

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 05:30:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231820.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_SRR6231820 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231820.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 05:30:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231820.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,185,497
Mapped reads	771,396 / 65.07%
Unmapped reads	414,101 / 34.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,353 / 0.45%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	50,661 / 4.27%
Duplication rate	5.25%
Clipped reads	419,200 / 35.36%

2.2. ACGT Content

Number/percentage of A's	13,734,559 / 27.88%
Number/percentage of C's	8,115,426 / 16.48%
Number/percentage of T's	16,585,034 / 33.67%
Number/percentage of G's	10,817,724 / 21.96%
Number/percentage of N's	5,768 / 0.01%
GC Percentage	38.44%

2.3. Coverage

Mean	0.0159

Standard Deviation	0.2375
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2.4. Mapping Quality

Mean Mapping Quality	46.24
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2.5. Mismatches and indels

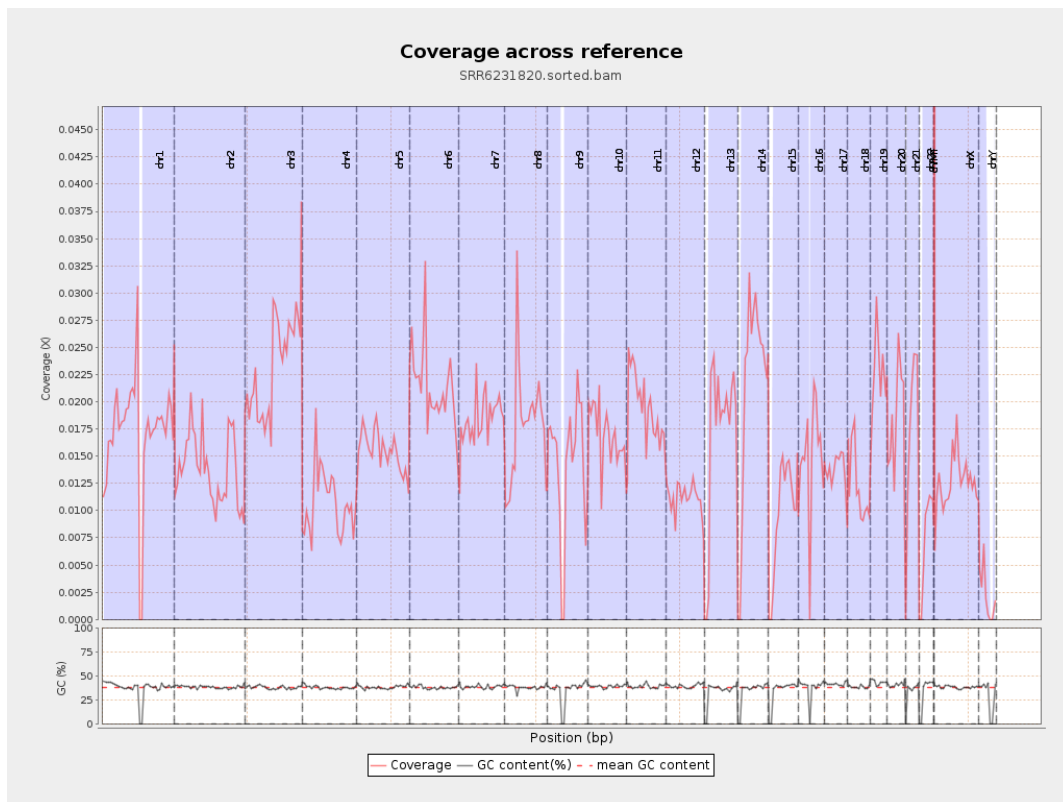
General error rate	1.02%
Mismatches	494,283
Insertions	4,292
Mapped reads with at least one insertion	0.55%
Deletions	17,987
Mapped reads with at least one deletion	2.3%
Homopolymer indels	44.21%

2.6. Chromosome stats

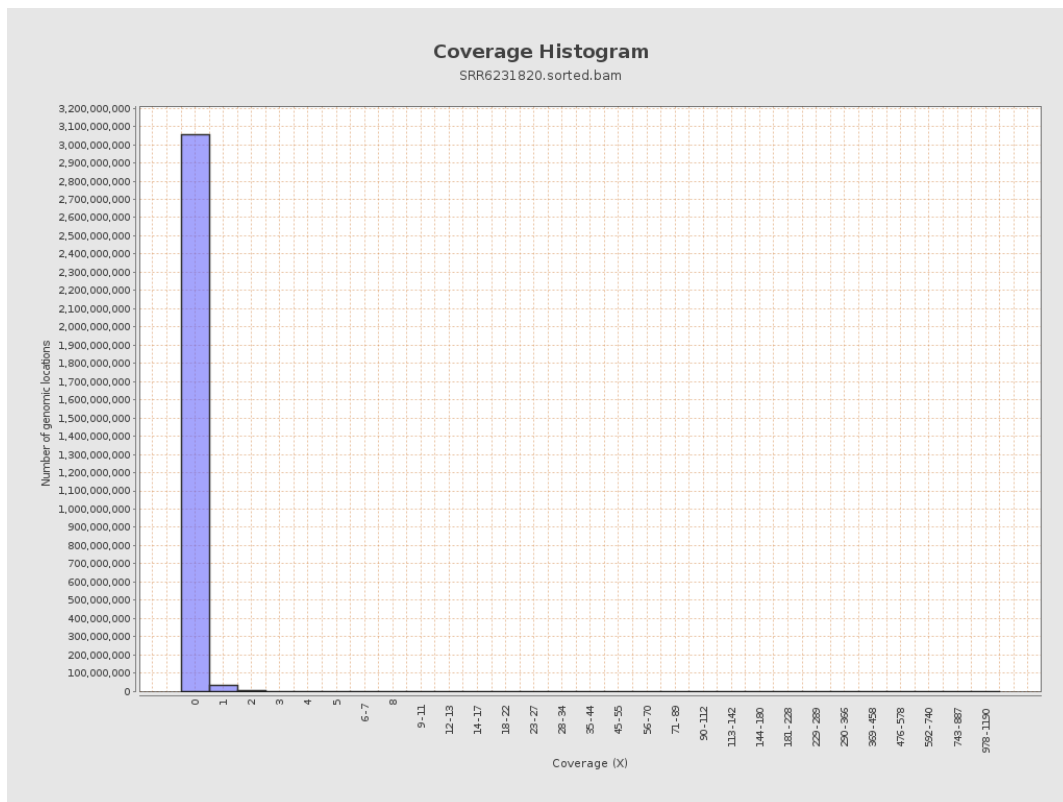
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4291070	0.0172	0.3171
chr2	243199373	3362938	0.0138	0.2155
chr3	198022430	4584456	0.0232	0.1814
chr4	191154276	2051506	0.0107	0.1246
chr5	180915260	2822287	0.0156	0.1477
chr6	171115067	3655479	0.0214	0.1917
chr7	159138663	2932671	0.0184	0.1952

chr8	146364022	2617632	0.0179	0.7137
chr9	141213431	2018392	0.0143	0.1543
chr10	135534747	2283651	0.0168	0.1692
chr11	135006516	2641719	0.0196	0.1789
chr12	133851895	1492020	0.0111	0.127
chr13	115169878	1944219	0.0169	0.1531
chr14	107349540	2324490	0.0217	0.1761
chr15	102531392	998600	0.0097	0.1177
chr16	90354753	1336710	0.0148	0.1467
chr17	81195210	1109538	0.0137	0.1403
chr18	78077248	944879	0.0121	0.2067
chr19	59128983	1345111	0.0227	0.2246
chr20	63025520	1149282	0.0182	0.1635
chr21	48129895	851336	0.0177	0.1573
chr22	51304566	379390	0.0074	0.0983
chrMT	16571	44050	2.6583	3.6852
chrX	155270560	1976003	0.0127	0.1358
chrY	59373566	132896	0.0022	0.0627

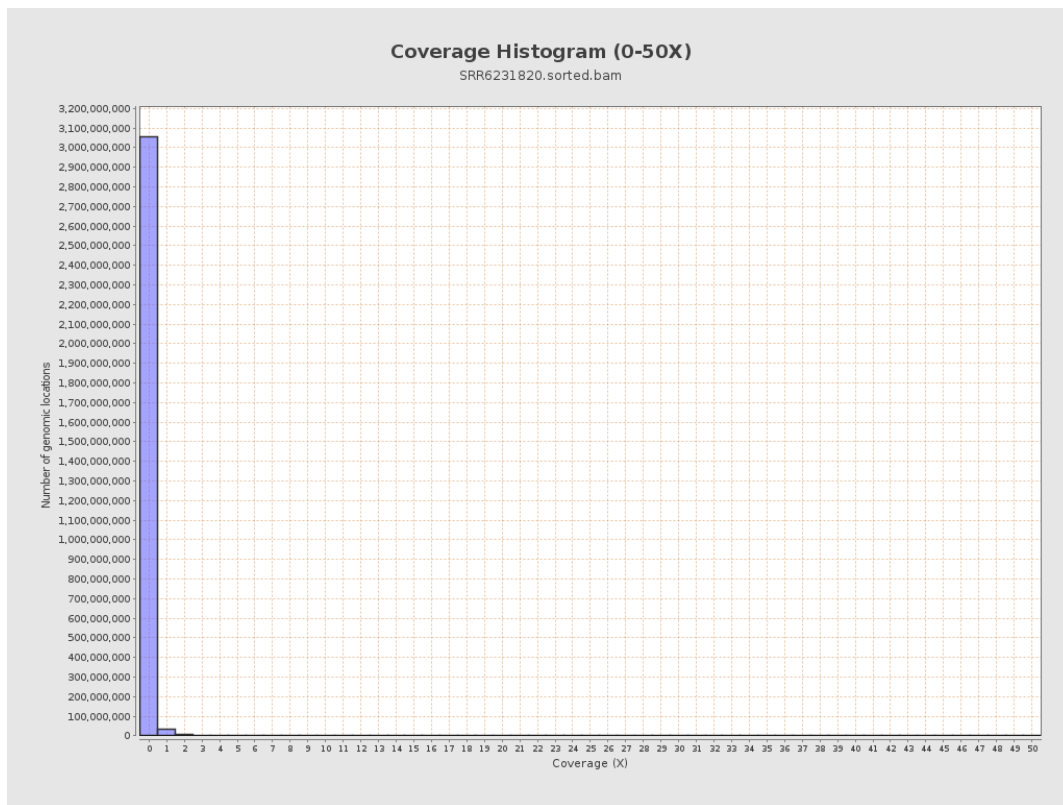
3. Results : Coverage across reference



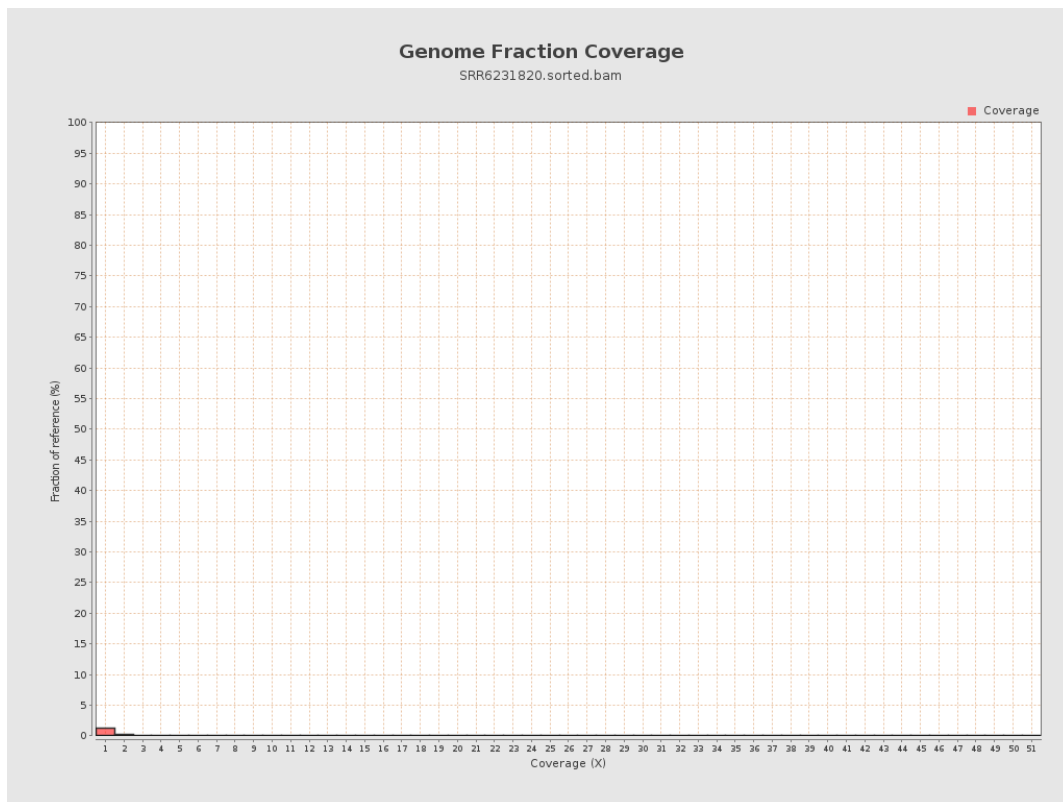
4. Results : Coverage Histogram



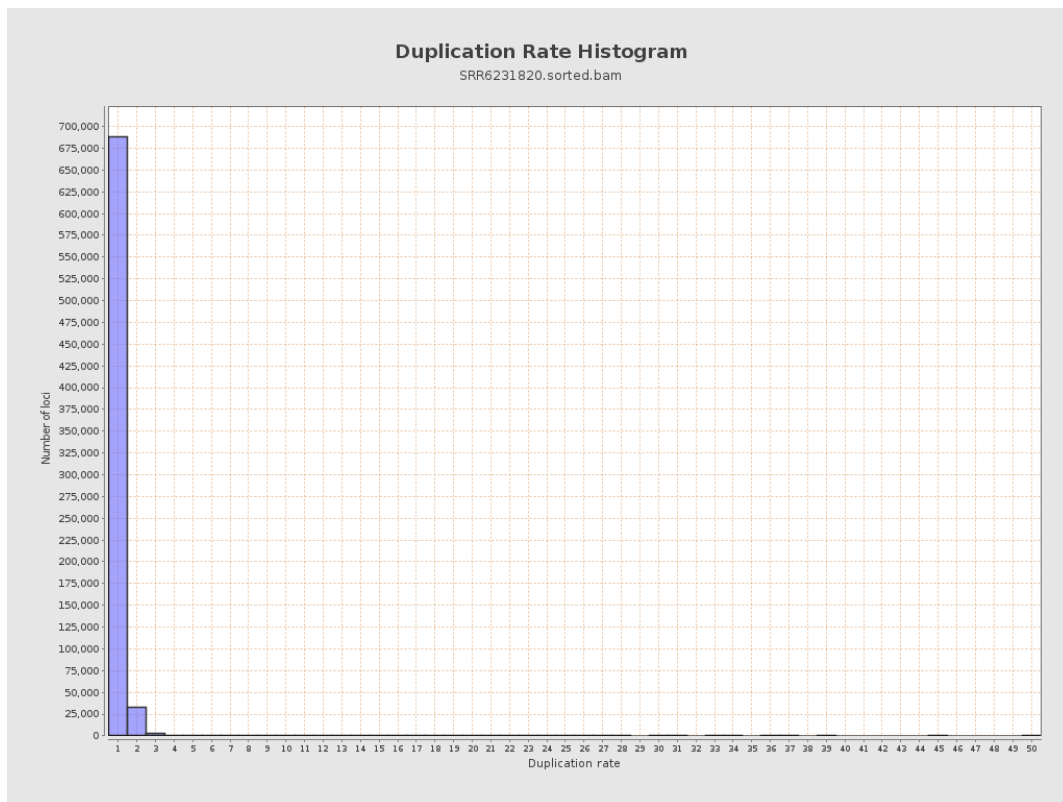
5. Results : Coverage Histogram (0-50X)



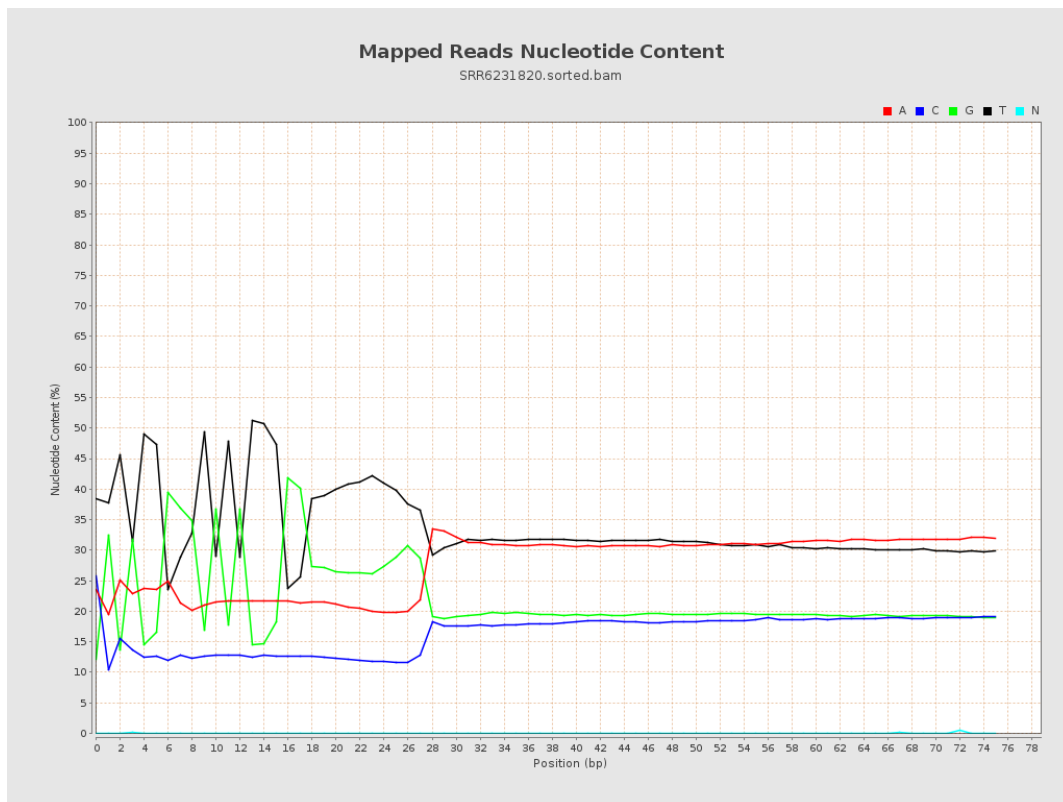
6. Results : Genome Fraction Coverage



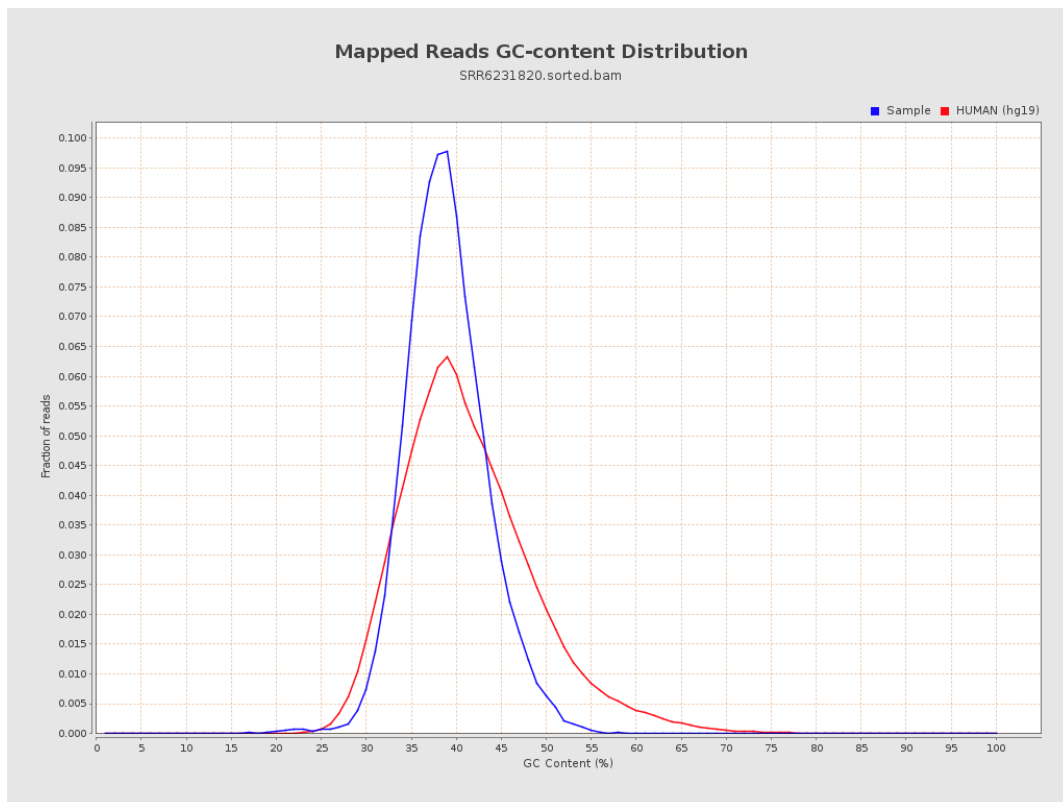
7. Results : Duplication Rate Histogram



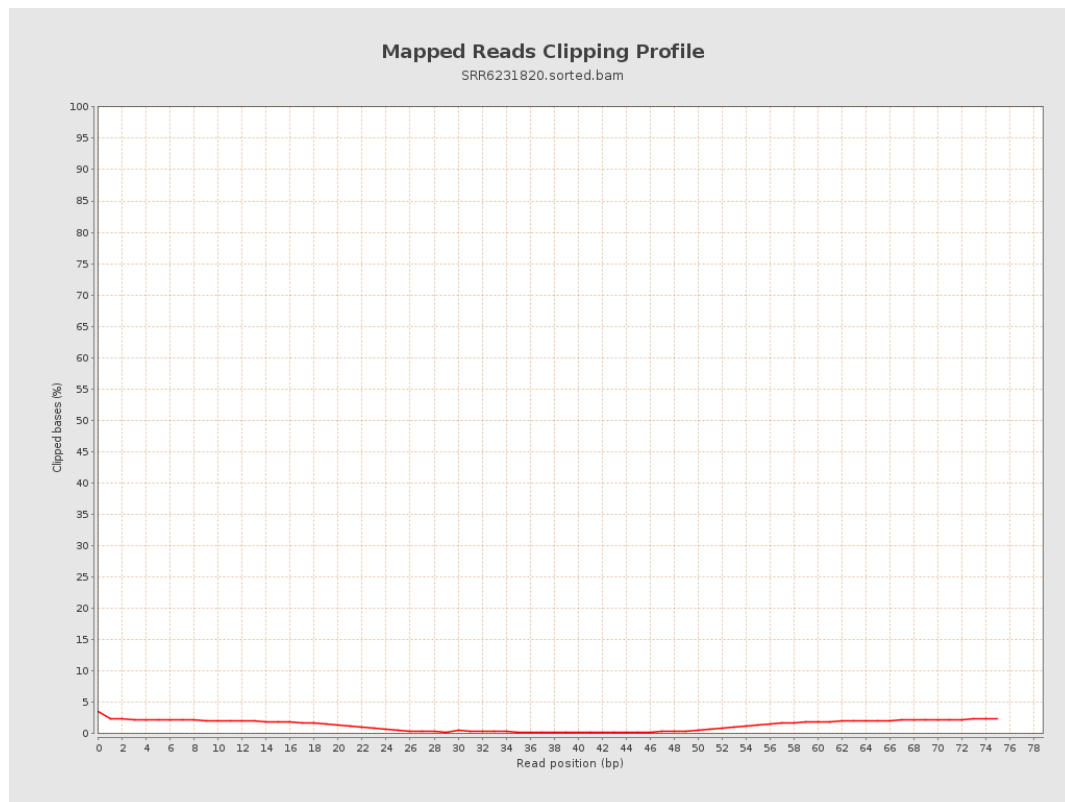
8. Results : Mapped Reads Nucleotide Content



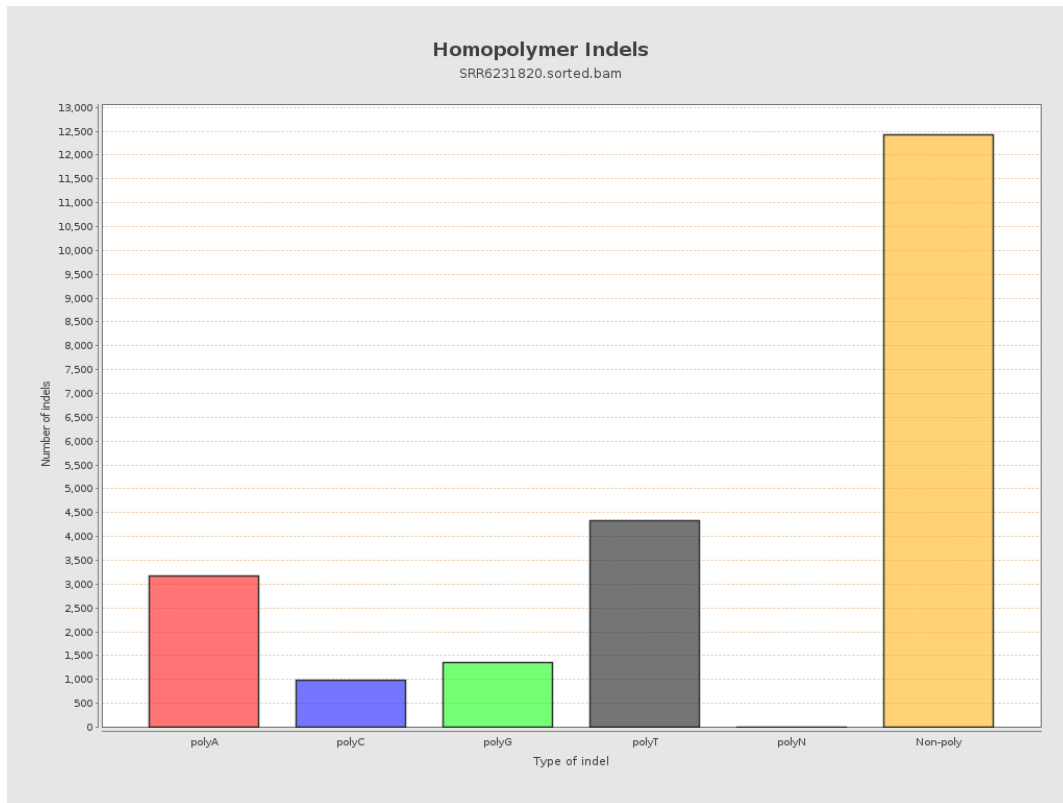
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

