

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 04:48:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231811.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_SRR6231811 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231811.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 04:48:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231811.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,409,381
Mapped reads	5,063,063 / 93.6%
Unmapped reads	346,318 / 6.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,714 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	607,937 / 11.24%
Duplication rate	9.92%
Clipped reads	2,709,697 / 50.09%

2.2. ACGT Content

Number/percentage of A's	84,584,687 / 26.01%
Number/percentage of C's	58,449,691 / 17.97%
Number/percentage of T's	106,229,049 / 32.66%
Number/percentage of G's	75,827,647 / 23.32%
Number/percentage of N's	125,338 / 0.04%
GC Percentage	41.29%

2.3. Coverage

Mean	0.1051

Standard Deviation	1.0035
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2.4. Mapping Quality

Mean Mapping Quality	45.07
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2.5. Mismatches and indels

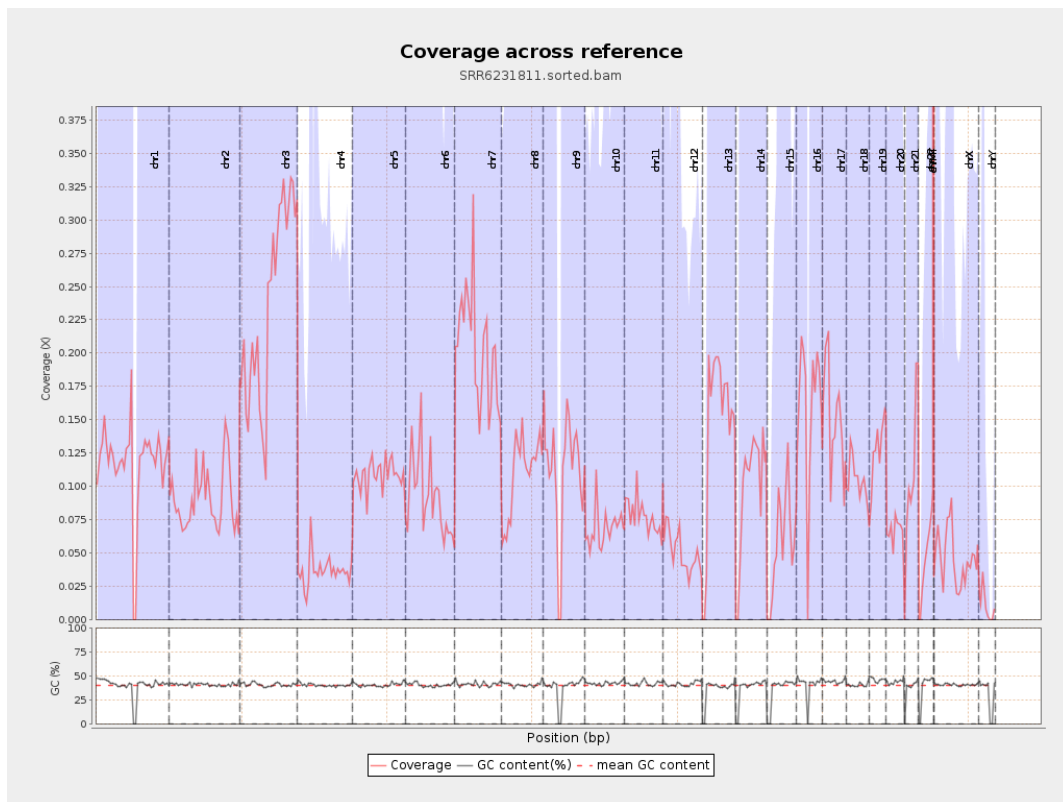
General error rate	0.62%
Mismatches	1,992,821
Insertions	20,697
Mapped reads with at least one insertion	0.41%
Deletions	68,019
Mapped reads with at least one deletion	1.33%
Homopolymer indels	44.64%

