

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 20:41:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236102.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_SRR6236102 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236102.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 20:41:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236102.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,889,532
Mapped reads	1,682,262 / 89.03%
Unmapped reads	207,270 / 10.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,807 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	73,362 / 3.88%
Duplication rate	3.15%
Clipped reads	718,834 / 38.04%

2.2. ACGT Content

Number/percentage of A's	31,380,834 / 27.97%
Number/percentage of C's	20,288,720 / 18.08%
Number/percentage of T's	35,818,970 / 31.92%
Number/percentage of G's	24,656,566 / 21.97%
Number/percentage of N's	59,557 / 0.05%
GC Percentage	40.06%

2.3. Coverage

Mean	0.0363

Standard Deviation	0.3941
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2.4. Mapping Quality

Mean Mapping Quality	44.26
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2.5. Mismatches and indels

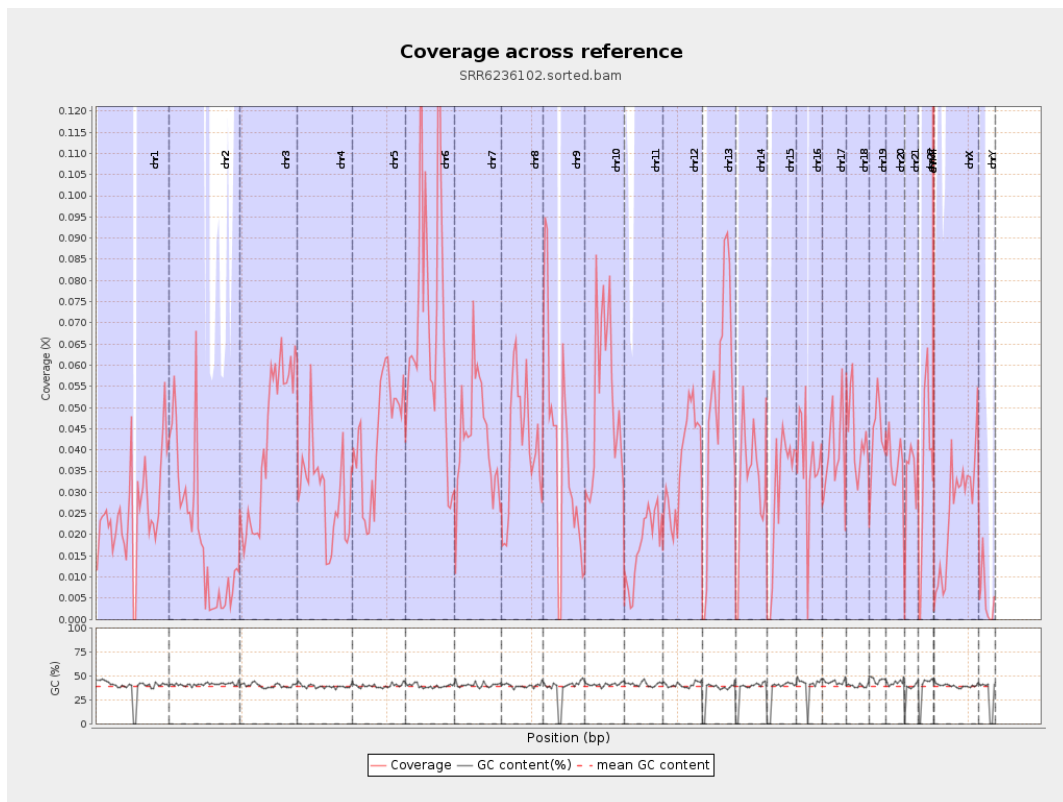
General error rate	0.85%
Mismatches	933,520
Insertions	8,883
Mapped reads with at least one insertion	0.52%
Deletions	32,548
Mapped reads with at least one deletion	1.91%
Homopolymer indels	46.51%

2.6. Chromosome stats

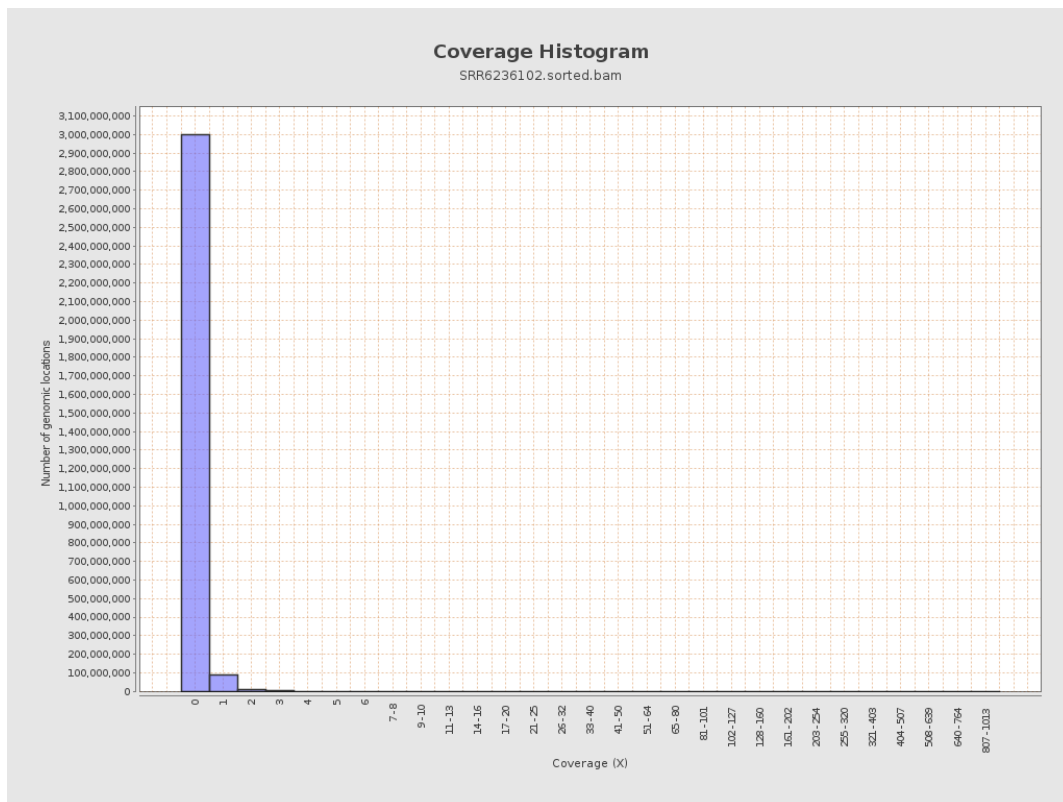
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6371076	0.0256	0.6117
chr2	243199373	4802846	0.0197	0.3824
chr3	198022430	8310935	0.042	0.2282
chr4	191154276	5687124	0.0298	0.2328
chr5	180915260	7874116	0.0435	0.2364
chr6	171115067	11722330	0.0685	0.6414
chr7	159138663	6937612	0.0436	0.4285

chr8	146364022	5928558	0.0405	0.6834
chr9	141213431	5468565	0.0387	0.4068
chr10	135534747	6974192	0.0515	0.4161
chr11	135006516	2351330	0.0174	0.2227
chr12	133851895	4962172	0.0371	0.2213
chr13	115169878	5903085	0.0513	0.2512
chr14	107349540	3383113	0.0315	0.2244
chr15	102531392	3049033	0.0297	0.1929
chr16	90354753	3329080	0.0368	0.2625
chr17	81195210	3164681	0.039	0.2564
chr18	78077248	3406073	0.0436	0.6893
chr19	59128983	2604161	0.044	0.4105
chr20	63025520	2309366	0.0366	0.2206
chr21	48129895	1597453	0.0332	0.2496
chr22	51304566	1781538	0.0347	0.2051
chrMT	16571	94060	5.6762	4.0201
chrX	155270560	3955950	0.0255	0.2099
chrY	59373566	293812	0.0049	0.1711

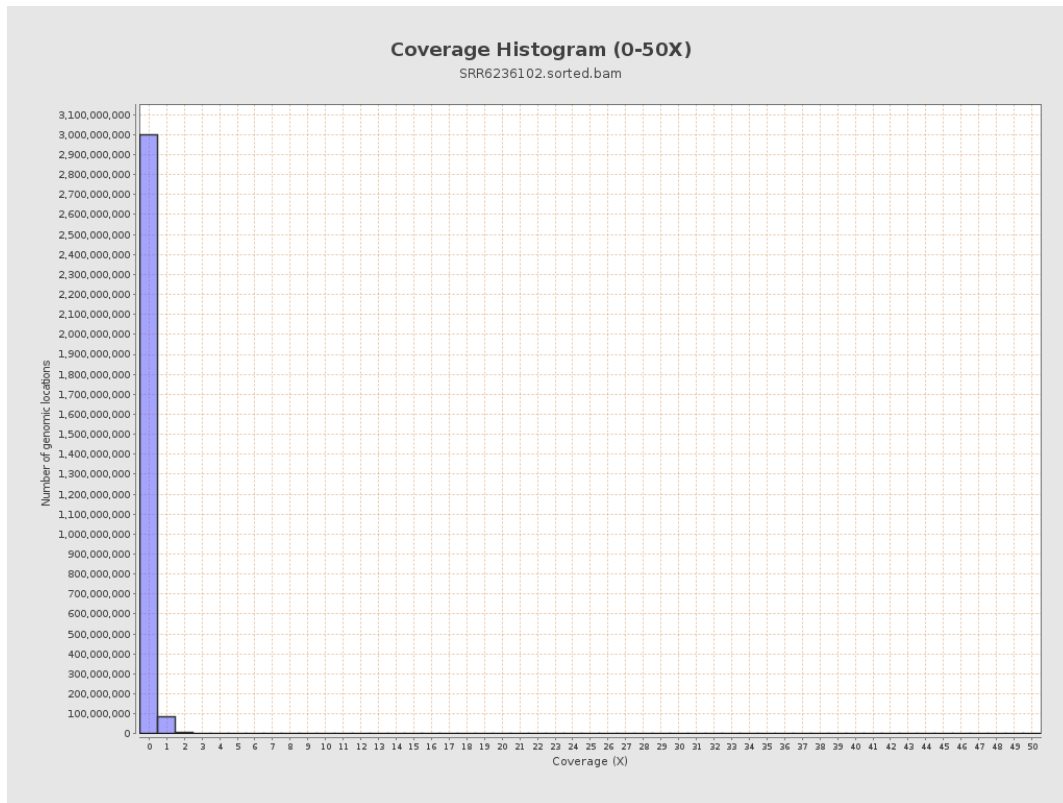
3. Results : Coverage across reference



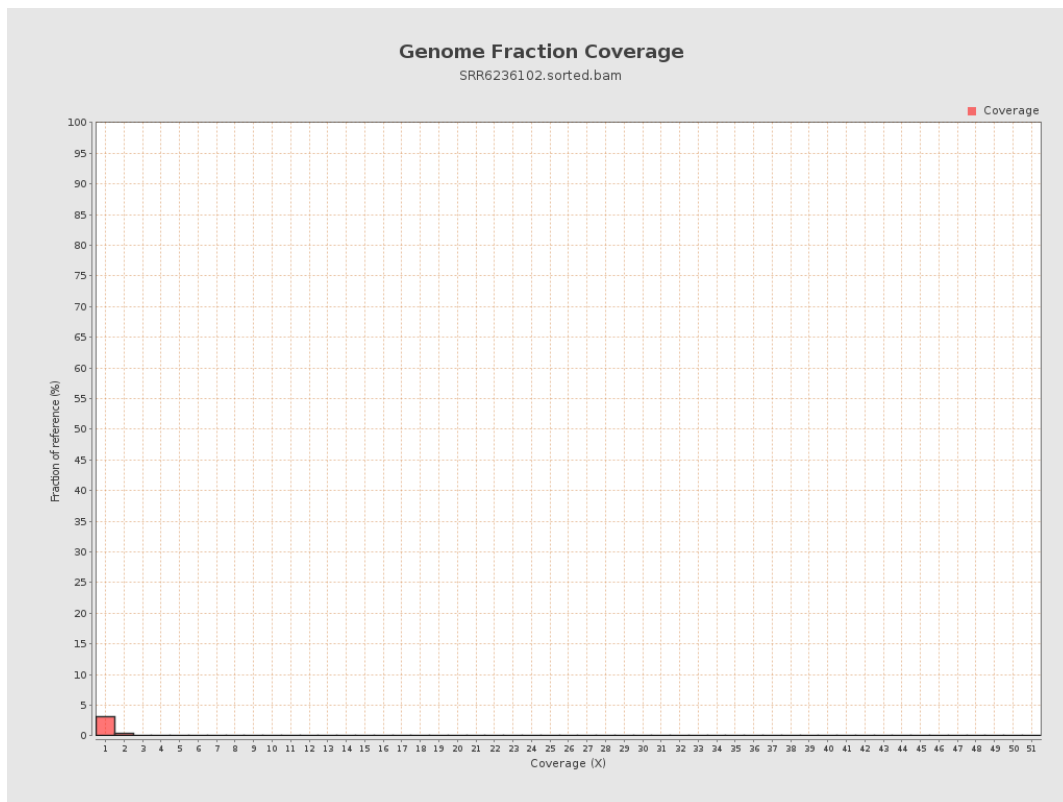
4. Results : Coverage Histogram



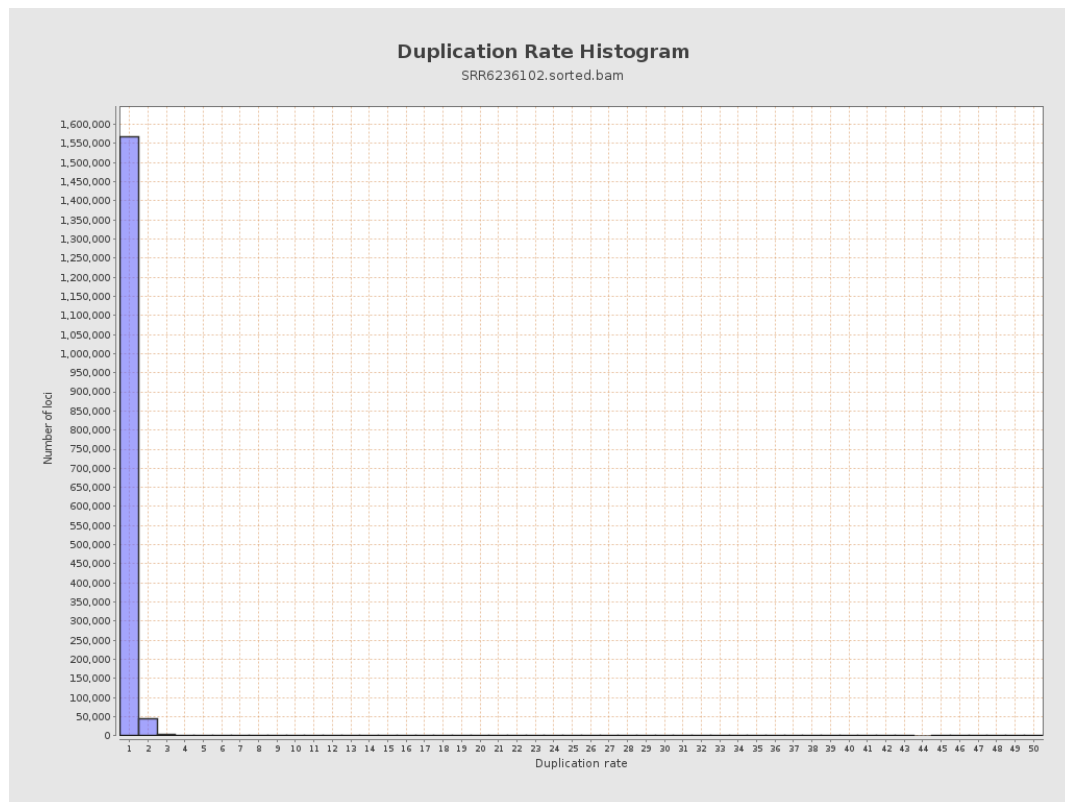
5. Results : Coverage Histogram (0-50X)



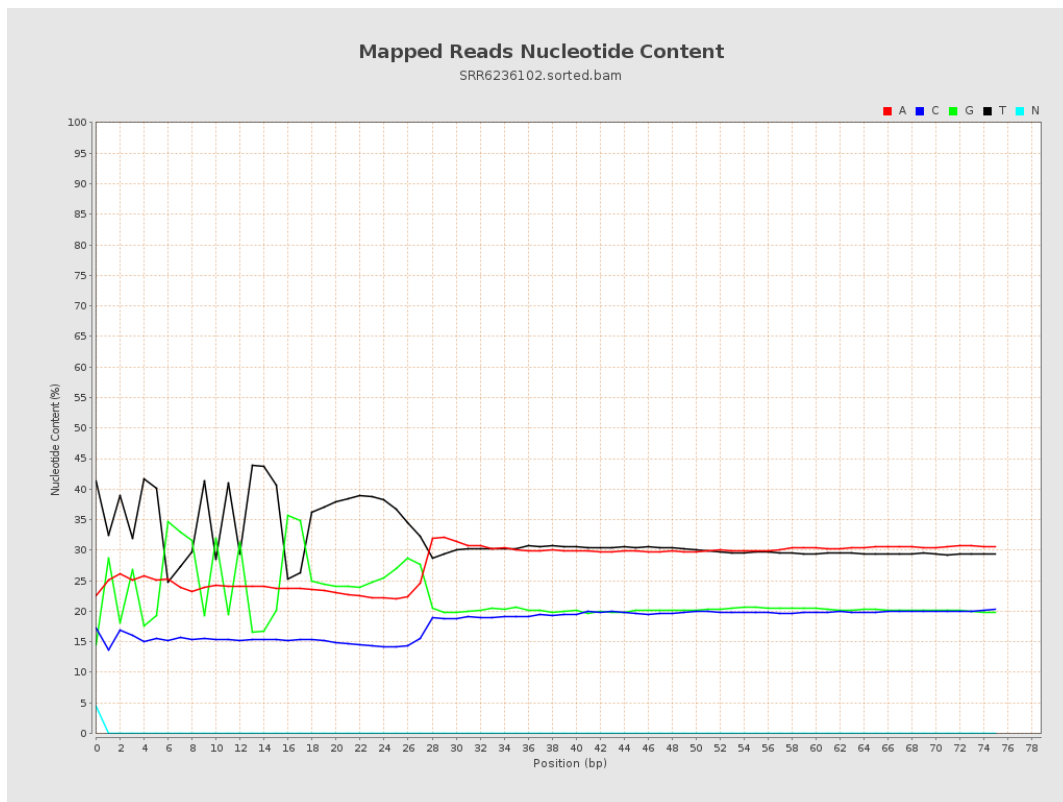
6. Results : Genome Fraction Coverage



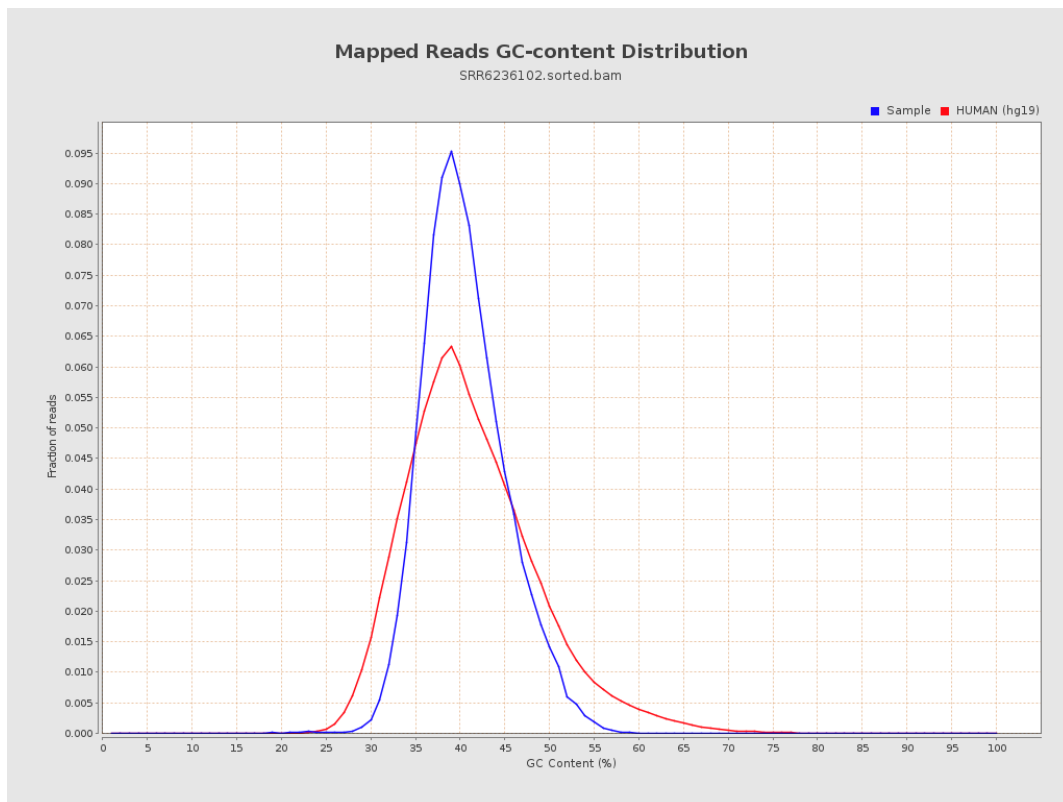
7. Results : Duplication Rate Histogram



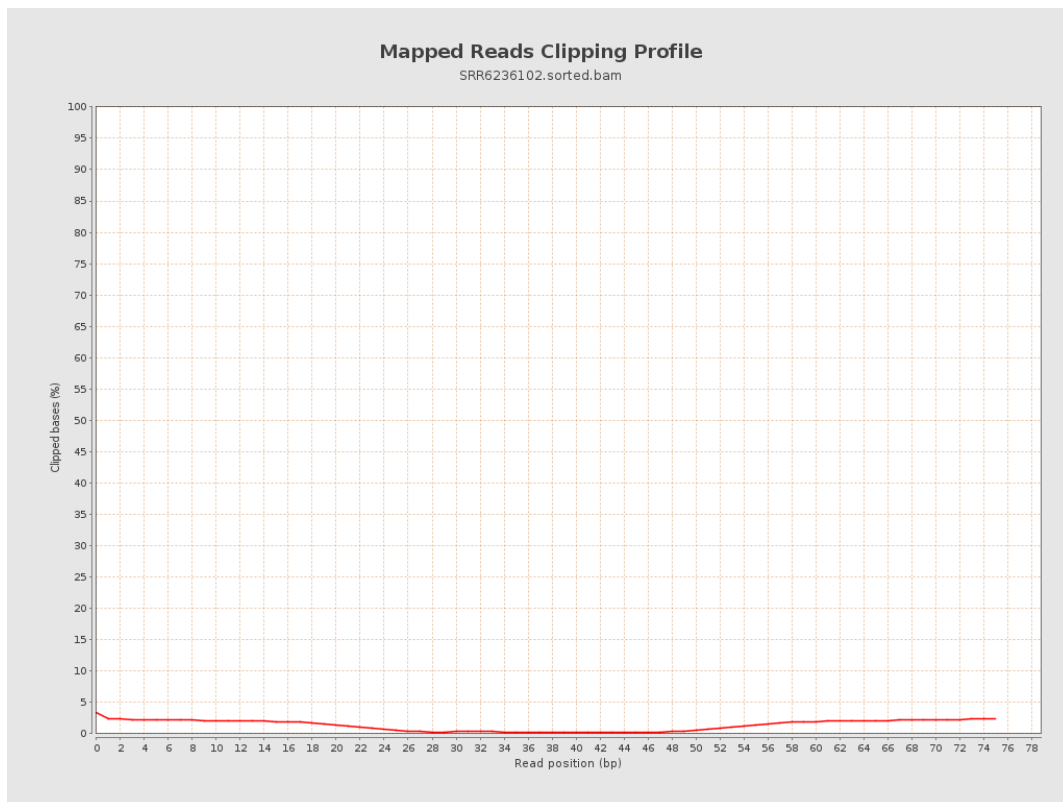
8. Results : Mapped Reads Nucleotide Content



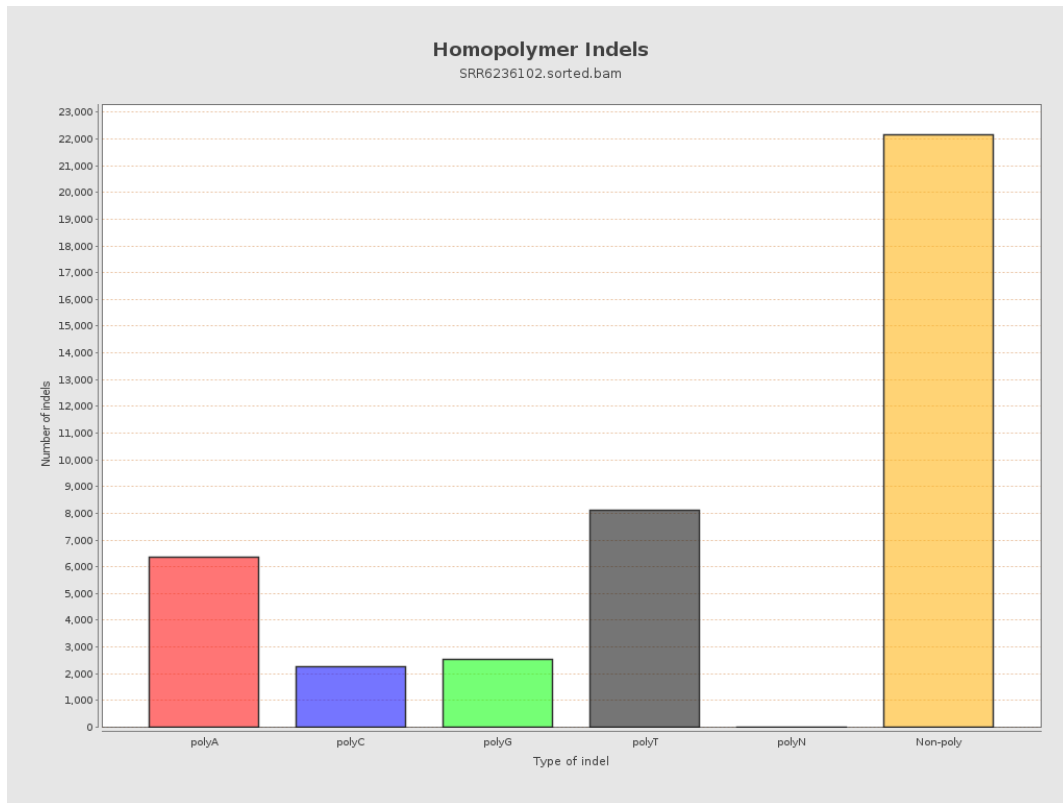
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

