

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/01 01:49:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
output/UF802/UF802_f4_q37_sortc_markdup.rescaled.bam -nw 400 -hm 3
```

1.2. Alignment

Command line:	bwa samse -r @RG\tID:UF802\tSM:UF802\tLB:nan\ tPL:ILLUMINA /data/stonelab/references/M_leprae_ TN/M_leprae_TN.fasta output/UF802/UF802-ancient.sai output/UF802/UF802- ancient.trimmed.fq
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 01 01:49:42 MST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	output/UF802/UF802_f4_q37_sortc_ markdup.rescaled.bam

2. Summary

2.1. Globals

Reference size	3,268,203
Number of reads	260
Mapped reads	260 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	30 / 139 / 48.01
Duplicated reads (estimated)	39 / 15%
Duplication rate	14.03%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	3,004 / 24.15%
Number/percentage of C's	3,290 / 26.44%
Number/percentage of T's	2,395 / 19.25%
Number/percentage of G's	3,752 / 30.16%
Number/percentage of N's	0 / 0%
GC Percentage	56.6%

2.3. Coverage

Mean	0.0038
Standard Deviation	0.2289

2.4. Mapping Quality

Mean Mapping Quality	2.22
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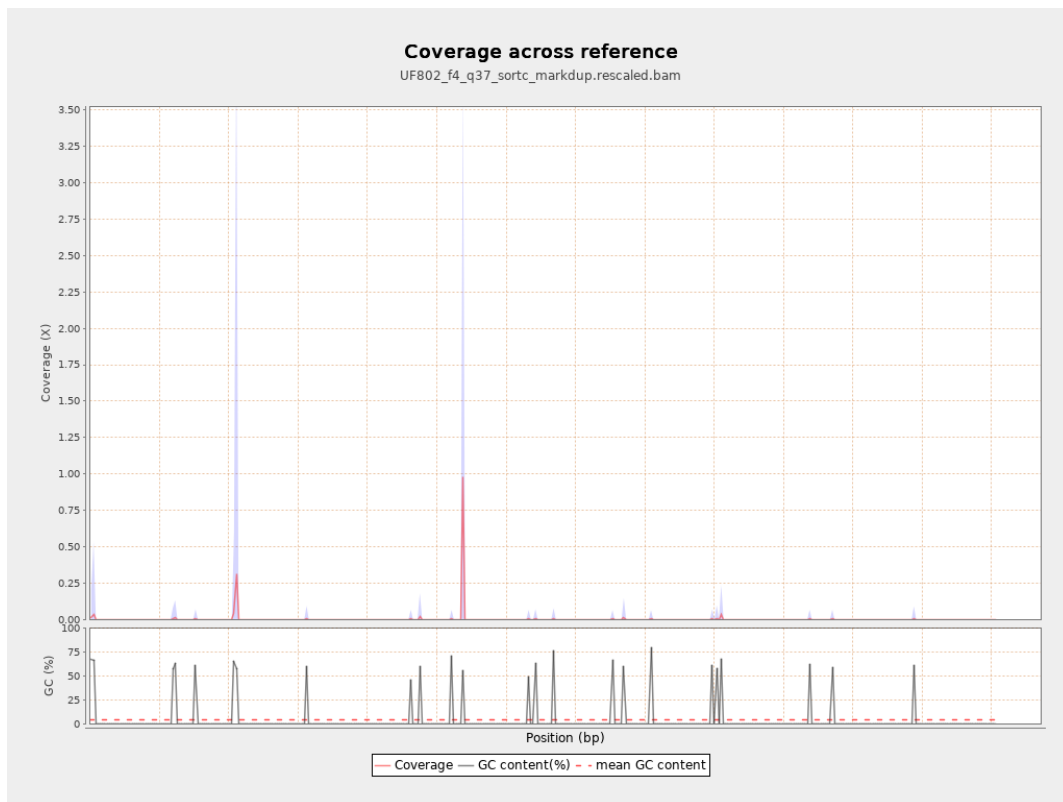
2.5. Mismatches and indels

General error rate	4.8%
Mismatches	556
Insertions	41
Mapped reads with at least one insertion	15.77%
Deletions	2
Mapped reads with at least one deletion	0.77%
Homopolymer indels	6.98%

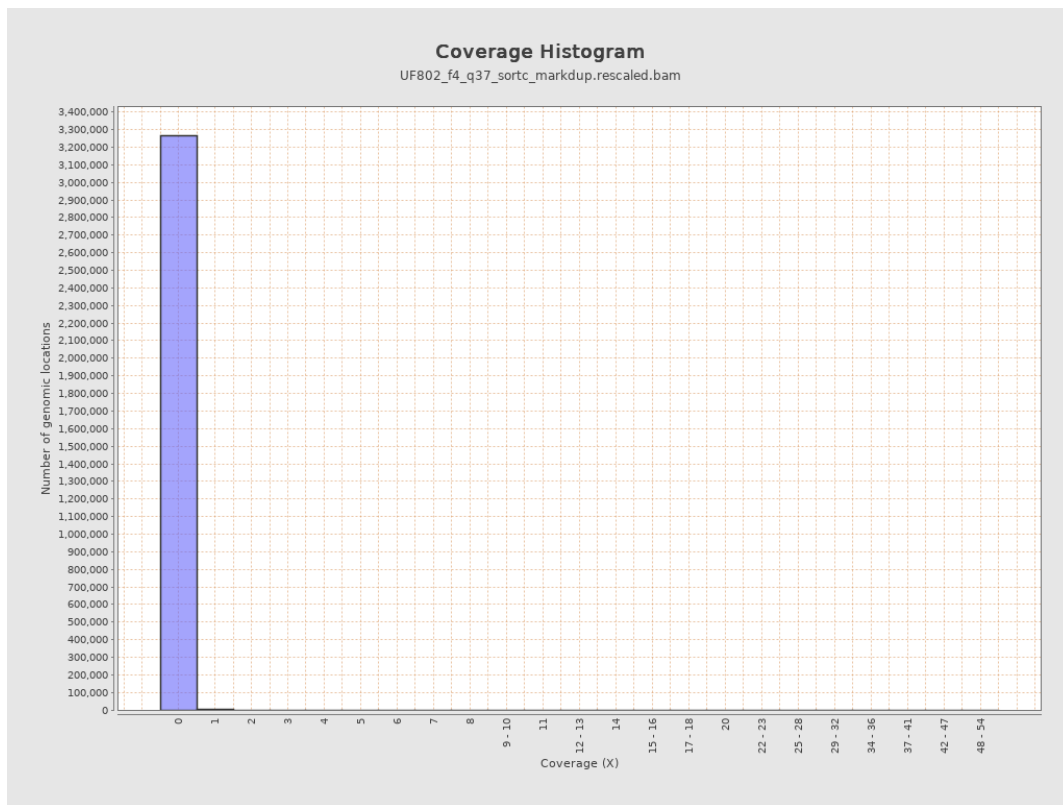
2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
ENA AL450380 AL450380.1	3268203	12443	0.0038	0.2289

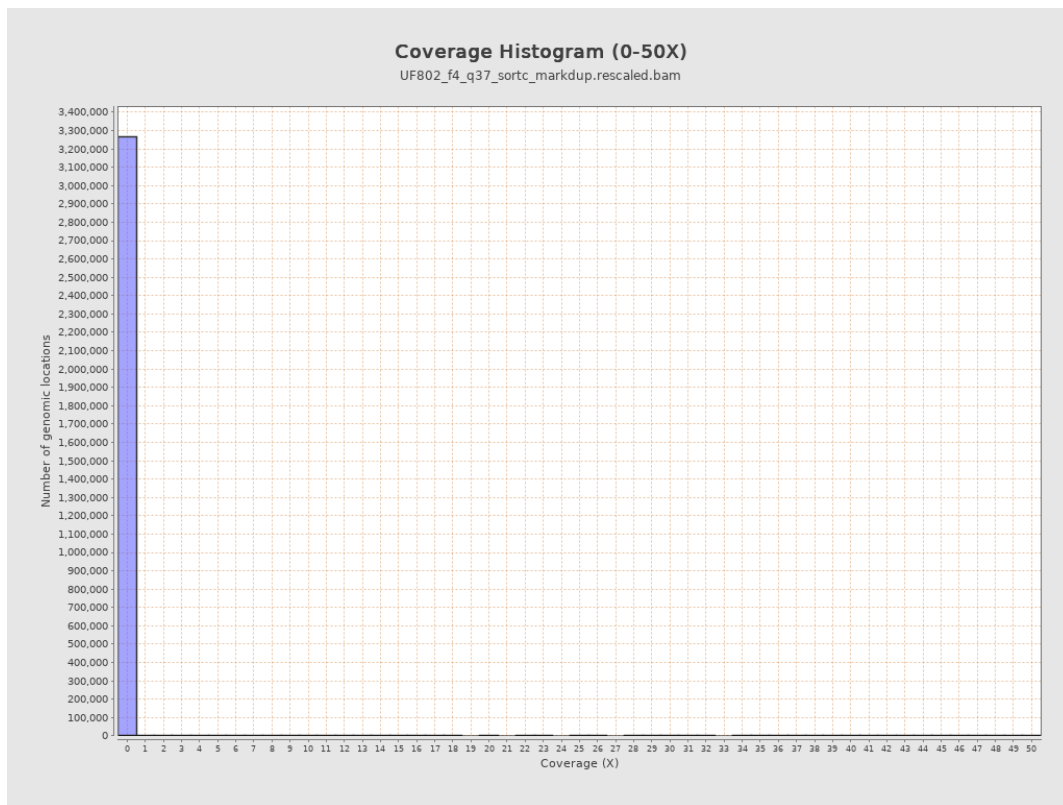
3. Results : Coverage across reference



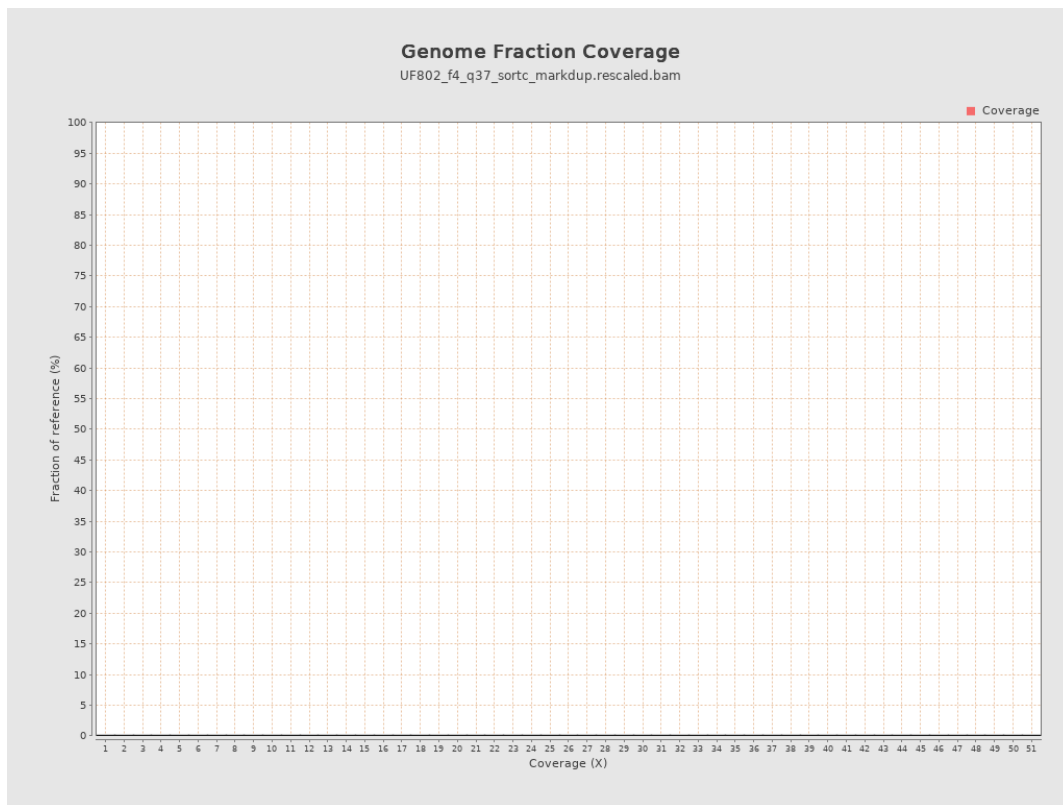
4. Results : Coverage Histogram



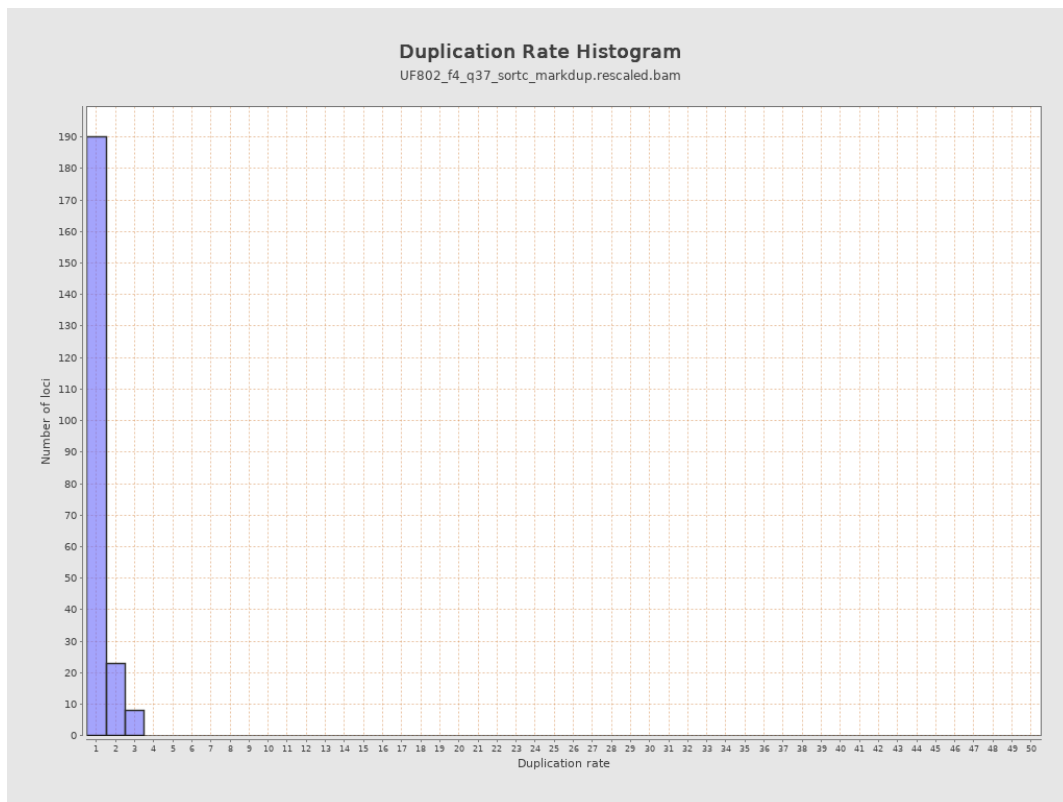
5. Results : Coverage Histogram (0-50X)



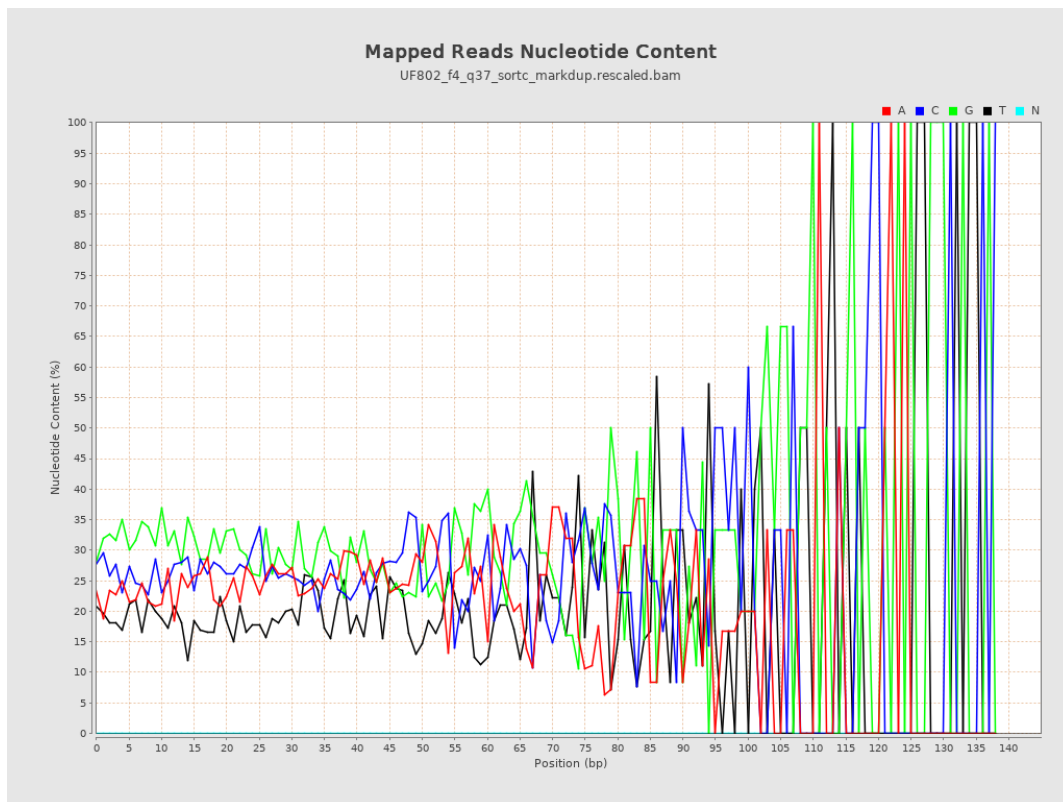
6. Results : Genome Fraction Coverage



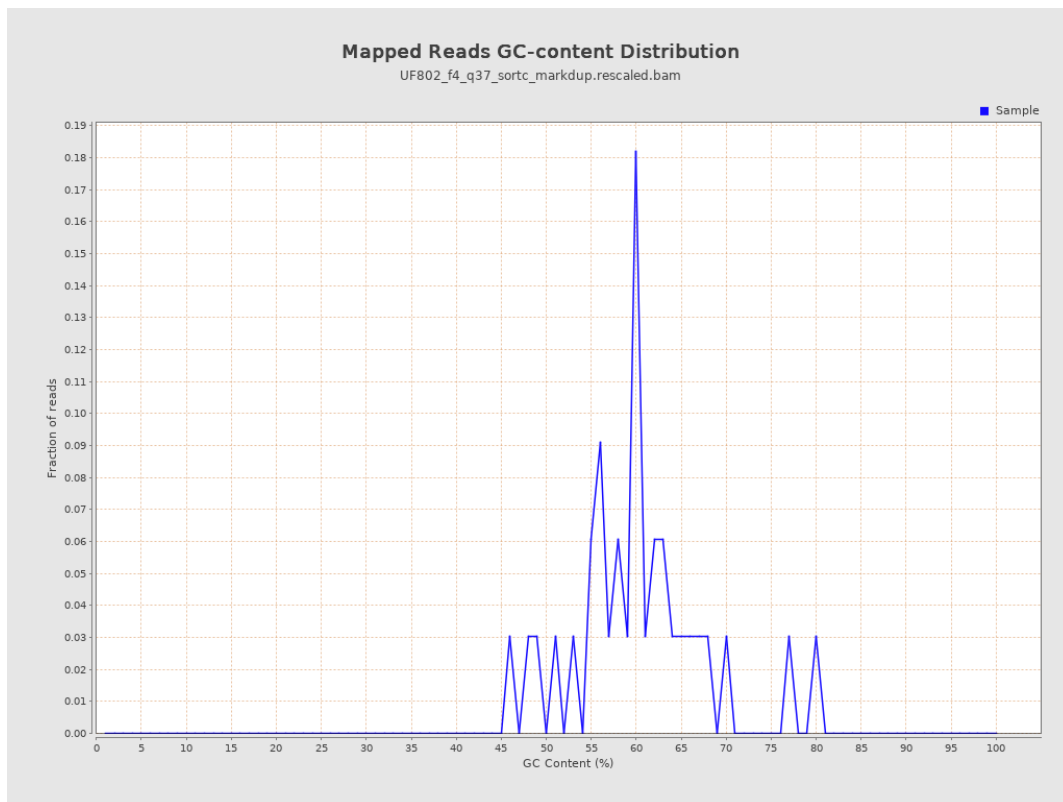
7. Results : Duplication Rate Histogram



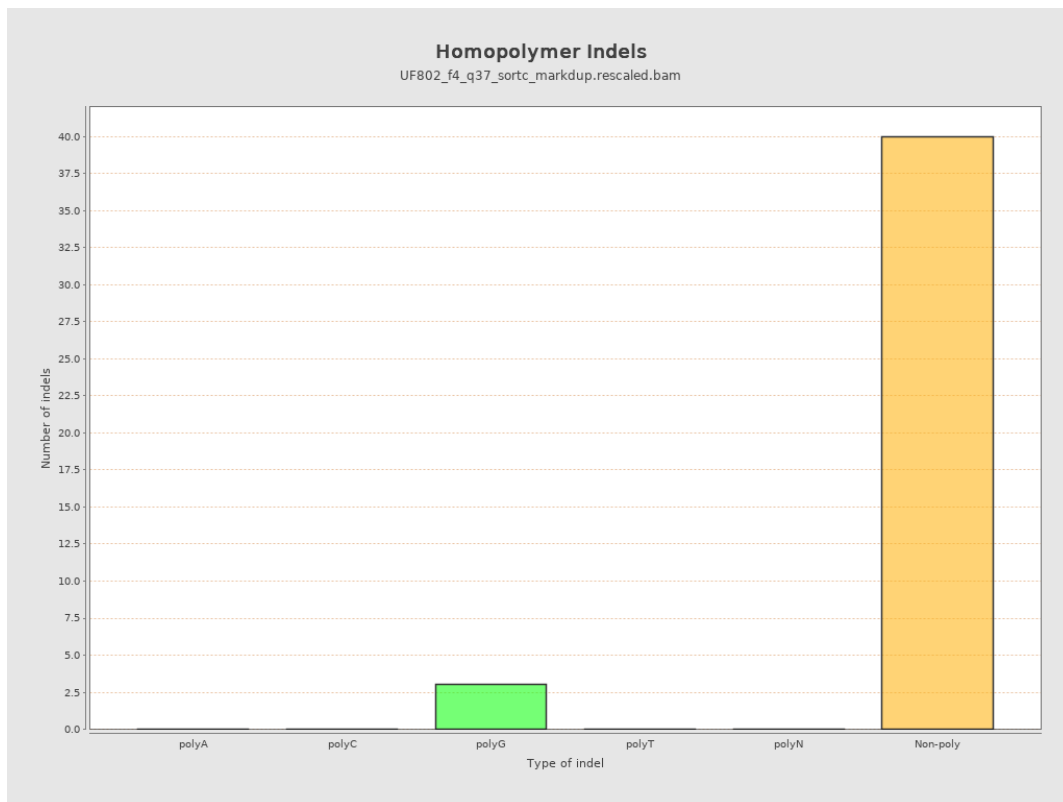
8. Results : Mapped Reads Nucleotide Content



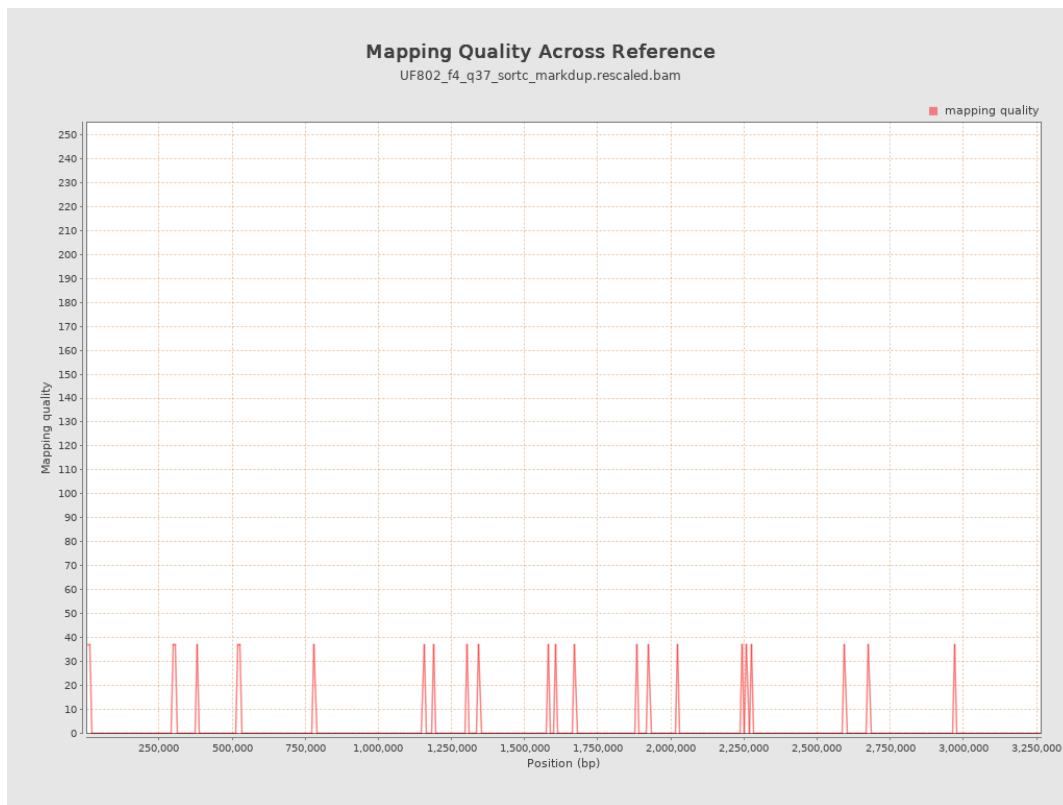
9. Results : Mapped Reads GC-content Distribution



10. Results : Homopolymer Indels



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

