Producing genus level table to use in sample-classifier (random Forest):
(qiime2-2019.7) lozuponelabs-MacBook-Pro:combinedCohortsAnalysis
Nancy$ qiime taxa collapse --i-table /Users/Nancy/Documents/
Autism_Project/qiime2redo/mergedTables/combinedCohortsAnalysis/id-
filtered-table.qza --i-taxonomy /Users/Nancy/Documents/Autism_Project/
qiime2redo/mergedTables/combinedCohortsAnalysis/taxonomy.qza --p-level
6 --o-collapsed-table genusLevelCollapsedTable.qza
Saved FeatureTable[Frequency] to: genusLevelCollapsedTable.qza

Running random forest with this table:
(qiime2-2019.7) lozuponelabs-MacBook-Pro:randomForest1016 Nancy$ qiime
sample-classifier classify-samples --i-table /Users/Nancy/Documents/
Autism_Project/qiime2redo/mergedTables/combinedCohortsAnalysis/
genusLevelCollapsedTable.qza --m-metadata-file /Users/Nancy/Documents/
Autism_Project/qiime2redo/mergedTables/combinedCohortsAnalysis/
metadata/combineCohorts_metadata.tsv --m-metadata-column ASD --p-
optimize-feature-selection --p-estimator RandomForestClassifier --p-n-
estimators 5000 --p-n-jobs 6 --p-random-state 123 --output-dir
randomForest1016
Saved SampleEstimator[Classifier] to: randomForest1016/
sample_estimator.qza
Saved FeatureData[Importance] to: randomForest1016/
feature_importance.qza
Saved SampleData[ClassifierPredictions] to: randomForest1016/
predictions.qza
Saved Visualization to: randomForest1016/model_summary.qzv
Saved Visualization to: randomForest1016/accuracy_results.qzv
Saved SampleData[Probabilities] to: randomForest1016/probabilities.qza

Exporting feature_importance.qza to see which features were 0.01 or
greater:
(qiime2-2019.7) lozuponelabs-MacBook-Pro:randomForest1016 Nancy$ qiime
tools export --input-path /Users/Nancy/Documents/Autism_Project/
qiime2redo/mergedTables/combinedCohortsAnalysis/randomForest1016/
randomForestOutput/feature_importance.qza --output-path /Users/Nancy/
Documents/Autism_Project/qiime2redo/mergedTables/
combinedCohortsAnalysis/randomForest1016/randomForestOutput/

Exporting genus level table to add count data to the metadata table:
(qiime2-2019.7) lozuponelabs-MacBook-Pro:randomForest1016 Nancy$ qiime
tools export --input-path /Users/Nancy/Documents/Autism_Project/
qiime2redo/mergedTables/combinedCohortsAnalysis/
genusLevelCollapsedTable.qza --output-path /Users/Nancy/Documents/
Autism_Project/qiime2redo/mergedTables/combinedCohortsAnalysis/
randomForest1016/randomForestOutput/

*** only added coprococcus and prevotella

Running sample-classifier (random Forest) with ASV table (counts):

```
(qiime2-2019.7) lozuponelabs-MacBook-Pro:tableRandomForest Nancy$
qiime sample-classifier classify-samples --i-table /Users/Nancy/
Documents/Autism_Project/qiime2redo/mergedTables/
combinedCohortsAnalysis/id-filtered-table.qza --m-metadata-file /
Users/Nancy/Documents/Autism_Project/qiime2redo/mergedTables/
combinedCohortsAnalysis/metadata/combineCohorts_metadata.tsv --m-
metadata-column ASD --p-optimize-feature-selection --p-estimator
RandomForestClassifier --p-n-estimators 5000 --p-n-jobs 6 --p-random-
state 123 --output-dir randomForestOutput
```

Saved SampleEstimator[Classifier] to: randomForestOutput/
sample_estimator.qza
Saved FeatureData[Importance] to: randomForestOutput/
feature_importance.qza
Saved SampleData[ClassifierPredictions] to: randomForestOutput/
predictions.qza
Saved Visualization to: randomForestOutput/model_summary.qzv
Saved Visualization to: randomForestOutput/accuracy_results.qzv
Saved SampleData[Probabilities] to: randomForestOutput/
probabilities.qza

Filter feature table with to only have the features that were
important:
```
(qiime2-2019.7) lozuponelabs-MacBook-Pro:tableRandomForest Nancy$
qiime feature-table filter-features --i-table /Users/Nancy/Documents/
Autism_Project/qiime2redo/mergedTables/combinedCohortsAnalysis/id-
filtered-table.qza --m-metadata-file /Users/Nancy/Documents/
Autism_Project/qiime2redo/mergedTables/combinedCohortsAnalysis/
randomForest1016/tableRandomForest/randomForestOutput/
feature_importance.qza --o-filtered-table id_important-feature-
table.qza
```
Saved FeatureTable[Frequency] to: id_important-feature-table.qza

Exporting important features:
```
(qiime2-2019.7) lozuponelabs-MacBook-Pro:tableRandomForest Nancy$
qiime tools export --input-path /Users/Nancy/Documents/Autism_Project/
qiime2redo/mergedTables/combinedCohortsAnalysis/randomForest1016/
tableRandomForest/id_important-feature-table.qza --output-path .
```

Convert export to tsv to add to metadata:
```
(qiime2-2019.7) lozuponelabs-MacBook-Pro:tableRandomForest Nancy$ biom
convert -i /Users/Nancy/Documents/Autism_Project/qiime2redo/
mergedTables/combinedCohortsAnalysis/randomForest1016/
tableRandomForest/feature-table.biom --to-tsv -o feature-table.tsv
```