Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 21:03:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975284.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR975284 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975284_1.fastq.gz SRR975284_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 21:03:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975284.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,321,822
Mapped reads	5,270,559 / 99.04%
Unmapped reads	51,263 / 0.96%
Mapped paired reads	5,270,559 / 99.04%
Mapped reads, first in pair	2,634,505 / 49.5%
Mapped reads, second in pair	2,636,054 / 49.53%
Mapped reads, both in pair	5,251,286 / 98.67%
Mapped reads, singletons	19,273 / 0.36%
Secondary alignments	0
Supplementary alignments	35,247 / 0.66%
Read min/max/mean length	30 / 101 / 101.27
Duplicated reads (estimated)	339,674 / 6.38%
Duplication rate	3.44%
Clipped reads	3,117,989 / 58.59%

2.2. ACGT Content

Number/percentage of A's	144,326,877 / 29.17%
Number/percentage of C's	100,097,017 / 20.23%
Number/percentage of T's	144,295,826 / 29.16%
Number/percentage of G's	106,117,664 / 21.44%
Number/percentage of N's	14,025 / 0%

GC Percentage	41.67%

2.3. Coverage

Mean	0.16
Standard Deviation	1.8384

2.4. Mapping Quality

Mean Mapping Quality	52.88

2.5. Insert size

Mean	89,767.01
Standard Deviation	2,858,809.56
P25/Median/P75	146 / 179 / 225

2.6. Mismatches and indels

General error rate	0.9%
Mismatches	4,254,382
Insertions	93,647
Mapped reads with at least one insertion	1.74%
Deletions	173,061
Mapped reads with at least one deletion	3.21%
Homopolymer indels	44.75%

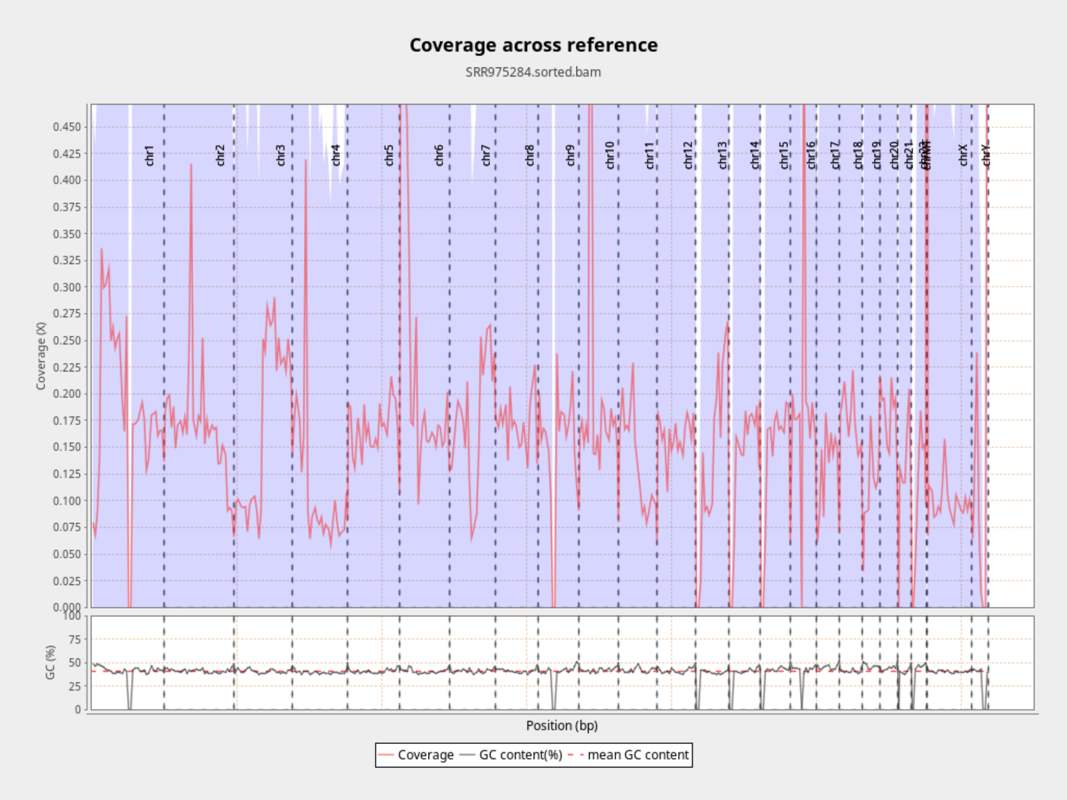
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

