS5, 4-SUBSTITUTED BENZOATES-GLUTAMATE LIGASE GH3.12, and NIM1-INTERACTING 2 (NIMIN-2), all of which play a role in the regulation of SA synthesis or the activation of genes downstream in the SAR pathway (Carviel et al. 2014; Hermann et al. 2013; Jagadeeswaran et al. 2007; Nawrath et al. 2002; Nobuta et al. 2007; Zwicker et al. 2007), whereby DTX47 was shown to be directly involved in the defense against viruses (Ishihara et al. 2008). Another highly induced gene encodes TARGET OF AVRB OPERATION1 (TAO1), a TIR-NB-LRR receptor-like protein previously known to also contribute to disease resistance induced by the *Pseudomonas syringae* effector AvrB (Eitas et al. 2008). Efficient progression of virus infection in Drakkar correlates with high levels of transcripts involved in membrane transport, the suppression of plant defense responses, and, potentially, in the regulation of plasmodesmata (PD)-mediated intercellular transport. For example, we found a strong induction of expression of the coatomer alpha-2 subunit of the COPI coatomer complex (Ahn et al. 2015), which is consistent with the role COPI vesicles in the replication of TuMV and other potyviruses (Wei and Wang 2008). The strongly induced NAC domain-containing protein 60 (NAC60) is a transcription factor activated at the ER that attenuates the sensitivity to abscisic acid (ABA). ABA has been shown to inhibit virus infection and is implicated to play a role in antiviral silencing and callose deposition at PD (Alazem and Lin 2017). NAC60 also reduces expression of ABI4 gene, which has been implicated in viral resistance (Alazem et al. 2014). The induction of transcripts encoding the leucine-rich repeat (LRR) receptor-like serine/threonine-protein kinase RPK2 is of particular interest as this protein forms heteromeric complexes with BAM1 which was recently shown to localize to PD, to promote the spread of the RNA silencing signal, and is targeted by a viral protein to inhibit antiviral RNA-silencing signaling (Rosas-Diaz et al. 2018). Thus, RPK2 may be induced during TuMV infection to regulate BAM1 and thereby control antiviral RNA silencing signaling through PD. A gene that is induced in Drakkar as well as in Tanto encodes a protein homologous to Arabidopsis PATELLIN-6 (PATL6), which was shown to be involved in resistance against *Alfalfa mosaic virus*, to interact with the viral movement protein (MP) and to prevent the targeting of MP to PD (Peiro et al. 2014). Other

induced transcripts encode TOPLESS-RELATED PROTEIN 2 (TPR2) and CYTOKININ DEHYDROGENASE 3 (CKX3), both of which are involved in the suppression of defense responses. TPX2 is a transcriptional corepressor and negative regulator of jasmonate responses (Pauwels et al. 2010), whereas CKX3 is a cytokinin-degrading enzyme that may control cytokinin levels implicated to determine the amplitude of immune responses and the outcome of plant-pathogen interactions (Argueso et al. 2012; Choi et al. 2010). Consistent with efficient systemic movement of the virus, TuMV-infection in Drakkar downregulates a transcript for PHLOEM PROTEIN 2-LIKE A2 (PP2A2) that together with PP2A1 can form high-molecular mass polymers to block phloem sieve plate pores (Fu et al. 2014).

The virus-induced differential expression profiles of several genes were validated by RT-qPCR using RNA samples of mock- and virus-treated Drakkar and Tanto plants of five independent biological experiments. The results generally confirmed the virus-induced changes in gene expression (Fig. S2) indicated by RNAseq data.

mRNA cleavage by miRNAs

The replicative sRNAseq datasets provided 27-52 Mio clean and quality-filtered (18-30 nt) reads per sample (Table S1). The sRNA size profiles within the libraries showed the expected changes in distribution of sizes upon RNA virus infection (Fig. S3). Mock-treated Drakkar and Tanto plants showed typical and very similar sRNA size profiles of predominantly 21nt – 24 nt long sRNAs, with likely DCL3-derived 24 nt sRNAs representing the major species. In contrast, the sRNA profiles in the virus-treated plants were dominated by virus-derived 21 nt and 22 nt siRNAs (84% and 74% of the 21 nt sRNAs are virus-derived in infected Drakkar and Tanto plants, respectively), which is consistent with the presence of the virus and the processing of viral dsRNA by DCL4 and DCL2, respectively. Moreover, host-derived sRNAs showed a strong increase in the number of 21 nt sRNAs, whereas the number of sRNAs belonging to other size classes, except the 22 nt size class, was strongly reduced. These alterations in the pattern of host sRNAs may represent an accumulation of miRNAs in virus-infected tissues, as previously observed (Hu et al. 2011; Tagami et al. 2007; Vogler et al. 2007). The virus-derived siRNAs aligned to the TuMV genome along its entire length, on both plus (+) and minus (-) strands. (Fig. S4)". The virus-genome aligned siRNA profiles of peaks and valleys are almost identical between Drakkar and Tanto, thus demonstrating that the cultivar-specific differences in the susceptibility for the virus cannot be explained by obvious differences in vsRNA processing or accumulation.

Host-derived miRNAs were identified by mapping the sRNA reads to *Brassicacea* mature miRNA family sequences deposited in miRBase (Kozomara and Griffiths-Jones 2014) and by analyzing them for miRNA prediction with ShortStack (Axtell 2013; Shahid and Axtell 2014). ShortStack annotates miRNAs on the basis of specific criteria, including a requirement of the corresponding star sequence present in the sRNA data and its mapping near the candidate miRNA sequence within the same gene. Our list of known and predicted miRNAs was complemented by *B. napus* miRNAs reported in publications and contained 1047 miRNAs to which our sRNAs were aligned (Table S8). Around 8 million sRNA reads per condition could be mapped to 652 expressed miRNA species and, of these, 53 miRNAs and 47 miRNAs were present only in either Drakkar and Tanto, respectively.

To identify mRNAs targeted for cleavage by miRNAs and other sRNAs expressed in the mock- and virus-treated plants the replicate DM, DT, TM and TT samples were also used for the sequencing of the mRNA degradome by PAREseq. The PAREseq reads consist of 20 nt signatures derived from mono-phosphorylated, non-capped 5' ends of the 3' fragments of mRNAs following cleavage by RISC, Dicer, or other degradation processes. By applying the combination of PAREseq, mRNAseq, and sRNAseq reads for degradome analysis with PAREsnip software (Folkes et al. 2012), we identified sRNA:mRNA pairs that are functional in sRNA-mediated RNA cleavage events. Our degradome and sRNA data sets derived from leaf samples of twelve independent replicate biological experiments with non-infected mock and TuMV-infected Drakkar and Tanto plants were consistent with the activity of numerous *B. napus* miRNAs involved in the RISC-mediated cleavage of mRNA targets known already in Arabidopsis and other species. The analysis agreed the activity of previously known *B. napus* members (annotated in miRbase) of miRNA families targeting the mRNA transcripts for SQUAMOSA PROMOTER-BINDING-LIKE (SPL) proteins (bna-miR156), Auxin response factors (ARFs) (bna-miR160), SCARECROW-LIKE (SCL) proteins (bna-miR171), Ethylene-responsive transcription factor (ERF) RELATED TO APETALA 2 (RAP2), TARGET OF EAT 2 (TOE2), and APETALA 2 (bna-miR172), Auxin signaling F-box (TIR1/AFB2/AFB3) proteins (bna-miR393), CHLOROPLASTIC SUPEROXIDE DISMUTASE (bna-miR398), and ARGONAUTE 2 (bna-miR403) (Table S9). Several members of these mRNA target families are also presumably targeted by previously unknown *B. napus* miRNAs identified by ShortStack (Table S10) or by miRNAs sequences present in miRbase but previous described only in other species (Table S11). Our degradome data also indicate the cleavage of several predicted targets by sRNAs that we annotated as "miRNA-related sRNAs" since they carry small mismatches to miRNA sequences in other species (Table S12). Some of these sequences were identified by ShortStack as genuine *B. napus* miRNAs (Table S13). Our replicate degradome data also

indicate that certain known miRNAs likely cause the cleavage of mRNA transcripts that were previously unknown as specific targets (Table S14). For example, a miRNA homologous to the *B. rapa* bra-miR1885b targets transcripts of BIOGENESIS OF LYSOSOME-RELATED ORGANELLES COMPLEX 1 SUBUNIT 2 (BLOS2), and the mRNA of the cytochrome c oxidase assembly protein COX19 is indicated as a target of the *B. napus* miRNA bna-miRC23a-3.

The cleavage breakpoints indicated by several miRNA:mRNA target pairs were confirmed RLM-5'RACE assays with independent, newly created, biological samples (Figs. S5-S9). For example, the targeting of ARF10 mRNA by bna-miR160c produced a highly defined degradome signature along the transcript in mock as well as infected Drakkar and Tanto samples, and the respective cleavage site could be clearly mapped also by 5'RACE (Fig.S5). Other examples of miRNA:mRNA target pairs confirmed by 5'RACE are bna-miR1885:TAO1 (Fig. S6), bna-miR403:AGO2 (Fig. S7), bna-mi1885b:BLOS2 (Fig. S8), or bna-miR172:APETALA2 (Fig. S9).

miRNA and mRNA target levels are not always correlated

Infection by TuMV-GFP leads to varying changes in the levels of the specific miRNAs and these changes are conspicuously similar between infection foci in Drakkar and Tanto. However, the virus-induced changes in the levels of the miRNAs does not always correspond to the expected reduction in the steady state level of the respective target mRNA. The complete data describing identified miRNA:mRNA target pairs and the respective miRNA and mRNA target expression levels in the two cultivars are summarized in Table S15 and an overview over miRNA and mRNA target expression levels is provided in Table S16. Several miRNA:mRNA target pairs follow the expected rule that an increase, or decrease, in the level of a specific miRNA should lead to a decrease, or increase, in level of the corresponding mRNA target, respectively. Amongst the targets showing cleavage in at least three of the twelve total samples, the miRNAs of the miRNA:mRNA target pairs miR403:AGO2, miR172:ERF RAP2-7, miR160c:ARF16, miR393:ASB2/3, miR156:SPL11, and miR172:APETALA2, are down-regulated upon infection and lead to a corresponding increase in the amount of the corresponding mRNA (Table S15). Conversely, the levels of miRNAs of other miRNA:mRNA target pairs, such as miR171:SCL, are increased and show a corresponding decrease of the corresponding mRNA. On the other hand, several other target pairs did not show these expected results. For example, the mRNAs of the target pairs miR1885b:BLOS2 or miR398:Superoxide dismutase 2 [Cu-Zn] (CSD2) accumulated upon infection, although their corresponding miRNAs increased. Similarly, several miRNA:mRNA target pairs correlated with lower levels of both the miRNAs and mRNAs.

Some miRNA:mRNA target pairs showed the expected results in mRNA levels in only one of the two cultivars but not in the other. These findings demonstrate that miRNA levels do not necessarily correspond to miRNA activity in mRNA target cleavage. Moreover, RISC-mediated cleavage is only one of several mechanisms by which cellular mRNA levels are regulated.

TuMV uses vsiRNAs to target host genes

The sRNA data analysis revealed that TuMV-infected cells produce about 300000 unique siRNA sequences derived from the positive and negative strands of the virus. The replicative PAREsnip data indicated the presence of 205 sRNA:mRNA target pairs (that involve 87 virus-derived siRNAs (vsiRNAs) that occur exclusively in the infected tissues and show 100% sequence homology to the virus and no significant sequence homology to the host (Table S17). As is shown in Fig. 2, the vsiRNA with the potential to interact with host mRNA cleavage are derived from both the minus and plus strands of the virus and map at various positions along the viral genome. Eight of the vsiRNAs stand out as they are repetitively associated with cleavage events in 17 different transcripts and were detected in at least two of the six independent degradomes of infected plants studied by PAREseq/PAREsnip (Table S18, vsiRNA:mRNA target pairs highlighted in Figure 2). Among the 17 different vsiRNA:mRNA target pairs, we found one unique vsiRNA (AAGAATCTGATGATGCTGT) capable of interacting with transcripts of eight genes encoding the ethylene response factors (ERFs) RAP2-7, TOE2, and APETALA2 (Table S18, Fig. 2G). Given that the ERFs targeted by the vsiRNA AAGAATCTGATGATGCTGT are also regulated by miR172, we wondered whether the vsiRNA could mimic the function of miR172. As is shown in Fig. 2b, and more in detail in Fig. S10, this vsiRNA indeed shows high homology to bna-miR172 and would cleaves exactly the same position within target sequence. Since the host downregulates miR172 levels upon infection (Fig. S10, d), the vsiRNA may complement this reduced amount of miR172 in order to control the expression of these ERFs. The PAREseq/PAREsnip data for host mRNA targets of vsiRNA (Table S18) provide evidence for specific roles of vsiRNA targeting mRNAs particularly in Drakkar, such as mRNAs encoding the pseudokinase ZED1, the cysteine-protease aleurain, and the serine/arginine-rich (SR) splicing factor RS31A. The pseudokinase ZED1 is an important mediator of effector-triggered immunity (Lewis et al. 2013; Seto et al. 2017), whereas the cysteine-protease aleurain plays an important role in hypersensitive responses and programmed cell death (Lu et al. 2015). SR proteins are essential factors in regulating pre-mRNA constitutive and alternative splicing (Jeong 2017). They also act in RNA surveillance and promote RNA degradation through the nonsense-mediated RNA decay

pathway (Zhang and Krainer 2004). In plants, SR proteins play numerous roles in stress tolerance (Duque 2011), and were shown to be involved in the splicing of RNA encoding plant immune receptors (Xu et al. 2011b). Nevertheless, the identified vsiRNA:mRNA target pairs are correlated with rather moderate yet significant downregulation of some of the target genes, thus indicating that the virus may use specific vsiRNAs to prevent a strong induction of these defense-related genes in infected cells.

TuMV infection triggers the widespread targeting of mRNAs through activation of secondary siRNA production from PHAS loci.

In addition to AGO1, also other AGO proteins, particularly AGO2, play important roles in antiviral defense (Carbonell and Carrington 2015; Garcia-Ruiz et al. 2015). The expression of AGO2 is controlled by AGO1 through miR403 (Harvey et al. 2011). Consistently, our PARE analysis predicted cleavage of AGO2 mRNAs (BnaCnng68320D and BnaA05g14760D) by miR403 (Fig. S7) in both mock-treated and TuMV-infected *B. napus* samples BnaC06g41790D). Nevertheless, infection triggered the downregulation of miR403 and upregulation of AGO2 mRNA levels. Interestingly, infection also caused a strong production of secondary, phased siRNAs (phasiRNAs) from AGO2 mRNA in both Drakkar and Tanto plants (Fig. 3a). The TuMV-associated activation of phased siRNA production from coding genes has been described in Arabidopsis (Cao et al. 2014) and may as well occur in *B. napus*. To identify other coding genes that produce virus-associated phasiRNAs (va-phasiRNAs) upon TuMV infection, we mapped the virus-induced siRNAs found in our sRNA data to the Drakkar and Tanto coding genes and filtering these genes by applying thresholds for the number of siRNAs mapped to the coding regions of genes (>100 reads), the gene-specific PHAS score calculated by Shortstack (>30), and for the ratio in the number of specific va-phasiRNAs found in infected tissues versus mock-treated tissues (rpm infected / rpm mock >2). Using this approach, we identified 128 coding genes that act as PHAS loci and produce va-phasiRNAs in Drakkar (Table S19) and 253 coding genes that that act as PHAS loci and produce va-phasiRNAs in Tanto (Table S20), and of which 98 coding genes produce va-phasiRNAs in both cultivars (Table S21). As has been shown in detail for tasiRNAs in Arabidopsis, phasiRNAs are produced by conversion of the gene transcript into dsRNA followed by phased cleavage into phasiRNA duplexes (Fei et al. 2013). The production of phasiRNAs from coding genes can have varying effects, from controlling the homeostasis of the specific mRNA and encoded protein to the suppression of the specific gene and other homologous members of the same gene families (Fei et al. 2013). As known by the prototype example of trans-acting siRNAs

(tasiRNAs (Vazquez et al. 2004)) and by several new examples involving coding genes such as NB-LRR, PPR and MYB genes, phasiRNAs may also act *in trans* by directing AGO-dependent slicing of mRNAs of genes other than that of their source mRNA (Fei et al. 2013). To determine whether the va-phasiRNAs found in our analysis are functional and cause the cleavage of secondary mRNA targets *in trans*, we used them as query in our PAREsnip analysis of our sequenced degradome libraries prepared from mock-treated and virus-infected tissues. We could not find any of the AGO2 mRNA-derived va-phasiRNAs in our PARE analysis, thus indicating that the AGO2 va-phasiRNAs do not act in RISC-mediated slicer activity. va-phasiRNAs produced by several other genes [for example BnaC02g40260D encoding Elongation factor 2 (EF2) (Fig. 3b) or BnaA05g28710D encoding CDC48E (Fig. 3c)] were similarly absent in our PAREsnip database and may similarly be inactive in guiding RISC-mediated target RNA cleavage. However, among other va-PHAS genes, we found members of three small gene families particularly involved in the production of va-phasiRNAs and engaged in secondary mRNA target cleavage. These three gene families are predicted to encode Chlorophyll a-b binding protein 1 (BnaA04g20150D, BnaAnng22920D, BnaC03g59520D, BnaA07g07560D, BnaA03g15830D, BnaC03g18980D, BnaA09g26570D, BnaA08g17660D, BnaC05g22880D, BnaC04g10770D, BnaC04g10780D), NBR1 homolog (NBR1, BnaA01g14050D, BnaA03g46880D, BnaC07g39070D, BnaC01g16550D, BnaC08g11760D), and a protein with homology to yeast ART1/TAR1 (Transcript Antisense to Ribosomal RNA) (Galopier and Hermann-Le Denmat 2011) (BnaAnng22160D, BnaA09g04420D, BnaC08g46150D, BnaAnng21760D). These three gene families alone were found to produce 415 different unique va-phasiRNAs induced upon infection (Tables S22-S24) and associated with 969 unique va-phasiRNA:RNA target pairs targeting 413 different genes upon infection. Whereas va-phasiRNAs derived from both dsRNA strands of genes for Chlorophyll a-b binding protein 1 were found to target their own transcript or other highly homologous transcripts of the same gene family (Table S25), va-phasiRNAs derived from NBR1 and TAR1 genes also target the mRNAs of other genes (Table S26 and Table 27). A predominant group of target genes for NBR1 va-phasiRNAs that was redundantly identified in several PARE analysis replicates encodes ACTIN DEPOLYMERIZATION FACTOR 3 (ADF3) (Table S26). ADF3 was recently shown to play an important role in plant defense against aphids (Mondal et al. 2018). It is interesting that the trans-acting NBR1-derived va-phasiRNAs with secondary gene targets map exactly to the peaks of va-phasiRNA production along the NBR1 transcript (Fig. 4). This suggests that the efficient cleavage of va-phasiRNA targets is already programmed at the level of the va-phasiRNA-producing

gene or that the va-phasiRNAs associated with target cleavage are stabilized by association with their effector complexes.

Taken together, these observations demonstrate that virus infection in rapeseed triggers the production of secondary siRNAs from numerous coding genes. Some of these genes, like those encoding AGO2, EF2, or CDC48E produce secondary siRNAs that do not participate in guiding RISC and, therefore, may represent end-products of an RDR-dependent mRNA degradation pathway to maintain mRNA homeostasis upon infection. Other genes like those encoding Chlorophyll a-b binding protein 1, NBR1, and TAR1, produce trans-acting siRNAs with the predicted potential to target mRNAs of homologous genes within the same gene family or mRNAs of other genes.

Targeting of viral RNA by virus- and host-derived sRNAs

Although antiviral defense relies to some extent on the degradation of viral dsRNA by DCL enzymes, virus-derived siRNAs were found in association with AGO proteins (Garcia-Ruiz et al. 2015; Pantaleo et al. 2007; Zhang et al. 2006), thus suggesting a role of RISC-mediated viral RNA cleavage. Given that the viral genomic RNA of TuMV is polyadenylated in infected cells and degradome analysis by PARE relies on the analysis of polyadenylated RNA fragments, we wondered whether we can find virus-specific degradome signatures of the viral (+) and (-) strands in our degradome data from infected samples. PAREsnip analysis revealed 56 unique vsiRNAs derived from the negative strand of the virus present in unique vsiRNA:vRNA target pairs, thus suggesting that viral genomic RNA is indeed cleaved by vsiRNA-programmed RISC. We found 36 unique vsiRNA:vRNA target pairs in Drakkar (Table S28) and 58 unique vsiRNA:vRNA target pairs in Tanto (Table 29). Of these, 26 unique vsiRNAs:vRNA target pairs were commonly found in both Drakkar and Tanto, whereas four and 26 of the unique pairs were Drakkar- and Tanto-specific, respectively. Although most of the cultivar-specific pairs rank relatively low with respect to the number of their specific vRNA cleavage fragments, the vsiRNA CAGTGCTGCTGCTTTCATCTG was associated with vRNA cleavage events at relatively high frequencies specifically in Tanto.

Interestingly, in addition these vsiRNA derived from the virus, we identified 87 unique virus-targeting sRNAs that were derived from the host (hsRNAs, host-derived siRNAs). We found 45 unique hsRNA:vRNA target pairs in Drakkar (Table S30) and 64 unique hsRNA:vRNA target pairs in Tanto (Table S31). 23 of the unique hsRNA:vRNA target pairs occurred in both cultivars and 22 and 41 of them were Drakkar- and Tanto-specific, respectively. The most frequent RISC-mediated vRNA cleavage events potentially involving vsiRNAs and hsRNAs were detected in the 3’ region of the viral

RNA (Fig. 5), which may be caused by a limitation in the length of cDNAs synthesized for PAREseq analysis. vsiRNA:vRNA and hsRNA:vRNA pairs found in both cultivars and associated with cleavage events found at the same positions of the vRNA in both cultivars provide mutual support for the significance of these viral sites of RISC-mediated cleavage. Cultivar-specific sites of vRNA cleavage may be related to the difference in viral susceptibility between Drakkar and Tanto. Interestingly, several of the hsRNA-mediated cleavage events were found to involve trans-acting va-phasiRNAs derived from NBR1 and TAR1 genes (Table S30 and Table S31). However, the large majority of the cleavage events were associated with unique hsRNAs derived from genes annotated as disease resistance genes TAO1 and RPP5, both encoding TIR-NB-LRR receptor-like proteins. These and several other genes associated with hsRNA-mediated antiviral vRNA cleavage produce numerous secondary siRNAs in both mock-treated as well as TuMV-infected plants (Figure S11). Thus, these genes produce antiviral siRNAs already before infection.

Discussion

sRNAs have emerged as key players of RNA silencing in the regulation of various biological processes, including plant growth and development, host immunity and pathogen virulence. As viruses replicate within plant cells viruses become an integrated part of this sRNA-mediated regulatory network. The plant host silencing machinery is known to process the double-stranded viral replication intermediates into primary and secondary vsiRNAs to use them as guides for cleavage of vRNA by AGO-RISC and that viruses suppress this antiviral host activity with their VSRs. However, although sRNAs and protein effectors in fungi, oomycetes, and bacteria have been shown to function in promoting pathogen virulence (Weiberg et al. 2014), much less is known about the potential of viruses to use their vsiRNAs and VSRs to target the expression of host genes. While the general impact of viral infection on host transcriptomes, the profiles of sRNAs, the methylation of sRNAs, and activities of specific miRNAs and few virus- or viroid-derived siRNAs have been described (e.g. Hu et al. 2011; Huang et al. 2016; Niu et al. 2015; Ruiz-Ferrer and Voinnet 2009; Varallyay et al. 2010; Whitham et al. 2006), a deep understanding of host and viral sRNA activities in mutual regulation within the viral niche of infected leaf cells engaged in local viral replication and spread has not yet been achieved. The current study has applied a combination of different replicate RNA profiling approaches to the analysis of distinct local sites of early TuMV infection in rapeseed leaves. By using rapeseed cultivars strongly differing in susceptibility to this economically important virus (Edwardson and Christie 1991; Shattuck 1992) the data distinguish general mechanisms involved in

virus infection from those that may correspond to resistance. Transcriptional RNAseq profiling revealed the regulation of virus-responsive genes whereas the combination of sRNAseq with PAREseq profiles allowed us to correlate the occurrence of cleaved mRNA 5'ends with corresponding sRNA:mRNA target pairs and thereby identify the virus-induced activity of sRNAs, including previously unknown miRNAs and siRNAs, in RISC-mediated RNA target cleavage. Collectively, the results draw a novel picture of interactions between a virus and its host (Fig. 6) in which the mutual regulation of host mRNAs and the viral RNA genome by host and virus-derived small RNAs plays a central role.

First of all, the results establish the novel finding that the host apparently uses endogenous siRNAs to target the virus, whereas the virus, in turn, uses vsiRNAs to target the host. The host-derived siRNAs that target the virus are derived from genes that convert all or part of their mRNA transcripts into secondary siRNAs. Such production of phased secondary siRNAs (phasiRNAs) has emerged as a regulatory mechanism for coding genes, particularly of nucleotide-binding, leucine-rich repeat (NB-LRR) disease resistance genes (Fei et al. 2013). Consistently, we found that siRNAs that target the virus are predominantly derived from resistance genes TAO1 and RPP5. This finding indicates that by conversion of their transcripts to siRNAs, resistance genes have the capacity to provide RNA-based immunity in addition to protein-based immunity. Interestingly, TAO1 and RPP5 produce phasiRNAs also in the absence of the virus suggesting that antiviral siRNA production from these genes serves to provide basal antiviral immunity already in naïve plants. Additional siRNAs targeting the virus derive from genes that produce siRNAs only upon infection, such as the Chroropylll a, b-binding protein 1 and NBR1 genes, or produce additional siRNAs upon infection such as the TAR1 genes. As previously noted in Arabidopsis and other viral host systems (Cao et al. 2014; Zheng et al. 2015), we found that virus infection indeed promotes a dramatic induction of phased secondary siRNA (va-phasiRNA) production from coding genes. According to our results, the va-phasiRNAs induced by TuMV infection in rapeseed greatly differ in their activity as guides for RISC in a manner dependent on the gene of origin. Some genes produce va-phasiRNAs not participating in RISC-mediated mRNA target cleavage (e.g. AGO2 genes), whereas other genes produce phasiRNAs that do participate in RISC-mediated mRNA target cleavage and target the gene of origin as well as homologous genes in the same gene family (e.g. Chorophyll-a,b-binding protein 1 genes). Yet other genes produce va-phasiRNAs that target other genes (e.g. NBR1 and TAR genes). The induction of va-phasiRNAs likely serves to dampen the effects of infection on transcript homeostasis. This might be particularly true for va-phasiRNAs that do not participate in RISC-mediated target cleavage, or

target only the gene of origin or genes within the same family. On the other hand, the loci that produce trans-acting va-phasiRNAs may be induced by the virus to modify the expression of secondary mRNA targets. This is supported, for example, by the virus-induced targeting of genes for ACTIN-DEPOLYMERIZING FACTOR 3 by NBR1-derived va-phasiRNAs, which may represent a virus-induced mechanism to lower defense against aphids that the virus needs for plant-to-plant transmission. These and other genes targeted by virus-induced and predominantly NBR1-derived va-phasiRNAs identify NBR1 genes as virus-inducible hubs for secondary trans-acting siRNA production and for the virus-induced manipulation of secondary mRNA targets. As NBR1-derived va-phasiRNAs also target the virus, the evolution of NBR1 genes as virus-inducible hubs for secondary trans-acting siRNA production may have occurred on the basis of the precondition that the va-phasiRNAs derived from the same hub will, in turn, also control the virus. It is intriguing that the *B. napus* NBR1 genes are highly homologous to the selective autophagy receptor protein AT4G24690/NBR1 gene in Arabidopsis (81-84% identity), which has been implicated in antiviral defenses involving the degradation of viral proteins and particles by autophagy (Hafren et al. 2017; Hafren and Hofius 2017) This protein was in particular shown to suppress TuMV infection in Arabidopsis by targeting the VSR of the virus (HcPro) (Hafren et al. 2018). Thus, by conversion of NBR1 mRNA into secondary siRNAs the virus gains widespread control over host gene expression and also suppresses NBR1 mRNA levels to control the antiviral functions of the NBR1 protein (Fig. 7).

Among the host mRNAs targeted by virus-derived siRNAs (vsRNAs), we identified 17 unique transcripts representing the most significant targets in both Drakkar and Tanto. Interestingly, all these transcripts encode ethylene responsive factors (ERFs) and are targeted by a specific unique vsiRNA. The targeted ERFs all contain a repression domain and therefore can act to actively inhibit transcription (Licausi et al. 2013). The vsiRNA mediates the cleavage of these transcripts at exactly the site usually cleaved by miR172. Since this miRNA is downregulated upon infection, this vsiRNA may mimic miR172 to maintain efficient control over the expression of ERFs, which regulate plant responses to biotic and abiotic stresses (Licausi et al. 2013; Muller and Munne-Bosch 2015). It is interesting that this vsiRNA is only 19 nucleotides (nt) in length. This particular length may have been selected to evade capturing by the TuMV VSR (HcPro), which specifically binds 21 and 22 nt sRNAs (Del Toro et al. 2017; Valli et al. 2018). Thus, unlike the 21 nt long miR172, which is prone to capturing by HcPro, the vsiRNA may remain active even at high VSR levels (Fig. 8). The observation that the mRNAs for ERFs and other host mRNA targets of vsiRNAs are only moderately

downregulated during infection suggests that the vsiRNA-mediated interaction of the virus with these genes may have evolved to interfere with a strong induction of these defense-related genes in infected cells.

The sRNA-mediated mechanisms described here were identified in two different rapeseed cultivars, which confirms the significance of the observations. Although these cultivars differ strongly in their susceptibility towards TuMV, the sRNA-mediated mechanisms seem rather be unrelated to these differences. Although we found cultivar specific cleavage sites in the vRNA, infection in these cultivars generally cause rather similar changes in the levels of host sRNAs and their mRNA targets. The specific susceptibility of the cultivars for TuMV infection is rather correlated with strong differences in the virus-induced mRNA levels of other genes. Resistance in Tanto is correlated with the cultivar-specific or pronounced expression of several important defense-related genes, (e.g. DTX47/EDS5, GH3.12, NIMIN-2, TAO1), whereas promoted infection in Drakkar correlates with the cultivar-specific or pronounced expression of genes involved in virus replication and movement (e.g. a COP-I subunit), the down -regulation of genes with potential to inhibit systemic movement (e.g. PPA2), or the attenuation of plant defenses (e.g. NAC60, RPK2, TPR2, CKX3). These genes, and also the NBR1 and TAR1 genes that spawn virus-induced secondary siRNAs for widespread virus-induced gene regulation, may represent important targets for plant engineering.

Materials and Methods

Plant materials, plant growth conditions, virus inoculation, and RNA extraction

Brassica napus cv. Drakkar and *Brassica napus* cv. Tanto plants grown for 4-5 weeks in a growth chamber at 24 ^{o}C with a 16h photoperiod were mechanically inoculated with freshly prepared crude extract (sap) of donor *B. napus* cv Drakkar plants systemically infected with TuMV-GFP. The donor plants were mechanically inoculated with sap from systemically infected *Nicotiana benthamiana* plants. Sap was always created by grinding infected leaves in 75 mM potassium phosphate buffer pH 7.5 in a cooled mortar. To create the original *N. benthamiana* donor plants, five weeks old *N. benthamiana* plants grown at 25^{o}C with a 16h photoperiod were inoculated by agroinfiltration of two leaves per plant with *A. tumefaciens* strain GV3101 containing the binary plasmid pCB-TuMV-GFP (Dunoyer et al. 2004; Lellis et al. 2002). The agrobacteria were grown over night and pressure-injected at an OD_{600nm} of 0.5 using a syringe without needle. The TuMV (UK1) construct present in plasmid pCB-TuMV-GFP (GenBank: EF028235.1) has been verified by sequencing before use.

Inoculated leaves were monitored with a handheld UV lamp (UVP Blak-Ray B-100) to reveal GFP fluorescent infection sites. TuMV-GFP infection sites in the inoculated leaves of *B. napus* cv Drakkar and *B. napus* cv Tanto plants were carefully isolated at 12 dpi with a 0.5 cm micropunch and immediately frozen in liquid nitrogen. Leaf disks of mock treated *B. napus* cv Drakkar (sample DM) and mock-treated *B. napus* cv Tanto plants (sample TM) as well as infection sites on virus-treated *B. napus* cv Drakkar (sample DT) and infection sites on virus-treated *B. napus* cv Tanto plants (sample TT) were dissected from three independent inoculation experiments. Thus, three samples each of DM, DT, TM, and TT, were created.

Total RNA of each sample was extracted from ca 200 dissected leaf-disks / infection foci. Two grams (2 g) of these were ground in liquid nitrogen and RNA was purified using the RNAeasy Mini Kit (Qiagen). The quality of each RNA sample was verified by gel electrophoresis and BioAnalyzer (Agilent technologies) techniques. The relative number of viral genomes in the samples was determined by RT-qPCR amplifying the TuMV CP cistron using oligonucleotide TGTTCGGCTTGGATGGAA as forward primer and oligonucleotide TTAACGTCCTCGGTCGTATGC as reverse primer within 30 ng total RNA. sRNAseq and mRNAseq sequencing libraries were constructed and sequenced (Illumina HiSeq2000) by aScidea Computational Biology Solutions (http://www.ascidea.com/). mRNA and sRNA reads were created by (2x100bp) paired-end sequencing and (1x50bp) sequencing, respectively.

Degradome sequencing

Degradome libraries were constructed from each RNA sample essentially as described previously (German et al. 2009). Briefly, mRNA was purified from 75-150 µg of total RNA using the Dynabeads mRNA direct purification kit (Ambion). 1 µg of the isolated mRNA was ligated to a 5' RNA adapter, purified using Dynabeads and used for the cDNA synthesis, PCR amplification and MmeI digestion. The 20 nt DNA fragments resulting from MmeI digestion were purified by polyacrylamide gel electrophoresis (PAGE) and 3’ ligated to a dsDNA adapter. The ligation products were further purified by PAGE and amplified by PCR using indexed Illumina primers (Illumina primers RPI1 to RPI4) to allow multiplexing during sequencing. The final libraries consisting of amplicons of approximately 125 bp were again purified by PAGE. The suitability of our libraries for high-throughput sequencing was tested by cloning them into TOPO vector and low-scale sequencing of individual clones. After quantification using Nanodrop, the degradome libraries were sequenced (1x 50 bp) on an Illumina HiSeq2000 platform by aScidea.

Whole genome re-sequencing

DNA isolated from 1.9 g fast-frozen leaf tissue of *B. napus* cv Drakkar and *B. napus* cv Tanto plants was used for creation of 800 bp insert PCR-free libraries and subsequent paired-end sequencing (2*150 bp) on an Illumina HiSeq 4000 platform (BGI Tech Solutions, Hongkong). The 123 Mio clean reads obtained for each cultivar were mapped to the *B.napus* "Darmor-bzh" reference genome sequence (Genoscope v4.1; (Chalhoub et al. 2014)) with the Burrows-Wheeler Aligner **BWA-MEM** algorithm ((Li and Durbin 2009); RRID:SCR_010910) version **v0.7.15-r1142**, using default parameters. Duplicated reads were marked with **Picard-tools** (RRID:SCR_006525; http://broadinstitute.github.io/picard/) version **v1.140** and SNPs calling was performed with GATK **HaplotypeCaller** ((McKenna et al. 2010), RRID:SCR_001876) version **v3.3-0**. Only high-quality homozygous SNPs were kept using the filters: QD < 2.0 || FS > 60.0 || MQ < 40.0 || MQRankSum < -12.5 || ReadPosRankSum < -8.0 || DP < 4. Representative genomes for Drakkar and Tanto cultivars were constructed by inferring these cultivar-specific high confidence SNPs into the reference sequence with GATK FastaAlternateReferenceMaker (RRID:SCR_001876; https://software.broadinstitute.org/gatk/documentation/tooldocs/3.8-0/org_broadinstitute_gatk_tools_walkers_fasta_FastaAlternateReferenceMaker.php). The reconstructed Drakkar and Tanto genomes were used for the rest of the analysis.

Bioinformatic analysis of mRNA, sRNA, and degradome profiles

mRNAseq raw reads libraries were quality checked with **FastQC** (RRID:SCR_014583) version **v0.11.2** and cleaned with **cutadapt** (RRID:SCR_011841) version **v1.8.1** for adapter removal, N removal and quality filtering. Reads longer than 60 bp and with a Phred score greater than 30 where kept. The clean RNAseq reads from the Tanto and Drakkar samples were then aligned to the reconstructed Tanto and Drakkar genomes, respectively, using **Tophat2** ((Kim et al. 2013), https://ccb.jhu.edu/software/tophat/index.shtml) version **v2.0.13**, allowing one mismatch and applying **Bowtie2** ((Langmead and Salzberg 2012), http://bowtie-bio.sourceforge.net/bowtie2/index.shtml) as its read-alignment engine. Genes were re-annotated with **blastx** against the *Arabidopsis thaliana* genome (with default parameters) and the Arabidopsis gene identifiers were used receive the gene ontology (GO) annotations from the protein knowledgebase (UniProtKB). For differential expression analysis the mapped reads were counted using the **SAMtools** (Li et al. 2009) (RRID:SCR_002105) **idxstats tool** version **v1.1**, and analyzed using **Bioconductor - DESeq2** (Love et al. 2014)(RRID:SCR_015687) version **v1.10.0**. The results were

filtered for expressed transcripts with at least 150 mean reads and showing statistically significant changes (p-value < 0.05) in expression between conditions.

sRNAseq raw read libraries were quality checked and reads were filtered like the mRNAseq read libraries. Clean reads that were 18 nt to 30 nt in length and that had a Phred score higher than 30 were kept and then annotated by mapping them with no mismatches to TuMV-GFP and to miRNAs of *Brassicacea* (*B. napus*, *B. oleracea*, *B. rapa*, *A. thaliana*, *A. lyrate*) compiled from miRbase (Kozomara and Griffiths-Jones 2014) using **Bowtie2** (Langmead and Salzberg 2012) version **v2.2.9** and applying the option "-t -N 0 --end-to-end --very-sensitive --score-min C,0,0" with no mismatch for virus -derived sRNAs. The set of miRNAs derived from miRbase was complemented by miRNAs described in recent publications (Jiang et al. 2014; Lukasik et al. 2013; Xu et al. 2012) and by miRNAs derived from miRNA genes predicted by **ShortStack** (Axtell, 2013)(RRID:SCR_010834). We used ShortStack version **v3.4.** in *de novo* mode and the list of predicted miRNAs was filtered to keep only clusters with: Dicer call 21, 22, 24nt, and MIRNAs step Y_N15. The total list of known miRNAs contained 1047 miRNAs, against which the sRNA reads were aligned. sRNA reads that were strongly induced by infection and could be mapped to both strands of *B. napus* coding genes but not to the viral genome likely represent a specific class of RDR1-dependent siRNAs identified in Arabidopsis and known as vasiRNAs (virus-associated siRNAs, (Cao et al. 2014)). Although the virus-induced *B. napus* siRNAs show phasing along the transcript of origin like vasiRNAs, we do not know the specific RDR by which these siRNAs are produced. Therefore, we refer to these siRNAs as "va-phasiRNAs" rather than to vasiRNAs. We focused our analysis on va-phasiRNAs that were 21 nt in length and represented by at least 100 reads in the samples from infected tissues. Moreover, va-phasiRNA-producing genes had a PHAS Score higher than 30 (determined by **ShortStack**). The virus-induced and phased production of the va-phasiRNAs was verified by visualization of the gene-specific siRNA pattern with the Integrated Genome Viewer tool IGV 2.3 (Thorvaldsdottir et al. 2013).

Similar as for mRNAseq and siRNAseq reads, also the sequenced degradome read libraries were cleaned with **cutadapt** (RRID:SCR_011841) version **v1.8.1** for adapter removal, N removal and quality filtering. Clean libraries were then analysed with **PAREsnip** (Folkes et al. 2012) implemented in the UEA sRNA Workbench (http://srna-workbench.cmp.uea.ac.uk/; (Stocks et al. 2018) version v4.2.1 alphaD, with min read abundance set to 100 and default parameters, and using the sRNAseq and mRNAseq data as inputs to predict sRNA:mRNA pairs associated with identified monophosphorylated mRNA 5'ends and consistent with sRNA-mediated RNA target cleavage. Specific cleavage events were normalized and compared between samples in reads per million (rpm;

number of specific cleavage events multiplied by10^6 and divided by the total number of cleavage events in the degradome library). The sums of normalized cleavage events occurring in the three replicates per condition (specific cultivar/specific treatment) were used to compare specific cleavage events between conditions. The gene or viral origins of the sRNAs associated with specific mRNA or viral RNA cleavage events were identified by extracting the sRNA associated with a specific cleavage event from PAREsnip and by aligning its sequence to the cultivar/viral transcriptome without mismatch, using **Bowtie 2**. A role of a given sRNA (e.g. miRNA, vasiRNA, vsRNA) in specific RNA target cleavage was determined by searching the sRNA:RNA target pair outputs of PAREsnip with the specific sRNA query sequence(s).

Quantitative RT-PCR

Total RNA was isolated from ca 150 leaf disk samples of infection sites or of mock-treated, non-infected control tissues each pooled from ten plants, respectively. After grinding, 0.1 g fine powder was homogenized and extracted with Trizol reagent (Invitrogen, USA) following the manufacturer's instructions. RNA quantities were determined by spectrophotometric analysis using Nanodrop equipment (Thermo Scientific, USA). 1-2 µg of the RNA preparations were reverse-transcribed using an oligo dT primer and SuperScript IV reverse transcriptase (200 U/µl) (Invitrogen). The abundance of specific transcript was measured by probing the cDNA by quantitative real-time PCR using a SYBR-green master mix (Roche) and allele-specific primers (Table S32) in a Lightcycler 480 (Roche). Because the mRNAseq data refer to changes in the expression of specific A- or-C-genome-specific alleles, the analysis was performed with genes for which allele-specific, intron-spanning primer sets showing no homology to any other paralogs or homologous sequences could be designed. The specific transcript levels were measured in five independent biological replicate samples for each cultivar and respective mock-treated and virus-infected conditions. Each RNA sample was analyzed by three technical replicates and specific RNA levels were normalized against the levels of transcripts produced by two known housekeeping genes (Bra011516 encoding a TIP41-like protein and BnaA08g11790D ('BnaUP1'; unknown function) (Wang et al. 2014; Zhang et al. 2014)). Significant differences in mRNA abundance between samples of the mock- and virus-treated conditions were determined by an F-test (test for homoscedasticity) followed by a t-test. The statistical significance levels in figures are shown with asterisks: $p<0.05$ = *; $p<0.01$ = **; $p<0.001$ =***.

5' RACE

mRNA 5'ends were analyzed by 5'RACE as described previously (Llave et al. 2011; Llave et al. 2002). poly(A)$^+$ mRNA was purified from 1-5 µg total RNA using a magnetic isolation module (NEBNext®, BioLabs) and ligated to the GeneRacer RNA oligo 5'RACE adapter (Invitrogen) using T4 RNA ligase (New England BioLabs). The ligation product was purified using Illustra Microspin S-300 Sephacryl columns (GE Healthcare) and reverse transcribed into cDNA using an oligo(dT)$_{20}$ primer and SuperScript IV reverse transcriptase (200 U/µl, Invitrogen). Each cDNA was then used of PCR amplification using the GeneRacer 5'RACE outer primer mapping to a sequence within the 5' adapter and two nested, gene specific primers (Table S33). The PCR products were purified with a PCR clean-up kit (Macherey-Nagel) and sequenced with an ABI3130xl sequencer (Applied Life Technologies).

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Figures:

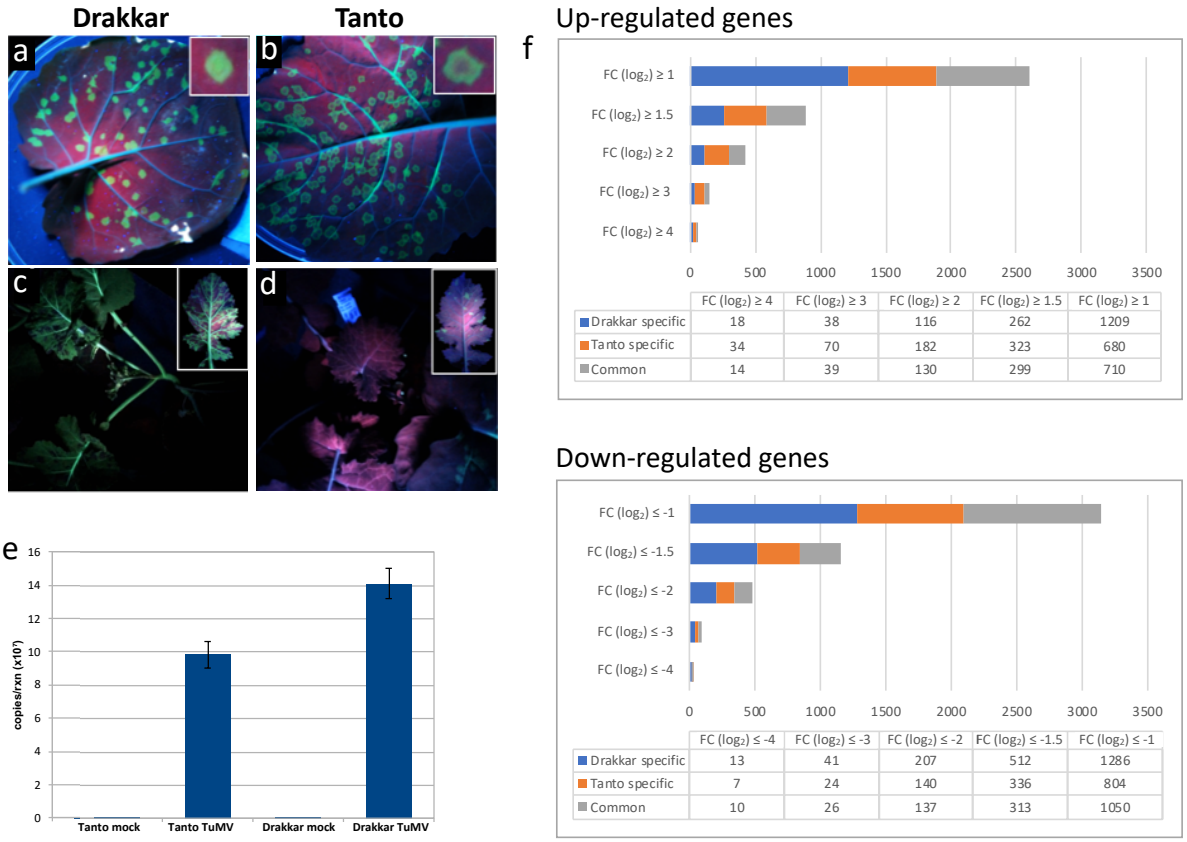


Fig. 1. TuMV-GFP infection in *B. napus*. a-d, local (6 dpi; **a**, **b**) and systemic (14 dpi; **c**, **d**) TuMV-GFP infection in Drakkar (**a**, **c**) and Tanto (**b**, **d**). Local infection foci in leaves have a disk-shaped appearance in Drakkar (**a**) and halo-shaped appearance in Tanto (**b**). TuMV exhibits efficient systemic spread in Drakkar (**c**) but not in Tanto (**d**). **e**, number of TuMV-GFP genome copies within expanded local infection foci at 12 dpi determined by RT-qPCR. Genome copies present in 30 ng total RNA were calculated using a RT-qPCR standard curve obtained for samples with known concentrations of *in vitro*-transcribed TuMV RNA. **f**, number of up-and down-regulated genes within infection foci of infected Drakkar and Tanto plants. The number of differentially expressed genes differs according to the applied fold change (FC) threshold (log_2 values). Considered mRNAs were represented by at least 150 mean reads (treatment and control) in each replicate experiment and showing statistically significant changes (p-value < 0.05) in expression between control and treatment conditions.

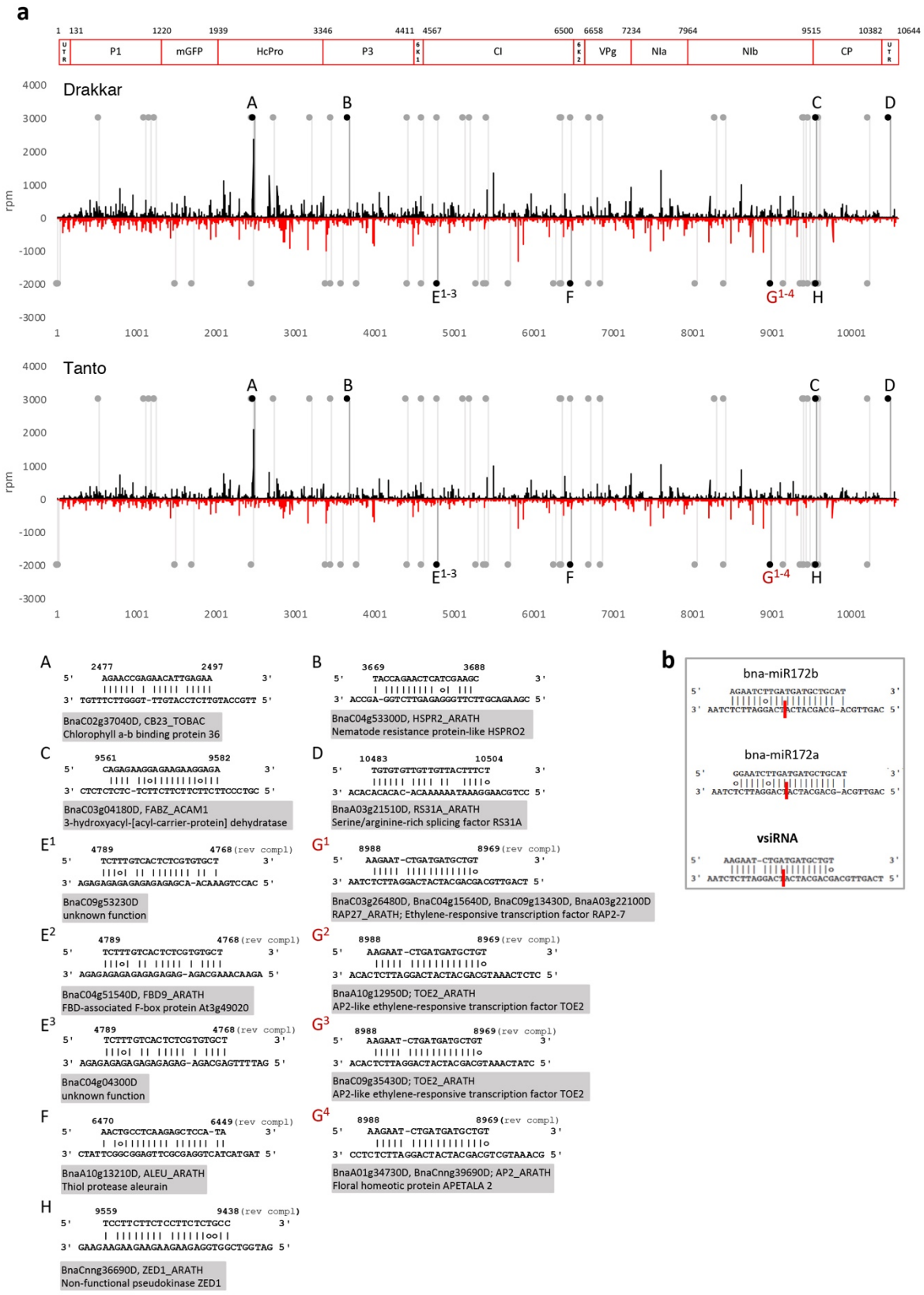
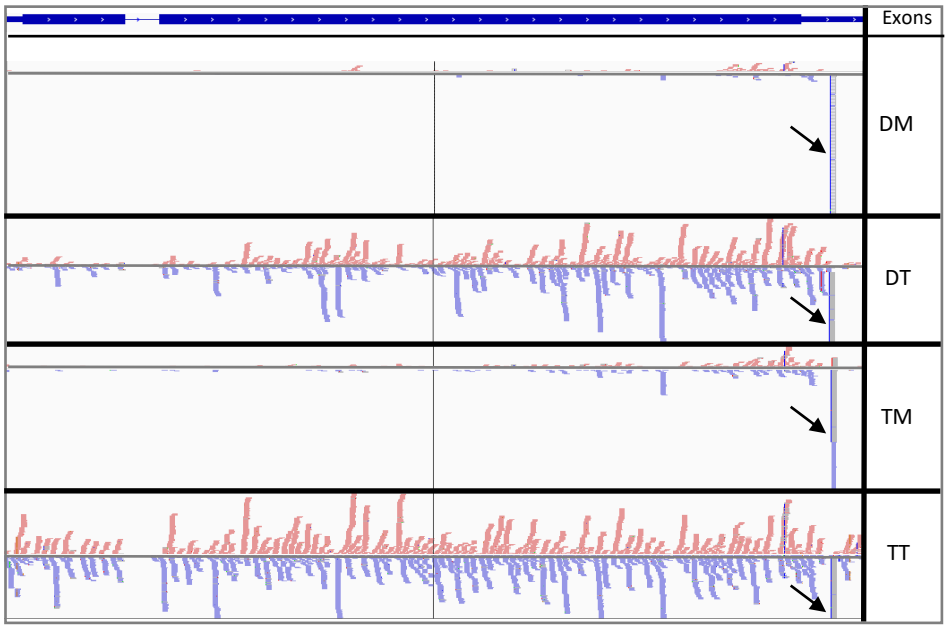


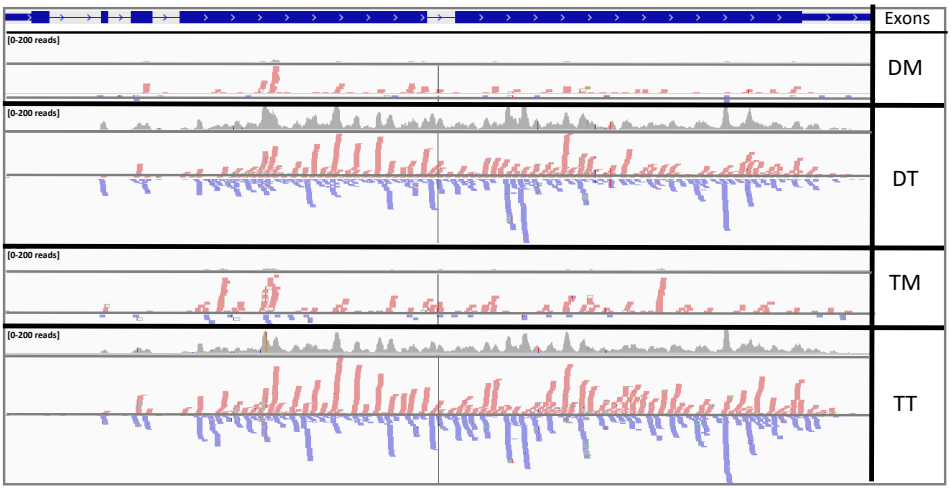
Fig. 2. vsiRNA profile and trans-acting vsiRNAs that target host genes. a, vsiRNAs found in Drakkar and Tanto aligned along the viral genome. vsiRNAs derived from the positive and negative strand of viral dsRNA are shown in black and red respectively. Untranslated regions (UTR) and proteins

encoded by the viral RNA are indicated on top of the figure. The vsiRNA profiles as well as the profiles of vsiRNAs associated with host mRNA cleavage (grey and black dots with lines indicating the position along the viral RNA) are almost identical between Drakkar and Tanto. The vsiRNA:mRNA target pairs of most significant vsiRNAs (black dots) are shown and indicated by capital letters. The vsiRNA labelled with G mimics miR172 and was found associated with cleavage of different mRNAs encoding ethylene-responsive factors (G^{1-4}). **b**, the vsiRNA labeled with 'G' in figure **a** is similar in sequence to bna-miR172a and bna-miR172b and is associated with cleavage at exactly the same site of target mRNA.

a BnaA05g14760D (AGO2)



b BnaC02g40260D (EF2, Elongation factor 2)



c BnaA05g28710D (CDC48E)

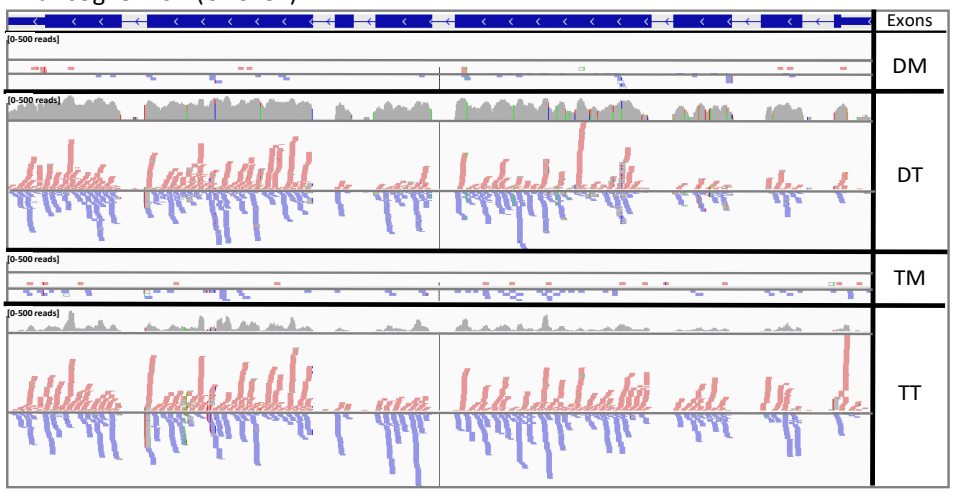


Fig. 3. Virus infection triggers the production of secondary va-phasiRNA from coding genes. a-c, Examples of va-phasiRNA-producing genes. The va-phasiRNAs of these genes were not associated with RISC-mediated RNA cleavage. For each example, the exon-intron structure of the mRNA and the alignment to the length of the mRNA of unique sRNAs sequenced in DM, DT, TM, and TT samples is shown. Unique sRNA reads derived from the positive and negative strand of the dsRNA are shown in red and blue, respectively. **b** and **c** show the amount of aligned sRNA reads (in grey). Arrows in **a**, position of miR403.

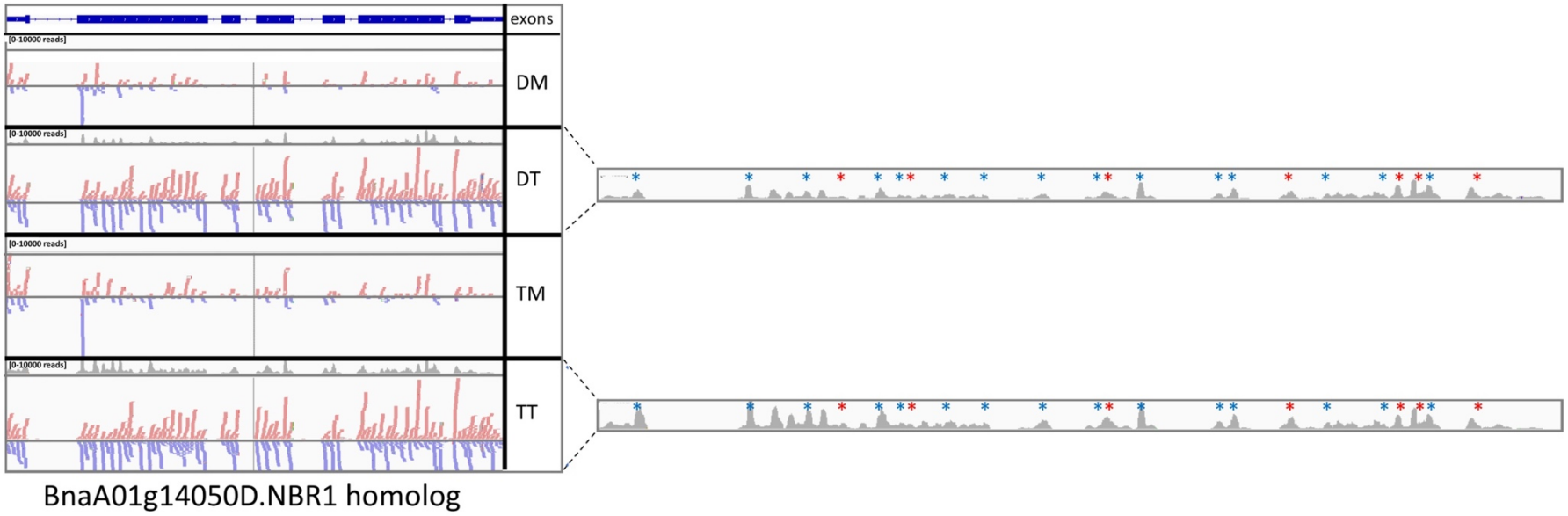


Fig. 4. NBR1-derived trans-acting va-phasiRNAs. NBR1-derived va-phasiRNAs associated with mRNA-target cleavage are derived from peaks of va-phasiRNA production. va-phasiRNAs derived from the positive and negative strand of NBR1 dsRNA are shown in red and blue, respectively.

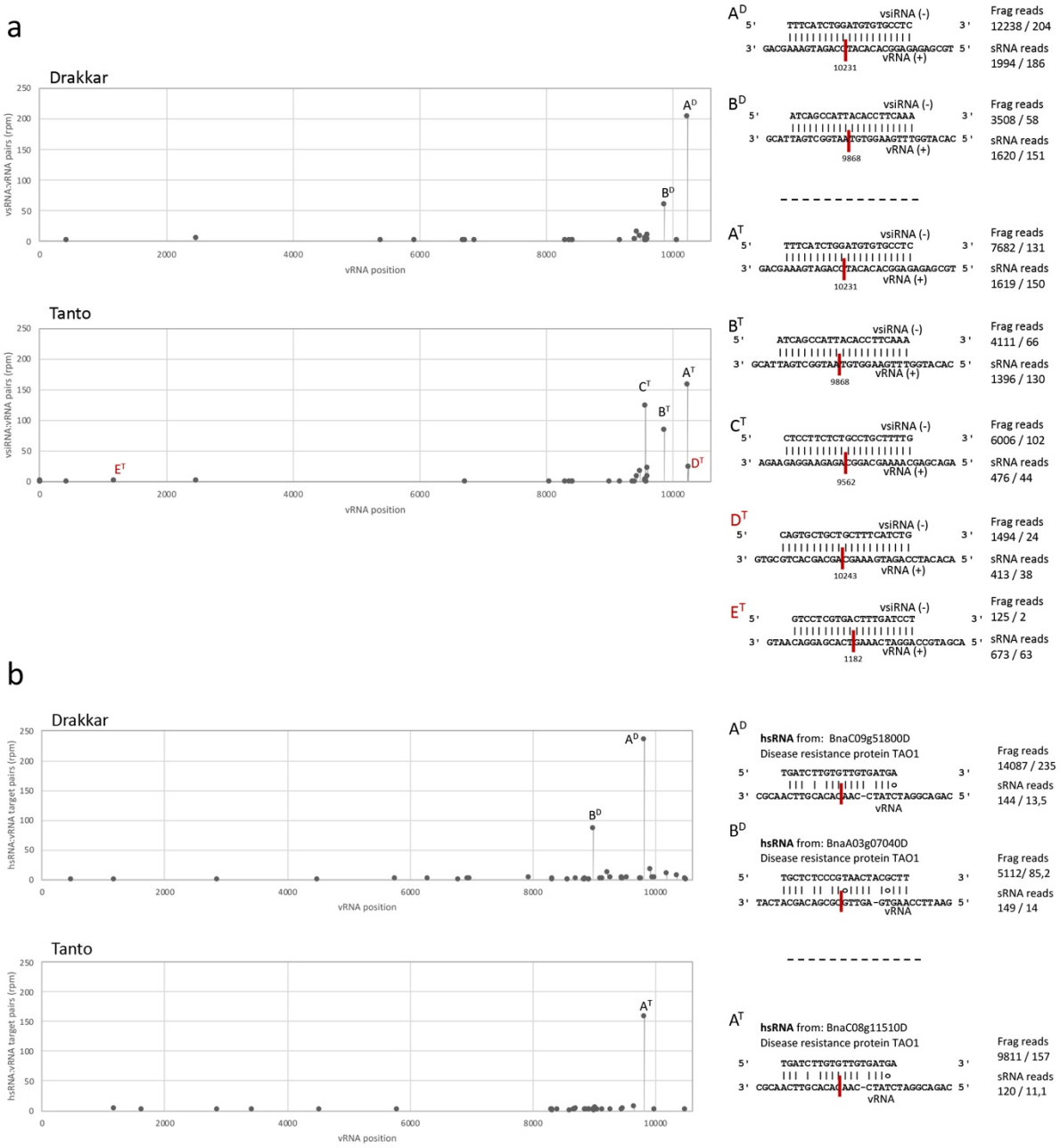


Fig. 5. RISC-mediated cleavage of viral RNA by virus and host siRNAs. a, vRNA cleavage by vsiRNAs; **b**, vRNA cleavage by host-derived siRNAs (hsRNAs). The distribution of vsiRNA:vRNA target pairs (rpm) and hsRNA:vRNA target pairs (rpm) along the vRNA is shown. The pattern of vRNA cleavage by vsiRNAs and hsRNAs is very similar between Drakkar and Tanto. vsiRNA:vRNA target pairs D^T and E^T were found in Tanto but not in Drakkar. Target pair alignments are shown together with the numbers for specific PARE signature fragment reads (Frag reads: total reads / rpm) and respective vsiRNA and hsRNA reads (sRNA reads: total reads / rpm).

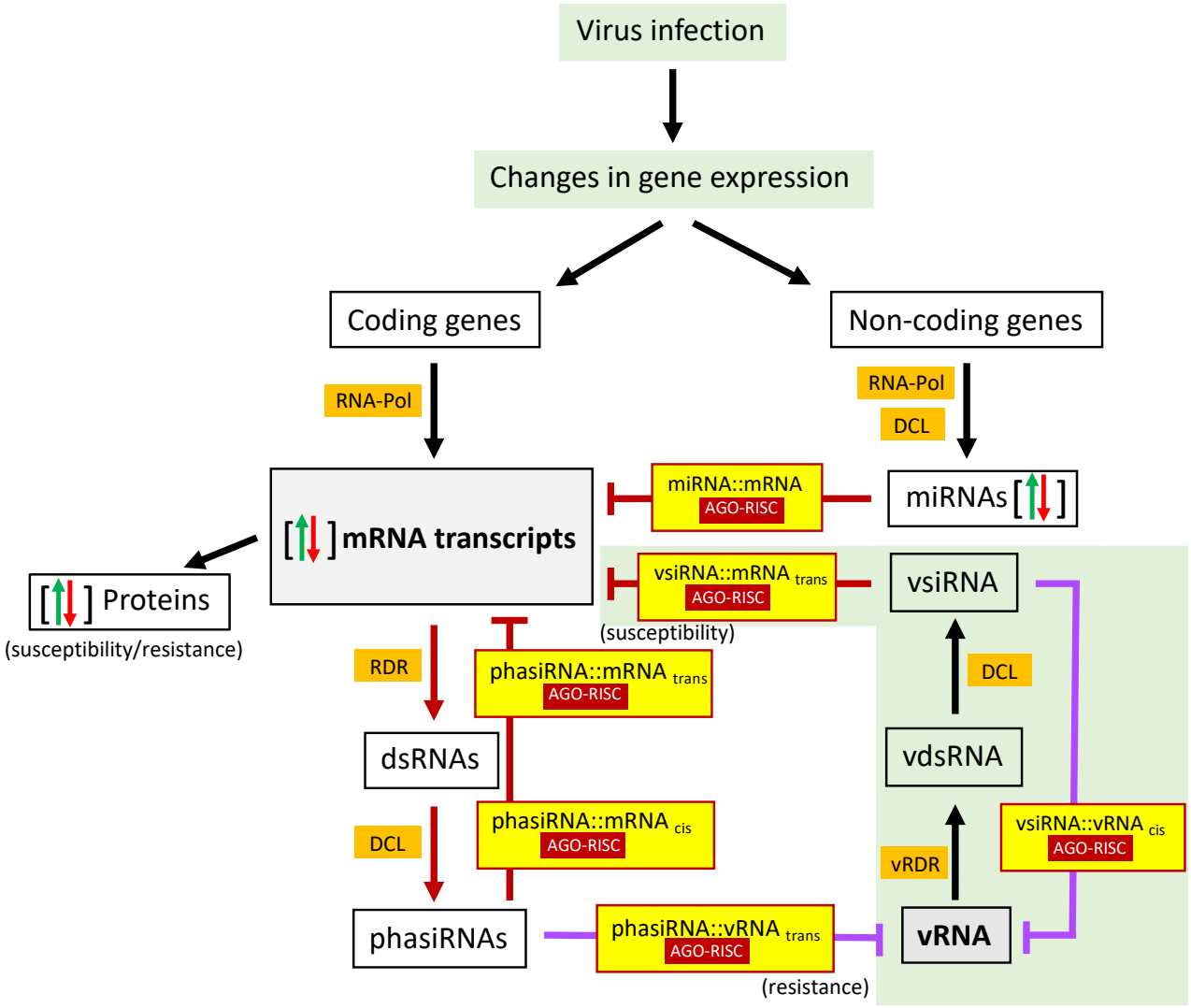


Fig. 6. Model of multiple virus:host interactions involving sRNAs. Virus infection causes changes in expression of coding and non-coding genes. Resulting changes in the levels of mRNA transcripts can lead to changes in the levels of encoded proteins that may play an important role in the determination of host susceptibility and resistance. Changes in the expression of non-coding genes leads to changes in the levels of miRNAs, which, in turn, control the levels of their mRNA targets by miRNA guided, RISC-mediated mRNA cleavage. Virus infection also triggers the ability of some genes to convert their mRNA transcripts via the formation of dsRNA into va-phasiRNAs. For some genes, va-phasiRNAs are the end product of a virus-induced pathway to control the transcript level (e.g. AGO2), whereas for other genes va-phasiRNAs engage RISC-mediated cleavage of either the transcript of origin, the transcript of origin as well as the transcripts of homologous genes in the same family, or of transcripts of other genes. The induction of va-phasiRNAs thus allows the virus to induce widespread regulation of secondary gene targets. The replicating virus, in turn, is primarily

controlled by DCL-mediated cleavage. However, DCL cleavage, again in turn, allows the virus to use its own vsiRNAs for RISC-mediated cleavage of host mRNA transcripts. The virus-induced RISC-mediated cleavage of host transcripts by va-phasiRNAs and vsiRNAs is, once again in turn, balanced by the ability of the host to also use vsiRNAs and va-phasiRNAs to target the viral RNA.

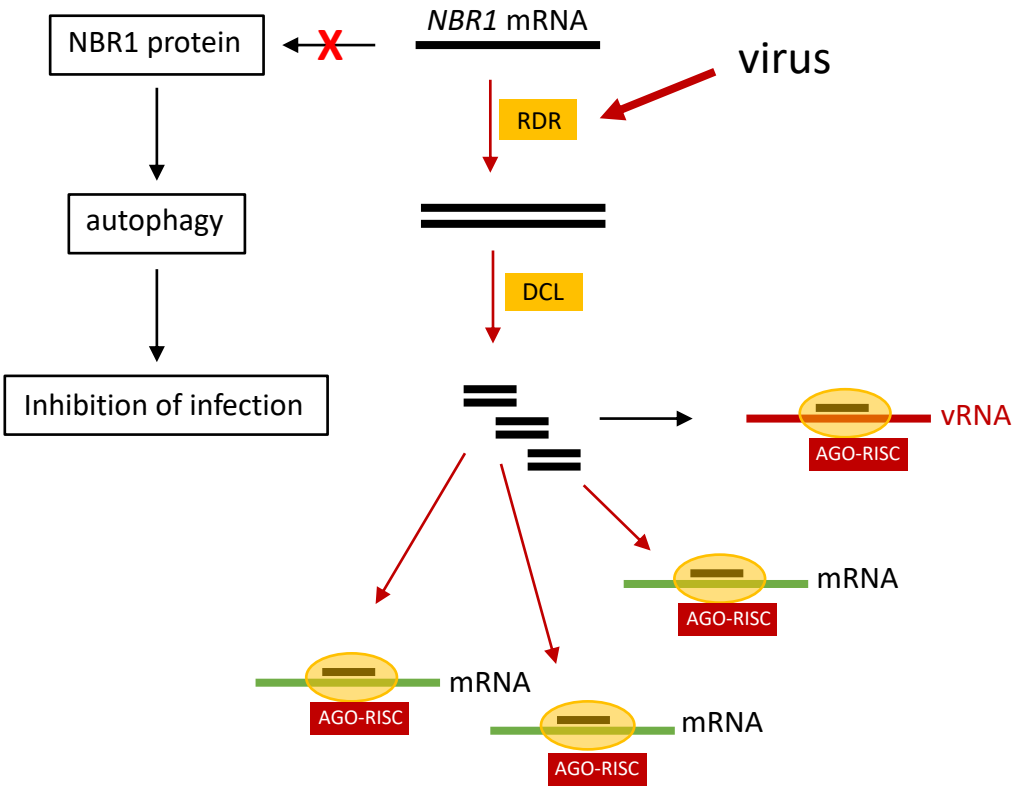


Fig. 7. NBR1 is a regulatory hub for plant:virus interactions. The NBR1 protein controls virus infection by targeting viral effector proteins (e.g. the VSR of TuMV) and viral particles for degradation by autophagy. The virus, in turn, triggers conversion of NBR1 mRNA into trans-acting va-phasiRNAs to induce widespread control over NBR1 and other gene targets. However, NBR1 va-phasi-RNAs also target the virus. Thus, the evolution of NBR1 as a virus-inducible hub for transacting siRNA production may be counterbalanced by an ability of the host to use the same locus to target the virus.

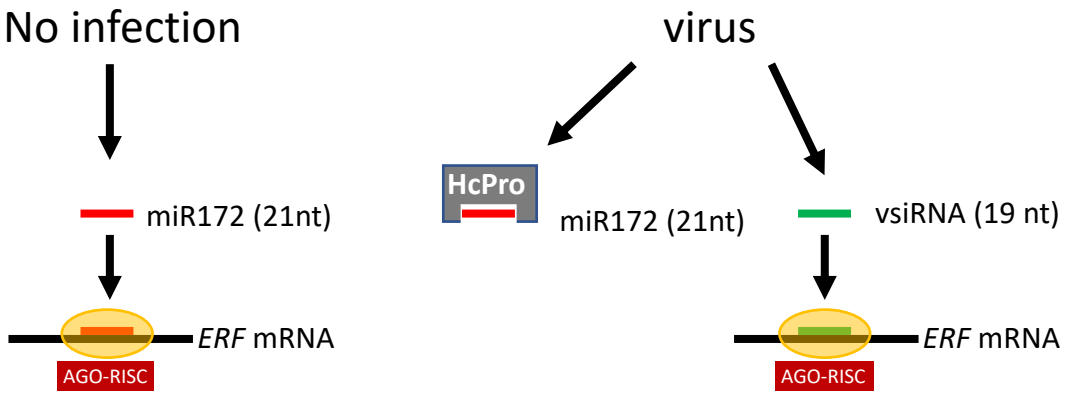


Fig. 8. A vsiRNA mimics and complements bna-miR172. In the absence of infection, the 21 nt long bna-miR172 controls the levels of mRNAs for ethylene-responsive transcription factor (ERF). During infection, bna-miR172 is trapped and inactivated by the VSR of the virus (HcPro). To keep ERF expression low, TuMV encodes a vsiRNA that mimics miR172. Because this vsiRNA is only 19 nt in length it escapes sequestration by HcPro and therefore remains active in the presence of the VSR.

Supplementary Figures and Tables are shown in APPENDIX 1.

Chapter III: Plant-virus infection and disease symptoms

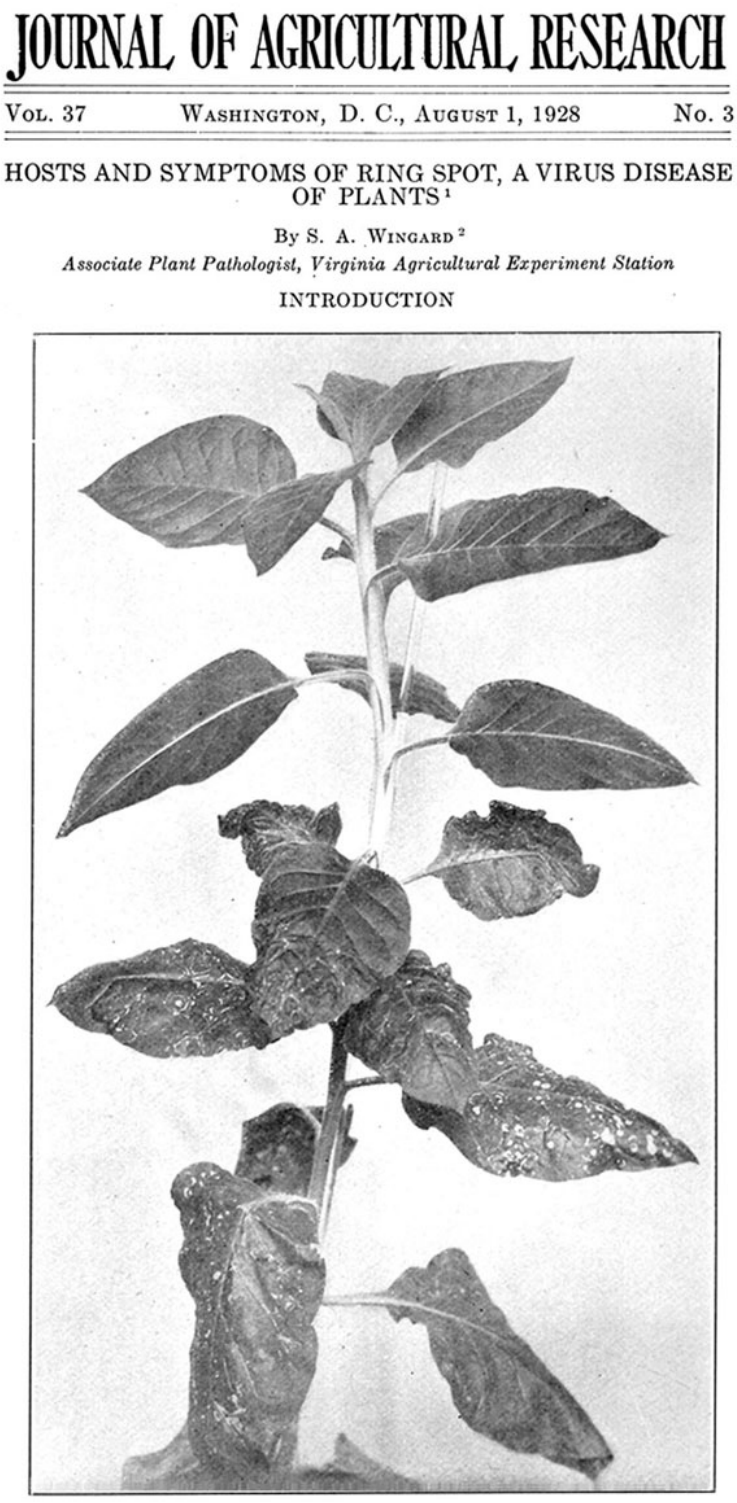
1. Introduction

Viral accumulation as well as the viral recruitment of host factors and membranes, and the interference of viral proteins with normal host cell processes can lead to various effects on plant growth and physiology. However, while certain plant:virus combinations lead to disease, other plant:virus interactions remain free of symptoms and undergo tolerance, a state in which the plant and the virus can coexist (Roossinck and Bazán 2017). Diseases caused by viruses and other pathogens in cultivated crop plants and associated losses in yield represent a global threat for food security (Calil and Fontes 2017). Thus, studies to achieve an understanding of the mechanisms that determine disease versus tolerance are of utmost importance.

A key to the mechanisms determining disease versus tolerance is provided by the phenomenon of “disease symptoms recovery”. This phenomenon describes the occurrence of heathy, “recovered” leaves on a diseased plant. Although symptoms recovery was generally believed to be caused by a strong host response able to overcome the pathogen, our team could show that Arabidopsis plants infected with ORMV undergo recovery without interfering with viral propagation. Therefore, this work showed that symptoms recovery can occur through an achievement of a tolerant state in which the virus and its host can coexist without disease (Kørner et al. 2018). The aim of his chapter is to draw the historical context of recovery, its correlation with RNA silencing, and the recent findings about this phenomenon. This chapter is followed by a description of my authorship contribution to the attached publication of Kørner et al. (2018).

1.1. The phenomenon of disease symptoms recovery

The phenomenon of symptoms recovery was described already 90 years ago for a *Tobacco ringspot virus* (*Nepovirus* genus) infection in tobacco plants (Wingard 1928) (Figure 6). Recovery in these plants occurred after 23 days of ringspot virus infection. The recovered leaves were reported immune to a second infection by the same virus. However, 90 years ago the underlying mechanism was a total mystery.



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HOSTS AND SYMPTOMS OF RING SPOT, A VIRUS DISEASE OF PLANTS[1]

By S. A. WINGARD[2]

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INTRODUCTION

Figure 6: Recovery: occurrence of healthy leaves on symptomatic plants.
Symptoms recovery in tobacco plants infected with *Tobacco ringspot virus*. Recovered leaves are immune to a second infection with the same type of virus. Crude extract preparation of these leaves is infectious to other plants (From Baulcombe 2004).

Research on recovery only started more than 60 years later, when it was found that infection of tobacco plants that were transgenic for either the *Tobacco etch virus* (TEV) CP or the *Potatovirus Y* (PVY) CP with TEV or PVY, respectively, first led to disease and then to recovery (Lindbo et al. 1993; Smith 1994). Similar to the original observations by Wingard, 1928, both transgenic plants showed immunity to a secondary infection.

Interestingly, resistance was only against the same virus used in the initial infection but not against the other virus. Thus, the recovered leaves of the plants infected with TEV showed resistance against secondary infection by TEV but were susceptible to PVY infection. Similarly, the recovered leaves of PVY-infected plants were susceptible for TEV or *Tobacco vein mottling virus* (TVMV) but resistant against secondary infection by PVY. These findings indicated that the resistance occurring in recovered leaves is virus-specific (Lindbo et al. 1993; Smith 1994). Interestingly, transgenic plants expressing a non-translatable PVY CP ORF also showed symptoms recovery upon infection with the cognate virus. This was the strong sign indicating that the mechanism behind symptoms recovery was sequence-specific and RNA-based (Smith 1994). Although today one may immediately consider RNA silencing as the responsible mechanism, the TGS and PTGS pathways and the role of small RNAs in these pathways were not yet known at this time. However, three publications established that recovery during infection by *Cauliflower mosaic virus* (CaMV) in *Brassica oleracea gongylodes*, by *Tomato black ring virus* (TBRV, *Nepovirus*) in *Nicotiana clevelandii*, and by *Tobacco rattle virus* (TRV) in *N. benthamiana* plants was correlated with reduced vRNA levels in recovered leaves as compared to symptomatic tissues, which suggesting that recovery may be related to transgene-induced gene silencing and cross-protection (Covey et al. 1997; Ratcliff et al. 1997; Ratcliff et al. 1999).

It was then soon realized that the occurrence of symptoms recovery depends on specific plant-virus combinations and is influenced by environmental factors such as daylength and temperature (Ghoshal and Sanfaçon 2014). Moreover, a reduction in vRNA levels during symptoms recovery was not always observed. This was reported, for example, in recovered tissues developed in tobacco plants infected with *Tobacco streak virus* (TSV) (Xin and Ding 2003) or in recovered tissues of *N. benthamiana* plants infected with *Tomato ringspot virus* (ToRSV) (Jovel et al. 2007). These findings suggested that symptoms recovery may not necessarily correlate with reduced viral replication or the degradation of vRNA.

1.2. Role of VSR function in the formation of disease symptoms and recovery

Understanding recovery also depends on an understanding of mechanisms that cause disease in the first place. Here, the VSRs play a specific role, because the mechanisms through which they act to suppress antiviral silencing (e.g. sequestration of small RNAs or degradation of AGO protein) are prone to also affect RNA silencing-based pathways involved in controlling host gene expression. The involvement of VSR activity in pathogenicity and symptom severity has been highlighted in several studies (e.g. Voinnet et al. 1999; Moissiard and Voinnet 2004; Voinnet 2005; Csorba et al. 2015). For example, Arabidopsis leaves constitutively expressing VSRs such as the pecluviral P15, the potyviral Hc-Pro, or the closteroviral P21 show disease symptoms with similarity to disease symptoms produced during viral infection, and the severity of the disease symptoms induced by expression of a specific VSR correlated with the efficiency by which the respective VSR controls antiviral RNA silencing (Voinnet 2005). Consistent with the role of VSR activity in disease symptom development, ectopic over-expression of Hc-Pro (PVY) or P25 (PVX) was shown to prevent recovery usually seen in tobacco plants infected with nepoviruses (Santovito et al. 2014; Siddiqui et al. 2008). In addition, the VSR of *Cucumber mosaic virus* (CMV), the 2b protein, is fundamental for disease symptom formation in *N. tabacum* or *A. thaliana* (Col-0), as a corresponding virus with compromised VSR activity (CMVΔ2b) did not trigger symptoms (Lewsey et al. 2009). Consistently, infection also with other viruses carrying mutations in their VSRs often resulted in recovery phenotypes (Hormuzdi and Bisaro 1995; Chu et al. 2000; Szittya et al. 2002; Omarov et al. 2006; Raja et al. 2008; Wu et al. 2010). This indicates that symptoms are induced by VSR activity and that a lack of VSR activity can allow recovery. However, this conclusion does not hold for all viruses, or virus strains. For example, for the subgroup IA strain Fny-CMV, both the wildtype and the VSR-deficient Fny-CMVΔ2b induced symptoms in *Chenopodium* species, *N. occidentalis* and five different *A. thaliana* ecotypes; Fny-CMVΔ2b allowed recovery only in the Arabidopsis C24 ecotype (Lewsey et al. 2009). Nevertheless, symptoms recovery is often permitted by viruses that express only weak VSRs and are not able to suppress the RNA silencing pathway efficiently (Martin-Hernandez and Baulcombe 2008; Ghoshal and Sanfaçon 2015). Thus, collectively, these findings indicated that disease symptoms are likely provoked by a strong VSR and that symptoms recovery may occur if the VSR is weak or weakened by mutation. However, as already mentioned, although a weak or

weakened VSR should be correlated with vRNA degradation, lower vRNA levels were not always observed. Translational repression rather than RNA degradation was proposed for recovery of *N. benthamiana* plants infected by *Tobacco ringspot virus* (ToRSV) (Jovel et al. 2007) since a temperature-dependent enhancement of recovery was correlated with a requirement for AGO1 and reduced translation of viral proteins despite the presence of enhanced levels of viral RNA and siRNAs (Ghoshal and Sanfacon 2014). Thus, recovery may involve a mechanism that weakens VSR activity without necessarily causing an effect on vRNA.

1.3. A potential role of antiviral meristem resistance in recovery

Since leaves emerge from the shoot apical meristem (SAM), the mechanism leading to the emergence of a healthy leaf rather than a diseased leaf on a systemically infected and diseased plant must be localized to the SAM. Interestingly, some viruses are unable to infect the meristem. The underlying mechanism of meristem resistance in these cases may be related to the mechanism of recovery in cases allowing virus entry. The failure of *Potato virus X* (PVX) to infect the *N. benthamiana* meristem was correlated with RDR6 activity, as shown with silenced RDR6 RNAi plants (Schwach et al. 2005). Since RDR6 is required for secondary siRNA production and the amplification of antiviral RNA silencing (Himber et al. 2003; Vazquez 2006), it was proposed that meristem resistance against the virus is due to secondary virus-derived siRNAs that spread systemically and immunize the meristem ahead of the virus (Schwach et al. 2005). An RDR polymerase activity was also invoked to explain the resistance of the tobacco apical meristem against invasion by CMV (Mochizuki and Ohki 2004). Interestingly, using immunohistochemical staining and *in situ* hybridization, it was shown that CMV was not excluded from the SAM. Rather, this virus was initially present at 7 days post-inoculation (dpi) and only later cleared (at 14 dpi). Consistent with this clearance, CMV-derived siRNAs were present in the SAM up to 24 dpi. Based on these observations, the authors concluded that the SAM in tobacco can clear viral infection by RNA silencing.

This case is one example showing that infected plants can undergo symptom recovery initiated in the SAM even if the infecting virus initially entered the SAM (Ghoshal and Sanfaçon 2015). In these cases, symptoms recovery may be due to a weak VSR or recovery from VSR activity (as described further above) rather than by recovery from the virus. For example, TRV

expresses a weak VSR called 16K. This virus is able to infect and systemically spread into the SAM of *N. benthamiana* plants whereas a mutant TRV with a inactivated VSR (TRV:stop) fails to reach the SAM (Martin-Hernandez and Baulcombe 2008). Interestingly, neither wild type TRV nor TRV:stop trigger symptoms or recovery. Based on these observations, it was proposed that viruses expressing only a weak VSRs are nevertheless able to enter the meristem and induce the accumulation of vRNA similar to viruses with a strong VSR. However, as compared to viruses with a strong VSR, viruses like TRV accumulate only transiently and to a lower level, which consequently will trigger weaker antiviral silencing responses and less damage, thus allowing recovery (Martin-Hernandez and Baulcombe 2008; Ghoshal and Sanfaçon 2015).

1.4. The role of PTGS and TGS in recovery

A decrease in vRNA concentration in recovered tissues (which is not seen in all cases of recovery) and the described role of RDR6, secondary siRNAs, and VSRs in recovery indicates that recovery can involve the degradation of the viral genome by antiviral PTGS. Antiviral RNA silencing acts through DCL and AGO-RISC mediated cleavage (Szittya et al. 2002). A role of RISC-mediated cleavage of viral RNA in symptoms recovery has been indicated by the analysis of infection of *N. benthamiana* plants with *Cymbidium ringspot tombusvirus* (CymRSV). A VSR-defective CymRSV mutant (CymRSV19stop), which is unable to express the VSR p19, was shown to allow symptoms recovery. The recovered leaves showed an accumulation of 21- to 25-nt long vsiRNAs indicating a role of vsiRNAs in recovery. Moreover, evidence was presented indicating that these vsiRNAs are used as guides for the cleavage of co-replicating defective interfering (DI) RNAs *in trans* thus suggesting their incorporation into RISC (Szittya et al. 2002). Pantaleo et al. (2007), used the expression of a sensor construct consisting of a GFP-encoding RNA fused to viral RNA in recovered leaves of an CymRSV19stop-infected plant to demonstrate that the virus-derived siRNAs target the sensor construct by RISC-mediated RNA cleavage. Using size fractionation, vsiRNAs and miRNAs were found to be bound by the same protein complex consistent with the size of the RISC complex. Based on these observations, the authors concluded that PTGS employing RISC-mediated cleavage of vRNA was responsible for symptoms recovery in leaves. The correlation of vRNA cleavage with

recovered tissues was corroborated with other plant-virus systems (Omarov et al. 2007; Scholthof et al. 2011).

In some cases, symptom recovery in plants infected with RNA viruses has been associated with RISC-mediated translational repression rather with cleavage of the vRNA. For example, recovery in *N. benthamiana* plant infected with *Tomato ringspot virus* (ToRSV) involved the translational inhibition of ToRSV-encoded CP and MP genes (Ghoshal and Sanfaçon 2014). Consistent with a role of AGO1 in antiviral RISC (Carbonell and Carrington 2015; Garcia-Ruiz et al. 2015; Morel et al. 2002), symptom recovery was blocked in *N. benthamiana* in which AGO1 was silenced by RNAi.

There is experimental evidence indicating that plant recovery from symptoms of infection by DNA viruses is caused by viral silencing involving components of the TGS pathway. Direct evidence of a role of TGS in recovery came from observations with a VSR-deficient *Beet curly top virus* (BCTV L2^{-}) in Arabidopsis (Raja et al. 2008). Using BCTV infection and chromatin immunoprecipitation (ChIP), the authors showed that Arabidopsis plants impaired in DNA methylation, exhibited reduced viral methylation and increased susceptibility to the virus. In contrast, BCTV L2^{-} infection led to the development of recovered leaves and these leaves contained hypermethylated viral DNA. Furthermore, symptom recovery was blocked in plants mutant for AGO4, a central component of the RdDM pathway (Zheng et al. 2007; Havecker et al. 2010; Gao et al. 2010; Blevins et al. 2015). Using the same ChIP procedure, the authors demonstrated that viral DNA methylation was abolished in these plants. These observations demonstrated the role of TGS in viral DNA methylation, which reduced the virulence of the virus and resulted in recovery of infected plants from disease symptoms.

Other studies revealed that antiviral defense and symptoms recovery in plants infected with DNA viruses also involves PTGS in addition to TGS (Rodriguez-Negrete et al. 2009; Pooggin 2013). Initial findings showed that infection of Arabidopsis with the geminivirus *Cabbage leaf curl virus* (CalCuV) triggered symptoms recovery and that 21-, 22-, and 24-nt long siRNAs accumulated in these symptom-free leaves (Blevins et al. 2006). The 21- nt and 22-nt long siRNAs and the 24 -nt long siRNAs represent central components of PTGS and TGS pathways, respectively. Moreover, recovery was inhibited in the PTGS mutants *dcl4*, *rdr6*, *sgs3* and *hen1* (Muangsan et al. 2004; Blevins et al. 2006). Small RNAs of the 21nt and 22nt sizes classes as well as of the 24 nt size category were also present in the recovered leaves of pepper plants

infected with the geminivirus *Pepper golden mosaic virus* (PepGMV) (Rodriguez-Negrete et al. 2009). Many of these siRNAs were derived from the virus and could be mapped all along the viral genome. It is interesting that the 21-22 nt vsiRNAs mapped to the coding genes of the virus, whereas the 24 nt siRNAs were derived from a strongly methylated viral intergenic region. The methylation level of this intergenic region was lower in the symptomatic leaves as compared to recovered leaves, which suggested a role of viral DNA methylation in recovery. Using bisulfite sequencing for the profiling of BCTV L2^{-} DNA methylation in systemically infected Arabidopsis wildtype plants and mutants affected in RdDM such as *drb3*, *dcl3*, and *ago4* demonstrated that these mutants failed to show symptom recovery and also were impaired in inducing strong cytosine methylation of the viral DNA genome (Raja et al. 2014). Consistent with a role of DCL3 and AGO4 in RdDM (Raja et al. 2008; Blevins et al. 2011), CoIP and biomolecular fluorescence complementation (BiFC) experiments demonstrated a direct interaction of DRB3 with DCL3 and AGO4 (Raja et al. 2014).

1.5. Disease symptoms recovery in ORMV-infected Arabidopsis plants

Although the role of PTGS in symptoms recovery in plants infected with RNA viruses and the role of both PTGS and TGS in symptoms recovery in plants infected with DNA viruses has been established, the full network of RNA-silencing based interactions between viruses and their plant hosts remains unclear. The publication of Kørner et al. (2018) to which I have contributed and which is attached herein, describes the interaction between Arabidopsis plants and the tobamovirus ORMV and provides deep insights into the mechanisms and genetic requirements involved in disease symptom formation and symptoms recovery.

ORMV belongs to the same virus family as the well-known TMV, but unlike TMV, ORMV produces strong disease symptoms in Arabidopsis. Importantly, we found that ORMV first induces symptoms and later allows symptoms recovery (Kørner et al. 2018; Fig. 1a-b; Fig. S1), which opened the way for genetic analysis of this phenomenon. Infected plants show severe disease symptoms at 14 dpi and start to develop recovered leaves at 23-25 dpi. As shown in Fig.1b of Kørner et al. (2018), the leaves of the infected plants were categorized at 28 dpi according to their symptom types to facilitate their analysis. The oldest leaves at the bottom of the plant were already present before inoculation and remained non-symptomatic but showed signs of necrosis presumably due to age (symptom type 1, ST1). Leaves that were still

young and physiological sinks at the time of inoculation were symptomatic. The lower, older leaves in this category showed different degrees of curling (symptom type 2, ST2), whereas the younger, more upper leaves showed stronger symptoms with strongly serrated margins (symptom type 3, ST3). Interestingly, several of the ST3 leaves showed a transition between leaf areas with symptoms restricted the tip and symptom-free areas at the leaf base. This transition occurred along a very distinct line at which a decision between disease and recovery apparently was made. Finally, the youngest leaves at the top of the plant were fully recovered and completely free of disease symptoms (symptom type 4, ST4). The transition between the diseased and healthy areas in ST3 "transition leaves" and the observation that symptoms in these leaves were limited to the leaf base suggested that the transition to recovery occurred along the border between source and sink tissues. This hypothesis was corroborated by infection of AtSUC:GFP plants as a source/sink marker (Imlau, 1999), which demonstrated that recovery indeed occurs in sink leaves and that leaves showing both diseases and recovered areas undergo the sink-to-source transition (Supplementary Fig. 14).
To determine whether symptom recovery was correlated with a decrease in the level of viral RNA, the different symptom types were probed by *in situ* hybridization (Kørner et al. 2018; Fig. 1c) and northern blotting (Kørner et al. 2018; Fig. 1d) using probes against the virus. Interestingly, the results showed that the recovered leaves contained viral RNA to the same level as the symptomatic leaves. The northern blot analysis also demonstrated that the RNA was full-length and, furthermore, that both strands of the viral RNA were present, thus indicating that the virus was actively replicating in recovered leaves as well as in symptomatic leaves.
I already mentioned evidence indicating a role of the VSR in the formation of disease symptoms and that recovery may occur in the presence of a weak or weakened VSR (see paragraph 1.2). To determine whether disease symptoms and disease recovery in ORMV-infected Arabidopsis plants correlate with VSR activity, we infected plants of Arabidopsis line 8z2, which expresses a continuously silenced, double 35S promoter-driven GFP transgene (Glazov et al. 2003). Using this approach we could show that ORMV infection restores GFP expression form this gene (Kørner et al. 2018; Fig. 1 e-g), thus indicating that the VSR activity, which is known to reside in the small replicase subunit [125k protein of ORMV (Hu et al. 2011; Malpica-López et al. 2018); 126k protein of TMV (Vogler et al. 2007); 122k protein of crTMV (Csorba et al. 2007)], suppresses PTGS activity. Importantly, green fluorescence coincided

with symptomatic tissues but was absent in recovered tissues demonstrating that that VSR activity is active in the symptomatic leaves and suppressed in the recovered leaves. RT-qPCR measurements were used to confirm that GFP mRNA levels were high in symptomatic leaves and low in the recovered leaves (Kørner et al. 2018; Fig. S2a). The correlation between symptom phenotypes and VSR activity was investigated by specific detection of viral and endogenous sRNAs. As shown previously (Hu et al. 2011), miR398 accumulated in ORMV-infected tissues. However, accumulation of this miRNA was restricted to symptomatic tissues with VSR activity, whereas recovered tissues with low or absent VSR activity also showed low levels of this miRNA. Also, ORMV-derived siRNAs accumulated to higher levels in symptomatic tissue and showed lower levels in recovered tissues (Kørner et al. 2018; Fig. S2). These findings are consistent with previous described correlations between tobamoviral VSR activity and specific sRNA accumulation (Blevins et al. 2006; Csorba et al. 2007; Hu et al. 2011). The correlation between symptoms and VSR activity were further demonstrated by infecting the *A. thaliana* suc:sul line (Himber et al. 2003), whose vein-centered chlorosis phenotype disappeared in the symptomatic leaves thus indicating the presence of VSR activity (ST2-ST3), but was distinctly visible along the veins in the recovered ST4 leaves, thus indicating the absence of VSR activity (Kørner et al. 2018; Fig. S3).

The analysis to this point demonstrated that recovery from symptoms in ORMV-infected plants occurs in sink tissues and is associated with the loss or strong reduction in VSR activity. However, given that the recovered leaves contained normal levels of replicating viral RNA, recovery was not caused by antiviral RNA silencing, but rather due to the silencing of VSR activity. Western blot assays using antibodies against the 125k-VSR protein demonstrated that the VSR was present in recovered leaves (Kørner et al. 2018; Fig. S13). Thus, recovery could not be correlated with translational repression of VSR expression. Rather, recovery was indeed due to the inhibition of the functional activity of the expressed protein. Based on the finding that symptoms recovery is restricted to sink tissues, we proposed that the suppression of VSR activity occurs in sink tissues.

The pathway leading to VSR inactivation in sink tissues was finally highlighted by genetic analysis using a library of known mutants affected in PTGS and TGS pathways (Kørner et al. 2018; Table 1, Table 2, Table S1, Table S2).

Infection of these mutants with ORMV was used to identify mutants showing impaired or enhanced symptoms recovery. In essence, the results of this analysis demonstrated that the

occurrence of symptoms recovery depends on the DCL4/RDR6/SGS3 pathway, which produces primary and secondary endogenous and viral siRNAs (Bologna and Voinnet, 2014). Moreover, mutants accumulating higher levels of secondary vsiRNAs (*dcl3-1* and *xrn4/ein5*) recovered earlier, thus indicating that recovery is the more likely the more vsiRNAs are produced. The analysis also showed that recovery in our system is independent of TGS pathway components, except for Pol IV and RDR2. Interestingly, these two proteins have been implicated to play a role in the spread or reception of systemic silencing signals (Dunoyer et al. 2007; Brosnan et al. 2007; Smith et al. 2007; Eamens et al. 2008). Based on our findings, we proposed that the mechanism that leads to VSR inactivation and symptoms recovery involves the trafficking of mobile vsiRNAs from source to sink and that the vsiRNAs that accumulate in sink tissues saturate the VSR so that its ability to sequester and interfere with the activity of other sRNAs, such as the GFP-mRNA derived siRNAs in the z82 line or miRNAs involved in the regulation of plant development, is suppressed (Kørner et al. 2018; Fig. 3).
Because the virus remains mostly unaffected by these mechanisms leading to symptoms recovery and continues to propagate, our study clearly demonstrated that plants can use sRNAs and intercellular communication to overcome an established disease and achieve a tolerant state in which both virus and host can coexist.

2. My contributing role to the publication by Kørner et al. (2018)

In the context of this work, I conducted experiments of ORMV infection in several *A. thaliana* PTGS and TGS mutants, analyzed the symptom phenotypes and performed molecular characterization by northern and western blot analysis (Figure 1d; Figure S12, and Figure S13), which aimed to answer several main questions in the understanding of the recovery phenomenon (see APPENDIX 2 for Supplementary Figures and Tables of Kørner et al. 2018).

Figure 1d shows a northern blot analysis of recovered leaves (except second lane from the left, symptomatic leaves) of wildtype plants and of single (*dcl3*, *ein5*, *rdr2*, *rdr6*) as well as of double mutants (*ein5 rdr6*, dcl2 dcl4) in which I have used radiolabeled probes to detect positive-sense (+) and negative sense (-) viral RNA. The result demonstrates that recovered leaves contain full-length genomic and subgenomic viral RNAs. The detection of negative sense viral RNA showed that the virus was actively replicating in recovered tissues. Moreover,

levels of viral RNAs appeared almost unchanged in the RNA silencing pathway mutants. However, the same mutants were shown to affect recovery in other experiments. Thus, recovery was found to occur independently from effects on viral RNA or viral replication.

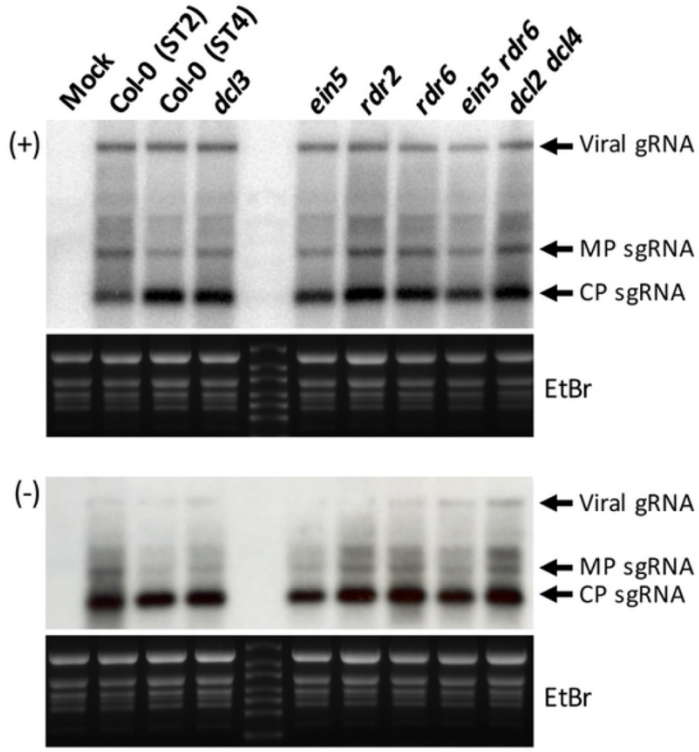


Figure 1d. Two independent northern blots showing viral plus (+) and minus (−)-sense genomic and sub-genomic viral RNAs in RNA extracts of non-recovered ST2 and recovered ST4 leaves of WT Col-0 plants and in recovered ST4 leaves of different silencing pathway mutants. The viral RNA pattern is identical to the viral RNA patterns reported in previous publications. The blot combines independent samples (each sample representing 20 infected plants, that is, recovery experiments) from WT plants (Col-0) and mutants undergoing recovery (dcl3, ein5 and ein5 rdr6) or not undergoing recovery (rdr2, rdr6 and dcl2 dcl4) in upper leaves, and demonstrates that upper leaves contain full-length plus and minus-sense viral RNA irrespective of recovery.

Figure S12 shows a small RNA northern blot in which I confirmed the expected effects of specific RNA pathway mutations on the synthesis and accumulation of specific sRNAs. The same small RNA blot was probed several times with different radiolabeled oligonucleotide probes to detect different sRNA species in the same samples. Probing siRNAs derived from the 5S repeat (ra-si1003) reports on the functionality of the TGS pathway, whereas probing tasiRNA255, miRNA160, and ORMV vsiRNA, reports on the functionality of PTGS pathways involved in tasiRNA, miRNA, and vsiRNA synthesis. As expected and previously shown (Blevins et al. 2006; Blevins et al. 2015), *dcl3* and *rdr2* mutants are defective in the production of 24 nt

siRNAs and repeat-associated siRNAs associated with TGS but do not affect any of the sRNA species associated with PTGS. In contrast the other mutants tested do not affect 24 nt species involved in TGS but specific classes of 21-22 nt sRNA involved in PTGS. Thus, *rdr6*, *ein5-rdr6, as well as dcl2-dcl4* were defective in the production of 21nt trans-acting siRNAs, as expected. Moreover, *dcl2-dcl4* affected the production of vsiRNAs. As expected, mutant *ein5* showed a strong increase in the level of vsiRNAs as expected. *ein5* plants are defective in exonuclease 4 (XRN4) activity (Olmedo et al. 2006; Potuschak et al. 2006; De Vleesschauwer et al. 2014) involved in RNA decay and thus provide increased levels of RNA template for secondary vsiRNA production. These increase levels of secondary vsiRNAs are consistent with enhanced recovery in the *ein5* plants (Kørner et al. 2018, Fig S8).

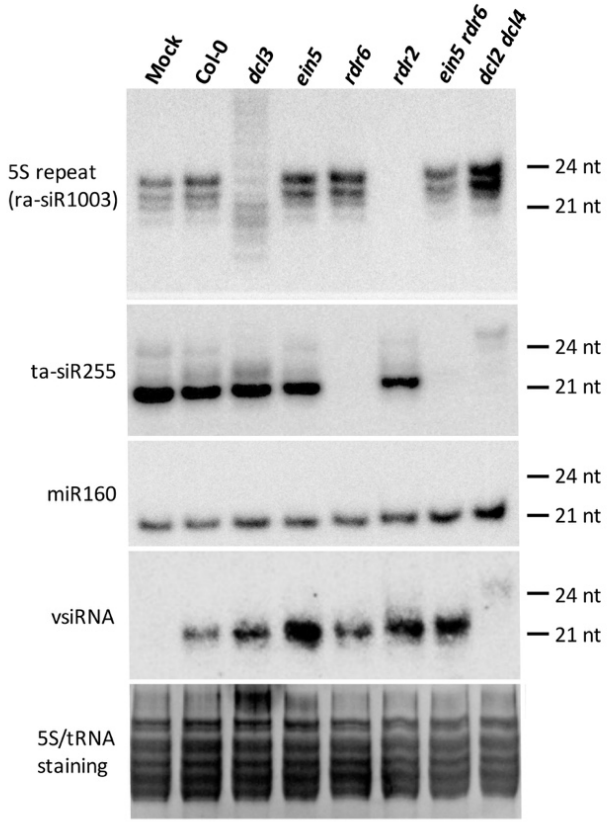


Figure S12: sRNA analysis of infected Col-0 wild type plants and silencing pathway mutants.
sRNA species in recovered ST4 (Col-0, *dcl3*, *ein5*) and corresponding non-recovered leaves of mutants (*rdr6*, *rdr2*, *ein5 rdr6*, *dcl2 dcl4*), in which recovery is absent, were analyzed. The analysis was performed with the same RNA samples also used for viral RNA analysis (Fig. 1d). The mutants affected the accumulation of specific sRNA species as expected. None of the mutants affected the accumulation of miR160. The accumulation of 5S rDNA repeat-derived ra-siR1003 was affected in *dcl3* and *rdr2* mutants but not in *rdr6* mutants, whereas the production of tasiR255 was affected in *rdr6*, *ein5 rdr6, and dcl2 dcl4* mutants but not in *rdr2* or *dcl3* mutants. As is also expected, production of vsiRNAs was abolished in *dcl2 dcl4*, as is consistent with the lack of recovery in this double mutant. Relative to Col-0 wild type, the vsiRNA levels were higher in mutants showing enhanced recovery (*ein 5*, *dcl3*) and reduced in *rdr6,* which interferes with the formation of secondary siRNAs and does not support recovery.

Figure S13 represents a western blot analysis to detect the 125k-VSR in samples taken from recovered leaves of wild type and mutant plants infected with ORMV. The results show that the VSR is expressed in infected tissues irrespective of recovery, thus demonstrating that the absence of VSR activity in recovered leaves cannot be ascribed to translational suppression of the protein.

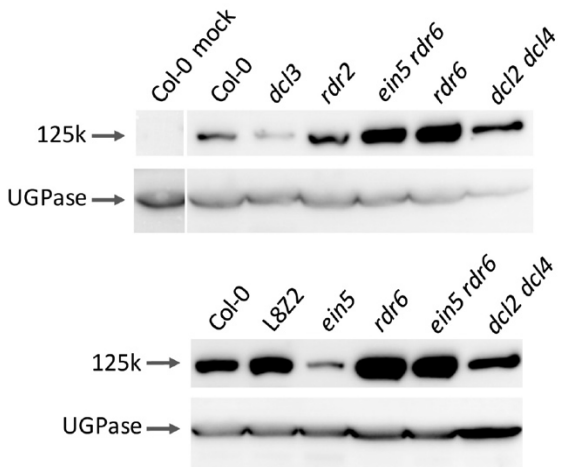


Figure S13: VSR expression in recovered leaves of infected Col-0 wild type plants and silencing pathway mutants.
The 125k-VSR is expressed in infected tissues irrespective of recovery. The amount of the VSR in recovered leaves is lower in mutants undergoing early recovery (*ein5*, *dcl3*) and higher in the upper leaves of *rdr6* mutants in which recovery is inhibited. L8z2 plants, which contain a continuously active silencing system, produce relatively high levels of the VSR whereas *dcl2 dcl4* plants, in which siRNA synthesis is inhibited, contain relatively low levels of the VSR. UGPase, UDP-glucose pyrophosphorylase.

In addition to these northern blots and western blots, I also performed experiments demonstrating the inhibition of symptoms recovery in transgenic plants expressing the VSR from a closterovirus (P21) or the VSR from a tombusvirus (P19) (Kørner et al. 2018; Fig. S4).

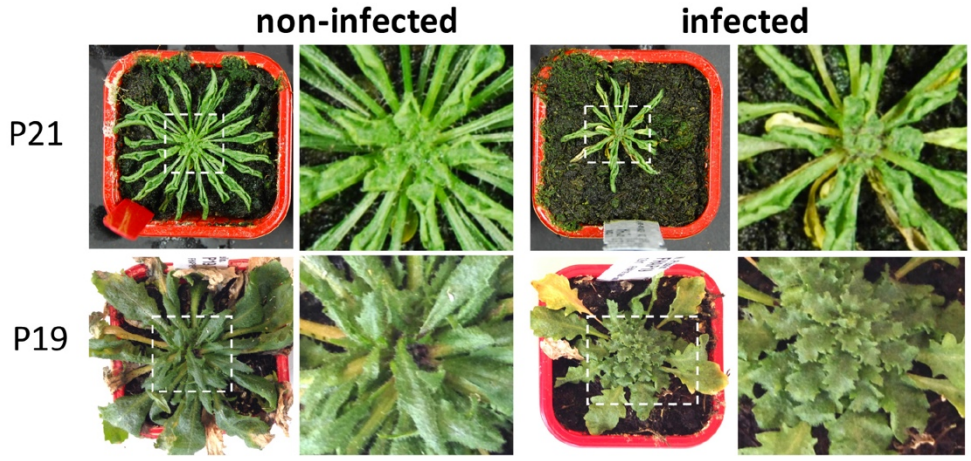


Figure S4: Suppression of recovery in VSR-expressing transgenic plants.
Mock- and ORMV-infected plants expressing either closterovirus P21-VSR or the tombusvirus P19-VSR. Plant areas within the dashed rectangles are shown enlarged. Neither P21 nor P19 plants allow disease recovery.

3. Conclusion

In this paper, the phenomenon of symptoms recovery in Arabidopsis was studied. This led to the identification of RNA silencing pathway genes that are involved and also unraveled the importance of an interesting interplay between a virus-encoded VSR and small RNAs in the determination of health versus disease.

The results demonstrate that symptoms recovery can occur in leaves undergoing normal virus replication and accumulation. Thus, plants have the capacity to achieve a state of tolerance and recover from an established disease despite the presence of an ongoing virus replication. Moreover, recovery can occur simply through inhibition of VSR activity. This may imply that plants could be protected against disease through strategies aiming at the inhibition of the VSR. Based on our observations and genetic requirements for recovery, we propose that the VSR is inhibited by mobile vsiRNAs that accumulate by systemic transport from source to sink. The sharp border between recovered and non-recovered tissues occurs along the sink-to-source transition suggests that the symptom-free sink-tissues will undergo disease as soon as these tissues mature and undergo the transition from sink to source. This may imply that the tolerance of plants for viruses could be supported by strengthening vsiRNA production (as shown in *dcl3* and *ein5/xrn4* mutants for ORMV) and by choosing growth conditions that support sink strength and a prolongation of juvenile growth.

KØRNER ET AL. 2018. CROSSTALK BETWEEN PTGS AND TGS PATHWAYS IN NATURAL ANTIVIRAL IMMUNITY AND DISEASE. NATURE PLANTS 4, 157-164.

General conclusion

The major goal of this thesis was to gain new insights into plant-virus interactions by elucidating the role of virus- and host-derived small RNAs in the regulation of gene expression during the local spread of virus infection in leaves and also in mechanisms determining plant disease and recovery. As part of my thesis I also contributed to a review article discussing current models of virus movement through PD (Pitzalis and Heinlein 2017).

The role of virus-and host-derived small RNAs in plant-virus interactions

The cellular events involved in local viral replication and cell-to-cell-movement have been intensely studied in recent years. However, we still know very little about plant:virus interactions playing a role in orchestrating these processes at the level of gene expression. Thus, as described in Chapter II of this thesis, different deep sequencing approaches (RNAseq, sRNAseq, PAREseq) were used to investigate the virus-induced changes in the host transcriptome and the regulation of genes and of the virus by virus- and host-encoded sRNAs. Using bioinformatic analysis of the sequencing data, the focus was laid on the identification of host-or virus-derived sRNAs that target host mRNA transcripts or viral RNA by RISC-mediated cleavage. The work was applied to TuMV infection in rapeseed (*B. napus*), which represents an economically important crop-pathosystem. To gain information related to the process of ongoing virus replication and spread, we used a GFP-tagged version of the virus, which allowed us to isolate RNA samples from local sites of spreading infection in the inoculated leaves. Reliable data and conclusions were achieved through the analysis of samples from three independent biological experiments. Moreover, the use of samples from two different cultivars allowed us to interpret the results in relation to the cultivar-specific susceptibility for the virus. Importantly, the different NGS approaches (RNAseq, sRNAseq, PAREseq) were always applied to the same individual RNA samples, so that the different levels of analysis and respective results for a given sample could be combined, mutually correlated and interpreted.

Genome-wide mRNAseq analysis revealed numerous genes showing differences in the accumulation of their transcripts between mock-treated and virus-treated samples. Among these, numerous virus-induced genes were significantly up or down-regulated either in both

cultivars or in a cultivar-specific manner. Some of the differentially expressed transcripts are predicted to encode proteins that are known to play important roles in pathogen defense. One example is CALMODULIN-BINDING PROTEIN 60G (CB60G), which is induced in both cultivars and known to act as a master immune regulator that promotes the expression of key genes involved in salicylic acid (SA) biosynthesis and in regulating PAMP-PTI, ETI and systemic acquired resistance (SAR) (Sun et al. 2015). Viral susceptibility in the cultivar Drakkar correlated, for example, with a strong induction of expression of the coatomer alpha-2 subunit of the COPI coatomer complex (Ahn et al. 2015), which may play a role in the formation of vesicles involved in TuMV replication and movement (Wei and Wang 2008) (see Chapter I). On the other hand, the more resistant phenotype of the cultivar Tanto was correlated, for example, with the specific induction of transcripts encoding TARGET OF AVRB OPERATION1 (TAO1), a TIR-NB-LRR receptor-like protein (Eitas et al. 2008). The general validity of our mRNAseq data was confirmed by testing the expression of several genes by RT-qPCR analysis, in which both the original RNA that was analyzed by NGS-mRNAseq as well as novel RNA samples from four new and independent infection experiments were used. This part of the work provided lists of genes with induced or suppressed transcript levels in local TuMV-GFP infection sites formed in two different cultivars differing in virus susceptibility, and these lists are ranked according to the strength of the observed changes.

To reveal mRNAs that might be targeted by virus-induced host-or-virus-derived sRNA, the sRNA reads were first counted and aligned to both the viral genome and the Tanto and Drakkar transcriptomes and annotated. As has been noted by previous studies (e.g. Hu et al. 2011; Tagami et al. 2007; Vogler et al. 2007), virus infection triggered drastic changes in the sRNA length profile. Whereas the sRNAs from Tanto and Drakkar mock samples showed identical and typical profiles of predominantly 21 nt - 24 nt long sRNAs, the profiles were greatly dominated by virus-derived 21 nt and 22 nt siRNAs upon infection (vsiRNAs). These profiles as well as the profiles of vsiRNAs aligned to the TuMV genome were almost identical between both *B. napus* cultivars, indicating that the differences in susceptibility for the virus cannot be explained by obvious differences in sRNA processing. By mapping the host-derived sRNAs to *Brassicacea* miRNAs in the miRbase database (Kozomara and Griffiths-Jones 2014), several of the reads could be annotated to known miRNAs. Moreover, by using Shortstack software (Axtell 2013), numerous previously unknown miRNAs were identified.

The sRNA and mRNA data were finally combined with the results of PAREseq analysis to reveal sRNAs that align to cleaved mRNA 5' ends and satisfy the conditions of RISC pairing using PAREsnip software (Folkes et al. 2012). The analysis revealed already known miRNAs:mRNA target pairs, such as miRNAs targeting the mRNAs for specific Squamosa promoter-binding-like (SPL) proteins, Auxin response factors (ARFs), Scarecrow-like (SCL) proteins, Ethylene-responsive transcription factors (RAP2-7, AP2), Auxin signaling F-box proteins (AFB2, AFB3), and Superoxide dismutase proteins (Llave et al. 2002 ; Rhoades et al. 2002 ; Allen et al. 2005 ; Wang et al. 2005a ; Wang et al. 2005b ; Kim et al. 2006; Gandikota et al. 2007; Vidal et al. 2010; Si-Ammour et al. 2011; Yu et al. 2012; Lu et al. 2013; Ma et al. 2014; Jung et al. 2014; Xu et al. 2016) and thereby confirmed the accuracy of PARE analysis. In addition, the analysis led to the identification of new miRNA:mRNA target pair candidates, such as miR1885b:BLOS2 or miRC23a:COX19. The cleavage activity of some of the known and predicted miRNA:mRNA target pairs was confirmed by gene-specific 5' RACE assays using repetitive, newly created biological samples.

One of the important aims was to determine whether the infecting virus may use vsiRNAs processed from its genome as RNA effectors for the RISC-mediated targeting of host genes. The analysis indeed revealed the presence of vsiRNAs in predicted vsiRNA:mRNA target pairs which appeared only after infection. A predominant vsiRNA was found in predicted vsiRNA:mRNA target pairs involving transcripts of ERF genes that are also targeted by miR172. This specific vsiRNA was found similar in sequence to miR172 and to engage in predicted cleavage of exactly the same site in the target mRNA. This suggests that viruses may encode vsiRNAs evolved to mimic the activity of host miRNAs and, thereby, to control the specific miRNA target genes during infection.

The mapping of sRNAs to the two cultivar transcriptomes and the analysis of the alignment with the ShortStack program (Axtell 2013) led to the identification of numerous *PHAS* loci that produce phased, secondary, small interfering RNAs (phasiRNAs). PhasiRNAs are produced by conversion of a transcript into dsRNA by RDR6 or RDR1 and subsequently processing of the dsRNA into phased siRNAs by DCL4 (Fei et al. 2013). The production of phasiRNAs is thought to represent a mechanism to down-regulate the specific transcript from which they are derived as well as to produce siRNAs able to target homologous sequences *in trans* (Fei et al. 2013). Thus, unlike the non-coding TAS genes in *Arabidopsis*, which were among the first loci known to produce phased tasiRNAs (Vazquez et al. 2004), *PHAS* loci refer to coding genes,

many of which are NB-LRR family genes involved in pathogen defense, as well as genes of the PPR and MYB families, as shown in *Arabidopsis*, *Medicago*, and peach (Fei et al. 2013; Zhai et al. 2011). The analysis of *PHAS* loci in mock-treated and TuMV-infected *B. napus* plants revealed that certain *PHAS* loci produce phasiRNAs only after infection. The production of virus-associated secondary siRNAs (vasiRNAs) from coding genes upon virus infection has been previously noted in *Arabidopsis* and found to require RDR1 for vasiRNA synthesis and AGO2 for mRNA target cleavage (Cao et al. 2014a). Thus, the vaPHAS loci identified in our analysis may represent vasiRNA-producing loci. However, because the pathway for the synthesis of the phasiRNAs in *B. napus* is not clarified, it is preferable to distinguish them as va-phasiRNAs. Our study indicates that virus infection in rapeseed stimulates the production of phasiRNAs at numerous defense-related coding genes (e.g. TAO1, AGO2, NBR1 homolog). Among these genes we found family members of three small gene families (encoding Chlorophyll a-b binding protein 1, NBR1 homolog, and TAR1) that produce va-phasiRNAs associated with cleavage of their own transcript or of transcripts of homologous genes in the same gene family. This suggests that the process of va-phasiRNA production may represent a mechanism to dampen the effects of infection on transcript homeostasis. Interestingly, members of the NBR1 and TAR1 family also produce va-phasiRNAs with potential to target mRNA transcripts of other genes. The data suggest that particularly NBR1 may represent a virus-induced hub for siRNA synthesis and the virus-induced targeting of a whole network of other genes.

The results of PAREsnip analysis indicate that also the viral genome can be cleaved by virus- and host-derived siRNAs (siRNAs, hsRNA). The large majority of the cleavage events were associated with unique hsRNAs derived from genes annotated as disease resistance genes TAO1 and RPP5, both encoding TIR-NB-LRR receptor-like proteins. The cleavage of the vRNA though vsiRNAs or hsRNAs may contribute to cultivar-specific susceptibility for the virus, as some cleavage sites are predicted in a cultivar-specific manner. Interestingly, some of the predicted hsRNA:vRNA target pairs include trans-acting va-phasiRNAs derived from NBR1 and TAR1 genes, which may support the hypothesis that the evolution of NBR1 genes as virus-inducible hubs for secondary tasiRNA production may have occurred on the precondition that the va-phasiRNAs derived from the same hub will, in turn, also control the virus. It is intriguing also that the *B. napus* NBR1 genes are highly homologous to the selective autophagy receptor

protein AT4G24690/NBR1 gene in Arabidopsis (81-84% identity), which has been implicated in antiviral defenses involving the degradation of viral proteins and particles by autophagy (Hafren et al. 2017; Hafren and Hofius 2017). This protein was shown to suppress TuMV infection in Arabidopsis by targeting the VSR of the virus (HcPro) (Hafren et al. 2018). Thus, by inducing the conversion of NBR1 mRNA into secondary siRNAs the virus may have gained the possibility to achieve widespread control over host gene expression and at the same time also to suppresses NBR1 mRNA levels and thereby control the antiviral functions of the NBR1 protein.

In conclusion, this study involved NGS analysis and *in vivo* experiments performed in *B. napus,* the most widely produced oilseed crop in the European Union. The results highlight differential expressed genes and virus- or host-derived sRNAs correlated with cleaved mRNA 5' ends indicating their role in RISC-mediated cleavage. Collectively, the data suggest that *B. napus* uses endogenous siRNAs derived from resistance genes to target the virus, whereas the virus, in turn, uses its own vsiRNAs to target the host. Moreover, by inducing the production of secondary siRNAs from coding genes, the virus appears to gain the possibility to target other genes. The virus-responsive genes and particularly the genes predicted as targets of vsiRNAs or va-phasiRNAs may play an important role during virus infection in *B. napus* and could represent important new candidate loci for crop improvement. However, it is important to note that the identified sRNA:RNA target pairs are predicted and that additional experiments are needed to prove that these target pairs are indeed functional in RISC-mediated RNA cleavage. One approach to gain supporting evidence could be by using AGO- immunoprecipitation for determining whether specific sRNAs in question are indeed present in AGO-RISC complexes. RISC-mediated cleavage of an mRNA target is usually confirmed by expression of a reporter construct in which the sRNA target sequence (and in a control construct, a mutant target sequence) is fused to a reporter, for example a transcript for GFP, and by comparing reporter expression (which is reduced by reporter RNA cleavage) between infected and control tissues. However, this approach may require the production of transgenic plants, since *B. napus* is not suitable for transient expression assays based on agroinfiltration. Given that the DNA genomes of Drakkar and Tanto were sequenced as part of this project, it may be possible to identify cultivar-specific SNPs that map to cultivar-specific sRNA:mRNA target pairs and use these SNPs in genetic crosses to correlate the SNPs and

specific mRNA cleavage by gene-specific 5'RACE experiments. The role of genes during virus infection should be tested using gene-specific mutants. However, given that *B. napus* is an allotetraploid species with an highly amplified genome (Chalhoub et al. 2014), it is almost impossible to create recessive mutants in which a given function is no longer expressed. The functional analysis of genes rather depends on dominant approaches such as VIGS, RNAi or CRISPR/CAS9, all of which have the potential to affect the expression of all members of a given gene family.

Nevertheless, the findings obtained in this study have revealed a complex network of potential sRNA-mediated interactions between *B. napus* and invading virus and led to the identification of important new gene targets for crop improvement.

Processes that lead to viral symptom recovery and promote plant health

Viruses are obligate intracellular parasites, and most studies of viruses have focused on describing their association with diseases. However, viral infection does not always trigger diseases. Although virus diversity surveys demonstrated that viruses were present in thousands of plants, no disease symptoms were seen that could be correlated with the presence of virus, even if the plants contained viruses related to important crop pathogens (Roossinck 2012; Roossinck and Bazán 2017; Roossinck and García-Arenal 2015). Thus, most plants in the wild appear to be tolerant to viruses and pathology from virus infection can be seen as an exception, rather than the rule. Given that viruses produce diseases and important yield losses in crops, it is very important to gain an understanding of the processes by which plants can promote their health in the presence of viruses. To gain such insight, the phenomenon of "symptoms recovery", thus the ability of plants to recover from disease, was studied. Using ORMV infection in Arabidopsis as a model, it was found that recovery occurred in the presence of replicating virus thus indicating that recovered leaves had gained a state of tolerance. By further analysis we showed that disease symptoms correlated with VSR activity and that the plant achieved tolerance through the ability to gain control over this activity. By screening Arabidopsis mutants affected in varies defense- and hormone-related pathways the underlying mechanism was found to involve post-transcriptional RNA silencing pathway genes that are required for the synthesis of primary and secondary siRNAs as well as transcriptional silencing pathway genes previously implied in systemic RNA silencing

signaling. Moreover, mutants that support enhanced siRNA production also showed enhanced recovery. Together with the additional finding that recovery was restricted to sink tissues, this led us to the model that recovery occurs upon transport of virus-derived siRNAs (vsiRNAs) from source to sink and that the vsiRNAs that accumulate in sink tissues finally cause saturation and inhibition of the VSR activity responsible for disease.

Overall, this study demonstrates that plants can use RNA silencing coupled to intercellular communication and systemic regulation to (gain) control (over) VSR activity in the distant, young tissues and thereby control (overcome an established) disease. This conclusion implies that plant health can be promoted by sink strength and by controlling the activity of genes that act against efficient vsiRNA production (e.g. EIN5/XRN4). The results are consistent with previous reports indicating the importance of RNA silencing and of a “weak” VSR in recovery. However, unlike in these previous reports, our findings argue against a requirement of viral inhibition or clearance as a precondition for recovery; we rather show that the virus itself is not affected during this process. Thus, recovery does not depend on the “killing of the pathogen” but rather on the ability of the infected plants to properly “deal” with the virus. This ability of plants to remain healthy despite the ubiquitous presence of viruses in the environment should indeed be expected as a result of virus-host co-evolution. To support propagation, a virus should not kill its host but rather promote its fitness. The occurrence of serious viral diseases in cultivated plants may be the result of extensive crop breeding that may have led to the loss of important mechanisms evolved during co-evolution.

Materials and methods

I. Materials

1. Plant species

1.1. *Brassica napus*

In this work, two different *B. napus* cultivars were used. Both cultivars are spring rapeseed varieties stemming from french breeding programs and developed by the company SERASEM (France). The cultivar 'Drakkar' is a 'double low' cultivar (low for toxic glucosinolates and erucic acid) approved for research in France in 1986. It has been used as an experimental host for genetic transformation (for example, Han et al. 2001) and the profiling of phloem sap contents (Buhtz et al. 2008; Hanhart et al. 2017). Seeds for this cultivar were provided by Michael Wassenegger (RLP AgroScience GmbH, AlPLanta - Institute for Plant Research, Neustadt an der Weinstrasse, Germany). The cultivar 'Tanto' has been approved in 1990 for research and used by INRA for the development of a *B. napus* Tilling platform using a collection of collection of 8500 EMS mutant lines. Seeds of this cultivar were provided by the company ANOVA$^+$ (Evry, France).

1.2. *Arabidopsis thaliana*

1.2.1. T-DNA mutants

T-DNA mutants mentioned in the publication by Kørner et al. (2018) were provided by Franck Vazquez (University of Basel, Switzerland). Tables 2 provide all recovery T-DNA mutants used for my contribution in Kørner et al. (2018).

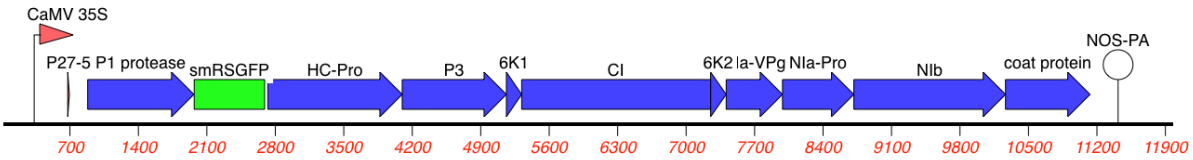
Tables 2: T-DNA mutants

Locus in Arabidopsis	T-DNA lines	Background	Annotations
AT3G43920	dcl3-1	Col 0	Dicer-Like 3
AT1G54490	ein5-1	Col 0	Ethylene Insensitive 5
AT4G11130	rdr2-2	Col 0	RNA-Dependent RNA Polymerase 2
AT3G49500	rdr6-15	Col 0	RNA-Dependent RNA Polymerase 6
	double mutant ein5-Rdr6	Col 0	-
	double mutant dcl2-4	Col 0	-
	P19 expressing lines	Col 0	-
	P21 expressing lines	Col 0	-
	Line 8z2	Col 0	-

2. Viral strain and constructs

2.1. pCB-TuMV-GFP

The binary plasmid pCB-TuMV-GFP (Lellis et al. 2002; Dunoyer et al. 2004; GenBank: EF028235.1) encodes the UK1 strain of TuMV modified by a Green Fluorescent Protein (GFP) cistron cloned between the P1 and HCpro sequences of the polyprotein (Fig. X). The binary plasmid is based on a pGREEN II backbone providing resistance to kanamycin and gives rise to infectious RNA upon transcription from an upstream 35S promoter in plant cells. The TuMV-GFP coding sequence was verified by DNA sequencing before use.



2.2. ORMV virions

ORMV virions were purified from systemically infected *Nicotiana benthamiana* leaves that were mechanically inoculated with infectious RNA produced by *in vitro* transcription of viral RNA from the pBTI ORMV IC clone (provided by Greg Pogue (Large Scale Biosciences, Vacaville) and were used for inoculation of *N. benthamiana* and *A. thaliana* plants as

described in previous publications of the team (Hu et al. 2011; Kørner et al. 2013; Niehl et al. 2014).

3. Antibodies

Antibody	Name	Detection	Oirign	Host / Clonality	Use
Primary antibody	UGPase	Anti-UDP glucose pyrophosphorylase	Agrisera (Vännäs, Sweden)	Rabbit / Polyclonal	1:5000 TBS-T 0.5% milk
	125k	125k ORMV replicase	Malpica-Lopez et al., 2018	Rabbit / Polyclonal	1:3500 TBS-T 5% milk
Secondary antibody	GAR	Goat Anti Rabbit antibody conjugated to **HoR**seradish **P**eroxidase (HRP)	Invitrogen	Goat / Polyclonal	1:10000 TBS-T 5% milk

4. Primers

Tables 3: Primers for nested PCR during 5'RACE

	Name	Nucleic acid sequences (5' - 3')	Gene annotations
5' RACE adapter	5'RACE Adapter	GCUGAUGGCGAUGAAUGAACACUGCGUUUGCUGGCUUUGAUGAAA	-
5' RACE adapter primers	5'RACE outer primer	GCTGATGGCGATGAATGAACACTG	-
	5'RACE inner primer	CGCGGATCCGAACACTGCGTTTGCTGGCTTTGATG	
Gene-specific primers	BnaA07g13830D-1	TTTCTCCTCCTTCTCCGC	Auxin response factor 10
	BnaA07g13830D-2	CTTTCTCCTCCTTCTCCGCCTC	
	BnaAnng18540D-1	GGGAGAAGCGAAGACAGT	Scarecrow-like protein 6
	BnaAnng18540D-2	GTCGGGAGAAGCGAAGACAGTG	
	BnaCnng68320D-1	CACCATAAGTAGTCTCCGCTC	Protein argonaute 2
	BnaA05g14760D-1	CCATTACATAATGCAGTCTCTGCTCC	Protein argonaute 2
	BnaA09g14980D-1	GACCAACCTCTTCCCTG	Disease resistance protein TAO1 {ECO:0000305}
	BnaA09g14980D-2	CACACAGGTTTCATCAAAGG	
	BnaCnng44780D-1	GTTTGGTTCAGACACAATGAAACG	Biogenesis of lysosome-related organelles complex 1 subunit 2
	BnaCnng44780D-2	CGATGTTGATGATGACGACACTCAG	
	BnaA01g34730D-1	CATGAGAGAAGGTTGGAAGC	Floral homeotic protein APETALA 2

II. Methods

1. Plant culture

Seeds were sown on soil. 5 to 7 days after germination, *B. napus* seedlings were transplanted into 13 cm pots; Arabidopsis seedlings were transplanted at 15 days after germination into 7 cm pots. Before using them for experiments (i.e. infection with virus), the plants were further grown for 4-5 weeks in a growth chamber with a 16h photoperiod at 24°C and 70% humidity.

2. Inoculation of plants with virus

Four weeks old *Brassica napus* plants were mechanically inoculated with TuMV using crude extract (sap) of previously infected plants and rubbing 2 leaves per plant with a gloved finger covered with sap in the presence of an abrasive (Celite®545). The sap was created from leaves that were previously harvested (at 20 days post inoculation, dpi) from systemically infected

B. napus cv Drakkar plants and by grinding them in 10 mM K_2HPO_4 buffer pH 7.5 (using 3 ml buffer per gram leaf material). These TuMV donor plants were initially mechanically inoculated with sap from systemically infected *Nicotiana benthamiana* plants. To create the original *N. benthamiana* donor plants, five weeks old *N. benthamiana* plants grown at 25°C with a 16h photoperiod were inoculated by agroinfiltration of two leaves per plant with *A. tumefaciens* strain GV3101 transformed with plasmid pCB-TuMV-GFP as described in Dunoyer et al. (2004) paragraph "Virus and plant material" in Materials and Methods. For agroinfiltration, the agrobacteria were grown over night and pressure-injected into leaves at an OD_{600nm} of 0.5 using a syringe without needle.

Three weeks old Arabidopsis plants were inoculated with ORMV by rubbing three leaves (pre-powdered with Celite®545) with a cotton tip in the presence of 150 ng purified ORMV virions per leaf (Kørner et al. 2018).

3. Measurement of specific RNA levels by reverse transcription followed by quantitative Polymerase Chain Reaction analysis (RT-qPCR)

3.1. Total RNA extraction and cDNA synthesis

TuMV-GFP infection sites developed in the inoculated leaves of *B. napus* plants were revealed by monitoring GFP fluorescence with a handheld UV lamp (UVP Blak-Ray B-100). At 12 dpi, fluorescent foci were carefully isolated by cutting leaf discs with a 0.5 cm micropunch and immediately frozen in liquid nitrogen. Leaf discs were also harvested from control plants treated with buffer without virus.

Total RNA was isolated from ca 150 leaf disk samples of infection sites or of mock (buffer)-treated, non-infected control tissues, each pooled from ten plants, respectively. After grinding in N_2, 0.1 g fine powder was homogenized and extracted with 1.4 ml Trizol reagent (Invitrogen, USA) until defrosting. After addition of chloroform to 20% (volume to volume) (300 µl), the sample was strongly vortexed for 40 sec. Following centrifugation at 9000 g for 15 min, the upper aqueous phase was transferred to a new tube and after mixing with an equal volume of cold pure isopropanol stored for 30 min at -20°C. After centrifugation at 10150 g (4°C) the lower aqueous phase was kept and supplemented with 1.4 ml cold 70% ethanol. This was followed by centrifugation at 9000 g for 5 min, after which the supernatant

was discarded and the pellet dried for 15-20 min at room temperature. Finally, the RNA in the pellet was resolubilized in 50 µl RNAse-free water heated to 60°C. The concentration of the isolated RNA was quantified by spectrophotometric measurement at 260 nm absorbance using Nanodrop equipment (Thermo Scientific, USA) (Purity: $A_{260}/A_{280} > 1.8$, $A_{260}/A_{230} > 2.0$) and stored at -20°C. For cDNA synthesis, the quality of the RNA sample was verified by an 1% agarose gel electrophoresis in 1x TBE [(90 mM Tris-base, 90 mM Boric acid, 2 mM EDTA (Ethylene Diamine Tetraacetic Acid, pH 8.3)] at constant voltage (100 V). 1-2 µg of the RNA was reverse-transcribed in the presence of an oligo$(dT)_{20}$ primer and the SuperScript IV reverse transcriptase (200 U/µl) following the manufacturer's instructions (Invitrogen).

3.2. cDNA quantification by RT-qPCR

PCR is an *in vitro* polymerase chain reaction technique that allows the exponential amplification of a DNA sequence by a thermostable DNA polymerase. It requires a pair of oligonucleotide primers hybridizing to flanking regions of the sequence selected for amplification, a complementary DNA strand as template and deoxynucleotide triphosphates (dGTPs, dCTPs, dATPs and dTTPs) for primer extension DNA synthesis. The abundance of specific transcript was measured by probing 1 µl cDNA by quantitative real-time PCR using 5 µl SYBR-green master mix (Roche) and 2 µl of 2.5 µM allele-specific oligonucleotide primers (12.5 µl forward and reverse primer in 475 µl water; see Table 3 for a list of primers used) in a Lightcycler 480 (Roche). The PCR program used for cDNA amplification and measurement is shown in table 4.

Table 4: qRT-PCR amplification conditions

Steps	Temp (°C)	Time	Cycles
Initiale denaturation	95	5 min	1
Denaturation	95	10 s	
Hybridization	60	15 s	45
Elongation	72	15 s	
	95	5 s	
Final cycle	55	1 min	1
	95	Continuous	
Cooling	40	30 s	1

The specific transcript levels were measured by applying three technical replicates for each sample. To compare different samples, the measured transcript level quantified as cycle threshold (Ct) values was normalized against the Ct values for RNA transcripts of two known "housekeeping" genes [TIP41-like protein; BnaA08g11790D (Zhang et al. 2014; Wang et al. 2014)]. The RT-qPCR analysis was performed the same way for each sample (e.g. virus- versus buffer-treated, one *B. napus* cultivar versus another). Assuming a Normal distribution of the data, a statistical Fisher's F-test was performed to determine variance equality (homoscedastic or heteroscedastic variance), which was needed for a subsequent student's T-test to calculate the probability of difference between populations and, thus, to determine whether mRNA abundances between control and treated samples were significantly different ($p<0.05$ = *; $p<0.01$=**; $p<0.001$ = ***).

4. 5'RACE (Rapid Analysis of cDNA Ends)

Non-capped mRNA 5'ends that occur upon RISC-mediated RNA cleavage were analyzed by 5'RACE as described previously (Llave et al. 2002; Llave et al. 2011). RLM (RNA Ligase-Mediated)-RACE kits are usually optimized for the cloning of cDNA of capped full-length mRNA molecules. In this procedure, the RNA is treated with calf intestinal phosphatase (CIP) to avoid the cloning of non-capped molecules carrying a 5' monophosphate (degraded mRNA, rRNA, tRNA and DNA) and with tobacco acid pyrophosphatase (TAP) to remove the cap structure on the full-length mRNA. Sine we aimed to apply 5'RACE for the cloning and identification of mRNA molecules that are non-capped and 5' monophosphorylated due to RISC-mediated cleavage, these two enzymatic steps were avoided. Instead, poly-adenylated RNA was used to ligate the 5'RACE RNA adapter to available mono-phosphorylated 5' RNA ends. As shown in figure 7, the ligation product was then reverse transcribed into cDNA using an oligo dT primer. The cDNA was then amplified with nested RACE adapter-specific and gene-specific primers to create gene-specific cDNA fragments that were further analyzed by electrophoresis through an 1% agarose gel in 1x TBE [(90 mM Tris-base, 90 mM Boric acid, 2 mM EDTA (Ethylene Diamine Tetraacetic Acid) pH 8.3] at constant voltage (100 V) and sequenced the IBMP platform with gene-specific primers and the ABI3130xl sequencer (Applied Life Technologies).

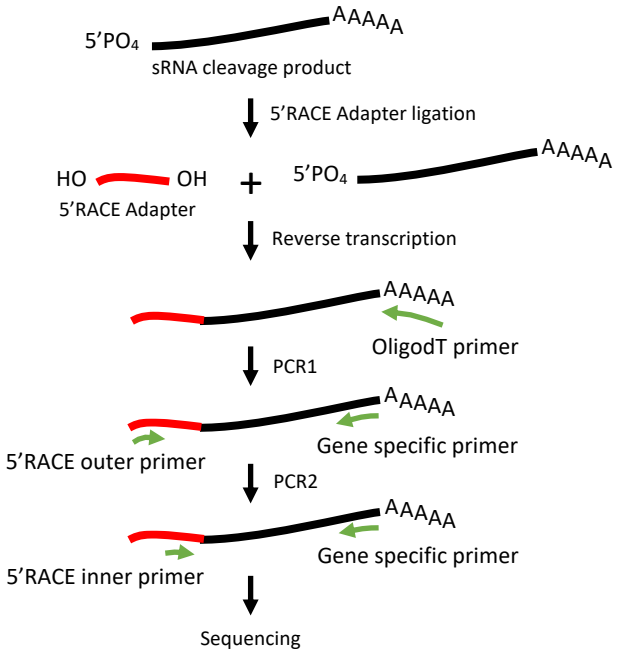


Figure 7: 5'RACE analysis of mRNA molecules with monophosphorylated, non-capped 5' ends.

4.1. Total RNA extraction

Total RNA was extracted as described under paragraph 3.1

4.2. Purification of mRNA from total RNA

Polyadenylated mRNA was purified from 1-5 µg total RNA by binding to oligo $d(T)_{25}$ -coupled paramagnetic beads and separation with a magnetic isolation module [NEBNext® Poly(A) RNA Magnetic Isolation Module (E7490L), BioLabs] according to the manufacturer's instructions. Each purified mRNA sample was quantified and the quality was measured according to the RNA Integrity Number (RIN) and 18S/28S ribosomal ratio using the Agilent RNA 6000 Pico Chip kit and by running the electrophoretic assays with the 2100 Bioanalyzer system (Agilent Technologies).

4.3. Adapter ligation

Ligation of the GeneRacer RNA oligo 5'RACE adapter (Invitrogen; see Table 2) to mRNA molecules carrying a monophosphate at the 5' end was performed as described in Llave et al. 2011 and following the manufacturer's instructions of T4 RNA ligase (New England BioLabs).

In a sterile Eppendorf tube were mixed 2 ng of RNA oligonucleotide adapter and 1 ng Poly(A) purified RNA, incubated for 5 min at 65°C to relax secondary structures. After incubation, the mixture was supplemented with 1 µl 10X ligation buffer, 1 µl RNAseOUT (40 U/µl), 1 µl T4 RNA ligase, 1 µl ATP (10 mM) and filled up with sterilized miliQ water to 10 µl final volume. After incubation at 37°C for 1h, the ligation products were separated from non-incorporated adapter molecules using an Illustra Microspin S-300 Sephacryl size filtration column (GE Healthcare) and centrifugation for 1 min at 735 g.

4.4. Reverse transcription

Eight µl of the RACE adapter-ligated RNA were used for cDNA synthesis as described in paragraph 3.1 with the exception that the reaction with SuperScript IV reverse transcriptase was done for 20 min at 60°C.

4.5. cDNA fragment amplification by PCR (nested PCR)

Sample preparation and conditions used for 5'RACE nested PCR amplification are detailed in table 5 and represent the same conditions used in Llave et al. 2011 and follows the manufacturer's instructions of the GoTaq® G2 Hot Start Polymerase (Promega). The sample preparation has been performed on ice and directly placed in 94°C pre-heated PCR block for amplification. Nested PCR requires two independent amplifications starting first with a gene-specific outer primer amplification followed by a second gene-specific inner primer amplification as shown in figure 7.

Table 5: Sample preparation and nested PCR conditions for 5'RACE.

Nested PCR amplification	Volumes
Colorless GoTaq®Flexi Buffer PCR buffer (5x)	10 µl
MgCl2 (25 mM)	3 µl
dNTP mix (10 mM each)	1 µl
GSP (10 mM)	1 µl
5'RACE Outer Primer (10 mM)	1 µl
5'END cDNA	1 - 2 µl
Taq DNA polymerase (5 U/ml)	0.5 µl
Final volume	50 µl

Steps	Temp (°C)	Time	Cycles
Initiale denaturation	94	5 min	1
Denaturation	94	30 s	5
Hybridization	70	1 min	
Denaturation	94	30 s	5
Hybridization	65	1 min	
Denaturation	94	30 s	
Hybridization	60	30 s	20–25
Elongation	72	1 min	
Final elongation	72	10 min	1

5. DNA genome sequencing

The genomes of the *B. napus* cultivars Drakkar and Tanto were analyzed by paired-end (2x 100 bp) sequencing and the reads were aligned to the published transcriptome of *B. napus* cultivar "Darmor-bzh" (Chalhoub et al. 2014; Genoscope v4.1, http://www.genoscope.cns.fr/brassicanapus/). Identified SNPs were inferred into the Darmor transcriptome to create the cultivar-specific transcriptomes that were used for the cultivar specific mapping of the mRNAseq, sRNAseq, and PAREseq reads.

5.1. DNA isolation

DNA was isolated by aScidea Computational Biology Solutions (http://www.ascidea.com/) from 1.9 g fast-frozen leaf tissue of *B. napus* cv Drakkar and *B. napus* cv *Tanto* plants.

5.2. Sequencing and quality control

The sequencing was performed with 800 bp insert PCR-free libraries and subsequent paired-end sequencing (2*100 bp) on an Illumina HiSeq 4000 platform (BGI Tech Solutions, Hongkong). Raw libraries were quality checked with FastQC (RRID:SCR_014583) version v0.11.2 and cleaned with cutadapt (RRID:SCR_011841) version v1.8.1 to remove adapters, ambiguous bases, and low-quality reads. Reads longer than 60 bp and with a Phred score greater than 30 were kept. The Phred quality scores reflect the nucleotide error probabilities. A Phred score of 30 reflects a base call accuracy of 99,9%.

5.3. Alignment of DNA reads to the *Brassica napus* reference genome

The 123 Mio clean reads obtained for each cultivar were mapped to the genome of European winter oilseed *B. napus* Darmor-bzh using the Burrows-Wheeler Aligner (Li and Durbin 2009); RRID:SCR_010910) version v0.7.15-r1142. The BWA-MEM algorithm was used with default parameters. Duplicated reads where marked and removed with Picard-tools (RRID:SCR_006525; http://broadinstitute.github.io/picard/) version v1.140 (Illumina sequencing involves several PCR amplification steps that may produce duplicated reads. If there is a wrongly sequenced nucleotide in these reads, the error is multiplied. Picard-tools identify and remove these reads derived from PCR duplicates to increase sequencing quality and to increase the reliability of the given sequence data and SNP calling).

5.4. SNP calling and cultivar-specific transcriptome construction

SNPs present in the DNA of Drakkar and Tanto in comparison to the DNA of Darmor-bzh were identified using GATK HaplotypeCaller (McKenna et al. 2010), RRID:SCR_001876) version v3.3-0. Only high-quality homozygous SNPs were kept using the following filters: QD < 2.0 || FS > 60.0 || MQ < 40.0 || MQRankSum < -12.5 || ReadPosRankSum < -8.0 || DP < 4.

Representative transcriptome genomes of Drakkar and Tanto cultivars were constructed by inferring each cultivar-specific high confidence SNPs into the Darmor-bzh reference genome using GATK FastaAlternateReferenceMaker (RRID:SCR_001876) https://software.broadinstitute.org/gatk/documentation/tooldocs/3.8-0/org_broadinstitute_gatk_tools_walkers_fasta_FastaAlternateReferenceMaker.php).

6. RNA sequencing

6.1. Total RNA isolation and quality control

For deep sequencing profiling of RNA, total RNA of each sample was extracted as described in paragraph 3.1, except that ca. 200 dissected leaf-disks were harvested at 12 dpi. Two grams (2 g) of these leaf disks were ground in liquid nitrogen and RNA was purified using the RNAeasy Mini Kit (Qiagen). The quality of each RNA sample was verified by gel electrophoresis and BioAnalyzer (Agilent technologies) techniques as described (paragraph 4.2). Each individual total RNA sample was divided into three aliquots, each used for further analysis by mRNAseq (transcriptome profiling), sRNAseq (small RNA profiling), and PAREseq (mRNA degradome profiling using Parallel Analysis of RNA ends (PARE)).

6.2. mRNA sequencing and quality control

The total RNA preparations were used for mRNA isolation, the construction of mRNAseq paired-end libraries (2*100bp) and Illumina HiSeq2000 sequencing by the company “aScidea Computational Biology Solutions” (http://www.ascidea.com/; Barcelona, Spain). The mRNAseq raw reads libraries were quality-checked with FastQC (RRID:SCR_014583) version v0.11.2 and cleaned with cutadapt (RRID:SCR_011841) version v1.8.1 for adapter removal,

"N" base removal, and quality filtering. Reads longer than 60 bp and with a Phred score greater than 30 where kept.

6.3. Alignment and annotation of mRNAseq reads

Tanto and Drakkar clean mRNAseq reads were aligned to the reconstructed Tanto and Drakkar transcriptome, respectively, using Tophat2 (Kim et al. 2013, https://ccb.jhu.edu/software/tophat/index.shtml) version v2.0.13. The Bowtie2 aligner was chosen allowing one mismatch (Langmead and Salzberg 2012, http://bowtie-bio.sourceforge.net/bowtie2/index.shtml). Genes were annotated using blastx on the *Arabidopsis thaliana* genome with default parameters. The *Arabidopsis* TAIR10 gene identifiers were used to retrieve the gene ontology (GO) annotations from the UniProtKB database.

6.4. Differential expression analysis

After mapping to the transcriptome the unique mapped RNAseq reads were counted using the SAMtools (Li et al. 2009, RRID:SCR_002105) idxstats tool version v1.1. The counts of mapped reads were then used for differential expression analysis with DESeq2 (Love et al. 2014), RRID:SCR_015687) version v1.10.0.

7. sRNA sequencing

sRNAseq paired-end libraries (1*50 bp) were constructed and sequenced on an Illumina HiSeq2000 sequencer by aScidea Computational Biology Solutions (http://www.ascidea.com/, Barcelona, Spain). The sRNAseq raw read libraries were quality checked and remaining reads were filtered like the mRNAseq read libraries. Clean reads that were 18 nt to 30 nt in length and that had a Phred score higher than 30 were kept.

7.1. vsiRNA alignment

Virus-derived siRNAs were identified by mapping the clean sRNAseq reads to the TuMV-GFP genome (described in paragraph 2.1 pCB-TuMV-GFP) with Bowtie2 (Langmead and Salzberg

2012) version v2.2.9 using the following options "-t -N 0 --end-to-end --very-sensitive --score-min C,0,0" with no mismatch for virus-derived sRNAs. These reads have been re-mapped to the cultivar-specific transcriptomes to verify the absence of homology in the plants.

7.2. Identification of miRNAs

Reads were mapped to miRNAs of *B. napus*, *B. oleracea*, *B. rapa*, *A. thaliana* and *A. lyrata* annotated in miRbase21 as well as to new Brassica miRNAs described in three publications (Xu et al. 2012; Lukasik et al. 2013; Jiang et al. 2014).

7.3. *De novo* miRNA and va-phasiRNA detection

To identify *B. napus* miRNAs that are still unknown, we analyzed the reads with ShortStack (Axtell 2013) (v3.4, RRID:SCR_010834) in *de novo* mode. ShortStack annotates miRNAs on the basis of specific criteria, including a requirement of the corresponding star sequence present in the sRNA data and its mapping near the candidate miRNA sequence within the same gene. The list of predicted miRNAs was filtered to keep only candidates (clusters) with: DicerCall 21, 22, 24nt, and MIRNAs step Y_N15. The DicerCall reflects the predominant RNA size observed in the locus (not necessarily the majority). The N15 step is the last step in the analysis. By choosing the option Y-N15, only the sRNA reads that have passed all selective steps of miRNA identification, including the sequencing of the exact miRNA star sequences, are selected and identified as miRNAs.

We focused our analysis of sequenced sRNAs also on the identification of siRNAs that are particularly induced upon virus infection. Similar to virus-associated, RDR1-dependent siRNAs (vasiRNAs) reported for Arabidopsis (Cao et al. 2014a), we found siRNAs that derive from coding genes that convert their transcripts into dsRNA followed by phased DCL-mediated cleavage and which we named “virus-associated phased siRNAs (va-phasiRNAs)”. The unique va-phasiRNAs in our database were predominantly 21 nt in length, represented by at least 100 reads in the samples from virus-infected tissues, and exceeded their normalized abundance in virus-treated tissues over their abundance in non-infected control tissues (mock) by at least a factor of 2 (rpm infected / rpm mock >2) (read per million (rpm); number of reads are multiplied by 10^6 and divided by the total number of cleavage events in the

corresponding sequenced library). Moreover, the corresponding va-phasiRNA-producing genes showed a PhaseScore (the quality of the phasing register) higher than 30 (determined by Shortstack). The virus-induced and phased production of the va-phasiRNAs was verified by visualization of the gene-specific siRNA pattern with the Integrated Genome Viewer tool IGV 2.3 (Thorvaldsdóttir et al. 2013).

7.4. Short read abundance and differential expression (DE) analysis

The abundance of our known and predicted miRNAs and va-phasiRNAs was estimated after mapping using idxstats command of SAMtools v1.1 (Li et al. 2009) (RRID:SCR_002105). The differential expression analysis for miRNAs was performed with DESeq2 (Love et al. 2014), RRID:SCR_015687) version v1.10.0.

8. mRNA degradome sequencing

The construction of PARE libraries was performed according to the protocol of German et al. (2009) with modifications, which concerned particularly the purification of each intermediate reaction product during the procedure. This part of the work was done by Khalid Amari (former Post-doc) in collaboration with Livia Donaire and César Llave in the CIB-CSIC Institute, Madrid (Spain). Similar to 5'RACE, the construction of PARE libraries involves mRNA purification (affinity binding to oligo dT-coated beads), 5'RNA adapter ligation, reverse transcription, an additional MmeI enzyme treatment causing cleavage of the cDNAs at a position 20 bp downstream of the original 5' end of the mRNA, subsequent 3'RNA adapter ligation to the new cDNA3' ends, PCR amplification, and high-throughput sequencing.

Thus, the procedure started by ligating 1 ug of purified mRNA to a 5' RNA adapter. After a new purification step of mRNA again using oligo dT-coupled Dynabeads, cDNA synthesis, short PCR amplification and MmeI digestion were performed as described (German et al. 2009). Digested fragments of ≈20 nt were then purified by PAGE, and 3' ligated to a dsDNA adapter. The ligation products were further purified by PAGE and amplified using Illumina primers. The final amplicons of approximately 125 bp were again purified by PAGE. To allow sample multiplexing in the sequencing reaction, different indexed primers were used in the amplification step (Illumina primers RPI1 to RPI4). The amplicon structure was then checked

by cloning into TOPO vector and low-scale sequencing of individual clones. All clones analyzed contained inserts according to the predicted structure when libraries prepared from Drakkar were tested.

8.1. Sequencing of PAREseq libraries and quality control

The PAREseq libraries were sequenced (1x 50 bp) on an Illumina HiSeq2000 platform by aScidea Computational Biology Solutions (http://www.ascidea.com/). The sequenced PAREseq read libraries were cleaned with cutadapt (RRID:SCR_011841) version v1.8.1 for adapter removal, 'removal of reads with "N" bases, and quality filtering.

8.2. Association of cleaved mRNA 5'ends with RISC-mediated mRNA cleavage

To determine whether the cleaved 5' mRNA ends identified by PAREseq analysis could be caused by RISC-mediated RNA cleavage, the sample-specific PAREseq library was aligned to the cultivar-specific transcriptome and correlated with sRNAs (determined by sRNAseq) from the same original total RNA sample with PAREsnip software (Folkes et al. 2012) implemented in the UEA sRNA Workbench version v4.2.1a (Stocks et al. 2018). The default parameters were used except for the "min read abundance" option set to 100. The analysis with this software allows the identification of potential mRNA:sRNA target pairs involved in sRNA-mediated RNA cleavage. Since the RNA genome of TuMV is polyadenylated, the PARE analysis included the analysis of 5' ends of viral RNA.

To compare predicted cleavage events between samples, the specific PAREseq reads associated with RISC-mediated mRNA cleavage events were normalized as reads per million. The sums of normalized cleavage events that occurred in the three biological replicates per condition (specific *B. napus* cultivar/specific treatment) were used to compare the occurrence and abundance of specific cleavage events between conditions. The gene or viral origins of sRNAs associated with specific mRNA or vRNA cleavage were identified by extracting the sRNA associated with a specific cleavage event from the PAREsnip analysis and by aligning its sequence to the transcriptome or viral genome without mismatch.

9. RNA analysis using the northern blotting technique

9.1. Total RNA extraction and size fractionation

RNA extraction from Arabidopsis plants was performed essentially as described under paragraph 3.1 for RNA from *B. napus* leaves. Here, total RNA was extracted by homogenizing 0.7 g Arabidopsis leaf material derived from the pools of several ORMV-infected (35 dpi) or non-infected Arabidopsis leaves, into fine powder in liquid N_2. In contrast to the protocol described in paragraph 3.1, the volumes of chemicals were adapted to the weight of Arabidopsis grinded tissues. Thus, 10 ml of TRI REAGENT® (MRC) were add to the crude extract and supplemented with 2 ml Chloroform in the suspension followed by strong vortexing to create a homogenous mixture. After centrifugation and precipitation, the pellet was washed with 10 ml of 70% EtOH and after discarding of the supernatant, the pellet was dried for 15-20 min at room temperature and finally resuspended in 150 µL RNAse-free water heated to 60°C. The RNA in the resuspended pellet was quantified with a NanoDrop microvolume spectrophotometer at 260 nm absorbance.

To separate high molecular weight (HMW) RNA (e.g. mRNA) from low molecular weight (LMW) RNA (e.g. small RNAs), the isolated total RNA was size-fractionated with the RNAeasy Mini Kit® (QIAGEN) by applying the RNA cleanup protocol with some modifications, as described by Blevins (2017). For instance, the RTL buffer was supplemented with 10 µl β-mercaptoethanol (β-ME) per ml nd the sample was adjusted to 90 µg total RNA. Moreover, all the flow-through was kept for collecting the LMW RNA.

Eluted HMW and LMW RNA fractions were precipitated by addition of an equal volume of isopropanol, overnight incubation at -20°C and centrifugation at 14 000 g in the cold (4°C). The precipitated RNA was resuspended in RNAse-free water and the concentration was determined with a NanoDrop microvolume spectrophotometer at 260 nm.

9.2. RNA blotting

The procedure of Northern blotting for the detection of specific HMW and LMW RNA molecules is mentioned in Kørner et al. (2018) and followed exactly the steps described in J. Sambrook, D. William Russell CSHL Press, 2006 (Volume 1, Chapter 7, Protocol 6 and 7) for

HMW RNA and the procedures described by Akbergenov et al. (2006) and Blevins (2017) for LMW RNA.

For the specific probing of HMW RNA, 8 μg of HMW RNA where used for electrophoresis through the formaldehyde agarose gel. The RNA was then transferred and fixed onto nitrocellulose membrane as described in J. Sambrook, D. William Russell CSHL Press, 2006 (Volume 1, Chapter 7, Protocol 6 and 7). The RNA was crosslinked to the membrane by UV irradiation (1400 x 100 μJ/cm^2). For detection of abundant, HMW, positive sense, genomic viral RNA, the RNA on the blot was probed by hybridization with a sequence-specific mix of oligonucleotide probes (with sequences complementary to the viral RNA) that were end-labelled with γ[^{32}P]-dATP. The probes were prepared in 20 μl reactions containing 1 μl T4 Polynucleotide-Kinase (Thermo Scientific), 0.3 μl 100 μM oligo-nucleotides, 2 μl 10X PNK buffer A, 4.5 μl γ[^{32}P]-dATP (~ 50 μCi) and 12 μl H_20 that were incubated for 30 min at 37°C. For detection of rare molecules such as negative strand viral RNA, a 200 bp long RNA probe generated by T7 promoter-driven *in vitro* transcription in the presence of α[^{32}P]-dUTP was used. The short oligonucleotide probes were purified through illustra MicroSpin G-25 Columns (GE Healthcare Life Sciences) and centrifugation at 735g for 1 min, whereas the longer probe was cleaned by phenol/chloroform extraction and 100% ethanol precipitation. The probes were applied to a nitrocellulose membrane (N+, Amersham) previously pre-hybridized for 4 hours in 10 ml PerfectHyb^{TM} Plus buffer (Sigma). The specific probes were then added and the membrane followed by incubation in this solution overnight at 37°C for detection of abundant viral positive RNA strand and 70°C for detection of the less abundant negative strand. The membranes probed with oligonucleotide or in vitro transcript probes were washed in 2x SSC (300mM NaCl, 30mM Na-Citrate, pH 7) containing 2% SDS (Sodium Dodecyl Sulphate) at 50°C for 5 min or 10 min at 60°C, respectively. To visualize the hybridized probes on the membrane, the membranes were exposed to a storage phosphor screen (for 1h to visualize the viral genomic RNA; for one week to visualize the viral negative strand RNA). The storage phosphor screen was then imaged with a Typhoon FLA-7000 laser scanner (GE Healthcare).

For probing of LMW RNA, 5 μg of the LMW RNAs were separated by electrophoresis through a 16 % polyacrylamide urea gel [12.0 ml 30% acrylamide bisacrylamide (19:1), 18 ml urea solution (11.1 g urea, 6.0 ml 5x TBE (54 g Tris-base, 27.5 g boric acid, 20 ml 0.5 M EDTA pH 8.0

in 1 L miliQ water)) supplemented with 30 µl of TEMED (N,N,N',N'-TEtraMEthyl-1-,2-Diaminométhane), 300 µl APS (ammonium persulfate) (10%)]. The polyacrylamide gel was pre-run in 1x TBE for 20 min at 15W before loading of the sample and the wells were washed using a syringae to remove any excess of urea. The samples were dried for 40 min at room temperature by sublimation in a SpeedVac Concentrator (Thermo Scientific) and resuspended in 8 µl RNA loading buffer (95% formamide, 0.025% bromophenol blue, 0.025% xylene cyanol FF, 5 mM EDTA, 0.025% SDS, pH 8.5). Before loading, the samples were heated to 95°C for 3 min and cooled on ice. The electrophoresis was run for 1h30 at 15W in 1X TBE. After electrophoresis, the RNA in the gel was stained for 8 min in Ethidium bromide (EtBr) solution (400 ml 1X TBE, 20 µl EtBr (from a 10 mg/ml stock) photographed (GelDoc 2000, Bio-Rad), and washed for 20 min in 1X TBE.

Next, the gel was blotted overnight onto a Hybond N+ membrane (GE Healthcare, UK) by capillarity blotting in 0.5X TBE buffer followed by crosslinking the RNA to the membrane by UV (140 mJ/cm^2). Oligonucleotide probes were prepared and purified as described for HMW probes. The membrane was pre-hybridized for 4 hours in 10 ml Perfect-Hyb buffer (Sigma, USA) at 40°C, followed by the overnight hybridization in the same buffer with the specific probes at 37 °C. Blots were washed three to five times in 0.5% SDS; 2x SSC at 37 °C. For detection of different sRNAs in the same RNA extract, the blots were stripped by three consecutive washes with boiling 0.5% SDS each for 20 min before re-probing. The membrane was exposed two- to seven-days to a storage phosphor screen, which was then imaged with a Typhoon FLA-7000 laser scanner (GE Healthcare).

10. Protein analysis using the western blot technique

10.1. Total protein extraction and quantification

As described in Kørner et al. (2018), 0.1g Arabidopsis leaf tissues were homogenized to fine powder in liquid N_2. After addition of 400-600 µl extraction buffer (10% glycerol, 5% β-ME, 75 mM Tris-HCl pH 6.8) and homogenization with the help of a Silimat® shaking machine, the sample was heated at 95°C with 2% SDS for 5 min and centrifuged at 14 000 g for 10 min. The aqueous phase was extracted, boiled 10 min at 95°C for their denaturation and quantified using the Bradford protein assay (Bio-Rad). The protein extract was then mixed to 1x with

Laemmli buffer (62,5 mM Tris-HCl pH 6.8, 3% SDS, 10% glycerol, 0.1% bromophenol blue, 5% β-ME), boiled again 5 min at 95°C before loading into a polyacrylamide gel.

10.2. SDS-PAGE

Proteins were separated by PAGE under denaturing conditions in the presence of SDS using Bio-Rad electrophoresis equipment. The acrylamide gel was polymerized in the presence of APS as a radical initiator and TEMED as catalyst. The acrylamide/bisacrylamide percentage in the separation gel was chosen according to the size of the proteins to be analyzed (generally between 8 % and 15%).

Protein samples were heated in Laemmli buffer for 10 min at 95 °C, mixed and cleared by centrifugation at 14,000 g for 10 min. Between 5 and 25 µL (≈ 20 µg) of protein solution were loaded per well. Protein size markers (PageRuler™ 10-170 kDa, Thermo Scientific, 7 µL) were loaded in parallel. The electrophoresis was performed in 1x Tris-Glycine-SDS buffer (25 mM Tris-base, pH 8.3, 192 mM Glycine) at constant voltage (90 V).

10.3. Protein transfer and luminescent detection

The protein gel was rinsed in transfer buffer (25 mM Tris-base, pH 8.3; glycine 250 mM) to partially remove the remaining SDS. Immobilon-P (Millipore) membrane was cut to the size of the gel, activated in 96% ethanol for 15 sec and briefly rinsed in transfer buffer. The gel and the membrane were placed in a transfer system (Mini Trans-Blot Cell, Bio-Rad) between Whatmann papers and sponges. The transfer was carried out at 90V for 130 min. The membrane was then rinsed for 10 min in TBS-T buffer (1x TBS and 0.1% Tween20®) and pre-incubated in TBS-T / 5% milk powder for 60 min at room temperature to saturate the unspecific sites. After addition of primary antibodies and further incubation at 10 rpm shaking on a Duomax 1030 (Heidolph) apparatus overnight at 4 °C (for dilutions see Material paragraph 4), the membrane was washed 3 times in TBS-T / 5% milk buffer for 10 min. The membrane was then incubated for 1h in the same buffer and in the presence of horseradish peroxidase-coupled secondary antibodies (see Material paragraph 4) at room temperature and again washed for 3 times in TBS-T buffer for 10 min. The location of the antibody-labeled proteins on the membrane was revealed by chemiluminescent detection using "Lumi-Light^{PLUS}

Western Blotting Substrate" (Roche Diagnostics) according to the manufacturer's recommendations (volume to volume black and white solution, 1 min contact with the membrane) and documented by imaging with a FUSION FX western blot and chemiluminescence imaging system (VIlber Lourmat, France). The membrane was stained with Coomassie blue (50% ethanol, 10% acetic acid, 0.25% Coomassie R250 blue) to visualize the amount of transferred protein.

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APPENDIX 1: SUPPLEMENTARY FIGURES AND TABLES OF DRAFT MANUSCRIPT: "VIRUS- AND HOST-DERIVED SMALL RNAS COORDINATE INFECTION IN OILSEED RAPE" BY PITZALIS ET AL.

Supplementary Figures:

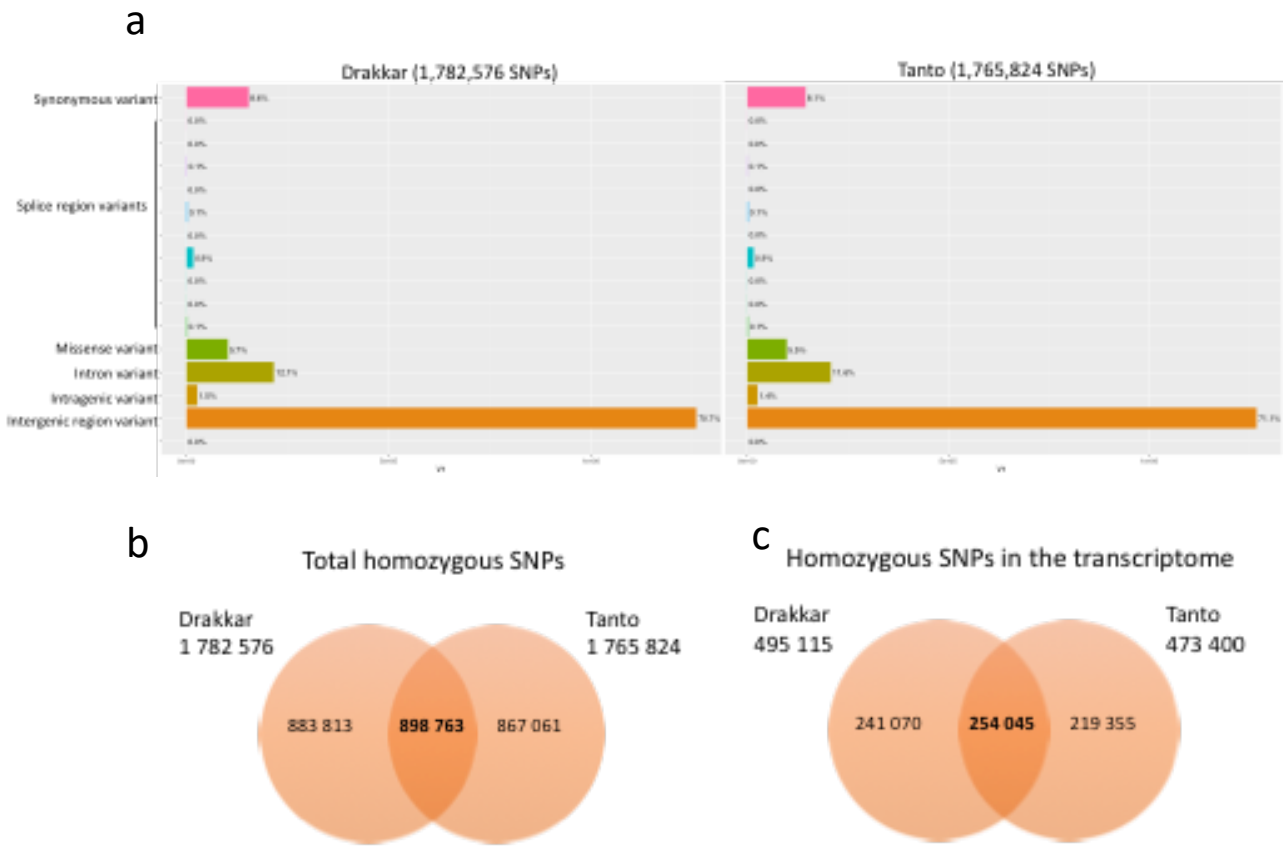

Fig. S1. Homozygous SNPs by which *B. napus* cvs. Drakkar and Tanto differ from the reference sequence of *B. napus* cv. Darmor-bzh. a, Distribution of SNP categories. Most SNPs are from intergenic regions. **b**, Total homozygous SNPs that are shared by or specific to the Drakkar and Tanto cultivars. **c**, Homozygous SNPs that map to transcribed genes and are either shared by or specific to the Drakkar and Tanto cultivars respectively.

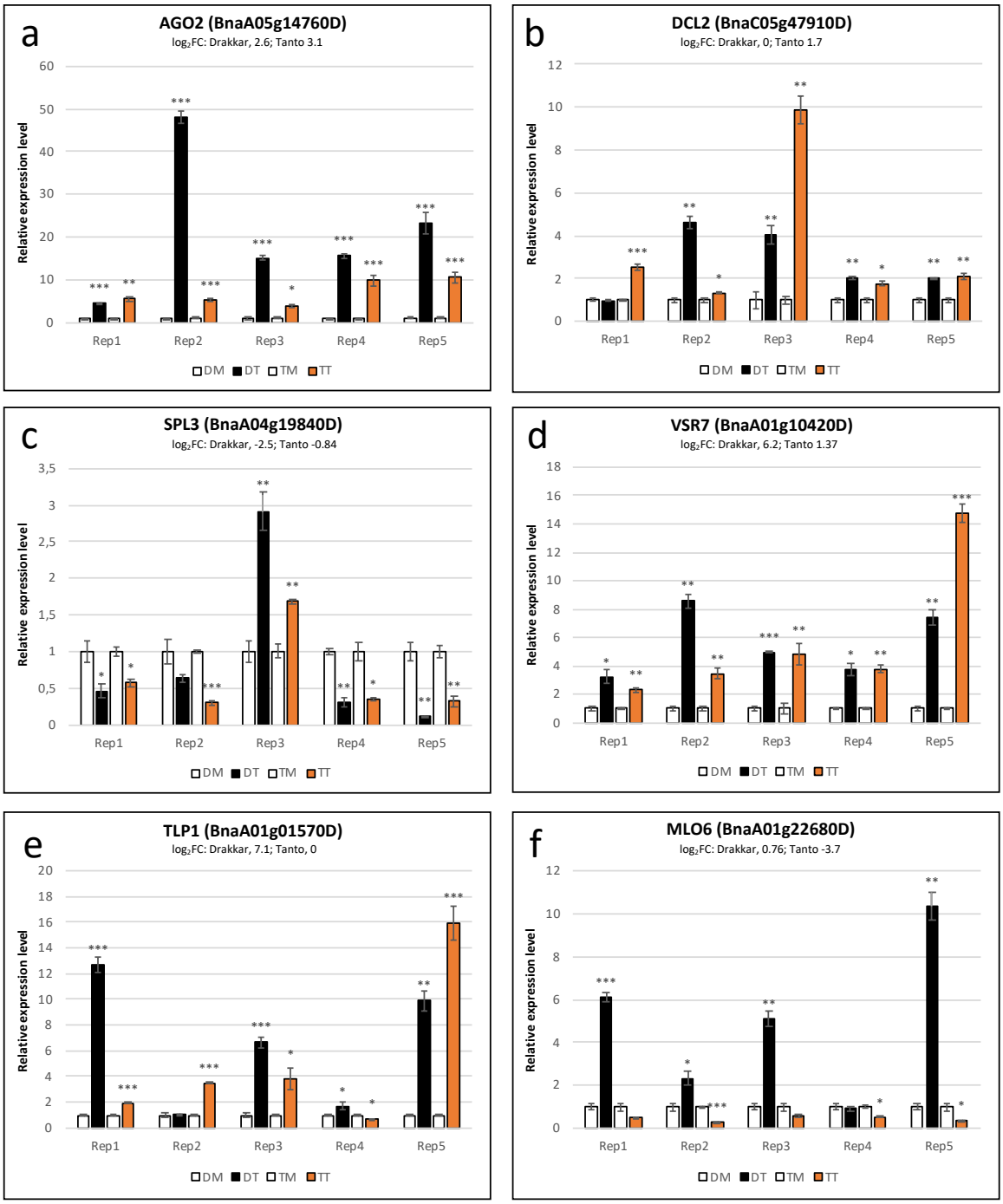

Fig. S2. Confirmation of RNAseq-based DEseq data by q-RT-PCR. Relative expression levels in local sites of virus-infected leaves in comparison to expression levels in mock-control tissues (set to 1) are shown. qRT-PCR assays were performed with original polyA RNA used for RNAseq (Rep1) as well as with polyA RNA isolated from new biological samples derived from four new independent experiments (Rep2-Rep5). **a**, RNAseq-based DEseq data indicated that a transcript for AGO2 (BnaA05g14760D) is induced by TuMV infection in both Drakkar (fold change [log_2]: 2.6) and Tanto (fold change [log_2]: 3.1). This upregulation in both cultivars is confirmed by qRT-PCR using independent RNA samples derived from the five independent experiments Rep1-Rep5. **b**, RNAseq-based DEseq data indicated that a transcript for DCL2 (BnaC05g47910D) is induced by TuMV

infection in Tanto (fold change [log_2]: 1.7) but not in Drakkar RNAseq-based (fold change [log_2]: 0.0). This upregulation Tanto is confirmed by qRT-PCR using independent RNA samples derived from the five independent experiments Rep1-Rep5. However, unlike the original sample (Rep1), samples Rep2-Rep5 indicate that DCL2 may also be virus-induced in Drakkar. **c**, RNAseq-based DEseq data indicated that a transcript for SPL3 (BnaA04g19840D) is downregulated by TuMV infection in both Drakkar (fold change [log_2]: -2.5) and Tanto (fold change [log_2]: -0.84). This downregulation in both cultivars is confirmed by qRT-PCR with samples from all replicative experiments except Rep3. **d**, RNAseq-based DEseq data indicated that a transcript for VSR7 (BnaA01g10420D) is induced by TuMV infection in both Drakkar (fold change [log_2]: 6.2) and Tanto (fold change [log_2]: 1.37). This induction in both cultivars is confirmed by qRT-PCR with samples from all replicative experiments. **e**, RNAseq-based DEseq data indicated that a transcript for TLP1 (BnaA01g01570D) is induced by TuMV infection in Drakkar (fold change [log_2]: 7.1) but not in Tanto (fold change [log_2]: 0.0). qRT-PCR analysis confirms the strong induction of this gene in Drakkar, although the induction is lower in the new repetitive samples. The RT-qPCR experiments also confirm a low or absent induction of this gene in Tanto, except in the Rep5 sample. **f**, RNAseq-based DEseq data indicated that a transcript for MLO6 (BnaA01g22680D) is induced by TuMV infection in Drakkar (fold change [log_2]: 0.76) and suppressed in Tanto (fold change [log_2]: -3.7). qRT-PCR analysis confirms the strong induction of this gene in Drakkar (except in Rep4), and the suppression of this gene in Tanto.

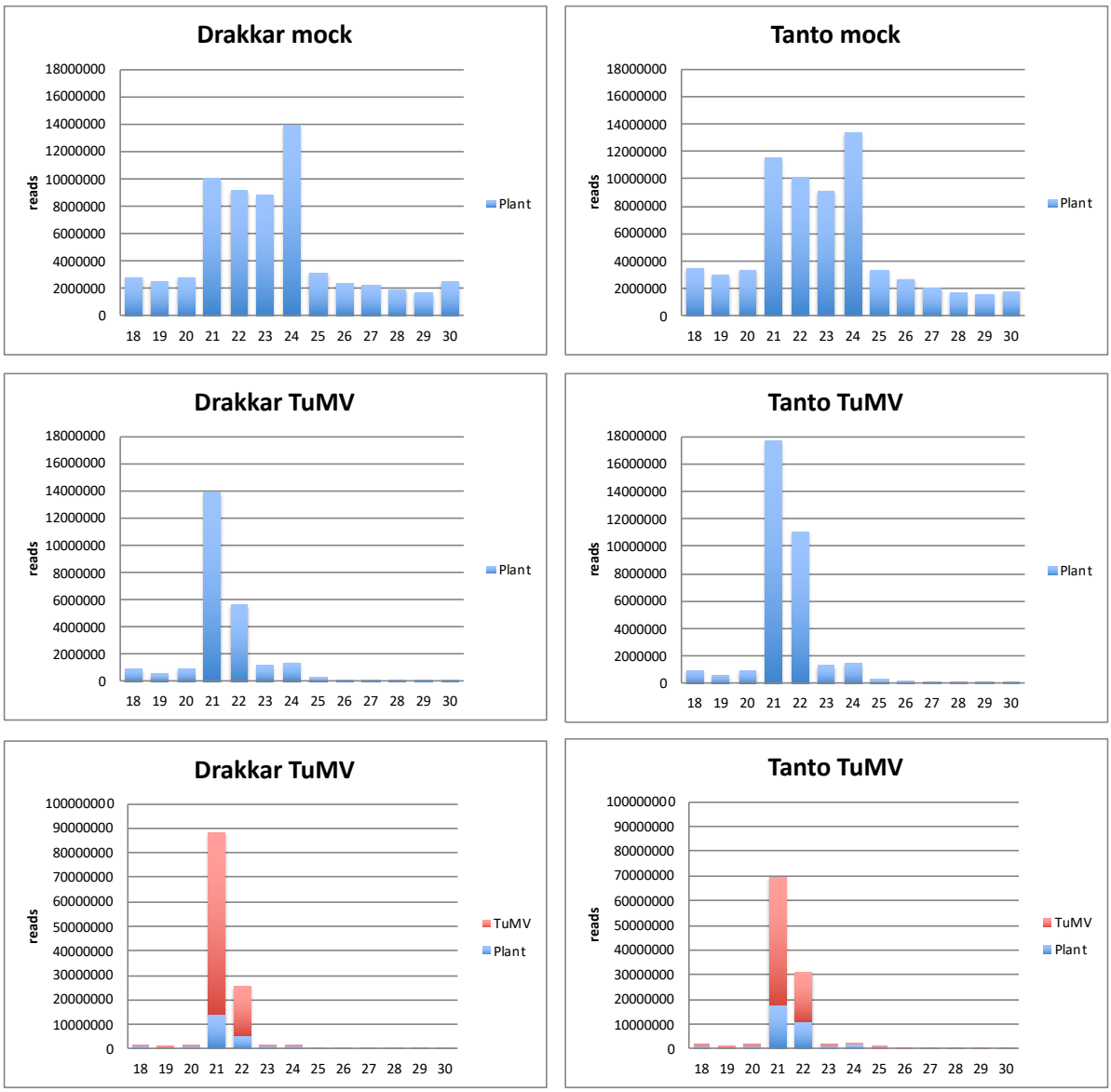

Fig. S3. Small RNA size distribution before and after TuMV infection in Drakkar and Tanto. Sizes of sRNAs within local infection sites in leaves and mock-treated control samples. The sRNA size distribution is very similar between Drakkar and Tanto. Panels at the top show the distribution of sRNAs in mock-treated control samples. The panels in the middle and at the bottom show the distribution of sRNAs within local infection sites. The panels in the middle show the sRNA size distribution only for host sRNAs, whereas the panels at the bottom show the size distribution for both host and viral sRNA. In comparison to the panels at the top, the panels in the middle illustrate the impact of virus infection on the host sRNA profile.

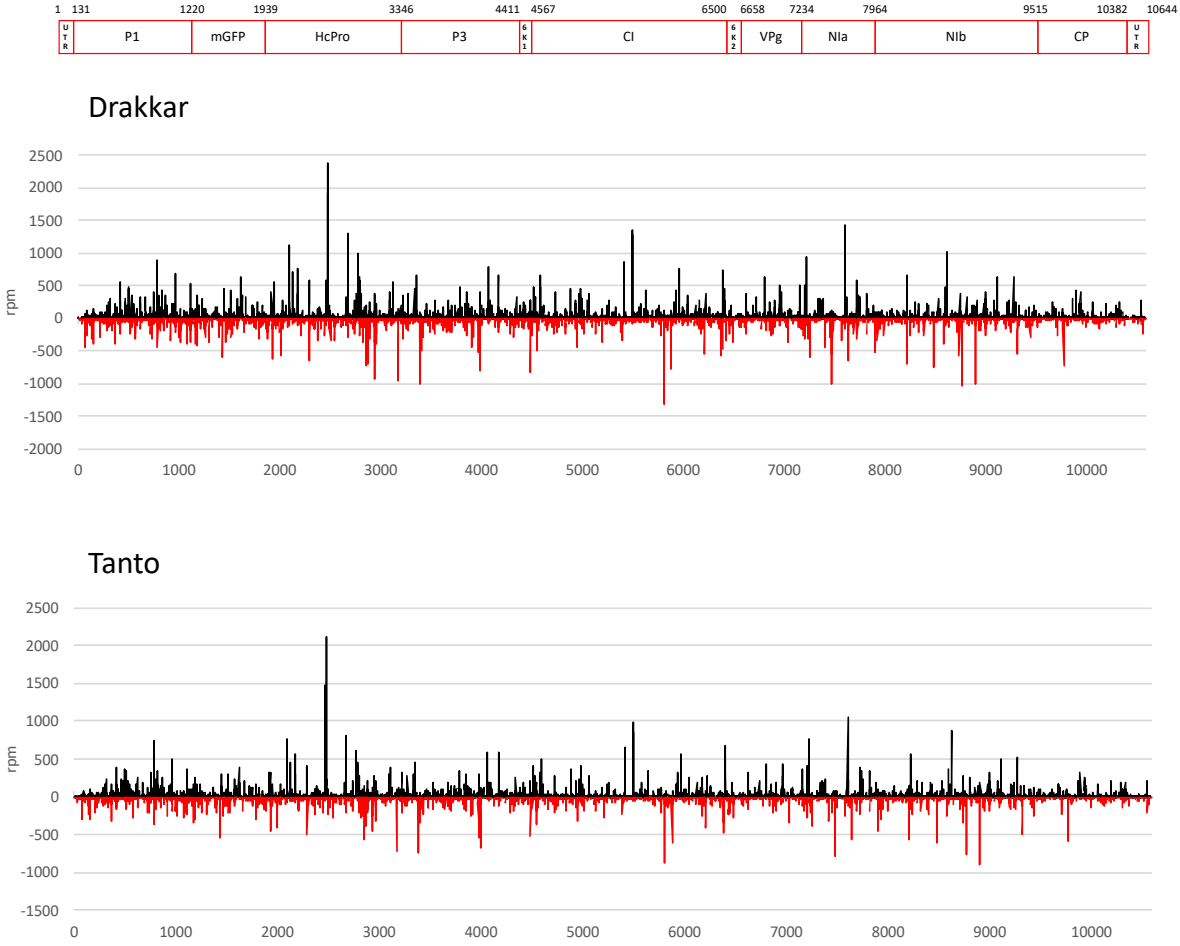

Fig. S4. Alignment of vsiRNAs to the TuMV genome. The pattern of vsiRNA shows the origin of vsiRNAs derived from DCL cleavage of viral dsRNA. All reads were mapped without mismatch to the 10644 bases long viral RNA. vsiRNA reads derived from the viral (+) strand are shown in black; vsiRNA reads derived from the viral (-) strand are shown in red. The UTRs and protein-coding regions of the viral RNA are shown at the top of the figure.

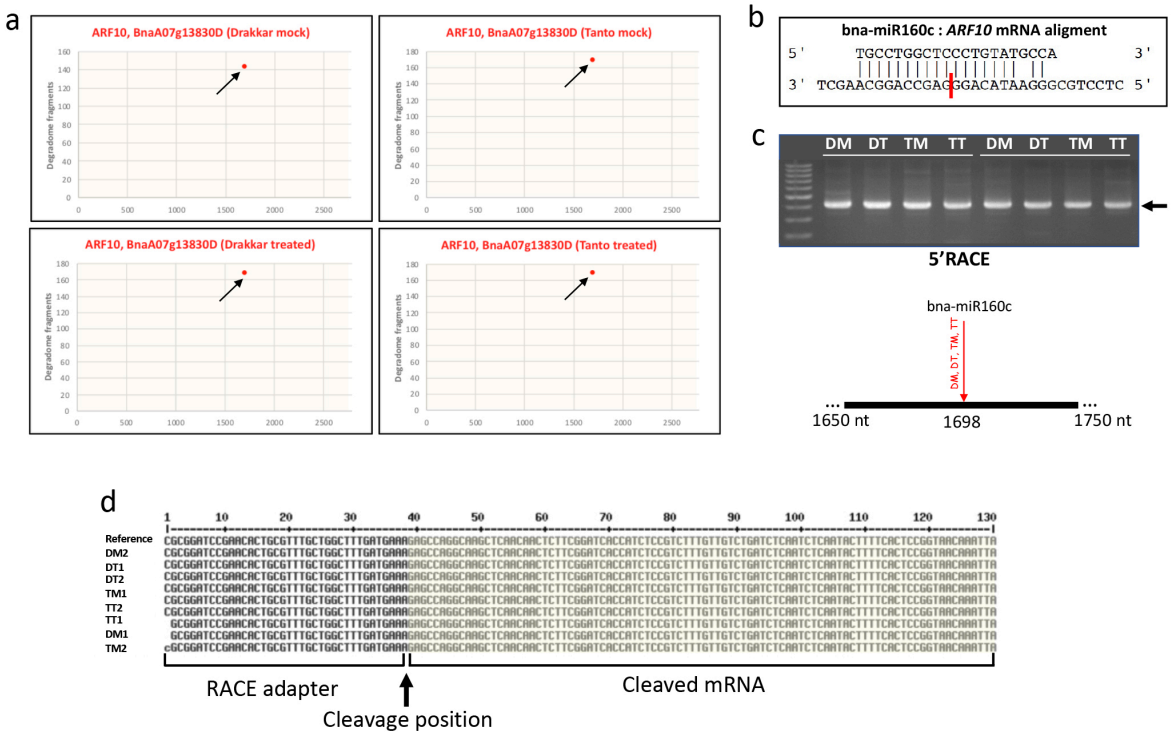

Fig. S5. Targeting of *ARF10* mRNA by bna-miR160c. a, Targeting of *ARF10* mRNA by bna-miR160c produced a highly defined PAREseq degradome signature (arrow) in mock (DM, TM) as well as infected Drakkar (DT) and Tanto (TT) samples. The T-plots generated by PAREsnip show the total number of degradome fragments (y axis) found for *ARF10* mRNA in the three replicate samples per condition analyzed by PAREseq and their mapping along the length of the *ARF10* mRNA (z-axis). **b**, Alignment of bna-miR160c to the *ARF10* mRNA by PAREsnip. The cleavage site within the miRNA:mRNA target pair behind nucleotide 1698 of the mRNA is indicated by a red line. **c**, 5' RACE analysis of independent biological samples confirmed the exact cleavage site at position 1698 of the transcript. The electrophoresis gel shows the RACE DNA fragment of corresponding size (arrow). **d**, Verification of the cleavage site by DNA sequencing of the RACE DNA fragment.

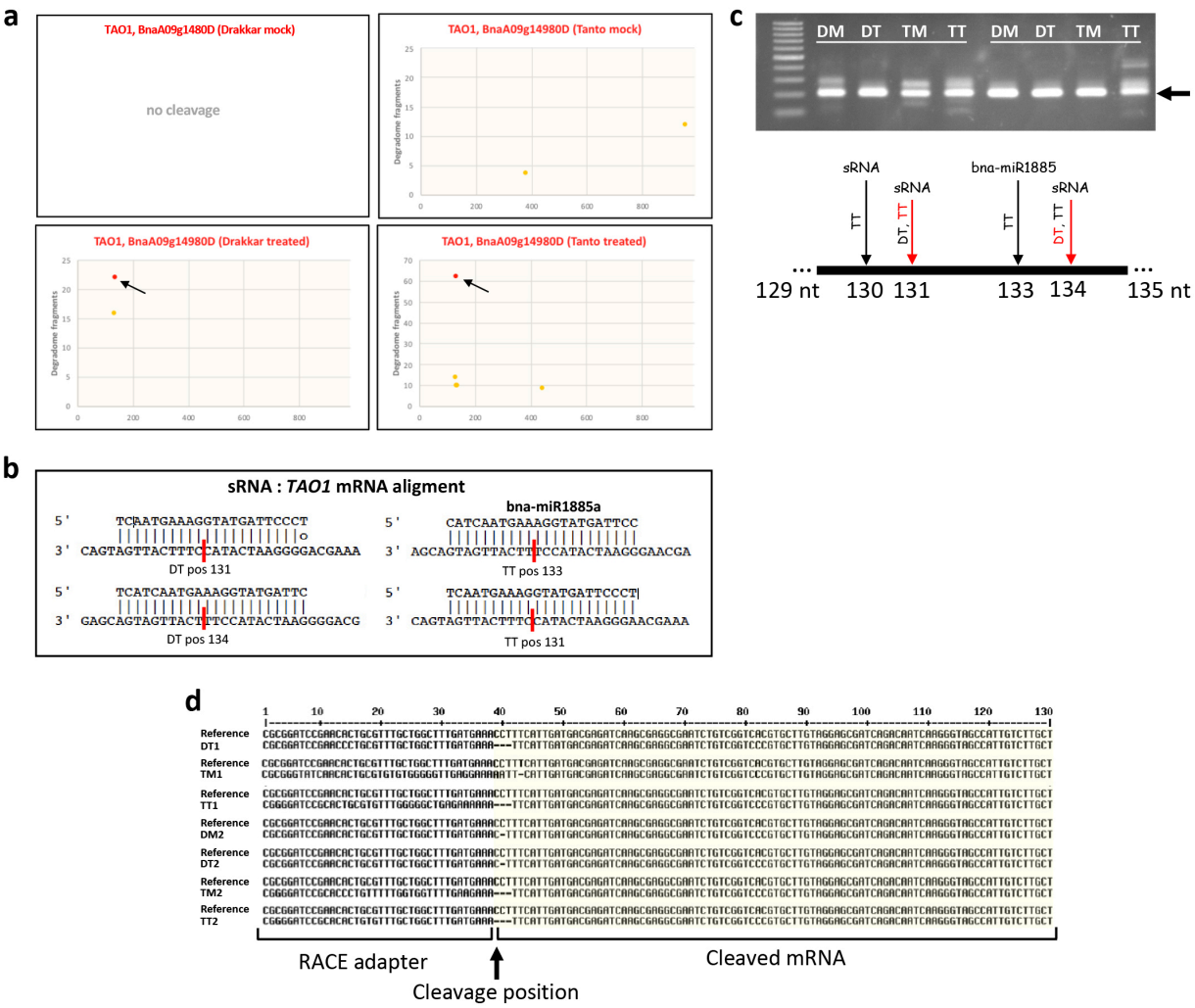

Fig. S6. Targeting of *Target of Avtb Operation 1 (TAO1)* mRNA by bna-miR1885a and related sRNAs. **a**, Targeting of *TAO1*mRNA by bna-miR1885a produced a highly defined PAREseq degradome signature (arrow) in TM as well as infected Drakkar (DT) and Tanto (TT) samples. The T-plots generated by PAREsnip show the total number of degradome fragments (y axis) found for *TAO1* mRNA in the three replicate samples per condition analyzed by PAREseq and their mapping along the length of the *TAO1* mRNA (z-axis). **b**, Alignment of bna-miR1885a and related siRNAs to the *TAO1* mRNA by PAREsnip. The specific cleavage sites within the miRNA:mRNA target pair behind nucleotide positions 131-134 of the mRNA are indicated by a red line. **c**, 5' RACE analysis of independent biological samples confirmed the exact cleavage sites at these positions of the transcript. Cleavage sites shown in red are the most dominant category 0 cleavage events indicated by the red dots and arrows in (**a**). The electrophoresis gel shows the RACE DNA fragment of corresponding size (arrow). **d**, The specific cleavage sites were confirmed by DNA sequencing of the RACE DNA fragment.

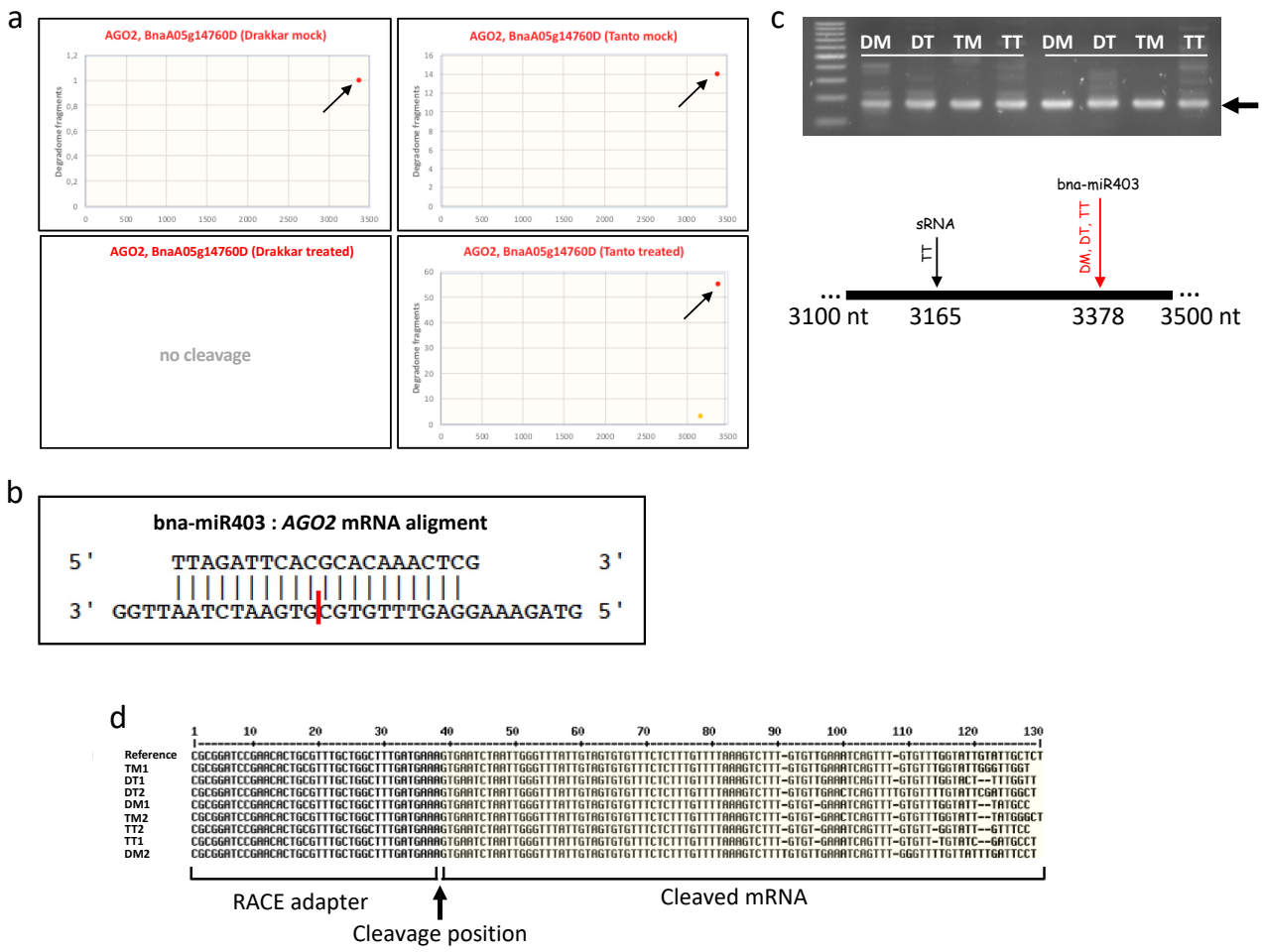

Fig. S7. Targeting of *AGO2* mRNA by bna-miR403. a, Targeting of *AGO2* mRNA by bna-miR403 produced a highly defined PAREseq degradome signature (arrow) in mock (DM, TM) as well as infected Tanto (TT) samples. The T-plots generated by PAREsnip show the total number of degradome fragments (y axis) found for *AGO2* mRNA in the three replicate samples per condition analyzed by PAREseq and their mapping along the length of the *AGO2* mRNA (z-axis). **b**, Alignment of bna-miR403 to the *AGO2* mRNA by PAREsnip. The specific cleavage site within the miR403:AGO2mRNA pair behind nucleotide positions 3378 of the mRNA is indicated by a red line. **c**, 5' RACE analysis of independent biological samples confirmed the exact cleavage sites at this position of the transcript. The cleavage sites shown in red is the most dominant category 0 cleavage event indicated by the red dots and arrow in (**a)**. The electrophoresis gel shows the RACE DNA fragment of corresponding size (arrow). PAREsnip analysis indicates a second cleavage site at position 3165 of the *Ago2* mRNA. **d**, The specific cleavage site at position 3378 was confirmed by DNA sequencing of the RACE DNA fragment.

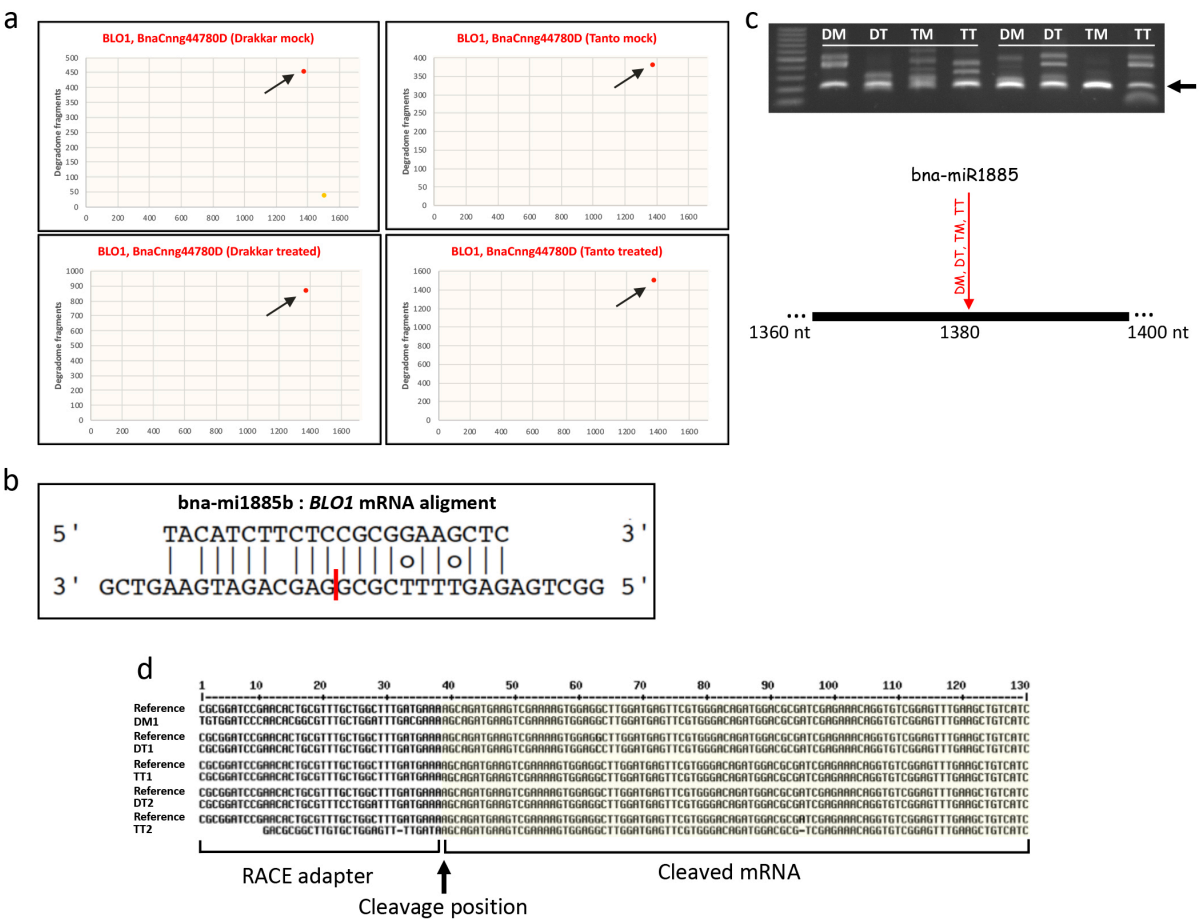

Fig. S8. Targeting of *Biogenesis of Lysosome-related organelles complex 1 subunit 2 (BLOS2)* mRNA by bna-miR1885b. a, Targeting of *BLOS2* mRNA by bna-miR1885b produced a highly defined PAREseq degradome signature (arrow) in mock (DM, TM) and infected (DT, TT) samples. The T-plots generated by PAREsnip show the total number of degradome fragments (y axis) found for *BLOS2* mRNA in the three replicate samples per condition analyzed by PAREseq and their mapping along the length of the *BLOS2* mRNA (z-axis). **b**, Alignment of bna-miR1885b to the *AGO2* mRNA by PAREsnip. The specific cleavage site within the miR1885b:AGO2mRNA pair behind nucleotide positions 1380 of the mRNA is indicated by a red line. **c**, 5' RACE analysis of independent biological samples confirmed the exact cleavage sites at this position of the transcript. The cleavage sites shown in red is the most dominant category 0 cleavage event indicated by the red dots and arrow in (**a)**. The electrophoresis gel shows the RACE DNA fragment of corresponding size (arrow). **d,** The specific cleavage site at position 1380 of the mRNA was confirmed by DNA sequencing of the RACE DNA fragment.

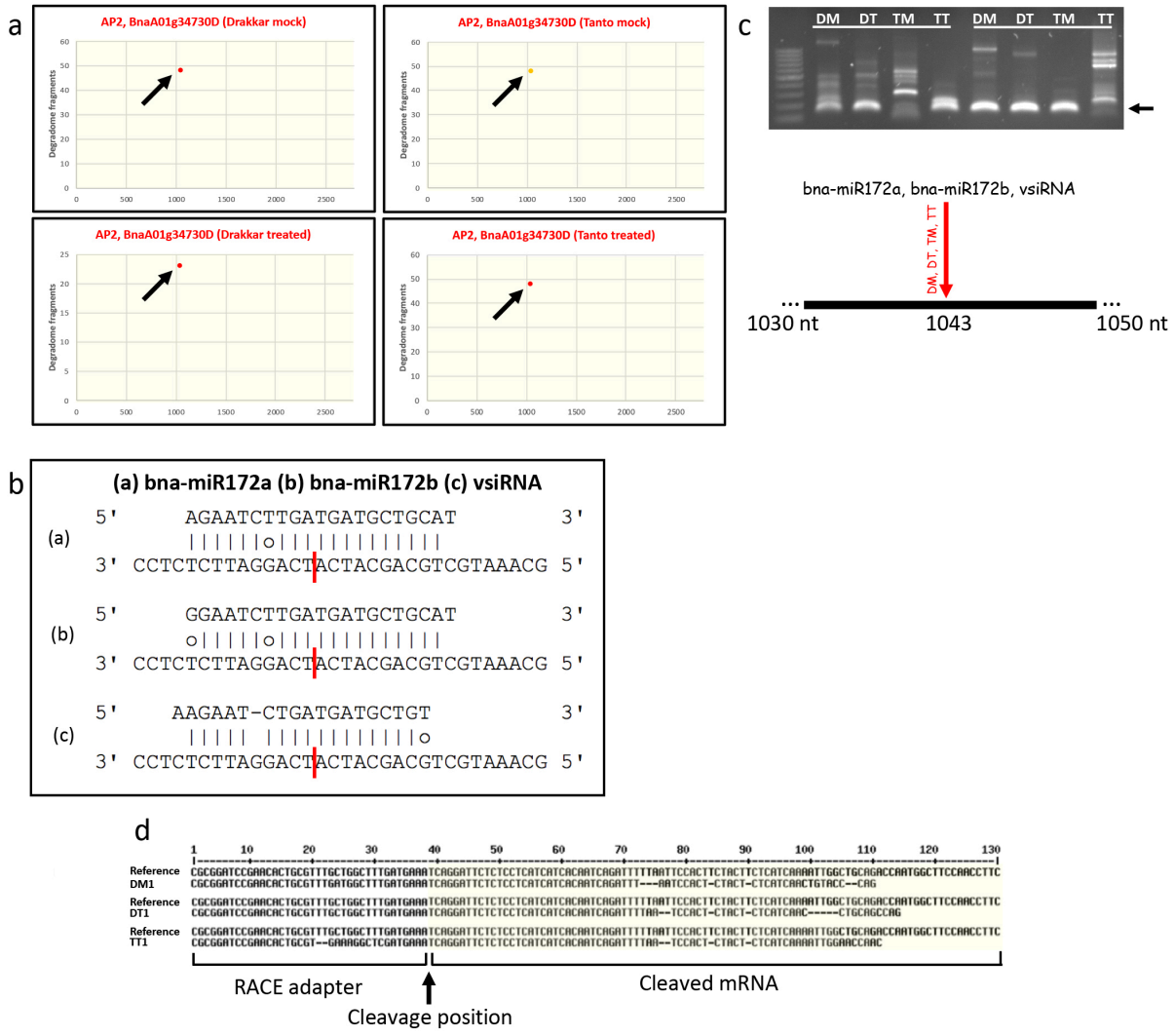

Fig. S9. Targeting of *AP2* mRNA by bna-miR172a, bna-miR172b and TuMV vsiRNA. **a,** Cleavage of *APETALA2* (AP2) mRNA produced a highly defined PAREseq degradome signature (arrow) in mock (DM, TM) and infected (DT, TT) samples. The T-plots generated by PAREsnip show the total number of degradome fragments (y axis) found for *AP2* mRNA in the three replicate samples per condition analyzed by PAREseq and their mapping along the length of the *AP2* mRNA (z-axis). **b**, AP2 cleavage by bna-miR172a, bna-miR172b and a specific TuMV vsiRNAs. The alignment of bna-miR172a, bna-miR172b and vsiRNA to the *AP2* mRNA by PAREsnip is shown. The specific cleavage site associated with the three target pairs and its location behind nucleotide positions 1043 of the mRNA is indicated by a red line. **c**, 5' RACE analysis of independent biological samples confirmed the exact cleavage sites at this position of the transcript. The cleavage sites shown in red is the category 0 cleavage event indicated by the red dots and arrow in (**a)**. The electrophoresis gel shows a RACE DNA fragment of corresponding size (arrow). **d,** The specific cleavage site at position 1043 of the mRNA was confirmed by DNA sequencing of the RACE DNA fragment.

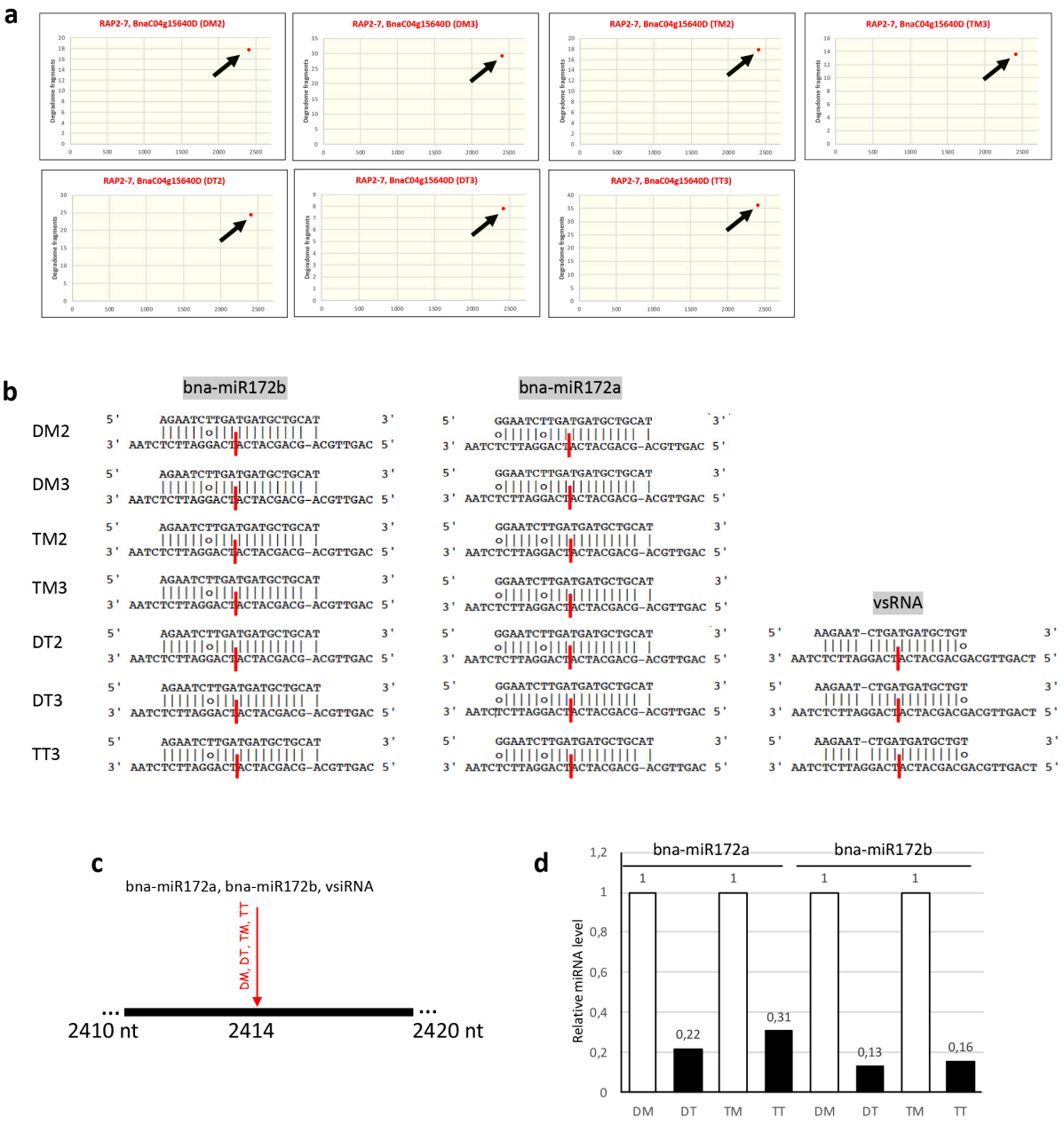

Fig. S10. Targeting of ERF *RAP2-7* mRNA by bna-miR172a, bna-miR172b, and TuMV vsRNA. Cleavage of *RAP2-7* mRNA produced a highly defined PAREseq degradome signature (arrow) in the seven PARE analysis replicates (DM2, DM3, DT2, DT3, TM2, TM3, TT3). The T-plots generated by PAREsnip show the total number of degradome fragments (y axis) found for *RAP2-7* mRNA in these samples in alignment along the length of the *RAP2-7* mRNA (z-axis). **b**, *RAP2-7* mRNA cleavage by bna-miR172a, bna-miR172b and a specific TuMV vsiRNA. The alignment of bna-miR172a, bna-miR172b and the vsiRNA to the *RAP2-7* mRNA as identified by PAREsnip analysis in the respective PARE analysis sample shown. As expected, the vsiRNA:RAP2-7 mRNA target pair occurred only in the infected samples (DT2, DT3, TT3). The specific cleavage site in the mRNA is indicated by a red line **c,** location of the specific cleavage site at nucleotide positions 2414. **d**, Levels of bna-miR172a

and bna-miR172b in the different samples, as determined by sRNAseq. Infection causes a strong reduction in the levels of these miRNAs. Cleavage of the same mRNA target by vsiRNA may complement this reduction in miR172 levels to maintain control over the expression of *RAP2-7*.

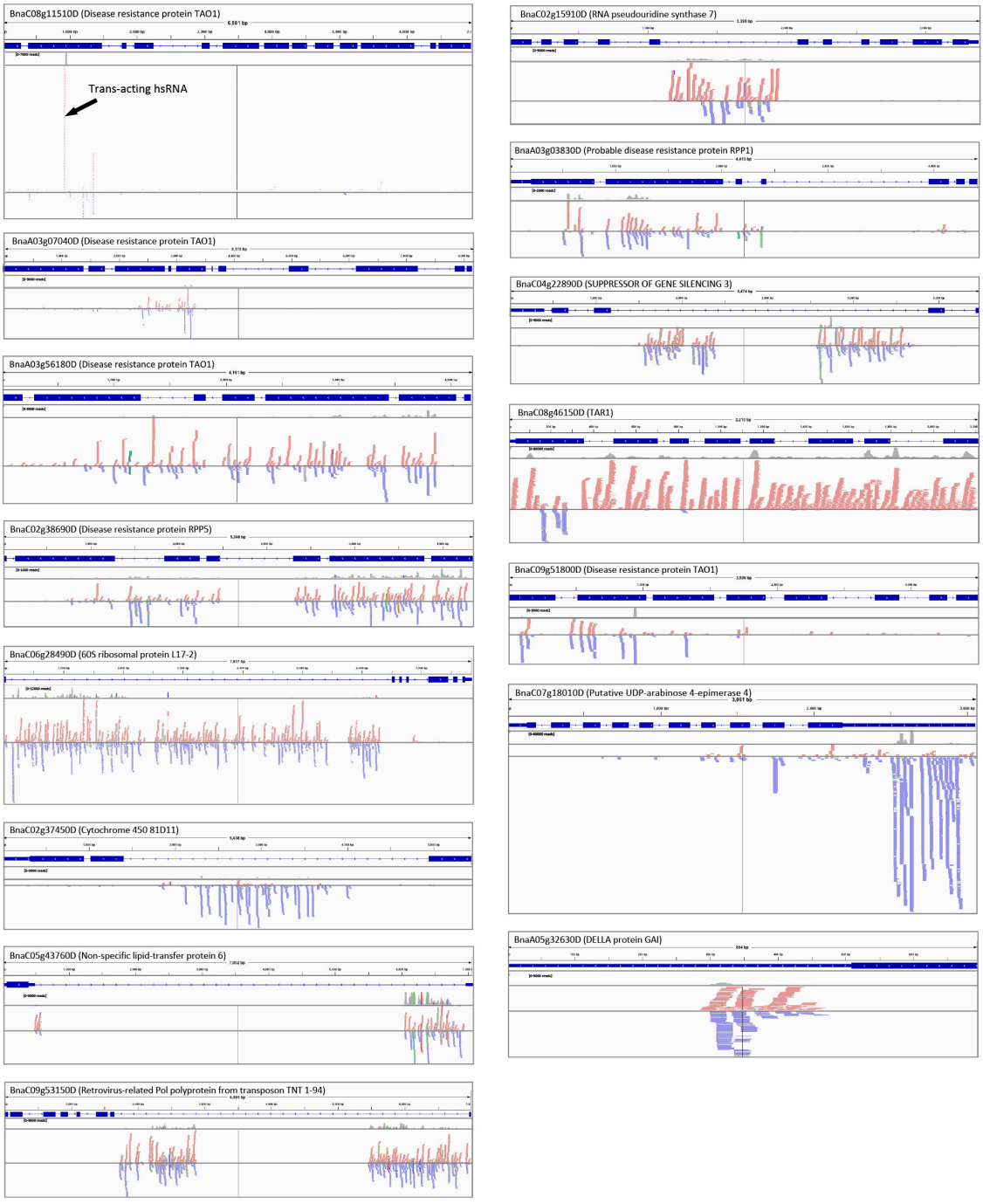

Fig. S11. Examples of host genes that produce trans-acting siRNAs associated with antiviral vRNA cleavage. The different panels show the identity of the host siRNA (hsRNA)-producing gene, the exon-intron structure of the mRNA and the alignment of hsRNAs to the mRNA. Thee panels show hsRNAs from mock-treated Drakkar samples. Thus, unlike va-phasiRNAs, the hsRNAs shown here

are expressed before infection. hsRNAs that target TuMV RNA for cleavage may constitute an antiviral defense layer that is already active before infection.

Supplementary Tables:

Table S1. RNAseq, sRNAseq, and PAREseq read and mapping statistics

RNAseq			Tophat 1mm		Tophat 0mm
sample	raw read pairs	read pairs after filtering	mapped to Drakkar transcriptome (%)	mapped to Tanto transcriptome (%)	mapped to virus (%)
DM1	43 912 453	41058168 (93.5%)	83.5%		
DM2	72 061 780	63849830 (88.6%)	84.9%		
DM3	77 108 467	69053540 (89.6%)	85.2%		
DT1	56 371 395	52684838 (93.5%)	82.7%		1.00%
DT2	79 992 678	71436541 (89.3%)	84.2%		0.90%
DT3	81 059 545	72219626 (89.1%)	83.4%		1.10%
TM1	52 507 664	49215556 (93.7%)		84.5%	
TM2	78 864 932	70708215 (89.7%)		85.1%	
TM3	80 875 384	72703910 (89.9%)		86.1%	
TT1	37 860 785	35427931 (93.6%)		83.3%	0.90%
TT2	74 880 253	66737776 (89.1%)		84.3%	0.80%
TT3	70 132 740	61864732 (88.2%)		84.3%	0.80%

sRNAseq			bowtie2 -t -N 0 --end-to-end --very-sensitive --score-min C,0,0		
sample	raw reads	reads after filtering	mapped to Drakkar transcriptome (%)	mapped to Tanto transcriptome (%)	mapped to virus (%)
DM1	56 025 255	27037795 (48.3%)	48.59%		0.01%
DM2	48 296 781	29994399 (62.1%)	41.92%		0.02%
DM3	66 801 262	49791620 (74.5%)	47.64%		0.06%
DT1	53 665 478	51503121 (96.0%)	13.38%		68.23%
DT2	50 094 688	42003172 (83.8%)	15.25%		64.56%
DT3	54 154 789	49288670 (91.0%)	14.30%		65.28%
TM1	56 422 412	40102411 (71.1%)		48.74%	0.01%
TM2	53 210 994	37955105 (71.3%)		44.33%	0.02%
TM3	56 518 524	36275037 (64.2%)		45.62%	0.06%
TT1	54 042 539	51476472 (95.3%)		21.27%	54.24%
TT2	40 112 100	34302205 (85.5%)		21.85%	52.24%
TT3	57 396 907	52282103 (91.1%)		21.99%	50.91%

PAREseq			bowtie2 -t -N 0 --end-to-end --very-sensitive --score-min C,0,0		
sample	raw reads	reads after filtering	mapped to Drakkar transcriptome (%)	mapped to Tanto transcriptome (%)	mapped to virus (%)
DM1	39 360 296	33032811 (83.9%)	15.76%		0.56%
DM2	10 330 179	7596192 (73.5%)	66.07%		0.00%
DM3	19 291 097	15995324 (82.9%)	72.80%		0.03%
DT1	31 138 488	26715785 (85.8%)	25.05%		2.36%
DT2	14 934 860	11254877 (75.4%)	57.97%		9.13%
DT3	27 356 001	22031176 (80.5%)	68.46%		8.23%
TM1	36 739 520	30524077 (83.1%)		66.68%	3.94%
TM2	8 138 303	6283685 (77.2%)		69.28%	0.00%
TM3	20 196 721	16981513 (84.1%)		74.20%	0.02%
TT1	37 590 376	33071083 (88.0%)		64.50%	0.89%
TT2	10 172 194	7663383 (75.3%)		61.07%	4.36%
TT3	25 146 645	21606965 (85.9%)		60.70%	6.62%

Table S2. DNA resequencing statistics

	Sequencing		Mapping to Darmor				Variant calling					
	read length (bases)	clean reads	mapped reads	% mapped	properly paired reads	% properly mapped	Raw SNPs	Good SNPs	Homozygous SNPs	heterozygous SNPs	Raw Indels	Good Indels
Drakkar	150	122 831 012	120 977 458	98.49	107 240 576	87.31	3 716 045	3 452 779	1 782 576 (1.5 np/kb)	1 670 203	767 119	714 714
Tanto	150	122 855 282	119 497 306	97.27	106 738 002	86.88	3 625 707	3 388 281	1 765 824 (1.5 snp/kb)	1 622 457	751 700	705 132

Table S3. Genes that are most strongly and significantly regulated within sites of local TuMV infection in both Drakkar and Tanto leaves.

	Foldchange (log_2)			% identity		
	Drakkar	**Tanto**	**UniProt**	**Drakkar**	**Tanto**	**Annotation**
BnaA02g31430D	6.53	8.18	CB60G_ARATH	71.73	71.20	Calmodulin-binding protein 60 G
BnaA02g26270D	5.97	7.49	PP2B1_ARATH	56.73	56.74	F-box protein PP2-B1
BnaA02g12230D	5.89	7.41	unknown	-	-	-
BnaA02g04960D	5.52	7.28	GL33_ARATH	92.89	92.89	Germin-like protein subfamily 3 member 3
BnaA02g06790D	5.40	6.78	ZAT12_ARATH	84.76	85.37	Zinc finger protein ZAT12
BnaA01g35960D	4.90	6.42	DF206_ARATH	62.50	62.50	Defensin-like protein 206
BnaA01g35950D	4.86	6.16	DF207_ARATH	62.50	62.50	Defensin-like protein 207
BnaA01g34060D	4.81	6.00	BGL25_ARATH	91.76	91.77	Probable inactive beta-glucosidase 25
BnaA01g31270D	4.74	5.79	RLP12_ARATH	43.27	43.05	Receptor-like protein 12
BnaA01g34050D	4.61	5.57	BGL25_ARATH	67.34	67.34	Probable inactive beta-glucosidase 25
BnaA01g14050D	4.52	5.51	NBR1_ARATH	74.29	74.29	Protein NBR1 homolog
BnaA01g15320D	4.28	5.19	unknown	#N/A	#N/A	Unknown
BnaA01g05320D	4.14	4.82	RD19A_ARATH	93.75	93.75	Cysteine proteinase RD19a
BnaA01g26340D	4.03	4.64	MHCKB_DICDI	27.08	27.91	Myosin heavy chain kinase B
BnaA01g14380D	-5.45	-4.64	unknown	-	-	-
BnaA01g11840D	-5.39	-4.64	APR3_ARATH	92.60	92.60	5'-adenylylsulfate reductase 3, chloroplastic
BnaA01g12340D	-5.34	-4.56	SAU36_ARATH	40.51	40.51	Auxin-responsive protein SAUR36
BnaA01g11780D	-5.06	-4.47	unknown	#N/A	#N/A	Unknown
BnaA01g13280D	-4.62	-4.41	CORI3_ARATH	83.48	84.35	Cystine lyase CORI3
BnaA01g10740D	-4.39	-4.35	CASL1_CANSA	43.27	43.28	Cannabidiolic acid synthase-like 1
BnaA01g06540D	-4.33	-4.32	GGP1_ARATH	84.55	84.55	Gamma-glutamyl peptidase 1
BnaA01g05120D	-4.33	-4.30	IGMT4_ARATH	50.96	50.96	Indole glucosinolate O-methyltransferase 4
BnaA01g05540D	-4.31	-4.23	SK2_ARATH	50.96	50.96	Shikimate kinase 2, chloroplastic
BnaA01g05060D	-4.18	-4.18	WRK18_ARATH	73.10	73.10	WRKY transcription factor 18

These genes respond significantly to TuMV infection in both Drakkar and Tanto. The fold-change values (log_2) represent significant differences between transcript levels within infection sites and transcript levels in mock-treated tissue samples (p-value: <0.05). These values are based on three independent infection experiments (biological replicates) for both Drakkar and Tanto. In each experiment, transcripts were detected with at least 150 mean reads. Only genes with strongest fold-changes ($[log_2] \geq +4 / -4$) are shown.

Table S4: Genes that are most strongly and significantly regulated within sites of local TuMV infection in Tanto leaves but not in Drakkar leaves. These genes respond significantly to TuMV infection in Tanto but not in Drakkar. The fold-change values (log_2) represent significant differences between transcript levels within infection sites and transcript levels in mock-treated tissue samples (p-value: <0.05). These values are based on three independent infection experiments (biological replicates) for both Drakkar and Tanto. In each experiment, transcripts were detected with at least 150 mean reads. Only genes with strongest fold-changes ($[log_2] \geq +4 / -4$) are shown.

	Foldchange (log_2)	UniProt	% identity	Annotation
BnaA01g00520D	8.30	C81F1_ARATH	83.63	Cytochrome P450 81F1
BnaA01g05280D	8.28	DTX47_ARATH	61.157	Protein DETOXIFICATION 47, chloroplastic
BnaA01g13360D	7.73	CHX17_ARATH	76.2	Cation/H(+) antiporter 17
BnaA01g15420D	7.40	PFKA3_ARATH	66.667	ATP-dependent 6-phosphofructokinase 3
BnaA01g33750D	6.52	TAO1_ARATH	58.311	Disease resistance protein TAO1
BnaA02g01560D	5.73	GH312_ARATH	87.547	4-substituted benzoates-glutamate ligase GH3.12
BnaA02g04040D	5.58	NC100_ARATH	83.696	NAC domain-containing protein 100
BnaA02g05170D	5.57	ALDO1_ARATH	78.508	Indole-3-acetaldehyde oxidase
BnaA02g05340D	5.52	CKX7_ARATH	89.024	Cytokinin dehydrogenase 7
BnaA02g09030D	5.50	unknown	-	-
BnaA02g10950D	5.38	ADF12_ARATH	94.253	Actin-depolymerizing factor 12
BnaA02g11760D	5.26	NRT31_ARATH	76.22	High-affinity nitrate transporter 3.1
BnaA02g13260D	5.11	YUID_BACSU	35	Uncharacterized membrane protein YuiD
BnaA02g15280D	5.09	DNJB6_XENTR	57.143	DnaJ homolog subfamily B member 6
BnaA02g17240D	5.08	C96AF_ARATH	54.237	Alkane hydroxylase MAH1
BnaA02g19960D	5.00	unknown	-	-
BnaA02g19970D	4.98	unknown	-	-
BnaA02g25150D	4.92	NIMI2_ARATH	76.147	Protein NIM1-INTERACTING 2
BnaA02g25550D	4.91	TDT_ARATH	89.46	Tonoplast dicarboxylate transporter
BnaA02g27620D	4.77	unknown	-	-
BnaA02g29990D	4.69	NSP5_ARATH	85.256	Nitrile-specifier protein 5
BnaA02g30040D	4.68	COL10_ARATH	68.584	Zinc finger protein CONSTANS-LIKE 10
BnaA02g31620D	4.51	PWD_ARATH	93.069	Phosphoglucan, water dikinase, chloroplastic
BnaA02g34380D	4.39	RGF9_ARATH	64.815	Root meristem growth factor 9
BnaA03g00550D	4.38	unknown	-	-
BnaA03g03700D	4.35	unknown	-	-
BnaA03g03710D	4.33	unknown	-	-
BnaA03g03740D	4.31	HS176_ARATH	89.677	17.6 kDa class II heat shock protein
BnaA03g05550D	4.30	FB244_ARATH	65.394	F-box protein At4g22390
BnaA03g12520D	4.23	unknown	-	-
BnaA03g13610D	4.16	PHF5B_ARATH	98.182	PHD finger-like domain-containing protein 5B
BnaA03g18980D	4.12	T5AT_TAXWC	31.735	Taxadien-5-alpha-ol O-acetyltransferase
BnaA03g19850D	4.10	SD16_ARATH	71.392	Receptor-like serine/threonine-protein kinase SD1-6
BnaA03g20310D	4.10	CHI4_BRANA	91.156	Basic endochitinase CHB4
BnaA01g00310D	-5.88	unknown	-	-
BnaA01g00740D	-5.11	YODA_ARATH	38.636	Mitogen-activated protein kinase kinase kinase YODA
BnaA01g10690D	-4.42	CML42_ARATH	81.579	Calcium-binding protein CML42
BnaA01g12860D	-4.25	PR1B1_ARATH	86.047	PRA1 family protein B1
BnaA01g12870D	-4.25	unknown	-	-
BnaA01g15080D	-4.12	AAPC_CENCI	38.415	Putative glucose-6-phosphate 1-epimerase
BnaA01g15130D	-4.04	AB10B_ARATH	65.835	ABC transporter B family member 10

Table S5: Genes that are most strongly and significantly regulated within sites of local TuMV infection in Drakkar leaves but not in Tanto leaves. These genes respond significantly to TuMV infection in Drakkar but not in Tanto. The fold-change values (log_2) represent significant differences between transcript levels within infection sites and transcript levels in mock-treated tissue samples (p-value: <0.05). These values are based on three independent infection experiments (biological replicates) for both Drakkar and Tanto. In each experiment, transcripts were detected with at least 150 mean reads. Only genes with strongest fold-changes ($[log_2] \geq +4 / -4$) are shown.

	Foldchange (log_2)	**UniProt**	**% identity**	**Annotation**
BnaA01g01570D	7.17	TLP1_PRUPE	54.24	Thaumatin-like protein 1
BnaA01g01780D	6.85	DIN1_RAPSA	54.24	Senescence-associated protein DIN1
BnaA01g05610D	6.48	COPA2_ARATH	92.27	Coatomer subunit alpha-2
BnaA01g21570D	5.64	PATL1_DANRE	26.57	Protein PAT1 homolog 1
BnaA01g30530D	5.50	AGL97_ARATH	29.37	Agamous-like MADS-box protein AGL97
BnaA01g33090D	5.33	NAC60_ARATH	73.02	NAC domain-containing protein 60
BnaA01g33110D	5.30	NAC60_ARATH	70.15	NAC domain-containing protein 60
BnaA01g33140D	5.21	RPK2_ARATH	88.27	LRR receptor-like serine/threonine-protein kinase RPK2
BnaA01g35500D	4.84	GRXS4_ARATH	98.04	Monothiol glutaredoxin-S4
BnaA01g36060D	4.74	VIP5_ARATH	86.68	Protein RTF1 homolog
BnaA01g37020D	4.72	TPR2_ARATH	82.12	Topless-related protein 2
BnaA02g04780D	4.65	RFS6_ARATH	82.95	Probable galactinol--sucrose galactosyltransferase 6
BnaA02g06780D	4.61	ZAT12_ARATH	86.25	Zinc finger protein ZAT12
BnaA02g08420D	4.45	CKX3_ARATH	65.84	Cytokinin dehydrogenase 3
BnaA02g09670D	4.41	unknown	-	-
BnaA02g10970D	4.31	LTI65_ARATH	47.77	Low-temperature-induced 65 kDa protein
BnaA02g25380D	4.16	MY1R1_SOLTU	75.95	Transcription factor MYB1R1
BnaA02g29540D	4.08	AIG2_ARATH	55.29	Protein AIG2
BnaA01g02570D	-6.09	BZP53_ARATH	50	bZIP transcription factor 53
BnaA01g03580D	-5.89	DRL29_ARATH	85.17	Probable disease resistance protein At4g33300
BnaA01g04010D	-5.66	U587_DROPS	28.91	UPF0587 protein GA18326
BnaA01g08750D	-4.89	MYC4_ARATH	72.4	Transcription factor MYC4
BnaA01g09070D	-4.88	E1314_ARATH	50.58	Glucan endo-1,3-beta-glucosidase 14
BnaA01g09200D	-4.81	unknown	-	-
BnaA01g10260D	-4.72	P2A02_ARATH	62.44	Protein PHLOEM PROTEIN 2-LIKE A2
BnaA01g13950D	-4.28	PUMP4_ARATH	87.15	Mitochondrial uncoupling protein 4
BnaA01g14340D	-4.21	TPD1_ARATH	85.09	Protein TAPETUM DETERMINANT 1
BnaA01g16090D	-4.14	FAD4_ARATH	77.61	Fatty acid desaturase 4, chloroplastic }
BnaA01g16380D	-4.06	DYL2_RAT	50	Dynein light chain 2, cytoplasmic
BnaA01g18170D	-4.01	ERF39_ARATH	81.97	Ethylene-responsive transcription factor ERF039
BnaA01g18680D	-4.01	BBX32_ARATH	55.36	B-box zinc finger protein 32

Table S6: Genes that are more strongly and significantly regulated within sites of local TuMV infection in Tanto leaves than in Drakkar leaves. These genes respond to TuMV infection more strongly in Tanto than in Drakkar. The fold-change values (log_2) represent significant differences between transcript levels within infection sites and transcript levels in mock-treated tissue samples (p-value: <0.05). These values are based on three independent infection experiments (biological replicates) for both Drakkar and Tanto. In each experiment, transcripts were detected with at least 150 mean reads. The table is based on genes with strongest fold-changes in Tanto ($[log_2] \geq +4 / -3,8$).

	Foldchange (log_2)			**% identity**		
	Drakkar	**Tanto**	**UniProt**	**Drakkar**	**Tanto**	**Annotations**
BnaA01g02270D	0.36	8.29	NFD4_ARATH	46.88	46.88	Protein NUCLEAR FUSION DEFECTIVE 4
BnaA01g05410D	0.76	8.04	GRP10_BRANA	95.92	95.92	Glycine-rich RNA-binding protein 10
BnaA01g08170D	1.13	7.98	YUC8_ARATH	92.2	92.20	Probable indole-3-pyruvate monooxygenase YUCCA8
BnaA01g08550D	-1.05	7.89	unknown	-	-	-
BnaA01g10250D	0.94	7.79	PATL6_ARATH	87.03	87.03	Patellin-6
BnaA01g13210D	-1.28	7.78	unknown	-	-	-
BnaA01g13700D	1.31	7.52	VEP1_ARATH	85.98	85.98	3-oxo-Delta(4,5)-steroid 5-beta-reductase
BnaA01g19210D	0.87	7.34	CIPK4_ARATH	78.66	78.90	CBL-interacting serine/threonine-protein kinase 4
BnaA01g20660D	0.78	7.32	PER34_ARATH	82.57	84.23	Peroxidase 34
BnaA01g27800D	0.52	7.28	DPYD_ARATH	73.23	73.23	Dihydropyrimidine dehydrogenase (NADP(+)), chloroplastic
BnaA01g27930D	1.08	7.15	CHX19_ARATH	65.52	71.68	Cation/H(+) antiporter 19
BnaA01g28680D	1.02	7.14	unknown	-	-	-
BnaA01g30490D	0.91	7.08	MD37C_ARATH	96.92	96.92	Probable mediator of RNA polymerase II transcription subunit 37c
BnaA01g31030D	0.90	7.05	RLP12_ARATH	42.26	42.15	Receptor-like protein 12
BnaA01g31190D	0.33	7.04	RLP12_ARATH	41.02	39.82	Receptor-like protein 12
BnaA01g31210D	0.90	6.91	RLP12_ARATH	40.09	40.20	Receptor-like protein 12
BnaA01g02860D	-0.39	-5.09	FUCO2_ARATH	85.42	86.11	Alpha-L-fucosidase 2
BnaA01g02460D	-0.43	-5.09	SPE2_ARATH	85.4	85.71	Arginine decarboxylase 2
BnaA01g03200D	-1.07	-4.77	RNHX1_ARATH	56.63	56.63	Putative ribonuclease H protein At1g65750
BnaA01g04750D	-0.77	-4.65	unknown	-	-	-
BnaA01g07460D	-0.80	-4.44	unknown	-	-	-
BnaA01g14730D	0.51	-4.12	TBL18_ARATH	83.63	83.63	Protein trichome birefringence-like 18
BnaA01g15810D	-0.68	-4.01	GPDL3_ARATH	84.95	59.06	Glycerophosphodiester phosphodiesterase GDPDL3
BnaA01g17700D	-0.95	-3.96	GAT17_ARATH	56.91	56.91	GATA transcription factor 17
BnaA01g19120D	-0.79	-3.91	APS3_ARATH	70.54	70.12	ATP-sulfurylase 3, chloroplastic

Table S7: Genes that are more strongly and significantly regulated within sites of local TuMV infection in Drakkar leaves than in Tanto leaves. These genes respond to TuMV infection more strongly in Drakkar than in Tanto. The fold-change values (log_2) represent significant differences between transcript levels within infection sites and transcript levels in mock-treated tissue samples (p-value: <0.05). These values are based on three independent infection experiments (biological replicates) for both Drakkar and Tanto. In each experiment, transcripts were detected with at least 150 mean reads. The table is based on genes with strongest fold-changes in Tanto ($[log_2] \geq +4 / -4$).

	Foldchange (log_2)			**% identity**		
	Drakkar	**Tanto**	**UniProt**	**Drakkar**	**Tanto**	**Annotation DT**
BnaA01g01000D	8.69	0.90	unknown	-	-	-
BnaA01g01300D	7.37	-0.41	UBC17_ARATH	94.59	91.89	Probable ubiquitin-conjugating enzyme E2 17
BnaA01g01690D	6.86	1.06	NIP1_ARATH	67.89	67.89	NEP1-interacting protein 1
BnaA01g10420D	6.22	1.38	VSR7_ARATH	92.67	92.67	Vacuolar-sorting receptor 7
BnaA01g13080D	6.20	1.08	unknown	-	-	-
BnaA01g13540D	6.01	0.52	UGE2_ARATH	67.11	67.11	UDP-glucose 4-epimerase 2
BnaA01g14240D	5.93	1.19	PPA24_ARATH	76.57	76.57	Probable inactive purple acid phosphatase 24
BnaA01g16400D	5.81	-0.60	NAC72_ARATH	72.7	72.70	NAC domain-containing protein 72
BnaA01g16910D	5.71	-0.54	ERF54_ARATH	69.77	69.44	Ethylene-responsive transcription factor ERF054
BnaA01g22310D	5.62	1.49	NRX1_ARATH	86.1	86.10	Probable nucleoredoxin 1
BnaA01g32540D	5.40	0.79	unknown	-	-	-
BnaA01g00140D	-7.25	-1.24	CADH7_ARATH	84.04	84.04	Cinnamyl alcohol dehydrogenase 7
BnaA01g01220D	-6.63	-1.01	unknown	-	-	-
BnaA01g02550D	-6.24	-0.86	unknown	-	-	-
BnaA01g02780D	-5.94	-1.48	ISPH_ARATH	50.63	50.63	4-hydroxy-3-methylbut-2-enyl diphosphate reductase, chloroplastic
BnaA01g03830D	-5.88	1.24	GRXC6_ARATH	91.67	91.67	Glutaredoxin-C6
BnaA01g04070D	-5.55	-0.89	LFS_ALLCE	36.15	36.15	Lachrymatory-factor synthase
BnaA01g05720D	-5.22	-0.80	PNSL4_ARATH	85.71	85.71	Photosynthetic NDH subunit of lumenal location 4, chloroplastic
BnaA01g06190D	-5.07	-1.25	FAD6C_BRANA	68.84	68.84	Omega-6 fatty acid desaturase, chloroplastic
BnaA01g06600D	-5.05	-0.72	unknown	-	-	-
BnaA01g08240D	-5.01	-0.91	TYDC2_ARATH	61.69	61.69	Probable tyrosine decarboxylase 2
BnaA01g08260D	-4.93	-1.39	PSB28_ARATH	88.75	85.71	Photosystem II reaction center PSB28 protein, chloroplastic
BnaA01g08510D	-4.90	0.81	CNBL1_ARATH	79.59	79.59	Calcineurin B-like protein 1
BnaA01g09270D	-4.74	-0.84	CHLI1_ARATH	96.57	96.57	Magnesium-chelatase subunit ChlI-1, chloroplastic
BnaA01g09550D	-4.74	-0.71	unknown	-	-	-
BnaA01g10480D	-4.65	-0.64	C71AF_ARATH	67.57	67.57	Cytochrome P450 71A15
BnaA01g10670D	-4.63	-0.97	YCP9_SCHPO	32.56	32.56	Uncharacterized oxidoreductase C663.09c

Table S8: Known and newly identified *B. napus* miRNAs.

Known miRNAs (miRbase) & size (nt)											
TTGGATTTATAGTTGGATAAG	athmiR56323p	21	AGAAGCAAAATGACGACTCGG	athmiR3933	21	ACTGGACGACTTACACGGAAG	bolmiR9411	21	TGAACCAGATAGAGTGGGACT	bnamiR6033	21
TTATGTCTTGTTGATCTCAAT	athmiR8635p	21	CGAACCATCACCTTCCAAACC	alymiR34455p	21	TTGTGTTGCGTTTCTGTTGATT	athmiR8182	22	TCCAATAGGTCGAGCATGTGC	athmiR8625p	21
TTCGATGTCTAGCAGTGCCA	athmiR775	20	GGCAGTCTCTTTGGCTATC	alymiR169n3p	19	TCATCGTAAGAGATCTGCATT	bramiR95683p	21	CAGGGAACAAGCAGAGCATGG	alymiR4085p	21
TTTGTTATTTTCGCATGCTCC	athmiR4239	21	GGCAGTCTCCTTGGCTATC	alymiR169k3p	19	GCTCACTGCTCTATCTGTCAGA	bramiR156g3p	22	TAAAAGTTAAGAGACAAGTTA	bramiR9563a3p	21
ACAGTGGTCATCTGGTGGGCT	athmiR5638b	21	TGACAGAAGAGAGAGAGCAG	athmiR156i	20	TGGAGAAGCAGGGCACGTGCAA	bramiR164e5p	22	TCATGGTCAGATCCGTCATCC	athmiR842	21
GATCTTTTGAGAGGGTTCCAG	athmiR2938	21	CCTTCTCATCGATGGTCTAGA	athmiR8243p	21	TTAGATGACCATCAACAAACT	athmiR827	21	AGCAAAAGCTAAGGAAAAGGAA	athmiR855	22
TGAAATTATAGATTTCGTACA	alymiR4243	21	TGACTAGACCCGTAACATTAC	athmiR4240	21	TCTTGCTTAAATGAGTATTCCA	athmiR828	22	CCCGCCTTGTATCAAGTGAAT	bramiR168a3p	21
TTGAAGAGGACTTGGAACTTCGAT	athmiR163	24	AGGTGGGCATACTGCCAATAG	athmiR394b3p	21	ATGTGCTGATTCGAGGTGGGA	athmiR8173	21	CTTTGGGATTTTCTTACAGCGA	alymiR4241	22
GGACTGTTGTCTGGCTCGAGG	athmiR166b5p	21	GAAACAACATACGTTACATCC	alymiR8223p	21	TGTTAAGGAGTGTTAACGGTG	athmiR5635c	21	TCATCTTCATCATCATCGTCA	athmiR414	21
ACTGTATATATGTAAGTGACA	athmiR5025	21	GCGTACAGAGTAGTCAAGCATG	alymiR160b3p	22	TACCCATATCTCCATCTCCAA	alymiR774a3p	21	TGAGCCAAGGATGACTTGCCG	athmiR169e	21
TAAGATCCGGACTACAACAAAG	athmiR850	22	GCGTACAGAGTAGTCAAGCATA	BnamiR160a*	22	GAGAGACTCTGAAAGACTCACC	bramiR95613p	22	CATTCAAGGACTTCTATTCAG	athmiR8465p	21
TGGCTTGGTTTATGTACACCG	athmiR778	21	TACGAGCCACTTGAAACTGAA	athmiR841a5p	21	AGGGACTTTGTGAATTTAGGG	athmiR5634	21	CGGCTCTGATACCAATTGATG	athmiR845a	21
GGCAGTCTCCTTGGATATC	alymiR169i3p	19	GGCAGTCTCCTTGGCTATT	alymiR169h3p	19	TGACAGAAGATAGAGAGCAC	athmiR157d	20	ACTGAAAACACTACAACCCCT	alymiR4235	21
TGAAACCAAGTAGCTAAATAG	athmiR5997	21	TTCGCAGGAGAGATAGCGCCA	bramiR3915p	21	TGTTTGTTGTACTCGGTCTAGT	athmiR833a5p	22	AAAAAACAAGGATCCACGGAT	alymiR34375p	21
GGCAATCCCATGTCAAA	alymiR8485p	17	GGCAAGTCATCTCTGGCTATG	alymiR169c3p	21	GTTCCCTTAAACGCTTTATTG	alymiR395f5p	21	TTGGTGGACAAGATCTGGGAT	athmiR5665	21
TAGACCATTTGTGAGAAGGGA	bnamiR824	21	AAACTTTCACCATACAAAATA	alymiR8575p	21	TTGGTGTTATGTGTAGTCTTC	athmiR5015	21	GATCCCCGGCAACGGCGCCA	athmiR8175	20
TGTTTTGTGGGTTTCTACCGA	bramiR5711	21	CATCCAAGGTGTTTGTAGAAA	athmiR29343p	21	TTTTTCCTCAAATTTATCCAA	athmiR8653p	21	AATCTCATCAATCTCCCAATA	alymiR3444a3p	21
GGGAGCCAGGGAAGAGGCAGT	bramiR4085p	21	AACAGAGCAGAAACAGAACAT	athmiR415	21	TTGTACAAATTTAAGTGTACG	athmiR5014a3p	21	ATATAGTCCAATCTATTGAAG	alymiR8605p	21
TTCGCTTGGTGCAGGTCGGGA	BnamiR168b	21	TTATTTGTTACCCATATCTCC	alymiR774a3p	21	GAGCTTTCTTCGGTCCACTC	BnamiR319a	20	AGGGTTGATATGAGAACACAC	athmiR398c5p	21
TGCCAAAGGAGATTTGTCCGG	bnamiR399c	21	TTTCCCGTAAAGCTTAGAACC	bramiR9555a3p	21	CACGTGCTCCACTCCTCCAAC	bramiR164ap3	21	TGTTCTGGTTTGATTTTGAAC	bramiR5718p5	21
AACTTTGTGATGACAACGAAG	athmiR3932b3p	21	TGGGTGGTGATCATATAAGAT	athmiR823	21	CGGTGGATCTTGTTTTTTGT	alymiR34373p	20	TGGCATAATTCTGTCAATTCC	alymiR34355p	21
AGATGTGGAGATCGTGGGGATG	athmiR8167a	22	GGGCATCTTTCTATTGGCAGG	athmiR399c5p	21	TGATTCTCTGTGTAAGCGAAA	athmiR1733p	21	TTGGGGACGAGATGTTTTGTTG	athmiR447b	22
AGAGCTTTCTTCGGTCCACTC	alymiR319b5p	21	TCTGCTGGTCGTTCCATGTTAA	bramiR60323p	22	TGAAGAAGATACGCAAGAAAG	alymiR8353p	21	AAGAACTCGTCTCTTAACTTTTAA	bramiR9563b5p	24
CCCTCAATGATGTTTTGAAGC	alymiR34413p	21	ATGGGACATCGAGCATTTAAT	athmiR5666	21	CGCAAATGCGGATATCAATGT	athmiR21125p	21	GCTTACTCTCTCTCTGTCACC	bramiR156a3p	21
TTCAGAGTCTAAACATGGTGT	alymiR34423p	21	GAAATCGGAGAGGAAATTCGCC	athmiR2933a	22	CCTGGGTTTGAGATAATTGAC	alymiR8693p	21	GTGGCATCATCAAGATTCACA	alymiR172a5p	21
AACCGCCGGTTTGATAATAGC	bramiR5724	21	TTGACAGAAGATAGAGAGCAC	bnamiR156g	21	AAATCCAATTTTCATTGCTTAA	alymiR4246	22	TGGCAGGAAAGACATAATTTT	athmiR5631	21
GCAGCATCATTAAGATTCACA	bramiR172d5p	21	CATTGTTTCTTGTTTTTTTCA	alymiR8375p	21	GGAATGTTGTCTGGATCGAGG	athmiR165a5p	21	GAGCTCCTTGAAGTTCAATGG	athmiR159b5p	21
CACGTACTCCCCTTCTCCAAC	alymiR164a3p	21	TCGCTCTGATACCAAATTGATG	athmiR845b	22	TCTCGCGCTTGTACGGCTTT	athmiR5642b	20	CTATCGGTCTACTTGGTCAGC	bramiR9552b5p	21
TTGTTTAGGTCCCTTAGTTTCT	alymiR8403p	22	GCGTACAAGGAGCCAAGCATG	alymiR160c3p	21	TTAGAGTTTTCTGGATACTTA	athmiR781a	21	TGCTCACTGCTCTTTCTGTCAGA	bramiR156f3p	23
ATCTGAAGAAAATAGCGGCAT	athmiR56483p	21	ATTAACGCTGGCGGTTGCGGCAGC	athmiR404	24	ATTGAATATGTTGGTTACTAT	athmiR5649a	21	CTGCTATCCTTTTCCTGTTGCA	alymiR8535p	22
CACTTATCTCAACCCTAGTGA	alymiR8695p	21	TTGTTTTGGATCTTAGATACA	athmiR5650	21	GGGTTGATATGAGGACACATG	alymiR398b5p	21	TTGGGGTTTCGAAATCAAGAG	alymiR34395p	21
CACGTGCTCCCCTCCTCCAAC	bramiR164e3p	21	GACTTATAATGATCTCATGAA	bramiR4003p	21	TTTTCTTCTACTTCTTGCACA	athmiR838	21	ACCGGTTGGAACTTGCCTTAA	athmiR5027	21
TTGCTTAAAGATTTTCTATGT	athmiR81703p	21	TAGCCAAGGATGACTTGCCTG	athmiR169h	21	TCAATAGATTGGACTATGTAT	athmiR860	21	TGAGCCTCTGTGGCAGCCCTC	alymiR7715p	21
CATCCATATTTTCATCTCGAA	athmiR774b3p	21	CGTACAAGGAGTCAAGCATGA	athmiR160c3p	21	TAATTCCACCAATAACTTCAGC	alymiR8565p	22	AAGTAGACACATAAGAAGGAG	athmiR5655	21
GGAGATTCTTTCAGTCCAGTC	alymiR319c5p	21	TTTTCTTCTTCTTCTTGCACA	alymiR8383p	21	CGTGACGAACATAATCAAACG	alymiR34475p	21	TTGTGATTTGGTTGGAATATC	bramiR5720	21
TCAATAGATTGGACTATATAT	alymiR8603p	21	CCTTGGAGAAATATGCGTCAA	athmiR8615p	21	GCTCTCTATACTTCTGTCACC	athmiR157c3p	21	CAAATTAAAGCTTCAAGGTAG	athmiR8293p	21
AATGTGCTGCAATATCTCTGC	bramiR5723	21	CTGAAGCTAGTGAAAGAGAGA	bramiR95653p	21	GCAGCACCATCAAGATTCACA	alymiR172b5p	21	TTTGAGTGTGTTTGTTATGAA	alymiR34473p	21
GATGGATATATCTTCAAGAAC	alymiR8613p	21	ACTTTGAAGCTTTGATTTGAA	athmiR8295p	21	ACCATGTTTAGACTCTGAATT	alymiR34425p	21	CAACAACGATTTTTGGGTCGTT	alymiR34363p	22
TCGCTTGGTGCAGGTCGAGAA	bnamiR168b	21	TTTGCTTCCAGCTTTTGTCTC	athmiR773a	21	TTGGATAATTGAAGATATAAA	bramiR5716	21	CACCAACCTCTCATCGTTCCC	alymiR8395p	21
AGAATCTTGATGATGCTGCAG	bnamiR172d	21	AAATTAAGAGATGAATTCTTAC	bramiR9563b3p	22	AGGCTTAGAAGAACGTTTGTT	bramiR5713	21	TGATTTTACAATAGATAGATA	alymiR8593p	21
TATGATCATCAGAAAACAGTG	athmiR5633	21	AGAAGCGTACAAGGAGATGAGG	athmiR8315p	22	TGGAGGCAGCGGTTCATCGATC	athmiR162a5p	22	GGGCGAATCCTCTATTGGCAGG	alymiR399e5p	22
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AGATAGAAAGCAATCTGGATA	alymiR34493p	21	TTTCCAAATGTAGACAAAGCA	bramiR1583p	21	GGAGGCAGCGGTTCATCGATC	bramiR1625p	21	TTGGACTGAAGGGAGCTCCTT	athmiR319c	21
CCGTATCTTGGCCTTGTCATT	athmiR50243p	21	TTAGATGACCATCAACAAACG	alymiR8273p	21	TTAGGGTAGTTAACGGAAGTTA	athmiR5629	22	TGGAGAAGCAGGGCACGTGCA	bnamiR164a	21
AAACTATATGTGTTGCTTAGA	bramiR95673p	21	ATCATGCTATCTCTTTGGATT	athmiR393a3p	21	AACATGGAGCATCAACAGATC	bramiR60325p	21	GCTCACTCTCTTTCTGTCATA	alymiR156d3p	21

Known miRNAs (miRbase) & size (nt)												
TGGAGAAGCAGGGCACGTGCG	bnamiR164d	21	ATAGTACTAGTACTTGCATGATCA	bnamiR6036	24	TTGTGATGATAATACGACTTC	bramiR5719	21	ATCATGCGATCTCTTTGGATT	athmiR393b3p	21
TCCGTTATTTCCGCATGCTCC	alymiR4239	21	GTTCGAGGCACGTTGGGAGG	athmiR5646	20	ATACCAAAACTCTCTCACTTT	athmiR5638a	21	ATTTGAGTCATGTCGTTAAG	athmiR5645a	20
CTTCTTAAGTGCTGATAATGC	athmiR8683p	21	TCAAAATCAGAGAATCAACCA	alymiR34343p	21	GGAATGTTGTCTGGCACGAGG	athmiR166e5p	21	AGAAGGACTAGTAAGATGGCT	alymiR8445p	21
GTTTGGAGAAATATGCATCAT	alymiR8615p	21	TCATTGAGTGCATCGTTGATG	athmiR397b	21	TGGTTTCCCTGGCCAATCCACT	alymiR34405p	22	ATGAATTTGGATCTAATTGAG	athmiR8655p	21
TGCCTGGCTCCCTGTATGCCA	bnamiR160c	21	TAGAATGCTATTGTAATCCAG	athmiR406	21	CCATCTTACTAGTCTTTCTTT	alymiR8443p	21	AAACGAACAAGAAACTGATGA	alymiR8373p	21
AACGACTTCATCTTCTTTGCT	alymiR34413p	21	TAATTTGGTGTTTCTTCGATC	athmiR8703p	21	TTTGGAAATATTTGGCTTGACT	athmiR56485p	22	TCACAGTTCTTGATTACCCAC	alymiR34333p	21
CCCCTTACAATGTCGAGTAAA	athmiR447c5p	21	AATGGAGGCAAGTGTGAAGGA	athmiR8165	21	TTTAAATCATATACTTTTGGT	athmiR407	21	GCTGATTCTCTGATTTTGAAC	alymiR34345p	21
TTTGGTCTGATTACGAATGTA	athmiR8184	21	TTCTTCGTGAATATCTGGCAT	athmiR780	21	TAAACTCCTCGTACTCTTCTTG	alymiR8313p	22	GACTTATAATAATCTCATGAA	alymiR4003p	21
GGGCGCCTCTCCATTGGCAGG	alymiR399b5p	21	GGGCAAATACTCCATTGGCAGA	alymiR399i5p	22	TCTCTCCGTTGTAAAATCAAA	alymiR8595p	21	AGATGCTCATTTGAGCAAGCAA	alymiR8283p	22
TGGAGTAGAAAATGCAGTCGT	bnamiR6035	21	AACCTATTTAACGACATGACT	athmiR5645c	21	CTTGATAGTGAGAAAGACCCA	alymiR34453p	21	TTTTGGAAATTTGTCCTTACG	athmiR426	21
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TTTTACTGCTACTTGTGTTCC	athmiR5012	21	TCTAGATTGCTTTCGGTCTGT	alymiR34495p	21	ACAAACACCTTGGATGTTCTT	athmiR782	21	GAATGATACTTGGATATAATC	bramiR95545p	21
TGGGTTGAGTTGAGTTGAGTTGGC	athmiR5653	24	TCTTGATGAAGAGGAATGGAA	alymiR8475p	21	TAATCTGCATCCTGGGGTTTA	bnamiR2111c	21	TTTTCCTCTGTTGAATTCTTGC	athmiR4221	22
ACTCATAAGATCGTGACACGT	athmiR5026	21	CAACTGAGCTTCCTCATCTCT	alymiR4224	21	GGCAAGTTGTCCTTCGGCTACA	athmiR169b3p	22	GGCAATAACTTGAGCAAACA	athmiR773b5p	20
CATTAATTTGTTCCCCTCCTA	alymiR4236	21	CGGCTCTGATACCAGTTGATG	alymiR845a3p	21	ATAGTTTCTCTTGTTCTGCAC	athmiR413	21	AGCTCTGATACCAAATGATGGAAT	athmiR8293p	24
TCTAGCAGCTGTTGAGCAGGT	athmiR780	21	TTTTGCGTTTCAACTCGGTCC	bramiR95575p	21	GGAATGTTGTTTGGCTCGAAG	BnamiR166a*	21	GCAAGTTGACTTTGGCTCTGT	BnamiR169n	21
TCTTTCTGCAAACGCCTTGGA	athmiR29345p	21	TGACAGAAGAAAGAGAGCAC	athmiR156h	20	CAGCCAAGGATGACTTGCCGG	bnamiR169n	21	TGTTGGGAAAGAAAAACTCTT	athmiR5019	21
TACTTAATTATAAGTCGTCTGG	bolmiR9410	22	TCATATCCAAGTATCATTCCT	bramiR95543p	21	TTTGTGACATCTAGGTGCTTT	athmiR5013	21	TTTGTTGATTGACATCTATAC	alymiR8275p	21
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GCTTACTCTCTTCTTGTCTCC	alymiR156g3p	21	AATAAAGCTGTGGGAAGATAC	BnamiR396	21	GACTTTAGCAACAACGATTTC	alymiR1635p	21	ACAATGAACGAAATCCAAATC	bramiR95593p	21
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TGAGATGAAATCTTTGATTGG	athmiR1886	21	TAACTATTTTGAGAAGAAGTG	athmiR8303p	21	CAACCGGAAAGGGGAGCAGCA	alymiR8533p	21	AATGCGCAACTCTATATTTCC	athmiR5637	21
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TGTTTTGTGCTTGAATCTAATT	athmiR4035p	22	ACAAAACGATTACACAGCTCGGTC	bramiR95645p	24	TTCTAATCCCGCCATGCACCG	alymiR34435p	21	ATGTAGTCCAATCTATTGAAG	bramiR8605p	21
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TGCTCACCTCTCTTTCTGTCAGT	bramiR156e3p	23	GGAATCTTGATGATGCTGCAT	bnamiR172b	21	GGCAAGTTGTCCTTGGCTACA	alymiR169a3p	21	TTCGAGGCCTATTAAACCTCTG	athmiR402	22
ACTTGGCTGATTCTATTATT	athmiR34345p	20	TGGTAAGATTGCTTATAAGCT	athmiR8445p	21	ACAGTTTGTGTTTTGTTTTGT	athmiR5998a	21	TTGAATTGAAGTGCTTGAATT	athmiR8463p	21
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GCAACATCTTCAAGATTCAGA	athmiR172d5p	21	ATCATGCGATCTCTTCGGATT	BnamiR393*	21	TGACCAAGTAGACCGATAGTC	bramiR9552a3p	21	ATAGGTGGGCCAGTGGTAGGA	athmiR8171	21
GGAGCATCATCAAGATTCACA	alymiR172c5p	21	GTCAATTGGTGATAGTAGTTC	bramiR95565p	21	GGGCAAGATCTCTATTGGCAGG	alymiR399h5p	22	GGTCATTTGAGAACTGTGATG	alymiR34335p	21
TGAATTTGAGAAGTTGAGGTA	alymiR4249	21	TTAGATTCACGCACAAACTCG	bnamiR403	21	CTGAAGTGTTTGGGGGAACTC	bnamiR395b	21	TTGTGCGGTTCAAATAGTAAC	athmiR5651	21
CTTTCTCGGCACTTGAGGATGT	alymiR8685p	22	TTTTGTTCATGACTGCATTTTC	bolmiR9409	22	ACACTAAAGGACCTAAACTAAC	alymiR8405p	22	TACAAGATGCATTCGAGCAATA	alymiR4226	22
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GGTCTTTCTCCCTATCAAGCG	alymiR34455p	21	CACATCATCAACATCAACTCC	alymiR4233	21	TGCGGGAAGCATTTGCACATG	athmiR8225p	21	TCTTCACTATTAGACGGACAA	athmiR5999	21
TCAGCGTTGCATTCAATTATG	alymiR397b3p	21	TGACAGAAGAGAGAGAGCAC	athmiR156j	20	TTTTGTATGTTGAAGGTGTAT	athmiR857	21	AAGCTCAGGAGGGATAGCGCC	bnamiR390c	21
TCCCCTCTTTAGCTTGGAGAAG	athmiR853	22	CTGAAGTGTTTGGAGGAACTC	alymiR395i	21	GCTGAGTTGGAACGCAAAATC	bramiR95573p	21	ATAGACAGAGTCACTCACAGA	athmiR8169	21
TGAAGCTGCCAGCATGATCT	bnamiR167d	20	TCTGATTTTCGAAGTCCCAAAA	alymiR34393p	22	GGCAAGTTGTCCTTGGCTAC	athmiR169a3p	20	AGGTGCTGAGTGTGCTAGTGC	athmiR8168	21

Known miRNAs (miRbase) & size (nt)												
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ACAGCCTAAACCAATCGGAGC	bnamiR1140	21	TGATTGAGCCGCGCCAATATCT	bnamiR171g	22	AGAGCTTCCTTGAGTCCATTC	bramiR3195p	21	TACGAGCCACTGGAAACTGAA	athmiR841b5p	21
GGGCGAATACTCCTATGGCAGA	alymiR399d5p	22	ATGAGTTGGGTCTAACCCATAACT	athmiR405b	24	CGATGAAGGTCTTTGGAACGGTA	athmiR5659	23	TGGATTGGTCAAGAGAACCGCA	alymiR34403p	22
TGTGGGTGGCAAACAAAGACGACA	alymiR8513p	24	TGATTGAGCCGCGCCAATATC	bnamiR171f	21	AAGATAAGCGCCTTAGTTCTG	athmiR852	21	ACATGCTGGATCTACTTGAAG	alymiR8623p	21
TCAATGCATTGAAAGTGACTA	athmiR161	21	ATATGCTGGATCTACTTGAAG	athmiR8623p	21	ACTTTGAATCTTTGATTTGAA	alymiR8295p	21	TGACAGAAGAGAGTGAGCACA	bnamiR156a	21
GGGCTCCTTATAGTTCAAACG	BnamiR159*	21	ACATTTTATTTTTGGCAATCA	alymiR4248b	21	AGATATGGGTGACTAATACTT	alymiR774a5p	21	TGAGAGAAGTGAGATGAAATC	athmiR1886	21
ATCCTCGGGATACGGATTACC	bramiR2111b3p	21	ATAAGAGCTGTTGAAGGAGTC	athmiR2937	21	TGAGTCTCTCACCAGTCTTTCAC	bramiR95615p	23	TGAGATGAAGATTTGGATGAC	alymiR774b5p	21
GCAAGTTGACCTTGGCTCTGC	athmiR169f3p	21	ACAGGTGGTGGAACAAATATGAGT	bramiR9560b5p	24	GGGCAAGATCACCATTGGCAGA	alymiR399f5p	22	TCCACCCATACCATACAGACCC	bnamiR6030	22
GAATGTTGTTTGGATCGAGG	alymiR165b5p	20	TGGGTGGCAAACAAAGACGAC	athmiR8513p	21	AAAGTATAATGGTTTAGTGGTTTG	athmiR8121	24	GTTCTCCCGAACACTTCATTG	alymiR395d5p	21
TAACTAAACATTGGTGTAGTA	athmiR849	21	ACCCGTCTCTTAATTTTTAAC	bramiR9563a5p	21	GTGTGATGATGTGTCATTTATA	athmiR8177	22	TACATCTTCTCCGCGGAAGCTC	bramiR1885b	22
GCAAGTTGACCTTGGCTCTGT	alymiR169e3p	21	AGGCTTTTAAGATCTGGTTGC	athmiR5643b	21	TCATATTAGTTCTACCTCCTGTTG	bramiR9560a3p	24	CGAGCAAAAATCATTGTTGAT	alymiR34365p	21
TGACATCCAGATAGAAGCTTTG	athmiR5996	22	TAGACCTTTGTGTTGCCATCG	alymiR4231	21	CCCGTCTTGTATCAACTGAAT	athmiR168b3p	21	TCACTCCTCTTCTTCATGATG	alymiR8473p	21
TGATTGGAAATTTCGTTGACT	athmiR779	21	TCGATTGGTGTCAGAGCCACG	alymiR845a5p	21	TTAGAAACTTGCAATTATATA	bramiR9555b3p	21	GCTCTCTAGCCTTCTGTCATCA	alymiR157a3p	22
TTAGGCTAAGATTTGTGAAGA	athmiR1888b	21	TCAAGCACCAGCTCGAAGAAGC	alymiR8255p	22	TTTGGATTGAAGGGAGCTCCT	athmiR159c	21	TTTGGATTGAAGGGAGCTCTT	athmiR159b3p	21
TGACCGAGTAGACCGATAGTC	bramiR9552b3p	21	TAATCCTACCAATAACTTCAGC	athmiR856	22	TTCTTGTGGATTCCTTGGAAA	athmiR5016	21	TCACTCCTCTTCTTCTTGATG	athmiR847	21
TGAGATGAAGATATGGGTGAT	athmiR774b5p	21	TCTTCTCCAAATAGTTTAGGTT	athmiR8305p	22	TCTGAGGATTTTTTTTGTGGTC	alymiR34483p	22	ATGGCATGAAAGAAGGTGAGA	athmiR5020b	21
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TGCTGGGATCGGGAATCGAAA	athmiR8325p	21	TGGAGCATCAACAGATCTCGG	bnamiR6032	21	ATTTCTAGTGGGTCGTATTCA	athmiR841a3p	21	GCAGCACCATTAAGATTCAC	athmiR172b5p	20
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TGAAGAGGACTTGGAACTCGATC	alymiR1633p	23	TTGGCATTCTGTCCACCTCC	bnamiR394a	20	TCAAGGATTAAGCTATGAAGC	alymiR34385p	21	TCCGATTGGCTTTAGGCTGTTG	bramiR1140p5	22
GCAAGTCGACTTTGGCTCTG	BnamiR161*	20	TGCCAAAGGAGATTTGCCTCG	athmiR399e	21	TACCAACCTTTCATCGTTCCC	athmiR8395p	21	ATTGGTAGTGGATAAGGGGGC	athmiR5023	21
TGCAAGAATGAGAAGCAAAGC	alymiR8385p	21	AATGAGAGAGAACACTGCAAA	athmiR5029	21	GGTCATGCTCTGACAGCCTCACT	alymiR167b3p	23	CGCTATCCATCCTGAGTTCC	athmiR390b3p	20
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CATGTGCCCATCTTCACCATC	athmiR164b3p	21	CATCAATGAAAGGTATGATTCC	bramiR1885a	22	AATTGGGTTTATGCTAGAGTT	athmiR5028	21	ATGGTCGAAGTAGGCAAAATC	athmiR4725p	21
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GAAATAGCGAAGATATGATTA	athmiR5628	21	TCAATGCACTGAAAGTGACTA	bnamiR161	21	CAACAGTCTCAGGATGGAAAA	bramiR94085p	21	GGTCGAGCAGACAACGAAGAT	alymiR8583p	21
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CGAAGAAAATGAAGTCGTTTT	alymiR34415p	21	TGCCACTCTTTTAGCTTCCGAATC	alymiR34463p	24	TTTGACGTGCTCGATCTGCTC	athmiR3932b5p	21	CTCGGAAGCTAGACGTGTGGCAGG	alymiR34465p	24
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GAAGGTAGTGAATTTGTTCGA	athmiR417	21	ACTGAAGTAGAGATTGGGTTT	athmiR5656	21	ATAGTCAATTTTATCGGTCTG	athmiR5664	21	TCCCAAATGTAGACAAAGCA	athmiR158a3p	20
AAAGCCTTGAACGCTGTCGTT	alymiR4228	21	GTGGGTTGCGGATAACGGTA	athmiR5644	20	TCGGACCAGGCTTCATCCCC	alymiR165b3p	20	ATAGCCTTGAACGCCGTCGTT	athmiR42285p	21
TGCCAAAGGAGATTTGCCCGG	bnamiR399b	21	AATTGTTCATTCAAGGATATT	alymiR773b3p	21	GCTCTCTAAGCTTCTGTCATCA	alymiR157b3p	22	AAACGAACAAAAAACTGATGG	athmiR8373p	21

Known miRNAs (miRbase) & size (nt)											
TGGAGAAGATACGCAAGAAAG	athmiR8353p	21	GGCAGTCTTCTTGGCTATC	alymiR169m3p	19	CTGAAGTGTTTGGGGGGACTC	bnamiR395f	21	TTGGACTGAAGGGAGCTCCCT	bramiR3193p	21
GATCATGTTCGTAGTTTCACC	BnamiR167e*	21	TAGTCCACTGTGGTCTAAGGC	athmiR56395p	21	GCTCTCTAGCCTTCTGTCATC	athmiR157a3p	21	TAATCTGCATCCTGAGGTTTA	bnamiR2111a5p	21
TTTTTCCTACTCCGCCCATACC	athmiR4723p	22	TTCAGGGACTTCAATTCAGAA	alymiR8465p	21	TCATTTGTGCCAATCATTCTA	alymiR4227	21	TTCTCAAGAAGGTGCATGAAC	athmiR825	21
TGTGTTCTCAGGTCACCCCTT	bolmiR398a3p	21	TCAGGTATGATTGACTTCAAA	athmiR8645p	21	CCAGGAAAACATCTTCAGACA	alymiR34485p	21	TAACAGAGTAATTGTACAGTG	athmiR8178	21
TTCCACAGCTTTCTTGAACTT	bnamiR396a	21	TGAAGCTGCCAGCATGATCTA	bnamiR167c	21	GAGCTCCCTTCCTCCAAAACG	alymiR159c5p	21	ACAGAGTTCCGTAGACCACGG	alymiR4023p	21
GGAATGTTGTCTGGCTCGAGG	alymiR166c5p	21	TGAGTTATCATTGGTCTTGTG	bramiR95695p	21	GCTCACTGCTCTTTCTGTCAGA	athmiR156a3p	22	ATGCACTGCCTCTTCCCTGGC	athmiR4083p	21
TAGCCAAGGATGACTTGCCTGC	bnamiR169h	22	CGAGACGAAGATATGGGTGAC	alymiR774a5p	21	ATGATGGATCCGACCATGATG	alymiR8425p	21	TCGATAAACCTCTGCATCCAG	bramiR1623p	21
TTGTTGATTCCTTGGAGATTG	alymiR4244	21	TACGCATTGAGTTTCGTTGCTT	athmiR777	22	CTGAAGTGTTTGGGGGGACTT	alymiR395c3p	21			
TGTTTTGTGCGTGACTCTAATT	alymiR403b5p	22	ACACTGAAGGACCTAAACTAAC	athmiR8405p	22	TCTCGTTCTCTCGTTTCAGCT	bramiR95655p	21			
AAACGTAAACATATATAATCGA	alymiR4237	22	TTATAAGCCATCTTACTAGTT	athmiR8443p	21	TTCGCTTGCAGAGAGAAATCAC	athmiR1735p	22			
AGAGGTACATCATGTAGTCTG	athmiR5661	21	TACTAAGTAGAGTCTAAGAGA	athmiR1887	21	TTGAAATTGTAGATTTCGTAC	athmiR4243	21			
TTCCACAGCTTTCTTGAACTG	athmiR396a5p	21	TTGAAAGTGACTACATCGGGG	alymiR1615p	21	CGAGCTGTGTAATCGTTTTGTT	bramiR95643p	22			
TGGACAAGGTTAGATTTGGTG	athmiR5657	21	TGGAGAGTAAGGACATTCAGA	bnamiR6028	21	ATCCTCGGGATACAGATTACC	bnamiR2111b3p	21			
TTATGAATGCTGAGGATGTTG	athmiR419	21	AGATATTGGTGCGGTTCAATC	athmiR171c5p	21	TTTCGTTGTCTGTTCGACCTT	athmiR858a	21			
GCTCAAGAAAGCTGTGGGAAA	bramiR3963p	21	TAAACTAATCACGGAAATGCA	athmiR420	21	CACCCAAATCTTCCTCTCAGG	alymiR774b3p	21			
TCATTGAGTGCAGCGTTGATG	athmiR397a	21	TGCGGATATCTTAGGATGAGGT	bramiR95685p	22	GTCACTTTCAATGCGTTGATC	bramiR1613p	21			
GCTCACCTCTCTTTCTGTCAGT	alymiR156b3p	22	GTCCTCGGGATGCGGATTACC	bnamiR2111a3p	21	TCTCGGTTCGCGATCCACAAG	athmiR8515p	21			
GAGATTCTTTCAGTCCAGTCA	BnamiR319b2	21	CCCCAAATGTAGACAAAGCA	athmiR158b	20	GAATCTTGATGATGCTGCAT	alymiR172e3p	20			
TGGTTTTGGACACGTGAAAAT	athmiR826b	21	ATGTGTATAGGGAAGCTAATC	athmiR8174	21	TTGAATGTGAATGAATCGGGC	athmiR5652	21			
ACCACAGCTTCTGCTACGAAC	alymiR8345p	21	TTTGATTCCAGCTTTTGTCTC	athmiR773b3p	21	AAGAACATCAAATTAGAATGT	athmiR8705p	21			
TTGTTGACAAATACTTAGGCTC	bramiR95665p	22	TGAGAAGAAGAAGAAGAAAA	athmiR5021	20	ATCTCATCAATCTCCCAATAC	alymiR3444b	21			
TAGGTTGGTGATCATATAGGAT	alymiR8233p	22	AGGTGGACATATTGCCAACA	alymiR394b3p	20	TAGTCCGGTTTTGGATACGTG	athmiR826a	21			
CAATTTCTAGTGGGTCGTATT	athmiR841b3p	21	GGGCTCCTCAGATGTTCATG	alymiR7713p	20	TCCTGTGTTTCCTTTGATGCGTGG	athmiR836	24			
GAGCTCCTTGAAGTTCAAACG	alymiR159a5p	21	TTGGGGACGACATCTTTTGTTG	athmiR447c3p	22	TAAAGTCAATAATACCTTGAAG	athmiR8643p	22			
TCCGGCAAGTTGACCTTGGCT	athmiR169g3p	21	TCCAAAGGCACAAGAACATCA	alymiR4250	21	AGAGGTGACCATTGGAGATG	athmiR5662	20			
GTTCAATAAAGCTGTGGGAAG	athmiR396a3p	21	TGGATTGGTCAAGGGAAGCGT	athmiR3440b3p	21	ATGGAATTTGATAAATAAACAC	alymiR4223	22			
ACGGTATCTCTCCTACGTAGC	bramiR3913p	21	TGACTGCATTAACTTGATCGT	athmiR8179	21	TTGATTCTCTTATCCAACTGT	athmiR56325p	21			
GGTTCGTACGTACACTGTTCA	athmiR416	21	TTATTCACAACTGCATAATTC	bramiR95623p	21	TGCCAAAGGAGATTTGCCCTG	athmiR399a	21			
CAAAGGTTGCTTGAATAAGGT	bramiR5726	21	TGTGTTAACTCAGGTCACCCCTG	alymiR398c3p	23	CACTTAGATTGTTCTTAGTATGAG	alymiR1887	24			
TGTGCAAATGCTTTCTACAGG	athmiR8223p	21	TGAAAGTGACTACATCGGGGT	athmiR161	21	AGATATTAGTGCGGTTCAATC	athmiR171b5p	21			
TCCAATAGGTCTAGCATGTGC	alymiR8625p	21	TCTGATGTATATAGCTTTGGG	bnamiR6034	21	AGTATCCAGAAAACTCTAATT	alymiR7813p	21			
GGGTCGACATGAGAACATATG	alymiR398c5p	21	GCTCACTCTCTTTTTGTCATAAC	athmiR156d3p	23	ATGACAAGGCCAAGATATAACA	athmiR50245p	22			
AAAAATGGAGTGAGAAATGGA	bramiR5721	21	GCTCTCTATGCTTCTGTCATC	alymiR157d3p	21	CACGTGTTCTACTCCTCCAAC	alymiR164c3p	21			
CGCTATCCATCCTGAGTTCCA	alymiR390b3p	21	GGGTAAGATCTCTATTGGCAGG	alymiR399a5p	22	TTTCATTCGAAATTGTTACCGC	alymiR4222	22			
TCAATTGGTATCAGAGCAACG	alymiR845b5p	21	GCTCACTCTCTATCCGTCACC	athmiR156f3p	21	TCAAGGAACGGATTTTGTTAA	athmiR8665p	21			
ATCAGTTTCTTGTTCGTTTCA	athmiR8375p	21	TAATCAGCTCCAGCTATGTACA	bramiR95533p	22	ATTTGTTACTAATTTGGAATG	athmiR50175p	21			
TCCAAAGGGATCGCATTGATC	bnamiR393	21	TCGGACCAGGCTTCATCCCCC	bnamiR166f	21	CTTTATATCCGCATTTGCGCA	athmiR21123p	21			
GTGCCTTGTGAGATTAGAGTT	alymiR34433p	21	GGGTCGACATGAGAACACATG	bramiR3985p	21	TAAGCTGCCAGCATGATCTTG	athmiR167c5p	21			
GATCATGTTCGCAGTTTCACC	athmiR167a3p	21	CCGGCGTTGCGCTCAATTATG	alymiR397a3p	21	GGCCGGTGGTCGCGAGAGGGA	athmiR8176	21			
TGAAGCTGCCAGCATGATCTT	BnamiR167f	21	TTGGGAGCTCGATGAGATCGA	alymiR3444a5p	21	TGGGGGTGGGGGGGTGACAG	athmiR8181	20			
GTCACTTTCACTGCATTAATC	alymiR1613p	21	TGATCTCTTCGTACTCTTCTTG	athmiR8313p	22	TCTGGTGTTGAGATAGTTGAC	athmiR869	21			
CGACAGAAGAGAGTGAGCAC	athmiR156g	20	ACAGGGAACAAGCAGAGCATG	athmiR4085p	21	AGGTGGGTATACTGCCAATA	alymiR394a3p	20			
TGAAGCTGCCAGCATGATCTAA	bnamiR167b	22	GAATGTTGTCTGGATCGAGG	alymiR165a5p	20	TTTTTGCAAATTAAAACCCCAA	alymiR4238	22			
TAACGCACAACACTAAGCCAT	athmiR2939	21	TCAGAACCAAACACAGAACAAG	bramiR5718	22	TATGAGAGTATTATAAGTCAC	bramiR4005p	21			
GGAATGTTGTTTGGCTCGAGG	alymiR166g5p	21	ATGGCTAGAGTGACTAGACCCG	alymiR4240	22	TTTGGATTTTGGTCATTGTTG	bramiR95595p	21			

Published miRNAs (not present in miRbase) & size (nt)					
TGCCTGGCTCCCTGTATACCA	BnamiRC9	21	AGAGTTTCCTTAAGTCCATTC	BnamiRC25*	21
TGTGTTGTGATGATAATCCGA	BnamiRC51	21	CCATACTAAATCTGGATCATTT	BnamiRC1	22
TCTTGTGTTGTGATGATAATC	BnamiRC53*	21	TATCTACTGCTTATGCCACCA	BnamiRC23a3	21
TTTCATCTTAGAGAATGTTGTC	BnamiRC45	22	TCGGATTATCATCACAACACT	BnamiRC56	21
TGATAATCCGACTTCTATGAC	BnamiRC54	21	ACATTGGACTACATATATTAC	BnamiRC151	21
GGGTCGATATGAGAACACATG	BnamiRC12	21	GCTGAGTTGGAACACAAAATC	bramiRn73p	21
TTGGTTTGGATCTTGGAAATC	BnamiRC55	21	CAAATGTAGACAAAGCAAAAC	BnamiRC47	21
ATGGTGTAGGTACTGAGCAGA	BnamiRC35	21	TTTTGCCTACTCCTCCCATACC	BnamiRC33	22
TTGGATTTATAGTTGGATAAG	athmiR56323p	21	TTATCATCACAACACTAGATC	BnamiRC53	21
NGCGGATATCTTAGGATGAGGT	bramiRn215p	22	ACCCTGTTGAGCTTGTCTCTA	BnamiRC13	21
GAATGATACTTGGATATGATC	bramiRn45p	21	TTGGACTGAAGGGAACTCCCT	BnamiRC25	21
CGTCCGGGGAAAGCAAAGTCG	BnamiRC36	21	ATGGATCCGCCGGATAAGGAT	BnamiRC28	21
TTAGAAACCTGCAATTATATA	bramiRn123p	21	AGATCATCCTGCGGCTTCATT	BnamiRC31	21
ATAGATCCTTCTGATGACGCA	BnamiRC6	21	TTGGCCACAACGGATTTAACA	BnamiRC44	21
TTTCCAAATGTAGACAAAGCT	bramiRn233p	21	TTACAGAACAGCAACAAGCTGT	BnamiRC23a2	22
AAACTAAGAGATGAATTCTTAC	bramiRn203p	22	TGGGATTGGCTTTGGGCTTTTC	BnamiRC3	22
TCAATGTTGGCTCAATTATGT	BnamiRC10	21	CAAATCCTGTCATCCCTACCA	BnamiRC7	21
ATCCTCGGGACACAGATTACC	BnamiRC34	21	TTCCCCGGACGACTTTAAATT	BnamiRC42	21
TAAGATGATGGGACGTTGGATC	BnamiRC39	22	CAGGAGAGATTGTTGGATCCA	BnamiRC8	21
ACTTGTCTCACTCATCAGTT	BnamiRC46	20	CAGCTGGACGACTTAGTAGAC	BnamiRC14	21
TTGGACGACTTTGTAGACGAC	BnamiRC22a3	21	TTAGGATTGAGATCTTAGCGA	BnamiRC24	21
TCAACCAAATACACATTGTGG	BnamiRC52	21	CTCTCGTGGAGCGTCTCGAGG	BnamiRC20	21
TTGAGGTTTTGAGGACTGGCC	BnamiRC29	21	TCGCGATCTTAGATCCTCTAA	BnamiRC18	21
TCAGAACCAAACCCAGAACAAG	BnamiRC23a1	22			
ATAAAACGATTACACAGCTCGGTC	bramiRn165p	24			
GTTTTGAGAGATTGGGAAGCT	BnamiRC16	21			
TGTGAATGATGCGGGAGATGT	BnamiRC43	21			
CGAGTTGGTCGGGAAAGACGG	BnamiRC19	21			
TAAGATGATGGAACACTGGCC	BnamiRC27	21			
TGAGCCAAAGATGACTTGTCG	BnamiRC26	21			
CAAGTAGACTACTTTCCAGACG	BnamiRC38	22			
TGATTTATCCAAGGGTTCAGG	BnamiRC37	21			
GCAAGTTGACTTTGGCTCCGT	BnamiRC32	21			
GGCGAGTCACCGGTGTCGGTC	BnamiRC11	21			
CGAGCTGTGTAATCGTTTTGTTA	bramiRn163p	23			
TTTCAGTCGTCATAGGTTAGT	BnamiRC4	21			
TTTTGGAGAAGGCTGTAGGCA	BnamiRC41	21			
AATCGGATTATCATCACAACA	BnamiRC51*	21			
TCCTGGACGACTTTCAAGTAAG	BnamiRC30	22			
CGCTCACAGCATCTGAACTCT	BnamiRC40	21			
GATGCATAACCACTAGATACG	BnamiRC23a3*	21			
TAAACAACACATATACTTTGC	bramiRn195p	21			
TTATATCCAAGTATCATTCCT	bramiRn43p	21			
CGTGGTCGTCCAAGTAGACGA	BnamiRC22a2	21			
CAAGTAGACGACTTTCCAGAC	BnamiRC22a1	21			

Previously unknown miRNAs identified with Shortstack & size (nt)												
ATAGAGGATCTAGAAACTGGGTTT	TM_Cluster_25078	24	ATCATGCGATCTATTTGGATT	TT_Cluster_60884	21	TCTGATGGCCTTGATGAGCTC	DT_Cluster_9519	21	ACCAGTCCTGAGATCATCGTTC	DT_Cluster_40687	22
ACGAGCTGTTACTCGCTGCCT	DM_Cluster_15438	21	TCTAAGATTCCTGTCTCTATC	TM_Cluster_75018	21	GCTGTGCTCTCTTCCCGCGTA	DT_Cluster_100403	21	AATTTTGTAGAAAACTATAAGA	TT_Cluster_22502	22
TTGTGATGAGAGCTCTTGCCT	TT_Cluster_140820	21	TATTGTTATATGTTTTGTTGA	TT_Cluster_79458	21	AGACTTCGTAGAAGACTTCCT	TT_Cluster_129316	21	GAGAAAAAAATAGGTATGGAT	TT_Cluster_2892	21
TCTATTAAGGTAACATCAGACT	DT_Cluster_86175	22	CTTGTCGGAGTTTATGATCTC	TM_Cluster_45056	21	TCGTTCCGTGTTGTTACCATC	DT_Cluster_85961	21	AGAGTTAAGTGGAGTCGAAGA	TM_Cluster_55184	21
AAAAGCTTCTCTGATTGATCT	TM_Cluster_54203	21	ATGAAAATACAATAGTGTTAGGAT	TM_Cluster_31975	24	ATCGACGAGAGATACGAAGAAACG	DM_Cluster_36769	24	AAAGAAAAAGAACTTCAAGCC	TT_Cluster_154549	21
AGAGGAACCTCTTCGTCGATT	TM_Cluster_58223	21	TTTTGGATTTGATTTTGAACA	TT_Cluster_115082	21	ATCCAATGTGTGTATTTGCTACTT	DT_Cluster_43752	24	TATTTTTTTTTTTATGTTATGT	TT_Cluster_162493	22
AGACTGTATCTTATATTAAGC	DM_Cluster_71480	21	AAGGATTGAGACTTGAGAGAG	TT_Cluster_149505	21	GATTTGTTTTCTCTTTGAACT	DT_Cluster_106347	21	GCAGATGATGTGAGCTGAGCA	TM_Cluster_32708	21
AAGGGGAAGGAACAGAAACGAGAA	TM_Cluster_23765	24	GTTATTGGAGTTAATAGAGAACCG	DM_Cluster_72295	24	CGGAGAATTATGATGAACAAG	TT_Cluster_12548	21	ATAAATGGATCATCTGGATGAAGA	TT_Cluster_8816	24
ATTGCAAGTGTCGTTTTAGATT	TM_Cluster_129	22	CGCATGTTTCTTTAGGAGATC	TT_Cluster_53036	21	TTCACGGCTCGAACTCGGGA	DT_Cluster_91815	20	TTGCTCCAAATAATTAAGACG	TT_Cluster_83274	21
AGAAGAAGGAGAGAGAGAAGG	TT_Cluster_123360	21	TGGCGACGTCGAAGATAGAGA	DT_Cluster_65219	21	TTGGACGACTTTGTAGACGACT	TM_Cluster_88781	22	TCAAGAAAGCTTACCAGAGGA	DM_Cluster_68457	21
TTTCATCAGTTTTATTTTGGG	DM_Cluster_39202	21	AAAAGGATCGAGGATTAAAAA	DT_Cluster_48080	21	TTTCCTACAGAAACAGGCGTA	TM_Cluster_27816	21	TTGACAGAAGAGAGTGAGCAC	TM_Cluster_40901	21
TTTTTTCTTTTTCTTTTCTTT	DT_Cluster_45893	21	AGTTTGGTTATTTTGGTCAGG	TM_Cluster_60327	21	TTTTTTTTAAATGTTATGTTG	TT_Cluster_48679	21	CCAGTAGTTCGTTAGGTTTGAC	TM_Cluster_14381	22
CACGGAATGGTATATGTAGCT	DT_Cluster_56508	21	TATTAAGATTGTGACATGTGT	TM_Cluster_51896	21	TACCTGATGAGATCTAGACGT	TM_Cluster_33867	21	AATTTATCACTTAAAAGGCACG	TM_Cluster_18970	22
TGAAGTTGTCATGAAGTCTTC	DM_Cluster_54050	21	ATTATGCAGTTGTGAATAAAC	DT_Cluster_8963	21	TCCATTAGTATCAGACGATCT	DM_Cluster_74956	21	AACGGAATATAAGAACTCATCTCT	TT_Cluster_121736	24
TAATTCACGTGTTGTTAACTCA	DT_Cluster_91375	22	CAATGAGAGTGATGTATGAGCCT	DM_Cluster_44186	23	CTTCCTATAAATATGCAAGCT	DM_Cluster_66235	21	ATGGAGTAGAAAATGCAGTCG	TT_Cluster_71899	21
TTGACAGAAGAGAGCGAGCAC	DM_Cluster_11733	21	AAGAATCTCGGTTAAGAGACT	DM_Cluster_52703	21	ACCATGTGGATGTTACGGACT	TT_Cluster_10076	21	AATTTGCTTCAATGTATGTCT	DT_Cluster_60726	21
AATCTGTTGAGATCTATGCCT	TT_Cluster_70886	21	TTTGAGAAGCATTCTGAGTGAGAA	DM_Cluster_59766	24	CCGAGTTTAATGTACCTGGTT	TM_Cluster_31961	21	TTCAGAATGAGATTGTGAAGG	TT_Cluster_87159	21
AGAGGTGTAAGAAAAGTTACC	DT_Cluster_90549	21	GGTAAAAGCCTTCAGAATATG	TT_Cluster_75425	21	CTGGCTCTGATACCATGTGAAAGT	DM_Cluster_58696	24	TACGGTAGACGAATTCGAATT	DT_Cluster_48536	21
ATTGGACAACTTTATTTTTTGGTC	TM_Cluster_31327	24	AGGCGGATTTGAATTTGAGGC	TT_Cluster_125992	21	TCGCTTGGTGCAGGTCGGGAAC	DM_Cluster_69056	22	TTCGGCTTGAGCTCGGTCGCT	TT_Cluster_99626	21
TTCCTGTTGTCGTTGACGACTC	TT_Cluster_61752	22	TGAAGATGACGATGACTTGAT	DT_Cluster_21302	21	TTCATTCATTTTCTTTGGCGCAAG	TM_Cluster_33492	24	TTGATCTGAATCAAGAGGGTC	TT_Cluster_101146	21
CGGATCTTCGCCGTGTAGCTAA	TT_Cluster_6709	22	ATTCATGTCATATGCTACTAC	TT_Cluster_155319	21	TAGTTATCAAGTGCATATATT	TM_Cluster_24345	21	AAAAAGGACGGATCTTGGCGC	TM_Cluster_32824	21
TCAGGTTTTTGGTATAGTTCC	DM_Cluster_3672	21	AAGATCTCTTTTATGCTTCCG	DT_Cluster_48947	21	ATTCACTAATCTTCAGGATAG	DM_Cluster_4681	21	TTGGCACAGTACTCGATCAGT	TT_Cluster_149038	21
ATTTATGGCTTCTCTTTTTTT	DM_Cluster_14659	21	TCATATGAGAAACGCATCCGTGA	TM_Cluster_648	23	TTGCTTGACTAGAGAAACTCAG	TM_Cluster_86300	22	TCCAAAGCCTTTCTATGTCTT	TM_Cluster_20495	21
AGACATCGTAGAAGACTTCCT	DT_Cluster_73601	21	AACAACGAATCGTTGAGGCGT	DM_Cluster_42401	21	AATGAAGAGTTCCTAGACTGTA	TT_Cluster_66922	22	TTTTGTTACTATTACGACTGCACC	TM_Cluster_30020	24
ACCTTATCATCTCTCTATCCCCTC	DM_Cluster_15748	24	TTAGAATACTCTTATTTACGTAGA	TT_Cluster_4536	24	CTTTGCTTTTAGGGTTTCTGTT	TT_Cluster_98357	22	ACGAGACCGCTGTAGATTAGACGA	TM_Cluster_30741	24
AACTGATTTACAACGATTTAGACC	TM_Cluster_65244	24	GAAACTTTGGGTTGGTTTTCC	TT_Cluster_94899	21	TTATCGAGGTCGGATTAGAATC	TM_Cluster_37650	22	CTTGTCGGAGTTTACGATCTC	DM_Cluster_29058	21
CTGGACGACTTAGTAGAAGGTCGT	TM_Cluster_86431	24	AATCTGTGTGAATAAAACTATAAC	DM_Cluster_264	24	GCAGACCCCTCTGACTCAGGCT	TM_Cluster_81182	22	AATGACCTTCTTTTTCTTCTT	DM_Cluster_28298	21
ATCGTCAATAAGTTTTAAGTTGGA	DM_Cluster_39689	24	ACTCATAGACGCACTGAAACC	DT_Cluster_69998	21	TTTTGTTACTATTACGACTGC	TT_Cluster_57302	21	TATTTTTGTTAGTGCCTTTCT	TM_Cluster_8390	21
AGCCTGGCTCTGATACCATGAAGT	TM_Cluster_16924	24	ACGGAAGCATAAAACAGATCT	TT_Cluster_71140	21	ATTCCAATGATTTCTTTTGAC	TT_Cluster_50452	21	TTTTGTTGTTTATTGTATATT	TT_Cluster_128447	21
AGGGATAACGACTACTGTAAAAGG	DM_Cluster_63218	24	TGACACATGCAGAGCCGTGAC	TT_Cluster_160692	21	GTGGTCATGGTCATCGTCATC	DT_Cluster_16177	21	TGATTGAGAGAATTCTGGAGT	TT_Cluster_84234	21
TACACAAATTTTTTTTTGTGT	TT_Cluster_117274	21	TAAAAGTAGAAACGCTGCCAG	DM_Cluster_21884	21	AAACCGGAGTAACTGAACTAACCA	TM_Cluster_24871	24	AAGAAAAAAACAGAACACCGAGGG	TM_Cluster_91189	24
ACATGTATTGTCGTTGATATA	TT_Cluster_120913	21	TTGTTCCTCGGAATTTCCTCG	DT_Cluster_51067	21	TATATGCACTTGATAGCTAAA	DT_Cluster_31915	21	ATAGAATAGCTCGTTACAAGA	TM_Cluster_37527	21
AGGACTTATCAGATATGAAAGA	TT_Cluster_93529	22	AGAATCTTGATGATGCTGCATT	TM_Cluster_35275	22	AGAAAGCATCTGTTGAAGCCA	TT_Cluster_11782	21	GTTTTGTTTGTTTGATATGTT	TT_Cluster_96434	21
TCTGAGGTCTATTTTTGTGAC	DT_Cluster_75500	21	TTCCTCCACTTCATGGCCTTCT	TM_Cluster_44652	22	GGAGCAGAACCAAGTTAGTCT	TT_Cluster_79242	21	CGGAAGACATGGTTCAAACTG	TM_Cluster_16626	21
TCGAGGGAGACACAATAACTG	TT_Cluster_160404	21	AGATCAAAACACTTGAGAGAG	DM_Cluster_37963	21	CAAACAAAAAAGCAATCAGTT	TT_Cluster_45521	21	TTTTTTTTTTTATGTTATGTTG	TT_Cluster_146472	22
TAGTGGAAGCAGCAACGAGAA	TM_Cluster_11636	21	CATTGGTATTGCTGTGGCCGA	TT_Cluster_56504	21	TGTCAGATCGTGTTCACGTCGGTC	TT_Cluster_87517	24	TTCAGATCCTAAGATGTGGACC	TT_Cluster_91710	22
TGATTGAGCCGCGTCAATATC	TM_Cluster_31773	21	AGTAGTTCGTTAGGTTTGACC	TT_Cluster_110546	21	ATTGTTGTATGTATATATATA	TT_Cluster_115914	21	AGACTCATCGTTTAGTTGGCC	TT_Cluster_153264	21
TTTTTGATTTAGAATTTAGGA	TT_Cluster_31043	21	CTTATATTCTAGTAAGAACCT	DM_Cluster_24381	21	GTAGCTAACTGTGTACATGTGTAG	TM_Cluster_62213	24	ACAGATCTGTCTCCTCTTCTC	TM_Cluster_10927	21
TTGAACCCAAGATCTCACCCT	TM_Cluster_18741	21	CAATTAAATATTAATATTTAT	DT_Cluster_52593	21	AGCGGAATATAAGAACTTGTCTCT	TM_Cluster_44506	24	CAAAGAGAAGATTGTCACACA	DT_Cluster_4696	21
AAACTAAGAGGACATGTAATC	TT_Cluster_31175	21	TCTAAAATAGAATATCATTGGAAC	TM_Cluster_20159	24	GAAGAGGCTAGAGAAGAGGCT	TM_Cluster_23018	21	CTTTTTTGCTTCTGTAAACTT	TM_Cluster_39415	21
GCAAGTAGACTTTGGCTCTGT	TT_Cluster_49493	21	TCTTGAGATTCGTCATGGAGA	TT_Cluster_26154	21	TTGGATCTCCAAGAGGACTCT	TM_Cluster_392	21	AACTGGATCAATTGTTGTTGT	TT_Cluster_127969	21
ATCATGCTATCCCTTTCGATT	TM_Cluster_14180	21	AAAAATCGGTTTAGGCAGCGC	TM_Cluster_51706	21	TCTTTTATATGGTTGTTGTAT	DM_Cluster_53371	21	TGTTTGACTTGTAGCTCAAGT	TT_Cluster_54797	21
CCGGGTGAAGATCTTCAAATC	TT_Cluster_49373	21	AAAGGAGATCGAAGATGAAGA	DT_Cluster_90643	21	AAGGGAATCGTCAATGCTCAGAGA	DM_Cluster_73944	24	TCTCGAAGATCAATGTATAGT	DM_Cluster_23013	21
CTATACTATTGATTGGCACCAG	DM_Cluster_65227	22	CTTTTCAACTTTATCAAAAACTGT	TM_Cluster_34784	24	ATAGAGAGAGAGATAGACTGA	DM_Cluster_62902	21	CCGTAACAAAAGTTAGTCAAC	TT_Cluster_7437	21
TAAATTAATAATATTGGGACT	TM_Cluster_35249	21	AGCGGAATATAAGAAACTGTTTCT	DM_Cluster_37332	24	AAAGCTGTAGATAAAAATTAAAGC	TT_Cluster_81900	24	AGCGGAATATAAGAACCTGTTTCT	DM_Cluster_63658	24

Previously unknown miRNAs identified with Shortstack & size (nt)								
GATGATGCTTGGGATTTATTT	DT_Cluster_99712	21	TCACTACGTTACAATATGCCA	DM_Cluster_32823	21	TATATGTAGACGGTAGGTACA	TT_Cluster_79511	21
TTGGTGATAATTGGATTGGCA	DT_Cluster_24117	21	ATGGGATATGGAGATCTTCTTC	DM_Cluster_21155	22	CTAGGCCGTAGCTATGCGCTT	TT_Cluster_7092	21
AGTATGATTTGTGATTTGACA	DT_Cluster_29179	21	AATCAAGCTTCTCCGCCTCTC	DM_Cluster_54440	21	TCGAACCGCCTTCAACAAGAG	DM_Cluster_65288	21
ATACGAGGATCATAAAGAACATGT	DM_Cluster_64248	24	TTTGAGATCTTCTACATGGTA	TT_Cluster_31983	21	ACCTGCTTTCCTGTTATAACC	TT_Cluster_6710	21
AAAATAACATTCATTAAAAGGTAA	DM_Cluster_35980	24	AATATAAAAACCCGTCTTTGA	TT_Cluster_122926	21	AGAGGTGTCAGAAGAGTTACC	TT_Cluster_129180	21
GTAGAATCCTTTTATTTTTTT	TT_Cluster_21225	21	GAAAGACCAGAGAAGCTGAAT	TT_Cluster_107573	21	TTTTAGTGTGAAATATAGATG	TM_Cluster_90838	21
TTTCTTTGTCTGTACGTTAGC	TM_Cluster_89694	21	TACCTACCGTCTACATATATG	TT_Cluster_79512	21	ACCGGATCTGAAAAGAAGACG	TT_Cluster_85098	21
TTATGCCCTGCCTAAACCGAT	DM_Cluster_7814	21	TGCCGGACGACATGTTGTGCC	TT_Cluster_111347	21	TTATGTTATGTTATGTTGAGT	TT_Cluster_113382	21
TTTTGTTCCATTTGCGTTTTGA	TM_Cluster_6643	22	GATGACTTACTGGTAAGTCGT	DT_Cluster_81732	21	AAGATATATATATATGTAGACACT	TM_Cluster_22037	24
ATTCGGTAAGCTCGTAGAGATTGC	DM_Cluster_39510	24	CCAACTACCAATGTTGAGACC	DT_Cluster_17185	21			
TTAACTAAAAAACTAAGAACC	TT_Cluster_90833	21	ATCAATGATTGTGGTGAAAGT	DM_Cluster_65653	21			
ATCTGATCACAAGTTTAATCT	TM_Cluster_69182	21	TTTGACTTGCATCTCAAGTTG	DT_Cluster_37598	21			
AACCCATCGTTGTGTGACAGA	TM_Cluster_41428	21	TATCGGTAAATCTTTAGTTTA	DT_Cluster_23782	21			
AAGAGAGAAGTGGACAGAAGC	TT_Cluster_122750	21	TCGAGTAACGCCAAGCGCACC	TT_Cluster_64173	21			
ATTTCATGTGGCTTTGTCGTAACG	DM_Cluster_23809	24	ATCCATTAGTATCAGACGATC	TT_Cluster_158092	21			
TGAGATTTGAGATTGTTCTTG	TT_Cluster_26085	21	TCTCCTCGCAAACTATCAGGT	TM_Cluster_17285	21			
TTTGATTGTTGGCCGGTTCGA	TT_Cluster_28252	21	AGGGATAAACATTCCATGGTC	DT_Cluster_80569	21			
ACGAAGCATAGAACAGATCTTTCT	TM_Cluster_77026	24	AACCCTGACGATTTGAAGAAC	TT_Cluster_111866	21			
AGGACTATACTCCGGCACCAGC	DT_Cluster_63465	22	AATTAGATAAGTCACAGACCT	TT_Cluster_11273	21			
AAAAAAAAGAACAATGATCCT	DT_Cluster_108551	21	TTTGGTTTGAATTAAAGTGACAGT	DM_Cluster_43468	24			
GCTATGAGATCAAAGGGTTGT	DT_Cluster_32516	21	CGATAAAAGACTCAAAACATT	TM_Cluster_91467	21			
GTGAGTCATAAAGTCTCAAACTTT	TM_Cluster_74925	24	GTTCGGTGGGGGGTCTTATTCT	TM_Cluster_4095	22			
CTGCAGCTGCTCTCATGGCTG	TT_Cluster_159252	21	GAAGACTGTAGTTGTTGTTGT	DM_Cluster_73929	21			
AAAACCGGAACCGAACCAAAAACC	TM_Cluster_51842	24	GGAGAGACATATTCGGGCTGA	TM_Cluster_57845	21			
ATCCAAAAAGTATTTCGTGTTATT	DM_Cluster_59926	24	ATTCGAGGACAGAGACGTACC	TM_Cluster_21042	21			
ATCAAAATATAGTGGTTGTTATTT	DM_Cluster_1748	24	TAACTAAAAAAAACTAAGAACC	DT_Cluster_1457	22			
TCAGACGACTTATATATAAGT	DM_Cluster_76911	21	ACTTGGTCATTGTTGTATGTAG	TM_Cluster_30515	22			
AATAAGTCGTCTGGAAAGTCTTCC	DM_Cluster_49871	24	TCTGAATCCAAGTAAGTTATT	TM_Cluster_29410	21			
ACTAGGAGATTTGACGCGACG	TT_Cluster_107634	21	GCCGGTCCTGAGATTTTGGGGAGG	DM_Cluster_58756	24			
TGCACTGCCTCTTCCCTGGCT	DM_Cluster_72862	21	TACTTTACTAATAATTAGGAT	TM_Cluster_58070	21			
TGTAAACCGGTTAATCTCTCT	DM_Cluster_58765	21	TATAGTACCGGTTATTGTTGG	TT_Cluster_103224	21			
TATTACTTAAAATCTCTTCCC	TT_Cluster_39048	21	TTGGTGAACGCAGCTAGTTGC	TM_Cluster_81969	21			
TTGATGATGCTTCTGTTGATG	DM_Cluster_33373	21	GAGAATTATTGCGACTTGCATCGT	TM_Cluster_84305	24			
ATGTTATATTTTAATAGTTAGACT	DM_Cluster_75967	24	TCAGTGATTTACAGAGCCAGC	DM_Cluster_67885	21			
GTCAAGATCTCATCAAGTAGA	TT_Cluster_64750	21	GGAGCACGGGTTTGTTTACCG	TT_Cluster_24622	21			
TGTTCTGTGGGTTTTTACCGA	TM_Cluster_25944	21	TAAGAACCCACATTAATCATG	TT_Cluster_107352	21			
AACCCTCTGATCTCATAGCTC	DM_Cluster_20384	21	AGAGACGCGACTGACATTGA	DT_Cluster_90935	20			
CATGAAGACTTCATGAAGACT	DM_Cluster_54243	21	AGTCTGAAACTTTGTGACATTGC	DT_Cluster_95086	23			
ATATTCCGTTAAGAACTTCACC	TT_Cluster_120084	22	TCACGGATTTATTTTTGGATC	TM_Cluster_63388	21			
AACTATACTAAAACCTTGAAC	DT_Cluster_5829	21	TTGAGGGACCAGTTTGAAGCT	TT_Cluster_157642	21			
ACGAAGCATAGAACAGATCTT	TT_Cluster_139251	21	CCGTGGGGCGGAACCGTTGAGC	TT_Cluster_129472	22			
ATTAATAATTATACTGAGGAA	TM_Cluster_87465	21	ACATGATCATCATTGGTGATG	TT_Cluster_44854	21			
TATAGTAATATAGTACTGTCT	TM_Cluster_72019	21	CGAGGACAATGAGACACAAGA	TT_Cluster_104489	21			
CATCGGTATAATTATTAATTA	TT_Cluster_157177	21	TTTCCCTTTTCGTTTATGTTT	TM_Cluster_70129	21			
GCTACGTAACGACCAAGCGGGA	TT_Cluster_23157	22	CCACAGAGATCTCAAGCCTGA	DT_Cluster_10323	21			

Table S9: bna-miRNA:mRNA pairs in *B. napus*.

						Fragment signatures (rpm)			
miRNA[a]	Target transcript ID	Predicted gene function	Cleavage position	miRNA:mRNA target pair (5'-3' : 3'-5')	Cleavage found in PAREseq replicates	DM	DT	TM	TT
bna-miR156	BnaA06g36780D	SPL 2[1]	3011	TGACAGAAGAGAGTGAGCAC |||||||||||||||| TTAAACTGTCTTCTCTCTCTCGTGGTAGTTCT	DT2 DT3 TT3	0.00	1.13	0.00	0.37
bna-miR156	BnaA06g36780D	SPL 2[1]	3012	TTGACAGAAGATAGAGAGCAC ||||||||||||||||| CTTAAACTGTCTTCTCTCTCTCGTGGTAGTTC	DT2 DT3 TT3	0.00	2.04	1.59	3.93
bna-miR156	BnaA04g19840D	SPL 3[2]	560	TGACAGAAGAGAGTGAGCAC ||||||||||||oo|||| TCTGACTGTCTTCTCTCGTTCGTTTCCGATTT	DM3 DT3 TT3	1.19	3.31	0.00	1.48
bna-miR156	BnaC04g44230D	SPL 3[2]	619	TGACAGAAGAGAGTGAGCAC ||||||||||||oo|||| TCTGACTGTCTTCTCTCGTTCGTTTCCCGAAT	DM3 DT3 TT3	1.19	3.31	0.00	1.48
bna-miR156	BnaC02g19100D	SPL 6[3]	1116	TGACAGAAGAGAGTGAGCAC |||||||||||||||| CTCGACTGTCTTCTCTCTCTCGTGTTCATCTC	DM3 DT2 DT3 TM3 TT3	4.50	17.09	5.12	4.07
bna-miR156	BnaC02g14000D	SPL 6[3]	1095	TGACAGAAGAGAGTGAGCAC |||||||||||||||| CTCGACTGTCTTCTCTCTCTCGTGTTCATCTC	DM3 DT2 DT3 TM3 TT3	4.50	17.09	5.12	4.07
bna-miR156	BnaC02g19100D	SPL 6[3]	1116	TGACAGAAGAGAGTGAGCAC |||||||||||||||| CTCGACTGTCTTCTCTCTCTCGTGTTCATCTC	DM3 DT2 DT3 TM3 TT3	4.50	17.09	5.12	4.07
bna-miR156	BnaC02g14000D	SPL 6[3]	1095	TGACAGAAGAGAGTGAGCAC |||||||||||||||| CTCGACTGTCTTCTCTCTCTCGTGTTCATCTC	DM3 DT2 DT3 TM3 TT3	4.50	17.09	5.12	4.07
bna-miR156	BnaA07g27730D	SPL 6[3]	639	TGACAGAAGAGAGTGAGCAC |||||||||||||||||| CTCGACTGTCTTCTCTCACTCGTGTTCATCTT	DM3 DT2 DT3	4.50	17.09	0.00	0.00
bna-miR156	BnaA02g14580D	SPL 6[3]	1083	TTGACAGAAGATAGAGAGCAC o|||||||||| ||||||||| ACTCGACTGTCTTCTCTCTCTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21
bna-miR156	BnaA07g27730D	SPL 6[3]	640	TTGACAGAAGATAGAGAGCAC o||||||||| || |||||| ACTCGACTGTCTTCCCTCACTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21
bna-miR156	BnaC02g19100D	SPL 6[3]	1117	TTGACAGAAGATAGAGAGCAC o|||||||||| ||||||||| ACTCGACTGTCTTCTCTCTCTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21
bna-miR156	BnaCnng61400D	SPL 6[3]	771	TTGACAGAAGATAGAGAGCAC o|||||||||| || |||||| ACTCGACTGTCTTCTCTCACTCGTGTTCATAT	DM3 TM3 TT3	1.75	0.00	1.06	1.43
bna-miR156	BnaC02g14000D	SPL 6[3]	1096	TTGACAGAAGATAGAGAGCAC o|||||||||| ||||||||| ACTCGACTGTCTTCTCTCTCTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21
bna-miR156	BnaC07g11380D	SPL 10[3]	1568	TTGACAGAAGATAGAGAGCAC ||||||||||| ||||||||| CTTCAACTGTCTTCTCTCTCTCGTGCCACCTT	DM2 DM3 DT2 DT3 TM2 TM3 TT2 TT3	18.84	0.86	14.61	34.85
bna-miR156	BnaA07g08830D	SPL 10[3]	1632	TTGACAGAAGATAGAGAGCAC ||||||||||| ||||||||| CTGCAACTGTCTTCTCTCTCTCGTGACATCTT	DM3 DT3 TM2 TM3 TT3	19.51	8.58	33.17	31.01
bna-miR156	BnaC07g11380D	SPL 10[3]	1567	TGACAGAAGAGAGTGAGCAC |||||||||||||||| TTCAACTGTCTTCTCTCTCTCGTGCCACCTTA	DM3 DT3 TM3 TT3	0.19	0.27	1.00	2.96
bna-miR156	BnaA07g08830D	SPL 10[3]	1631	TGACAGAAGAGAGTGAGCAC |||||||||||||||| TGCAACTGTCTTCTCTCTCTCGTGACATCTTT	DM3 TM3 TT3	5.00	0.00	0.77	3.89
bna-miR156	BnaAnng25050D	SPL 11[3]	1341	TTGACAGAAGATAGAGAGCAC ||||||||||| ||||||||| CTGCAACTGTCTTCTCTCTCTCGTGACATCTT	DM3 DT3 TM2 TM3 TT3	19.51	8.58	33.17	31.01
bna-miR156	BnaC05g21270D	SPL 11[3]	1690	TGACAGAAGAGAGTGAGCAC |||||||||||| o||||| TTCAACTGTCTTCTCTCTTTCGTGCCACCTTT	DM3 DT3 TM3 TT3	0.19	0.27	1.00	3.01
bna-miR156	BnaAnng25050D	SPL 11[3]	1340	TGACAGAAGAGAGTGAGCAC |||||||||||||||| TGCAACTGTCTTCTCTCTCTCGTGACATCTTT	DM3 TM3 TT3	5.00	0.00	0.77	3.89
bna-miR156	BnaC04g23930D	SPL 15[3]	952	TTGACAGAAGATAGAGAGCAC ||||||||||| ||||||||| CTCAAACTGTCTTCTCTCTCTCGTGTCGAACT	DM2 DM3 DT3 TM3 TT3	2.80	3.00	0.82	1.90
bna-miR160	BnaA07g13830D	ARF 10[4]	1698	TGCCTGGCTCCCTGTATGCCA |||||||||||||||||| || TCGAACGGACCGAGGGACATAAGGGCGTCCTC	DM3 DT2 DT3 TM2 TM3 TT2 TT3	8.94	12.50	18.38	20.22
bna-miR160	BnaA01g06910D	ARF 16[4]	2341	TGCCTGGCTCCCTGTATGCCA |||||||||||||||| o|| TAATACGGACCGAGGGACATTTGGGTGCCCTT	DM3 DT2 DT3 TM2 TM3 TT2 TT3	8.06	22.86	18.60	32.45
bna-miR160	BnaC01g08330D	ARF 16[4]	2324	TGCCTGGCTCCCTGTATGCCA |||||||||||||||| o|| TAATACGGACCGAGGGACATTTGGGTGCCCTT	DM3 DT2 DT3 TM2 TM3 TT2 TT3	8.06	22.86	18.60	32.45
bna-miR171	BnaAnng18550D	SCL 6[5]	840	TTGAGCCGTGCCAATATCACG ||||||||o||||||||| AACTAACTCGGCGCGGTTATAGGGGACACGGT	DM3 DT2 DT3 TM3 TT3	4.13	4.22	5.30	0.97
bna-miR171	BnaAnng18540D	SCL 6[5]	851	TTGAGCCGTGCCAATATCACG ||||||||o||||||||| AACTAACTCGGCGCGGTTATAGGGGACACGGT	DM3 DT2 DT3 TM3 TT3	4.13	4.22	5.30	0.97
bna-miR171	BnaC04g22080D	SCL 22[6]	816	TTGAGCCGTGCCAATATCACG ||||||||o||||||||| AACTAACTCGGCGCGGTTATAGGGAACGCGCT	DM3 DT2 TM3 TT3	14.50	4.53	1.06	0.60
bna-miR172	BnaC09g13430D	ERF RAP2-7[7]	1039	AGAATCTTGATGATGCTGCAT ||||||o||||||||||| AATCTCTTAGGACTACTACGACG-ACGTTGAC	DM2 DM3 DT2 DT3 TM2 TM3 TT3	16.60	10.03	14.48	6.66

bna-miR172	BnaA03g22100D	ERF RAP2-7[7]	2284	AGAATCTTGATGATGCTGCAT	|||||o|||||||||	AATCTCTTAGGACTACTACGACG-ACGTTGAC	DM2 DM3 DT2 DT3 TM2 TM3 TT3	16.60	10.03	14.48	6.66
bna-miR172	BnaC03g26480D	ERF RAP2-7[7]	2328	AGAATCTTGATGATGCTGCAT	|||||o|||||||||	AATCTCTTAGGACTACTACGACG-ACGTTGAC	DM2 DM3 DT2 DT3 TM2 TM3 TT3	16.60	10.03	14.48	6.66
bna-miR172	BnaC04g15640D	ERF RAP2-7[7]	2414	AGAATCTTGATGATGCTGCAT	|||||o|||||||||	AATCTCTTAGGACTACTACGACG-ACGTTGAC	DM2 DM3 DT2 DT3 TM2 TM3 TT3	16.60	10.03	14.48	6.66
bna-miR172	BnaC03g26480D	ERF RAP2-7[7]	2328	GGAATCTTGATGATGCTGCAT	o||||o|||||||||	AATCTCTTAGGACTACTACGACG-ACGTTGAC	DM2 DM3 DT2 DT3 TM2 TM3 TT3	16.60	10.03	14.48	6.66
bna-miR172	BnaA03g22100D	ERF RAP2-7[7]	2284	GGAATCTTGATGATGCTGCAT	o||||o|||||||||	AATCTCTTAGGACTACTACGACG-ACGTTGAC	DM2 DM3 DT2 DT3 TM2 TM3 TT3	16.60	10.03	14.48	6.66
bna-miR172	BnaC04g15640D	ERF RAP2-7[7]	2414	GGAATCTTGATGATGCTGCAT	o||||o|||||||||	AATCTCTTAGGACTACTACGACG-ACGTTGAC	DM2 DM3 DT2 DT3 TM2 TM3 TT3	16.60	10.03	14.48	6.66
bna-miR172	BnaC09g13430D	ERF RAP2-7[7]	1039	GGAATCTTGATGATGCTGCAT	o||||o|||||||||	AATCTCTTAGGACTACTACGACG-ACGTTGAC	DM2 DM3 DT2 DT3 TM2 TM3 TT3	16.60	10.03	14.48	6.66
bna-miR172	BnaA10g12950D	AP2-like ERF TOE2[8]	2933	AGAATCTTGATGATGCTGCAT	|||||o|||||||||||	ACACTCTTAGGACTACTACGACGTAAACTCTC	DM3 DT2 DT3 TM2 TM3 TT3	0.75	5.00	11.14	9.95
bna-miR172	BnaC09g35430D	AP2-like ERF TOE2[8]	2671	AGAATCTTGATGATGCTGCAT	|||||o|||||||||||	ACACTCTTAGGACTACTACGACGTAAACTATC	DM3 DT2 DT3 TM2 TM3 TT3	0.75	5.00	11.14	9.95
bna-miR172	BnaA10g12950D	AP2-like ERF TOE2[8]	2933	GGAATCTTGATGATGCTGCAT	o||||o|||||||||||	ACACTCTTAGGACTACTACGACGTAAACTCTC	DM3 DT2 DT3 TM2 TM3 TT3	0.75	5.00	11.14	9.95
bna-miR172	BnaC09g35430D	AP2-like ERF TOE2[8]	2671	GGAATCTTGATGATGCTGCAT	o||||o|||||||||||	ACACTCTTAGGACTACTACGACGTAAACTATC	DM3 DT2 DT3 TM2 TM3 TT3	0.75	5.00	11.14	9.95
bna-miR172	BnaA07g12050D	AP2-like ERF TOE3[9]	2227	AGAATCTTGATGATGCTGC-AT	|||||o||||||||o|| ||	CCTCTCTTAGGACTACTACGGCGGTAAGGGTG	DM3 TM2 TT3	1.56	0.00	8.75	0.46
bna-miR172	BnaC07g16190D	AP2-like ERF TOE3[9]	2185	AGAATCTTGATGATGCTGCAT	|||||o|||||||||	CCTCTCTTAGGACTACTACGTCGTCGGTAAGG	DM3 TM2 TT3	1.56	0.00	8.75	0.46
bna-miR172	BnaA07g12050D	AP2-like ERF TOE3[9]	2227	GGAATCTTGATGATGCTGC-AT	o||||o||||||||o|| ||	CCTCTCTTAGGACTACTACGGCGGTAAGGGTG	DM3 TM2 TT3	1.56	0.00	8.75	0.46
bna-miR172	BnaCnng39690D	ERF APETALA 2[7]	2233	GGAATCTTGATGATGCTGCAT	o||||o||||||||||	CCTCTCTTAGGACTACTACGACGTCGTAAACG	DT2 DT3 TT3	0.00	0.53	0.71	1.25
bna-miR172	BnaCnng39690D	ERF APETALA 2[7]	2233	AGAATCTTGATGATGCTGCAT	|||||o||||||||||	CCTCTCTTAGGACTACTACGACGTCGTAAACG	DT2 DT3 TT3	0.00	0.53	0.71	1.25
bna-miR172	BnaA01g34730D	ERF APETALA 2[7]	1043	AGAATCTTGATGATGCTGCAT	|||||o||||||||||	CCTCTCTTAGGACTACTACGACGTCGTAAACG	DM2 DM3 DT2 TM3 TT3	3.62	2.04	0.47	1.62
bna-miR172	BnaA01g34730D	ERF APETALA 2[7]	1043	GGAATCTTGATGATGCTGCAT	o||||o||||||||||	CCTCTCTTAGGACTACTACGACGTCGTAAACG	DM2 DM3 DT2 TM3 TT3	3.62	2.04	0.47	1.62
bna-miR393	BnaC02g36370D	AUXIN SIGNALING F-BOX 2[10]	2591	TCCAAAGGGATCGCATTGATC	||||||||||||||||||	CTGTAGGTTTCCCTAGCGTAACAAAGTATGAA	DM2 DM3 DT2 DT3 TM3 TT3	7.08	2.00	5.77	8.70
bna-miR393	BnaA02g28290D	AUXIN SIGNALING F-BOX 2[10]	2531	TCCAAAGGGATCGCATTGATC	||||||||||||||||||	CTGTAGGTTTCCCTAGCGTAACAAAGTATGAA	DM2 DM3 DT2 DT3 TM3 TT3	7.08	2.00	5.77	8.70
bna-miR393	BnaC08g40890D	AUXIN SIGNALING F-BOX 3[11]	2468	TCCAAAGGGATCGCATTGATC	|||||||||||||||||||	CTGTAGGTTTCCCTAGCGTAACAAGACATGAA	DM3 DT3 TM3 TT3	2.63	4.63	9.30	12.08
bna-miR393	BnaA08g24570D	AUXIN SIGNALING F-BOX 3[11]	2640	TCCAAAGGGATCGCATTGATC	||||||||||||||||||	CTGTAGGTTTCCCTAGCGTAACAAAGCATGAA	DM3 DT3 TM3 TT3	2.63	4.63	9.30	12.08
bra-miR398	BnaA04g16310D	Superoxide dismutase [Cu-Zn], chloroplastic[12]	776	TGTGTTCTCAGGTCACCCCTG	||| |||o||||||||| oo	TATTACA-AAGGGTCCAGTGGGCGTACTGCCT	DM2 TM3 TT3	3.42	0.00	1.35	0.23
bna-miR403	BnaCnng68320D	ARGONAUTE 2[13]	3030	TTAGATTCACGCACAAACTCG	||||||||||||||||||	GGTTAATCTAAGTGCGTGTTTGAGGAACTCTA	DM1 DM3 DT1 DT2 DT3 TM2 TM3 TT3	62.32	9.04	9.78	5.46
bna-miR403	BnaA05g14760D	ARGONAUTE 2[13]	3378	TTAGATTCACGCACAAACTCG	||||||||||||||||||	GGTTAATCTAAGTGCGTGTTTGAGGAAAGATG	DM1 TM3 TT3	0.03	0.00	0.82	2.55

[a] *Brassica napus* miRNA identified in sRNAseq and PAREseq data

SPL = SQUAMOSA PROTEIN-BINDING LIKE; ARF = auxin response factor; SCL = SCARECROW-LIKE; ERF = ethylene-responsive transcription factor;

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Table S10: miRNA:mRNA target pairs involving miRNAs previously unknown in *B. napus* and identified by Shortstack.

						Fragment signatures (rpm)			
miRNA[a]	Target transcript ID	Predicted gene function	Cleavage position	miRNA:mRNA target pair (5'-3' : 3'-5')	Cleavage found in PAREseq replicates	DM	DT	TM	TT
gma-miR156k	BnaA06g36780D	SPL 2[1]	1568	TTGACAGAAGAGAGTGAGCAC |||||||||||||||| |||||| CTTAAACTGTCTTCTCTCTCTCGTGGTAGTTC	DT2 DT3 TT3	0.00	2.04	1.59	3.93
gma-miR156k	BnaCnng61400D	SPL 6[2]	1380	TTGACAGAAGAGAGTGAGCAC o|||||||||||||||||||| ACTCGACTGTCTTCTCTCACTCGTGTTCATAT	DM3 TM3 TT3	1.75	0.00	1.06	1.43
gma-miR156k	BnaA02g14580D	SPL 6[2]	2328	TTGACAGAAGAGAGTGAGCAC o||||||||||||| |||||| ACTCGACTGTCTTCTCTCTCTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21
gma-miR156k	BnaC02g19100D	SPL 6[2]	1039	TTGACAGAAGAGAGTGAGCAC o||||||||||||| |||||| ACTCGACTGTCTTCTCTCTCTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21
gma-miR156k	BnaC02g14000D	SPL 6[2]	2284	TTGACAGAAGAGAGTGAGCAC o||||||||||||| |||||| ACTCGACTGTCTTCTCTCTCTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21
gma-miR156k	BnaA07g27730D	SPL 6[2]	2284	TTGACAGAAGAGAGTGAGCAC o|||||||| ||||||||| ACTCGACTGTCTTCCCTCACTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21
gma-miR156k	BnaC07g11380D	SPL 10[2]	2328	TTGACAGAAGAGAGTGAGCAC |||||||||||||||| |||||| CTTCAACTGTCTTCTCTCTCTCGTGCCACCTT	DM2 DM3 DT2 DT3 TM2 TM3 TT2 TT3	18.84	0.86	14.61	34.85
gma-miR156k	BnaA07g08830D	SPL 10[2]	2414	TTGACAGAAGAGAGTGAGCAC |||||||||||||||| |||||| CTGCAACTGTCTTCTCTCTCTCGTGACATCTT	DM3 DT3 TM2 TM3 TT3	19.51	8.58	33.17	31.01
gma-miR156k	BnaAnng25050D	SPL 11[2]	2414	TTGACAGAAGAGAGTGAGCAC |||||||||||||||| |||||| CTGCAACTGTCTTCTCTCTCTCGTGACATCTT	DM3 DT3 TM2 TM3 TT3	19.51	8.58	33.17	31.01
gma-miR156k	BnaC04g23930D	SPL 15[2]	1039	TTGACAGAAGAGAGTGAGCAC |||||||||||||||| |||||| CTCAAACTGTCTTCTCTCTCTCGTGTCGAACT	DM2 DM3 DT3 TM3 TT3	2.80	3.00	0.82	1.90
ath-miR393	BnaC02g36370D	AUXIN SIGNALING F-BOX 2[3]	2341	TCCAAAGGGATCGCATTGATCC |||||||||||||||||| | | CTGTAGGTTTCCCTAGCGTAACAAAGTATGAA	DM2 DM3 DT2 DT3 TM3 TT3	7.08	4.13	5.77	8.70
ath-miR393	BnaA02g28290D	AUXIN SIGNALING F-BOX 2[3]	2324	TCCAAAGGGATCGCATTGATCC |||||||||||||||||| | | CTGTAGGTTTCCCTAGCGTAACAAAGTATGAA	DM2 DM3 DT2 DT3 TM3 TT3	7.08	4.13	5.77	8.70
ath-miR393	BnaA08g24570D	AUXIN SIGNALING F-BOX 3[4]	1698	TCCAAAGGGATCGCATTGATCC |||||||||||||||||| | | CTGTAGGTTTCCCTAGCGTAACAAAGCATGAA	DM3 DT3 TM3 TT3	2.63	4.63	9.30	12.08
ath-miR393	BnaC08g40890D	AUXIN SIGNALING F-BOX 3[4]	2591	TCCAAAGGGATCGCATTGATCC |||||||||||||||||| | CTGTAGGTTTCCCTAGCGTAACAAGACATGAA	DM3 DT3 TM3 TT3	2.63	4.63	9.30	12.08

[a] miRNA from other species and homologous to miRNA found in the *B. napus* sRNAseq and DEGseq data and identified by ShortStack

SPL = SQUAMOSA PROTEIN-BINDING LIKE

References

1 Rhoades, M. W. *et al.* Prediction of plant MicroRNA targets. *Cell* **110**, 513-520 (2002).

2 Xu, M. *et al.* Developmental Functions of miR156-Regulated SQUAMOSA PROMOTER BINDING PROTEIN-LIKE (SPL) Genes in Arabidopsis thaliana. *PLoS Genet* **12**, e1006263 (2016).

3 Si-Ammour, A. *et al.* miR393 and secondary siRNAs regulate expression of the TIR1/AFB2 auxin receptor clade and auxin-related development of Arabidopsis leaves. *Plant Physiol* **157**, 683-691 (2011).

4 Vidal, E. A. *et al.* Nitrate-responsive miR393/AFB3 regulatory module controls root system architecture in Arabidopsis thaliana. *Proc Natl Acad Sci U S A* **107**, 4477-4482, (2010).

Table S11: miRNA:mRNA target pairs involving miRNA sequences identical to miRNAs previously identified in other species

						Fragment signatures (rpm)			
miRNA[a]	Target transcript ID	Predicted gene function	Cleavage position	miRNA:mRNA target pair (5'-3' : 3'-5')	Cleavage found in PAREseq replicates	DM	DT	TM	TT
gma-miR156q	BnaA06g36780D	SPL 2	3011	TGACAGAAGAGAGTGAGCACT |||||||||||| |||||o3' TTAAACTGTCTTCTCTCTCTCGTGGTAGTTCT	DT2 DT3 TT3	0.00	1.13	0.00	0.37
smo-miR156c	BnaA06g36780D	SPL 2	3012	TTGACAGAAGAAAGAGAGCAC ||||||||||| |||||||||3' CTTAAACTGTCTTCTCTCTCTCGTGGTAGTTC	DT2 DT3 TT3	0.00	2.04	1.59	3.93
gma-miR156q	BnaA04g19840D	SPL 3	560	TGACAGAAGAGAGTGAGCACT ||||||||||||oo|||3' TCTGACTGTCTTCTCTCGTTCGTTTCCGATTT	DM3 DT3 TT3	1.19	3.31	0.00	1.48
gma-miR156q	BnaC04g44230D	SPL 3	619	TGACAGAAGAGAGTGAGCACT ||||||||||||oo|||3' TCTGACTGTCTTCTCTCGTTCGTTTCCCGAAT	DM3 DT3 TT3	1.19	3.31	0.00	1.48
gma-miR156q	BnaA07g27730D	SPL 6	639	TGACAGAAGAGAGTGAGCACT ||||||||||||||||||3' CTCGACTGTCTTCTCTCACTCGTGTTCATCTT	DM3 DT2 DT3	4.50	17.09	0.00	0.00
smo-miR156c	BnaCnng61400D	SPL 6	771	TTGACAGAAGAAAGAGAGCAC o|||||||||| || ||||||3' ACTCGACTGTCTTCTCTCACTCGTGTTCATAT	DM3 TM3 TT3	1.75	0.00	1.06	1.43
smo-miR156c	BnaC02g14000D	SPL 6	1096	TTGACAGAAGAAAGAGAGCAC o|||||||||| |||||||||3' ACTCGACTGTCTTCTCTCTCTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21
smo-miR156c	BnaA02g14580D	SPL 6	1083	TTGACAGAAGAAAGAGAGCAC o|||||||||| |||||||||3' ACTCGACTGTCTTCTCTCTCTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21
smo-miR156c	BnaC02g19100D	SPL 6	1117	TTGACAGAAGAAAGAGAGCAC o|||||||||| |||||||||3' ACTCGACTGTCTTCTCTCTCTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21
smo-miR156c	BnaA07g27730D	SPL 6	640	TTGACAGAAGAAAGAGAGCAC o||||||||| || ||||||3' ACTCGACTGTCTTCCCTCACTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21
gma-miR156q	BnaC02g19100D	SPL 6	1116	TGACAGAAGAGAGTGAGCACT ||||||||||||| ||||||3' CTCGACTGTCTTCTCTCTCTCGTGTTCATCTC	DM3 DT2 DT3 TM3 TT3	4.50	17.09	5.12	4.07
gma-miR156q	BnaA02g14580D	SPL 6	1082	TGACAGAAGAGAGTGAGCACT ||||||||||||| ||||||3' CTCGACTGTCTTCTCTCTCTCGTGTTCATCTC	DM3 DT2 DT3 TM3 TT3	4.50	17.09	5.12	4.07
gma-miR156q	BnaCnng61400D	SPL 6	770	TGACAGAAGAGAGTGAGCACT ||||||||||||||||||||3' CTCGACTGTCTTCTCTCACTCGTGTTCATATT	DM3 DT2 DT3 TM3 TT3	4.50	17.09	5.12	4.07
gma-miR156q	BnaC02g14000D	SPL 6	1095	TGACAGAAGAGAGTGAGCACT ||||||||||||| ||||||3' CTCGACTGTCTTCTCTCTCTCGTGTTCATCTC	DM3 DT2 DT3 TM3 TT3	4.50	17.09	5.12	4.07
gma-miR156q	BnaA07g08830D	SPL 10	1631	TGACAGAAGAGAGTGAGCACT ||||||||||||| |||||||3' TGCAACTGTCTTCTCTCTCTCGTGACATCTTT	DM3 TM3 TT3	5.00	0.00	0.77	3.89
smo-miR156c	BnaC07g11380D	SPL 10	1568	TTGACAGAAGAAAGAGAGCAC ||||||||||| |||||||||3' CTTCAACTGTCTTCTCTCTCTCGTGCCACCTT	DM2 DM3 DT2 DT3 TM2 TM3 TT2 TT3	18.84	0.86	14.61	34.85
smo-miR156c	BnaA07g08830D	SPL 10	1632	TTGACAGAAGAAAGAGAGCAC ||||||||||| |||||||||3' CTGCAACTGTCTTCTCTCTCTCGTGACATCTT	DM3 DT3 TM2 TM3 TT3	19.51	8.58	33.17	31.01
gma-miR156q	BnaC07g11380D	SPL 10	1567	TGACAGAAGAGAGTGAGCACT ||||||||||||| ||||||3' TTCAACTGTCTTCTCTCTCTCGTGCCACCTTA	DM3 DT3 TM3 TT3	0.19	0.27	1.00	2.96
gma-miR156q	BnaAnng25050D	SPL 11	1340	TGACAGAAGAGAGTGAGCACT ||||||||||||| |||||||3' TGCAACTGTCTTCTCTCTCTCGTGACATCTTT	DM3 TM3 TT3	5.00	0.00	0.77	3.89
gma-miR156q	BnaC05g21270D	SPL 11	1690	TGACAGAAGAGAGTGAGCACT ||||||||||||| o||||3' TTCAACTGTCTTCTCTCTTTCGTGCCACCTTT	DM3 DT3 TM3 TT3	0.19	0.27	1.00	3.01
smo-miR156c	BnaAnng25050D	SPL 11	1341	TTGACAGAAGAAAGAGAGCAC ||||||||||| |||||||||3' CTGCAACTGTCTTCTCTCTCTCGTGACATCTT	DM3 DT3 TM2 TM3 TT3	19.51	8.58	33.17	31.01
smo-miR156c	BnaC04g23930D	SPL 15	952	TTGACAGAAGAAAGAGAGCAC ||||||||||| |||||||||3' CTCAAACTGTCTTCTCTCTCTCGTGTCGAACT	DM2 DM3 DT3 TM3 TT3	2.80	3.00	0.82	1.90
gma-miR160b	BnaA07g13830D	ARF 10	1698	TGCCTGGCTCCCTGTATGCC |||||||||||||||| ||3' TCGAACGGACCGAGGGACATAAGGGCGTCCTC	DM3 DT2 DT3 TM2 TM3 TT2 TT3	8.94	12.50	18.38	20.22
gma-miR160b	BnaC01g08330D	ARF 16	2324	TGCCTGGCTCCCTGTATGCC |||||||||||||||| o||3' TAATACGGACCGAGGGACATTTGGGTGCCCTT	DM3 DT2 DT3 TM2 TM3 TT2 TT3	8.06	22.86	18.60	32.45
gma-miR160b	BnaA01g06910D	ARF 16	2341	TGCCTGGCTCCCTGTATGCC |||||||||||||||| o||3' TAATACGGACCGAGGGACATTTGGGTGCCCTT	DM3 DT2 DT3 TM2 TM3 TT2 TT3	8.06	22.86	18.60	32.45
aof-miR393a	BnaA02g28290D	AUXIN SIGNALING F-BOX 2	2531	TCCAAAGGGATCGCATTGATTC |||||||||||||||||| |||3' CTGTAGGTTTCCCTAGCGTAACAAAGTATGAA	DM2 DM3 TM3	7.08	0.00	5.77	0.00
osa-miR393b-5p	BnaC02g36370D	AUXIN SIGNALING F-BOX 2	2591	TCCAAAGGGATCGCATTGATCT |||||||||||||||||| ||3' CTGTAGGTTTCCCTAGCGTAACAA-ATAATGA	DM2 DM3 TM3	7.08	0.00	5.77	0.00
aof-miR393a	BnaC02g36370D	AUXIN SIGNALING F-BOX 2	2591	TCCAAAGGGATCGCATTGATTC |||||||||||||||||| |||3' CTGTAGGTTTCCCTAGCGTAACAAAGTATGAA	DM2 DM3 TM3	7.08	0.00	5.77	0.00
osa-miR393b-5p	BnaA02g28290D	AUXIN SIGNALING F-BOX 2	2531	TCCAAAGGGATCGCATTGATCT |||||||||||||||||| ||3' CTGTAGGTTTCCCTAGCGTAACAA-ATAATGA	DM2 DM3 TM3	7.08	0.00	5.77	0.00
ahy-miR398	BnaA04g16310D	Superoxide dismutase [Cu-Zn], chloroplastic	776	TGTGTTCTCAGGTCACCCCT ||| |||o||||||||| o3' TATTACA-AAGGGTCCAGTGGGCGTACTGCCT	DM2 TM3 TT3	3.42	0.00	1.35	0.23
cas-miR403	BnaCnng68320D	ARGONAUTE 2	3030	TTAGATTCACGCACAAACTCGT ||||||||||||||||||| |3' GGTTAATCTAAGTGCGTGTTTGAGGAACTCTA	DM1 DM3 TM2 TM3	62.32	0.00	9.78	0.00

[a] miRNA in other species identical to miRNA identified in *B. napus* and present in sRNAseq and PAREseq data

SPL = SQUAMOSA PROTEIN-BINDING LIKE; ARF = auxin response factor; SCL = SCARECROW-LIKE; ERF = ethylene-responsive transcription factor;

Table S12: miRNA-like sRNAs found in sRNA:mRNA target pairs

								Fragment signatures (rpm)			
miRNA [a]	miRNA sequence [b]	sRNA found in sRNA:mRNA target pair [c]	Target transcript ID	Predicted gene function	Cleavage position	miRNA:mRNA target pair (5'-3' : 3'-5')	Cleavage found in PAREseq replicates	DM	DT	TM	TT
bra-miR1885b	TACATCTTCTCCGCGGAAGCTC	TACATCTTCTCCGCGGAAGCTCT	BnaCnng44780D	BLOCS2	1380	TACATCTTCTCCGCGGAAGCTCT GCTGAAGTAGACGAGGCGCTTTTGAGAGTCGG	DM2 DM3 DT2 DT3 TM2 TM3 TT2 TT3	32.90	66.25	33.05	116.04
bna-miR403	TTAGATTCACGCACAAACTCG	TTAGATTCACGCACAAACTCA	BnaCnng68320D	ARGONAUTE 2	3030	TTAGATTCACGCACAAACTCA GGTTAATCTAAGTGCGTGTTTGAGGAACTCTA	DM1 DM3 DT1 DT2 DT3 TM2 TM3	62.32	9.04	9.78	0.00
bna-miR156b,c,g	TTGACAGAAGATAGAGAGCAC	TTGACAGAAGATAGAGAGCACT	BnaC07g11380D	SPL 10	1568	TTGACAGAAGATAGAGAGCACT CTTCAACTGTCTTCTCTCTCGTGCCACCTT	DM2 DM3 DT2 DT3 TM2 TM3 TT3	18.84	0.86	14.61	6.66
bra-miR1885b	TACATCTTCTCCGCGGAAGCTC	TACATCTTCTCCGCGGAAGCT	BnaCnng44780D	BLOCS2	1380	TACATCTTCTCCGCGGAAGCT GCTGAAGTAGACGAGGCGCTTTTGAGAGTCGG	DM2 DM3 DT3 TM2 TM3 TT2 TT3	32.90	10.98	33.05	116.04
bna-miR403	TTAGATTCACGCACAAACTCG	TTAGATTCACGCACAAACTC	BnaCnng68320D	ARGONAUTE 2	3030	TTAGATTCACGCACAAACTC GGTTAATCTAAGTGCGTGTTTGAGGAACTCTA	DM1 DM3 DT1 DT3 TM2 TM3	62.32	1.40	9.78	0.00
bna-miR156b,c,g	TTGACAGAAGATAGAGAGCAC	TTGACAGAAGATAGAGAGCACT	BnaC04g23930D	SPL 15	952	TTGACAGAAGATAGAGAGCACT CTCAAACTGTCTTCTCTCTCTCGTGTCGAACT	DM2 DM3 DT3 TM3 TT3	2.80	3.00	0.82	1.90
bna-miR403	TTAGATTCACGCACAAACTCG	TTAGATTCACGCACAAACT	BnaCnng68320D	ARGONAUTE 2	3030	TTAGATTCACGCACAAACT GGTTAATCTAAGTGCGTGTTTGAGGAACTCTA	DM3 DT2 DT3 TM2 TM3	2.50	9.00	9.78	0.00
bna-miR156b,c,g	TTGACAGAAGATAGAGAGCAC	TTGACAGAAGATAGAGAGCACT	BnaA07g08830D	SPL 10	1632	TTGACAGAAGATAGAGAGCACT CTGCAACTGTCTTCTCTCTCTCGTGACATCTT	DM3 DT3 TM2 TM3 TT3	19.51	8.58	33.17	31.01
bna-miR156b,c,g	TTGACAGAAGATAGAGAGCAC	TTGACAGAAGATAGAGAGCACT	BnaAnng25050D	SPL 11	1341	TTGACAGAAGATAGAGAGCACT CTGCAACTGTCTTCTCTCTCGTGACATCTT	DM3 DT3 TM2 TM3 TT3	19.51	8.58	33.17	31.01
bna-miR403	TTAGATTCACGCACAAACTCG	TTAGATTCACGCACAAACTCT	BnaCnng68320D	ARGONAUTE 2	3030	TTAGATTCACGCACAAACTCT GGTTAATCTAAGTGCGTGTTTGAGGAACTCTA	DM1 DM3 TM2 TM3	62.32	0.00	9.78	0.00
ath-miR393a-5p	TCCAAAGGGATCGCATTGATCC	TCCAAAGGGATCGCATTGATTT	BnaC02g36370D	AUXIN SIGNALING F-BOX 2	2591	TCCAAAGGGATCGCATTGATTT CTGTAGGTTTCCCTAGCGTAAC-AAAGTATGA	DM2 DM3 TM3 TT3	7.08	0.00	5.77	8.70
ath-miR393a-5p	TCCAAAGGGATCGCATTGATCC	TCCAAAGGGATCGCATTGATTTT	BnaA02g28290D	AUXIN SIGNALING F-BOX 2	2531	TCCAAAGGGATCGCATTGATTTT CTGTAGGTTTCCCTAGCGTAAC-AAAGTATGA	DM2 DM3 TM3 TT3	7.08	0.00	5.77	8.70
ath-miR393a-5p	TCCAAAGGGATCGCATTGATCC	TCCAAAGGGATCGCATTGATTTT	BnaC02g36370D	AUXIN SIGNALING F-BOX 2	2591	TCCAAAGGGATCGCATTGATTTT CTGTAGGTTTCCCTAGCGTAAC-AAAGTATGA	DM2 DM3 TM3 TT3	7.08	0.00	5.77	8.70
ath-miR393a-5p	TCCAAAGGGATCGCATTGATCC	TCCAAAGGGATCGCATTGATTT	BnaA02g28290D	AUXIN SIGNALING F-BOX 2	2531	TCCAAAGGGATCGCATTGATTT CTGTAGGTTTCCCTAGCGTAAC-AAAGTATGA	DM2 DM3 TM3 TT3	7.08	0.00	5.77	8.70
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC05g45520D	unknown	4343	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCCCAAATCCCAAATCTC	DM2 DM3 TM2	14.17	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC01g37940D	ABC TRANSPORTER C FAMILY MEMBER 6	5485	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCTCAAATCCCAAATCTC	DM2 DM3 TM2	5.51	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC03g09670D	probable SULFATE TRANSPORTER 3.5	5213	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCTCAAATCCCAAATCCC	DM2 DM3 TM2	14.17	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC09g45640D	ASPARTIC PROTEASE IN GUARD CELL 2	352	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCTCAAATCCCAAATCCC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC03g50960D	FLC EXPRESSOR	549	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCCCAAATTTCAAATCCC	DM2 DM3 TM2	12.04	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC08g24620D	ASPARTATE-TRNA LIGASE 2, cytoplasmic	1361	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCTCAAATCCCAAATTCC	DM2 DM3 TM2	14.17	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC07g04220D	unknown	1300	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCTCAATTCCCCACCCAA	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC04g50800D	JASMONIC ACID-AMIDO SYNTHETASE JAR1	2484	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCCTAAATCTCAAATCTC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC09g14920D	NADPH-DEPENDENT CODEINONE REDUCTASE 1-2	2030	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCCCAAATCTCAAATCCC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC03g11870D	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG 12	1594	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCCCAAATCTCAAATCCC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaCnng40640D	probable PROTEIN PHOSPHATASE 2C 65	86	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATTTTAAATCCCAAATCCT	DM2 DM3 TM2	17.23	0.00	0.16	0.00

stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC03g70840D	uncharacterized protein at4g26485	1266	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCTCAAATCCCAAATTCC	DM2 DM3 TM2	14.17	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaCnng53590D	FRUCTOSE-1,6-BISPHOSPHATASE, cytosolic	2962	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCCCAAATCTCAAATCTC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC06g28920D	HISTONE-LYSINE N-METHYLTRANSFERASE, H3 lysine-9 specific SUVH7	427	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCCCAAATCCCAAATCCC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC05g17240D	UDP-GLYCOSYLTRANSFERASE 72B3	2528	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCCCAAATCTCAAATCCC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC07g33840D	unknown	534	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCCCAAATCCCAAATCCT	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC09g14510D	SPLICING FACTOR U2AF large subunit B	2134	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCCCAAATCTCAAATCCC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC04g21710D	F-BOX/KELCH-repeat protein AT3G61590	3241	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCGCAAATCTCAAATCCC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC09g16870D	Histone-lysine n-methyltransferase ATXR7	558	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCCCAAATCTCAAATCTC	DM2 DM3 TM2	12.04	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC08g20210D	Toll/interleukin-1 receptor-like protein	1829	TTTAGGGTTTAGGGTTTAGAGTT TCTCAAATCTCAAATCCTAAATCCTAAATTTC	DM2 DM3 TM2	17.23	0.00	4.93	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC08g03760D	PTO-INTERACTING PROTEIN 1	337	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCCCAAATCCCAAATCCC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC05g16440D	unknown	528	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCCCAAATCTCAAATCCC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC08g43030D	EPSIN	1184	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCTCAAATCCCAAATCCC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC01g32070D	unknown	2296	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCCCAAATCTCAAATCCC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC07g21320D	PURPLE ACID PHOSPHATASE 7	5825	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCTCAAATCCCAAATCCC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC04g30340D	15.7 kda heat shock protein, peroxisomal	357	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCCCAAATCTCAAATCCT	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC02g08880D	unknown	708	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCTCAAATCCCAAATTCC	DM2 DM3 TM2	14.17	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC06g18020D	unknown	517	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCTAAAATCCCAAATCCC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC06g20530D	SYNAPTONEMAL COMPLEX 2	5207	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCTCAAATCCCAAATCTA	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC05g30190D	LINOLEATE 9S-LIPOXYGENASE 5, chloroplastic	3792	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCTAAAATCCCAAATCCC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC06g06260D	uncharacterized protein At1g24485	4115	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATTCCAAATCTCAAATACC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaCnng10820D	unknown	5333	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCCCAAATCTTAACTCTT	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaA10g01220D	Histone-lysine n-methyltransferase MEDEA	2903	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCTCAAATCCCAAATCCC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC07g18670D	ALPHA-GLUCAN WATER DIKINASE 2	1317	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCCCAAATCTCAAATCTC	DM2 DM3 TM2	12.04	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC01g10210D	CALCINEURIN B-LIKE PROTEIN 1	1463	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATCCCAAATCTCAAATCCCAAATCTC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC06g06620D	Proteasome subunit alpha type-5-A	2881	TTTAGGGTTTAGGGTTTAGAGTT TCCCAAATTCCAAATCTCAACTTTTTACTCTA	DM2 DM3 TM2	14.17	0.00	4.14	0.00

stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC07g05560D	Probable disease resistance protein RPP1	1324	TTTAGGGTTTAGGGTTTAGAGTT ||||||||||oo|||||| ||| TCCCAAATCCCAAATTTCAAATCCCAAATCCC	DM2 DM3 TM2	12.04	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC07g01030D	ALPHA-DIOXYGENASE 1	518	TTTAGGGTTTAGGGTTTAGAGTT ||||||||||o|||||| ||| TCCCAAATCCCAAATCTCAAATCCCAAATCCC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC06g12110D	NDR1/HIN1-LIKE 3	1415	TTTAGGGTTTAGGGTTTAGAGTT |||||||||||||||||||||| TCCCAAATCCCAAATCCCAAATCTCAACTCTT	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC09g48090D	FORMIN-LIKE 20	1726	TTTAGGGTTTAGGGTTTAGAGTT |||||||||||||||||||||| TCCCAAATCCCAAATCCCAAATCTCAAATCCC	DM2 DM3 TM2	12.04	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC09g52700D	unknown	1488	TTTAGGGTTTAGGGTTTAGAGTT ||||||||||o|||||| ||| TCCCAAATCCCAAATCTCAAATCCCAAATCCC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC06g27140D	PROTEASE DO-LIKE 4, mitochondrial	621	TTTAGGGTTTAGGGTTTAGAGTT ||||||||||o||||o||| TCCCAAATCCCAAATCTCAAATTCCAAATCCC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC09g43620D	ATP SYNTHASE subunit O, mitochondrial	1382	TTTAGGGTTTAGGGTTTAGAGTT ||||||||||o ||||| ||| TCCCAAATCCCAAATCTAAAATCCCAAATCCC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC08g03730D	unknown	1572	TTTAGGGTTTAGGGTTTAGAGTT ||||||||||||||||||o|| TCCCAAATCCCAAATCCCAAATCTTAAATCCC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC01g04980D	MYOSIN-15	563	TTTAGGGTTTAGGGTTTAGAGTT ||||||||||oo||||o||| TCCCAAATCCCAAATCTTAAATTCCAAATCCC	DM2 DM3 TM2	14.17	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC04g05580D	DA1-RELATED 2	1014	TTTAGGGTTTAGGGTTTAGAGTT |||||||||||||||||||||| TCCCAAATCCCAAATCCCAAATCCCAAATTTT	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC02g23510D	GIBBERELLIN-REGULATED PROTEIN 1	413	TTTAGGGTTTAGGGTTTAGAGTT ||||||||||o||||| o|| TCCCAAATCCCAAATCTCAAATCCTAAATCCC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC03g03580D	Lipoyl synthase, chloroplastic	329	TTTAGGGTTTAGGGTTTAGAGTT ||||||||||o||||| ||| TCCCAAATCCCAAATCTCAAATCCCAAATCCC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC02g10540D	DEHYDRODOLICHYL DIPHOSPHATE SYNTHASE 2	1113	TTTAGGGTTTAGGGTTTAGAGTT |||||||||||||||||o|| TCCCAAATCCCAAATCCCAAATCTTAAATCCC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC06g26670D	LIPOXYGENASE 6, chloroplastic	1004	TTTAGGGTTTAGGGTTTAGAGTT ||||||||||o|||||| ||| TCCCAAATCCCAAATCTCAAATCCCAAATCCC	DM2 DM3 TM2	5.51	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC09g37860D	IMPORTIN-5	1806	TTTAGGGTTTAGGGTTTAGAGTT |||||o|||||o||||||| ||| TCTCAAATCTCAAATTCCAAATCACAAATCTC	DM2 DM3 TM2	17.23	0.00	4.93	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC07g00720D	MONOTHIOL GLUTAREDOXIN-S12, chloroplastic	1162	TTTAGGGTTTAGGGTTTAGAGTT |||||||||||||||||||||| TCCCAAATCCCAAATCCCAAATCCCAAATCTC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaCnng23260D	SUCROSE SYNTHASE 3	1339	TTTAGGGTTTAGGGTTTAGAGTT ||||||||||o|||||| ||| TCCCAAATCCCAAATCTCAAATCCCAAATCCC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC08g31090D	CYTOCHROME P450 76C3	607	TTTAGGGTTTAGGGTTTAGAGTT |||||||||||||||||||||| TCCCAAATCCCAAATCCCAAATCCCAAATCTC	DM2 DM3 TM2	17.23	0.00	0.16	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaCnng17780D	unknown	1371	TTTAGGGTTTAGGGTTTAGAGTT |||||o||||||||||||| ||| TCTCAAATCTCAAATCCCAAATCCCAAATCTC	DM2 DM3 TM2	17.23	0.00	4.93	0.00
stu-miR8005a	TTTAGAGTTTAAGGTTTAGAGTTT	TTTAGGGTTTAGGGTTTAGAGTT	BnaC08g21260D	tRNA-DIHYDROURIDINE(20) SYNTHASE [NAD(P)+]-like	5585	TTTAGGGTTTAGGGTTTAGAGTT |||||||||||||||||||||| TCCCAAATCCCAAATCCCAAATCTCAACTCTT	DM2 DM3 TM2	17.23	0.00	0.16	0.00
ath-miR393a-5p	TCCAAAGGGATCGCATTGATCC	TCCAAAGGGATCGCATTGATTTTT	BnaA02g28290D	AUXIN SIGNALING F-BOX 2	2531	TCCAAAGGGATCGCATTGATTTTT ||||||||||||||||||o | CTGTAGGTTTCCCTAGCGTAACAAAGTATGAA	DM2 DM3 TM3	7.08	0.00	5.77	0.00
ath-miR393a-5p	TCCAAAGGGATCGCATTGATCC	TCCAAAGGGATCGCATTGATTTTT	BnaC02g36370D	AUXIN SIGNALING F-BOX 2	2591	TCCAAAGGGATCGCATTGATTTTT ||||||||||||||||||o | CTGTAGGTTTCCCTAGCGTAACAAAGTATGAA	DM2 DM3 TM3	7.08	0.00	5.77	0.00
ath-miR393a-5p	TCCAAAGGGATCGCATTGATCC	TCCAAAGGGATCGCATTGATT	BnaA02g28290D	AUXIN SIGNALING F-BOX 2	2531	TCCAAAGGGATCGCATTGATT ||||||||||||||||| || CTGTAGGTTTCCCTAGCGTAACAAAGTATGAA	DM2 DM3 TM3	7.08	0.00	5.77	0.00
ath-miR393a-5p	TCCAAAGGGATCGCATTGATCC	TCCAAAGGGATCGCATTGATT	BnaC02g36370D	AUXIN SIGNALING F-BOX 2	2591	TCCAAAGGGATCGCATTGATT ||||||||||||||||| || CTGTAGGTTTCCCTAGCGTAACAAAGTATGAA	DM2 DM3 TM3	7.08	0.00	5.77	0.00
bra-miR398-3p	TGTGTTCTCAGGTCACCCCTG	TGTGTTCTCAGGTCACCCC	BnaA04g16310D	SUPEROXIDE DISMUTASE [CU-ZN], chloroplastic	776	TGTGTTCTCAGGTCACCCC ||| |||o||||||||| TATTACA-AAGGGTCCAGTGGGCGTACTGCCT	DM2 TM3 TT3	3.42	0.00	1.35	0.23
bra-miR1885b	TACATCTTCTCCGCGGAAGCTC	TACATCTTCTCCGCGGAAGCTCT	BnaA06g29450D	BLOCS2	319	TACATCTTCTCCGCGGAAGCTCT | ||||| |||||oo||o||| GTTGAAGTAGACGAGGCGTTTTTGAGACTCGG	DM3 DT2 TT3	0.13	0.18	0.00	0.19
bna-miR160a,b,c,d	TGCCTGGCTCCCTGTATGCCA	TGCCTGGCTCCCTGTATGCCT	BnaA07g13830D	AUXIN RESPONSE FACTOR 10	1698	TGCCTGGCTCCCTGTATGCCT |||||||||||||||| ||o TCGAACGGACCGAGGGACATAAGGGCGTCCTC	DM3 TM2 TM3	8.94	0.00	18.38	0.00

bna-miR160a,b,c,d	TGCCTGGCTCCCTGTATGCCA	TGCCTGGCTCCCTGTATGCCT	BnaA01g06910D	AUXIN RESPONSE FACTOR 16	2341	TGCCTGGCTCCCTGTATGCCT |||||||||||||||| o||o TAATACGGACCGAGGGACATTTGGGTGCCCTT	DM3 TM2 TM3	8.06	0.00	18.60	0.00
bna-miR160a,b,c,d	TGCCTGGCTCCCTGTATGCCA	TGCCTGGCTCCCTGTATGCCT	BnaC01g08330D	AUXIN RESPONSE FACTOR 16	2324	TGCCTGGCTCCCTGTATGCCT |||||||||||||||| o||o TAATACGGACCGAGGGACATTTGGGTGCCCTT	DM3 TM2 TM3	8.06	0.00	18.60	0.00
ath-miR393a-5p	TCCAAAGGGATCGCATTGATCC	TCCAAAGGGATCGCATTGATTTT	BnaC08g40890D	AUXIN SIGNALING F-BOX 3	2468	TCCAAAGGGATCGCATTGATTTT ||||||||||||||||||| ||o| CTGTAGGTTTCCCTAGCGTAAC-AAGACATGA	DM3 TM3 TT3	2.63	0.00	9.30	12.08
ath-miR393a-5p	TCCAAAGGGATCGCATTGATCC	TCCAAAGGGATCGCATTGATTTT	BnaA08g24570D	AUXIN SIGNALING F-BOX 3	2640	TCCAAAGGGATCGCATTGATTTT ||||||||||||||||||| |||o CTGTAGGTTTCCCTAGCGTAAC-AAAGCATGA	DM3 TM3 TT3	2.63	0.00	9.30	12.08
bna-miR156b,c,g	TTGACAGAAGATAGAGAGCAC	TTGACAGAAGATAGAGAGCACT	BnaC02g19100D	SPL 6	1117	TTGACAGAAGATAGAGAGCACT o|||||||||| ||||||||| ACTCGACTGTCTTCTCTCTCTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21
ath-miR393a-5p	TCCAAAGGGATCGCATTGATCC	TCCAAAGGGATCGCATTGATTT	BnaA08g24570D	AUXIN SIGNALING F-BOX 3	2640	TCCAAAGGGATCGCATTGATTT |||||||||||||||||| ||| CTGTAGGTTTCCCTAGCGTAAC-AAAGCATGA	DM3 TM3 TT3	2.63	0.00	9.30	12.08
ath-miR393a-5p	TCCAAAGGGATCGCATTGATCC	TCCAAAGGGATCGCATTGATTT	BnaC08g40890D	AUXIN SIGNALING F-BOX 3	2468	TCCAAAGGGATCGCATTGATTT |||||||||||||||||| |o| CTGTAGGTTTCCCTAGCGTAACAAGACATGAA	DM3 TM3 TT3	2.63	0.00	9.30	12.08
bna-miR156b,c,g	TGACAGAAGAGAGTGAGCAC	TTGACAGAAGATAGAGAGCACT	BnaA02g14580D	SPL 6	1083	TTGACAGAAGATAGAGAGCACT o|||||||||| ||||||||| ACTCGACTGTCTTCTCTCTCTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21
bna-miR156b,c,g	TGACAGAAGAGAGTGAGCAC	TTGACAGAAGATAGAGAGCACT	BnaA07g27730D	SPL 6	640	TTGACAGAAGATAGAGAGCACT o|||||||| || |||||| ACTCGACTGTCTTCCCTCACTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21
bna-miR156b,c,g	TGACAGAAGAGAGTGAGCAC	TTGACAGAAGATAGAGAGCACT	BnaC02g14000D	SPL 6	1096	TTGACAGAAGATAGAGAGCACT o|||||||||| ||||||||| ACTCGACTGTCTTCTCTCTCTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21
bra-miR1885a	CATCAATGAAAGGTATGATTCC	TCAATGAAAGGTATGATTCCC	BnaA09g14980D	Disease resistance protein TAO1	131	TCAATGAAAGGTATGATTCCC ||||||||||||||||||| CAGTAGTTACTTTCCATACTAAGGGAACGAAA	DT2 DT3 TT3	0.00	0.99	0.00	2.87
bra-miR1885a	CATCAATGAAAGGTATGATTCC	TCAATGAAAGGTATGATTCCCT	BnaA09g14980D	Disease resistance protein TAO1	131	TCAATGAAAGGTATGATTCCCT |||||||||||||||||||| CAGTAGTTACTTTCCATACTAAGGGAACGAAA	DT2 DT3 TT3	0.00	0.99	0.00	2.87
bra-miR1885a	CATCAATGAAAGGTATGATTCC	TCAATGAAAGGTATGATTCCCA	BnaA09g14980D	Disease resistance protein TAO1	131	TCAATGAAAGGTATGATTCCCA ||||||||||||||||||| CAGTAGTTACTTTCCATACTAAGGGAACGAAA	DT2 DT3 TT3	0.00	0.99	0.00	2.87
bna-miR156b,c,g	TTGACAGAAGATAGAGAGCAC	TTGACAGAAGATAGAGAGCACT	BnaA06g36780D	SPL 2	3012	TTGACAGAAGATAGAGAGCACT ||||||||||| ||||||||o CTTAAACTGTCTTCTCTCTCTCGTGGTAGTTC	DT2 DT3 TT3	0.00	2.04	1.59	3.93
ath-miR414	TCATCTTCATCATCATCGTCA	TCATCATCGTCATCATTGTGA	BnaC08g30150D	F-BOX/KELCH-repeat protein SKIP20	1162	TCATCATCGTCATCATTGTGA |||||||o||||||o|| CAGTAGTAGTAGTAGTAGCAGGGCGAAAG	TM1 TM2 TT1	0.00	0.00	7.35	172.81

[a] miRNAs from *B. napus* and other species matching the sRNA found in sRNAseq and PAREseq data with mismatches

[b] Nucleotides that are missing the in the relavant sRNA found in PAREse data are indicated in green color

[c] sRNA found in *B. napus* sRNAseq and PAREseq data with mismatches to known miRNAs

SPL = SQUAMOSA PROMOTER-BINDING LIKE; BLOCS 2 = BLOCS2 = BIOGENESIS OF LYSOSOME-RELATED ORGANELLES COMPLEX 1 subunit 2

Table S13: Transcripts cleaved by a miRNA-like sRNA identified by ShortStack

							Fragment signatures (rpm)			
miRNA [a]	miRNA-like [b]	Target transcript ID	Predicted gene function	Cleavage position	miRNA:mRNA target pair (5'-3' : 3'-5')	Cleavage found in PAREseq replicates	DM	DT	TM	TT
bra-miR156a,b,d,f-5p	TTGACAGAAGAGAGCGAGCAC	BnaA06g36780D	SPL 2	3012	TTGACAGAAGATAGAGAGCAC CTTAAACTGTCTTCTCTCTCTCGTGGTAGTTC	DT2 DT3 TT3	0.00	2.04	1.59	3.93
bra-miR156a,b,d,f-5p	TTGACAGAAGAGAGCGAGCAC	BnaA02g14580D	SPL 6	1083	TTGACAGAAGATAGAGAGCAC ACTCGACTGTCTTCTCTCTCTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21
bra-miR156a,b,d,f-5p	TTGACAGAAGAGAGCGAGCAC	BnaCnng61400D	SPL 6	771	TTGACAGAAGATAGAGAGCAC ACTCGACTGTCTTCTCTCACTCGTGTTCATAT	DM3 TM3 TT3	1.75	0.00	1.06	1.43
bra-miR156a,b,d,f-5p	TTGACAGAAGAGAGCGAGCAC	BnaA07g27730D	SPL 6	640	TTGACAGAAGATAGAGAGCAC ACTCGACTGTCTTCCCTCACTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21
bra-miR156a,b,d,f-5p	TTGACAGAAGAGAGCGAGCAC	BnaC02g14000D	SPL 6	1096	TTGACAGAAGATAGAGAGCAC ACTCGACTGTCTTCTCTCTCTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21
bra-miR156a,b,d,f-5p	TTGACAGAAGAGAGCGAGCAC	BnaC02g19100D	SPL 6	1117	TTGACAGAAGATAGAGAGCAC ACTCGACTGTCTTCTCTCTCTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21
bra-miR156a,b,d,f-5p	TTGACAGAAGAGAGCGAGCAC	BnaA07g08830D	SPL 10	1632	TTGACAGAAGATAGAGAGCAC CTGCAACTGTCTTCTCTCTCTCGTGACATCTT	DM3 DT3 TM2 TM3 TT3	19.51	8.58	33.17	31.01
bra-miR156a,b,d,f-5p	TTGACAGAAGAGAGCGAGCAC	BnaC07g11380D	SPL 10	1568	TTGACAGAAGATAGAGAGCAC CTTCAACTGTCTTCTCTCTCTCGTGCCACCTT	DM2 DM3 DT2 DT3 TM2 TM3 TT2 TT3	18.84	0.86	14.61	34.85
bra-miR156a,b,d,f-5p	TTGACAGAAGAGAGCGAGCAC	BnaAnng25050D	SPL 11	1341	TTGACAGAAGATAGAGAGCAC CTGCAACTGTCTTCTCTCTCTCGTGACATCTT	DM3 DT3 TM2 TM3 TT3	19.51	8.58	33.17	31.01
bra-miR156a,b,d,f-5p	TTGACAGAAGAGAGCGAGCAC	BnaC04g23930D	SPL 15	952	TTGACAGAAGATAGAGAGCAC CTCAAACTGTCTTCTCTCTCTCGTGTCGAACT	DM2 DM3 DT3 TM3 TT3	2.80	3.00	0.82	1.90

[a] Known *B. rapa* miRNA homologous to the miRNA-like sRNA found in *B. napus* sRNA sRNAseq and PAREseq data

[b] miRNA-like sRNA present in B. napus but carrying mismatches (highlighted in red color) relative to the known bra-miRNA

SPL = SQUAMOSA PROTEIN-BINDING LIKE

Table S14: New mRNA targets of known miRNAs

						Fragment signatures (rpm)			
miRNA[a]	Transcript ID	Predicted gene function	Cleavage position	miRNA:mRNA target pair (5'-3' : 3'-5')	Cleavage found in PAREseq replicates	DM	DT	TM	TT
bra-miR1885b	BnaCnng44780D	BLOCS 2	1380	TACATCTTCTCCGCGGAAGCTC GCTGAAGTAGACGAGGCGCTTTTGAGAGTCGG	DM2 DM3 DT2 DT3 TM2 TM3 TT2 TT3	32.90	66.25	33.05	116.04
bra-miR1885b	BnaA06g29450D	BLOCS 2	319	TACATCTTCTCCGCGGAAGCTC GTTGAAGTAGACGAGGCGTTTTTGAGACTCGG	DM3 DT2 TT3	0.13	0.18	0.00	0.19
Bna-miRC23a-3	BnaA07g28290D	Cytochrome c oxidase assembly protein COX19	996	TATCTACTGCTTATGCCACCA GTCTGTATAGGACGAA-ACGGTAGTTCAAGGA	DM2 DM3 TM2 TM3 TT3	0.26	0.00	0.22	0.32
bna-miR6030	BnaA02g16970D	unknown	984	TCCACCCATACCATACAGACCC CTTCAGGTAGGTTTTGT-TGTCTGGGTTGGTT	DM3 DT3 TM2 TM3	0.56	0.59	5.40	0.00

[a] miRNA present in *B. napus* sRNAseq and PAREseq data

BLOCS2 = BIOGENESIS OF LYSOSOME-RELATED ORGANELLES COMPLEX 1 subunit 2

Table S15: Targeting of host mRNA transcripts by miRNAs

miRNA					host mRNA targets								DE target mRNA			
miRNA species	miRNA reads & FC(log2)				Target transcript ID	Predicted gene function	Cleavage position	miRNA:mRNA target pair (5'-3' : 3'-5')	Cleavage found in PAREseq replicates	Fragment signatures (rpm)				mRNA reads & FC(log2)			
	DM	DT	TM	TT						DM	DT	TM	TT	DM	DT	TM	TT
bna-miR403	107384	-1.72	31065	-1.19	BnaCnng68320D	Protein argonaute 2	3030	TTAGATTCACGCACAAACTCG GGTTAATCTAAGTGCGTGTTTGAGGAACTCTA	DM1 DM3 DT1 DT2 DT3 TM2 TM3 TT3	62.32	9.04	9.78	5.46	1200	1.50	1793	1.27
DM_Cluster_11733	907	-1.13	913	-1.70	BnaC07g11380D	SPL 10	1568	TTGACAGAAGAGAGCGAGCAC CTTCAACTGTCTTCTCTCTCTCGTGCCACCTT	DM2 DM3 DT2 DT3 TM2 TM3 TT2 TT3	18.84	0.86	14.61	34.85	363	-0.54	470	-0.34
bna-miR156g	8555	-1.13	11778	-1.65	BnaC07g11380D	SPL 10	1568	TTGACAGAAGATAGAGAGCAC CTTCAACTGTCTTCTCTCTCTCGTGCCACCTT	DM2 DM3 DT2 DT3 TM2 TM3 TT2 TT3	18.84	0.86	14.61	34.85	363	-0.54	470	-0.34
TM_Cluster_40901	2027	-1.23	2789	-1.44	BnaC07g11380D	SPL 10	1568	TTGACAGAAGAGAGTGAGCAC CTTCAACTGTCTTCTCTCTCTCGTGCCACCTT	DM2 DM3 DT2 DT3 TM2 TM3 TT2 TT3	18.84	0.86	14.61	34.85	363	-0.54	470	-0.34
bra-miR1885b	68093	2.29	75658	2.85	BnaCnng44780D	BLOCS 2	1380	TACATCTTCTCCGCGGAAGCTC GCTGAAGTAGACGAGGCGCTTTTGAGAGTCGG	DM2 DM3 DT2 DT3 TM2 TM3 TT2 TT3	32.90	66.25	33.05	116.04	1110	0.44	916	0.64
bna-miR172b	359	-1.72	440	-1.73	BnaC03g26480D	ERF RAP2-7	2328	GGAATCTTGATGATGCTGCAT AATCTCTTAGGACTACTACGACG-ACGTTGAC	DM2 DM3 DT2 DT3 TM2 TM3 TT3	16.60	10.03	14.48	6.66	815	-0.39	1202	0.43
bna-miR172a	591	-1.02	477	-0.70	BnaC09g13430D	ERF RAP2-7	1039	AGAATCTTGATGATGCTGCAT AATCTCTTAGGACTACTACGACG-ACGTTGAC	DM2 DM3 DT2 DT3 TM2 TM3 TT3	16.60	10.03	14.48	6.66	652	0.30	3166	-1.57
bna-miR172a	591	-1.02	477	-0.70	BnaA03g22100D	ERF RAP2-7	2284	AGAATCTTGATGATGCTGCAT AATCTCTTAGGACTACTACGACG-ACGTTGAC	DM2 DM3 DT2 DT3 TM2 TM3 TT3	16.60	10.03	14.48	6.66	413	0.53	317	1.04
bna-miR172b	359	-1.72	440	-1.73	BnaA03g22100D	ERF RAP2-7	2284	GGAATCTTGATGATGCTGCAT AATCTCTTAGGACTACTACGACG-ACGTTGAC	DM2 DM3 DT2 DT3 TM2 TM3 TT3	16.60	10.03	14.48	6.66	413	0.53	317	1.04
bna-miR172a	591	-1.02	477	-0.70	BnaC03g26480D	ERF RAP2-7	2328	AGAATCTTGATGATGCTGCAT AATCTCTTAGGACTACTACGACG-ACGTTGAC	DM2 DM3 DT2 DT3 TM2 TM3 TT3	16.60	10.03	14.48	6.66	815	-0.39	1202	0.43
bna-miR172b	359	-1.72	440	-1.73	BnaC04g15640D	ERF RAP2-7	2414	GGAATCTTGATGATGCTGCAT AATCTCTTAGGACTACTACGACG-ACGTTGAC	DM2 DM3 DT2 DT3 TM2 TM3 TT3	16.60	10.03	14.48	6.66	1538	0.78	45574	-1.74
bna-miR172a	591	-1.02	477	-0.70	BnaC04g15640D	ERF RAP2-7	2414	AGAATCTTGATGATGCTGCAT AATCTCTTAGGACTACTACGACG-ACGTTGAC	DM2 DM3 DT2 DT3 TM2 TM3 TT3	16.60	10.03	14.48	6.66	1538	0.78	45574	-1.74
bna-miR172b	359	-1.72	440	-1.73	BnaC09g13430D	ERF RAP2-7	1039	GGAATCTTGATGATGCTGCAT AATCTCTTAGGACTACTACGACG-ACGTTGAC	DM2 DM3 DT2 DT3 TM2 TM3 TT3	16.60	10.03	14.48	6.66	652	0.30	3166	-1.57
bna-miR160c	12249	-1.03	11890	-0.98	BnaA01g06910D	ARF 16	2341	TGCCTGGCTCCCTGTATGCCA TAATACGGACCGAGGGACATTTGGGTGCCCTT	DM3 DT2 DT3 TM2 TM3 TT2 TT3	8.06	22.86	18.60	32.45	395	0.60	647	1.21
bna-miR160c	12249	-1.03	11890	-0.98	BnaC01g08330D	ARF 16	2324	TGCCTGGCTCCCTGTATGCCA TAATACGGACCGAGGGACATTTGGGTGCCCTT	DM3 DT2 DT3 TM2 TM3 TT2 TT3	8.06	22.86	18.60	32.45	730	0.52	685	0.79
bna-miR160c	12249	-1.03	11890	-0.98	BnaA07g13830D	ARF 10	1698	TGCCTGGCTCCCTGTATGCCA TCGAACGGACCGAGGGACATAAGGGCGTCCTC	DM3 DT2 DT3 TM2 TM3 TT2 TT3	8.94	12.50	18.38	20.22	1006	-0.63	717	0.01
ath-miR393b-5p	15380	-0.14	15066	-0.54	BnaC02g36370D	Protein AUXIN SIGNALING F-BOX 2	2591	TCCAAAGGGATCGCATTGATCC CTGTAGGTTTCCCTAGCGTAACAAAGTATGAA	DM2 DM3 DT2 DT3 TM3 TT3	7.08	4.13	5.77	8.70	1128	0.35	1232	0.12
ath-miR393b-5p	15380	-0.14	15066	-0.54	BnaA02g28290D	Protein AUXIN SIGNALING F-BOX 2	2531	TCCAAAGGGATCGCATTGATCC CTGTAGGTTTCCCTAGCGTAACAAAGTATGAA	DM2 DM3 DT2 DT3 TM3 TT3	7.08	4.13	5.77	8.70	664	0.50	860	0.24
bna-miR172b	359	-1.72	440	-1.73	BnaA10g12950D	AP2-like ERF TOE2	2933	GGAATCTTGATGATGCTGCAT ACACTCTTAGGACTACTACGACGTAAACTCTC	DM3 DT2 DT3 TM2 TM3 TT3	0.75	5.00	11.14	9.95	297	0.33	443	-0.04
bna-miR172a	591	-1.02	477	-0.70	BnaA10g12950D	AP2-like ERF TOE2	2933	AGAATCTTGATGATGCTGCAT ACACTCTTAGGACTACTACGACGTAAACTCTC	DM3 DT2 DT3 TM2 TM3 TT3	0.75	5.00	11.14	9.95	297	0.33	443	-0.04
bna-miR172a	591	-1.02	477	-0.70	BnaC09g35430D	AP2-like ERF TOE2	2671	AGAATCTTGATGATGCTGCAT ACACTCTTAGGACTACTACGACGTAAACTATC	DM3 DT2 DT3 TM2 TM3 TT3	0.75	5.00	11.14	9.95	232	0.01	342	-0.22
bna-miR172b	359	-1.72	440	-1.73	BnaC09g35430D	AP2-like ERF TOE2	2671	GGAATCTTGATGATGCTGCAT ACACTCTTAGGACTACTACGACGTAAACTATC	DM3 DT2 DT3 TM2 TM3 TT3	0.75	5.00	11.14	9.95	232	0.01	342	-0.22
bna-miR172a	591	-1.02	477	-0.70	BnaA01g34730D	Floral homeotic protein APETALA 2	1043	AGAATCTTGATGATGCTGCAT CCTCTCTTAGGACTACTACGACGTCGTAAACG	DM2 DM3 DT2 TM3 TT3	3.62	2.04	0.47	1.62	460	-0.44	487	0.12
bna-miR172b	359	-1.72	440	-1.73	BnaA01g34730D	Floral homeotic protein APETALA 2	1043	GGAATCTTGATGATGCTGCAT CCTCTCTTAGGACTACTACGACGTCGTAAACG	DM2 DM3 DT2 TM3 TT3	3.62	2.04	0.47	1.62	460	-0.44	487	0.12
DM_Cluster_11733	907	-1.13	913	-1.70	BnaC04g23930D	SPL 15	952	TTGACAGAAGAGAGCGAGCAC CTCAAACTGTCTTCTCTCTCTCGTGTCGAACT	DM2 DM3 DT3 TM3 TT3	2.80	3.00	0.82	1.90	206	-0.32	65	-0.83
TM_Cluster_40901	2027	-1.23	2789	-1.44	BnaC04g23930D	SPL 15	952	TTGACAGAAGAGAGTGAGCAC CTCAAACTGTCTTCTCTCTCTCGTGTCGAACT	DM2 DM3 DT3 TM3 TT3	2.80	3.00	0.82	1.90	206	-0.32	65	-0.83

bna-miR393	190	-2.00	269	-2.10	BnaC02g36370D	Protein AUXIN SIGNALING F-BOX 2	2591	TCCAAAGGGATCGCATTGATC CTGTAGGTTTCCCTAGCGTAACAAAGTATGAA	DM2 DM3 DT3 TM3 TT3	7.08	2.00	5.77	8.70	1128	0.35	1232	0.12
bna-miR156g	8555	-1.13	11778	-1.65	BnaC04g23930D	SPL 15	952	TTGACAGAAGATAGAGAGCAC CTCAAACTGTCTTCTCTCTCTCGTGTCGAACT	DM2 DM3 DT3 TM3 TT3	2.80	3.00	0.82	1.90	206	-0.32	65	-0.83
bna-miR393	190	-2.00	269	-2.10	BnaA02g28290D	Protein AUXIN SIGNALING F-BOX 2	2531	TCCAAAGGGATCGCATTGATC CTGTAGGTTTCCCTAGCGTAACAAAGTATGAA	DM2 DM3 DT3 TM3 TT3	7.08	2.00	5.77	8.70	664	0.50	860	0.24
Bna-miRC23a-3	418	-0.13	573	0.60	BnaA07g28290D	Cytochrome c oxidase assembly protein COX19	996	TATCTACTGCTTATGCCACCA o GTCTGTATAGGACGAA-ACGGTAGTTCAAGGA	DM2 DM3 TM2 TM3 TT3	0.26	0.00	0.22	0.32	735	-0.40	658	-0.35
bna-miR156d	681	-0.65	436	-0.95	BnaC02g19100D	SPL 6	1116	TGACAGAAGAGAGTGAGCAC CTCGACTGTCTTCTCTCTCTCGTGTTCATCTC	DM3 DT2 DT3 TM3 TT3	4.50	17.09	5.12	4.07	329	-0.27	316	0.23
bna-miR156d	681	-0.65	436	-0.95	BnaC02g14000D	SPL 6	1095	TGACAGAAGAGAGTGAGCAC CTCGACTGTCTTCTCTCTCTCGTGTTCATCTC	DM3 DT2 DT3 TM3 TT3	4.50	17.09	5.12	4.07	119	-0.15	150	0.01
bna-miR156d	681	-0.65	436	-0.95	BnaCnng61400D	SPL 6	770	TGACAGAAGAGAGTGAGCAC CTCGACTGTCTTCTCTCACTCGTGTTCATATT	DM3 DT2 DT3 TM3 TT3	4.50	17.09	5.12	4.07	509	-0.62	401	-0.05
bna-miR171a	796	2.20	753	1.93	BnaAnng18550D	Scarecrow-like protein 6	840	TTGAGCCGTGCCAATATCACG AACTAACTCGGCGCGGTTATAGGGGACACGGT	DM3 DT2 DT3 TM3 TT3	4.13	4.22	5.30	0.97	1895	-0.60	1146	-0.25
bna-miR171a	796	2.20	753	1.93	BnaAnng18540D	Scarecrow-like protein 6	851	TTGAGCCGTGCCAATATCACG AACTAACTCGGCGCGGTTATAGGGGACACGGT	DM3 DT2 DT3 TM3 TT3	4.13	4.22	5.30	0.97	2152	-0.61	1286	-0.23
bna-miR156d	681	-0.65	436	-0.95	BnaA02g14580D	SPL 6	1082	TGACAGAAGAGAGTGAGCAC CTCGACTGTCTTCTCTCTCTCGTGTTCATCTC	DM3 DT2 DT3 TM3 TT3	4.50	17.09	5.12	4.07	197	-0.16	227	0.12
bna-miR156g	8555	-1.13	11778	-1.65	BnaAnng25050D	SPL 11	1341	TTGACAGAAGATAGAGAGCAC CTGCAACTGTCTTCTCTCTCTCGTGACATCTT	DM3 DT3 TM2 TM3 TT3	19.51	8.58	33.17	31.01	68	0.70	73	0.71
TM_Cluster_40901	2027	-1.23	2789	-1.44	BnaAnng25050D	SPL 11	1341	TTGACAGAAGAGAGTGAGCAC CTGCAACTGTCTTCTCTCTCTCGTGACATCTT	DM3 DT3 TM2 TM3 TT3	19.51	8.58	33.17	31.01	68	0.70	73	0.71
DM_Cluster_11733	907	-1.13	913	-1.70	BnaA07g08830D	SPL 10	1632	TTGACAGAAGAGAGCGAGCAC CTGCAACTGTCTTCTCTCTCTCGTGACATCTT	DM3 DT3 TM2 TM3 TT3	19.51	8.58	33.17	31.01	341	-0.61	213	0.57
TM_Cluster_40901	2027	-1.23	2789	-1.44	BnaA07g08830D	SPL 10	1632	TTGACAGAAGAGAGTGAGCAC CTGCAACTGTCTTCTCTCTCTCGTGACATCTT	DM3 DT3 TM2 TM3 TT3	19.51	8.58	33.17	31.01	341	-0.61	213	0.57
bna-miR156g	8555	-1.13	11778	-1.65	BnaA07g08830D	SPL 10	1632	TTGACAGAAGATAGAGAGCAC CTGCAACTGTCTTCTCTCTCTCGTGACATCTT	DM3 DT3 TM2 TM3 TT3	19.51	8.58	33.17	31.01	341	-0.61	213	0.57
DM_Cluster_11733	907	-1.13	913	-1.70	BnaAnng25050D	SPL 11	1341	TTGACAGAAGAGAGCGAGCAC CTGCAACTGTCTTCTCTCTCTCGTGACATCTT	DM3 DT3 TM2 TM3 TT3	19.51	8.58	33.17	31.01	68	0.70	73	0.71
bna-miR171a	796	2.20	753	1.93	BnaC04g22080D	Scarecrow-like protein 22	816	TTGAGCCGTGCCAATATCACG AACTAACTCGGCGCGGTTATAGGGAACGCGCT	DM3 DT2 TM3 TT3	14.50	4.53	1.06	0.60	1330	-0.97	568	0.05
bna-miR6030	2879	-0.09	3092	-0.17	BnaA02g16970D	unknown	984	TCCACCCATACCATACAGACCC CTTCAGGTAGGTTTTGT-TGTCTGGGTTGGTT	DM3 DT3 TM2 TM3	0.56	0.59	5.40	0.00	3328	-0.78	1502	-0.72
ath-miR393b-5p	15380	-0.14	15066	-0.54	BnaA08g24570D	Protein AUXIN SIGNALING F-BOX 3	2640	TCCAAAGGGATCGCATTGATCC CTGTAGGTTTCCCTAGCGTAACAAAGCATGAA	DM3 DT3 TM3 TT3	2.63	4.63	9.30	12.08	2530	-0.19	2985	0.31
ath-miR393b-5p	15380	-0.14	15066	-0.54	BnaC08g40890D	Protein AUXIN SIGNALING F-BOX 3	2468	TCCAAAGGGATCGCATTGATCC CTGTAGGTTTCCCTAGCGTAACAAGACATGAA	DM3 DT3 TM3 TT3	2.63	4.63	9.30	12.08	2634	0.55	3065	0.56
bna-miR156d	681	-0.65	436	-0.95	BnaC05g21270D	SPL 11	1690	TGACAGAAGAGAGTGAGCAC TTCAACTGTCTTCTCTCTTTCGTGCCACCTTT	DM3 DT3 TM3 TT3	0.19	0.27	1.00	3.01	521	-0.73	346	0.50
bna-miR393	190	-2.00	269	-2.10	BnaC08g40890D	Protein AUXIN SIGNALING F-BOX 3	2468	TCCAAAGGGATCGCATTGATC CTGTAGGTTTCCCTAGCGTAACAAGACATGAA	DM3 DT3 TM3 TT3	2.63	4.63	9.30	12.08	2634	0.55	3065	0.56
bna-miR393	190	-2.00	269	-2.10	BnaA08g24570D	Protein AUXIN SIGNALING F-BOX 3	2640	TCCAAAGGGATCGCATTGATC CTGTAGGTTTCCCTAGCGTAACAAAGCATGAA	DM3 DT3 TM3 TT3	2.63	4.63	9.30	12.08	2530	-0.19	2985	0.31
bna-miR156d	681	-0.65	436	-0.95	BnaC07g11380D	SPL 10	1567	TGACAGAAGAGAGTGAGCAC TTCAACTGTCTTCTCTCTCGTGCCACCTTA	DM3 DT3 TM3 TT3	0.19	0.27	1.00	2.96	363	-0.54	470	-0.34
bna-miR403	107384	-1.72	31065	-1.19	BnaA05g14760D	Protein argonaute 2	3378	TTAGATTCACGCACAAACTCG GGTTAATCTAAGTGCGTGTTTGAGGAAAGATG	DM1 TM3 TT3	0.03	0.00	0.82	2.55	255	2.60	378	3.13
bra-miR398-3p	128022	4.09	73186	4.34	BnaA04g16310D	Superoxide dismutase [Cu-Zn], chloroplastic	776	TGTGTTCTCAGGTCACCCCTG TATTACA-AAGGGTCCAGTGGGCGTACTGCCT	DM2 TM3 TT3	3.42	0.00	1.35	0.23	259	2.75	10832	0.67
bna-miR156d	681	-0.65	436	-0.95	BnaA07g27730D	SPL 6	639	TGACAGAAGAGAGTGAGCAC CTCGACTGTCTTCTCTCACTCGTGTTCATCTT	DM3 DT2 DT3	4.50	17.09	0.00	0.00	149	-0.17	308	0.33
bra-miR1885b	68093	2.29	75658	2.85	BnaA06g29450D	BLOCS 2	319	TACATCTTCTCCGCGGAAGCTC GTTGAAGTAGACGAGGCGTTTTTGAGACTCGG	DM3 DT2 TT3	0.13	0.18	0.00	0.19	79	0.10	113	0.63
bna-miR156d	681	-0.65	436	-0.95	BnaA04g19840D	SPL 3	560	TGACAGAAGAGAGTGAGCAC TCTGACTGTCTTCTCTCGTTCGTTTCCGATTT	DM3 DT3 TT3	1.19	3.31	0.00	1.48	2043	-2.52	210	-0.84

bna-miR156d	681	-0.65	436	-0.95	BnaC04g44230D	SPL 3	619	TGACAGAAGAGAGTGAGCAC ||||||||||||oo|||| TCTGACTGTCTTCTCTCGTTCGTTTCCCGAAT	DM3 DT3 TT3	1.19	3.31	0.00	1.48	153	-1.42	84	-0.83
bna-miR172b	359	-1.72	440	-1.73	BnaA07g12050D	AP2-like ERF TOE3	2227	GGAATCTTGATGATGCTGC-AT o||||o||||||||o|| || CCTCTCTTAGGACTACTACGGCGGTAAGGGTG	DM3 TM2 TT3	1.56	0.00	8.75	0.46	254	-0.25	513	0.08
bna-miR172a	591	-1.02	477	-0.70	BnaA07g12050D	AP2-like ERF TOE3	2227	AGAATCTTGATGATGCTGC-AT |||||o||||||||o|||| CCTCTCTTAGGACTACTACGGCGGTAAGGGTG	DM3 TM2 TT3	1.56	0.00	8.75	0.46	254	-0.25	513	0.08
bna-miR172a	591	-1.02	477	-0.70	BnaC07g16190D	AP2-like ERF TOE3	2185	AGAATCTTGATGATGCTGCAT |||||o|||||||||| CCTCTCTTAGGACTACTACGTCGTCGGTAAGG	DM3 TM2 TT3	1.56	0.00	8.75	0.46	429	-0.24	932	-0.05
TM_Cluster_40901	2027	-1.23	2789	-1.44	BnaCnng61400D	SPL 6	771	TTGACAGAAGAGAGTGAGCAC o||||||||||||||||||| ACTCGACTGTCTTCTCTCACTCGTGTTCATAT	DM3 TM3 TT3	1.75	0.00	1.06	1.43	509	-0.62	401	-0.05
bna-miR156g	8555	-1.13	11778	-1.65	BnaA02g14580D	SPL 6	1083	TTGACAGAAGATAGAGAGCAC o||||||||| |||||||| ACTCGACTGTCTTCTCTCTCTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21	197	-0.16	227	0.12
bna-miR156g	8555	-1.13	11778	-1.65	BnaA07g27730D	SPL 6	640	TTGACAGAAGATAGAGAGCAC o||||||||| || |||||| ACTCGACTGTCTTCCCTCACTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21	149	-0.17	308	0.33
TM_Cluster_40901	2027	-1.23	2789	-1.44	BnaA02g14580D	SPL 6	1083	TTGACAGAAGAGAGTGAGCAC o||||||||||||| |||||| ACTCGACTGTCTTCTCTCTCTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21	197	-0.16	227	0.12
TM_Cluster_40901	2027	-1.23	2789	-1.44	BnaC02g19100D	SPL 6	1117	TTGACAGAAGAGAGTGAGCAC o||||||||||||| |||||| ACTCGACTGTCTTCTCTCTCTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21	329	-0.27	316	0.23
DM_Cluster_11733	907	-1.13	913	-1.70	BnaA07g27730D	SPL 6	640	TTGACAGAAGAGAGCGAGCAC o|||||||||| |||||| ACTCGACTGTCTTCCCTCACTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21	149	-0.17	308	0.33
DM_Cluster_11733	907	-1.13	913	-1.70	BnaC02g14000D	SPL 6	1096	TTGACAGAAGAGAGCGAGCAC o||||||||||||| |||||| ACTCGACTGTCTTCTCTCTCTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21	119	-0.15	150	0.01
DM_Cluster_11733	907	-1.13	913	-1.70	BnaC02g19100D	SPL 6	1117	TTGACAGAAGAGAGCGAGCAC o||||||||||||| |||||| ACTCGACTGTCTTCTCTCTCTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21	329	-0.27	316	0.23
bna-miR156d	681	-0.65	436	-0.95	BnaAnng25050D	SPL 11	1340	TGACAGAAGAGAGTGAGCAC ||||||||||||| |||||| TGCAACTGTCTTCTCTCTCGTGACATCTTT	DM3 TM3 TT3	5.00	0.00	0.77	3.89	68	0.70	73	0.71
DM_Cluster_11733	907	-1.13	913	-1.70	BnaCnng61400D	SPL 6	771	TTGACAGAAGAGAGCGAGCAC o||||||||||||||||||| ACTCGACTGTCTTCTCTCACTCGTGTTCATAT	DM3 TM3 TT3	1.75	0.00	1.06	1.43	509	-0.62	401	-0.05
TM_Cluster_40901	2027	-1.23	2789	-1.44	BnaC02g14000D	SPL 6	1096	TTGACAGAAGAGAGTGAGCAC o||||||||||||| |||||| ACTCGACTGTCTTCTCTCTCTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21	119	-0.15	150	0.01
DM_Cluster_11733	907	-1.13	913	-1.70	BnaA02g14580D	SPL 6	1083	TTGACAGAAGAGAGCGAGCAC o||||||||||||| |||||| ACTCGACTGTCTTCTCTCTCTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21	197	-0.16	227	0.12
bna-miR156g	8555	-1.13	11778	-1.65	BnaC02g19100D	SPL 6	1117	TTGACAGAAGATAGAGAGCAC o||||||||| |||||||| ACTCGACTGTCTTCTCTCTCTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21	329	-0.27	316	0.23
TM_Cluster_40901	2027	-1.23	2789	-1.44	BnaA07g27730D	SPL 6	640	TTGACAGAAGAGAGTGAGCAC o||||||||| |||||||| ACTCGACTGTCTTCCCTCACTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21	149	-0.17	308	0.33
bna-miR156g	8555	-1.13	11778	-1.65	BnaC02g14000D	SPL 6	771	TTGACAGAAGATAGAGAGCAC o||||||||| || |||||| ACTCGACTGTCTTCTCACTCGTGTTCATAT	DM3 TM3 TT3	1.75	0.00	1.06	1.43	509	-0.62	401	-0.05
bna-miR156d	681	-0.65	436	-0.95	BnaA07g08830D	SPL 10	1631	TGACAGAAGAGAGTGAGCAC ||||||||||||| |||||| TGCAACTGTCTTCTCTCTCGTGACATCTTT	DM3 TM3 TT3	5.00	0.00	0.77	3.89	341	-0.61	213	0.57
bna-miR156g	8555	-1.13	11778	-1.65	BnaC02g14000D	SPL 6	1096	TTGACAGAAGATAGAGAGCAC o|||||||||| |||||||| ACTCGACTGTCTTCTCTCTCTCGTGTTCATCT	DM3 TM3 TT3	2.56	0.00	0.94	4.21	119	-0.15	150	0.01
bna-miR156d	681	-0.65	436	-0.95	BnaA06g36780D	SPL 2	3011	TGACAGAAGAGAGTGAGCAC ||||||||||||| |||||| TTAAACTGTCTTCTCTCTCTCGTGGTAGTTCT	DT2 DT3 TT3	0.00	1.13	0.00	0.37	247	-0.41	234	0.38
bna-miR172a	591	-1.02	477	-0.70	BnaCnng39690D	Floral homeotic protein APETALA 2	2233	AGAATCTTGATGATGCTGCAT ||||||o||||||||||| CCTCTCTTAGGACTACTACGACGTCGTAAACG	DT2 DT3 TT3	0.00	0.53	0.71	1.25	485	0.19	639	0.28
TM_Cluster_40901	2027	-1.23	2789	-1.44	BnaA06g36780D	SPL 2	3012	TTGACAGAAGAGAGTGAGCAC |||||||||||||||||| CTTAAACTGTCTTCTCTCTCTCGTGGTAGTTC	DT2 DT3 TT3	0.00	2.04	1.59	3.93	247	-0.41	234	0.38
bna-miR156g	8555	-1.13	11778	-1.65	BnaA06g36780D	SPL 2	3012	TTGACAGAAGATAGAGAGCAC ||||||||||| ||||||||| CTTAAACTGTCTTCTCTCTCTCGTGGTAGTTC	DT2 DT3 TT3	0.00	2.04	1.59	3.93	247	-0.41	234	0.38
DM_Cluster_11733	907	-1.13	913	-1.70	BnaA06g36780D	SPL 2	3012	TTGACAGAAGAGAGCGAGCAC ||||||||||||||| |||||| CTTAAACTGTCTTCTCTCTCTCGTGGTAGTTC	DT2 DT3 TT3	0.00	2.04	1.59	3.93	247	-0.41	234	0.38
bna-miR172b	359	-1.72	440	-1.73	BnaCnng39690D	Floral homeotic protein APETALA 2	2233	GGAATCTTGATGATGCTGCAT o||||o|||||||||| CCTCTCTTAGGACTACTACGACGTCGTAAACG	DT2 DT3 TT3	0.00	0.53	0.71	1.25	485	0.19	639	0.28
bna-miR166f	10405	-3.09	14049	-2.47	BnaC04g10480D	Homeobox-leucine zipper protein ATHB-8	1374	TCGGACCAGGCTTCATCCCCC o||||||||||||||| CTTAGGCCTGGTCCGATGTTGGTGTATTTTCT	DM1 TT1	49.71	0.00	0.00	0.06	108	-1.01	60	-0.04
TM_Cluster_20495	388	0.89	809	1.33	BnaA09g24940D	Formin-like protein 14	4123	TCCAAAGCCTTTCTATGTCTT |||||||||||||| o TGAAAGG-TTCGTAAAGAAACAGTGGCCATAT	DM2 DM3	4.80	0.00	0.00	0.00	130	0.03	324	0.09

TT_Cluster_158092	4303	5.32	3718	4.23	BnaC03g01750D	Pentatricopeptide repeat-containing protein At5g04780	669	AT-CCATTAGTATCAGACGATC CTCTACGGTGATCACAGTCTGTAAGGTTCCCT	DM2 DM3	14.64	0.00	0.00	0.00	1583	-0.80	1121	-0.26
bna-miR172a	591	-1.02	477	-0.70	BnaA08g21860D	Plastocyanin major isoform, chloroplastic	1506	AGAATCTTGATGATGCTGCAT ATGGTCGTGGGACTACTCCG-CGTGTCATCTT	DM2 TT2	6.19	0.00	0.00	32.49	59514	-0.94	37006	0.06
bna-miR168a	11932	-0.46	12265	-0.50	BnaC03g19180D	Flavin-dependent oxidoreductase FOX2	1408	TCGCTTGGTGCAGGTCGGGAA CCTTAGGGAACGAC-TCTGGCCTTTTTCAATC	DM2 TT3	6.19	0.00	0.00	0.14	27	-2.03	1	0.21
bna-miR6030	2879	-0.09	3092	-0.17	BnaA05g35220D	Protein usf	1388	TCCACCCATACCATACAGACCC GTGTAGGTGTGT-TTGTATGTTTGGTGAAACA	DM3 DT2	1.63	1.78	0.00	0.00	5526	-0.43	4177	-0.50
Bna-miRC5-3	6298	0.80	7492	0.23	BnaA10g27170D	Metallothionein-like protein type 2, MT2-22	513	TTATCATCACAACACTAGATC CGGTAATAAT-GTGTTGTAATCTATATAACGT	DM3 DT2	5.44	2.22	0.00	0.00	18693	0.10	35745	-0.15
bna-miR172b	359	-1.72	440	-1.73	BnaC07g16190D	AP2-like ERF TOE3	2185	GGAATCTTGATGATGCTGCAT CCTCTCTTAGGACTACTACGTCGTCGGTAAGG	DM3 TM2	1.56	0.00	8.75	0.00	429	-0.24	932	-0.05
DM_Cluster_72862	1184	-2.45	894	-2.68	BnaA02g05230D	L-ascorbate oxidase	919	TGCACTGCCTCTTCCCTGGCT TTGCACGTGACGGAGAAGGGAAGCAACGAATT	DM3 TM3	1.00	0.00	0.47	0.00	291	-3.54	1237	0.05
bna-miR6030	2879	-0.09	3092	-0.17	BnaA08g24820D	Disease resistance protein RPS5	540	TCCACCCATACCATACAGACCC GATGAGGTGGGTATGGCATATCTGGGTACTAT	DM3 TT3	2.19	0.00	0.00	0.14	775	-0.25	881	-0.41
Bna-miRC5-1	1687	1.15	2129	0.82	BnaC06g43790D	Patellin-1	1513	TGTGTTGTGATGATA-ATCCGA GGAACCACTACACTACTATCTAGGCTTACAAA	DM3 TT3	2.13	0.00	0.00	0.19	6297	1.16	10892	-0.44
bna-miR6030	2879	-0.09	3092	-0.17	BnaC09g10770D	Putative disease resistance protein At1g63350	546	TCCACCCATACCATACAGACCC GATGAGGTGGGTATGGTACCTCTGGGTATTAT	DM3 TT3	2.19	0.00	0.00	0.14	0	-0.09	0	NA
TT_Cluster_99626	82	2.24	129	0.96	BnaA03g47470D	Probable transcriptional regulator SLK3	2843	TTCGGCTTGAGCTCGGTCGCT GACGACGCCGAACTCGACTCGGTAAGTATCGA	DT2 DT3	0.00	3.72	0.00	0.00	176	1.25	316	0.20
bra-miR161-3p	2462	5.83	2802	5.89	BnaA06g39650D	Probable disease resistance RPP8-like protein 2	3040	GTCACTTTCAATGCGTTGATC TTACTAGTGATAGTTTCGTAAC-AGTATGTTT	DT2 DT3	0.00	3.29	0.00	0.00	2510	0.13	1262	-0.44
bna-miR1140	610	-2.58	1448	-2.24	BnaA01g02940D	Stress enhanced protein 1, chloroplastic	536	ACAGCCTAAACCAATCGGAGC CCGCTGTC-GTTTTGGTTGGTATCGCGGTGCT	DT2 TM3	0.00	1.69	0.77	0.00	22908	-0.90	21622	-0.19
bra-miR1885b	68093	2.29	75658	2.85	BnaC01g40310D	Probable disease resistance protein RPP1	198	TACATCTTCTCCGCGGAAGCTC ATGCCTGTAGACGAGGCACCTTCGAGCCTTTC	DT3 TT3	0.00	1.00	0.00	0.19	109	0.50	98	1.04
bna-miR156d	681	-0.65	436	-0.95	BnaC04g23930D	SPL 15	951	TGACAGAAGAGAGTGAGCAC TCAAACTGTCTTCTCTCTCTCGTGTCGAACTC	DT3 TT3	0.00	0.45	0.00	0.19	206	-0.32	65	-0.83
bna-miR156d	681	-0.65	436	-0.95	BnaC03g18800D	SPL 3	706	TGACAGAAGAGAGTGAGCAC CTGAACTGTCTTCTCTCGTTCGTTTCGGACAA	DT3 TT3	0.00	0.64	0.00	0.56	269	-1.04	202	-0.29
bna-miR1140	610	-2.58	1448	-2.24	BnaA07g07430D	unknown	1143	ACAGCCTAAACCAATCGGAGC CTCGTGTCTGGTTTCGTTAGCCTCGACCAACT	DT3 TT3	0.00	0.54	0.00	0.05	35088	0.12	23165	0.00
bna-miR169m	627	-0.01	273	-1.44	BnaA09g36260D	Autophagy-related protein 3	250	TGAGCCA-AAGATGACTTGCCG AGTACTCGGTGTTCTATTCAACTGACTTCTCA	TM3 TT3	0.00	0.00	1.65	0.97	27	0.25	2	-0.34
bna-miR156g	8555	-1.13	11778	-1.65	BnaA04g24340D	SPL 9	2050	TTGACAGAAGATAGAGAGCAC CCTAAACTGTCTTCTCTCTCTCGTGTCAAACT	TM3 TT3	0.00	0.00	0.29	0.09	216	-0.89	102	-0.18
bna-miR6030	2879	-0.09	3092	-0.17	BnaCnng50410D	Probable disease resistance protein At4g14610	63	TCCACCCATACCATACAGACCC GTTGAGGTGGGTATGGCATATTAGGGTATTAT	TM3 TT3	0.00	0.00	0.77	0.14	1	-0.25	2	0.63
bna-miR6030	2879	-0.09	3092	-0.17	BnaCnng64090D	Disease resistance protein RPS5	549	TCCACCCATACCATACAGACCC GTTGAGGTGGGTATGGTATGTTTGGGTTTTGG	TM3 TT3	0.00	0.00	0.77	0.14	234	-0.41	281	-0.41
bna-miR156g	8555	-1.13	11778	-1.65	BnaA07g16180D	Protein NRT1/ PTR FAMILY 5.7	2279	TTGACAGAAGATAGAGAGCAC CTGCGGCTGTTTTCTGCCTCTCGTGCTCCCTC	TM3 TT3	0.00	0.00	1.53	0.23	1962	0.55	1355	-0.82
DM_Cluster_11733	907	-1.13	913	-1.70	BnaA04g24340D	SPL 9	2050	TTGACAGAAGAGAGCGAGCAC CCTAAACTGTCTTCTCTCTCTCGTGTCAAACT	TM3 TT3	0.00	0.00	0.29	0.09	216	-0.89	102	-0.18
bna-miR156g	8555	-1.13	11778	-1.65	BnaC04g48150D	SPL 9	2021	TTGACAGAAGATAGAGAGCAC CCTAAACTGTCTTCTCTCTCTCGTGTCAAACT	TM3 TT3	0.00	0.00	0.29	0.09	140	-0.95	103	0.49
DM_Cluster_11733	907	-1.13	913	-1.70	BnaC04g48150D	SPL 9	2021	TTGACAGAAGAGAGCGAGCAC CCTAAACTGTCTTCTCTCTCTCGTGTCAAACT	TM3 TT3	0.00	0.00	0.29	0.09	140	-0.95	103	0.49
TM_Cluster_40901	2027	-1.23	2789	-1.44	BnaC04g48150D	SPL 9	2021	TTGACAGAAGAGAGTGAGCAC CCTAAACTGTCTTCTCTCTCTCGTGTCAAACT	TM3 TT3	0.00	0.00	0.29	0.09	140	-0.95	103	0.49
TM_Cluster_40901	2027	-1.23	2789	-1.44	BnaA04g24340D	SPL 9	2050	TTGACAGAAGAGAGTGAGCAC CCTAAACTGTCTTCTCTCTCTCGTGTCAAACT	TM3 TT3	0.00	0.00	0.29	0.09	216	-0.89	102	-0.18
DT_Cluster_32516	1168	3.98	94	4.66	BnaC02g04920D	GTP-binding protein TypA/BipA homolog	3262	GCTATGAGATCAAAGGGTTGT GGTCTGATATTC-AGTTACCTCACAGTTCGTG	DM2	13.16	0.00	0.00	0.00	1746	-0.25	2807	-0.69
TT_Cluster_158092	4303	5.32	3718	4.23	BnaC04g55930D	Photosystem I reaction center subunit XI, chloroplastic	1301	ATCCATTAGTATCAGACGATC CTTCTAGGT-ATCATAATGTGTTACTGCTGGG	DM2	4.74	0.00	0.00	0.00	154153	-0.92	72410	-0.28

Bna-miRC5-3	6298	0.80	7492	0.23	BnaCnng24080D	unknown	1713	TTATCATCACAACACTAGATC |o|||||||||||| ||| GTCAAGTAATAATGTTTTGAT-TAGACGAACG	DM2	7.50	0.00	0.00	0.00	1271	-0.44	1322	-0.92
Bna-miRC5-3*	7608	1.26	9375	0.51	BnaA05g32900D	unknown	2034	TCTTGTGTT-GTGATGATAATC ||o||||||||||||| TCAAGGACAGAATCACAACTTTTAGTATGTTT	DM2	11.85	0.00	0.00	0.00	886	0.96	818	0.33
TT_Cluster_31983	71	-0.87	103	-0.41	BnaC02g21170D	Uncharacterized mitochondrial protein	5849	TTTGAGATCTTCTACATGGTA |o||||||| o|||o|| TAGAAGA-TCTAGAAAGAGTACTATGTGGAGT	DM2	2.11	0.00	0.00	0.00	40	0.22	86	-0.34
bol-miR398a-3p	10530	1.57	1850	2.48	BnaA04g16310D	Superoxide dismutase [Cu-Zn], chloroplastic	776	TGTGTTCTCAGGTCACCCCTT |||||o||||||||| o TATTACA-AAGGGTCCAGTGGGCGTACTGCCT	DM2	3.42	0.00	0.00	0.00	259	2.75	10832	0.67
ath-miR158a-3p	2664	0.22	2942	0.53	BnaC04g11790D	Protein disulfide-isomerase like 2-2	2754	TCCCAAATGTAGACAAAGCA ||||||||||||||| TGTTA-GGTTTTCATCTTTTTAGTCCAGTTTG	DM2	4.08	0.00	0.00	0.00	796	0.27	702	0.05
ath-miR158a-3p	2664	0.22	2942	0.53	BnaA05g35030D	Protein disulfide-isomerase 2-3	2932	TCCCAAATGTAGACAAAGCA ||||||||||||||| TGTTA-GGTTTTCATCTTTTTAGTCCAGTTTG	DM2	3.16	0.00	0.00	0.00	283	0.42	296	0.51
bna-miR168a	11932	-0.46	12265	-0.50	BnaAnng29170D	Flavin-dependent oxidoreductase FOX5	1594	TCGCTTGGTGCAGGTCGGGAA || |||||||oo||o|| CCTTAGGGAACGAC-TCTGGCCTTTTTTAATC	DM2	6.19	0.00	0.00	0.00	2733	-1.94	468	-1.91
bna-miR156d	681	-0.65	436	-0.95	BnaCnng60270D	Putative F-box/kelch-repeat protein	1247	TGACAGAAGAGAGTGAGCAC ||||||||| o||| TCTCACTGTCTT-TCTCTTACGTTTTGGAAGA	DM2	8.16	0.00	0.00	0.00	292	0.42	101	0.36
TT_Cluster_158092	4303	5.32	3718	4.23	BnaA03g49900D	unknown	898	ATCCATTAGTATCAGACGATC || |||o|o|||||||| GTAATAAGTAGTTATAGT-TGGTAGTCAAAAT	DM2	0.13	0.00	0.00	0.00	2841	-0.54	1722	0.12
bna-miR156d	681	-0.65	436	-0.95	BnaC08g47240D	Serine/arginine-rich splicing factor RS40	2533	TGACAGAAGAGAGTGAGCAC |||| |||||| o|o||| GTCTTCTGT-TTCTCTGATTTGTGTCCTGTGT	DM2	4.61	0.00	0.00	0.00	1178	0.79	1912	0.02
TM_Cluster_20495	388	0.89	809	1.33	BnaA07g02880D	unknown	613	TCCAAAGCCTTTCTATGTCTT | ||||||||||||o| AAAGAAGTTTCGCAAACAT-CAGGAGTAGGAC	DM2	9.61	0.00	0.00	0.00	8990	0.19	12198	0.89
TM_Cluster_20495	388	0.89	809	1.33	BnaA09g25140D	Formin-like protein 14	4002	TCCAAAGCCTTTCTATGTCTT |||||||||||| o TGAAAGG-TTCGTAAAGAAACAGTGGCCATAT	DM2	3.42	0.00	0.00	0.00	157	-0.50	396	-0.22
TM_Cluster_20495	388	0.89	809	1.33	BnaC08g08440D	Formin-like protein 14	4444	TCCAAAGCCTTTCTATGTCTT |||||||||||| o TGAAAGG-TTCGTAAAGAAACAGTGGTCATAT	DM2	3.42	0.00	0.00	0.00	329	0.20	601	-0.04
TM_Cluster_31773	230	-3.02	282	-2.30	BnaAnng18550D	Scarecrow-like protein 6	843	TGATTGAGCCGCGTCAATATC |||||||||||o|||||| GACAACTAACTCGGCGCGGTTATAGGGGACAC	DM3	2.00	0.00	0.00	0.00	1895	-0.60	1146	-0.25
bna-miR393	190	-2.00	269	-2.10	BnaC03g26040D	Calvin cycle protein CP12-1, chloroplastic	441	TCCAAAGGGATCGCATTGATC ||||||||||| ||o |o| AAGAAGGTTT-CCTAGCCTAGGTGGTCGAAAG	DM3	1.25	0.00	0.00	0.00	26188	-0.31	15773	0.36
bol-miR398a-3p	10530	1.57	1850	2.48	BnaC04g39580D	Superoxide dismutase [Cu-Zn] 2, chloroplastic	1049	TGTGTTCTCAGGTCACCCCTT ||||o||||||||| o CATTACA-AAGGGTCCAGTGGGCGTACTGCCT	DM3	0.50	0.00	0.00	0.00	9215	1.34	8232	0.61
bna-miR171f	250	-3.02	206	-2.82	BnaAnng18550D	Scarecrow-like protein 6	843	TGATTGAGCCGCGCCAATATC ||||||||||||||||||| GACAACTAACTCGGCGCGGTTATAGGGGACAC	DM3	2.00	0.00	0.00	0.00	1895	-0.60	1146	-0.25
bra-miR398-3p	128022	4.09	73186	4.34	BnaC04g39580D	Superoxide dismutase [Cu-Zn] 2, chloroplastic	1049	TGTGTTCTCAGGTCACCCCTG |||||o||||||||| oo CATTACA-AAGGGTCCAGTGGGCGTACTGCCT	DM3	0.50	0.00	0.00	0.00	9215	1.34	8232	0.61
bna-miR160c	12249	-1.03	11890	-0.98	BnaA06g28020D	Ferrochelatase-1, chloroplastic/mitochondrial	1857	TGCCTGGCTCCCTGTATGCCA |||o||||||||o ||| GGTTTC-GATCGAGGGACATGAGGTACAGATA	DM3	2.13	0.00	0.00	0.00	3618	-0.99	4983	-0.82
bra-miR162-5p	777	4.43	893	4.05	BnaC04g28440D	Calmodulin-like protein 9	949	GGAGGCAGCGGTTCATCGATC o||||||||o| |||o| TTATTCTCCGTCGCTA-GTAGTAAAACCTCTT	DM3	1.19	0.00	0.00	0.00	21150	-0.21	15480	-0.74
TM_Cluster_31773	230	-3.02	282	-2.30	BnaAnng18540D	Scarecrow-like protein 6	854	TGATTGAGCCGCGTCAATATC |||||||||||o|||||| GACAACTAACTCGGCGCGGTTATAGGGGACAC	DM3	2.00	0.00	0.00	0.00	2152	-0.61	1286	-0.23
bra-miR161-3p	2462	5.83	2802	5.89	BnaA05g00560D	Probable glutamyl endopeptidase, chloroplastic	3771	GTCACTTTCAATGCGTTGATC ||||||| ||||||| GGCACAG-GAAAGTCACGCAACTTCTTAGACA	DM3	1.81	0.00	0.00	0.00	1644	0.44	1883	-0.19
TM_Cluster_14180	1157	4.24	1274	3.62	BnaC05g12750D	unknown	2844	ATCATGCTATCCCTTTCGATT | ||o||o|||o||o||o CAGAT-GTGCGGTAAGGGAAGTTAGTTTTTTC	DM3	1.88	0.00	0.00	0.00	704	-0.25	718	-0.32
bna-miR171f	250	-3.02	206	-2.82	BnaAnng18540D	Scarecrow-like protein 6	854	TGATTGAGCCGCGCCAATATC ||||||||||||||||||| GACAACTAACTCGGCGCGGTTATAGGGGACAC	DM3	2.00	0.00	0.00	0.00	2152	-0.61	1286	-0.23
DM_Cluster_72862	1184	-2.45	894	-2.68	BnaA08g00080D	Nucleolar protein 56	2111	TGCACTGCCTC-TTCCCTGGCT ||||||||| ||||| || CCGGAGGTGACGGAGGAAGGGAAGGAGTAGAT	DM3	2.44	0.00	0.00	0.00	915	-0.51	1422	-0.27
TT_Cluster_49373	205	0.75	16	0.89	BnaC01g20440D	Acyl-CoA-binding domain-containing protein 2	492	CCGGGTGAAGAT-CTTCAAATC |||| |||||| |||||| TGGAGGCCAAATTCTAAGAAGTTAAGGCCAAG	DM3	2.19	0.00	0.00	0.00	967	0.01	1288	0.19
bna-miR393	190	-2.00	269	-2.10	BnaA03g21770D	Calvin cycle protein CP12-1, chloroplastic	430	TCCAAAGGGATCGCATTGATC |||||||||| ||o |o| AAGAAGGTTT-CCTAGCCTAGGTGGTCGAAAG	DM3	1.25	0.00	0.00	0.00	30535	-0.29	23325	0.41
DM_Cluster_63658	2715	-3.31	1915	-2.16	BnaC07g44720D	Probable E3 ubiquitin ligase SUD1	674	AGCGGAAT-ATAAGAACCTGTTTCT | ||||||||||||||o TCATGGCCTTACTATTCTTGGACAAGTCATTC	DM3	1.50	0.00	0.00	0.00	2	-0.05	0	-0.02
DT_Cluster_32516	1168	3.98	94	4.66	BnaA05g16130D	unknown	139	GCTATGAGATCAAAGGGTTGT || |o||||||||||| CCGCCGCTGCTCTAGTTGCCAATCAAAGTGTT	DT1	0.00	93.47	0.00	0.00	3900	0.58	414	-2.43

DM_Cluster_74956	333	-0.42	288	-0.07	BnaA05g22300D	unknown	287	TCCATTAGTATCAGACGATCT TGTTAGGTAAT-ATGTTCTGAGAGAAGCGGCG	DT2	0.00	1.24	0.00	0.00	12638	-0.64	10065	-0.32
ath-miR399c-3p	1166	4.07	308	2.23	BnaC03g10360D	unknown	500	TGCCAAAGGAGAGTTGCCCTG ATTCAAGGTTACCTCTCAGCTTGACGGGTGTT	DT2	0.00	0.71	0.00	0.00	1325	-1.09	836	0.07
ath-miR393b-5p	15380	-0.14	15066	-0.54	BnaC02g46810D	Chlorophyll a-b binding protein CP26, chloroplastic	1211	TCCAAAGGGATCGCATTGATCC GTTCAGGGTTCCCTAGTTTACCT-GGAGGACC	DT2	0.00	2.93	0.00	0.00	120529	-0.31	70742	-0.17
Bna-miRC5-6	8054	0.26	9232	0.03	BnaC03g06050D	Uncharacterized protein At5g39865	1247	TCGGATTATCATCACAACACT TGGTTGCCTAAT-GTAGTGTAGTGTTGTGTTT	DT2	0.00	3.47	0.00	0.00	1268	0.29	1497	0.51
DM_Cluster_11733	907	-1.13	913	-1.70	BnaA03g50880D	CBS domain-containing protein CBSX2, chloroplastic	139	TTGACAGAAGAGAGCGAGCAC CTTAAACTGTC-TCTCTAGCTTGGGTACTAAT	DT2	0.00	2.13	0.00	0.00	5775	-0.42	3625	-0.16
ath-miR399c-3p	1166	4.07	308	2.23	BnaA03g08160D	unknown	510	TGCCAAAGGAGAGTTGCCCTG ATTCAAGGTTACCTCTCAGCTTGACGGGTGTT	DT2	0.00	0.71	0.00	0.00	989	-0.66	383	-0.04
Bna-miRC5-3*	7608	1.26	9375	0.51	BnaC02g18950D	Cation/calcium exchanger 2	674	TCTTGTGTTGTGATGATAATC ATCGAGAACGCGACTCTAC-ATTGAGGTACAG	DT2	0.00	5.78	0.00	0.00	44	-0.44	42	-0.04
bna-miR160c	12249	-1.03	11890	-0.98	BnaAnng09100D	Zinc finger protein GIS2	1260	TGCCTGGCTCCCTGTA-TGCCA TGCACCGGACCGAGAGACGTCAAGGTCGTGGC	DT2	0.00	2.84	0.00	0.00	2561	0.59	2548	0.19
Bna-miRC5-3*	7608	1.26	9375	0.51	BnaA02g03730D	Cation/calcium exchanger 2	1211	TCTTGTGTTGTGATGATAATC ATCGAGAACGCGACTCTAC-ATTGAGGTACAG	DT2	0.00	5.78	0.00	0.00	60	-0.12	156	-0.40
DM_Cluster_74956	333	-0.42	288	-0.07	BnaA01g17170D	Aspartic proteinase nepenthesin-2	1310	TCCATTAGTATCAGACGATCT TGGCAAGTAGTCGTAGTTTG-TAGGTTGGAAG	DT2	0.00	0.36	0.00	0.00	1133	1.36	3902	0.53
DM_Cluster_20384	1208	-0.60	136	-1.17	BnaC01g11390D	Uncharacterized WD repeat-containing protein C17D11.16	1379	AACCCTCTGATCTCATAGCTC CCGCTTAGGAAACTAGGTTATCGATGTTTTAA	DT2	0.00	4.44	0.00	0.00	381	0.21	601	-0.10
DT_Cluster_99712	303	5.45	306	6.22	BnaA09g25260D	Photosystem I reaction center subunit III, chloroplastic	137	GATGATGCTTGGGATTTATTT TTCTCTACT-CGAAATCTAAAGAAATGTTCTG	DT2	0.00	2.31	0.00	0.00	88880	-0.39	91654	-0.08
DM_Cluster_11733	907	-1.13	913	-1.70	BnaC07g44730D	CBS domain-containing protein CBSX2, chloroplastic	84	TTGACAGAAGAGAGCGAGCAC CTTAAACTGTC-TCTCTAGCTTGGGTAACTAA	DT2	0.00	2.13	0.00	0.00	4431	-0.55	3079	-0.73
bra-miR168a-3p	3941	0.39	3743	-0.22	BnaA02g15710D	Transcription factor TCP22	1126	CCCGCCTTGTATCAAGTGAAT TGTTGGGCGGGACAGGGTTGGCCTATTGAGGG	DT2	0.00	7.11	0.00	0.00	2214	-0.29	1308	-0.20
DM_Cluster_74956	333	-0.42	288	-0.07	BnaA06g02940D	Probable disease resistance protein At1g15890	534	TCCATTAGTATCAGACGATCT GGTAAGGTATTTATGGATTGCAAGAAGGAAGT	DT2	0.00	0.98	0.00	0.00	142	0.36	191	-0.24
TM_Cluster_40901	2027	-1.23	2789	-1.44	BnaA03g50880D	CBS domain-containing protein CBSX2, chloroplastic	139	TTGACAGAAGAGAGTGAGCAC CTTAAACTGTC-TCTCTAGCTTGGGTACTAAT	DT2	0.00	2.13	0.00	0.00	5775	-0.42	3625	-0.16
bna-miR156d	681	-0.65	436	-0.95	BnaC05g38350D	SPL 5	643	TGACAGAAGAGAGTGAGCAC ATCTACTGTCTTCTCTCTCTCGCCAACCCACA	DT3	0.00	1.00	0.00	0.00	134	-0.26	242	-0.74
bra-miR161-3p	2462	5.83	2802	5.89	BnaAnng35590D	Transcription initiation factor TFIID subunit 7	1162	GTCACTTTCAATGCGTTGATC CGTTCAGAGAGAGTTGCGCGACATGTTCGAGG	DT3	0.00	0.59	0.00	0.00	180	-0.06	185	0.34
Bna-miRC5-3*	7608	1.26	9375	0.51	BnaC06g34090D	Toll/interleukin-1 receptor-like protein	1028	TCTTGTGTTGTGATGATAATC GAACAGAACACATCACTACTATT-GATATGAG	DT3	0.00	0.73	0.00	0.00	38	0.20	93	0.81
TT_Cluster_49373	205	0.75	16	0.89	BnaAnng02740D	Nuclear transcription factor Y subunit A-2	1389	CCGGGTGAAGATCTTCAAATC GAAAGGCCTACTTCTTGAAGTCTCAAGACTCT	DT3	0.00	0.05	0.00	0.00	307	-1.22	466	-0.15
bna-miR1140	610	-2.58	1448	-2.24	BnaC01g04200D	Stress enhanced protein 1, chloroplastic	517	ACAGCCTAAACCAATCGGAGC CCGCTGTC-GTTTTGGTTGGTATCGCGGTGCT	DT3	0.00	0.09	0.00	0.00	23010	-0.54	19812	-0.11
ath-miR824-3p	1668	0.27	1940	0.33	BnaC06g07880D	Putative methylesterase 14, chloroplastic	1674	CCTTCT-CATCGATGGTCTAGA AATGGAAGAGGTAGTAACCAGGTTCACCATGT	DT3	0.00	1.41	0.00	0.00	544	0.85	853	0.78
Bna-miRC18	1100	4.32	1708	5.12	BnaA09g10810D	RHOMBOID-like protein 3	1623	TCGCGATCT-TAGATCCTCTAA GACAGAGTTAGAGAACAAGGAGATTATCAGAT	DT3	0.00	0.23	0.00	0.00	2537	0.14	5131	-0.84
bna-miR156d	681	-0.65	436	-0.95	BnaA05g24340D	SPL 5	1905	TGACAGAAGAGAGTGAGCAC ATCTACTGTCTTCTCTCTCTCGCAAACCCACT	DT3	0.00	1.00	0.00	0.00	225	0.35	258	-0.97
bna-miR171a	796	2.20	753	1.93	BnaC08g32280D	unknown	475	TTGAGCCGTG-CCAATATCACG CTCTAGCTCGGTACTGGCTAAGGTGCTCGAGC	DT3	0.00	6.85	0.00	0.00	3015	-0.89	23462	-0.31
Bna-miR168b	10600	0.84	8401	0.90	BnaCnng11330D	DIS3-like exonuclease 2	3782	TTCGCTTGGTGCAGGTCGGGA AGAGAGGCGAGCCACCTC-AGCCATTGTCTGT	DT3	0.00	0.36	0.00	0.00	368	0.91	979	-0.98
TT_Cluster_110546	594	6.07	647	6.37	BnaC07g20110D	DeSI-like protein At4g17486	1007	AGTAGTTCGTTAGGTTTGACC GGACCCGTCAAGGA-TCCAAGTTGGAGTTTGT	DT3	0.00	0.05	0.00	0.00	1304	0.02	1138	-0.04
Bna-miRC5-3*	7608	1.26	9375	0.51	BnaA07g30510D	Toll/interleukin-1 receptor-like protein	1023	TCTTGTGTTGTGATGATAATC GAACAGAACACATCACTACTATT-GATATGAG	DT3	0.00	0.73	0.00	0.00	1	0.39	0	NA
TT_Cluster_79242	173	-0.38	67	-1.00	BnaA01g05240D	Kinesin-like protein NACK2	4543	GGAGCAGAACCAAGTTAGTCT TCTTCTTCTTCTTGGTTTAGTCATCTCGTCTC	DT3	0.00	0.09	0.00	0.00	25	0.07	2114	0.23

