Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 22:10:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975290.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_SRR975290 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975290_1.fastq.gz SRR975290_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 22:10:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975290.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,327,746
Mapped reads	3,294,312 / 99%
Unmapped reads	33,434 / 1%
Mapped paired reads	3,294,312 / 99%
Mapped reads, first in pair	1,646,759 / 49.49%
Mapped reads, second in pair	1,647,553 / 49.51%
Mapped reads, both in pair	3,283,614 / 98.67%
Mapped reads, singletons	10,698 / 0.32%
Secondary alignments	0
Supplementary alignments	17,433 / 0.52%
Read min/max/mean length	30 / 101 / 101.21
Duplicated reads (estimated)	153,695 / 4.62%
Duplication rate	2.67%
Clipped reads	2,067,678 / 62.13%

2.2. ACGT Content

Number/percentage of A's	86,866,069 / 28.84%
Number/percentage of C's	57,932,604 / 19.24%
Number/percentage of T's	91,341,624 / 30.33%
Number/percentage of G's	65,014,336 / 21.59%
Number/percentage of N's	6,634 / 0%

GC Percentage	40.82%

2.3. Coverage

Mean	0.0973
Standard Deviation	1.0386

2.4. Mapping Quality

Mean Mapping Quality	52.86

2.5. Insert size

Mean	48,558.97
Standard Deviation	2,101,040.46
P25/Median/P75	137 / 171 / 217

2.6. Mismatches and indels

General error rate	0.85%
Mismatches	2,451,470
Insertions	49,440
Mapped reads with at least one insertion	1.47%
Deletions	100,419
Mapped reads with at least one deletion	2.99%
Homopolymer indels	46.54%

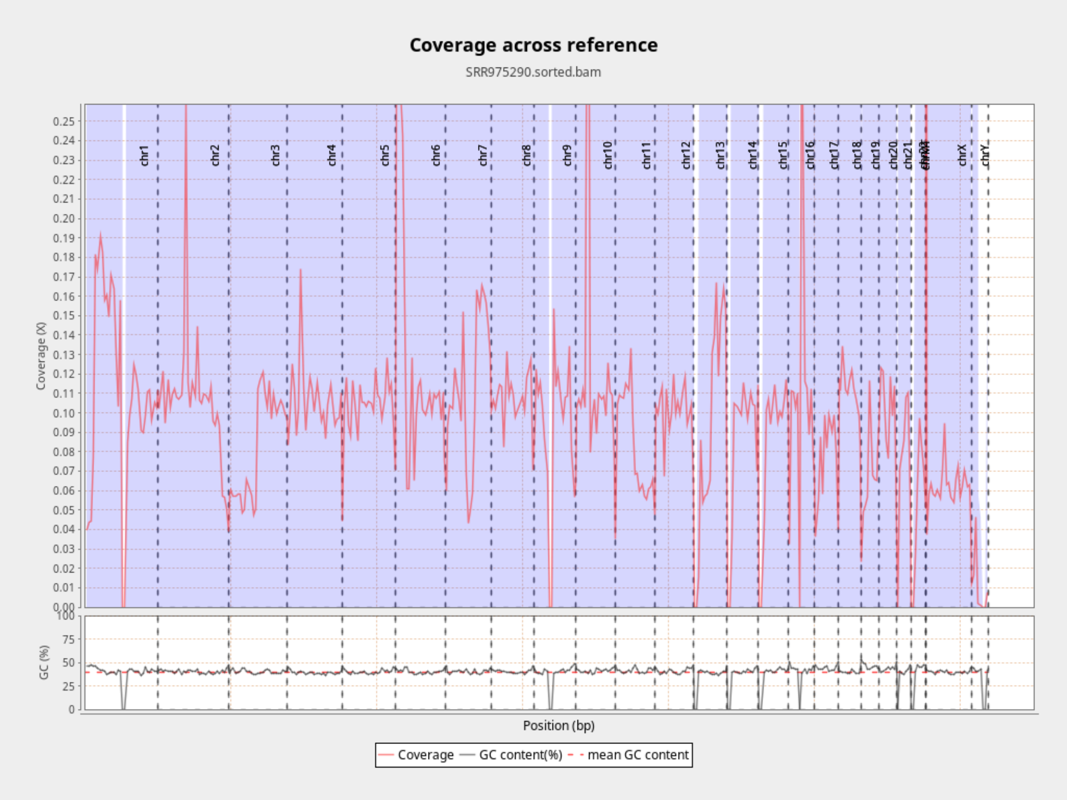
2.7. Chromosome stats

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

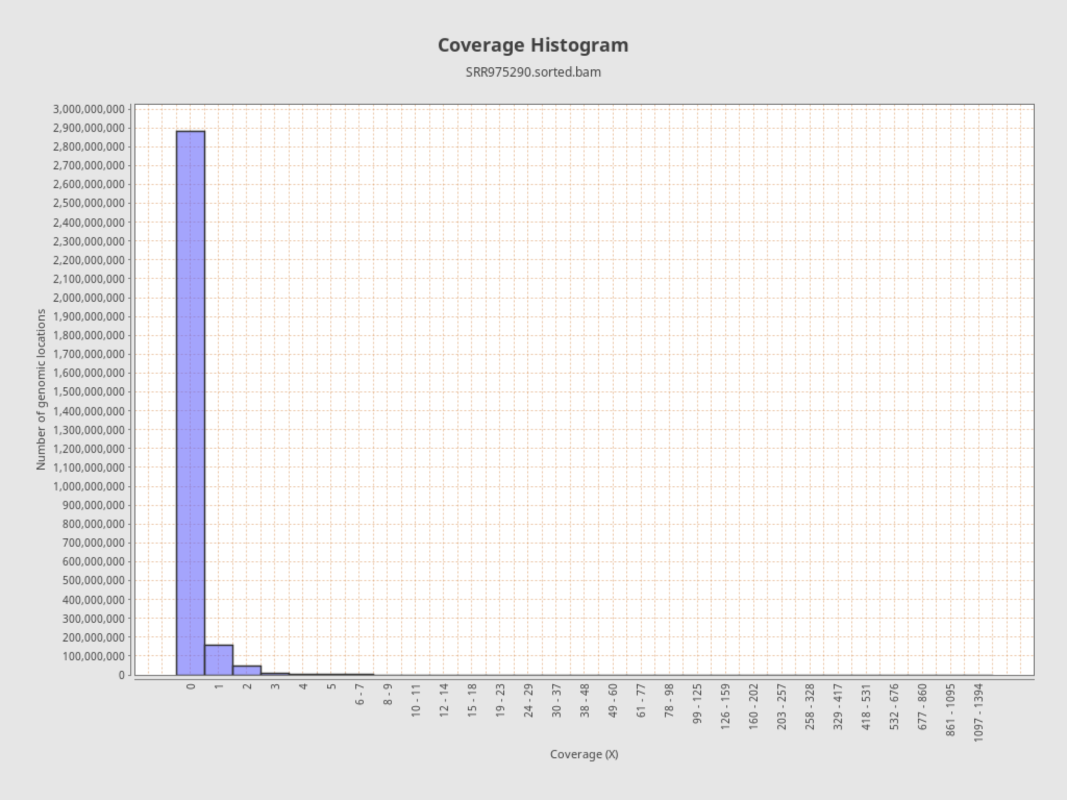
		bases	**coverage**	**deviation**
chr1	249250621	27910274	0.112	1.0798
chr2	243199373	26132793	0.1075	1.0733
chr3	198022430	16356902	0.0826	0.3875
chr4	191154276	20336679	0.1064	0.658
chr5	180915260	19126508	0.1057	0.4113
chr6	171115067	21972641	0.1284	0.87
chr7	159138663	17916688	0.1126	1.1735
chr8	146364022	15801970	0.108	0.5186
chr9	141213431	13222114	0.0936	1.4104
chr10	135534747	16827815	0.1242	3.0079
chr11	135006516	11319695	0.0838	0.9393
chr12	133851895	13647058	0.102	0.4055
chr13	115169878	10657745	0.0925	0.3805
chr14	107349540	9027392	0.0841	0.4054
chr15	102531392	8670617	0.0846	0.3672
chr16	90354753	9977207	0.1104	1.4788
chr17	81195210	6239640	0.0768	0.7916
chr18	78077248	8766740	0.1123	1.4773
chr19	59128983	3905168	0.066	0.6576
chr20	63025520	6369952	0.1011	0.4363
chr21	48129895	3794634	0.0788	0.4801
chr22	51304566	2747641	0.0536	0.2931
chrMT	16571	261688	15.7919	25.1912
chrX	155270560	9707636	0.0625	0.4518

chrY	59373566	628447	0.0106	0.5999

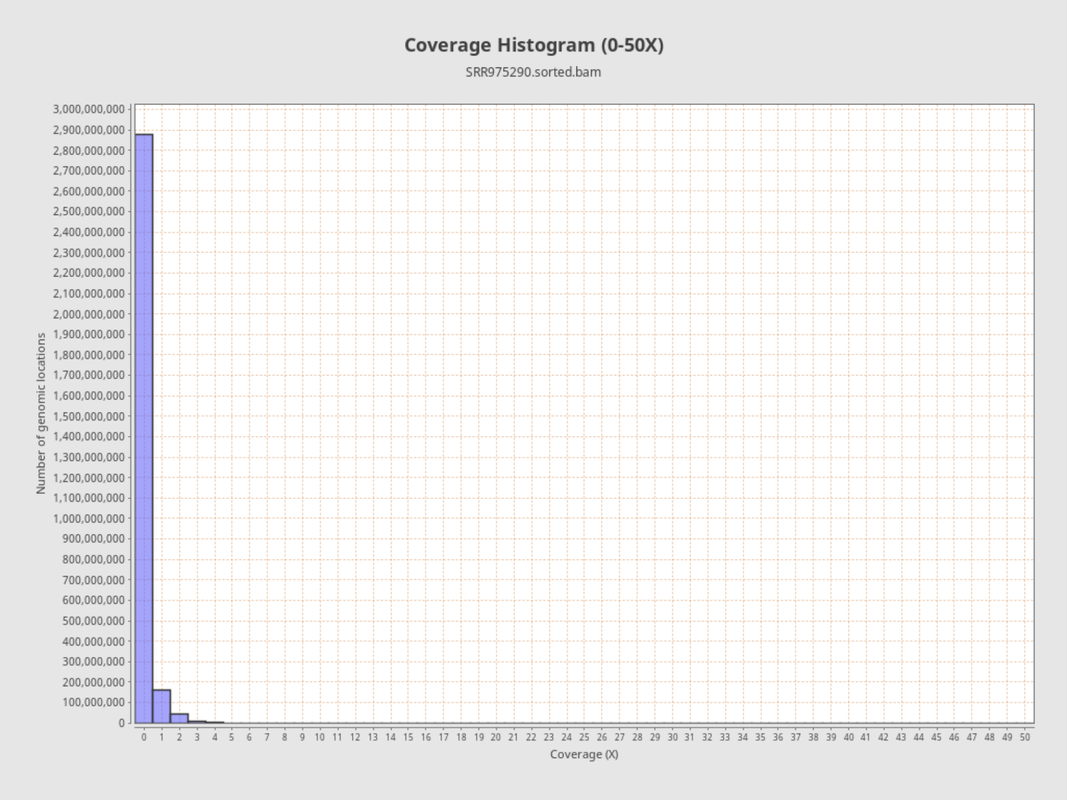
3. Results : Coverage across reference



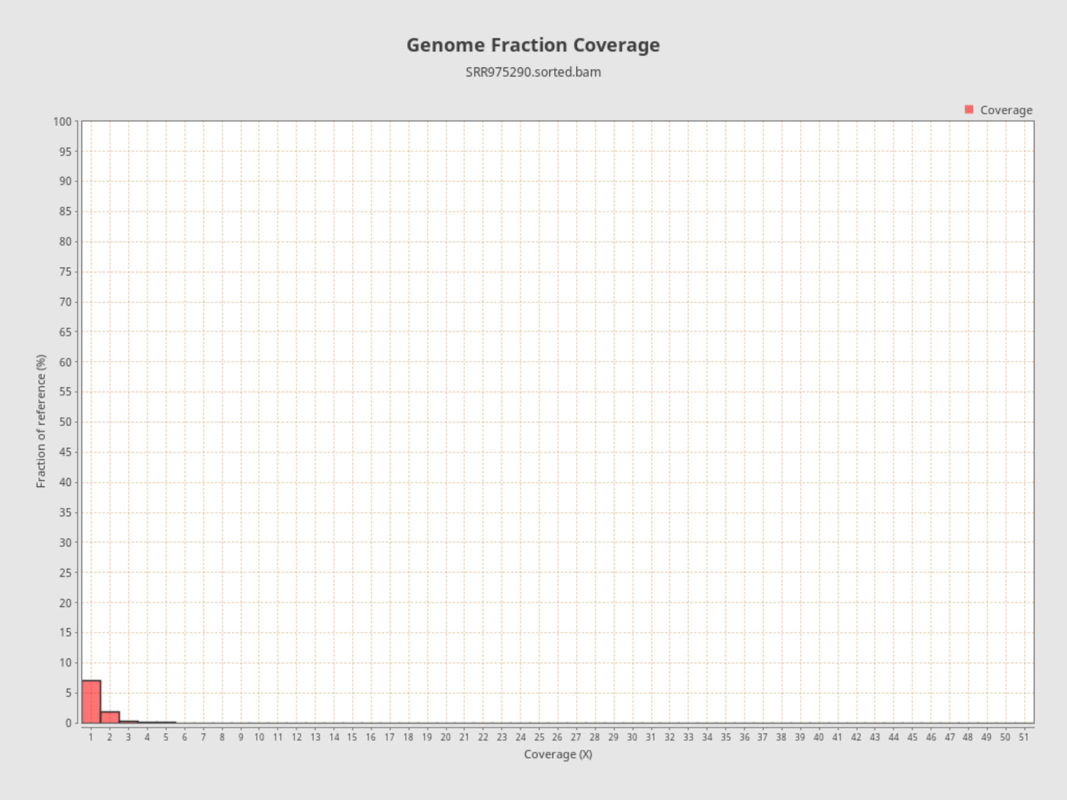
4. Results : Coverage Histogram



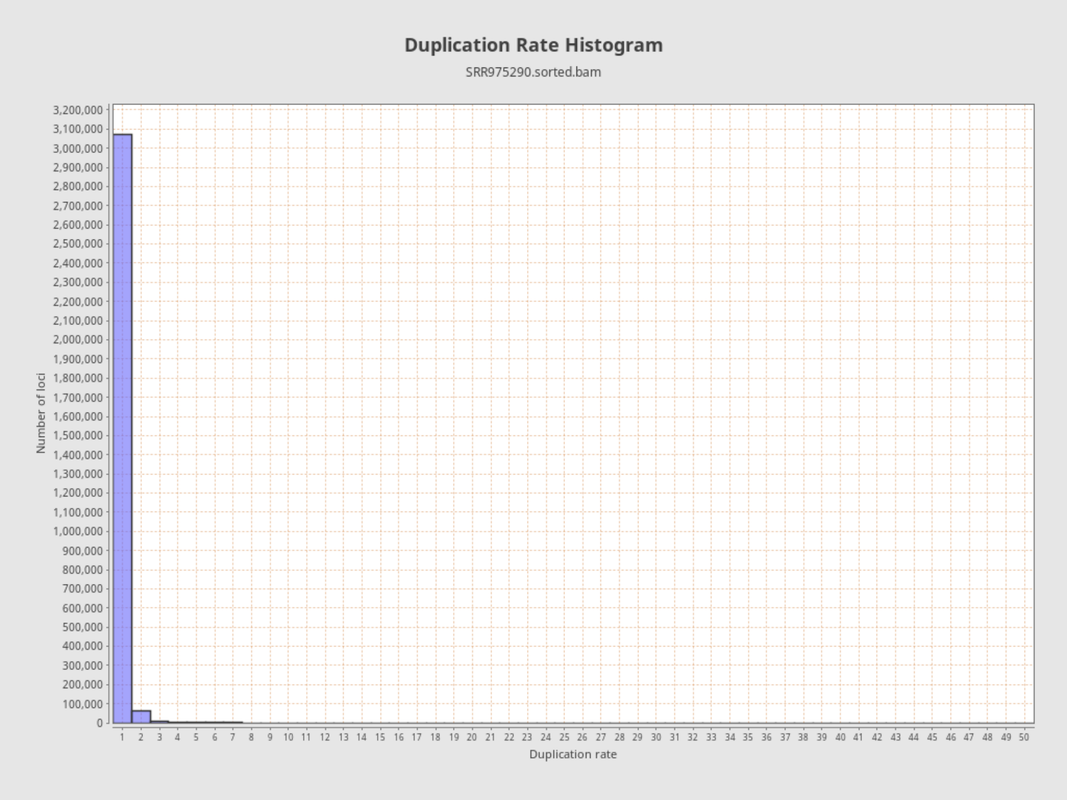
5. Results : Coverage Histogram (0-50X)



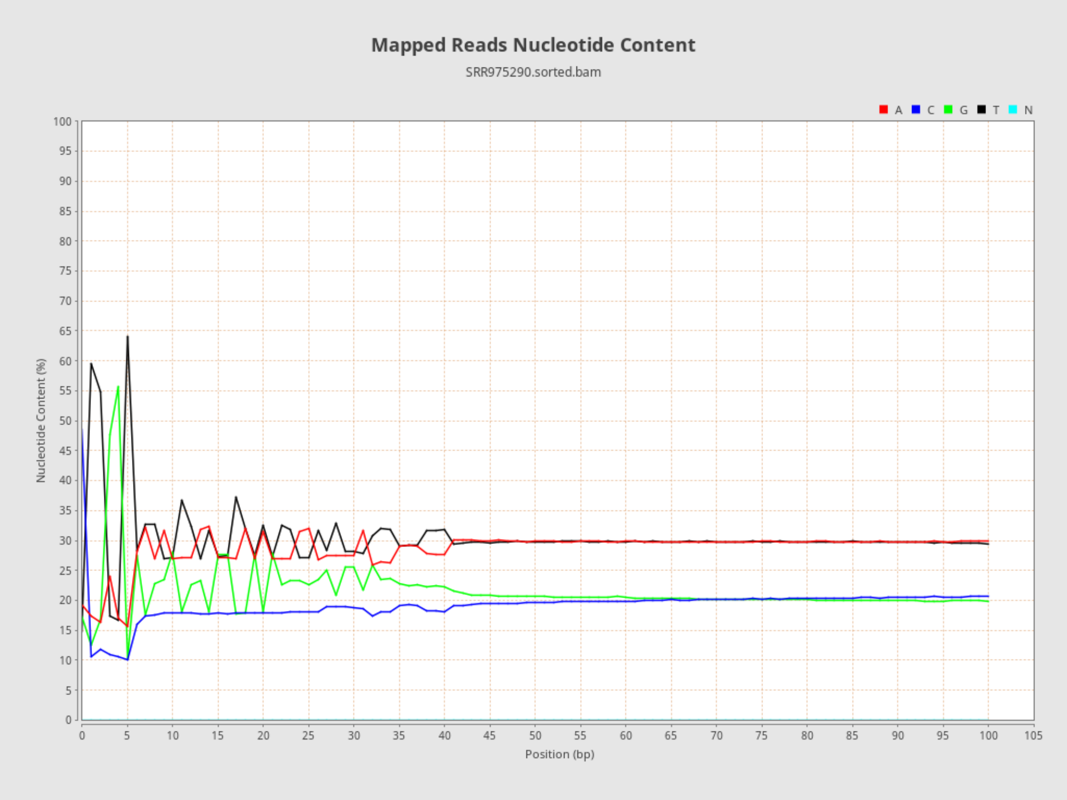
6. Results : Genome Fraction Coverage



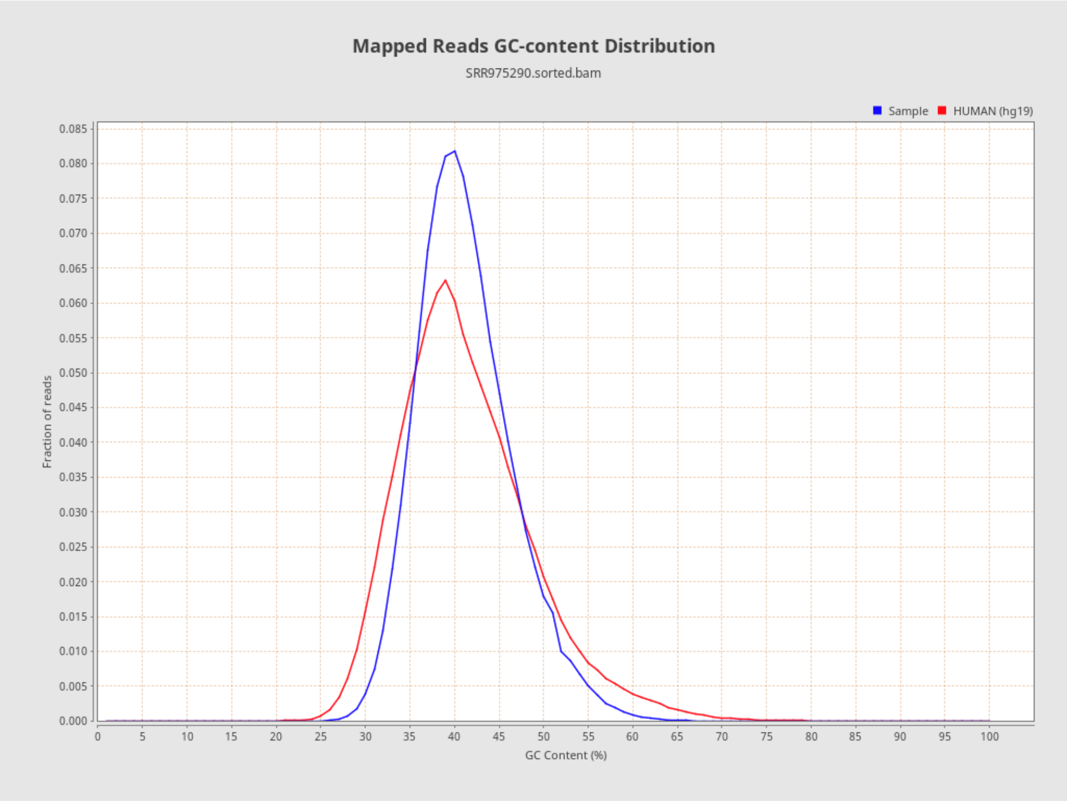
7. Results : Duplication Rate Histogram



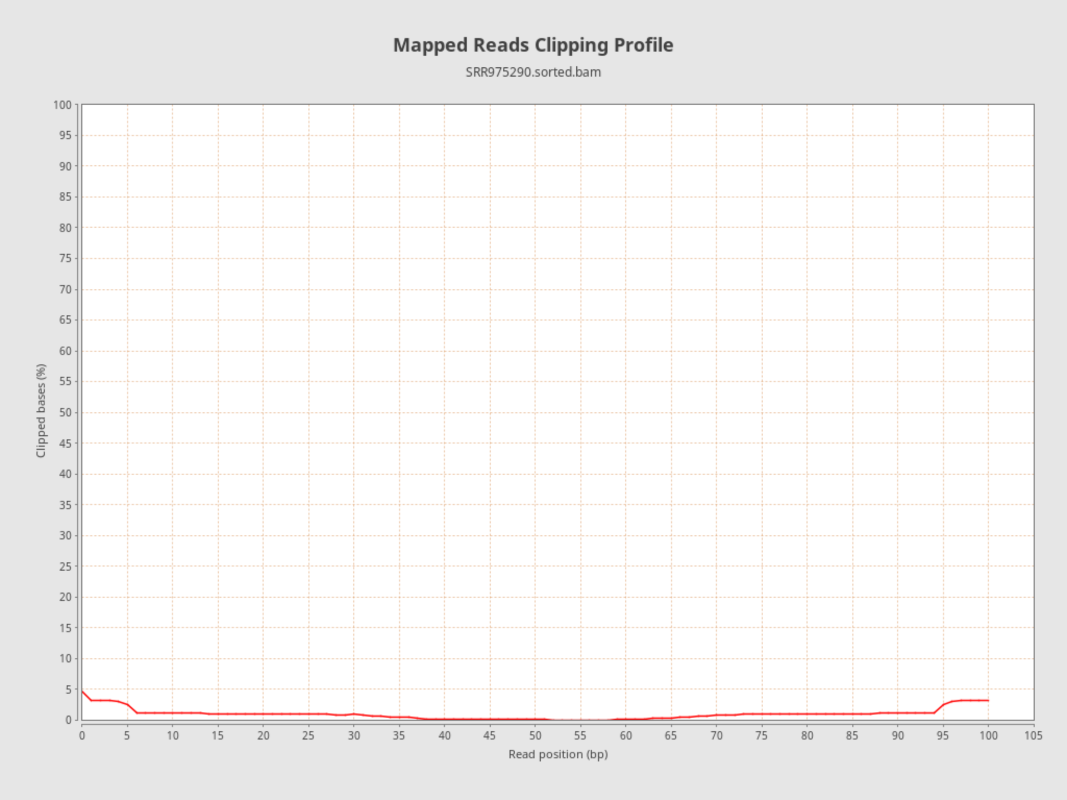
8. Results : Mapped Reads Nucleotide Content



