Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 05:21:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975328.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_SRR975328 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975328_1.fastq.gz SRR975328_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 05:21:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975328.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,501,394
Mapped reads	3,457,100 / 98.73%
Unmapped reads	44,294 / 1.27%
Mapped paired reads	3,457,100 / 98.73%
Mapped reads, first in pair	1,727,585 / 49.34%
Mapped reads, second in pair	1,729,515 / 49.4%
Mapped reads, both in pair	3,443,132 / 98.34%
Mapped reads, singletons	13,968 / 0.4%
Secondary alignments	0
Supplementary alignments	18,705 / 0.53%
Read min/max/mean length	30 / 101 / 101.21
Duplicated reads (estimated)	207,878 / 5.94%
Duplication rate	3%
Clipped reads	2,137,140 / 61.04%

2.2. ACGT Content

Number/percentage of A's	92,137,184 / 29.32%
Number/percentage of C's	59,973,430 / 19.08%
Number/percentage of T's	95,714,051 / 30.45%
Number/percentage of G's	66,465,834 / 21.15%
Number/percentage of N's	7,340 / 0%

GC Percentage	40.23%

2.3. Coverage

Mean	0.1016
Standard Deviation	1.4235

2.4. Mapping Quality

Mean Mapping Quality	52.58

2.5. Insert size

Mean	81,091.53
Standard Deviation	2,753,666.61
P25/Median/P75	135 / 168 / 213

2.6. Mismatches and indels

General error rate	0.84%
Mismatches	2,503,933
Insertions	59,043
Mapped reads with at least one insertion	1.66%
Deletions	104,041
Mapped reads with at least one deletion	2.94%
Homopolymer indels	44.27%

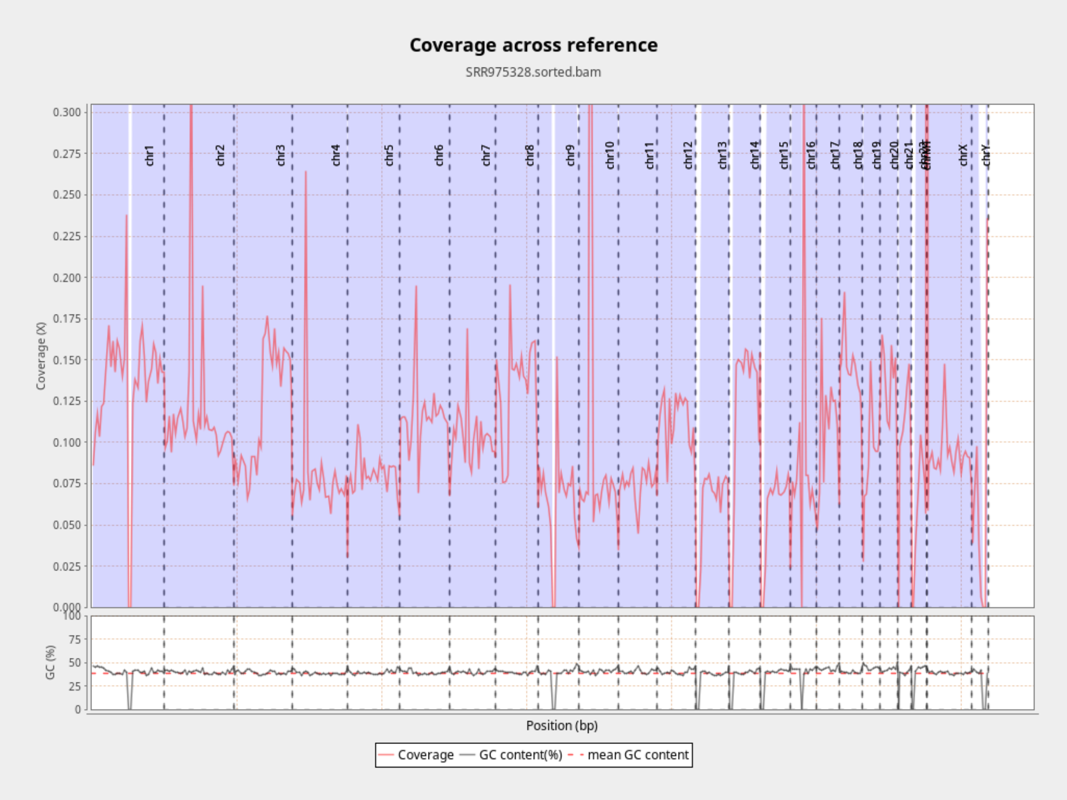
2.7. Chromosome stats

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

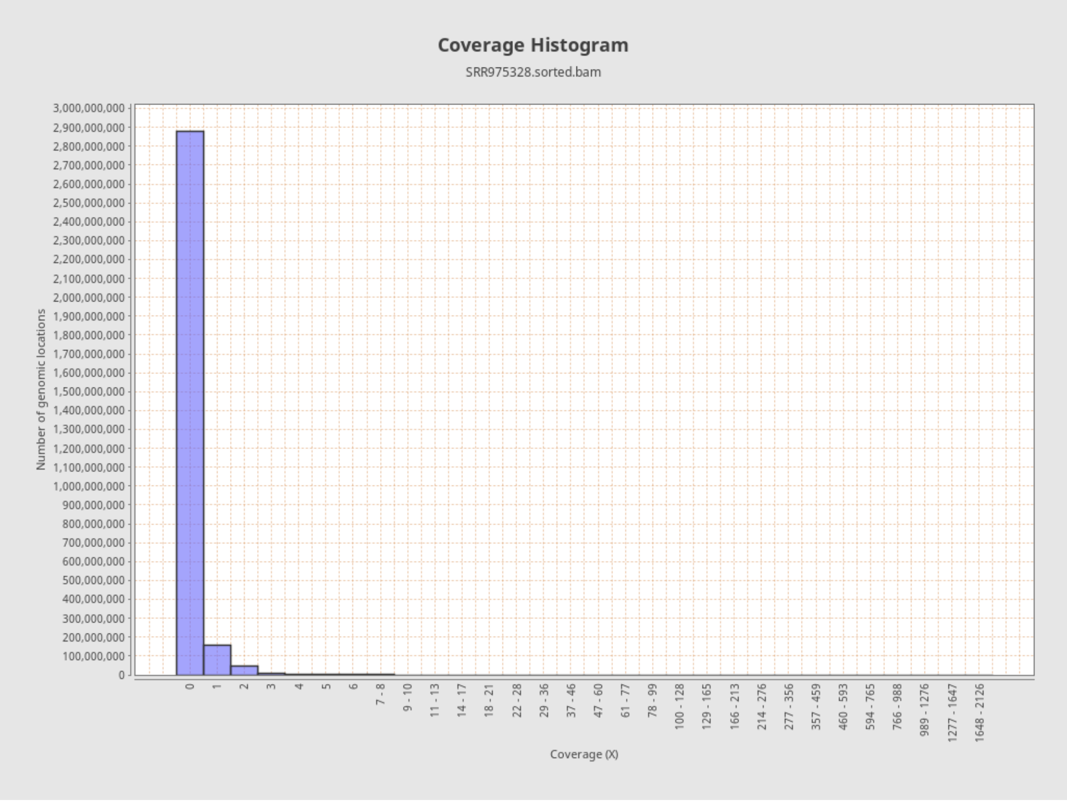
		bases	coverage	deviation
chr1	249250621	33497533	0.1344	1.5238
chr2	243199373	28810292	0.1185	1.7505
chr3	198022430	24145837	0.1219	0.5137
chr4	191154276	15454194	0.0808	1.0698
chr5	180915260	14710204	0.0813	0.3673
chr6	171115067	19788607	0.1156	0.9675
chr7	159138663	16389176	0.103	1.3841
chr8	146364022	19652439	0.1343	0.7112
chr9	141213431	9297492	0.0658	1.5765
chr10	135534747	13284291	0.098	4.4172
chr11	135006516	10059572	0.0745	0.6171
chr12	133851895	15157529	0.1132	0.4301
chr13	115169878	7075134	0.0614	0.3059
chr14	107349540	12849297	0.1197	0.4774
chr15	102531392	5996323	0.0585	0.3029
chr16	90354753	8048688	0.0891	1.787
chr17	81195210	8753179	0.1078	1.5452
chr18	78077248	11441139	0.1465	1.8787
chr19	59128983	5373852	0.0909	0.7817
chr20	63025520	8536952	0.1355	0.5255
chr21	48129895	5114459	0.1063	0.5238
chr22	51304566	3073300	0.0599	0.3482
chrMT	16571	86274	5.2063	4.5199
chrX	155270560	14332333	0.0923	0.5448

