# Supplementary File S6. Sequencing Quality Summary Report

This file summarizes the sequencing quality and per-sample read metrics for the 10 pooled high-touch surface samples sequenced in this study (Azenta project 30-1192731958; Illumina NovaSeq X Plus, 25B flow cell, 2×150 bp). It has two parts:

### Part A — Provider sequencing statistics (Azenta)

Per-sample raw read counts, yield (Mbases), mean quality score, and percentage of bases ≥ Q30, together with the overall run statistics.

### Part B — Pre- and post-trimming quality control (MultiQC / fastp)

Aggregated per-sample quality metrics including reads passing filter, adapter content, duplication, GC content, sequence quality before and after fastp trimming, insert-size distribution, and the fraction of reads classified as human (Homo sapiens) versus microbial/unclassified. Trimming: fastp v0.24.0; host removal: bwa-mem2 v2.2.1 against GRCh38; taxonomic classification: Kraken2 v2.17.1 (database k2_pluspf_20250714).

*Note: read counts are reported as sequenced by the provider; Kraken2 processes paired reads, so classification counts are expressed in read pairs elsewhere in the manuscript. The per-pool host fraction plotted in Figure 1 and tabulated in Supplementary Table S4 is derived from bwa-mem2 alignment to GRCh38 and is methodologically distinct from the Kraken2-based "% Homo sapiens" column reported below.*

# AZENTA NGS DATA REPORT

## 1. PROJECT SUMMARY

| | |
|---|---|
| Customer | Mohamad Taisir Ghiba |
| Email | 443105998@student.ksu.edu.sa |
| Sample | |
| QuoteNumber | 30-1192731958 |
| Configuration | Illumina 2x150bp |

## 2. SAMPLE SEQUENCING STATISTICS

Show 10 entries Search:

Table 2.1 Sample Sequencing Statistics

| Project | Sample ID | Barcode Sequence | # Reads | Yield (Mbases) | Mean Quality Score | % Bases >= 30 |
|---|---|---|---|---|---|---|
| 30-1192731958 | CP18 | ACATACAC+AGCACAAG | 19,183,830 | 5,755 | 38.50 | 92.75 |
| 30-1192731958 | AP5 | TATCAGTA+TTACTACT | 18,520,878 | 5,556 | 38.61 | 93.25 |
| 30-1192731958 | AP9 | TTTCCATC+TCCGAATG | 18,745,092 | 5,624 | 37.92 | 90.00 |
| 30-1192731958 | HP10 | CAAGAAGT+CGACTAGG | 18,836,098 | 5,651 | 38.60 | 93.20 |
| 30-1192731958 | HP6 | ACACGTAT+TTACATCG | 18,393,883 | 5,518 | 38.65 | 93.42 |
| 30-1192731958 | AP7 | CGAGTCAG+CCTTAGTA | 19,538,103 | 5,862 | 38.54 | 92.93 |
| 30-1192731958 | HP2 | GCTTAAGT+TGTTTACT | 19,096,697 | 5,729 | 38.52 | 92.90 |
| 30-1192731958 | CP8 | CCAATGAA+TAGCTCAC | 24,730,059 | 7,419 | 36.87 | 84.87 |
| 30-1192731958 | CP17 | ATCAGTTG+CCCGCGTT | 18,833,688 | 5,650 | 38.32 | 91.86 |
| 30-1192731958 | CP20 | CTCCATAT+GGGTAAGC | 20,709,688 | 6,213 | 38.47 | 92.52 |

Select Columns Download

Showing 1 to 10 of 10 entries Previous 1 Next

## 3. OVERALL SEQUENCING STATISTICS

Table 3.1 Overall Sequencing Statistics

| Project | # Reads | Yield (Mbases) | Mean Quality Score | % Bases >= 30 |
|---|---|---|---|---|
| 30-1192731958 | 196,588,016 | 58,977 | 38.26 | 91.57 |

## 4. FAQS

If you have any further questions or concerns, please consider examining our FAQ page located here.

Azenta Life Sciences
Next Generation Sequencing
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MultiQC

A modular tool to aggregate results from bioinformatics analyses across many samples into a single report.

Report generated on 2025-11-25, 09:56 +03 based on data in: `/ssr/analysis/Virology_Ghiba/processed_data`

# General Statistics

Copy table | Configure Columns | Plot | Showing 20/20 rows and 8/10 columns.

| Sample Name | % Homo sapiens | % Top 5 Species | % Unclassified | % Duplication | M Reads After Filtering | GC content | % PF | % Adapter |
|---|---|---|---|---|---|---|---|---|
| AP5_R1_001 | | | | 31.0% | 35.2 | 53.5% | 94.9% | 20.6% |
| AP5_krak | 41.0% | 53.9% | 8.0% | | | | | |
| AP7_R1_001 | | | | 34.8% | 36.5 | 52.5% | 93.5% | 24.0% |
| AP7_krak | 39.6% | 51.6% | 8.7% | | | | | |
| AP9_R1_001 | | | | 42.9% | 32.3 | 53.0% | 86.1% | 24.2% |
| AP9_krak | 22.7% | 27.5% | 50.7% | | | | | |
| CP17_R1_001 | | | | 34.1% | 35.2 | 57.9% | 93.3% | 17.3% |
| CP17_kral | 26.9% | 27.3% | 24.2% | | | | | |
| CP18_R1_001 | | | | 23.9% | 36.7 | 50.7% | 95.8% | 17.3% |
| CP18_kral | 51.3% | 53.1% | 23.6% | | | | | |
| CP20_R1_001 | | | | 36.3% | 38.9 | 53.9% | 93.9% | 12.6% |
| CP20_kral | 22.8% | 33.7% | 14.6% | | | | | |
| CP8_R1_001 | | | | 46.8% | 33.5 | 56.8% | 67.7% | 32.4% |
| CP8_krak | 15.3% | 21.8% | 37.6% | | | | | |
| HP10_R1_001 | | | | 28.3% | 35.9 | 53.7% | 95.2% | 19.2% |
| HP10_kral | 45.3% | 54.8% | 6.6% | | | | | |
| HP2_R1_001 | | | | 32.8% | 36.0 | 50.5% | 94.2% | 20.3% |
| HP2_krak | 60.9% | 64.3% | 7.2% | | | | | |
| HP6_R1_001 | | | | 35.6% | 34.7 | 47.5% | 94.2% | 19.4% |

| Sample Name | % Homo sapiens | % Top 5 Species | % Unclassified | % Duplication | M Reads After Filtering | GC content | % PF | % Adapter |
|---|---|---|---|---|---|---|---|---|
| HP6_krak | 66.8% | ort | 69.3% | 5.1% | | | | |

# Kraken

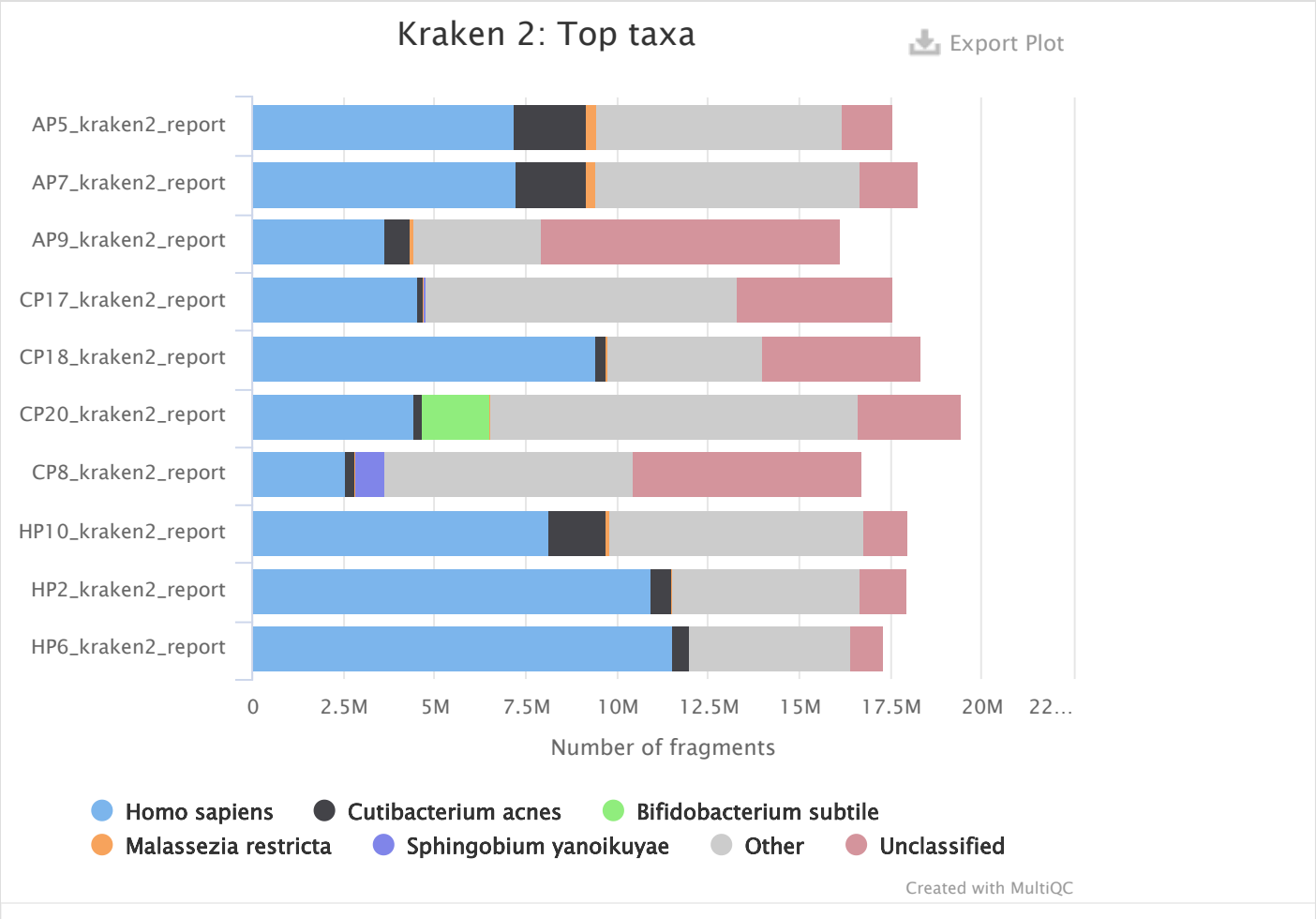
Kraken is a taxonomic classification tool that uses exact k-mer matches to find the lowest common ancestor (LCA) of a given sequence. *DOI: 10.1186/gb-2014-15-3-r46.*

## Top taxa

The number of reads falling into the top 5 taxa across different ranks.

Counts | Percentages

Species | Genus | Family | Order | Class | Phylum | Kingdom | Domain | Root



# fastp

fastp An ultra-fast all-in-one FASTQ preprocessor (QC, adapters, trimming, filtering, splitting...). *DOI: 10.1093/bioinformatics/bty560.*

## Filtered Reads

Filtering statistics of sampled reads.

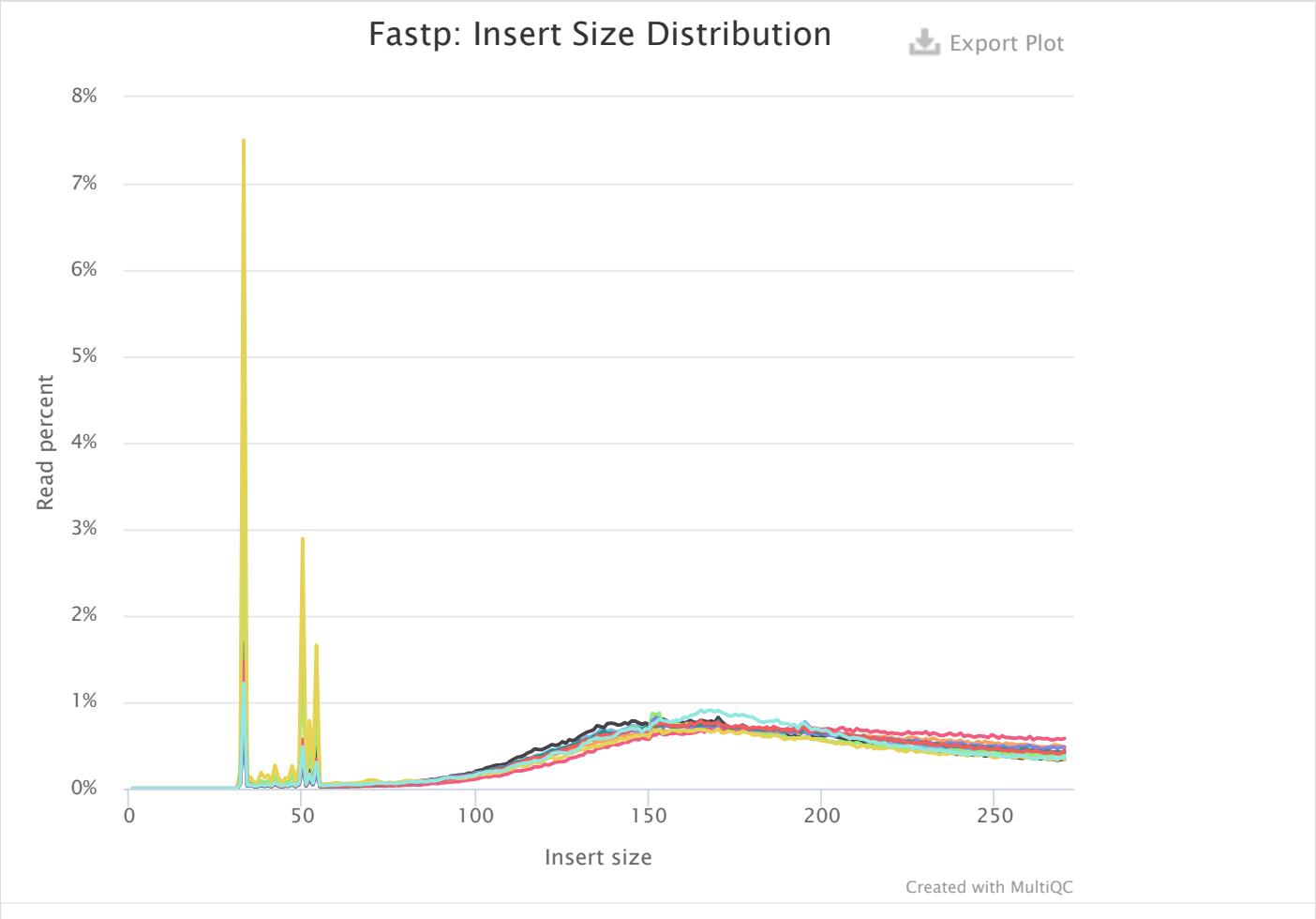
Number of Reads | Percentages



# Insert Sizes

Insert size estimation of sampled reads.

Y-Limits: on

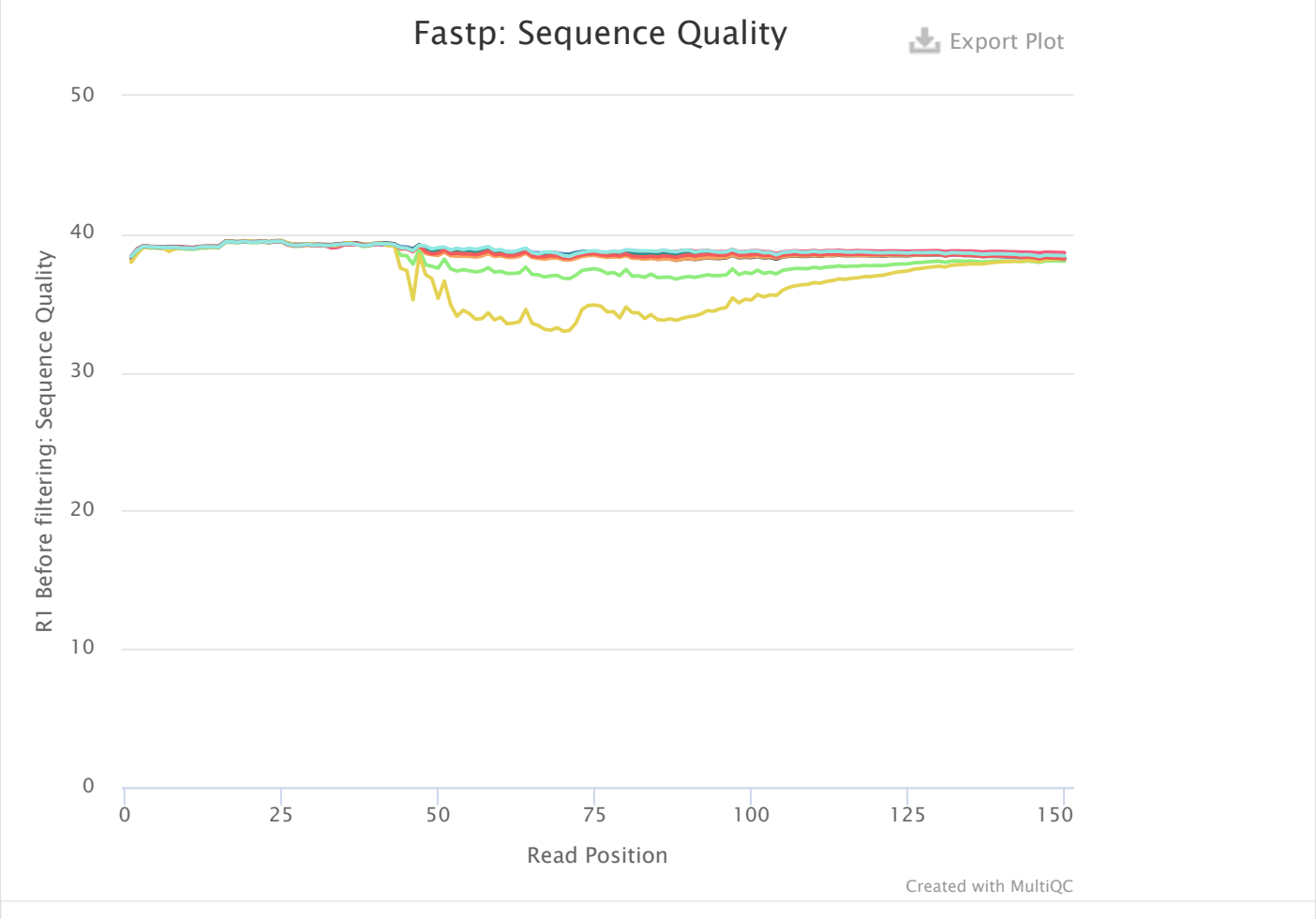


# Sequence Quality

Average sequencing quality over each base of all reads.

Y-Limits: on

Read 1: Before filtering | Read 1: After filtering | Read 2: Before filtering | Read 2: After filtering

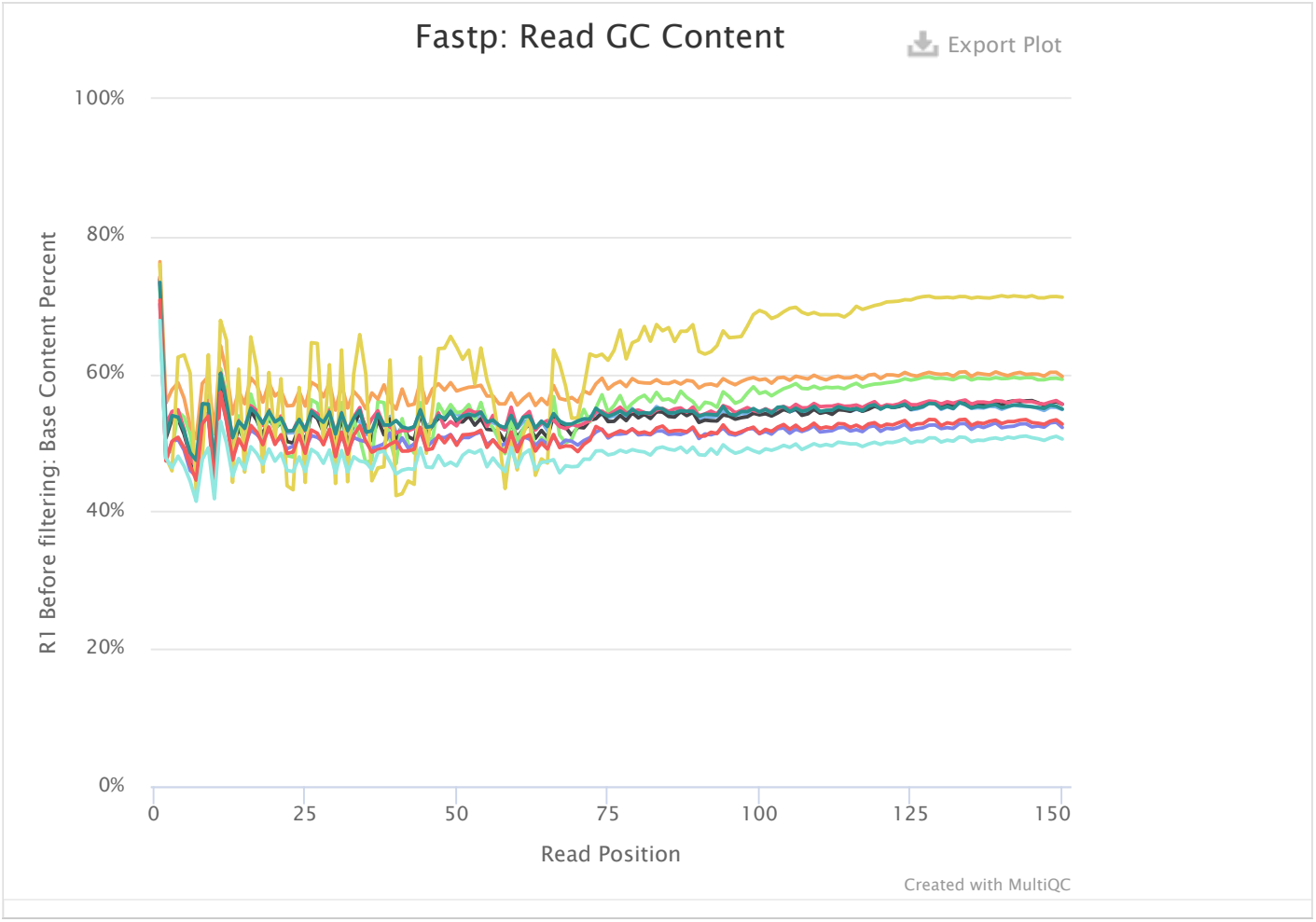


# GC Content

Average GC content over each base of all reads.

Y-Limits: on

Read 1: Before filtering | Read 1: After filtering | Read 2: Before filtering | Read 2: After filtering

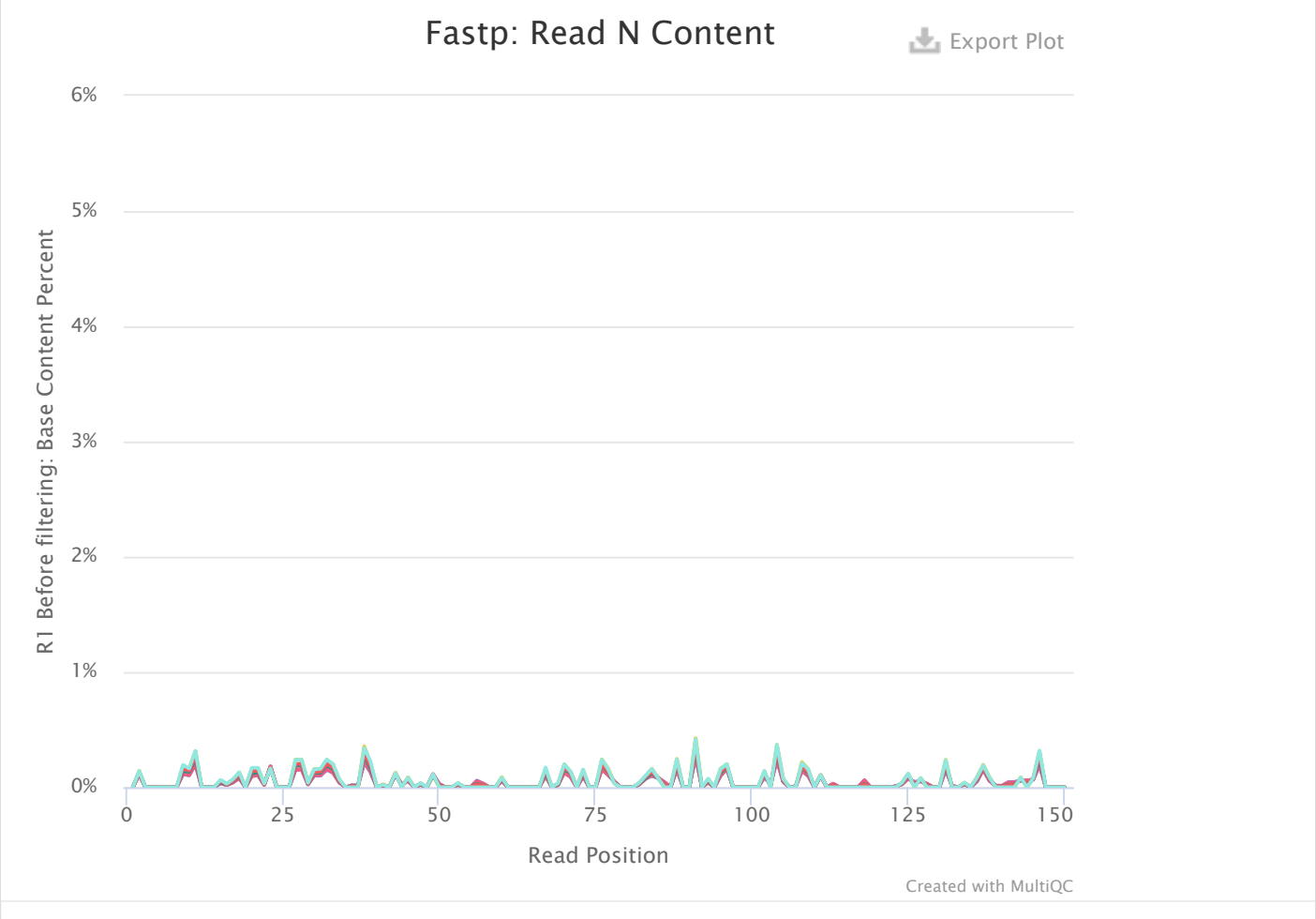


# N content

Average N content over each base of all reads.

Y-Limits: on

Read 1: Before filtering | Read 1: After filtering | Read 2: Before filtering | Read 2: After filtering




**MultiQC v1.14** - Written by Phil Ewels, available on GitHub.
This report uses HighCharts, jQuery, jQuery UI, Bootstrap, FileSaver.js and clipboard.js.

seqeralabs