Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2022/03/01 01:48:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
output/UF100/UF100_f4_q37_sortc_markdup.rescaled.bam -nw 400 -hm 3
```

1.2. Alignment

Command line:	bwa samse -r @RG\tID:UF100\tSM:UF100\tLB:nan\tPL:ILLUMINA /data/stonelab/references/M_leprae_TN/M_leprae_TN.fasta output/UF100/UF100-ancient.sai output/UF100/UF100-ancient.trimmed.fq
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 01 01:48:36 MST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	output/UF100/UF100_f4_q37_sortc_markdup.rescaled.bam

2. Summary

2.1. Globals

Reference size	3,268,203
Number of reads	369
Mapped reads	369 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	30 / 106 / 46.96
Duplicated reads (estimated)	47 / 12.74%
Duplication rate	12.11%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	4,287 / 24.74%
Number/percentage of C's	4,216 / 24.33%
Number/percentage of T's	3,210 / 18.53%
Number/percentage of G's	5,613 / 32.4%
Number/percentage of N's	0 / 0%
GC Percentage	56.73%

2.3. Coverage

Mean	0.0053
Standard Deviation	0.2789

2.4. Mapping Quality

Mean Mapping Quality	3.05

2.5. Mismatches and indels

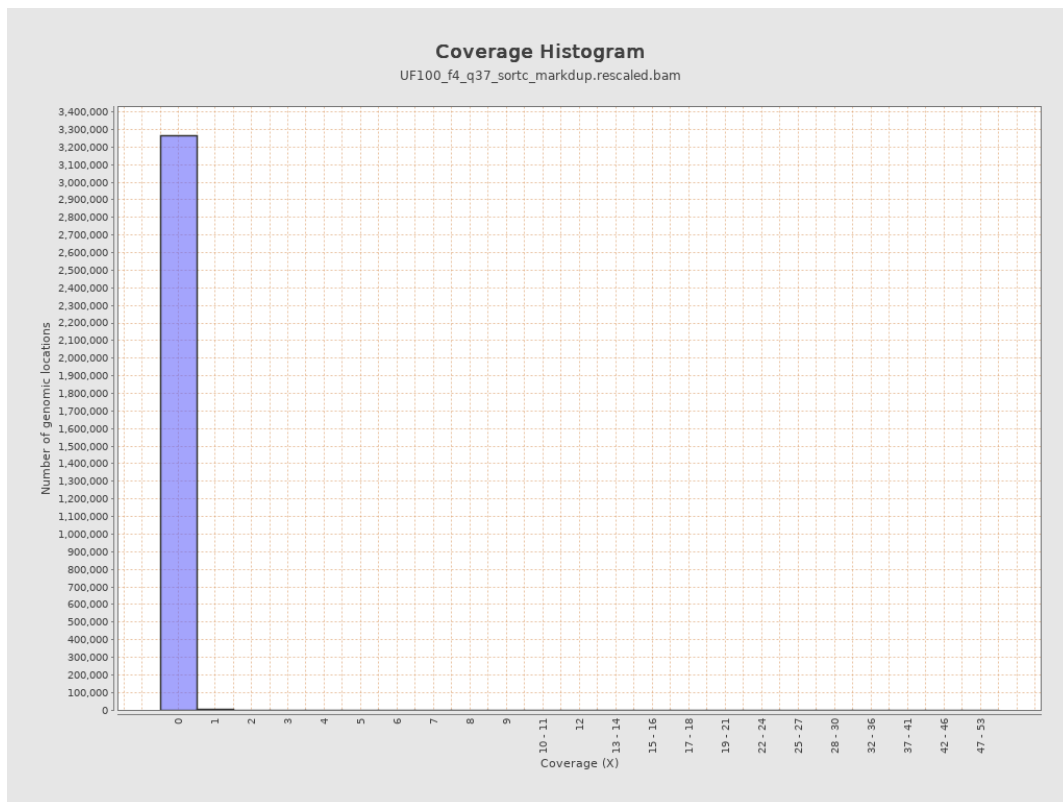|	
General error rate	4.06%
Mismatches	700
Insertions	3
Mapped reads with at least one insertion	0.81%
Deletions	8
Mapped reads with at least one deletion	2.17%
Homopolymer indels	9.09%

2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
ENA|AL450380|AL450380.1	3268203	17334	0.0053	0.2789

3. Results : Coverage across reference

Coverage across reference
UF100_f4_q37_sortc_markdup.rescaled.bam

4. Results : Coverage Histogram

Coverage Histogram
UF100_f4_q37_sortc_markdup.rescaled.bam

5. Results : Coverage Histogram (0-50X)
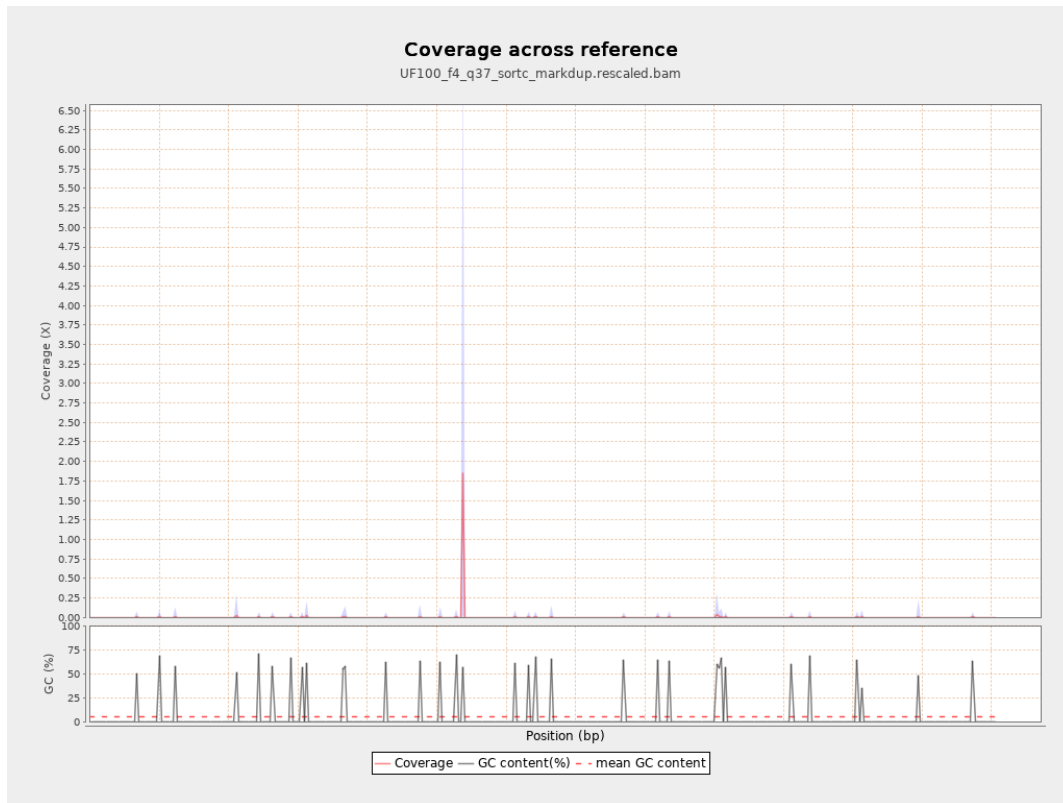
Coverage Histogram (0-50X)
UF100_f4_q37_sortc_markdup.rescaled.bam
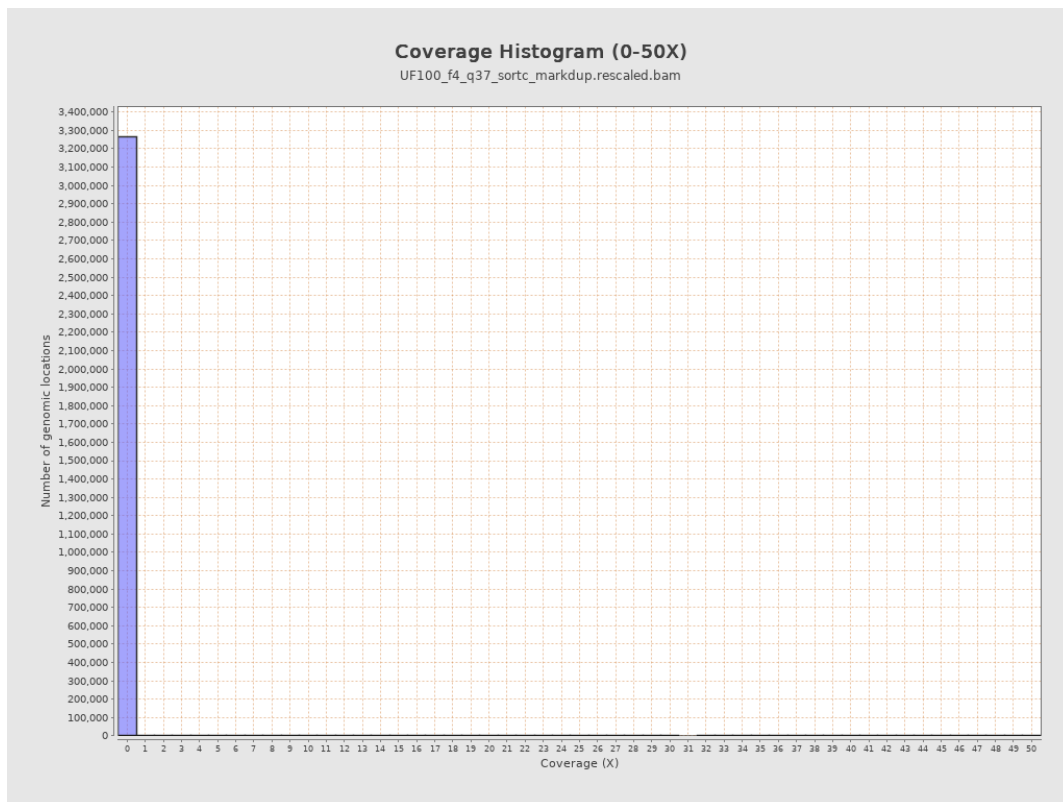
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
UF100_f4_q37_sortc_markdup.rescaled.bam
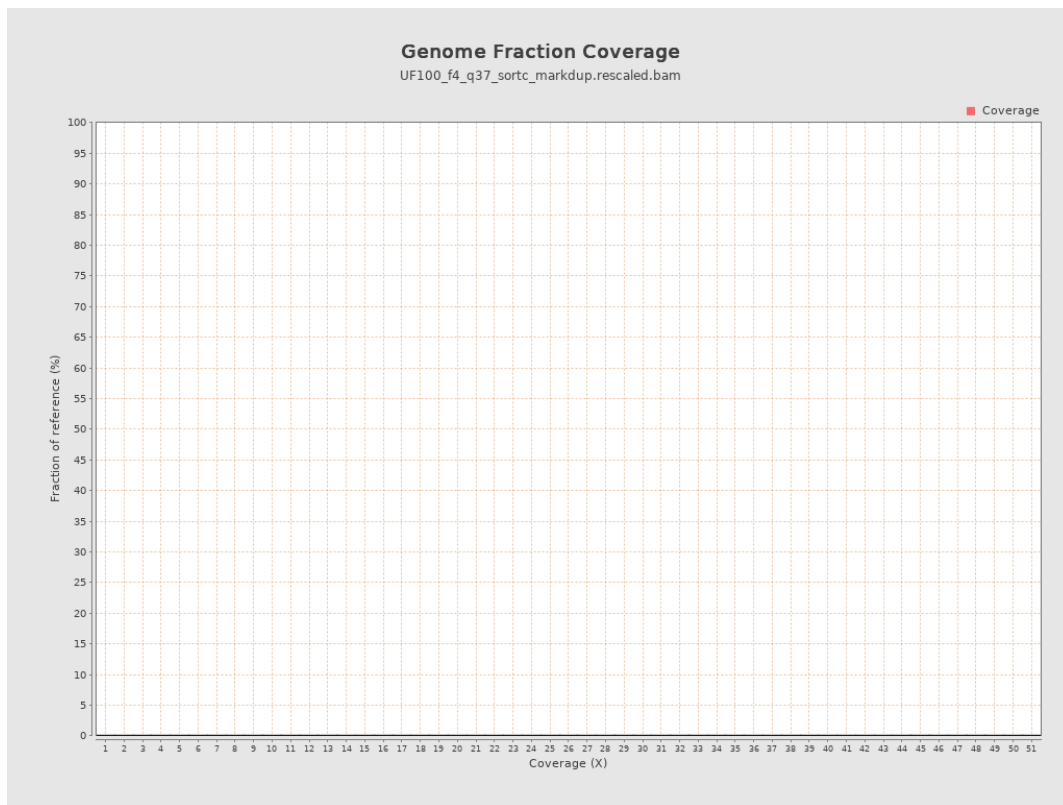
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
UF100_f4_q37_sortc_markdup.rescaled.bam
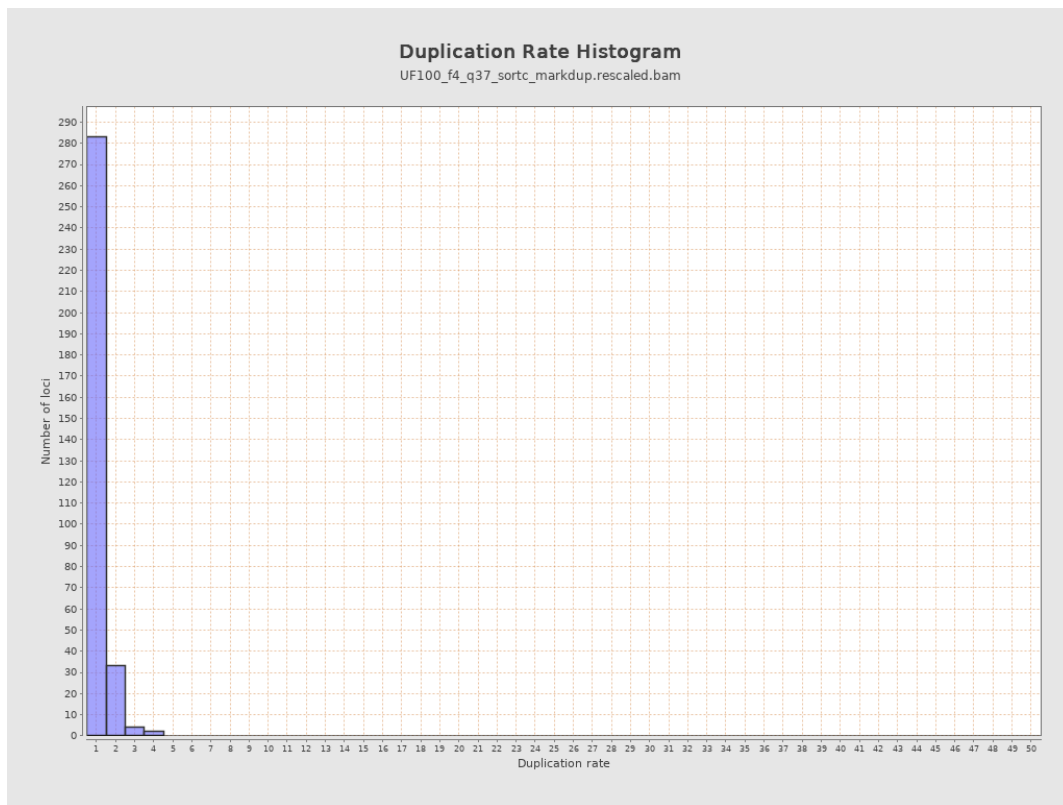
8. Results : Mapped Reads Nucleotide Content

9. Results : Mapped Reads GC-content Distribution

Mapped Reads GC-content Distribution
UF100_f4_q37_sortc_markdup.rescaled.bam
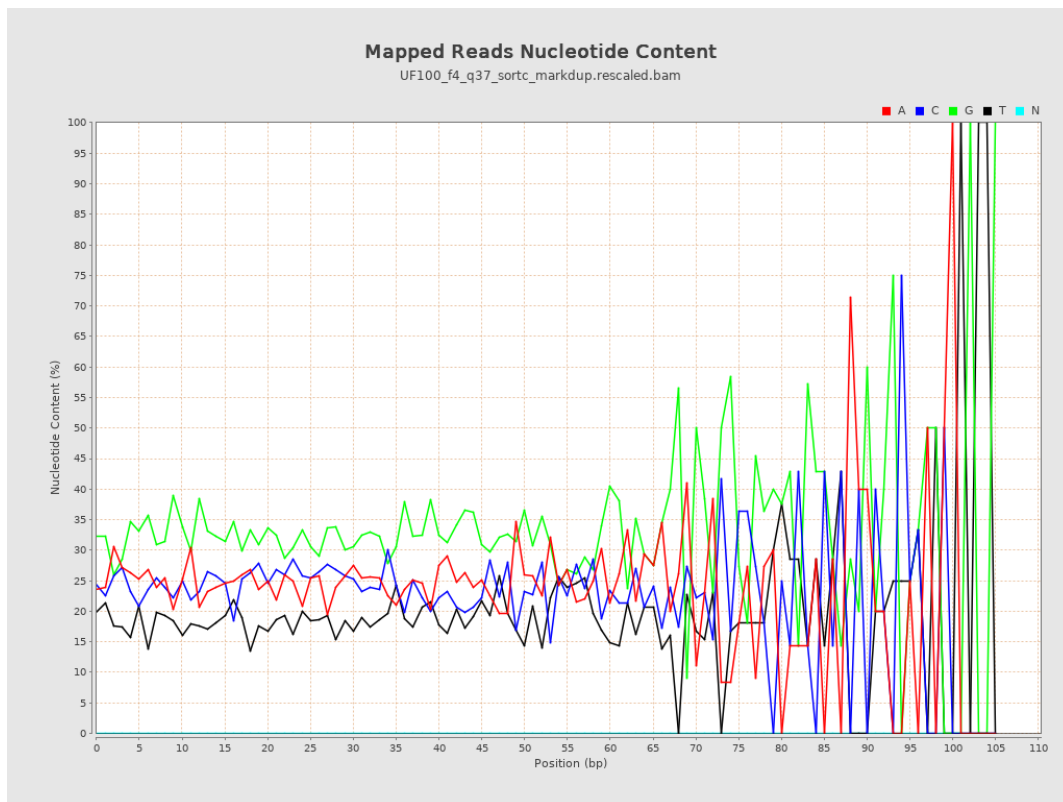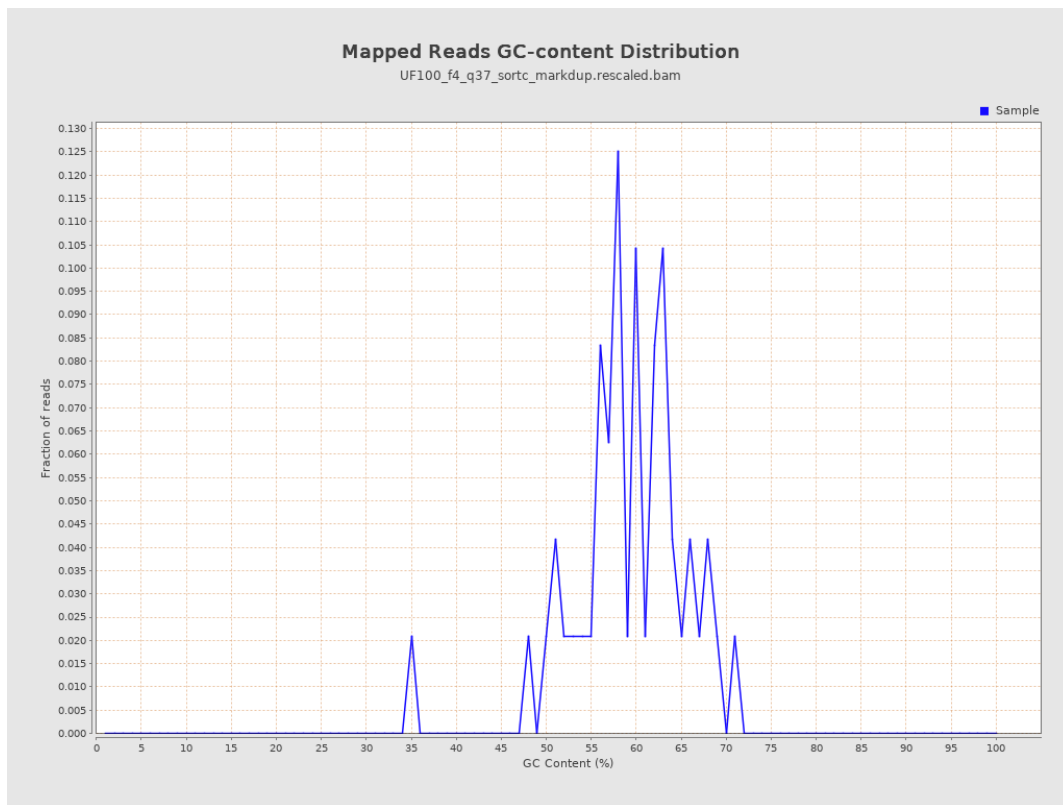
10. Results : Homopolymer Indels
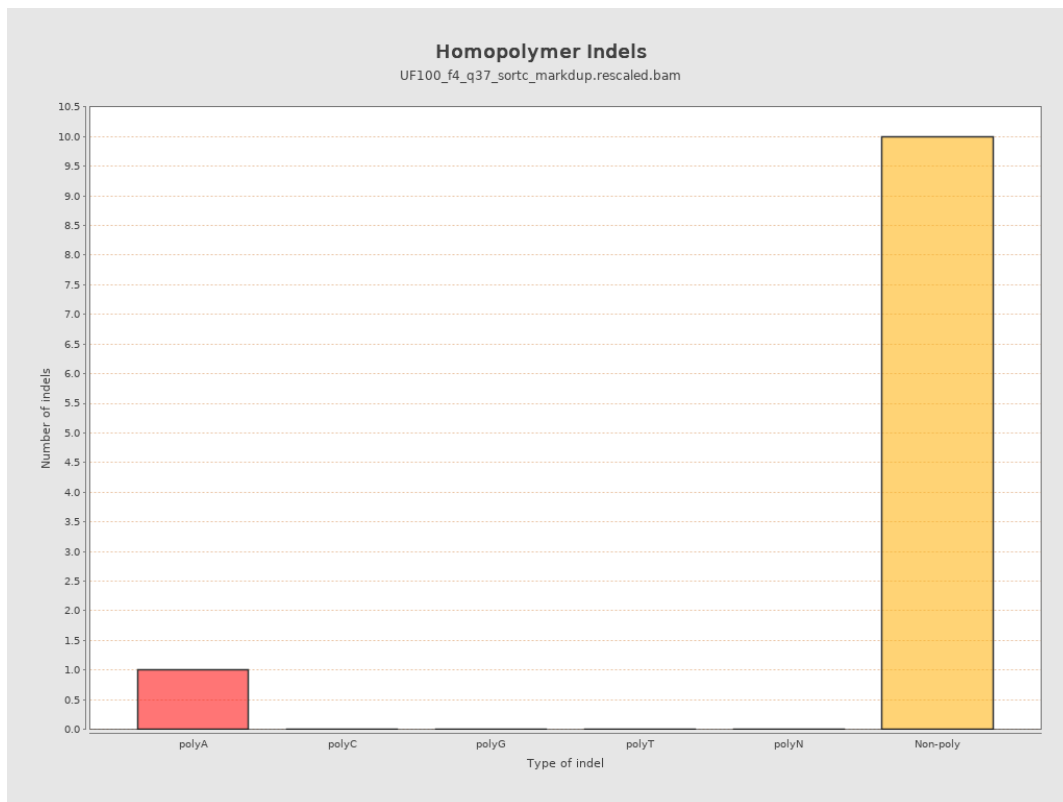
11. Results : Mapping Quality Across Reference

12. Results : Mapping Quality Histogram

Mapping Quality Histogram
UF100_f4_q37_sortc_markdup.rescaled.bam