

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 03:30:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231797.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_SRR6231797 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231797.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 03:30:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231797.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,730,592
Mapped reads	4,647,570 / 81.1%
Unmapped reads	1,083,022 / 18.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	43,932 / 0.77%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	550,278 / 9.6%
Duplication rate	7.38%
Clipped reads	3,110,388 / 54.28%

2.2. ACGT Content

Number/percentage of A's	83,334,387 / 29.17%
Number/percentage of C's	55,408,294 / 19.4%
Number/percentage of T's	80,581,245 / 28.21%
Number/percentage of G's	66,336,625 / 23.22%
Number/percentage of N's	21,015 / 0.01%
GC Percentage	42.62%

2.3. Coverage

Mean	0.0923

Standard Deviation	15.0337
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2.4. Mapping Quality

Mean Mapping Quality	43.92
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2.5. Mismatches and indels

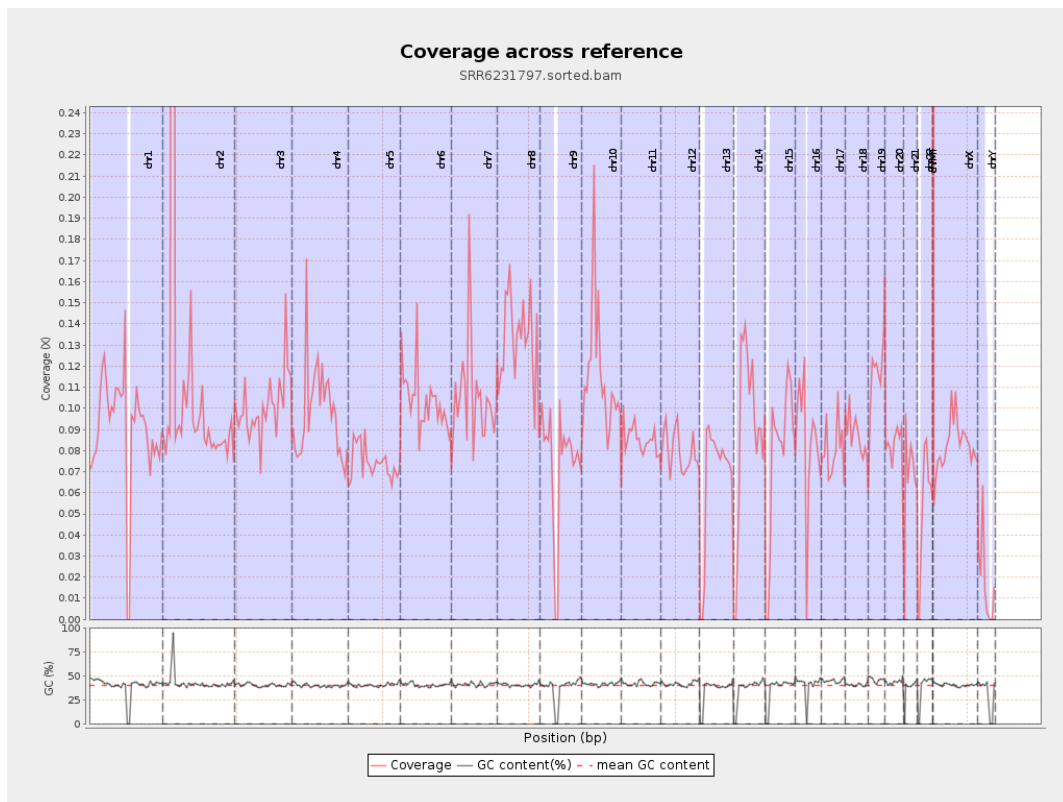
General error rate	0.63%
Mismatches	1,759,854
Insertions	22,036
Mapped reads with at least one insertion	0.47%
Deletions	58,575
Mapped reads with at least one deletion	1.25%
Homopolymer indels	44.74%

2.6. Chromosome stats

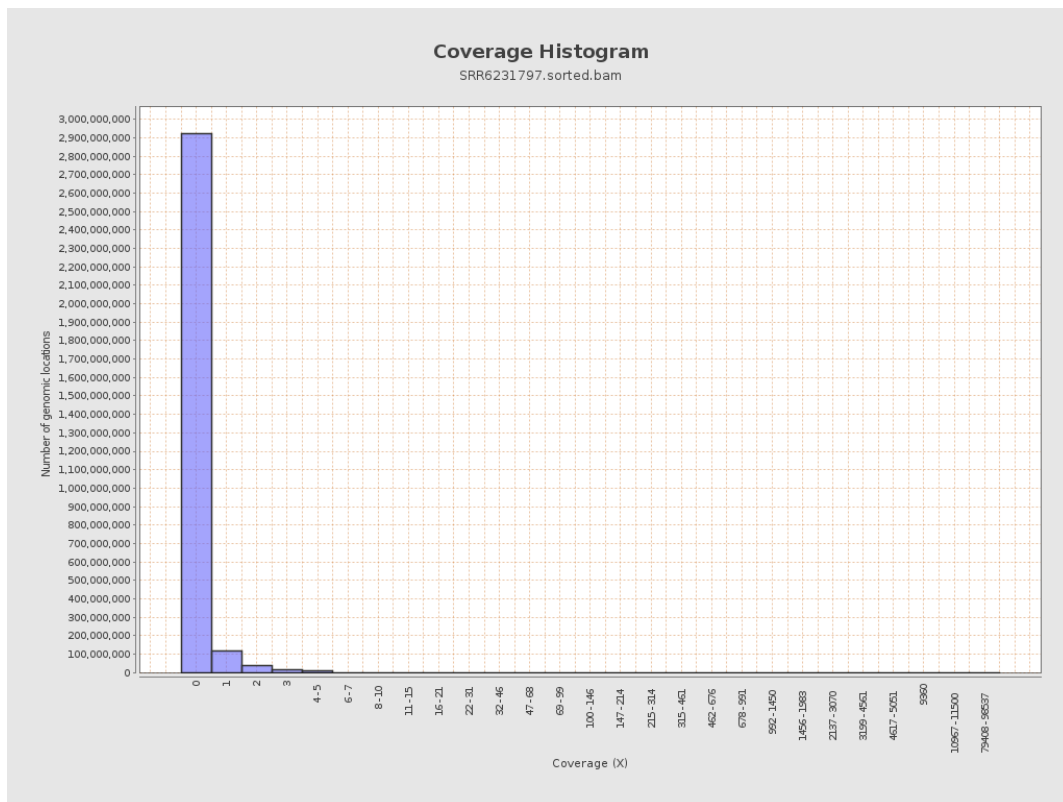
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	22533828	0.0904	1.3928
chr2	243199373	30345251	0.1248	53.5659
chr3	198022430	20076484	0.1014	0.4681
chr4	191154276	18652339	0.0976	0.584
chr5	180915260	13435750	0.0743	0.4066
chr6	171115067	17703577	0.1035	0.5705
chr7	159138663	16737593	0.1052	1.2519

chr8	146364022	19384386	0.1324	1.4705
chr9	141213431	10526111	0.0745	0.6513
chr10	135534747	15625200	0.1153	0.8604
chr11	135006516	11471805	0.085	0.6029
chr12	133851895	10712484	0.08	0.4259
chr13	115169878	7667336	0.0666	0.3823
chr14	107349540	9750535	0.0908	0.6123
chr15	102531392	7891029	0.077	0.4154
chr16	90354753	7527558	0.0833	0.4768
chr17	81195210	6575873	0.081	0.4744
chr18	78077248	6804207	0.0871	1.2199
chr19	59128983	6923770	0.1171	1.0321
chr20	63025520	5214759	0.0827	0.4523
chr21	48129895	3296968	0.0685	0.4732
chr22	51304566	2701765	0.0527	0.3238
chrMT	16571	340513	20.5487	13.5903
chrX	155270560	12815710	0.0825	0.4733
chrY	59373566	1065922	0.018	0.4369

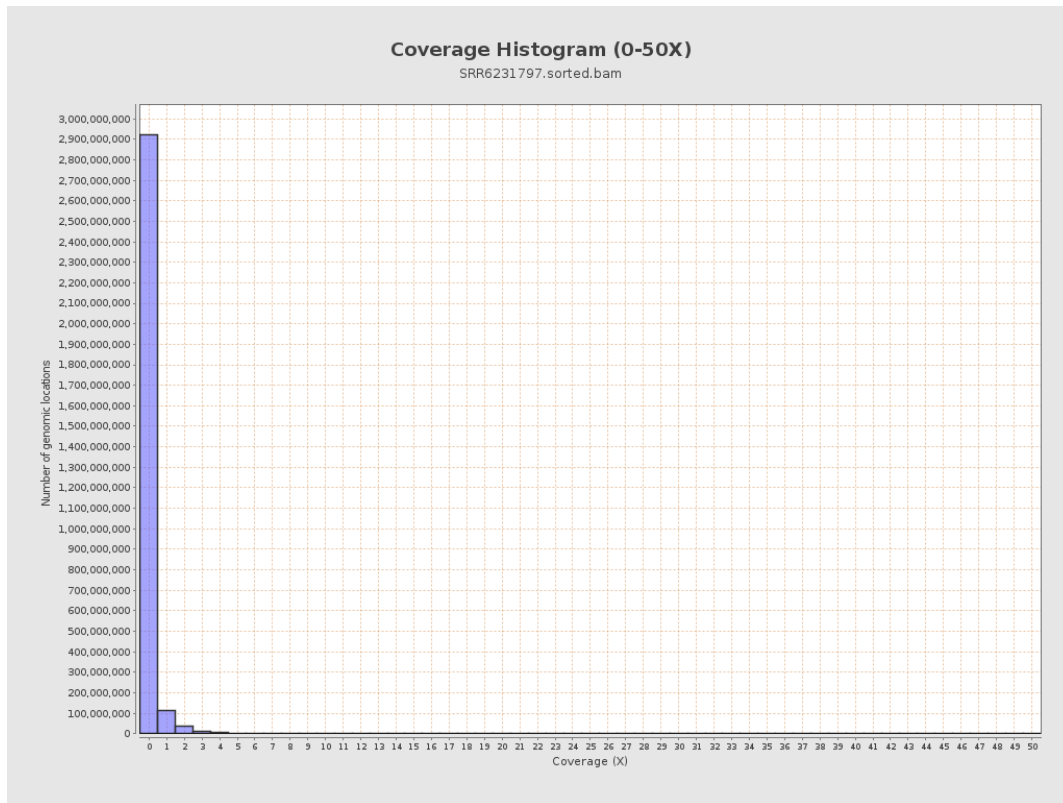
3. Results : Coverage across reference



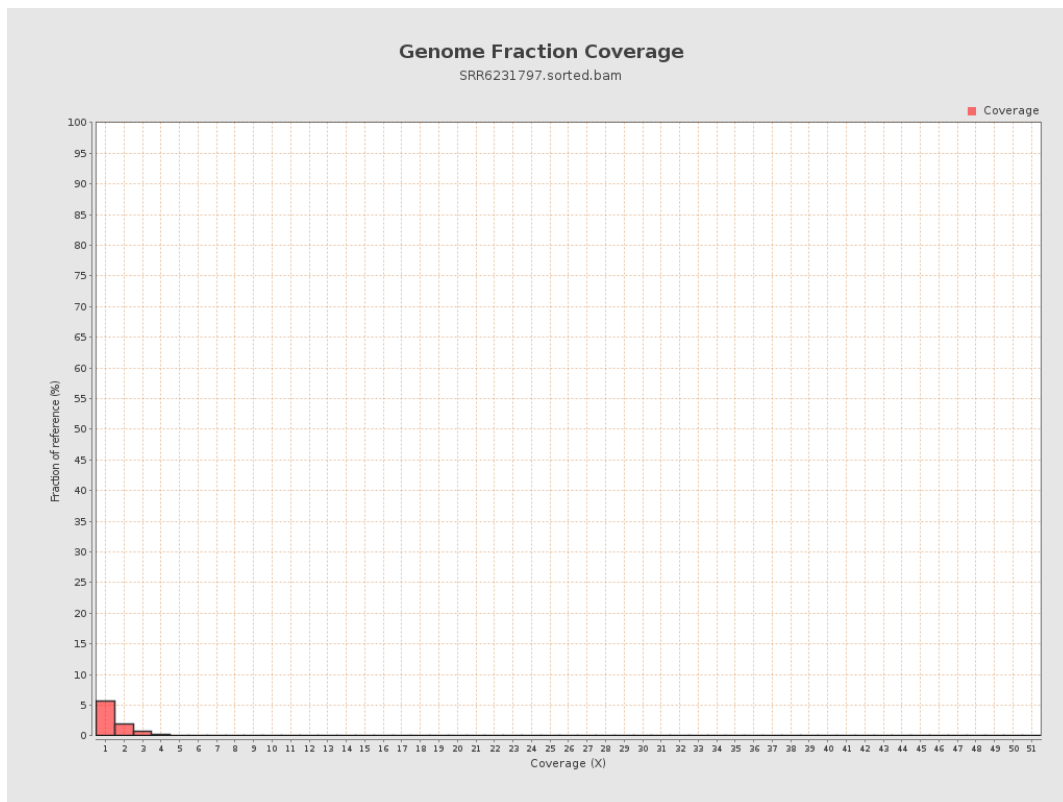
4. Results : Coverage Histogram



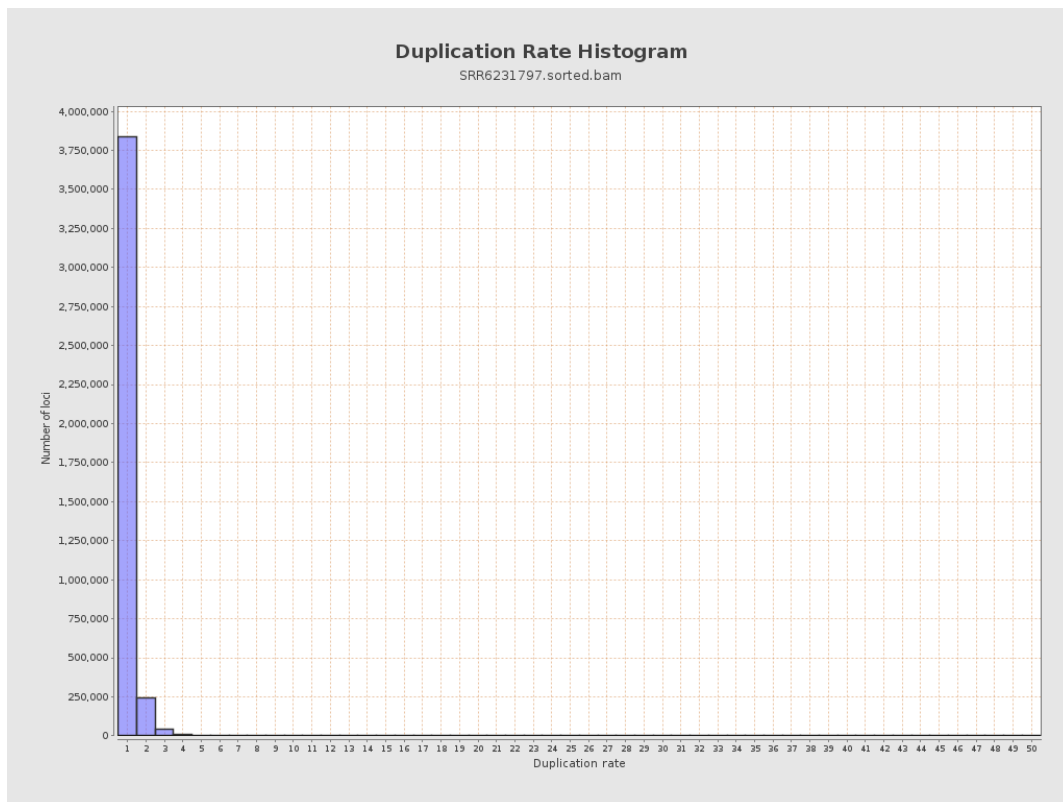
5. Results : Coverage Histogram (0-50X)



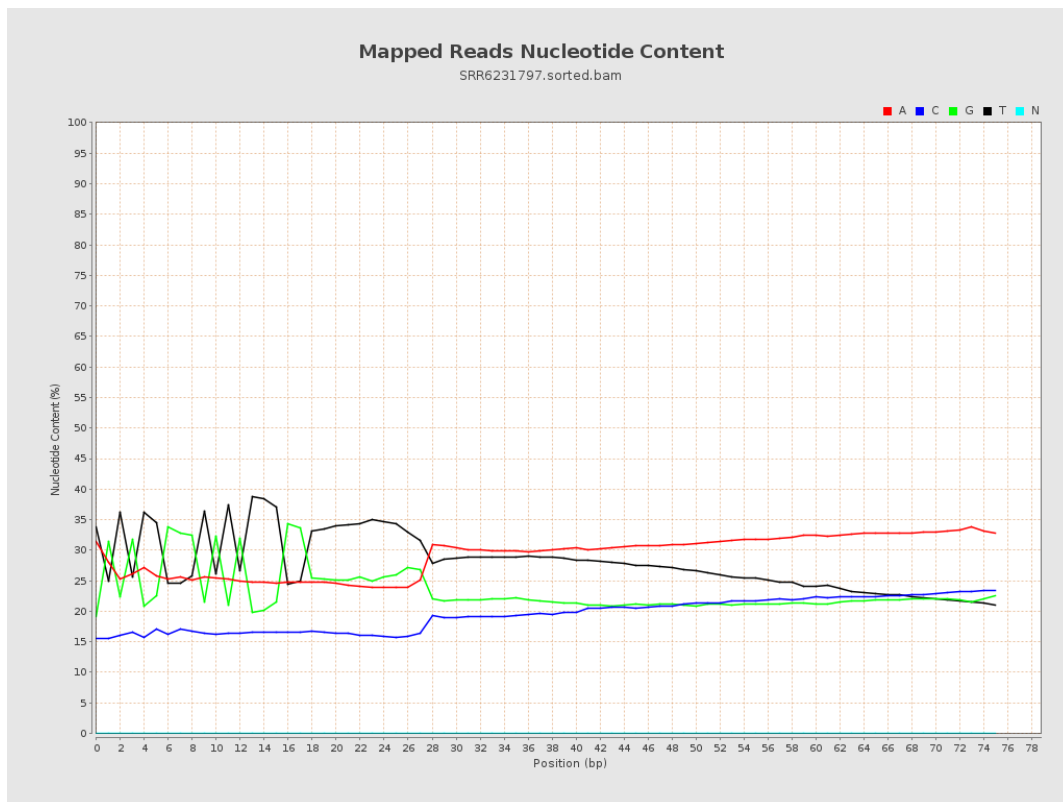
6. Results : Genome Fraction Coverage



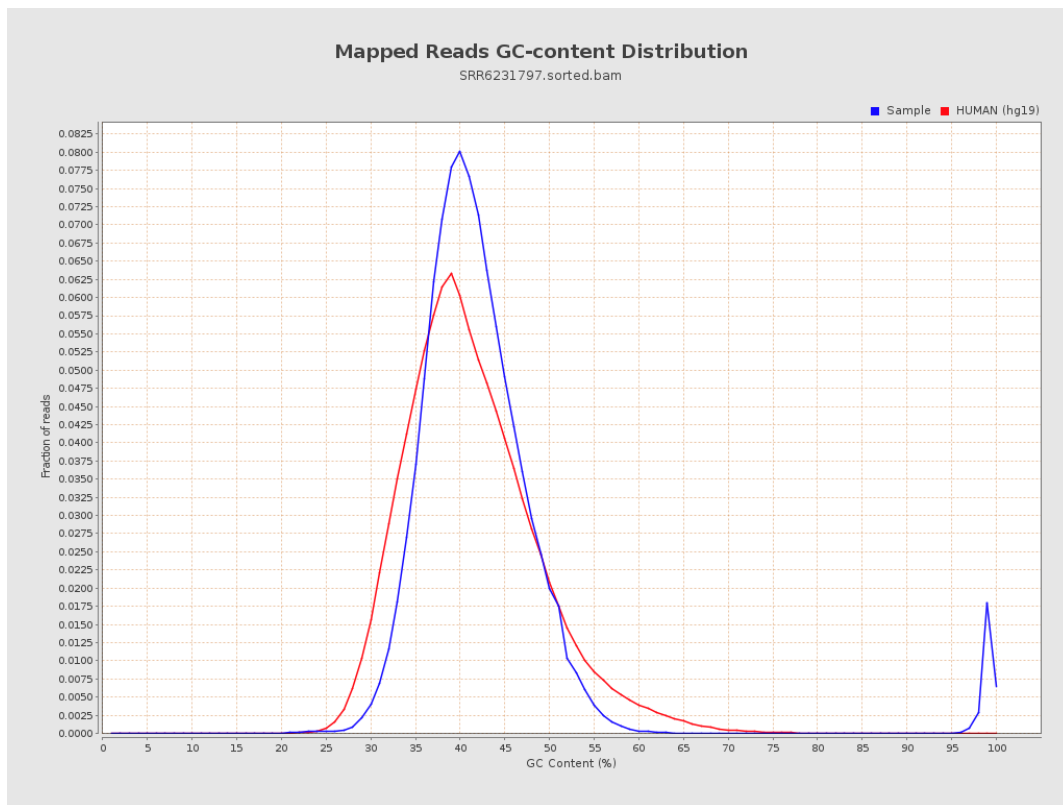
7. Results : Duplication Rate Histogram



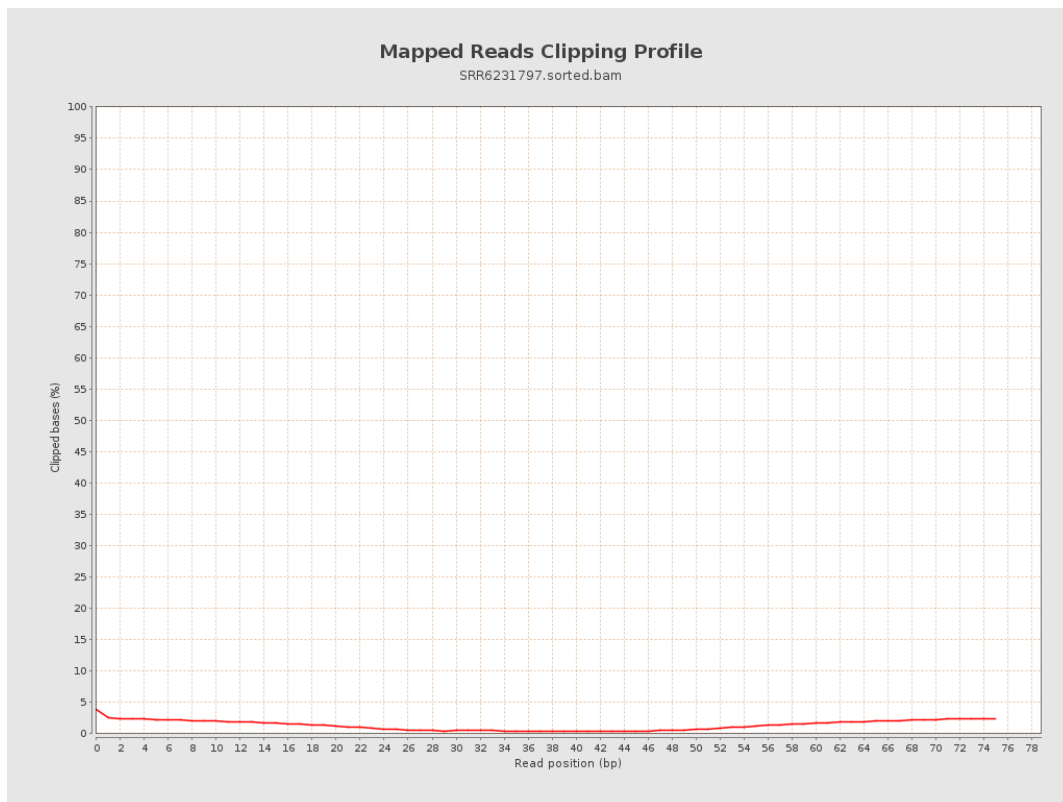
8. Results : Mapped Reads Nucleotide Content



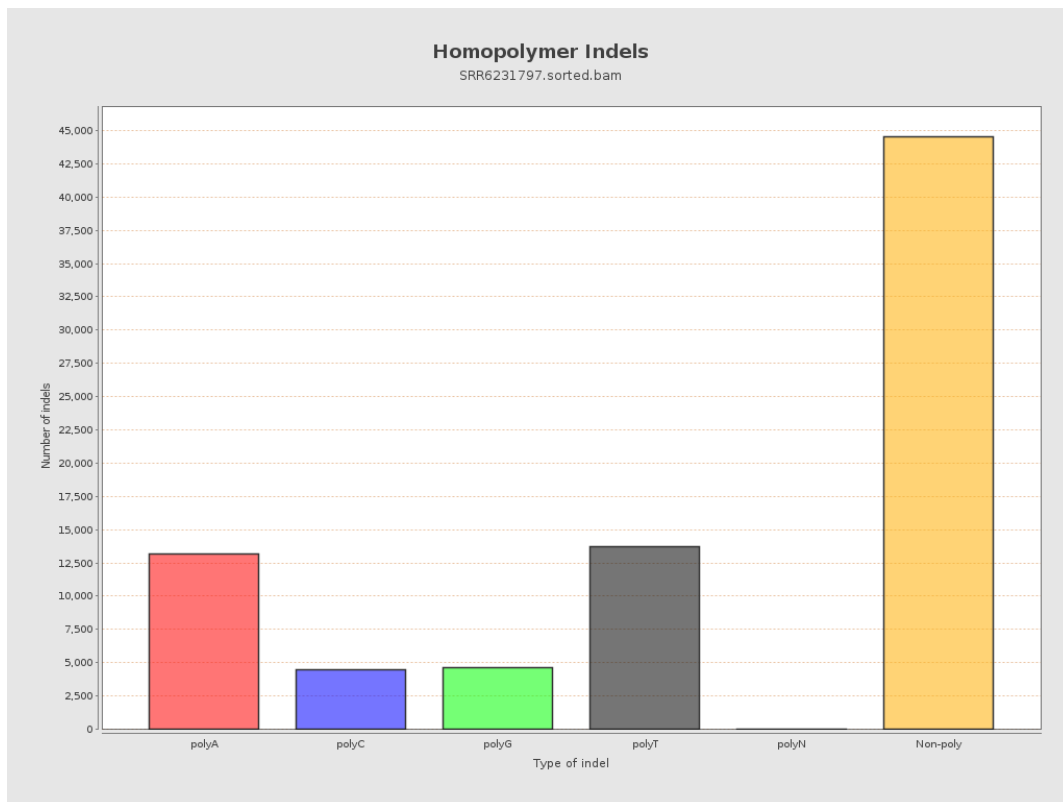
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

