

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/12 10:42:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695913.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/seu_share/home/tujing/220232460/software/bwa-0.7.18/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1695913 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695913.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Thu Sep 12 10:42:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695913.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,875,388
Mapped reads	11,535,658 / 89.59%
Unmapped reads	1,339,730 / 10.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	169,122 / 1.31%
Read min/max/mean length	8 / 360 / 124
Duplicated reads (estimated)	2,192,579 / 17.03%
Duplication rate	16.04%
Clipped reads	2,882,312 / 22.39%

2.2. ACGT Content

Number/percentage of A's	425,477,969 / 28.38%
Number/percentage of C's	322,301,376 / 21.5%
Number/percentage of T's	420,342,345 / 28.04%
Number/percentage of G's	331,007,103 / 22.08%
Number/percentage of N's	0 / 0%
GC Percentage	43.58%

2.3. Coverage

Mean	0.4876

Standard Deviation	1.3534
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2.4. Mapping Quality

Mean Mapping Quality	51.08
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2.5. Mismatches and indels

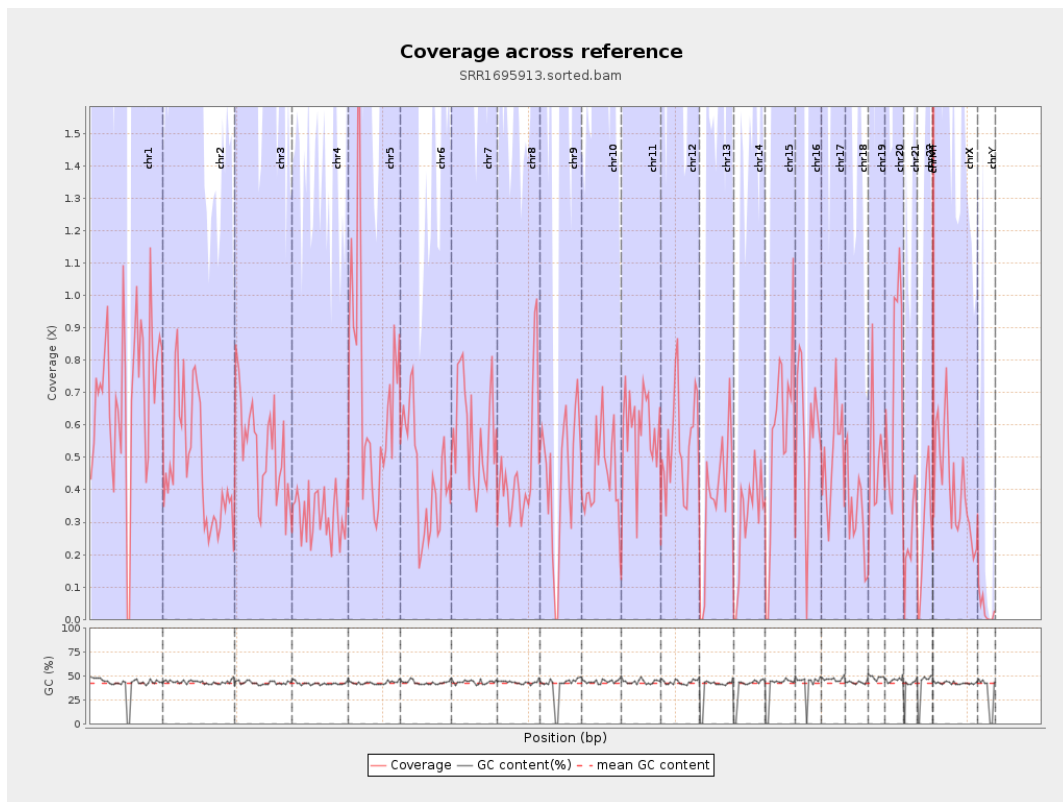
General error rate	1.73%
Mismatches	16,039,763
Insertions	9,037,794
Mapped reads with at least one insertion	47.43%
Deletions	9,296,275
Mapped reads with at least one deletion	48.72%
Homopolymer indels	36.3%

2.6. Chromosome stats

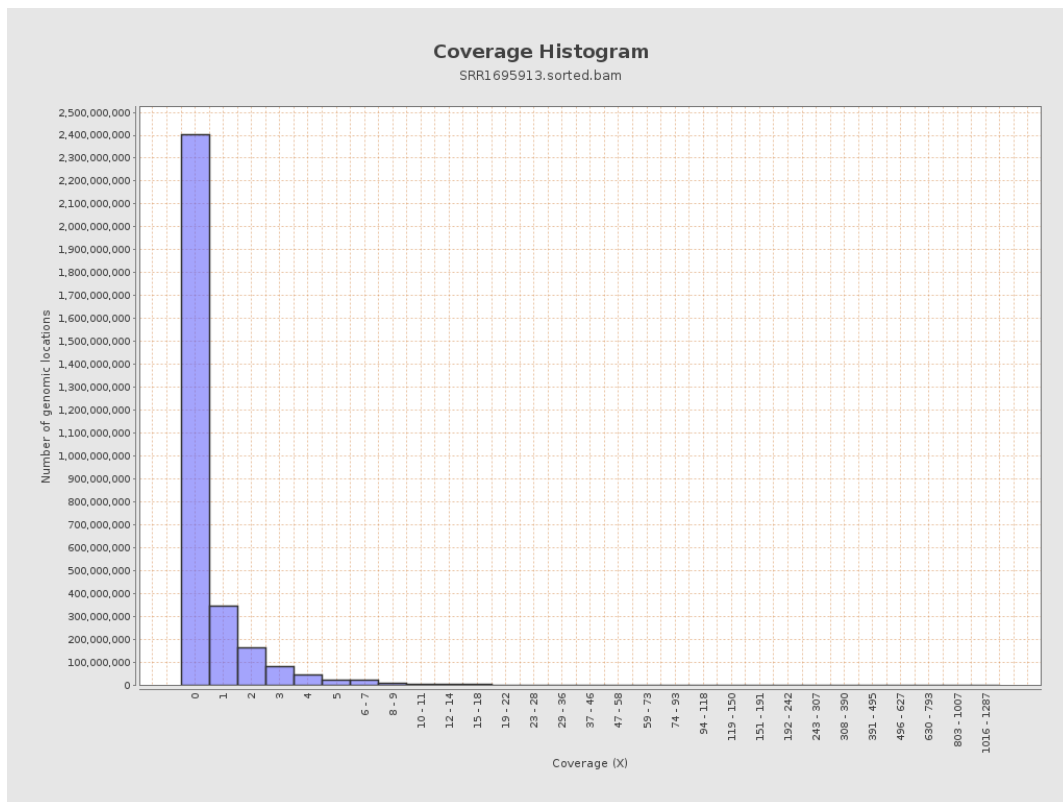
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	171761020	0.6891	2.0207
chr2	243199373	115097051	0.4733	1.2508
chr3	198022430	103675655	0.5236	1.2824
chr4	191154276	61651662	0.3225	0.9944
chr5	180915260	127244985	0.7033	1.5942
chr6	171115067	74904666	0.4377	1.2167
chr7	159138663	91370310	0.5742	1.3498

chr8	146364022	68588190	0.4686	1.2218
chr9	141213431	61873100	0.4382	1.2418
chr10	135534747	61238610	0.4518	1.325
chr11	135006516	79060263	0.5856	1.3841
chr12	133851895	73556363	0.5495	1.3666
chr13	115169878	44066155	0.3826	1.0858
chr14	107349540	33744827	0.3143	0.9695
chr15	102531392	57293163	0.5588	1.379
chr16	90354753	51242931	0.5671	1.3629
chr17	81195210	41282314	0.5084	1.338
chr18	78077248	25725891	0.3295	1.2813
chr19	59128983	29396521	0.4972	1.6922
chr20	63025520	45474561	0.7215	1.6401
chr21	48129895	12194518	0.2534	0.9381
chr22	51304566	14245002	0.2777	0.9531
chrMT	16571	194814	11.7563	7.0026
chrX	155270560	62761867	0.4042	1.107
chrY	59373566	1778045	0.0299	0.5962

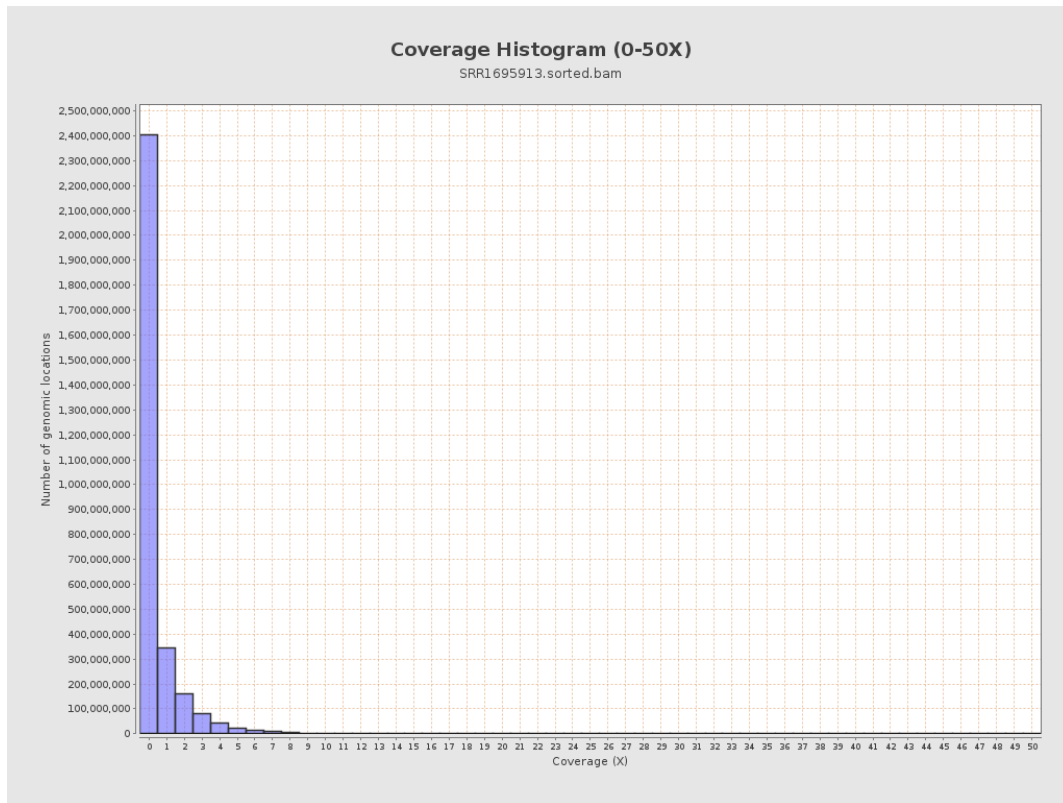
3. Results : Coverage across reference



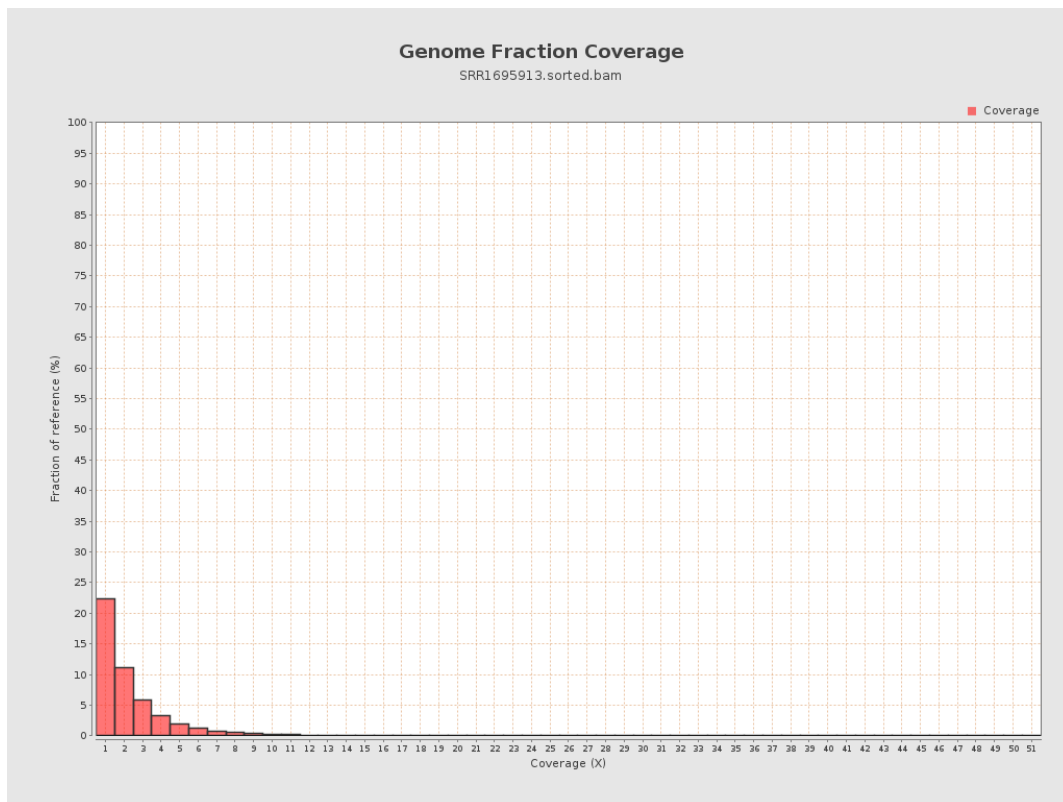
4. Results : Coverage Histogram



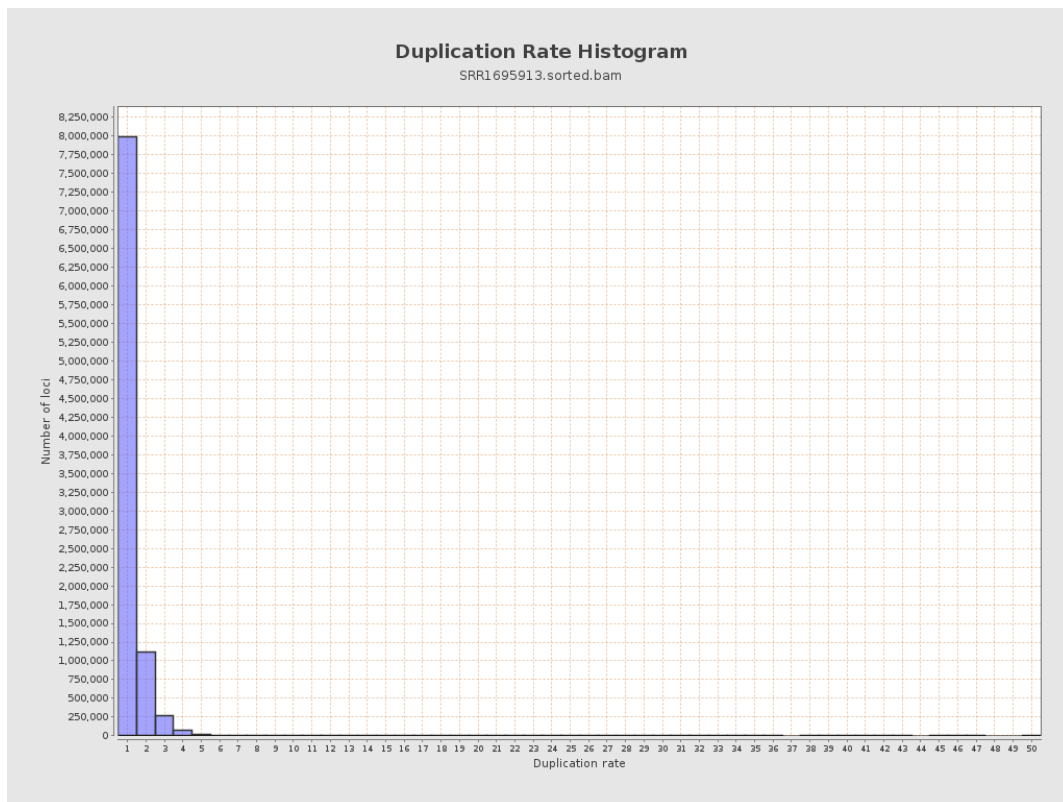
5. Results : Coverage Histogram (0-50X)



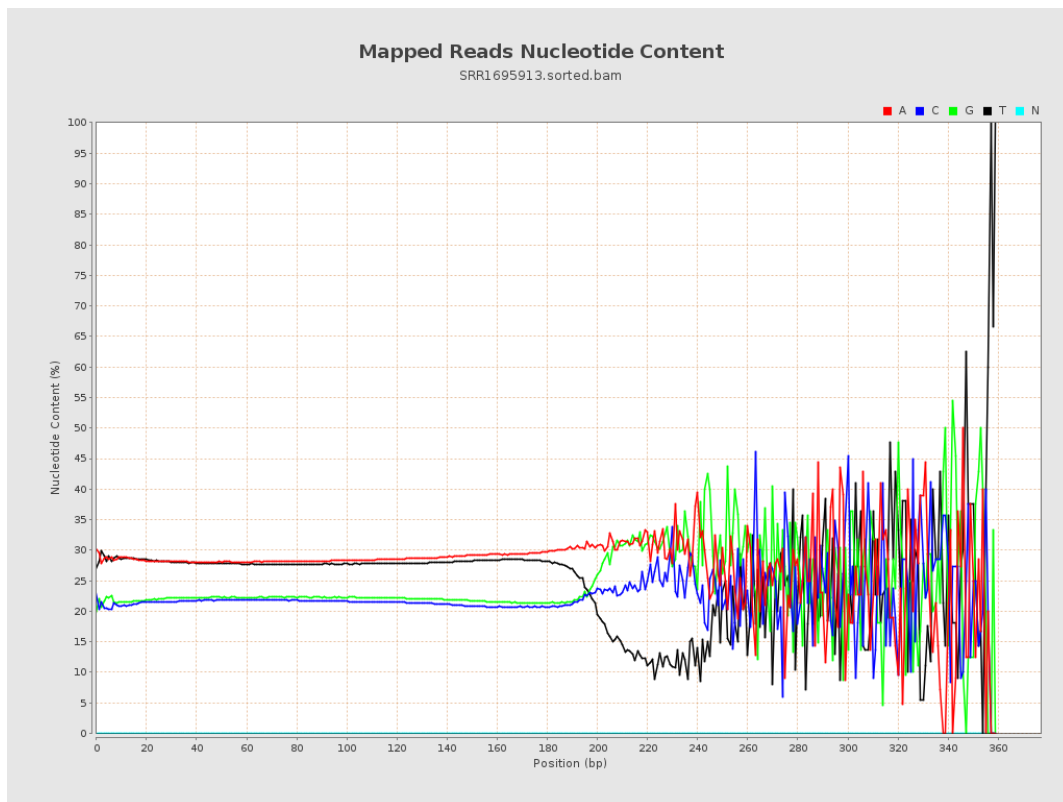
6. Results : Genome Fraction Coverage



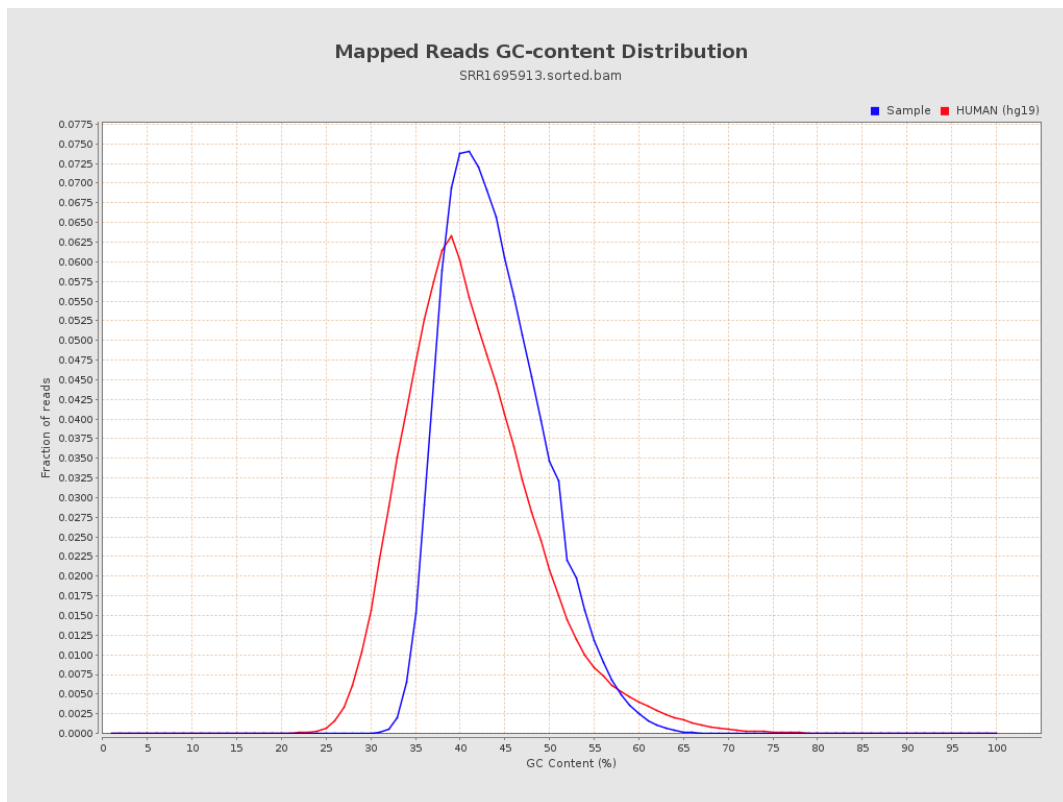
7. Results : Duplication Rate Histogram



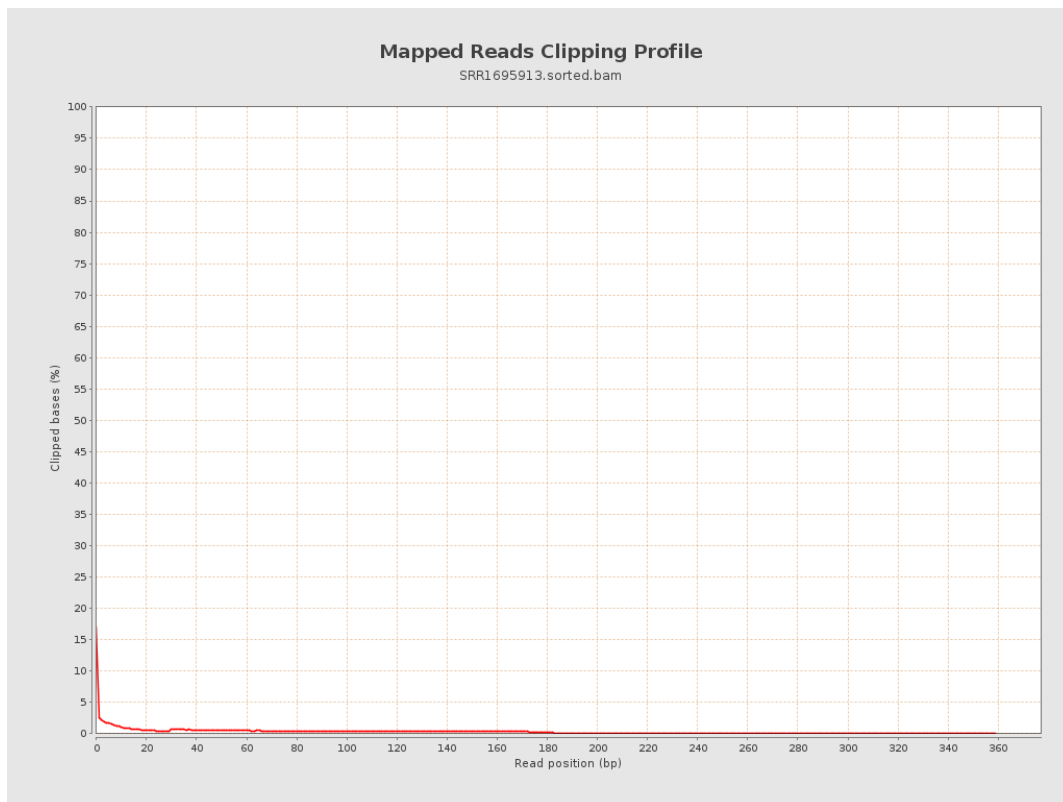
8. Results : Mapped Reads Nucleotide Content



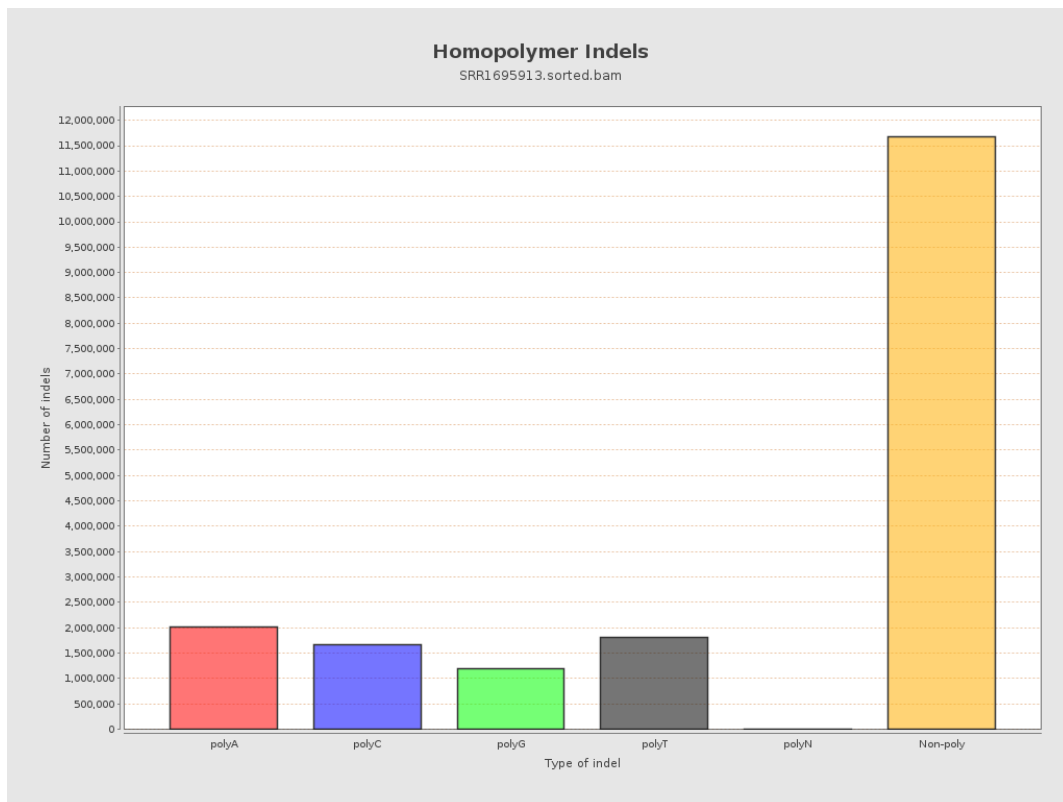
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

