#Activate QIIME1 conda

conda create -n qiime1 python=2.7 qiime matplotlib=1.4.3 mock nose -c bioconda

source activate qiime1

#separate reads from barcodes

extract\_barcodes.py --fastq1 ~/FL103/AllReads\_unfiltered.fastq --bc1\_len 8 -m ~/FL103/FL103\_MapFile.txt -o ~/FL103/barcodes\_unfiltered

conda deactivate

#Zip barcode file

gzip ~/FL103/barcodes\_unfiltered/barcodes.fastq -r ~/FL103/barcodes\_unfiltered/barcodes.fastq.gz

#Rename “reads” to “sequences” for QIIME2 formatting

mv ~/FL103/barcodes\_unfiltered/reads.fastq ~/FL103/barcodes\_unfiltered/sequences.fastq

#Zip sequences file

gzip ~/FL103/barcodes\_unfiltered/sequences.fastq -r ~/FL103/barcodes\_unfiltered/sequences.fastq.gz