

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/08 09:34:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam RCL415.bam -nw 400 -hm 3
```

1.2. Alignment

Command line:	bwa-mem2 mem -t 4 PY79.fasta RAW_DATA/RCL415_R1.fastq.gz RAW_DATA/RCL415_R2.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa-mem2 (2.2.1)
Analysis date:	Thu Aug 08 09:34:44 CEST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	RCL415.bam

2. Summary

2.1. Globals

Reference size	4 033 459
Number of reads	23 899 288
Mapped reads	23 188 425 / 97,03%
Unmapped reads	710 863 / 2,97%
Mapped paired reads	23 188 425 / 97,03%
Mapped reads, first in pair	11 616 511 / 48,61%
Mapped reads, second in pair	11 571 914 / 48,42%
Mapped reads, both in pair	23 138 631 / 96,82%
Mapped reads, singletons	49 794 / 0,21%
Secondary alignments	0
Supplementary alignments	10 418 / 0,04%
Read min/max/mean length	30 / 126 / 125,96
Duplicated reads (estimated)	19 208 403 / 80,37%
Duplication rate	95,5%
Clipped reads	383 632 / 1,61%

2.2. ACGT Content

Number/percentage of A's	817 344 554 / 28,08%
Number/percentage of C's	637 362 330 / 21,9%
Number/percentage of T's	819 139 796 / 28,14%
Number/percentage of G's	637 096 744 / 21,89%
Number/percentage of N's	59 346 / 0%

GC Percentage	43,78%
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2.3. Coverage

Mean	721,7271
Standard Deviation	107,6403

2.4. Mapping Quality

Mean Mapping Quality	59,35
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2.5. Insert size

Mean	16 820,21
Standard Deviation	188 062,71
P25/Median/P75	259 / 324 / 408

2.6. Mismatches and indels

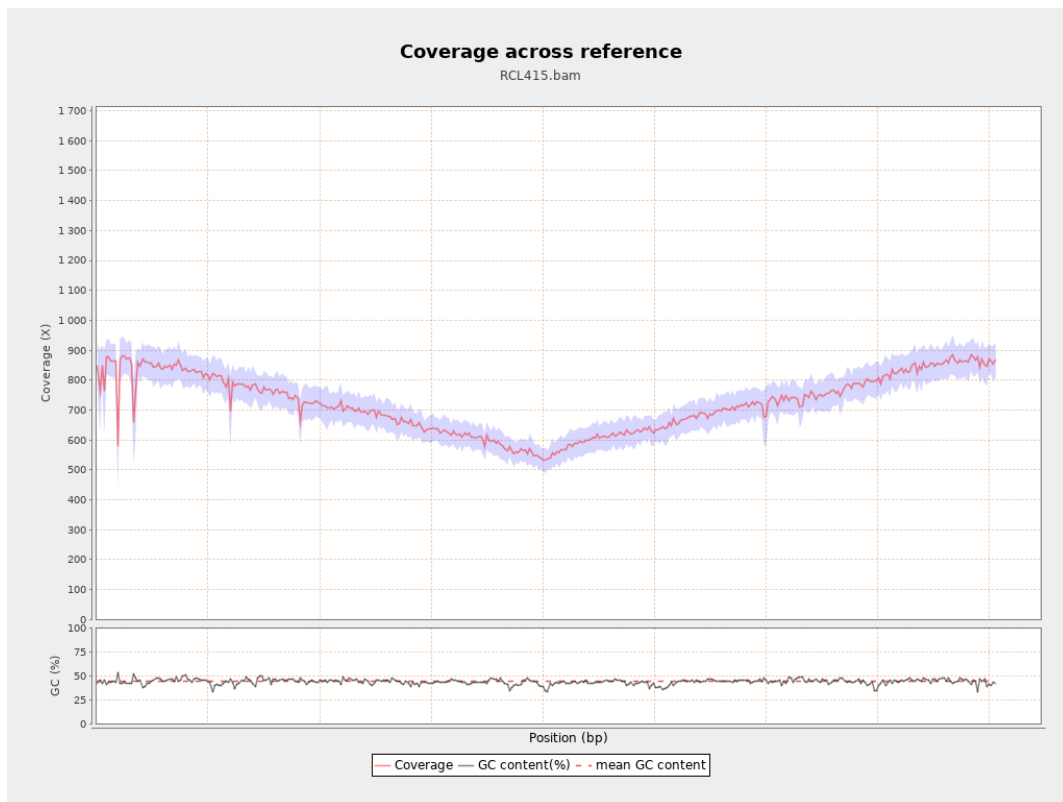
General error rate	0,26%
Mismatches	7 583 013
Insertions	7 971
Mapped reads with at least one insertion	0,03%
Deletions	10 670
Mapped reads with at least one deletion	0,05%
Homopolymer indels	59,4%

2.7. Chromosome stats

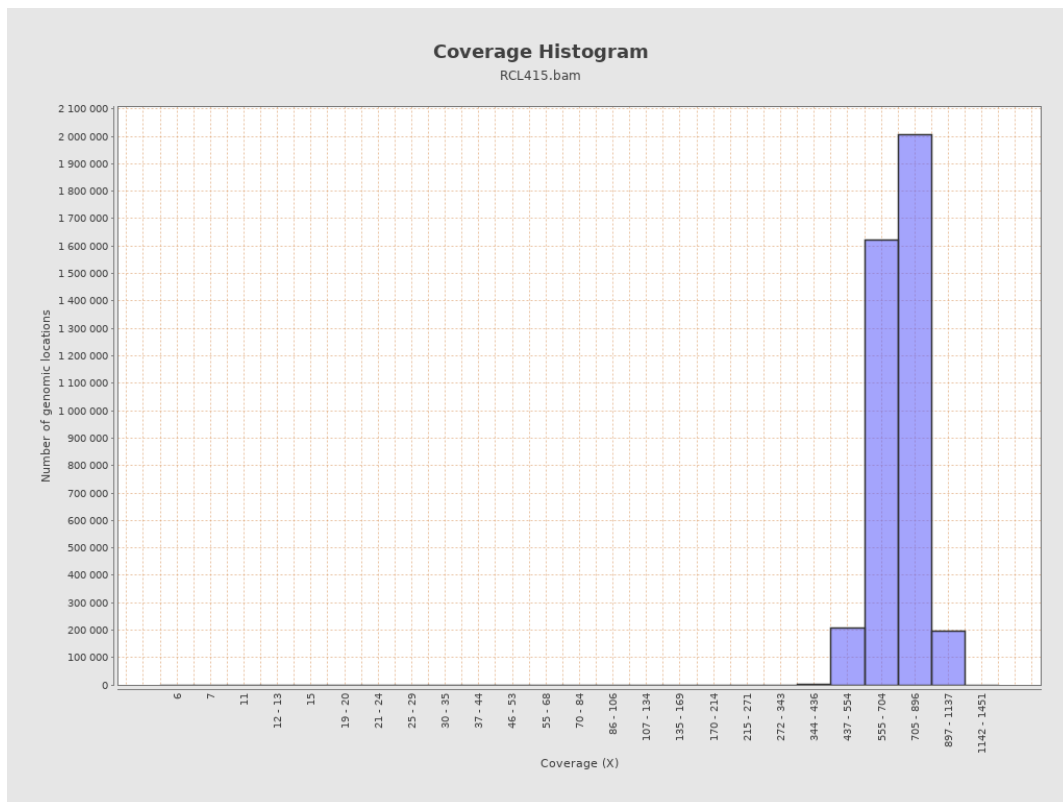
Name	Length	Mapped	Mean	Standard
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		bases	coverage	deviation
CP006881.1	4033459	2911056836	721,7271	107,6403

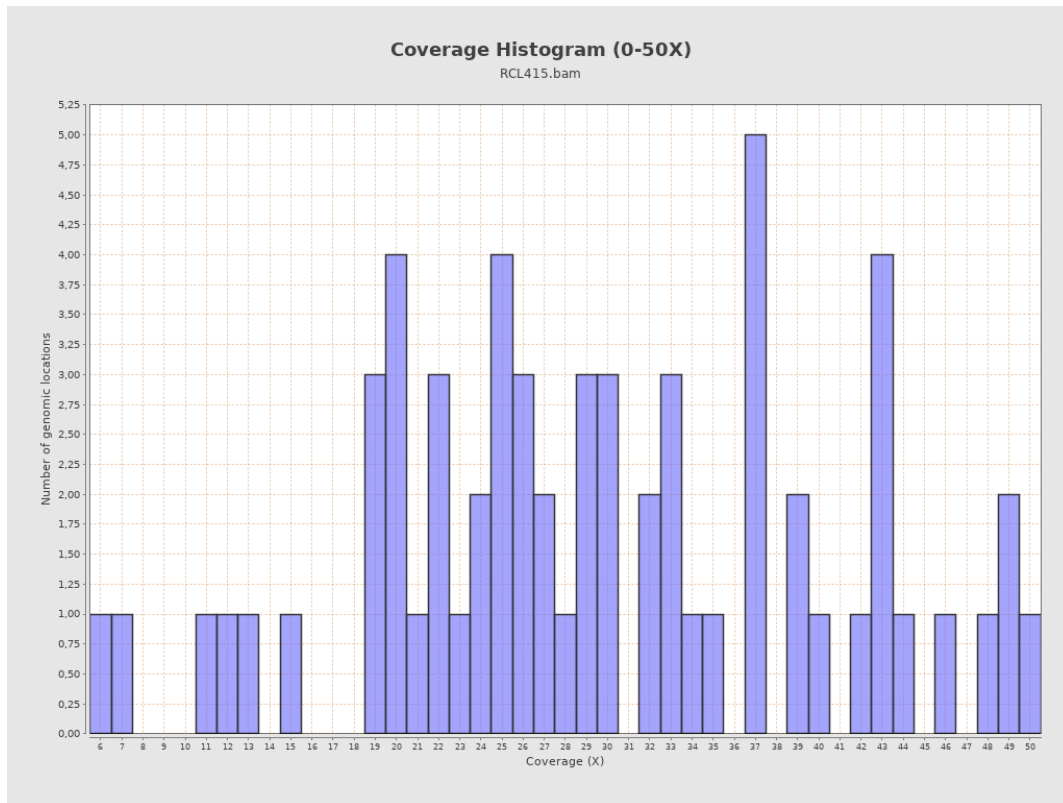
3. Results : Coverage across reference



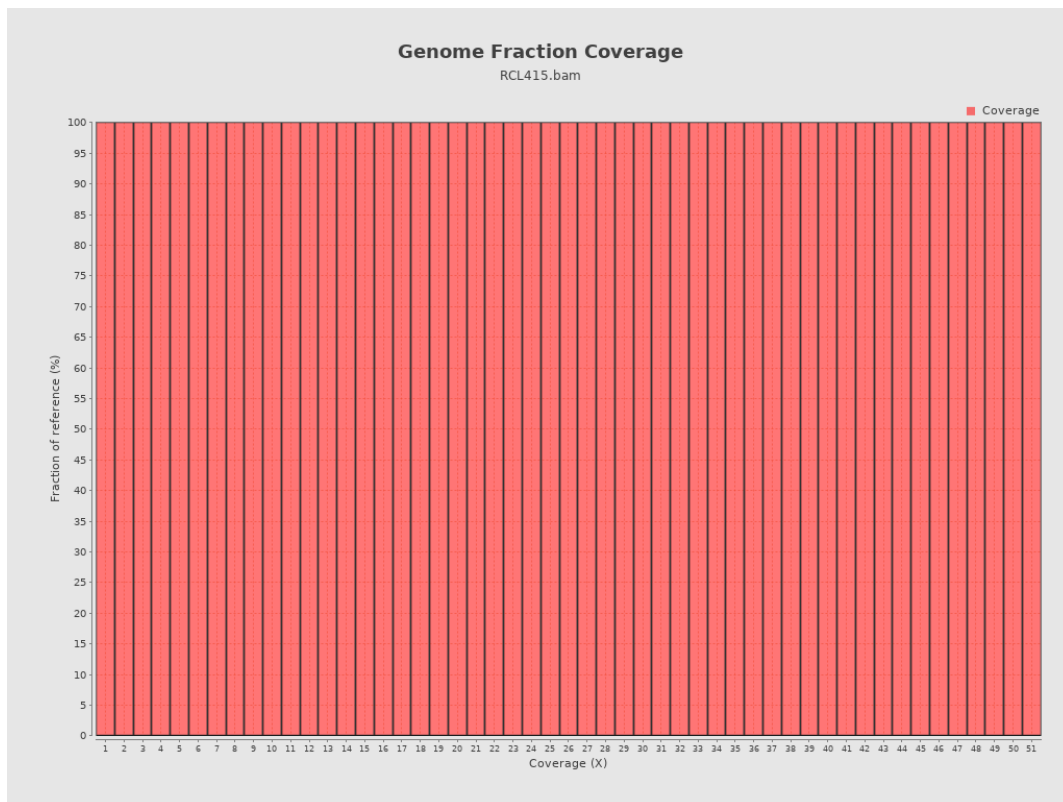
4. Results : Coverage Histogram



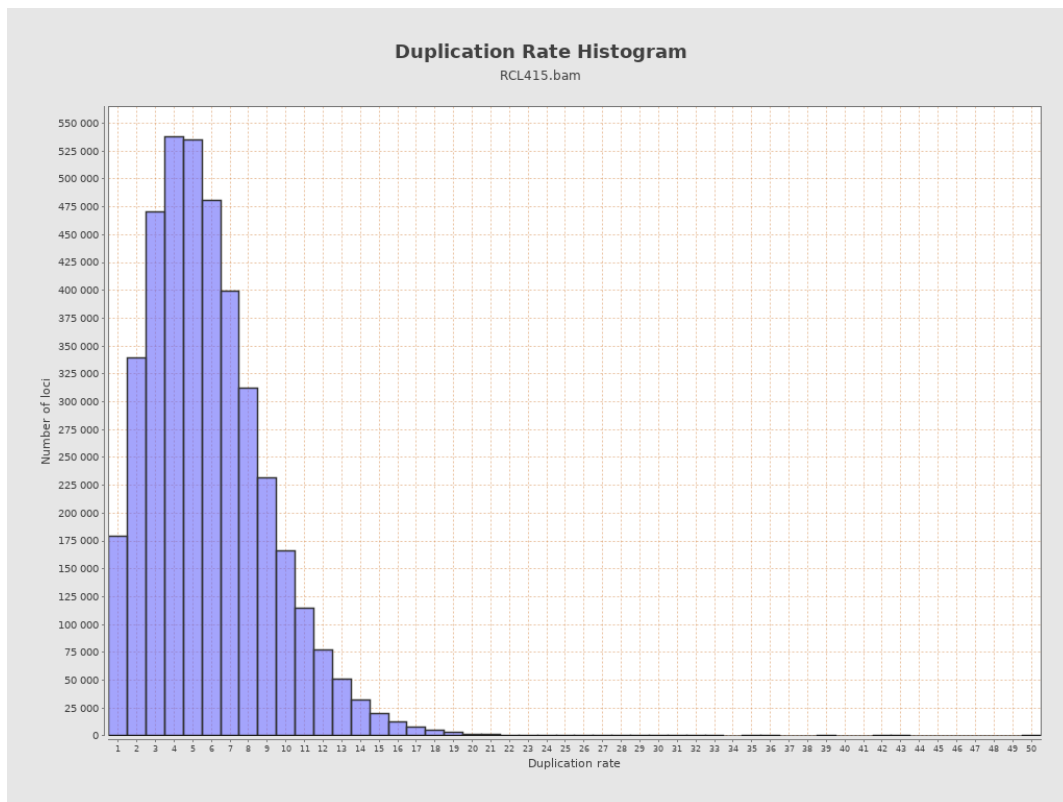
5. Results : Coverage Histogram (0-50X)



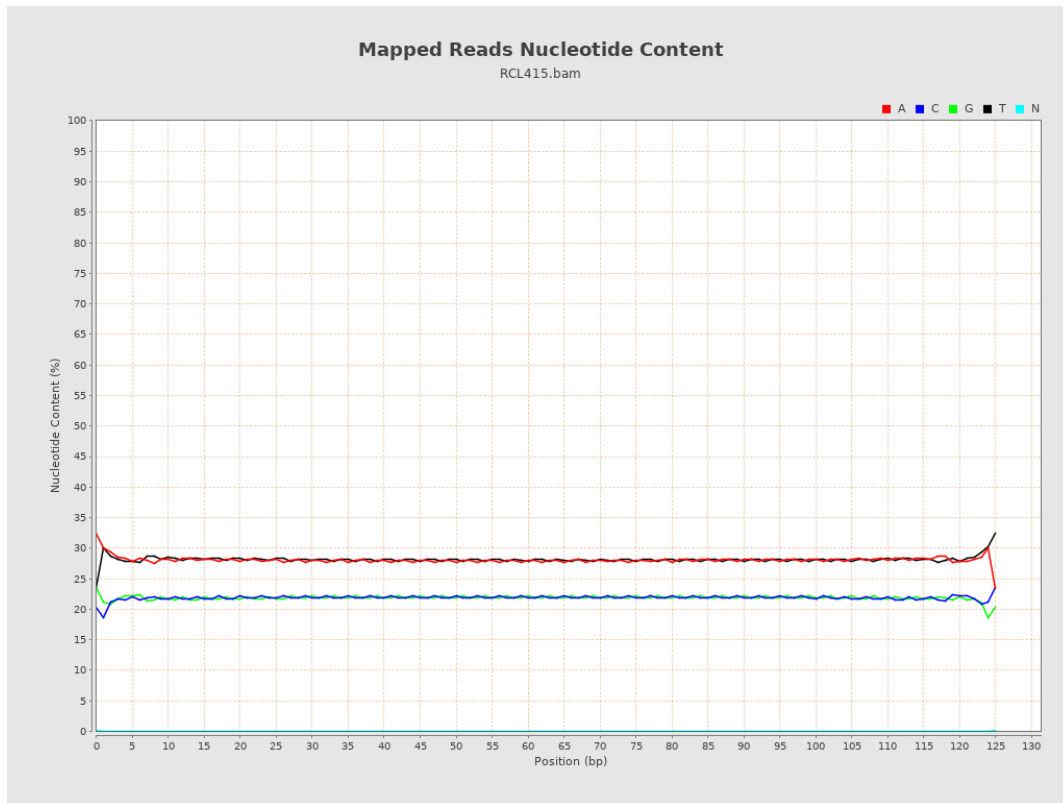
6. Results : Genome Fraction Coverage



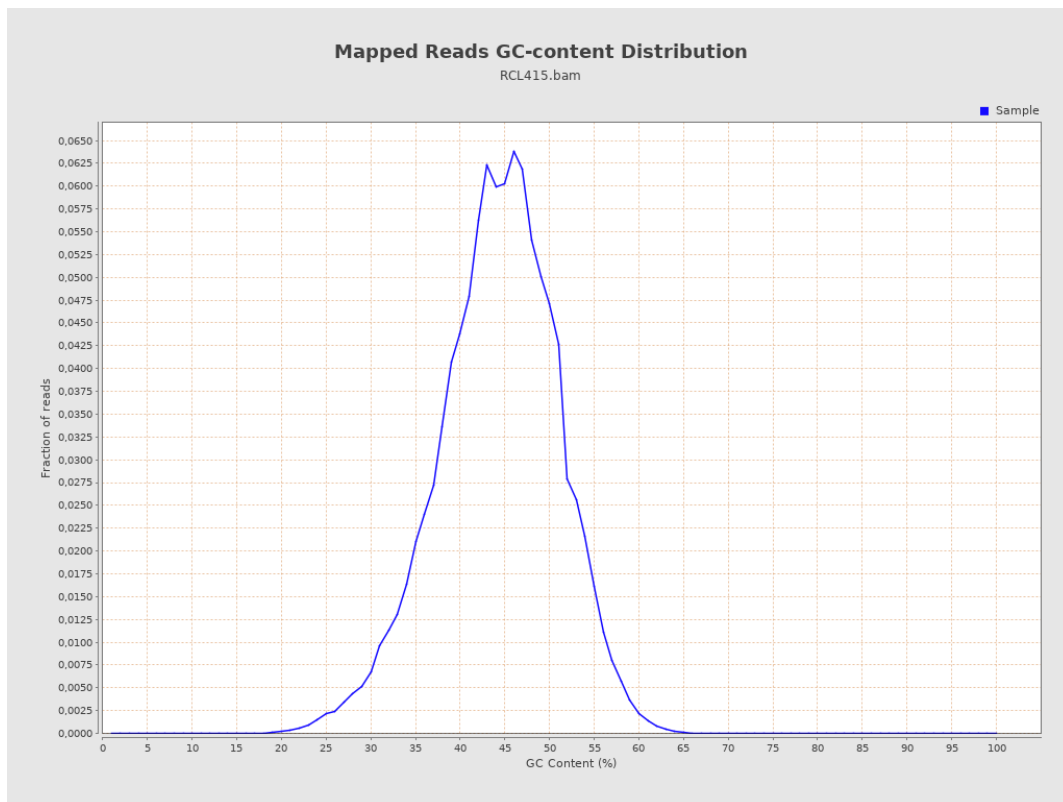
7. Results : Duplication Rate Histogram



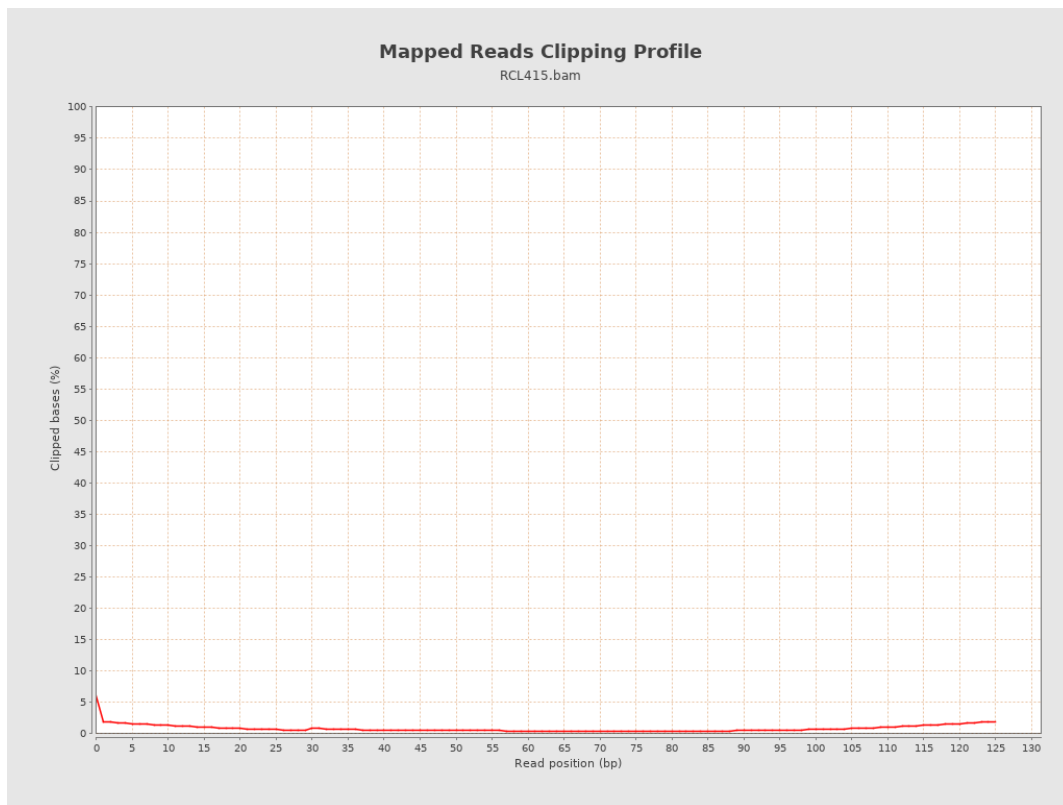
8. Results : Mapped Reads Nucleotide Content



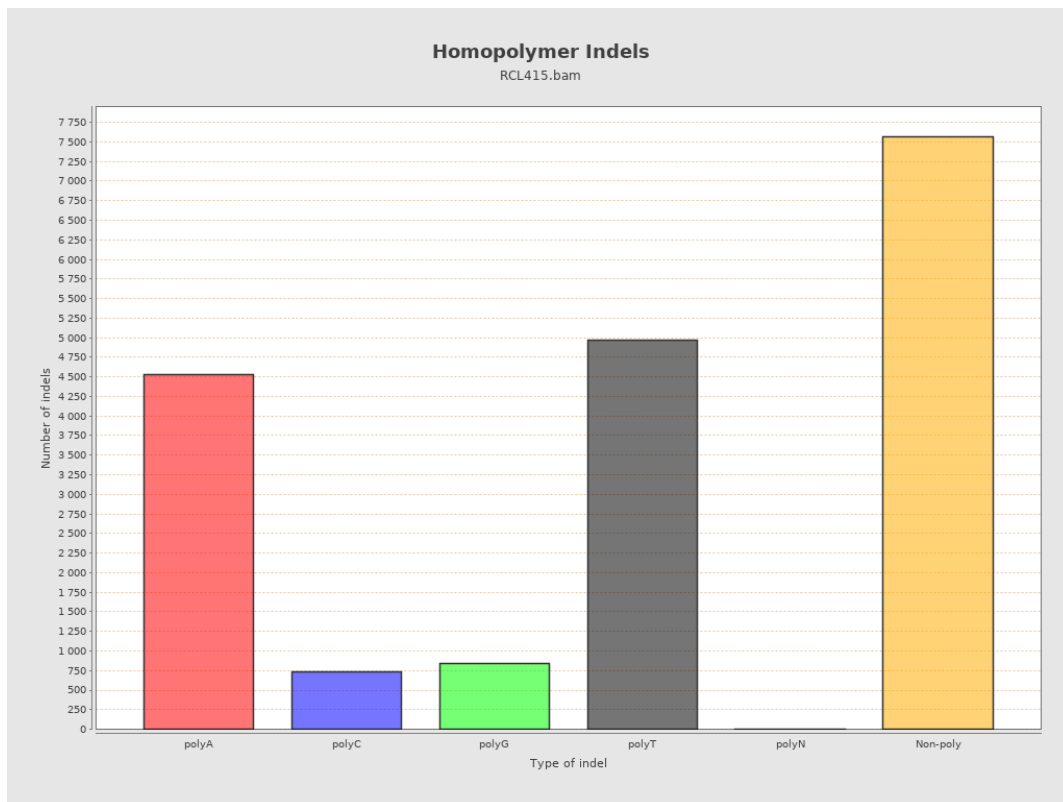
9. Results : Mapped Reads GC-content Distribution



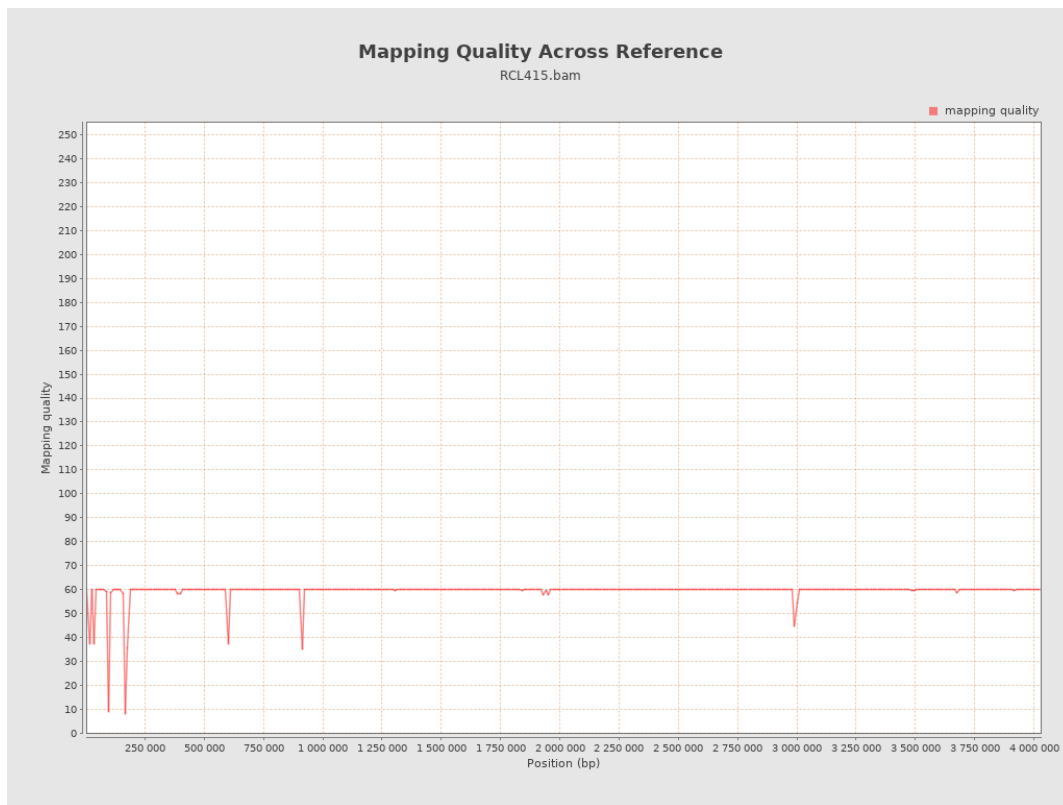
10. Results : Mapped Reads Clipping Profile



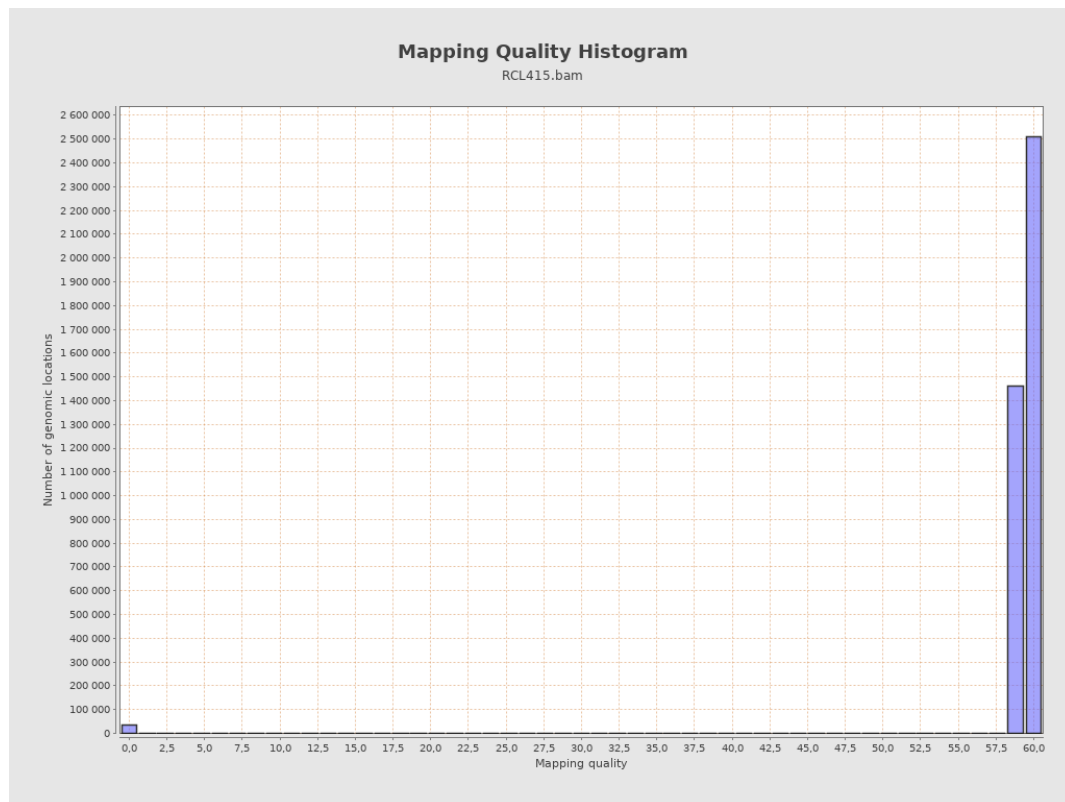
11. Results : Homopolymer Indels



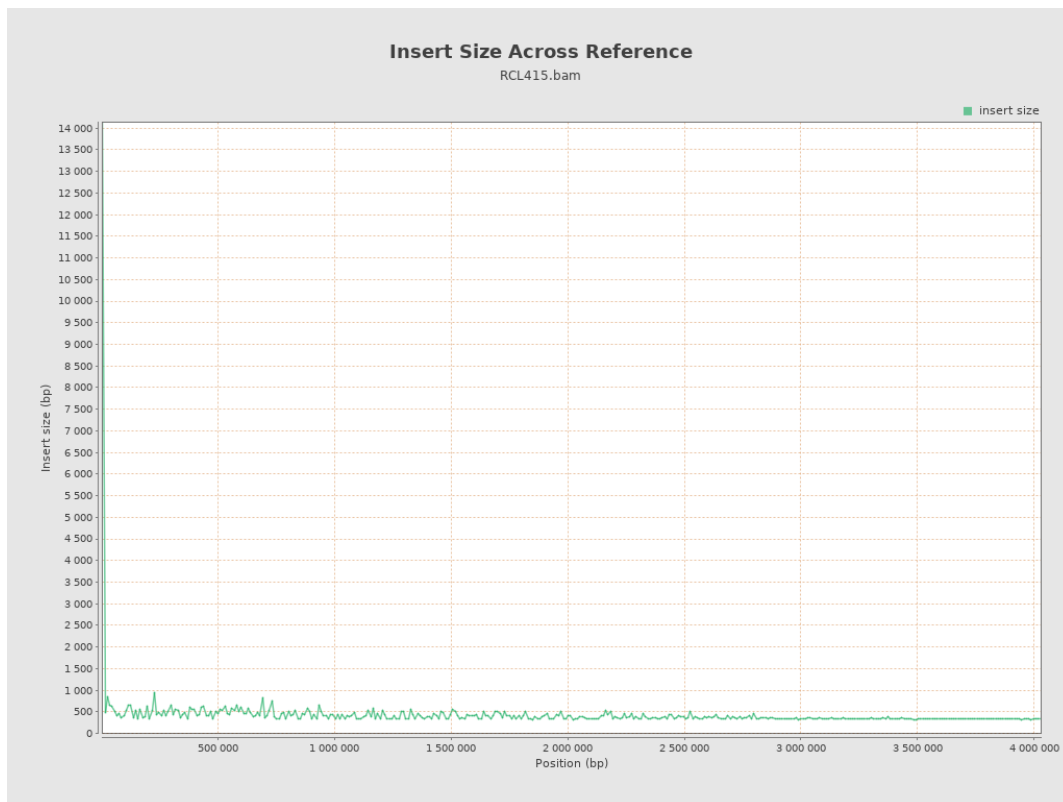
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

