

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/01 02:03:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
output/UF8/UF8_f4_q37_sortc_markdup.rescaled.bam -nw 400 -hm 3
```

1.2. Alignment

Command line:	bwa samse -r @RG\tID:UF8\tSM:UF8\tLB:nan\tPL:ILLUMINA /data/stonelab/references/M_leprae_TN/M_leprae_TN.fasta output/UF8/UF8-ancient.sai output/UF8/UF8-ancient.trimmed.fq
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 01 02:03:11 MST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	output/UF8/UF8_f4_q37_sortc_markdup.rescaled.bam

2. Summary

2.1. Globals

Reference size	3,268,203
Number of reads	63,177
Mapped reads	63,177 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	30 / 140 / 67.45
Duplicated reads (estimated)	4,099 / 6.49%
Duplication rate	3.71%
Clipped reads	1 / 0%

2.2. ACGT Content

Number/percentage of A's	956,884 / 22.46%
Number/percentage of C's	1,113,450 / 26.13%
Number/percentage of T's	951,037 / 22.32%
Number/percentage of G's	1,239,112 / 29.08%
Number/percentage of N's	1 / 0%
GC Percentage	55.22%

2.3. Coverage

Mean	1.3038
Standard Deviation	3.5916

2.4. Mapping Quality

Mean Mapping Quality	37
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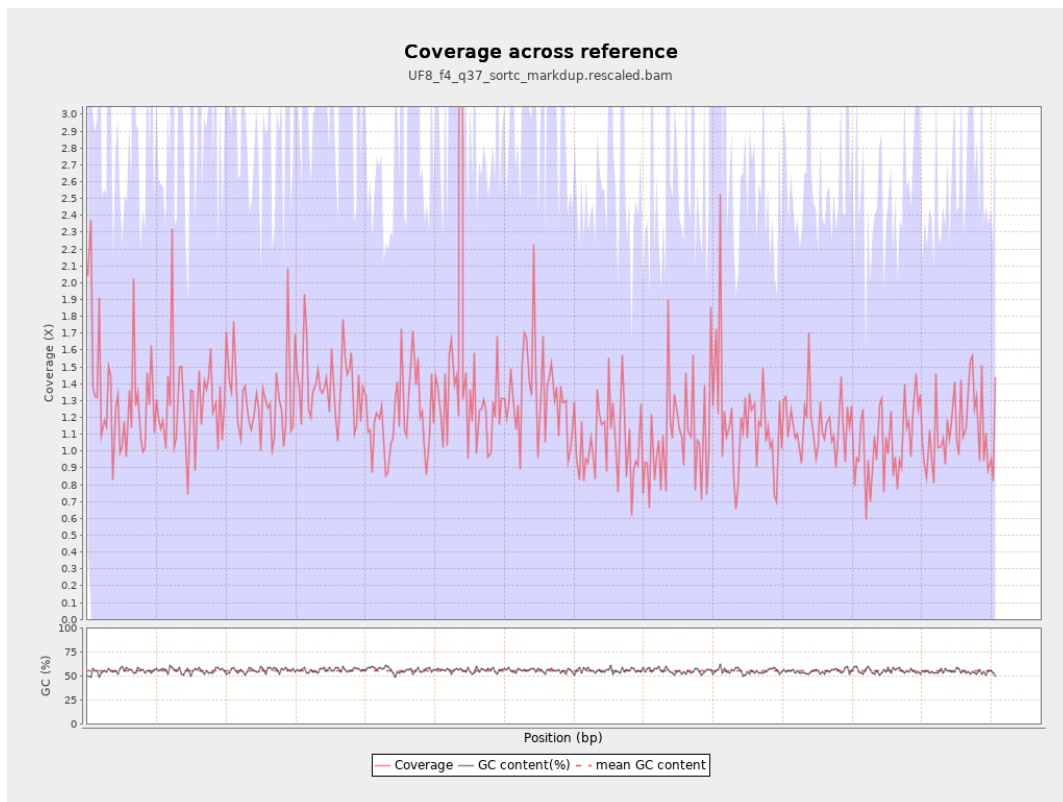
2.5. Mismatches and indels

General error rate	0.66%
Mismatches	27,574
Insertions	453
Mapped reads with at least one insertion	0.72%
Deletions	665
Mapped reads with at least one deletion	1.05%
Homopolymer indels	35.78%

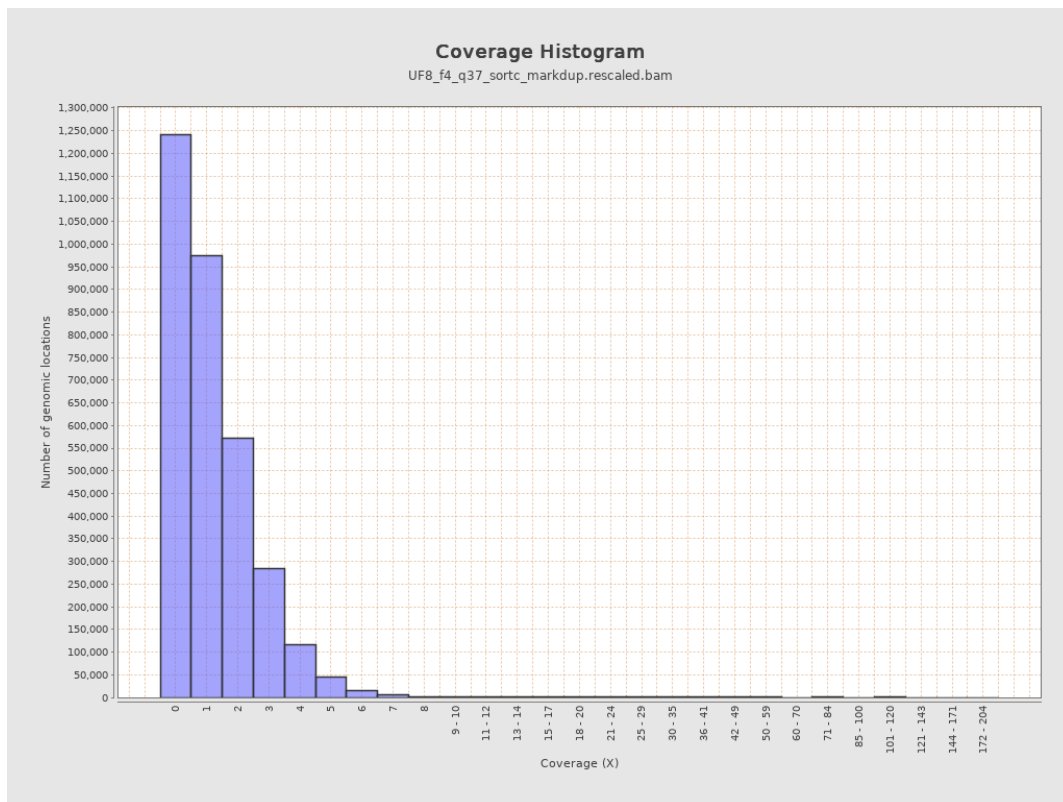
2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
ENA AL450380 AL450380.1	3268203	4261222	1.3038	3.5916

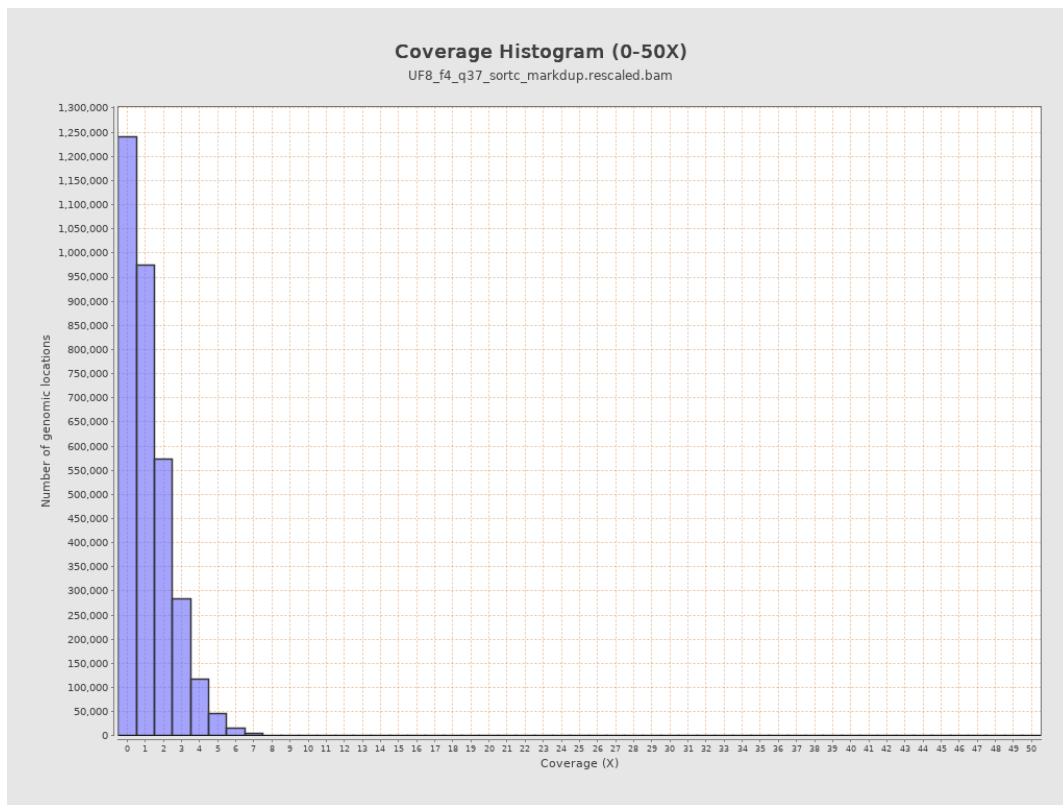
3. Results : Coverage across reference



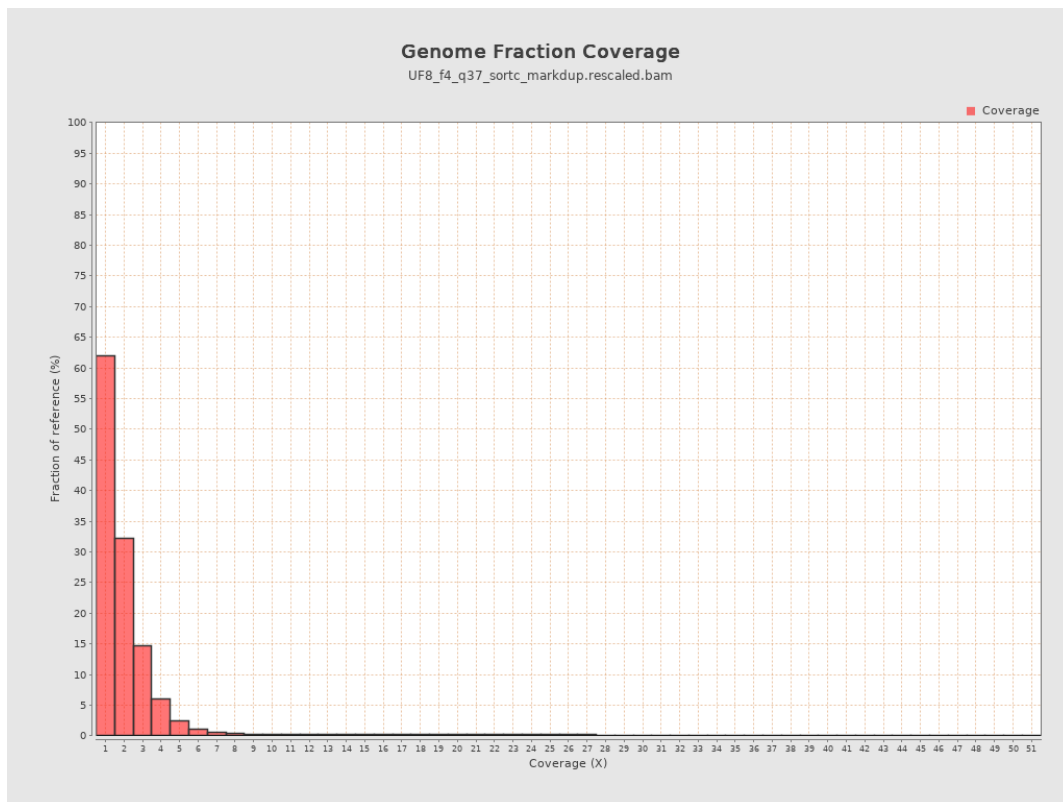
4. Results : Coverage Histogram



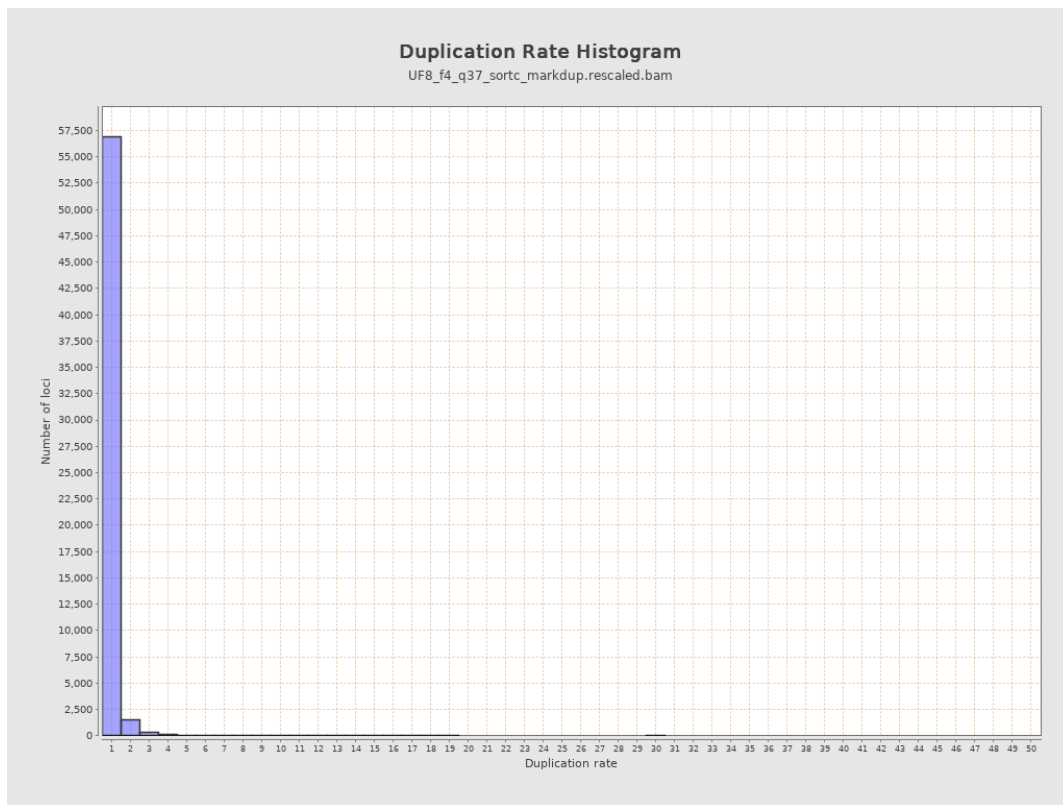
5. Results : Coverage Histogram (0-50X)



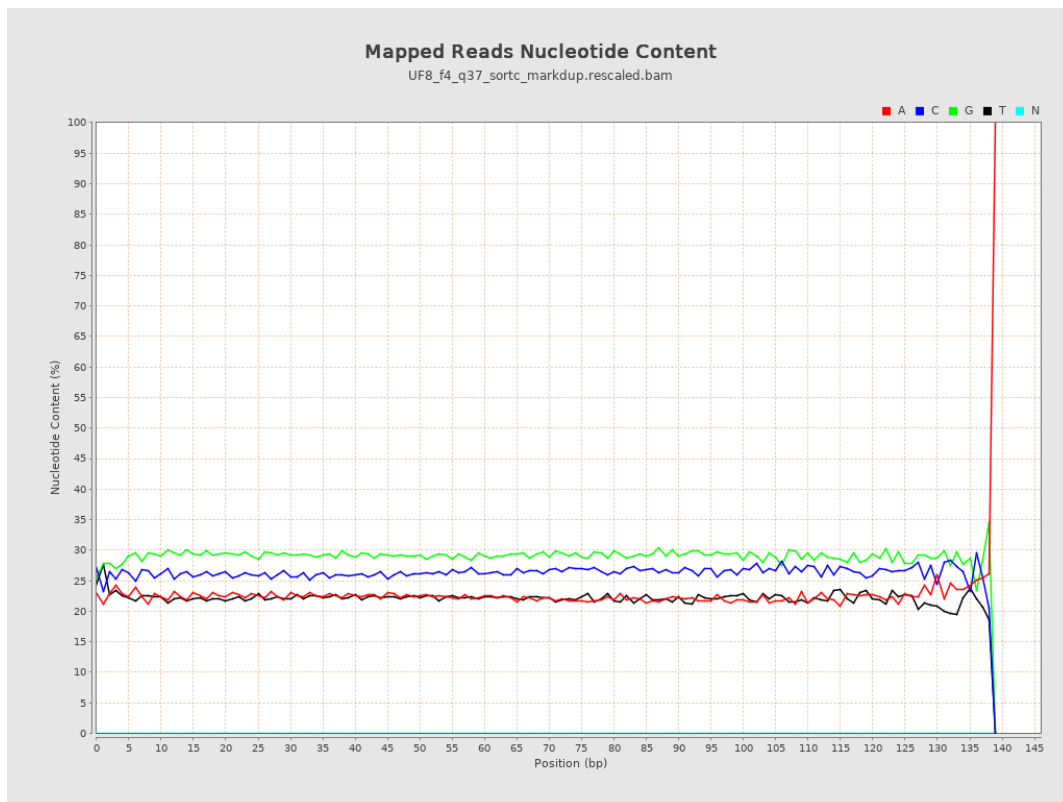
6. Results : Genome Fraction Coverage



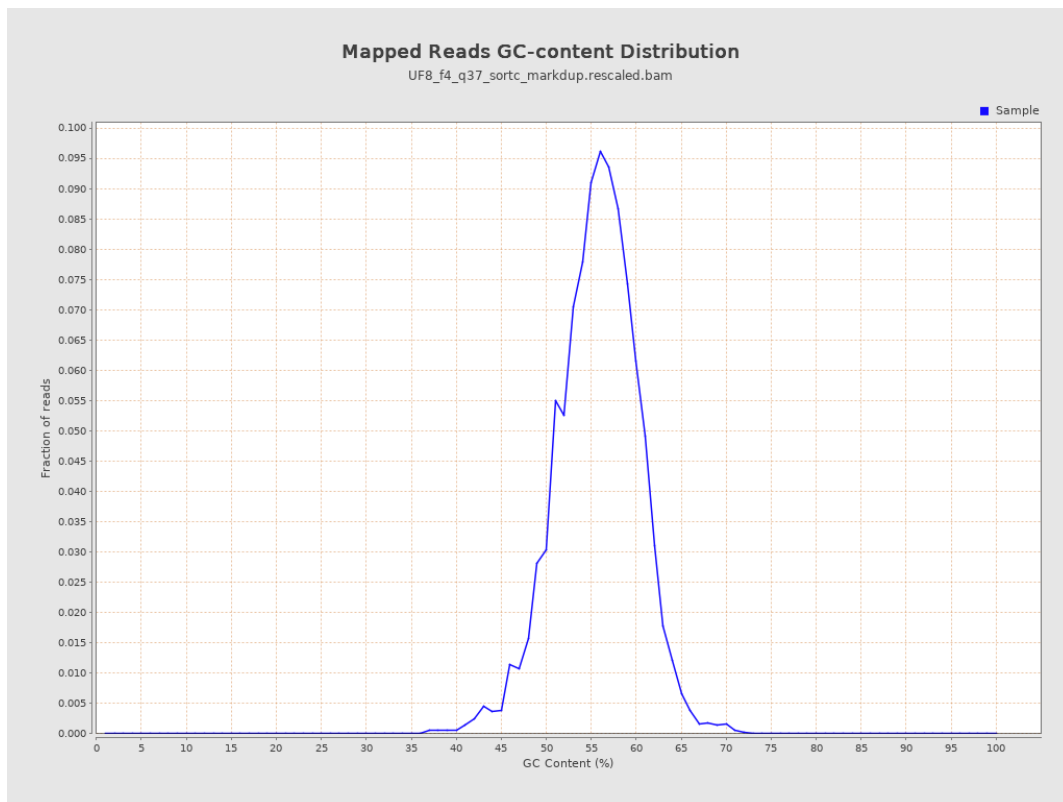
7. Results : Duplication Rate Histogram



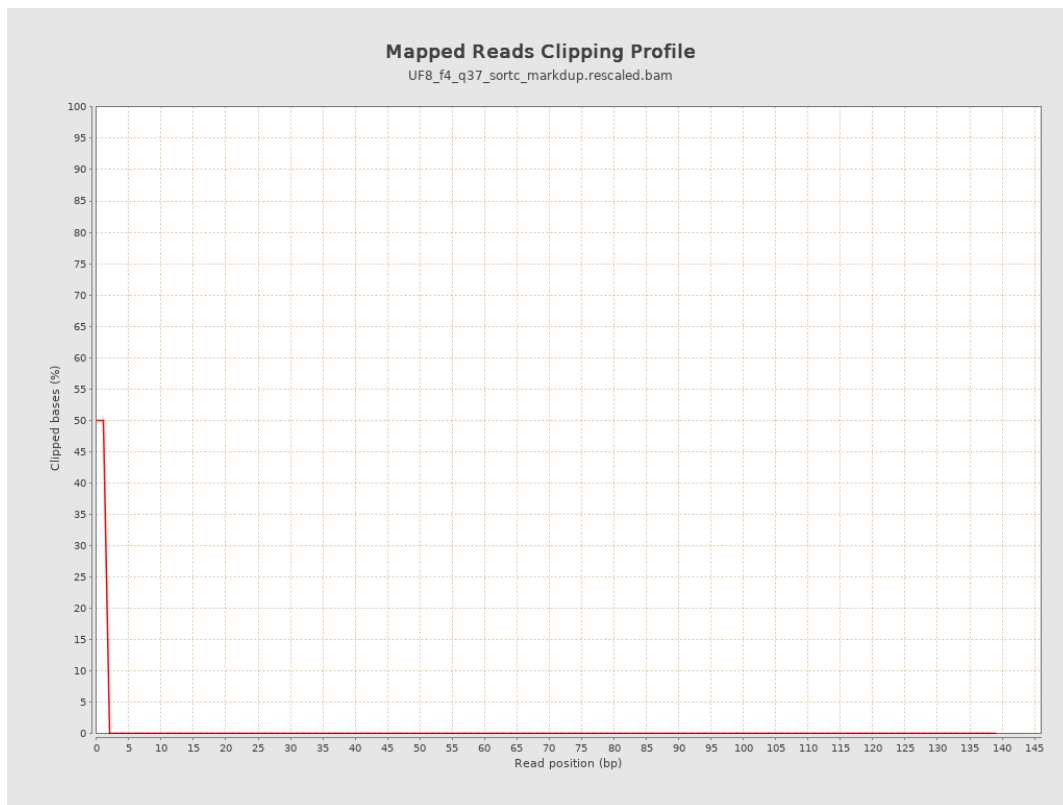
8. Results : Mapped Reads Nucleotide Content



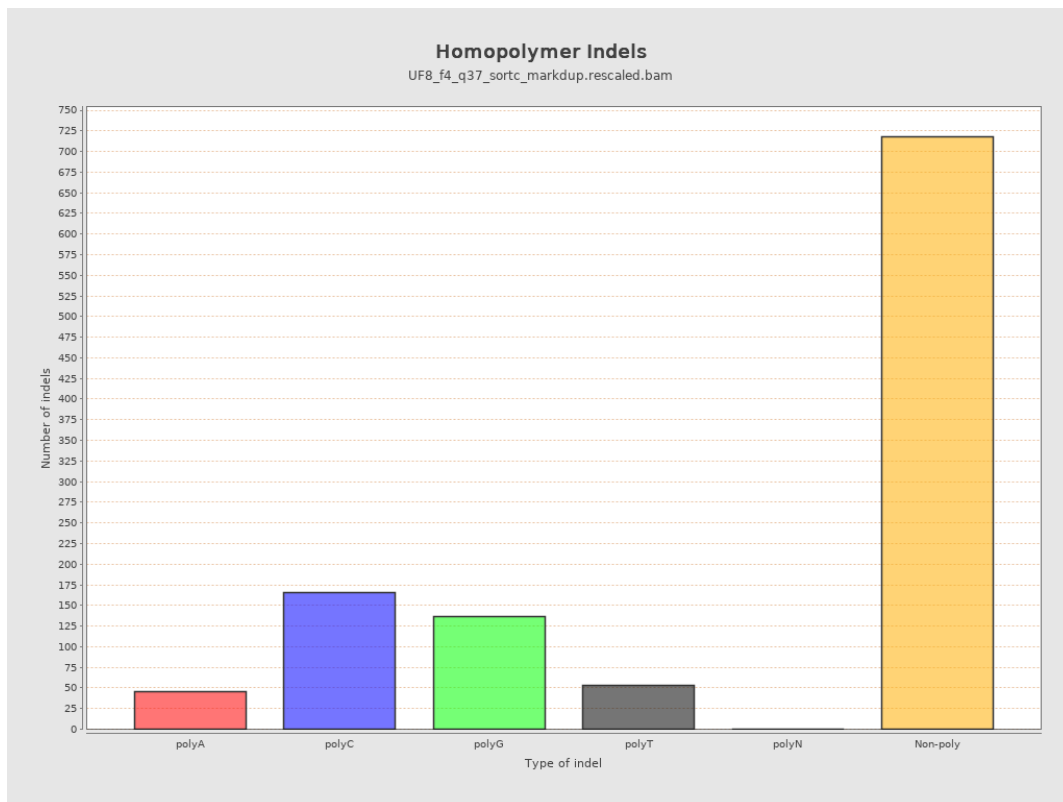
9. Results : Mapped Reads GC-content Distribution



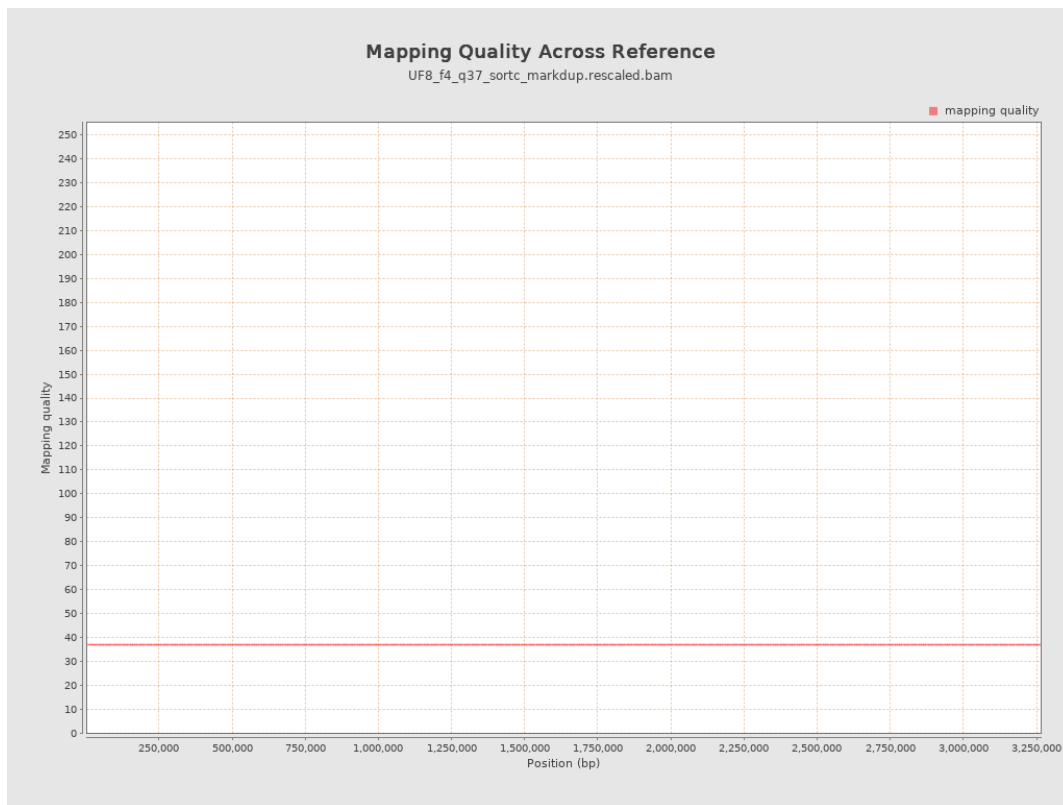
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

