

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 19:40:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230366.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_SRR6230366 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230366.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 19:40:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230366.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,013,709
Mapped reads	2,891,186 / 95.93%
Unmapped reads	122,523 / 4.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,482 / 0.78%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	189,349 / 6.28%
Duplication rate	4.99%
Clipped reads	638,013 / 21.17%

2.2. ACGT Content

Number/percentage of A's	62,811,734 / 29.96%
Number/percentage of C's	42,813,846 / 20.42%
Number/percentage of T's	61,439,196 / 29.31%
Number/percentage of G's	42,461,449 / 20.25%
Number/percentage of N's	123,807 / 0.06%
GC Percentage	40.68%

2.3. Coverage

Mean	0.0678

Standard Deviation	0.893
--------------------	-------

2.4. Mapping Quality

Mean Mapping Quality	46.17
----------------------	-------

2.5. Mismatches and indels

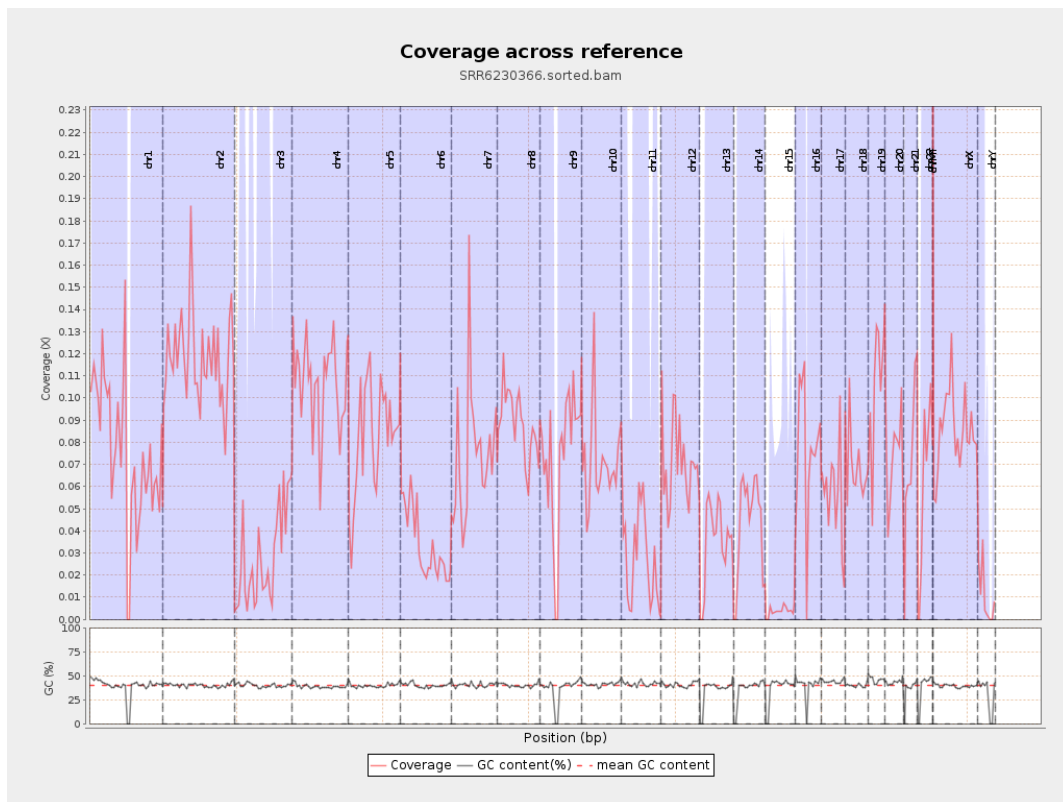
General error rate	0.89%
Mismatches	1,831,630
Insertions	19,458
Mapped reads with at least one insertion	0.67%
Deletions	61,982
Mapped reads with at least one deletion	2.12%
Homopolymer indels	47.19%

