Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 23:36:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975298.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_SRR975298 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975298_1.fastq.gz SRR975298_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 23:36:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975298.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,600,194
Mapped reads	2,564,837 / 98.64%
Unmapped reads	35,357 / 1.36%
Mapped paired reads	2,564,837 / 98.64%
Mapped reads, first in pair	1,285,279 / 49.43%
Mapped reads, second in pair	1,279,558 / 49.21%
Mapped reads, both in pair	2,554,142 / 98.23%
Mapped reads, singletons	10,695 / 0.41%
Secondary alignments	0
Supplementary alignments	29,912 / 1.15%
Read min/max/mean length	30 / 151 / 151.54
Duplicated reads (estimated)	408,774 / 15.72%
Duplication rate	15.59%
Clipped reads	1,902,503 / 73.17%

2.2. ACGT Content

Number/percentage of A's	100,948,462 / 29.37%
Number/percentage of C's	68,603,698 / 19.96%
Number/percentage of T's	101,846,087 / 29.63%
Number/percentage of G's	72,288,027 / 21.03%
Number/percentage of N's	21,821 / 0.01%

GC Percentage	40.99%

2.3. Coverage

Mean	0.1111
Standard Deviation	1.1894

2.4. Mapping Quality

Mean Mapping Quality	53.47

2.5. Insert size

Mean	77,431.48
Standard Deviation	2,649,449.91
P25/Median/P75	135 / 167 / 211

2.6. Mismatches and indels

General error rate	0.97%
Mismatches	3,168,039
Insertions	62,681
Mapped reads with at least one insertion	2.3%
Deletions	113,558
Mapped reads with at least one deletion	4.26%
Homopolymer indels	45.97%

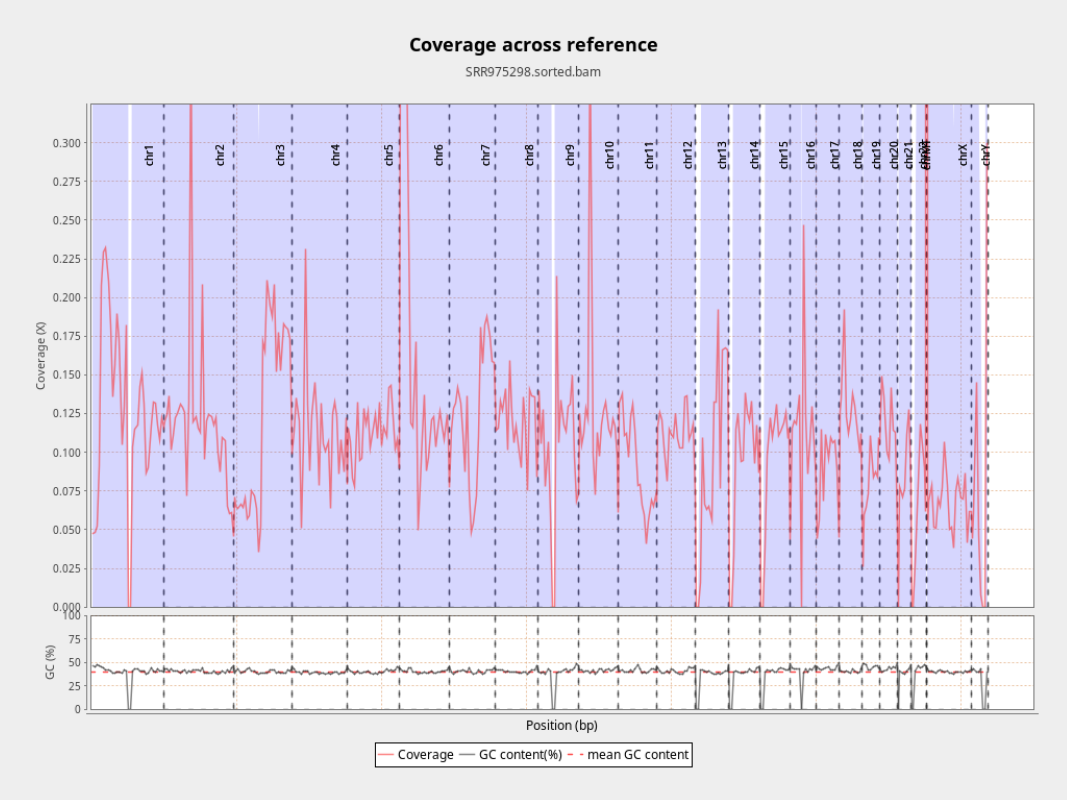
2.7. Chromosome stats

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

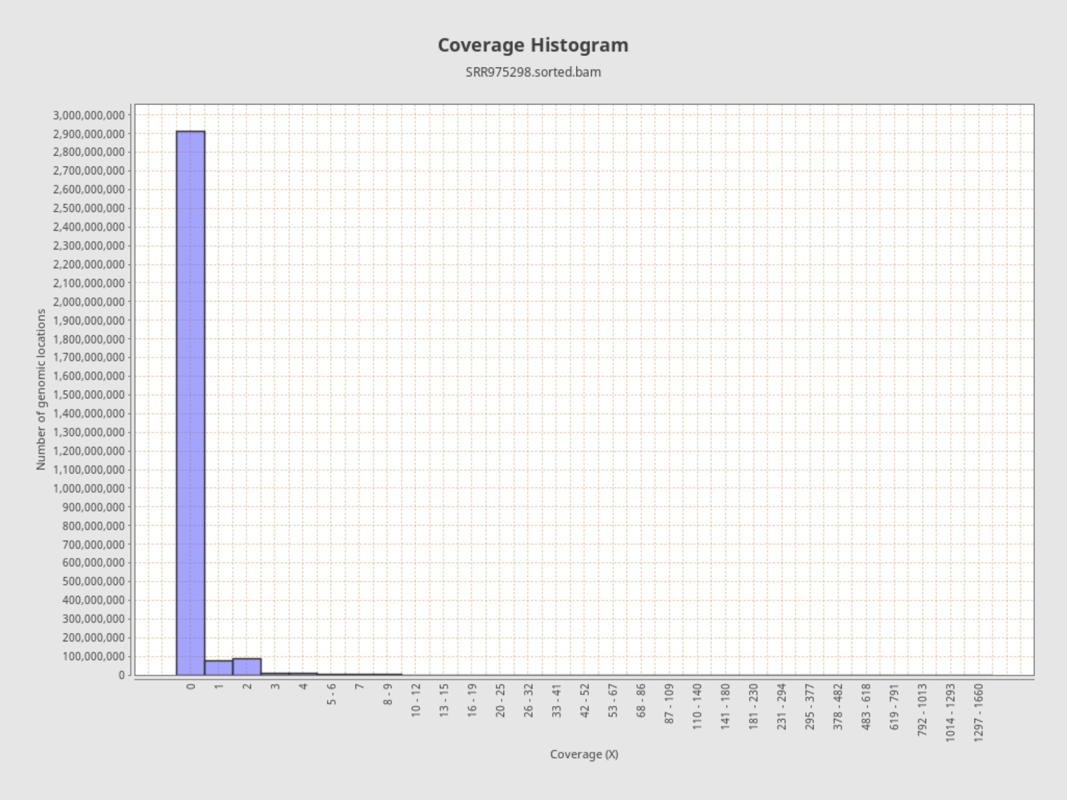
		bases	coverage	deviation
chr1	249250621	31454464	0.1262	1.1556
chr2	243199373	29312848	0.1205	1.8195
chr3	198022430	24288658	0.1227	0.5146
chr4	191154276	21727749	0.1137	1.0203
chr5	180915260	20471065	0.1132	0.4893
chr6	171115067	27680459	0.1618	0.8822
chr7	159138663	20002588	0.1257	1.0124
chr8	146364022	17408503	0.1189	0.6933
chr9	141213431	14718809	0.1042	2.4588
chr10	135534747	17278957	0.1275	1.9964
chr11	135006516	12163394	0.0901	1.0399
chr12	133851895	15106609	0.1129	0.485
chr13	115169878	11099341	0.0964	0.4522
chr14	107349540	9994400	0.0931	0.4633
chr15	102531392	9602018	0.0936	0.4425
chr16	90354753	10137205	0.1122	1.229
chr17	81195210	7170508	0.0883	1.0689
chr18	78077248	9990681	0.128	2.2111
chr19	59128983	4672506	0.079	0.826
chr20	63025520	7340176	0.1165	0.5738
chr21	48129895	3990450	0.0829	0.62
chr22	51304566	3383890	0.066	0.3777
chrMT	16571	90191	5.4427	4.2235
chrX	155270560	10299996	0.0663	0.4989

chrY	59373566	4560284	0.0768	1.8512

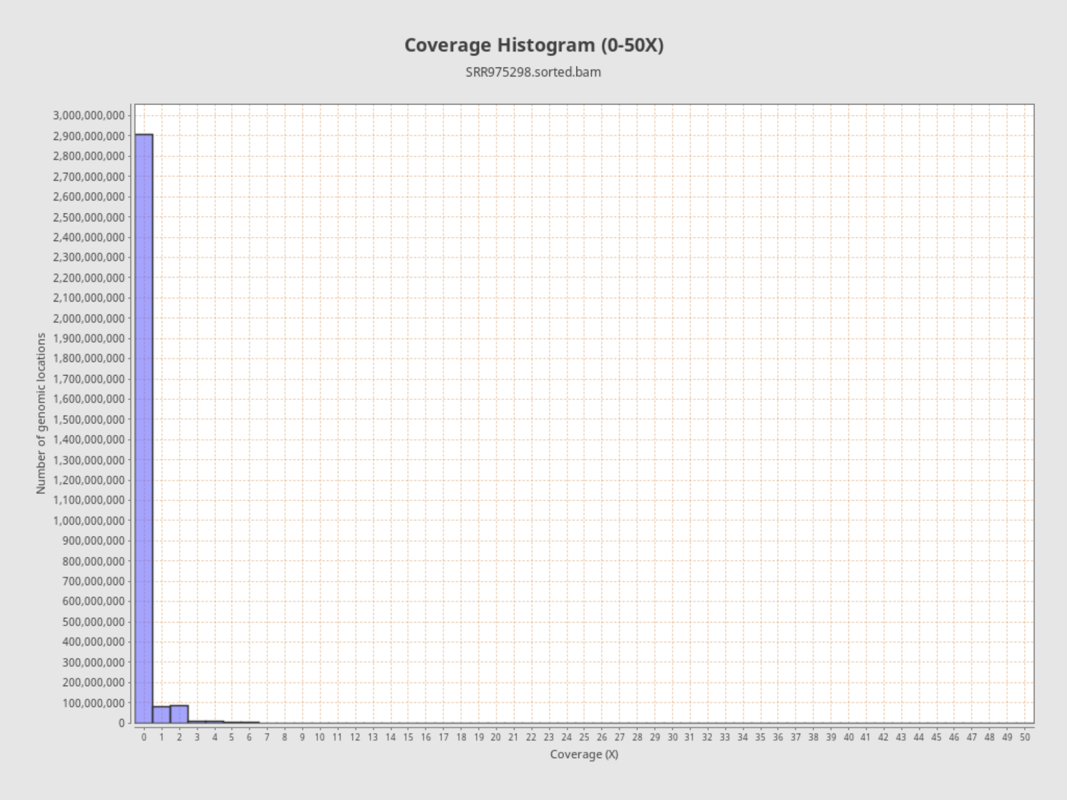
3. Results : Coverage across reference



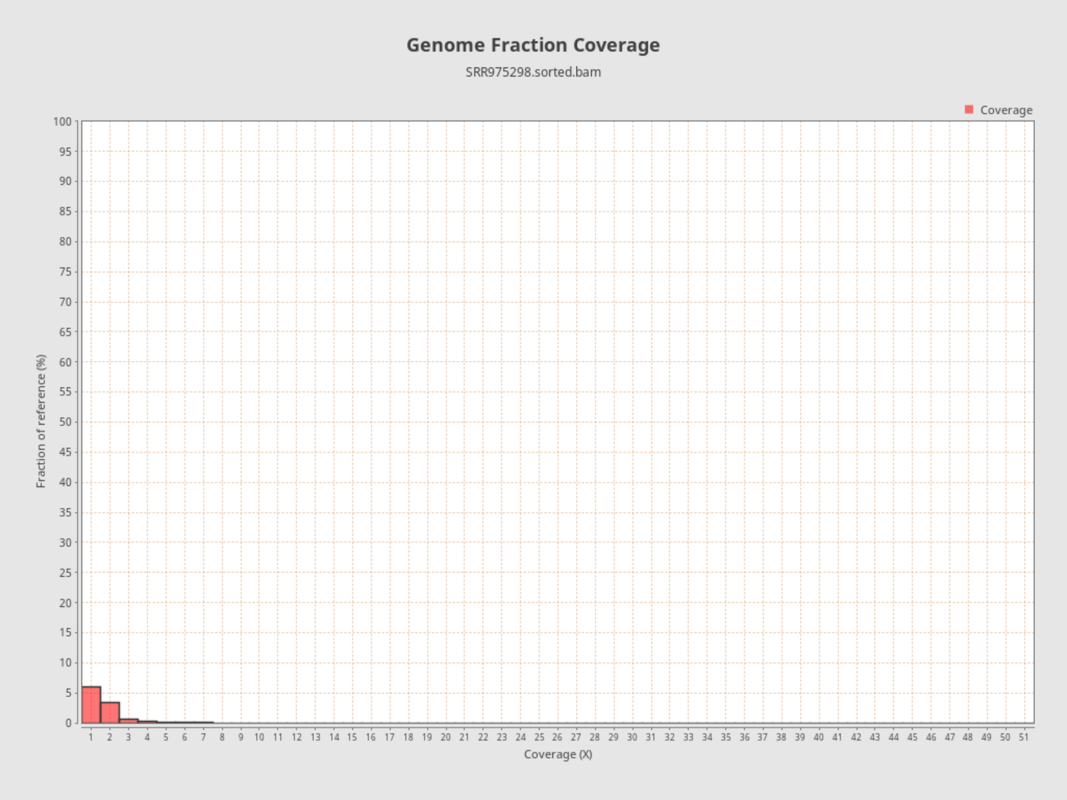
4. Results : Coverage Histogram



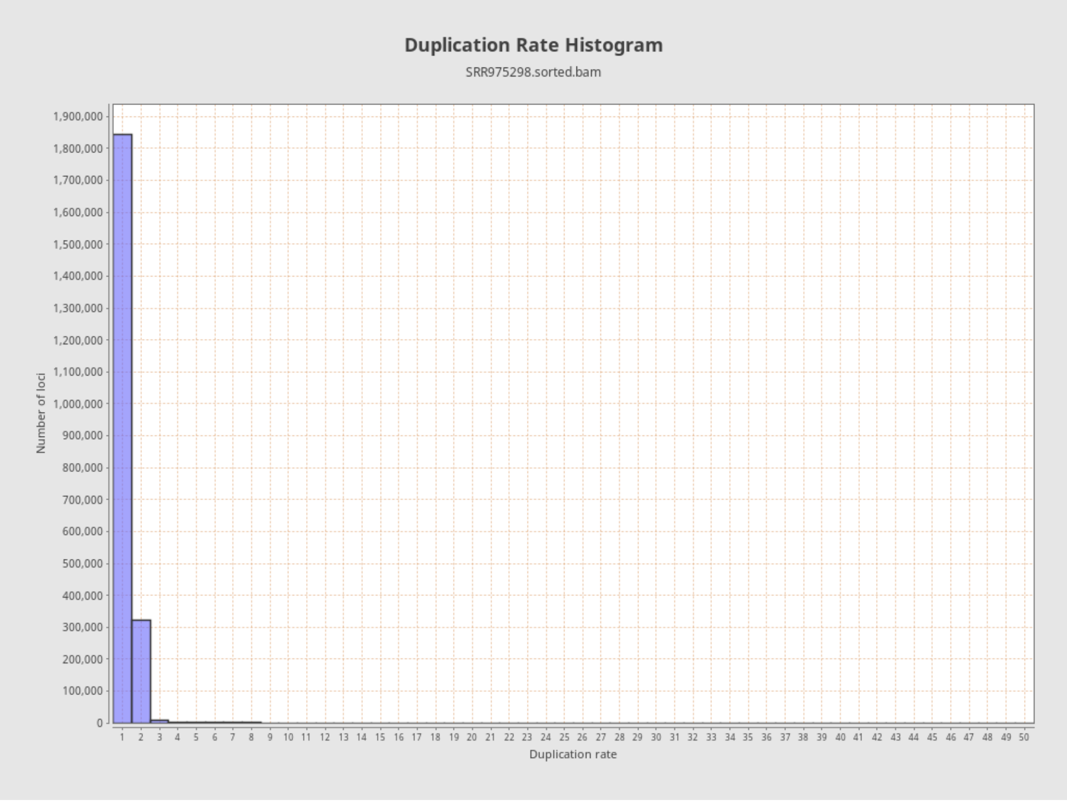
5. Results : Coverage Histogram (0-50X)



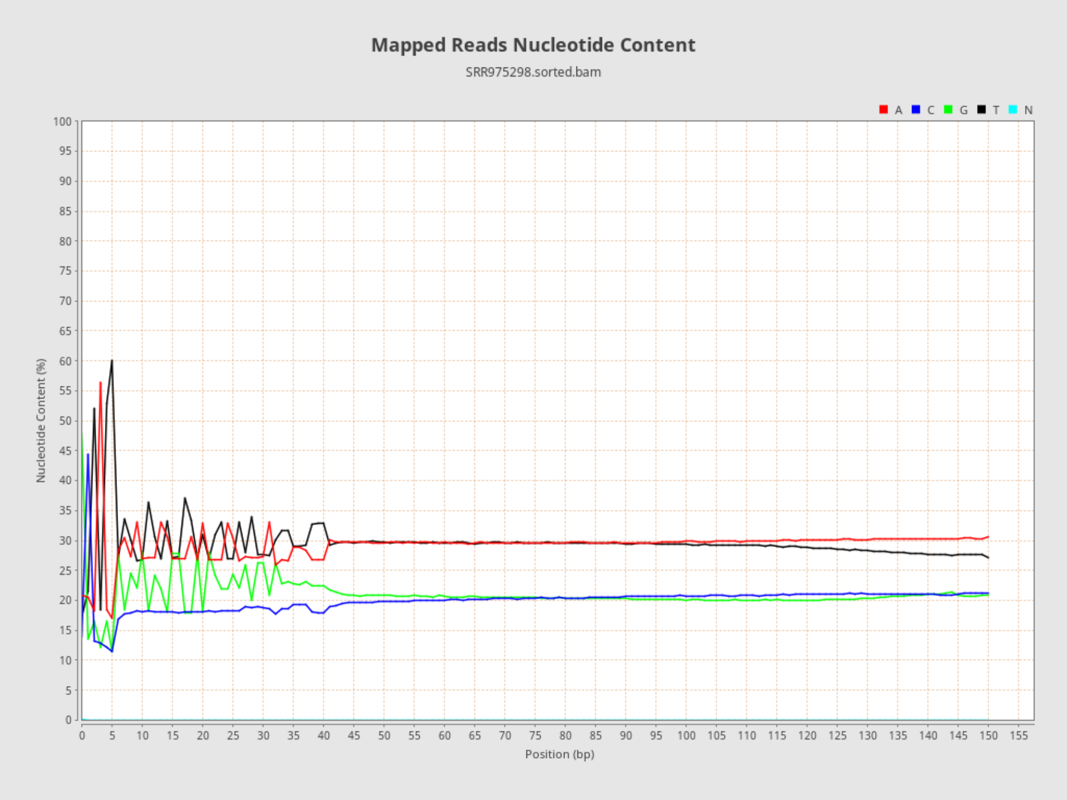
6. Results : Genome Fraction Coverage



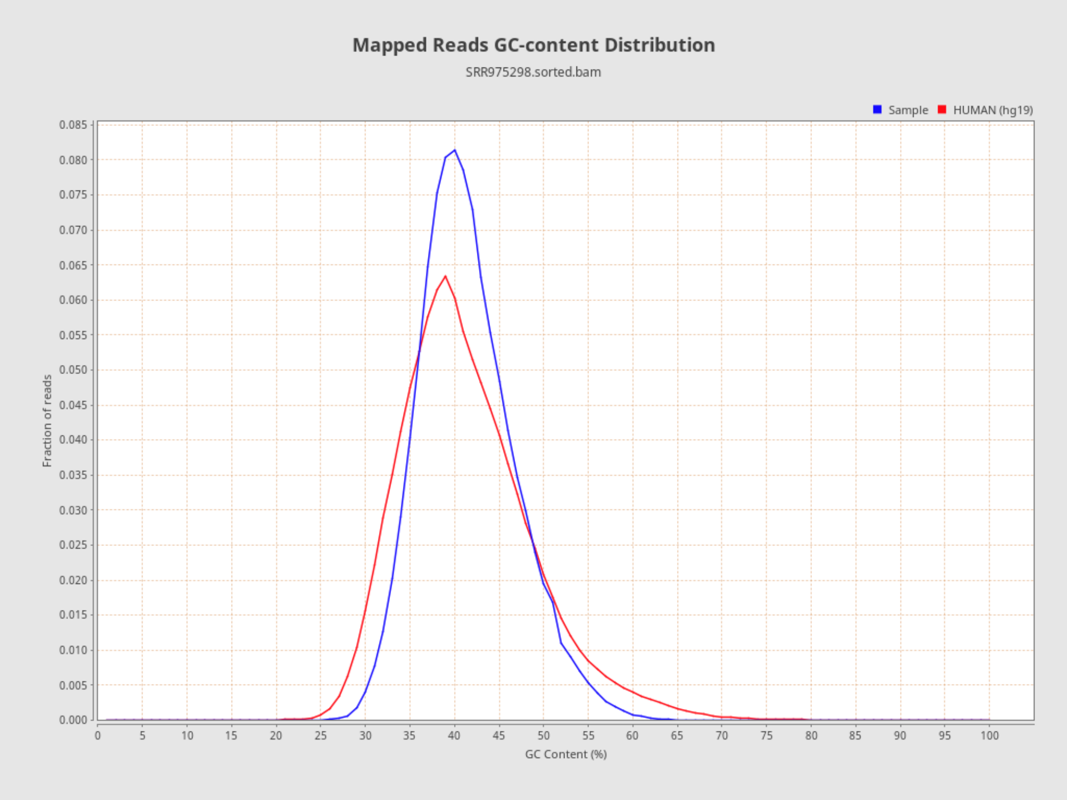
7. Results : Duplication Rate Histogram



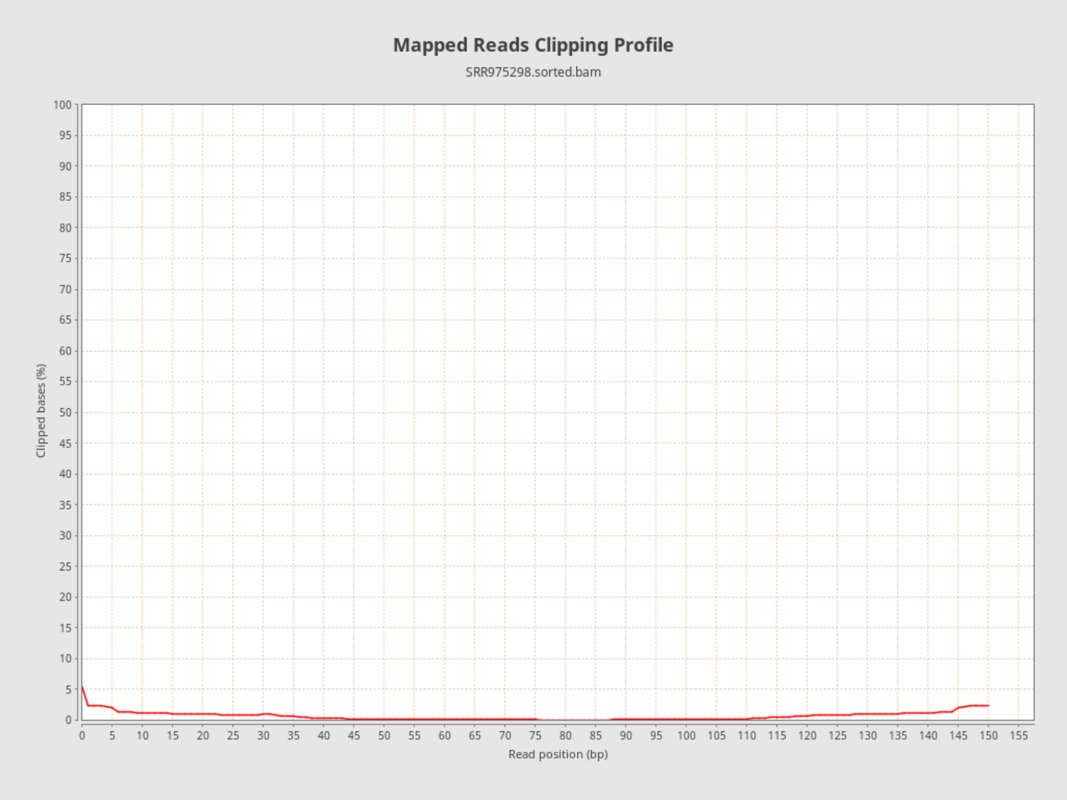
8. Results : Mapped Reads Nucleotide Content



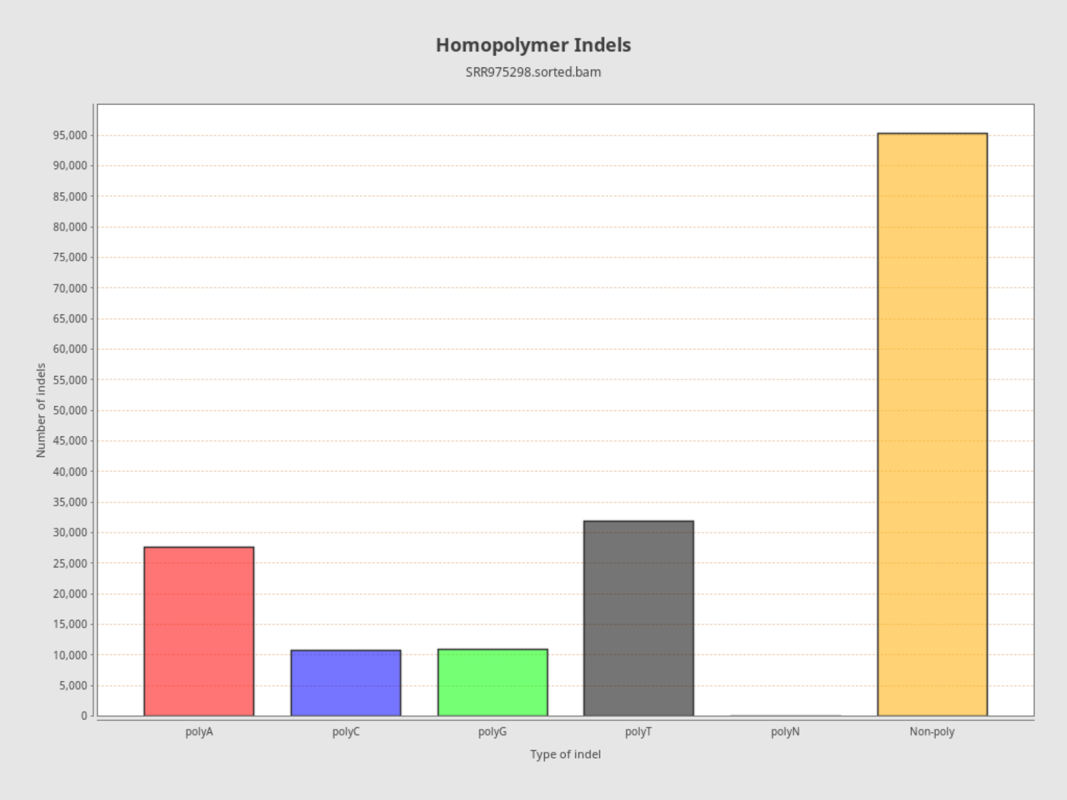
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

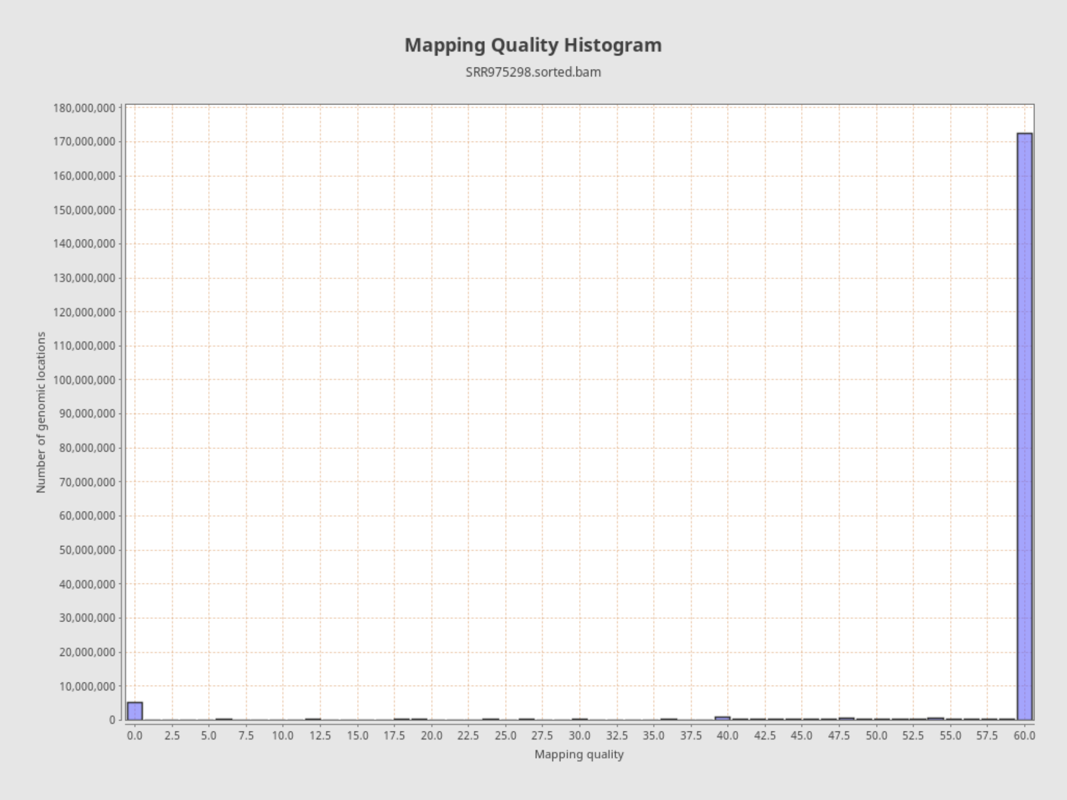


11. Results : Homopolymer Indels

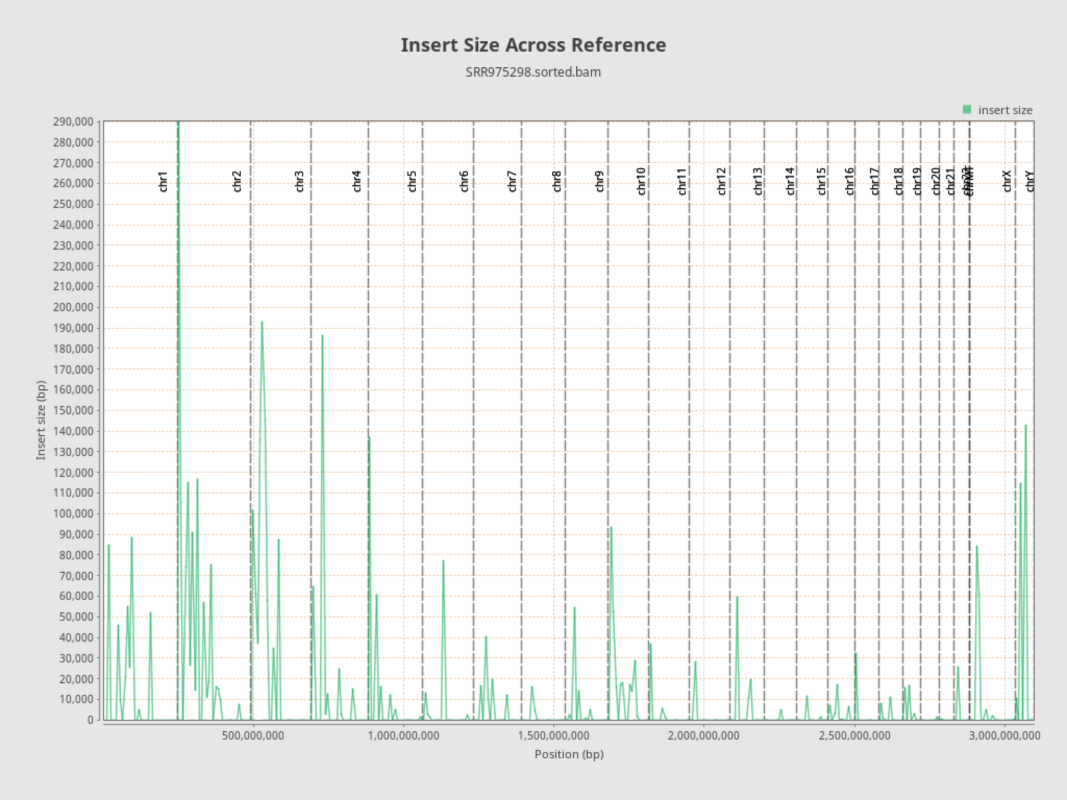


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram