

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 09:13:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231871.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_SRR6231871 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231871.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 09:13:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231871.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,146,513
Mapped reads	3,913,671 / 94.38%
Unmapped reads	232,842 / 5.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,137 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	438,338 / 10.57%
Duplication rate	9.47%
Clipped reads	1,965,339 / 47.4%

2.2. ACGT Content

Number/percentage of A's	68,060,193 / 26.72%
Number/percentage of C's	45,376,561 / 17.82%
Number/percentage of T's	83,351,531 / 32.73%
Number/percentage of G's	57,783,392 / 22.69%
Number/percentage of N's	99,667 / 0.04%
GC Percentage	40.51%

2.3. Coverage

Mean	0.0823

Standard Deviation	0.7204
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2.4. Mapping Quality

Mean Mapping Quality	46.06
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2.5. Mismatches and indels

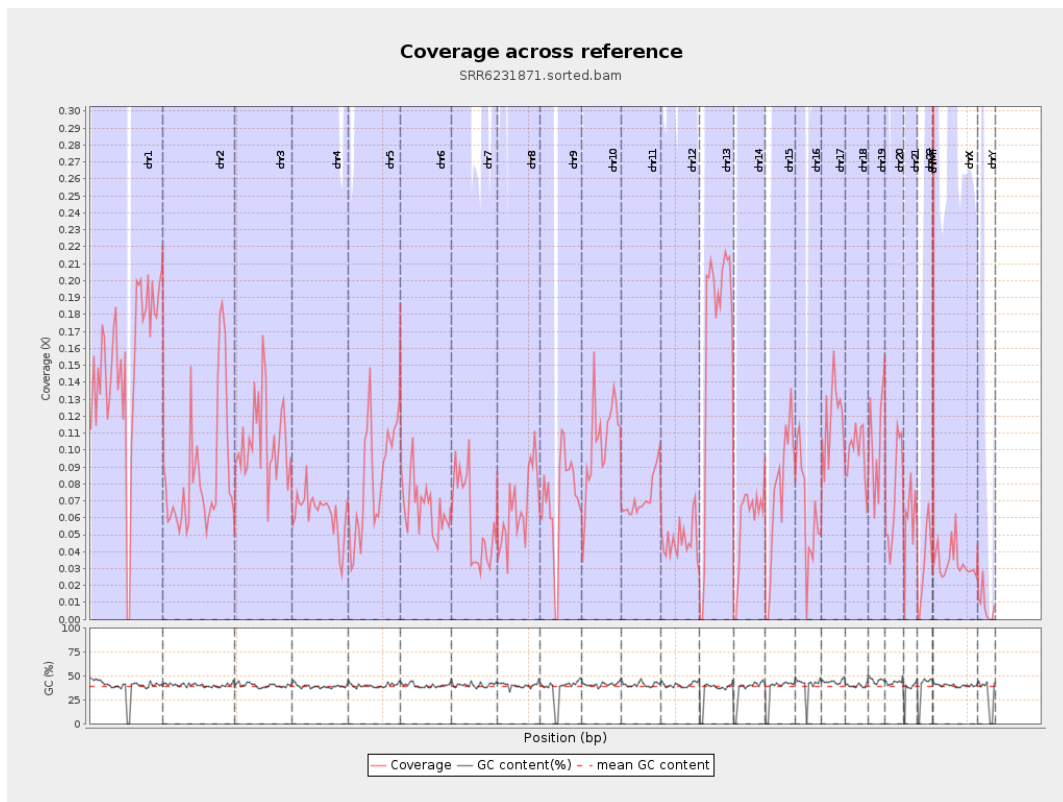
General error rate	0.62%
Mismatches	1,540,527
Insertions	16,704
Mapped reads with at least one insertion	0.42%
Deletions	57,380
Mapped reads with at least one deletion	1.45%
Homopolymer indels	44.94%

2.6. Chromosome stats

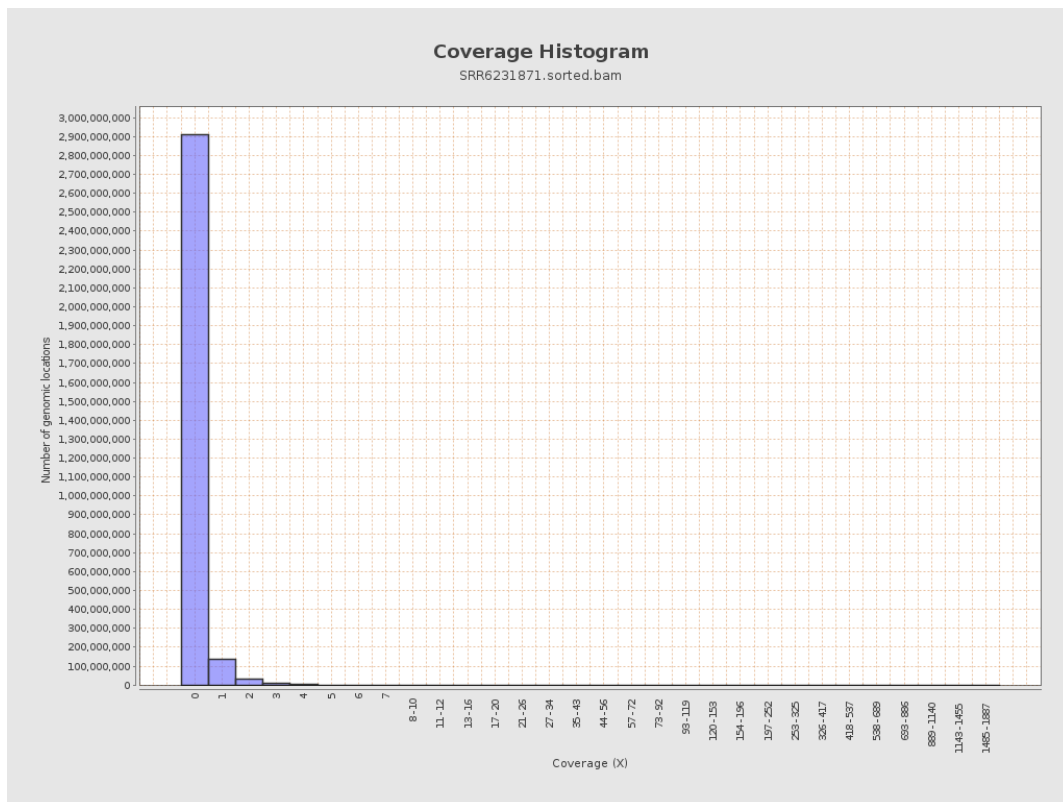
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	38061075	0.1527	1.3728
chr2	243199373	20784881	0.0855	1.0258
chr3	198022430	20710131	0.1046	0.4218
chr4	191154276	12069143	0.0631	0.3571
chr5	180915260	15276899	0.0844	0.3853
chr6	171115067	11360869	0.0664	0.4448
chr7	159138663	9245860	0.0581	0.7279

chr8	146364022	9748118	0.0666	1.1765
chr9	141213431	10123262	0.0717	0.5623
chr10	135534747	14152446	0.1044	0.6741
chr11	135006516	9738749	0.0721	0.4457
chr12	133851895	6278431	0.0469	0.312
chr13	115169878	19163061	0.1664	0.5519
chr14	107349540	6101384	0.0568	0.377
chr15	102531392	7482731	0.073	0.3809
chr16	90354753	5699722	0.0631	0.4155
chr17	81195210	9770516	0.1203	0.5158
chr18	78077248	7712494	0.0988	1.3006
chr19	59128983	6167427	0.1043	0.9245
chr20	63025520	4623685	0.0734	0.4133
chr21	48129895	2832854	0.0589	0.3339
chr22	51304566	1749285	0.0341	0.2328
chrMT	16571	153020	9.2342	6.006
chrX	155270560	5281108	0.034	0.3212
chrY	59373566	485813	0.0082	0.1889

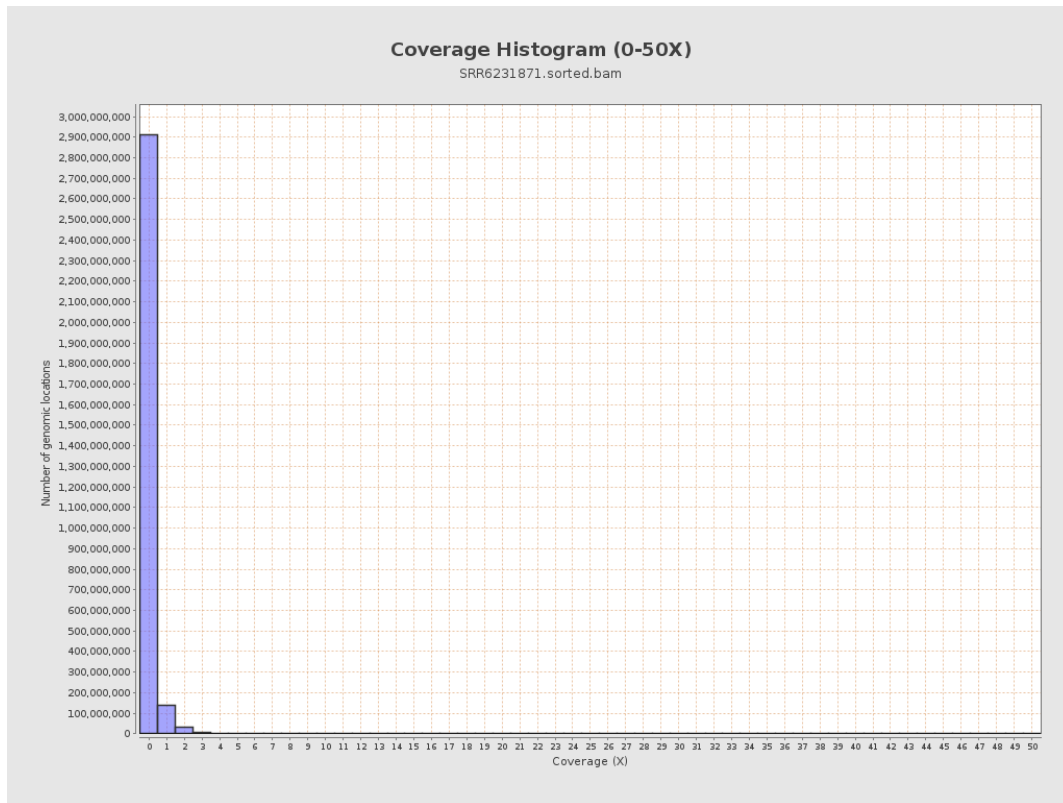
3. Results : Coverage across reference



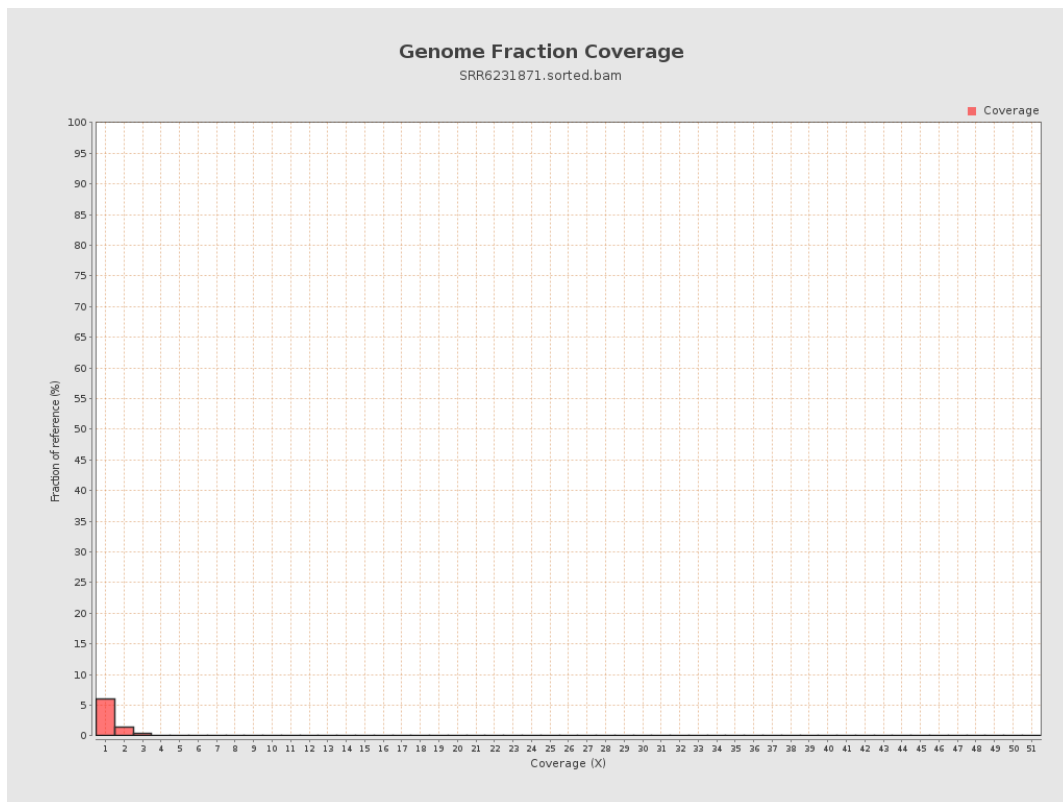
4. Results : Coverage Histogram



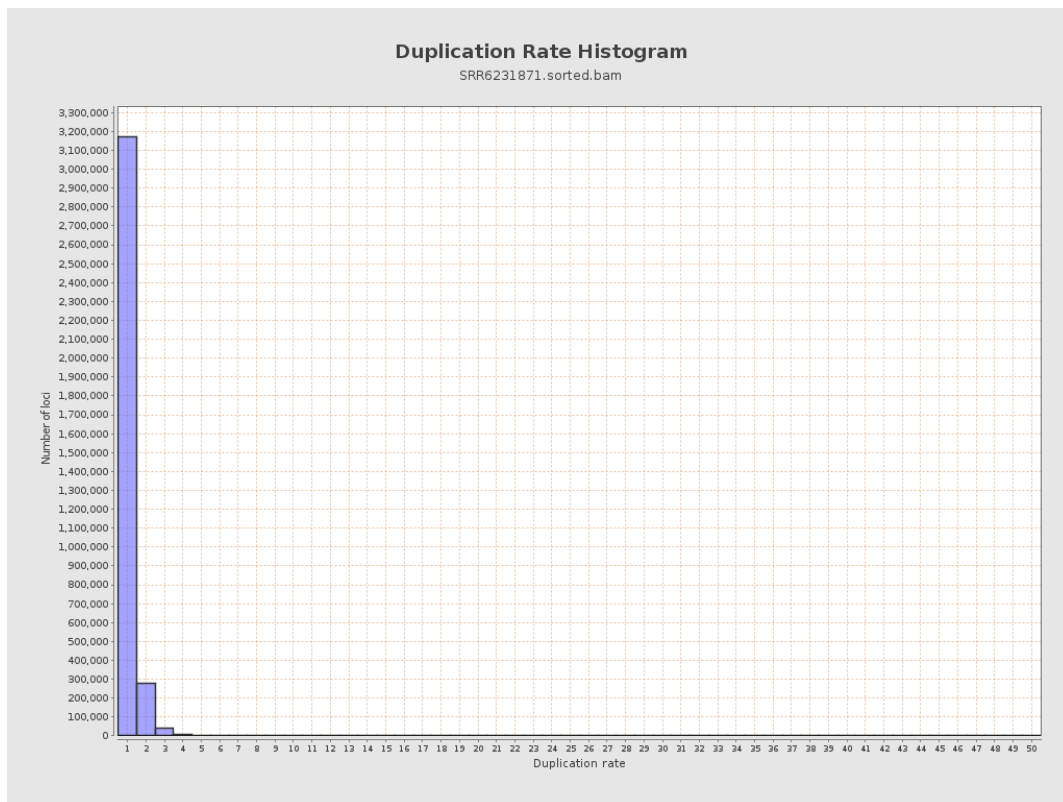
5. Results : Coverage Histogram (0-50X)



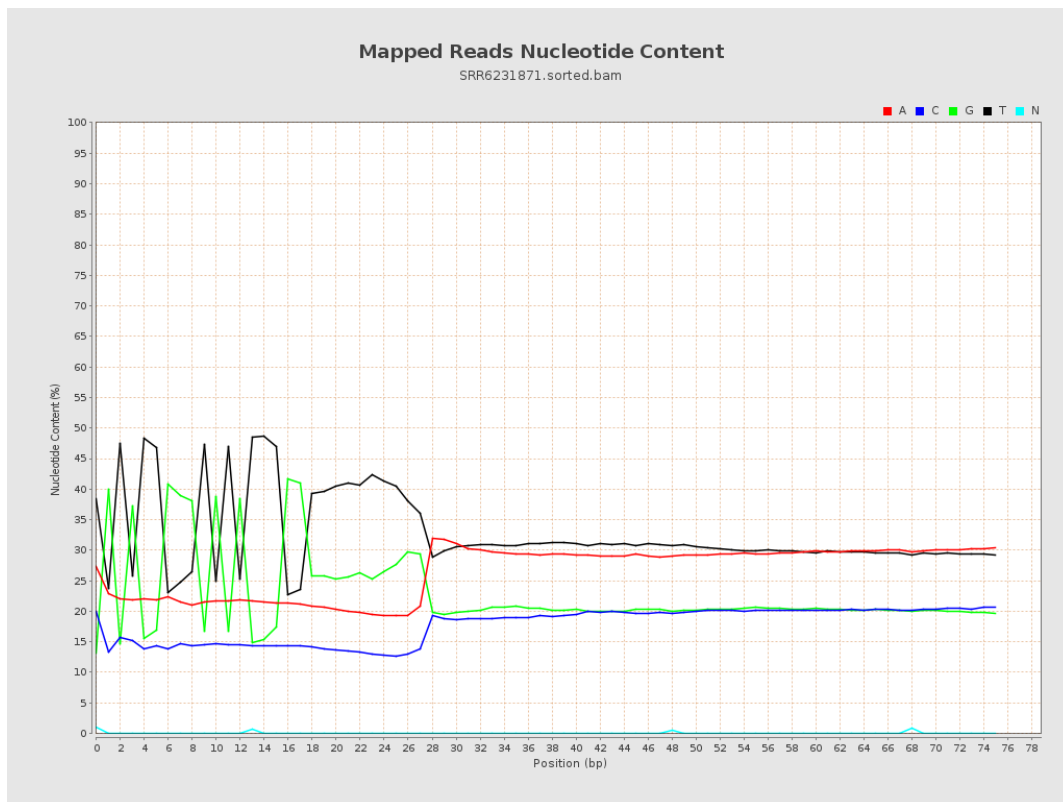
6. Results : Genome Fraction Coverage



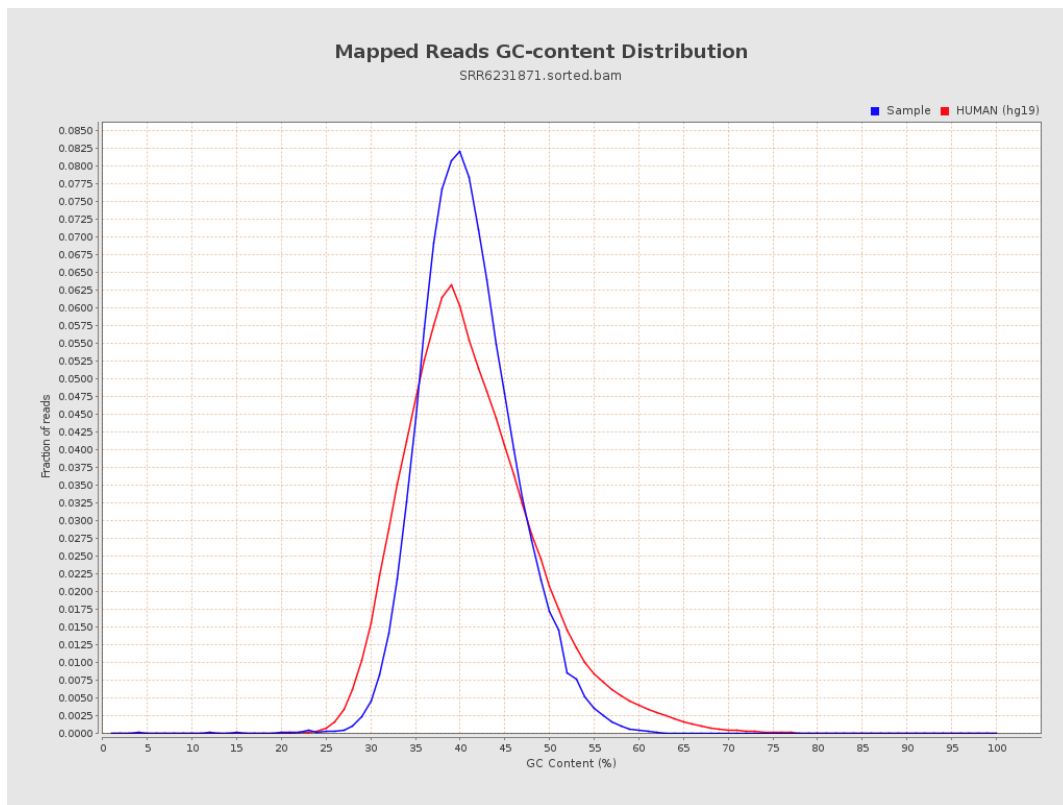
7. Results : Duplication Rate Histogram



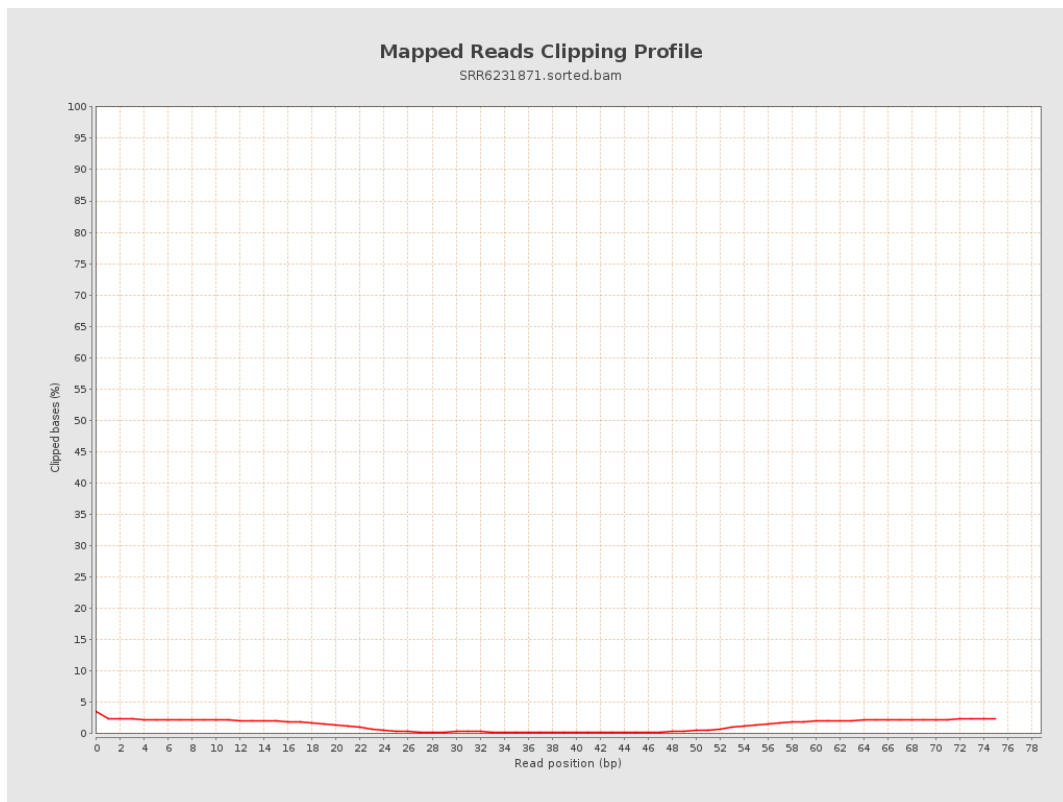
8. Results : Mapped Reads Nucleotide Content



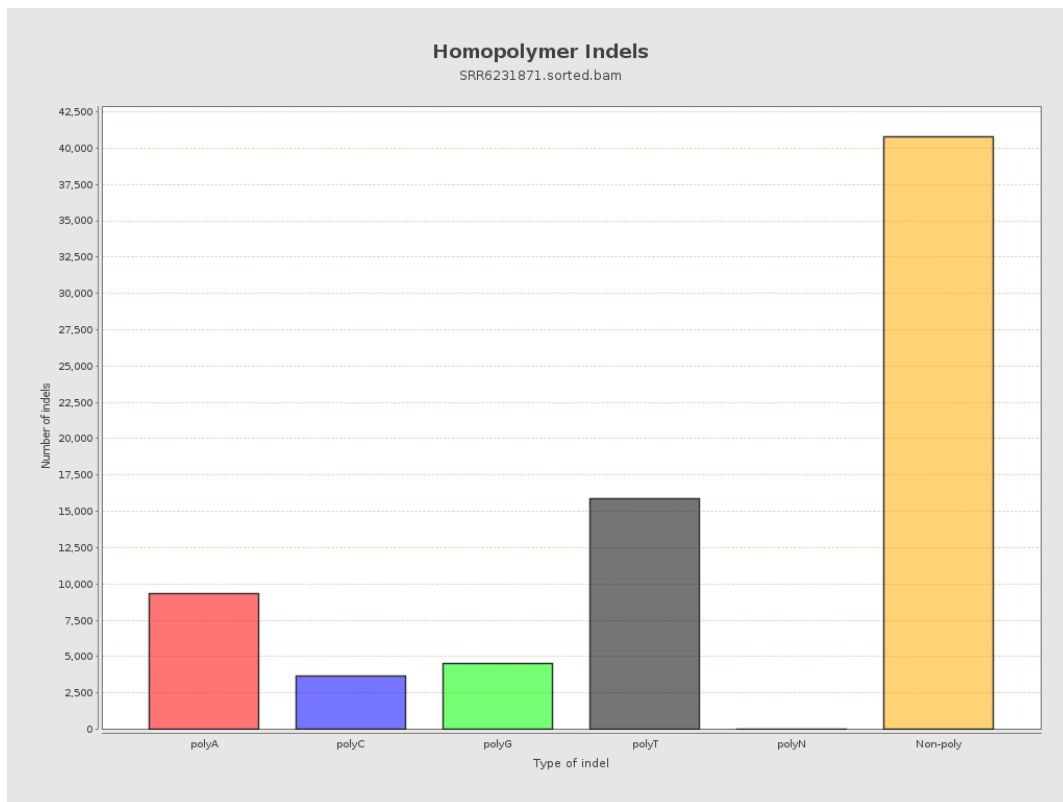
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

