Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2022/03/02 02:56:28

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
output/UF8/UF8_f4_q37_sortc_markdup.rescaled.bam -nw 400 -hm 3

1.2. Alignment

Command line:	bwa samse -r @RG\tID:UF8\tSM:UF8\tLB:nan\tPL:ILLUMINA /data/stonelab/references/Human_mitochondrial/NC_012920.1.fasta output/UF8/UF8-ancient.sai output/UF8/UF8-ancient.trimmed.fq
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 02 02:56:28 MST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	output/UF8/UF8_f4_q37_sortc_markdup.rescaled.bam

2. Summary

2.1. Globals

Reference size	16,569
Number of reads	80
Mapped reads	80 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	30 / 126 / 57.25
Duplicated reads (estimated)	0 / 0%
Duplication rate	0%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	1,458 / 31.83%
Number/percentage of C's	1,446 / 31.57%
Number/percentage of T's	1,142 / 24.93%
Number/percentage of G's	534 / 11.66%
Number/percentage of N's	0 / 0%
GC Percentage	43.23%

2.3. Coverage

Mean	0.2765
Standard Deviation	0.5841

2.4. Mapping Quality

Mean Mapping Quality	11.92

2.5. Mismatches and indels

General error rate	1.55%
Mismatches	71
Insertions	0
Mapped reads with at least one insertion	0%
Deletions	2
Mapped reads with at least one deletion	2.5%
Homopolymer indels	50%

2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
NC_012920.1	16569	4582	0.2765	0.5841

3. Results : Coverage across reference

Coverage across reference
UF8_f4_q37_sortc_markdup.rescaled.bam

4. Results : Coverage Histogram

Coverage Histogram
UF8_f4_q37_sortc_markdup.rescaled.bam

5. Results : Coverage Histogram (0-50X)
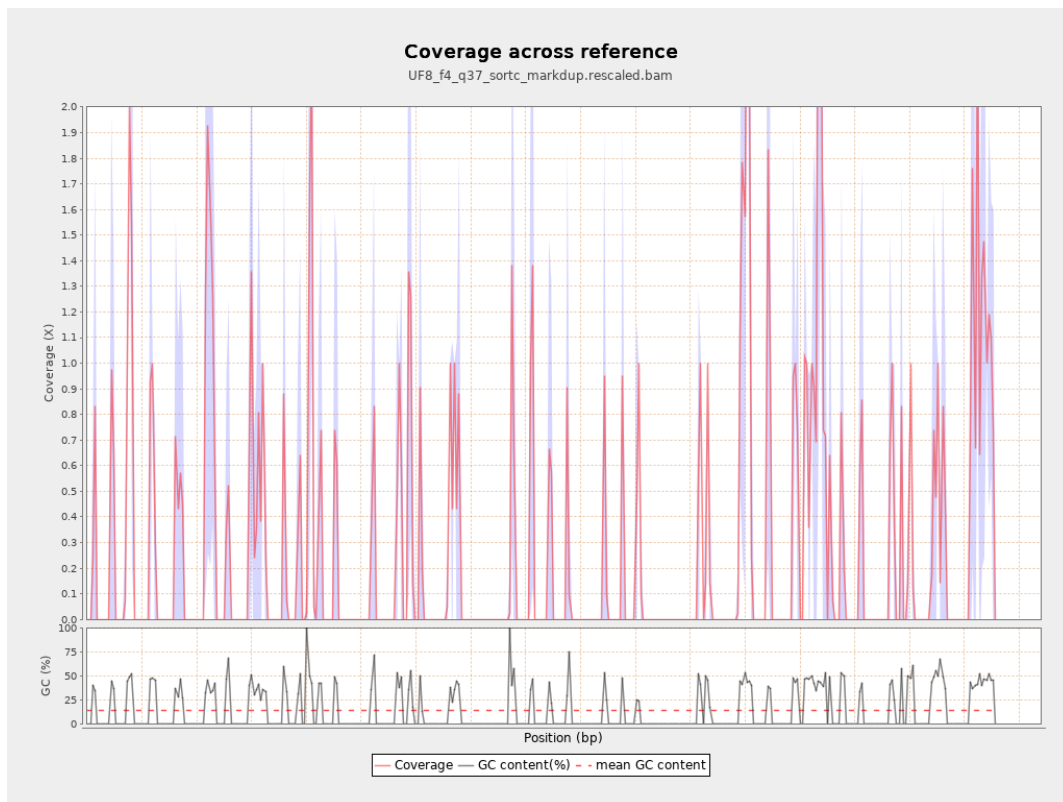
Coverage Histogram (0-50X)
UF8_f4_q37_sortc_markdup.rescaled.bam
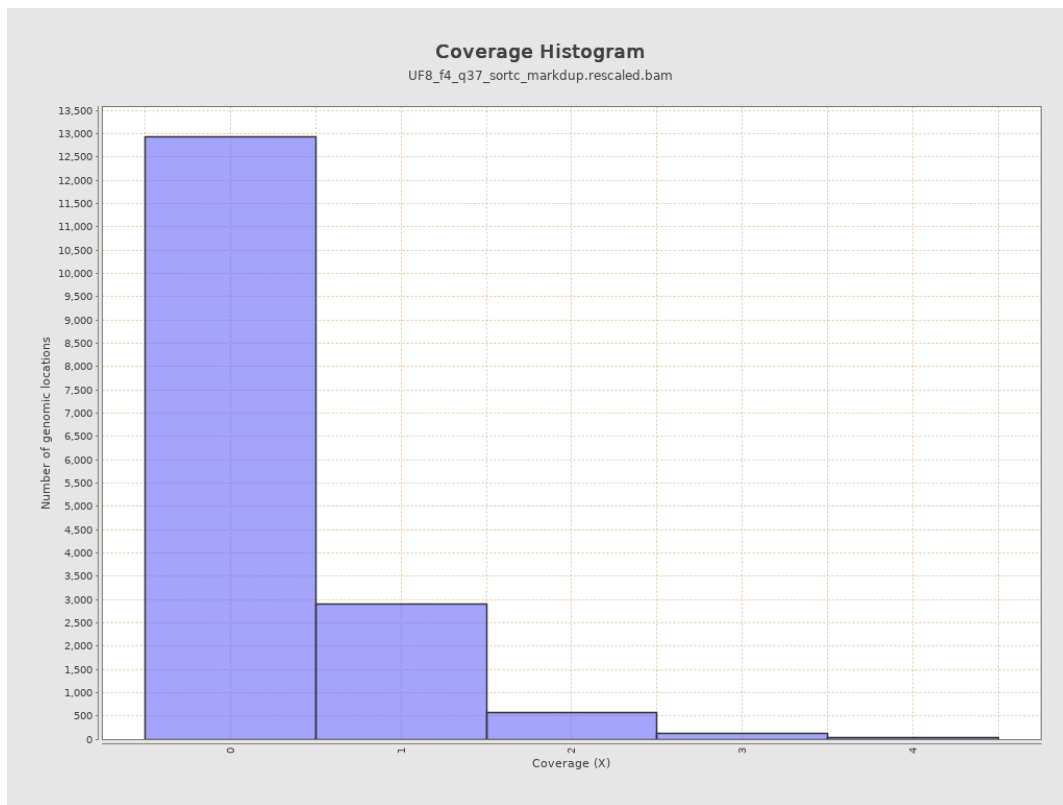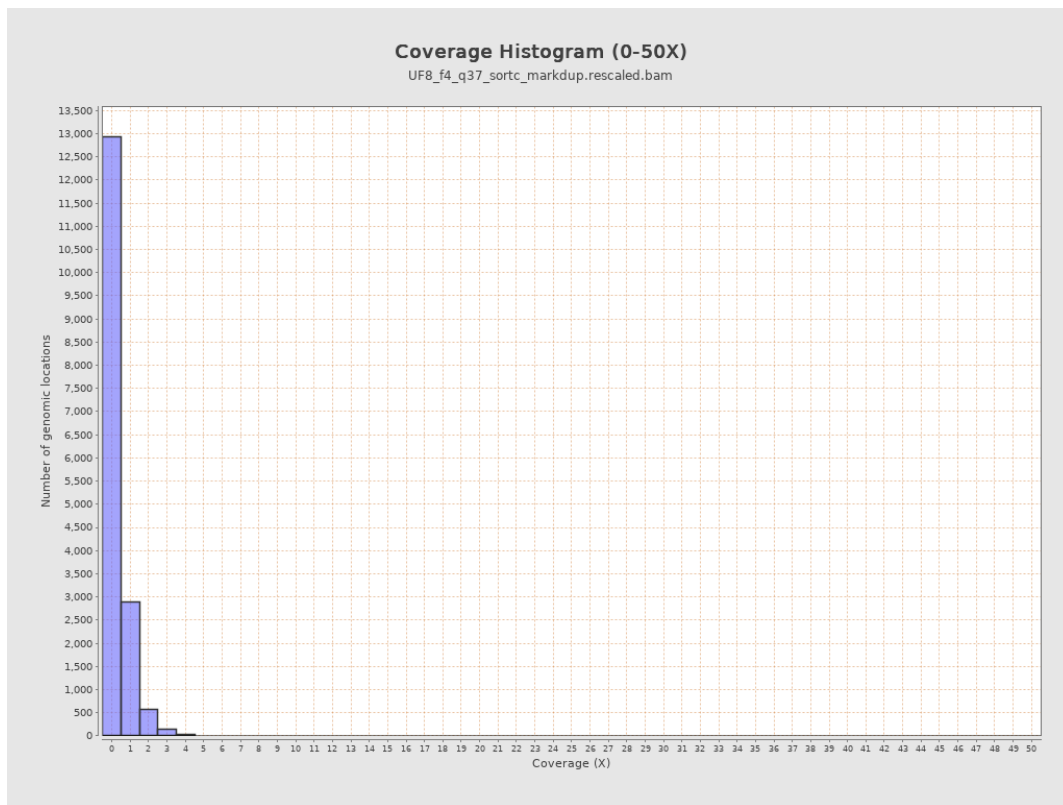
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
UF8_f4_q37_sortc_markdup.rescaled.bam
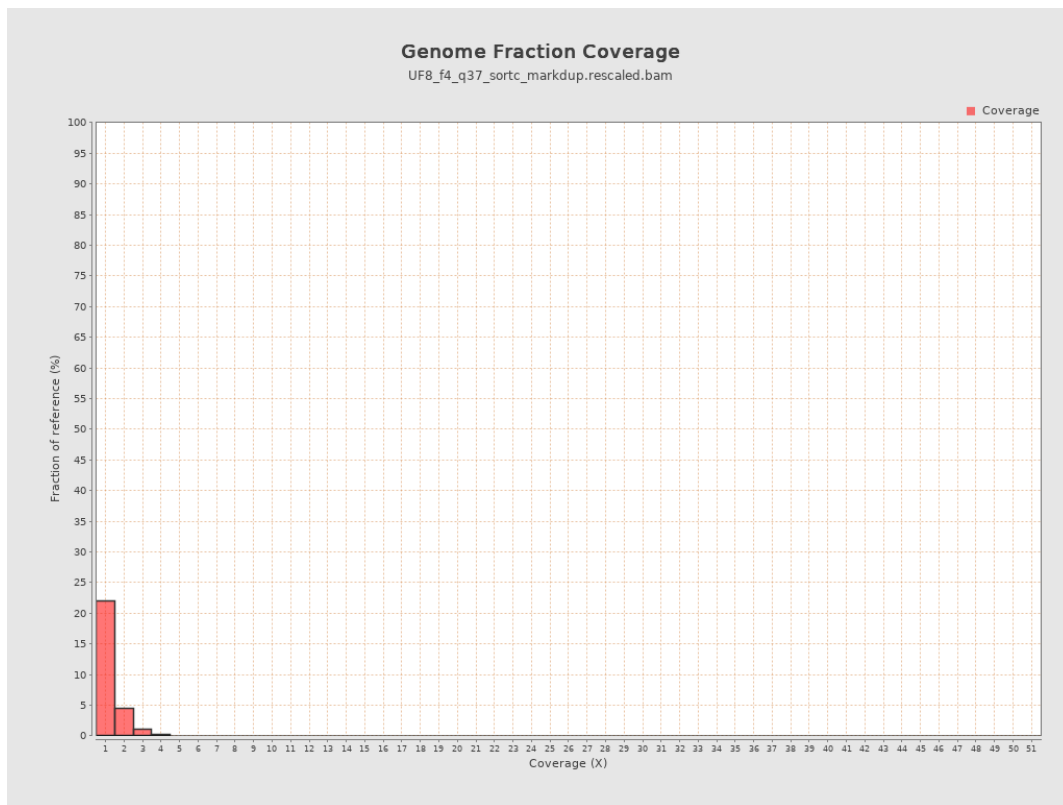
7. Results : Duplication Rate Histogram
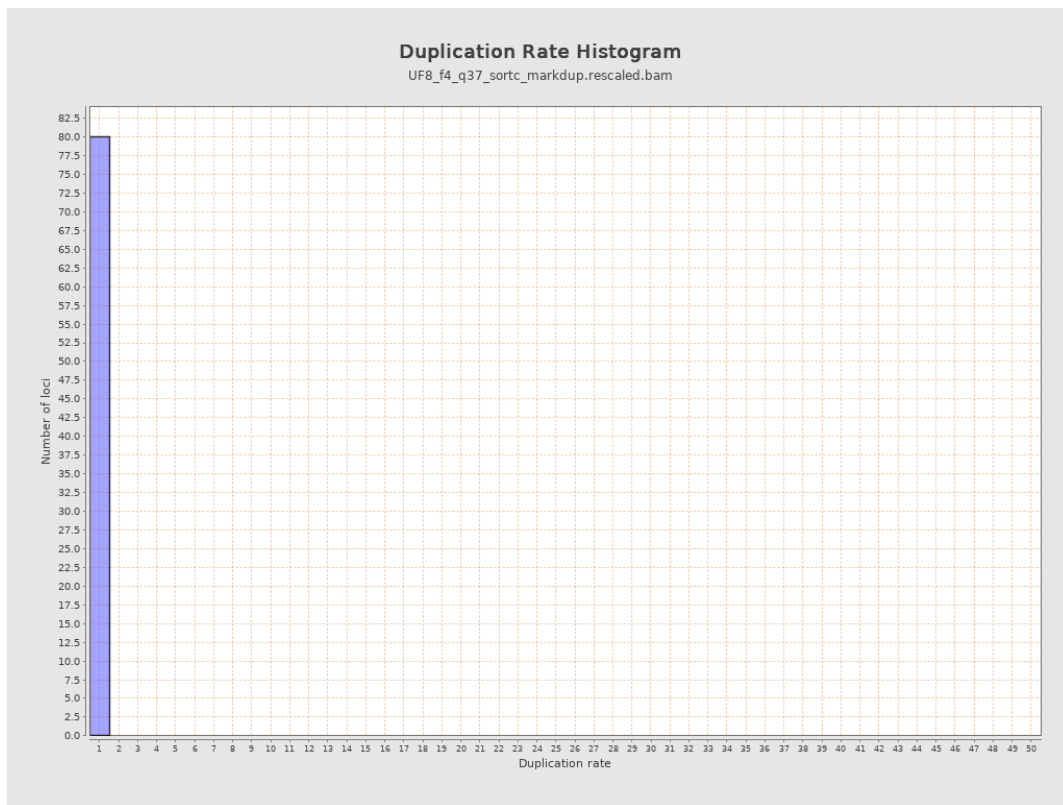
Duplication Rate Histogram
UF8_f4_q37_sortc_markdup.rescaled.bam

8. Results : Mapped Reads Nucleotide Content

Mapped Reads Nucleotide Content
UF8_f4_q37_sortc_markdup.rescaled.bam

9. Results : Mapped Reads GC-content Distribution

Mapped Reads GC-content Distribution
UF8_f4_q37_sortc_markdup.rescaled.bam
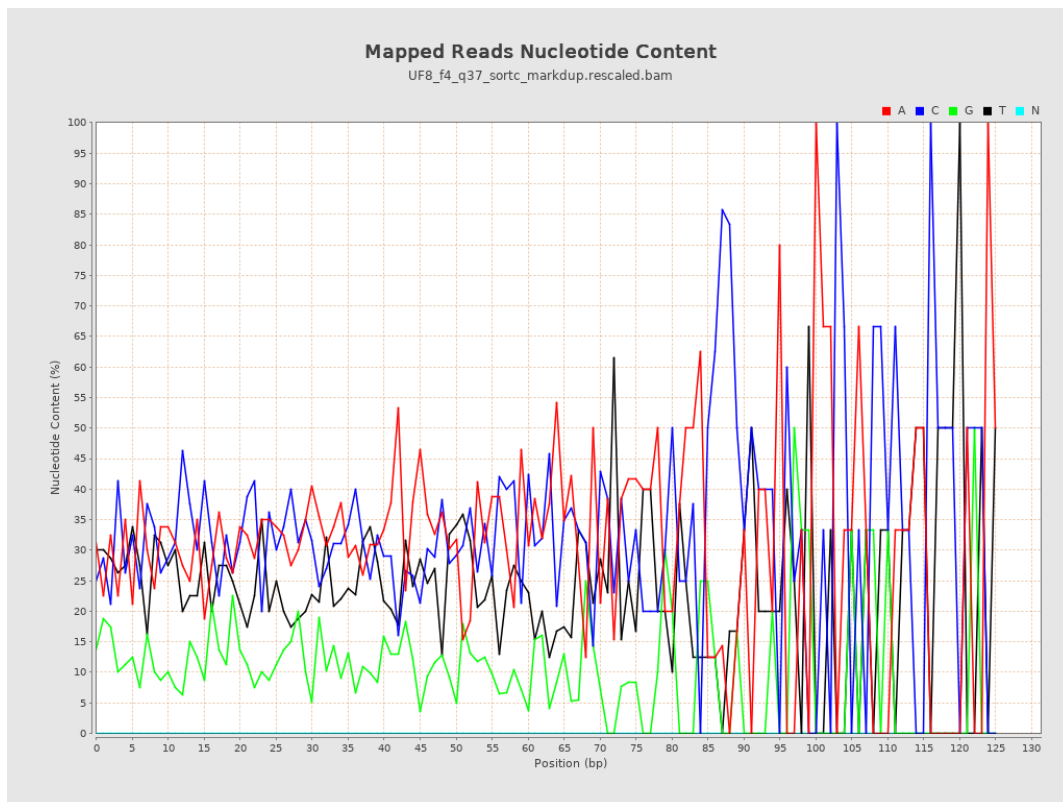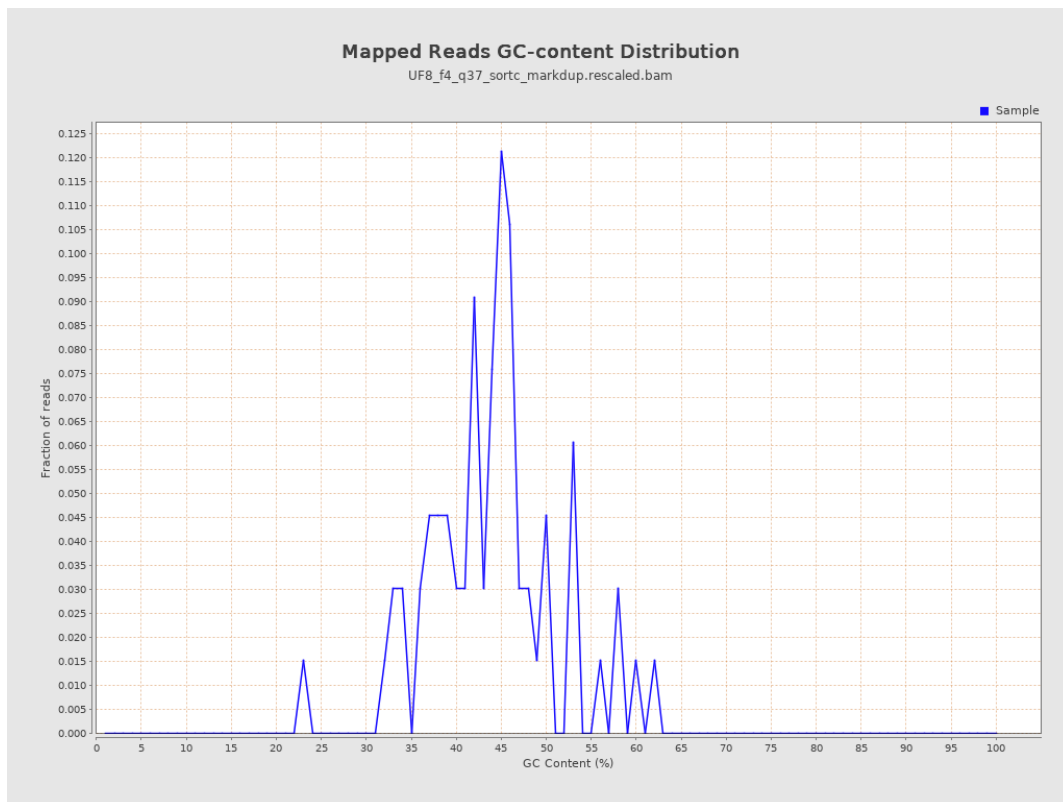
10. Results : Homopolymer Indels

Homopolymer Indels
UF8_f4_q37_sortc_markdup.rescaled.bam

11. Results : Mapping Quality Across Reference

Mapping Quality Across Reference
UF8_f4_q37_sortc_markdup.rescaled.bam

12. Results : Mapping Quality Histogram

Mapping Quality Histogram
UF8_f4_q37_sortc_markdup.rescaled.bam