Bacteroides vulgatus 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 Bacteroide vulgatus from the annotation of de novo assembled contigs.

Read in metaphlan2 results

Dominance

Bacteroides vulgatus

The Escherichia coli genome was found to be a circular DNA molecule 4.7 million base pairs in length, containing 4288 annotated protein-coding genes (organized into 2584 operons), seven ribosomal RNA (rRNA) operons, and 86 transfer RNA (tRNA) genes.

- also need an outgroup**

- https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3147508/

Sample Selections

- write 20171122_Bvulgatus.txt
- write 20171122_SampleID_Bvulgatus.txt

Assembly summary

- read in 20171122_Bvulgatus/assembly_summary.txt
- write 20171122_Bvulgatuss_accession.txt

External genome

- need to double check for `.` in the name

- write 20171122_vulgatus-external-genomes.txt