

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

Report generated on 2024-07-24, 16:58 CEST based on data in: /Users/noecrespo/Desktop/quality\_check\_results

### **General Statistics**

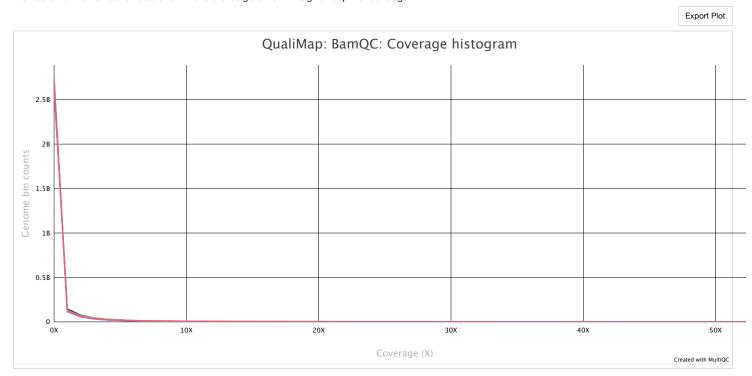
♣ Copy table	ble Configure columns		Scatter plot		<b>■</b> Violin plot	Showing $^6/_6$ rows and $^6/_{15}$ columns.						Export as CS
Sample Name	9,	% GC		≥ 30X	[	Median cov		Mean cov		% Aligned	Reads	mapped
D0_10X	4	18 %		1.2 %		0 X		65.7 X		91.3 %	337.9 M	
D12_10X	4	18 %		1.6 %		0 X		99.1 X		92.3 %	385.0 M	
D16+_10X	4	18 %		1.6 %		0 X		79.1 X		94.7 %	394.8 M	
D1610X		17 %	1.4 %		0 X		79.2 X		94.1 %	392.0 M		
D2_10X	4	18 %	1.2 %		0 X		65.0 X		89.9 %	338.3 M		
D8_10X		17 %		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/btv566; 10.1093/bioinformatics/btv503.

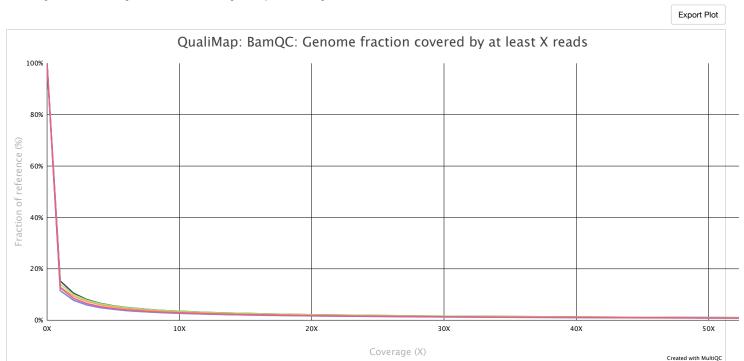
#### Coverage histogram

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



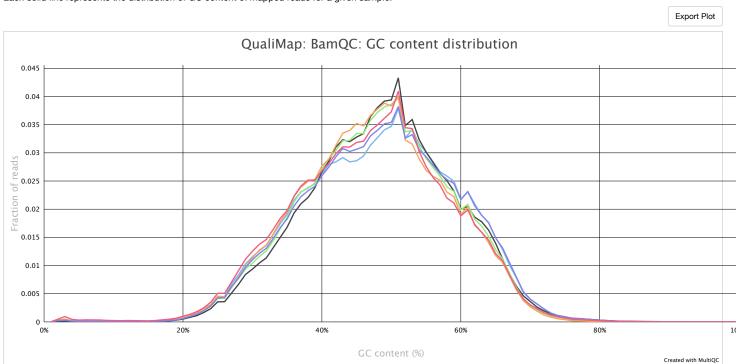
## Cumulative genome coverage

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



#### GC content distribution

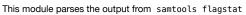
Each solid line represents the distribution of GC content of mapped reads for a given sample.

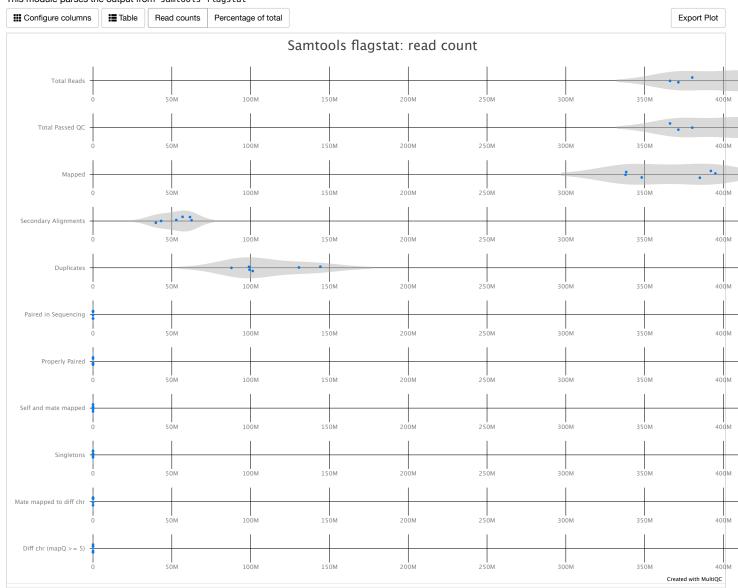


### **Samtools**

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

#### **Flagstat**





<u>MultiQC v1.23</u> - Written by <u>Phil Ewels</u>, available on <u>GitHub</u>.

This report uses <u>Plotly</u>, <u>jQuery</u>, <u>jQuery</u> <u>UI</u>, <u>Bootstrap</u>, <u>FileSaver.js</u> and <u>clipboard.js</u>.

