MultiQC

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

Report generated on 2022-07-21, 14:00 based on data in: `/Users/pp/Documents/H3K27ac/fastq`

General Statistics

Copy table | Configure Columns | Plot | Showing 21/21 rows and 4/5 columns.

Sample Name	% Dups	% GC	Read Length	M Seqs
GSM3752845_Y-15T-H3K27ac	31.1%	46%	35 bp	22.7
GSM3752848_Y-13A-H3K27ac	33.6%	47%	28 bp	21.8
GSM3752849_Y-18T-H3K27ac	30.0%	46%	34 bp	25.0
GSM3752850_Y-14A-H3K27ac	33.7%	46%	27 bp	22.2
GSM3752851_Y-19T-H3K27ac	30.8%	45%	34 bp	25.1
GSM3752852_Y-15A-H3K27ac	26.9%	48%	36 bp	23.8
GSM3752854_O-8A-H3K27ac	34.2%	48%	29 bp	22.9
GSM3752855_O-10T-H3K27ac	29.9%	43%	37 bp	22.4
GSM3752856_O-6A-H3K27ac	28.7%	46%	35 bp	23.8
GSM3752857_O-11T-H3K27ac	0.0%	0%	0 bp	0.0
GSM3752858_O-7A-H3K27ac	33.7%	46%	33 bp	24.7
GSM3752861_O-9A-H3K27ac	26.8%	46%	38 bp	21.4
GSM3752862_O-10A-H3K27ac	29.4%	45%	35 bp	24.6
GSM3752863_O-11A-H3K27ac	24.0%	44%	43 bp	20.0
GSM3752864_AD-1T-H3K27ac	35.4%	46%	30 bp	26.3
GSM3752866_AD-2T-H3K27ac	39.5%	47%	28 bp	28.0
GSM3752867_AD-2A-H3K27ac	29.5%	44%	37 bp	22.9
GSM3752868_AD-3T-H3K27ac	26.1%	46%	37 bp	22.6
GSM3752870_AD-3A-H3K27ac	32.5%	44%	34 bp	25.6
GSM3752871_AD-5A-H3K27ac	39.0%	48%	28 bp	28.4
GSM3752872_AD-8T-H3K27ac	33.0%	45%	35 bp	25.0

