

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/01 01:55:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
output/UF700/UF700_f4_q37_sortc_markdup.rescaled.bam -nw 400 -hm 3
```

1.2. Alignment

Command line:	bwa samse -r @RG\tID:UF700\tSM:UF700\tLB:nan\ \tPL:ILLUMINA /data/stonelab/references/M_leprae_ TN/M_leprae_TN.fasta output/UF700/UF700-ancient.sai output/UF700/UF700- ancient.trimmed.fq
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 01 01:55:42 MST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	output/UF700/UF700_f4_q37_sortc_ markdup.rescaled.bam

2. Summary

2.1. Globals

Reference size	3,268,203
Number of reads	277,699
Mapped reads	277,699 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	30 / 141 / 75.57
Duplicated reads (estimated)	23,362 / 8.41%
Duplication rate	8.21%
Clipped reads	1 / 0%

2.2. ACGT Content

Number/percentage of A's	4,769,733 / 22.73%
Number/percentage of C's	5,493,082 / 26.18%
Number/percentage of T's	4,801,343 / 22.88%
Number/percentage of G's	5,921,580 / 28.22%
Number/percentage of N's	9 / 0%
GC Percentage	54.39%

2.3. Coverage

Mean	6.4216
Standard Deviation	4.4704

2.4. Mapping Quality

Mean Mapping Quality	37
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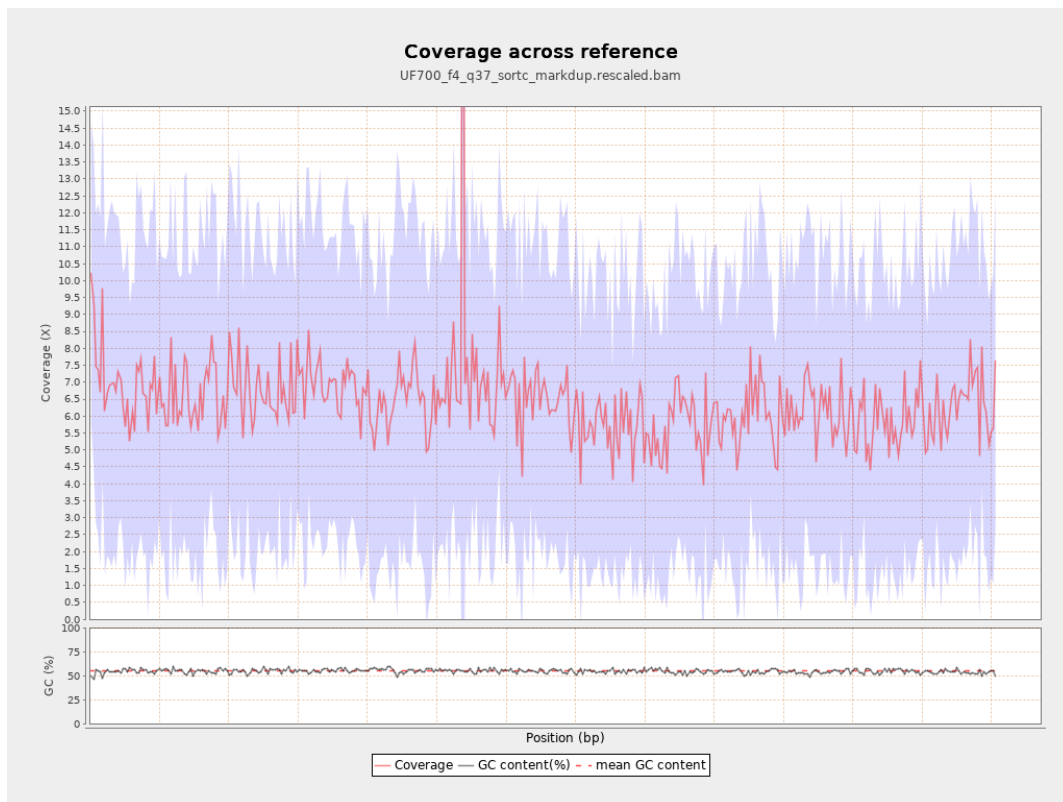
2.5. Mismatches and indels

General error rate	0.99%
Mismatches	207,383
Insertions	694
Mapped reads with at least one insertion	0.25%
Deletions	1,026
Mapped reads with at least one deletion	0.37%
Homopolymer indels	47.44%

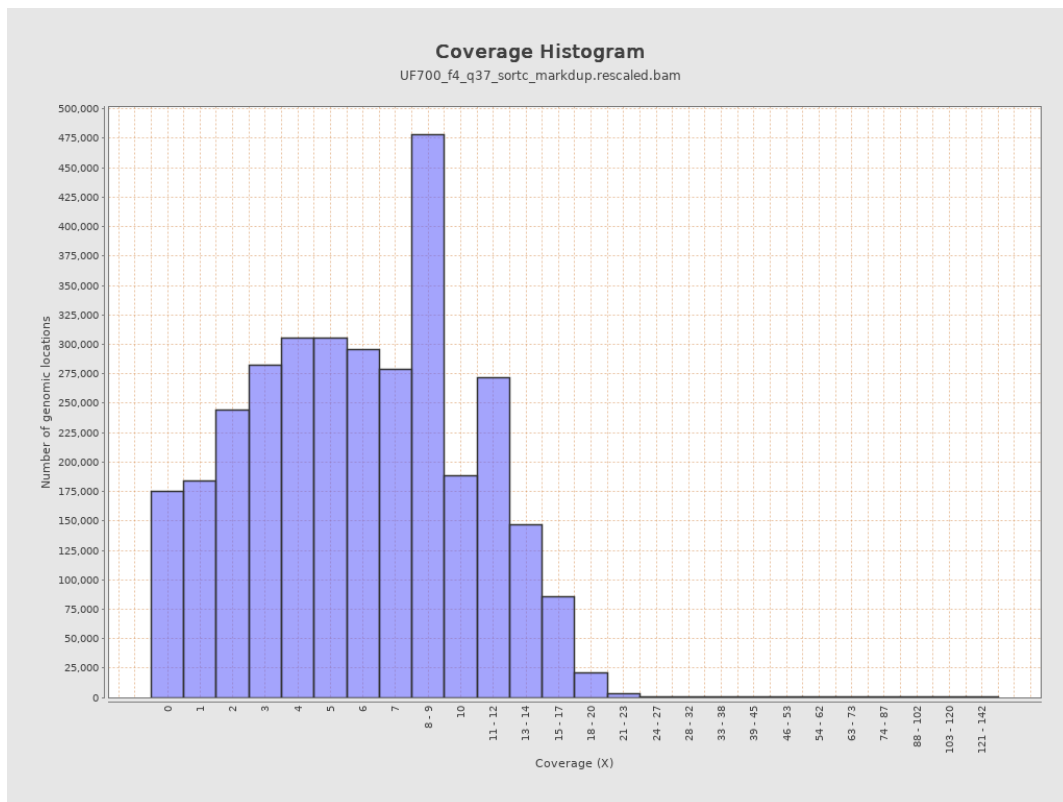
2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
ENA AL450380 AL450380.1	3268203	20986938	6.4216	4.4704

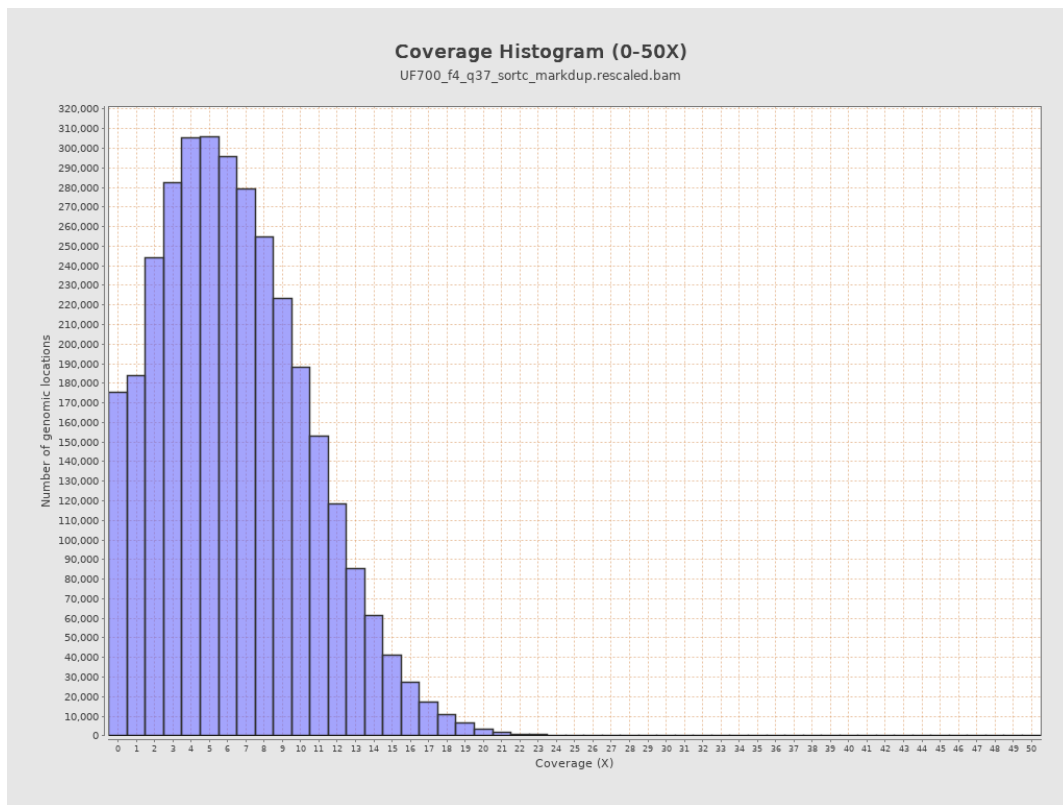
3. Results : Coverage across reference



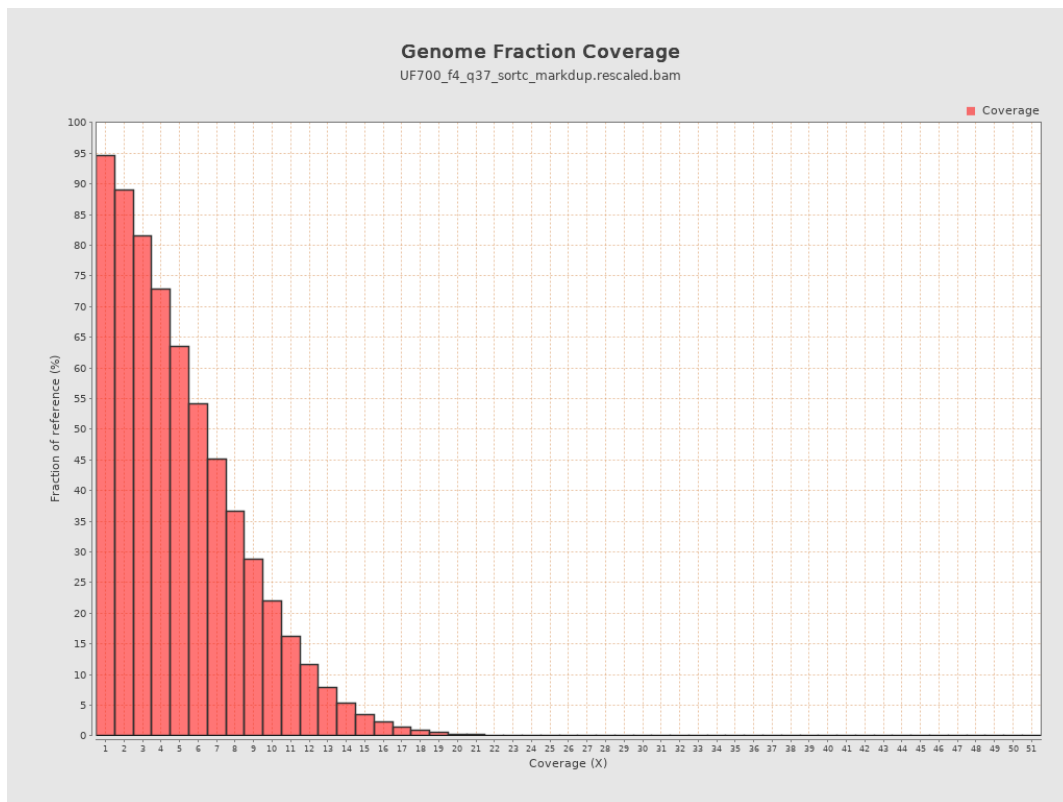
4. Results : Coverage Histogram



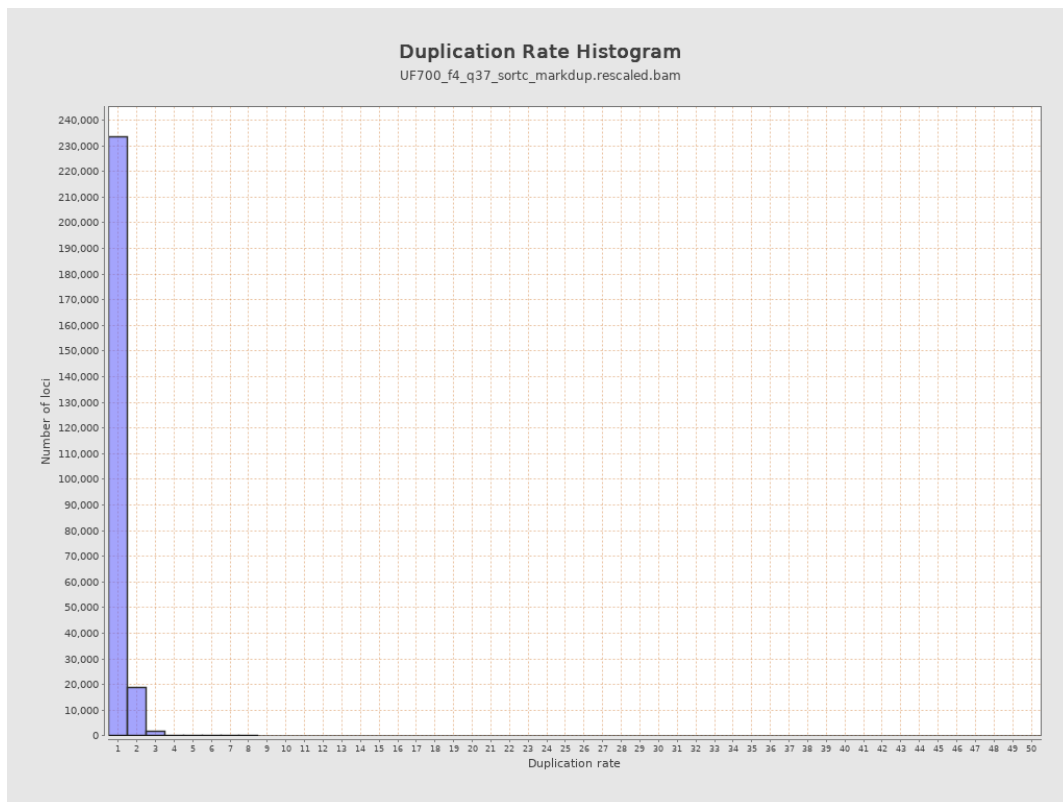
5. Results : Coverage Histogram (0-50X)



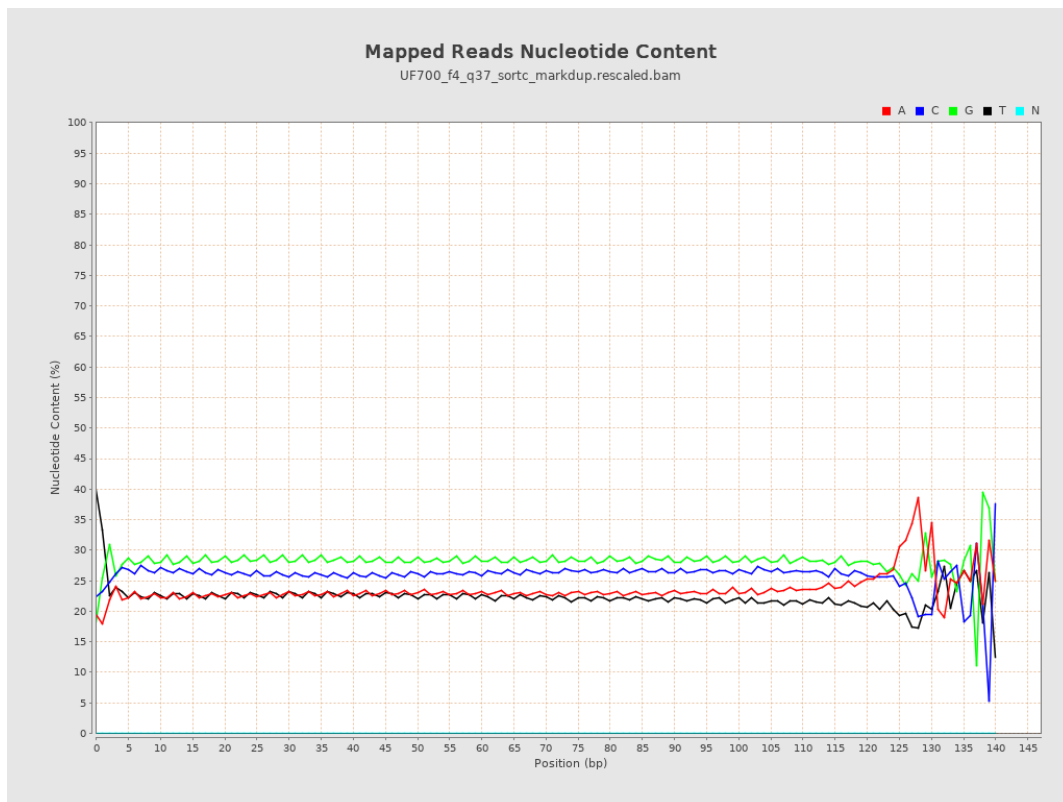
6. Results : Genome Fraction Coverage



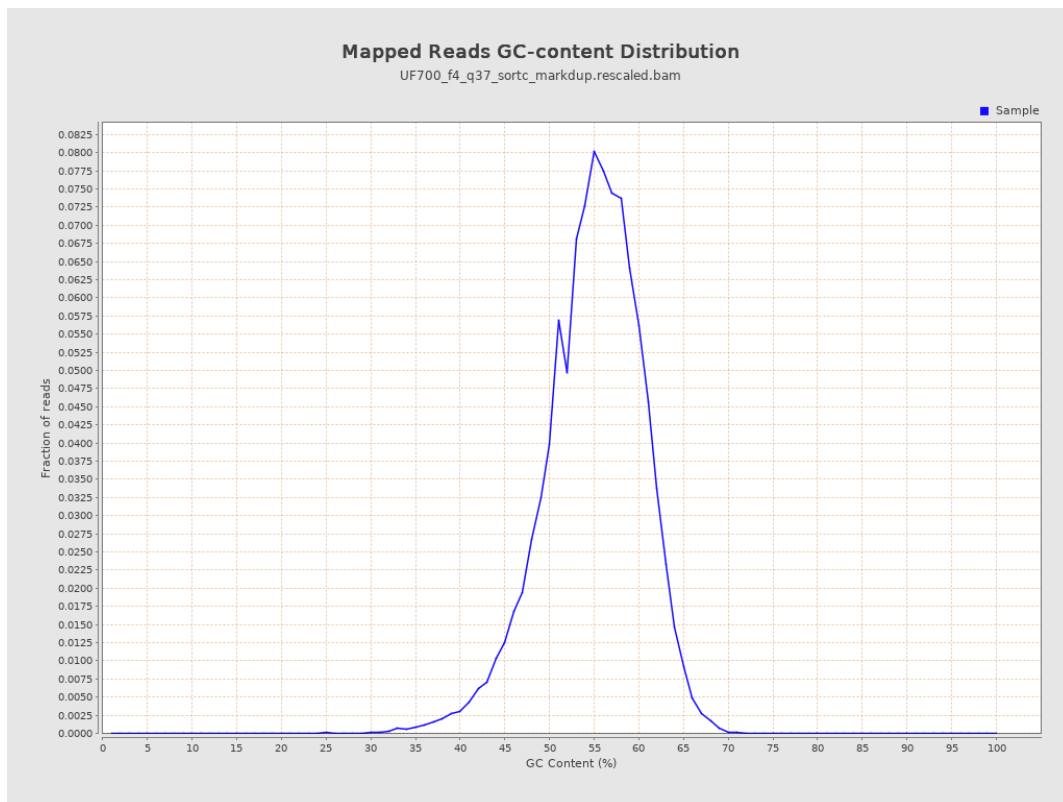
7. Results : Duplication Rate Histogram



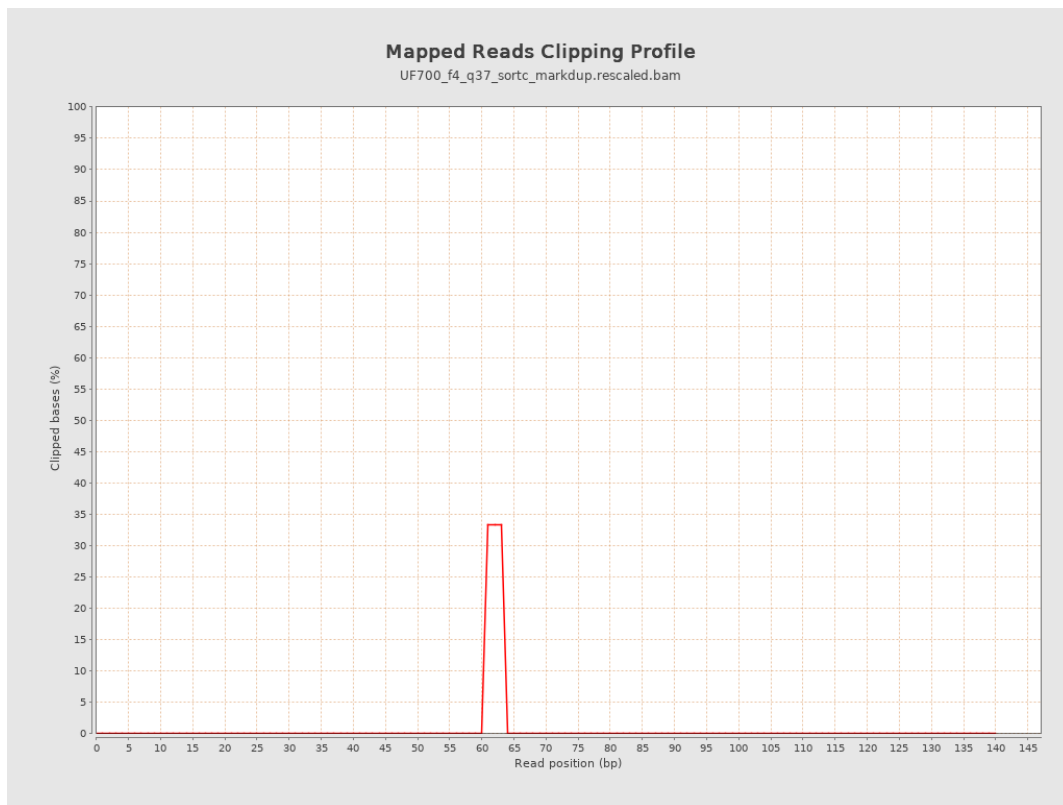
8. Results : Mapped Reads Nucleotide Content



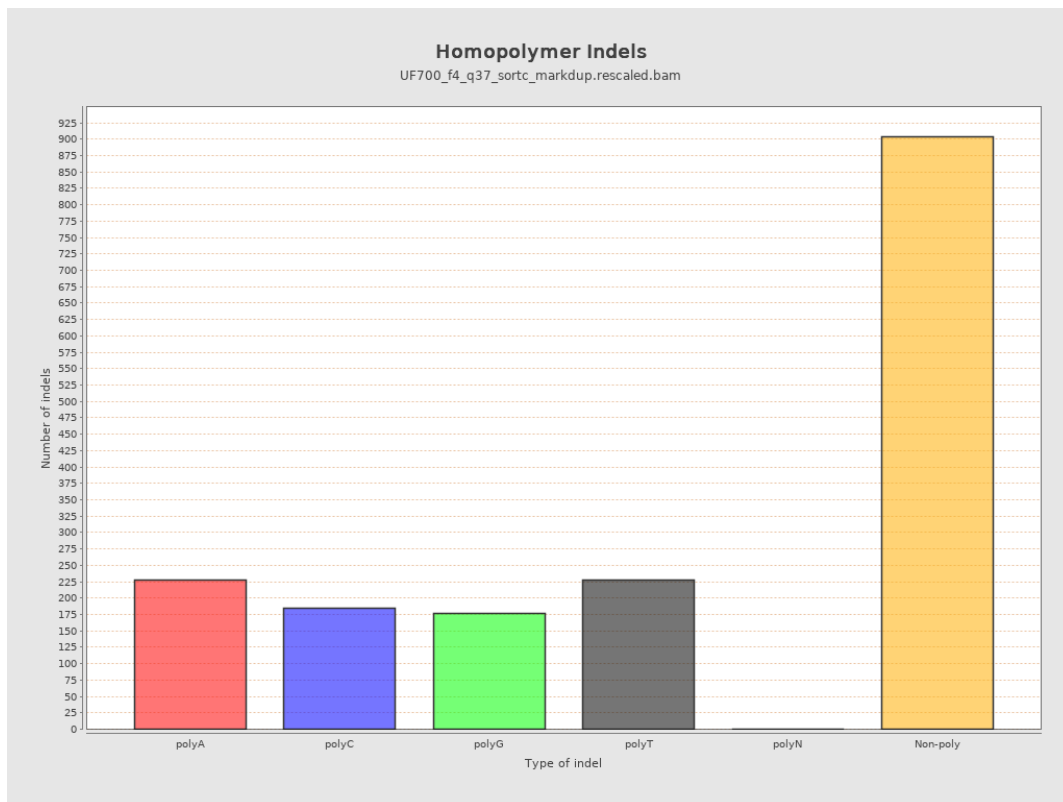
9. Results : Mapped Reads GC-content Distribution



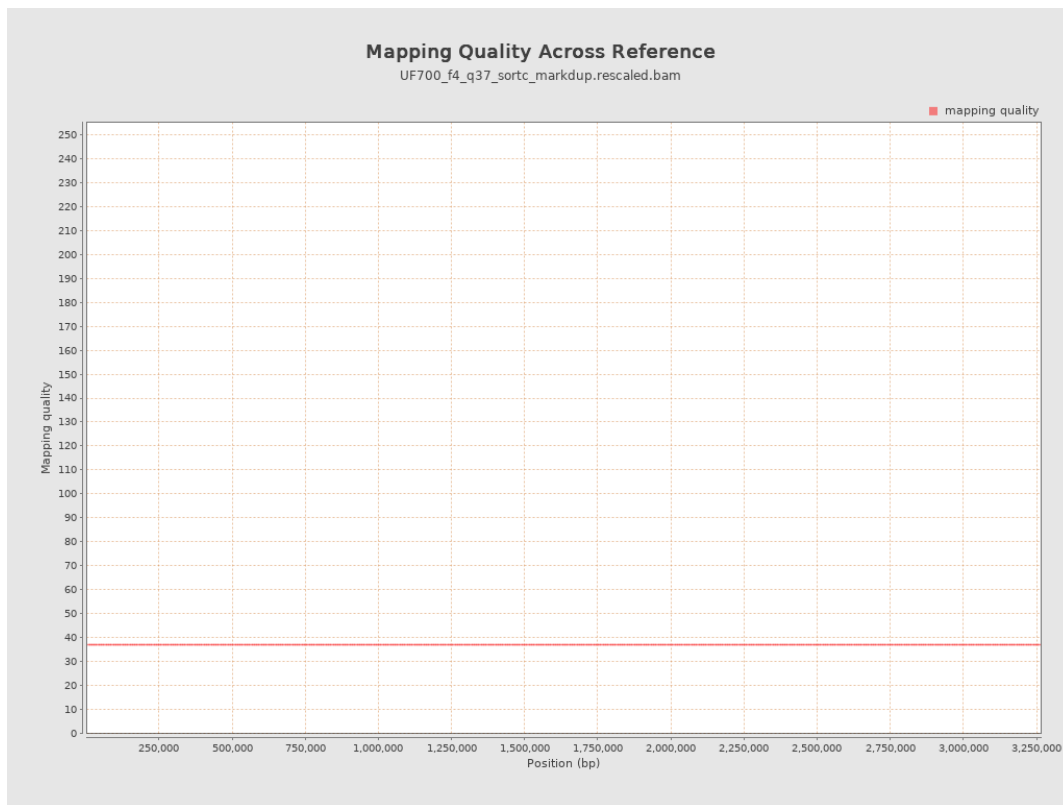
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

