

Pipeline Run

Pipeline user: {user-id}

Study name: {study_name}

Study link:
<{pipeline-run-url}>

Pipeline: Metatranscriptomics Pipeline

Pipeline version: v1.1

2.1 Run Duration

Start Time (UTC)	Finish Time (UTC)
{date & time}	2023-08-08 10:38:09.882861

2.2 Samples filtered out from the analysis

Note - to pass the FastQC filter samples must have a percentage GC content within a specified range (≥ 25 and $\leq 75\%$), a minimum average base quality (default 20), a minimum sequence length (default 70nt) and a minimum number of sequences (default 500).

If the table below is blank, all samples have passed filtering.

Sample name	Problem

2.3 Sequence and Contig counts

Pipeline step	Mean (SEM)	Percentage (SEM)
Starting Sequences	110000.0 (10000.00)	100
Sequences remaining after quality filtering (fastp)	108416.9 (9858.01)	98.56
Sequences remaining after human decontamination (Bowtie2)	53126.1 (5332.49)	48.30

2.4 Metatranscriptome coverage

Coverage (%)
39.40%