Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 04:33:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975322.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_SRR975322 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975322_1.fastq.gz SRR975322_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 04:33:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975322.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,099,056
Mapped reads	4,053,995 / 98.9%
Unmapped reads	45,061 / 1.1%
Mapped paired reads	4,053,995 / 98.9%
Mapped reads, first in pair	2,026,231 / 49.43%
Mapped reads, second in pair	2,027,764 / 49.47%
Mapped reads, both in pair	4,038,856 / 98.53%
Mapped reads, singletons	15,139 / 0.37%
Secondary alignments	0
Supplementary alignments	30,210 / 0.74%
Read min/max/mean length	30 / 101 / 101.3
Duplicated reads (estimated)	312,714 / 7.63%
Duplication rate	3.79%
Clipped reads	2,411,392 / 58.83%

2.2. ACGT Content

Number/percentage of A's	113,110,040 / 29.56%
Number/percentage of C's	77,436,949 / 20.24%
Number/percentage of T's	111,405,466 / 29.12%
Number/percentage of G's	80,629,660 / 21.07%
Number/percentage of N's	7,757 / 0%

GC Percentage	41.31%

2.3. Coverage

Mean	0.1237
Standard Deviation	2.1614

2.4. Mapping Quality

Mean Mapping Quality	52.57

2.5. Insert size

Mean	91,712.56
Standard Deviation	2,884,149.47
P25/Median/P75	141 / 174 / 222

2.6. Mismatches and indels

General error rate	0.84%
Mismatches	3,068,718
Insertions	74,145
Mapped reads with at least one insertion	1.79%
Deletions	140,318
Mapped reads with at least one deletion	3.38%
Homopolymer indels	47.08%

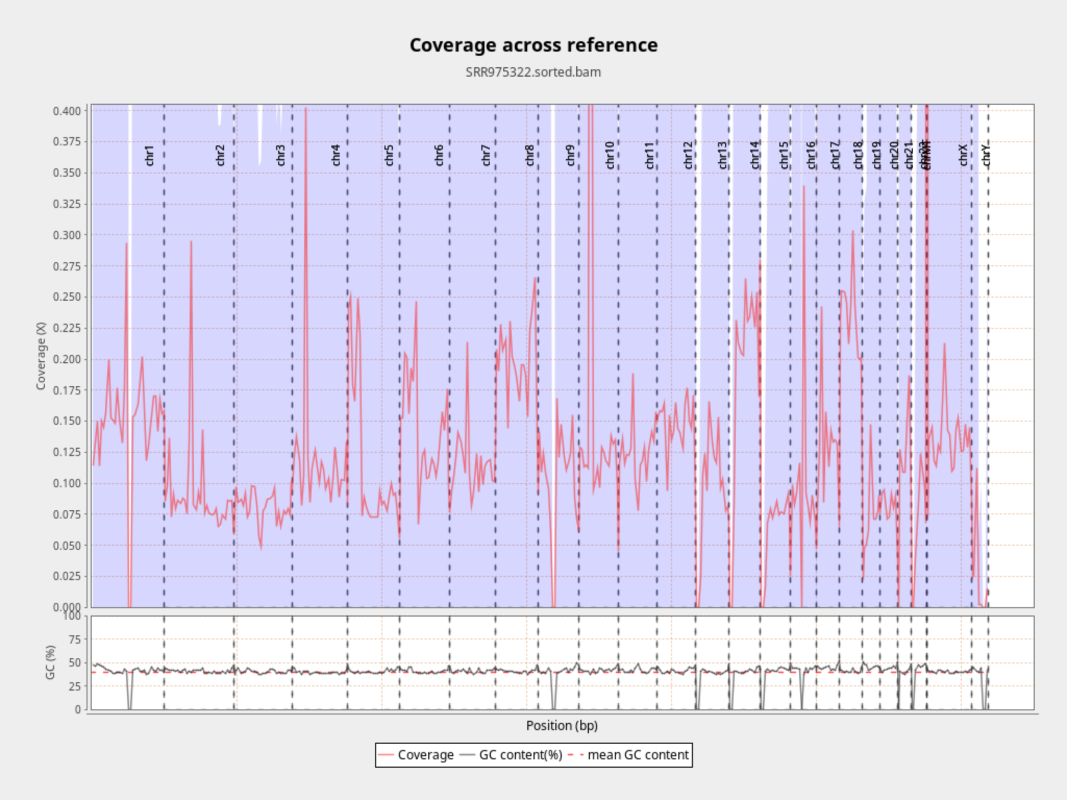
2.7. Chromosome stats

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

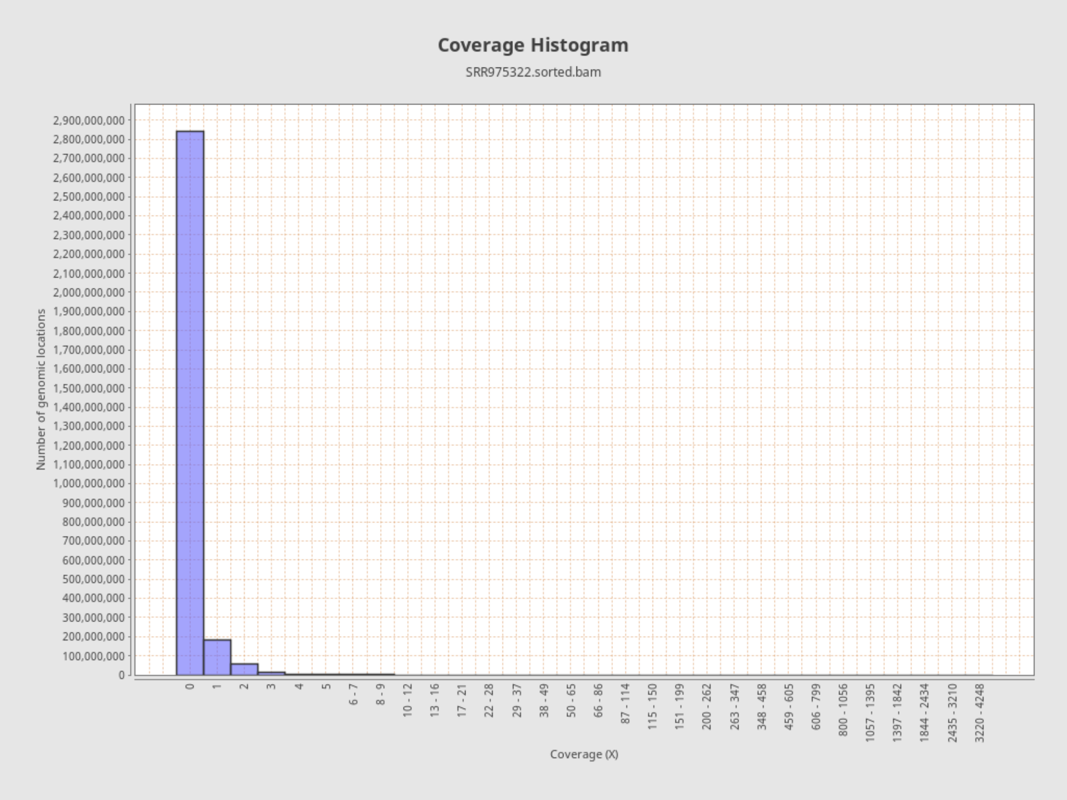
		bases	**coverage**	**deviation**
chr1	249250621	37215562	0.1493	1.8674
chr2	243199373	22520804	0.0926	1.5039
chr3	198022430	15959677	0.0806	0.5869
chr4	191154276	23036281	0.1205	1.6418
chr5	180915260	21111351	0.1167	0.4527
chr6	171115067	24604317	0.1438	1.4982
chr7	159138663	18236306	0.1146	1.9365
chr8	146364022	29128915	0.199	0.7937
chr9	141213431	14581084	0.1033	1.6902
chr10	135534747	23037153	0.17	8.202
chr11	135006516	16742918	0.124	1.5293
chr12	133851895	19869552	0.1484	0.5013
chr13	115169878	10954021	0.0951	0.3931
chr14	107349540	20119433	0.1874	0.6068
chr15	102531392	6436394	0.0628	0.3142
chr16	90354753	8912300	0.0986	1.6849
chr17	81195210	10674696	0.1315	2.1936
chr18	78077248	18497400	0.2369	2.3299
chr19	59128983	4335083	0.0733	1.0092
chr20	63025520	5132514	0.0814	0.527
chr21	48129895	5723346	0.1189	0.762
chr22	51304566	3650923	0.0712	0.3575
chrMT	16571	98624	5.9516	5.24
chrX	155270560	20914877	0.1347	0.8121

chrY	59373566	1342440	0.0226	1.4151

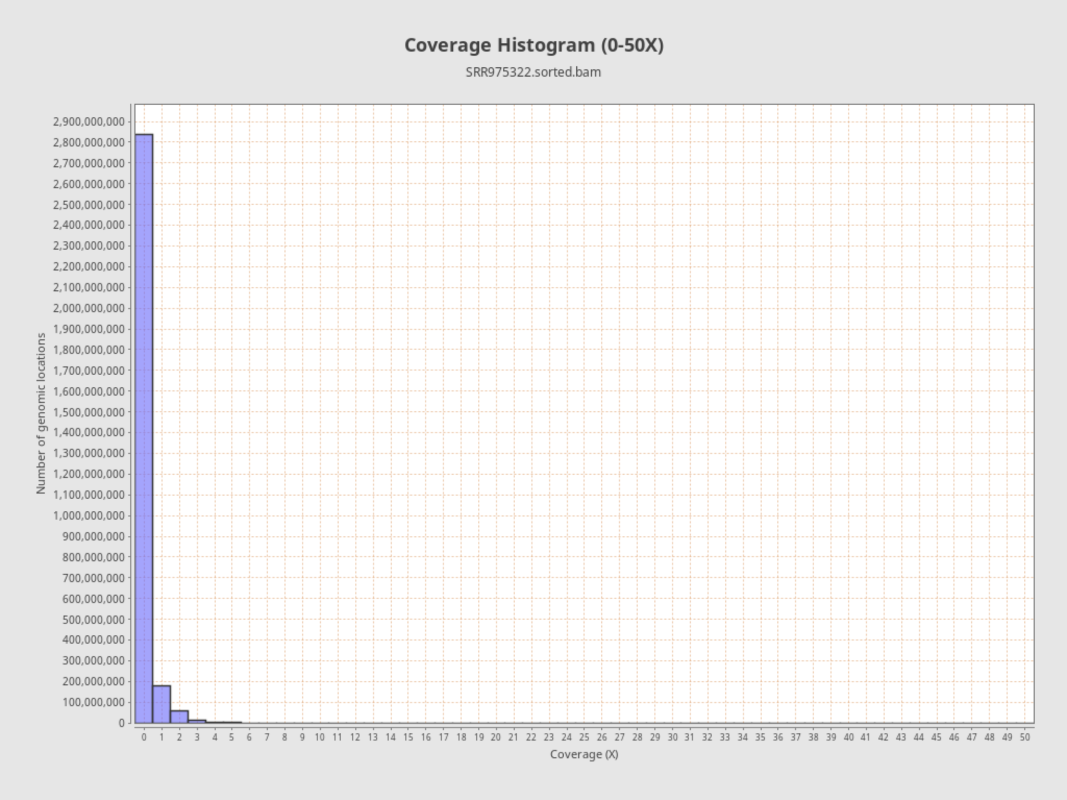
3. Results : Coverage across reference



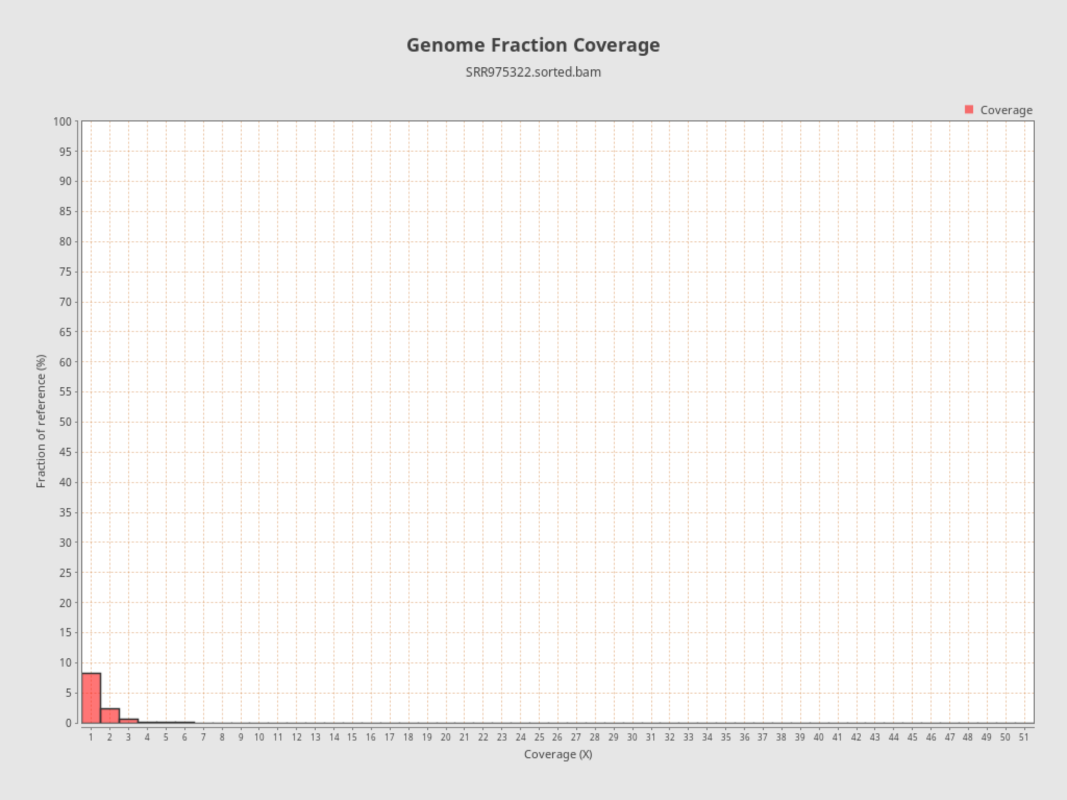
4. Results : Coverage Histogram



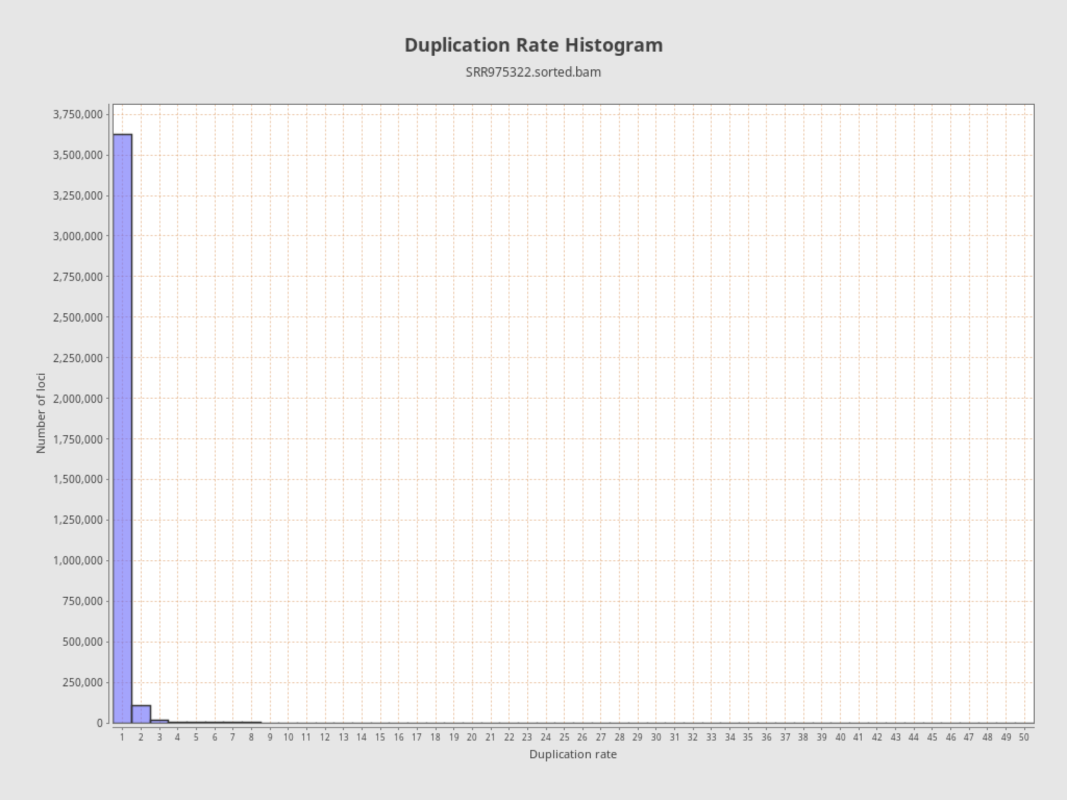
5. Results : Coverage Histogram (0-50X)



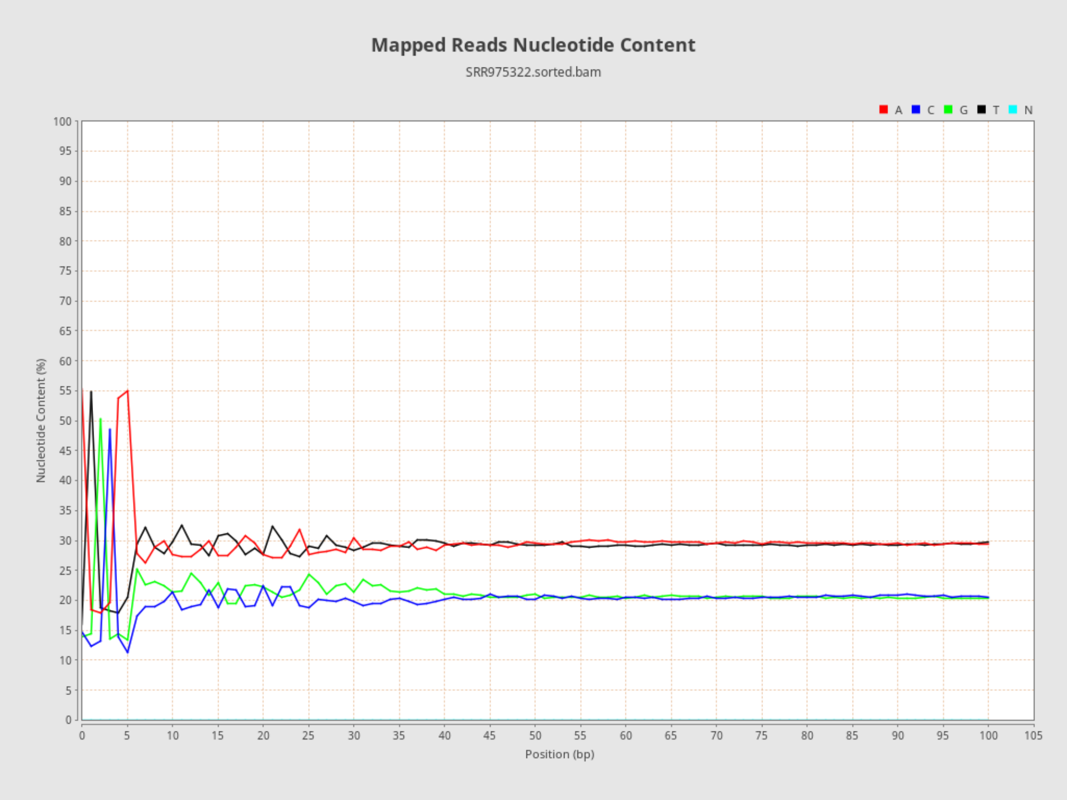
6. Results : Genome Fraction Coverage



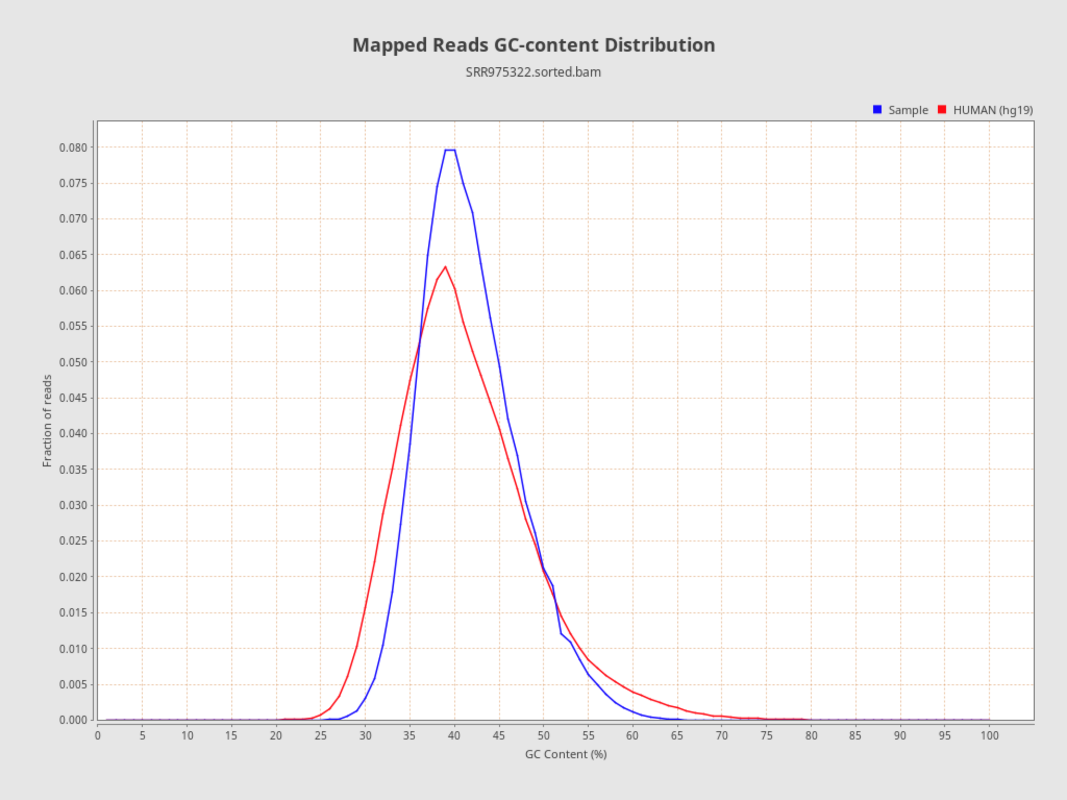
7. Results : Duplication Rate Histogram



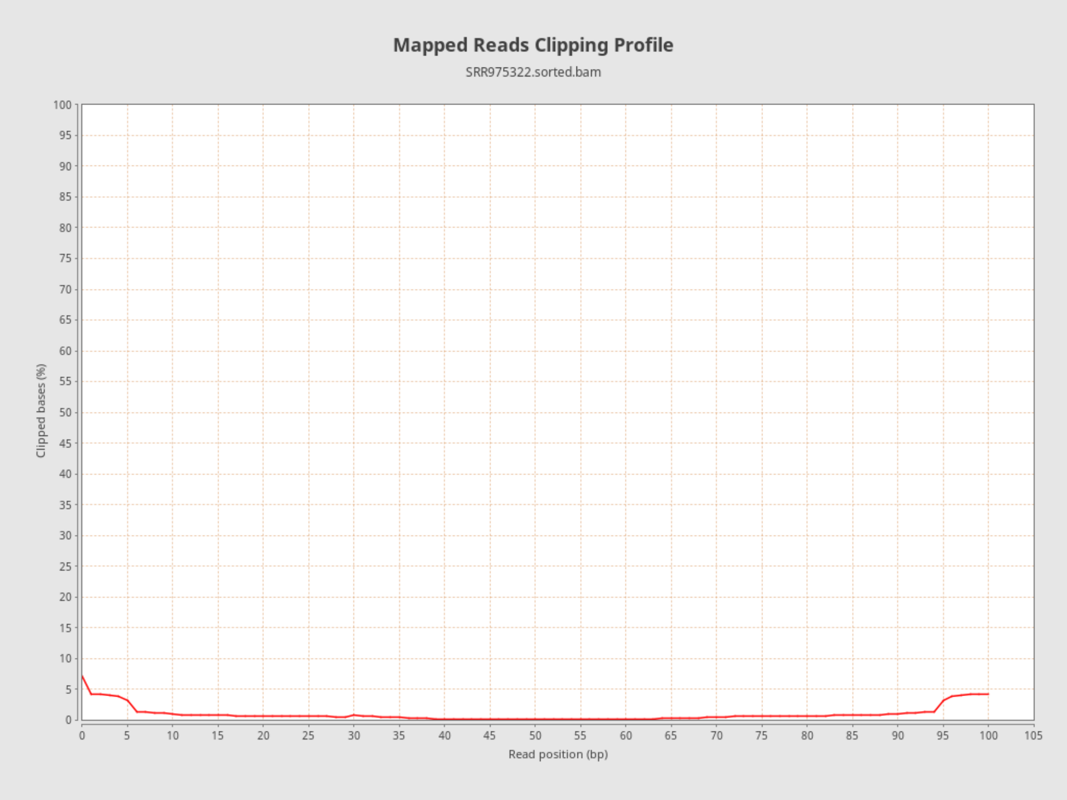
8. Results : Mapped Reads Nucleotide Content



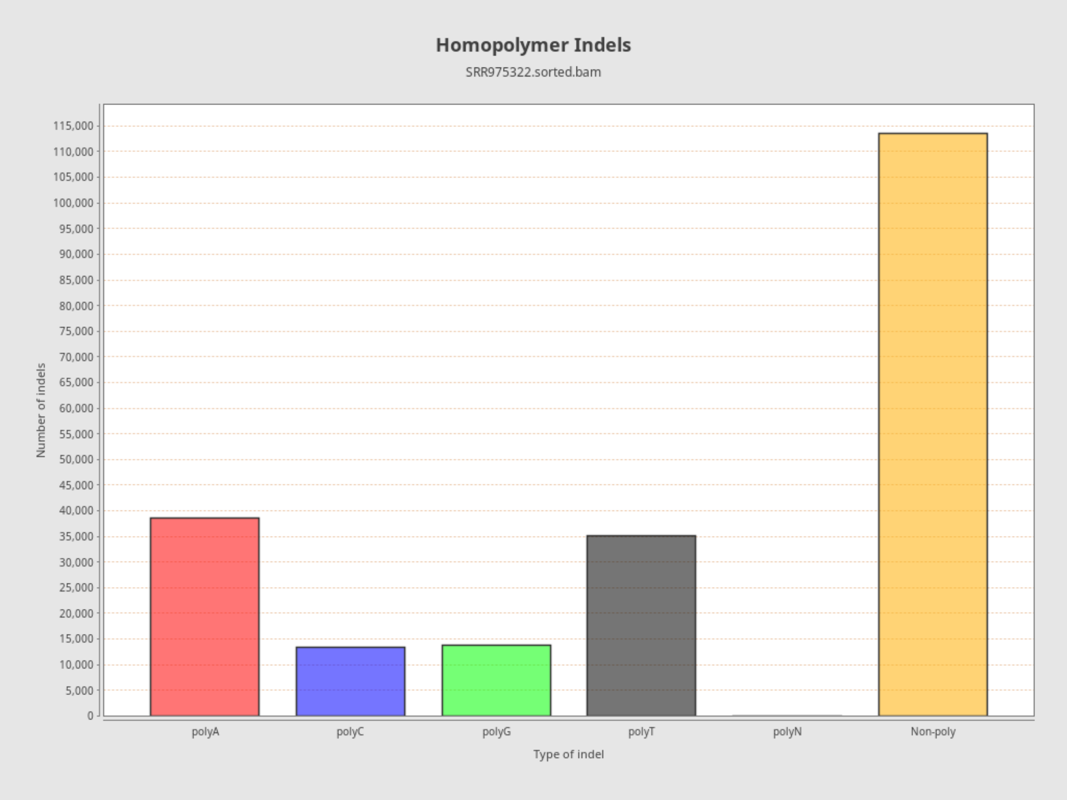
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

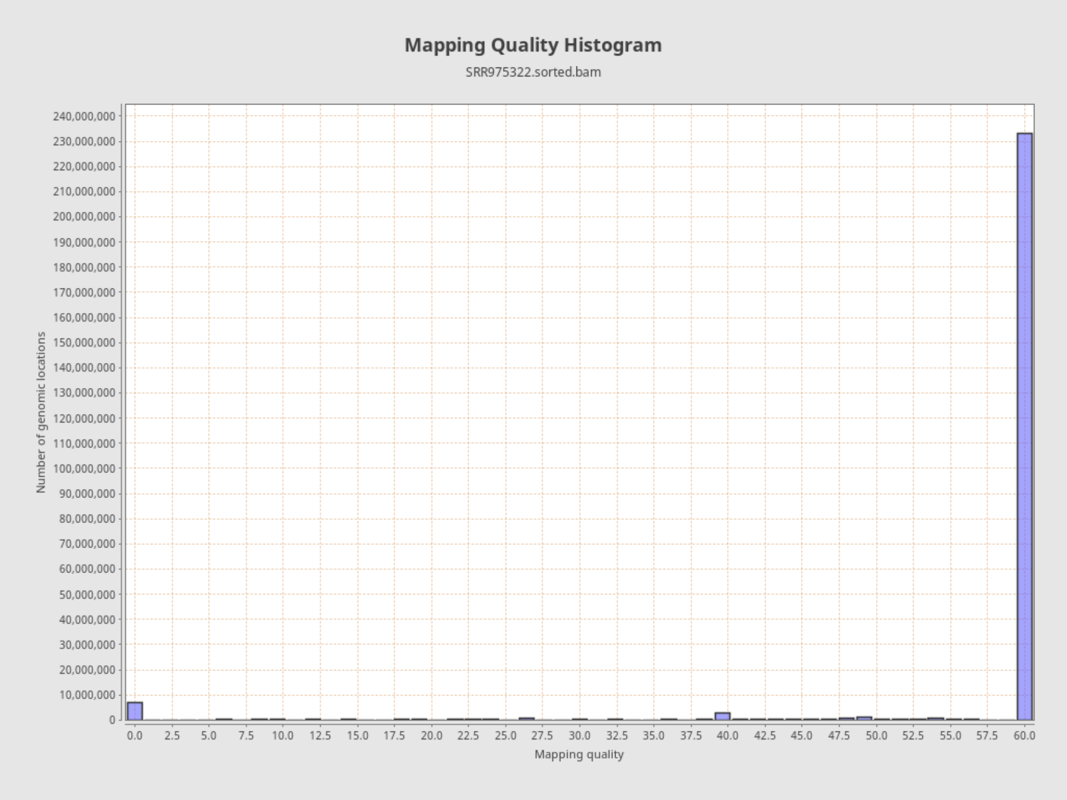


11. Results : Homopolymer Indels

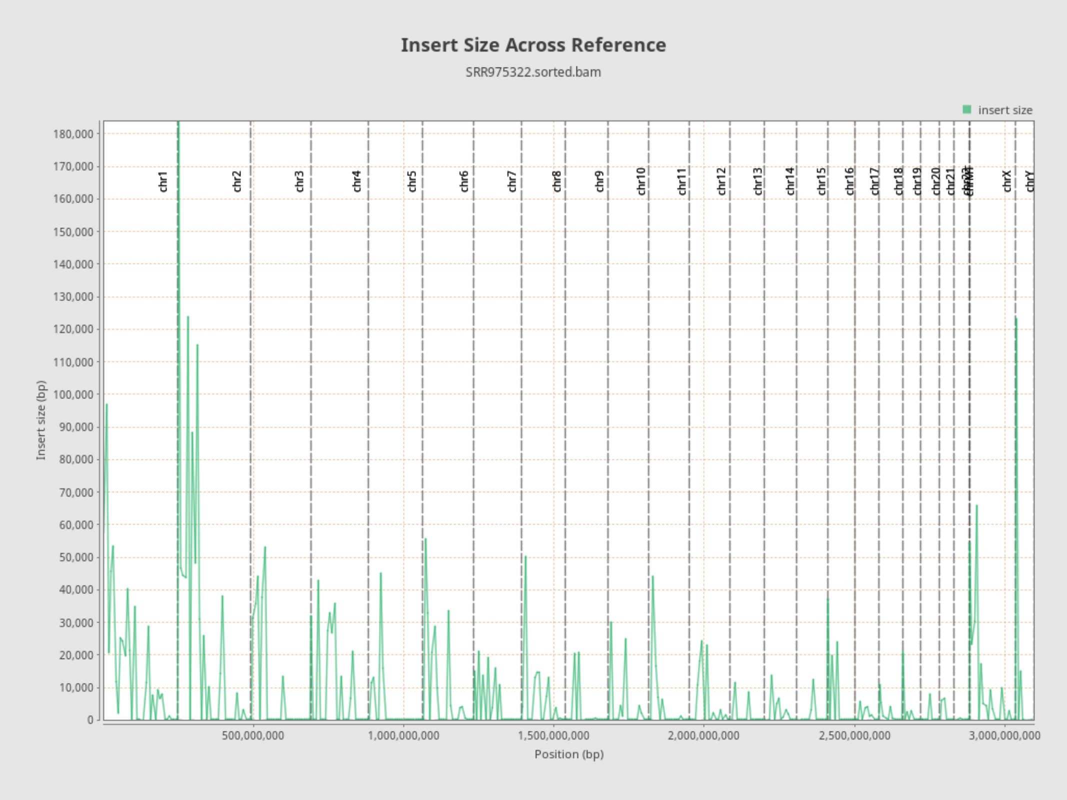


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram