

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/14 09:31:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695990.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_SRR1695990 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695990.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Sat Sep 14 09:31:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695990.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,998,809
Mapped reads	12,919,925 / 92.29%
Unmapped reads	1,078,884 / 7.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	185,922 / 1.33%
Read min/max/mean length	8 / 360 / 143.68
Duplicated reads (estimated)	2,893,525 / 20.67%
Duplication rate	19.2%
Clipped reads	3,180,220 / 22.72%

2.2. ACGT Content

Number/percentage of A's	546,991,612 / 28.69%
Number/percentage of C's	402,924,410 / 21.14%
Number/percentage of T's	543,894,884 / 28.53%
Number/percentage of G's	412,606,388 / 21.64%
Number/percentage of N's	0 / 0%
GC Percentage	42.78%

2.3. Coverage

Mean	0.6201

Standard Deviation	1.7195
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2.4. Mapping Quality

Mean Mapping Quality	52.07
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2.5. Mismatches and indels

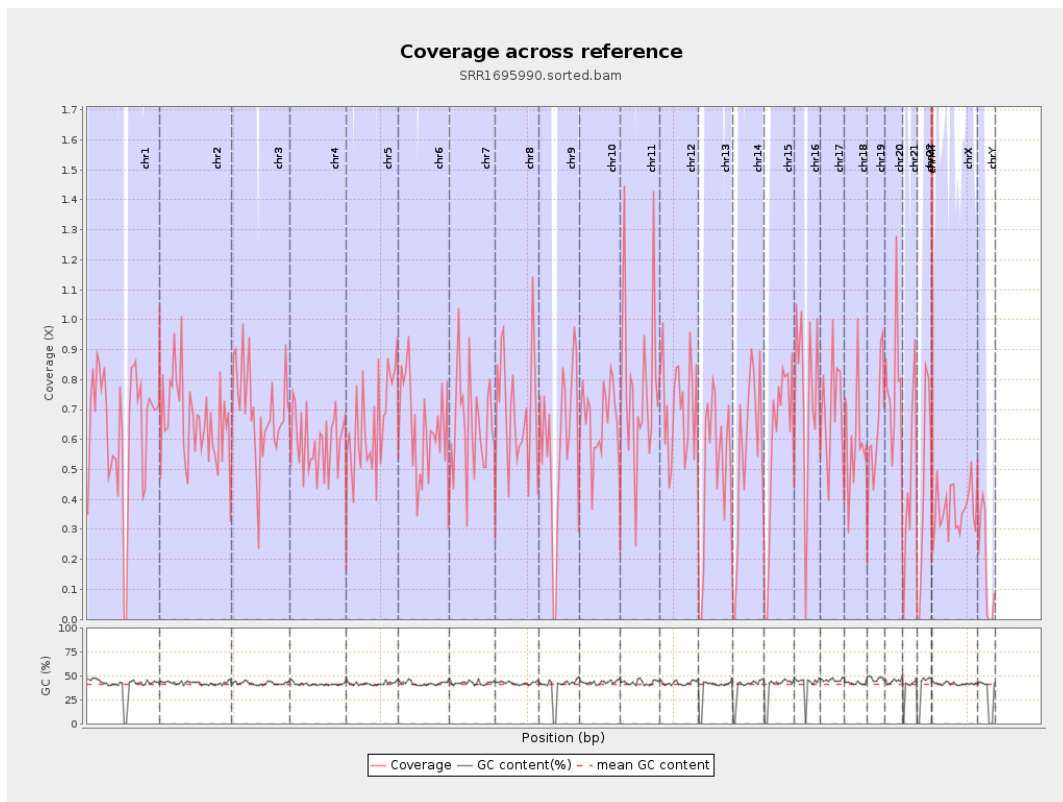
General error rate	1.63%
Mismatches	19,923,449
Insertions	10,379,984
Mapped reads with at least one insertion	45.7%
Deletions	11,857,453
Mapped reads with at least one deletion	52.46%
Homopolymer indels	37.39%

2.6. Chromosome stats

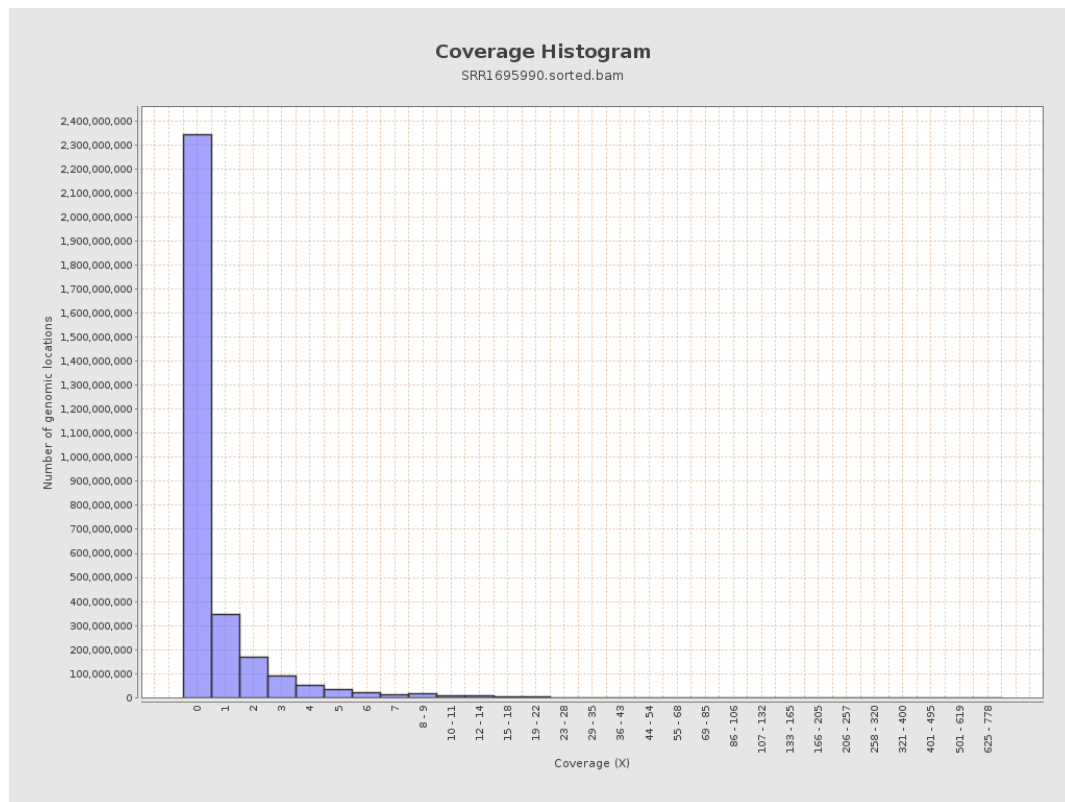
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	159799970	0.6411	1.8667
chr2	243199373	161055474	0.6622	1.7198
chr3	198022430	137491108	0.6943	1.752
chr4	191154276	112980696	0.591	1.5539
chr5	180915260	118267995	0.6537	1.7136
chr6	171115067	109691409	0.641	1.7827
chr7	159138663	102086041	0.6415	1.6376

chr8	146364022	102487375	0.7002	1.7291
chr9	141213431	81638144	0.5781	1.6016
chr10	135534747	90261313	0.666	1.7348
chr11	135006516	102888778	0.7621	2.2228
chr12	133851895	95139436	0.7108	1.8102
chr13	115169878	58270822	0.506	1.489
chr14	107349540	58985870	0.5495	1.5751
chr15	102531392	60325025	0.5884	1.5896
chr16	90354753	65079725	0.7203	1.8203
chr17	81195210	55678349	0.6857	1.8929
chr18	78077248	47126135	0.6036	1.7699
chr19	59128983	38400080	0.6494	1.9114
chr20	63025520	48353581	0.7672	1.9064
chr21	48129895	22936205	0.4765	1.5992
chr22	51304566	22507826	0.4387	1.4677
chrMT	16571	558721	33.7168	21.164
chrX	155270560	56829272	0.366	1.2768
chrY	59373566	10750189	0.1811	1.1025

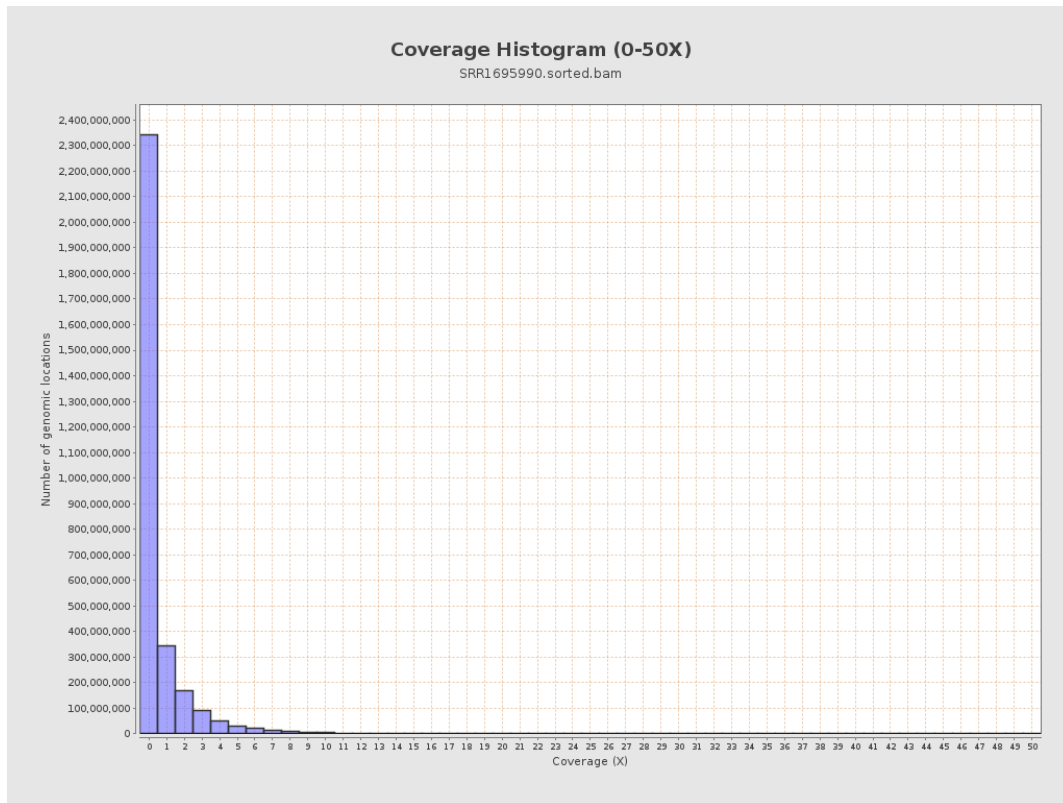
3. Results : Coverage across reference



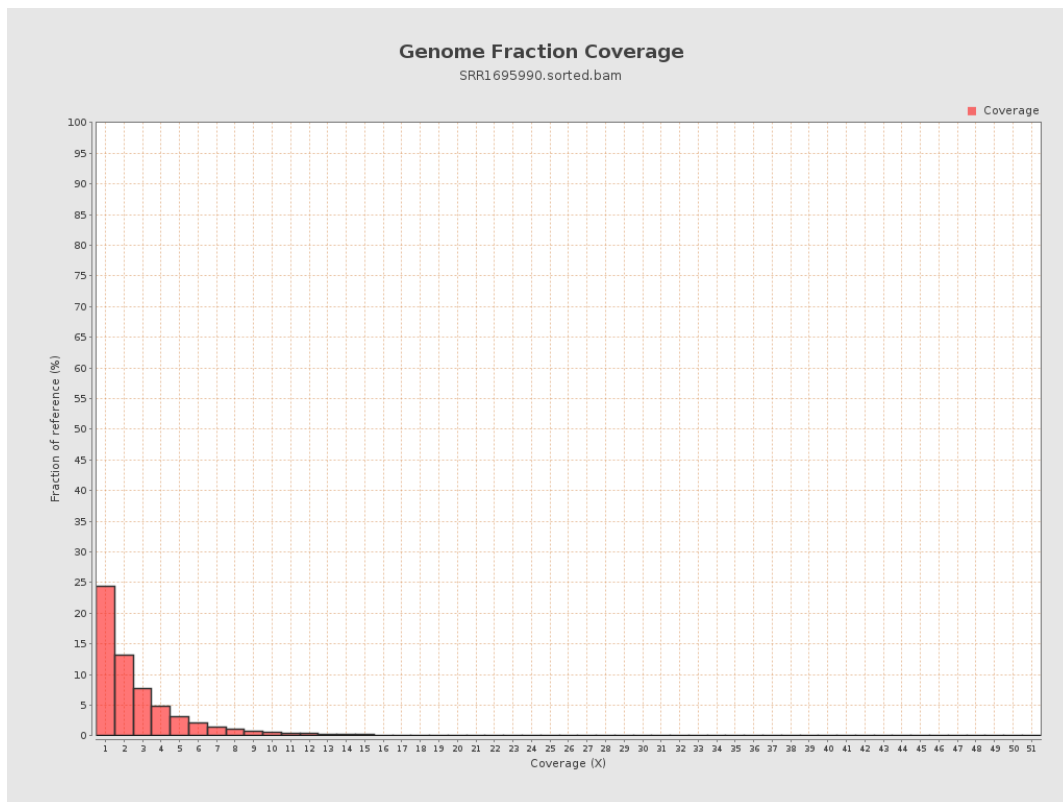
4. Results : Coverage Histogram



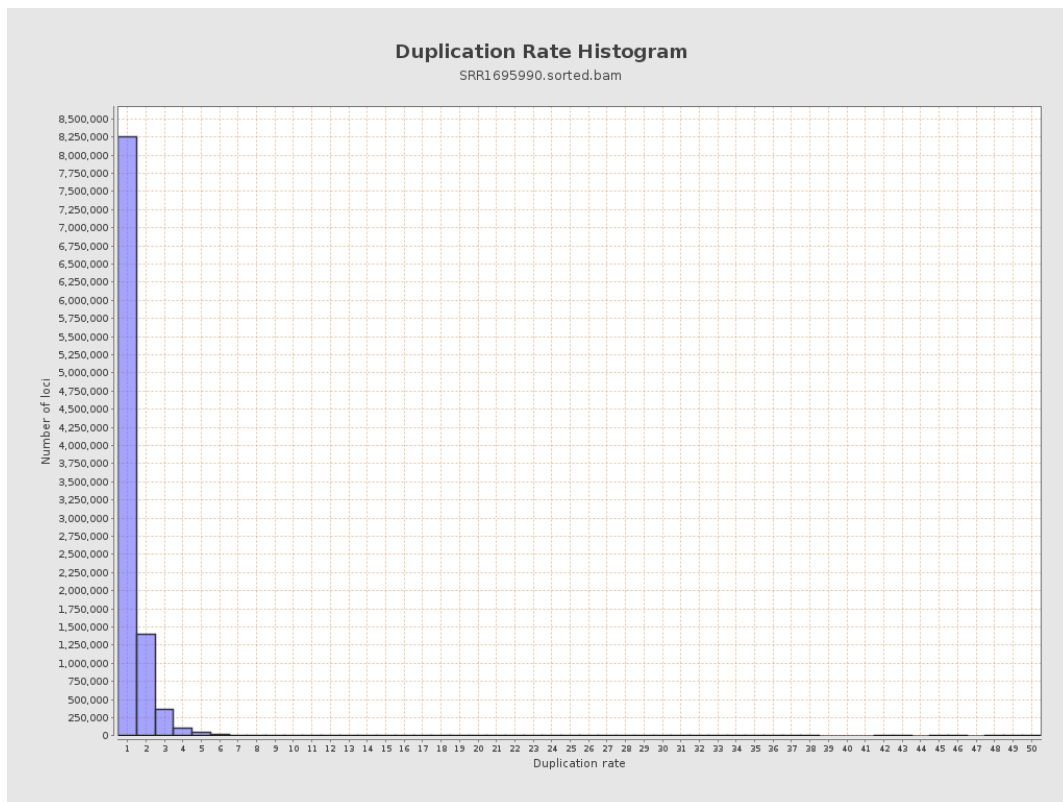
5. Results : Coverage Histogram (0-50X)



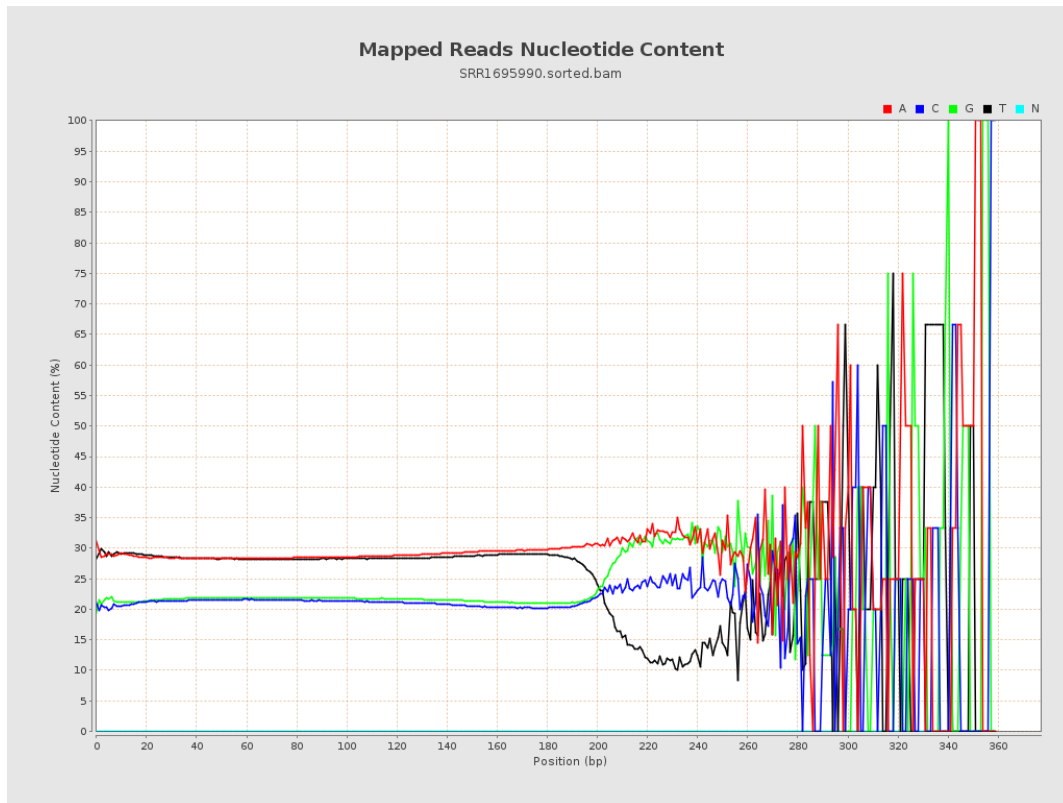
6. Results : Genome Fraction Coverage



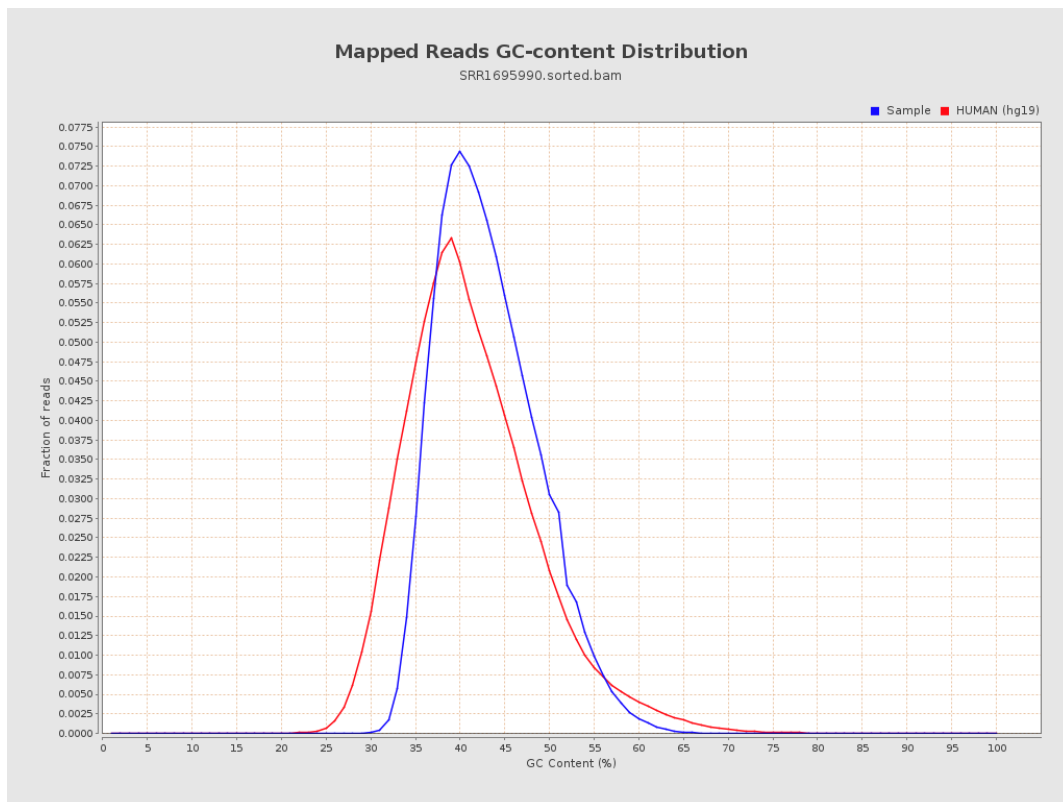
7. Results : Duplication Rate Histogram



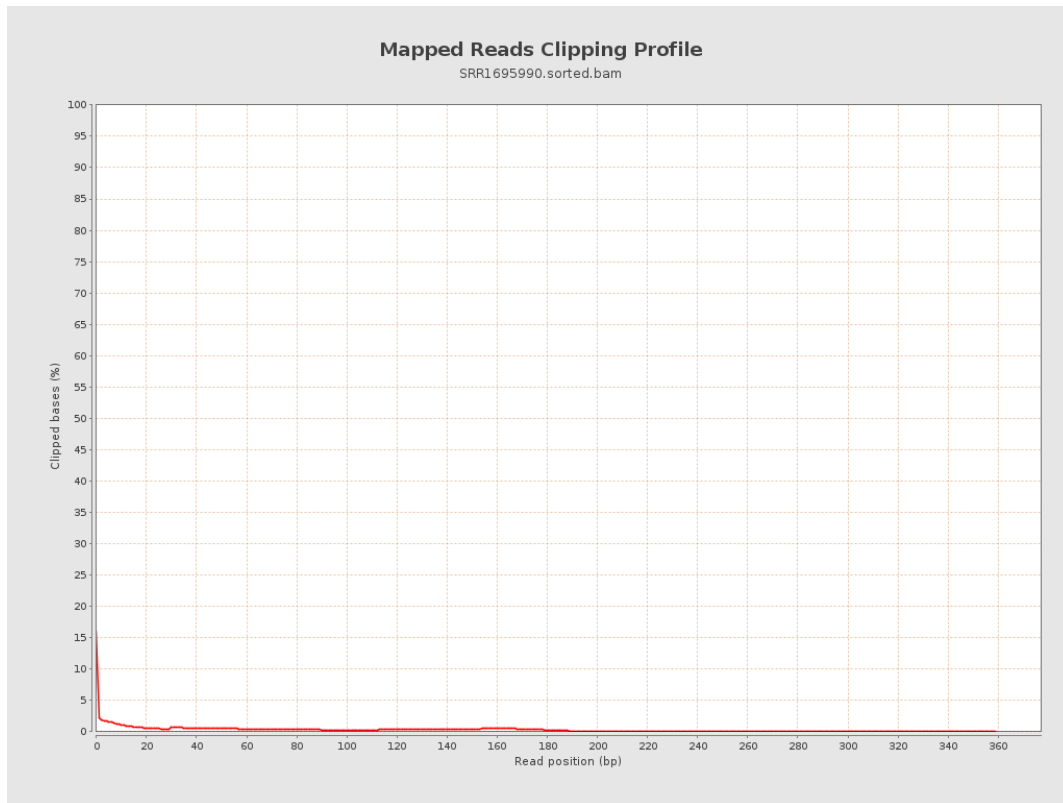
8. Results : Mapped Reads Nucleotide Content



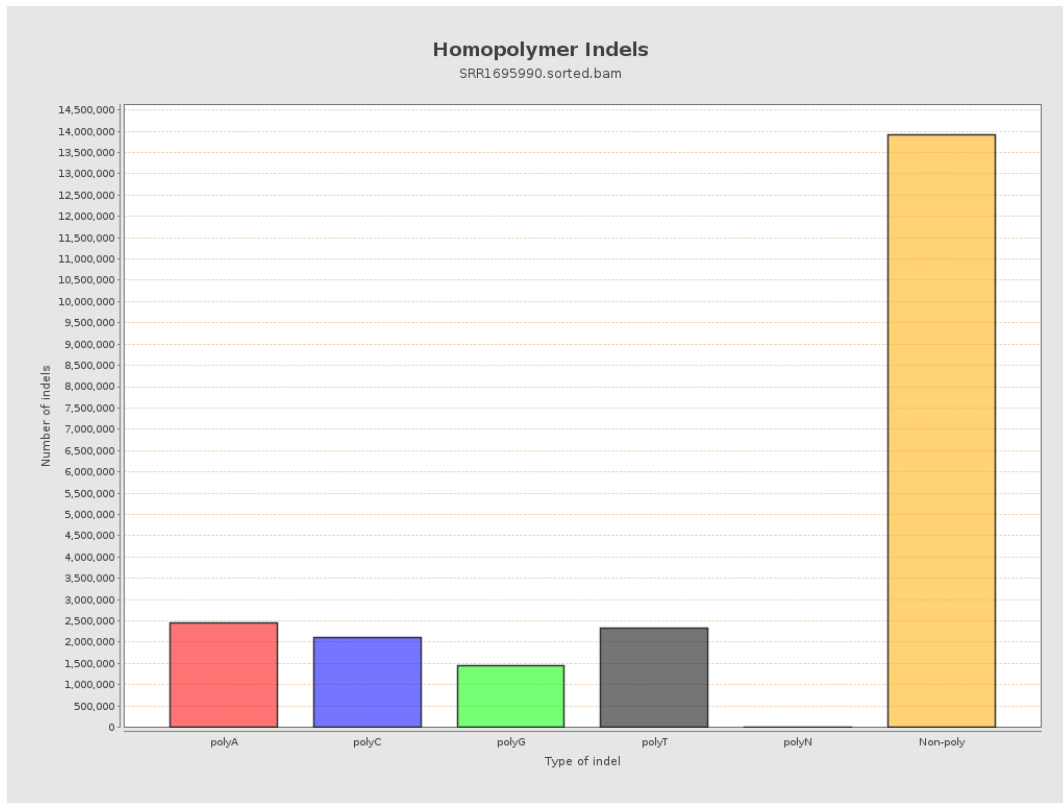
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

