

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/08 09:30:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam RCL368.bam -nw 400 -hm 3
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1.2. Alignment

Command line:	bwa-mem2 mem -t 4 PY79.fasta RAW_DATA/RCL368_R1.fastq.gz RAW_DATA/RCL368_R2.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa-mem2 (2.2.1)
Analysis date:	Thu Aug 08 09:30:52 CEST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	RCL368.bam

2. Summary

2.1. Globals

Reference size	4 033 459
Number of reads	18 158 535
Mapped reads	17 803 507 / 98,04%
Unmapped reads	355 028 / 1,96%
Mapped paired reads	17 803 507 / 98,04%
Mapped reads, first in pair	8 914 348 / 49,09%
Mapped reads, second in pair	8 889 159 / 48,95%
Mapped reads, both in pair	17 773 953 / 97,88%
Mapped reads, singletons	29 554 / 0,16%
Secondary alignments	0
Supplementary alignments	6 549 / 0,04%
Read min/max/mean length	30 / 126 / 125,97
Duplicated reads (estimated)	13 896 906 / 76,53%
Duplication rate	90,96%
Clipped reads	264 185 / 1,45%

2.2. ACGT Content

Number/percentage of A's	628 033 129 / 28,09%
Number/percentage of C's	489 277 189 / 21,88%
Number/percentage of T's	629 139 541 / 28,14%
Number/percentage of G's	489 445 783 / 21,89%
Number/percentage of N's	46 261 / 0%

GC Percentage	43,77%
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2.3. Coverage

Mean	554,3591
Standard Deviation	84,4327

2.4. Mapping Quality

Mean Mapping Quality	59,32
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2.5. Insert size

Mean	11 896,59
Standard Deviation	158 412,55
P25/Median/P75	260 / 321 / 394

2.6. Mismatches and indels

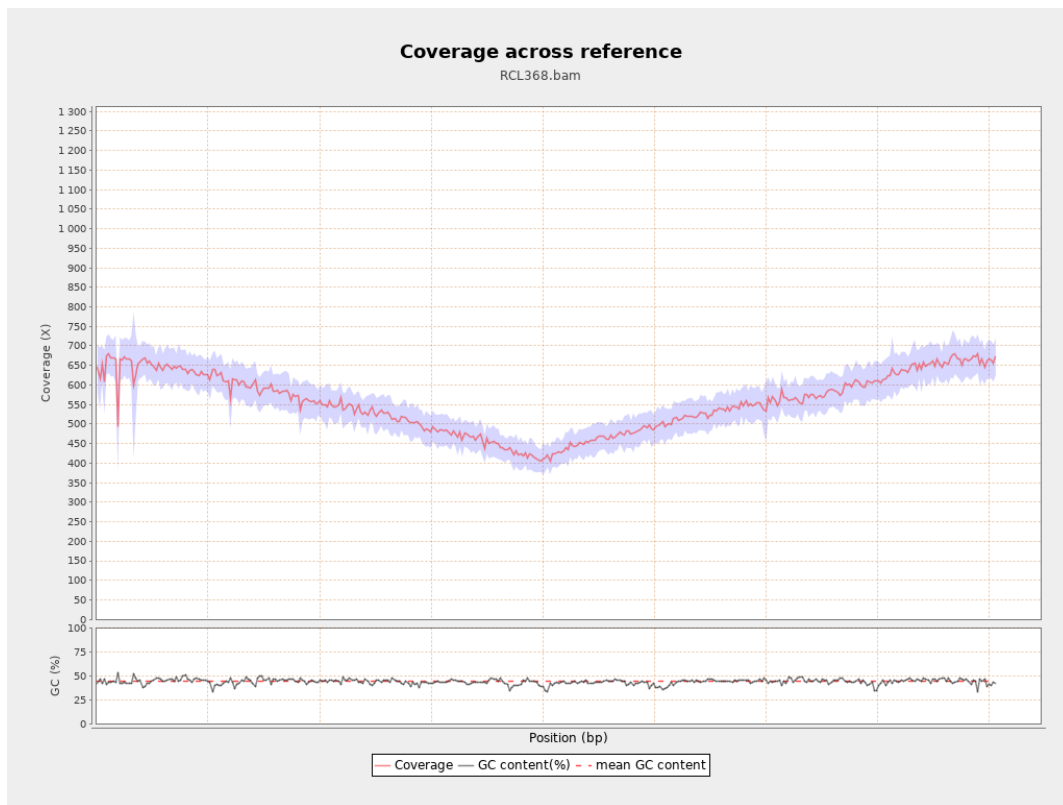
General error rate	0,24%
Mismatches	5 273 812
Insertions	6 597
Mapped reads with at least one insertion	0,04%
Deletions	8 138
Mapped reads with at least one deletion	0,05%
Homopolymer indels	60,55%

2.7. Chromosome stats

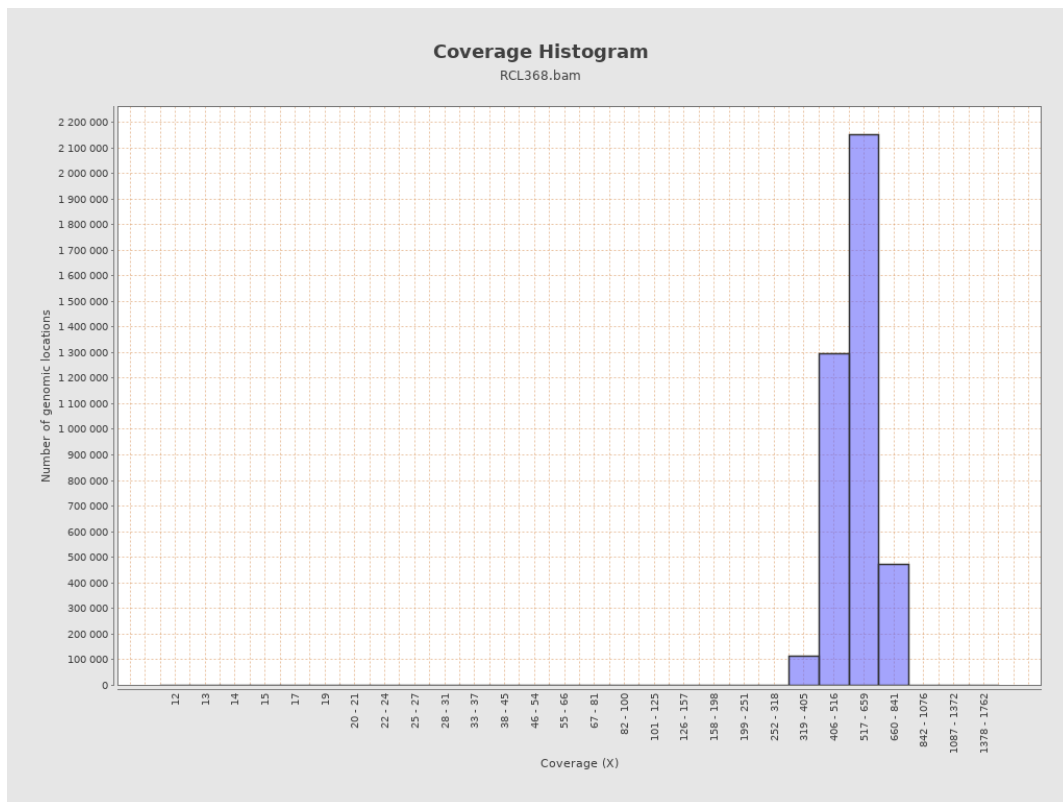
Name	Length	Mapped	Mean	Standard
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		bases	coverage	deviation
CP006881.1	4033459	2235984895	554,3591	84,4327

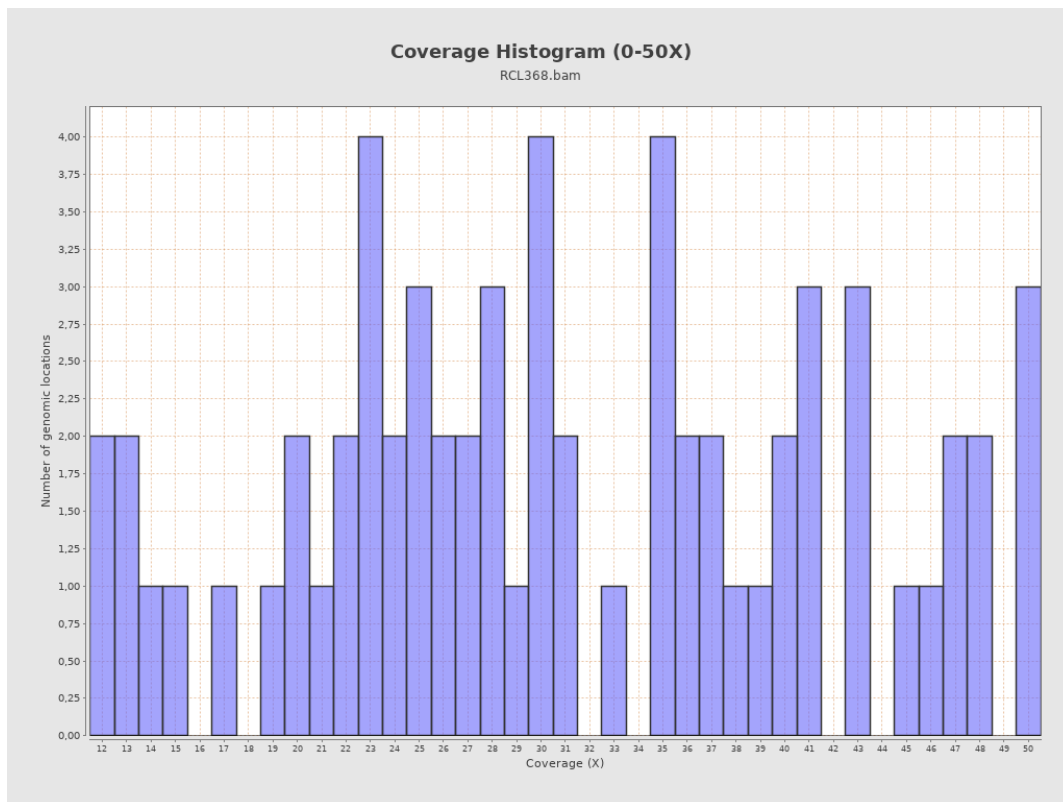
3. Results : Coverage across reference



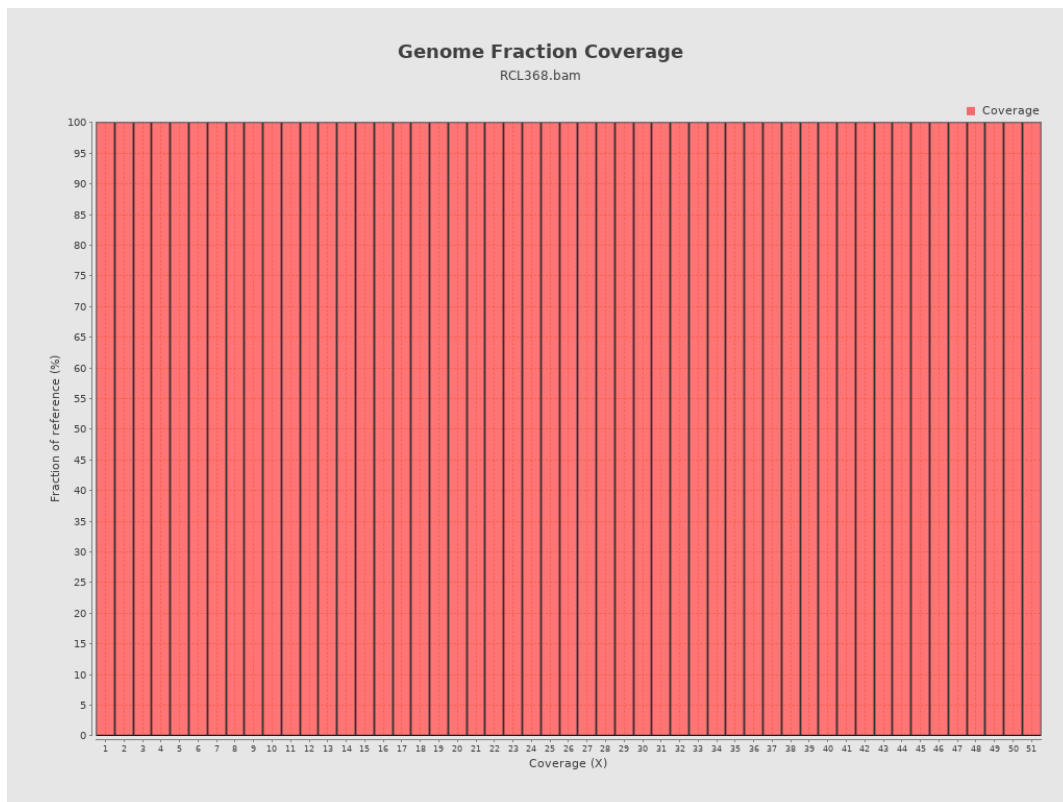
4. Results : Coverage Histogram



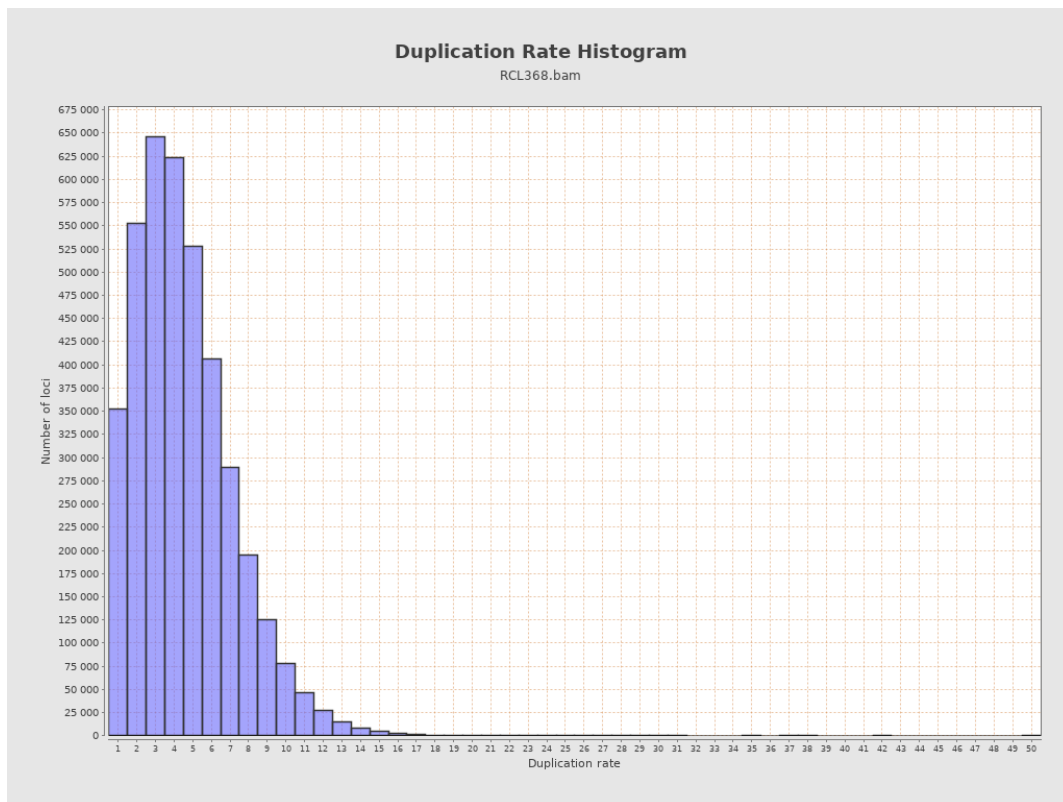
5. Results : Coverage Histogram (0-50X)



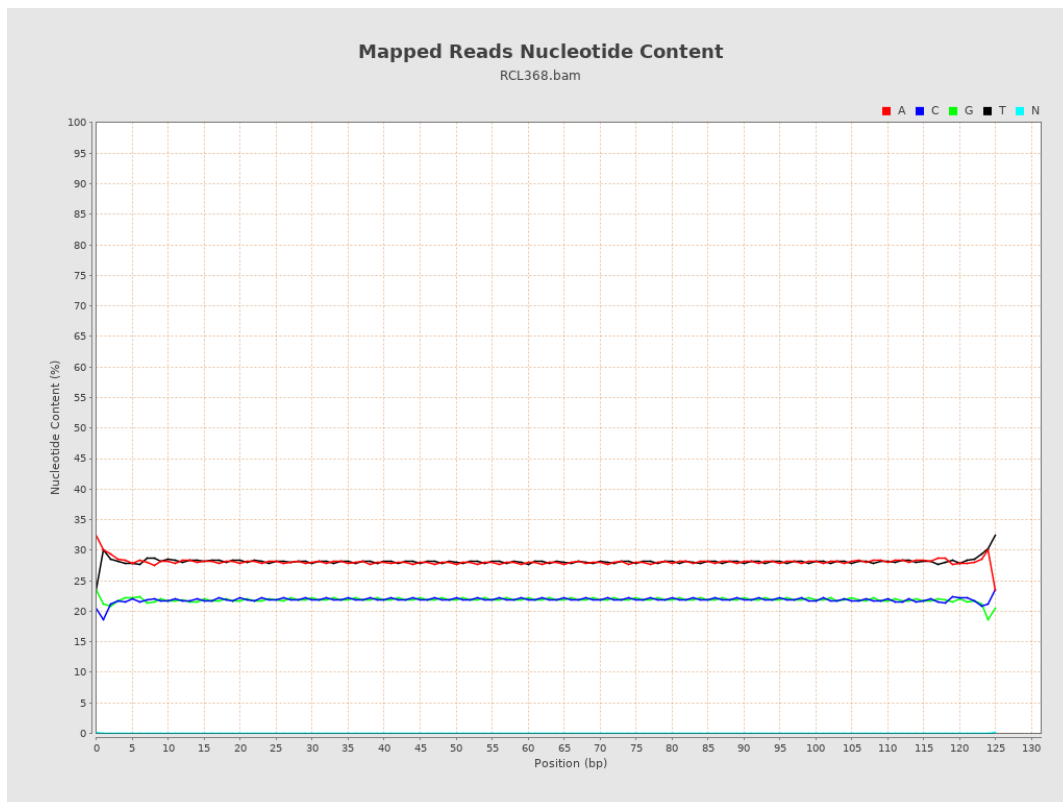
6. Results : Genome Fraction Coverage



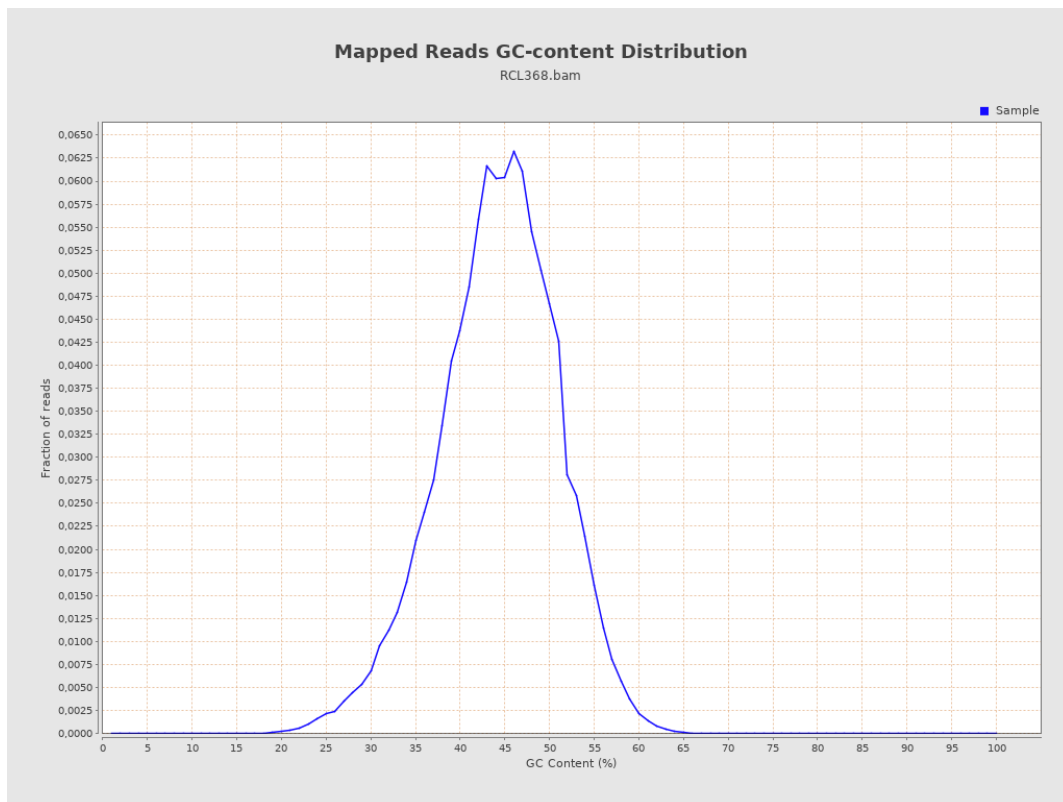
7. Results : Duplication Rate Histogram



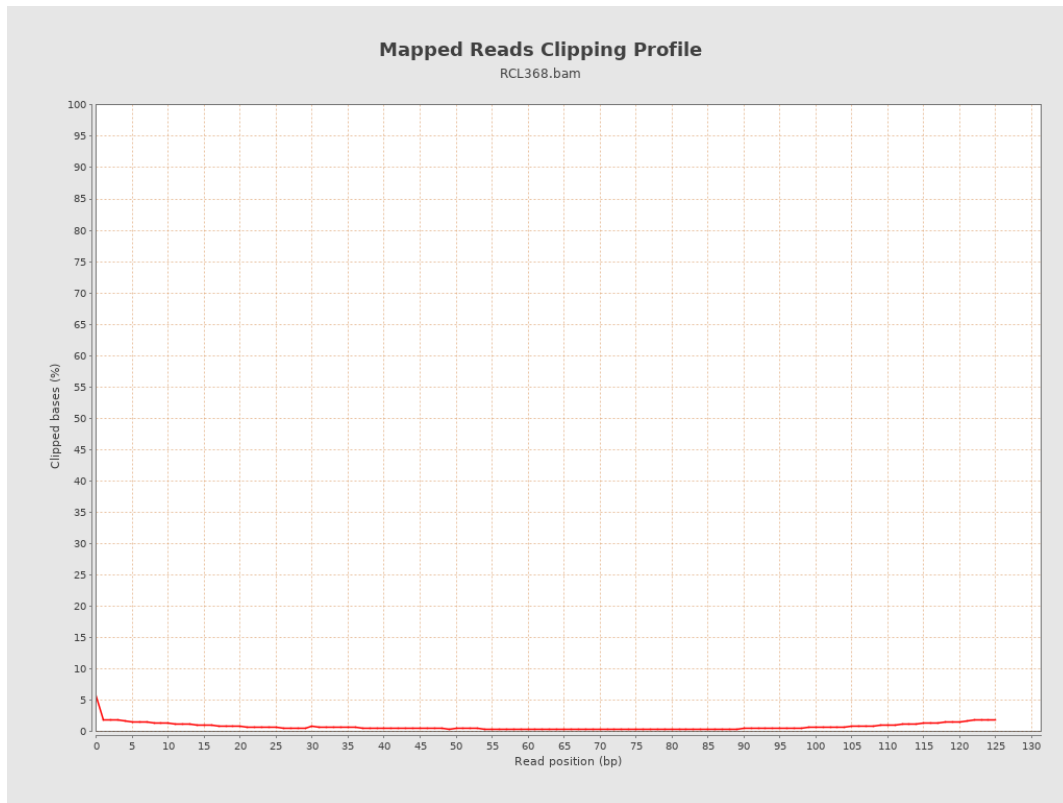
8. Results : Mapped Reads Nucleotide Content



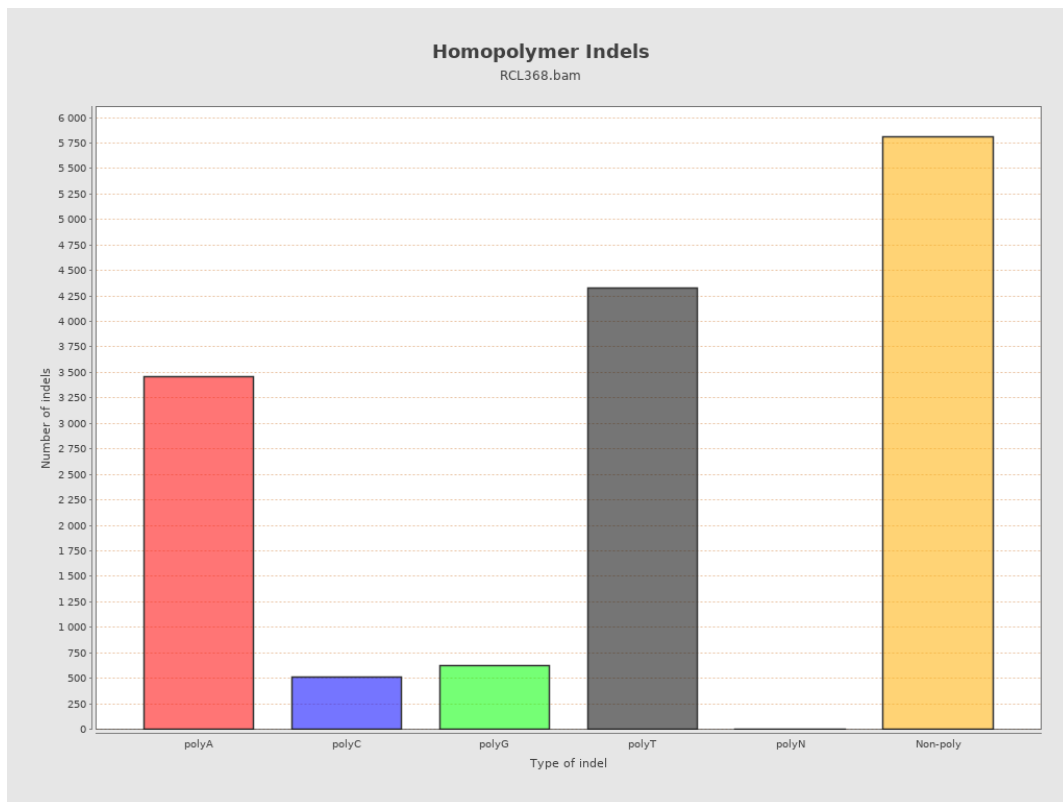
9. Results : Mapped Reads GC-content Distribution



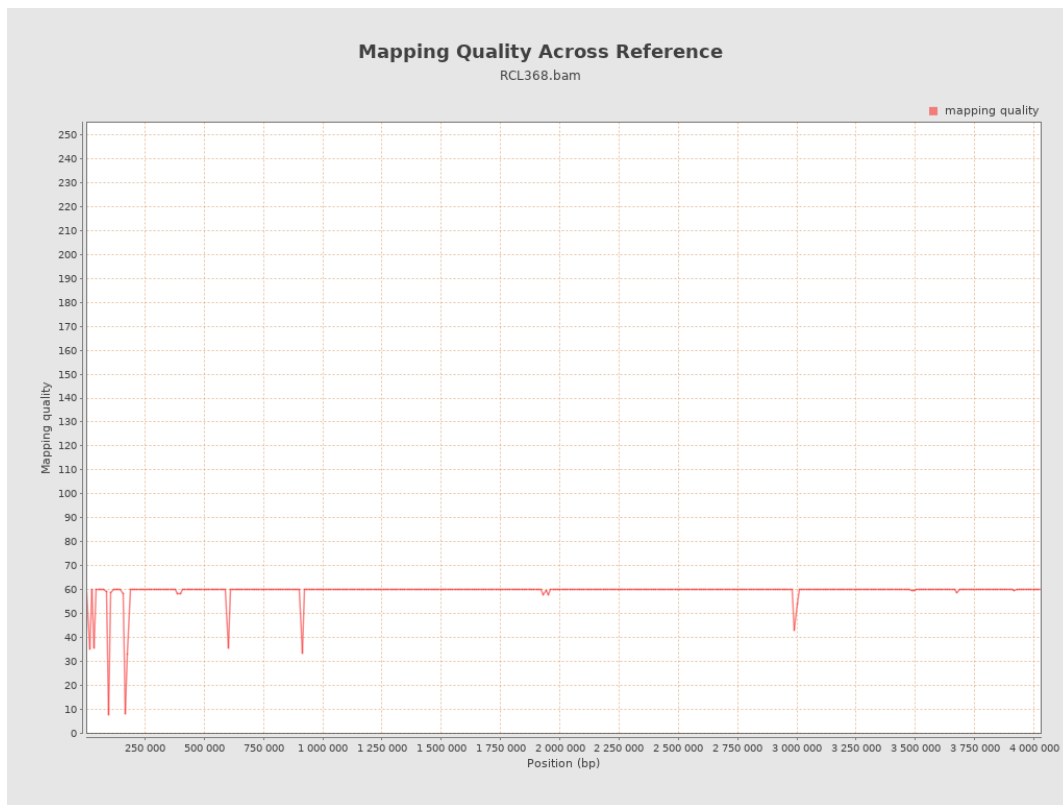
10. Results : Mapped Reads Clipping Profile



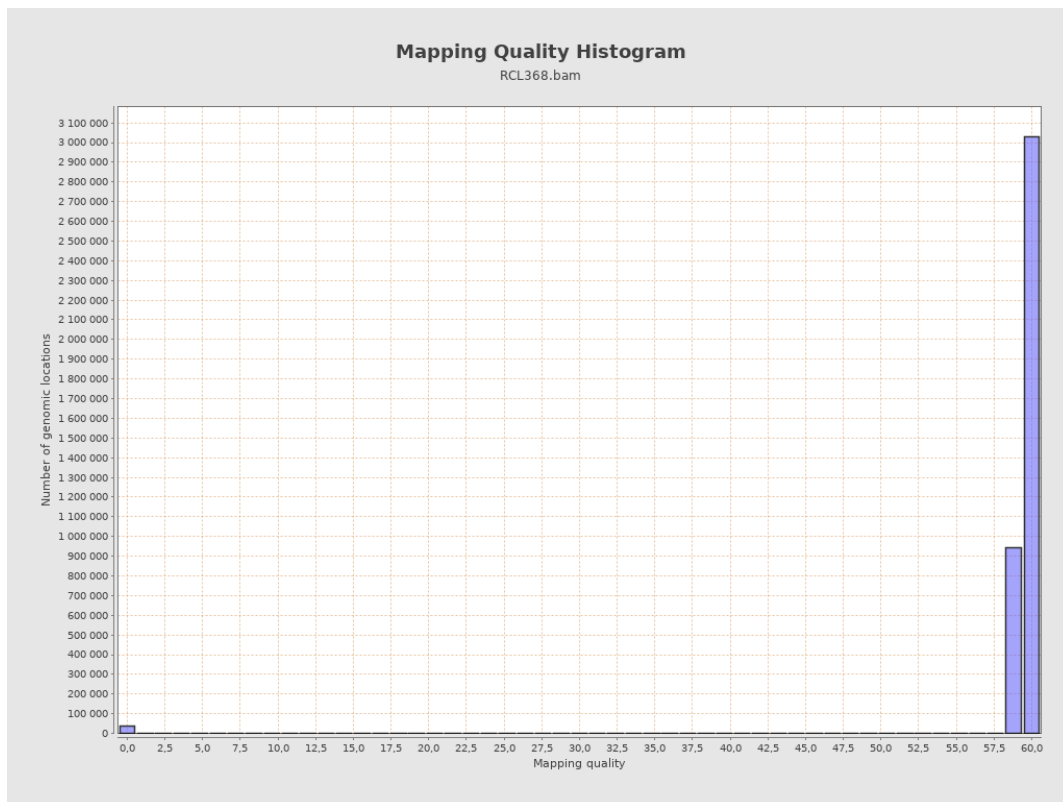
11. Results : Homopolymer Indels



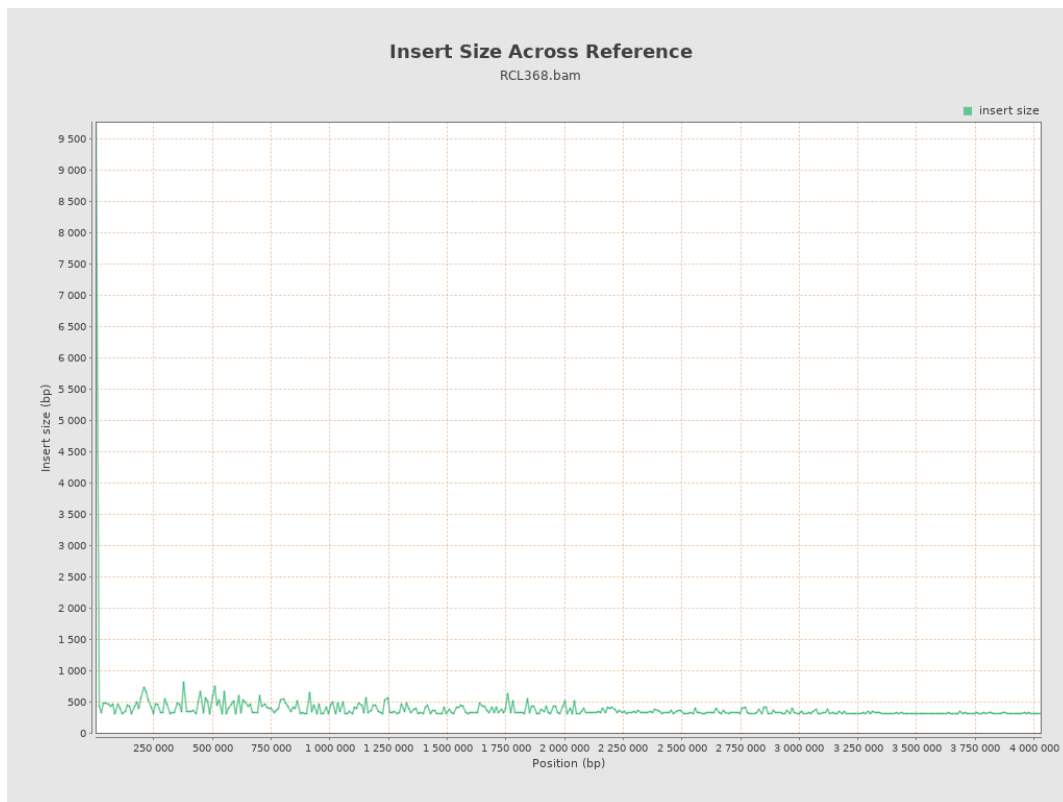
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

