Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 16:13:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975259.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_SRR975259 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975259_1.fastq.gz SRR975259_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 16:13:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975259.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,868,670
Mapped reads	3,832,412 / 99.06%
Unmapped reads	36,258 / 0.94%
Mapped paired reads	3,832,412 / 99.06%
Mapped reads, first in pair	1,915,964 / 49.53%
Mapped reads, second in pair	1,916,448 / 49.54%
Mapped reads, both in pair	3,822,954 / 98.82%
Mapped reads, singletons	9,458 / 0.24%
Secondary alignments	0
Supplementary alignments	27,041 / 0.7%
Read min/max/mean length	30 / 101 / 101.29
Duplicated reads (estimated)	117,227 / 3.03%
Duplication rate	1.38%
Clipped reads	2,011,052 / 51.98%

2.2. ACGT Content

Number/percentage of A's	110,615,832 / 29.68%
Number/percentage of C's	75,676,476 / 20.31%
Number/percentage of T's	109,878,201 / 29.48%
Number/percentage of G's	76,493,329 / 20.53%
Number/percentage of N's	5,394 / 0%

GC Percentage	40.83%

2.3. Coverage

Mean	0.1204
Standard Deviation	1.355

2.4. Mapping Quality

Mean Mapping Quality	53.38

2.5. Insert size

Mean	111,692.4
Standard Deviation	3,178,292.92
P25/Median/P75	145 / 180 / 228

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	1,863,603
Insertions	52,100
Mapped reads with at least one insertion	1.33%
Deletions	48,457
Mapped reads with at least one deletion	1.23%
Homopolymer indels	37.59%

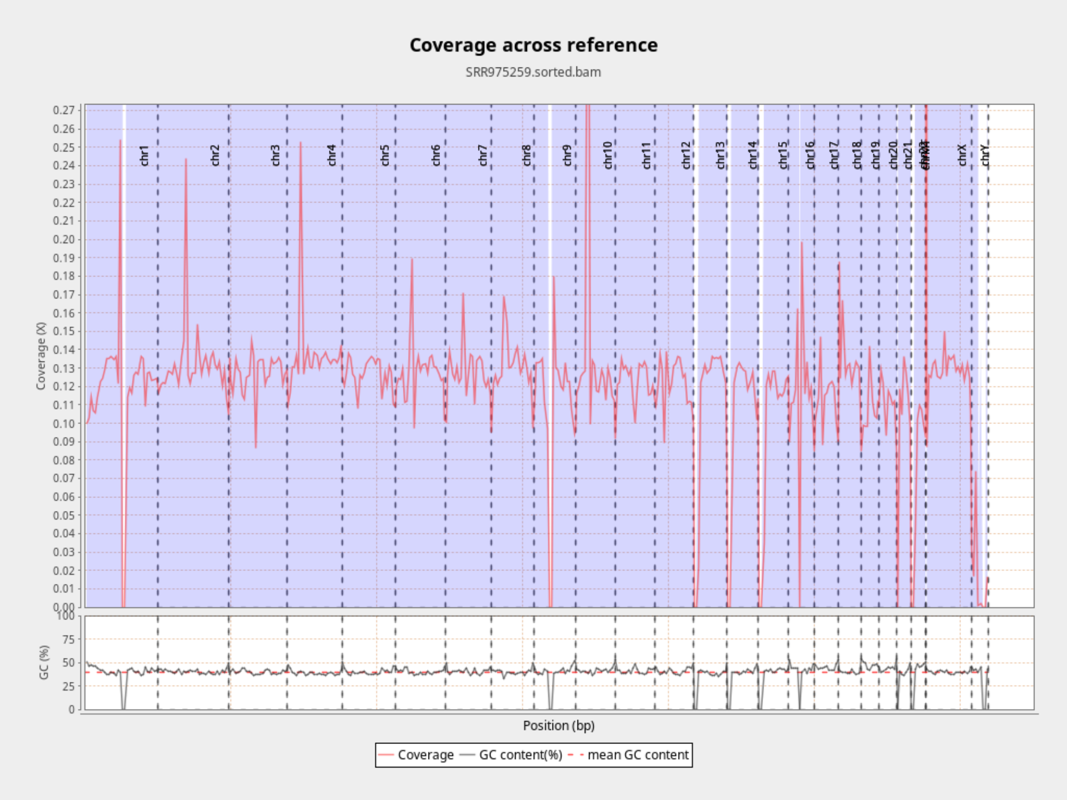
2.7. Chromosome stats

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

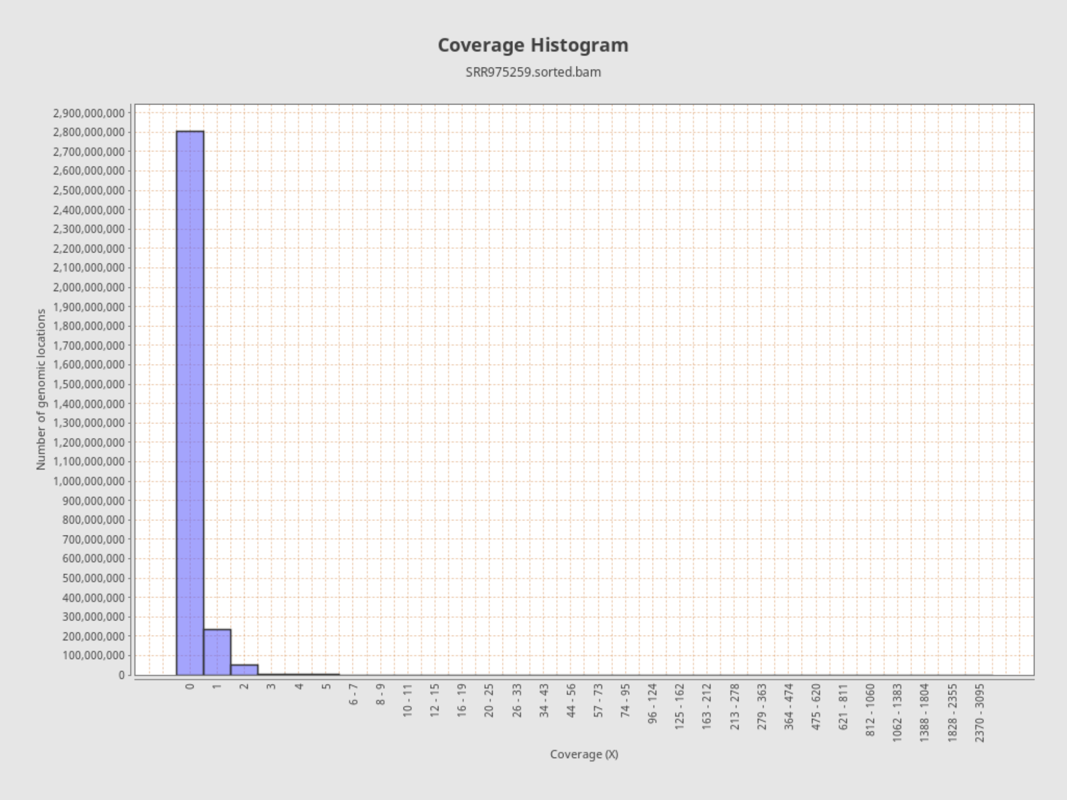
		bases	coverage	deviation
chr1	249250621	29694769	0.1191	3.0138
chr2	243199373	32198544	0.1324	0.9009
chr3	198022430	25156214	0.127	0.4361
chr4	191154276	26270299	0.1374	1.0721
chr5	180915260	22994262	0.1271	0.4111
chr6	171115067	21961626	0.1283	0.7591
chr7	159138663	20378182	0.1281	1.0453
chr8	146364022	19198381	0.1312	2.2777
chr9	141213431	15687836	0.1111	1.3372
chr10	135534747	19069282	0.1407	2.7348
chr11	135006516	16611705	0.123	0.7114
chr12	133851895	16358081	0.1222	0.4008
chr13	115169878	12455834	0.1082	0.3744
chr14	107349540	11089099	0.1033	0.3808
chr15	102531392	9996774	0.0975	0.3557
chr16	90354753	10382559	0.1149	0.7899
chr17	81195210	9224313	0.1136	0.6081
chr18	78077248	10450914	0.1339	1.592
chr19	59128983	6320772	0.1069	1.2773
chr20	63025520	7081410	0.1124	0.4439
chr21	48129895	5150960	0.107	0.5081
chr22	51304566	3755613	0.0732	0.3133
chrMT	16571	347345	20.961	5.7977
chrX	155270560	19931407	0.1284	0.5239

chrY	59373566	1016952	0.0171	0.8155

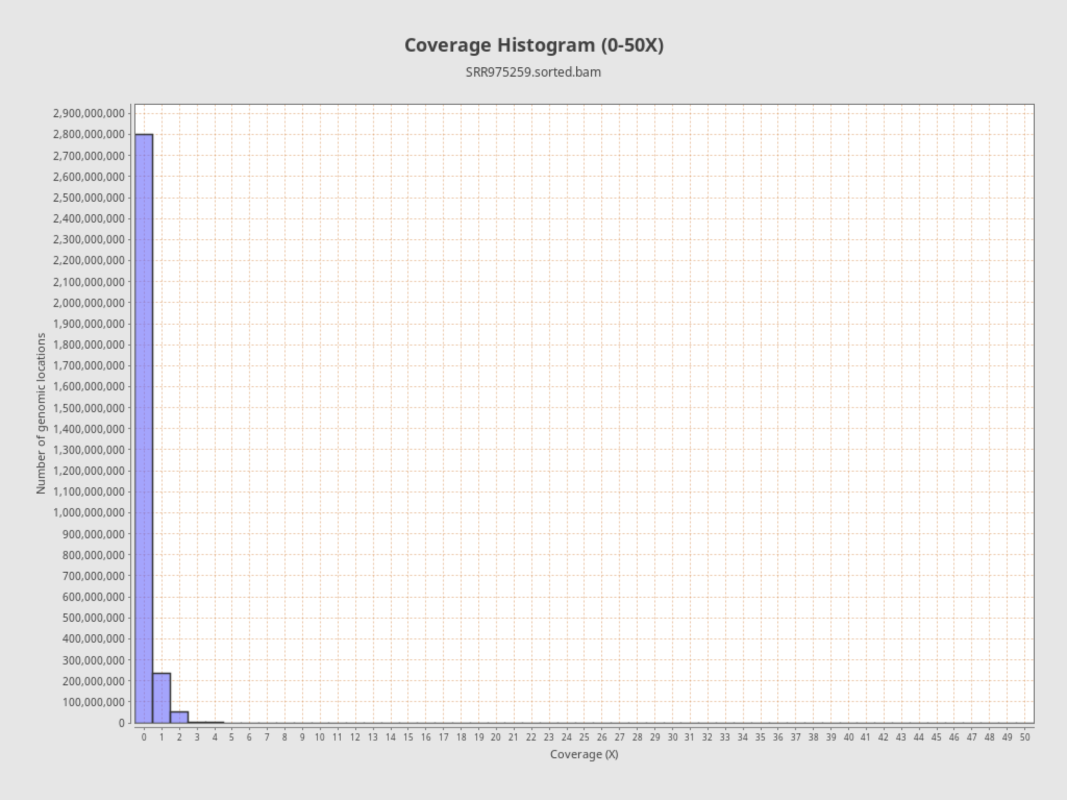
3. Results : Coverage across reference



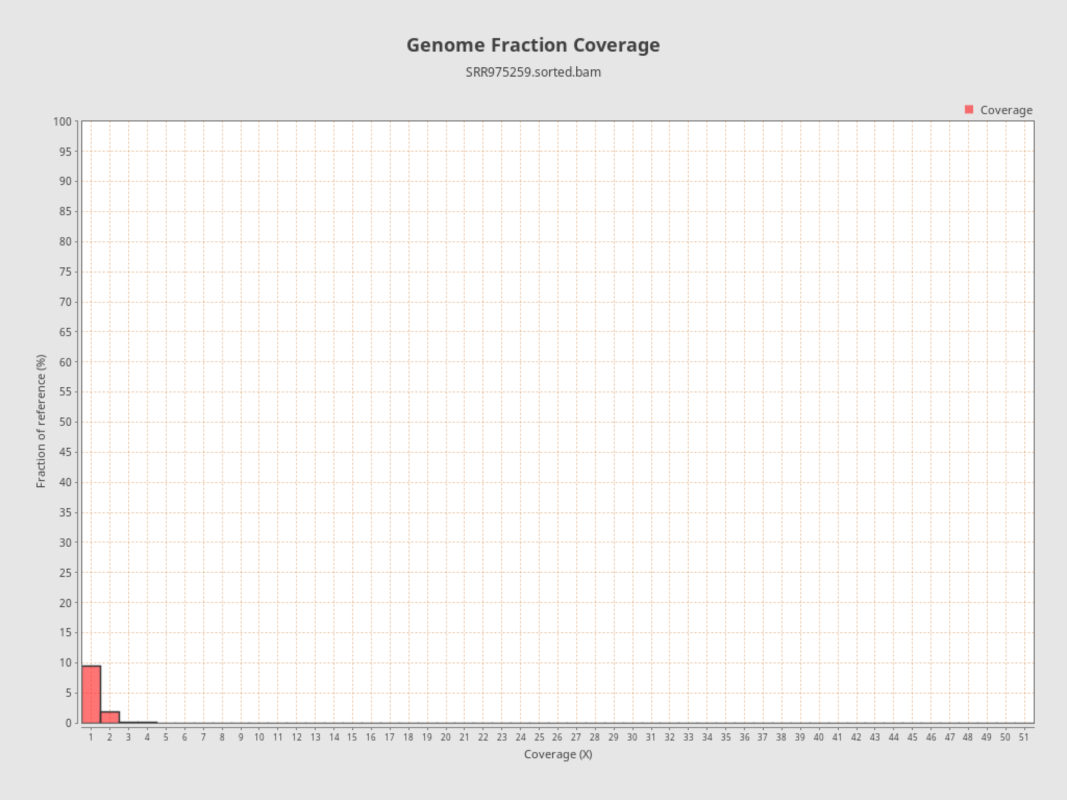
4. Results : Coverage Histogram



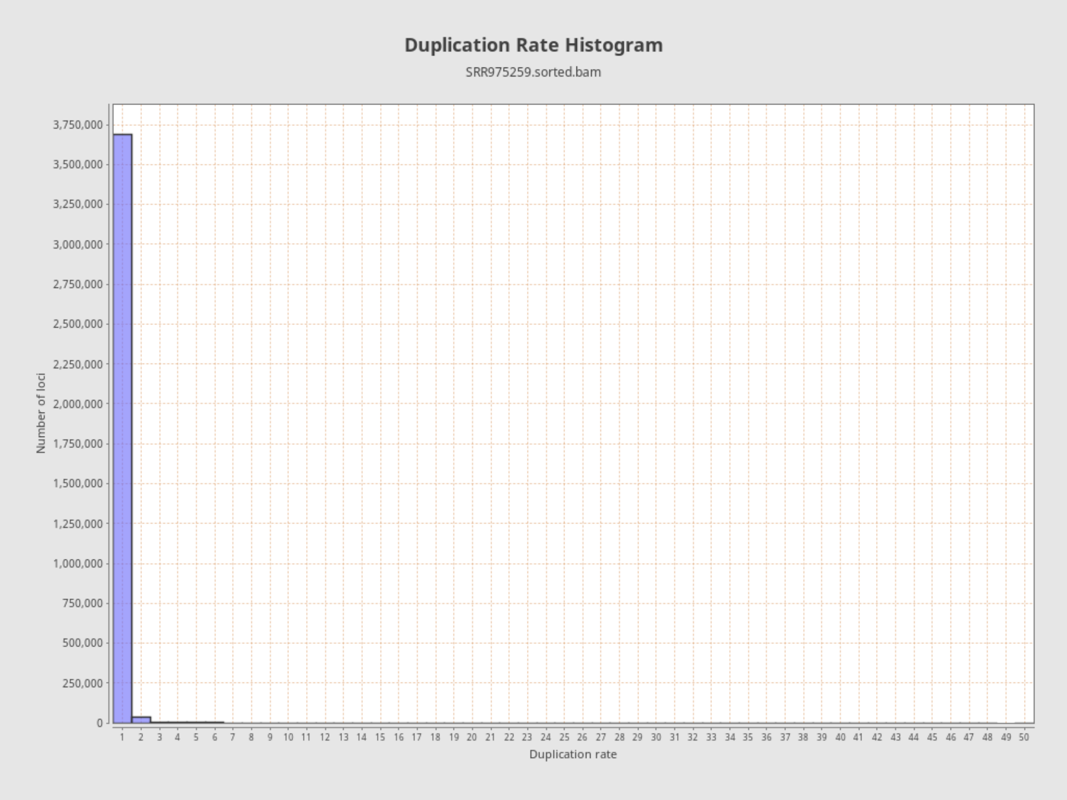
5. Results : Coverage Histogram (0-50X)



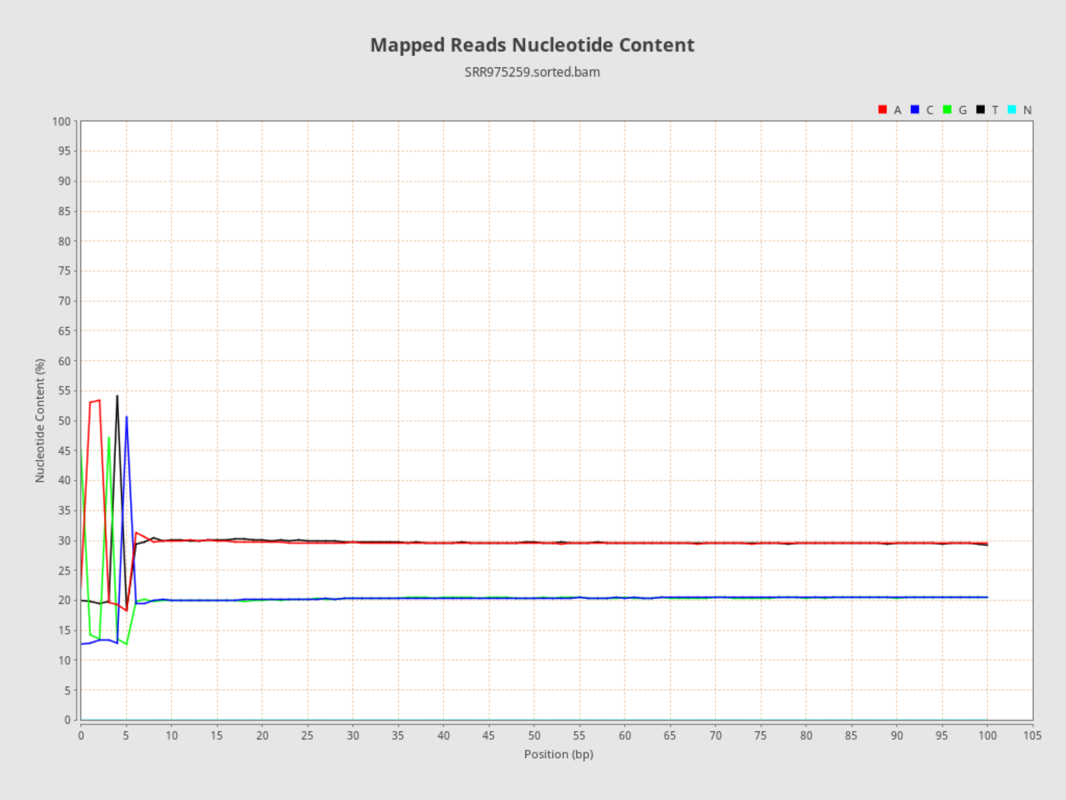
6. Results : Genome Fraction Coverage



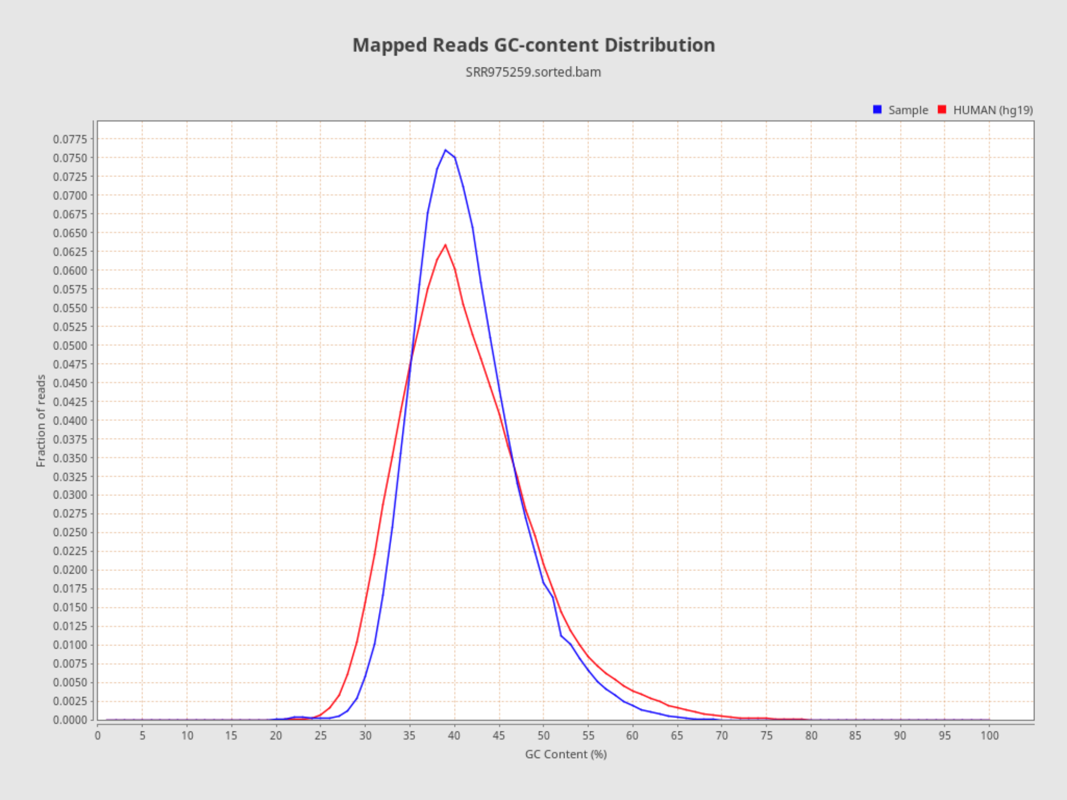
7. Results : Duplication Rate Histogram



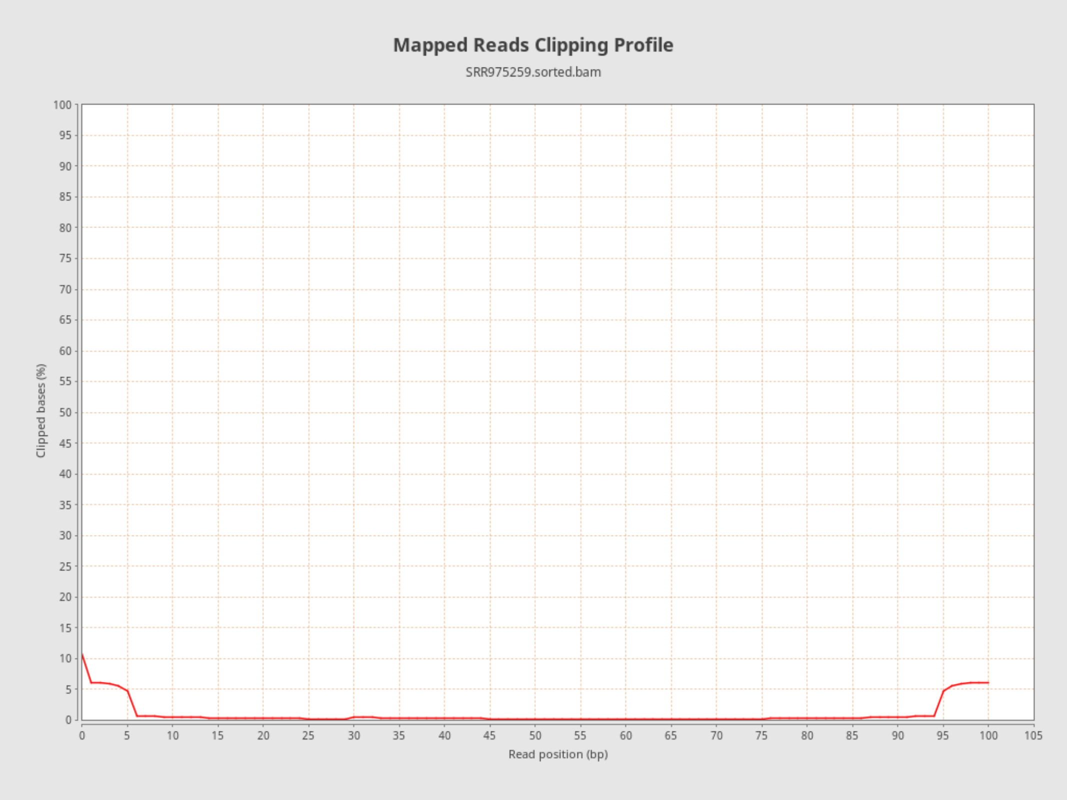
8. Results : Mapped Reads Nucleotide Content



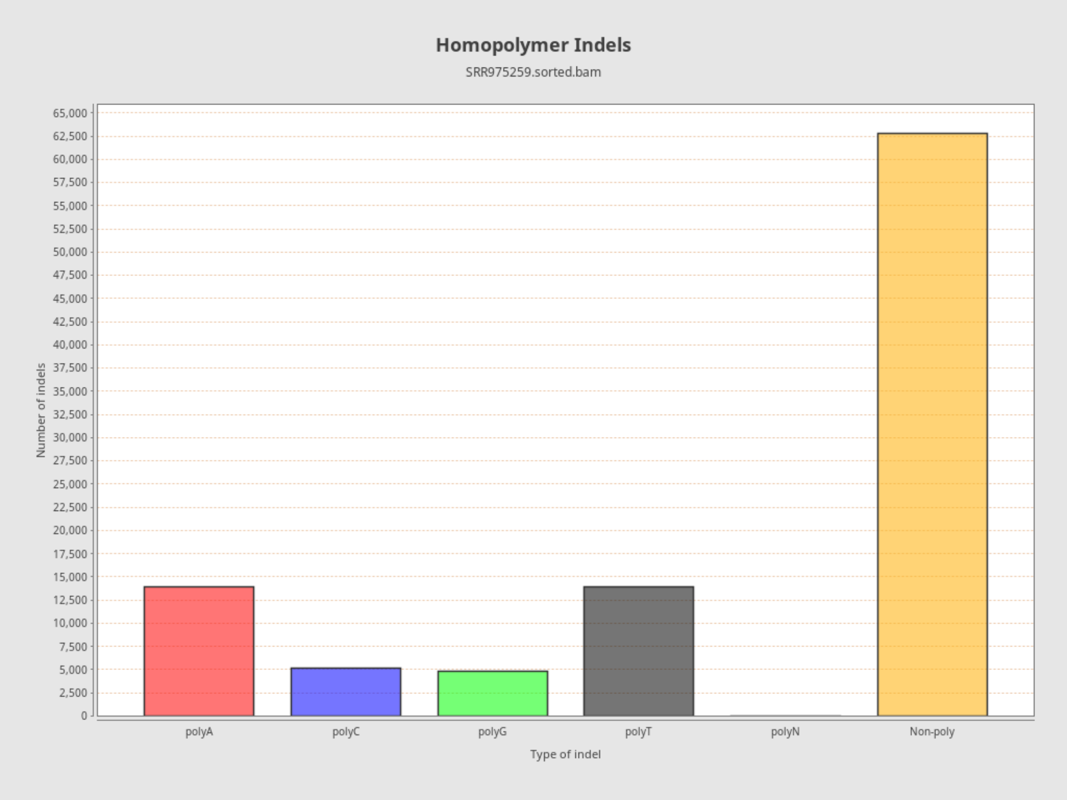
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

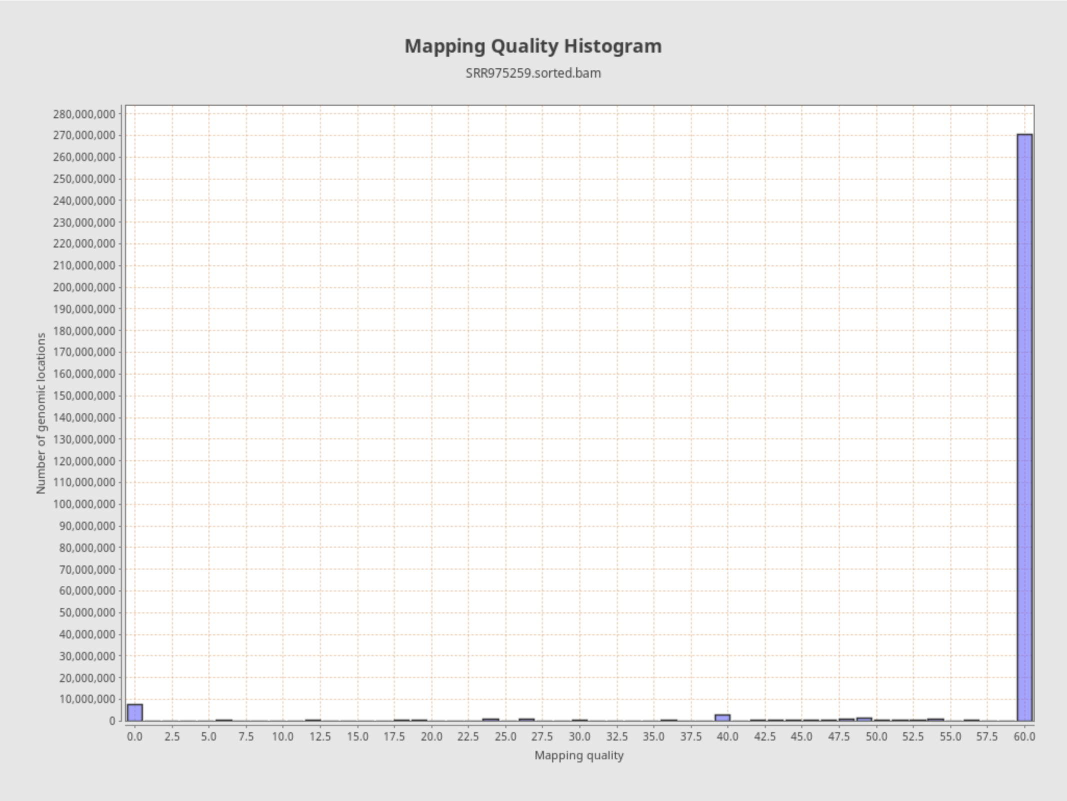


11. Results : Homopolymer Indels

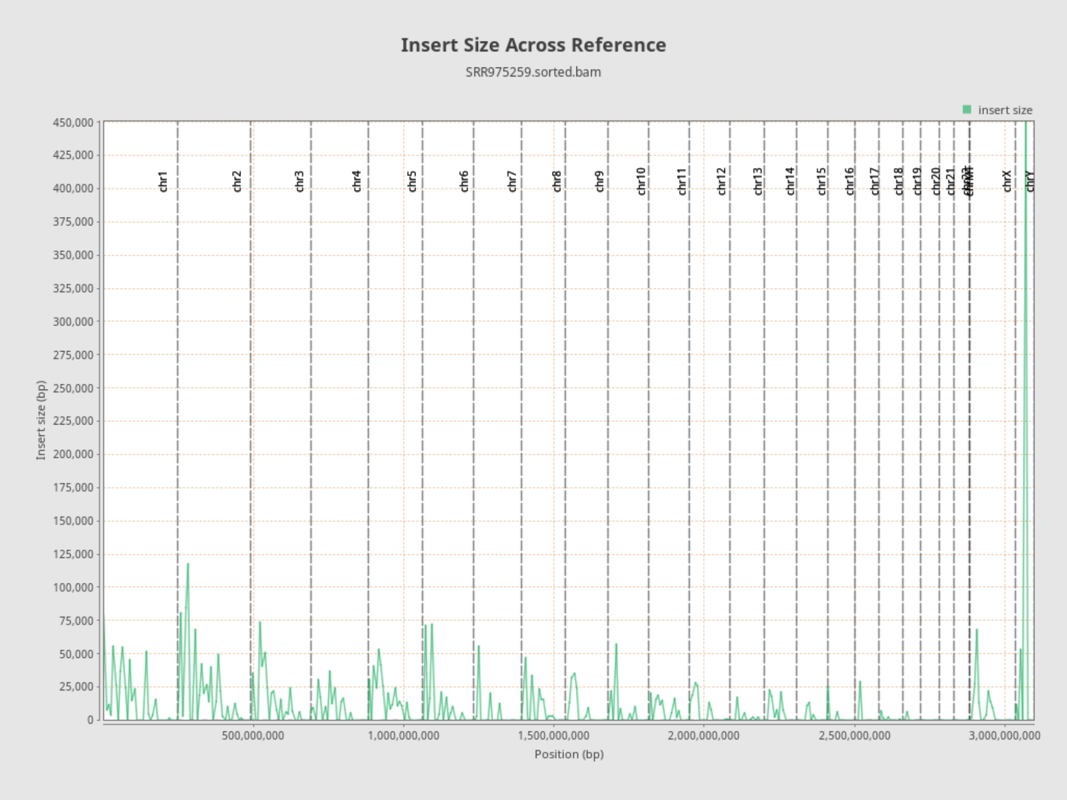


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram