

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 09:35:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231875.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_SRR6231875 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231875.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 09:35:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231875.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,463,111
Mapped reads	4,225,846 / 94.68%
Unmapped reads	237,265 / 5.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,204 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	346,112 / 7.75%
Duplication rate	6.55%
Clipped reads	1,830,686 / 41.02%

2.2. ACGT Content

Number/percentage of A's	78,677,683 / 27.85%
Number/percentage of C's	51,555,338 / 18.25%
Number/percentage of T's	90,572,030 / 32.06%
Number/percentage of G's	61,630,607 / 21.81%
Number/percentage of N's	115,873 / 0.04%
GC Percentage	40.06%

2.3. Coverage

Mean	0.0913

Standard Deviation	1.0321
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2.4. Mapping Quality

Mean Mapping Quality	45.68
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2.5. Mismatches and indels

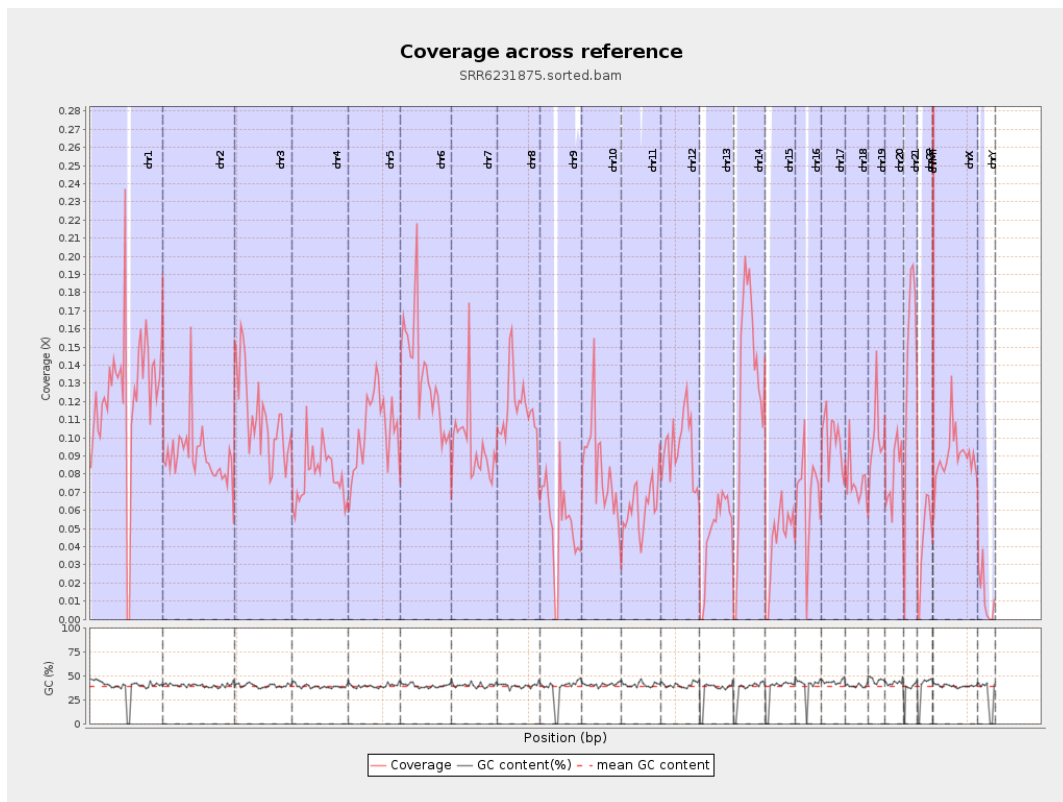
General error rate	0.65%
Mismatches	1,806,199
Insertions	19,855
Mapped reads with at least one insertion	0.47%
Deletions	67,109
Mapped reads with at least one deletion	1.57%
Homopolymer indels	45.08%

2.6. Chromosome stats

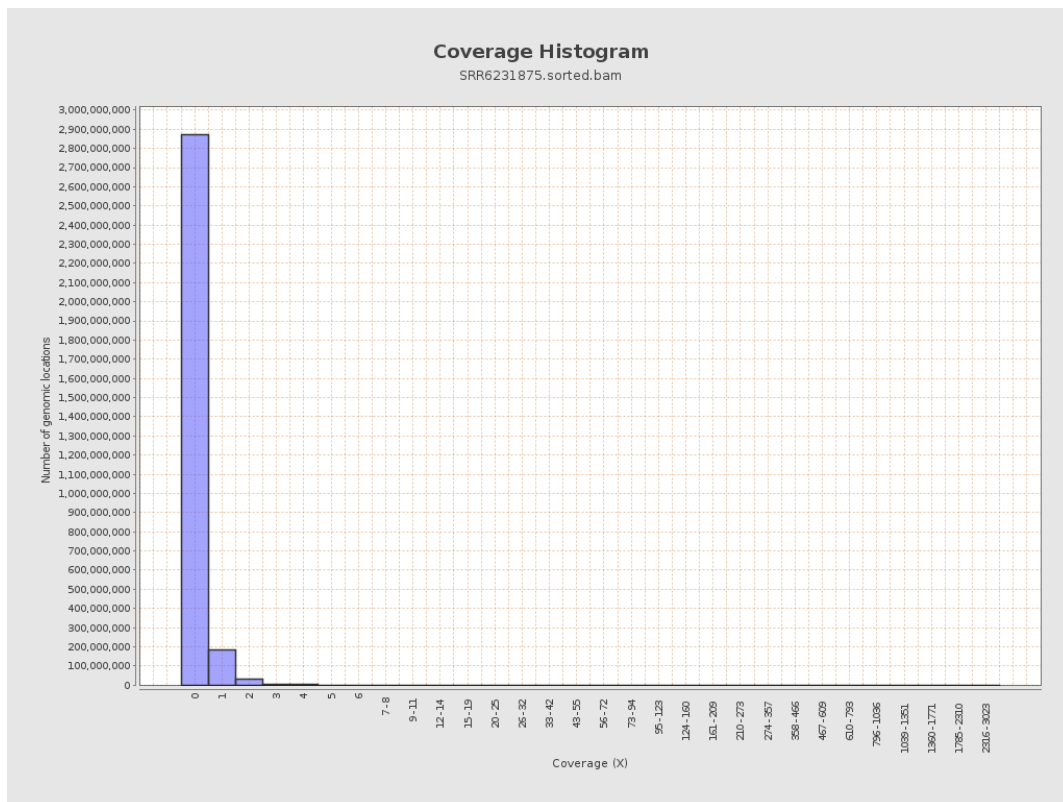
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	30975709	0.1243	2.5069
chr2	243199373	21882979	0.09	0.8828
chr3	198022430	22070856	0.1115	0.4014
chr4	191154276	15216817	0.0796	0.3988
chr5	180915260	18727553	0.1035	0.3978
chr6	171115067	22997164	0.1344	0.6905
chr7	159138663	15180539	0.0954	1.2208

chr8	146364022	16885705	0.1154	1.8907
chr9	141213431	7476227	0.0529	0.5877
chr10	135534747	11188186	0.0825	0.773
chr11	135006516	8393333	0.0622	0.565
chr12	133851895	12582910	0.094	0.3802
chr13	115169878	5527127	0.048	0.2768
chr14	107349540	13856368	0.1291	0.4579
chr15	102531392	4454450	0.0434	0.2797
chr16	90354753	6035414	0.0668	0.3989
chr17	81195210	8121046	0.1	0.4508
chr18	78077248	5949092	0.0762	1.4608
chr19	59128983	5957082	0.1007	1.3677
chr20	63025520	4991272	0.0792	0.3736
chr21	48129895	6928681	0.144	0.4903
chr22	51304566	2253897	0.0439	0.2439
chrMT	16571	337484	20.3659	11.5559
chrX	155270560	13943000	0.0898	0.4464
chrY	59373566	737268	0.0124	0.2334

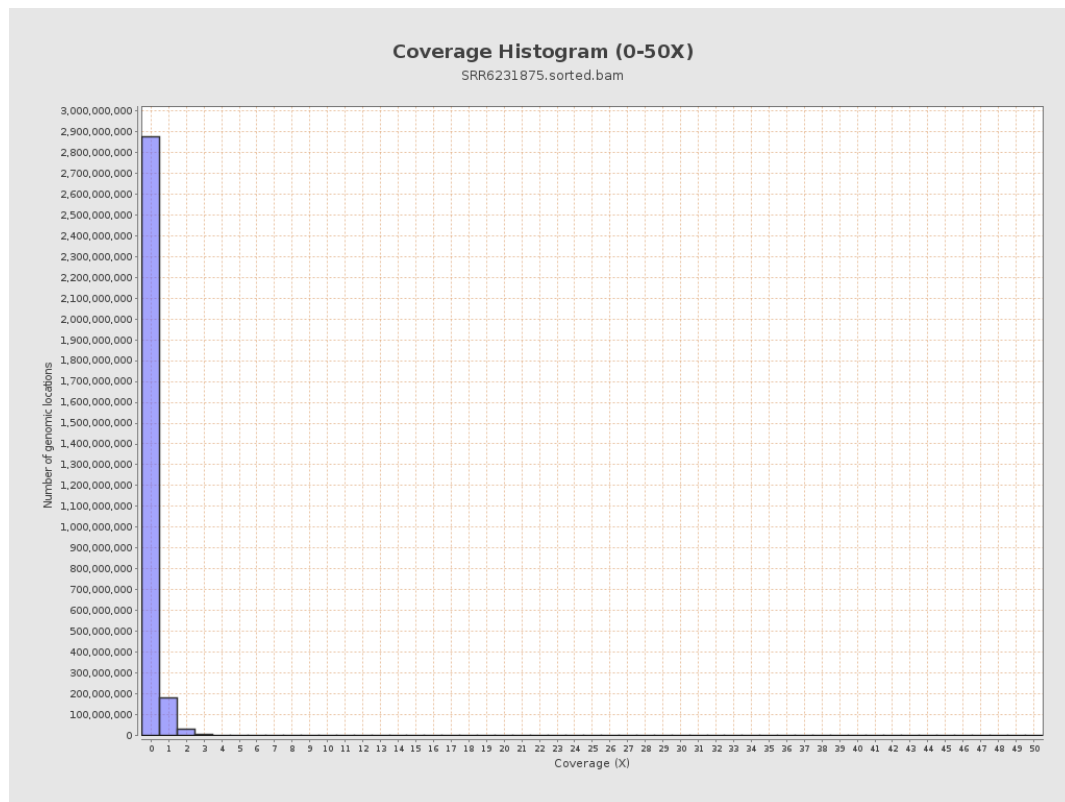
3. Results : Coverage across reference



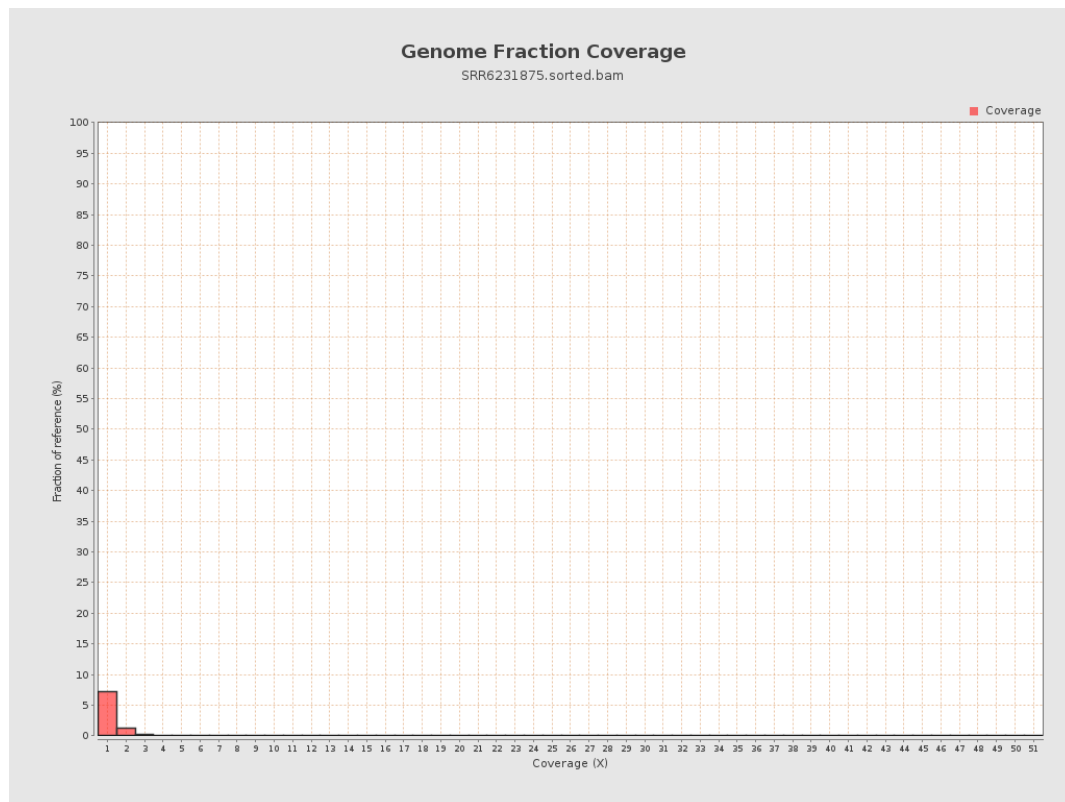
4. Results : Coverage Histogram



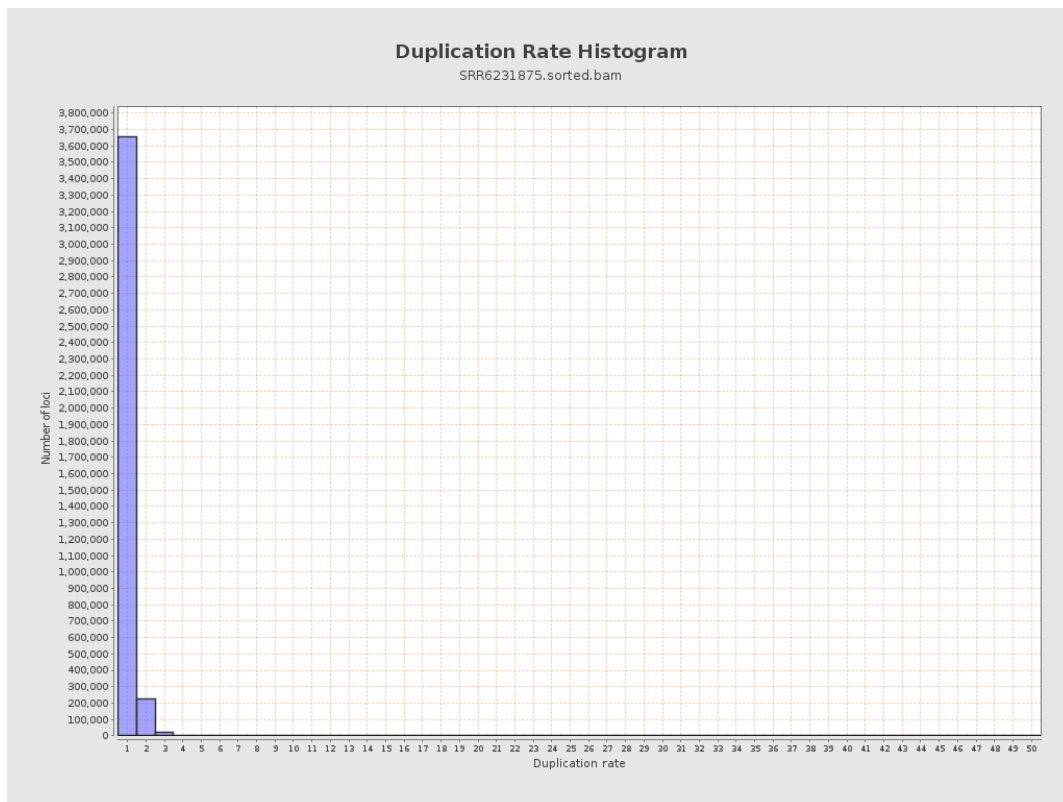
5. Results : Coverage Histogram (0-50X)



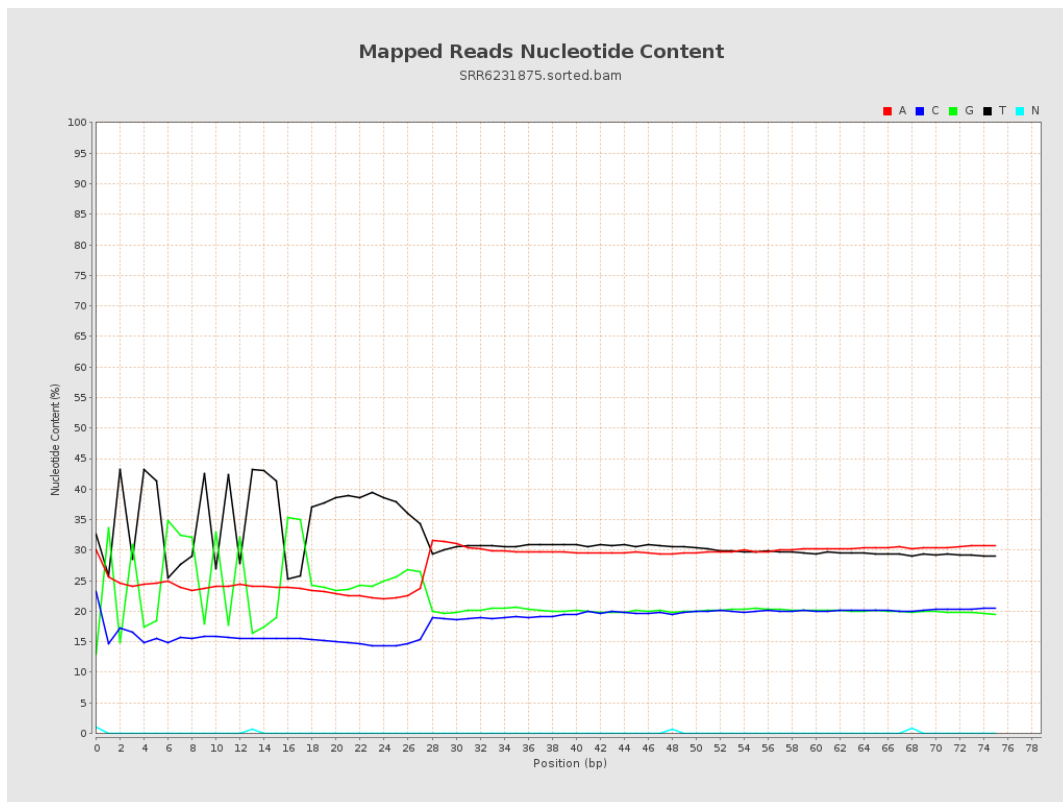
6. Results : Genome Fraction Coverage



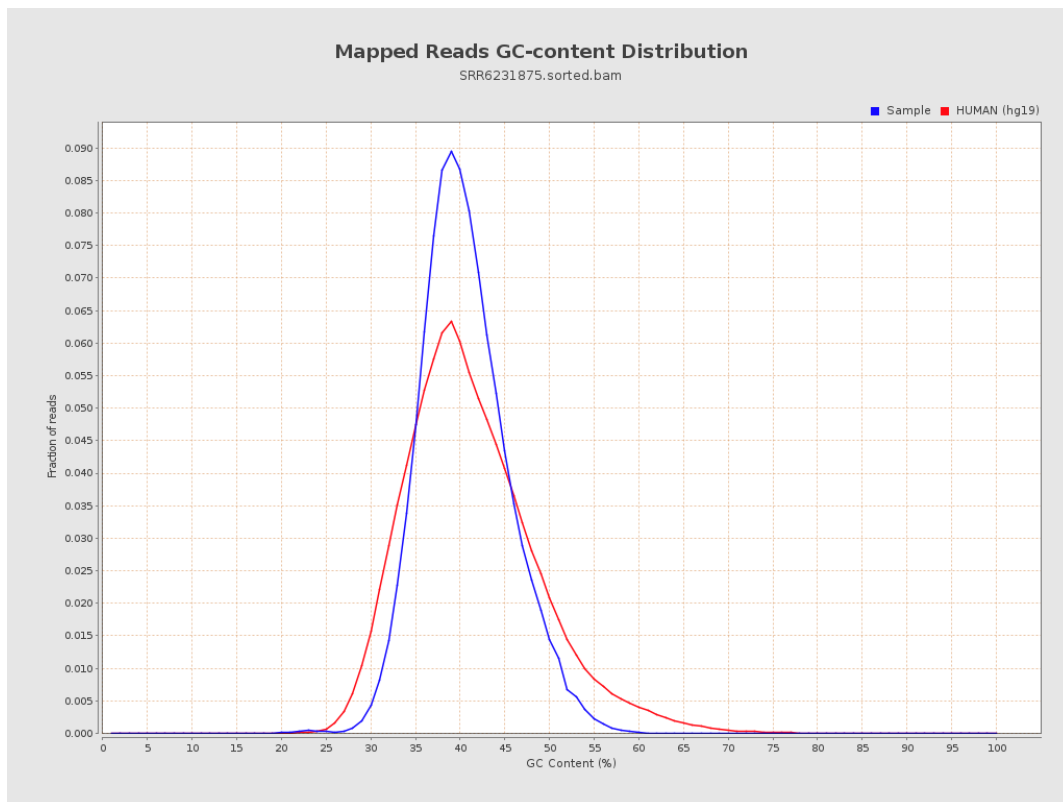
7. Results : Duplication Rate Histogram



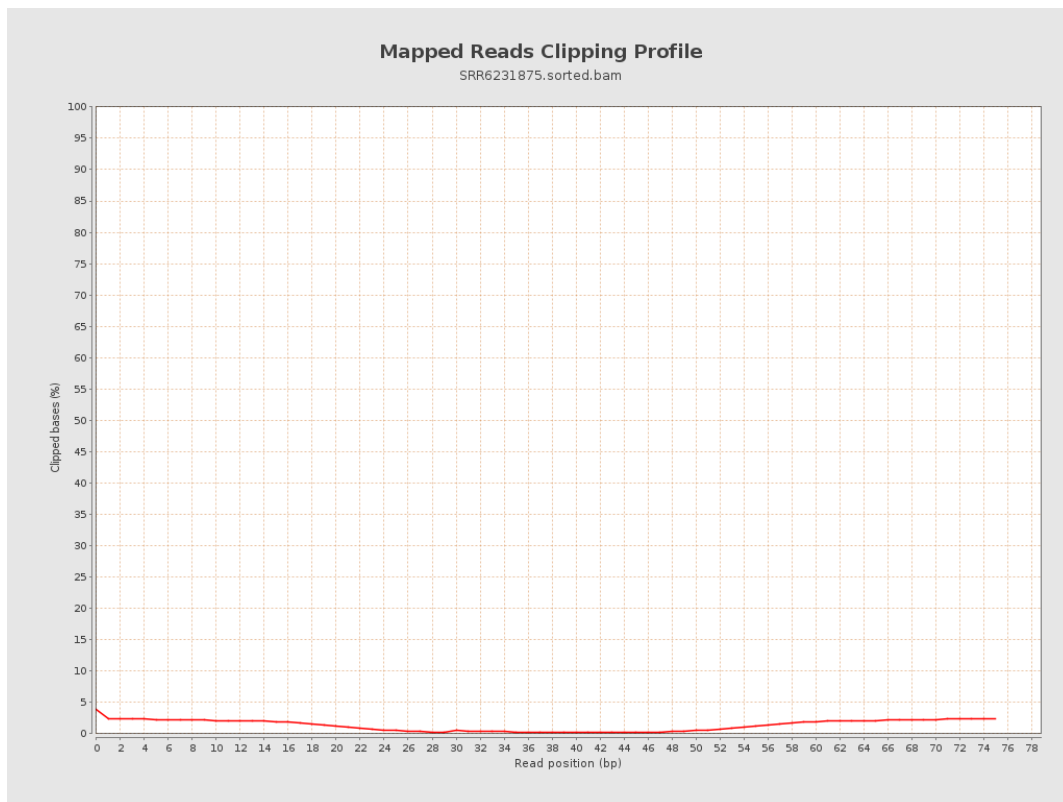
8. Results : Mapped Reads Nucleotide Content



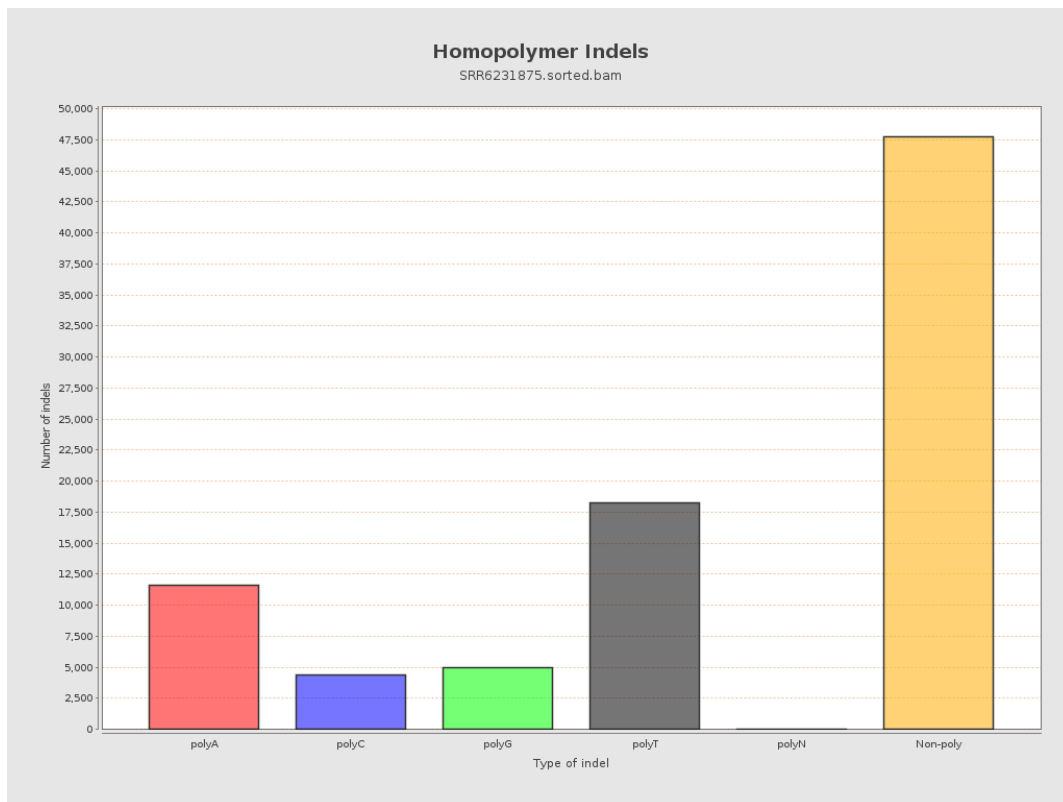
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

