

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/14 08:38:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695982.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_SRR1695982 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695982.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Sat Sep 14 08:38:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695982.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,858,678
Mapped reads	9,762,598 / 89.91%
Unmapped reads	1,096,080 / 10.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	160,423 / 1.48%
Read min/max/mean length	8 / 359 / 125.33
Duplicated reads (estimated)	1,829,317 / 16.85%
Duplication rate	15.74%
Clipped reads	2,526,676 / 23.27%

2.2. ACGT Content

Number/percentage of A's	363,099,542 / 28.42%
Number/percentage of C's	273,107,095 / 21.38%
Number/percentage of T's	360,097,187 / 28.19%
Number/percentage of G's	281,278,146 / 22.02%
Number/percentage of N's	0 / 0%
GC Percentage	43.39%

2.3. Coverage

Mean	0.4157

Standard Deviation	1.196
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2.4. Mapping Quality

Mean Mapping Quality	51.06
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2.5. Mismatches and indels

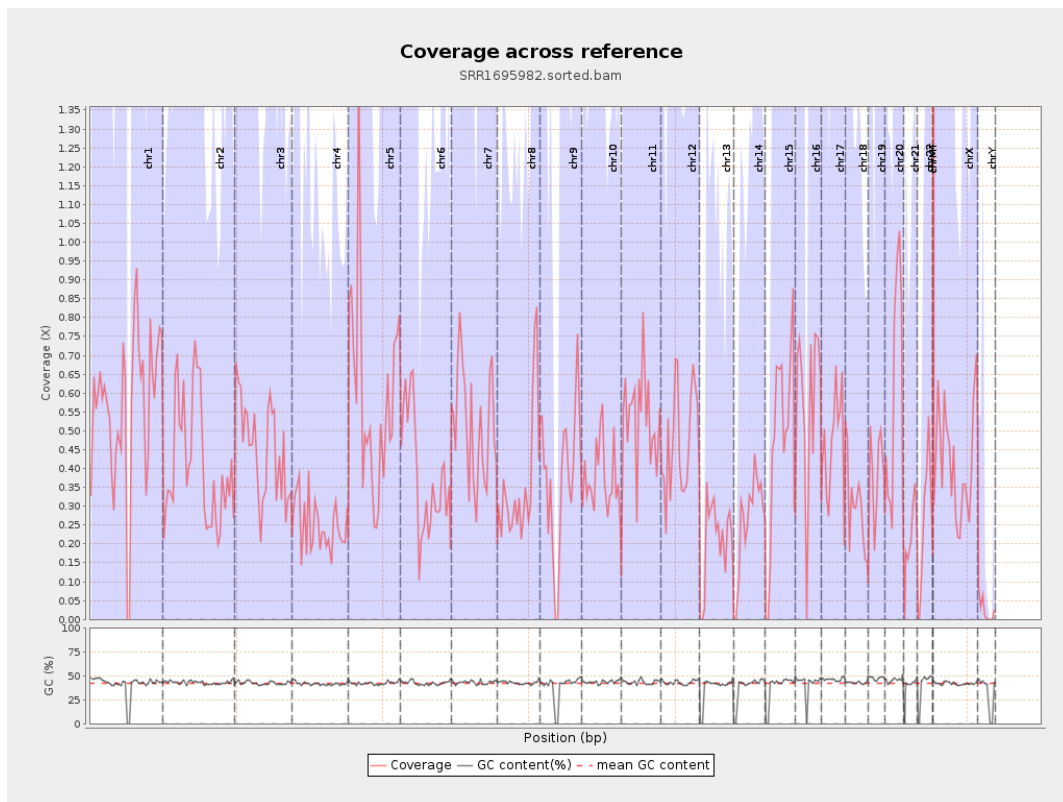
General error rate	1.77%
Mismatches	14,245,739
Insertions	7,634,889
Mapped reads with at least one insertion	47.45%
Deletions	8,325,872
Mapped reads with at least one deletion	50.44%
Homopolymer indels	36.43%

