

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 08:33:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231861.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_SRR6231861 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231861.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 08:33:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231861.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	838,383
Mapped reads	509,015 / 60.71%
Unmapped reads	329,368 / 39.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,625 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	13,380 / 1.6%
Duplication rate	2.2%
Clipped reads	245,598 / 29.29%

2.2. ACGT Content

Number/percentage of A's	9,346,954 / 28.07%
Number/percentage of C's	5,754,678 / 17.28%
Number/percentage of T's	10,818,585 / 32.49%
Number/percentage of G's	7,379,282 / 22.16%
Number/percentage of N's	1,491 / 0%
GC Percentage	39.44%

2.3. Coverage

Mean	0.0108

Standard Deviation	0.1349
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2.4. Mapping Quality

Mean Mapping Quality	44.05
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2.5. Mismatches and indels

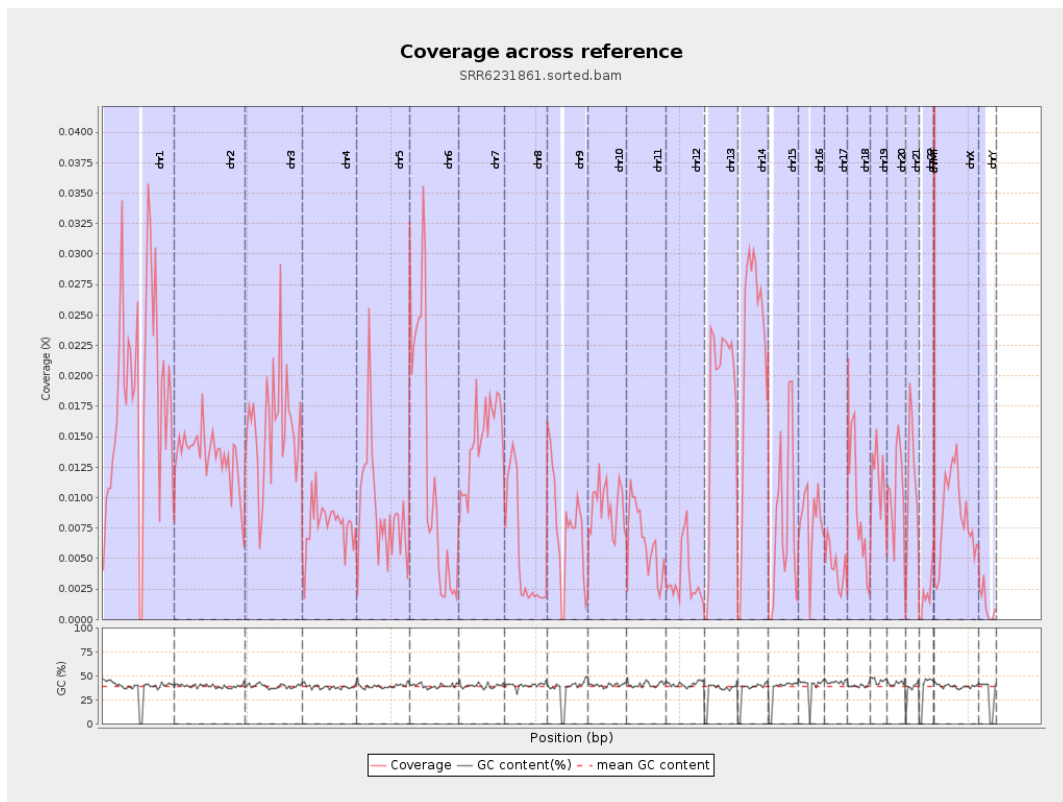
General error rate	0.92%
Mismatches	301,616
Insertions	2,819
Mapped reads with at least one insertion	0.55%
Deletions	10,403
Mapped reads with at least one deletion	2.02%
Homopolymer indels	44.34%

2.6. Chromosome stats

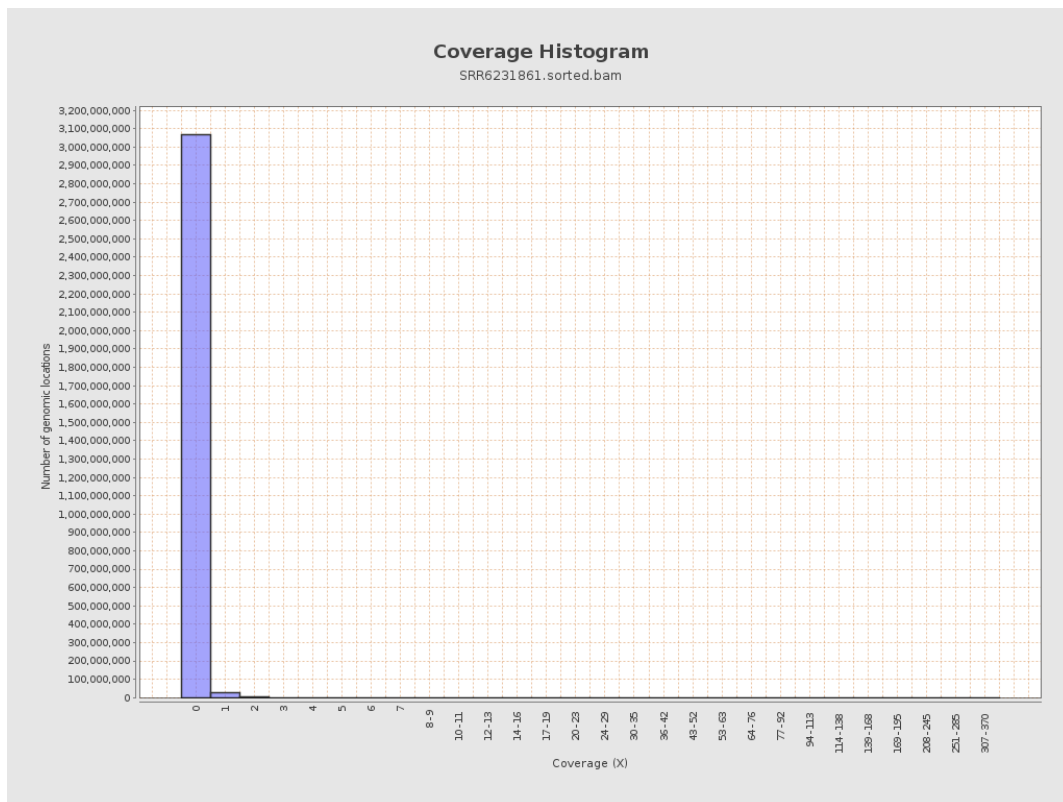
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4490183	0.018	0.2002
chr2	243199373	3258124	0.0134	0.152
chr3	198022430	3148855	0.0159	0.1341
chr4	191154276	1483199	0.0078	0.0938
chr5	180915260	1636033	0.009	0.1012
chr6	171115067	2136463	0.0125	0.1339
chr7	159138663	2345900	0.0147	0.163

chr8	146364022	777717	0.0053	0.2362
chr9	141213431	1091940	0.0077	0.102
chr10	135534747	1248024	0.0092	0.1105
chr11	135006516	862101	0.0064	0.0892
chr12	133851895	442565	0.0033	0.0617
chr13	115169878	2072027	0.018	0.143
chr14	107349540	2355809	0.0219	0.1603
chr15	102531392	766339	0.0075	0.0924
chr16	90354753	728820	0.0081	0.0998
chr17	81195210	350296	0.0043	0.0707
chr18	78077248	725466	0.0093	0.1555
chr19	59128983	667304	0.0113	0.1315
chr20	63025520	661393	0.0105	0.1109
chr21	48129895	552201	0.0115	0.1145
chr22	51304566	114028	0.0022	0.049
chrMT	16571	16934	1.0219	1.1666
chrX	155270560	1315980	0.0085	0.0996
chrY	59373566	71679	0.0012	0.0404

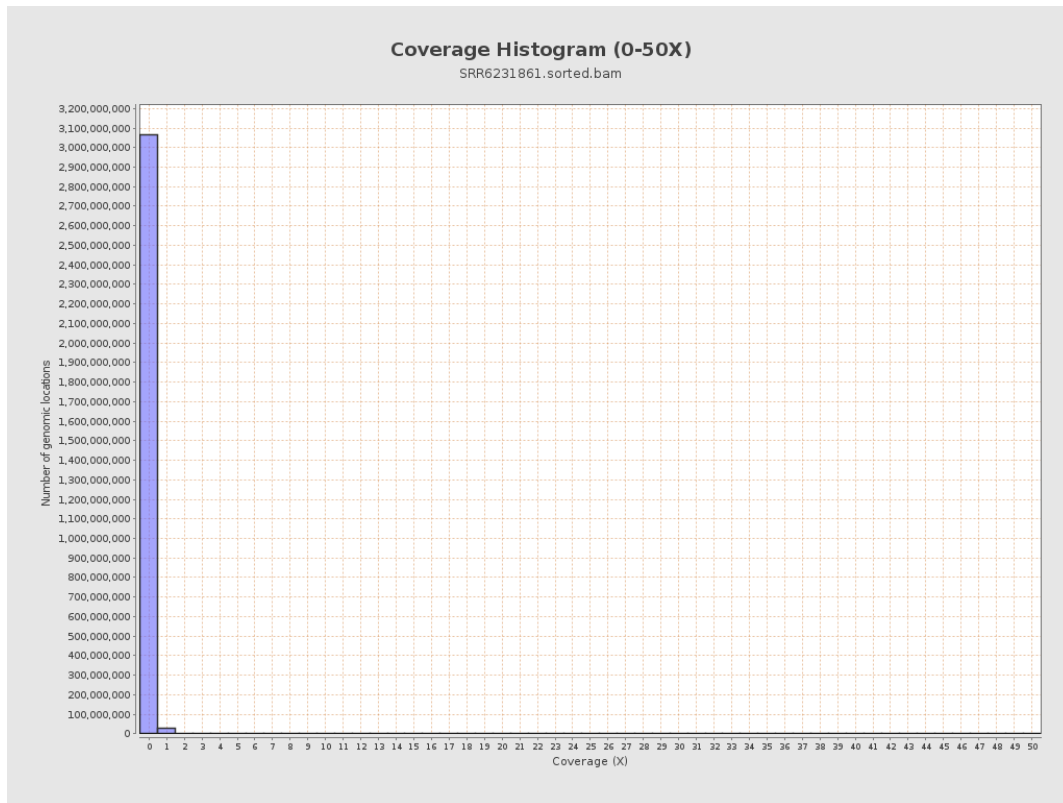
3. Results : Coverage across reference



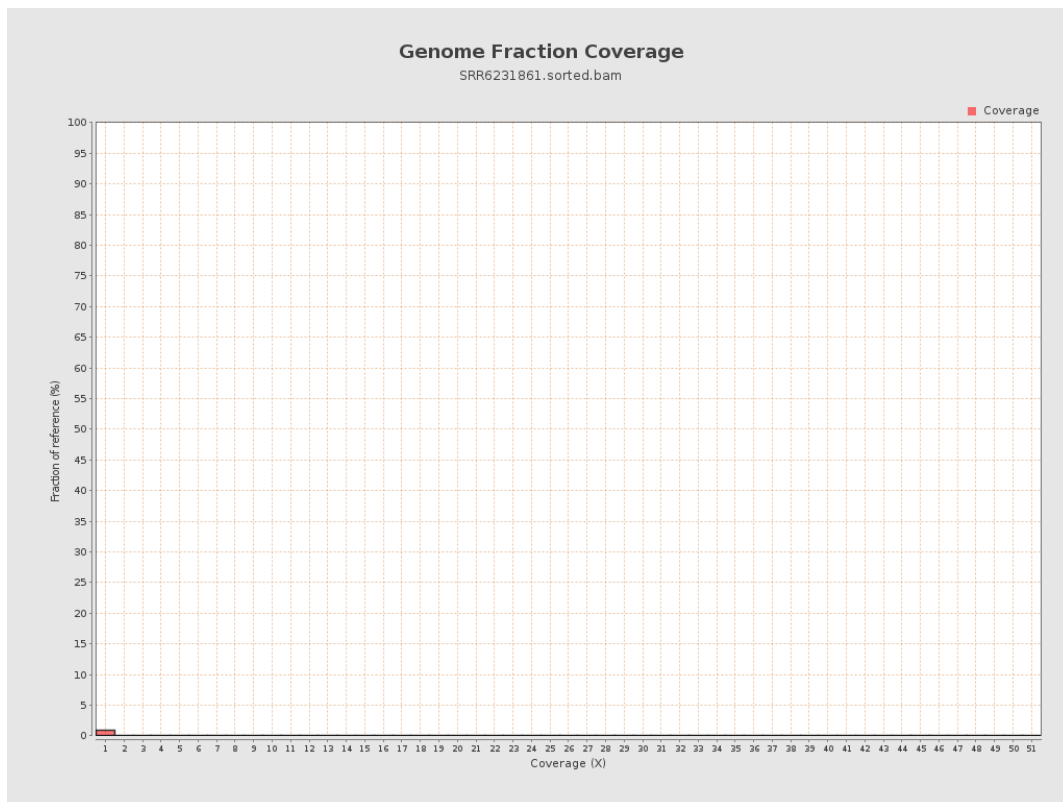
4. Results : Coverage Histogram



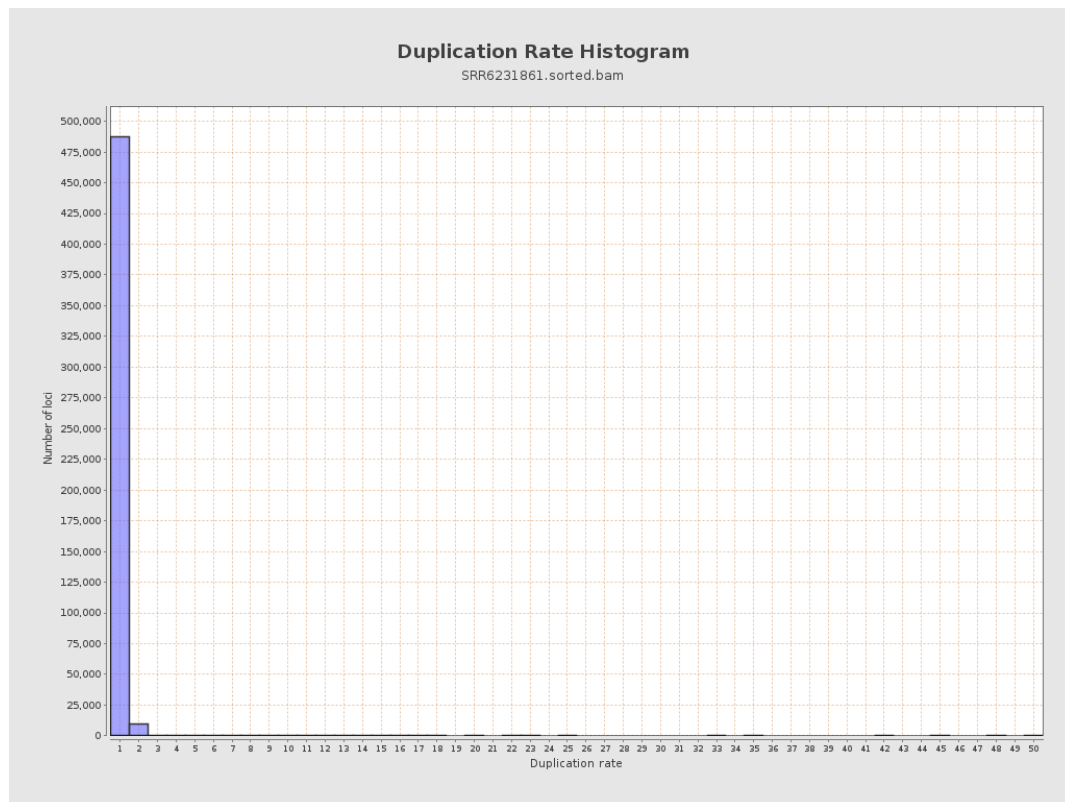
5. Results : Coverage Histogram (0-50X)



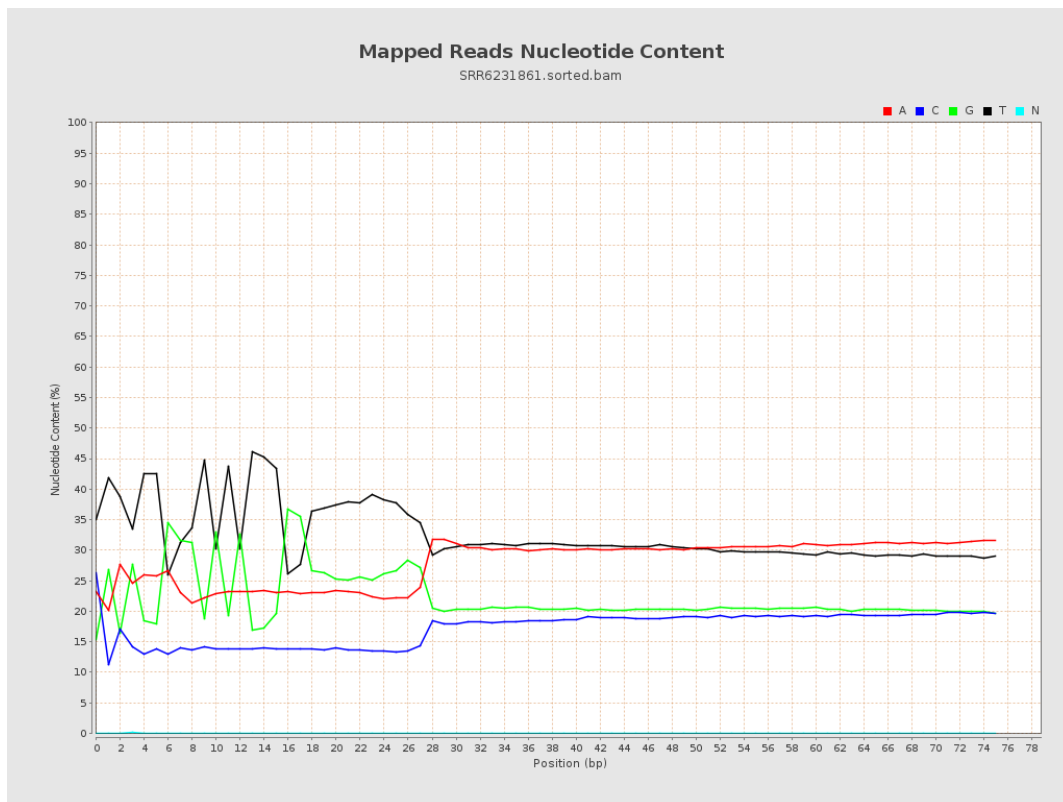
6. Results : Genome Fraction Coverage



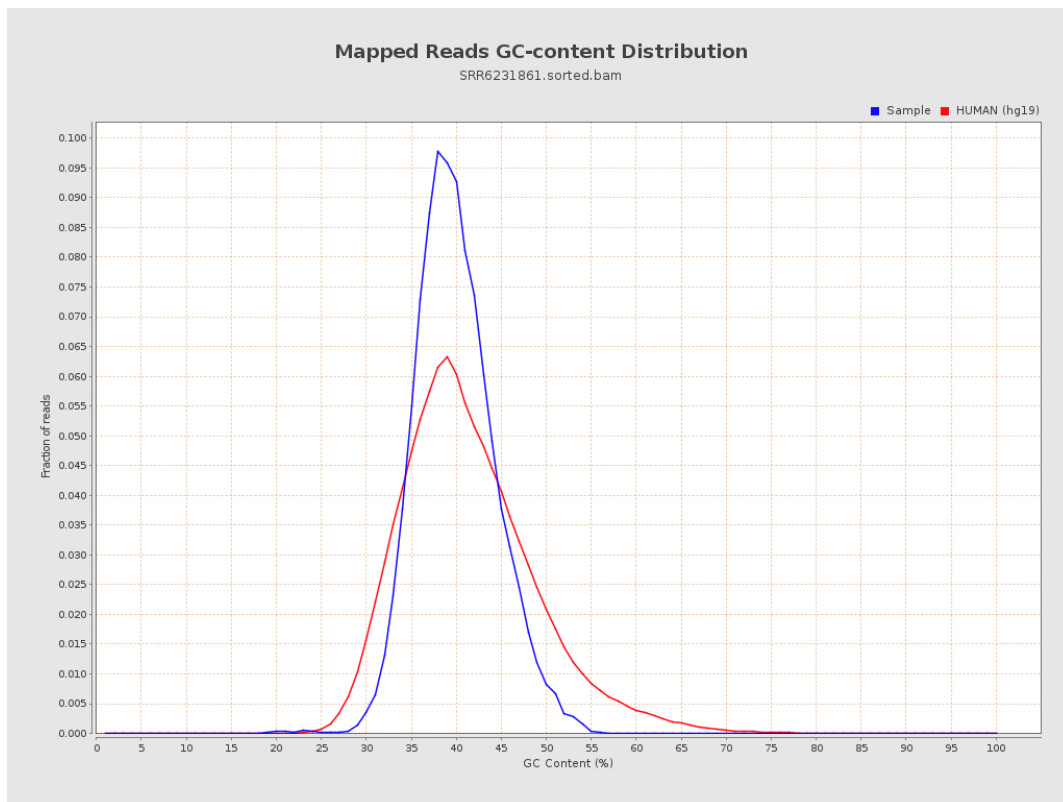
7. Results : Duplication Rate Histogram



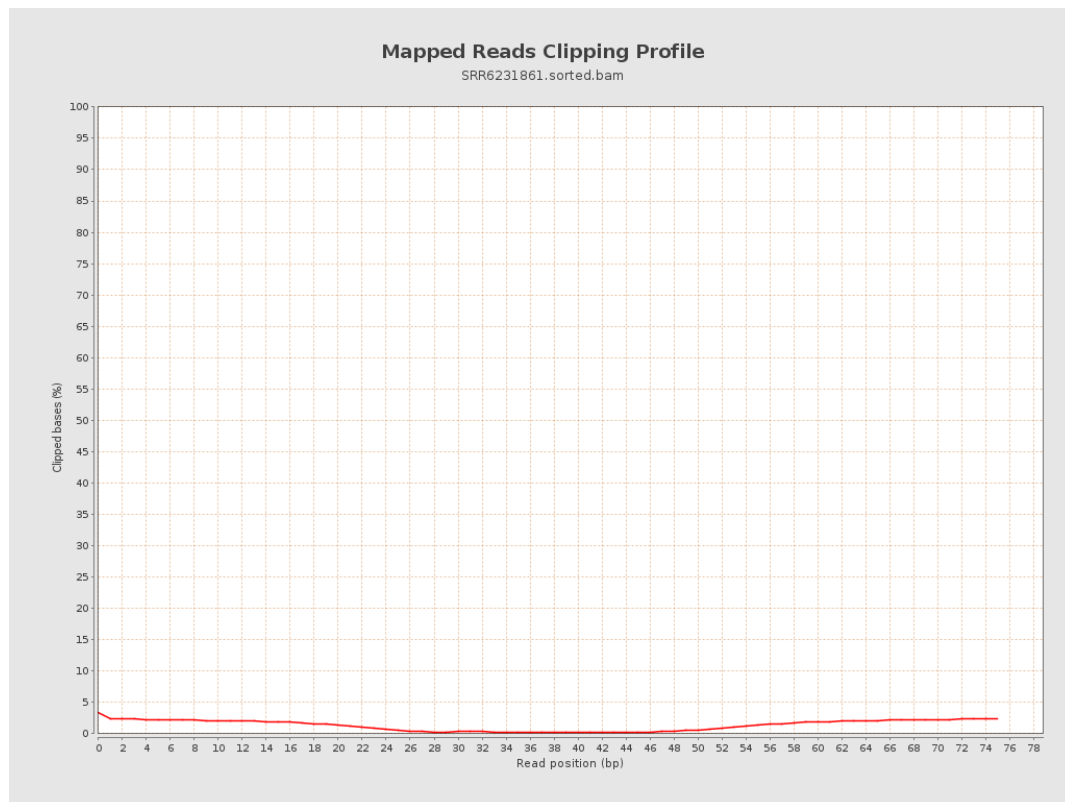
8. Results : Mapped Reads Nucleotide Content



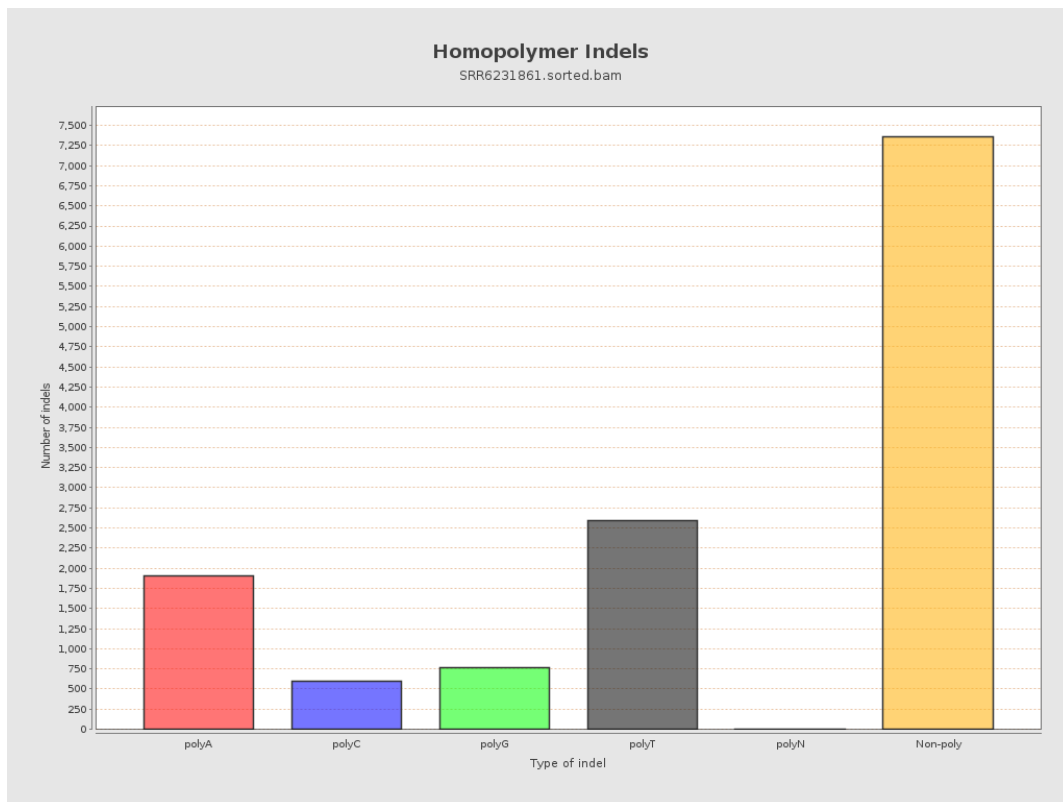
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

