Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2024/09/07 05:41:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975331.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_SRR975331 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975331_1.fastq.gz SRR975331_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 05:41:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975331.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,371,266
Mapped reads	3,260,542 / 96.72%
Unmapped reads	110,724 / 3.28%
Mapped paired reads	3,260,542 / 96.72%
Mapped reads, first in pair	1,629,567 / 48.34%
Mapped reads, second in pair	1,630,975 / 48.38%
Mapped reads, both in pair	3,241,604 / 96.15%
Mapped reads, singletons	18,938 / 0.56%
Secondary alignments	0
Supplementary alignments	26,006 / 0.77%
Read min/max/mean length	30 / 101 / 101.3
Duplicated reads (estimated)	250,085 / 7.42%
Duplication rate	4.09%
Clipped reads	2,146,591 / 63.67%

2.2. ACGT Content

Number/percentage of A's	84,489,453 / 28.9%
Number/percentage of C's	56,091,153 / 19.19%
Number/percentage of T's	88,688,368 / 30.34%
Number/percentage of G's	63,073,985 / 21.57%
Number/percentage of N's	6,776 / 0%

GC Percentage	40.76%

2.3. Coverage

Mean	0.0945
Standard Deviation	1.3545

2.4. Mapping Quality

Mean Mapping Quality	52.29

2.5. Insert size

Mean	88,898.5
Standard Deviation	2,928,797.73
P25/Median/P75	131 / 163 / 207

2.6. Mismatches and indels

General error rate	0.86%
Mismatches	2,371,709
Insertions	59,101
Mapped reads with at least one insertion	1.74%
Deletions	103,670
Mapped reads with at least one deletion	3.1%
Homopolymer indels	44.12%

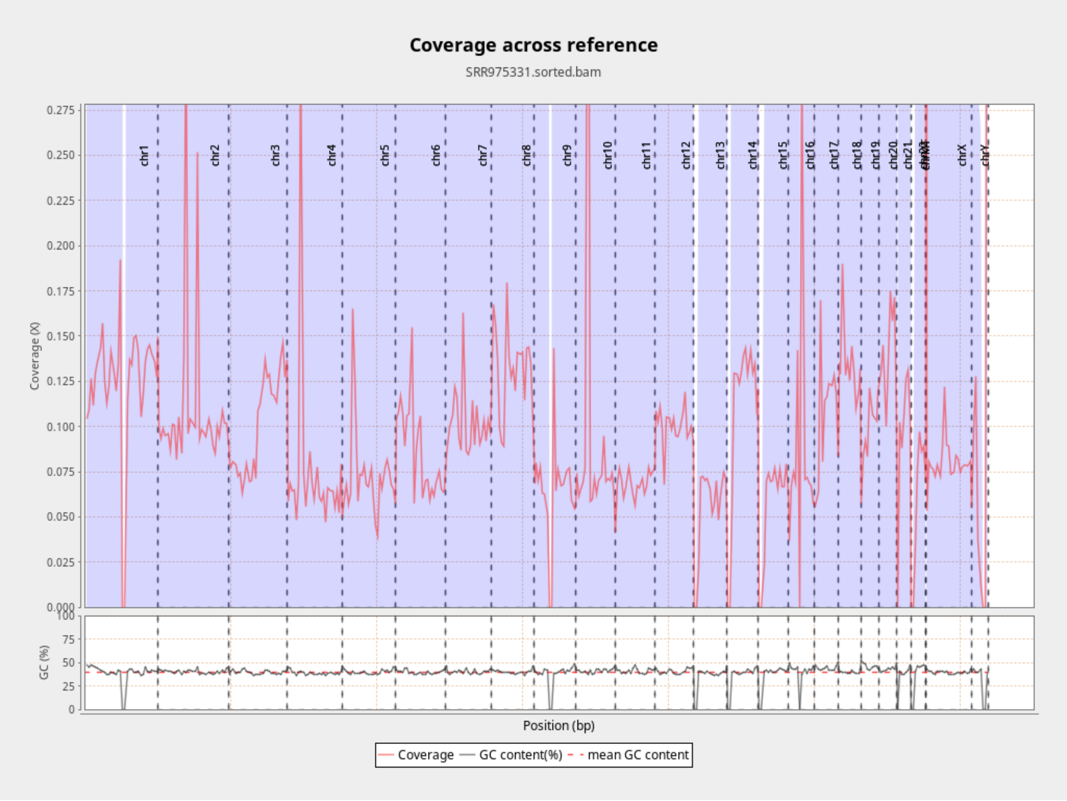
2.7. Chromosome stats

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

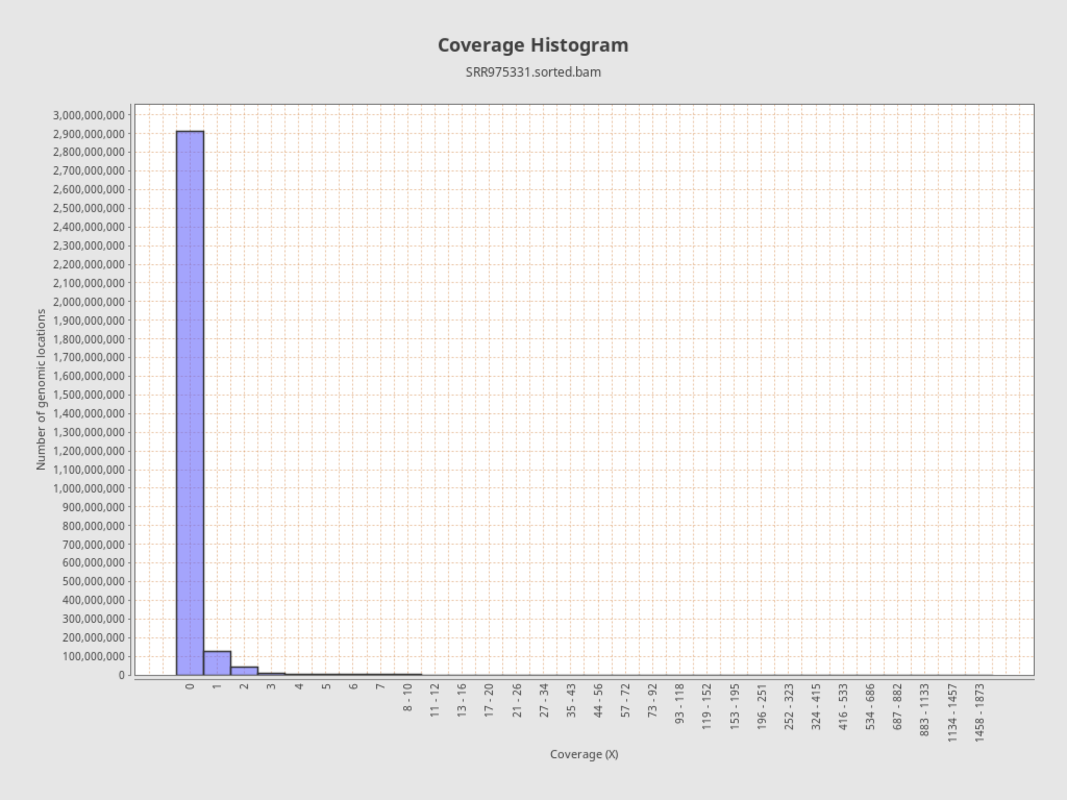
		bases	coverage	deviation
chr1	249250621	30988495	0.1243	1.1104
chr2	243199373	26898219	0.1106	2.149
chr3	198022430	19929708	0.1006	0.4636
chr4	191154276	14195963	0.0743	1.3252
chr5	180915260	13236005	0.0732	0.4036
chr6	171115067	14712092	0.086	0.718
chr7	159138663	16113041	0.1013	1.2061
chr8	146364022	19287763	0.1318	0.6926
chr9	141213431	9124383	0.0646	1.5537
chr10	135534747	12734605	0.094	3.4839
chr11	135006516	9210029	0.0682	0.5443
chr12	133851895	13416470	0.1002	0.4458
chr13	115169878	6355716	0.0552	0.3184
chr14	107349540	11665572	0.1087	0.5416
chr15	102531392	5905388	0.0576	0.3252
chr16	90354753	7888046	0.0873	1.9449
chr17	81195210	8796149	0.1083	1.473
chr18	78077248	10537113	0.135	1.928
chr19	59128983	5793037	0.098	0.6833
chr20	63025520	8887521	0.141	0.6175
chr21	48129895	4796774	0.0997	0.6203
chr22	51304566	3116884	0.0608	0.4557
chrMT	16571	294767	17.7881	13.5755
chrX	155270560	12519686	0.0806	0.5438

chrY	59373566	6154476	0.1037	2.595

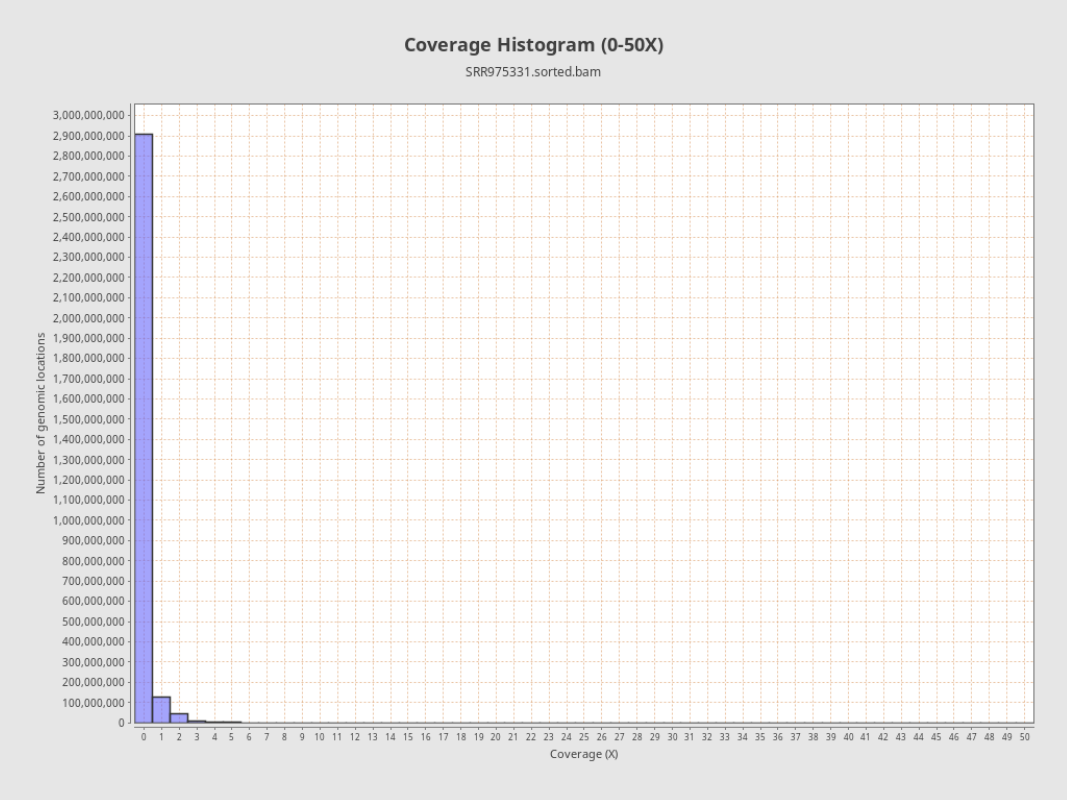
3. Results : Coverage across reference



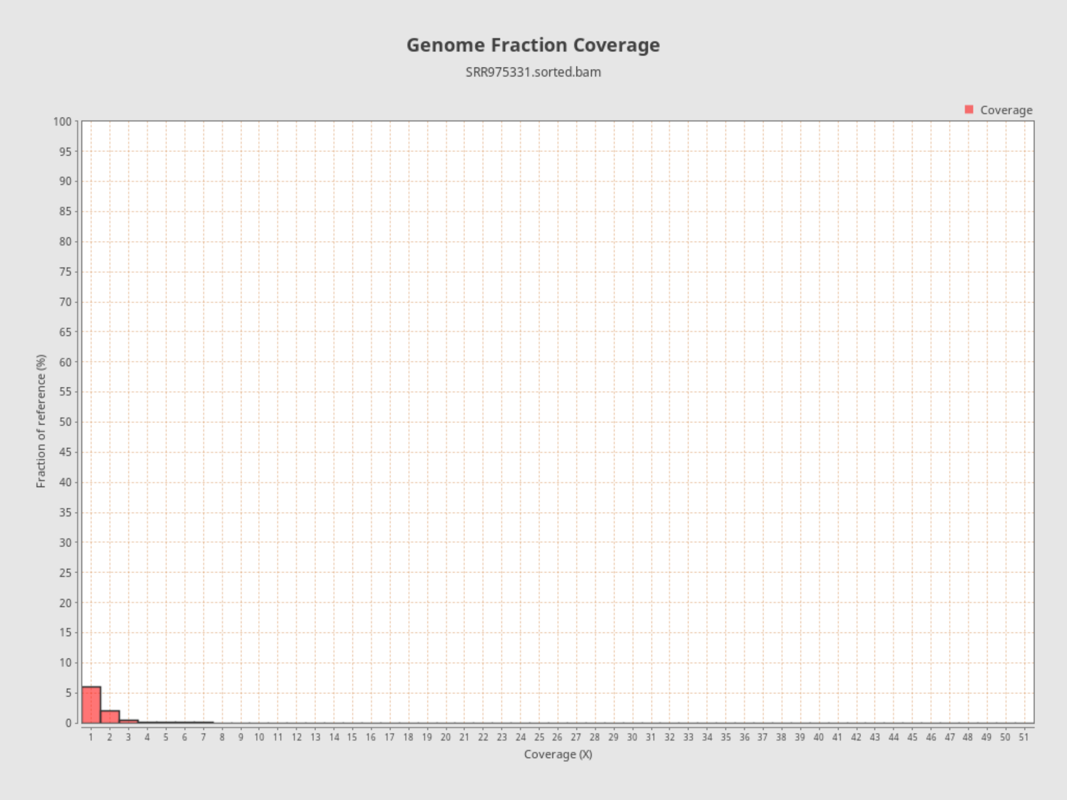
4. Results : Coverage Histogram



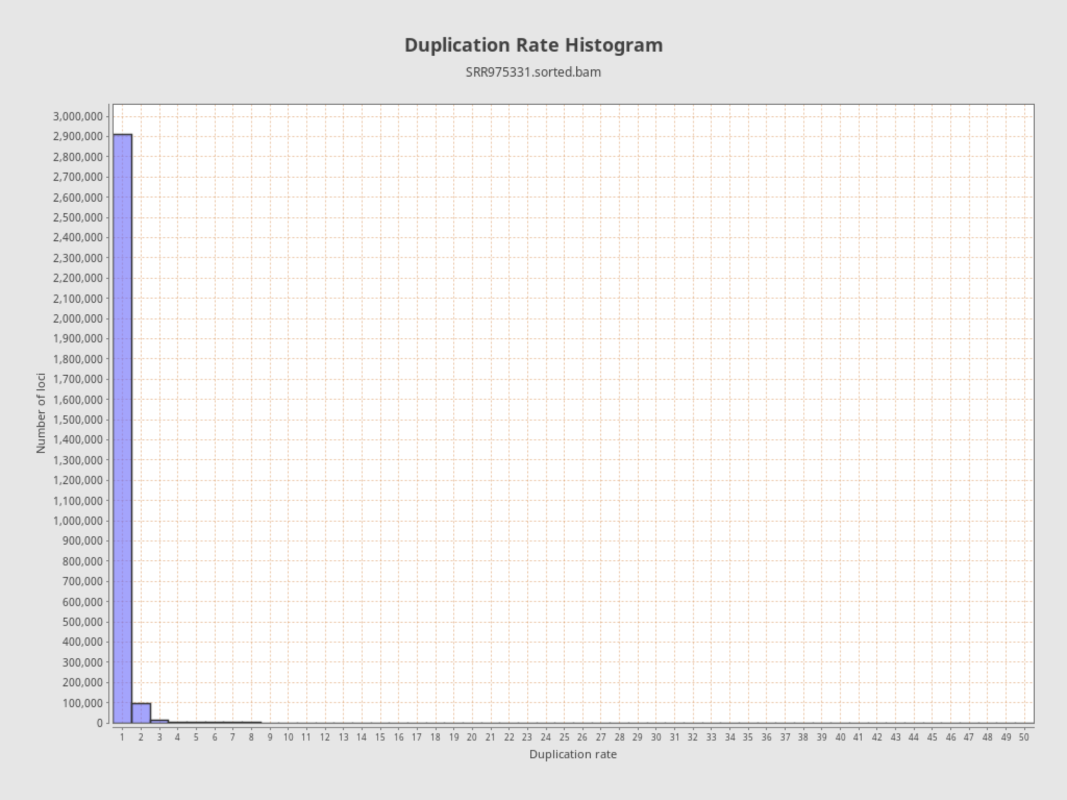
5. Results : Coverage Histogram (0-50X)



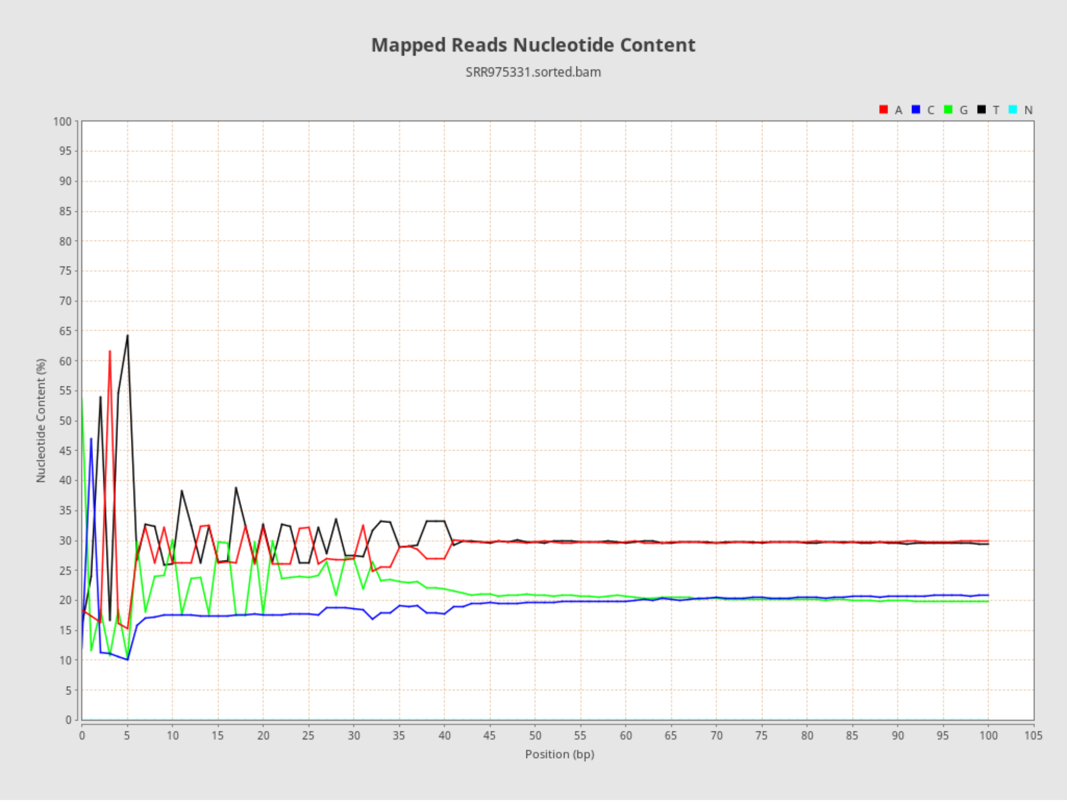
6. Results : Genome Fraction Coverage



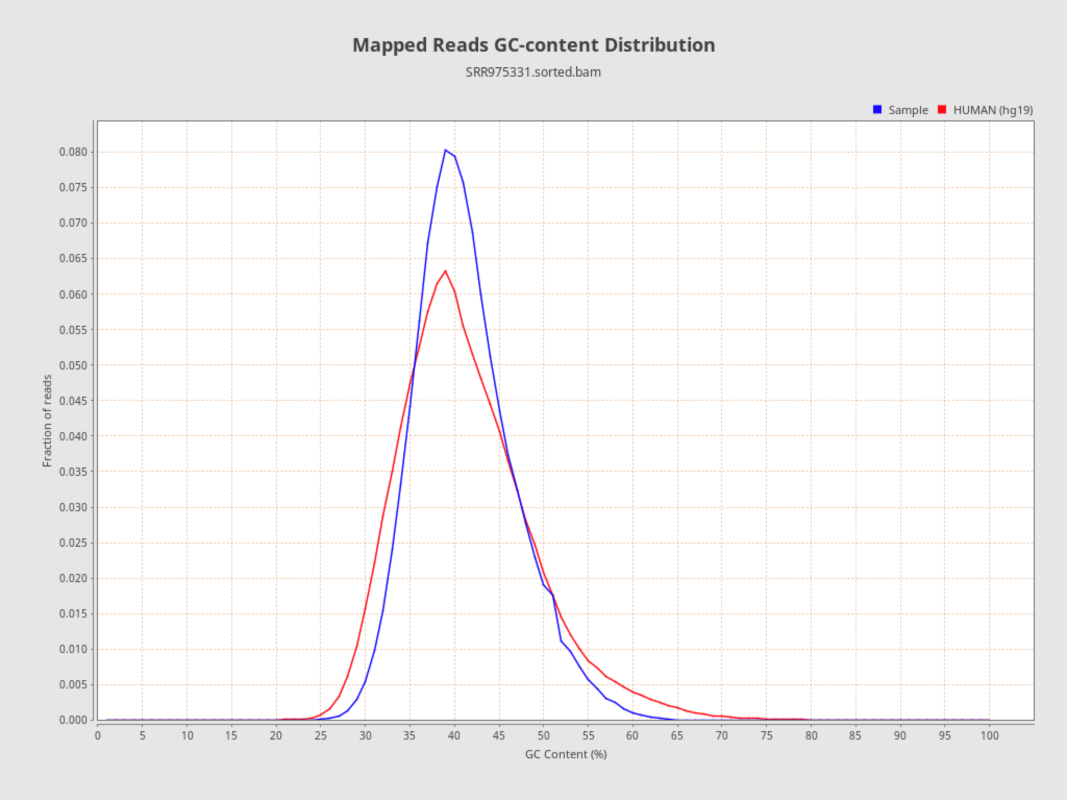
7. Results : Duplication Rate Histogram



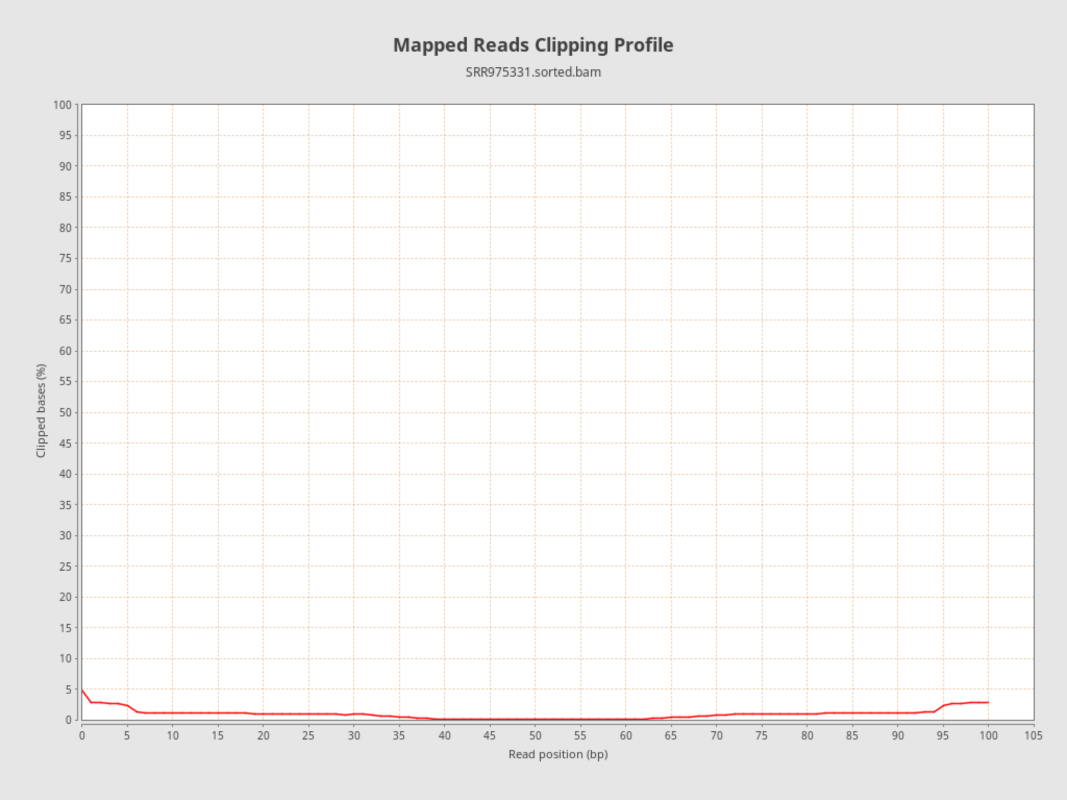
8. Results : Mapped Reads Nucleotide Content



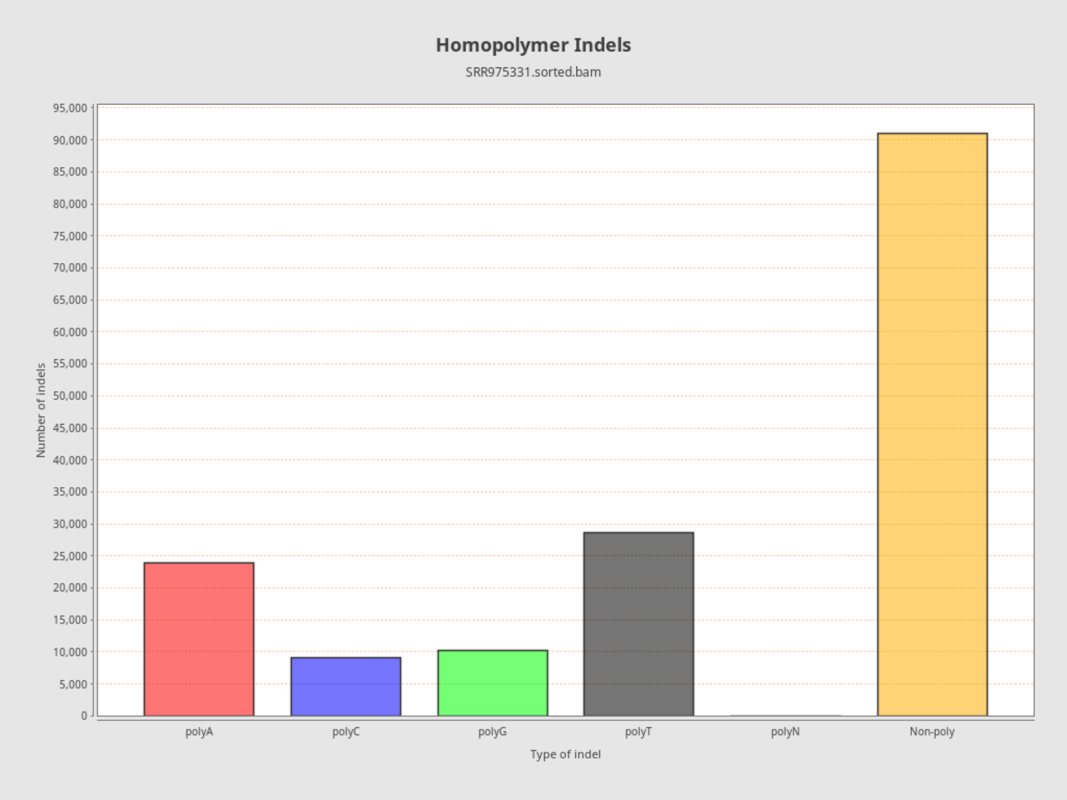
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

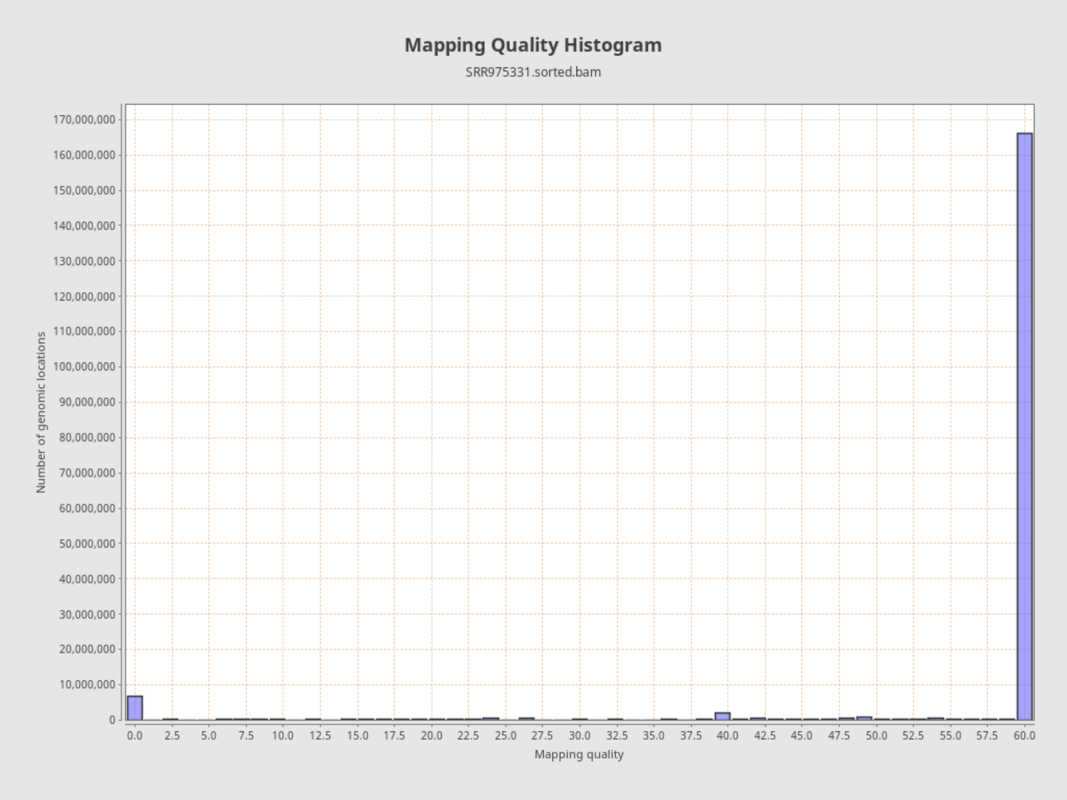


11. Results : Homopolymer Indels

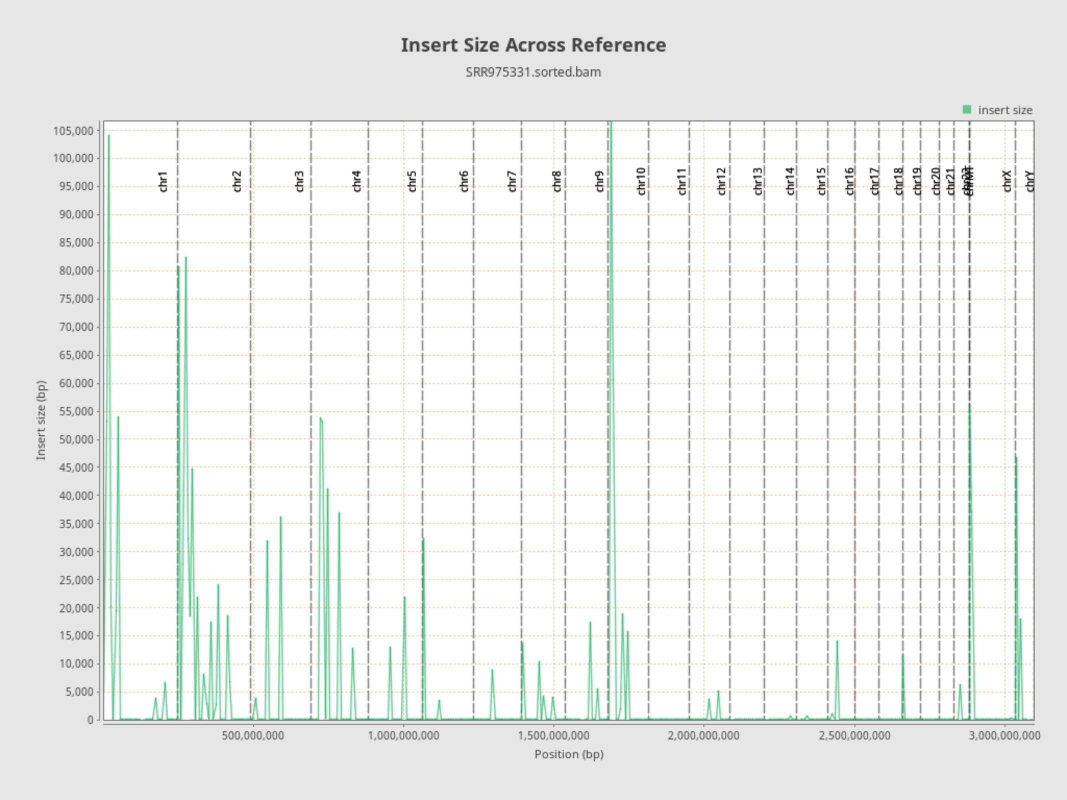


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram