

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 08:34:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231862.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_SRR6231862 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231862.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 08:34:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231862.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	873,133
Mapped reads	607,201 / 69.54%
Unmapped reads	265,932 / 30.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,368 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	17,940 / 2.05%
Duplication rate	2.38%
Clipped reads	255,938 / 29.31%

2.2. ACGT Content

Number/percentage of A's	11,668,299 / 28.7%
Number/percentage of C's	7,140,574 / 17.56%
Number/percentage of T's	13,305,071 / 32.73%
Number/percentage of G's	8,538,044 / 21%
Number/percentage of N's	2,183 / 0.01%
GC Percentage	38.57%

2.3. Coverage

Mean	0.0131

Standard Deviation	0.1822
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2.4. Mapping Quality

Mean Mapping Quality	45.31
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2.5. Mismatches and indels

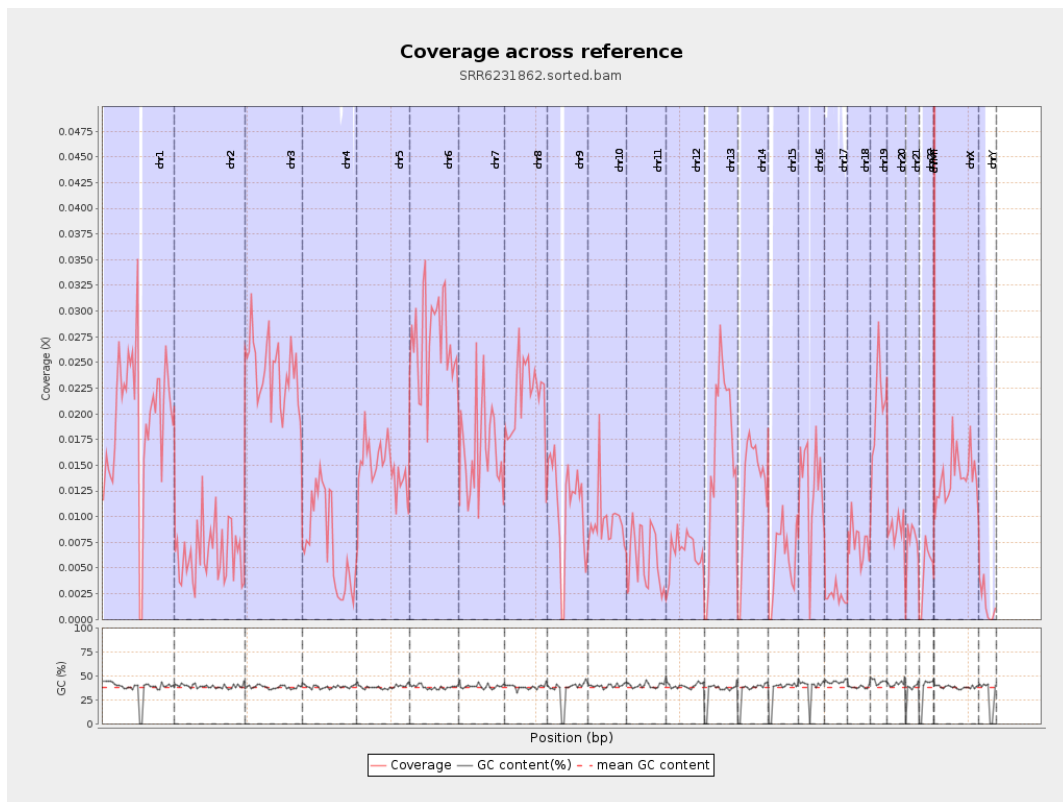
General error rate	0.84%
Mismatches	336,908
Insertions	3,346
Mapped reads with at least one insertion	0.54%
Deletions	15,576
Mapped reads with at least one deletion	2.52%
Homopolymer indels	43.99%

2.6. Chromosome stats

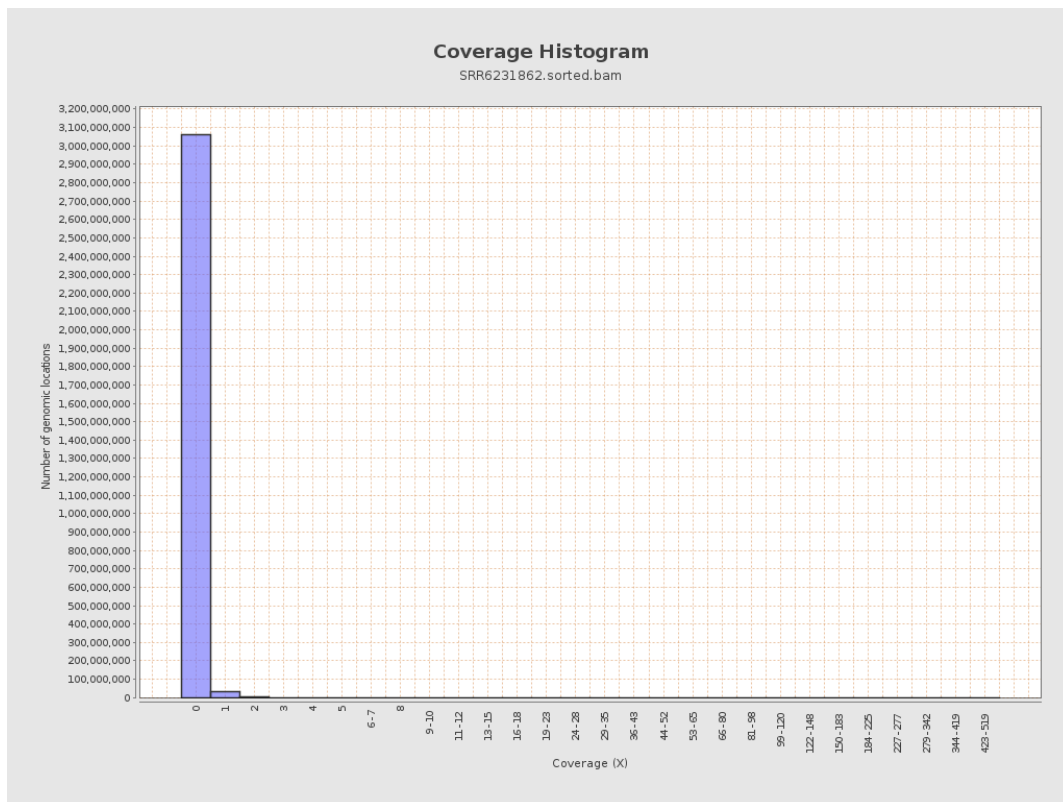
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4833225	0.0194	0.3701
chr2	243199373	1549681	0.0064	0.1194
chr3	198022430	4766764	0.0241	0.1672
chr4	191154276	1415079	0.0074	0.0936
chr5	180915260	2698589	0.0149	0.1321
chr6	171115067	4645156	0.0271	0.1964
chr7	159138663	2609344	0.0164	0.1964

chr8	146364022	3158829	0.0216	0.3501
chr9	141213431	1574114	0.0111	0.1252
chr10	135534747	1291429	0.0095	0.1434
chr11	135006516	794646	0.0059	0.0966
chr12	133851895	885885	0.0066	0.0885
chr13	115169878	1892109	0.0164	0.139
chr14	107349540	1379387	0.0128	0.1246
chr15	102531392	603525	0.0059	0.0823
chr16	90354753	1152778	0.0128	0.1265
chr17	81195210	179948	0.0022	0.0528
chr18	78077248	587582	0.0075	0.1904
chr19	59128983	1229624	0.0208	0.2418
chr20	63025520	551319	0.0087	0.1015
chr21	48129895	356510	0.0074	0.0933
chr22	51304566	245653	0.0048	0.0737
chrMT	16571	10799	0.6517	0.9321
chrX	155270560	2177942	0.014	0.1306
chrY	59373566	91531	0.0015	0.0449

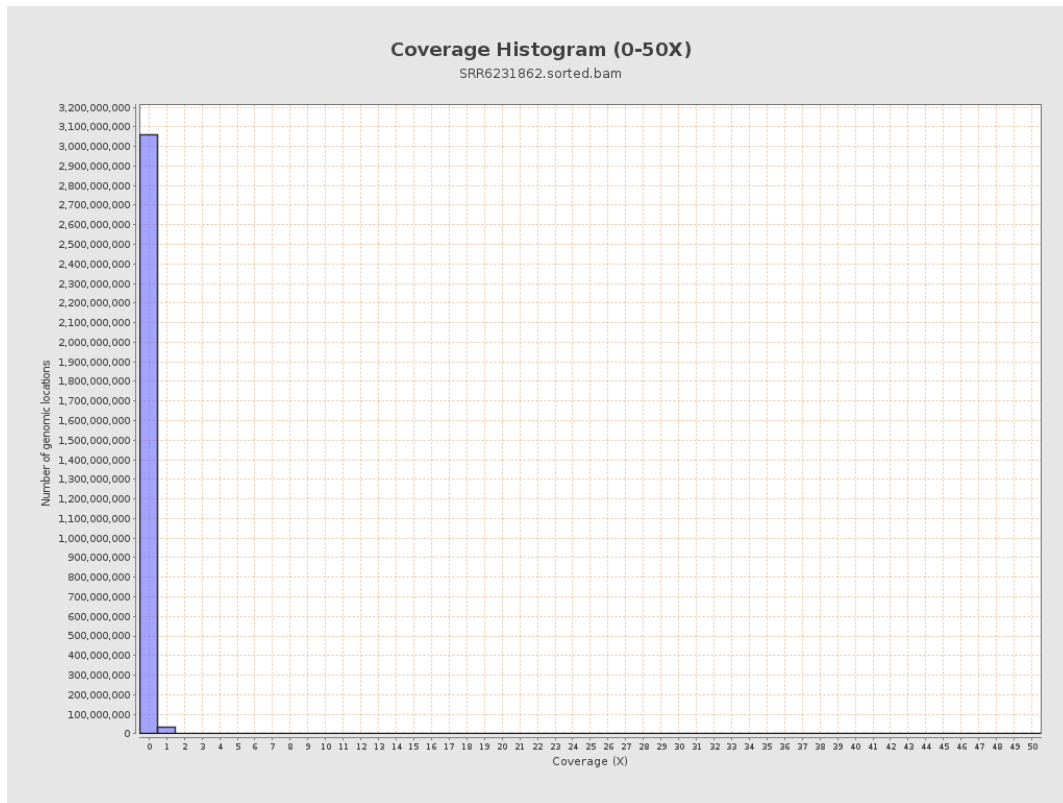
3. Results : Coverage across reference



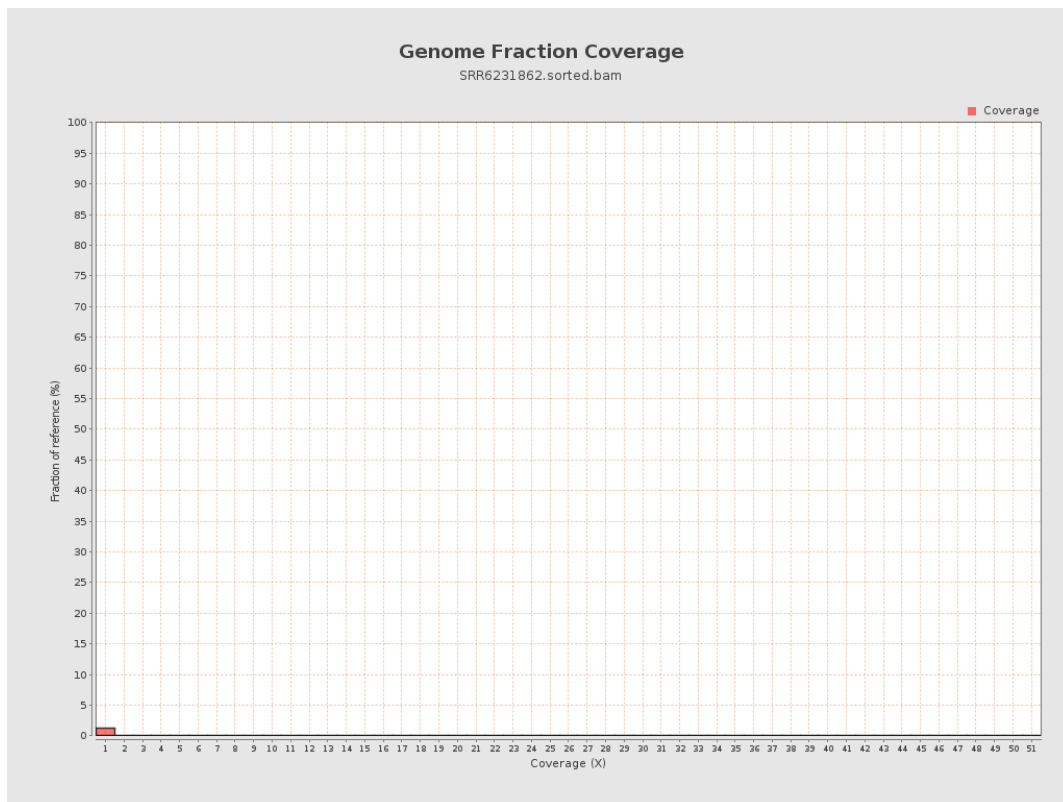
4. Results : Coverage Histogram



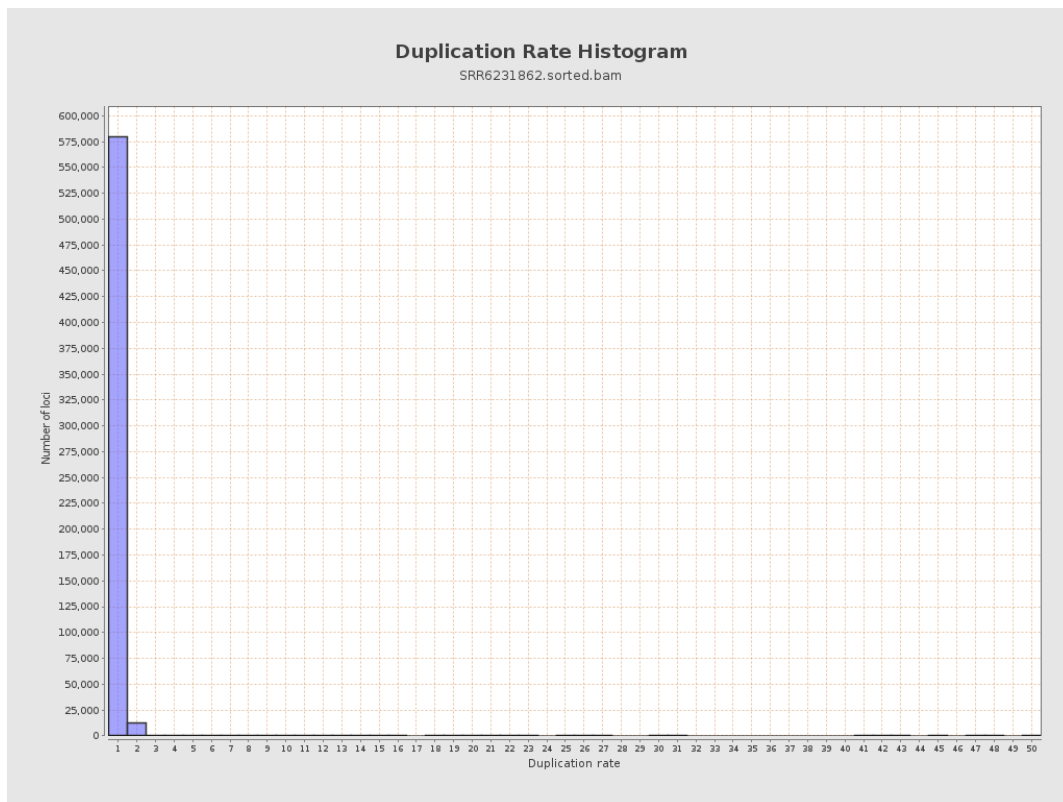
5. Results : Coverage Histogram (0-50X)



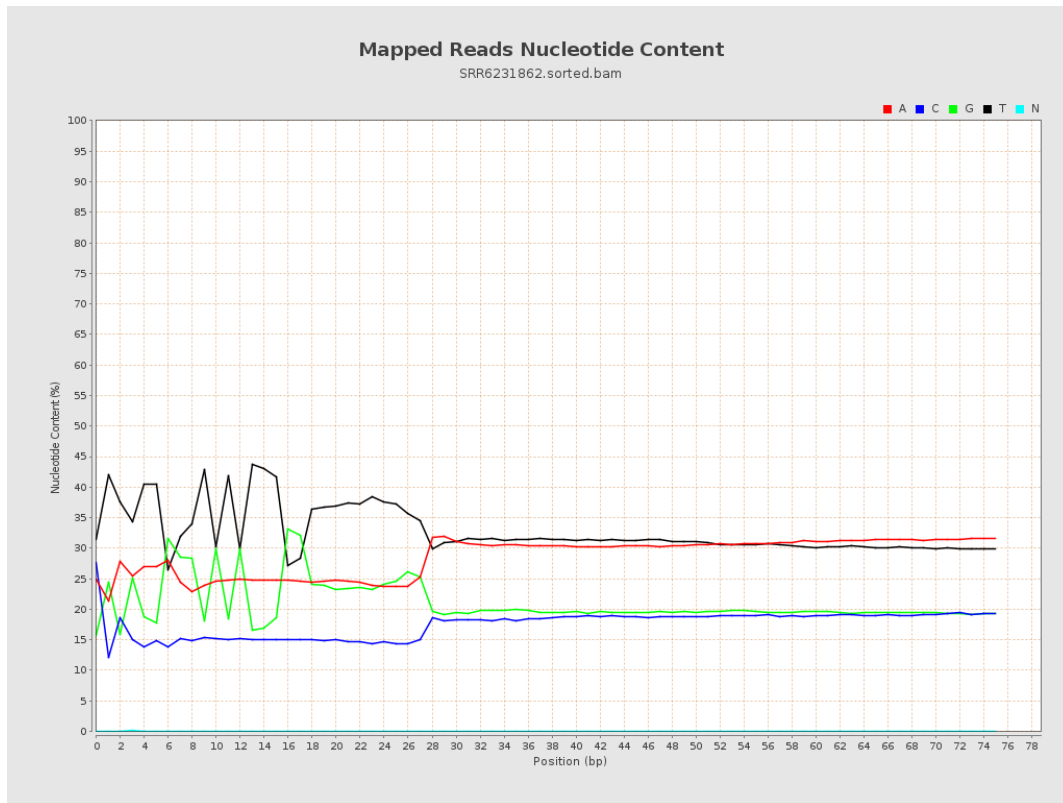
6. Results : Genome Fraction Coverage



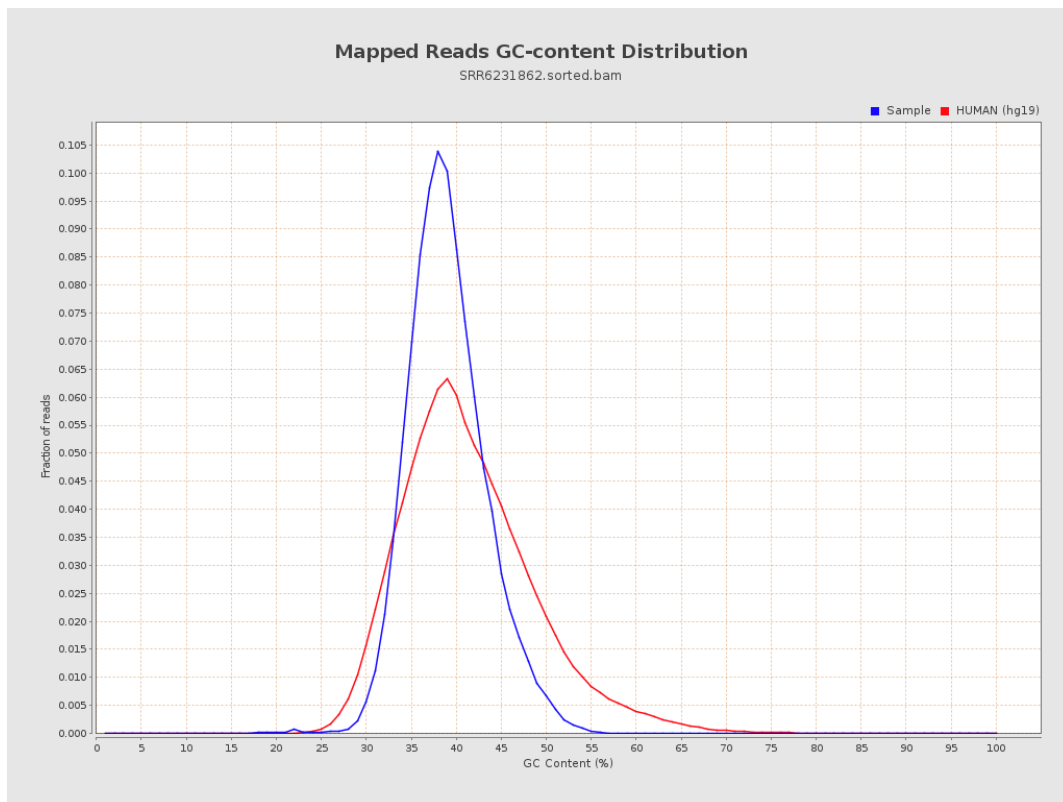
7. Results : Duplication Rate Histogram



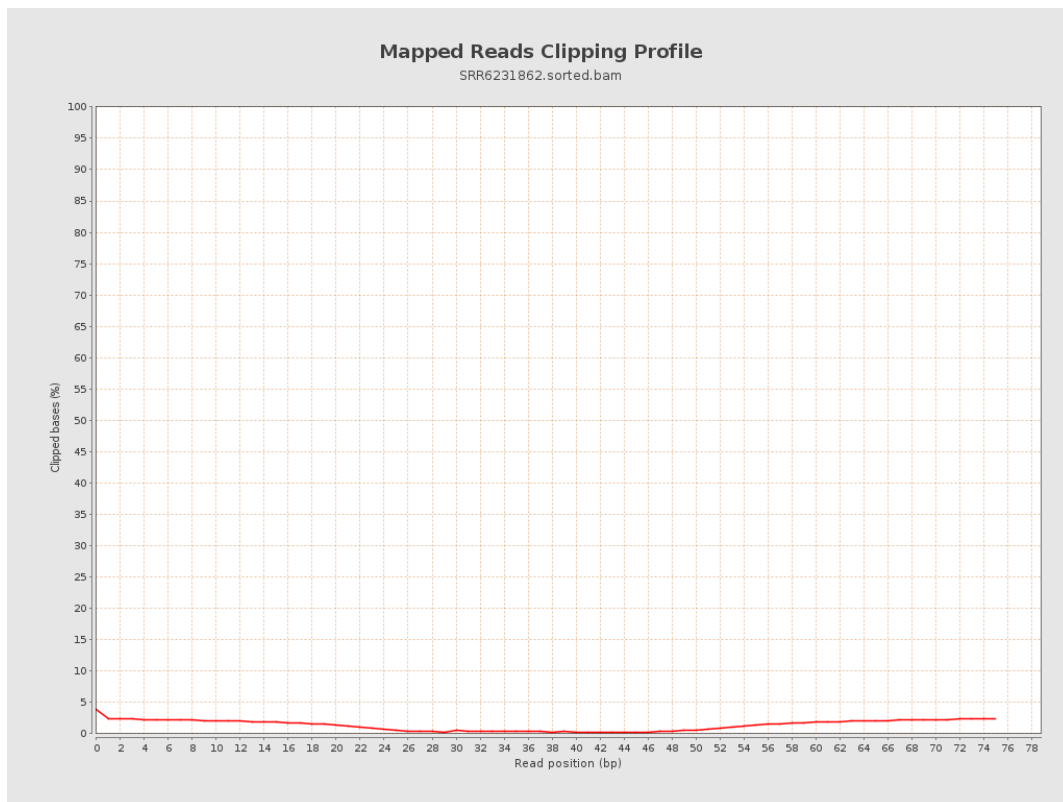
8. Results : Mapped Reads Nucleotide Content



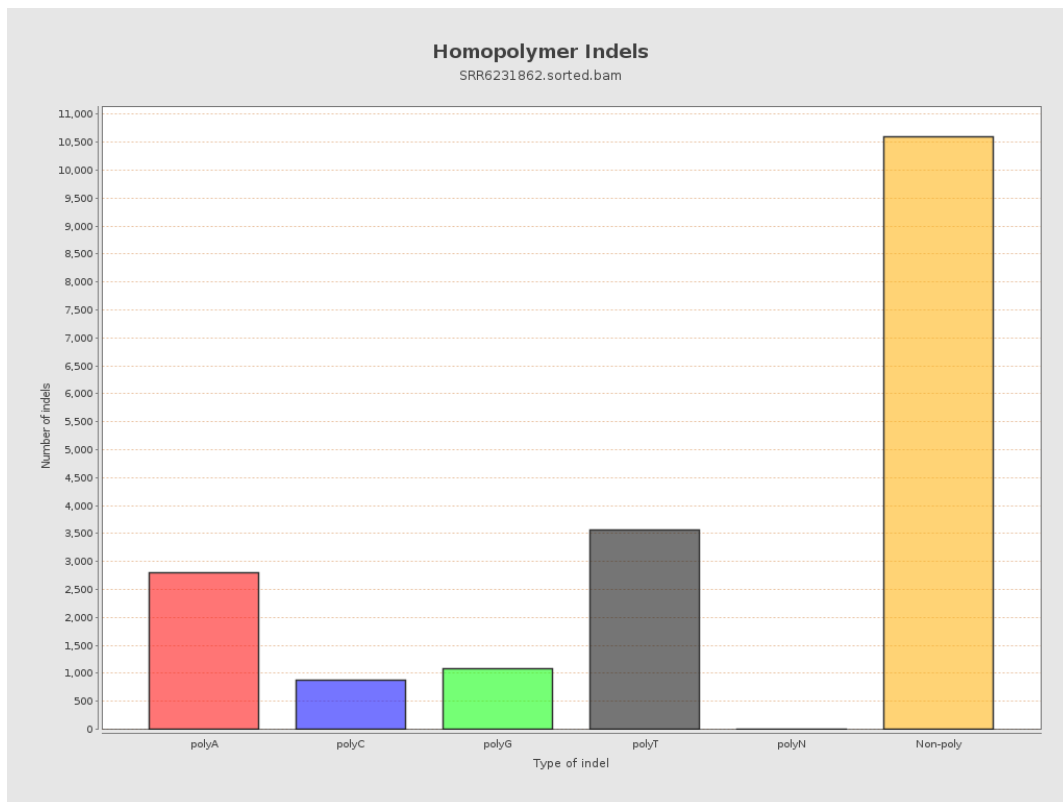
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