2.6. Chromosome stats

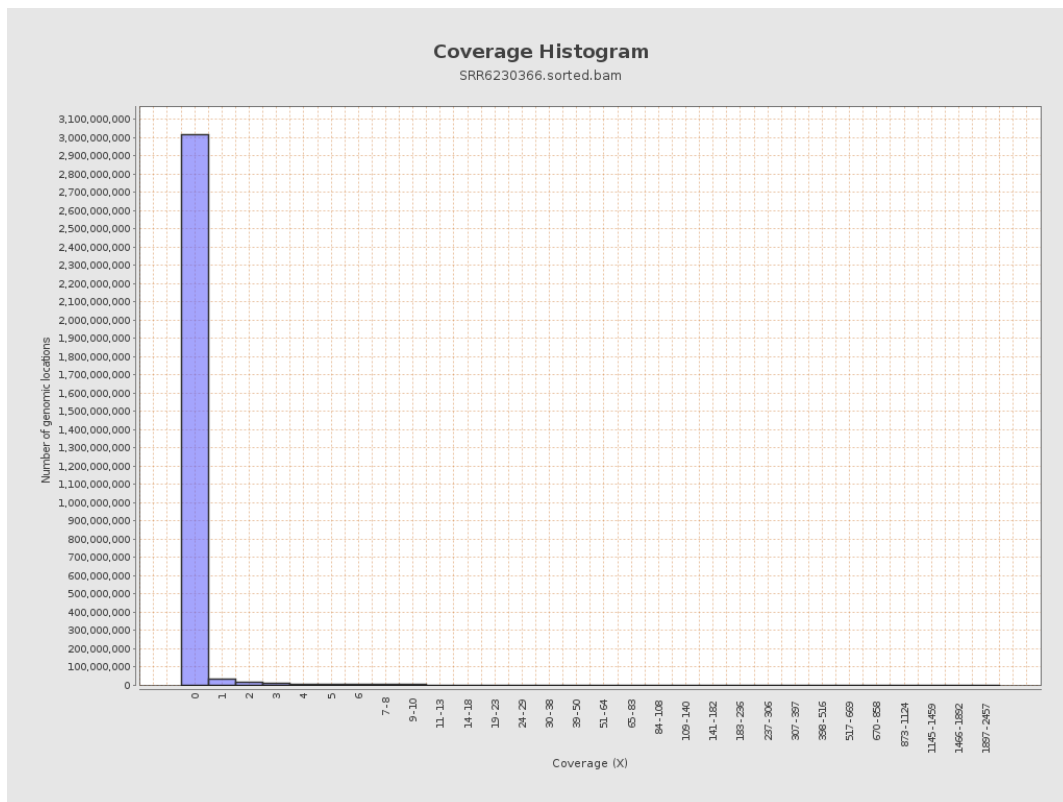
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	18814379	0.0755	1.9389
chr2	243199373	29006219	0.1193	0.9666
chr3	198022430	5439972	0.0275	0.3437
chr4	191154276	20298649	0.1062	0.77
chr5	180915260	14898708	0.0824	0.6093
chr6	171115067	5762544	0.0337	0.4123
chr7	159138663	11832763	0.0744	1.3023

chr8	146364022	12977826	0.0887	0.8234
chr9	141213431	10367613	0.0734	0.745
chr10	135534747	9448112	0.0697	0.8055
chr11	135006516	3840397	0.0284	0.4084
chr12	133851895	9505137	0.071	0.5679
chr13	115169878	4133831	0.0359	0.3938
chr14	107349540	4822979	0.0449	0.5014
chr15	102531392	379242	0.0037	0.0987
chr16	90354753	6833437	0.0756	0.6247
chr17	81195210	4618948	0.0569	0.5107
chr18	78077248	5385588	0.069	1.4411
chr19	59128983	6221352	0.1052	1.1061
chr20	63025520	4662788	0.074	0.5978
chr21	48129895	3538371	0.0735	0.6603
chr22	51304566	3138666	0.0612	0.5079
chrMT	16571	5103	0.3079	0.8957
chrX	155270560	13209731	0.0851	0.6495
chrY	59373566	613750	0.0103	0.3776

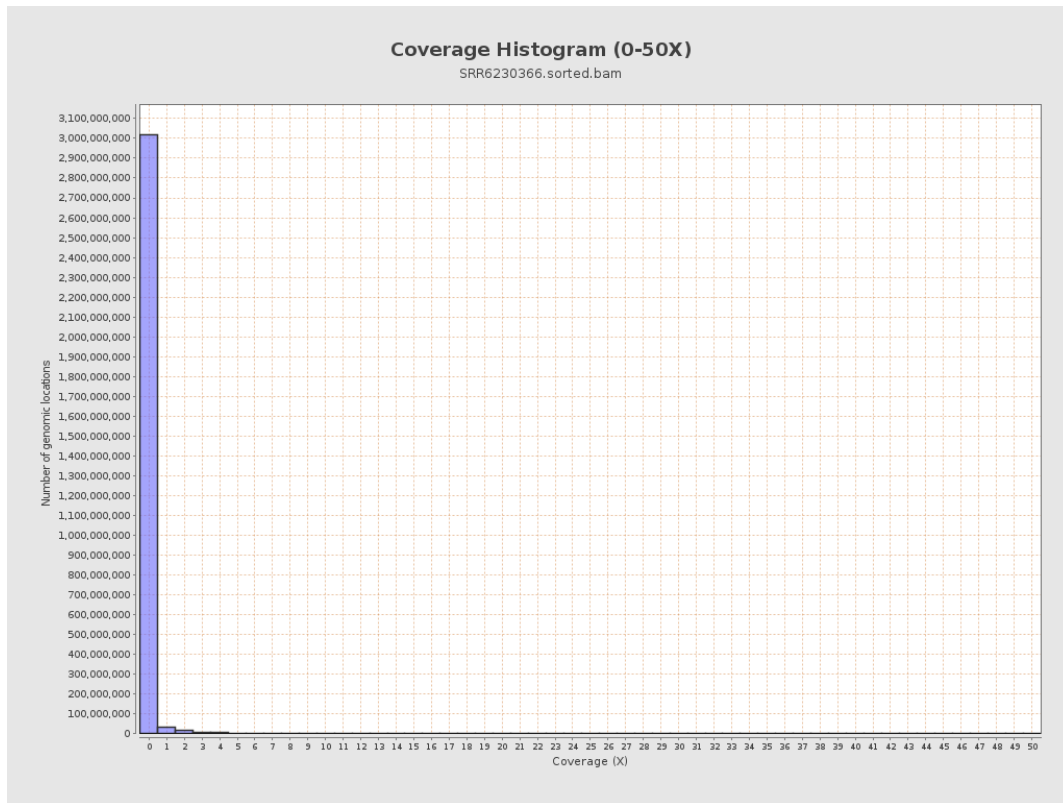
3. Results : Coverage across reference



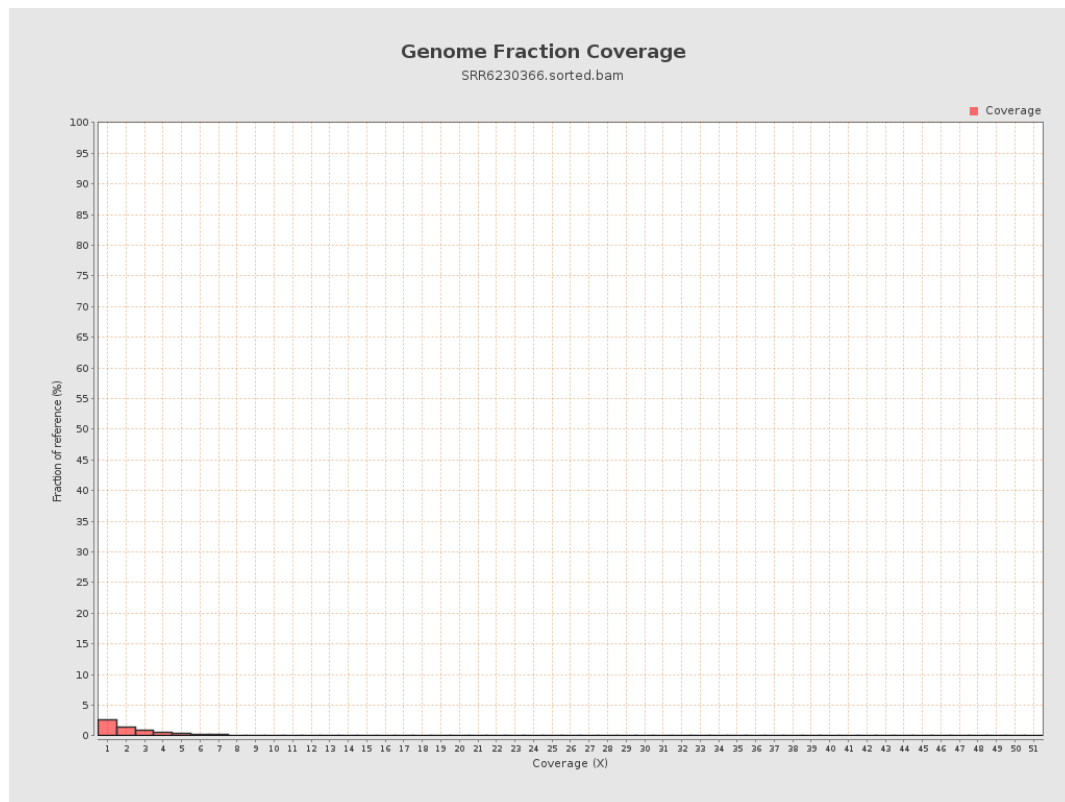
4. Results : Coverage Histogram



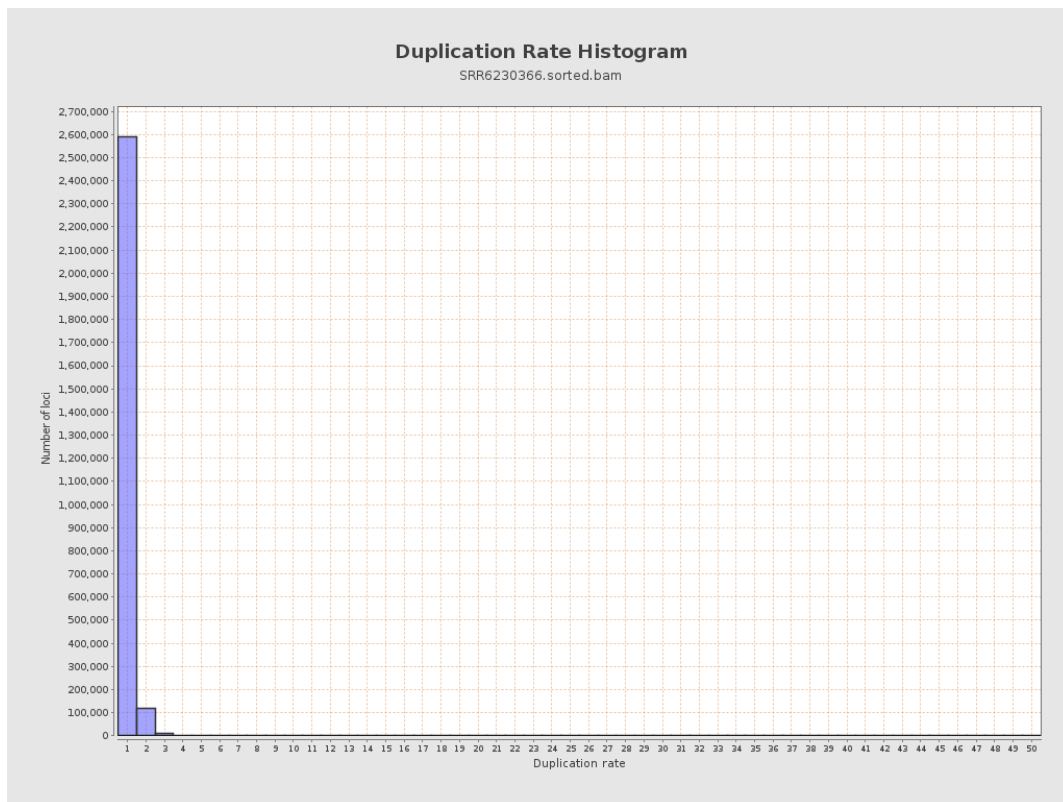
5. Results : Coverage Histogram (0-50X)



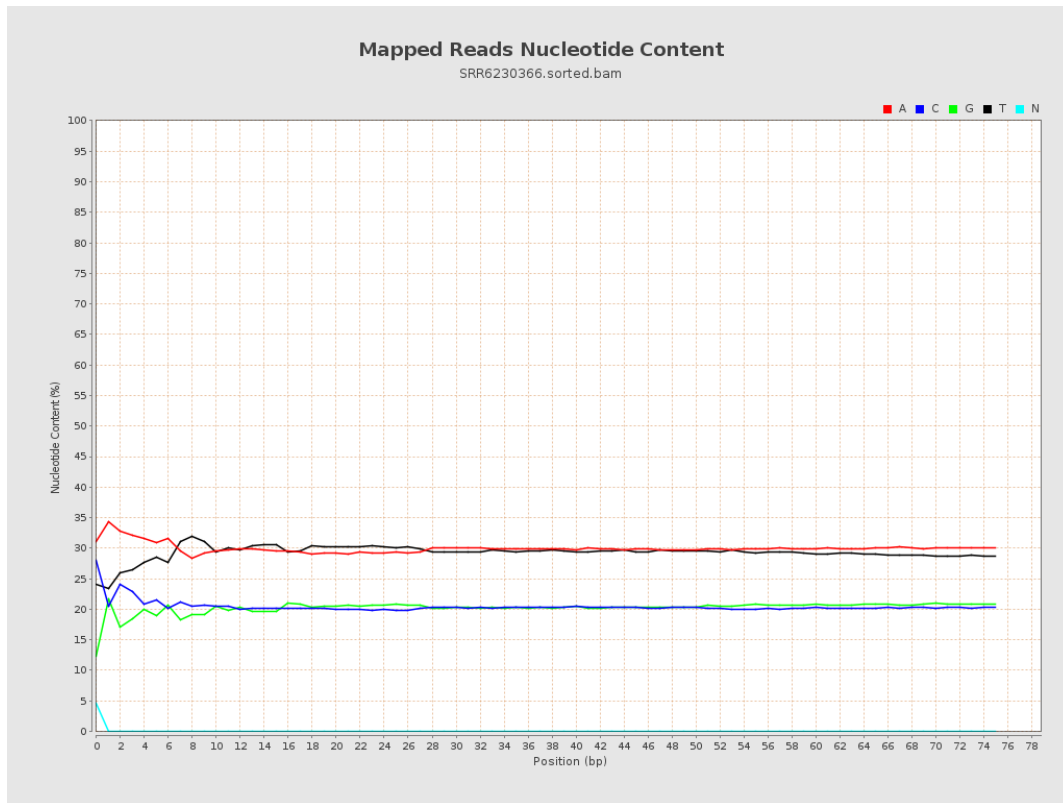
6. Results : Genome Fraction Coverage



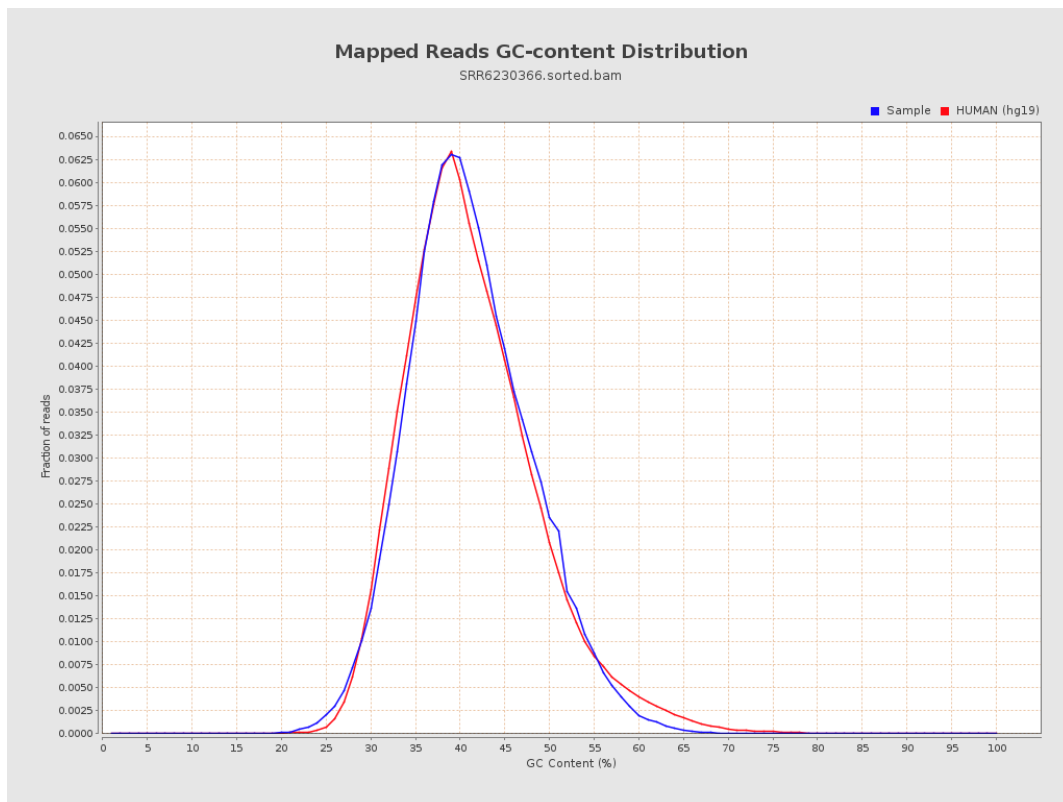
7. Results : Duplication Rate Histogram



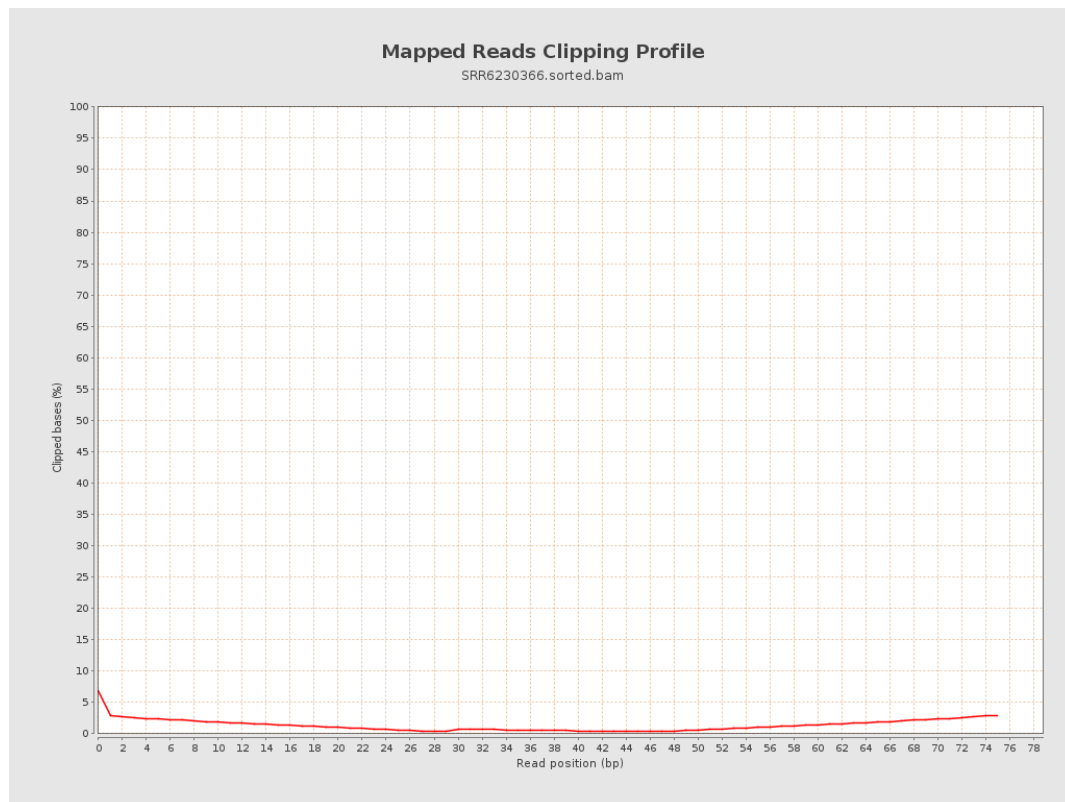
8. Results : Mapped Reads Nucleotide Content



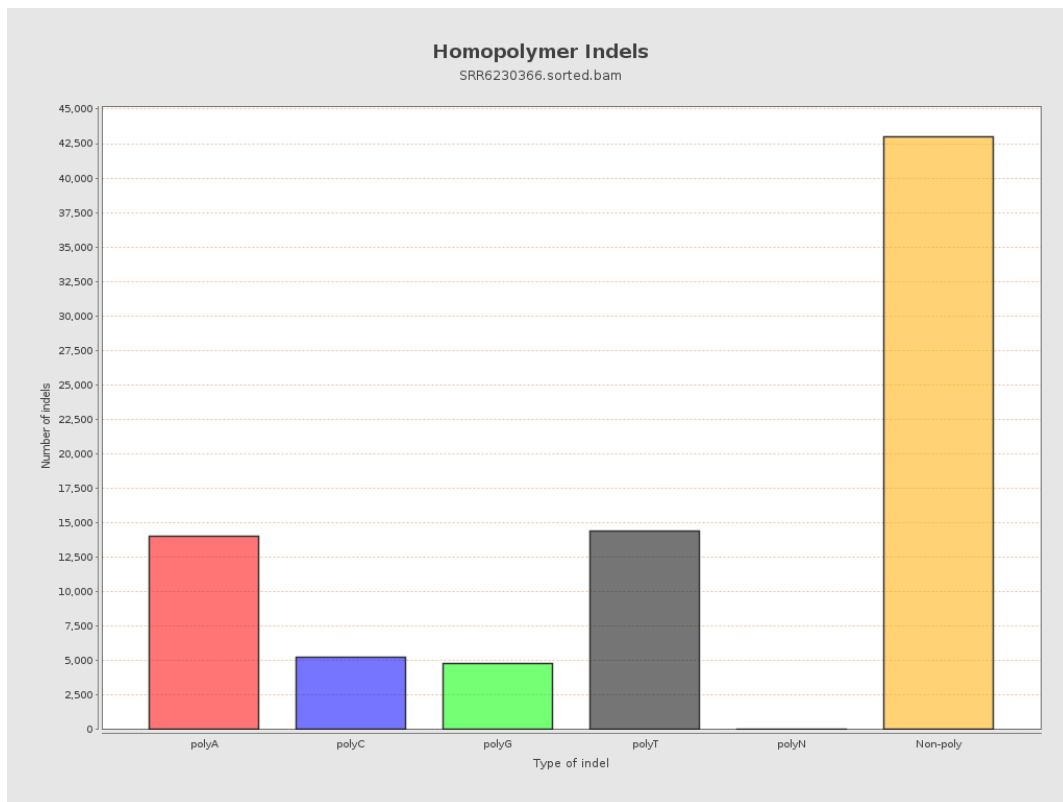
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

