Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2022/03/02 02:56:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
output/UF101/UF101_f4_q37_sortc_markdup.rescaled.bam -nw 400 -hm 3
```

1.2. Alignment

Command line:	bwa samse -r @RG\tID:UF101\tSM:UF101\tLB:nan\tPL:ILLUMINA /data/stonelab/references/Human_mitochondrial/NC_012920.1.fasta output/UF101/UF101-ancient.sai output/UF101/UF101-ancient.trimmed.fq
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 02 02:56:40 MST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	output/UF101/UF101_f4_q37_sortc_markdup.rescaled.bam

2. Summary

2.1. Globals

Reference size	16,569
Number of reads	6,648
Mapped reads	6,648 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	30 / 129 / 73.22
Duplicated reads (estimated)	1,315 / 19.78%
Duplication rate	20.4%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	153,461 / 31.53%
Number/percentage of C's	151,022 / 31.03%
Number/percentage of T's	127,957 / 26.29%
Number/percentage of G's	54,275 / 11.15%
Number/percentage of N's	0 / 0%
GC Percentage	42.18%

2.3. Coverage

Mean	29.3775
Standard Deviation	15.41

2.4. Mapping Quality

Mean Mapping Quality	36.35

2.5. Mismatches and indels

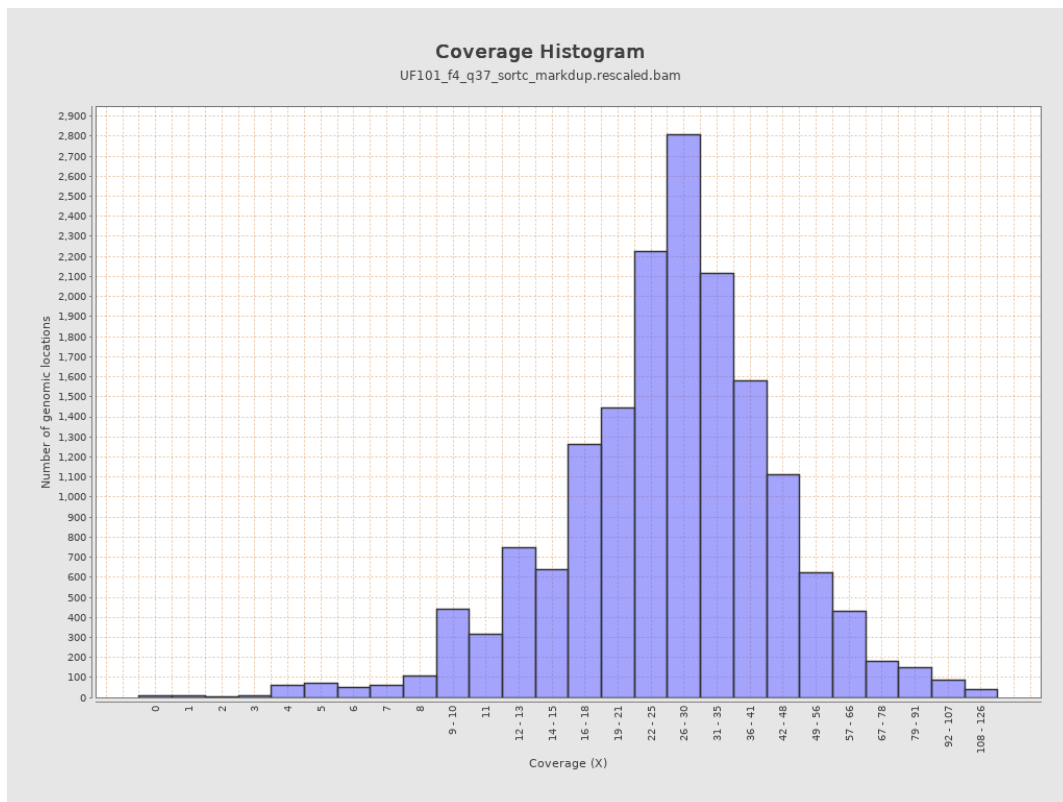|	
General error rate	2.15%
Mismatches	10,461
Insertions	23
Mapped reads with at least one insertion	0.3%
Deletions	37
Mapped reads with at least one deletion	0.56%
Homopolymer indels	38.33%

2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
NC_012920.1	16569	486756	29.3775	15.41

3. Results : Coverage across reference

Coverage across reference
UF101_f4_q37_sortc_markdup.rescaled.bam

4. Results : Coverage Histogram

Coverage Histogram
UF101_f4_q37_sortc_markdup.rescaled.bam

5. Results : Coverage Histogram (0-50X)
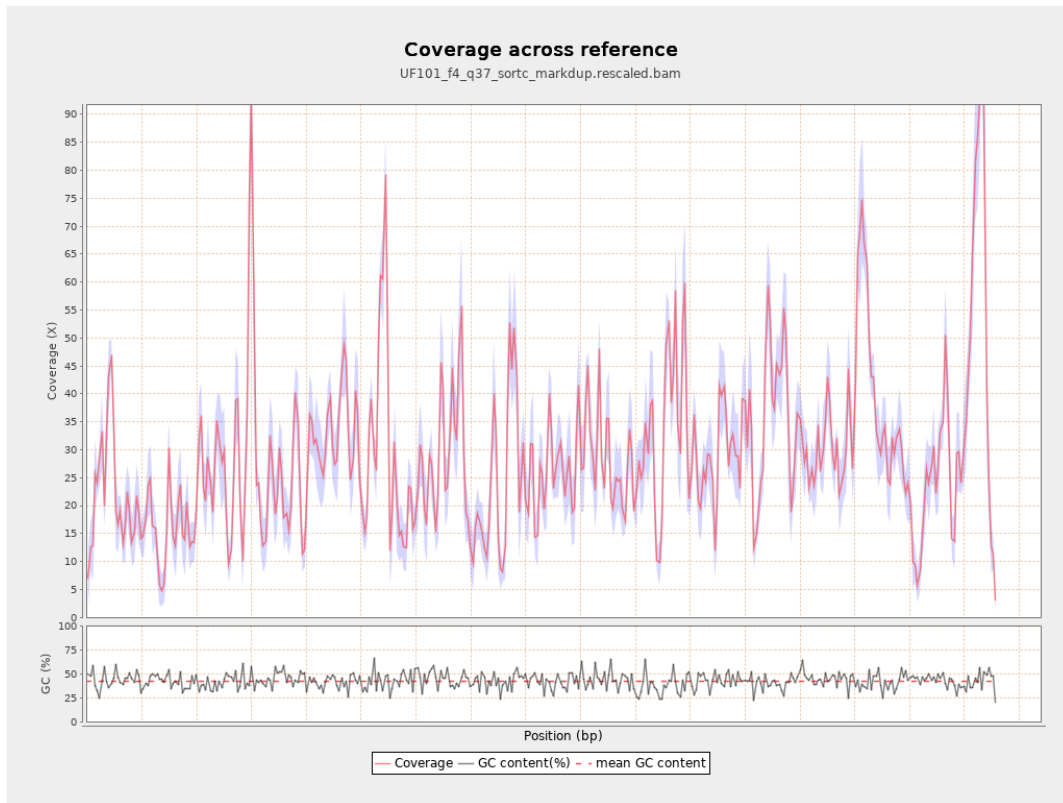
Coverage Histogram (0-50X)
UF101_f4_q37_sortc_markdup.rescaled.bam
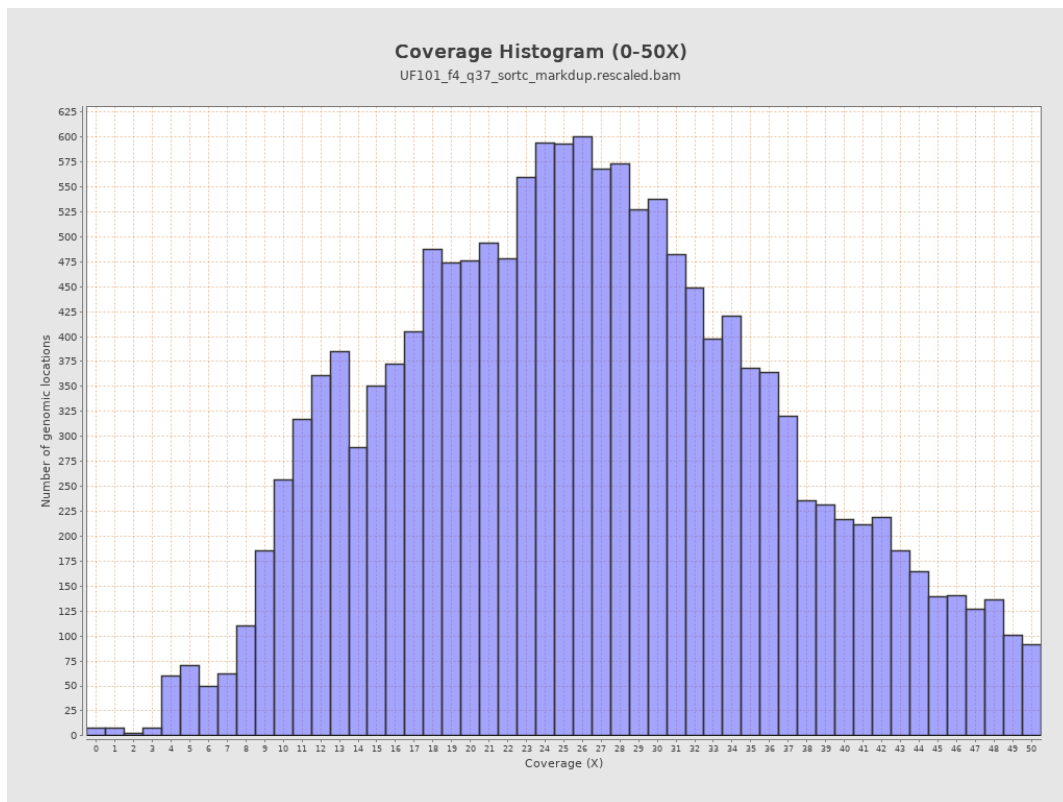
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
UF101_f4_q37_sortc_markdup.rescaled.bam
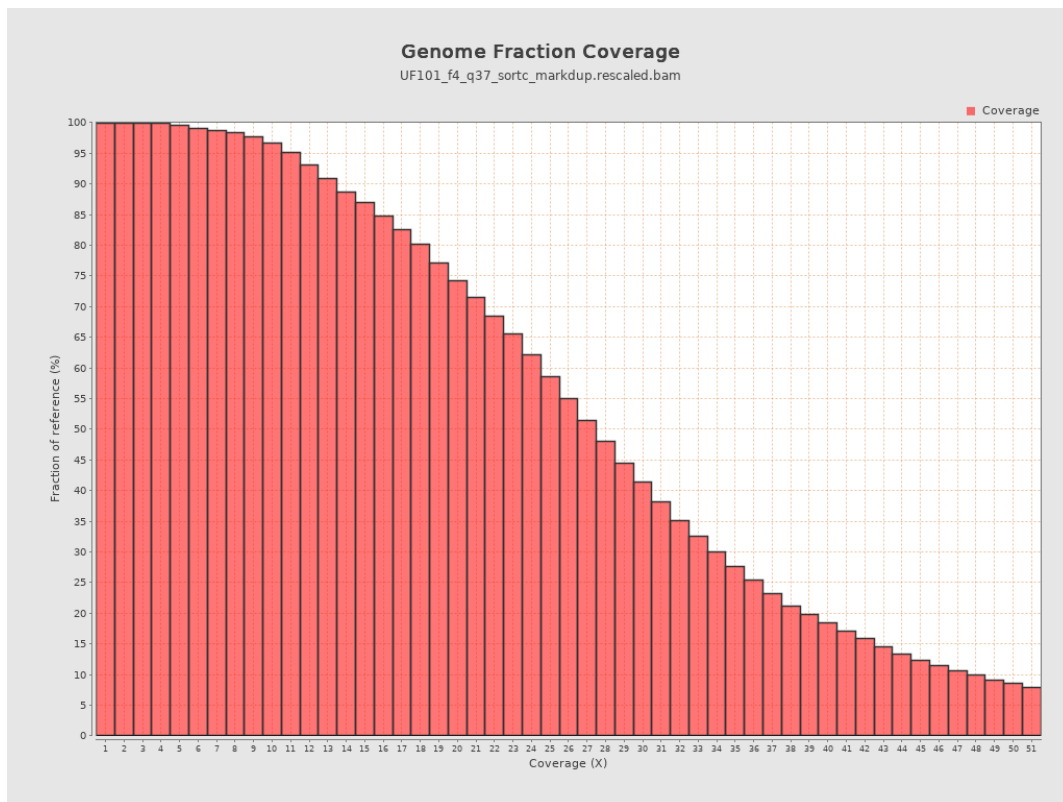
7. Results : Duplication Rate Histogram
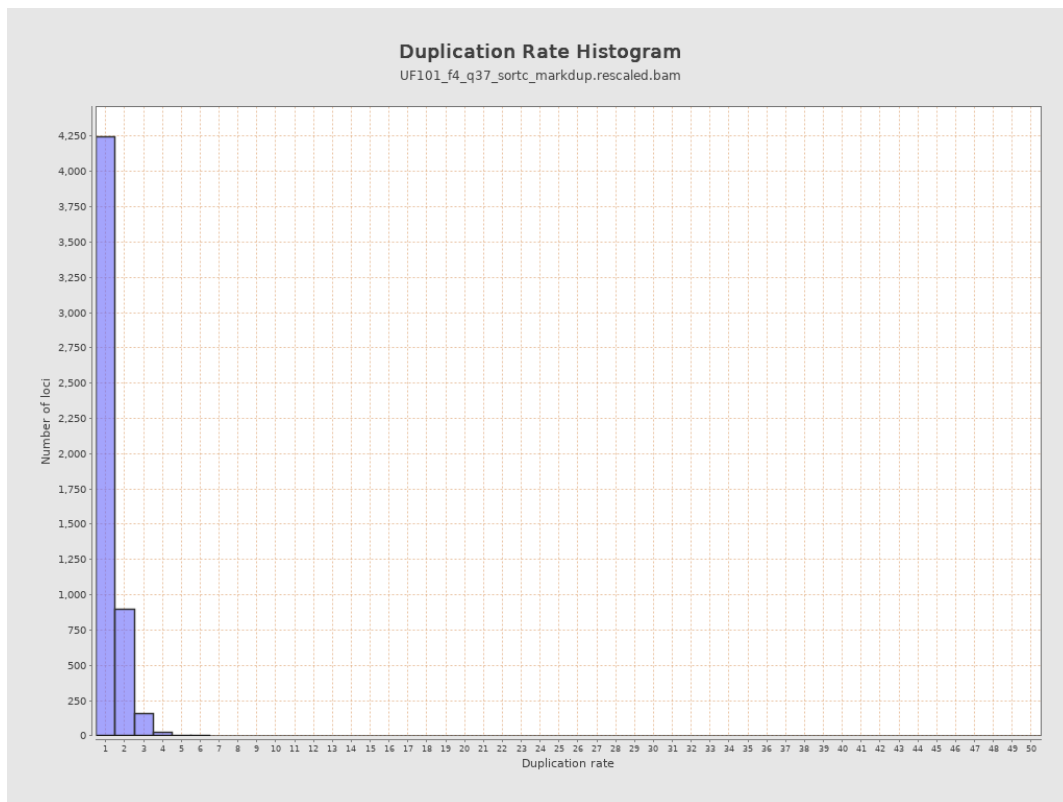
Duplication Rate Histogram
UF101_f4_q37_sortc_markdup.rescaled.bam

8. Results : Mapped Reads Nucleotide Content

Mapped Reads Nucleotide Content
UF101_f4_q37_sortc_markdup.rescaled.bam

9. Results : Mapped Reads GC-content Distribution

Mapped Reads GC-content Distribution
UF101_f4_q37_sortc_markdup.rescaled.bam
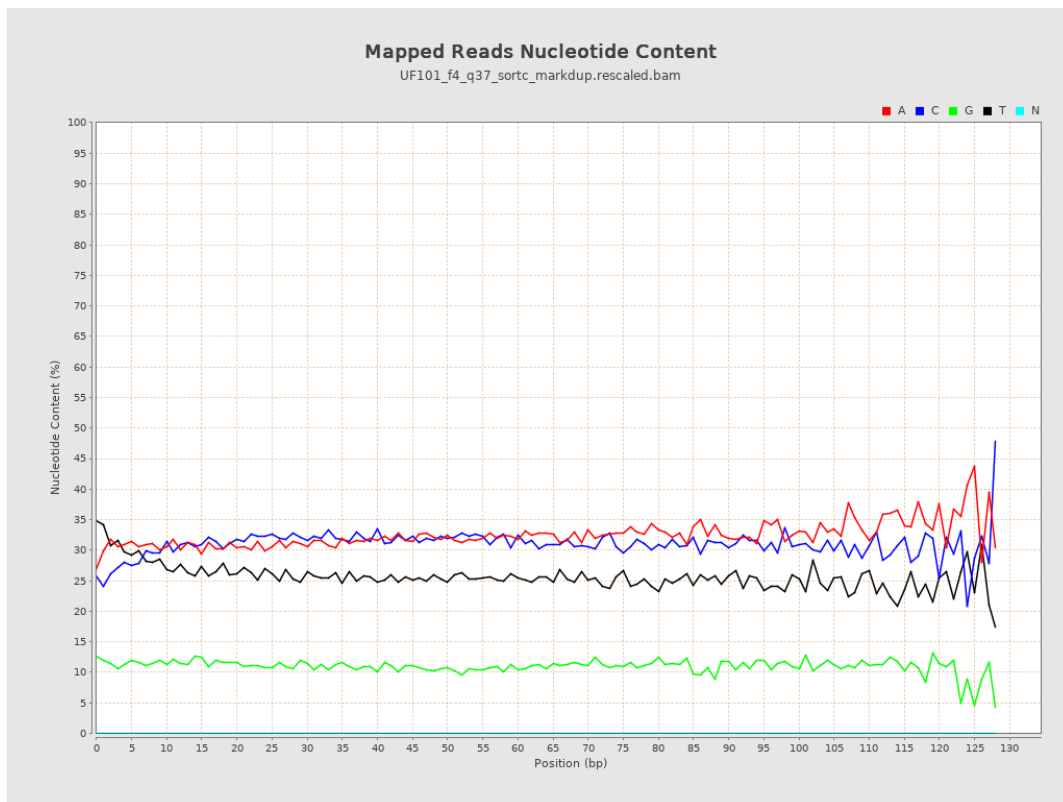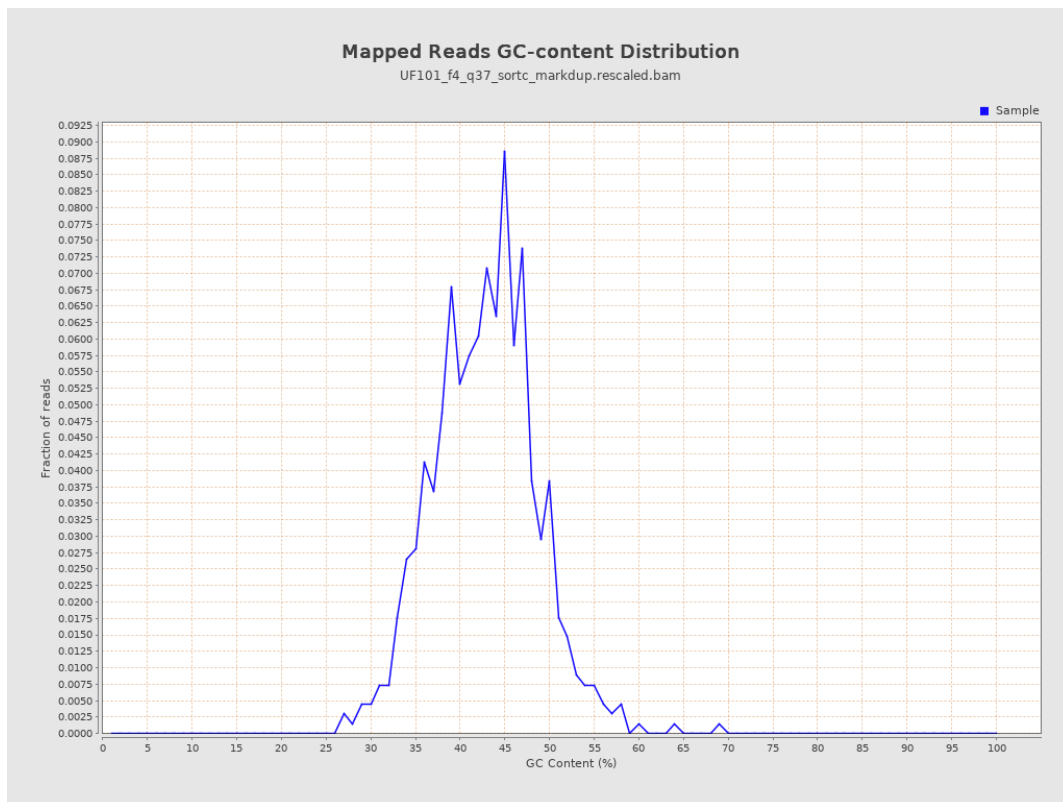
10. Results : Homopolymer Indels

11. Results : Mapping Quality Across Reference

Mapping Quality Across Reference
UF101_f4_q37_sortc_markdup.rescaled.bam

12. Results : Mapping Quality Histogram

Mapping Quality Histogram
UF101_f4_q37_sortc_markdup.rescaled.bam