

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/14 08:32:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695981.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_SRR1695981 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695981.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Sat Sep 14 08:32:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695981.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,536,127
Mapped reads	9,462,216 / 89.81%
Unmapped reads	1,073,911 / 10.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	143,748 / 1.36%
Read min/max/mean length	8 / 360 / 125.87
Duplicated reads (estimated)	1,718,469 / 16.31%
Duplication rate	15.27%
Clipped reads	2,439,298 / 23.15%

2.2. ACGT Content

Number/percentage of A's	351,418,458 / 28.21%
Number/percentage of C's	270,016,131 / 21.68%
Number/percentage of T's	348,972,108 / 28.02%
Number/percentage of G's	275,135,657 / 22.09%
Number/percentage of N's	0 / 0%
GC Percentage	43.77%

2.3. Coverage

Mean	0.4053

Standard Deviation	1.1066
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2.4. Mapping Quality

Mean Mapping Quality	51.24
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2.5. Mismatches and indels

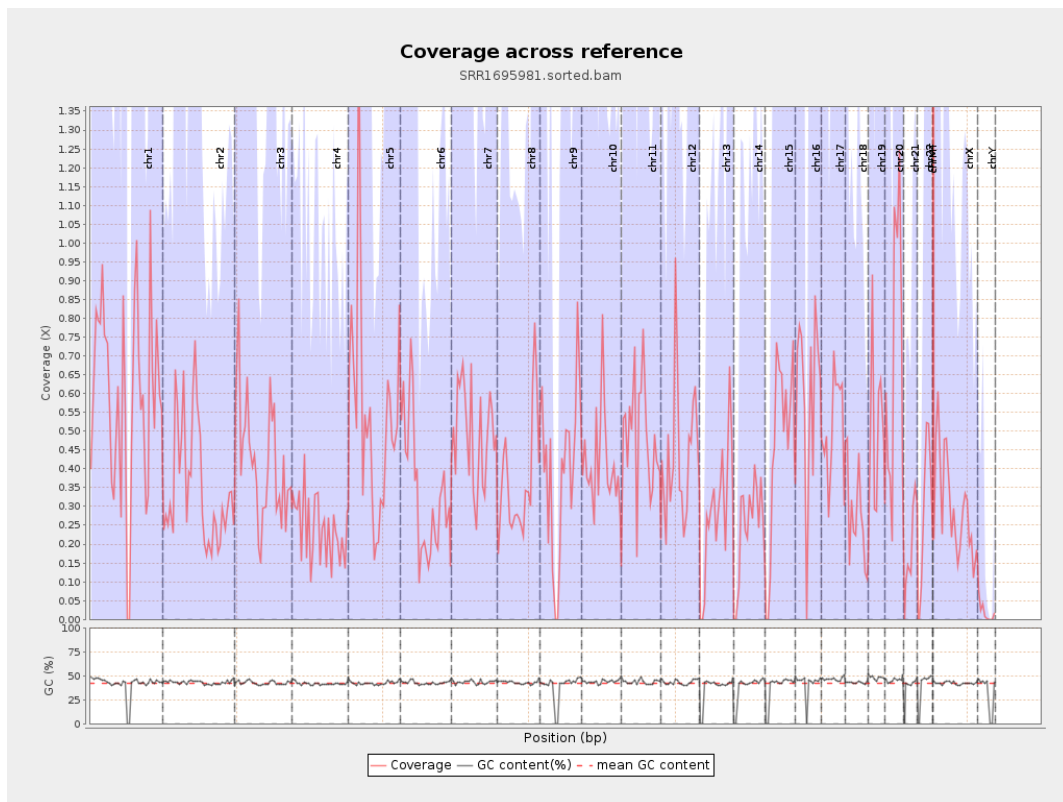
General error rate	1.78%
Mismatches	14,105,239
Insertions	7,407,419
Mapped reads with at least one insertion	47.45%
Deletions	8,371,418
Mapped reads with at least one deletion	51.44%
Homopolymer indels	36.7%

2.6. Chromosome stats

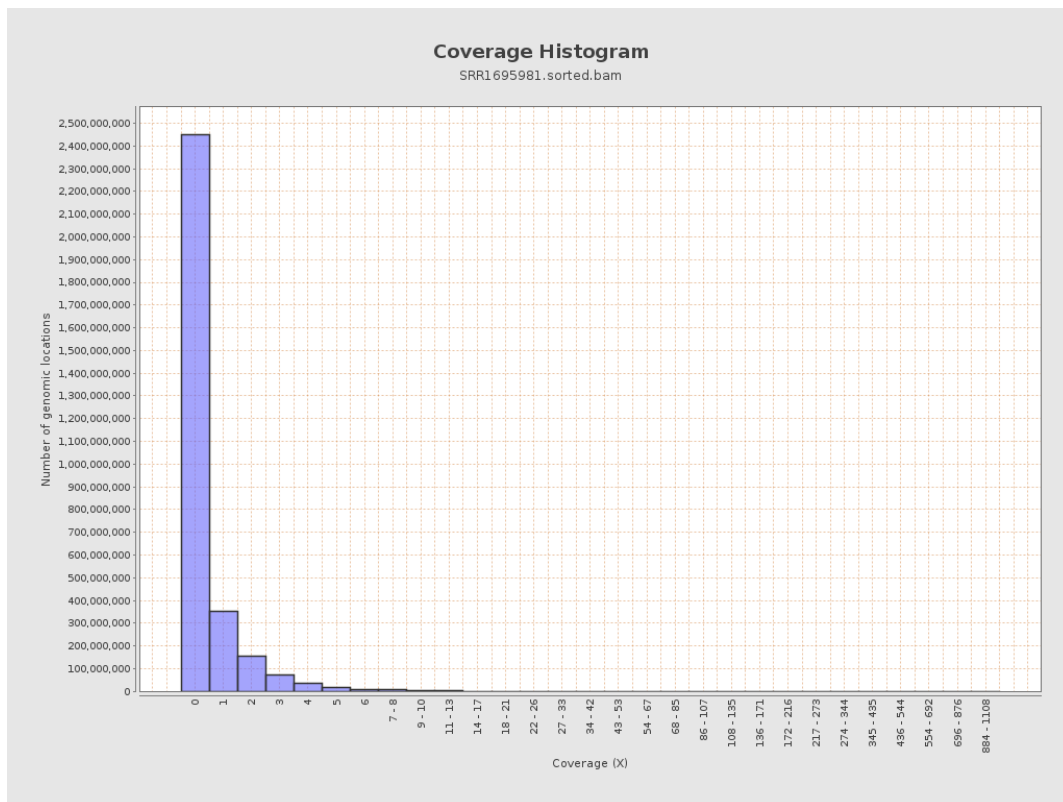
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	146893477	0.5893	1.6732
chr2	243199373	85678382	0.3523	0.9601
chr3	198022430	82188818	0.415	1.033
chr4	191154276	45401470	0.2375	0.7679
chr5	180915260	99764093	0.5514	1.2775
chr6	171115067	57143011	0.3339	0.9348
chr7	159138663	77775560	0.4887	1.1331

chr8	146364022	54306802	0.371	0.9821
chr9	141213431	54304675	0.3846	1.0205
chr10	135534747	56801088	0.4191	1.1219
chr11	135006516	64747125	0.4796	1.1355
chr12	133851895	59742265	0.4463	1.0894
chr13	115169878	33626438	0.292	0.869
chr14	107349540	26835005	0.25	0.7819
chr15	102531392	47190603	0.4603	1.1078
chr16	90354753	52637427	0.5826	1.256
chr17	81195210	42254541	0.5204	1.2069
chr18	78077248	21409665	0.2742	0.9112
chr19	59128983	29667263	0.5017	1.4645
chr20	63025520	44475716	0.7057	1.4546
chr21	48129895	9382153	0.1949	0.7142
chr22	51304566	15093464	0.2942	0.8806
chrMT	16571	208996	12.6122	7.6564
chrX	155270560	46217621	0.2977	0.8619
chrY	59373566	1091919	0.0184	0.3274

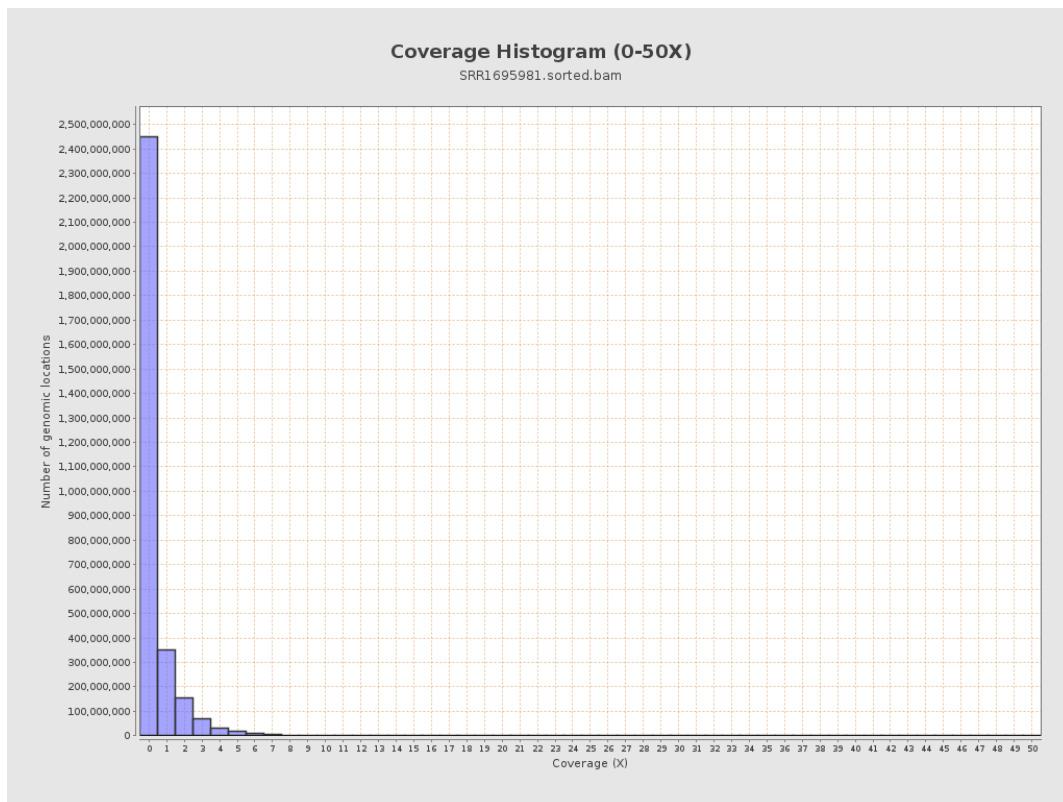
3. Results : Coverage across reference



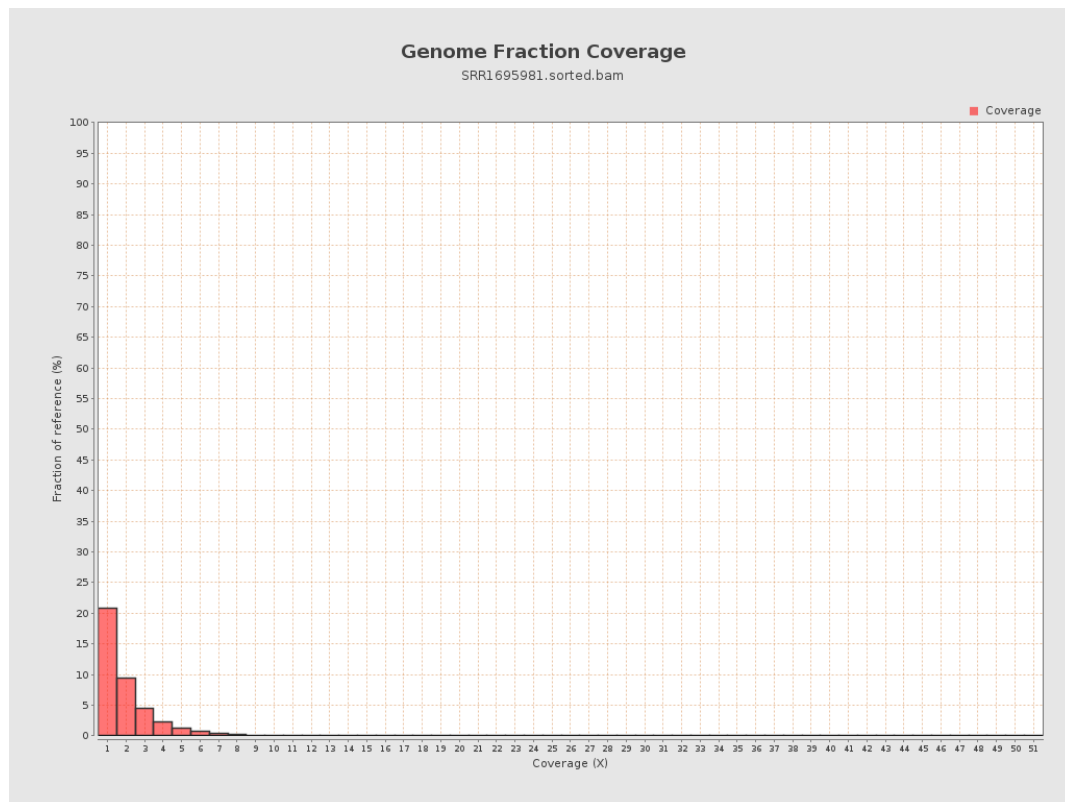
