Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 23:48:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975302.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_SRR975302 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975302_1.fastq.gz SRR975302_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 23:48:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975302.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,449,046
Mapped reads	2,423,456 / 98.96%
Unmapped reads	25,590 / 1.04%
Mapped paired reads	2,423,456 / 98.96%
Mapped reads, first in pair	1,213,139 / 49.54%
Mapped reads, second in pair	1,210,317 / 49.42%
Mapped reads, both in pair	2,416,690 / 98.68%
Mapped reads, singletons	6,766 / 0.28%
Secondary alignments	0
Supplementary alignments	25,058 / 1.02%
Read min/max/mean length	30 / 151 / 151.5
Duplicated reads (estimated)	370,606 / 15.13%
Duplication rate	15.25%
Clipped reads	1,767,066 / 72.15%

2.2. ACGT Content

Number/percentage of A's	95,675,894 / 29.23%
Number/percentage of C's	66,353,166 / 20.27%
Number/percentage of T's	95,676,408 / 29.23%
Number/percentage of G's	69,572,496 / 21.26%
Number/percentage of N's	20,785 / 0.01%

GC Percentage	41.53%

2.3. Coverage

Mean	0.1058
Standard Deviation	1.1589

2.4. Mapping Quality

Mean Mapping Quality	53.67

2.5. Insert size

Mean	68,882.98
Standard Deviation	2,557,841.76
P25/Median/P75	136 / 168 / 212

2.6. Mismatches and indels

General error rate	1.01%
Mismatches	3,188,773
Insertions	55,824
Mapped reads with at least one insertion	2.2%
Deletions	112,737
Mapped reads with at least one deletion	4.5%
Homopolymer indels	47.15%

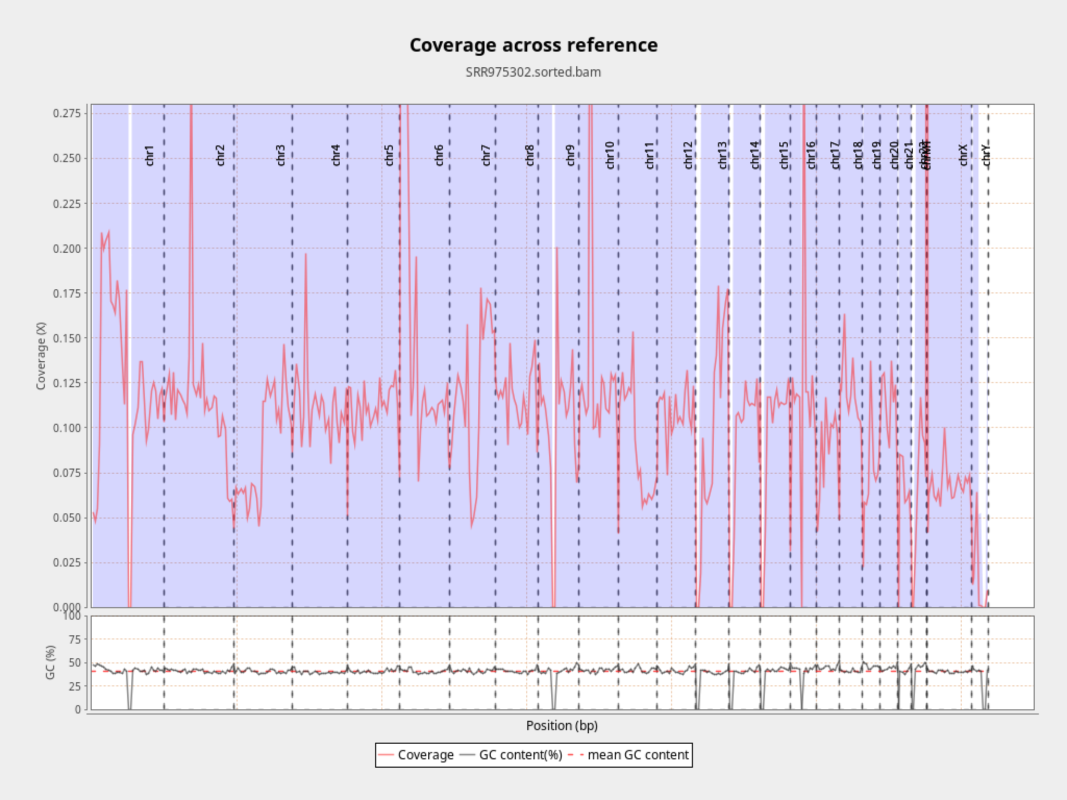
2.7. Chromosome stats

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

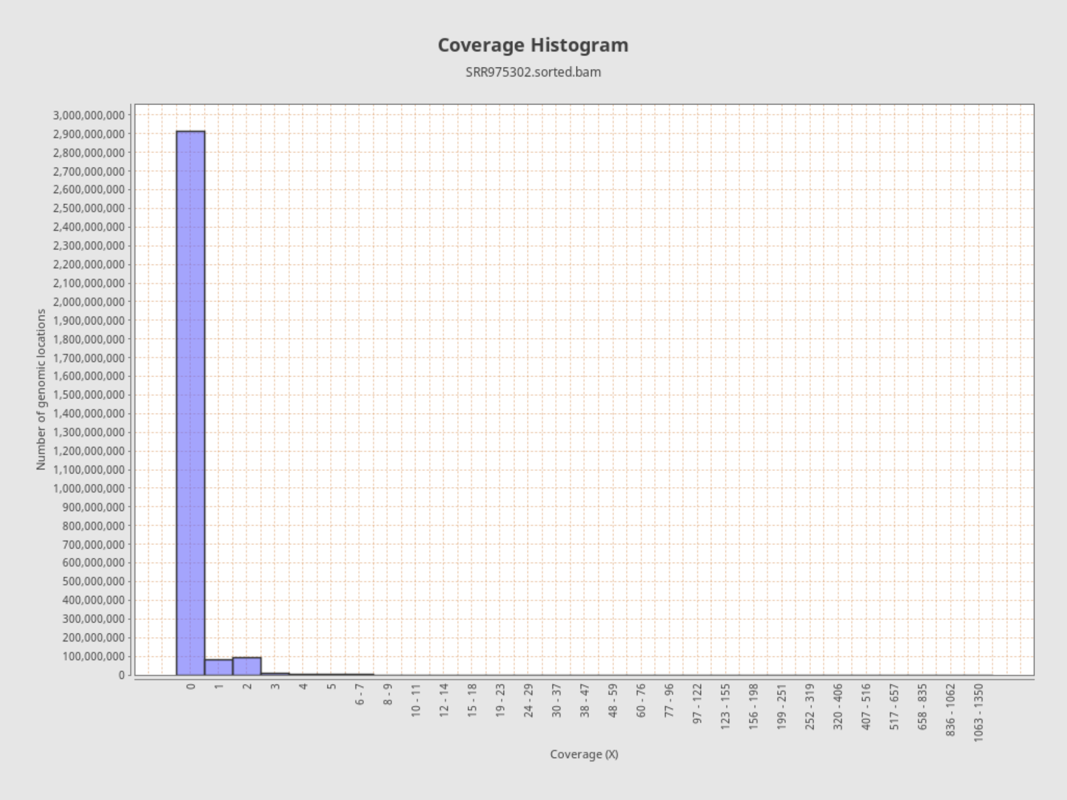
		bases	coverage	deviation
chr1	249250621	30760969	0.1234	1.2313
chr2	243199373	28116107	0.1156	1.3171
chr3	198022430	17764421	0.0897	0.4314
chr4	191154276	21384812	0.1119	0.8015
chr5	180915260	20333360	0.1124	0.4672
chr6	171115067	26800292	0.1566	1.0304
chr7	159138663	18931246	0.119	1.2343
chr8	146364022	17108791	0.1169	0.5982
chr9	141213431	14526038	0.1029	2.0186
chr10	135534747	18064100	0.1333	2.8412
chr11	135006516	12123152	0.0898	1.1643
chr12	133851895	14614406	0.1092	0.4595
chr13	115169878	11242687	0.0976	0.4375
chr14	107349540	9805160	0.0913	0.4268
chr15	102531392	9616163	0.0938	0.4273
chr16	90354753	10859596	0.1202	1.5896
chr17	81195210	7006038	0.0863	0.9622
chr18	78077248	9385084	0.1202	1.8566
chr19	59128983	4394964	0.0743	0.8037
chr20	63025520	7098861	0.1126	0.5182
chr21	48129895	2919845	0.0607	0.5351
chr22	51304566	3386971	0.066	0.3596
chrMT	16571	35359	2.1338	2.3995
chrX	155270560	10457855	0.0674	0.5016

chrY	59373566	771907	0.013	0.9342

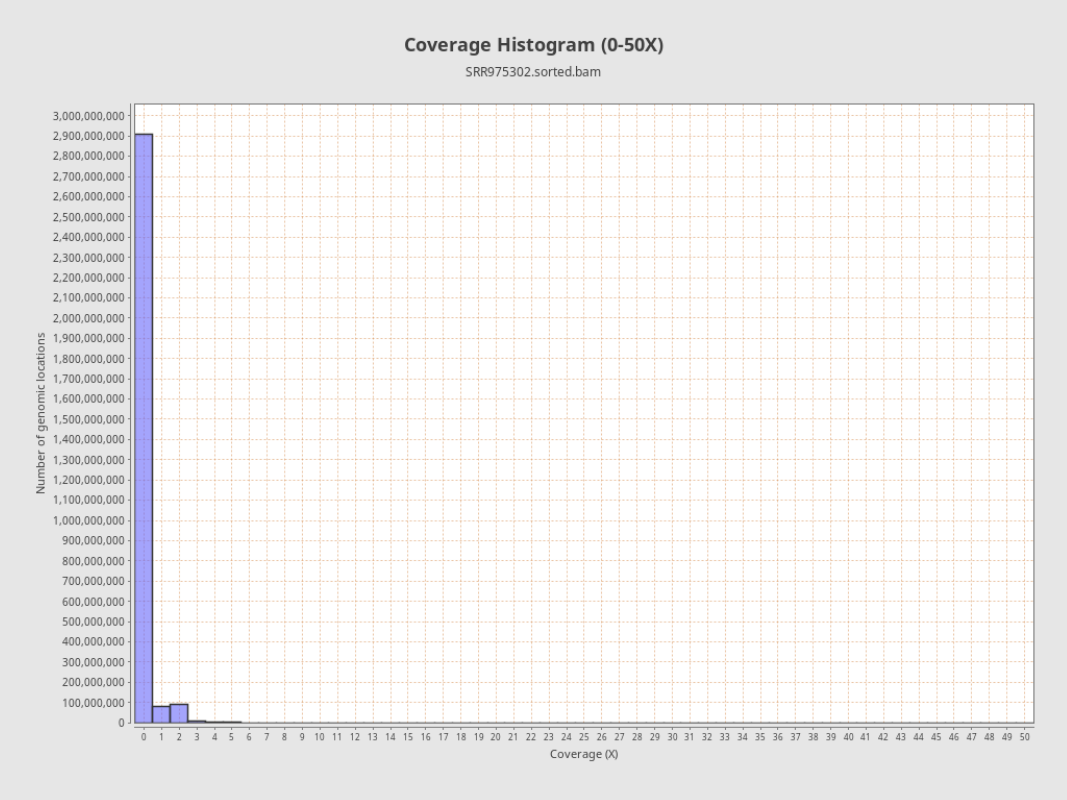
3. Results : Coverage across reference



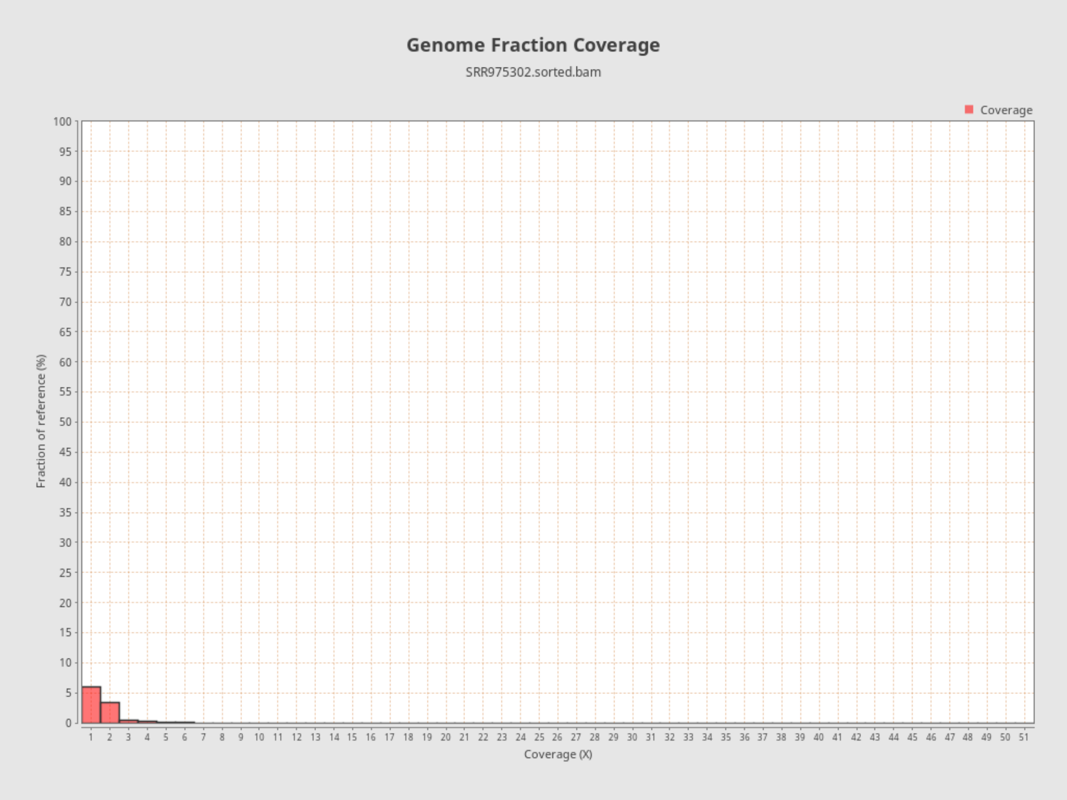
4. Results : Coverage Histogram



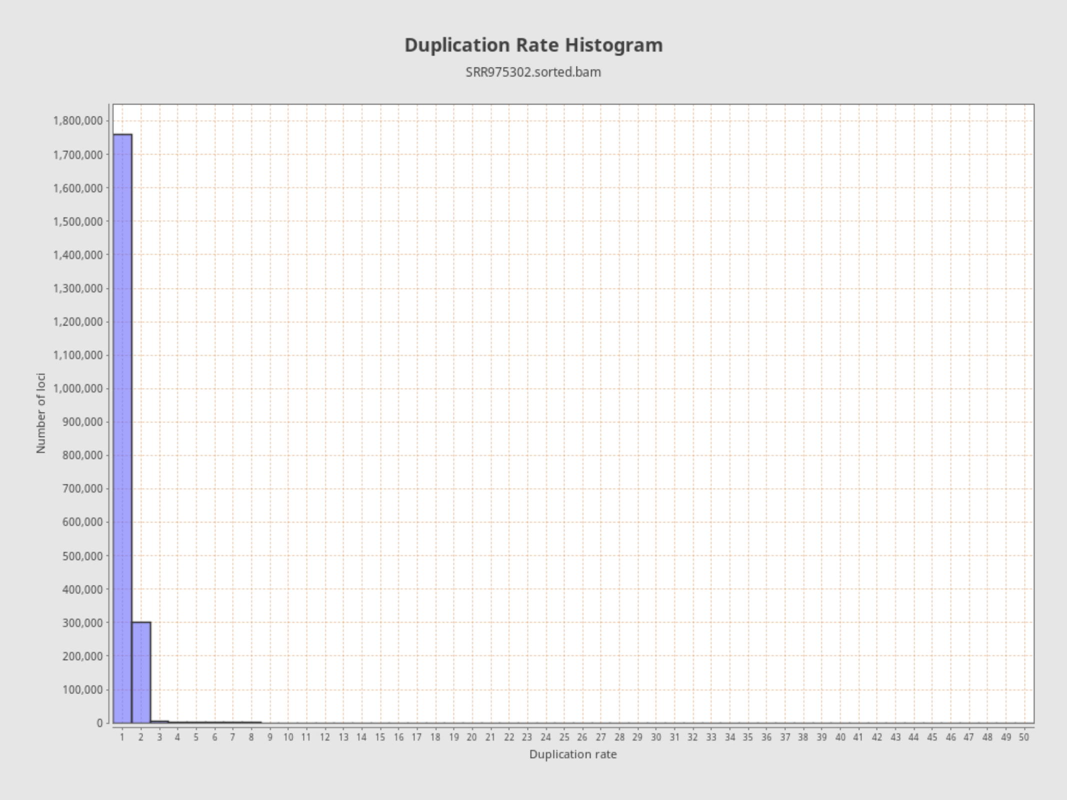
5. Results : Coverage Histogram (0-50X)



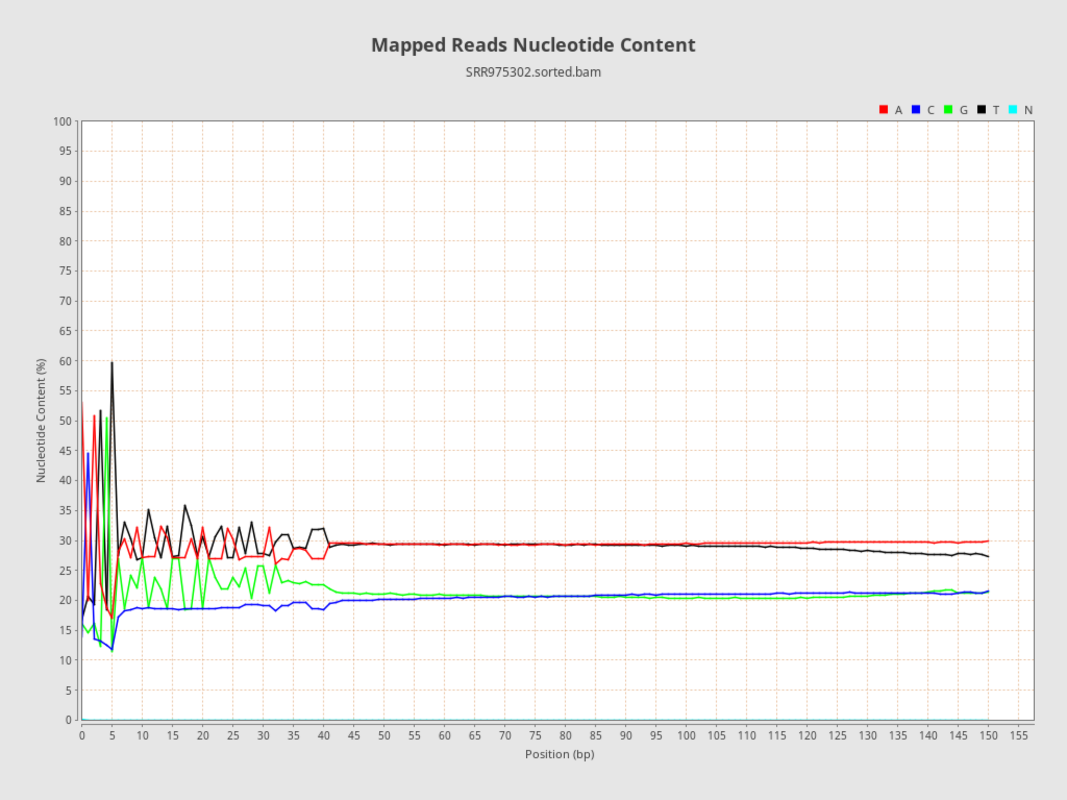
6. Results : Genome Fraction Coverage



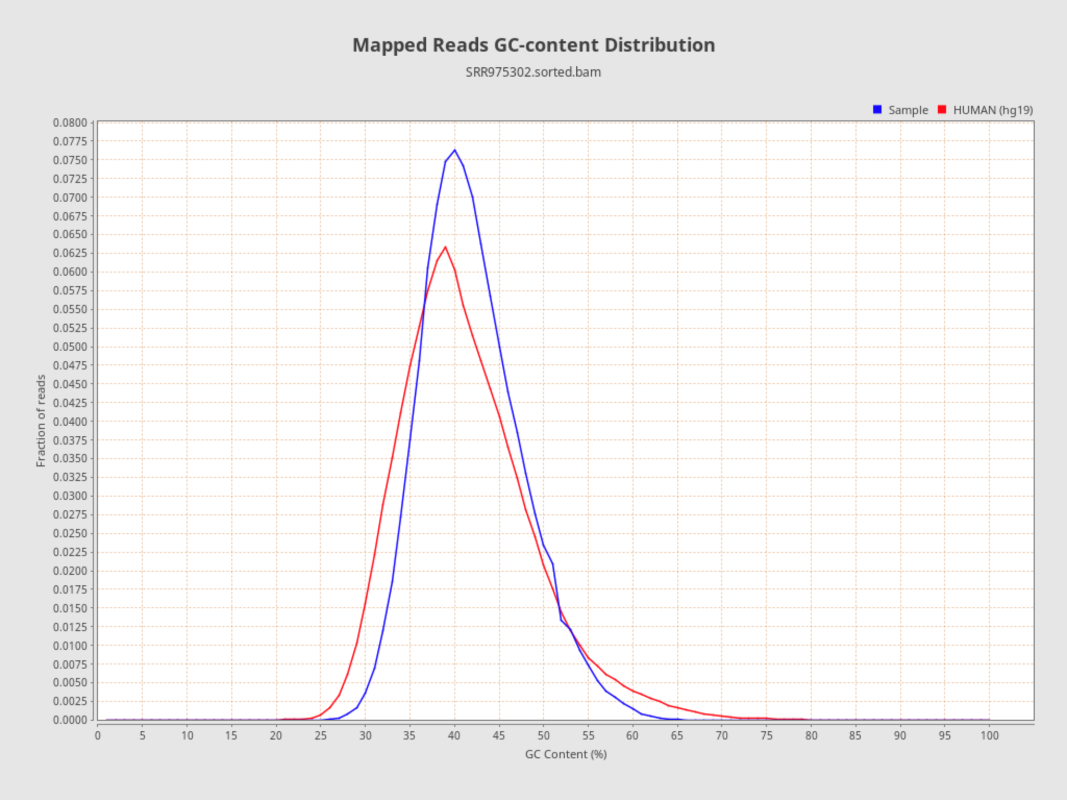
7. Results : Duplication Rate Histogram



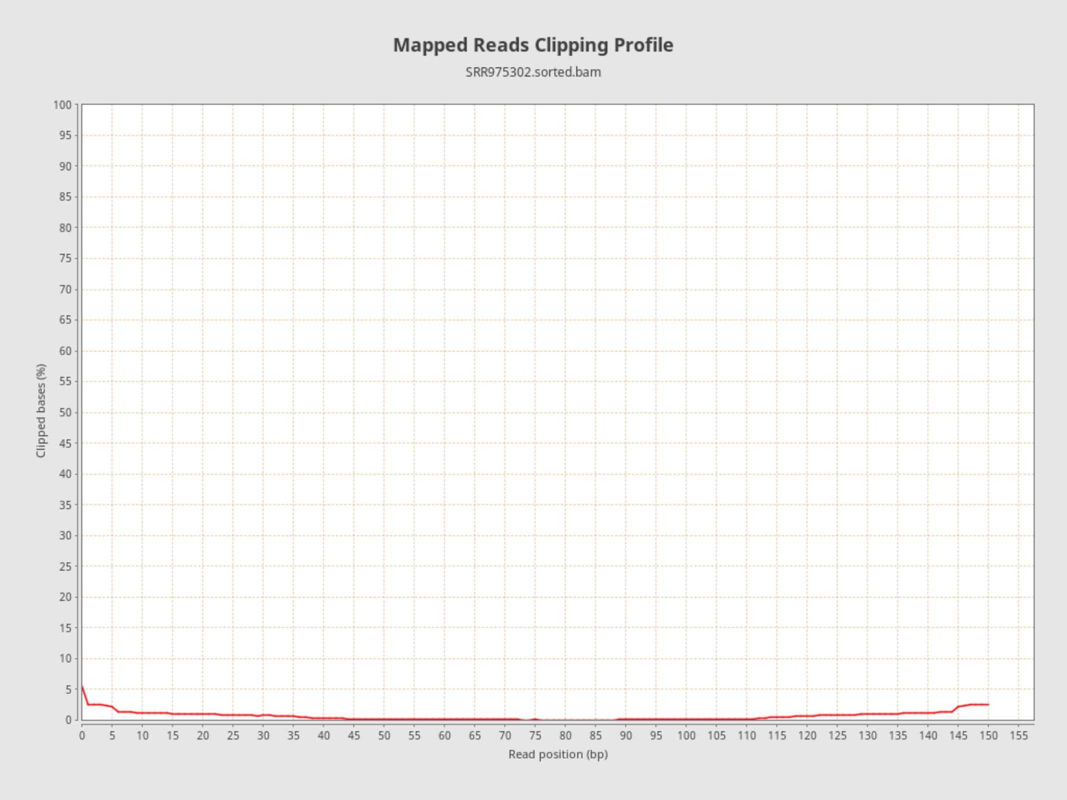
8. Results : Mapped Reads Nucleotide Content



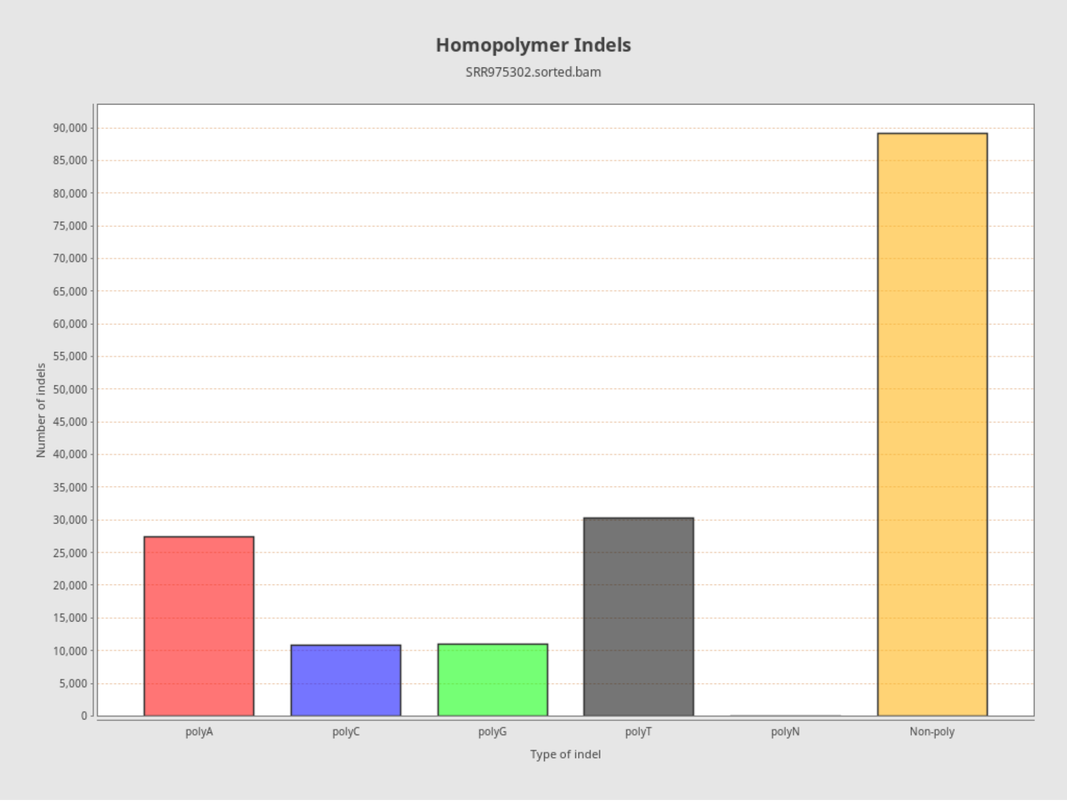
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

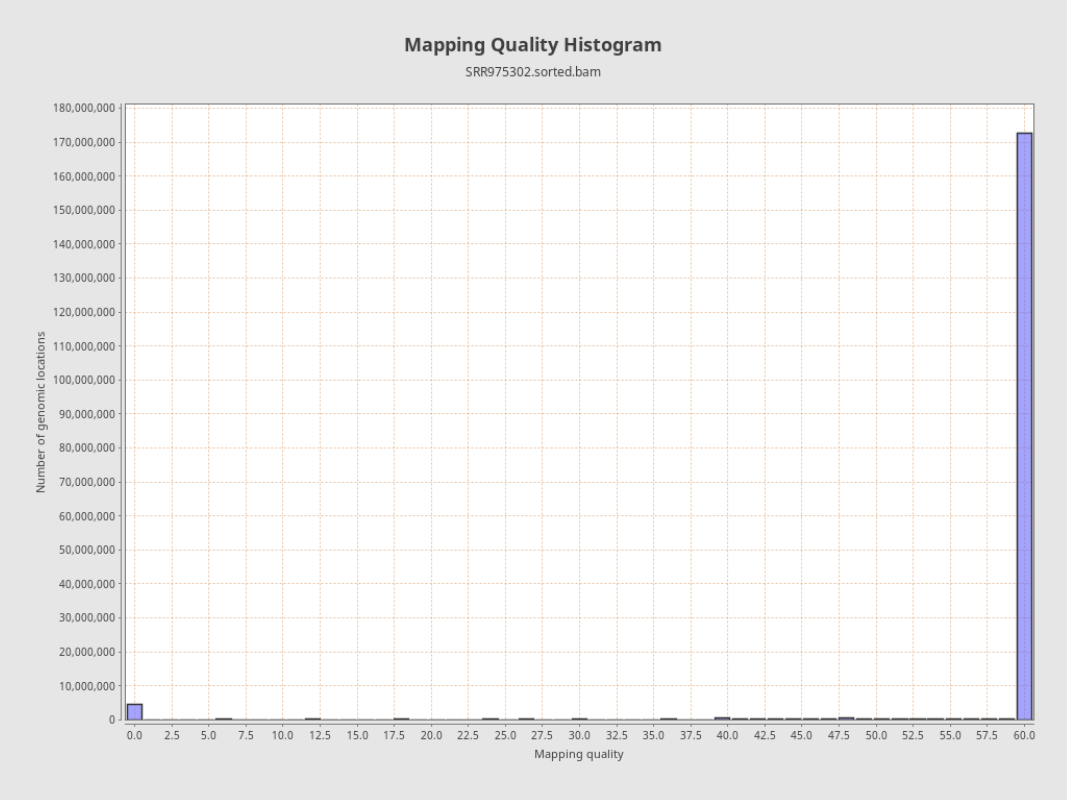


11. Results : Homopolymer Indels

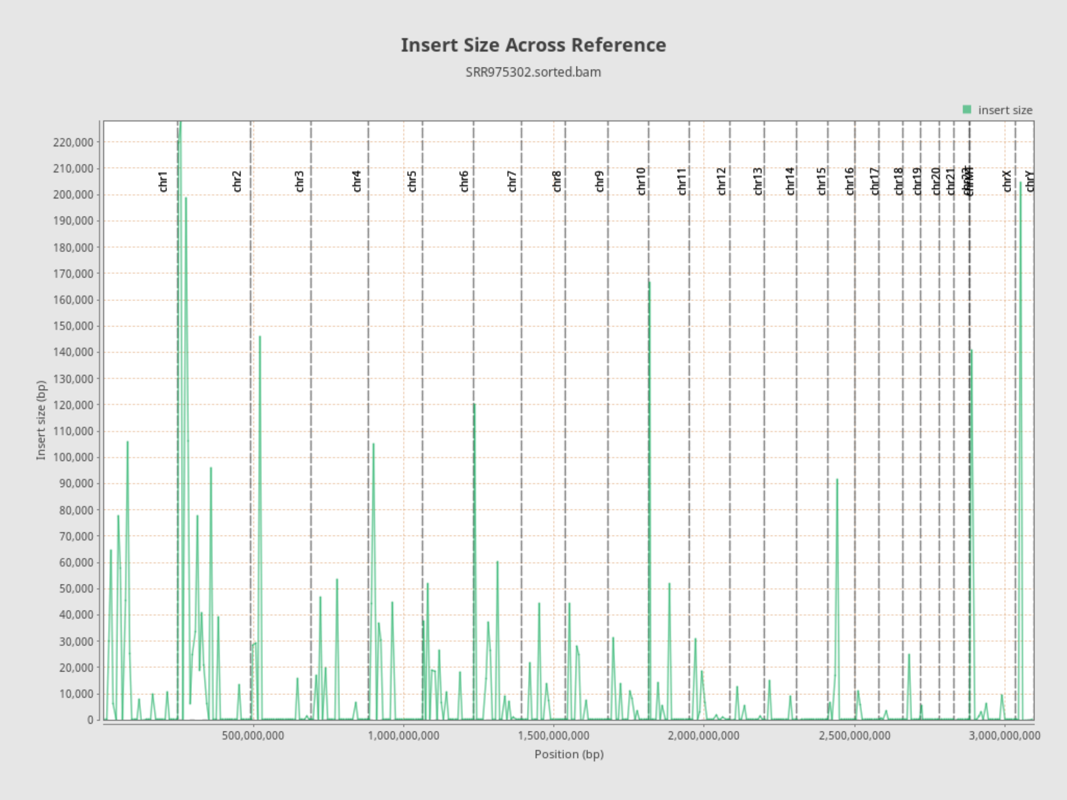


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram