

General Stats

FastQC

Sequence Counts

Sequence Quality Histograms

Per Sequence Quality Scores

Per Base Sequence Content

Per Sequence GC Content

Per Base N Content

Sequence Length Distribution

Sequence Duplication Levels

Overrepresented sequences

Adapter Content



(<http://multiqc.info>)

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

Report generated on 2019-05-08, 17:22 based on data in: /home/stan/FinalProject/fastqc

General Statistics

Copy table

Configure Columns

Plot

Showing 44/44 rows and 4/5 columns.

Sample Name	% Dups	% GC	Length	M Seqs
SRR8489594				
SRR8489595				
SRR8489596				
SRR8489597				
SRR8489598				
SRR8489603				
SRR8489604				
SRR8489605				
SRR8489606				
SRR8489608				
SRR8489614_1				
SRR8489614_2				
SRR8489617_2				
SRR8489619_1				
SRR8489620_1				



FastQC

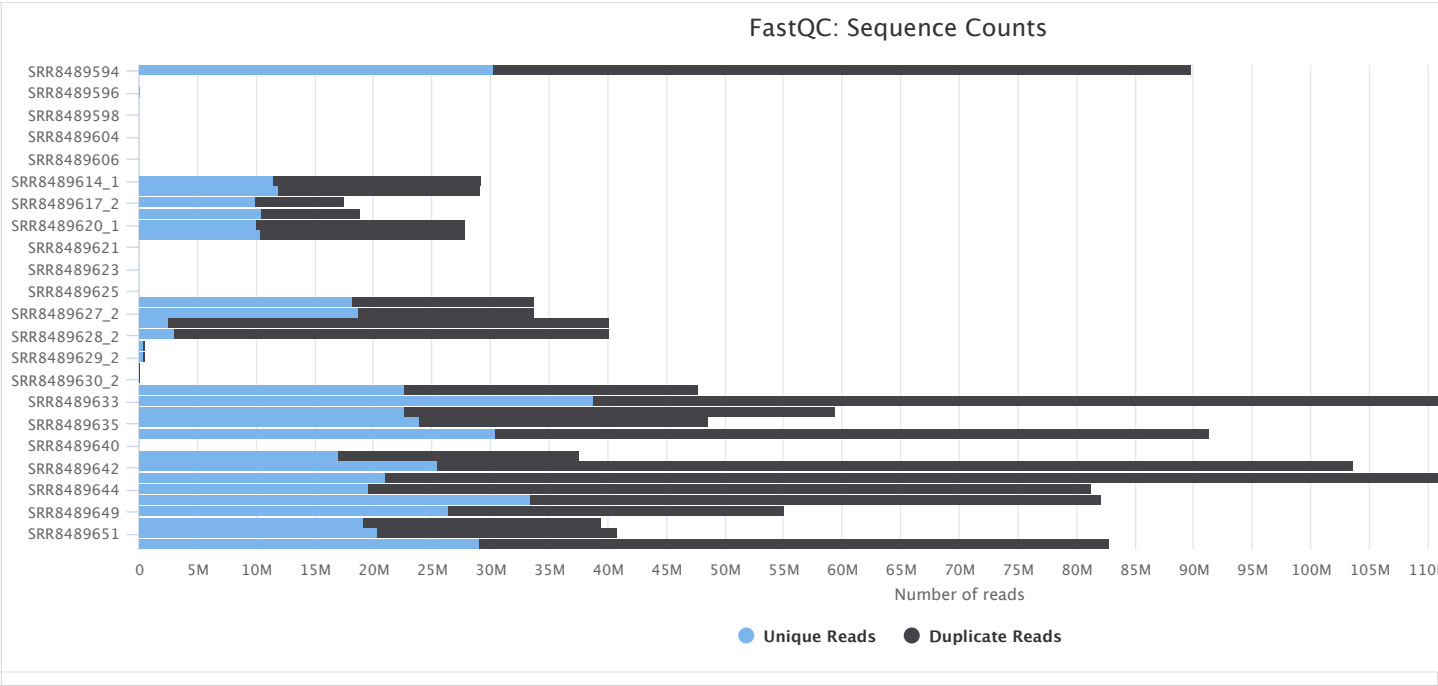
Sequence Counts

Help

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

Number of reads

Percentages



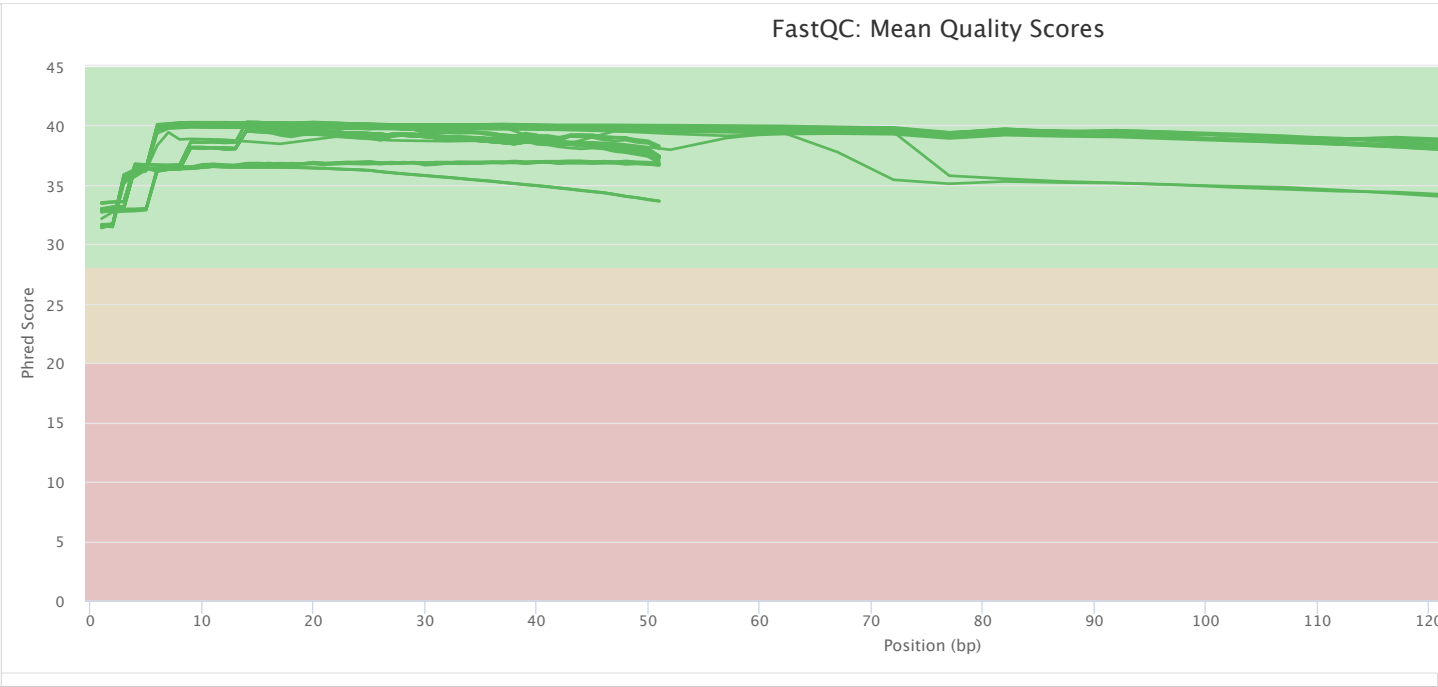
Sequence Quality Histograms

44

Help

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

Y-Limits: ☒ on



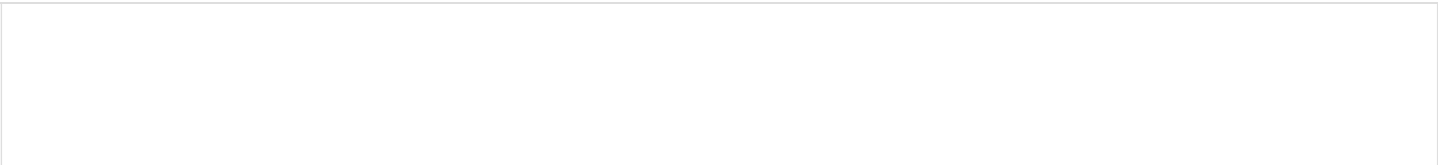
Per Sequence Quality Scores

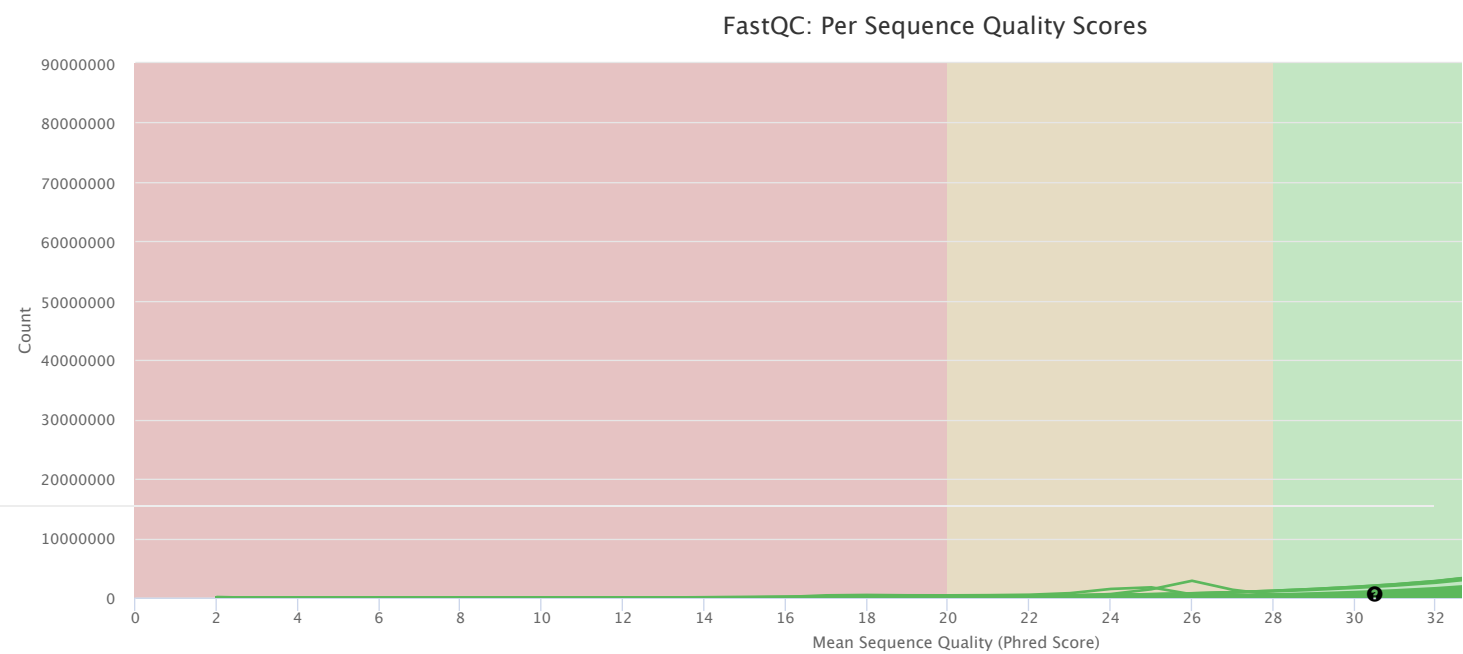
44

Help

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

Y-Limits: ☐ on





🖱️ Click a sample row to see a line plot for that dataset.

📘 Rollover for sample name

Position: -

%T: -

%C: -

%A: -

%G: -

📄 Export Plot

Per Sequence GC Content

3482

📘 Help

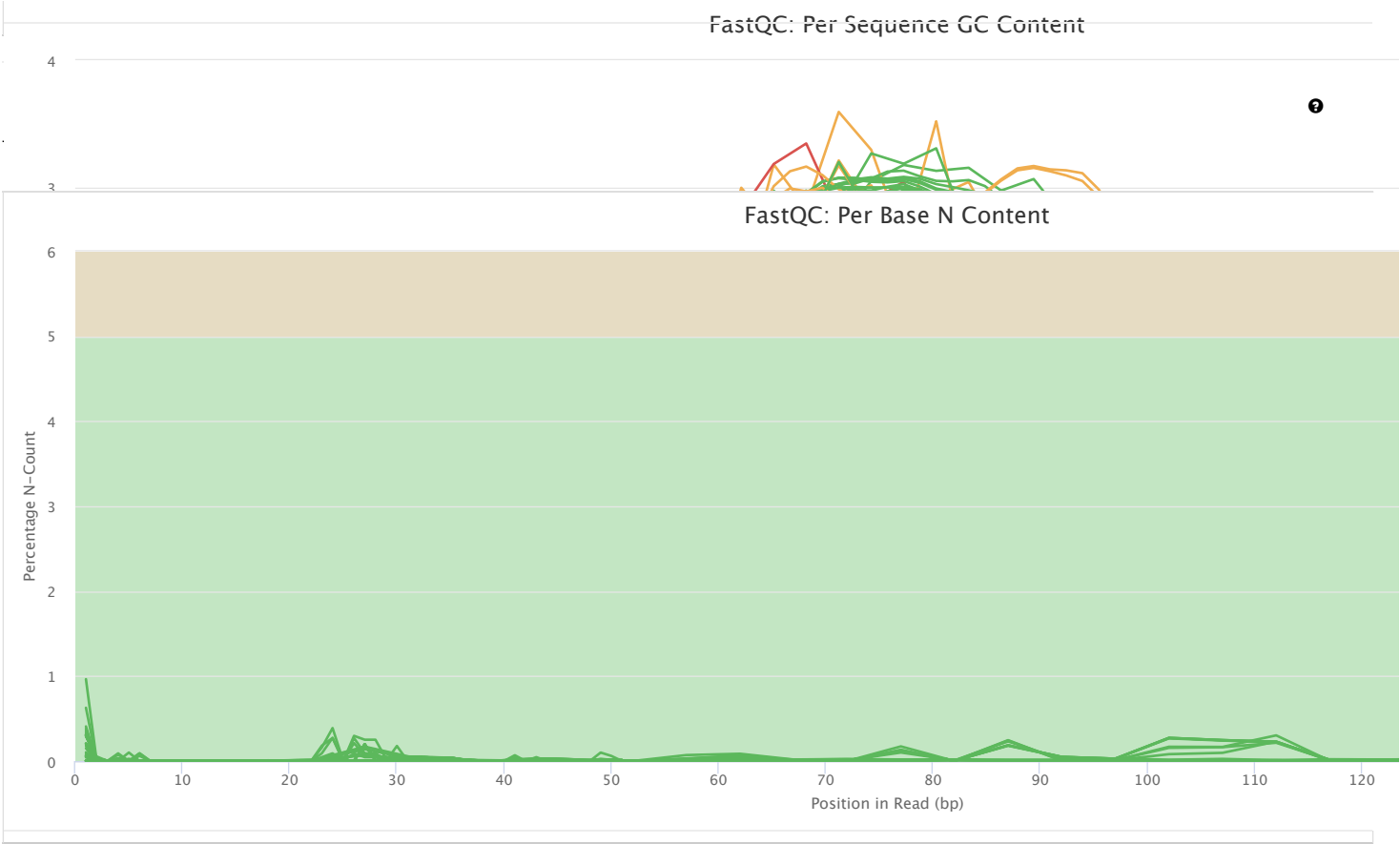
The average GC content of reads. Normal random library typically have a roughly normal distribution of GC content.

Y-Limits: on

Percentages

Counts





Sequence Length Distribution

44

All samples have sequences of a single length (51bp , 151bp). See the General Statistics Table.

