Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 20:00:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975276.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_SRR975276 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975276_1.fastq.gz SRR975276_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 20:00:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975276.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,229,748
Mapped reads	3,188,263 / 98.72%
Unmapped reads	41,485 / 1.28%
Mapped paired reads	3,188,263 / 98.72%
Mapped reads, first in pair	1,593,695 / 49.34%
Mapped reads, second in pair	1,594,568 / 49.37%
Mapped reads, both in pair	3,177,858 / 98.39%
Mapped reads, singletons	10,405 / 0.32%
Secondary alignments	0
Supplementary alignments	15,479 / 0.48%
Read min/max/mean length	30 / 101 / 101.19
Duplicated reads (estimated)	133,251 / 4.13%
Duplication rate	2.45%
Clipped reads	2,001,277 / 61.96%

2.2. ACGT Content

Number/percentage of A's	83,791,711 / 28.89%
Number/percentage of C's	56,205,081 / 19.38%
Number/percentage of T's	86,493,189 / 29.82%
Number/percentage of G's	63,572,061 / 21.92%
Number/percentage of N's	6,385 / 0%

GC Percentage	41.29%

2.3. Coverage

Mean	0.0938
Standard Deviation	0.9559

2.4. Mapping Quality

Mean Mapping Quality	52.85

2.5. Insert size

Mean	51,230.88
Standard Deviation	2,182,346.49
P25/Median/P75	137 / 171 / 216

2.6. Mismatches and indels

General error rate	0.83%
Mismatches	2,299,509
Insertions	49,545
Mapped reads with at least one insertion	1.52%
Deletions	100,175
Mapped reads with at least one deletion	3.08%
Homopolymer indels	45.81%

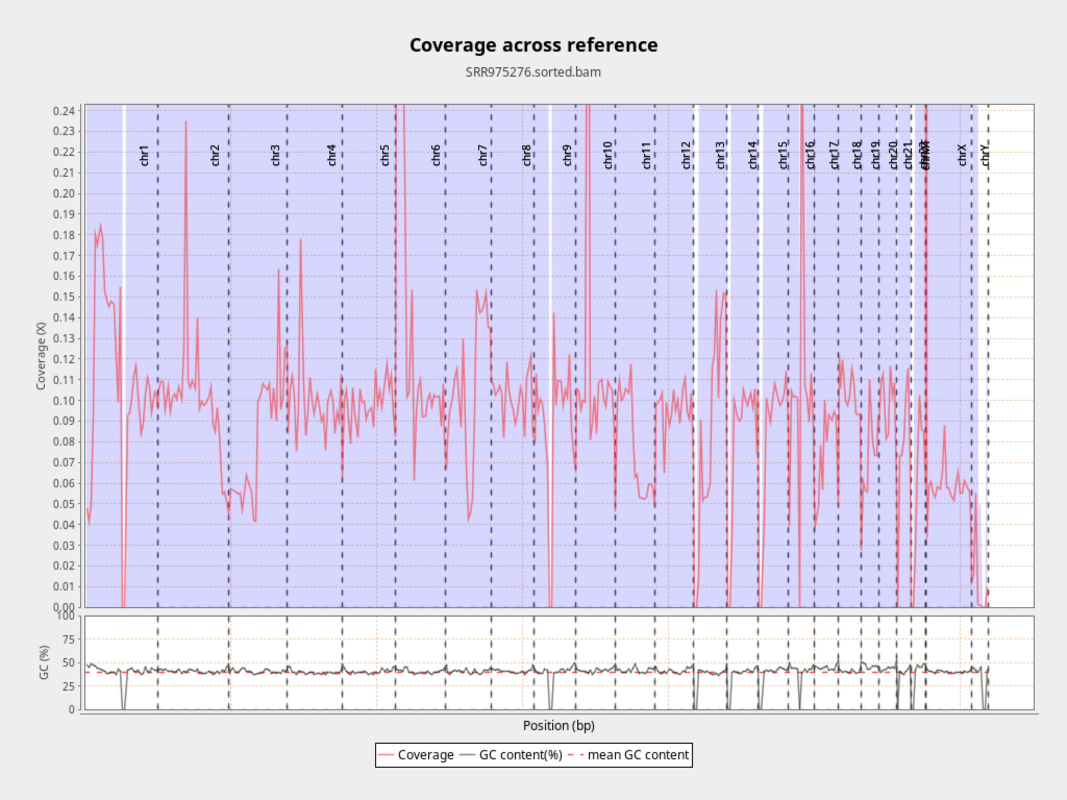
2.7. Chromosome stats

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

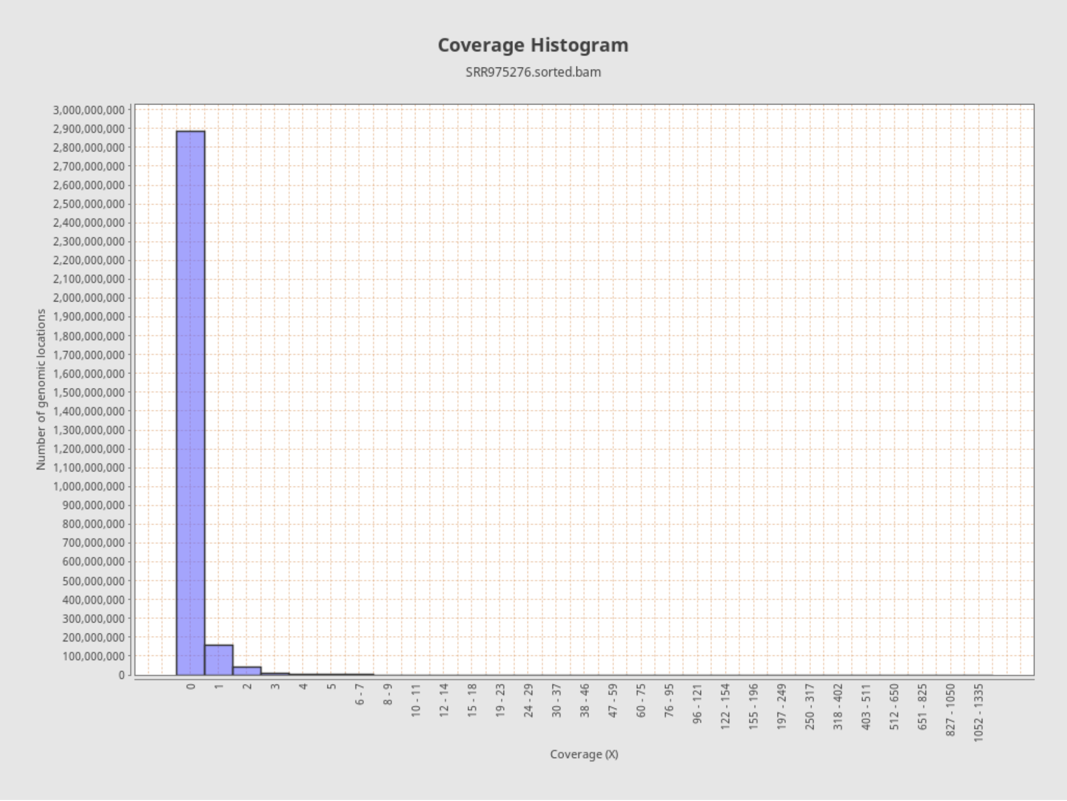
		bases	coverage	deviation
chr1	249250621	27071479	0.1086	1.075
chr2	243199373	24671210	0.1014	0.9657
chr3	198022430	16198344	0.0818	0.3797
chr4	191154276	19041876	0.0996	0.6711
chr5	180915260	17900743	0.0989	0.3863
chr6	171115067	23882796	0.1396	0.7657
chr7	159138663	16795282	0.1055	0.9053
chr8	146364022	14872148	0.1016	0.4731
chr9	141213431	12563052	0.089	1.2171
chr10	135534747	16075486	0.1186	2.8728
chr11	135006516	10516638	0.0779	0.8491
chr12	133851895	12851750	0.096	0.3821
chr13	115169878	9896023	0.0859	0.3598
chr14	107349540	8553804	0.0797	0.3726
chr15	102531392	8407240	0.082	0.3511
chr16	90354753	9529725	0.1055	1.3314
chr17	81195210	6176649	0.0761	0.6193
chr18	78077248	8125176	0.1041	1.2556
chr19	59128983	4209943	0.0712	0.6239
chr20	63025520	6207816	0.0985	0.4102
chr21	48129895	3805914	0.0791	0.4514
chr22	51304566	2997083	0.0584	0.3005
chrMT	16571	126070	7.6079	6.7072
chrX	155270560	9045142	0.0583	0.4192

chrY	59373566	713491	0.012	0.6944

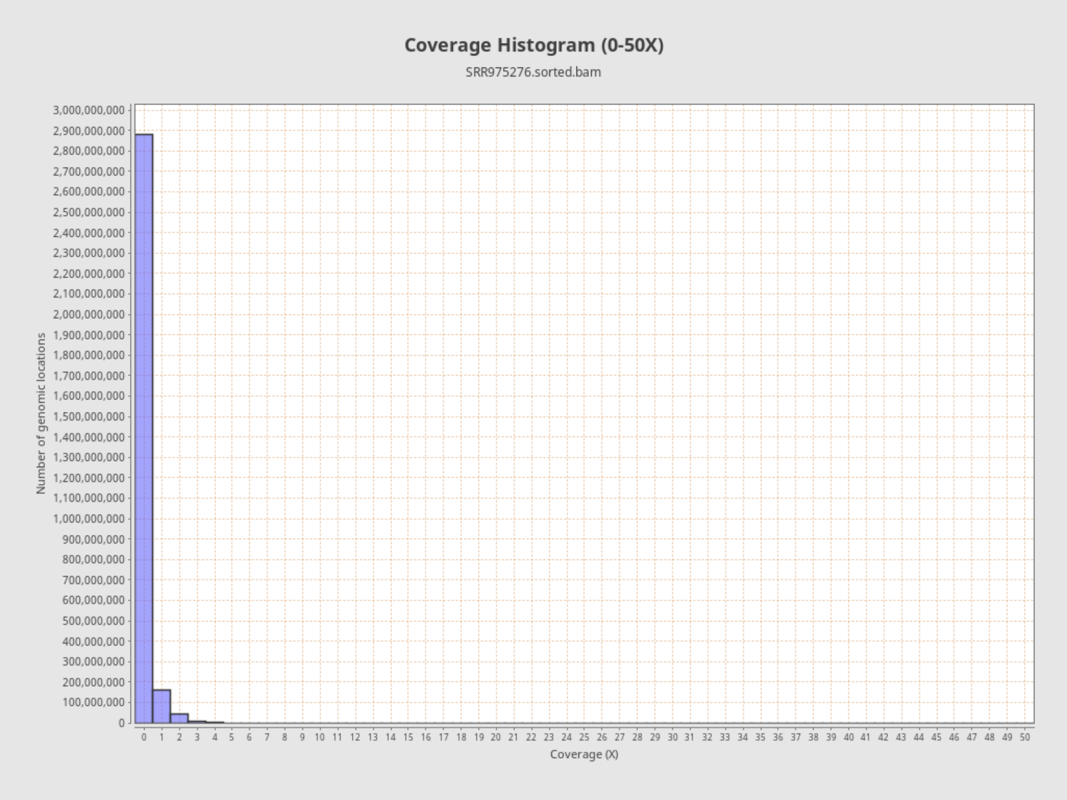
3. Results : Coverage across reference



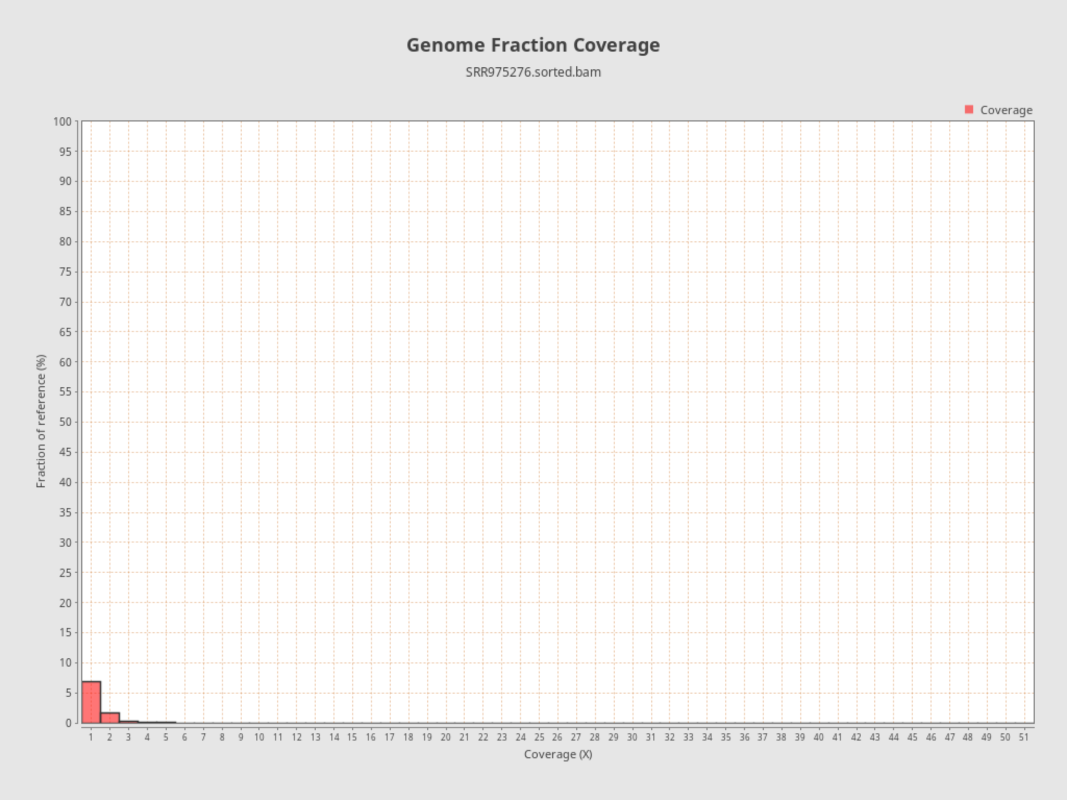
4. Results : Coverage Histogram



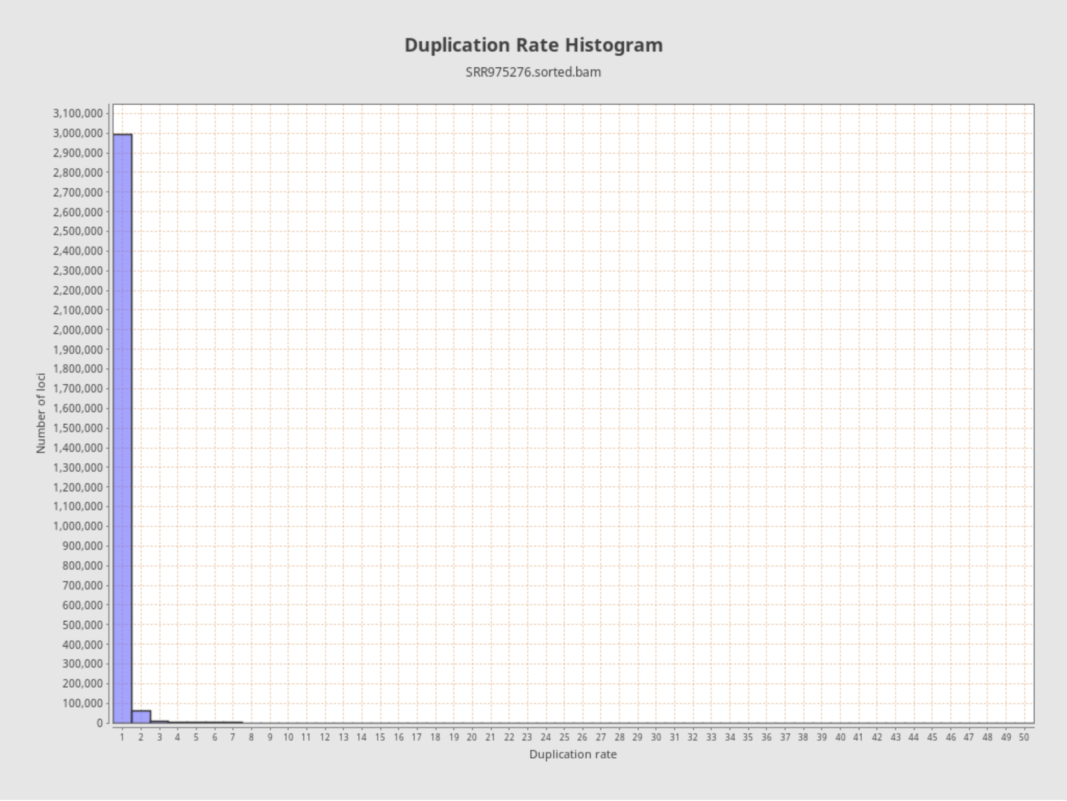
5. Results : Coverage Histogram (0-50X)



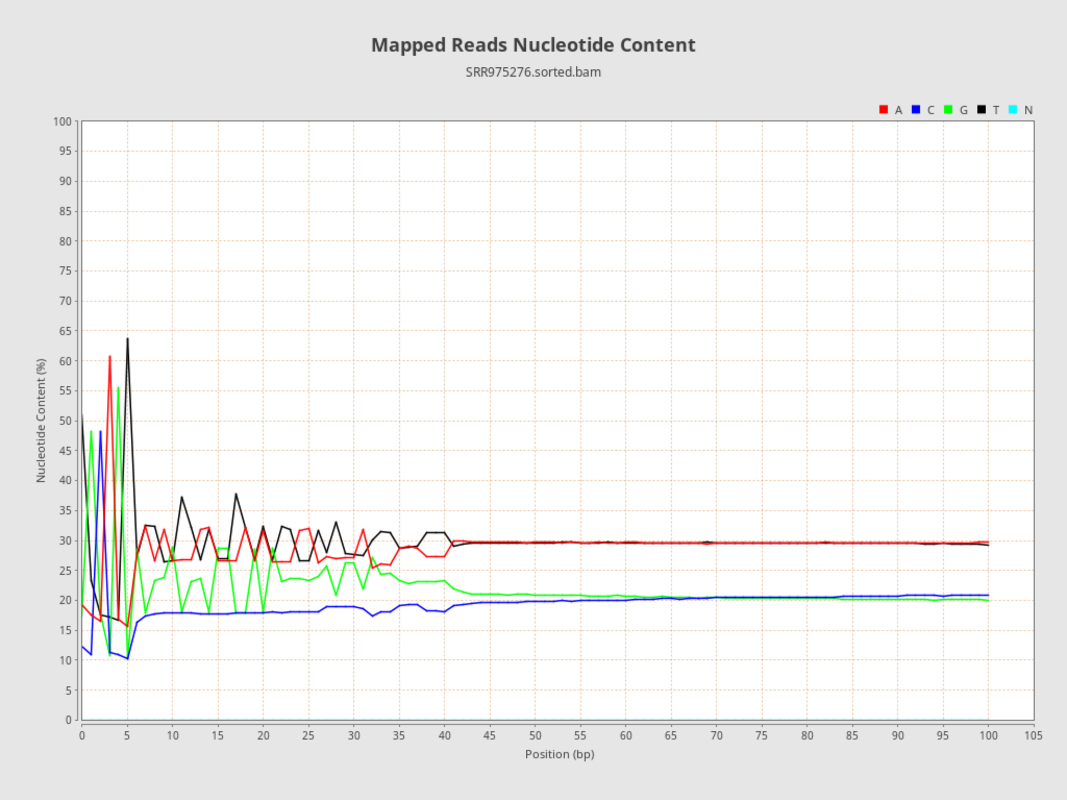
6. Results : Genome Fraction Coverage



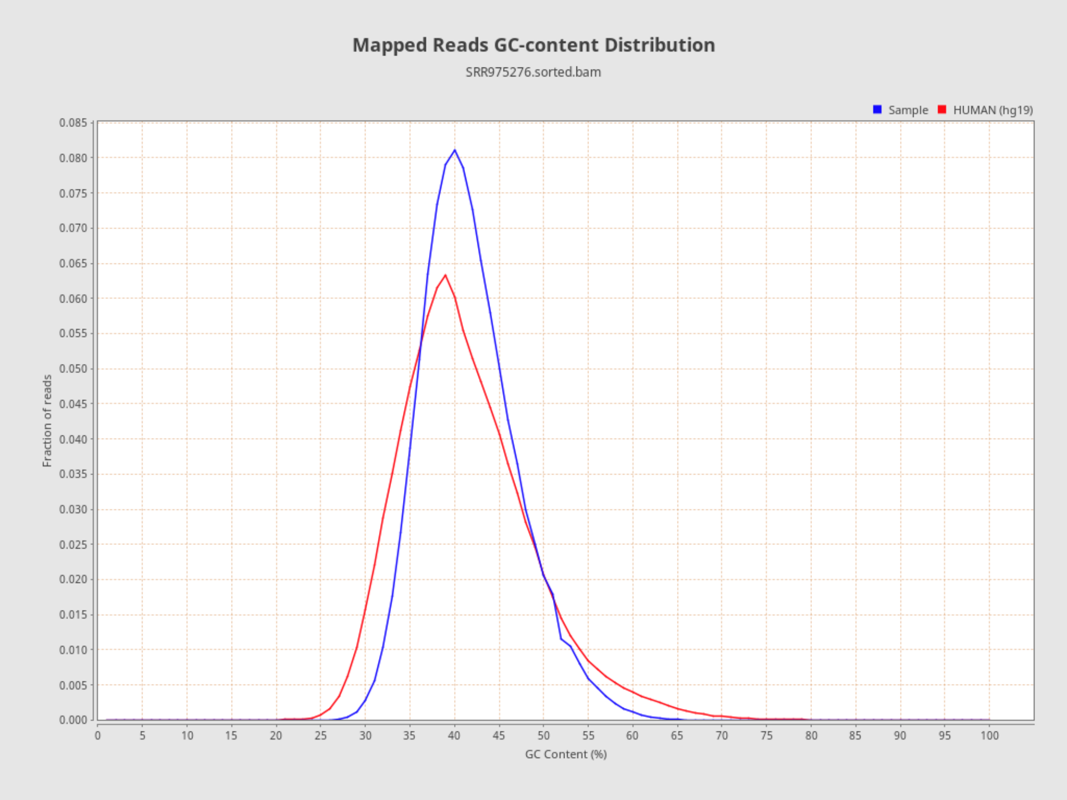
7. Results : Duplication Rate Histogram



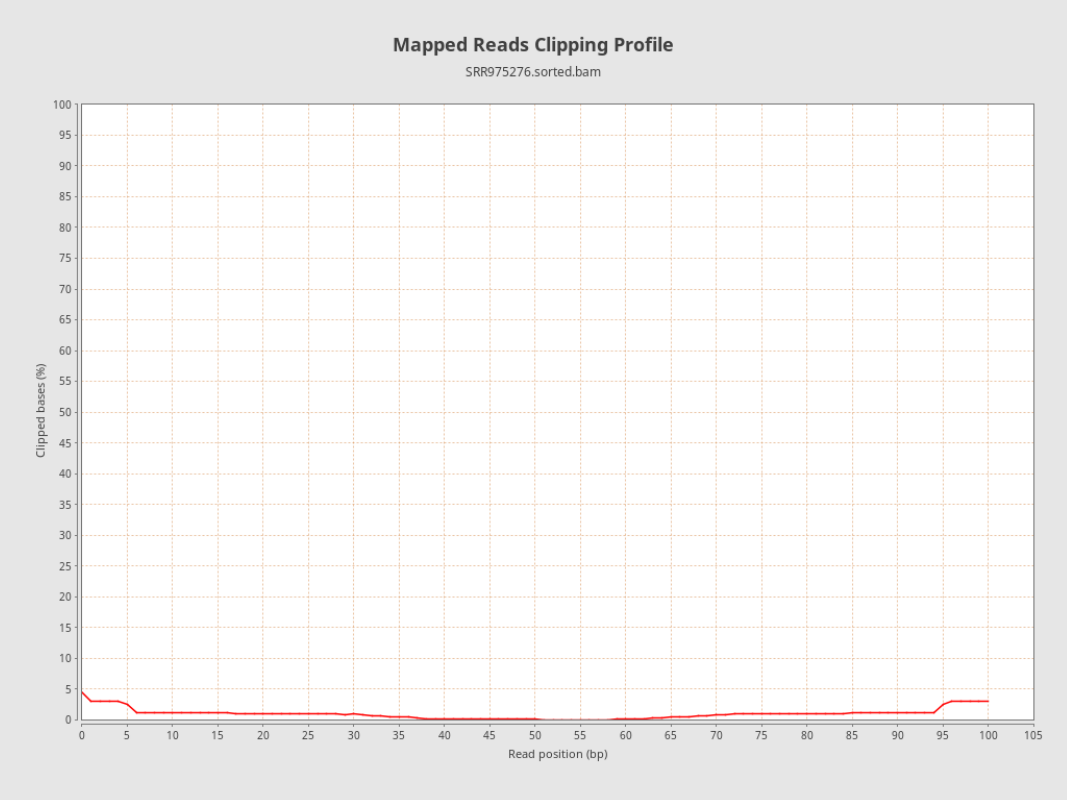
8. Results : Mapped Reads Nucleotide Content



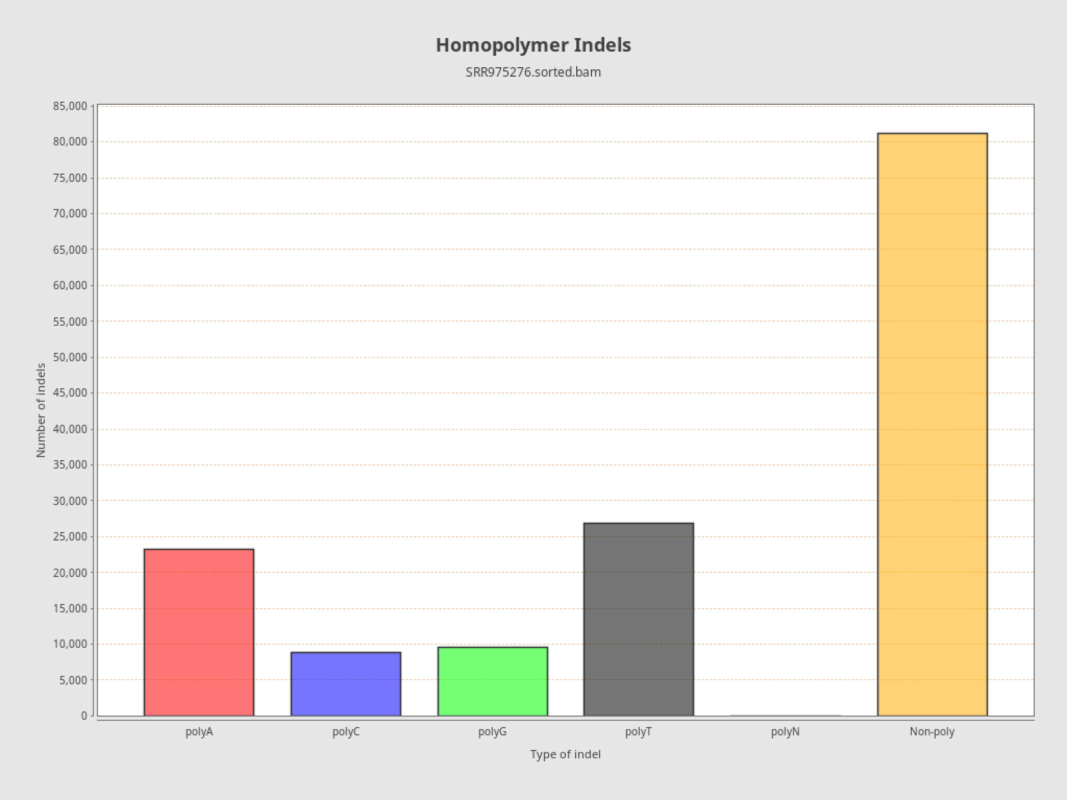
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

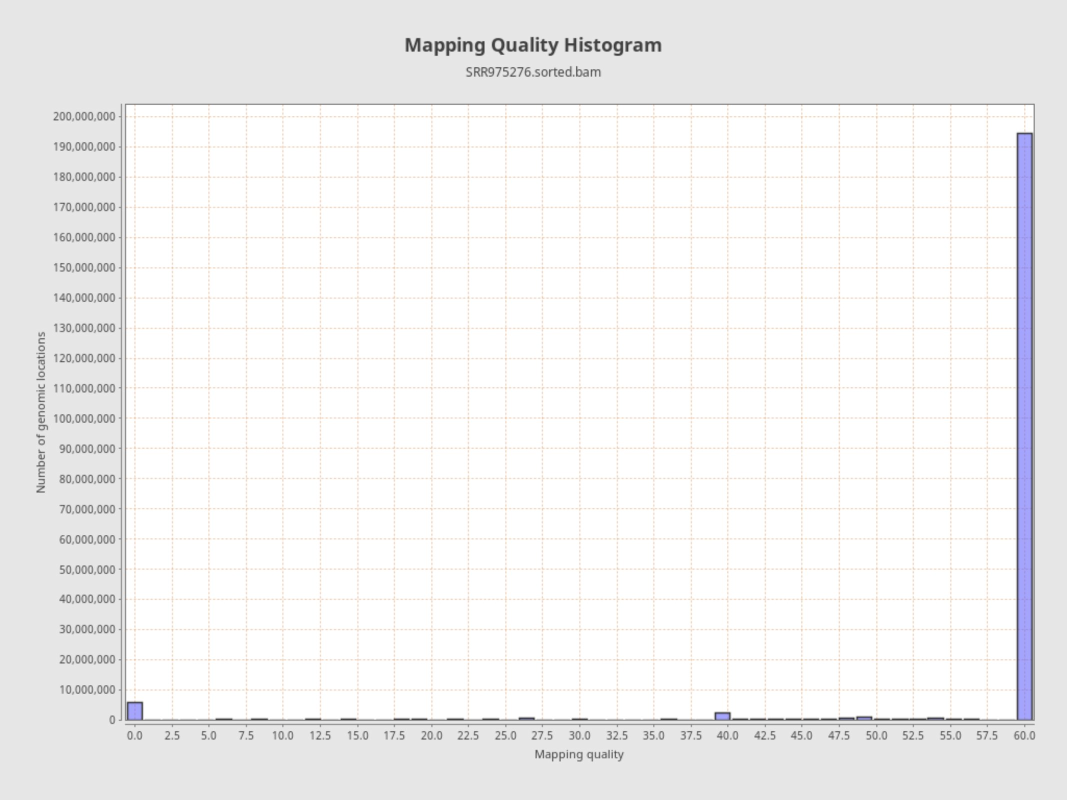


11. Results : Homopolymer Indels

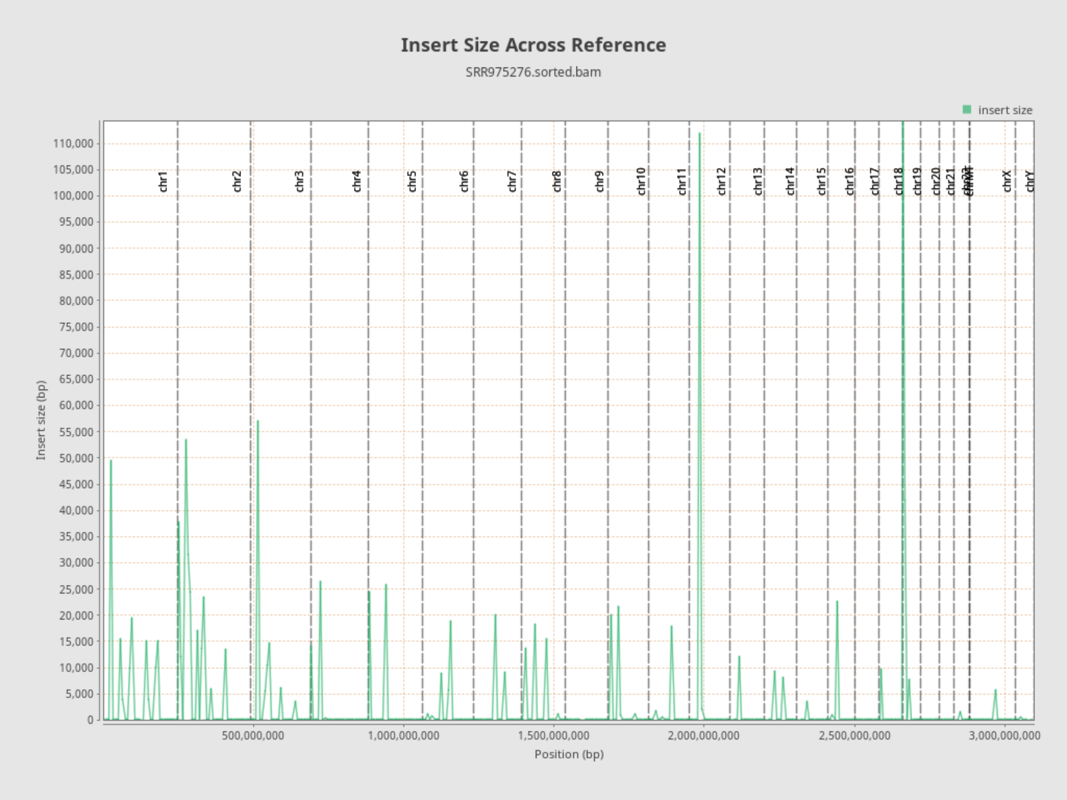


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram