

E faecalis refseq/external genomes

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Read in sunbeam pipeline and metadata

In this report, we looked at the `meconium` samples from IGRAM run1, and identified the strain of E faecalis from the annotation of de novo assembled contigs.

Read in metaphlan2 results

Dominance

Enterococcus faecalis

The E. faecalis genome consists of 3.22 million base pairs with 3,113 protein-coding genes.[19]

Sample Selections

- write 20171117_Efaecalis.txt
- write 20171117_SampleID_Efaecalis.txt

Assembly summary

- read in 20171117_Efaecalis/assembly_summary.txt
- write 20171117_Efaecalis_accession.txt

External genome

- write 20171117_faecalis-external-genomes.txt