

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 00:54:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231760.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_SRR6231760 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231760.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 00:54:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231760.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,829,024
Mapped reads	4,285,886 / 88.75%
Unmapped reads	543,138 / 11.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	44,392 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	359,573 / 7.45%
Duplication rate	5.87%
Clipped reads	2,039,956 / 42.24%

2.2. ACGT Content

Number/percentage of A's	82,202,455 / 29.09%
Number/percentage of C's	53,378,887 / 18.89%
Number/percentage of T's	85,503,339 / 30.26%
Number/percentage of G's	61,500,891 / 21.76%
Number/percentage of N's	20,283 / 0.01%
GC Percentage	40.65%

2.3. Coverage

Mean	0.0913

Standard Deviation	5.5237
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2.4. Mapping Quality

Mean Mapping Quality	41.53
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2.5. Mismatches and indels

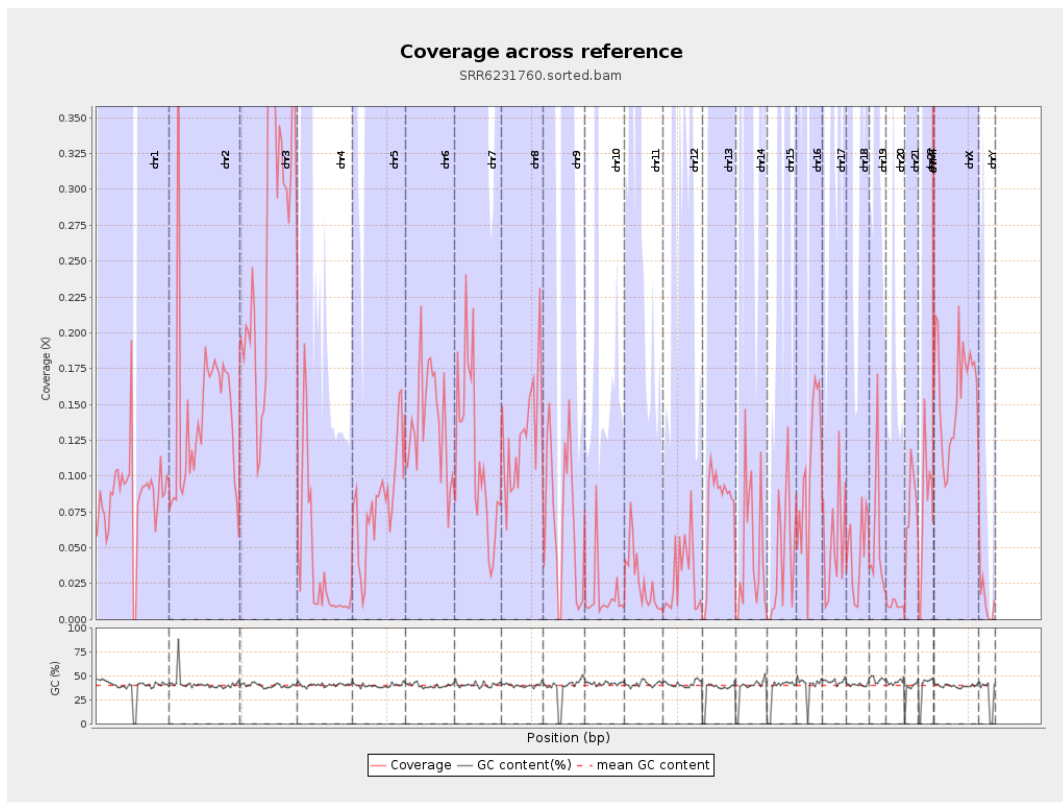
General error rate	0.61%
Mismatches	1,697,408
Insertions	18,920
Mapped reads with at least one insertion	0.44%
Deletions	72,485
Mapped reads with at least one deletion	1.67%
Homopolymer indels	46.21%

2.6. Chromosome stats

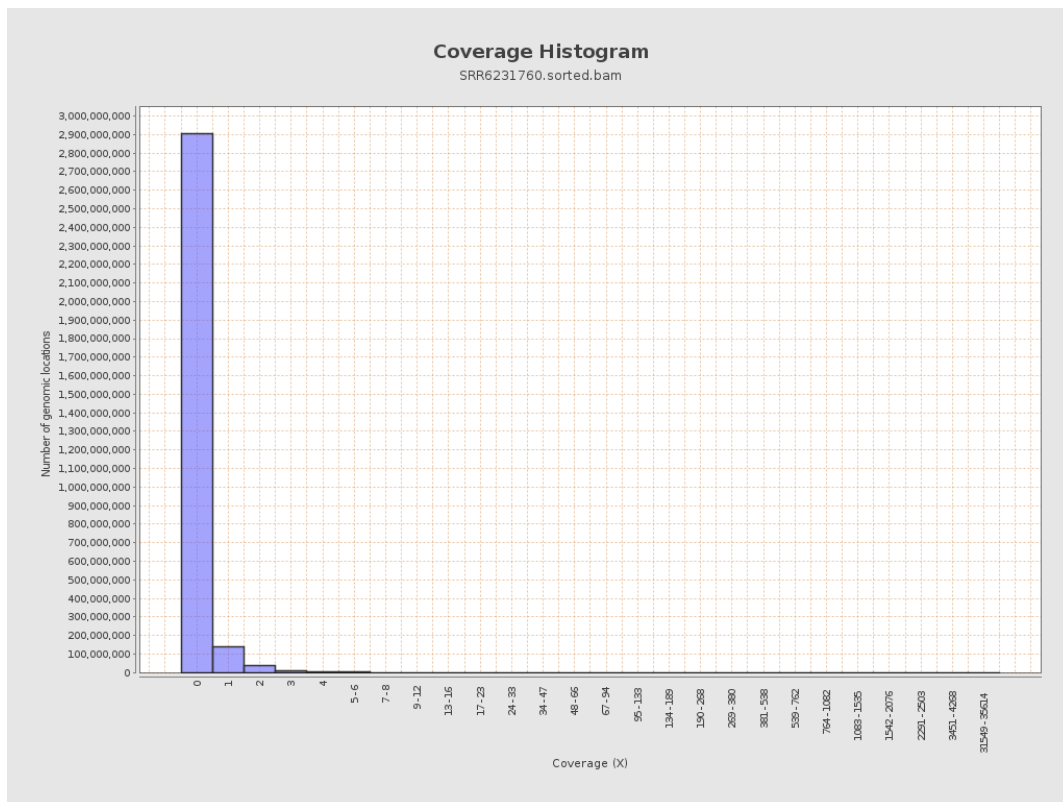
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	21356290	0.0857	2.1055
chr2	243199373	34820820	0.1432	19.4621
chr3	198022430	51487826	0.26	0.703
chr4	191154276	7049579	0.0369	0.2866
chr5	180915260	14609668	0.0808	0.3874
chr6	171115067	23390909	0.1367	0.7085
chr7	159138663	17997642	0.1131	1.4644

chr8	146364022	18992053	0.1298	0.7844
chr9	141213431	9605058	0.068	0.6063
chr10	135534747	2108723	0.0156	0.6422
chr11	135006516	3607343	0.0267	0.4872
chr12	133851895	4062053	0.0303	0.2772
chr13	115169878	8853193	0.0769	0.3653
chr14	107349540	5321550	0.0496	0.3842
chr15	102531392	4455554	0.0435	0.2862
chr16	90354753	9502598	0.1052	0.5136
chr17	81195210	4477190	0.0551	0.3157
chr18	78077248	3676909	0.0471	1.4496
chr19	59128983	3443262	0.0582	1.2276
chr20	63025520	626576	0.0099	0.1784
chr21	48129895	3627344	0.0754	0.3925
chr22	51304566	3960636	0.0772	0.3696
chrMT	16571	323925	19.5477	11.2121
chrX	155270560	24547150	0.1581	0.6196
chrY	59373566	825464	0.0139	0.1828

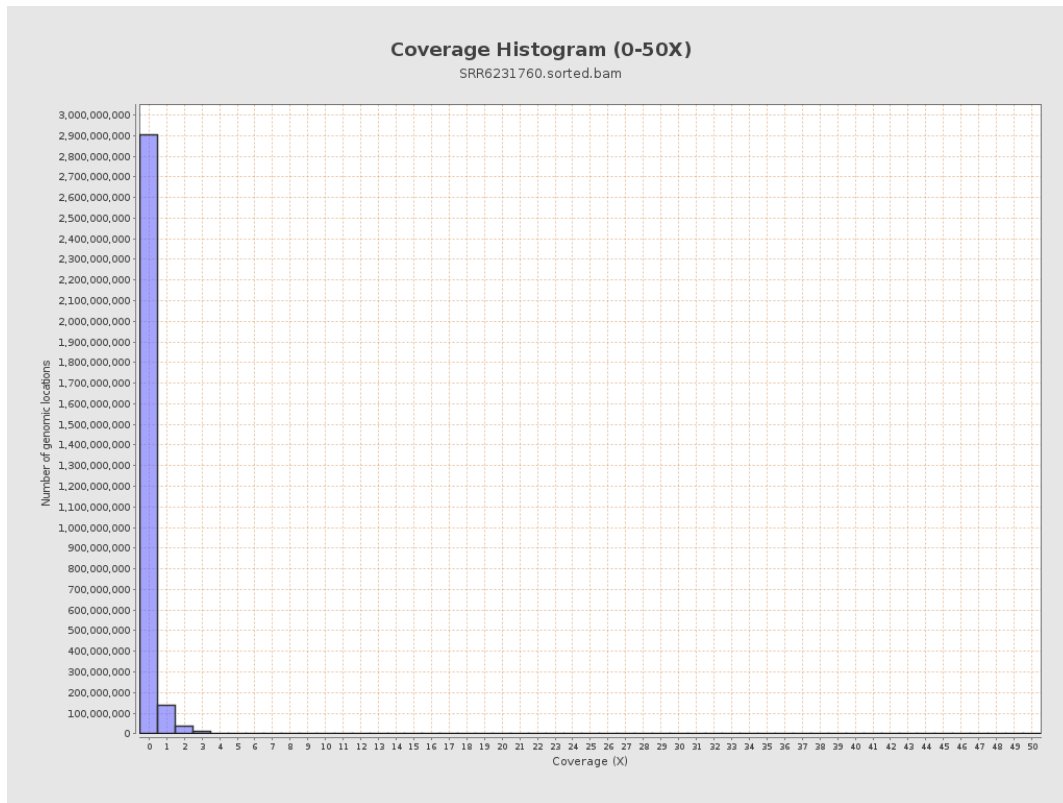
3. Results : Coverage across reference



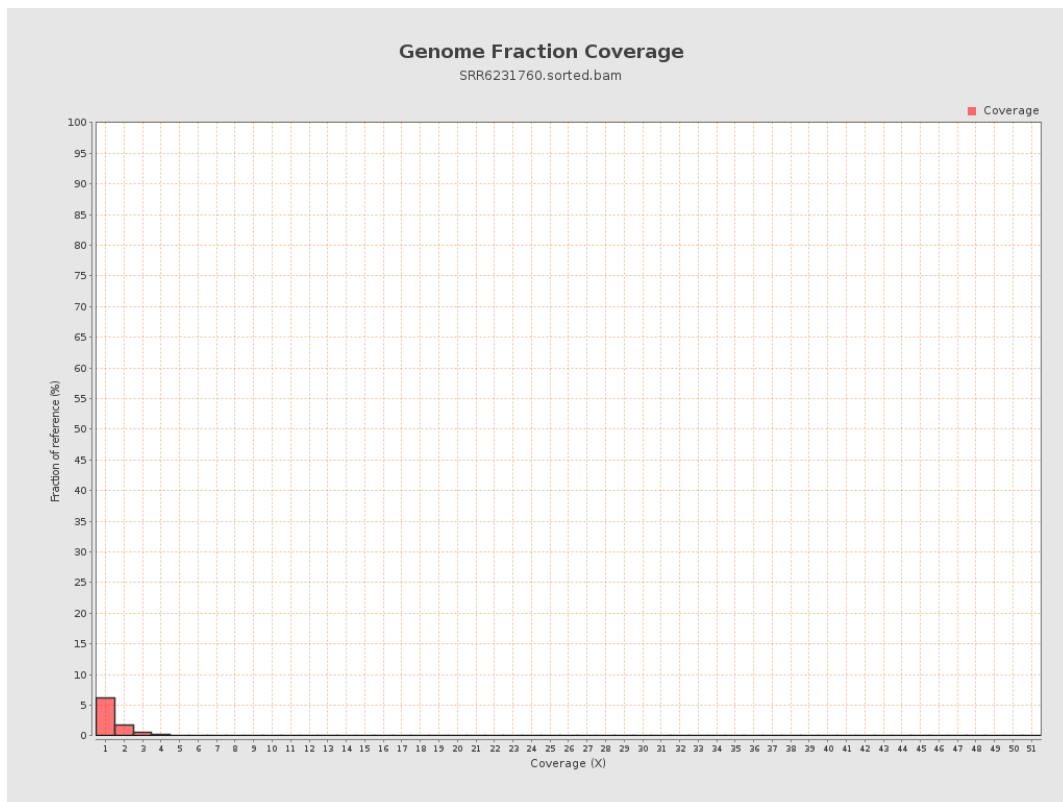
4. Results : Coverage Histogram



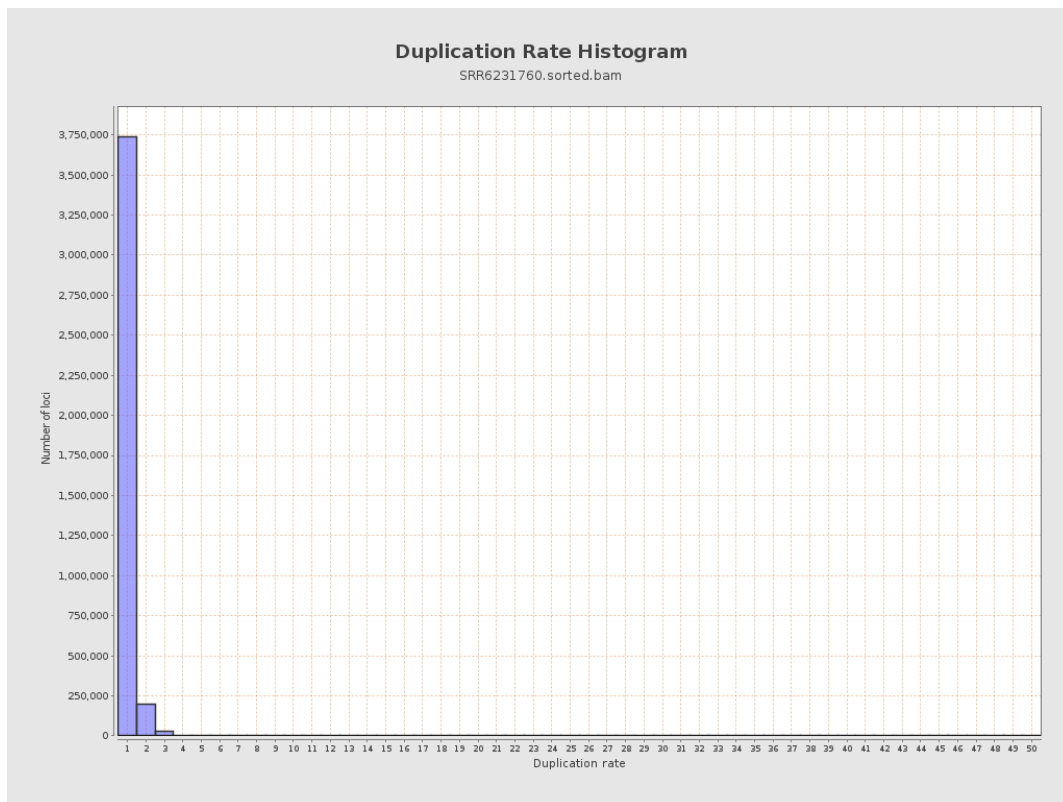
5. Results : Coverage Histogram (0-50X)



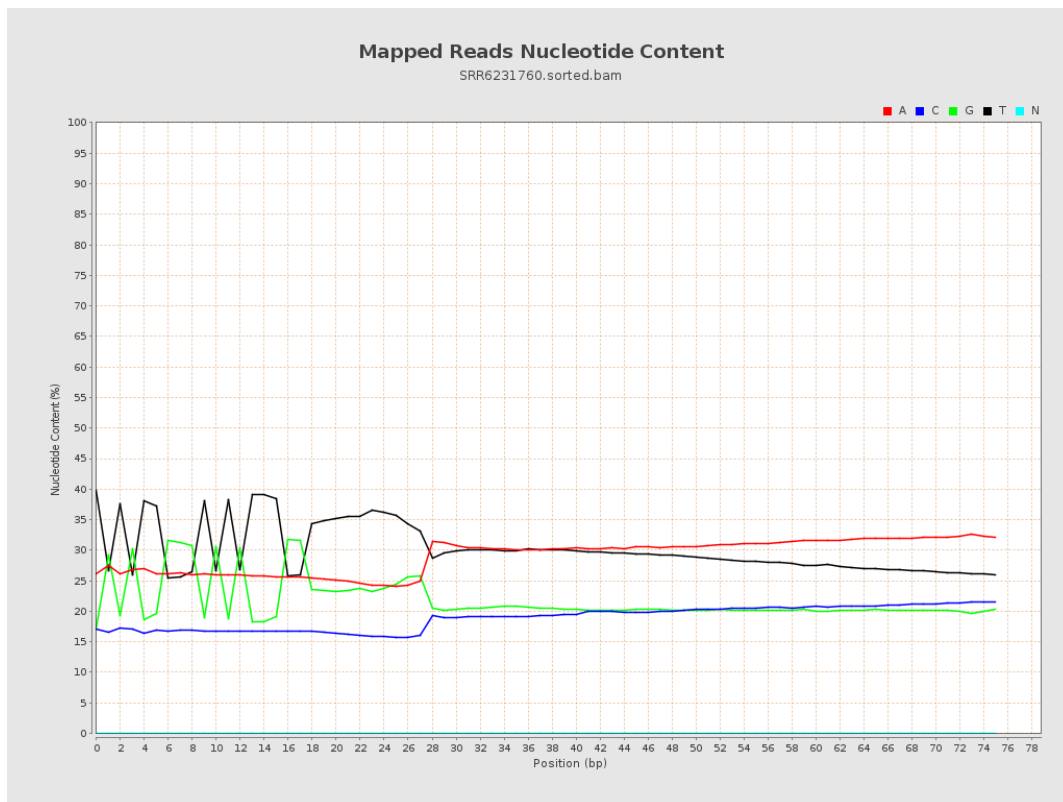
6. Results : Genome Fraction Coverage



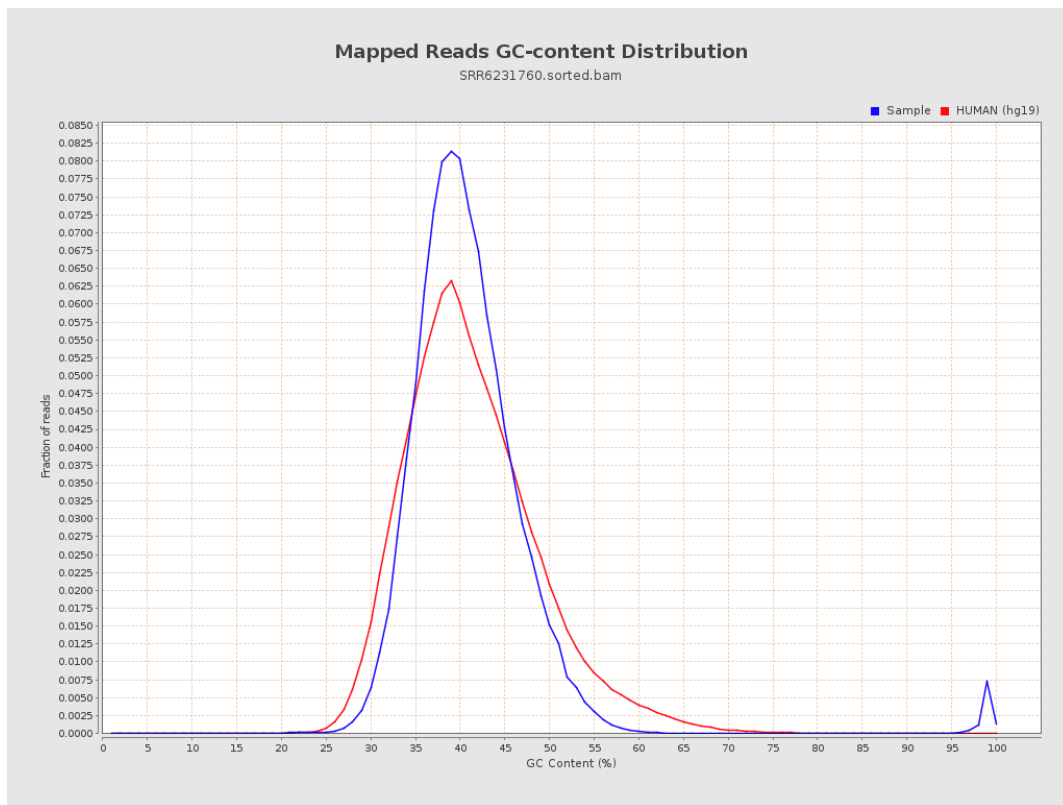
7. Results : Duplication Rate Histogram



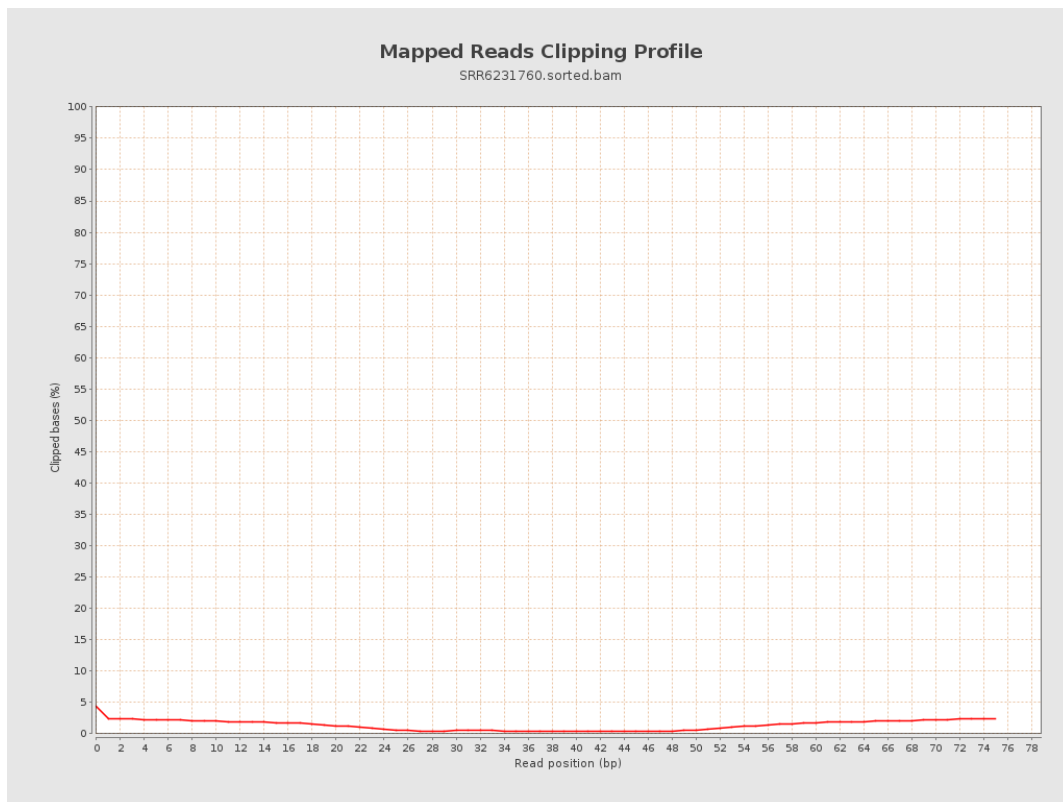
8. Results : Mapped Reads Nucleotide Content



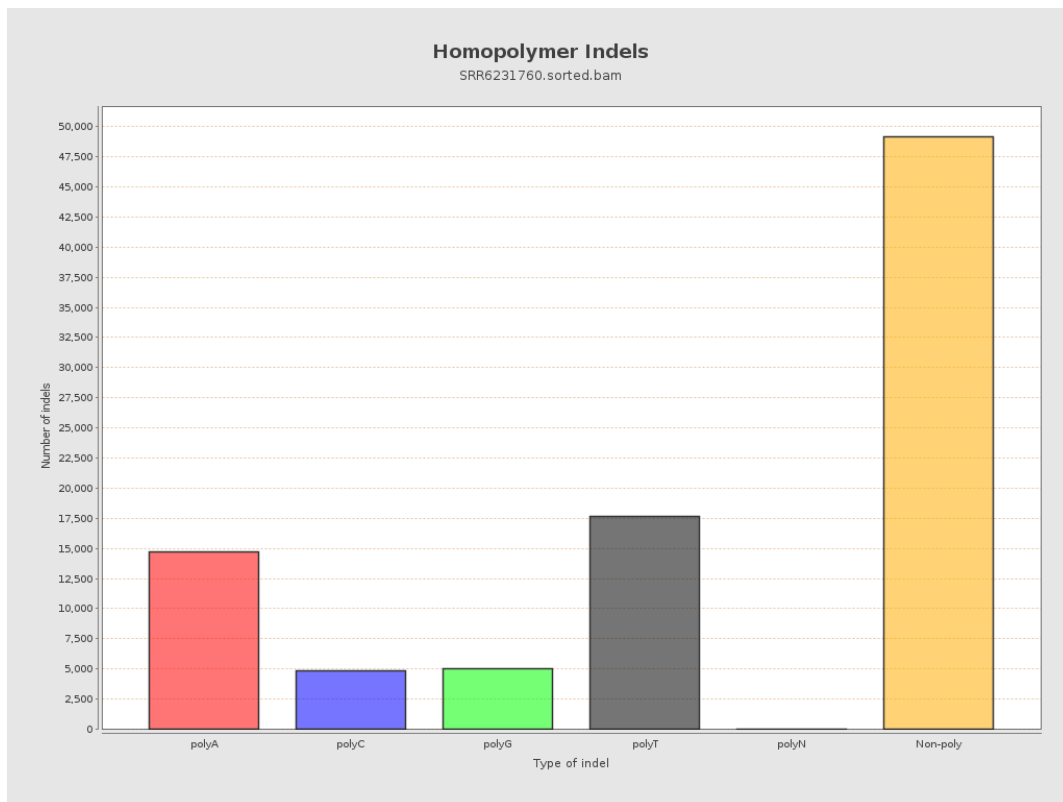
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

