



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

Report generated on 2025-11-07, 11:07 GMT based on data in: /data/home/ha25679/20251103-DNAseq/QC

General Statistics

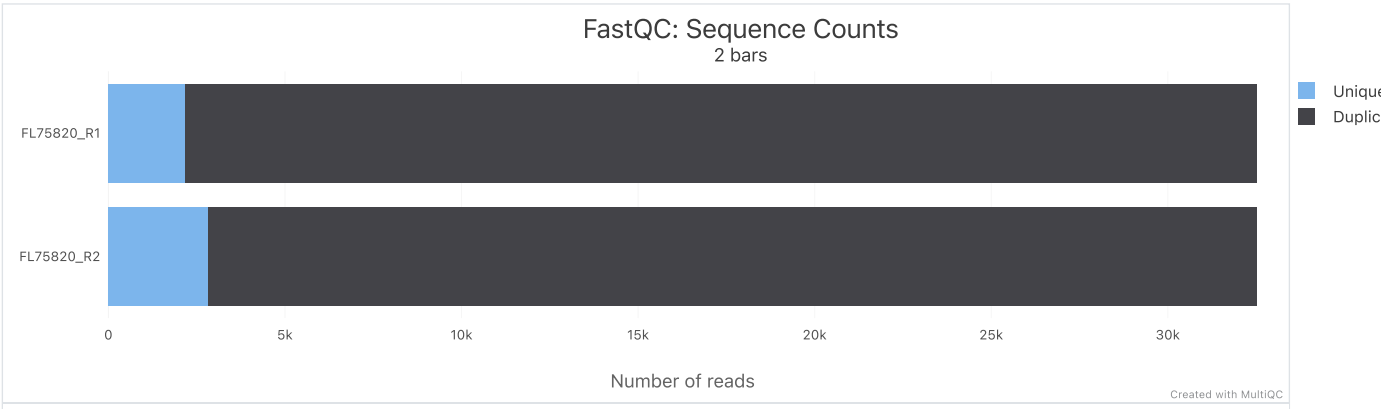
Sample Name	Dups	GC	Seqs
FL75820_R1	93.3 %	55.0 %	0.0 M
FL75820_R2	91.3 %	54.0 %	0.0 M

FastQC Version: 0.12.1

Quality control tool for high throughput sequencing data. <http://www.bioinformatics.babraham.ac.uk/projects/fastqc>

Sequence Counts

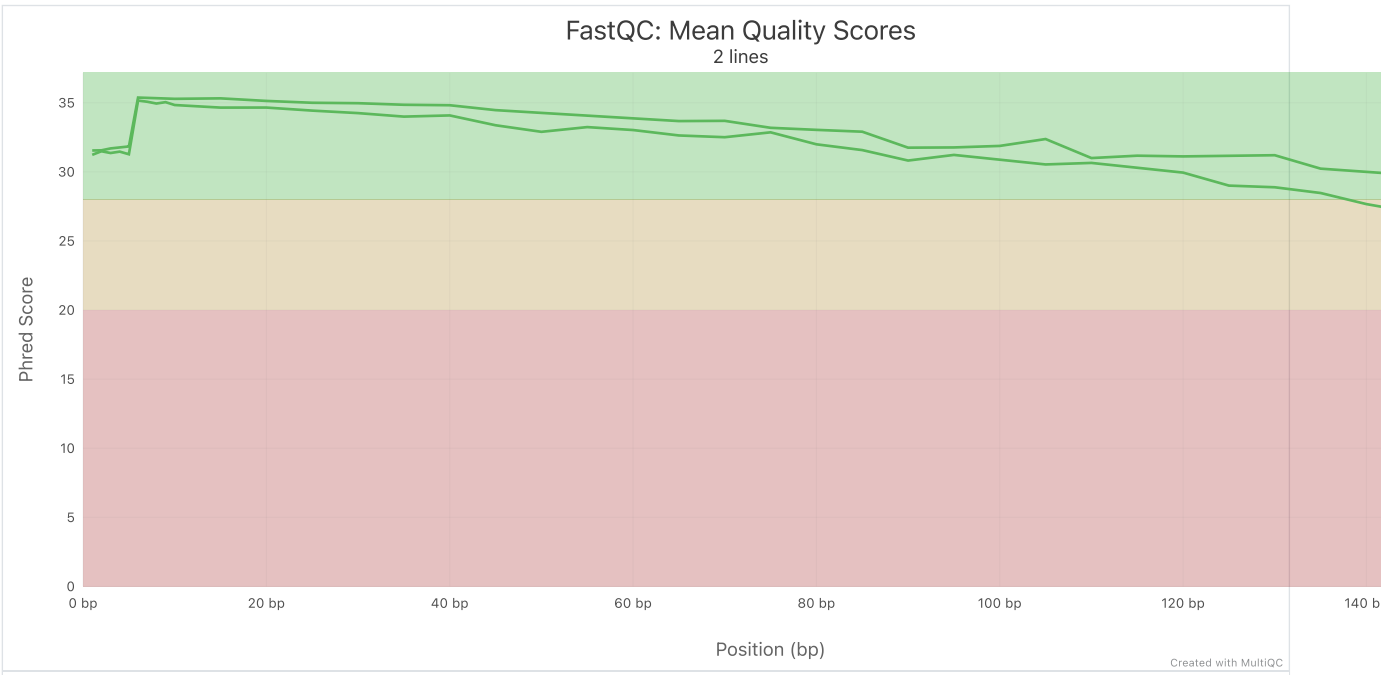
Sequence counts for each sample. Duplicate read counts are an estimate only.