2.6. Chromosome stats

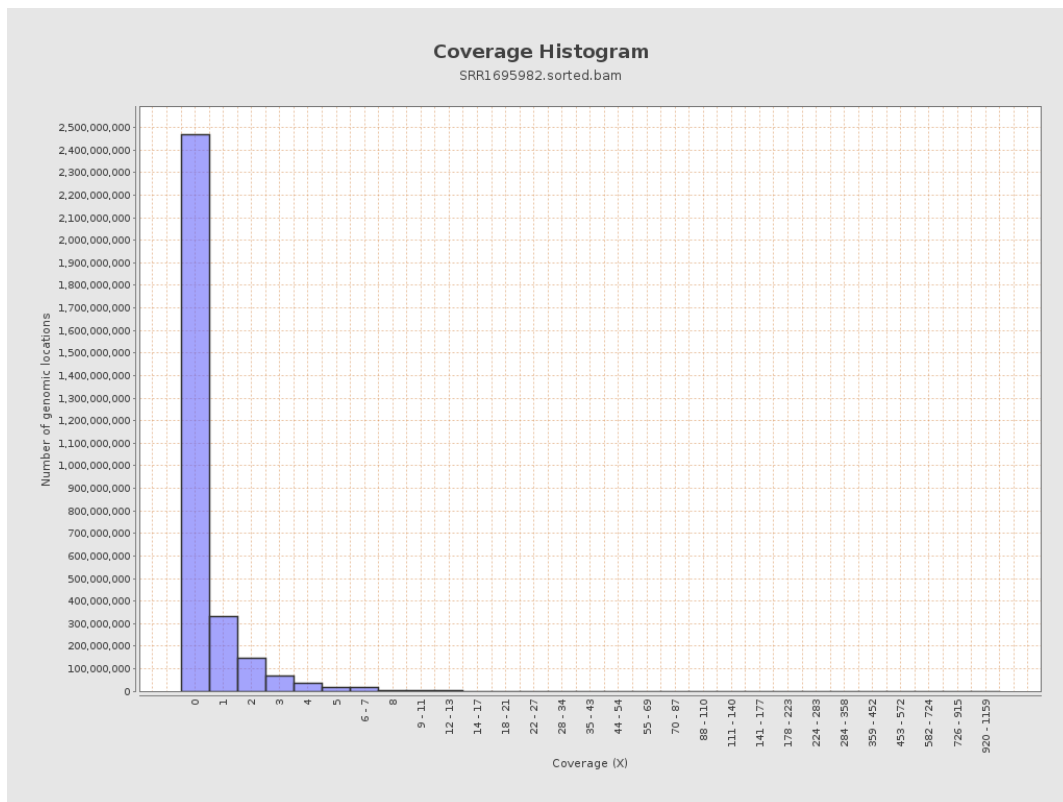
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	139872183	0.5612	1.7657
chr2	243199373	99820971	0.4104	1.1147
chr3	198022430	88944503	0.4492	1.1347
chr4	191154276	48096547	0.2516	0.8563
chr5	180915260	107440358	0.5939	1.3607
chr6	171115067	64763498	0.3785	1.0894
chr7	159138663	81440717	0.5118	1.2493

chr8	146364022	53283091	0.364	1.0196
chr9	141213431	51922854	0.3677	1.0485
chr10	135534747	51357972	0.3789	1.1922
chr11	135006516	71394494	0.5288	1.2793
chr12	133851895	63783198	0.4765	1.1795
chr13	115169878	24159221	0.2098	0.7506
chr14	107349540	28239852	0.2631	0.858
chr15	102531392	48458093	0.4726	1.2138
chr16	90354753	50615098	0.5602	1.3425
chr17	81195210	38763867	0.4774	1.256
chr18	78077248	23295934	0.2984	1.1248
chr19	59128983	22247780	0.3763	1.4358
chr20	63025520	38417754	0.6096	1.4163
chr21	48129895	10513142	0.2184	0.8449
chr22	51304566	13593486	0.265	0.9157
chrMT	16571	181908	10.9775	6.4463
chrX	155270560	64746540	0.417	1.0972
chrY	59373566	1466421	0.0247	0.4869

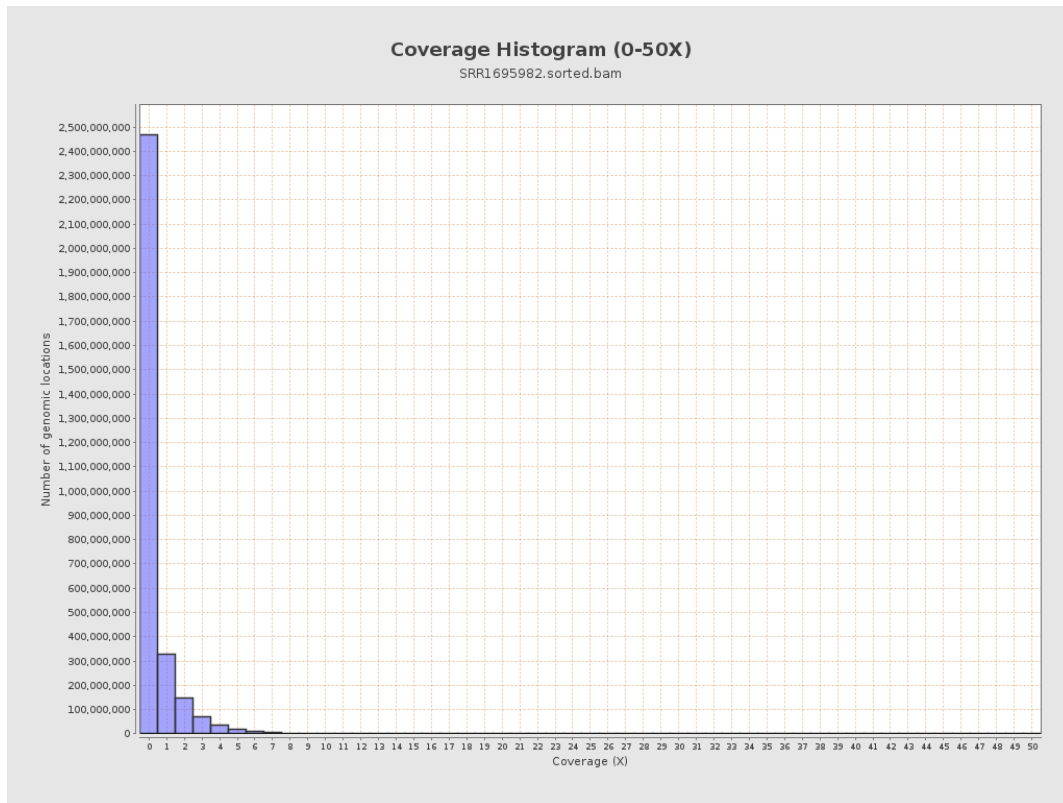
3. Results : Coverage across reference



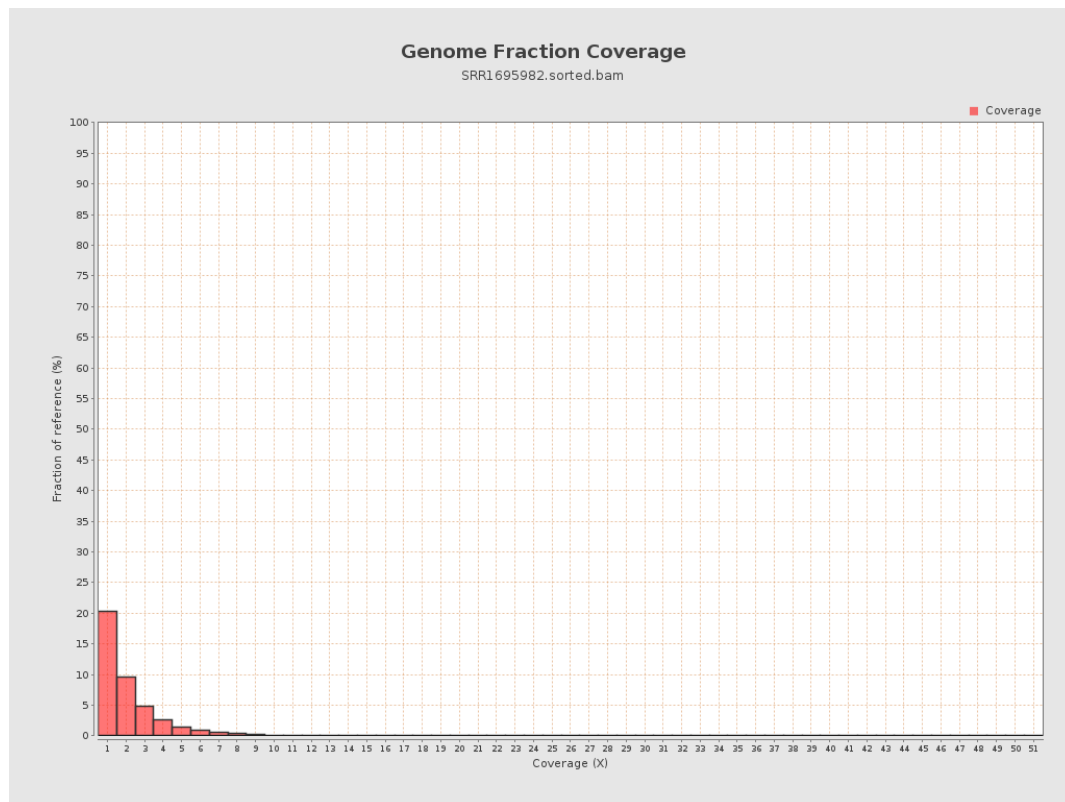
4. Results : Coverage Histogram



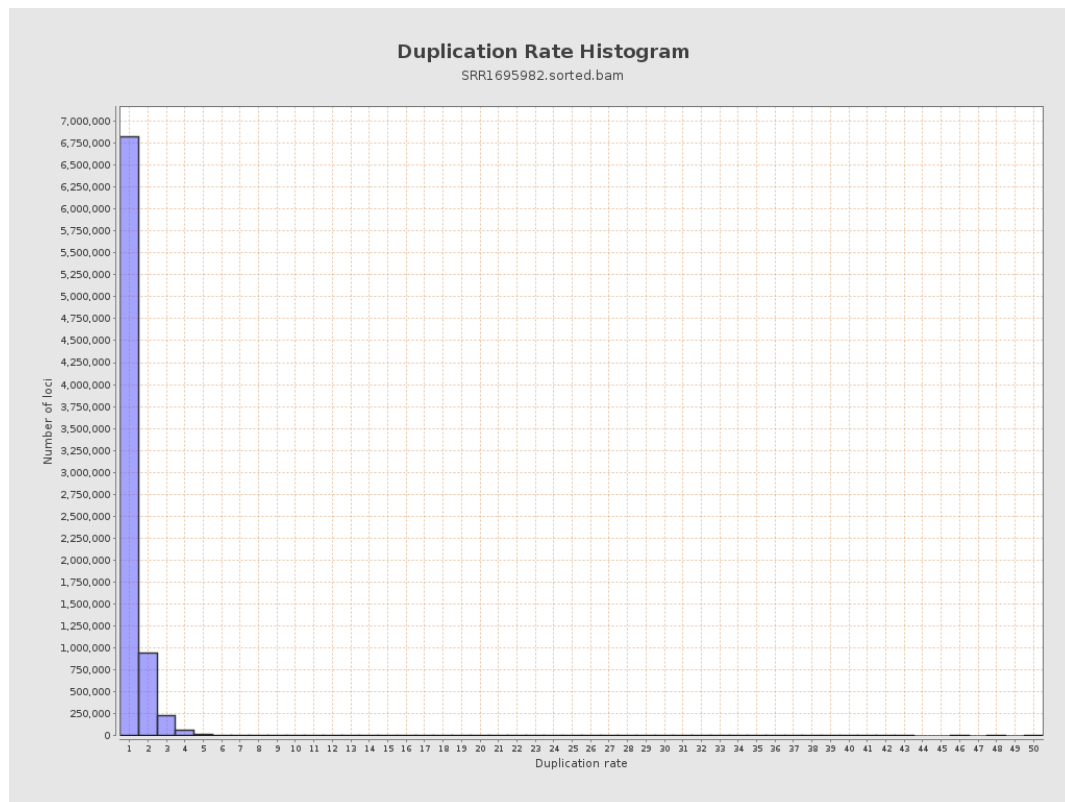
5. Results : Coverage Histogram (0-50X)



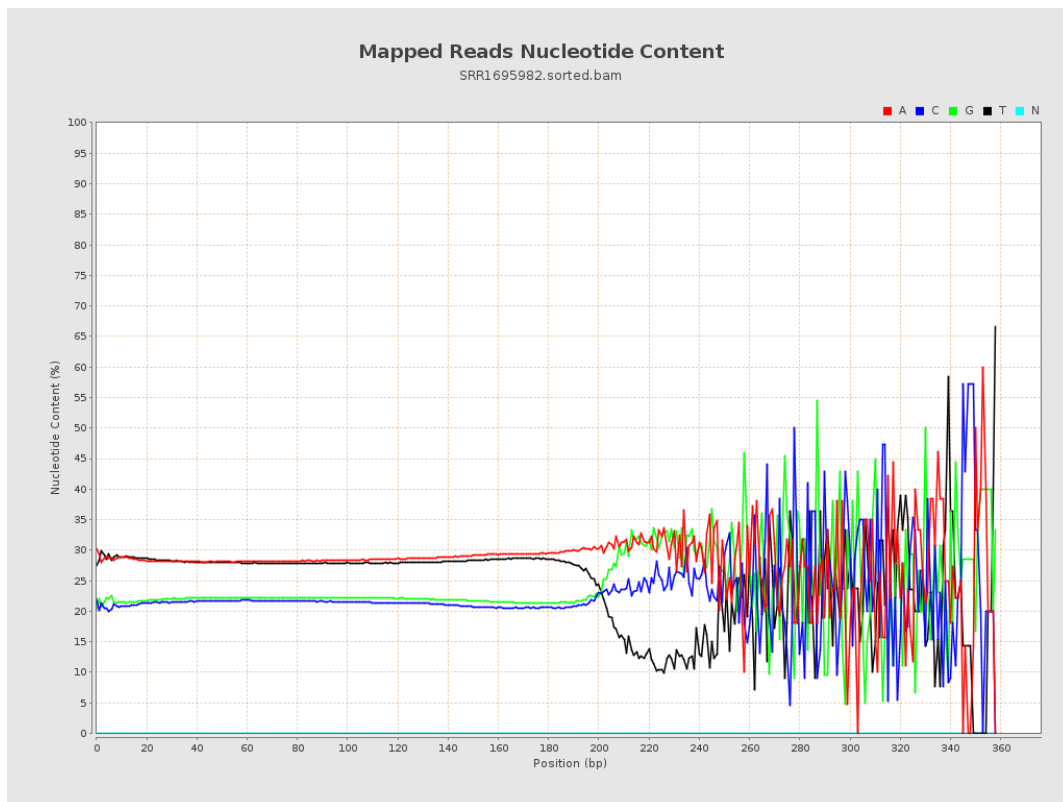
6. Results : Genome Fraction Coverage



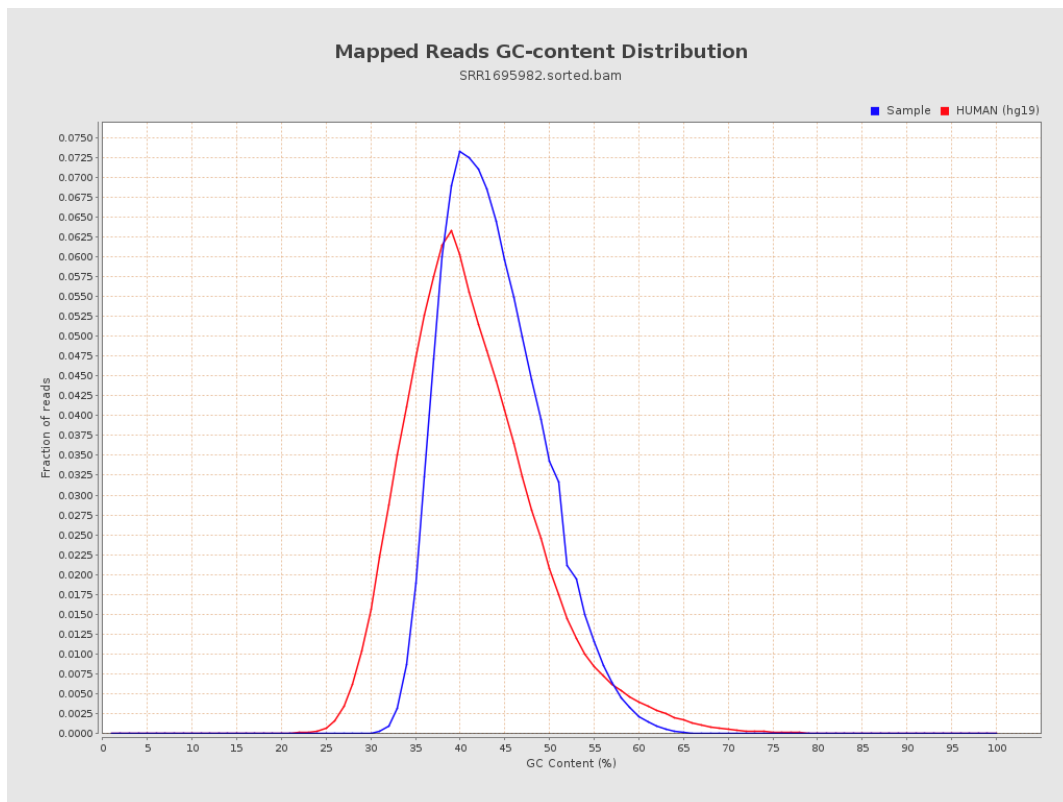
7. Results : Duplication Rate Histogram



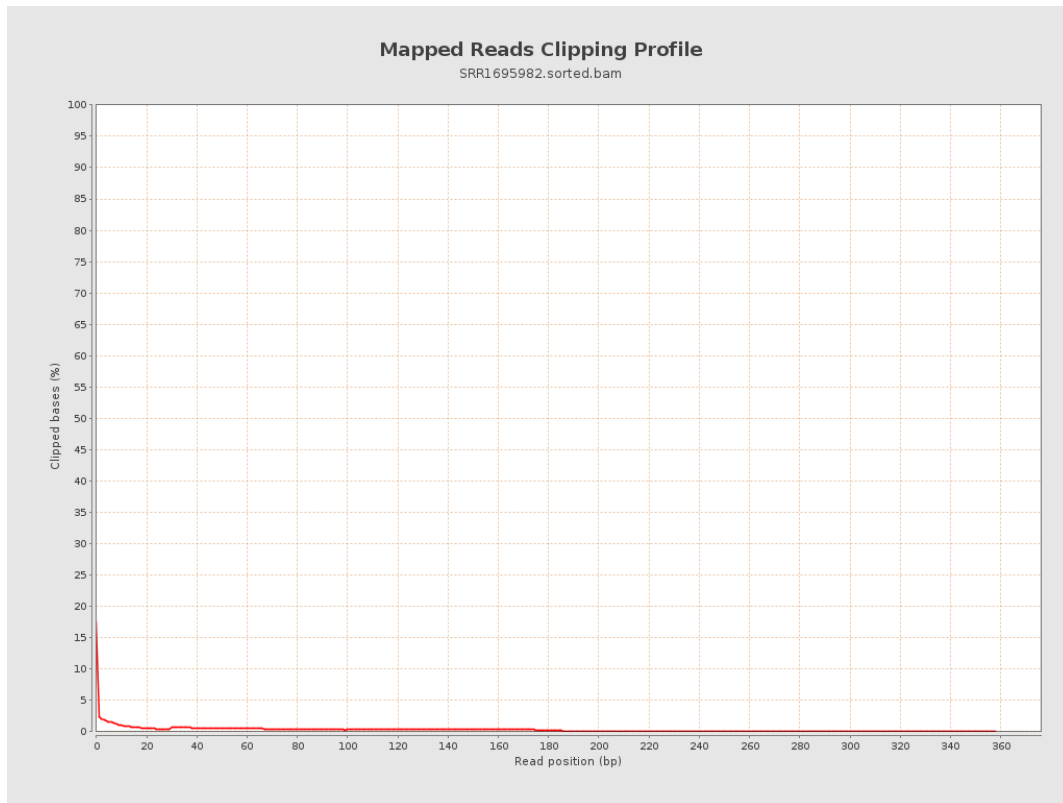
8. Results : Mapped Reads Nucleotide Content



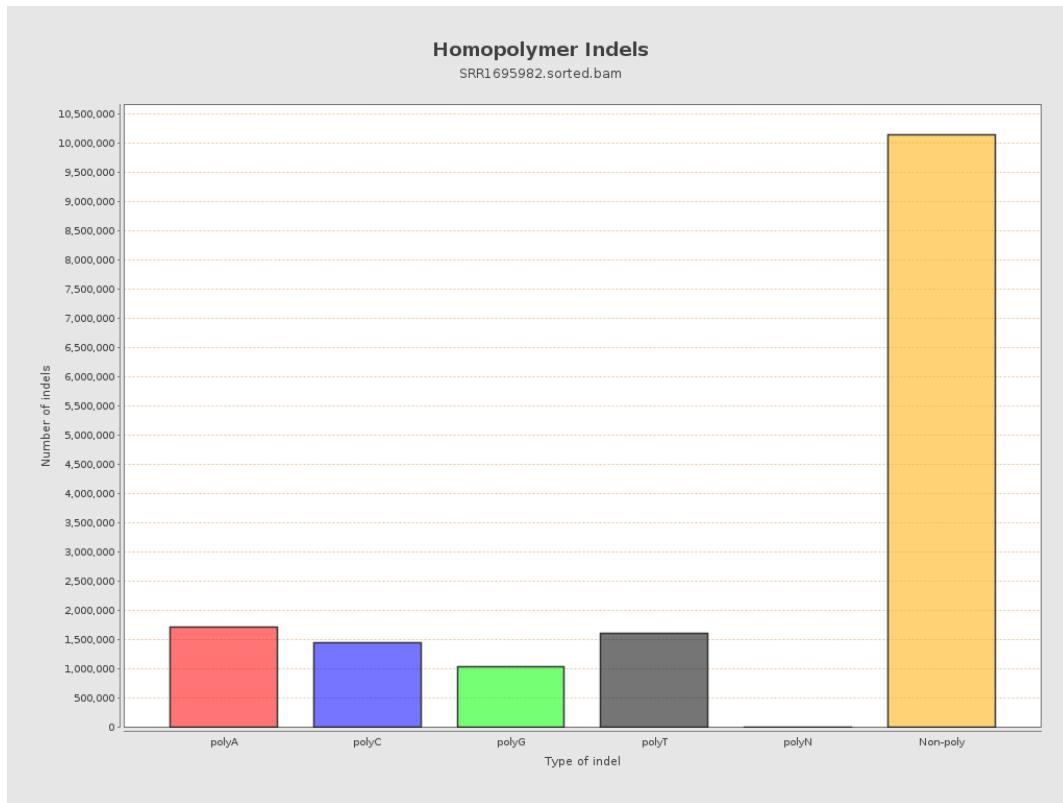
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

