Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 20:14:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975280.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_SRR975280 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975280_1.fastq.gz SRR975280_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 20:14:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975280.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,349,142
Mapped reads	2,320,899 / 98.8%
Unmapped reads	28,243 / 1.2%
Mapped paired reads	2,320,899 / 98.8%
Mapped reads, first in pair	1,162,366 / 49.48%
Mapped reads, second in pair	1,158,533 / 49.32%
Mapped reads, both in pair	2,312,674 / 98.45%
Mapped reads, singletons	8,225 / 0.35%
Secondary alignments	0
Supplementary alignments	34,080 / 1.45%
Read min/max/mean length	30 / 151 / 151.7
Duplicated reads (estimated)	392,971 / 16.73%
Duplication rate	15.62%
Clipped reads	1,714,568 / 72.99%

2.2. ACGT Content

Number/percentage of A's	91,401,402 / 29.51%
Number/percentage of C's	61,975,856 / 20.01%
Number/percentage of T's	91,492,474 / 29.54%
Number/percentage of G's	64,812,342 / 20.93%
Number/percentage of N's	19,395 / 0.01%

GC Percentage	40.94%

2.3. Coverage

Mean	0.1001
Standard Deviation	1.4747

2.4. Mapping Quality

Mean Mapping Quality	53.48

2.5. Insert size

Mean	86,513.13
Standard Deviation	2,754,292.42
P25/Median/P75	134 / 167 / 212

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	3,085,910
Insertions	63,952
Mapped reads with at least one insertion	2.59%
Deletions	102,321
Mapped reads with at least one deletion	4.23%
Homopolymer indels	44.34%

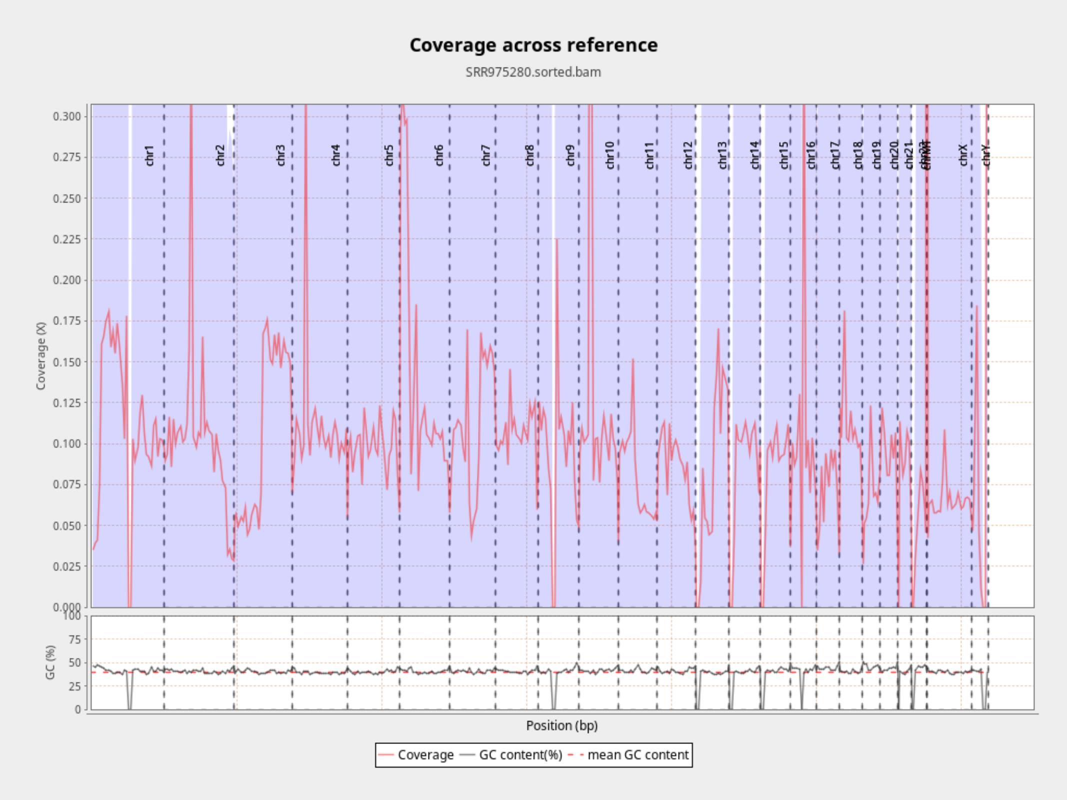
2.7. Chromosome stats

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

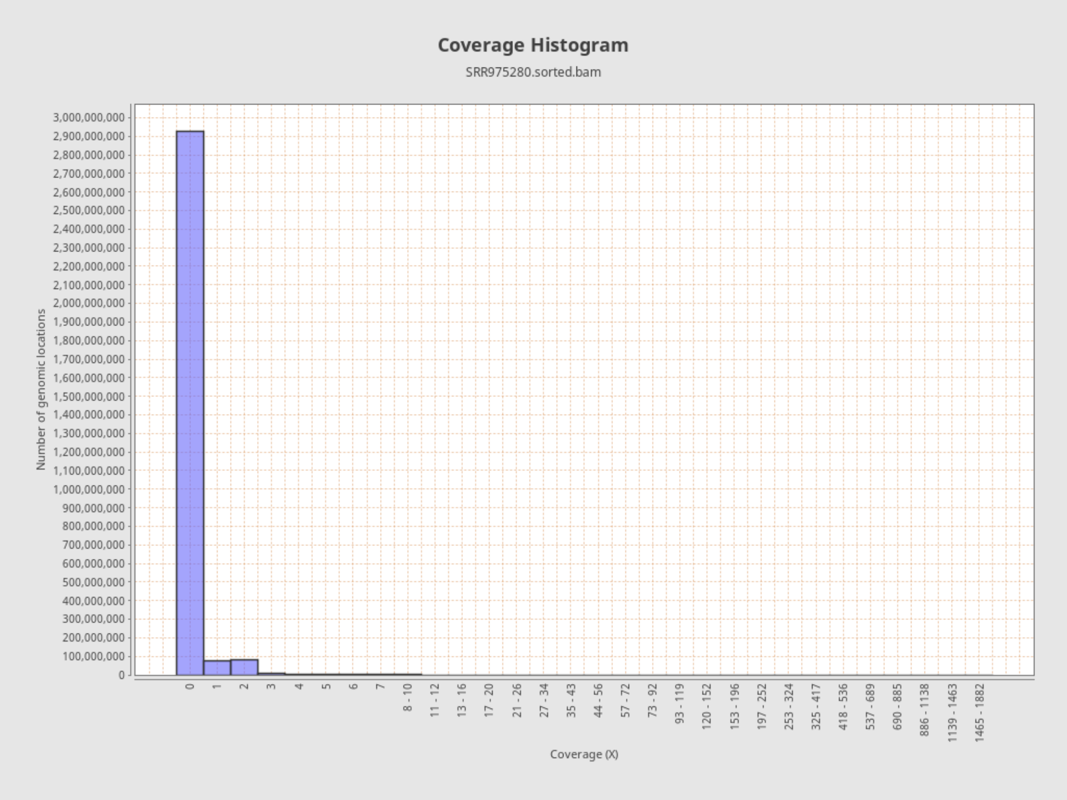
		bases	coverage	deviation
chr1	249250621	27624673	0.1108	1.4161
chr2	243199373	25370694	0.1043	1.6339
chr3	198022430	21552958	0.1088	0.5038
chr4	191154276	21427256	0.1121	1.4341
chr5	180915260	17870335	0.0988	0.4391
chr6	171115067	24427949	0.1428	0.9793
chr7	159138663	17904024	0.1125	1.2798
chr8	146364022	15618765	0.1067	0.6363
chr9	141213431	13545284	0.0959	2.4105
chr10	135534747	17450054	0.1287	4.0037
chr11	135006516	10779082	0.0798	1.1706
chr12	133851895	11710049	0.0875	0.4118
chr13	115169878	9861238	0.0856	0.4096
chr14	107349540	9042266	0.0842	0.4266
chr15	102531392	8296686	0.0809	0.3942
chr16	90354753	9582548	0.1061	1.8287
chr17	81195210	5838370	0.0719	0.7886
chr18	78077248	8746688	0.112	2.156
chr19	59128983	4065597	0.0688	0.9136
chr20	63025520	5967444	0.0947	0.6345
chr21	48129895	4080186	0.0848	0.8746
chr22	51304566	2525380	0.0492	0.3183
chrMT	16571	65881	3.9757	3.1937
chrX	155270560	10114160	0.0651	0.4908

