Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2022/03/02 02:57:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
output/UF25/UF25_f4_q37_sortc_markdup.rescaled.bam -nw 400 -hm 3
```

1.2. Alignment

Command line:	bwa samse -r @RG\tID:UF25\tSM:UF25\tLB:nan\tPL:ILLUMINA /data/stonelab/references/Human_mitochondrial/NC_012920.1.fasta output/UF25/UF25-ancient.sai output/UF25/UF25-ancient.trimmed.fq
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 02 02:57:58 MST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	output/UF25/UF25_f4_q37_sortc_markdup.rescaled.bam

2. Summary

2.1. Globals

Reference size	16,569
Number of reads	856
Mapped reads	856 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	30 / 115 / 50.9
Duplicated reads (estimated)	41 / 4.79%
Duplication rate	4.42%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	13,499 / 30.98%
Number/percentage of C's	14,068 / 32.29%
Number/percentage of T's	11,054 / 25.37%
Number/percentage of G's	4,949 / 11.36%
Number/percentage of N's	0 / 0%
GC Percentage	43.65%

2.3. Coverage

Mean	2.6299
Standard Deviation	2.9106

2.4. Mapping Quality

Mean Mapping Quality	34.51

2.5. Mismatches and indels

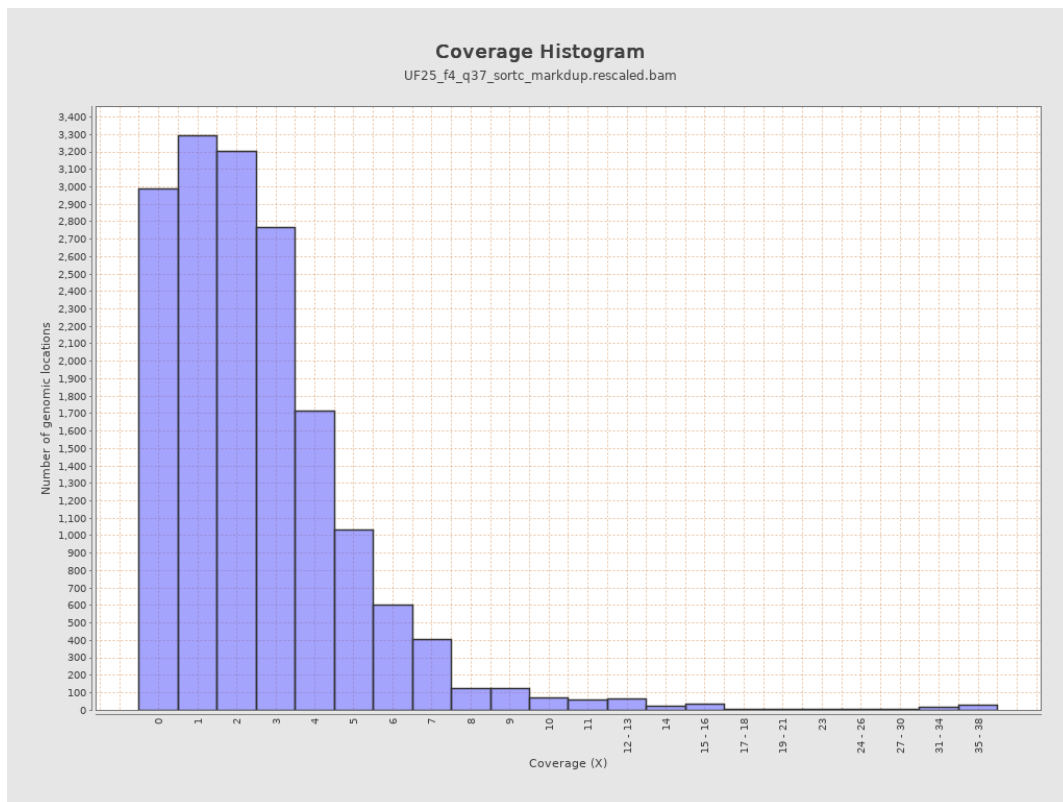| General error rate	0.42%
Mismatches	182
Insertions	1
Mapped reads with at least one insertion	0.12%
Deletions	4
Mapped reads with at least one deletion	0.47%
Homopolymer indels	20%

2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
NC_012920.1	16569	43574	2.6299	2.9106

3. Results : Coverage across reference

Coverage across reference
UF25_f4_q37_sortc_markdup.rescaled.bam

4. Results : Coverage Histogram

Coverage Histogram
UF25_f4_q37_sortc_markdup.rescaled.bam

5. Results : Coverage Histogram (0-50X)
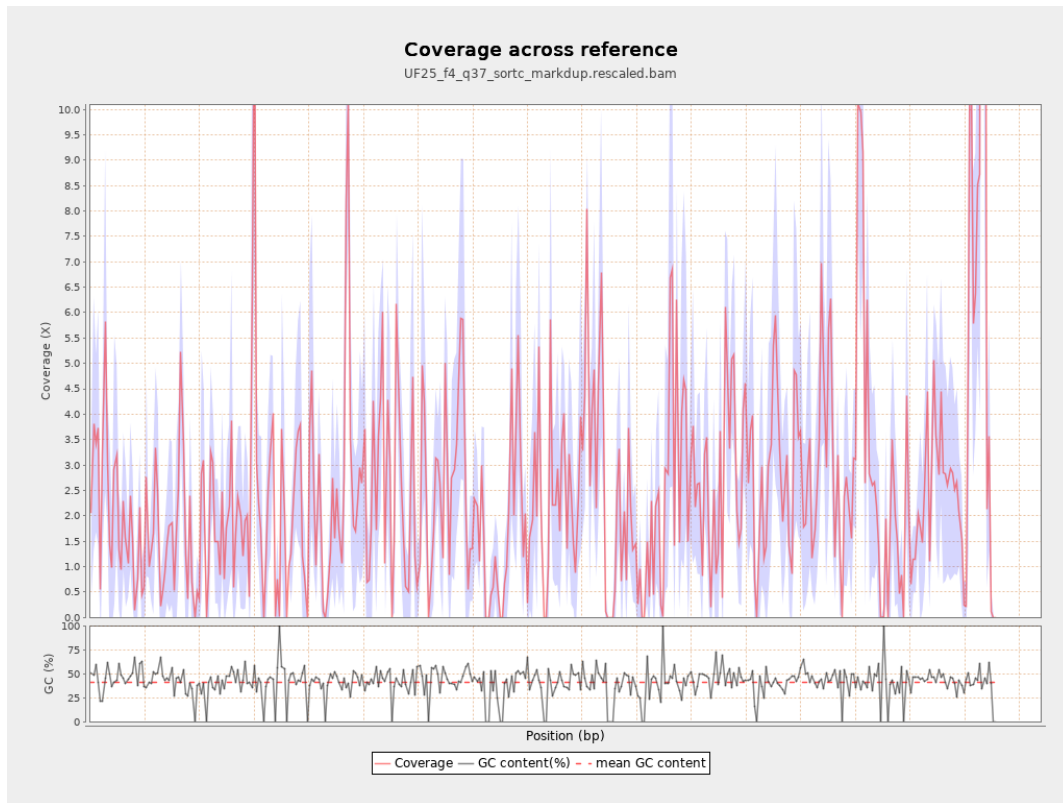
Coverage Histogram (0-50X)
UF25_f4_q37_sortc_markdup.rescaled.bam
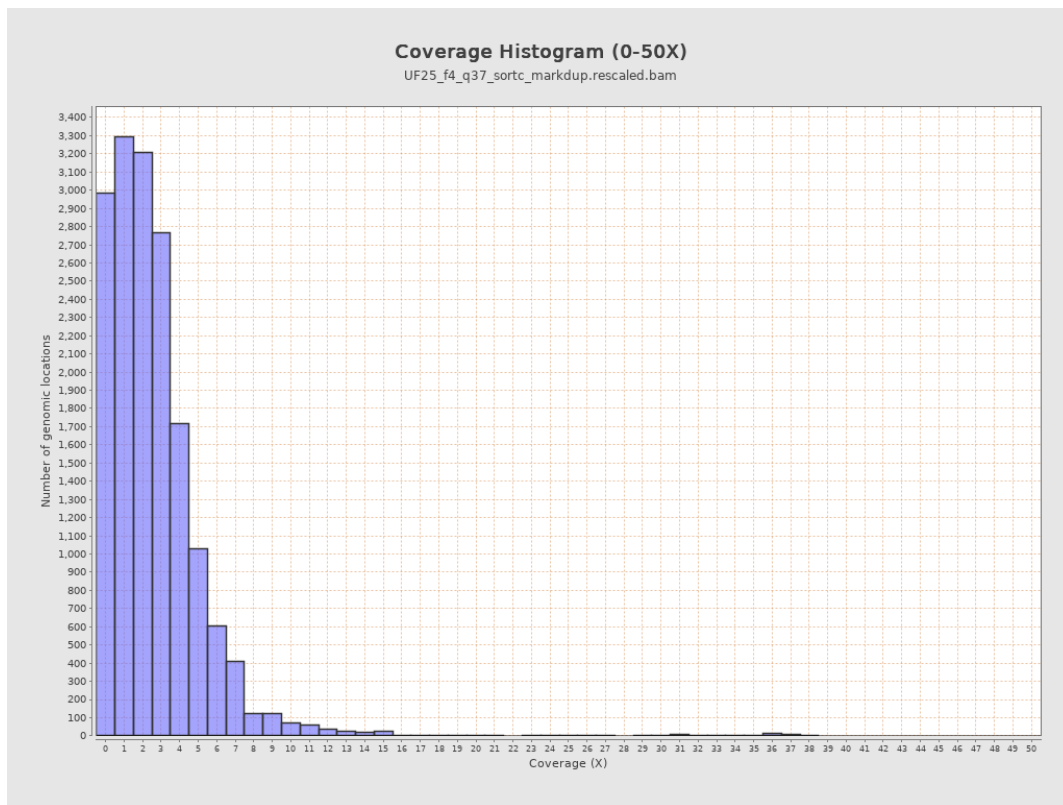
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
UF25_f4_q37_sortc_markdup.rescaled.bam
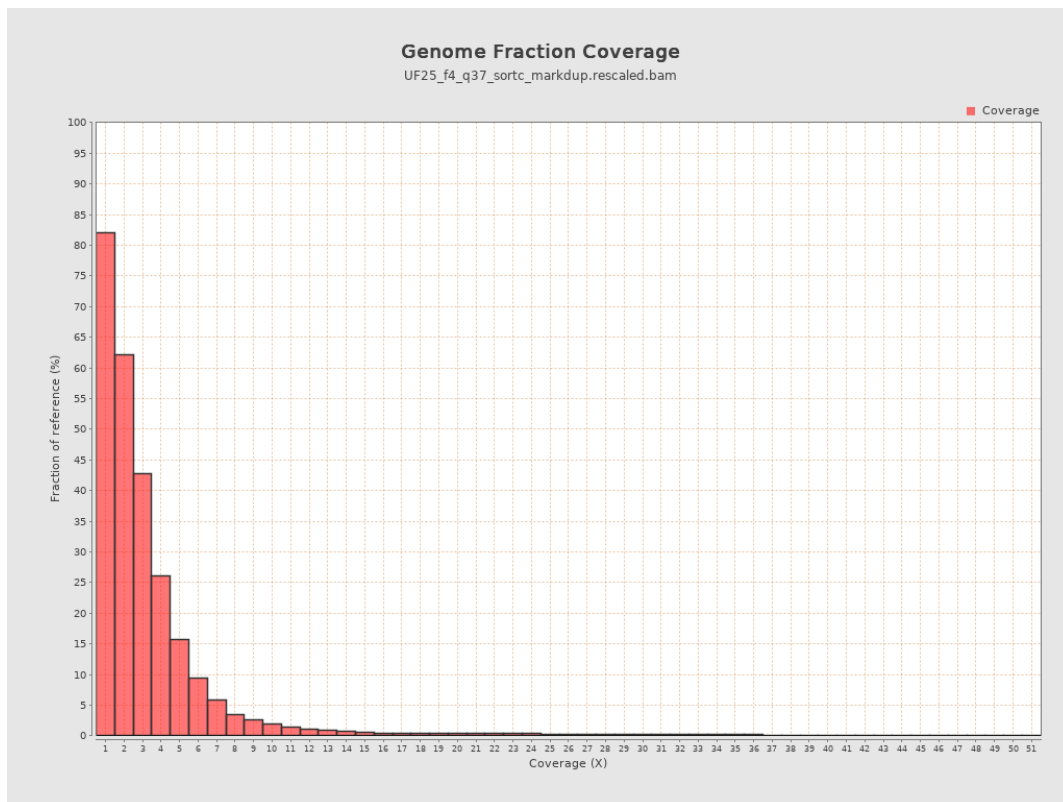
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
UF25_f4_q37_sortc_markdup.rescaled.bam

8. Results : Mapped Reads Nucleotide Content

Mapped Reads Nucleotide Content
UF25_f4_q37_sortc_markdup.rescaled.bam
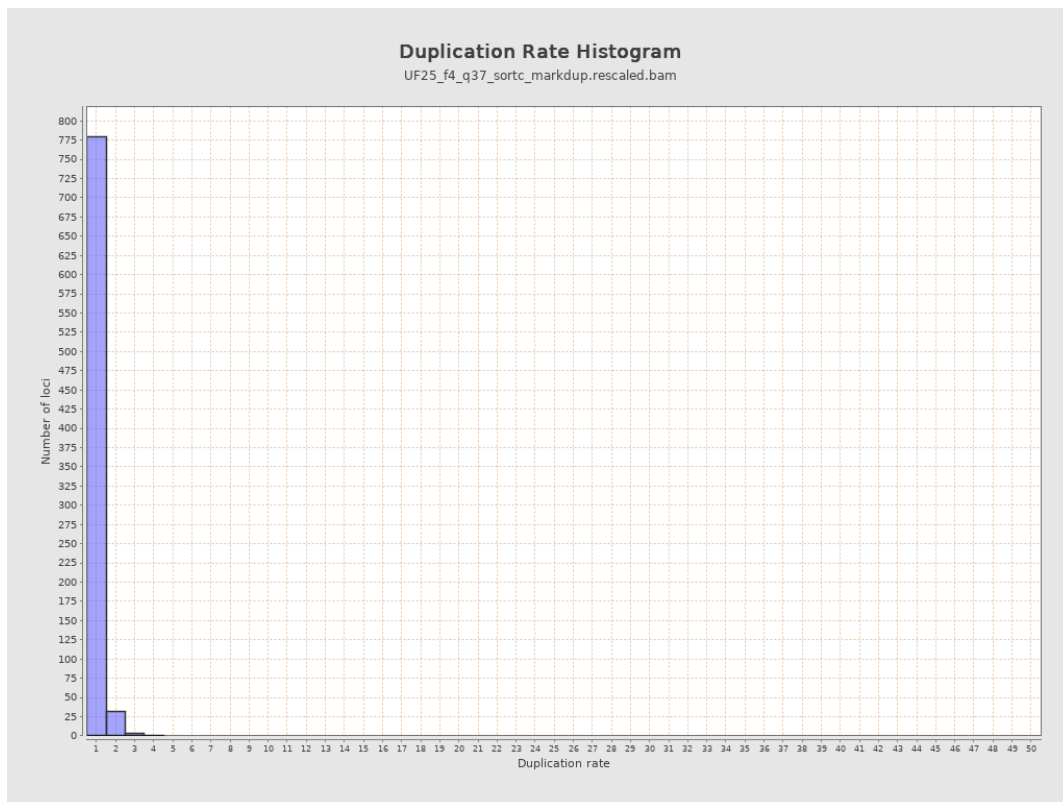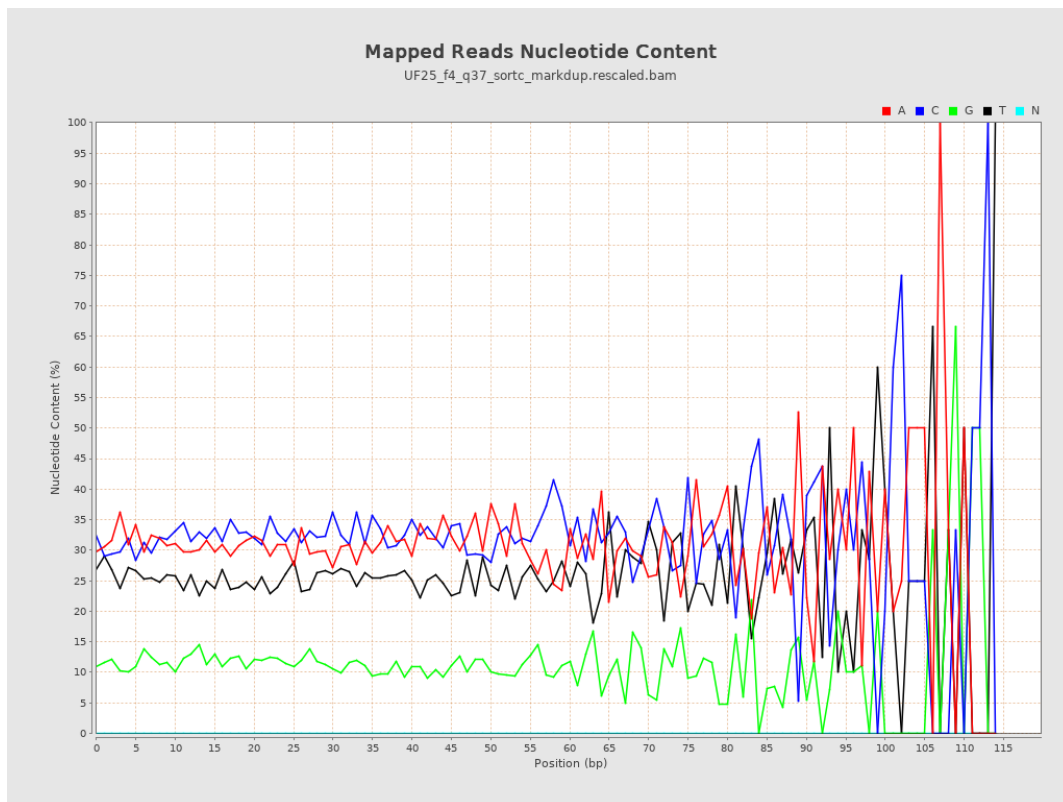
9. Results : Mapped Reads GC-content Distribution
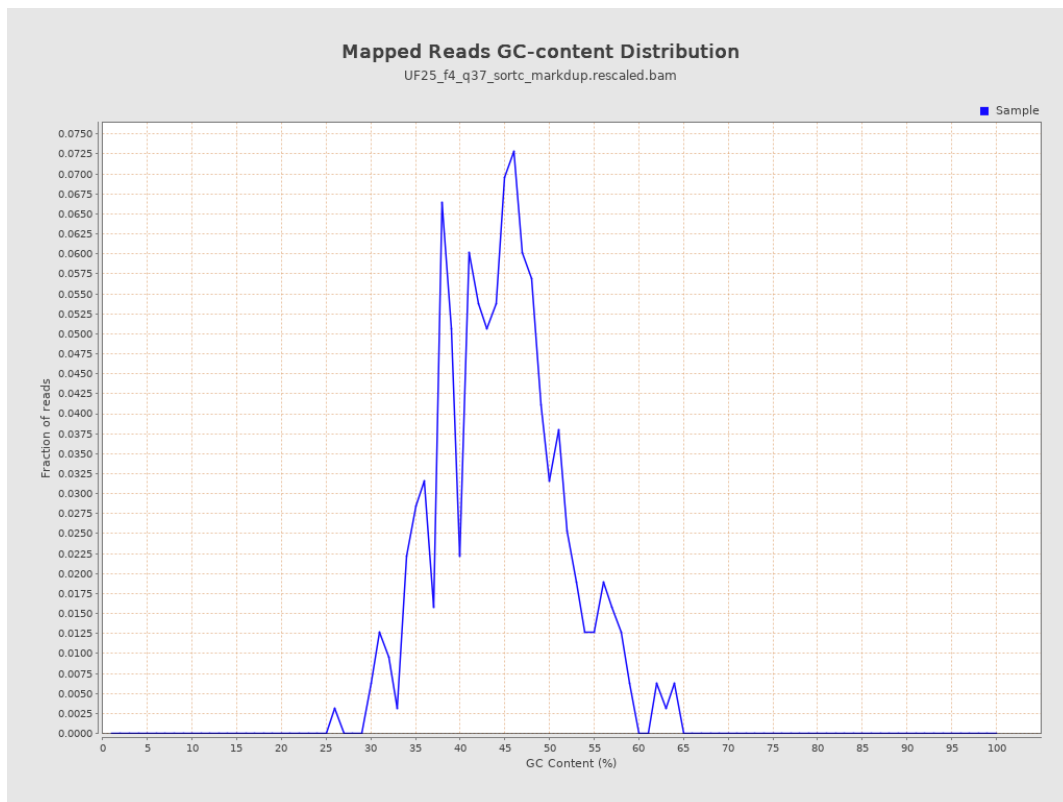
10. Results : Homopolymer Indels

Homopolymer Indels
UF25_f4_q37_sortc_markdup.rescaled.bam

11. Results : Mapping Quality Across Reference

Mapping Quality Across Reference
UF25_f4_q37_sortc_markdup.rescaled.bam

12. Results : Mapping Quality Histogram

Mapping Quality Histogram
UF25_f4_q37_sortc_markdup.rescaled.bam