Sequence Quality Histograms

2

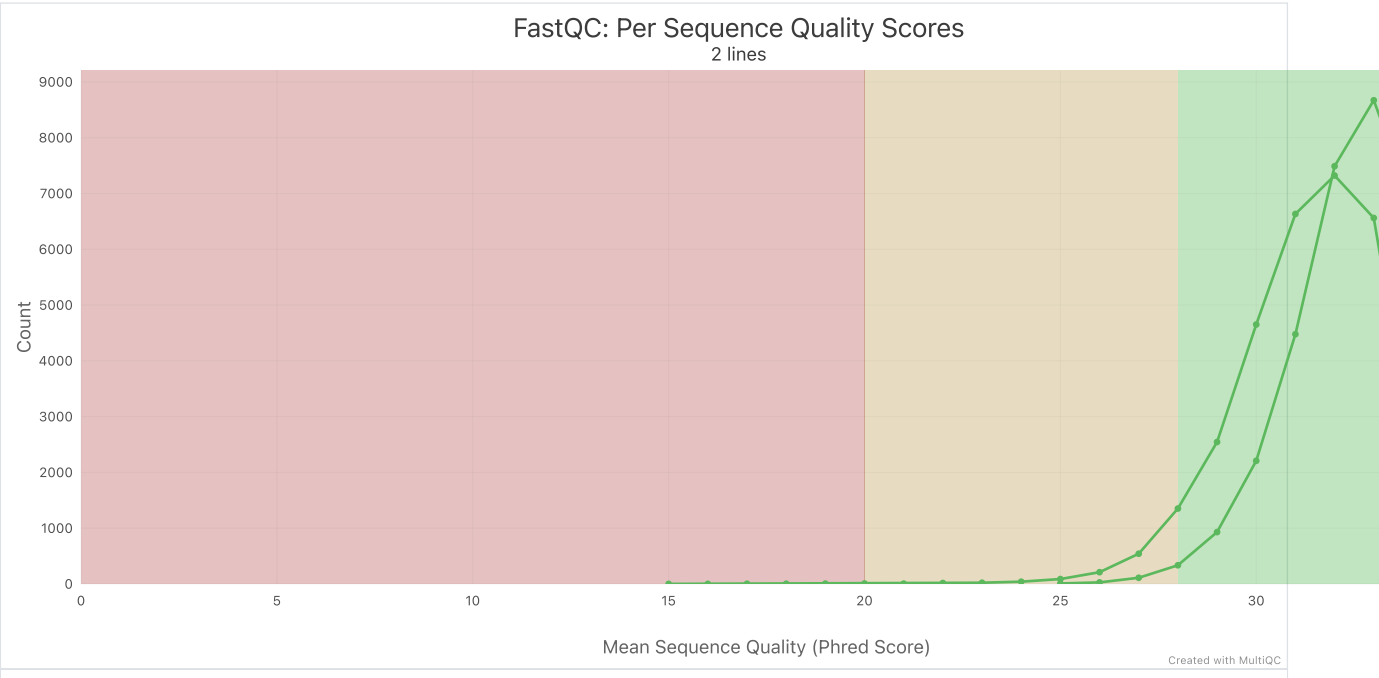
The mean quality value across each base position in the read.



Per Sequence Quality Scores

2

The number of reads with average quality scores. Shows if a subset of reads has poor quality.

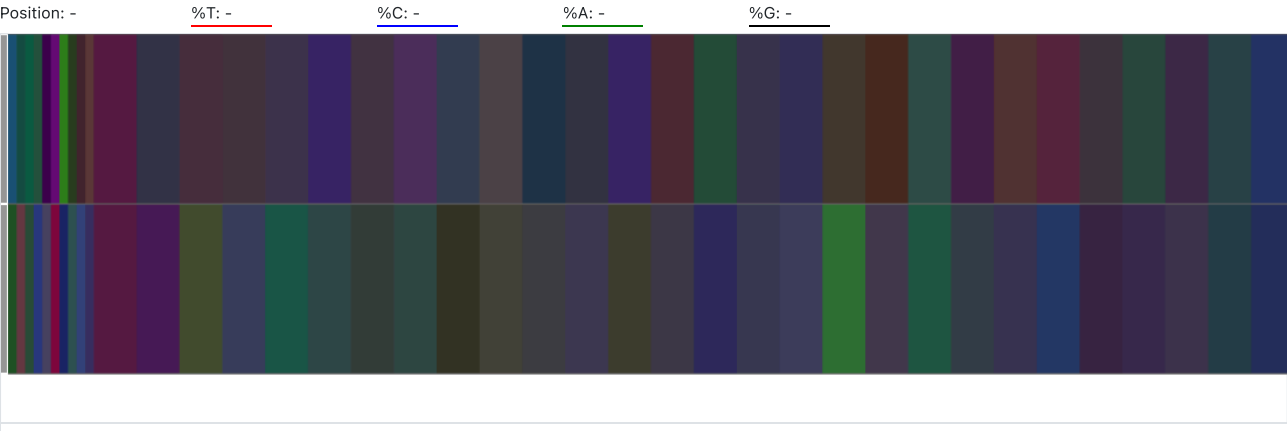


Per Base Sequence Content

The proportion of each base position for which each of the four normal DNA bases has been called.

\$👇 Click a sample row to see a line plot for that dataset.

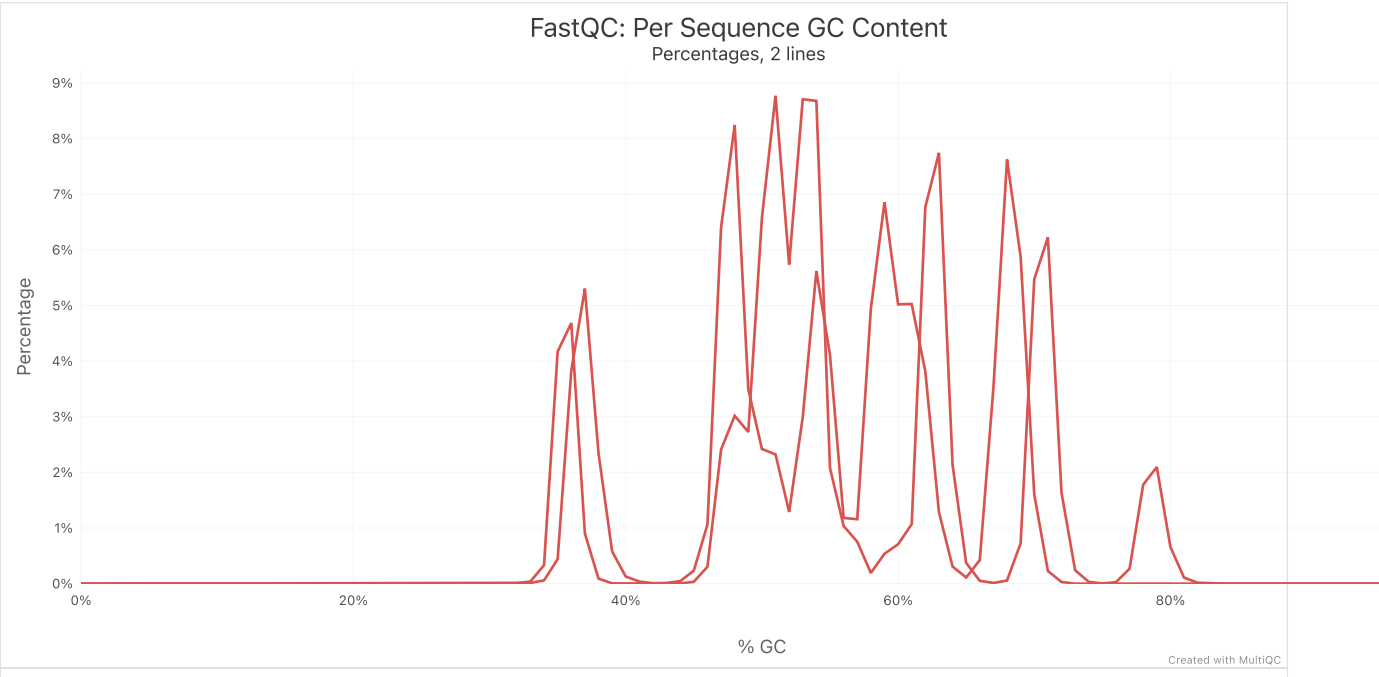
Rollover for sample name



Per Sequence GC Content

2

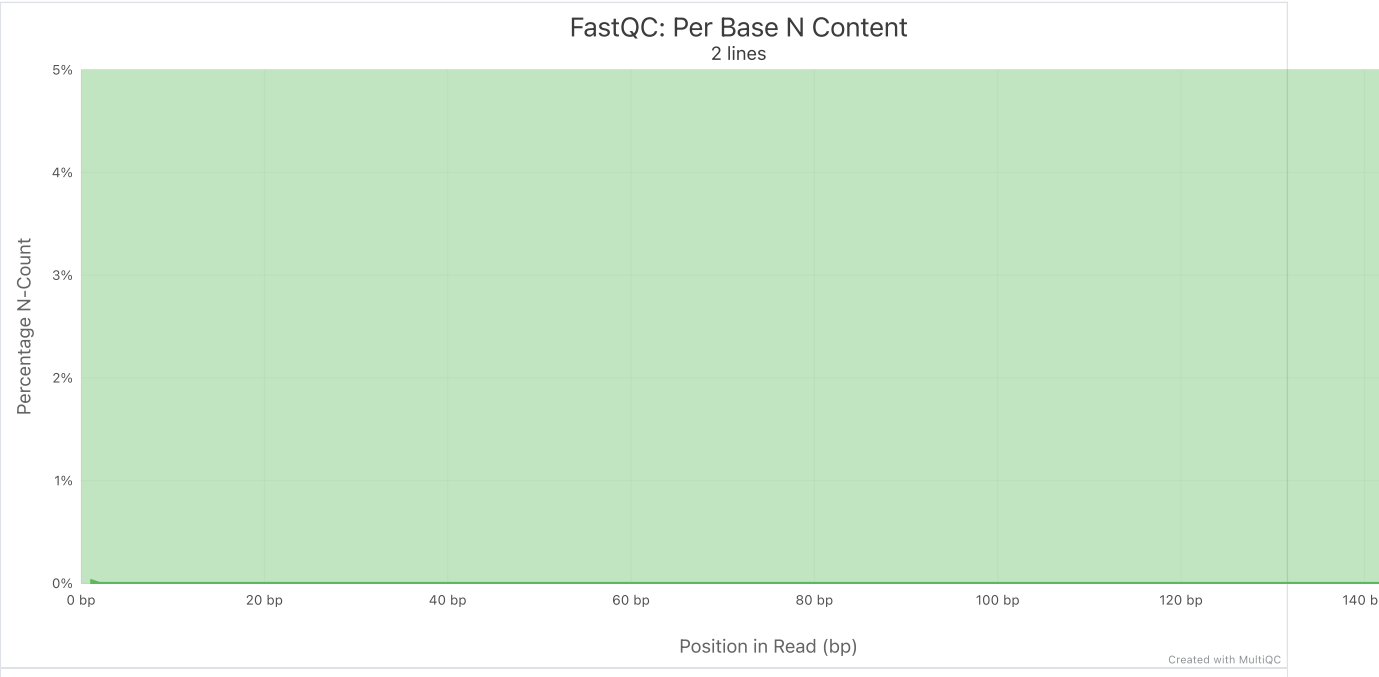
The average GC content of reads. Normal random library typically have a roughly normal distribution of GC content.



Per Base N Content

2

The percentage of base calls at each position for which an N was called.



Sequence Length Distribution

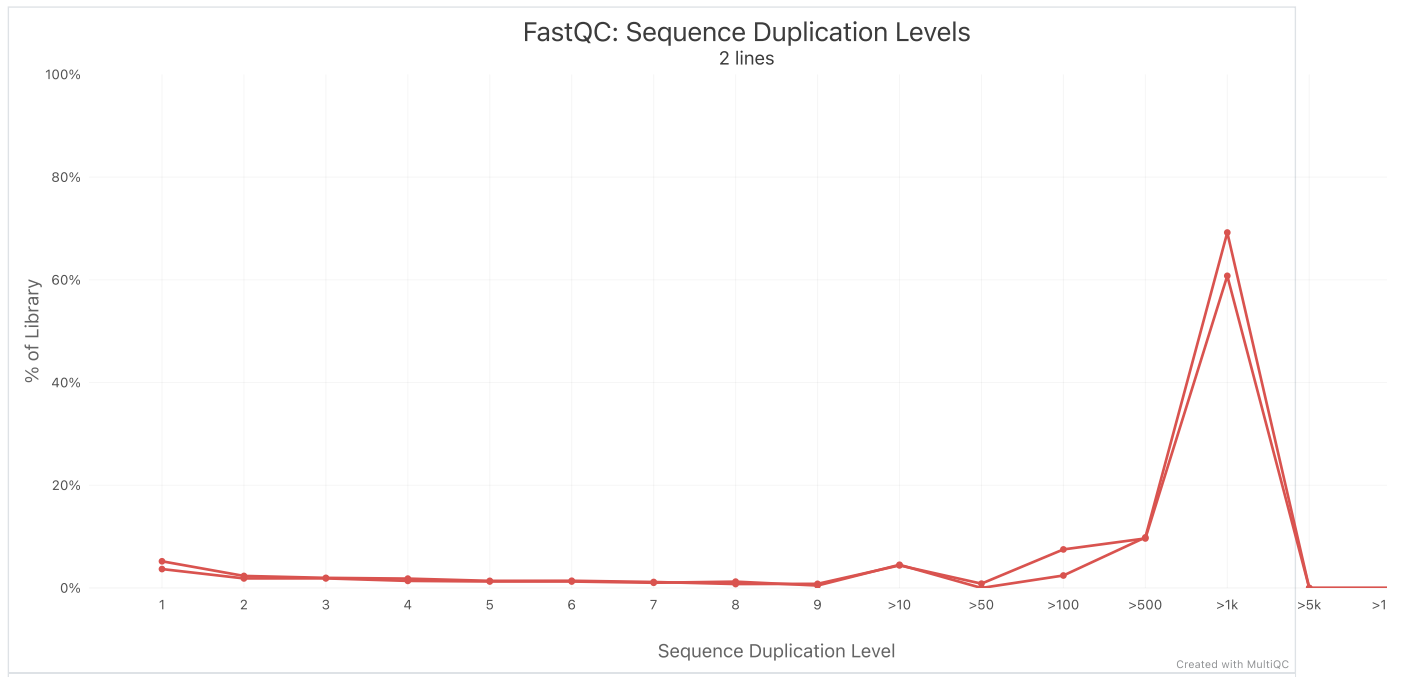
2

All samples have sequences of a single length (151bp)

Sequence Duplication Levels

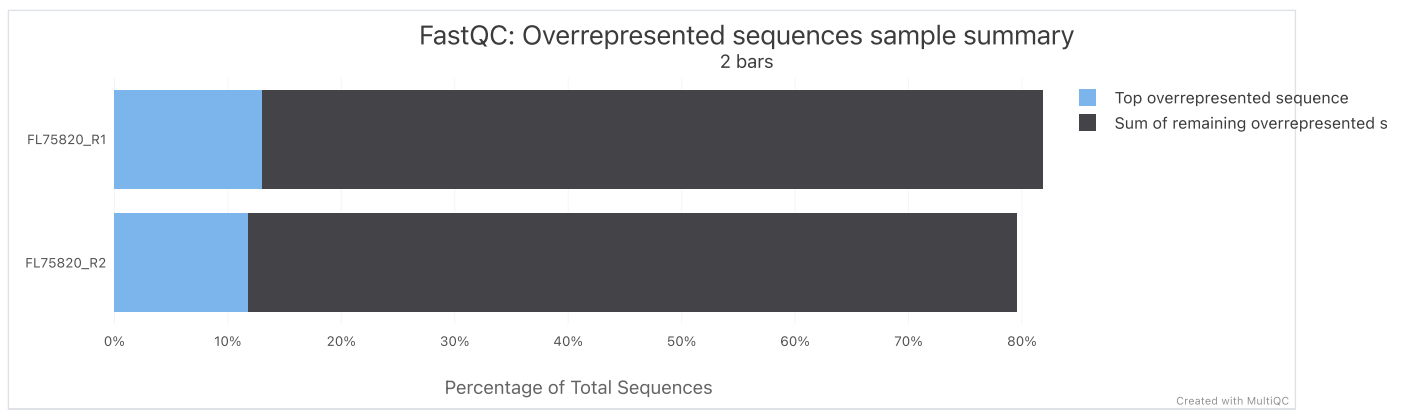
2

The relative level of duplication found for every sequence.



Overrepresented sequences by sample

The total amount of overrepresented sequences found in each library.



Top overrepresented sequences

Top overrepresented sequences across all samples. The table shows 20 most overrepresented sequences across all samples, ranked by the number of samples they occur in.

Overrepresented sequence	Reports ▾	Occurrences ▾	% of all reads
CCACTCAGTTTTCTTTCTCTGGCTTTGGGACCTCTTAACCTGTGGCTTC	4	231	6.5060 %
AGAGCTGAGGAAGCCGGCGCCAGTTCGCGGGGCTCCGGGCCGCCACTCA	3	87	6.1308 %
GCACCTCAAAGCTGTTCCGTCCCAGTAGATTACCACTACTCAGGATAGGA	3	837	5.9002 %
GTCCTCAGCGTCGCGCTTGTCTGTGAAGCGAACGAAGCGAAGCCGCGG	3	679	5.6572 %
CACAGCAGGCCAGTGTGCAGGGTGCCAAGTGGCTCCTGACCTGGAGTCTT	3	638	5.5942 %
AGGTGTATTAATCCATTTTCAACTTACAATATTTTCAACTTACGACGAG	2	749	4.2271 %
AGGAGCTGGTGTGTTGGGCGAGTGCTAGGAAAGAGGCAAGGAAAGGTGA	2	188	3.3645 %
TCCAGTTGCTTTATCTGTTCACCTTGTGCCCTGACTTTCAACTCTGTCTCC	1	1572	2.4173 %
GAAGCGAAAATTCCATGGGACTGAOTTTCTGCTCTTGTCTTTCAGACTTC	1	1529	2.3512 %
GAGGCTGTCAGTGGGGAACAAGAAGTGGAGAATGTCAGTCTGAGTCAGGC	1	314	2.0205 %
CCGCCTCCCGGGTCCCCTCAGCCCGGTTTACCTGCGGCTCCGGCGCTCC	1	297	1.9944 %
CTCCTCCAGAGACCCAGTTGCAATACCAGACCTCAGGCGGCTCATAGG	1	389	1.5208 %
CTTTTATCACCTTTCCTTGCCTCTTTCCTAGCACTGCCCAACAACACCAG	1	947	1.4562 %
TAGGGCCAGGAAGGGGCTGAGGTCACTCACCTGGAGTGAGCCCTGCTCC	1	385	1.0533 %
CACAGCAGGCCAGTGTGCACGGTGCCAAGTGGCTCCTGACCTGGAGTCT	1	178	0.8888 %
TTCAGGAAGTCTGAAAGACAAGAGCAGAAAGTCAGTCCCATGGAATTTT	1	213	0.6351 %
CATGGAAGCCAGCCCTCAGGGCAACTGACCGTGCAAGTCACAGACTTC	1	376	0.5782 %
CCGCCACCCGCGGTCCCCTCAGCCCGGTTTACCTGCGGCTCCGGCGCTCC	1	25	0.0707 %
CCACTCAGTTTTCTTTCTCTGGCTTTGGGACCTCTTAACCTGTGGCTTC	1	33	0.0507 %
TAGAGCTGAGGAAGCCGGCGCCAGTTCGCGGGGCTCCGGGCCGCCACTCA	1		0.0507 %

Adapter Content

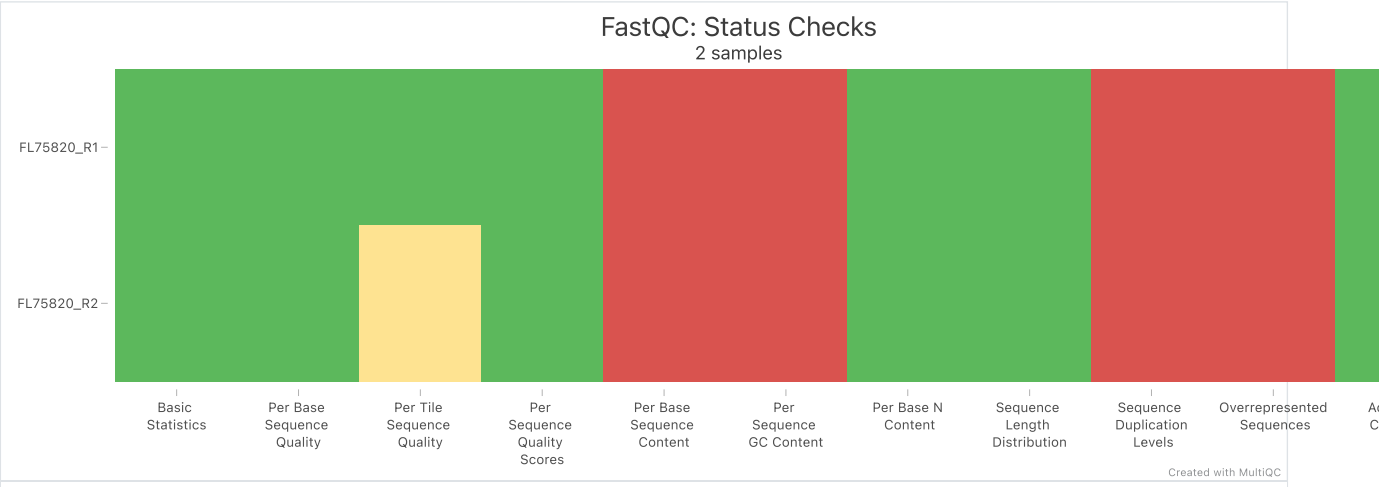
2

The cumulative percentage count of the proportion of your library which has seen each of the adapter sequences at each position.

No samples found with any adapter contamination > 0.1%

Status Checks

Status for each FastQC section showing whether results seem entirely normal (green), slightly abnormal (orange) or very unusual (red).



Software Versions

Software Versions lists versions of software tools extracted from file contents.

Software	Version
FastQC	0.12.1

MultiQC v1.32 - Written by [Phil Ewels](#), available on [GitHub](#).
This report uses [Plotly](#), [jQuery](#), [jQuery UI](#), [Bootstrap](#) and [FileSaver.js](#).