Bna-miRC5-2	57	4.51	34	4.49	BnaC08g01880D	Oxygen-evolving enhancer protein 2, chloroplastic	1456	TCAACCAAATACACATTGTGG ||||||||||||||o TTCTAGATGGTTTATAT-TAAAACTTTTTCGG	DT3	0.00	0.05	0.00	0.00	89725	-0.35	80069	0.11
bna-miR156d	681	-0.65	436	-0.95	BnaAnng20610D	unknown	1457	TGACAGAAGAGAGTGAGCAC |||||||o|o||o|| CTCAACTGTGTTCTTTTA-TTTTGTGCTTTAC	TM1	0.00	0.00	0.07	0.00	1158	1.26	150	2.18
bna-miR169m	627	-0.01	273	-1.44	BnaA07g28040D	unknown	1598	TGAG-CCAAAGATGACTTGCCG |||||||||||o||| ACAAGTCAGGTTTCTACTCGACGACTCAAGTC	TM2	0.00	0.00	9.87	0.00	74223	-1.05	69421	-0.68
bna-miR172a	591	-1.02	477	-0.70	BnaA05g05600D	Eukaryotic translation initiation factor 3 subunit F	1481	AGAATCTTGATGATGCTGCAT |o|||||||o||o||o AGGCTTTCAGAA-TACTGCGATGTGGTAGGTA	TM2	0.00	0.00	7.16	0.00	297	0.11	601	-0.21
bra-miR168b-3p	18213	0.54	19036	0.59	BnaC01g40140D	unknown	2680	CCCGCCTTGCATCAACTGAAT |||o||||||||||| GGCCGGGTGG-ACGTCGATGACTAAGTAGGCA	TM2	0.00	0.00	3.18	0.00	704	0.24	851	-0.20
bna-miR156g	8555	-1.13	11778	-1.65	BnaA08g07870D	SH3 domain-containing protein 1	2557	TTGACAGAAGATAGAGAGCAC ||||||||||||||| TTATAA-TGTCTTCTTTGTCTCTTGGGTAGTT	TM2	0.00	0.00	9.23	0.00	1285	-0.04	2171	-0.11
bna-miR6029	23	0.18	89	-0.56	BnaA05g05840D	Ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic	614	TGGGGTTGTGATTTCAGGCTT o|||||||||||||| TCCTGCCGCAACACTCAAGGCC-AAGGGTATC	TM2	0.00	0.00	14.48	0.00	17408	-0.50	4594	-2.46
TM_Cluster_20495	388	0.89	809	1.33	BnaA10g17910D	Glutamine synthetase cytosolic isozyme 1-4	2161	TCCAAAGCCTTTCTATGTCTT ||||||o||||||||| CGTTAGG-TTCGAAGAGATAGCGAAAGAAATA	TM2	0.00	0.00	9.71	0.00	2233	-1.28	1113	-1.44
DM_Cluster_11733	907	-1.13	913	-1.70	BnaA08g07870D	SH3 domain-containing protein 1	2557	TTGACAGAAGAGAGCGAGCAC ||||||||o||||| TTATAA-TGTCTTCTTTGTCTCTTGGGTAGTT	TM2	0.00	0.00	9.23	0.00	1285	-0.04	2171	-0.11
bol-miR398a-3p	10530	1.57	1850	2.48	BnaA03g26510D	Protein TolB {ECO:0000255|HAMAP-Rule:MF_00671}	565	TGTGTTCTCAGGTCACCCCTT o|o||||||oo|||||o GGCGGCGCAAGCGTCTGGTGGTGAGAGAAGAG	TM2	0.00	0.00	11.62	0.00	4814	-0.02	4286	-0.99
bra-miR168b-3p	18213	0.54	19036	0.59	BnaA01g33620D	unknown	2923	CCCGCCTTGCATCAACTGAAT |||o||||||||||| GGCCGGGTGG-ACGTCGATGACTAAGTAGGCA	TM2	0.00	0.00	3.18	0.00	150	0.93	226	-0.59
bna-miR171a	796	2.20	753	1.93	BnaA04g01210D	Scarecrow-like protein 22	668	TTGAGCCGTGCCAATATCACG |||||||o||||||||| CACTAACTCGGCGCGGTTATAGGGAACGCGCT	TM3	0.00	0.00	1.41	0.00	342	-0.73	265	-0.46
ath-miR8175	992	-0.77	1495	-1.66	BnaA06g24600D	Phosphoenolpyruvate carboxykinase [ATP]	930	GATCCCCGGCAACGGCGCCA ||||o|||||||| AAACCGA-GGGCTGTTGCAGCGGTTGCGTGGC	TM3	0.00	0.00	0.53	0.00	1701	2.34	682	-2.30
bol-miR398a-3p	10530	1.57	1850	2.48	BnaA09g47090D	Copper chaperone for superoxide dismutase, chloroplastic/cytosolic	1238	TGTGTTCTCAGGTCACCCCTT |||||o||||||||| GAGATCACAAGGGTCCAGCGGGTTACCGACAG	TM3	0.00	0.00	4.65	0.00	152	1.04	345	0.89
bna-miR393	190	-2.00	269	-2.10	BnaC03g71780D	Thiamine thiazole synthase, chloroplastic	1581	TCCAAAGGGATCGCATTGATC |||||||||o|| |||o| ACCGAGGTTTCCCTGGCAGCACTGGCGTGCTC	TM3	0.00	0.00	1.00	0.00	52131	-0.89	75887	-0.80
Bna-miRC5-1	1687	1.15	2129	0.82	BnaCnng38210D	Probable disease resistance protein RPP1	1187	TGTGTTGTGATGATAATCCGA |||||||o|o|||||||| TAGAACACAACATTGCTATTAGGCTGAGGGCC	TM3	0.00	0.00	0.59	0.00	99	0.54	70	-0.16
bna-miR156g	8555	-1.13	11778	-1.65	BnaC01g36290D	SPL 5	756	TTGACAGAAGATAGAGAGCAC ||||||||||||||||| CATCTACTGTCTTCTATCTCTCGACCACACAA	TM3	0.00	0.00	0.53	0.00	180	-0.81	182	-1.85
TM_Cluster_18741	137	-1.82	238	-1.45	BnaC04g43510D	ATP synthase subunit gamma, mitochondrial	849	TTGAACCCAAGATCTCACCCT o|o|||||o|o|o||||| TTAGGATTTGGGATTTGGGGTGGGAAATTGAG	TM3	0.00	0.00	0.18	0.00	4109	-0.39	2652	-0.11
Bna-miRC5-3	6298	0.80	7492	0.23	BnaC05g24000D	Protein neuralized	2581	TTATCATCA-CAACACTAGATC |o|||||||||||||| AGTAGTAGTAGTAGTAGTGCTCGAGAAATTTA	TM3	0.00	0.00	0.59	0.00	89	-0.69	159	-0.51
TT_Cluster_99626	82	2.24	129	0.96	BnaA03g35150D	F-box/kelch-repeat protein SKIP30	999	TTCGGCTTGAGCTCGGTCGCT o|||||o|o|o||o|||o TTAGGAGCCGAATTTGAGTCTGCGGCTGCGTT	TM3	0.00	0.00	0.41	0.00	572	0.98	876	0.35
bol-miR398a-3p	10530	1.57	1850	2.48	BnaC08g41150D	Copper chaperone for superoxide dismutase, chloroplastic/cytosolic	1295	TGTGTTCTCAGGTCACCCCTT |||||o|||||||| GAGATCACAAGGGTCCAGCGGGTTACCGACAG	TM3	0.00	0.00	4.65	0.00	423	1.41	671	0.86
bra-miR168b-5p	22226	0.73	23408	1.78	BnaA05g26160D	ABC transporter C family member 7	630	TCGCTTGGTGCAGGTCGGGAC |||o|||||o|||| CTGCATCG-ACTACGTCCGGCCCAGTGCGAGG	TM3	0.00	0.00	0.94	0.00	4458	-0.32	4397	-0.53
Bna-miRC5-5	298	-1.49	276	0.50	BnaA05g18000D	unknown	277	TTGGTTTGGATCTTGGAAATC |o|o|||||o|||| CGGTAGCTAAAACTAGAGGCTTT-GCGTCCAA	TM3	0.00	0.00	0.35	0.00	32	-0.93	24	0.15
ath-miR408-5p	192	-1.86	240	-1.88	BnaC09g28020D	Protein NSP-INTERACTING KINASE 2	2953	ACAGGGAACAAGCAGAGCATG ||||||||||||||| GTTCT-TCCCTTTTTCGTCTCGTAGAAAAGAA	TM3	0.00	0.00	0.18	0.00	147	-1.16	114	-1.52
Bna-miRC5-5	298	-1.49	276	0.50	BnaCnng56620D	LOB domain-containing protein 37	730	TTGGTT-TGGATCTTGGAAATC o|||||o||||o|||| CTAGACCAAGATCTCGAACTTTTAGATCTCAC	TM3	0.00	0.00	0.47	0.00	8789	-0.17	7977	0.34
TM_Cluster_25944	18779	-0.56	9010	-0.75	BnaA06g23990D	Protein MADS AFFECTING FLOWERING 5	4323	TGTTCTGTGGGTTTTTACCGA ||o||||o||||||| TCTCAGAGGCCACCTAACAATGGCTTAGATAT	TM3	0.00	0.00	0.88	0.00	1290	-0.54	1602	-0.21
bna-miR172a	591	-1.02	477	-0.70	BnaC02g20120D	Protein TIFY 7	1566	AGAATCTTGATGATGCTGCAT ||||||||||||o||| ACCGTC-TCGAACTACTACGGCGTCGTCGTCG	TM3	0.00	0.00	0.53	0.00	671	-1.85	338	-1.83
TM_Cluster_18741	137	-1.82	238	-1.45	BnaC05g28760D	Putative F-box protein At1g33020	1811	TTGAACCCAAGATCTCACCCT o|o|||||o|o|o||||o TTAGGATTTGGGATTTGGGGTGGGGATTTGAG	TM3	0.00	0.00	0.18	0.00	26	-0.46	13	-0.20
Bna-miR168b	10600	0.84	8401	0.90	BnaC09g33650D	Phototropin-2	4236	TTCGCTTGGTGCAGGTCGGGA |||||||||||||o| AAGCAAACGATCCACGTCCA-CCTTATTATTC	TM3	0.00	0.00	0.35	0.00	2037	-0.15	3086	-0.46

Bna-miRC5-5	298	-1.49	276	0.50	BnaC05g28430D	unknown	289	TTGGTTTGGATCTTGGAAATC |o|o||||||o|||| | CGGTAGCTAAAACTAGAGGCTTT-GCGGCCAA	TM3	0.00	0.00	0.35	0.00	135	0.37	126	1.21
TT_Cluster_90833	824	1.96	804	1.76	BnaA03g13140D	Non-specific lipid-transfer protein 3	651	TTAACTAAAAAACTAAGAACC |o|||| |||| |||o|| GAAAAGTTGATGTTTT-ATTTTTGTTCTGTTT	TM3	0.00	0.00	0.18	0.00	38973	-0.64	39416	-0.65
ath-miR157c-3p	96	-2.06	150	-2.40	BnaA07g10750D	COP9 signalosome complex subunit 7	1592	GCTCTCTATACTTCTGTCACC ||||| |||o| ||||| AGAGAGAGAGAGATGGA-AGAGTGGCCTACGG	TM3	0.00	0.00	0.06	0.00	767	0.28	963	0.05
bna-miR156d	681	-0.65	436	-0.95	BnaA01g08150D	Photosystem I reaction center subunit IV A, chloroplastic	2536	TGACAGAAGAGAGTGAGCAC |||||o||||||| | CAAGTCTGTCCTTTCTCACTCAAGAATCTAAC	TT2	0.00	0.00	0.00	7.83	60807	-0.84	42677	0.05
TM_Cluster_40901	2027	-1.23	2789	-1.44	BnaAnng20610D	unknown	1458	TTGACAGAAGAGAGTGAGCAC |||||| |||o|o| |o|| TCTCAACTGTGTTCTTTTA-TTTTGTGCTTTA	TT2	0.00	0.00	0.00	41.24	1158	1.26	150	2.18
bna-miR156d	681	-0.65	436	-0.95	BnaC03g06730D	Probable receptor-like protein kinase At5g15080	868	TGACAGAAGAGAGTGAGCAC |||||| ||||o|||| CAAAACTGTCGT-TGTCATTCGGGTCATGGCC	TT2	0.00	0.00	0.00	17.22	936	0.80	1419	0.39
bna-miR156d	681	-0.65	436	-0.95	BnaC09g04210D	unknown	33	TGACAGAAGAGAGTGAGCAC ||||||||||||| CGTTACCGTCTTCTCTCTCTC-TCTCTCTCTC	TT2	0.00	0.00	0.00	25.32	11100	0.47	10215	-0.41
Bna-miRC23a-1	595	-2.11	812	-1.35	BnaC02g04190D	Omega-amidase, chloroplastic	693	TCAGAACCAAACCCAGAACAAG |||||||||| ||||||| TGGTAGTCTTGGTTTCTGTGTTGTTCACAATA	TT3	0.00	0.00	0.00	0.23	6	-0.23	9	0.15
Bna-miRC5-1	1687	1.15	2129	0.82	BnaA02g15820D	Patellin-1	1404	TGTGTTGTGATGATA-ATCCGA |o| |||||||||| |||||| GGAACCGCTACACTACTATCTAGGCTTACAAA	TT3	0.00	0.00	0.00	0.14	17903	0.71	29654	-0.12
bna-miR393	190	-2.00	269	-2.10	BnaA06g05730D	unknown	345	TCCAAAGGGATCGCATTGATC o| |||o|||||||| ||| CTTGGGCTTTCTCTAGCGTAAGTAGCTGCACC	TT3	0.00	0.00	0.00	0.14	32	0.02	29	-0.23
Bna-miRC5-1	1687	1.15	2129	0.82	BnaC01g40310D	Probable disease resistance protein RPP1	1202	TGTGTTGTGATGATAATCCGA ||o||||o|o|||||||| TAGAACGCAACATTGCTATTAGGCTGAAGGTA	TT3	0.00	0.00	0.00	0.37	109	0.50	98	1.04
bna-miR171a	796	2.20	753	1.93	BnaA07g01720D	Scarecrow-like protein 15	608	TTGAGCCGTGCCAATATCACG |||||||||| ||||||||| AACTAACTCGGCACTGTTATAGTGGACTCGCA	TT3	0.00	0.00	0.00	0.28	191	-0.39	181	-0.16
bna-miR156g	8555	-1.13	11778	-1.65	BnaA05g24340D	SPL 5	1906	TTGACAGAAGATAGAGAGCAC ||||||||||| |||||||| CATCTACTGTCTTCTCTCTCTCGCAAACCCAC	TT3	0.00	0.00	0.00	2.92	225	0.35	258	-0.97
TM_Cluster_40901	2027	-1.23	2789	-1.44	BnaC03g18800D	SPL 3	707	TTGACAGAAGAGAGTGAGCAC |||||||||||||oo|||| TCTGAACTGTCTTCTCTCGTTCGTTTCGGACA	TT3	0.00	0.00	0.00	0.23	269	-1.04	202	-0.29
bna-miR160c	12249	-1.03	11890	-0.98	BnaA07g33740D	ARF 17	302	TGCCTGGCTCCCTGTATGCCA ||||||||||||o||||| CATTACGGACCGAGGGACGTACGGTCGTCCTT	TT3	0.00	0.00	0.00	0.65	38	0.21	52	1.77
bna-miR156d	681	-0.65	436	-0.95	BnaC03g16490D	SPL 13B	1168	TGACAGAAGAGAGTGAGCAC |||||||||||||| | TACTACTGTCTTCTCTCTCTCGCGTTAGTCTC	TT3	0.00	0.00	0.00	0.09	216	-0.86	140	0.41
TM_Cluster_58223	4175	11.67	4550	11.82	BnaC05g16520D	Nematode resistance protein-like HSPRO2	85	AGAGGAACCTCTTCGTCGATT |||o||||||||o| |oo CGCTTCTTCTTGGAGAAGCGG-TGGCGAAGGT	TT3	0.00	0.00	0.00	0.09	0	NA	3	0.63
Bna-miRC5-1	1687	1.15	2129	0.82	BnaC07g51220D	Nicotinate phosphoribosyltransferase 1	42	TGTGTTGTGATGATAATCCGA ||||||||||||||||||| TAGATCACAACACTACTATTAGGCTCAAGGTT	TT3	0.00	0.00	0.00	0.05	1075	-0.96	838	-0.17
ath-miR158a-3p	2664	0.22	2942	0.53	BnaC03g71700D	Two-pore potassium channel 1	1707	TCCCAAATGTAGACAAAGCA ||||||o||o||||o|| GGTCA-GGTTTATATTTGTTTTGTAAGTTTCT	TT3	0.00	0.00	0.00	0.19	651	-0.26	297	0.40
TT_Cluster_121736	3998	-3.49	2711	-2.20	BnaC03g72850D	unknown	7088	AACGGAATATAAGAACTCATCTCT |||||||||||||||o ||| AGAATTGCCTTATATTCTTGGACAAAGAATTA	TT3	0.00	0.00	0.00	0.05	1	-0.51	3	0.76
TM_Cluster_58223	4175	11.67	4550	11.82	BnaA01g06670D	Probable cyclic nucleotide-gated ion channel 17	2558	AGAGGAACCTCTTCGTCGATT || |||||||||||o|o| ACATCCT-CTTGGAGAAGCAGTTGAGGAGAAC	TT3	0.00	0.00	0.00	0.14	837	0.81	1946	0.81
TT_Cluster_121736	3998	-3.49	2711	-2.20	BnaA03g25520D	Cysteine-rich receptor-like protein kinase 37	1134	AACGGAATATAAGAACTCATCTCT |||||||||||||| ||||| AGAATTGCCTTATATTCTTAAACAGAGAATTA	TT3	0.00	0.00	0.00	0.05	2	1.29	4	0.11
TM_Cluster_40901	2027	-1.23	2789	-1.44	BnaC05g21270D	SPL 11	1691	TTGACAGAAGAGAGTGAGCAC |||||||||||||o||||| CTTCAACTGTCTTCTCTCTTTCGTGCCACCTT	TT3	0.00	0.00	0.00	0.97	521	-0.73	346	0.50
bra-miR9558-5p	1908	6.71	439	6.50	BnaCnng02130D	Probable methyltransferase PMT13	2508	AGAGATGTCTGGCTTGCAACA ||||| || ||||||||| GAGGTCTCTCCAAACC-AACGTTGTTCCTAGA	TT3	0.00	0.00	0.00	0.09	13	0.54	15	0.08
bna-miR393	190	-2.00	269	-2.10	BnaA04g22760D	Proline transporter 1	5146	TCCAAAGGGATCGCATTGATC ||||||||||||||||||| TCCTAGGTTTCCCTAGCGTAACTAGGATTCAG	TT3	0.00	0.00	0.00	1.11	70	-1.86	60	-0.90
bra-miR400-5p	1090	0.47	1001	0.30	BnaA09g49860D	Pentatricopeptide repeat-containing protein At1g06580	357	TATGAGAGTATTATAAGTCAC |||||||||||||||||| GCAATTACTCTCATAATATTCAGTGGTCTAAG	TT3	0.00	0.00	0.00	0.05	15	0.71	20	-1.17
TT_Cluster_121736	3998	-3.49	2711	-2.20	BnaC02g47980D	Probable WRKY transcription factor 3	1154	AACGGAATATAAGAACTCATCTCT ||||||||||||o||||| AGAATCGCCTTATATTATTGGGCAGAGAATTG	TT3	0.00	0.00	0.00	0.23	0	0.17	1	0.52
DM_Cluster_11733	907	-1.13	913	-1.70	BnaC03g18800D	SPL 3	707	TTGACAGAAGAGAGCGAGCAC |||||||||||||o|||| TCTGAACTGTCTTCTCTCGTTCGTTTCGGACA	TT3	0.00	0.00	0.00	0.23	269	-1.04	202	-0.29
Bna-miRC5-1	1687	1.15	2129	0.82	BnaA03g53820D	Nicotinate phosphoribosyltransferase 1	231	TGTGTTGTGATGATAATCCGA |||||||||||||||||| TAGATCACAACACTACTATTAGGCTAAAGGTT	TT3	0.00	0.00	0.00	0.05	1350	-1.27	1008	-1.06
TM_Cluster_58223	4175	11.67	4550	11.82	BnaC08g27070D	Nematode resistance protein-like HSPRO2	85	AGAGGAACCTCTTCGTCGATT |||o|||||||||o| |oo CGCTTCTTCTTGGAGAAGCGG-TGGCGAAGGT	TT3	0.00	0.00	0.00	0.09	0	NA	48	0.50

bna-miR6030	2879	-0.09	3092	-0.17	BnaCnng20410D	Putative disease resistance protein At4g10780	552	TCCACCCATACCATACAGACCC GATGAGGTGGGTATGGTATTTCCGGGTATTAA	TT3	0.00	0.00	0.00	0.19	0	NA	0	NA
TT_Cluster_99626	82	2.24	129	0.96	BnaCnng72810D	unknown	236	TTCGGCTTGAGCTCGGTCGCT AGAGAGGCCG-ACTAGAGCAAGTGGTAGAGGC	TT3	0.00	0.00	0.00	0.28	170	-0.89	159	0.22
bra-miR5718	997	-4.30	1115	-3.86	BnaC02g04190D	Omega-amidase, chloroplastic	693	TCAGAACCAAACACAGAACAAG TGGTAGTCTTGGTTTCTGTGTTGTTCACAATA	TT3	0.00	0.00	0.00	0.23	6	-0.23	9	0.15
Bna-miRC5-5	298	-1.49	276	0.50	BnaC03g29750D	Plastid lipid-associated protein 1, chloroplastic	209	TTGGTTTGGATCTTGGAAATC CAGTGACCGAGCCTAGAAC-TTTAGCACGGCT	TT3	0.00	0.00	0.00	0.28	1422	-1.81	7584	-1.28
DM_Cluster_11733	907	-1.13	913	-1.70	BnaC05g21270D	SPL 11	1691	TTGACAGAAGAGAGCGAGCAC CTTCAACTGTCTTCTCTCTTTCGTGCCACCTT	TT3	0.00	0.00	0.00	0.97	521	-0.73	346	0.50
TT_Cluster_121736	3998	-3.49	2711	-2.20	BnaC04g56920D	Phosphoglycerate mutase-like protein 4	929	AACGGAATATAAGAACTCATCTCT AGAATTGCCTTATATTATTGGGCAGAGAATTG	TT3	0.00	0.00	0.00	0.05	0	NA	0	-0.18
bna-miR156d	681	-0.65	436	-0.95	BnaA03g13580D	SPL 13B	1157	TGACAGAAGAGAGTGAGCAC TACTACTGTCTTCTCTCTCGCGTTAGTCTC	TT3	0.00	0.00	0.00	0.05	57	-1.77	36	-0.81
bna-miR156d	681	-0.65	436	-0.95	BnaC03g27870D	SPL 13B	1014	TGACAGAAGAGAGTGAGCAC TACTACTGTCTTCTCTCTCTCGTTTTAGTCTC	TT3	0.00	0.00	0.00	0.05	10	1.42	12	0.82
TM_Cluster_58223	4175	11.67	4550	11.82	BnaC01g08680D	Nematode resistance protein-like HSPRO2	85	AGAGGAACCTCTTCGTCGATT CGCTTCTTCTTGGAGAAGCGG-TGGCGAAGGT	TT3	0.00	0.00	0.00	0.09	0	NA	48	0.50
Bna-miRC5-1	1687	1.15	2129	0.82	BnaC01g40270D	Disease resistance protein TAO1	1181	TGTGTTGTGATGATAATCCGA TAGAACGCAACATTGCTATTAGGCTGAAGGTA	TT3	0.00	0.00	0.00	0.37	230	0.10	475	0.12
bra-miR9558-5p	1908	6.71	439	6.50	BnaA03g26990D	Probable methyltransferase PMT13	2692	AGAGATGTCTGGCTTGCAACA AAGGTCTCTCCAAACC-AACGTTGTTCTTAGA	TT3	0.00	0.00	0.00	0.42	1313	0.82	1629	0.20
bna-miR824	393	-0.34	651	-0.01	BnaC01g04170D	Agamous-like MADS-box protein AGL16	2881	TAGACCATTTGTGAGAAGGGA ACGGATCTGGTAAACACTCTTCTCTTTAAAAG	TT3	0.00	0.00	0.00	0.14	1026	0.33	1154	-0.04
bna-miR403	107384	-1.72	31065	-1.19	BnaA10g17020D	AAA-ATPase At5g17760	887	TTAGATTCACGCA-CAAACTCG GTCCAGTCTCAGTGCGTAGTGTGAGCGCTCGA	TT3	0.00	0.00	0.00	0.05	60	1.71	306	2.32
TT_Cluster_121736	3998	-3.49	2711	-2.20	BnaC03g37420D	Ras-related protein RABA4d	1122	AACGGAATATAAGAACTCATCTCT AGAATCGCCTTATATTCTTGGGCA-ATAAATT	TT3	0.00	0.00	0.00	0.23	0	NA	0	NA
ath-miR393b-5p	15380	-0.14	15066	-0.54	BnaA04g22760D	Proline transporter 1	5146	TCCAAAGGGATCGCATTGATCC TCCTAGGTTTCCCTAGCGTAACTAGGATTCAG	TT3	0.00	0.00	0.00	1.11	70	-1.86	60	-0.90
bra-miR162-3p	2634	0.33	3868	0.03	BnaA02g18750D	F-box protein At1g78100	396	TCGATAAACCTCTGCATCCAG AGGCGGC-ATTTTGAGGTGTAGGTCCAAGGCC	TT3	0.00	0.00	0.00	0.05	37	1.35	126	3.24
ath-miR408-3p	1270	-1.94	1812	-2.56	BnaCnng09320D	Peptide chain release factor 1	1341	ATGCACTGCCTCTTCCCTGGC AGGGTACGTGACGGAGAAGGGACCGAGGGAAA	TT3	0.00	0.00	0.00	0.28	154	-0.40	101	-0.34
TM_Cluster_40901	2027	-1.23	2789	-1.44	BnaA04g19840D	SPL 3	561	TTGACAGAAGAGAGTGAGCAC CTCTGACTGTCTTCTCTCGTTCGTTTCCGATT	TT3	0.00	0.00	0.00	0.28	2043	-2.52	210	-0.84
bra-miR398-3p	128022	4.09	73186	4.34	BnaC09g42920D	unknown	3114	TGTGTTCTCAGGTCACCCCTG AAGTACACAAGAGTCCAGTGGGGACGACTCGA	TT3	0.00	0.00	0.00	0.05	668	-1.18	410	-0.35
bna-miR160c	12249	-1.03	11890	-0.98	BnaC06g38360D	ARF 17	1854	TGCCTGGCTCCCTGTATGCCA CATTACGGACCGAGGGACGTACGGCCGTCCTT	TT3	0.00	0.00	0.00	0.65	101	0.63	118	1.48
TT_Cluster_121736	3998	-3.49	2711	-2.20	BnaCnng68400D	Paired amphipathic helix protein Sin3-like 2	1132	AACGGAATATAAGAACTCATCTCT AGAATTGCCTTATATTCTTGGGCAGAGAATTG	TT3	0.00	0.00	0.00	0.05	1	-0.06	0	-0.25
bna-miR156g	8555	-1.13	11778	-1.65	BnaC05g21270D	SPL 11	1691	TTGACAGAAGATAGAGAGCAC CTTCAACTGTCTTCTCTCTTTCGTGCCACCTT	TT3	0.00	0.00	0.00	0.97	521	-0.73	346	0.50
DM_Cluster_11733	907	-1.13	913	-1.70	BnaC05g38350D	SPL 5	644	TTGACAGAAGAGAGCGAGCAC CATCTACTGTCTTCTCTCTCGCCAACCCAC	TT3	0.00	0.00	0.00	2.92	134	-0.26	242	-0.74
Bna-miRC5-1	1687	1.15	2129	0.82	BnaA01g33750D	Disease resistance protein TAO1	1198	TGTGTTGTGATGATAATCCGA TAGAACGCAACATTACTATTAGGCTGAAGGTA	TT3	0.00	0.00	0.00	0.37	2	0.19	193	6.52
Bna-miRC18	1100	4.32	1708	5.12	BnaA03g27440D	Transcription factor MYB57	581	TCGCGATCTTAGATCCTCTAA ACAAAGCGTTAGAAGCTGGTGGATATATATAA	TT3	0.00	0.00	0.00	0.09	134	-0.65	64	-0.41
bra-miR1885a	35126	0.13	34337	1.09	BnaA09g14980D	Disease resistance protein TAO1	133	CATCAATGAAAGGTATGATTCC AGCAGTAGTTACTTTCCATACTAAGGGAACGA	TT3	0.00	0.00	0.00	0.46	540	-1.01	1072	0.50
bna-miR824	393	-0.34	651	-0.01	BnaA01g02900D	Agamous-like MADS-box protein AGL16	2899	TAGACCATTTGTGAGAAGGGA ACGGATCTGGTAAACACTCTTCTCTTTAAAAG	TT3	0.00	0.00	0.00	0.14	433	0.10	610	0.23
bra-miR9558-5p	1908	6.71	439	6.50	BnaC03g31950D	Probable methyltransferase PMT13	2756	AGAGATGTCTGGCTTGCAACA AAGGTCTCTCCAAACC-AACGTTGTTCTTAGA	TT3	0.00	0.00	0.00	0.42	1819	0.56	1912	0.06
bra-miR5718	997	-4.30	1115	-3.86	BnaA03g03750D	Omega-amidase, chloroplastic	693	TCAGAACCAAACACAGAACAAG TGGTAGTCTTGGTTTCTGTGTCGTTCACAATA	TT3	0.00	0.00	0.00	0.23	2644	0.18	2748	0.46
bna-miR169m	627	-0.01	273	-1.44	BnaC04g36060D	unknown	219	TGAGCCAAAGATGACTTGCCG CCGGCCTCGGTATCTGCTGAGCGGCGGAGGCG	TT3	0.00	0.00	0.00	0.32	180	0.26	111	-0.06

Bna-miRC5-1	1687	1.15	2129	0.82	BnaA01g33710D	Disease resistance protein TAO1	2124	TGTGTTGTGATGATAATCCGA ||o||||o||||||||||| TAGAACGCAACATTACTATTAGGCTGAAGGTA	TT3	0.00	0.00	0.00	0.37	44	1.06	48	0.35
bol-miR398a-3p	10530	1.57	1850	2.48	BnaC09g42920D	unknown	3114	TGTGTTCTCAGGTCACCCCTT |||||||||||||||||| AAGTACACAAGAGTCCAGTGGGGACGACTCGA	TT3	0.00	0.00	0.00	0.05	668	-1.18	410	-0.35
Bna-miRC5-1	1687	1.15	2129	0.82	BnaC01g40280D	Probable disease resistance protein RPP1	4154	TGTGTTGTGATGATAATCCGA ||o||||o|o||||||||| TAGAACGCAACATTGCTATTAGGCTGAAGGTA	TT3	0.00	0.00	0.00	0.37	89	1.56	206	0.80
bna-miR172a	591	-1.02	477	-0.70	BnaC04g05700D	Ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic	452	AGAATCTTGATGATGCTGCAT ||||||||||||||o|| ACCCTCTTAGAACTACTACAATGTTGAAAGAA	TT3	0.00	0.00	0.00	0.09	18086	-0.55	317	-1.75
TM_Cluster_40901	2027	-1.23	2789	-1.44	BnaC04g44230D	SPL 3	620	TTGACAGAAGAGAGTGAGCAC o||||||||||||oo|||| CTCTGACTGTCTTCTCTCGTTCGTTTCCCGAA	TT3	0.00	0.00	0.00	0.28	153	-1.42	84	-0.83
Bna-miRC5-1	1687	1.15	2129	0.82	BnaA01g33780D	Disease resistance protein TAO1	1319	TGTGTTGTGATGATAATCCGA ||o||||o|||||||||| TAGAACGCAACATTACTATTAGGCTGAAGGTA	TT3	0.00	0.00	0.00	0.37	19	0.97	854	-0.12
DM_Cluster_11733	907	-1.13	913	-1.70	BnaC04g44230D	SPL 3	620	TTGACAGAAGAGAGCGAGCAC o||||||||||||||o|||| CTCTGACTGTCTTCTCTCGTTCGTTTCCCGAA	TT3	0.00	0.00	0.00	0.28	153	-1.42	84	-0.83
TT_Cluster_160692	24	4.76	65	4.10	BnaA07g25530D	Glutamate decarboxylase 2	3786	TGAC-ACATGCAGAGCCGTGAC |||| |||o|||||o|||||| ATTACTGTTGTGCGTCTTGGCACTACACGACG	TT3	0.00	0.00	0.00	0.28	2363	1.18	7086	1.05
bna-miR394a	429	-2.17	509	-2.10	BnaC07g11360D	F-box only protein 6	1771	TTGGCATTCTGTCCACCTCC ||||||||||||| |||||| TGCAAACCGTAAGACAGTTGGAGGAAGGTGTC	TT3	0.00	0.00	0.00	0.09	399	0.39	343	0.32
bna-miR6030	2879	-0.09	3092	-0.17	BnaC08g41340D	Probable disease resistance protein At1g12290	555	TCCACCCATACCATACAGACCC |||||||||||| || |||||| GATGAGGTGGGTATGGCATATCTGGGTACTAG	TT3	0.00	0.00	0.00	0.19	23	2.49	27	2.86
bna-miR156g	8555	-1.13	11778	-1.65	BnaAnng21160D	Retrovirus-related Pol polyprotein from transposon TNT 1-94	5714	TTGACAGAAGATAGAGAGCAC o|o||| ||||o|||||| ||| AAGAGATTGTGTTCTGTCTCT-GTGCCTTTGA	TT3	0.00	0.00	0.00	0.28	5	0.55	0	-0.08
DM_Cluster_11733	907	-1.13	913	-1.70	BnaA04g19840D	SPL 3	561	TTGACAGAAGAGAGCGAGCAC o||||||||||||||o|||| CTCTGACTGTCTTCTCTCGTTCGTTTCCGATT	TT3	0.00	0.00	0.00	0.28	2043	-2.52	210	-0.84
bna-miR172b	359	-1.72	440	-1.73	BnaC04g05700D	Ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic	452	GGAATCTTGATGATGCTGCAT o|||||||||||||o|| ACCCTCTTAGAACTACTACAATGTTGAAAGAA	TT3	0.00	0.00	0.00	0.09	18086	-0.55	317	-1.75
TM_Cluster_31773	230	-3.02	282	-2.30	BnaA07g01720D	Scarecrow-like protein 15	611	TGATTGAGCCGCGTCAATATC |||||||||| ||||||| GGCAACTAACTCGGCACTGTTATAGTGGACTC	TT3	0.00	0.00	0.00	0.23	191	-0.39	181	-0.16
bna-miR172b	359	-1.72	440	-1.73	BnaC07g26670D	unknown	498	GGAATCTTGATGATGCTGCAT |||||||o||||||| CAAGACCTAGAACTGCTACGA-GTACTCTAAT	TT3	0.00	0.00	0.00	0.05	104	-0.59	125	-0.16
ath-miR408-3p	1270	-1.94	1812	-2.56	BnaC04g00470D	Peptide chain release factor 1	2279	ATGCACTGCCTCTTCCCTGGC |||||||||||||||||| AGGGTACGTGACGGAGAAGGGACCGAGGGACA	TT3	0.00	0.00	0.00	0.28	352	0.15	317	-0.52
bna-miR6030	2879	-0.09	3092	-0.17	BnaA07g17000D	Putative disease resistance protein At4g10780	552	TCCACCCATACCATACAGACCC |||||||||||||| || ||| GATGAGGTGGGTATGGTATTTCGGGGTATTAA	TT3	0.00	0.00	0.00	0.19	14	1.08	5	0.65
bra-miR1885a	35126	0.13	34337	1.09	BnaC09g39550D	Probable disease resistance protein RPP1	121	CATCAATGAAAGGTATGATTCC |||||||||||| ||||||| AGGAATAGTTACTTTCCTGACTAAGGTAACGA	TT3	0.00	0.00	0.00	0.05	0	NA	430	-0.66
Bna-miRC5-3*	7608	1.26	9375	0.51	BnaC06g26630D	Signal recognition particle subunit SRP72	395	TCTTGTGTTGTGATGATAATC |||||||||||||| |||o| GTCGAGAACACAACACTAAAATTGGTTCAGGA	TT3	0.00	0.00	0.00	0.14	14	1.34	105	-0.15

SPL = SQUAMOSA PROTEIN-BINDING LIKE; ARF = auxin response factor; SCL = SCARECROW-LIKE; ERF = ethylene-responsive transcription factor; BLOCS 2 = BLOCS2 = BIOGENESIS OF LYSOSOME-RELATED ORGANELLES COMPLEX 1 subunit 2

Table S16: Overview over levels of miRNAs and their corresponding mRNA targets

						miRNA fold change (log_2)		mRNA target fold change (log_2)	
Virus-induced miRNA and target levels	**miRNA**	**miRNA sequence**	**Target transcript ID**	**Annotation**	**Clevage found in PAREseq replicates**	**Drakkar**	**Tanto**	**Drakkar**	**Tanto**
miRNA↓ target mRNA↑	miR403	TTAGATTCACGCACAAACTCG	BnaCnng68320D	AGO2	DM1 DM3 DT1 DT2 DT3 TM2 TM3 TT3	-1.72	-1.19	1.50	1.27
	miR403	TTAGATTCACGCACAAACTCG	BnaA05g14760D	AGO2	DM1 TM3 TT3	-1.72	-1.19	2.60	3.13
	miR396	TCCAAAGGGATCGCATTGATC	BnaA02g28290D	AFB2	DM2 DM3 DT3 TM3 TT3	-2.00	-2.10	0.50	0.24
	miR395	TCCAAAGGGATCGCATTGATC	BnaC02g36370D	AFB2	DM2 DM3 DT3 TM3 TT3	-2.00	-2.10	0.35	0.12
	miR394	TCCAAAGGGATCGCATTGATCC	BnaA02g28290D	AFB2	DM2 DM3 DT2 DT3 TM3 TT3	-0.14	-0.54	0.50	0.24
	miR393	TCCAAAGGGATCGCATTGATCC	BnaC02g36370D	AFB2	DM2 DM3 DT2 DT3 TM3 TT3	-0.14	-0.54	0.35	0.12
	miR393	TCCAAAGGGATCGCATTGATCC	BnaC08g40890D	AFB3	DM3 DT3 TM3 TT3	-0.14	-0.54	0.55	0.56
	miR393	TCCAAAGGGATCGCATTGATC	BnaC08g40890D	AFB2	DM3 DT3 TM3 TT3	-2.00	-2.10	0.55	0.56
	miR172	AGAATCTTGATGATGCTGCAT	BnaA03g22100D	ERF RAP2-7	DM2 DM3 DT2 DT3 TM2 TM3 TT3	-1.02	-0.70	0.53	1.04
	miR172	GGAATCTTGATGATGCTGCAT	BnaA03g22100D	ERF RAP2-7	DM2 DM3 DT2 DT3 TM2 TM3 TT3	-1.72	-1.73	0.53	1.04
	miR172	AGAATCTTGATGATGCTGCAT	BnaCnng39690D	APETALA 2	DT2 DT3 TT3	-1.02	-0.70	0.19	0.28
	miR172	GGAATCTTGATGATGCTGCAT	BnaCnng39690D	APETALA 2	DT2 DT3 TT3	-1.72	-1.73	0.19	0.28
	miR160	TGCCTGGCTCCCTGTATGCCA	BnaA01g06910D	ARF16	DM3 DT2 DT3 TM2 TM3 TT2 TT3	-1.03	-0.98	0.60	1.21
	miR160	TGCCTGGCTCCCTGTATGCCA	BnaC01g08330D	ARF16	DM3 DT2 DT3 TM2 TM3 TT2 TT3	-1.03	-0.98	0.52	0.79
	miR156	TTGACAGAAGATAGAGAGCAC	BnaAnng25050D	SPL11	DM3 DT3 TM2 TM3 TT3	-1.13	-1.65	0.70	0.71
	miR156	TGACAGAAGAGAGTGAGCAC	BnaAnng25050D	SPL11	DM3 TM3 TT3	-0.65	-0.95	0.70	0.71
	miR (Shortstack)	TTGACAGAAGAGAGTGAGCAC	BnaAnng25050D	SPL11	DM3 DT3 TM2 TM3 TT3	-1.23	-1.44	0.70	0.71
	miR (Shortstack)	TTGACAGAAGAGAGCGAGCAC	BnaAnng25050D	SPL11	DM3 DT3 TM2 TM3 TT3	-1.13	-1.70	0.70	0.71
miRNA↑ target mRNA↓	bna-miR171	TTGAGCCGTGCCAATATCACG	BnaAnng18550D	SCL6	DM3 DT2 DT3 TM3 TT3	2.20	1.93	-0.60	-0.25
	bna-miR171	TTGAGCCGTGCCAATATCACG	BnaAnng18540D	SCL6	DM3 DT2 DT3 TM3 TT3	2.20	1.93	-0.61	-0.23
miRNA↑ target mRNA↑	miR1885	TACATCTTCTCCGCGGAAGCTC	BnaCnng44780D	BLOC1S2	DM2 DM3 DT2 DT3 TM2 TM3 TT2 TT3	2.29	2.85	0.44	0.64
	miR398	TGTGTTCTCAGGTCACCCCTG	BnaA04g16310D	SODC2	DM2 TM3 TT3	4.09	4.34	2.75	0.67
	miR1885	TACATCTTCTCCGCGGAAGCTC	BnaA06g29450D	BLOC1S2	DM3 DT2 TT3	2.29	2.85	0.10	0.63
miRNA↓ target mRNA↓	miR (Shortstack)	TTGACAGAAGAGAGCGAGCAC	BnaC07g11380D	SPL10	DM2 DM3 DT2 DT3 TM2 TM3 TT2 TT3	-1.13	-1.70	-0.54	-0.34
	miR156	TTGACAGAAGATAGAGAGCAC	BnaC07g11380D	SPL10	DM2 DM3 DT2 DT3 TM2 TM3 TT2 TT3	-1.13	-1.65	-0.54	-0.34
	miR (Shortstack)	TTGACAGAAGAGAGTGAGCAC	BnaC07g11380D	SPL10	DM2 DM3 DT2 DT3 TM2 TM3 TT2 TT3	-1.23	-1.44	-0.54	-0.34
	miR (Shortstack)	TTGACAGAAGAGAGCGAGCAC	BnaC04g23930D	SPL15	DM2 DM3 DT3 TM3 TT3	-1.13	-1.70	-0.32	-0.83
	miR (Shortstack)	TTGACAGAAGAGAGTGAGCAC	BnaC04g23930D	SPL15	DM2 DM3 DT3 TM3 TT3	-1.23	-1.44	-0.32	-0.83
	miR156	TTGACAGAAGATAGAGAGCAC	BnaC04g23930D	SPL15	DM2 DM3 DT3 TM3 TT3	-1.13	-1.65	-0.32	-0.83
	miR156	TGACAGAAGAGAGTGAGCAC	BnaCnng61400D	SPL6	DM3 DT2 DT3 TM3 TT3	-0.65	-0.95	-0.62	-0.05
	miR6030	TCCACCCATACCATACAGACCC	BnaA02g16970D	unknown	DM3 DT3 TM2 TM3	-0.09	-0.17	-0.78	-0.72
	miR156	TGACAGAAGAGAGTGAGCAC	BnaC07g11380D	SPL10	DM3 DT3 TM3 TT3	-0.65	-0.95	-0.54	-0.34
	miR156	TGACAGAAGAGAGTGAGCAC	BnaA04g19840D	SPL3	DM3 DT3 TT3	-0.65	-0.95	-2.52	-0.84
	miR156	TGACAGAAGAGAGTGAGCAC	BnaC04g44230D	SPL3	DM3 DT3 TT3	-0.65	-0.95	-1.42	-0.83
	miR172	AGAATCTTGATGATGCTGCAT	BnaC07g16190D	AP2	DM3 TM2 TT3	-1.02	-0.70	-0.24	-0.05
	miR (Shortstack)	TTGACAGAAGAGAGTGAGCAC	BnaCnng61400D	SPL6	DM3 TM3 TT3	-1.23	-1.44	-0.62	-0.05
	miR (Shortstack)	TTGACAGAAGAGAGCGAGCAC	BnaCnng61400D	SPL6	DM3 TM3 TT3	-1.13	-1.70	-0.62	-0.05
	miR156	TTGACAGAAGATAGAGAGCAC	BnaCnng61400D	SPL6	DM3 TM3 TT3	-1.13	-1.65	-0.62	-0.05
miRNA↑ target mRNA only in one cultivar↓	miRC5-3	TTATCATCACAACACTAGATC	BnaA10g27170D	MT23	DM3 DT2	0.80	0.23	0.10	-0.15
	miRC5-1	TGTGTTGTGATGATAATCCGA	BnaC06g43790D	PATL1	DM3 TT3	1.15	0.82	1.16	-0.44
	miR161	GTCACTTTCAATGCGTTGATC	BnaA06g39650D	RPP8-like2	DT2 DT3	5.83	5.89	0.13	-0.44
	miRC5-3	TTATCATCACAACACTAGATC	BnaA10g27170D	MT23	DM3 DT2	0.80	0.23	0.10	-0.15
	miRC5-1	TGTGTTGTGATGATAATCCGA	BnaC06g43790D	PATL1	DM3 TT3	1.15	0.82	1.16	-0.44
	miR161	GTCACTTTCAATGCGTTGATC	BnaA06g39650D	RPP8-like2	DT2 DT3	5.83	5.89	0.13	-0.44
	miR171	TTGAGCCGTGCCAATATCACG	BnaC04g22080D	SCL22	DM3 DT2 TM3 TT3	2.20	1.93	-0.97	0.05
miRNA↓ target mRNA only in one cultivar↑	miR172	AGAATCTTGATGATGCTGCAT	BnaC09g13430D	ERF RAP2-7	DM2 DM3 DT2 DT3 TM2 TM3 TT3	-1.02	-0.70	0.30	-1.57
	miR172	GGAATCTTGATGATGCTGCAT	BnaC04g15640D	ERF RAP2-7	DM2 DM3 DT2 DT3 TM2 TM3 TT3	-1.72	-1.73	0.78	-1.74
	miR172	AGAATCTTGATGATGCTGCAT	BnaC04g15640D	ERF RAP2-7	DM2 DM3 DT2 DT3 TM2 TM3 TT3	-1.02	-0.70	0.78	-1.74
	miR172	GGAATCTTGATGATGCTGCAT	BnaC09g13430D	ERF RAP2-7	DM2 DM3 DT2 DT3 TM2 TM3 TT3	-1.72	-1.73	0.30	-1.57
	miR172	GGAATCTTGATGATGCTGCAT	BnaA10g12950D	AP2	DM3 DT2 DT3 TM2 TM3 TT3	-1.72	-1.73	0.33	-0.04
	miR172	AGAATCTTGATGATGCTGCAT	BnaA10g12950D	AP2	DM3 DT2 DT3 TM2 TM3 TT3	-1.02	-0.70	0.33	-0.04
	miR172	AGAATCTTGATGATGCTGCAT	BnaC09g35430D	AP2	DM3 DT2 DT3 TM2 TM3 TT3	-1.02	-0.70	0.01	-0.22
	miR172	GGAATCTTGATGATGCTGCAT	BnaC09g35430D	AP2	DM3 DT2 DT3 TM2 TM3 TT3	-1.72	-1.73	0.01	-0.22
corresponding changes in only one cultivar	miRC23a-3	TATCTACTGCTTATGCCACCA	BnaA07g28290D	COX19	DM2 DM3 TM2 TM3 TT3	-0.13	0.60	-0.40	-0.35

Table S17: Targeting of host mRNA transcripts by vsiRNAs

vsiRNA						Host mRNA targets									DE target mRNA			
vsiRNA (strand)	Length	vsiRNA reads & FC(log2)				Target transcript ID	Predicted gene function	Cleavage position	vsiRNA:mRNA target pair (5'-3' : 3'-5')	Cleavage found in PAREseq replicates	Fragment signatures (rpm)				mRNA reads & FC(log2)			
		DM	DT	TM	TT						DM	DT	TM	TT	DM	DT	TM	TT
AAGAATCTGATGATGCTGT (-)	19	0.00	2.13	0.00	1.60	BnaC03g26480D	ERF RAP2-7	2328	AAGAAT-CTGATGATGCTGT AATCTCTTAGGACTACTACGACGACGTTGACT	DT2 DT3 TT3	0.00	10.03	0.00	6.66	815	-0.39	1202	0.43
AAGAATCTGATGATGCTGT (-)	19	0.00	2.13	0.00	1.60	BnaC04g15640D	ERF RAP2-7	2414	AAGAAT-CTGATGATGCTGT AATCTCTTAGGACTACTACGACGACGTTGACT	DT2 DT3 TT3	0.00	10.03	0.00	6.66	1538	0.78	45574	-1.74
AAGAATCTGATGATGCTGT (-)	19	0.00	2.13	0.00	1.60	BnaA10g12950D	AP2-like ERF TOE2	2933	AAGAAT-CTGATGATGCTGT ACACTCTTAGGACTACTACGACGTAAACTCTC	DT2 DT3 TT3	0.00	5.00	0.00	9.95	297	0.33	443	-0.04
AAGAATCTGATGATGCTGT (-)	19	0.00	2.13	0.00	1.60	BnaC09g35430D	AP2-like ERF TOE2	2671	AAGAAT-CTGATGATGCTGT ACACTCTTAGGACTACTACGACGTAAACTATC	DT2 DT3 TT3	0.00	5.00	0.00	9.95	232	0.01	342	-0.22
AAGAATCTGATGATGCTGT (-)	19	0.00	2.13	0.00	1.60	BnaC09g13430D	ERF RAP2-7	1039	AAGAAT-CTGATGATGCTGT AATCTCTTAGGACTACTACGACGACGTTGACT	DT2 DT3 TT3	0.00	10.03	0.00	6.66	652	0.30	3166	-1.57
TCTTTGTCACTCTCGTGTGCT (-)	21	0.01	54.27	0.02	40.69	BnaC09g53230D	unknown	219	TCTTTGTCACTCTCGTGTGCT AGAGAGAGAGAGAGAGAGCA-ACAAAGTCCAC	DT2 DT3	0.00	13.49	0.00	0.00	3	-0.02	5	-0.27
TCCTTCTTCTCCTTCTCTGCC (-)	21	0.01	11.63	0.00	9.29	BnaCnng36690D	Non-functional pseudokinase ZED1	62	TCCTTCTTCTCCTTCTCTGCC GAAGAAGAAGAAGAAGAAGAGGTGGCTGGTAG	DT2 DT3	0.00	4.17	0.00	0.00	197	-0.18	186	-0.35
TCTTTGTCACTCTCGTGTGCT (-)	21	0.01	54.27	0.02	40.69	BnaC04g51540D	FBD-associated F-box protein At3g49020	114	TCTTTGTCACTCTCGTGTGCT AGAGAGAGAGAGAGAGAG-AGACGAAACAAGA	DT2 DT3	0.00	13.49	0.00	0.00	1	-0.54	0	-0.18
TCTTTGTCACTCTCGTGTGCT (-)	21	0.01	54.27	0.02	40.69	BnaC04g04300D	unknown	213	TCTTTGTCACTCTCGTGTGCT AGAGAGAGAGAGAGAGAG-AGACGAGTTTTAG	DT2 DT3	0.00	13.49	0.00	0.00	1	0.63	4	-0.04
AAGAATCTGATGATGCTGT (-)	19	0.00	2.13	0.00	1.60	BnaA03g22100D	ERF RAP2-7	2284	AAGAAT-CTGATGATGCTGT AATCTCTTAGGACTACTACGACGACGTTGACT	DT2 DT3	0.00	10.03	0.00	0.00	413	0.53	317	1.04
AACTGCCTCAAGAGCTCCATA (-)	21	0.01	32.88	0.04	29.44	BnaA10g13210D	Thiol protease aleurain	1221	AACTGCCTCAAGAGCTCCA-TA CTATTCGGCGGAGTTCGCGAGGTCATCATGAT	DT2 DT3	0.00	3.52	0.00	0.00	45621	-0.63	51819	0.27
AAGAATCTGATGATGCTGT (-)	19	0.00	2.13	0.00	1.60	BnaA01g34730D	Floral homeotic protein APETALA 2	1043	AAGAAT-CTGATGATGCTGT CCTCTCTTAGGACTACTACGACGTCGTAAACG	DT2 TT3	0.00	2.04	0.00	1.62	460	-0.44	487	0.12
AAGAATCTGATGATGCTGT (-)	19	0.00	2.13	0.00	1.60	BnaCnng39690D	Floral homeotic protein APETALA 2	2233	AAGAAT-CTGATGATGCTGT CCTCTCTTAGGACTACTACGACGTCGTAAACG	DT2 TT3	0.00	0.53	0.00	1.25	485	0.19	639	0.28
TGTGTGTTGTTGTTACTTTCT (+)	21	0.01	8.67	0.00	7.24	BnaA03g21510D	Serine/arginine-rich splicing factor RS31A	356	TGTGTGTTGTTGTTACTTTCT ACACACACAC-ACAAAAAATAAAGGAACGTCC	DT1 DT2	0.00	0.13	0.00	0.00	4	-0.19	4	0.19
TACCAGAACTCATCGAAGC (+)	19	0.00	1.79	0.00	2.25	BnaC04g53300D	Nematode resistance protein-like HSPRO2	1241	TACCAGAACTCATCGAAGC ACCGA-GGTCTTGAGAGGGTTCTTGCAGAAGC	DT1 TT1	0.00	0.04	0.00	170.97	24819	-0.46	11586	0.49
AGAACCGAGAACATTGAGAA (+)	20	0.01	4.14	0.00	4.01	BnaC02g37040D	Chlorophyll a-b binding protein 36, chloroplastic	863	AGAACCGAGAACATTGAGAA TGTTTCTTGGGT-TTGTACCTCTTGTACCGTT	DT2 DT3	0.00	10.41	0.00	0.00	535655	-0.48	315782	-0.03
CAGAGAAGGAGAAGAAGGAGA (+)	21	0.00	16.42	0.00	12.78	BnaC03g04180D	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	90	CAGAGAAGGAGAAGAAGGAGA CTCTCTCTC-TCTTCTTCTTCTTCCCTGC	DT2 TT2	0.00	0.18	0.00	0.65	603	-0.17	401	0.13
CAGAGAAGGAGAAGAAGGAGA (+)	21	0.00	16.42	0.00	12.78	BnaA01g09950D	unknown	203	CAGAGAAGGAGAAGAAGGAGA TCTTCT-TCTTCTTCTTCTTCTGCTGCCA	DT1	0.00	0.04	0.00	0.00	1	-0.04	3	0.51
AGTGGACCATAAGACAAAGA (+)	20	0.00	2.40	0.00	2.44	BnaCnng71720D	NAD(P)H-quinone oxidoreductase subunit S, chloroplastic	63	AGTGGACCATAAGACAAAGA TTCTTCAGC-GGTAATCTGTTTCTTTTCAAAA	DT1	0.00	0.04	0.00	0.00	2632	-0.92	1831	0.34
CAGAGAAGGAGAAGAAGGAGA (+)	21	0.00	16.42	0.00	12.78	BnaC08g39950D	Phosphate transporter PHO1 homolog 3	3327	CAGAGAAGGAGAAGAAGGAGA TCTTCT-TCTTCTTCTTCTTCTTAGTTTA	DT1	0.00	0.22	0.00	0.00	436	-0.75	421	1.46
TGTGTGTTGTTGTTACTTTCT (+)	21	0.01	8.67	0.00	7.24	BnaC01g07420D	unknown	66	TGTGTGTTGTTGTTACTTTCT ACACACACAC-ACAATGGGGAGAGGTAACAAC	DT1	0.00	0.04	0.00	0.00	3855	-0.32	3867	0.18
TCTTCTCCTTCTCTGCCTGCT (-)	21	0.00	14.53	0.00	10.41	BnaC04g03350D	60S ribosomal protein L7-3	1583	TCTTCTCCTTCTCTGC-CTGCT AAGAAGAAGAAGAAGAGACGCGGCGCGAGAGA	DT1	0.00	0.04	0.00	0.00	1877	-0.50	2166	-0.59
TCCTTCTTCTCCTTCTCTGCC (-)	21	0.01	11.63	0.00	9.29	BnaC02g09670D	Probable WRKY transcription factor 38	958	TCCTTCTTCTCCTTCTCTGCC GAAGAAGAGGAAGAGGAAGAGAAGGGGTCTCT	DT1	0.00	0.04	0.00	0.00	181	0.25	178	-0.30
AAAAGGAACGAGAGAGGCAAA (+)	21	0.00	8.38	0.01	5.55	BnaC06g38600D	Trehalose-phosphate phosphatase B	1252	AAAAGGAACGAGAGAGGCAAA CAGCTTTTACATGC-CTGTCTGTTTTGAACAA	DT2	0.00	6.57	0.00	0.00	23	1.61	54	0.92
AGAAATACTGAAACAAAGTTG (+)	21	0.00	3.65	0.00	2.67	BnaC05g04590D	Oxygen-evolving enhancer protein 2, chloroplastic	1213	AGAAATACTGAAACAAAGTTG AAGTTCGTTGTGACTTTCTT-CACCGACGAAA	DT2	0.00	12.97	0.00	0.00	84174	-0.31	77609	-0.12
AGAAGAACTTTTCACTGGAG (+)	20	0.00	3.11	0.00	3.12	BnaC03g07170D	F-box/kelch-repeat protein At5g15710	1324	AGAAGAACTTTTCACTGGAG CATGTCTTC-TGGAAAGGGAACTAAGGTGCTG	DT2	0.00	1.95	0.00	0.00	868	0.74	1116	0.05
TCCTGAAGATTTCTCTGCA (+)	19	0.00	2.72	0.01	2.18	BnaUnng02970D	Ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic	58	TCCTGAAGATTTCTCTGCA AGCCAGGACTTCTATGGGAACGTTTGTGGCTA	DT2	0.00	3.91	0.00	0.00	3584	0.02	5721	-0.81

CAACAAAATGGGTAGAGAAGT (+)	21	0.00	4.09	0.01	2.72	BnaC05g40970D	Omega-6 fatty acid desaturase, endoplasmic reticulum	2690	CAACAAAATGGGTAGAGAAGT ||||||||||o||| ||| TTGTGTTGTTTTACCTATCAATTCTAATAACT	DT2	0.00	2.49	0.00	0.00	6262	-0.09	5587	0.08
TTGATAAGGAACCAGCTCAAG (+)	21	0.00	3.37	0.00	2.38	BnaC06g08100D	Uncharacterized oxidoreductase At4g09670	1692	TTGATA-AGGAACCAGCTCAAG o||||| |o||||| |||||| CCGGACTATGTTCTTGGGCAAGTTCCAATAAT	DT2	0.00	4.26	0.00	0.00	153	1.41	235	0.98
GTCCCAACGAACTTCGAAGT (+)	20	0.01	2.47	0.00	1.97	BnaC06g03660D	Formate--tetrahydrofolate ligase	1639	GTCCCAACGAACTTCGAAGT |||||||||o||o GGTCCAGGG-TGGTCGAAGTTTCGTTAAAATA	DT2	0.00	0.09	0.00	0.00	3378	0.47	5957	-0.17
TCCTGAAGATTTCTCTGCA (+)	19	0.00	2.72	0.01	2.18	BnaC05g04590D	Oxygen-evolving enhancer protein 2, chloroplastic	1014	TCCTGAAGATTTCTCTGCA |||||| |||| |||| TTGCAGGACTTGTAAACAGAGGTCTTACAAAC	DT2	0.00	0.44	0.00	0.00	84174	-0.31	77609	-0.12
CGAGAACATATCAGTGCTTGAA (+)	22	0.00	5.81	0.00	7.81	BnaC02g01060D	Translation factor GUF1 homolog, chloroplastic	4254	CGAGAACATATCAGTGCTTGAA ||||| ||||| oo|o|||| GAAGGCTCTT-TATAGAGGTGGACTTGGTTAG	DT2	0.00	2.40	0.00	0.00	3411	-0.63	4747	-1.09
CGAGAACATATCAGTGCTTG (+)	20	0.00	1.85	0.00	1.18	BnaAnng06020D	Translation factor GUF1 homolog, chloroplastic	4437	CGAGAACATATCAGTGCTTG |||||| ||||| oo|o|| GAAGGCTCTT-TATAGAGGTGGACTTGGTTAG	DT2	0.00	2.40	0.00	0.00	3770	-0.31	5245	-1.00
AGCAGGCAGAGAAGGAGAAGA (+)	21	0.01	16.08	0.00	11.04	BnaC05g44310D	Zinc finger protein CONSTANS-LIKE 9	2805	AGCAGGCAGAGAAGGAGAAGA || |o||||||||o|o ||| TCTCTC-TTCGTCTCTTCTTTCTCTTTCATC	DT2	0.00	3.02	0.00	0.00	260	1.64	608	0.70
TTGATCCTGAAGATTTCTCTG (+)	21	0.01	8.69	0.00	5.64	BnaA09g29410D	Transcription factor PRE6	138	TTGATCCTGAAGATTTCTCTG |||| ||||||o| |||| ACAGAACTTGCACTACTAGA-AGACGAGCTGT	DT2	0.00	3.55	0.00	0.00	195	-1.07	45	1.38
CGAGAACATATCAGTGCTTGAA (+)	22	0.00	5.81	0.00	7.81	BnaAnng06020D	Translation factor GUF1 homolog, chloroplastic	4437	CGAGAACATATCAGTGCTTGAA ||||| ||||| oo|o|||| GAAGGCTCTT-TATAGAGGTGGACTTGGTTAG	DT2	0.00	2.40	0.00	0.00	3770	-0.31	5245	-1.00
AGAACCGAGAACATTGAGAA (+)	20	0.01	4.14	0.00	4.01	BnaC02g03830D	unknown	834	AGAACCGAGAACATTGAGAA |||| |o||||||||| GAAGTCTTCGTTCTTGTA-CTCAGTCAAATCG	DT2	0.00	1.33	0.00	0.00	56	0.00	128	-0.15
CGAAGCAGAAGTCCATCAGAG (+)	21	0.02	49.63	0.02	27.47	BnaA08g22510D	Phosphoserine phosphatase, chloroplastic	1905	CGAAGCAGAAGTCCATCAGAG ||||| ||| ||||||| AAGTGCTTCGACTTGAGGTCGTATCGTATACT	DT2	0.00	2.84	0.00	0.00	117	-0.26	88	-0.68
GGCAGAGAAGGAGAAGAAGGA (+)	21	0.00	14.92	0.00	15.67	BnaC04g10180D	Retrovirus-related Pol polyprotein from transposon TNT 1-94	8639	GGCAGA-GAAGGAGAAGAAGGA |||||||o||| ||||| TCTCCTTCTCCTTCTTCTGCTTCCTCTCTATC	DT2	0.00	0.09	0.00	0.00	742	0.37	604	0.42
TATGGAGCTCTTGAGGCAGTT (+)	21	0.01	32.53	0.04	21.34	BnaC08g19360D	Catalase-3	1541	TATGGAGCTCTTGAGGCAGTT o |||||||| |||| |||o TTGTGGACCTCGAGA-CTCCTTCAGTCGTGTT	DT2	0.00	2.49	0.00	0.00	206744	0.47	335599	0.67
TCTTCTCCTTCTCTGCCTGCT (-)	21	0.00	14.53	0.00	10.41	BnaC04g03420D	unknown	1664	TCTTCTCCTTCTCTGCCTGCT ||||||| ||||||| ||| AGTTAGAAGAGGTAGAGACG-AGGAGCACGTG	DT2	0.00	2.84	0.00	0.00	400	0.41	667	0.12
CACTTCTCTACCCATTTTGTT (-)	21	0.00	2.88	0.01	1.75	BnaC05g19100D	E3 ubiquitin-protein ligase Topors	1368	CACTTCT-CTACCCATTTTGTT ||o||| ||||||||o| GTGGTGGAGATGATGGGTATAATTATTCAGAT	DT2	0.00	3.02	0.00	0.00	264	-0.16	421	-0.08
TCTTTGTCACTCTCGTGTGCT (-)	21	0.01	54.27	0.02	40.69	BnaCnng04170D	G-type lectin S-receptor-like serine/threonine-protein kinase At1g61420	217	TCTTTGTCACTCTCGTGTGCT |||o| || |||||| o||| AGAGAGAGAGAGAGAGAGCAAGCGATCGCCAT	DT2	0.00	9.95	0.00	0.00	0	NA	0	NA
ATCTCGATGTTTCCAACTTTC (-)	21	0.01	6.48	0.01	5.29	BnaA02g19290D	Syntaxin-52	737	ATCTCGATGTTTCCAACTTTC |||||o| |||o||||o| AAACTAGAGTT-CAAGGGTTGGTATAGGAATG	DT2	0.00	0.09	0.00	0.00	1252	1.14	1631	0.45
TTCAAGCACTGATATGTTCTC (-)	21	0.00	11.41	0.01	7.87	BnaA03g58480D	unknown	2595	TTCAAGCACTGATATGTTCTC ||| |o|| |||||||| AGAAAAGGTTGTAAGTATACTAGAGCACGCAC	DT2	0.00	3.38	0.00	0.00	76	0.29	243	3.53
TGCTCGGATTGTCTCTTCGCT (-)	21	0.01	48.09	0.03	30.95	BnaC03g09700D	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	5107	TGCTCGGATTGTCTCTTCGCT || |||||| | ||||o|| ATGTAGGTGCCTAAGA-AGAAGTGACTAAAAC	DT2	0.00	5.15	0.00	0.00	999	0.24	1692	0.78
CTTGAGCTGGTTCCTTATCAA (-)	21	0.00	3.15	0.00	1.84	BnaC06g34600D	unknown	1752	CTTGAGCTGGTTCCTTATCAA ||||||o|||| || | | TCACGAACTCGGCCAAGAAAGATATATTGTTT	DT2	0.00	2.75	0.00	0.00	3064	-0.76	2866	0.53
AGAGATTTCAAAACGACCAAC (-)	21	0.01	39.61	0.03	25.54	BnaC03g37640D	Protein ABIL3	1889	AGAGATTTCAAAACGACCAAC |||o||||||| | ||| AACGTCTTTAAACTTTTG-TTATTGTTTTGAG	DT2	0.00	2.40	0.00	0.00	745	-0.54	853	-0.79
TCTTTGTCACTCTCGTGTGCT (-)	21	0.01	54.27	0.02	40.69	BnaC07g21160D	unknown	1202	TCTTTGTCACTCTCGTGTGCT |||o| || |||||o||| | AGAGAGAGAGAGAGAGAGCGCACTATTTTGTA	DT2	0.00	9.95	0.00	0.00	2354	0.19	91	0.62
ATCTCGATGTTTCCAACTTTC (-)	21	0.01	6.48	0.01	5.29	BnaA07g35020D	Syntaxin-52	833	ATCTCGATGTTTCCAACTTTC |||||o| |||o||||o| AAACTAGAGTT-CAAGGGTTGGTATAGGAACG	DT2	0.00	0.09	0.00	0.00	6895	0.08	11581	0.17
TCTTTGTCACTCTCGTGTGCT (-)	21	0.01	54.27	0.02	40.69	BnaC01g20600D	Cytochrome c oxidase subunit 6b-2	1095	TCTTTGTCACTCTCGTGTGCT |||o| || ||||||| ||| AGAGAGAGAGAGAGAGAGCAAA-GAAGAATAT	DT2	0.00	9.95	0.00	0.00	2123	-0.31	2419	0.03
TGCACCACTGTGGATTATC (-)	19	0.00	3.07	0.00	3.75	BnaC02g33150D	Sulfite oxidase	503	TGCACCACTGTGGATTATC o||| |||||o|| || | ATGGGCGT-GTGACATCTCATCGTCACTGTAA	DT2	0.00	0.09	0.00	0.00	5754	-0.28	6669	-0.47
ATCTCGATGTTTCCAACTTTC (-)	21	0.01	6.48	0.01	5.29	BnaC06g39950D	Syntaxin-52	875	ATCTCGATGTTTCCAACTTTC ||||o| |||o||||o| AAACTAGAGTT-CAAGGGTTGGTATAGGAACG	DT2	0.00	0.09	0.00	0.00	2984	0.40	3077	0.33
TCTCCTTCTTCTCCTTCTCTG (-)	21	0.00	3.37	0.00	2.64	BnaC07g28010D	F-box/LRR-repeat/kelch-repeat protein At1g09650	973	TCTCCTTCTTCTCCTTCTCTG ||||||||||||||oo TTGAAGAAGAAGAAGAAGAAGAGGTGTTTTTA	DT2	0.00	2.58	0.00	0.00	0	NA	0	NA
TCCTTCTTCTCCTTCTCTGCC (-)	21	0.01	11.63	0.00	9.29	BnaC09g48790D	unknown	510	TCCTTCTTCTCCTTCTCTGCC |||||||| |||| |||| GAAGAAGAAGAAGAAGAAGAAACGGTAGAAAT	DT2	0.00	2.22	0.00	0.00	411	-1.55	965	-1.54
TTCAAGCACTGATATGTTCTCG (-)	22	0.01	16.85	0.00	15.92	BnaA03g58480D	unknown	2595	TTCAAGCACTGATATGTTCTCG ||| |o|| ||||| |||| AGAAAAGGTTGTAAGTATACTAGAGCACGCAC	DT2	0.00	3.38	0.00	0.00	76	0.29	243	3.53
TCTTTGTCACTCTCGTGTGCT (-)	21	0.01	54.27	0.02	40.69	BnaA09g45920D	Ankyrin repeat domain-containing protein 49	1497	TCTTTGTCACTCTCGTGTGCT |||o| || |||||| |||| AGAGAGAGAGAGAGAGAGAAAACGACAATCGA	DT2	0.00	9.95	0.00	0.00	1639	0.46	3125	0.46
TTCAAGCACTGATATGTTCTCG (-)	22	0.01	16.85	0.00	15.92	BnaA03g38950D	Cold-regulated 413 plasma membrane protein 4	872	TTCAAGCACTGATATGTTCTCG o|||| ||o|||||||| GGTGGACTTCGAGATTATACAAGAACCTCGTT	DT2	0.00	4.71	0.00	0.00	13485	0.00	12495	0.25
TCCTTCTTCTCCTTCTCTGCC (-)	21	0.01	11.63	0.00	9.29	BnaC04g03350D	60S ribosomal protein L7-3	1587	TCCTTCTTCTCCTTCTCTGCC |||||||| |||||||| GAAGAAGAAGAAGAAGAAGACGCGGCGCGA	DT2	0.00	2.22	0.00	0.00	1877	-0.50	2166	-0.59

TCTTTGTCACTCTCGTGTGCT (-)	21	0.01	54.27	0.02	40.69	BnaC04g09270D	unknown	2394	TCTTTGTCACTCTCGTGTGCT |||o| || |||||||| AGAGAGAGAGAGAGAGAGAACACAACACGAAG	DT2	0.00	9.95	0.00	0.00	424	0.03	505	-0.28
AACTGCCTCAAGAGCTCCATA (-)	21	0.01	32.88	0.04	29.44	BnaA06g22690D	UPF0235 protein At5g63440	6830	AACTGCCTCAAGA-GCTCCATA ||| ||||||||| ||| | o| TATGTTGCCGGAGTTCTTCGAAGAGTATGTGG	DT2	0.00	0.09	0.00	0.00	618	0.57	1058	0.24
TCTTTGTCACTCTCGTGTGCT (-)	21	0.01	54.27	0.02	40.69	BnaC06g22550D	Mitochondrial import inner membrane translocase subunit Tim13	438	TCTTTGTCACTCTCGTGTGCT |||o| || ||||||||o| AGAGAGAGAGAGAGAGAGCACATCAACTTATA	DT2	0.00	9.95	0.00	0.00	266	0.03	233	0.72
TTCAAGCACTGATATGTTCTC (-)	21	0.00	11.41	0.01	7.87	BnaA07g12810D	Heme oxygenase 1, chloroplastic	1196	TTCAAGCACTGATATGTTCTC |o||o|| ||||| |||| GAGAAGGTTTGTTACTA-AGAAGAGAAGAGAG	DT2	0.00	2.04	0.00	0.00	5165	0.09	6234	-0.16
TCCTTCTTCTCCTTCTCTGCC (-)	21	0.01	11.63	0.00	9.29	BnaA05g11520D	Transcription factor bHLH10	1041	TCCTTCTTCTCCTTCTCTGCC |||||||| |||||oo|| GAAGAAGAAGAAGAAGAAGAGGTGGTTGAGAT	DT2	0.00	2.22	0.00	0.00	2	0.52	0	-0.18
AGGAGCTTTCCCTTCTTGTGC (-)	21	0.00	5.80	0.02	3.28	BnaA08g23210D	unknown	467	AGGAGCTTTCCCTTCTTGTGC ||||| ||||| |||||||| TCCCTCCTC-AAAGGACAGAACACGCCACTCT	DT2	0.00	1.16	0.00	0.00	229	0.84	298	0.38
GTTTGCCAACATGTCTTCTTT (-)	21	0.01	6.52	0.01	4.24	BnaC03g33070D	Putative lipid phosphate phosphatase 3, chloroplastic	1487	GTTTGCCAACATGTCTTCTTT ||o|o|||| ||o||||| GCGCCAGATGGTTG-ACGCAAGAAATAGCTTA	DT2	0.00	0.09	0.00	0.00	192	-0.51	84	-0.79
TCGGTTCTGTTCTTCAGGTAT (-)	21	0.00	4.80	0.00	2.98	BnaA10g29460D	Zinc finger CCCH domain-containing protein 66	2046	TCGGTTCTGTTCTTCAGGTAT || ||||||| ||o||||| TGCCAGACAAGACA-GAGGTACATACTAACGA	DT2	0.00	2.75	0.00	0.00	2099	1.16	1610	0.45
TCTTTGTCACTCTCGTGTGCT (-)	21	0.01	54.27	0.02	40.69	BnaC08g06970D	unknown	2974	TCTTTGTCACTCTCGTGTGCT |||o| || ||||||o|| AGAGAGAGAGAGAGAGAGCATACCAATTTCTA	DT2	0.00	9.95	0.00	0.00	33	1.24	41	0.86
TCTTTGTCACTCTCGTGTGCT (-)	21	0.01	54.27	0.02	40.69	BnaC05g47830D	Protease Do-like 7	5308	TCTTTGTCACTCTCGTGTGCT |||o| || |||||||| AGAGAGAGAGAGAGAGAG-ACACGTAAAGTAA	DT2	0.00	9.95	0.00	0.00	161	0.89	685	-0.03
GTTTGCCAACATGTCTTCTTT (-)	21	0.01	6.52	0.01	4.24	BnaA03g28040D	Putative lipid phosphate phosphatase 3, chloroplastic	1107	GTTTGCCAACATGTCTTCTTT ||o|o|||| ||o||||| GCGCCAGATGGTTG-ACGCAAGAAATAGCTTA	DT2	0.00	0.09	0.00	0.00	1071	-0.42	758	-0.75
TCTTTGTCACTCTCGTGTGCT (-)	21	0.01	54.27	0.02	40.69	BnaC03g14000D	WEB family protein At5g55860	987	TCTTTGTCACTCTCGTGTGCT |||o| || |||||||| AGAGAGAGAGAGAGAGAGAACAC-ATTATTTT	DT2	0.00	9.95	0.00	0.00	44	1.55	142	0.48
GCTCGGATTGTCTCTTCGCTT (-)	21	0.00	19.90	0.01	8.93	BnaC01g20330D	ATPase family AAA domain-containing protein 1-A	1185	GCTCGGATTGTCTCTTCGCTT |||| ||| |||||||| || AGCTCGAGACTACCAGACAAGC-AACGTCGTT	DT2	0.00	5.24	0.00	0.00	1392	-0.17	1457	0.00
TCTTTGTCACTCTCGTGTGCT (-)	21	0.01	54.27	0.02	40.69	BnaAnng12590D	Serine/threonine-protein kinase Nek4	1004	TCTTTGTCACTCTCGTGTGCT |||o| || |||||| |||| AGAGAGAGAGAGAGAGAGC-CACGACACACAC	DT2	0.00	9.95	0.00	0.00	107	0.28	168	0.51
TTTGCCTCTCTCGTTCCTTTT (-)	21	0.02	12.25	0.00	9.24	BnaC09g21210D	unknown	1674	TTTGCCTCTCTCGTTCCTTTT ||||| |||||||||||o| CGAGAAACGAAAAGAGCAAGGAAGAGGGCGAG	DT2	0.00	2.13	0.00	0.00	418	0.23	618	0.04
TCCTTCTTCTCCTTCTCTGCC (-)	21	0.01	11.63	0.00	9.29	BnaC06g10270D	26S protease regulatory subunit 7 homolog A	90	TCCTTCTTCTCCTTCTCTGCC |||||||| ||||| |||| GAAGAAGAAGAAGAAGAAGA-ACGGTCCTCGA	DT2	0.00	2.22	0.00	0.00	26	0.35	14	0.48
TCTTCTCCTTCTCTGCCTGCT (-)	21	0.00	14.53	0.00	10.41	BnaA03g20710D	unknown	1607	TCTTCTCCTTCTCTGCCTGCT ||||||| ||||||| ||| AGTTAGAAGAGGTAGAGACG-AGGAGTACGTG	DT2	0.00	2.84	0.00	0.00	53	0.73	79	-0.44
TCTTTGTCACTCTCGTGTGCT (-)	21	0.01	54.27	0.02	40.69	BnaC08g40790D	unknown	133	TCTTTGTCACTCTCGTGTGCT |||o| || ||||o|o||| AGAGAGAGAGAGAGAGTTTACGACAGAGAA	DT2	0.00	9.95	0.00	0.00	110	0.51	260	0.80
CAGATTCCCTCTCTTTTGTGC (-)	21	0.00	13.10	0.00	10.58	BnaC09g09560D	bZIP transcription factor 27	352	CAGATTCCCTCTCTTTTGTGC ||||||||| o|||| | CGTCGTCTAAGAGACAAGAAACA-GTATGCCA	DT2	0.00	1.95	0.00	0.00	281	1.12	101	-0.60
TCTTTGTCACTCTCGTGTGCT (-)	21	0.01	54.27	0.02	40.69	BnaC06g33580D	40S ribosomal protein SA	1555	TCTTTGTCACTCTCGTGTGCT |||o| || ||||||||o| AGAGAGAGAGAGAGAGAGCACATTAAAAGTTG	DT2	0.00	9.95	0.00	0.00	1108	-0.18	1374	-0.28
TCTTTGTCACTCTCGTGTGCT (-)	21	0.01	54.27	0.02	40.69	BnaC08g49820D	Uncharacterized protein At4g28440	189	TCTTTGTCACTCTCGTGTGCT |||o| || |||||| |||| AGAGAGAGAGAGAGAGAG-AGACGAAACTCAA	DT2	0.00	9.95	0.00	0.00	715	-0.15	794	-0.17
TTCAAGCACTGATATGTTCTC (-)	21	0.00	11.41	0.01	7.87	BnaA03g38950D	Cold-regulated 413 plasma membrane protein 4	872	TTCAAGCACTGATATGTTCTC o| |||| ||o|||||||| GGTGGACTTCGAGATTATACAAGAACCTCGTT	DT2	0.00	4.71	0.00	0.00	13485	0.00	12495	0.25
TCTTTGTCACTCTCGTGTGCT (-)	21	0.01	54.27	0.02	40.69	BnaC02g46260D	Eukaryotic initiation factor 4A-3	3361	TCTTTGTCACTCTC-GTGTGCT |||o| || ||||| |||o|| AGAGAGAGAGAGAGAGAGACACATGAAACACA	DT2	0.00	1.24	0.00	0.00	34	-0.77	44	-0.45
TCTTTGTCACTCTCGTGTGCT (-)	21	0.01	54.27	0.02	40.69	BnaA01g16060D	Polyadenylate-binding protein RBP45C	2947	TCTTTGTCACTCTCGTGTGCT |||o| || |||||||| AGAGAGAGAGAGAGAGAG-ACAGGAAACGGGA	DT2	0.00	9.95	0.00	0.00	1264	0.94	1553	0.36
AGCTTCCTCAGCGCTGTTTCC (-)	21	0.00	3.00	0.00	2.05	BnaA03g26510D	Protein TolB	1799	AGCTTCCTCAGCGCTGTTTCC |||o|||||o| ||||| GCAGTCGGAGGAGTTGGGTCAA-GGCAGGTTG	DT2	0.00	1.24	0.00	0.00	4814	-0.02	4286	-0.99
CATCTTCATAATCCTCAAAGA (-)	21	0.02	25.23	0.00	20.64	BnaC03g34850D	unknown	297	CATCTTCATAATCCTCAAAGA |||o|| || ||||| |||| AGGAGGAGGAGGATGAGGAGGTTCTAGGAGGC	DT2	0.00	2.93	0.00	0.00	40	-1.63	13	0.15
TCTTCTCCTTCTCTGCCTGCT (-)	21	0.00	14.53	0.00	10.41	BnaA05g03810D	unknown	1698	TCTTCTCCTTCTCTGCCTGCT ||||||| ||||||| ||| AGTTAGAAGAGGTAGAGACG-AGGAGCACGTG	DT2	0.00	2.84	0.00	0.00	141	0.81	451	-0.01
TGCACCACTGTGGATTATC (-)	19	0.00	3.07	0.00	3.75	BnaA02g25010D	Sulfite oxidase	1193	TGCACCACTGTGGATTATC o||| |||||o|| ||| ATGGGCGT-GTGACATCTCATCGTCACTGTAA	DT2	0.00	0.09	0.00	0.00	5337	-0.49	6854	-0.14
CTTTGAGGATTATGAAGATGG (+)	21	0.01	15.65	0.01	11.75	BnaCnng78640D	Callose synthase 2	1268	CTTTGAGGATTATGAAGATGG ||||||||| |||||| AAAAAAAACTCCTAAATCTTCTACAGAGTTTG	DT3	0.00	0.36	0.00	0.00	254	0.50	1035	0.03
ATGAGATGTTTGCTACATGAG (+)	21	0.05	90.54	0.04	77.55	BnaC07g15020D	Nascent polypeptide-associated complex subunit alpha-like protein 4	1105	ATGAGATGTTTGCTACATGAG |||||o|||o|| |||o TCTTTACTCTGCAAATTAT-TACTTTTCTCCT	DT3	0.00	0.91	0.00	0.00	4080	-0.26	2578	-0.40
AAAGTTGGAAACATCGAGATC (+)	21	0.01	41.93	0.01	34.07	BnaC02g08490D	Serine/threonine-protein kinase EDR1	143	AAAGTTGGAAACATCGAGATC |||o|| ||| |||o| GAGGTTTCGACATTTATAG-TCTGGACATAGT	DT3	0.00	0.91	0.00	0.00	22	-0.20	0	NA
GAACCGAGAACATTGAGAA (+)	19	0.00	2.65	0.00	1.82	BnaA03g32780D	Uncharacterized WD repeat-containing protein C2A9.03	1462	GAACCGAGAACATTGAGAA |||||||||||||||| TGTAC-TGGCGCTTGTAACTCTTGAAGGAAGA	DT3	0.00	0.05	0.00	0.00	2628	1.05	3580	0.19

ATGTCACTGATGAGAATGACA (+)	21	0.03	75.41	0.02	65.78	BnaA05g05400D	PRA1 family protein B2	781	ATGTCACTGATGAGAATGACA TGGGTACA-TTACTACTCTTGTTGTTCTCATA	DT3	0.00	0.64	0.00	0.00	177	0.20	292	0.16
ATCAAAGTCACGAGGACAA (+)	19	0.01	5.36	0.00	4.18	BnaA02g21580D	Hydroxymethylglutaryl-CoA synthase	3053	ATCAAAGTCACGAGGACAA GATTTAGTTTCATTGTTCTTGGAATATTTTTG	DT3	0.00	0.54	0.00	0.00	574	0.48	474	0.13
GAACCGAGAACATTGAGAA (+)	19	0.00	2.65	0.00	1.82	BnaC03g37880D	Uncharacterized WD repeat-containing protein C2A9.03	823	GAACCGAGAACATTGAGAA TGTAC-TGGCGCTTGTAACTCTTGAAGGAAGA	DT3	0.00	0.05	0.00	0.00	4820	0.92	5107	0.19
CAGAGAAGGAGAAGAAGGAGA (+)	21	0.00	16.42	0.00	12.78	BnaA08g20540D	Probable alanine aminotransferase, mitochondrial	2827	CAGAGAAGGAGAAGAAGGAGA TATTGT-TCTTCTTCTTCTTCTTCTTCTT	DT3	0.00	0.68	0.00	0.00	52960	0.16	60702	-0.60
ATGTGTGTTGTTGTTACTTTC (+)	21	0.00	6.98	0.00	5.84	BnaC04g32090D	Ferredoxin-thioredoxin reductase catalytic chain, chloroplastic	1649	ATGTGTGTTGTTGTTACTTTC AGTGTACACTCGACAACAAAGAAACTAAAGTA	DT3	0.00	1.54	0.00	0.00	21191	-0.76	17515	0.27
GGCAGAGAAGGAGAAGAAGGA (+)	21	0.00	14.92	0.00	15.67	BnaAnng12610D	Selenocysteine Se-methyltransferase	2165	GGCAGA-GAAGGAGAAGAAGGA AAACCGTTTCCTTCCTTTTTTTTTTTGTTTC	DT3	0.00	0.82	0.00	0.00	32	-0.25	157	0.67
ATGTGTGTTGTTGTTACTTTC (+)	21	0.00	6.98	0.00	5.84	BnaA04g09900D	Ferredoxin-thioredoxin reductase catalytic chain, chloroplastic	1765	ATGTGTGTTGTTGTTACTTTC AGTGTACACTCGACAACAAAGAAACTAAAGTA	DT3	0.00	1.54	0.00	0.00	10879	-1.20	23141	0.16
GAACCGAGAACATTGAGAA (+)	19	0.00	2.65	0.00	1.82	BnaC08g31360D	Aquaporin PIP1.1	1209	GAACCGAGAACATTGAGAA TTCACTTGGTTCTTTTGACGTTTGGGCTAACC	DT3	0.00	0.05	0.00	0.00	23730	-1.23	420	-1.59
GGAGAAGAACTTTTCACTGGA (+)	21	0.00	9.17	0.01	5.49	BnaA08g04820D	Photosystem I reaction center subunit XI, chloroplastic	1177	GGAGAAGAACTTTTCACTGGA GAGGCTTCTTCTTGGGAGGTCATTTGAATCGG	DT3	0.00	0.27	0.00	0.00	165917	-0.97	71693	-0.26
CAGAGAAGGAGAAGAAGGAGAG (+)	22	0.00	2.00	0.00	2.18	BnaA08g20540D	Probable alanine aminotransferase, mitochondrial	2827	CAGAGAAGGAGAAGAAGGAGAG TCTTCTTCTTCTTCTTCTTCTT	DT3	0.00	0.68	0.00	0.00	52960	0.16	60702	-0.60
GAACCGAGAACATTGAGAA (+)	19	0.00	2.65	0.00	1.82	BnaC02g24930D	F-box protein At1g78280	6954	GAACCGAGAACATTGAGAA TTGAATTGTCTTTTGTTATTCTTTTCATTCTT	DT3	0.00	0.41	0.00	0.00	0	0.22	25	-1.93
TTGATCCTGAAGATTTCTCTG (+)	21	0.01	8.69	0.00	5.64	BnaA05g02670D	unknown	1265	TTGATCCTGAAGATTTCTCTG CAAGAACTAGTATTTCAAAAGAGTTTGAGGTA	DT3	0.00	0.50	0.00	0.00	1558	-1.01	940	-0.26
ATGAGATGTTTGCTACATGAG (+)	21	0.05	90.54	0.04	77.55	BnaC07g15050D	Nascent polypeptide-associated complex subunit alpha-like protein 4	818	ATGAGATGTTTGCTACATGAG TCTTTACTCTGCAAATTAT-TACTTTTCTCCT	DT3	0.00	0.91	0.00	0.00	3121	-0.25	1749	-0.39
GAGGCACACATCCAGATGAAA (+)	21	0.00	3.90	0.00	3.21	BnaA06g19730D	Nicalin	3926	GAGGCACACATCCAGATGAAA TTGTCTCCGTATGTTG-TCTTCTTTCTCAATT	DT3	0.00	0.05	0.00	0.00	1642	0.58	1687	0.40
GAGAAGTTGAGTTCTCCACTC (+)	21	0.00	4.51	0.00	3.28	BnaC08g35000D	E3 ubiquitin-protein ligase ORTHRUS 1	1059	GAGAAGTTGAGTTCTCCACTC TACGCCCTTC-ACTCGAGGGGTGACGGCCGTG	DT3	0.00	1.27	0.00	0.00	508	1.57	2122	-0.18
GTTTGCCAACATGTCTTCTTT (-)	21	0.01	6.52	0.01	4.24	BnaA02g35780D	ACT domain-containing protein ACR4	1404	GTTTGCCAACATGTCTTCTTT AGTGCAAACTGTTGTTCGGATGAGATAGGCAG	DT3	0.00	0.05	0.00	0.00	118	1.08	154	0.21
TCTTTGTCACTCTCGTGTGCT (-)	21	0.01	54.27	0.02	40.69	BnaCnng74000D	unknown	1178	TCTTTGTCACTCTCGTGTGCT TCTAAGAAACAGTGGGAGCTTAGGAAGTAGAG	DT3	0.00	0.05	0.00	0.00	1540	0.00	2383	-1.10
TCAAGCACTGATATGTTCTCG (-)	21	0.00	23.20	0.02	13.86	BnaA03g46010D	unknown	1154	TCAAGCACTGATATGTTCTCG AACTAGTTCGTGGCTCTGTTAGAGATCAGACG	DT3	0.00	1.18	0.00	0.00	517	-0.94	368	0.15
TCTCCTTCTTCTCCTTCTCTG (-)	21	0.00	3.37	0.00	2.64	BnaA09g40650D	FATTY ACID EXPORT 7	94	TCTCCTTCTTCTCCTTCTCTG AAGAAGAAGAAGAAGAAGAAGAGACACAAGAG	DT3	0.00	0.73	0.00	0.00	1069	0.54	1826	0.00
CAGATTCCCTCTCTTTTGTGC (-)	21	0.00	13.10	0.00	10.58	BnaC07g39310D	Magnesium protoporphyrin IX methyltransferase, chloroplastic	36	CAGATTCCCTCTCTTTTGTGC TTGAGTCTTAGTGAGAGAAGAGACGATTTCTT	DT3	0.00	0.05	0.00	0.00	0	NA	0	NA
TGCAGAGAAATCTTCAGGATC (-)	21	0.02	40.38	0.00	31.94	BnaA03g28370D	unknown	916	TGCAGAGAAATCTTCAGGATC TAAAACGT-TCTTTAAAAGTCTTAATGTAAAT	DT3	0.00	0.50	0.00	0.00	101257	1.32	5	-0.08
CTTGAGCTGGTTCCTTATCAA (-)	21	0.00	3.15	0.00	1.84	BnaC04g01050D	DNA-directed RNA polymerase II subunit 2	5525	CTTGAGCTGGTT-CCTTATCAA GCGGGAAGTCGACCAACGGAACAATTCTAAAC	DT3	0.00	2.54	0.00	0.00	741	0.77	1011	0.04
AATCGACGAAGAGGTTCCTCT (-)	21	0.01	6.25	0.00	3.43	BnaA06g13620D	BRASSINAZOLE-RESISTANT 2	836	AATCGACGAAGAGGTTCCTCT CTCCTTCGCTGCTTCCCTAGGGGGGCAAGGAC	DT3	0.00	0.09	0.00	0.00	4541	-0.94	5546	-0.61
GCTCGGATTGTCTCTTCGCTT (-)	21	0.00	19.90	0.01	8.93	BnaC07g39750D	Pre-mRNA cleavage factor Im 25 kDa subunit 2	1098	GCTCGGATTGTCTCTTCGCTT TGGTCG-GCTTAACGGAGGTTCGAATGACCAG	DT3	0.00	0.05	0.00	0.00	1069	-0.13	971	0.36
TCGGTTCTGTTCTTCAGGTAT (-)	21	0.00	4.80	0.00	2.98	BnaA10g04730D	unknown	2694	TCGGTTCTGTTCTTCAGGTAT GAAGAGTCGAGACAA-ATGTCTATTCTTTTTT	DT3	0.00	0.05	0.00	0.00	13875	0.43	20448	0.46
GTTTGCCAACATGTCTTCTTT (-)	21	0.01	6.52	0.01	4.24	BnaA10g09960D	unknown	1271	GTTTGCCAACATGTCTTCTTT GGCCCAAACGGTGG-ACAGAAAAAGAGTAGGG	DT3	0.00	0.91	0.00	0.00	2550	0.37	2408	0.58
TAATTTTGAAGTTAGCTTTGA (-)	21	0.01	5.86	0.00	5.20	BnaA09g32000D	STRICTOSIDINE SYNTHASE-LIKE 5	1512	TAATTTTGAAGTTAGCTTTGA GAATATTATAACTT-ATTTGAAACTATATCTT	DT3	0.00	0.32	0.00	0.00	450	0.20	305	0.57
CTCCTTCTCTGCCTGCTTTTG (-)	21	0.00	3.86	0.00	3.42	BnaA07g37840D	Triosephosphate isomerase, cytosolic	362	CTCCTTCTCTGCCTGCTTTTG GAGAGAGGGAGAGAGGGAGGAATACATGTACT	DT3	0.00	0.05	0.00	0.00	9	0.00	2	0.20
AATCGACGAAGAGGTTCCTCT (-)	21	0.01	6.25	0.00	3.43	BnaA03g56710D	14-3-3-like protein GF14 mu	443	AATCGACGAAGAGGTTCCTCT CGAGCTAGCTGC-TCTTCTAGGAGGTGCTTCG	DT3	0.00	0.82	0.00	0.00	20660	-0.42	17262	0.02
GTTTGCCAACATGTCTTCTTT (-)	21	0.01	6.52	0.01	4.24	BnaC09g32420D	unknown	1067	GTTTGCCAACATGTCTTCTTT GGCCCAAACGGTGGT-CAGAAAAAGAGTAGGG	DT3	0.00	0.91	0.00	0.00	1265	0.60	1241	1.16
TTGCAATACAACTTGGAACTT (-)	21	0.07	147.07	0.10	122.43	BnaA09g03890D	60S ribosomal protein L18-2	1802	TTGCAATACAACTTGGAACTT TTGGAGCGTTGT-TGGAATCTGGAACTTTGGT	DT3	0.00	0.95	0.00	0.00	5462	-0.45	4250	-0.33

TCCTGAAGATTTCTCTGCA (+)	19	0.00	2.72	0.01	2.18	BnaC05g02020D	Probable serine/threonine-protein kinase At1g54610	3025	TCCTGAAGATTTCTCTGCA TTTAAGGACTTCGACGGACA-GTACAAGGAGT	TT1	0.00	0.00	0.00	0.03	374	0.79	937	-0.24
TACCAGAACTCATCGAAGC (+)	19	0.00	1.79	0.00	2.25	BnaA05g05590D	Nematode resistance protein-like HSPRO2	1238	TACCAGAACTCATCGAAGC ACCGA-GGTCTTGAGAGGGTTCTTGCAGAAGC	TT1	0.00	0.00	0.00	170.97	20946	-0.27	12277	0.61
TACCAGAACTCATCGAAGC (+)	19	0.00	1.79	0.00	2.25	BnaC05g16520D	Nematode resistance protein-like HSPRO2	227	TACCAGAACTCATCGAAGC ACCGA-GGTCTTGAGAGGGTTCTTGCAGAATC	TT1	0.00	0.00	0.00	0.12	0	NA	3	0.63
TACCAGAACTCATCGAAGC (+)	19	0.00	1.79	0.00	2.25	BnaC04g05370D	Nematode resistance protein-like HSPRO2	572	TACCAGAACTCATCGAAGC ACCGA-GGTCTTGAGAGGGTTCTTACAGAATC	TT1	0.00	0.00	0.00	170.97	0	NA	153	0.54
TGAAGAACAGAACCGAGAA (+)	19	0.00	2.77	0.00	2.00	BnaA05g06490D	Vacuolar cation/proton exchanger 1	3799	TGAAGAACAGAACCGAGAA TCTTACTT-TTATCTTGTCTTTCGTATGTATC	TT1	0.00	0.00	0.00	0.06	56218	0.06	37596	0.41
TACCAGAACTCATCGAAGC (+)	19	0.00	1.79	0.00	2.25	BnaC01g08680D	Nematode resistance protein-like HSPRO2	227	TACCAGAACTCATCGAAGC ACCGA-GGTCTTGAGAGGGTTCTTGCAGAATC	TT1	0.00	0.00	0.00	0.12	0	NA	48	0.50
TACCAGAACTCATCGAAGC (+)	19	0.00	1.79	0.00	2.25	BnaC08g27070D	Nematode resistance protein-like HSPRO2	227	TACCAGAACTCATCGAAGC ACCGA-GGTCTTGAGAGGGTTCTTGCAGAATA	TT1	0.00	0.00	0.00	0.12	0	NA	48	0.50
TCCTGAAGATTTCTCTGCA (+)	19	0.00	2.72	0.01	2.18	BnaA10g02110D	Probable serine/threonine-protein kinase At1g54610	2920	TCCTGAAGATTTCTCTGCA TTTAAGGACTTCGACGGACA-GTACAAGAAGT	TT1	0.00	0.00	0.00	0.03	168	1.22	896	-0.45
TCCTTCTTCTCCTTCTCTGCC (-)	21	0.01	11.63	0.00	9.29	BnaC05g12820D	FAM32A	647	TCCTTCTTCTCCTTCTCTGCC AACAAAGAAGAAGAAGAAGA-ACTGAGGTGGA	TT1	0.00	0.00	0.00	169.36	4196	-0.39	2181	0.07
ATGTTGAGTTTTTATATTTT (-)	20	0.00	0.34	0.00	2.48	BnaC03g17480D	Pentatricopeptide repeat-containing protein At2g31400, chloroplastic	2750	ATGTTGAGTTTTTATATTTT AAAAAAAAACTCAAAAACATAATAGAGCACTG	TT1	0.00	0.00	0.00	0.09	549	-0.66	529	0.33
TTTTCCTTTAACTGTGTGCTT (-)	21	0.00	31.87	0.01	19.91	BnaC07g43040D	CBL-interacting serine/threonine-protein kinase 6	1156	TTTTCCTTTAACTGTGTGCTT TCAGAGAAGGAATTTGA-ACACGTGCCTCTCT	TT1	0.00	0.00	0.00	0.03	7528	-1.29	4024	-0.65
TCCTTCTTCTCCTTCTCTGCC (-)	21	0.01	11.63	0.00	9.29	BnaA07g01940D	Nucleolar complex protein 2 homolog	3649	TCCTTCTTCTCCTTCTCTGCC ACCAAAGAAGAAGAAGAAGAAGAAGGAGACGGA	TT1	0.00	0.00	0.00	0.18	99	-0.23	182	-0.01
TTTGAAATCACATCACAATTG (-)	21	0.04	106.27	0.04	74.96	BnaA06g04090D	Dihydrolipoyl dehydrogenase 1, mitochondrial	1479	TTTGAAATCACATCAC-AATTG ACCAGGACCTTAGTGTAGAGGTTAGCGTATGT	TT1	0.00	0.00	0.00	0.21	6339	-0.50	7445	-0.28
CAGAGAAGGAGAAGAAGGAGA (+)	21	0.00	16.42	0.00	12.78	BnaC04g45550D	Phosphatidylinositol:ceramide inositolphosphotransferase 2	27	CAGAGAAGGAGAAGAAGGAGA CTCTCTCTC-TCTTCTACTTCTTTTATCTAAA	TT2	0.00	0.00	0.00	0.65	11056	-1.12	10110	-0.78
CAAGCGAAGAGACAATCCGAGC (+)	22	0.00	6.69	0.01	6.13	BnaC03g72010D	Aquaporin PIP2-2	42	CAAGCGAAGAGACAATCCGAGC GAACGCTCGGTTCT-TGTTCGGCTTGCAGTGG	TT2	0.00	0.00	0.00	18.14	837	-1.76	1138	-1.75
TTGATCCTGAAGATTTCTCTG (+)	21	0.01	8.69	0.00	5.64	BnaA03g39650D	Calcium sensing receptor, chloroplastic	152	TTGATCCTGAAGATTTCTCTG CGTCAACAATGACTTCTGAAGTAACGGTAGAG	TT2	0.00	0.00	0.00	20.62	34860	-0.90	25557	-1.10
CAGAGAAGGAGAAGAAGGAGA (+)	21	0.00	16.42	0.00	12.78	BnaA06g32100D	Eukaryotic translation initiation factor 3 subunit I	1675	CAGAGAAGGAGAAGAAGGAGA CTCTCTCTC-TCTTCTTCTTTGTTTTGTATAG	TT2	0.00	0.00	0.00	0.65	676	-0.11	768	0.33
TTGATCCTGAAGATTTCTCTG (+)	21	0.01	8.69	0.00	5.64	BnaCnng40790D	Calcium sensing receptor, chloroplastic	146	TTGATCCTGAAGATTTCTCTG CGTCAACAATGACTTCTGAAGTAACGGTAGAG	TT2	0.00	0.00	0.00	20.62	31417	-1.08	19182	-1.15
GGCAGAGAAGGAGAAGAAGGA (+)	21	0.00	14.92	0.00	15.67	BnaC01g02600D	Chaperone protein dnaJ 11, chloroplastic	53	GGCAGAGAAGGAGAAGA-AGGA CTCTCCGCCTCTTCTTCTCCTCTCCTTCCCTA	TT2	0.00	0.00	0.00	0.13	14229	0.09	11688	0.24
GTTTGCCAACATGTCTTCTTT (-)	21	0.01	6.52	0.01	4.24	BnaC02g18910D	ACT domain-containing protein ACR4	1806	GTTTGCCAACATGTCTTCTTT AGTGCAAGCTGTTGTTCGGATGAGATAGGCAG	TT2	0.00	0.00	0.00	13.70	123	1.28	183	-0.08
TCTTCTCCTTCTCTGCCTGCT (-)	21	0.00	14.53	0.00	10.41	BnaA06g03470D	Zinc finger CCCH domain-containing protein 38	2657	TCTTCTCCTTCTCTGCCTGCT AAGAAGAAGAAGAAGAGA-GAAAGAGAGACAG	TT2	0.00	0.00	0.00	0.13	214	0.34	388	0.11
TCCTTCTTCTCCTTCTCTGCCT (-)	22	0.00	1.17	0.00	1.92	BnaA03g06780D	unknown	4415	TCCTTCTTCTCCTTCTCTGCCT GAACAGGAAGAAGAAGAACAGGAAGAAGAAGA	TT2	0.00	0.00	0.00	13.18	181	0.98	357	0.45
CCTTCTTCTCCTTCTCTGCCT (-)	21	0.00	11.17	0.00	8.13	BnaAnng29350D	unknown	559	CCTTCTTCTCCTTCTCTGCCT TGTCAGAAGAGGAG-AAGAGGTCGAACGAATT	TT2	0.00	0.00	0.00	14.48	2639	-0.04	5680	1.49
TCCTTCTTCTCCTTCTCTGCC (-)	21	0.01	11.63	0.00	9.29	BnaC06g00930D	DNA replication licensing factor MCM2	167	TCCTTCTTC-TCCTTCTCTGCC TAGAAGAAGAAGAAGGAGGAGGCCGAGTAGAG	TT2	0.00	0.00	0.00	0.13	57	-0.33	29	0.12
TCCTTCTTCTCCTTCTCTGCCT (-)	22	0.00	1.17	0.00	1.92	BnaA01g14170D	unknown	29	TCCTTCTTCTCCTTCTCTGCCT AGCTGTGAAGAA-AGGAAGAAACCGATCATCA	TT2	0.00	0.00	0.00	3.26	1837	-0.13	1248	-0.42
TCTCCTTCTTCTCCTTCTCTG (-)	21	0.00	3.37	0.00	2.64	BnaA07g22880D	Anoctamin-like protein At1g73020	138	TCTCCTTCTTCTCCTTCTCTG AAGAAGAAGAAGAAGAAGAAGAAGAG-CTCAGGAG	TT2	0.00	0.00	0.00	0.13	0	NA	0	NA
TCTCCTTCTTCTCCTTCTCTG (-)	21	0.00	3.37	0.00	2.64	BnaCnng17860D	unknown	2377	TCTCCTTCTTCTCCTTCTCTG TAGAAGAAGAAGAAGAAGAAGAAATAGTAGTA	TT2	0.00	0.00	0.00	22.57	2425	-0.38	3587	-0.59
TCTCCTTCTTCTCCTTCTCTG (-)	21	0.00	3.37	0.00	2.64	BnaC07g15380D	Dehydrin ERD10	787	TCTCCTTCTTCTCCTTCTC-TG TCTTAGGGAAAGAAGAGGAGGCGTACGAGGCG	TT2	0.00	0.00	0.00	15.40	16379	-0.33	24732	-0.42
TCCTTCTTCTCCTTCTCTGCCT (-)	22	0.00	1.17	0.00	1.92	BnaC06g00930D	DNA replication licensing factor MCM2	167	TCCTTCTTC-TCCTTCTCTGCCT TAGAAGAAGAAGAAGGAGGAGGCCGAGTAGAG	TT2	0.00	0.00	0.00	0.13	57	-0.33	29	0.12
GAAGAGACACAGTTGGAGG (-)	19	0.00	2.47	0.00	3.06	BnaC05g17050D	Proteasome subunit beta type-3-A	60	GAAGAGA-CACAGTTGGAGG CTTCTTCTTTAGAGTCTGCCTCCTCTCTCTCT	TT2	0.00	0.00	0.00	5.74	2360	0.23	2410	0.96
TCCTTCTTCTCCTTCTCTGCCT (-)	22	0.00	1.17	0.00	1.92	BnaAnng29030D	Dehydrin ERD14	527	TCCTTCTTCTCCTTC-TCTGCCT GAACAGGAAGAAGAAGAAGGAGAAGAGTGGTA	TT2	0.00	0.00	0.00	13.18	92939	-0.04	94652	-1.37
TCCTTCTTCTCCTTCTCTGCC (-)	21	0.01	11.63	0.00	9.29	BnaAnng29030D	Dehydrin ERD14	527	TCCTTCTTCTCCTTC-TCTGCC GAACAGGAAGAAGAAGAAGGAGAAGAGTGGTA	TT2	0.00	0.00	0.00	13.18	92939	-0.04	94652	-1.37

GAAGAGACACAGTTGGAGG (-)	19	0.00	2.47	0.00	3.06	BnaC08g05980D	Cytochrome c oxidase subunit 6b-1	191	GAAGAGACACAG-TTGGAGG o ||||||||||||o TCTCTCTCTCTCTGTCGAACCTCTTCTTATTA	TT2	0.00	0.00	0.00	1.17	740	-0.66	610	-0.40
TCCTTCTTCTCCTTCTCTGCCT (-)	22	0.00	1.17	0.00	1.92	BnaA02g36030D	Dehydrin ERD14	517	TCCTTCTTCTCCTTC-TCTGCCT ||||||||| ||| ||| | o GAACAGGAAGAAGAAGAAGGAGAAGAGTGGTA	TT2	0.00	0.00	0.00	13.18	56906	0.21	128884	-1.36
TCCTTCTTCTCCTTCTCTGCC (-)	21	0.01	11.63	0.00	9.29	BnaA02g36030D	Dehydrin ERD14	517	TCCTTCTTCTCCTTC-TCTGCC ||||||||| ||| ||| | GAACAGGAAGAAGAAGAAGGAGAAGAGTGGTA	TT2	0.00	0.00	0.00	13.18	56906	0.21	128884	-1.36
AGAGGAACCTCTTCGTCGATT (+)	21	0.08	168.57	0.10	150.66	BnaC05g16520D	Nematode resistance protein-like HSPRO2	85	AGAGGAACCTCTTCGTCGATT |||o|||||||||o| |oo CGCTTCTTCTTGGAGAAGCGG-TGGCGAAGGT	TT3	0.00	0.00	0.00	0.09	0	NA	3	0.63
AGAAATACTGAAACAAAGTTG (+)	21	0.00	3.65	0.00	2.67	BnaC07g45570D	CMP-sialic acid transporter 4	520	AGAAATACTGAAACAAAGTTG |o| |||||||||| || o| TACGTTTATATGACTTTGTCTCTGCTGGGACG	TT3	0.00	0.00	0.00	0.23	61	-0.35	12	0.35
GGCAGAGAAGGAGAAGAAGGA (+)	21	0.00	14.92	0.00	15.67	BnaC09g07830D	Protein indeterminate-domain 1	973	GGCAGAGAAGGAGAAGAAGGA ||||||||||||||||||| TCCGCCGCCTCTTCCTCTTCCTCCTCCTCTTA	TT3	0.00	0.00	0.00	0.05	251	0.00	557	0.38
GGAAACAGCGCTGAGGAAGCT (+)	21	0.04	25.98	0.02	20.14	BnaAnng07000D	NAC domain-containing protein 100	873	GGAAACAGCGCTGAGGAAGCT o| |||||||||| ||||o CAATTC-TTGTCCCGACTACTTCGGTAACTCA	TT3	0.00	0.00	0.00	0.37	600	0.12	252	2.22
AGAGGAACCTCTTCGTCGATT (+)	21	0.08	168.57	0.10	150.66	BnaA01g06670D	Probable cyclic nucleotide-gated ion channel 17	2558	AGAGGAACCTCTTCGTCGATT ||||||||||||o|o| ACATCCT-CTTGGAGAAGCAGTTGAGGAGAAC	TT3	0.00	0.00	0.00	0.14	837	0.81	1946	0.81
CAACAAAATGGGTAGAGAAGT (+)	21	0.00	4.09	0.01	2.72	BnaCnng07130D	UDP-glycosyltransferase 71B2	1528	CAACAAAATGGGTAGAGAAGT |||| |||||||||o| ||o| ATTGGTTGCTTTACCCATTTGTTTACTATCGC	TT3	0.00	0.00	0.00	0.69	601	-0.97	519	0.69
AAAGTTGGAAACATCGAGATC (+)	21	0.01	41.93	0.01	34.07	BnaCnng32250D	Serine/threonine-protein kinase EDR1	1551	AAAGTTGGAAACATCGAGATC |||o|| ||||||| |||o| GAGGTTTCGACATTTGTAG-TCTGGACATAAT	TT3	0.00	0.00	0.00	0.05	0	NA	0	NA
TGAGGACGAGAAGGTTGTAAT (+)	21	0.02	37.99	0.02	23.40	BnaA03g39650D	Calcium sensing receptor, chloroplastic	1917	TGAGGACGAGAAGGTTGTAAT || |o|||||||||||| GGACACGCTTGCTCTTC-AACATTCTTAGTCA	TT3	0.00	0.00	0.00	0.05	34860	-0.90	25557	-1.10
AGCACACGAGAGTGACAAAGA (+)	21	0.01	1.11	0.00	1.39	BnaA07g33880D	unknown	978	AGCACACGAGAGTGACAAAGA |o||||||||||| ||| GGTGTTGTGTGCTCTCACTAATTGTTGTCCAA	TT3	0.00	0.00	0.00	1.25	8919	-0.65	9072	0.04
AATTATGTCACTGATGAGAAT (+)	21	0.01	6.59	0.01	2.41	BnaC02g28890D	unknown	1569	AATTATGTC-ACTGATGAGAAT |||o|o|||||o||o||||| CATTTAGTGCAGCTTATTATTCTTAGTTTTTG	TT3	0.00	0.00	0.00	0.74	1916	0.22	2503	0.01
AGAGGAACCTCTTCGTCGATT (+)	21	0.08	168.57	0.10	150.66	BnaC08g27070D	Nematode resistance protein-like HSPRO2	85	AGAGGAACCTCTTCGTCGATT |||o|||||||||o| |oo CGCTTCTTCTTGGAGAAGCGG-TGGCGAAGGT	TT3	0.00	0.00	0.00	0.09	0	NA	48	0.50
AGAAATACTGAAACAAAGTTG (+)	21	0.00	3.65	0.00	2.67	BnaA07g37360D	LOB domain-containing protein 37	438	AG-AAATACTGAAACAAAGTTG || |||||||||||||o|| ATCTCGTTTCTGACTTTGTTTCGACGCGTCTT	TT3	0.00	0.00	0.00	0.79	14521	-0.27	6914	0.24
GGCAGAGAAGGAGAAGAAGGA (+)	21	0.00	14.92	0.00	15.67	BnaA07g25910D	E3 ubiquitin-protein ligase SINA-like 2	274	GGCAG-AGAAGGAGAAGAAGGA o| ||||||o|||||||o| TCTTCTTCTTCTTCTTCTTCTTCTTCTTCGAC	TT3	0.00	0.00	0.00	0.14	1	-0.03	1	0.30
AGAAATACTGAAACAAAGTTG (+)	21	0.00	3.65	0.00	2.67	BnaA03g40660D	LOB domain-containing protein 38	425	AG-AAATACTGAAACAAAGTTG || |||||||||||||o|| ATCTCGTTTCTGACTTTGTTTCGACGTTTACT	TT3	0.00	0.00	0.00	0.79	93	0.06	69	-0.56
AGAGGAACCTCTTCGTCGATT (+)	21	0.08	168.57	0.10	150.66	BnaC01g08680D	Nematode resistance protein-like HSPRO2	85	AGAGGAACCTCTTCGTCGATT |||o|||||||||o| |oo CGCTTCTTCTTGGAGAAGCGG-TGGCGAAGGT	TT3	0.00	0.00	0.00	0.09	0	NA	48	0.50
CAAGCGAAGAGACAATCCGAGC (+)	22	0.00	6.69	0.01	6.13	BnaC04g47810D	Putative fluoride ion transporter CrcB 2	1422	CAAGCGAAGAGACAATCCGAGC | ||| |||o|||||||| CTCGGCTCG-TTCTTTGGTAGACTCGGTCTGT	TT3	0.00	0.00	0.00	0.56	1057	-0.23	945	-0.13
AAAGAAGACATGTTGGCAAAC (+)	21	0.01	23.82	0.00	11.75	BnaA08g22410D	NAP1-related protein 2	1939	AAAGAAGACATGTTGGCAAAC | |||||||||||o|||| ACAATATCTTCTGTACATTCGTTTACCACCAA	TT3	0.00	0.00	0.00	0.09	2302	-1.14	1840	-0.58
ATCCTGAAGATTTCTCTGCAG (+)	21	0.02	78.87	0.02	46.04	BnaA10g00130D	UDP-glucuronate 4-epimerase 3	3686	ATCCTGAAGATTTCTCTGCAG ||||||| |||||||| || GAATTAGGACTT-TAAAGAGAGGTATTATGTT	TT3	0.00	0.00	0.00	0.23	462	-0.09	1129	-0.03
AGAAATACTGAAACAAAGTTG (+)	21	0.00	3.65	0.00	2.67	BnaCnng56620D	LOB domain-containing protein 37	442	AG-AAATACTGAAACAAAGTTG || |||||||||||||o|| ATCTCGTTTCTGACTTTGTTTCGACGCGTGTT	TT3	0.00	0.00	0.00	0.79	8789	-0.17	7977	0.34
GAGAACATATCAGTGCTTGAA (+)	21	0.00	5.87	0.01	3.82	BnaCnng15900D	Tetraspanin-3	577	GAGAACATATCAGTGCTTGAA o||||||||||oo||| | GACCTTCTTGTATAGTCGTGAAAGTCCCTGCG	TT3	0.00	0.00	0.00	0.09	12239	-0.31	15096	0.58
ATACCTGAAGAACAGAACCGA (+)	21	0.02	107.91	0.06	79.43	BnaC01g13020D	unknown	372	ATACCTGAAGAACAGAACCGA |||||o||||| o|||o| AGGCTATGGATTTCTTTATTTGGTTTCACTTT	TT3	0.00	0.00	0.00	0.09	319	-1.17	112	-0.88
AAAGGAACGAGAGAGGCAAAA (+)	21	0.00	11.54	0.01	8.84	BnaA09g12090D	Putative pentatricopeptide repeat-containing protein At1g64310	1269	AAAGGAACGAGAGAGGCAAAA |||o| || |||| ||||||| CACATTTTC-TGGTCTCACCGTTTTACATGTT	TT3	0.00	0.00	0.00	0.09	12	-0.51	8	-0.88
CGAGAACATATCAGTGCTTGAA (+)	22	0.00	5.81	0.00	7.81	BnaA05g34080D	Cystathionine gamma-synthase 1, chloroplastic	1101	CGAGAACATATCAGTGCTTGAA |o|o| |||| |||||||||| TTCGGTTTTCGTATTGTCACGAACGTGTGTAG	TT3	0.00	0.00	0.00	0.05	16483	-0.89	7249	-0.88
CAGAGAAGGAGAAGAAGGAGAG (+)	22	0.00	2.00	0.00	2.18	BnaC09g17310D	Thioredoxin H-type	788	CAGAGAAGGAGAAGAAGGAGAG ||||||o|||||||o|||o ATCCATCTCTTCTTCTTCTTCTTCCTATT	TT3	0.00	0.00	0.00	0.14	72375	-0.95	58061	-0.35
GAAAGTTGGAAACATCGAGAT (+)	21	0.00	5.75	0.00	2.41	BnaC02g27970D	unknown	1650	GAAAGTTGGAAACATCGAGAT | ||||||||||| o||o TATGC-TTCAACCTTTGTTTTTCTGTCTTTCG	TT3	0.00	0.00	0.00	0.37	3	-0.08	20	-0.25
AAAGTTGGAAACATCGAGATC (+)	21	0.01	41.93	0.01	34.07	BnaC01g01120D	Protein RMD5 homolog A	2177	AAAGTTGGAAACATCGAGATC ||| ||||||o||||| | CTACCTTC-ACCTTAGTGGCTCTCGACGATGG	TT3	0.00	0.00	0.00	0.14	2018	1.10	2342	0.43
AGAATTGTGTATCCACCATCCG (-)	22	0.00	6.19	0.00	5.51	BnaA02g00880D	DEAD-box ATP-dependent RNA helicase 56	484	AGAATTGTGTATCCACCATCCG |||o|||||||||o o TAGGTCTTGACACATAGG-GGTGCATTGGAGA	TT3	0.00	0.00	0.00	0.19	3026	0.46	5327	0.53
AGAATTGTGTATCCACCATCC (-)	21	0.00	4.51	0.00	2.37	BnaC09g20450D	unknown	2001	AGAATTGTGTATCCACCATCC |o||||| ||||||| ||| TAGGTTTTAACA-ATAGGTAGAAGGAACACAC	TT3	0.00	0.00	0.00	0.14	211	0.72	853	0.40

CATCTTCATAATCCTCAAAGA (-)	21	0.02	25.23	0.00	20.64	BnaA09g47450D	Aspartic proteinase A1	2386	CATCTTCATAATCCTCAAAGA ||||o|| ||||o|||| AGTCGTAGAGGTCTTAGGGGTT-CTGGCATTG	TT3	0.00	0.00	0.00	0.19	58685	0.94	92695	1.33
CAGATTCCCTCTCTTTTGTGC (-)	21	0.00	13.10	0.00	10.58	BnaC09g42190D	unknown	137	CAGATTCCCTCTCTTTTGTGC ||||||||||o|| ||| TAATGTCTAAGGGAGAAAGAA-ACGCTGAACC	TT3	0.00	0.00	0.00	0.28	0	NA	1	0.11
CTGCACGTATCCCTCAGGCAT (-)	21	0.00	5.97	0.00	3.05	BnaC06g41130D	unknown	2663	CTGCACGTATCCCTCAGGCAT |o|||| |||||||||| GAGGGGCGTGGATAGGGAGTC-GAAGTAGAGG	TT3	0.00	0.00	0.00	0.28	465	1.00	906	0.59
CATCTTCATAATCCTCAAAGA (-)	21	0.02	25.23	0.00	20.64	BnaC08g41720D	Aspartic proteinase	790	CATCTTCATAATCCTCAAAGA ||||o|| ||||o|||| AGTCGTAGAGGTCTTAGGGGTT-CTGGCATTG	TT3	0.00	0.00	0.00	0.19	37930	0.46	48931	0.66
CTTTAATCGTTTTGTGTATGT (-)	21	0.00	8.28	0.00	10.97	BnaA08g18480D	Purine permease 1	83	CTTTAATCGTTTTGTGTATGT |||| |||||||||| ||| AATGGAAACTA-CAAAACACAAACACAACAAC	TT3	0.00	0.00	0.00	0.05	2275	-0.08	3497	0.37
AGAATTGTGTATCCACCATCC (-)	21	0.00	4.51	0.00	2.37	BnaA09g18520D	unknown	2007	AGAATTGTGTATCCACCATCC |o||||| |||||||| TAGGTTTTAACA-ATAGGTAGAAGGAACACAC	TT3	0.00	0.00	0.00	0.14	565	-0.69	766	-0.38
TTATGTTGAGTTTTTATATT (-)	20	0.00	1.71	0.00	30.26	BnaA01g22950D	unknown	1566	TTATGTTGAGTTTTTATATT ||||||||||||| TCAGATTACAACTCAAAAAAAAAAAAGGTTAGT	TT3	0.00	0.00	0.00	0.14	280	1.15	233	0.36
AACTTTGTTTCAGTATTTCTT (-)	21	0.00	4.54	0.00	2.19	BnaC05g10240D	unknown	45	AACTTTGTTTCAGTATTTCTT |||||||||o||||o TGTCTTGAAAGAAAGTTA-AAAGAGCCCTTTT	TT3	0.00	0.00	0.00	0.09	475	0.46	4591	1.14
TCAAGCACTGATATGTTCTCG (-)	21	0.00	23.20	0.02	13.86	BnaA10g05040D	AP-2 complex subunit sigma	976	TCAAGCACTGATATGTTCTCG |||||| |o||o||o|||| GAAGAGTTCGAGGCTGTAGGAGAGCTACTAGC	TT3	0.00	0.00	0.00	0.05	1166	-0.47	959	0.13
TTTGCCTCTCTCGTTCCTTTT (-)	21	0.02	12.25	0.00	9.24	BnaC04g41100D	Thylakoidal processing peptidase 1, chloroplastic	2000	TTTGCCTCTCTCGTTCCTTTT ||||| ||||o|o||||||| TGTCAAACGTAGAGGGTAAGGAAAAAGATGTG	TT3	0.00	0.00	0.00	0.05	10971	-0.19	8170	-0.52
TTTCATCTGGATGTGTGCCTC (-)	21	0.02	14.11	0.00	11.95	BnaA03g13310D	Superoxide dismutase [Fe] 2, chloroplastic	1136	TTTCATCTGGATGTGTGCCTC |o||||o|||||||| CTGTTAGGTAGATCTAGACACGGATCCTAAAC	TT3	0.00	0.00	0.00	0.51	320	0.13	224	-0.40
TCAAGCACTGATATGTTCTCG (-)	21	0.00	23.20	0.02	13.86	BnaC05g20230D	unknown	3275	TCAAGCACTGATATGTTCTCG o||| |||||||o|o|||o TTCGGGTTGGTGACTATGCGAGAGTCCGACGC	TT3	0.00	0.00	0.00	0.23	347	1.06	619	0.13
TTTGCCTCTCTCGTTCCTTTT (-)	21	0.02	12.25	0.00	9.24	BnaA04g17540D	Thylakoidal processing peptidase 1, chloroplastic	2341	TTTGCCTCTCTCGTTCCTTTT ||||| |||o|o||||||| TGTCAAACGTAGAGGGTAAGGAAAAAGATGTG	TT3	0.00	0.00	0.00	0.05	2020	-0.58	9542	-0.61
AGAATTGTGTATCCACCATCC (-)	21	0.00	4.51	0.00	2.37	BnaA09g38720D	Transketolase-1, chloroplastic	2325	AGAATTGTGTATCCACCATCC || ||||||||||||| AGTCTC-TAACACATAGGTGGGAAGAGGTGAG	TT3	0.00	0.00	0.00	0.09	14311	-0.83	13711	-0.77
TGACTTTGAAGTCTCTTTCAA (-)	21	0.00	2.89	0.00	2.45	BnaA05g31990D	Sugar transporter ERD6-like 10	2442	TGACTTTGAAGTCTCTTTCAA o||||||||| |||o|||| TTGAGCTGAAACTT-AGAAGAAGTTCGGAAAA	TT3	0.00	0.00	0.00	0.14	5234	-0.52	6252	-0.37
TGCACGTATCCCTCAGGCA (-)	19	0.00	2.30	0.00	1.82	BnaA03g21090D	Autophagy-related protein 8e	489	TGCACGTATCCCTCAGGCA |||| ||||||||oo|| CATAACGTACATAGAGAGTTTGTTTGTTTCTA	TT3	0.00	0.00	0.00	0.05	24300	0.64	4689	0.13
TGCAGAGAAATCTTCAGGATC (-)	21	0.02	40.38	0.00	31.94	BnaA01g14050D	NBR1 homolog	708	TGCAGAGAAATCTTCAGGATC ||||||||||||o||| GCTGACGTGTCATTAGAAGTTCTTGAATTCTG	TT3	0.00	0.00	0.00	0.05	2959	5.97	279	7.49
TTTTGCCTCTCTCGTTCCTTT (-)	21	0.01	15.07	0.01	11.06	BnaC04g29080D	U-box domain-containing protein 11	1379	TTTTGCCTCTCTC-GTTCCTTT |o|||||||||| |||||| AAGGAGAACGGAGAGAGACAAGGCAAGAAGCA	TT3	0.00	0.00	0.00	0.14	0	NA	0	NA
CCTTCTTCTCCTTCTCTGCCT (-)	21	0.00	11.17	0.00	8.13	BnaA02g05030D	Probable pollen receptor-like kinase 6	1004	CCTTCTTCTCCTTCTCTGCCT |||o||o||||o|||o ||| AGGAGGAGGAGGAGGAGGAGGAGGATGTGGTG	TT3	0.00	0.00	0.00	0.69	0	0.22	1	0.18
TCAAGCACTGATATGTTCTCG (-)	21	0.00	23.20	0.02	13.86	BnaCnng48180D	Glucose-6-phosphate 1-dehydrogenase 1, chloroplastic	1159	TC-AAGCACTGATATGTTCTCG || |||||||||| |||||o CTTAGCTTCGTGACTTTCCAAGAGTTGCTCAA	TT3	0.00	0.00	0.00	0.14	2094	0.00	3135	-0.45

Table S18: Most significant targeting of host mRNA transcripts by vsiRNAs

vsRNA (strand)	Mean reads (rpm)		Target transcript ID	Predicted gene function	Cleavage position	vsiRNA:mRNA target pair (5'-3' : 3'-5')	Cleavage found in PAREseq replicates	Fragment signatures (rpm)		FC(log2)	
	DT	TT						DT	TT	DT	TT
AAGAATCTGATGATGCTGT (-)	2.13	1.60	BnaC03g26480D	ERF RAP2-7	2328	AAGAAT-CTGATGATGCTGT AATCTCTTAGGACTACTACGACGACGTTGACT	DT2 DT3 TT3	10.03	6.66	-0.39	0.43
AAGAATCTGATGATGCTGT (-)	2.13	1.60	BnaC04g15640D	ERF RAP2-7	2414	AAGAAT-CTGATGATGCTGT AATCTCTTAGGACTACTACGACGACGTTGACT	DT2 DT3 TT3	10.03	6.66	0.78	-1.74
AAGAATCTGATGATGCTGT (-)	2.13	1.60	BnaA10g12950D	AP2-like ERF TOE2	2933	AAGAAT-CTGATGATGCTGT ACACTCTTAGGACTACTACGACGTAAACTCTC	DT2 DT3 TT3	5.00	9.95	0.33	-0.04
AAGAATCTGATGATGCTGT (-)	2.13	1.60	BnaC09g35430D	AP2-like ERF TOE2	2671	AAGAAT-CTGATGATGCTGT ACACTCTTAGGACTACTACGACGTAAACTATC	DT2 DT3 TT3	5.00	9.95	0.01	-0.22
AAGAATCTGATGATGCTGT (-)	2.13	1.60	BnaC09g13430D	ERF RAP2-7	1039	AAGAAT-CTGATGATGCTGT AATCTCTTAGGACTACTACGACGACGTTGACT	DT2 DT3 TT3	10.03	6.66	0.30	-1.57
AAGAATCTGATGATGCTGT (-)	2.13	1.60	BnaA03g22100D	ERF RAP2-7	2284	AAGAAT-CTGATGATGCTGT AATCTCTTAGGACTACTACGACGACGTTGACT	DT2 DT3	10.03	0.00	0.53	1.04
AAGAATCTGATGATGCTGT (-)	2.13	1.60	BnaA01g34730D	Floral homeotic protein APETALA 2	1043	AAGAAT-CTGATGATGCTGT CCTCTCTTAGGACTACTACGACGTCGTAAACG	DT2 TT3	2.04	1.62	-0.44	0.12
AAGAATCTGATGATGCTGT (-)	2.13	1.60	BnaCnng39690D	Floral homeotic protein APETALA 2	2233	AAGAAT-CTGATGATGCTGT CCTCTCTTAGGACTACTACGACGTCGTAAACG	DT2 TT3	0.53	1.25	0.19	0.28
TCTTTGTCACTCTCGTGTGCT (-)	54.27	40.69	BnaC09g53230D	unknown	219	TCTTTGTCACTCTCGTGTGCT AGAGAGAGAGAGAGAGAGCA-ACAAAGTCCAC	DT2 DT3	13.49	0.00	-0.02	-0.27
TCTTTGTCACTCTCGTGTGCT (-)	54.27	40.69	BnaC04g51540D	FBD-associated F-box protein At3g49020	114	TCTTTGTCACTCTCGTGTGCT AGAGAGAGAGAGAGAGAG-AGACGAAACAAGA	DT2 DT3	13.49	0.00	-0.54	-0.18
TCTTTGTCACTCTCGTGTGCT (-)	54.27	40.69	BnaC04g04300D	unknown	213	TCTTTGTCACTCTCGTGTGCT AGAGAGAGAGAGAGAGAG-AGACGAGTTTTAG	DT2 DT3	13.49	0.00	0.63	-0.04
TCCTTCTTCTCCTTCTCTGCC (-)	11.63	9.29	BnaCnng36690D	Non-functional pseudokinase ZED1	62	TCCTTCTTCTCCTTCTCTGCC GAAGAAGAAGAAGAAGAAGAGGTGGCTGGTAG	DT2 DT3	4.17	0.00	-0.18	-0.35
AACTGCCTCAAGAGCTCCATA (-)	32.88	29.44	BnaA10g13210D	Thiol protease aleurain	1221	AACTGCCTCAAGAGCTCCA-TA CTATTCGGCGGAGTTCGCGAGGTCATCATGAT	DT2 DT3	3.52	0.00	-0.63	0.27
TGTGTGTTGTTGTTACTTTCT (+)	8.67	7.24	BnaA03g21510D	Serine/arginine-rich splicing factor RS31A	356	TGTGTGTTGTTGTTACTTTCT ACACACACAC-ACAAAAAATAAAGGAACGTCC	DT1 DT2	0.13	0.00	-0.19	0.19
TACCAGAACTCATCGAAGC (+)	1.79	2.25	BnaC04g53300D	Nematode resistance protein-like HSPRO2	1241	TACCAGAACTCATCGAAGC ACCGA- GGTCTTGAGAGGGTTCTTGCAGAAGC	DT1 TT1	0.04	170.97	-0.46	0.49
AGAACCGAGAACATTGAGAA (+)	4.14	4.01	BnaC02g37040D	Chlorophyll a-b binding protein 36, chloroplastic	863	AGAACCGAGAACATTGAGAA TGTTTCTTGGGT-TTGTACCTCTTGTACCGTT	DT2 DT3	10.41	0.00	-0.48	-0.03
CAGAGAAGGAGAAGAAGGAGA (+)	16.42	12.78	BnaC03g04180D	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	90	CAGAGAAGGAGAAGAAGGAGA CTCTCTCTC-TCTTCTTCTTCTTCCCTGC	DT2 TT2	0.18	0.65	-0.17	0.13

Table S19: PHAS loci that produce va-phasiRNAs in Drakkar

			siRNA reads & rpm & ratio & PHAS Score					
PHAS locus	Predicted gene function	transcript length	DM (reads, rpm)		DT (reads, rpm)		DT rpm / DM rpm	PHAS Score
BnaA01g14050D	NBR1 homolog	2109	91	570	83110	250229	439	210.5
BnaC01g16550D	NBR1 homolog	2118	90	564	74021	222864	395	227.4
BnaA04g20150D	Chlorophyll a-b binding protein 1, chloroplastic	804	460	2882	18293	55077	19	178.9
BnaA04g12130D	Probable fructose-bisphosphate aldolase 1, chloroplastic	1173	79	495	10287	30972	63	42.1
BnaAnng22920D	Chlorophyll a-b binding protein 1, chloroplastic	804	277	1736	10046	30247	17	164.2
BnaC03g59520D	Chlorophyll a-b binding protein 1, chloroplastic	804	375	2350	9349	28148	12	98.7
BnaC04g33570D	Fructose-bisphosphate aldolase, chloroplastic	1173	79	495	8934	26899	54	47.6
BnaA02g05040D	unknown	753	206	1291	8803	26504	21	117
BnaA05g29390D	Chlorophyll a-b binding protein CP29.2, chloroplastic	867	161	1009	8490	25562	25	100
BnaA07g07560D	Chlorophyll a-b binding protein 1, chloroplastic	804	324	2030	8429	25378	13	86.5
BnaA07g19610D	ABC transporter G family member 35	4173	108	677	7975	24011	35	61.6
BnaA03g15830D	Chlorophyll a-b binding protein 1, chloroplastic	801	249	1560	7690	23153	15	75.4
BnaC03g18980D	Chlorophyll a-b binding protein 1, chloroplastic	801	253	1585	6797	20465	13	38.9
BnaC05g10980D	RNA-dependent RNA polymerase 1	3282	45	282	6467	19471	69	74.9
BnaA09g26570D	Chlorophyll a-b binding protein 1, chloroplastic	804	198	1241	6307	18989	15	61.1
BnaA08g17660D	Chlorophyll a-b binding protein 1, chloroplastic	804	248	1554	6017	18116	12	64.9
BnaC05g22880D	Chlorophyll a-b binding protein 1, chloroplastic	804	175	1097	5702	17168	16	52.1
BnaC06g14450D	Probable pectate lyase 22	1611	661	4142	5481	16502	4	443.6
BnaAnng23670D	ATPase 2, plasma membrane-type	2757	51	320	5457	16430	51	45.2
BnaA09g47880D	Zinc transporter 4, chloroplastic	1194	10	63	5290	15927	254	65.4
BnaC08g42250D	Zinc transporter 4, chloroplastic	1191	6	38	5248	15801	420	67.1
BnaC08g16670D	unknown	591	723	4530	4752	14307	3	934.2
BnaC07g09400D	Chlorophyll a-b binding protein 1, chloroplastic	804	234	1466	4742	14277	10	47.3
BnaA09g00390D	S-adenosylmethionine synthase	1098	29	182	4716	14199	78	120.1
BnaC07g39070D	NBR1 homolog	2076	12	75	4664	14042	187	42
BnaC04g08360D	S-adenosylmethionine synthase 3	1122	34	213	4646	13988	66	83.5
BnaC04g10770D	Chlorophyll a-b binding protein 1, chloroplastic	990	503	3152	4644	13982	4	105.3
BnaA02g22660D	Tubulin beta-4 chain	1341	30	188	4585	13805	73	97.4
BnaC05g27560D	Probable LRR receptor-like serine/threonine-protein kinase At4g08850	2241	50	313	4387	13208	42	51.9

BnaC04g10780D	Chlorophyll a-b binding protein 1, chloroplastic	801	238	1491	4242	12772	9	69.8
BnaC09g37170D	unknown	759	35	219	4176	12573	57	59.5
BnaC07g29410D	EIN3-binding F-box protein 2	1866	20	125	4169	12552	100	97.4
BnaC06g41790D	ARGONAUTE 2	3108	71	445	4024	12116	27	76.1
BnaA06g37230D	Probable fructose-bisphosphate aldolase 2, chloroplastic	1182	109	683	3934	11845	17	30.2
BnaAnng14520D	Subtilisin-like protease SBT1.7	2283	32	201	3924	11814	59	67.2
BnaC05g17000D	Protein TolB	2121	14	88	3918	11796	134	71.4
BnaC03g60280D	Probable fructose-bisphosphate aldolase 2, chloroplastic	1152	131	821	3810	11471	14	43.2
BnaA10g14810D	unknown	747	63	395	3708	11164	28	36.9
BnaA05g09400D	Chlorophyll a-b binding protein 1, chloroplastic	801	105	658	3640	10959	17	46.5
BnaA07g17260D	Putative calcium-transporting ATPase 11, plasma membrane-type	3078	15	94	3609	10866	116	75.4
BnaC04g42010D	Probable mediator of RNA polymerase II transcription subunit 37e	783	22	138	3579	10776	78	110.4
BnaC04g37750D	EIN3-binding F-box protein 1	1800	88	551	3555	10703	19	92.2
BnaC02g31030D	Tubulin beta-1 chain	1338	21	132	3523	10607	81	42
BnaA06g38620D	Pyrophosphate-energized vacuolar membrane proton pump	1821	778	4875	3370	10146	2	53.1
BnaA06g35940D	unknown	5187	14	88	3180	9574	109	62.7
BnaC03g05980D	Magnesium-chelatase subunit ChlH, chloroplastic	4155	126	790	3124	9406	12	31
BnaA06g04440D	Elongation factor 1-alpha 4	1383	16	100	3119	9391	94	79.6
BnaC04g50850D	Phosphatidylinositol 4-kinase gamma 4	1470	10	63	3083	9282	148	63.8
BnaCnng64010D	ABC transporter G family member 36	2145	25	157	3070	9243	59	43.4
BnaCnng07470D	Putative calcium-transporting ATPase 11, plasma membrane-type	3078	18	113	3065	9228	82	36.7
BnaC01g21920D	Cysteine proteinase RD19a	1107	28	175	3045	9168	52	60.9
BnaA06g15400D	Protein TolB	2004	26	163	2988	8996	55	45.5
BnaC04g42020D	Probable mediator of RNA polymerase II transcription subunit 37e	723	12	75	2895	8716	116	79
BnaA05g28710D	Cell division control protein 48 homolog E	2427	15	94	2862	8617	92	30.4
BnaA03g10790D	Heat shock protein 90-4	1728	30	188	2762	8316	44	87.1
BnaC07g15280D	Catalase-3	1479	105	658	2710	8159	12	40.1
BnaCnng74930D	24-methylenesterol C-methyltransferase 2	1071	22	138	2654	7991	58	36.6
BnaA04g14890D	EIN3-binding F-box protein 1	1872	57	357	2597	7819	22	47.4
BnaCnng20770D	24-methylenesterol C-methyltransferase 2	1071	17	107	2592	7804	73	40.4

BnaA09g26890D	U-box domain-containing protein 17	2115	7	44	2588	7792	178	43.3
BnaAnng01730D	ABC transporter G family member 22	2157	20	125	2547	7669	61	30.8
BnaAnng35580D	Glycine-rich RNA-binding protein GRP2A	507	149	934	2377	7157	8	38.2
BnaC07g21430D	Protein NRT1/ PTR FAMILY 8.3	1758	11	69	2366	7124	103	45.6
BnaC07g19250D	unknown	5082	17	107	2347	7066	66	44.7
BnaC07g15930D	Subtilisin-like protease SBT1.7	2283	23	144	2329	7012	49	34.9
BnaA06g24650D	Leucine-rich repeat receptor-like serine/threonine-protein kinase BAM1	2916	42	263	2238	6738	26	61.8
BnaC08g38660D	Chlorophyll a-b binding protein CP24 10B, chloroplastic	780	61	382	2233	6723	18	54.9
BnaCnng03470D	Probable mediator of RNA polymerase II transcription subunit 37e	783	16	100	2198	6618	66	54.1
BnaC06g38300D	Nitrate reductase [NADH], clone PBNBR1405	2685	211	1322	2185	6579	5	32.8
BnaC05g40290D	ABC transporter C family member 7	5214	21	132	2070	6232	47	40
BnaC09g32520D	Transmembrane protein 245	1953	26	163	2053	6181	38	49.2
BnaC08g36330D	Transcription activator GLK1	3066	94	589	1950	5871	10	125.2
BnaAnng04540D	Probable LRR receptor-like serine/threonine-protein kinase At4g08850	1626	3	19	1899	5718	304	50.4
BnaC03g25510D	Aquaporin PIP1-2	861	32	201	1863	5609	28	32.7
BnaC01g38940D	Cell division control protein 48 homolog E	2433	8	50	1856	5588	111	33.1
BnaC02g40260D	Elongation factor 2	2517	21	132	1853	5579	42	48.8
BnaA03g26530D	S-adenosylmethionine synthase	1098	22	138	1773	5338	39	38.5
BnaA01g29630D	Subtilisin-like protease SBT1.4	2328	62	388	1766	5317	14	31.2
BnaC01g37240D	Subtilisin-like protease SBT1.4	2328	63	395	1766	5317	13	38.6
BnaA09g56570D	Chlorophyll a-b binding protein CP24 10B, chloroplastic	780	74	464	1694	5100	11	55.3
BnaC04g20690D	Calcium-transporting ATPase 12, plasma membrane-type	3102	23	144	1664	5010	35	37.8
BnaA03g00850D	Cell division control protein 48 homolog E	2397	5	31	1658	4992	159	31.1
BnaA01g22310D	Probable nucleoredoxin 1	1737	94	589	1639	4935	8	38.1
BnaA07g19580D	2-methyl-6-phytyl-1,4-hydroquinone methyltransferase, chloroplastic	1014	11	69	1632	4914	71	36
BnaC01g03600D	unknown	438	276	1729	1600	4817	3	30.3
BnaC01g33900D	Actin-2	1134	48	301	1593	4796	16	34.6
BnaA02g27980D	Thiamine thiazole synthase, chloroplastic	843	96	602	1593	4796	8	43
BnaC01g43180D	Probable nucleoredoxin 1	1737	45	282	1583	4766	17	37.6
BnaA09g04600D	EIN3-binding F-box protein 2	1851	16	100	1556	4685	47	34.8

BnaAnng33970D	Elongation factor 2	1530	15	94	1542	4643	49	56.3
BnaA07g07430D	unknown	744	174	1090	1522	4582	4	36.9
BnaCnng38780D	Elongation factor 1-alpha 4	1287	21	132	1521	4579	35	31.4
BnaA09g05850D	Probable mediator of RNA polymerase II transcription subunit 37e	795	21	132	1480	4456	34	34.1
BnaC09g14730D	unknown	264	215	1347	1480	4456	3	352.5
BnaA04g21850D	Vacuolar cation/proton exchanger 1	1398	32	201	1451	4369	22	30.2
BnaA03g49610D	Cytidine deaminase 1	873	72	451	1369	4122	9	31
BnaC03g13470D	Heat shock protein 90-2	1614	24	150	1351	4068	27	31.7
BnaC02g01960D	ABC transporter G family member 22	2259	13	81	1341	4038	50	169.7
BnaAnng09960D	Tubulin beta-4 chain	1338	12	75	1307	3935	52	30.3
BnaAnng07150D	unknown	699	11	69	1302	3920	57	41.9
BnaC04g06480D	Inorganic phosphate transporter 1-4	1524	53	332	1290	3884	12	34.4
BnaC03g76150D	Elongation factor 2	1200	21	132	1243	3742	28	30.3
BnaA10g29460D	Zinc finger CCCH domain-containing protein 66	1560	17	107	1234	3715	35	33.4
BnaA07g33680D	Nitrate reductase [NADH], clone PBNBR1405	840	203	1272	1224	3685	3	32.7
BnaCnng23930D	Cytochrome P450 89A2	1488	1	6	1124	3384	540	32
BnaC07g23740D	Pentatricopeptide repeat-containing protein At3g26630, chloroplastic	1359	21	132	1089	3279	25	43.4
BnaCnng44170D	UDP-glucuronate 4-epimerase 6	1383	208	1303	879	2647	2	34.7
BnaC04g44100D	DEAD-box ATP-dependent RNA helicase 21	1773	12	75	858	2583	34	33.4
BnaA08g21730D	Catalase-3	1479	87	545	841	2532	5	32.4
BnaA01g26070D	unknown	1320	18	113	822	2475	22	33.9
BnaC08g37970D	Cationic amino acid transporter 8, vacuolar	1758	3	19	810	2439	130	31.5
BnaC07g36920D	GPN-loop GTPase 1	87	71	445	809	2436	5	310.5
BnaA07g00390D	Shikimate O-hydroxycinnamoyltransferase	1302	30	188	798	2403	13	49.1
BnaA05g24750D	Probable leucine-rich repeat receptor-like serine/threonine-protein kinase	627	70	439	703	2117	5	45.1
BnaC09g23240D	unknown	306	87	545	699	2105	4	43.8
BnaC06g37290D	3-hydroxy-3-methylglutaryl-coenzyme A reductase 1	1725	18	113	656	1975	18	62.5
BnaA07g32810D	3-hydroxy-3-methylglutaryl-coenzyme A reductase 1	1731	16	100	624	1879	19	64.7
BnaC09g15730D	unknown	417	45	282	529	1593	6	33.1
BnaC08g14130D	Pentatricopeptide repeat-containing protein At1g10270	2466	5	31	283	852	27	60.5
BnaC04g10550D	unknown	357	22	138	173	521	4	48.1

BnaC07g29950D	TRANSPARENT TESTA GLABRA 1	717	4	25	2241	6747	269	42.6
BnaC03g51090D	Probable inactive purple acid phosphatase 29	1272	5	31	945	2845	91	47.8
BnaA08g25040D	Aspartic proteinase A1	1581	15	94	872	2625	28	58.2
BnaC01g06430D	unknown	630	20	125	150	452	4	64.6
BnaC07g43630D	unknown	543	15	94	102	307	3	33
BnaC07g00300D	Transcription activator GLK1	1341	37	232	437	1316	6	40.1
BnaC04g46560D	Ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic	1320	265	1661	2830	8521	5	75.3
BnaC04g30870D	Ribulose bisphosphate carboxylase small chain F1, chloroplastic	546	174	1090	940	2830	3	35.9

Table S20: PHAS loci that produce va-phasiRNAs in Tanto

			siRNA reads & rpm & ratio & PHAS Score					
PHAS locus	Predicted gene function	transcript length	TM (reads, rpm)		TT (reads, rpm)		TT rpm / TM rpm	PHAS Score
BnaA01g14050D	NBR1 homolog	2109	135	691	114844	232160	336	377
BnaC01g16550D	NBR1 homolog	2118	102	522	106357	215003	412	386.9
BnaC06g41790D	ARGONAUTE 2	3108	280	1433	19302	39019	27	273
BnaA07g19610D	ABC transporter G family member 36	4173	261	1336	16033	32411	24	139.3
BnaA04g20150D	Chlorophyll a-b binding protein 1, chloroplastic	804	966	4944	15481	31295	6	224.5
BnaC05g10980D	RNA-dependent RNA polymerase 1	3282	131	670	15172	30671	46	219
BnaA02g05040D	unknown	753	886	4534	13153	26589	6	155.9
BnaA10g27060D	Probable mediator of RNA polymerase II transcription subunit 37e	1365	113	578	11312	22867	40	38.1
BnaC05g48370D	Auxin transport protein BIG	15231	154	788	10170	20559	26	96.3
BnaC03g59520D	Chlorophyll a-b binding protein 1, chloroplastic	804	720	3685	9663	19534	5	93.3
BnaA08g17660D	Chlorophyll a-b binding protein 1, chloroplastic	804	628	3214	8176	16528	5	95.7
BnaAnng22920D	Chlorophyll a-b binding protein 1, chloroplastic	804	500	2559	7981	16134	6	207.7
BnaC07g39070D	NBR1 homolog	2076	18	92	7264	14684	159	93.6
BnaC03g18980D	Chlorophyll a-b binding protein 1, chloroplastic	801	498	2549	7218	14591	6	94.3
BnaCnng68320D	ARGONAUTE 2	2664	100	512	7091	14335	28	596
BnaC07g19250D	unknown	5082	34	174	7067	14286	82	149.3
BnaA07g07560D	Chlorophyll a-b binding protein 1, chloroplastic	804	532	2723	7018	14187	5	105.1
BnaCnng64010D	ABC transporter G family member 36	2145	110	563	6938	14025	25	72.8
BnaC04g42010D	Probable mediator of RNA polymerase II transcription subunit 37e	783	36	184	6884	13916	76	173.9
BnaC07g29410D	EIN3-binding F-box protein 2	1866	55	281	6858	13864	49	157
BnaC06g01910D	ABC transporter C family member 4	4497	28	143	6776	13698	96	63.5
BnaA09g25290D	ARGONAUTE 2	3072	86	440	6633	13409	30	374.5
BnaA04g12130D	Probable fructose-bisphosphate aldolase 1, chloroplastic	1173	222	1136	6384	12905	11	47.8
BnaC06g14450D	Probable pectate lyase 22	1611	1054	5394	6333	12802	2	475.3
BnaAnng23670D	ATPase 2, plasma membrane-type	2757	119	609	6257	12649	21	49
BnaC09g00800D	Callose synthase 12	5352	25	128	6234	12602	98	86.2
BnaA01g06820D	ATPase 2, plasma membrane-type	2847	105	537	6214	12562	23	32.6
BnaA09g26570D	Chlorophyll a-b binding protein 1, chloroplastic	804	483	2472	6184	12501	5	59.1
BnaA03g15830D	Chlorophyll a-b binding protein 1, chloroplastic	801	417	2134	6117	12366	6	119.6

BnaA06g09600D	RNA-dependent RNA polymerase 1	3330	47	241	5863	11852	49	42.3
BnaA03g32690D	ABC transporter C family member 3	3696	44	225	5849	11824	53	69.1
BnaA04g14890D	EIN3-binding F-box protein 1	1872	115	589	5744	11612	20	106.8
BnaC05g22880D	Chlorophyll a-b binding protein 1, chloroplastic	804	416	2129	5639	11399	5	53.6
BnaA02g05430D	Chaperone protein dnaJ 2	1272	42	215	5606	11333	53	85.1
BnaC05g43180D	Cell division control protein 48 homolog E	2427	16	82	5495	11108	136	59.8
BnaC04g46560D	Ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic	1320	641	3280	5436	10989	3	132.9
BnaA03g10790D	Heat shock protein 90-4	1728	36	184	5314	10742	58	117.1
BnaC08g16670D	unknown	591	994	5087	5301	10716	2	984.3
BnaA06g03880D	ABC transporter C family member 4	4557	34	174	5242	10597	61	47
BnaC04g33570D	Probable fructose-bisphosphate aldolase 1, chloroplastic	1173	201	1029	5199	10510	10	44.7
BnaA09g01630D	Callose synthase 12	5352	28	143	5197	10506	73	37.9
BnaC04g37750D	EIN3-binding F-box protein 1	1800	131	670	5101	10312	15	98.9
BnaC09g05190D	unknown	2046	5	26	4924	9954	389	36
BnaC03g05980D	Magnesium-chelatase subunit ChlH, chloroplastic	4155	261	1336	4648	9396	7	37.7
BnaAnng35580D	Glycine-rich RNA-binding protein GRP2A	507	255	1305	4601	9301	7	79.7
BnaC04g01000D	BAG family molecular chaperone regulator 6	2733	5	26	4517	9131	357	88.8
BnaC04g42020D	Probable mediator of RNA polymerase II transcription subunit 37e	723	27	138	4488	9073	66	83.5
BnaA06g34380D	Protein NRT1/ PTR FAMILY 8.3	1974	9	46	4443	8982	195	47.8
BnaA10g27080D	Probable mediator of RNA polymerase II transcription subunit 37e	783	31	159	4349	8792	55	39.4
BnaA02g22660D	Tubulin beta-4 chain	1341	47	241	4295	8682	36	107
BnaA05g28710D	Cell division control protein 48 homolog E	2427	9	46	4276	8644	188	50.2
BnaA09g05630D	unknown	2169	4	20	4263	8618	421	50.9
BnaA03g39600D	Sacsin	13023	58	297	4144	8377	28	53.1
BnaCnng03470D	Probable mediator of RNA polymerase II transcription subunit 37e	783	28	143	4143	8375	58	89
BnaC02g12750D	Heat shock protein 90-4	1722	26	133	4084	8256	62	102.8
BnaA05g29390D	Chlorophyll a-b binding protein CP29.2, chloroplastic	867	304	1556	4033	8153	5	66.7
BnaC04g10780D	Chlorophyll a-b binding protein 1, chloroplastic	801	398	2037	3885	7854	4	78
BnaA10g27070D	Probable mediator of RNA polymerase II transcription subunit 37e	723	26	133	3884	7852	59	55.1
BnaC07g15280D	Catalase-3	1479	246	1259	3846	7775	6	40.6
BnaA03g49610D	Cytidine deaminase 1	873	155	793	3793	7668	10	84.1
BnaA07g17260D	Putative calcium-transporting ATPase 11, plasma membrane-type	3078	19	97	3758	7597	78	85.2
BnaAnng02450D	REF/SRPP-like protein At3g05500	711	12	61	3742	7565	123	113.4

BnaC01g40400D	unknown	768	132	676	3722	7524	11	87.1
BnaC04g10770D	Chlorophyll a-b binding protein 1, chloroplastic	990	610	3122	3682	7443	2	85.2
BnaA09g26890D	U-box domain-containing protein 17	2115	14	72	3653	7385	103	69.9
BnaA06g04440D	Elongation factor 1-alpha 4	1383	29	148	3617	7312	49	112.5
BnaA06g27640D	EIN3-binding F-box protein 2	1869	41	210	3584	7245	35	63
BnaAnng03650D	unknown	5613	39	200	3579	7235	36	56.9
BnaC04g50850D	Phosphatidylinositol 4-kinase gamma 4	1470	31	159	3530	7136	45	78
BnaC09g21440D	Beta-amylase 1, chloroplastic	1695	185	947	3423	6920	7	79
BnaC02g31030D	Tubulin beta-1 chain	1338	42	215	3393	6859	32	66.6
BnaCnng71820D	ABC transporter C family member 3	1521	20	102	3382	6837	67	58.8
BnaC03g13930D	Heat shock protein 90-3	1731	15	77	3378	6829	89	73.5
BnaC03g37870D	Proteasome activator subunit 4	5355	11	56	3373	6819	121	38.3
BnaC03g37680D	Probable mediator of RNA polymerase II transcription subunit 37c	1953	18	92	3355	6782	74	60.5
BnaA06g37230D	Probable fructose-bisphosphate aldolase 2, chloroplastic	1182	251	1285	3276	6623	5	37.1
BnaA06g35940D	unknown	5187	15	77	3256	6582	86	69.8
BnaA10g14810D	unknown	747	119	609	3238	6546	11	49.7
BnaC07g21430D	NRT1/ PTR FAMILY 8.3	1758	14	72	3223	6515	91	39.5
BnaC01g38940D	Cell division control protein 48 homolog E	2433	11	56	3220	6509	116	71.3
BnaA03g32320D	Probable mediator of RNA polymerase II transcription subunit 37c	1959	14	72	3213	6495	91	52.2
BnaC05g05630D	Elongation factor 1-alpha 4	1464	42	215	3082	6230	29	45
BnaC03g13470D	Heat shock protein 90-2	1614	20	102	3069	6204	61	85.7
BnaC03g77220D	Polyadenylate-binding protein 2	1854	425	2175	3026	6117	3	60.3
BnaC09g37170D	unknown	759	118	604	3020	6105	10	55.8
BnaC08g36330D	Transcription activator GLK1	3066	336	1720	2982	6028	4	96.8
BnaC08g21780D	unknown	5628	41	210	2973	6010	29	42.3
BnaA09g05850D	Probable mediator of RNA polymerase II transcription subunit 37e	795	29	148	2941	5945	40	96.6
BnaCnng24140D	Chlorophyll a-b binding protein CP29.2, chloroplastic	870	278	1423	2870	5802	4	33.1
BnaC03g13870D	Heat shock protein 90-2	1095	30	154	2859	5780	38	54
BnaA03g32640D	ABC transporter C family member 6	1509	18	92	2806	5672	62	37.8
BnaC02g40260D	Elongation factor 2	2517	50	256	2776	5612	22	76.5
BnaA09g26850D	Protein MEI2-like 5	2322	19	97	2701	5460	56	40
BnaC09g54000D	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (ferredoxin), chloroplastic	2211	41	210	2699	5456	26	30.5
BnaC07g50780D	Cytidine deaminase 1	942	119	609	2697	5452	9	58.6

BnaA03g00850D	Cell division control protein 48 homolog E	2397	10	51	2695	5448	106	60
BnaA03g14760D	SOBIR1	1938	25	128	2668	5393	42	72.2
BnaA08g15160D	U-box domain-containing protein 5	5406	28	143	2660	5377	38	48.6
BnaCnng03460D	Probable mediator of RNA polymerase II transcription subunit 37e	723	13	67	2593	5242	79	30.5
BnaC03g73610D	ABC transporter C family member 3	2385	18	92	2586	5228	57	54.5
BnaA05g33630D	Auxin transport protein BIG	6681	33	169	2570	5195	31	37.4
BnaA07g05790D	Beta-amylase 1, chloroplastic	1713	138	706	2570	5195	7	31.5
BnaAnng07150D	unknown	699	12	61	2564	5183	84	48.8
BnaC05g17890D	QUIRKY	3024	39	200	2519	5092	26	48.7
BnaC08g14030D	NF-X1-type zinc finger protein NFXL1	2898	29	148	2518	5090	34	47.6
BnaC04g30810D	Ribulose bisphosphate carboxylase small chain 1A, chloroplastic	546	252	1290	2501	5056	4	45.4
BnaA09g00390D	S-adenosylmethionine synthase	1098	51	261	2483	5019	19	71.1
BnaC05g11440D	ALG-2 interacting protein X	2571	22	113	2464	4981	44	37.4
BnaC04g30870D	Ribulose bisphosphate carboxylase small chain F1, chloroplastic	546	309	1581	2452	4957	3	62.3
BnaA02g08820D	Heat shock protein 90-2	1656	18	92	2427	4906	53	75.1
BnaC03g17800D	SOBIR1	1935	31	159	2426	4904	31	37.1
BnaA01g15810D	GDPDL2	2274	30	154	2422	4896	32	35.9
BnaC07g29950D	TRANSPARENT TESTA GLABRA 1	717	9	46	2418	4888	106	40.7
BnaC06g06400D	Heat shock 70 kDa protein 14	2871	34	174	2384	4819	28	35.4
BnaC08g49360D	Glycine-rich RNA-binding protein 7	504	157	803	2383	4817	6	33.9
BnaC01g27600D	Probable mediator of RNA polymerase II transcription subunit 37e	1254	20	102	2369	4789	47	32.7
BnaA01g32030D	Cell division control protein 48 homolog A	2433	7	36	2312	4674	130	32.8
BnaCnng26360D	unknown	438	122	624	2310	4670	7	42.8
BnaC06g38300D	Nitrate reductase [NADH], clone PBNBR1405	2685	421	2155	2293	4635	2	35.2
BnaC09g41970D	Probable endo-1,3(4)-beta-glucanase ARB_01444	2151	16	82	2262	4573	56	39.4
BnaC05g43540D	unknown	1104	1	5	2255	4559	891	41.3
BnaA06g00870D	Heat shock 70 kDa protein 14	2577	14	72	2156	4358	61	35.7
BnaCnng38780D	Elongation factor 1-alpha 4	1287	31	159	2154	4354	27	77.8
BnaA08g25950D	NF-X1-type zinc finger protein NFXL1	2676	28	143	2150	4346	30	34
BnaC08g32100D	Probable protein phosphatase 2C 49	1128	10	51	2134	4314	84	49.1
BnaAnng01730D	ABC transporter G family member 22	2157	52	266	2122	4290	16	43.4
BnaC02g46810D	Chlorophyll a-b binding protein CP26, chloroplastic	846	245	1254	2119	4284	3	30.7
BnaA09g05860D	Probable mediator of RNA polymerase II transcription subunit 37e	717	21	107	2117	4280	40	52.9

BnaC09g34840D	E3 ubiquitin-protein ligase RING1-like	1068	21	107	2113	4271	40	36.9
BnaC01g01110D	Heat shock 70 kDa protein 9, mitochondrial	2043	7	36	2112	4269	119	45
BnaC01g31710D	Proteasome subunit alpha type-4-A	606	9	46	2102	4249	92	60.1
BnaA05g28110D	unknown	741	118	604	2097	4239	7	45.9
BnaC04g07660D	L-type lectin-domain containing receptor kinase IV.1	2022	23	118	2090	4225	36	40.3
BnaC03g11130D	ABC transporter F family member 1	2760	21	107	2033	4110	38	35.5
BnaC04g20690D	Calcium-transporting ATPase 12, plasma membrane-type	3102	36	184	2022	4088	22	40.9
BnaA10g00830D	NAC domain-containing protein 1	1428	17	87	2001	4045	46	48
BnaC09g32520D	Transmembrane protein 245	1953	43	220	1993	4029	18	51.9
BnaC05g40290D	ABC transporter C family member 7	5214	64	328	1964	3970	12	40.2
BnaAnng33970D	Elongation factor 2	1530	38	194	1946	3934	20	47.3
BnaC01g21920D	Cysteine proteinase RD19a	1107	61	312	1932	3906	13	46.4
BnaC03g51090D	Probable inactive purple acid phosphatase 29	1272	17	87	1919	3879	45	51.2
BnaCnng36540D	Tubulin beta-4 chain	1338	30	154	1916	3873	25	35.8
BnaC06g28800D	ATP-dependent zinc metalloprotease FTSH 1, chloroplastic	2109	121	619	1856	3752	6	33.9
BnaC05g17000D	TolB	2121	37	189	1837	3714	20	53.4
BnaA03g11140D	Heat shock protein 90-2	1092	14	72	1820	3679	51	37.2
BnaC02g44790D	Auxin-responsive protein SAUR32	387	7	36	1811	3661	102	45.1
BnaC03g01160D	Cell division control protein 48 homolog E	2430	9	46	1809	3657	79	43.5
BnaAnng12070D	Probable mediator of RNA polymerase II transcription subunit 37e	771	10	51	1805	3649	71	51.7
BnaA09g39770D	Probable protein phosphatase 2C 49	1125	12	61	1773	3584	58	88.9
BnaA10g14240D	Chaperone protein dnaJ 3	1269	7	36	1764	3566	100	36.6
BnaA09g22540D	Chlorophyll a-b binding protein CP26, chloroplastic	630	201	1029	1751	3540	3	31.3
BnaAnng04540D	Probable LRR receptor-like serine/threonine-protein kinase At4g08850	1626	4	20	1739	3515	172	62.9
BnaC05g30200D	TIME FOR COFFEE	4650	100	512	1734	3505	7	30.3
BnaA04g18310D	Pentatricopeptide repeat-containing protein At2g31400, chloroplastic	2190	23	118	1731	3499	30	36.2
BnaA01g30060D	ABC transporter C family member 3	3483	8	41	1725	3487	85	30.8
BnaA06g31350D	unknown	2055	22	113	1721	3479	31	36.9
BnaA03g32250D	ELC	1812	11	56	1680	3396	60	32
BnaA01g30490D	Probable mediator of RNA polymerase II transcription subunit 37c	1953	15	77	1652	3340	44	34.7
BnaC04g08360D	S-adenosylmethionine synthase 3	1122	60	307	1636	3307	11	42.1
BnaAnng09960D	Tubulin beta-4 chain	1338	33	169	1623	3281	19	43.5
BnaC05g09210D	Glyceraldehyde-3-phosphate dehydrogenase GAPA2, chloroplastic	1200	313	1602	1598	3230	2	32.3

BnaA08g18750D	Calcium-transporting ATPase 1, chloroplastic	3054	8	41	1596	3226	79	41.4
BnaA09g04600D	EIN3-binding F-box protein 2	1851	53	271	1593	3220	12	39.9
BnaC03g76150D	Elongation factor 2	1200	35	179	1562	3158	18	42.8
BnaC04g44100D	DEAD-box ATP-dependent RNA helicase 21	1773	17	87	1561	3156	36	49.6
BnaC09g06290D	Splicing factor 3B subunit 1	3627	19	97	1553	3139	32	34.4
BnaA07g15900D	Fructose-bisphosphate aldolase, cytoplasmic isozyme 2	1077	5	26	1545	3123	122	51
BnaA01g29630D	Subtilisin-like protease SBT1.4	2328	221	1131	1533	3099	3	37.2
BnaC06g14270D	Fructose-bisphosphate aldolase, cytoplasmic isozyme 2	1077	16	82	1517	3067	37	37.9
BnaC01g05230D	Glycine dehydrogenase (decarboxylating) 1, mitochondrial	3138	281	1438	1516	3065	2	30.6
BnaA07g07430D	unknown	744	278	1423	1502	3036	2	39.2
BnaC07g22660D	Phosphatidylinositol 4-kinase gamma 7	1848	60	307	1494	3020	10	32.3
BnaC03g37540D	Protein ELC	1779	9	46	1477	2986	65	33.9
BnaC08g42250D	Zinc transporter 4, chloroplastic	1191	2	10	1464	2960	289	33.5
BnaA06g33610D	Phosphatidylinositol 4-kinase gamma 7	1851	45	230	1462	2955	13	31.8
BnaC04g47650D	Probable calcium-binding protein CML35	654	35	179	1455	2941	16	35.6
BnaA09g06770D	Splicing factor 3B subunit 1	3705	25	128	1455	2941	23	39.3
BnaC02g45020D	Ferredoxin--NADP reductase, leaf isozyme 1, chloroplastic	3015	31	159	1441	2913	18	46.2
BnaA10g18410D	Probable endo-1,3(4)-beta-glucanase ARB_01444	2139	15	77	1432	2895	38	38.3
BnaA07g13530D	RuBisCO large subunit-binding protein subunit alpha, chloroplastic	1791	16	82	1432	2895	35	45.8
BnaA10g25550D	Probable disease resistance protein At4g33300	1971	13	67	1425	2881	43	31.1
BnaAnng14520D	Subtilisin-like protease SBT1.7	2283	31	159	1422	2875	18	44.8
BnaA09g56570D	Chlorophyll a-b binding protein CP24 10B, chloroplastic	780	175	896	1415	2860	3	44.6
BnaA08g25040D	Aspartic proteinase A1	1581	37	189	1412	2854	15	60.7
BnaA10g11620D	Chaperone protein ClpB	2826	52	266	1400	2830	11	31.6
BnaA01g24250D	CBL-interacting serine/threonine-protein kinase 7	1245	86	440	1376	2782	6	43.6
BnaA01g22310D	Probable nucleoredoxin 1	1737	46	235	1334	2697	11	48.1
BnaA08g18140D	26S proteasome non-ATPase regulatory subunit 11 homolog	1260	5	26	1319	2666	104	31.5
BnaC05g47720D	unknown	768	35	179	1315	2658	15	48.1
BnaA10g12520D	E3 ubiquitin-protein ligase RING1-like	1029	11	56	1302	2632	47	30.1
BnaA07g00390D	Shikimate O-hydroxycinnamoyltransferase	1302	117	599	1287	2602	4	54.5
BnaC09g15730D	unknown	417	52	266	1240	2507	9	71.8
BnaCnng73290D	NDR1/HIN1-Like protein 3	714	49	251	1215	2456	10	32
BnaC03g61170D	Heat shock 70 kDa protein 9, mitochondrial	2046	8	41	1210	2446	60	84

BnaA03g26530D	S-adenosylmethionine synthase	1098	35	179	1166	2357	13	30.1
BnaA01g26500D	Actin-8	1134	62	317	1104	2232	7	37.7
BnaC07g23740D	Pentatricopeptide repeat-containing protein At3g26630, chloroplastic	1359	44	225	1101	2226	10	34.2
BnaA07g06190D	UDP-glucuronate 4-epimerase 6	1362	130	665	1099	2222	3	32.5
BnaA09g13710D	Photosystem I chlorophyll a/b-binding protein 3-1, chloroplastic	816	86	440	1086	2195	5	35.2
BnaCnng39500D	SOBIR1	1926	18	92	1083	2189	24	33.5
BnaA02g10190D	Auxin-responsive protein SAUR32	387	8	41	1064	2151	53	39.3
BnaCnng19190D	L-type lectin-domain containing receptor kinase IV.4	1716	18	92	1063	2149	23	47.8
BnaCnng70090D	Phenolic glucoside malonyltransferase 1	1401	5	26	1052	2127	83	34.4
BnaA10g00410D	BPS1, chloroplastic	1053	95	486	1043	2108	4	31.3
BnaAnng33460D	Polyubiquitin	315	50	256	1040	2102	8	46
BnaA04g24870D	unknown	2367	65	333	1031	2084	6	34.9
BnaC03g32940D	S-adenosylmethionine decarboxylase proenzyme 3	1104	84	430	1022	2066	5	36.9
BnaC09g47020D	unknown	1428	36	184	1012	2046	11	31.9
BnaC03g26530D	unknown	1098	1	5	1005	2032	397	30.2
BnaA01g33660D	Glyceraldehyde-3-phosphate dehydrogenase, cytosolic	1026	1	5	999	2020	395	34.5
BnaA03g50170D	UDP-glucuronate 4-epimerase 1	1293	31	159	971	1963	12	36
BnaC05g12070D	Chlorophyll a-b binding protein CP24 10B, chloroplastic	777	117	599	966	1953	3	33.6
BnaC09g44830D	unknown	195	19	97	963	1947	20	46.5
BnaA09g51620D	NAC domain-containing protein 68	1278	4	20	958	1937	95	33.6
BnaAnng12060D	Probable mediator of RNA polymerase II transcription subunit 37e	432	2	10	946	1912	187	47.2
BnaA08g15870D	Heat shock 70 kDa protein 9, mitochondrial	2037	9	46	938	1896	41	55.5
BnaA05g37180D	unknown	777	26	133	936	1892	14	33
BnaC09g33600D	Temperature-induced lipocalin-1	558	4	20	921	1862	91	38.5
BnaC07g12870D	Probable galacturonosyltransferase-like 8	1149	33	169	888	1795	11	37.1
BnaA01g26070D	unknown	1320	39	200	817	1652	8	32.6
BnaA01g10750D	Reticuline oxidase-like protein	1707	36	184	812	1641	9	53.7
BnaC03g68420D	Tubulin alpha chain	1353	44	225	807	1631	7	34.9
BnaC06g37290D	3-hydroxy-3-methylglutaryl-coenzyme A reductase 1	1725	28	143	792	1601	11	43.1
BnaC03g13880D	Heat shock protein 90-3	438	11	56	773	1563	28	37.7
BnaA07g32810D	3-hydroxy-3-methylglutaryl-coenzyme A reductase 1	1731	24	123	742	1500	12	34.9
BnaA03g09920D	Temperature-induced lipocalin-1	564	2	10	728	1472	144	33.5
BnaA09g35490D	Putative serine/threonine-protein kinase-like protein CCR3	2376	8	41	728	1472	36	30.5

BnaC08g39050D	E3 ubiquitin-protein ligase RHA2A	504	72	368	721	1458	4	41.6
BnaA02g34980D	unknown	195	9	46	654	1322	29	41
BnaA06g40330D	Transcription factor MYC3	1350	21	107	650	1314	12	30.2
BnaA03g31400D	Transcription factor LUX	408	1	5	639	1292	252	40.8
BnaC08g08080D	Bifunctional purple acid phosphatase 26	1428	10	51	622	1257	25	119.1
BnaC08g14130D	Pentatricopeptide repeat-containing protein At1g10270	2466	6	31	599	1211	39	90.4
BnaA01g04620D	Probable sugar phosphate/phosphate translocator At4g32390	1056	15	77	596	1205	16	30.6
BnaA08g04620D	bZIP transcription factor 60	702	5	26	524	1059	41	47.6
BnaA09g29100D	Probable mediator of RNA polymerase II transcription subunit 37e	384	1	5	512	1035	202	30.1
BnaC01g06430D	unknown	630	37	189	455	920	5	123.4
BnaC07g43630D	unknown	543	17	87	375	758	9	79.2
BnaA02g01510D	GEM-like protein 5	819	7	36	349	706	20	30.7
BnaC08g22890D	Receptor-like protein kinase FERONIA	3531	12	61	349	706	11	166.8
BnaC05g11770D	Periodic tryptophan protein 2 homolog	2763	8	41	345	697	17	144.1
BnaA03g07990D	unknown	312	13	67	299	604	9	42.4
BnaC07g51300D	Tubulin-folding cofactor C	369	3	15	283	572	37	65.6
BnaA01g04890D	unknown	591	21	107	273	552	5	56.8
BnaA03g51870D	unknown	540	13	67	242	489	7	34.4
BnaA04g08510D	unknown	111	6	31	171	346	11	66.8
BnaA07g28470D	Glutathione S-transferase U11	705	1	5	158	319	62	38.8
BnaC06g26810D	unknown	369	19	97	138	279	3	33.8
BnaC03g60280D	Probable fructose-bisphosphate aldolase 2, chloroplastic	1152	321	1643	3705	7490	5	35.9
BnaC09g14730D	unknown	264	318	1627	2752	5563	3	706.3
BnaC02g01960D	ABC transporter G family member 22	2259	31	159	819	1656	10	64.8
BnaC07g36920D	GPN-loop GTPase 1	87	264	1351	1590	3214	2	427
BnaC07g00300D	Transcription activator GLK1	1341	94	481	945	1910	4	66.8

Table S21: PHAS loci that produce va-phasiRNAs in both Drakkar and Tanto

			siRNA reads & rpm & ratio & PHAS Score												mRNA reads & FC(log2)			
PHAS locus	Predicted gene function	transcript length	DM (reads, rpm)		DT (reads, rpm)		DT rpm / DM rpm	PHAS Score	TM (reads, rpm)		TT (reads, rpm)		TT rpm / TM rpm	PHAS Score	DT		TT	
BnaA01g14050D	NBR1 homolog	2109	91	570	83110	250229	439	210.5	135	691	114844	232160	336	377	2959	5.97	279	7.49
BnaC01g16550D	NBR1 homolog	2118	90	564	74021	222864	395	227.4	102	522	106357	215003	412	386.9	7201	1.42	15409	0.96
BnaA04g20150D	Chlorophyll a-b binding protein 1, chloroplastic	804	460	2882	18293	55077	19	178.9	966	4944	15481	31295	6	224.5	1094135	-0.31	1114135	0.27
BnaA04g12130D	Probable fructose-bisphosphate aldolase 1, chloroplastic	1173	79	495	10287	30972	63	42.1	222	1136	6384	12905	11	47.8	94780	-0.96	56836	-0.91
BnaAnng22920D	Chlorophyll a-b binding protein 1, chloroplastic	804	277	1736	10046	30247	17	164.2	500	2559	7981	16134	6	207.7	1104783	-0.36	569076	0.15
BnaC03g59520D	Chlorophyll a-b binding protein 1, chloroplastic	804	375	2350	9349	28148	12	98.7	720	3685	9663	19534	5	93.3	417531	0.02	305188	0.73
BnaC04g33570D	Probable fructose-bisphosphate aldolase 1, chloroplastic	1173	79	495	8934	26899	54	47.6	201	1029	5199	10510	10	44.7	128831	-0.68	56212	-0.96
BnaA02g05040D	unknown	753	206	1291	8803	26504	21	117	886	4534	13153	26589	6	155.9	9906	-0.40	27852	1.49
BnaA05g29390D	Chlorophyll a-b binding protein CP29.2, chloroplastic	867	161	1009	8490	25562	25	100	304	1556	4033	8153	5	66.7	270995	0.12	261389	-0.13
BnaA07g07560D	Chlorophyll a-b binding protein 1, chloroplastic	804	324	2030	8429	25378	13	86.5	532	2723	7018	14187	5	105.1	403662	-0.74	229128	0.32
BnaA07g19610D	ABC transporter G family member 36	4173	108	677	7975	24011	35	61.6	261	1336	16033	32411	24	139.3	11558	0.64	29843	-0.98
BnaA03g15830D	Chlorophyll a-b binding protein 1, chloroplastic	801	249	1560	7690	23153	15	75.4	417	2134	6117	12366	6	119.6	267044	-0.34	199603	-0.18
BnaC03g18980D	Chlorophyll a-b binding protein 1, chloroplastic	801	253	1585	6797	20465	13	38.9	498	2549	7218	14591	6	94.3	384220	-0.18	242674	0.08
BnaC05g10980D	**RNA-dependent RNA polymerase 1**	3282	45	282	6467	19471	69	74.9	131	670	15172	30671	46	219	192	1.68	2967	1.75
BnaA09g26570D	Chlorophyll a-b binding protein 1, chloroplastic	804	198	1241	6307	18989	15	61.1	483	2472	6184	12501	5	59.1	325731	-0.25	212798	0.26
BnaA08g17660D	Chlorophyll a-b binding protein 1, chloroplastic	804	248	1554	6017	18116	12	64.9	628	3214	8176	16528	5	95.7	278219	-0.23	317665	0.62
BnaC05g22880D	Chlorophyll a-b binding protein 1, chloroplastic	804	175	1097	5702	17168	16	52.1	416	2129	5639	11399	5	53.6	179754	-0.12	117020	0.42
BnaC06g14450D	Probable pectate lyase 22	1611	661	4142	5481	16502	4	443.6	1054	5394	6333	12802	2	475.3	1	-0.21	0	-0.23
BnaAnng23670D	ATPase 2, plasma membrane-type	2757	51	320	5457	16430	51	45.2	119	609	6257	12649	21	49	8812	0.86	15284	0.00
BnaC08g42250D	Zinc transporter 4, chloroplastic	1191	6	38	5248	15801	420	67.1	2	10	1464	2960	289	33.5	12455	1.01	262	1.59
BnaC08g16670D	unknown	591	723	4530	4752	14307	3	934.2	994	5087	5301	10716	2	984.3	262	1.58	249	0.59
BnaA09g00390D	S-adenosylmethionine synthase	1098	29	182	4716	14199	78	120.1	51	261	2483	5019	19	71.1	10063	1.39	9795	-0.35
BnaC07g39070D	NBR1 homolog	2076	12	75	4664	14042	187	42	18	92	7264	14684	159	93.6	2241	1.36	5953	1.44
BnaC04g08360D	S-adenosylmethionine synthase 3	1122	34	213	4646	13988	66	83.5	60	307	1636	3307	11	42.1	20377	0.26	14311	-0.36
BnaC04g10770D	Chlorophyll a-b binding protein 1, chloroplastic	990	503	3152	4644	13982	4	105.3	610	3122	3682	7443	2	85.2	425070	-0.17	199007	0.94
BnaA02g22660D	Tubulin beta-4 chain	1341	30	188	4585	13805	73	97.4	47	241	4295	8682	36	107	15463	0.76	15551	0.03
BnaC04g10780D	Chlorophyll a-b binding protein 1, chloroplastic	801	238	1491	4242	12772	9	69.8	398	2037	3885	7854	4	78	524035	-0.12	299557	0.39
BnaC09g37170D	unknown	759	35	219	4176	12573	57	59.5	118	604	3020	6105	10	55.8	12900	-0.53	12768	1.25
BnaC07g29410D	EIN3-binding F-box protein 2	1866	20	125	4169	12552	100	97.4	55	281	6858	13864	49	157	3690	1.38	6255	-0.30
BnaC06g41790D	**ARGONAUTE 2**	3108	71	445	4024	12116	27	76.1	280	1433	19302	39019	27	273	515	1.62	275	1.68
BnaA06g37230D	Probable fructose-bisphosphate aldolase 2, chloroplastic	1182	109	683	3934	11845	17	30.2	251	1285	3276	6623	5	37.1	156206	-0.63	136158	-0.82
BnaAnng14520D	Subtilisin-like protease SBT1.7	2283	32	201	3924	11814	59	67.2	31	159	1422	2875	18	44.8	21663	1.26	391	2.19

BnaC05g17000D	TolB	2121	14	88	3918	11796	134	71.4	37	189	1837	3714	20	53.4	4889	0.82	6470	0.96
BnaC03g60280D	Probable fructose-bisphosphate aldolase 2, chloroplastic	1152	131	821	3810	11471	14	43.2	321	1643	3705	7490	5	35.9	337891	-0.41	265827	-1.31
BnaA10g14810D	unknown	747	63	395	3708	11164	28	36.9	119	609	3238	6546	11	49.7	4259	-0.08	221	2.32
BnaA07g17260D	Putative calcium-transporting ATPase 11, plasma membrane-type	3078	15	94	3609	10866	116	75.4	19	97	3758	7597	78	85.2	1651	0.36	2516	-0.10
BnaC04g42010D	Probable mediator of RNA polymerase II transcription subunit 37e	783	22	138	3579	10776	78	110.4	36	184	6884	13916	76	173.9	7494	0.58	8197	0.02
BnaC04g37750D	EIN3-binding F-box protein 1	1800	88	551	3555	10703	19	92.2	131	670	5101	10312	15	98.9	5497	1.08	5577	0.50
BnaC02g31030D	Tubulin beta-1 chain	1338	21	132	3523	10607	81	42	42	215	3393	6859	32	66.6	11143	0.52	10691	-0.14
BnaA06g35940D	unknown	5187	14	88	3180	9574	109	62.7	15	77	3256	6582	86	69.8	85	0.27	135	0.96
BnaC03g05980D	Magnesium-chelatase subunit ChlH, chloroplastic	4155	126	790	3124	9406	12	31	261	1336	4648	9396	7	37.7	6999	0.05	13921	-0.36
BnaA06g04440D	Elongation factor 1-alpha 4	1383	16	100	3119	9391	94	79.6	29	148	3617	7312	49	112.5	15039	0.36	20329	0.69
BnaC04g50850D	Phosphatidylinositol 4-kinase gamma 4	1470	10	63	3083	9282	148	63.8	31	159	3530	7136	45	78	1119	0.68	2158	0.05
BnaCnng64010D	ABC transporter G family member 36	2145	25	157	3070	9243	59	43.4	110	563	6938	14025	25	72.8	9022	0.35	19316	-1.24
BnaC01g21920D	Cysteine proteinase RD19a	1107	28	175	3045	9168	52	60.9	61	312	1932	3906	13	46.4	71963	0.57	107705	0.91
BnaC04g42020D	Probable mediator of RNA polymerase II transcription subunit 37e	723	12	75	2895	8716	116	79	27	138	4488	9073	66	83.5	2467	1.07	5877	-0.17
BnaA05g28710D	Cell division control protein 48 homolog E	2427	15	94	2862	8617	92	30.4	9	46	4276	8644	188	50.2	2722	1.41	4360	1.04
BnaC04g46560D	Ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic	1320	265	1661	2830	8521	5	75.3	641	3280	5436	10989	3	132.9	330879	0.04	528385	-0.83
BnaA03g10790D	Heat shock protein 90-4	1728	30	188	2762	8316	44	87.1	36	184	5314	10742	58	117.1	8390	0.61	9912	-0.36
BnaC07g15280D	Catalase-3	1479	105	658	2710	8159	12	40.1	246	1259	3846	7775	6	40.6	91411	0.90	169486	1.06
BnaA04g14890D	EIN3-binding F-box protein 1	1872	57	357	2597	7819	22	47.4	115	589	5744	11612	20	106.8	3940	0.48	6751	0.31
BnaA09g26890D	U-box domain-containing protein 17	2115	7	44	2588	7792	178	43.3	14	72	3653	7385	103	69.9	1984	-1.28	1588	-0.16
BnaAnng01730D	ABC transporter G family member 22	2157	20	125	2547	7669	61	30.8	52	266	2122	4290	16	43.4	224	1.96	15994	0.01
BnaAnng35580D	Glycine-rich RNA-binding protein GRP2A	507	149	934	2377	7157	8	38.2	255	1305	4601	9301	7	79.7	1087	1.91	313	2.15
BnaC07g21430D	NRT1/ PTR FAMILY 8.3	1758	11	69	2366	7124	103	45.6	14	72	3223	6515	91	39.5	293	1.61	6929	0.61
BnaC07g19250D	unknown	5082	17	107	2347	7066	66	44.7	34	174	7067	14286	82	149.3	77	0.91	156	1.66
BnaC07g29950D	TRANSPARENT TESTA GLABRA 1	717	4	25	2241	6747	269	42.6	9	46	2418	4888	106	40.7	1587	0.85	1823	1.48
BnaCnng03470D	Probable mediator of RNA polymerase II transcription subunit 37e	783	16	100	2198	6618	66	54.1	28	143	4143	8375	58	89	13013	0.10	7825	-0.55
BnaC06g38300D	Nitrate reductase [NADH], clone PBNBR1405	2685	211	1322	2185	6579	5	32.8	421	2155	2293	4635	2	35.2	24180	0.66	49284	-0.85
BnaC05g40290D	ABC transporter C family member 7	5214	21	132	2070	6232	47	40	64	328	1964	3970	12	40.2	10665	0.19	7900	-0.31
BnaC09g32520D	Transmembrane protein 245	1953	26	163	2053	6181	38	49.2	43	220	1993	4029	18	51.9	3386	0.29	3458	0.16
BnaC08g36330D	Transcription activator GLK1	3066	94	589	1950	5871	10	125.2	336	1720	2982	6028	4	96.8	12057	0.65	12947	0.47
BnaAnng04540D	Probable LRR receptor-like serine/threonine-protein kinase At4g08850	1626	3	19	1899	5718	304	50.4	4	20	1739	3515	172	62.9	1030	1.44	2189	0.49
BnaC01g38940D	Cell division control protein 48 homolog E	2433	8	50	1856	5588	111	33.1	11	56	3220	6509	116	71.3	192	1.85	3854	1.28
BnaC02g40260D	Elongation factor 2	2517	21	132	1853	5579	42	48.8	50	256	2776	5612	22	76.5	2593	1.15	5719	0.28
BnaA03g26530D	S-adenosylmethionine synthase	1098	22	138	1773	5338	39	38.5	35	179	1166	2357	13	30.1	2317	1.20	2959	-0.24
BnaA01g29630D	Subtilisin-like protease SBT1.4	2328	62	388	1766	5317	14	31.2	221	1131	1533	3099	3	37.2	7030	0.36	9424	0.33

BnaA09g56570D	Chlorophyll a-b binding protein CP24 10B, chloroplastic	780	74	464	1694	5100	11	55.3	175	896	1415	2860	3	44.6	76392	-0.42	45146	0.80
BnaC04g20690D	Calcium-transporting ATPase 12, plasma membrane-type	3102	23	144	1664	5010	35	37.8	36	184	2022	4088	22	40.9	256	1.72	2154	1.84
BnaA03g00850D	Cell division control protein 48 homolog E	2397	5	31	1658	4992	159	31.1	10	51	2695	5448	106	60	648	3.73	1290	0.94
BnaA01g22310D	Probable nucleoredoxin 1	1737	94	589	1639	4935	8	38.1	46	235	1334	2697	11	48.1	1188	5.62	2130	1.49
BnaA09g04600D	EIN3-binding F-box protein 2	1851	16	100	1556	4685	47	34.8	53	271	1593	3220	12	39.9	224	2.07	7390	0.07
BnaAnng33970D	Elongation factor 2	1530	15	94	1542	4643	49	56.3	38	194	1946	3934	20	47.3	6638	0.65	8159	-0.02
BnaA07g07430D	unknown	744	174	1090	1522	4582	4	36.9	278	1423	1502	3036	2	39.2	35088	0.12	23165	0.00
BnaCnng38780D	Elongation factor 1-alpha 4	1287	21	132	1521	4579	35	31.4	31	159	2154	4354	27	77.8	8532	0.45	12216	0.02
BnaA09g05850D	Probable mediator of RNA polymerase II transcription subunit 37e	795	21	132	1480	4456	34	34.1	29	148	2941	5945	40	96.6	5815	0.34	7181	-0.29
BnaC09g14730D	unknown	264	215	1347	1480	4456	3	352.5	318	1627	2752	5563	3	706.3	116	0.44	71	0.58
BnaA03g49610D	Cytidine deaminase 1	873	72	451	1369	4122	9	31	155	793	3793	7668	10	84.1	1697	0.13	2609	0.38
BnaC03g13470D	Heat shock protein 90-2	1614	24	150	1351	4068	27	31.7	20	102	3069	6204	61	85.7	2550	0.61	5285	0.39
BnaC02g01960D	ABC transporter G family member 22	2259	13	81	1341	4038	50	169.7	31	159	819	1656	10	64.8	4529	0.29	8863	-0.66
BnaAnng09960D	Tubulin beta-4 chain	1338	12	75	1307	3935	52	30.3	33	169	1623	3281	19	43.5	5538	0.80	7420	-0.26
BnaAnng07150D	unknown	699	11	69	1302	3920	57	41.9	12	61	2564	5183	84	48.8	216	1.95	780	2.22
BnaC03g76150D	Elongation factor 2	1200	21	132	1243	3742	28	30.3	35	179	1562	3158	18	42.8	4213	1.22	6895	0.13
BnaC07g23740D	Pentatricopeptide repeat-containing protein At3g26630, chloroplastic	1359	21	132	1089	3279	25	43.4	44	225	1101	2226	10	34.2	3016	0.03	2363	0.03
BnaC03g51090D	Probable inactive purple acid phosphatase 29	1272	5	31	945	2845	91	47.8	17	87	1919	3879	45	51.2	12544	-0.18	18233	-1.17
BnaC04g30870D	Ribulose bisphosphate carboxylase small chain F1, chloroplastic	546	174	1090	940	2830	3	35.9	309	1581	2452	4957	3	62.3	827514	-1.02	394604	-0.74
BnaA08g25040D	Aspartic proteinase A1	1581	15	94	872	2625	28	58.2	37	189	1412	2854	15	60.7	28771	0.81	39528	0.65
BnaC04g44100D	DEAD-box ATP-dependent RNA helicase 21	1773	12	75	858	2583	34	33.4	17	87	1561	3156	36	49.6	662	1.07	1189	0.59
BnaA01g26070D	unknown	1320	18	113	822	2475	22	33.9	39	200	817	1652	8	32.6	1459	0.85	1384	0.70
BnaC07g36920D	GPN-loop GTPase 1	87	71	445	809	2436	5	310.5	264	1351	1590	3214	2	427	117	0.46	49	0.23
BnaA07g00390D	Shikimate O-hydroxycinnamoyltransferase	1302	30	188	798	2403	13	49.1	117	599	1287	2602	4	54.5	2532	-0.07	2504	-1.07
BnaC06g37290D	3-hydroxy-3-methylglutaryl-coenzyme A reductase 1	1725	18	113	656	1975	18	62.5	28	143	792	1601	11	43.1	4092	0.69	4820	-0.37
BnaA07g32810D	3-hydroxy-3-methylglutaryl-coenzyme A reductase 1	1731	16	100	624	1879	19	64.7	24	123	742	1500	12	34.9	5438	0.30	6236	-0.64
BnaC09g15730D	unknown	417	45	282	529	1593	6	33.1	52	266	1240	2507	9	71.8	3367	1.05	2684	0.55
BnaC07g00300D	Transcription activator GLK1	1341	37	232	437	1316	6	40.1	94	481	945	1910	4	66.8	3752	-0.49	3161	1.05
BnaC08g14130D	Pentatricopeptide repeat-containing protein At1g10270	2466	5	31	283	852	27	60.5	6	31	599	1211	39	90.4	132	0.87	236	0.80
BnaC01g06430D	unknown	630	20	125	150	452	4	64.6	37	189	455	920	5	123.4	18010	-0.27	17667	0.15
BnaC07g43630D	unknown	543	15	94	102	307	3	33	17	87	375	758	9	79.2	30948	-0.95	16634	0.02

Table S22: va-phasiRNAs derived from NBR1 genes and associated with mRNA target cleavage

		Normalised reads						Normalised reads						Normalised reads			
va-phasiRNA	dsRNA strand	DM	DT	TM	TT	va-phasiRNA	dsRNA strand	DM	DT	TM	TT	va-phasiRNA	dsRNA strand	DM	DT	TM	TT
AAGAGATTGATCTGAACAAGGA	+	2.20	138.96	1.41	165.40	TCACGTCAAGCTCACTGTTGA	-	0.00	42.37	0.00	55.12	CAGAGAGCGTCAACAGACTGCT	-	0.00	17.54	0.00	24.02
AAGAGATTGATCTGAACAAGG	+	0.26	250.83	0.80	287.10	ACTAATCGAGGATTTGGAATC	-	0.90	19.36	1.42	25.26	ACGAGTGCAGTAGTAGAATCC	-	2.61	45.10	4.12	73.73
GTCAATGTACTTGATGGAACC	+	0.00	58.25	0.00	59.62	AGAGAGCGTCAACAGACTGCT	-	0.00	29.47	0.00	25.53	CTGTCCATTAGCTTTGAAAGGC	-	0.00	4.85	0.00	22.20
TGAGGGACAACGAGTACAACT	+	1.77	108.08	0.80	100.16	CTGCTCCAAGTTGTACTCGTT	-	0.00	23.69	0.00	19.11	CACCAACGTTCGACTGCACAGT	-	0.00	13.61	0.00	39.88
AGGGACAACGAGTACAACTTG	+	0.00	56.57	0.00	48.26	TTCACGTCAAGCTCACTGTTGA	-	0.00	26.27	0.00	49.38	TTAGGAACAACAGGCTCAACT	-	0.00	47.07	4.12	53.62
AAGAAGAACAATGGAAGCATT	+	0.00	252.60	0.00	250.67	AGAATCCATCGTTCACGGATT	-	0.00	35.91	6.14	87.55	TCCAATAAGATATGTATCGGCC	-	0.00	22.43	0.00	43.37
ACGAGTTTCATGGACTGAACT	+	0.00	110.77	0.00	185.32	TCAGGCATAACCGAGGCGGATG	-	0.00	16.33	1.23	27.60	AGGACAAAGCGACTGTCTAGCT	-	0.00	12.37	0.00	22.87
GAAGAATGACGTCGAGATAAC	+	0.00	91.46	0.00	80.70	CAGAGAGCGTCAACAGACTGC	-	0.00	48.37	1.42	52.41	TCCACAGAGAGCGTCAACAGAC	-	0.00	26.80	0.00	44.02
TGATCTGACGAACAAGAGGCT	+	0.26	72.59	0.71	56.83	AACAGGTCATCTTTCATCGGA	-	0.00	48.42	0.00	53.63	TGCAGATGAGGAACCGCCACC	-	0.00	38.92	0.00	36.10
AACGAGTTTCATGGACTGAAC	+	0.00	81.35	0.00	77.95	TTTAGACTTGAATCTAGGCCC	-	0.85	65.13	1.23	91.94	CAGTAGTAGAATCCATCGTTCA	-	0.00	10.80	0.00	22.35
CATGGCACGCAGATCGTTTGGA	+	0.00	52.42	0.00	127.05	CCACAGAGAGCGTCAACAGAC	-	0.00	58.95	0.00	40.73	ACCACCGATCCAAACGATCTG	-	0.90	24.93	4.08	40.98
ATGGACTGAACTTGAATGCCT	+	0.00	131.39	2.32	121.20	CCAATAAGATATGTATCGGCC	-	0.00	34.13	0.00	40.65	CATCGGAATGTTTGATCCCGA	-	0.85	80.22	2.06	80.75
CTACTACTGTTGAGGCCTTGG	+	0.00	61.33	0.71	68.36	TCTGGTTCAACATCAGCACCT	-	0.00	18.07	0.00	19.29	AGGACTTGAGAGCTTCCCGAG	-	0.00	34.60	2.06	61.12
AACGAGTTTCATGGACTGAACT	+	0.26	63.53	0.71	138.84	GGCATAACCGAGGCGGATGAA	-	0.00	21.46	0.00	35.26	TTGAGATTCGTTGGATTTGGA	-	0.00	15.30	0.00	21.64
ACAACGAGTACAACTTGGAGC	+	0.00	63.11	0.81	54.52	TTAGCTTTGAAAGGCACCCTGA	-	4.45	23.84	6.18	50.49	AGGCGGATGAACTCCCACTGCT	-	0.00	8.19	0.00	23.24
ATACATATCTTATTGGAGGATG	+	1.68	123.57	0.71	139.20	GACGAGTGCAGTAGTAGAATC	-	4.41	29.70	2.47	46.93	CTTTAGACTTGAATCTAGGCCC	-	0.00	22.11	0.00	41.59
TTGATGCATCCTTGAAGGGCT	+	0.00	24.58	0.00	39.09	GTACACCTGAAATGTAAACCT	-	0.90	14.22	0.00	13.94	TTTGAAAGGCACCCTGAAGCGC	-	0.85	6.92	1.42	24.45
TGCCCGTCGTGTATGTCACTC	+	0.00	40.75	0.71	62.96	TAACCGAGGCGGATGAACTCC	-	0.90	25.63	3.48	65.72	GTCCATTAGCTTTGAAAGGCAC	-	0.00	6.27	0.00	11.96
TAACACTGTTGTGCCTAACACT	+	0.52	26.45	0.00	40.38	TAACCGAGGCGGATGAACTCCC	-	0.00	31.47	0.00	82.52	TTCACCAGCGGAAGGAACTTC	-	0.00	22.83	0.00	35.89
CCACTGCACTCGTCGTCAAGG	+	1.68	21.06	0.80	55.42	CGACGAGTGCAGTAGTAGAATC	-	4.36	57.24	4.90	153.24	TAGAATCCATCGTTCACGGAT	-	2.61	37.55	2.66	80.66
CATGGACTGAACTTGAATGCC	+	0.00	179.80	0.81	192.60	TCCATTAGCTTTGAAAGGCACC	-	3.55	29.98	5.69	59.03	AAGAGGTCGTTGTCATCAACA	-	0.85	20.62	0.00	35.10
ACAGCTTGATCTGGACATGGC	+	1.77	42.41	2.34	99.09	ATTGGCTTTGAAAGGCACCCT	-	0.85	32.30	5.50	47.72	AAACACTAATCGAGGATTTGGA	-	0.85	12.80	2.47	38.72
ACAGCTTGATCTTGACATGGC	+	1.67	19.47	0.00	38.63	ATTAGCTTTGAAAGGCACCCT	-	0.00	29.35	6.77	43.56	GAGAGGTCGTTGTCATCAACA	-	0.00	17.03	0.00	26.18
TGATGTTATGATGGCTGTGCC	+	0.00	22.74	0.00	61.16	TCCACAGAGAGCGTCAACAGA	-	0.85	71.95	0.00	68.09	TTAGCTTTGAAAGGCACCCTG	-	0.00	15.43	0.00	25.52
AAGGATGTATCTAAGAAGACC	+	0.00	35.76	0.00	55.46	AAGGGATGTAGCTGTTGAGCT	-	0.00	34.19	0.00	47.26	AGGACTTGAGAGCTTCCCGAGC	-	0.85	8.07	0.00	38.00
TACATATCTTATTGGAGGATG	+	0.00	72.42	0.00	77.68	GTACATTGACATCAAGGACAA	-	0.00	31.92	0.00	35.29	TAGAATCCATCGTTCACGGATT	-	0.85	31.93	0.00	127.67
ATGGACAGCTTGATCTGGACA	+	0.26	38.41	0.00	72.73	ACGAAGACGAAGATGAAGATG	-	0.85	5.36	0.00	19.56	CCCAGTTATTGGAAGAACGCC	-	0.85	16.76	0.00	32.43
AAGAATGACGTCGAGATAACC	+	0.00	61.06	0.00	48.51	GAGAACTCAGCATCCAGAGGG	-	0.00	16.09	2.47	37.77						
CAACTTGGAGCAGTCTGTTGAC	+	0.00	52.70	0.81	83.99	CCTGAGGACTTGAGAGCTTCC	-	0.00	25.99	0.00	39.81						
AACAAGAGGCTGCTGAAGAAG	+	0.00	39.73	0.00	34.17	GTAGAATCCATCGTTCACGGAT	-	0.00	38.86	0.00	94.43						
CTGAGGGACAACGAGTACAACT	+	0.00	54.36	0.00	77.18	TTGGCTTTGAAAGGCACCCTGA	-	2.61	19.48	10.66	37.65						

Table S23: va-phasiRNAs derived from Chlorophyll a-b binding protein 1 genes and associated with mRNA target cleavage

		Normalised reads						Normalised reads						Normalised reads			
va-phasiRNA	dsRNA strand	DM	DT	TM	TT	va-phasiRNA	dsRNA strand	DM	DT	TM	TT	va-phasiRNA	dsRNA strand	DM	DT	TM	TT
TGAAGATCTGTGAACCAGCCT	+	20.96	133.72	46.38	88.70	TTCTGGGTCGGTAGCGAGGCC	+	9.09	79.41	19.57	51.47	ACAATGGCTTGAACAAAGAAT	-	7.91	20.02	9.43	14.35
TAAGATGCTCTGAGCGTGGACC	+	11.46	136.08	26.68	108.25	GTGGACCAAGCTCGGGTTGCC	+	0.52	57.53	0.80	37.80	GTGGACCAAGCTCGGGTTGCC	-	1.71	27.01	1.23	18.63
CTGAAGATCTGTGAACCAGCC	+	1.15	72.60	5.34	49.11	AAATGGTCGGCGAGATTCTCC	+	1.77	42.17	0.00	36.11	TCTGCGAACCGGCCTTGAACC	-	6.20	18.94	23.54	29.15
AATGGACCCAAGTACTTGACT	+	18.37	72.33	46.63	46.52	TCTGCGAACCGGCCTTGAACC	+	3.72	37.53	12.61	58.49	CCATGGGCTGCCTGATGGGCC	-	0.90	22.99	1.42	17.98
AAGATGCTCTGAGCGTGGACC	+	3.08	178.85	16.77	127.30	TCTGTGAACCAGCCTTGAACC	+	41.17	299.14	97.17	243.71	GAGGCCGAGGACTTGCTTTACC	-	4.41	7.52	15.01	15.56
AATGGACCTAAGTACTTGACT	+	1.68	67.65	9.91	28.85	TCCGAGAGAGTCAAGTACTTG	+	25.80	74.67	23.30	45.23	CGAACCGGCCTTGAACCAAACC	-	0.90	18.48	1.42	31.28
CTTCCAAGGACTTCTGATGCT	+	81.76	197.98	223.18	147.39	CCATGGGCTGCCTGATGGGCC	+	0.89	46.54	0.81	36.31	ATGAGGATCACCTGAGTAGCC	-	3.55	23.32	7.18	20.89
CGGCCTTGAACCAAACCGCCT	+	24.72	45.46	58.66	45.77	CCGAGGACTTGCTTTACCCAG	+	14.02	40.90	45.03	54.25	CGTGGACCAAGCTCGGGTTGCC	-	0.00	16.65	0.00	25.11
TGAACCAGCCTTGAACCAAAC	+	2.57	45.15	7.88	49.07	GAGGCCGAGGACTTGCTTTACC	+	1.94	15.69	5.85	31.33	TCTCGGGATCGGCTGAGAGACC	-	3.55	16.27	0.00	24.58
ATGGACCCAAGTACTTGACCC	+	13.18	44.55	29.91	43.27	CGAACCGGCCTTGAACCAAACC	+	0.89	38.54	0.81	63.34	TGAACAAAGAATCCAAACATA	-	2.69	12.21	3.89	16.26
TTCGCTGAAGATCTGCGAACC	+	3.44	34.66	9.38	45.70	ATGAGGATCACCTGAGTAGCC	+	1.68	47.44	3.91	42.09	AGAAGAAACGTTCTAATGGCT	-	4.36	12.13	27.25	16.82
TGAACCAGCCTTGAACCAAACG	+	0.00	48.61	1.61	32.52	CGTGGACCAAGCTCGGGTTGCC	+	0.00	35.21	0.00	50.90	AAGAAGAAACGTTCTAATGGC	-	2.56	23.17	49.29	22.53
AATGGCTAAGATGCTCTGAGC	+	1.68	34.77	0.00	35.24	TCTCGGGATCGGCTGAGAGACC	+	1.68	33.98	0.00	49.84	AGGCCGAGGACTTGCTTTACC	-	4.31	16.91	30.62	15.44
CCGGCCTTGAACCAAACCGCC	+	1.15	47.94	5.54	66.69	TGAACAAAGAATCCAAACATA	+	2.66	23.48	2.41	32.46						
TGAACCAGCCTTGAACCAAACC	+	0.89	40.02	7.92	39.29	CTGAAGATCTGTGAACCAGCCT	+	1.67	25.03	0.00	50.89						
TTCGCTGAAGATCTGTGAACC	+	17.41	302.45	36.62	219.25	AGGCCGAGGACTTGCTTTACC	+	1.93	33.99	12.61	30.98						
GGAAGACGCAGCCTAGGGCTC	+	0.52	38.54	3.93	42.68	TAAGATGCTCTGAGCGTGGACC	-	23.65	68.26	49.99	53.79						
ATCTGTGAACCAGCCTTGAAC	+	0.00	63.13	7.15	43.34	AATGGACCCAAGTACTTGACT	-	34.34	34.76	93.41	22.97						
ATCTGTGAACCAGCCTTGAACC	+	8.28	38.44	30.33	53.02	AAGATGCTCTGAGCGTGGACC	-	6.07	91.12	29.83	63.38						
AAGGTAGCTCGGTGGCTCGCC	+	0.26	45.84	5.58	27.97	AATGGACCTAAGTACTTGACT	-	3.55	32.73	21.93	14.26						
CCTAGGGCTCCGAGCATGGCC	+	3.09	50.71	4.46	37.55	AAGATGCTCTGAGCGTGAACC	-	0.85	24.10	2.66	16.12						
ACTCAGGTGATCCTCATGGGA	+	1.04	37.07	11.27	33.62	TTCGCTGAAGATCTGCGAACC	-	5.25	17.98	18.23	22.86						
TTCTGGGTCGGTAGCGAGACC	+	19.16	75.82	64.40	84.07	AATGGCTAAGATGCTCTGAGC	-	3.55	17.93	0.00	17.51						
CCTTCGCTGAAGATCTGTGAA	+	0.00	59.00	0.00	31.14	CCGGCCTTGAACCAAACCGCC	-	1.75	22.81	10.03	32.90						
TCTGTGAGCCAGCCTTGAACC	+	7.93	33.66	9.69	25.51	GGAAGACGCAGCCTAGGGCTC	-	1.71	19.33	7.37	21.16						
CTAGGGCTCCGAGCATGGCCC	+	1.41	54.60	3.91	41.28	AAGGTAGCTCGGTGGCTCGCC	-	0.85	22.99	10.41	13.88						
GTCGGCGAGATTCTCCAACGG	+	1.77	31.41	3.99	26.54	CCTAGGGCTCCGAGCATGGCC	-	6.16	25.34	11.08	18.64						
ATGGTCGGCGAGATTCTCCAA	+	9.18	55.51	20.22	29.70	ACTCAGGTGATCCTCATGGGA	-	3.42	19.43	18.41	16.85						
ACAATGGCTTGAACAAAGAAT	+	4.24	40.76	4.64	29.02	CTAGGGCTCCGAGCATGGCCC	-	2.61	27.16	7.18	20.50						

Table S24: va-phasiRNAs derived from TAR1 genes and associated with mRNA target cleavage

		Normalised reads						Normalised reads						Normalised reads			
va-phasiRNA	dsRNA strand	DM	DT	TM	TT	va-phasiRNA	dsRNA strand	DM	DT	TM	TT	va-phasiRNA	dsRNA strand	DM	DT	TM	TT
CGAGCTAAGGACGTCAGGAGCG	+	#N/A	#N/A	28.61	63.94	GTCGCTGCAAAACCTAGGGCG	+	7.93	37.07	9.47	60.64	CAATGTCCTCGACCTATTCTC	+	76.06	128.34	134.24	250.33
CCCCATCCTCTCGAGGATATG	+	1.41	105.00	6.22	132.85	ACCCGTCTGATAGCGCTTATG	+	23.46	95.40	122.66	166.83	AGGAAGCTGATTGGCTGGATC	+	74.43	124.57	136.07	260.72
CATCCTCTCGAGGATATGGGAC	+	1.41	65.82	6.96	261.61	GCACTTGCACATGGGTTAGTC	+	11.88	45.74	20.56	90.87	TATTCAACGAGTTCACACCTTG	+	96.30	160.73	598.68	538.61
GTTGGCCAAAATCCGAGCTAA	+	1.93	90.11	3.24	33.75	GGTTAGTCGATCCTAAGAGTC	+	53.33	197.69	146.20	378.64	CCTCGATGAGTAGGAGGGCGC	+	16.81	27.95	50.20	52.33
TGTGTTACCGCACGCGGTTGGC	+	9.35	297.89	32.46	563.56	AGAGGCATCGGGGACGCAATG	+	19.59	70.58	23.71	101.14	GTTAAAATTCCGGAACCGGGA	+	63.63	102.89	115.62	225.72
TCCGAGCTAAGAACGTCAGGA	+	5.64	174.13	0.00	0.67	CCGAAGAGGGGAAAGGTTCCA	+	17.03	60.41	40.25	103.44	GATCCTAAGAGTCGGGGGAAAC	+	38.38	61.22	44.84	145.48
TCGAGGATATGGGACGGAAGC	+	43.26	1122.33	111.30	928.51	AGTTCACACCTTGGCCGACAG	+	12.69	45.00	122.06	75.33	AATGGATGGCGCTGAAGCGCG	+	114.78	180.52	373.41	479.41
CGCACGCGGTTGGCCAAAATC	+	8.11	194.14	5.31	102.73	CCAAGGAAGTTTGAGGCAATA	+	99.10	341.97	277.03	668.17	AGTTCTATCGGGTAAAGCCAA	+	9.95	15.47	44.67	30.00
TCGAGGATATGGGACGGAAGCT	+	28.59	542.56	44.06	384.72	CGGTTGGCCAAAATCCGAGCT	+	15.20	50.45	20.51	28.58	CAAATGAGAACTTTGAAGGCA	+	23.01	34.98	59.69	41.18
GAACGTCAGGAGCGTCTTGACA	+	3.09	54.08	0.00	0.25	GCCGTCTGCGACGTCGCGAGA	+	365.18	1204.80	1283.32	2941.70	CGGCCGTCGGTGCAGATCTTG	+	48.72	72.47	95.81	127.91
GTTCACACCTTGGCCGACAGG	+	18.42	311.96	69.83	615.48	GATCCTAAGAGTCGGGGGAAA	+	16.64	52.81	33.77	88.65	TGAACGGCACTTGCACATGGG	+	92.95	137.53	249.60	236.34
ATGGGACGGAAGCTGATCTCC	+	44.51	721.86	77.21	419.08	CGGCTTCTTAGAGGGACTATG	+	38.29	112.07	61.04	195.35	TGGTGTCCGGTGCATTCCCGG	+	17.40	25.67	27.59	60.16
GTCTGCGACGTCGCGAGAAGTC	+	177.74	2794.55	301.43	7106.17	CGTCTGCGACGTCGCGAGAAG	+	109.87	319.01	216.40	447.47	AACCCGTCTGATAGCGCTTATG	+	50.71	74.37	134.66	178.54
TAAGAACGTCAGGAGCGTCT	+	4.44	56.99	0.00	0.40	CGGTCGCTGCAAAACCTAGGG	+	22.65	64.99	48.32	119.78	GTTGAGCCATCCCACGGAATC	+	10.09	14.69	31.56	26.99
GTTGGCCAAAATCCGAGCT	+	2.04	24.42	6.45	13.01	ACGCAATGTCCTCGACCTATT	+	15.51	43.45	32.48	63.72	CGCGAACTTCGAAAGGGGATCC	+	130.62	185.41	284.46	587.28
TGTGTTACCGCACGCGGTTGGCC	+	10.78	120.29	7.65	112.79	CGTGGTGTCCGGTGCATTCCC	+	21.08	57.98	96.27	105.81	GCCTCGATGAGTAGGAGGGCG	+	38.73	54.85	109.75	77.18
GTCTGCGACGTCGCGAGAAGT	+	101.30	1128.77	181.66	1889.19	CGTGGGTGGTTCGCCGTCTGC	+	955.47	2530.07	3144.52	3516.77	TTAAATAGGTAGGACGGGGTGG	+	14.19	19.90	50.70	45.29
TGTATTCAACGAGTTCACACC	+	35.11	379.00	77.07	643.71	CTGATCTCCCGTGTGTTACCG	+	120.84	301.33	152.25	252.46	ATTCAACGAGTTCACACCTTG	+	54.98	76.67	279.65	156.88
GTTCGCCGTCTGCGACGTCGC	+	29.87	302.31	74.39	413.97	TGATCTCCCGTGTGTTACCGC	+	25.95	64.56	48.99	55.05	CAGGCCTCGATGAGTAGGAGG	+	59.62	79.40	155.58	204.14
TATGGGACGGAAGCTGATCTCC	+	37.80	377.74	93.06	415.63	CATGTGAACGGCACTTGCACA	+	830.30	1959.98	2077.74	3318.76	GGATAGCTGGAGCTCGGAAAC	+	25.54	33.74	81.52	75.29
GAACGACCTGAGAACGATGAA	+	14.30	132.60	113.19	241.21	AAGGTTCCATGTGAACGGCAC	+	44.54	104.68	119.79	220.04	CCGTCTGCGACGTCGCGAGAA	+	464.02	597.62	1711.42	900.63
AGGATATGGGACGGAAGCTGA	+	59.45	517.07	105.38	247.38	GATGGCGCTGAAGCGCGCGAC	+	17.62	39.44	49.46	74.32	AAGGCCGAAGAGGGGAAAGGT	+	40.25	51.83	163.42	151.43
CGCGGTTGGCCAAAATCCGAG	+	10.50	90.11	27.48	56.01	CGGAGACGTCGGCGGGAATTC	+	21.24	47.42	36.61	108.15	CGCGCTAACCTAGAACCCACA	+	38.14	45.73	93.98	83.38
AGCTGATCTCCCGTGTGTTAC	+	18.44	154.03	50.81	109.28	AATTCCGGAAAGAGTTATCTT	+	39.22	85.38	102.58	130.26	GCCGTCTGCGACGTCGCGAGAA	+	45.58	54.35	104.25	142.83
CGCGAACTTCGAAAGGGGATC	+	107.19	863.03	259.07	2036.74	GGTCGCTGCAAAACCTAGGGC	+	12.79	27.32	18.88	67.41	TGCGGGATGAACCGGAAGCCG	+	253.07	296.40	613.72	498.18
AGGCCTCGATGAGTAGGAGGG	+	13.90	106.85	50.09	229.85	CTGAAGCGCGCGACCTATACC	+	151.29	318.14	405.04	555.55	AGAGCCAGGCCTCGATGAGTA	+	228.08	255.20	771.91	533.14
AGCTGATCTCCCGTGTGTTACC	+	31.33	238.62	49.87	126.22	CTGGAGCTCGGAAACGAGTTC	+	40.26	81.04	92.73	101.54	AAGAGCCAGGCCTCGATGAGT	+	29.79	32.74	75.04	64.03
CTAAGAACGTCAGGAGCGTCT	+	74.08	532.19	0.00	0.88	TAGGCCAAGGAAGTTTGAGGCA	+	130.02	259.46	407.50	566.27	GGTTAGTCGATCCTAAGAGTCG	+	108.00	117.16	151.96	304.33
GGCCGAAGAGGGGAAAGGTTC	+	11.17	79.65	38.65	149.09	GGGTGGTTCGCCGTCTGCGAC	+	65.80	129.54	125.25	169.79	ACGGAATCGAGAGCTCCAAGT	+	1236.13	1339.37	2708.65	2249.48
GATCTCCCGTGTGTTACCGCA	+	28.71	186.86	44.09	119.75	TGATTGGCTGGATCCCTCACG	+	19.86	38.79	41.58	129.90	CTTATGCGCGAACTTCGAAAGG	+	29.10	31.37	77.89	128.69
AGGAGCGTCTTGACATGCGGT	+	18.02	92.36	139.92	67.53	TCGATCCTAAGAGTCGGGGGA	+	80.35	153.36	229.65	270.06	TCGATTAAGACAGCAGGACGG	+	82.26	88.01	155.41	179.30
GCGGTCGCTGCAAAACCTAGG	+	29.72	152.11	63.89	287.58	ATGGCCGTTTAGGCCAAGGAAG	+	38.83	72.55	104.51	182.04	TTCCATGTGAACGGCACTTGC	+	73.01	77.99	163.72	124.07
GTTGGCCAAAATCCGAGCTAAG	+	6.37	31.77	4.02	35.32	TTGGTCGATTAAGACAGCAGG	+	67.80	122.62	163.65	221.13	ATGAACCGGAAGCCGGGTTACG	+	85.30	90.44	175.86	215.73
TGGCCGTTTAGGCCAAGGAAG	+	31.56	157.36	128.60	450.85	AAACTTTAAATAGGTAGGACG	+	75.35	135.48	141.44	335.15	CATCCCACGGAATCGAGAGCT	+	74.64	78.81	197.83	155.07
TATGGGACGGAAGCTGATCTC	+	119.99	563.81	182.12	368.24	TGCGGAAGGATCATTGTCGTA	+	289.94	497.11	1953.41	384.34	TGCGCGCTAACCTAGAACCCA	+	18.51	19.51	53.80	39.41

		Normalised reads						Normalised reads						Normalised reads			
va-phasiRNA	dsRNA strand	DM	DT	TM	TT	va-phasiRNA	dsRNA strand	DM	DT	TM	TT	va-phasiRNA	dsRNA strand	DM	DT	TM	TT
TGTTGAGCCATCCCACGGAATC	+	19.17	20.14	27.45	36.82	TAGCTCGGATTTTGGCCAACC	-	13.93	255.39	76.00	163.78	ACCAAGATCTGCACCGACGGC	-	17.58	123.69	38.09	209.00
ACTTCGAAAGGGGATCCGGTT	+	26.97	28.31	78.82	65.73	CCACCAAGATCTGCACCGACG	-	4.36	79.19	5.35	115.18	TTTGAGAATAGGTCGAGGACA	-	203.27	1363.51	538.52	2860.41
GCTGAAGCGCGCGACCTATACC	+	42.50	44.19	147.43	141.61	AGATCTGCACCGACGGCCGCT	-	0.85	15.22	3.48	33.56	TACTCATCGAGGCCTGGCTCT	-	13.20	88.31	35.05	355.83
AATGAGAACTTTGAAGGCCGAAT	+	103.76	106.61	157.43	81.45	TAGTCCCTCTAAGAAGCCGGCC	-	1.75	29.80	10.03	119.14	AGCACGCAGATGCCGAGGCAC	-	0.00	6.51	4.08	14.09
TTAAGGTGGTGACCTAAGCCCG	+	13.32	13.45	31.21	35.31	AGAAGCCGGCCGTGAAGGGATG	-	1.80	30.06	27.28	53.97	GTCCCTCTAAGAAGCCGGCCG	-	6.20	40.25	13.09	105.07
TCCTAAGAGTCGGGGGAAACC	+	297.22	291.49	406.86	528.42	AAGATCTGCACCGACGGCCGCT	-	0.90	14.86	1.23	44.97	TAATCGACCAACACCCTTTGT	-	1.80	11.34	6.14	17.68
AAGAGTCGGGGGAAACCCGTC	+	115.43	110.68	232.08	246.67	TGAGAATAGGTCGAGGACATTG	-	0.90	14.50	0.00	43.83	AAAGTTTGAGAATAGGTCGAG	-	8.63	53.52	63.69	75.79
AACCCACAAAGGGTGTTGGTC	+	813.37	739.76	1886.74	1963.55	TTGGCTTTACCCGATAGAACTC	-	4.31	66.36	9.24	217.09	AACCCGACTCGTAGACAGCGC	-	14.23	78.93	102.12	105.59
CGGCCGTCGGTGCAGATCTTGG	+	871.20	764.03	1259.97	1756.44	TCGACCAACACCCTTTGTGGG	-	3.46	52.42	26.46	89.84	ACCCGACTCGTAGACAGCGCC	-	10.47	56.44	56.17	124.16
TAAAGCCAATGATTAGAGGCA	+	28.49	23.41	30.16	41.57	ACCACCAAGATCTGCACCGACG	-	0.00	15.07	0.00	71.22	TAGGTTAGCGCGCAGTTGGGCA	-	0.90	4.72	1.42	23.80
CAATGTCCTCGACCTATTCTCA	+	39.41	28.06	84.22	88.50	AACTTCCTTGGCCTAAACGGCC	-	1.71	25.61	2.66	162.61	GCAGACGGCGAACCACCCACG	-	9.53	47.34	4.08	80.94
GGTAAGCAGAACTGGCGATGC	+	39.95	27.14	61.99	68.14	GACTTCTCGCGACGTCGCAGAC	-	4.27	63.16	13.74	109.62	CCAAGATCTGCACCGACGGCC	-	22.02	105.38	32.79	154.52
ATTAGAGGCATCGGGGACGCAA	+	29.99	19.33	36.02	59.45	ACAACCCGACTCGTAGACAGCG	-	0.00	14.24	33.42	97.89	ATTCCGTGGGATGGCTCAACAA	-	0.00	4.70	2.47	33.52
GCTAAGGACGTCAGGAGCGTC	+	0.00	0.31	36.10	497.05	GTAACACACGGGAGATCAGCT	-	3.50	47.28	8.79	35.72	TGTCGGCCAAGGTGTGAACTC	-	32.29	149.93	148.96	290.43
AGCTAAGGACGTCAGGAGCGTC	+	0.00	0.13	39.44	662.83	CAACGCGAGCTGATGACTCGA	-	0.90	12.10	12.72	26.69	ACTCATCGAGGCCTGGCTCTT	-	4.40	20.17	13.73	31.60
TGCTCCGTTCCGCATTCGACC	-	#N/A	#N/A	44.07	58.66	ACTTCGGAGGGAACCAGCTACT	-	0.90	11.26	6.18	24.51	TAGCTCGGATTTTGGCCAACCG	-	4.41	19.97	33.01	20.37
CGTCCTTAGCTCGGATTTTGGC	-	#N/A	#N/A	121.64	188.13	TGAGAATAGGTCGAGGACATT	-	5.30	64.62	14.18	90.52	TTTAAAGTTTGAGAATAGGTC	-	16.77	72.02	27.29	124.88
GAATAGGTCGAGGACATTGCG	-	0.85	55.66	3.48	105.77	GTCGGCTGTGCACCCGTGAGG	-	1.71	20.77	1.42	49.47	CTTAGGATCGACTAACCCATG	-	8.71	37.09	34.06	52.79
CTCATCGAGGCCTGGCTCTTG	-	1.71	83.91	4.90	143.58	ACCAAGATCTGCACCGACGGCC	-	1.75	21.24	2.66	71.73	GTCGCAGACGGCGAACCACCCA	-	28.57	118.70	47.63	205.21
AGAATAGGTCGAGGACATTGC	-	0.85	38.20	16.17	67.47	GATAGAACTCGTTTCCGAGCT	-	14.20	166.23	38.77	336.70	GGTAACACACGGGAGATCAGCT	-	8.80	36.47	17.84	24.79
GACTCTTAGGATCGACTAACC	-	0.85	30.23	6.14	42.37	TAACGTTGCCGTCAACCGCCA	-	0.00	11.46	12.09	26.52	TATTTAAAGTTTGAGAATAGG	-	8.72	35.65	12.94	55.73
GTCCTGCTGTCTTAATCGACC	-	0.00	31.04	15.75	50.98	CACCAAGATCTGCACCGACGGC	-	2.61	29.45	15.19	131.87	AGATAACTCTTTCCGGAATTC	-	1.80	7.27	16.76	16.88
GTGTGAACTCGTTGAATACATC	-	0.00	30.35	16.42	87.19	CCTCTAATCATTGGCTTTACC	-	1.80	20.05	1.23	36.26	GCCCTAGGTTTTGCAGCGACC	-	2.61	9.92	2.66	24.18
CTCATCGAGGCCTGGCTCTTGC	-	0.00	28.28	2.85	109.43	GAGAATAGGTCGAGGACATTGC	-	6.20	68.62	11.04	358.72	TCAAGGTCGGTCGGCTGTGCA	-	3.46	13.07	12.09	28.36
ACTTCCTTGGCCTAAACGGCC	-	4.27	120.42	77.86	237.77	CGACTCTTAGGATCGACTAACC	-	9.70	106.91	27.24	232.10	GATCAGCTTCCGTCCCATATC	-	6.07	21.39	8.16	13.25
AGAATAGGTCGAGGACATTGCG	-	0.00	27.11	1.42	106.78	TTAGCGCGCAGTTGGGCACCG	-	5.35	58.26	11.87	135.48	TACTCATCGAGGCCTGGCTCTT	-	15.90	52.44	35.10	189.02
CGACGTCGCAGACGGCGAACC	-	32.30	849.78	61.44	2765.49	CATCGAGGCCTGGCTCTTGCC	-	10.51	110.09	31.36	144.62	ATAGAACTCGTTTCCGAGCTC	-	48.88	160.72	160.84	277.69
CTGTCTTAATCGACCAACACC	-	0.00	26.30	0.00	38.80	GACGCTCCTGACGTTCTTAGC	-	1.75	18.31	#N/A	#N/A	TAGACAGCGCCTCGTGGTGCGA	-	0.85	2.64	3.70	14.08
GCATGTCAAGACGCTCCTGACG	-	0.00	25.25	35.81	23.33	GAAGATCAAGGTCGGTCGGCTG	-	0.00	9.38	0.00	28.61	TAAAGTTTGAGAATAGGTCGA	-	11.32	34.87	18.63	38.80
GGTATAGGTCGCGCGCTTCAGC	-	0.85	18.78	3.48	37.68	ACCCGATAGAACTCGTTTCCG	-	1.80	15.70	24.85	22.98	AAACAACCCGACTCGTAGACA	-	3.50	10.58	30.53	25.16
CCGTGGGATGGCTCAACAAAGC	-	0.90	19.60	14.78	53.66	CGGTTCCGGAATTTTAACCGGA	-	0.85	7.22	0.00	25.46	TTAATCGACCAACACCCTTTG	-	3.55	10.61	4.08	20.18
TCTTAGCTCGGATTTTGGCCA	-	1.80	38.19	0.00	0.12	GAGCTCTCGATTCCGTGGGATG	-	0.00	8.18	2.06	28.99	TTGAGAATAGGTCGAGGACATT	-	10.47	30.82	14.37	92.73
ACTCATCGAGGCCTGGCTCTTG	-	0.85	17.89	2.66	53.35	GTCGGCCAAGGTGTGAACTCG	-	6.92	52.47	4.08	91.32	AATAGGTCGAGGACATTGCGT	-	5.34	15.67	24.55	40.98
GAGAATAGGTCGAGGACATTG	-	4.45	87.04	5.69	123.35	ATTGCCTCAAACTTCCTTGGCC	-	4.40	32.88	74.00	119.08	TCCGTCCCATATCCTCGAGAGG	-	13.16	37.29	20.43	36.11
CAAGATCTGCACCGACGGCCG	-	0.85	16.10	1.23	30.11	TAGGTTAGCGCGCAGTTGGGC	-	0.00	7.41	4.27	21.52	AGCTCGGATTTTGGCCAACCG	-	52.80	148.67	378.81	63.63

		Normalised reads						Normalised reads			
va-phasiRNA	dsRNA strand	DM	DT	TM	TT	va-phasiRNA	dsRNA strand	DM	DT	TM	TT
ACTCTTAGGATCGACTAACCC	-	6.07	16.29	26.01	20.45	TCTCGCGACGTCGCAGACGGCG	-	306.51	451.31	1402.23	1422.22
CCCCGAATCGATCGGCGGACC	-	25.40	67.54	47.53	195.45	AAAATGGCCCACTTGGAGCTCT	-	4.45	6.53	0.00	25.41
TCGCGCCCTAGGTTTTGCAGCG	-	0.90	2.35	1.23	15.53	TCTAATCATTGGCTTTACCCGA	-	2.61	3.73	14.77	32.25
CTACCTATTTAAAGTTTGAGA	-	8.85	23.08	11.04	36.70	TTCTTAGCTCGGATTTTGGCC	-	203.59	289.71	2.85	1.60
TTTGTGGGTTCTAGGTTAGCG	-	6.25	16.23	5.35	19.64	ATCGAGGCCTGGCTCTTGCCC	-	57.01	79.21	214.29	161.12
GTTCTTAGCTCGGATTTTGGCC	-	20.19	49.70	0.00	0.06	ATTGCCTCAAACTTCCTTGGC	-	62.22	86.00	382.64	140.59
GTCGAGGACATTGCGTCCCCGA	-	0.00	2.46	1.42	21.25	TTGCCTCAAACTTCCTTGGCCT	-	14.87	20.28	75.69	83.48
CTTTCGAAGTTCGCGCATAAG	-	14.15	33.08	26.30	55.27	CAGCGCCATCCATTTTCGGGGC	-	3.46	4.69	12.50	24.52
TGAACTCGTTGAATACATCAG	-	77.13	171.22	229.34	411.16	GAGATCAGCTTCCGTCCCATA	-	23.90	32.30	32.58	22.82
CGCTCCTGACGTTCTTAGCTC	-	48.70	101.28	0.00	0.48	TACCCGATAGAACTCGTTTCC	-	46.92	62.92	49.09	102.58
TTTCGAAGTTCGCGCATAAGC	-	28.22	58.56	131.51	111.70	TTTGAGAATAGGTCGAGGACAT	-	4.41	5.81	2.66	27.40
CACCAAGATCTGCACCGACGG	-	126.72	262.92	283.96	459.48	TAGCTCGGATTTTGGCCAACCGC	-	20.42	26.86	83.91	39.74
TCCTACTCATCGAGGCCTGGC	-	6.20	12.83	9.01	29.82	TGTCGGCCAAGGTGTGAACTCG	-	30.41	37.07	133.79	108.00
ACAACCCGACTCGTAGACAGC	-	29.34	60.34	151.21	135.51	TCAGCGCCATCCATTTTCGGGG	-	4.45	5.39	8.20	41.24
CGCGACGTCGCAGACGGCG	-	47.38	95.44	350.64	151.98	CAACCCGACTCGTAGACAGCA	-	7.90	9.54	56.28	20.80
TTTAGTGGACTTCTCGCGACT	-	29.02	57.90	73.90	60.37	CCGGTTCCGGAATTTTAACCG	-	19.50	23.29	53.55	45.95
TCAGCGCCATCCATTTTCGGG	-	15.92	31.73	50.07	48.38	CTTAGCTCGGATTTTGGCCAAC	-	15.77	18.63	120.87	26.98
CGCCCCGAATCGATCGGCGGA	-	28.94	56.58	34.73	147.85	ATTTTCAAGGGCCGCCGGGAA	-	16.68	19.48	47.60	24.65
CGATAGAACTCGTTTCCGAGC	-	71.55	136.47	44.75	238.06	TCGATCGGCGGACCGGATTGC	-	13.22	15.32	9.01	23.56
CGTCCCATATCCTCGAGAGGA	-	172.94	326.00	311.97	170.30	TTAGCTCGGATTTTGGCCAACC	-	175.30	202.64	366.78	173.10
CGCATGTCAAGACGCTCCT	-	6.02	10.90	622.23	22.79	TCTAATCATTGGCTTTACCCG	-	8.80	9.99	6.36	23.51
GTCCCATATCCTCGAGAGGATG	-	151.56	274.16	284.93	270.58	ATCGATCGGCGGACCGGATTG	-	14.16	15.28	43.14	32.82
CAACCCGACTCGTAGACAGCGC	-	18.38	32.64	75.89	103.29	ATTCCGTGGGATGGCTCAACA	-	43.20	44.37	171.08	62.96
ACGCTCCTGACGTTCTTAGCT	-	10.51	18.57	0.00	0.12	CCAAGGTGTGAACTCGTTGAA	-	81.80	82.59	215.93	175.72
ATCTGCACCGACGGCCGCTCC	-	4.36	7.22	0.00	18.55	CCGAATCGATCGGCGGACCGGA	-	51.11	48.82	88.62	213.26
CCTACTCATCGAGGCCTGGCTC	-	6.20	10.18	20.50	28.76	CCACCAAGATCTGCACCGACGG	-	34.10	23.72	82.59	103.97
ACGCCCCGAATCGATCGGCGGA	-	6.16	10.09	3.70	48.21	GCGGACCGGATTGCTCCGTTC	-	134.30	88.02	64.08	173.69
CCGATAGAACTCGTTTCCGAG	-	156.45	255.46	181.14	370.66	AACAACCCGACTCGTAGACAG	-	20.28	12.59	33.00	35.37
AACCCGACTCGTAGACAGCGCC	-	3.50	5.68	11.53	41.18	CGGTCCGTCGCTGAGGACGCT	-	36.12	17.95	45.24	48.94
AGCTCGGATTTTGGCCAACCGC	-	46.60	75.27	379.96	39.84	ACCCGACTCGTAGACAGCGCCT	-	9.58	4.27	28.93	29.64
CTCAAACTTCCTTGGCCTAAA	-	18.42	29.66	26.60	49.83	CCCGGGCTTAGGTCACCACCT	-	58.29	25.16	43.78	49.41
TTGGTCCGTGTTACAAGACA	-	3.42	5.42	13.06	30.96	CGTAGACAGCGCCTCGTGGTGC	-	8.63	2.33	14.74	29.31
CTGAGGACGCTTCTCCAGACT	-	19.40	29.77	49.58	45.93	TCAAGACGCTCCTGACGTCCT	-	0.00	0.15	20.88	23.56
TGAACTCGTTGAATACATCAGT	-	90.74	136.42	503.35	395.98						
CAGTTGGGCACCGTAACCCGG	-	34.13	50.77	48.64	103.11						

Table S25: va-phasiRNAs produced from genes encoding 'Chlorophyll a-b binding protein 1' and targeting mRNAs within the gene family for cleavage

va-phasiRNA[1]									Host mRNA targets[2]									DE target mRNA[3]					
va-phasiRNA	dsRNA (+) / (-) strand va-phasiRNA	Origin (gene family)	Normalized reads (positive / negative)						Target transcript ID	Predicted gene function	Cleavage position	vsiRNA:mRNA target pair (5'-3' : 3'-5')	Cleavage found in PAREseq replicates	Fragment signatures (rpm)				mRNA reads & FC(log2)					
			DM	DT	DT/DM reads	TM	TT	TT/TM reads						DM	DT	TM	TT	DM	DT	TM	TT		
TGAAGATCTGTGAACCAGCCT	+	Chloro[4]	20.96 / -	133.72 / -	6.38 / -	46.38 / -	88.70 / -	1.91 / -	BnaC03g59520D	CABBP1	519	TGAAGATCTGTGAACCAGCCT AGCGACTTCTAGACGCTTGGCCGGAACTTGGT	DT2 DT3 TT2 TT3	0.00	25.42	0.00	44.55	417531	0.02	305188	0.73		
TAAGATGCTCTGAGCGTGGACC	+ / -	Chloro	11.46 / 23.65	136.08 / 68.26	11.87 / 2.89	26.68 / 49.99	108.25 / 53.79	4.06 / 1.08	BnaC04g10780D	CABBP1	465	TAAGATGCTCTGAGCGTGGACC ACCGATTCTACGAGACTCGCACCTGGTTCGAG	DT2 DT3 TT2 TT3	0.00	16.13	0.00	32.99	524035	-0.12	299557	0.39		
TGAAGATCTGTGAACCAGCCT	+	Chloro	20.96 / -	133.72 / -	6.38 / -	46.38 / -	88.70 / -	1.91 / -	BnaC04g10780D	CABBP1	406	TGAAGATCTGTGAACCAGCCT AGCGACTTCTAGACGCTTGGCCGGAACTTGGT	DT2 DT3 TT2 TT3	0.00	34.98	0.00	43.95	524035	-0.12	299557	0.39		
TAAGATGCTCTGAGCGTGGACC	+ / -	Chloro	11.46 / 23.65	136.08 / 68.26	11.87 / 2.89	26.68 / 49.99	108.25 / 53.79	4.06 / 1.08	BnaA09g26570D	CABBP1	534	TAAGATGCTCTGAGCGTGGACC ACCGATTCTACGAGACTCGCACCTGGTTCGAG	DT2 DT3 TT2 TT3	0.00	16.13	0.00	32.99	325731	-0.25	212798	0.26		
TAAGATGCTCTGAGCGTGGACC	+ / -	Chloro	11.46 / 23.65	136.08 / 68.26	11.87 / 2.89	26.68 / 49.99	108.25 / 53.79	4.06 / 1.08	BnaA05g09410D	CABBP1	465	TAAGATGCTCTGAGCGTGGACC ACCGATTCTACGAGACTCGCACCTGGTTCGAG	DT2 DT3 TT2 TT3	0.00	16.13	0.00	32.99	185278	-0.12	131779	1.16		
TGAAGATCTGTGAACCAGCCT	+	Chloro	20.96 / -	133.72 / -	6.38 / -	46.38 / -	88.70 / -	1.91 / -	BnaA05g09410D	CABBP1	406	TGAAGATCTGTGAACCAGCCT AGCGACTTCTAGACGCTTGGCCGGAACTTGGT	DT2 DT3 TT2 TT3	0.00	34.98	0.00	43.95	185278	-0.12	131779	1.16		
CTGAAGATCTGTGAACCAGCC	+	Chloro	1.15 / -	72.60 / -	63.24 / -	5.34 / -	49.11 / -	9.19 / -	BnaC03g59520D	CABBP1	520	CTGAAGATCTGTGAACCAGCC AAGCGACTTCTAGACGCTTGGCCGGAACTTGG	DT1 DT3 TT3	0.00	3.52	0.00	5.04	417531	0.02	305188	0.73		
CTGAAGATCTGTGAACCAGCC	+	Chloro	1.15 / -	72.60 / -	63.24 / -	5.34 / -	49.11 / -	9.19 / -	BnaA05g09410D	CABBP1	407	CTGAAGATCTGTGAACCAGCC AAGCGACTTCTAGACGCTTGGCCGGAACTTGG	DT1 DT3 TT3	0.00	84.41	0.00	6.16	185278	-0.12	131779	1.16		
CTGAAGATCTGTGAACCAGCC	+	Chloro	1.15 / -	72.60 / -	63.24 / -	5.34 / -	49.11 / -	9.19 / -	BnaC04g10780D	CABBP1	407	CTGAAGATCTGTGAACCAGCC AAGCGACTTCTAGACGCTTGGCCGGAACTTGG	DT1 DT3 TT3	0.00	84.41	0.00	6.16	524035	-0.12	299557	0.39		
AATGGACCCAAGTACTTGACT	+ / -	Chloro	18.37 / 34.34	72.33 / 34.76	3.94 / 1.01	46.63 / 93.41	46.52 / 22.97	1.00 / 0.25	BnaA05g09410D	CABBP1	173	AATGGACCCAAGTACTTGACT CCTCTTACCTGGGTTCATGAATTGGGACAGCC	DT2 DT3 TT3	0.00	2.73	0.00	0.32	185278	-0.12	131779	1.16		
AAGATGCTCTGAGCGTGGACC	+ / -	Chloro	3.08 / 6.07	178.85 / 91.12	58.09 / 15.02	16.77 / 29.83	127.30 / 63.38	7.59 / 2.12	BnaC04g10780D	CABBP1	464	AAGATGCTCTGAGCGTGGACC CCGATTCTACGAGACTCGCACCTGGTTCGAGC	DT2 DT3 TT3	0.00	10.86	0.00	3.24	524035	-0.12	299557	0.39		
AATGGACCCAAGTACTTGACT	+ / -	Chloro	18.37 / 34.34	72.33 / 34.76	3.94 / 1.01	46.63 / 93.41	46.52 / 22.97	1.00 / 0.25	BnaC04g10780D	CABBP1	173	AATGGACCCAAGTACTTGACT CCTCTTACCTGGGTTCATGAATTGGGACAGCC	DT2 DT3 TT3	0.00	2.73	0.00	0.32	524035	-0.12	299557	0.39		
AAGATGCTCTGAGCGTGGACC	+ / -	Chloro	3.08 / 6.07	178.85 / 91.12	58.09 / 15.02	16.77 / 29.83	127.30 / 63.38	7.59 / 2.12	BnaA05g09410D	CABBP1	464	AAGATGCTCTGAGCGTGGACC CCGATTCTACGAGACTCGCACCTGGTTCGAGC	DT2 DT3 TT3	0.00	10.86	0.00	3.24	185278	-0.12	131779	1.16		
AAGATGCTCTGAGCGTGGACC	+ / -	Chloro	3.08 / 6.07	178.85 / 91.12	58.09 / 15.02	16.77 / 29.83	127.30 / 63.38	7.59 / 2.12	BnaA09g26570D	CABBP1	533	AAGATGCTCTGAGCGTGGACC CCGATTCTACGAGACTCGCACCTGGTTCGAGC	DT2 DT3 TT3	0.00	10.86	0.00	3.24	325731	-0.25	212798	0.26		
AATGGACCTAAGTACTTGACT	+ / -	Chloro	1.68 / 3.55	67.65 / 32.73	40.24 / 9.21	9.91 / 21.93	28.85 / 14.26	2.91 / 0.65	BnaC04g10780D	CABBP1	173	AATGGACCTAAGTACTTGACT CCTCTTACCTGGGTTCATGAATTGGGACAGCC	DT2 DT3	0.00	2.73	0.00	0.00	524035	-0.12	299557	0.39		
AAGATGCTCTGAGCGTGAACC	-	Chloro	- / -	24.10 / 24.10	- / 28.22	2.66 / 2.66	16.12 / 16.12	6.07 / 6.07	BnaC04g10780D	CABBP1	464	AAGATGCTCTGAGCGTGAACC CCGATTCTACGAGACTCGCACCTGGTTCGAGC	DT2 DT3	0.00	10.86	0.00	0.00	524035	-0.12	299557	0.39		
AAGATGCTCTGAGCGTGAACC	-	Chloro	- / -	24.10 / 24.10	- / 28.22	2.66 / 2.66	16.12 / 16.12	6.07 / 6.07	BnaA05g09410D	CABBP1	464	AAGATGCTCTGAGCGTGAACC CCGATTCTACGAGACTCGCACCTGGTTCGAGC	DT2 DT3	0.00	10.86	0.00	0.00	185278	-0.12	131779	1.16		
AATGGACCTAAGTACTTGACT	+ / -	Chloro	1.68 / 3.55	67.65 / 32.73	40.24 / 9.21	9.91 / 21.93	28.85 / 14.26	2.91 / 0.65	BnaA05g09410D	CABBP1	173	AATGGACCTAAGTACTTGACT CCTCTTACCTGGGTTCATGAATTGGGACAGCC	DT2 DT3	0.00	2.73	0.00	0.00	185278	-0.12	131779	1.16		
AAGATGCTCTGAGCGTGAACC	-	Chloro	- / -	24.10 / 24.10	- / 28.22	2.66 / 2.66	16.12 / 16.12	6.07 / 6.07	BnaA09g26570D	CABBP1	533	AAGATGCTCTGAGCGTGAACC CCGATTCTACGAGACTCGCACCTGGTTCGAGC	DT2 DT3	0.00	10.86	0.00	0.00	325731	-0.25	212798	0.26		
CTTCCAAGGACTTCTGATGCT	+	Chloro	81.76 / -	197.98 / -	2.42 / -	223.18 / -	147.39 / -	- / -	BnaA09g26570D	CABBP1	146	CTTCCAAGGACTTCTGATGCT CGGCGAAGGTTCCTGAAGACTACGACGTCCTC	DT2 TT3	0.00	3.82	0.00	0.42	325731	-0.25	212798	0.26		
CTTCCAAGGACTTCTGATGCT	+	Chloro	81.76 / -	197.98 / -	2.42 / -	223.18 / -	147.39 / -	- / -	BnaC03g59520D	CABBP1	190	CTTCCAAGGACTTCTGATGCT CGGCGAAGGTTCCTGAAGACTACGACGACCCC	DT2 TT3	0.00	3.82	0.00	0.42	417531	0.02	305188	0.73		
TGAACCAGCCTTGAACCAAAC	+	Chloro	2.57 / -	45.15 / -	17.58 / -	7.88 / -	49.07 / -	6.23 / -	BnaC03g59520D	CABBP1	509	TGAACCAGCCTTGAACCAAAC o AGACGCTTGGCCGGAACTTGGTTTGGCGGAGA	DT3 TT3	0.00	3.50	0.00	0.28	417531	0.02	305188	0.73		
ATGGACCCAAGTACTTGACCC	+	Chloro	13.18 / -	44.55 / -	3.38 / -	29.91 / -	43.27 / -	1.45 / -	BnaC04g10780D	CABBP1	172	ATGGACCCAAGTACTTGACCC CTCTTACCTGGGTTCATGAATTGGGACAGCCT	DT3 TT3	0.00	0.95	0.00	0.51	524035	-0.12	299557	0.39		
TTCGCTGAAGATCTGCGAACC	+ / -	Chloro	3.44 / 5.25	34.66 / 17.98	10.06 / 3.42	9.38 / 18.23	45.70 / 22.86	4.87 / 1.25	BnaC04g10780D	CABBP1	411	TTCGCTGAAGATCTGCGAACC GAGGAAGCGACTTCTAGACGCTTGGCCGGAAC	DT3 TT3	0.00	5.40	0.00	2.08	524035	-0.12	299557	0.39		
CGGCCTTGAACCAAACCGCCT	+	Chloro	24.72 / -	45.46 / -	1.84 / -	58.66 / -	45.77 / -	0.78 / -	BnaA05g09410D	CABBP1	391	CGGCCTTGAACCAAACCGCCT CTTGGCCGGAACTTGGTTTGGCGGAAGAGGCTT	DT3 TT3	0.00	4.99	0.00	3.38	185278	-0.12	131779	1.16		
TGAACCAGCCTTGAACCAAACG	+	Chloro	0.00 / -	48.61 / -	48.61 / -	1.61 / -	32.52 / -	20.17 / -	BnaA05g09410D	CABBP1	396	TGAACCAGCCTTGAACCAAACG o AGACGCTTGGCCGGAACTTGGTTTGGCGAAGA	DT3 TT3	0.00	3.50	0.00	0.28	185278	-0.12	131779	1.16		
AATGGCTAAGATGCTCTGAGC	+ / -	Chloro	1.68 / 3.55	34.77 / 17.93	20.68 / 5.04	0.00 / 0.00	35.24 / 17.51	35.24 / 17.51	BnaA09g26570D	CABBP1	540	AATGGCTAAGATGCTCTGAGC GGGTTTACCGATTCTACGAGACTCGCACCTGG	DT3 TT3	0.00	9.76	0.00	7.82	325731	-0.25	212798	0.26		

AATGGACCCAAGTACTTGACT	+ / -	Chloro	18.37 / 34.34	72.33 / 34.76	3.94 / 1.01	46.63 / 93.41	46.52 / 22.97	1.00 / 0.25	BnaC03g59520D	CABBP1	286	AATGGACCCAAGTACTTGACT ||||| |||||||||||||| CCTCTTACCCGGGTTCATGAACTGAGAGAGCC	DT3 TT3	0.00	0.86	0.00	0.60	417531	0.02	305188	0.73
TGAACCAGCCTTGAACCAAACG	+	Chloro	0.00 / -	48.61 / -	48.61 / -	1.61 / -	32.52 / -	20.17 / -	BnaC04g10780D	CABBP1	396	TGAACCAGCCTTGAACCAAACG o|||||||||||||||||o AGACGCTTGGCCGGAACTTGGTTTGTCGGAGA	DT3 TT3	0.00	3.50	0.00	0.28	524035	-0.12	299557	0.39
AATGGCTAAGATGCTCTGAGC	+ / -	Chloro	1.68 / 3.55	34.77 / 17.93	20.68 / 5.04	0.00 / 0.00	35.24 / 17.51	35.24 / 17.51	BnaC04g10780D	CABBP1	471	AATGGCTAAGATGCTCTGAGC ||||||||||||||||||| GGGTTTACCGATTCTACGAGACTCGCACCTGG	DT3 TT3	0.00	1.72	0.00	5.60	524035	-0.12	299557	0.39
CCGGCCTTGAACCAAACCGCC	+ / -	Chloro	1.15 / 1.75	47.94 / 22.81	41.75 / 13.03	5.54 / 10.03	66.69 / 32.90	12.03 / 3.28	BnaA05g09410D	CABBP1	392	CCGGCCTTGAACCAAACCGCC ||||||||||||||||||| GCTTGGCCGGAACTTGGTTTGGCGAAGAGGCT	DT3 TT3	0.00	3.77	0.00	0.74	185278	-0.12	131779	1.16
TGAACCAGCCTTGAACCAAACG	+	Chloro	0.00 / -	48.61 / -	48.61 / -	1.61 / -	32.52 / -	20.17 / -	BnaC03g59520D	CABBP1	509	TGAACCAGCCTTGAACCAAACG o||||||||||||||||| AGACGCTTGGCCGGAACTTGGTTTGGCGGAGA	DT3 TT3	0.00	3.50	0.00	0.28	417531	0.02	305188	0.73
CCGGCCTTGAACCAAACCGCC	+ / -	Chloro	1.15 / 1.75	47.94 / 22.81	41.75 / 13.03	5.54 / 10.03	66.69 / 32.90	12.03 / 3.28	BnaC03g59520D	CABBP1	505	CCGGCCTTGAACCAAACCGCC ||||||||||||||||||| GCTTGGCCGGAACTTGGTTTGGCGGAGAGGCT	DT3 TT3	0.00	3.77	0.00	0.74	417531	0.02	305188	0.73
ATGGACCCAAGTACTTGACCC	+	Chloro	13.18 / -	44.55 / -	3.38 / -	29.91 / -	43.27 / -	1.45 / -	BnaC03g59520D	CABBP1	285	ATGGACCCAAGTACTTGACCC ||||||||||||||||| CTCTTACCCGGGTTCATGAACTGAGAGAGCCT	DT3 TT3	0.00	0.27	0.00	0.32	417531	0.02	305188	0.73
ATGGACCCAAGTACTTGACCC	+	Chloro	13.18 / -	44.55 / -	3.38 / -	29.91 / -	43.27 / -	1.45 / -	BnaA05g09410D	CABBP1	172	ATGGACCCAAGTACTTGACCC |||||||||||||o||| CTCTTACCTGGGTTCATGAATTGGGACAGCCT	DT3 TT3	0.00	0.95	0.00	0.51	185278	-0.12	131779	1.16
TGAACCAGCCTTGAACCAAACC	+	Chloro	0.89 / -	40.02 / -	45.11 / -	7.92 / -	39.29 / -	4.96 / -	BnaC04g10780D	CABBP1	396	TGAACCAGCCTTGAACCAAACC o||||||||||||||||| AGACGCTTGGCCGGAACTTGGTTTGTCGGAGA	DT3 TT3	0.00	3.50	0.00	0.28	524035	-0.12	299557	0.39
CCGGCCTTGAACCAAACCGCC	+ / -	Chloro	1.15 / 1.75	47.94 / 22.81	41.75 / 13.03	5.54 / 10.03	66.69 / 32.90	12.03 / 3.28	BnaC04g10780D	CABBP1	392	CCGGCCTTGAACCAAACCGCC ||||||||||||||||||| GCTTGGCCGGAACTTGGTTTGTCGGAGAGGCT	DT3 TT3	0.00	3.77	0.00	0.74	524035	-0.12	299557	0.39
TTCGCTGAAGATCTGTGAACC	+	Chloro	17.41 / -	302.45 / -	17.37 / -	36.62 / -	219.25 / -	5.99 / -	BnaC04g10780D	CABBP1	411	TTCGCTGAAGATCTGTGAACC |||||||||||||o||||| GAGGAAGCGACTTCTAGACGCTTGGCCGGAAC	DT3 TT3	0.00	5.40	0.00	2.08	524035	-0.12	299557	0.39
TGAACCAGCCTTGAACCAAACC	+	Chloro	0.89 / -	40.02 / -	45.11 / -	7.92 / -	39.29 / -	4.96 / -	BnaC03g59520D	CABBP1	509	TGAACCAGCCTTGAACCAAACC o||||||||||||||||| AGACGCTTGGCCGGAACTTGGTTTGGCGGAGA	DT3 TT3	0.00	3.50	0.00	0.28	417531	0.02	305188	0.73
TGAACCAGCCTTGAACCAAAC	+	Chloro	2.57 / -	45.15 / -	17.58 / -	7.88 / -	49.07 / -	6.23 / -	BnaC04g10780D	CABBP1	396	TGAACCAGCCTTGAACCAAAC o|||| ||||||||||| AGACGCTTGGCCGGAACTTGGTTTGTCGGAGA	DT3 TT3	0.00	3.50	0.00	0.28	524035	-0.12	299557	0.39
TGAACCAGCCTTGAACCAAAC	+	Chloro	2.57 / -	45.15 / -	17.58 / -	7.88 / -	49.07 / -	6.23 / -	BnaA05g09410D	CABBP1	396	TGAACCAGCCTTGAACCAAAC o|||| ||||||||||| AGACGCTTGGCCGGAACTTGGTTTGGCGAAGA	DT3 TT3	0.00	3.50	0.00	0.28	185278	-0.12	131779	1.16
GGAAGACGCAGCCTAGGGCTC	+ / -	Chloro	0.52 / 1.71	38.54 / 19.33	73.87 / 11.32	3.93 / 7.37	42.68 / 21.16	10.86 / 2.87	BnaA09g26570D	CABBP1	403	GGAAGACGCAGCCTAGGGCTC ||||||o||||||||||| AGGCCCTTCTGTGTCGGATCCCGAGGTTCGTA	DT3 TT3	0.00	0.36	0.00	0.14	325731	-0.25	212798	0.26
AAGATGCTCTGAGCGTGGACC	+ / -	Chloro	3.08 / 6.07	178.85 / 91.12	58.09 / 15.02	16.77 / 29.83	127.30 / 63.38	7.59 / 2.12	BnaC03g59520D	CABBP1	577	AAGATGCTCTGAGCGTGGACC |||||||||||||||o||| TCGGTTCTACGAGACTCGCACTTGGTTCGATC	DT3 TT3	0.00	1.13	0.00	2.31	417531	0.02	305188	0.73
TGAACCAGCCTTGAACCAAACC	+	Chloro	0.89 / -	40.02 / -	45.11 / -	7.92 / -	39.29 / -	4.96 / -	BnaA05g09410D	CABBP1	396	TGAACCAGCCTTGAACCAAACC o||||||||||||||||| AGACGCTTGGCCGGAACTTGGTTTGGCGAAGA	DT3 TT3	0.00	3.50	0.00	0.28	185278	-0.12	131779	1.16
CGGCCTTGAACCAAACCGCCT	+	Chloro	24.72 / -	45.46 / -	1.84 / -	58.66 / -	45.77 / -	0.78 / -	BnaC04g10780D	CABBP1	391	CGGCCTTGAACCAAACCGCCT |||||||||||||||| CTTGGCCGGAACTTGGTTTGTCGGAGAGGCTT	DT3 TT3	0.00	4.99	0.00	3.38	524035	-0.12	299557	0.39
CGGCCTTGAACCAAACCGCCT	+	Chloro	24.72 / -	45.46 / -	1.84 / -	58.66 / -	45.77 / -	0.78 / -	BnaC03g59520D	CABBP1	504	CGGCCTTGAACCAAACCGCCT ||||||||||||||||||| CTTGGCCGGAACTTGGTTTGGCGGAGAGGCTT	DT3 TT3	0.00	4.99	0.00	3.38	417531	0.02	305188	0.73
ATCTGTGAACCAGCCTTGAAC	+	Chloro	0.00 / -	63.13 / -	63.13 / -	7.15 / -	43.34 / -	6.06 / -	BnaC03g59520D	CABBP1	514	ATCTGTGAACCAGCCTTGAAC |||||o|||| |||||||| CTTCTAGACGCTTGGCCGGAACTTGGTTTGGC	TT1 TT3	0.00	0.00	0.00	0.59	417531	0.02	305188	0.73
ATCTGTGAACCAGCCTTGAACC	+	Chloro	8.28 / -	38.44 / -	4.64 / -	30.33 / -	53.02 / -	1.75 / -	BnaC04g10780D	CABBP1	401	ATCTGTGAACCAGCCTTGAACC |||||o||||| ||||||||| CTTCTAGACGCTTGGCCGGAACTTGGTTTGTC	TT1 TT3	0.00	0.00	0.00	0.59	524035	-0.12	299557	0.39
ATCTGTGAACCAGCCTTGAACC	+	Chloro	8.28 / -	38.44 / -	4.64 / -	30.33 / -	53.02 / -	1.75 / -	BnaA05g09410D	CABBP1	401	ATCTGTGAACCAGCCTTGAACC |||||o||||| ||||||||| CTTCTAGACGCTTGGCCGGAACTTGGTTTGGC	TT1 TT3	0.00	0.00	0.00	0.59	185278	-0.12	131779	1.16
ATCTGTGAACCAGCCTTGAACC	+	Chloro	8.28 / -	38.44 / -	4.64 / -	30.33 / -	53.02 / -	1.75 / -	BnaC03g59520D	CABBP1	514	ATCTGTGAACCAGCCTTGAACC |||||o||||| ||||||||| CTTCTAGACGCTTGGCCGGAACTTGGTTTGGC	TT1 TT3	0.00	0.00	0.00	0.59	417531	0.02	305188	0.73
ATCTGTGAACCAGCCTTGAAC	+	Chloro	0.00 / -	63.13 / -	63.13 / -	7.15 / -	43.34 / -	6.06 / -	BnaC04g10780D	CABBP1	401	ATCTGTGAACCAGCCTTGAAC |||||o|||| ||||||||| CTTCTAGACGCTTGGCCGGAACTTGGTTTGTC	TT1 TT3	0.00	0.00	0.00	0.59	524035	-0.12	299557	0.39
ATCTGTGAACCAGCCTTGAAC	+	Chloro	0.00 / -	63.13 / -	63.13 / -	7.15 / -	43.34 / -	6.06 / -	BnaA05g09410D	CABBP1	401	ATCTGTGAACCAGCCTTGAAC |||||o|||| ||||||||| CTTCTAGACGCTTGGCCGGAACTTGGTTTGGC	TT1 TT3	0.00	0.00	0.00	0.59	185278	-0.12	131779	1.16
AAGGTAGCTCGGTGGCTCGCC	+ / -	Chloro	0.26 / 0.85	45.84 / 22.99	175.72 / 26.93	5.58 / 10.41	27.97 / 13.88	5.02 / 1.33	BnaC03g59520D	CABBP1	311	AAGGTAGCTCGGTGGCTCGCC ||||||||||||||||||| GCCATTCCATCGAGCCACCGAGCGGCCTCTTA	DT2	0.00	1.42	0.00	0.00	417531	0.02	305188	0.73
CCTAGGGCTCCGAGCATGGCC	+ / -	Chloro	3.09 / 6.16	50.71 / 25.34	16.41 / 4.11	4.46 / 11.08	37.55 / 18.64	8.43 / 1.68	BnaA05g09410D	CABBP1	323	CCTAGGGCTCCGAGCATGGCC |||||||||o||||||||| TGTCGGATCCCGAGGTTCGTACCGGGTAGACG	DT2	0.00	3.47	0.00	0.00	185278	-0.12	131779	1.16
CCTTCGCTGAAGATCTGTGAA	+	Chloro	0.00 / -	59.00 / -	59.00 / -	0.00 / -	31.14 / -	31.14 / -	BnaA05g09410D	CABBP1	413	CCTTCGCTGAAGATCTGTGAA ||||||||||||||||o||| GGGAGGAAGCGACTTCTAGACGCTTGGCCGGA	DT3	0.00	1.91	0.00	0.00	185278	-0.12	131779	1.16
ATGGTCGGCGAGATTCTCCAA	+	Chloro	9.18 / -	55.51 / -	6.04 / -	20.22 / -	29.70 / -	1.47 / -	BnaC04g10780D	CABBP1	729	ATGGTCGGCGAGATTCTCCAA |||||o||||||||||| GGTTTACCAGTCGCTCTAAGAGGTTGCCAGGG	DT3	0.00	23.60	0.00	0.00	524035	-0.12	299557	0.39
AAGATGCTCTGAGCGTGAACC	-	Chloro	0.85 / 0.85	24.10 / 24.10	28.22 / 28.22	2.66 / 2.66	16.12 / 16.12	6.07 / 6.07	BnaC03g59520D	CABBP1	577	AAGATGCTCTGAGCGTGAACC ||||||||||||||||||| TCGGTTCTACGAGACTCGCACTTGGTTCGATC	DT3	0.00	1.13	0.00	0.00	417531	0.02	305188	0.73
TTCTGGGTCGGTAGCGAGGCC	+	Chloro	9.09 / -	79.41 / -	8.73 / -	19.57 / -	51.47 / -	2.63 / -	BnaA07g07570D	CABBP1	2055	TTCTGGGTCGGTAGCGAGGCC o|||||||||||||o||| TTCGGAGACCCAGCCATCGGTTCGGGTTACCC	DT3	0.00	0.18	0.00	0.00	213712	-0.76	117162	0.37
AAATGGTCGGCGAGATTCTCC	+	Chloro	1.77 / -	42.17 / -	23.76 / -	0.00 / -	36.11 / -	36.11 / -	BnaA09g26570D	CABBP1	800	AAATGGTCGGCGAGATTCTCC |||||||o||o|| |||||| TCGGTTTACCAGTCGTTCCAAGAGGTTGCCAG	DT3	0.00	14.89	0.00	0.00	325731	-0.25	212798	0.26
ACAATGGCTTGAACAAAGAAT	+ / -	Chloro	4.24 / 7.91	40.76 / 20.02	9.62 / 2.53	4.64 / 9.43	29.02 / 14.35	6.26 / 1.52	BnaA05g09410D	CABBP1	692	ACAATGGCTTGAACAAAGAAT || |||||o|| |||||||| TCACTGCTACCGGACATGTTTCTTAGGTTTGT	DT3	0.00	8.49	0.00	0.00	185278	-0.12	131779	1.16
GTGGACCAAGCTCGGGTTGCC	+ / -	Chloro	0.52 / 1.71	57.53 / 27.01	110.27 / 15.82	0.80 / 1.23	37.80 / 18.63	47.40 / 15.10	BnaC04g10780D	CABBP1	450	GTGGACCAAGCTCGGGTTGCC ||||||||||||||||||| CTCGCACCTGGTTCGAGCCCAACGGGTTCATC	DT3	0.00	3.31	0.00	0.00	524035	-0.12	299557	0.39
AATGGACCTAAGTACTTGACT	+ / -	Chloro	1.68 / 3.55	67.65 / 32.73	40.24 / 9.21	9.91 / 21.93	28.85 / 14.26	2.91 / 0.65	BnaC03g59520D	CABBP1	286	AATGGACCTAAGTACTTGACT ||||| ||o|||||||||| CCTCTTACCCGGGTTCATGAACTGAGAGAGCC	DT3	0.00	0.86	0.00	0.00	417531	0.02	305188	0.73

AATGGACCTAAGTACTTGACT	+ / -	Chloro	1.68 / 3.55	67.65 / 32.73	40.24 / 9.21	9.91 / 21.93	28.85 / 14.26	2.91 / 0.65	BnaC03g59520D	CABBP1	286	AATGGACCTAAGTACTTGACT ||||||o|||||||||||| CCTCTTACCCGGGTTCATGAACTGAGAGAGCC	DT3	0.00	0.86	0.00	0.00	417531	0.02	305188	0.73
TTCGCTGAAGATCTGTGAACC	+	Chloro	17.41 / -	302.45 / -	17.37 / -	36.62 / -	219.25 / -	5.99 / -	BnaA09g26570D	CABBP1	480	TTCGCTGAAGATCTGTGAACC o||||||||||||||||||| GAGGGAGCGACTTCTAAACACTCGGCCGGAAC	DT3	0.00	1.72	0.00	0.00	325731	-0.25	212798	0.26
AAATGGTCGGCGAGATTCTCC	+	Chloro	1.77 / -	42.17 / -	23.76 / -	0.00 / -	36.11 / -	36.11 / -	BnaA05g09410D	CABBP1	731	AAATGGTCGGCGAGATTCTCC |||||||o||o|||||||| TCGGTTTACCAGTCGTTCTAAGAGGTTTCCAG	DT3	0.00	14.89	0.00	0.00	185278	-0.12	131779	1.16
CCTTCGCTGAAGATCTGTGAA	+	Chloro	0.00 / -	59.00 / -	59.00 / -	0.00 / -	31.14 / -	31.14 / -	BnaC04g10780D	CABBP1	413	CCTTCGCTGAAGATCTGTGAA |||||||||||||||o||| GGGAGGAAGCGACTTCTAGACGCTTGGCCGGA	DT3	0.00	5.08	0.00	0.00	524035	-0.12	299557	0.39
GTCGGCGAGATTCTCCAACGG	+	Chloro	1.77 / -	31.41 / -	17.70 / -	3.99 / -	26.54 / -	6.66 / -	BnaC04g10780D	CABBP1	726	GTCGGCGAGATTCTCCAACGG ||o||||||||||||||| TTACCAGTCGCTCTAAGAGGTTGCCAGGGAAA	DT3	0.00	1.82	0.00	0.00	524035	-0.12	299557	0.39
GTGGACCAAGCTCGGGTTGCC	+ / -	Chloro	0.52 / 1.71	57.53 / 27.01	110.27 / 15.82	0.80 / 1.23	37.80 / 18.63	47.40 / 15.10	BnaA09g26570D	CABBP1	519	GTGGACCAAGCTCGGGTTGCC ||||||||||||||||||| CTCGCACCTGGTTCGAGCCCAACGGGTTCATC	DT3	0.00	3.31	0.00	0.00	325731	-0.25	212798	0.26
AAATGGTCGGCGAGATTCTCC	+	Chloro	1.77 / -	42.17 / -	23.76 / -	0.00 / -	36.11 / -	36.11 / -	BnaC04g10780D	CABBP1	731	AAATGGTCGGCGAGATTCTCC |||||||o||||||||||| TCGGTTTACCAGTCGCTCTAAGAGGTTGCCAG	DT3	0.00	14.89	0.00	0.00	524035	-0.12	299557	0.39
TTCGCTGAAGATCTGCGAACC	+ / -	Chloro	3.44 / 5.25	34.66 / 17.98	10.06 / 3.42	9.38 / 18.23	45.70 / 22.86	4.87 / 1.25	BnaA09g26570D	CABBP1	480	TTCGCTGAAGATCTGCGAACC o||||||||||| || || || GAGGGAGCGACTTCTAAACACTCGGCCGGAAC	DT3	0.00	1.72	0.00	0.00	325731	-0.25	212798	0.26
GTGGACCAAGCTCGGGTTGCC	+ / -	Chloro	0.52 / 1.71	57.53 / 27.01	110.27 / 15.82	0.80 / 1.23	37.80 / 18.63	47.40 / 15.10	BnaA05g09410D	CABBP1	450	GTGGACCAAGCTCGGGTTGCC ||||||||||||||||||| CTCGCACCTGGTTCGAGCCCAACGGGTTCATC	DT3	0.00	3.31	0.00	0.00	185278	-0.12	131779	1.16
AAATGGTCGGCGAGATTCTCC	+	Chloro	1.77 / -	42.17 / -	23.76 / -	0.00 / -	36.11 / -	36.11 / -	BnaC03g59520D	CABBP1	844	AAATGGTCGGCGAGATTCTCC |||||||o||o|||||||| TCGGTTTACCAGTCGTTCTAAGAGGTTTCCAG	DT3	0.00	14.89	0.00	0.00	417531	0.02	305188	0.73
ATGGACCCAAGTACTTGACCC	+	Chloro	13.18 / -	44.55 / -	3.38 / -	29.91 / -	43.27 / -	1.45 / -	BnaA09g26570D	CABBP1	241	ATGGACCCAAGTACTTGACCC ||||||||||||||||||| CTCTTACCTGGGTTCATGAACTGAGAAAGCCT	DT3	0.00	0.64	0.00	0.00	325731	-0.25	212798	0.26
TTCTGGGTCGGTAGCGAGACC	+	Chloro	19.16 / -	75.82 / -	3.96 / -	64.40 / -	84.07 / -	1.31 / -	BnaA07g07570D	CABBP1	2055	TTCTGGGTCGGTAGCGAGACC o|||||||||||||o || TTCGGAGACCCAGCCATCGGTTCGGGTTACCC	DT3	0.00	0.18	0.00	0.00	213712	-0.76	117162	0.37
ACAATGGCTTGAACAAAGAAT	+ / -	Chloro	4.24 / 7.91	40.76 / 20.02	9.62 / 2.53	4.64 / 9.43	29.02 / 14.35	6.26 / 1.52	BnaC03g59520D	CABBP1	805	ACAATGGCTTGAACAAAGAAT ||||o|||||||||||| TCACTGTTATCGAACTTGTTTCTTAGGTTTGT	DT3	0.00	1.63	0.00	0.00	417531	0.02	305188	0.73
CCATGGGCTGCCTGATGGGCC	+ / -	Chloro	0.89 / 0.90	46.54 / 22.99	52.46 / 25.61	0.81 / 1.42	36.31 / 17.98	44.57 / 12.64	BnaA09g26570D	CABBP1	207	CCATGGGCTGCCTGATGGGCC |||||||||||||||||| GCATGGTACCCGACGGACTACCAGGGAAACCG	DT3	0.00	1.77	0.00	0.00	325731	-0.25	212798	0.26
CCTAGGGCTCCGAGCATGGCC	+ / -	Chloro	3.09 / 6.16	50.71 / 25.34	16.41 / 4.11	4.46 / 11.08	37.55 / 18.64	8.43 / 1.68	BnaC03g59520D	CABBP1	436	CCTAGGGCTCCGAGCATGGCC ||||||||||||||||||| CGTCGGATCCCGAGGCTCGTACCGGGTGGACG	DT3	0.00	0.54	0.00	0.00	417531	0.02	305188	0.73
GGAAGACGCAGCCTAGGGCTC	+ / -	Chloro	0.52 / 1.71	38.54 / 19.33	73.87 / 11.32	3.93 / 7.37	42.68 / 21.16	10.86 / 2.87	BnaC04g10780D	CABBP1	334	GGAAGACGCAGCCTAGGGCTC ||||o|||| |||||||||| AGTCCCTTTTGCGTAGGATCCCGAGGTTCGTA	TT3	0.00	0.00	0.00	0.28	524035	-0.12	299557	0.39
AATGGCTAAGATGCTCTGAGC	+ / -	Chloro	1.68 / 3.55	34.77 / 17.93	20.68 / 5.04	0.00 / 0.00	35.24 / 17.51	35.24 / 17.51	BnaA05g09410D	CABBP1	471	AATGGCTAAGATGCTCTGAGC ||||||||||||||||||| GGGTTTACCGATTCTACGAGACTCGCACCTGG	TT3	0.00	0.00	0.00	5.23	185278	-0.12	131779	1.16
CGAACCGGCCTTGAACCAAACC	+ / -	Chloro	0.89 / 0.90	38.54 / 18.48	43.44 / 20.59	0.81 / 1.42	63.34 / 31.28	77.75 / 21.99	BnaC03g59520D	CABBP1	509	CGAACCGGCCTTGAACCAAACC ||||||||||||||||||||||| AGACGCTTGGCCGGAACTTGGTTTGGCGGAGA	TT3	0.00	0.00	0.00	0.28	417531	0.02	305188	0.73
ATGAGGATCACCTGAGTAGCC	+ / -	Chloro	1.68 / 3.55	47.44 / 23.32	28.22 / 6.56	3.91 / 7.18	42.09 / 20.89	10.76 / 2.91	BnaA05g09410D	CABBP1	494	ATGAGGATCACCTGAGTAGCC |||||o|||||||| ||||| AGGGTACTCTTAGTGGACGCAACGGGTTTACC	TT3	0.00	0.00	0.00	0.23	185278	-0.12	131779	1.16
TTCGCTGAAGATCTGTGAACC	+	Chloro	17.41 / -	302.45 / -	17.37 / -	36.62 / -	219.25 / -	5.99 / -	BnaA05g09410D	CABBP1	411	TTCGCTGAAGATCTGTGAACC |||||||||||||o|||| GAGGAAGCGACTTCTAGACGCTTGGCCGGAAC	TT3	0.00	0.00	0.00	0.83	185278	-0.12	131779	1.16
CGTGGACCAAGCTCGGGTTGCC	+ / -	Chloro	0.00 / 0.00	35.21 / 16.65	35.21 / 16.65	0.00 / 0.00	50.90 / 25.11	50.90 / 25.11	BnaC04g10780D	CABBP1	451	CGTGGACCAAGCTCGGGTTGCC ||||||||||||||||||| ACTCGCACCTGGTTCGAGCCCAACGGGTTCAT	TT3	0.00	0.00	0.00	0.83	524035	-0.12	299557	0.39
CGAACCGGCCTTGAACCAAACC	+ / -	Chloro	0.89 / 0.90	38.54 / 18.48	43.44 / 20.59	0.81 / 1.42	63.34 / 31.28	77.75 / 21.99	BnaC04g10780D	CABBP1	396	CGAACCGGCCTTGAACCAAACC ||||||||||||||||||| AGACGCTTGGCCGGAACTTGGTTTGTCGGAGA	TT3	0.00	0.00	0.00	0.28	524035	-0.12	299557	0.39
ATGAGGATCACCTGAGTAGCC	+ / -	Chloro	1.68 / 3.55	47.44 / 23.32	28.22 / 6.56	3.91 / 7.18	42.09 / 20.89	10.76 / 2.91	BnaA07g07570D	CABBP1	1943	ATGAGGATCACCTGAGTAGCC || |o|||||| |||||||| AGGGTAGTTCTAGTGAACTCATCGGGTTTATC	TT3	0.00	0.00	0.00	0.51	213712	-0.76	117162	0.37
CGTGGACCAAGCTCGGGTTGCC	+ / -	Chloro	0.00 / 0.00	35.21 / 16.65	35.21 / 16.65	0.00 / 0.00	50.90 / 25.11	50.90 / 25.11	BnaA09g26570D	CABBP1	520	CGTGGACCAAGCTCGGGTTGCC ||||||||||||||||||| ACTCGCACCTGGTTCGAGCCCAACGGGTTCAT	TT3	0.00	0.00	0.00	0.83	325731	-0.25	212798	0.26
CCGGCCTTGAACCAAACCGCC	+ / -	Chloro	1.15 / 1.75	47.94 / 22.81	41.75 / 13.03	5.54 / 10.03	66.69 / 32.90	12.03 / 3.28	BnaA09g26570D	CABBP1	461	CCGGCCTTGAACCAAACCGCC ||||||||||||||||||| ACTCGGCCGGAACTTGGTTTGGCGGAGAGGCT	TT3	0.00	0.00	0.00	0.05	325731	-0.25	212798	0.26
CTGAAGATCTGTGAACCAGCCT	+	Chloro	1.67 / -	25.03 / -	14.99 / -	0.00 / -	50.89 / -	50.89 / -	BnaA05g09410D	CABBP1	407	CTGAAGATCTGTGAACCAGCCT |||||||||o|||| |||| AAGCGACTTCTAGACGCTTGGCCGGAACTTGG	TT3	0.00	0.00	0.00	6.16	185278	-0.12	131779	1.16
CTGAAGATCTGTGAACCAGCCT	+	Chloro	1.67 / -	25.03 / -	14.99 / -	0.00 / -	50.89 / -	50.89 / -	BnaC03g59520D	CABBP1	520	CTGAAGATCTGTGAACCAGCCT ||||||||||o|||| |||| AAGCGACTTCTAGACGCTTGGCCGGAACTTGG	TT3	0.00	0.00	0.00	5.04	417531	0.02	305188	0.73
CGAACCGGCCTTGAACCAAACC	+ / -	Chloro	0.89 / 0.90	38.54 / 18.48	43.44 / 20.59	0.81 / 1.42	63.34 / 31.28	77.75 / 21.99	BnaA05g09410D	CABBP1	396	CGAACCGGCCTTGAACCAAACC ||||||||||||||||||| AGACGCTTGGCCGGAACTTGGTTTGGCGAAGA	TT3	0.00	0.00	0.00	0.28	185278	-0.12	131779	1.16
ATGAGGATCACCTGAGTAGCC	+ / -	Chloro	1.68 / 3.55	47.44 / 23.32	28.22 / 6.56	3.91 / 7.18	42.09 / 20.89	10.76 / 2.91	BnaC04g10780D	CABBP1	494	ATGAGGATCACCTGAGTAGCC ||||||||||||||||||| AGGGTACTCCTAGTGGACTCATCGGGTTTACC	TT3	0.00	0.00	0.00	2.59	524035	-0.12	299557	0.39
TTCGCTGAAGATCTGTGAACC	+	Chloro	17.41 / -	302.45 / -	17.37 / -	36.62 / -	219.25 / -	5.99 / -	BnaC03g59520D	CABBP1	524	TTCGCTGAAGATCTGTGAACC |||||||||||||o|||| GAGGAAGCGACTTCTAGACGCTTGGCCGGAAC	TT3	0.00	0.00	0.00	0.37	417531	0.02	305188	0.73
TTCGCTGAAGATCTGCGAACC	+ / -	Chloro	3.44 / 5.25	34.66 / 17.98	10.06 / 3.42	9.38 / 18.23	45.70 / 22.86	4.87 / 1.25	BnaA05g09410D	CABBP1	411	TTCGCTGAAGATCTGCGAACC ||||||||||||||||||| GAGGAAGCGACTTCTAGACGCTTGGCCGGAAC	TT3	0.00	0.00	0.00	0.83	185278	-0.12	131779	1.16
TGAACAAAGAATCCAAACATA	+ / -	Chloro	2.66 / 2.69	23.48 / 12.21	8.82 / 4.53	2.41 / 3.89	32.46 / 16.26	13.47 / 4.18	BnaC04g10780D	CABBP1	683	TGAACAAAGAATCCAAACATA ||||||||||||||||||| ACGGACTTGCTTCTTAGGTTTGTACCTCTTGT	TT3	0.00	0.00	0.00	0.09	524035	-0.12	299557	0.39
CGGCCTTGAACCAAACCGCCT	+	Chloro	24.72 / -	45.46 / -	1.84 / -	58.66 / -	45.77 / -	0.78 / -	BnaA09g26570D	CABBP1	460	CGGCCTTGAACCAAACCGCCT ||||||||||||||||||| CTCGGCCGGAACTTGGTTTGGCGGAGAGGCTT	TT3	0.00	0.00	0.00	0.28	325731	-0.25	212798	0.26
TGAACAAAGAATCCAAACATA	+ / -	Chloro	2.66 / 2.69	23.48 / 12.21	8.82 / 4.53	2.41 / 3.89	32.46 / 16.26	13.47 / 4.18	BnaA07g07570D	CABBP1	2132	TGAACAAAGAATCCAAACATA ||||||||||||||||||| CCGAACTTGTTTCTTAGGTTTGTATCTCTTGT	TT3	0.00	0.00	0.00	0.09	213712	-0.76	117162	0.37
TGAACAAAGAATCCAAACATA	+ / -	Chloro	2.66 / 2.69	23.48 / 12.21	8.82 / 4.53	2.41 / 3.89	32.46 / 16.26	13.47 / 4.18	BnaA09g26570D	CABBP1	752	TGAACAAAGAATCCAAACATA ||||||||||||||||||| CCGAACTTGTTTCTTAGGTTTGTATCTCTTGT	TT3	0.00	0.00	0.00	0.09	325731	-0.25	212798	0.26
TAAGATGCTCTGAGCGTGGACC	+ / -	Chloro	11.46 / 23.65	136.08 / 68.26	11.87 / 2.89	26.68 / 49.99	108.25 / 53.79	4.06 / 1.08	BnaC03g59520D	CABBP1	578	TAAGATGCTCTGAGCGTGGACC o|||||||||||||||o||| ATCGGTTCTACGAGACTCGCACTTGGTTCGAT	TT3	0.00	0.00	0.00	0.79	417531	0.02	305188	0.73

TGAACAAAGAATCCAAACATA	+ / -	Chloro	2.66 / 2.69	23.48 / 12.21	8.82 / 4.53	2.41 / 3.89	32.46 / 16.26	13.47 / 4.18	BnaA05g09410D	CABBP1	683	TGAACAAAGAATCCAAACATA CCGGACATGTTTCTTAGGTTTGTACCTCTTGT	TT3	0.00	0.00	0.00	1.80	185278	-0.12	131779	1.16
CTAGGGCTCCGAGCATGGCCC	+ / -	Chloro	1.41 / 2.61	54.60 / 27.16	38.76 / 10.42	3.91 / 7.18	41.28 / 20.50	10.55 / 2.85	BnaA05g09410D	CABBP1	322	CTAGGGCTCCGAGCATGGCCC GTCGGATCCCGAGGTTCGTACCGGGTAGACGT	TT3	0.00	0.00	0.00	0.23	185278	-0.12	131779	1.16
TCTCGGGATCGGCTGAGAGACC	+ / -	Chloro	1.68 / 3.55	33.98 / 16.27	20.21 / 4.58	0.00 / 0.00	49.84 / 24.58	49.84 / 24.58	BnaC03g59520D	CABBP1	372	TCTCGGGATCGGCTGAGAGACC TTGCAGAGCCCTAGCCGACTCTCTGGACGCCA	TT3	0.00	0.00	0.00	0.60	417531	0.02	305188	0.73
CTGAAGATCTGTGAACCAGCCT	+	Chloro	1.67 / -	25.03 / -	14.99 / -	0.00 / -	50.89 / -	50.89 / -	BnaC04g10780D	CABBP1	407	CTGAAGATCTGTGAACCAGCCT AAGCGACTTCTAGACGCTTGGCCGGAACTTGG	TT3	0.00	0.00	0.00	6.16	524035	-0.12	299557	0.39
ATGAGGATCACCTGAGTAGCC	+ / -	Chloro	1.68 / 3.55	47.44 / 23.32	28.22 / 6.56	3.91 / 7.18	42.09 / 20.89	10.76 / 2.91	BnaC03g59520D	CABBP1	607	ATGAGGATCACCTGAGTAGCC AGGGTAGTTCTAGTGAACTCATCGGGTTTATC	TT3	0.00	0.00	0.00	0.51	417531	0.02	305188	0.73
CGTGGACCAAGCTCGGGTTGCC	+ / -	Chloro	0.00 / 0.00	35.21 / 16.65	35.21 / 16.65	0.00 / 0.00	50.90 / 25.11	50.90 / 25.11	BnaA05g09410D	CABBP1	451	CGTGGACCAAGCTCGGGTTGCC ACTCGCACCTGGTTCGAGCCCAACGGGTTCAT	TT3	0.00	0.00	0.00	0.83	185278	-0.12	131779	1.16
CTAGGGCTCCGAGCATGGCCC	+ / -	Chloro	1.41 / 2.61	54.60 / 27.16	38.76 / 10.42	3.91 / 7.18	41.28 / 20.50	10.55 / 2.85	BnaC03g59520D	CABBP1	435	CTAGGGCTCCGAGCATGGCCC GTCGGATCCCGAGGCTCGTACCGGGTGGACGT	TT3	0.00	0.00	0.00	0.05	417531	0.02	305188	0.73
AATGGCTAAGATGCTCTGAGC	+ / -	Chloro	1.68 / 3.55	34.77 / 17.93	20.68 / 5.04	0.00 / 0.00	35.24 / 17.51	35.24 / 17.51	BnaC03g59520D	CABBP1	584	AATGGCTAAGATGCTCTGAGC GGGTTTATCGGTTCTACGAGACTCGCACTTGG	TT3	0.00	0.00	0.00	3.15	417531	0.02	305188	0.73

[1] sRNA seq / DESeq2 data

[2] PAREseq / PAREsnip data

[3] RNAseq / DESeq2 data

[4] 'Chloro' stands for genes predicted to encode "Chlorophyll a-b binding protein 1" (BnaC03g59520D, BnaC04g10780D, BnaA09g26570D, BnaA05g09410D, BnaA07g07570D)

CABBP1 = Chlorophyll a-b binding protein 1, chloroplastic

Table S26: va-phasiRNAs produced from genes for 'NBR1 homolog' and targeting mRNAs within the gene family as well as mRNAs of other genes for cleavage

va-phasiRNA[1]									Host mRNA targets[2]									DE target mRNA[3]				
va-phasiRNA	dsRNA (+) / (-) strand va-phasiRNA	Origin (gene family)	Normalized reads (positive / negative)						Target transcript ID	Predicted gene function	Cleavage position	vsiRNA:mRNA target pair (5'-3' : 3'-5')	Cleavage found in PAREseq replicates	Fragment signatures (rpm)				mRNA reads & FC(log2)				
			DM	DT	DT/DM reads	TM	TT	TT/TM reads						DM	DT	TM	TT	DM	DT	TM	TT	
TCACGTCAAGCTCACTGTTGA	-	NBR1[4]	0.00	42.37	42.37	0.00	55.12	55.12	BnaA10g12850D	Actin-depolymerizing factor 3	828	TCACGTCAAGCTCACTGTTGA CTTAAG-GCAGTTCGAGAGAGAACTTGGACAG	DT2 DT3 TT2 TT3	0.00	9.15	0.00	30.42	19836	-0.82	11518	-0.67	
ACTAATCGAGGATTTGGAATC	-	NBR1	0.90	19.36	21.57	1.42	25.26	17.75	BnaA07g28860D	NAD(P)H-quinone oxidoreductase subunit I, chloroplastic	960	ACTAATCGAGGATTTGGAATC ACACTGATTA-CTCCTATATGTCAGTGTTGAC	DT1 TT1	0.00	0.37	0.00	0.21	4231	-1.42	6245	-0.45	
AGAGAGCGTCAACAGACTGCT	-	NBR1	0.00	29.47	29.47	0.00	25.53	25.53	BnaA01g14050D	NBR1 homolog	2865	AGAGAGCGTCAACAGACTGCT GGTGTCTCTCGCAGTTGTCTGACGAGGTTCAA	DT2 TT3	0.00	3.20	0.00	1.25	2959	5.97	279	7.49	
CTGCTCCAAGTTGTACTCGTT	-	NBR1	0.00	23.69	23.69	0.00	19.11	19.11	BnaA03g46880D	NBR1 homolog	2701	CTGCTCCAAGTTGTACTCGTT GTCTGACGAGGTTCAACATGAGCAACAGGGAG	DT3 TT3	0.00	3.54	0.00	0.79	2740	0.77	4843	0.45	
CTGCTCCAAGTTGTACTCGTT	-	NBR1	0.00	23.69	23.69	0.00	19.11	19.11	BnaC07g39070D	NBR1 homolog	3667	CTGCTCCAAGTTGTACTCGTT GTCTGACGAGGTTCAACATGAGTAAAAGGAAG	DT3 TT3	0.00	3.54	0.00	0.79	2241	1.36	5953	1.44	
TTCACGTCAAGCTCACTGTTGA	-	NBR1	0.00	26.27	26.27	0.00	49.38	49.38	BnaC09g35260D	Actin-depolymerizing factor 3	8174	TTCACGTCAAGCTCACTGTTGA ACTTAAG-GTAGTTCGAGAGAGAACTTGGACA	DT3 TT3	0.00	0.64	0.00	0.28	31652	-0.66	22464	-0.59	
TTCACGTCAAGCTCACTGTTGA	-	NBR1	0.00	26.27	26.27	0.00	49.38	49.38	BnaA10g12850D	Actin-depolymerizing factor 3	829	TTCACGTCAAGCTCACTGTTGA ACTTAAG-GCAGTTCGAGAGAGAACTTGGACA	DT3 TT3	0.00	1.36	0.00	0.65	19836	-0.82	11518	-0.67	
AGAATCCATCGTTCACGGATT	-	NBR1	0.00	35.91	35.91	6.14	87.55	14.26	BnaA02g27010D	Probable ribose-5-phosphate isomerase 2	979	AGAATC-CATCGTTCACGGATT GAGTCTTAGCGTAGCGAGTGCCGGGGGTTTAG	DT3 TT3	0.00	0.64	0.00	0.09	8358	-0.70	5388	-1.06	
TCAGGCATAACCGAGGCGGATG	-	NBR1	0.00	16.33	16.33	1.23	27.60	22.37	BnaC08g19950D	disulfide isomerase-like 1-1	1799	TCAGGCATAACCGAGGCGGATG CAAGAGT-CGTAGTGGCTCTTCCTTCGATTCT	DT1	0.00	0.04	0.00	0.00	628	0.98	958	0.59	
AAGAGATTGATCTGAACAAGGA	+	NBR1	2.20	138.96	63.08	1.41	165.40	116.99	BnaC06g27630D	Heme oxygenase 1, chloroplastic	1402	AAGAGATTGATCTGAACAAGGA TTTATTCTCAAACTATGTTTGTTCGTCTTCGC	DT2	0.00	7.82	0.00	0.00	2525	0.05	5615	-0.13	
AAGAGATTGATCTGAACAAGG	+	NBR1	0.26	250.83	961.57	0.80	287.10	360.05	BnaC07g16850D	Heme oxygenase 1, chloroplastic	1402	AAGAGATTGATCTGAACAAGG TTTATTCTCAAACTATGTTTGTTCGTCTTCGC	DT2	0.00	7.82	0.00	0.00	2525	0.05	5615	-0.13	
GTCAATGTACTTGATGGAACC	+	NBR1	0.00	58.25	58.25	0.00	59.62	59.62	BnaC07g25880D	COBRA-like protein 2	1691	GTCAATGTACT-TGATGGAACC TGTACGGTTACTTGAGACTACCCTGTGTATAC	DT2	0.00	0.27	0.00	0.00	3541	-0.07	2677	-1.26	
CAGAGAGCGTCAACAGACTGC	-	NBR1	0.00	48.37	48.37	1.42	52.41	36.84	BnaA04g14370D	unknown	3327	CAGAGAGCGTCAACAGACTGC ACGTGTCTCTCGAAGTTGTTTTGTTTTTTTTG	DT2	0.00	3.20	0.00	0.00	81	0.30	174	0.71	
AACAGGTCATCTTTCATCGGA	-	NBR1	0.00	48.42	48.42	0.00	53.63	53.63	BnaC02g20670D	Tubulin-folding cofactor E	259	AACAGGTCATCTTTCATCGGA GGTGTTGTCTAGTAGAAA-TAACTAAGACTAT	DT2	0.00	3.29	0.00	0.00	0	-0.15	0	0.20	
TTTAGACTTGAATCTAGGCCC	-	NBR1	0.85	65.13	76.27	1.23	91.94	74.52	BnaA06g15370D	unknown	949	TTTAGACTTGAATCTAGGCCC CGGAAAATCTAAACCT-GAGTCGGGACGGCTC	DT2	0.00	1.69	0.00	0.00	205	-0.70	130	-0.18	
CCACAGAGAGCGTCAACAGAC	-	NBR1	0.00	58.95	58.95	0.00	40.73	40.73	BnaC08g19430D	High mobility group B protein 3	493	CCACAGAGAGCGTCAACAGAC AACCGGTGTCTCTCGGATTAGT-TGTTTGCAT	DT2	0.00	2.84	0.00	0.00	23448	0.16	33959	0.61	
TGAGGGACAACGAGTACAACT	+	NBR1	1.77	108.08	60.91	0.80	100.16	125.61	BnaC07g33200D	60S ribosome subunit biogenesis protein NIP7 homolog	509	TGAGGGACAACGAGTACAACT GACTACTTCGTGTTGCT-ATGGTAAGCCTAGG	DT2	0.00	3.11	0.00	0.00	81	-0.16	101	0.21	
AAGAGATTGATCTGAACAAGGA	+	NBR1	2.20	138.96	63.08	1.41	165.40	116.99	BnaC07g16850D	Heme oxygenase 1, chloroplastic	1402	AAGAGATTGATCTGAACAAGGA TTTATTCTCAAACTATGTTTGTTCGTCTTCGC	DT2	0.00	7.82	0.00	0.00	2525	0.05	5615	-0.13	
CCAATAAGATATGTATCGGCC	-	NBR1	0.00	34.13	34.13	0.00	40.65	40.65	BnaA09g29590D	unknown	1760	CCAATAAGATATGTATCGGCC CGTAGGCTATTTTATATATA-CCGTTGTGTGT	DT2	0.00	1.24	0.00	0.00	276	-2.06	17878	-1.44	
TCTGGTTCAACATCAGCACCT	-	NBR1	0.00	18.07	18.07	0.00	19.29	19.29	BnaC09g31710D	unknown	423	TCTGGTTCAACATCAGCACCT GAGAAGGCGAAGTTGGAGTCTTGGGAATCGTG	DT2	0.00	3.47	0.00	0.00	684	-0.26	672	-0.84	
GTCAATGTACTTGATGGAACC	+	NBR1	0.00	58.25	58.25	0.00	59.62	59.62	BnaC03g16870D	COBRA-like protein 2	243	GTCAATGTACT-TGATGGAACC TGTACGGTTACTTGAGACTACCCTGTGTATAC	DT2	0.00	0.27	0.00	0.00	2	0.45	4	0.26	
AGGGACAACGAGTACAACTTG	+	NBR1	0.00	56.57	56.57	0.00	48.26	48.26	BnaA09g39460D	Uncharacterized membrane protein YuiD	171	AGGGACAACGAGT-ACAACTTG TCTCTCTCTTTTTCTCAATGTTCAACTCACAC	DT2	0.00	3.02	0.00	0.00	861	-0.85	473	0.29	
AAGAGATTGATCTGAACAAGG	+	NBR1	0.26	250.83	961.57	0.80	287.10	360.05	BnaC06g27630D	Heme oxygenase 1, chloroplastic	1402	AAGAGATTGATCTGAACAAGG TTTATTCTCAAACTATGTTTGTTCGTCTTCGC	DT3	0.00	0.73	0.00	0.00	2525	0.05	5615	-0.13	
AAGAAGAACAATGGAAGCATT	+	NBR1	0.00	252.60	252.60	0.00	250.67	250.67	BnaA02g06380D	Exonuclease V, chloroplastic	2591	AAGAAGAACAATGGAAGCATT TCCGTTCTTCTTGTTGACTTTGCGAGACCTAG	DT3	0.00	0.64	0.00	0.00	76	-0.16	542	0.37	
ACGAGTTTCATGGACTGAACT	+	NBR1	0.00	110.77	110.77	0.00	185.32	185.32	BnaA05g24200D	unknown	699	ACGAGTTTCATGGACTGAACT TCTATACTCGAGGTATCT-ACTTGAGTGTAGT	DT3	0.00	0.50	0.00	0.00	116435	-0.83	116567	-0.30	
TTCACGTCAAGCTCACTGTTGA	-	NBR1	0.00	26.27	26.27	0.00	49.38	49.38	BnaC03g68570D	Protease 2	3630	TTCA-CGTCAAGCTCACTGTTGA TACAGGTCGCGGTTCGAGTGTAAACTTGTTTT	DT3	0.00	0.36	0.00	0.00	3	0.80	4	0.86	
TTCACGTCAAGCTCACTGTTGA	-	NBR1	0.00	26.27	26.27	0.00	49.38	49.38	BnaC06g03570D	Protease 2	3743	TTCA-CGTCAAGCTCACTGTTGA TACAGGTCGCGGTTCGAGTGTAAACTTGTTTT	DT3	0.00	0.36	0.00	0.00	1215	0.93	1754	0.17	

GGCATAACCGAGGCGGATGAA	-	NBR1	0.00	21.46	21.46	0.00	35.26	35.26	BnaA07g32110D	unknown	134	GGCATAACCGAGGCGGATGAA CTGCCGGCATTGGCTCTGC-TGTTTCTACTTA	DT3	0.00	1.63	0.00	0.00	133	-1.85	118	-0.73
TTAGCTTTGAAAGGCACCCTGA	-	NBR1	4.45	23.84	5.35	6.18	50.49	8.17	BnaA03g01940D	Trichome birefringence-like 9	5529	TTAGCTTTGAAAGGCACC-CTGA ACGAAACCGAGACTTTCTGCGGAGATTTTTAA	DT3	0.00	0.82	0.00	0.00	1124	0.06	2295	-0.22
AAGAGATTGATCTGAACAAGG	+	NBR1	0.26	250.83	961.57	0.80	287.10	360.05	BnaA09g04340D	ALFIN-LIKE 4	1679	AAGAGAT-TGATCTGAACAAGG TGGTTGTTTAGACTAGATTGGTTTCTCATTCC	DT3	0.00	0.05	0.00	0.00	2354	0.07	2274	-0.13
GACGAGTGCAGTAGTAGAATC	-	NBR1	4.41	29.70	6.74	2.47	46.93	19.02	BnaA02g34140D	Classical arabinogalactan protein 1	307	GACGAGTGCAGTAGTAGAATC TCGGCTGCTTA-GTCTTCCTCTTAGTCGATTT	DT3	0.00	0.82	0.00	0.00	393	-0.10	114	1.21
GAAGAATGACGTCGAGATAAC	+	NBR1	0.00	91.46	91.46	0.00	80.70	80.70	BnaC03g05120D	unknown	677	GAAGAATGACGTCGAGATAAC GCGGCTTCAT-CTGCAGCGCTAGTGCGAGGAT	DT3	0.00	0.09	0.00	0.00	392	0.45	493	0.62
GTACACCTGAAATGTAAACCT	-	NBR1	0.90	14.22	15.85	0.00	13.94	13.94	BnaC02g35340D	unknown	512	GTACACCTGAAATGTAAACCT GGCTCAT-TGGACTTTATGTATGTGTGGTGCC	DT3	0.00	1.04	0.00	0.00	109	-0.62	78	-0.58
TAACCGAGGCGGATGAACTCC	-	NBR1	0.90	25.63	28.55	3.48	65.72	18.88	BnaC05g17820D	NRT1/ PTR FAMILY 5.10	1153	TAACCGAGGCGGATGAACTCC CGATGTTGGCTTCGACTATTAGAGGTCAAGAA	DT3	0.00	0.86	0.00	0.00	1729	-0.06	1192	-0.35
TAACCGAGGCGGATGAACTCCC	-	NBR1	0.00	31.47	31.47	0.00	82.52	82.52	BnaC05g17820D	NRT1/ PTR FAMILY 5.10	1153	TAACCGAGGCGGATGAACTCCC CGATGTTGGCTTCGACTATTAGAGGTCAAGAA	DT3	0.00	0.86	0.00	0.00	1729	-0.06	1192	-0.35
CGACGAGTGCAGTAGTAGAATC	-	NBR1	4.36	57.24	13.14	4.90	153.24	31.25	BnaA02g34140D	Classical arabinogalactan protein 1	308	CGACGAGTGCAGTAGTAGAATC GTCGGCTGCTTA-GTCTTCCTCTTAGTCGATT	DT3	0.00	0.09	0.00	0.00	393	-0.10	114	1.21
TCCATTAGCTTTGAAAGGCACC	-	NBR1	3.55	29.98	8.44	5.69	59.03	10.37	BnaA06g15400D	TolB	1628	TCCATTAGCTTTGAAAGGC-ACC TGGAAGGCAATTGAAGGTTTCTGGTGGCCAGA	DT3	0.00	0.45	0.00	0.00	16652	0.59	19929	1.17
TGATCTGACGAACAAGAGGCT	+	NBR1	0.26	72.59	278.29	0.71	56.83	80.40	BnaC03g04590D	Histone H3.3	523	TGATCTGACGAACAAGAGGCT ACTCGTTAGAGTGCTTGTTCTGCGACCTTGCC	DT3	0.00	0.05	0.00	0.00	1764	0.21	1874	0.88
TTAGCTTTGAAAGGCACCCTGA	-	NBR1	4.45	23.84	5.35	6.18	50.49	8.17	BnaCnng46650D	unknown	302	TTAGCTTTGAAAGGCACCCTGA GCCCAACCGAAGCTTTCCACGGGA-TCCTTAT	DT3	0.00	0.09	0.00	0.00	30330	-0.52	7478	-0.52
AACGAGTTTCATGGACTGAAC	+	NBR1	0.00	81.35	81.35	0.00	77.95	77.95	BnaA06g05780D	Cysteine proteinase RD21a	1653	AACGAGTTTCATGGACTGAAC GTCGTTGTTCAGAGTAGTCGACTTGTTATCCA	DT3	0.00	1.41	0.00	0.00	315	0.81	439	0.67
ATTGGCTTTGAAAGGCACCCT	-	NBR1	0.85	32.30	37.83	5.50	47.72	8.67	BnaCnng46650D	unknown	303	ATTGGCTTTGAAAGGCACCCT AGCCCAACCGAAGCTTTCCACGGGATCCTTAT	DT3	0.00	5.04	0.00	0.00	30330	-0.52	7478	-0.52
AAGAGATTGATCTGAACAAGGA	+	NBR1	2.20	138.96	63.08	1.41	165.40	116.99	BnaA09g04340D	ALFIN-LIKE 4	1679	AAGAGAT-TGATCTGAACAAGGA TGGTTGTTTAGACTAGATTGGTTTCTCATTCC	DT3	0.00	0.05	0.00	0.00	2354	0.07	2274	-0.13
ATTAGCTTTGAAAGGCACCCT	-	NBR1	0.00	29.35	29.35	6.77	43.56	6.43	BnaA10g09070D	Thioredoxin Y2, chloroplastic	522	ATTAGCTTTGAAAGGCACCCT CAACCAATCG-AACGTTCCGAGGGAGGACGGT	DT3	0.00	0.68	0.00	0.00	1255	-0.73	959	-0.10
CATGGCACGCAGATCGTTTGGA	+	NBR1	0.00	52.42	52.42	0.00	127.05	127.05	BnaA09g02120D	Chlorophyll a-b binding protein 36, chloroplastic	998	CATGGCACGCAGATCGTT-TGGA TCTTGTACCGTTCGGCTGGCAAGAACTCGAGG	DT3	0.00	0.82	0.00	0.00	281901	-0.39	186238	-0.53
AAGAAGAACAATGGAAGCATT	+	NBR1	0.00	252.60	252.60	0.00	250.67	250.67	BnaC08g47950D	unknown	526	AAGAAGAACAATGGAAGCATT TCCGTTCTTCTTGTTGACTTCGCGAGACCCAC	DT3	0.00	0.64	0.00	0.00	8	0.12	4	0.38
TTAGCTTTGAAAGGCACCCTGA	-	NBR1	4.45	23.84	5.35	6.18	50.49	8.17	BnaC03g02490D	unknown	3359	TTAGCTTTGAAAGGCACC-CTGA ACGAAACCGAGACTTTCTGCGGAGATTTTTAA	DT3	0.00	0.82	0.00	0.00	1147	-0.04	2399	-0.48
ATGGACTGAACTTGAATGCCT	+	NBR1	0.00	131.39	131.39	2.32	121.20	52.27	BnaA09g16230D	Thioredoxin H5	791	ATGGACTGAAC-TTGAATGCCT GCCGTACCGGACTTGTAGCTTGAGGAAACGTT	DT3	0.00	2.63	0.00	0.00	74599	-0.30	61037	-0.34
TCCACAGAGAGCGTCAACAGA	-	NBR1	0.85	71.95	84.25	0.00	68.09	68.09	BnaA09g42630D	ATHB-6	1373	TCCACAGAGAGCGTCAACAGA GCTTAGGTGTCTTTTTTA-TTGTCTCGTAAAA	DT3	0.00	0.54	0.00	0.00	36527	0.09	27823	0.23
ATTAGCTTTGAAAGGCACCCT	-	NBR1	0.00	29.35	29.35	6.77	43.56	6.43	BnaCnng46650D	unknown	303	ATTAGCTTTGAAAGGCACCCT AGCCCAACCGAAGCTTTCCACGGGATCCTTAT	DT3	0.00	5.04	0.00	0.00	30330	-0.52	7478	-0.52
AAGGGATGTAGCTGTTGAGCT	-	NBR1	0.00	34.19	34.19	0.00	47.26	47.26	BnaA01g14050D	NBR1 homolog	1538	AAGGGATGTAGCTGTTGAGCT AGACTTCCCTACATCGACAACTCGACTCTGCC	DT3	0.00	0.23	0.00	0.00	2959	5.97	279	7.49
GTACATTGACATCAAGGACAA	-	NBR1	0.00	31.92	31.92	0.00	35.29	35.29	BnaC09g21010D	ALFIN-LIKE 6	2494	GTACATTGACATCAAGGACAA TCATCACGTAACTGTAATTGTTGTTGTTGTTT	DT3	0.00	0.05	0.00	0.00	3112	-0.19	3311	0.07
CTACTACTGTTGAGGCCTTGG	+	NBR1	0.00	61.33	61.33	0.71	68.36	96.71	BnaC01g40190D	Probable UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase SEC	5660	CTACTACTGTTGAGGCCTTGG AAAAGGTGATGA-AACTTCACAACTCCGAAGA	DT3	0.00	0.05	0.00	0.00	1771	0.70	5582	0.03
AACGAGTTTCATGGACTGAACT	+	NBR1	0.26	63.53	243.54	0.71	138.84	196.41	BnaA06g05780D	Cysteine proteinase RD21a	1653	AACGAGTTTCATGGACTGAACT GTCGTTGTTCAGAGTAGTCGACTTGTTATCCA	DT3	0.00	1.41	0.00	0.00	315	0.81	439	0.67
ACGAAGACGAAGATGAAGATG	-	NBR1	0.85	5.36	6.28	0.00	19.56	19.56	BnaAnng36210D	Ribulose bisphosphate carboxylase small chain F1, chloroplastic	1064	ACGAAGACGAAGATGAAGATG TCATTGGTTCTGCTTCTTCGT-TATATCTCTA	TT1	0.00	0.00	0.00	0.09	439500	-1.05	249908	-0.85
GAGAACTCAGCATCCAGAGGG	-	NBR1	0.00	16.09	16.09	2.47	37.77	15.31	BnaA04g19440D	Heterogeneous nuclear ribonucleoprotein 1	1421	GAGAACTCAGCATCCAGAGGG TTCATGC-TGAGTCGTAGTTCTCACGGACTTG	TT2	0.00	0.00	0.00	25.45	353	-0.10	624	0.29
ATTGGCTTTGAAAGGCACCCT	-	NBR1	0.85	32.30	37.83	5.50	47.72	8.67	BnaC03g02490D	unknown	3360	ATTGGCTTTGAAAGGCACCCT GACGAAACCGAGACTTTCTGCGG-AGATTTTT	TT2	0.00	0.00	0.00	17.62	1147	-0.04	2399	-0.48
CCTGAGGACTTGAGAGCTTCC	-	NBR1	0.00	25.99	25.99	0.00	39.81	39.81	BnaC08g30150D	F-box/kelch-repeat protein SKIP20	43	CCTGAGGACT-TGAGAGCTTCC TTTAGGGCTGCTGAGACTTTCGGAGGACAATG	TT2	0.00	0.00	0.00	14.88	26454	-0.07	26280	0.19
ACAACGAGTACAACTTGGAGC	+	NBR1	0.00	63.11	63.11	0.81	54.52	66.93	BnaA06g38980D	Nitrilase 2	1537	ACAACG-AGTACAACTTGGAGC TGGTGTAGCTTCATATTGAACCGTGCACGCTA	TT2	0.00	0.00	0.00	22.18	25815	0.19	27259	-0.32
ATTGGCTTTGAAAGGCACCCT	-	NBR1	0.85	32.30	37.83	5.50	47.72	8.67	BnaA03g01940D	Trichome birefringence-like 9	5530	ATTGGCTTTGAAAGGCACCCT GACGAAACCGAGACTTTCTGCGG-AGATTTTT	TT2	0.00	0.00	0.00	17.62	1124	0.06	2295	-0.22
GAGAACTCAGCATCCAGAGGG	-	NBR1	0.00	16.09	16.09	2.47	37.77	15.31	BnaC04g43830D	Heterogeneous nuclear ribonucleoprotein 1	1513	GAGAACTCAGCATCCAGAGGG TTCATGC-TGAGTCGTAGTTCTCACGGACTTG	TT2	0.00	0.00	0.00	25.45	1323	-0.02	1141	0.02
ATTGGCTTTGAAAGGCACCCT	-	NBR1	0.85	32.30	37.83	5.50	47.72	8.67	BnaA10g30500D	unknown	2858	ATTGGCTTTGAAAGGCACCCT GACGAAACCGAGACTTTCTGCGG-AGGTTTTT	TT2	0.00	0.00	0.00	17.62	17	0.83	6	0.57
ATACATATCTTATTGGAGGATG	+	NBR1	1.68	123.57	73.50	0.71	139.20	196.92	BnaA09g06820D	Beta-ureidopropionase	923	ATACATATCTTATTGGAGGATG GCACTAGGTATAGAGAAAGCTCCTATCCTAAG	TT3	0.00	0.00	0.00	0.09	166	0.24	275	0.49

GTAGAATCCATCGTTCACGGAT	-	NBR1	0.00	38.86	38.86	0.00	94.43	94.43	BnaA08g28040D	3-ketoacyl-CoA thiolase 1, peroxisomal	1613	GTAGAAT-CCATCGTTCACGGAT ||||| |||||||o||o|| ATCCAGCTTAGGGTAGCAGGTGTCTTTGACAA	TT3	0.00	0.00	0.00	0.05	482	0.12	654	0.38
TTGGCTTTGAAAGGCACCCTGA	-	NBR1	2.61	19.48	7.48	10.66	37.65	3.53	BnaCnng46650D	unknown	302	TTGGCTTTGAAAGGCACCCTGA ||||||o||||| ||||| GCCCAACCGAAGCTTTCCACGGGA-TCCTTAT	TT3	0.00	0.00	0.00	0.14	30330	-0.52	7478	-0.52
CAGAGAGCGTCAACAGACTGCT	-	NBR1	0.00	17.54	17.54	0.00	24.02	24.02	BnaC07g39070D	NBR1 homolog	3684	CAGAGAGCGTCAACAGACTGCT ||o|||| ||||||||||| AGGTGTTTCTCGGAGTTGTCTGACGAGGTTCA	TT3	0.00	0.00	0.00	0.05	2241	1.36	5953	1.44
ACGAGTGCAGTAGTAGAATCC	-	NBR1	2.61	45.10	17.31	4.12	73.73	17.91	BnaC08g14680D	unknown	1152	ACGAGTGCAGTAGTAGAATCC ||| |||||||||o TAACGGCT-ACGTCATCATCTTGCCCTACCCT	TT3	0.00	0.00	0.00	0.23	282	-0.32	311	0.34
CTGTCCATTAGCTTTGAAAGGC	-	NBR1	0.00	4.85	4.85	0.00	22.20	22.20	BnaA05g33370D	Probable protein phosphatase 2C 33	2361	CTGTCCATTAGCTTTGAAAGGC |||||||o|||||||| GAGAGACAGGT-ATTGAAACTTTCGGAATTCT	TT3	0.00	0.00	0.00	0.05	5394	0.00	3387	0.21
TCTGGTTCAACATCAGCACCT	-	NBR1	0.00	18.07	18.07	0.00	19.29	19.29	BnaC01g16550D	NBR1 homolog	2645	TCTGGTTCAACATCAGCACCT ||||||||||||||||||| TCGAAGACCAAGTTGTAGTCGTGGAAAGTGAT	TT3	0.00	0.00	0.00	0.19	7201	1.42	15409	0.96
CACCAACGTTCGACTGCACAGT	-	NBR1	0.00	13.61	13.61	0.00	39.88	39.88	BnaC03g32940D	S-adenosylmethionine decarboxylase proenzyme 3	880	CACCAACGTTCGACTGCACAGT ||||||o|||| ||||||o AAGCGAGGTTGCGAGCTCACGTGTCGGTGTCT	TT3	0.00	0.00	0.00	0.60	60577	-0.22	56260	-0.16
CAGAGAGCGTCAACAGACTGC	-	NBR1	0.00	48.37	48.37	1.42	52.41	36.84	BnaC07g39070D	NBR1 homolog	3684	CAGAGAGCGTCAACAGACTGC ||o|||| ||||||||||| AGGTGTTTCTCGGAGTTGTCTGACGAGGTTCA	TT3	0.00	0.00	0.00	0.05	2241	1.36	5953	1.44
TTAGGAACAACAGGCTCAACT	-	NBR1	0.00	47.07	47.07	4.12	53.62	13.02	BnaA03g46880D	NBR1 homolog	2454	TTAGGAACAACAGGCTCAACT ||||||||||||||||||| TCACAATCCTTGTTGTCCGAGTTGCAGTGGTT	TT3	0.00	0.00	0.00	0.05	2740	0.77	4843	0.45
TCCAATAAGATATGTATCGGCC	-	NBR1	0.00	22.43	22.43	0.00	43.37	43.37	BnaC07g39070D	NBR1 homolog	3028	TCCAATAAGATATGTATCGGCC |||||||||| |||||||o|| TAGTAGGTTATTCTTTACATAGCTGGTCCATT	TT3	0.00	0.00	0.00	0.09	2241	1.36	5953	1.44
AGGACAAAGCGACTGTCTAGCT	-	NBR1	0.00	12.37	12.37	0.00	22.87	22.87	BnaC08g11760D	NBR1 homolog	1744	AGGACAAAGCGACTGTCTAGCT || |||||||| |||| |||| TAGTTCGTGTTTCGCCGACAGTTCGAATCCGG	TT3	0.00	0.00	0.00	0.32	1275	1.12	1941	0.66
TTGATGCATCCTTGAAGGGCT	+	NBR1	0.00	24.58	24.58	0.00	39.09	39.09	BnaA01g17500D	DOWNY MILDEW RESISTANCE 6	833	TTGATGCATCCTTGAAGGGCT ||||| ||||||| |oo||| CGGTAACTA-GTAGGAACATTTCGACTTCTGG	TT3	0.00	0.00	0.00	0.19	883	0.90	1333	1.24
TCCACAGAGAGCGTCAACAGAC	-	NBR1	0.00	26.80	26.80	0.00	44.02	44.02	BnaA03g46880D	NBR1 homolog	2722	TCCACAGAGAGCGTCAACAGAC |||||o|||||||||||| ATTGAGGTGTTTCTCGGAGTTGTCTGACGAGG	TT3	0.00	0.00	0.00	0.09	2740	0.77	4843	0.45
TGCAGATGAGGAACCGCCACC	-	NBR1	0.00	38.92	38.92	0.00	36.10	36.10	BnaA01g04130D	unknown	9400	TGCAGATGAGGAACCGCCACC |||||||| |||o| || GACCACGTCTACACCTCGGTGTTGATAGGGGT	TT3	0.00	0.00	0.00	0.69	162	0.10	368	0.12
CTGCTCCAAGTTGTACTCGTT	-	NBR1	0.00	23.69	23.69	0.00	19.11	19.11	BnaC07g36330D	Leucine-rich repeat receptor-like serine/threonine-protein kinase BAM3	2673	CTGCTCC-AAGTTGTACTCGTT ||o||||o||||| |o|o CATGATGAGGTTTCGACATGTGTAGCGAGAAG	TT3	0.00	0.00	0.00	0.37	131	-0.33	81	-0.34
CAGTAGTAGAATCCATCGTTCA	-	NBR1	0.00	10.80	10.80	0.00	22.35	22.35	BnaC04g33980D	WAT1-related protein At4g15540	1604	CAGTAGTAGAATCCATCGTTCA ||||| |||||||| |o||| TAGTGTCAT-ATCTTAGGTTTCGAGTTATAGT	TT3	0.00	0.00	0.00	0.37	3644	0.44	7641	1.19
TGCCCGTCGTGTATGTCACTC	+	NBR1	0.00	40.75	40.75	0.71	62.96	89.07	BnaA01g04910D	Aspartate aminotransferase, chloroplastic	2379	TGCCCGTCGTGTATGTCACTC || ||||o||| |o||||| GTGAACAGGCAGTACA-ATAGTGAGACGGTGC	TT3	0.00	0.00	0.00	0.28	672	0.41	1134	0.78
AGAGAGCGTCAACAGACTGCT	-	NBR1	0.00	29.47	29.47	0.00	25.53	25.53	BnaA03g46880D	NBR1 homolog	2717	AGAGAGCGTCAACAGACTGCT |o||||| ||||||||||| GGTGTTTCTCGGAGTTGTCTGACGAGGTTCAA	TT3	0.00	0.00	0.00	0.14	2740	0.77	4843	0.45
GTAGAATCCATCGTTCACGGAT	-	NBR1	0.00	38.86	38.86	0.00	94.43	94.43	BnaC08g00920D	3-ketoacyl-CoA thiolase 2, peroxisomal	1494	GTAGAAT-CCATCGTTCACGGAT ||||| |||||||o||o|| ATCCAGCTTAGGGTAGCAGGTGTCTTTGACAA	TT3	0.00	0.00	0.00	0.05	406	0.20	674	0.66
TCCACAGAGAGCGTCAACAGAC	-	NBR1	0.00	26.80	26.80	0.00	44.02	44.02	BnaC07g39070D	NBR1 homolog	3688	TCCACAGAGAGCGTCAACAGAC |||||o|||||||||||| ATTGAGGTGTTTCTCGGAGTTGTCTGACGAGG	TT3	0.00	0.00	0.00	0.09	2241	1.36	5953	1.44
TCACGTCAAGCTCACTGTTGA	-	NBR1	0.00	42.37	42.37	0.00	55.12	55.12	BnaA01g14050D	NBR1 homolog	2144	TCACGTCAAGCTCACTGTTGA ||||||||||||||||||| TGAAAGTGCAGTTCGAGTGACAACTATCCGTG	TT3	0.00	0.00	0.00	0.14	2959	5.97	279	7.49
TTAGGAACAACAGGCTCAACT	-	NBR1	0.00	47.07	47.07	4.12	53.62	13.02	BnaA01g14050D	NBR1 homolog	2590	TTAGGAACAACAGGCTCAACT ||||||||||||||||||| TCACAATCCTTGTTGTCCGAGTTGAAGTGGTT	TT3	0.00	0.00	0.00	0.09	2959	5.97	279	7.49
TCCACAGAGAGCGTCAACAGA	-	NBR1	0.85	71.95	84.25	0.00	68.09	68.09	BnaA03g46880D	NBR1 homolog	2722	TCCACAGAGAGCGTCAACAGA |||||o|||| |||||||| ATTGAGGTGTTTCTCGGAGTTGTCTGACGAGG	TT3	0.00	0.00	0.00	0.09	2740	0.77	4843	0.45
ACCACCGATCCAAACGATCTG	-	NBR1	0.90	24.93	27.77	4.08	40.98	10.05	BnaA05g35060D	Beta-glucosidase 33	2311	ACCACCGATCCAAACGATCTG || ||||||||||o||oo AGTCTCG-GGCTAGGTTTGTTAGGTTGGGCTA	TT3	0.00	0.00	0.00	0.14	67	0.19	56	-0.12
CATCGGAATGTTTGATCCCGA	-	NBR1	0.85	80.22	93.94	2.06	80.75	39.22	BnaA01g14050D	NBR1 homolog	2546	CATCGGAATGTTTGATCCCGA ||||||||||||||||||| GAAAGTAGCCTTACAAACTAGGGCTTCTTCGA	TT3	0.00	0.00	0.00	0.14	2959	5.97	279	7.49
AGGACAAAGCGACTGTCTAGCT	-	NBR1	0.00	12.37	12.37	0.00	22.87	22.87	BnaC07g39070D	NBR1 homolog	2576	AGGACAAAGCGACTGTCTAGCT ||||||||||||||| || TAGTTCGTGTTTCGCTGACAGCTCAAATCAGG	TT3	0.00	0.00	0.00	0.32	2241	1.36	5953	1.44
CAGAGAGCGTCAACAGACTGCT	-	NBR1	0.00	17.54	17.54	0.00	24.02	24.02	BnaA03g46880D	NBR1 homolog	2718	CAGAGAGCGTCAACAGACTGCT ||o|||| ||||||||||| AGGTGTTTCTCGGAGTTGTCTGACGAGGTTCA	TT3	0.00	0.00	0.00	0.05	2740	0.77	4843	0.45
CATCGGAATGTTTGATCCCGA	-	NBR1	0.85	80.22	93.94	2.06	80.75	39.22	BnaC01g16550D	NBR1 homolog	2673	CATCGGAATGTTTGATCCCGA ||||||||||||||||||| GAAAGTAGCCTTACAAACTAGGGCTTCTTCGA	TT3	0.00	0.00	0.00	0.14	7201	1.42	15409	0.96
AGGACTTGAGAGCTTCCCGAG	-	NBR1	0.00	34.60	34.60	2.06	61.12	29.69	BnaC07g47570D	Auxin-responsive protein SAUR23	26	AGGACTTGAGAGCTTCCCGAG ||o|||||o||||||| GACGTCTTGCACTCTTGAACGACTCGTATCTC	TT3	0.00	0.00	0.00	0.93	1127	0.63	454	-0.16
TTAGGAACAACAGGCTCAACT	-	NBR1	0.00	47.07	47.07	4.12	53.62	13.02	BnaC01g16550D	NBR1 homolog	2717	TTAGGAACAACAGGCTCAACT ||||||||||||||||||| TCACAATCCTTGTTGTCCGAGTTGAAGTGGTT	TT3	0.00	0.00	0.00	0.05	7201	1.42	15409	0.96
TTAGGAACAACAGGCTCAACT	-	NBR1	0.00	47.07	47.07	4.12	53.62	13.02	BnaC03g43120D	Auxin-responsive protein IAA2	733	TTAGGAACAACAGGC-TCAACT |||o| ||||o|| ||||| ACGCAATCTTCGTTGTTCGCAGTTGATGTTTC	TT3	0.00	0.00	0.00	0.05	2515	0.12	10032	-1.77
TAACACTGTTGTGCCTAACACT	+	NBR1	0.52	26.45	50.70	0.00	40.38	40.38	BnaC01g03280D	NLP2	3196	TAACACTGTTGTGCCTAACACT ||||| |||||| |o||||o AAGGATTGTCACAA-ACAGGTTGTGGTTTCCT	TT3	0.00	0.00	0.00	0.14	172	-0.32	302	0.20
TTGAGATTCGTTGGATTTGGA	-	NBR1	0.00	15.30	15.30	0.00	21.64	21.64	BnaA01g14050D	NBR1 homolog	1200	TTGAGATTCGTTGGATTTGGA ||||||||||||||||||| GGACAACTCTAAGCAACCTAAACCTAAACCTC	TT3	0.00	0.00	0.00	0.09	2959	5.97	279	7.49
TCCAATAAGATATGTATCGGCC	-	NBR1	0.00	22.43	22.43	0.00	43.37	43.37	BnaA01g14050D	NBR1 homolog	2195	TCCAATAAGATATGTATCGGCC ||||||||||||||||||| TAGGAGGTTATTCTATACATAGCCGGTCCACT	TT3	0.00	0.00	0.00	0.37	2959	5.97	279	7.49
CTGCTCCAAGTTGTACTCGTT	-	NBR1	0.00	23.69	23.69	0.00	19.11	19.11	BnaA01g14050D	NBR1 homolog	2849	CTGCTCCAAGTTGTACTCGTT ||||||||||||||||||| GTCTGACGAGGTTCAACATGAGCAACAGGGAG	TT3	0.00	0.00	0.00	0.05	2959	5.97	279	7.49

CCACTGCACTCGTCGTCAAGG	+	NBR1	1.68	21.06	12.53	0.80	55.42	69.51	BnaC05g04590D	Oxygen-evolving enhancer protein 2, chloroplastic	981	CCACTGCACTCGTCGTCAAGG CAACGGTGACGT-AACAACAGTTTCGGAGGGA	TT3	0.00	0.00	0.00	14.02	84174	-0.31	77609	-0.12
CATGGACTGAACTTGAATGCC	+	NBR1	0.00	179.80	179.80	0.81	192.60	236.42	BnaC07g43040D	CBL-interacting serine/threonine-protein kinase 6	1633	CATGGACTGAA-CTTGAATGCC CTTAGTGCTTGACTTAGAACTTAGGTTGTTAT	TT3	0.00	0.00	0.00	0.05	7528	-1.29	4024	-0.65
AGGCGGATGAACTCCCACTGCT	-	NBR1	0.00	8.19	8.19	0.00	23.24	23.24	BnaA09g56240D	Serine/arginine-rich splicing factor SR45	2851	AGGCGGATGAACTCCCACTGCT CTCCTCCGCC-ACTCGACGATGACGACGACAA	TT3	0.00	0.00	0.00	0.19	487	0.34	350	-0.32
TTAGGAACAACAGGCTCAACT	-	NBR1	0.00	47.07	47.07	4.12	53.62	13.02	BnaC07g39070D	NBR1 homolog	3429	TTAGGAACAACAGGCTCAACT TCACAATCCTTGTTGTCCGAGTTGCAGTGGTT	TT3	0.00	0.00	0.00	0.05	2241	1.36	5953	1.44
CTTTAGACTTGAATCTAGGCCC	-	NBR1	0.00	22.11	22.11	0.00	41.59	41.59	BnaA10g00700D	3-ketoacyl-CoA synthase 1	1480	CT-TTAGACTTGAATCTAGGCCC CGTGACAATGTGAACTTTGGTCTGGGTTTGCG	TT3	0.00	0.00	0.00	0.23	461	-2.01	2947	-1.43
ACAGCTTGATCTGGACATGGC	+	NBR1	1.77	42.41	23.90	2.34	99.09	42.41	BnaC09g45610D	CBS domain-containing protein CBSX3, mitochondrial	1733	ACAGCTTG-ATCTGGACATGGC TAGTGTCGAACGTAGAACTGGATTGTAGTCTA	TT3	0.00	0.00	0.00	0.09	19107	0.02	24881	0.61
TTTGAAAGGCACCCTGAAGCGC	-	NBR1	0.85	6.92	8.10	1.42	24.45	17.18	BnaC03g44440D	Probable E3 ubiquitin-protein ligase XERICO	299	TTTGAAAGGCACCCTGAAGCGC CTTAAAGCTGTCCGTGTGACTT-GTGAGCGAC	TT3	0.00	0.00	0.00	0.09	1	-0.85	10	0.44
TCCACAGAGAGCGTCAACAGA	-	NBR1	0.85	71.95	84.25	0.00	68.09	68.09	BnaC08g11760D	NBR1 homolog	2781	TCCACAGAGAGCGTCAACAGA ATTGAGGTGTTTCTCGTAGTTGTCTGACGAGG	TT3	0.00	0.00	0.00	0.09	1275	1.12	1941	0.66
AGAGAGCGTCAACAGACTGCT	-	NBR1	0.00	29.47	29.47	0.00	25.53	25.53	BnaC07g39070D	NBR1 homolog	3683	AGAGAGCGTCAACAGACTGCT GGTGTTTCTCGGAGTTGTCTGACGAGGTTCAA	TT3	0.00	0.00	0.00	0.14	2241	1.36	5953	1.44
ACAGCTTGATCTTGACATGGC	+	NBR1	1.67	19.47	11.66	0.00	38.63	38.63	BnaA10g21510D	CBS domain-containing protein CBSX3, mitochondrial	882	ACAGCTTG-ATCTTGACATGGC TAGTGTCGAACGTAGAACTGGATTGTAGTCTA	TT3	0.00	0.00	0.00	0.09	7046	0.26	27404	0.73
TGATGTTATGATGGCTGTGCC	+	NBR1	0.00	22.74	22.74	0.00	61.16	61.16	BnaA01g34100D	50S ribosomal protein L2, chloroplastic	736	TGATGTTATG-ATGGCTGTGCC TAAAGATATAATACATACCGGCACGGATTCCC	TT3	0.00	0.00	0.00	0.14	159	-0.95	233	-0.64
CCACAGAGAGCGTCAACAGAC	-	NBR1	0.00	58.95	58.95	0.00	40.73	40.73	BnaC01g16550D	NBR1 homolog	2993	CCACAGAGAGCGTCAACAGAC TTGAGGTGTCTCTCGCAGTTGTCTGACGAGGT	TT3	0.00	0.00	0.00	0.19	7201	1.42	15409	0.96
GTCCATTAGCTTTGAAAGGCAC	-	NBR1	0.00	6.27	6.27	0.00	11.96	11.96	BnaA10g13100D	L-type lectin-domain containing receptor kinase I.7	373	GTCCATTAGCTTTGAAAGGCAC CTTCGAGGTAACCGCAACTTTTCGGGCTTCTT	TT3	0.00	0.00	0.00	0.09	26	1.30	35	0.40
TTCACCAGCGGAAGGAACTTC	-	NBR1	0.00	22.83	22.83	0.00	35.89	35.89	BnaC09g44810D	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	1442	TTCACCAGCGGAAGGAACTTC AACAAGGTGGTCACGTTCTTT-AGGAACGCGG	TT3	0.00	0.00	0.00	6.43	2646	-0.57	3936	-0.03
AAGGATGTATCTAAGAAGACC	+	NBR1	0.00	35.76	35.76	0.00	55.46	55.46	BnaA01g29510D	Phosphoinositide phosphatase SAC2	4811	AAGGATGTATCTAAGAAGACC AGAGTTTCTATATAGGTTGTTCTAGATTCAAT	TT3	0.00	0.00	0.00	0.05	321	-0.70	824	-0.49
TAGAATCCATCGTTCACGGAT	-	NBR1	2.61	37.55	14.41	2.66	80.66	30.36	BnaCnng36390D	Ethylene-responsive transcription factor ERF106	851	TAGAATCCATCGTTCACGGAT TACAAT-TTACGTAGTAAGTGTCTAGTGAACT	TT3	0.00	0.00	0.00	0.14	5421	0.31	4671	-0.67
CTACTACTGTTGAGGCCTTGG	+	NBR1	0.00	61.33	61.33	0.71	68.36	96.71	BnaA04g26770D	Transcription factor bHLH70	901	CTACTACTGTTGAGGCCTTGG CGAGGAGGATGATAACTGCGGA-CCAGAGGGA	TT3	0.00	0.00	0.00	0.19	6	0.77	2	0.45
TACATATCTTATTGGAGGATG	+	NBR1	0.00	72.42	72.42	0.00	77.68	77.68	BnaC04g36680D	F-box/kelch-repeat protein At1g64840	1066	TACATATCTTATTGGAGGATG GGTGAGGTATA-AATATCTGCCTACAAGGTGA	TT3	0.00	0.00	0.00	0.14	0	NA	0	NA
TTAGGAACAACAGGCTCAACT	-	NBR1	0.00	47.07	47.07	4.12	53.62	13.02	BnaC01g13810D	Mitochondrial pyruvate carrier 4	1196	TTAGGAACAACAGGCTCAACT AAGAAACCGTTGTTGTCCGAGGTGAAGTCTAC	TT3	0.00	0.00	0.00	0.14	510	-0.31	627	0.25
CTTTAGACTTGAATCTAGGCCC	-	NBR1	0.00	22.11	22.11	0.00	41.59	41.59	BnaC05g00780D	3-ketoacyl-CoA synthase 1	913	CT-TTAGACTTGAATCTAGGCCC CGTGACAATGTGAACTTTGGTCTGGGTTTGCG	TT3	0.00	0.00	0.00	0.23	555	-1.39	1255	-1.31
TCCACAGAGAGCGTCAACAGA	-	NBR1	0.85	71.95	84.25	0.00	68.09	68.09	BnaA01g14050D	NBR1 homolog	2870	TCCACAGAGAGCGTCAACAGA ATTGAGGTGTCTCTCGCAGTTGTCTGACGAGG	TT3	0.00	0.00	0.00	0.14	2959	5.97	279	7.49
TGATGTTATGATGGCTGTGCC	+	NBR1	0.00	22.74	22.74	0.00	61.16	61.16	BnaC09g16640D	50S ribosomal protein L2, chloroplastic	736	TGATGTTATG-ATGGCTGTGCC TAAAGATATAATACATACCGGCACGGATTCCC	TT3	0.00	0.00	0.00	0.14	119	-1.08	175	-0.77
ATGGACAGCTTGATCTGGACA	+	NBR1	0.26	38.41	147.26	0.00	72.73	72.73	BnaC09g37830D	unknown	518	ATGGACAG-CTTGATCTGGACA GCTTACTTGTCAGAACTTGACCAGTTATAGCT	TT3	0.00	0.00	0.00	0.05	1778	0.17	2181	0.97
CAGAGAGCGTCAACAGACTGC	-	NBR1	0.00	48.37	48.37	1.42	52.41	36.84	BnaA03g46880D	NBR1 homolog	2718	CAGAGAGCGTCAACAGACTGC AGGTGTTTCTCGGAGTTGTCTGACGAGGTTCA	TT3	0.00	0.00	0.00	0.05	2740	0.77	4843	0.45
AAGAGGTCGTTGTCATCAACA	-	NBR1	0.85	20.62	24.14	0.00	35.10	35.10	BnaA05g25510D	Eukaryotic initiation factor 4A-1	1829	AAGAGGTC-GTTGTCATCAACA CGGTTCTCTAGTCAGCACTAGTTGTGTGCTCT	TT3	0.00	0.00	0.00	0.05	5805	0.09	8038	0.09
AAACACTAATCGAGGATTTGGA	-	NBR1	0.85	12.80	14.99	2.47	38.72	15.69	BnaC02g10220D	Ras-related protein RABA2d	402	AAACACTAATCGAGGATTTGGA TTAAGTTGTGGTTACCACCTGAACCTAAGGTT	TT3	0.00	0.00	0.00	0.09	320	-1.19	767	-1.83
AACGAGTTTCATGGACTGAAC	+	NBR1	0.00	81.35	81.35	0.00	77.95	77.95	BnaA03g10910D	Probable pyruvate kinase, cytosolic isozyme	492	AACGAGTTTCATGGACTGAAC AGGATTG-TCAAAGGACTGGACTTGGTTCAGG	TT3	0.00	0.00	0.00	0.05	722	1.19	1399	0.71
GAGAGGTCGTTGTCATCAACA	-	NBR1	0.00	17.03	17.03	0.00	26.18	26.18	BnaA05g25510D	Eukaryotic initiation factor 4A-1	1829	GAGAGGTC-GTTGTCATCAACA CGGTTCTCTAGTCAGCACTAGTTGTGTGCTCT	TT3	0.00	0.00	0.00	0.05	5805	0.09	8038	0.09
TCCACAGAGAGCGTCAACAGAC	-	NBR1	0.00	26.80	26.80	0.00	44.02	44.02	BnaA01g14050D	NBR1 homolog	2870	TCCACAGAGAGCGTCAACAGAC ATTGAGGTGTCTCTCGCAGTTGTCTGACGAGG	TT3	0.00	0.00	0.00	0.14	2959	5.97	279	7.49
TGCCCGTCGTGTATGTCACTC	+	NBR1	0.00	40.75	40.75	0.71	62.96	89.07	BnaC01g06460D	Aspartate aminotransferase, chloroplastic	2966	TGCCCGTCGTGTATGTCACTC GTGAACAGGCAGTACA-ATAGTGAGACGGTGC	TT3	0.00	0.00	0.00	0.28	2305	0.33	2777	0.34
TGCAGATGAGGAACCGCCACC	-	NBR1	0.00	38.92	38.92	0.00	36.10	36.10	BnaC01g05590D	unknown	9565	TGCAGATGAGGAACCGCCACC GACCACGTCTACACCTTGGTGTTGATAGGGGT	TT3	0.00	0.00	0.00	0.69	195	-0.14	360	0.04
TTAGCTTTGAAAGGCACCCTG	-	NBR1	0.00	15.43	15.43	0.00	25.52	25.52	BnaA10g16590D	Myb family transcription factor APL	103	TTAGCTTTGAAAGGCACCCTG TTAGAATCAAAATTTTACGTCGGACGAAGAGA	TT3	0.00	0.00	0.00	0.05	268	0.54	329	0.31
AAGAATGACGTCGAGATAACC	+	NBR1	0.00	61.06	61.06	0.00	48.51	48.51	BnaA06g06600D	AP-1 complex subunit mu-2	101	AAGAATGACGTCGAGATAACC TCTCTTCTTACT-CGACTCTAGTAGTAGTACT	TT3	0.00	0.00	0.00	0.37	1947	0.21	2563	0.00
TCCAATAAGATATGTATCGGCC	-	NBR1	0.00	22.43	22.43	0.00	43.37	43.37	BnaC05g33790D	Cyclin-dependent kinase inhibitor 6	497	TCCAATAAGATATGTATCGGCC ATCGAGGCTATTCT-TACGAAGCTGGAGGAGT	TT3	0.00	0.00	0.00	0.14	612	-0.06	523	0.45
TCCAATAAGATATGTATCGGCC	-	NBR1	0.00	22.43	22.43	0.00	43.37	43.37	BnaC08g11760D	NBR1 homolog	2128	TCCAATAAGATATGTATCGGCC TAGGAGGTTATTCTTTACATAGCTGGTCCATT	TT3	0.00	0.00	0.00	0.37	1275	1.12	1941	0.66

TTAGGAACAACAGGCTCAACT	-	NBR1	0.00	47.07	47.07	4.12	53.62	13.02	BnaC03g43130D	Auxin-responsive protein IAA2	2944	TTAGGAACAACAGGC-TCAACT ACGCAATCTTCGTTGTTCGCAGTTGATGTTTC	TT3	0.00	0.00	0.00	0.05	272	0.65	395	-1.77
AACGAGTTTCATGGACTGAACT	+	NBR1	0.26	63.53	243.54	0.71	138.84	196.41	BnaC03g13590D	Probable pyruvate kinase, cytosolic isozyme	1807	AACGAGTTTCATGGACTGAACT AGGATTG-TCAAAGGACTGGACTTGGTTCAGG	TT3	0.00	0.00	0.00	0.05	866	1.07	2235	0.29
AGGACTTGAGAGCTTCCCGAGC	-	NBR1	0.85	8.07	9.45	0.00	38.00	38.00	BnaC07g47570D	Auxin-responsive protein SAUR23	26	AGGACTTGAGAGCTTCCCGAGC GACGTCTTGCACTCTTGAACGACTCGTATCTC	TT3	0.00	0.00	0.00	0.93	1127	0.63	454	-0.16
CAACTTGGAGCAGTCTGTTGAC	+	NBR1	0.00	52.70	52.70	0.81	83.99	103.10	BnaC07g32720D	unknown	1031	CAACTTGGAGCAGTCTGTTGAC TCTGGTTGAACTTCGAGAGAGAA-TGTGTGTT	TT3	0.00	0.00	0.00	0.23	5449	0.03	4478	0.00
CTGCTCCAAGTTGTACTCGTT	-	NBR1	0.00	23.69	23.69	0.00	19.11	19.11	BnaA07g06830D	unknown	1260	CTGCTCCAAGTTGTACTCGTT ATACGACGAGTTTCAACGCGAGTGAGACGGTA	TT3	0.00	0.00	0.00	0.09	518	0.10	540	0.27
CTGCTCCAAGTTGTACTCGTT	-	NBR1	0.00	23.69	23.69	0.00	19.11	19.11	BnaC01g16550D	NBR1 homolog	2973	CTGCTCCAAGTTGTACTCGTT GTCTGACGAGGTTCAACATGAGCAACAGGGAG	TT3	0.00	0.00	0.00	0.05	7201	1.42	15409	0.96
CCTGAGGACTTGAGAGCTTCC	-	NBR1	0.00	25.99	25.99	0.00	39.81	39.81	BnaA01g14050D	NBR1 homolog	971	CCTGAGGACTTGAGAGCTTCC GAAAGGACTCCTGAACTCTCGAAGGGATCGAA	TT3	0.00	0.00	0.00	0.05	2959	5.97	279	7.49
TCACGTCAAGCTCACTGTTGA	-	NBR1	0.00	42.37	42.37	0.00	55.12	55.12	BnaC01g16550D	NBR1 homolog	2269	TCACGTCAAGCTCACTGTTGA TGAAAGTGCAGTTCGAGTGACAACTATCCGTG	TT3	0.00	0.00	0.00	0.14	7201	1.42	15409	0.96
AACAAGAGGCTGCTGAAGAAG	+	NBR1	0.00	39.73	39.73	0.00	34.17	34.17	BnaA03g19060D	NRT1/ PTR FAMILY 5.1	5994	AACAAGAGGCTGCTGAAGAAG ACAGTGGTTCTTCGATAAGTTCTTCAAGGGTT	TT3	0.00	0.00	0.00	0.69	2097	-0.03	1312	0.10
CACCAACGTTCGACTGCACAGT	-	NBR1	0.00	13.61	13.61	0.00	39.88	39.88	BnaA09g38220D	Methylenetetrahydrofolate reductase 1	2677	CACCAACGTTCGACTGCACAGT CGAAGTGGTTGCAAACT-ATGGGTCAAGGGAC	TT3	0.00	0.00	0.00	0.14	1670	-0.10	2002	-0.64
TCTGGTTCAACATCAGCACCT	-	NBR1	0.00	18.07	18.07	0.00	19.29	19.29	BnaA01g14050D	NBR1 homolog	2518	TCTGGTTCAACATCAGCACCT TCGAAGACCAAGTTGTAGTCGTGGAAAGTGAT	TT3	0.00	0.00	0.00	0.19	2959	5.97	279	7.49
TTGGCTTTGAAAGGCACCCTGA	-	NBR1	2.61	19.48	7.48	10.66	37.65	3.53	BnaA03g01940D	Trichome birefringence-like 9	5529	TTGGCTTTGAAAGGCACC-CTGA ACGAAACCGAGACTTTCTGCGGAGATTTTTAA	TT3	0.00	0.00	0.00	0.37	1124	0.06	2295	-0.22
CCAATAAGATATGTATCGGCC	-	NBR1	0.00	34.13	34.13	0.00	40.65	40.65	BnaCnng06320D	unknown	890	CCAATAAGATATGTATCGGCC GATAGGTT-TTGTATACGTATCTGGAGGGGCT	TT3	0.00	0.00	0.00	0.09	97	0.27	335	0.84
TGATGTTATGATGGCTGTGCC	+	NBR1	0.00	22.74	22.74	0.00	61.16	61.16	BnaA06g19320D	50S ribosomal protein L2, chloroplastic	858	TGATGTTATG-ATGGCTGTGCC TAAAGATATAATACATACCGGCACGGATTCCC	TT3	0.00	0.00	0.00	0.14	134	-1.21	191	-0.79
TAGAATCCATCGTTCACGGATT	-	NBR1	0.85	31.93	37.40	0.00	127.67	127.67	BnaCnng36390D	Ethylene-responsive transcription factor ERF106	851	TAGAATCCATCGTTCACGGATT TACAAT-TTACGTAGTAAGTGTCTAGTGAACT	TT3	0.00	0.00	0.00	0.14	5421	0.31	4671	-0.67
AGGACAAAGCGACTGTCTAGCT	-	NBR1	0.00	12.37	12.37	0.00	22.87	22.87	BnaA03g46880D	NBR1 homolog	1603	AGGACAAAGCGACTGTCTAGCT TAGTTCGTGTTTCGCTGACAGCTCAAATCAGG	TT3	0.00	0.00	0.00	0.32	2740	0.77	4843	0.45
CTGAGGGACAACGAGTACAACT	+	NBR1	0.00	54.36	54.36	0.00	77.18	77.18	BnaA05g17450D	UV-B-induced protein At3g17800, chloroplastic	1611	CTGAG-GGACAACGAGTACAACT CATGACTCTCTTGTTGTTTATGTTCAACCAGG	TT3	0.00	0.00	0.00	0.05	2941	0.06	3349	-0.12
CAGAGAGCGTCAACAGACTGC	-	NBR1	0.00	48.37	48.37	1.42	52.41	36.84	BnaC08g11760D	NBR1 homolog	2777	CAGAGAGCGTCAACAGACTGC AGGTGTTTCTCGTAGTTGTCTGACGAGGTTCA	TT3	0.00	0.00	0.00	0.51	1275	1.12	1941	0.66
CAGAGAGCGTCAACAGACTGCT	-	NBR1	0.00	17.54	17.54	0.00	24.02	24.02	BnaA01g14050D	NBR1 homolog	2866	CAGAGAGCGTCAACAGACTGCT AGGTGTCTCTCGCAGTTGTCTGACGAGGTTCA	TT3	0.00	0.00	0.00	1.25	2959	5.97	279	7.49
AACGAGTTTCATGGACTGAAC	+	NBR1	0.00	81.35	81.35	0.00	77.95	77.95	BnaC03g13590D	Probable pyruvate kinase, cytosolic isozyme	1807	AACGAGTTTCATGGACTGAAC AGGATTG-TCAAAGGACTGGACTTGGTTCAGG	TT3	0.00	0.00	0.00	0.05	866	1.07	2235	0.29
AGAGAGCGTCAACAGACTGCT	-	NBR1	0.00	29.47	29.47	0.00	25.53	25.53	BnaC01g16550D	NBR1 homolog	2989	AGAGAGCGTCAACAGACTGCT GGTGTCTCTCGCAGTTGTCTGACGAGGTTCAA	TT3	0.00	0.00	0.00	0.14	7201	1.42	15409	0.96
ACAGCTTGATCTTGACATGGC	+	NBR1	1.67	19.47	11.66	0.00	38.63	38.63	BnaC09g45610D	CBS domain-containing protein CBSX3, mitochondrial	1733	ACAGCTTG-ATCTTGACATGGC TAGTGTCGAACGTAGAACTGGATTGTAGTCTA	TT3	0.00	0.00	0.00	0.09	19107	0.02	24881	0.61
CCCAGTTATTGGAAGAACGCC	-	NBR1	0.85	16.76	19.63	0.00	32.43	32.43	BnaA03g53450D	Probable serine/threonine-protein kinase Cx32, chloroplastic	2240	CCCAGTTATTGGAAGAACGCC GGCCGGCTTAATTACCTTCTTGCCGGACCCTG	TT3	0.00	0.00	0.00	0.05	2692	0.65	3435	0.10
TCCAATAAGATATGTATCGGCC	-	NBR1	0.00	22.43	22.43	0.00	43.37	43.37	BnaC01g16550D	NBR1 homolog	2320	TCCAATAAGATATGTATCGGCC TAGGAGGTTATTCTTTACATAGCTGGTCCACT	TT3	0.00	0.00	0.00	0.37	7201	1.42	15409	0.96
CAGAGAGCGTCAACAGACTGCT	-	NBR1	0.00	17.54	17.54	0.00	24.02	24.02	BnaC08g11760D	NBR1 homolog	2777	CAGAGAGCGTCAACAGACTGCT AGGTGTTTCTCGTAGTTGTCTGACGAGGTTCA	TT3	0.00	0.00	0.00	0.51	1275	1.12	1941	0.66
AGAATCCATCGTTCACGGATT	-	NBR1	0.00	35.91	35.91	6.14	87.55	14.26	BnaA03g15990D	Probable protein phosphatase 2C 28	255	AGAATCCATCGTTCACGGATT AAGGTTTTA-GTAGTAAGTACATAGATAGATA	TT3	0.00	0.00	0.00	0.23	0	NA	0	NA
CAGAGAGCGTCAACAGACTGC	-	NBR1	0.00	48.37	48.37	1.42	52.41	36.84	BnaA01g14050D	NBR1 homolog	2866	CAGAGAGCGTCAACAGACTGC AGGTGTCTCTCGCAGTTGTCTGACGAGGTTCA	TT3	0.00	0.00	0.00	1.25	2959	5.97	279	7.49
TCTGGTTCAACATCAGCACCT	-	NBR1	0.00	18.07	18.07	0.00	19.29	19.29	BnaA06g22550D	Probable inactive purple acid phosphatase 29	3508	TCTGGTTCAACATCAGCACCT GGGAAGAACAAGTT-TAGTCGTTGATGTTGAG	TT3	0.00	0.00	0.00	0.14	31	0.76	0	0.24
TCCACAGAGAGCGTCAACAGAC	-	NBR1	0.00	26.80	26.80	0.00	44.02	44.02	BnaC08g11760D	NBR1 homolog	2781	TCCACAGAGAGCGTCAACAGAC ATTGAGGTGTTTCTCGTAGTTGTCTGACGAGG	TT3	0.00	0.00	0.00	0.09	1275	1.12	1941	0.66
TCCAATAAGATATGTATCGGCC	-	NBR1	0.00	22.43	22.43	0.00	43.37	43.37	BnaA03g46880D	NBR1 homolog	2055	TCCAATAAGATATGTATCGGCC TAGTAGGTTATTCTTTACATAGCTGGTCCATT	TT3	0.00	0.00	0.00	0.14	2740	0.77	4843	0.45
TCCACAGAGAGCGTCAACAGA	-	NBR1	0.85	71.95	84.25	0.00	68.09	68.09	BnaC07g39070D	NBR1 homolog	3688	TCCACAGAGAGCGTCAACAGA ATTGAGGTGTTTCTCGGAGTTGTCTGACGAGG	TT3	0.00	0.00	0.00	0.09	2241	1.36	5953	1.44

[1] sRNA seq / DEseq data

[2] PAREseq / PAREsnip data

[3] RNAseq / Deseq data

[4] "NBR1" stands for a small gene family predicted to encode a homolog of NBR1 (BnaA01g14050D, BnaA03g46880D, BnaC07g39070D, BnaC01g16550D, BnaC08g11760D)

Table S27: va-phasiRNAs produced from genes for 'TAR1' and targeting mRNAs within the gene family and other genes

va-phasiRNA[1]									Host mRNA targets[2]									DE target mRNA[3]			
va-phasiRNA	dsRNA (+) / (-) strand va-phasiRNA	Origin (gene family)	Normalized reads (positive / negative)						Target transcript ID	Predicted gene function	Cleavage position	vsiRNA:mRNA target pair (5'-3' : 3'-5')	Cleavage found in PAREseq replicates	Fragment signatures (rpm)				mRNA reads & FC(log2)			
			DM	DT	DT/DM reads	TM	TT	TT/TM reads						DM	DT	TM	TT	DM	DT	TM	TT
CCGAAGAGGGGAAAGGTTCCA	+	TAR1[4]	17.03	60.41	3.55	40.25	103.44	2.57	BnaA04g08570D	Ribulose bisphosphate carboxylase small chain 1A, chloroplastic	907	CCGAAGAGGGGAAAGGTTCCA ||||| |o||||| ||||| CGTAGGCTTGTTCCCTT-CGAAGGTGTAACAG	DT2 DT3 TT1 TT2 TT3	0.00	548.73	0.00	135.27	329765	-1.19	100342	-0.88
CCGAAGAGGGGAAAGGTTCCA	+	TAR1	17.03	60.41	3.55	40.25	103.44	2.57	BnaAnng36210D	Ribulose bisphosphate carboxylase small chain F1, chloroplastic	756	CCGAAGAGGGGAAAGGTTCCA ||||| |o||||| ||||| CGTAGGCTTGTTCCCTT-CGAAGGTGTAACAG	DT2 DT3 TT1 TT2	0.00	548.73	0.00	40.77	439500	-1.05	249908	-0.85
CAACCCGACTCGTAGACAGCGC	-	TAR1	18.38	32.64	1.78	75.89	103.29	1.36	BnaA09g04420D	TAR1	614	CAACCCGACTCGTAGACAGCGC |||||||||||||||||||| GTTTGTTGGGCTGAGCATCTGTCGCGGAGCAC	DT2 DT3 TT3	0.00	5.72	0.00	1.20	239430	-1.00	101442	-0.78
CAACCCGACTCGTAGACAGCGC	-	TAR1	18.38	32.64	1.78	75.89	103.29	1.36	BnaC08g46150D	TAR1	610	CAACCCGACTCGTAGACAGCGC |||||||||||||||||||| GTTTGTTGGGCTGAGCATCTGTCGCGGAGCAC	DT2 DT3 TT3	0.00	5.72	0.00	1.20	143979	-1.14	60510	-0.80
ACCCGACTCGTAGACAGCGCC	-	TAR1	10.47	56.44	5.39	56.17	124.16	2.21	BnaA09g04420D	TAR1	612	ACCCGACTCGTAGACAGCGCC ||||||||||||||||||| TTGTTGGGCTGAGCATCTGTCGCGGAGCACCA	DT2 DT3 TT3	0.00	7.99	0.00	12.59	239430	-1.00	101442	-0.78
CAACCCGACTCGTAGACAGCGC	-	TAR1	18.38	32.64	1.78	75.89	103.29	1.36	BnaAnng36730D	Putative uncharacterized protein ART3	614	CAACCCGACTCGTAGACAGCGC |||||||||||||||||||| GTTTGTTGGGCTGAGCATCTGTCGCGGAACAC	DT2 DT3 TT3	0.00	5.72	0.00	1.20	32584	-0.17	17996	-0.74
GGTAACACACGGGAGATCAGCT	-	TAR1	8.80	36.47	4.14	17.84	24.79	1.39	BnaA09g04420D	TAR1	213	GGTAACACACGGGAGATCAGCT |||||||||||||||||||| CACGCCATTGTGTGCCCTCTAGTCGAAGGCAG	DT2 DT3 TT3	0.00	6.91	0.00	0.79	239430	-1.00	101442	-0.78
ACCCGACTCGTAGACAGCGCC	-	TAR1	10.47	56.44	5.39	56.17	124.16	2.21	BnaC08g46150D	TAR1	608	ACCCGACTCGTAGACAGCGCC ||||||||||||||||||| TTGTTGGGCTGAGCATCTGTCGCGGAGCACCA	DT2 DT3 TT3	0.00	7.99	0.00	12.59	143979	-1.14	60510	-0.80
GGTAACACACGGGAGATCAGCT	-	TAR1	8.80	36.47	4.14	17.84	24.79	1.39	BnaAnng36730D	Putative uncharacterized protein ART3	213	GGTAACACACGGGAGATCAGCT |||||||||||||||||||| CACGCCATTGTGTGCCCTCTAGTCGAAGGCAG	DT2 DT3 TT3	0.00	6.91	0.00	0.79	32584	-0.17	17996	-0.74
GGTAACACACGGGAGATCAGCT	-	TAR1	8.80	36.47	4.14	17.84	24.79	1.39	BnaAnng22160D	TAR1	1213	GGTAACACACGGGAGATCAGCT |||||||||||||o||||| CACGCCATTGTGTGCCCTCTGGTCGAAGGCAG	DT2 DT3 TT3	0.00	6.91	0.00	0.79	257765	-1.01	114234	-0.85
CAACCCGACTCGTAGACAGCGC	-	TAR1	18.38	32.64	1.78	75.89	103.29	1.36	BnaAnng22160D	TAR1	1614	CAACCCGACTCGTAGACAGCGC |||||||||||||||||||| GTTTGTTGGGCTGAGCATCTGTCGCGGAGCAC	DT2 DT3 TT3	0.00	5.72	0.00	1.20	257765	-1.01	114234	-0.85
GGTAACACACGGGAGATCAGCT	-	TAR1	8.80	36.47	4.14	17.84	24.79	1.39	BnaC08g46150D	TAR1	209	GGTAACACACGGGAGATCAGCT |||||||||||||o||||| CACGCCATTGTGTGCCCTCAGGTCGAAGGTAG	DT2 DT3 TT3	0.00	6.91	0.00	0.79	143979	-1.14	60510	-0.80
ACCCGACTCGTAGACAGCGCC	-	TAR1	10.47	56.44	5.39	56.17	124.16	2.21	BnaAnng36730D	Putative uncharacterized protein ART3	612	ACCCGACTCGTAGACAGCGCC ||||||||||||||||||| TTGTTGGGCTGAGCATCTGTCGCGGAACACCA	DT2 DT3 TT3	0.00	7.99	0.00	12.59	32584	-0.17	17996	-0.74
CGCGACGTCGCAGACGGCG	-	TAR1	47.38	95.44	2.01	350.64	151.98	0.43	BnaAnng22160D	TAR1	650	CGCGACGTCGCAGACGGCG ||||| ||||||o||| TGTTGGGCTG-AGCATCTGTCGCGGAGCACCA	DT2 DT3 TT3	0.00	14.03	0.00	2.68	257765	-1.01	114234	-0.85
ACCCGACTCGTAGACAGCGCC	-	TAR1	10.47	56.44	5.39	56.17	124.16	2.21	BnaAnng22160D	TAR1	1612	ACCCGACTCGTAGACAGCGCC ||||||||||||||||||| TTGTTGGGCTGAGCATCTGTCGCGGAGCACCA	DT2 DT3 TT3	0.00	7.99	0.00	12.59	257765	-1.01	114234	-0.85
CCAAGGAAGTTTGAGGCAATA	+	TAR1	99.10	341.97	3.45	277.03	668.17	2.41	BnaC03g61150D	Serine hydroxymethyltransferase 1, mitochondrial	3042	CCAAGGAAGTTTGAGGCAATA |||||||||oo|o|||| GTAAGGTACCTTCAAGTTTCGT-ATTATTTTT	DT2 DT3 TT3	0.00	5.15	2.64	0.00	43289	-0.26	69289	-0.79
CTCATCGAGGCCTGGCTCTTGC	-	TAR1	0.00	28.28	28.28	2.85	109.43	38.45	BnaC06g42820D	Casein kinase II subunit beta	1443	CTCATCGAGGCCTGGCTCTTGC |o|| |||||||||||| GGCGGGGTCGCT-CGGTCCGACAACGGTAGTC	DT3 TT2 TT3	0.00	9.53	0.00	78.23	1090	-0.24	960	-0.08
CTTTCGAAGTTCGCGCATAAG	-	TAR1	14.15	33.08	2.34	26.30	55.27	2.10	BnaA03g39180D	Actin-depolymerizing factor 5	146	CTTTCGAAGTTCGCGCATAAG |o|||| ||| ||||||| GGTCGGAAGCTGCAA-CGCATATTCTAGAAAC	DT2 DT3	0.00	6.99	0.00	0.00	91	0.95	58	-0.13
CATCGAGGCCTGGCTCTTGCC	-	TAR1	10.51	110.09	10.47	31.36	144.62	4.61	BnaC06g42820D	Casein kinase II subunit beta	1441	CATCGAGGCCTGGCTCTTGCC ||||| ||||| ||||| CGGGGTCGCT-CGGTCCGACAACGGTAGTCAA	DT2 DT3	0.00	4.34	0.00	0.00	1090	-0.24	960	-0.08
CTTTCGAAGTTCGCGCATAAG	-	TAR1	14.15	33.08	2.34	26.30	55.27	2.10	BnaC03g46510D	Actin-depolymerizing factor 5	1066	CTTTCGAAGTTCGCGCATAAG |o|||| ||| ||||||| GGTCGGAAGCTGCAA-CGCATATTCTAGAAAC	DT2 DT3	0.00	6.99	0.00	0.00	1669	0.97	1200	-0.06
CCACCAAGATCTGCACCGACG	-	TAR1	4.36	79.19	18.17	5.35	115.18	21.52	BnaC03g20170D	unknown	130	CCACCAAGATCTGCACCG-ACG ||||||||| |||||| GGAGGGTGGTTCTACAATTGGCATGCATGAAA	DT2 DT3	0.00	3.55	0.00	0.00	0	NA	0	NA
TACTCATCGAGGCCTGGCTCT	-	TAR1	13.20	88.31	6.69	35.05	355.83	10.15	BnaAnng22160D	TAR1	3274	TACTCATCGAGGCCTGGCTCT ||||||||||||||||||| GAGGATGAGTAGCTCCGGACCGAGAACGGGGC	DT2 DT3	0.00	3.59	0.00	0.00	257765	-1.01	114234	-0.85
CGGTTGGCCAAAATCCGAGCT	+	TAR1	15.20	50.45	3.32	20.51	28.58	1.39	BnaA08g29260D	Nuclear pore complex protein NUP214	7841	CGGTTGGCCAAAATCCGAGCT ||||||||||| || || CGCTGCCAACCGGTTT-AGGCGGGACTCACCC	DT2 DT3	0.00	4.01	0.00	0.00	126	0.74	285	0.12
AGGCCTCGATGAGTAGGAGGG	+	TAR1	13.90	106.85	7.69	50.09	229.85	4.59	BnaA03g07490D	Stem-specific protein TSJT1	1821	AGGCCTCGATGAGTAGGAGGG |o||||o|||o|o|||oo AACATTCGGAGTTACTGGTTCTCTTGGAGCAA	DT2 DT3	0.00	5.44	0.00	0.00	44213	-0.31	27325	0.63
TACTCATCGAGGCCTGGCTCTT	-	TAR1	15.90	52.44	3.30	35.10	189.02	5.39	BnaA09g04420D	TAR1	1720	TACTCATCGAGGCCTGGCTCTT ||||||||||||||||||| GAGGATGAGTAGCTCCGGACCGAGAACGGGGC	DT2 DT3	0.00	3.59	0.00	0.00	239430	-1.00	101442	-0.78
TACTCATCGAGGCCTGGCTCT	-	TAR1	13.20	88.31	6.69	35.05	355.83	10.15	BnaA09g04420D	TAR1	1720	TACTCATCGAGGCCTGGCTCT ||||||||||||||||||| GAGGATGAGTAGCTCCGGACCGAGAACGGGGC	DT2 DT3	0.00	3.59	0.00	0.00	239430	-1.00	101442	-0.78
TACTCATCGAGGCCTGGCTCTT	-	TAR1	15.90	52.44	3.30	35.10	189.02	5.39	BnaAnng22160D	TAR1	3274	TACTCATCGAGGCCTGGCTCTT ||||||||||||||||||| GAGGATGAGTAGCTCCGGACCGAGAACGGGGC	DT2 DT3	0.00	3.59	0.00	0.00	257765	-1.01	114234	-0.85
TTGAGAATAGGTCGAGGACATT	-	TAR1	10.47	30.82	2.95	14.37	92.73	6.46	BnaA06g04090D	Dihydrolipoyl dehydrogenase 1, mitochondrial	1447	TTGAGA-ATAGGTCGAGGACATT o||||| |||||||o||o GCGGACTCTGTAACCAGCTCTTGGAGAGCAAG	DT2 DT3	0.00	7.75	0.00	0.00	6339	-0.50	7445	-0.28
CCACCAAGATCTGCACCGACG	-	TAR1	4.36	79.19	18.17	5.35	115.18	21.52	BnaA03g56370D	unknown	130	CCACCAAGATCTGCACCG-ACG ||||||||| |||||| GGAGGGTGGTTCTACAATTGGCATGCATGAAA	DT2 DT3	0.00	3.55	0.00	0.00	0	NA	0	NA
CCCGGGCTTAGGTCACCACCT	-	TAR1	58.29	25.16	0.43	43.78	49.41	1.13	BnaC03g72010D	Aquaporin PIP2-2	15	CCCGGGCTTAGGTCACCACCT ||||| ||||| ||||||| GTGGCGGCCCAAATACACTGGTGGAAGT	DT2 TT3	0.00	0.27	0.00	0.09	837	-1.76	1138	-1.75
CCACCAAGATCTGCACCGACG	-	TAR1	4.36	79.19	18.17	5.35	115.18	21.52	BnaC08g46150D	TAR1	1790	CCACCAAGATCTGCACCGACG ||||||||||||||||||| TGATGGTGGTTCTAGACGTGGCTGCCGGCGAG	DT2 TT3	0.00	2.75	0.00	0.09	143979	-1.14	60510	-0.80
CTCAAACTTCCTTGGCCTAAA	-	TAR1	18.42	29.66	1.61	26.60	49.83	1.87	BnaA02g04300D	Aspartate aminotransferase, cytoplasmic isozyme 1	3462	CTCAAACTTCCTTGGCCTAAA |||||| ||||||||| ||| AACCAAGTTTGTAGGAACCGGTTTTTCTATAC	DT2 TT3	0.00	1.42	0.00	0.28	1641	-0.15	1805	-0.03

CTCAAACTTCCTTGGCCTAAA	-	TAR1	18.42	29.66	1.61	26.60	49.83	1.87	BnaA02g04300D	Aspartate aminotransferase, cytoplasmic isozyme 1	3462	CTCAAACTTCCTTGGCCTAAA AACCAAGTTTGTAGGAACCGGTTTTTCTATAC	DT2 TT3	0.00	1.42	0.00	0.28	1641	-0.15	1805	-0.03
CCACCAAGATCTGCACCGACG	-	TAR1	4.36	79.19	18.17	5.35	115.18	21.52	BnaC02g36110D	unknown	389	CCACCAAGATCTGCACCGACG TGATGGTGGTTCTAGACGTGGCTGTCGGTGAG	DT2 TT3	0.00	2.75	0.00	0.09	25737	-1.12	12547	-0.80
CCCGGGCTTAGGTCACCACCT	-	TAR1	58.29	25.16	0.43	43.78	49.41	1.13	BnaA03g17030D	Aquaporin PIP2-2	508	CCCGGGCTTAGGTCACCACCT GTGGCGGCCCAAATACACTGGTGGAAGTGTAT	DT2 TT3	0.00	0.27	0.00	0.09	10540	-1.26	1150	-2.83
CCACCAAGATCTGCACCGACG	-	TAR1	4.36	79.19	18.17	5.35	115.18	21.52	BnaA09g04420D	TAR1	1794	CCACCAAGATCTGCACCGACG TGATGGTGGTTCTAGACGGGGCTGCCGGCGAG	DT2 TT3	0.00	2.75	0.00	0.09	239430	-1.00	101442	-0.78
CTCATCGAGGCCTGGCTCTTG	-	TAR1	1.71	83.91	49.13	4.90	143.58	29.28	BnaC06g42820D	Casein kinase II subunit beta	1443	CTCATCGAGGCCTGGCTCTTG GGCGGGGTCGCT-CGGTCCGACAACGGTAGTC	DT3 TT2	0.00	9.53	0.00	74.25	1090	-0.24	960	-0.08
CCCGGGCTTAGGTCACCACCT	-	TAR1	58.29	25.16	0.43	43.78	49.41	1.13	BnaC03g71780D	Thiamine thiazole synthase, chloroplastic	1986	CCCGGGCTTAGGTCACC-ACCT GTCGAGGCCCGAATCCAGAGGCTGTATCCAAG	DT3 TT2	0.00	6.04	0.00	21.01	52131	-0.89	75887	-0.80
GAGATCAGCTTCCGTCCCATA	-	TAR1	23.90	32.30	1.35	32.58	22.82	0.70	BnaA09g04420D	TAR1	201	GAGATCAGCTTCCGTCCCATA TGCCCTCTAGTCGAAGGCAGGGTATAGGAGCT	DT3 TT3	0.00	0.86	0.00	0.23	239430	-1.00	101442	-0.78
ATGAACCGGAAGCCGGGTTACG	+	TAR1	85.30	90.44	1.06	175.86	215.73	1.23	BnaA08g07920D	F-box/kelch-repeat protein SKIP25	1208	ATGAACCGGAAGCCGGGTTACG TATGTACTTGGCTTT-GGCCAAGTTCGGGAAG	DT3 TT3	0.00	0.50	0.00	0.14	210	-1.45	110	-0.14
CGTGGTGTCCGGTGCATTCCC	+	TAR1	21.08	57.98	2.75	96.27	105.81	1.10	BnaC02g37040D	Chlorophyll a-b binding protein 36, chloroplastic	412	CGTGGTGTCCGGTGCATTCCC GTTGGCATCAGAGGCCCCATAAGTGGCCATTC	DT3 TT3	0.00	0.05	0.00	0.05	535655	-0.48	315782	-0.03
AGATCTGCACCGACGGCCGCT	-	TAR1	0.85	15.22	17.82	3.48	33.56	9.64	BnaC02g04990D	Protein ZINC INDUCED FACILITATOR-LIKE 1	3957	AGATCTGCACCGACGGCCGCT GCACTCTCGATGTGGCTGGTGGTGATAGTGTA	DT3 TT3	0.00	0.54	0.00	0.19	129	1.66	39	1.31
CCGAATCGATCGGCGGACCGGA	-	TAR1	51.11	48.82	0.96	88.62	213.26	2.41	BnaAnng36730D	Putative uncharacterized protein ART3	830	CCGAATCGATCGGCGGACCGGA GCGGGGGCTTAGCTAGCCGCCTGGCCTAACGAG	DT3 TT3	0.00	2.27	0.00	1.34	32584	-0.17	17996	-0.74
CCAAGATCTGCACCGACGGCC	-	TAR1	22.02	105.38	4.78	32.79	154.52	4.71	BnaC02g36110D	unknown	386	CCAAGATCTGCACCGACGGCC TGGTGGTTCTAGACGTGGCTGTCGGTGAGGGG	DT3 TT3	0.00	1.41	0.00	0.37	25737	-1.12	12547	-0.80
ACCCGACTCGTAGACAGCGCC	-	TAR1	10.47	56.44	5.39	56.17	124.16	2.21	BnaA08g23760D	Chlorophyll a-b binding protein CP24 10A, chloroplastic	957	ACCCGACTCGTAGACAGCGCC GGGATAGGCGGAGCATTTGTGGCGGTGCACAG	DT3 TT3	0.00	2.54	0.00	0.46	10588	-0.34	5425	0.68
GAGATCAGCTTCCGTCCCATA	-	TAR1	23.90	32.30	1.35	32.58	22.82	0.70	BnaAnng36730D	Putative uncharacterized protein ART3	201	GAGATCAGCTTCCGTCCCATA TGCCCTCTAGTCGAAGGCAGGGTATAGGAGCT	DT3 TT3	0.00	0.86	0.00	0.23	32584	-0.17	17996	-0.74
GTCCCATATCCTCGAGAGGATG	-	TAR1	151.56	274.16	1.81	284.93	270.58	0.95	BnaAnng36730D	Putative uncharacterized protein ART3	188	GTCCCATATCCTCGAGAGGATG AAGGCAGGGTATAGGAGCTCTCCTACCCCCCT	DT3 TT3	0.00	5.13	0.00	0.37	32584	-0.17	17996	-0.74
AGATCTGCACCGACGGCCGCT	-	TAR1	0.85	15.22	17.82	3.48	33.56	9.64	BnaC08g46150D	TAR1	1784	AGATCTGCACCGACGGCCGCT TGGTTCTAGACGTGGCTGCCGGCGAGGCGGGC	DT3 TT3	0.00	1.41	0.00	0.69	143979	-1.14	60510	-0.80
CCAAGGTGTGAACTCGTTGAA	-	TAR1	81.80	82.59	1.01	215.93	175.72	0.81	BnaAnng22160D	TAR1	430	CCAAGGTGTGAACTCGTTGAA AGCCGGTTCCACACTTGAGCAACTTATGTAGT	DT3 TT3	0.00	2.45	0.00	0.19	257765	-1.01	114234	-0.85
CGTCCCATATCCTCGAGAGGA	-	TAR1	172.94	326.00	1.89	311.97	170.30	0.55	BnaAnng36730D	Putative uncharacterized protein ART3	189	CGTCCCATATCCTCGAGAGGA GAAGGCAGGGTATAGGAGCTCTCCTACCCCCC	DT3 TT3	0.00	0.86	0.00	0.28	32584	-0.17	17996	-0.74
AGATCTGCACCGACGGCCGCT	-	TAR1	0.85	15.22	17.82	3.48	33.56	9.64	BnaA02g01850D	Protein ZINC INDUCED FACILITATOR 1	1218	AGATCTGCACCGACGGCCGCT GCACTCTCGATGTGGCTGGTGGTGATAGTGTA	DT3 TT3	0.00	0.54	0.00	0.19	4	0.83	0	-0.20
AGGCCTCGATGAGTAGGAGGG	+	TAR1	13.90	106.85	7.69	50.09	229.85	4.59	BnaC05g28700D	Stem-specific protein TSJT1	1499	AGGCCTCGATGAGTAGGAGGG AACATTCGGAGCTACTGGTTCTCTTGGAGCAA	DT3 TT3	0.00	0.91	0.00	0.09	177	-0.05	1096	0.51
CCGAATCGATCGGCGGACCGGA	-	TAR1	51.11	48.82	0.96	88.62	213.26	2.41	BnaC08g46150D	TAR1	826	CCGAATCGATCGGCGGACCGGA GCGGGGCTTAGCTAGCCGCCTGGCCTAACGAG	DT3 TT3	0.00	2.27	0.00	1.34	143979	-1.14	60510	-0.80
GCAGACGGCGAACCACCCACG	-	TAR1	9.53	47.34	4.97	4.08	80.94	19.84	BnaA06g30390D	Nitrile-specifier protein 5	1053	GCAGACGGCGAACCACCCACG TTGTCGTTTG-CGCGTGGTGGGTGCACCCGTG	DT3 TT3	0.00	0.73	0.00	0.65	11635	1.14	16852	1.14
CCAAGATCTGCACCGACGGCC	-	TAR1	22.02	105.38	4.78	32.79	154.52	4.71	BnaC08g46150D	TAR1	1787	CCAAGATCTGCACCGACGGCC TGGTGGTTCTAGACGTGGCTGCCGGCGAGGCG	DT3 TT3	0.00	1.41	0.00	0.37	143979	-1.14	60510	-0.80
CCCCGAATCGATCGGCGGACC	-	TAR1	25.40	67.54	2.66	47.53	195.45	4.11	BnaAnng22160D	TAR1	1832	CCCCGAATCGATCGGCGGACC GTGCGGGGCTTAGCTAGCCGCCTGGCCTAACG	DT3 TT3	0.00	2.36	0.00	0.32	257765	-1.01	114234	-0.85
AGGCCTCGATGAGTAGGAGGG	+	TAR1	13.90	106.85	7.69	50.09	229.85	4.59	BnaC02g08540D	Stem-specific protein TSJT1	1866	AGGCCTCGATGAGTAGGAGGG AACATTCGGAGCTACTGGTTCTCTTGGAGCAA	DT3 TT3	0.00	0.91	0.00	0.09	42710	0.13	42762	0.74
CCCCGAATCGATCGGCGGACC	-	TAR1	25.40	67.54	2.66	47.53	195.45	4.11	BnaA09g04420D	TAR1	832	CCCCGAATCGATCGGCGGACC GTGCGGGGCTTAGCTAGCCGCCTGGCCTAACG	DT3 TT3	0.00	2.36	0.00	0.32	239430	-1.00	101442	-0.78
CCAAGATCTGCACCGACGGCC	-	TAR1	22.02	105.38	4.78	32.79	154.52	4.71	BnaA09g04420D	TAR1	1791	CCAAGATCTGCACCGACGGCC TGGTGGTTCTAGACGGGGCTGCCGGCGAGGCG	DT3 TT3	0.00	1.41	0.00	0.37	239430	-1.00	101442	-0.78
CCCCGAATCGATCGGCGGACC	-	TAR1	25.40	67.54	2.66	47.53	195.45	4.11	BnaAnng36730D	Putative uncharacterized protein ART3	832	CCCCGAATCGATCGGCGGACC GTGCGGGGCTTAGCTAGCCGCCTGGCCTAACG	DT3 TT3	0.00	2.36	0.00	0.32	32584	-0.17	17996	-0.74
GTCCCATATCCTCGAGAGGATG	-	TAR1	151.56	274.16	1.81	284.93	270.58	0.95	BnaA09g04420D	TAR1	188	GTCCCATATCCTCGAGAGGATG AAGGCAGGGTATAGGAGCTCTCCTACCCCCCT	DT3 TT3	0.00	5.13	0.00	0.37	239430	-1.00	101442	-0.78
CCGAATCGATCGGCGGACCGGA	-	TAR1	51.11	48.82	0.96	88.62	213.26	2.41	BnaA09g04420D	TAR1	830	CCGAATCGATCGGCGGACCGGA GCGGGGCTTAGCTAGCCGCCTGGCCTAACGAG	DT3 TT3	0.00	2.27	0.00	1.34	239430	-1.00	101442	-0.78
CGTCCCATATCCTCGAGAGGA	-	TAR1	172.94	326.00	1.89	311.97	170.30	0.55	BnaA09g04420D	TAR1	189	CGTCCCATATCCTCGAGAGGA GAAGGCAGGGTATAGGAGCTCTCCTACCCCCC	DT3 TT3	0.00	0.86	0.00	0.28	239430	-1.00	101442	-0.78

CCCCGAATCGATCGGCGGACC	-	TAR1	25.40	67.54	2.66	47.53	195.45	4.11	BnaC08g46150D	TAR1	828	CCCCGAATCGATCGGCGGACC GTGCGGGGCTTAGCTAGCCGCCTGGCCTAACG	DT3 TT3	0.00	2.36	0.00	0.32	143979	-1.14	60510	-0.80
AGATCTGCACCGACGGCCGCT	-	TAR1	0.85	15.22	17.82	3.48	33.56	9.64	BnaC02g36110D	unknown	383	AGATCTGCACCGACGGCCGCT TGGTTCTAGACGTGGCTGTCGGTGAGGGGGCC	DT3 TT3	0.00	1.41	0.00	0.69	25737	-1.12	12547	-0.80
CCGAATCGATCGGCGGACCGGA	-	TAR1	51.11	48.82	0.96	88.62	213.26	2.41	BnaAnng22160D	TAR1	1830	CCGAATCGATCGGCGGACCGGA GCGGGGCTTAGCTAGCCGCCTGGCCTAACGAG	DT3 TT3	0.00	2.27	0.00	1.34	257765	-1.01	114234	-0.85
AACAACCCGACTCGTAGACAG	-	TAR1	20.28	12.59	0.62	33.00	35.37	1.07	BnaC08g46150D	TAR1	612	AACAACCCGACTCGTAGACAG GGGTTTGTTGGGCTGAGCATCTGTCGCGGAGC	TT2 TT3	0.00	0.00	0.00	22.33	143979	-1.14	60510	-0.80
AACAACCCGACTCGTAGACAG	-	TAR1	20.28	12.59	0.62	33.00	35.37	1.07	BnaAnng36730D	Putative uncharacterized protein ART3	616	AACAACCCGACTCGTAGACAG GGGTTTGTTGGGCTGAGCATCTGTCGCGGAAC	TT2 TT3	0.00	0.00	0.00	22.33	32584	-0.17	17996	-0.74
AACAACCCGACTCGTAGACAG	-	TAR1	20.28	12.59	0.62	33.00	35.37	1.07	BnaAnng22160D	TAR1	1616	AACAACCCGACTCGTAGACAG GGGTTTGTTGGGCTGAGCATCTGTCGCGGAGC	TT2 TT3	0.00	0.00	0.00	22.33	257765	-1.01	114234	-0.85
AACAACCCGACTCGTAGACAG	-	TAR1	20.28	12.59	0.62	33.00	35.37	1.07	BnaA09g04420D	TAR1	616	AACAACCCGACTCGTAGACAG GGGTTTGTTGGGCTGAGCATCTGTCGCGGAGC	TT2 TT3	0.00	0.00	0.00	22.33	239430	-1.00	101442	-0.78
CTGAGGACGCTTCTCCAGACT	-	TAR1	19.40	29.77	1.53	49.58	45.93	0.93	BnaAnng00930D	unknown	1389	CTGAGGACGCTTCTCCAGACT CCACGTCTCCT-CGCAGAGATCTGACATCTTT	DT2	0.00	1.87	0.00	0.00	2942	-0.20	2085	0.00
GTTAAAATTCCGGAACCGGGA	+	TAR1	63.63	102.89	1.62	115.62	225.72	1.95	BnaA06g39060D	Puromycin-sensitive aminopeptidase	2000	GTTAAAATTCCGGAACCGGGA TGTACAATTTT-AGACCTTGCCGCTGTTACAA	DT2	0.00	2.31	0.00	0.00	4126	1.02	7452	0.36
GGTTAGTCGATCCTAAGAGTCG	+	TAR1	108.00	117.16	1.08	151.96	304.33	2.00	BnaA08g11840D	Probable disease resistance protein At4g33300	3113	GGTTAGTCGATCCTAAGAGTCG ATATCCAATTA-CTAGGATGAGCAGCTCGGTT	DT2	0.00	0.09	0.00	0.00	5912	0.01	8859	0.28
AGGAGCGTCTTGACATGCGGT	+	TAR1	18.02	92.36	5.13	139.92	67.53	0.48	BnaA03g24640D	RNA polymerase II transcriptional coactivator KELP	210	AGGAGCGTCTTGAC-ATGCGGT AAGCTCCTTGCTGAACTGCTACGGCGCATGCT	DT2	0.00	0.89	0.00	0.00	1223	0.03	1319	0.13
GAACGACCTGAGAACGATGAA	+	TAR1	14.30	132.60	9.27	113.19	241.21	2.13	BnaCnng51140D	Transcription repressor OFP15	714	GAACGACCTG-AGAACGATGAA TTCTTGTGCTGCACATCTTGCTGTTTCCTCTA	DT2	0.00	3.20	0.00	0.00	125	-1.01	21	-1.01
CGACGTCGCAGACGGCGAACC	-	TAR1	32.30	849.78	26.31	61.44	2765.49	45.01	BnaAnng22160D	TAR1	648	CGACGTCGCAGACGGCGAACC GAGCGCTGCAGCGTCTGCCGCTTGGTGGGTGC	DT2	0.00	1.33	0.00	0.00	257765	-1.01	114234	-0.85
ATTGCCTCAAACTTCCTTGGCC	-	TAR1	4.40	32.88	7.47	74.00	119.08	1.61	BnaA10g17340D	2-hydroxyacyl-CoA lyase	1403	ATTGCCTCAAACTTCCTTGGCC ACAATGATGGAGTT-GAAGGTACCGCGACTTA	DT2	0.00	1.69	0.00	0.00	3693	0.29	3325	0.34
GACGCTCCTGACGTTCTTAGC	-	TAR1	1.75	18.31	10.46	#N/A	#N/A	#N/A	BnaC04g41350D	Histone H1.2	846	GACGCTCCTGACGTTCTTAGC GTGTCGGCGACGAC-GAAAGAATCGTCCTCGT	DT2	0.00	4.80	0.00	0.00	5973	0.67	4998	1.03
GGCCGAAGAGGGGAAAGGTTC	+	TAR1	11.17	79.65	7.13	38.65	149.09	3.86	BnaAnng21760D	TAR1	832	GGCCGAAGA-GGGGAAAGGTTC CTTCCGGCTTCTCCCCTTTCCAAGGTACACTT	DT2	0.00	0.18	0.00	0.00	47012	-1.01	20912	-0.79
CGACGTCGCAGACGGCGAACC	-	TAR1	32.30	849.78	26.31	61.44	2765.49	45.01	BnaC05g18830D	ADP-ribosylation factor 1	906	CGACGTCGCAGACGGCGAACC GGGGGCTGTAGGGTCTGACACTTTGACTACAA	DT2	0.00	3.29	0.00	0.00	2747	-0.95	1994	-0.57
GTCGCTGCAAAACCTAGGGCG	+	TAR1	7.93	37.07	4.67	9.47	60.64	6.40	BnaC02g04560D	GEM-like protein 5	1177	GTCGCTGCAAAACCTAGGGCG CTGCCAGCGATGTTTTTCGTTGCGCTTGTAAT	DT2	0.00	1.78	0.00	0.00	9378	-1.30	10291	-0.23
GTCGCTGCAAAACCTAGGGCG	+	TAR1	7.93	37.07	4.67	9.47	60.64	6.40	BnaA02g01510D	GEM-like protein 5	1141	GTCGCTGCAAAACCTAGGGCG CTGCCAGCGATGTTTTTCGTTGCGCTTGTAAT	DT2	0.00	1.78	0.00	0.00	8779	-0.33	12866	0.21
GAACGACCTGAGAACGATGAA	+	TAR1	14.30	132.60	9.27	113.19	241.21	2.13	BnaA05g08210D	Transcription repressor OFP15	761	GAACGACCTG-AGAACGATGAA TTCTTGTGCTGCACATCTTGCTGTTTCCTCTA	DT2	0.00	3.20	0.00	0.00	349	-0.10	310	-1.37
AGAATAGGTCGAGGACATTGC	-	TAR1	0.85	38.20	44.74	16.17	67.47	4.17	BnaCnng03470D	Probable mediator of RNA polymerase II transcription subunit 37e	369	AGAATAGGTCGAGGACA-TTGC ACAGGCTCATCCAGCTCTTGTGAACGAGGAAG	DT2	0.00	2.22	0.00	0.00	13013	0.10	7825	-0.55
TTCTTAGCTCGGATTTTGGCC	-	TAR1	203.59	289.71	1.42	2.85	1.60	0.56	BnaC09g49110D	unknown	3724	TTCTTAGCTCGGATTTTGGCC CCGTAAG-ATTGAGCTAAAAAGCGGGACTAAA	DT2	0.00	3.73	0.00	0.00	2447	0.25	3898	0.21
TATGGGACGGAAGCTGATCTCC	+	TAR1	37.80	377.74	9.99	93.06	415.63	4.47	BnaC04g38650D	Abscisic-aldehyde oxidase	4210	TATGGGACGGAAGCTGATCTCC TATGGTACACTGCCTTGGACT-GAAGAGGTAG	DT2	0.00	2.04	0.00	0.00	242	0.69	592	0.85
AGGAAGCTGATTGGCTGGATC	+	TAR1	74.43	124.57	1.67	136.07	260.72	1.92	BnaA04g27920D	Ribulose bisphosphate carboxylase small chain F1, chloroplastic	800	AGGAAGCTGATTGGCTGGATC CCGCTACTTTGACTACGTGACCTGGACTGCCA	DT2	0.00	2.58	0.00	0.00	153	-2.47	68959	-1.12
TAAAGTTTGAGAATAGGTCGA	-	TAR1	11.32	34.87	3.08	18.63	38.80	2.08	BnaC01g42660D	Casein kinase II subunit alpha-2	2276	TA-AAGTTTGAGAATAGGTCGA AAGATGTTCAAACTTTTATCTACTTTCGTCAG	DT2	0.00	4.26	0.00	0.00	3956	0.18	4929	0.14
ATTGCCTCAAACTTCCTTGGC	-	TAR1	62.22	86.00	1.38	382.64	140.59	0.37	BnaC09g40570D	2-hydroxyacyl-CoA lyase	1394	ATTGCCTCAAACTTCCTTGGC ACAATGATGGAGTT-GAAGGTACCGCGACTTA	DT2	0.00	1.69	0.00	0.00	5556	0.31	6178	0.27
TGTCGGCCAAGGTGTGAACTCG	-	TAR1	30.41	37.07	1.22	133.79	108.00	0.81	BnaA04g08110D	Aspartic proteinase PCS1	934	TGTCGGCCAAG-GTGTGAACTCG CGGTGCAGCTGGTTCACTCACTTAAGCCTTGG	DT2	0.00	0.09	0.00	0.00	2668	-1.34	8138	-0.73
ATGGGACGGAAGCTGATCTCC	+	TAR1	44.51	721.86	16.22	77.21	419.08	5.43	BnaA07g13340D	60S acidic ribosomal protein P2-2	540	ATGGGACGGAAGCTGATCTCC GGCGAACCTTGCCTTCGGTT-GAAGAGGGAAG	DT2	0.00	0.98	0.00	0.00	3567	-0.78	2075	-0.44
GATCCTAAGAGTCGGGGGAAA	+	TAR1	16.64	52.81	3.17	33.77	88.65	2.63	BnaCnng49000D	Geranylgeranyl diphosphate reductase, chloroplastic	1119	GATCC-TAAGAGTCGGGGGAAA TGGGTAGGCATTTTTAGCCCTCTGTGCAGTAG	DT2	0.00	3.38	0.00	0.00	51471	-0.43	41448	-0.08
GACGCTCCTGACGTTCTTAGC	-	TAR1	1.75	18.31	10.46	#N/A	#N/A	#N/A	BnaA09g04420D	TAR1	257	GACGCTCCTGACGTTCTTAGC AGTTCTGCGAGGACTGCAAGAATCGAGCCTAA	DT2	0.00	5.42	0.00	0.00	239430	-1.00	101442	-0.78
GTTGGCCAAAATCCGAGCT	+	TAR1	2.04	24.42	12.00	6.45	13.01	2.02	BnaC03g26840D	Protein TIC 55, chloroplastic	1985	GTTGGCCAAAATCCGAGCT TCGCCAATCGGTTTAACCCTCGGACGTATCAT	DT2	0.00	2.31	0.00	0.00	12179	-0.22	13798	-0.01
GTTCACACCTTGGCCGACAGG	+	TAR1	18.42	311.96	16.94	69.83	615.48	8.81	BnaC02g09010D	Tubulin alpha-5 chain	1247	GTTCACACCTTGGCCGACAGG GAGCCCAGTGT-GAACCGGTAGTACGATCGAC	DT2	0.00	1.07	0.00	0.00	1652	-0.03	2624	-0.55
TCCGAGCTAAGAACGTCAGGA	+	TAR1	5.64	174.13	30.90	0.00	0.67	0.67	BnaC09g19270D	La-related protein 6A	1022	TCCGAGCTAAGAACGT-CAGGA GAGTAGGCTTGATTGTTGGACGTCCAAACTCG	DT2	0.00	0.98	0.00	0.00	4571	0.64	4208	0.68
TATTTAAAGTTTGAGAATAGG	-	TAR1	8.72	35.65	4.09	12.94	55.73	4.31	BnaA06g01690D	CURVATURE THYLAKOID 1C, chloroplastic	1122	TATTTAAAGTTTGAGAATAGG TATCATAAATGTCAAAGTCATGTACTTTGATC	DT2	0.00	4.09	0.00	0.00	58754	-0.47	33630	0.00
CGCGGTTGGCCAAAATCCGAG	+	TAR1	10.50	90.11	8.58	27.48	56.01	2.04	BnaA06g13930D	Probable purine permease 14	717	CGCGGTTGGCCAAAATCCGAG GGCCGCGGCTACCGCTTTT-GGTTCCTCTAAT	DT2	0.00	0.18	0.00	0.00	15550	-1.02	12616	-0.47

TGAGAATAGGTCGAGGACATT	-	TAR1	5.30	64.62	12.20	14.18	90.52	6.38	BnaC03g70870D	unknown	1600	TGAGAATAGGTCGAGGACATT o||||||| || ||||||| TTCGGCTCTTATACATCCCCTGTAACTGTTAC	DT2	0.00	5.06	0.00	0.00	358	-0.03	411	0.46
CTGGAGCTCGGAAACGAGTTC	+	TAR1	40.26	81.04	2.01	92.73	101.54	1.09	BnaCnng73370D	unknown	2166	CTGGAGCTCGGAAACGAGTTC |||o|o|||o||||| GTATGACTTTGAGCTTTTG-TGAATAATGAAC	DT2	0.00	7.20	0.00	0.00	663	0.89	852	-0.03
AGAATAGGTCGAGGACATTGCG	-	TAR1	0.00	27.11	27.11	1.42	106.78	75.05	BnaCnng03470D	Probable mediator of RNA polymerase II transcription subunit 37e	369	AGAATAGGTCGAGGACA-TTGCG || |||||||o||| |||| ACAGGCTCATCCAGCTCTTGTGAACGAGGAAG	DT2	0.00	2.22	0.00	0.00	13013	0.10	7825	-0.55
CGGAGACGTCGGCGGGAATTC	+	TAR1	21.24	47.42	2.23	36.61	108.15	2.95	BnaCnng61690D	Cyclin-dependent kinase G1	177	CGGAGACGTCGGCGGGAATTC |o||||||oo|||||o| GGGAGTCTCTGCAGTTTCCCTTAGGCATGAGA	DT2	0.00	1.60	0.00	0.00	290	0.90	640	-0.46
GGCCGAAGAGGGGAAAGGTTC	+	TAR1	11.17	79.65	7.13	38.65	149.09	3.86	BnaC08g47040D	unknown	371	GGCCGAAGA-GGGGAAAGGTTC |||||||| |||o|||o||| CTTCGGCTTCTCCCCTTTCCAAGGTACACTT	DT2	0.00	3.55	0.00	0.00	127	-1.10	34	-1.09
GGATAGCTGGAGCTCGGAAAC	+	TAR1	25.54	33.74	1.32	81.52	75.29	0.92	BnaC05g14260D	Probable galacturonosyltransferase 11	2461	GGATAGCTGGAGCTCGGAAAC |||| ||| |||||oo|||| TATTCCTACCGAGCTCAAGTTTTTGGAATTGG	DT2	0.00	5.24	0.00	0.00	583	0.98	1381	0.85
CTGTCTTAATCGACCAACACC	-	TAR1	0.00	26.30	26.30	0.00	38.80	38.80	BnaA01g02530D	unknown	269	CTGTCTTAATCGACCAACACC |o||||||| ||||||| TAGTGGCAGCAGTAGC-GGTCGTGGCAGCTCT	DT2	0.00	2.31	0.00	0.00	5501	-0.97	2576	0.40
GAACGTCAGGAGCGTCTTGACA	+	TAR1	3.09	54.08	17.50	0.00	0.25	0.25	BnaC03g37980D	Chaperonin 60 subunit beta 2, chloroplastic	2807	GAACGTCAGGAGCGTCTTGACA |||o||o||o||||| || CAGTC-TGTAGTTCTTGCAGAAACGTTGGCTC	DT2	0.00	3.55	0.00	0.00	2	-0.16	1	0.23
AGAGCCAGGCCTCGATGAGTA	+	TAR1	228.08	255.20	1.12	771.91	533.14	0.69	BnaA07g10020D	Glutamate--glyoxylate aminotransferase 1	1752	AGAGCCAGGCCTCGATGAGTA |||||||| o ||||| TAGGTCTCGGTCCGTGACAACTC-TAAGGACA	DT2	0.00	1.16	0.00	0.00	2159	-1.15	156	-0.95
GATCAGCTTCCGTCCCATATC	-	TAR1	6.07	21.39	3.53	8.16	13.25	1.62	BnaA07g13420D	unknown	661	GATCAGCTTCCGTCCCATATC ||||||||| |||||| CGCTCTAGTCGAAGACAAGGGA-AGGATATGG	DT2	0.00	1.60	0.00	0.00	8994	-0.47	9332	-0.59
CCGATAGAACTCGTTTCCGAG	-	TAR1	156.45	255.46	1.63	181.14	370.66	2.05	BnaA02g22450D	Probable inactive histone-lysine N-methyltransferase SUVR2	3067	CCGATAGAACTCGTTTCCGAG |||o||||||o| ||o o GTAAGGCTGTCTTGAGCGATGGTGTAACTGTT	DT2	0.00	0.09	0.00	0.00	51	1.06	90	-0.27
AAACTTTAAATAGGTAGGACG	+	TAR1	75.35	135.48	1.80	141.44	335.15	2.37	BnaC05g08610D	Sugar transport protein 1	2547	AAACTTTAAATAGGTAGGACG |||||o|||||o|oo |o CGGGTTTGAAGTTTA-CCGTTTCGTAACAGTT	DT2	0.00	5.60	0.00	0.00	10496	0.70	19013	-0.36
CAGGCCTCGATGAGTAGGAGG	+	TAR1	59.62	79.40	1.33	155.58	204.14	1.31	BnaC02g08540D	Stem-specific protein TSJT1	1867	CAGGCCTCGATGAGTAGGAGG |o|||||||| o|o|||o GAACATTCGGAGCTACTGGTTCTCTTGGAGCA	DT2	0.00	2.58	0.00	0.00	42710	0.13	42762	0.74
ACGCAATGTCCTCGACCTATT	+	TAR1	15.51	43.45	2.80	32.48	63.72	1.96	BnaA10g08550D	Thiamine thiazole synthase, chloroplastic	1390	ACGCAATG-TCCTCGACCTATT || ||||| || ||o|||| || AGTTGGGTTACGAGAAGTTGGAGAAGTGTGGC	DT2	0.00	1.78	0.00	0.00	34190	0.04	80064	-0.13
CCGATAGAACTCGTTTCCGAG	-	TAR1	156.45	255.46	1.63	181.14	370.66	2.05	BnaC02g30730D	Probable inactive histone-lysine N-methyltransferase SUVR2	3807	CCGATAGAACTCGTTTCCGAG |||o||||||o| ||o o GTAAGGCTGTCTTGAGCGATGGTGTAACTGTT	DT2	0.00	0.09	0.00	0.00	108	0.84	172	-0.12
CGCGACGTCGCAGACGGCG	-	TAR1	47.38	95.44	2.01	350.64	151.98	0.43	BnaA09g04420D	TAR1	612	CGCGACGTCGCAGACGGCG ||||| ||||||o|| TGTTGGGCTG-AGCATCTGTCGCGGAGCACCA	DT2	0.00	3.91	0.00	0.00	239430	-1.00	101442	-0.78
AAGAGTCGGGGGAAACCCGTC	+	TAR1	115.43	110.68	0.96	232.08	246.67	1.06	BnaA05g09410D	Chlorophyll a-b binding protein 1, chloroplastic	343	AAGAG-TCGGGGGAAACCCGTC |||| ||o||o|||| |o| CGGTTCTCGAGTCCCTTTTGTGTCGGATCCCG	DT2	0.00	0.62	0.00	0.00	185278	-0.12	131779	1.16
GACGCTCCTGACGTTCTTAGC	-	TAR1	1.75	18.31	10.46	#N/A	#N/A	#N/A	BnaAnng36730D	Putative uncharacterized protein ART3	257	GACGCTCCTGACGTTCTTAGC |||||||||||o||||| AGTTCTGCGAGGACTGCAGGAATCGAGCCTAA	DT2	0.00	5.42	0.00	0.00	32584	-0.17	17996	-0.74
GACGCTCCTGACGTTCTTAGC	-	TAR1	1.75	18.31	10.46	#N/A	#N/A	#N/A	BnaAnng22160D	TAR1	1257	GACGCTCCTGACGTTCTTAGC |||||||||||||||||| AGTTCTGCGAGGACTGCAAGAATCGAGCCTAA	DT2	0.00	5.42	0.00	0.00	257765	-1.01	114234	-0.85
AGGAAGCTGATTGGCTGGATC	+	TAR1	74.43	124.57	1.67	136.07	260.72	1.92	BnaC04g34390D	Ribulose bisphosphate carboxylase small chain F1, chloroplastic	836	AGGAAGCTGATTGGCTGGATC |||o|||| o||||o| CCGCTACTTTGACTACGTGACCTGGACTGCCA	DT2	0.00	2.58	0.00	0.00	1052	-1.72	68447	-1.29
AAGGCCGAAGAGGGGAAAGGT	+	TAR1	40.25	51.83	1.29	163.42	151.43	0.93	BnaC03g45990D	Cold-regulated 413 plasma membrane protein 4	117	AAGGCCGAAGAGGGGAAAGGT |||||||||ooo|||| CTCCTTCCTGCTTCTCTTTTTACAATCTCGAA	DT2	0.00	1.24	0.00	0.00	23257	0.14	24229	0.31
GCCTCGATGAGTAGGAGGGCG	+	TAR1	38.73	54.85	1.42	109.75	77.18	0.70	BnaA07g03740D	Cold-regulated 413 plasma membrane protein 1	736	GCCTCGATGAGTAGGAGGGCG o||o||||||||| ||o TCGGTGGTGTTACTCATCCTAGCGTCGTCGGC	DT2	0.00	1.07	0.00	0.00	19875	-0.06	35061	0.47
TTCCATGTGAACGGCACTTGC	+	TAR1	73.01	77.99	1.07	163.72	124.07	0.76	BnaA10g18700D	UDP-glucose 6-dehydrogenase 3	872	TTCCATGTGAACGGCACTTGC |o||| |o|||o||||| GCGCAGGGTTCGCTGGCTCTGAACGAAGTGTC	DT2	0.00	4.35	0.00	0.00	1438	-0.78	1872	-0.80
TAAAGTTTGAGAATAGGTCGA	-	TAR1	11.32	34.87	3.08	18.63	38.80	2.08	BnaA03g11160D	ER membrane protein complex subunit 8/9 homolog	1542	TAAAGTTTGAGAATAGGTCGA ||| ||||||||||| TTTGATTCCAAACTCT-ATACTGCTAATTATC	DT2	0.00	0.98	0.00	0.00	1358	0.29	676	0.19
GCCGTCTGCGACGTCGCGAGAA	+	TAR1	45.58	54.35	1.19	104.25	142.83	1.37	BnaC02g16080D	F-box protein At5g50450	651	GCCGTCTGCGACGTCGCGAGAA o|| || |||||||||||| CTGCTGGAAGCCGCTGCAGCGCTCCTTGCGGC	DT2	0.00	2.67	0.00	0.00	7727	0.91	8707	0.46
ACCAAGATCTGCACCGACGGC	-	TAR1	17.58	123.69	7.04	38.09	209.00	5.49	BnaC08g25640D	U-box domain-containing protein 14	7945	AC-CAAGATCTGCACCGACGGC || ||| ||||||||o|| | AGTTGCGTTGTAGACGTGGTTGGAGAGAGCGA	DT2	0.00	5.78	0.00	0.00	4241	-0.08	4365	0.08
GATAGAACTCGTTTCCGAGCT	-	TAR1	14.20	166.23	11.71	38.77	336.70	8.68	BnaC05g18220D	T-complex protein 11 homolog	4014	GATAGAACTCGTTTCCGAGCT o|||o|||||o||||| TCGGTTATTTTGAGGAGAGTCACGAAACATAT	DT2	0.00	1.16	0.00	0.00	1028	0.04	5321	0.71
AGGAAGCTGATTGGCTGGATC	+	TAR1	74.43	124.57	1.67	136.07	260.72	1.92	BnaA07g19360D	unknown	387	AGGAAGCTGATTGGCTGGATC ||| ||||||o||| || GTCTTCCCTCGAATAATCGACACAGCGCAACG	DT2	0.00	2.22	0.00	0.00	1636	-0.81	1587	0.11
TATGGGACGGAAGCTGATCTC	+	TAR1	119.99	563.81	4.70	182.12	368.24	2.02	BnaC04g38650D	Abscisic-aldehyde oxidase	4210	TATGGGACGGAAGCTGATCTC o||| ||||||||o|| TATGGTACACTGCCTTGGACTGAAGAGGTAGT	DT2	0.00	2.04	0.00	0.00	242	0.69	592	0.85
ACCAAGATCTGCACCGACGGC	-	TAR1	17.58	123.69	7.04	38.09	209.00	5.49	BnaA09g34680D	U-box domain-containing protein 14	2714	AC-CAAGATCTGCACCGACGGC || ||| ||||||||o|| | AGTTGCGTTGTAGACGTGGTTGGAGAGAGCGA	DT2	0.00	5.78	0.00	0.00	507	1.22	1092	0.40
CTCAAACTTCCTTGGCCTAAA	-	TAR1	18.42	29.66	1.61	26.60	49.83	1.87	BnaC02g08820D	Aspartate aminotransferase, cytoplasmic	3372	CTCAAACTTCCTTGGCCTAAA ||||| ||||o|||| AACCAAGTTGTAGGAATCGGTTTTTCTATGC	DT2	0.00	1.42	0.00	0.00	748	0.08	1147	0.02
ATTGCCTCAAACTTCCTTGGC	-	TAR1	62.22	86.00	1.38	382.64	140.59	0.37	BnaA10g17340D	2-hydroxyacyl-CoA lyase	1403	ATTGCCTCAAACTTCCTTGGC |o|o||||| |||| |||| ACAATGATGGAGTT-GAAGGTACCGCGACTTA	DT2	0.00	1.69	0.00	0.00	3693	0.29	3325	0.34
TTTCGAAGTTCGCGCATAAGC	-	TAR1	28.22	58.56	2.08	131.51	111.70	0.85	BnaA03g39180D	Actin-depolymerizing factor 5	145	TTTCGAAGTTCGCGCATAAGC o|||||||| ||||| GTCGGAAGCTGCAA-CGCATATTCTAGAAACG	DT2	0.00	0.53	0.00	0.00	91	0.95	58	-0.13
CAGGCCTCGATGAGTAGGAGG	+	TAR1	59.62	79.40	1.33	155.58	204.14	1.31	BnaAnng08700D	Stem-specific protein TSJT1	1768	CAGGCCTCGATGAGTAGGAGG |o|||||||| o|o|||o GAACATTCGGAGCTACTGGTTCTCTTGGAGCA	DT2	0.00	2.58	0.00	0.00	76196	0.07	92666	0.70
CTGAGGACGCTTCTCCAGACT	-	TAR1	19.40	29.77	1.53	49.58	45.93	0.93	BnaC02g02570D	unknown	1509	CTGAGGACGCTTCTCCAGACT ||||||||| |||||| CCACGTCTCCT-CGCAGAGATCTGACATCTAT	DT2	0.00	1.87	0.00	0.00	3856	-0.24	6573	-0.04

TTCCATGTGAACGGCACTTGC	+	TAR1	73.01	77.99	1.07	163.72	124.07	0.76	BnaCnng71670D	31 kDa ribonucleoprotein, chloroplastic	1366	TTCCATGTGAACGGCACTTGC ||||o||||||||| | GGCTTAGGTGCACTTGCCG-GACAGAGCGCCA	DT2	0.00	2.67	0.00	0.00	7724	-1.30	3373	-1.23
ATTGCCTCAAACTTCCTTGGCC	-	TAR1	4.40	32.88	7.47	74.00	119.08	1.61	BnaC09g40570D	2-hydroxyacyl-CoA lyase	1394	ATTGCCTCAAACTTCCTTGGCC |o|o||||| ||||||| ACAATGATGGAGTT-GAAGGTACCGCGACTTA	DT2	0.00	1.69	0.00	0.00	5556	0.31	6178	0.27
CGATAGAACTCGTTTCCGAGC	-	TAR1	71.55	136.47	1.91	44.75	238.06	5.32	BnaC05g18220D	T-complex protein 11 homolog	4015	CGATAGAACTCGTTTCCGAGC |o||o|||| |o|||| GTCGGTTATTTTGAGGAGAGTCACGAAACATA	DT2	0.00	1.07	0.00	0.00	1028	0.04	5321	0.71
GGTTAGTCGATCCTAAGAGTC	+	TAR1	53.33	197.69	3.71	146.20	378.64	2.59	BnaA08g11840D	Probable disease resistance protein At4g33300	3113	GGTTAGTCGATCCTAAGAGTC |||||o| ||||||| ||| ATATCCAATTA-CTAGGATGAGCAGCTCGGTT	DT2	0.00	0.09	0.00	0.00	5912	0.01	8859	0.28
CAGGCCTCGATGAGTAGGAGG	+	TAR1	59.62	79.40	1.33	155.58	204.14	1.31	BnaC05g28700D	Stem-specific protein TSJT1	1500	CAGGCCTCGATGAGTAGGAGG |o||||||||o|o||o GAACATTCGGAGCTACTGGTTCTCTTGGAGCA	DT2	0.00	2.58	0.00	0.00	177	-0.05	1096	0.51
TTTCGAAGTTCGCGCATAAGC	-	TAR1	28.22	58.56	2.08	131.51	111.70	0.85	BnaC03g46510D	Actin-depolymerizing factor 5	1065	TTTCGAAGTTCGCGCATAAGC o||||||||||||| GTCGGAAGCTGCAA-CGCATATTCTAGAAACG	DT2	0.00	0.53	0.00	0.00	1669	0.97	1200	-0.06
GGCCGAAGAGGGGAAAGGTTC	+	TAR1	11.17	79.65	7.13	38.65	149.09	3.86	BnaCnng04230D	Photosystem I chlorophyll a/b-binding protein 3-1, chloroplastic	793	GGCCGAAGAGGG-GAAAGGTTC |||o|||||||||| AGCTCCTGTTTCTCCCACATTCCCAGACGGGT	DT2	0.00	0.09	0.00	0.00	145090	-0.27	5799	-0.70
GCCGTCTGCGACGTCGCGAGA	+	TAR1	365.18	1204.80	3.30	1283.32	2941.70	2.29	BnaC02g16080D	F-box protein At5g50450	651	GCCGTCTGCGACGTCGCGAGA o|||||||||||||| CTGCTGGAAGCCGCTGCAGCGCTCCTTGCGGC	DT2	0.00	2.67	0.00	0.00	7727	0.91	8707	0.46
TGTCGGCCAAGGTGTGAACTC	-	TAR1	32.29	149.93	4.64	148.96	290.43	1.95	BnaA04g08110D	Aspartic proteinase PCS1	934	TGTCGGCCAAG-GTGTGAACTC o|||o|||||||||| CGGTGCAGCTGGTTCACTCACTTAAGCCTTGG	DT2	0.00	0.09	0.00	0.00	2668	-1.34	8138	-0.73
CAATGTCCTCGACCTATTCTC	+	TAR1	76.06	128.34	1.69	134.24	250.33	1.86	BnaC09g41340D	Glutamine synthetase leaf isozyme, chloroplastic	2485	CAATGTCCTCGACCTATTCTC ||||||||||o||| ACGAGTCACAGG-GCTGGTTGAGATTAGCTAC	DT2	0.00	0.09	0.00	0.00	3389	-1.45	5095	-0.45
CACCAAGATCTGCACCGACGGC	-	TAR1	2.61	29.45	11.30	15.19	131.87	8.68	BnaC08g46150D	TAR1	1789	CACCAAGATCTGCACCGACGGC ||||||||||||||||||| GATGGTGGTTCTAGACGTGGCTGCCGGCGAGG	DT3	0.00	0.45	0.00	0.00	143979	-1.14	60510	-0.80
TCGACCAACACCCTTTGTGGG	-	TAR1	3.46	52.42	15.15	26.46	89.84	3.40	BnaA07g12810D	Heme oxygenase 1, chloroplastic	952	TCGACCAACACCCTTTGTGGG ||||||| || |o| |||| AGTAAGCTGGTGGTCGCGA-CACCCGCTTCAT	DT3	0.00	0.05	0.00	0.00	5165	0.09	6234	-0.16
ATTCAACGAGTTCACACCTTG	+	TAR1	54.98	76.67	1.39	279.65	156.88	0.56	BnaC07g20450D	C2-DOMAIN ABA-RELATED 11	661	ATTCAACGAGTTCACACCTTG ||||||| ||o|||| ||| GGGCTAAGTTG-TCGCGTGTCGAAGTCGGTGT	DT3	0.00	1.45	0.00	0.00	242	-0.78	402	-1.08
CACCAAGATCTGCACCGACGG	-	TAR1	126.72	262.92	2.07	283.96	459.48	1.62	BnaC02g36110D	unknown	388	CACCAAGATCTGCACCGACGG ||||||||||||||||o| GATGGTGGTTCTAGACGTGGCTGTCGGTGAGG	DT3	0.00	0.45	0.00	0.00	25737	-1.12	12547	-0.80
CGGTTGGCCAAAATCCGAGCT	+	TAR1	15.20	50.45	3.32	20.51	28.58	1.39	BnaC03g26820D	Protein TIC 55, chloroplastic	1977	CGGTTGGCCAAAATCCGAGCT ||||o||||| | |||o CATCGCCAATCGGTTTAACCCTCGGACGTATC	DT3	0.00	3.90	0.00	0.00	10972	-0.21	13105	0.00
CACCAAGATCTGCACCGACGG	-	TAR1	126.72	262.92	2.07	283.96	459.48	1.62	BnaC08g46150D	TAR1	1789	CACCAAGATCTGCACCGACGG ||||||||||||||||||| GATGGTGGTTCTAGACGTGGCTGCCGGCGAGG	DT3	0.00	0.45	0.00	0.00	143979	-1.14	60510	-0.80
CAGTTGGGCACCGTAACCCGG	-	TAR1	34.13	50.77	1.49	48.64	103.11	2.12	BnaA05g23870D	Monothiol glutaredoxin-S15, mitochondrial	385	CAGTTGGGCACCGTAACCCGG ||||o|||o|||||oo AATTGTCAATCC-TAGTATTGGGTTTTCCGTA	DT3	0.00	1.23	0.00	0.00	2049	-0.34	1914	-0.08
ATTCAACGAGTTCACACCTTG	+	TAR1	54.98	76.67	1.39	279.65	156.88	0.56	BnaC02g33470D	Protein C2-DOMAIN ABA-RELATED 11	1375	ATTCAACGAGTTCACACCTTG ||||||| ||o|||| ||| GGGCTAAGTTG-TCGCGTGTCGAAGTCGGTGT	DT3	0.00	1.45	0.00	0.00	822	-0.35	470	-1.07
CGTGGTGTCCGGTGCATTCCC	+	TAR1	21.08	57.98	2.75	96.27	105.81	1.10	BnaC03g44110D	Chlorophyll a-b binding protein 151, chloroplastic	374	CGTGGTGTCCGGTGCATTCCC ||o|| ||||| |||| GTCGGCATCAGAGGCCCCATAAGAGGTCAATC	DT3	0.00	0.05	0.00	0.00	291224	-0.22	195401	0.08
TCTCGCGACGTCGCAGACGGCG	-	TAR1	306.51	451.31	1.47	1402.23	1422.22	1.01	BnaC02g04080D	unknown	593	TCTCGCGACGTCGCAGACGGCG || ||||| |||||||| GTCGAGTGCGCGGCCGCGTCTGCGGCGCTAGT	DT3	0.00	0.73	0.00	0.00	22	-0.49	17	-0.04
GTTCTTAGCTCGGATTTTGGCC	-	TAR1	20.19	49.70	2.46	0.00	0.06	0.06	BnaA03g55850D	26S proteasome non-ATPase regulatory subunit 12 homolog A	1367	GTTCTTAGCT-CGGATTTTGGCC o||||o||| |o|||o||o|| TTACTAAGAGTCGAAGTCTAGAAGTGGTCGGA	DT3	0.00	0.41	0.00	0.00	292	0.91	457	0.62
TATTTAAAGTTTGAGAATAGG	-	TAR1	8.72	35.65	4.09	12.94	55.73	4.31	BnaC08g47760D	AB hydrolase superfamily protein YfhM	899	TATTTAAAGTTTGAGAATAGG |||||| ||oo|o|||| AAAAAAAAATTTAAAGTTTTTATCAAAGTTTT	DT3	0.00	0.05	0.00	0.00	39	-0.96	29	-0.69
GCGGTCGCTGCAAAACCTAGG	+	TAR1	29.72	152.11	5.12	63.89	287.58	4.50	BnaA04g18820D	Nitrile-specifier protein 2	1332	GCGGTCGCTGCAAAACCTAGG o|||o||o|||||||o GTAGTGCCGGCGGC-TTTTGCATCTCACATCT	DT3	0.00	0.86	0.00	0.00	789	-2.53	158	-0.94
AACCCGTCTGATAGCGCTTATG	+	TAR1	50.71	74.37	1.47	134.66	178.54	1.33	BnaA09g08380D	Probable protein S-acyltransferase 23	5674	AACCCGTCTGATAG-CGCTTATG |||||||o|||||o||||o GTGTTTGGGCAGGCTACCTGTTAATATAGTAT	DT3	0.00	2.00	0.00	0.00	134	0.89	172	-0.25
AACCCGTCTGATAGCGCTTATG	+	TAR1	50.71	74.37	1.47	134.66	178.54	1.33	BnaA09g52690D	Probable protein S-acyltransferase 23	4011	AACCCGTCTGATAG-CGCTTATG |||||||o|||||o||||o GTGTTTGGGCAGGCTACCTGTTAATATAGTAT	DT3	0.00	2.00	0.00	0.00	214	0.86	283	-0.28
CGTGGTGTCCGGTGCATTCCC	+	TAR1	21.08	57.98	2.75	96.27	105.81	1.10	BnaC07g24660D	Chlorophyll a-b binding protein 36, chloroplastic	384	CGTGGTGTCCGGTGCATTCCC ||o|| ||||| |||| GTTGGCATCAGAGGCCCCATAAGTGGTCAATC	DT3	0.00	0.05	0.00	0.00	197988	-0.38	124155	-0.61
ACGCTCCTGACGTTCTTAGCT	-	TAR1	10.51	18.57	1.77	0.00	0.12	0.12	BnaAnng22160D	TAR1	1256	ACGCTCCTGACGTTCTTAGCT ||||||||||||||||||| GTTCTGCGAGGACTGCAAGAATCGAGCCTAAA	DT3	0.00	1.63	0.00	0.00	257765	-1.01	114234	-0.85
AAACTTTAAATAGGTAGGACG	+	TAR1	75.35	135.48	1.80	141.44	335.15	2.37	BnaAnng07730D	unknown	1978	AAACTTTAAA-TAGGTAGGACG ||||o||||||oo||o TTTGTTTCAAGTTTTATCCATTTTGTATCTTT	DT3	0.00	0.14	0.00	0.00	489	-0.33	1318	0.04
GTTCGCCGTCTGCGACGTCGC	+	TAR1	29.87	302.31	10.12	74.39	413.97	5.57	BnaC03g38850D	Transcription factor TCP4	633	GTTCGCCGTCTGCGACGTCGC |||||| |o| ||||||| GCGGCAAGCGACGGAGGCTGCATCGCGCCGCA	DT3	0.00	0.73	0.00	0.00	3079	0.71	3165	0.84
GATCCTAAGAGTCGGGGGAAAC	+	TAR1	38.38	61.22	1.60	44.84	145.48	3.24	BnaCnng49000D	Geranylgeranyl diphosphate reductase, chloroplastic	1119	GATCC-TAAGAGTCGGGGGAAAC |||| ||o|o||||o||| TGGGTAGGCATTTTTAGCCCTCTGTGCAGTAG	DT3	0.00	0.41	0.00	0.00	51471	-0.43	41448	-0.08
AATTCCGGAAAGAGTTATCTT	+	TAR1	39.22	85.38	2.18	102.58	130.26	1.27	BnaC09g45480D	unknown	485	AATTCCGGAAAGAGTTATCTT ||||| |o|||||o|||o| CACTTTAAGCCTTTTCTTTGTAGGAGCATGCG	DT3	0.00	0.41	0.00	0.00	10796	-0.43	6420	0.17
TTAGCGCGCAGTTGGGCACCG	-	TAR1	5.35	58.26	10.89	11.87	135.48	11.42	BnaA04g08570D	Ribulose bisphosphate carboxylase small chain 1A, chloroplastic	1072	TTAGCGCGCAGTTGGGCACCG oo|o|||| |o||oo||||| AGAAGGTTGCGC-TTAATTCGTGGCCACTTCG	DT3	0.00	1.54	0.00	0.00	329765	-1.19	100342	-0.88
CGGTTGGCCAAAATCCGAGCT	+	TAR1	15.20	50.45	3.32	20.51	28.58	1.39	BnaA03g22780D	Protein TIC 55, chloroplastic	1983	CGGTTGGCCAAAATCCGAGCT ||||o||||| | |||o CATCGCCAATCGGTTTAACCCTCGGACGTATC	DT3	0.00	3.90	0.00	0.00	13773	-0.21	13394	-0.07
GCATGTCAAGACGCTCCTGACG	-	TAR1	0.00	25.25	25.25	35.81	23.33	0.65	BnaC05g09210D	Glyceraldehyde-3-phosphate dehydrogenase GAPA2, chloroplastic	567	GCATGTCAAGACGCTCCTGACG |||| ||||||| |||||| CGGTCGTAGAGTTCTTCAAGGACGGCTAGGAT	DT3	0.00	0.86	0.00	0.00	95743	-1.27	48838	-0.64
ATAGAACTCGTTTCCGAGCTC	-	TAR1	48.88	160.72	3.29	160.84	277.69	1.73	BnaAnng22010D	Heat shock protein 90-5, chloroplastic	912	ATAGAACTCGTTTCCGAGCTC ||o||||o|||||| AGAGTATTTAGAACAAGGGGTCGAGTCGGCCC	DT3	0.00	0.05	0.00	0.00	5	-0.63	13	-1.13

GATCTCCCGTGTGTTACCGCA	+	TAR1	28.71	186.86	6.51	44.09	119.75	2.72	BnaA01g26430D	Polyol transporter 5	5087	GATCTCCCGTGTGTTACCG-CA ||o||||||o||o||||| TTCGCTGGAGGGAACGCAGAGGCCGTTCTTTC	DT3	0.00	0.32	0.00	0.00	2772	0.37	1660	0.48
ACCCGTCTGATAGCGCTTATG	+	TAR1	23.46	95.40	4.07	122.66	166.83	1.36	BnaA01g30450D	Probable protein phosphatase 2C 38	1641	ACCCGTCTGATAGCGCTTATG ||||||||||o|||| GTATTCGGCAGACTA-CGTTTATACTCTTTGA	DT3	0.00	0.05	0.00	0.00	807	0.45	1155	0.42
TCTCGCGACGTCGCAGACGGCG	-	TAR1	306.51	451.31	1.47	1402.23	1422.22	1.01	BnaA06g22540D	unknown	601	TCTCGCG-ACGTCGCAGACGGCG ||||||||o||||||| TATAGAGGGCATGCGGCTGCTGCCGCTCAAGC	DT3	0.00	2.63	0.00	0.00	492	-0.68	244	-0.32
AAGAGCCAGGCCTCGATGAGT	+	TAR1	29.79	32.74	1.10	75.04	64.03	0.85	BnaA08g15450D	BEL1-like homeodomain protein 2	2204	AAGAGCCAGGCCTCGATGAGT ||||||o|||||o| GAGCTTCTCGGTTCG-AGCTTCCTATAATTGC	DT3	0.00	0.23	0.00	0.00	1214	0.17	1051	1.06
GCCTCGATGAGTAGGAGGGCG	+	TAR1	38.73	54.85	1.42	109.75	77.18	0.70	BnaC03g57550D	unknown	517	GCCTCGATGAGTAGGAGGGCG ||||||||o|o||o|||| GGGAAGGAGCTACTTTTTCTTCCGCCGCCGCA	DT3	0.00	0.59	0.00	0.00	5979	-0.15	4557	-0.17
TCTTAGCTCGGATTTTGGCCA	-	TAR1	1.80	38.19	21.27	0.00	0.12	0.12	BnaC01g28840D	Splicing factor U2af large subunit B	767	TCTTA-GCTCGGATTTTGGCCA |o|||||||||o|||o|| ATGCGGATACGAGCCTAGAACTGGATGCAAGT	DT3	0.00	1.95	0.00	0.00	815	0.16	1378	0.03
CGGCCGTCGGTGCAGATCTTGG	+	TAR1	871.20	764.03	0.88	1259.97	1756.44	1.39	BnaC05g11930D	Pyrophosphate-energized vacuolar membrane proton pump 1	2502	CGGCCGTCGGTGCAGATCTTGG o|||||||| |||||||o TACCTTC-GCAGCCACCTCTAGAACTGCGTGC	DT3	0.00	1.04	0.00	0.00	7046	0.31	11121	0.43
TGAGAATAGGTCGAGGACATT	-	TAR1	5.30	64.62	12.20	14.18	90.52	6.38	BnaA09g14090D	Phosphatidylinositol 4-phosphate 5-kinase 8	2356	TGAGAATAGGTCGAGGACATT ||||||||||o|||o| CAGCACTCTT-TCCATCTTCTATGACGGTGAA	DT3	0.00	0.05	0.00	0.00	394	0.61	566	0.35
ACGGAATCGAGAGCTCCAAGT	+	TAR1	1236.13	1339.37	1.08	2708.65	2249.48	0.83	BnaC09g37030D	Phosphoinositide phosphatase SAC4	6586	ACGGAATCGAGAGCTCCAAGT ||o||||||||||oo ATGTTGTCTTAACTCT-GAAGTTTGTATTTGT	DT3	0.00	0.91	0.00	0.00	380	0.51	699	0.08
ATTGCCTCAAACTTCCTTGGC	-	TAR1	62.22	86.00	1.38	382.64	140.59	0.37	BnaAnng22160D	TAR1	353	ATTGCCTCAAACTTCCTTGGC |||||||||||||||||| ACAATAACGGAGTTTGAAGGAACCGGATTTGC	DT3	0.00	1.00	0.00	0.00	257765	-1.01	114234	-0.85
TGTATTCAACGAGTTCACACC	+	TAR1	35.11	379.00	10.80	77.07	643.71	8.35	BnaC08g20820D	Peroxidase 34	3919	TGTATTCAACGAGTTCACACC o|||||||||||||| GATTGCTTTAGTTGCTCAAGT-TGGTGTAGAA	DT3	0.00	0.45	0.00	0.00	9451	-1.42	10030	-1.21
ATTGCCTCAAACTTCCTTGGCC	-	TAR1	4.40	32.88	7.47	74.00	119.08	1.61	BnaAnng22160D	TAR1	353	ATTGCCTCAAACTTCCTTGGCC |||||||||||||||||||| ACAATAACGGAGTTTGAAGGAACCGGATTTGC	DT3	0.00	1.00	0.00	0.00	257765	-1.01	114234	-0.85
ATAGAACTCGTTTCCGAGCTC	-	TAR1	48.88	160.72	3.29	160.84	277.69	1.73	BnaC09g22180D	Heat shock protein 90-5, chloroplastic	3772	ATAGAACTCGTTTCCGAGCTC ||||| |||o|||||| AGAGTATCTAGAACAAGGGGTCGAGTCGGCCC	DT3	0.00	1.72	0.00	0.00	1202	-0.77	1696	-1.27
CATCCCACGGAATCGAGAGCT	+	TAR1	74.64	78.81	1.06	197.83	155.07	0.78	BnaA04g04090D	Uridine 5'-monophosphate synthase	1988	CATCCCACGGAATCGAGAGCT ||o|||o||||o|o|| GTTGGTGGAGTGTCTTAGTTTT-GATGACTCT	DT3	0.00	1.91	0.00	0.00	471	-0.27	893	-0.13
GTCGGCTGTGCACCCGTGAGG	-	TAR1	1.71	20.77	12.16	1.42	49.47	34.77	BnaAnng22160D	TAR1	2101	GTCGGCTGTGCACCCGTGAGG |||||||||||||||||| CAGCCAGCCGACACGTGGGCACTCCCTAGGTC	DT3	0.00	1.50	0.00	0.00	257765	-1.01	114234	-0.85
AGCTCGGATTTTGGCCAACCGC	-	TAR1	46.60	75.27	1.62	379.96	39.84	0.10	BnaA09g04420D	TAR1	239	AGCTCGGATTTTGGCCAACCGC |||||||||||||||||| AGAATCGAGCCTAAAACCGGTTGGCGCACGCC	DT3	0.00	0.45	0.00	0.00	239430	-1.00	101442	-0.78
ATAGAACTCGTTTCCGAGCTC	-	TAR1	48.88	160.72	3.29	160.84	277.69	1.73	BnaA09g19450D	Heat shock protein 90-5, chloroplastic	3720	ATAGAACTCGTTTCCGAGCTC ||||| |||o|||||| AGAGTATCTAGAACAAGGGGTCGAGTCGGCCC	DT3	0.00	1.72	0.00	0.00	651	-0.81	1452	-1.36
TCGAGGATATGGGACGGAAGCT	+	TAR1	28.59	542.56	18.98	44.06	384.72	8.73	BnaC07g24760D	50S ribosomal protein L12-1, chloroplastic	231	TCGAGGATATGGGACGGAAGCT o||||||||||||||| AGCTGCCGCCTATACCCTGCCTCC-ACCCAAC	DT3	0.00	2.13	0.00	0.00	5886	-0.82	2379	-0.49
ATAGAACTCGTTTCCGAGCTC	-	TAR1	48.88	160.72	3.29	160.84	277.69	1.73	BnaC07g22680D	Heat shock protein 90-5, chloroplastic	3658	ATAGAACTCGTTTCCGAGCTC |||o|||||o|||||| AGAGTATTTAGAACAAGGGGTCGAGCCGGCCT	DT3	0.00	0.05	0.00	0.00	763	0.10	1059	-1.04
CACCAAGATCTGCACCGACGG	-	TAR1	126.72	262.92	2.07	283.96	459.48	1.62	BnaA09g04420D	TAR1	1793	CACCAAGATCTGCACCGACGG ||||||||||||||| GATGGTGGTTCTAGACGGGGCTGCCGGCGAGG	DT3	0.00	0.45	0.00	0.00	239430	-1.00	101442	-0.78
CGTGGTGTCCGGTGCATTCCC	+	TAR1	21.08	57.98	2.75	96.27	105.81	1.10	BnaA02g29010D	Chlorophyll a-b binding protein 36, chloroplastic	381	CGTGGTGTCCGGTGCATTCCC |||o|||||||||| GTCGGCATCAGAGGCCCCATAAGAGGCCAATC	DT3	0.00	0.05	0.00	0.00	544923	-0.38	395149	-0.03
TCGAGGATATGGGACGGAAGC	+	TAR1	43.26	1122.33	25.94	111.30	928.51	8.34	BnaC07g24760D	50S ribosomal protein L12-1, chloroplastic	231	TCGAGGATATGGGACGGAAGC o|||||||||||||| AGCTGCCGCCTATACCCTGCCTCCACCCAACG	DT3	0.00	2.13	0.00	0.00	5886	-0.82	2379	-0.49
TGATCTCCCGTGTGTTACCGC	+	TAR1	25.95	64.56	2.49	48.99	55.05	1.12	BnaC02g03410D	IQ-DOMAIN 1	2068	TGATCTCCCGTGTGTTACCGC o||||||||||||o| GGTAGCAAGAGGACACACCATGGTGGTGGCGA	DT3	0.00	1.72	0.00	0.00	2322	-0.09	3269	-0.65
CGCCCCGAATCGATCGGCGGA	-	TAR1	28.94	56.58	1.95	34.73	147.85	4.26	BnaA04g09380D	Vesicle transport v-SNARE 11	1258	CGCCCCGAATCGATCGGCGGA |||||||||||| || TCAAGCTGGG-TTAGCTAGCCAACTGTAGTAG	DT3	0.00	0.41	0.00	0.00	2923	-0.42	4783	0.29
CGCTCCTGACGTTCTTAGCTC	-	TAR1	48.70	101.28	2.08	0.00	0.48	0.48	BnaC03g11200D	Adenylate kinase isoenzyme 6 homolog	113	CGCTCCTGACGTTCTTAGCTC ||||o| |o||||||| || ACAATCGAGGGCGGTAAGAATC-AGAAACCTT	DT3	0.00	1.32	0.00	0.00	180	-0.40	826	-0.44
AGCTCGGATTTTGGCCAACCGC	-	TAR1	46.60	75.27	1.62	379.96	39.84	0.10	BnaAnng22160D	TAR1	1239	AGCTCGGATTTTGGCCAACCGC |||||||||||||||||| AGAATCGAGCCTAAAACCGGTTGGCGCACGCC	DT3	0.00	0.45	0.00	0.00	257765	-1.01	114234	-0.85
CGGCCGTCGGTGCAGATCTTG	+	TAR1	48.72	72.47	1.49	95.81	127.91	1.34	BnaC05g11930D	Pyrophosphate-energized vacuolar membrane proton pump 1	2502	CGGCCGTCGGTGCAGATCTTG o|||||||| ||||||| TACCTTC-GCAGCCACCTCTAGAACTGCGTGC	DT3	0.00	1.04	0.00	0.00	7046	0.31	11121	0.43
GATCTCCCGTGTGTTACCGCA	+	TAR1	28.71	186.86	6.51	44.09	119.75	2.72	BnaC01g33830D	Polyol transporter 5	2850	GATCTCCCGTGTGTTACCG-CA ||o||||||o||o||||| TTCGCTGGAGGGAACGCAGAGGCCGTTCTTTC	DT3	0.00	0.32	0.00	0.00	3720	0.10	2823	-0.09
AAGAGCCAGGCCTCGATGAGT	+	TAR1	29.79	32.74	1.10	75.04	64.03	0.85	BnaC04g25580D	Beta-hexosaminidase 1	3542	AAGAGCCAGGCCTCGATGAGT |||||||||o||||| ATCGTTCTCGGTCCAGGTCTCC-CACCAGAAG	DT3	0.00	1.82	0.00	0.00	437	0.55	397	0.04
GCGGTCGCTGCAAAACCTAGG	+	TAR1	29.72	152.11	5.12	63.89	287.58	4.50	BnaCnng21640D	Nitrile-specifier protein 2	1239	GCGGTCGCTGCAAAACCTAGG o||o||o|||||||o GTAGTGCCGGCGGC-TTTTGCATCTCACATCT	DT3	0.00	0.86	0.00	0.00	343	-1.54	136	0.00
TTCCATGTGAACGGCACTTGC	+	TAR1	73.01	77.99	1.07	163.72	124.07	0.76	BnaCnng47960D	60S ribosomal protein L10a-3	3124	TTCCATGTG-AACGGCACTTGC ||||||||||||oo| CTAAAGGTACACTTTTCCGTGCGTGCGGTAGA	DT3	0.00	0.82	0.00	0.00	3211	-0.21	3247	0.25
GTCGGCTGTGCACCCGTGAGG	-	TAR1	1.71	20.77	12.16	1.42	49.47	34.77	BnaA09g04420D	TAR1	1101	GTCGGCTGTGCACCCGTGAGG |||||||||||||||||| CAGCCAGCCGACACGTGGGCACTCCCTAGGTC	DT3	0.00	1.50	0.00	0.00	239430	-1.00	101442	-0.78
CCGGTTCCGGAATTTTAACCG	-	TAR1	19.50	23.29	1.19	53.55	45.95	0.86	BnaA08g00450D	RuBisCO large subunit-binding protein subunit beta, chloroplastic	4241	CCGGTTCCGGAATTTTAACCG ||||||o|||||||| GAACGGCCAACGTCGTAACATTGGCTTGAAGT	DT3	0.00	2.41	0.00	0.00	1782	0.23	1832	-0.68
AAGGCCGAAGAGGGGAAAGGT	+	TAR1	40.25	51.83	1.29	163.42	151.43	0.93	BnaAnng19780D	Long chain base biosynthesis protein 1b	3306	AAGGCCGAAGAGGGGA-AAGGT ||||||||o|||||| GCCCTGCCGTCTTCTCTCCTGTTCCAAAAAAA	DT3	0.00	2.00	0.00	0.00	4369	0.07	728	-0.17
ACGCTCCTGACGTTCTTAGCT	-	TAR1	10.51	18.57	1.77	0.00	0.12	0.12	BnaAnng36730D	Putative uncharacterized protein ART3	256	ACGCTCCTGACGTTCTTAGCT ||||||||||o||||||| GTTCTGCGAGGACTGCAGGAATCGAGCCTAAA	DT3	0.00	1.63	0.00	0.00	32584	-0.17	17996	-0.74

GTTGGCCAAAATCCGAGCTAAG	+	TAR1	6.37	31.77	4.99	4.02	35.32	8.78	BnaC01g36130D	Lectin-like protein At3g16530	855	GTTGGCCAAAATCCGAGCTAAG ||o|||||| |||o|o||o CTTTGAATCGGTTTT-GGCTTGGTTTTTGGTT	DT3	0.00	0.50	0.00	0.00	4899	0.07	357	-1.85
AGCTCGGATTTTGGCCAACCG	-	TAR1	52.80	148.67	2.82	378.81	63.63	0.17	BnaAnng22160D	TAR1	1239	AGCTCGGATTTTGGCCAACCG ||||||||||||||||||| AGAATCGAGCCTAAAACCGGTTGGCGCACGCC	DT3	0.00	0.45	0.00	0.00	257765	-1.01	114234	-0.85
ACGCTCCTGACGTTCTTAGCT	-	TAR1	10.51	18.57	1.77	0.00	0.12	0.12	BnaA09g04420D	TAR1	256	ACGCTCCTGACGTTCTTAGCT ||||||||||||||||||| GTTCTGCGAGGACTGCAAGAATCGAGCCTAAA	DT3	0.00	1.63	0.00	0.00	239430	-1.00	101442	-0.78
CCCGGGCTTAGGTCACCACCT	-	TAR1	58.29	25.16	0.43	43.78	49.41	1.13	BnaA02g27980D	Thiamine thiazole synthase, chloroplastic	2263	CCCGGGCTTAGGTCACC-ACCT ||||||||||||||| TTCGAGGCCCGAATCCAGAGGCTGTATCCTAG	DT3	0.00	1.77	0.00	0.00	96019	-0.45	80064	-0.23
GCACTTGCACATGGGTTAGTC	+	TAR1	11.88	45.74	3.85	20.56	90.87	4.42	BnaC07g39400D	Mediator-associated protein 1	941	GCACTTGCACATGGGTTAGTC |||||o||| |o|oo|o|| TTGGCGTGAATGTG-ATCTGAGTAGGTTTGGG	DT3	0.00	1.72	0.00	0.00	158	1.18	385	0.32
TGAACGGCACTTGCACATGGG	+	TAR1	92.95	137.53	1.48	249.60	236.34	0.95	BnaA01g02530D	unknown	681	TGAACGGCACTTGCACATGGG o|| |o|||||||||o| TGGTGCTAGTCGTGAACTTGAACTCCGGCTCT	DT3	0.00	2.27	0.00	0.00	5501	-0.97	2576	0.40
CGTGGTGTCCGGTGCATTCCC	+	TAR1	21.08	57.98	2.75	96.27	105.81	1.10	BnaA09g02120D	Chlorophyll a-b binding protein 36, chloroplastic	567	CGTGGTGTCCGGTGCATTCCC |||o||||||||| GTCGGCATCAGAGGCCCCATAAGTGGCCAATC	DT3	0.00	0.05	0.00	0.00	281901	-0.39	186238	-0.53
GTCGGCCAAGGTGTGAACTCG	-	TAR1	6.92	52.47	7.58	4.08	91.32	22.39	BnaC09g36950D	Probable disease resistance protein RPP1	157	GTCGGCCAAGGTGTGAACTCG || |||||||o o||||| GCGTCA-CCGGTTCCGAGCTTGATCCCCTCCC	DT3	0.00	1.00	0.00	0.00	54	-1.35	109	-0.07
AGAGGCATCGGGGACGCAATG	+	TAR1	19.59	70.58	3.60	23.71	101.14	4.27	BnaC02g48620D	Serine/threonine protein phosphatase 2A 57 kDa regulatory subunit B' iota isoform	941	AGAGGCATCGGGGACGCAATG ||||||||o|||| ||| CGCAGCTCCGT-GCCTCTGCACTACTTGAATT	DT3	0.00	2.45	0.00	0.00	1263	0.06	1054	0.46
GTCGGCTGTGCACCCGTGAGG	-	TAR1	1.71	20.77	12.16	1.42	49.47	34.77	BnaAnng36730D	Putative uncharacterized protein ART3	1101	GTCGGCTGTGCACCCGTGAGG ||||||||||||||||||| CAGCCAGCCGACACGTGGGCACTCCCTAGGTC	DT3	0.00	1.50	0.00	0.00	32584	-0.17	17996	-0.74
TTTAAAGTTTGAGAATAGGTC	-	TAR1	16.77	72.02	4.29	27.29	124.88	4.58	BnaC01g42660D	Casein kinase II subunit alpha-2	2278	TTTA-AAGTTTGAGAATAGGTC |o|| |||||||o||||o| TCAAGATGTTCAAACTTTTATCTACTTTCGTC	DT3	0.00	0.82	0.00	0.00	3956	0.18	4929	0.14
AGCTCGGATTTTGGCCAACCG	-	TAR1	52.80	148.67	2.82	378.81	63.63	0.17	BnaA09g04420D	TAR1	239	AGCTCGGATTTTGGCCAACCG ||||||||||||||||||| AGAATCGAGCCTAAAACCGGTTGGCGCACGCC	DT3	0.00	0.45	0.00	0.00	239430	-1.00	101442	-0.78
CGTCCCATATCCTCGAGAGGA	-	TAR1	172.94	326.00	1.89	311.97	170.30	0.55	BnaA09g32850D	Coatomer subunit gamma	478	CGTCCCATATCCTCGAGAGGA || |||||| |||||||| AAGTGCCGTGTATATGAGCTCCCCTACTTAGT	DT3	0.00	0.05	0.00	0.00	206	-0.14	282	-0.29
GTTCTTAGCTCGGATTTTGGCC	-	TAR1	20.19	49.70	2.46	0.00	0.06	0.06	BnaC09g46790D	26S proteasome non-ATPase regulatory subunit 12 homolog A	1992	GTTCTTAGCT-CGGATTTTGGCC o|||o||| |o||o|| ||| TTACTAAGAGTCGAAGTCTAGAAGCGGTCGAA	DT3	0.00	0.41	0.00	0.00	2538	0.36	2744	0.16
AGGATATGGGACGGAAGCTGA	+	TAR1	59.45	517.07	8.70	105.38	247.38	2.35	BnaC03g38850D	Transcription factor TCP4	2011	AGGATATGGGACGGAAGCTGA ||||||| ||||||| |||||| CCAGTCCTATAACCTTC-TTGGACTTTACCAC	DT3	0.00	2.00	0.00	0.00	3079	0.71	3165	0.84
AGGAAGCTGATTGGCTGGATC	+	TAR1	74.43	124.57	1.67	136.07	260.72	1.92	BnaC03g09140D	Serine/threonine-protein kinase PBS1	2941	AGGAAGCTGA-TTGGCTGGATC |o||||o|||o||||| TCTTTCTTCGGCTGAATCGACCTCAAAGAAA	DT3	0.00	1.00	0.00	0.00	185	0.99	444	-0.30
TGAGAATAGGTCGAGGACATT	-	TAR1	5.30	64.62	12.20	14.18	90.52	6.38	BnaC09g14450D	Phosphatidylinositol 4-phosphate 5-kinase 8	3348	TGAGAATAGGTCGAGGACATT ||||| ||||o|| |o| CAGCACTCTT-TCCATCTTCTATGACGGTGAA	DT3	0.00	0.05	0.00	0.00	330	0.88	583	0.76
CACCAAGATCTGCACCGACGGC	-	TAR1	2.61	29.45	11.30	15.19	131.87	8.68	BnaC02g36110D	unknown	388	CACCAAGATCTGCACCGACGGC |||||||||||||||o|| GATGGTGGTTCTAGACGTGGCTGTCGGTGAGG	DT3	0.00	0.45	0.00	0.00	25737	-1.12	12547	-0.80
CCGGTTCCGGAATTTTAACCG	-	TAR1	19.50	23.29	1.19	53.55	45.95	0.86	BnaA05g13740D	RuBisCO large subunit-binding protein subunit beta, chloroplastic	2977	CCGGTTCCGGAATTTTAACCG ||||||o||| |||||| GAACGGCCAACGTCGTAACATTGGCATAAAGT	DT3	0.00	2.41	0.00	0.00	1127	-0.52	327	-2.44
CATCCCACGGAATCGAGAGCT	+	TAR1	74.64	78.81	1.06	197.83	155.07	0.78	BnaC04g26270D	Uridine 5'-monophosphate synthase	1958	CATCCCACGGAATCGAGAGCT ||o| |||o||||||o| || GTTGGTGGAGTGTCTTAGCTTT-GATGACTCT	DT3	0.00	1.91	0.00	0.00	2292	0.28	1336	0.21
TGATCTCCCGTGTGTTACCGC	+	TAR1	25.95	64.56	2.49	48.99	55.05	1.12	BnaC08g20540D	Coiled-coil domain-containing protein SCD2	4052	TGATCTCCCGTGTGTTACCGC |||| |||||||o||| || ATCAACTAAAGGGCA-ACGATGCCGACTAGGT	DT3	0.00	1.68	0.00	0.00	2339	0.62	5507	0.12
CACCAAGATCTGCACCGACGGC	-	TAR1	2.61	29.45	11.30	15.19	131.87	8.68	BnaA09g04420D	TAR1	1793	CACCAAGATCTGCACCGACGGC ||||||||||||||||||| GATGGTGGTTCTAGACGGGGCTGCCGGCGAGG	DT3	0.00	0.45	0.00	0.00	239430	-1.00	101442	-0.78
CGCACGCGGTTGGCCAAAATC	+	TAR1	8.11	194.14	23.94	5.31	102.73	19.35	BnaA07g22280D	Probable xyloglucan 6-xylosyltransferase 5	279	CGCACGCGGTTGGCCAAAATC || |||||||oo||| |o CGCGGC-TGCGCCAATTGGTCTTGTAGTAGCT	DT3	0.00	0.18	0.00	0.00	263	-0.25	278	-0.60
GGGTGGTTCGCCGTCTGCGAC	+	TAR1	65.80	129.54	1.97	125.25	169.79	1.36	BnaA06g06060D	Dynamin-2B	6834	GGGTGGTTCGCCGTCTGCGAC ||||||| |||||||| || AAGCCCCACCACGCCGCCGACGATGGTCTCGG	DT3	0.00	2.27	0.00	0.00	758	0.95	1669	0.24
CTAAGAACGTCAGGAGCGTCT	+	TAR1	74.08	532.19	7.18	0.00	0.88	0.88	BnaA05g03490D	Stearoyl-[acyl-carrier-protein] 9-desaturase, chloroplastic	2325	CTAAGAACGTCAGGAGCGTCT |o||||| |||o|o |||o GGCTGGTTCTTG-AGTTCTTACAGGCGTATTA	DT3	0.00	0.36	0.00	0.00	633	-0.81	747	-1.15
GTCGGCCAAGGTGTGAACTCG	-	TAR1	6.92	52.47	7.58	4.08	91.32	22.39	BnaA03g53860D	unknown	389	GTCGGCCAAGGTGTGAACTCG || |||||||o o|||o|o GCGTCA-CCGGTTCCGAGCTTGGGTCCCCGCC	DT3	0.00	1.00	0.00	0.00	7	-0.89	12	0.14
TAAGAACGTCAGGAGCGTCT	+	TAR1	4.44	56.99	12.85	0.00	0.40	0.40	BnaC06g38520D	DOWNSTREAM OF FLC	866	TAAGA-ACGTCAGGAGCGTCT o|o| ||o|||o|o|o||| CTCGTTTTGTGTAGTCTTTGTAGAAAGAGCTT	DT3	0.00	0.82	0.00	0.00	13959	-0.62	6927	-0.98
ATGAACCGGAAGCCGGGTTACG	+	TAR1	85.30	90.44	1.06	175.86	215.73	1.23	BnaC08g09120D	F-box/kelch-repeat protein SKIP25	1098	ATGAACCGGAAGCCGGGTTACG |||||||o|| |||| |o| | TATGTACTTGGCTTT-GGCCAAGTTCGGGAAC	DT3	0.00	0.50	0.00	0.00	933	-1.11	465	-0.45
GTTGGCCAAAATCCGAGCTAA	+	TAR1	1.93	90.11	46.67	3.24	33.75	10.41	BnaC01g36130D	Lectin-like protein At3g16530	855	GTTGGCCAAAATCCGAGCTAA ||o||||| |||o|o|| CTTGAATCGGTTTT-GGCTTGGTTTTTGGTT	DT3	0.00	0.50	0.00	0.00	4899	0.07	357	-1.85
GAGAATAGGTCGAGGACATTG	-	TAR1	4.45	87.04	19.55	5.69	123.35	21.67	BnaA03g12990D	unknown	2007	GAGAATAGGTCGAGGACATTG o||| |o||||||| |||| CTTCTTCTTCTTCAGCTCC-GTAAAACCTCGC	DT3	0.00	0.05	0.00	0.00	225	0.71	382	0.31
AGGCCTCGATGAGTAGGAGGG	+	TAR1	13.90	106.85	7.69	50.09	229.85	4.59	BnaAnng08700D	Stem-specific protein TSJT1	1767	AGGCCTCGATGAGTAGGAGGG |o|||||||| o|o||oo AACATTCGGAGCTACTGGTTCTCTTGGAGCAA	DT3	0.00	0.91	0.00	0.00	76196	0.07	92666	0.70
TGTTGAGCCATCCCACGGAATC	+	TAR1	19.17	20.14	1.05	27.45	36.82	1.34	BnaA01g21230D	Caltractin	1154	TGTTGAGCCATCCCACGGAATC |||o|||| |||| |||| TCGAAGAAGTTGGTAGAGTGC-TTAGAGTCGT	TT1	0.00	0.00	0.00	0.12	6744	-0.37	5615	0.12
TGGTGTCCGGTGCATTCCCGG	+	TAR1	17.40	25.67	1.48	27.59	60.16	2.18	BnaA02g29010D	Chlorophyll a-b binding protein 36, chloroplastic	379	TGGTGTCCGGTGCATTC-CCGG |o|| ||||| ||||| |||| CGGCATCAGAGGCCCCATAAGAGGCCAATCCA	TT1	0.00	0.00	0.00	0.18	544923	-0.38	395149	-0.03
TGGTGTCCGGTGCATTCCCGG	+	TAR1	17.40	25.67	1.48	27.59	60.16	2.18	BnaA09g02120D	Chlorophyll a-b binding protein 36, chloroplastic	565	TGGTGTCCGGTGCATTC-CCGG |o|| ||||| ||||| |||| CGGCATCAGAGGCCCCATAAGTGGCCAATCCA	TT1	0.00	0.00	0.00	0.18	281901	-0.39	186238	-0.53
TGAGAATAGGTCGAGGACATTG	-	TAR1	0.90	14.50	16.15	0.00	43.83	43.83	BnaC07g19130D	CTD small phosphatase-like protein 2	1442	TGAGAATAGGTCGAGGACATTG ||||o||||oo|||| AGTAAGTCTTGTCCA-CTTTTATAACATAGTC	TT2	0.00	0.00	0.00	32.62	914	0.67	1763	-0.20

CGGTCGCTGCAAAACCTAGGG	+	TAR1	22.65	64.99	2.87	48.32	119.78	2.48	BnaCnng63660D	unknown	146	CGGTCGCTGCAAAACCTAGGG CGGTGCCACCGATGTTTTTGCTGCCGTTTGAA	TT2	0.00	0.00	0.00	39.15	29982	-1.02	11225	-0.81
GGTCGCTGCAAAACCTAGGGC	+	TAR1	12.79	27.32	2.14	18.88	67.41	3.57	BnaCnng63660D	unknown	145	GGTCGCTGCAAAACCTAGGGC GGTGCCACCGATGTTTTTGCTGCCGTTTGAAG	TT2	0.00	0.00	0.00	13.44	29982	-1.02	11225	-0.81
GGTCGCTGCAAAACCTAGGGC	+	TAR1	12.79	27.32	2.14	18.88	67.41	3.57	BnaA01g26300D	unknown	57	GGTCGCTGCAAAACCTAGGGC GGTGCCACCGATGTTTTTGCTGCCGTTTGAAG	TT2	0.00	0.00	0.00	13.44	8209	-0.62	2309	-1.04
GATCTCCCGTGTGTTACCGCA	+	TAR1	28.71	186.86	6.51	44.09	119.75	2.72	BnaA05g29460D	Probable receptor-like protein kinase At5g15080	2794	GATCT-CCCGTGTGTTACCGCA GAGCTAGAGGGGTATACGAAGGAGTGGCGCCG	TT2	0.00	0.00	0.00	10.31	2857	1.00	5496	0.09
ATTTTCAAGGGCCGCCGGGAA	-	TAR1	16.68	19.48	1.17	47.60	24.65	0.52	BnaC02g14410D	Ubiquitin-conjugating enzyme E2-17 kDa	1291	ATTTTCAAGGGCCGCCGGGAA TCTTTAAAATTTTCCTGCTGTCTTTGTCTACA	TT2	0.00	0.00	0.00	20.62	32408	-0.83	28647	-0.28
CGGTCGCTGCAAAACCTAGGG	+	TAR1	22.65	64.99	2.87	48.32	119.78	2.48	BnaA01g26300D	unknown	58	CGGTCGCTGCAAAACCTAGGG CGGTGCCACCGATGTTTTTGCTGCCGTTTGAA	TT2	0.00	0.00	0.00	39.15	8209	-0.62	2309	-1.04
TGAGAATAGGTCGAGGACATT	-	TAR1	5.30	64.62	12.20	14.18	90.52	6.38	BnaC07g19130D	CTD small phosphatase-like protein 2	1442	TGAGAATAGGTCGAGGACATT AGTAAGTCTTGTCCA-CTTTTATAACATAGTC	TT2	0.00	0.00	0.00	32.62	914	0.67	1763	-0.20
CCTCGATGAGTAGGAGGGCGC	+	TAR1	16.81	27.95	1.66	50.20	52.33	1.04	BnaA07g03740D	Cold-regulated 413 plasma membrane protein 1	735	CCTCGATGAGTAGGAGGGC-GC CGGTGGTGTTACTCATCCTAGCGTCGTCGGCC	TT2	0.00	0.00	0.00	1.96	19875	-0.06	35061	0.47
CGGTCCGTCGCTGAGGACGCT	-	TAR1	36.12	17.95	0.50	45.24	48.94	1.08	BnaC03g44110D	Chlorophyll a-b binding protein 151, chloroplastic	150	CGGTCCGTCGCTGAGGACGCT CTGCGCC-GGCGGCGGCCTCTGTGGCTGGAAC	TT2	0.00	0.00	0.00	43.71	291224	-0.22	195401	0.08
CGCGCTAACCTAGAACCCACA	+	TAR1	38.14	45.73	1.20	93.98	83.38	0.89	BnaC04g12290D	unknown	766	CGCGCTAACCTAGAACCCACA GTCAGTGTGGTTGGATAGTGG-TGTAAAAATC	TT2	0.00	0.00	0.00	9.26	6623	-0.43	4072	-0.38
TCCTAAGAGTCGGGGGGAAACC	+	TAR1	297.22	291.49	0.98	406.86	528.42	1.30	BnaCnng49000D	Geranylgeranyl diphosphate reductase, chloroplastic	1117	TCC-TAAGAGTCGGGGGAAACC GGTAGGCATTTTTAGCCCTCTGTGCAGTAGAG	TT2	0.00	0.00	0.00	4.18	51471	-0.43	41448	-0.08
TCGATCCTAAGAGTCGGGGGA	+	TAR1	80.35	153.36	1.91	229.65	270.06	1.18	BnaCnng49000D	Geranylgeranyl diphosphate reductase, chloroplastic	1121	TCGATCC-TAAGAGTCGGGGGA TTTGGGTAGGCATTTTTAGCCCTCTGTGCAGT	TT2	0.00	0.00	0.00	8.61	51471	-0.43	41448	-0.08
AAAGTTTGAGAATAGGTCGAG	-	TAR1	8.63	53.52	6.20	63.69	75.79	1.19	BnaC05g42720D	Exocyst complex component SEC8	6660	AAAGTTTGAGAATAGGTCGAG GCCGTTT-AAATTCTTATCAAGTGTCTCAAGA	TT2	0.00	0.00	0.00	5.09	914	0.92	1864	-0.32
CGCATGTCAAGACGCTCCT	-	TAR1	6.02	10.90	1.81	622.23	22.79	0.04	BnaC03g44110D	Chlorophyll a-b binding protein 151, chloroplastic	807	CGCATGTCAAGACGCTCCT GCTCTTGTACCGTTCTGC-AGGCAAGAACTCG	TT2	0.00	0.00	0.00	9.53	291224	-0.22	195401	0.08
GTCCTGCTGTCTTAATCGACC	-	TAR1	0.00	31.04	31.04	15.75	50.98	3.24	BnaC02g36110D	unknown	180	GTCCTGCTGTCTTAATCGACC GTGGCAGGACGACAGAATTAGCTGGTTGTGGG	TT3	0.00	0.00	0.00	0.19	25737	-1.12	12547	-0.80
TCCGTCCCATATCCTCGAGAGG	-	TAR1	13.16	37.29	2.83	20.43	36.11	1.77	BnaA09g04420D	TAR1	191	TCCGTCCCATATCCTCGAGAGG TCGAAGGCAGGGTATAGGAGCTCTCCTACCCC	TT3	0.00	0.00	0.00	1.43	239430	-1.00	101442	-0.78
GTCCTGCTGTCTTAATCGACC	-	TAR1	0.00	31.04	31.04	15.75	50.98	3.24	BnaAnng22160D	TAR1	3137	GTCCTGCTGTCTTAATCGACC GTGGCAGGACGACAGAATTAGCTGGTTGTGGG	TT3	0.00	0.00	0.00	0.19	257765	-1.01	114234	-0.85
TGTCGGCCAAGGTGTGAACTC	-	TAR1	32.29	149.93	4.64	148.96	290.43	1.95	BnaC04g55960D	Aspartic proteinase PCS1	934	TGTCGGCCAAG-GTGTGAACTC CGGTGCAGCTGGTTCACACACTTAAGCCTTGG	TT3	0.00	0.00	0.00	0.46	7524	-0.72	8197	-0.94
CCCGGGCTTAGGTCACCACCT	-	TAR1	58.29	25.16	0.43	43.78	49.41	1.13	BnaA06g39230D	Thioredoxin reductase 2	721	CCCGGGCTTAGGTCACCACCT AGCATGGTCCGAATC-AGTGGTGTATGGGTAG	TT3	0.00	0.00	0.00	0.23	4554	-0.24	4040	-0.34
GGTCGCTGCAAAACCTAGGGC	+	TAR1	12.79	27.32	2.14	18.88	67.41	3.57	BnaA09g24650D	Pinoresinol reductase 1	116	GGTCGCTGCAAAACCTAGGGC GAGACCGGCGACGTTTTGCATCCAGTGCACTG	TT3	0.00	0.00	0.00	0.14	7	-1.02	6	-1.56
TAGGTTAGCGCGCAGTTGGGCA	-	TAR1	0.90	4.72	5.26	1.42	23.80	16.73	BnaA09g04420D	TAR1	1544	TAGGTTAGCGCGCAGTTGGGCA CAAGATCCAATCGCGCGTCAACCCGTGGCATT	TT3	0.00	0.00	0.00	0.28	239430	-1.00	101442	-0.78
TTTGTGGGTTCTAGGTTAGCG	-	TAR1	6.25	16.23	2.60	5.35	19.64	3.67	BnaC02g36110D	unknown	152	TTTGTGGGTTCTAGGTTAGCG TGGGAAACACCCAAGATCCAATCGCGCGTCAA	TT3	0.00	0.00	0.00	0.19	25737	-1.12	12547	-0.80
AGCTAAGGACGTCAGGAGCGTC	+	TAR1	0.00	0.13	0.13	39.44	662.83	16.80	BnaAnng21760D	TAR1	2421	AGCTAAGGACGTCAGGAGCGTC AGGCTCGATTCCTGCAGTCCTCGCAGAACTGT	TT3	0.00	0.00	0.00	0.37	47012	-1.01	20912	-0.79
AGCACGCAGATGCCGAGGCAC	-	TAR1	0.00	6.51	6.51	4.08	14.09	3.45	BnaA07g03530D	Putative polyol transporter 1	762	AGCACGCAGATGCCGAGGCAC ACGGTTGTGAGGCTACCGATCCGTGTGACTCC	TT3	0.00	0.00	0.00	0.37	0	NA	167	0.75
CGCGAACTTCGAAAGGGGATCC	+	TAR1	130.62	185.41	1.42	284.46	587.28	2.06	BnaA02g31580D	Elongation factor 2	1585	CGCGAACTTCGAAAGGGGATCC TGCAGCGTTTGGAGCTT-CGTCTAGGGAGAGT	TT3	0.00	0.00	0.00	0.14	2906	0.75	5480	0.27
GGTAAGCAGAACTGGCGATGC	+	TAR1	39.95	27.14	0.68	61.99	68.14	1.10	BnaC07g47710D	Trafficking protein particle complex subunit 2-like protein	438	GGTA-AGCAGAACTGGCGATGC GACCCATATCGTCTGGATCTTTACGGAGCAAG	TT3	0.00	0.00	0.00	0.09	1897	-0.12	1562	0.12
TTAGCGCGCAGTTGGGCACCG	-	TAR1	5.35	58.26	10.89	11.87	135.48	11.42	BnaA09g04420D	TAR1	1540	TTAGCGCGCAGTTGGGCACCG ATCCAATCGCGCGTCAACCCGTGGCATTGGGC	TT3	0.00	0.00	0.00	0.28	239430	-1.00	101442	-0.78
TAAAGTTTGAGAATAGGTCGA	-	TAR1	11.32	34.87	3.08	18.63	38.80	2.08	BnaA09g04420D	TAR1	1404	TAAAGTTTGAGAATAGGTCGA ATAAATTTCAAACTCTTATCCAGCTCCTGTAA	TT3	0.00	0.00	0.00	0.05	239430	-1.00	101442	-0.78
AGCTGATCTCCCGTGTGTTAC	+	TAR1	18.44	154.03	8.35	50.81	109.28	2.15	BnaC05g16310D	unknown	3109	AGCTGATCTCCCGTGTGTTAC TTCCTCGACTTGAGGGGACTTAATGTTCTTGT	TT3	0.00	0.00	0.00	0.23	1059	-0.63	942	-0.28
CCACCAAGATCTGCACCGACGG	-	TAR1	34.10	23.72	0.70	82.59	103.97	1.26	BnaC08g46150D	TAR1	1790	CCACCAAGATCTGCACCGACGG TGATGGTGGTTCTAGACGTGGCTGCCGGCGAG	TT3	0.00	0.00	0.00	0.09	143979	-1.14	60510	-0.80
TCAGCGCCATCCATTTTCGGG	-	TAR1	15.92	31.73	1.99	50.07	48.38	0.97	BnaA09g04420D	TAR1	1668	TCAGCGCCATCCATTTTCGGG GCGAAGTCGCGGTAGGTAAAAGCCCCGATCAA	TT3	0.00	0.00	0.00	0.19	239430	-1.00	101442	-0.78
CCTCTAATCATTGGCTTTACC	-	TAR1	1.80	20.05	11.17	1.23	36.26	29.39	BnaC08g46150D	TAR1	1360	CCTCTAATCATTGGCTTTACC CTACGGAGATTAGTAACCGAAATGGGCTATCT	TT3	0.00	0.00	0.00	0.05	143979	-1.14	60510	-0.80
CCGTGGGATGGCTCAACAAAGC	-	TAR1	0.90	19.60	21.83	14.78	53.66	3.63	BnaAnng36730D	Putative uncharacterized protein ART3	1447	CCGTGGGATGGCTCAACAAAGC CTAAGGCACCCTACCGAGTTGTTTCGTCGGTG	TT3	0.00	0.00	0.00	0.37	32584	-0.17	17996	-0.74
CAGCGCCATCCATTTTCGGGGC	-	TAR1	3.46	4.69	1.36	12.50	24.52	1.96	BnaC08g46150D	TAR1	1663	CAGCGCCATCCATTTTCGGGGC CGAAGTCGCGGTAGGTAAAAGCCCCGATCAAC	TT3	0.00	0.00	0.00	0.14	143979	-1.14	60510	-0.80
CAGCGCCATCCATTTTCGGGGC	-	TAR1	3.46	4.69	1.36	12.50	24.52	1.96	BnaAnng22160D	TAR1	3221	CAGCGCCATCCATTTTCGGGGC CGAAGTCGCGGTAGGTAAAAGCCCCGATCAAC	TT3	0.00	0.00	0.00	0.14	257765	-1.01	114234	-0.85

TCGAGGATATGGGACGGAAGC	+	TAR1	43.26	1122.33	25.94	111.30	928.51	8.34	BnaA09g21880D	Protein SGT1 homolog B	79	TCGAGGATATGGGACGGAAGC AGAAAGCTCCTATACC-TCTCTACGTCTTCTT	TT3	0.00	0.00	0.00	0.05	1270	0.98	1945	0.25
ACAACCCGACTCGTAGACAGC	-	TAR1	29.34	60.34	2.06	151.21	135.51	0.90	BnaA09g04420D	TAR1	615	ACAACCCGACTCGTAGACAGC GGTTTGTTGGGCTGAGCATCTGTCGCGGAGCA	TT3	0.00	0.00	0.00	1.43	239430	-1.00	101442	-0.78
GCCTCGATGAGTAGGAGGGCG	+	TAR1	38.73	54.85	1.42	109.75	77.18	0.70	BnaC02g08540D	Stem-specific protein TSJT1	1864	GCCTCGATGAGTAGGAGGGCG CATTCGGAGCTACTGGTTCTCTTGGAGCAAAC	TT3	0.00	0.00	0.00	0.14	42710	0.13	42762	0.74
TAACGTTGCCGTCAACCGCCA	-	TAR1	0.00	11.46	11.46	12.09	26.52	2.19	BnaC03g00280D	Pyridoxal 5'-phosphate synthase subunit PDX1.3	154	TAACGTTGCCGTCAACCGCCA TAGCGTGGCAATGGCATTTGGCGGTGCTGCGA	TT3	0.00	0.00	0.00	0.09	208	-1.84	7652	-0.58
GAGCTCTCGATTCCGTGGGATG	-	TAR1	0.00	8.18	8.18	2.06	28.99	14.08	BnaAnng36730D	Putative uncharacterized protein ART3	1459	GAGCTCTCGATTCCGTGGGATG GAACCTCGAGAGCTAAGGCACCCTACCGAGTT	TT3	0.00	0.00	0.00	0.05	32584	-0.17	17996	-0.74
CTTAGGATCGACTAACCCATG	-	TAR1	8.71	37.09	4.26	34.06	52.79	1.55	BnaAnng16700D	unknown	951	CTTAGGATCGACTAACCCATG CTGAGAATCCTAGCTGATTGGGTACACGTTCA	TT3	0.00	0.00	0.00	0.23	0	0.17	2	0.44
ACTCTTAGGATCGACTAACCC	-	TAR1	6.07	16.29	2.69	26.01	20.45	0.79	BnaC02g36110D	unknown	484	ACTCTTAGGATCGACTAACCC GGGCTGAGAATCCTAGCTGATTGGGTACACGT	TT3	0.00	0.00	0.00	0.32	25737	-1.12	12547	-0.80
CAACCCGACTCGTAGACAGCA	-	TAR1	7.90	9.54	1.21	56.28	20.80	0.37	BnaC08g46150D	TAR1	610	CAACCCGACTCGTAGACAGCA GTTTGTTGGGCTGAGCATCTGTCGCGGAGCAC	TT3	0.00	0.00	0.00	1.20	143979	-1.14	60510	-0.80
TCAGCGCCATCCATTTTCGGG	-	TAR1	15.92	31.73	1.99	50.07	48.38	0.97	BnaAnng22160D	TAR1	3222	TCAGCGCCATCCATTTTCGGG GCGAAGTCGCGGTAGGTAAAAGCCCCGATCAA	TT3	0.00	0.00	0.00	0.19	257765	-1.01	114234	-0.85
AATAGGTCGAGGACATTGCGT	-	TAR1	5.34	15.67	2.93	24.55	40.98	1.67	BnaA02g26360D	unknown	1535	AATAGGTCGAGGACATTGCGT GGCGTTA-CTAGTTCCTCTAATGCAACATGTG	TT3	0.00	0.00	0.00	0.14	516	0.35	631	0.52
TGAACTCGTTGAATACATCAGT	-	TAR1	90.74	136.42	1.50	503.35	395.98	0.79	BnaAnng22160D	TAR1	422	TGAACTCGTTGAATACATCAGT CCACACTTGAGCAACTTATGTAGTCACATCGC	TT3	0.00	0.00	0.00	0.32	257765	-1.01	114234	-0.85
TCCGTCCCATATCCTCGAGAGG	-	TAR1	13.16	37.29	2.83	20.43	36.11	1.77	BnaAnng36730D	Putative uncharacterized protein ART3	191	TCCGTCCCATATCCTCGAGAGG TCGAAGGCAGGGTATAGGAGCTCTCCTACCCC	TT3	0.00	0.00	0.00	1.43	32584	-0.17	17996	-0.74
GAGCTCTCGATTCCGTGGGATG	-	TAR1	0.00	8.18	8.18	2.06	28.99	14.08	BnaC02g36110D	unknown	56	GAGCTCTCGATTCCGTGGGATG GAACCTCGAGAGCTAAGGCACCCTACCGAGTT	TT3	0.00	0.00	0.00	0.05	25737	-1.12	12547	-0.80
ATCTGCACCGACGGCCGCTCC	-	TAR1	4.36	7.22	1.66	0.00	18.55	18.55	BnaC02g36110D	unknown	381	ATCTGCACCGACGGCCGCTCC GTTCTAGACGTGGCTGTCGGTGAGGGGGCCGA	TT3	0.00	0.00	0.00	0.32	25737	-1.12	12547	-0.80
TTGGCTTTACCCGATAGAACTC	-	TAR1	4.31	66.36	15.39	9.24	217.09	23.49	BnaAnng36730D	Putative uncharacterized protein ART3	1354	TTGGCTTTACCCGATAGAACTC TAGTAACCGAAATGGGCTATCTTGAGTAAAGG	TT3	0.00	0.00	0.00	0.09	32584	-0.17	17996	-0.74
CTACCTATTTAAAGTTTGAGA	-	TAR1	8.85	23.08	2.61	11.04	36.70	3.32	BnaAnng22160D	TAR1	2967	CTACCTATTTAAAGTTTGAGA GCAGGATGGATAAATTTCAAACTCTTATCCAG	TT3	0.00	0.00	0.00	0.56	257765	-1.01	114234	-0.85
GAGCTCTCGATTCCGTGGGATG	-	TAR1	0.00	8.18	8.18	2.06	28.99	14.08	BnaC08g46150D	TAR1	1455	GAGCTCTCGATTCCGTGGGATG GAACCTCGAGAGCTAAGGCACCCTACCGAGTT	TT3	0.00	0.00	0.00	0.05	143979	-1.14	60510	-0.80
TGCGCGCTAACCTAGAACCCA	+	TAR1	18.51	19.51	1.05	53.80	39.41	0.73	BnaA05g18020D	Transcription factor MYC2	508	TGCGCGCTAACCTAGAACC-CA CGGAATGGGCGGTTGGGTCTTGGCGTTCGCTT	TT3	0.00	0.00	0.00	0.14	2021	-0.41	4517	-0.82
TTTAGTGGACTTCTCGCGACT	-	TAR1	29.02	57.90	2.00	73.90	60.37	0.82	BnaAnng22160D	TAR1	664	TTTAGTGGACTTCTCGCGACT TTCCAAATCACCTGAAGAGCGCTGCAGCGTCT	TT3	0.00	0.00	0.00	0.14	257765	-1.01	114234	-0.85
CCGGTTCCGGAATTTTAACCG	-	TAR1	19.50	23.29	1.19	53.55	45.95	0.86	BnaC02g26290D	unknown	513	CCGGTTCCGGAATTTTAACCG AGGTGTCGAGGGCCTTAAAGTTGGCCAAAGAG	TT3	0.00	0.00	0.00	1.25	1336	0.02	483	2.03
TCAGCGCCATCCATTTTCGGGG	-	TAR1	4.45	5.39	1.21	8.20	41.24	5.03	BnaA09g04420D	TAR1	1668	TCAGCGCCATCCATTTTCGGGG GCGAAGTCGCGGTAGGTAAAAGCCCCGATCAA	TT3	0.00	0.00	0.00	0.19	239430	-1.00	101442	-0.78
AATAGGTCGAGGACATTGCGT	-	TAR1	5.34	15.67	2.93	24.55	40.98	1.67	BnaC02g34430D	unknown	2230	AATAGGTCGAGGACATTGCGT GGCGTTA-CTAGTTCCTCTAATGCAACATGTG	TT3	0.00	0.00	0.00	0.14	691	0.39	795	0.62
AACCCGACTCGTAGACAGCGCC	-	TAR1	3.50	5.68	1.62	11.53	41.18	3.57	BnaAnng22160D	TAR1	1613	AACCCGACTCGTAGACAGCGCC TTTGTTGGGCTGAGCATCTGTCGCGGAGCACC	TT3	0.00	0.00	0.00	0.93	257765	-1.01	114234	-0.85
TTAAGGTGGTGACCTAAGCCCG	+	TAR1	13.32	13.45	1.01	31.21	35.31	1.13	BnaAnng21760D	TAR1	1808	TTAAGGTGGTGACCTAAGCCCG GCCTAATTCCACCACTGGATTCGGGCCCGAAA	TT3	0.00	0.00	0.00	0.23	47012	-1.01	20912	-0.79
AAACAACCCGACTCGTAGACA	-	TAR1	3.50	10.58	3.02	30.53	25.16	0.82	BnaA09g04420D	TAR1	617	AAACAACCCGACTCGTAGACA AGGGTTTGTTGGGCTGAGCATCTGTCGCGGAG	TT3	0.00	0.00	0.00	2.45	239430	-1.00	101442	-0.78
TGCTCCGTTCCGCATTCGACC	-	TAR1	#N/A	#N/A	#N/A	44.07	58.66	1.33	BnaC06g00260D	Cysteine proteinase RD21a	1684	TGCTCCGTTCCGCATTCGACC CGGTAAGAGACAAGGCATAGGCTGGCGGTGTT	TT3	0.00	0.00	0.00	0.23	18560	1.24	37108	1.39
CTTAGGATCGACTAACCCATG	-	TAR1	8.71	37.09	4.26	34.06	52.79	1.55	BnaC02g36110D	unknown	481	CTTAGGATCGACTAACCCATG CTGAGAATCCTAGCTGATTGGGTACACGTTCA	TT3	0.00	0.00	0.00	0.23	25737	-1.12	12547	-0.80
TCTAATCATTGGCTTTACCCG	-	TAR1	8.80	9.99	1.13	6.36	23.51	3.70	BnaC08g46150D	TAR1	1358	TCTAATCATTGGCTTTACCCG ACGGAGATTAGTAACCGAAATGGGCTATCTTG	TT3	0.00	0.00	0.00	0.28	143979	-1.14	60510	-0.80
TTAATCGACCAACACCCTTTG	-	TAR1	3.55	10.61	2.98	4.08	20.18	4.95	BnaAnng22160D	TAR1	3126	TTAATCGACCAACACCCTTTG ACAGAATTAGCTGGTTGTGGGAAACACCCAAG	TT3	0.00	0.00	0.00	0.14	257765	-1.01	114234	-0.85
CGACGTCGCAGACGGCGAACC	-	TAR1	32.30	849.78	26.31	61.44	2765.49	45.01	BnaC03g25930D	ADP-ribosylation factor 2	289	CGACGTCGCAGACGGCGAACC GGGGGCTGTAGGGTCTGCCATTTCGATTACAA	TT3	0.00	0.00	0.00	0.56	5095	-0.17	4045	0.12
CTTAGGATCGACTAACCCATG	-	TAR1	8.71	37.09	4.26	34.06	52.79	1.55	BnaC08g46150D	TAR1	1882	CTTAGGATCGACTAACCCATG CTGAGAATCCTAGCTGATTGGGTACACGTTCA	TT3	0.00	0.00	0.00	0.23	143979	-1.14	60510	-0.80
ACCCGACTCGTAGACAGCGCCT	-	TAR1	9.58	4.27	0.45	28.93	29.64	1.02	BnaA09g04420D	TAR1	612	ACCCGACTCGTAGACAGCGCCT TTGTTGGGCTGAGCATCTGTCGCGGAGCACCA	TT3	0.00	0.00	0.00	12.59	239430	-1.00	101442	-0.78
ACTCATCGAGGCCTGGCTCTT	-	TAR1	4.40	20.17	4.58	13.73	31.60	2.30	BnaAnng22160D	TAR1	3273	ACTCATCGAGGCCTGGCTCTT AGGATGAGTAGCTCCGGACCGAGAACGGGGCT	TT3	0.00	0.00	0.00	0.51	257765	-1.01	114234	-0.85
TCAGCGCCATCCATTTTCGGG	-	TAR1	15.92	31.73	1.99	50.07	48.38	0.97	BnaC02g36110D	unknown	265	TCAGCGCCATCCATTTTCGGG GCGAAGTCGCGGTAGGTAAAAGCCCCGATCAA	TT3	0.00	0.00	0.00	0.19	25737	-1.12	12547	-0.80
GTGTGAACTCGTTGAATACATC	-	TAR1	0.00	30.35	30.35	16.42	87.19	5.31	BnaAnng22160D	TAR1	425	GTGTGAACTCGTTGAATACATC GTTCCACACTTGAGCAACTTATGTAGTCACAT	TT3	0.00	0.00	0.00	0.09	257765	-1.01	114234	-0.85

AGTTCTATCGGGTAAAGCCAA	+	TAR1	9.95	15.47	1.55	44.67	30.00	0.67	BnaA02g22400D	VAN3-binding protein	1931	AGTTCTATCGGGTAAAGCCAA |o||||o||o|||||| GTCGTTAAGATGGCATATT-CGGGTAGGAAAT	TT3	0.00	0.00	0.00	0.19	2536	-1.03	1553	-1.35
TGTCGGCCAAGGTGTGAACTCG	-	TAR1	30.41	37.07	1.22	133.79	108.00	0.81	BnaC04g55960D	Aspartic proteinase PCS1	934	TGTCGGCCAAG-GTGTGAACTCG o|||o||||| ||||||||| CGGTGCAGCTGGTTCACACACTTAAGCCTTGG	TT3	0.00	0.00	0.00	0.46	7524	-0.72	8197	-0.94
GATGGCGCTGAAGCGCGCGAC	+	TAR1	17.62	39.44	2.24	49.46	74.32	1.50	BnaA09g33120D	unknown	555	GATGGCGCTGAAGCGCGCGAC o|||||||||| ||||| ACTTTTACCGAGACTTCCAGCGCTTTTTGGGC	TT3	0.00	0.00	0.00	0.19	300	1.04	586	-0.15
CGCGAACTTCGAAAGGGGATCC	+	TAR1	130.62	185.41	1.42	284.46	587.28	2.06	BnaC02g40260D	Elongation factor 2	2663	CGCGAACTTCGAAAGGGGATCC |||o|||o|| ||||o|||| TGCAGCGTTTGGAG-TTTCGTCTAGGGAGAGT	TT3	0.00	0.00	0.00	0.14	2593	1.15	5719	0.28
TGGCCGTTTAGGCCAAGGAAG	+	TAR1	31.56	157.36	4.99	128.60	450.85	3.51	BnaC03g04540D	Transmembrane 9 superfamily member 8	2084	TGGCCGTTTAGGCCAAGGAAG o| ||||||||o||| TACTCTC-GCAAATCCTGTTTCTTCTACCTCC	TT3	0.00	0.00	0.00	0.05	1131	0.47	1631	0.04
AGCTCGGATTTTGGCCAACCG	-	TAR1	52.80	148.67	2.82	378.81	63.63	0.17	BnaAnng36730D	Putative uncharacterized protein ART3	239	AGCTCGGATTTTGGCCAACCG |||||||||||||||||| GGAATCGAGCCTAAAACCGGTTGGCGCACGCC	TT3	0.00	0.00	0.00	0.05	32584	-0.17	17996	-0.74
ACCCGATAGAACTCGTTTCCG	-	TAR1	1.80	15.70	8.75	24.85	22.98	0.92	BnaC02g28770D	Dihydroflavonol-4-reductase	1212	ACCCGATAGAACTCGTTTCCG ||||||o|||o|| o|| GGCTTGGGCTATTTTGGGCTTGGCCAGGGCTT	TT3	0.00	0.00	0.00	0.14	42	-0.32	17	-0.45
TTGGTCCGTGTTACAAGACA	-	TAR1	3.42	5.42	1.59	13.06	30.96	2.37	BnaC08g46150D	TAR1	1005	TTGGTCCGTGTTACAAGACA |||||||||||||||| GAGGAACCAGGCACAAAGTTCTGTCCAGCTTA	TT3	0.00	0.00	0.00	0.79	143979	-1.14	60510	-0.80
GACTCTTAGGATCGACTAACC	-	TAR1	0.85	30.23	35.40	6.14	42.37	6.90	BnaC08g46150D	TAR1	1886	GACTCTTAGGATCGACTAACC |||||||||||||||||| GGGGCTGAGAATCCTAGCTGATTGGGTACACG	TT3	0.00	0.00	0.00	0.23	143979	-1.14	60510	-0.80
CCTACTCATCGAGGCCTGGCTC	-	TAR1	6.20	10.18	1.64	20.50	28.76	1.40	BnaA09g04420D	TAR1	1722	CCTACTCATCGAGGCCTGGCTC ||||||||||||||||||| GGGAGGATGAGTAGCTCCGGACCGAGAACGGG	TT3	0.00	0.00	0.00	0.74	239430	-1.00	101442	-0.78
TGTTGAGCCATCCCACGGAATC	+	TAR1	19.17	20.14	1.05	27.45	36.82	1.34	BnaA01g22570D	Pentatricopeptide repeat-containing protein At1g60770	721	TGTTGAGCCATCCCACGGAATC ||||o|||||| ||||o| GTAAAGAACTTGGTAGGG-GCCTTGGGAGAGC	TT3	0.00	0.00	0.00	0.19	14	-0.14	16	-0.16
TAGGTTAGCGCGCAGTTGGGCA	-	TAR1	0.90	4.72	5.26	1.42	23.80	16.73	BnaC08g46150D	TAR1	1540	TAGGTTAGCGCGCAGTTGGGCA |||||||||||||||||| CAAGATCCAATCGCGCGTCAACCCGTGGCATT	TT3	0.00	0.00	0.00	0.28	143979	-1.14	60510	-0.80
CGACGTCGCAGACGGCGAACC	-	TAR1	32.30	849.78	26.31	61.44	2765.49	45.01	BnaC03g45530D	Probable plastid-lipid-associated protein 11	2170	CGACGTCGCAGACGGCGAACC |||| |||||o||||| CAGAGGTGCACCGTCTGTCGCTTAGAGGACAC	TT3	0.00	0.00	0.00	0.14	277	0.27	300	-0.06
ATCGATCGGCGGACCGGATTG	-	TAR1	14.16	15.28	1.08	43.14	32.82	0.76	BnaC07g50850D	Cytokinin dehydrogenase 4	2548	ATC-GATCGGCGGACCGGATTG |o| ||||o|||| ||o||oo AAATGGCCTAGCTGCCTAGCTTAGTCTATAGG	TT3	0.00	0.00	0.00	0.14	0	NA	1	0.02
TAGACAGCGCCTCGTGGTGCGA	-	TAR1	0.85	2.64	3.09	3.70	14.08	3.80	BnaC08g46150D	TAR1	598	TAGACAGCGCCTCGTGGTGCGA |||||||||||||||||| GAGCATCTGTCGCGGAGCACCACGCTGTCCCA	TT3	0.00	0.00	0.00	2.55	143979	-1.14	60510	-0.80
CCTACTCATCGAGGCCTGGCTC	-	TAR1	6.20	10.18	1.64	20.50	28.76	1.40	BnaAnng22160D	TAR1	3276	CCTACTCATCGAGGCCTGGCTC |||||||||||||||||| GGGAGGATGAGTAGCTCCGGACCGAGAACGGG	TT3	0.00	0.00	0.00	0.74	257765	-1.01	114234	-0.85
AAACAACCCGACTCGTAGACA	-	TAR1	3.50	10.58	3.02	30.53	25.16	0.82	BnaAnng36730D	Putative uncharacterized protein ART3	617	AAACAACCCGACTCGTAGACA |||||||||||||||||| AGGGTTTGTTGGGCTGAGCATCTGTCGCGGAA	TT3	0.00	0.00	0.00	2.45	32584	-0.17	17996	-0.74
TAGGTTAGCGCGCAGTTGGGC	-	TAR1	0.00	7.41	7.41	4.27	21.52	5.04	BnaAnng22160D	TAR1	3098	TAGGTTAGCGCGCAGTTGGGC |||||||||||||||||| CAAGATCCAATCGCGCGTCAACCCGTGGCATT	TT3	0.00	0.00	0.00	0.28	257765	-1.01	114234	-0.85
ACCACCAAGATCTGCACCGACG	-	TAR1	0.00	15.07	15.07	0.00	71.22	71.22	BnaC08g46150D	TAR1	1791	ACCACCAAGATCTGCACCGACG |||||||||||||||||| ATGATGGTGGTTCTAGACGTGGCTGCCGGCGA	TT3	0.00	0.00	0.00	0.51	143979	-1.14	60510	-0.80
ATTCCGTGGGATGGCTCAACAA	-	TAR1	0.00	4.70	4.70	2.47	33.52	13.59	BnaC09g05890D	ROOT PRIMORDIUM DEFECTIVE 1	665	ATTCCGTGGGATGGCTCAACAA |||||o||||| |||||| ACGAGAAGGCATCCTACAGAGGTGTCAGAACT	TT3	0.00	0.00	0.00	0.19	70	-0.07	89	-0.71
GTCGAGGACATTGCGTCCCCGA	-	TAR1	0.00	2.46	2.46	1.42	21.25	14.94	BnaC02g16050D	NUCLEAR FUSION DEFECTIVE 4	116	GTCGAGGACATTGCGTCCCCGA |o|| ||||||| |o|||| CTAGCGGCCCCTGTAACTCGGTGGCTTATTTA	TT3	0.00	0.00	0.00	0.09	1351	0.57	1550	0.23
CCCCATCCTCTCGAGGATATG	+	TAR1	1.41	105.00	74.53	6.22	132.85	21.37	BnaAnng21760D	TAR1	2493	CCCCATCCTCTCGAGGATATG |||||||||||||||||| CAGGGGGGTAGGAGAGCTCCTATACCCTGCCT	TT3	0.00	0.00	0.00	0.14	47012	-1.01	20912	-0.79
GAAGATCAAGGTCGGTCGGCTG	-	TAR1	0.00	9.38	9.38	0.00	28.61	28.61	BnaCnng62280D	Rab3 GTPase-activating protein catalytic subunit	3713	GAAGATCAAGGTCGGTCGGCTG |||||| ||||o|o|||| GCGCCTTCTACTTCGAGTCGGCGGACTTGGCG	TT3	0.00	0.00	0.00	0.09	355	0.46	518	-0.10
TTTGTGGGTTCTAGGTTAGCG	-	TAR1	6.25	16.23	2.60	5.35	19.64	3.67	BnaAnng22160D	TAR1	3109	TTTGTGGGTTCTAGGTTAGCG |||||||||||||||||| TGGGAAACACCCAAGATCCAATCGCGCGTCAA	TT3	0.00	0.00	0.00	0.19	257765	-1.01	114234	-0.85
CGTAGACAGCGCCTCGTGGTGC	-	TAR1	8.63	2.33	0.27	14.74	29.31	1.99	BnaC08g46150D	TAR1	600	CGTAGACAGCGCCTCGTGGTGC |||||||||||||||||| CTGAGCATCTGTCGCGGAGCACCACGCTGTCC	TT3	0.00	0.00	0.00	0.23	143979	-1.14	60510	-0.80
TTTGTGGGTTCTAGGTTAGCG	-	TAR1	6.25	16.23	2.60	5.35	19.64	3.67	BnaC08g46150D	TAR1	1551	TTTGTGGGTTCTAGGTTAGCG |||||||||||||||||| TGGGAAACACCCAAGATCCAATCGCGCGTCAA	TT3	0.00	0.00	0.00	0.19	143979	-1.14	60510	-0.80
AACTTCCTTGGCCTAAACGGCC	-	TAR1	1.71	25.61	15.00	2.66	162.61	61.21	BnaAnng22160D	TAR1	344	AACTTCCTTGGCCTAAACGGCC |||||||||||||||||| GAGTTTGAAGGAACCGGATTTGCCGGTATCAG	TT3	0.00	0.00	0.00	0.09	257765	-1.01	114234	-0.85
TCAAGACGCTCCTGACGTCCT	-	TAR1	0.00	0.15	0.15	20.88	23.56	1.13	BnaC04g03780D	Beta-glucosidase 26, peroxisomal	2001	TCAAGACGCTCCTGACGTCCT |||o||| ||||| ||||| ATGAAGTTTTGCAAAGACT-CAGGACAACCTA	TT3	0.00	0.00	0.00	0.05	5922	0.21	2492	-0.85
TAAAGCCAATGATTAGAGGCA	+	TAR1	28.49	23.41	0.82	30.16	41.57	1.38	BnaCnng67370D	unknown	363	TAAAGCCAATGATTAGAGGCA |||||||||||||||||| GCCCATTTCGGTTACTAATCTCCGTAGCCCCT	TT3	0.00	0.00	0.00	0.05	3342	-1.03	1416	-1.00
ACTTCGAAAGGGGATCCGGTT	+	TAR1	26.97	28.31	1.05	78.82	65.73	0.83	BnaC06g39320D	unknown	246	ACTTCGAAAGGGGATCCGGTT || |||||o|||||o|| TCGAAGACGCTTTCTCCTAGGCTAACGCTGAC	TT3	0.00	0.00	0.00	0.09	936	-0.10	801	0.20
TAGGTTAGCGCGCAGTTGGGC	-	TAR1	0.00	7.41	7.41	4.27	21.52	5.04	BnaA09g04420D	TAR1	1544	TAGGTTAGCGCGCAGTTGGGC |||||||||||||||||| CAAGATCCAATCGCGCGTCAACCCGTGGCATT	TT3	0.00	0.00	0.00	0.28	239430	-1.00	101442	-0.78
ACTCTTAGGATCGACTAACCC	-	TAR1	6.07	16.29	2.69	26.01	20.45	0.79	BnaA09g04420D	TAR1	1889	ACTCTTAGGATCGACTAACCC |||||||||||||||||| GGGCTGAGAATCCTAGCTGATTGGGTACACGT	TT3	0.00	0.00	0.00	0.32	239430	-1.00	101442	-0.78
CGAGCTAAGGACGTCAGGAGCG	+	TAR1	#N/A	#N/A	#N/A	28.61	63.94	2.24	BnaA09g52700D	Receptor-like protein kinase 2	89	CGAGCTAAG-GACGTCAGGAGCG ||||||||| ||| || |o|||| CTCGCTCGATTCACTGAAGCCTTCGCTGGGCC	TT3	0.00	0.00	0.00	0.42	542	-0.14	431	-0.36
CAAGATCTGCACCGACGGCCG	-	TAR1	0.85	16.10	18.85	1.23	30.11	24.40	BnaC02g36110D	unknown	385	CAAGATCTGCACCGACGGCCG ||||||||||||||o||o GGTGGTTCTAGACGTGGCTGTCGGTGAGGGGG	TT3	0.00	0.00	0.00	0.32	25737	-1.12	12547	-0.80
AACCCGACTCGTAGACAGCGCC	-	TAR1	3.50	5.68	1.62	11.53	41.18	3.57	BnaC08g46150D	TAR1	609	AACCCGACTCGTAGACAGCGCC ||||||||||||||||||| TTTGTTGGGCTGAGCATCTGTCGCGGAGCACC	TT3	0.00	0.00	0.00	0.93	143979	-1.14	60510	-0.80

ATCTGCACCGACGGCCGCTCC	-	TAR1	4.36	7.22	1.66	0.00	18.55	18.55	BnaC08g46150D	TAR1	1782	ATCTGCACCGACGGCCGCTCC ||||||||||||||||||| GTTCTAGACGTGGCTGCCGGCGAGGCGGGCCC	TT3	0.00	0.00	0.00	0.32	143979	-1.14	60510	-0.80
CTTATGCGCGAACTTCGAAAGG	+	TAR1	29.10	31.37	1.08	77.89	128.69	1.65	BnaA08g08960D	Probable serine/threonine-protein kinase drkB	2648	CTTATGCGCGAACTTC-GAAAGG |||||||||||||||| AAAAGAACACGAGCTTGAAGACTTTCGTACAG	TT3	0.00	0.00	0.00	0.05	11	0.84	14	1.00
CAATGTCCTCGACCTATTCTC	+	TAR1	76.06	128.34	1.69	134.24	250.33	1.86	BnaC06g04310D	Probable plastid-lipid-associated protein 12, chloroplastic	2088	CAATGTCCTCGACCTATTCTC |||||||||| ||||||| AATAGTTTC-GGAGCTGAATAAGAGTAGAAGA	TT3	0.00	0.00	0.00	0.14	10886	-0.27	12333	-0.07
GTCGAGGACATTGCGTCCCCGA	-	TAR1	0.00	2.46	2.46	1.42	21.25	14.94	BnaA02g11610D	Leucine-rich repeat receptor-like serine/threonine-protein kinase BAM2	143	GTCGAGGACATTGCGTCCCCGA |o|||||||| |o|||| CTAGCGGCCCCTGTAACTCGGTGGCTTATTTA	TT3	0.00	0.00	0.00	0.09	104	0.10	675	0.95
GAACGACCTGAGAACGATGAA	+	TAR1	14.30	132.60	9.27	113.19	241.21	2.13	BnaA08g26380D	Putative disease resistance protein At4g10780	1730	GAACGACCTGAGAACGATGAA |||||||||||| o o o|| AACTCTTGCTGGACTCTTATAGTTTCGTACTA	TT3	0.00	0.00	0.00	0.19	930	-0.12	1295	-0.36
ATTAGAGGCATCGGGGACGCAA	+	TAR1	29.99	19.33	0.64	36.02	59.45	1.65	BnaC06g41830D	unknown	383	ATTAGAGGC-ATCGGGGACGCAA ||o|||o||||o|||||| CTATAGTCTTCGCTCGGCTCTGCGTTAGCGAC	TT3	0.00	0.00	0.00	0.09	4895	-0.09	4041	-0.75
TGTCGGCCAAGGTGTGAACTCG	-	TAR1	30.41	37.07	1.22	133.79	108.00	0.81	BnaC08g26570D	Retrovirus-related Pol polyprotein from transposon TNT 1-94	3435	TGTCGGCCAAGGTGTGAACTCG ||| ||||||o o|||o|| GGCAACA-CCGGTTCCGAGCTTGGGCCCACCG	TT3	0.00	0.00	0.00	0.05	3336	-0.03	3904	0.53
GCGGACCGGATTGCTCCGTTC	-	TAR1	134.30	88.02	0.66	64.08	173.69	2.71	BnaC07g17170D	Putative SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 3-like 3	4851	GCGGACCGGATTGCTCCGTTC |||||||o||||| AGACCGGCTGGCCTGAAGAAGCA-GTCAGTTT	TT3	0.00	0.00	0.00	1.16	0	0.24	325	0.12
AGCTGATCTCCCGTGTGTTACC	+	TAR1	31.33	238.62	7.62	49.87	126.22	2.53	BnaC07g27440D	Basic leucine zipper 63	1694	AGCTGATCTCCCGTGT-GTTACC |||||||||| ||||o|| GAACTCGACTAGAGGCCACATCAGTGAACCCT	TT3	0.00	0.00	0.00	0.32	7103	0.61	11840	-0.02
TGTCGGCCAAGGTGTGAACTCG	-	TAR1	30.41	37.07	1.22	133.79	108.00	0.81	BnaA02g30270D	Transcription factor bHLH78	847	TGTCGGCCAAGGTGTGAACTCG ||| ||||||oo o|||o|| GGCAACA-CCGGTTCTGAGCTTGGGCCCACCG	TT3	0.00	0.00	0.00	0.05	24	0.27	12	-0.34
TTGGTCCGTGTTACAAGACA	-	TAR1	3.42	5.42	1.59	13.06	30.96	2.37	BnaA09g04420D	TAR1	1009	TTGGTCCGTGTTACAAGACA ||||||||||||||| GAGGAACCAGGCACAAAGTTCTGCCCAGCTTA	TT3	0.00	0.00	0.00	0.79	239430	-1.00	101442	-0.78
AGCTGATCTCCCGTGTGTTAC	+	TAR1	18.44	154.03	8.35	50.81	109.28	2.15	BnaC07g27440D	Basic leucine zipper 63	1694	AGCTGATCTCCCGTGT-GTTAC ||||||||||| |||||o|| GAACTCGACTAGAGGCCACATCAGTGAACCCT	TT3	0.00	0.00	0.00	0.32	7103	0.61	11840	-0.02
CAAGATCTGCACCGACGGCCG	-	TAR1	0.85	16.10	18.85	1.23	30.11	24.40	BnaC08g46150D	TAR1	1786	CAAGATCTGCACCGACGGCCG ||||||||||||||||||| GGTGGTTCTAGACGTGGCTGCCGGCGAGGCGG	TT3	0.00	0.00	0.00	0.32	143979	-1.14	60510	-0.80
TCAAGACGCTCCTGACGTCCT	-	TAR1	0.00	0.15	0.15	20.88	23.56	1.13	BnaA05g04060D	Beta-glucosidase 26, peroxisomal	5030	TCAAGACGCTCCTGACGTCCT |||o||| |||| ||||| ATGAAGTTTTGCAAAGACT-CAGGACAACCTA	TT3	0.00	0.00	0.00	0.05	13312	0.04	8542	-0.77
CTGAAGCGCGCGACCTATACC	+	TAR1	151.29	318.14	2.10	405.04	555.55	1.37	BnaA09g12720D	unknown	1643	CTGAAGCGCGCGACCTATACC ||||||o||| |||| o || TCTTGACTTCGTGCG-TGGAAGAGGTACATTA	TT3	0.00	0.00	0.00	0.05	1227	-2.09	4409	-0.42
CGTAGACAGCGCCTCGTGGTGC	-	TAR1	8.63	2.33	0.27	14.74	29.31	1.99	BnaA09g04420D	TAR1	604	CGTAGACAGCGCCTCGTGGTGC ||||||||||||||||||| CTGAGCATCTGTCGCGGAGCACCACGCTGTCC	TT3	0.00	0.00	0.00	0.23	239430	-1.00	101442	-0.78
ACTTCCTTGGCCTAAACGGCC	-	TAR1	4.27	120.42	28.20	77.86	237.77	3.05	BnaAnng22160D	TAR1	343	ACTTCCTTGGCCTAAACGGCC ||||||||||||||||||| AGTTTGAAGGAACCGGATTTGCCGGTATCAGG	TT3	0.00	0.00	0.00	0.42	257765	-1.01	114234	-0.85
TGTGTTACCGCACGCGGTTGGCC	+	TAR1	10.78	120.29	11.15	7.65	112.79	14.75	BnaAnng21760D	TAR1	2452	TGTGTTACCGCACGCGGTTGGCC |||||||||||||||||||| GGGCACACAATGGCGTGCGCCAACCGGTTTTA	TT3	0.00	0.00	0.00	0.32	47012	-1.01	20912	-0.79
CGTGGGTGGTTCGCCGTCTGC	+	TAR1	955.47	2530.07	2.65	3144.52	3516.77	1.12	BnaC04g55760D	Probable pectate lyase 15	1370	CGTGGGTGGTTCGCCGTCTGC o||||o|||||| ||o|| TGTCTTACCCATCAAGCGG-AGGCGAACCGCA	TT3	0.00	0.00	0.00	0.28	695	-0.88	1156	-1.25
TAGACAGCGCCTCGTGGTGCGA	-	TAR1	0.85	2.64	3.09	3.70	14.08	3.80	BnaAnng22160D	TAR1	1602	TAGACAGCGCCTCGTGGTGCGA |||||||||||||||||||| GAGCATCTGTCGCGGAGCACCACGCTGTCCCA	TT3	0.00	0.00	0.00	2.55	257765	-1.01	114234	-0.85
ACTTCGGAGGGAACCAGCTACT	-	TAR1	0.90	11.26	12.54	6.18	24.51	3.97	BnaC04g08100D	Aquaporin PIP2-7	1259	ACTTCGGAGGGAACC-AGCTACT |||||o||||||| ||| GGCGTGAAGACTTCCTTGGCTCCCTGAACCTT	TT3	0.00	0.00	0.00	0.23	59251	-0.87	3399	-1.75
CAGCGCCATCCATTTTCGGGGC	-	TAR1	3.46	4.69	1.36	12.50	24.52	1.96	BnaC02g36110D	unknown	264	CAGCGCCATCCATTTTCGGGGC ||||||||||||||||||| CGAAGTCGCGGTAGGTAAAAGCCCCGATCAAC	TT3	0.00	0.00	0.00	0.14	25737	-1.12	12547	-0.80
ACCAAGATCTGCACCGACGGCC	-	TAR1	1.75	21.24	12.13	2.66	71.73	27.00	BnaC02g36110D	unknown	387	ACCAAGATCTGCACCGACGGCC ||||||||||||||||o|| ATGGTGGTTCTAGACGTGGCTGTCGGTGAGGG	TT3	0.00	0.00	0.00	0.14	25737	-1.12	12547	-0.80
TGTTGAGCCATCCCACGGAATC	+	TAR1	19.17	20.14	1.05	27.45	36.82	1.34	BnaCnng75490D	Nitrilase 2	195	TGTTGAGCCATCCCACGGAATC ||||| |||||| ||o|o| CCTACCAACTAGGTAGGG-GCTTTGGGGTCTA	TT3	0.00	0.00	0.00	0.05	654	-0.29	6707	-0.06
ACCAAGATCTGCACCGACGGC	-	TAR1	17.58	123.69	7.04	38.09	209.00	5.49	BnaA09g04420D	TAR1	1792	ACCAAGATCTGCACCGACGGC ||||||||||| |||||||| ATGGTGGTTCTAGACGGGGCTGCCGGCGAGGC	TT3	0.00	0.00	0.00	0.14	239430	-1.00	101442	-0.78
CAAGATCTGCACCGACGGCCG	-	TAR1	0.85	16.10	18.85	1.23	30.11	24.40	BnaA09g04420D	TAR1	1790	CAAGATCTGCACCGACGGCCG |||||||||| ||||||||| GGTGGTTCTAGACGGGGCTGCCGGCGAGGCGG	TT3	0.00	0.00	0.00	0.32	239430	-1.00	101442	-0.78
CGTAGACAGCGCCTCGTGGTGC	-	TAR1	8.63	2.33	0.27	14.74	29.31	1.99	BnaAnng36730D	Putative uncharacterized protein ART3	604	CGTAGACAGCGCCTCGTGGTGC ||||||||||||||||||| CTGAGCATCTGTCGCGGAACACCCACGCTGTCC	TT3	0.00	0.00	0.00	0.23	32584	-0.17	17996	-0.74
TGCGGAAGGATCATTGTCGTA	+	TAR1	289.94	497.11	1.71	1953.41	384.34	0.20	BnaC05g50090D	unknown	3188	TGCGGAAGGATCATTGTC-GTA || |||||||| |oo|| |o| TCGTACACCTTCCTAGCAGTAGTCGTAGAAGG	TT3	0.00	0.00	0.00	0.14	1	0.48	0	-0.14
AACCCGACTCGTAGACAGCGC	-	TAR1	14.23	78.93	5.55	102.12	105.59	1.03	BnaA09g04420D	TAR1	613	AACCCGACTCGTAGACAGCGC ||||||||||||||||||| TTTGTTGGGCTGAGCATCTGTCGCGGAGCACC	TT3	0.00	0.00	0.00	0.93	239430	-1.00	101442	-0.78
TTAGCGCGCAGTTGGGCACCG	-	TAR1	5.35	58.26	10.89	11.87	135.48	11.42	BnaA04g26950D	SWR1-complex protein 4	1176	TTAGCGCGCAGTTGGGCACCG o|||o||||o |||||| TCGAGATCGTGCGTCGTCCCG-GGCTCAGTGA	TT3	0.00	0.00	0.00	0.09	352	-0.10	532	0.00
GACTCTTAGGATCGACTAACC	-	TAR1	0.85	30.23	35.40	6.14	42.37	6.90	BnaAnng16700D	unknown	955	GACTCTTAGGATCGACTAACC ||||||||||||||||||| GGGGCTGAGAATCCTAGCTGATTGGGTACACG	TT3	0.00	0.00	0.00	0.23	0	0.17	2	0.44
CCGTGGGATGGCTCAACAAAGC	-	TAR1	0.90	19.60	21.83	14.78	53.66	3.63	BnaAnng22160D	TAR1	3001	CCGTGGGATGGCTCAACAAAGC |||||||||||||||||||| CTAAGGCACCCTACCGAGTTGTTTCGTCGGTG	TT3	0.00	0.00	0.00	0.37	257765	-1.01	114234	-0.85
TATTCAACGAGTTCACACCTTG	+	TAR1	96.30	160.73	1.67	598.68	538.61	0.90	BnaC02g04340D	DDT domain-containing protein PTM	6397	TATTCAACGAGTTCACACCTTG o||||o|o|||||| ||o GTCGGTAAG-TGTTTAAGTGTCGAATCCTACC	TT3	0.00	0.00	0.00	0.05	132	0.51	308	0.20
TCAGCGCCATCCATTTTCGGGG	-	TAR1	4.45	5.39	1.21	8.20	41.24	5.03	BnaAnng22160D	TAR1	3222	TCAGCGCCATCCATTTTCGGGG ||||||||||||||||||| GCGAAGTCGCGGTAGGTAAAAGCCCCGATCAA	TT3	0.00	0.00	0.00	0.19	257765	-1.01	114234	-0.85
CGATAGAACTCGTTTCCGAGC	-	TAR1	71.55	136.47	1.91	44.75	238.06	5.32	BnaC04g07600D	NRT1/ PTR FAMILY 5.6	957	CGATAGAACTCGTTTCCGAGC ||||||||||||| o| CATTGCTATCTT-ACCAAAGGGATGCTCCTTA	TT3	0.00	0.00	0.00	0.09	6	-0.09	31	-0.97

CCGTGGGATGGCTCAACAAAGC	-	TAR1	0.90	19.60	21.83	14.78	53.66	3.63	BnaC02g36110D	unknown	44	CCGTGGGATGGCTCAACAAAGC CTAAGGCACCCTACCGAGTTGTTTCGTCGGTG	TT3	0.00	0.00	0.00	0.37	25737	-1.12	12547	-0.80
TGCGCGCTAACCTAGAACCCA	+	TAR1	18.51	19.51	1.05	53.80	39.41	0.73	BnaC05g28450D	Transcription factor MYC2	508	TGCGCGCTAACCTAGAACC-CA CGGAATGGGCGGTTGGGTCTTGGCGTTCGCTT	TT3	0.00	0.00	0.00	0.14	1261	0.05	3071	-0.87
ACTCATCGAGGCCTGGCTCTTG	-	TAR1	0.85	17.89	20.95	2.66	53.35	20.08	BnaA09g04420D	TAR1	1719	ACTCATCGAGGCCTGGCTCTTG AGGATGAGTAGCTCCGGACCGAGAACGGGGCT	TT3	0.00	0.00	0.00	0.51	239430	-1.00	101442	-0.78
TTGGCTTTACCCGATAGAACTC	-	TAR1	4.31	66.36	15.39	9.24	217.09	23.49	BnaAnng22160D	TAR1	2908	TTGGCTTTACCCGATAGAACTC TAGTAACCGAAATGGGCTATCTTGAGCAAAGG	TT3	0.00	0.00	0.00	0.09	257765	-1.01	114234	-0.85
ACCAAGATCTGCACCGACGGCC	-	TAR1	1.75	21.24	12.13	2.66	71.73	27.00	BnaC08g46150D	TAR1	1788	ACCAAGATCTGCACCGACGGCC ATGGTGGTTCTAGACGTGGCTGCCGGCGAGGC	TT3	0.00	0.00	0.00	0.14	143979	-1.14	60510	-0.80
AAAATGGCCCACTTGGAGCTCT	-	TAR1	4.45	6.53	1.47	0.00	25.41	25.41	BnaC02g36110D	unknown	71	AAAATGGCCCACTTGGAGCTCT TGGTTTTTACCGGGTGAACCTCGAGAGCTAAG	TT3	0.00	0.00	0.00	0.14	25737	-1.12	12547	-0.80
TAGACAGCGCCTCGTGGTGCGA	-	TAR1	0.85	2.64	3.09	3.70	14.08	3.80	BnaAnng36730D	Putative uncharacterized protein ART3	602	TAGACAGCGCCTCGTGGTGCGA GAGCATCTGTCGCGGAACACCACGCTGTCCCA	TT3	0.00	0.00	0.00	2.55	32584	-0.17	17996	-0.74
CCACCAAGATCTGCACCGACGG	-	TAR1	34.10	23.72	0.70	82.59	103.97	1.26	BnaA09g04420D	TAR1	1794	CCACCAAGATCTGCACCGACGG TGATGGTGGTTCTAGACGGGGCTGCCGGCGAG	TT3	0.00	0.00	0.00	0.09	239430	-1.00	101442	-0.78
CAACGCGAGCTGATGACTCGA	-	TAR1	0.90	12.10	13.48	12.72	26.69	2.10	BnaA07g02250D	Vacuolar-sorting receptor 2	5794	CAACGCGAGCTGATGACTCGA ATCAGTTGCGCTCGACTACTGAGCGCGAATGA	TT3	0.00	0.00	0.00	0.46	29	-0.87	42	-0.86
TGTCGGCCAAGGTGTGAACTCG	-	TAR1	30.41	37.07	1.22	133.79	108.00	0.81	BnaA02g10010D	PRA1 family protein H	917	TGTCGGCCAAGGTGTGAACTCG GGCAACA-CCGGTTCTGAGCTTGGGCCCACTA	TT3	0.00	0.00	0.00	0.05	0	NA	0	-0.18
ACAACCCGACTCGTAGACAGCG	-	TAR1	0.00	14.24	14.24	33.42	97.89	2.93	BnaC08g46150D	TAR1	611	ACAACCCGACTCGTAGACAGCG GGTTTGTTGGGCTGAGCATCTGTCGCGGAGCA	TT3	0.00	0.00	0.00	1.43	143979	-1.14	60510	-0.80
GAGCTCTCGATTCCGTGGGATG	-	TAR1	0.00	8.18	8.18	2.06	28.99	14.08	BnaA09g04420D	TAR1	1459	GAGCTCTCGATTCCGTGGGATG GAACCTCGAGAGCTAAGGCACCCTACCGAGTT	TT3	0.00	0.00	0.00	0.05	239430	-1.00	101442	-0.78
CCACCAAGATCTGCACCGACGG	-	TAR1	34.10	23.72	0.70	82.59	103.97	1.26	BnaC06g03610D	Helicase-like transcription factor CHR27	4217	CCACCAAGATCTGCACCGACGG CGGAGGTGGTACCAGAAGTGGTTTCCGTCTAC	TT3	0.00	0.00	0.00	0.37	293	0.43	545	0.14
AACCCGACTCGTAGACAGCGCC	-	TAR1	3.50	5.68	1.62	11.53	41.18	3.57	BnaA09g04420D	TAR1	613	AACCCGACTCGTAGACAGCGCC TTTGTTGGGCTGAGCATCTGTCGCGGAGCACC	TT3	0.00	0.00	0.00	0.93	239430	-1.00	101442	-0.78
CTGGAGCTCGGAAACGAGTTC	+	TAR1	40.26	81.04	2.01	92.73	101.54	1.09	BnaCnng67370D	unknown	391	CTGGAGCTCGGAAACGAGTTC TATCGACCTCGAGCCTTTGCTCAAGATAGCCC	TT3	0.00	0.00	0.00	0.37	3342	-1.03	1416	-1.00
GCGGACCGGATTGCTCCGTTC	-	TAR1	134.30	88.02	0.66	64.08	173.69	2.71	BnaAnng36730D	Putative uncharacterized protein ART3	818	GCGGACCGGATTGCTCCGTTC TAGCCGCCTGGCCTAACGAGGCAAGGCGTAGG	TT3	0.00	0.00	0.00	0.23	32584	-0.17	17996	-0.74
AAGATCTGCACCGACGGCCGCT	-	TAR1	0.90	14.86	16.56	1.23	44.97	36.45	BnaC09g37220D	Copper transporter 5	321	AAGATCTGCACCGACGGCCGCT CGGCTTTTCGTCGTGGCTGC-GTCGAAACCGC	TT3	0.00	0.00	0.00	0.14	2040	0.11	1542	0.51
TGTCGGCCAAGGTGTGAACTCG	-	TAR1	30.41	37.07	1.22	133.79	108.00	0.81	BnaC09g17830D	Glutathione gamma-glutamylcysteinyltransferase 1	1136	TGTCGGCCAAGGTGTGAACTCG GGCAACA-CCGGTTCCGAGCTTGGGCCCACCG	TT3	0.00	0.00	0.00	0.05	1	-0.47	1	0.32
CGGCTTCTTAGAGGGACTATG	+	TAR1	38.29	112.07	2.93	61.04	195.35	3.20	BnaA09g12590D	unknown	1669	CGGCTTCTTAGAGGGACT-ATG AGAAGGCGAAGAATCTCGGTGACTACAAGAAA	TT3	0.00	0.00	0.00	0.28	97	-0.55	132	-0.13
GCCCTAGGTTTTGCAGCGACC	-	TAR1	2.61	9.92	3.81	2.66	24.18	9.10	BnaA09g04420D	TAR1	1753	GCCCTAGGTTTTGCAGCGACC AGCGCGGGATCCAAAACGTCGCTGGCGGCGCG	TT3	0.00	0.00	0.00	0.28	239430	-1.00	101442	-0.78
CGCGAACTTCGAAAGGGGATC	+	TAR1	107.19	863.03	8.05	259.07	2036.74	7.86	BnaA02g31580D	Elongation factor 2	1585	CGCGAACTTCGAAAGGGGATC TGCAGCGTTTGGAGCTT-CGTCTAGGGAGAGT	TT3	0.00	0.00	0.00	0.14	2906	0.75	5480	0.27
ACCCGACTCGTAGACAGCGCCT	-	TAR1	9.58	4.27	0.45	28.93	29.64	1.02	BnaAnng22160D	TAR1	1612	ACCCGACTCGTAGACAGCGCCT TTGTTGGGCTGAGCATCTGTCGCGGAGCACCA	TT3	0.00	0.00	0.00	12.59	257765	-1.01	114234	-0.85
AACAACCCGACTCGTAGACAG	-	TAR1	20.28	12.59	0.62	33.00	35.37	1.07	BnaC02g16080D	F-box protein At5g50450	822	AACAACCCGACTCGTAGACAG GGTTTTGTTGGGCTGGGC-TTAGTTTGGTTAG	TT3	0.00	0.00	0.00	0.05	7727	0.91	8707	0.46
GACTTCTCGCGACGTCGCAGAC	-	TAR1	4.27	63.16	14.79	13.74	109.62	7.98	BnaAnng22160D	TAR1	657	GACTTCTCGCGACGTCGCAGAC TCACCTGAAGAGCGCTGCAGCGTCTGCCGCTT	TT3	0.00	0.00	0.00	0.05	257765	-1.01	114234	-0.85
TAAAGTTTGAGAATAGGTCGA	-	TAR1	11.32	34.87	3.08	18.63	38.80	2.08	BnaAnng22160D	TAR1	2958	TAAAGTTTGAGAATAGGTCGA ATAAATTTCAAACTCTTATCCAGCTCCTGTAA	TT3	0.00	0.00	0.00	0.05	257765	-1.01	114234	-0.85
TGTCGGCCAAGGTGTGAACTC	-	TAR1	32.29	149.93	4.64	148.96	290.43	1.95	BnaC08g26570D	Retrovirus-related Pol polyprotein from transposon TNT 1-94	3435	TGTCGGCCAAGGTGTGAACTC GGCAACA-CCGGTTCCGAGCTTGGGCCCACCG	TT3	0.00	0.00	0.00	0.05	3336	-0.03	3904	0.53
AAGAGTCGGGGGAAACCCGTC	+	TAR1	115.43	110.68	0.96	232.08	246.67	1.06	BnaC07g26260D	unknown	268	AAGA-GTCGGGGGAAACCCGTC GCCTTCTGCAGCTCTCTTTGATTAGCAAGGAA	TT3	0.00	0.00	0.00	0.69	57	1.19	119	0.89
AAGGTTCCATGTGAACGGCAC	+	TAR1	44.54	104.68	2.35	119.79	220.04	1.84	BnaC05g33170D	Zinc finger protein AZF2	103	AAGGTTCCATGTGAACGGCAC TCGGTTCCGAGGTACTTTTGCCGCAGCAAGCA	TT3	0.00	0.00	0.00	0.05	3767	-0.68	1821	0.55
GCGGACCGGATTGCTCCGTTC	-	TAR1	134.30	88.02	0.66	64.08	173.69	2.71	BnaA09g04420D	TAR1	818	GCGGACCGGATTGCTCCGTTC TAGCCGCCTGGCCTAACGAGGCAAGGCGTAGG	TT3	0.00	0.00	0.00	0.23	239430	-1.00	101442	-0.78
AATGAGAACTTTGAAGGCGAAT	+	TAR1	103.76	106.61	1.03	157.43	81.45	0.52	BnaA08g14100D	Stem-specific protein TSJT1	22	AATGAG-AACTTTGAAGGCCGAAT ATATTATTCTTTGAAACTTCCTTTTTACGTCT	TT3	0.00	0.00	0.00	0.05	56881	1.42	67607	0.16
TTTGAGAATAGGTCGAGGACA	-	TAR1	203.27	1363.51	6.71	538.52	2860.41	5.31	BnaA10g18670D	Nipped-B-like protein A	9074	TTTGAGAATAGGTC-GAGGACA AGGCAACCTCTTATCCGGACTCTTGTGTTAGT	TT3	0.00	0.00	0.00	0.09	222	0.32	477	0.05
CTGATCTCCCGTGTGTTACCG	+	TAR1	120.84	301.33	2.49	152.25	252.46	1.66	BnaC01g19630D	Protochlorophyllide reductase B, chloroplastic	1608	CTGATCTCCCGTGTGTTACCG GAGTGACTAGAGGGTGTGAAATG-CTCGGAAG	TT3	0.00	0.00	0.00	0.19	6869	0.56	7240	0.46
GTCCTGCTGTCTTAATCGACC	-	TAR1	0.00	31.04	31.04	15.75	50.98	3.24	BnaA09g04420D	TAR1	1583	GTCCTGCTGTCTTAATCGACC GTGGCAGGACGACAGAATTAGCTGGTTGTGGG	TT3	0.00	0.00	0.00	0.19	239430	-1.00	101442	-0.78
ACTTCGAAAGGGGATCCGGTT	+	TAR1	26.97	28.31	1.05	78.82	65.73	0.83	BnaC03g59890D	Disease resistance protein RPS6	1795	ACTTCGAAAGGGGATCCGGTT CCTGTGAGG-TCTCCCTTGGGCTGATTGCGGA	TT3	0.00	0.00	0.00	0.14	0	NA	9	0.74
AAGATCTGCACCGACGGCCGCT	-	TAR1	0.90	14.86	16.56	1.23	44.97	36.45	BnaA09g49870D	4-hydroxyphenylpyruvate dioxygenase	1616	AAGATCTGCACCGACGGCCGCT ACATTTCTAGACTTCGTTGCAGGGGACTAGTA	TT3	0.00	0.00	0.00	0.14	23362	0.72	31844	0.32

AGATAACTCTTTCCGGAATTC	-	TAR1	1.80	7.27	4.05	16.76	16.88	1.01	BnaA06g23380D	Protein EXORDIUM-like 2	1096	AGATAACTCTTTCCGGAATTC |o| |||||||o|||o| TTCGTTTCTTGAGATAGGTCTTAGGTTTGGGC	TT3	0.00	0.00	0.00	0.09	1459	-0.56	1509	-0.77
ACTTCGAAAGGGGATCCGGTT	+	TAR1	26.97	28.31	1.05	78.82	65.73	0.83	BnaA07g34480D	unknown	181	ACTTCGAAAGGGGATCCGGTT || |||||o|||||o|| TCGAAGACGCTTTCTCCTAGGCTAACGCTGAC	TT3	0.00	0.00	0.00	0.09	470	-0.80	965	0.02
TTGGCTTTACCCGATAGAACTC	-	TAR1	4.31	66.36	15.39	9.24	217.09	23.49	BnaC08g46150D	TAR1	1350	TTGGCTTTACCCGATAGAACTC ||||||||||||||||||| TAGTAACCGAAATGGGCTATCTTGAGCAAAGG	TT3	0.00	0.00	0.00	0.09	143979	-1.14	60510	-0.80
TTTAAAGTTTGAGAATAGGTC	-	TAR1	16.77	72.02	4.29	27.29	124.88	4.58	BnaC03g63280D	Disease resistance protein RRS1	3169	TTTAAAGTTTGAGAATAGGTC o||||o||||||o| TGTCGAA-TTCGAACTGTTATCTAAAGTTCAA	TT3	0.00	0.00	0.00	0.32	128	0.66	277	-0.01
TACCCGATAGAACTCGTTTCC	-	TAR1	46.92	62.92	1.34	49.09	102.58	2.09	BnaC04g38520D	ABC transporter G family member 32	6242	TACCCGATAGAACTCGTTTCC |||o||||||o|o||| CCAAACGGGTTATCATG-GTAGAGGTGGTATT	TT3	0.00	0.00	0.00	0.42	417	0.33	406	-0.67
TCTAATCATTGGCTTTACCCG	-	TAR1	8.80	9.99	1.13	6.36	23.51	3.70	BnaA09g04420D	TAR1	1362	TCTAATCATTGGCTTTACCCG ||||||||||||||||||| ACGGAGATTAGTAACCGAAATGGGCTATCTTG	TT3	0.00	0.00	0.00	0.28	239430	-1.00	101442	-0.78
CTCAAACTTCCTTGGCCTAAA	-	TAR1	18.42	29.66	1.61	26.60	49.83	1.87	BnaAnng22160D	TAR1	348	CTCAAACTTCCTTGGCCTAAA ||||||||||||||||||| AACGGAGTTTGAAGGAACCGGATTTGCCGGTA	TT3	0.00	0.00	0.00	0.14	257765	-1.01	114234	-0.85
CAGTTGGGCACCGTAACCCGG	-	TAR1	34.13	50.77	1.49	48.64	103.11	2.12	BnaA03g04730D	NUCLEAR FUSION DEFECTIVE 4}	2487	CAGTTGGGCACCGTAACCCGG ||||o||||||||o| TCGGGTC-ACTCGTGGCATGGGCTCAGGATAG	TT3	0.00	0.00	0.00	0.14	205	3.56	9473	-1.07
AGCTCGGATTTTGGCCAACCGC	-	TAR1	46.60	75.27	1.62	379.96	39.84	0.10	BnaAnng36730D	Putative uncharacterized protein ART3	239	AGCTCGGATTTTGGCCAACCGC ||||||||||||||||||| GGAATCGAGCCTAAAACCGGTTGGCGCACGCC	TT3	0.00	0.00	0.00	0.05	32584	-0.17	17996	-0.74
CAATGTCCTCGACCTATTCTCA	+	TAR1	39.41	28.06	0.71	84.22	88.50	1.05	BnaC06g04310D	Probable plastid-lipid-associated protein 12, chloroplastic	2088	CAATGTCCTCGACCTATTCTCA ||||||||||||||||||| AATAGTTTC-GGAGCTGAATAAGAGTAGAAGA	TT3	0.00	0.00	0.00	0.14	10886	-0.27	12333	-0.07
TGAACTCGTTGAATACATCAG	-	TAR1	77.13	171.22	2.22	229.34	411.16	1.79	BnaAnng22160D	TAR1	422	TGAACTCGTTGAATACATCAG ||||||||||||||||||| CCACACTTGAGCAACTTATGTAGTCACATCGC	TT3	0.00	0.00	0.00	0.32	257765	-1.01	114234	-0.85
TCTAATCATTGGCTTTACCCG	-	TAR1	8.80	9.99	1.13	6.36	23.51	3.70	BnaAnng22160D	TAR1	2916	TCTAATCATTGGCTTTACCCG ||||||||||||||||||| ACGGAGATTAGTAACCGAAATGGGCTATCTTG	TT3	0.00	0.00	0.00	0.28	257765	-1.01	114234	-0.85
TTAGCGCGCAGTTGGGCACCG	-	TAR1	5.35	58.26	10.89	11.87	135.48	11.42	BnaAnng22160D	TAR1	3094	TTAGCGCGCAGTTGGGCACCG ||||||||||||||||||| ATCCAATCGCGCGTCAACCCGTGGCATTGGGC	TT3	0.00	0.00	0.00	0.28	257765	-1.01	114234	-0.85
TCTAATCATTGGCTTTACCCGA	-	TAR1	2.61	3.73	1.43	14.77	32.25	2.18	BnaAnng22160D	TAR1	2916	TCTAATCATTGGCTTTACCCGA ||||||||||||||||||| ACGGAGATTAGTAACCGAAATGGGCTATCTTG	TT3	0.00	0.00	0.00	0.28	257765	-1.01	114234	-0.85
TCCTACTCATCGAGGCCTGGC	-	TAR1	6.20	12.83	2.07	9.01	29.82	3.31	BnaA04g26770D	Transcription factor bHLH70	901	TCCTACTCATCGAGGCCTGGC ||||||| || |||||||| GAGGAGGATGA-TAACTGCGGACCAGAGGGAT	TT3	0.00	0.00	0.00	0.19	6	0.77	2	0.45
GCCCTAGGTTTTGCAGCGACC	-	TAR1	2.61	9.92	3.81	2.66	24.18	9.10	BnaAnng22160D	TAR1	3307	GCCCTAGGTTTTGCAGCGACC ||||||||||||||||||| AGCGCGGGATCCAAAACGTCGCTGGCGGCGCG	TT3	0.00	0.00	0.00	0.28	257765	-1.01	114234	-0.85
GAAGATCAAGGTCGGTCGGCTG	-	TAR1	0.00	9.38	9.38	0.00	28.61	28.61	BnaA10g09330D	Rab3 GTPase-activating protein catalytic subunit	4278	GAAGATCAAGGTCGGTCGGCTG |||||||||o|o|||| GCGCCTTCTACTTCGAGTCGGCGGACTTGGCG	TT3	0.00	0.00	0.00	0.09	549	0.26	790	-0.10
TTAGCGCGCAGTTGGGCACCG	-	TAR1	5.35	58.26	10.89	11.87	135.48	11.42	BnaAnng36730D	Putative uncharacterized protein ART3	1540	TTAGCGCGCAGTTGGGCACCG ||||||||||||||||||| ATCCAATCGCGCGTCAACCCGTGGCATTGGGC	TT3	0.00	0.00	0.00	0.28	32584	-0.17	17996	-0.74
TCGCGCCCTAGGTTTTGCAGCG	-	TAR1	0.90	2.35	2.61	1.23	15.53	12.59	BnaC08g46150D	TAR1	1753	TCGCGCCCTAGGTTTTGCAGCG ||||||||||||||||||| CCCGAGCGCGGGATCCAAAACGTCGCTGGCGG	TT3	0.00	0.00	0.00	0.32	143979	-1.14	60510	-0.80
CTTAGCTCGGATTTTGGCCAAC	-	TAR1	15.77	18.63	1.18	120.87	26.98	0.22	BnaC01g28840D	Splicing factor U2af large subunit B	766	CTTA-GCTCGGATTTTGGCCAAC |o|||||||o||o|||| TGCGGATACGAGCCTAGAACTGGATGCAAGTC	TT3	0.00	0.00	0.00	0.42	815	0.16	1378	0.03
TCGCGCCCTAGGTTTTGCAGCG	-	TAR1	0.90	2.35	2.61	1.23	15.53	12.59	BnaA09g04420D	TAR1	1757	TCGCGCCCTAGGTTTTGCAGCG ||||||||||||||||||| CCCGAGCGCGGGATCCAAAACGTCGCTGGCGG	TT3	0.00	0.00	0.00	0.32	239430	-1.00	101442	-0.78
CAACGCGAGCTGATGACTCGA	-	TAR1	0.90	12.10	13.48	12.72	26.69	2.10	BnaAnng22160D	TAR1	540	CAACGCGAGCTGATGACTCGA ||||||||||||||||||| ATCAGTTGCGCTCGACTACTGAGCGCGAATGA	TT3	0.00	0.00	0.00	0.51	257765	-1.01	114234	-0.85
GACTCTTAGGATCGACTAACC	-	TAR1	0.85	30.23	35.40	6.14	42.37	6.90	BnaA09g04420D	TAR1	1890	GACTCTTAGGATCGACTAACC ||||||||||||||||||| GGGGCTGAGAATCCTAGCTGATTGGGTACACG	TT3	0.00	0.00	0.00	0.23	239430	-1.00	101442	-0.78
TGTGTTACCGCACGCGGTTGGC	+	TAR1	9.35	297.89	31.85	32.46	563.56	17.36	BnaAnng21760D	TAR1	2452	TGTGTTACCGCACGCGGTTGGC ||||||||||||||||||| GGGCACACAATGGCGTGCGCCAACCGGTTTTA	TT3	0.00	0.00	0.00	0.32	47012	-1.01	20912	-0.79
GTCTGCGACGTCGCGAGAAGT	+	TAR1	101.30	1128.77	11.14	181.66	1889.19	10.40	BnaA06g23560D	Beta-D-xylosidase 4	3068	GTCTGCGACGTCGCGAGAAGT |o|||||||||||oo AAAGCGGACGCTGCAGCGGCCTTTGGGTAGAG	TT3	0.00	0.00	0.00	0.42	763	0.93	555	0.73
GCTGAAGCGCGCGACCTATACC	+	TAR1	42.50	44.19	1.04	147.43	141.61	0.96	BnaC06g00260D	Cysteine proteinase RD21a	1520	GCTGAAGCGCGCGACCTATACC ||||o||o||||| o|| ATCTCGACCTTGCGTGCTGGTGGTGGGAGTTA	TT3	0.00	0.00	0.00	0.05	18560	1.24	37108	1.39
CTTAGCTCGGATTTTGGCCAAC	-	TAR1	15.77	18.63	1.18	120.87	26.98	0.22	BnaA01g23100D	Splicing factor U2af large subunit B	684	CTTA-GCTCGGATTTTGGCCAAC |o|||||||o||o|||| TGCGGATACGAGCCTAGAACTGGATGCAAGTC	TT3	0.00	0.00	0.00	0.28	442	0.12	599	-0.06
GACTCTTAGGATCGACTAACC	-	TAR1	0.85	30.23	35.40	6.14	42.37	6.90	BnaC04g09710D	Ribose-phosphate pyrophosphokinase 1, chloroplastic	2640	GACTCTTAGGATCGACTAACC ||||||| ||o||||||| TGGTCTGAGAAT-CTGGCTGATTGTTTTCGTT	TT3	0.00	0.00	0.00	0.32	1146	-0.07	1096	-0.33
TTAGCGCGCAGTTGGGCACCG	-	TAR1	5.35	58.26	10.89	11.87	135.48	11.42	BnaC08g46150D	TAR1	1536	TTAGCGCGCAGTTGGGCACCG ||||||||||||||||||| ATCCAATCGCGCGTCAACCCGTGGCATTGGGC	TT3	0.00	0.00	0.00	0.28	143979	-1.14	60510	-0.80
AGCACGCAGATGCCGAGGCAC	-	TAR1	0.00	6.51	6.51	4.08	14.09	3.45	BnaA07g03520D	Putative polyol transporter 1	849	AGCACGCAGATGCCGAGGCAC |o||||||||||||| ACGGTTGTGAGGCTACCGATCCGTGTGACTCC	TT3	0.00	0.00	0.00	0.37	0	NA	88	0.68
TAGCTCGGATTTTGGCCAACCG	-	TAR1	4.41	19.97	4.53	33.01	20.37	0.62	BnaAnng36730D	Putative uncharacterized protein ART3	240	TAGCTCGGATTTTGGCCAACCG ||||||||||||||||||| AGGAATCGAGCCTAAAACCGGTTGGCGCACGC	TT3	0.00	0.00	0.00	0.14	32584	-0.17	17996	-0.74
CTGATCTCCCGTGTGTTACCG	+	TAR1	120.84	301.33	2.49	152.25	252.46	1.66	BnaA01g16440D	Protochlorophyllide reductase B, chloroplastic	1701	CTGATCTCCCGTGTGTTACCG |||||||||oooo||||| GAGTGACTAGAGGGTGTGAAATG-CTCGGAAG	TT3	0.00	0.00	0.00	0.19	2167	1.05	3120	0.80
GCTAAGGACGTCAGGAGCGTC	+	TAR1	0.00	0.31	0.31	36.10	497.05	13.77	BnaC08g03530D	Probable serine/threonine protein kinase IRE3	4082	GCTAAGGACGTCAGGAGCGTC ||o||||||||||o| GCCGCGGTTCAT-CAGTCCTCACGGGTGACGT	TT3	0.00	0.00	0.00	0.05	382	1.12	757	0.55
TAGGTTAGCGCGCAGTTGGGCA	-	TAR1	0.90	4.72	5.26	1.42	23.80	16.73	BnaAnng22160D	TAR1	3098	TAGGTTAGCGCGCAGTTGGGCA ||||||||||||||||||| CAAGATCCAATCGCGCGTCAACCCGTGGCATT	TT3	0.00	0.00	0.00	0.28	257765	-1.01	114234	-0.85
ACCCGACTCGTAGACAGCGCCT	-	TAR1	9.58	4.27	0.45	28.93	29.64	1.02	BnaAnng36730D	Putative uncharacterized protein ART3	612	ACCCGACTCGTAGACAGCGCCT ||||||||||||||||||| TTGTTGGGCTGAGCATCTGTCGCGGAACACCA	TT3	0.00	0.00	0.00	12.59	32584	-0.17	17996	-0.74

TCAGCGCCATCCATTTTCGGG	-	TAR1	15.92	31.73	1.99	50.07	48.38	0.97	BnaC08g46150D	TAR1	1664	TCAGCGCCATCCATTTTCGGG GCGAAGTCGCGGTAGGTAAAAGCCCCGATCAA	TT3	0.00	0.00	0.00	0.19	143979	-1.14	60510	-0.80
TCGATTAAGACAGCAGGACGG	+	TAR1	82.26	88.01	1.07	155.41	179.30	1.15	BnaC01g37490D	PRA1 family protein F4	488	TCGATTAAG-ACAGCAGGACGG TGCAGCCAGTTCTTGTCGTCTTGCTACCAATA	TT3	0.00	0.00	0.00	0.05	1084	-0.19	14	-0.65
ACCCGATAGAACTCGTTTCCG	-	TAR1	1.80	15.70	8.75	24.85	22.98	0.92	BnaC01g04840D	Protein TIC 22, chloroplastic	304	ACCCGATAGAACTCGTTTCCG TCGTTTGGCTATCT-GAACAGAGGCCATCCTA	TT3	0.00	0.00	0.00	0.09	612	-0.54	596	-0.08
GTCCTGCTGTCTTAATCGACC	-	TAR1	0.00	31.04	31.04	15.75	50.98	3.24	BnaCnng51480D	Cytochrome P450 89A2	1271	GTCCTGCTGTCTTAATCGACC AGGGCAGGGCGATAGAAGCAGC-GGTTGCCGA	TT3	0.00	0.00	0.00	0.32	4	-0.21	12	1.18
CCTCTAATCATTGGCTTTACC	-	TAR1	1.80	20.05	11.17	1.23	36.26	29.39	BnaA09g04420D	TAR1	1364	CCTCTAATCATTGGCTTTACC CTACGGAGATTAGTAACCGAAATGGGCTATCT	TT3	0.00	0.00	0.00	0.05	239430	-1.00	101442	-0.78
CCTCTAATCATTGGCTTTACC	-	TAR1	1.80	20.05	11.17	1.23	36.26	29.39	BnaAnng22160D	TAR1	2918	CCTCTAATCATTGGCTTTACC CTACGGAGATTAGTAACCGAAATGGGCTATCT	TT3	0.00	0.00	0.00	0.05	257765	-1.01	114234	-0.85
ATGGCCGTTTAGGCCAAGGAAG	+	TAR1	38.83	72.55	1.87	104.51	182.04	1.74	BnaC03g44110D	Chlorophyll a-b binding protein 151, chloroplastic	98	ATGGCCGTTTAGGCCAAGGAAG GAACTCCCGGCAAA-CCGGTCGCTTCCTCCTA	TT3	0.00	0.00	0.00	0.28	291224	-0.22	195401	0.08
ACAACCCGACTCGTAGACAGCG	-	TAR1	0.00	14.24	14.24	33.42	97.89	2.93	BnaAnng22160D	TAR1	1615	ACAACCCGACTCGTAGACAGCG GGTTTGTTGGGCTGAGCATCTGTCGCGGAGCA	TT3	0.00	0.00	0.00	1.43	257765	-1.01	114234	-0.85
AACCCGACTCGTAGACAGCGC	-	TAR1	14.23	78.93	5.55	102.12	105.59	1.03	BnaAnng36730D	Putative uncharacterized protein ART3	613	AACCCGACTCGTAGACAGCGC TTTGTTGGGCTGAGCATCTGTCGCGGAACACC	TT3	0.00	0.00	0.00	0.93	32584	-0.17	17996	-0.74
TGGCCGTTTAGGCCAAGGAAG	+	TAR1	31.56	157.36	4.99	128.60	450.85	3.51	BnaC02g02650D	unknown	1815	TGGCCGTTTAGGCCAAGGAAG GGTCACGGTCAAATCCAGTTTCTTCATCATTT	TT3	0.00	0.00	0.00	0.05	1506	0.96	3550	-0.57
ACCACCAAGATCTGCACCGACG	-	TAR1	0.00	15.07	15.07	0.00	71.22	71.22	BnaA09g04420D	TAR1	1795	ACCACCAAGATCTGCACCGACG ATGATGGTGGTTCTAGACGGGGCTGCCGGCGA	TT3	0.00	0.00	0.00	0.51	239430	-1.00	101442	-0.78
TTAATCGACCAACACCCTTTG	-	TAR1	3.55	10.61	2.98	4.08	20.18	4.95	BnaC08g46150D	TAR1	1568	TTAATCGACCAACACCCTTTG ACAGAATTAGCTGGTTGTGGGAAACACCCAAG	TT3	0.00	0.00	0.00	0.14	143979	-1.14	60510	-0.80
TCAGCGCCATCCATTTTCGGGG	-	TAR1	4.45	5.39	1.21	8.20	41.24	5.03	BnaA09g05840D	Auxin response factor 2	3746	TCAGCGCCATCCATTTTCGGGG TGATAGTCG-GTTAGGAAGAAGCCTCGGTAGT	TT3	0.00	0.00	0.00	0.19	1569	0.82	4618	-0.39
CATCCTCTCGAGGATATGGGAC	+	TAR1	1.41	65.82	46.71	6.96	261.61	37.60	BnaAnng21760D	TAR1	2490	CATCCTCTCGAGGATATGGGAC GGGGGTAGGAGAGCTCCTATACCCTGCCTTCG	TT3	0.00	0.00	0.00	0.23	47012	-1.01	20912	-0.79
GAATAGGTCGAGGACATTGCG	-	TAR1	0.85	55.66	65.18	3.48	105.77	30.38	BnaA03g12990D	unknown	2005	GAATAGGTCGAGGACATTGCG TCTTCTTCTTCAGCTCC-GTAAAACCTCGCCA	TT3	0.00	0.00	0.00	0.14	225	0.71	382	0.31
TTGGTCGATTAAGACAGCAGG	+	TAR1	67.80	122.62	1.81	163.65	221.13	1.35	BnaC08g17080D	ACT domain-containing protein ACR11	626	TTGGTCGATTAAGACAGCAGG TTAGAACCAGCTAATACTGGTGACCACAGCCT	TT3	0.00	0.00	0.00	0.19	43675	-0.96	34325	-0.49
TAATCGACCAACACCCTTTGT	-	TAR1	1.80	11.34	6.31	6.14	17.68	2.88	BnaC06g31760D	Zinc finger protein VAR3, chloroplastic	1799	TAATCGACCAACACCCTTTGT CACTAGTAG-TGGTTGTGAGAAGCTTAGGCCA	TT3	0.00	0.00	0.00	0.09	22	-0.28	21	-0.32
CATGTGAACGGCACTTGCACA	+	TAR1	830.30	1959.98	2.36	2077.74	3318.76	1.60	BnaC08g24660D	Soluble inorganic pyrophosphatase 4	2579	CATGTGAACG-GCACTTGCACA TGTGTTACACTTTCACGTCAACGTGTGCAAGA	TT3	0.00	0.00	0.00	0.23	548	0.33	1032	0.57
CTGGAGCTCGGAAACGAGTTC	+	TAR1	40.26	81.04	2.01	92.73	101.54	1.09	BnaAnng21760D	TAR1	1341	CTGGAGCTCGGAAACGAGTTC TATCGACCTCGAGCCTTGCTTAAGATAGCCC	TT3	0.00	0.00	0.00	0.37	47012	-1.01	20912	-0.79
TTTGTGGGTTCTAGGTTAGCG	-	TAR1	6.25	16.23	2.60	5.35	19.64	3.67	BnaA09g04420D	TAR1	1555	TTTGTGGGTTCTAGGTTAGCG TGGGAAACACCCAAGATCCAATCGCGCGTCAA	TT3	0.00	0.00	0.00	0.19	239430	-1.00	101442	-0.78
TCGATCGGCGGACCGGATTGC	-	TAR1	13.22	15.32	1.16	9.01	23.56	2.61	BnaC01g19970D	unknown	1798	TCGATCGGCGGACCGGATTGC TTGTAGAT-GCCGCCTAGCCTGTCGTCATTGC	TT3	0.00	0.00	0.00	0.42	1155	-0.08	1964	-0.21
TTTGAGAATAGGTCGAGGACAT	-	TAR1	4.41	5.81	1.32	2.66	27.40	10.32	BnaA10g18670D	Nipped-B-like protein A	9074	TTTGAGAATAGGTC-GAGGACAT AGGCAACCTCTTATCCGGACTCTTGTGTTAGT	TT3	0.00	0.00	0.00	0.09	222	0.32	477	0.05
AACCCACAAAGGGTGTTGGTC	+	TAR1	813.37	739.76	0.91	1886.74	1963.55	1.04	BnaC08g47040D	unknown	597	AACCCACAAAGGGTGTTGGTC GATCTTGGGTGTTTCCCACAACCAGCTAATTC	TT3	0.00	0.00	0.00	0.05	127	-1.10	34	-1.09
CAGTTGGGCACCGTAACCCGG	-	TAR1	34.13	50.77	1.49	48.64	103.11	2.12	BnaC03g06270D	Protein NUCLEAR FUSION DEFECTIVE 4	2462	CAGTTGGGCACCGTAACCCGG TCGGGTC-ACTCGTGGCATGGGCTCAGGATAG	TT3	0.00	0.00	0.00	0.14	5984	1.18	564	-1.80
TAACGTTGCCGTCAACCGCCA	-	TAR1	0.00	11.46	11.46	12.09	26.52	2.19	BnaA03g00380D	Pyridoxal 5'-phosphate synthase subunit PDX1.3	142	TAACGTTGCCGTCAACCGCCA TAGCGTGGCAATGGCATTTGGCGGTGCTGCGA	TT3	0.00	0.00	0.00	0.09	29735	-1.22	19962	-0.38
TCGCGCCCTAGGTTTTGCAGCG	-	TAR1	0.90	2.35	2.61	1.23	15.53	12.59	BnaAnng22160D	TAR1	3311	TCGCGCCCTAGGTTTTGCAGCG CCCGAGCGCGGGATCCAAAACGTCGCTGGCGG	TT3	0.00	0.00	0.00	0.32	257765	-1.01	114234	-0.85
TTTGTGGGTTCTAGGTTAGCG	-	TAR1	6.25	16.23	2.60	5.35	19.64	3.67	BnaAnng36730D	Putative uncharacterized protein ART3	1555	TTTGTGGGTTCTAGGTTAGCG TGGGAAACACCCAAGATCCAATCGCGCGTCAA	TT3	0.00	0.00	0.00	0.19	32584	-0.17	17996	-0.74
CAACCCGACTCGTAGACAGCA	-	TAR1	7.90	9.54	1.21	56.28	20.80	0.37	BnaAnng36730D	Putative uncharacterized protein ART3	614	CAACCCGACTCGTAGACAGCA GTTTGTTGGGCTGAGCATCTGTCGCGGAACAC	TT3	0.00	0.00	0.00	1.20	32584	-0.17	17996	-0.74
TAGACAGCGCCTCGTGGTGCGA	-	TAR1	0.85	2.64	3.09	3.70	14.08	3.80	BnaA09g04420D	TAR1	602	TAGACAGCGCCTCGTGGTGCGA GAGCATCTGTCGCGGAGCACCACGCTGTCCCA	TT3	0.00	0.00	0.00	2.55	239430	-1.00	101442	-0.78
CCGTGGGATGGCTCAACAAAGC	-	TAR1	0.90	19.60	21.83	14.78	53.66	3.63	BnaA09g04420D	TAR1	1447	CCGTGGGATGGCTCAACAAAGC CTAAGGCACCCTACCGAGTTGTTTCGTCGGTG	TT3	0.00	0.00	0.00	0.37	239430	-1.00	101442	-0.78
GTTGAGCCATCCCACGGAATC	+	TAR1	10.09	14.69	1.46	31.56	26.99	0.86	BnaCnng75490D	Nitrilase 2	194	GTTGAGCCATCCCACGGAATC CTACCAACTAGGTAGGG-GCTTTGGGGTCTAC	TT3	0.00	0.00	0.00	0.32	654	-0.29	6707	-0.06
CTTAGGATCGACTAACCCATG	-	TAR1	8.71	37.09	4.26	34.06	52.79	1.55	BnaA09g04420D	TAR1	1886	CTTAGGATCGACTAACCCATG CTGAGAATCCTAGCTGATTGGGTACACGTTCA	TT3	0.00	0.00	0.00	0.23	239430	-1.00	101442	-0.78
GCGGACCGGATTGCTCCGTTC	-	TAR1	134.30	88.02	0.66	64.08	173.69	2.71	BnaAnng22160D	TAR1	1818	GCGGACCGGATTGCTCCGTTC TAGCCGCCTGGCCTAACGAGGCAAGGCGTAGG	TT3	0.00	0.00	0.00	0.23	257765	-1.01	114234	-0.85
GTCCCTCTAAGAAGCCGGCCG	-	TAR1	6.20	40.25	6.50	13.09	105.07	8.02	BnaA04g13660D	Extra-large guanine nucleotide-binding protein 1	2064	GTCCCTCTAAGAAGCCGGCCG AGTGCAGGGAG-TTCTTCGTATGGCTCTATTG	TT3	0.00	0.00	0.00	0.05	996	0.40	2059	0.63
TCAAGGTCGGTCGGCTGTGCA	-	TAR1	3.46	13.07	3.78	12.09	28.36	2.35	BnaCnng40810D	Probable acyl-activating enzyme 17, peroxisomal	2562	TCAAGGTCGGTCGGCTGTGCA GGTGGGTTCCAACCAGCCGGTTCGTTGTTGTA	TT3	0.00	0.00	0.00	0.09	5014	0.84	8505	0.73

AACCCACAAAGGGTGTTGGTC	+	TAR1	813.37	739.76	0.91	1886.74	1963.55	1.04	BnaAnng21760D	TAR1	1113	AACCCACAAAGGGTGTTGGTC GATCTTGGGTGTTTCCCACAACCAGTTAAATC	TT3	0.00	0.00	0.00	0.05	47012	-1.01	20912	-0.79
TTAGCTCGGATTTTGGCCAACC	-	TAR1	175.30	202.64	1.16	366.78	173.10	0.47	BnaAnng36730D	Putative uncharacterized protein ART3	241	TTAGCTCGGATTTTGGCCAACC CAGGAATCGAGCCTAAAACCGGTTGGCGCACG	TT3	0.00	0.00	0.00	0.28	32584	-0.17	17996	-0.74
AGAAGCCGGCCGTGAAGGGATG	-	TAR1	1.80	30.06	16.74	27.28	53.97	1.98	BnaA10g07430D	DETOXIFICATION 16	3069	AGAAGCCGGCCGTGAAGGGATG TCTCTCTTCGACCGGCACT-CACTACTTTGCA	TT3	0.00	0.00	0.00	0.05	3602	-0.25	3542	-0.28
TTAAATAGGTAGGACGGGGTGG	+	TAR1	14.19	19.90	1.40	50.70	45.29	0.89	BnaA06g15350D	NAD kinase 2, chloroplastic	2879	TTAAATAGGTAGGACGGGGTGG GTCCAATTTA-CTATGTTGCCCTCCCTGTCGA	TT3	0.00	0.00	0.00	0.09	2920	0.26	6023	-0.02
GAGAATAGGTCGAGGACATTGC	-	TAR1	6.20	68.62	11.06	11.04	358.72	32.49	BnaA09g19150D	IQ-DOMAIN 31	2532	GAGAATAGGTCGAGGACATTGC ATTTCTCTTGTACAGTTTCTG-AGTGGTGTGG	TT3	0.00	0.00	0.00	0.14	14	0.41	8	0.03
ACAACCCGACTCGTAGACAGC	-	TAR1	29.34	60.34	2.06	151.21	135.51	0.90	BnaAnng36730D	Putative uncharacterized protein ART3	615	ACAACCCGACTCGTAGACAGC GGTTTGTTGGGCTGAGCATCTGTCGCGGAACA	TT3	0.00	0.00	0.00	1.43	32584	-0.17	17996	-0.74
TAGGTTAGCGCGCAGTTGGGCA	-	TAR1	0.90	4.72	5.26	1.42	23.80	16.73	BnaAnng36730D	Putative uncharacterized protein ART3	1544	TAGGTTAGCGCGCAGTTGGGCA CAAGATCCAATCGCGCGTCAACCCGTGGCATT	TT3	0.00	0.00	0.00	0.28	32584	-0.17	17996	-0.74
GTAACACACGGGAGATCAGCT	-	TAR1	3.50	47.28	13.50	8.79	35.72	4.06	BnaC05g20570D	Mediator of RNA polymerase II transcription subunit 25	3880	GTAACACACGGGAGATCAGCT CGGGCTTTGTGTTCCTTC-AGTCGAAACGGTT	TT3	0.00	0.00	0.00	0.42	654	1.09	1569	0.40
TCAGCGCCATCCATTTTCGGGG	-	TAR1	4.45	5.39	1.21	8.20	41.24	5.03	BnaC08g46150D	TAR1	1664	TCAGCGCCATCCATTTTCGGGG GCGAAGTCGCGGTAGGTAAAAGCCCCGATCAA	TT3	0.00	0.00	0.00	0.19	143979	-1.14	60510	-0.80
ACCAAGATCTGCACCGACGGCC	-	TAR1	1.75	21.24	12.13	2.66	71.73	27.00	BnaA09g04420D	TAR1	1792	ACCAAGATCTGCACCGACGGCC ATGGTGGTTCTAGACGGGGCTGCCGGCGAGGC	TT3	0.00	0.00	0.00	0.14	239430	-1.00	101442	-0.78
TTAAGGTGGTGACCTAAGCCCG	+	TAR1	13.32	13.45	1.01	31.21	35.31	1.13	BnaC05g37680D	Monothiol glutaredoxin-S15, mitochondrial	688	TTAAGG-TGGTGACCTAAGCCCG GAGAATGCCGATCACTCGATTTGGGTGTGACT	TT3	0.00	0.00	0.00	0.05	77	-0.15	100	-0.18
GCCCTAGGTTTTGCAGCGACC	-	TAR1	2.61	9.92	3.81	2.66	24.18	9.10	BnaC08g46150D	TAR1	1749	GCCCTAGGTTTTGCAGCGACC AGCGCGGGATCCAAAACGTCGCTGGCGGCGCG	TT3	0.00	0.00	0.00	0.28	143979	-1.14	60510	-0.80
CTTAGCTCGGATTTTGGCCAAC	-	TAR1	15.77	18.63	1.18	120.87	26.98	0.22	BnaAnng36730D	Putative uncharacterized protein ART3	242	CTTAGCTCGGATTTTGGCCAAC GCAGGAATCGAGCCTAAAACCGGTTGGCGCAC	TT3	0.00	0.00	0.00	0.65	32584	-0.17	17996	-0.74
AAACAACCCGACTCGTAGACA	-	TAR1	3.50	10.58	3.02	30.53	25.16	0.82	BnaAnng22160D	TAR1	1617	AAACAACCCGACTCGTAGACA AGGGTTTGTTGGGCTGAGCATCTGTCGCGGAG	TT3	0.00	0.00	0.00	2.45	257765	-1.01	114234	-0.85
TTAATCGACCAACACCCTTTG	-	TAR1	3.55	10.61	2.98	4.08	20.18	4.95	BnaC02g36110D	unknown	169	TTAATCGACCAACACCCTTTG ACAGAATTAGCTGGTTGTGGGAAACACCCAAG	TT3	0.00	0.00	0.00	0.14	25737	-1.12	12547	-0.80
CAACCCGACTCGTAGACAGCA	-	TAR1	7.90	9.54	1.21	56.28	20.80	0.37	BnaA09g04420D	TAR1	614	CAACCCGACTCGTAGACAGCA GTTTGTTGGGCTGAGCATCTGTCGCGGAGCAC	TT3	0.00	0.00	0.00	1.20	239430	-1.00	101442	-0.78
ATTTTCAAGGGCCGCCGGGAA	-	TAR1	16.68	19.48	1.17	47.60	24.65	0.52	BnaCnng60170D	Putative cytochrome c oxidase subunit 5b-like	29	ATTTTCAAGGGCCGCCGGGAA CGGCTAAGAGTTACCGTTTGCCCTTTCTCCTT	TT3	0.00	0.00	0.00	0.05	165	-0.51	158	-0.29
ATCGAGGCCTGGCTCTTGCCC	-	TAR1	57.01	79.21	1.39	214.29	161.12	0.75	BnaA09g04420D	TAR1	1715	ATCGAGGCCTGGCTCTTGCCC TGAGTAGCTCCGGACCGAGAACGGGGCTGCCG	TT3	0.00	0.00	0.00	0.14	239430	-1.00	101442	-0.78
GTCGCAGACGGCGAACCACCCA	-	TAR1	28.57	118.70	4.15	47.63	205.21	4.31	BnaAnng22160D	TAR1	644	GTCGCAGACGGCGAACCACCCA GCTGCAGCGTCTGCCGCTTGGTGGGTGCAGCG	TT3	0.00	0.00	0.00	0.46	257765	-1.01	114234	-0.85
TCAAGGTCGGTCGGCTGTGCA	-	TAR1	3.46	13.07	3.78	12.09	28.36	2.35	BnaA03g39660D	Probable acyl-activating enzyme 17, peroxisomal	2278	TCAAGGTCGGTCGGCTGTGCA GGTGGGTTCCAACCAGCCGGTTCGTTGTTGTA	TT3	0.00	0.00	0.00	0.09	1885	1.18	2946	0.03
TCTAATCATTGGCTTTACCCGA	-	TAR1	2.61	3.73	1.43	14.77	32.25	2.18	BnaAnng36730D	Putative uncharacterized protein ART3	1362	TCTAATCATTGGCTTTACCCGA ACGGAGATTAGTAACCGAAATGGGCTATCTTG	TT3	0.00	0.00	0.00	0.28	32584	-0.17	17996	-0.74
AAAATGGCCCACTTGGAGCTCT	-	TAR1	4.45	6.53	1.47	0.00	25.41	25.41	BnaA09g04420D	TAR1	1474	AAAATGGCCCACTTGGAGCTCT TGGTTTTTACCGGGTGAACCTCGAGAGCTAAG	TT3	0.00	0.00	0.00	0.14	239430	-1.00	101442	-0.78
ACTCTTAGGATCGACTAACCC	-	TAR1	6.07	16.29	2.69	26.01	20.45	0.79	BnaC08g46150D	TAR1	1885	ACTCTTAGGATCGACTAACCC GGGCTGAGAATCCTAGCTGATTGGGTACACGT	TT3	0.00	0.00	0.00	0.32	143979	-1.14	60510	-0.80
ACTCATCGAGGCCTGGCTCTTG	-	TAR1	0.85	17.89	20.95	2.66	53.35	20.08	BnaAnng22160D	TAR1	3273	ACTCATCGAGGCCTGGCTCTTG AGGATGAGTAGCTCCGGACCGAGAACGGGGCT	TT3	0.00	0.00	0.00	0.51	257765	-1.01	114234	-0.85
ACTCATCGAGGCCTGGCTCTT	-	TAR1	4.40	20.17	4.58	13.73	31.60	2.30	BnaA09g04420D	TAR1	1719	ACTCATCGAGGCCTGGCTCTT AGGATGAGTAGCTCCGGACCGAGAACGGGGCT	TT3	0.00	0.00	0.00	0.51	239430	-1.00	101442	-0.78
ACAACCCGACTCGTAGACAGC	-	TAR1	29.34	60.34	2.06	151.21	135.51	0.90	BnaAnng22160D	TAR1	1615	ACAACCCGACTCGTAGACAGC GGTTTGTTGGGCTGAGCATCTGTCGCGGAGCA	TT3	0.00	0.00	0.00	1.43	257765	-1.01	114234	-0.85
AATGGATGGCGCTGAAGCGCG	+	TAR1	114.78	180.52	1.57	373.41	479.41	1.28	BnaC03g26080D	60S ribosomal protein L7a-1	243	AATGGATGGCGCTGAAG-CGCG ACGTTTGCCTGCCGCGACTTCAGCTTTTTACT	TT3	0.00	0.00	0.00	0.05	478	0.55	771	0.10
AAGGTTCCATGTGAACGGCAC	+	TAR1	44.54	104.68	2.35	119.79	220.04	1.84	BnaC01g33270D	Zinc finger protein AZF2	94	AAGGTTCCATGTGAACGGCAC TCGGTTCCGAGGTACTTTTGCCGCAGCAAGTA	TT3	0.00	0.00	0.00	0.05	2968	-0.97	2325	0.03
ACAACCCGACTCGTAGACAGCG	-	TAR1	0.00	14.24	14.24	33.42	97.89	2.93	BnaA09g04420D	TAR1	615	ACAACCCGACTCGTAGACAGCG GGTTTGTTGGGCTGAGCATCTGTCGCGGAGCA	TT3	0.00	0.00	0.00	1.43	239430	-1.00	101442	-0.78
TCTAATCATTGGCTTTACCCG	-	TAR1	8.80	9.99	1.13	6.36	23.51	3.70	BnaAnng36730D	Putative uncharacterized protein ART3	1362	TCTAATCATTGGCTTTACCCG ACGGAGATTAGTAACCGAAATGGGCTATCTTG	TT3	0.00	0.00	0.00	0.28	32584	-0.17	17996	-0.74
CGCATGTCAAGACGCTCCT	-	TAR1	6.02	10.90	1.81	622.23	22.79	0.04	BnaC07g44630D	unknown	1221	CGCATGTCAAGACGCTCCT TAAAGCGTACAGTTTCGAAAGGAAACTAGAAG	TT3	0.00	0.00	0.00	0.28	185	-0.27	200	0.27
GTCCTGCTGTCTTAATCGACC	-	TAR1	0.00	31.04	31.04	15.75	50.98	3.24	BnaC08g46150D	TAR1	1579	GTCCTGCTGTCTTAATCGACC GTGGCAGGACGACAGAATTAGCTGGTTGTGGG	TT3	0.00	0.00	0.00	0.19	143979	-1.14	60510	-0.80
TTAATCGACCAACACCCTTTG	-	TAR1	3.55	10.61	2.98	4.08	20.18	4.95	BnaA09g04420D	TAR1	1572	TTAATCGACCAACACCCTTTG ACAGAATTAGCTGGTTGTGGGAAACACCCAAG	TT3	0.00	0.00	0.00	0.14	239430	-1.00	101442	-0.78
TCTAATCATTGGCTTTACCCGA	-	TAR1	2.61	3.73	1.43	14.77	32.25	2.18	BnaC08g46150D	TAR1	1358	TCTAATCATTGGCTTTACCCGA ACGGAGATTAGTAACCGAAATGGGCTATCTTG	TT3	0.00	0.00	0.00	0.28	143979	-1.14	60510	-0.80
TAAAGTTTGAGAATAGGTCGA	-	TAR1	11.32	34.87	3.08	18.63	38.80	2.08	BnaC08g46150D	TAR1	1400	TAAAGTTTGAGAATAGGTCGA ATAAATTTCAAACTCTTATCCAGCTCCTGTAA	TT3	0.00	0.00	0.00	0.05	143979	-1.14	60510	-0.80

TGATTGGCTGGATCCCTCACG	+	TAR1	19.86	38.79	1.95	41.58	129.90	3.12	BnaC03g49830D	Peptidyl-prolyl cis-trans isomerase FKBP12	1068	TGATTGGCTGGATCCCTCACG |||||||||||o|||| TGGCTCAAACCGACCTAAGGGGTGCGGCCTTT	TT3	0.00	0.00	0.00	0.69	12410	-0.68	21342	-0.06
CGTCCCATATCCTCGAGAGGA	-	TAR1	172.94	326.00	1.89	311.97	170.30	0.55	BnaA05g01180D	GATA transcription factor 25	411	CGTCCCATATCCTCGAGAGGA ||||||||| ||| o|||| TATAGCA-GGTATAGCAGCATTCCTTACACTG	TT3	0.00	0.00	0.00	0.19	0	0.19	42	0.21
TGTCGGCCAAGGTGTGAACTCG	-	TAR1	30.41	37.07	1.22	133.79	108.00	0.81	BnaA05g35790D	Protein NRT1/ PTR FAMILY 7.3	2649	TGTCGGCCAAGGTGTGAACTCG ||| |||||||oo o||||o|| GGCAACA-CCGGTTCTGAGCTTGGGCCCACCG	TT3	0.00	0.00	0.00	0.05	206	-1.05	331	-1.42
CTACCTATTTAAAGTTTGAGA	-	TAR1	8.85	23.08	2.61	11.04	36.70	3.32	BnaC08g46150D	TAR1	1409	CTACCTATTTAAAGTTTGAGA |||||||||||||||||| GCAGGATGGATAAATTTCAAACTCTTATCCAG	TT3	0.00	0.00	0.00	0.56	143979	-1.14	60510	-0.80
CAACCCGACTCGTAGACAGCA	-	TAR1	7.90	9.54	1.21	56.28	20.80	0.37	BnaAnng22160D	TAR1	1614	CAACCCGACTCGTAGACAGCA |||||||||||||||||| GTTTGTTGGGCTGAGCATCTGTCGCGGAGCAC	TT3	0.00	0.00	0.00	1.20	257765	-1.01	114234	-0.85
TAGCTCGGATTTTGGCCAACC	-	TAR1	13.93	255.39	18.33	76.00	163.78	2.16	BnaAnng36730D	Putative uncharacterized protein ART3	240	TAGCTCGGATTTTGGCCAACC |||||||||||||||||| AGGAATCGAGCCTAAAACCGGTTGGCGCACGC	TT3	0.00	0.00	0.00	0.14	32584	-0.17	17996	-0.74
CGTAGACAGCGCCTCGTGGTGC	-	TAR1	8.63	2.33	0.27	14.74	29.31	1.99	BnaAnng22160D	TAR1	1604	CGTAGACAGCGCCTCGTGGTGC |||||||||||||||||||| CTGAGCATCTGTCGCGGAGCACCACGCTGTCC	TT3	0.00	0.00	0.00	0.23	257765	-1.01	114234	-0.85
ACAACCCGACTCGTAGACAGCG	-	TAR1	0.00	14.24	14.24	33.42	97.89	2.93	BnaAnng36730D	Putative uncharacterized protein ART3	615	ACAACCCGACTCGTAGACAGCG |||||||||||||||||||| GGTTTGTTGGGCTGAGCATCTGTCGCGGAACA	TT3	0.00	0.00	0.00	1.43	32584	-0.17	17996	-0.74
CCCGGGCTTAGGTCACCACCT	-	TAR1	58.29	25.16	0.43	43.78	49.41	1.13	BnaA09g09110D	Thioredoxin reductase 2	828	CCCGGGCTTAGGTCACCACCT ||o||||||| ||||||| ATCATGGTCCGAATC-AGTGGTGTATTGGTAG	TT3	0.00	0.00	0.00	0.19	1005	0.48	1074	0.05
ACCAAGATCTGCACCGACGGC	-	TAR1	17.58	123.69	7.04	38.09	209.00	5.49	BnaC08g46150D	TAR1	1788	ACCAAGATCTGCACCGACGGC |||||||||||||||||||| ATGGTGGTTCTAGACGTGGCTGCCGGCGAGGC	TT3	0.00	0.00	0.00	0.14	143979	-1.14	60510	-0.80
TAGGTTAGCGCGCAGTTGGGC	-	TAR1	0.00	7.41	7.41	4.27	21.52	5.04	BnaAnng36730D	Putative uncharacterized protein ART3	1544	TAGGTTAGCGCGCAGTTGGGC |||||||||||||||||| CAAGATCCAATCGCGCGTCAACCCGTGGCATT	TT3	0.00	0.00	0.00	0.28	32584	-0.17	17996	-0.74
ACCCGACTCGTAGACAGCGCCT	-	TAR1	9.58	4.27	0.45	28.93	29.64	1.02	BnaC08g46150D	TAR1	608	ACCCGACTCGTAGACAGCGCCT |||||||||||||||||||| TTGTTGGGCTGAGCATCTGTCGCGGAGCACCA	TT3	0.00	0.00	0.00	12.59	143979	-1.14	60510	-0.80
CAGCGCCATCCATTTTCGGGGC	-	TAR1	3.46	4.69	1.36	12.50	24.52	1.96	BnaA09g04420D	TAR1	1667	CAGCGCCATCCATTTTCGGGGC |||||||||||||||||||| CGAAGTCGCGGTAGGTAAAAGCCCCGATCAAC	TT3	0.00	0.00	0.00	0.14	239430	-1.00	101442	-0.78
ACGCCCCGAATCGATCGGCGGA	-	TAR1	6.16	10.09	1.64	3.70	48.21	13.03	BnaCnng65030D	unknown	1101	ACGCCCCGAATCGATCGGCGGA |||||||||| |o|||| CGAGTACGGGGCTTA-CTTGTCGCATGTCGAA	TT3	0.00	0.00	0.00	0.05	136	0.89	143	1.16
TCAGCGCCATCCATTTTCGGGG	-	TAR1	4.45	5.39	1.21	8.20	41.24	5.03	BnaC02g36110D	unknown	265	TCAGCGCCATCCATTTTCGGGG ||||||||||||||||||| GCGAAGTCGCGGTAGGTAAAAGCCCCGATCAA	TT3	0.00	0.00	0.00	0.19	25737	-1.12	12547	-0.80
ACCACCAAGATCTGCACCGACG	-	TAR1	0.00	15.07	15.07	0.00	71.22	71.22	BnaC02g36110D	unknown	390	ACCACCAAGATCTGCACCGACG ||||||||||||||||||o ATGATGGTGGTTCTAGACGTGGCTGTCGGTGA	TT3	0.00	0.00	0.00	0.51	25737	-1.12	12547	-0.80
CGTCCTTAGCTCGGATTTTGGC	-	TAR1	#N/A	#N/A	#N/A	121.64	188.13	1.55	BnaA01g24160D	unknown	1728	CGTCCTTAGCTCGGATTTTGGC ||o||||o|o|o|| |||o|| CTATGCGGGAATTGGGTCTCAAATCGAAAAAC	TT3	0.00	0.00	0.00	0.46	4547	1.24	6710	-0.23
ACAACCCGACTCGTAGACAGC	-	TAR1	29.34	60.34	2.06	151.21	135.51	0.90	BnaC08g46150D	TAR1	611	ACAACCCGACTCGTAGACAGC |||||||||||||||||| GGTTTGTTGGGCTGAGCATCTGTCGCGGAGCA	TT3	0.00	0.00	0.00	1.43	143979	-1.14	60510	-0.80
AACCCGACTCGTAGACAGCGCC	-	TAR1	3.50	5.68	1.62	11.53	41.18	3.57	BnaAnng36730D	Putative uncharacterized protein ART3	613	AACCCGACTCGTAGACAGCGCC |||||||||||||||||||| TTTGTTGGGCTGAGCATCTGTCGCGGAACACC	TT3	0.00	0.00	0.00	0.93	32584	-0.17	17996	-0.74
TTGGTCCGTGTTACAAGACA	-	TAR1	3.42	5.42	1.59	13.06	30.96	2.37	BnaAnng36730D	Putative uncharacterized protein ART3	1009	TTGGTCCGTGTTACAAGACA |||||||||||||||| GAGGAACCAGGCACAAAGTTCTGCCCAGCTTA	TT3	0.00	0.00	0.00	0.79	32584	-0.17	17996	-0.74
ACCCGATAGAACTCGTTTCCG	-	TAR1	1.80	15.70	8.75	24.85	22.98	0.92	BnaA02g18740D	Trehalose-phosphate phosphatase B	1492	ACCCGATAGAACTCGTTTCCG ||||||||||o|| o|| GGCTTGGGCTATCTTGGGCTTGGCCAGGGCTT	TT3	0.00	0.00	0.00	0.14	95	-0.97	46	-1.42
TGCGGGATGAACCGGAAGCCG	+	TAR1	253.07	296.40	1.17	613.72	498.18	0.81	BnaA03g38530D	unknown	1108	TGCGGGATGAACCGGAAGCCG ||| |||||||||o|o GAAAACGACCTACTTGGACTTTGTTTTTGTTT	TT3	0.00	0.00	0.00	0.05	1083	-0.45	897	-0.33
CTACCTATTTAAAGTTTGAGA	-	TAR1	8.85	23.08	2.61	11.04	36.70	3.32	BnaA09g04420D	TAR1	1413	CTACCTATTTAAAGTTTGAGA |||||||||||||||||| GCAGGATGGATAAATTTCAAACTCTTATCCAG	TT3	0.00	0.00	0.00	0.56	239430	-1.00	101442	-0.78
TAGTCCCTCTAAGAAGCCGGCC	-	TAR1	1.75	29.80	17.01	10.03	119.14	11.88	BnaAnng22160D	TAR1	321	TAGTCCCTCTAAGAAGCCGGCC |||||||||||||||||| CGGTATCAGGGAGATTCTTCGGCCGGCACTTC	TT3	0.00	0.00	0.00	0.09	257765	-1.01	114234	-0.85
CGTCCTTAGCTCGGATTTTGGC	-	TAR1	#N/A	#N/A	#N/A	121.64	188.13	1.55	BnaA08g12620D	Serine/threonine-protein kinase HT1	2037	CGTCCTTAGCTCGGATTTTGGC |||| ||||||||oo|| GTCAGCAGTAATGGAGCC-AAAGTCGAGGGAG	TT3	0.00	0.00	0.00	0.05	980	0.53	1395	0.20
GATCTCCCGTGTGTTACCGCA	+	TAR1	28.71	186.86	6.51	44.09	119.75	2.72	BnaA03g18910D	Zinc finger CCCH domain-containing protein 29	20	GATCTCCCGTGTGTTACCGCA |||||||| oo|o||||| ACTCCTAGAGCGCAAGTAGTGGCGTCGACGGT	TT3	0.00	0.00	0.00	0.23	499	-0.53	489	0.09
CGGTTCCGGAATTTTAACCGGA	-	TAR1	0.85	7.22	8.46	0.00	25.46	25.46	BnaC02g26290D	unknown	512	CGG-TTCCGGAATTTTAACCGGA |o| |o|||||||o||||| GGTGTCGAGGGCCTTAAAGTTGGCCAAAGAGG	TT3	0.00	0.00	0.00	0.79	1336	0.02	483	2.03
AAAATGGCCCACTTGGAGCTCT	-	TAR1	4.45	6.53	1.47	0.00	25.41	25.41	BnaAnng22160D	TAR1	3028	AAAATGGCCCACTTGGAGCTCT ||||||||||||||||||| TGGTTTTTACCGGGTGAACCTCGAGAGCTAAG	TT3	0.00	0.00	0.00	0.14	257765	-1.01	114234	-0.85
TAGGTTAGCGCGCAGTTGGGC	-	TAR1	0.00	7.41	7.41	4.27	21.52	5.04	BnaC02g36110D	unknown	141	TAGGTTAGCGCGCAGTTGGGC |||||||||||||||||| CAAGATCCAATCGCGCGTCAACCCGTGGCATT	TT3	0.00	0.00	0.00	0.28	25737	-1.12	12547	-0.80
CTGGAGCTCGGAAACGAGTTC	+	TAR1	40.26	81.04	2.01	92.73	101.54	1.09	BnaCnng72040D	Purple acid phosphatase 10	834	CTGGAGCTCGGAAACGAGTTC |||o||||||| || ||||| GACGGACTTCGAGCCATTCCTCATGCCATGGA	TT3	0.00	0.00	0.00	0.09	176	0.29	95	-0.95
TAGGTTAGCGCGCAGTTGGGCA	-	TAR1	0.90	4.72	5.26	1.42	23.80	16.73	BnaC02g36110D	unknown	141	TAGGTTAGCGCGCAGTTGGGCA ||||||||||||||||||| CAAGATCCAATCGCGCGTCAACCCGTGGCATT	TT3	0.00	0.00	0.00	0.28	25737	-1.12	12547	-0.80
CGTCTGCGACGTCGCGAGAAG	+	TAR1	109.87	319.01	2.90	216.40	447.47	2.07	BnaC08g26820D	unknown	139	CGTCTGCGACGTCGCGAGAAG |||||||||| ||||| TACCGCAGACGCTGCCGCTC-CTTCTATCCTC	TT3	0.00	0.00	0.00	0.05	1857	-0.78	2002	-0.05
CCGTGGGATGGCTCAACAAAGC	-	TAR1	0.90	19.60	21.83	14.78	53.66	3.63	BnaC08g46150D	TAR1	1443	CCGTGGGATGGCTCAACAAAGC |||||||||||||||||||| CTAAGGCACCCTACCGAGTTGTTTCGTCGGTG	TT3	0.00	0.00	0.00	0.37	143979	-1.14	60510	-0.80
CTCAAACTTCCTTGGCCTAAA	-	TAR1	18.42	29.66	1.61	26.60	49.83	1.87	BnaC07g15020D	Nascent polypeptide-associated complex subunit alpha-like protein 4	959	CTCAAACTTCCTTGGCCTAAA ||| |||||||||| || GCTCGAG-TTGTAGGAACCGAAGTTGTGGCCA	TT3	0.00	0.00	0.00	0.05	4080	-0.26	2578	-0.40
ATTCCGTGGGATGGCTCAACA	-	TAR1	43.20	44.37	1.03	171.08	62.96	0.37	BnaC09g05890D	ROOT PRIMORDIUM DEFECTIVE 1	665	ATTCCGTGGGATGGCTCAACA |||||o||||| ||| ||| ACGAGAAGGCATCCTACAGAGGTGTCAGAACT	TT3	0.00	0.00	0.00	0.19	70	-0.07	89	-0.71

TAGGTTAGCGCGCAGTTGGGC	-	TAR1	0.00	7.41	7.41	4.27	21.52	5.04	BnaC08g46150D	TAR1	1540	TAGGTTAGCGCGCAGTTGGGC CAAGATCCAATCGCGCGTCAACCCGTGGCATT	TT3	0.00	0.00	0.00	0.28	143979	-1.14	60510	-0.80
GCGGACCGGATTGCTCCGTTC	-	TAR1	134.30	88.02	0.66	64.08	173.69	2.71	BnaC08g46150D	TAR1	814	GCGGACCGGATTGCTCCGTTC TAGCCGCCTGGCCTAACGAGACAAGGCGGTAGA	TT3	0.00	0.00	0.00	0.23	143979	-1.14	60510	-0.80
CGACTCTTAGGATCGACTAACC	-	TAR1	9.70	106.91	11.02	27.24	232.10	8.52	BnaC04g09710D	Ribose-phosphate pyrophosphokinase 1, chloroplastic	2640	CGACTCTTAGGATCGACTAACC TTGGTCTGAGAATC-TGGCTGATTGTTTTCGT	TT3	0.00	0.00	0.00	0.32	1146	-0.07	1096	-0.33
ACCAAGATCTGCACCGACGGC	-	TAR1	17.58	123.69	7.04	38.09	209.00	5.49	BnaC02g36110D	unknown	387	ACCAAGATCTGCACCGACGGC ATGGTGGTTCTAGACGTGGCTGTCGGTGAGGG	TT3	0.00	0.00	0.00	0.14	25737	-1.12	12547	-0.80
TTAGCGCGCAGTTGGGCACCG	-	TAR1	5.35	58.26	10.89	11.87	135.48	11.42	BnaC02g36110D	unknown	137	TTAGCGCGCAGTTGGGCACCG ATCCAATCGCGCGTCAACCCGTGGCATTGGGC	TT3	0.00	0.00	0.00	0.28	25737	-1.12	12547	-0.80
TCTAATCATTGGCTTTACCCGA	-	TAR1	2.61	3.73	1.43	14.77	32.25	2.18	BnaA09g04420D	TAR1	1362	TCTAATCATTGGCTTTACCCGA ACGGAGATTAGTAACCGAAATGGGCTATCTTG	TT3	0.00	0.00	0.00	0.28	239430	-1.00	101442	-0.78
GACTCTTAGGATCGACTAACC	-	TAR1	0.85	30.23	35.40	6.14	42.37	6.90	BnaC02g36110D	unknown	485	GACTCTTAGGATCGACTAACC GGGGCTGAGAATCCTAGCTGATTGGGTACACG	TT3	0.00	0.00	0.00	0.23	25737	-1.12	12547	-0.80
GATCTCCCGTGTGTTACCGCA	+	TAR1	28.71	186.86	6.51	44.09	119.75	2.72	BnaC03g22460D	Zinc finger CCCH domain-containing protein 29	1554	GATCTCCCGTGTGTTACCGCA ACTCCTAGAGCGCAAGTAGTGGCGTCGACGGT	TT3	0.00	0.00	0.00	0.23	1862	-0.79	1591	-0.23
TTCCATGTGAACGGCACTTGC	+	TAR1	73.01	77.99	1.07	163.72	124.07	0.76	BnaC09g11200D	Probable LRR receptor-like serine/threonine-protein kinase At1g63430	2637	TTCCATGTGAACGGCACTTGC GTTCAAGGTATACTT-CCATGAACTCTGGTGC	TT3	0.00	0.00	0.00	0.05	419	0.11	479	-0.07
AGATCTGCACCGACGGCCGCT	-	TAR1	0.85	15.22	17.82	3.48	33.56	9.64	BnaA09g03360D	Calmodulin-4	270	AGATCTGCACCGACG-GCCGCT GTGGTCTAGACGTGGGTGCGCCGCGGCGAAGC	TT3	0.00	0.00	0.00	0.14	1215	-1.27	641	-0.30
TGCGGAAGGATCATTGTCGTA	+	TAR1	289.94	497.11	1.71	1953.41	384.34	0.20	BnaA05g01900D	unknown	2932	TGCGGAAGGATCATTGTC-GTA TCGTACACCTTCCTAGCAGTAGTCGTAGAAGG	TT3	0.00	0.00	0.00	0.14	0	0.26	0	-0.25
ACCCGATAGAACTCGTTTCCG	-	TAR1	1.80	15.70	8.75	24.85	22.98	0.92	BnaA02g07420D	Subtilisin-like protease SBT4.9	3700	ACCCGATAGAACTCGTTTCCG GGCTTGGGCTATCTTGGGCTTGGCCAGGGCTT	TT3	0.00	0.00	0.00	0.14	2	-0.54	1	0.09
AAACAACCCGACTCGTAGACA	-	TAR1	3.50	10.58	3.02	30.53	25.16	0.82	BnaC02g16080D	F-box protein At5g50450	823	AAACAACCCGACTCGTAGACA CGGTTTTGTTGGGCTGGGC-TTAGTTTGGTTA	TT3	0.00	0.00	0.00	0.19	7727	0.91	8707	0.46
CCACCAAGATCTGCACCGACG	-	TAR1	4.36	79.19	18.17	5.35	115.18	21.52	BnaC06g03610D	Helicase-like transcription factor CHR27	4217	CCACCAAGATCTGCACCGACG CGGAGGTGGTACCAGAAGTGGTTTCCGTCTAC	TT3	0.00	0.00	0.00	0.37	293	0.43	545	0.14
AAAATGGCCCACTTGGAGCTCT	-	TAR1	4.45	6.53	1.47	0.00	25.41	25.41	BnaC08g46150D	TAR1	1470	AAAATGGCCCACTTGGAGCTCT TGGTTTTTACCGGGTGAACCTCGAGAGCTAAG	TT3	0.00	0.00	0.00	0.14	143979	-1.14	60510	-0.80
AACTTCCTTGGCCTAAACGGCC	-	TAR1	1.71	25.61	15.00	2.66	162.61	61.21	BnaA06g40090D	Homeobox-leucine zipper protein HAT1	835	AACTTCCTTGGCCTAAACGGCC CAAGTTGAA-GAACCGGTTTCGCTCGAAGACA	TT3	0.00	0.00	0.00	0.09	2137	0.10	3490	-0.76
GTCGGCCAAGGTGTGAACTCG	-	TAR1	6.92	52.47	7.58	4.08	91.32	22.39	BnaAnng22160D	TAR1	435	GTCGGCCAAGGTGTGAACTCG CGGACAGCCGGTTCCACACTTGAGCAACTTAT	TT3	0.00	0.00	0.00	0.23	257765	-1.01	114234	-0.85
AGTTCACACCTTGGCCGACAG	+	TAR1	12.69	45.00	3.55	122.06	75.33	0.62	BnaA10g30530D	Ankyrin repeat-containing protein At5g02620	651	AGTTCACACCTTGG-CCGACAG CGATTCAGGTGTGGAAACAGGTTGTCCTTTGT	TT3	0.00	0.00	0.00	0.09	577	1.97	2083	0.61
TTGGCTTTACCCGATAGAACTC	-	TAR1	4.31	66.36	15.39	9.24	217.09	23.49	BnaA09g04420D	TAR1	1354	TTGGCTTTACCCGATAGAACTC TAGTAACCGAAATGGGCTATCTTGAGCAAAGG	TT3	0.00	0.00	0.00	0.09	239430	-1.00	101442	-0.78
ATCGAGGCCTGGCTCTTGCCC	-	TAR1	57.01	79.21	1.39	214.29	161.12	0.75	BnaAnng22160D	TAR1	3269	ATCGAGGCCTGGCTCTTGCCC TGAGTAGCTCCGGACCGAGAACGGGGCTGCCG	TT3	0.00	0.00	0.00	0.14	257765	-1.01	114234	-0.85
ACGCCCCGAATCGATCGGCGGA	-	TAR1	6.16	10.09	1.64	3.70	48.21	13.03	BnaC08g31010D	unknown	1134	ACGCCCCGAATCGATCGGCGGA CGAGTACGGGGCTTA-CTTGTCGCATGTAGAAA	TT3	0.00	0.00	0.00	0.05	430	0.80	710	0.16
GAGCTCTCGATTCCGTGGGATG	-	TAR1	0.00	8.18	8.18	2.06	28.99	14.08	BnaAnng22160D	TAR1	3013	GAGCTCTCGATTCCGTGGGATG GAACCTCGAGAGCTAAGGCACCCTACCGAGTT	TT3	0.00	0.00	0.00	0.05	257765	-1.01	114234	-0.85
CCGTCTGCGACGTCGCGAGAA	+	TAR1	464.02	597.62	1.29	1711.42	900.63	0.53	BnaC02g16080D	F-box protein At5g50450	650	CCGTCTGCGACGTCGCGAGAA TGCTGGAAGCCGCTGCAGCGCTCCTTGCGGCA	TT3	0.00	0.00	0.00	0.23	7727	0.91	8707	0.46
AACCCGACTCGTAGACAGCGC	-	TAR1	14.23	78.93	5.55	102.12	105.59	1.03	BnaAnng22160D	TAR1	1613	AACCCGACTCGTAGACAGCGC TTTGTTGGGCTGAGCATCTGTCGCGGAGCACC	TT3	0.00	0.00	0.00	0.93	257765	-1.01	114234	-0.85
TCCTAAGAGTCGGGGGAAACC	+	TAR1	297.22	291.49	0.98	406.86	528.42	1.30	BnaC04g38970D	Transcription factor LHW	3803	TCCTAAGAG-TCGGGGGAAACC TTCAGGGTTCTCTAGCCCCCTTTTTTTCGTTTA	TT3	0.00	0.00	0.00	0.05	869	-0.64	775	-0.30
AGTTCTATCGGGTAAAGCCAA	+	TAR1	9.95	15.47	1.55	44.67	30.00	0.67	BnaCnng67370D	unknown	375	AGTTCTATCGGGTAAAGCCAA TTGCTCAAGATAGCCCATTTCGGTTACTAATC	TT3	0.00	0.00	0.00	0.09	3342	-1.03	1416	-1.00
ACGGAATCGAGAGCTCCAAGT	+	TAR1	1236.13	1339.37	1.08	2708.65	2249.48	0.83	BnaC03g64120D	Vacuolar protein sorting-associated protein 28 homolog 1	899	ACGGAATCGAGAGCTCCAAGT TTGTTGCCTTCG-TCTCGAGCTTCATCTCCGG	TT3	0.00	0.00	0.00	0.05	2249	-0.12	2417	0.72
TATGGGACGGAAGCTGATCTCC	+	TAR1	37.80	377.74	9.99	93.06	415.63	4.47	BnaC04g12310D	Membrane metalloprotease ARASP, chloroplastic	287	TATGGGACGGAAGCTGATCTCC AACCAGACTCTGCCT-CGGCAAGAGGTACGCC	TT3	0.00	0.00	0.00	0.09	6263	-0.65	4246	-0.12
AAACAACCCGACTCGTAGACA	-	TAR1	3.50	10.58	3.02	30.53	25.16	0.82	BnaC08g46150D	TAR1	613	AAACAACCCGACTCGTAGACA AGGGTTTGTTGGGCTGAGCATCTGTCGCGGAG	TT3	0.00	0.00	0.00	2.45	143979	-1.14	60510	-0.80
TTGCCTCAAACTTCCTTGGCCT	-	TAR1	14.87	20.28	1.36	75.69	83.48	1.10	BnaAnng22160D	TAR1	352	TTGCCTCAAACTTCCTTGGCCT CAATAACGGAGTTTGAAGGAACCGGATTTGCC	TT3	0.00	0.00	0.00	0.32	257765	-1.01	114234	-0.85
TTAATCGACCAACACCCTTTG	-	TAR1	3.55	10.61	2.98	4.08	20.18	4.95	BnaAnng36730D	Putative uncharacterized protein ART3	1572	TTAATCGACCAACACCCTTTG ACAGAATTAGCTGGTTGTGGGAAACACCCAAG	TT3	0.00	0.00	0.00	0.14	32584	-0.17	17996	-0.74
GTCCTGCTGTCTTAATCGACC	-	TAR1	0.00	31.04	31.04	15.75	50.98	3.24	BnaAnng36730D	Putative uncharacterized protein ART3	1583	GTCCTGCTGTCTTAATCGACC GTGGCAGGACGACAGAATTAGCTGGTTGTGGG	TT3	0.00	0.00	0.00	0.19	32584	-0.17	17996	-0.74
CAAATGAGAACTTTGAAGGCA	+	TAR1	23.01	34.98	1.52	59.69	41.18	0.69	BnaC08g47040D	unknown	389	CAAATGAGAACTTTGAAGGCA ATAAGTTTACTCTTGAAACTTCCGGCTTCTCC	TT3	0.00	0.00	0.00	0.14	127	-1.10	34	-1.09
CCACCAAGATCTGCACCGACGG	-	TAR1	34.10	23.72	0.70	82.59	103.97	1.26	BnaC02g36110D	unknown	389	CCACCAAGATCTGCACCGACGG TGATGGTGGTTCTAGACGTGGCTGTCGGTGAG	TT3	0.00	0.00	0.00	0.09	25737	-1.12	12547	-0.80
TGTCGGCCAAGGTGTGAACTC	-	TAR1	32.29	149.93	4.64	148.96	290.43	1.95	BnaC09g17830D	Glutathione gamma-glutamylcysteinyltransferase 1	1136	TGTCGGCCAAGGTGTGAACTC GGCAACA-CCGGTTCCGAGCTTGGGCCCACCG	TT3	0.00	0.00	0.00	0.05	1	-0.47	1	0.32