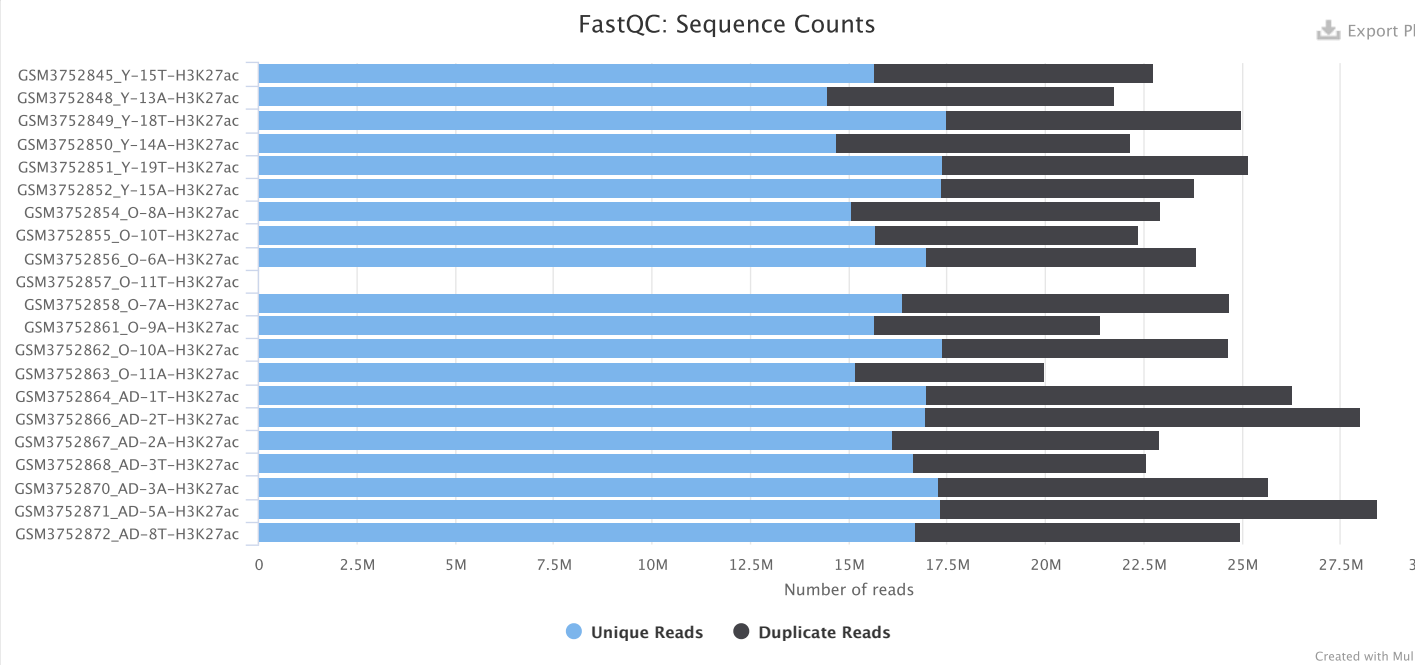
FastQC

FastQC is a quality control tool for high throughput sequence data, written by Simon Andrews at the Babraham Institute in Cambridge.

Sequence Counts

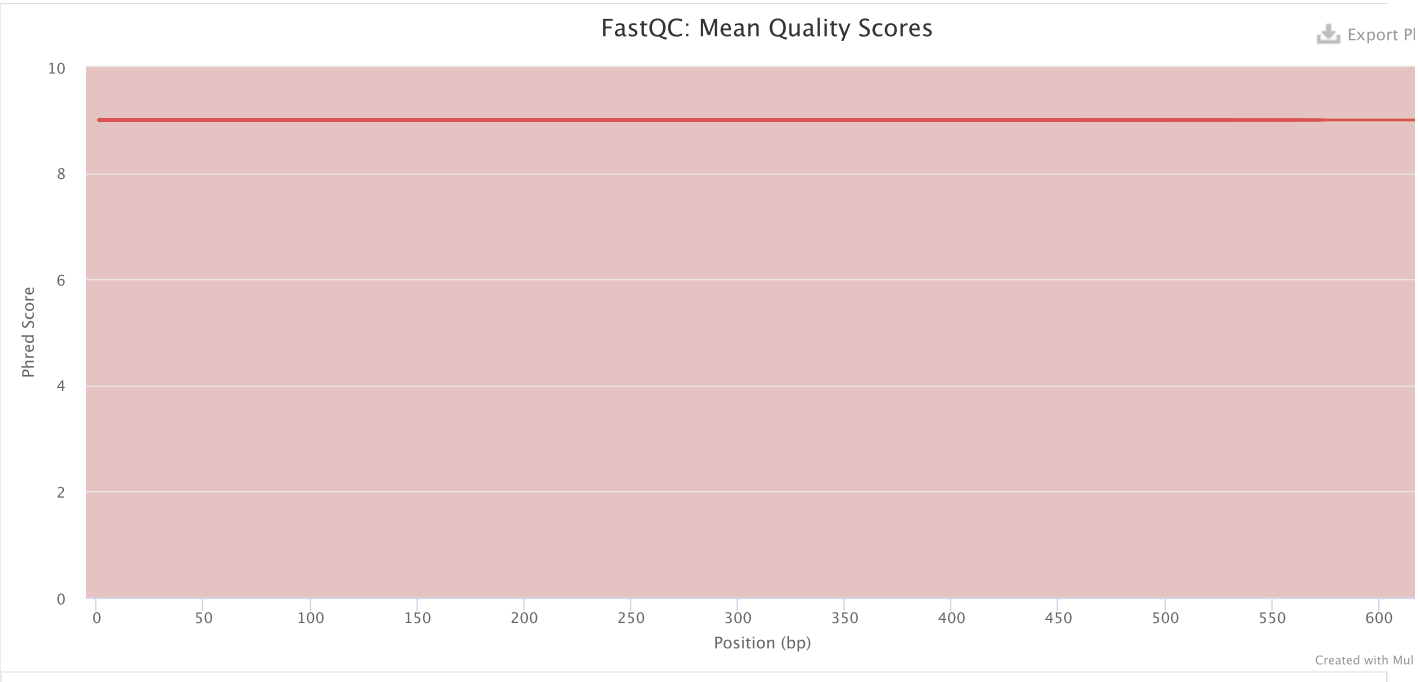
Sequence counts for each sample. Duplicate read counts are an estimate only.

Number of reads | Percentages



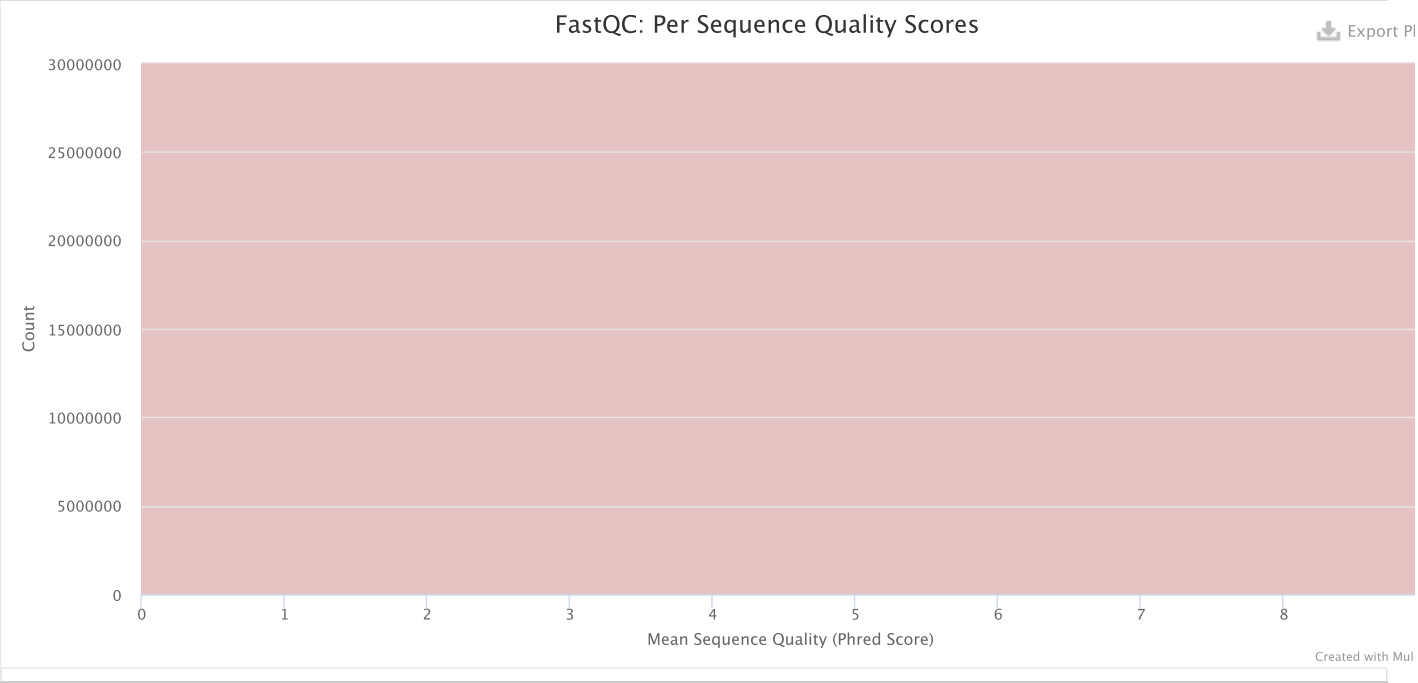
Sequence Quality Histograms

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



Per Sequence Quality Scores

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



Per Base Sequence Content

7

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.

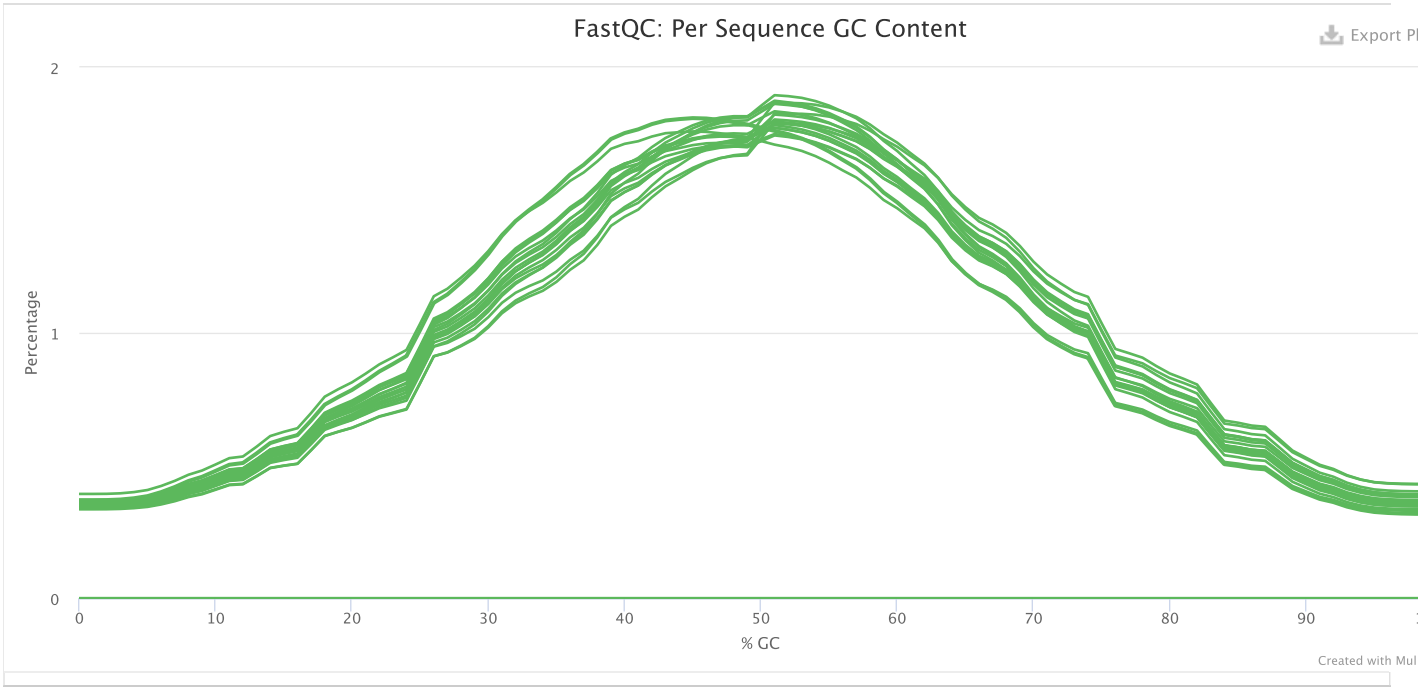
Rollover for sample name

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

Per Sequence GC Content 21

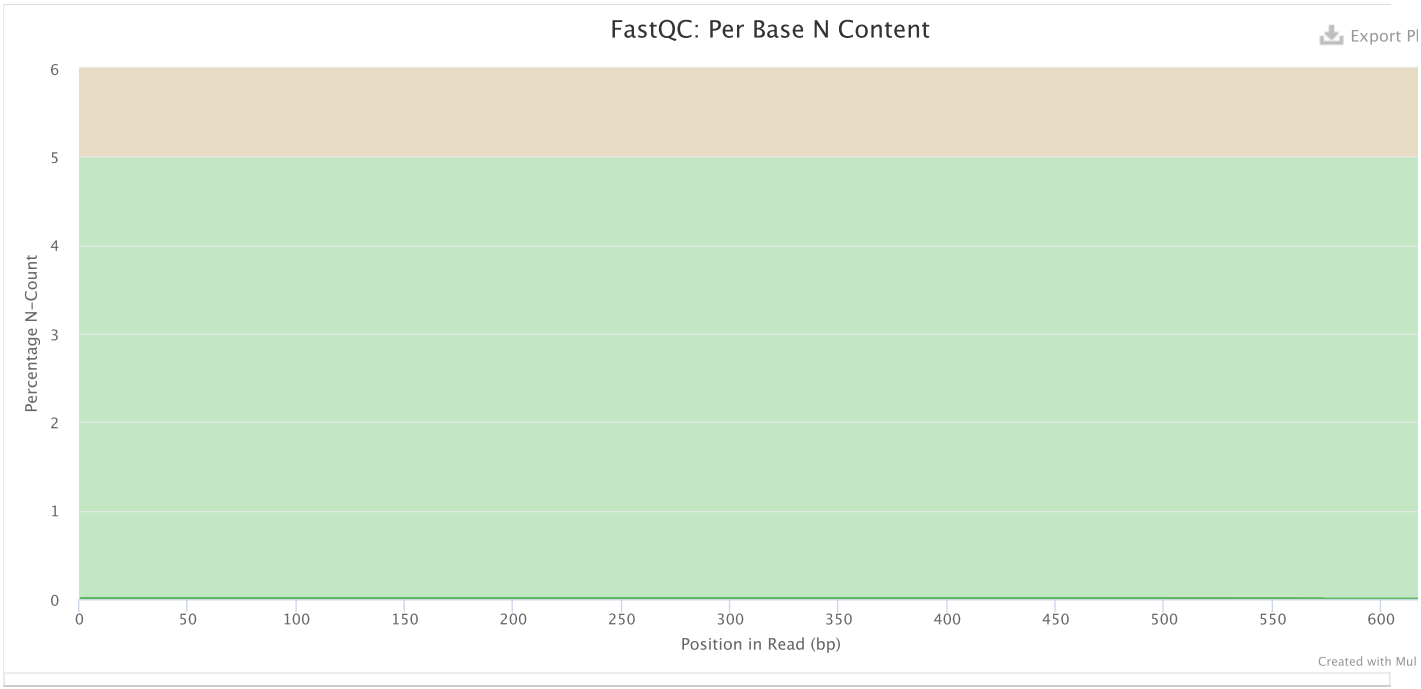
The average GC content of reads. Normal random library typically have a roughly normal distribution of GC content.

Percentages | Counts



Per Base N Content 21

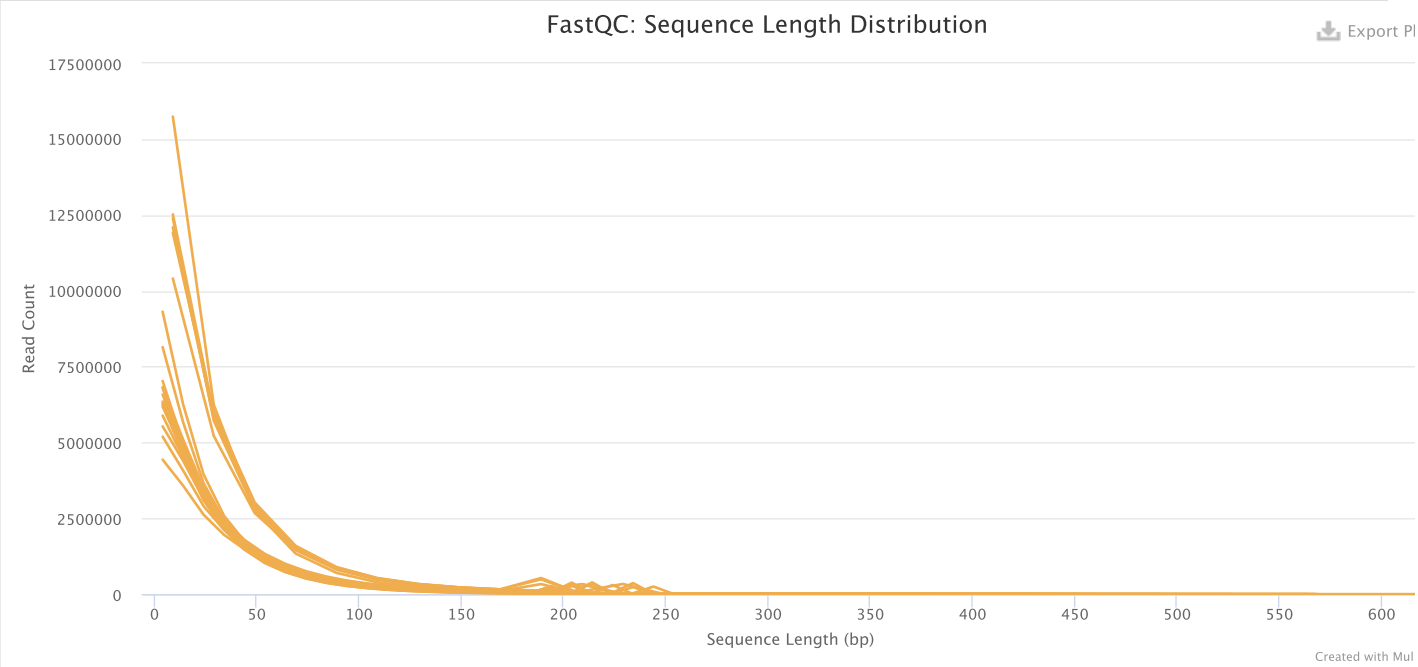
The percentage of base calls at each position for which an `N` was called.



Sequence Length Distribution

20

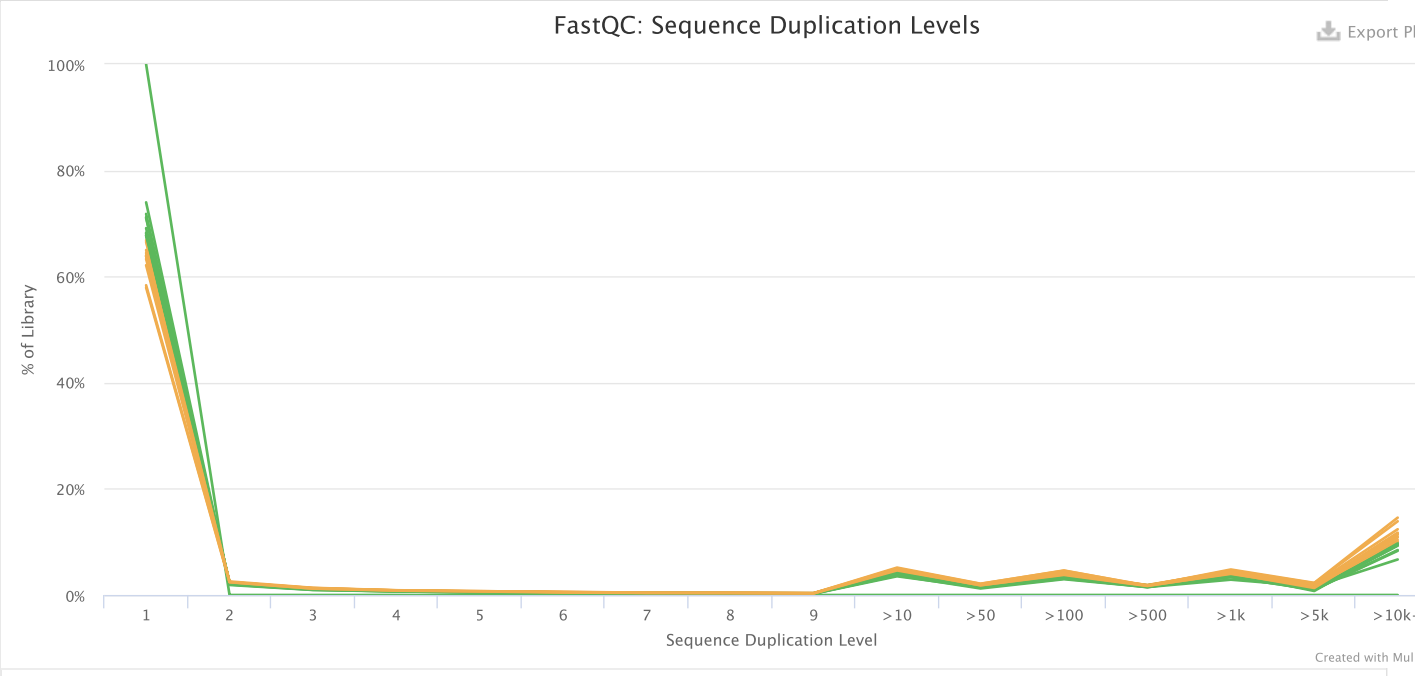
The distribution of fragment sizes (read lengths) found. See the FastQC help



Sequence Duplication Levels

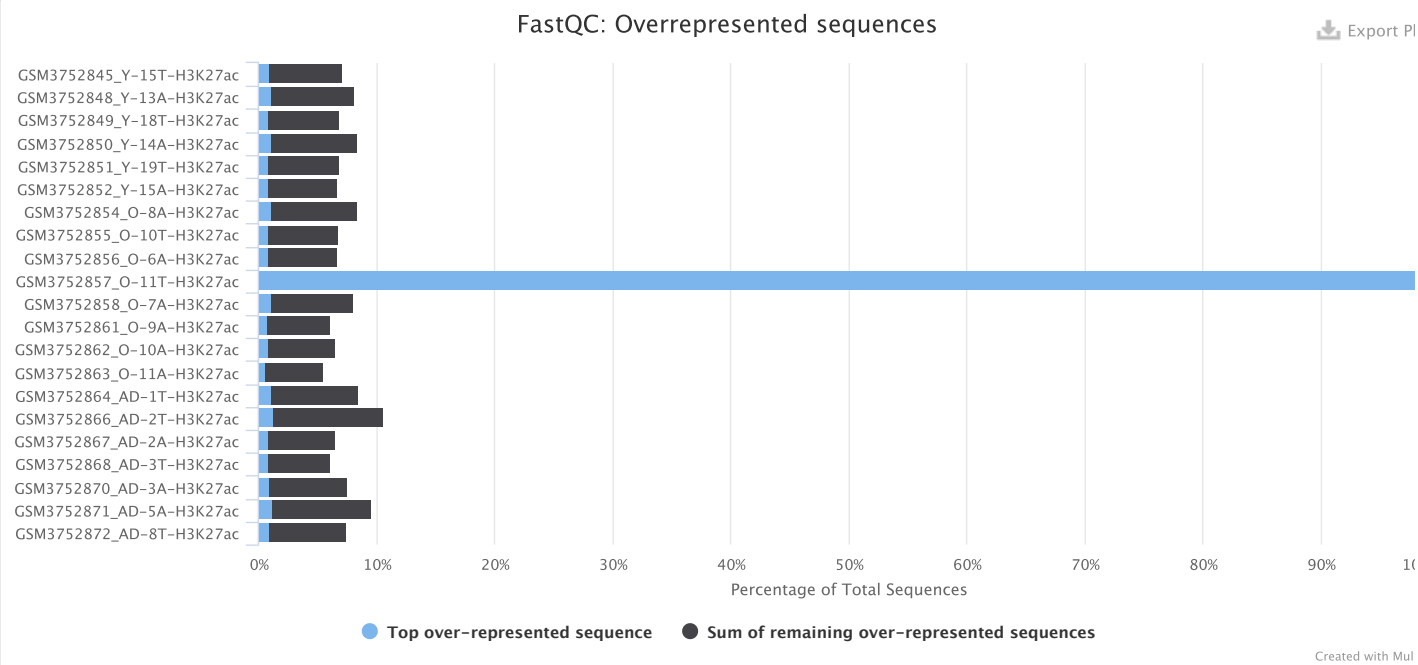
10 11

The relative level of duplication found for every sequence.



Overrepresented sequences 11

The total amount of overrepresented sequences found in each library.

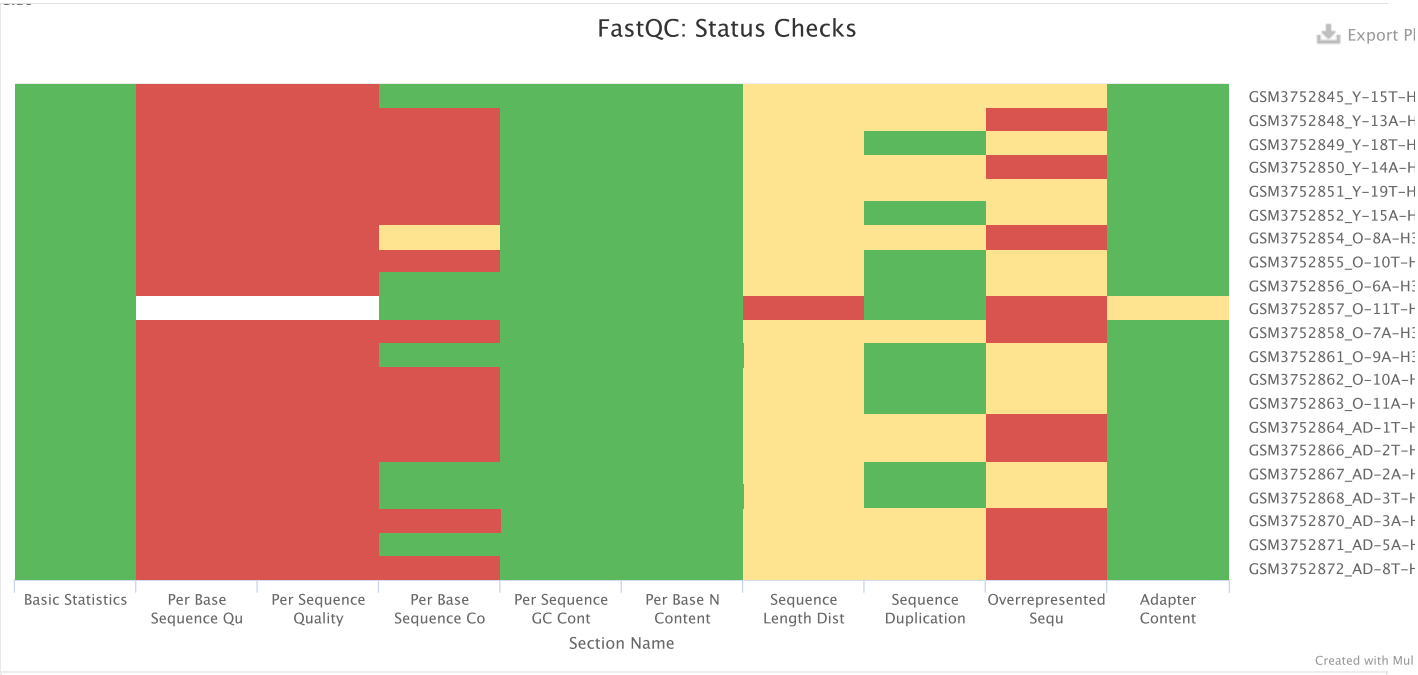


Adapter Content 20

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).

Sort by highlight **Min:** 0 **Max:** 1