#building phylogenetic tree

#Conduct alignment for tree building

qiime alignment mafft \

--i-sequences ~/FL103/DADA2\_350\_unfiltered/representative\_sequences.qza \

--o-alignment ~/FL103/DADA2\_350\_unfiltered/representative\_sequences\_aligned.qza

#Mask (i.e., filter) unconserved and highly gapped columns from an alignment.

qiime alignment mask \

--i-alignment ~/FL103/DADA2\_350\_unfiltered/representative\_sequences\_aligned.qza \

--o-masked-alignment ~/FL103/DADA2\_350\_unfiltered/representative\_sequences\_aligned\_masked.qza

#Generate a tree for phylogenetic diversity analyses

qiime phylogeny fasttree \

--i-alignment ~/FL103/DADA2\_350\_unfiltered/representative\_sequences\_aligned\_masked.qza \

--o-tree ~/FL103/DADA2\_350\_unfiltered/unrooted-tree.qza

#place the root at the midpoint of the longest tip-to-tip distance on the tree

qiime phylogeny midpoint-root \

--i-tree ~/FL103/DADA2\_350\_unfiltered/unrooted-tree.qza \

--o-rooted-tree ~/FL103/DADA2\_350\_unfiltered/rooted-tree.qza