

General Statistics

Copy table

Configure columns

Scatter plot

Violin plot

Showing 6/6 rows and 6/15 columns.

Export as CSV

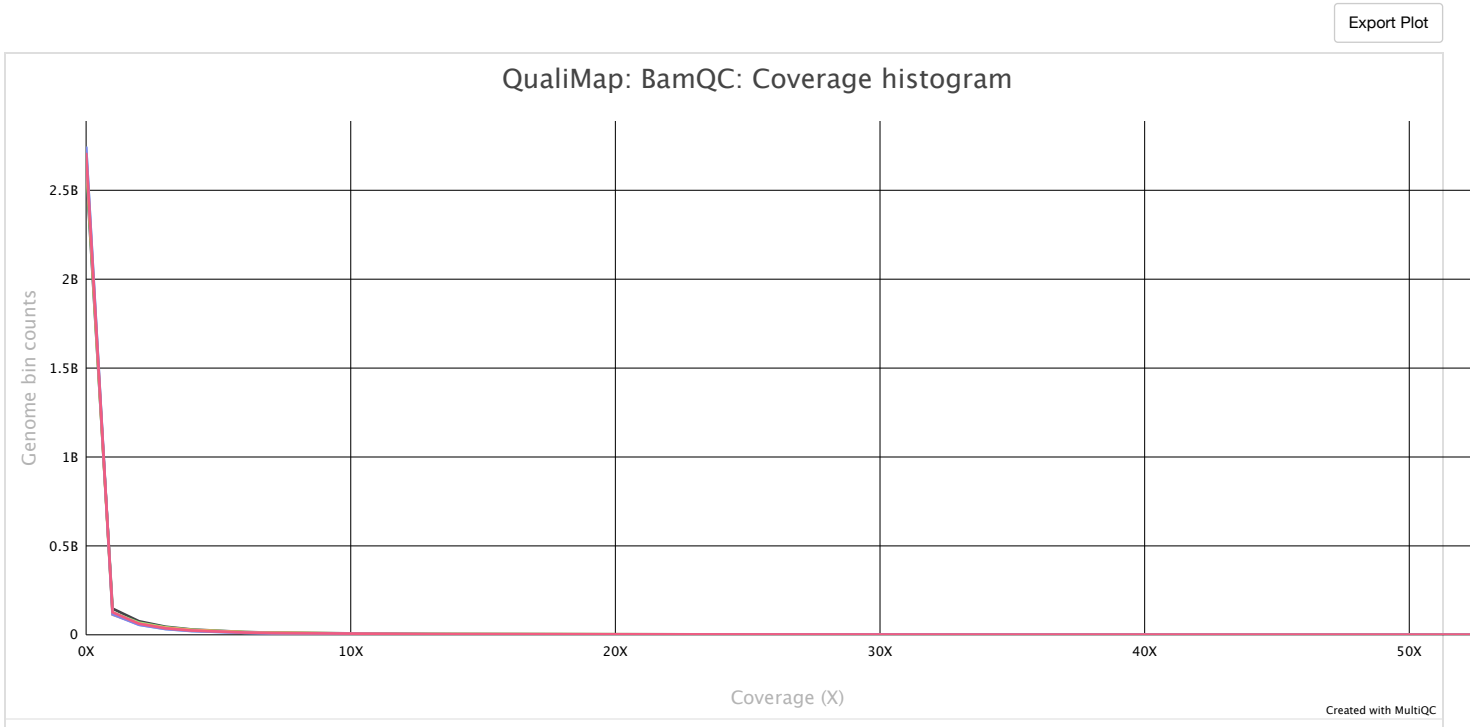
Sample Name	% GC	≥ 30X	Median cov	Mean cov	% Aligned	Reads mapped
D0_10X	48 %	1.2 %	0 X	65.7 X	91.3 %	337.9 M
D12_10X	48 %	1.6 %	0 X	99.1 X	92.3 %	385.0 M
D16+_10X	48 %	1.6 %	0 X	79.1 X	94.7 %	394.8 M
D16-_10X	47 %	1.4 %	0 X	79.2 X	94.1 %	392.0 M
D2_10X	48 %	1.2 %	0 X	65.0 X	89.9 %	338.3 M
D8_10X	47 %	1.3 %	0 X	88.3 X	90.2 %	348.1 M

QualiMap

QualiMap is a platform-independent application to facilitate the quality control of alignment sequencing data and its derivatives like feature counts. DOI: 10.1093/bioinformatics/btv566; 10.1093/bioinformatics/bts503.

Coverage histogram

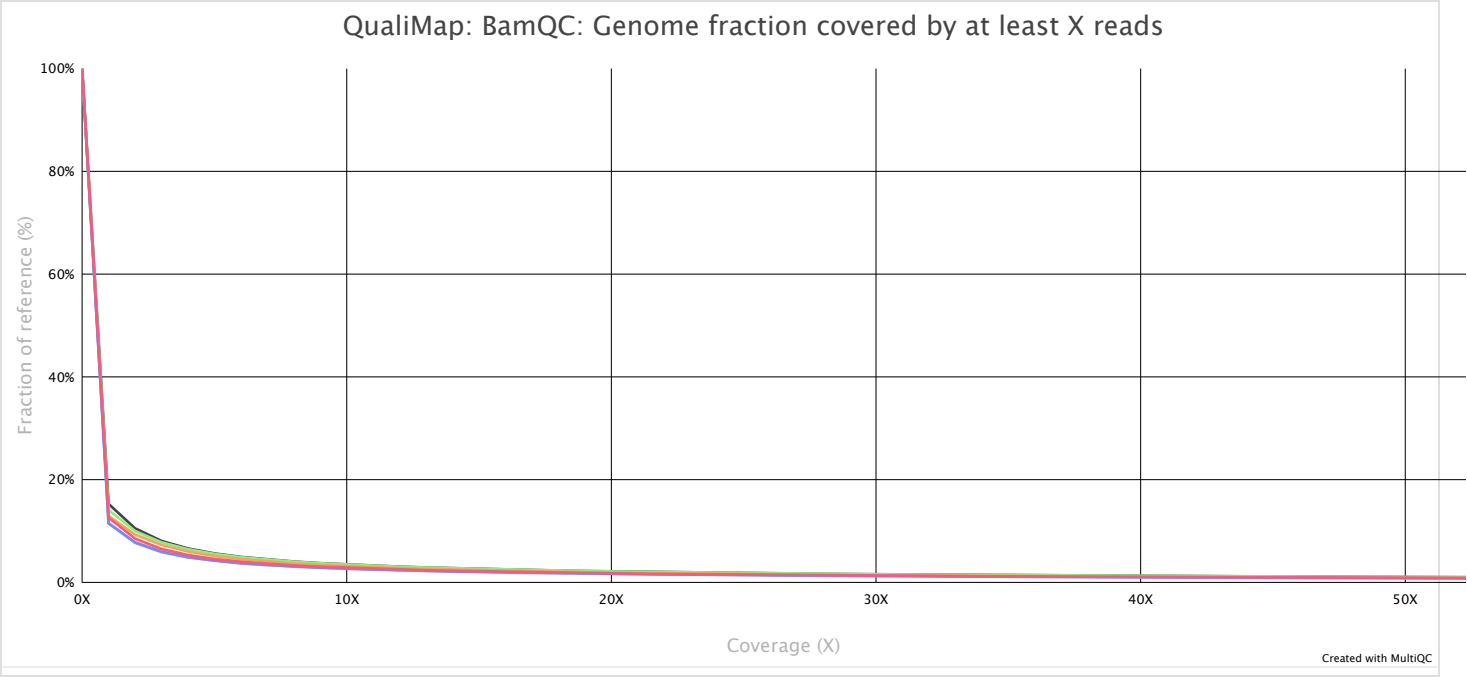
Distribution of the number of locations in the reference genome with a given depth of coverage.



Cumulative genome coverage

Percentage of the reference genome with at least the given depth of coverage.

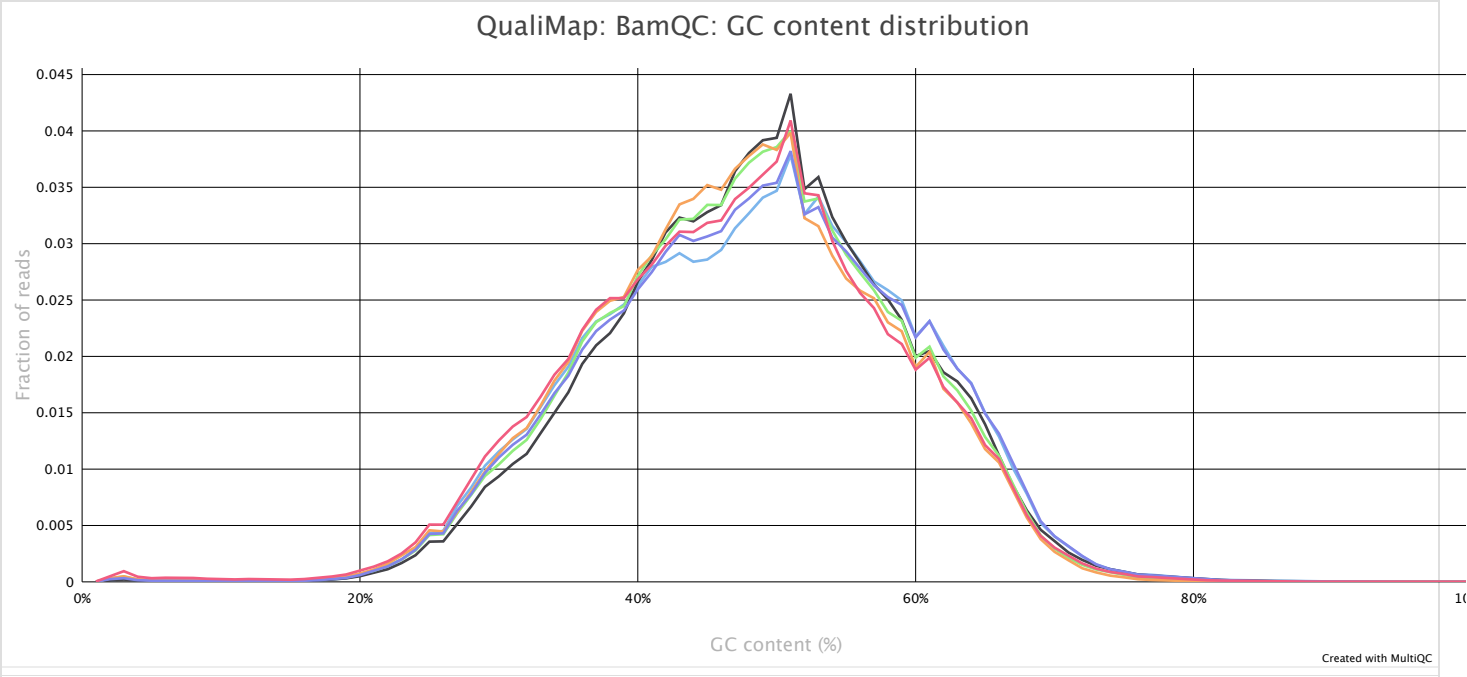
Export Plot



GC content distribution

Each solid line represents the distribution of GC content of mapped reads for a given sample.

Export Plot



Samtools

samtools is a suite of programs for interacting with high-throughput sequencing data. DOI: 10.1093/bioinformatics/btp352.

Flagstat

This module parses the output from samtools flagstat

