

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/01 02:20:45

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/M_leprae_ TN/M_leprae_TN.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:	Tue Mar 01 02:20:44 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	3,268,203
Number of reads	61,399
Mapped reads	61,399 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	30 / 141 / 74.2
Duplicated reads (estimated)	3,108 / 5.06%
Duplication rate	3.71%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	1,045,673 / 22.95%
Number/percentage of C's	1,160,907 / 25.48%
Number/percentage of T's	1,050,296 / 23.06%
Number/percentage of G's	1,298,643 / 28.51%
Number/percentage of N's	2 / 0%
GC Percentage	53.99%

2.3. Coverage

Mean	1.3941
Standard Deviation	3.2916

2.4. Mapping Quality

Mean Mapping Quality	37
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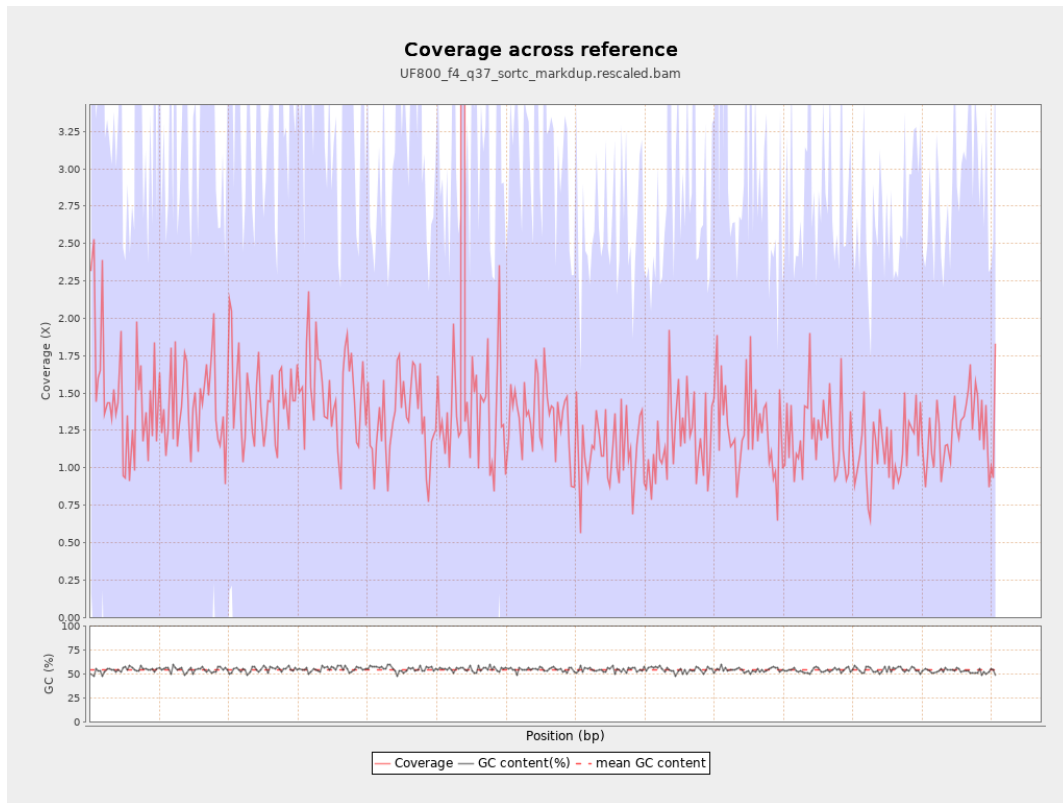
2.5. Mismatches and indels

General error rate	0.81%
Mismatches	36,816
Insertions	262
Mapped reads with at least one insertion	0.43%
Deletions	541
Mapped reads with at least one deletion	0.88%
Homopolymer indels	38.85%

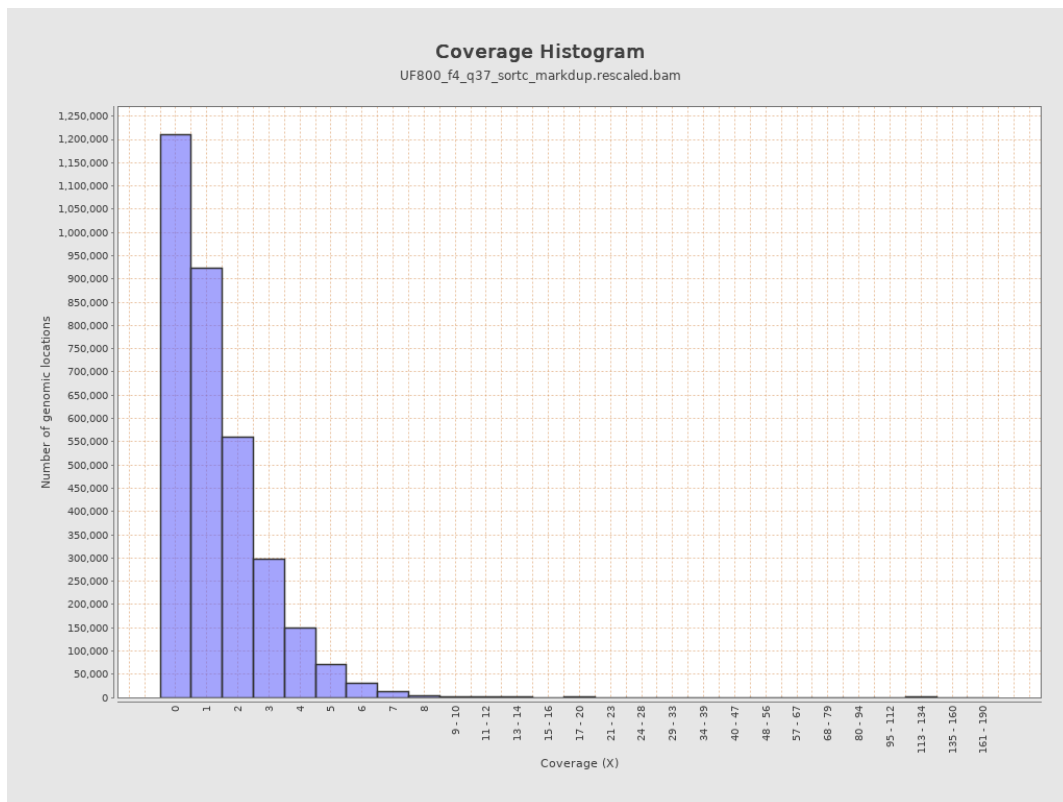
2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
ENA AL450380 AL450380.1	3268203	4556103	1.3941	3.2916

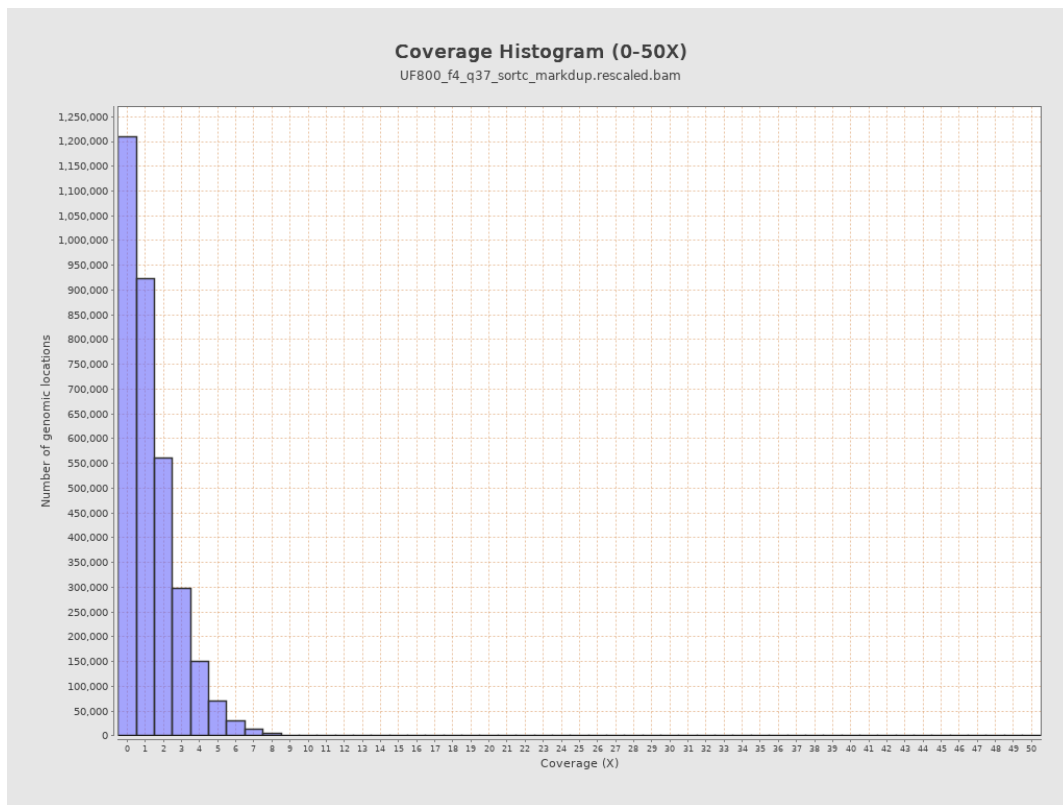
3. Results : Coverage across reference



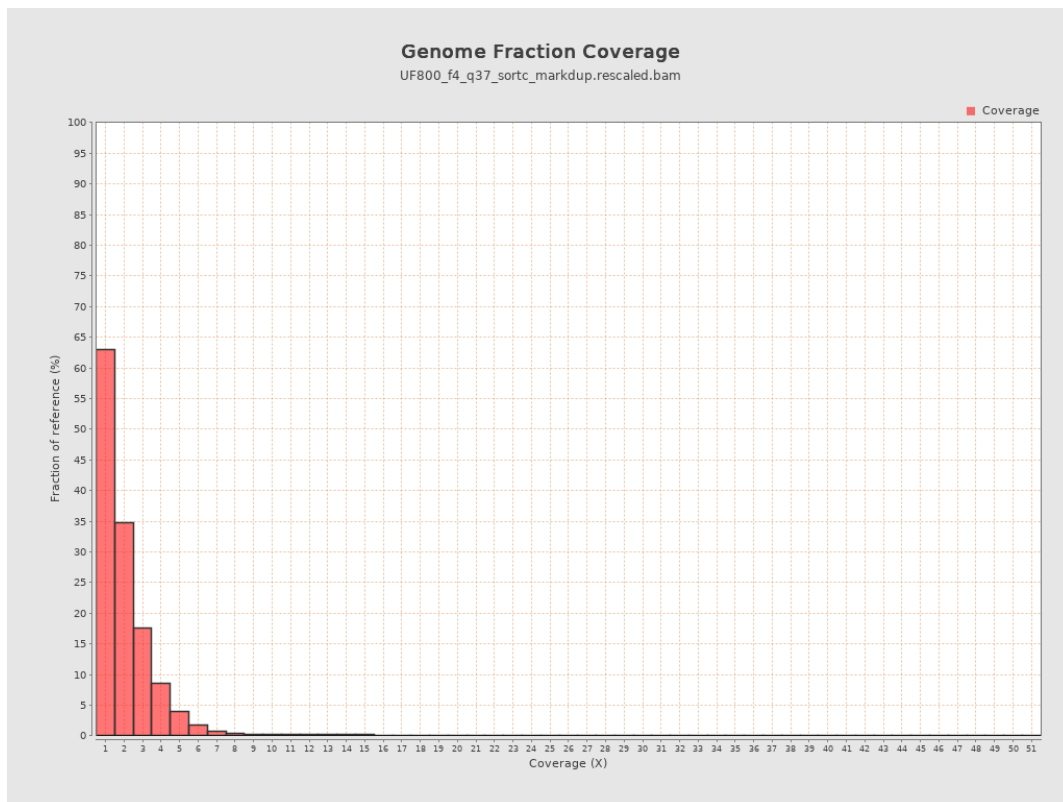
4. Results : Coverage Histogram



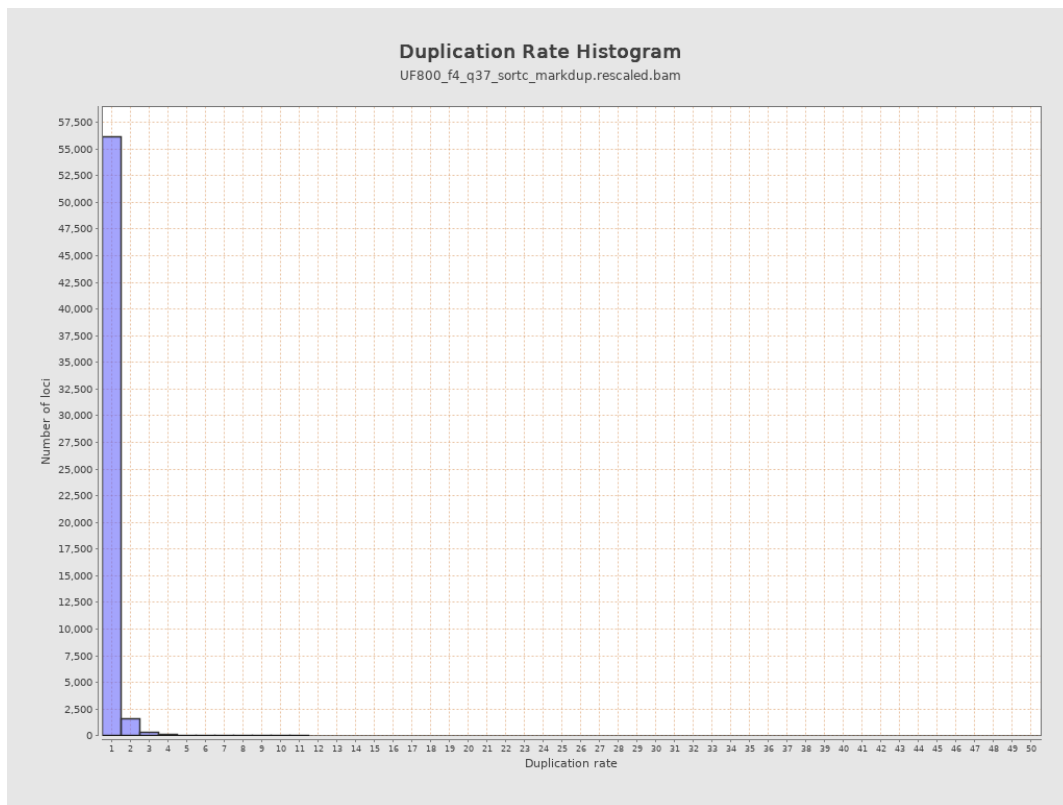
5. Results : Coverage Histogram (0-50X)



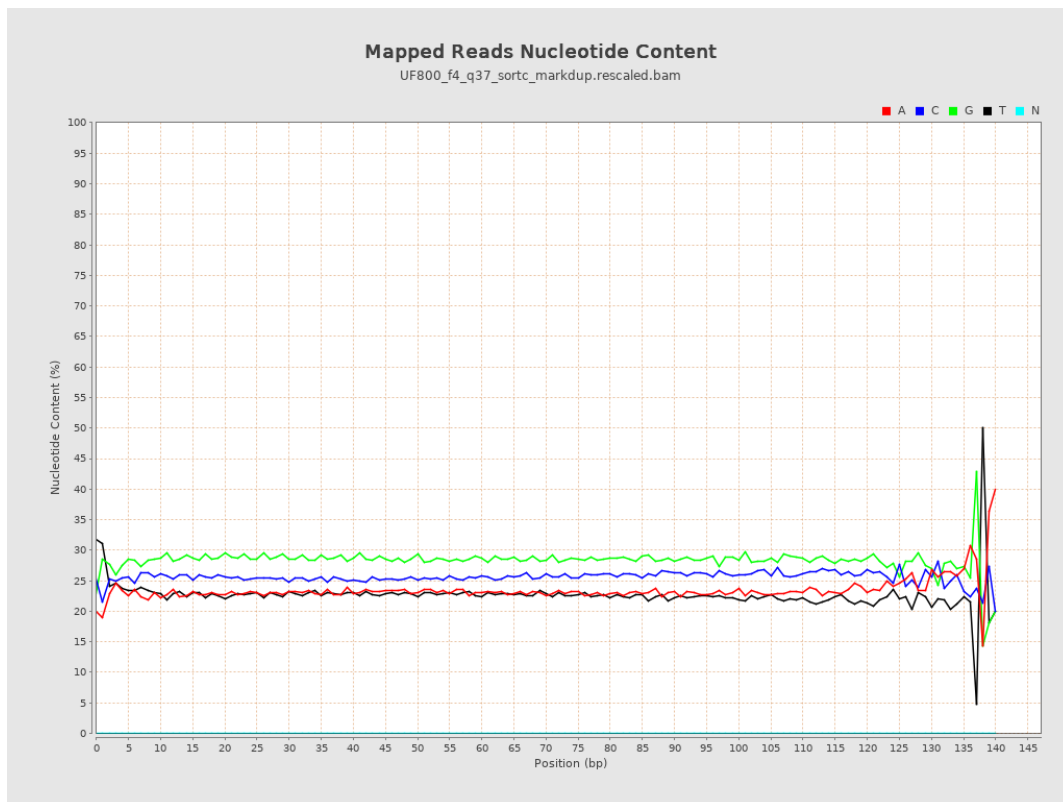
6. Results : Genome Fraction Coverage



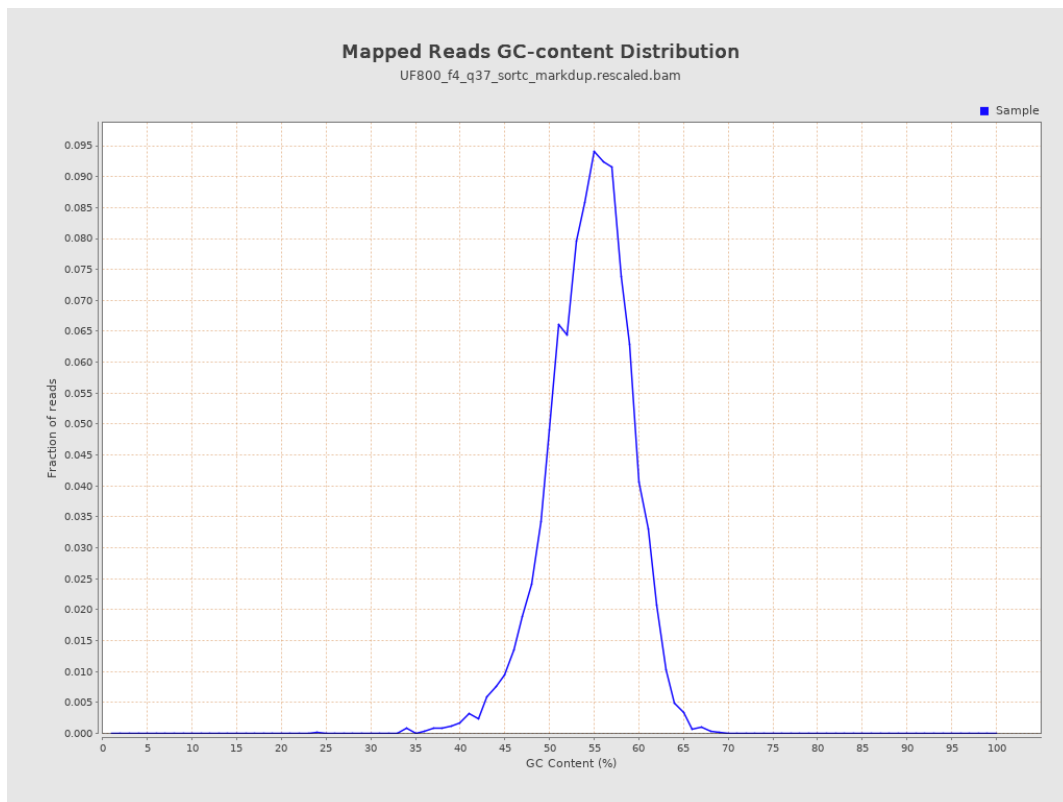
7. Results : Duplication Rate Histogram



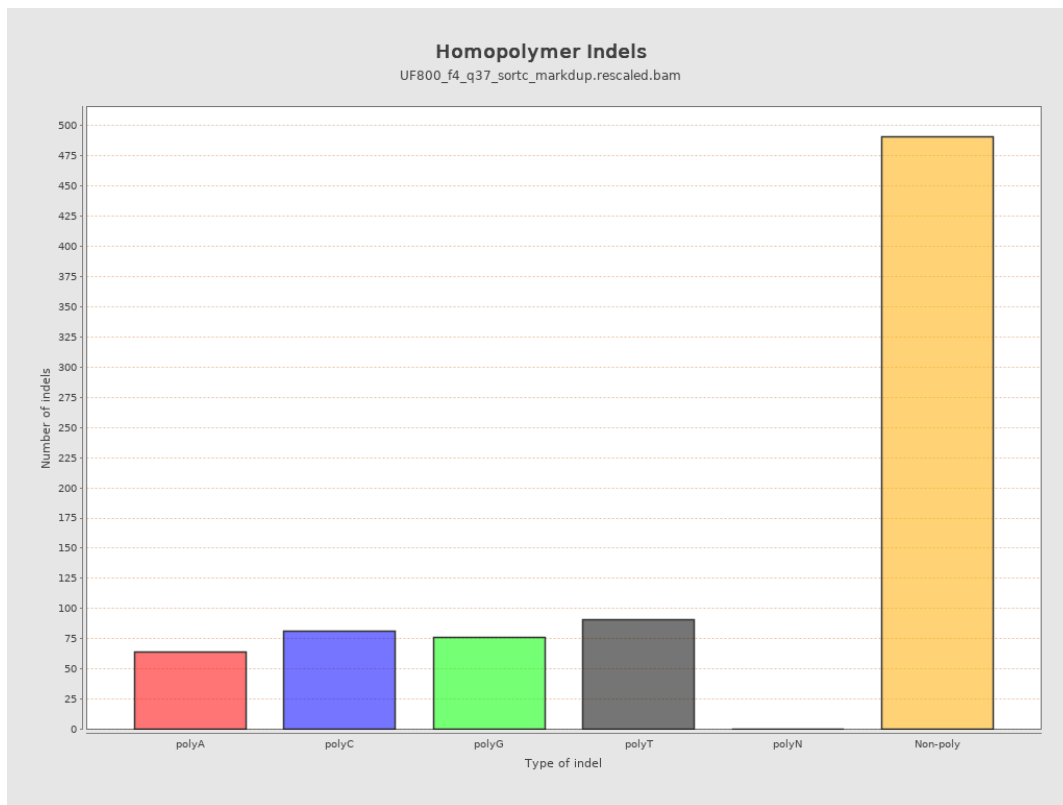
8. Results : Mapped Reads Nucleotide Content



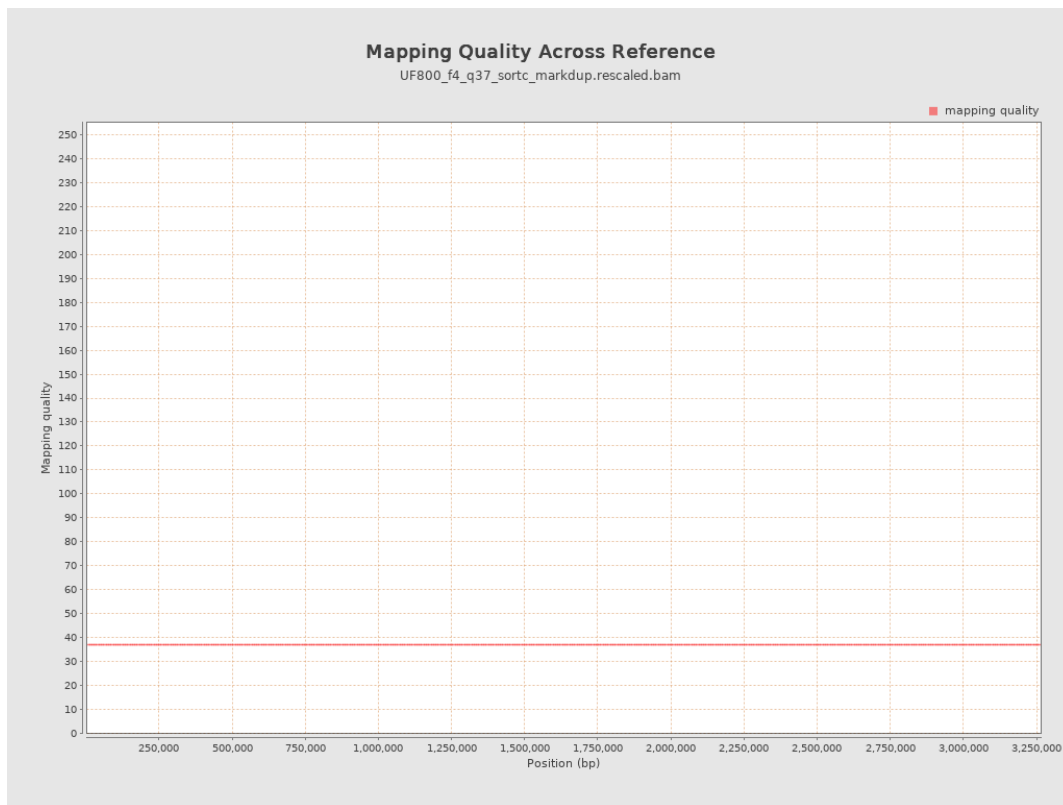
9. Results : Mapped Reads GC-content Distribution



10. Results : Homopolymer Indels



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