2.6. Chromosome stats

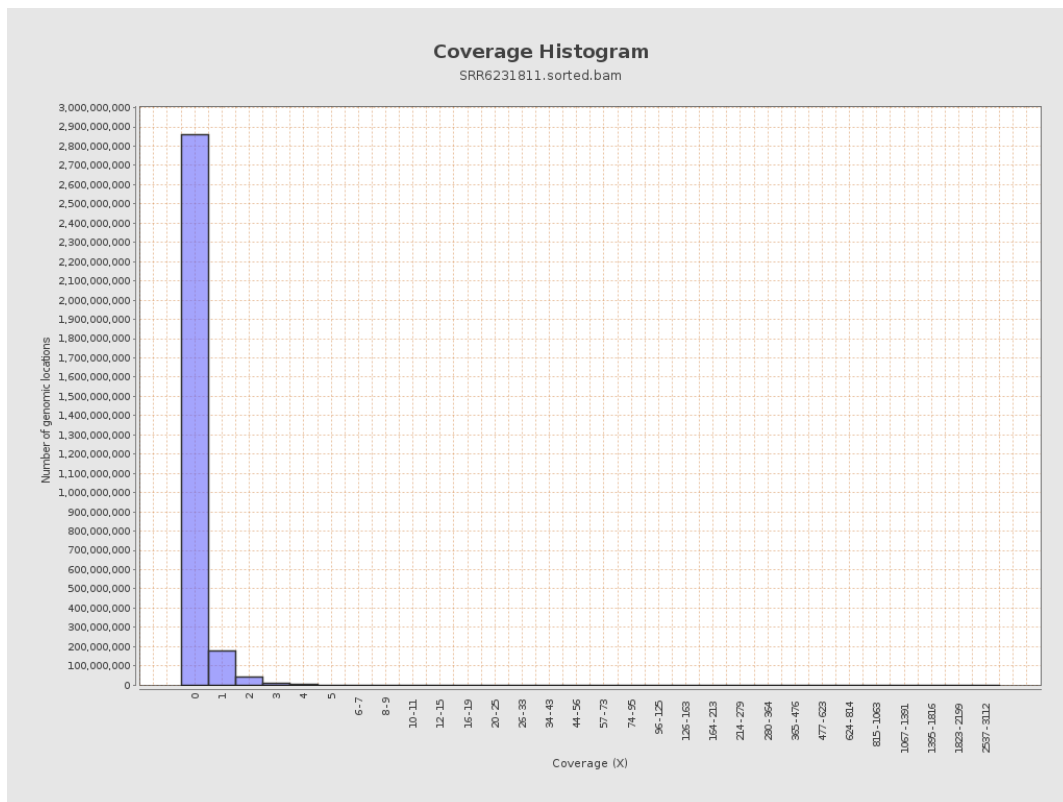
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	29152174	0.117	1.7805
chr2	243199373	21968871	0.0903	1.4954
chr3	198022430	46439267	0.2345	0.6447
chr4	191154276	6867987	0.0359	0.329
chr5	180915260	19606827	0.1084	0.4391
chr6	171115067	15777081	0.0922	0.6411
chr7	159138663	32302078	0.203	2.1486

chr8	146364022	16097254	0.11	1.1287
chr9	141213431	15440881	0.1093	0.6564
chr10	135534747	9202083	0.0679	0.6213
chr11	135006516	10381281	0.0769	0.4839
chr12	133851895	6724014	0.0502	0.3411
chr13	115169878	16801278	0.1459	0.534
chr14	107349540	10598108	0.0987	0.4982
chr15	102531392	5908779	0.0576	0.3623
chr16	90354753	14603407	0.1616	0.6143
chr17	81195210	12042400	0.1483	0.6565
chr18	78077248	8252347	0.1057	1.6158
chr19	59128983	7492437	0.1267	1.1713
chr20	63025520	4151861	0.0659	0.4249
chr21	48129895	5229698	0.1087	0.4613
chr22	51304566	2293003	0.0447	0.2654
chrMT	16571	242642	14.6426	8.6076
chrX	155270560	7169897	0.0462	0.3997
chrY	59373566	590200	0.0099	0.235

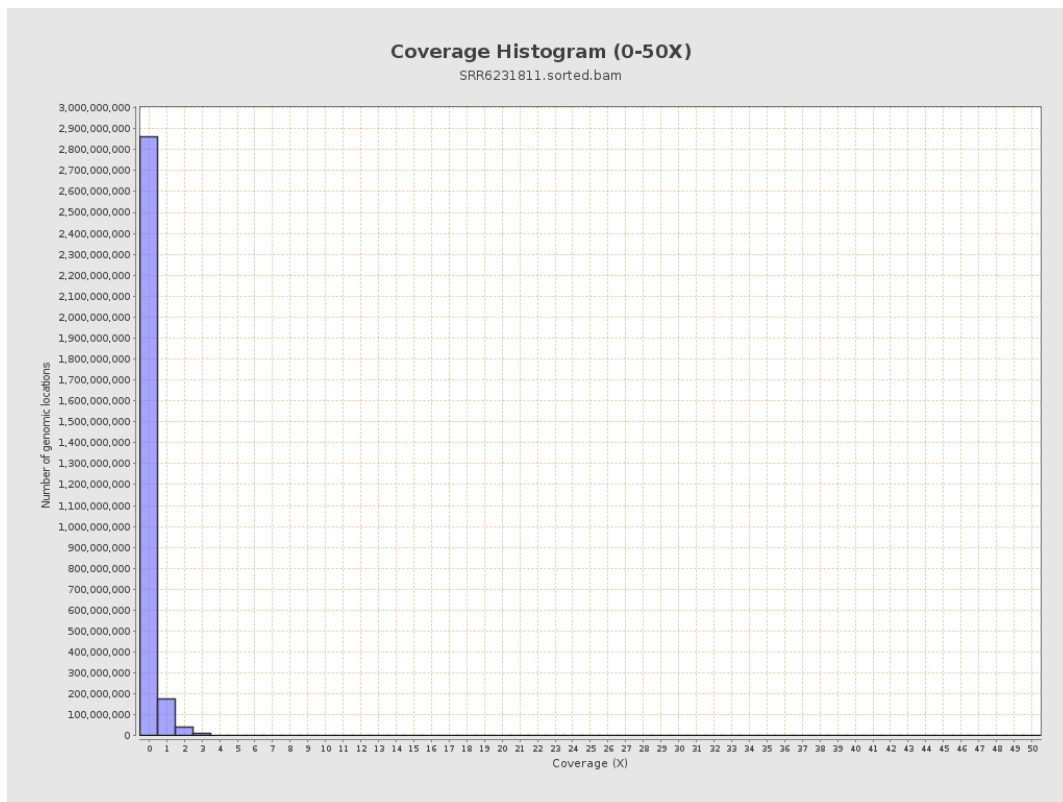
3. Results : Coverage across reference



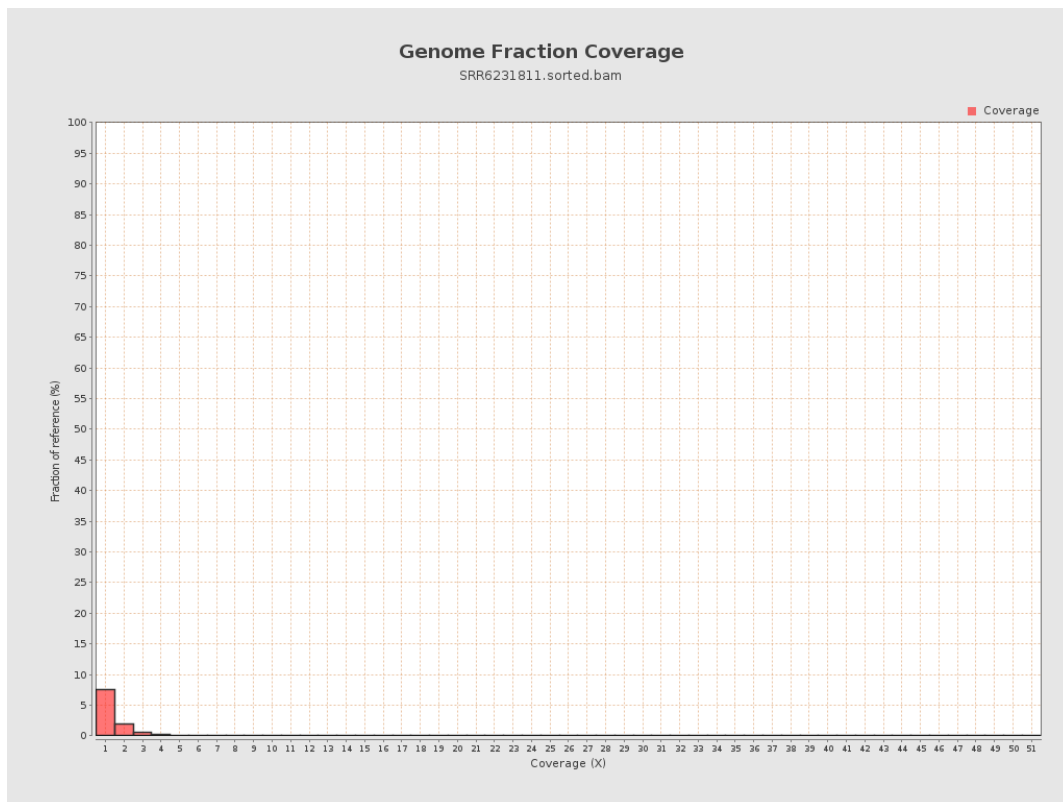
4. Results : Coverage Histogram



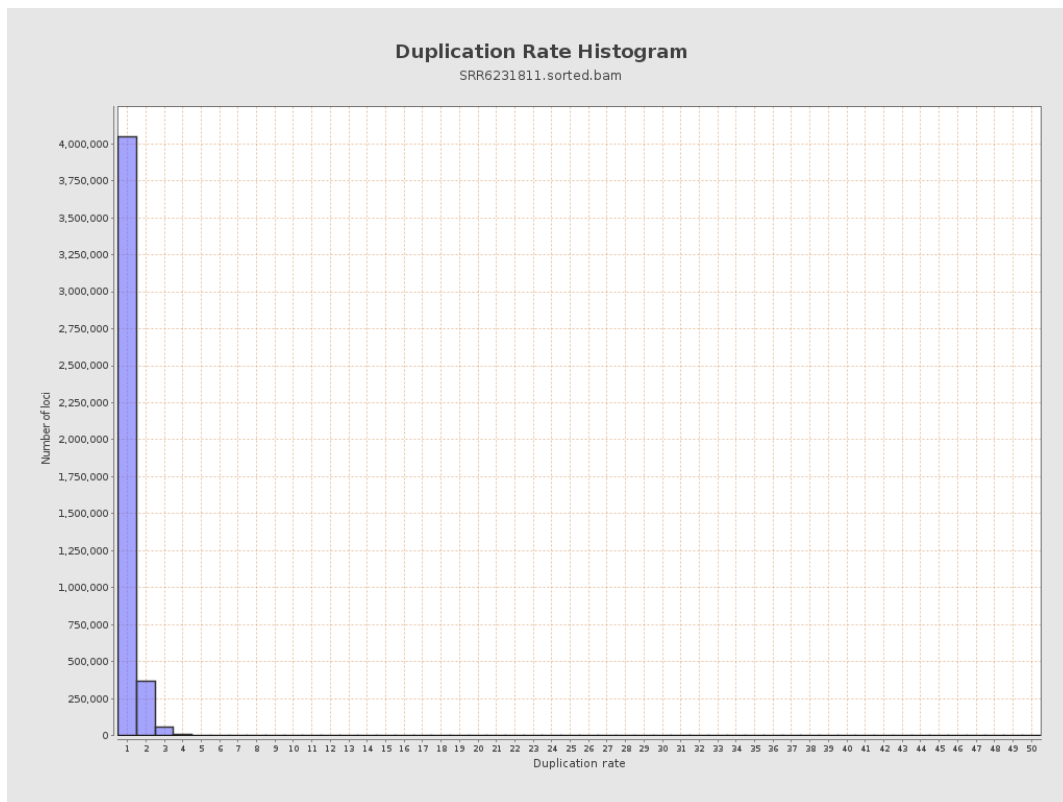
5. Results : Coverage Histogram (0-50X)



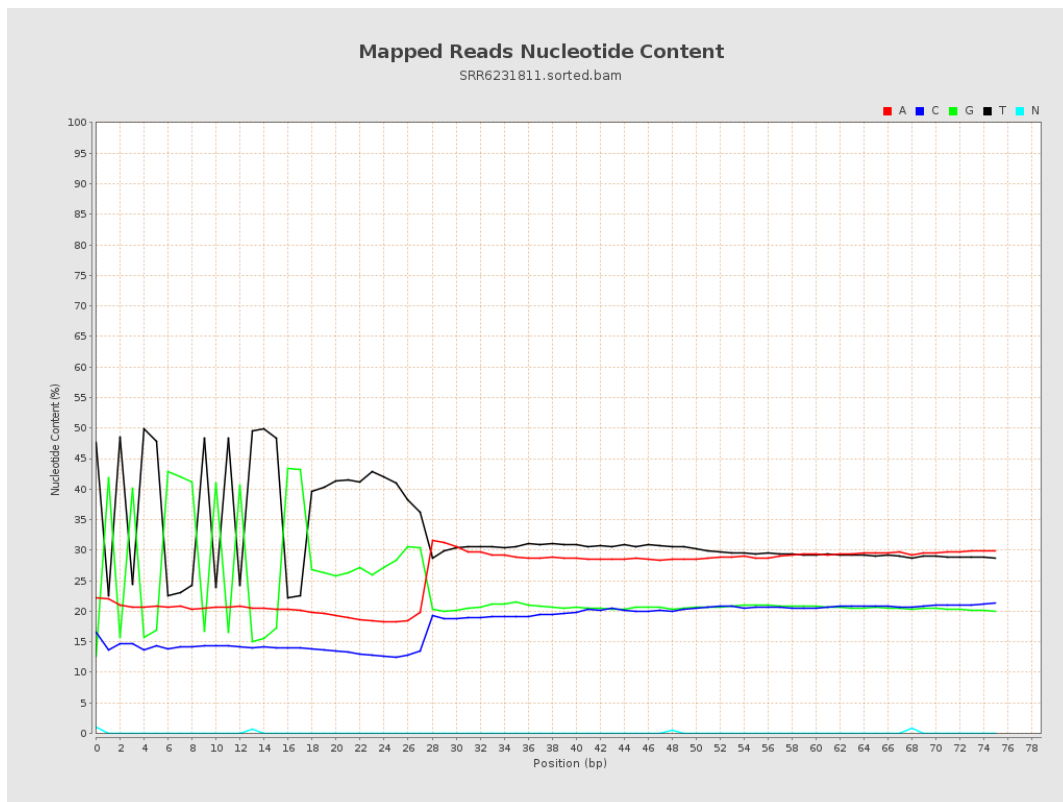
6. Results : Genome Fraction Coverage



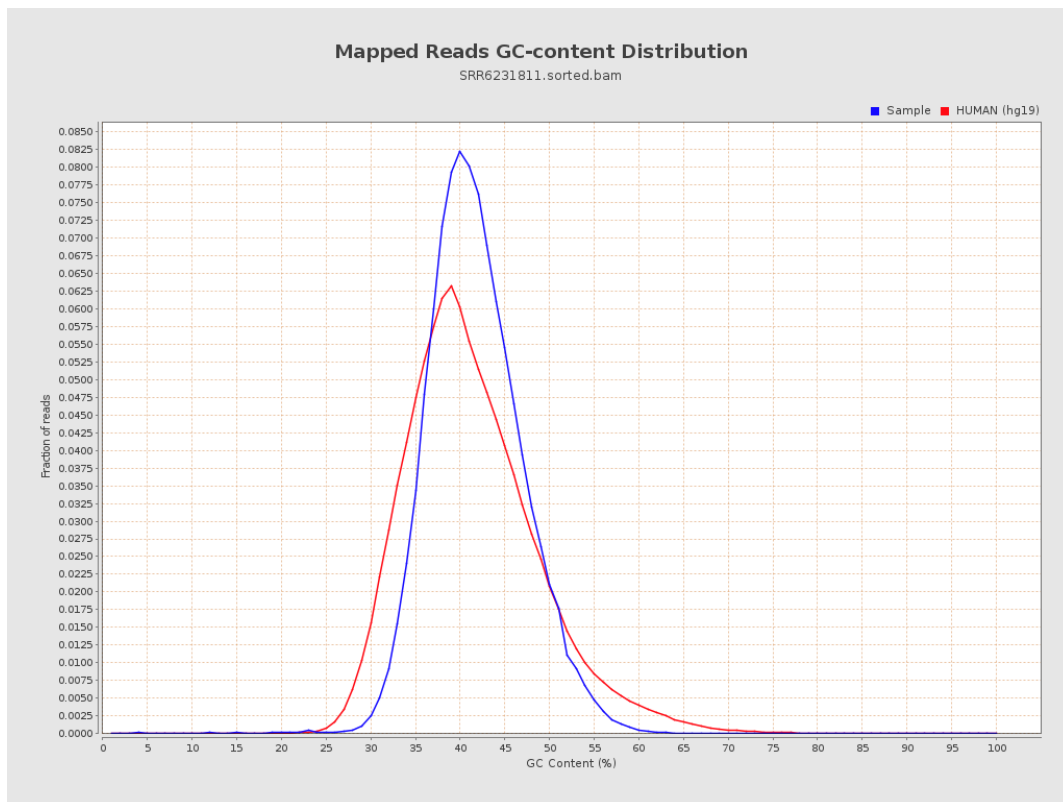
7. Results : Duplication Rate Histogram



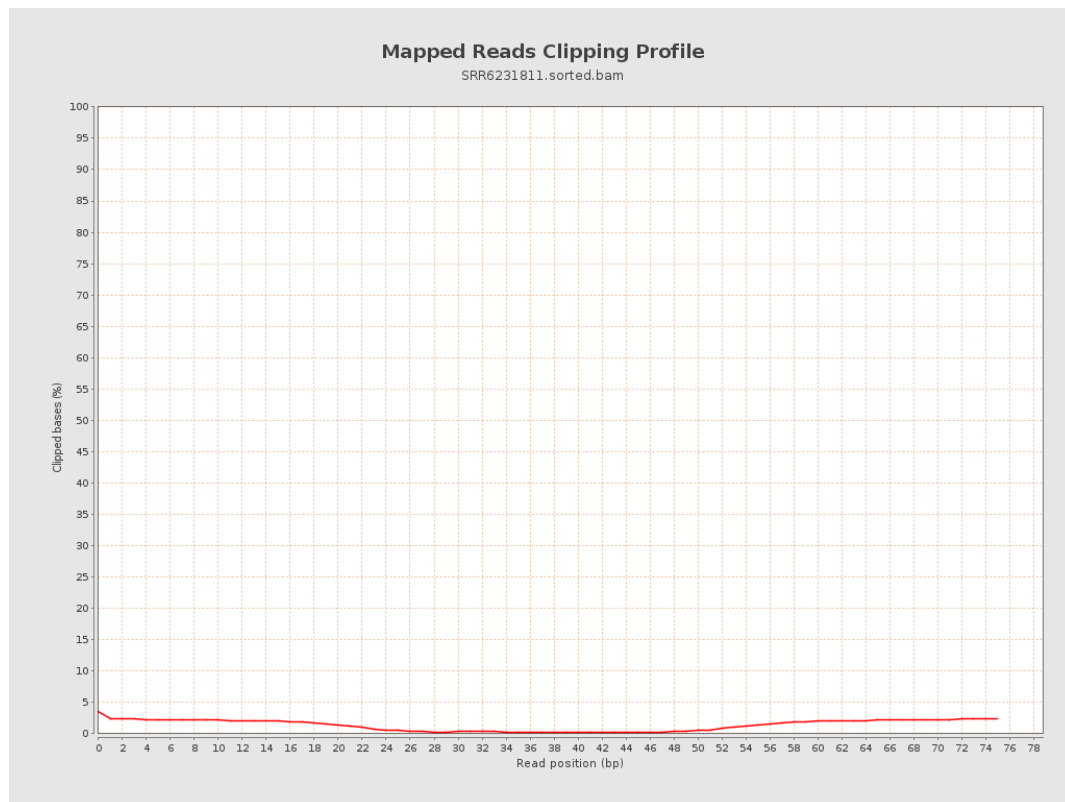
8. Results : Mapped Reads Nucleotide Content



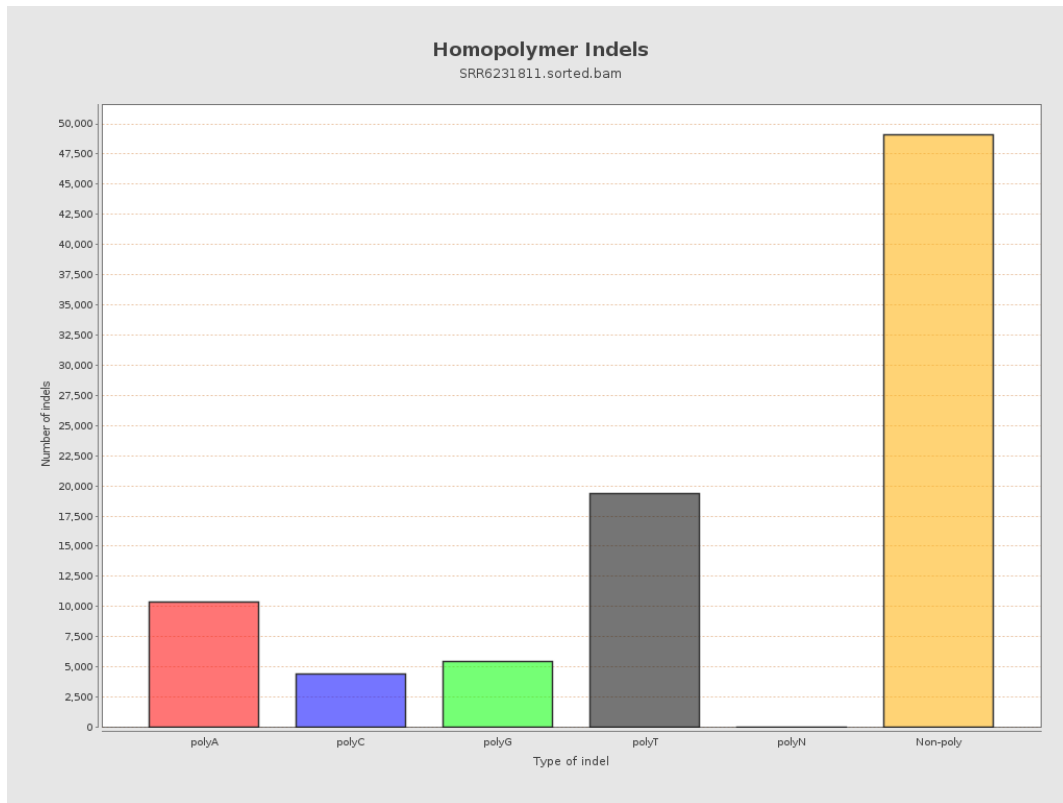
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

