

Hifiasm-meta analysis using environmental samples

Sequence statistics

Feature	
Mean read length	14,405.2
Median read length	13,861.0
Mean read quality	35.8
Median read quality	35.3
Number of reads	1,988,560
Read length N50	14,617
Total bases	28,645,567,667

Feature	
Mean read length	28,692.2
Median read length	16,306.0
Mean read quality	N/A
Median read quality	N/A
Number of reads	15,606
Read length N50	29,883
Total bases	447,770,496

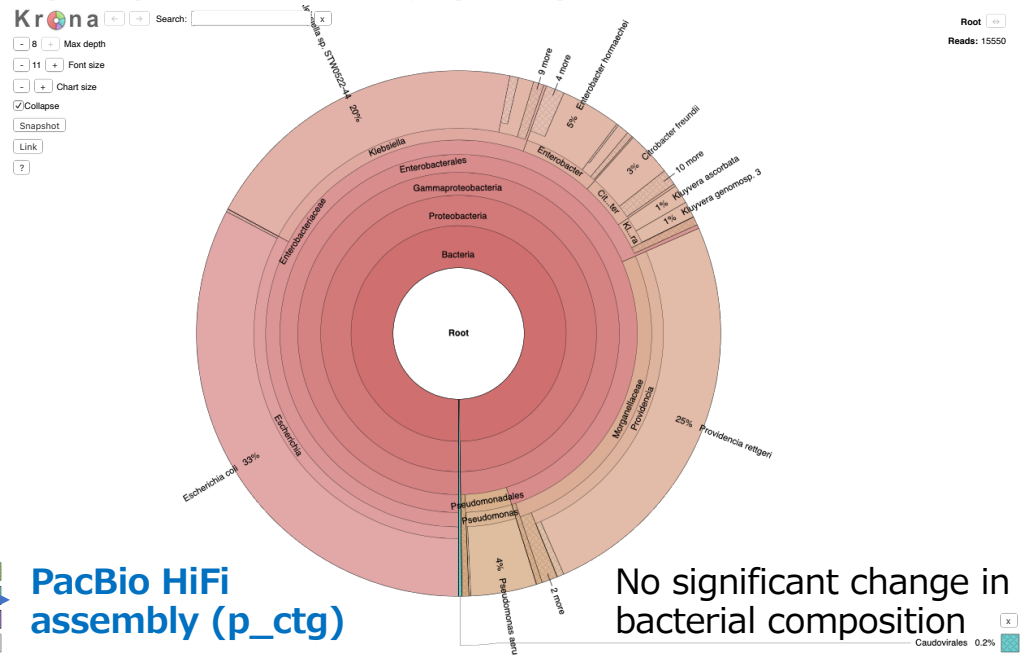
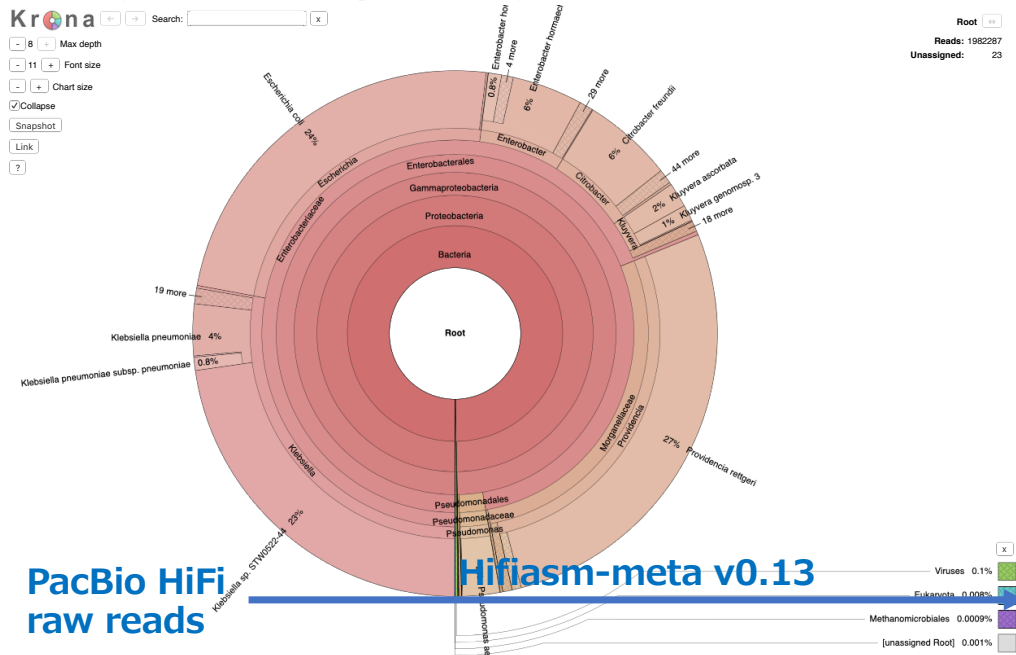
Sequencing depth: **x63.97**
(enough?)

PacBio HiFi
raw reads

Hifiasm-meta v0.13

PacBio HiFi
assembly (p_ctg)

Metagenomic analysis using Kraken2 v2.1.1 w/ standard plus protozoa & fungi (2021) libraries



PacBio HiFi
raw reads

Hifiasm-meta v0.13

PacBio HiFi
assembly (p_ctg)