

Exercise 3: example report (You can change the format and include any extra information you find important)

Our team selected the SRA run ERR12302112 from NCBI, part of the bioproject PRJEB69695. The focus of this project is to explore the fecal microbiota associated with acute COVID-19 infection, specifically analyzing gut microbiome samples. This particular sample was sequenced using the Illumina MiSeq platform, targeting the 16S rRNA gene region, and comprises 19,844 reads.

<https://www.ncbi.nlm.nih.gov/bioproject/PRJEB69695>

Fecal microbiota in relation to acute COVID-19 infection

Accession: PRJEB69695 ID: 1042070

People with acute COVID-19 due to SARS-CoV-2 infection experience a range of symptoms, but major factors contributing to severe clinical outcomes remain to be understood. Emerging evidence suggests associations between the gut microbiome and the severity and progression of COVID-19. To better understand the host-microbiota interactions in acute COVID-19, we characterized the intestinal microbiome of patients with active SARS-CoV-2 infection in comparison to recovered patients and uninfected healthy controls. We performed 16S rRNA sequencing of fecal samples collected between May 2020 and January 2021 from 20 COVID- positive patients, 20 COVID-recovered subjects and 20 healthy controls. COVID-19-positive patients had altered microbiome community characteristics compared to the recovered and control subjects, as assessed by α - and β -diversity differences. In COVID-positive patients, we observed depletion of Bacteroidaceae, Ruminococcaceae, and Lachnospiraceae, as well as decreased relative abundances of the genera Faecalibacterium, Adlercreutzia, and the Eubacterium brachy group. The enrichment of Prevotellaceae with COVID-19 infection continued after viral clearance; antibiotic use further induced gut microbiota perturbations in COVID-positive patients. In total, we present evidence that acute COVID-19 induces gut microbiota dysbiosis with depletion of particular populations of commensal bacteria, a phenomenon heightened by antibiotic exposure, but the general effects do not persist post-recovery. [Less...](#)

Accession	PRJEB69695
Scope	Monoisolate
Publications	Yin YS <i>et al.</i> , "Alterations of the fecal microbiota in relation to acute COVID-19 infection and recovery.", <i>Mol Biomed</i> , 2022 Nov 28;3(1):36
Submission	Registration date: 18-Nov-2023 University of California San Diego Microbiome Initiative

<https://www.ncbi.nlm.nih.gov/sra/ERX11679108>

[ERX11679108](#): qita_ptid_16151:14812.CV19.012

1 ILLUMINA (Illumina MiSeq) run: 19,844 spots, 3M bases, 1.7Mb downloads

Design: Fecal microbiota in relation to acute COVID-19 infection

Submitted by: University of California San Diego Microbiome Initiative (University of California San Diego Microbiome Init)

Study: Fecal microbiota in relation to acute COVID-19 infection

[PRJEB69695](#) • [ERP154635](#) • [All experiments](#) • [All runs](#)

[show Abstract](#)

Sample: 14812.CV19.012; Fecal microbiota in relation to acute COVID-19 infection

[SAMEA114630795](#) • [ERS17015066](#) • [All experiments](#) • [All runs](#)

Organism: [human gut metagenome](#)

Library:

Name: 14812.CV19.012

Instrument: Illumina MiSeq

Strategy: AMPLICON

Source: METAGENOMIC

Selection: PCR

Layout: SINGLE

Construction protocol: Illumina EMP protocol 515f, 806rbc amplification of 16S rRNA V4

Experiment attributes: [\(show all 12 attributes...\)](#)

Runs: 1 run, 19,844 spots, 3M bases, [1.7Mb](#)

Run	# of Spots	# of Bases	Size	Published
ERR12302112	19,844	3M	1.7Mb	2023-11-17

For data processing, we employed Kraken2. Upon analysis, we identified the five most prevalent species, as follows:

6.10	1211	1211	S	2211140	Acidobacteriaceae bacterium SBC82
6.08	1206	1206	S	39488	[Eubacterium] hallii
4.68	929	929	S	853	Faecalibacterium prausnitzii
3.44	683	683	S	2109690	Lachnospiraceae bacterium Choco86
2.77	550	550	S	239935	Akkermansia muciniphila

- Acidobacteriaceae bacterium: Notably, we found limited information regarding this species.
- Eubacterium hallii: Recognized for its significant role in maintaining intestinal metabolic balance. It can metabolize glucose, acetate, and lactate to produce butyrate and hydrogen. Its presence in this gut microbiome dataset is logical, aligning with our research focus.
- Faecalibacterium. prausnitzii is an important bacterium for human health but, members of this species are very sensitive to changes in gut environment which ...(Reference: <https://www.nature.com/articles/ismej2016176>)