4. Results : Coverage Histogram



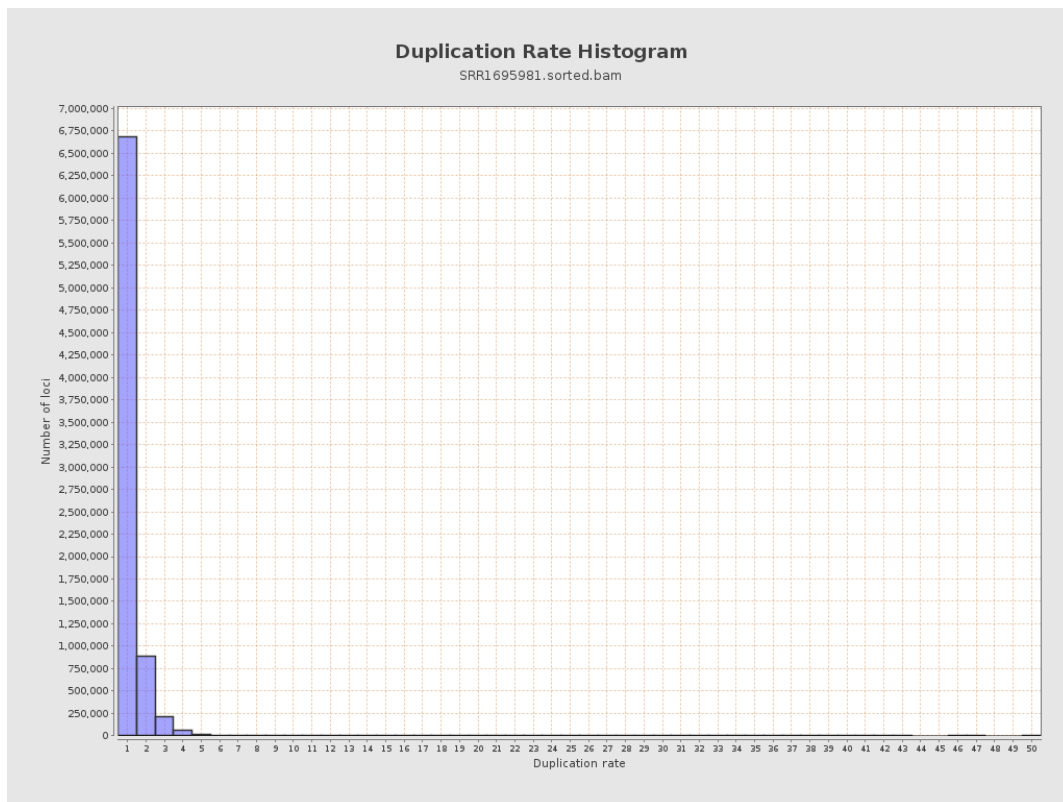
5. Results : Coverage Histogram (0-50X)



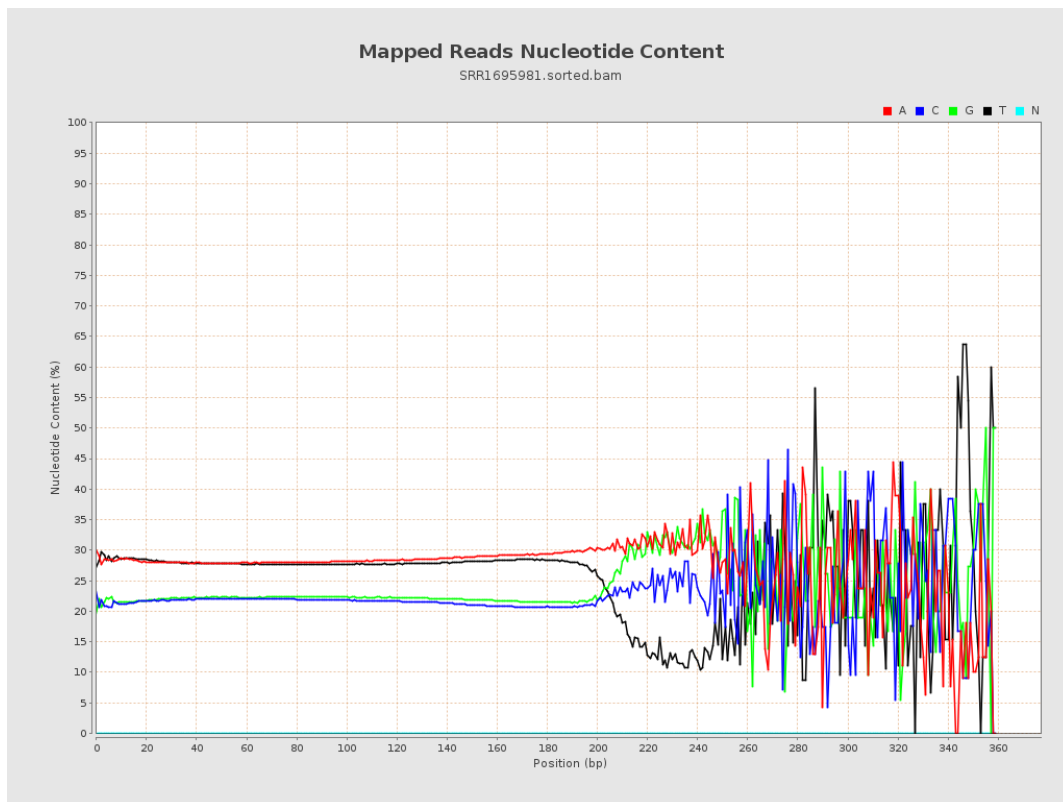
6. Results : Genome Fraction Coverage



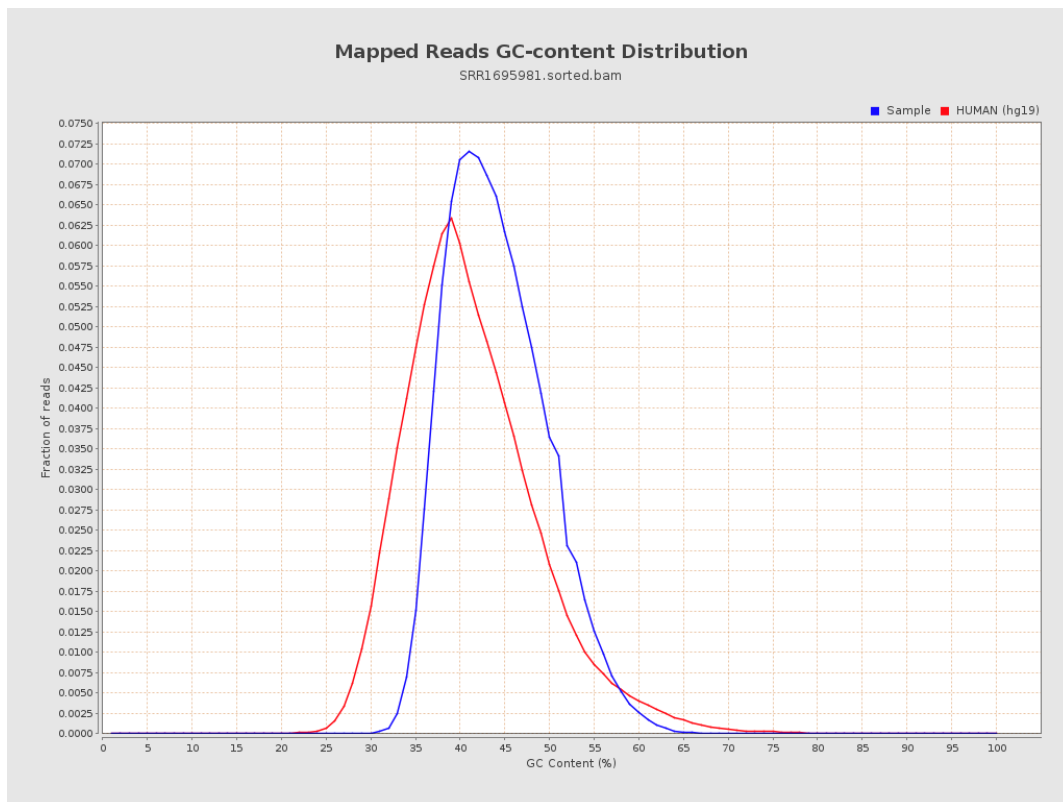
7. Results : Duplication Rate Histogram



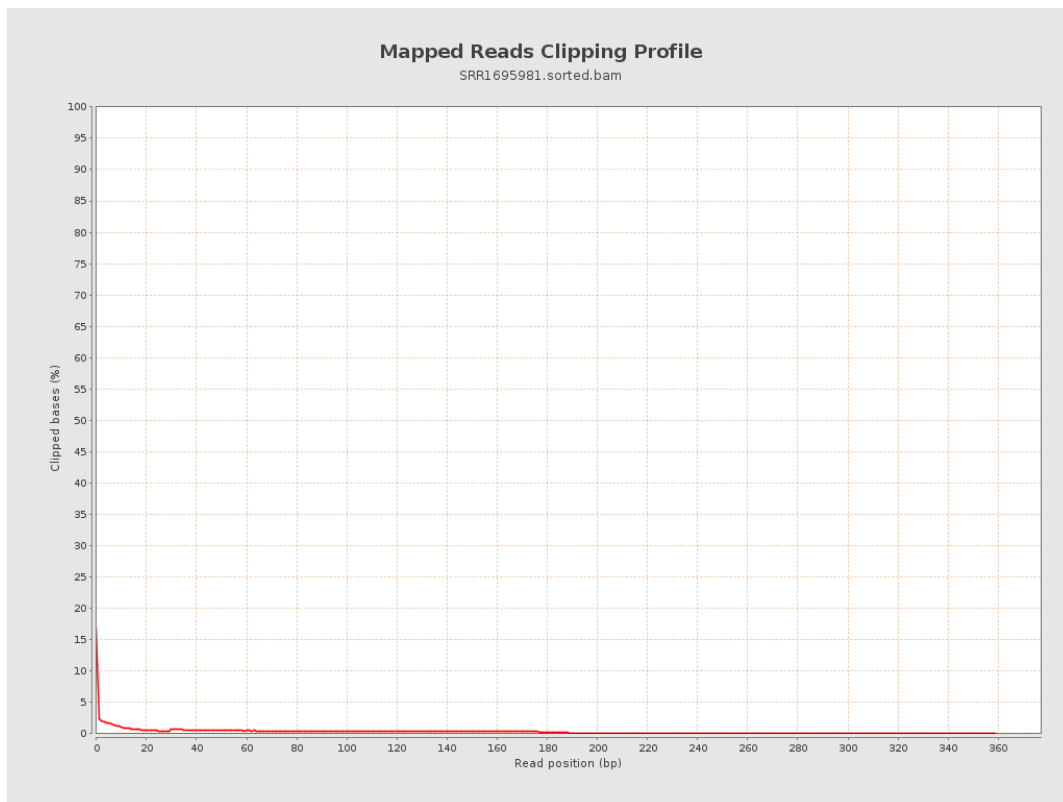
8. Results : Mapped Reads Nucleotide Content



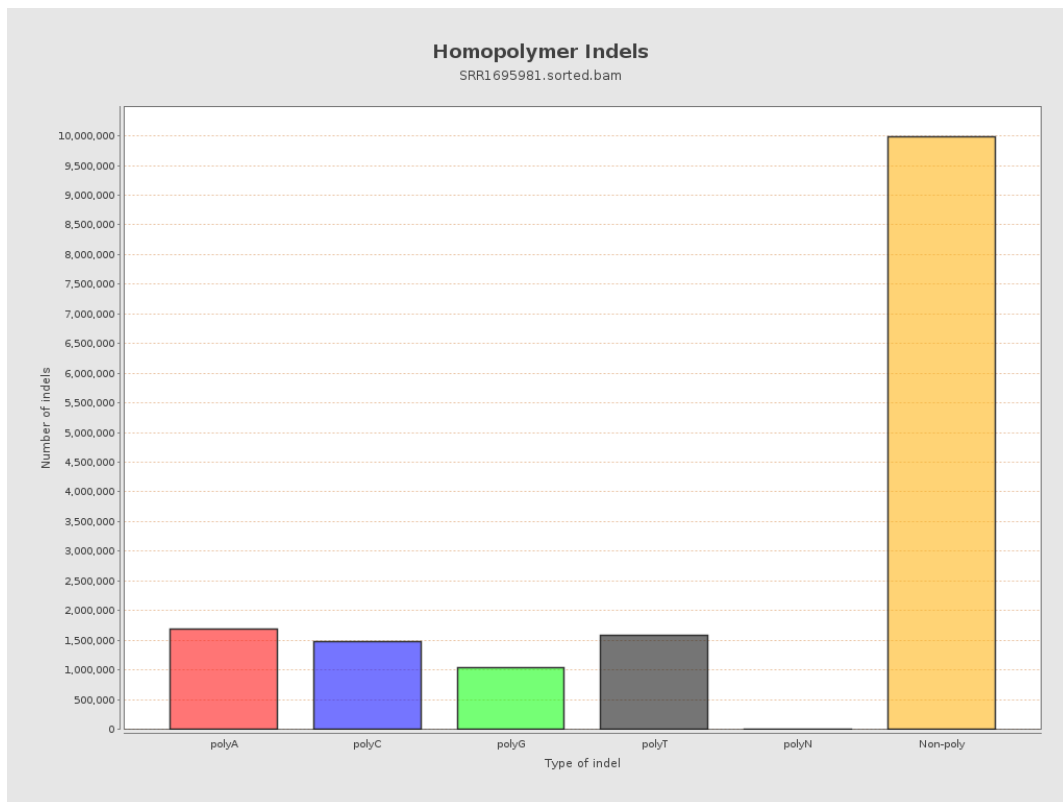
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

