

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/01 02:04:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
output/UF801/UF801_f4_q37_sortc_markdup.rescaled.bam -nw 400 -hm 3
```

1.2. Alignment

Command line:	bwa samse -r @RG\tID:UF801\tSM:UF801\tLB:nan\ tPL:ILLUMINA /data/stonelab/references/M_leprae_ TN/M_leprae_TN.fasta output/UF801/UF801-ancient.sai output/UF801/UF801- ancient.trimmed.fq
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 01 02:04:52 MST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	output/UF801/UF801_f4_q37_sortc_ markdup.rescaled.bam

2. Summary

2.1. Globals

Reference size	3,268,203
Number of reads	188,788
Mapped reads	188,788 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	30 / 141 / 72.24
Duplicated reads (estimated)	12,885 / 6.83%
Duplication rate	6.33%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	3,222,308 / 23.63%
Number/percentage of C's	3,415,566 / 25.05%
Number/percentage of T's	3,228,486 / 23.68%
Number/percentage of G's	3,770,238 / 27.65%
Number/percentage of N's	5 / 0%
GC Percentage	52.69%

2.3. Coverage

Mean	4.1729
Standard Deviation	4.5767

2.4. Mapping Quality

Mean Mapping Quality	37
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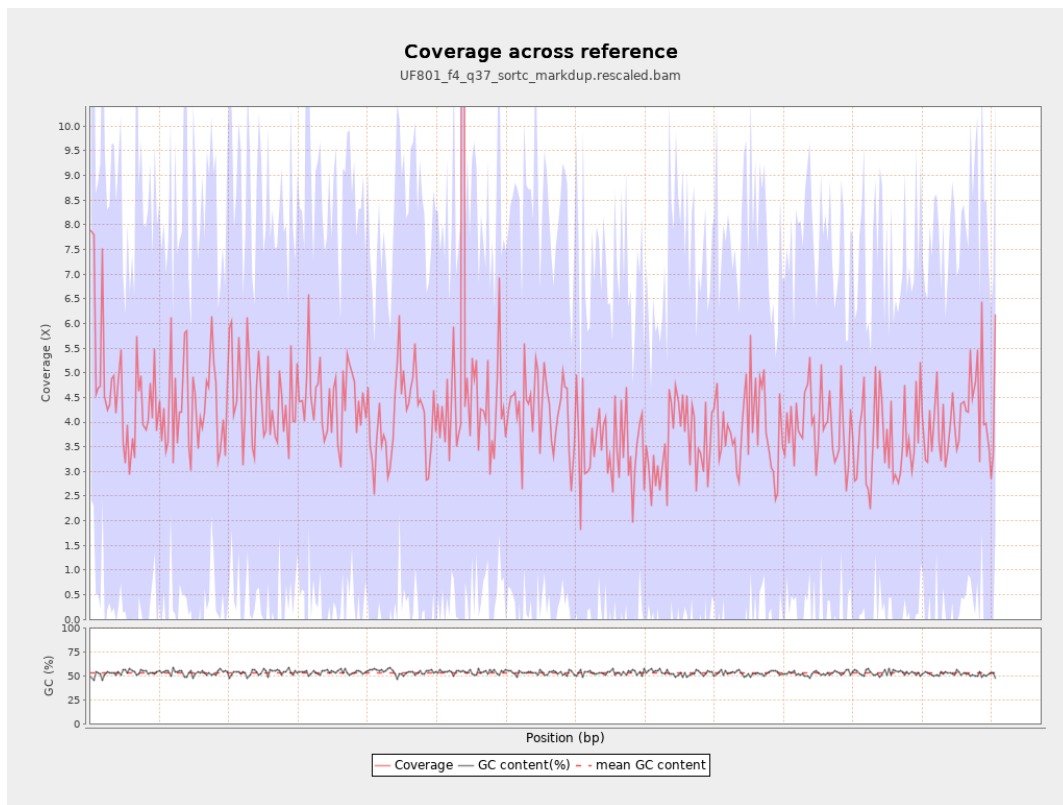
2.5. Mismatches and indels

General error rate	1.24%
Mismatches	168,024
Insertions	472
Mapped reads with at least one insertion	0.25%
Deletions	1,091
Mapped reads with at least one deletion	0.58%
Homopolymer indels	43.31%

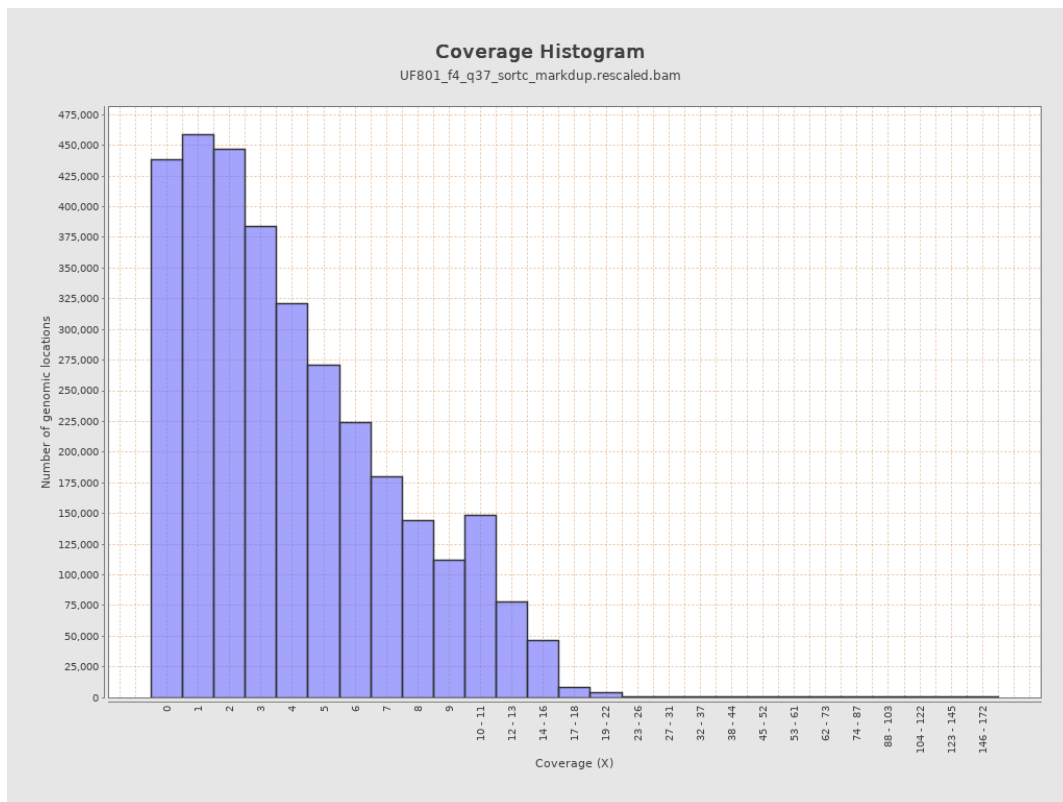
2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
ENA AL450380 AL450380.1	3268203	13637831	4.1729	4.5767

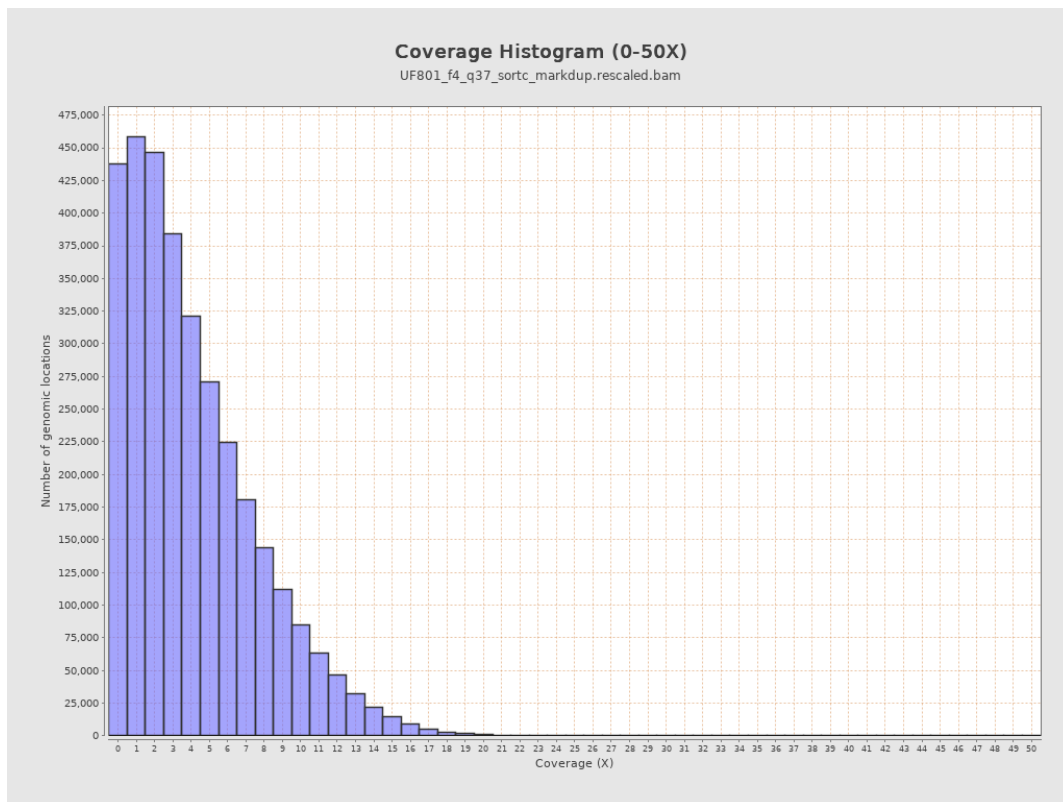
3. Results : Coverage across reference



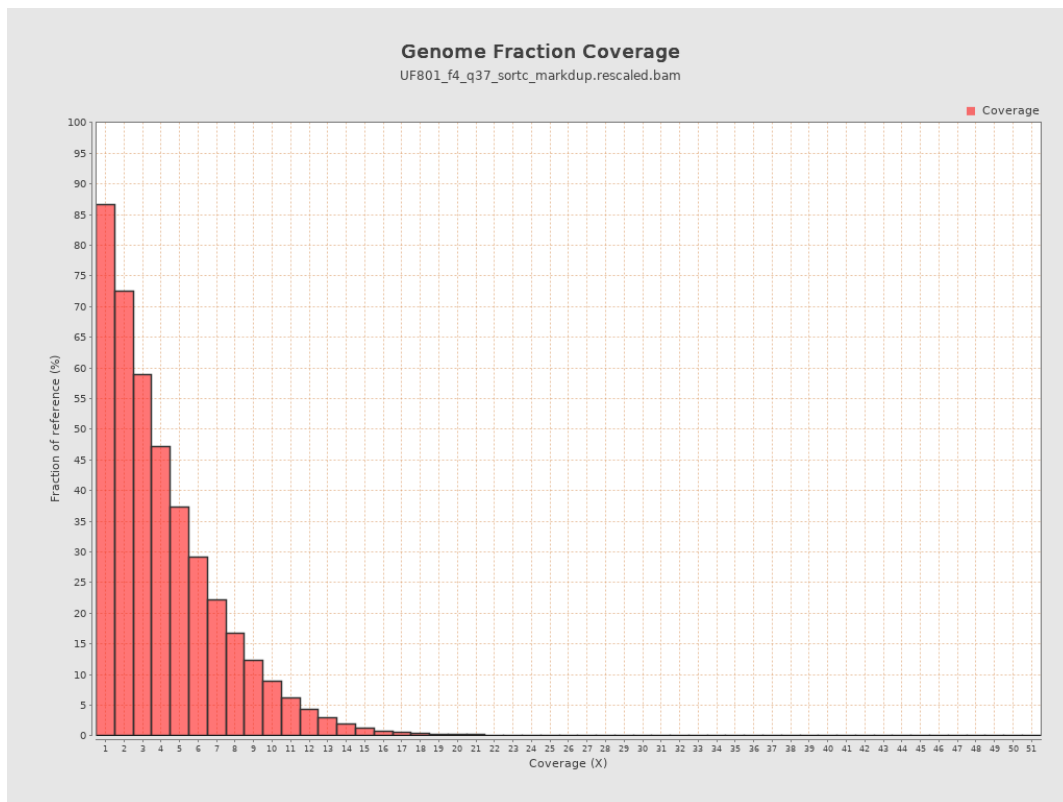
4. Results : Coverage Histogram



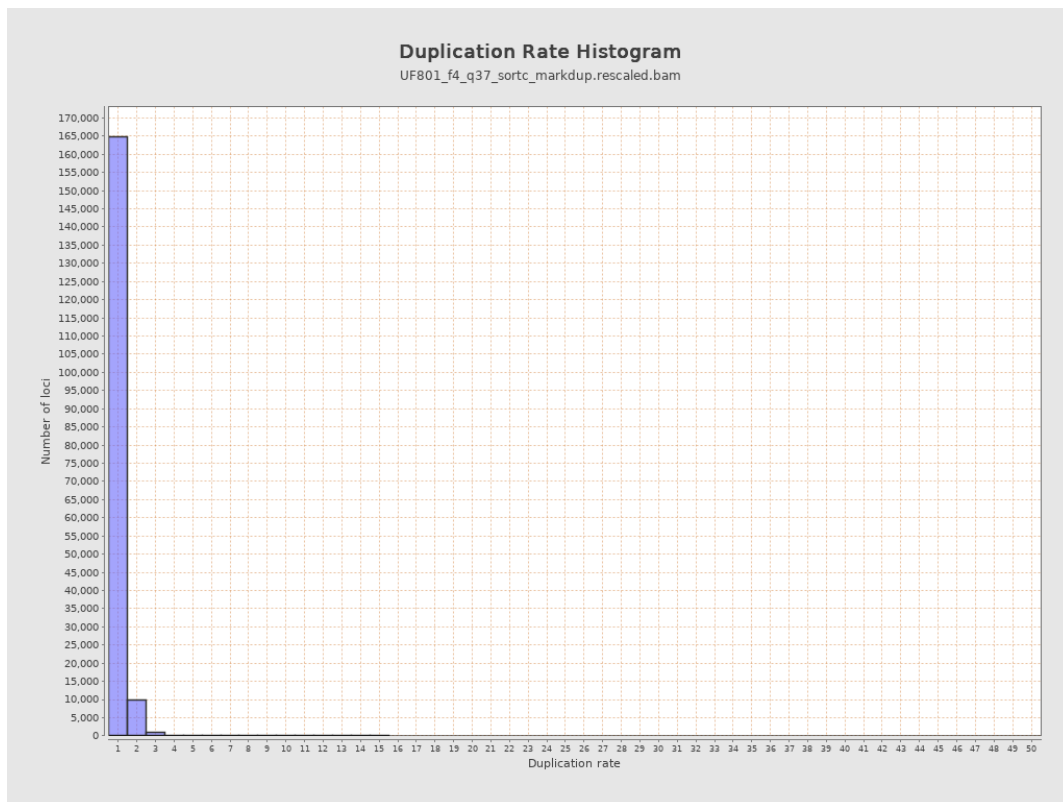
5. Results : Coverage Histogram (0-50X)



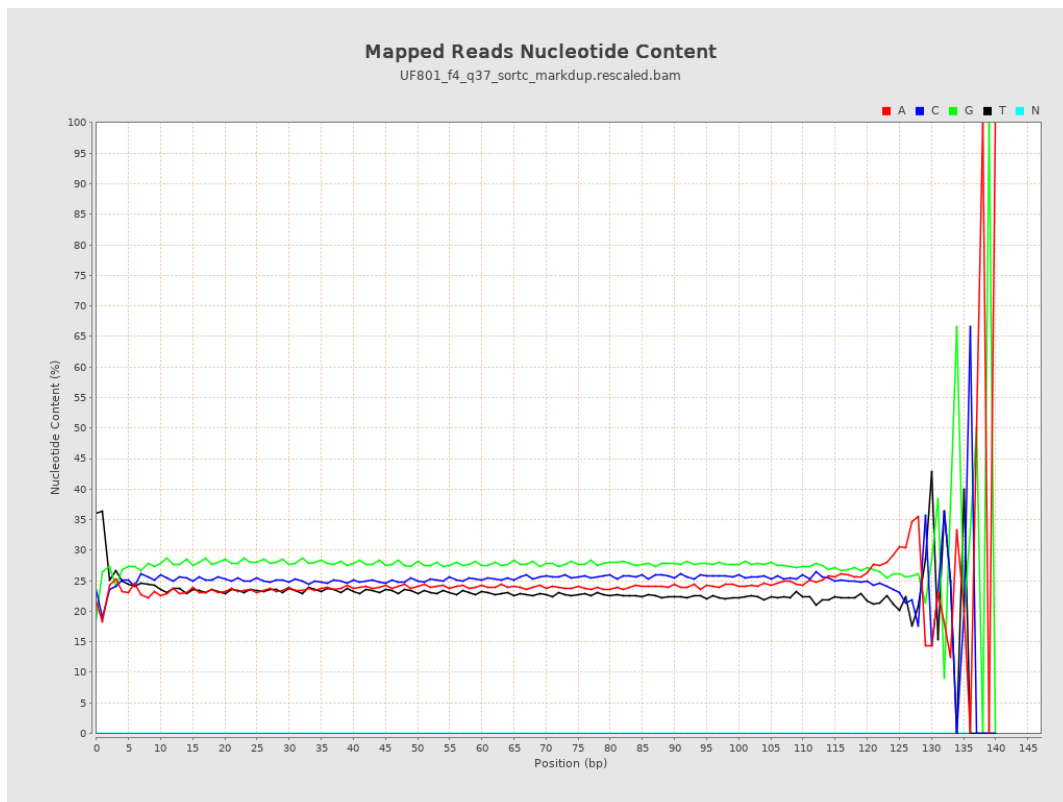
6. Results : Genome Fraction Coverage



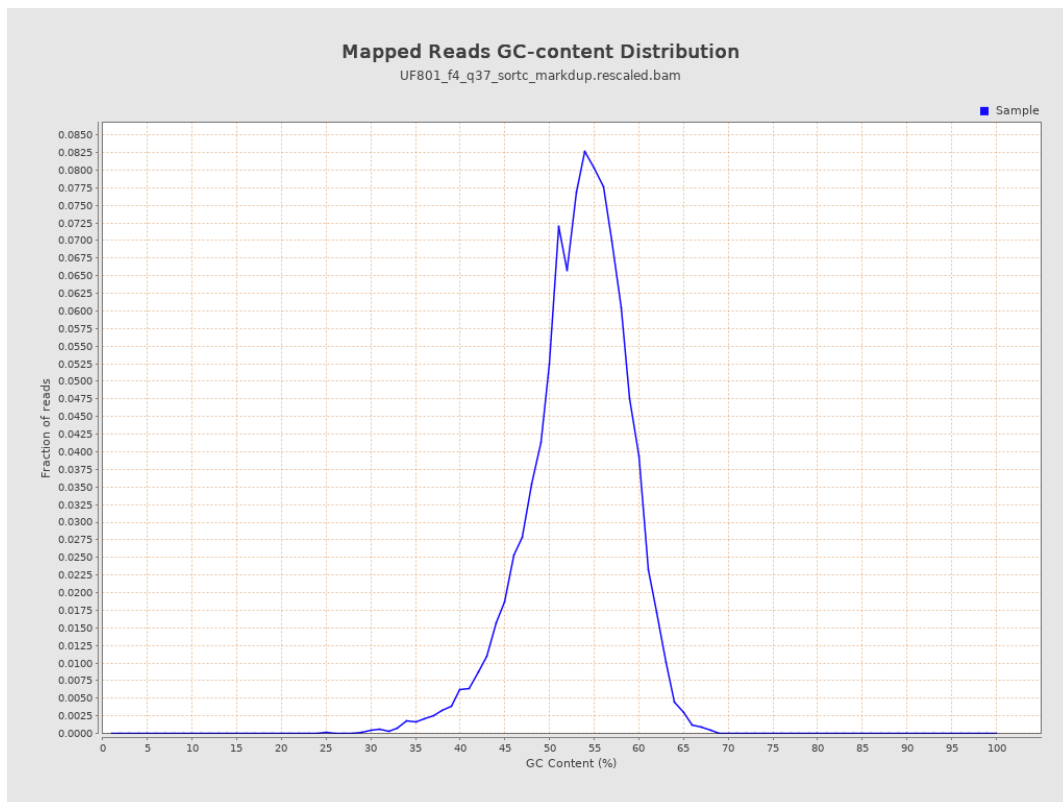
7. Results : Duplication Rate Histogram



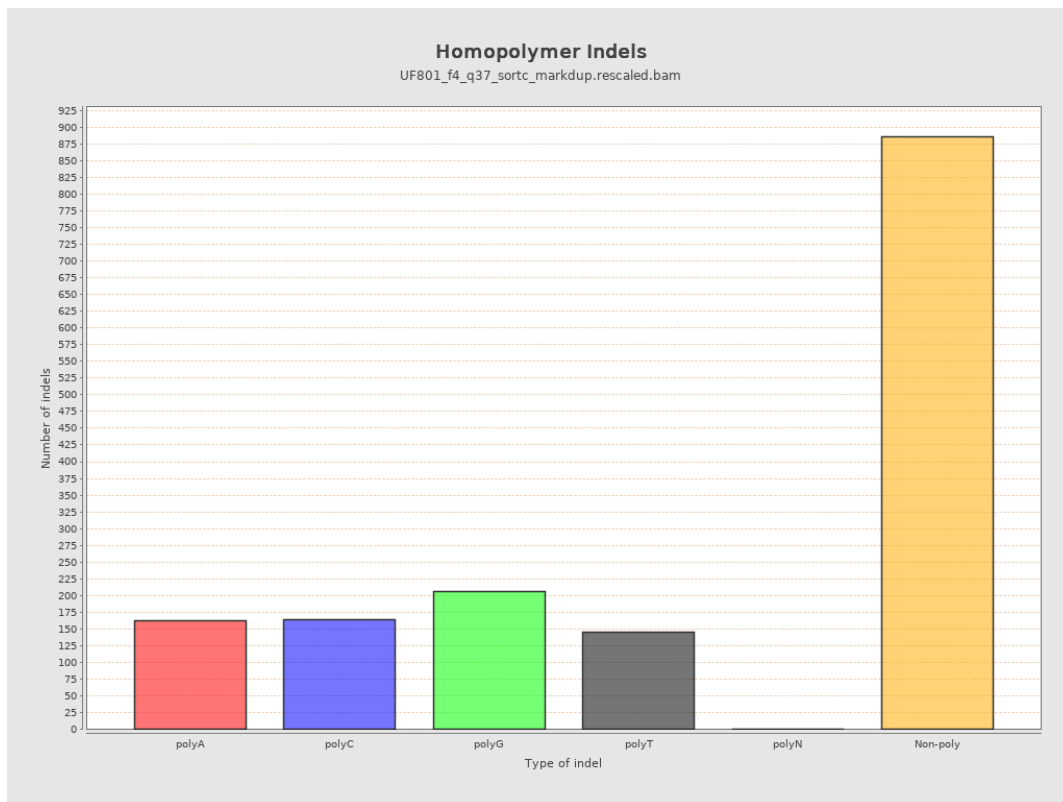
8. Results : Mapped Reads Nucleotide Content



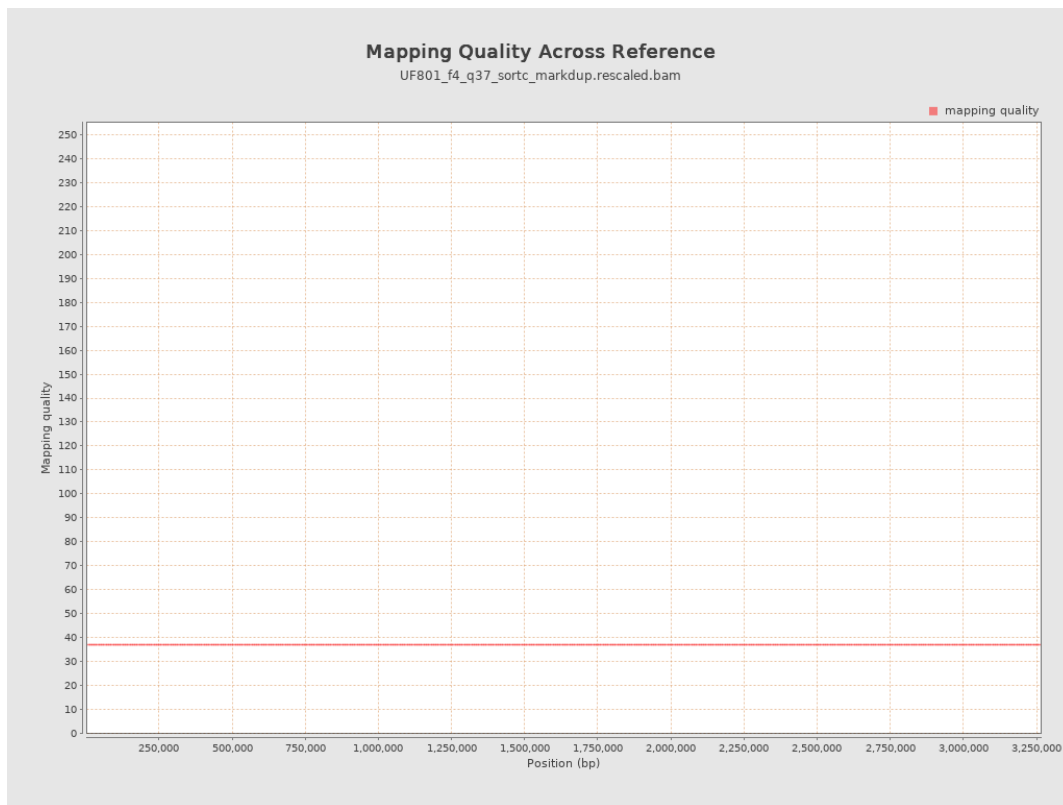
9. Results : Mapped Reads GC-content Distribution



10. Results : Homopolymer Indels



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

