APPENDIX IV : Sequence pre analysis: The command line codes used for both ITS and

D1/D2 28S rRNA. Of the epiphytic and endophytic sequence reads.

#! /bin/bash

For reads in `cat /home/user/&lt;file path&gt;/fastq.txt`

do

TrimmomaticPE-phred33

/home/user/cashew/cashew\_project/&lt;file.path&gt;/${reads}1.fastq.gz/home/user/cashew/cashew

\_project/&lt;file.path&gt;${reads}2.fastq.gz ./${reads}1.trim.fastq ./${reads}1.untrim.fastq

./${reads}2.trim.fastq ./${reads}2.untrim.fastq ILLUMINACLIP: NexteraPE-PE.fa:2:30:10

LEADING: 3 TRAILING: 3 SLIDINGWINDOW: 4:15 MINLEN: 36.

Done

#! /bin/bash

For reads in `cat /home/user/&lt;file. Path&gt;/fastq.txt`

do

Vsearch -fastq\_mergepairs /home/user/&lt;file. Path&gt;/${reads}\_1.trim.fastq -reverse

/home/user/&lt;file. Path&gt;/${reads}\_2.trim.fastq -fastq\_maxdiffs 10 -fastq\_minovlen 10 -

fastq\_truncqual 2 -fastq\_allowmergestagger -fastq\_minlen 1 -fastq\_minmergelen 1 -fastaout

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/home/user/&lt;file.path&gt;/${reads}.merged.fasta–eetabbedout/home/

user/&lt;file.path&gt;/${reads}.tb

done

#! /bin/bash

For reads in `cat /home/user/&lt;file. Path&gt;/fastq.txt`

Do

sed -e &quot;s/\(^@.\*\) .\*$/\1;sample=${reads%.\*};/&quot; ../&lt;file. Path&gt;/$reads &gt;&gt; &lt;file.name&gt;;

Done

APPENDIX V : Sequence processing: The command line codes used for both ITS and

D1/D2 28S rRNA. Of the epiphytic and endophytic quality sequence reads.

Read Filtering: (vsearch --fastx\_filter &lt;input.fastq/fasta&gt; --fastq\_maxee 1 –fastaout

&lt;output.fasta)

Removal of dulicate reads: (vsearch –derep\_fulllength &lt;input.fasta&gt; --output &lt;output.fasta

–sizeout –relabel ASV)

Read Denoising:  (vsearch –cluster\_unoise &lt;input.fasta&gt; --minsize 4 –unoise\_alpha 2

–centroids &lt;output.fasta&gt;)

Denovo chimera removal: (vsearch –uchime3\_denovo &lt;input.fasta –nonchimeras

&lt;output.fasta&gt;)

ASV Clustering into OUT: (vsearch –cluster\_size &lt;input.fasta&gt; --id 0.97 –centroids

&lt;otu.fasta&gt; --sizein –relabel out)

Mapping of OUTs to Raw reads (creation of OTU Table count): (vsearch –usearch\_global

&lt;reads.fasta&gt; -db out.fasta –id 0.97 –otutabout &lt;output.tsv)

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OTU Alignment: (mafft –thread 4 –globalpair –maxiterate 1000 &lt;input.fasta&gt;

&lt;output.fasta&gt;)

Tree building:  (Fastree –gtr –nt &lt;input.fasta&gt; &lt;output.tre&gt;)

Local BLAST database:  (makeblastdb –in &lt;input.fasta&gt; -out &lt;database name&gt; -dbtype

&lt;nucl&gt; -title &lt;”fungal database” &gt; -seqids)

Creating taxa file:  (blastn –query &lt;out.fasta&gt; -db ref\_seq.fasta –evalue 10e-21, -outfmt ‘6

std’ &lt;–output. Taxa&gt;

Taxa file cleaning: (removal of underscores): sed –I ”s/;/\t/g&quot; &lt;filename&gt;  and sed -i

&#39;s/\(\w\+\)\_\_//g&#39; &lt;filename&gt;.