Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 02:33:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975316.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_SRR975316 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975316_1.fastq.gz SRR975316_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 02:33:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975316.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,658,720
Mapped reads	2,622,815 / 98.65%
Unmapped reads	35,905 / 1.35%
Mapped paired reads	2,622,815 / 98.65%
Mapped reads, first in pair	1,313,496 / 49.4%
Mapped reads, second in pair	1,309,319 / 49.25%
Mapped reads, both in pair	2,613,574 / 98.3%
Mapped reads, singletons	9,241 / 0.35%
Secondary alignments	0
Supplementary alignments	30,377 / 1.14%
Read min/max/mean length	30 / 151 / 151.55
Duplicated reads (estimated)	418,963 / 15.76%
Duplication rate	15.75%
Clipped reads	1,943,802 / 73.11%

2.2. ACGT Content

Number/percentage of A's	102,710,324 / 29.2%
Number/percentage of C's	71,622,603 / 20.36%
Number/percentage of T's	102,723,187 / 29.21%
Number/percentage of G's	74,647,498 / 21.22%
Number/percentage of N's	21,672 / 0.01%

GC Percentage	41.59%

2.3. Coverage

Mean	0.1137
Standard Deviation	1.2578

2.4. Mapping Quality

Mean Mapping Quality	53.66

2.5. Insert size

Mean	86,903.75
Standard Deviation	2,838,056.01
P25/Median/P75	134 / 166 / 211

2.6. Mismatches and indels

General error rate	1.08%
Mismatches	3,619,111
Insertions	66,232
Mapped reads with at least one insertion	2.4%
Deletions	135,660
Mapped reads with at least one deletion	4.98%
Homopolymer indels	47.13%

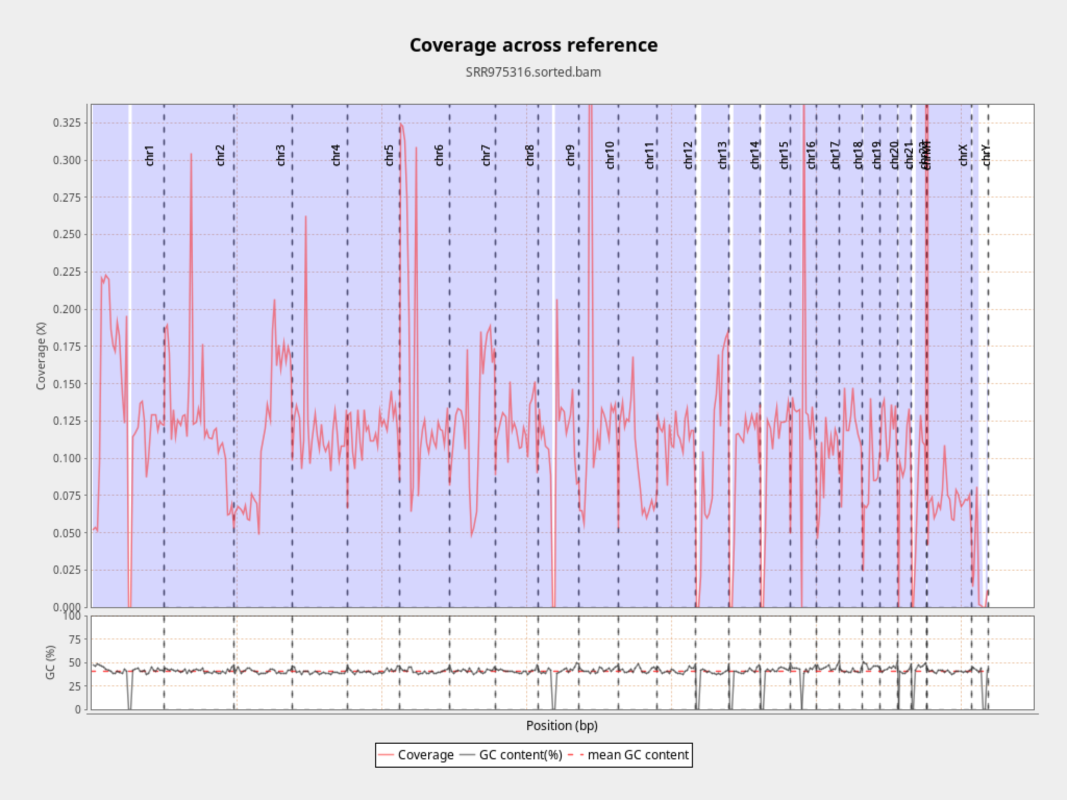
2.7. Chromosome stats

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

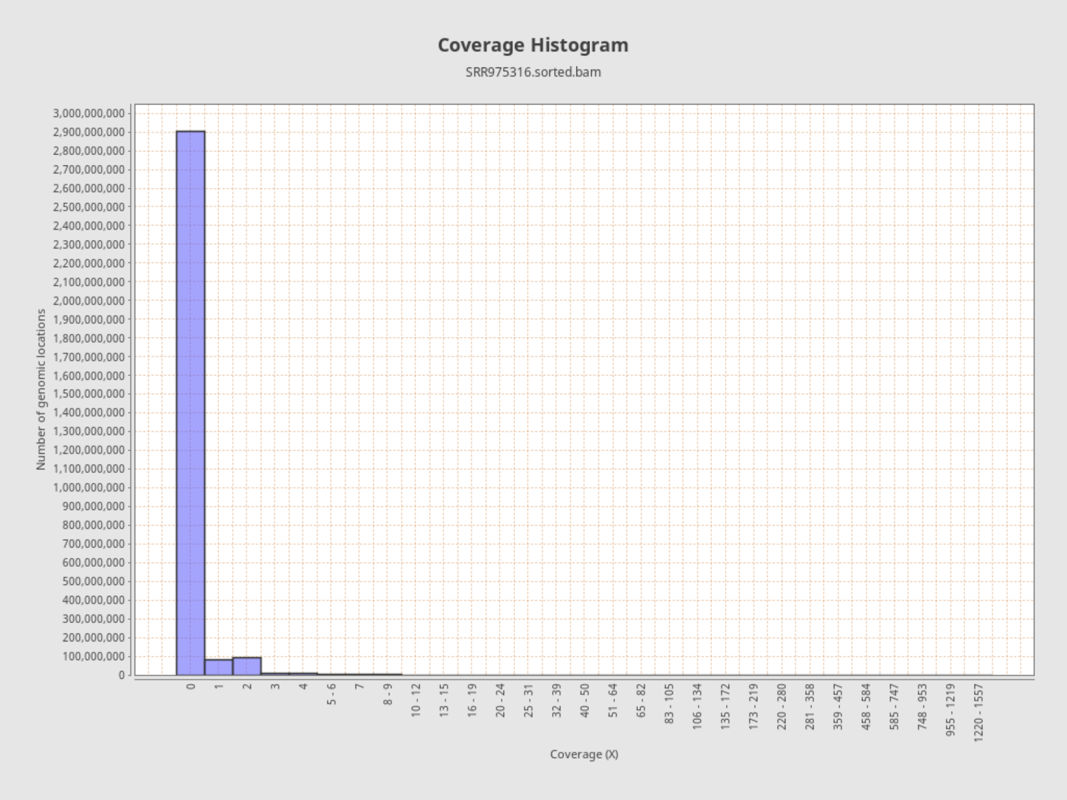
		bases	coverage	deviation
chr1	249250621	32673652	0.1311	1.3488
chr2	243199373	30799071	0.1266	1.3201
chr3	198022430	22784139	0.1151	0.4983
chr4	191154276	22916280	0.1199	1.0239
chr5	180915260	21720344	0.1201	0.4929
chr6	171115067	26441311	0.1545	1.0354
chr7	159138663	20420351	0.1283	1.3471
chr8	146364022	17672714	0.1207	0.606
chr9	141213431	15407629	0.1091	2.1086
chr10	135534747	17945925	0.1324	3.2243
chr11	135006516	13228531	0.098	1.2546
chr12	133851895	15497201	0.1158	0.4815
chr13	115169878	11729175	0.1018	0.4532
chr14	107349540	10531085	0.0981	0.457
chr15	102531392	10299061	0.1004	0.4491
chr16	90354753	11940293	0.1321	1.6887
chr17	81195210	7857029	0.0968	1.0511
chr18	78077248	9266702	0.1187	1.9426
chr19	59128983	4942460	0.0836	0.8495
chr20	63025520	7530534	0.1195	0.5797
chr21	48129895	4551498	0.0946	0.6514
chr22	51304566	3836725	0.0748	0.3926
chrMT	16571	71993	4.3445	3.4111
chrX	155270560	10939308	0.0705	0.5276

chrY	59373566	976994	0.0165	1.1163

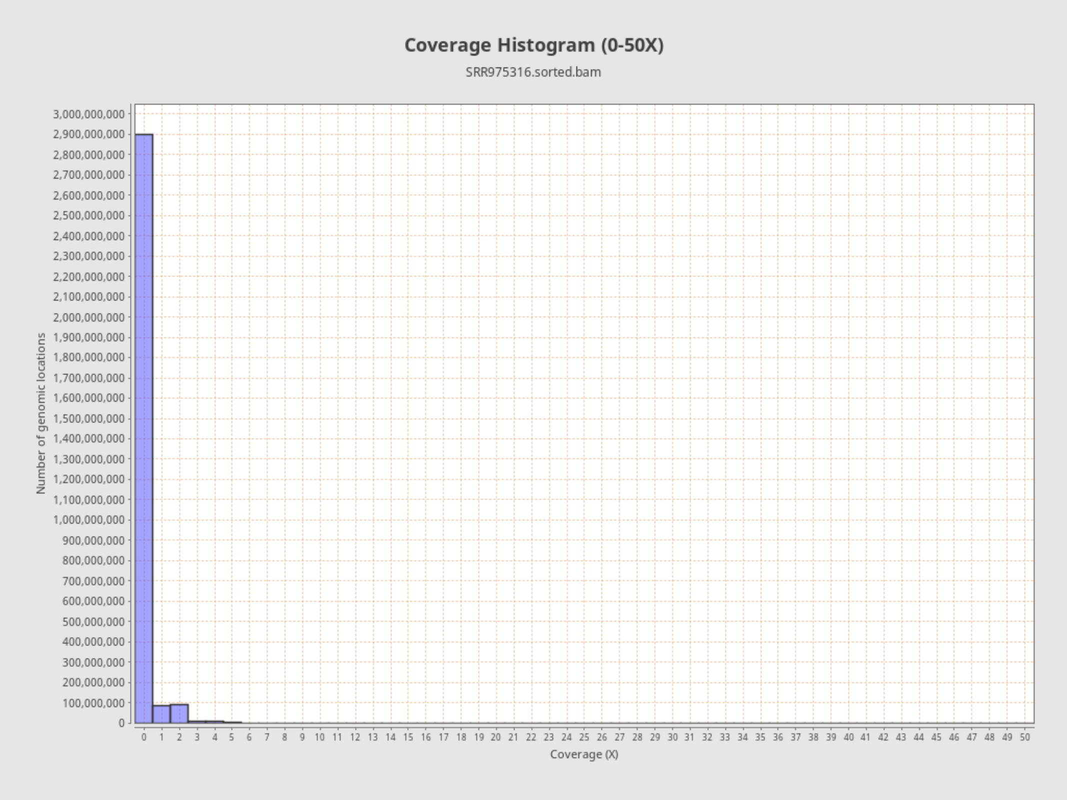
3. Results : Coverage across reference



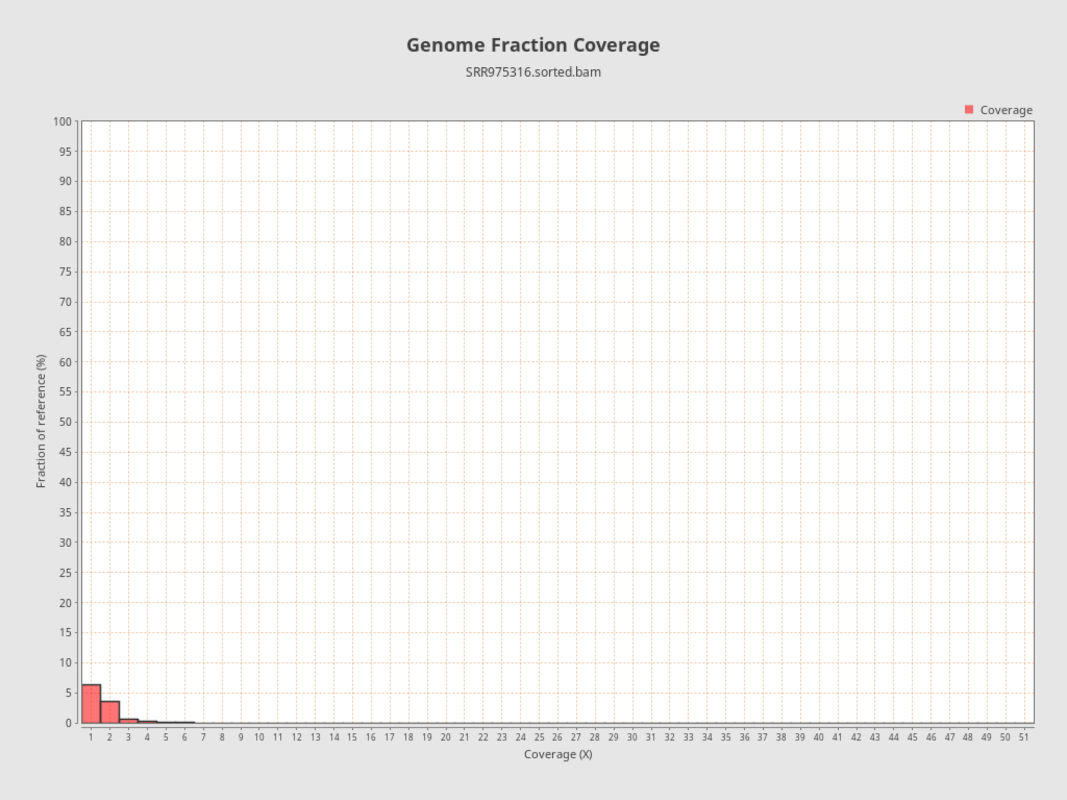
4. Results : Coverage Histogram



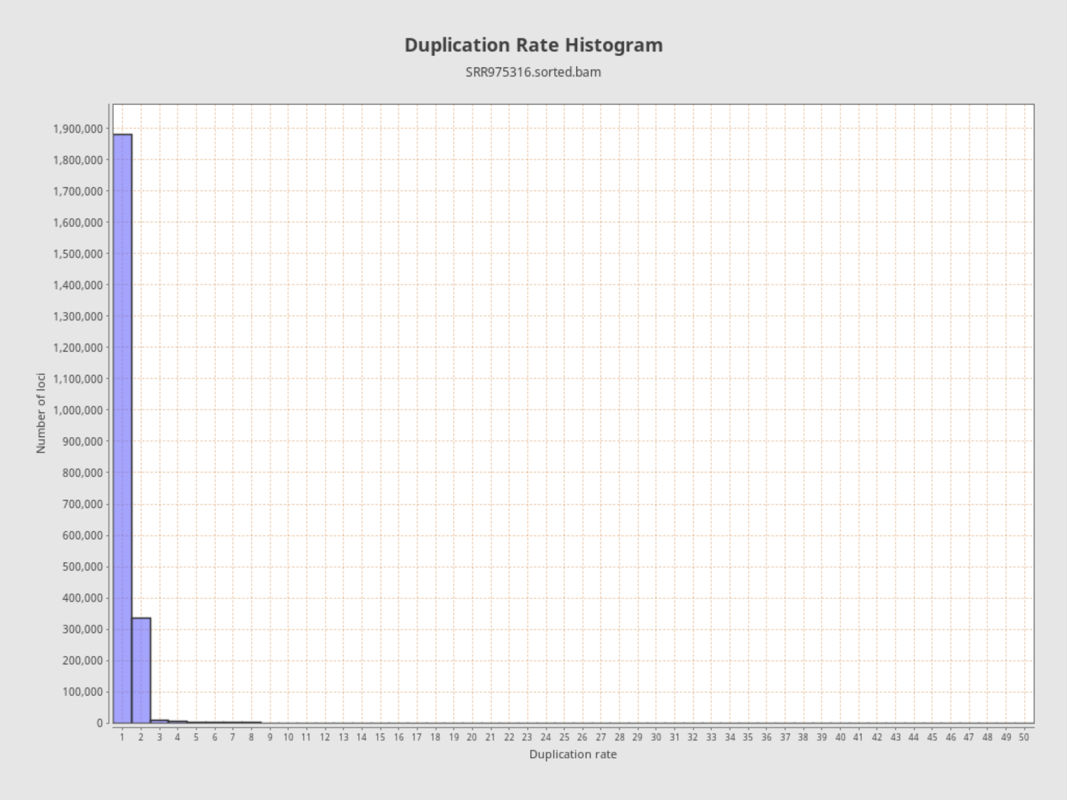
5. Results : Coverage Histogram (0-50X)



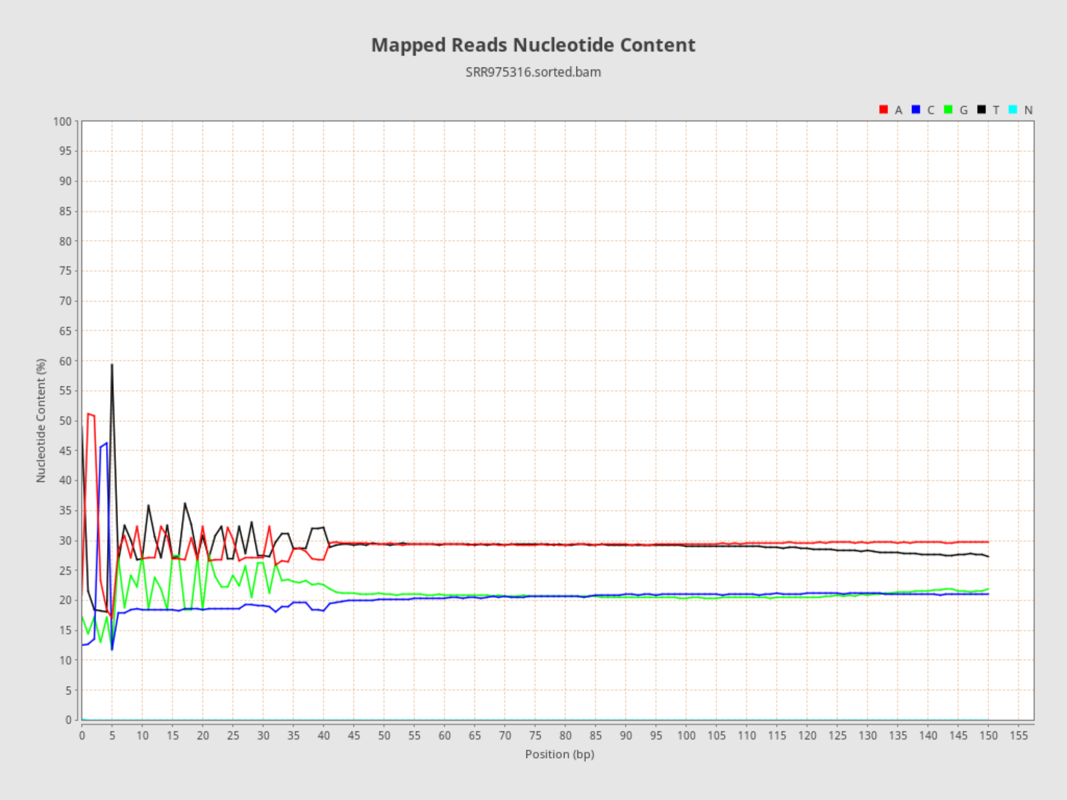
6. Results : Genome Fraction Coverage



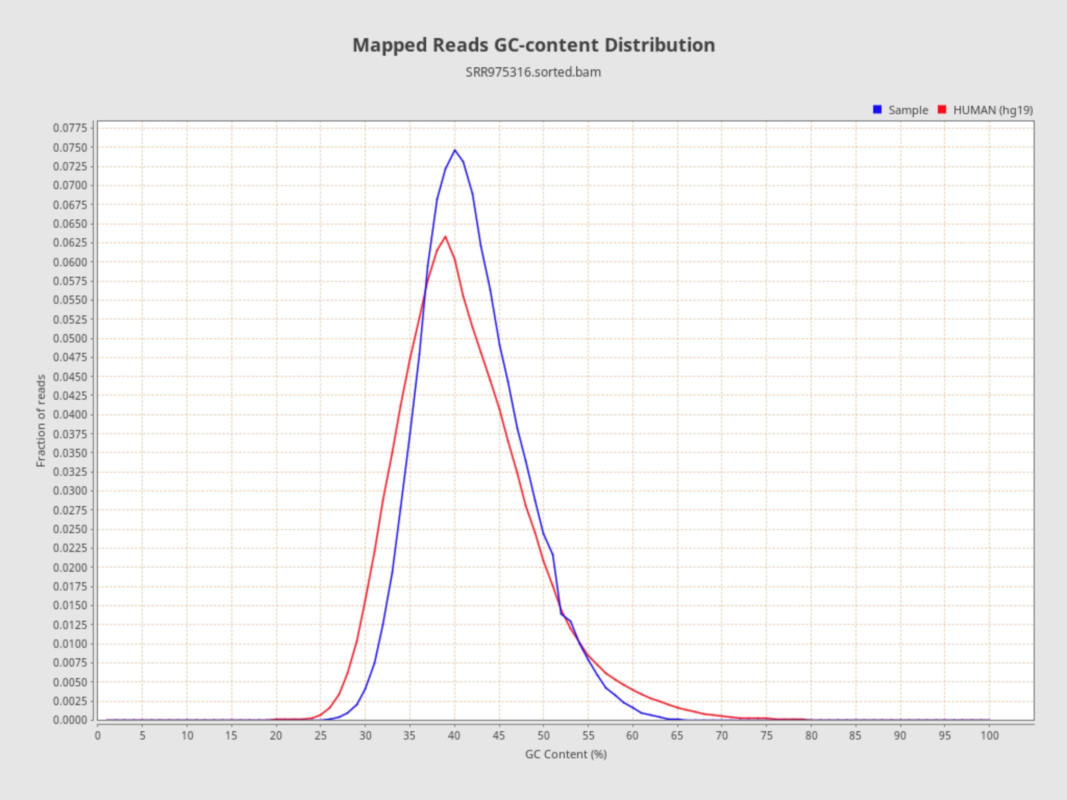
7. Results : Duplication Rate Histogram



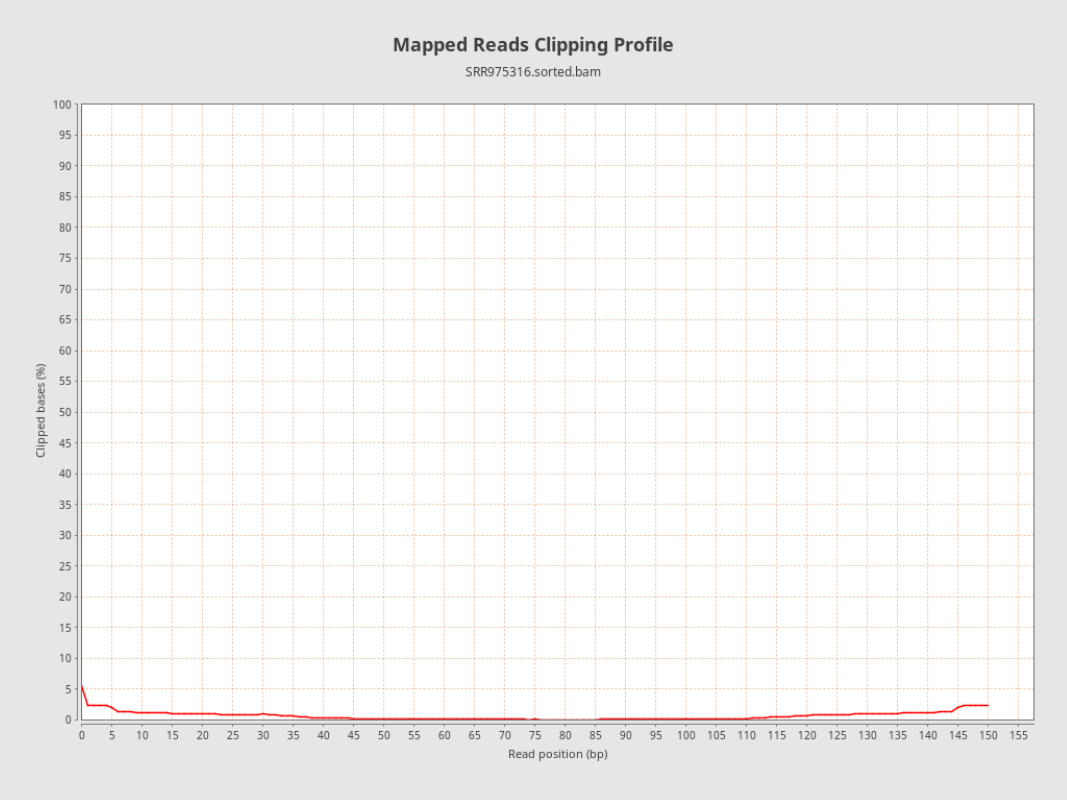
8. Results : Mapped Reads Nucleotide Content



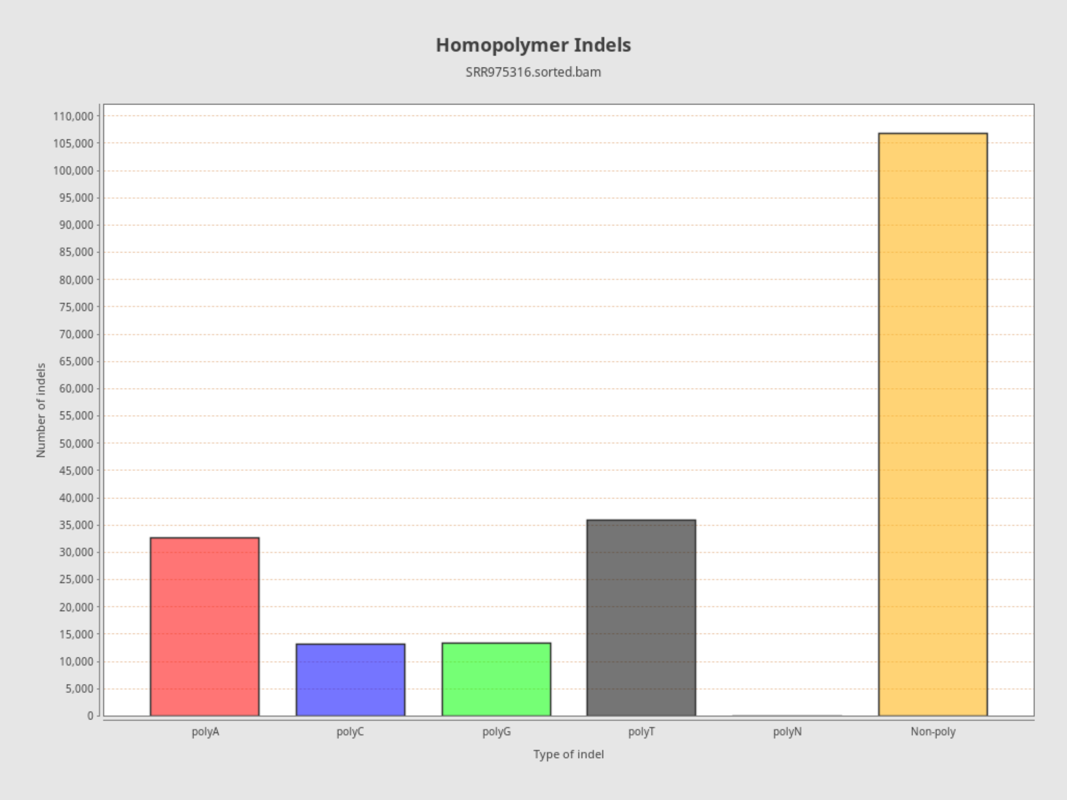
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

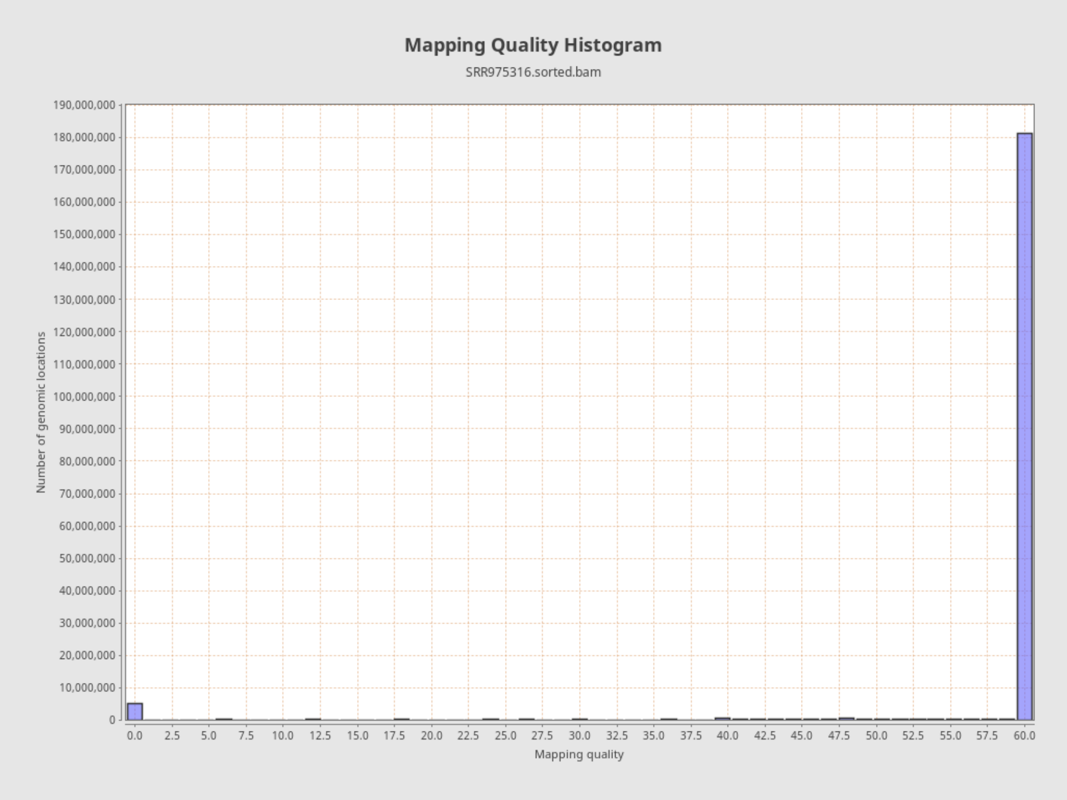


11. Results : Homopolymer Indels

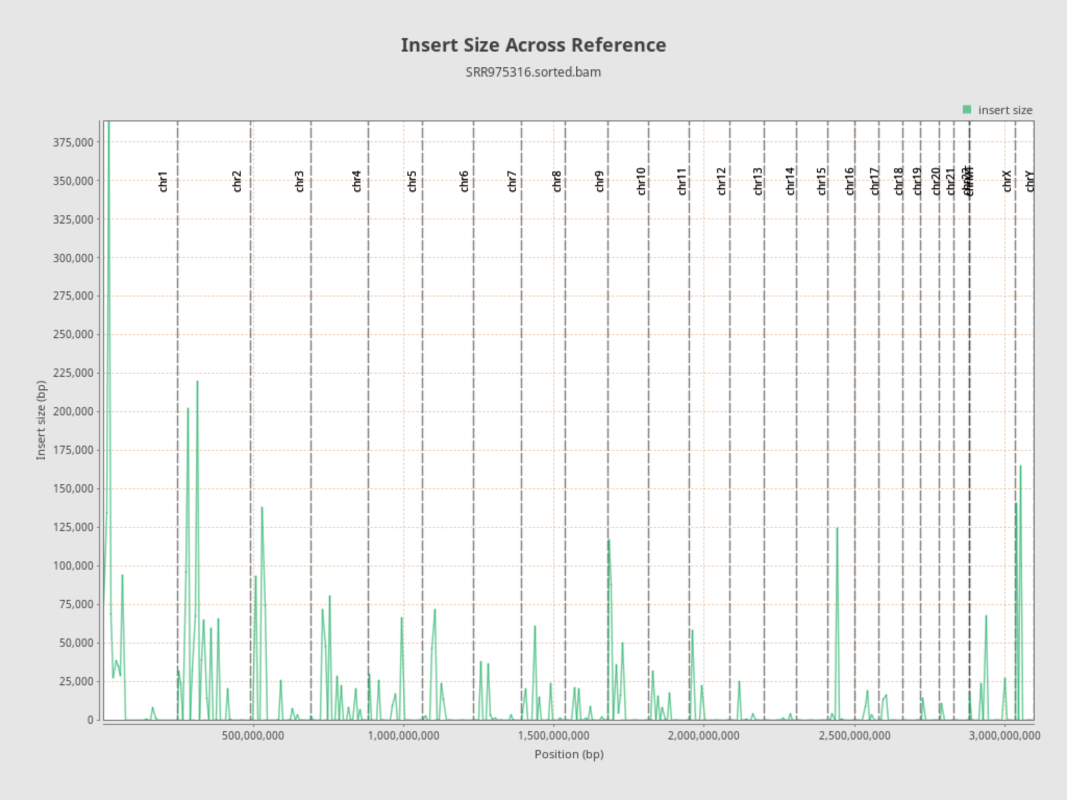


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram