

**Supplemental Figure legends:**

**Figure S1 Biotrophic growth of *Pestalotiopsis fici* in a tea branch.** A–C, longitudinal sections of a tea branch 21 days after inoculation with *P. fici* hyphae; A, fluorescent micrograph of tea and hyphae; B, brightfield micrograph of A; C, overlay of fluorescent and brightfield micrographs; D–F, cross sections of a tea branch 21 days after inoculation with *P. fici* hyphae; D, tea branch and hyphae; E, brightfield micrograph of D; F, overlay of fluorescent and brightfield micrographs. Scale bar = 100  $\mu\text{m}$ .

**Figure S2 Evidence for gene prediction accuracy in *Pestalotiopsis fici*.** Three types of evidences were combined: (i) Functional annotation (at least one domain/motif), (ii) Orthologous genes between *P. fici* and selected fungi, (iii) Solexa RNA-sequence support.

**Figure S3 Fold changes in di-nucleotide abundances for all repeat families of *Pestalotiopsis fici* compared to the nonrepetitive control sequence on a Log<sub>10</sub> scale.**

**Figure S4 Gene count per OrthoMCL family for each species.** Genes were clustered into families using OrthoMCL software. The x-axis bins indicate the number of genes per family, while the counts of y-axis indicate the total number of genes in each bin per species.

**Figure S5 Hierarchical clustering of the top 105 Z-scores for *Pestalotiopsis fici* gene family sizes.** The Z-scores scale indicates that the gene family size is smaller (blue) or the larger (red). So, the red blocks reflect gene family expansions. The gene families were constructed by OrthoMCL. Left: Gene family size in different sizes. Right: Gene family description (Pfam families); function annotation (FunCat).

**Figure S6 Biclustering of glycoside hydrolase gene families and polysaccharide lyase gene families in *Pestalotiopsis fici* and other selected fungi.** In the top tree, the fungi are

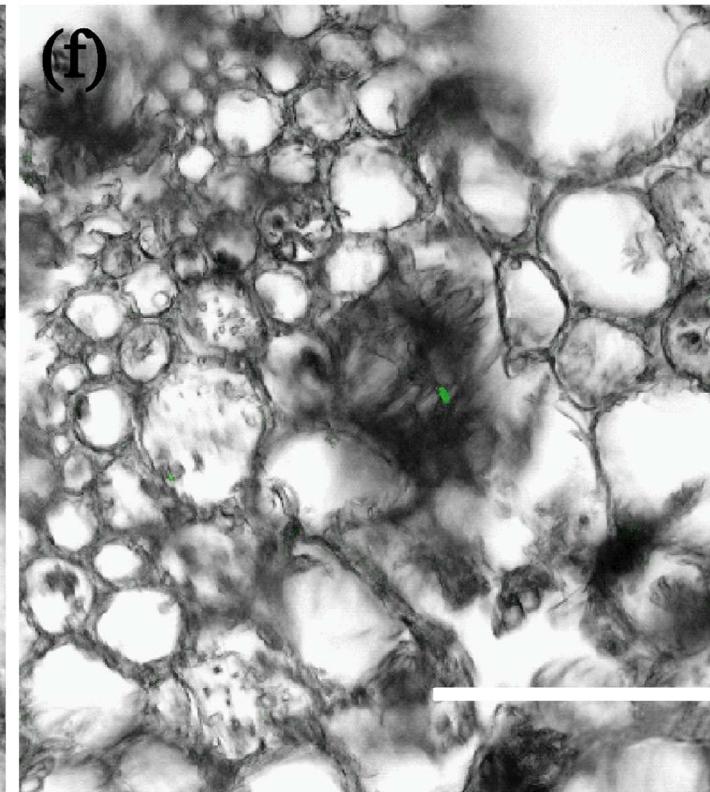
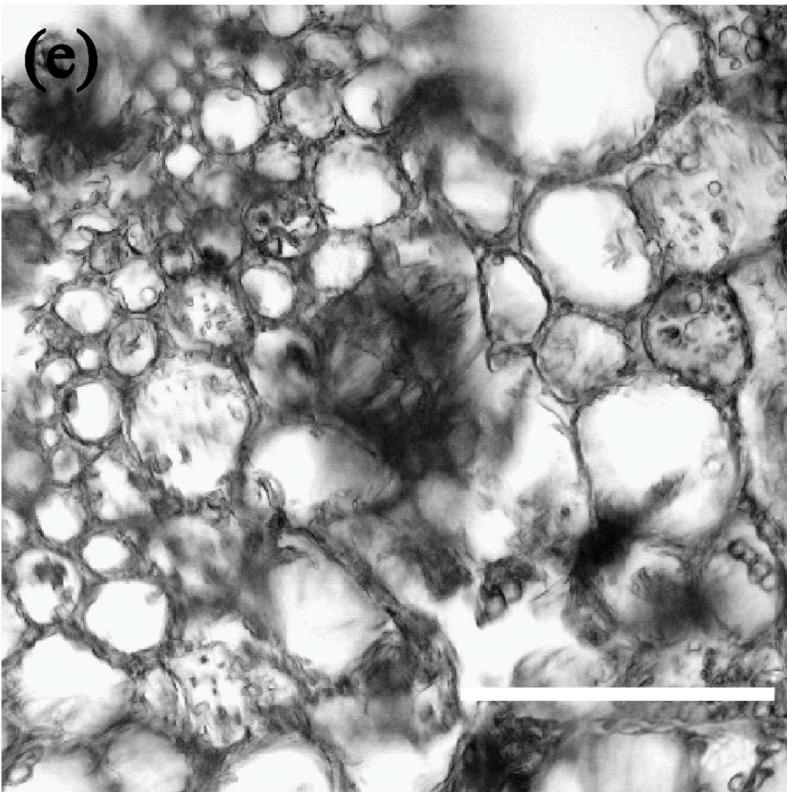
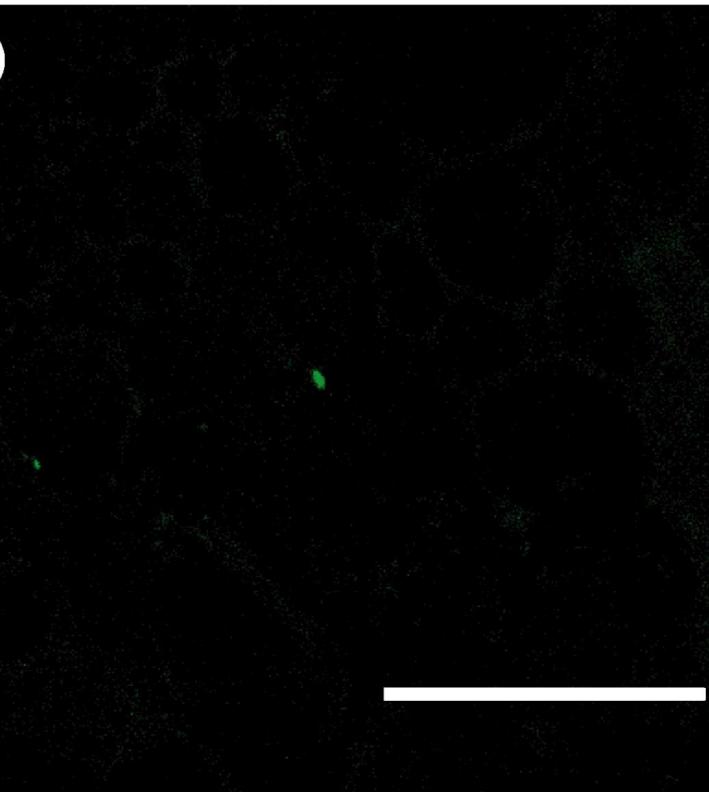
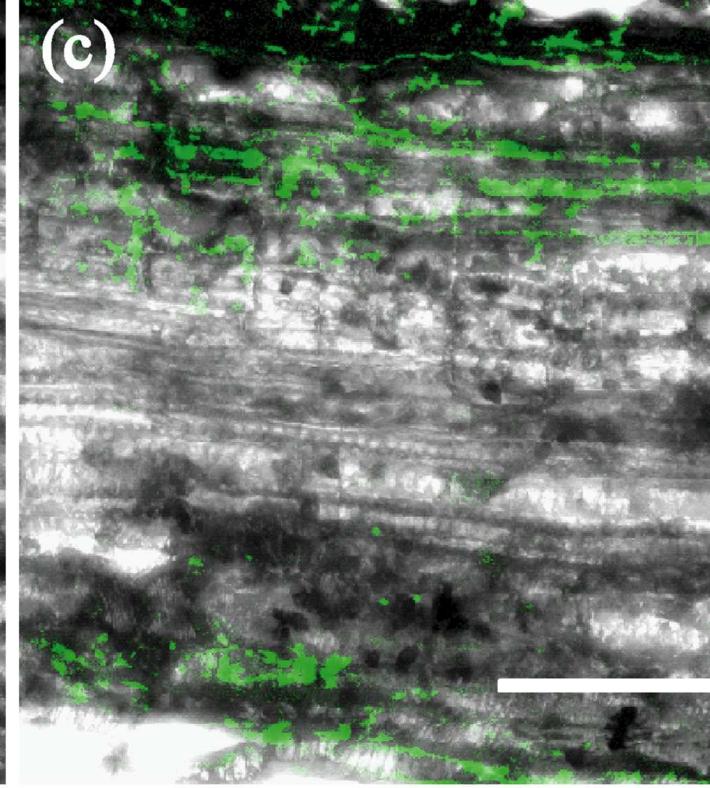
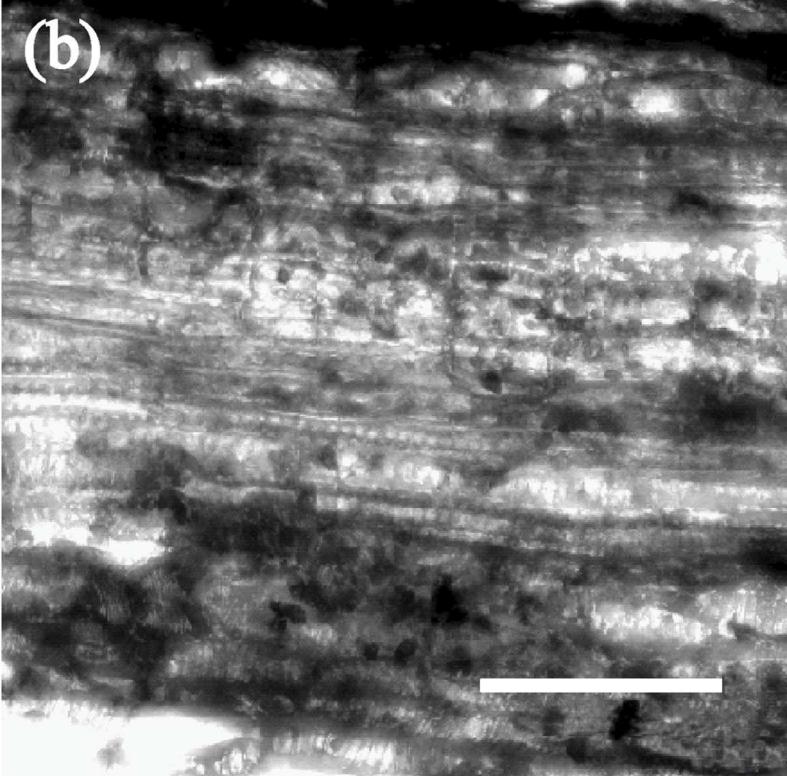
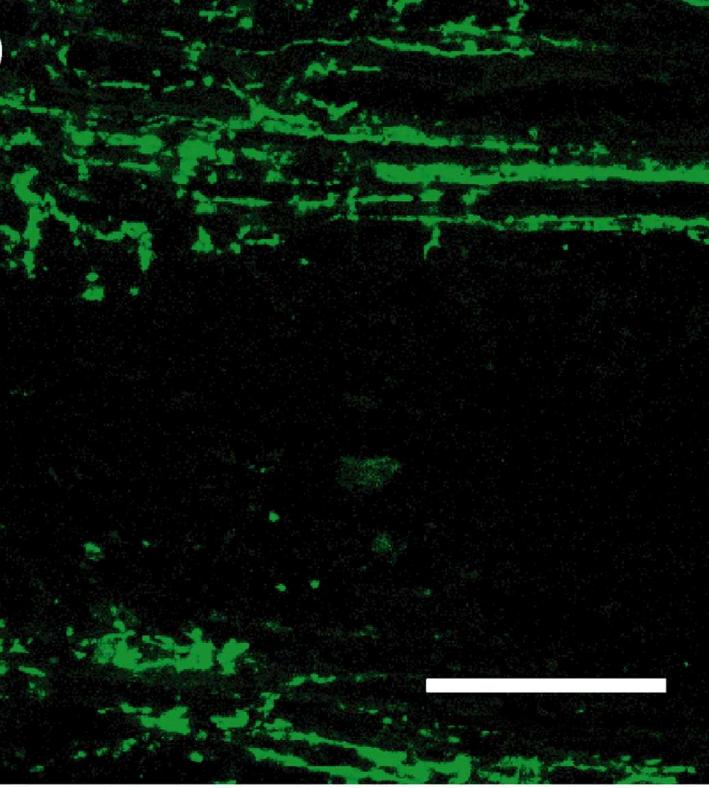
abbreviated as follows: *Pestalotiopsis fici* (PF), *Verticillium albo-atrum* (VA), *Magnaporthe oryzae* (MO), *Epichloë festucae* (EF), *Fusarium graminearum* (FG), *Glomerella graminicola* (GG), *Sclerotinia sclerotiorum* (SS), *Neurospora crassa* (NC), *Tuber melanosporum* (TM), *Ascocoryne sarcoides* (AS), *Piriformospora indica* (PI), *Saccharomyces cerevisiae* (SC), *Laccaria bicolor* (LB) and *Trichoderma reesei* (TR). The left tree shows the class number of the enzyme families according to the carbohydrate-active enzyme database. The values in the matrix indicate the number of gene encoding enzymes detected for each combination of enzyme family and fungus. A color scale from white (0 occurrences) to red (42 occurrences) indicates the abundance of the different enzymes per species.

**Figure S7 Phylogenetic tree of polyketide synthases (PKS) inferred by maximum likelihood analysis of the KS domain and the domain architecture of PKS proteins.** The accession numbers of the bacterial PKS genes (Bact) and the fatty acid synthase genes from animals (Fas) obtained from GenBank are shown in Table S9. Scale bar represents the number of substitutions per site. The KS number is indicated by protein IDs, as follows: PFICI: *Pestalotiopsis fici*, VDBG, *Verticillium albo-atrum*; MGG, *Magnaporthe oryzae*; EFQ, *Epichloë festucae*; FGSG, *Fusarium graminearum*; GSTUM, *Glomerella graminicola*; NCU, *Neurospora crassa*; sarcoides, *Ascocoryne sarcoides* and Trire2, *Trichoderma reesei*. The domain architecture of the proteins is shown on the right. Protein domain names are as follows: KS, ketoacyl synthase; AT, acyltransferase domain; ACP, acyl carrier domain; KR, ketoreductase; DH, dehydratase; ER, enoyl reductase; TD, terminal domain; TE, thioesterase; ME, methyl transferase and PP, 4'-phosphopantetheinyl transferase; C, condensation domain; AMP, adenylation domain; PCP, peptidyl carrier protein. Support values below 40% are not

shown.

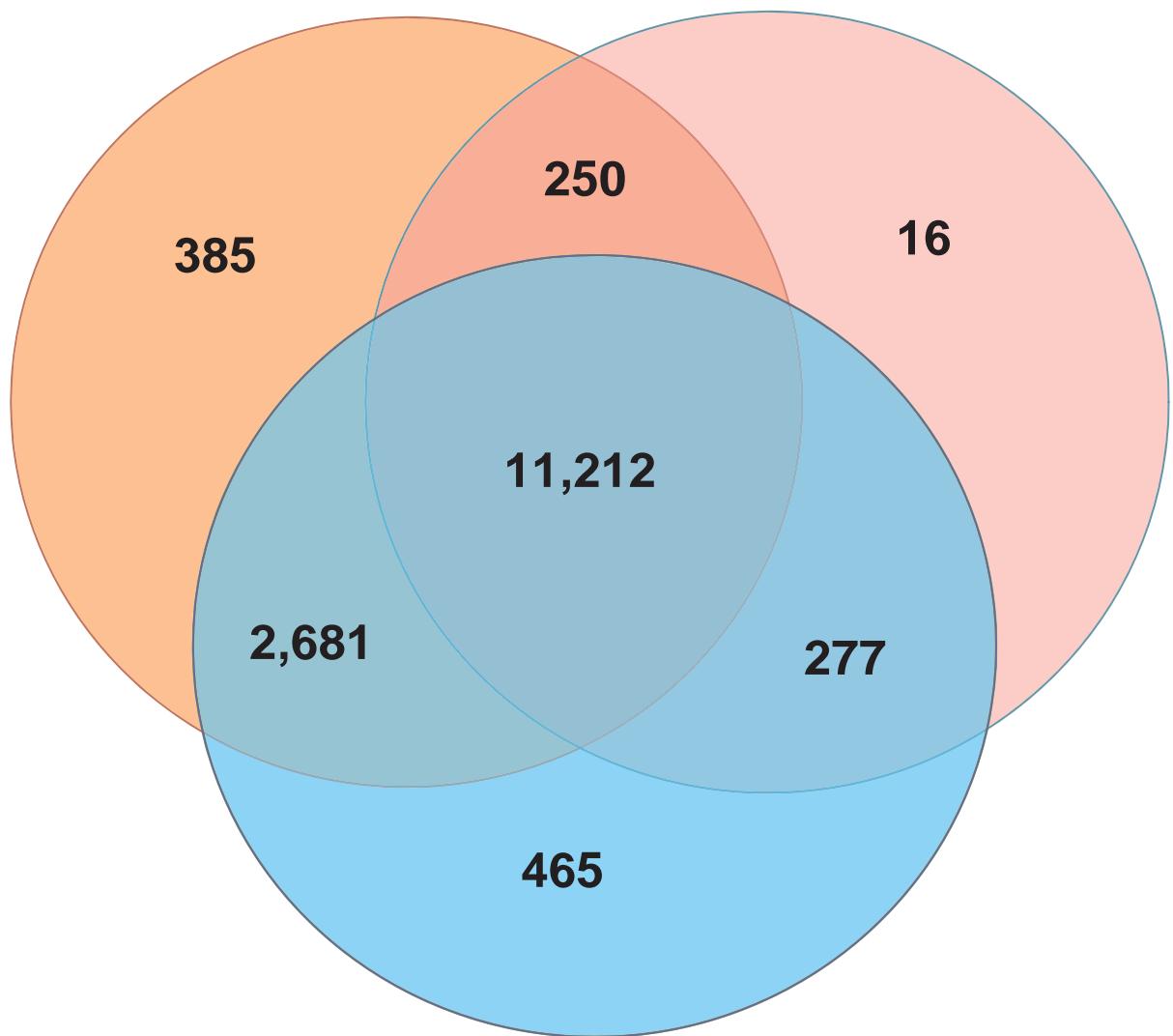
**Figure S8 Pestalotiopsis fici-specific expansion of genes that may encode Diels-Alderase.**

The fungi names are *Pestalotiopsis fici* (PFICI), *Verticillium albo-atrum* (VDBG), *Magnaporthe oryzae* (MGG, black color), *Epichloë festucae* (EFQ), *Fusarium graminearum* (FGSG), *Glomerella graminicola* (GSTUM).

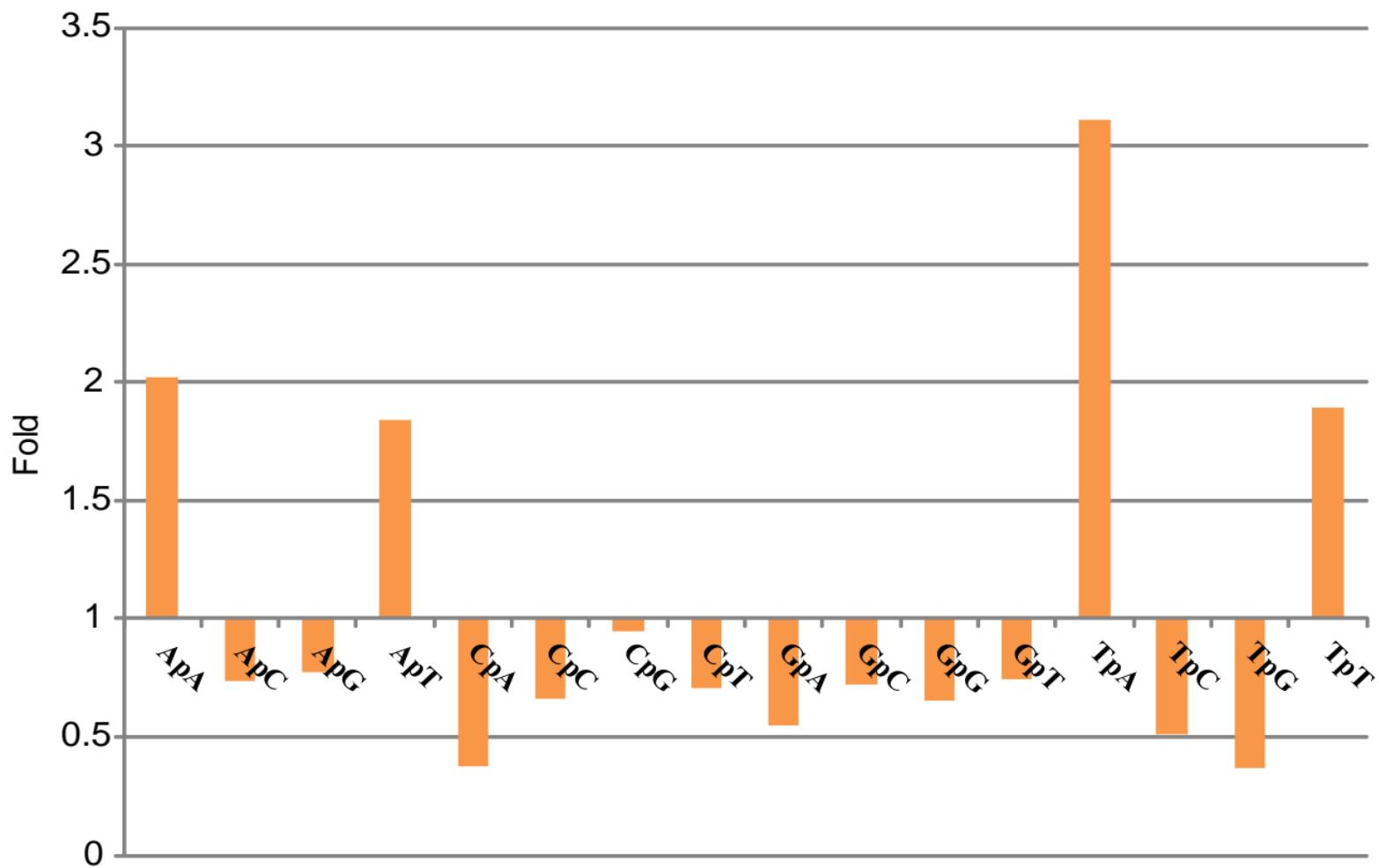


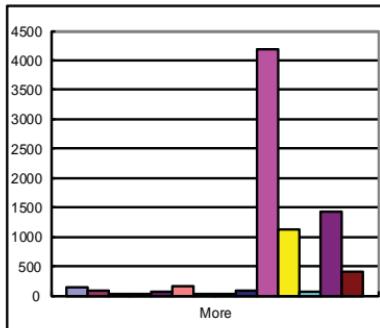
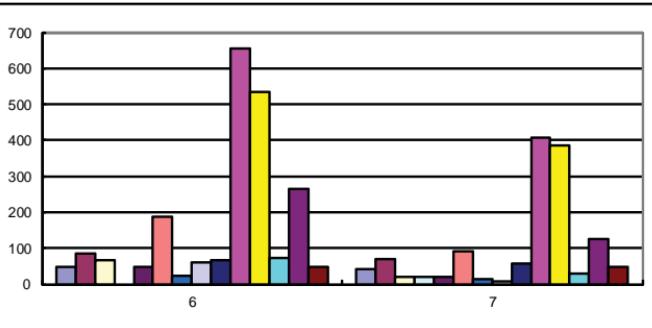
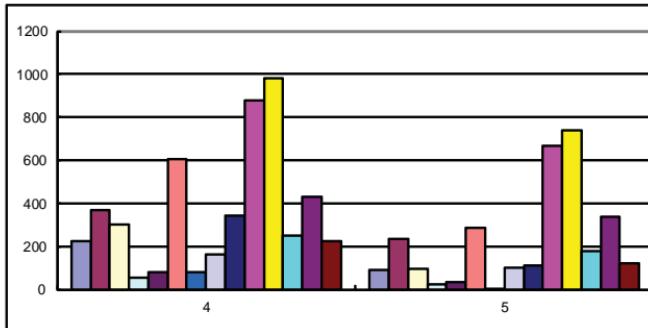
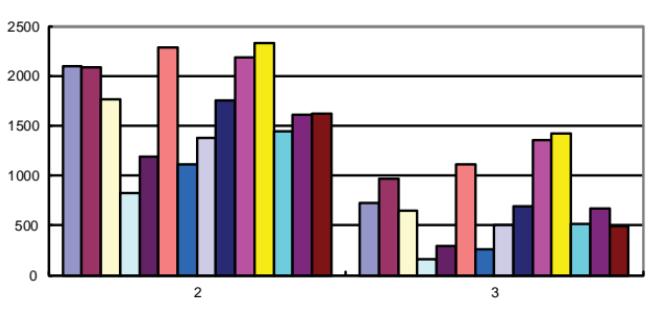
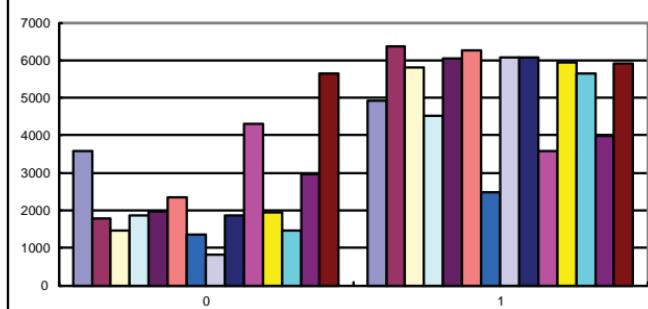
**Functional evidence**  
**(14,528 genes)**  
**(94%)**

**Orthology evidence**  
**(11,755 genes)**  
**(76%)**



**RNA-seq evidence**  
**(14,635 genes)**  
**(95%)**





- E. festucae*
- G. graminicola*
- V. albo-atrum*
- T. melanosporum*
- N. crassa*
- F. graminearum*
- S. cerevisiae*
- T. reesei*
- M. oryzae*
- L. bicolor*
- P. fici*
- A. sarcoides*
- P. indica*
- S. sclerotiorum*

A. sativus  
E. fetida  
P. gracilis  
O. granulosum  
L. bicolor  
M. oryzae  
N. crassa  
P. fiji  
P. indica  
S. cerevisiae  
S. pombe  
T. zuluensis  
T. reesei  
V. fibrosis

Dynamitin, GTPase domain	defense related proteins
hypothetical protein	
hypothetical protein	
Amidohydrolase 1	
Luciferase-like	
Major facilitator superfamily	
NACHT	
ATPase, AAA-type, core	
Ankyrin repeat	
Monoxygenase, FAD-binding	aerobic aromatic catabolism
SMP-30/Gluconolactonase/LRE-like region	
Cytochrome P450	detoxification involving cytochrome P450
regulation of amino acid metabolism	regulation of amino acid metabolism
Glutamine amidotransferase type I	nucleobase metabolism
GLEYA adhesin domain	
hypothetical protein	
Short-chain dehydrogenase	
Protein of unknown function	
Major facilitator superfamily	
Ankyrin repeat	
NACHT	
Hebesce	
Tetratricopeptide TPR-4	transcriptional control
Heterokaryon incompatibility	
Cytochrome P450	pheromone response, mating-type determination, sex-specific proteins
hypothetical protein	sesquiterpenes metabolism
Short-chain dehydrogenase	
Heterokaryon incompatibility	
Aldehyde-lyase domain	C-compound and carbohydrate metabolism
hypothetical protein	pheromone response, mating-type determination, sex-specific proteins
NmrA-like	biosynthesis metabolism of secondary products derived from L-phenylalanine
Alcohol dehydrogenase GroES-like	biosynthesis metabolism of phenylpropanoids
Major facilitator superfamily	
Oxoglutarate/iron-dependent oxygenase	drug/town transport
NADH:quinon oxidoreductase	
Major facilitator superfamily	
Methyltransferase type II	energy conversion and regeneration
Heterokaryon incompatibility	allantoin and allatoate transport
hypothetical protein	
Tyrosinase	
Intradiol ring-cleavage dioxygenase	biosynthesis metabolism of melanins
Cytochrome P450	
Intradiol ring-cleavage dioxygenase	detoxification involving cytochrome P450
Cytochrome P450	
ATPase, AAA-type, core	
hypothetical protein	
Alpha/beta hydrolase fold-3	
Heterokaryon incompatibility	
Flavin-containing monooxygenase-like	
Multicopper oxidase	
Short-chain dehydrogenase	
Chloroperoxidase	
Sulfatase	
hypothetical protein	
Monoxygenase, FAD-binding	
Tannase/feruloyl esterase	
FAD dependent oxidoreductase	
hypothetical protein	
Peptidase S15	
Cytochrome P450	
hypothetical protein	
Extracellular membrane protein, CFEM domain	
Protein of unknown function	
Phytanoyl-CoA dioxygenase	
Cytochrome P450	
Class II aldolase	
Pectate lyase	
Tannase/feruloyl esterase	
hypothetical protein	
Glucose-methanol-choline oxidoreductase	
Beta-lactamase-like	
NACHT	
Carboxylesterase, type B	
Transcription factor, fungi	
Major facilitator superfamily	
Short-chain dehydrogenase	
hypothetical protein	
O-methyltransferase, family 2	
Cytochrome P450	
O-methyltransferase, family 2	
Major facilitator superfamily	
Lipase, GDSL	
Putative cyclase	
FAD linked oxidase	
Arylsulfotransferase	
FAD linked oxidase	
Glycoside hydrolase, family 43	
PTA-like protein	
hypothetical protein	
Heterokaryon incompatibility	
ABC transporter-like	
Short-chain dehydrogenase	
Serine/threonine-protein kinase-like domain	
Aldehyde dehydrogenase domain	
Pepidase S8/S53	
Heterokaryon incompatibility	
Amino acid transporter, transmembrane	
Heterokaryon incompatibility	
Cytochrome P450	
Cytochrome P450	

