Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2022/03/02 03:10:40

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
output/UF803/UF803_f4_q37_sortc_markdup.rescaled.bam -nw 400 -hm 3

1.2. Alignment

Command line:	bwa samse -r @RG\tID:UF803\tSM:UF803\tLB:nan\tPL:ILLUMINA /data/stonelab/references/Human_mitochondrial/NC_012920.1.fasta output/UF803/UF803-ancient.sai output/UF803/UF803-ancient.trimmed.fq
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 02 03:10:39 MST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	output/UF803/UF803_f4_q37_sortc_markdup.rescaled.bam

2. Summary

2.1. Globals

Reference size	16,569
Number of reads	854
Mapped reads	854 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	30 / 138 / 67.54
Duplicated reads (estimated)	47 / 5.5%
Duplication rate	5.7%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	18,154 / 31.47%
Number/percentage of C's	18,435 / 31.96%
Number/percentage of T's	14,606 / 25.32%
Number/percentage of G's	6,483 / 11.24%
Number/percentage of N's	0 / 0%
GC Percentage	43.2%

2.3. Coverage

Mean	3.4813
Standard Deviation	3.5492

2.4. Mapping Quality

Mean Mapping Quality	34.74

2.5. Mismatches and indels

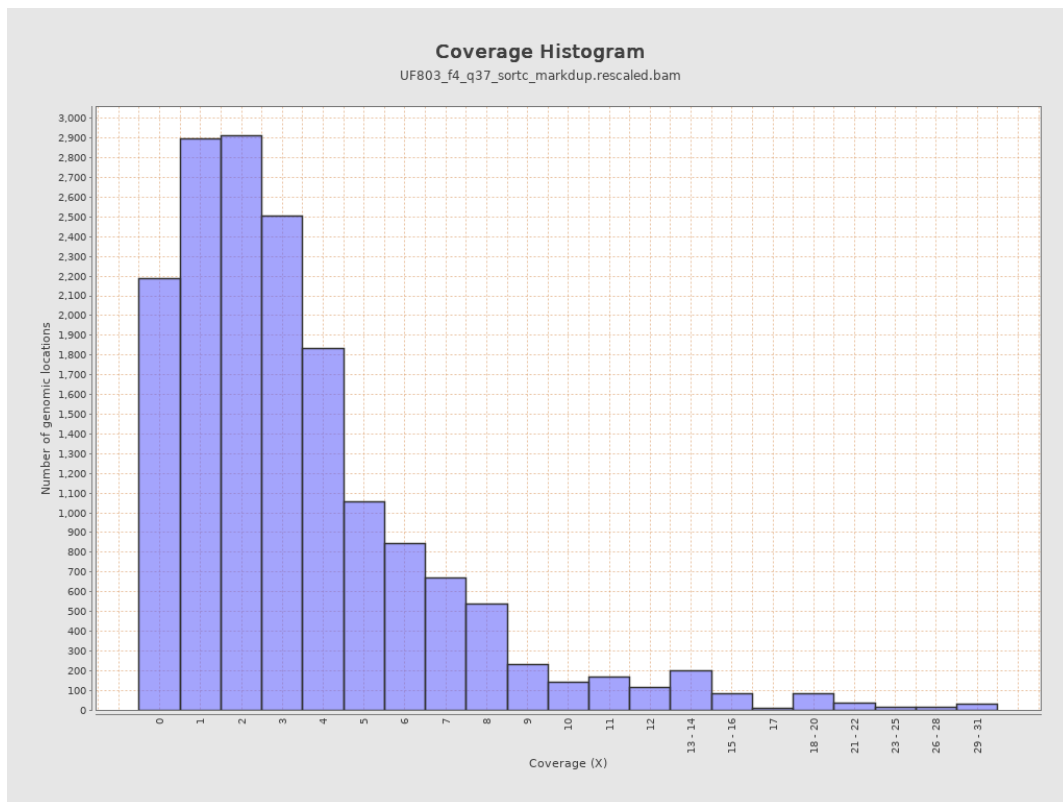| General error rate	0.41%
Mismatches	232
Insertions	3
Mapped reads with at least one insertion	0.35%
Deletions	3
Mapped reads with at least one deletion	0.35%
Homopolymer indels	50%

2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
NC_012920.1	16569	57681	3.4813	3.5492

3. Results : Coverage across reference

Coverage across reference
UF803_f4_q37_sortc_markdup.rescaled.bam

4. Results : Coverage Histogram

Coverage Histogram
UF803_f4_q37_sortc_markdup.rescaled.bam

5. Results : Coverage Histogram (0-50X)
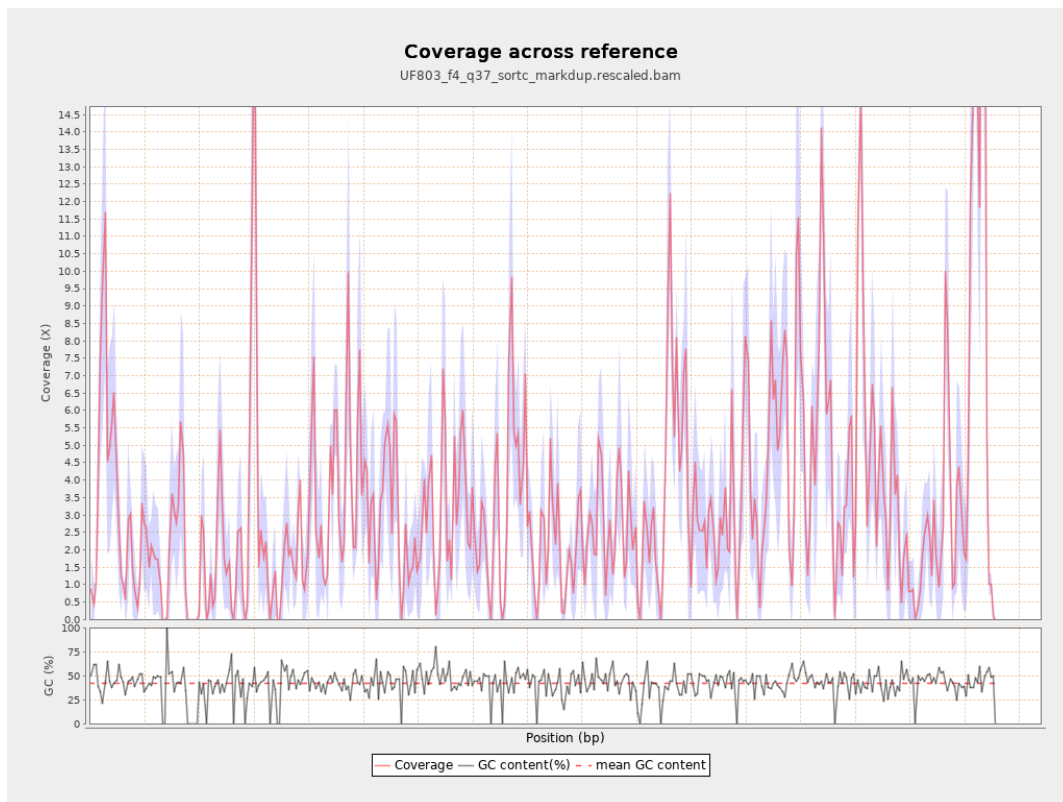
Coverage Histogram (0-50X)
UF803_f4_q37_sortc_markdup.rescaled.bam
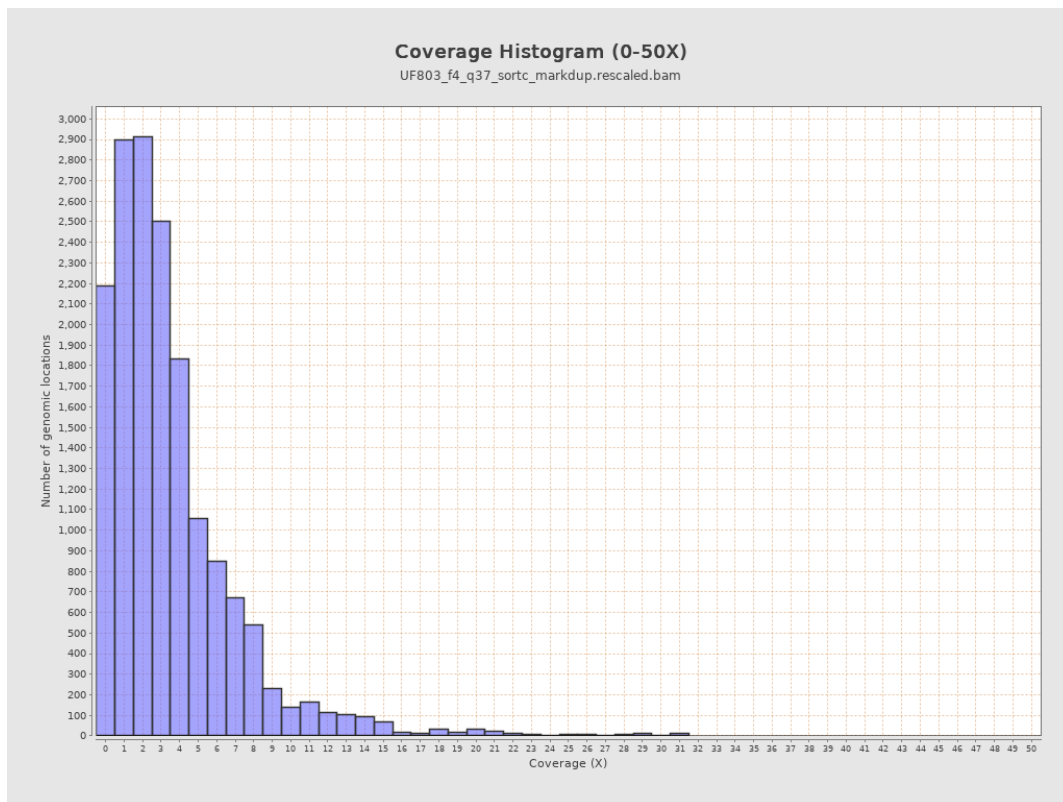
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
UF803_f4_q37_sortc_markdup.rescaled.bam
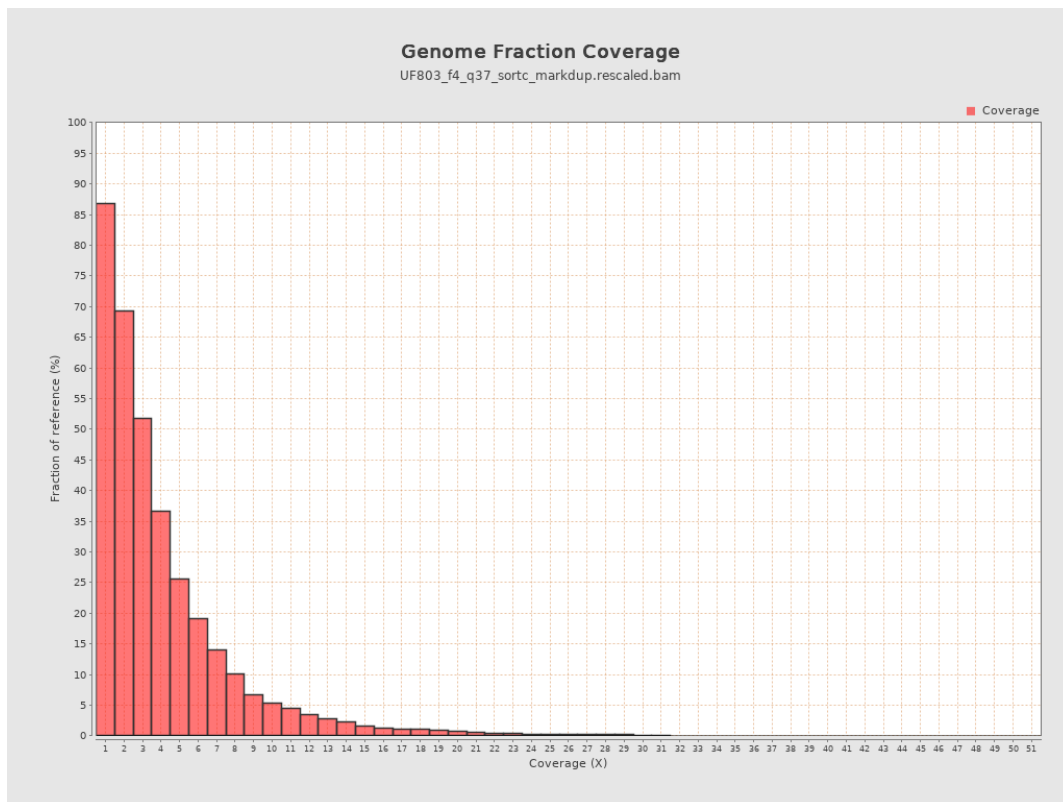
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
UF803_f4_q37_sortc_markdup.rescaled.bam

8. Results : Mapped Reads Nucleotide Content

Mapped Reads Nucleotide Content
UF803_f4_q37_sortc_markdup.rescaled.bam
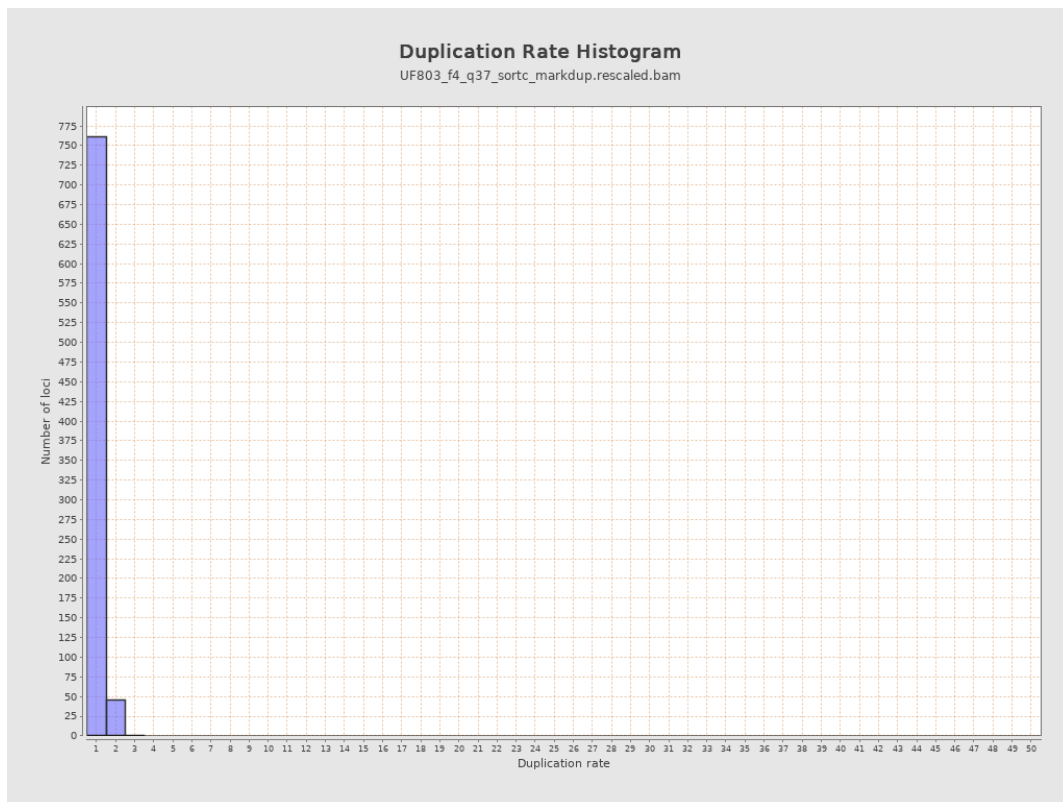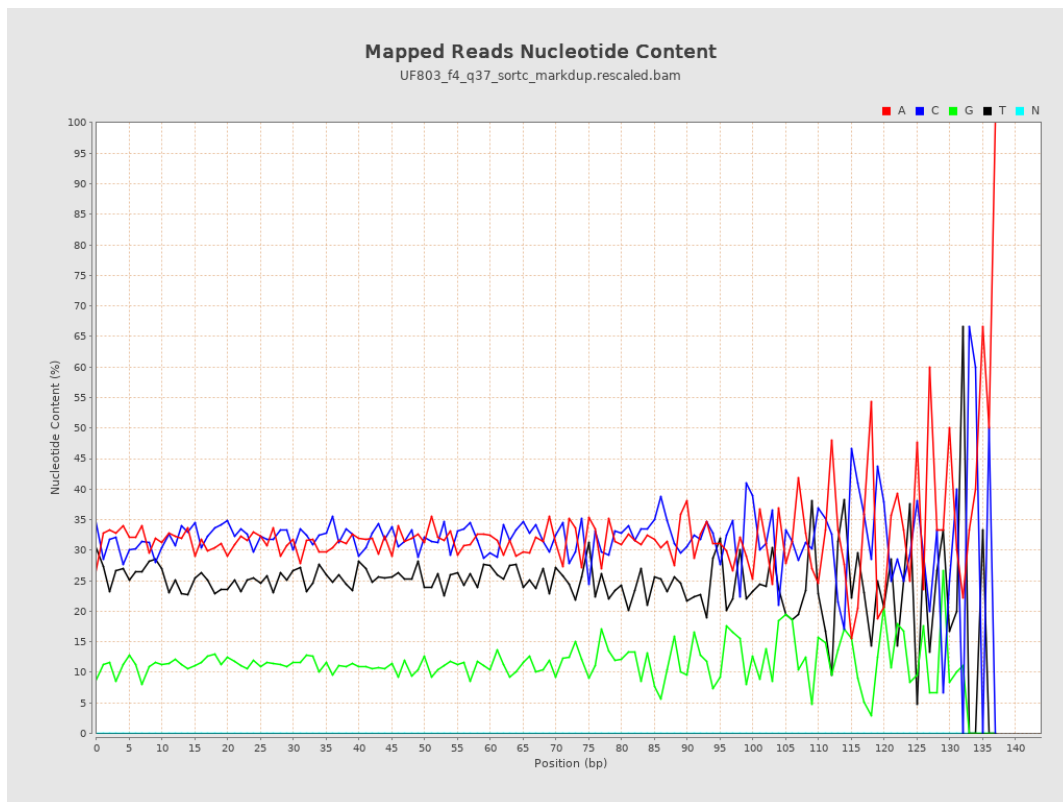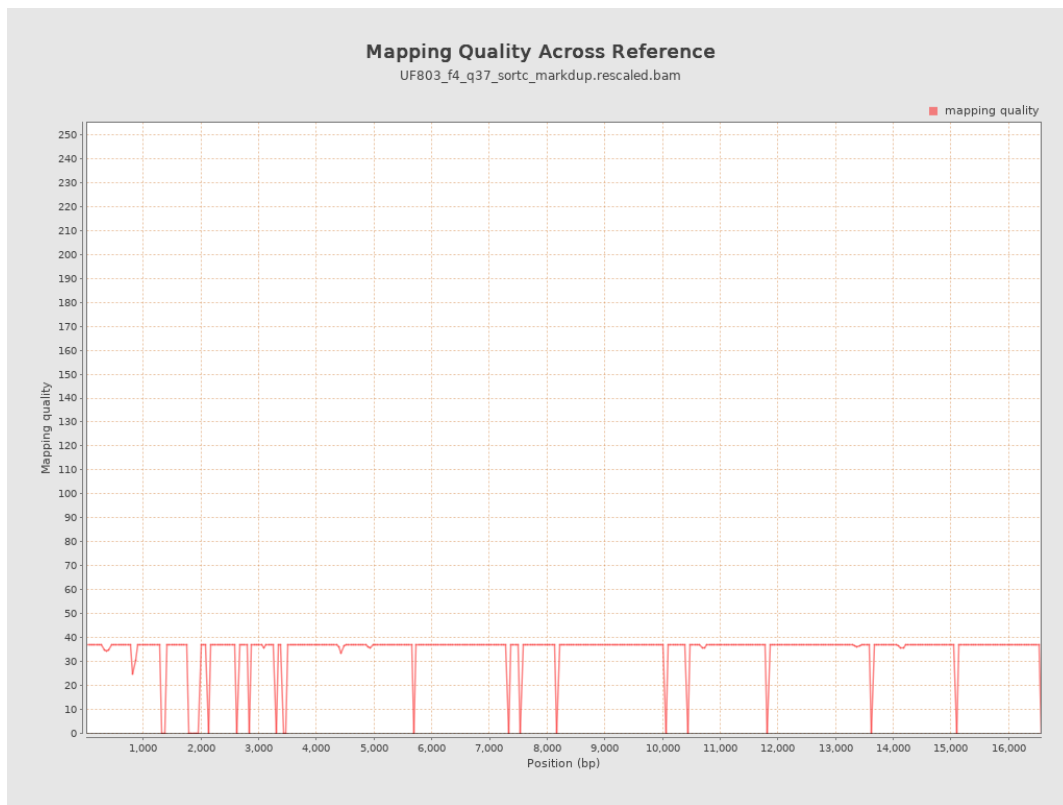
9. Results : Mapped Reads GC-content Distribution
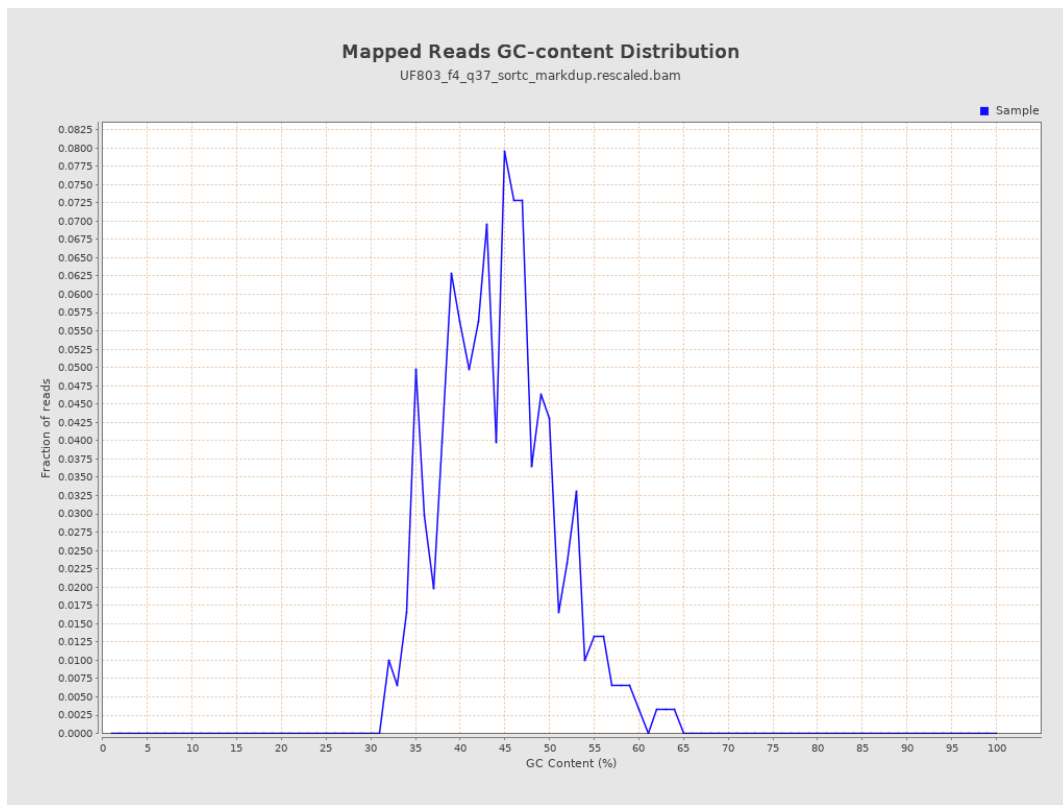
10. Results : Homopolymer Indels

11. Results : Mapping Quality Across Reference

Mapping Quality Across Reference
UF803_f4_q37_sortc_markdup.rescaled.bam

12. Results : Mapping Quality Histogram

Mapping Quality Histogram
UF803_f4_q37_sortc_markdup.rescaled.bam