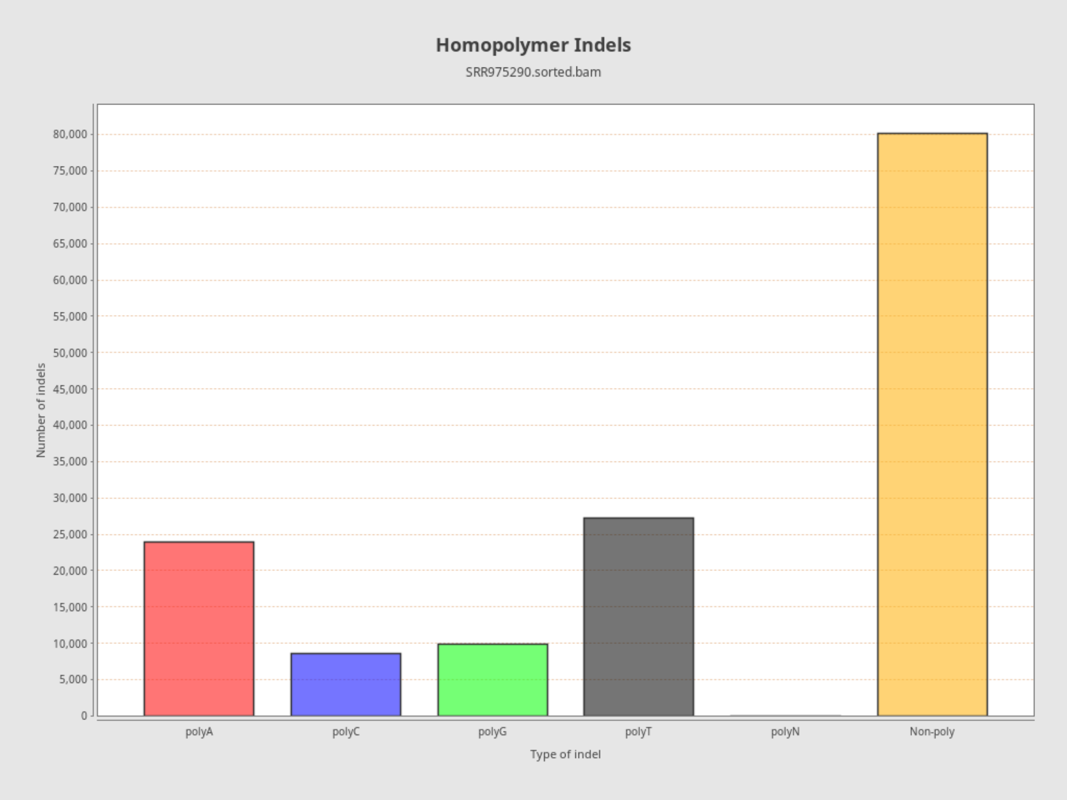
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

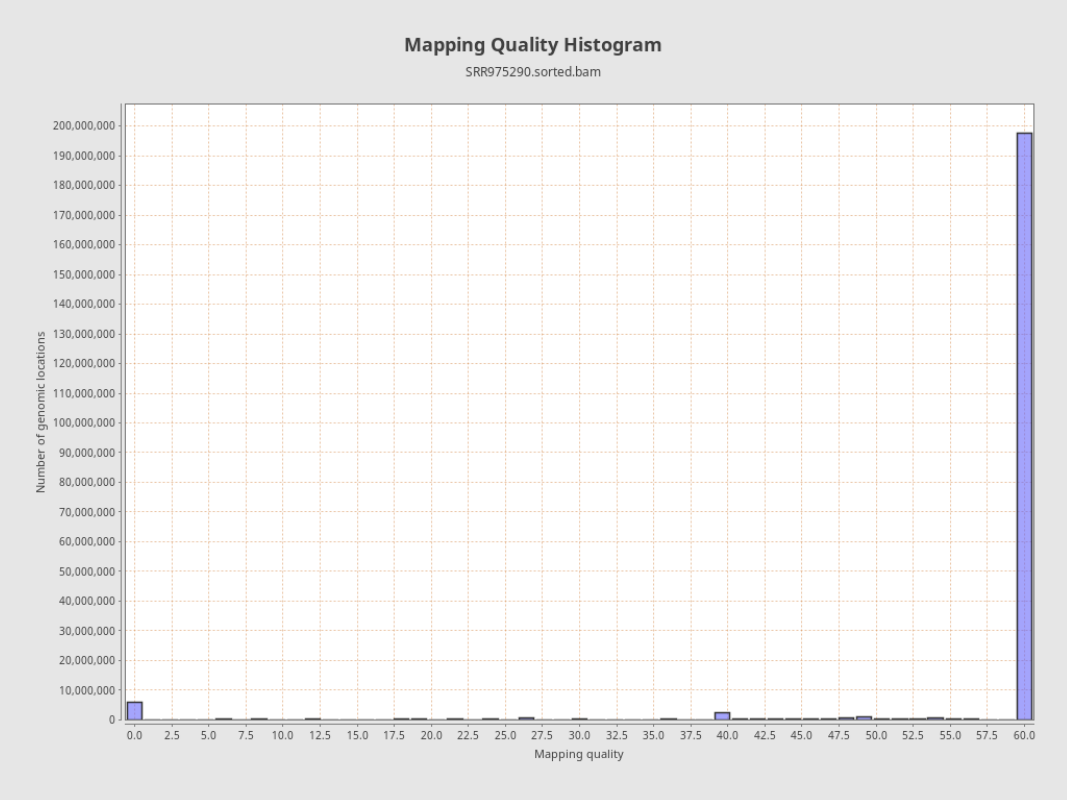


11. Results : Homopolymer Indels

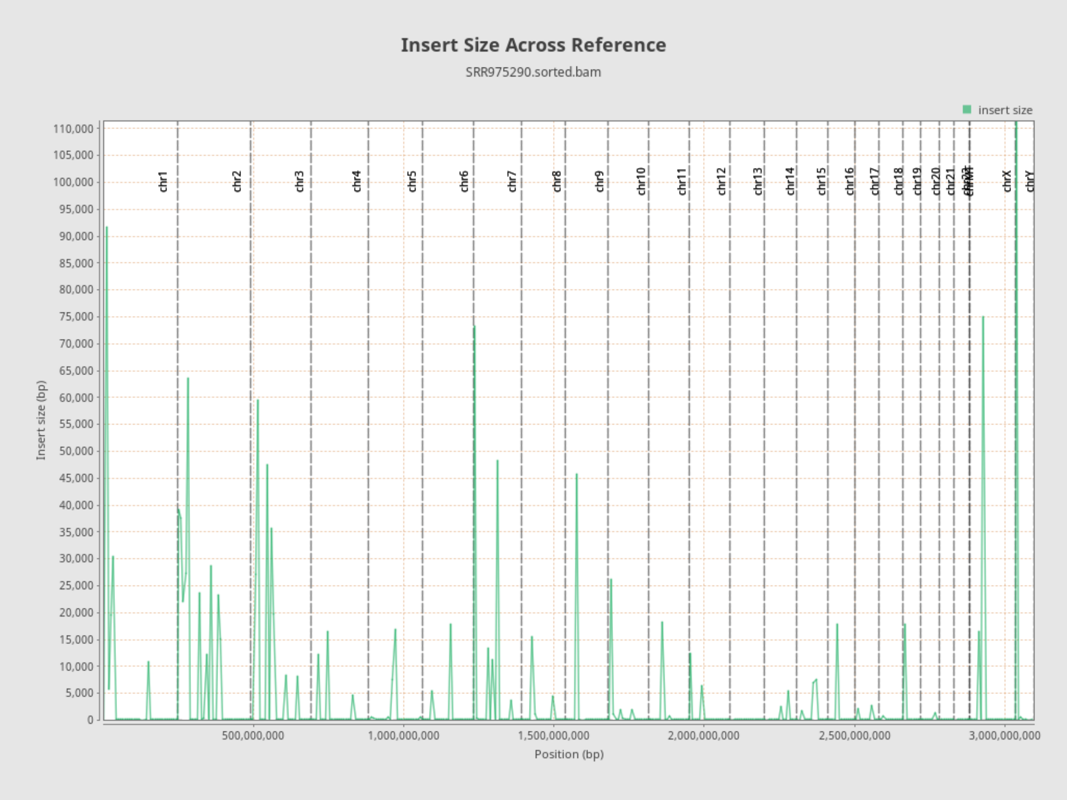


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram