

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 01:25:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231768.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_SRR6231768 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231768.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 01:25:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231768.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,057,036
Mapped reads	628,014 / 59.41%
Unmapped reads	429,022 / 40.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,088 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	16,878 / 1.6%
Duplication rate	2.11%
Clipped reads	362,631 / 34.31%

2.2. ACGT Content

Number/percentage of A's	11,103,268 / 28.16%
Number/percentage of C's	6,429,604 / 16.31%
Number/percentage of T's	12,788,126 / 32.43%
Number/percentage of G's	9,110,518 / 23.1%
Number/percentage of N's	736 / 0%
GC Percentage	39.41%

2.3. Coverage

Mean	0.0127

Standard Deviation	0.1597
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2.4. Mapping Quality

Mean Mapping Quality	46.04
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2.5. Mismatches and indels

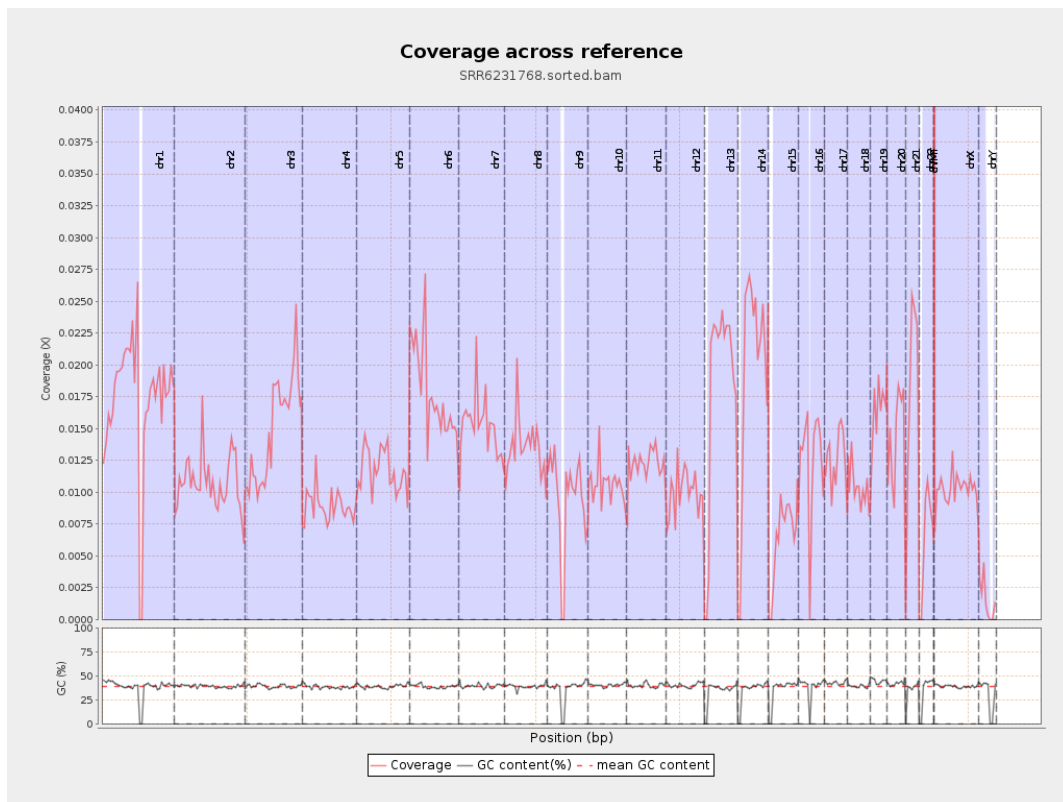
General error rate	1.09%
Mismatches	424,598
Insertions	3,082
Mapped reads with at least one insertion	0.49%
Deletions	14,333
Mapped reads with at least one deletion	2.25%
Homopolymer indels	44.18%

2.6. Chromosome stats

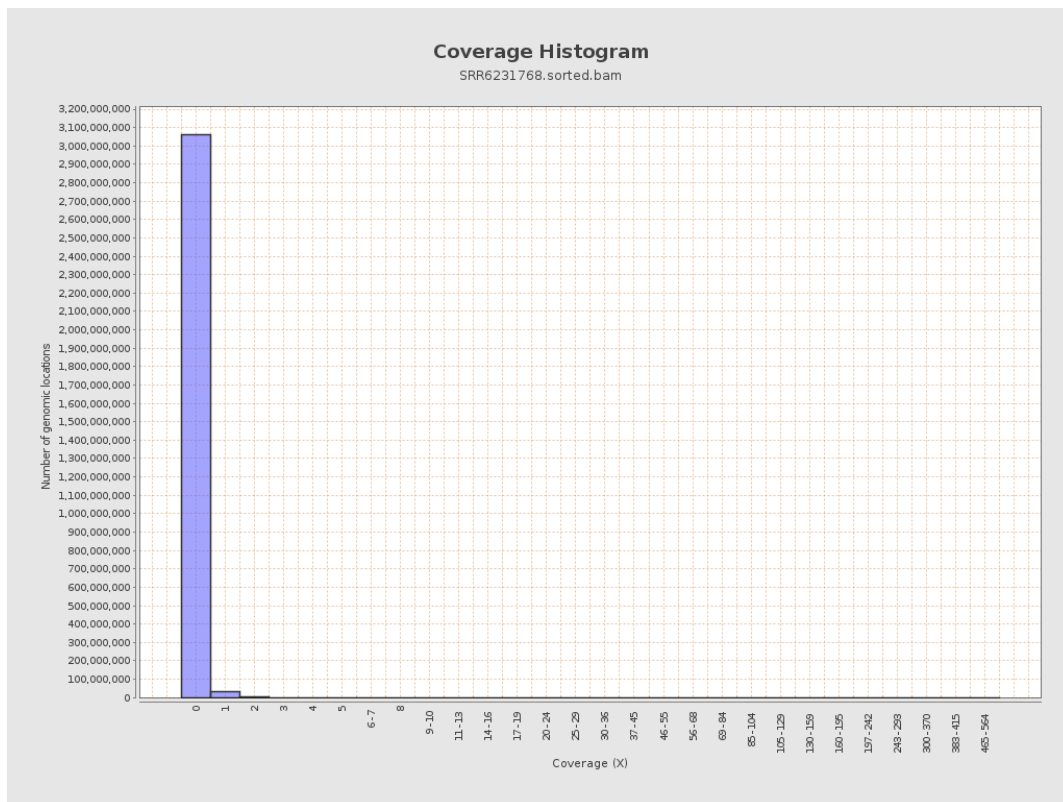
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4316393	0.0173	0.249
chr2	243199373	2619140	0.0108	0.1337
chr3	198022430	2957258	0.0149	0.1286
chr4	191154276	1693204	0.0089	0.0998
chr5	180915260	2122851	0.0117	0.1181
chr6	171115067	3042041	0.0178	0.1528
chr7	159138663	2405636	0.0151	0.1693

chr8	146364022	1975899	0.0135	0.3543
chr9	141213431	1345760	0.0095	0.1136
chr10	135534747	1430525	0.0106	0.1213
chr11	135006516	1659841	0.0123	0.1287
chr12	133851895	1323784	0.0099	0.1048
chr13	115169878	2081483	0.0181	0.1429
chr14	107349540	2101820	0.0196	0.1507
chr15	102531392	658232	0.0064	0.0844
chr16	90354753	1107441	0.0123	0.1207
chr17	81195210	1018907	0.0125	0.1204
chr18	78077248	807689	0.0103	0.1905
chr19	59128983	970774	0.0164	0.1675
chr20	63025520	895541	0.0142	0.1271
chr21	48129895	878958	0.0183	0.1438
chr22	51304566	331485	0.0065	0.0841
chrMT	16571	27109	1.6359	1.6337
chrX	155270560	1596661	0.0103	0.1107
chrY	59373566	88045	0.0015	0.0442

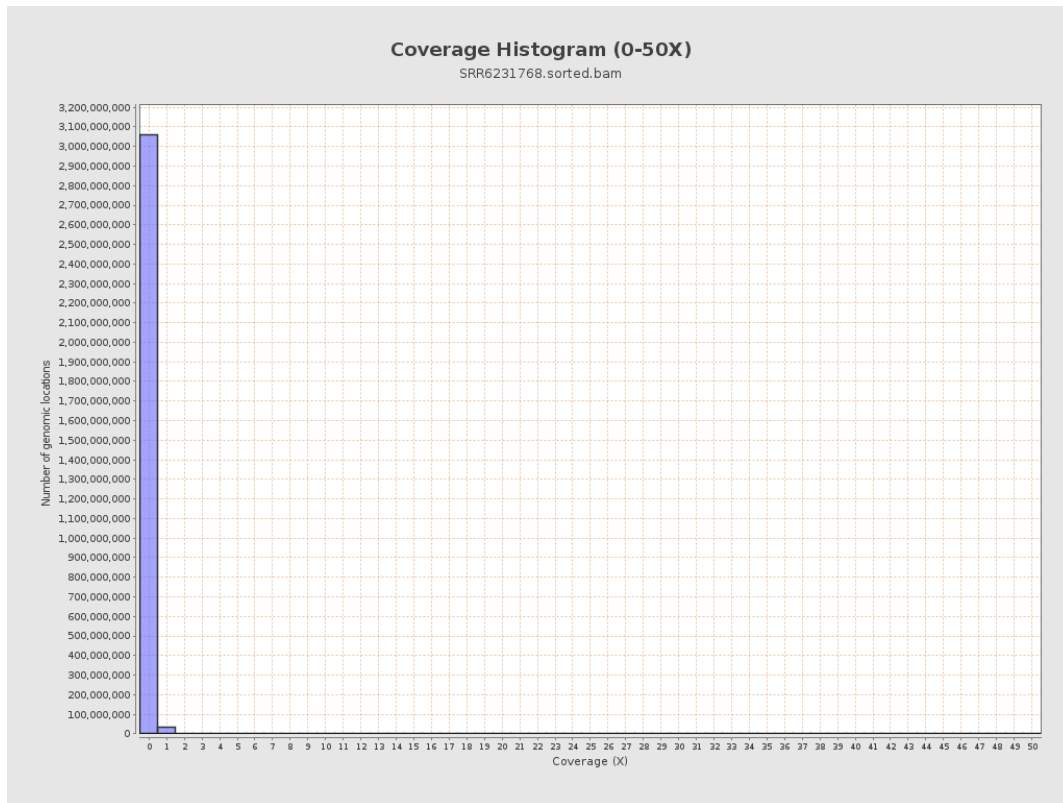
3. Results : Coverage across reference



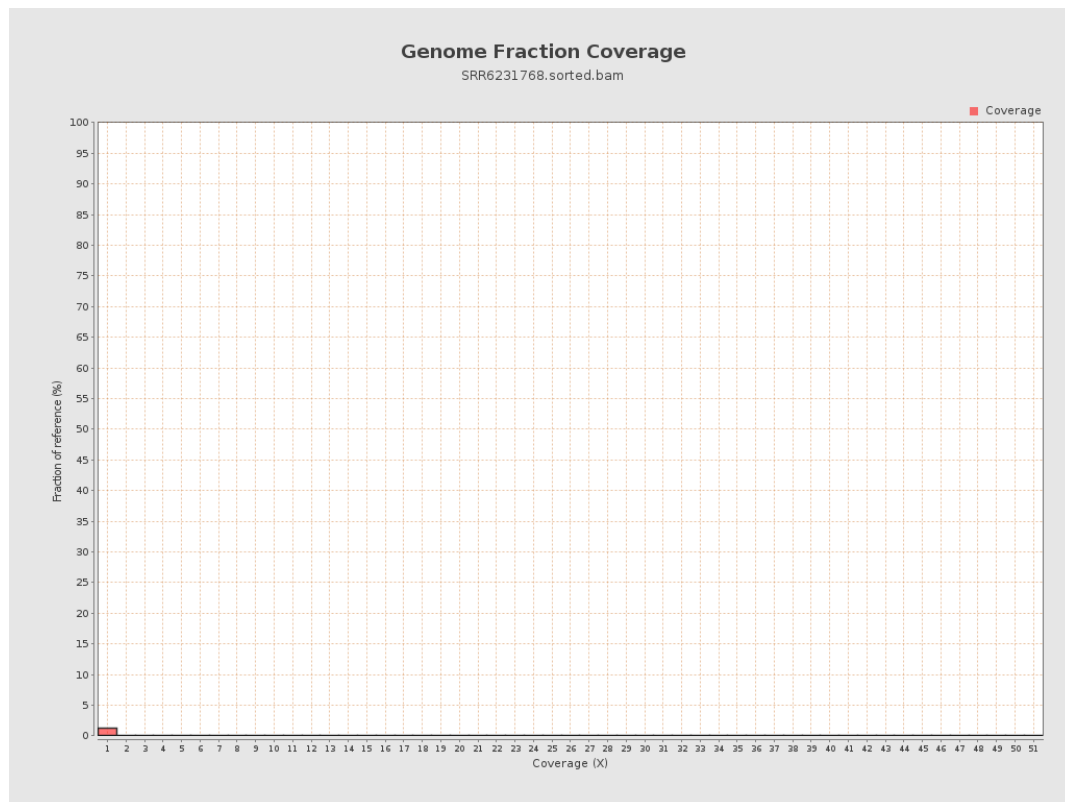
4. Results : Coverage Histogram



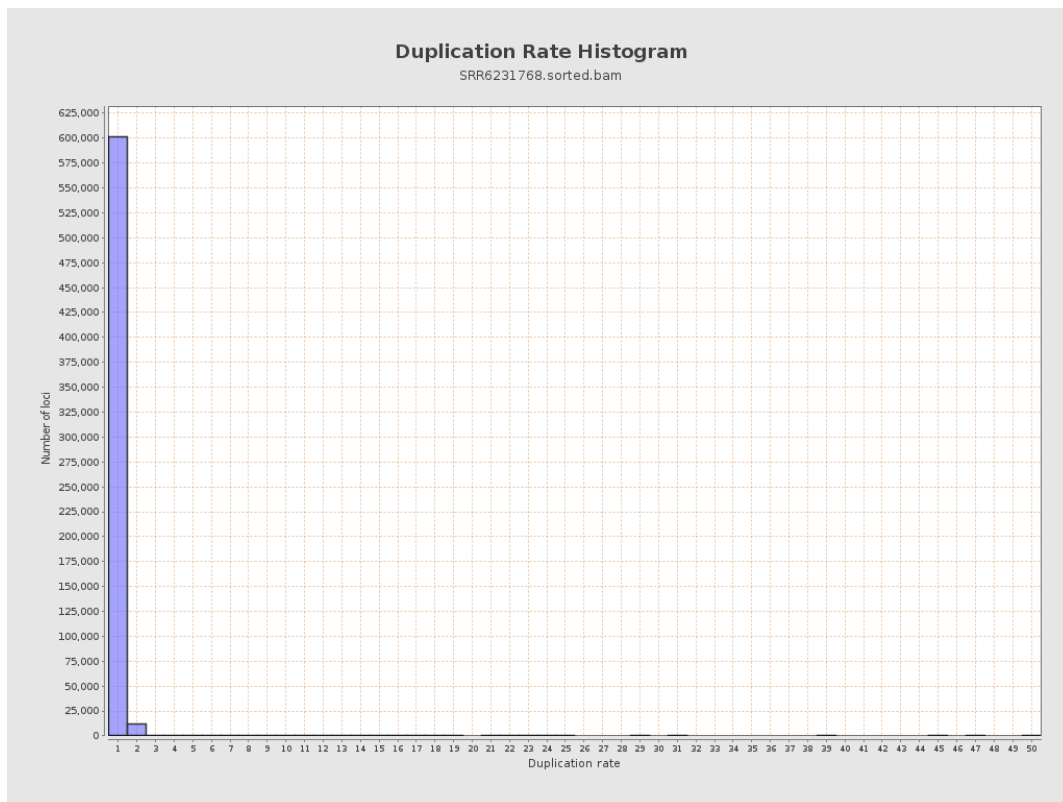
5. Results : Coverage Histogram (0-50X)



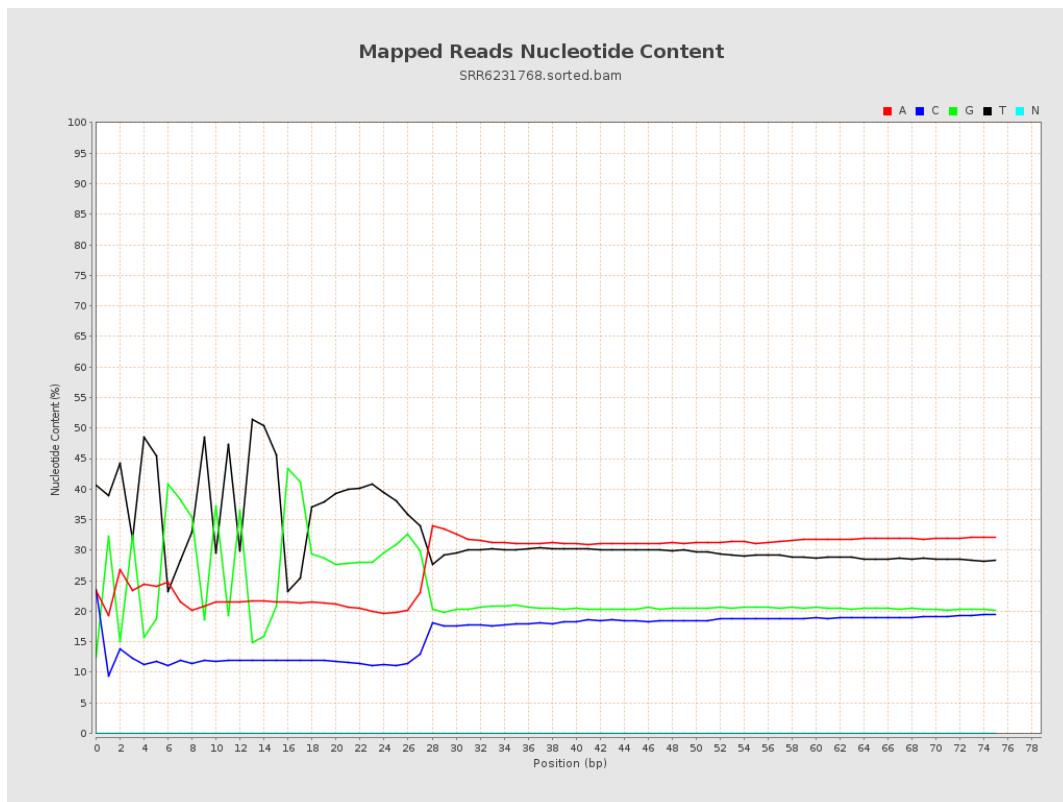
6. Results : Genome Fraction Coverage



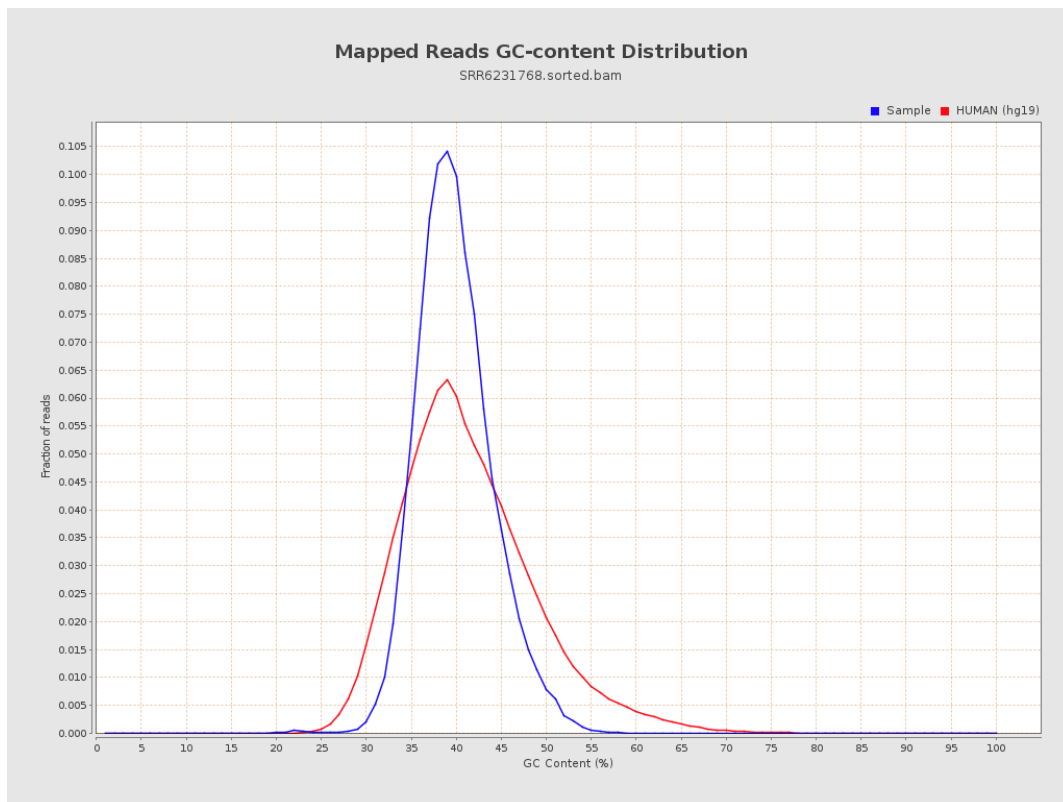
7. Results : Duplication Rate Histogram



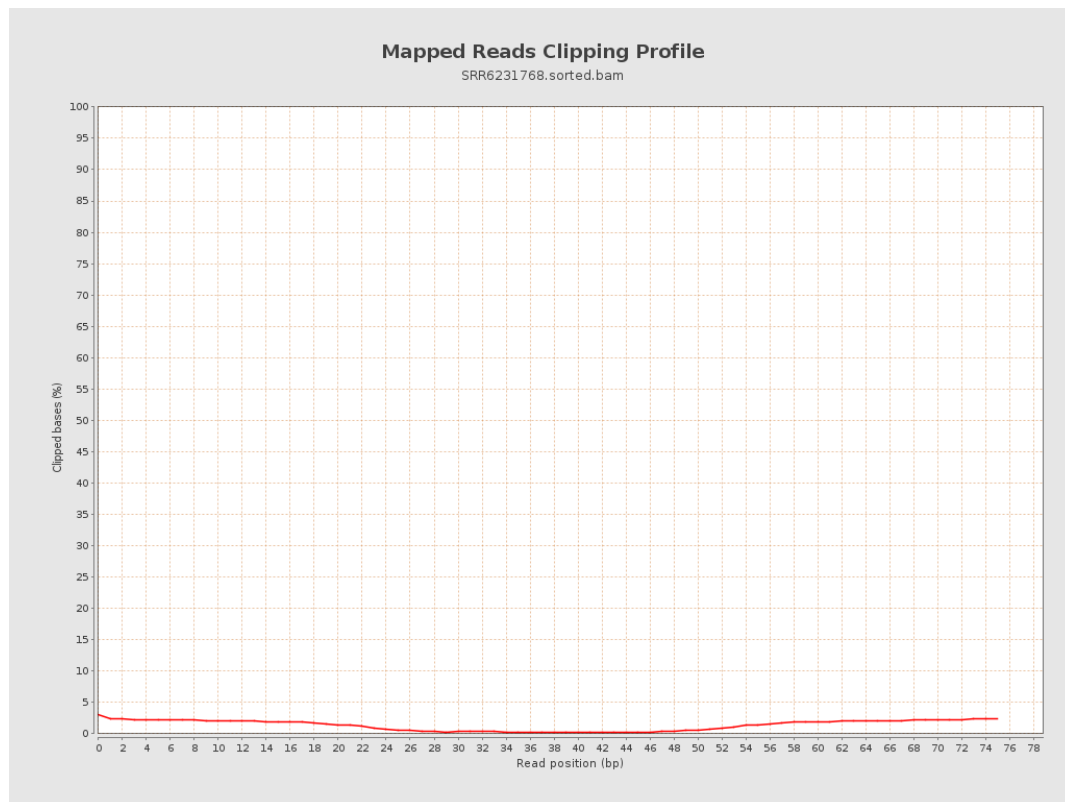
8. Results : Mapped Reads Nucleotide Content



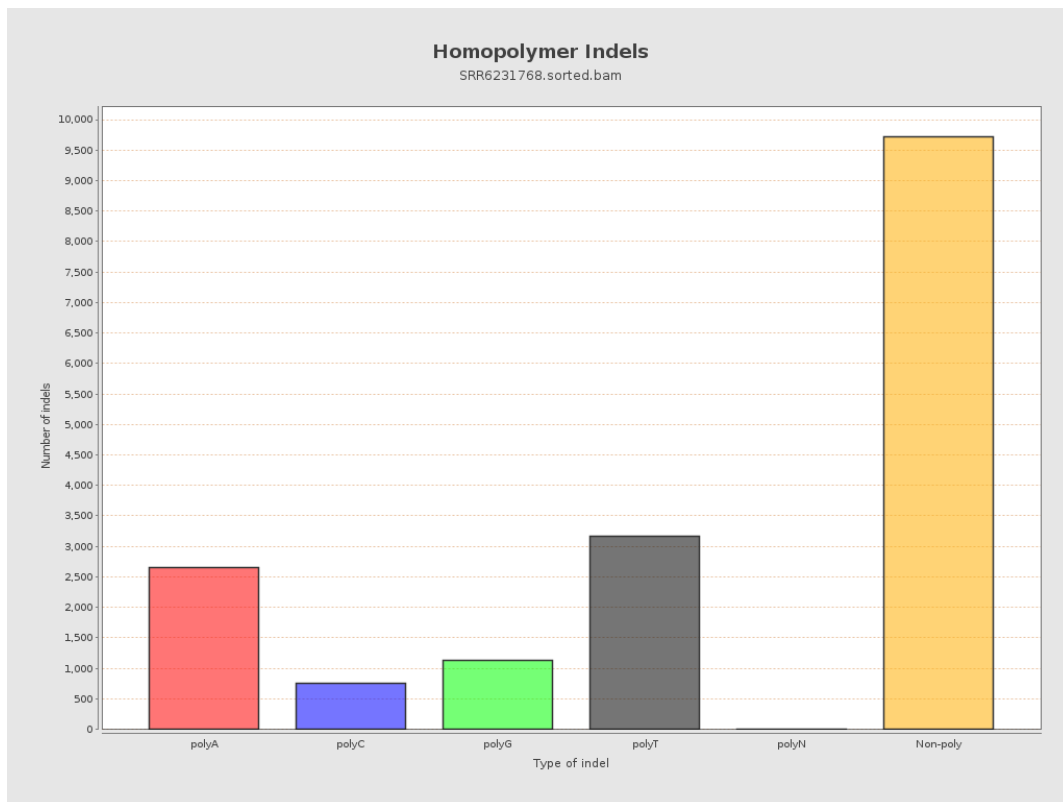
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

