

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 10:37:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231889.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_SRR6231889 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231889.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 10:37:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231889.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,981,439
Mapped reads	4,673,321 / 93.81%
Unmapped reads	308,118 / 6.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,454 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	447,946 / 8.99%
Duplication rate	3.25%
Clipped reads	1,943,913 / 39.02%

2.2. ACGT Content

Number/percentage of A's	81,803,194 / 25.92%
Number/percentage of C's	58,501,313 / 18.54%
Number/percentage of T's	89,543,407 / 28.37%
Number/percentage of G's	85,674,510 / 27.15%
Number/percentage of N's	66,459 / 0.02%
GC Percentage	45.68%

2.3. Coverage

Mean	0.102

Standard Deviation	32.5438
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2.4. Mapping Quality

Mean Mapping Quality	42.72
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2.5. Mismatches and indels

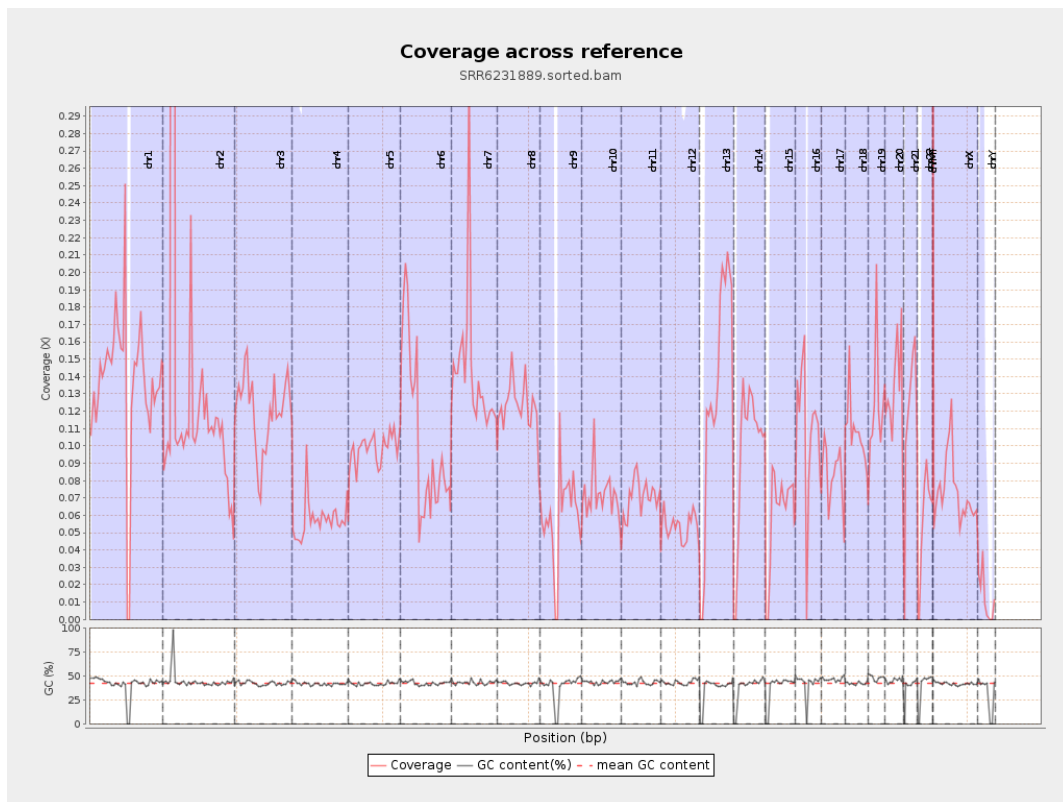
General error rate	0.71%
Mismatches	2,185,819
Insertions	23,277
Mapped reads with at least one insertion	0.49%
Deletions	74,169
Mapped reads with at least one deletion	1.57%
Homopolymer indels	45.59%

2.6. Chromosome stats

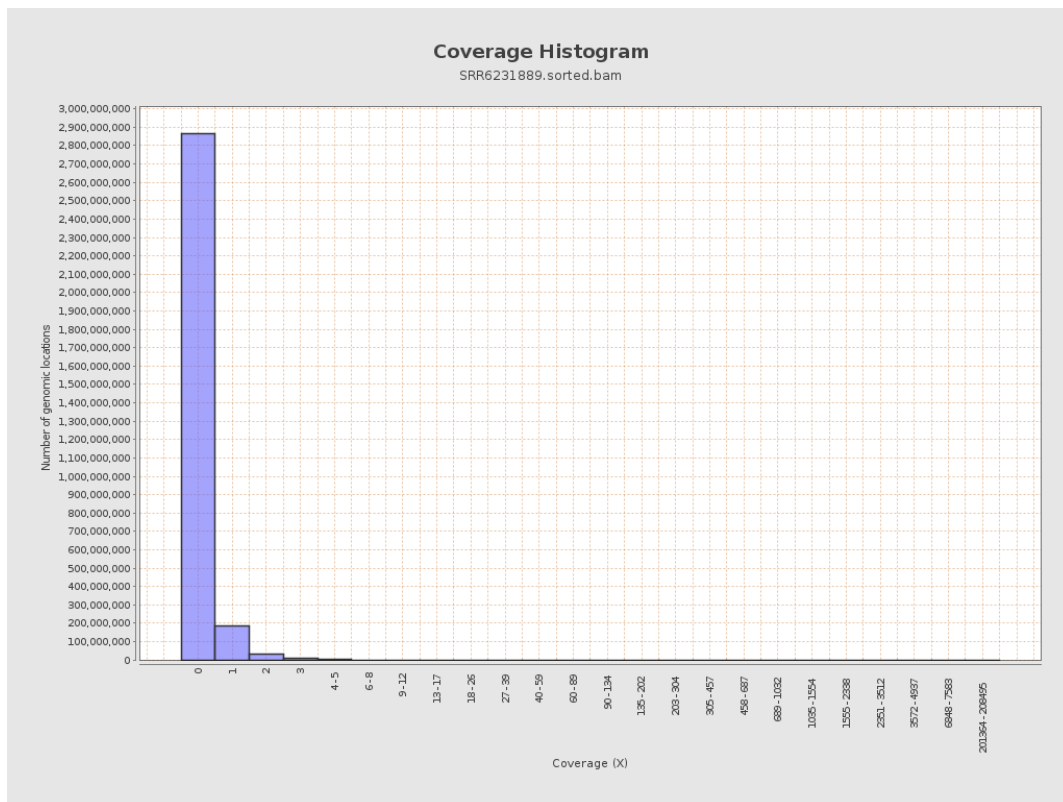
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	34108017	0.1368	2.1946
chr2	243199373	42318241	0.174	116.0472
chr3	198022430	23673462	0.1195	0.4354
chr4	191154276	11070873	0.0579	0.3521
chr5	180915260	17889380	0.0989	0.4123
chr6	171115067	17775688	0.1039	0.6178
chr7	159138663	22673208	0.1425	2.6314

chr8	146364022	17963632	0.1227	0.9006
chr9	141213431	8360495	0.0592	0.895
chr10	135534747	9724632	0.0718	0.5861
chr11	135006516	9467486	0.0701	0.8867
chr12	133851895	7223265	0.054	0.3093
chr13	115169878	15274563	0.1326	0.4649
chr14	107349540	10587333	0.0986	0.6002
chr15	102531392	6181446	0.0603	0.3161
chr16	90354753	9485055	0.105	0.5338
chr17	81195210	6892408	0.0849	0.4975
chr18	78077248	8494839	0.1088	1.9922
chr19	59128983	7361539	0.1245	1.4375
chr20	63025520	8437784	0.1339	0.5175
chr21	48129895	5709221	0.1186	0.4933
chr22	51304566	2884869	0.0562	0.2929
chrMT	16571	8704	0.5253	1.2206
chrX	155270560	11386250	0.0733	0.5574
chrY	59373566	758327	0.0128	0.2365

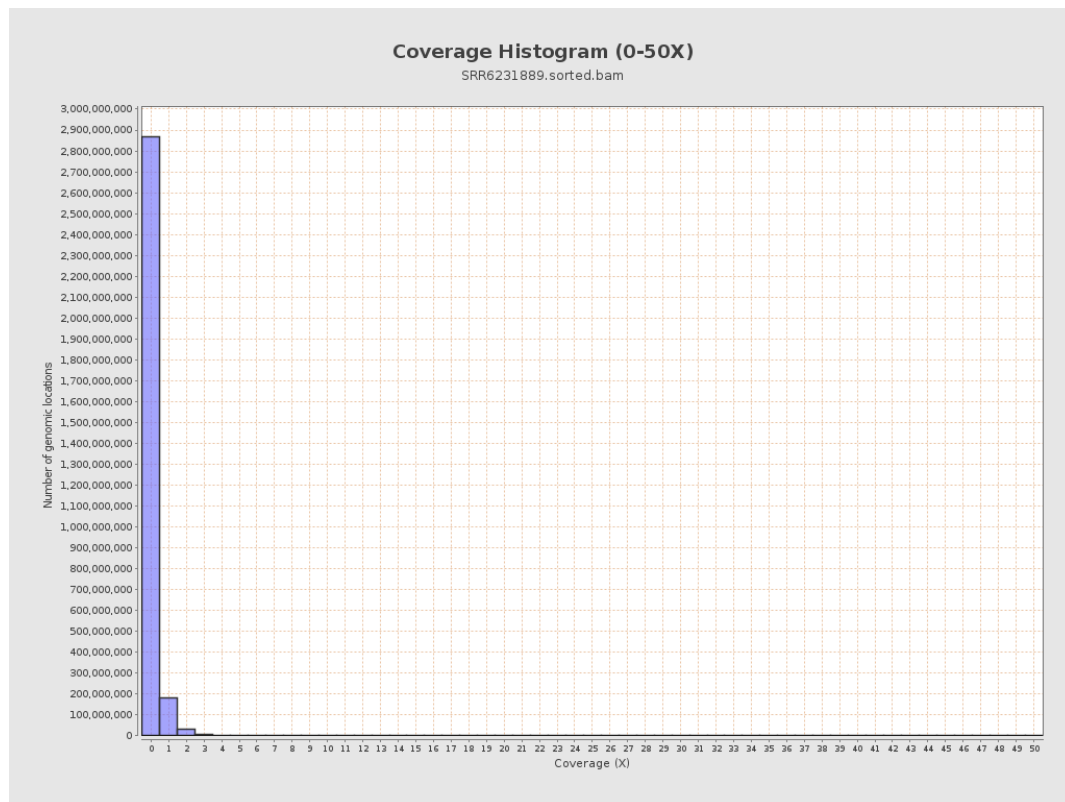
3. Results : Coverage across reference



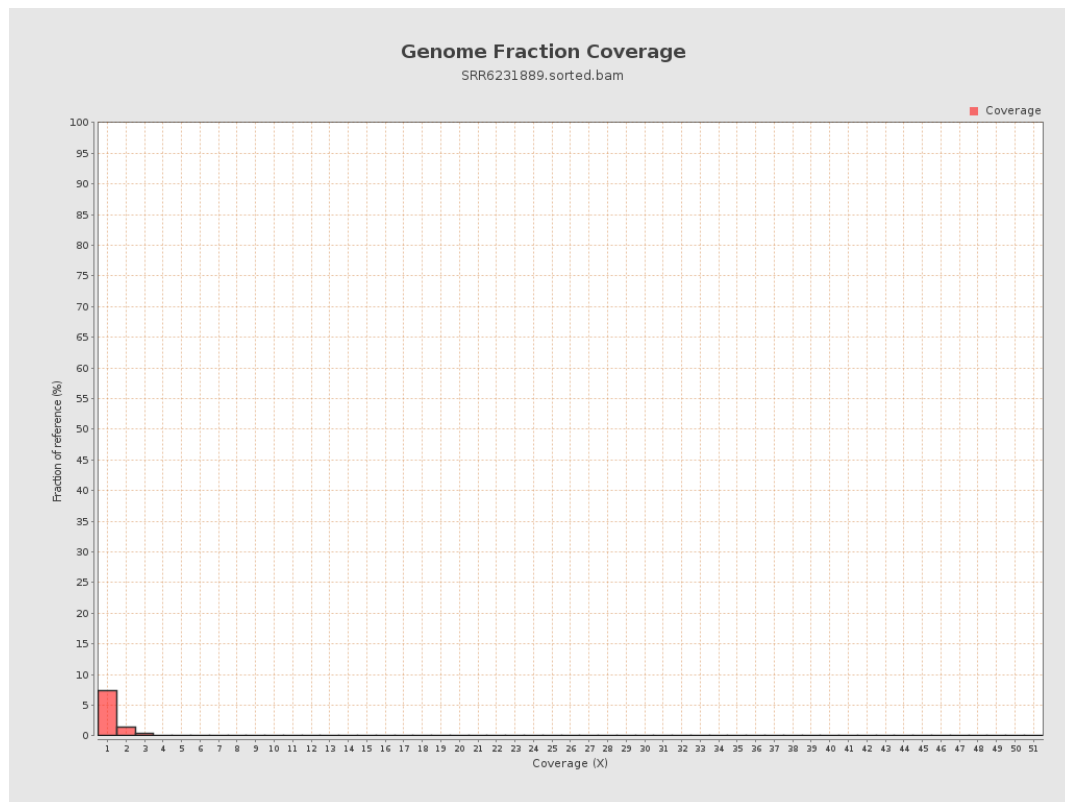
4. Results : Coverage Histogram



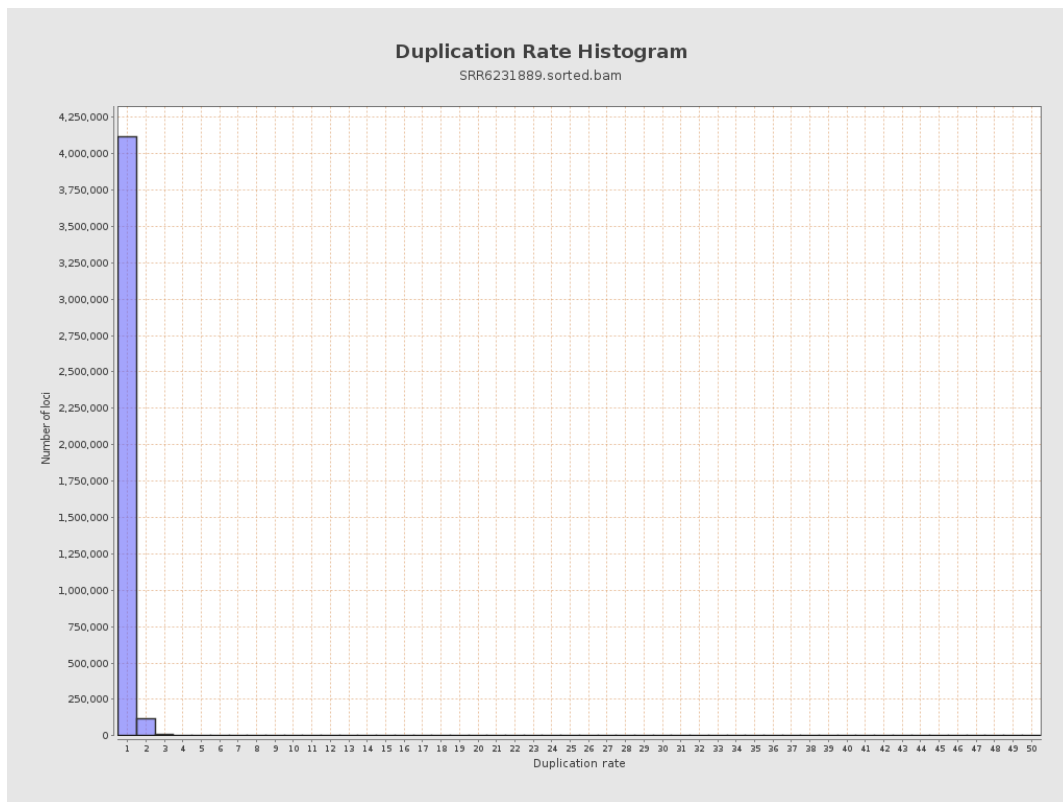
5. Results : Coverage Histogram (0-50X)



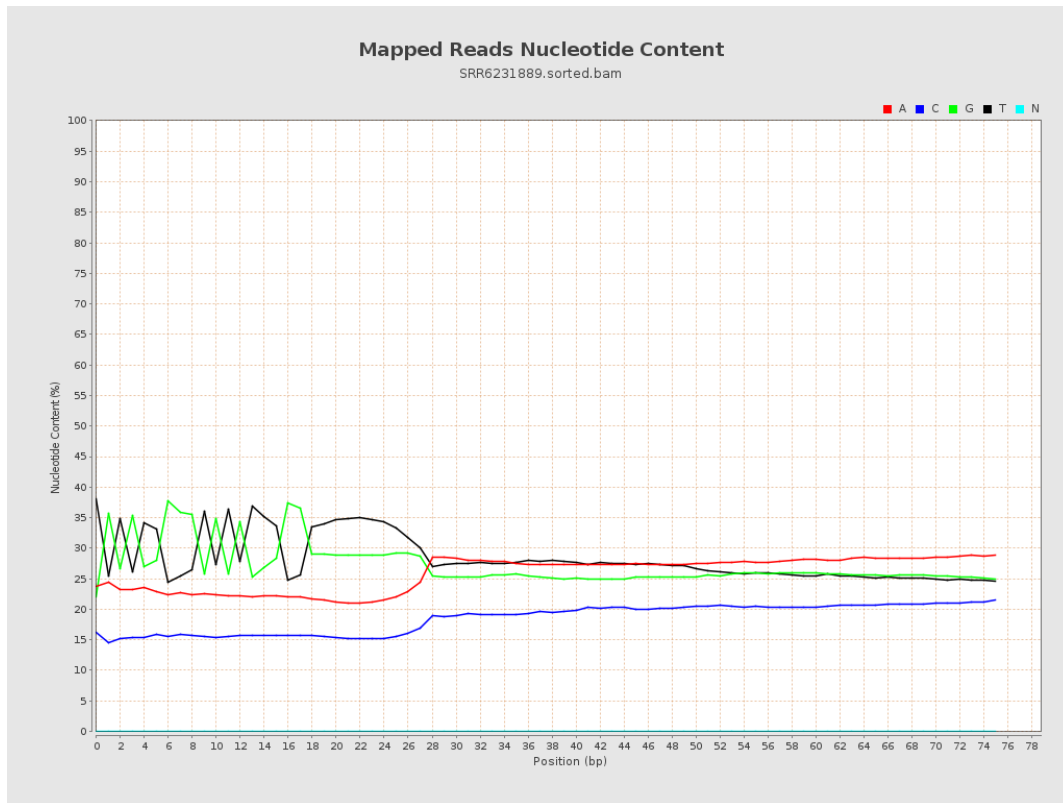
6. Results : Genome Fraction Coverage



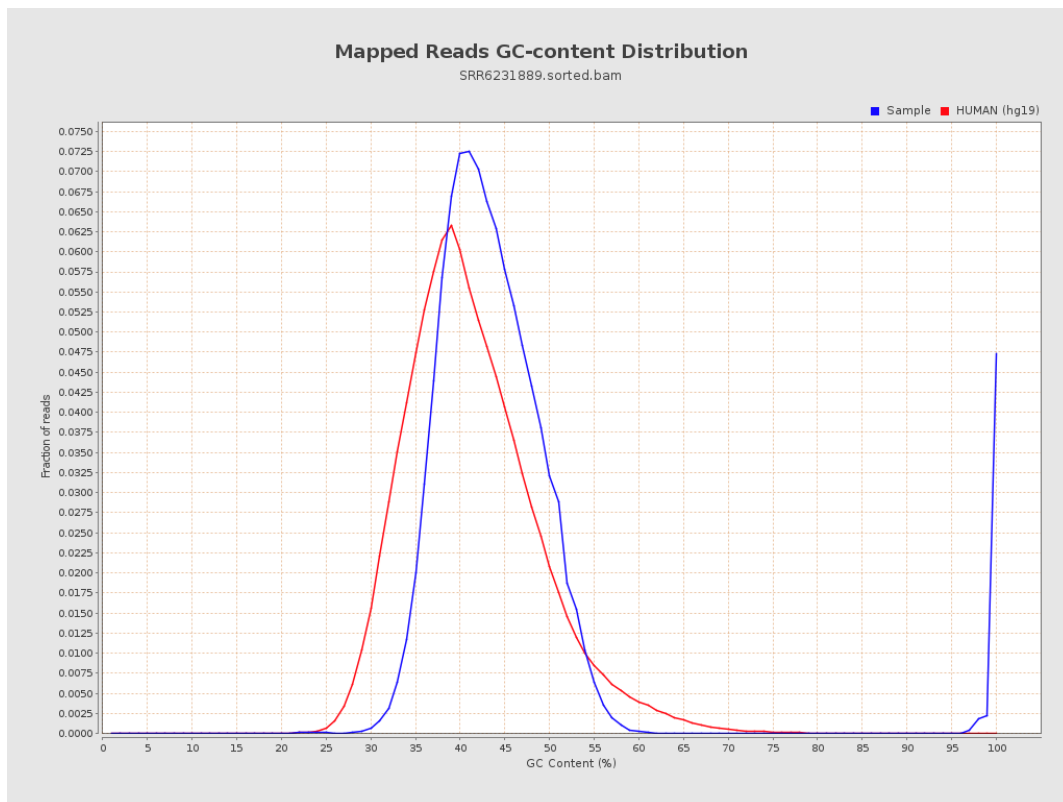
7. Results : Duplication Rate Histogram



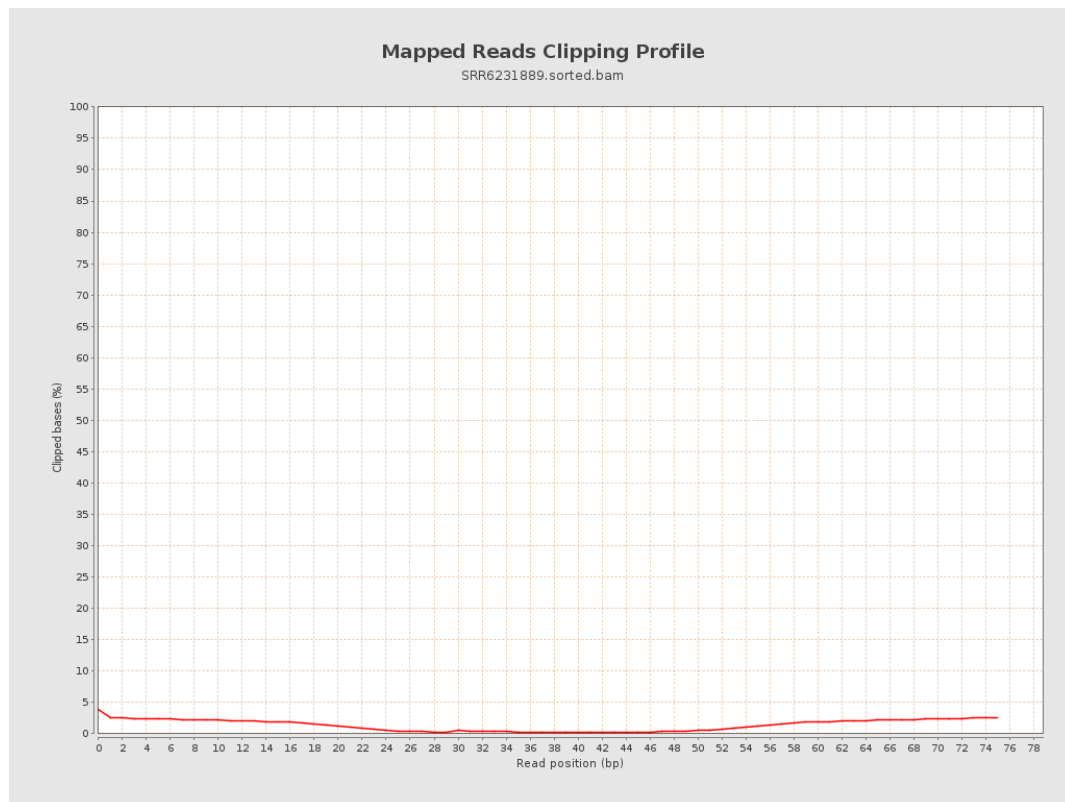
8. Results : Mapped Reads Nucleotide Content



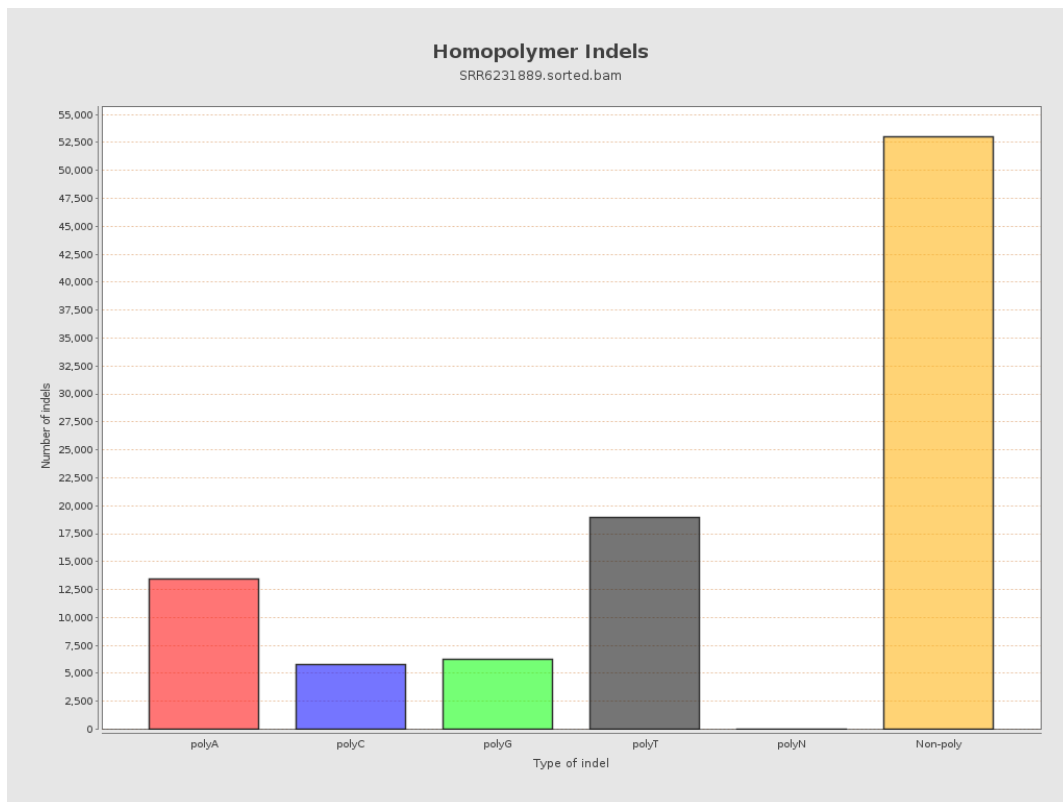
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

