

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/14 08:17:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695979.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_SRR1695979 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695979.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Sat Sep 14 08:17:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695979.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,021,589
Mapped reads	11,492,920 / 88.26%
Unmapped reads	1,528,669 / 11.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,069 / 0.12%
Read min/max/mean length	8 / 361 / 130.22
Duplicated reads (estimated)	2,529,788 / 19.43%
Duplication rate	18.39%
Clipped reads	2,975,601 / 22.85%

2.2. ACGT Content

Number/percentage of A's	426,219,648 / 27.5%
Number/percentage of C's	344,817,883 / 22.25%
Number/percentage of T's	426,641,274 / 27.53%
Number/percentage of G's	352,084,240 / 22.72%
Number/percentage of N's	0 / 0%
GC Percentage	44.97%

2.3. Coverage

Mean	0.5042

Standard Deviation	1.7385
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2.4. Mapping Quality

Mean Mapping Quality	52.16
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2.5. Mismatches and indels

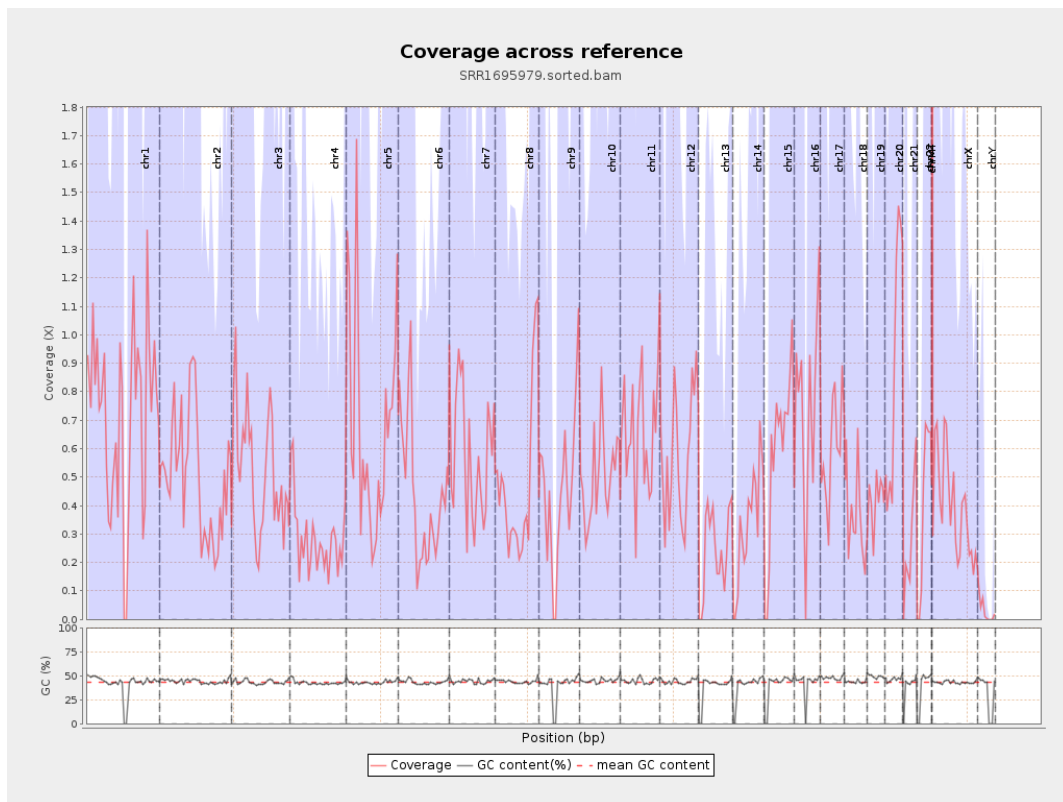
General error rate	2.08%
Mismatches	21,893,212
Insertions	9,527,862
Mapped reads with at least one insertion	49.07%
Deletions	9,951,589
Mapped reads with at least one deletion	51.73%
Homopolymer indels	36.7%

2.6. Chromosome stats

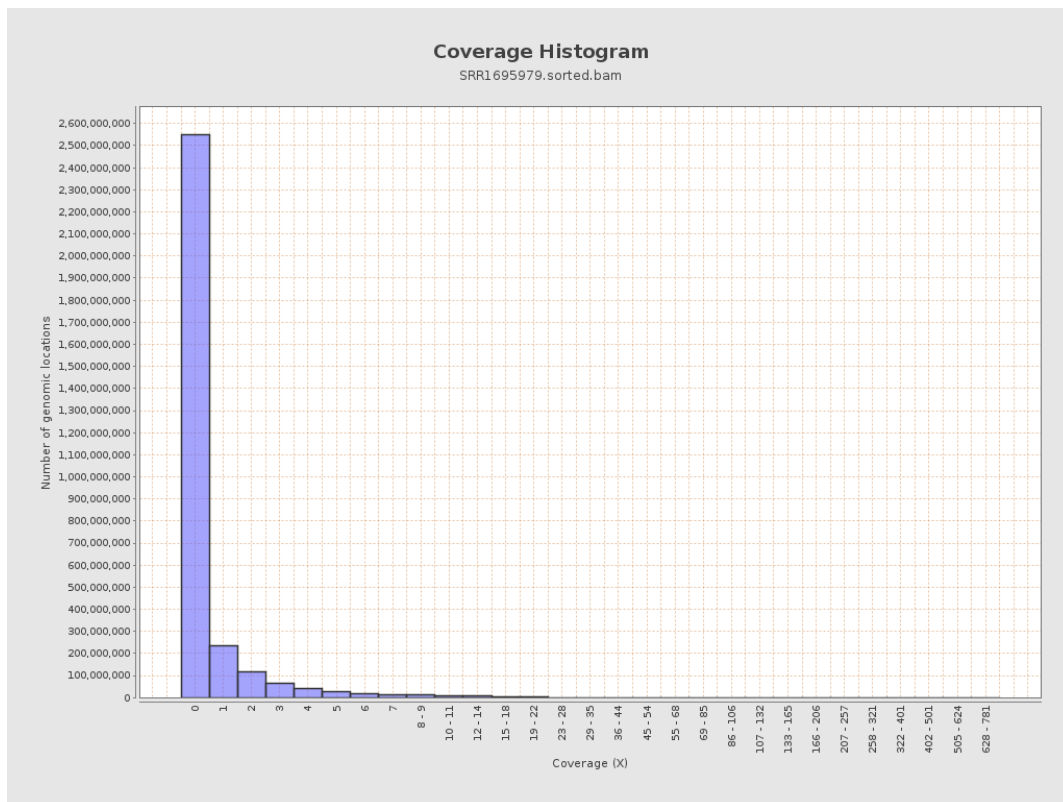
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	178321939	0.7154	2.3034
chr2	243199373	122339219	0.503	1.7424
chr3	198022430	103414654	0.5222	1.637
chr4	191154276	53285019	0.2788	1.1781
chr5	180915260	123240601	0.6812	2.0918
chr6	171115067	73924536	0.432	1.4618
chr7	159138663	92474542	0.5811	1.7807

chr8	146364022	68668798	0.4692	1.5691
chr9	141213431	65794535	0.4659	1.6597
chr10	135534747	68607655	0.5062	1.6247
chr11	135006516	87417370	0.6475	1.9153
chr12	133851895	76364330	0.5705	1.7793
chr13	115169878	28127023	0.2442	1
chr14	107349540	35226608	0.3281	1.2319
chr15	102531392	60367932	0.5888	1.9113
chr16	90354753	67034908	0.7419	2.3433
chr17	81195210	48960458	0.603	1.861
chr18	78077248	28822359	0.3692	1.4489
chr19	59128983	24838494	0.4201	1.5205
chr20	63025520	55805464	0.8854	2.5478
chr21	48129895	14120819	0.2934	1.892
chr22	51304566	20997295	0.4093	1.4635
chrMT	16571	248571	15.0004	15.788
chrX	155270560	60662685	0.3907	1.3547
chrY	59373566	1764813	0.0297	0.5783

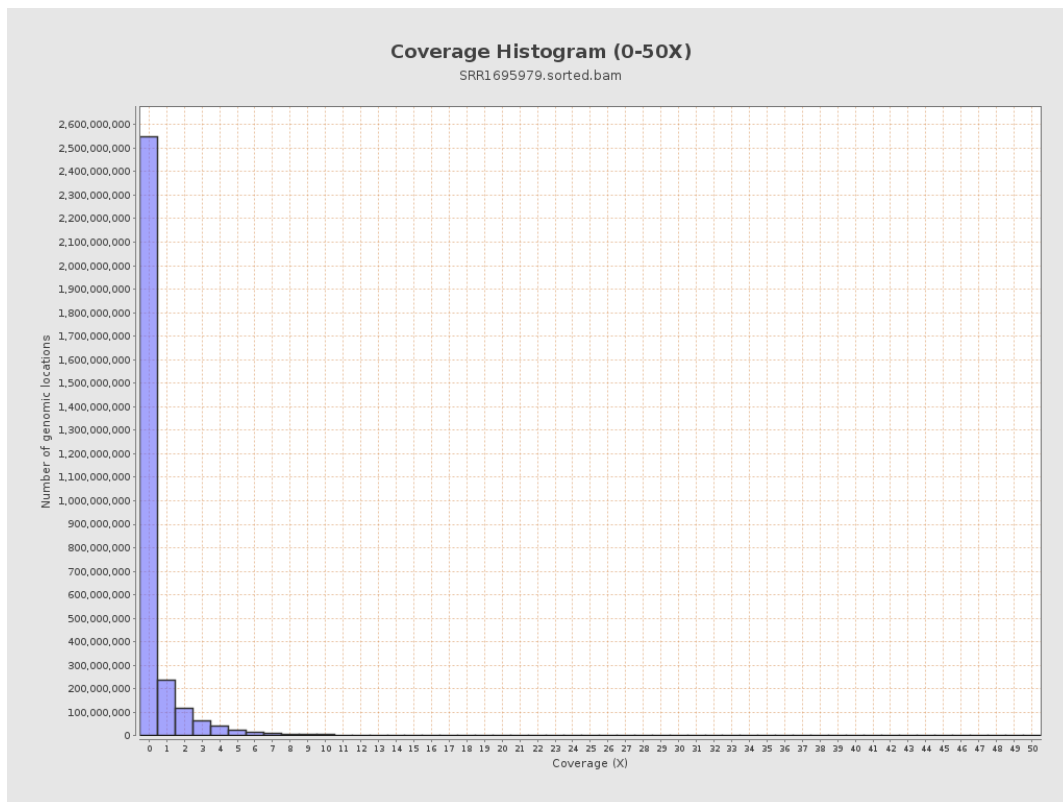
3. Results : Coverage across reference



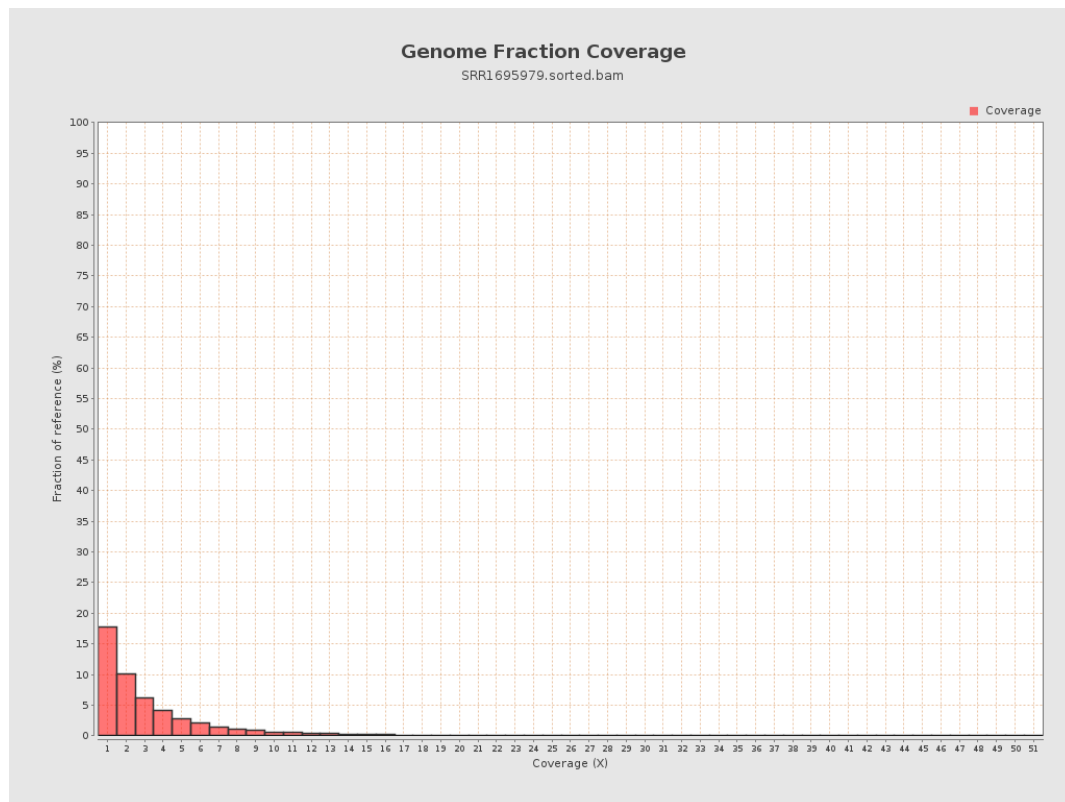
4. Results : Coverage Histogram



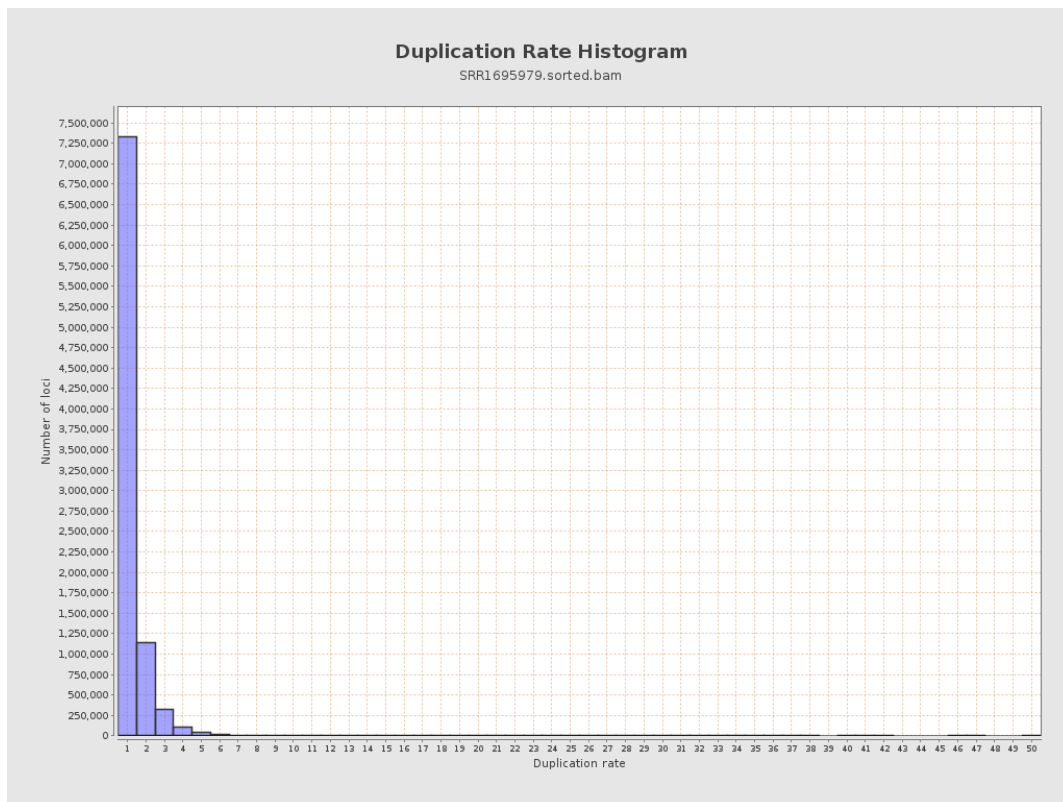
5. Results : Coverage Histogram (0-50X)



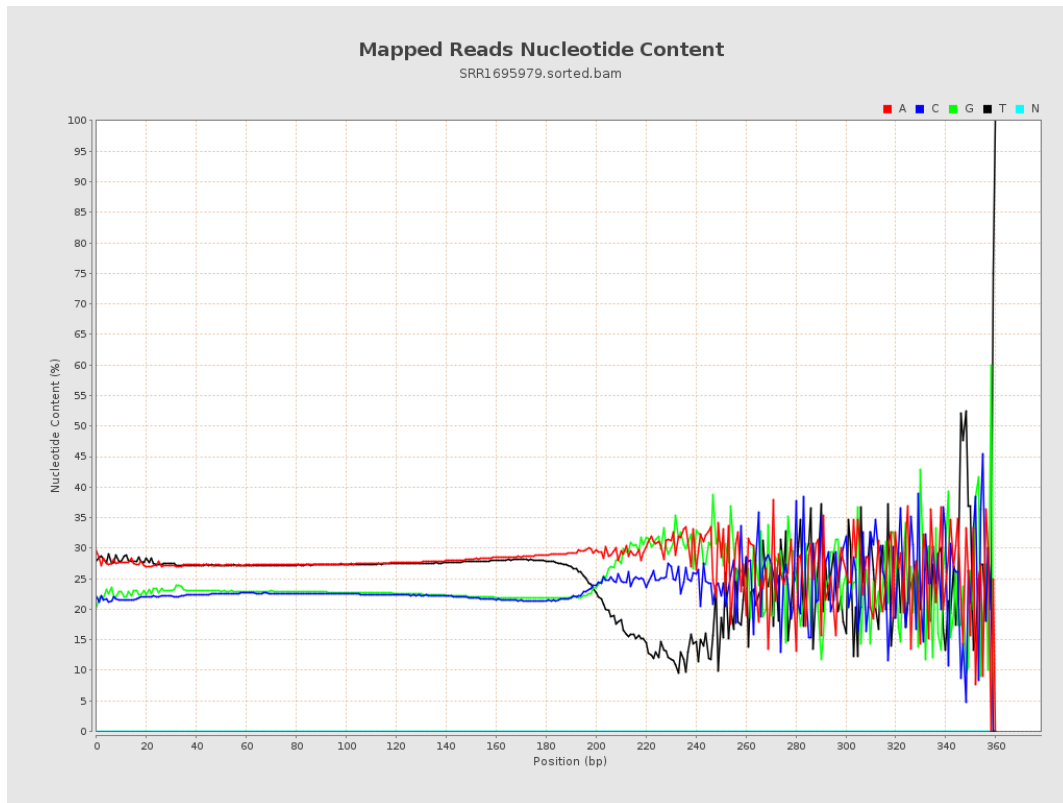
6. Results : Genome Fraction Coverage



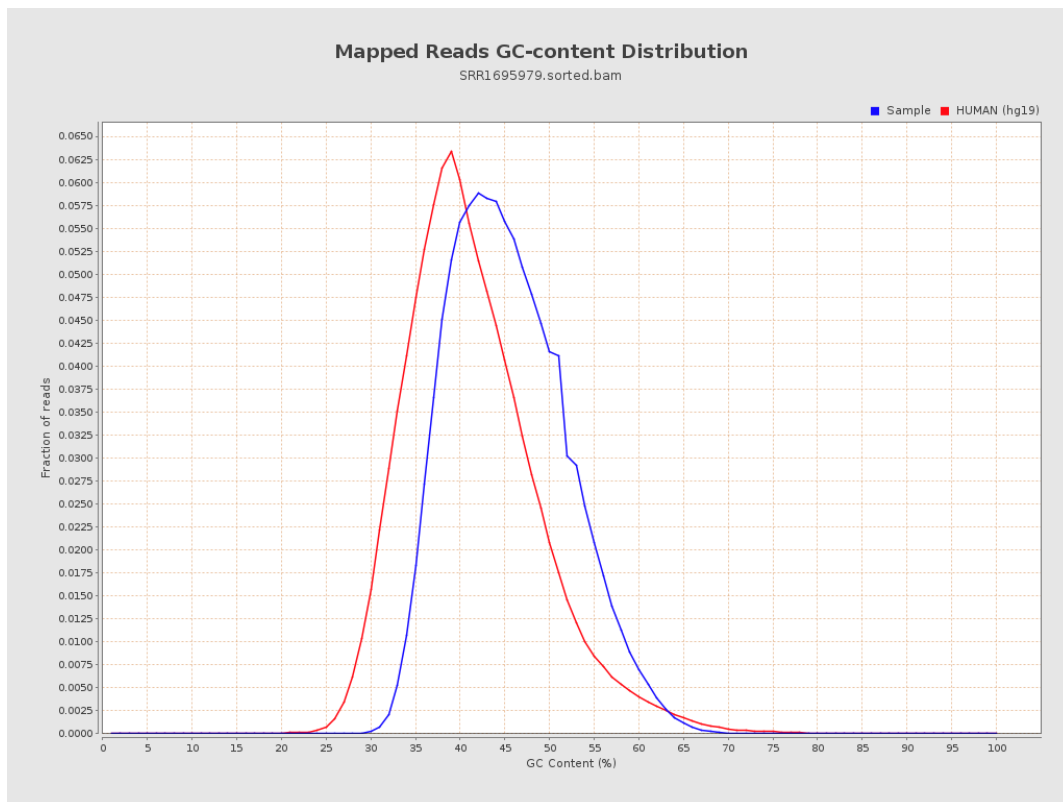
7. Results : Duplication Rate Histogram



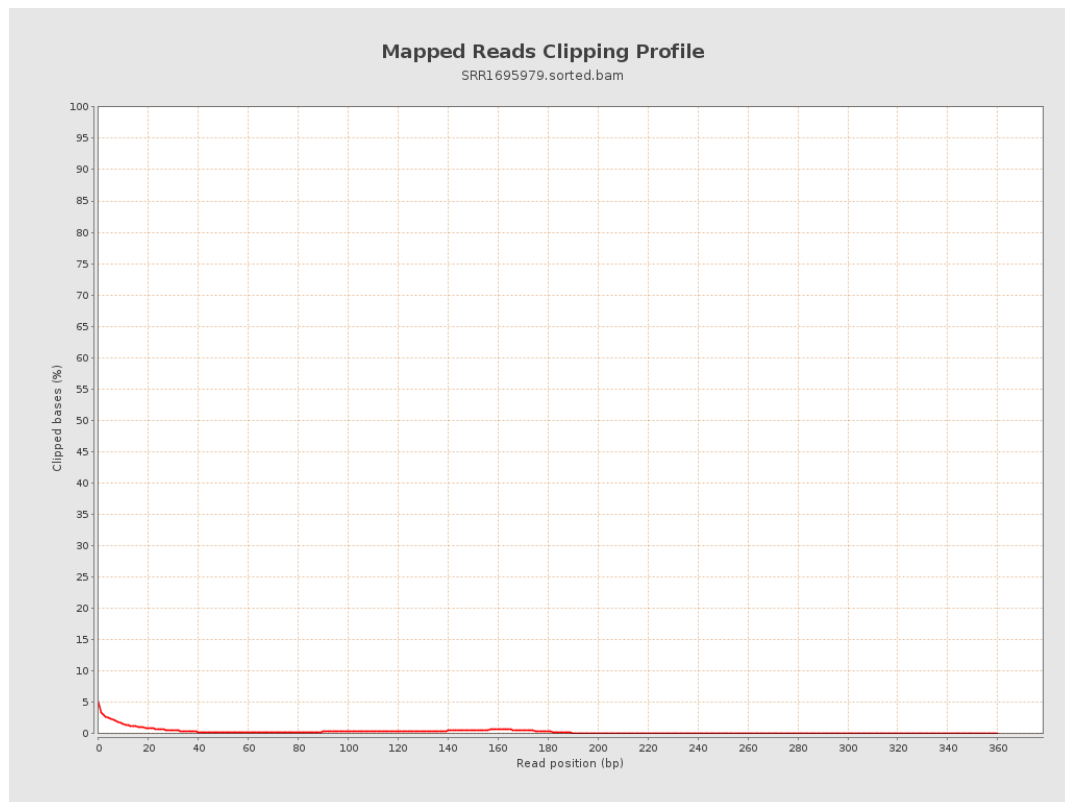
8. Results : Mapped Reads Nucleotide Content



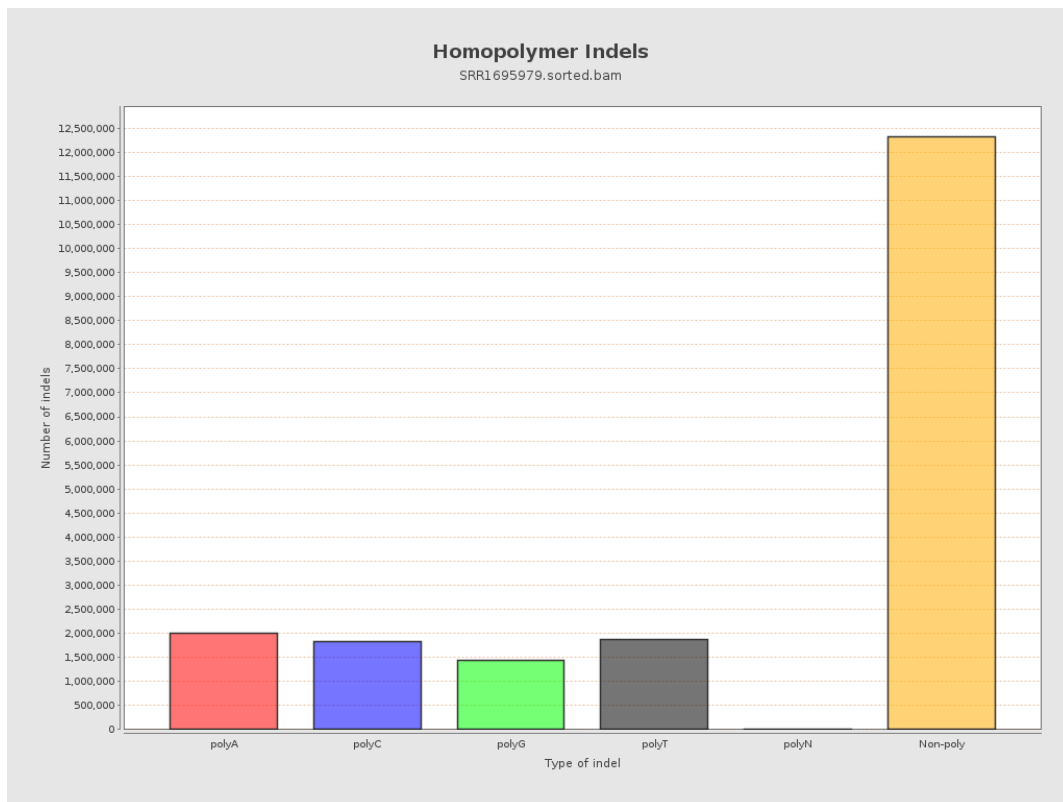
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

