

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/14 08:03:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695977.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_SRR1695977 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695977.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Sat Sep 14 08:03:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695977.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,668,259
Mapped reads	12,472,495 / 91.25%
Unmapped reads	1,195,764 / 8.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,477 / 0.14%
Read min/max/mean length	8 / 361 / 132.68
Duplicated reads (estimated)	2,788,607 / 20.4%
Duplication rate	18.78%
Clipped reads	3,281,801 / 24.01%

2.2. ACGT Content

Number/percentage of A's	470,313,075 / 27.65%
Number/percentage of C's	378,614,490 / 22.26%
Number/percentage of T's	468,747,647 / 27.55%
Number/percentage of G's	383,528,567 / 22.54%
Number/percentage of N's	0 / 0%
GC Percentage	44.8%

2.3. Coverage

Mean	0.5534

Standard Deviation	1.867
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2.4. Mapping Quality

Mean Mapping Quality	52.02
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2.5. Mismatches and indels

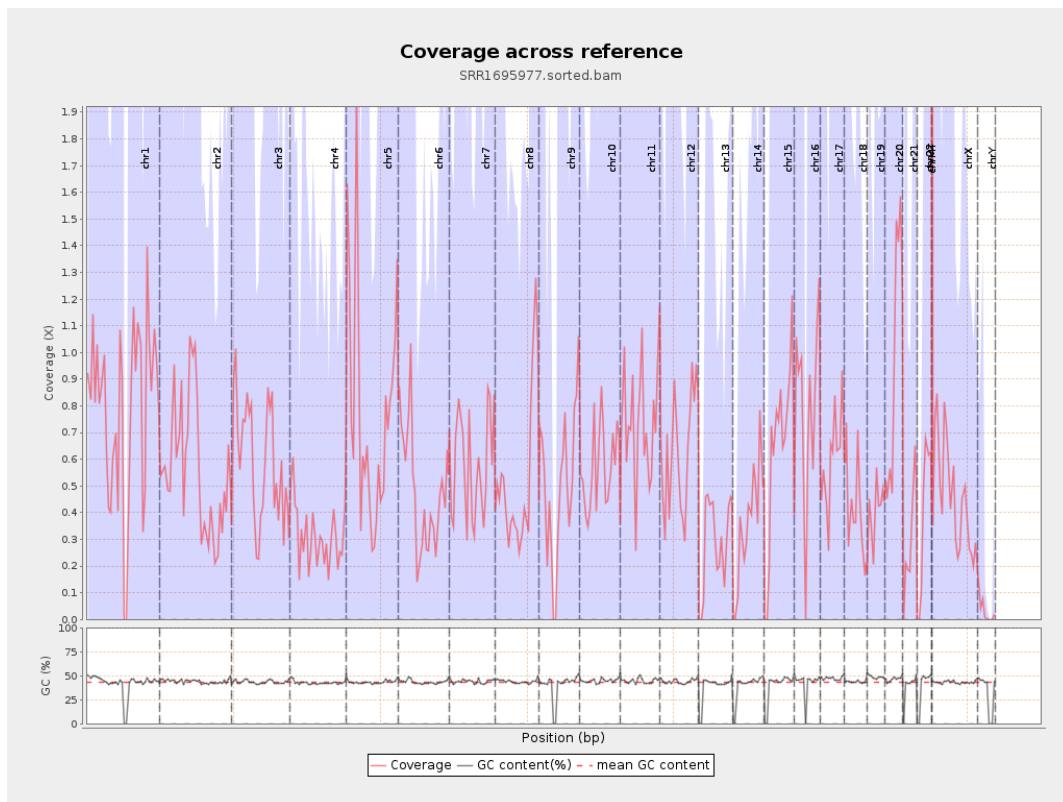
General error rate	2.03%
Mismatches	23,948,653
Insertions	9,780,546
Mapped reads with at least one insertion	47.11%
Deletions	10,771,435
Mapped reads with at least one deletion	51.65%
Homopolymer indels	36.69%

2.6. Chromosome stats

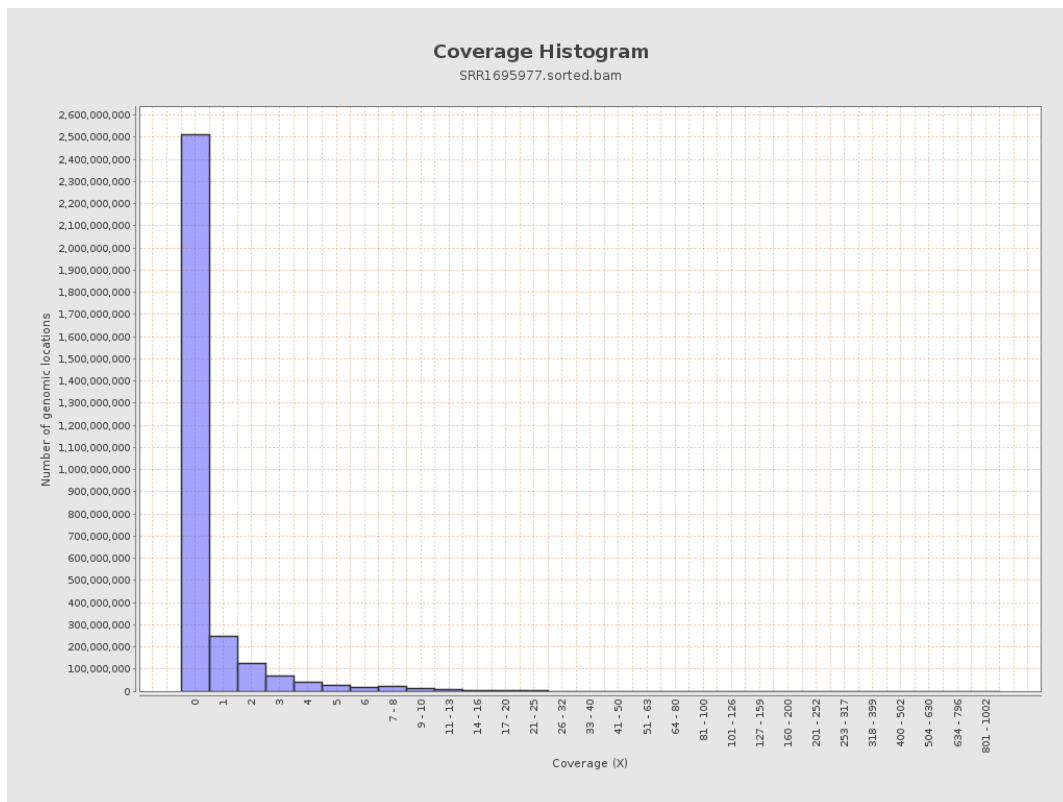
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	196488497	0.7883	2.5518
chr2	243199373	136320636	0.5605	1.9498
chr3	198022430	117461898	0.5932	1.786
chr4	191154276	59524418	0.3114	1.2523
chr5	180915260	141145258	0.7802	2.3236
chr6	171115067	82062943	0.4796	1.5502
chr7	159138663	92244968	0.5797	1.7597

chr8	146364022	76079160	0.5198	1.6746
chr9	141213431	72259951	0.5117	1.7882
chr10	135534747	77749408	0.5736	1.7846
chr11	135006516	97730289	0.7239	2.1059
chr12	133851895	83272326	0.6221	1.863
chr13	115169878	32986550	0.2864	1.1066
chr14	107349540	37777445	0.3519	1.2873
chr15	102531392	65902132	0.6428	2.0164
chr16	90354753	70605256	0.7814	2.3328
chr17	81195210	49067970	0.6043	1.8666
chr18	78077248	32553208	0.4169	1.6376
chr19	59128983	23982439	0.4056	1.5911
chr20	63025520	60646673	0.9623	2.6741
chr21	48129895	15133270	0.3144	2.0011
chr22	51304566	20196451	0.3937	1.4194
chrMT	16571	207039	12.4941	13.298
chrX	155270560	69929667	0.4504	1.4711
chrY	59373566	1854779	0.0312	0.6281

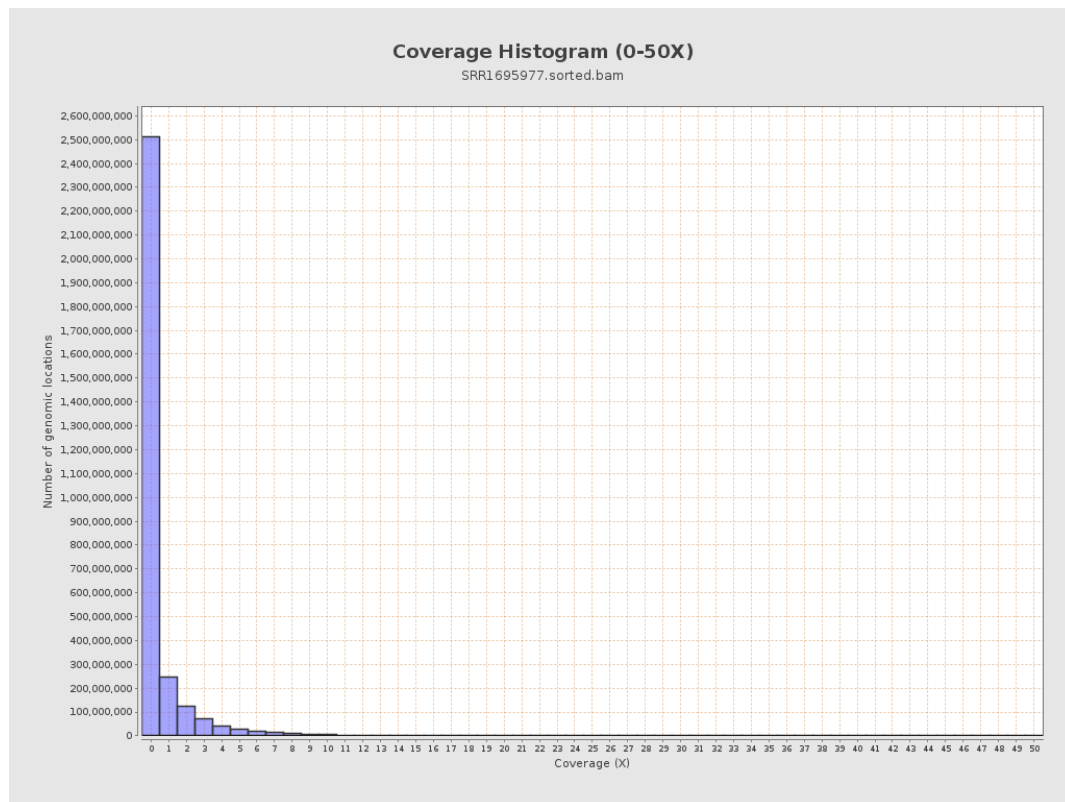
3. Results : Coverage across reference



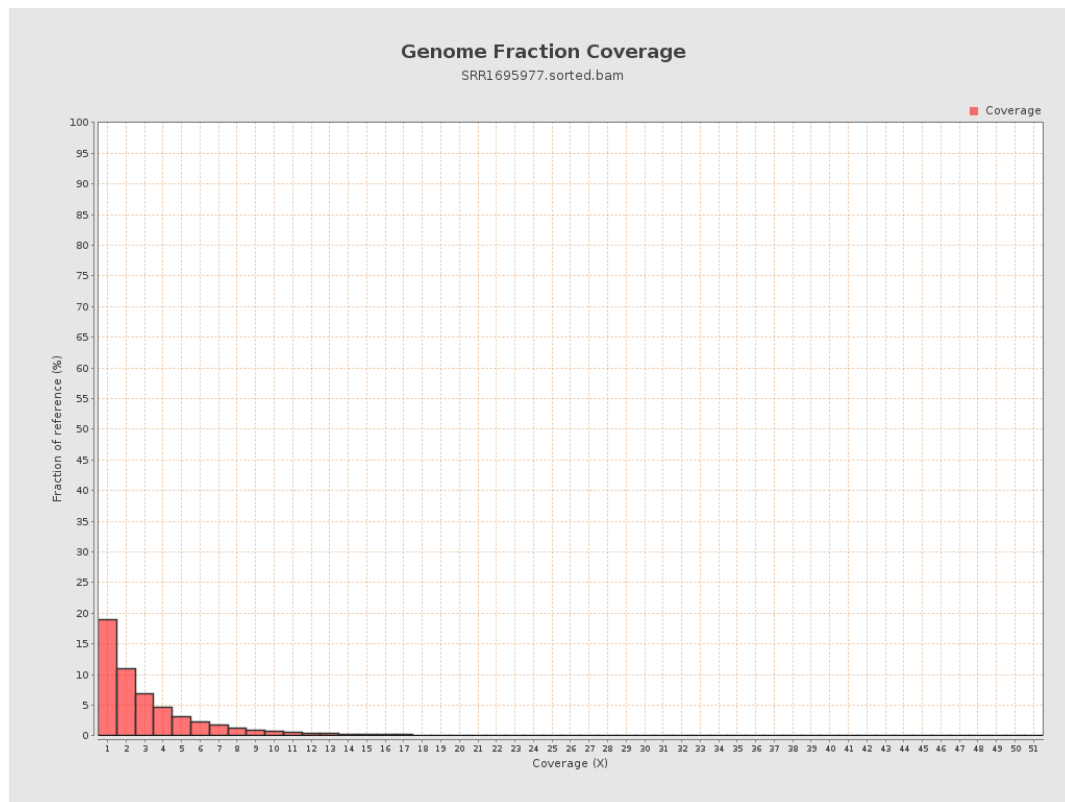
4. Results : Coverage Histogram



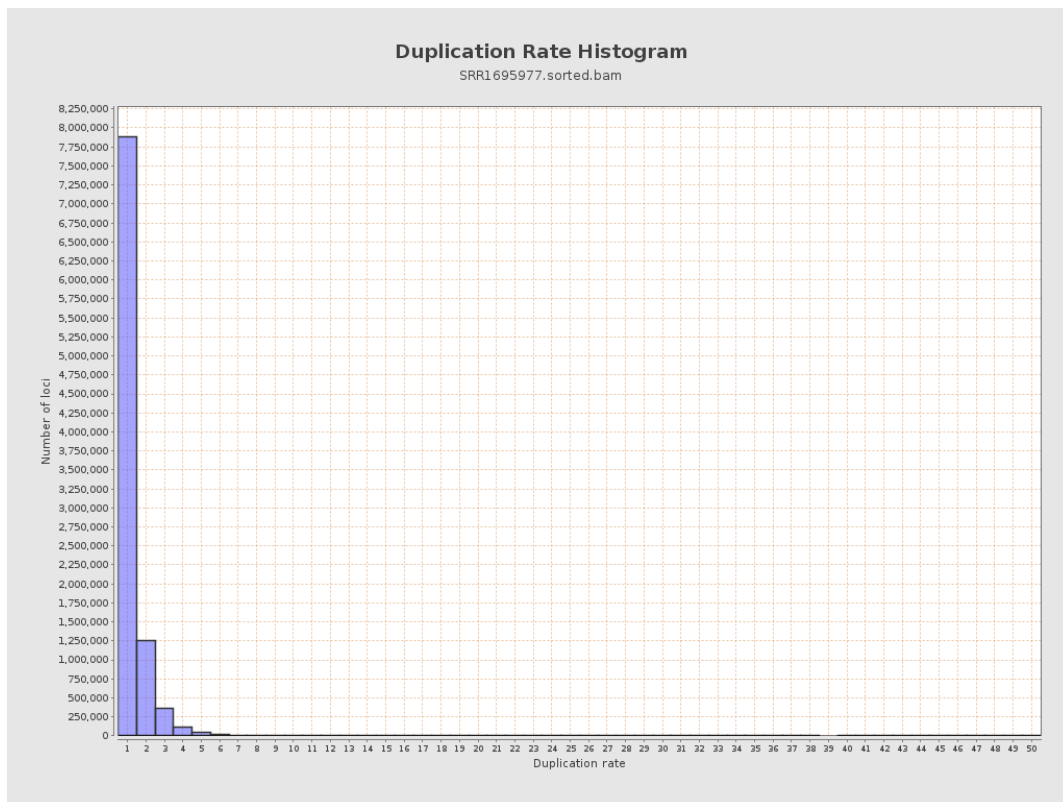
5. Results : Coverage Histogram (0-50X)



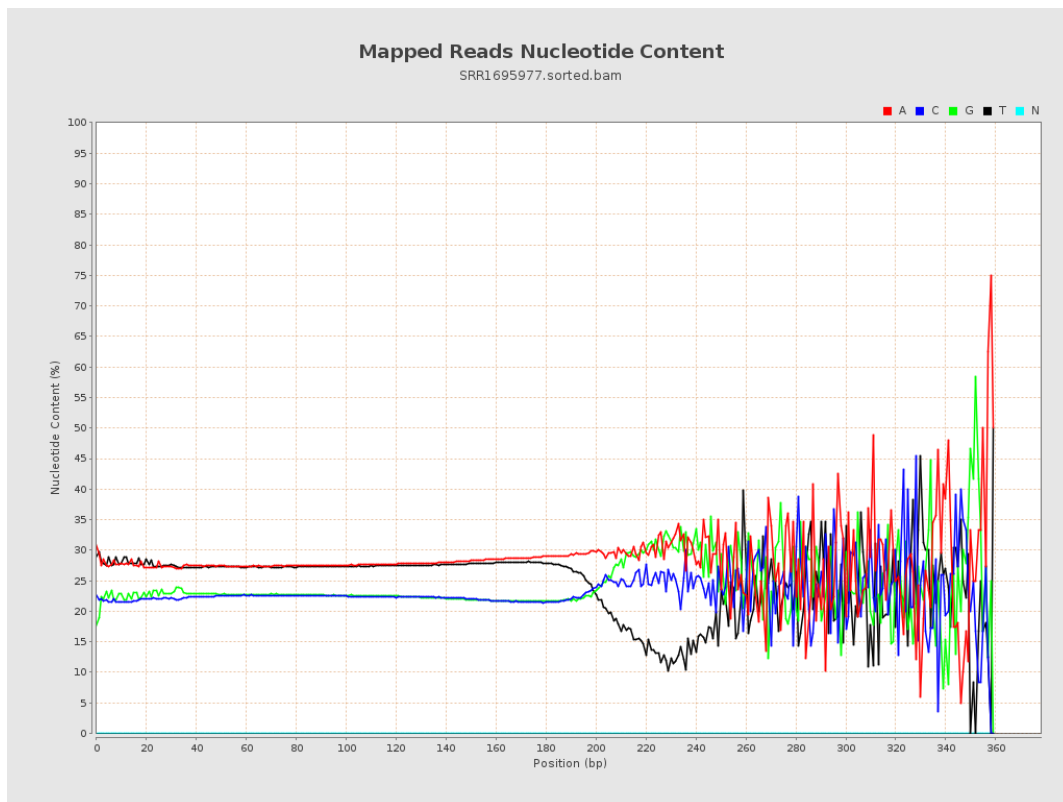
6. Results : Genome Fraction Coverage



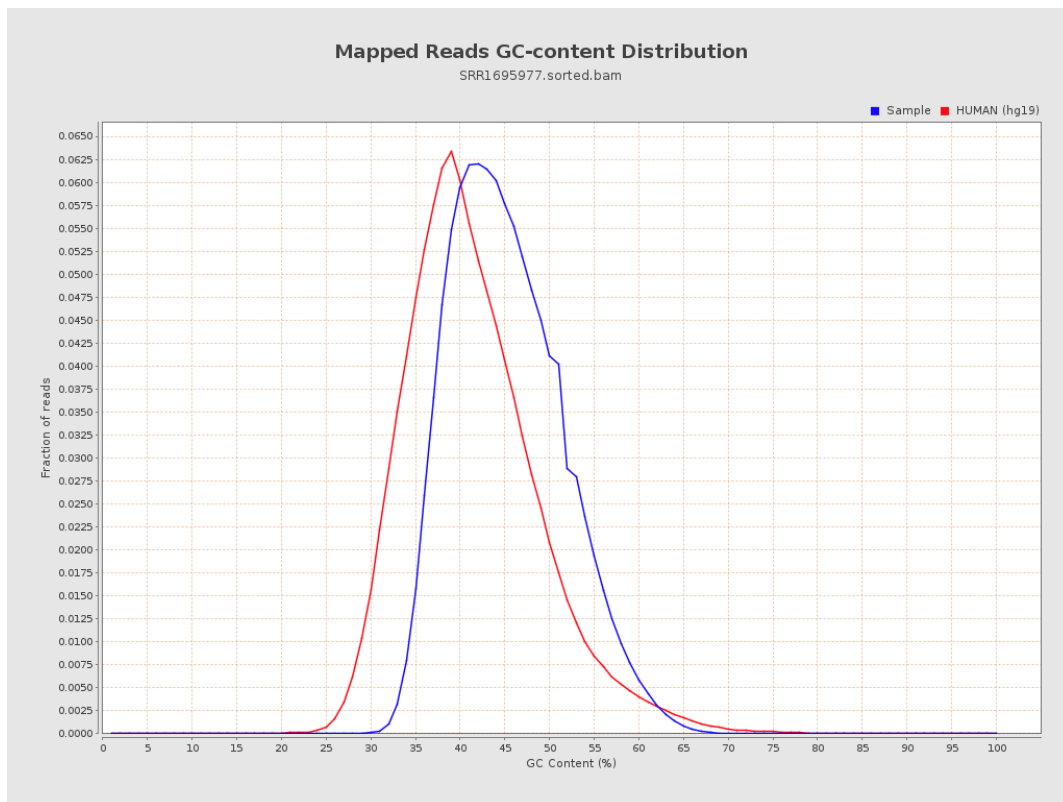
7. Results : Duplication Rate Histogram



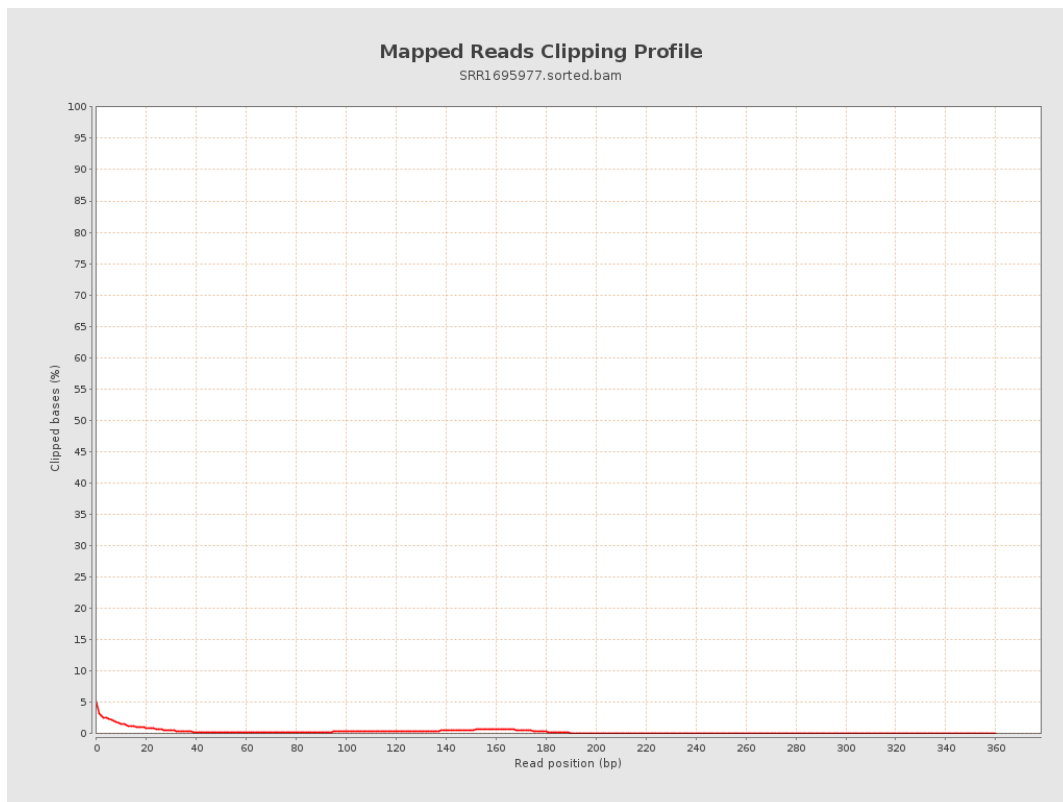
8. Results : Mapped Reads Nucleotide Content



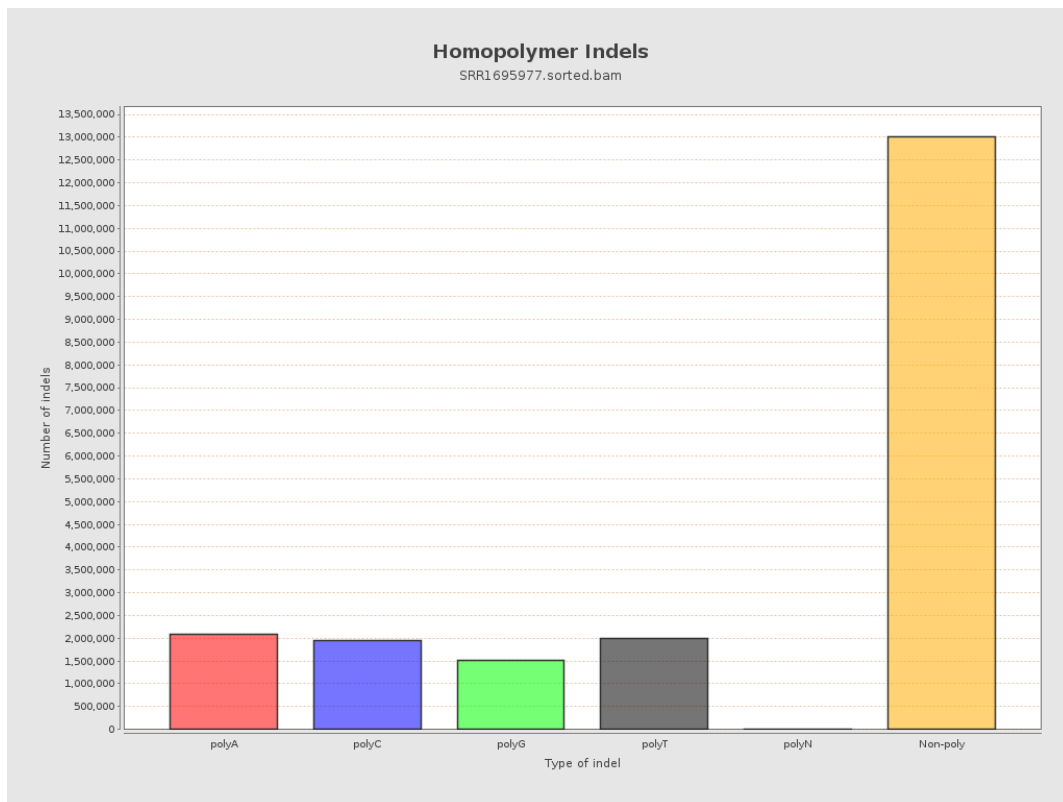
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

