Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 19:46:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975252.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_SRR975252 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975252_1.fastq.gz SRR975252_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 19:46:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975252.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	132,652,904
Mapped reads	131,486,058 / 99.12%
Unmapped reads	1,166,846 / 0.88%
Mapped paired reads	131,486,058 / 99.12%
Mapped reads, first in pair	65,739,490 / 49.56%
Mapped reads, second in pair	65,746,568 / 49.56%
Mapped reads, both in pair	130,963,562 / 98.73%
Mapped reads, singletons	522,496 / 0.39%
Secondary alignments	0
Supplementary alignments	309,658 / 0.23%
Read min/max/mean length	30 / 101 / 101.09
Duplicated reads (estimated)	88,606,916 / 66.8%
Duplication rate	47.89%
Clipped reads	83,035,117 / 62.6%

2.2. ACGT Content

Number/percentage of A's	3,300,015,626 / 27.54%
Number/percentage of C's	2,545,173,114 / 21.24%
Number/percentage of T's	3,345,666,244 / 27.92%
Number/percentage of G's	2,792,473,664 / 23.3%
Number/percentage of N's	331,687 / 0%

GC Percentage	44.54%

2.3. Coverage

Mean	3.8724
Standard Deviation	62.5066

2.4. Mapping Quality

Mean Mapping Quality	55.75

2.5. Insert size

Mean	61,761.61
Standard Deviation	2,413,518.58
P25/Median/P75	145 / 182 / 232

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	69,092,919
Insertions	1,304,173
Mapped reads with at least one insertion	0.98%
Deletions	2,785,528
Mapped reads with at least one deletion	2.09%
Homopolymer indels	47.03%

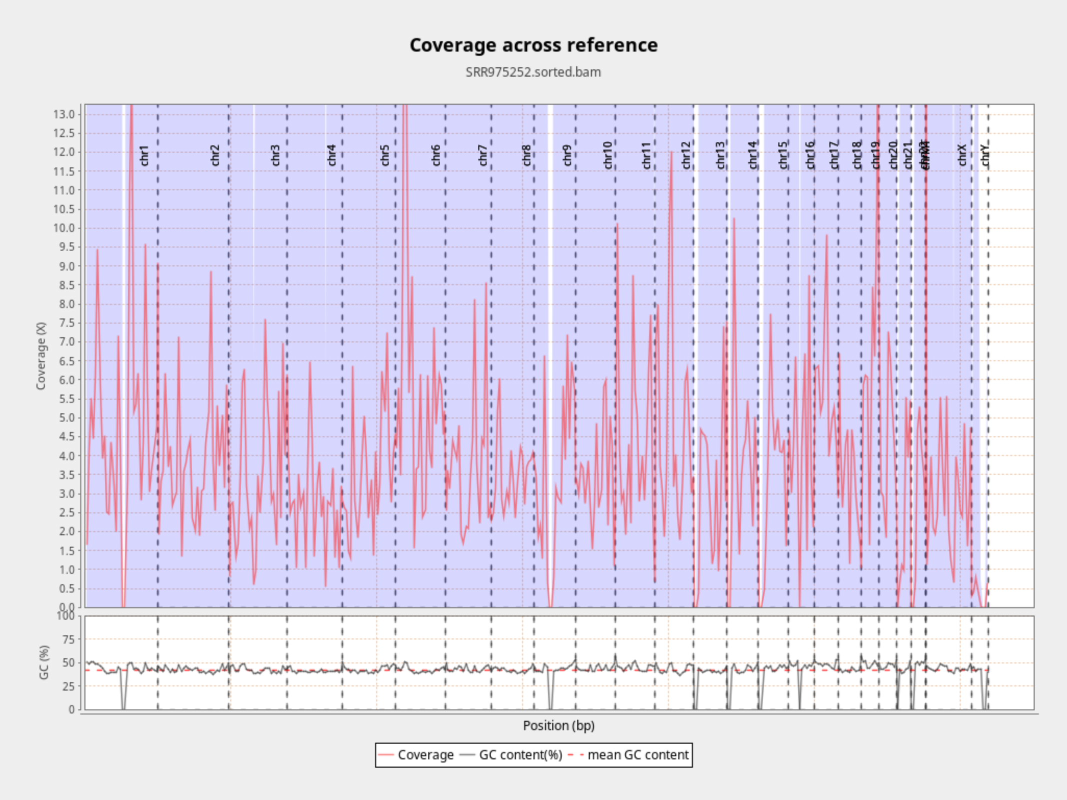
2.7. Chromosome stats

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

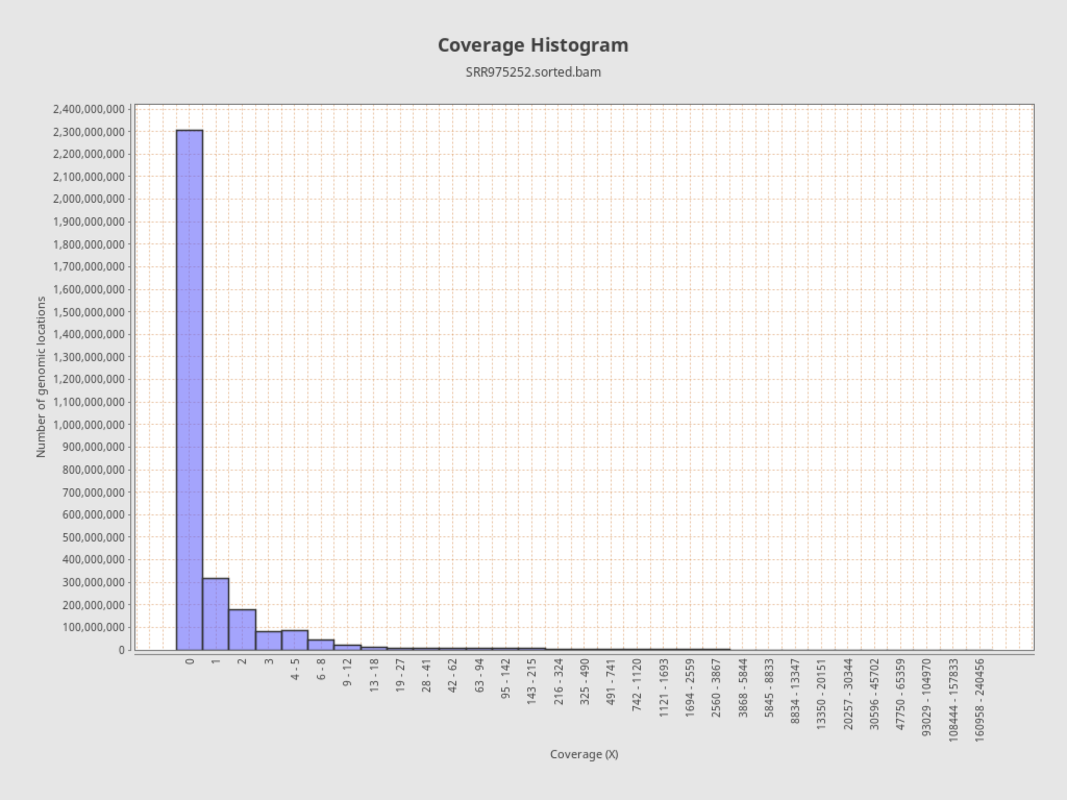
		bases	coverage	deviation
chr1	249250621	1213092762	4.867	56.4586
chr2	243199373	941116141	3.8697	47.6745
chr3	198022430	686904224	3.4688	44.6459
chr4	191154276	532648320	2.7865	146.8834
chr5	180915260	640167893	3.5385	47.4788
chr6	171115067	1042653415	6.0933	76.7311
chr7	159138663	600300302	3.7722	51.5267
chr8	146364022	519150483	3.547	46.5714
chr9	141213431	465204881	3.2943	45.4751
chr10	135534747	475326852	3.507	49.3373
chr11	135006516	615376806	4.5581	54.2175
chr12	133851895	658139937	4.9169	56.9492
chr13	115169878	333986788	2.8999	45.0795
chr14	107349540	387517595	3.6099	48.5714
chr15	102531392	347287911	3.3871	44.722
chr16	90354753	369433684	4.0887	49.516
chr17	81195210	469067575	5.777	59.9633
chr18	78077248	270860914	3.4691	51.5997
chr19	59128983	387428996	6.5523	95.1728
chr20	63025520	293787962	4.6614	58.7213
chr21	48129895	121692982	2.5284	38.4716
chr22	51304566	147392632	2.8729	47.8105
chrMT	16571	462689	27.9216	31.0934
chrX	155270560	449378543	2.8942	40.7418

chrY	59373566	19499947	0.3284	8.55

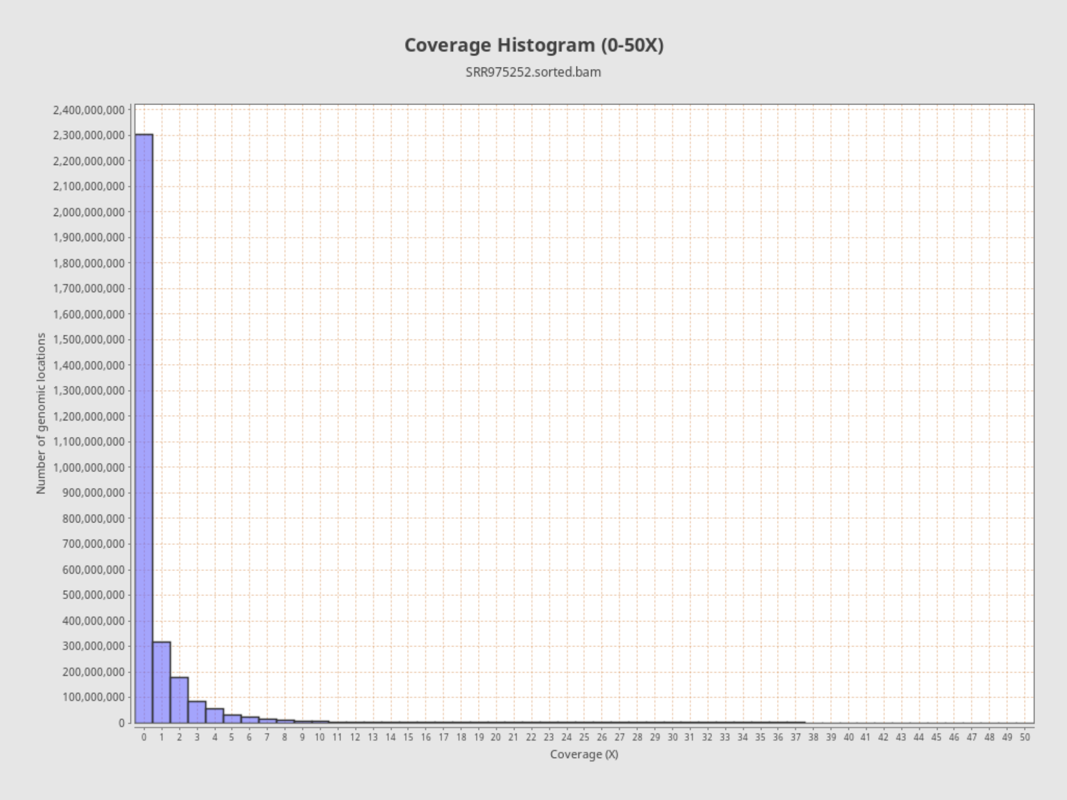
3. Results : Coverage across reference



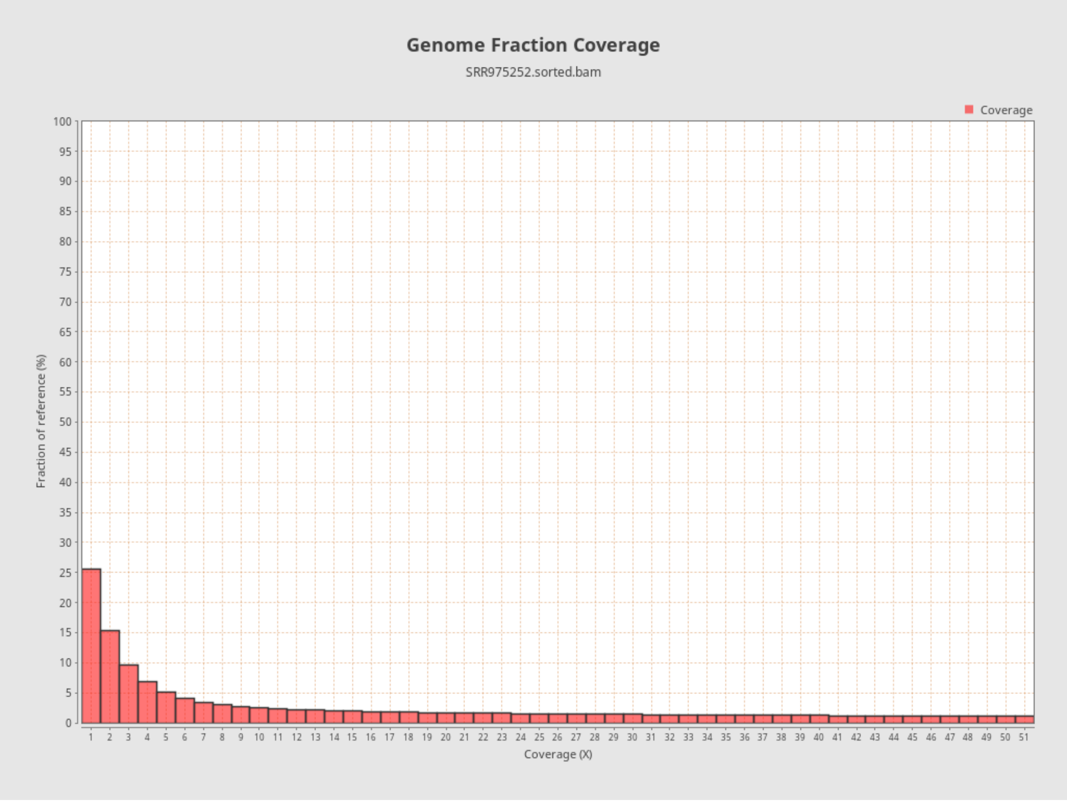
4. Results : Coverage Histogram



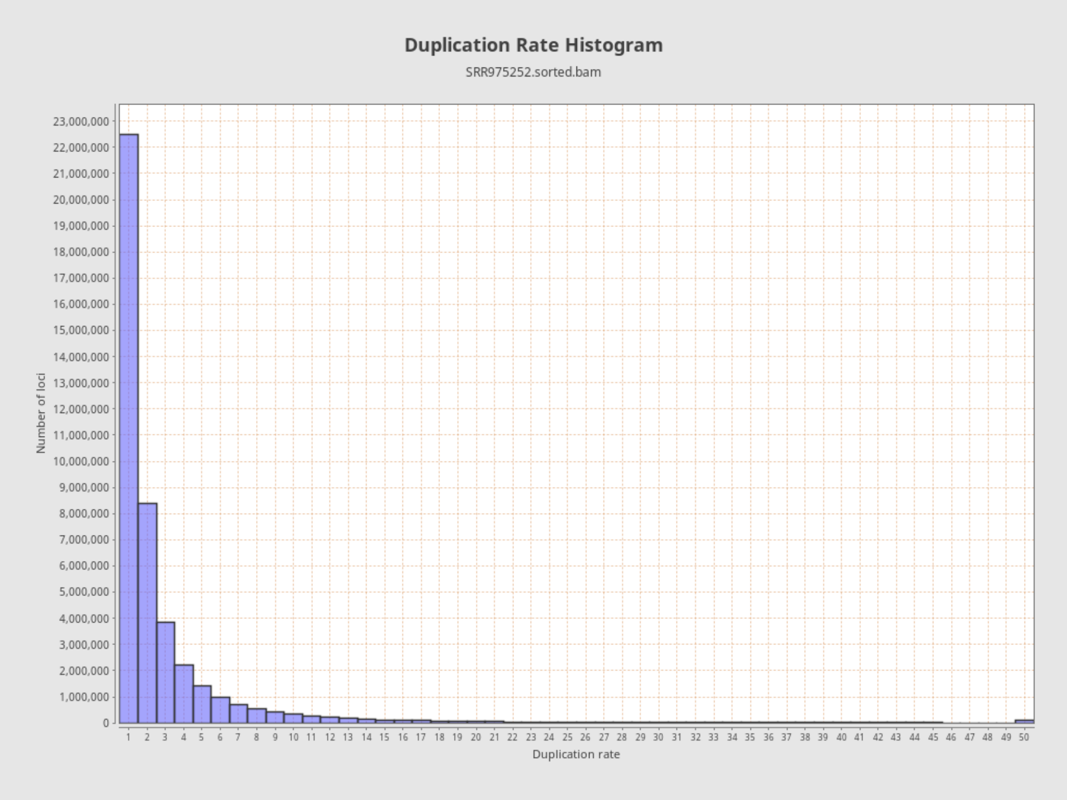
5. Results : Coverage Histogram (0-50X)



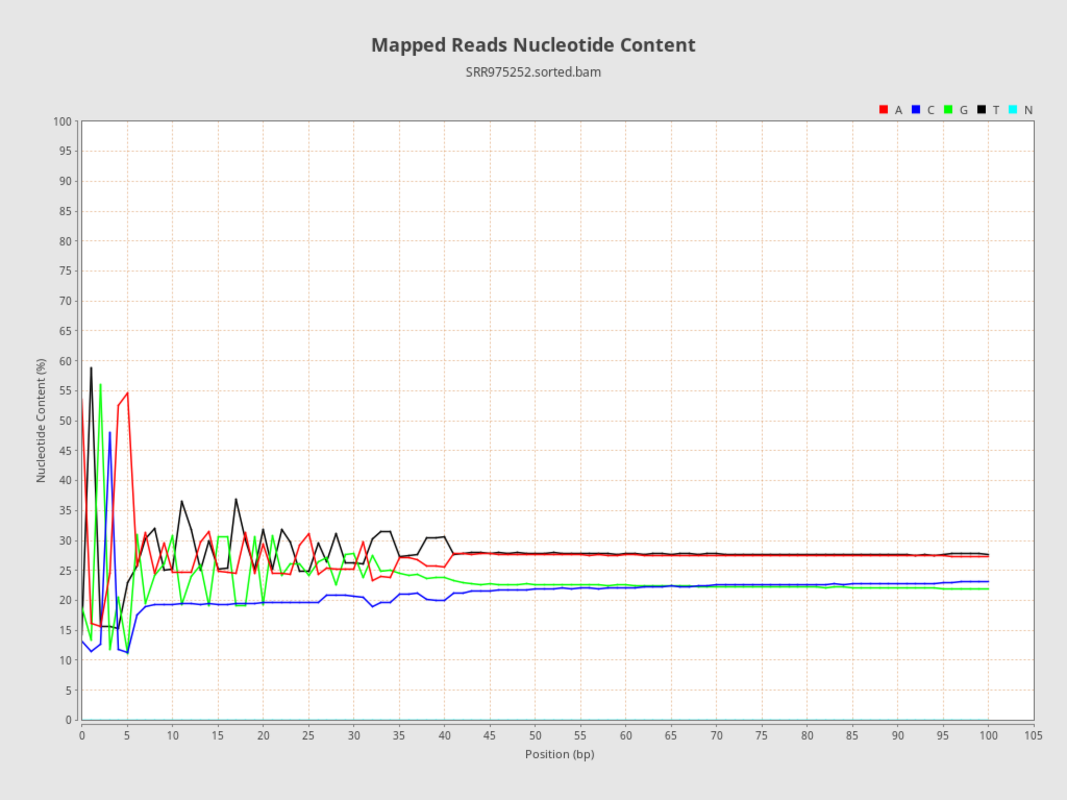
6. Results : Genome Fraction Coverage



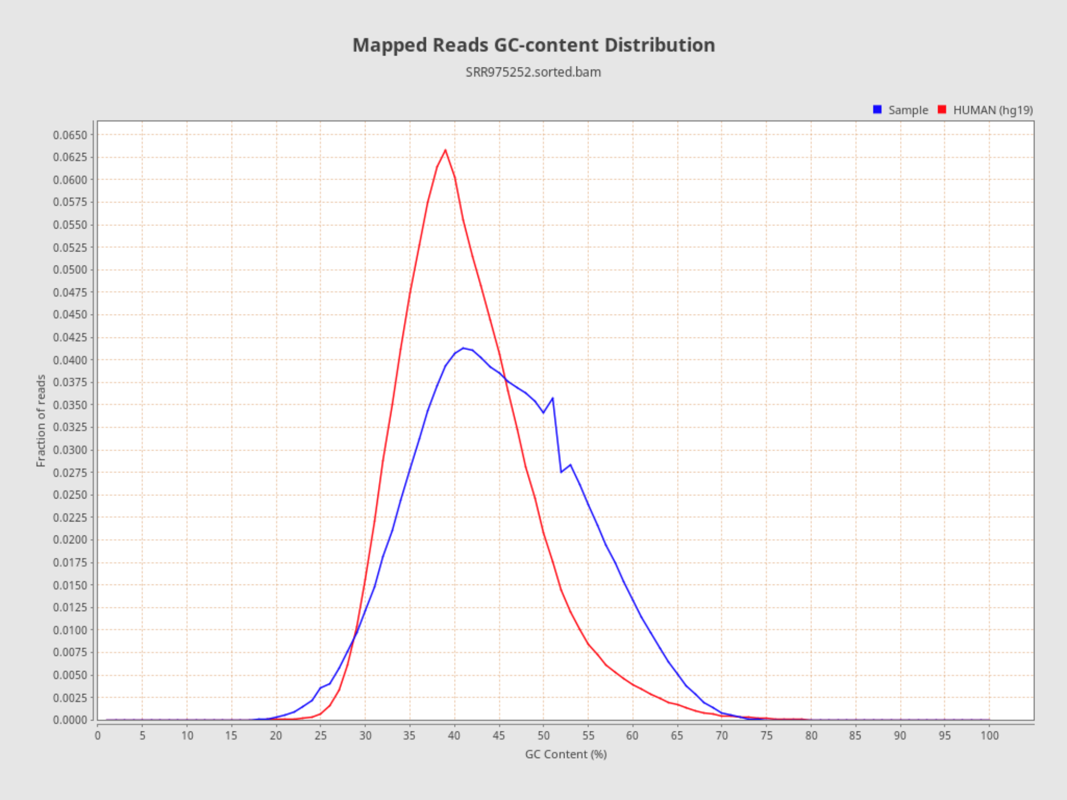
7. Results : Duplication Rate Histogram



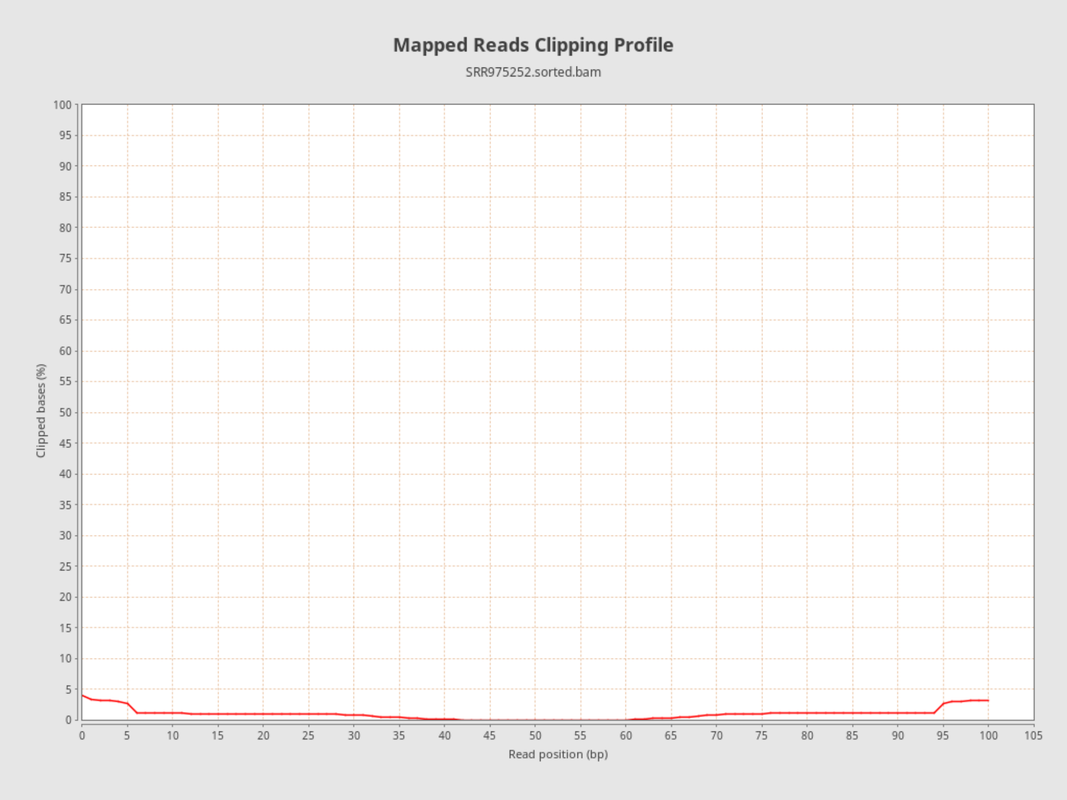
8. Results : Mapped Reads Nucleotide Content



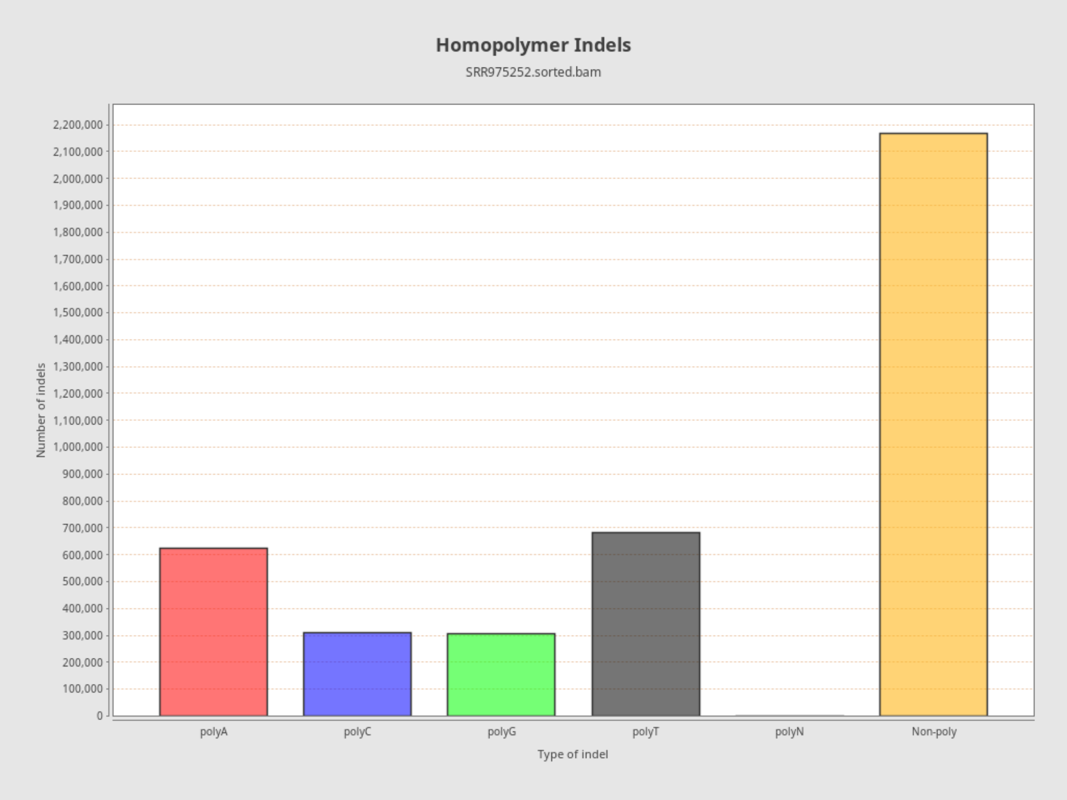
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

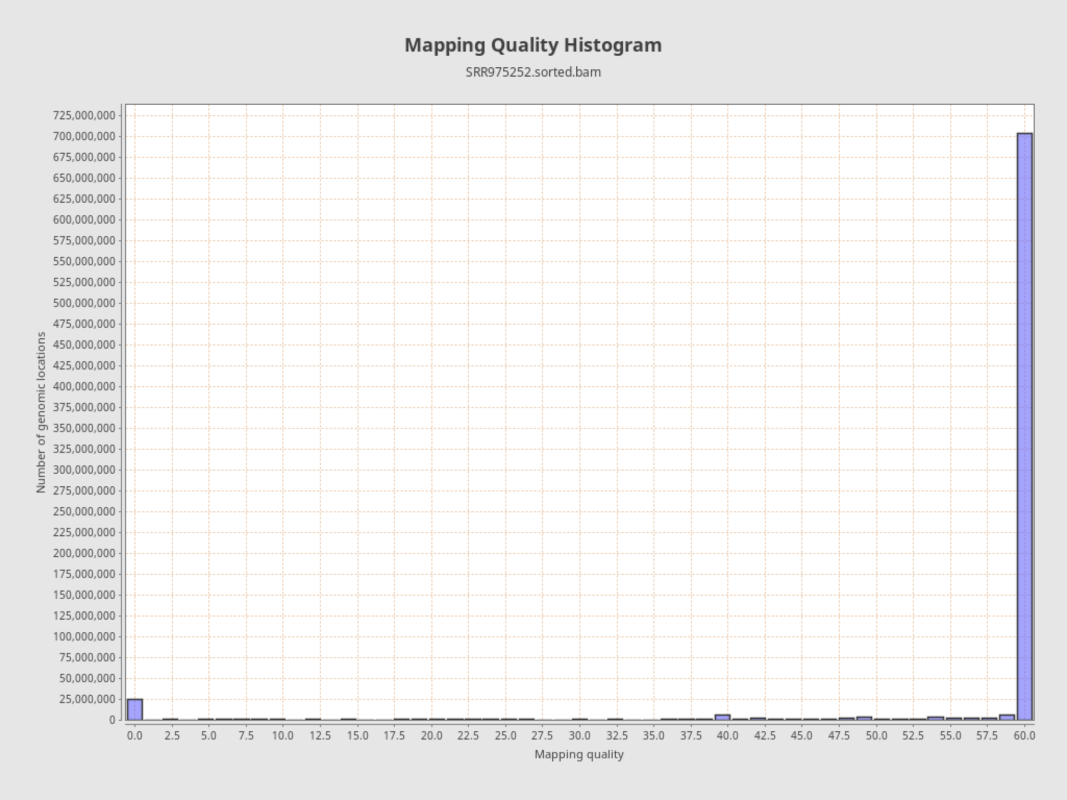


11. Results : Homopolymer Indels

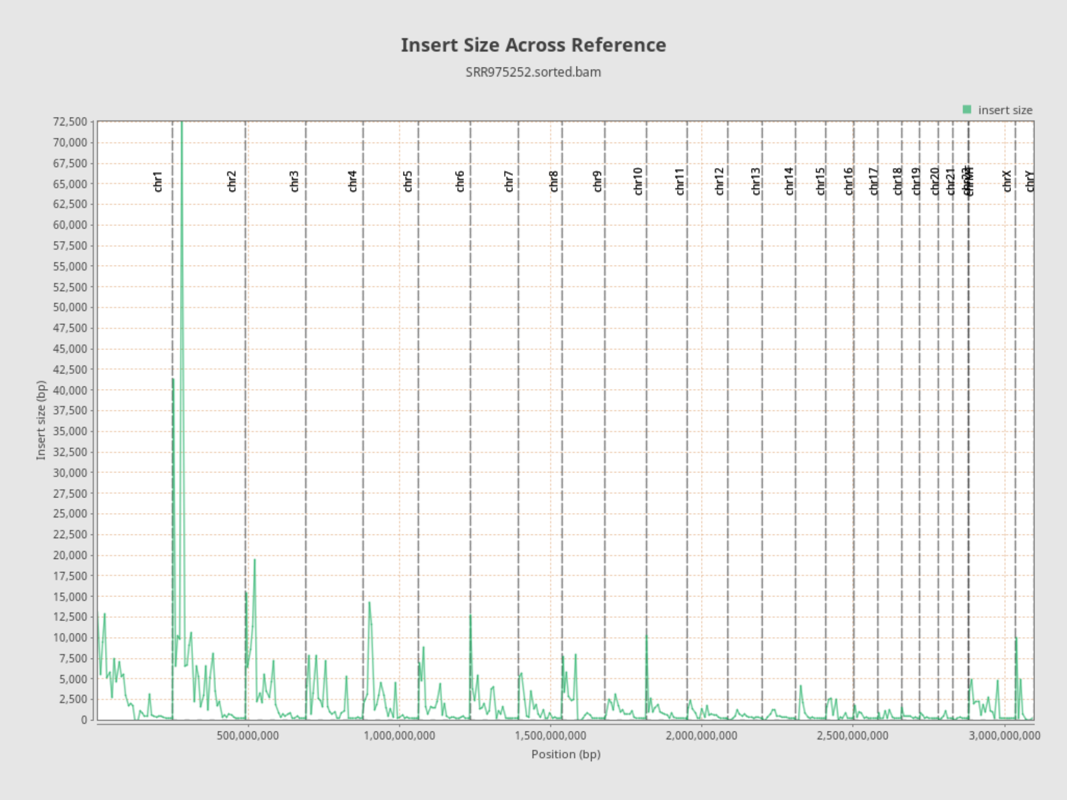


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram