Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 05:06:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975326.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_SRR975326 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975326_1.fastq.gz SRR975326_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 05:06:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975326.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,822,330
Mapped reads	4,782,501 / 99.17%
Unmapped reads	39,829 / 0.83%
Mapped paired reads	4,782,501 / 99.17%
Mapped reads, first in pair	2,390,830 / 49.58%
Mapped reads, second in pair	2,391,671 / 49.6%
Mapped reads, both in pair	4,770,392 / 98.92%
Mapped reads, singletons	12,109 / 0.25%
Secondary alignments	0
Supplementary alignments	59,144 / 1.23%
Read min/max/mean length	30 / 101 / 101.51
Duplicated reads (estimated)	219,164 / 4.54%
Duplication rate	1.77%
Clipped reads	2,580,986 / 53.52%

2.2. ACGT Content

Number/percentage of A's	139,139,787 / 29.95%
Number/percentage of C's	92,711,397 / 19.96%
Number/percentage of T's	139,872,677 / 30.11%
Number/percentage of G's	92,804,831 / 19.98%
Number/percentage of N's	9,722 / 0%

GC Percentage	39.94%

2.3. Coverage

Mean	0.1501
Standard Deviation	2.3699

2.4. Mapping Quality

Mean Mapping Quality	53.26

2.5. Insert size

Mean	121,558.62
Standard Deviation	3,331,003.14
P25/Median/P75	141 / 171 / 214

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	2,297,892
Insertions	57,195
Mapped reads with at least one insertion	1.17%
Deletions	62,876
Mapped reads with at least one deletion	1.28%
Homopolymer indels	38.77%

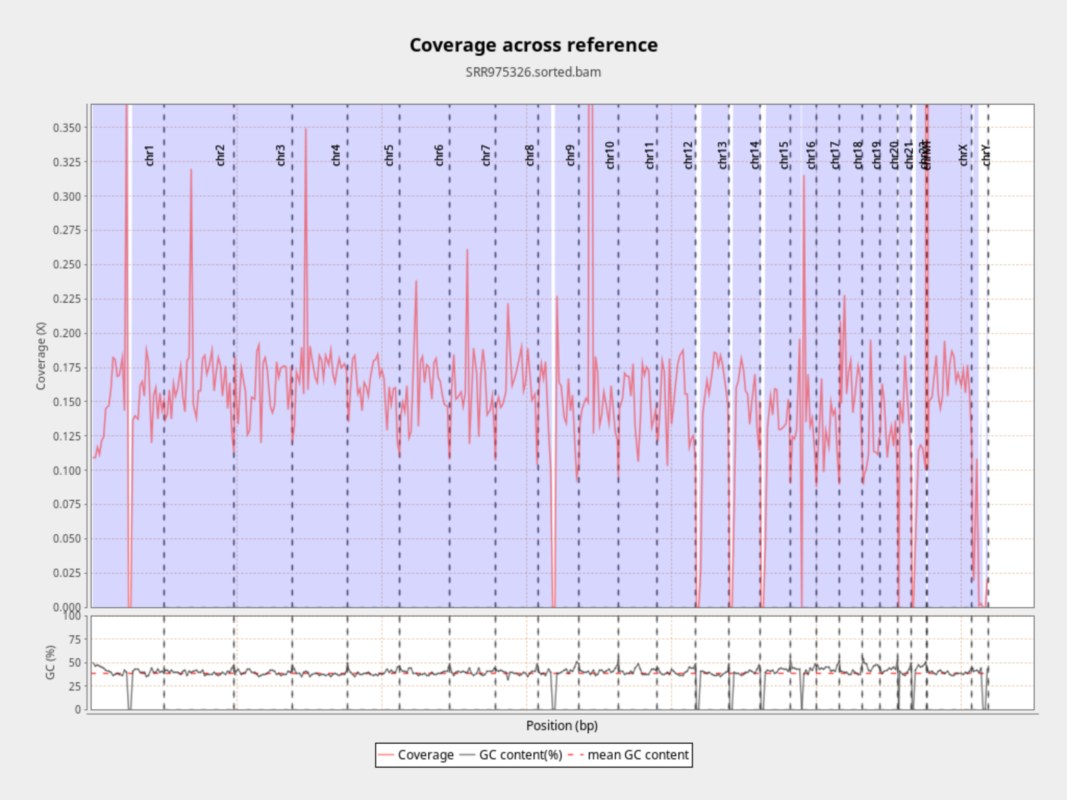
2.7. Chromosome stats

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

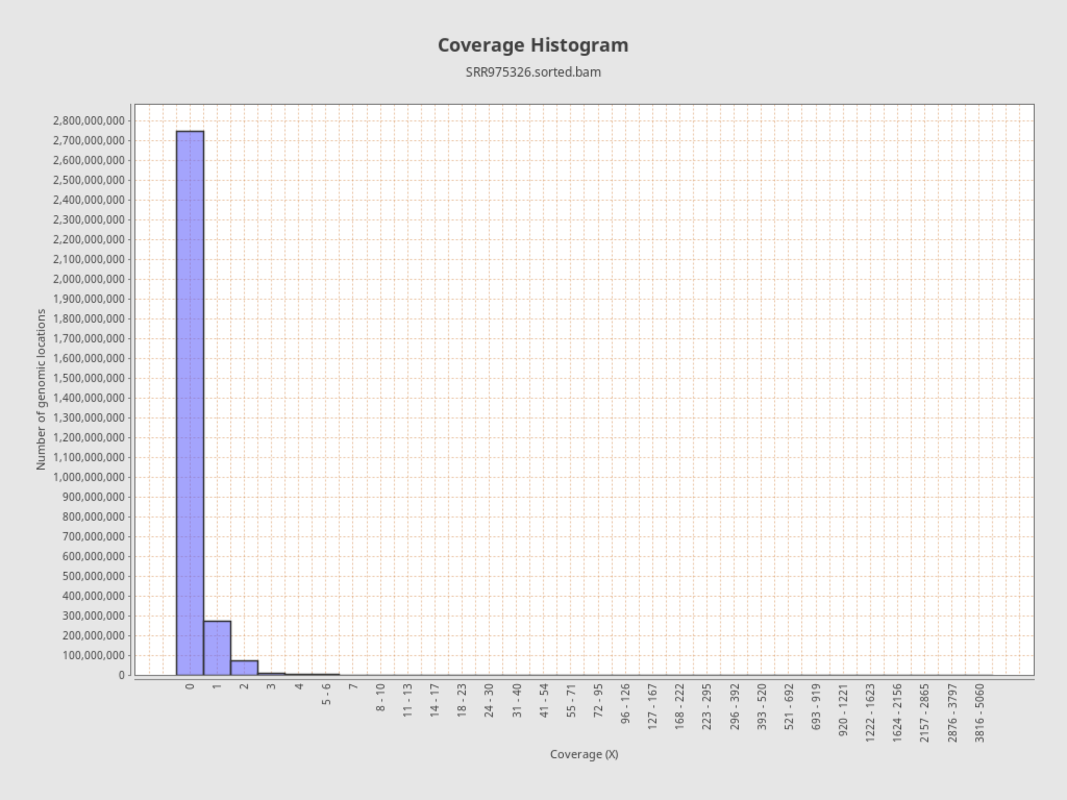
		bases	**coverage**	**deviation**
chr1	249250621	36492416	0.1464	4.9736
chr2	243199373	40278737	0.1656	1.2323
chr3	198022430	31728734	0.1602	0.6525
chr4	191154276	34046256	0.1781	1.5237
chr5	180915260	28984021	0.1602	0.4755
chr6	171115067	27618587	0.1614	0.9354
chr7	159138663	25440619	0.1599	2.0856
chr8	146364022	24124568	0.1648	3.5725
chr9	141213431	18992858	0.1345	1.8743
chr10	135534747	25489546	0.1881	6.4484
chr11	135006516	20637374	0.1529	1.0111
chr12	133851895	20182277	0.1508	0.459
chr13	115169878	15911705	0.1382	0.4305
chr14	107349540	13776547	0.1283	0.4507
chr15	102531392	11774763	0.1148	0.393
chr16	90354753	12617591	0.1396	1.3684
chr17	81195210	10369254	0.1277	0.7334
chr18	78077248	13178165	0.1688	2.4235
chr19	59128983	7047775	0.1192	2.279
chr20	63025520	8212481	0.1303	0.5499
chr21	48129895	6405654	0.1331	0.7244
chr22	51304566	4085370	0.0796	0.3394
chrMT	16571	525050	31.6849	8.1975
chrX	155270560	25398000	0.1636	0.6785

chrY	59373566	1363727	0.023	1.2646

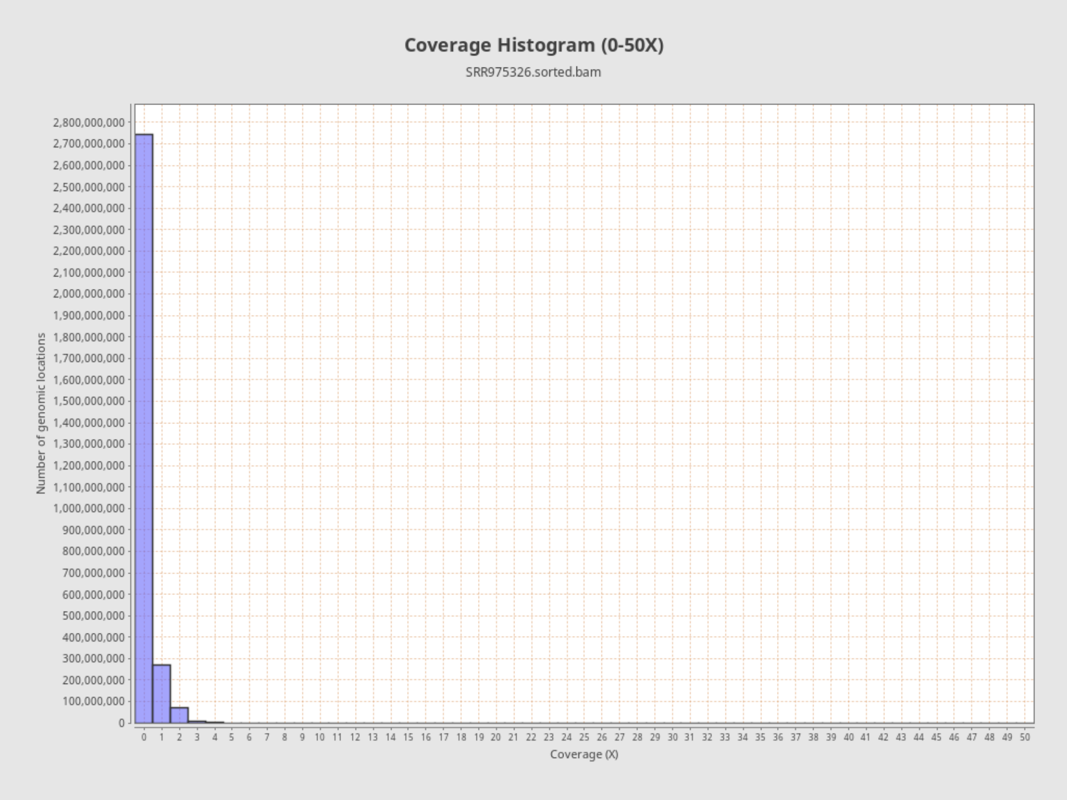
3. Results : Coverage across reference



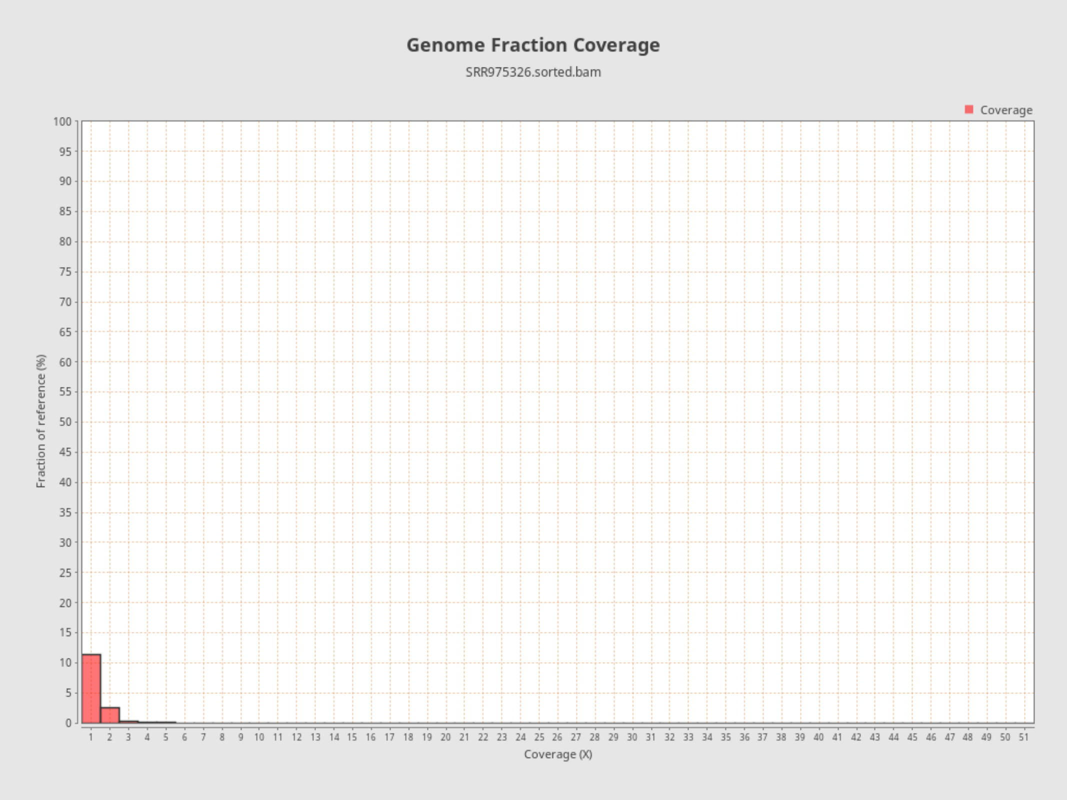
4. Results : Coverage Histogram



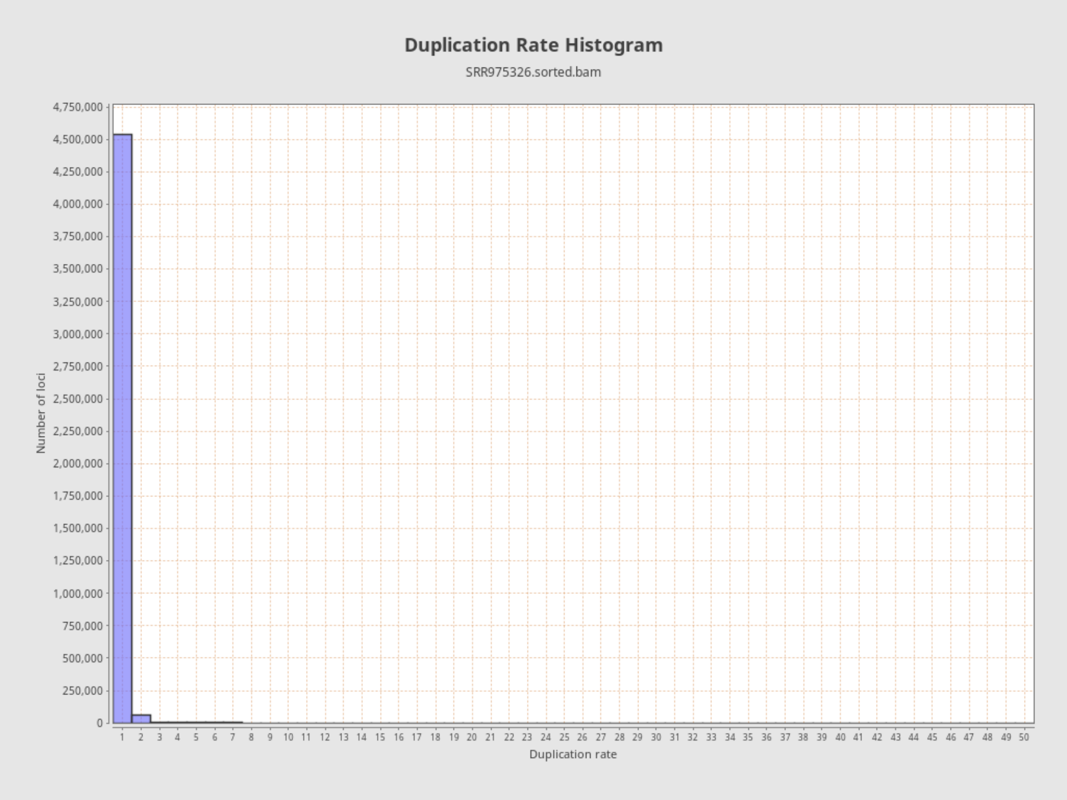
5. Results : Coverage Histogram (0-50X)



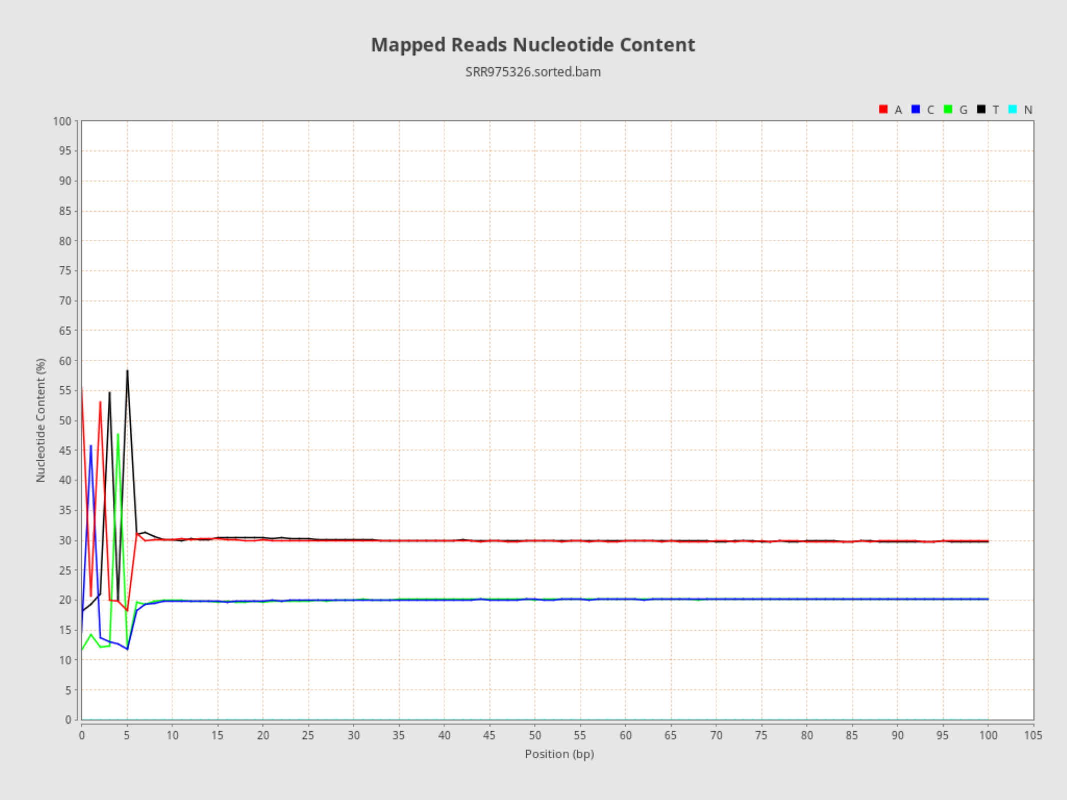
6. Results : Genome Fraction Coverage



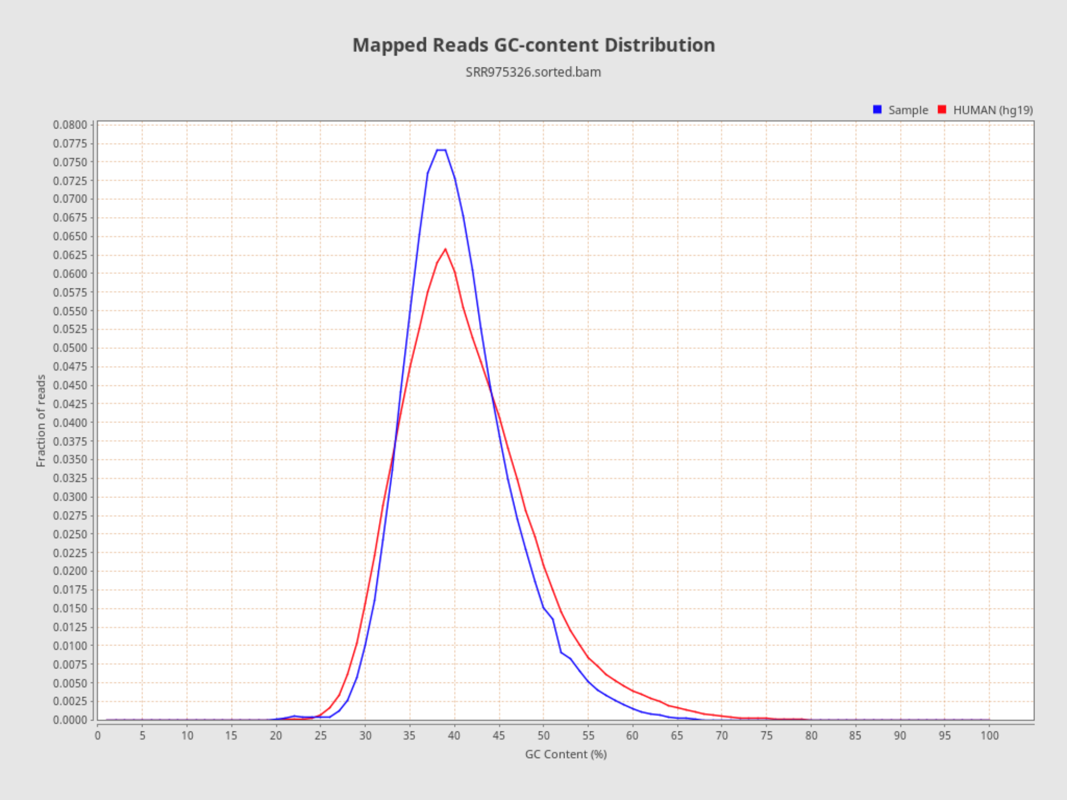
7. Results : Duplication Rate Histogram



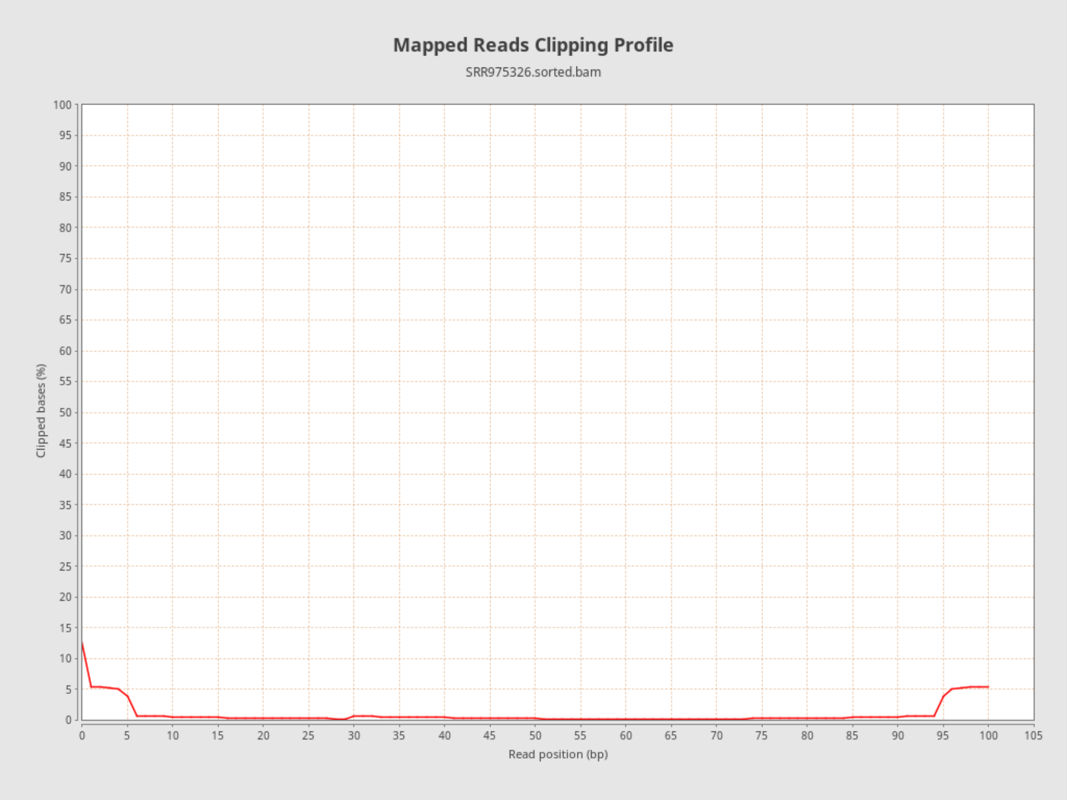
8. Results : Mapped Reads Nucleotide Content



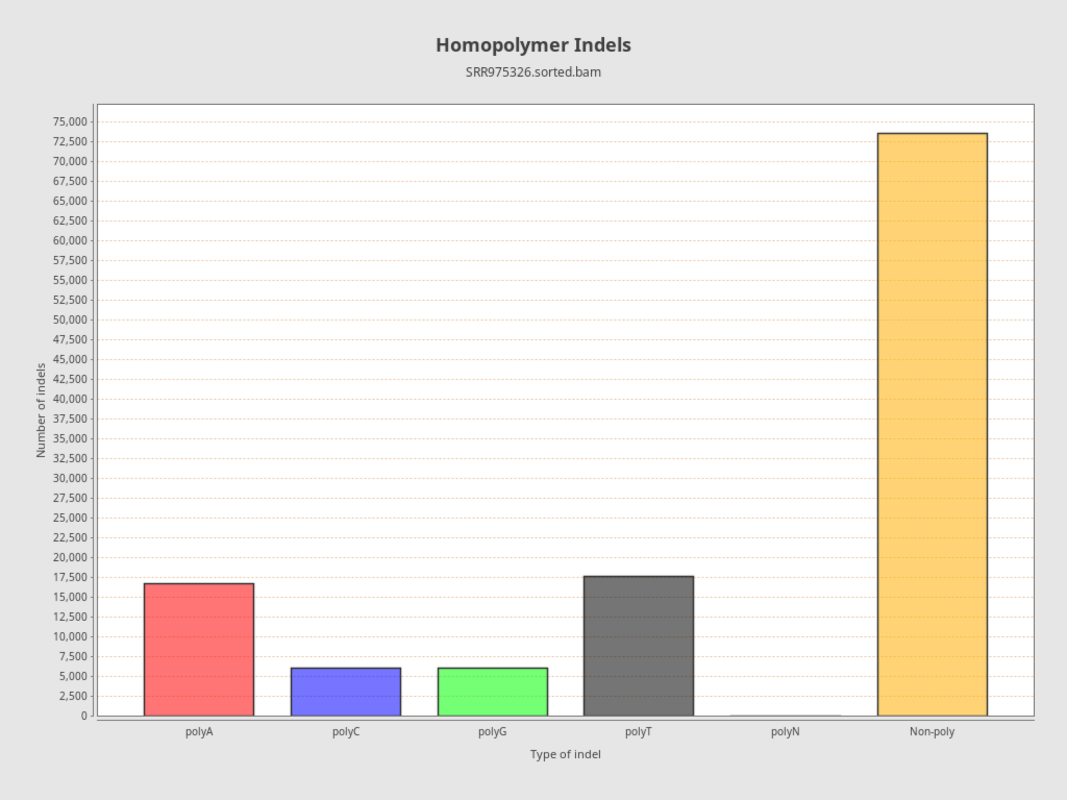
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

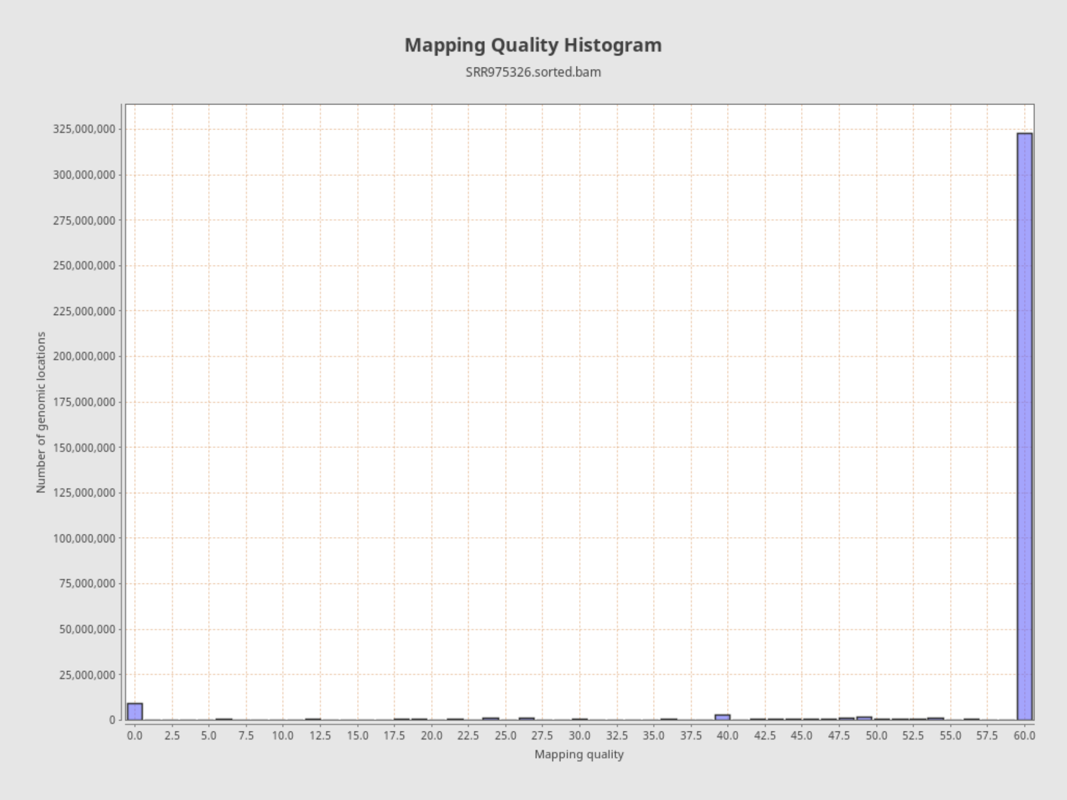


11. Results : Homopolymer Indels

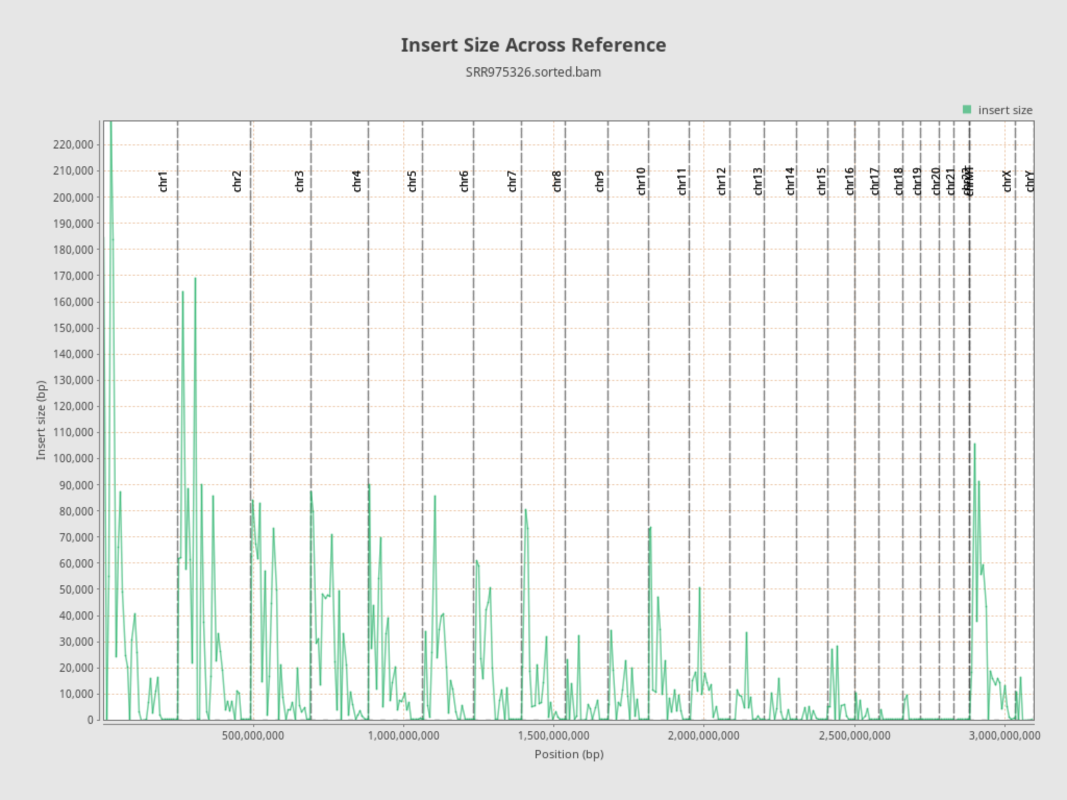


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram