Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 04:25:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975321.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_SRR975321 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975321_1.fastq.gz SRR975321_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 04:25:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975321.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,759,980
Mapped reads	3,713,917 / 98.77%
Unmapped reads	46,063 / 1.23%
Mapped paired reads	3,713,917 / 98.77%
Mapped reads, first in pair	1,856,578 / 49.38%
Mapped reads, second in pair	1,857,339 / 49.4%
Mapped reads, both in pair	3,704,386 / 98.52%
Mapped reads, singletons	9,531 / 0.25%
Secondary alignments	0
Supplementary alignments	60,298 / 1.6%
Read min/max/mean length	30 / 101 / 101.66
Duplicated reads (estimated)	178,182 / 4.74%
Duplication rate	2.61%
Clipped reads	2,069,934 / 55.05%

2.2. ACGT Content

Number/percentage of A's	103,577,056 / 28.83%
Number/percentage of C's	77,622,287 / 21.6%
Number/percentage of T's	103,458,706 / 28.79%
Number/percentage of G's	74,652,597 / 20.78%
Number/percentage of N's	7,621 / 0%

GC Percentage	42.38%

2.3. Coverage

Mean	0.1161
Standard Deviation	1.5971

2.4. Mapping Quality

Mean Mapping Quality	52.92

2.5. Insert size

Mean	143,604.66
Standard Deviation	3,612,288.3
P25/Median/P75	130 / 153 / 184

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	1,915,843
Insertions	47,875
Mapped reads with at least one insertion	1.25%
Deletions	55,310
Mapped reads with at least one deletion	1.45%
Homopolymer indels	40.27%

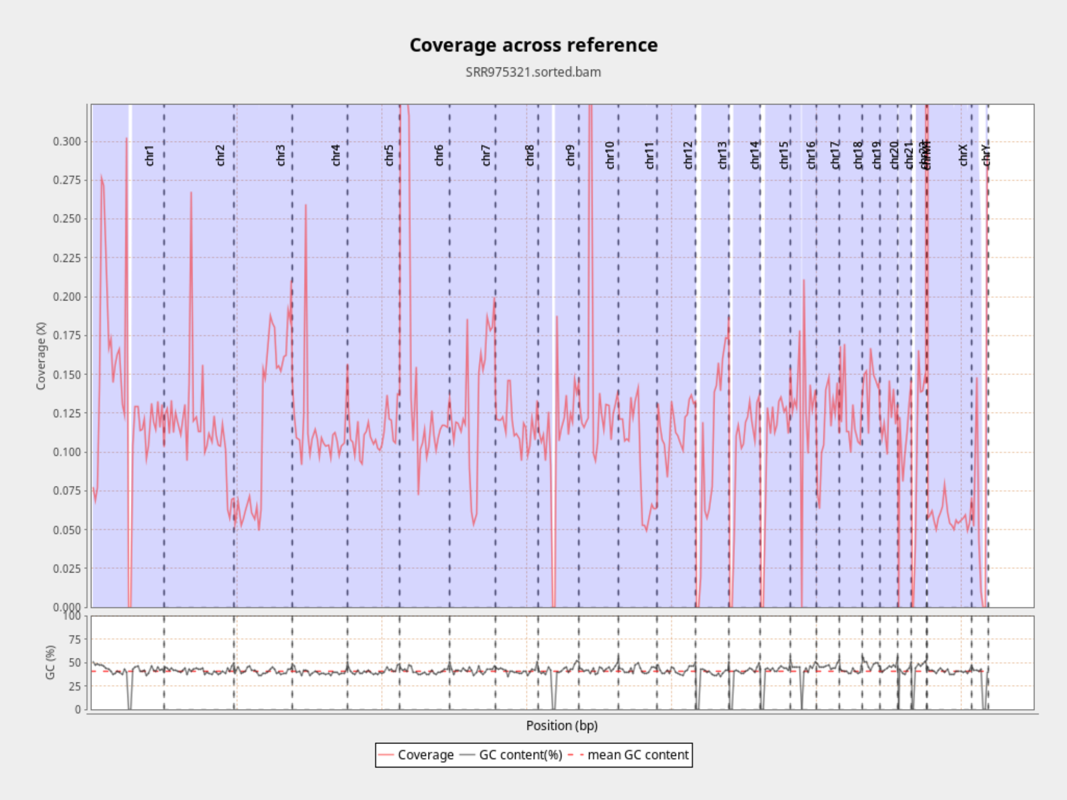
2.7. Chromosome stats

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

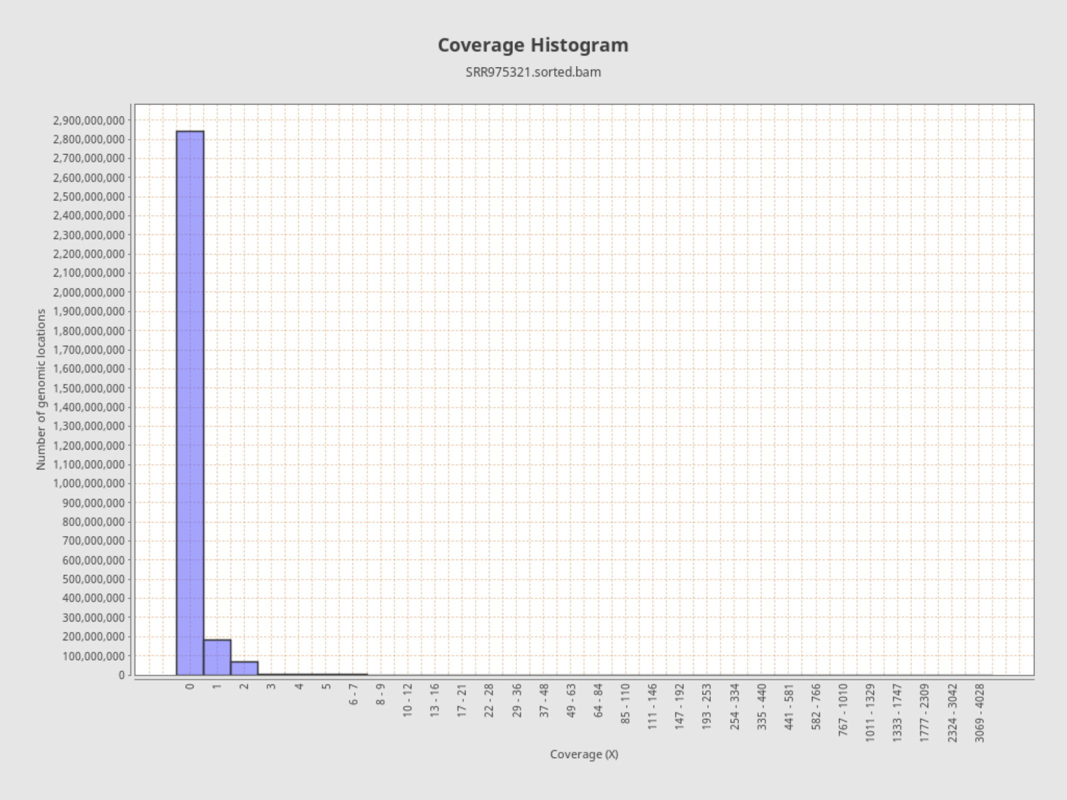
		bases	coverage	deviation
chr1	249250621	33653180	0.135	4.0441
chr2	243199373	28182306	0.1159	1.0454
chr3	198022430	23018078	0.1162	0.4611
chr4	191154276	22068105	0.1154	1.1249
chr5	180915260	20225841	0.1118	0.4105
chr6	171115067	27652461	0.1616	0.7484
chr7	159138663	21001473	0.132	1.2282
chr8	146364022	17207056	0.1176	1.5371
chr9	141213431	15328106	0.1085	1.6131
chr10	135534747	19030017	0.1404	2.9143
chr11	135006516	12717740	0.0942	0.8486
chr12	133851895	15669077	0.1171	0.5288
chr13	115169878	11858679	0.103	0.3902
chr14	107349540	10525935	0.0981	0.3954
chr15	102531392	10360283	0.101	0.3845
chr16	90354753	11715847	0.1297	0.8842
chr17	81195210	9345972	0.1151	0.597
chr18	78077248	9507642	0.1218	1.7125
chr19	59128983	8607464	0.1456	1.9711
chr20	63025520	7711305	0.1224	0.4993
chr21	48129895	4950287	0.1029	0.8616
chr22	51304566	5178589	0.1009	0.9305
chrMT	16571	461955	27.8773	9.45
chrX	155270560	8965056	0.0577	0.4693

chrY	59373566	4509378	0.0759	1.5953

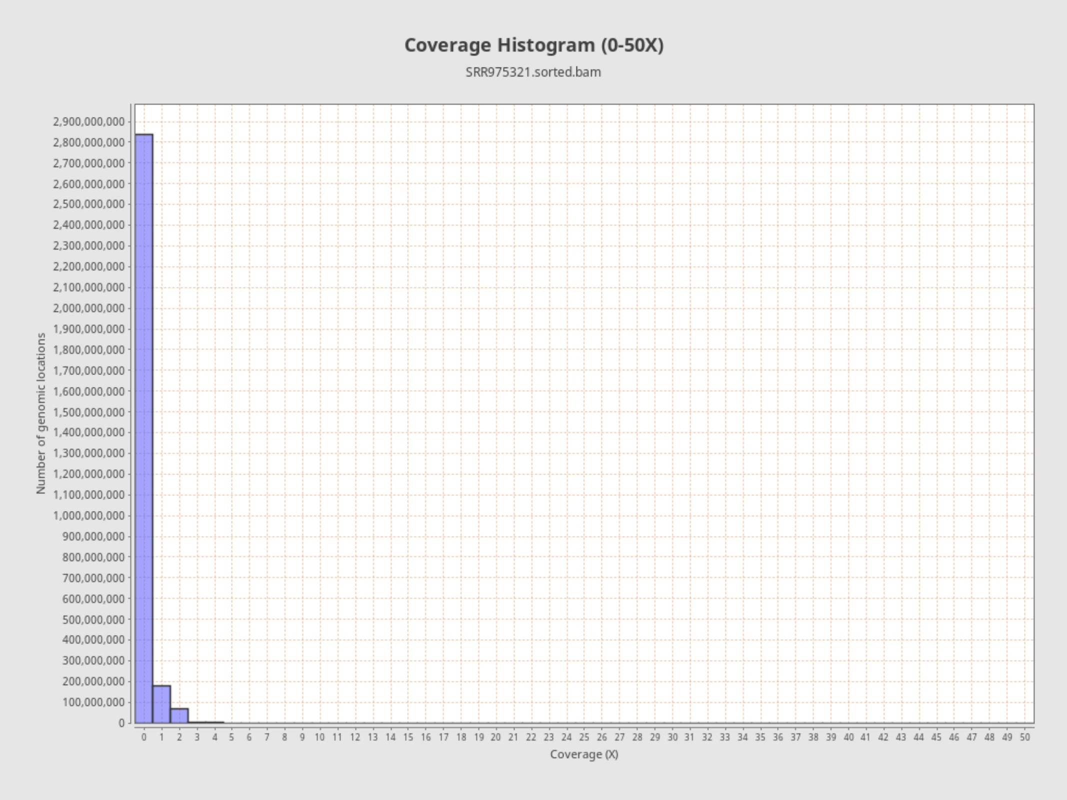
3. Results : Coverage across reference



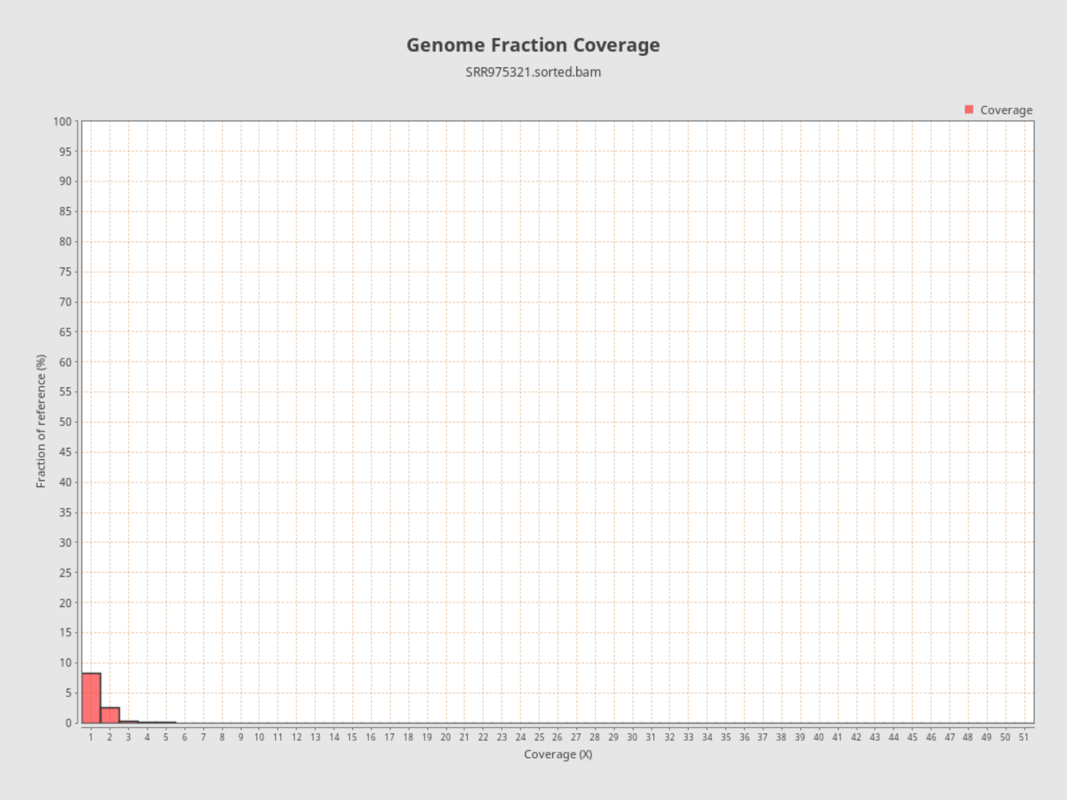
4. Results : Coverage Histogram



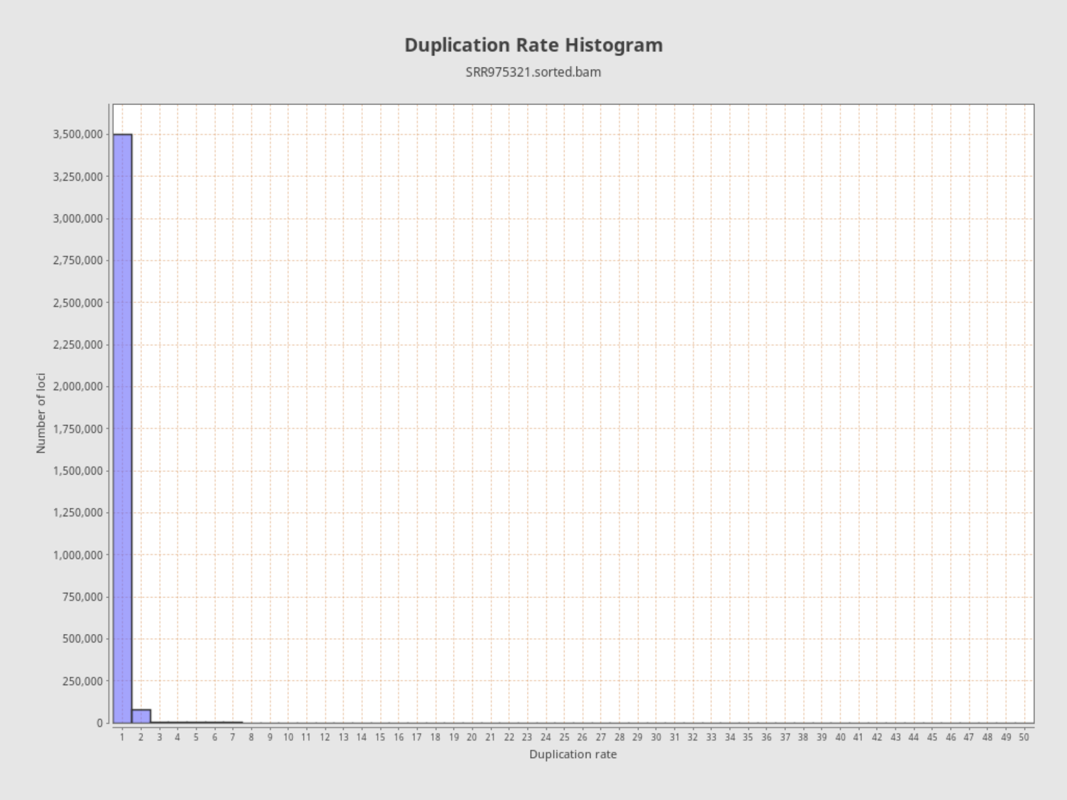
5. Results : Coverage Histogram (0-50X)



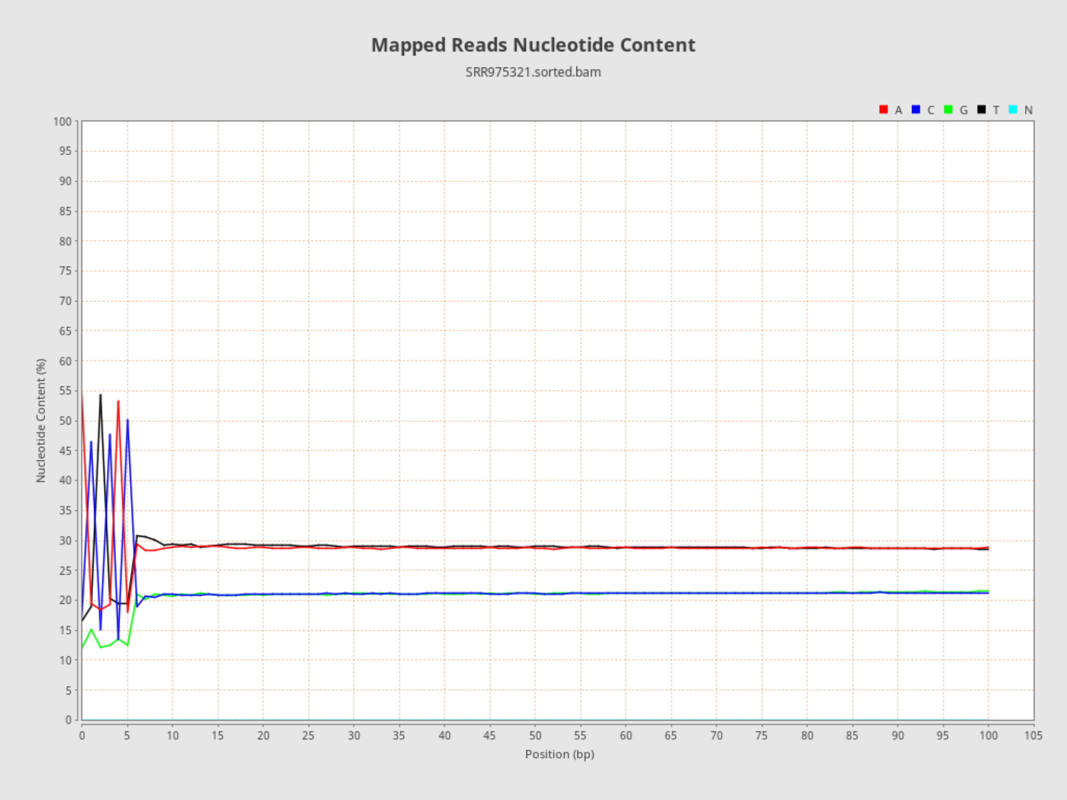
6. Results : Genome Fraction Coverage



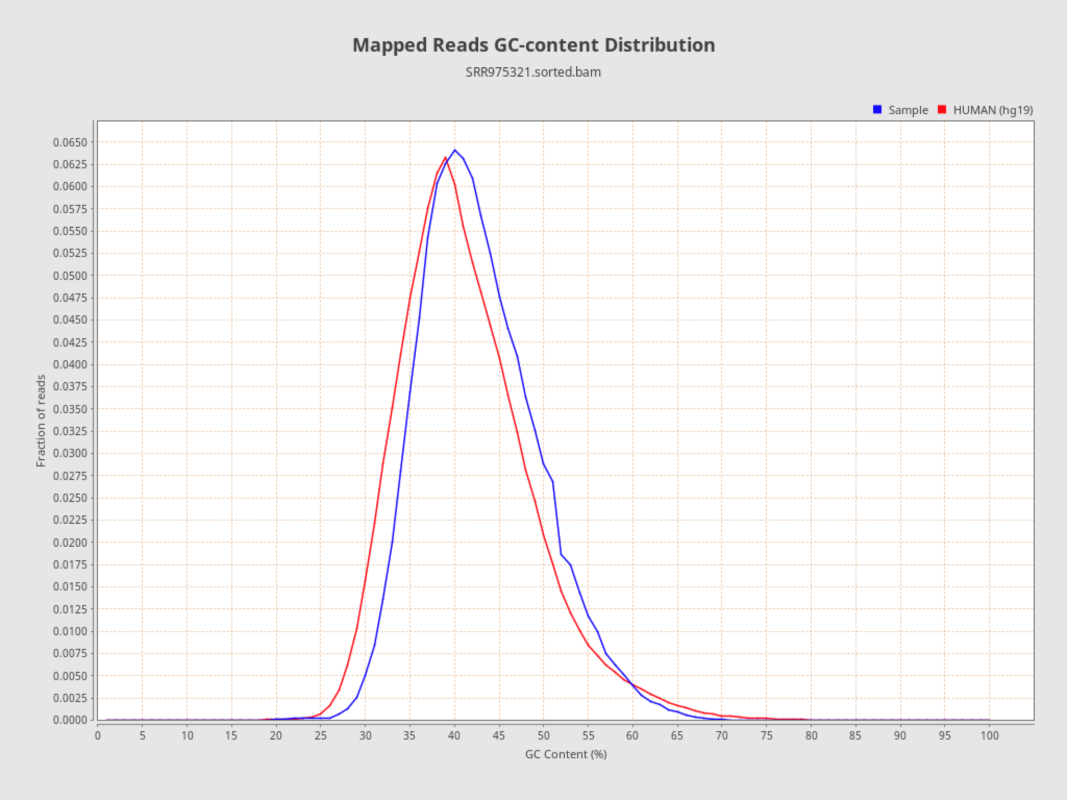
7. Results : Duplication Rate Histogram



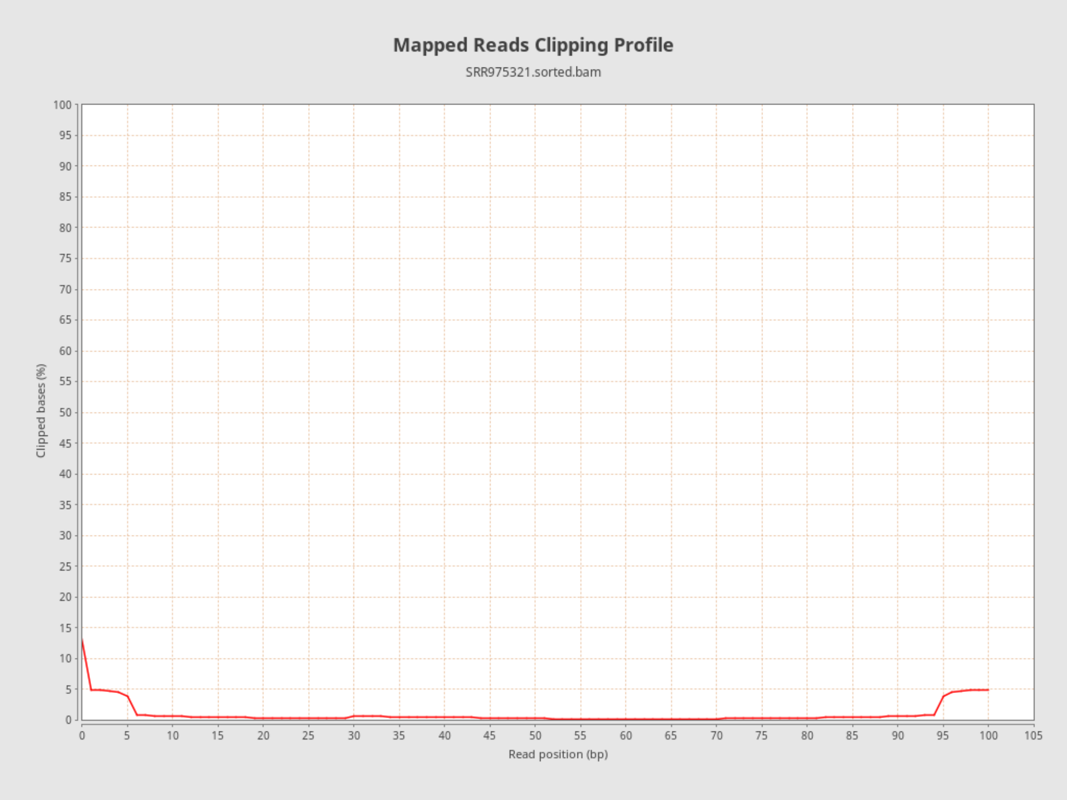
8. Results : Mapped Reads Nucleotide Content



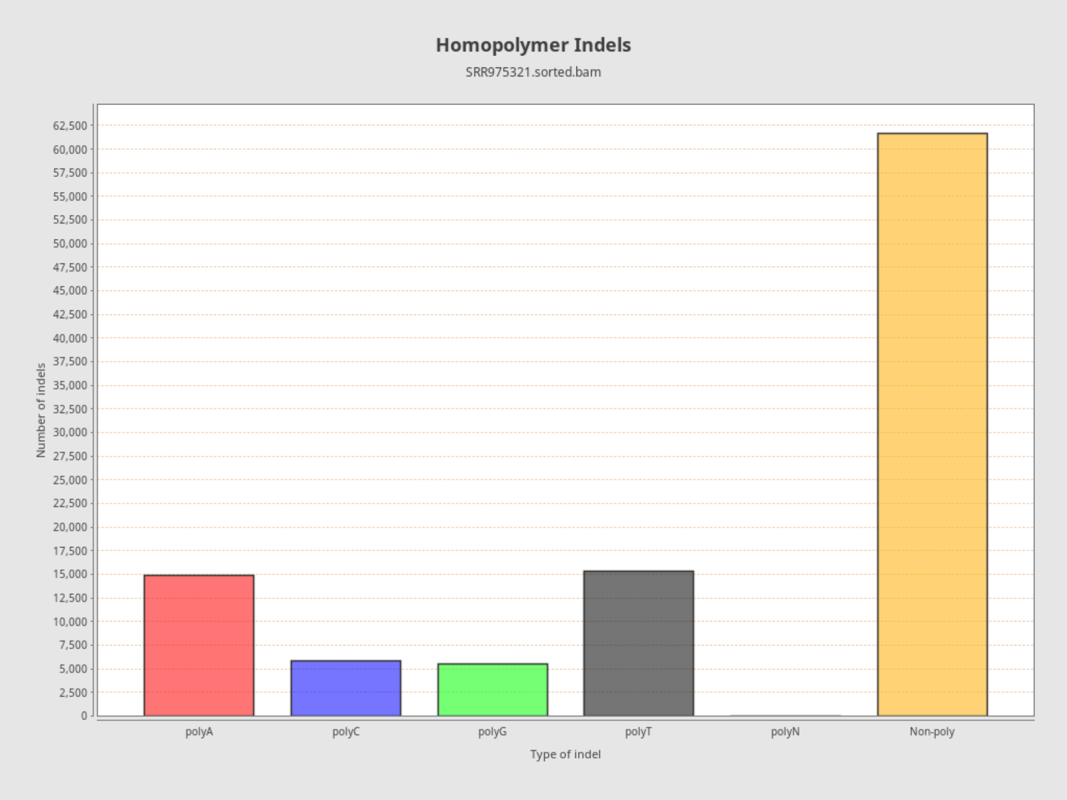
9. Results : Mapped Reads GC-content Distribution



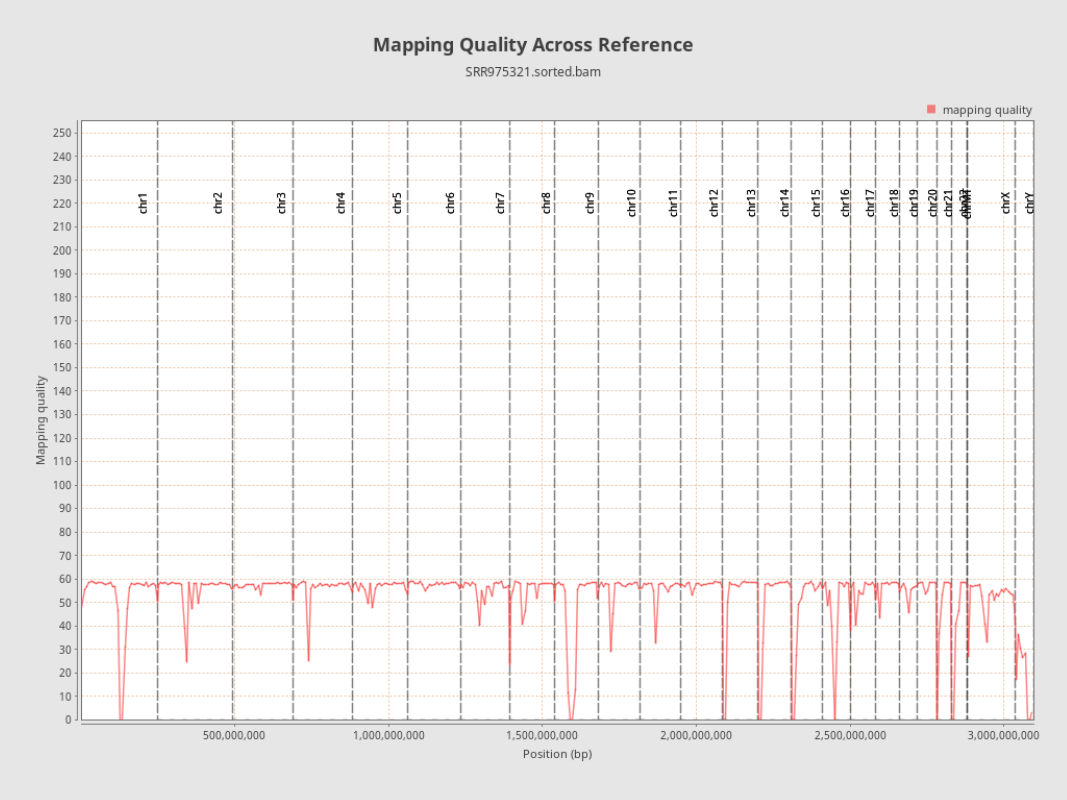
10. Results : Mapped Reads Clipping Profile



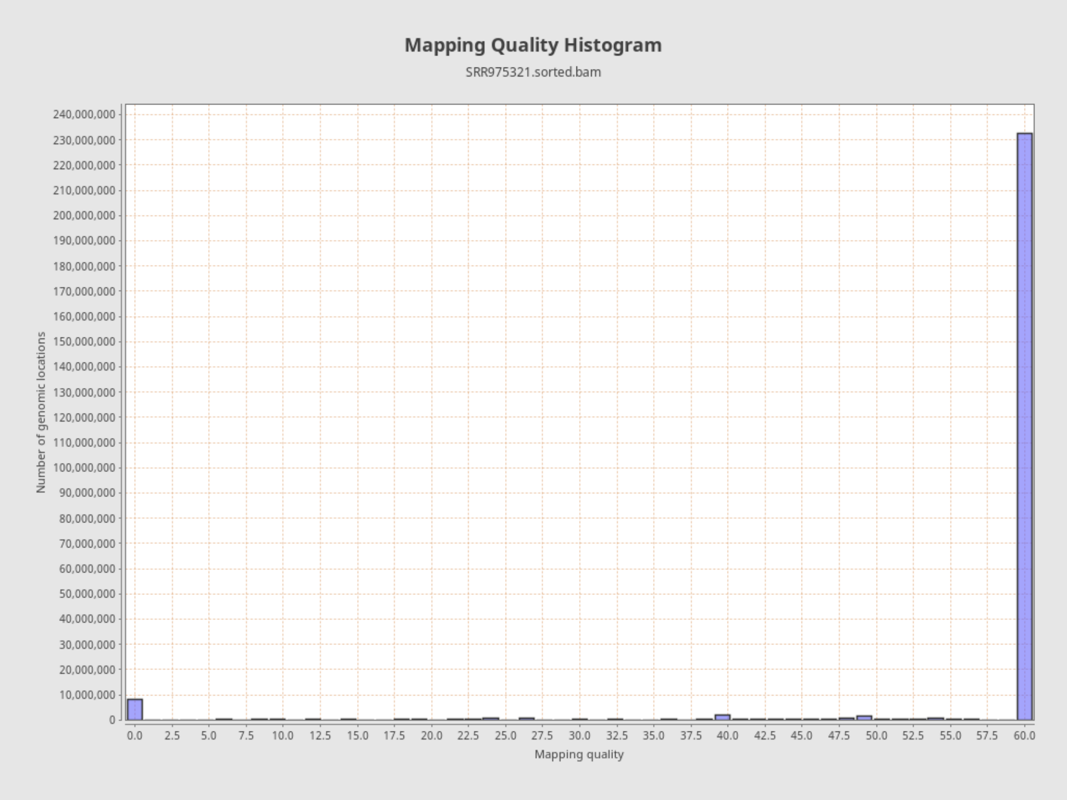
11. Results : Homopolymer Indels



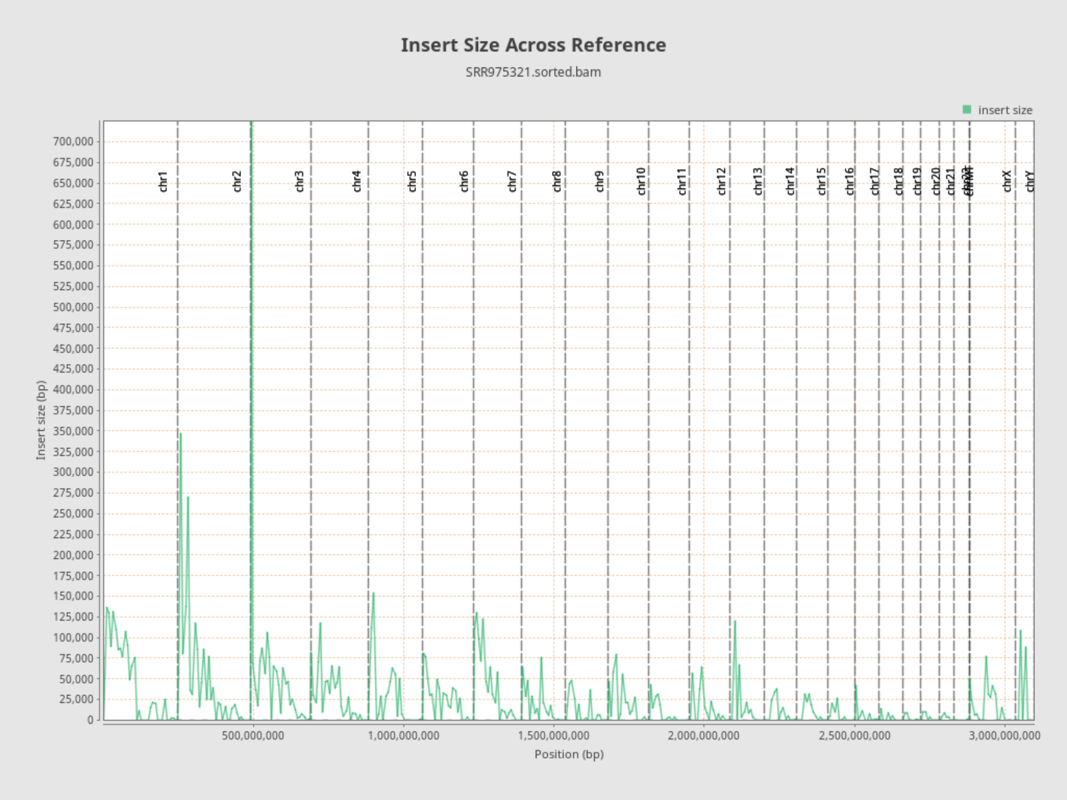
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram