**Supplementary Methods**

Supplementary Method S1: Scripts used in this study.

Supplementary Method S2: Keywords for retrieving fungal nutrient-related sequences from GenBank.

Supplementary Method S3: Keywords for extracting LRR/defense/symbiosis related transcripts from the top (photosynthetic) layer highly expressed transcripts.

***Supplementary Method S1***

Scripts used in this study. Program or pipeline names are underlined. All scripts are preceded with a # sign.

SortMeRNA

#/./bin/sortmerna-2.1-linux-64/sortmerna --ref /bin/sortmerna-2.1-linux-64/rRNA\_databases/silva-bac-23s-id98.fasta,/bin/sortmerna-2.1-linux-64/index/silva-bac-23s-db:/bin/sortmerna-2.1-linux-64/rRNA\_databases/silva-arc-16s-id95.fasta,/bin/sortmerna-2.1-linux-64/index/silva-arc-16s-db:/bin/sortmerna-2.1-linux-64/rRNA\_databases/silva-arc-23s-id98.fasta,/bin/sortmerna-2.1-linux-64/index/silva-arc-23s-db:/bin/sortmerna-2.1-linux-64/rRNA\_databases/rfam-5s-database-id98.fasta,/bin/sortmerna-2.1-linux-64/index/rfam-5s-db:/bin/sortmerna-2.1-linux-64/rRNA\_databases/rfam-5.8s-database-id98.fasta,/bin/sortmerna-2.1-linux-64/index/rfam-5.8s-db:/bin/sortmerna-2.1-linux-64/rRNA\_databases/silva-euk-28s-id98.fasta,/bin/sortmerna-2.1-linux-64/index/silva-euk-28s-db:/bin/sortmerna-2.1-linux-64/rRNA\_databases/silva-euk-18s-id95.fasta,/bin/sortmerna-2.1-linux-64/index/silva-euk-18s-db --reads 1B\_merge.fastq --fastx --aligned all\_1B\_rRNA --other all\_1B\_non\_rrna.fastq fastq --log -v

Trinity

-Assembly

#trinityrnaseq-2.1.1/Trinity --seqType fq --left forward/all\_1.fastq --right reverse/all\_2.fastq --CPU 1 --max\_memory 350G

-Find component utility, Misc directory of Trinity package getting the longest transcripts at component (gene level)

#get\_longest\_isoform\_seq\_per\_trinity\_gene.pl

CD-HIT

#./cd-hit-est -i RDP\_NC\_J\_CF\_ref\_D12\_clean.fasta -o sil\_NC\_J\_CF\_ref\_D12\_ref\_98.fas -c 0.98 -n 10 -d 0 -M 16000

BLAST Uniprot

#blastx -query ./g\_3.fasta -db /database/nr -out ./g\_3.fasta.uniall -outfmt 5 -max\_target\_seqs 1

BLAST results filtering

#grep -Pn "\<Hit\_def\>" $f -B 7| grep -Pn OC=fungi -B 7 | grep -Po TRINITY\_.+\] >> fungi.list\_1;

Transdecoder

#TransDecoder-2.1.0/TransDecoder.LongOrfs -t sed\_rename\_all\_98\_fungi.fasta

Trinotate pipeline

Transcripts: BLASTX Uniprot

#blastx -query ./15\_C5.fasta -db uni\_all\_oc -out ./15\_C5.fasta.uni -outfmt 6 -max\_target\_seqs 1 -evalue 1e-6

Protein BLASTP to uniprot

#blastp -query longest\_orfs.pep -db /work/kc178/ref/uni\_all/uni\_all\_oc -outfmt 6 -max\_target\_seqs 1 -evalue 1e-6

HMMER to pfam

#hmmscan --domtblout Trino.pfam Pfam-A.hmm longest\_orfs.pep > pfam.log

signalP

#signalp -f short -n signalp.out longest\_orfs.pep

Tmhmm

#tmhmm –short longest\_orfs.pep > tmhmm.log

Build sql database

#./Build\_Trinotate\_Boilerplate\_SQLite\_db.pl Trinotate

#/get\_Trinity\_gene\_to\_trans\_map.pl C5\_Trinity\_long.fasta > Trinity.fasta.gene\_trans\_map

Load search results

#Trinotate-Trinotate-v3.1.1/Trinotate Trinotate.sqlite init --gene\_trans\_map Trinity.fasta.gene\_trans\_map --transcript\_fasta uniq\_sidero\_sulfur.fasta --transdecoder\_pep longest\_orfs.pep

#Trinotate Trinotate.sqlite LOAD\_swissprot\_blastp BLASTP.uniprot

#Trinotate Trinotate.sqlite LOAD\_swissprot\_blastx unique.uniprot

#Trinotate Trinotate.sqlite LOAD\_pfam Trino.pfam

#Trinotate Trinotate.sqlite LOAD\_tmhmm C5\_Trinity\_long\_transdecoder\_dir/ tmhmm.log

#Trinotate Trinotate.sqlite LOAD\_signalp C5\_Trinity\_long\_transdecoder\_dir/signalp.out

GoSeq

#run\_GOseq.pl --factor\_labeling factor\_labeling.txt --GO\_assignments go\_annotations.txt --lengths gene.lengths.txt

***Supplementary Method S2***

Keywords for retrieving fungal nutrient-related sequences from GenBank (accessed in 2015 for amino acids, carbon, nitrogen and phosphorus, and in 2018 for sulfur).

Amino acids (organic nitrogen) (42604 sequences)

((((fungi[Organism]) AND amino acid transport) OR ((fungi[Organism]) AND amino acid metabolism)) Not shotgun)Not putative)Not hypothetical)Not unnamed) NOT unknown)

Carbon (28840 sequences):

(((((((((((fungi[Organism]) AND carbon transport) OR ((fungi[Organism]) AND carbon metabolism) OR ((fungi[Organism]) AND sugar transport)) OR ((fungi[Organism]) AND sugar metabolism transport)) OR ((fungi[Organism]) AND carbohydrate transport)) OR ((fungi[Organism]) AND carbohydrate metabolism)) Not shotgun)Not putative)Not hypothetical)Not unnamed) NOT unknown)

Inorganic nitrogen (3257 sequences):

(((((((((((fungi[Organism]) AND nitrogen transport) OR ((fungi[Organism]) AND ammonium transport) OR ((fungi[Organism]) AND nitrate transport)) OR ((fungi[Organism]) AND nitrite transport)) OR ((fungi[Organism]) AND urea transport)) OR ((fungi[Organism]) AND ammonia transport)) Not shotgun)Not putative)Not hypothetical)Not unnamed) NOT unknown)

Phosphorus (29247 sequences):

(((((((fungi[Organism]) AND phosphorus transport) OR ((fungi[Organism]) AND phosphate transport) Not shotgun)Not putative)Not hypothetical)Not unnamed) NOT unknown)

((((fungi[Organism]) AND amino acid transport) Not shotgun)Not putative)Not hypothetical)Not unnamed) NOT unknown)

Sulfur: (110 sequences)

((((((((((((((((((((sulfite transporter) AND fungi[Organism]) NOT draft genome)) NOT whole genome)) NOT chromosome))) NOT contig)) NOT scaffold))) NOT supercontig)) NOT assembly) NOT putative)) NOT cluster) NOT nickel

(((((((((((((((sulfate transporter) AND fungi[Organism]) NOT genome) NOT supercontig) NOT contig) NOT scaffold) NOT putative) NOT hypothetical) NOT draft))) NOT chromosome) NOT phosphate) NOT predicted)) NOT patent

((((((((((siderophore transporter) AND fungi[Organism]) NOT genome) NOT supercontig) NOT contig) NOT scaffold) NOT putative) NOT hypothetical) NOT draft))

***Supplementary Method S3***

Keywords for extracting LRR/defense/symbiosis related transcripts from the top (photosynthetic) layer highly expressed transcripts.

leucine rich

LRR

defense

symbiotic

symbiosis

defensive