

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/02 02:57:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
output/UF100/UF100_f4_q37_sortc_markdup.rescaled.bam -nw 400 -hm 3
```

1.2. Alignment

Command line:	bwa samse -r @RG\tID:UF100\tSM:UF100\tLB:nan\ \tPL:ILLUMINA /data/stonelab/references/Human_mit ochondrial/NC_012920.1.fasta output/UF100/UF100-ancient.sai output/UF100/UF100- ancient.trimmed.fq
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 02 02:57:46 MST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	output/UF100/UF100_f4_q37_sortc_ markdup.rescaled.bam

2. Summary

2.1. Globals

Reference size	16,569
Number of reads	91
Mapped reads	91 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	30 / 129 / 57.13
Duplicated reads (estimated)	0 / 0%
Duplication rate	0%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	1,656 / 31.88%
Number/percentage of C's	1,558 / 29.99%
Number/percentage of T's	1,306 / 25.14%
Number/percentage of G's	675 / 12.99%
Number/percentage of N's	0 / 0%
GC Percentage	42.98%

2.3. Coverage

Mean	0.3135
Standard Deviation	0.5571

2.4. Mapping Quality

Mean Mapping Quality	15.15
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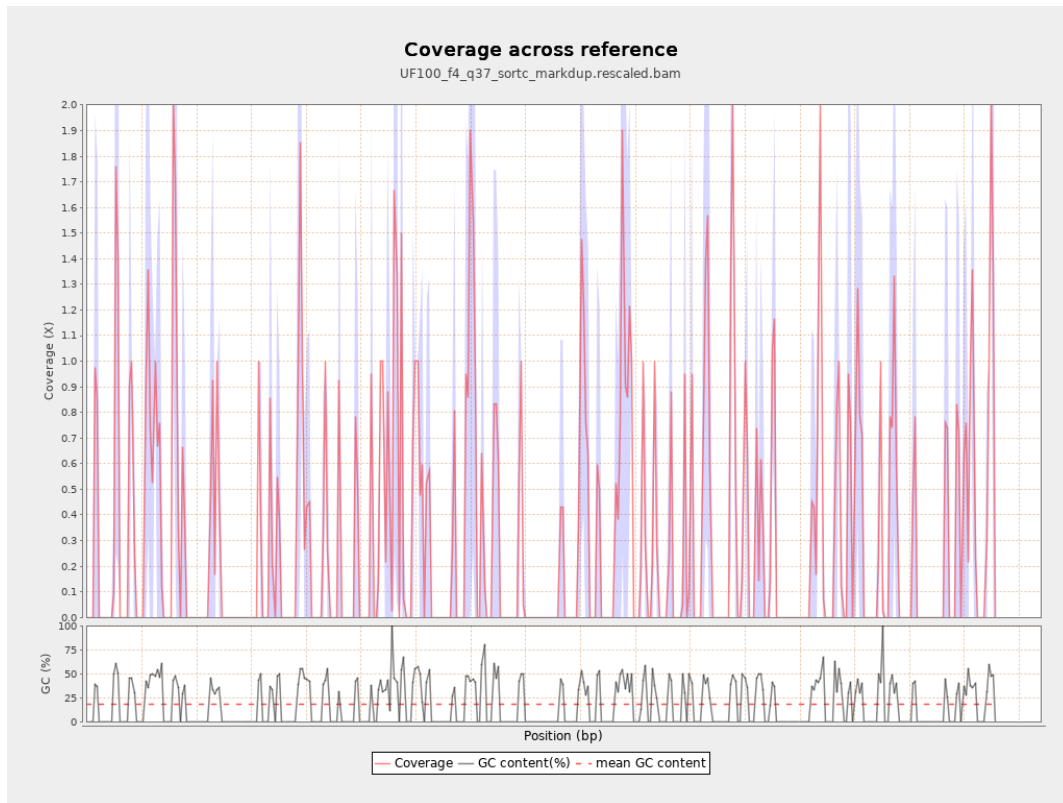
2.5. Mismatches and indels

General error rate	1.44%
Mismatches	71
Insertions	1
Mapped reads with at least one insertion	1.1%
Deletions	0
Mapped reads with at least one deletion	0%
Homopolymer indels	0%

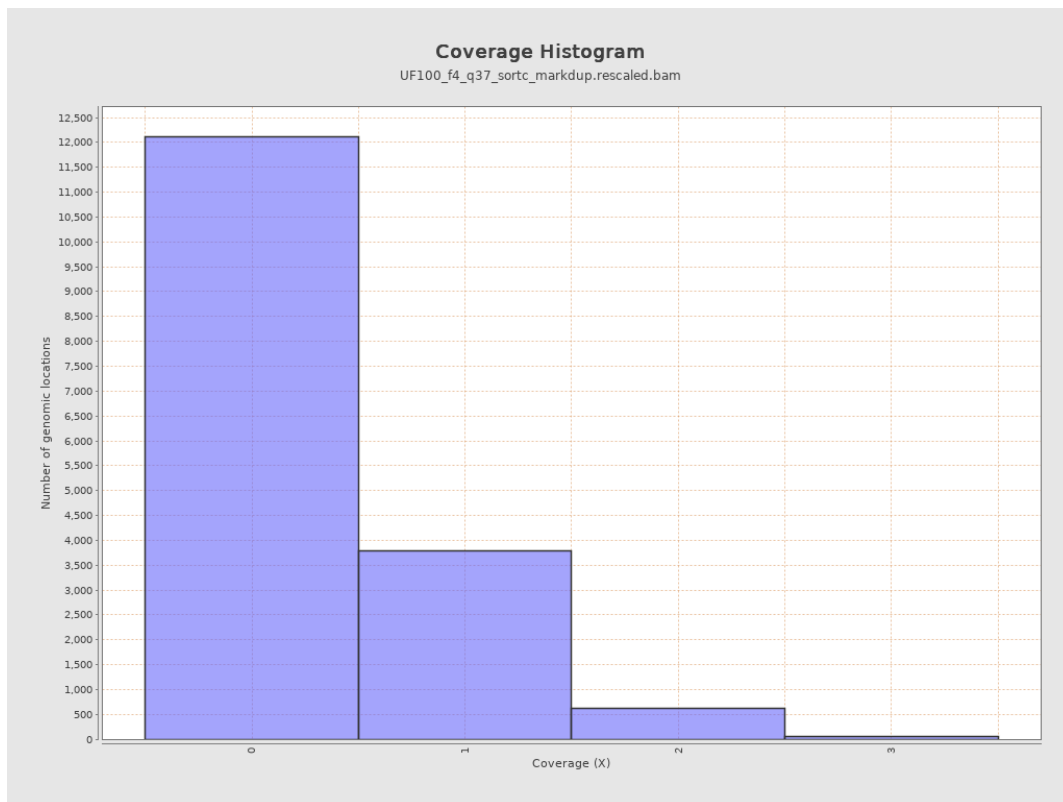
2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
NC_012920.1	16569	5195	0.3135	0.5571

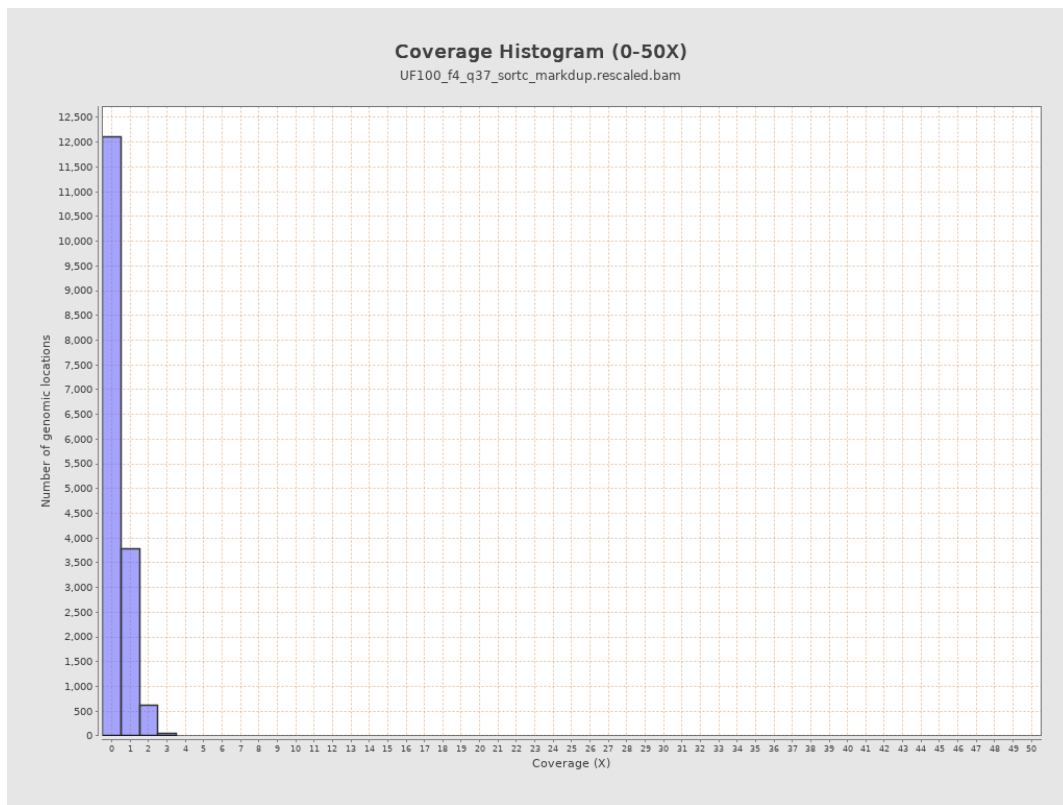
3. Results : Coverage across reference



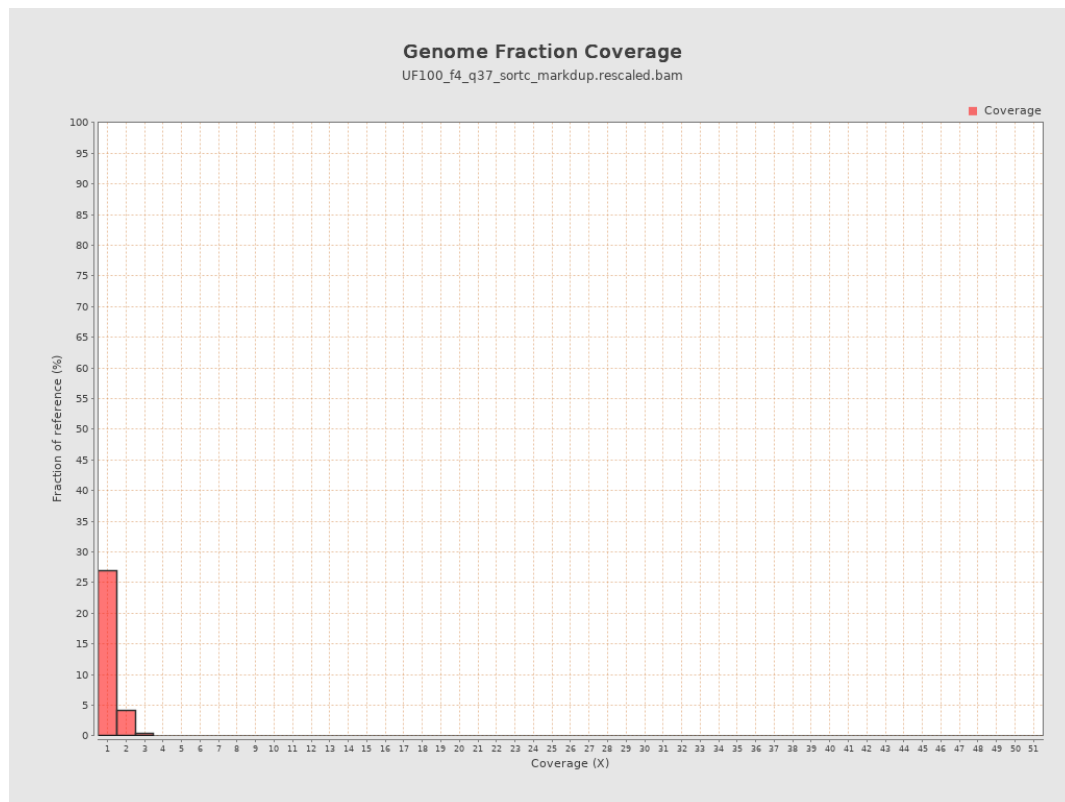
4. Results : Coverage Histogram



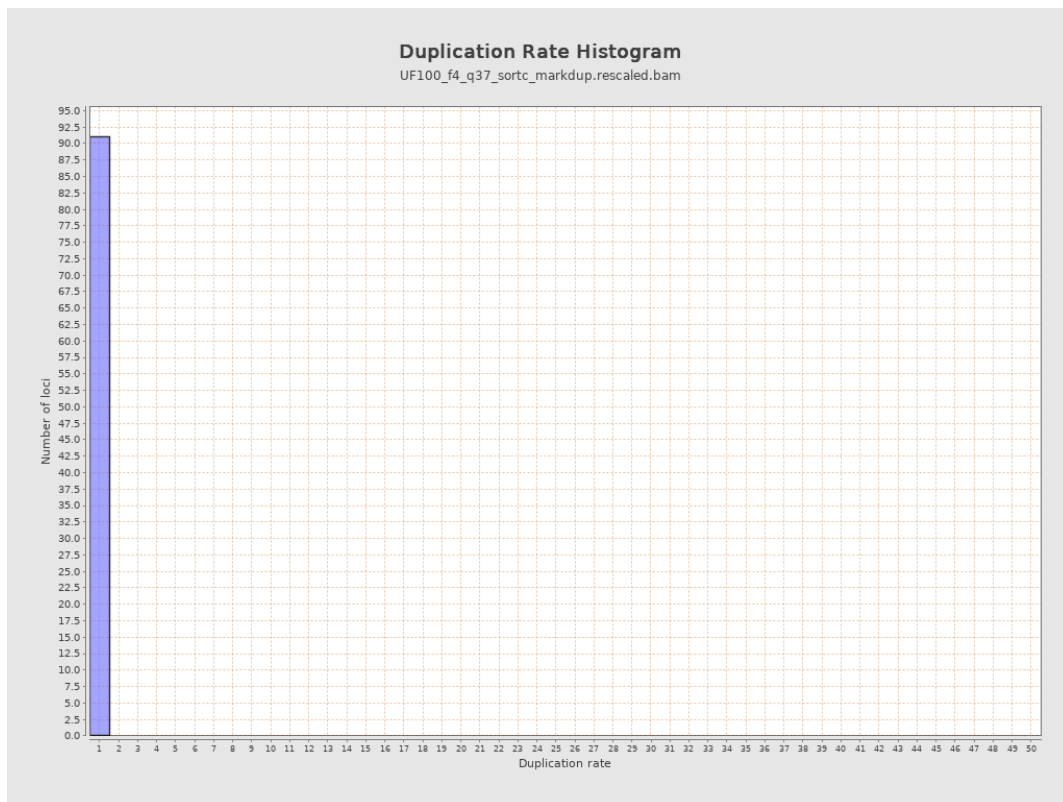
5. Results : Coverage Histogram (0-50X)



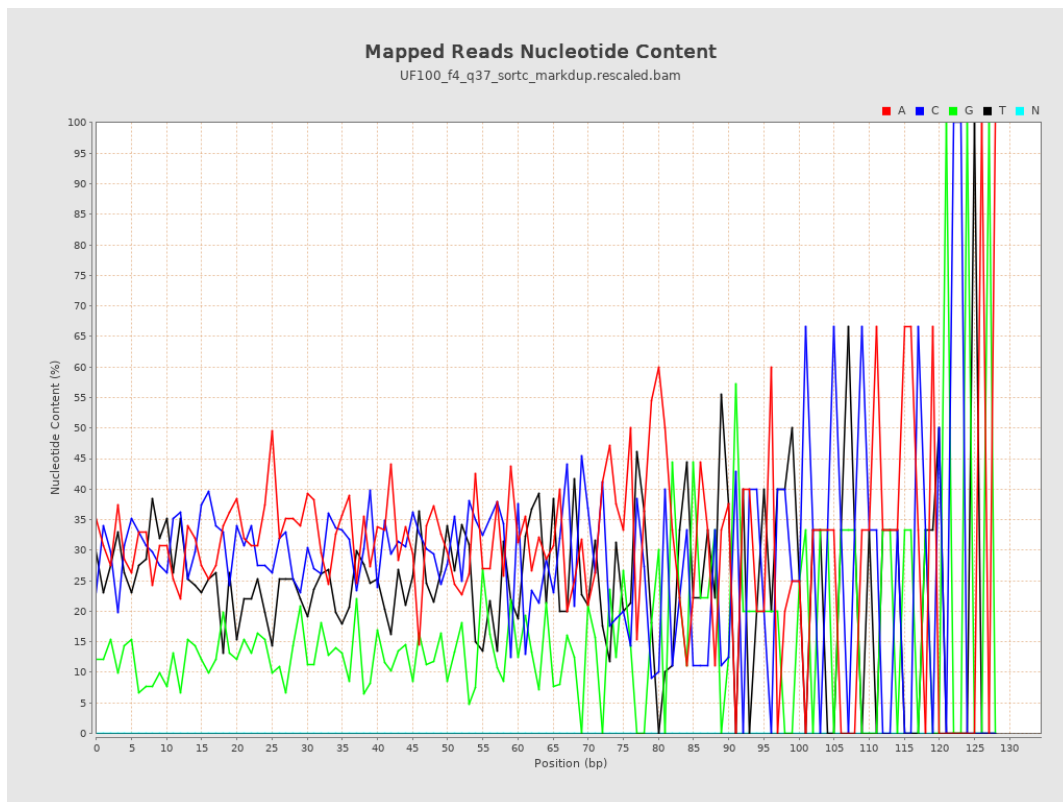
6. Results : Genome Fraction Coverage



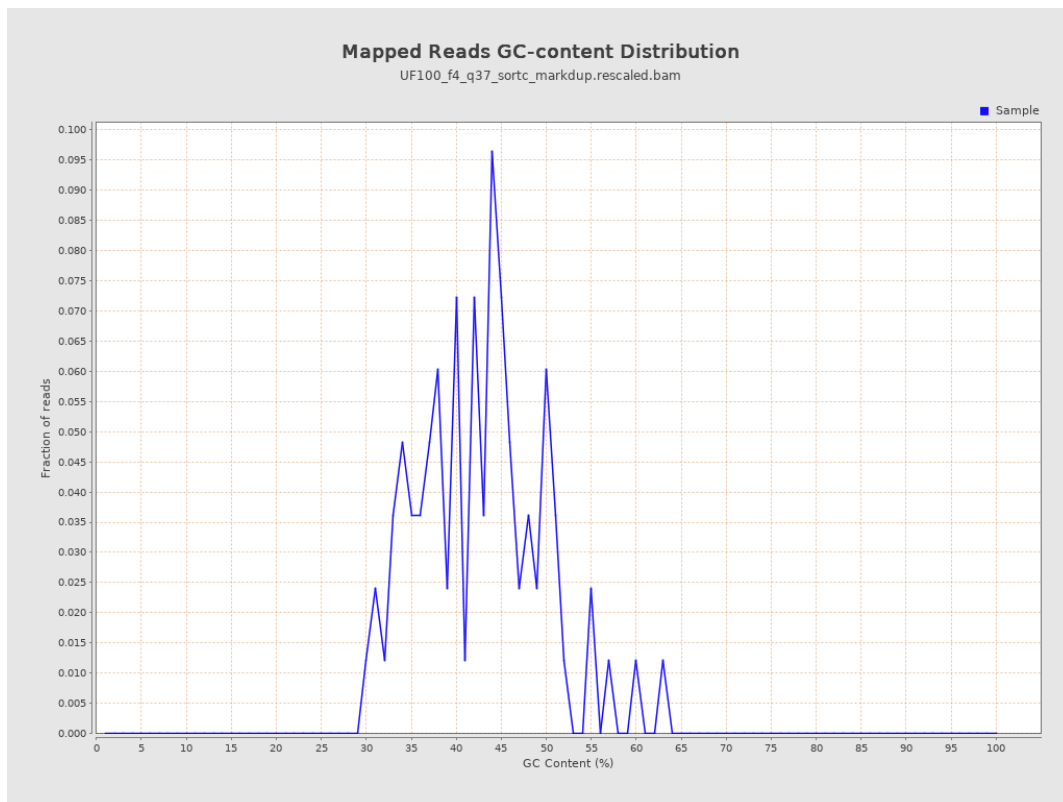
7. Results : Duplication Rate Histogram



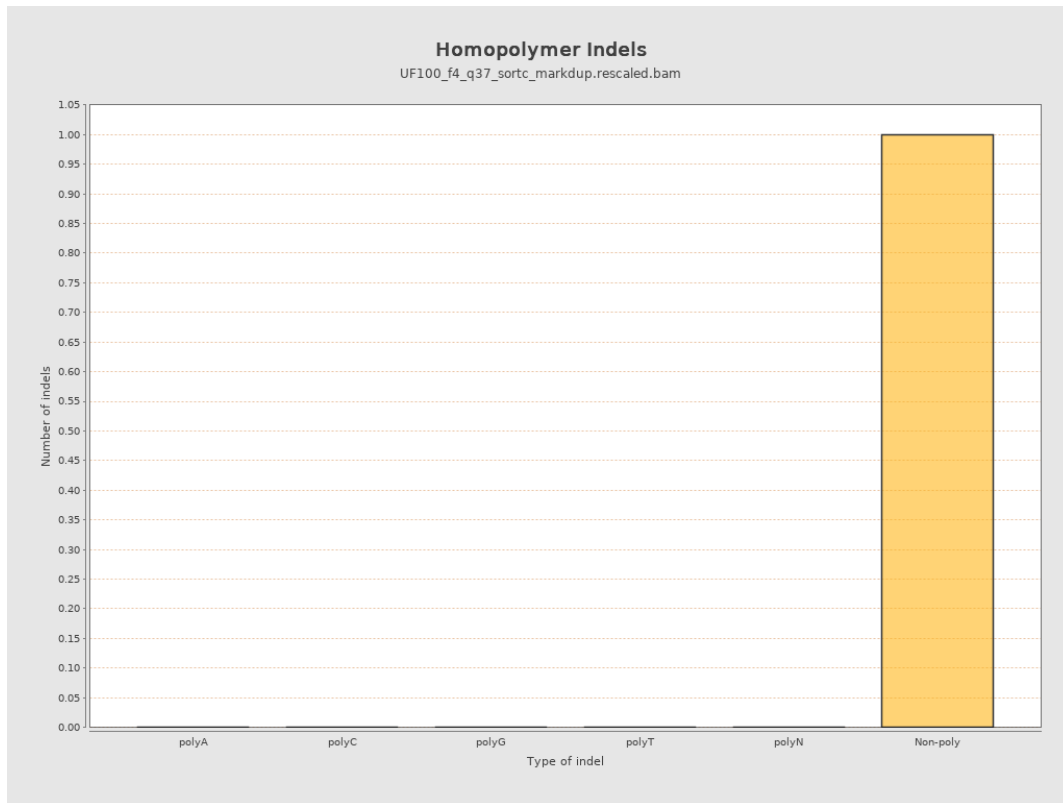
8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



10. Results : Homopolymer Indels



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

