Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2022/03/02 02:56:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
output/UF11/UF11_f4_q37_sortc_markdup.rescaled.bam -nw 400 -hm 3
```

1.2. Alignment

Command line:	bwa samse -r @RG\tID:UF11\tSM:UF11\tLB:nan\tPL:ILLUMINA /data/stonelab/references/Human_mitochondrial/NC_012920.1.fasta output/UF11/UF11-ancient.sai output/UF11/UF11-ancient.trimmed.fq
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 02 02:56:34 MST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	output/UF11/UF11_f4_q37_sortc_markdup.rescaled.bam

2. Summary

2.1. Globals

Reference size	16,569
Number of reads	416
Mapped reads	416 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	31 / 120 / 60.02
Duplicated reads (estimated)	12 / 2.88%
Duplication rate	2.48%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	8,072 / 32.33%
Number/percentage of C's	7,392 / 29.6%
Number/percentage of T's	6,382 / 25.56%
Number/percentage of G's	3,124 / 12.51%
Number/percentage of N's	0 / 0%
GC Percentage	42.11%

2.3. Coverage

Mean	1.507
Standard Deviation	2.6197

2.4. Mapping Quality

Mean Mapping Quality	31.11

2.5. Mismatches and indels

General error rate	2.12%
Mismatches	530

2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
NC_012920.1	16569	24970	1.507	2.6197

3. Results : Coverage across reference

Coverage across reference
UF11_f4_q37_sortc_markdup.rescaled.bam

4. Results : Coverage Histogram

Coverage Histogram
UF11_f4_q37_sortc_markdup.rescaled.bam

5. Results : Coverage Histogram (0-50X)
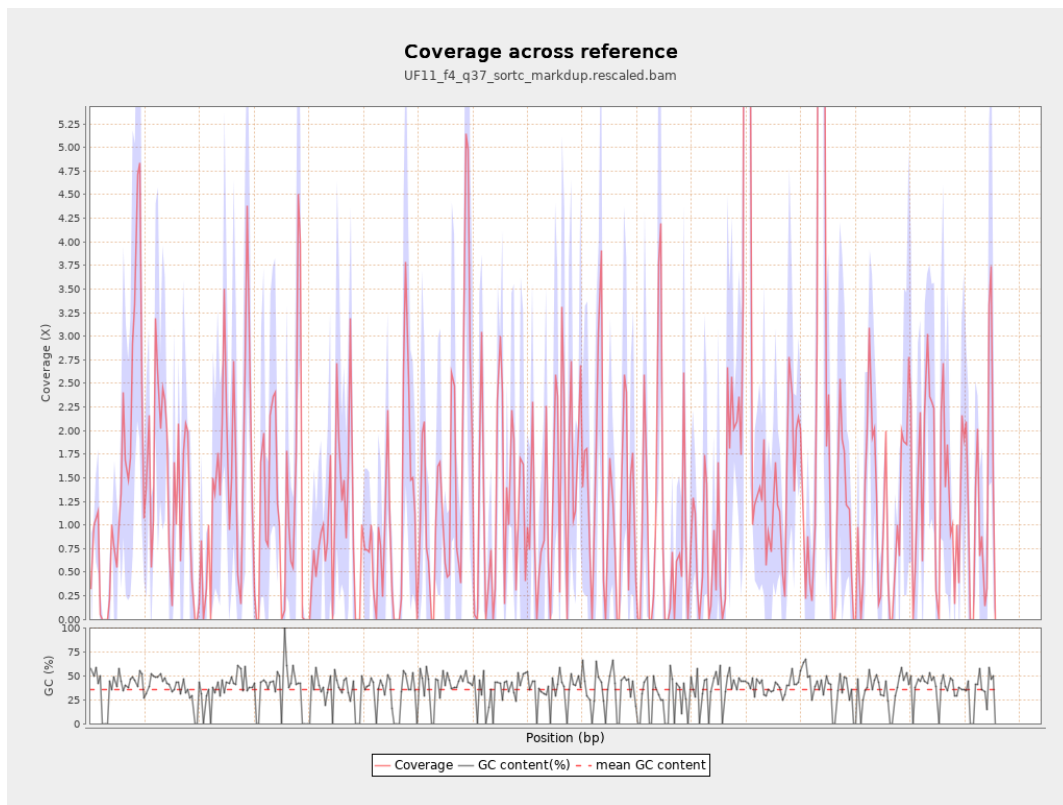
Coverage Histogram (0-50X)
UF11_f4_q37_sortc_markdup.rescaled.bam
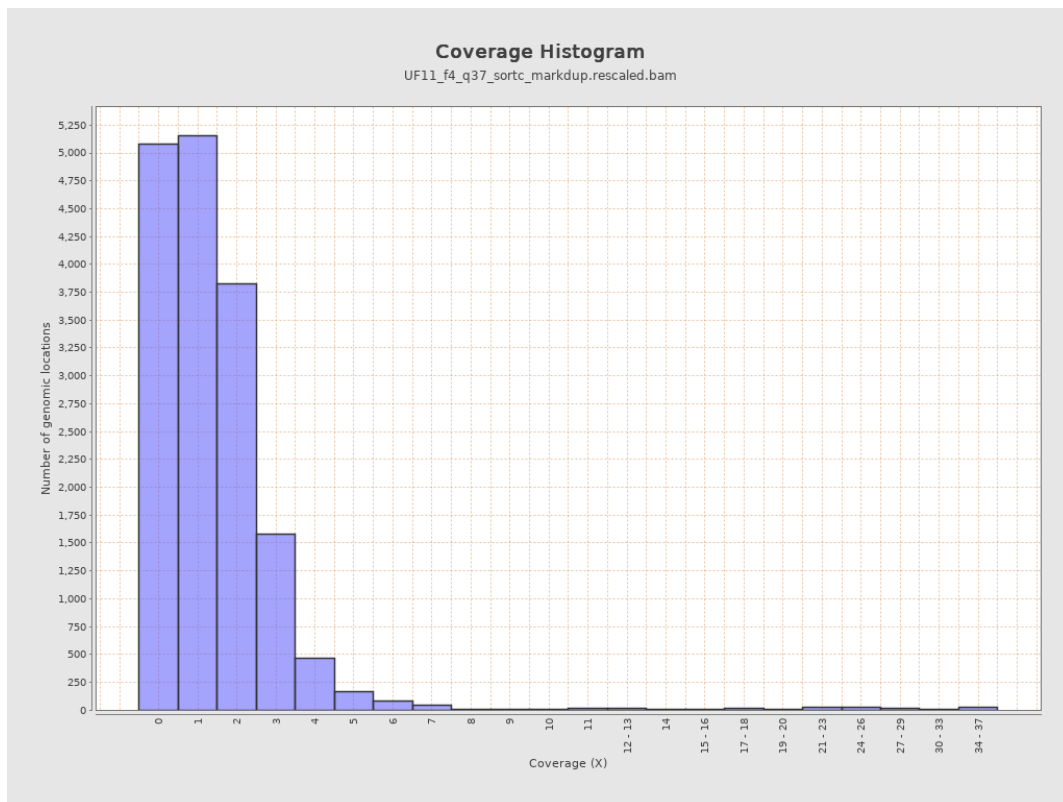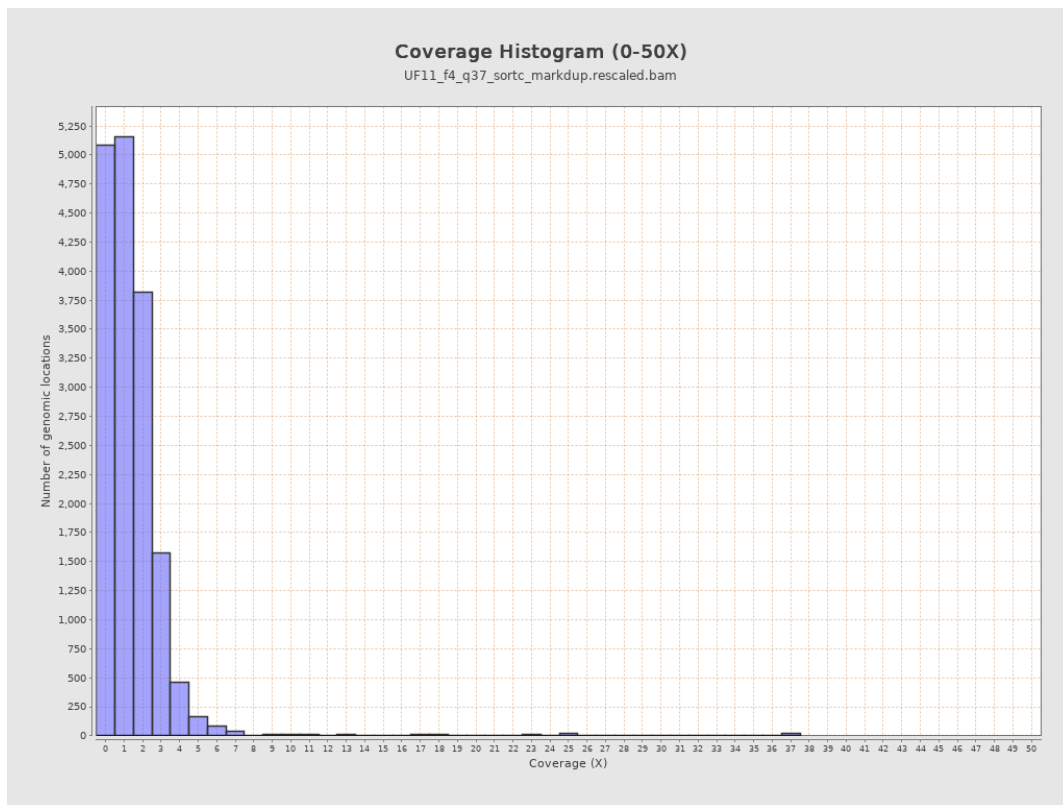
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
UF11_f4_q37_sortc_markdup.rescaled.bam
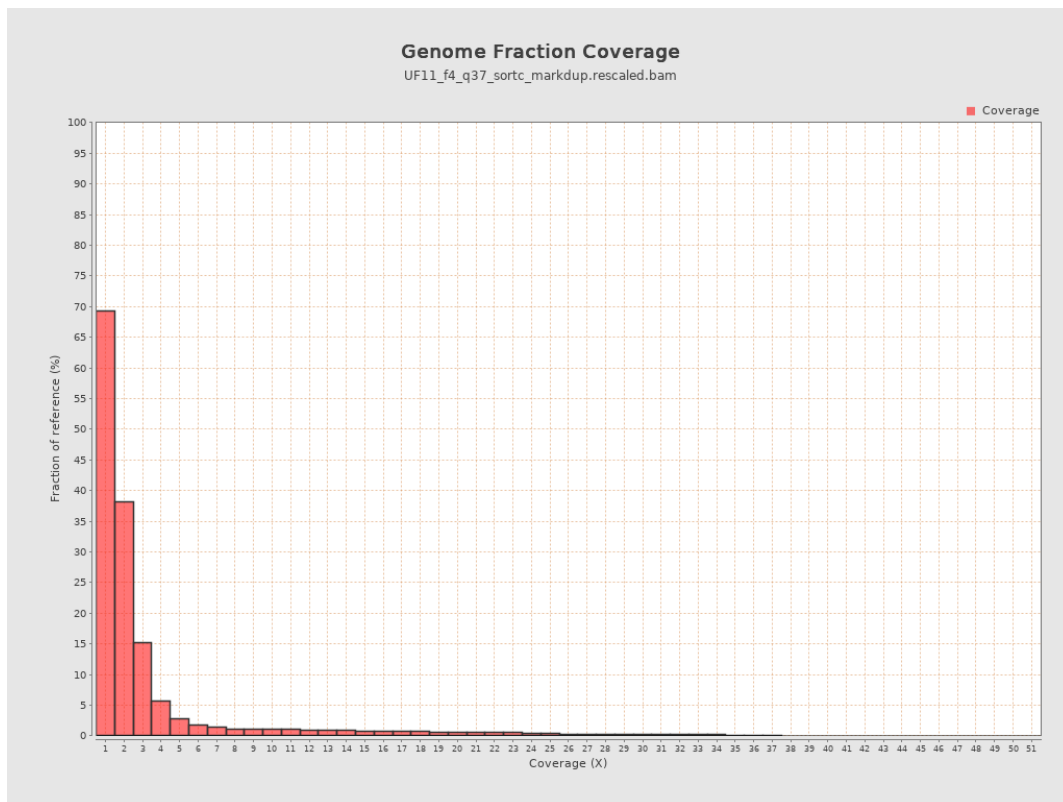
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
UF11_f4_q37_sortc_markdup.rescaled.bam
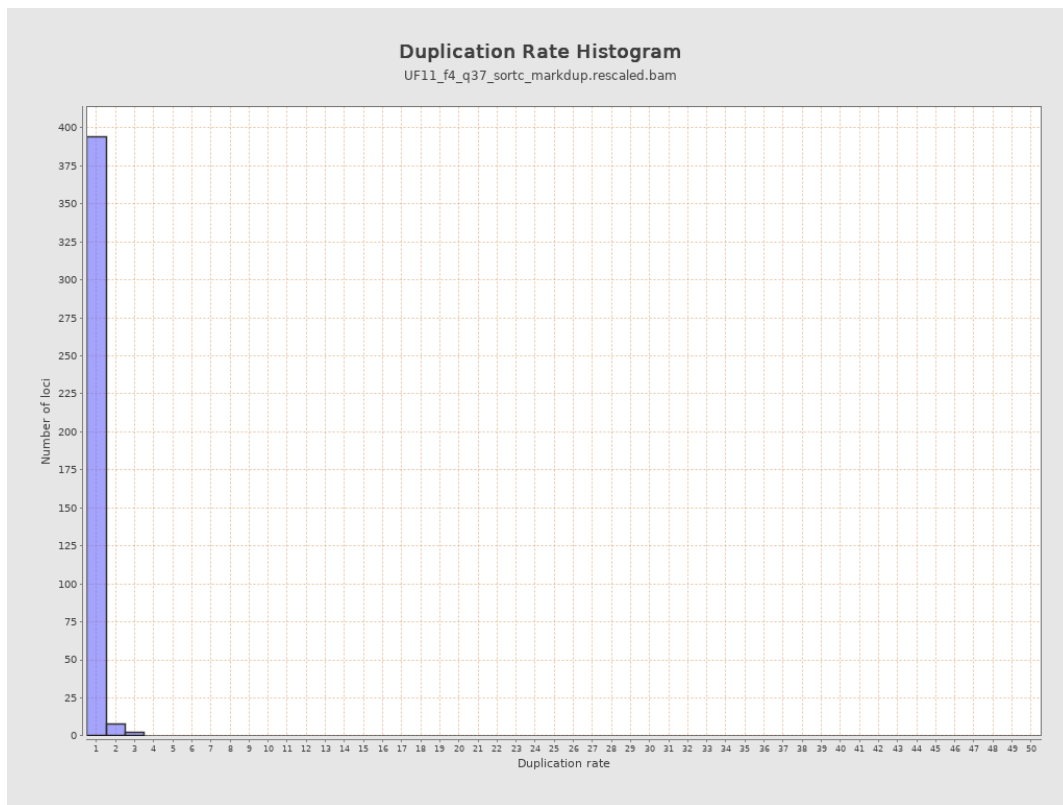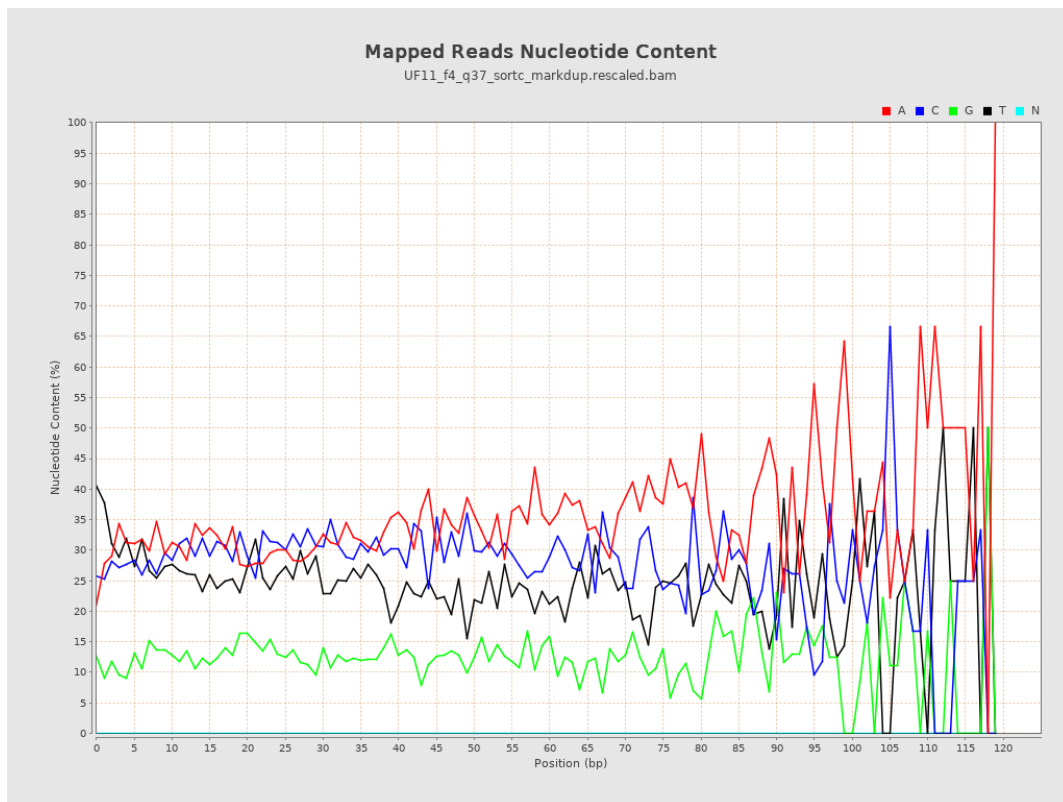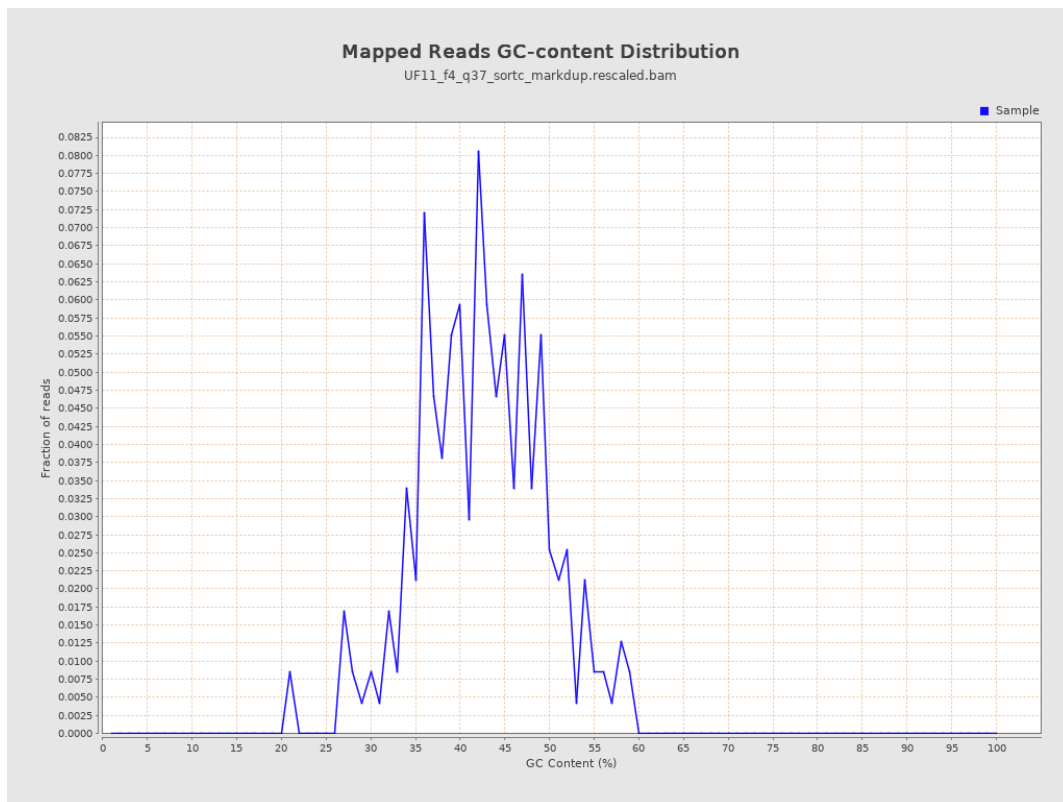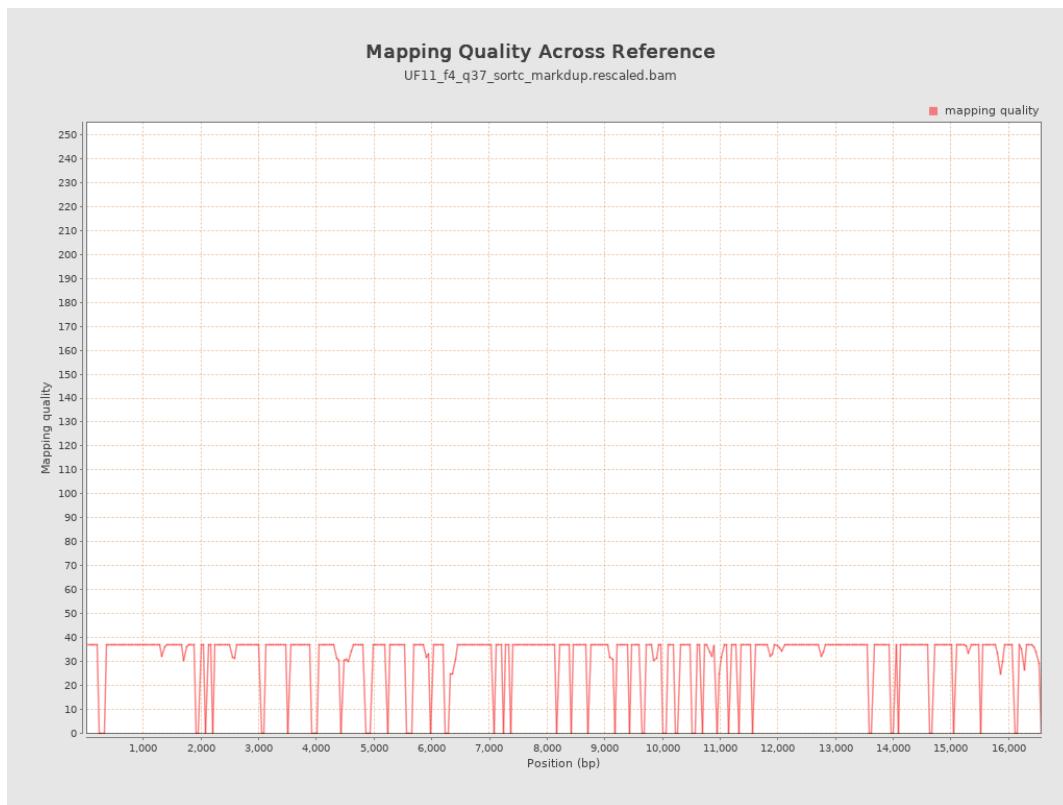
8. Results : Mapped Reads Nucleotide Content

9. Results : Mapped Reads GC-content Distribution

10. Results : Mapping Quality Across Reference

Mapping Quality Across Reference
UF11_f4_q37_sortc_markdup.rescaled.bam

11. Results : Mapping Quality Histogram

Mapping Quality Histogram
UF11_f4_q37_sortc_markdup.rescaled.bam