

# Amplicon result supplementary instruction

( 02 )

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## 02.FeatureAnalysis 【feature sequence and feature table】

### 1. feature.fasta 【feature sequence】

### 2. feature.tax\_assignments.txt 【annotation result】

Qiime2 software is used for annotation. For 16s and 18s, we use Silva 138.1 database, for ITS, we use Unite v9.0 database. For irregular region, we use micro\_NT database by default.

Mitochondria and chloroplast might appear in the annotation result, but here, these are their official name, they should not be defined as organelles, mitochondria belongs to Proteobacteria (phylum) , Alphaproteobacteria(class), Rickettsiales(order),it is one type of prokaryotic microorganism, and chloroplast is very common in cyanobacteria.

### 3. aligned-rep-seqs.qza 【multiple sequence alignment result】

### 4. denoisingTable.qza 【qza directory of ASV after denoise】

### 5. denoisingTable.qza 【qza file of ASV after denoise】

### 6. denoisingTable.qzv 【qzv directory of ASV after denoise】

### 7. denoisingTable.qzv 【qzv file of ASV after denoise】

### 8. featureSeqs.qza 【qza directory of feature sequence】

### 9. featureSeqs.qza 【qza file of feature sequence】

### 10. featureSeqs.qzv 【qzv directory of feature sequence】

### 11. featureSeqs.qzv 【qzv file of feature sequence】

### 12. featureTable.qza 【qza directory of feature table】

### 13. featureTable.qza 【qza file of feature table】

### 14. featureTable.qzv 【qzv directory of feature table】

### 15. featureTable.qzv 【qzv file of feature table】

### 16. masked-aligned-rep-seqs.qza 【multiple sequence alignment result after high variation removing】

### 17. rooted-tree.qza 【qza directory of rooted-tree】

### 18. rooted-tree.qza 【qza file of rooted-tree】

### 19. unrooted-tree.qza 【qza directory of unrooted-tree】

### 20. unrooted-tree.qza 【qza file of unrooted-tree】

### 21. seq\_taxonomy.qza 【qza directory of sequence annotation】

### 22. seq\_taxonomy.qza 【qzv file of sequence annotation】

### 23. seq\_taxonomy.qzv 【qza directory of sequence annotation】

### 24. seq\_taxonomy.qzv 【qzv file of sequence annotation】

## 25. tables 【feature table】

### 25.1 sample/group1/ 【feature table of sample or group】

#### 25.1.1 featureTable\_Absolute 【feature table of absolute abundance】

25.1.1.1 featureTable.\*.total.absolute.txt 【feature table of absolute abundance】

25.1.1.2 featureTable.\*.\*.absolute.xls 【feature table of absolute abundance at each taxonomy level {k,p,c,o,f,g,s}】

Column number	Column name	Instruction
1	Taxonomy	Annotation result
2	Sample/group name	Absolute abundance
3	Tax_detail	Detailed annotation result

#### 25.2 featureTable\_Relative 【feature table of relative abundance】

25.2.1 featureTable.\*.total.relative.xls 【feature table of relative abundance after normalization】

25.2.2 featureTable.\*.\*.relative.xls 【feature table of relative abundance at each taxonomy level】

#### 25.3 featureTable\_Even 【feature table of absolute abundance after normalization】

The meaning and method of normalization: owe to the different of sequencing depth, there are different sequence number among samples, in order to eliminate the experimental error and ensure comparability between sample data, we need to set a consistent depth

The method is set a threshold according to the sample that has the least sequence number, then the number of sequences set by this threshold are selected for analysis.

25.3.1 featureTable.\*.\*.total.even.txt 【feature table of absolute abundance after normalization】

Column number	Column name	Instruction
1	Taxonomy	Annotation result
2	Sample/group	Absolute abundance after normalization
3	Tax_detail	Detailed annotation result

25.3.2 featureTable.\*.\*.absolute.xls 【absolute abundance at each taxonomy level】

#### 25.4 featureTable\_Biom 【biom file】

25.4.1 featureTable.\*.total.absolute.txt.biom 【 absolute abundance table, biom format】

25.4.2 featureTable.\*.total.even.txt.biom 【 even abundance table, biom format】

25.4.3 featureTable.\*.total.relative.txt.biom 【 relative abundance table, biom formta】

25.4.4 featureTable.\*.total.absolute.txt.qza 【 absolute abundance table, qza format】

25.4.5 featureTable.\*.total.even.txt.qza 【 even abundance table, qza format】

25.4.6 featureTable.\*.total.relative.txt.qza 【 relative abundance table, qza format】

### 25.5. featureTable\_tableStat 【summary of annotation in sample or group】

25.5.1 featureTable.briefStatInfo.txt 【summary of brief annotation】

25.5.2 featureTable.relativeStat.\*.xls 【number of annotation at each taxonomy level  
(k,p,c,o,f,g,s)】

25.5.3 classifiedStat.sample.absolute.{xls,svg,png} 【statistical result and visual display of  
annotation number at each taxonomy level in sample】

Column number	Column name	Instruction
1	Sample_Name	Sample name
2	Kingdom	Tags number at Kingdom taxonomy level
3	Phylum	Tags number at Phylum taxonomy level
4	Class	Tags number at Class taxonomy level
5	Order	Tags number at Order taxonomy level
6	Family	Tags number at Family taxonomy level
7	Genus	Tags number at Genus taxonomy level
8	Species	Tags number at Species taxonomy level