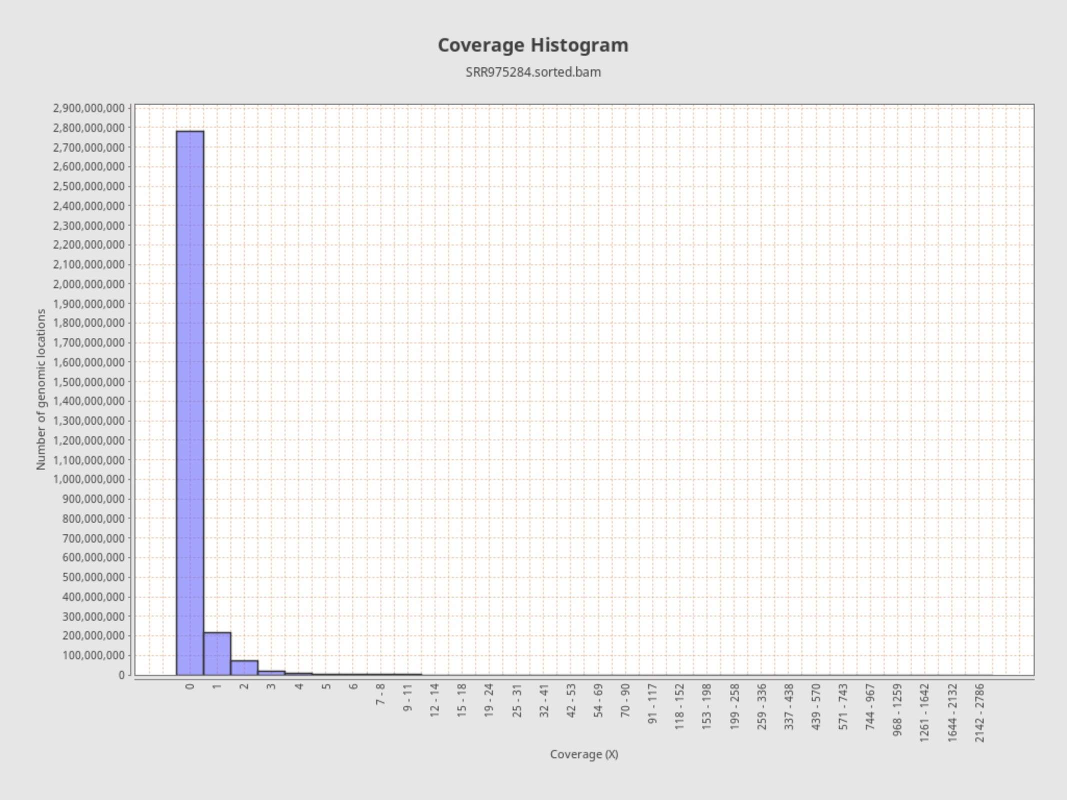
		bases	coverage	deviation
chr1	249250621	45861485	0.184	1.6997
chr2	243199373	41588449	0.171	1.7249
chr3	198022430	34127876	0.1723	0.6309
chr4	191154276	21635368	0.1132	1.5769
chr5	180915260	30557653	0.1689	0.5549
chr6	171115067	39651798	0.2317	1.3551
chr7	159138663	27967314	0.1757	1.5886
chr8	146364022	25176816	0.172	0.7386
chr9	141213431	21195917	0.1501	2.1581
chr10	135534747	27798768	0.2051	5.7312
chr11	135006516	18368728	0.1361	1.7087
chr12	133851895	21408583	0.1599	0.5385
chr13	115169878	16194898	0.1406	0.5055
chr14	107349540	14550070	0.1355	0.5351
chr15	102531392	14293458	0.1394	0.5033
chr16	90354753	17538394	0.1941	2.7423
chr17	81195210	10435215	0.1285	1.2641
chr18	78077248	13856581	0.1775	2.1659
chr19	59128983	6578128	0.1113	1.0531
chr20	63025520	11475128	0.1821	0.6757
chr21	48129895	6195688	0.1287	0.8014
chr22	51304566	5311928	0.1035	0.4537
chrMT	16571	104063	6.2798	5.3829
chrX	155270560	15219305	0.098	0.7298

chrY	59373566	8065029	0.1358	3.1418

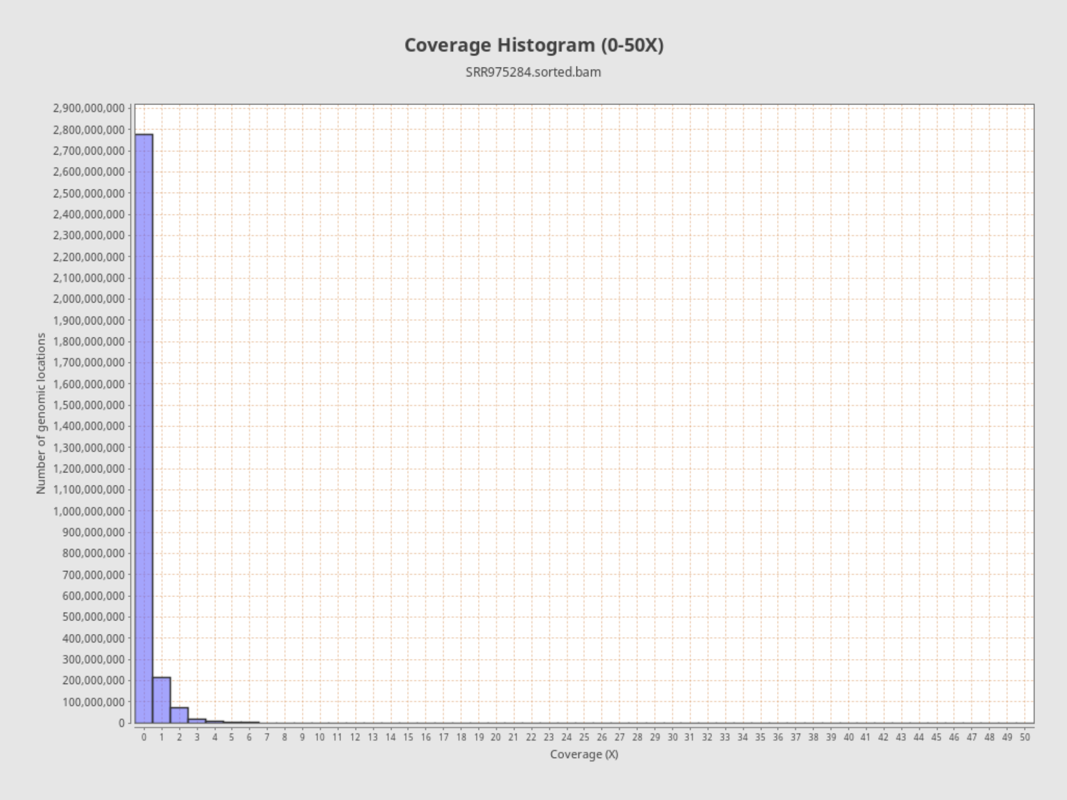
3. Results : Coverage across reference



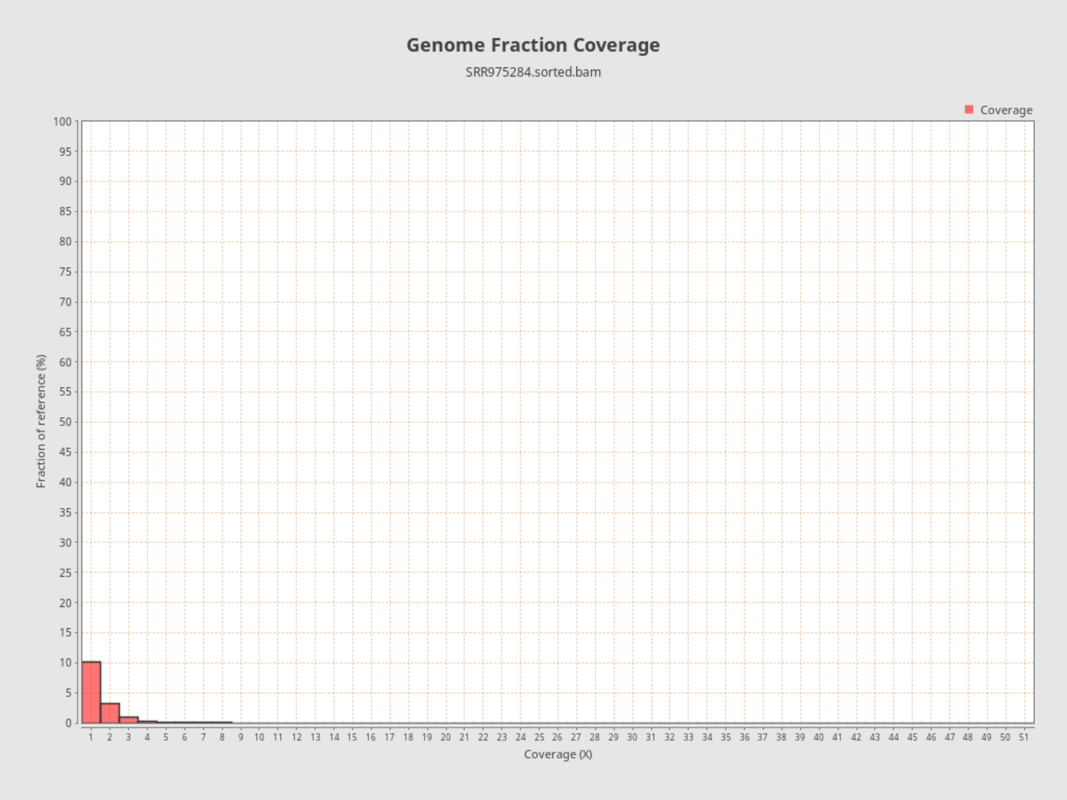
4. Results : Coverage Histogram



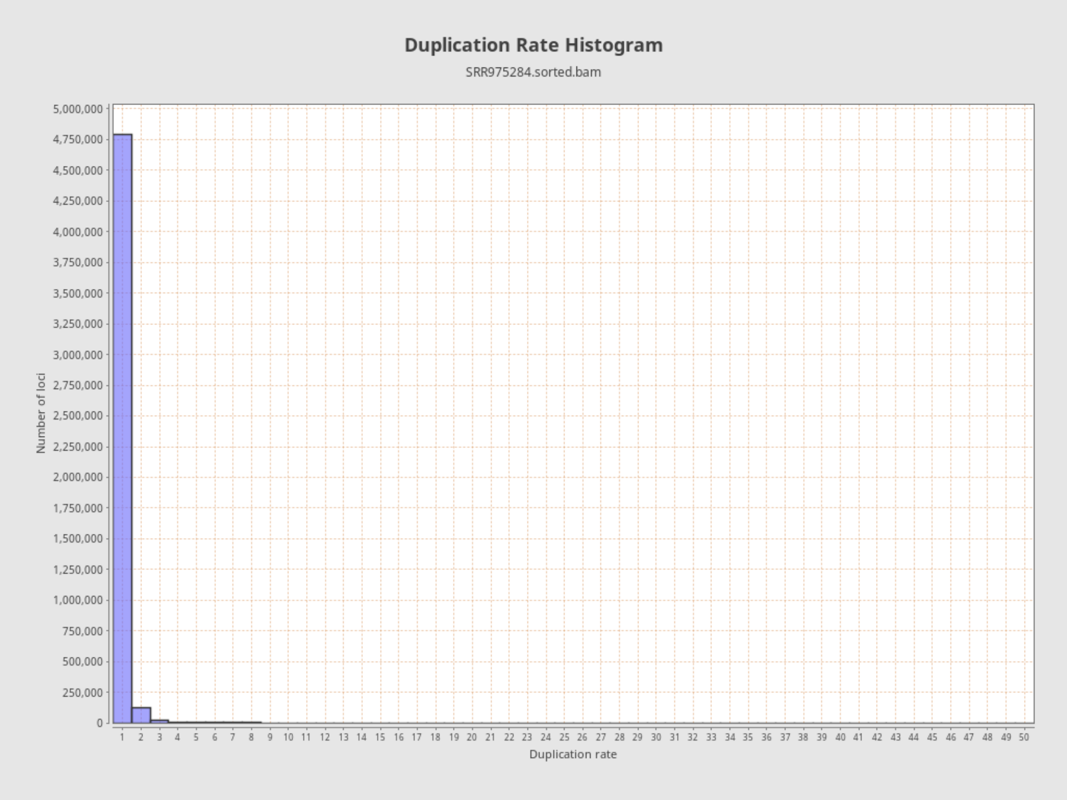
5. Results : Coverage Histogram (0-50X)



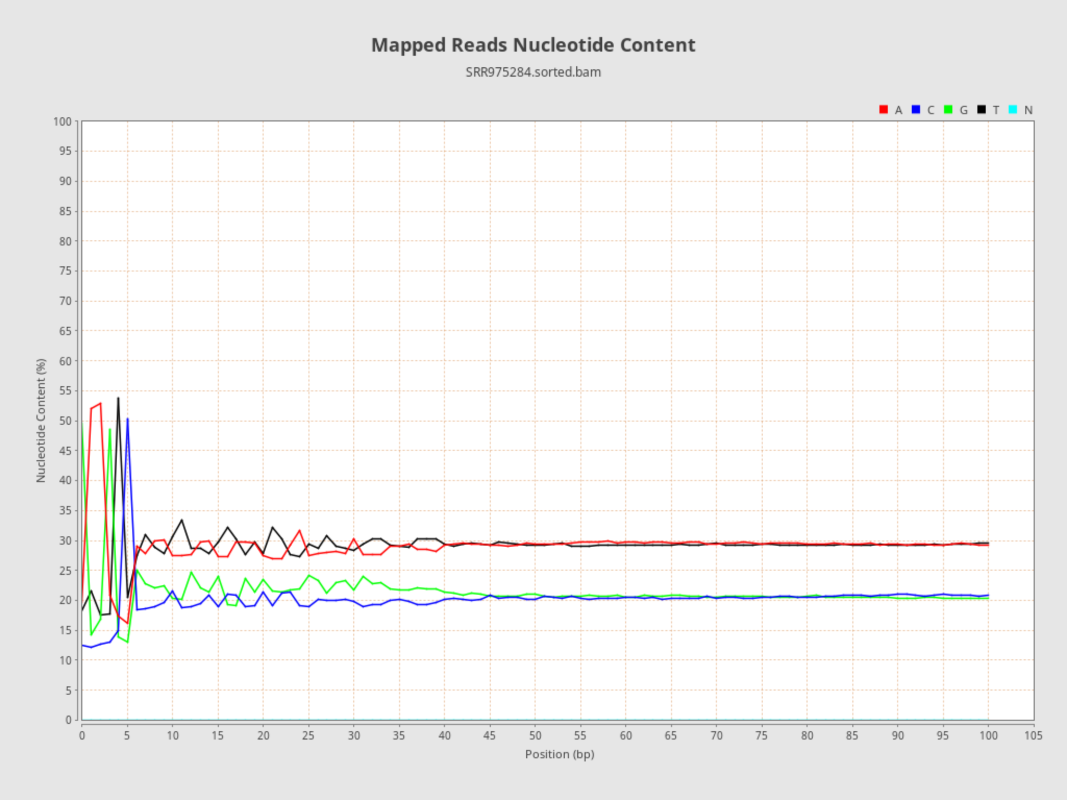
6. Results : Genome Fraction Coverage



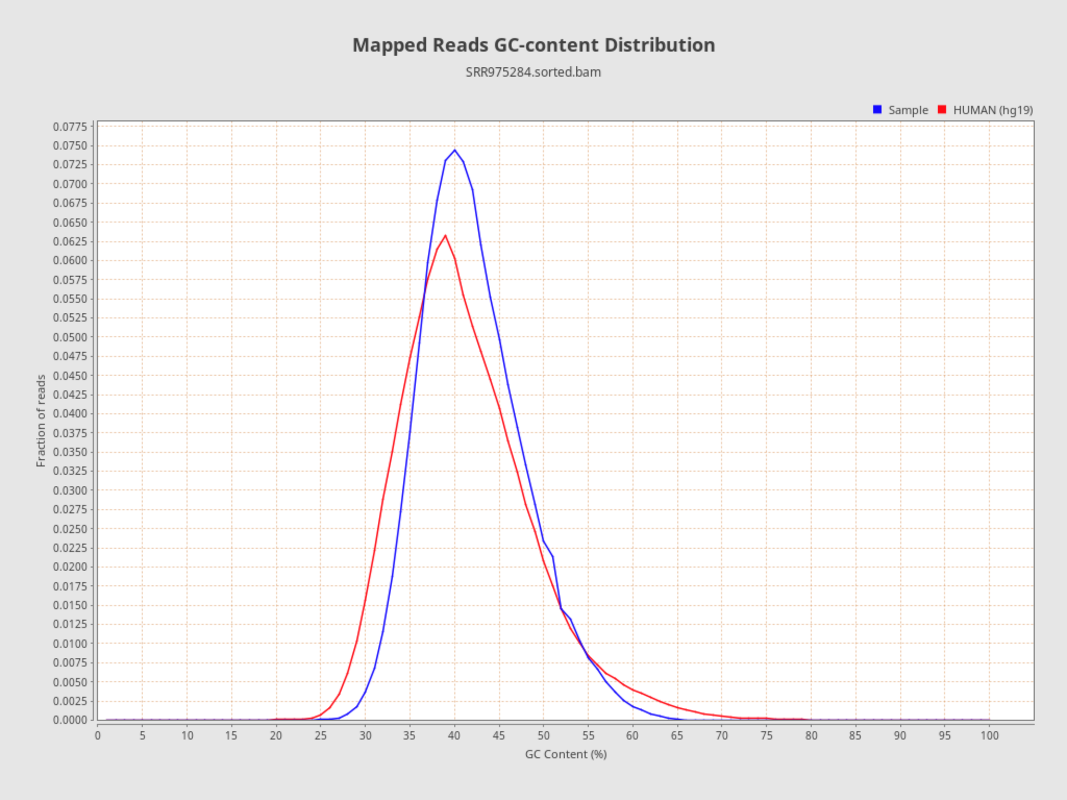
7. Results : Duplication Rate Histogram



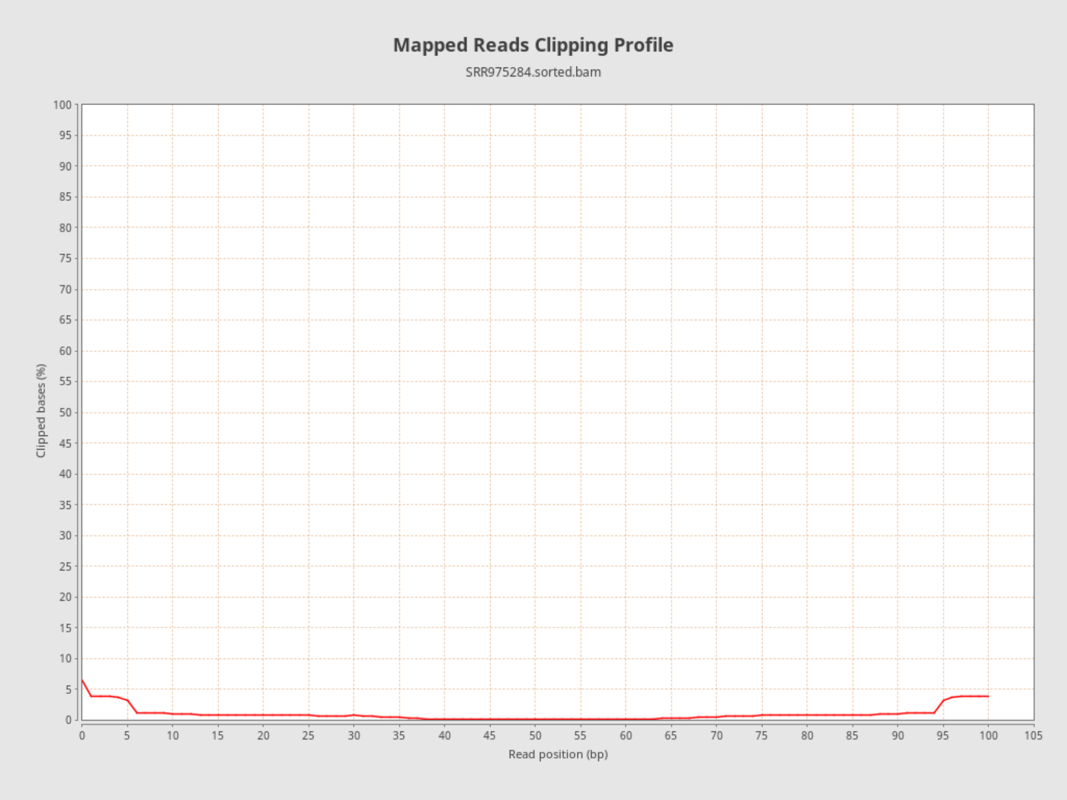
8. Results : Mapped Reads Nucleotide Content



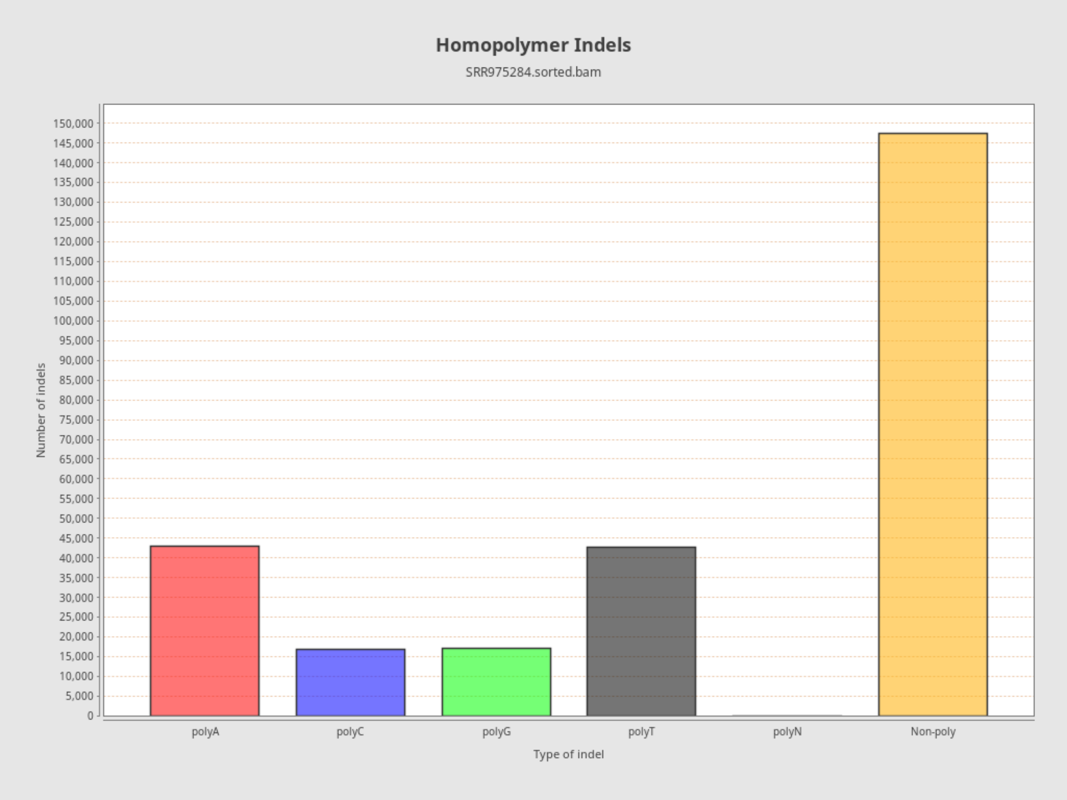
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

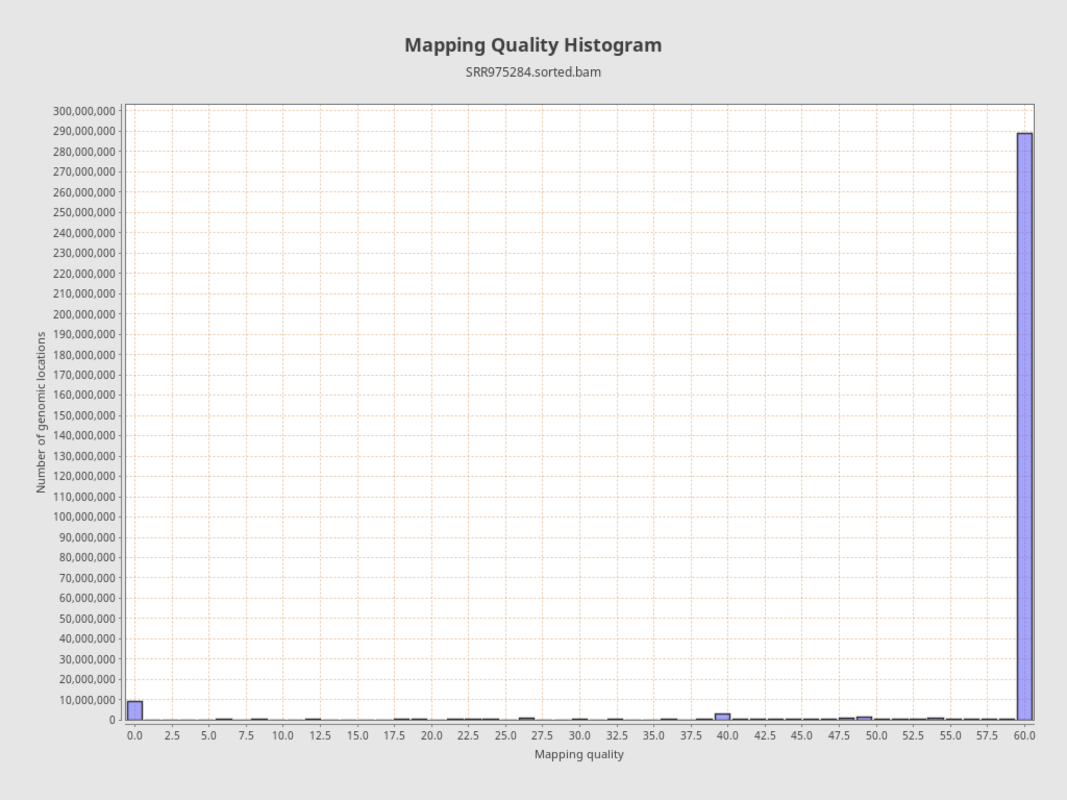


11. Results : Homopolymer Indels

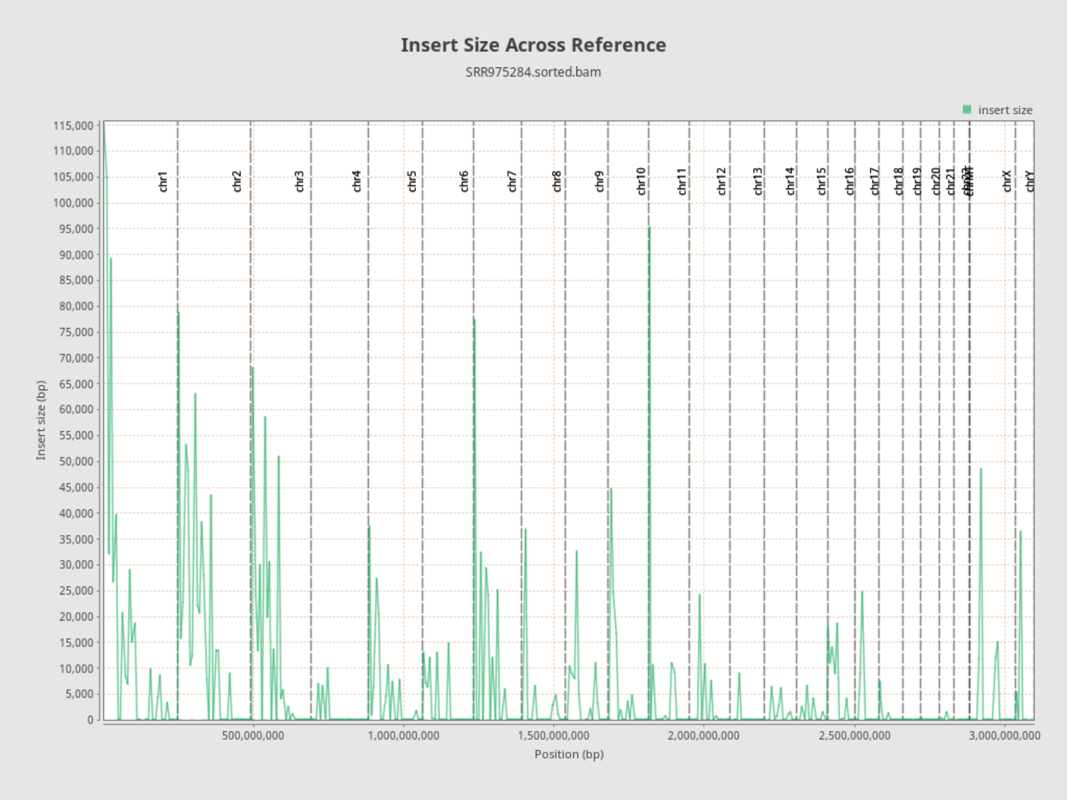


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram