Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 17:48:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975270.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_SRR975270 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975270_1.fastq.gz SRR975270_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 17:48:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975270.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,232,870
Mapped reads	2,208,621 / 98.91%
Unmapped reads	24,249 / 1.09%
Mapped paired reads	2,208,621 / 98.91%
Mapped reads, first in pair	1,106,383 / 49.55%
Mapped reads, second in pair	1,102,238 / 49.36%
Mapped reads, both in pair	2,201,118 / 98.58%
Mapped reads, singletons	7,503 / 0.34%
Secondary alignments	0
Supplementary alignments	22,487 / 1.01%
Read min/max/mean length	30 / 151 / 151.49
Duplicated reads (estimated)	320,780 / 14.37%
Duplication rate	14.67%
Clipped reads	1,608,185 / 72.02%

2.2. ACGT Content

Number/percentage of A's	85,611,772 / 28.7%
Number/percentage of C's	61,957,260 / 20.77%
Number/percentage of T's	85,893,264 / 28.79%
Number/percentage of G's	64,833,401 / 21.73%
Number/percentage of N's	18,306 / 0.01%

GC Percentage	42.5%

2.3. Coverage

Mean	0.0964
Standard Deviation	0.9837

2.4. Mapping Quality

Mean Mapping Quality	53.8

2.5. Insert size

Mean	75,066.99
Standard Deviation	2,611,427.39
P25/Median/P75	137 / 169 / 214

2.6. Mismatches and indels

General error rate	1%
Mismatches	2,866,634
Insertions	47,166
Mapped reads with at least one insertion	2.05%
Deletions	101,639
Mapped reads with at least one deletion	4.45%
Homopolymer indels	47.91%

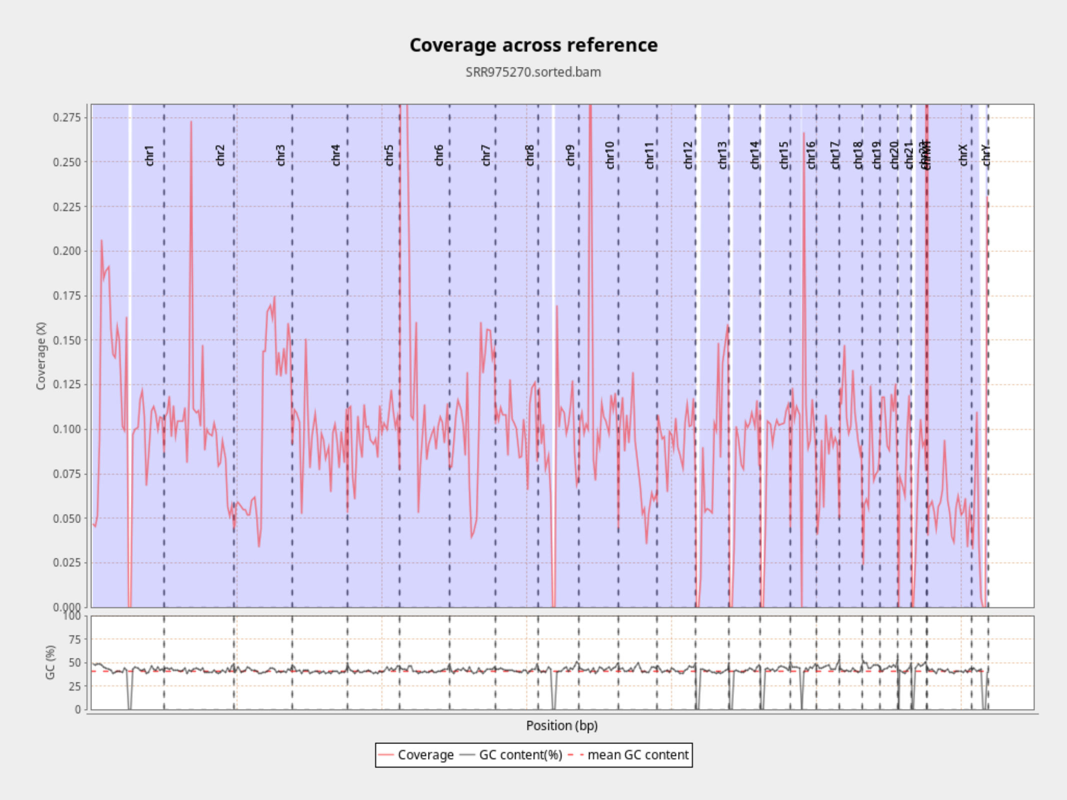
2.7. Chromosome stats

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

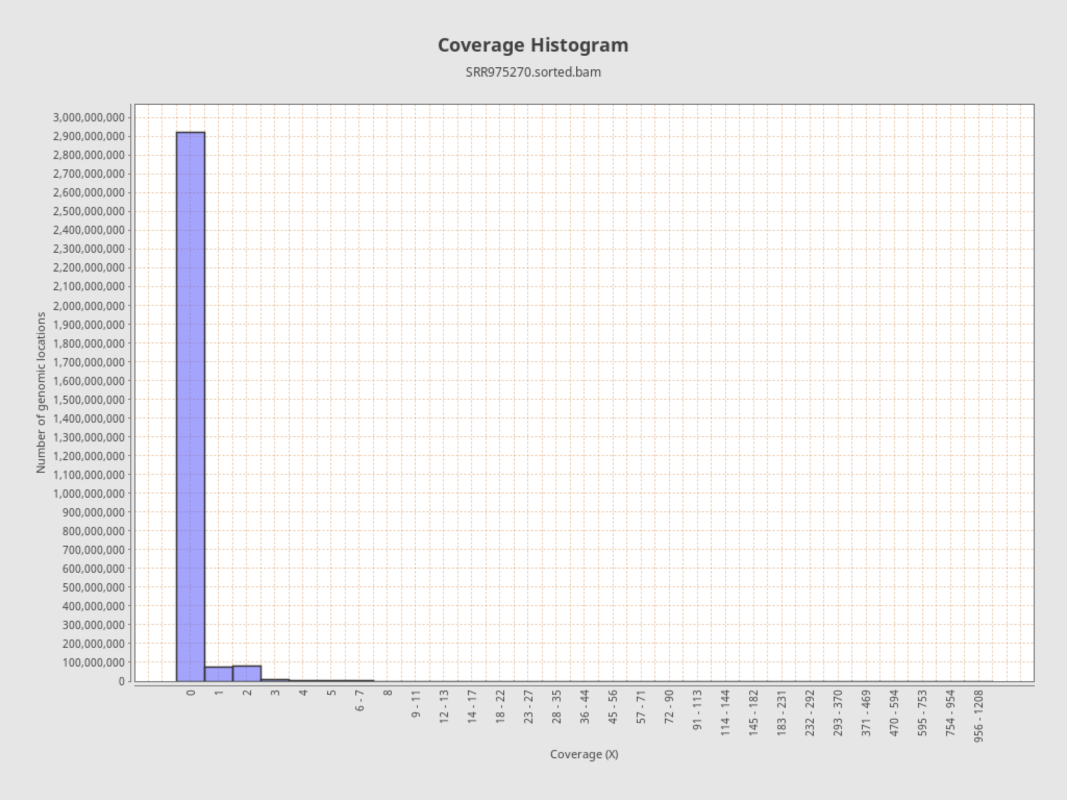
		bases	coverage	deviation
chr1	249250621	27681998	0.1111	1.1547
chr2	243199373	24858070	0.1022	1.1624
chr3	198022430	20354245	0.1028	0.4488
chr4	191154276	18117478	0.0948	0.5948
chr5	180915260	17927318	0.0991	0.4319
chr6	171115067	24065539	0.1406	0.8957
chr7	159138663	16973125	0.1067	1.0431
chr8	146364022	15017172	0.1026	0.5414
chr9	141213431	12799442	0.0906	1.7609
chr10	135534747	15681033	0.1157	2.0754
chr11	135006516	10767917	0.0798	1.0886
chr12	133851895	12894913	0.0963	0.425
chr13	115169878	9500350	0.0825	0.3961
chr14	107349540	8639837	0.0805	0.3985
chr15	102531392	8656732	0.0844	0.3974
chr16	90354753	9694123	0.1073	1.2431
chr17	81195210	6529452	0.0804	0.817
chr18	78077248	8536240	0.1093	1.6018
chr19	59128983	4277089	0.0723	0.7528
chr20	63025520	6690064	0.1061	0.4772
chr21	48129895	3622913	0.0753	0.5054
chr22	51304566	3226534	0.0629	0.3462
chrMT	16571	29432	1.7761	1.9127
chrX	155270560	8492014	0.0547	0.4591

chrY	59373566	3471582	0.0585	1.2228

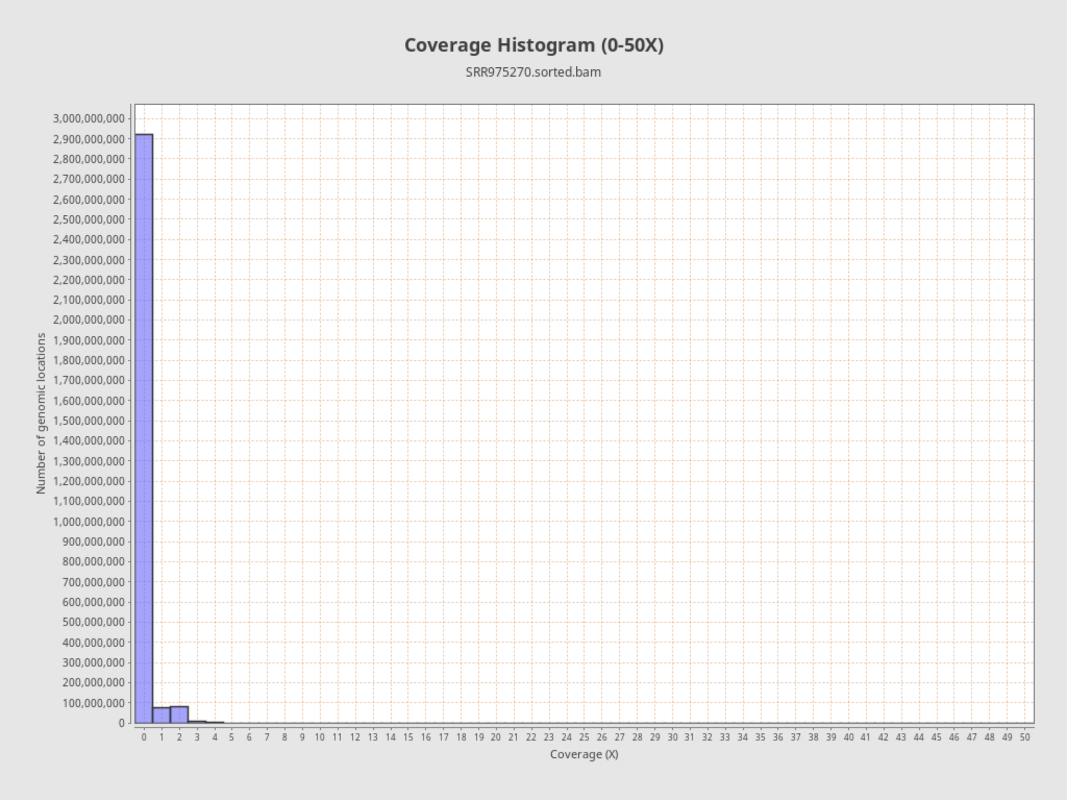
3. Results : Coverage across reference



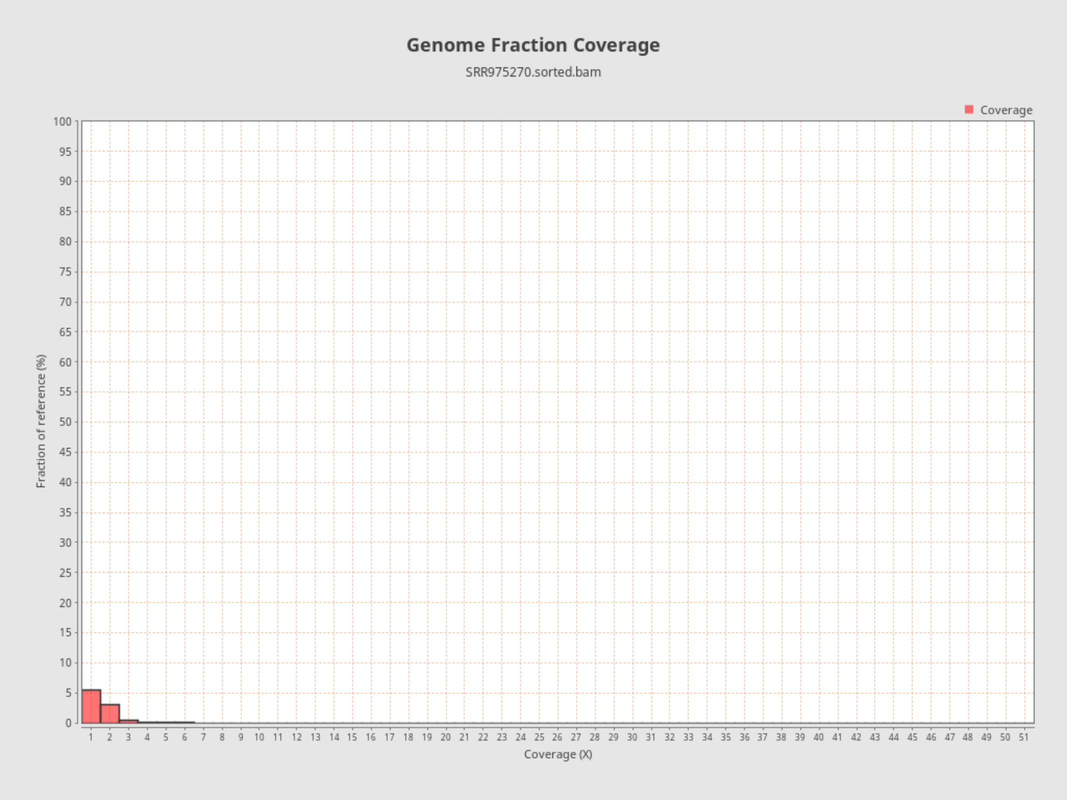
4. Results : Coverage Histogram



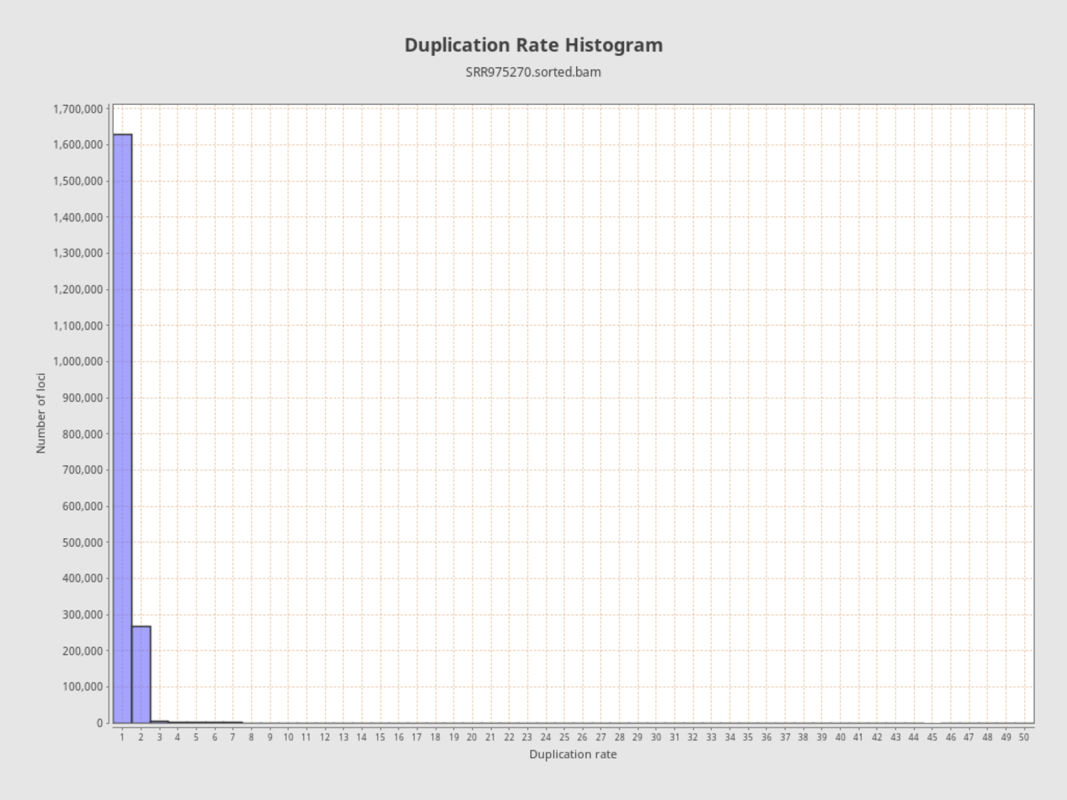
5. Results : Coverage Histogram (0-50X)



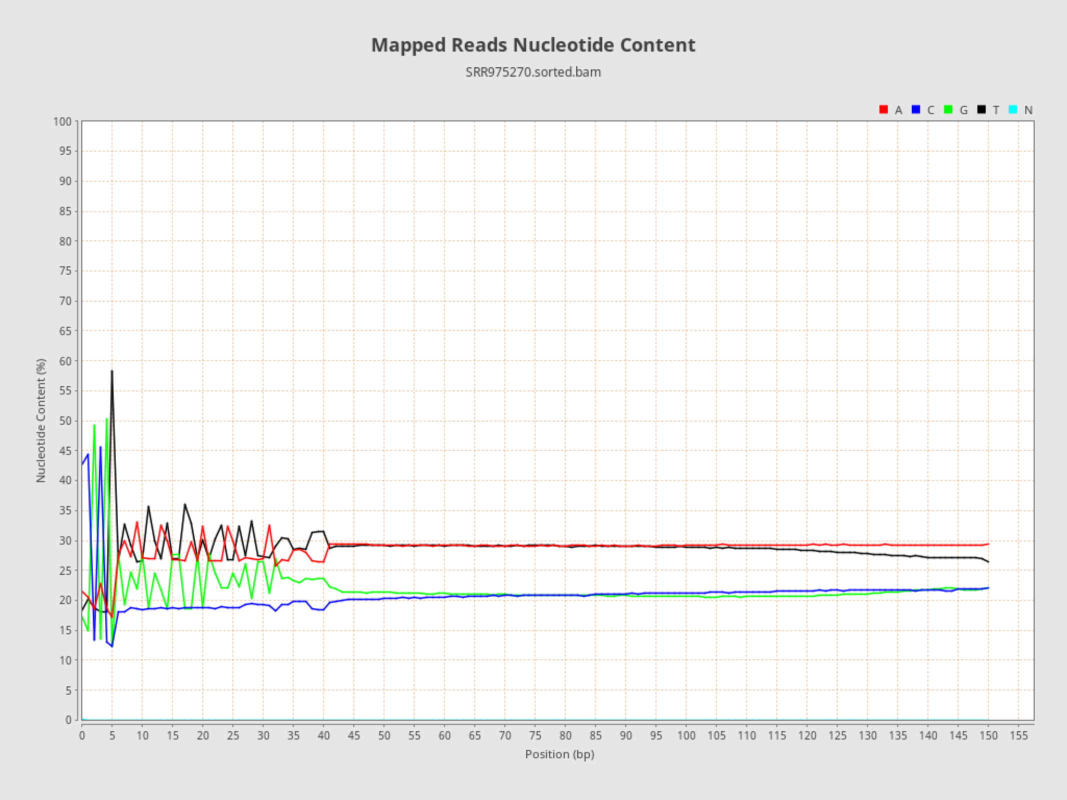
6. Results : Genome Fraction Coverage



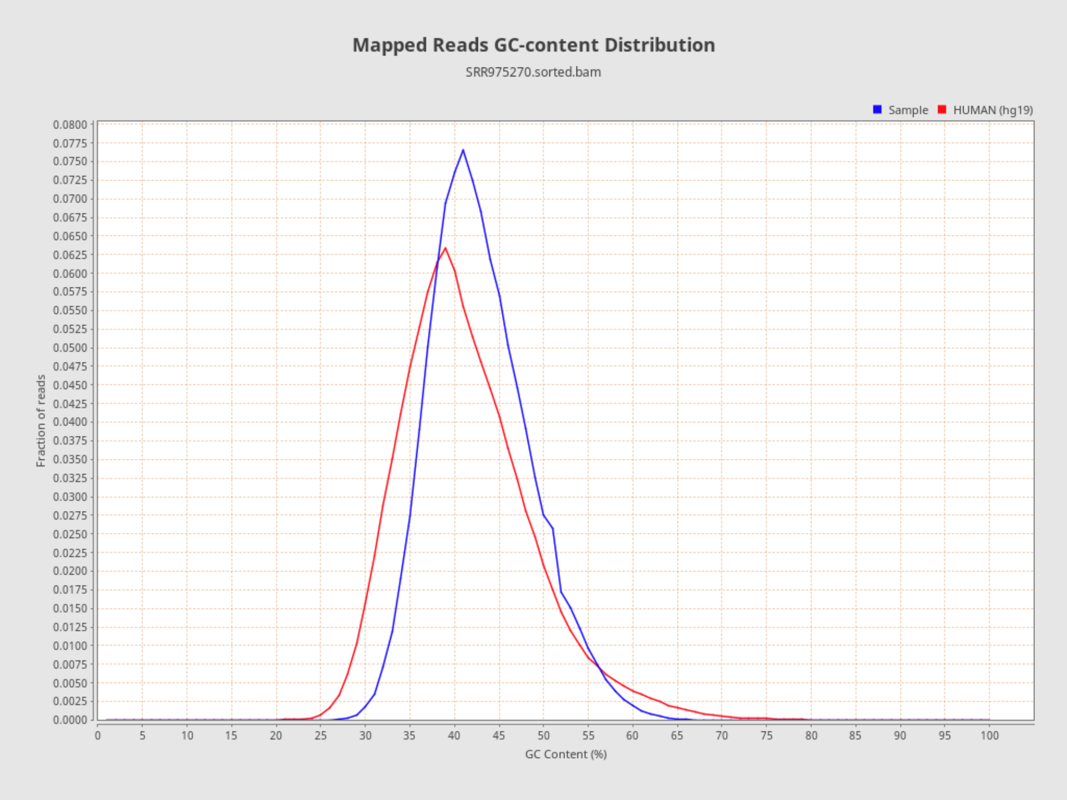
7. Results : Duplication Rate Histogram



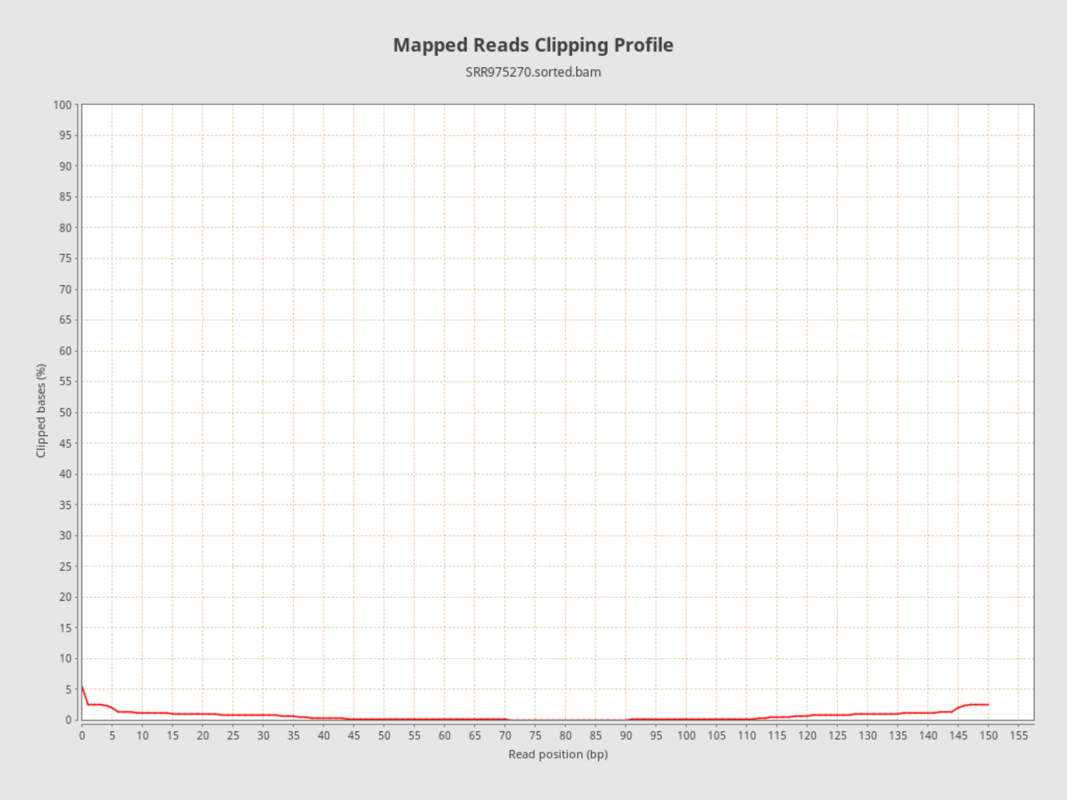
8. Results : Mapped Reads Nucleotide Content



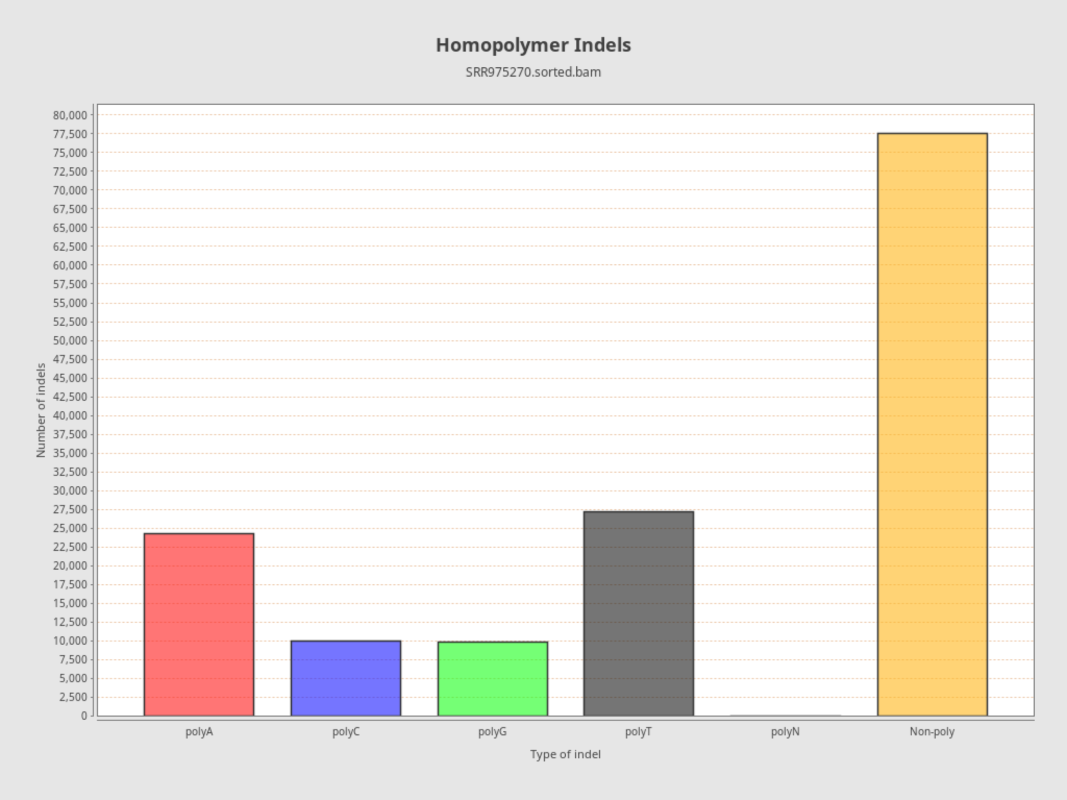
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

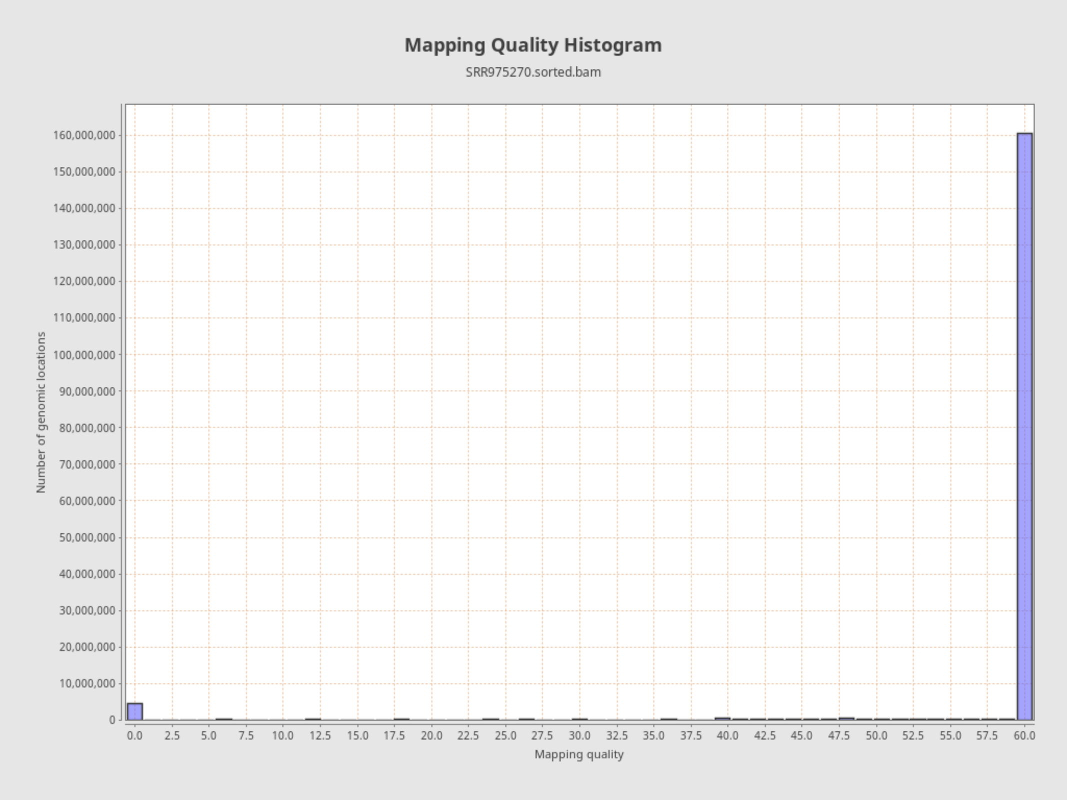


11. Results : Homopolymer Indels

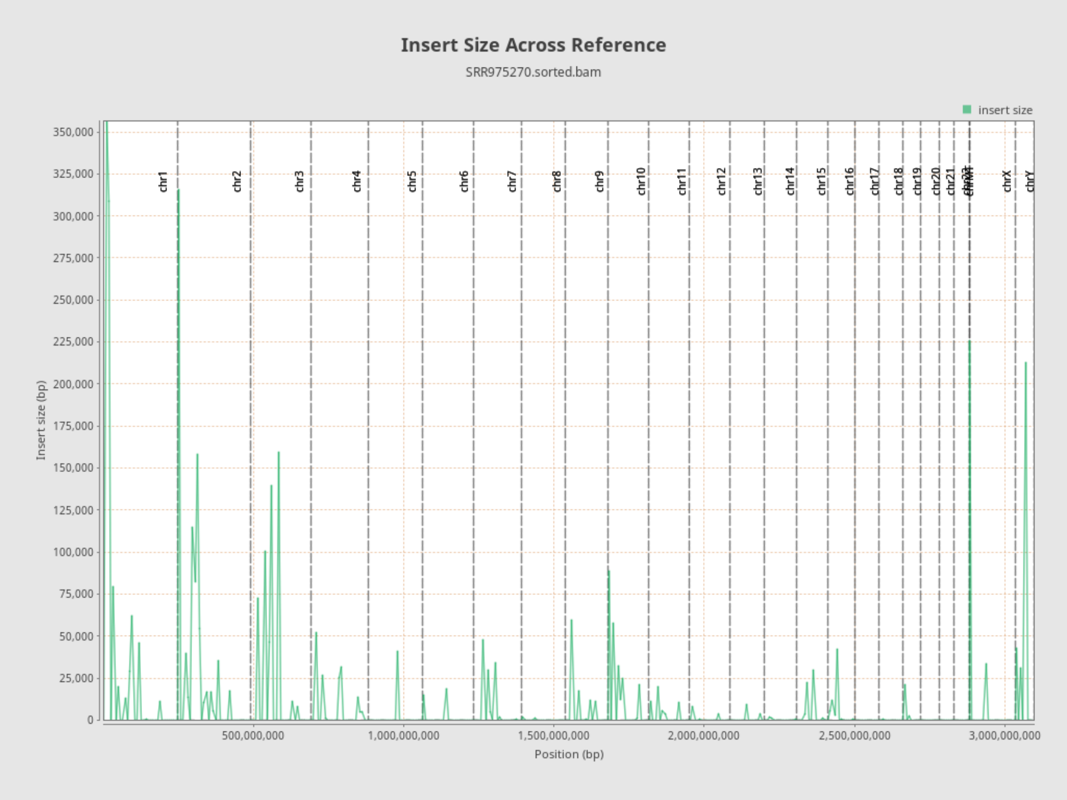


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram