multiple
reflect
infection
tissue
mediated
data
clusters
suggesting
example
terms
cinerea
generate
role
al
shown
defence
used
and/or
plant
mutants
processes
TGA3
identified
GO
series
time
process
up-regulated
GP2S
reduced
response
models
highlight
points
genome
generated
mm
lesion
ability
spatial
ET
majority
genes
experimentally
changes
Fig
SA
protein
profiling
autophagy
activation
also
test
may
several
early
help
biosynthetic
family
suggests
single
different
cluster
downstream
negative
important
pathogens
expression
resolve
Although
hormone
motif
interaction
types
modelling
conditions
cell
around
novel
hormones
Arabidopsis
ABA
direct
overrepresented
differentially
known
ANAC055
regulation
whole
JA
false
syringae
well
static
responses
period
necrotrophic
profiles
plants
due
roles
high-resolution
PAL
et
core
components
TF
function
two
one
leaf
down-regulated
NPR1
growth
likely
host
highlighted
TFs
specific
timing
differences
synthesis
hpi
levels
involved
leaves
key
biological
many
hypothesis
analysis
network
interactions
hence
clear
transcriptional
pathogen
signalling
TGA
compared
gene
susceptibility
expressed
regulatory
rate
leads
increased
number
clock
small