Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2022/03/01 01:48:28

1. Input data & parameters

1.1. QualiMap command line

> qualimap bamqc -bam
> output/UF18/UF18_f4_q37_sortc_markdup.rescaled.bam -nw 400 -hm 3

1.2. Alignment

Command line:	bwa samse -r @RG\tID:UF18\tSM:UF18\tLB:nan\tPL:ILLUMINA /data/stonelab/references/M_leprae_TN/M_leprae_TN.fasta output/UF18/UF18-ancient.sai output/UF18/UF18-ancient.trimmed.fq
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 01 01:48:27 MST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	output/UF18/UF18_f4_q37_sortc_markdup.rescaled.bam

2. Summary

2.1. Globals

Reference size	3,268,203
Number of reads	157
Mapped reads	157 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	30 / 132 / 56.5
Duplicated reads (estimated)	13 / 8.28%
Duplication rate	6.94%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	2,152 / 24.27%
Number/percentage of C's	2,301 / 25.95%
Number/percentage of T's	1,622 / 18.29%
Number/percentage of G's	2,793 / 31.5%
Number/percentage of N's	0 / 0%
GC Percentage	57.44%

2.3. Coverage

Mean	0.0027
Standard Deviation	0.1614

2.4. Mapping Quality

Mean Mapping Quality	3.61

2.5. Mismatches and indels

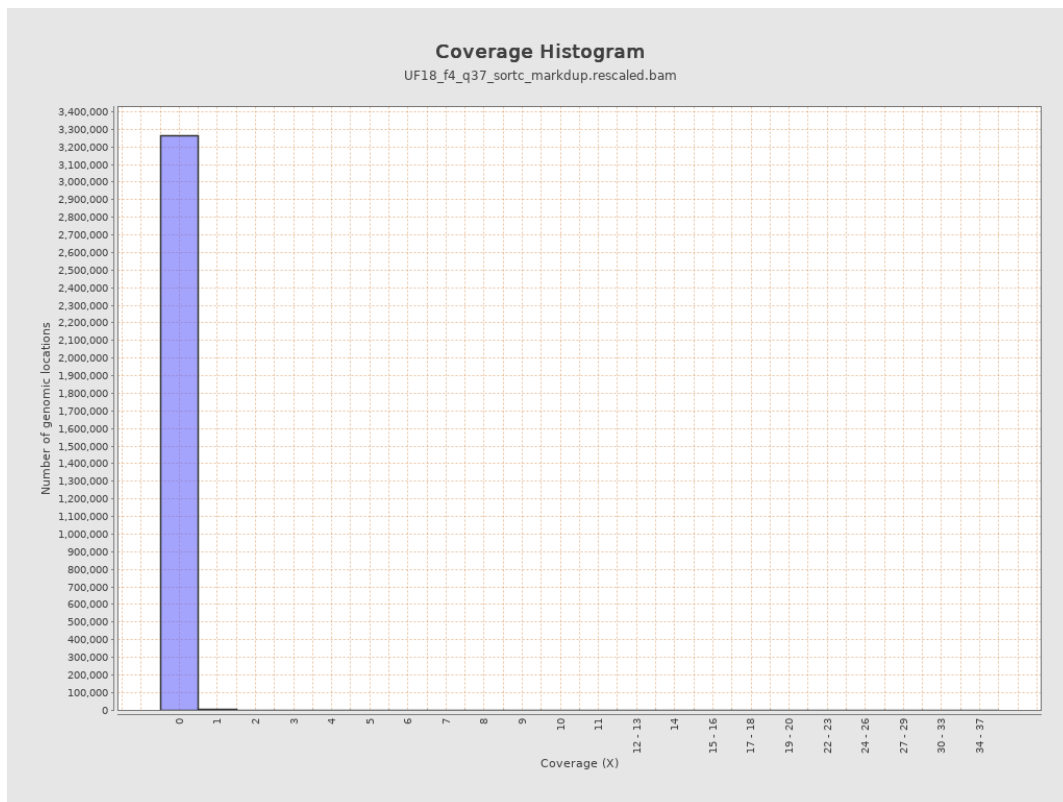|	
General error rate	3.84%
Mismatches	338
Insertions	3
Mapped reads with at least one insertion	1.91%
Deletions	3
Mapped reads with at least one deletion	1.91%
Homopolymer indels	33.33%

2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
ENA|AL450380|AL450380.1	3268203	8871	0.0027	0.1614

3. Results : Coverage across reference

Coverage across reference
UF18_f4_q37_sortc_markdup.rescaled.bam

4. Results : Coverage Histogram

Coverage Histogram
UF18_f4_q37_sortc_markdup.rescaled.bam

5. Results : Coverage Histogram (0-50X)
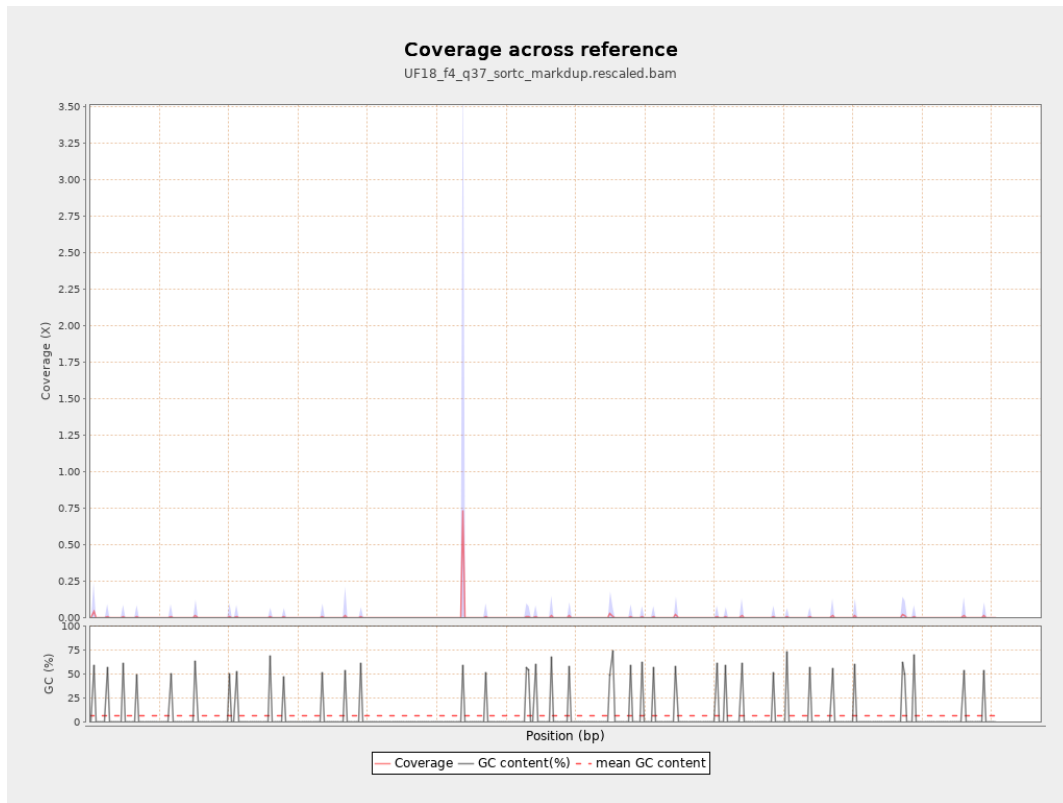
Coverage Histogram (0-50X)
UF18_f4_q37_sortc_markdup.rescaled.bam
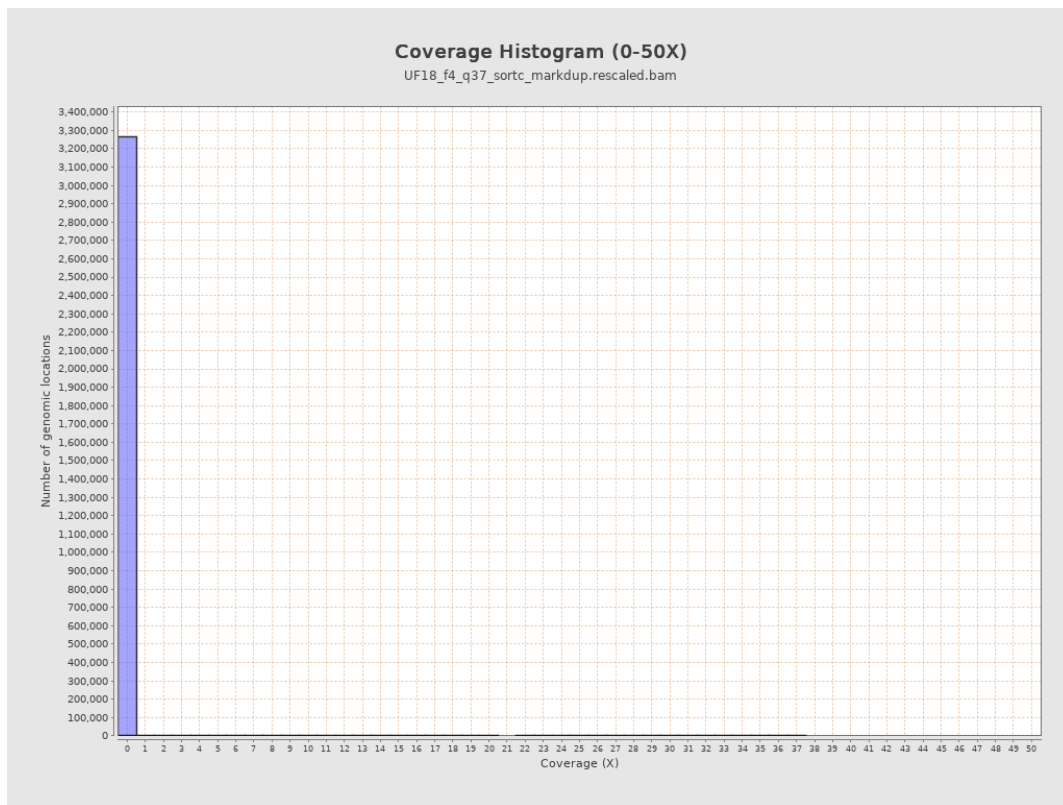
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
UF18_f4_q37_sortc_markdup.rescaled.bam
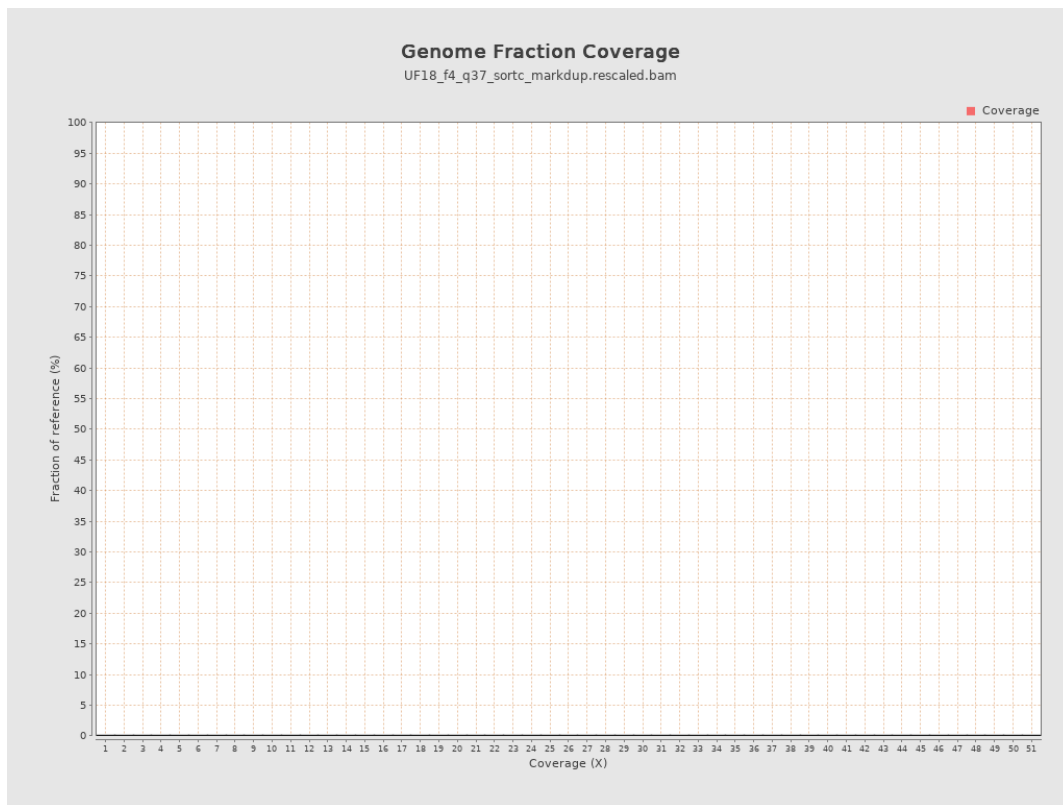
7. Results : Duplication Rate Histogram
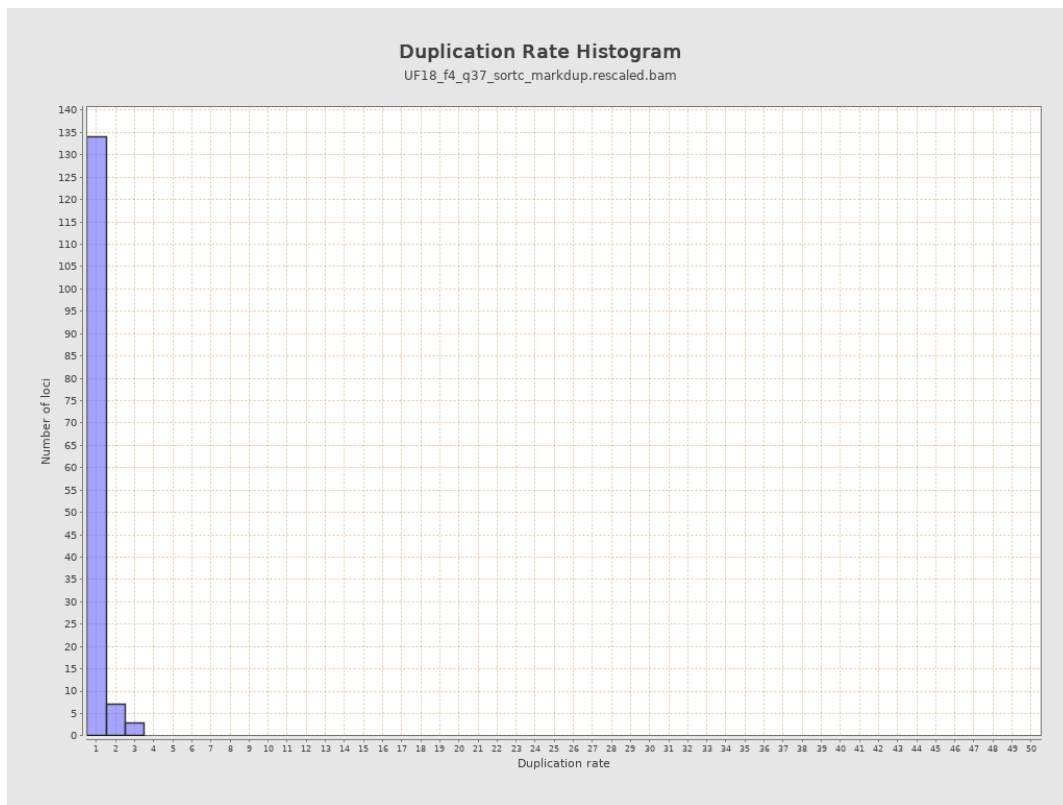
Duplication Rate Histogram
UF18_f4_q37_sortc_markdup.rescaled.bam

8. Results : Mapped Reads Nucleotide Content

Mapped Reads Nucleotide Content
UF18_f4_q37_sortc_markdup.rescaled.bam

9. Results : Mapped Reads GC-content Distribution

Mapped Reads GC-content Distribution
UF18_f4_q37_sortc_markdup.rescaled.bam
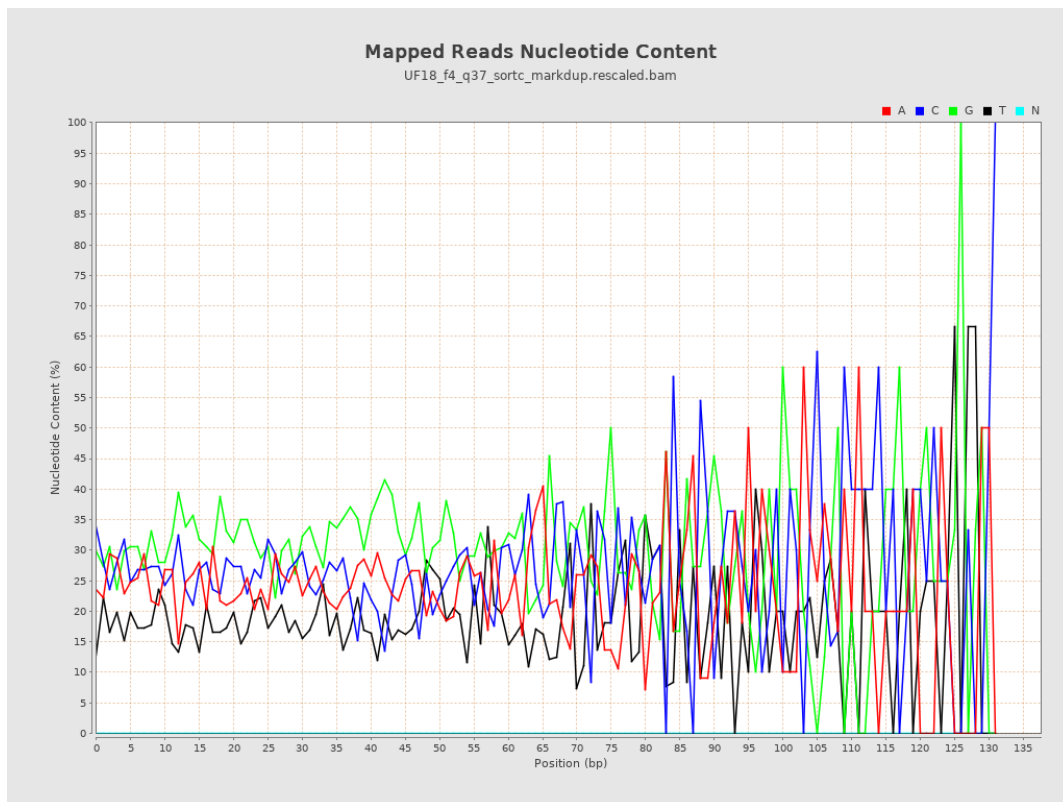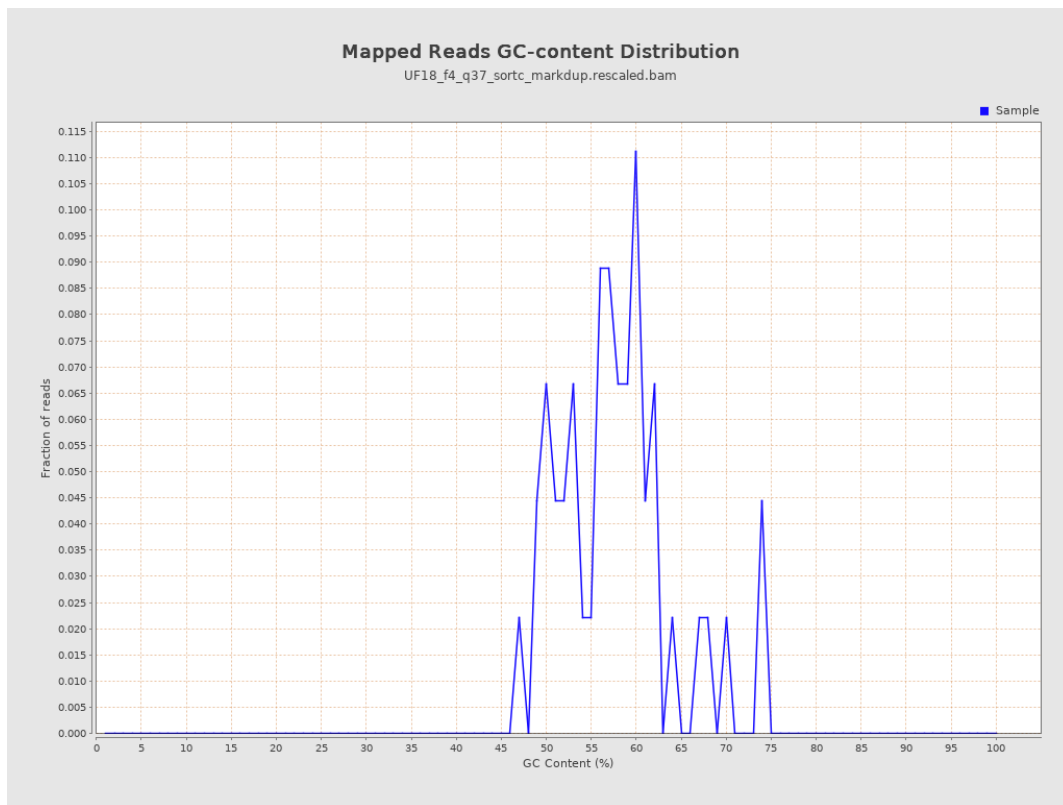
10. Results : Homopolymer Indels

Homopolymer Indels
UF18_f4_q37_sortc_markdup.rescaled.bam

11. Results : Mapping Quality Across Reference

Mapping Quality Across Reference
UF18_f4_q37_sortc_markdup.rescaled.bam

12. Results : Mapping Quality Histogram

Mapping Quality Histogram
UF18_f4_q37_sortc_markdup.rescaled.bam