

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/01 02:29:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
output/UF703/UF703_f4_q37_sortc_markdup.rescaled.bam -nw 400 -hm 3
```

1.2. Alignment

Command line:	bwa samse -r @RG\tID:UF703\tSM:UF703\tLB:nan\ tPL:ILLUMINA /data/stonelab/references/M_leprae_ TN/M_leprae_TN.fasta output/UF703/UF703-ancient.sai output/UF703/UF703- ancient.trimmed.fq
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 01 02:29:08 MST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	output/UF703/UF703_f4_q37_sortc_ markdup.rescaled.bam

2. Summary

2.1. Globals

Reference size	3,268,203
Number of reads	1,202,332
Mapped reads	1,202,332 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	30 / 141 / 68.31
Duplicated reads (estimated)	317,749 / 26.43%
Duplication rate	26.41%
Clipped reads	7 / 0%

2.2. ACGT Content

Number/percentage of A's	18,678,775 / 22.74%
Number/percentage of C's	21,083,849 / 25.67%
Number/percentage of T's	18,896,749 / 23.01%
Number/percentage of G's	23,463,775 / 28.57%
Number/percentage of N's	21 / 0%
GC Percentage	54.24%

2.3. Coverage

Mean	25.1313
Standard Deviation	17.6209

2.4. Mapping Quality

Mean Mapping Quality	36.99
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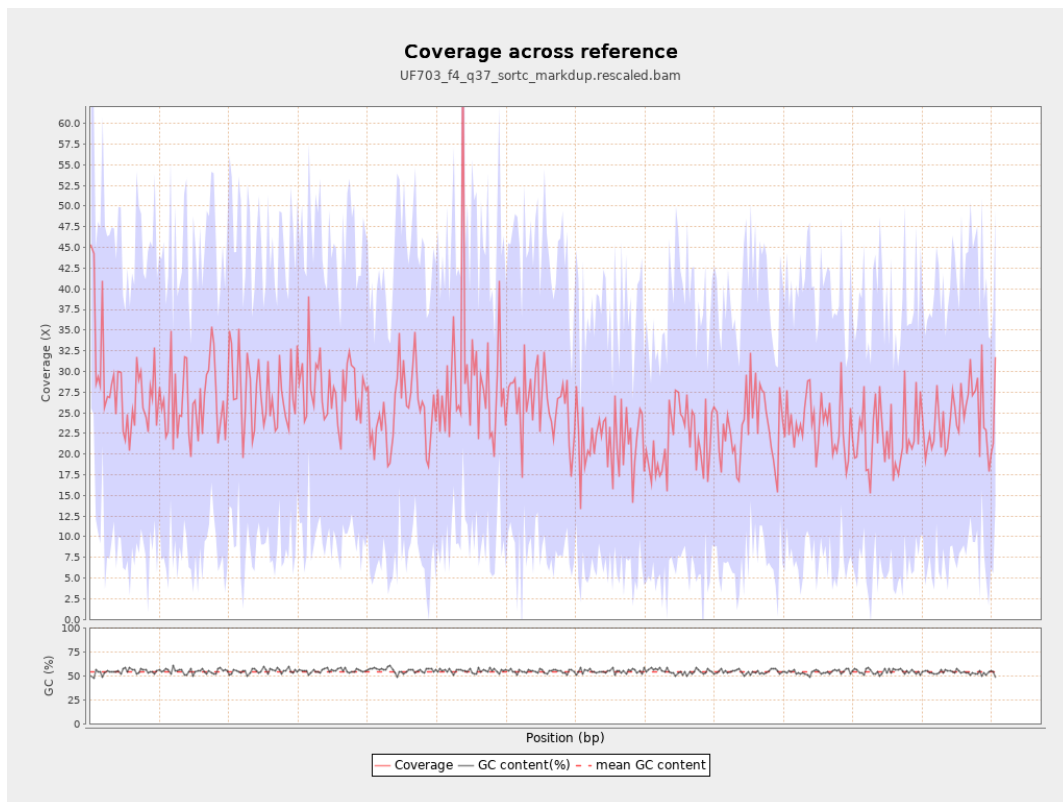
2.5. Mismatches and indels

General error rate	0.16%
Mismatches	129,154
Insertions	1,829
Mapped reads with at least one insertion	0.15%
Deletions	9,617
Mapped reads with at least one deletion	0.8%
Homopolymer indels	39.9%

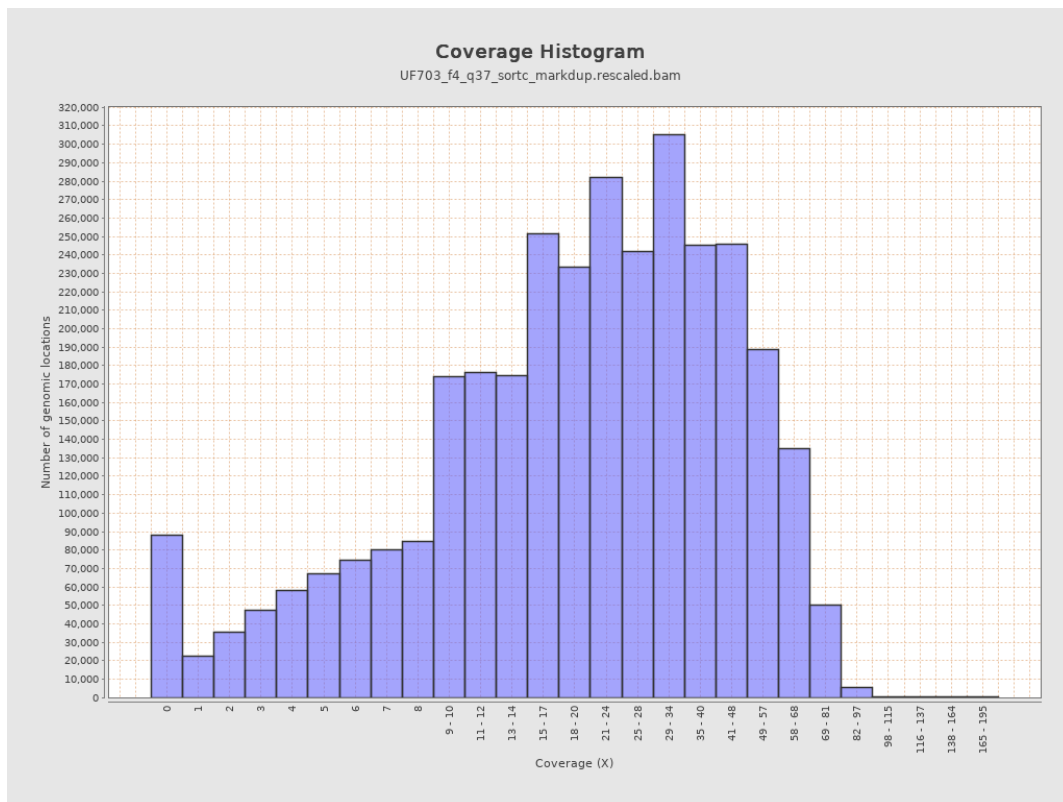
2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
ENA AL450380 AL450380.1	3268203	82134347	25.1313	17.6209

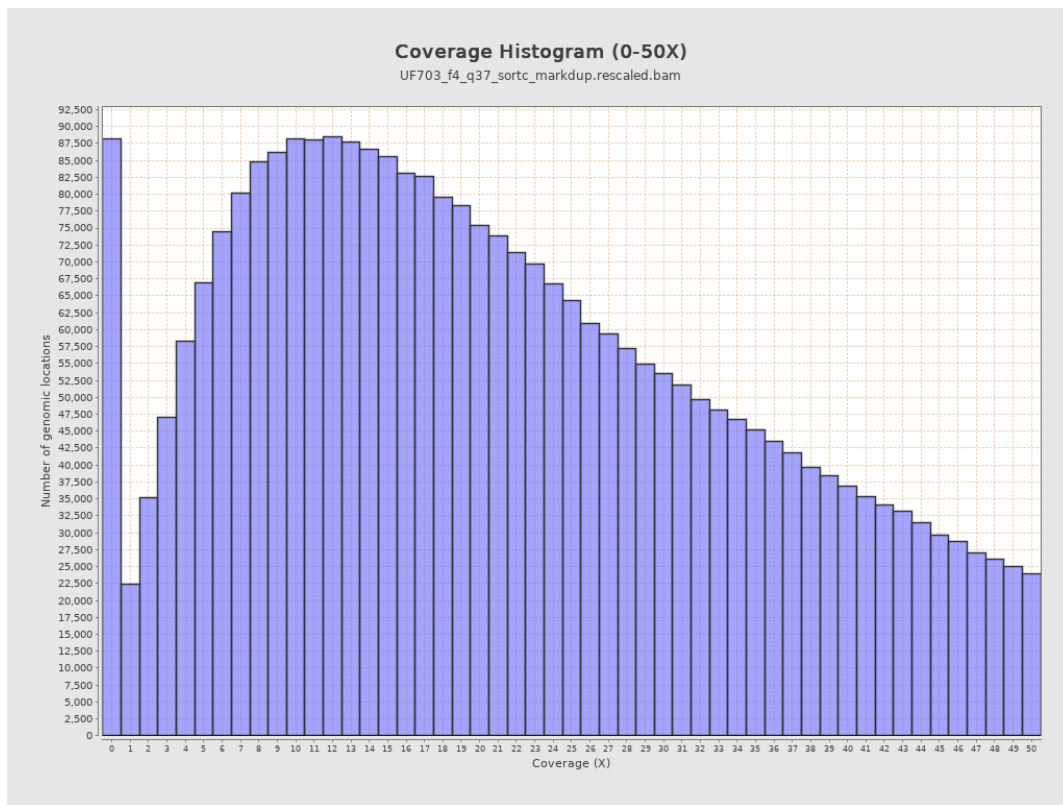
3. Results : Coverage across reference



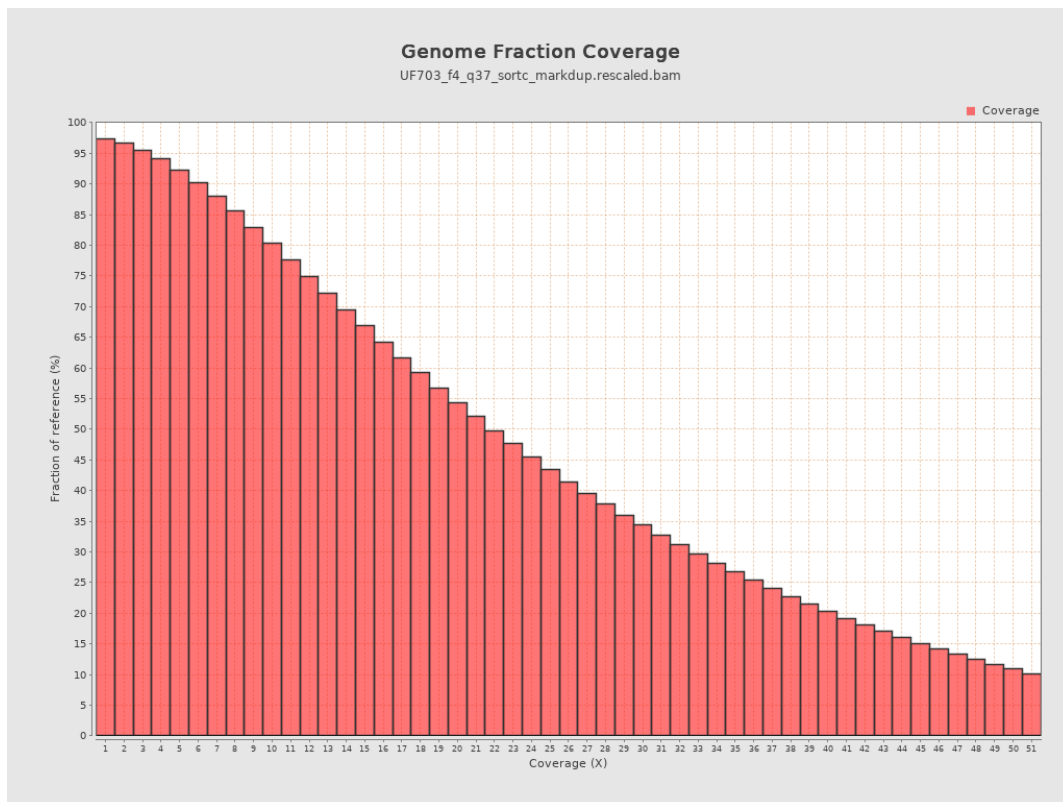
4. Results : Coverage Histogram



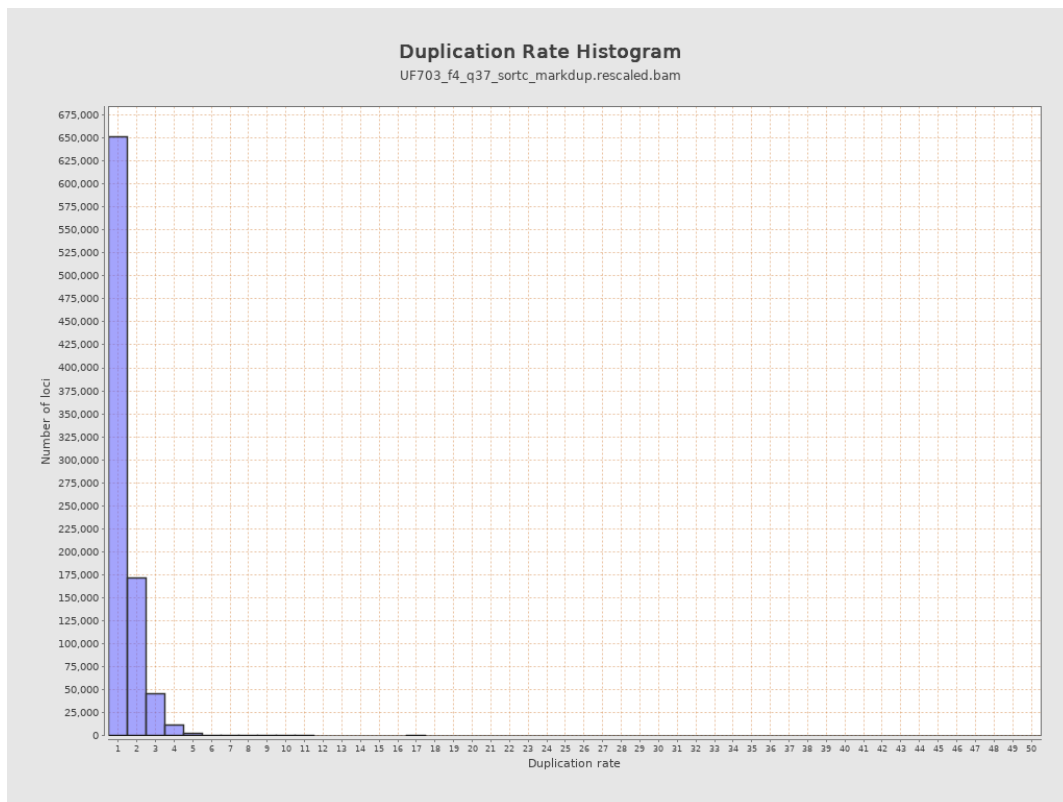
5. Results : Coverage Histogram (0-50X)



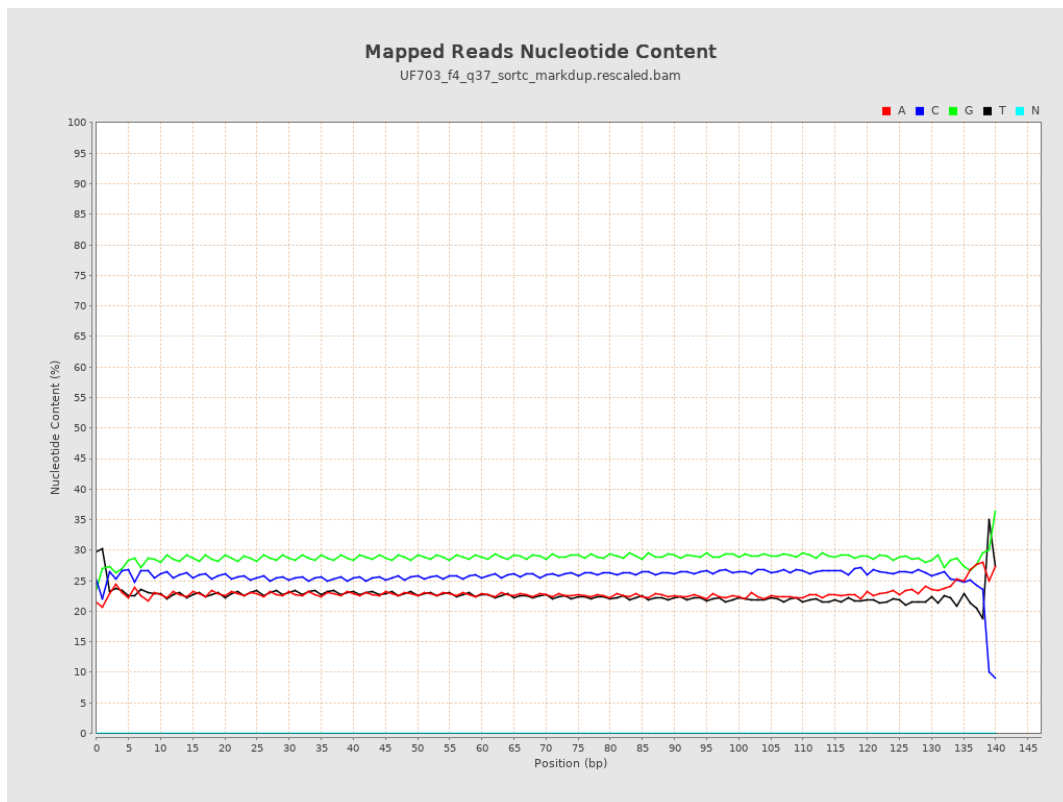
6. Results : Genome Fraction Coverage



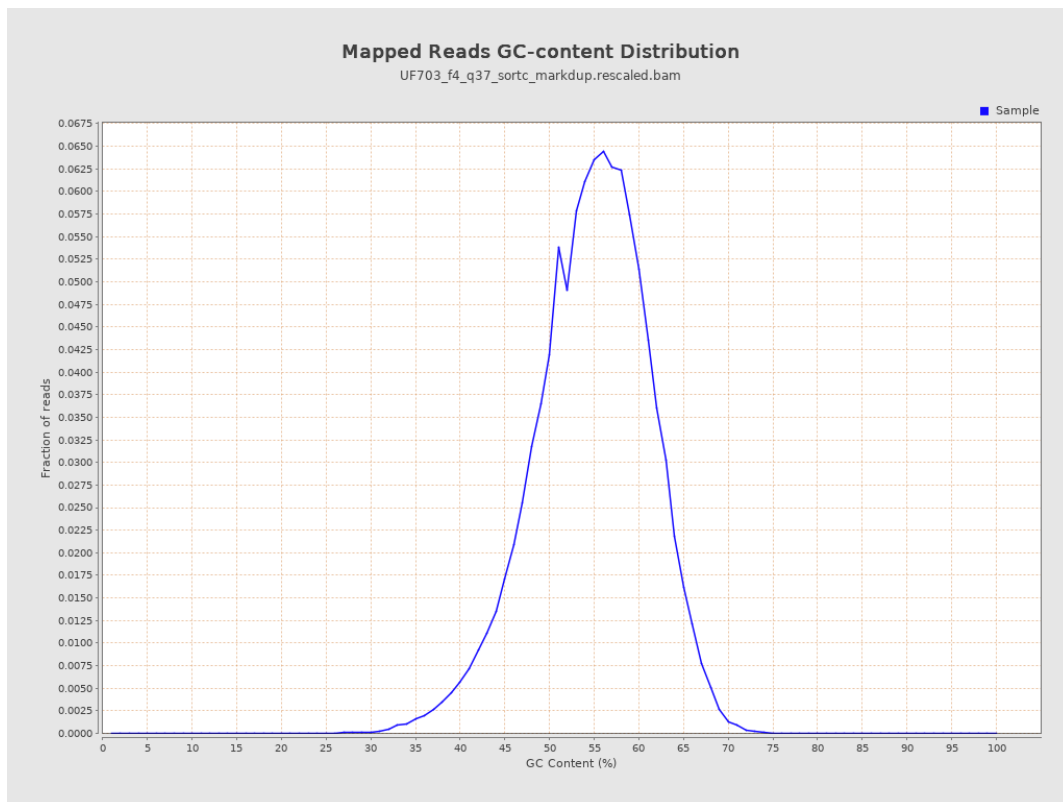
7. Results : Duplication Rate Histogram



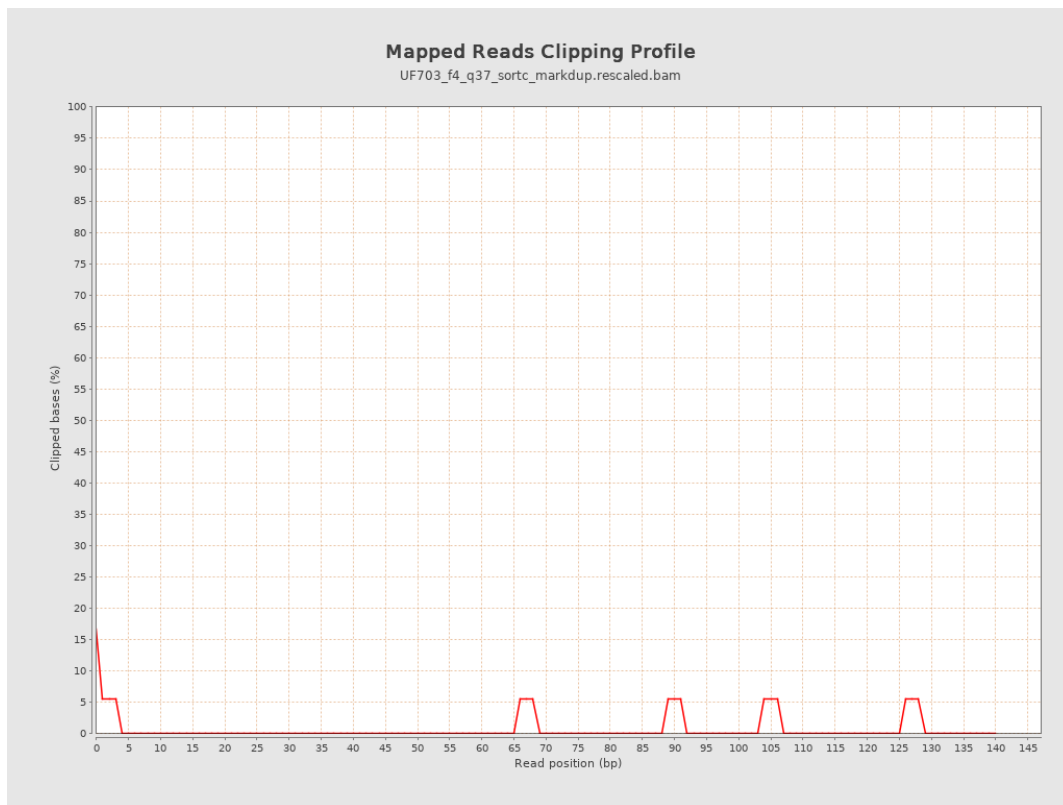
8. Results : Mapped Reads Nucleotide Content



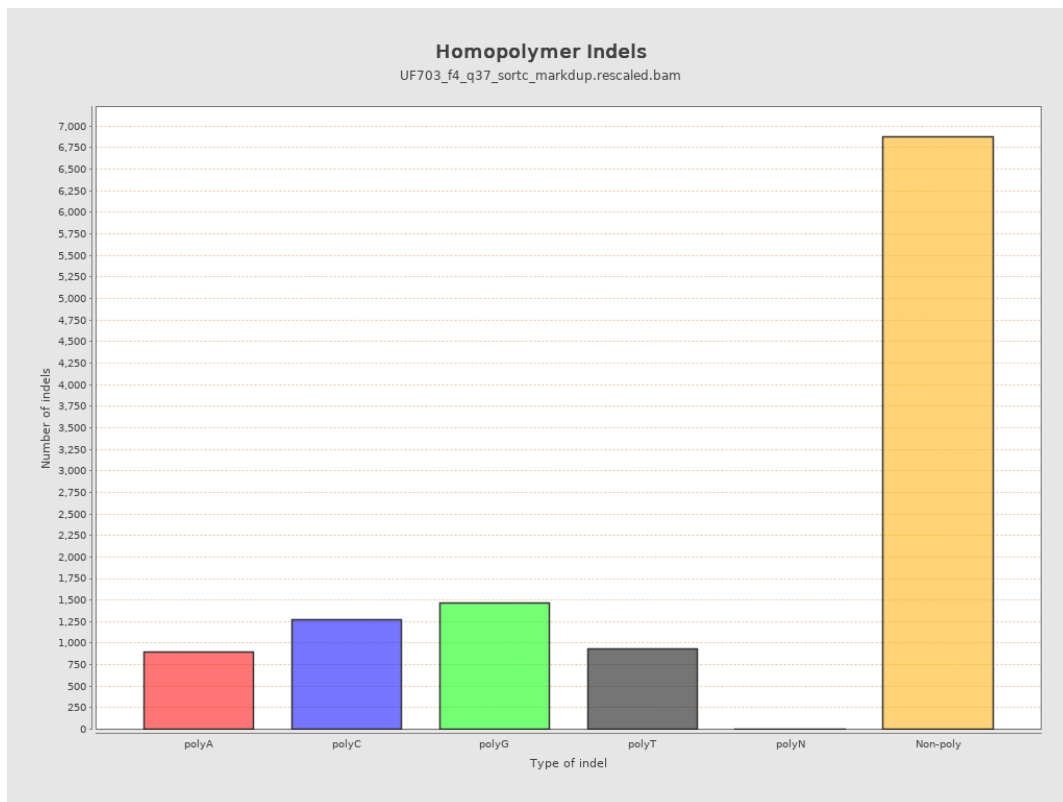
9. Results : Mapped Reads GC-content Distribution



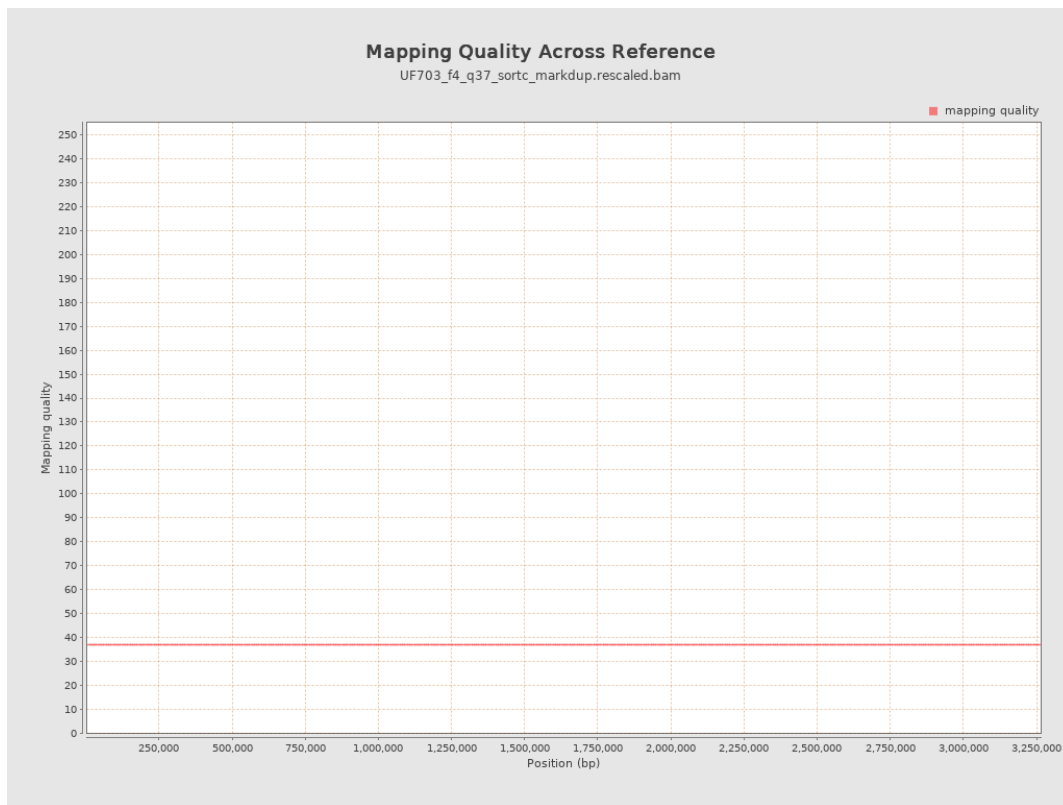
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

