Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2022/03/01 01:49:32

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
output/UF103/UF103_f4_q37_sortc_markdup.rescaled.bam -nw 400 -hm 3

1.2. Alignment

Command line:	bwa samse -r @RG\tID:UF103\tSM:UF103\tLB:nan\tPL:ILLUMINA /data/stonelab/references/M_leprae_TN/M_leprae_TN.fasta output/UF103/UF103-ancient.sai output/UF103/UF103-ancient.trimmed.fq
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 01 01:49:31 MST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	output/UF103/UF103_f4_q37_sortc_markdup.rescaled.bam

2. Summary

2.1. Globals

Reference size	3,268,203
Number of reads	1,859
Mapped reads	1,859 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	30 / 132 / 59.82
Duplicated reads (estimated)	647 / 34.8%
Duplication rate	31.11%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	26,568 / 23.9%
Number/percentage of C's	27,525 / 24.76%
Number/percentage of T's	21,533 / 19.37%
Number/percentage of G's	35,530 / 31.96%
Number/percentage of N's	0 / 0%
GC Percentage	56.73%

2.3. Coverage

Mean	0.034
Standard Deviation	1.4263

2.4. Mapping Quality

Mean Mapping Quality	6.84

2.5. Mismatches and indels

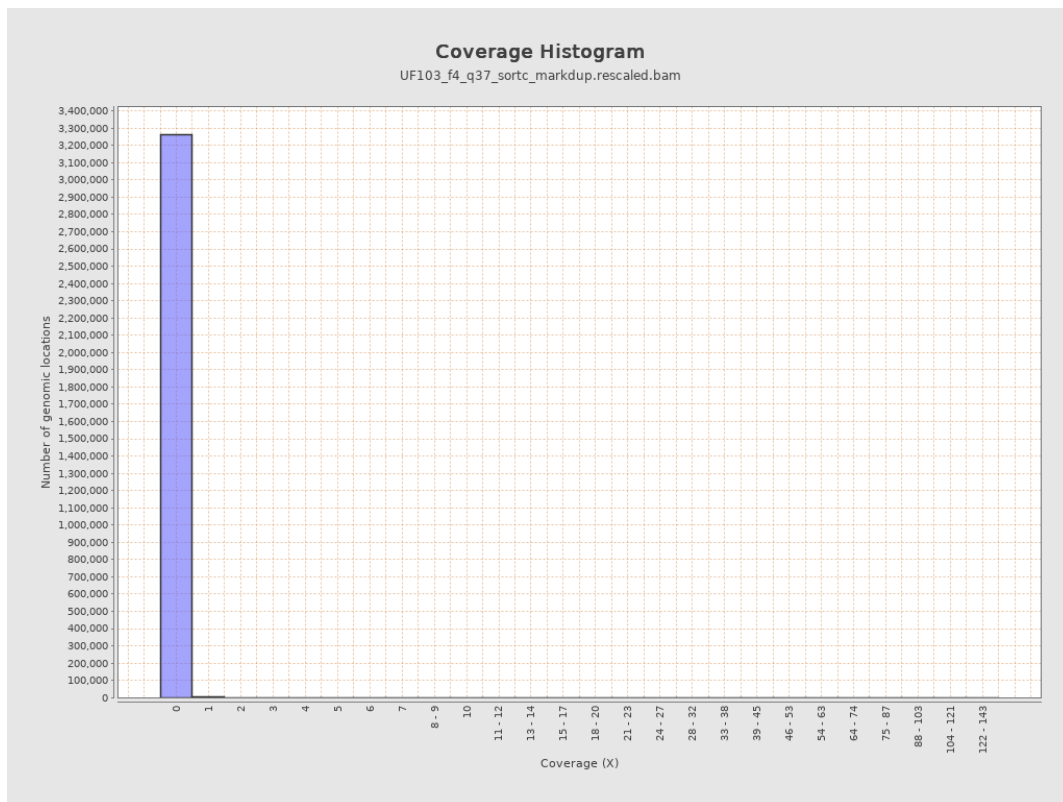|	
General error rate	4.22%
Mismatches	4,653
Insertions	44
Mapped reads with at least one insertion	2.37%
Deletions	40
Mapped reads with at least one deletion	2.15%
Homopolymer indels	13.1%

2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
ENA|AL450380|AL450380.1	3268203	111196	0.034	1.4263

3. Results : Coverage across reference

Coverage across reference
UF103_f4_q37_sortc_markdup.rescaled.bam
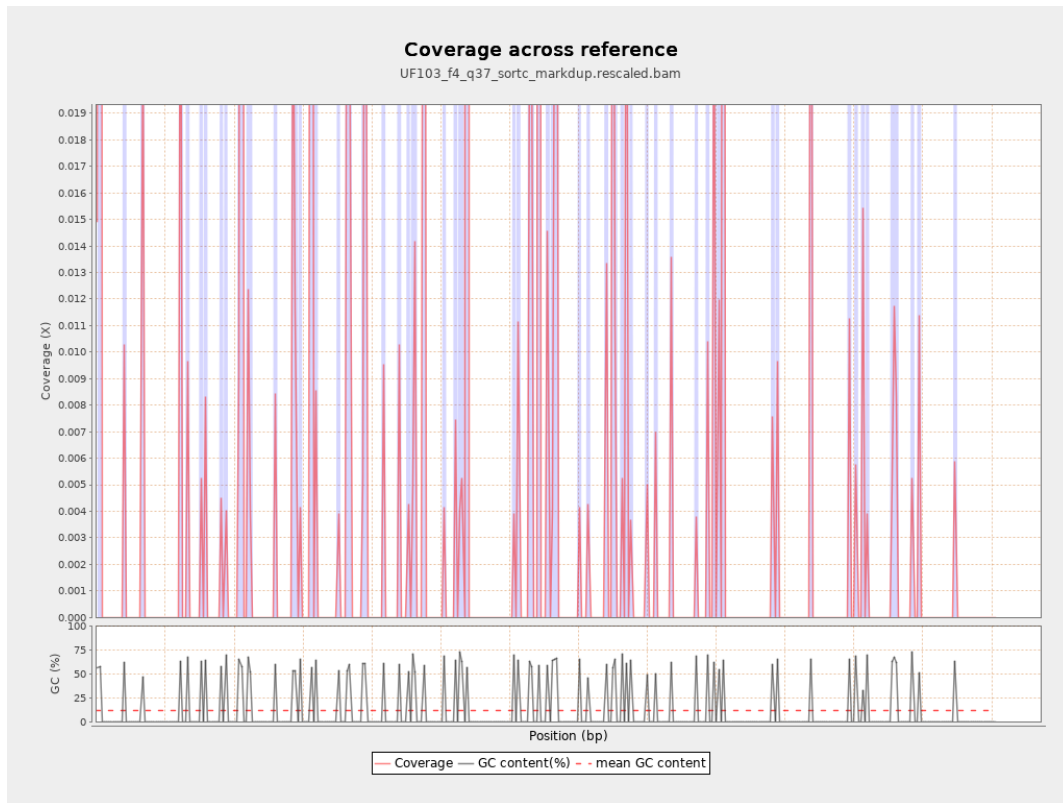
4. Results : Coverage Histogram

5. Results : Coverage Histogram (0-50X)

Coverage Histogram (0-50X)
UF103_f4_q37_sortc_markdup.rescaled.bam
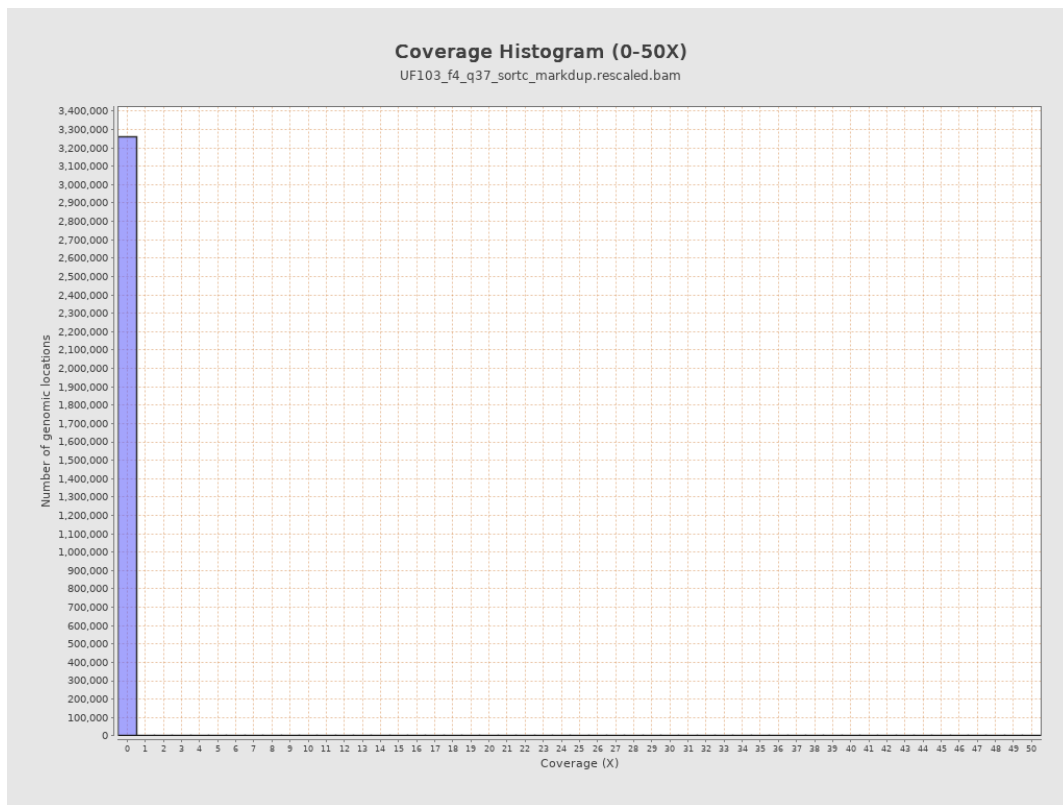
6. Results : Genome Fraction Coverage
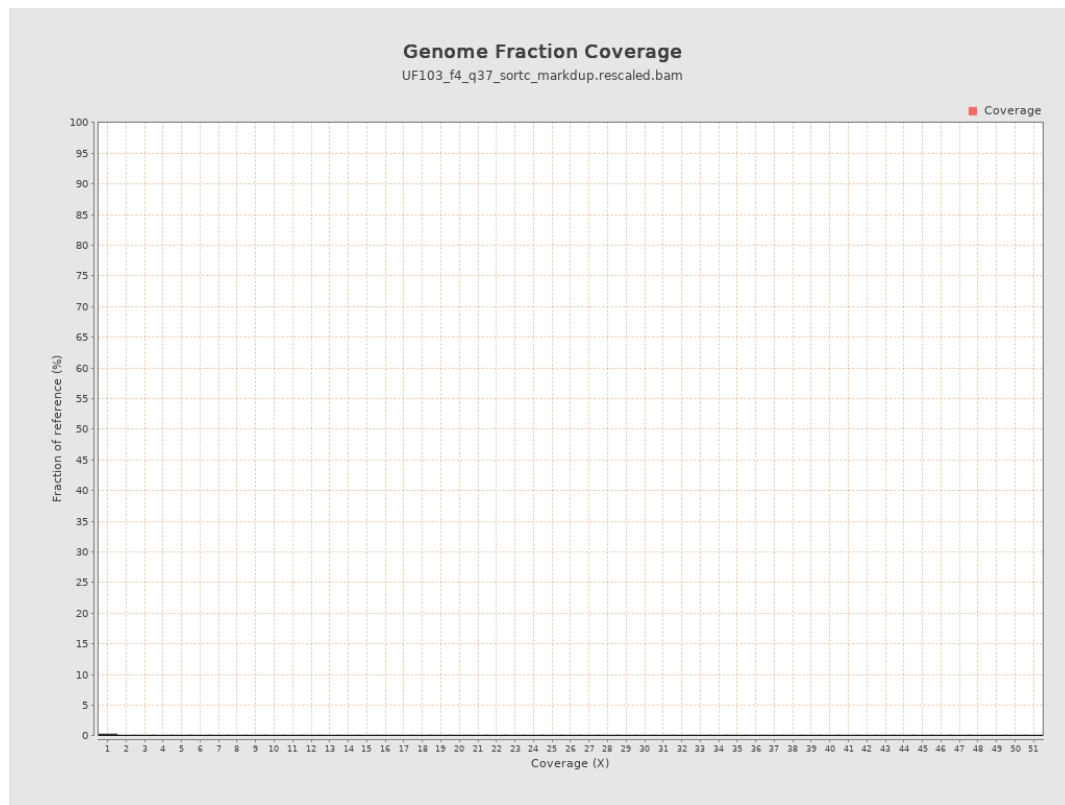
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
UF103_f4_q37_sortc_markdup.rescaled.bam

8. Results : Mapped Reads Nucleotide Content

Mapped Reads Nucleotide Content
UF103_f4_q37_sortc_markdup.rescaled.bam
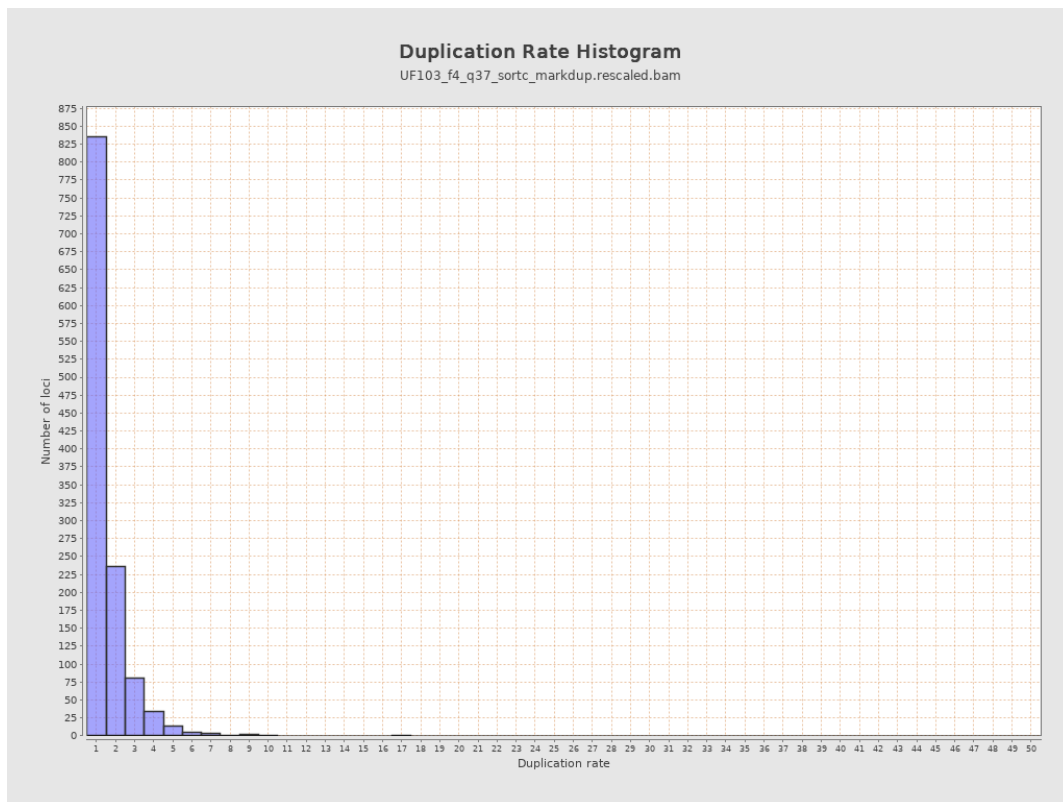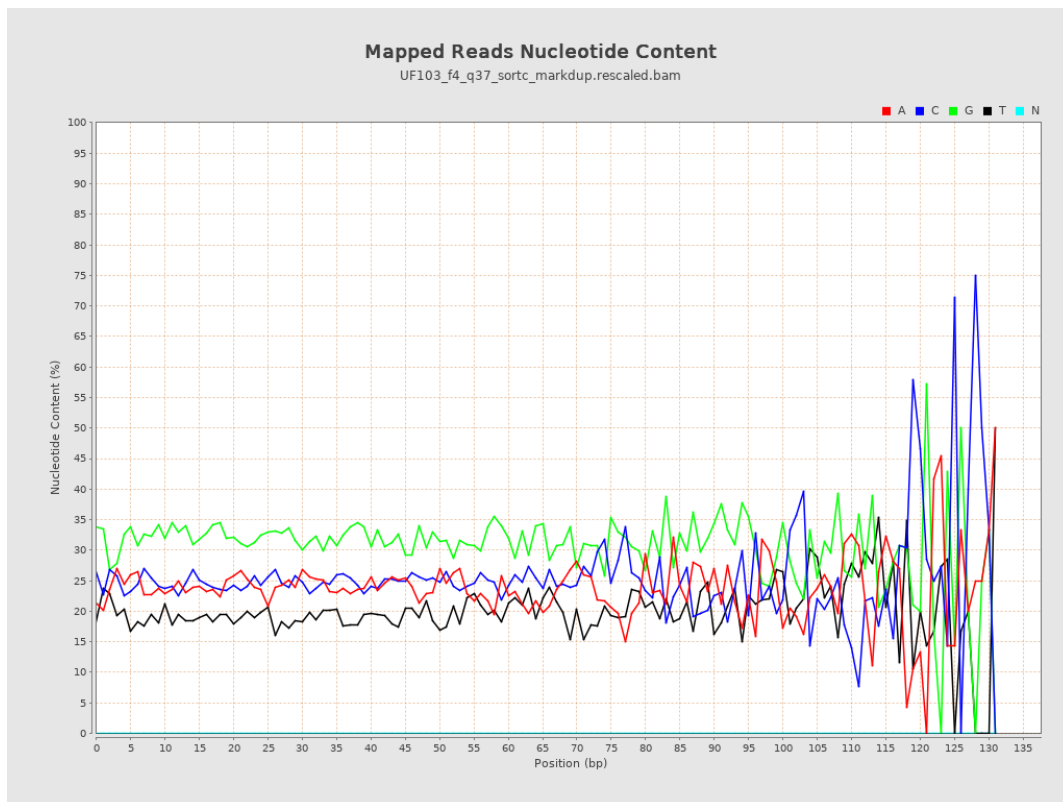
9. Results : Mapped Reads GC-content Distribution
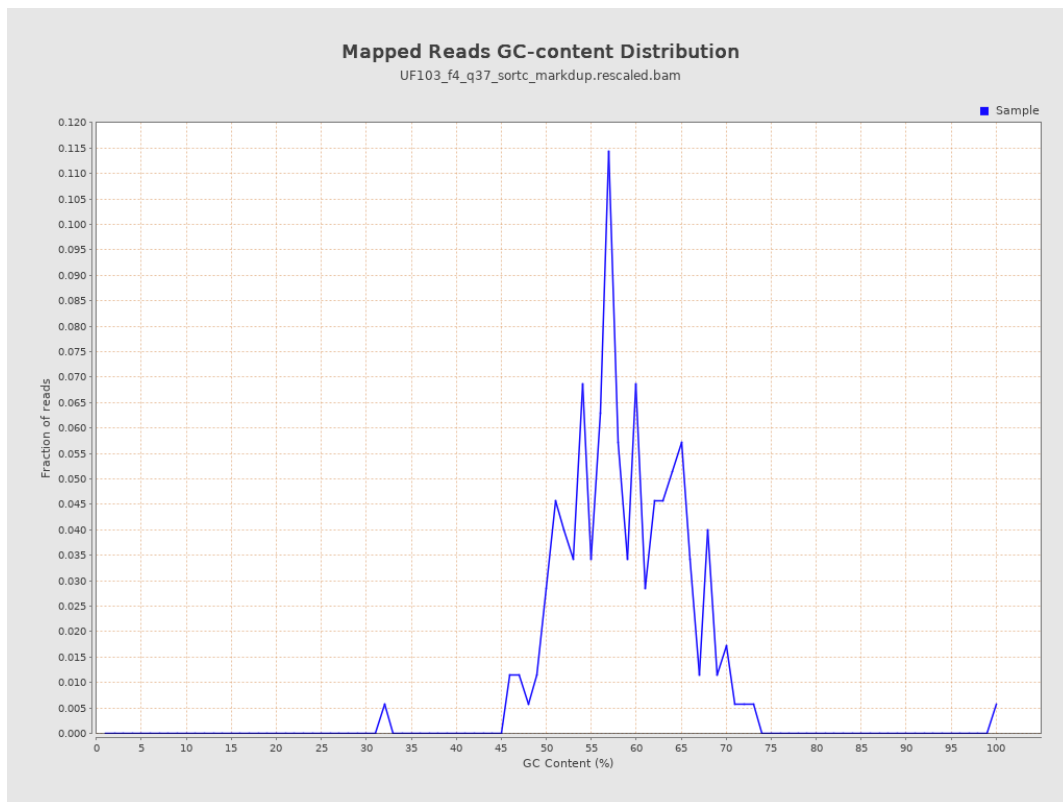
10. Results : Homopolymer Indels

Homopolymer Indels
UF103_f4_q37_sortc_markdup.rescaled.bam
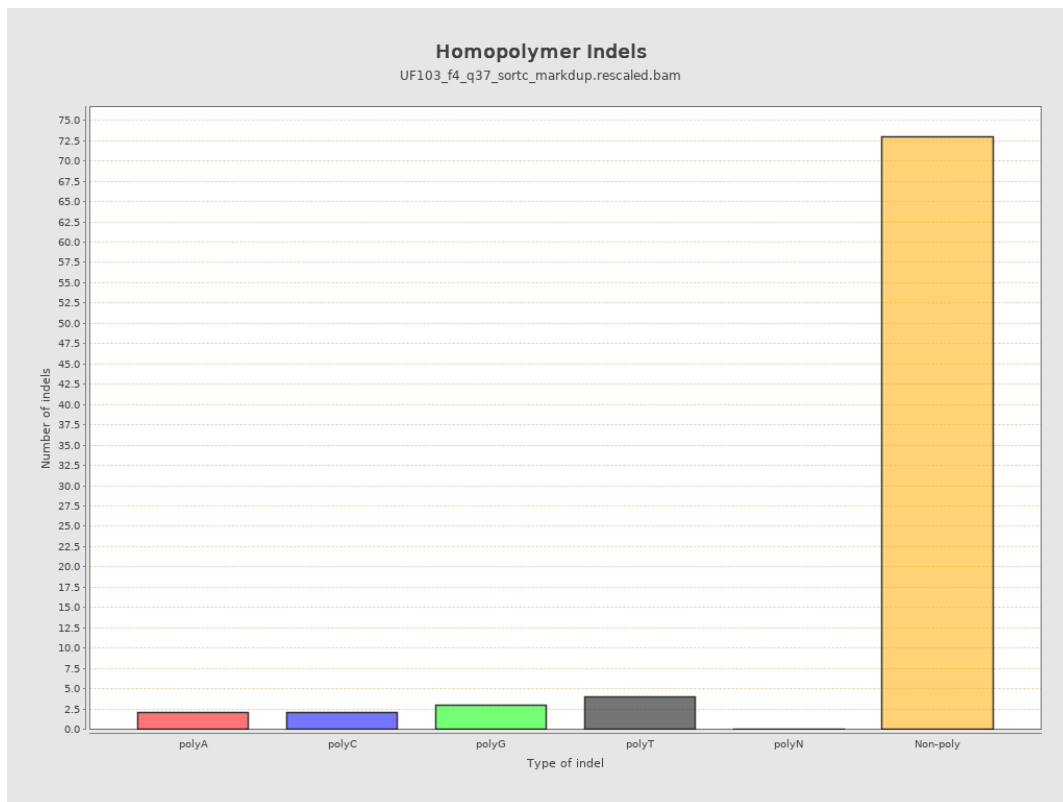
11. Results : Mapping Quality Across Reference

12. Results : Mapping Quality Histogram

Mapping Quality Histogram
UF103_f4_q37_sortc_markdup.rescaled.bam