

MultiQC

(<http://multiqc.info>)

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

Report generated on 2022-01-23, 19:54 based on data in: `/media/data04/gaye/workspace/rnaseq/alignments2/hisat2`

General Statistics

Copy tableConfigure ColumnsPlotShowing 6/6 rows and 4/6 columns.

Sample Name	% Aligned	% Dups	% GC	M Seqs
SRR12424243				
SRR12424244				
SRR12424245				
SRR12424255				
SRR12424256				
SRR12424257				

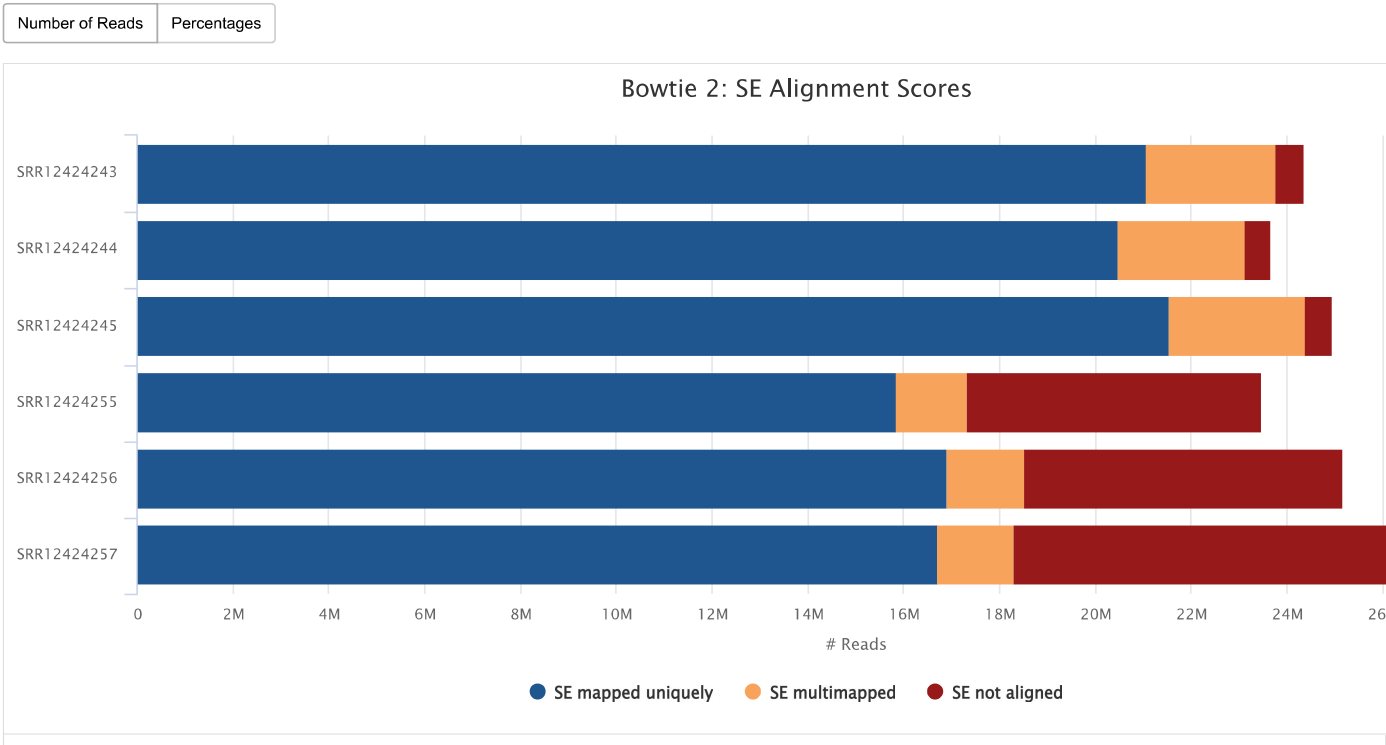
Bowtie 2 / HiSAT2

Bowtie 2 (<http://bowtie-bio.sourceforge.net/bowtie2/>) and HISAT2 (<https://ccb.jhu.edu/software/hisat2/>) are fast and memory-efficient tools for aligning sequencing reads against a reference genome. Unfortunately both tools have identical log output by default, so it is impossible to distinguish which tool was used.

Single-end alignments

Help

This plot shows the number of reads aligning to the reference in different ways.



FastQC

FastQC (<http://www.bioinformatics.babraham.ac.uk/projects/fastqc/>) is a quality control tool for high throughput sequence data, written by Simon Andrews at the Babraham Institute in Cambridge.

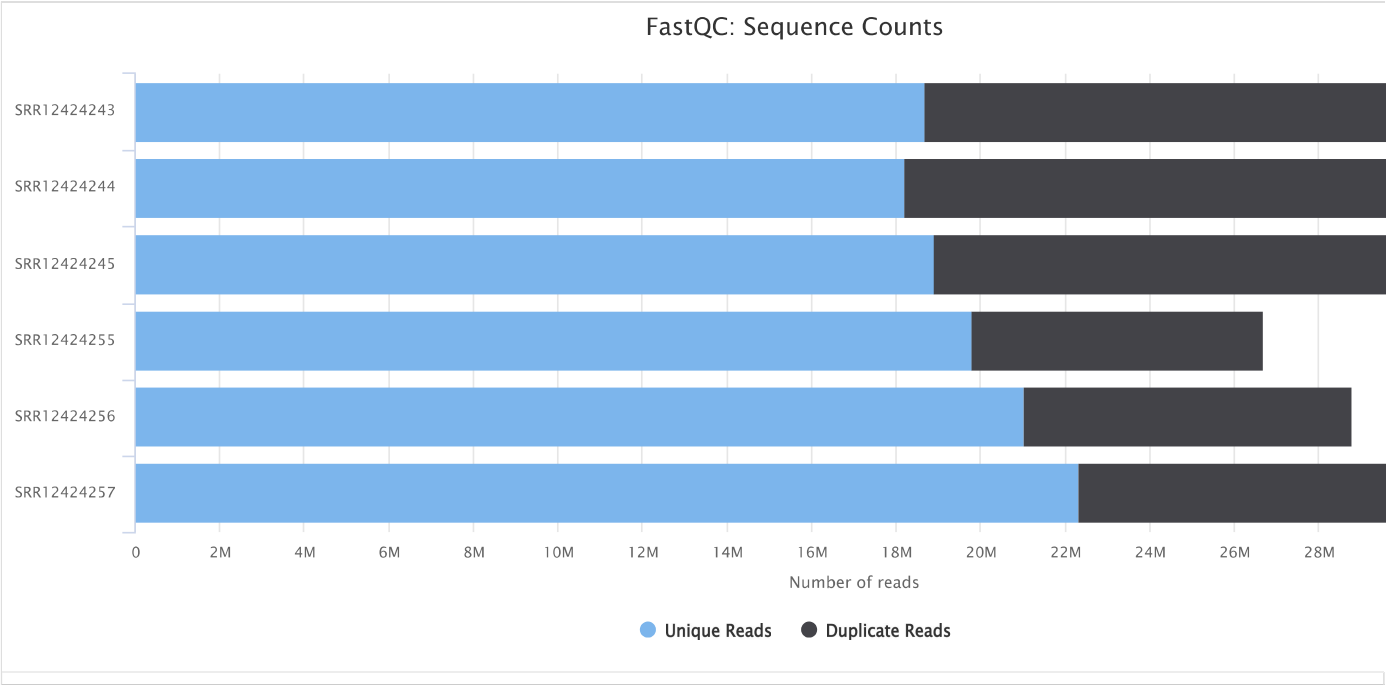
Sequence Counts

[Help](#)

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

Number of reads

Percentages



Sequence Quality Histograms

6

[Help](#)

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



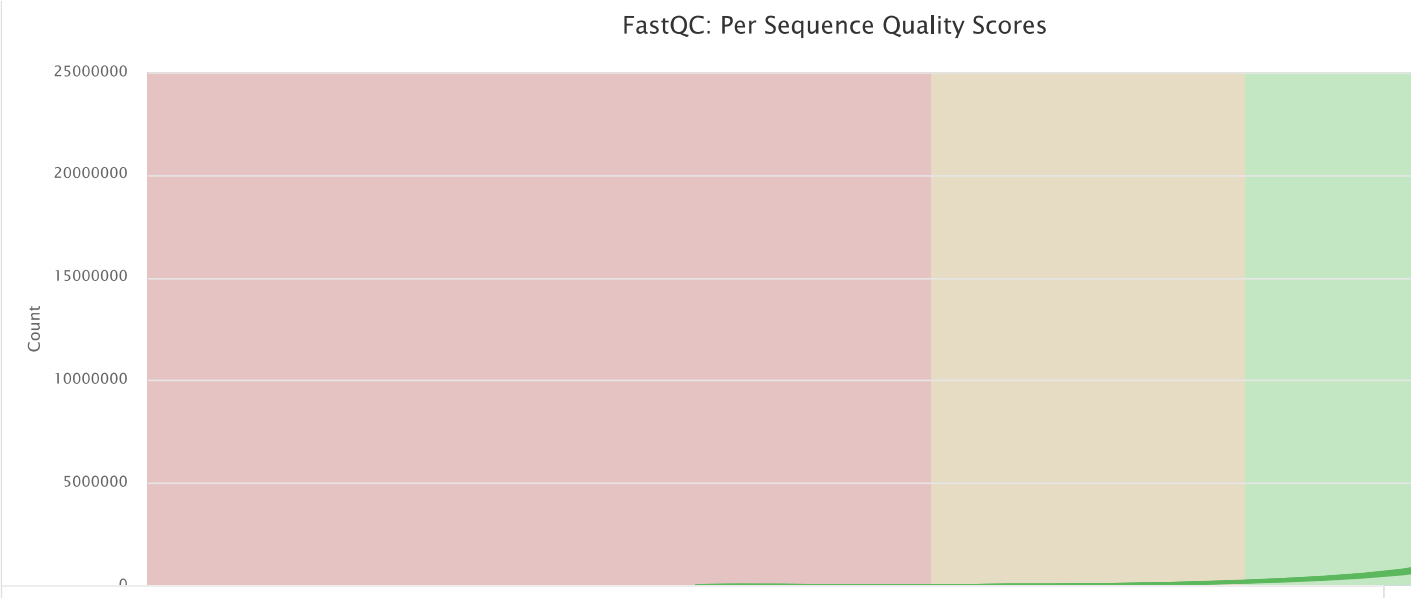
Per Sequence Quality Scores

6

[Help](#)

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





Per Base Sequence Content

0 2 4

Help

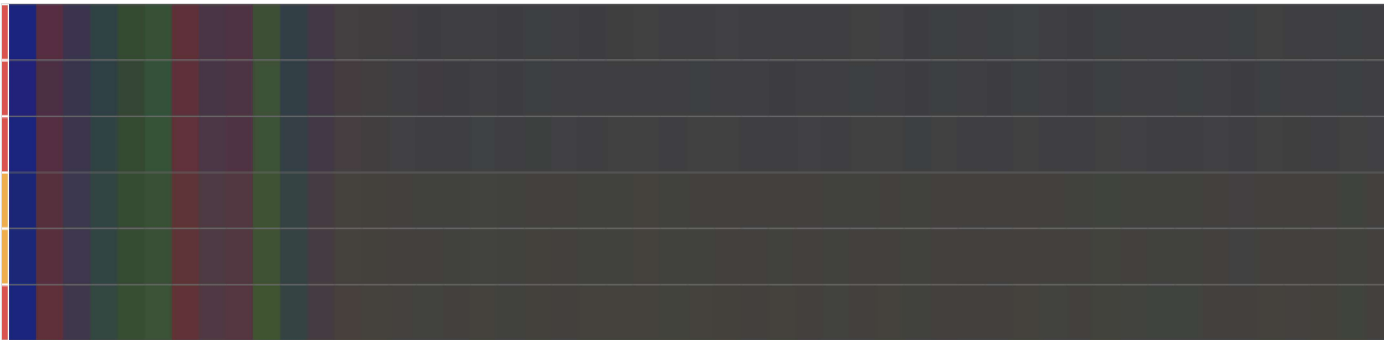
The proportion of each base position for which each of the four normal DNA bases has been called.

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

Rollover for sample name

Position: - %T: - %C: - %A: - %G: -

Export Plot



Per Sequence GC Content

3 3

Help

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

Percentages Counts

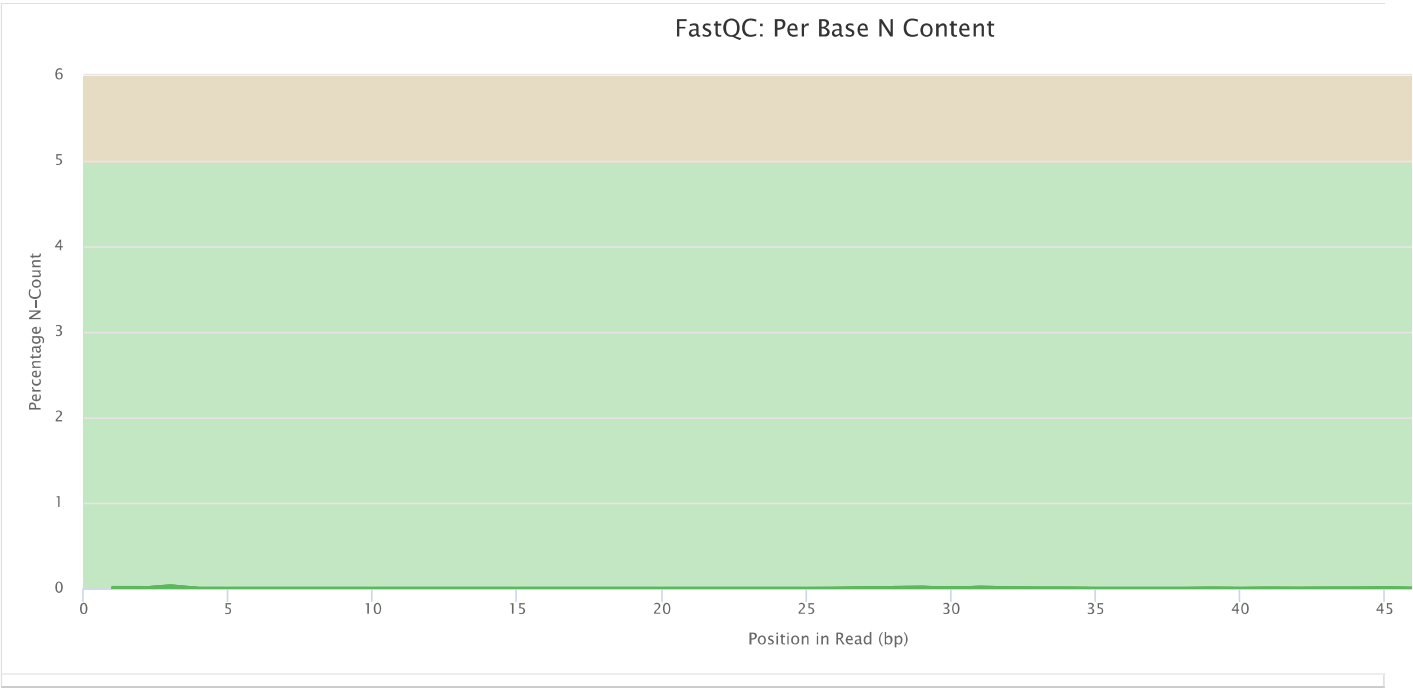


Per Base N Content

6

Help

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



Sequence Length Distribution

6

All samples have sequences of a single length (51bp).

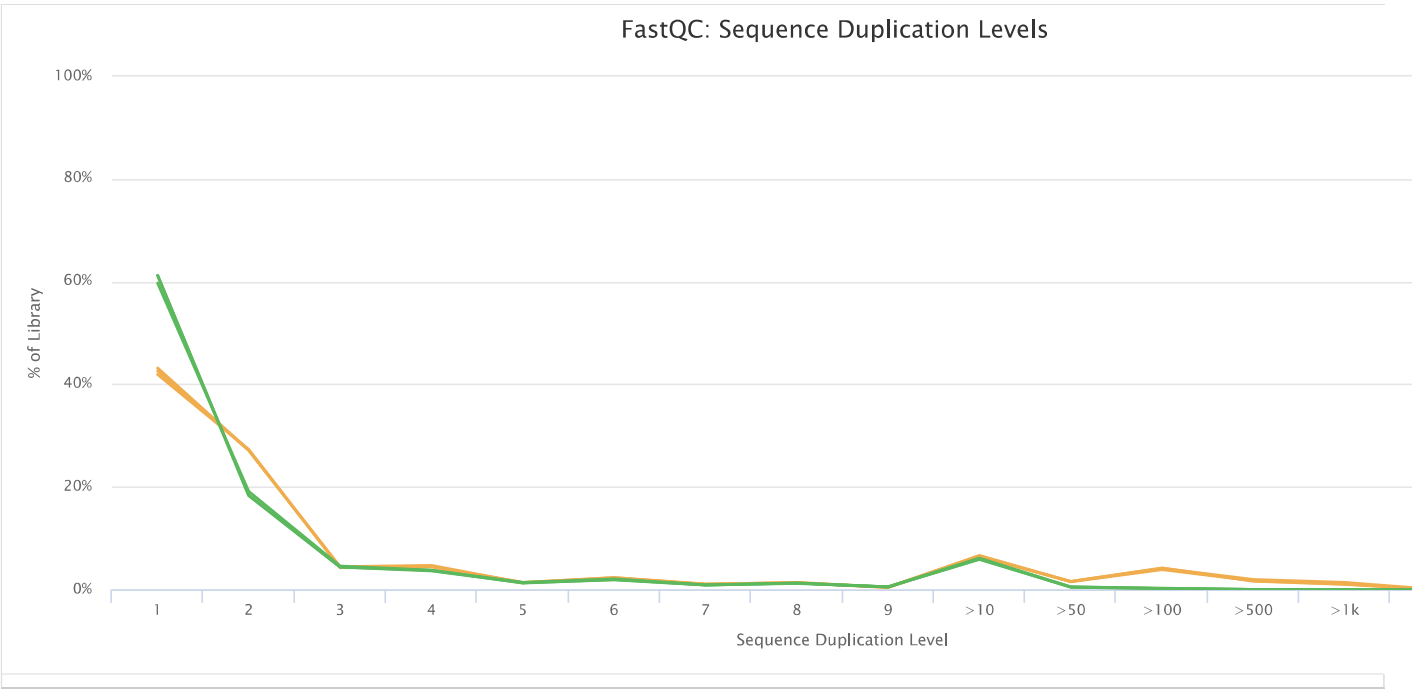
Sequence Duplication Levels

3

3

Help

The relative level of duplication found for every sequence.



Overrepresented sequences

6

Help

The total amount of overrepresented sequences found in each library.

6 samples had less than 1% of reads made up of overrepresented sequences

Adapter Content

6

Help

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

Help

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

Sort by highlight

