Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 17:42:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975268.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_SRR975268 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975268_1.fastq.gz SRR975268_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 17:42:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975268.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,121,466
Mapped reads	2,093,695 / 98.69%
Unmapped reads	27,771 / 1.31%
Mapped paired reads	2,093,695 / 98.69%
Mapped reads, first in pair	1,048,619 / 49.43%
Mapped reads, second in pair	1,045,076 / 49.26%
Mapped reads, both in pair	2,086,688 / 98.36%
Mapped reads, singletons	7,007 / 0.33%
Secondary alignments	0
Supplementary alignments	24,722 / 1.17%
Read min/max/mean length	30 / 151 / 151.56
Duplicated reads (estimated)	314,232 / 14.81%
Duplication rate	14.69%
Clipped reads	1,516,756 / 71.5%

2.2. ACGT Content

Number/percentage of A's	81,862,602 / 28.99%
Number/percentage of C's	58,165,938 / 20.6%
Number/percentage of T's	81,233,291 / 28.76%
Number/percentage of G's	61,139,811 / 21.65%
Number/percentage of N's	17,811 / 0.01%

GC Percentage	42.24%

2.3. Coverage

Mean	0.0913
Standard Deviation	1.0334

2.4. Mapping Quality

Mean Mapping Quality	53.78

2.5. Insert size

Mean	66,893.02
Standard Deviation	2,456,232.13
P25/Median/P75	137 / 169 / 214

2.6. Mismatches and indels

General error rate	1.08%
Mismatches	2,909,607
Insertions	56,399
Mapped reads with at least one insertion	2.55%
Deletions	106,468
Mapped reads with at least one deletion	4.89%
Homopolymer indels	46.09%

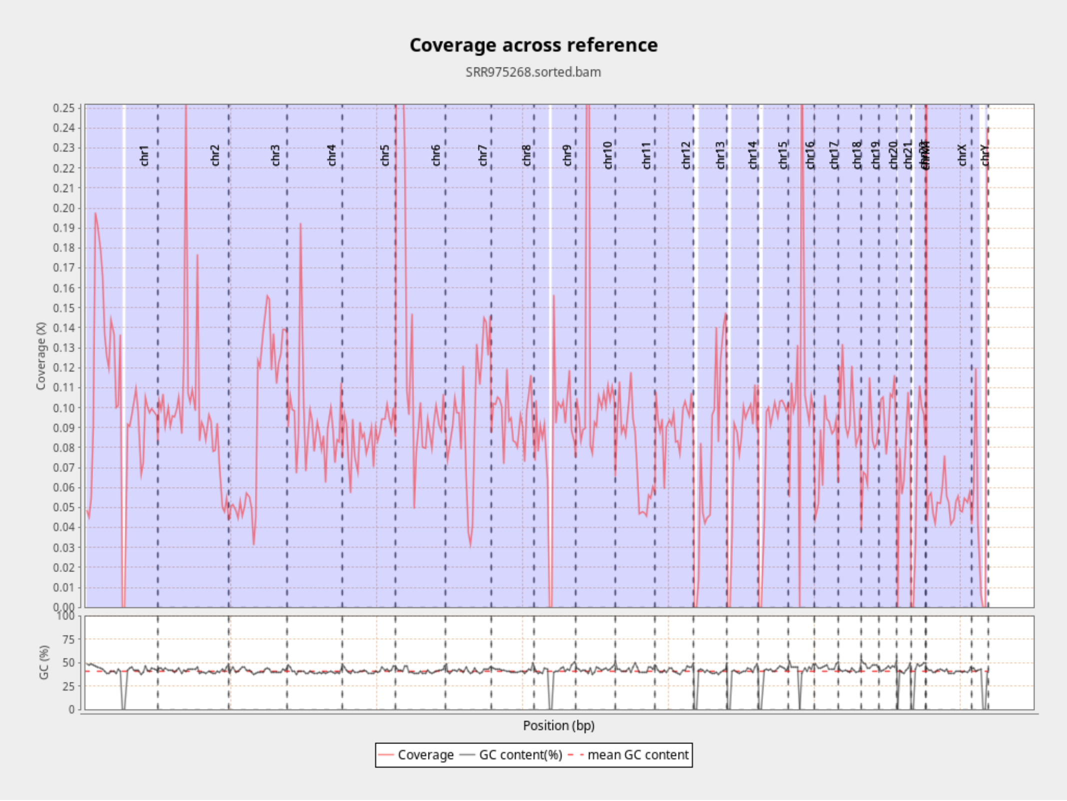
2.7. Chromosome stats

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

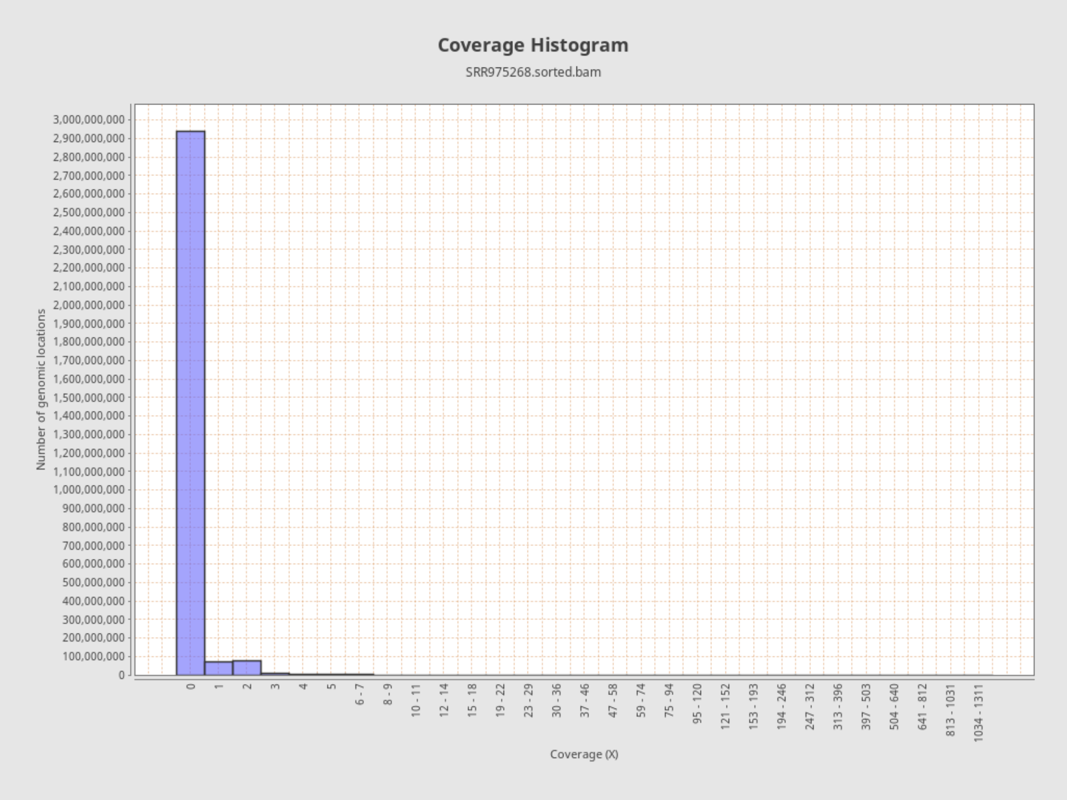
		bases	**coverage**	**deviation**
chr1	249250621	25665299	0.103	0.9898
chr2	243199373	23727508	0.0976	1.2179
chr3	198022430	18283902	0.0923	0.4444
chr4	191154276	17606663	0.0921	0.7873
chr5	180915260	15555871	0.086	0.4109
chr6	171115067	22741055	0.1329	0.83
chr7	159138663	15355105	0.0965	0.9152
chr8	146364022	13951339	0.0953	0.5091
chr9	141213431	12187133	0.0863	1.5698
chr10	135534747	15556931	0.1148	2.7985
chr11	135006516	10294191	0.0762	0.936
chr12	133851895	12296055	0.0919	0.4226
chr13	115169878	8781070	0.0762	0.3874
chr14	107349540	8350478	0.0778	0.4046
chr15	102531392	8301479	0.081	0.3968
chr16	90354753	9945655	0.1101	1.465
chr17	81195210	6520480	0.0803	0.7641
chr18	78077248	7778916	0.0996	1.4185
chr19	59128983	4604116	0.0779	0.6496
chr20	63025520	6166469	0.0978	0.4983
chr21	48129895	3461749	0.0719	0.5552
chr22	51304566	3461882	0.0675	0.3712
chrMT	16571	53066	3.2023	3.0589
chrX	155270560	8160189	0.0526	0.4103

chrY	59373566	3825703	0.0644	1.4962

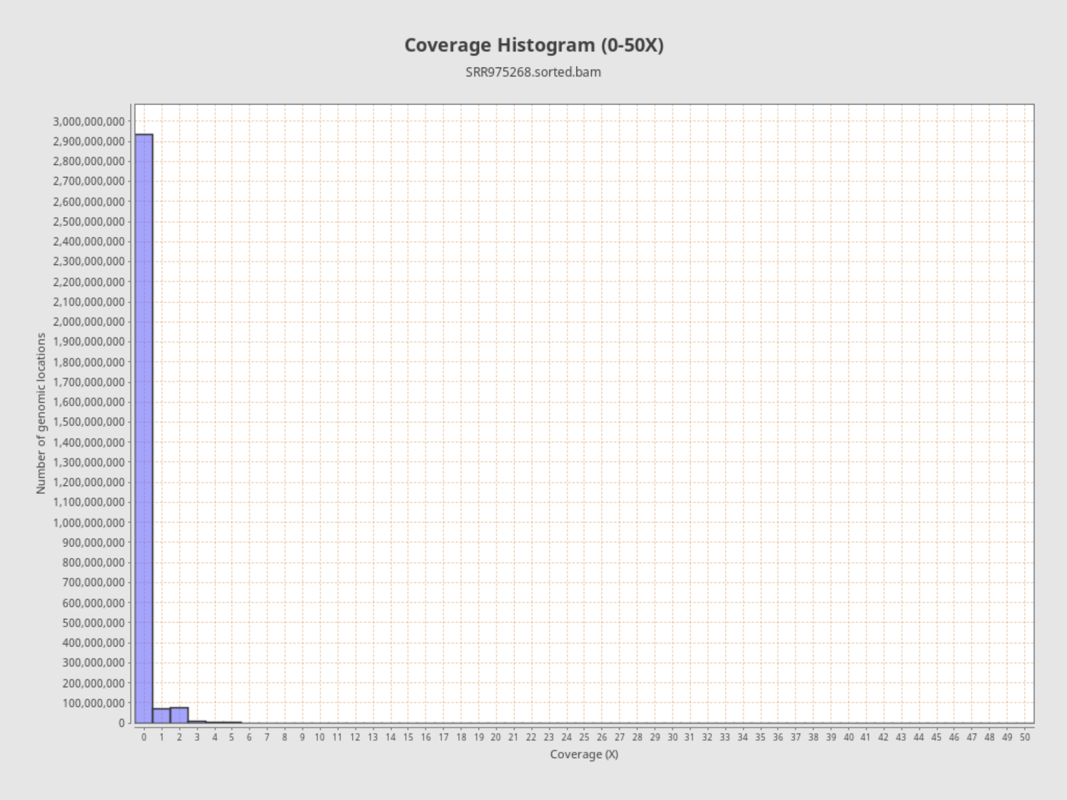
3. Results : Coverage across reference



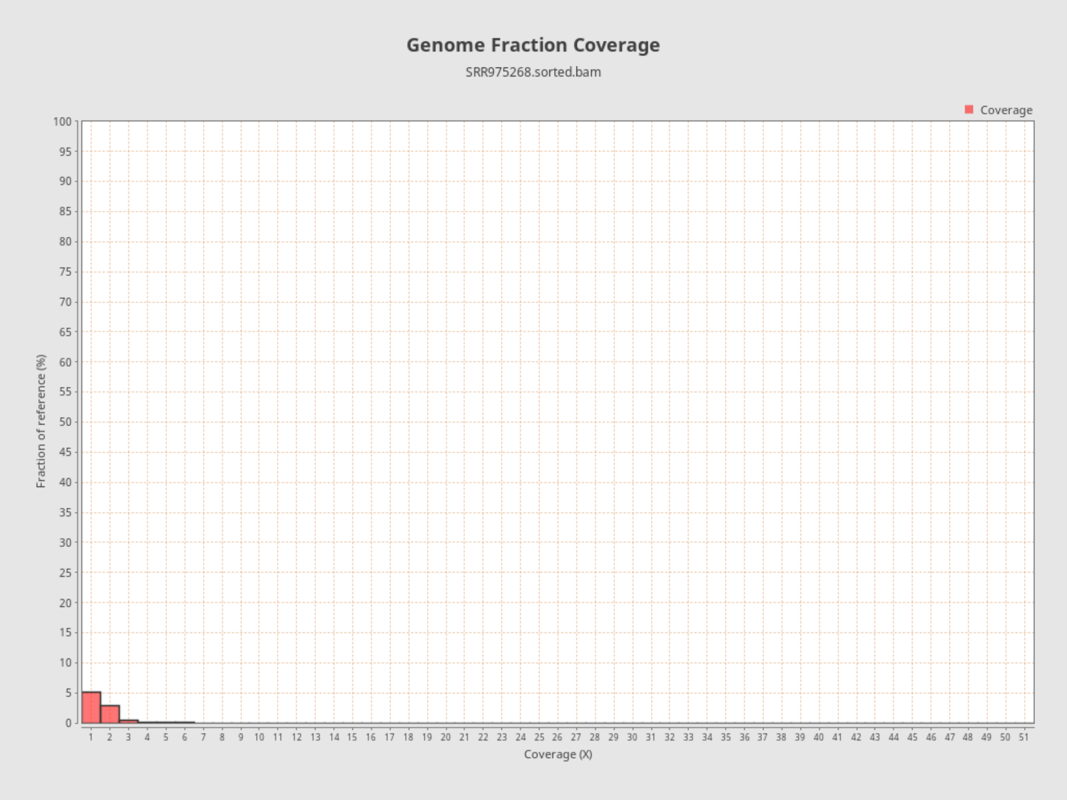
4. Results : Coverage Histogram



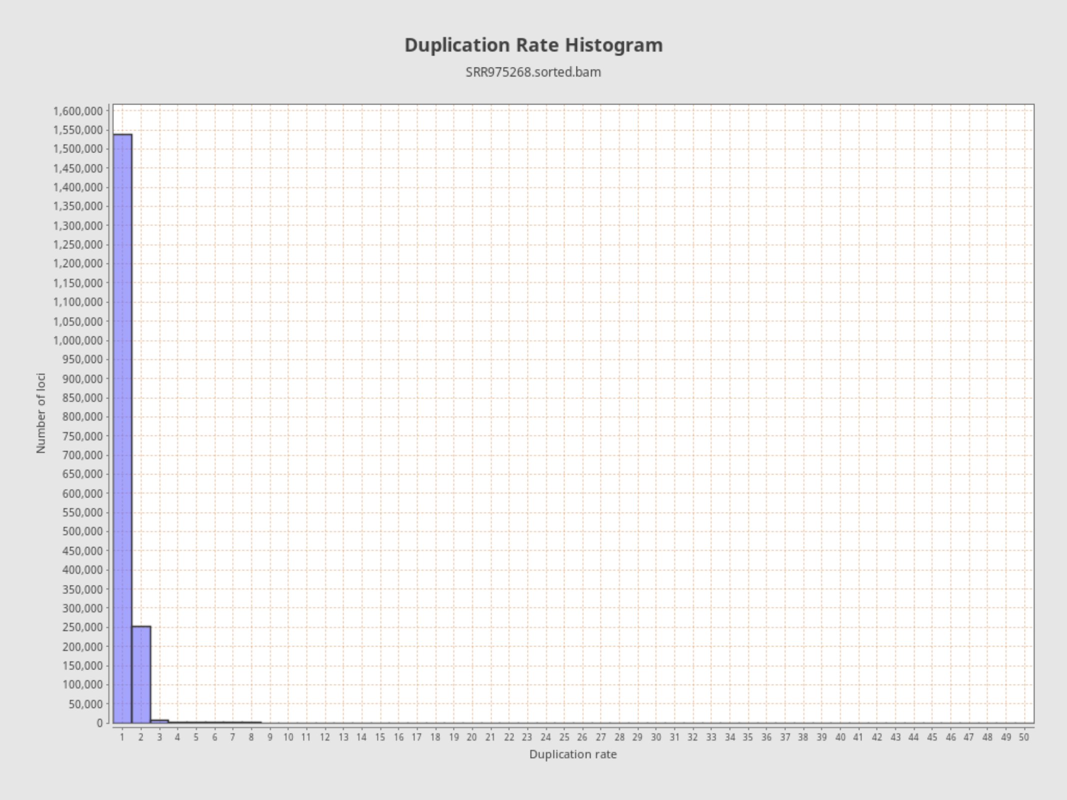
5. Results : Coverage Histogram (0-50X)



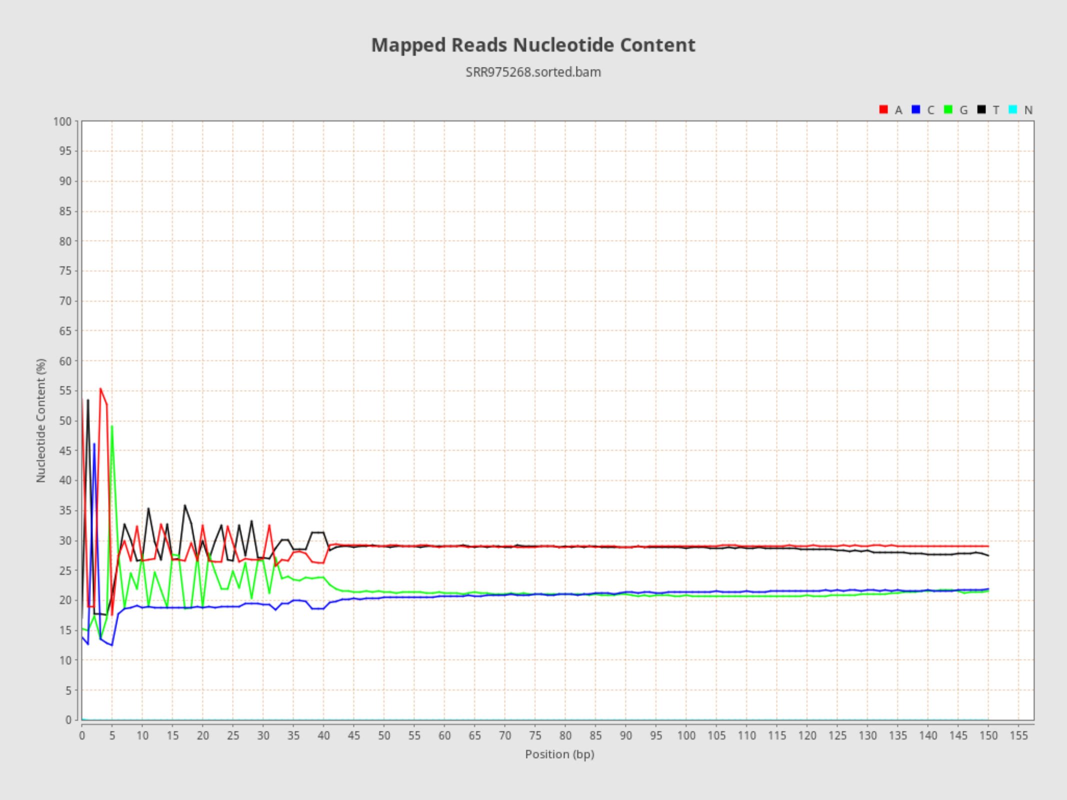
6. Results : Genome Fraction Coverage



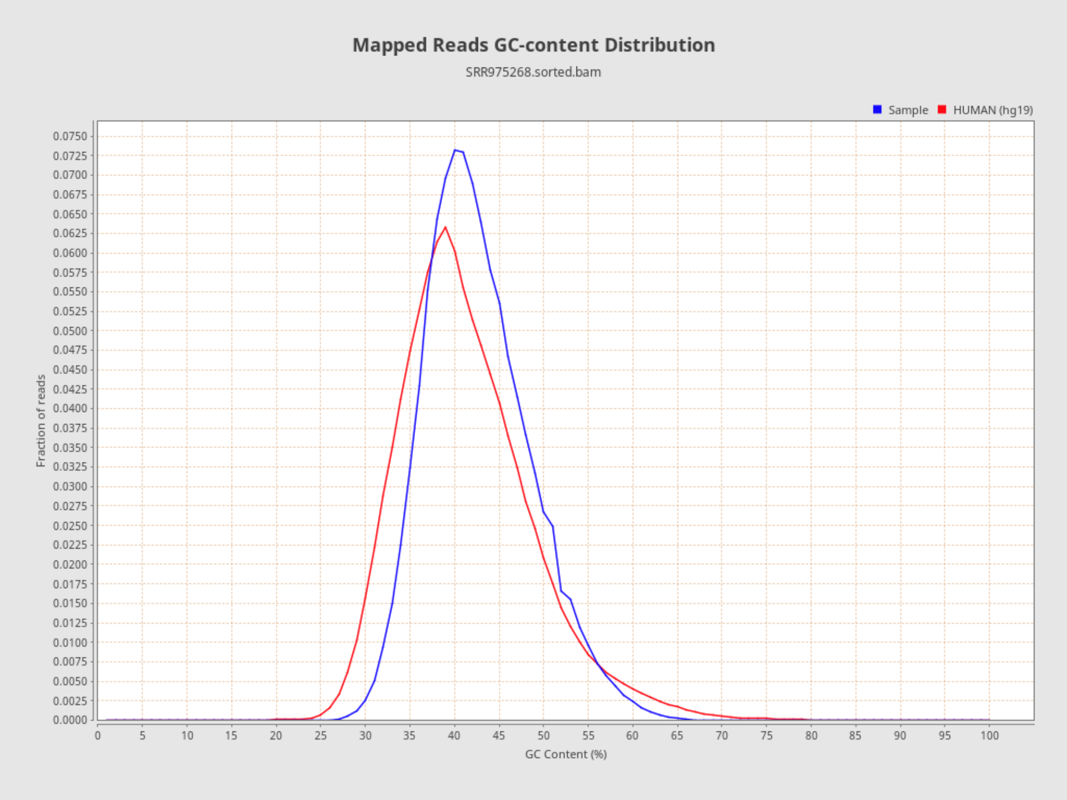
7. Results : Duplication Rate Histogram



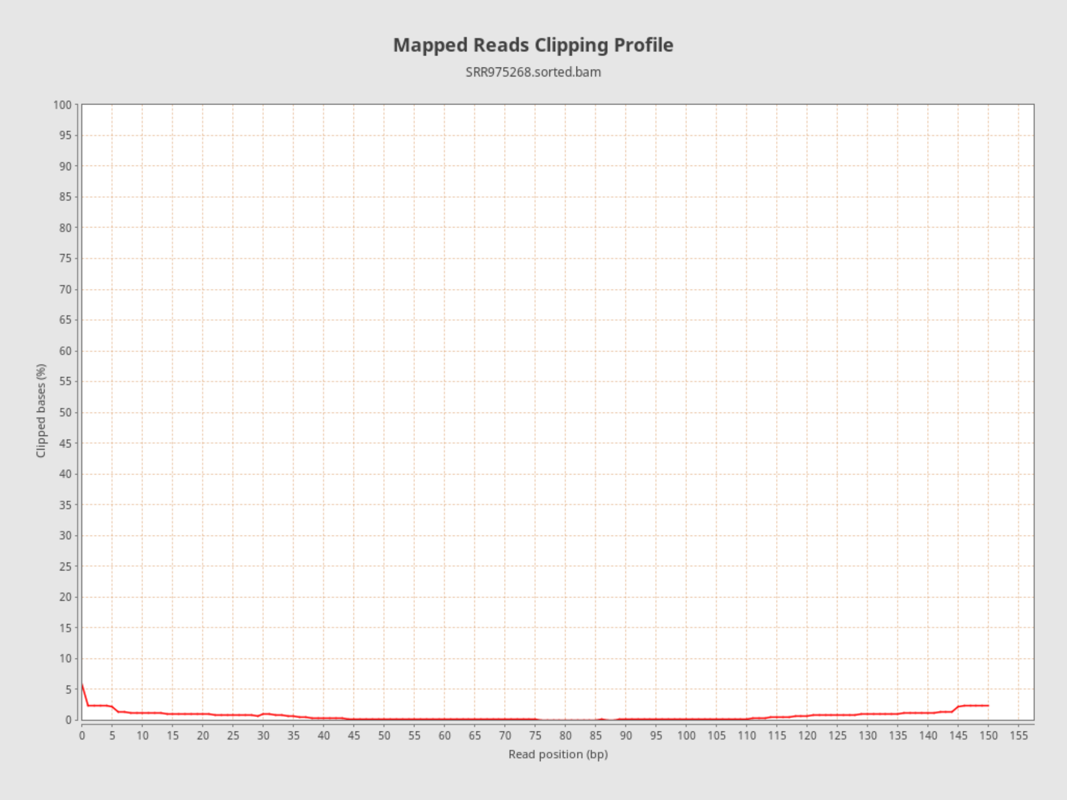
8. Results : Mapped Reads Nucleotide Content



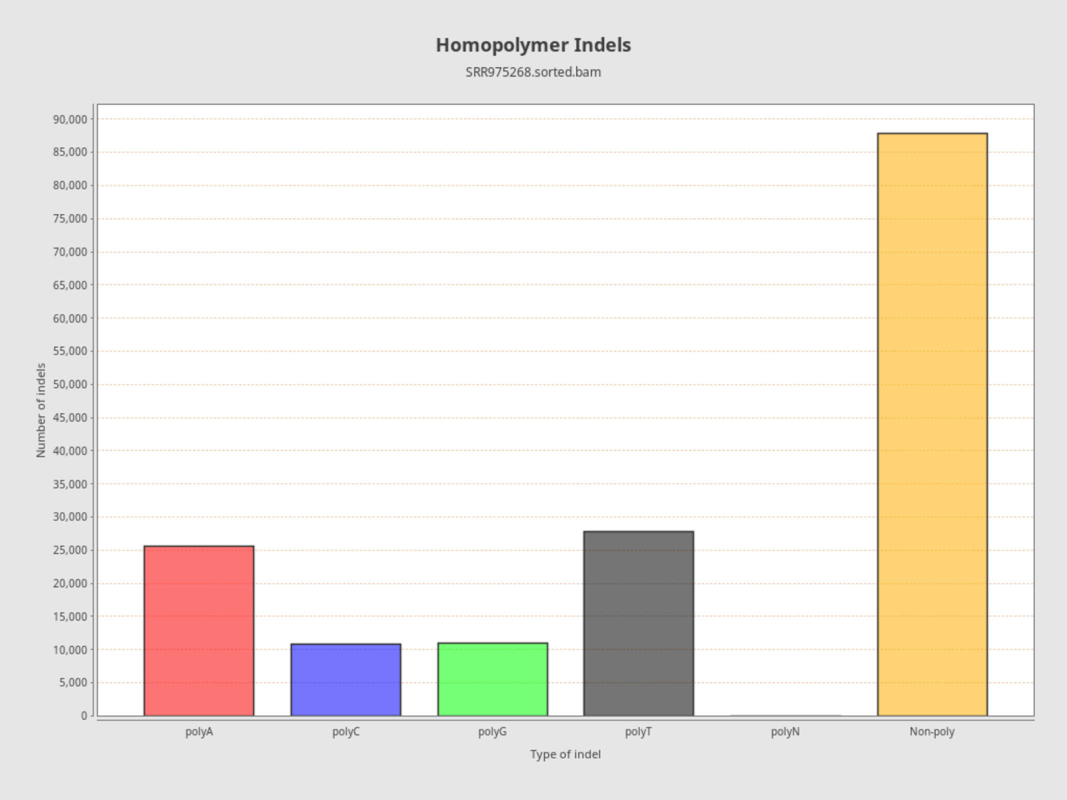
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

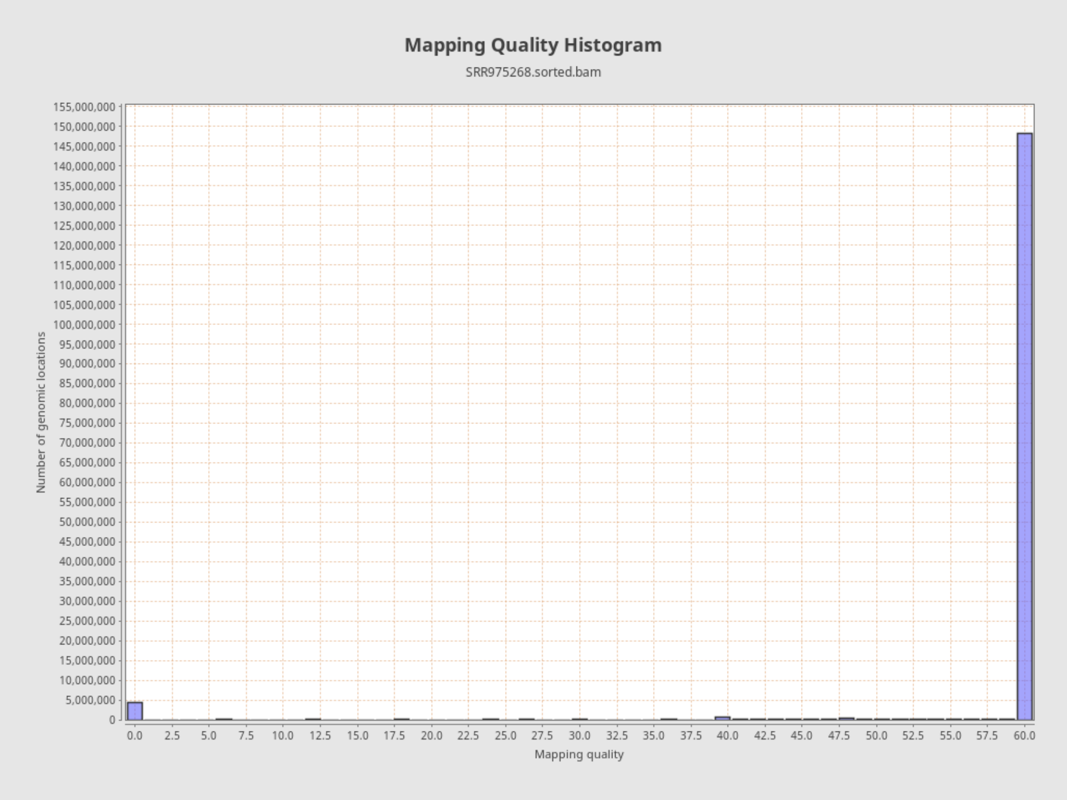


11. Results : Homopolymer Indels

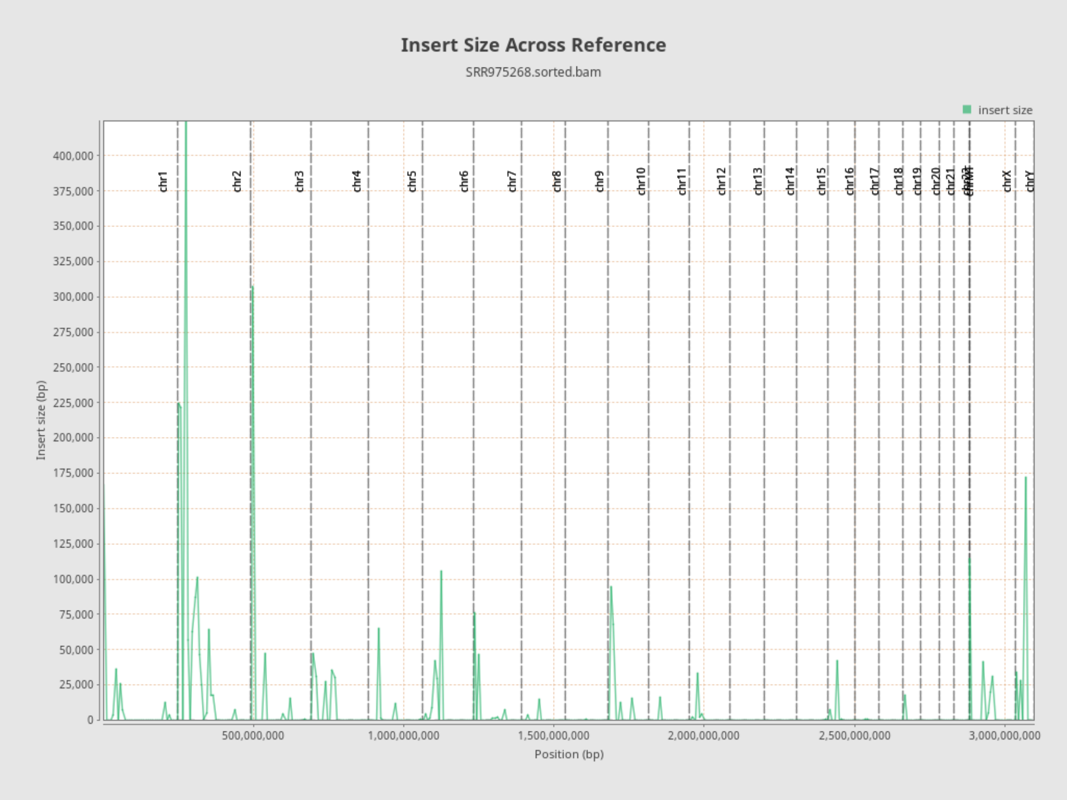


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram