

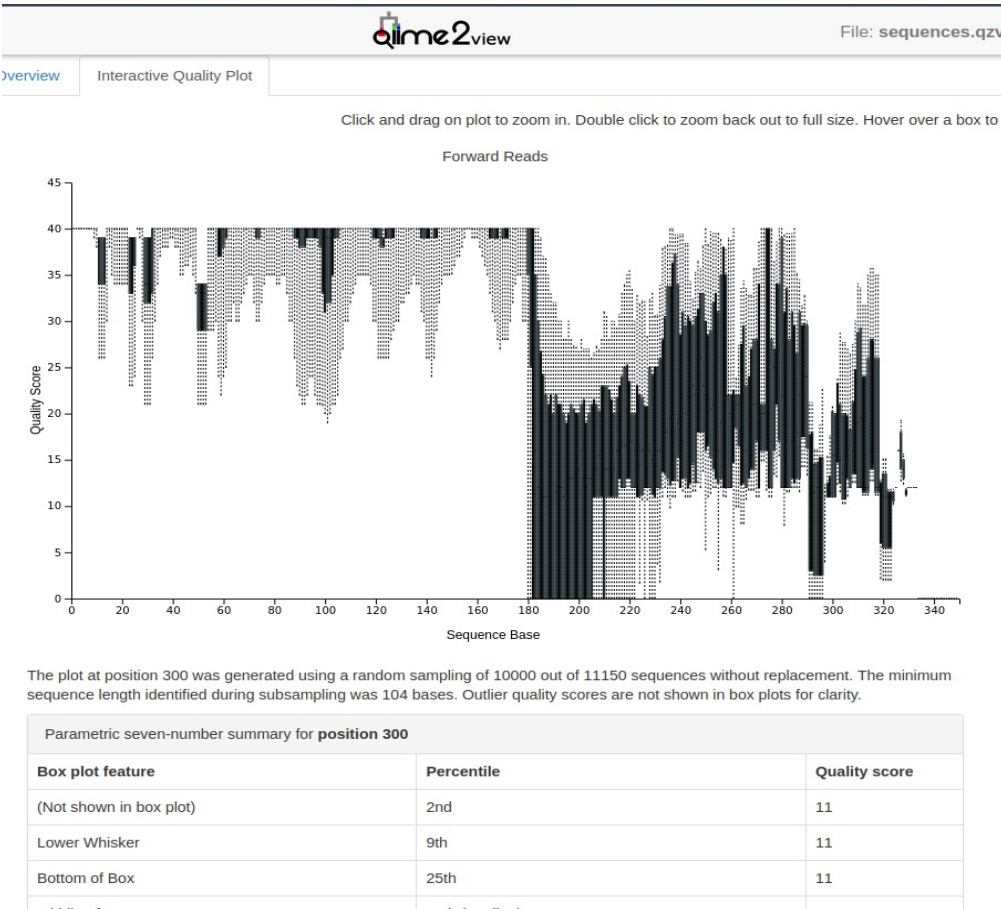
Data:

- SRX351237_calculus_sra_data.fastq - calculus.fastq
- SRX351242_bone_sra_data.fastq - root.fastq
- G12_contigs.fna

```
qiime tools import --type 'SampleData[SequencesWithQuality]' --input-path manifest.tsv
--output-path sequences.qza --input-format SingleEndFastqManifestPhred33V2
```

```
qiime tools validate sequences.qza
Result sequences.qza appears to be valid at level=max.
```

```
qiime demux summarize --i-data sequences.qza --o-visualization sequences.qzv
```



Demultiplexed sequence counts summary

	forward reads
Minimum	5362
Median	5575.0

Mean	5575.0
Maximum	5788
Total	11150

- qiime dada2 denoise-single --i-demultiplexed-seqs sequences.qza --p-trim-left **32** --p-trunc-len **147** --o-representative-sequences rep-seqs.qza --o-table table.qza --o-denoising-stats stats.qza
- qiime metadata tabulate --m-input-file stats.qza --o-visualization stats.qzv
- qiime feature-table summarize --i-table table.qza --o-visualization table.qzv --m-sample-metadata-file sample-metadata.tsv
- qiime feature-table tabulate-seqs --i-data rep-seqs.qza --o-visualization rep-seqs.qzv
- wget -o "gg-13-8-99-nb-classifier.qza" "<https://data.qiime2.org/2018.11/common/gg-13-8-99-nb-classifier.qza>"

Search

sample-id sq2-types	input numeric	filtered numeric	percentage of input passed filter numeric	denoised numeric	non-chimeric numeric	percentage of input non-chimeric numeric
bone	5788	5589	96.56	5425	5349	92.42
calculus	5362	5185	96.7	5044	4801	89.54

Showing 1 to 2 of 2 entries

Sequence Length Statistics						Seven-Number Summary of Sequence Lengths							
Download sequence-length statistics as a TSV						Download seven-number summary as a TSV							
Sequence Count	Min Length	Max Length	Mean Length	Range	Standard Deviation	Percentile:	2%	9%	25%	50%	75%	91%	98%
165	115	115	115.0	0	0.0	Length* (nts):	115	115	115	115	115	115	115

*Values rounded down to nearest whole number.

qiime feature-classifier classify-sklearn --i-classifier gg-13-8-99-nb-classifier.qza --i-reads rep-seqs.qza --o-classification taxonomy.qza

qiime metadata tabulate --m-input-file taxonomy.qza --o-visualization taxonomy.qzv

qiime taxa barplot \
 --i-table table.qza \
 --i-taxonomy taxonomy.qza \
 --m-metadata-file sample-metadata.tsv \
 --o-visualization taxa-bar-plots.qzv

1. Porphyromonas gingivalis
2. Tannerella forsythia

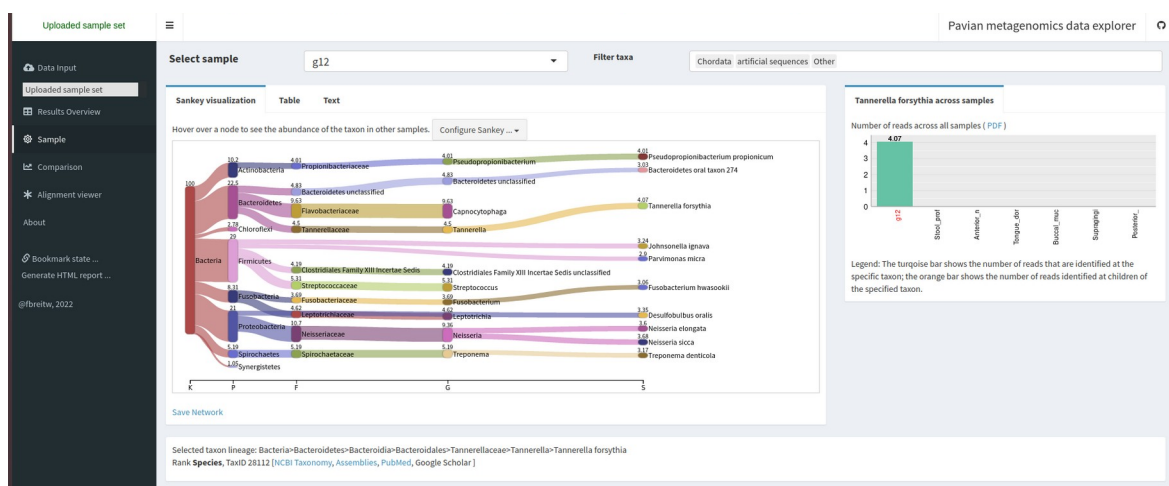
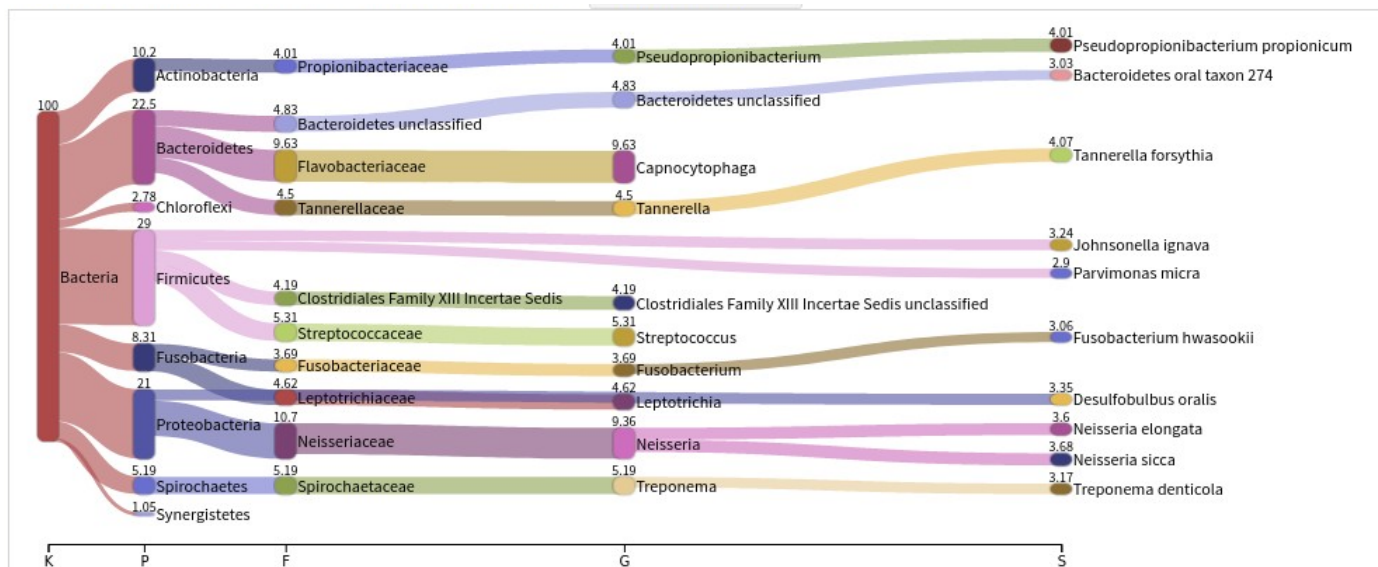
3. Treponema denticola

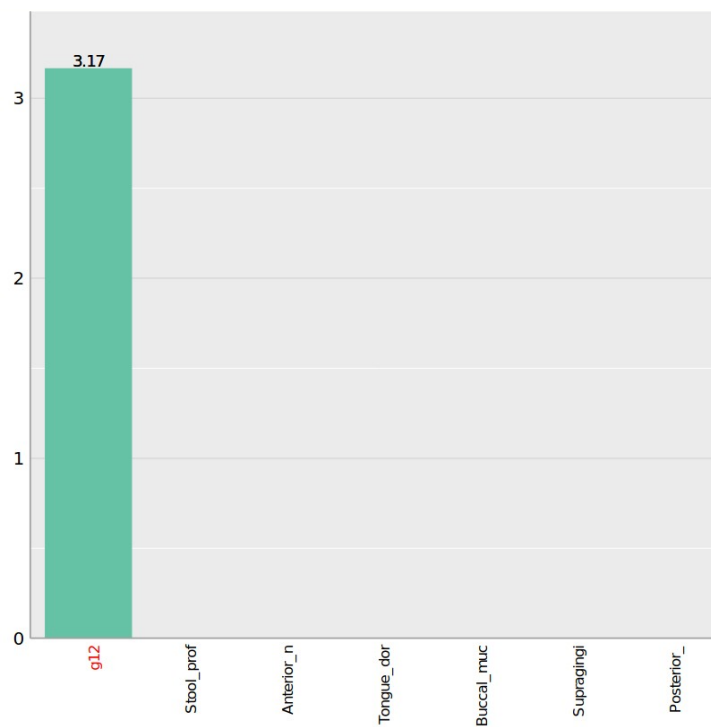
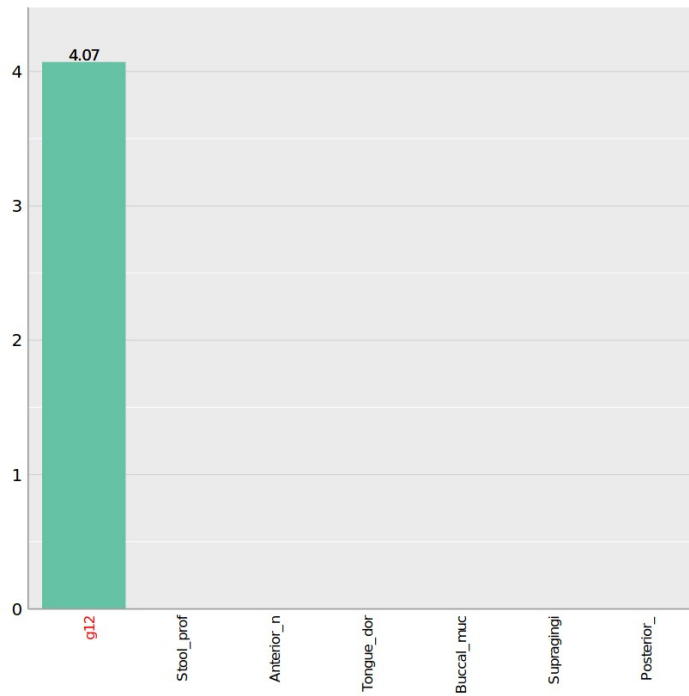
Shotgun-sequencing:

- metaphlan g12.fna --input_type fasta --nproc 6 > g12.txt

for f in *.fasta ; do metaphlan \$f --input_type fasta --nproc 6 > \${f%.fasta}_profile.txt ; done

merge_metaphlan_tables.py *.txt > merged_abundance_table.txt





- `bwa index forsythia.fasta`
- `bwa mem forsythia.fasta g12.fna > alignment.sam`
- `samtools view -S -b alignment.sam > alignment.bam`
- `samtools sort alignment.bam -o alignment_sorted.bam`
- `bedtools bamtobed -i alignment_sorted.bam > alignment_sorted.bed`
- `bedtools intersect -a sequence.gff3 -b alignment_sorted.bed -v > intersect_result.txt`

