

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

Report generated on 2022-12-28, 11:51 EST based on data in: /Users/austinherbert/Desktop/SF3B1/DMS_Seq/multiqc

🔔 Welcome! Not sure where to start?

[Watch a tutorial video](#) (6:08)

don't show again ✕

General Statistics

📄 Copy table

⚙️ Configure Columns

📊 Plot

Showing 25/25 rows and 3/3 columns.

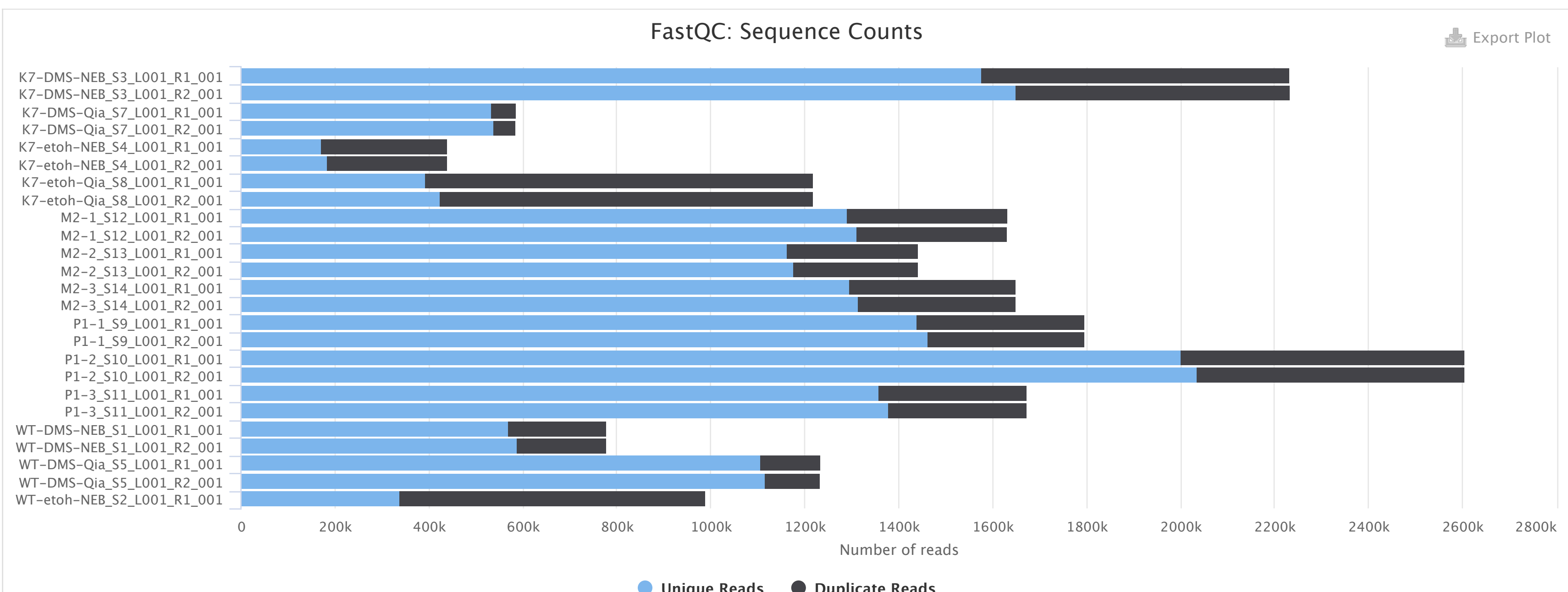
Sample Name	% Dups	% GC	M Seqs
K7-DMS-NEB_S3_L001_R1_001	29.4%	43%	2.2
K7-DMS-NEB_S3_L001_R2_001	26.2%	43%	2.2
K7-DMS-Qia_S7_L001_R1_001	8.7%	51%	0.6
K7-DMS-Qia_S7_L001_R2_001	7.8%	50%	0.6
K7-etoh-NEB_S4_L001_R1_001	60.7%	44%	0.4
K7-etoh-NEB_S4_L001_R2_001	58.3%	44%	0.4
K7-etoh-Qia_S8_L001_R1_001	67.7%	48%	1.2
K7-etoh-Qia_S8_L001_R2_001	65.2%	48%	1.2
M2-1_S12_L001_R1_001	20.9%	47%	1.6
M2-1_S12_L001_R2_001	19.7%	47%	1.6
M2-2_S13_L001_R1_001	19.4%	48%	1.4
M2-2_S13_L001_R2_001	18.5%	48%	1.4
M2-3_S14_L001_R1_001	21.4%	48%	1.7
M2-3_S14_L001_R2_001	20.3%	48%	1.7
P1-1_S9_L001_R1_001	19.8%	47%	1.8

FastQC

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

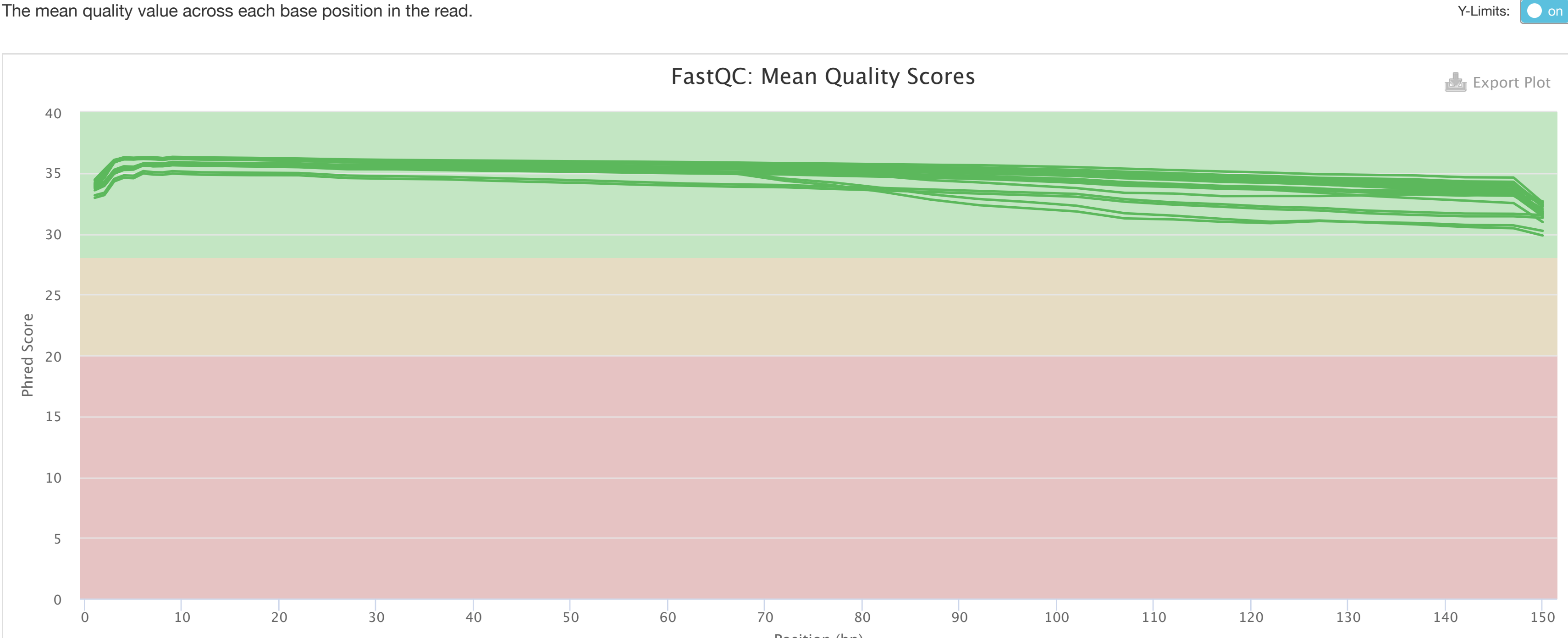
Sequence Counts

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



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.



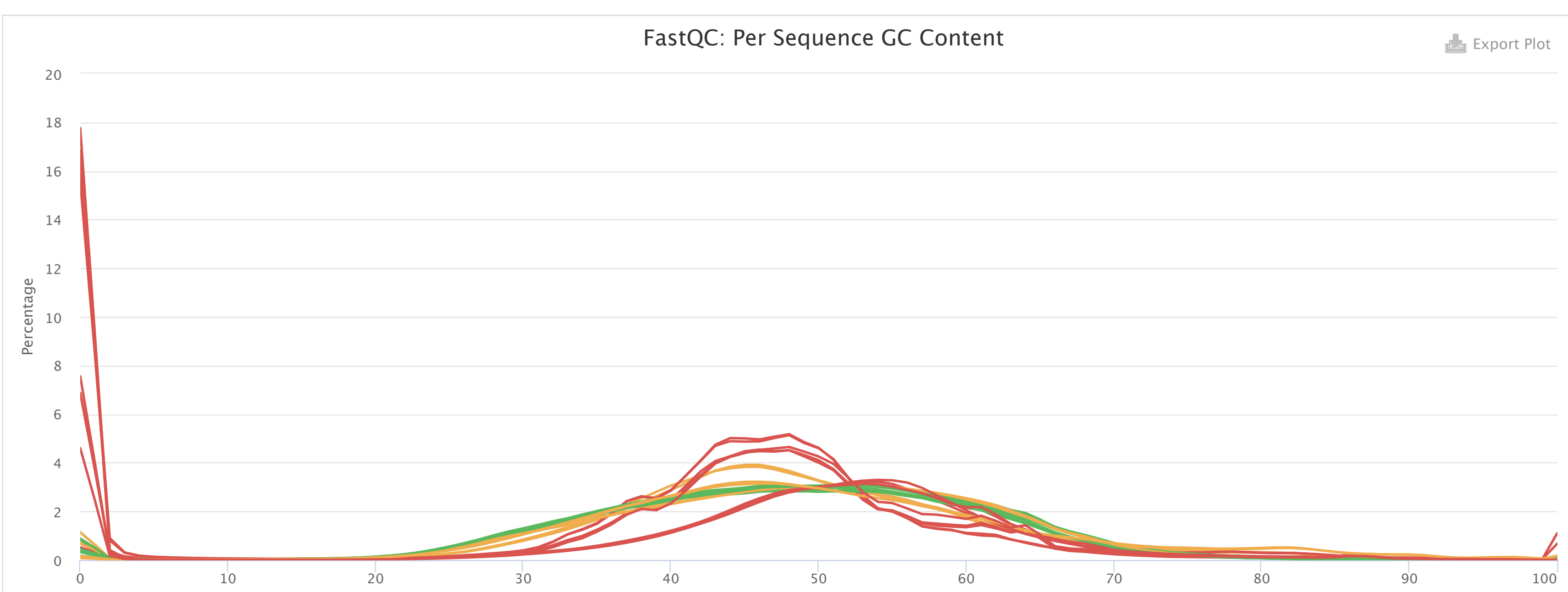
Per Base Sequence Content

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



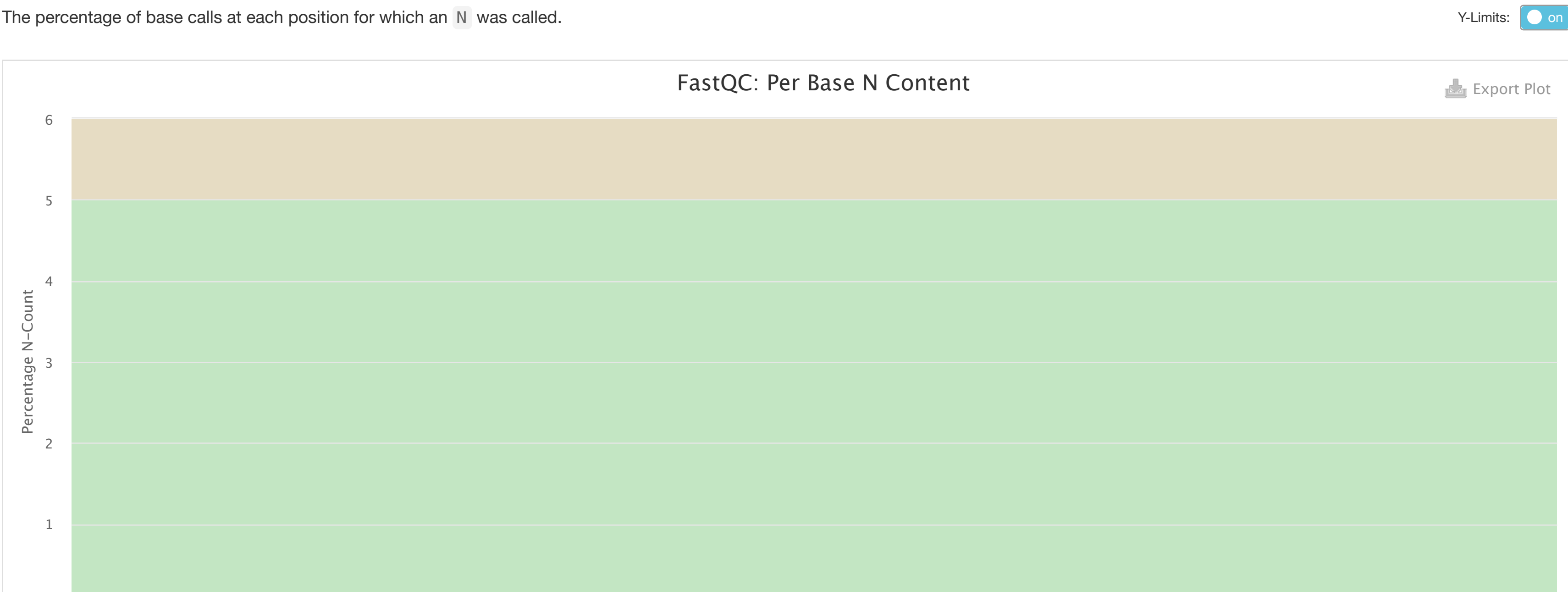
Per Sequence GC Content

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



Per Base N Content

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

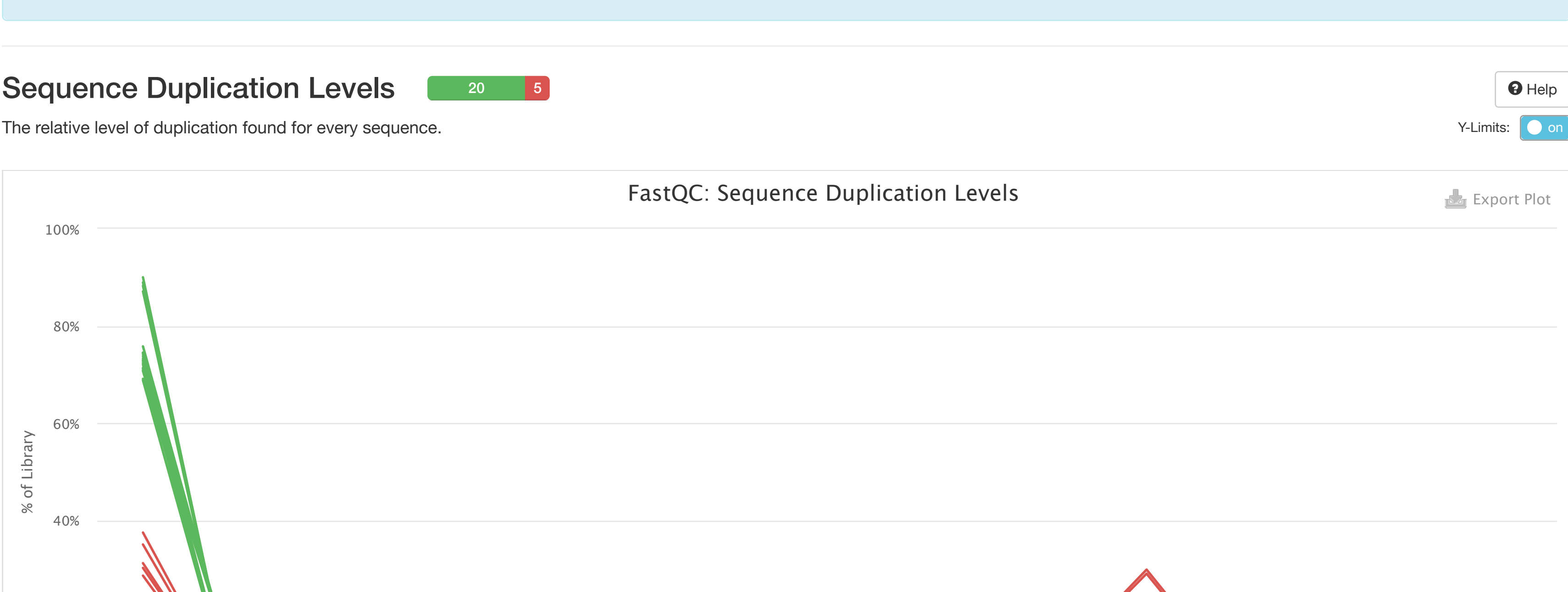


Sequence Length Distribution

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

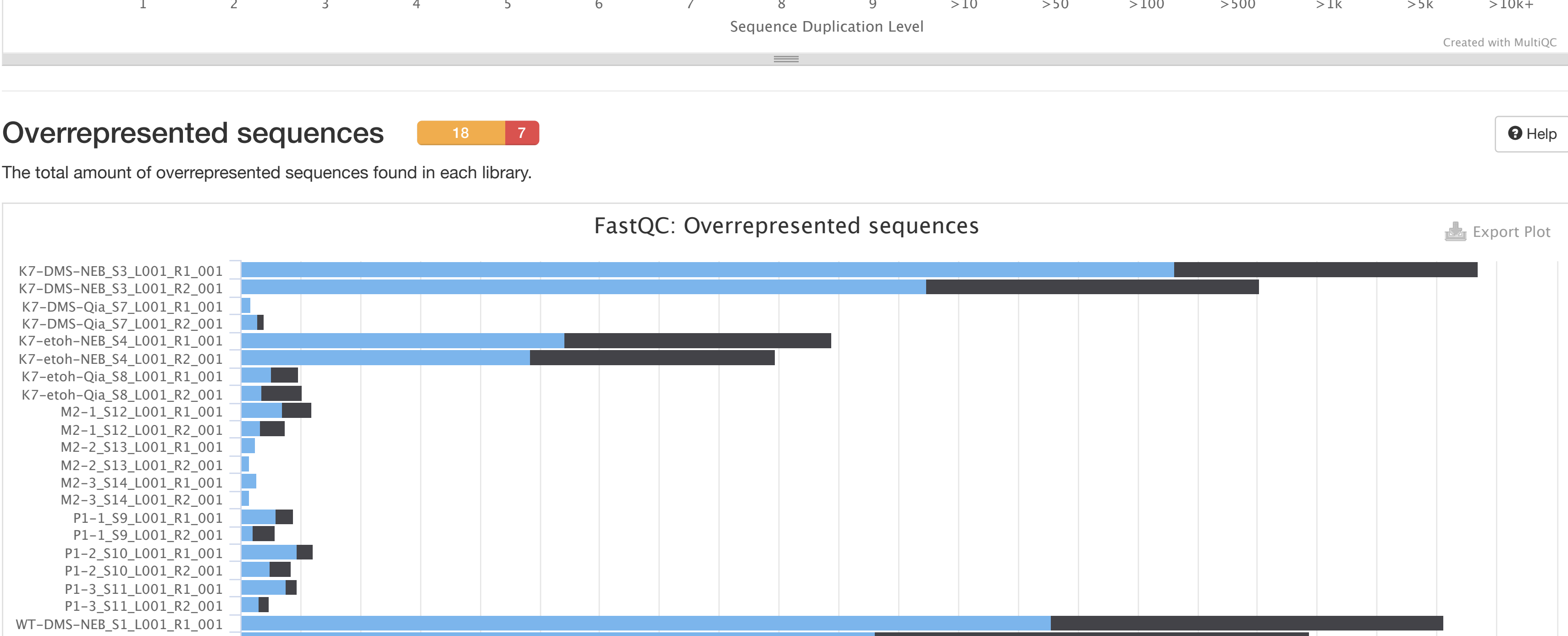
Sequence Duplication Levels

The relative level of duplication found for every sequence.



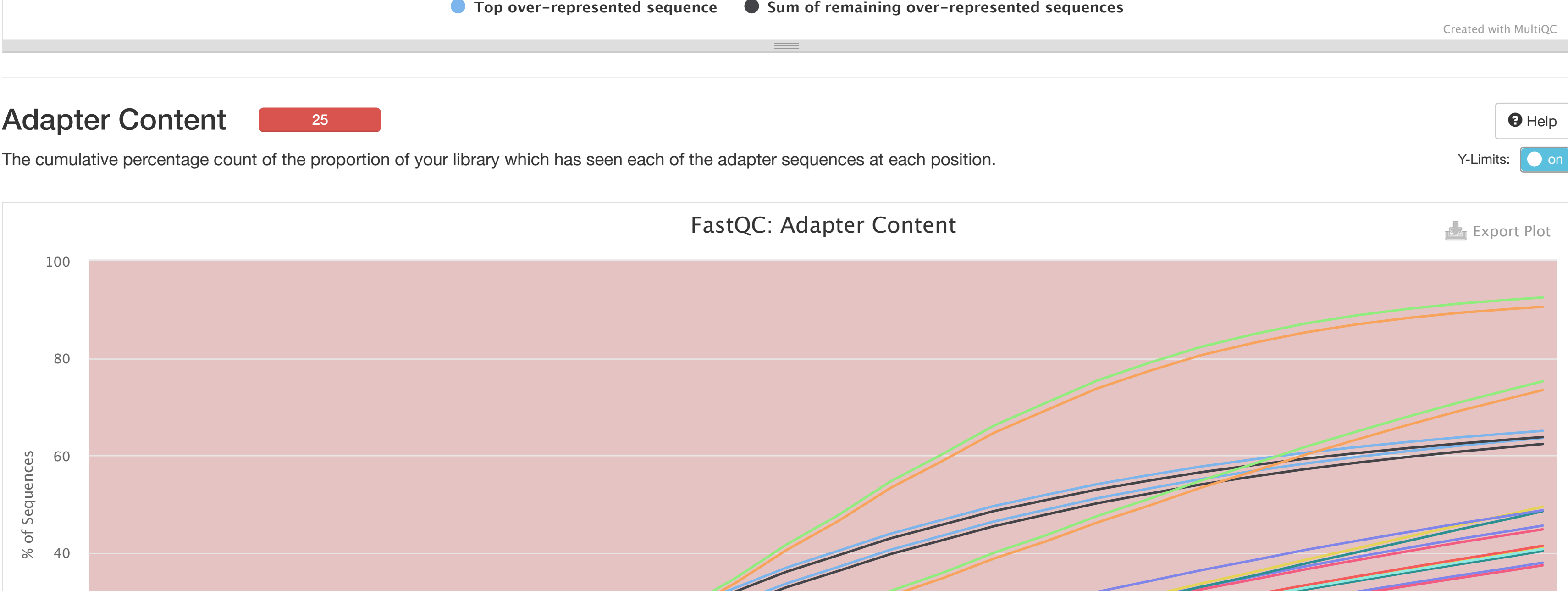
Overrepresented sequences

The total amount of overrepresented sequences found in each library.



Adapter Content

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



Status Checks

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

