

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 09:23:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081911.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR3081911 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081911.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 09:23:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081911.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,743,078
Mapped reads	2,550,428 / 92.98%
Unmapped reads	192,650 / 7.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,516 / 0.68%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	94,395 / 3.44%
Duplication rate	2.87%
Clipped reads	947,276 / 34.53%

2.2. ACGT Content

Number/percentage of A's	49,440,026 / 28.33%
Number/percentage of C's	32,767,649 / 18.78%
Number/percentage of T's	54,753,923 / 31.38%
Number/percentage of G's	37,549,301 / 21.52%
Number/percentage of N's	2,133 / 0%
GC Percentage	40.29%

2.3. Coverage

Mean	0.0564

Standard Deviation	0.426
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2.4. Mapping Quality

Mean Mapping Quality	46.94
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2.5. Mismatches and indels

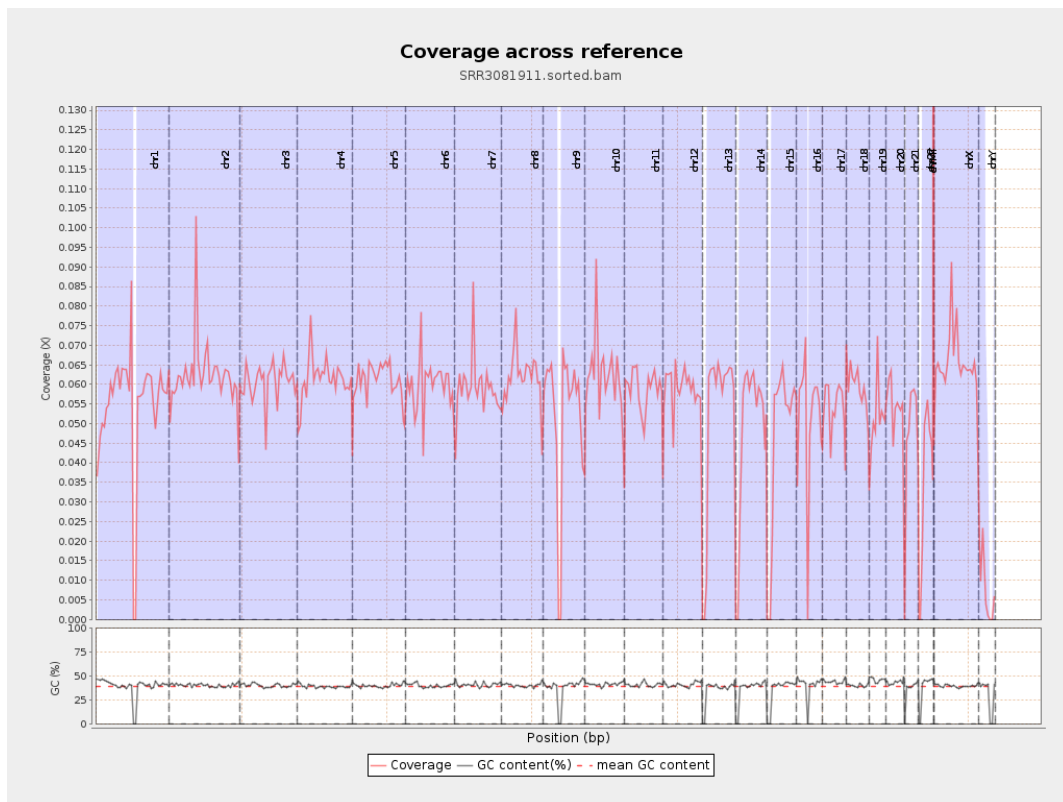
General error rate	0.87%
Mismatches	1,491,397
Insertions	13,768
Mapped reads with at least one insertion	0.53%
Deletions	40,133
Mapped reads with at least one deletion	1.56%
Homopolymer indels	48.04%

2.6. Chromosome stats

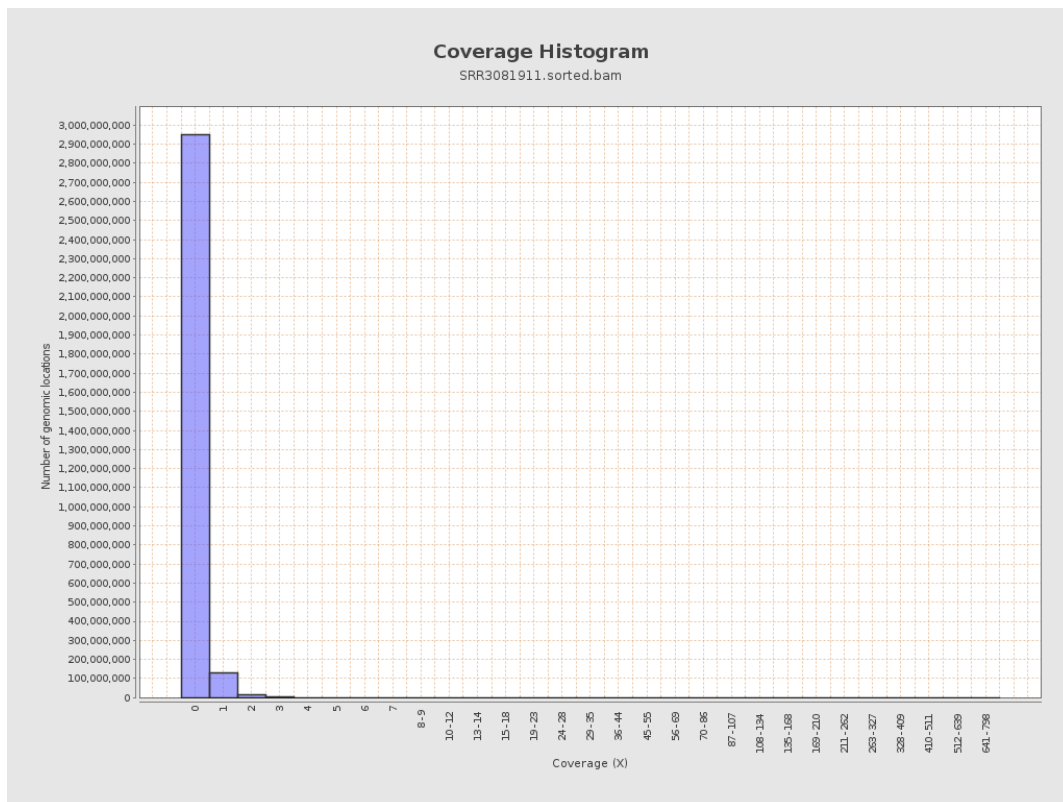
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13654079	0.0548	0.7261
chr2	243199373	15156820	0.0623	0.5041
chr3	198022430	12010666	0.0607	0.2797
chr4	191154276	11732256	0.0614	0.3066
chr5	180915260	11064607	0.0612	0.2819
chr6	171115067	10215540	0.0597	0.3273
chr7	159138663	9472285	0.0595	0.5476

chr8	146364022	9042159	0.0618	0.5856
chr9	141213431	7365904	0.0522	0.4027
chr10	135534747	8460700	0.0624	0.4369
chr11	135006516	7886059	0.0584	0.3663
chr12	133851895	7850164	0.0586	0.2789
chr13	115169878	5944715	0.0516	0.2583
chr14	107349540	5194400	0.0484	0.2635
chr15	102531392	4801372	0.0468	0.2475
chr16	90354753	4647634	0.0514	0.299
chr17	81195210	4338812	0.0534	0.2945
chr18	78077248	4653028	0.0596	0.7465
chr19	59128983	3055946	0.0517	0.552
chr20	63025520	3410587	0.0541	0.2741
chr21	48129895	2261188	0.047	0.2699
chr22	51304566	1760622	0.0343	0.2086
chrMT	16571	6813	0.4111	0.6605
chrX	155270560	10156170	0.0654	0.328
chrY	59373566	436863	0.0074	0.1625

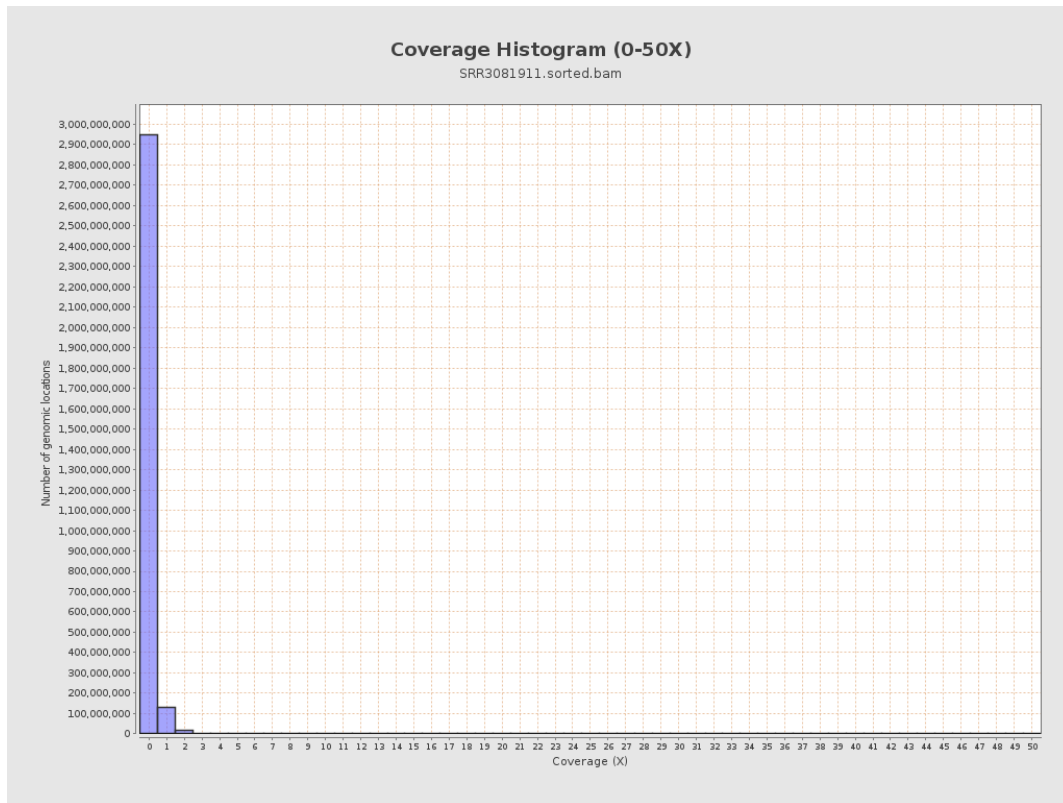
3. Results : Coverage across reference



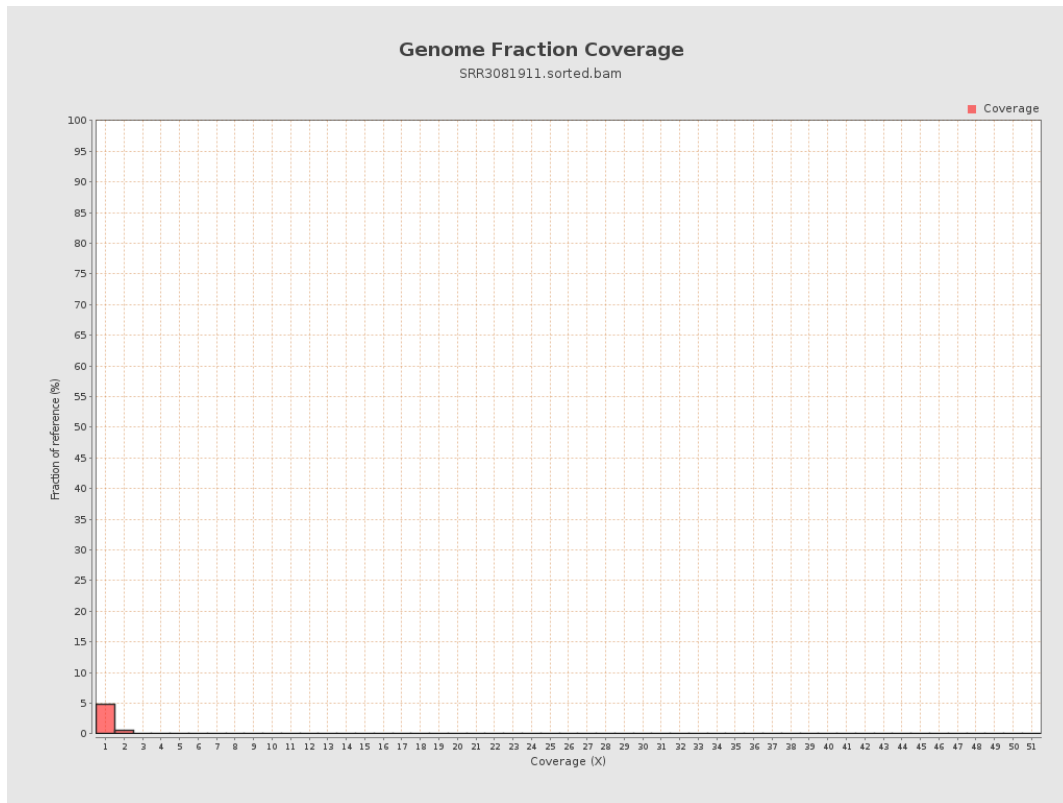
4. Results : Coverage Histogram



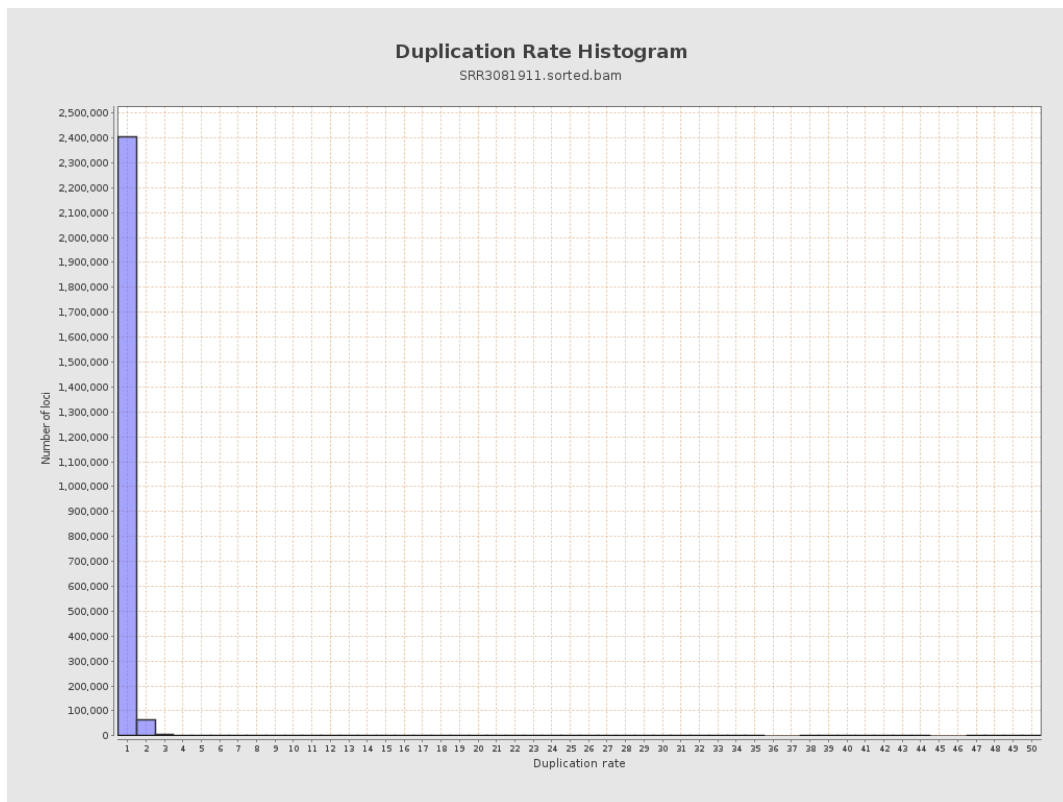
5. Results : Coverage Histogram (0-50X)



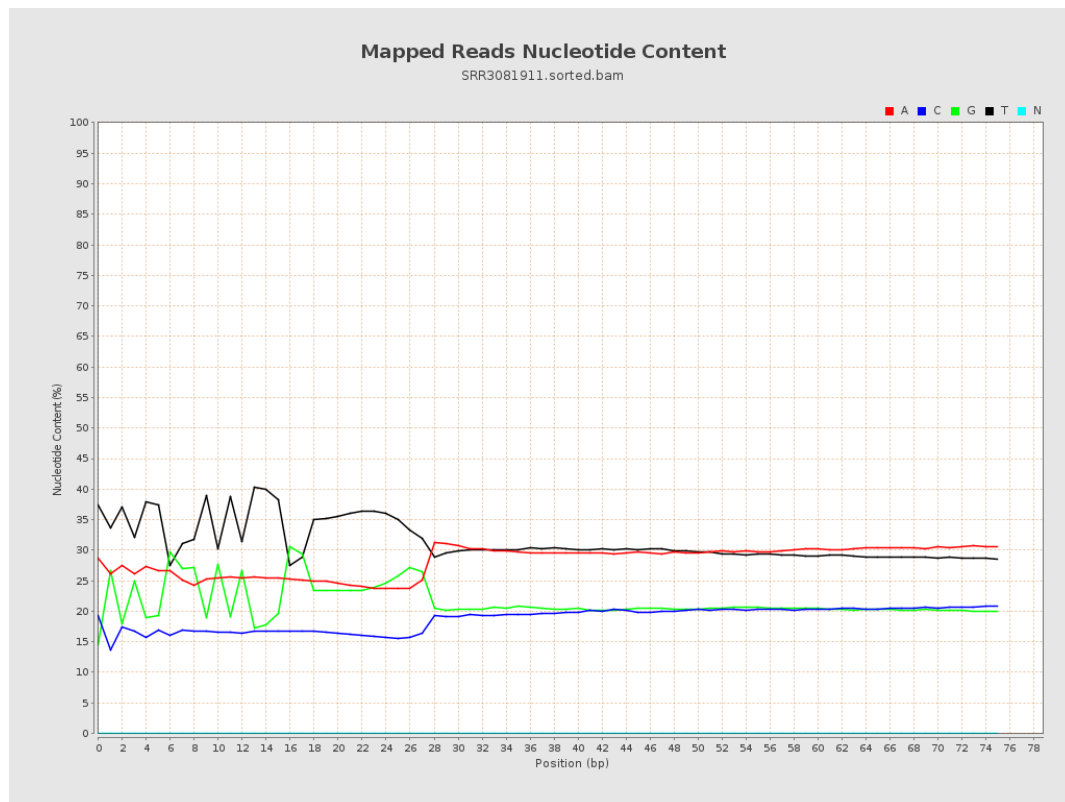
6. Results : Genome Fraction Coverage



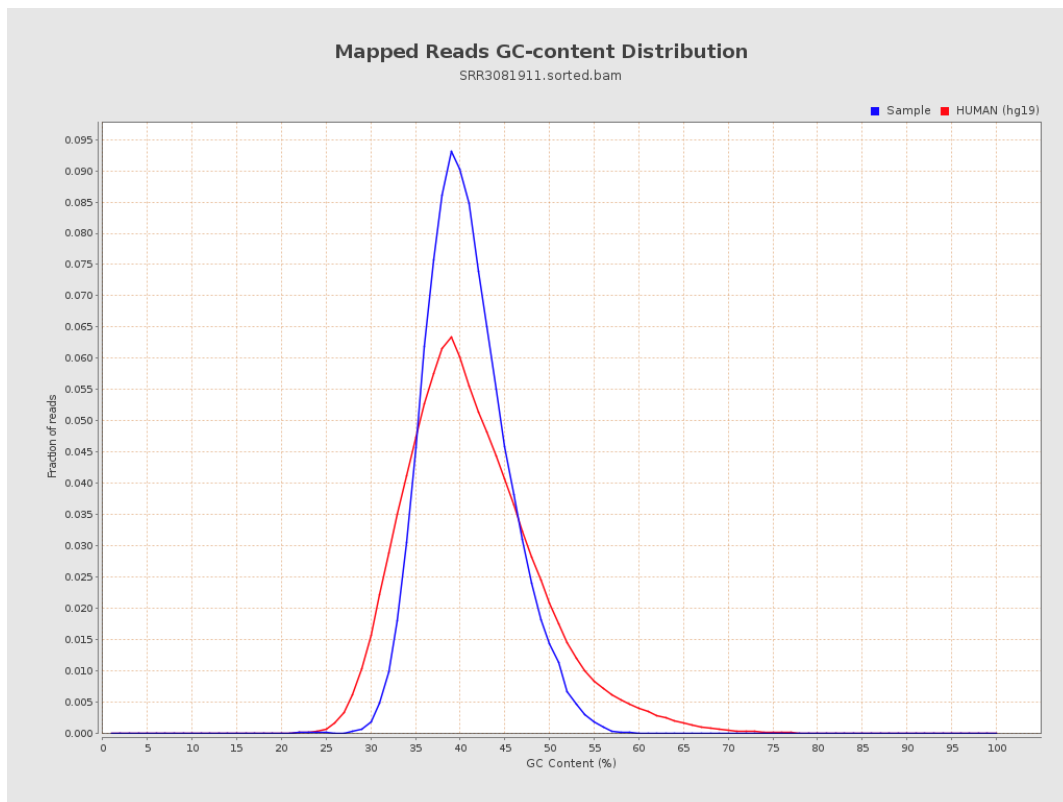
7. Results : Duplication Rate Histogram



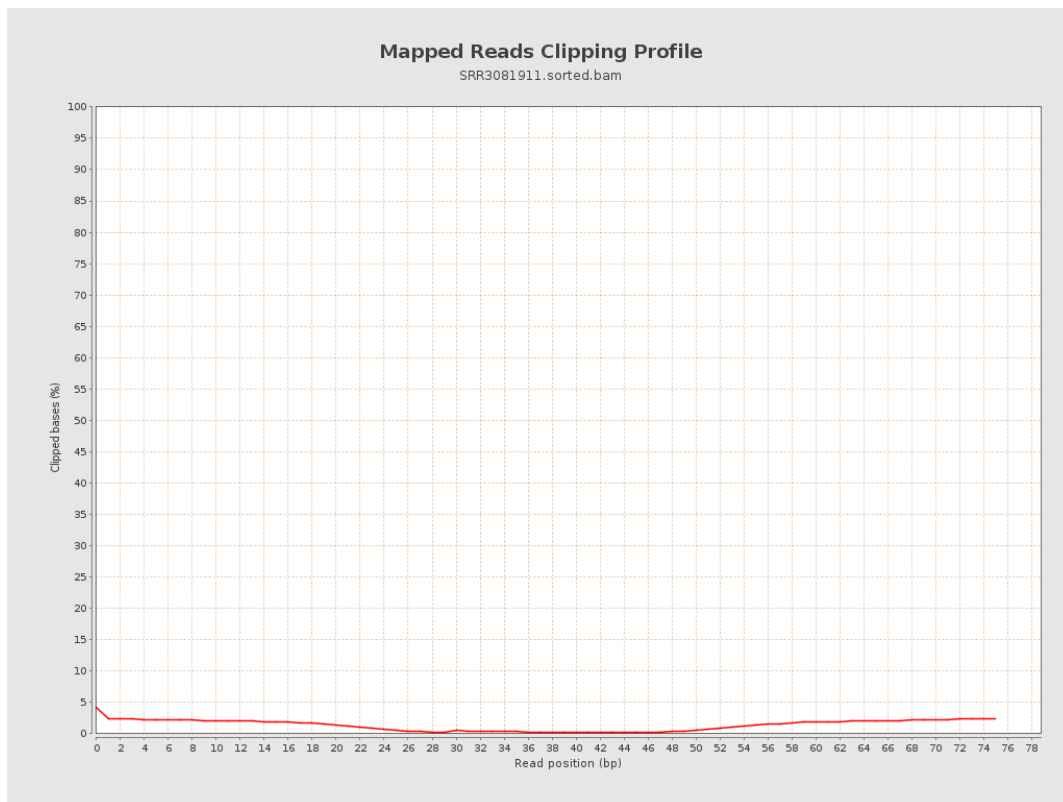
8. Results : Mapped Reads Nucleotide Content



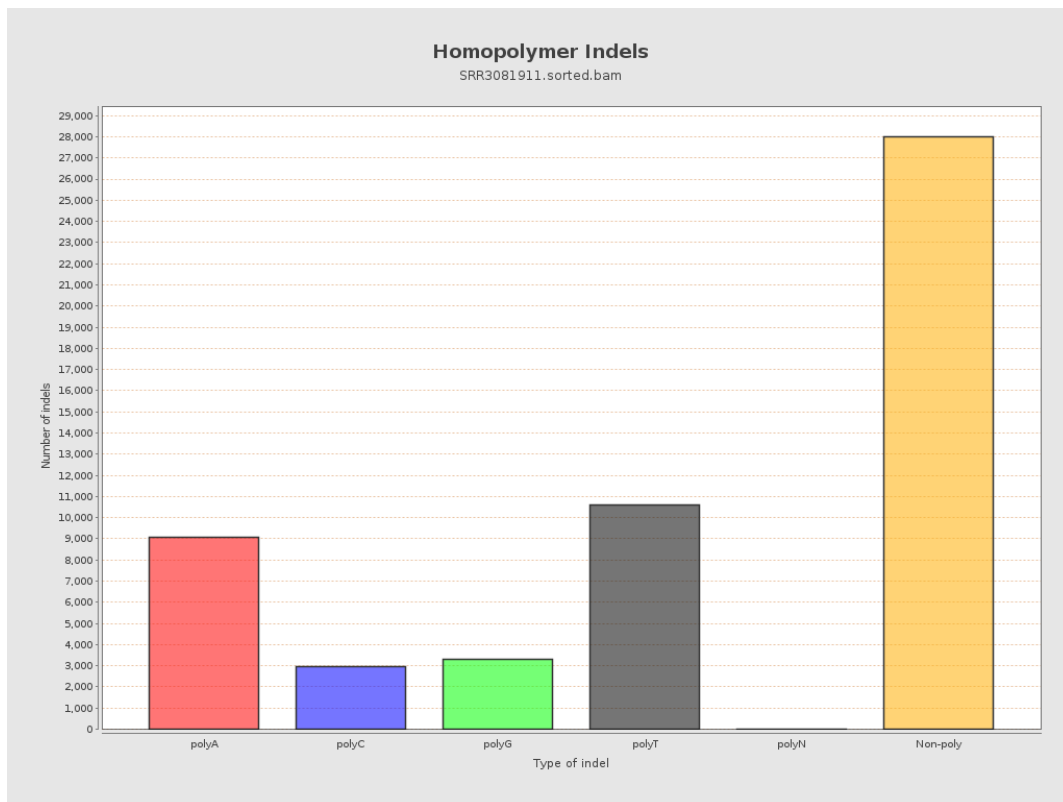
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

