# Qualimap Analysis Results

*BAM QC analysis*
*Generated by Qualimap v.2.2.2-dev*
*2022/03/02 02:57:56*

# 1. Input data & parameters

## 1.1. QualiMap command line

> qualimap bamqc -bam
> output/UF801/UF801_f4_q37_sortc_markdup.rescaled.bam -nw 400 -hm 3

## 1.2. Alignment

| | |
|---|---|
| Command line: | bwa samse -r @RG\tID:UF801\tSM:UF801\tLB:nan\tPL:ILLUMINA /data/stonelab/references/Human_mitochondrial/NC_012920.1.fasta output/UF801/UF801-ancient.sai output/UF801/UF801-ancient.trimmed.fq |
| Draw chromosome limits: | no |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Mar 02 02:57:55 MST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | output/UF801/UF801_f4_q37_sortc_markdup.rescaled.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 16,569 |
| Number of reads | 962 |
| Mapped reads | 962 / 100% |
| Unmapped reads | 0 / 0% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Read min/max/mean length | 30 / 129 / 62.36 |
| Duplicated reads (estimated) | 24 / 2.49% |
| Duplication rate | 2.56% |
| Clipped reads | 0 / 0% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 18,984 / 31.64% |
| Number/percentage of C's | 17,902 / 29.84% |
| Number/percentage of T's | 15,992 / 26.66% |
| Number/percentage of G's | 7,114 / 11.86% |
| Number/percentage of N's | 0 / 0% |
| GC Percentage | 41.7% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 3.6209 |
| Standard Deviation | 2.0308 |

## 2.4. Mapping Quality

| Mean Mapping Quality | 35.77 |
|---|---|

## 2.5. Mismatches and indels

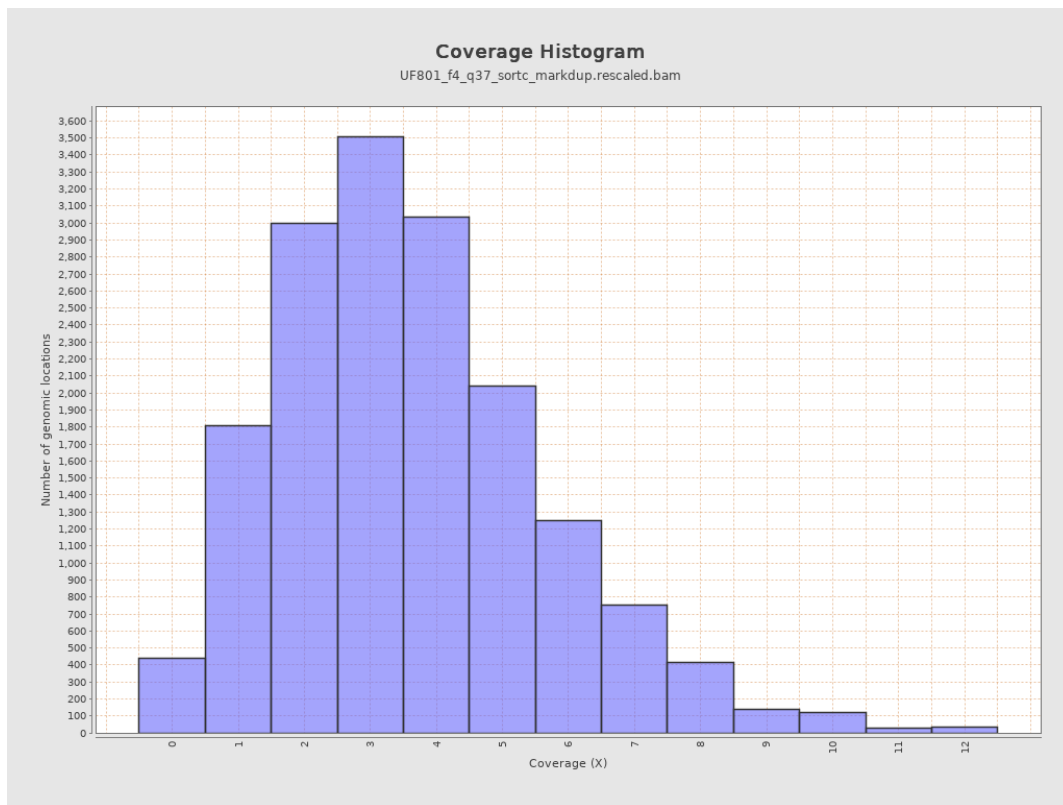| General error rate | 2.76% |
|---|---|
| Mismatches | 1,651 |
| Insertions | 2 |
| Mapped reads with at least one insertion | 0.1% |
| Deletions | 2 |
| Mapped reads with at least one deletion | 0.21% |
| Homopolymer indels | 25% |

## 2.6. Chromosome stats

| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| NC_012920.1 | 16569 | 59994 | 3.6209 | 2.0308 |

# 3. Results : Coverage across reference



**Coverage across reference**
UF801_f4_q37_sortc_markdup.rescaled.bam

# 4. Results : Coverage Histogram



**Coverage Histogram**
UF801_f4_q37_sortc_markdup.rescaled.bam

# 5. Results : Coverage Histogram (0-50X)
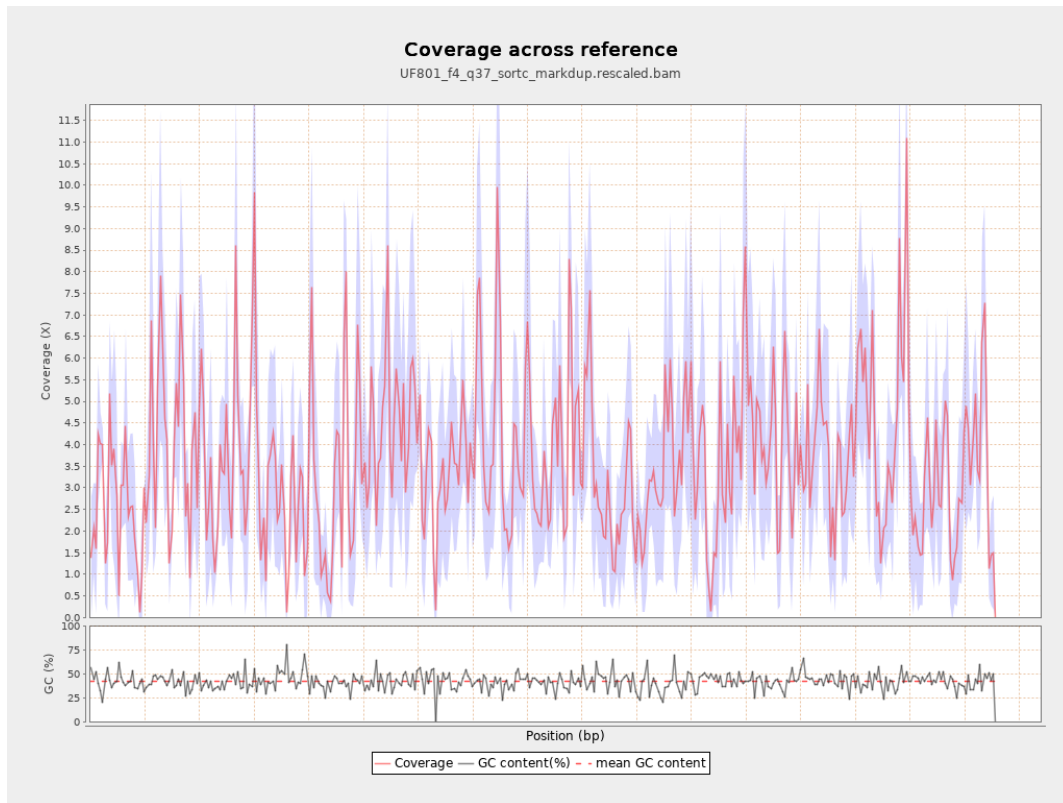


Coverage Histogram (0-50X)
UF801_f4_q37_sortc_markdup.rescaled.bam
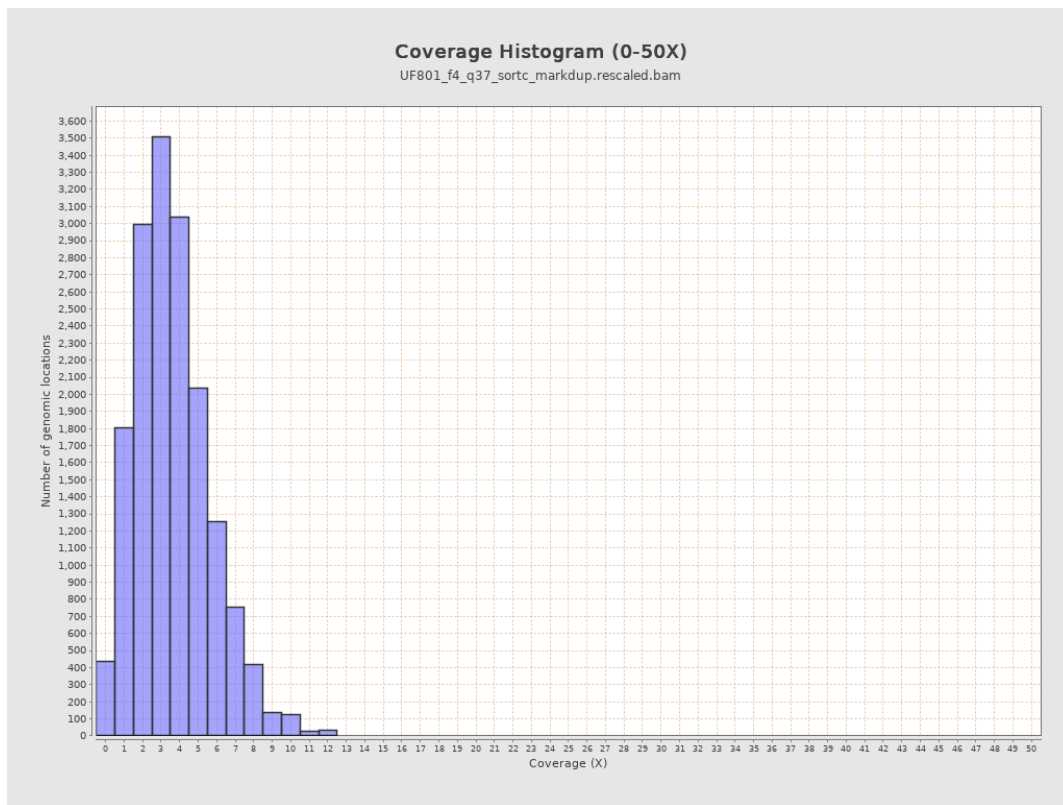
# 6. Results : Genome Fraction Coverage



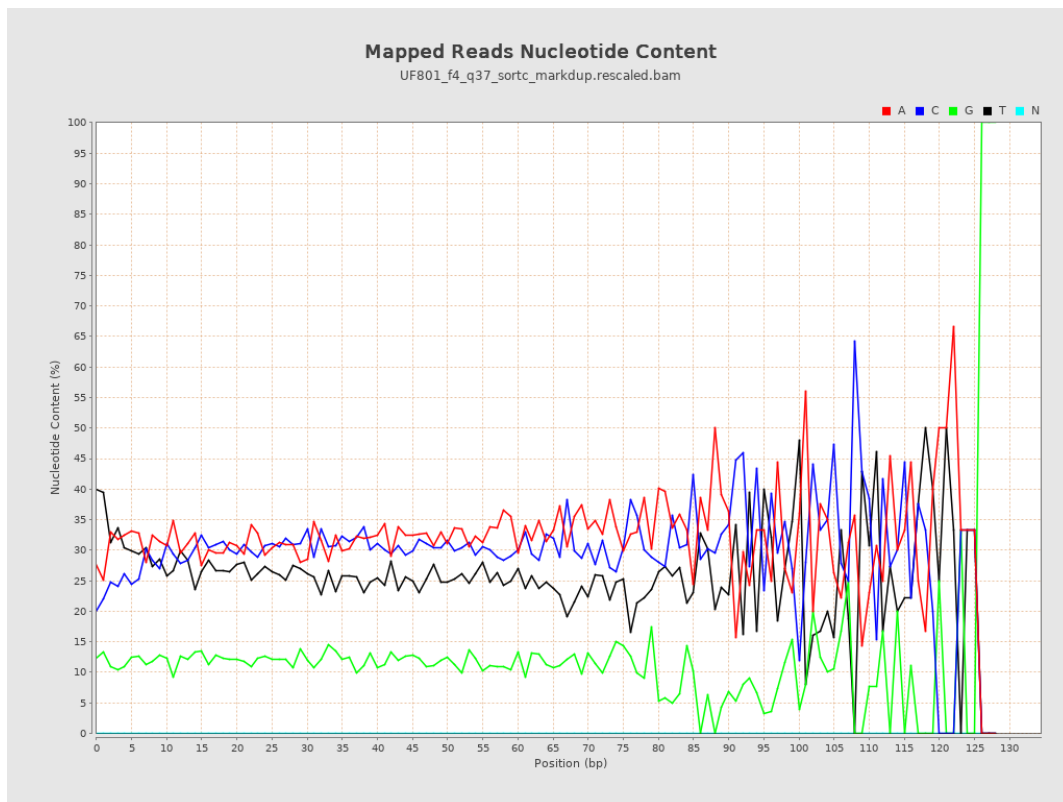**Genome Fraction Coverage**
UF801_f4_q37_sortc_markdup.rescaled.bam
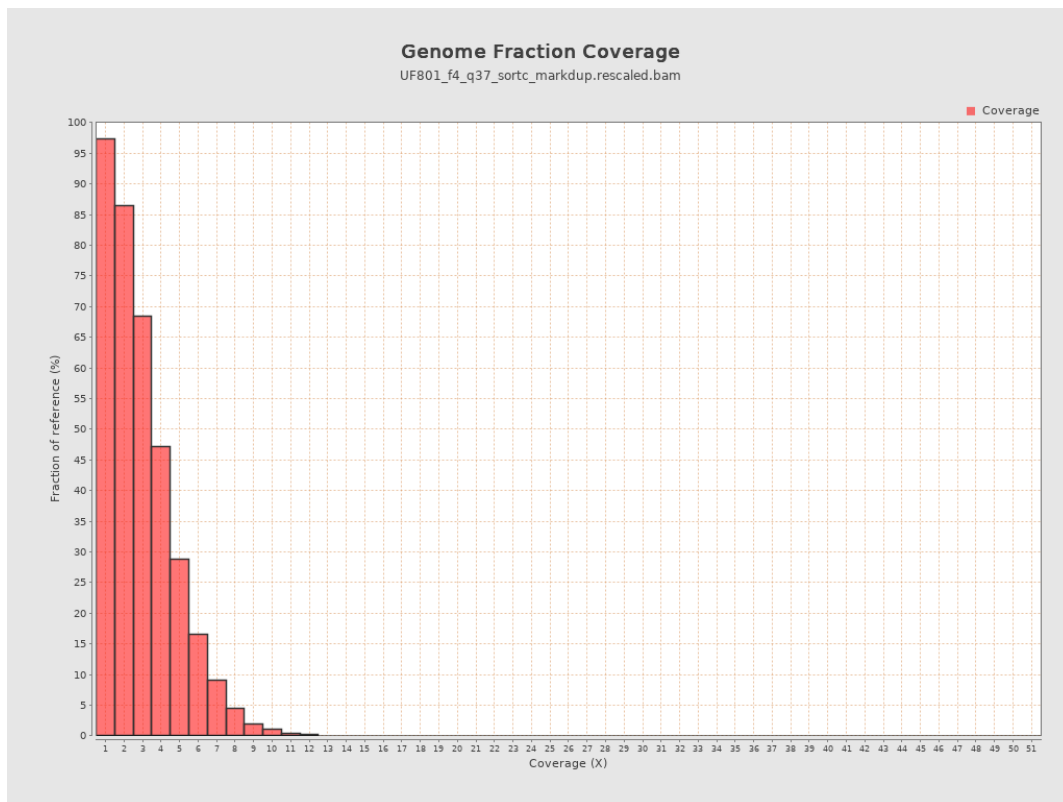
# 7. Results : Duplication Rate Histogram
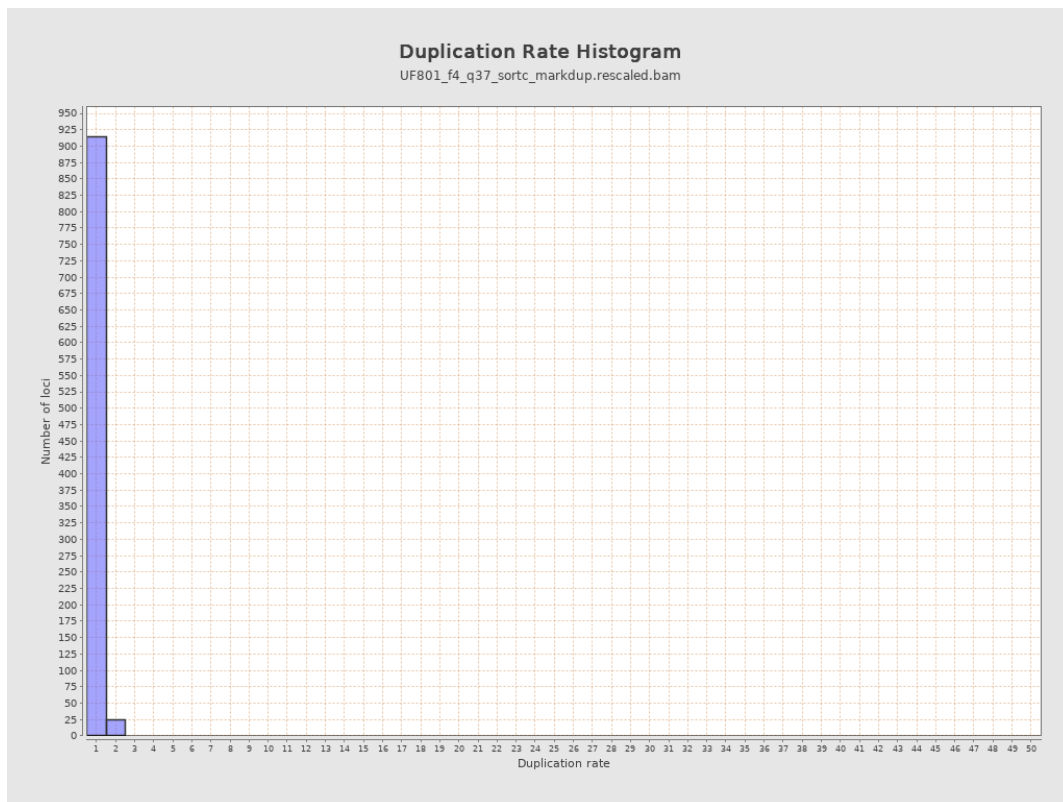
# 8. Results : Mapped Reads Nucleotide Content

**Mapped Reads Nucleotide Content**
UF801_f4_q37_sortc_markdup.rescaled.bam

# 9. Results : Mapped Reads GC-content Distribution



Mapped Reads GC-content Distribution
UF801_f4_q37_sortc_markdup.rescaled.bam
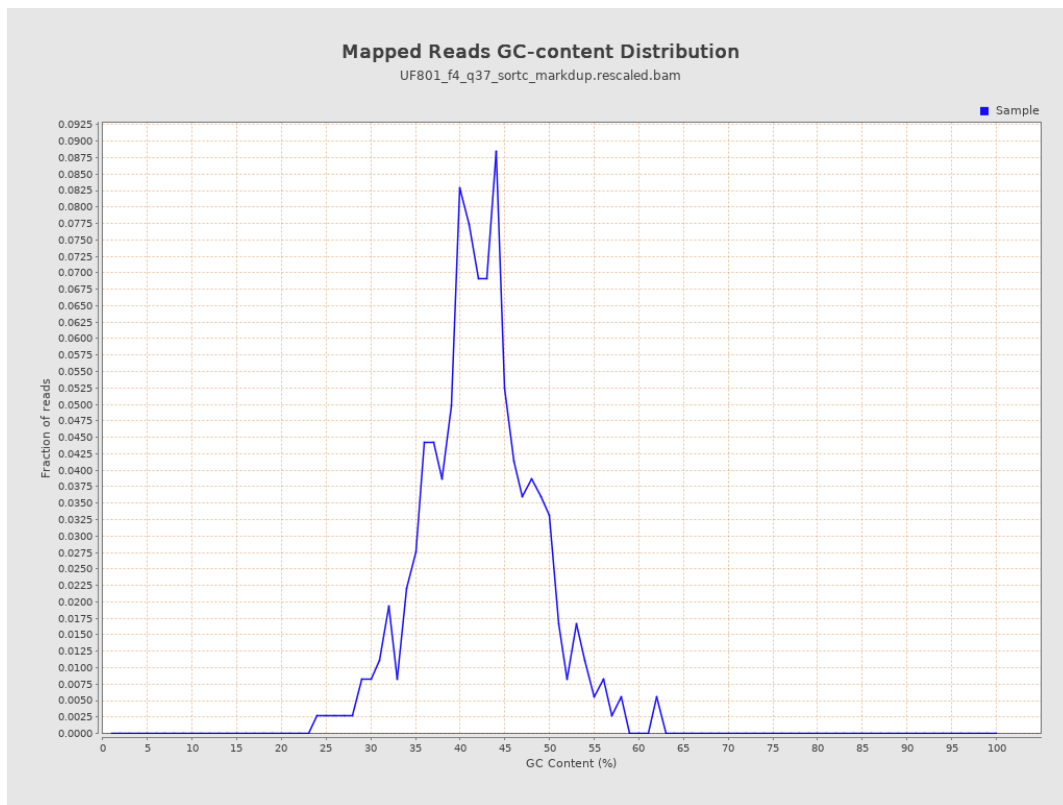
# 10. Results : Homopolymer Indels



**Homopolymer Indels**
UF801_f4_q37_sortc_markdup.rescaled.bam

# 11. Results : Mapping Quality Across Reference



Mapping Quality Across Reference
UF801_f4_q37_sortc_markdup.rescaled.bam

# 12. Results : Mapping Quality Histogram



**Mapping Quality Histogram**
UF801_f4_q37_sortc_markdup.rescaled.bam