CGTCTGCGACGTCGCGAGAAG	+	TAR1	109.87	319.01	2.90	216.40	447.47	2.07	BnaA09g35450D	unknown	211	CGTCTGCGACGTCGCGAGAAG TACCGCAGACGCTGCCGCTC-CTTCTATCCTC	TT3	0.00	0.00	0.00	0.05	2947	-0.44	2533	0.07
TTGGTCCGTGTTACAAGACA	-	TAR1	3.42	5.42	1.59	13.06	30.96	2.37	BnaAnng22160D	TAR1	2009	TTGGTCCGTGTTACAAGACA GAGGAACCAGGCACAAAGTTCTGCCCAGCTTA	TT3	0.00	0.00	0.00	0.79	257765	-1.01	114234	-0.85
TAGGCCAAGGAAGTTTGAGGCA	+	TAR1	130.02	259.46	2.00	407.50	566.27	1.39	BnaA08g02450D	unknown	1277	TAGGCCAAGGAAGTTTGAGGCA TTACCTCCGGCTCCTTCAA-CTACGTCTTCGT	TT3	0.00	0.00	0.00	0.09	119	1.03	750	-0.06
TAGCTCGGATTTTGGCCAACCGC	-	TAR1	20.42	26.86	1.32	83.91	39.74	0.47	BnaAnng36730D	Putative uncharacterized protein ART3	240	TAGCTCGGATTTTGGCCAACCGC AGGAATCGAGCCTAAAACCGGTTGGCGCACGC	TT3	0.00	0.00	0.00	0.14	32584	-0.17	17996	-0.74
GTCTGCGACGTCGCGAGAAGTC	+	TAR1	177.74	2794.55	15.72	301.43	7106.17	23.57	BnaA06g23560D	Beta-D-xylosidase 4	3068	GTCTGCGACGTCGCGAGAAGTC AAAGCGGACGCTGCAGCGGCCTTTGGGTAGAG	TT3	0.00	0.00	0.00	0.42	763	0.93	555	0.73
CGCGAACTTCGAAAGGGGATC	+	TAR1	107.19	863.03	8.05	259.07	2036.74	7.86	BnaC02g40260D	Elongation factor 2	2663	CGCGAACTTCGAAAGGGGATC TGCAGCGTTTGGAG-TTTCGTCTAGGGAGAGT	TT3	0.00	0.00	0.00	0.14	2593	1.15	5719	0.28
TATGGGACGGAAGCTGATCTC	+	TAR1	119.99	563.81	4.70	182.12	368.24	2.02	BnaC04g12310D	Membrane metalloprotease ARASP, chloroplastic	287	TATGGGACGGAAGCTGATCTC AACCAGACTCTGCCT-CGGCAAGAGGTACGCC	TT3	0.00	0.00	0.00	0.09	6263	-0.65	4246	-0.12
GGTATAGGTCGCGCGCTTCAGC	-	TAR1	0.85	18.78	22.00	3.48	37.68	10.82	BnaA07g32560D	Small nuclear ribonucleoprotein SmD3a	175	GGTATAGGTCGC-GCGCTTCAGC GGAGACATGTCGAGCGGCGAGAAGTCGAGGTG	TT3	0.00	0.00	0.00	0.09	526	-0.25	610	-0.05
ACTCTTAGGATCGACTAACCC	-	TAR1	6.07	16.29	2.69	26.01	20.45	0.79	BnaAnng16700D	unknown	954	ACTCTTAGGATCGACTAACCC GGGCTGAGAATCCTAGCTGATTGGGTACACGT	TT3	0.00	0.00	0.00	0.32	0	0.17	2	0.44
AACAACCCGACTCGTAGACAG	-	TAR1	20.28	12.59	0.62	33.00	35.37	1.07	BnaA08g21760D	4-coumarate--CoA ligase-like 5	1292	AACAACCCGACTCGTAGACAG CAGGTTCTTGGGCTGGGCA-CTGGCCTAGGTG	TT3	0.00	0.00	0.00	0.05	8252	-1.15	267	-2.10
AACCCGACTCGTAGACAGCGC	-	TAR1	14.23	78.93	5.55	102.12	105.59	1.03	BnaC08g46150D	TAR1	609	AACCCGACTCGTAGACAGCGC TTTGTTGGGCTGAGCATCTGTCGCGGAGCACC	TT3	0.00	0.00	0.00	0.93	143979	-1.14	60510	-0.80
CGTCTGCGACGTCGCGAGAAG	+	TAR1	109.87	319.01	2.90	216.40	447.47	2.07	BnaC02g16080D	F-box protein At5g50450	649	CGTCTGCGACGTCGCGAGAAG GCTGGAAGCCGCTGCAGCGCTCCTTGCGGCAT	TT3	0.00	0.00	0.00	0.05	7727	0.91	8707	0.46

[1] sRNA seq / DEseq data

[2] PAREseq / PAREsnip data

[3] RNAseq / Deseq data

[4] "TAR1" stands for a small gene family predicted to encode a homolog of the yeast Protein TAR1 gene (BnaAnng22160D, BnaA09g04420D, BnaC08g46150D, BnaAnng21760D)

Table S28: TuMV vsiRNAs associated with vRNA cleavage in Drakkar

vsiRNA	(-) strand	vsiRNA mean reads	vsiRNA mean reads (rpm)	Cleavage Position	vsiRNA:vRNA target pair (5'- 3' : 3'-5')	Fragment signatures	Fragment signatures (rpm)
TTTCATCTGGATGTGTGCCTC	y	1994	186	10231	TTTCATCTGGATGTGTGCCTC ||||||||||||||||||| GACGAAAGTAGACCTACACACGGAGAGAGCGT	12238	203.96
ATCAGCCATTACACCTTCAAA	y	1620	151	9868	ATCAGCCATTACACCTTCAAA ||||||||||||||||||| GCATTAGTCGGTAATGTGGAAGTTTGGTACAC	3508	58.46
CTTGAGCTGGTTCCTTATCAA	y	439	41	9431	CTTGAGCTGGTTCCTTATCAA ||||||||||||||||||| AGGAGAACTCGACCAAGGAATAGTTCCATCTC	861	14.35
TTTTGCCTCTCTCGTTCCTTT	y	2108	197	9606	TTTTGCCTCTCTCGTTCCTTT ||||||||||||||||||| GACGAAAACGGAGAGAGCAAGGAAAAGACGGA	573	9.55
TTTTGCCTCTCTCGTTCCTTTT	y	166	16	9606	TTTTGCCTCTCTCGTTCCTTTT |||||||||||||||||||| GACGAAAACGGAGAGAGCAAGGAAAAGACGGA	573	9.55
TTTGCCTCTCTCGTTCCTTTT	y	1716	160	9605	TTTGCCTCTCTCGTTCCTTTT ||||||||||||||||||| ACGAAAACGGAGAGAGCAAGGAAAAGACGGAA	541	9.02
TTTGCCTCTCTCGTTCCTTTTC	y	324	30	9605	TTTGCCTCTCTCGTTCCTTTTC |||||||||||||||||||| ACGAAAACGGAGAGAGCAAGGAAAAGACGGAA	541	9.02
CATCTTCATAATCCTCAAAGA	y	3525	329	9479	CATCTTCATAATCCTCAAAGA ||||||||||||||||||| CGTGGTAGAAGTATTAGGAGTTTCTAACGAAC	494	8.23
TCGGTTCTGTTCTTCAGGTAT	y	689	64	2475	TCGGTTCTGTTCTTCAGGTAT ||||||||||||||||||| CAAGAGCCAAGACAAGAAGTCCATAGCACGAT	240	4.00
TCCTTCTTCTCCTTCTCTGCC	y	1626	152	9570	TCCTTCTTCTCCTTCTCTGCC ||||||||||||||||||| AGAGAGGAAGAAGAGGAAGAGACGGACGAAAA	225	3.75
TCCTTCTTCTCCTTCTCTGCCT	y	165	15	9570	TCCTTCTTCTCCTTCTCTGCCT |||||||||||||||||||| AGAGAGGAAGAAGAGGAAGAGACGGACGAAAA	225	3.75
TCTCCTTCTTCTCCTTCTCTG	y	466	44	9572	TCTCCTTCTTCTCCTTCTCTG ||||||||||||||||||| AGAGAGAGGAAGAAGAGGAAGAGACGGACGAA	206	3.43
CTCCTTCTCTGCCTGCTTTTG	y	544	51	9562	CTCCTTCTCTGCCTGCTTTTG ||||||||||||||||||| AGAAGAGGAAGAGACGGACGAAAACGAGCAGA	180	3.00
TCTTCTCCTTCTCTGCCTGCT	y	2016	188	9596	TCTTCTCCTTCTCTGCCTGCT ||| ||||| ||||||| || AGAGAGCA-AGGAAAAGACGGAAGAGAGAGAG	113	1.88
AGCTTCCTCAGCGCTGTTTCC	y	419	39	9405	AGCTTCCTCAGCGCTGTTTCC ||||||||||||||||||| CATCTCGAAGGAGTCGCGACAAAGGCGATACA	102	1.70
TTTTGCCTCTCTCGTTCCTTT	y	2108	197	9585	TTTTGCC-TCTCTCGTTCCTTT ||o|||| |||||| o||||o GAAAAGACGGAAGAGAGAGAGGAAGAAGAGGA	60	1.00
TTTTGCCTCTCTCGTTCCTTTT	y	166	16	9585	TTTTGCC-TCTCTCGTTCCTTTT ||o|||| |||||| o||||o| GAAAAGACGGAAGAGAGAGAGGAAGAAGAGGA	60	1.00
AGTAATCCTTCTTCTTTCCTT	y	398	37	8372	AGTAATCCTTCTTCTTTCCTT ||||||||||||||||||| CGCTTCATTAGGAAGAAGAAAGGAAATATGTT	54	0.90
CAGATTCCCTCTCTTTTGTGC	y	1880	176	9171	CAGATTCCCTCTCTTTTGTGC ||||||||||||||||||| TTAGGTCTAAGGGAGAGAAAACACGGGGACCA	47	0.78
TTTGCCTCTCTCGTTCCTTTT	y	1716	160	9584	TTTGCC-TCTCTCGTTCCTTTT |o|||| |||||| o||||o| AAAAGACGGAAGAGAGAGAGGAAGAAGAGGAA	46	0.77
TTTGCCTCTCTCGTTCCTTTTC	y	324	30	9584	TTTGCC-TCTCTCGTTCCTTTTC |o|||| |||||| o||||o| AAAAGACGGAAGAGAGAGAGGAAGAAGAGGAA	46	0.77
CAACTTTGTTTCAGTATTTCT	y	349	33	8421	CAACTTTGTTTCAGTATTTCT ||||||||||||||||||| AAGTGTTGAAACAAAGTCATAAAGAAGAAAGT	41	0.68
CAACTTTGTTTCAGTATTTCTT	y	271	25	8421	CAACTTTGTTTCAGTATTTCTT |||||||||||||||||||| AAGTGTTGAAACAAAGTCATAAAGAAGAAAGT	41	0.68
CATTGCGAAATTTTAGTTTCT	y	181	17	6692	CATTGCGAAATTTTAGTTTCT ||||||||||||||||||| GCCCGTAACGCTTTAAAATCAAAGACGGAAAC	37	0.62
CATTCGATCTAGGTTTCGCA	y	211	20	425	CATTCGATCTAGGTTTCGCA ||||||||||||||||||| TGCCGTAAGCTAGATCCAAAGCGTTGGAGGTC	35	0.58
TCTTCTCCTTCTCTGCCTGCT	y	2016	188	9566	TCTTCTCCTTCTCTGCCTGCT ||||||||||||||||||| AGGAAGAAGAGGAAGAGACGGACGAAAACGAG	32	0.53
CACTTCTCTACCCATTTTGTT	y	415	39	6721	CACTTCTCTACCCATTTTGTT ||||||||||||||||||| GCATGTGAAGAGATGGGTAAAACAACAGAGCC	29	0.48
CACTTCTCTACCCATTTTGTTG	y	102	10	6721	CACTTCTCTACCCATTTTGTTG |||||||||||||||||||| GCATGTGAAGAGATGGGTAAAACAACAGAGCC	29	0.48
ATTCTCATCAGTGACATAATT	y	168	16	8302	ATTCTCATCAGTGACATAATT ||||||||||||||||||| ACAGTAAGAGTAGTCACTGTATTAACGTACAA	23	0.38
TGACTTTGAAGTCTCTTTCAA	y	418	39	5387	TGACTTTGAAGTCTCTTTCAA ||||||||||||||||||| AAGCACTGAAACTTCAGAGAAAGTTAATCTTC	22	0.37
CTTCTGCTTCGTTTCTGGG	y	104	10	10073	CTTCTGCTTCGTTTCTGGG |||| ||| |||o |||oo ATGCGAAGTCGATGCAGTGACTTTACCCGGTA	19	0.32
CCTTCTTCTCCTTCTCTGCCT	y	1573	147	9569	CCTTCTTCTCCTTCTCTGCCT ||||||||||||||||||| GAGAGGAAGAAGAGGAAGAGACGGACGAAAAC	18	0.30
TGACTTTGAAGTCTCTTTCAA	y	418	39	5913	TGACTTTGAAGTCTCTTTCAA ||| |||| |o|||||| | AGAGACTCAAAC-TTAGAGAAATTCTCACGCA	16	0.27
AACTTTGTTTCAGTATTTCTT	y	654	61	8420	AACTTTGTTTCAGTATTTCTT ||||||||||||||||||| AGTGTTGAAACAAAGTCATAAAGAAGAAAGTA	13	0.22
TGCAGAGAAATCTTCAGGATC	y	5840	546	6865	TGCAGAGAAATCTTCAGGATC ||||||||||||||||||| CTTGACGTCTCTTTAGAAGTCCTAGTTTGGGT	13	0.22
CTTTAATCGTTTTGTGTATGT	y	805	75	35	CTTTAATCGTTTTGTGTATGT ||||||||||||||||||| AAACGAAATTAGCAAAACACATACAATACAAC	1	0.02

Drakkar-specific

Table S29: TuMV vsiRNAs associated with vRNA cleavage in Tanto

vsiRNA	(-) strand	vsiRNA mean reads	vsiRNA mean reads (rpm)	Cleavage Position	vsiRNA:vRNA target pair (5'-3' : 3'-5')	Fragment signatures	Fragment signatures (rpm)
TTTCATCTGGATGTGTGCCTC	y	1619	150	10231	TTTCATCTGGATGTGTGCCTC ||||||||||||||||||| GACGAAAGTAGACCTACACACGGAGAGAGCGT	7682	123.22
CTCCTTCTCTGCCTGCTTTTG	y	476	44	9562	CTCCTTCTCTGCCTGCTTTTG ||||||||||||||||||| AGAAGAGGAAGAGACGGACGAAAACGAGCAGA	6006	96.34
ATCAGCCATTACACCTTCAAA	y	1396	130	9868	ATCAGCCATTACACCTTCAAA ||||||||||||||||||| GCATTAGTCGGTAATGTGGAAGTTTGGTACAC	4111	65.94
CAGTGCTGCTGCTTTCATCTG	y	413	38	10243	CAGTGCTGCTGCTTTCATCTG ||||||||||||||||||| GTGCGTCACGACGACGAAAGTAGACCTACACA	1494	23.96
TTTGCCTCTCTCGTTCCTTTT	y	1240	115	9605	TTTGCCTCTCTCGTTCCTTTT ||||||||||||||||||| ACGAAAACGGAGAGAGCAAGGAAAAGACGGAA	1144	18.35
TTTGCCTCTCTCGTTCCTTTTC	y	442	41	9605	TTTGCCTCTCTCGTTCCTTTTC |||||||||||||||||||| ACGAAAACGGAGAGAGCAAGGAAAAGACGGAA	1144	18.35
CATCTTCATAATCCTCAAAGA	y	2767	257	9479	CATCTTCATAATCCTCAAAGA ||||||||||||||||||| CGTGGTAGAAGTATTAGGAGTTTCTAACGAAC	889	14.26
CTTGAGCTGGTTCCTTATCAA	y	248	23	9431	CTTGAGCTGGTTCCTTATCAA ||||||||||||||||||| AGGAGAACTCGACCAAGGAATAGTTCCATCTC	435	6.98
TTTTGCCTCTCTCGTTCCTTT	y	1471	137	9606	TTTTGCCTCTCTCGTTCCTTT ||||||||||||||||||| GACGAAAACGGAGAGAGCAAGGAAAAGACGGA	426	6.83
TTTTGCCTCTCTCGTTCCTTTT	y	195	18	9606	TTTTGCCTCTCTCGTTCCTTTT |||||||||||||||||||| GACGAAAACGGAGAGAGCAAGGAAAAGACGGA	426	6.83
TCTCCTTCTTCTCCTTCTCTG	y	350	33	9572	TCTCCTTCTTCTCCTTCTCTG ||||||||||||||||||| AGAGAGAGGAAGAAGAGGAAGAGACGGACGAA	176	2.82
TCTCCTTCTTCTCCTTCTCTGC	y	113	10	9572	TCTCCTTCTTCTCCTTCTCTGC |||||||||||||||||||| AGAGAGAGGAAGAAGAGGAAGAGACGGACGAA	176	2.82
TCCTTCTTCTCCTTCTCTGCC	y	1208	112	9570	TCCTTCTTCTCCTTCTCTGCC ||||||||||||||||||| AGAGAGGAAGAAGAGGAAGAGACGGACGAAAA	144	2.31
TCCTTCTTCTCCTTCTCTGCCT	y	246	23	9570	TCCTTCTTCTCCTTCTCTGCCT |||||||||||||||||||| AGAGAGGAAGAAGAGGAAGAGACGGACGAAAA	144	2.31
TCGGTTCTGTTCTTCAGGTAT	y	411	38	2475	TCGGTTCTGTTCTTCAGGTAT ||||||||||||||||||| CAAGAGCCAAGACAAGAAGTCCATAGCACGAT	144	2.31
GTCCTCGTGACTTTGATCCT	y	673	63	1182	GTCCTCGTGACTTTGATCCT ||||||||||||||||||| GTAACAGGAGCACTGAAACTAGGACCGTAGCA	125	2.01
TCTTCTCCTTCTCTGCCTGCT	y	1377	128	9566	TCTTCTCCTTCTCTGCCTGCT ||||||||||||||||||| AGGAAGAAGAGGAAGAGACGGACGAAAACGAG	100	1.60
CCTTCTTCTCCTTCTCTGCCT	y	1072	100	9569	CCTTCTTCTCCTTCTCTGCCT ||||||||||||||||||| GAGAGGAAGAAGAGGAAGAGACGGACGAAAAC	89	1.43
TGTTGAGTTTTTATATTTT	y	460	43	12	TGTTGAGTTTTTATATTTT |||||||||||||||||| CAATACAACTCAAAAATATAAAAAA	89	1.43
TGTTGAGTTTTTATATTTTT	y	431	40	12	TGTTGAGTTTTTATATTTTT |||||||||||||||||| CAATACAACTCAAAAATATAAAAAA	89	1.43
TTATGTTGAGTTTTTATAT	y	209	19	15	TTATGTTGAGTTTTTATAT |||||||||||||||||| ATACAATACAACTCAAAAATATAAAAAA	79	1.27
TTATGTTGAGTTTTTATATT	y	4284	398	15	TTATGTTGAGTTTTTATATT |||||||||||||||||| ATACAATACAACTCAAAAATATAAAAAA	79	1.27
CAACTTTGTTTCAGTATTTCT	y	190	18	8421	CAACTTTGTTTCAGTATTTCT ||||||||||||||||||| AAGTGTTGAAACAAAGTCATAAAGAAGAAAGT	52	0.83
CAACTTTGTTTCAGTATTTCTT	y	186	17	8421	CAACTTTGTTTCAGTATTTCTT |||||||||||||||||||| AAGTGTTGAAACAAAGTCATAAAGAAGAAAGT	52	0.83
AACTTTGTTTCAGTATTTCTT	y	308	29	8420	AACTTTGTTTCAGTATTTCTT ||||||||||||||||||| AGTGTTGAAACAAAGTCATAAAGAAGAAAGTA	48	0.77
AGCTTCCTCAGCGCTGTTTCC	y	273	25	9405	AGCTTCCTCAGCGCTGTTTCC ||||||||||||||||||| CATCTCGAAGGAGTCGCGACAAAGGCGATACA	44	0.71
TTTGCCTCTCTCGTTCCTTTT	y	1240	115	9584	TTTGCC-TCTCTCGTTCCTTTT |o||| ||||| o||||o| AAAAGACGGAAGAGAGAGGAAGAAGAGGAA	22	0.35
CAGATTCCCTCTCTTTTGTGC	y	1483	138	9171	CAGATTCCCTCTCTTTTGTGC ||||||||||||||||||| TTAGGTCTAAGGGAGAGAAAACACGGGGACCA	20	0.32
AGTAATCCTTCTTCTTTCCTT	y	288	27	8372	AGTAATCCTTCTTCTTTCCTT ||||||||||||||||||| CGCTTCATTAGGAAGAAGAAAGGAAATATGTT	18	0.29
TTTTGCCTCTCTCGTTCCTTT	y	1471	137	9585	TTTTGCC-TCTCTCGTTCCTTT ||o||| ||||| o||||o GAAAAGACGGAAGAGAGAGGAAGAAGAGGA	17	0.27
TTTTGCCTCTCTCGTTCCTTTT	y	195	18	9585	TTTTGCC-TCTCTCGTTCCTTTT ||o||| ||||| o||||o| GAAAAGACGGAAGAGAGAGGAAGAAGAGGA	17	0.27
TATGTTGAGTTTTTATATT	y	172	16	14	TATGTTGAGTTTTTATATT |||||||||||||||||| TACAATACAACTCAAAAATATAAAAAA	16	0.26
AGGAGCTTTCCCTTCTTGTGC	y	431	40	9376	AGGAGCTTTCCCTTCTTGTGC ||||||||||||||||||| ACATTCCTCGAAAGGGAAGAACACGATCCCTC	12	0.19
ATGTTGAGTTTTTATATTTT	y	346	32	13	ATGTTGAGTTTTTATATTTT |||||||||||||||||| ACAATACAACTCAAAAATATAAAAAA	12	0.19
ATTCTCATCAGTGACATAATT	y	129	12	8302	ATTCTCATCAGTGACATAATT ||||||||||||||||||| ACAGTAAGAGTAGTCACTGTATTAACGTACAA	9	0.14
TTTTCCTTTAACTGTGTGCTT	y	2742	255	8056	TTTTCCTTTAACTGTGTGCTT ||||||||||||||||||| CTGTAAAAGGAAATTGACACACGAAACAGTGT	8	0.13
CATTCGATCTAGGTTTCGCA	y	148	14	425	CATTCGATCTAGGTTTCGCA ||||||||||||||||||| TGCCGTAAGCTAGATCCAAAGCGTTGGAGGTC	8	0.13
AAGAATCTGATGATGCTGT	y	205	19	8997	AAGAATCTGATGATGCTGT |||||||||||||||||| CTGCTTCTTAGACTACTACGACAGCGCGTTGA	7	0.11
TTTGAAATCACATCACAATTG	y	10697	993	8229	TTTGAAATCACATCACAATTG ||| ||| || ||||| |o| CAGAAAAGTTT-GTCTAGTGTCAGCTACAAAG	6	0.10
AGAATTGTGTATCCACCATCC	y	326	30	3798	AGAATTGTGTATCCACCATCC ||||||||||||||||||| GGAGTCTTAACACATAGGTGGTAGGCGTTCGA	6	0.10
AGAATTGTGTATCCACCATCCG	y	744	69	3798	AGAATTGTGTATCCACCATCCG |||||||||||||||||||| GGAGTCTTAACACATAGGTGGTAGGCGTTCGA	6	0.10
CACTTCTCTACCCATTTTGTT	y	251	23	6721	CACTTCTCTACCCATTTTGTT ||||||||||||||||||| GCATGTGAAGAGATGGGTAAAACAACAGAGCC	5	0.08
GGGATCTTTCGAAAGGGCA	y	160	15	1849	GGGATCTTTCGAAAGGGCA |||||||||||||||||| GCAACCCTAGAAAGCTTTCCCGTCTAACACAC	5	0.08
CTTATGCTCTGGATTTCTGCG	y	1966	183	2331	CTTATGCTCTGGATTTCTGCG ||||||||||||||||||| TAGCGAATACGAGACCTAAAGACGCTTTAGAA	4	0.06
CTTATGCTCTGGATTTCTGCGA	y	188	17	2331	CTTATGCTCTGGATTTCTGCGA |||||||||||||||||||| TAGCGAATACGAGACCTAAAGACGCTTTAGAA	4	0.06
TGACGAAGAATCTGATGATG	y	161	15	9002	TGACGAAGAATCTGATGATG |||||||||||||||||| GGCAACTGCTTCTTAGACTACTACGACAGCGC	3	0.05
TTTTCCTTTAACTGTGTGCTT	y	2742	255	8055	TTTTCCTTTAACTGTGTGCTT |||o| ||| ||||||||| TGTAAAAGGAAATT-GACACACGAAACAGTGT	3	0.05
TGACTTTGAAGTCTCTTTCAA	y	330	31	5912	TGACTTTGAAGTCTCTTTCAA ||| ||||| ||||||| AGAGACTCAAACTT-AGAGAAATTCTCACGCA	3	0.05
CCAGATTCCCTCTCTTTTGTG	y	117	11	9172	CCAGATTCCCTCTCTTTTGTG |||||||||||||||||| CTTAGGTCTAAGGGAGAGAAAACACGGGGACC	2	0.03
TGTTCTCGCACGTGTGATCTT	y	1070	99	6350	TGTTCTCGCACGTGTGATCTT ||||||||||||||||||| CTATACAAGAGCGTGCACACTAGAAAGTAGTA	2	0.03
TTTGAAATCACATCACAATTG	y	10697	993	5301	TTTGAAATCACATCACAATTG ||||||||||||||||||| AGGAAAACTTTAGTGTAGTGTTAACGAAGGTG	2	0.03
AGAGATTTCAAAACGACCAAC	y	3362	312	3597	AGAGATTTCAAAACGACCAAC ||||||||||||||||||| GCGATCTCTAAAGTTTTGCTGGTTGTTTTGCC	2	0.03
GTTTTCCAGTAGTGCAAATAA	y	133	12	1373	GTTTTCCAGTAGTGCAAATAA |||||||||||||||||| CCATCAAAAGGTCATCACGTTTATTTAAATTC	2	0.03
CTTTAATCGTTTTGTGTATGT	y	1154	107	35	CTTTAATCGTTTTGTGTATGT ||||||||||||||||||| AAACGAAATTAGCAAAACACATACAATACAAC	2	0.03
TGACTTTGAAGTCTCTTTCAA	y	330	31	5913	TGACTTTGAAGTCTCTTTCAA ||| |||| |o||||||| AGAGACTCAAAC-TTAGAGAAATTCTCACGCA	1	0.02
TGAGAATCTTTGTGACACAG	y	175	16	4508	TGAGAATCTTTGTGACACAG |||||||||||||||||| AACAACTCTTAGAAACACTGTGTCAGCGAAGC	1	0.02
TGCTCGGATTGTCTCTTCGCT	y	4206	391	4422	TGCTCGGATTGTCTCTTCGCT ||||||||||||||||||| AAGAACGAGCCTAACAGAGAAGCGAACTACTT	1	0.02
TGCTCGGATTGTCTCTTCGCTT	y	295	27	4422	TGCTCGGATTGTCTCTTCGCTT |||||||||||||||||||| AAGAACGAGCCTAACAGAGAAGCGAACTACTT	1	0.02

Table S30: vRNA cleavage by host-derived sRNAs in Drakkar

hsRNA	Origin of: Transcript ID	Origin of: Predicted gene function	hsRNA reads		Cleavage position in vRNA	hsRNA:vRNA target pair (5'-3' : 3'-5')	Fragment signatures	
			reads	rpm			reads	rpm
TGATCTTGTGTTGTGATGA	BnaC09g51800D	Disease resistance protein TAO1	144	2.40	9823	TGATCTTGTGTTGTGATGA CGCAACTTGCACACAAC-CTATCTAGGCAGAC	14087	234.78
TGCTCTCCCGTAACTACGCTT	BnaA03g07040D	Disease resistance protein TAO1	149	2.48	8984	TGCTCTCCCGTAACTACGCTT TACTACGACAGCGCGTTGA-GTGAACCTTAAG	5112	85.20
TCCAGATCCTTAAAGCAATTG	BnaC02g38690D	Disease resistance protein RPP5	113	1.88	9923	TCCAGATCCTTAAAGCAATTG TACGTGGTCTGGTAATTTGGT-AACTCTTACT	1010	16.83
GATCGATTCCATGTGTTGGAT	BnaC06g28490D	60S ribosomal protein L17-2	336	5.60	9225	GATCGATTCCATGTGTTGGAT AAAGCTGGCTAGGGTA-AGATCTTAGCTATGA	661	11.02
AGAAATCAGTTCATAAAGCTC	BnaC08g23700D	Unknown	239	3.98	10189	AGAAATCAGTTCATAAAGCTC AGGATCTTCAGTAAAGTATCTTTAGTTTACGC	548	9.13
AGTTATGCTTGTGTTGACTGA	BnaC04g51890D	Unknown	281	4.68	10349	AGTTATGCTTGTGTTGACTGA TCATTCAATACGTACAAGGCTAATTGCAGGAG	400	6.67
CTTAGCATCAATCATTTCACA	BnaC05g43760D	Non-specific lipid-transfer protein 6	154	2.57	9529	CTTAGCATCAATCATTTCACA GTTTGGA-CGTAGTTCGCAAAGTGGACGGACC	235	3.92
AGCTGCATCACGAGCTTCACT	BnaC09g53150D	Retrovirus-related Pol polyprotein from transposon TNT 1-94	219	3.65	9529	AGCTGCATCACGAGCTTCACT AGTTTGGACGTAGTTCGCAAAGTGGACGGACC	235	3.92
TGCGCAGAGTCTTTTTAAGTC	BnaAnng10090D	Putative UDP-arabinose 4-epimerase 4	134	2.23	9262	TGCGCAGAGTCTTTTTAAGTC AGCGACGCGTCTAACGGAGAT-CAGCTACCGT	166	2.77
TGCGCAGAGTCTTTCTAAGTC	BnaC07g18010D	Putative UDP-arabinose 4-epimerase 4	539	8.98	9262	TGCGCAGAGTCTTTCTAAGTC AGCGACGCGTCTAACGGAGAT-CAGCTACCGT	166	2.77
TCTTGGTCGTCCATATCAGCC	BnaAnng23890D	Unknown	221	3.68	9984	TCTTGGTCGTCCAT-ATCAGCC GACTAGCAGCGGCAGGTAGTAGTGGGTGTAAG	151	2.52
CGAGCTCTTGAGTGTATGAGA	BnaC04g39780D	Retrovirus-related Pol polyprotein from transposon TNT 1-94	123	2.05	7939	CGAGCTCTTGAGTGTATGAGA GACGGCACGACAGCTC-CAGACTCTAATCGAA	143	2.38
AATGGCTAAGATGCTCTGAGC	BnaA05g09400D	Chlorophyll a-b binding protein 1, chloroplastic	242	4.03	9446	AATGGCTAAGATGCTCT-GAGC TTTATTACCCACTCTAGGAGAACTCGACCAAG	142	2.37
TTATGTTGTGGGGATTTCGTT	BnaC04g22890D	SUPPRESSOR OF GENE SILENCING 3	150	2.50	9952	5' TTATGTT-GTGGGGATTTCGTT GCAAATACAAGCCCCTCCAAGGCAAGAGTTAC	136	2.27
GTCAACAACAACGCATGGGCC	BnaA03g15830D	Chlorophyll a-b binding protein 1, chloroplastic	144	2.40	10490	GTCAACAACAACGCATGGGCC CTTTCA-TTGTTGTTGTGTGTACTGTTTCAGT	127	2.12
GATGATTGGGATTTGGGGTCC	BnaA04g11150D	Disease resistance protein RML1B	111	1.85	9776	GATGATTGGGATTTGGGGTCC TAATCTACTAGCTCCAAATCTC-GGTGAGAAA	127	2.12
CGAAGAGGTCGTTGTCATCAA	BnaA01g14050D	Protein NBR1 homolog	158	2.63	8312	CGAAGAGGTCGTTGTCATCAA CGAAGCTTATACAGTAAGAGTAGTCACTGTAT	83	1.38
TGCGAGAGTATTCTTTGAGCC	BnaA04g09730D	Genome polyprotein	460	7.67	9103	TGCGAGAGTATTCTTTGAGCC ACTCA-GCTTTCATATGAAGTCCGGGTCAAGT	82	1.37
CCATTAGCTTTGAAAGGCACC	BnaA01g14050D	NBR1 homolog	436	7.27	8700	CCATTAGCTTTGAAAGGCACC ACTCGGTAGTCGTAGCGTTATGTGGGTTGGTA	81	1.35
CCATTAGCTTTGAAAGGCACCC	BnaA01g14050D	NBR1 homolog	106	1.77	8700	CCATTAGCTTTGAAAGGCACCC ACTCGGTAGTCGTAGCGTTATGTGGGTTGGTA	81	1.35
AGTGGATCCATCTGATGTGAA	BnaA03g03830D	Probable disease resistance protein RPP1	2120	35.33	8857	AGTGGATCCATCTGATGTGAA CTGCTCACAT-GGTAGACCACATCTTTATCCC	80	1.33
TCAACGATTGTGTGAAATGAT	BnaC05g43760D	Non-specific lipid-transfer protein 6	432	7.20	9465	TCAACGATTGTGTG-AAATGAT TAGGAGTTTCTAACGAACGTTTATTACCCACT	78	1.30
CTCGGATTTTGGCCAACCG	BnaA09g04420D	TAR1	101	1.68	9748	CTCGGATTTTGGCCAACCG AAAAGAGCATAGAACCG-TGCGCGTAGAACGA	73	1.22
TATGCTTTCACATGATGGATG	BnaC06g04850D	Defensin-like protein 19	195	3.25	9459	TATGCTTTCACATGATGGATG TTCTA-ACGAACGTTTATTACCCACTCTAGGA	61	1.02
AGGTTGTTGGTGAGCCTCGAA	BnaA03g29710D	Peroxisomal fatty acid beta-oxidation multifunctional protein	153	2.55	5763	AGGTTGTTGGTGAGC-CTCGAA GCTCTGCAACAACCACTAGTGACCTTCGGGTA	59	0.98
ATCTTCTCCGCGGAAGCTC	BnaAnng10090D	Putative UDP-arabinose 4-epimerase 4	525	8.75	6979	ATCTTCTCCGCGGAAGCTC CGAGTAGGAGGGGCTCATTC-AGGTAAGAATA	49	0.82
AGGTCGTTCTGTTTCCAGGGT	BnaAnng22160D	TAR1	103	1.72	9130	AGGTCGTTCTGTTTCCAGGGT GGTCTCCAG-AGGAAAAAGGGACCAAGAACTC	39	0.65
GCACTTGCACATGGGTTAGTC	BnaC02g36110D	Unknown	313	5.22	6941	GCACTTGCACATGGGTTA-GTC TTCACGAGAACGTGTTCCCACTACAGACACTC	37	0.62
AGGAAGTTCGAAGGATAGACT	BnaC09g53150D	Retrovirus-related Pol polyprotein from transposon TNT 1-94	151	2.52	6288	AGGAAGTTCGAAGGATAGACT TCACT-CTTCAAGCTTCTTCTCTGTGTCAACC	37	0.62
GTGGATCCATCTGATGTGAAA	BnaC03g05380D	Disease resistance protein TAO1	107	1.78	8856	GTGGATCCATCTGATGTGAAA TGCTCACAT-GGTAGACCACATCTTTATCCCC	27	0.45
TGCTCCGTTCCGCATCCGACC	BnaAnng22160D	TAR1	239	3.98	4487	TGCTCCGTTCCGCATCCGACC GTCAGCGAAGCAAGACGTAG-CTTGTAGTACT	26	0.43
CCAAGATGAGTGCTCTCCT	BnaC09g16480D	Unknown	39336	655.58	476	CCAAGATGAGTGCTCTCCT GTCAGGTTTTTCTCACGAGAG-AGGAACAAAC	25	0.42
TTGAGCCTGTTGTTCCTAACA	BnaC07g39070D	NBR1 homolog	186	3.10	8919	TTGAGCCTGTTGTTCCTAACA CTGGTACTCGCACAACAGGTGTTGTCAGCTAC	23	0.38
GAGCCTGTTGTTCCTAACACT	BnaC01g16550D	NBR1 homolog	153	2.55	8917	GAGCCTGTTGTTCCTAACACT GGTACTCGCACAACAGGTGTTGTCAGCTACCG	22	0.37
TCGGCGGGAATTCCGGAAAG	BnaA09g04420D	TAR1	114	1.90	10508	TCGGCGGGAATTCCGGAAAG TACAAGCCG-CTTTTATGTCTTTCATTGTTGT	19	0.32
TCGAAGAGGTCGTTGTCATCAA	BnaA01g14050D	NBR1 homolog	102	1.70	8313	TCGAAGAGGTCGTTGTCATCAA TCGAAGCTTATACAGTAAGAGTAGTCACTGTA	19	0.32
GTCCTTGTGACGTAGTTCTCT	BnaC02g37450D	Cytochrome P450 81D11	199	3.32	1182	GTCCTTGTGACGTAGTTCTCT GTAACAGGAGCACTGAAACTAG-GACCGTAGC	19	0.32
ATATAGAAATTGTGGGTATACG	BnaCnng34030D	Copia protein	121	2.02	8843	ATATAGAAATTGTGGGTATACG AGACCACATCTTTATC-CCCATATGTGCTAAA	17	0.28
ATTCTGTAGTGTCAGAGCGGC	BnaA08g22900D	Putative F-box/kelch-repeat protein At3g24610	252	4.20	2858	ATTCTGTAGTGTCAGAGCGGC GGACTAAGACAACACTGTGTTGTTGTACGTAC	15	0.25
GTAGATTTTTCCACTCATCGAG	BnaCnng34030D	Copia protein	320	5.33	8563	GTAGATTTTTCCACTCATCGAG GGTGCGTTTGAAAAGGTGGGTTG-TCACACAG	11	0.18
CATAACTCTTGCTCTTCTTCT	BnaC04g51890D	Unknown	107	1.78	6794	CATAACTCTTGCTCTTCTTCT CACAGGA-TGGGAACGAGAAGGGAAAGAAACA	11	0.18
TCGTAGATTTTTCCACTCATC	BnaCnng34030D	Copia protein	163	2.72	8565	TCGTAGATTTTTCCACTCATC TAGGTGCGTTTGAAAAGGTGGGTTGTCACACA	7	0.12
GGGATTAGTCCTTTGGGCCT	BnaC05g33180D	F-box protein At3g49510	287	4.78	4530	GGGATTAGTCCTTTGGGCCT TCACCGCTGATCAGGGAATTCGAACAACTCTT	5	0.08
CAGATTAGTCCCTTGGGCCTG	BnaC09g19010D	Inactive disease resistance protein RPS4	205	3.42	4530	CAGATTAGTCCCTTGGGCCTG CACCG-CTGATCAGGGAATTCGAACAACTCTT	5	0.08
TGAGCCTGTTGTTCCTAACACT	BnaA03g46880D	NBR1 homolog	167	2.78	8918	TGAGCCTGTTGTTCCTAACACT TGGTACTCGCACAACAGGTGTTGTCAGCTACC	2	0.03

Drakkar-specific

Table S31: vRNA cleavage by host-derived sRNAs in Tanto

hsRNA	Origin of: Transcript ID	Origin of: Predicted gene function	hsRNA reads		Cleavage position in vRNA	hsRNA:vRNA target pair (5'-3' : 3'-5')	Fragment signatures	
			reads	rpm			reads	rpm
TGATCTTGTGTTGTGATGA	BnaC08g11510D	Disease resistance protein TAO1	120	2	9823	TGATCTTGTGTTGTGATGA CGCAACTTGCACACAAC-CTATCTAGGCAGAC	9811	157.38
CTTCATGTGCTGCATCATTGT	BnaC02g15910D	RNA pseudouridine synthase 7	120	2	9647	CTTCATGTGCTGCATCATTGT GGGAGAAGAACACGTTGTAGGAACGGAAAGAA	368	5.90
TTACCAGTAAGTCGTCTCTGG	BnaC09g33120D	unknown	136	2	9023	TTACCAGTAAGTCGTCTCTGG TGCGAATCGTCATTTAGTAGAGGCAACTGCTT	287	4.60
CCATTAGCTTTGAAAGGCACC	BnaA01g14050D	NBR1 homolog	719	12	8700	CCATTAGCTTTGAAAGGCACC ACTCGGTAGTCGTAGCGTTATGTGGGTTGGTA	138	2.21
CCATTAGCTTTGAAAGGCACCC	BnaA01g14050D	NBR1 homolog	391	6	8700	CCATTAGCTTTGAAAGGCACCC ACTCGGTAGTCGTAGCGTTATGTGGGTTGGTA	138	2.21
GTCCTTGTGACGTAGTTCTCT	BnaC02g37450D	Cytochrome P450 81D11	285	5	1182	GTCCTTGTGACGTAGTTCTCT GTAACAGGAGCACTGAAACTAG-GACCGTAGC	125	2.01
TCAACGATTGTGTGAAATGAT	BnaC05g43760D	Non-specific lipid-transfer protein 6	124	2	9465	TCAACGATTGTGTG-AAATGAT TAGGAGTTTCTAACGAACGTTTATTACCCACT	123	1.97
AGTGGATCCATCTGATGTGAA	BnaA03g56180D	Disease resistance protein TAO1	964	15	8857	AGTGGATCCATCTGATGTGAA CTGCTCACAT-GGTAGACCACATCTTTATCCC	60	0.96
GTCAACAACAACGCATGGGCC	BnaC04g10770D	Chlorophyll a-b binding protein 1, chloroplastic	123	2	10490	GTCAACAACAACGCATGGGCC CTTTCA-TTGTTGTTGTGTGTACTGTTTCAGT	56	0.90
TCTTGGTCGTCCATATCAGCC	BnaAnng23890D	unknown	212	3	9984	TCTTGGTCGTCCAT-ATCAGCC GACTAGCAGCGGCAGGTAGTAGTGGGTGTAAG	56	0.90
CGAACTTCGAAAGGGGATC	BnaC08g46150D	TAR1	103	2	8666	CGAACTTCGAAAGGGGATC CGTTGC-TGAGGTTGTTCGCTAGGGTTGGTGT	38	0.61
AATGGCTAAGATGCTCTGAGC	BnaA05g09410D	Chlorophyll a-b binding protein 1, chloroplastic	259	4	9446	AATGGCTAAGATGCTCT-GAGC TTTATTACCCACTCTAGGAGAACTCGACCAAG	33	0.53
TTGAGCCTGTTGTTCCTAACA	BnaA01g14050D	NBR1 homolog	239	4	8919	TTGAGCCTGTTGTTCCTAACA CTGGTACTCGCACAACAGGTGTTGTCAGCTAC	29	0.47
GAGCCTGTTGTTCCTAACACT	BnaA03g46880D	NBR1 homolog	173	3	8917	GAGCCTGTTGTTCCTAACACT GGTACTCGCACAACAGGTGTTGTCAGCTACCG	28	0.45
TGAGCCTGTTGTTCCTAACACT	BnaA03g46880D	NBR1 homolog	353	6	8918	TGAGCCTGTTGTTCCTAACACT TGGTACTCGCACAACAGGTGTTGTCAGCTACC	28	0.45
CCGAGGAGGTTGTTGTCCTTG	BnaCnng03470D	Probable mediator of RNA polymerase II transcription subunit 37e	129	2	1629	CCGAGGAGGTTGTTGTCCTTG CACCGGCTCCTACAAAGGCAGGAGGAACTTTA	27	0.43
TTAATAATATACTCGTTACGTT	BnaA06g14780D	unknown	117	2	9054	TTAATAATATACTCGTTACGTT TCACAGTTCTTATATGAGTA-TGAGACCCACA	26	0.42
TAAGGATATATACATATACTC	BnaC05g43760D	Non-specific lipid-transfer protein 6	117	2	9055	TAAGGATATATACATATACTC TCACAGTTCT-TATATGAGTATGAGACCCACA	24	0.38
AGGTCGTTCTGTTTCCAGGGT	BnaAnng22160D	TAR1	143	2	9130	AGGTCGTTCTGTTTCCAGGGT GGTCTCCAG-AGGAAAAAGGGACCAAGAACTC	20	0.32
CGAAGAGGTCGTTGTCATCAA	BnaA01g14050D	NBR1 homolog	237	4	8312	CGAAGAGGTCGTTGTCATCAA CGAAGCTTATACAGTAAGAGTAGTCACTGTAT	19	0.30
TGCGCAGAGTCTTTTTAAGTC	BnaAnng10090D	Putative UDP-arabinose 4-epimerase 4	128	2	9262	TGCGCAGAGTCTTTTAAGTC AGCGACGCGTCTAACGGAGAT-CAGCTACCGT	18	0.29
TGCGCAGAGTCTTTCTAAGTC	BnaC07g18010D	Putative UDP-arabinose 4-epimerase 4	403	6	9262	TGCGCAGAGTCTTTCTAAGTC AGCGACGCGTCTAACGGAGAT-CAGCTACCGT	18	0.29
TGCTCTCCCGTAACTACGCTT	BnaA02g04080D	Disease resistance protein TAO1	402	6	8984	TGCTCTCCCGTAACTACGCTT TACTACGACAGCGCGTTGA-GTGAACCTTAAG	17	0.27
TCTTGTCGGAGTTTATGATC	BnaA01g23650D	Adenylate isopentenyltransferase 7, mitochondrial	1324	21	8865	TCTTGTCGGAGTTTATGATC TTGAAGAACTG-CTCACATGGTAGACCACATC	15	0.24
TCTTGTCGGAGTTTATGATCT	BnaC02g08450D	Adenylate isopentenyltransferase 5, chloroplastic	27771	445	8865	TCTTGTCGGAGTTTATGATCT TTGAAGAACTG-CTCACATGGTAGACCACATC	15	0.24
CCCAACTATCTCGAACGGCCC	BnaAnng23890D	unknown	101	2	8681	CCCAACTATCTCG-AACGGCCC ATGTGGGTTGGTAGACCGTTGCTGAGGTTGTT	15	0.24
TTCTTTCTTTCGTGTTGGATG	BnaC01g16550D	NBR1 homolog	103	2	8405	TTCTTTCTTTCGTGTTGGATG CATAAAG-AAGAAAGTAGAGCCCACACTTGAG	15	0.24
GGGATTAGTCCTTTGGGCCT	BnaA05g32630D	DELLA protein GAI	100	2	4530	GGGATTAGTCCTTTGGGCCT TCACCGCTGATCAGGGAATTCGAACAACTCTT	13	0.21
CCGTGATATTTCTGAGAAGAC	BnaCnng34030D	Copia protein	117	2	5792	CCGTGATATTTCTGAGAAGAC AAATGGCAATGTAATGGTTCTTATGAACAGCT	10	0.16
GCTTGTGGTTCGGACACTC	BnaA08g02720D	unknown	278	4	3432	GCTTGTGGTTCGGACACTC TCAACGAA-ACCAAACATCTGAGGAAAATACT	10	0.16
GCTTGTGGTTCGGACACTCT	BnaA08g02720D	unknown	541	9	3432	GCTTGTGGTTCGGACACTCT TCAACGAA-ACCAAACATCTGAGGAAAATACT	10	0.16
GCTTGTGGTTCGAACACTC	BnaA08g02450D	unknown	157	3	3432	GCTTGTGGTTCGAACACTC TCAACGAA-ACCAAACATCTGAGGAAAATACT	10	0.16
GCTTGTGGTTCGAACACTCT	BnaA08g02450D	unknown	239	4	3432	GCTTGTGGTTCGAACACTCT TCAACGAA-ACCAAACATCTGAGGAAAATACT	10	0.16
ATTCTCATCATCGTCATCATT	BnaA09g14980D	Disease resistance protein TAO1	152	2	8302	ATTCTCATCATCGTCATCATT ACAGTAAGAGTAGTCACTGTATTAACGTACAA	9	0.14
ATTCTGTAGTGTCAGAGCGGC	BnaA08g22900D	Putative F-box/kelch-repeat protein At3g24610	163	3	2858	ATTCTGTAGTGTCAGAGCGGC GGACTAAGACAACACTGTGTTGTTGTACGTAC	9	0.14
TCGAAGAGGTCGTTGTCATCAA	BnaA01g14050D	NBR1 homolog	583	9	8313	TCGAAGAGGTCGTTGTCATCAA TCGAAGCTTATACAGTAAGAGTAGTCACTGTA	8	0.13
GGAATCTTGATGATGCTGCAT	BnaC02g09940D	unknown	456	7	8997	GGAATCTTGATGATGCTGCAT TGCTTCTTAG-ACTACTACGACAGCGCGTTGA	7	0.11
CCAAGATTGTCATCGTAGAATC	BnaA02g05040D	unknown	166	3	8604	CCAAGATTGTCATCGTAGAATC TCGAGATTCCAACACTAGTATCTT-GACCAAC	7	0.11
GTTCCAAAGACCTCTGAGGCT	BnaC03g18980D	Chlorophyll a-b binding protein 1, chloroplastic	136	2	8617	GTTCCAAAGACCTCTGAGGCT GTTGCGAGGTTCCTCGAGATTCCAACACTAGT	5	0.08
TTTCATCGTTCTCAGGTCGTT	BnaAnng22160D	TAR1	209	3	7547	TTTCATCGTTCTCAGGTCGTT TAAGCAAGTGGAAAGAGTCCAACGGACTTTGG	5	0.08
GCTTGAAAATCGGACGTCT	BnaA09g04420D	TAR1	143	2	7107	GCTTGAAAATCGGACGTCT CCAACGCACTTCTAGTGTGTGGAACTCTCCAT	5	0.08
TTCATGACTTCCTTCTTCTT	BnaC07g18010D	Putative UDP-arabinose 4-epimerase 4	304	5	6242	TTCATGACTTCCTTCTTCTT TCATAAGGAC-GAAGGAAGAGAGGAGTCGCTA	5	0.08
TTCATGACTTCCTTCTTCTTT	BnaC07g18010D	Putative UDP-arabinose 4-epimerase 4	248	4	6242	TTCATGACTTCCTTCTTCTTT TCATAAGGAC-GAAGGAAGAGAGGAGTCGCTA	5	0.08
AACGACGTCAAATATTTCTGT	BnaA09g17530D	Vesicle-associated protein 1-4	120	2	3220	AACGACGTCAAATATTTCTGT TTAGTTGCTGTACTTAATAGAAACAGAATACC	5	0.08
GTAGATTTTTCCACTCATCGAG	BnaCnng34030D	Copia protein	416	7	8563	GTAGATTTTTCCACTCATCGAG GGTGCGTTTGAAAAGGTGGGTTG-TCACACAG	4	0.06
TCTTCTCAGAAATATCACGGTC	BnaC03g45030D	12-oxophytodienoate reductase 3	202	3	8231	TCTTCTCAGAAATATCACGGTC TGACAGAAAAGTTTGTCTAGTGTCAGCTACAA	4	0.06
TGTTGGTTTGGGTCTTGGAAC	BnaC07g51220D	Nicotinate phosphoribosyltransferase 1	2590	42	7583	TGTTGGTTTGGGTCTTGGAAC TACGAGAACCAAACCTTTAACCTGGGGTGGTA	4	0.06
GCACTTGCACATGGGTTAGTC	BnaC02g36110D	unknown	653	10	6941	GCACTTGCACATGGGTTA-GTC TTCACGAGAACGTGTTCCCACTACAGACACTC	4	0.06
GTGACATACACGACGGGCATG	BnaC01g16550D	NBR1 homolog	171	3	2851	GTGACATACACGACGGGCATG ACAACACTGTGT-TGTTGTACGTACCTGCTTC	4	0.06
TTTTAACCGGATCCCCTTTCG	BnaA09g04420D	TAR1	197	3	2780	TTTTAACCGGATCCCCTTTCG TACCAAGA-TGGCCAAGCGGAAAGTAGACAAG	4	0.06
TCGGCGGGAATTCCGGAAAG	BnaA09g04420D	TAR1	134	2	10508	TCGGCGGGAATTCCGGAAAG TACAAGCCG-CTTTTATGTCTTTCATTGTTGT	3	0.05
CACCGTCCTGCTGTCTTAATC	BnaAnng36730D	TAR1	194	3	5572	CACCGTCCTGCTGTCTTAATC ACGAGTCGTAAGACGACAGACATAGTTCTATA	3	0.05
TTGCTATAGATGGTTTCTGCT	BnaA03g16300D	TIM14-1	252	4	3681	TTGCTATAGATGGTTTCTGCT CGGAAACGA-AGCTACTCAAGACCATCTGAAG	3	0.05
TTCCGTGGGATGGCTCAACAA	BnaAnng22160D	TAR1	320	5	2165	TTCCGTGGGATGGCTCAACAA CGAACAGGAACCCTATCGAGT-GATAGACAAT	3	0.05

TTGTCTCTCCTTGTAATTGCT	BnaCnng34030D	Copia protein	123	2	1618	TTGTCTCTCCTTGTAATTGCT oo||| ||||||| |||o| | CAAAGGCAG-GAGGAACTTTAGCTAAGGGAAT	3	0.05
ATTGTTATGCCTAGGCTCAGA	BnaA09g16680D	Disease resistance protein TAO1	212	3	7620	ATTGTTATGCCTAGGCTCAGA |||o|| |o| ||| |||||| ACCGTAATAACATG-ATCAGAGTCTCTGATAT	2	0.03
ATTCCAGATGTCGAGATCAGA	BnaC05g10980D	RNA-dependent RNA polymerase 1	109	2	6085	ATTCCAGATGTCGAGATCAGA ||o||| ||||| ||||| | AGTGTAGGGTGTACAGATCTACT-TCAAAAAG	2	0.03
ATCACATATGTCTAGTGGACT	BnaC09g02400D	Glutamate receptor 1.2	370	6	6085	ATCACATATGTCTAG-TGGACT ||| ||o||||||| ||o| | AGTGTAGGGTGTACAGATCTACTTCAAAAAGA	2	0.03
AGAGATTGATCTGAACAAGGA	BnaC01g16550D	NBR1 homolog	4372	70	3008	AGAGATTGATCTGAACAAGGA ||| |||||| | ||||| o| TCCTTCTATAACTACA-TTGTTATTGGAAGAA	2	0.03
TCATTGAAACCCTTCTGGATC	BnaA01g14050D	NBR1 homolog	106	2	2499	TCATTGAAACCCTTCTGGATC ||| || ||||||||| o|| CTGAAGTCAC-TTGGGAAGAGTTACAAGAGCC	2	0.03
CGTTTTCCCTGAGCTCTTGGC	BnaAnng22920D	Chlorophyll a-b binding protein 1, chloroplastic	128	2	9122	CGTTTTCCCTGAGCTCTTGGC | |||||||| | |||||o AGAGGAAAAAGGGAC-CAAGAACTCAGCTTTC	1	0.02
TACTAATTCATGATCTGGC	BnaC09g29290D	30S ribosomal protein S7, chloroplastic	140	2	6462	TACTAATTCATGATCTGGC |||| |o||||| || | AGGTATGAGTGAGTACTTTACGGCTCTATAAG	1	0.02
TCGCTCCTACAAGCACGTGAC	BnaA09g14980D	Disease resistance protein TAO1	256	4	6371	TCGCTCCTACAAGCACGTGAC |||||||| |||||||| ||| CTGAAGCGAGGAAGTTCGTG-ACTATACAAGA	1	0.02
AGGATTCCCTTAGTAACGG	BnaC08g46150D	TAR1	101	2	1086	AGGATTCCCTTAGTAACGG ||o||||| || o|||o CCAATCTTAAGGTAAAGGTTGCTGATACGGTG	1	0.02

Tanto-specific

Table S32: Oligonucleotide primers used for RT-qPCR analysis

Gene type	Gene ID	Foward primer (5' - 3')	Reverse primer (5' - 3')	Gene annotation	Ref.
Housekeeping genes	BnaA08g11790D	AGCCTGAGGAGATATTAGCAGGAA	ATCTCACTGCAGCTCCACCAT	BnaUP1 - Unknown annotation	Zhang *et al* ., 2014
	Bra011516	TGAAGAGCAGATTGATTTGGCT	ACACTCCATTGTCAGCCAGTT	TIP41-like Protein	Wang *et al.*, 2014
Differentially expressed genes	BnaA07g16850D	CAAATTCCCAAGAAGTTACTTTAGG	TTCCGATGTATGTGATGCTG	Probable WRKY transcription factor 70	
	BnaA01g22680D	TATACGCTCTAGTTACTCAGATGG	GCTACTGCTACTCTCTCG	MLO-like protein 6	
	BnaA03g54590D	TCAGTCTGCTGCTCAATGTTTGTAG	CGATATGTATGTTACATGAAGTGTGATGGT	Lipid transfer protein EARLI 1	
	BnaA01g30490D	CAATCATTGCGAGAATGTACCAAGG	GGTAGGAACATCATCATCCATGCC	Probable mediator of RNA polymerase II transcription subunit 37c	
	BnaA01g10420D	CCGATCAAGATATTTGTATAGAGAGAAATG	ATTTGTAGAATAGATAACCAGCTAAACCC	Vacuolar-sorting receptor 7	
	BnaA01g08510D	ATGACACTCCCATATCTCAGGGATATTAC	TTCATGTGGCAATCTCATCGACC	Calcineurin B-like protein 1	
	BnaA01g01570D	TAACCCAAGTGTGAAGAGTGCAAAG	ACGCGGTAGATAGAGTTGGC	Thaumatin-like protein 1	
	BnaA07g19520D	TGCAGGAATCTGAAAGAGC	GGAAGTGTATGTATCAGGGAAATG	TRANSPORT INHIBITOR RESPONSE 1	
	BnaA08g30830D	AGTTTGTGGTATTGAATACGTTTGTATCT	ACGGACCTATATATAAGTAACCGTAAATGC	Pathogenesis-related protein PR-1	
	BnaA01g03580D	GGAAAGAACTGGGAAATGGATGA	CAACAGAACCTCTGCCTTAG	Probable disease resistance protein At4g33300	
	BnaAnng10090D	GCAATTAAAGGTGAAAGGAACAGACTAC	TTTACGTGAGCATCCACGAGG	Putative UDP-arabinose 4-epimerase 4	
	BnaA09g14980D	GCGGGGGTAAACAGAATGGAC	CTCATATCGAGTTGGTATATGATGGAGC	Disease resistance protein TAO1	
	BnaA04g19840D	TAGCAGGTTTCACGAGCTAAGT	TCATTGTGTCCAGCTAAGCGTC	Squamosa promoter-binding-like protein 3	
	BnaA01g00520D	GGCTAATGATGGCCATGATGC	TCAACACGTCAGGGTGTCTAAG	Cytochrome P450 81F1	
	BnaC05g47910D	TCCCAAAGGTTCTTGGAGATTTGATAG	CTACTTCCTTGTCGTAACCCGAG	DCL 2	
	BnaA06g12810D	CAAGTGCAAGTGGTAGTGGG	GGGTCTTGTGTTAGTTGTCGTAGG	PLASMODESMATA CALLOSE-BINDING PROTEIN 3	
	BnaA05g14760D	ATGCTATTATATTGATTATCGTAACAGCCC	ACAAAGAGAAACACACTACAATAAACCC	AGO2	

Table S33: Oligonucleotide adapters and primers used for 5'RACE analysis

	Name	Nucleic acid sequences (5' - 3')	Gene annotations
5' RACE adapter	5'RACE Adapter	GCUGAUGGCGAUGAAUGAACACUGCGUUUGCUGGCUUUGAUGAAA	-
5' RACE adapter primers	5'RACE outer primer	GCTGATGGCGATGAATGAACACTG	-
	5'RACE inner primer	CGCGGATCCGAACACTGCGTTTGCTGGCTTTGATG	
Gene-specific primers	BnaA07g13830D-1	TTTCTCCTCCTTCTCCGC	ARF10
	BnaA07g13830D-2	CTTTCTCCTCCTTCTCCGCCTC	
	BnaAnng18540D-1	GGGAGAAGCGAAGACAGT	SCL6
	BnaAnng18540D-2	GTCGGGAGAAGCGAAGACAGTG	
	BnaCnng68320D-1	CACCATAAGTAGTCTCCGCTC	AGO2
	BnaA05g14760D-1	CCATTACATAATGCAGTCTCTGCTCC	AGO2
	BnaA09g14980D-1	GACCAACCTCTTCCCTG	TAO1
	BnaA09g14980D-2	CACACAGGTTTCATCAAAGG	
	BnaCnng44780D-1	GTTTGGTTCAGACACAATGAAACG	BLOS2
	BnaCnng44780D-2	CGATGTTGATGATGACGACACTCAG	
	BnaA01g34730D-1	CATGAGAGAAGGTTGGAAGC	APETALA 2

APPENDIX 2: SUPPLEMENTARY FIGURES AND TABLES OF PUBLICATION: "CROSSTALK BETWEEN PTGS AND TGS PATHWAYS IN NATURAL ANTIVIRAL IMMUNITY AND DISEASE RECOVERY" KØRNER ET AL. 2018

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SUPPLEMENTARY INFORMATION

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Crosstalk between PTGS and TGS pathways in natural antiviral immunity and disease recovery

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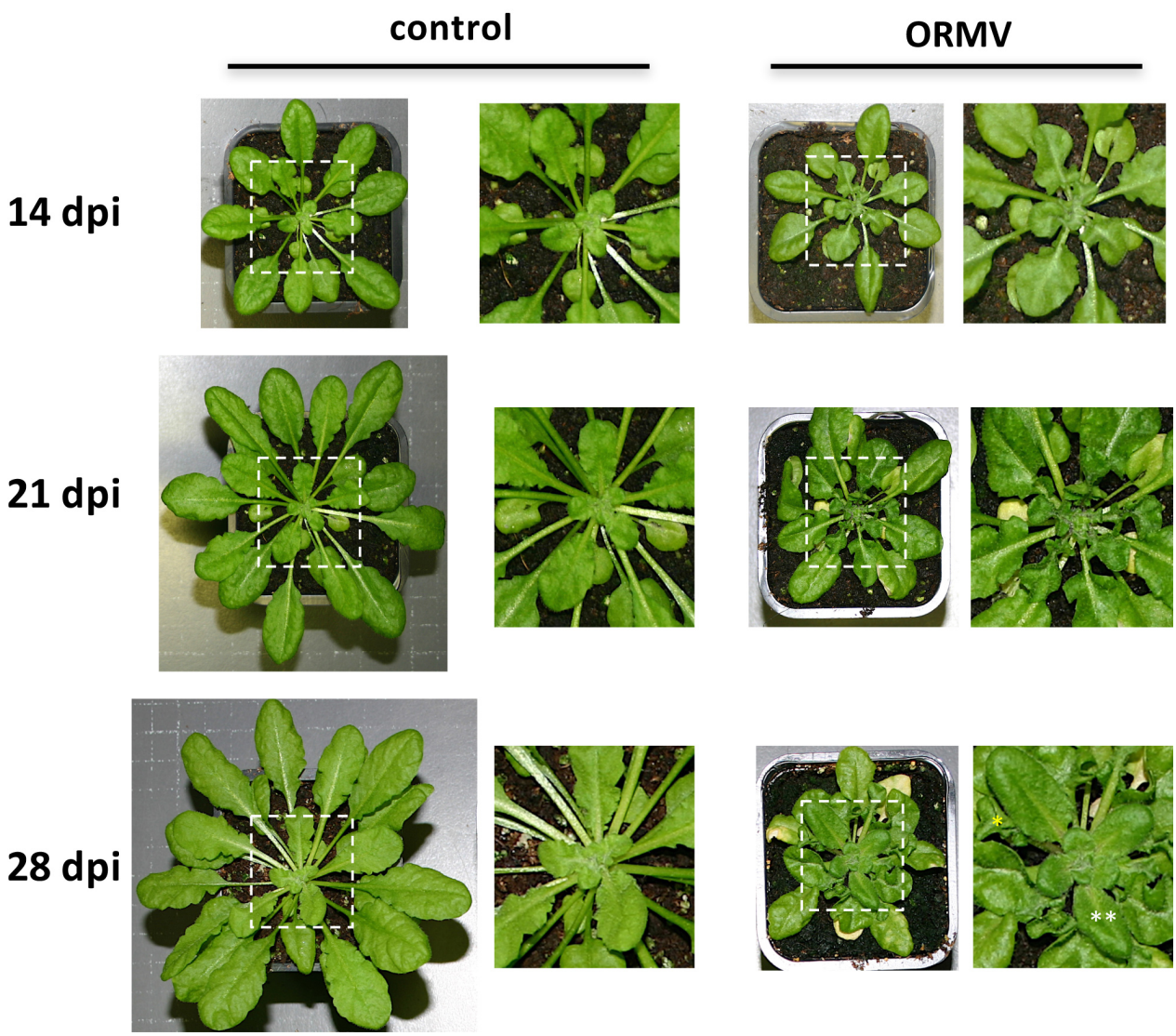
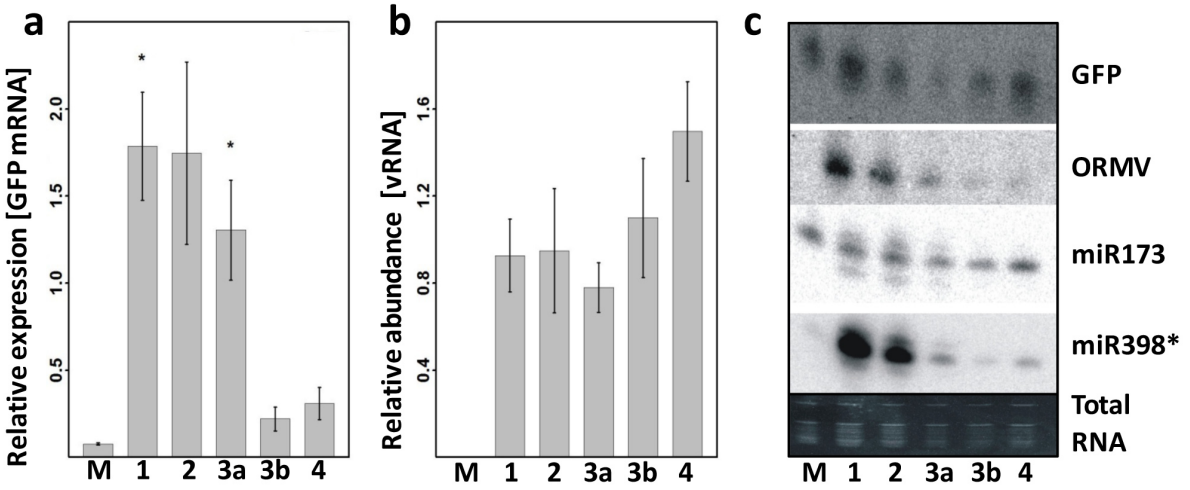
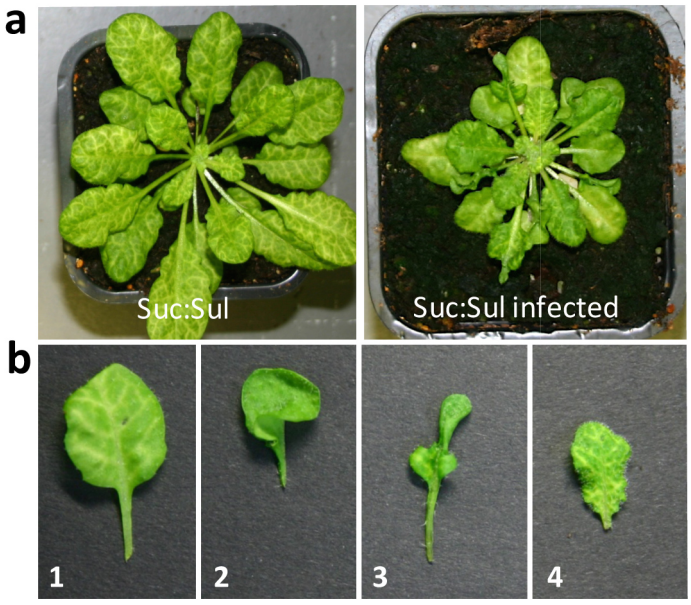


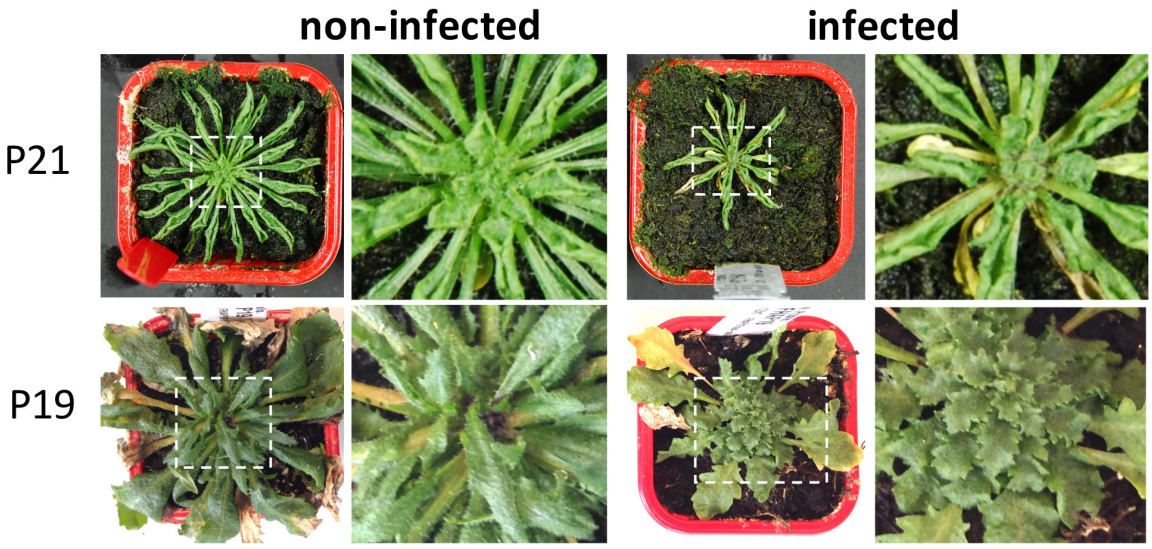
Supplementary Figure S1. Symptoms and symptom recovery during ORMV infection in Arabidopsis. Non-infected control plants and ORMV-infected plants at 14, 21, and 28 dpi. Whole plants and enlarged central parts (within the area delimited by white rectangle) are shown. As has been reproduced in several recovery experiments, leaves emerging of infected plants at 21 dpi show strong symptoms, whereas leaves emerging at 28 dpi and onwards are recovered and are free of symptoms. Examples of symptomatic and recovered leaves are labeled with one yellow and two white asterisks, respectively.



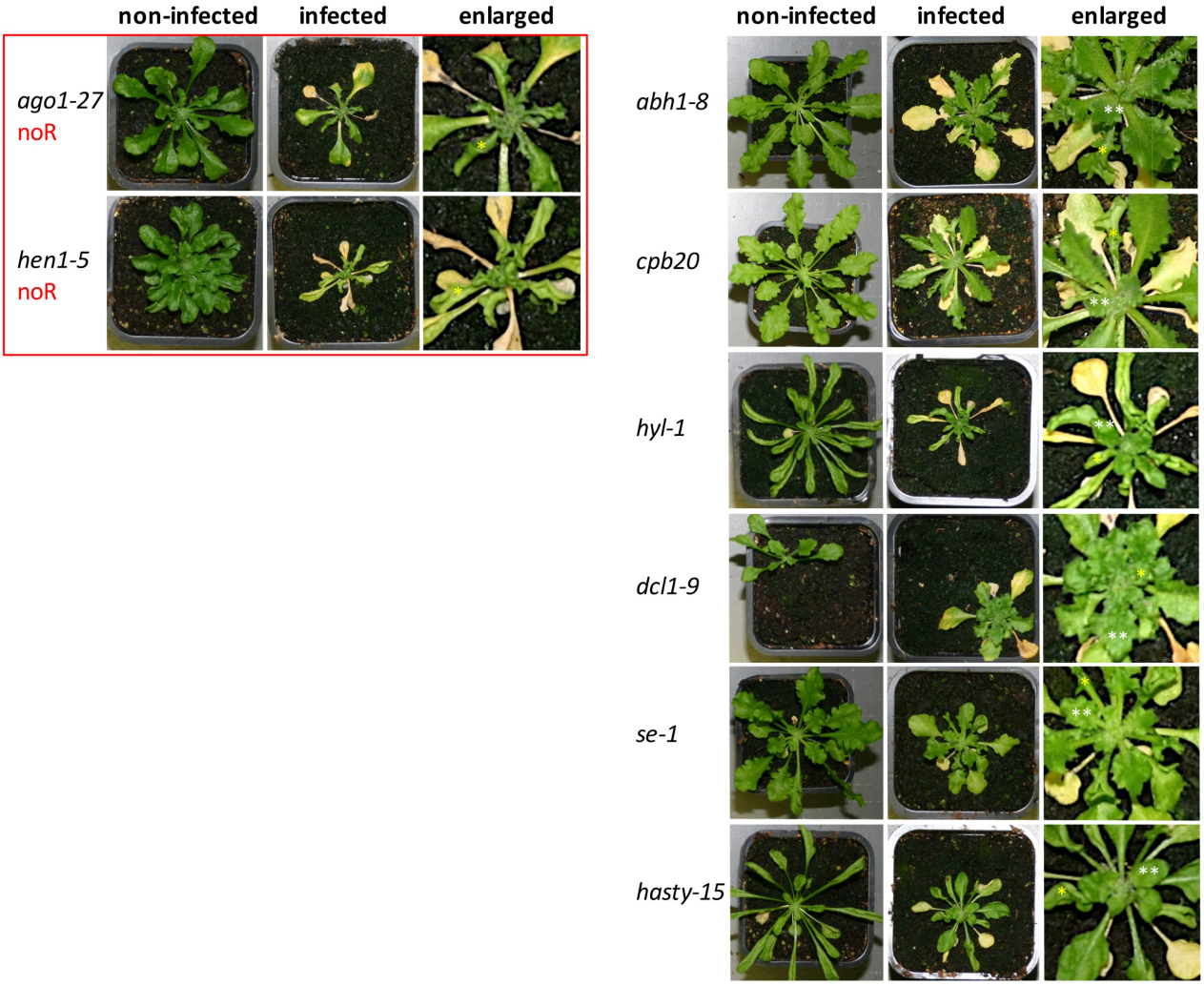
Supplementary Figure S2. Analysis of STs in L8z2 plants. Accumulation of GFP mRNA (**a**) and viral RNA (**b**) in leaves of the different STs, measured by RT-qPCR; n= 3 ± SE, Student's t-test * $p<0.05$. The level of GFP mRNA (**a**) in ST3a tissue was similar as in the other fluorescent symptom types (ST1 and ST2) and clearly higher than in mock-inoculated tissues. In contrast, GFP mRNA levels were similar to mock in the recovered, non-fluorescent tissues of ST3b and ST4. The amount of viral RNA (**b**) was similar in all infected tissues. (**c**), Northern blot showing the levels of GFP-derived siRNAs (GFP) and vsiRNAs (ORMV) as well as of miR173 and miR398*, in leaves of the different STs. Similar vsiRNA levels occur also in the different STs of infected wild type Col-0 plants (not shown). Stained total RNA is shown as loading control. M, mock.



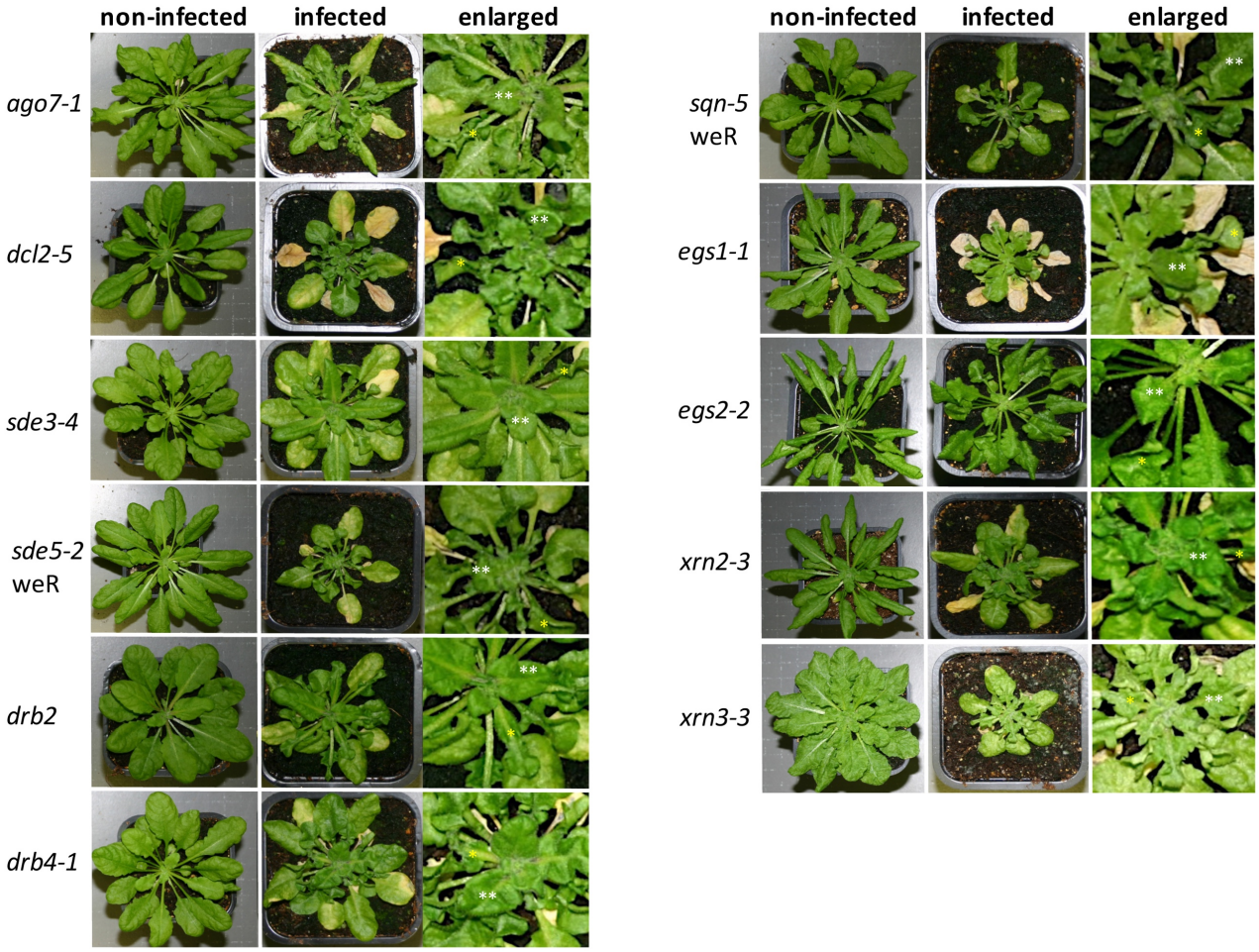
Supplementary Figure S3. Symptoms, recovery, and correlation with viral silencing suppression in ORMV-infected Arabidopsis Suc:Sul plants. (**a**), Non-infected and ORMV-infected Suc:Sul plants. (**b**) Examples of individual leaf STs of an infected Suc:Sul plant at 28 dpi. The virus suppresses vein bleaching (silencing of the *SULFUR* gene) in ST2 leaves, and partly also in ST3 leaves, whereas there is no suppression of *SULFUR* silencing in recovered ST4 leaves. These observations have been reproduced in several recovery experiments.



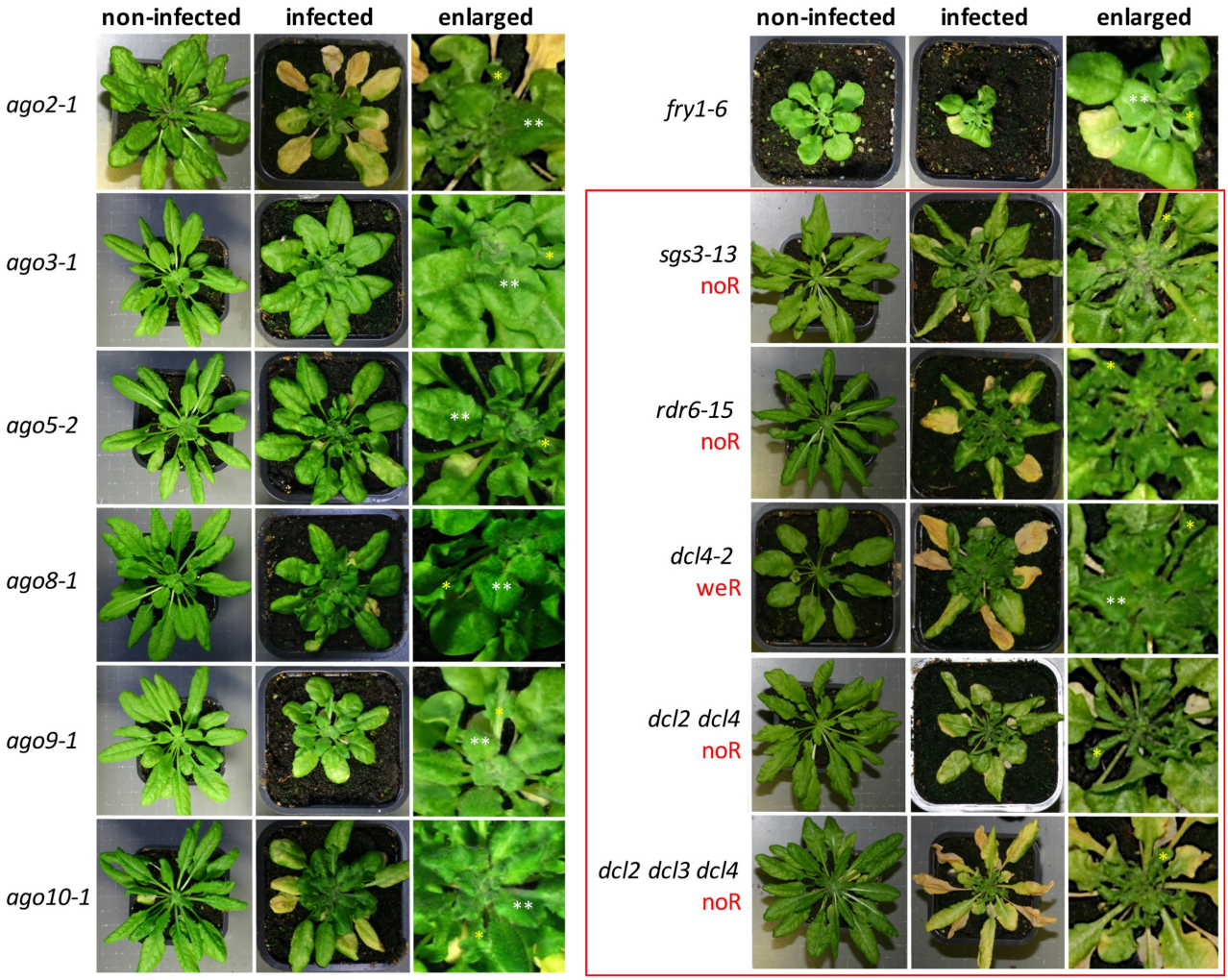
Supplementary Figure S4. Suppression of recovery in VSR-expressing transgenic plants. Examples of non- infected and ORMV-infected plants expressing either closterovirus P21-VSR or the tombusvirus P19-VSR. Plant areas within the dashed rectangles are shown enlarged. Neither P21 nor P19 plants allow disease recovery.



Supplementary Figure S5. **Recovery phenotypes of Arabidopsis mutants.** Non-infected and ORMV-infected plants at 28 dpi. The central parts of the infected plants are shown enlarged. Infected plants are usually stunted and are thus smaller than non-infected plants of the same age. For size comparison between infected and non-infected plants the pot size can serve as a reference. In the enlarged images, examples of symptomatic and recovered leaves are labelled with one (*) and two (**) asterisks, respectively.
ago1-27 and *hen1-5* mutants (left) impaired in components shared by several endogenous sRNA pathways do not show recovery. Mutants impaired in the biogenesis of miRNAs (right) recover normally. noR, no recovery.

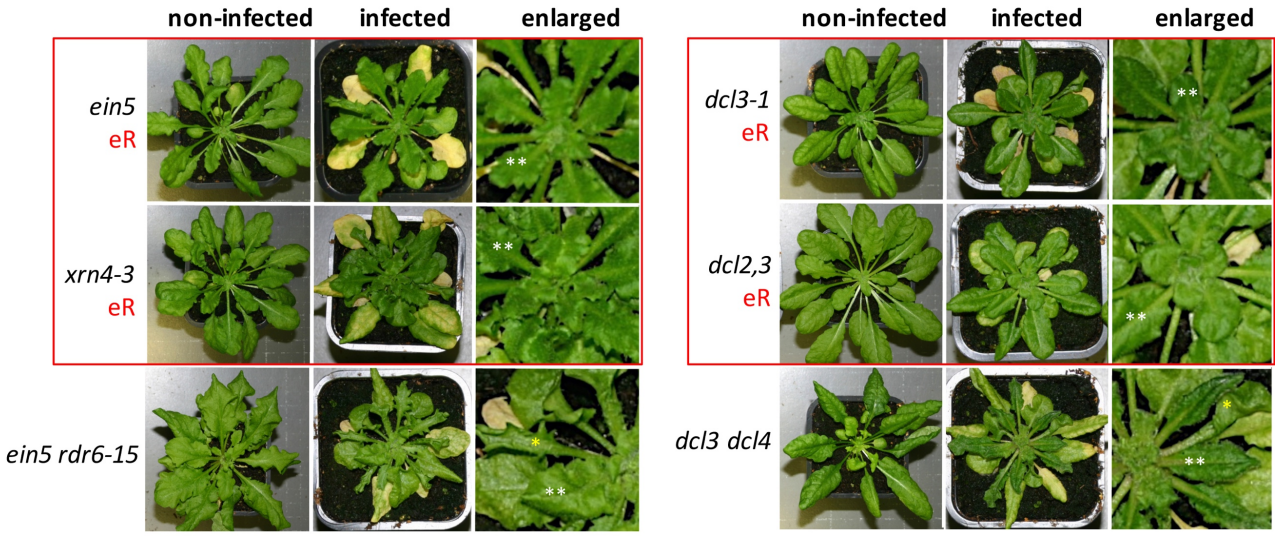


Supplementary Figure S6. Recovery phenotypes of Arabidopsis mutants impaired in the biogenesis of various classes of siRNAs. Non-infected and ORMV-infected plants at 28 dpi. The central parts of the infected plants are shown enlarged. Infected plants are usually stunted and are thus smaller than non-infected plants of the same age. For size comparison between infected and non-infected plants the pot size can serve as a reference. In the enlarged images, examples of symptomatic and recovered leaves are labelled with one (*) and two (**) asterisks, respectively.



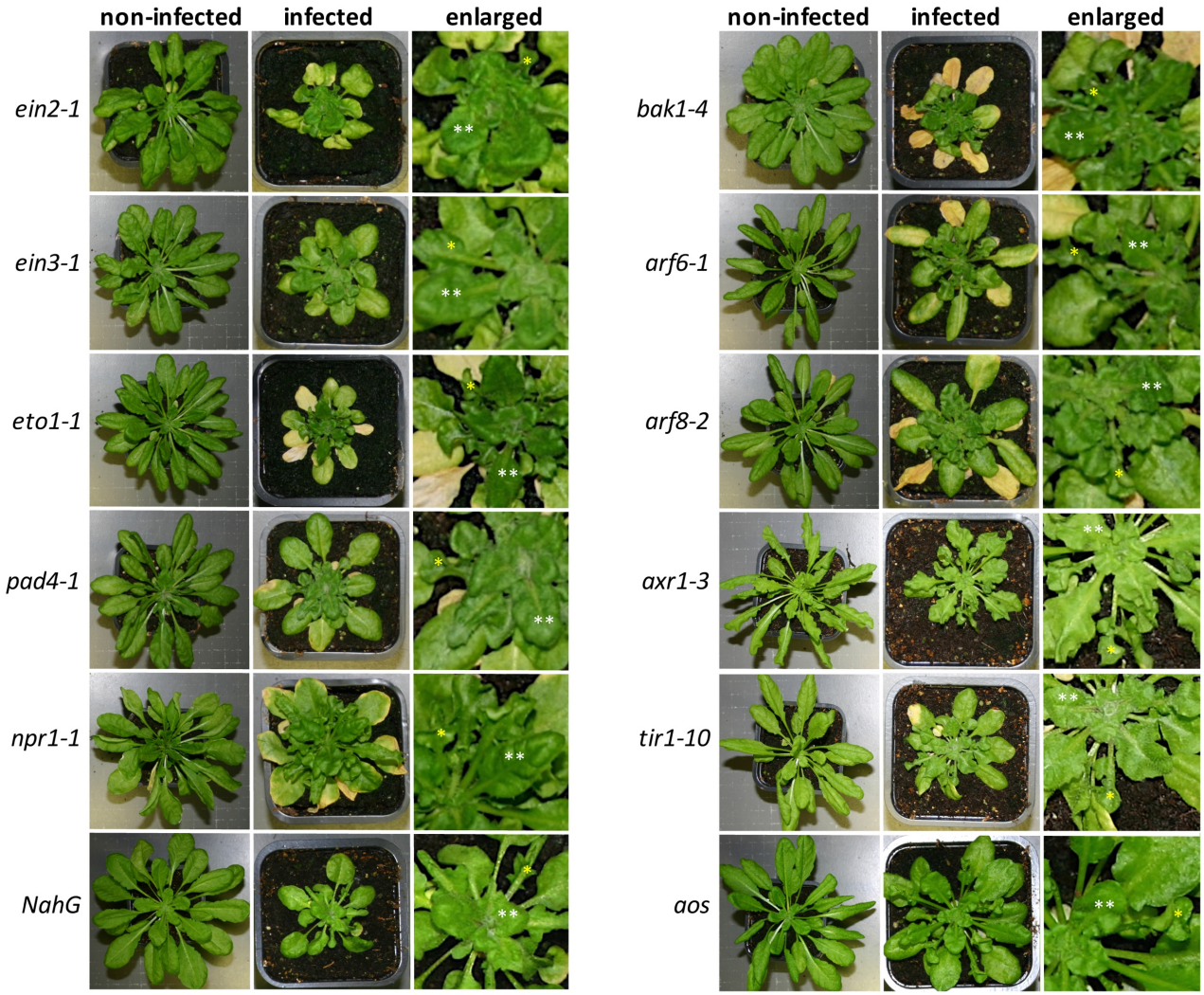
Supplementary Figure S7. **Recovery phenotypes of Arabidopsis mutants impaired in the biogenesis of various classes of siRNAs.** Non-infected and ORMV-infected plants at 28 dpi. The central parts of the infected plants are shown enlarged. Infected plants are usually stunted and are thus smaller than non-infected plants of the same age. For size comparison between infected and non-infected plants the pot size can serve as a reference. In the enlarged images, examples of symptomatic and recovered leaves are labelled with one (*) and two (**) asterisks, respectively.

Mutants affected in general factors needed for the production and amplification of various classes of siRNAs do not recover (*rdr6-15* and *sgs3-13*) or recover weakly (*dcl4-2*). noR; no recovery; weR, weak (delayed) recovery.



Supplementary Figure S8. Recovery phenotypes of Arabidopsis mutants affecting the steady state level of siRNAs. Non-infected and ORMV-infected plants at 28 dpi. The central parts of the infected plants are shown enlarged. Infected plants are usually stunted and are thus smaller than non-infected plants of the same age. For size comparison between infected and non-infected plants the pot size can serve as a reference. In the enlarged images, examples of symptomatic and recovered leaves are labelled with one (*) and two (**) asterisks, respectively.

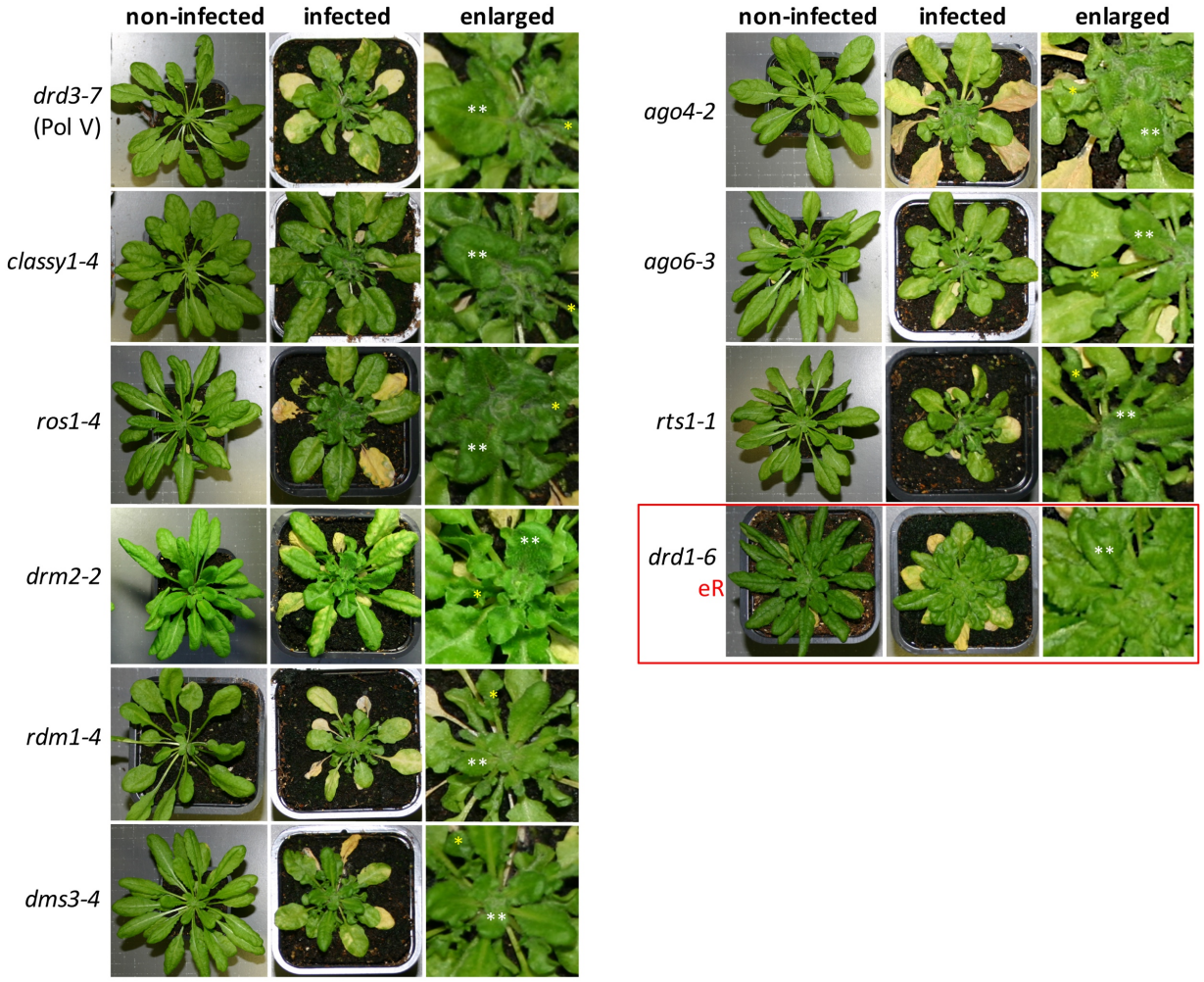
ein5 and *xrn4-3* mutants show enhanced (early) recovery (eR). This effect is RDR6-dependent as shown by normal recovery of the *ein5 rdr6-15* double mutant. *dcl3-1* single and *dcl2 dcl3* double mutants also show enhanced (early) recovery. This effect is DCL4-dependent, since the *dcl3 dcl4* double mutant recovers normally.



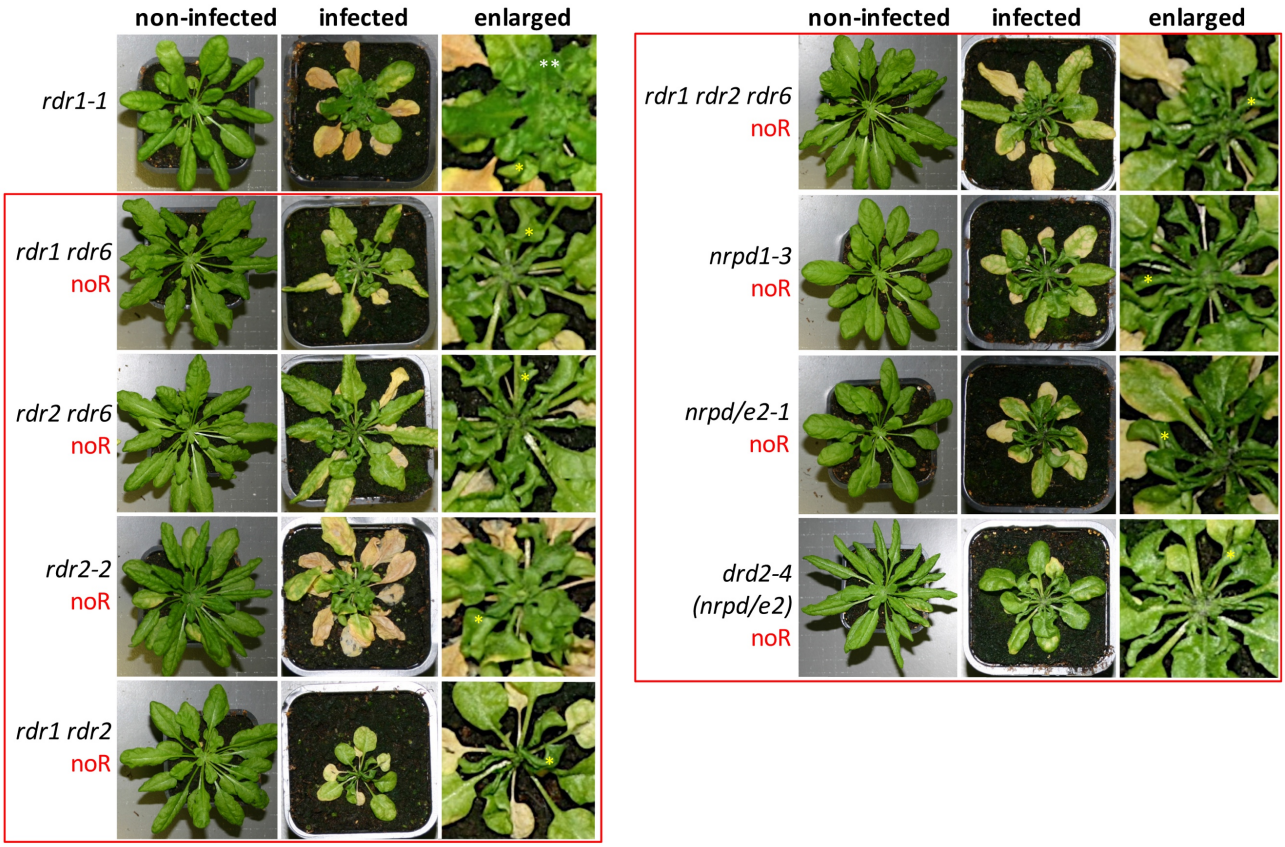
Supplementary Figure S9. Recovery phenotypes of Arabidopsis mutants affected in ethylene, salicylic acid (SA), jasmonic acid (JA) and auxin synthesis and signaling recover normally. Non-infected and ORMV-infected plants at 28 dpi. The central parts of the infected plants are shown enlarged. Infected plants are usually stunted and are thus smaller than non-infected plants of the same age. For size comparison between infected and non-infected plants the pot size can serve as a reference. In the enlarged images, examples of symptomatic and recovered leaves are labelled with one (*) and two (**) asterisks, respectively.

Supplementary Figures S10 and S11. Recovery phenotypes of Arabidopsis TGS mutants acting up- or downstream of DCL3. Non-infected and ORMV-infected plants at 28 dpi. The central parts of the infected plants are shown enlarged. Infected plants are usually stunted and are thus smaller than non-infected plants of the same age. For size comparison between infected and non-infected plants the pot size can serve as a reference. In the enlarged images, examples of symptomatic and recovered leaves are labelled with one (*) and two (**) asterisks, respectively.

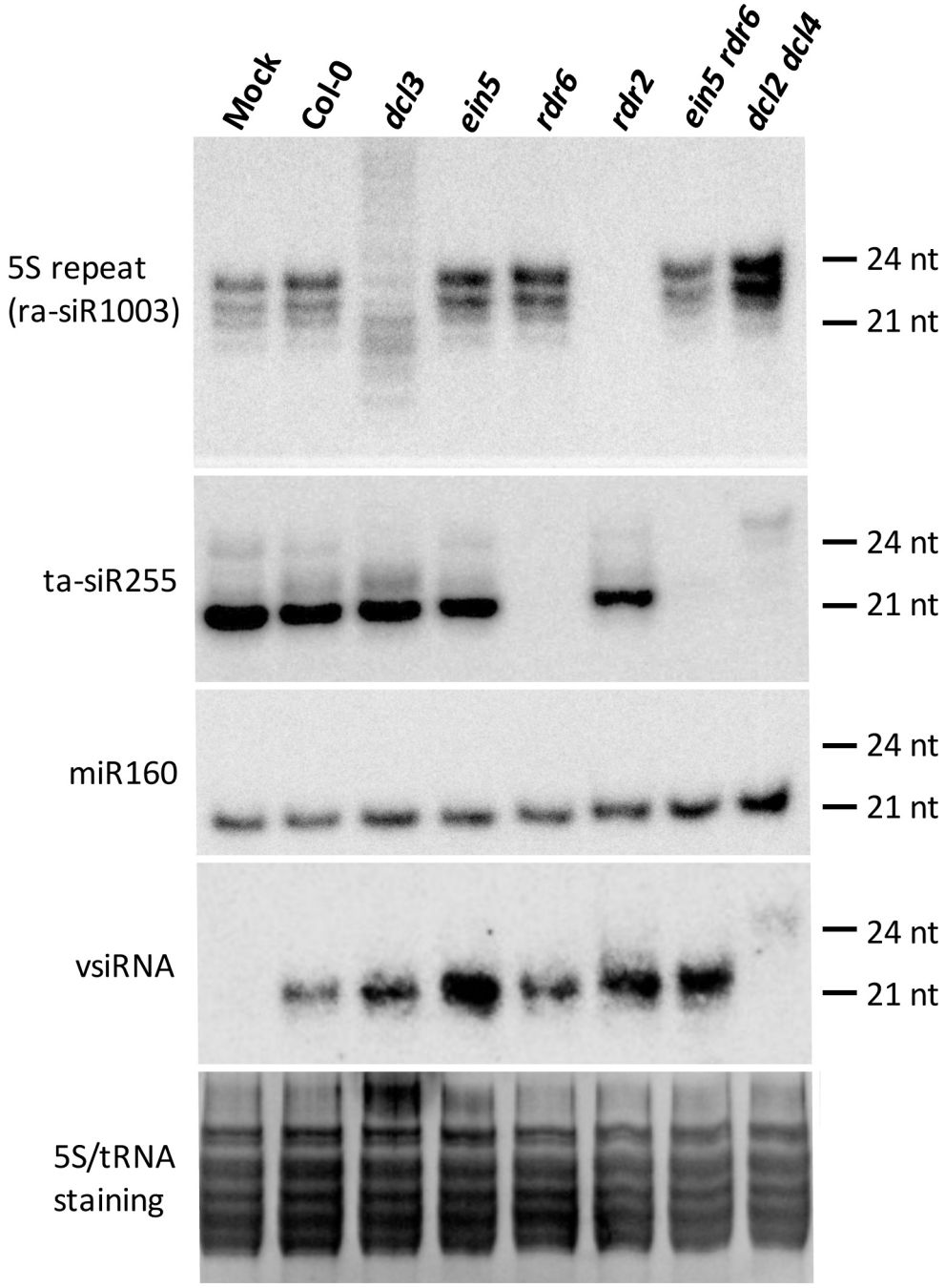
Mutants more directly involved in chromatin remodeling and DNA methylation (e.g. *rdm1*, *drd3*, *classy1*, *drm2*, *dms3*, *rts1*, *ago4*, *ago6*, *ros1*) recover normally. However, *rdr2-2* and several Pol IV-subunit mutants (*nrpd1-3*, *nrpd/e2-1, drd2-4*) do not recover. *drd1* shows enhanced (early) recovery. The DRD1 gene encodes a subunit of the chromatin-remodeling complex that mediates the recruitment of Pol IV and Pol V to chromatin. Enhanced recovery in the *drd1* mutant may indicate that the recruitment of Pol IV to chromatin competes with the role of Pol IV in recovery. eR, enhanced (early) recovery; noR, no recovery.



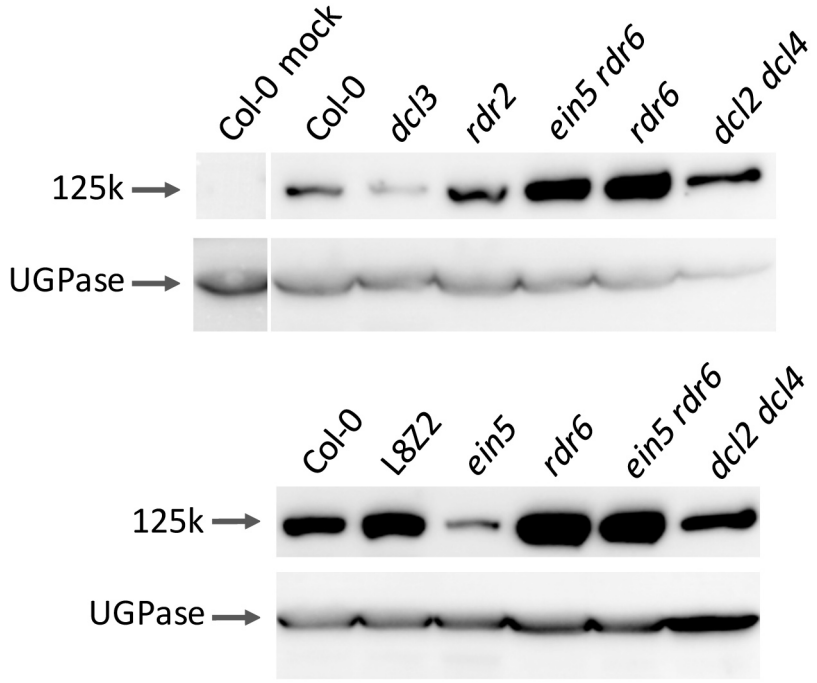
Supplementary Figure S10 (legend above)



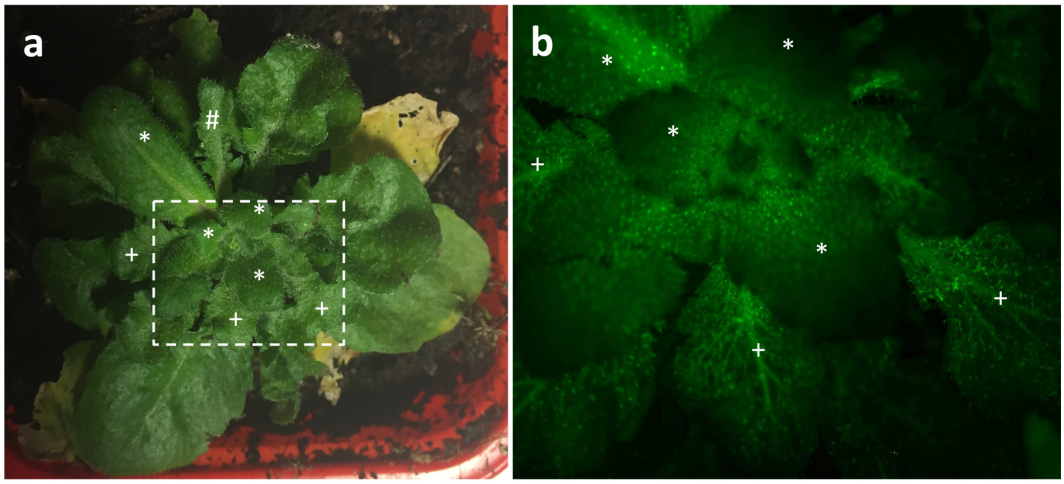
Supplementary Figure S11 (legend above



Supplementary Figure S12. sRNA analysis of ORMV-infected Col-0 wild type plants and silencing pathway mutants. sRNA species in recovered ST4 (Col-0, *dcl3*, *ein5, ein5 rdr6*) and corresponding non-recovered leaves of mutants (*rdr6*, *rdr2*, *dcl2 dcl4*), in which recovery is absent, were analyzed. The analysis was performed with the same RNA samples also used for viral RNA analysis (Fig. 1d). The mutants affected the accumulation of specific sRNA species as expected and shown previously [9]. None of the mutants affected the accumulation of miR160. The accumulation of 5S rDNA repeat-derived ra-siR1003 was affected in *dcl3* and *rdr2* mutants but not in *rdr6* mutants, whereas the production of tasiR255 was affected in *rdr6*, *ein5 rdr6, and dcl2 dcl4* mutants but not in *rdr2* or *dcl3* mutants. As is also expected, production of vsiRNAs was abolished in *dcl2 dcl4*, as is consistent with the lack of recovery in this double mutant. Relative to Col-0 wild type, the vsiRNA levels were higher in mutants showing enhanced recovery (*ein5*, *dcl3*) and reduced in *rdr6,* which interferes with the formation of secondary siRNAs and does not support recovery.



Supplementary Figure S13. VSR expression in recovered leaves of ORMV-infected Col-0 wild type plants and silencing pathway mutants. The 125k-VSR is expressed in infected tissues irrespective of recovery. The amount of the VSR in recovered leaves is lower in mutants undergoing early recovery (*ein5*, *dcl3*) and higher in the upper leaves of *rdr6* mutants in which recovery is inhibited. L8z2 plants, which contain a continuously active silencing system, produce relatively high levels of the VSR whereas *dcl2 dcl4* plants, in which siRNA synthesis is inhibited, contain relatively low levels of the VSR. The Western blot analysis was replicated two times. UGPase, UDP-glucose pyrophosphorylase.



Supplementary Figure S14. Recovery in sink tissues. (**a**), AtSUC:GFP plant infected with ORMV (28 dpi). The part of the plant within the rectangle is shown in (**b**). *, recovered ST4 leaves; +, partially symptomatic ST3/ST4 transition leaves; #, strongly symptomatic ST3 leaf. (**b**), GFP fluorescence of the plant parts highlighted by the rectangle in (**a**). Recovered leaves are sinks as shown by the diffusion of GFP throughout the leaf tissue; in ST3/ST4 transition leaves, GFP starts to remain within the phloem, thus indicating that these leaves undergo the sink-source transition. *, recovered ST4 leaves; +, partially symptomatic ST3/ST4 transition leaves. (**c**), Recovered leaf showing diffused GFP. (**d**) ST3/ST4 transition leaf showing diffused GFP in the leaf base (sink) and GFP remaining in the veins (source), thus indicating the sink-to-source transition. (**e**), Flattened ST2 leaf showing the typical source pattern with GFP retained in the veins.

Supplementary Table S1: Occurrence and timing of recovery in hormone pathway mutants

Timing	ATG number	Mutant	# plants[1]	Gene function
Early	AT1G54490	*ein5-1*	14/14	Ethylene signalling / RNA decay
		xrn4-3	21/22	
Normal	AT5G03280	*ein2-1*	4/4	Ethylene signaling
	AT3G20770	*ein3-1*	4/4	
	AT3G51770	*eto1-1*	4/4	
	AT3G52430	*pad4-1*	4/4	SA-defense signaling
	AT1G64280	*npr1-1*	5/7	
	-	*NahG*	3/8	
	AT4G33430	*bak1-4*	4/4	Innate immunity / brassinosteroid signaling
	AT1G30330	*arf6-1*	4/4	Auxin signaling
	AT5G37020	*arf8-2*	4/4	
	AT1G05180	*axr1-3*	4/4	
	AT3G62980	*tir1-10*	4/4	

[1] number of plants showing specific recovery phenotype / number of plants infected.

Supplementary Table S2: Table of nucleic acid qPCR primers and Northern blot hybridization probes

	Name	ATG number	Forward primer or probe	Reverse primer
qPCR	GAPDH	At1g13440	TTGGTGACAACAGGTCAAGCA	AAACTTGTCGCTCAATGCAATC
	EXP	At4g26410	GAGCTGAAGTGGCTTCCATGAC	GGTCCGACATACCCATGATCC
	18S	At3g41768	CGTCCCTGCCCTTTGTACAC	CGAACACTTCACCGGATCATT
	ORMV CP	-	CAAGCGGCAAGAGATACTGTTAGAC	GCTGGTTCGGTGTCACAATCG
	GFP 5	-	GCCCGACAACCACTACCTGAG	GGCGGCGGTCACGAACTC
Probe Fig S2c	ORMV_siRNA	-	AATTGGTGCTCGTTGATGGTGTTC	TCTACCGTCCTCACATTGTCCTTG
	GFP_siRNA	-	CACATGAAGCAGCACGACTT	TGCTCAGGTAGTGGTTGTCG
	miRNA398*	-	TGTTCACATGCCACTCCTTTG	
	miRNA173	-	GTGATTTCTCTCTGCAAGCGAA	
Probe Fig 1d	ORMV_subgen_as_1	-	TCTCCGGTCTATATCTATACTTATTACTATTTACATCCCT	
	ORMV_subgen_as_2	-	TTTTCTTCTTTATATTGTAACGAATCAGGACCGGCGTATC	
	ORMV_subgen_as_3	-	AAATACTGGTACTGATTCGAGCTCGTGATGTTGTAAACCA	
	ORMV_subgen_as_4	-	CTGGTTAAGCATCGCTGTGGGCTCTGCCCACATCGCTGCG	
	ORMV_subgen_as_5	-	CCGCTTGAGTTTGGTACGACTGCGACAACGCAGACACGCA	
	ORMV_subgen_as_6	-	CTCAGAAGGTTAGAGAACTGCTGTCTAACAGTATCTCTTG	
Probe Fig S12	siR1003	-	ATGCCAAGTTTGGCCTCACGGTCT	
	ta-siR255	-	TACGCTATGTTGGACTTAGAA	
	miR160	-	TGGCATACAGGGAGCCAGGCA	
	ORMV_1 s	-	GCACGCTCGAGACGCCCTAAGGTCCAT	
	ORMV_2 s	-	AGGCCGTACACTCCCTAGCGGGTGGTC	
	ORMV_3 s	-	CGCTGCGCACCTTTTCAAGGGACGCGA	

UNIVERSITE DE STRASBOURG
RESUME DE LA THESE DE DOCTORAT EN FRANCAIS

Discipline : Science du Vivant

Présentée par : Pitzalis Nicolas

Titre : Interactions plantes-virus : rôle des petits ARN non-codants dérivés du virus et de l'hôte au cours d'une infection et d'une maladie

Unité de recherche : UPR 2357, CNRS
Institut de Biologie Moléculaire des Plantes (IBMP)

Directeur de thèse : Dr. Manfred Heinlein, Directeur de recherche, IBMP-CNRS

L'objectif principal de cette thèse était d'acquérir de nouvelles connaissances sur les interactions plantes-virus en étudiant le rôle des petits ARN dérivés de virus et de l'hôte dans la régulation de l'expression génique lors de la propagation locale de l'infection virale dans les feuilles malades et guéries. Dans le cadre de ma thèse, j'ai également contribué à un article de synthèse sur les modèles actuels du mouvement des virus à travers les plasmodesmes (PD) (Pitzalis and Heinlein 2017).

Le rôle des petits ARN dérivés du virus et de l'hôte dans les interactions plantes-virus

Les événements cellulaires impliqués dans la réplication virale locale et le mouvement de cellule à cellule ont été intensément étudiés ces dernières années. Cependant, nous en savons encore très peu sur les interactions entre les plantes et les virus, qui jouent un rôle dans l'orchestration de ces processus au niveau de l'expression des gènes. Ainsi, comme décrit dans le chapitre II de cette thèse, différentes approches de séquençage profond (RNAseq, sRNAseq, PAREseq) ont été utilisées pour étudier les modifications induites par le virus dans le transcriptome de l'hôte, la régulation des gènes et du virus par de petits ARN (sRNA) codés par le virus et l'hôte. En utilisant une analyse bioinformatique des données de séquençage, l'accent a été mis sur l'identification des sRNA dérivés de l'hôte ou du virus qui ciblent les transcrits de l'ARN messager (mRNA) hôte ou l'ARN viral par clivage du complexe RISC (RNA-Induced Silencing Complex). Les travaux ont été appliqués chez le colza (*B. napus*) infecté par le TuMV, qui représente un pathosystème économique important. Pour obtenir des informations sur le processus de réplication et de propagation du virus en cours, nous avons utilisé une version du virus étiquetée GFP, ce qui nous a permis d'isoler des échantillons d'ARN des sites de propagation de l'infection dans les feuilles inoculées. Des données fiables et des conclusions ont été obtenues grâce à l'analyse d'échantillons provenant de trois expériences biologiques indépendantes. De plus, l'utilisation d'échantillons de deux cultivars différents

nous a permis d'interpréter les résultats en fonction de la sensibilité spécifique du cultivar face au virus. Fait important, les différentes approches NGS (RNAseq, sRNAseq, PAREseq) ont toujours été appliquées aux mêmes échantillons d'ARN individuels, de sorte que les différents niveaux d'analyse et les résultats respectifs pour un échantillon donné pouvaient être combinés, mutuellement corrélés et interprétés.

L'analyse du RNAseq à l'échelle du génome a révélé de nombreux gènes montrant des différences dans l'accumulation de leurs transcrits entre les échantillons contrôles traités par simulation et ceux traités par le virus. Parmi ceux-ci, de nombreux gènes induits par le virus étaient significativement positivement ou négativement régulés, soit chez les deux cultivars, soit de manière spécifique à un cultivar. Certains des transcrits différentiellement exprimés ont été prédit pour coder des protéines connues pour jouer des rôles importants dans la défense des agents pathogènes. Un exemple est la CALMODULIN-BINDING PROTEIN 60G (CB60G), induite chez les deux cultivars et connue pour agir en tant que régulateur immunitaire favorisant l'expression des gènes clés impliqués dans la biosynthèse de l'acide salicylique et régulant les méchanismes de "pathogen-associated molecular pattern (PAMP)-triggered immunity (PTI)", "effector-triggered immunity (ETI) et la "résistance systémique acquise" (SAR) (Sun et al. 2015). La susceptibilité virale chez le cultivar Drakkar a été corrélée, entre autres, à une forte induction de l'expression de la sous-unité alpha-2 du complexe coatomer COP I (Ahn et al. 2015), qui pourrait jouer un rôle dans la formation de vésicules de réplication et dans leur mouvement (Wei and Wang 2008) (voir chapitre I). Par ailleurs, le phénotype plus résistant du cultivar Tanto pourrait être corrélé, à l'induction spécifique de transcrits codant pour TARGET OF AVRB OPERATION1 (TAO1), une protéine similaire au récepteur TIR-NB-LRR (Eitas et al. 2008), cible activée lors d'une attaque pathogène. La validité générale de nos données mRNAseq a été confirmée en testant l'expression de plusieurs gènes par analyse RT-qPCR. L'ARN original analysé par NGS-mRNAseq a été comparé avec ceux de nouveaux échantillons provenant de quatre autres expériences d'infection indépendantes. Cette partie du travail a fourni des listes de gènes classés selon le degré d'induction ou de répression de la transcription dans les sites d'infection locale de TuMV-GFP. Deux cultivars différents présentant des susceptibilités virales différentes ont été analysés.

Pour révéler les mRNA qui pourraient être ciblés par les sRNAs dérivé de l'hôte ou du virus et induit par le virus, de petits fragments d'ARN (appelés "reads") ont d'abord été comptés et alignés sur le transcriptome du génome viral et celui de Tanto et Drakkar avant de réaliser les annotations. Comme découvert par des études antérieures (par exemple Tagami et al. 2007; Vogler et al. 2007, Hu et al. 2011), l'infection virale a provoqué des changements radicaux dans le profil de taille des sRNAs. Alors que les sRNAs des échantillons de Tanto et de Drakkar présentaient des profils identiques et typiques de sRNAs de 21 nt à 24 nt de long, les profils étaient fortement dominés par les ARN interférent (siRNA) de 21 nt et 22 nt dérivés du virus lors de l'infection (vsiRNA). Ces profils, ainsi que les profils de vsiRNAs alignés sur le génome du TuMV, étaient presque identiques entre les deux cultivars de *B. napus*, ce qui indique que

les différences de sensibilité au virus ne peuvent être expliquées par des différences évidentes dans le traitement (processing) des sRNAs. En mappant les sRNA dérivés de l'hôte sur les micro ARN (miRNA) des *Brassicacea* dans la base de données miRbase (Kozomara and Griffiths-Jones 2014), plusieurs petits fragments de sRNAs correspondaient à des miRNAs connus. De plus, en utilisant le logiciel Shortstack (Axtell, 2013), de nombreux miRNAs inconnus auparavant ont été identifiés.

Les données sur les sRNAs et les mRNAs ont finalement été combinées aux résultats de l'analyse PAREseq pour révéler les sRNAs alignés sur les extrémités 5' clivées des mRNAs et sont compatibles avec les conditions de jumelage RISC d'après le logiciel PAREsnip (Folkes et al. 2012). L'analyse a révélé des paires miRNAs:mRNA cibles déjà connues, telles que les miRNAs ciblant les mRNAs codant pour des protéines spécifiques de liaison au promoteur Squamosa (SPL), des facteurs de réponse aux auxines (ARF), des protéines Scarecrow-like (SCL), des facteurs de transcription sensibles à l'éthylène (ERF-RAP2-7, AP2), les protéines F-box de signalisation auxines (AFB2, AFB3) et les protéines Superoxyde dismutases (Llave et al. 2002; Rhoades et al. 2002; Allen et al. 2005; Wang et al. 2005a; Wang et al. 2005b, Kim et al. 2006; Gandikota et al. 2007; Vidal et al. 2010; Si Ammour et al. 2011; Yu et al. 2012; Lu et al. 2013; Ma et al. 2014; Jung et al. 2014; Xu et al. 2016), confirmant ainsi l'analyse PARE. De plus, ce travail a permis d'identifier de nouveaux candidats pour les paires de miRNA:mRNA, tels que miR1885b:BLOS2 ou miRC23a:COX19. L'activité de clivage de certaines paires miRNA:mRNA cibles, connues et prédites, a été confirmée par des tests 5'RACE (Rapid Amplification of cDNA Ends) spécifiques. Basé sur les résultats obtenus par le logiciel PAREsnip, ces expériences ont permis, en utilisant des échantillons biologiques indépendants, de confirmer certains sites de clivages, au sein de cibles mRNAs prédits.

L'un des objectifs importants était de déterminer si le virus infectieux pouvait utiliser, les siRNAs produits à partir de son génome, en tant qu'effecteurs d'ARN pour le ciblage par le complexe RISC des gènes de l'hôte. L'analyse a en effet révélé la présence de vsiRNAs dans les paires cibles vsiRNA:mRNA qui n'apparaissaient qu'après infection. Un vsiRNA prédominant a été trouvé dans les paires cibles vsiRNA:mRNA et implique des transcrits de gènes ERF également ciblés par miR172. Ce vsiRNA a été trouvé similaire à la séquence miR172 et de plus, est prédit être responsable du clivage exactement sur le même locus dans le transcrit cible. Cela suggère que les virus peuvent coder pour des vsiRNAs évolués pour imiter l'activité des miRNAs hôtes et, par conséquent, pour contrôler les gènes cibles spécifiques des miRNAs pendant l'infection.

La cartographie des sRNAs sur deux transcriptomes de cultivars différents et l'analyse de l'alignement avec le programme ShortStack (Axtell, 2013) ont conduit à l'identification de nombreux loci phasés (PHAS) qui produisent de petits ARN interférents secondaires (phasiRNA) en phase. Les phasiRNAs sont produits par la conversion d'un transcrit en ARN double brin (ARNdb) par des ARN polymérases dépendant de l'ARN (RDR6 ou RDR1). Ils sont traités ensuite de l'ARNdb en siRNAs phasés par DCL4 (Fei et al. 2013). Ceci est en faveur de l'hypothèse où la production de phasiRNAs représente un mécanisme permettant de réguler à la baisse le transcrit spécifique dont ces siRNAs sont issus et de produire des siRNAs capables

de cibler des séquences homologues en trans (Fei et al. 2013). Ainsi, à la différence des gènes TAS non-codants d'*Arabidopsis*, connus parmi les premiers loci permettant la production de siRNAs agissant en trans (tasiRNAs) (Vazquez et al. 2004), les loci PHAS se réfèrent à des gènes codants, dont font parties les gènes de la famille des LRR impliqués dans la défense contre des agents pathogènes, ainsi que les gènes des familles PPR et MYB, comme illustré chez *Arabidopsis thaliana*, *Medicago truncatula* et *Prunus persica* (Fei et al. 2013; Zhai et al. 2011). L'analyse des loci PHAS chez des plants de *B. napus* contrôles ou infectés par TuMV, a révélé que certains loci PHAS produisent des siRNAs phasiques seulement après l'infection. La production de siRNAs secondaires associés au virus (vasiRNA) à partir de gènes codants lors d'une infection virale, a été découverte chez Arabidopsis et nécessite RDR1 pour leurs synthèse et Argonaute (AGO) 2 pour le clivage de transcrits cibles (Cao et al. 2014). Ainsi, les loci induisant la production de siRNAs phasiques identifiés dans notre analyse, peuvent représenter des loci produisant des vasiRNAs. Cependant, comme la voie de synthèse des phasiRNAs dans *B. napus* n'est pas connu, il est préférable de les distinguer en tant que va-phasiRNAs et non vasiRNAs. Notre étude indique que l'infection virale chez le colza stimule la production de phasiRNAs sur de nombreux gènes codants qui sont liés à la défense (par exemple, homologue TAO1, AGO2, NBR1). Parmi ces gènes, nous avons trouvé des membres de trois petites familles de gènes (codant pour la protéine Chlorophyll a-b binding protein 1, NBR1 homolog, et TAR1) qui produisent des va-phasiRNAs associés au clivage de leurs propres transcrits ou de transcrits de gènes homologues. Cela suggère que le processus de production de va-phasiRNA pourrait représenter un mécanisme pour atténuer les effets de l'infection sur l'homéostasie transcriptionnelle. Il est intéressant de noter que les membres de la famille NBR1 et TAR1 produisent également des va-phasiRNAs avec le potentiel de cibler les transcrits d'autres gènes. Les données suggèrent que particulièrement NBR1 peut organiser des centres inductibles ("hub") par le virus pour la synthèse de siRNAs et le ciblage induit du virus par tout un réseau d'autres gènes.

Les résultats de l'analyse PAREsnip indiquent que le génome viral peut également être clivé par des siRNAs dérivés du virus et de l'hôte (vsiRNA, hsRNA). La grande majorité des événements de clivage était associée à des hsRNAs uniques, dérivés de gènes annotés comme étant des gènes de résistance aux maladies (TAO1 et RPP5), tous deux codant pour des protéines de type récepteur TIR-NB-LRR. Le clivage de l'ARN viral (vRNA) par le biais des vsiRNAs ou hsRNAs peut contribuer à la sensibilité spécifique du cultivar pour le virus, car certains sites de clivage sont prédits de manière spécifique à un cultivar. Il est intéressant de noter que certaines des paires cibles d'hsRNA:vRNA incluent des va-phasiRNAs actifs en trans et sont dérivés des gènes NBR1 et TAR1. Ce résultat pourrait corroborer l'hypothèse de l'évolution des gènes NBR1 en tant qu'hub induit par le virus induisant la production de siRNAs secondaires. Celui-ci pourrait avoir évolué, à condition, que les va-phasiRNAs dérivés du même hub soient capables de contrôler à leur tour le virus. Il est également intéressant de noter que les gènes NBR1 de *B. napus* sont hautement homologues du gène codant pour la protéine AT4G24690/NBR1 de l'autophagie chez *Arabidopsis* (identité de 81 à 84%), impliquée

dans les défenses antivirales impliquant la dégradation des protéines et des particules virales par autophagie (Hafren et al. 2017; Hafren and Hofius 2017). Il a été montré que cette protéine supprime l'infection du TuMV chez *Arabidopsis* en ciblant le VSR du virus (HcPro) (Hafren et al. 2018). Ainsi, en induisant la conversion de transcrit NBR1 en siRNAs secondaires, le virus peut avoir eu la possibilité d'obtenir un contrôle généralisé de l'expression du gène hôte, en supprimant les taux de transcrit NBR1 et en contrôlant les fonctions antivirales de la protéine NBR1.

En conclusion, cette étude a impliqué une analyse NGS et des expériences *in vivo* réalisées sur *B. napus*, la culture d'oléagineux la plus largement produite dans l'Union Européenne. Les résultats mettent en évidence des gènes exprimés différentiellement et des sRNAs dérivés du virus ou de l'hôte en corrélation avec les extrémités 5' des mRNAs clivés, indiquant leur rôle dans le clivage par RISC. Collectivement, les données suggèrent que *B. napus* utilise des siRNAs endogènes dérivés de gènes de résistance, pour cibler le virus, alors que le virus, à son tour, utilise ses propres siRNAs pour cibler l'hôte. De plus, en induisant la production de siRNAs secondaires à partir de gènes codants, le virus semble avoir la possibilité de cibler d'autres gènes. Les gènes sensibles au virus, et en particulier les gènes prédits comme cibles des siRNAs ou des va-phasiRNAs, peuvent avoir un rôle important dans l'infection virale chez *B. napus* et pourraient représenter d'importants nouveaux loci, candidats pour l'amélioration des cultures. Cependant, il est important de noter que les paires cibles de sRNA:RNA identifiées sont prédites et que des expériences supplémentaires sont nécessaires pour démontrer si ces paires de cibles sont effectivement fonctionnelles dans le clivage de l'ARN par RISC. Une approche pour obtenir des preuves à l'appui de cette hypothèse pourrait être d'utiliser l'immunoprécipitation de la protéine AGO pour déterminer si des sRNAs candidats, sont effectivement présents dans les complexes AGO-RISC. Le clivage par RISC d'une cible de mRNA est généralement éprouvé par l'utilisation d'une construction test et d'une construction témoin d'une séquence cible mutée dans laquelle la séquence mRNA cible de siRNA, est fusionnée à un rapporteur, par exemple le transcrit GFP. La fluorescence, réduite s'il y a clivage de l'ARN rapporteur, sera comparée entre les tissus infectés et les tissus témoins. Cependant, cette approche peut nécessiter la production de plantes transgéniques, étant donné que *B. napus* ne convient pas aux tests d'expression transitoire basés sur l'agroinfiltration. Comme les génomes d'ADN de Drakkar et Tanto ont été séquencés dans le cadre de ce projet, il pourrait être possible d'identifier des polymorphismes nucléotidiques (Single Nucleotide Polymorphisms, SNPs) spécifiques à des cultivars, qui correspondent aux paires cibles sRNA:mRNA, eux même présent dans un seul cultivar, et utiliser ces SNPs dans des croisements génétiques afin de corréler les SNPs spécifiques au clivage de transcrit par des expériences 5'RACE d'un gène. Le rôle des gènes au cours de l'infection virale doit être testé à l'aide de mutants spécifiques de ces gènes. Cependant, étant donné que *B. napus* est une espèce allotétraploïde avec un génome fortement amplifié (Chalhoub et al. 2014), il est presque impossible de créer des mutants récessifs dans lesquels une fonction donnée est abolie. L'analyse fonctionnelle des gènes dépend plutôt d'approches dominantes telles que

l'ARN interférence (RNAi) ou le CRISPR/CAS9, qui peuvent affecter l'expression de tous les membres d'une famille de gènes donnée.
Néanmoins, les résultats obtenus dans cette étude ont révélé un réseau complexe d'interactions potentielles médiées par les sRNAs entre *B. napus* et le virus et ont permis d'identifier de nouvelles cibles génétiques importantes pour l'amélioration des cultures.

Processus conduisant à la guérison des symptômes viraux et favorisant la santé des plantes
Les virus sont des parasites intracellulaires obligatoires et la plupart des études sur les virus se sont concentrés sur la symptomatologie des maladies virales. Cependant, l'infection virale ne déclenche pas toujours des maladies. Bien que des études sur la diversité virale aient démontré la présence de virus dans des milliers de plantes, souvent aucun symptôme de maladie pouvant être corrélé à la présence du virus n'a été observé, même si les plantes contenaient des virus liés à d'importants agents pathogènes (Roossinck 2012; Roossinck and Bazán 2017). Roossinck and García-Arenal 2015). Ainsi, la plupart des plantes à l'état sauvage, semblent tolérer les virus et la pathologie de l'infection virale peut être considérée comme une exception plutôt que comme une règle. Étant donné que les virus produisent des maladies et des pertes de rendement importantes dans les cultures, il est nécessaire de comprendre les processus par lesquels les plantes peuvent promouvoir leur santé en présence de virus. Pour obtenir une telle information, le phénomène d'"auto-guérison des symptômes", donc la capacité des plantes à se remettre de la maladie, a été étudié. En utilisant l'infection par ORMV chez *Arabidopsis* comme modèle, il a été constaté que la guérison se produisait en présence de virus répliquant, indiquant ainsi que les feuilles guéries avaient acquis un état de tolérance. Par une analyse plus poussée, nous avons montré que les symptômes de la maladie étaient corrélés à l'activité du suppresseur de silencing (VSR) et que la plante était capable de maîtriser cette activité. En examinant les mutants d'*Arabidopsis* affectés dans diverses voies liées à la défense et aux hormones, nous avons constaté que le mécanisme sous-jacent impliquait des gènes de voie de RNA silencing post-transcriptionnel (PTGS) nécessaires à la synthèse de siRNAs primaires et secondaires ainsi que des gènes de signalisation du RNA silencing. De plus, les mutants de gènes requis pour la production de siRNAs primaires et secondaires ont également montré une guérison plus rapide. Avec la découverte supplémentaire que la guérison était limitée aux tissus de destination (tissus "puits", les parties des feuilles importatrices de sucres), cela nous a conduit au modèle selon lequel la guérison se produit lors du transport des siRNAs dérivés du virus (vsiRNA) depuis leur source de production jusqu'à leurs tissus puits, et que les vsiRNAs qui s'accumulent dans ces tissus son responsables de la saturation et de l'inactivation du VSR responsable de la maladie.
Globalement, cette étude démontre que les plantes peuvent utiliser le RNA silencing couplé à une communication intercellulaire et à la régulation systémique pour prendre le contrôle de l'activité VSR dans les jeunes tissus éloignés du site d'infection pour contrôler (surmonter) la maladie établie. Cette conclusion implique que la santé des plantes peut être favorisée par la force d'importation des tissus puits et par le contrôle de l'activité des gènes qui agissent contre la production efficace de vsiRNAs (par exemple EIN5/XRN4). Les résultats sont

cohérents avec les rapports précédents indiquant l'importance du RNA silencing et d'un VSR "faible" dans la guérison des symptômes. Cependant, contrairement à ces rapports antérieurs, nos résultats plaident contre une exigence d'inhibition ou de suppression virale comme condition préalable à la guérison ; nous montrons plutôt que le virus lui-même n'est pas affecté pendant ce processus. Ainsi, l'auto-guérison des symptômes ne dépend pas de la "destruction" de l'agent pathogène mais plutôt de la capacité des plantes infectées à "gérer" correctement le virus. Cette capacité des plantes à rester en bonne santé malgré l'omniprésence du virus dans l'environnement, devrait en effet être attendue de par une coévolution virus-hôtes. Pour soutenir la propagation, un virus ne devrait pas tuer son hôte mais plutôt promouvoir son développement (sa santé). L'apparition de maladies virales graves chez les plantes cultivées peut être le résultat d'une surexploitation des croisements qui peut avoir entraîné la perte d'importants mécanismes mis en place au cours de la coévolution.

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Plant-virus interactions: role of virus- and host-derived small non-coding RNAs during infection and disease

Abstract: Virus infection in plants depends on the ability of viruses to replicate and spread their genomes between cells through plasmodesmata, and to overcome host antiviral defense responses, such as RNA silencing. RNA silencing relies on 21-24 nt long small RNAs (sRNAs) that are processed from double-stranded RNA (dsRNA) precursor molecules by Dicer-like (DCL) enzymes and guide Argonaute (AGO)-containing RNA-induced Silencing complexes (RISC) to homologous RNA targets (viral RNA or host RNA) for sequence-specific cleavage or translational repression. Antiviral RNA silencing is triggered by viral dsRNA produced during replication of the viral genome. The viral dsRNA is processed by DCL4 and DCL2 into virus-derived siRNAs (vsiRNAs). However, the functions of vsiRNAs and of the Virus-encoded Suppressor of RNA silencing (VSR) in plant-virus interactions is not well understood. In this thesis, I investigated the role of host- and virus-derived sRNAs during infection of Rapeseed (*Brassica napus*, Canola) by the UK1 strain of *Turnip mosaic virus* (TuMV-UK1). By using a TuMV derivative tagged with a gene encoding green fluorescent protein (TuMV-GFP), two rapeseed cultivars ('Drakkar' and 'Tanto') that differ in susceptibility to this virus were identified. Transcriptional profiling of local infection foci in Drakkar and Tanto leaves by next generation sequencing (NGS) revealed numerous differentially expressed genes. The same RNA samples from mock- and virus- treated Drakkar and Tanto leaves were also used for the global NGS profiling of sRNAs (sRNAseq) and their potential RNA targets (PAREseq). The bioinformatic analysis and their *in vivo* validation led to the identification of transcript cleavage events involving known and yet unknown miRNAs. Importantly, the results indicate that TuMV hijacks the host RNA silencing pathway with siRNAs derived from its own genome (vsiRNAs) to target host genes. The virus also triggers the widespread targeting of host messenger RNAs (mRNAs) through activation of phased, secondary siRNA production from PHAS loci. In turn, both vsiRNAs and host-derived siRNAs (hsRNAs) target and cleave the viral RNA by the RISC-mediated pathway. These observations illuminate the role of host and virus-derived sRNAs in the coordination of virus infection.
Another chapter of this thesis is dedicated to the analysis of virus-induced diseases by using Arabidopsis plants infected with the *Oilseed rape mosaic tobamovirus* (ORMV) as a model. Initially, the infected plants develop leaves with strong disease symptoms. However, at a later stage, disease-free, "recovered" leaves start to appear. Analysis of symptoms recovery led to the identification of a mechanism in which the VSR and virus derived-siRNAs play a central role. I used Arabidopsis mutants impaired in transcriptional and post-transcriptional silencing pathways (TGS and PTGS respectively) and a plant line carrying a promoter-driven GFP transgene silenced by PTGS (Arabidopsis line 8z2). Using various techniques able to monitor virus infection, small and long viral RNA molecules, VSR activity, as well as phloem-mediated transport with in these lines, this study led to the identification of genes required for disease symptoms and disease symptom recovery. Moreover, the observations allowed to propose a model in which symptoms recovery occurs upon robust delivery of antiviral secondary vsiRNAs from source to sink tissues, and establishment of a vsiRNA dosage able to block the VSR activity involved in the formation of disease symptoms.

Résumé : L'infection virale chez les plantes dépend de la capacité des virus à se répliquer, à diffuser leur génome à travers les cellules par le biais de plasmodesmes et à surmonter les réponses de défense antivirale de l'hôte, telles que le RNA silencing. Le RNA silencing repose sur des petits ARN (sRNA) de 21-24 nt créés à partir de molécules précurseurs d'ARN double brin (ARNdb) par des enzymes de type Dicer (DCL). En s'associant aux protéines Argonautes (AGO), faisant partie des complexes induisant le RNA silencing (RISC), ils sont guidés vers des cibles à ARN homologues (ARN viral ou hôte) pour induire soit leur clivage de manière séquence-spécifique, soit leur répression traductionnelle. Le RNA silencing antiviral est déclenché par les ARNdb viraux produits lors de la réplication du génome viral. L'ARNdb viral est traité par DCL4 et DCL2 en sRNA interférent (siRNA) dérivés du virus (vsiRNA). Cependant, les fonctions des vsiRNAs et du suppresseur de RNA silencing (VSR) codé par le virus, dans un contexte d'interactions plantes-virus, ne sont pas bien comprises. Dans cette thèse, j'ai étudié le rôle des sRNAs dérivés de l'hôte et du virus lors de l'infection du colza (*Brassica napus*, Canola) par la souche UK1 du virus de la mosaïque du navet (TuMV-UK1). En utilisant un dérivé de TuMV fusionné avec un gène codant pour la protéine fluorescente verte (TuMV-GFP), deux cultivars de colza ('Drakkar' et 'Tanto') qui diffèrent par leur susceptibilité à ce virus ont été identifiés. Le profil transcriptionnel des foyers d'infection locale, dans les feuilles de Drakkar et de Tanto, par séquençage nouvelle génération (NGS) a révélé de nombreux gènes exprimés de manière différentielle. Les mêmes échantillons d'ARN provenant de feuilles de Drakkar et de Tanto, traitées par des virus ou utilisées en contrôle, ont également servi à établir le profil NGS des sRNAs (sRNAseq) et de leurs cibles potentielles d'ARN (PAREseq). Les analyses bioinformatiques et leur validation *in vivo*, ont permis d'identifier les événements de clivage de transcrits impliquant des micro ARN (miRNA) connus et encore inconnus. Fait important, les résultats indiquent que TuMV détourne la voie du RNA silencing de l'hôte avec des siRNAs issus de son propre génome (vsiRNA) pour cibler les gènes de l'hôtes. Le virus déclenche également le ciblage à grande échelle des ARN messagers (ARNm) de l'hôte par l'activation de la production de siRNAs secondaires en phase, à partir de locus PHAS. À leur tour, les vsiRNAs et les siRNAs dérivés de l'hôte (hsRNAs) ciblent et clivent l'ARN viral par le complexe RISC. Ces observations éclairent le rôle des siRNAs dérivés de l'hôte et du virus dans la coordination de l'infection virale.
Un autre chapitre de cette thèse est consacré à l'analyse des maladies induites par des virus en utilisant comme modèle de plante Arabidopsis, infectée par un *tobamovirus*, le virus de la mosaïque du colza (ORMV). Initialement, les plantes infectées développent des feuilles présentant de forts symptômes de maladie. Cependant, à un stade ultérieur, des feuilles "guéries" et saines, commencent à apparaître. L'analyse de cette guérison des symptômes a permis d'identifier un mécanisme dans lequel, le VSR et les vsiRNAs, jouent un rôle central. J'ai utilisé des mutants d'Arabidopsis altérés dans les voies de silencing transcriptionnelle (TGS) et post-transcriptionnelle (PTGS) et une lignée végétale exprimant un transgène GFP sous contrôle d'un promoteur affaibli par PTGS (lignée Arabidopsis 8z2). Par diverses techniques d'analyse de l'infection virale, des petites et longues molécules d'ARN viral, de l'activité VSR, ainsi que du transport phloémien dans ces lignées, j'ai pu identifier des gènes nécessaires à l'apparition des symptômes de la maladie et du phénotype de guérison des symptômes. De plus, ces observations ont permis de proposer un modèle dans lequel cette guérison dépend d'un adressage important de vsiRNAs secondaires antiviraux depuis leur source de production jusqu'à leurs tissus de destination, et l'établissement d'un apport en vsiRNAs capable de bloquer l'activité VSR impliquée dans la formation des feuilles symptomatiques.