based on this thread: https://forum.qiime2.org/t/converting-biom-files-with-taxonomic-info-for-import-in-r-with-phyloseq/2542/5

 # How to export a feature (OTU) table and convert from biom to .tsv (use following codes in QIIME2)

 # Step 1, export OTU table

```
qiime tools export \
 table-no-mitochondria-no-chloroplast.qza \
 --output-dir phyloseq
```

 # OTU table exports as feature-table.biom so convert to .tsv

```
biom convert -i phyloseq/feature-table.biom -o phyloseq/otu_table.txt --to-tsv
```

 # now you have otu_table.txt

open it up in text edit and change #OTUID to OTUID

 # Step 2, export taxonomy table

```
qiime tools export \
taxonomy.qza\
 --output-dir phyloseq
```

 # now you have taxonomy.tsv

open it up in text edit and change Feature ID to OTUID

 # Step 3, export tree

```
qiime tools export \
 unrooted-tree.qza \
 --output-dir phyloseq
```

 # Step 4, if you filtered out any sequences (chloroplasts, mitochondria, etc) then your taxonomy and OTU tables are different lengths. QIIME2 doesn't filter out taxonomy, so you have to merge the two files in R and output a merged file.

(use following codes in R)

 # set working directory

```
setwd("~/QIIME2/WoodsHole_Sea_Cucumber/phyloseq")
```

 # read in OTU table

```
otu <- read.table(file = "otu_table.txt", header = TRUE)
head(otu)
```

 # read in taxonomy table

```
tax <- read.table(file = "taxonomy.tsv", sep = '\t', header = TRUE)
head(tax)
```

 # merge files

```
merged_file <- merge(otu, tax, by.x = c("OTUID"), by.y=c("OTUID"))
head(merged_file)
```

note: number of rows should equal your shortest file length, drops taxonomy for OTUs that don’t exist in your OTU table

 # output merged .txt file

```
write.table(merged_file, file = "combined_otu_tax", sep = '\t', col.names =
TRUE, row.names = FALSE)
```

It seems tedious but you need to open the merged .txt file in excel and split into two files: one for taxonomy (containing only the columns OTUID and taxonomic info) and the other for the OTU matrix (containing only OTUID and abundances in each sample). Note: for the taxonomy file, you need to use data —> text-to-columns in Excel and separate on semicolon to get columns for kingdom, phylum, class, etc… once you make these two separate files in excel, save each as a .csv

 # Step 5, Finally, upload all of your files into phyloseq in R!

 # load libraries

```
library("ggplot2")
library("phyloseq")
library("ape")
```

 # set working directory

```
setwd("~/QIIME_2/WoodsHole_Sea_Cucumber/phyloseq")

# read in otu table
otu_table = read.csv("otu_matrix.csv", sep=",", row.names=1)
otu_table = as.matrix(otu_table)

# read in taxonomy
# seperated by kingdom phylum class order family genus species
taxonomy = read.csv("taxonomy.csv", sep=",", row.names=1)
taxonomy = as.matrix(taxonomy)

# read in metadata
# variables = DateCuke  Site    Sample_type        Sample_type_day
# variables = Sample_type_site        Sample_method    Full_index
metadata = read.table("Sea_Cucumber_metadata.txt", row.names=1)

# read in tree
phy_tree = read_tree("tree.nwk")

# import as phyloseq objects
OTU = otu_table(otu_table, taxa_are_rows = TRUE)
TAX = tax_table(taxonomy)
META = sample_data(metadata)
# (tree was already imported as a phyloseq object)

# check that your OTU names are consistent across objects
taxa_names(TAX)
taxa_names(OTU)
taxa_names(phy_tree)

# make sure files have the same sample names
sample_names(OTU)
sample_names(META)
```

 # merge into one phyloseq object

```
physeq = phyloseq(OTU, TAX, META, phy_tree)
physeq
```

 # Now, continue to analysis in phyloseq!