chrY	59373566	3562673	0.06	1.4115

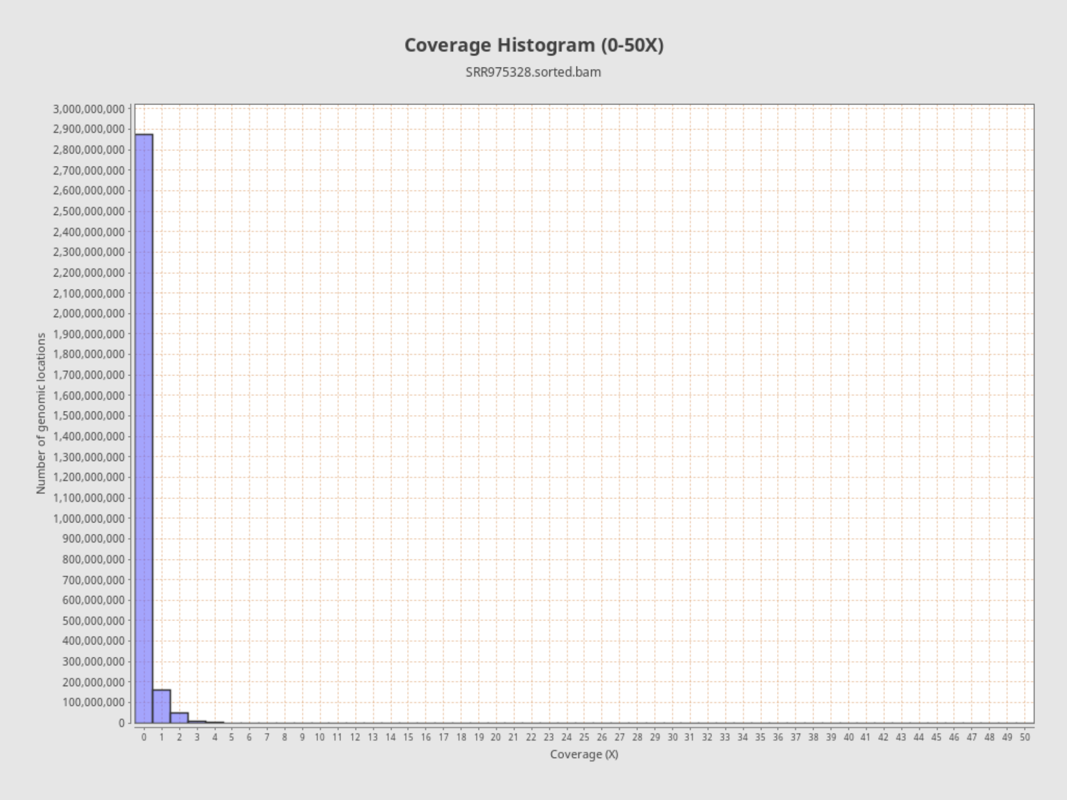
3. Results : Coverage across reference



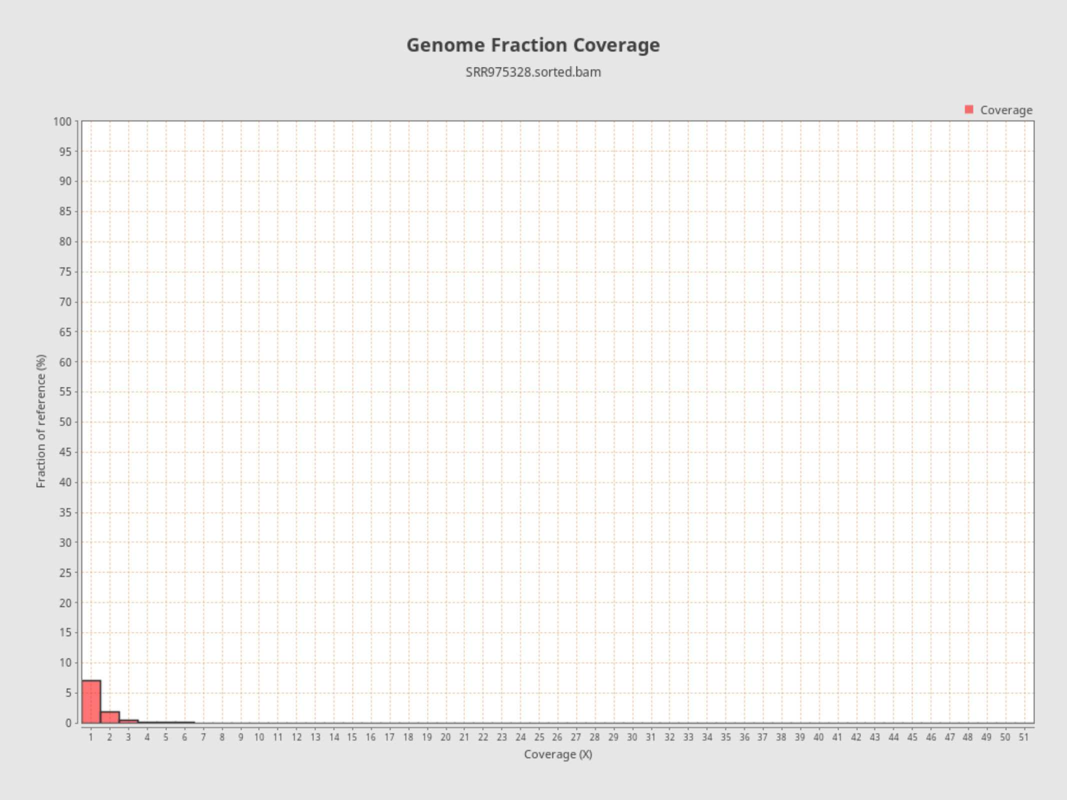
4. Results : Coverage Histogram



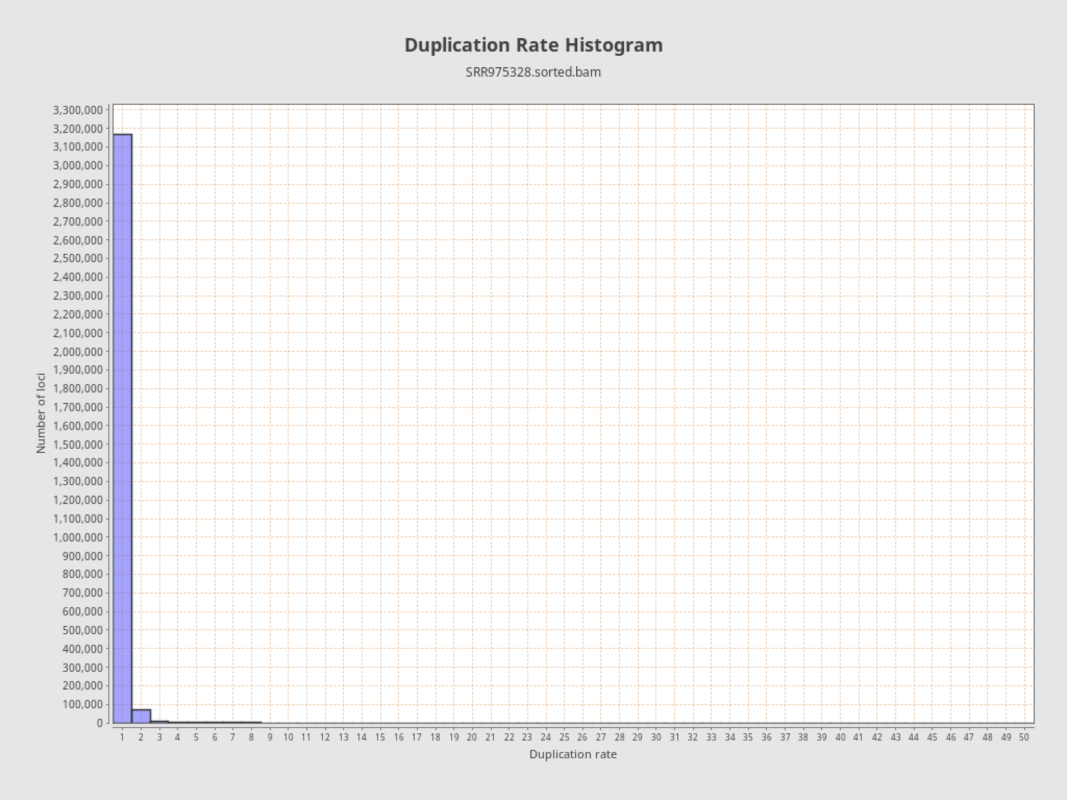
5. Results : Coverage Histogram (0-50X)



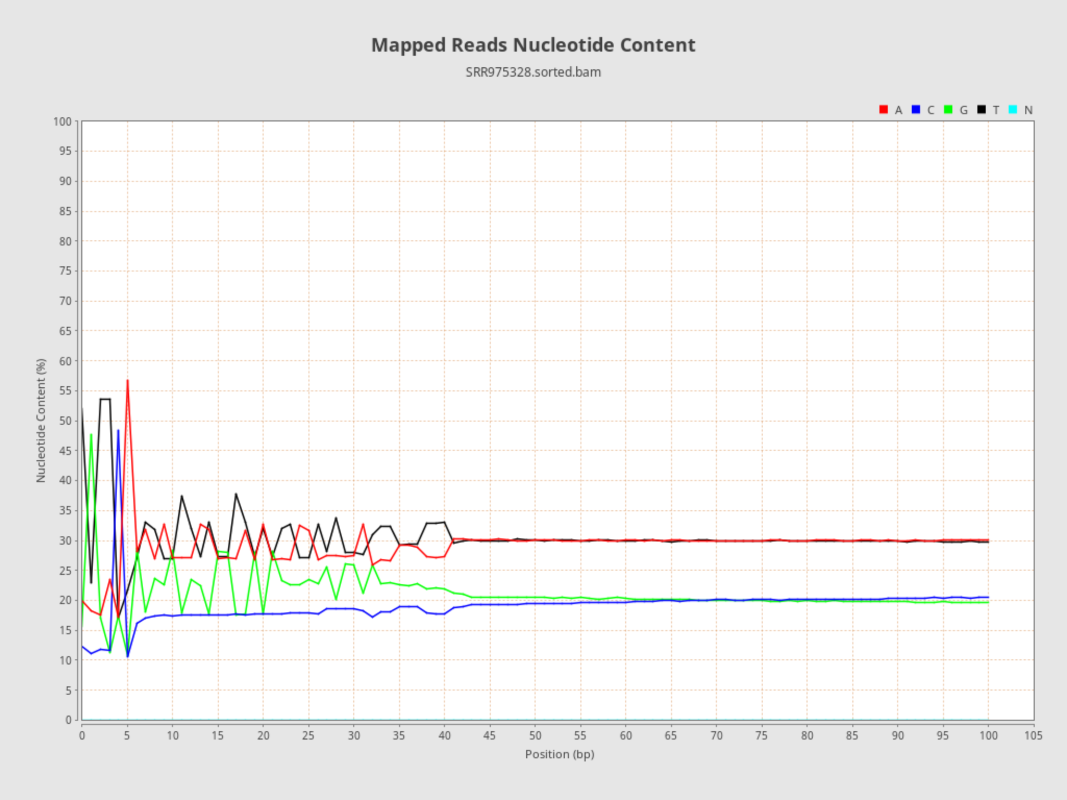
6. Results : Genome Fraction Coverage



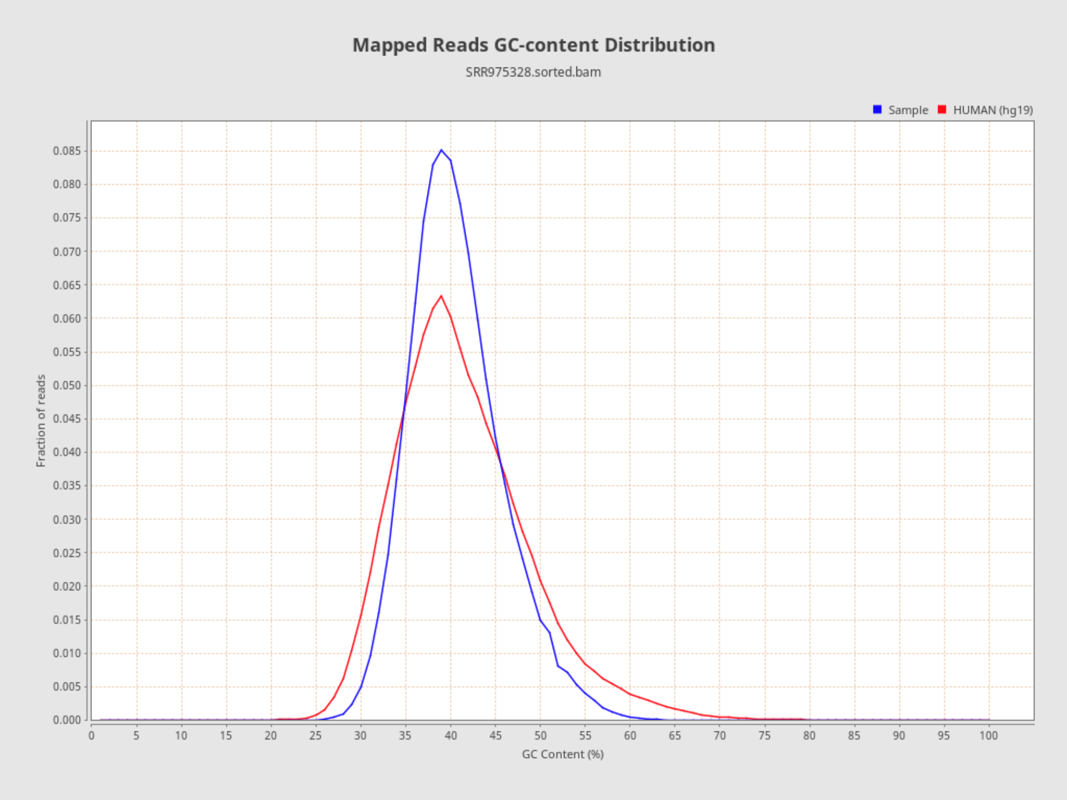
7. Results : Duplication Rate Histogram



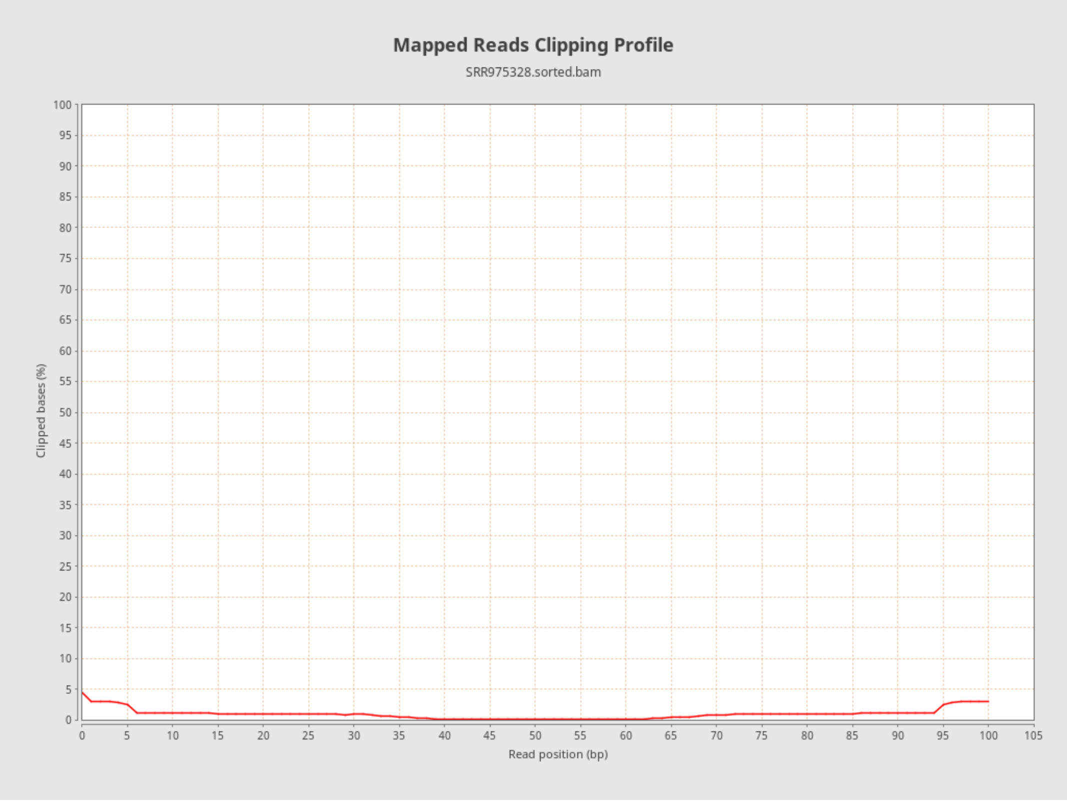
8. Results : Mapped Reads Nucleotide Content



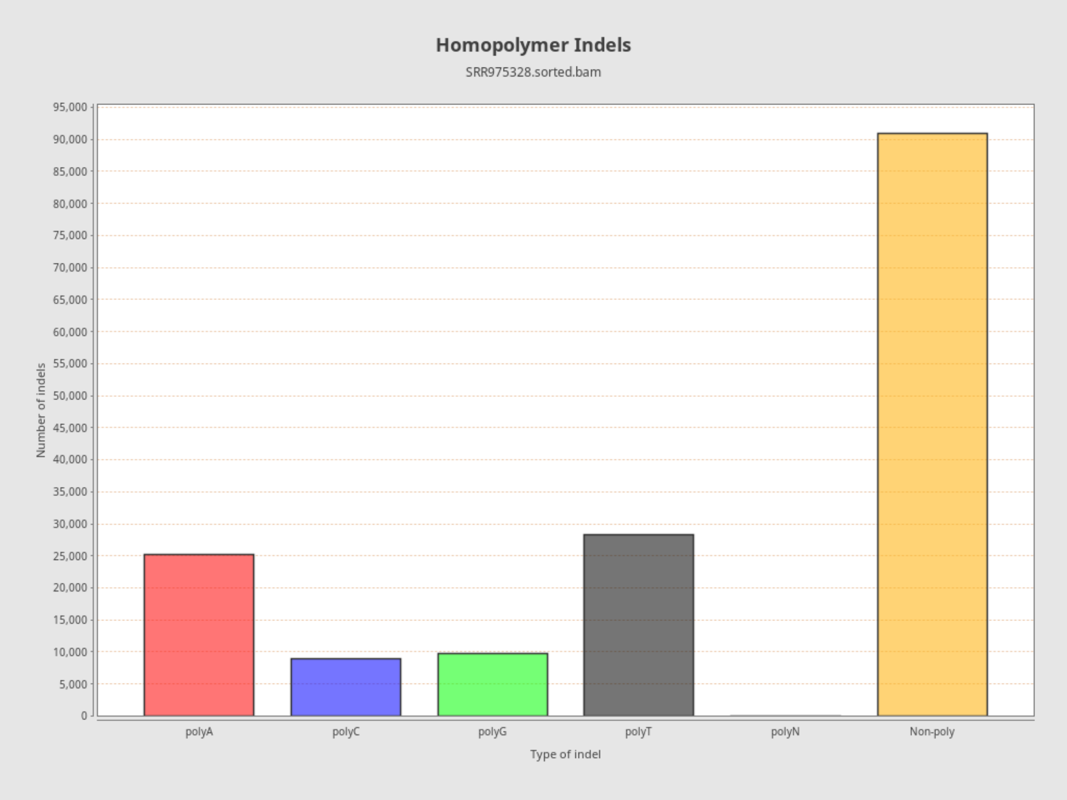
9. Results : Mapped Reads GC-content Distribution



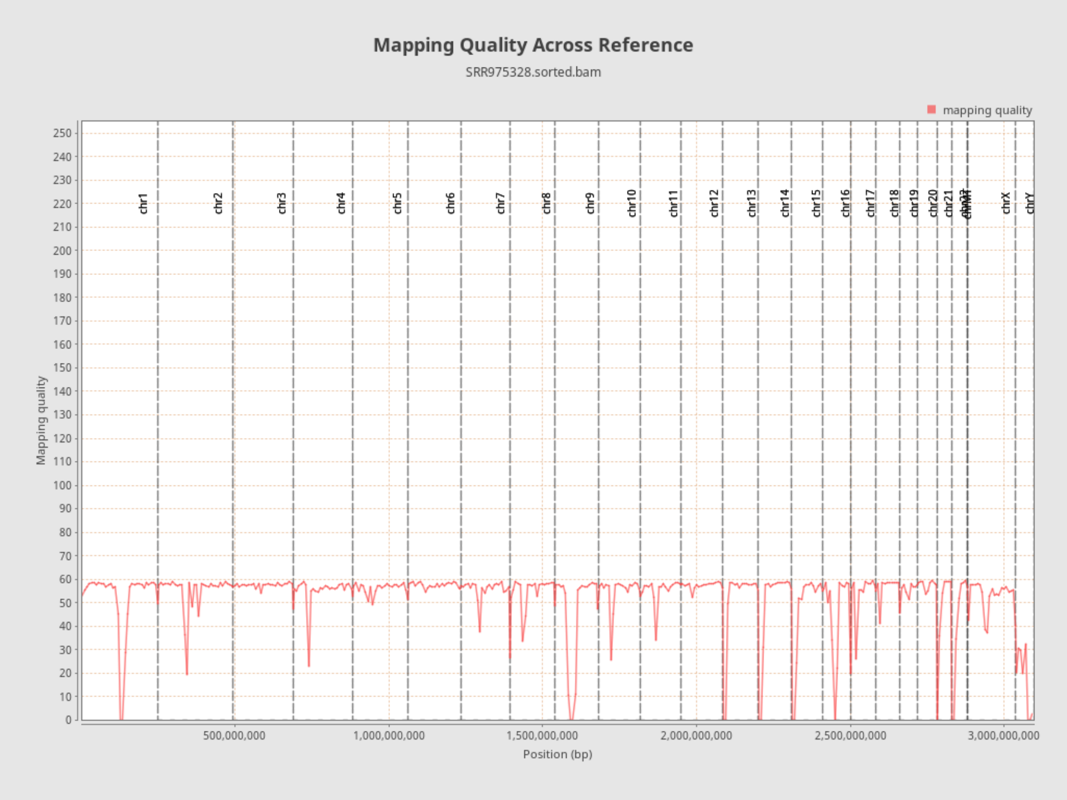
10. Results : Mapped Reads Clipping Profile



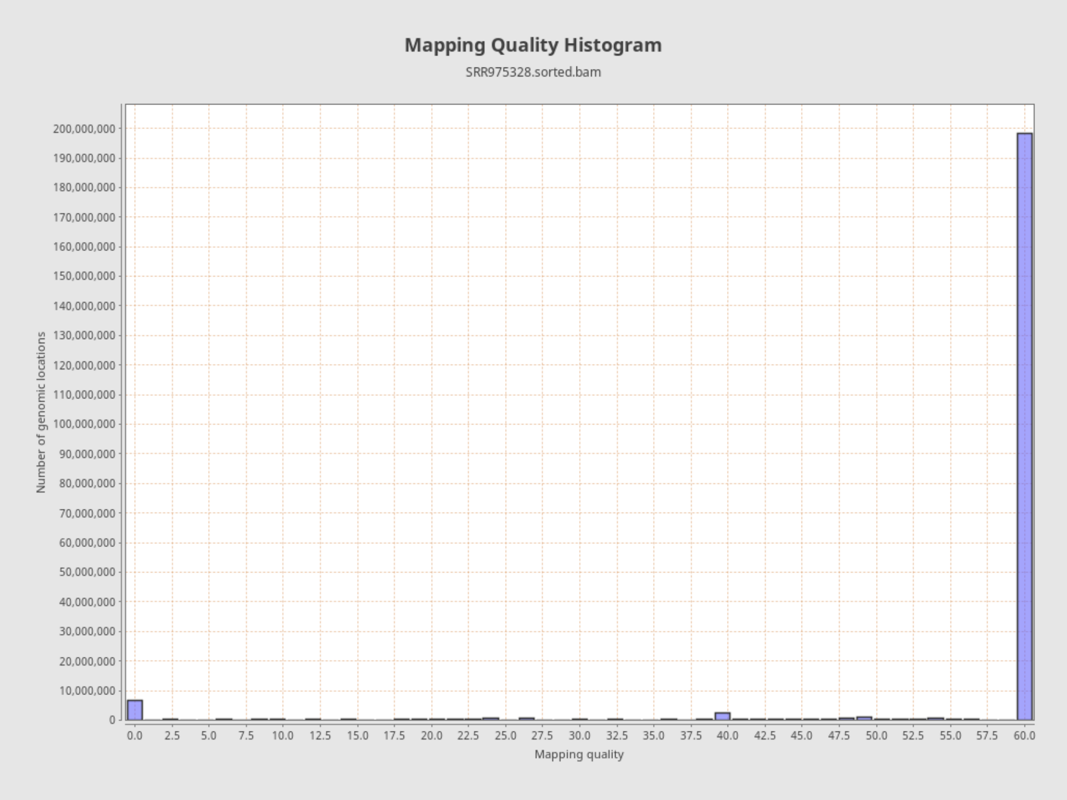
11. Results : Homopolymer Indels



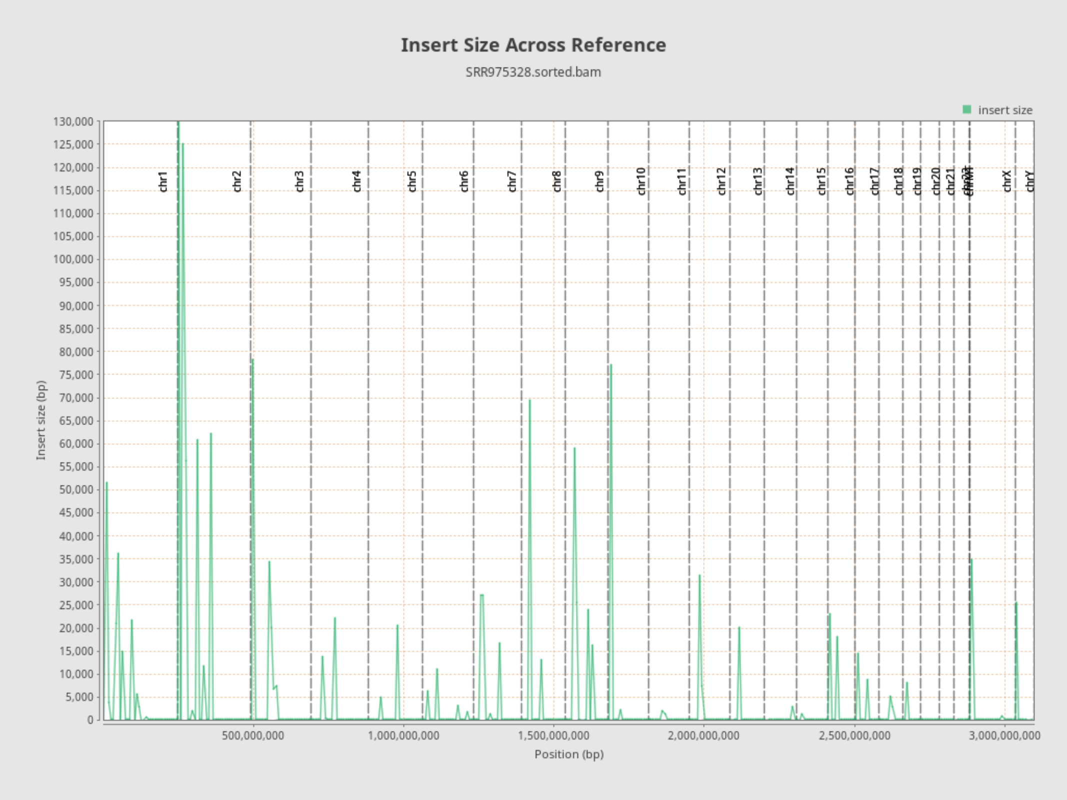
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram