Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2022/03/01 01:51:21

1. Input data & parameters

1.1. QualiMap command line

> qualimap bamqc -bam
> output/UF21/UF21_f4_q37_sortc_markdup.rescaled.bam -nw 400 -hm 3

1.2. Alignment

Command line:	bwa samse -r @RG\tID:UF21\tSM:UF21\tLB:nan\tPL:ILLUMINA /data/stonelab/references/M_leprae_TN/M_leprae_TN.fasta output/UF21/UF21-ancient.sai output/UF21/UF21-ancient.trimmed.fq
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 01 01:51:21 MST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	output/UF21/UF21_f4_q37_sortc_markdup.rescaled.bam

2. Summary

2.1. Globals

Reference size	3,268,203
Number of reads	2,262
Mapped reads	2,262 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	30 / 141 / 68.68
Duplicated reads (estimated)	116 / 5.13%
Duplication rate	4.01%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	35,352 / 22.76%
Number/percentage of C's	41,679 / 26.83%
Number/percentage of T's	34,456 / 22.18%
Number/percentage of G's	43,842 / 28.23%
Number/percentage of N's	0 / 0%
GC Percentage	55.06%

2.3. Coverage

Mean	0.0475
Standard Deviation	0.5304

2.4. Mapping Quality

Mean Mapping Quality	33.66

2.5. Mismatches and indels

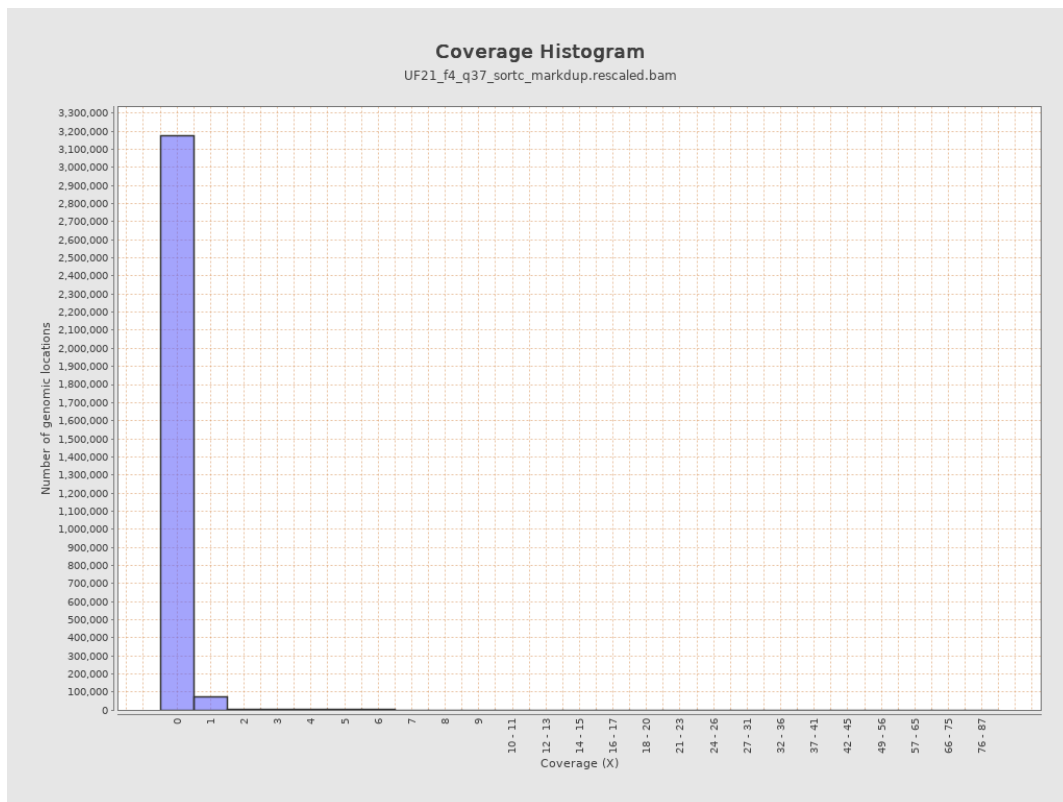|	
General error rate	1.37%
Mismatches	2,116
Insertions	10
Mapped reads with at least one insertion	0.44%
Deletions	29
Mapped reads with at least one deletion	1.28%
Homopolymer indels	20.51%

2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
ENA|AL450380|AL450380.1	3268203	155364	0.0475	0.5304

3. Results : Coverage across reference

Coverage across reference
UF21_f4_q37_sortc_markdup.rescaled.bam

4. Results : Coverage Histogram

Coverage Histogram
UF21_f4_q37_sortc_markdup.rescaled.bam

5. Results : Coverage Histogram (0-50X)
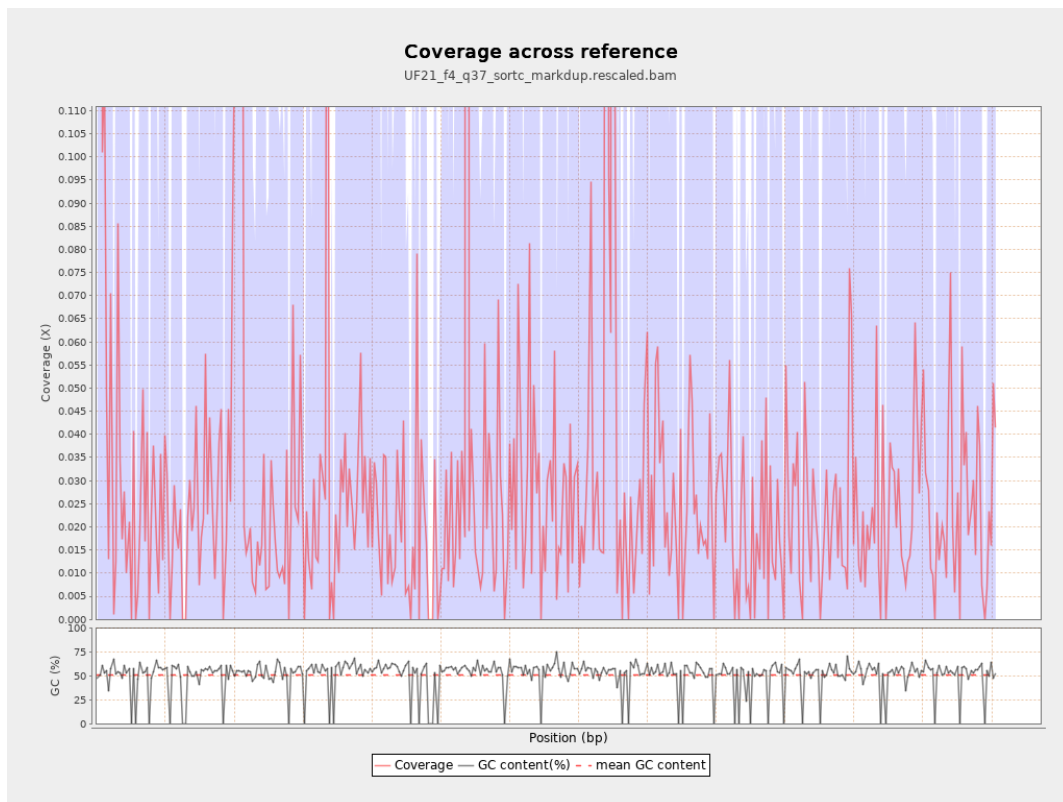
Coverage Histogram (0-50X)
UF21_f4_q37_sortc_markdup.rescaled.bam
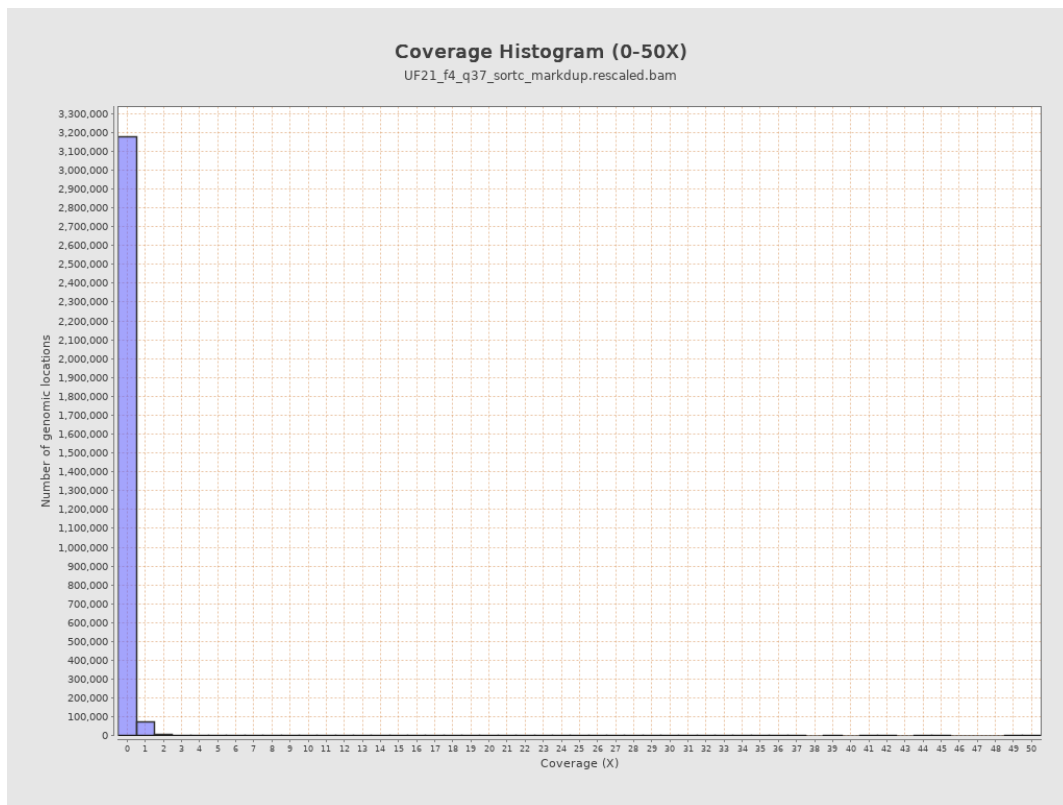
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
UF21_f4_q37_sortc_markdup.rescaled.bam
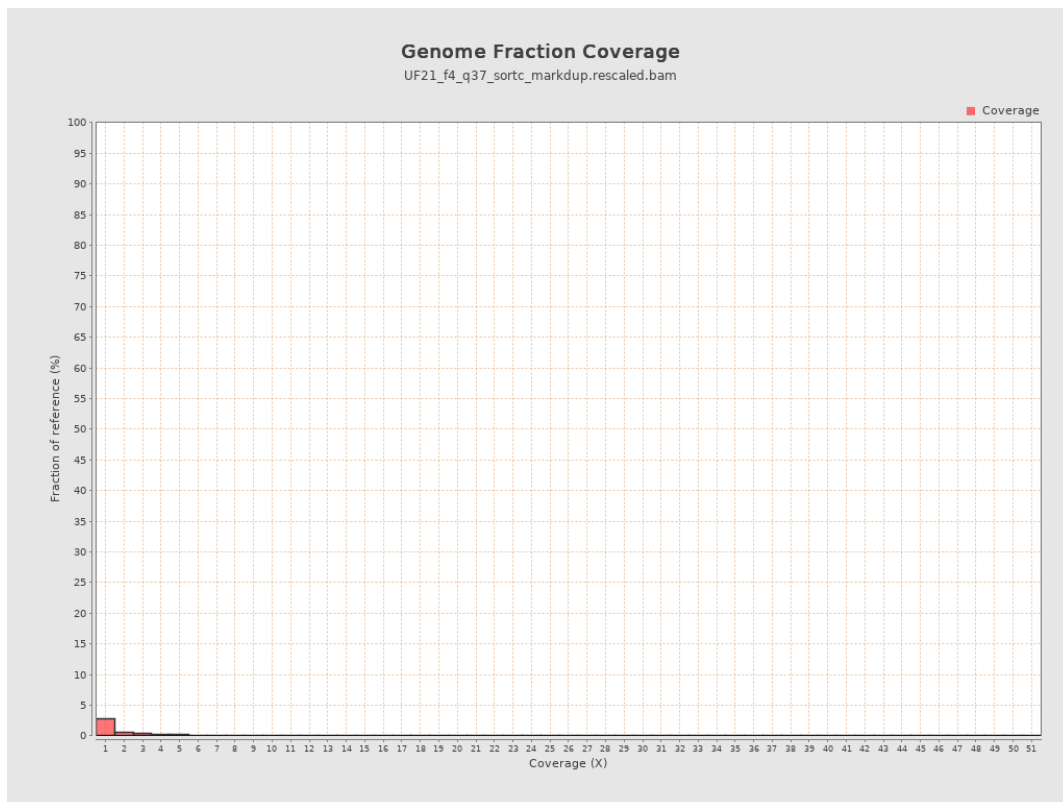
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
UF21_f4_q37_sortc_markdup.rescaled.bam
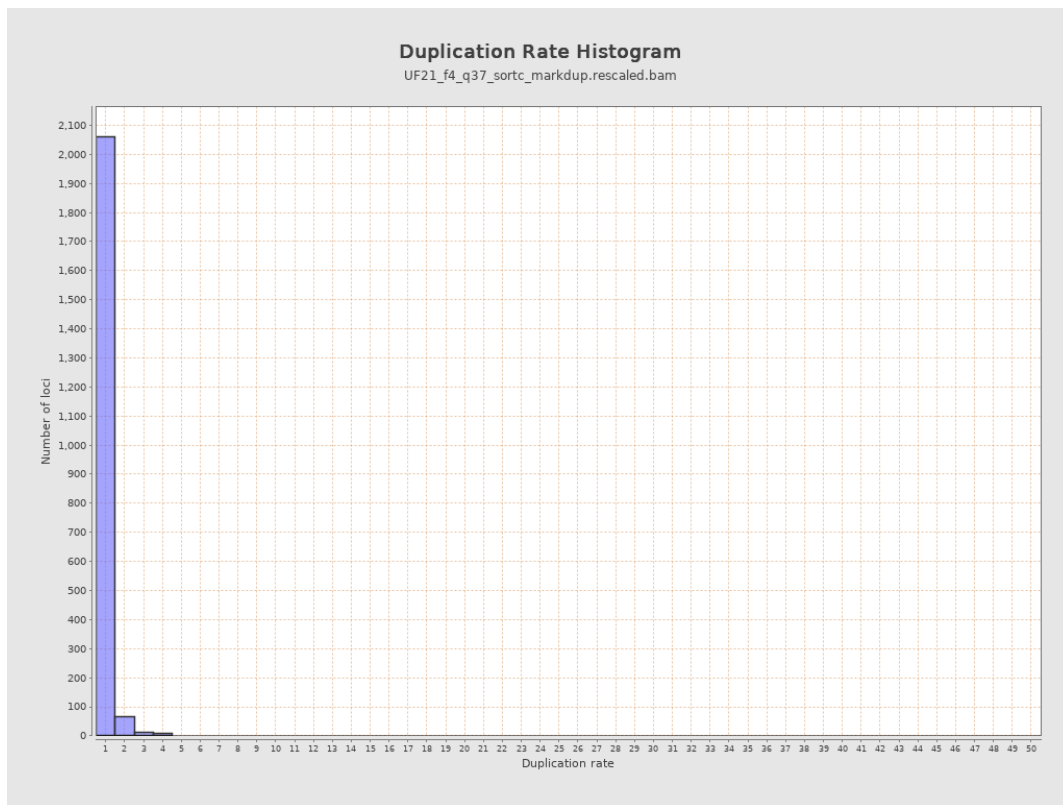
8. Results : Mapped Reads Nucleotide Content

9. Results : Mapped Reads GC-content Distribution

Mapped Reads GC-content Distribution
UF21_f4_q37_sortc_markdup.rescaled.bam
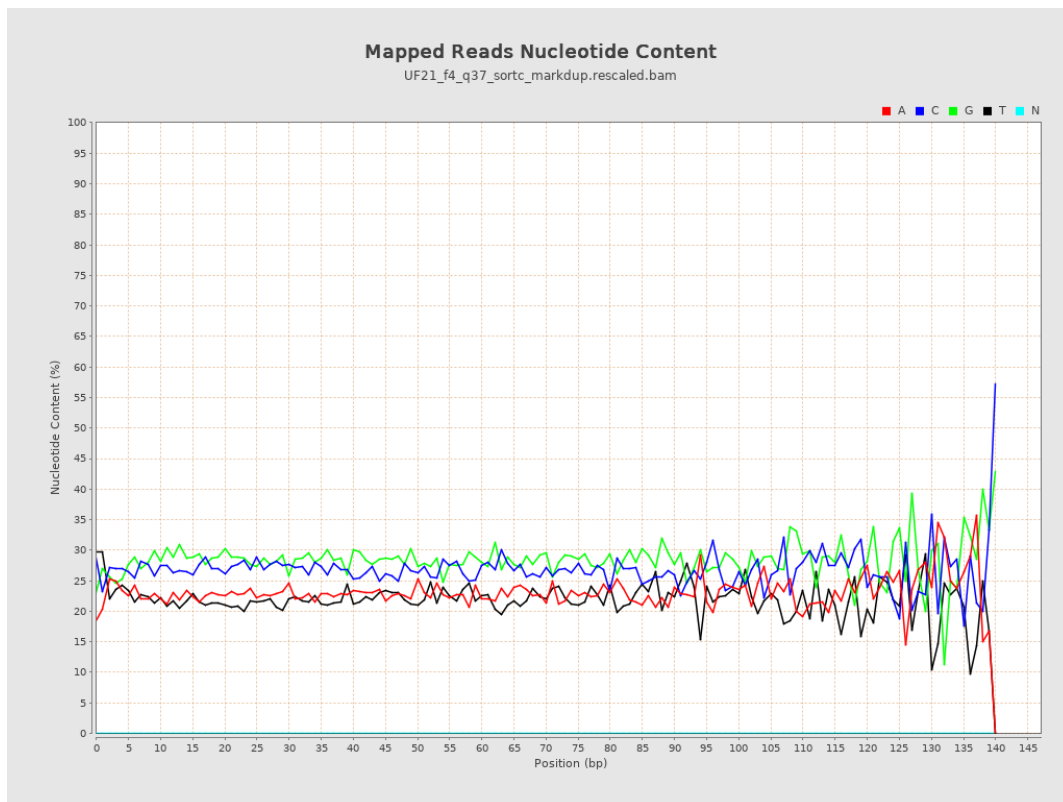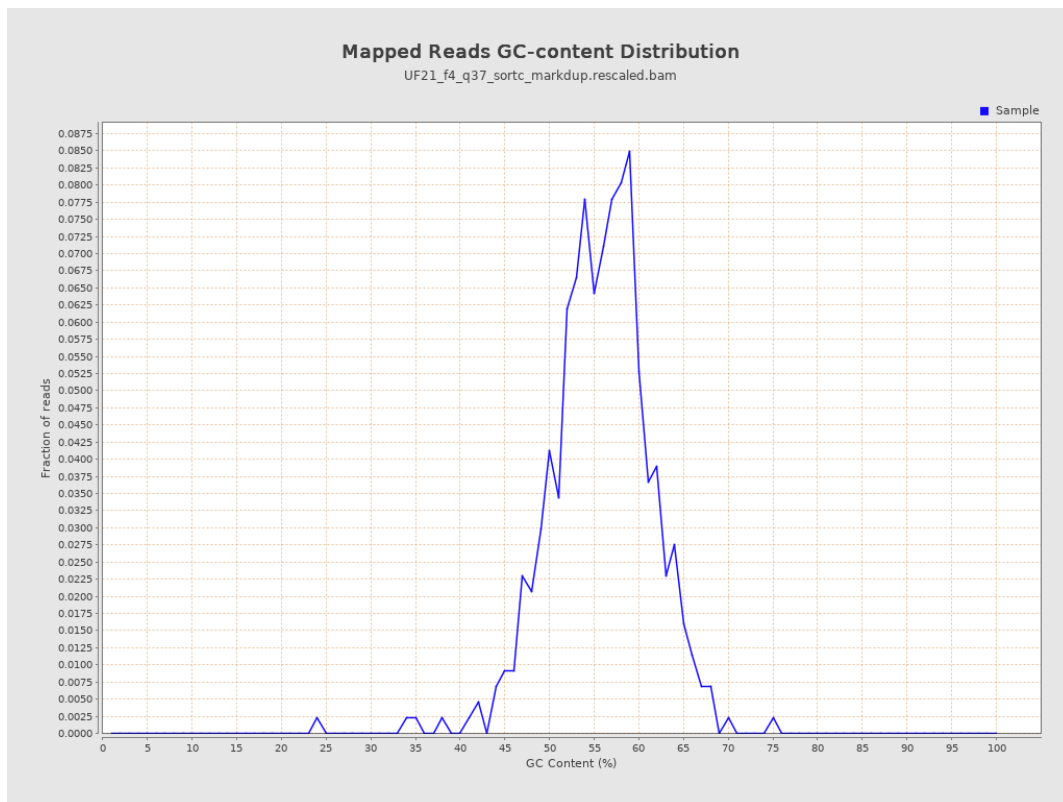
10. Results : Homopolymer Indels

11. Results : Mapping Quality Across Reference

Mapping Quality Across Reference
UF21_f4_q37_sortc_markdup.rescaled.bam

12. Results : Mapping Quality Histogram

Mapping Quality Histogram
UF21_f4_q37_sortc_markdup.rescaled.bam