chrY	59373566	6464337	0.1089	2.8851

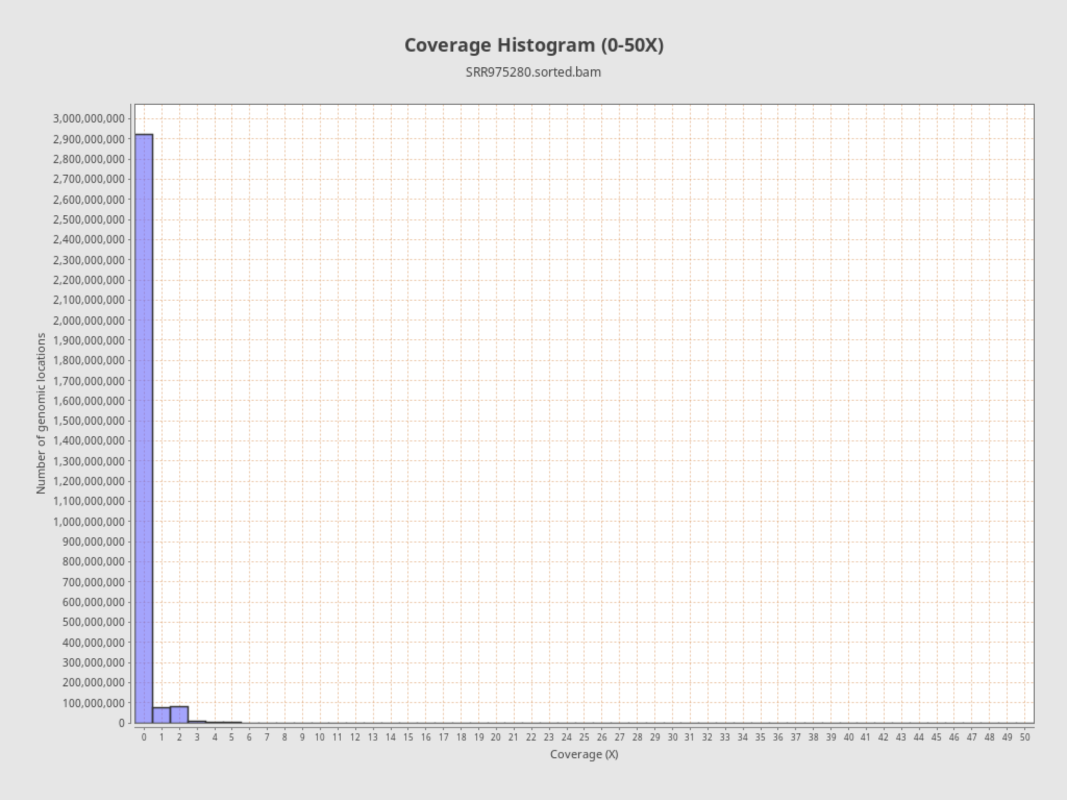
3. Results : Coverage across reference



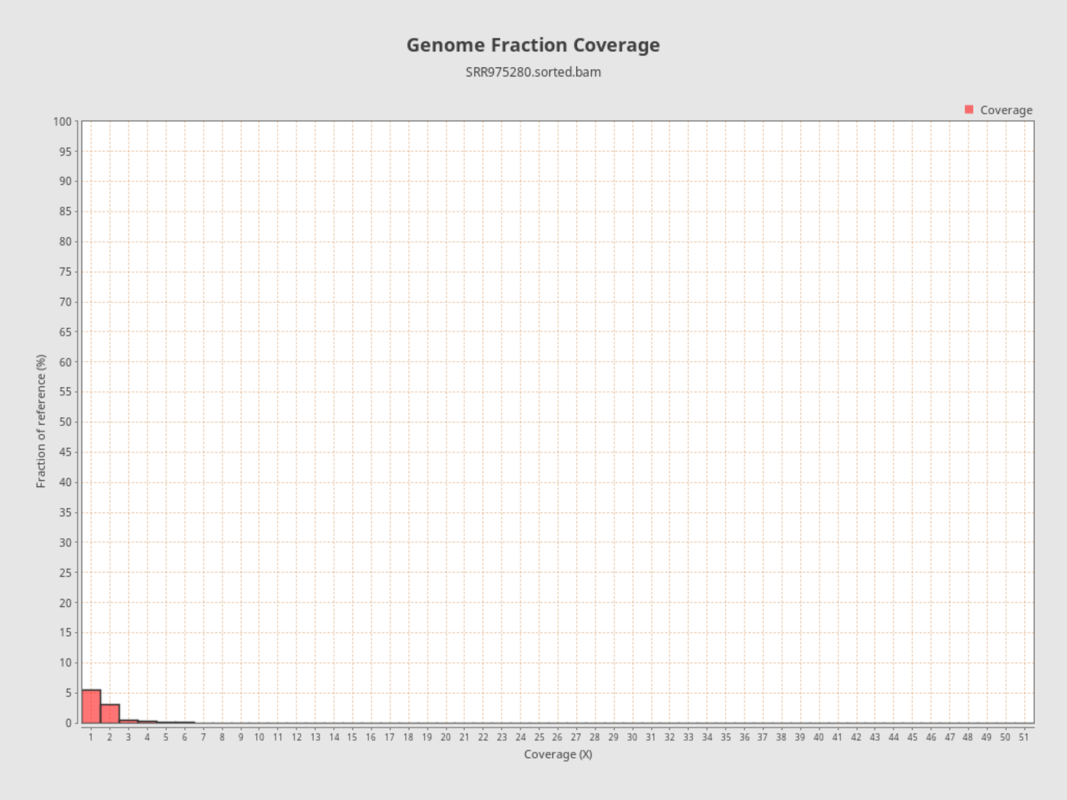
4. Results : Coverage Histogram



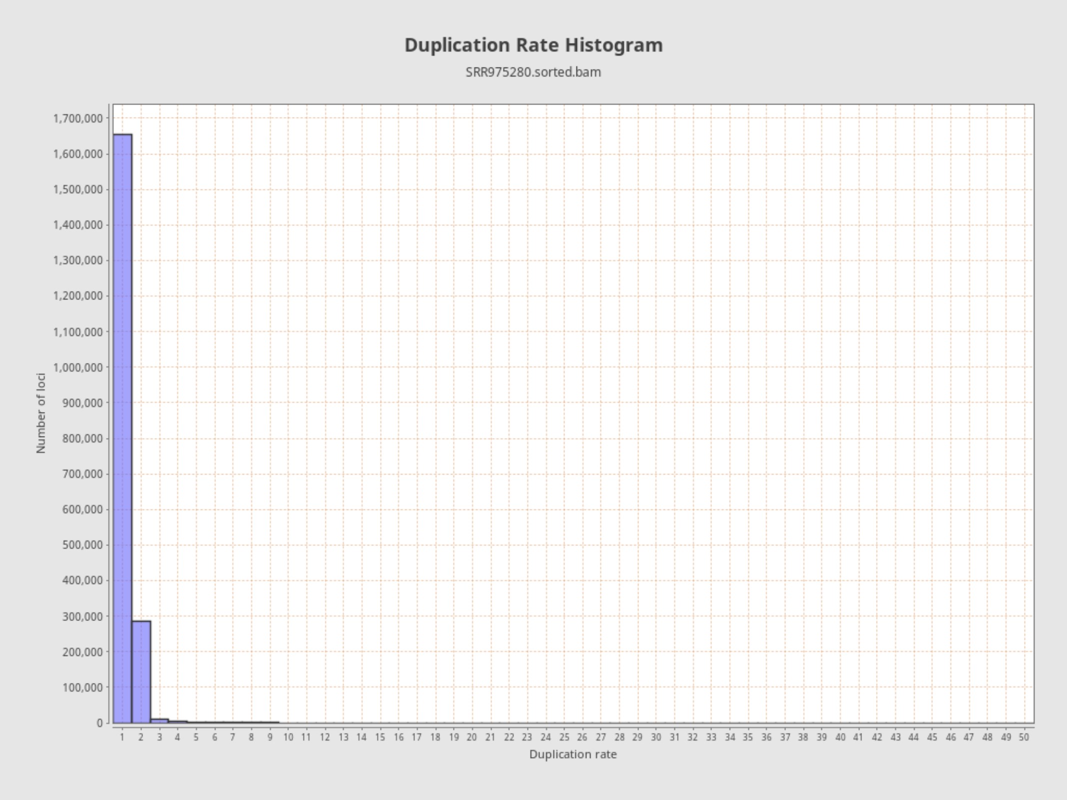
5. Results : Coverage Histogram (0-50X)



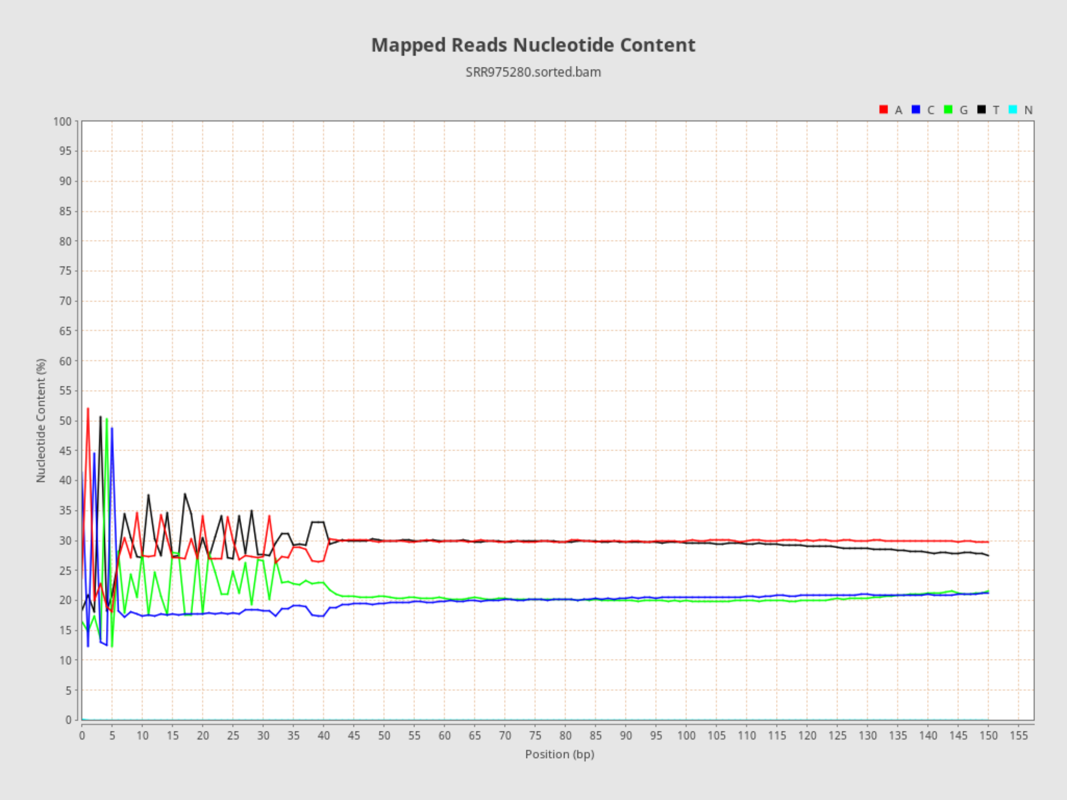
6. Results : Genome Fraction Coverage



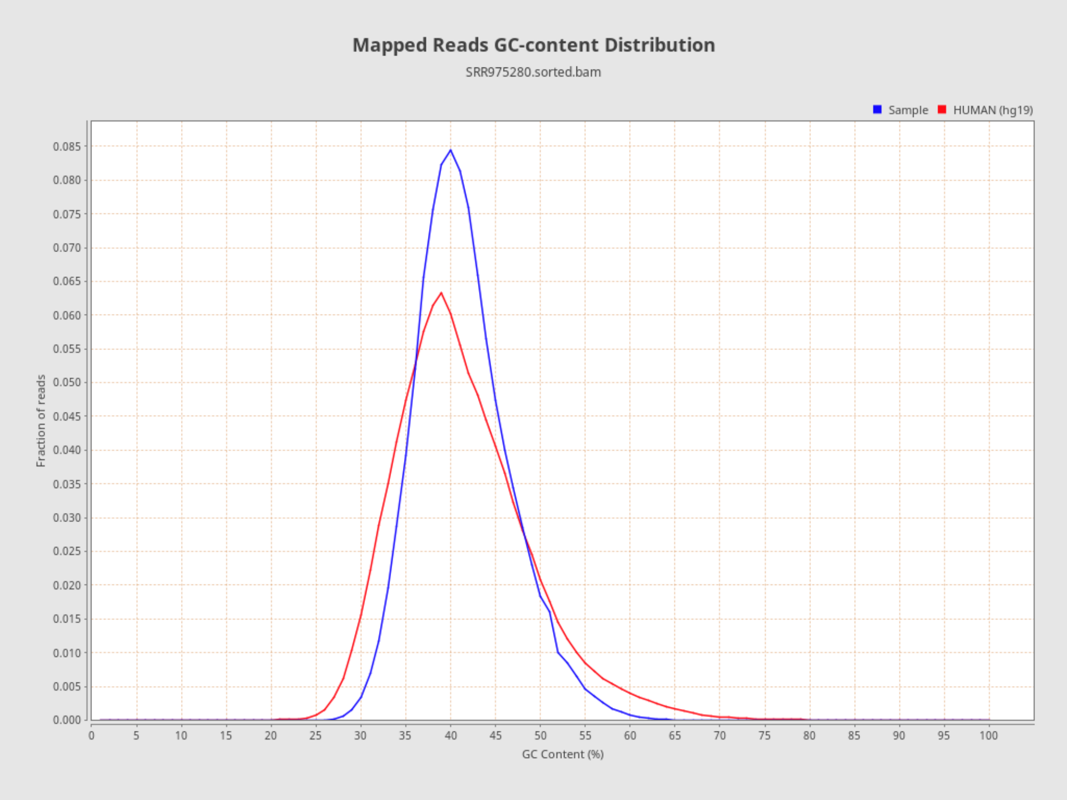
7. Results : Duplication Rate Histogram



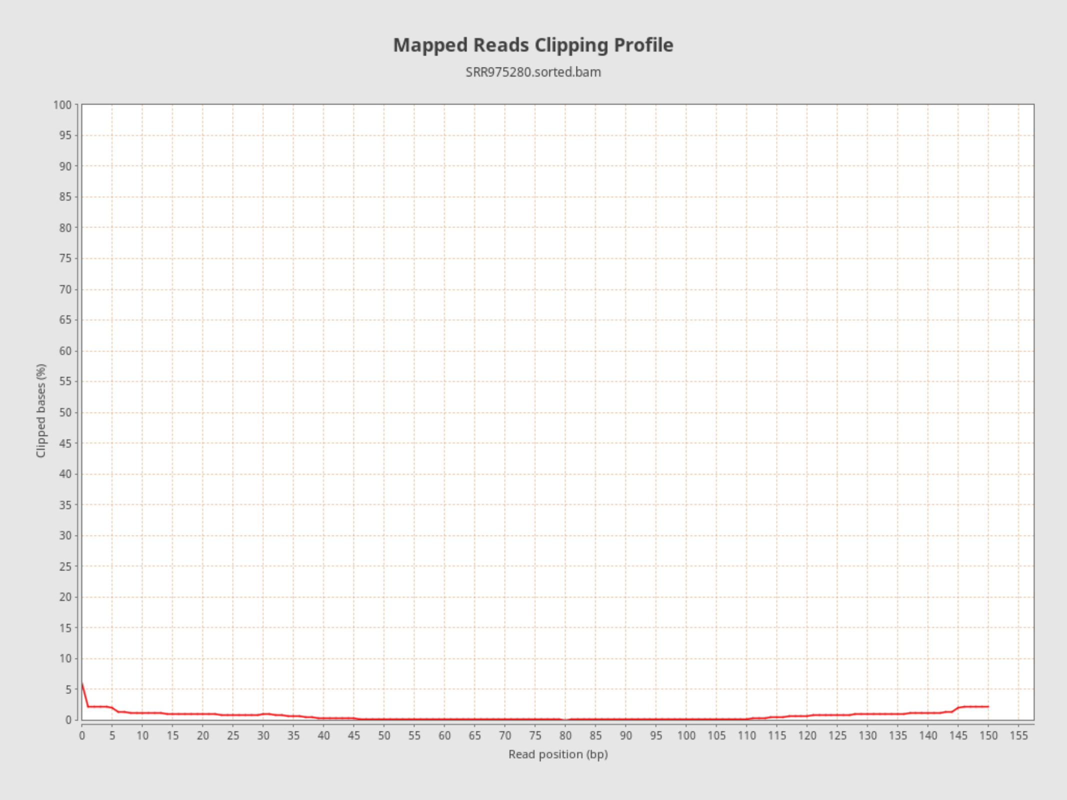
8. Results : Mapped Reads Nucleotide Content



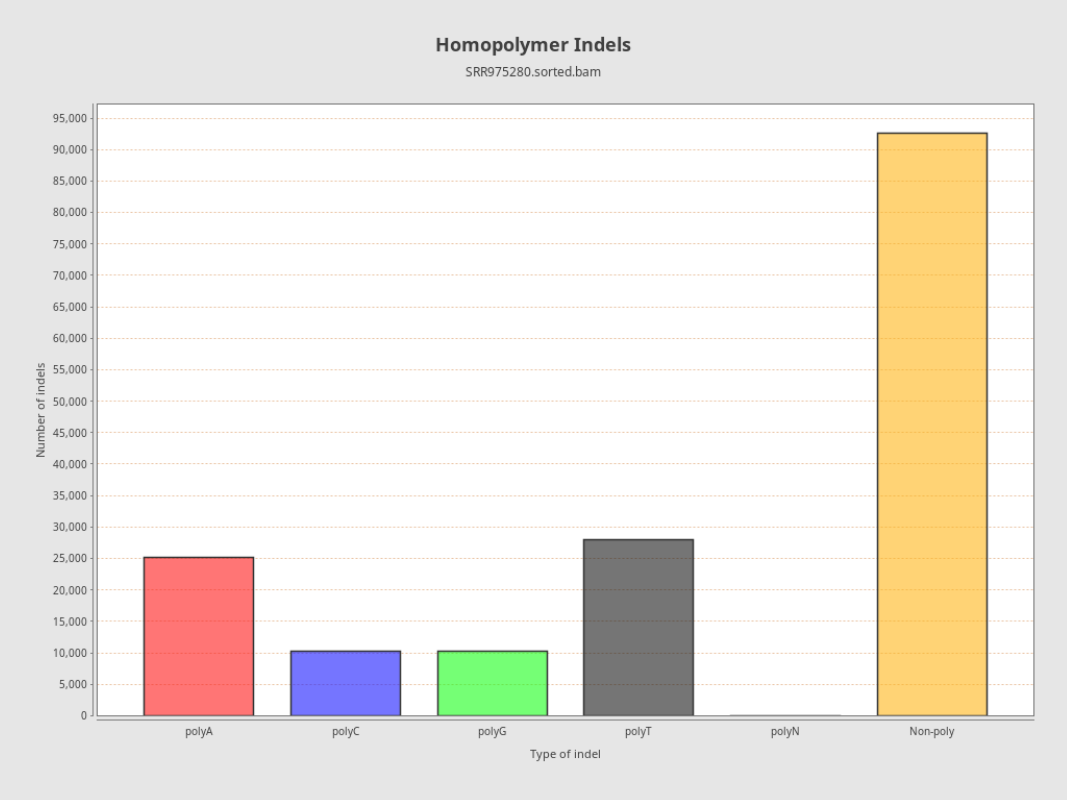
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

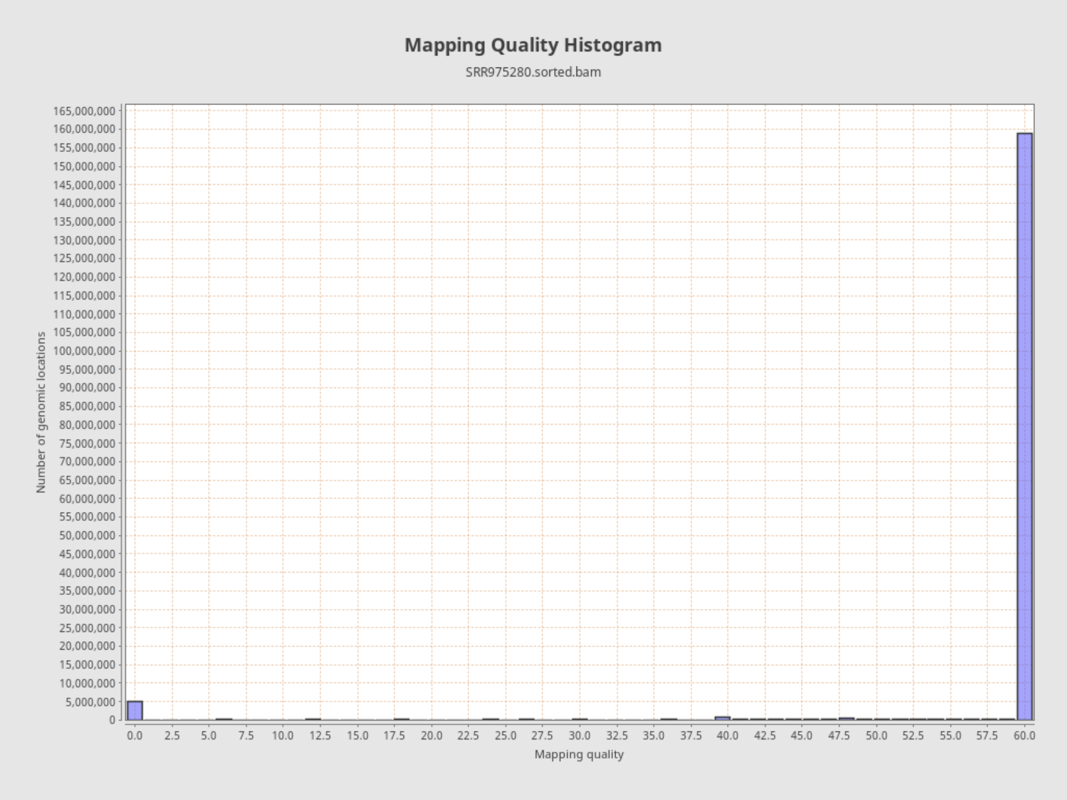


11. Results : Homopolymer Indels

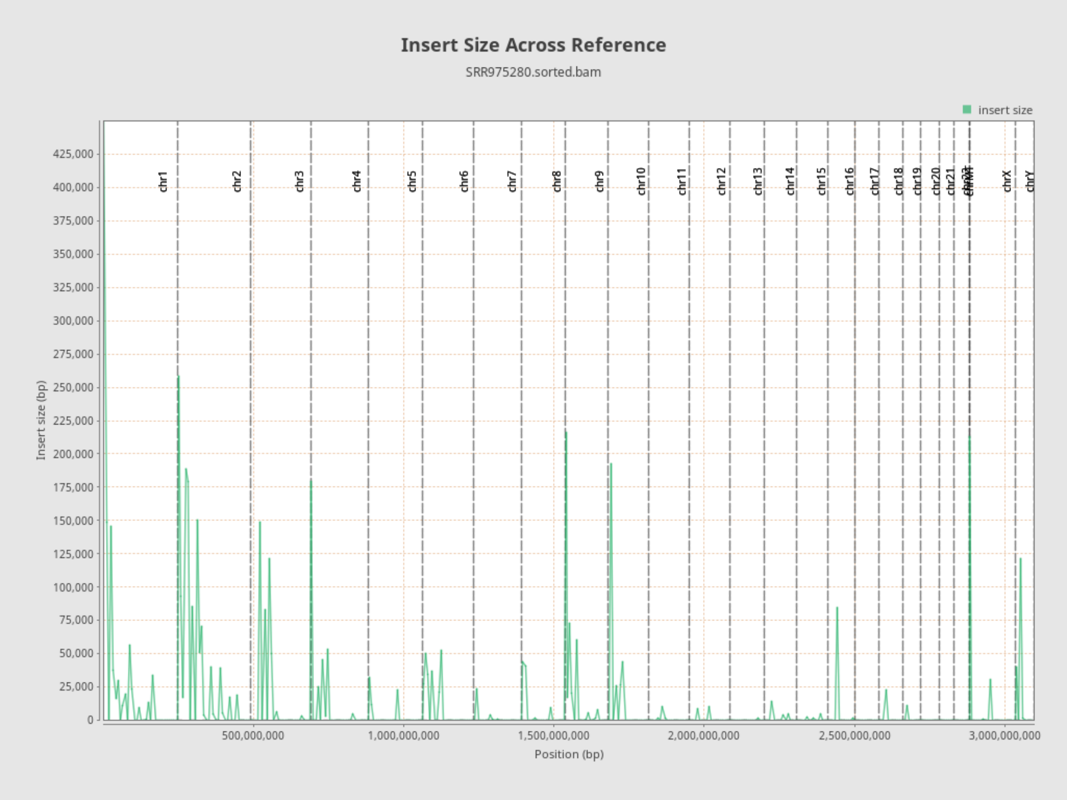


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram