

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/02 03:47:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
output/UF800/UF800_f4_q37_sortc_markdup.rescaled.bam -nw 400 -hm 3
```

1.2. Alignment

Command line:	bwa samse -r @RG\tID:UF800\tSM:UF800\tLB:nan\ \tPL:ILLUMINA /data/stonelab/references/Human_mit ochondrial/NC_012920.1.fasta output/UF800/UF800-ancient.sai output/UF800/UF800- ancient.trimmed.fq
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 02 03:47:16 MST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	output/UF800/UF800_f4_q37_sortc_ markdup.rescaled.bam

2. Summary

2.1. Globals

Reference size	16,569
Number of reads	31
Mapped reads	31 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	31 / 133 / 51.68
Duplicated reads (estimated)	0 / 0%
Duplication rate	0%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	519 / 32.4%
Number/percentage of C's	515 / 32.15%
Number/percentage of T's	416 / 25.97%
Number/percentage of G's	152 / 9.49%
Number/percentage of N's	0 / 0%
GC Percentage	41.64%

2.3. Coverage

Mean	0.0967
Standard Deviation	0.3312

2.4. Mapping Quality

Mean Mapping Quality	5.99
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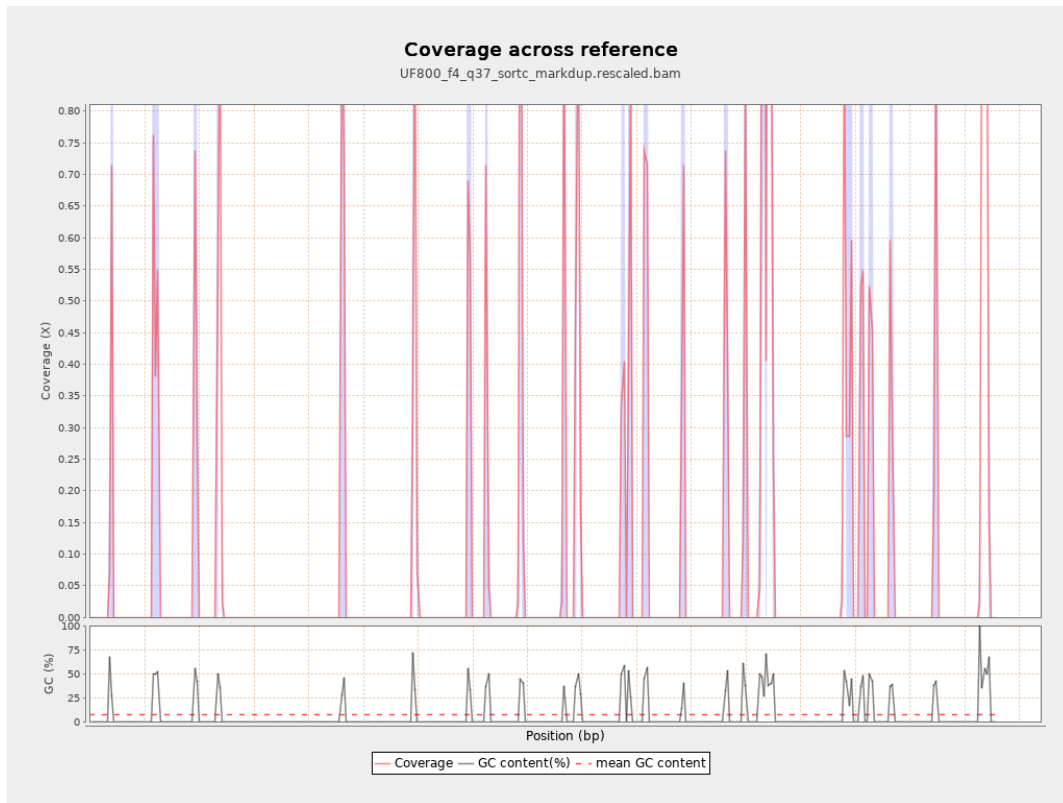
2.5. Mismatches and indels

General error rate	1.06%
Mismatches	17

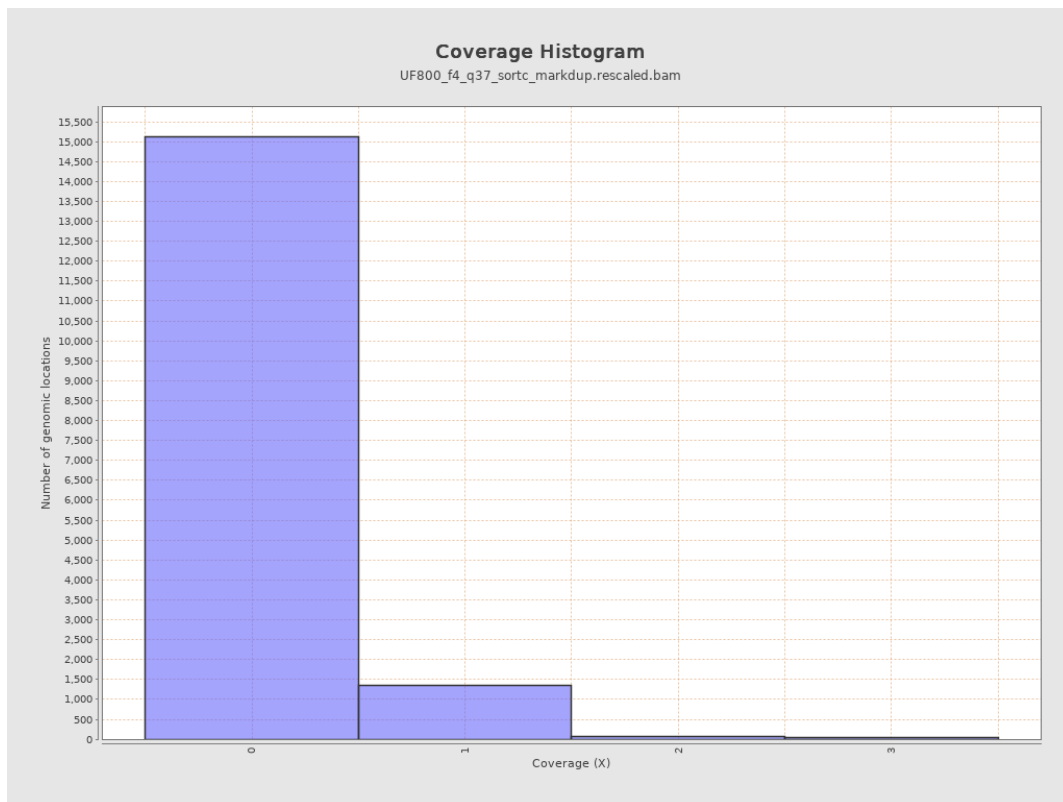
2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
NC_012920.1	16569	1602	0.0967	0.3312

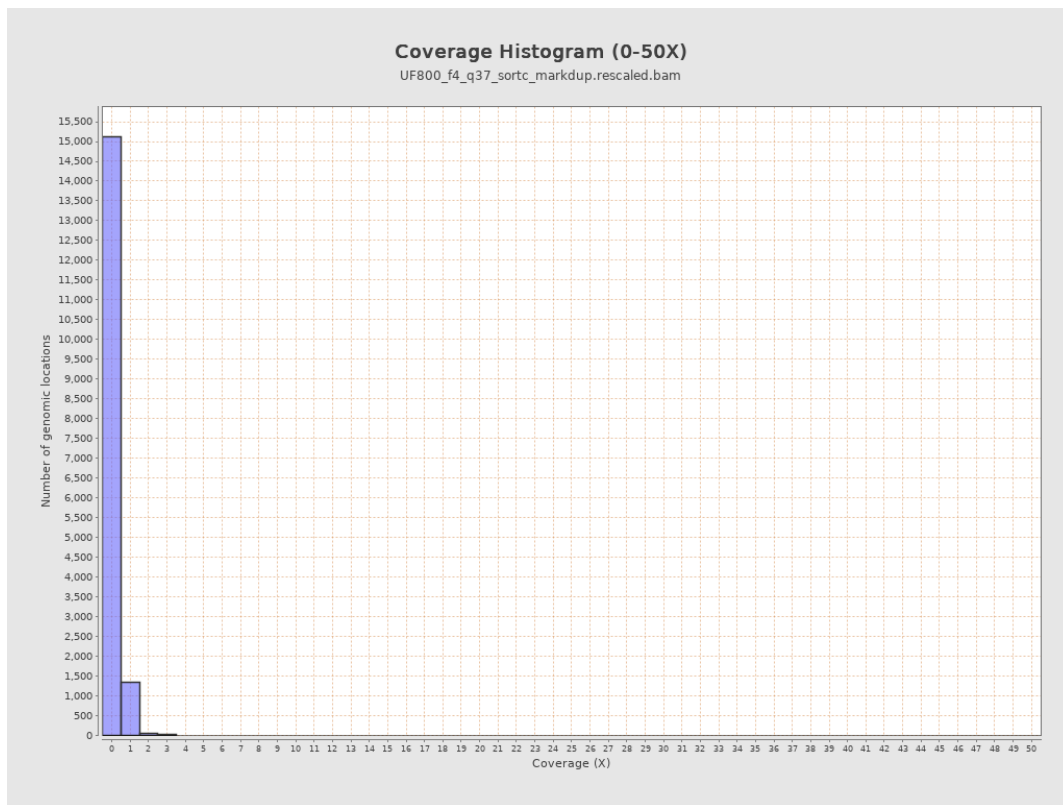
3. Results : Coverage across reference



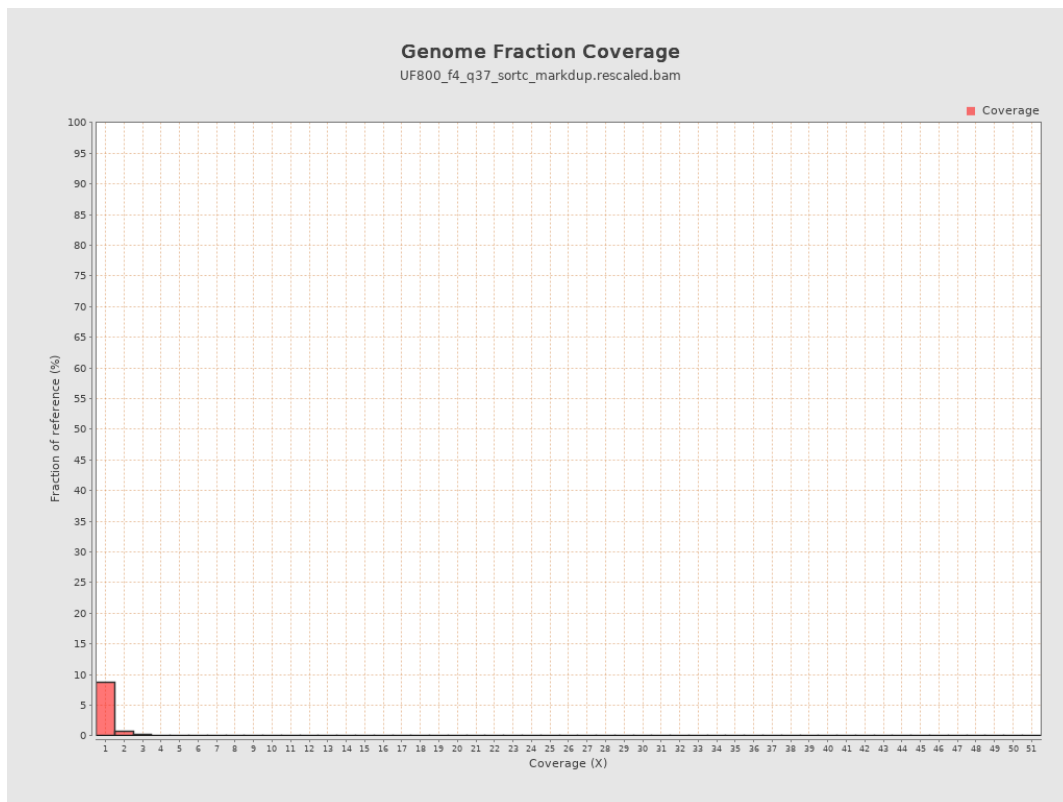
4. Results : Coverage Histogram



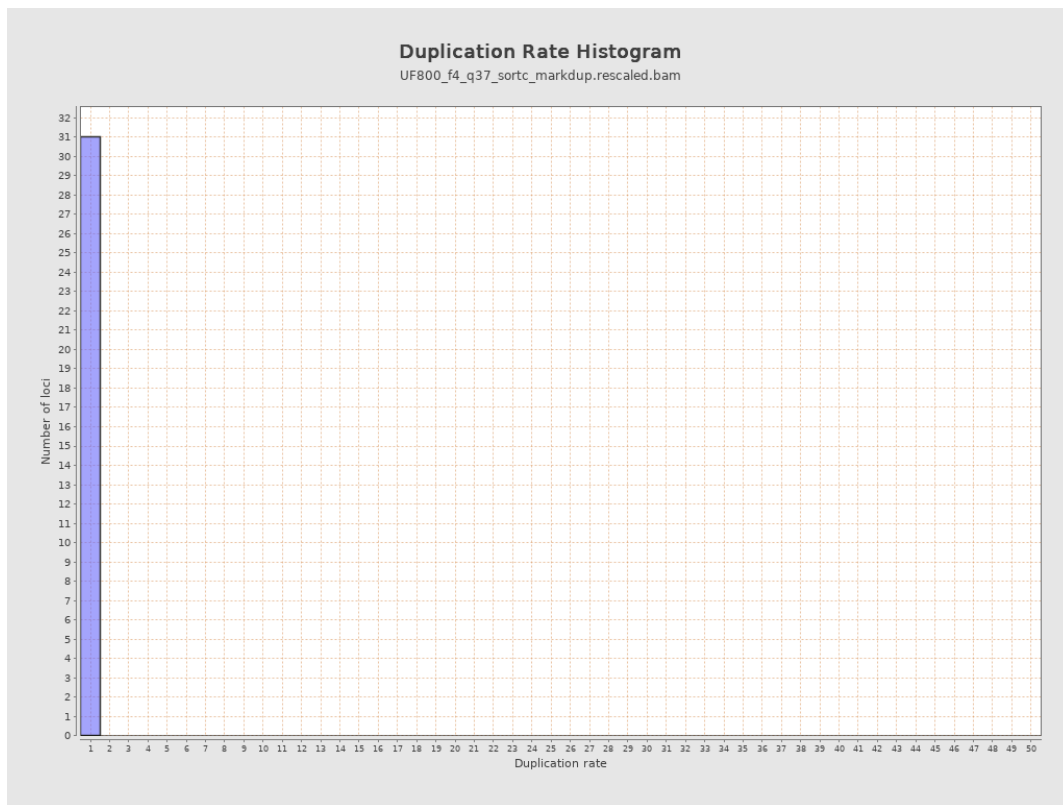
5. Results : Coverage Histogram (0-50X)



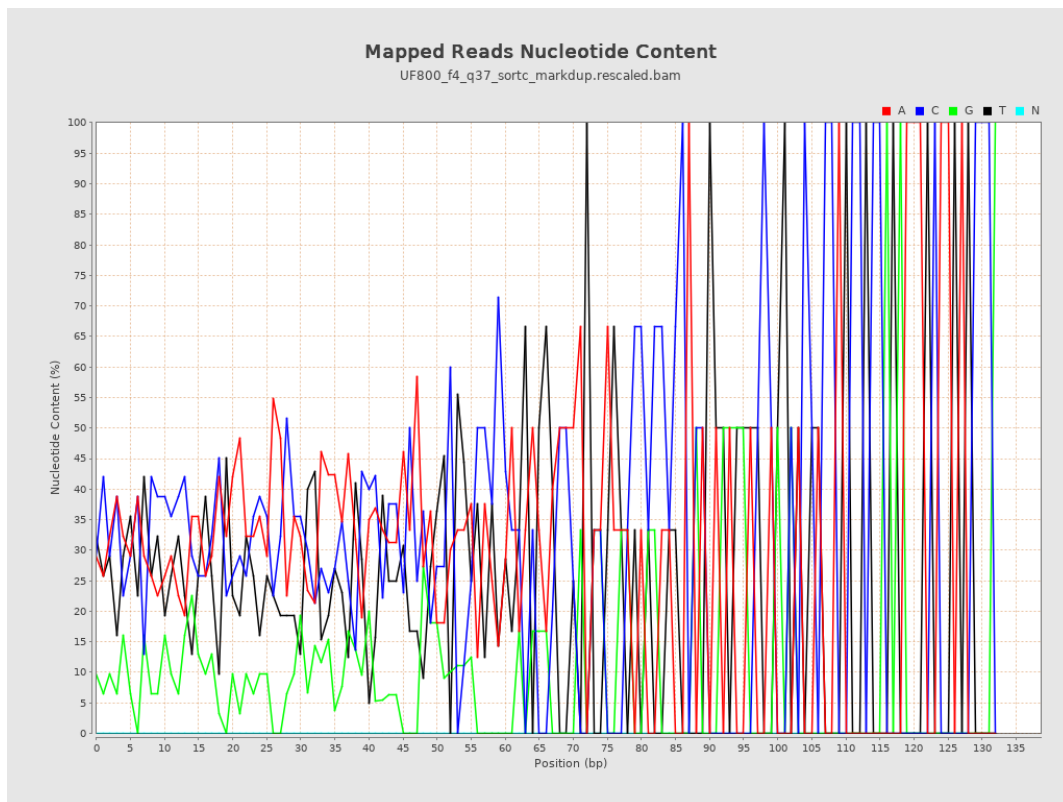
6. Results : Genome Fraction Coverage



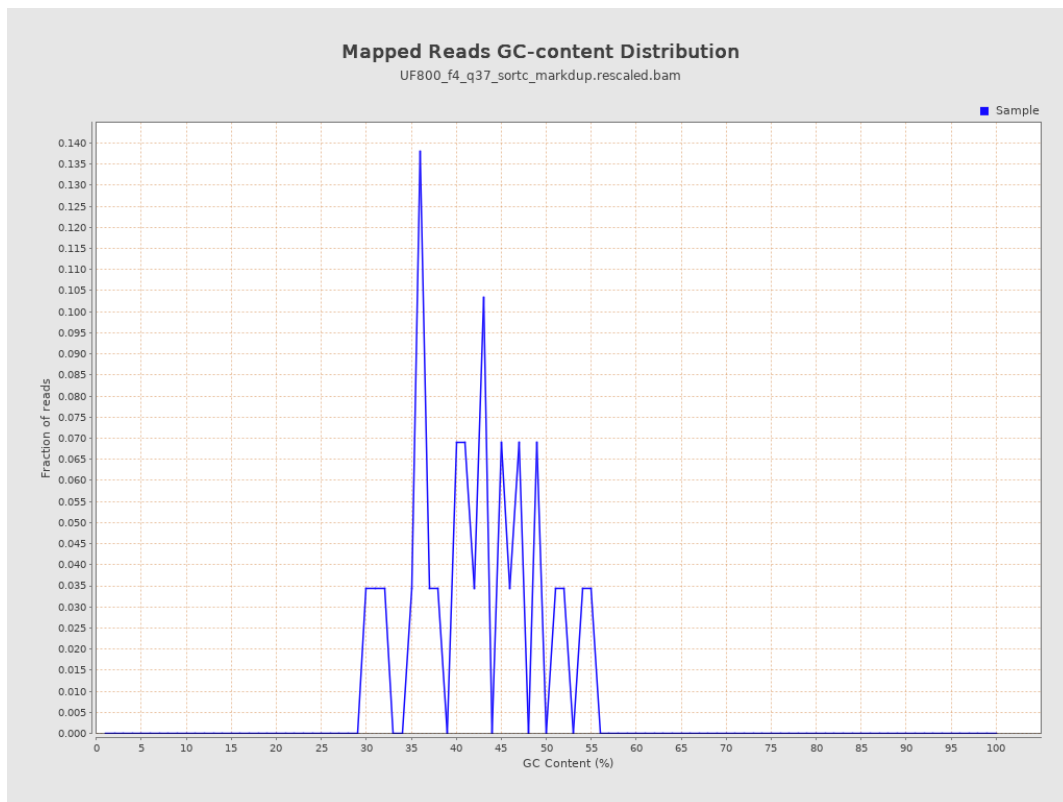
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



10. Results : Mapping Quality Across Reference



11. Results : Mapping Quality Histogram

