Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2022/03/02 02:57:25

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
output/UF104/UF104_f4_q37_sortc_markdup.rescaled.bam -nw 400 -hm 3

1.2. Alignment

Command line:	bwa samse -r @RG\tID:UF104\tSM:UF104\tLB:nan\tPL:ILLUMINA /data/stonelab/references/Human_mitochondrial/NC_012920.1.fasta output/UF104/UF104-ancient.sai output/UF104/UF104-ancient.trimmed.fq
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 02 02:57:24 MST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	output/UF104/UF104_f4_q37_sortc_markdup.rescaled.bam

2. Summary

2.1. Globals

Reference size	16,569
Number of reads	27
Mapped reads	27 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	33 / 124 / 70
Duplicated reads (estimated)	0 / 0%
Duplication rate	0%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	570 / 30.16%
Number/percentage of C's	552 / 29.21%
Number/percentage of T's	495 / 26.19%
Number/percentage of G's	273 / 14.44%
Number/percentage of N's	0 / 0%
GC Percentage	43.65%

2.3. Coverage

Mean	0.1141
Standard Deviation	0.3618

2.4. Mapping Quality

Mean Mapping Quality	5.62

2.5. Mismatches and indels

General error rate	0.58%
Mismatches	11
Insertions	0
Mapped reads with at least one insertion	0%
Deletions	1
Mapped reads with at least one deletion	3.7%
Homopolymer indels	0%

2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
NC_012920.1	16569	1891	0.1141	0.3618

3. Results : Coverage across reference

Coverage across reference
UF104_f4_q37_sortc_markdup.rescaled.bam

4. Results : Coverage Histogram

Coverage Histogram
UF104_f4_q37_sortc_markdup.rescaled.bam

5. Results : Coverage Histogram (0-50X)
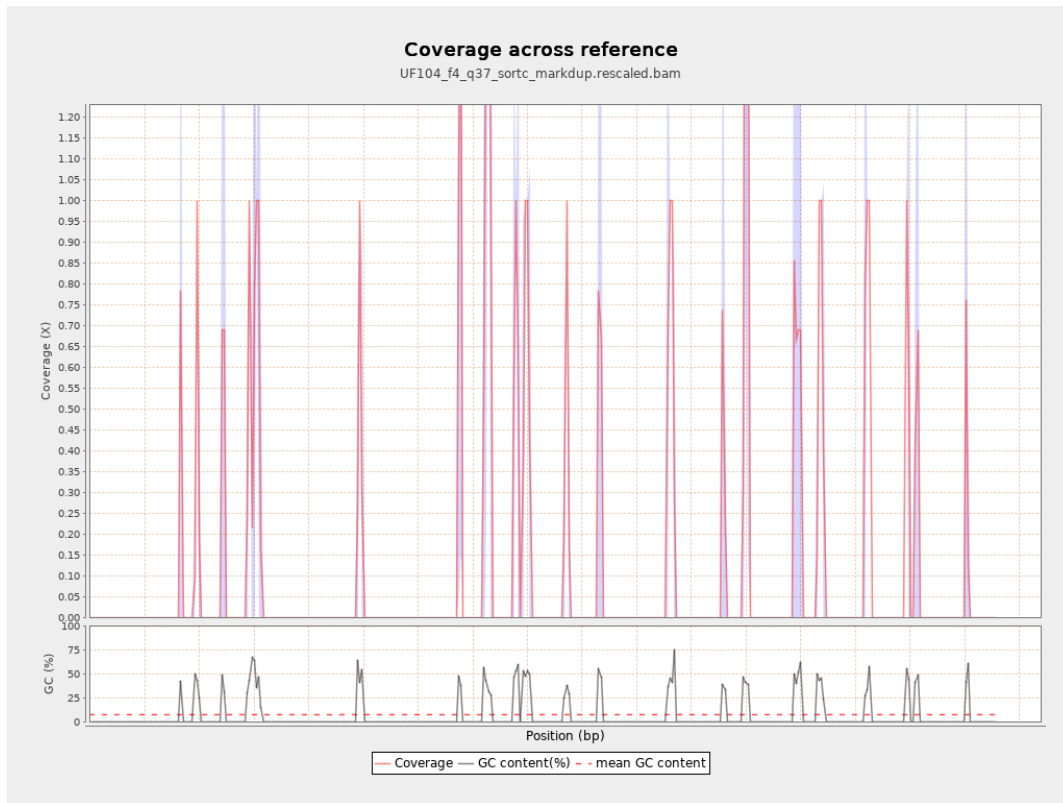
Coverage Histogram (0-50X)
UF104_f4_q37_sortc_markdup.rescaled.bam
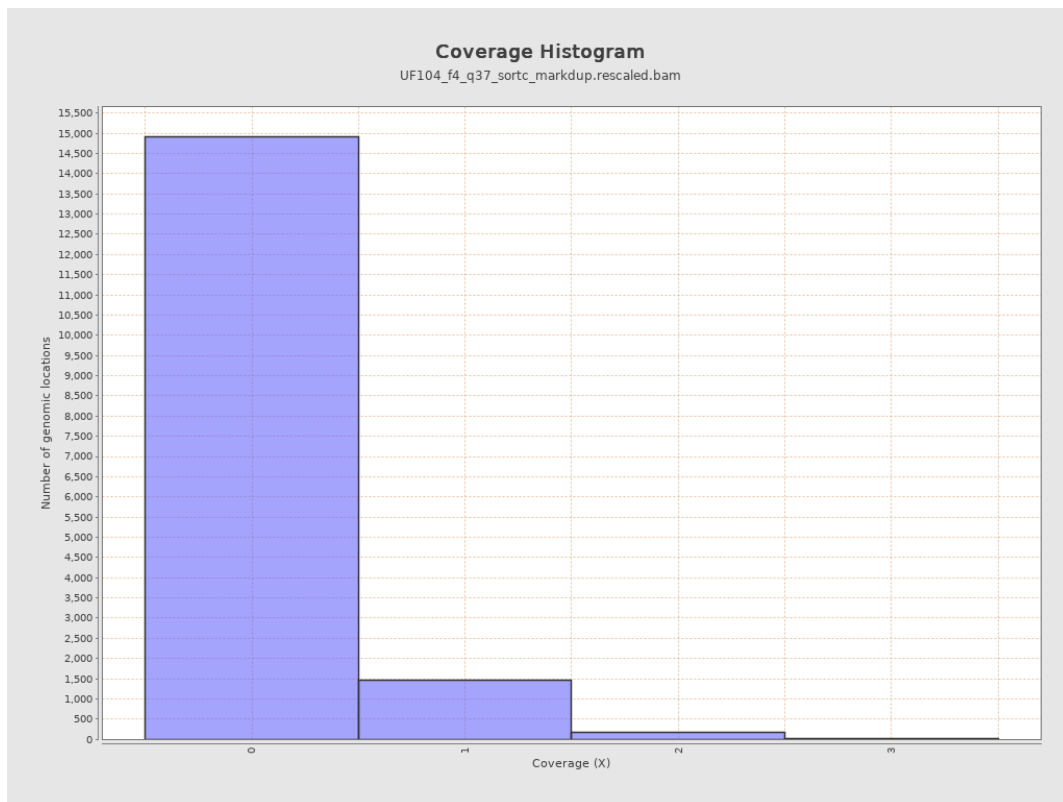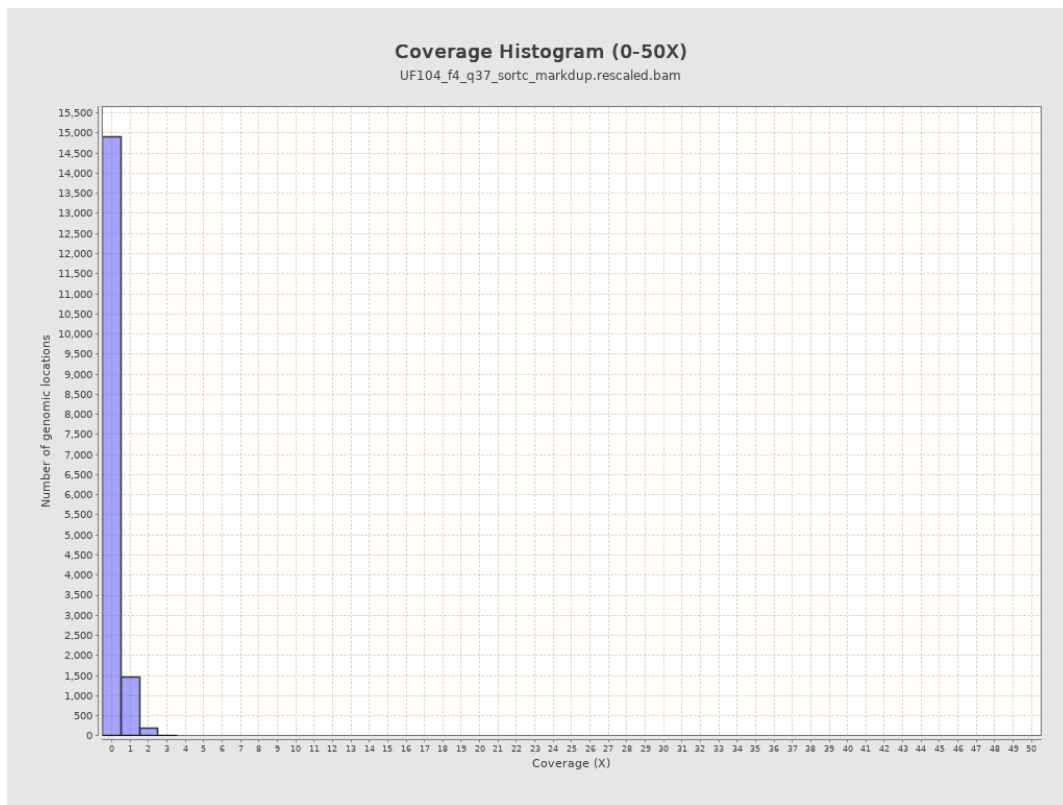
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
UF104_f4_q37_sortc_markdup.rescaled.bam
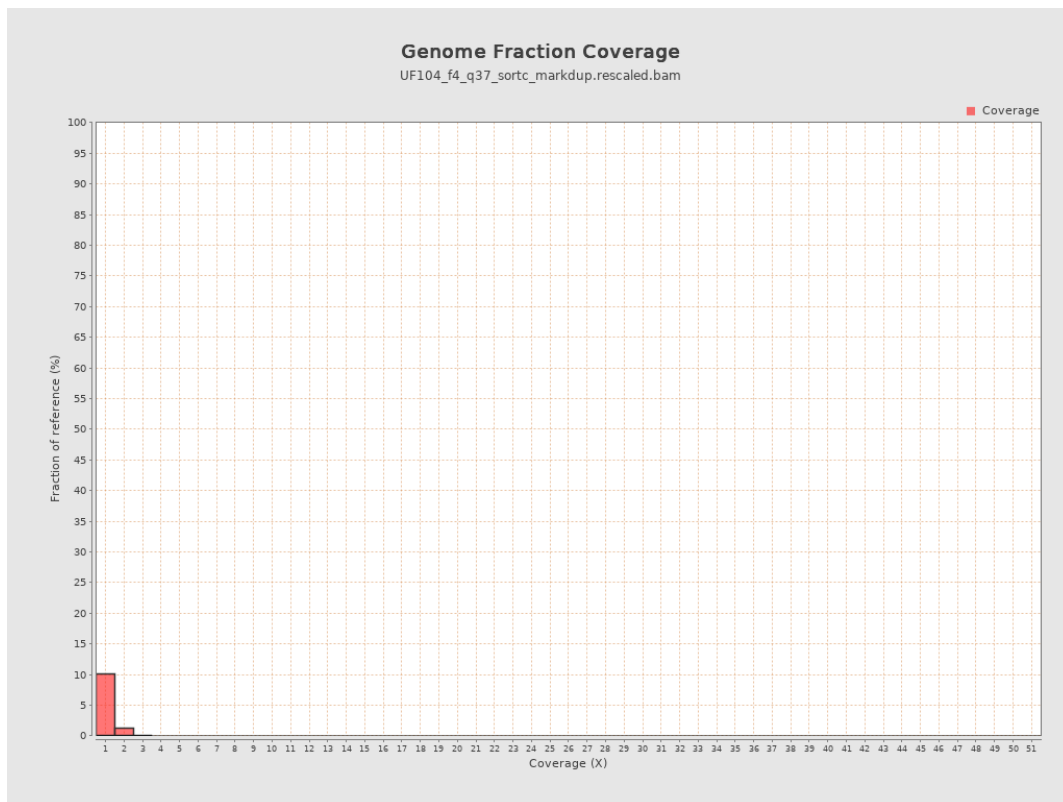
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
UF104_f4_q37_sortc_markdup.rescaled.bam
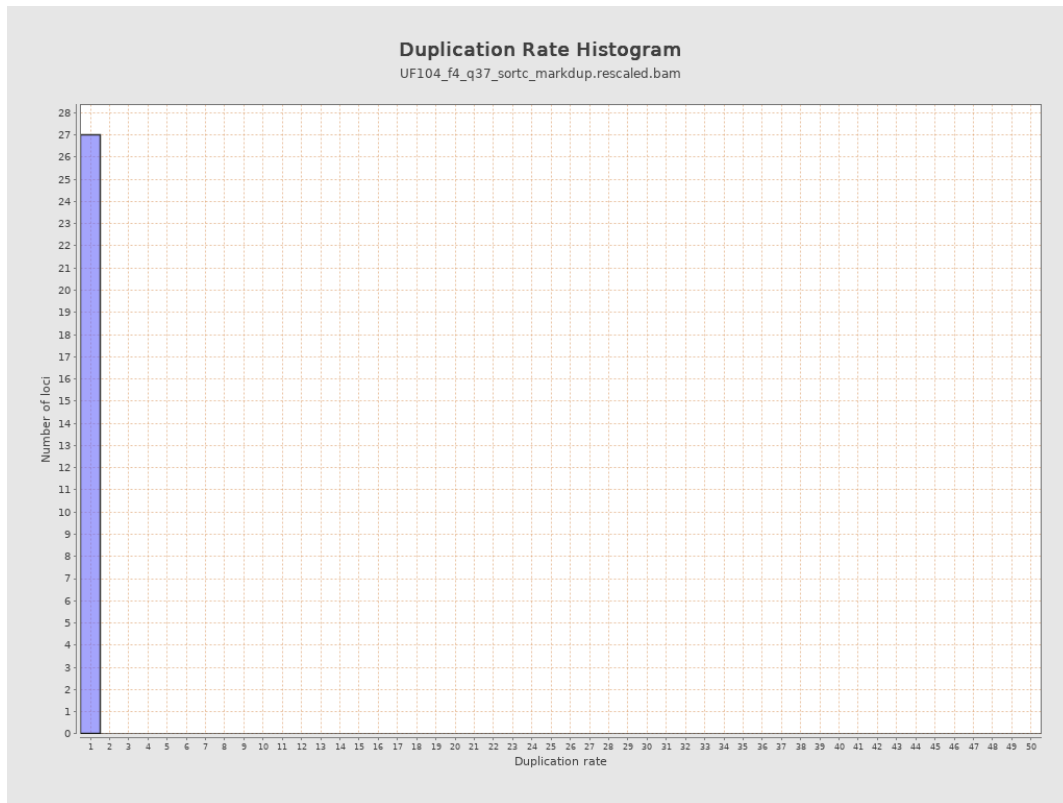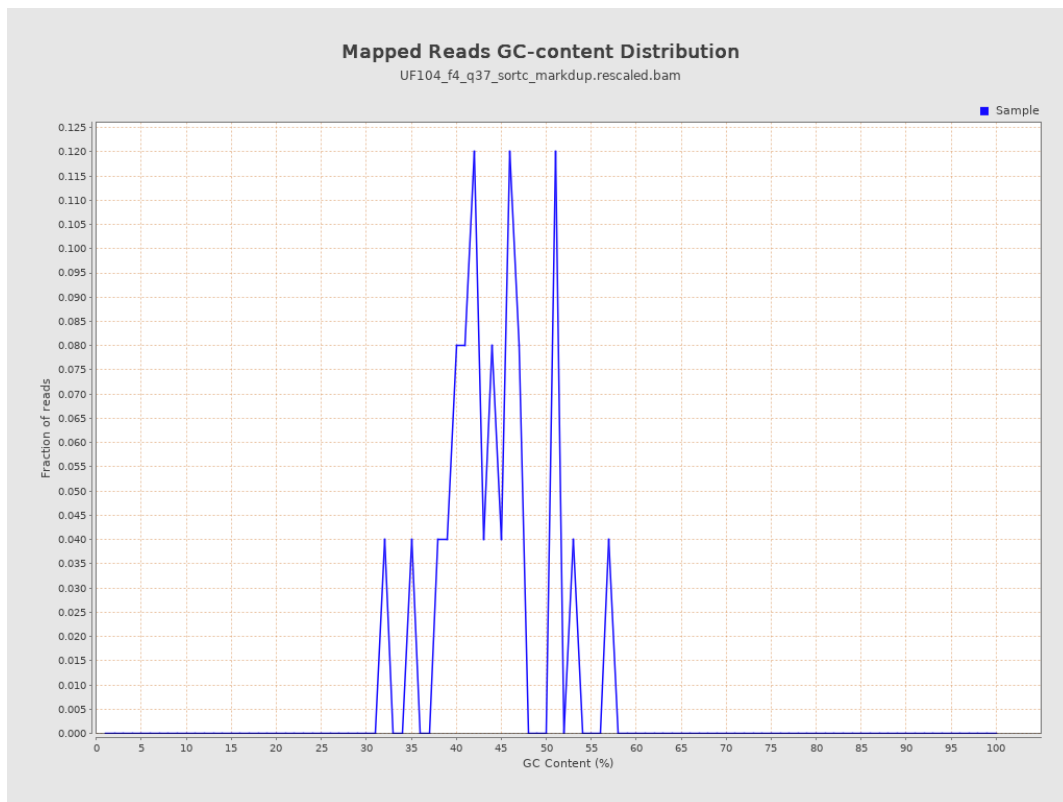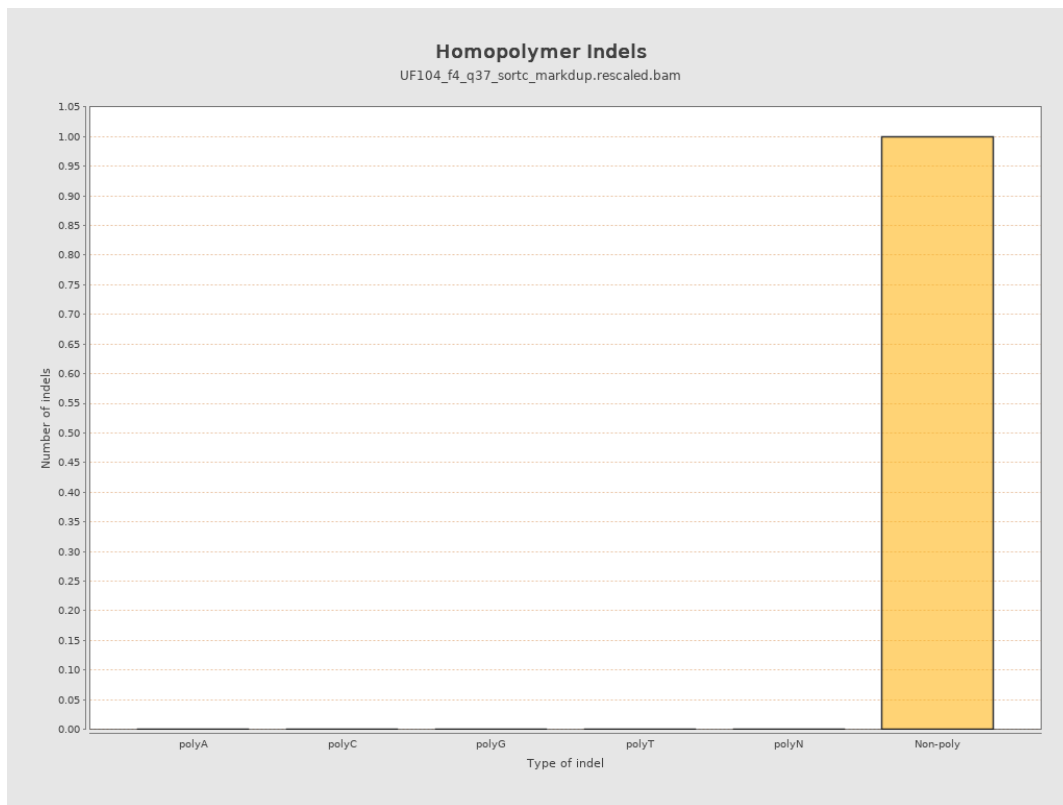
8. Results : Mapped Reads Nucleotide Content
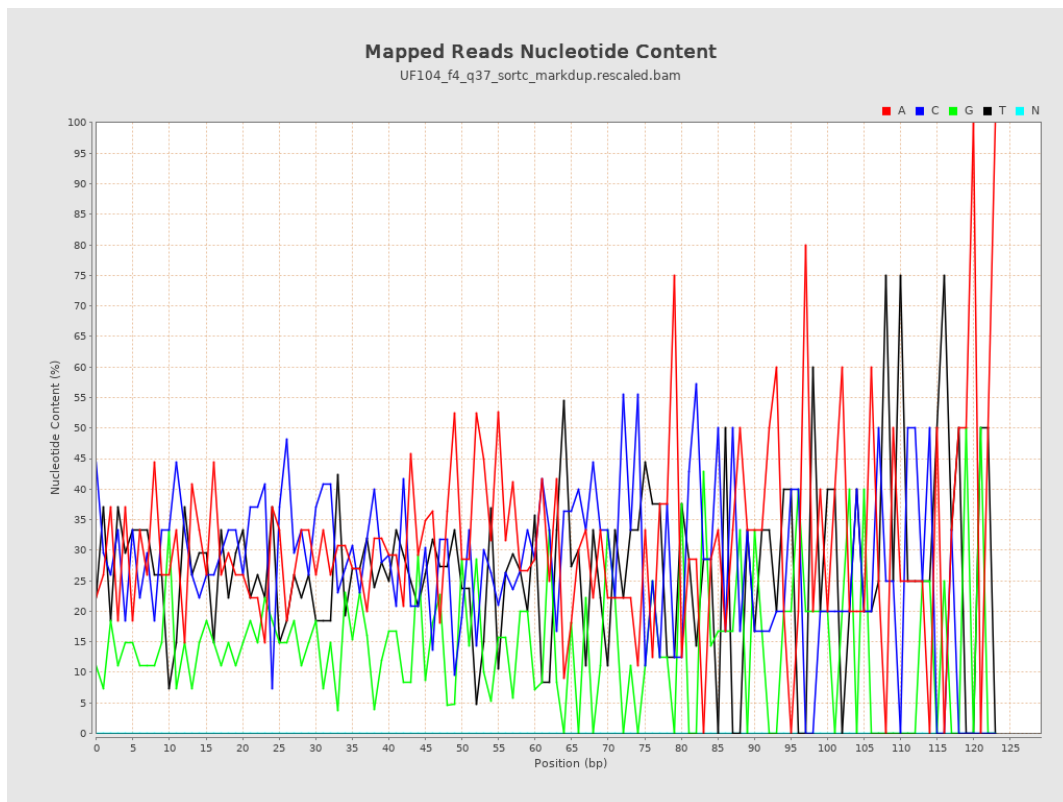
9. Results : Mapped Reads GC-content Distribution

10. Results : Homopolymer Indels

Homopolymer Indels
UF104_f4_q37_sortc_markdup.rescaled.bam

11. Results : Mapping Quality Across Reference

12. Results : Mapping Quality Histogram

Mapping Quality Histogram
UF104_f4_q37_sortc_markdup.rescaled.bam