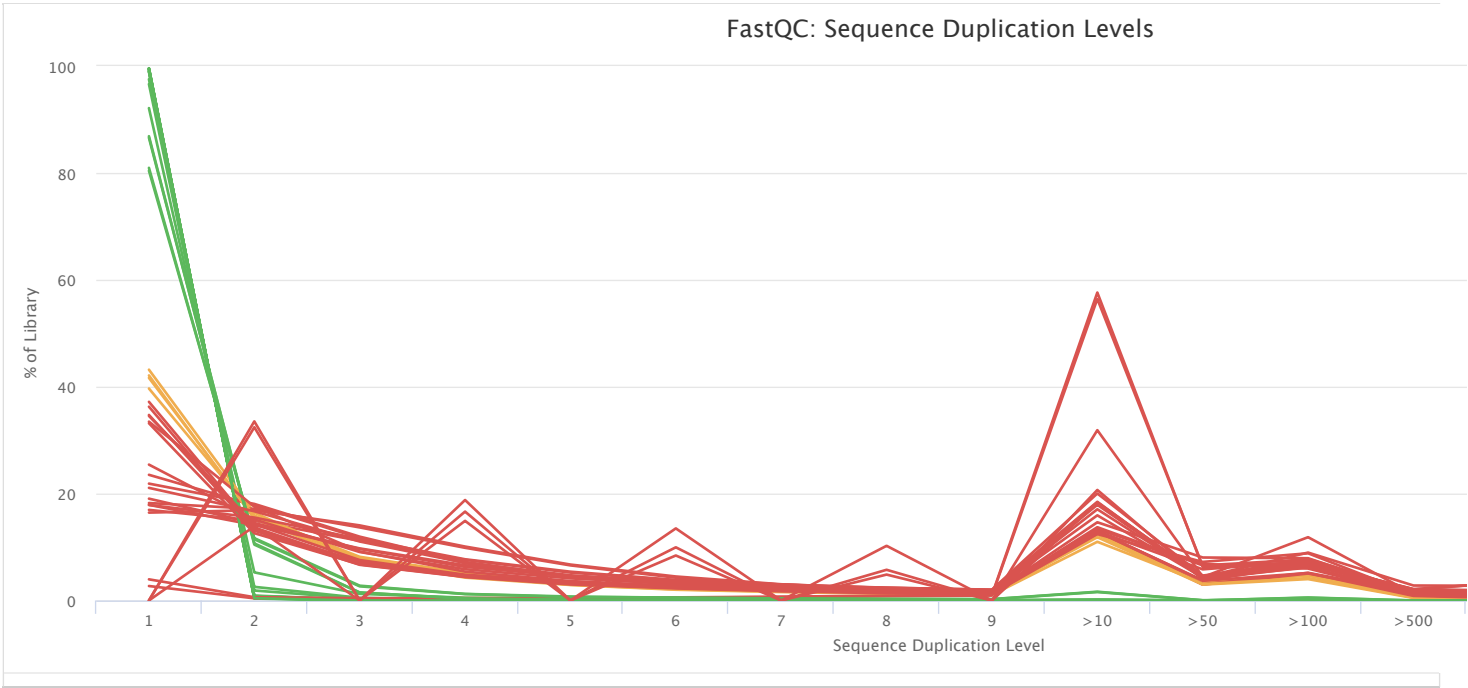
Sequence Duplication Levels

19 4 21

The relative level of duplication found for every sequence.

Help

Y-Limits: on



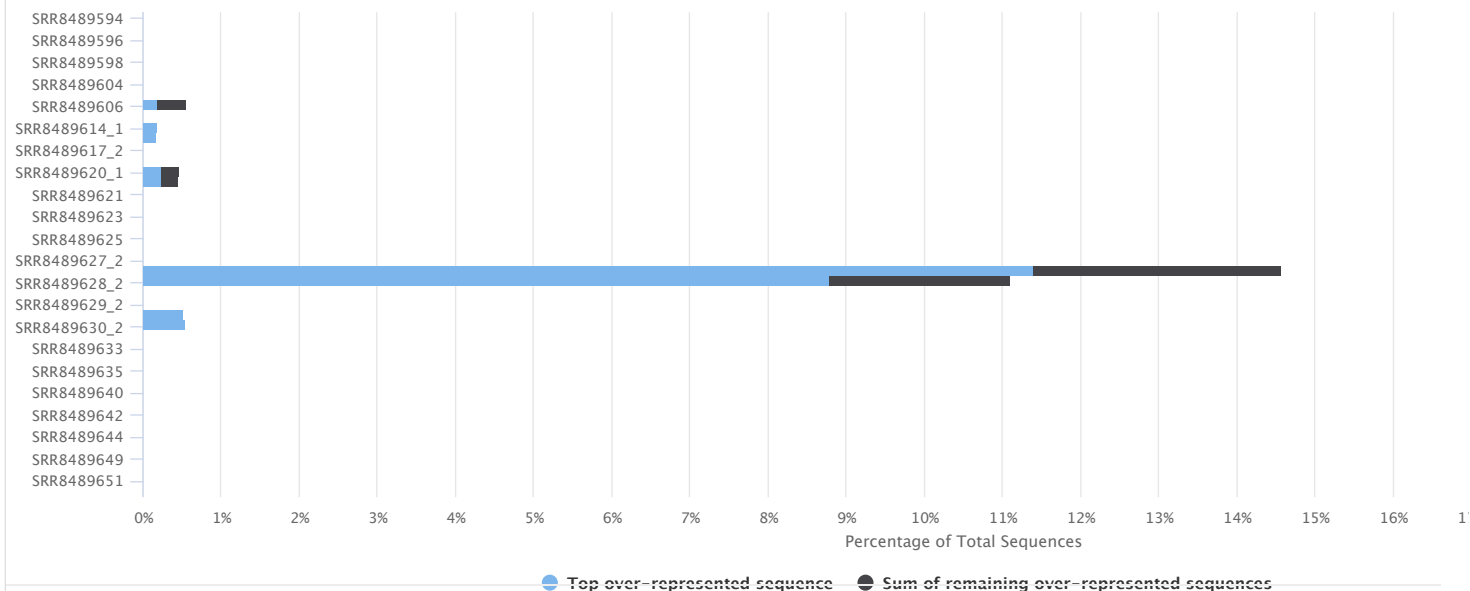
Overrepresented sequences

35 7 2

The total amount of overrepresented sequences found in each library.

Help

## FastQC: Overrepresented sequences



## Adapter Content

30 014

Help

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

Y-Limits: ☐ on

## FastQC: Adapter Content

