Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 02:20:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975312.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_SRR975312 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975312_1.fastq.gz SRR975312_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 02:20:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975312.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,399,276
Mapped reads	2,331,338 / 97.17%
Unmapped reads	67,938 / 2.83%
Mapped paired reads	2,331,338 / 97.17%
Mapped reads, first in pair	1,187,764 / 49.51%
Mapped reads, second in pair	1,143,574 / 47.66%
Mapped reads, both in pair	2,283,760 / 95.19%
Mapped reads, singletons	47,578 / 1.98%
Secondary alignments	0
Supplementary alignments	24,325 / 1.01%
Read min/max/mean length	30 / 151 / 151.49
Duplicated reads (estimated)	333,351 / 13.89%
Duplication rate	14.09%
Clipped reads	1,690,533 / 70.46%

2.2. ACGT Content

Number/percentage of A's	90,559,807 / 28.97%
Number/percentage of C's	63,983,172 / 20.47%
Number/percentage of T's	90,499,674 / 28.95%
Number/percentage of G's	67,542,008 / 21.61%
Number/percentage of N's	18,449 / 0.01%

GC Percentage	42.07%

2.3. Coverage

Mean	0.101
Standard Deviation	1.0656

2.4. Mapping Quality

Mean Mapping Quality	53.65

2.5. Insert size

Mean	71,303.26
Standard Deviation	2,555,826.64
P25/Median/P75	135 / 168 / 213

2.6. Mismatches and indels

General error rate	1.32%
Mismatches	3,991,411
Insertions	56,666
Mapped reads with at least one insertion	2.32%
Deletions	114,734
Mapped reads with at least one deletion	4.75%
Homopolymer indels	46.46%

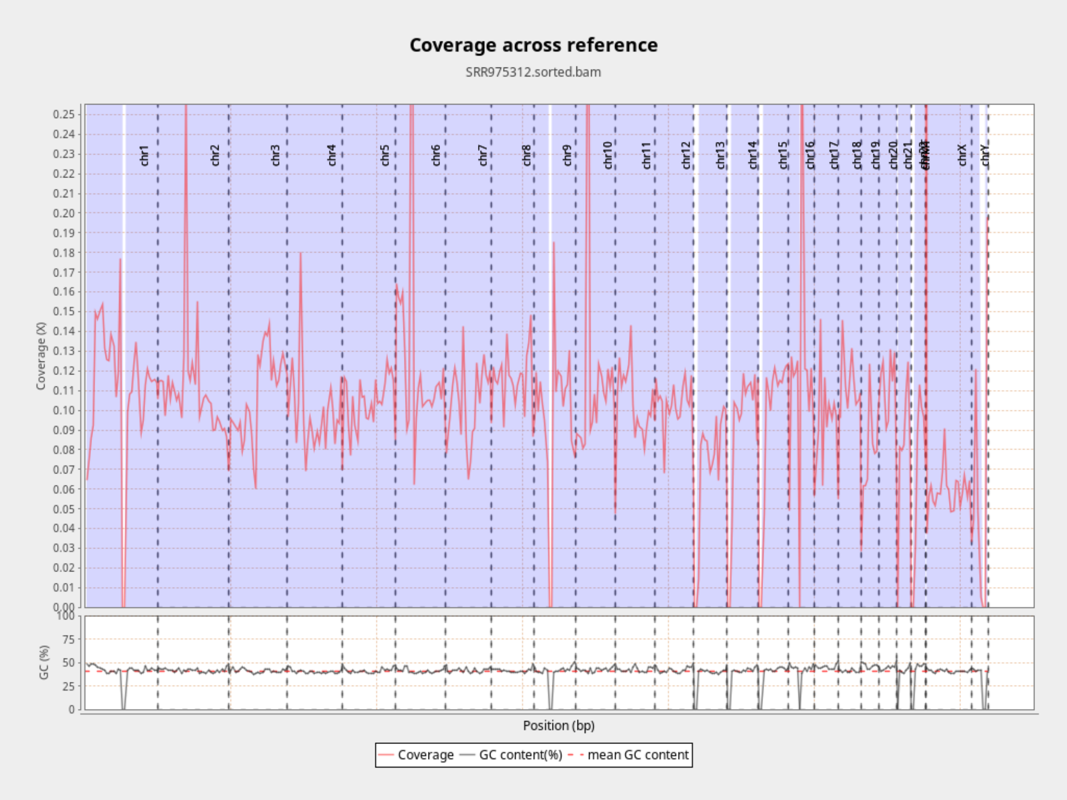
2.7. Chromosome stats

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

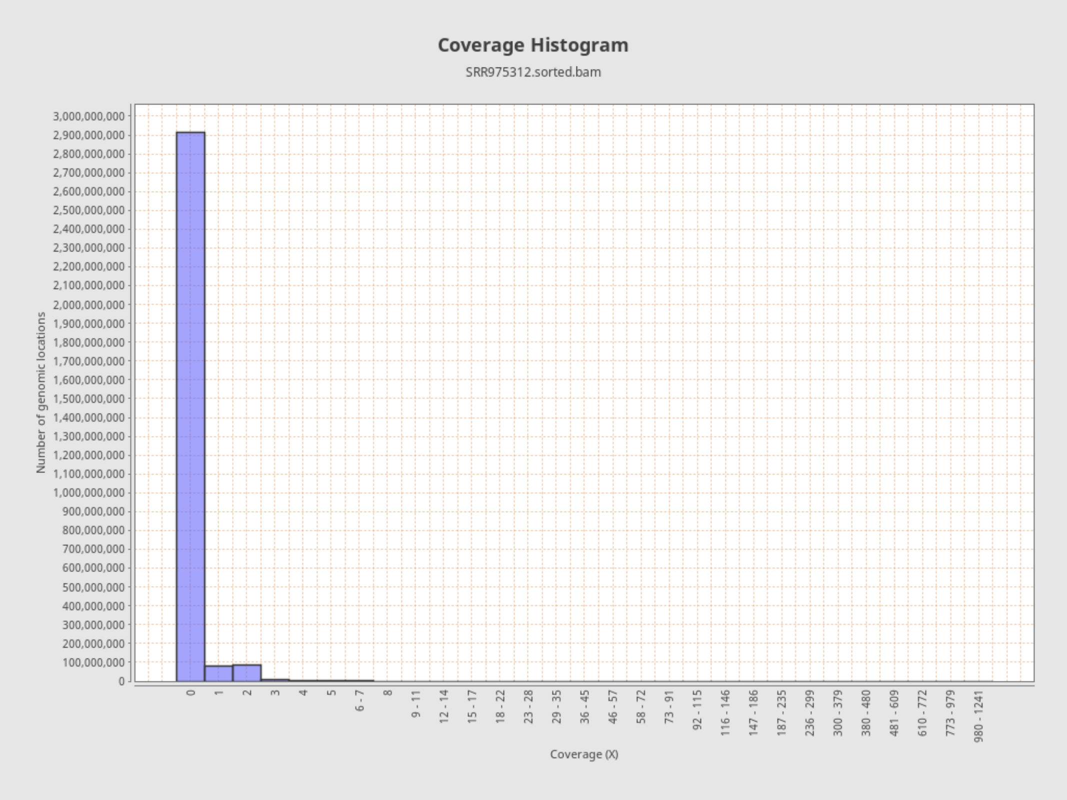
		bases	coverage	deviation
chr1	249250621	27607711	0.1108	1.1376
chr2	243199373	27075707	0.1113	1.1531
chr3	198022430	21307593	0.1076	0.4582
chr4	191154276	18907981	0.0989	0.7212
chr5	180915260	18983836	0.1049	0.449
chr6	171115067	21740065	0.127	1.2832
chr7	159138663	16515776	0.1038	1.1431
chr8	146364022	17094661	0.1168	0.5591
chr9	141213431	13754835	0.0974	1.8356
chr10	135534747	15780656	0.1164	2.3137
chr11	135006516	14055375	0.1041	1.0856
chr12	133851895	13811623	0.1032	0.4433
chr13	115169878	8096440	0.0703	0.3617
chr14	107349540	9397063	0.0875	0.4232
chr15	102531392	9605681	0.0937	0.4267
chr16	90354753	10773858	0.1192	1.4814
chr17	81195210	7717245	0.095	1.189
chr18	78077248	8821624	0.113	1.6447
chr19	59128983	4561477	0.0771	0.7134
chr20	63025520	7019632	0.1114	0.5053
chr21	48129895	4068515	0.0845	0.5363
chr22	51304566	3464303	0.0675	0.3611
chrMT	16571	94359	5.6942	4.1463
chrX	155270560	9160971	0.059	0.4625

chrY	59373566	3400391	0.0573	1.2356

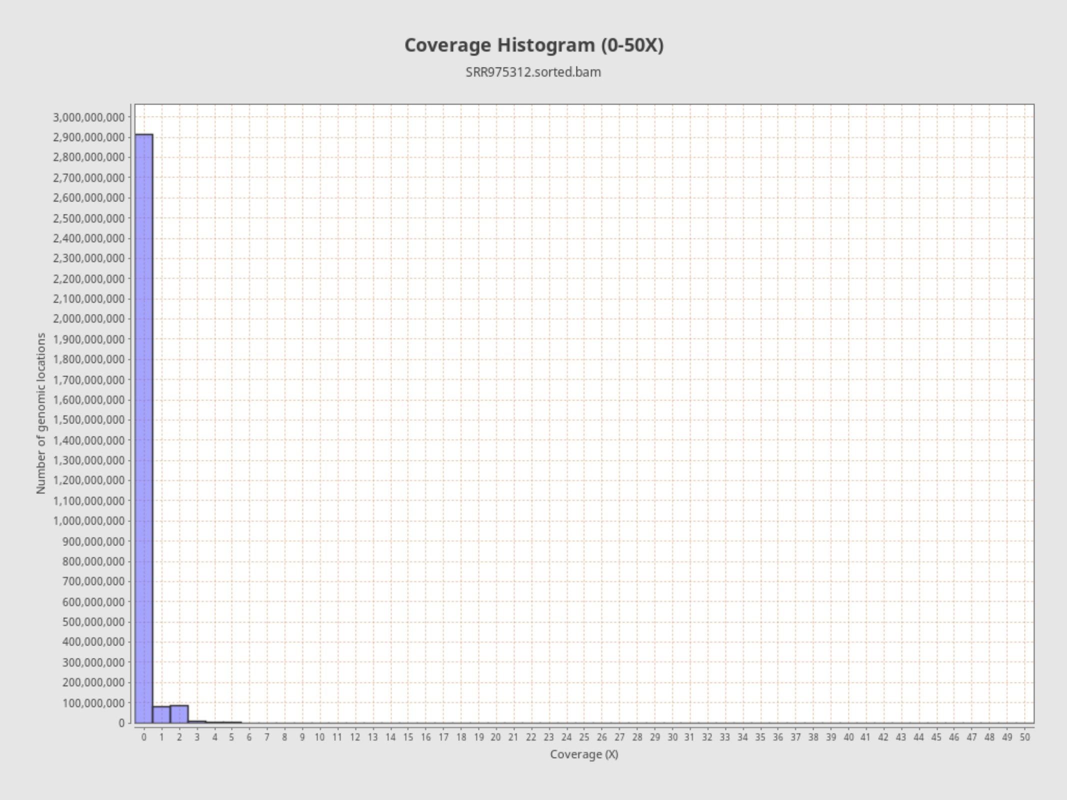
3. Results : Coverage across reference



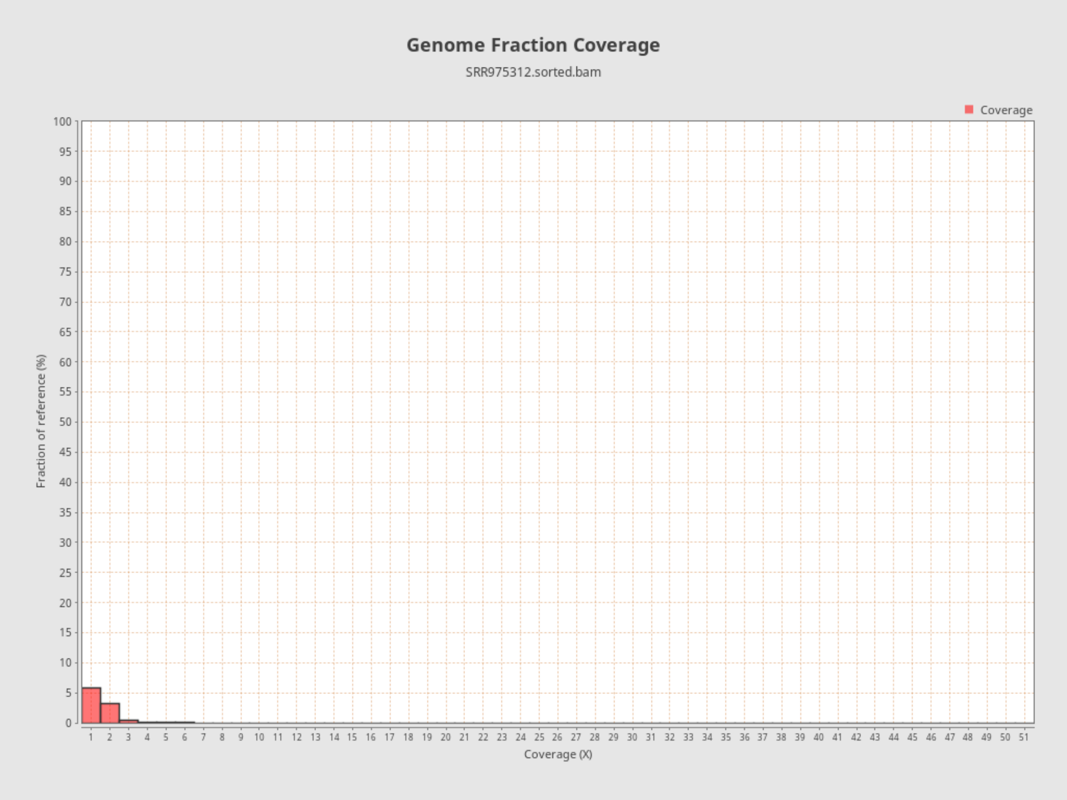
4. Results : Coverage Histogram



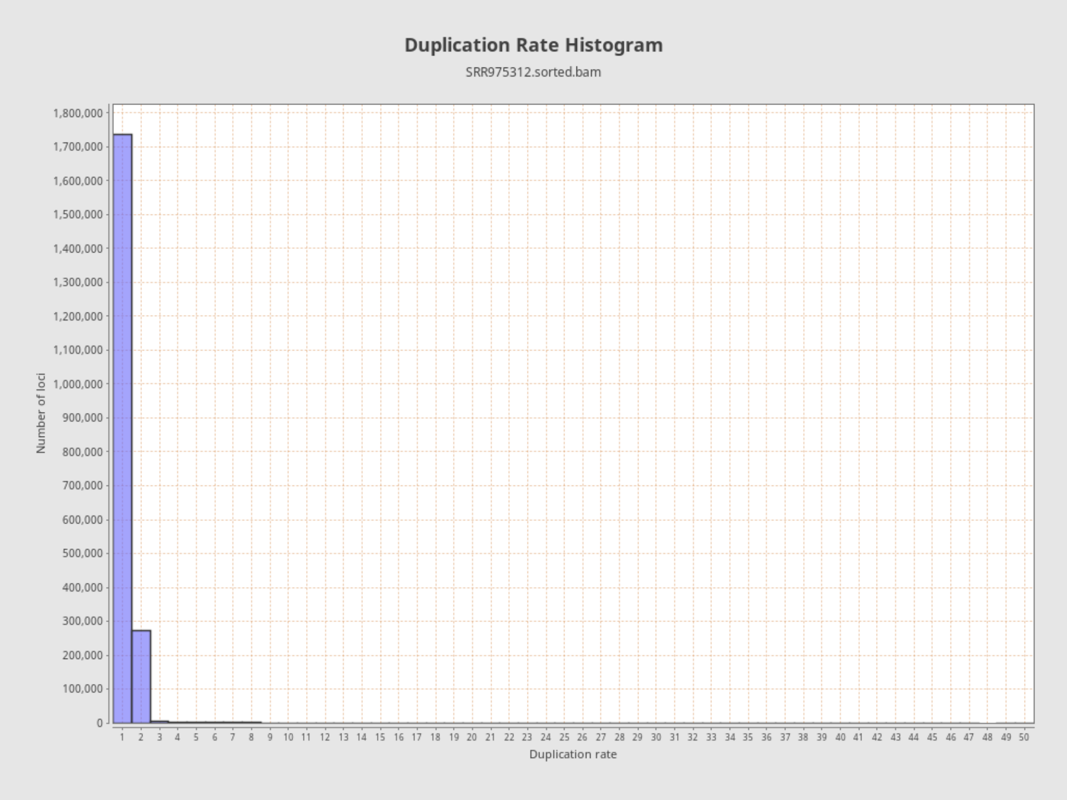
5. Results : Coverage Histogram (0-50X)



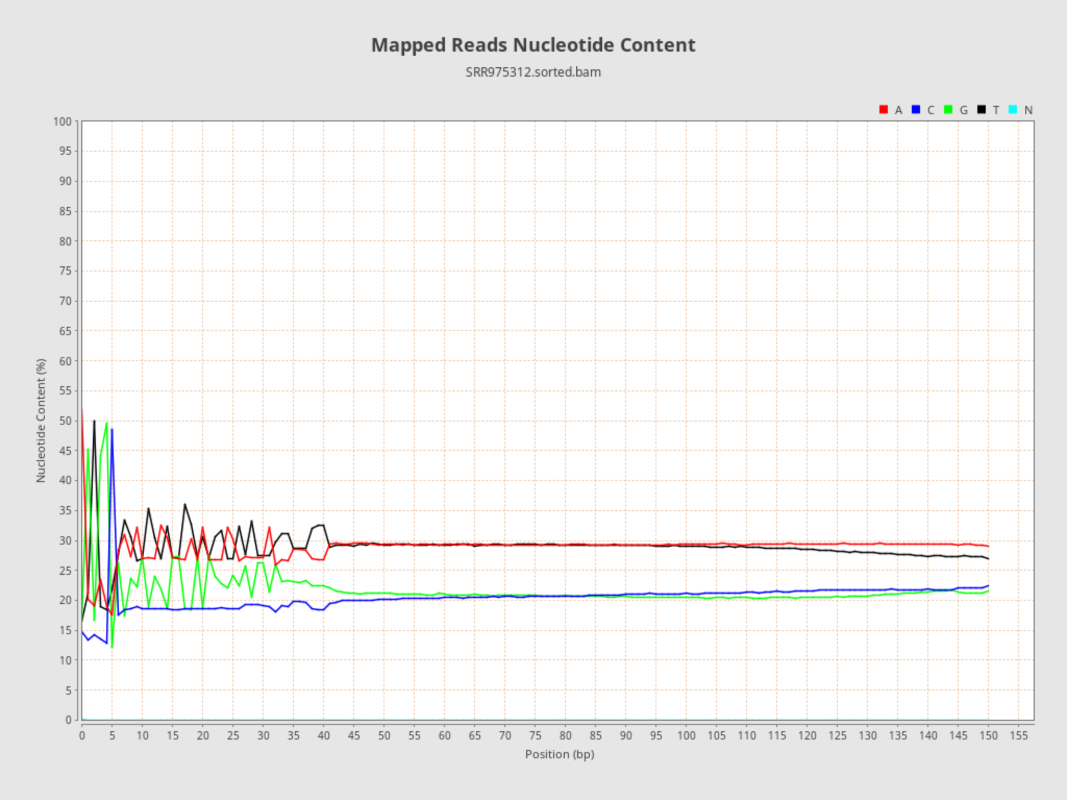
6. Results : Genome Fraction Coverage



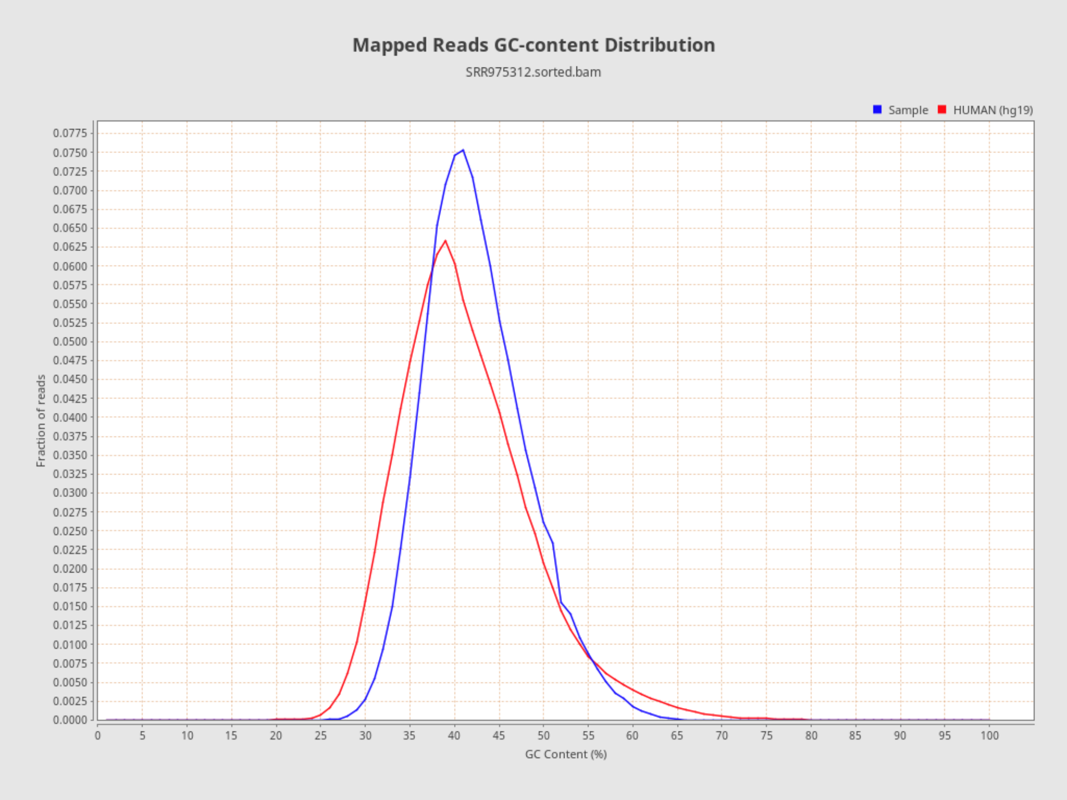
7. Results : Duplication Rate Histogram



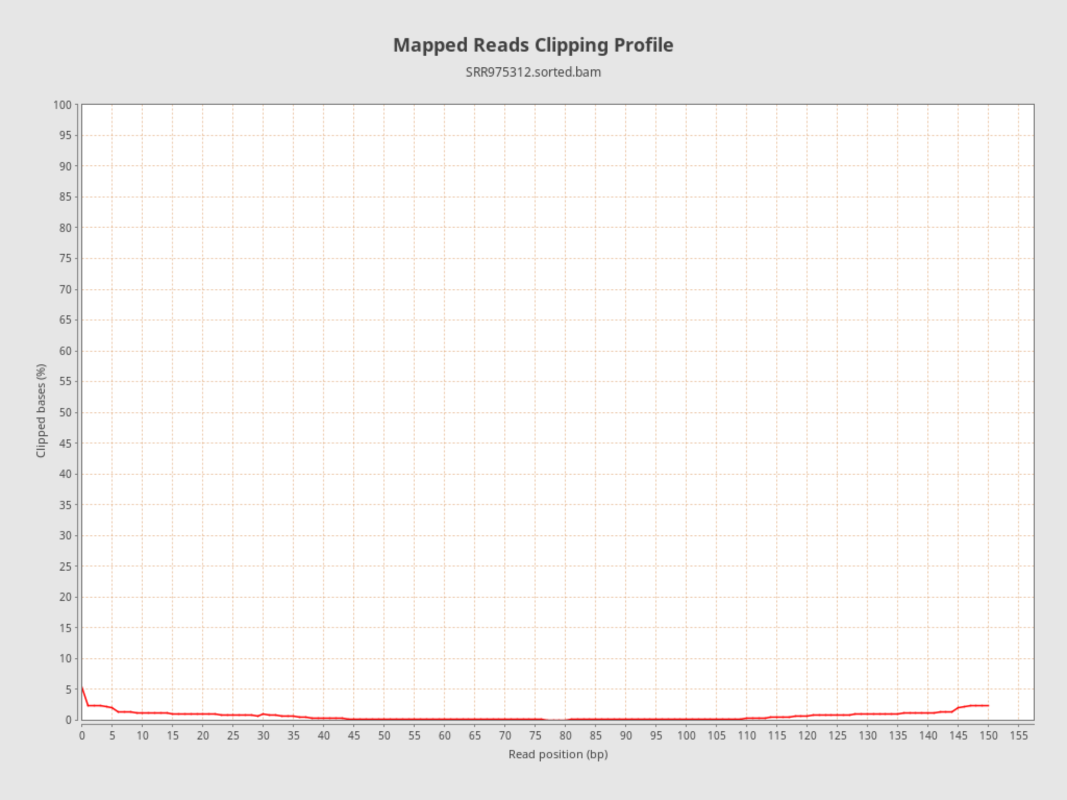
8. Results : Mapped Reads Nucleotide Content



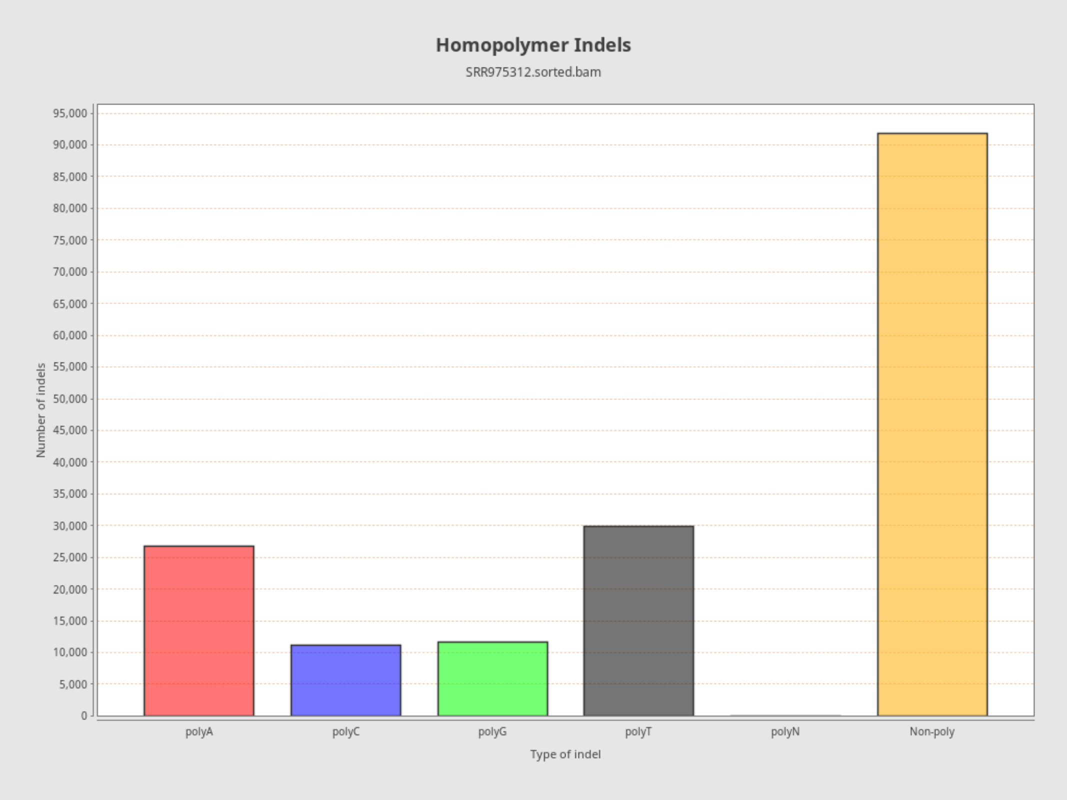
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

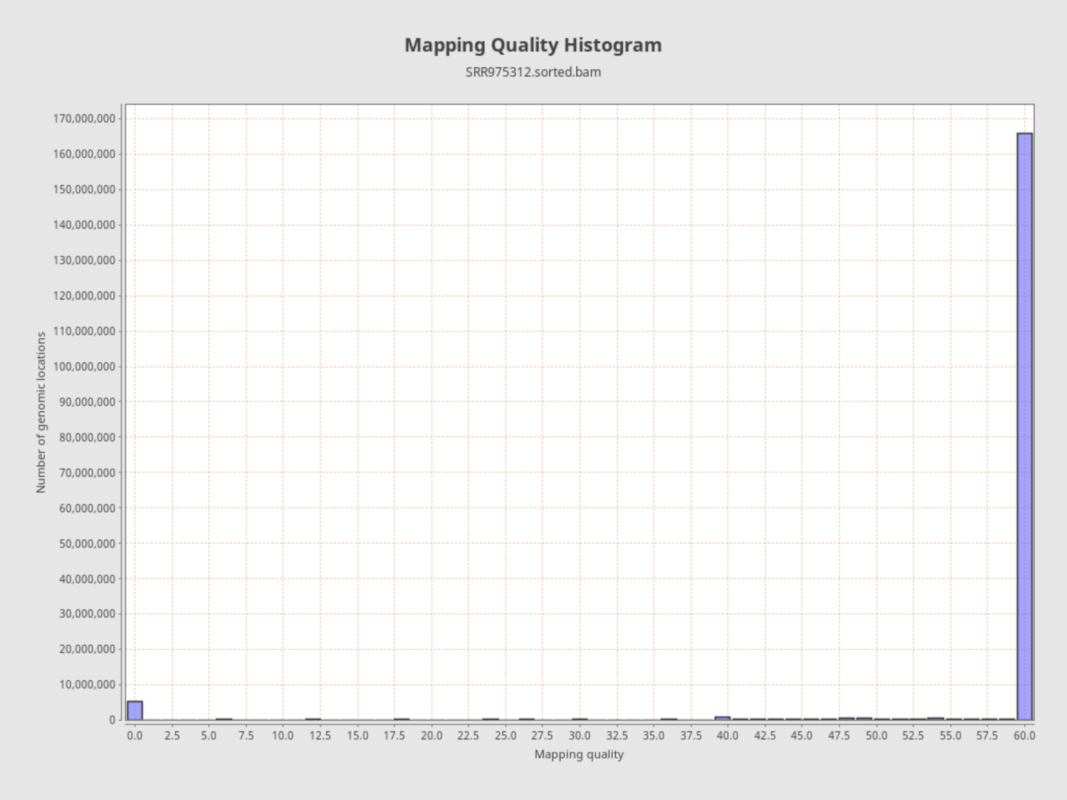


11. Results : Homopolymer Indels

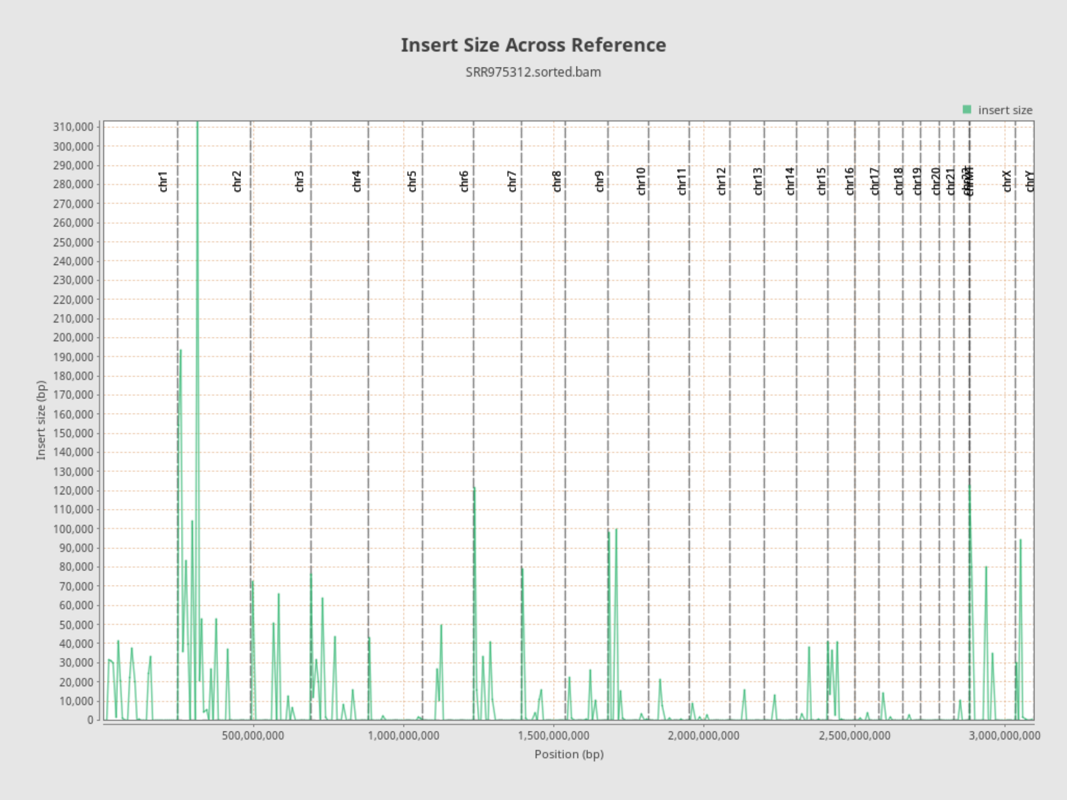


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram