Inputs

sample_ name	primer_ name
S1	rps10
S1	its
S2	rps10
S2	its

primer_ name	forward	reverse
rps10	GTT...	ATR...
its	GTG...	TCC...

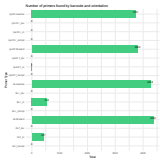
Outputs

Remove N's and create file structure

```
output <- prepare_reads(
data_directory = "data",
output_directory =
"demulticoder_outputs",
overwrite_existing = TRUE)
```

Primer sequence counts across samples

N's filtered from reads

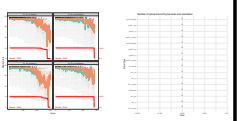


Remove primers and trim reads

```
cut_trim(output,
cutadapt_path="local/bin/
cutadapt")
```

Read quality plots; primer sequence counts after trimming

Demultiplexed and trimmed reads

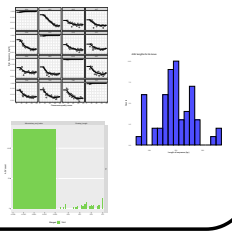


Make ASV abundance matrix

```
make_asv_abund_matrix(
output)
```

Quality plots after read merging; ASV abundance matrices

Merged read files



Assign taxonomy

```
assign_tax(output,
asv_abund_matrix,
db_its = "fungidb.fasta",
db_rps10 =
"oomycetedb.fasta")
```

Formatted databases; Final ASV matrices and taxonomic assignments

Convert matrix to phyloseq and taxmap objects

```
objs <-
convert_asv_matrix_to_objs(
output)
```

R objects for downstream analyses

Taxmap object