Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 05:28:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975329.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_SRR975329 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975329_1.fastq.gz SRR975329_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 05:28:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975329.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,381,998
Mapped reads	3,326,347 / 98.35%
Unmapped reads	55,651 / 1.65%
Mapped paired reads	3,326,347 / 98.35%
Mapped reads, first in pair	1,662,173 / 49.15%
Mapped reads, second in pair	1,664,174 / 49.21%
Mapped reads, both in pair	3,308,964 / 97.84%
Mapped reads, singletons	17,383 / 0.51%
Secondary alignments	0
Supplementary alignments	24,544 / 0.73%
Read min/max/mean length	30 / 101 / 101.29
Duplicated reads (estimated)	246,243 / 7.28%
Duplication rate	3.52%
Clipped reads	2,094,949 / 61.94%

2.2. ACGT Content

Number/percentage of A's	89,720,570 / 29.73%
Number/percentage of C's	58,074,591 / 19.24%
Number/percentage of T's	89,951,689 / 29.8%
Number/percentage of G's	64,060,286 / 21.23%
Number/percentage of N's	6,696 / 0%

GC Percentage	40.47%

2.3. Coverage

Mean	0.0976
Standard Deviation	1.5648

2.4. Mapping Quality

Mean Mapping Quality	52.46

2.5. Insert size

Mean	76,917.96
Standard Deviation	2,645,517.07
P25/Median/P75	134 / 166 / 211

2.6. Mismatches and indels

General error rate	0.89%
Mismatches	2,538,877
Insertions	61,766
Mapped reads with at least one insertion	1.79%
Deletions	103,796
Mapped reads with at least one deletion	3.04%
Homopolymer indels	44.21%

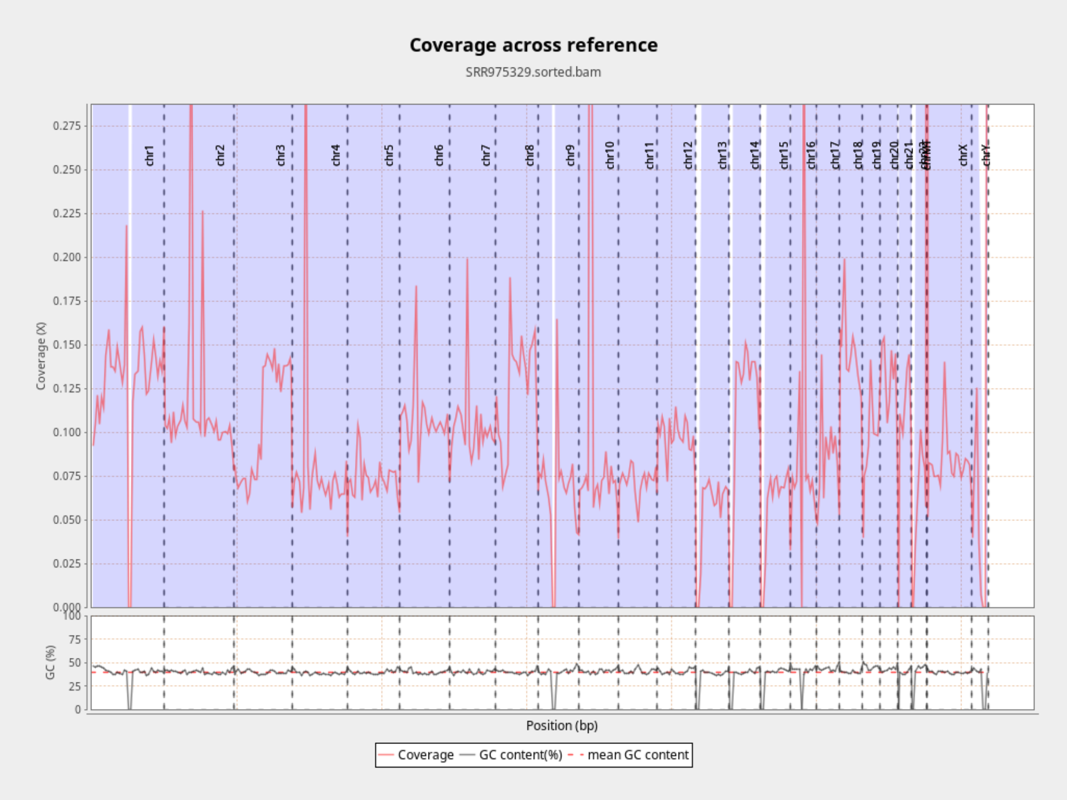
2.7. Chromosome stats

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

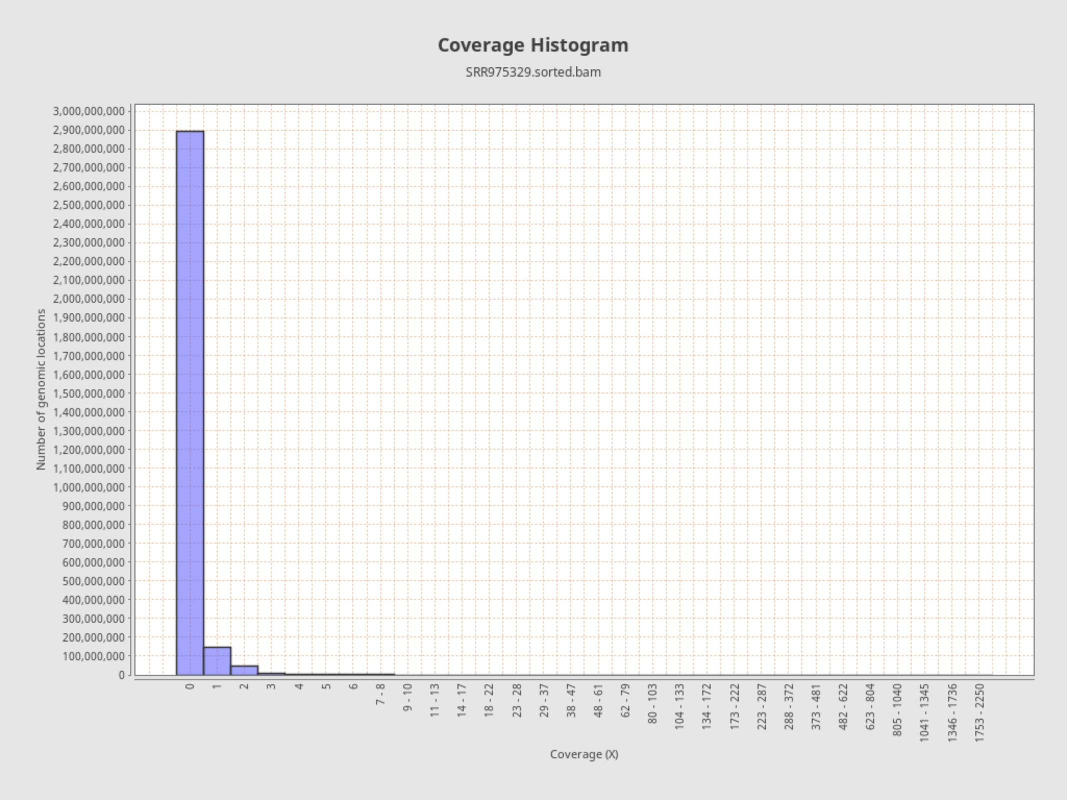
		bases	coverage	deviation
chr1	249250621	31881352	0.1279	1.4514
chr2	243199373	28564456	0.1175	2.0639
chr3	198022430	21223350	0.1072	0.4946
chr4	191154276	15685923	0.0821	1.6581
chr5	180915260	13354135	0.0738	0.3766
chr6	171115067	18353474	0.1073	0.9213
chr7	159138663	16451847	0.1034	1.5923
chr8	146364022	18526657	0.1266	0.7079
chr9	141213431	9396569	0.0665	1.7465
chr10	135534747	14052415	0.1037	4.6497
chr11	135006516	9721168	0.072	0.5909
chr12	133851895	13184878	0.0985	0.4097
chr13	115169878	6295383	0.0547	0.297
chr14	107349540	12107237	0.1128	0.5
chr15	102531392	5827597	0.0568	0.3002
chr16	90354753	8482151	0.0939	2.1084
chr17	81195210	6996381	0.0862	1.2168
chr18	78077248	11381957	0.1458	2.0582
chr19	59128983	5643112	0.0954	0.7841
chr20	63025520	8302616	0.1317	0.6074
chr21	48129895	5193669	0.1079	0.6249
chr22	51304566	3040964	0.0593	0.3884
chrMT	16571	80206	4.8401	5.6005
chrX	155270560	12843707	0.0827	0.5392

chrY	59373566	5430626	0.0915	2.3711

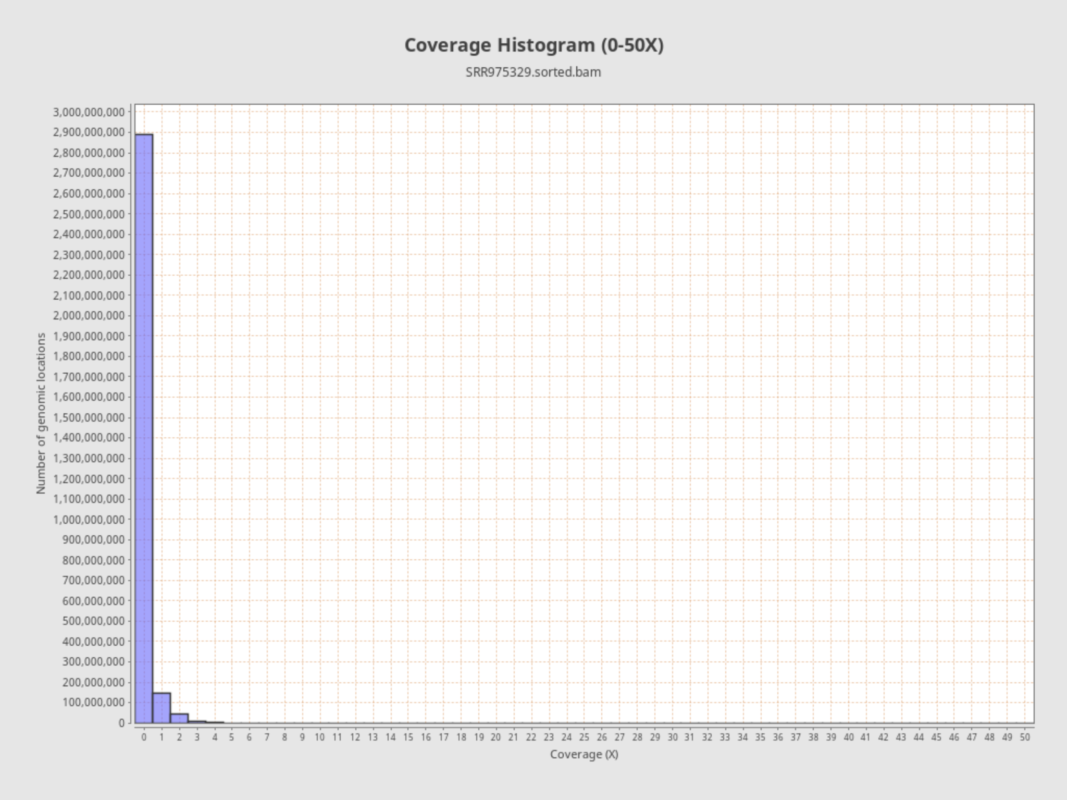
3. Results : Coverage across reference



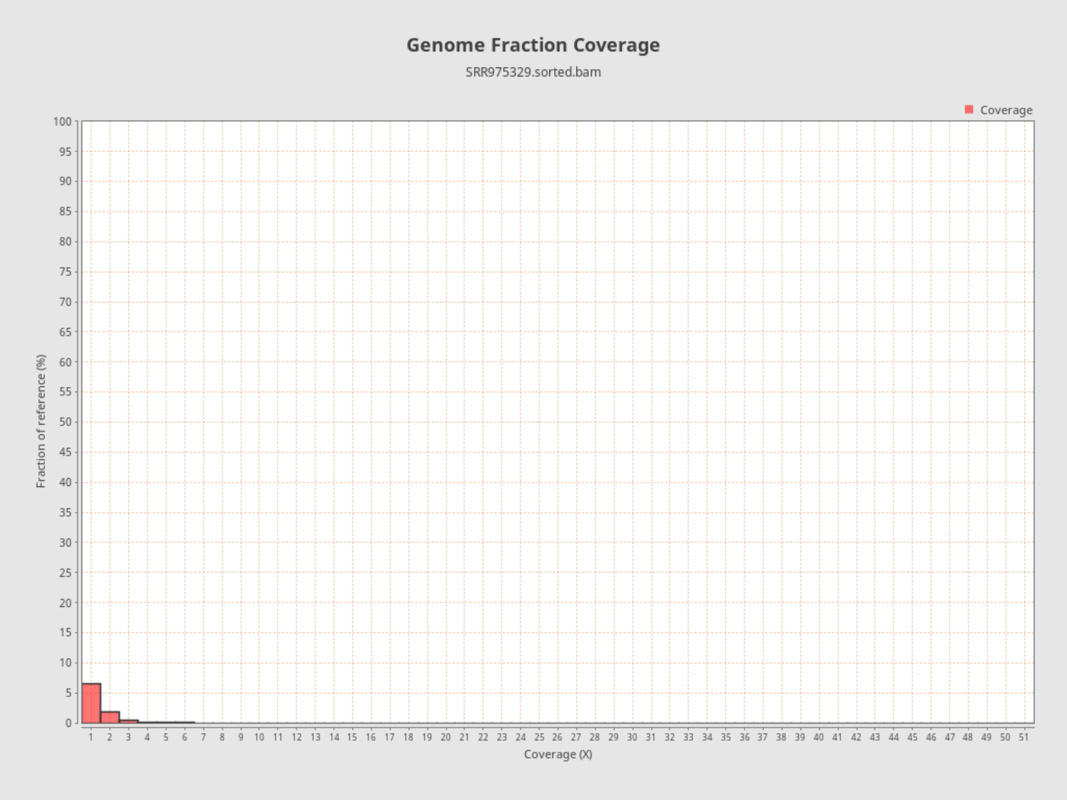
4. Results : Coverage Histogram



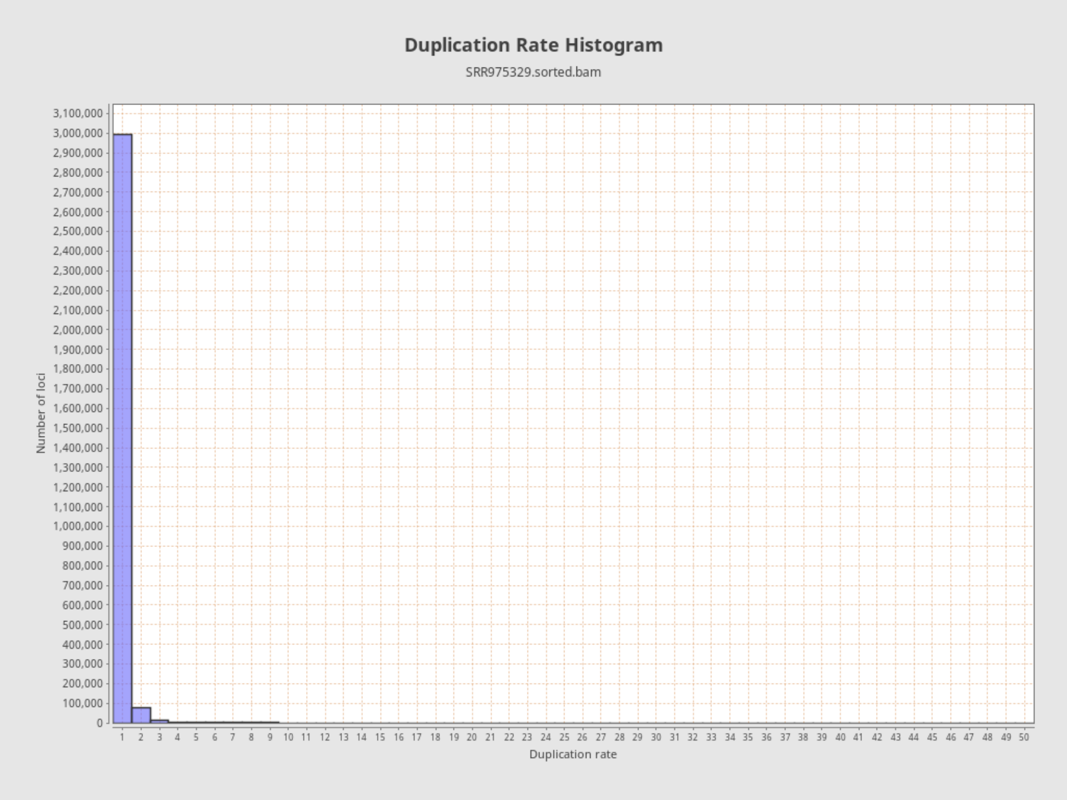
5. Results : Coverage Histogram (0-50X)



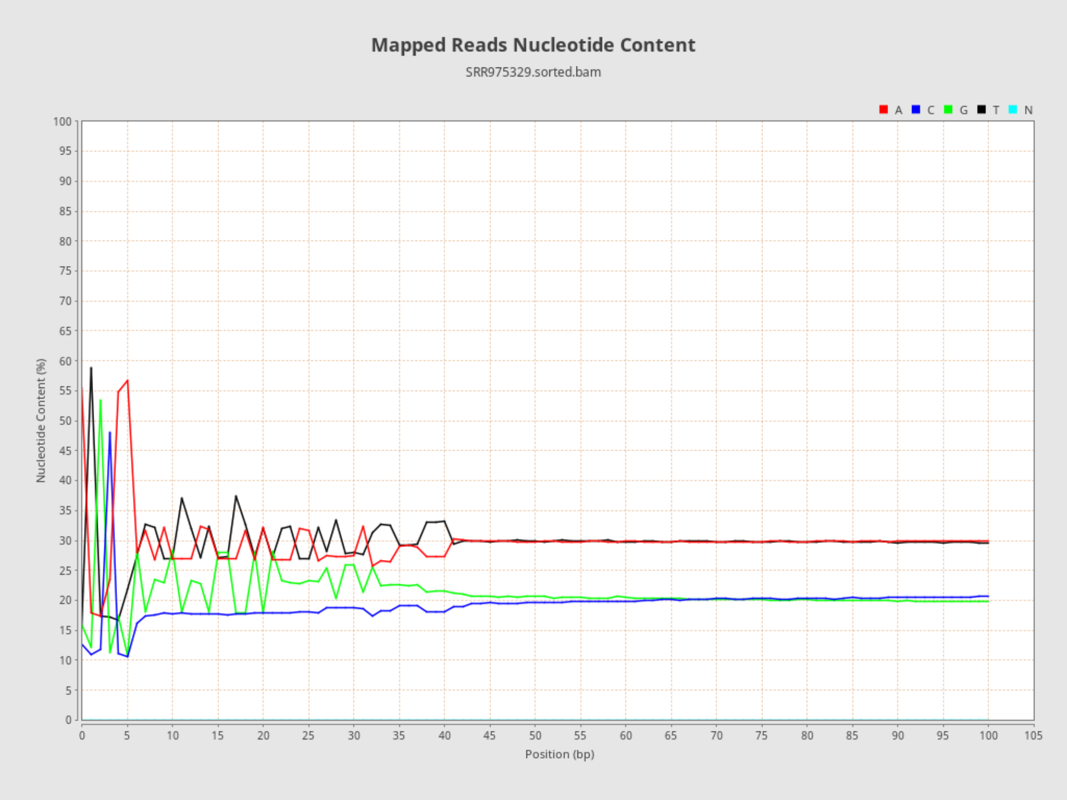
6. Results : Genome Fraction Coverage



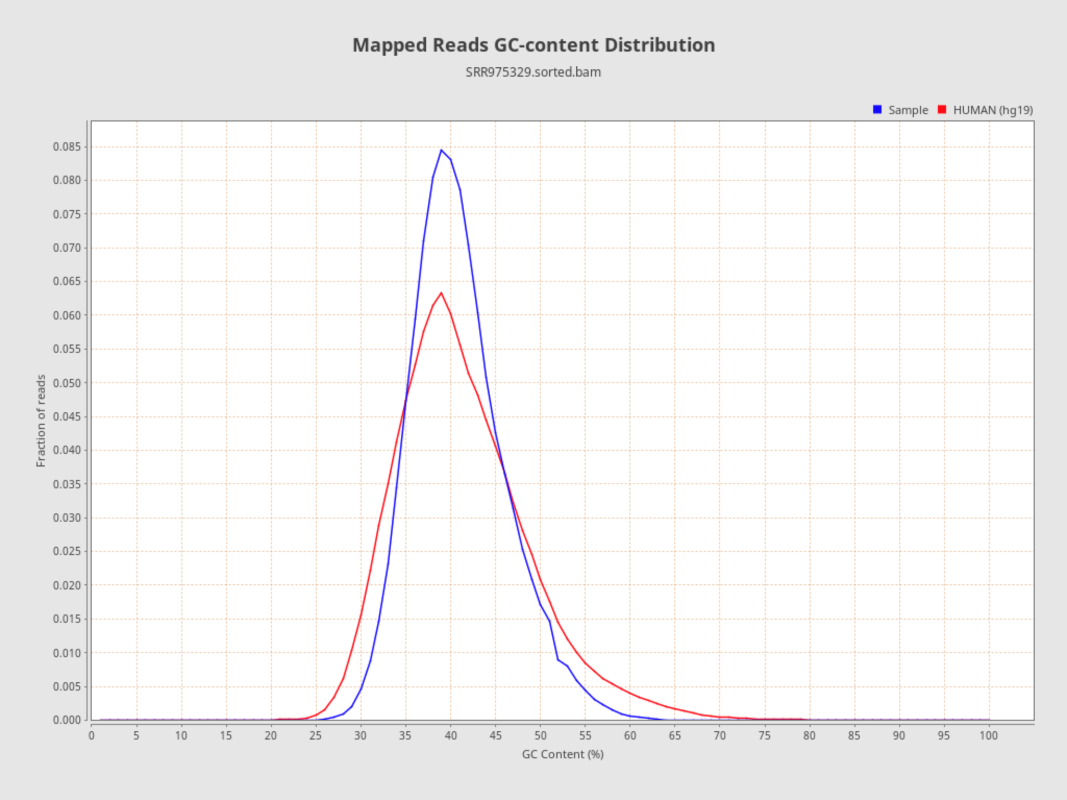
7. Results : Duplication Rate Histogram



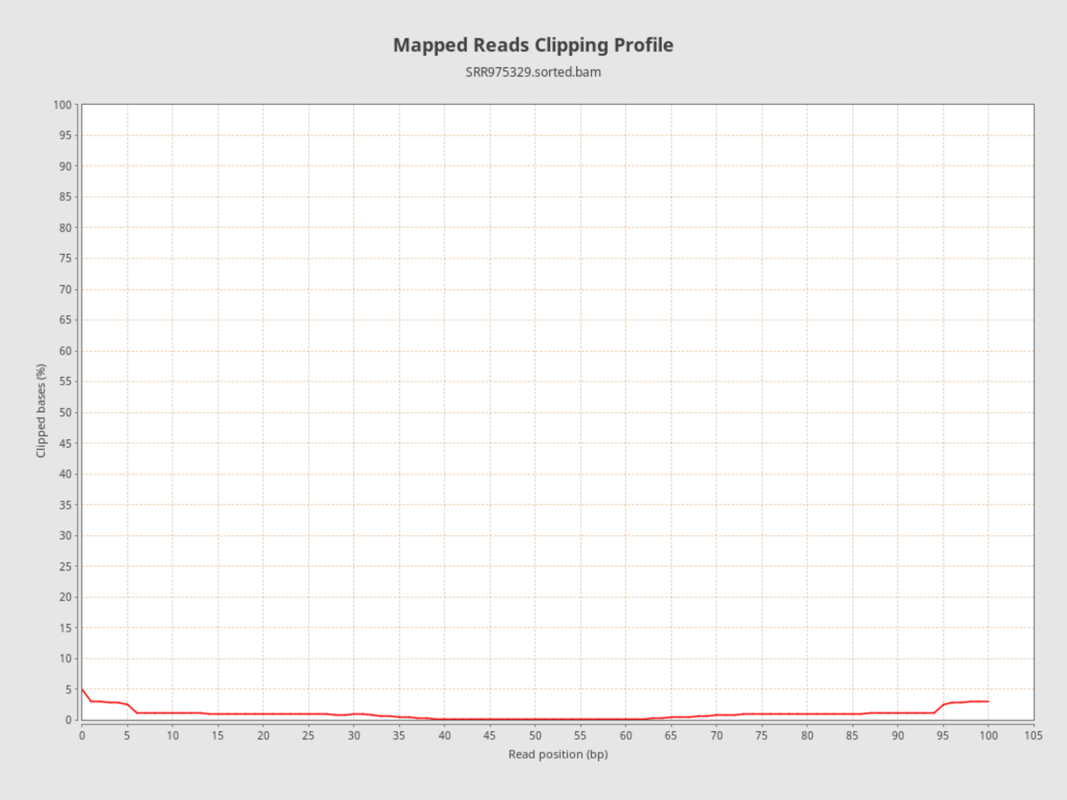
8. Results : Mapped Reads Nucleotide Content



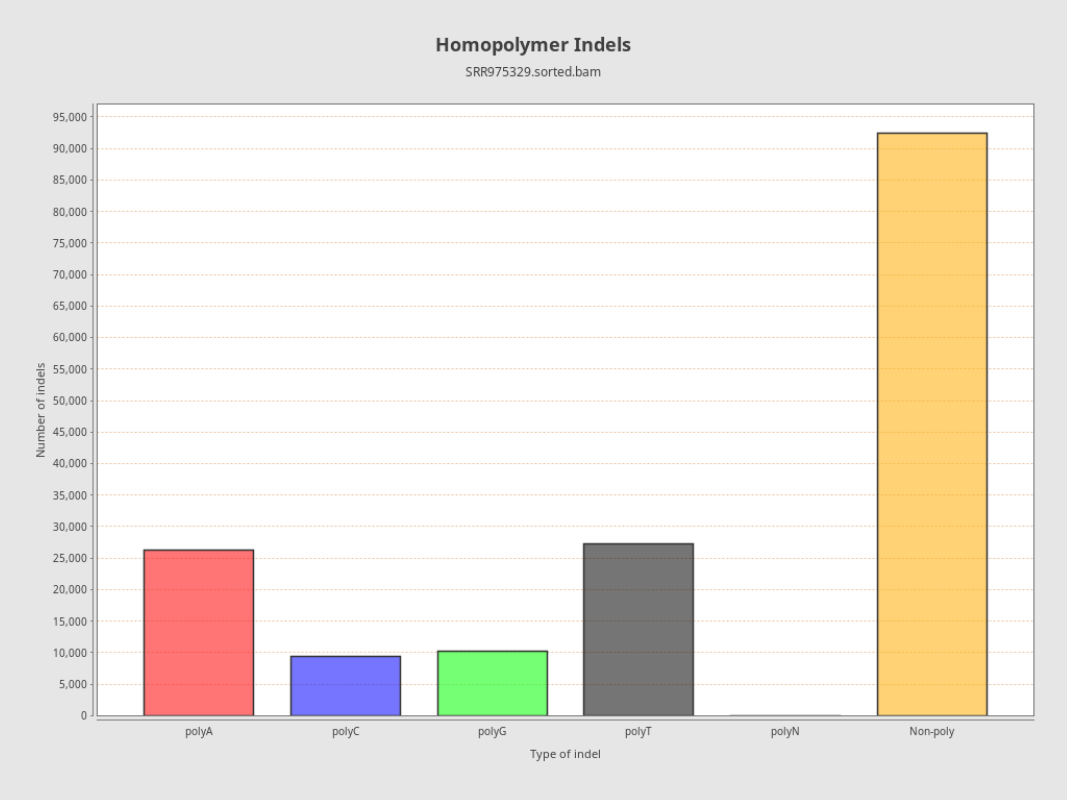
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

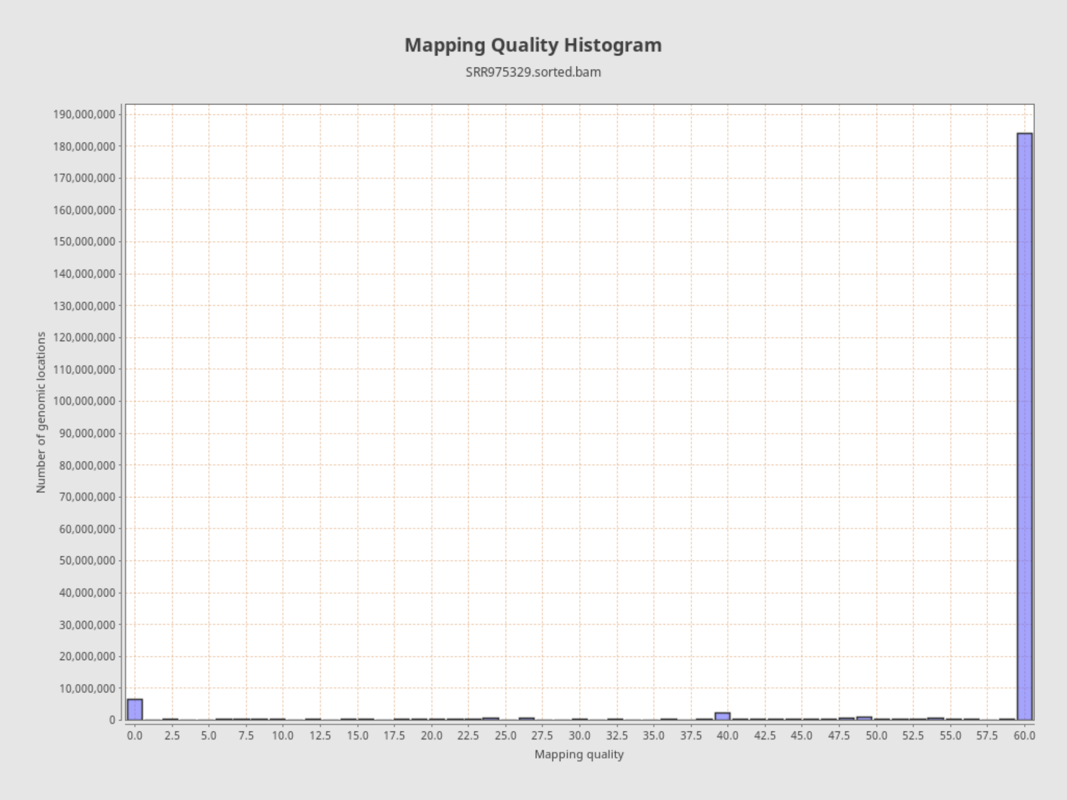


11. Results : Homopolymer Indels

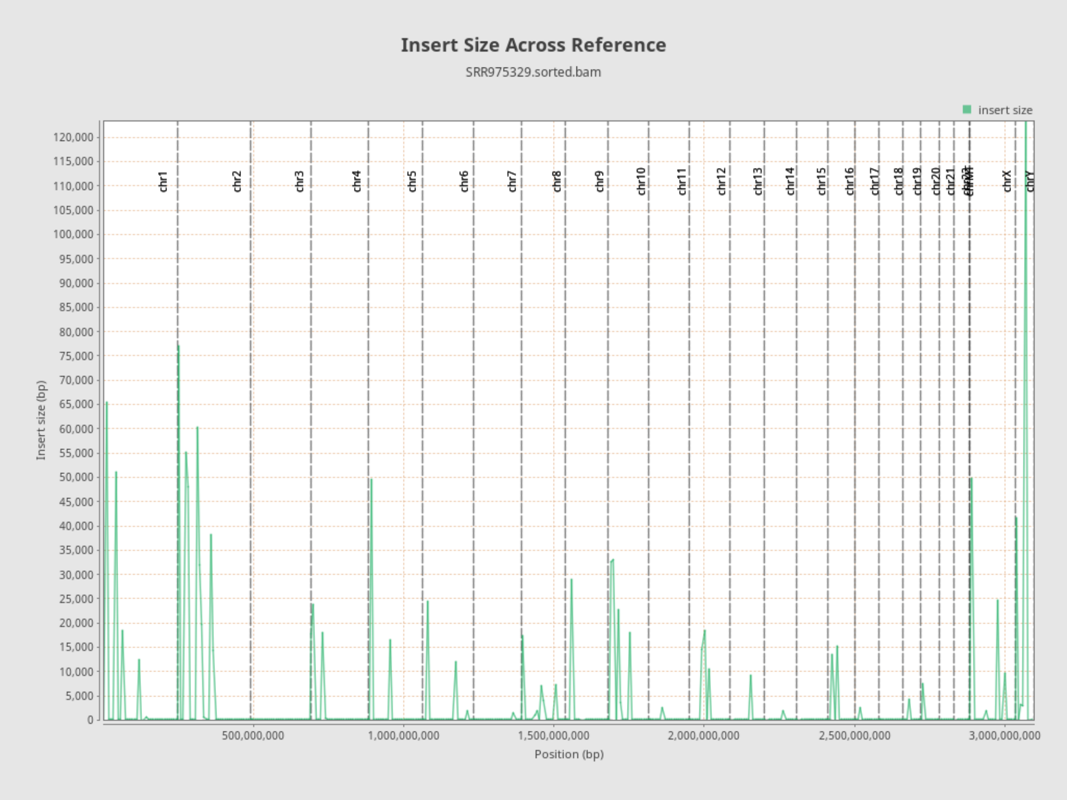


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram