MultiQC

(http://multiqc.info)

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

- /public/home/zhaoqq6/project/CHIP/SRR10085024_fastqc.zip
- /public/home/zhaoqq6/project/CHIP/SRR10085026_fastqc.zip
- /public/home/zhaoqq6/project/CHIP/SRR10085032_fastqc.zip

General Statistics

Sample Name	% Dups	% GC	Length	% Failed	M Seqs
SRR10085024					
SRR10085026					
SRR10085032					

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.

☐ Flat image plot. Toolbox functions such as highlighting / hiding samples will not work (see the docs (http://multiqc.info/docs/#flat--interactive-plots)).
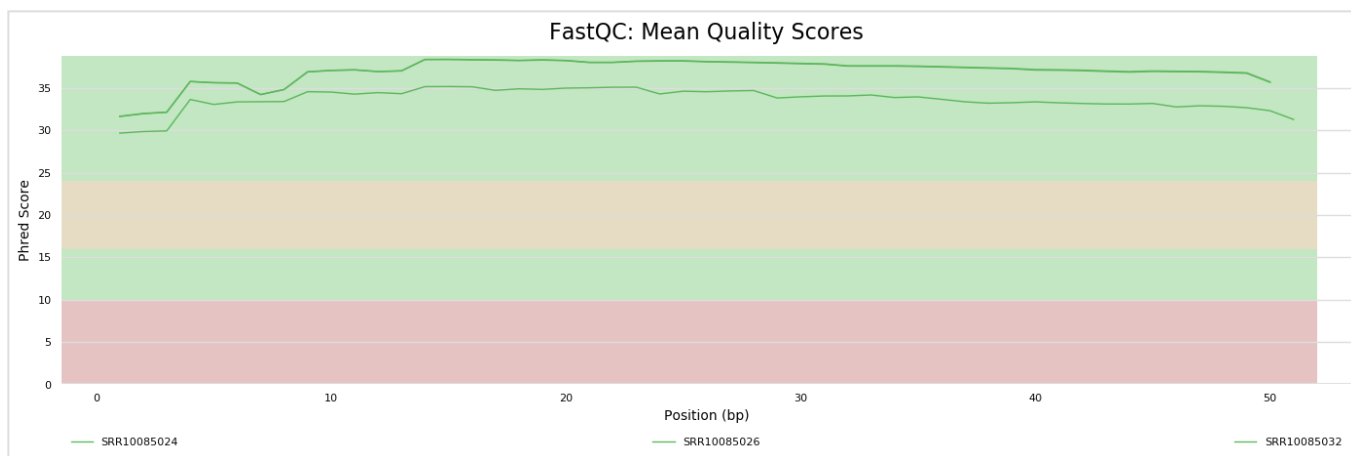
FastQC: Sequence Counts

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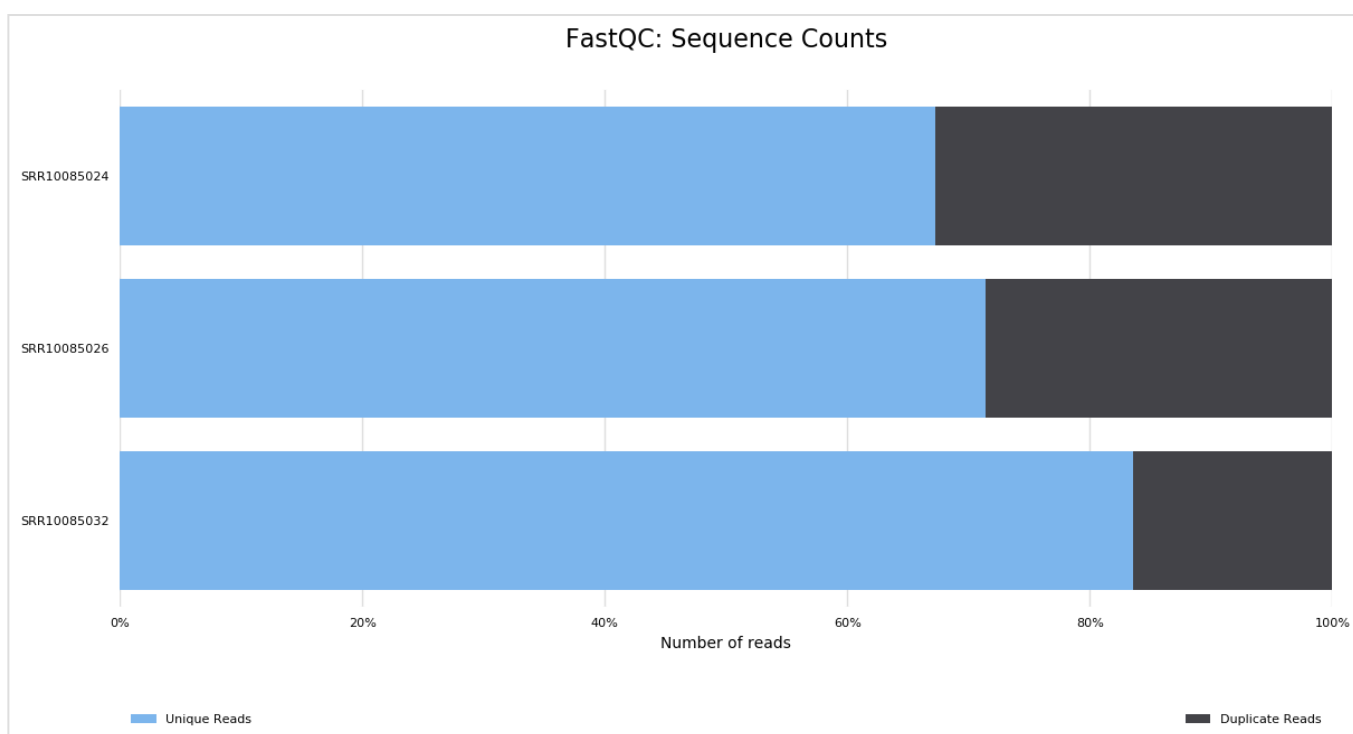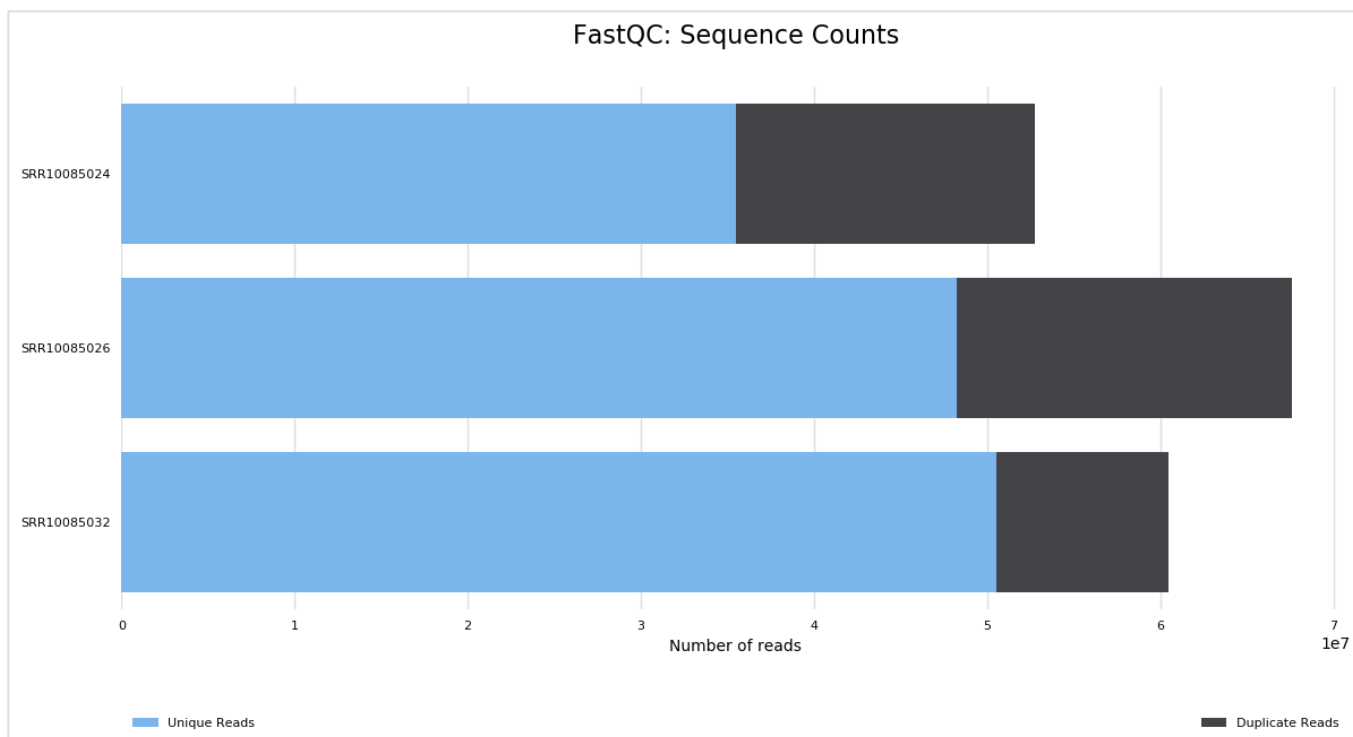
Sequence Quality Histograms

☐ Help

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

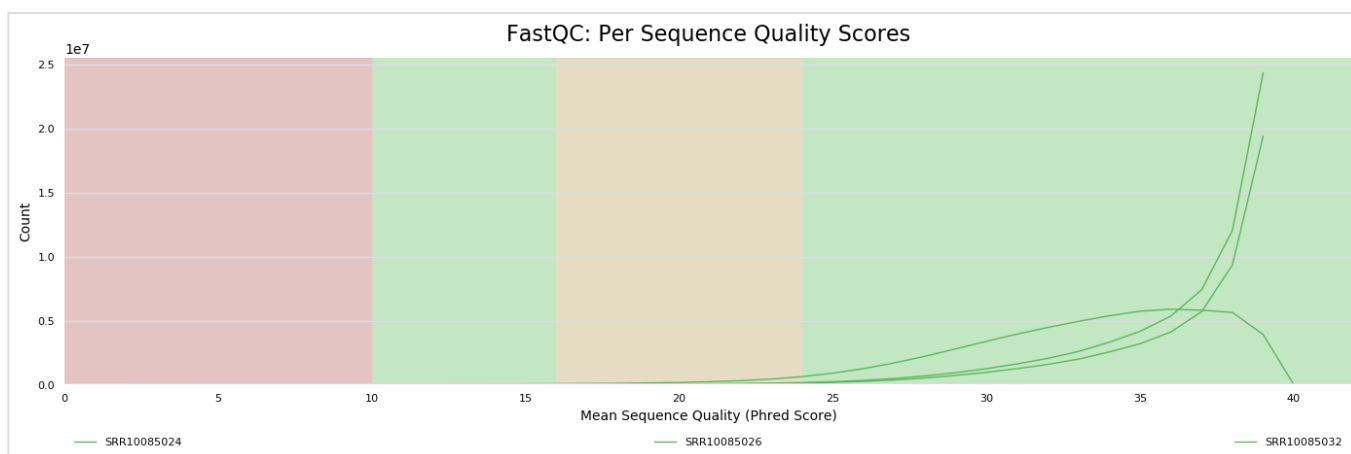☐ Flat image plot. Toolbox functions such as highlighting / hiding samples will not work (see the docs (http://multiqc.info/docs/#flat--interactive-plots)).

FastQC: Mean Quality Scores

SRR10085024   SRR10085026   SRR10085032

Per Sequence Quality Scores

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

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FastQC: Per Sequence Quality Scores

SRR10085024   SRR10085026   SRR10085032

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

Position: -   %T: -   %C: -   %A: -   ☐ Export Plot
    %G: -

Per Sequence GC Content

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

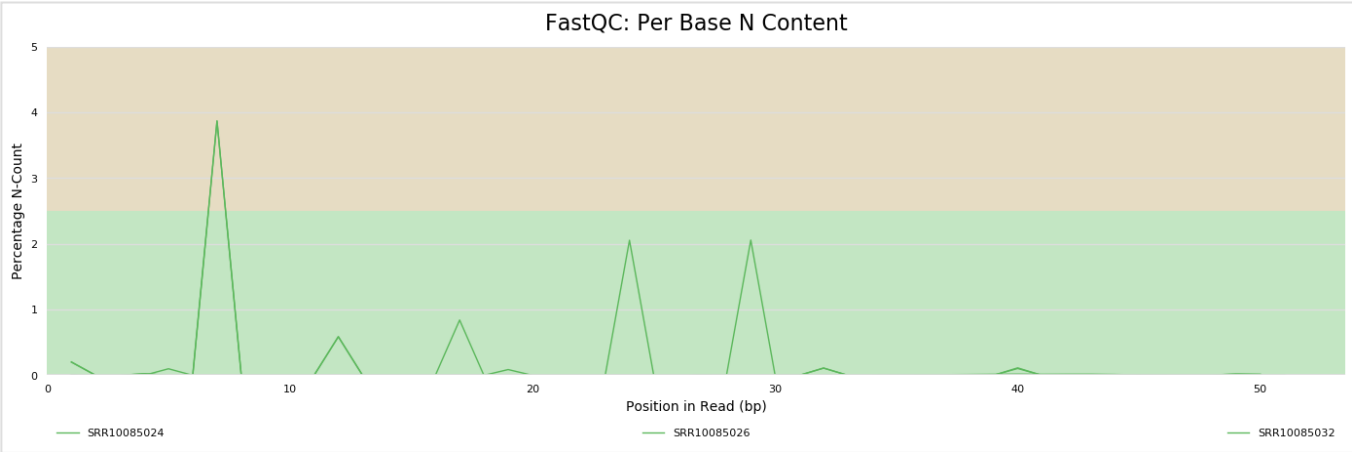☐ Flat image plot. Toolbox functions such as highlighting / hiding samples will not work (see the docs (http://multiqc.info/docs/#flat--interactive-plots)).

FastQC: Per Sequence GC Content

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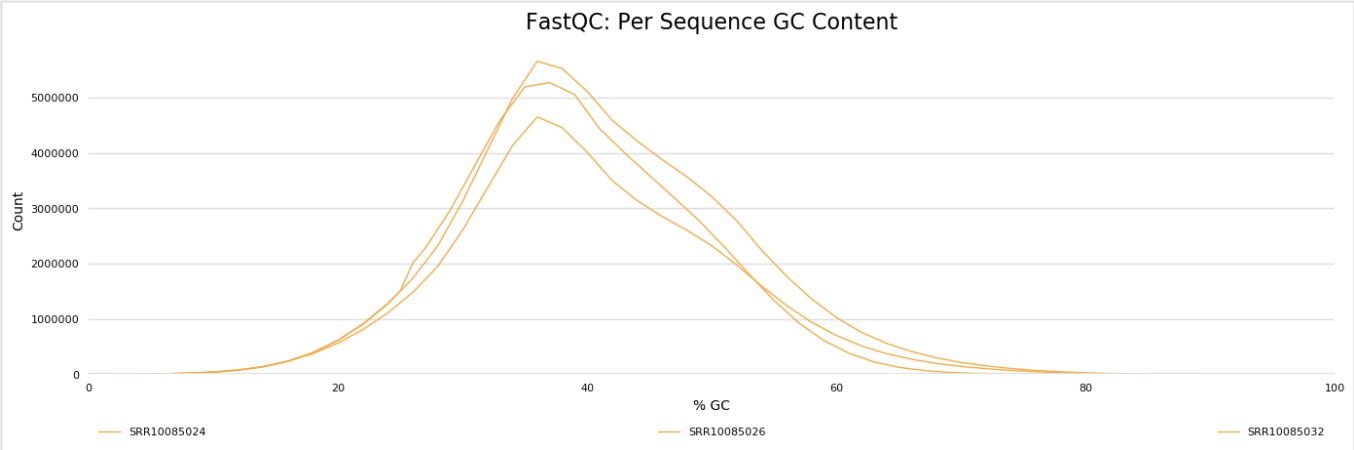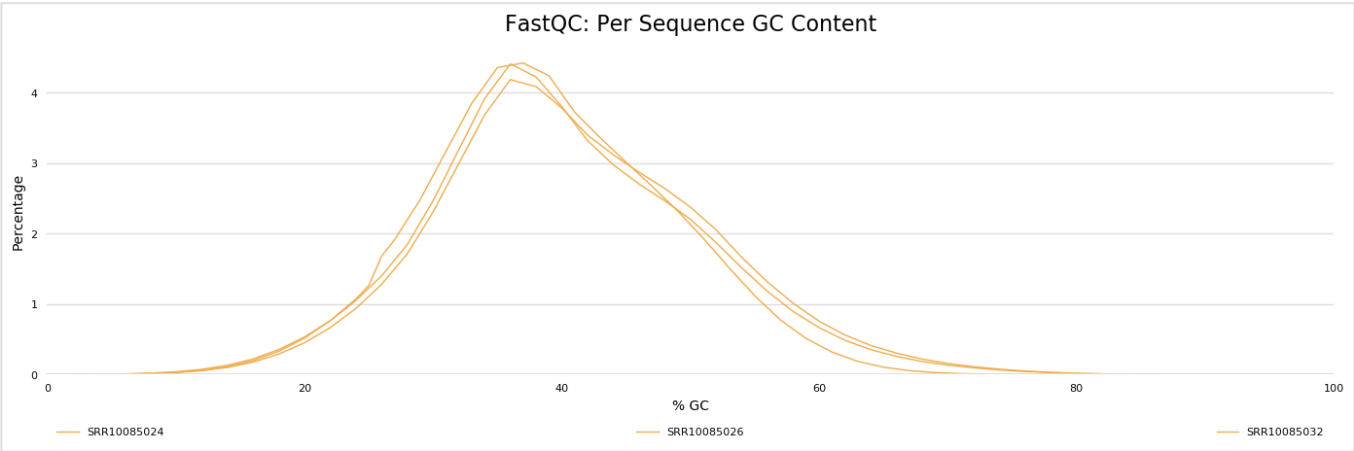
Per Base N Content

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

☐ Flat image plot. Toolbox functions such as highlighting / hiding samples will not work (see the docs (http://multiqc.info/docs/#flat--interactive-plots)).

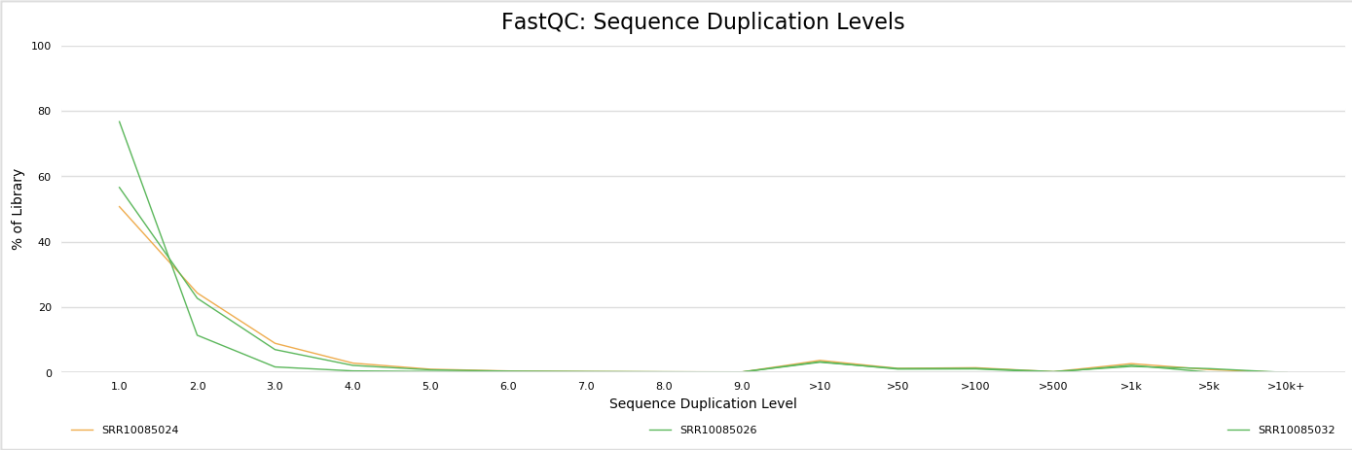## Sequence Length Distribution

All samples have sequences of a single length (50bp , 51bp). See the General Statistics Table.

Sequence Duplication Levels   ☐ Help

The relative level of duplication found for every sequence.

☐ Flat image plot. Toolbox functions such as highlighting / hiding samples will not work (see the docs (http://multiqc.info/docs/#flat--interactive-plots)).

Overrepresented sequences   ☐ Help

The total amount of overrepresented sequences found in each library.

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

Adapter Content

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%