

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 03:09:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231793.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_SRR6231793 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231793.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 03:09:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231793.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,823,431
Mapped reads	2,485,114 / 88.02%
Unmapped reads	338,317 / 11.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,073 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	370,992 / 13.14%
Duplication rate	12.74%
Clipped reads	1,409,641 / 49.93%

2.2. ACGT Content

Number/percentage of A's	40,438,413 / 25.78%
Number/percentage of C's	27,237,018 / 17.36%
Number/percentage of T's	52,719,317 / 33.6%
Number/percentage of G's	36,428,879 / 23.22%
Number/percentage of N's	58,456 / 0.04%
GC Percentage	40.58%

2.3. Coverage

Mean	0.0507

Standard Deviation	0.6098
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2.4. Mapping Quality

Mean Mapping Quality	36.69
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2.5. Mismatches and indels

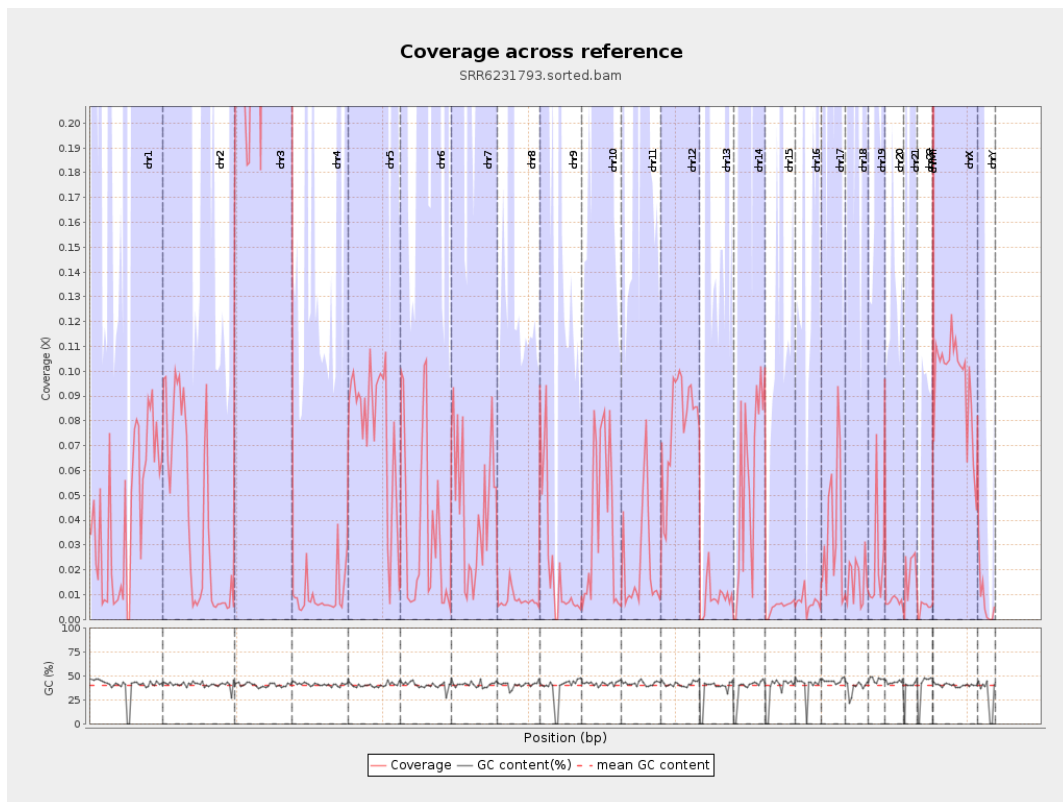
General error rate	0.65%
Mismatches	996,737
Insertions	10,381
Mapped reads with at least one insertion	0.41%
Deletions	35,748
Mapped reads with at least one deletion	1.43%
Homopolymer indels	45.06%

2.6. Chromosome stats

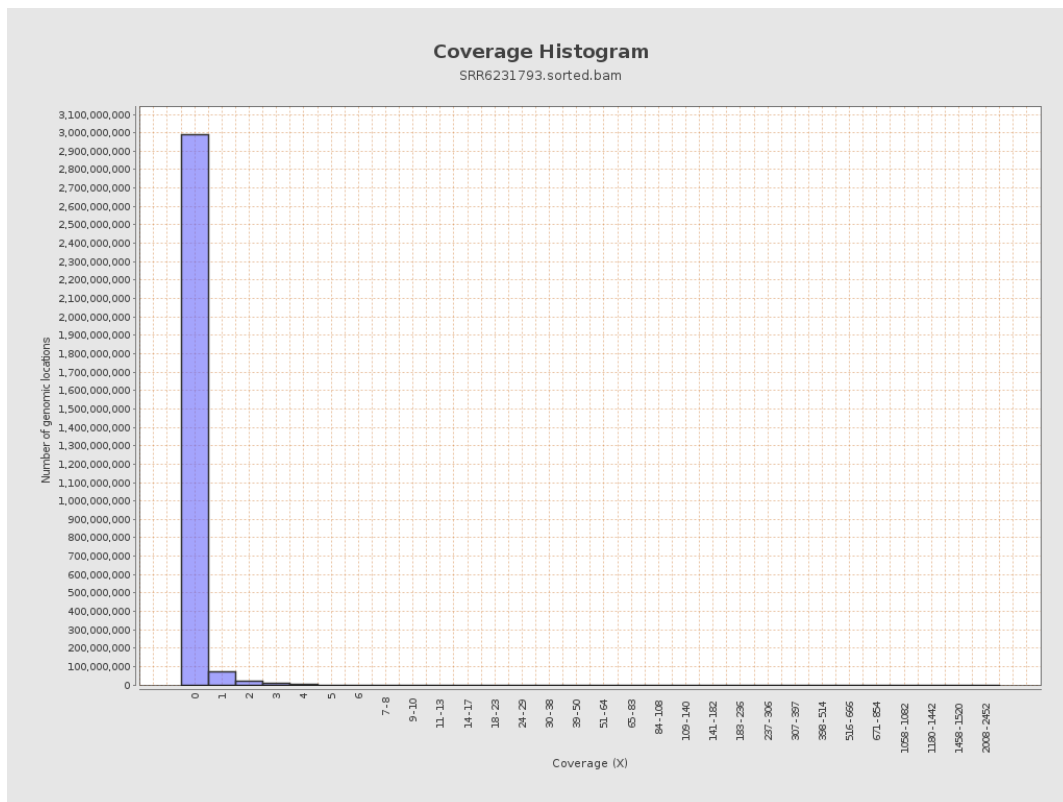
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10562876	0.0424	0.7154
chr2	243199373	9940188	0.0409	1.1397
chr3	198022430	53657221	0.271	0.7413
chr4	191154276	1886799	0.0099	0.1617
chr5	180915260	13704151	0.0757	0.381
chr6	171115067	5960900	0.0348	0.5057
chr7	159138663	7183104	0.0451	0.385

chr8	146364022	1142294	0.0078	0.3924
chr9	141213431	2875642	0.0204	0.2145
chr10	135534747	5290578	0.039	0.6524
chr11	135006516	2925841	0.0217	0.2224
chr12	133851895	10664468	0.0797	0.4033
chr13	115169878	1047748	0.0091	0.3216
chr14	107349540	6125461	0.0571	0.3296
chr15	102531392	510268	0.005	0.192
chr16	90354753	608497	0.0067	0.1665
chr17	81195210	3000429	0.037	0.2627
chr18	78077248	1209759	0.0155	1.8815
chr19	59128983	1458722	0.0247	0.5391
chr20	63025520	465345	0.0074	0.1253
chr21	48129895	907308	0.0189	0.1935
chr22	51304566	236518	0.0046	0.0823
chrMT	16571	171796	10.3673	10.8952
chrX	155270560	14958210	0.0963	0.4711
chrY	59373566	446268	0.0075	0.2005

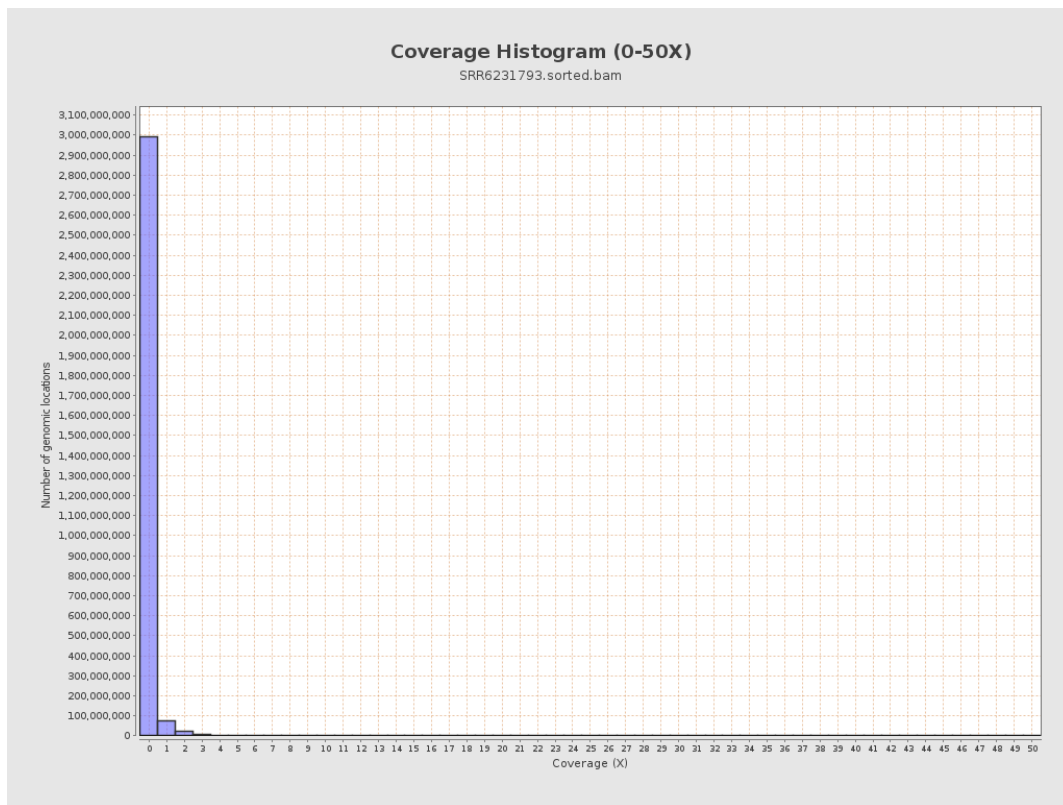
3. Results : Coverage across reference



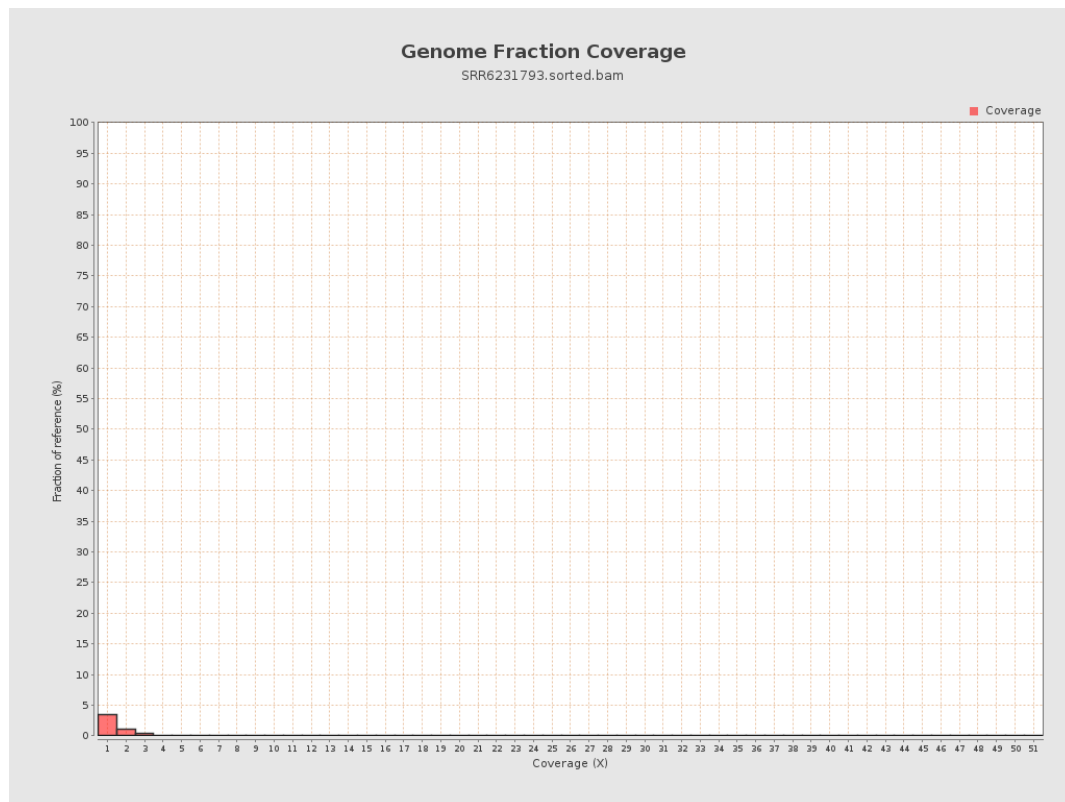
4. Results : Coverage Histogram



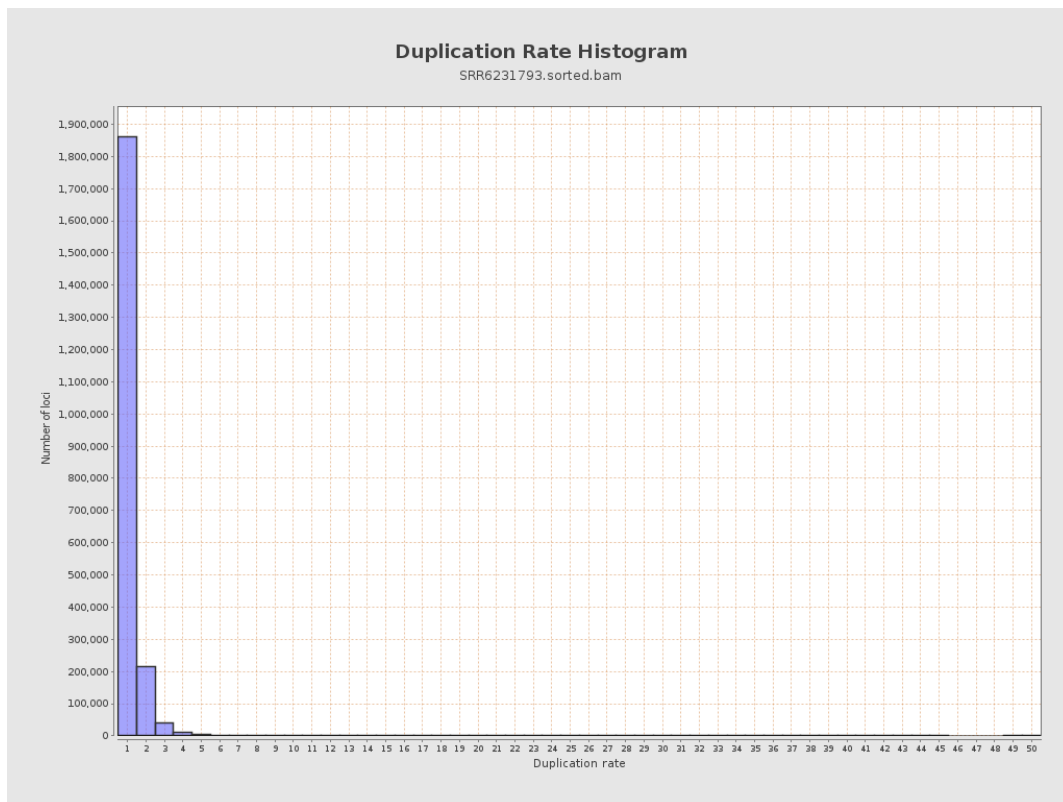
5. Results : Coverage Histogram (0-50X)



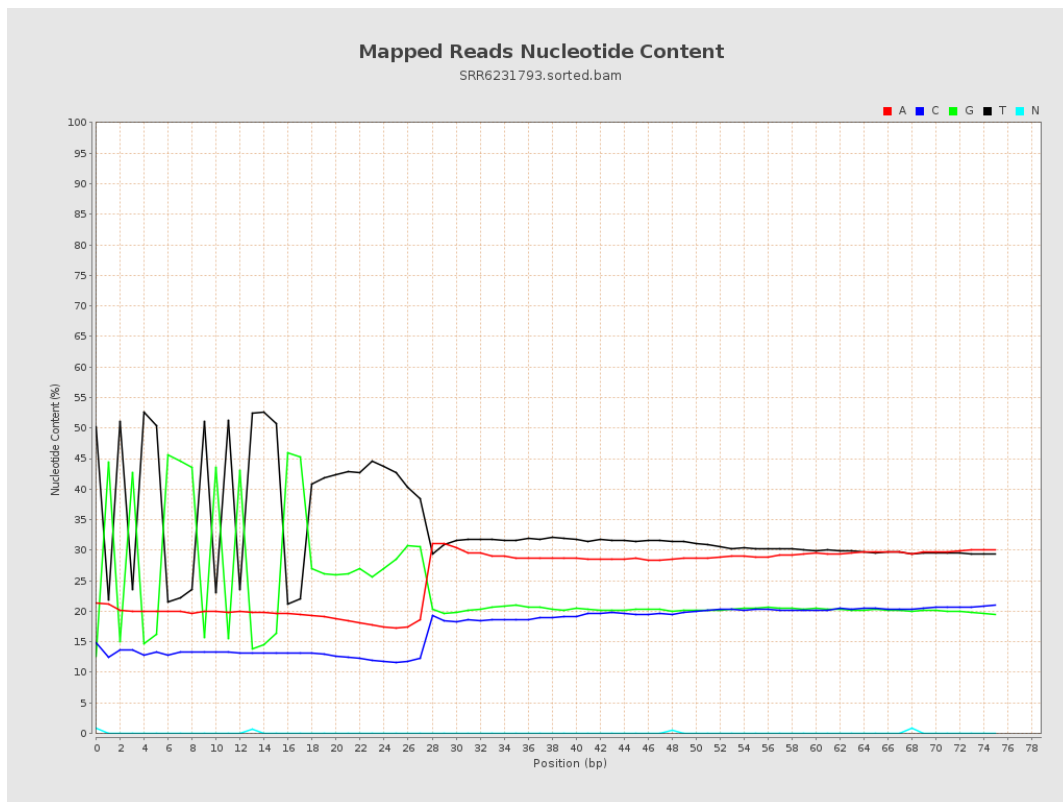
6. Results : Genome Fraction Coverage



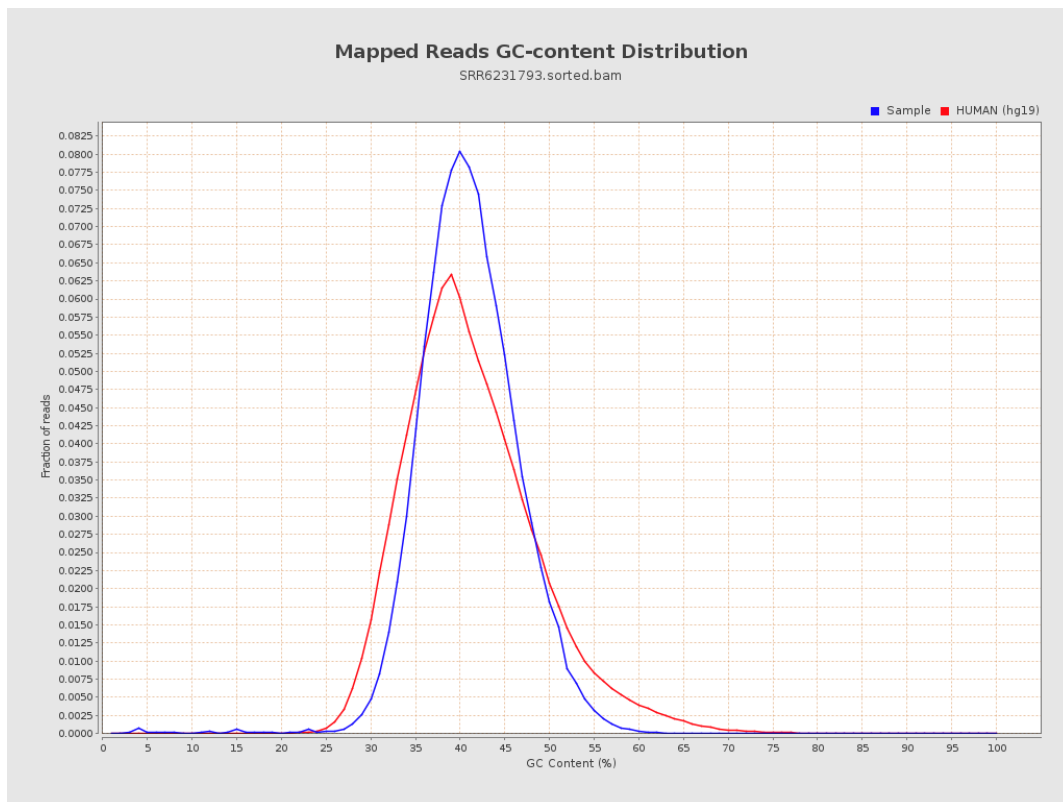
7. Results : Duplication Rate Histogram



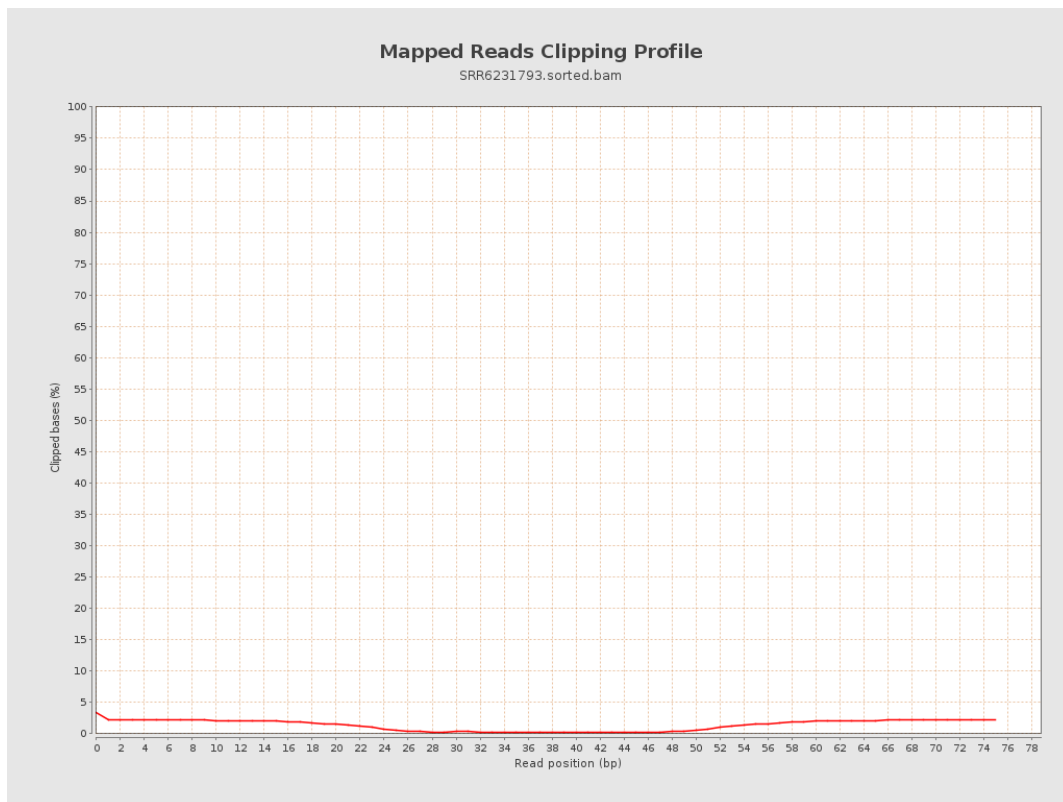
8. Results : Mapped Reads Nucleotide Content



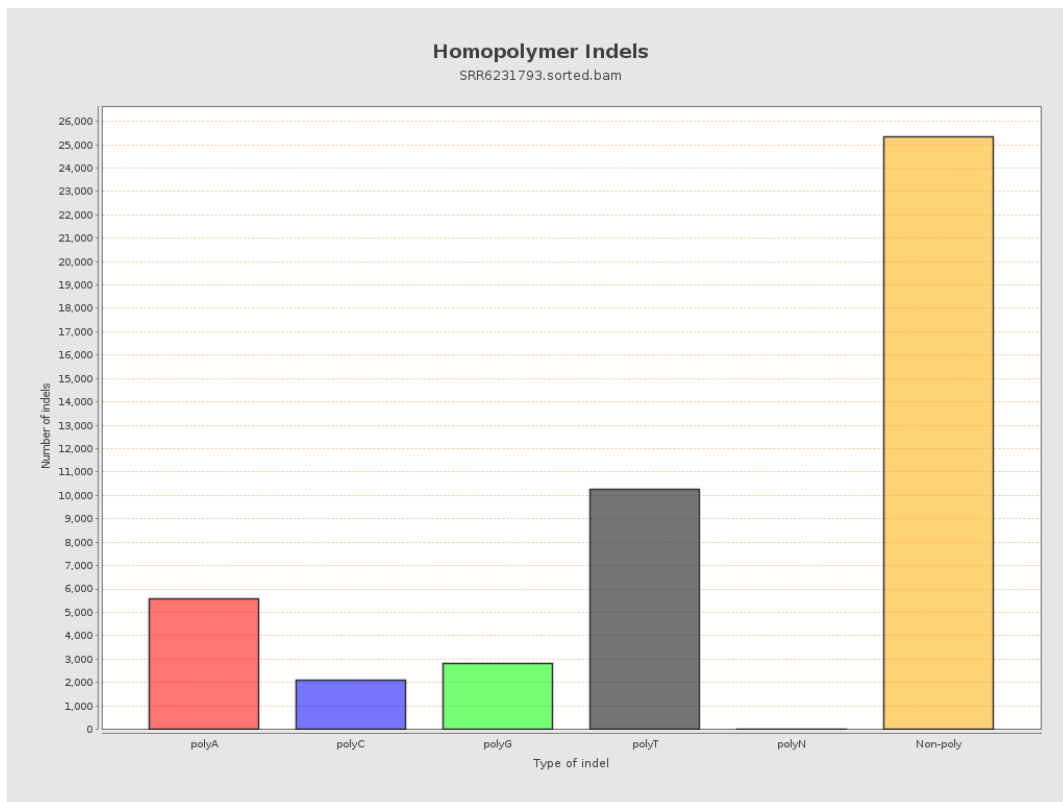
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

