#See cutadapt workflow for data prep

#QIIME1

#Validate mapping file

validate\_mapping\_file.py -m ~/Documents/Mock\_Spike\_In/2017-02-27\_MockSpikeIn\_mappingfile\_w\_dna\_conc.csv -o ~/Documents/Mock\_Spike\_In/QIIME1/check\_map

No errors or warnings were found in mapping file.

#Join paired ends

multiple\_join\_paired\_ends.py \

-i cutadapt\_trimtrim \

-o trimmed/join\_paired\_ends \

--read1\_indicator '\_R1' \

--read2\_indicator '\_R2'

#Delete unjoined files

cd ~/Documents/Mock\_Spike\_In/QIIME1/join\_paired\_ends\_param/

for f in ~/Documents/Mock\_Spike\_In/QIIME1/join\_paired\_ends\_param/\*; do

 cd $f

 rm fastqjoin.un1.fastq

 rm fastqjoin.un2.fastq

done

cd

#Split libraries

multiple\_split\_libraries\_fastq.py -i ~/Documents/Mock\_Spike\_In/QIIME1/join\_paired\_ends/ -o ~/Documents/Mock\_Spike\_In/QIIME1/split\_libraries\_def -m sampleid\_by\_file --read\_indicator '.join' --include\_input\_dir\_path --remove\_filepath\_in\_name

#Pick OTUs

#Parameters in param.txt: pick\_rep\_set:rep\_set\_picking\_method most\_abundant

pick\_open\_reference\_otus.py -i ~/Documents/Mock\_Spike\_In/QIIME1/split\_libraries\_def/seqs.fna -r ~/Documents/Mock\_Spike\_In/RefFiles/97\_otus.fasta -o ~/Documents/Mock\_Spike\_In/QIIME1/OTU\_picking\_def/ --parallel --jobs\_to\_start 16

#Identify chimeras

identify\_chimeric\_seqs.py \

-i OTU\_picking\_def/pynast\_aligned\_seqs/rep\_set\_aligned.fasta \

-a 97\_otus.fasta \

-o OTU\_picking\_def/chimeric\_seqs.txt

--split\_by\_sampleid

#Count lines in chimeras.txt

wc -l ~/Documents/Mock\_Spike\_In/QIIME1/slayer\_checked\_chimeras\_def/chimeras.txt

#Filter out chimeras

filter\_fasta.py \

-f OTU\_picking\_def/pynast\_aligned\_seqs/rep\_set\_aligned.fasta \

-o OTU\_picking\_def/non\_chimeric\_rep\_set\_aligned.fasta \

-s OTU\_picking\_def/chimeric\_seqs.txt \

-n

#Sequences remaining

grep -c ">" ~/Documents/Mock\_Spike\_In/QIIME1/OTU\_picking\_def/seqs\_chimeras\_filtered.fna

#Make filtered OTU biom file

make\_otu\_table.py \

-i OTU\_picking\_def/final\_otu\_map\_mc2.txt \

-o OTU\_picking\_def/otu\_table.biom \

-e OTU\_picking\_def/chimeric\_seqs.txt \

-t uclust\_assigned\_taxonomy/rep\_set\_tax\_assignments.txt