Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 05:48:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975332.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_SRR975332 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975332_1.fastq.gz SRR975332_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 05:48:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975332.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,300,008
Mapped reads	4,248,938 / 98.81%
Unmapped reads	51,070 / 1.19%
Mapped paired reads	4,248,938 / 98.81%
Mapped reads, first in pair	2,124,044 / 49.4%
Mapped reads, second in pair	2,124,894 / 49.42%
Mapped reads, both in pair	4,238,504 / 98.57%
Mapped reads, singletons	10,434 / 0.24%
Secondary alignments	0
Supplementary alignments	27,654 / 0.64%
Read min/max/mean length	30 / 101 / 101.27
Duplicated reads (estimated)	165,013 / 3.84%
Duplication rate	1.84%
Clipped reads	2,237,269 / 52.03%

2.2. ACGT Content

Number/percentage of A's	121,206,831 / 29.34%
Number/percentage of C's	84,340,557 / 20.42%
Number/percentage of T's	123,160,609 / 29.81%
Number/percentage of G's	84,371,788 / 20.42%
Number/percentage of N's	8,363 / 0%

GC Percentage	40.84%

2.3. Coverage

Mean	0.1335
Standard Deviation	1.5097

2.4. Mapping Quality

Mean Mapping Quality	53.46

2.5. Insert size

Mean	87,194.25
Standard Deviation	2,792,044.68
P25/Median/P75	137 / 168 / 211

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	2,022,139
Insertions	59,355
Mapped reads with at least one insertion	1.36%
Deletions	54,496
Mapped reads with at least one deletion	1.25%
Homopolymer indels	37.9%

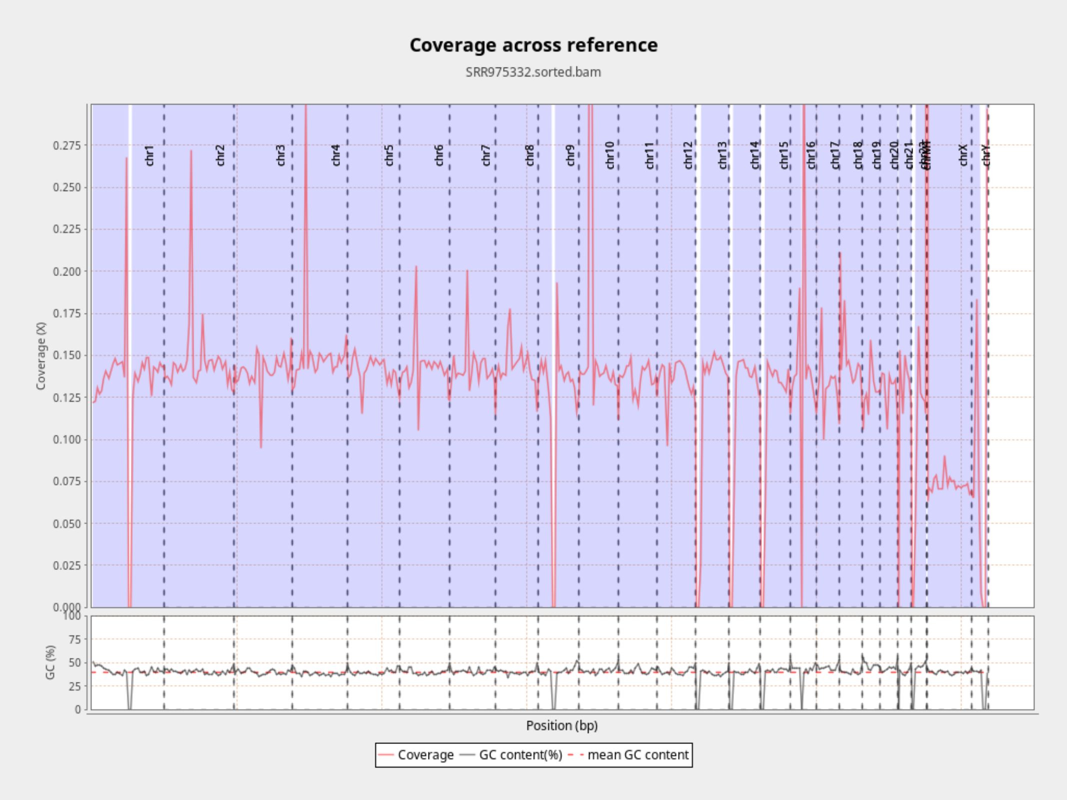
2.7. Chromosome stats

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

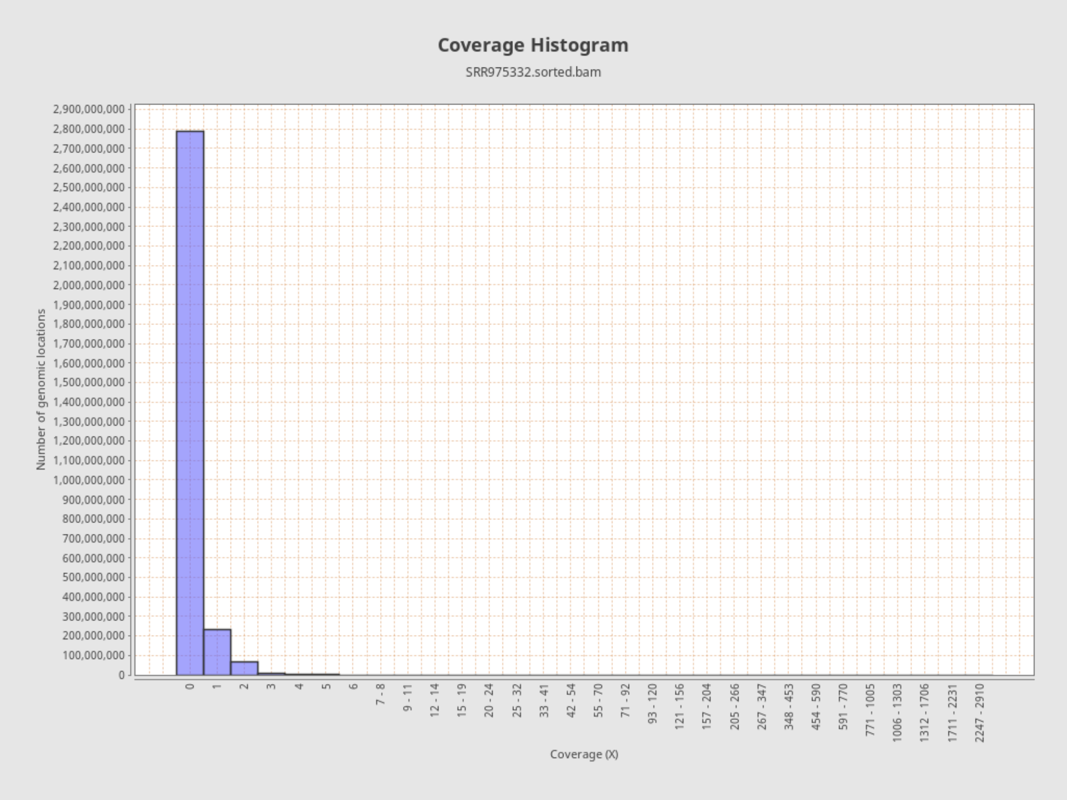
		bases	coverage	deviation
chr1	249250621	33360904	0.1338	3.0269
chr2	243199373	35793329	0.1472	1.0493
chr3	198022430	27794515	0.1404	0.4947
chr4	191154276	29073999	0.1521	1.3305
chr5	180915260	25477808	0.1408	0.4458
chr6	171115067	24430830	0.1428	0.822
chr7	159138663	22757817	0.143	1.3229
chr8	146364022	21136745	0.1444	1.7542
chr9	141213431	17453216	0.1236	1.382
chr10	135534747	22183538	0.1637	3.7082
chr11	135006516	18474742	0.1368	0.6572
chr12	133851895	18233514	0.1362	0.4405
chr13	115169878	13832771	0.1201	0.4048
chr14	107349540	12565416	0.1171	0.4176
chr15	102531392	11507493	0.1122	0.3927
chr16	90354753	13110300	0.1451	1.5075
chr17	81195210	10767823	0.1326	0.778
chr18	78077248	11570296	0.1482	1.7305
chr19	59128983	7654805	0.1295	1.3327
chr20	63025520	8234099	0.1306	0.5224
chr21	48129895	5971267	0.1241	1.1072
chr22	51304566	4806531	0.0937	1.2149
chrMT	16571	481748	29.0718	7.911
chrX	155270560	11361127	0.0732	0.4049

chrY	59373566	5185358	0.0873	1.7388

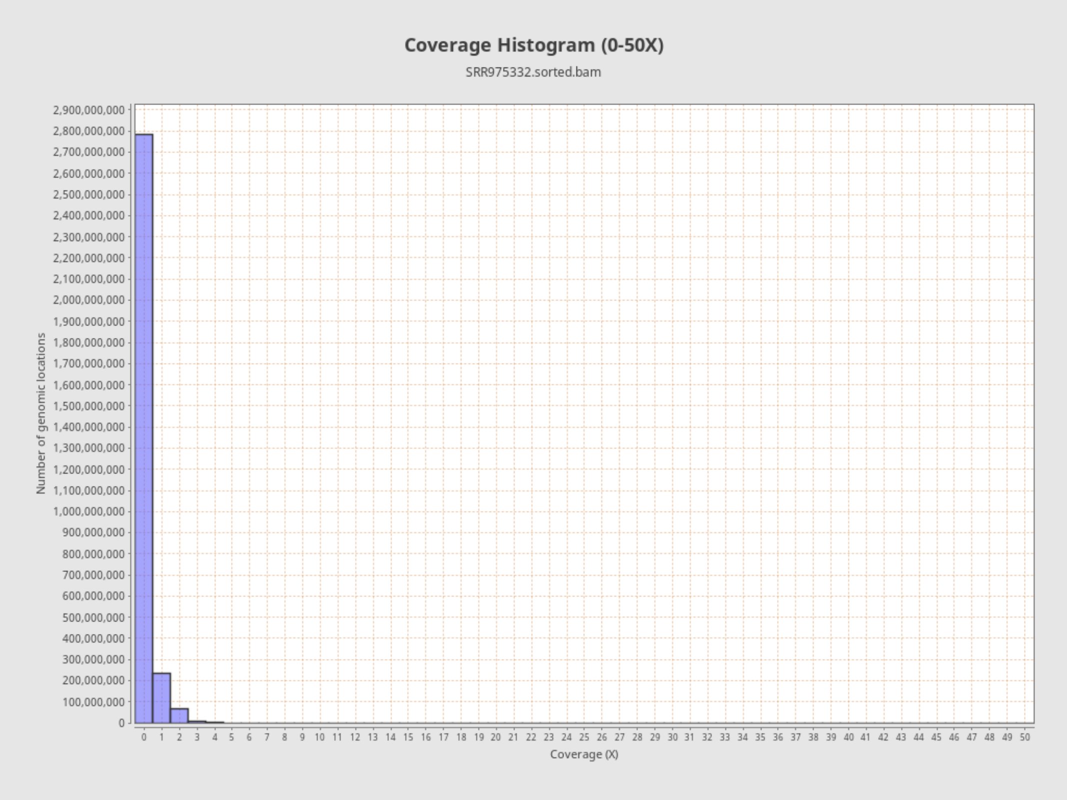
3. Results : Coverage across reference



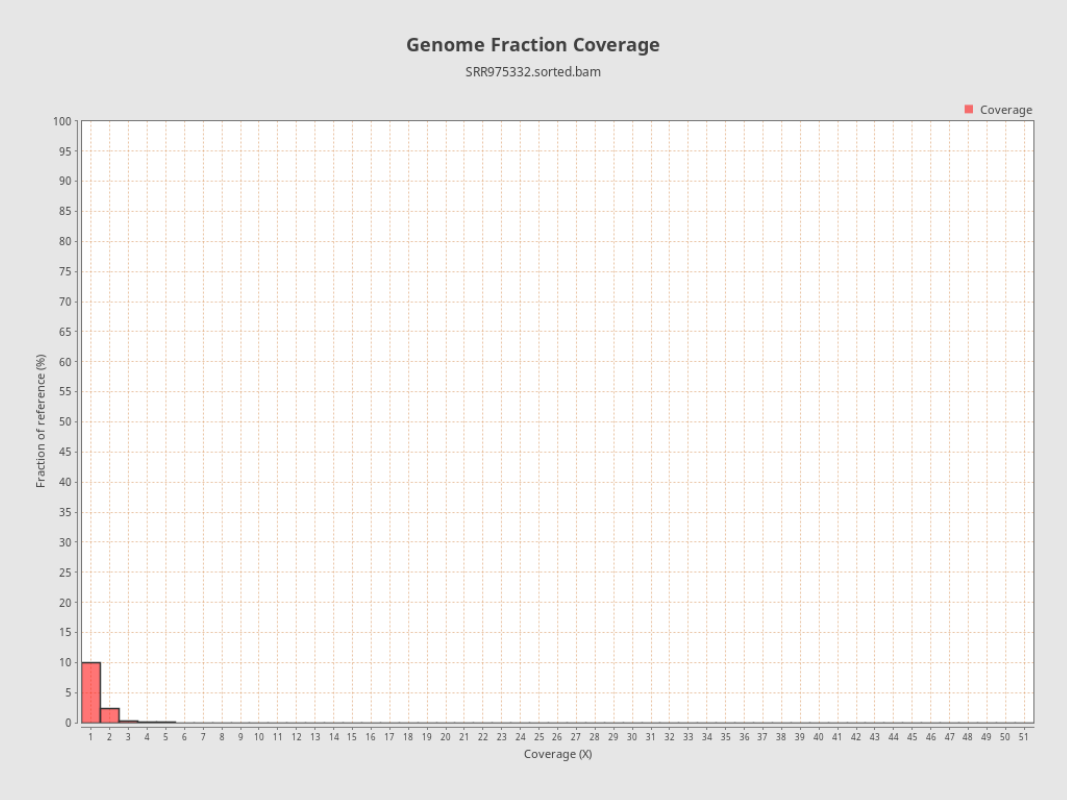
4. Results : Coverage Histogram



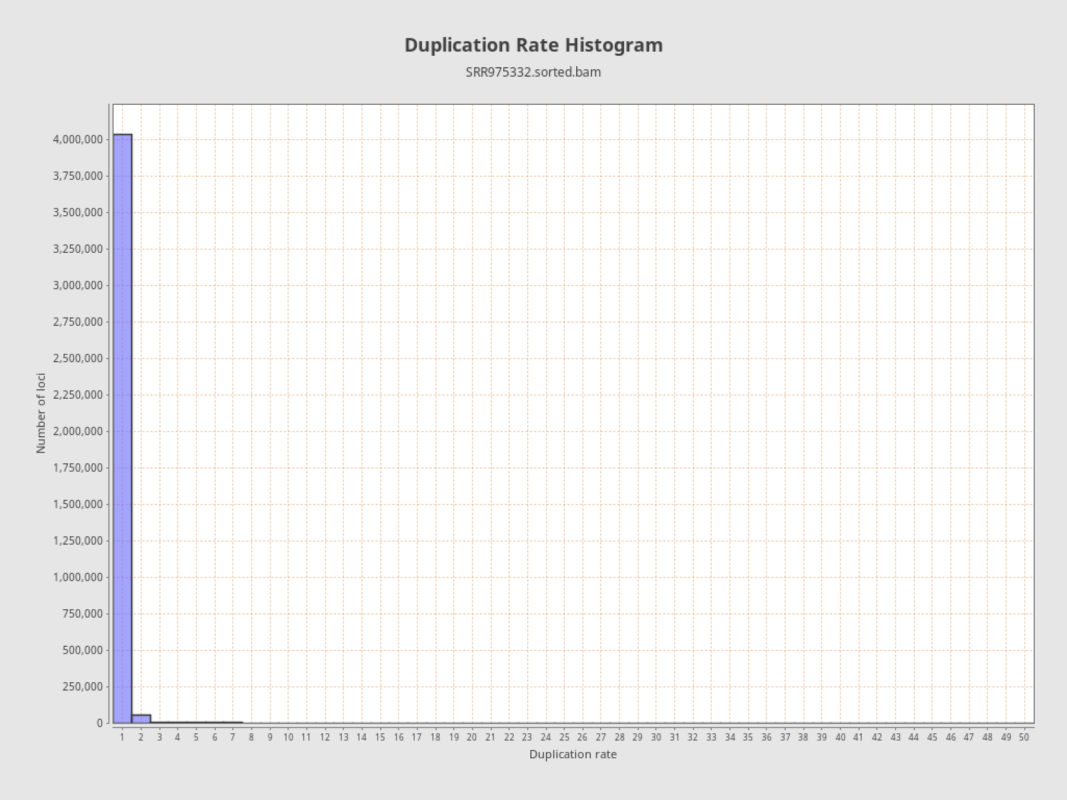
5. Results : Coverage Histogram (0-50X)



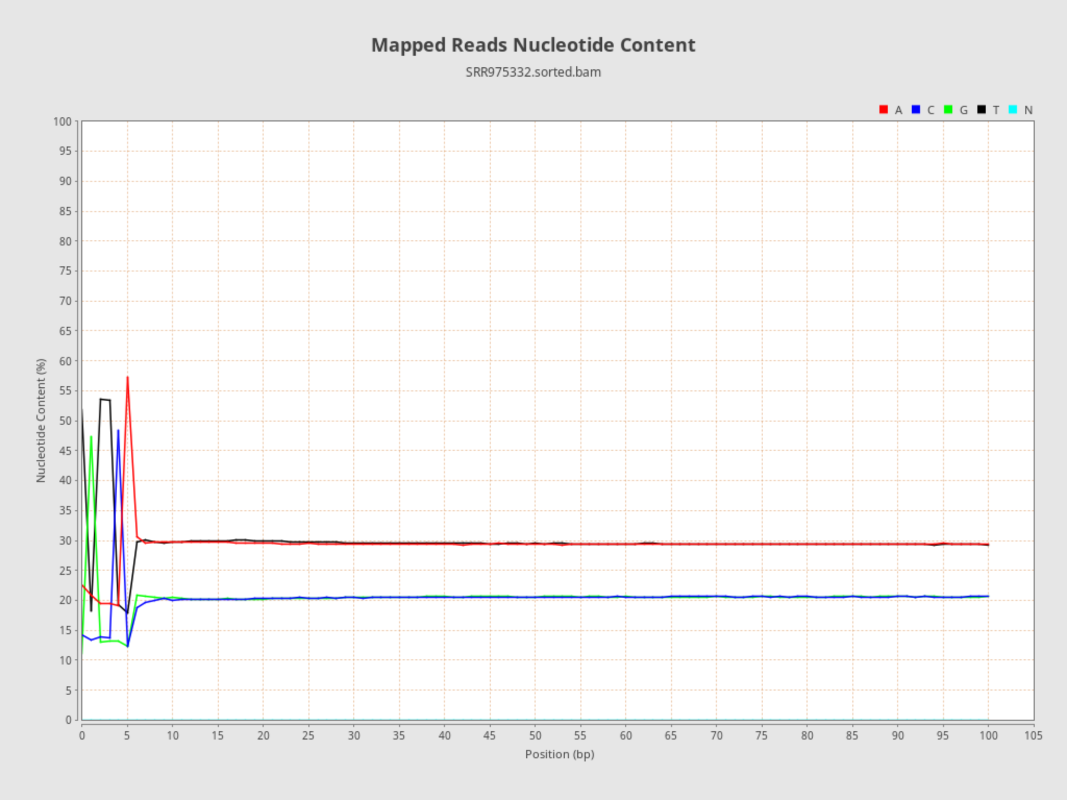
6. Results : Genome Fraction Coverage



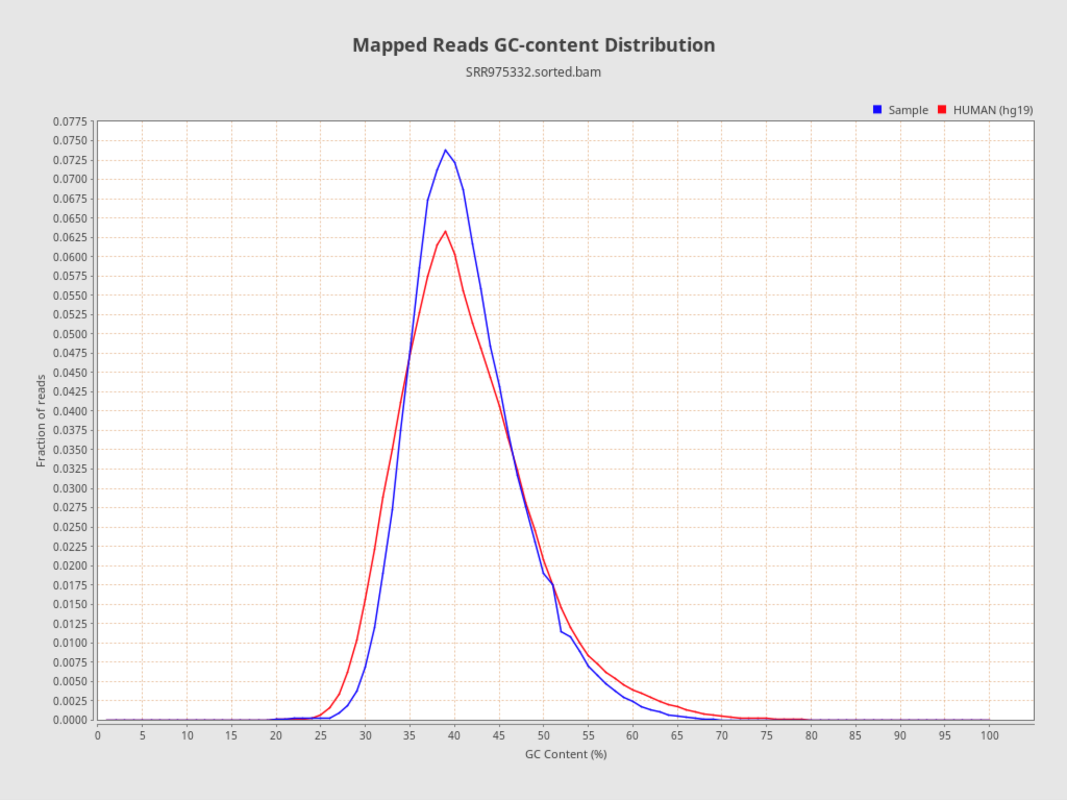
7. Results : Duplication Rate Histogram



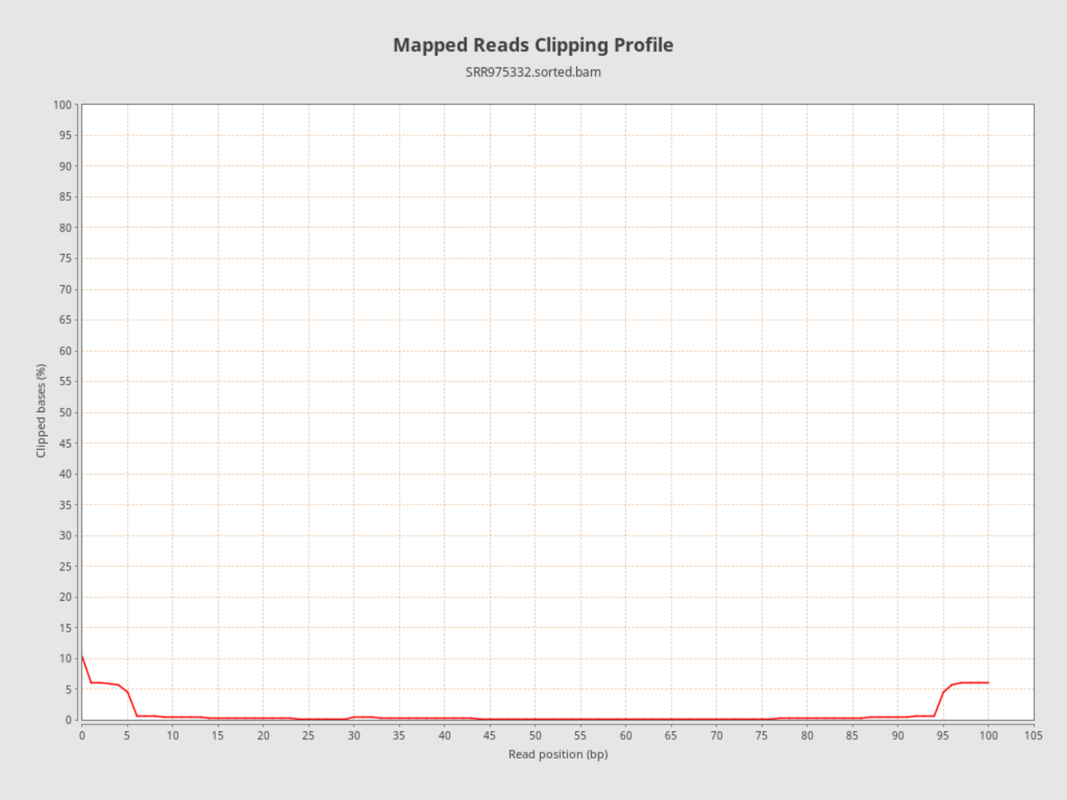
8. Results : Mapped Reads Nucleotide Content



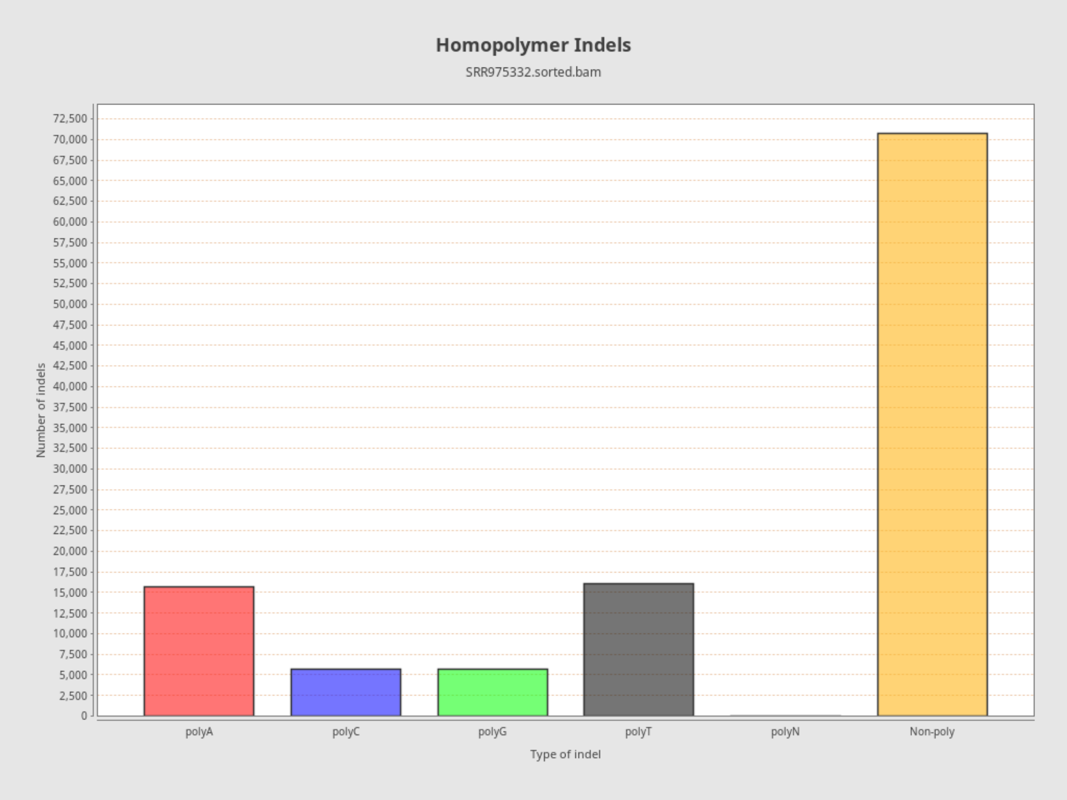
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

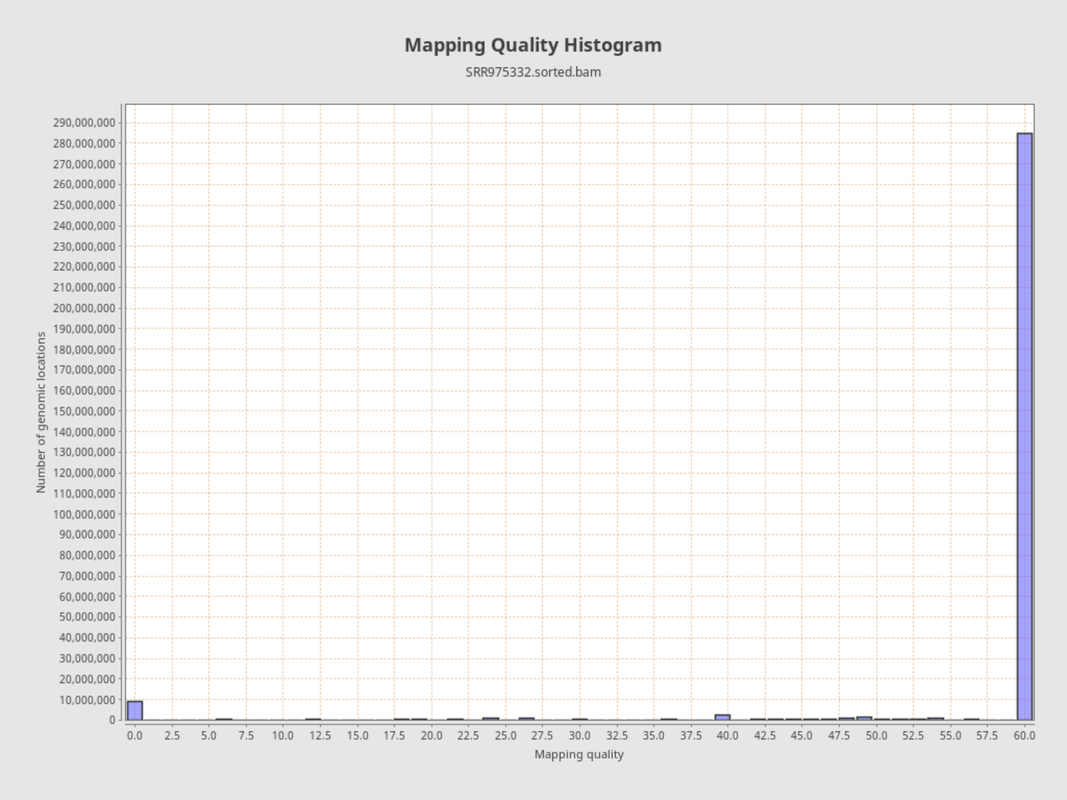


11. Results : Homopolymer Indels

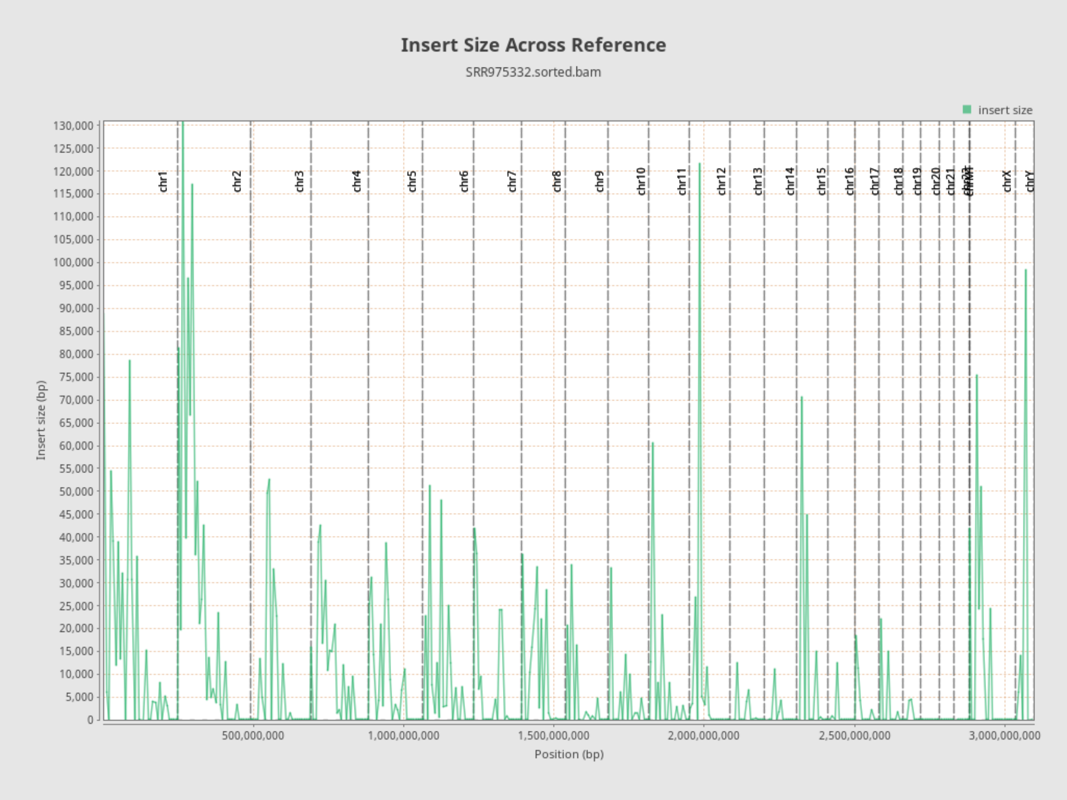


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram