

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 15:44:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068191.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_SRR6068191 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068191.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 15:44:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068191.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,147,955
Mapped reads	1,984,851 / 92.41%
Unmapped reads	163,104 / 7.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,858 / 0.78%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	148,203 / 6.9%
Duplication rate	5.55%
Clipped reads	809,955 / 37.71%

2.2. ACGT Content

Number/percentage of A's	39,035,387 / 28.95%
Number/percentage of C's	25,338,829 / 18.79%
Number/percentage of T's	42,224,777 / 31.31%
Number/percentage of G's	28,082,081 / 20.82%
Number/percentage of N's	169,269 / 0.13%
GC Percentage	39.61%

2.3. Coverage

Mean	0.0436

Standard Deviation	0.6681
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2.4. Mapping Quality

Mean Mapping Quality	43.68
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2.5. Mismatches and indels

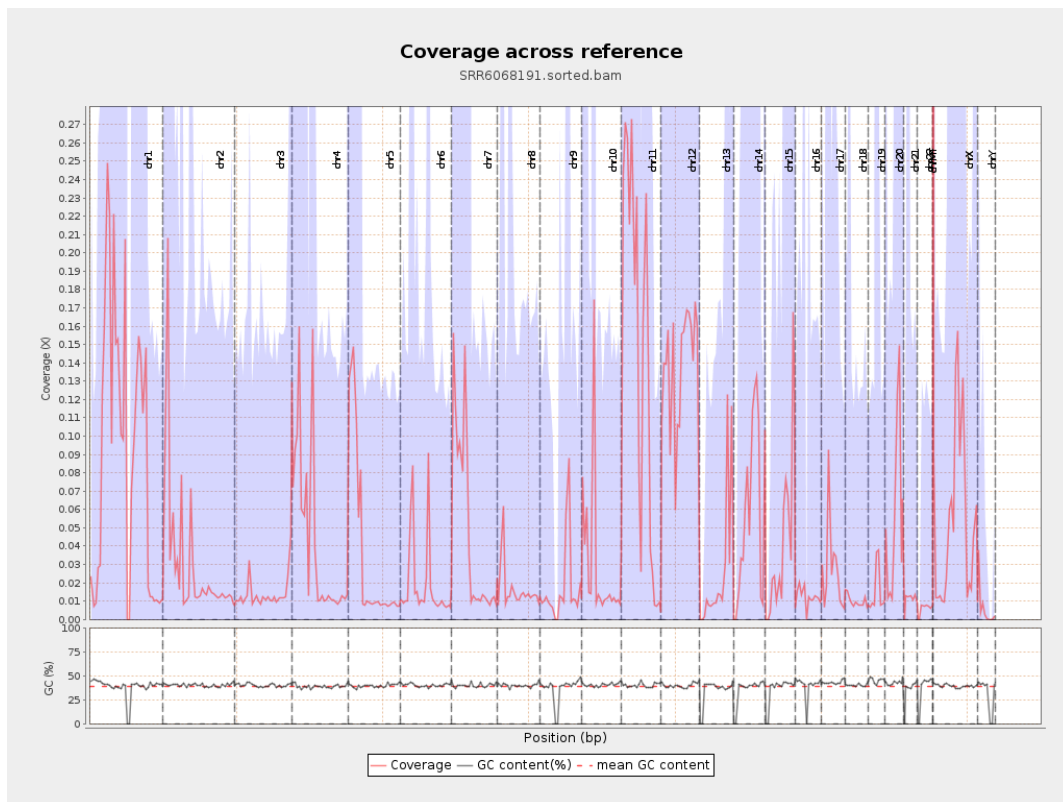
General error rate	0.86%
Mismatches	1,149,521
Insertions	8,684
Mapped reads with at least one insertion	0.43%
Deletions	35,722
Mapped reads with at least one deletion	1.78%
Homopolymer indels	46.73%

2.6. Chromosome stats

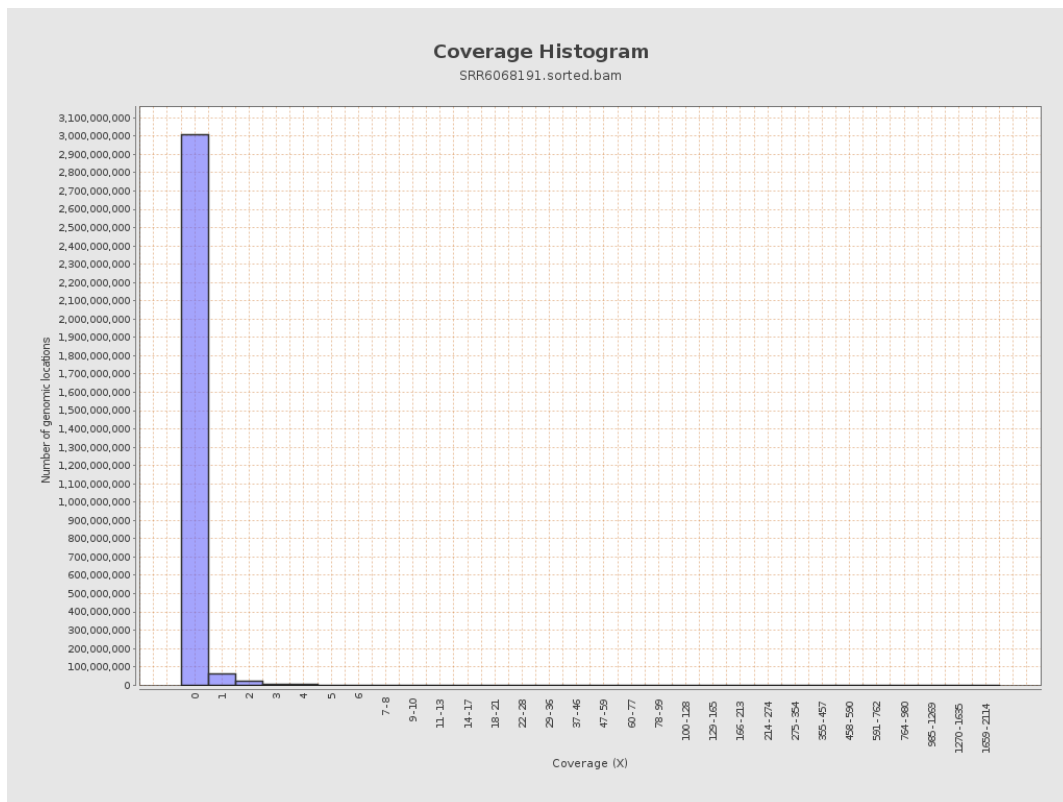
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	21888072	0.0878	1.3267
chr2	243199373	7557620	0.0311	0.2621
chr3	198022430	2899167	0.0146	0.3277
chr4	191154276	8173440	0.0428	0.302
chr5	180915260	6335833	0.035	0.2643
chr6	171115067	3418682	0.02	0.2032
chr7	159138663	7468261	0.0469	0.4074

chr8	146364022	2417193	0.0165	0.2218
chr9	141213431	2299081	0.0163	0.1846
chr10	135534747	3858467	0.0285	1.4854
chr11	135006516	18782556	0.1391	1.5844
chr12	133851895	18253613	0.1364	0.5278
chr13	115169878	3109857	0.027	0.2378
chr14	107349540	6110646	0.0569	0.3379
chr15	102531392	4269755	0.0416	0.2921
chr16	90354753	1089689	0.0121	0.198
chr17	81195210	2227190	0.0274	0.5773
chr18	78077248	780040	0.01	0.1789
chr19	59128983	935065	0.0158	0.8891
chr20	63025520	3506054	0.0556	0.3401
chr21	48129895	531248	0.011	0.2663
chr22	51304566	301714	0.0059	0.1017
chrMT	16571	102778	6.2023	5.6368
chrX	155270560	8263318	0.0532	0.4396
chrY	59373566	332509	0.0056	0.0998

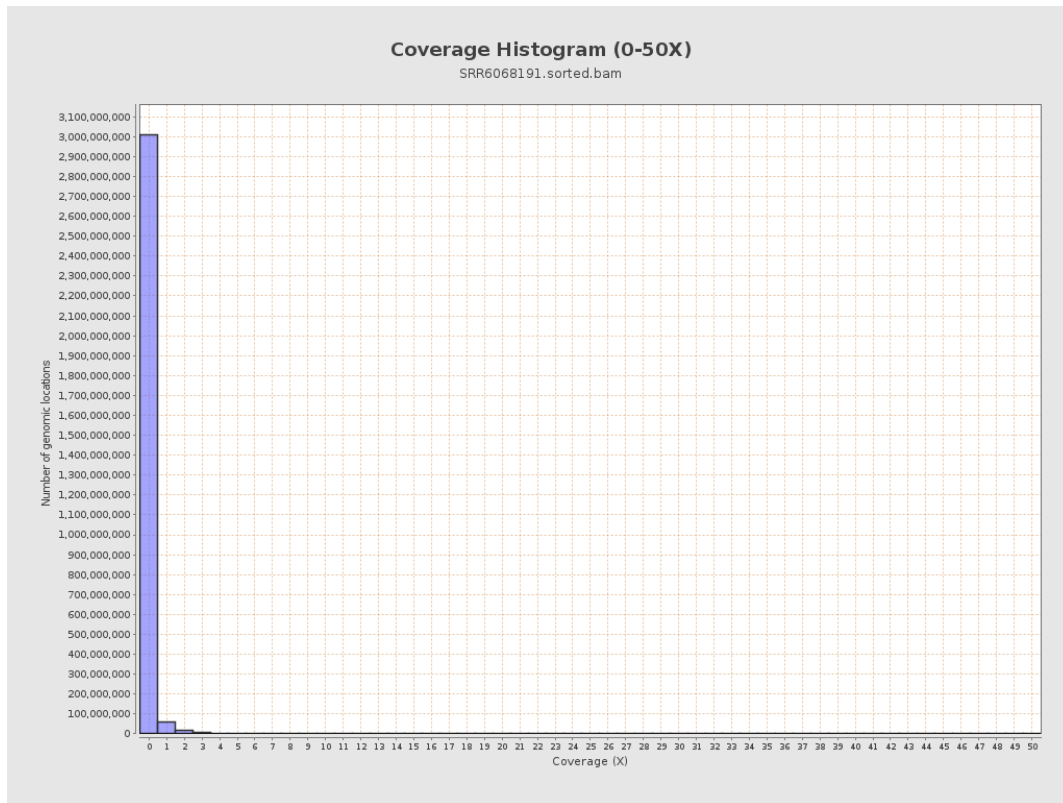
3. Results : Coverage across reference



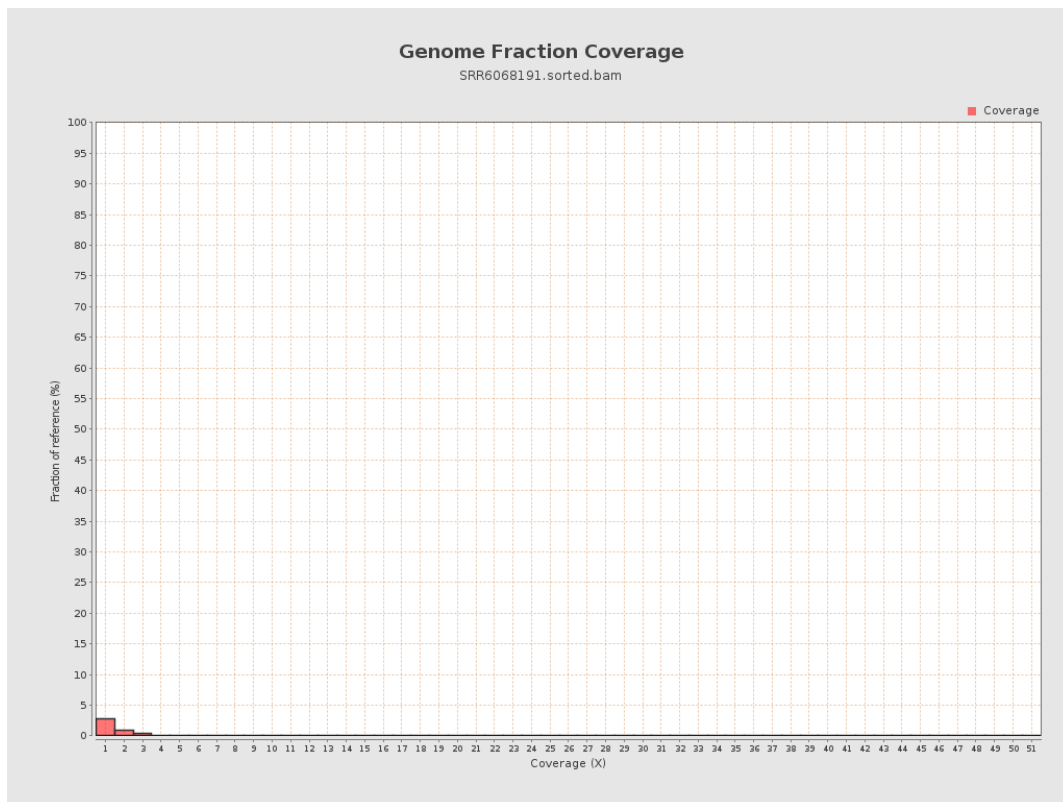
4. Results : Coverage Histogram



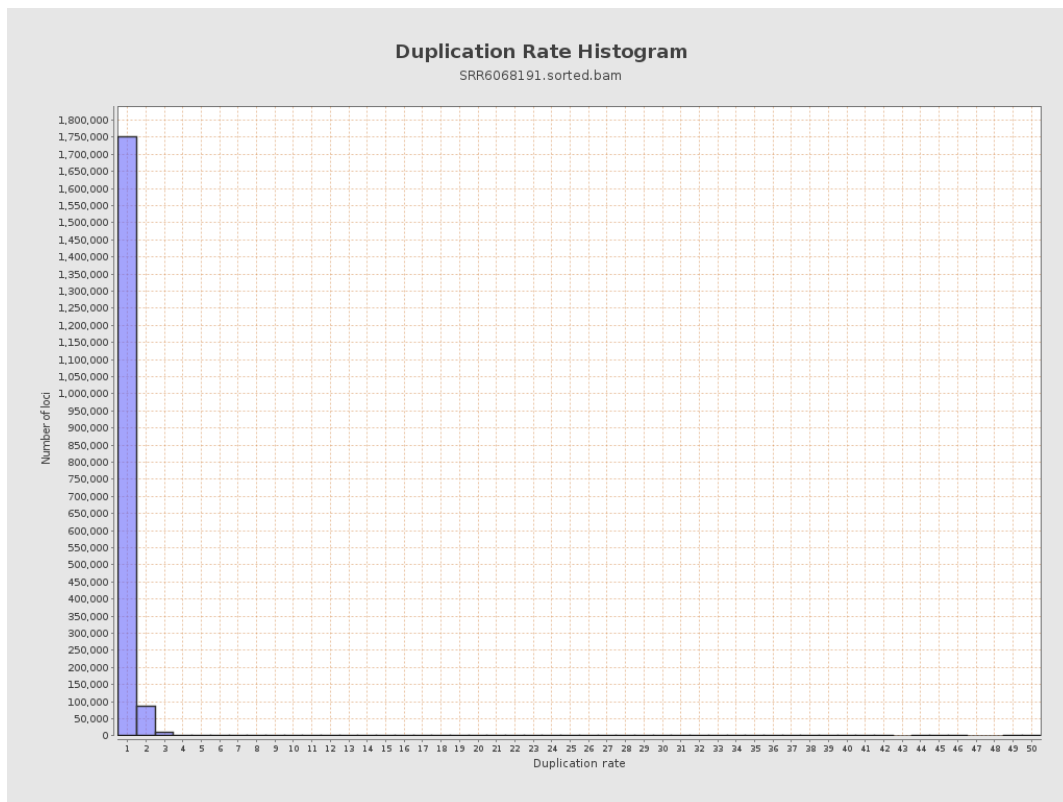
5. Results : Coverage Histogram (0-50X)



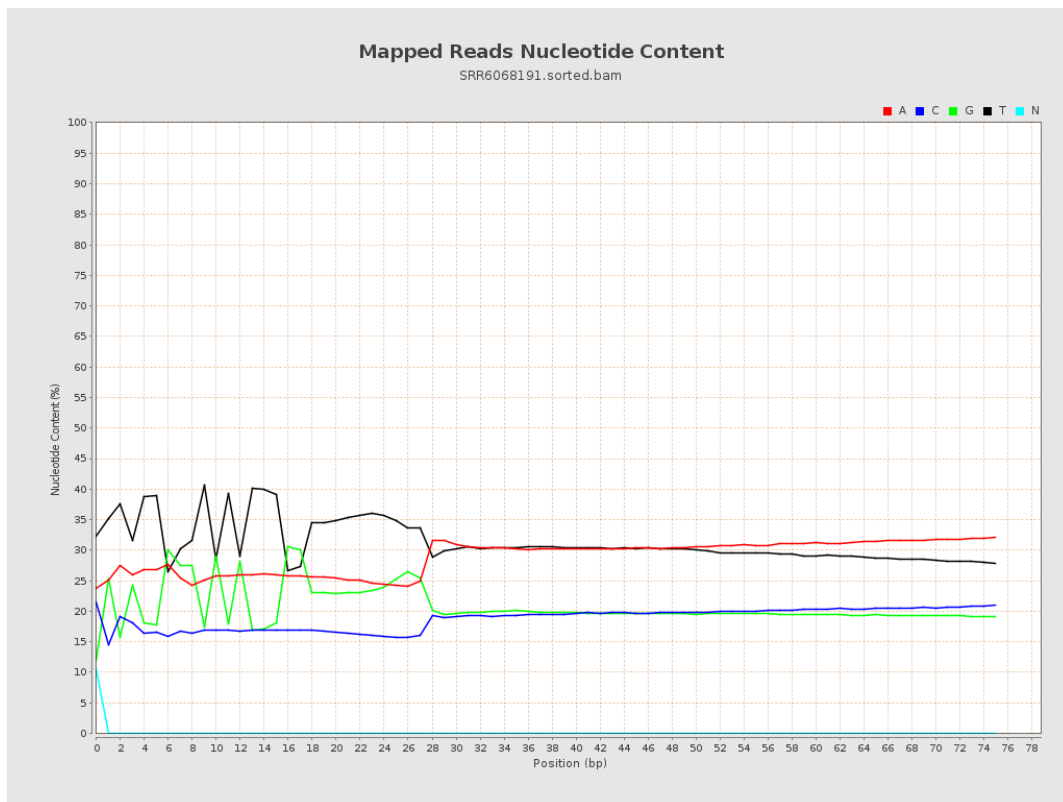
6. Results : Genome Fraction Coverage



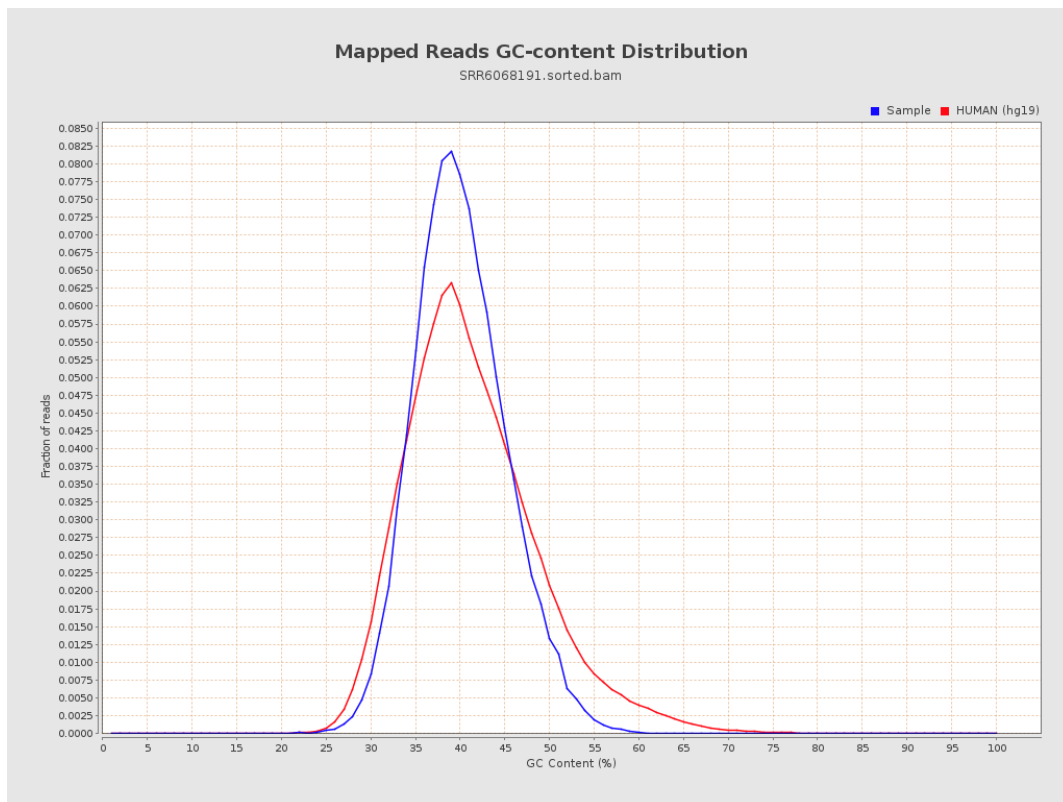
7. Results : Duplication Rate Histogram



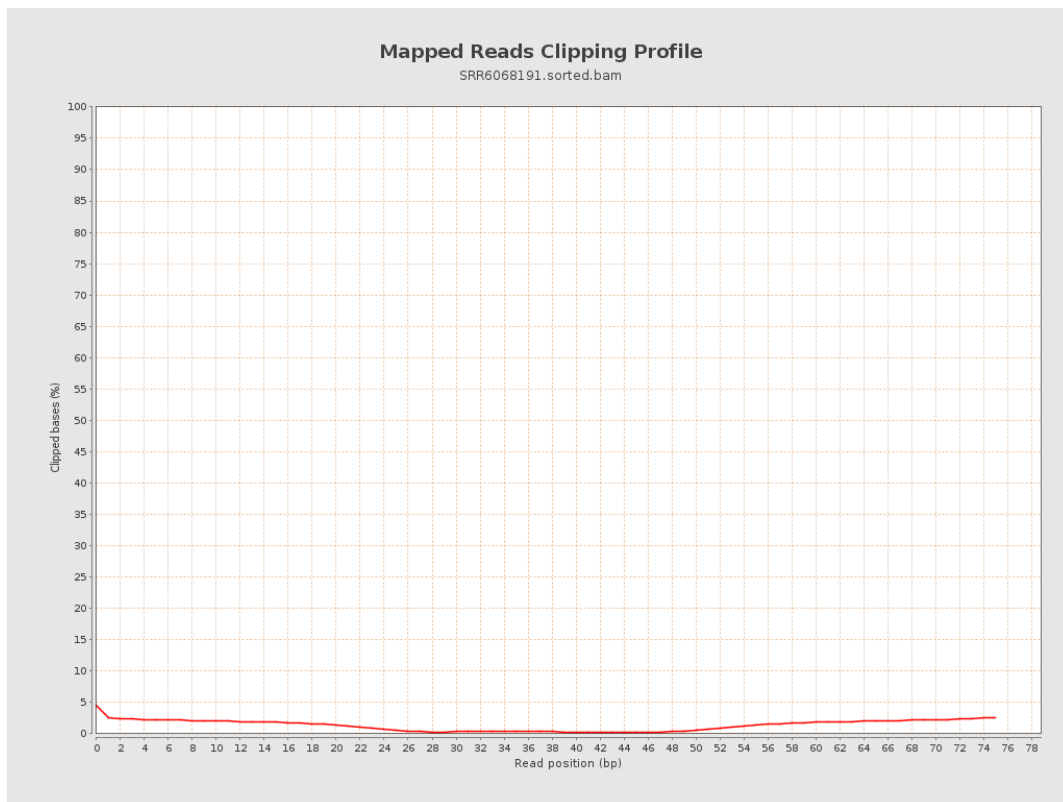
8. Results : Mapped Reads Nucleotide Content



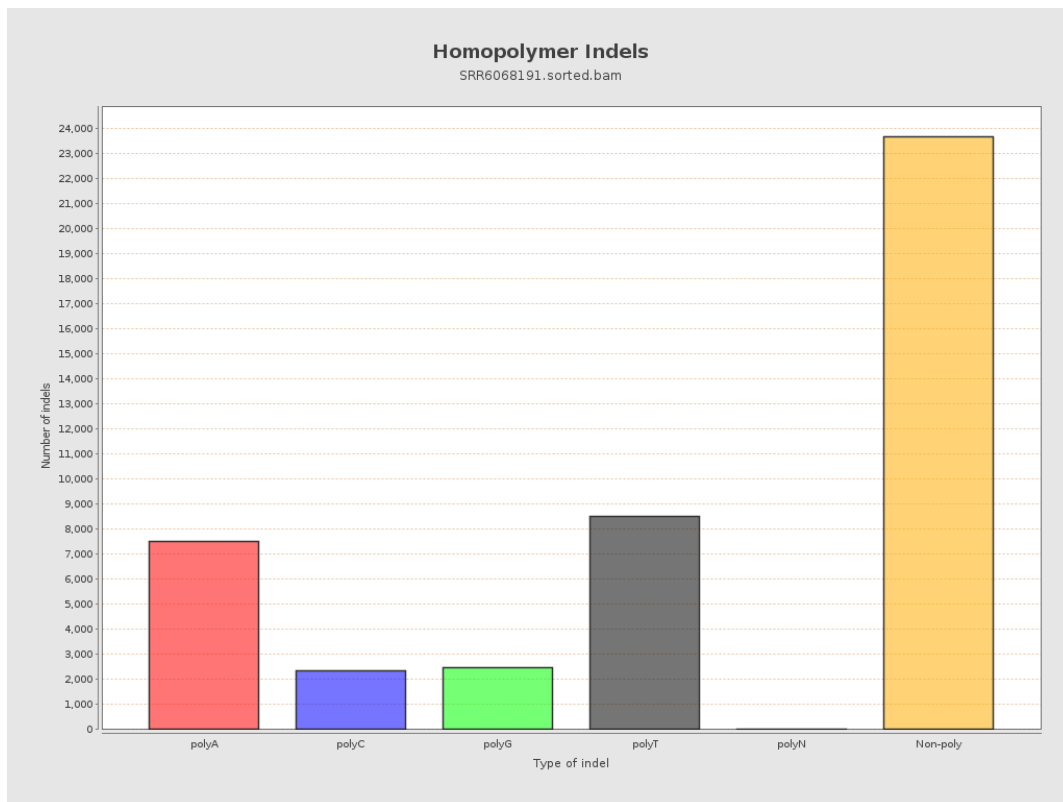
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

