

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/14 08:11:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695978.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_SRR1695978 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695978.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Sat Sep 14 08:11:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695978.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,602,712
Mapped reads	12,299,403 / 90.42%
Unmapped reads	1,303,309 / 9.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,761 / 0.15%
Read min/max/mean length	8 / 360 / 130.18
Duplicated reads (estimated)	2,751,025 / 20.22%
Duplication rate	18.58%
Clipped reads	3,238,050 / 23.8%

2.2. ACGT Content

Number/percentage of A's	456,246,707 / 27.57%
Number/percentage of C's	365,782,416 / 22.1%
Number/percentage of T's	454,203,605 / 27.44%
Number/percentage of G's	378,888,621 / 22.89%
Number/percentage of N's	0 / 0%
GC Percentage	44.99%

2.3. Coverage

Mean	0.5387

Standard Deviation	1.8232
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2.4. Mapping Quality

Mean Mapping Quality	51.94
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2.5. Mismatches and indels

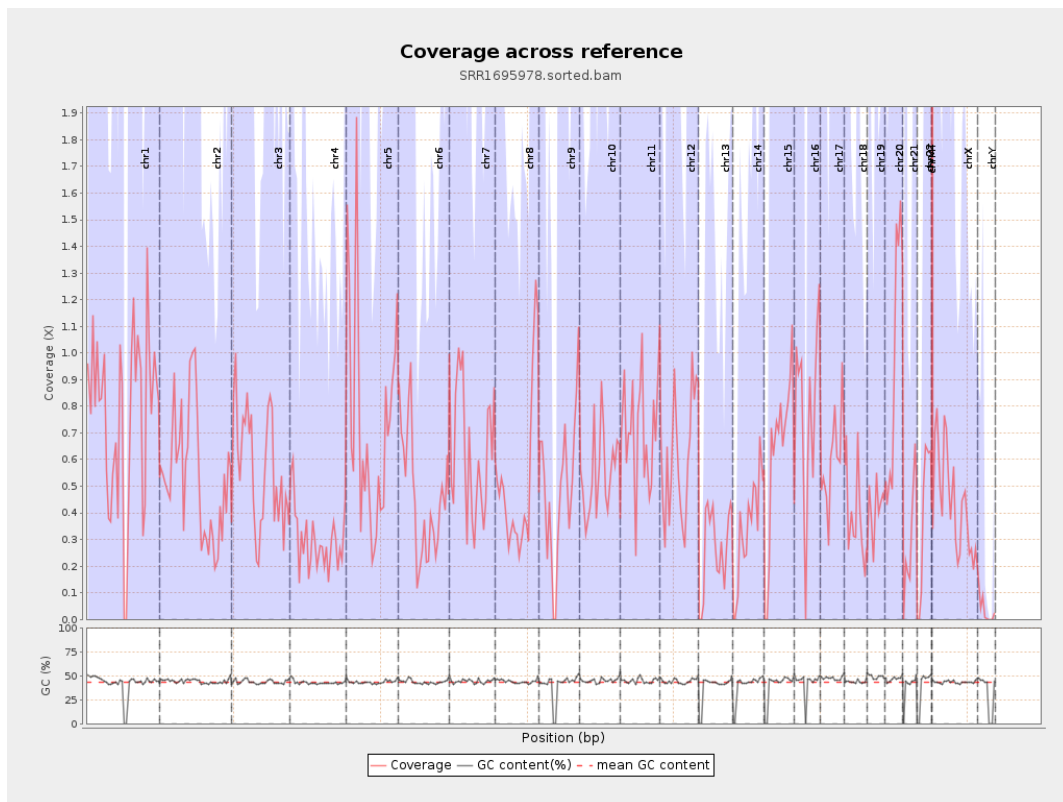
General error rate	2.1%
Mismatches	24,262,084
Insertions	9,788,723
Mapped reads with at least one insertion	47.67%
Deletions	11,191,450
Mapped reads with at least one deletion	53.24%
Homopolymer indels	36.6%

2.6. Chromosome stats

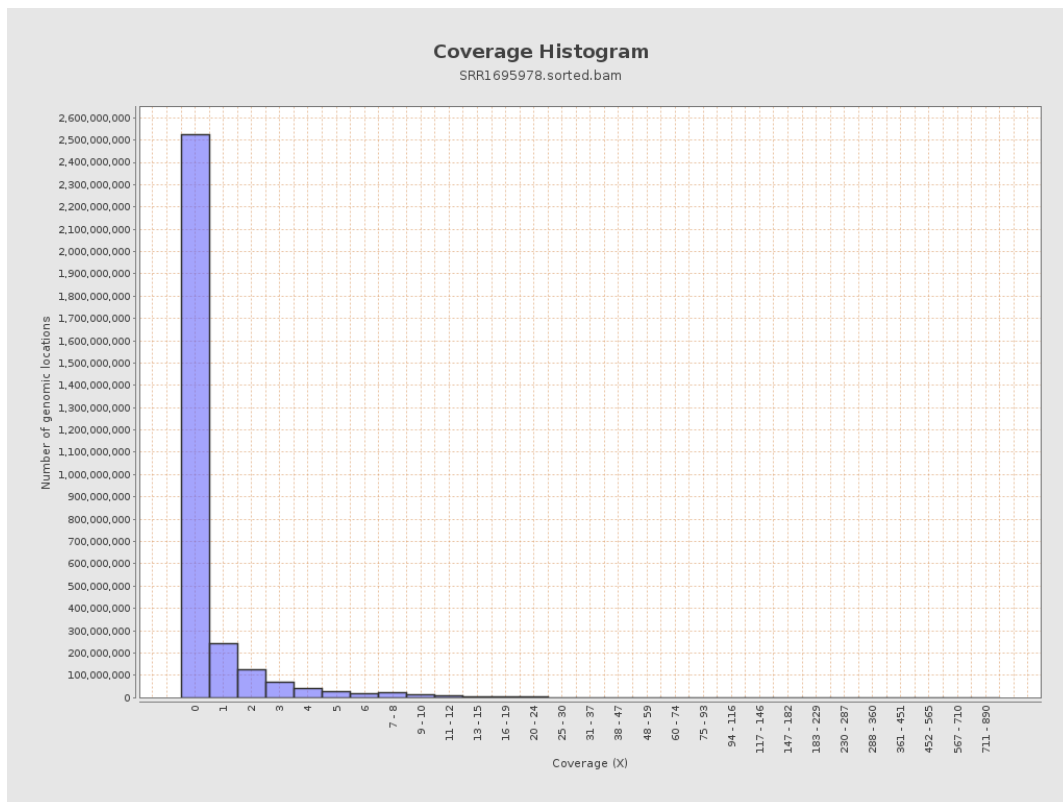
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	190604000	0.7647	2.4581
chr2	243199373	130557337	0.5368	1.8377
chr3	198022430	112669008	0.569	1.7294
chr4	191154276	56802567	0.2972	1.222
chr5	180915260	133563771	0.7383	2.2285
chr6	171115067	77885340	0.4552	1.5044
chr7	159138663	100132792	0.6292	1.8926

chr8	146364022	74274734	0.5075	1.6633
chr9	141213431	70690260	0.5006	1.7511
chr10	135534747	75169589	0.5546	1.7263
chr11	135006516	94403194	0.6992	2.0376
chr12	133851895	80876320	0.6042	1.8326
chr13	115169878	30716748	0.2667	1.0515
chr14	107349540	36329055	0.3384	1.2227
chr15	102531392	64195139	0.6261	1.9839
chr16	90354753	69818806	0.7727	2.3583
chr17	81195210	49068444	0.6043	1.8326
chr18	78077248	30648817	0.3925	1.5689
chr19	59128983	24450505	0.4135	1.6135
chr20	63025520	60307260	0.9569	2.6246
chr21	48129895	15118254	0.3141	1.9982
chr22	51304566	20223439	0.3942	1.3992
chrMT	16571	258556	15.6029	16.6067
chrX	155270560	66819602	0.4303	1.4211
chrY	59373566	1981175	0.0334	0.6653

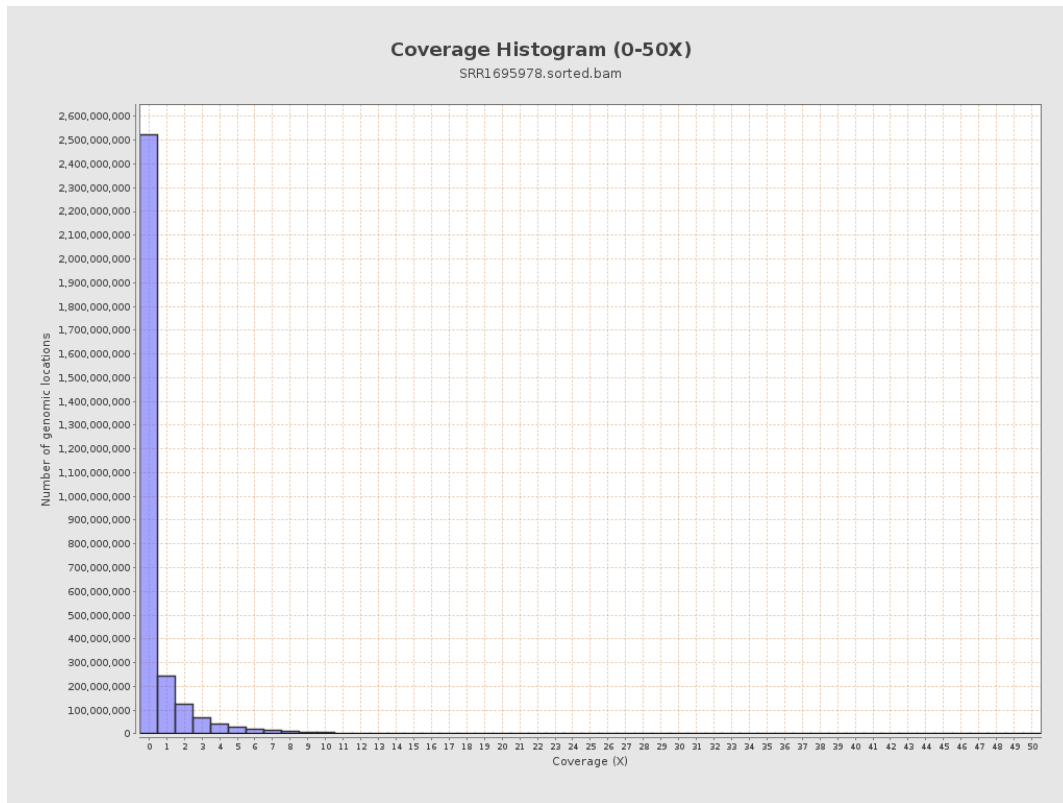
3. Results : Coverage across reference



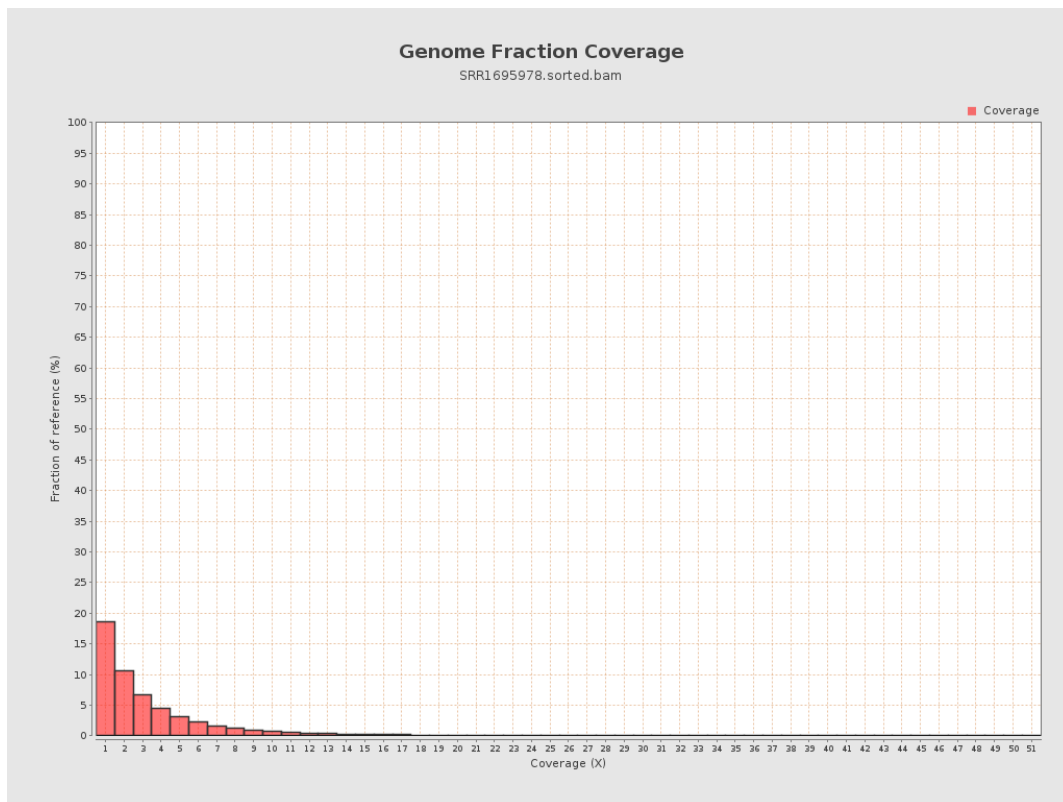
4. Results : Coverage Histogram



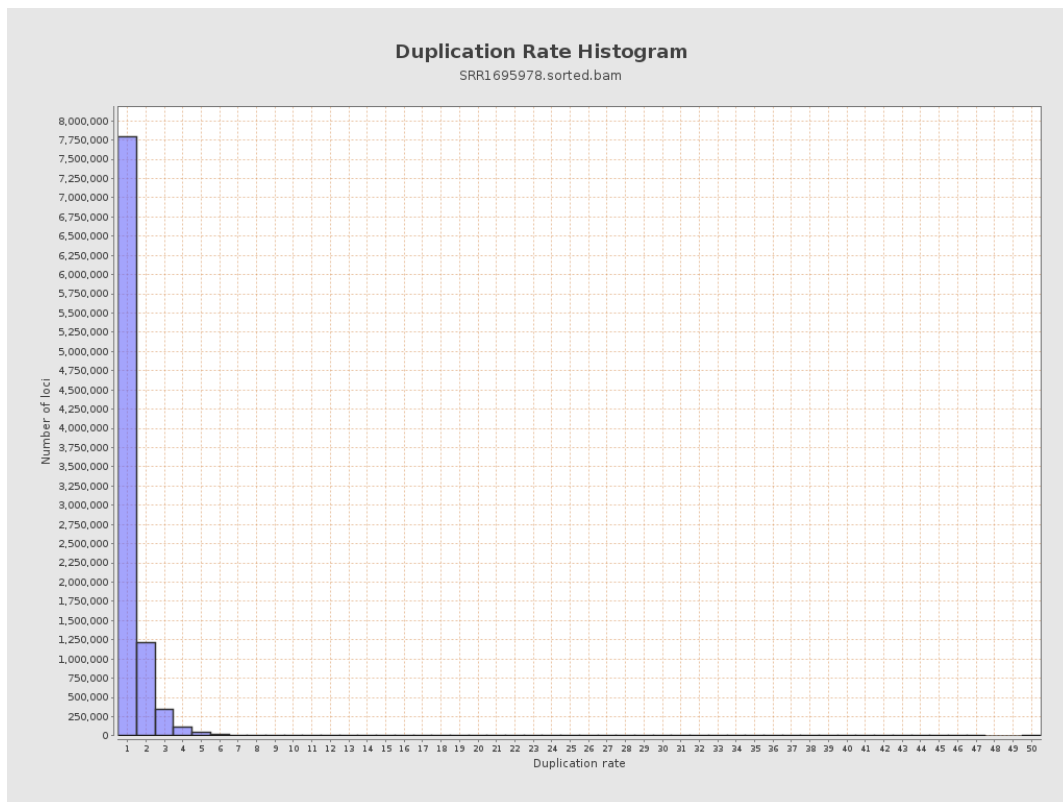
5. Results : Coverage Histogram (0-50X)



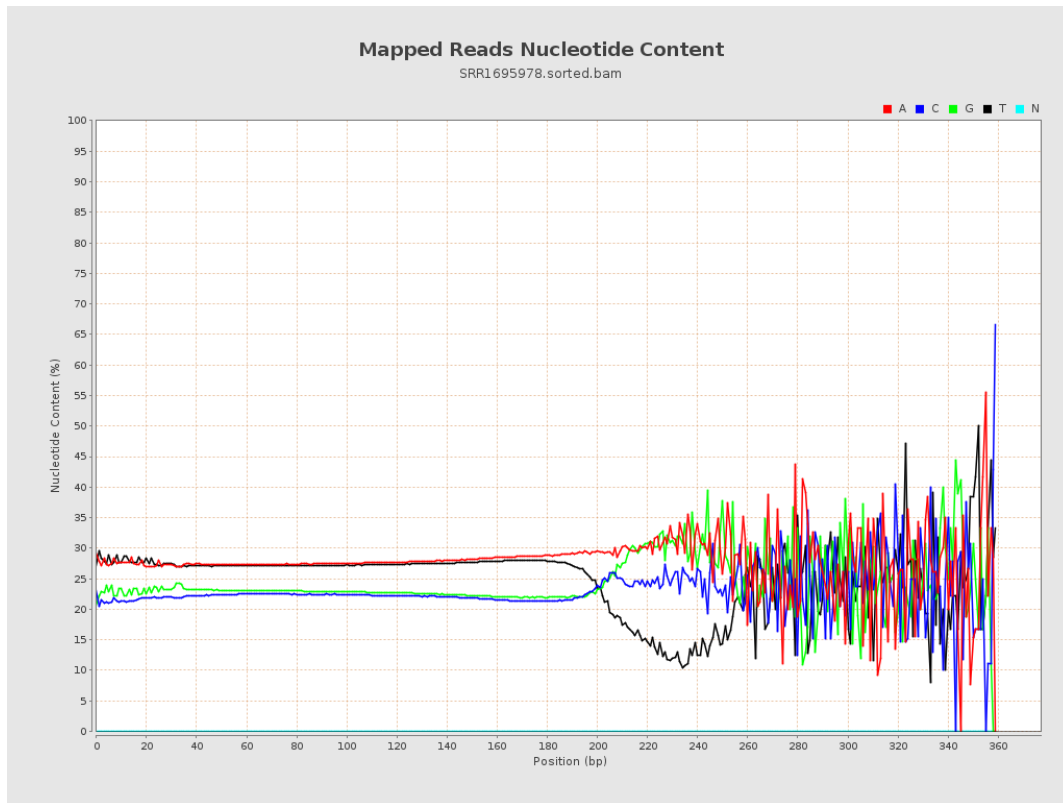
6. Results : Genome Fraction Coverage



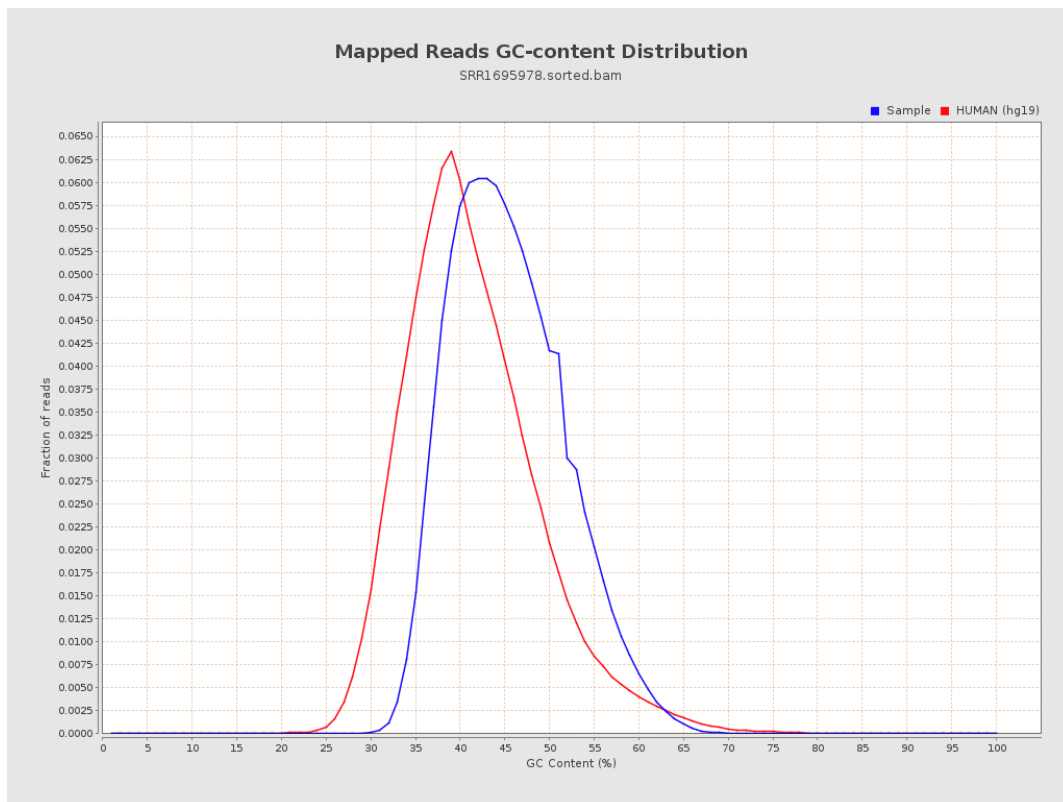
7. Results : Duplication Rate Histogram



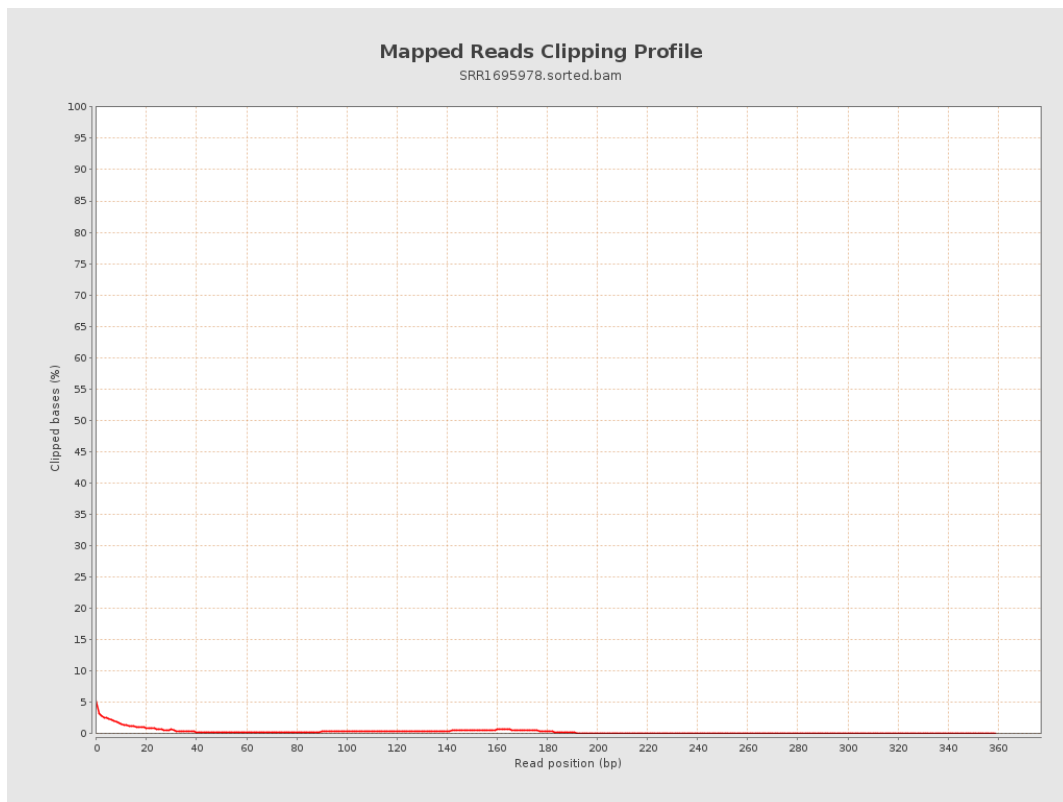
8. Results : Mapped Reads Nucleotide Content



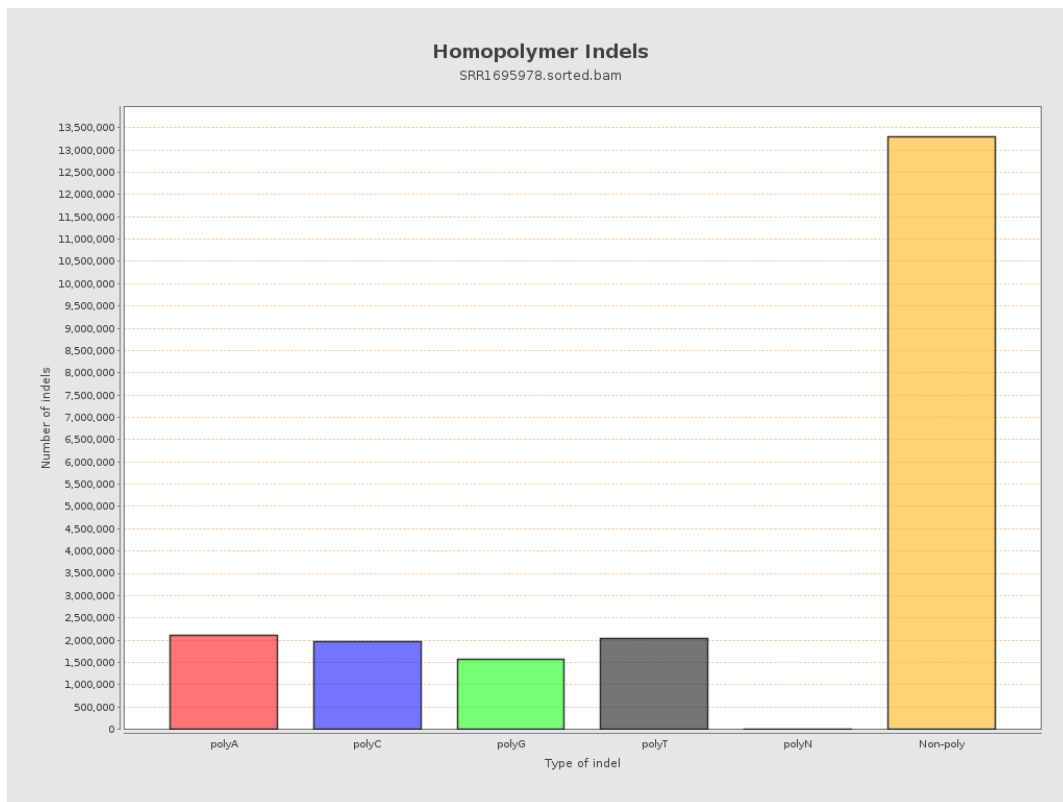
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

