Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/08 22:42:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975307.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_SRR975307 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975307_1.fastq.gz SRR975307_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 08 22:42:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975307.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	62,855,282
Mapped reads	62,611,270 / 99.61%
Unmapped reads	244,012 / 0.39%
Mapped paired reads	62,611,270 / 99.61%
Mapped reads, first in pair	31,285,768 / 49.77%
Mapped reads, second in pair	31,325,502 / 49.84%
Mapped reads, both in pair	62,488,234 / 99.42%
Mapped reads, singletons	123,036 / 0.2%
Secondary alignments	0
Supplementary alignments	129,324 / 0.21%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	37,207,806 / 59.2%
Duplication rate	42.23%
Clipped reads	38,477,968 / 61.22%

2.2. ACGT Content

Number/percentage of A's	1,490,513,416 / 26.44%
Number/percentage of C's	1,226,291,878 / 21.75%
Number/percentage of T's	1,510,684,901 / 26.8%
Number/percentage of G's	1,409,921,597 / 25.01%
Number/percentage of N's	102,558 / 0%

GC Percentage	46.76%

2.3. Coverage

Mean	1.8217
Standard Deviation	27.5214

2.4. Mapping Quality

Mean Mapping Quality	55.5

2.5. Insert size

Mean	67,417.31
Standard Deviation	2,560,120.12
P25/Median/P75	145 / 183 / 234

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	33,461,431
Insertions	619,683
Mapped reads with at least one insertion	0.98%
Deletions	1,355,894
Mapped reads with at least one deletion	2.13%
Homopolymer indels	45.61%

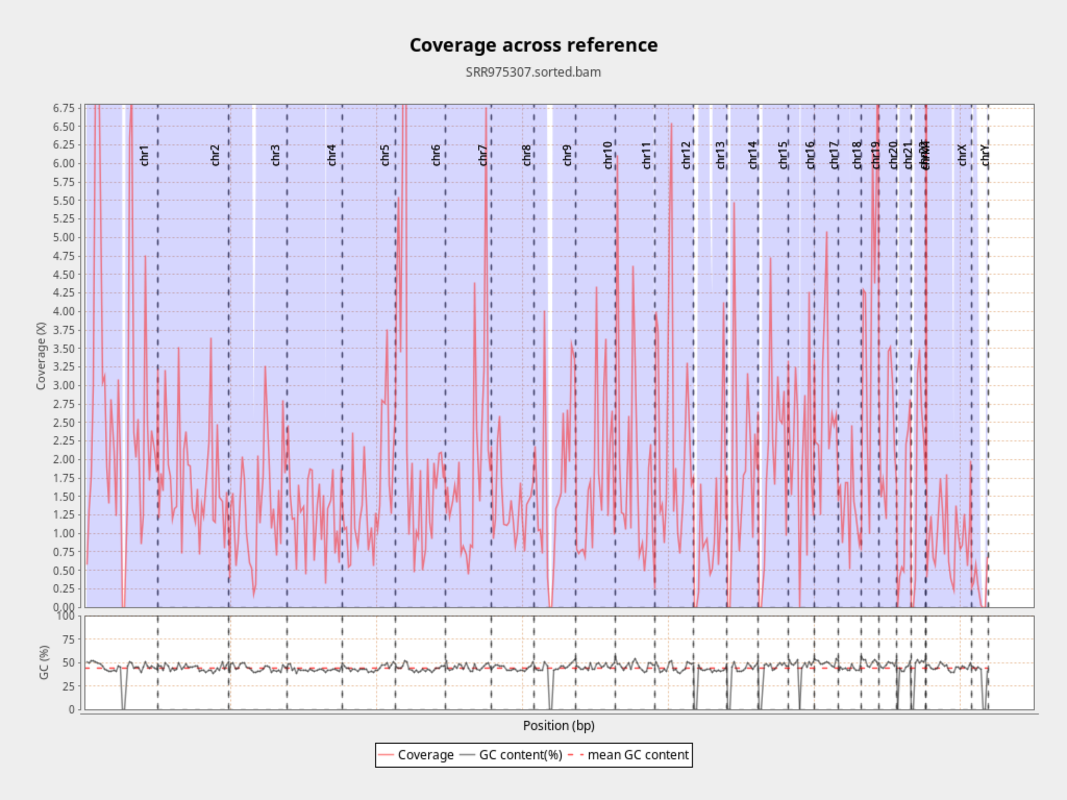
2.7. Chromosome stats

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

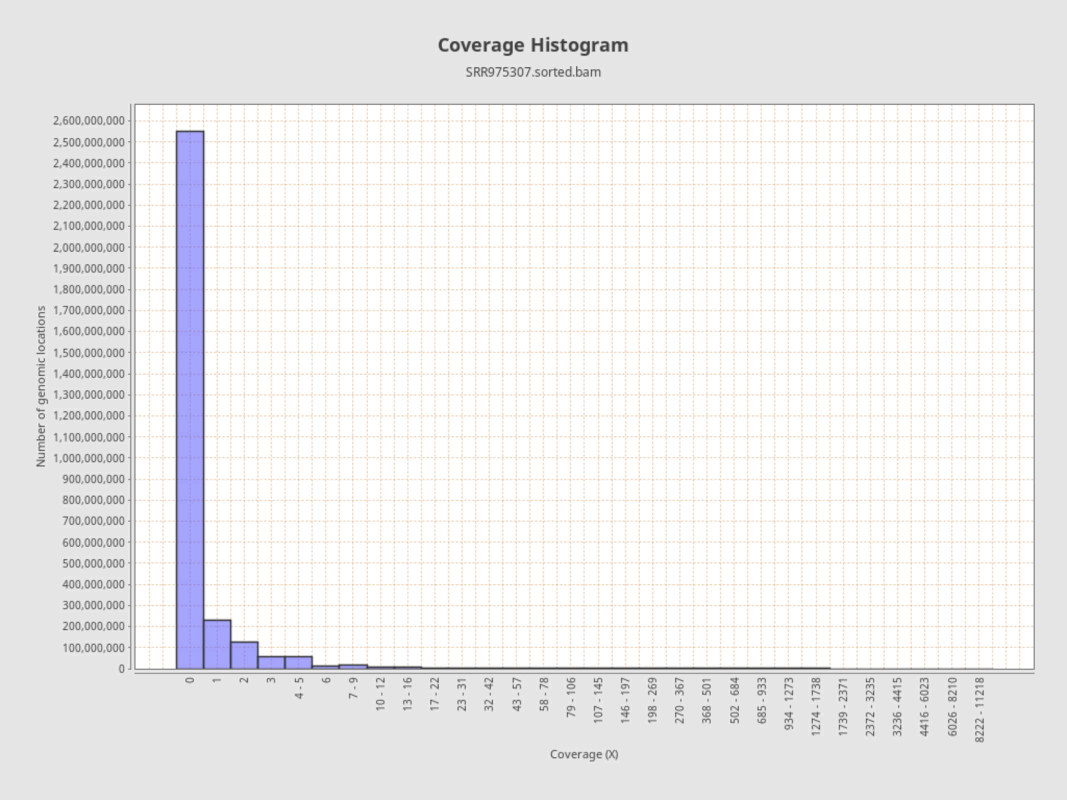
		bases	**coverage**	**deviation**
chr1	249250621	685467522	2.7501	37.1997
chr2	243199373	413215522	1.6991	23.8172
chr3	198022430	275629885	1.3919	20.5577
chr4	191154276	245477855	1.2842	19.6322
chr5	180915260	271611154	1.5013	21.1742
chr6	171115067	458191271	2.6777	40.3954
chr7	159138663	301937052	1.8973	31.7298
chr8	146364022	200821701	1.3721	19.1557
chr9	141213431	233355122	1.6525	23.5043
chr10	135534747	235934228	1.7408	25.4644
chr11	135006516	261012001	1.9333	27.9001
chr12	133851895	316862355	2.3673	31.2783
chr13	115169878	120754713	1.0485	18.0273
chr14	107349540	189084759	1.7614	26.5256
chr15	102531392	204760483	1.9971	29.2113
chr16	90354753	184817735	2.0455	27.237
chr17	81195210	220915951	2.7208	33.3628
chr18	78077248	106545077	1.3646	20.2171
chr19	59128983	242493412	4.1011	50.4412
chr20	63025520	149869769	2.3779	30.8338
chr21	48129895	60659815	1.2603	28.3197
chr22	51304566	96093897	1.873	28.2663
chrMT	16571	420729	25.3895	25.1359
chrX	155270560	147444500	0.9496	17.1707

chrY	59373566	16184232	0.2726	5.0414

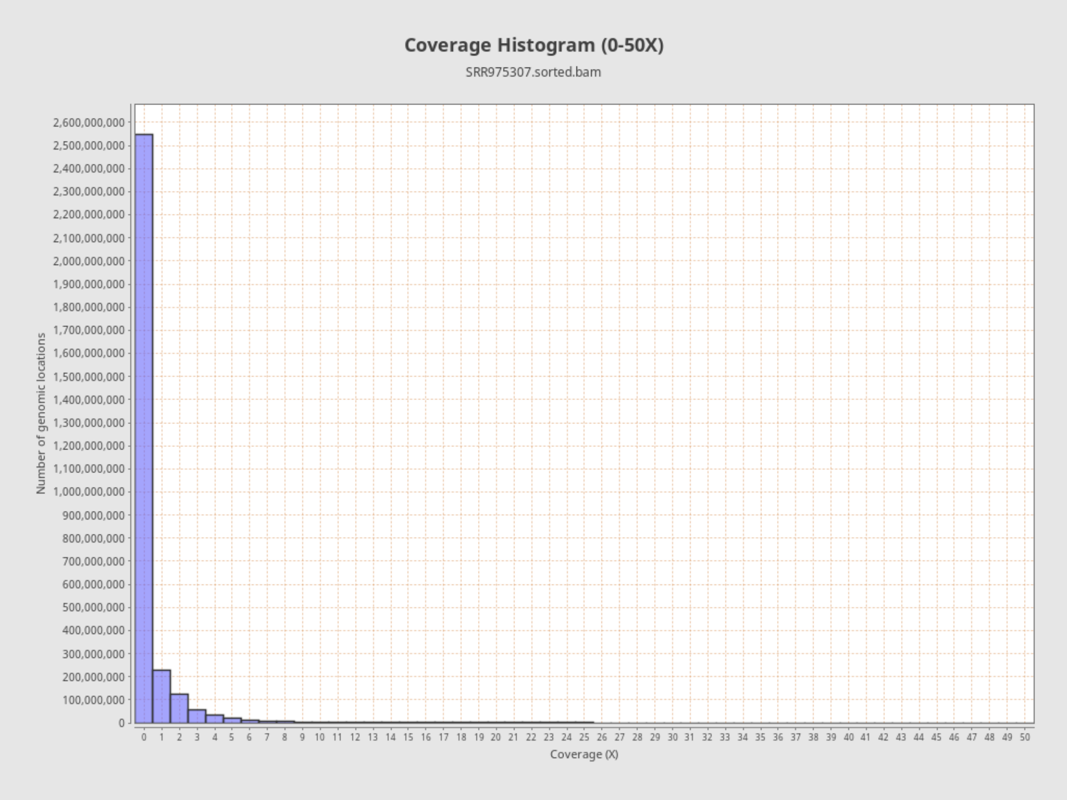
3. Results : Coverage across reference



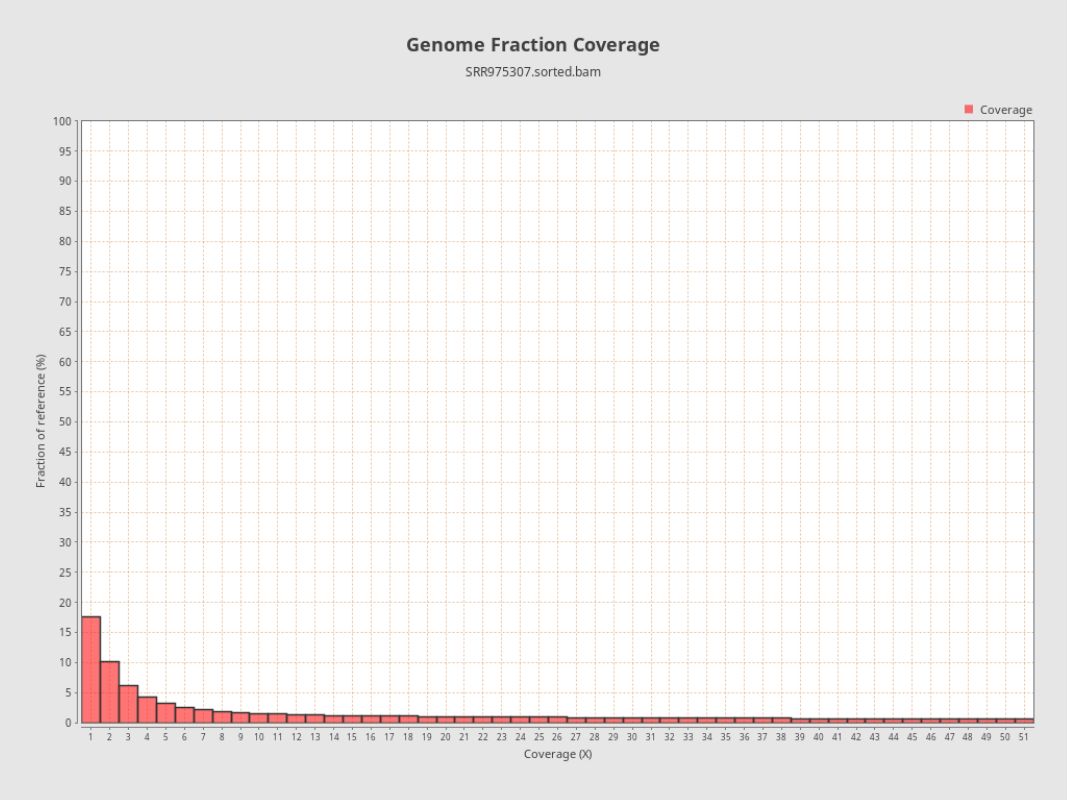
4. Results : Coverage Histogram



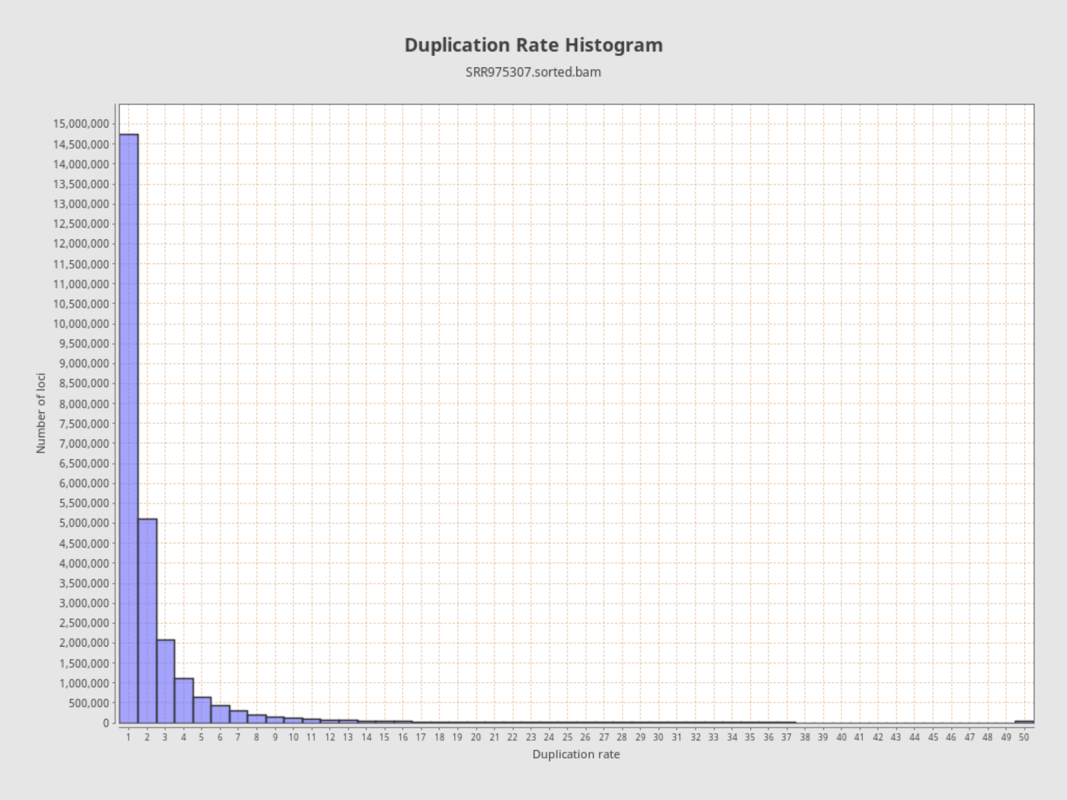
5. Results : Coverage Histogram (0-50X)



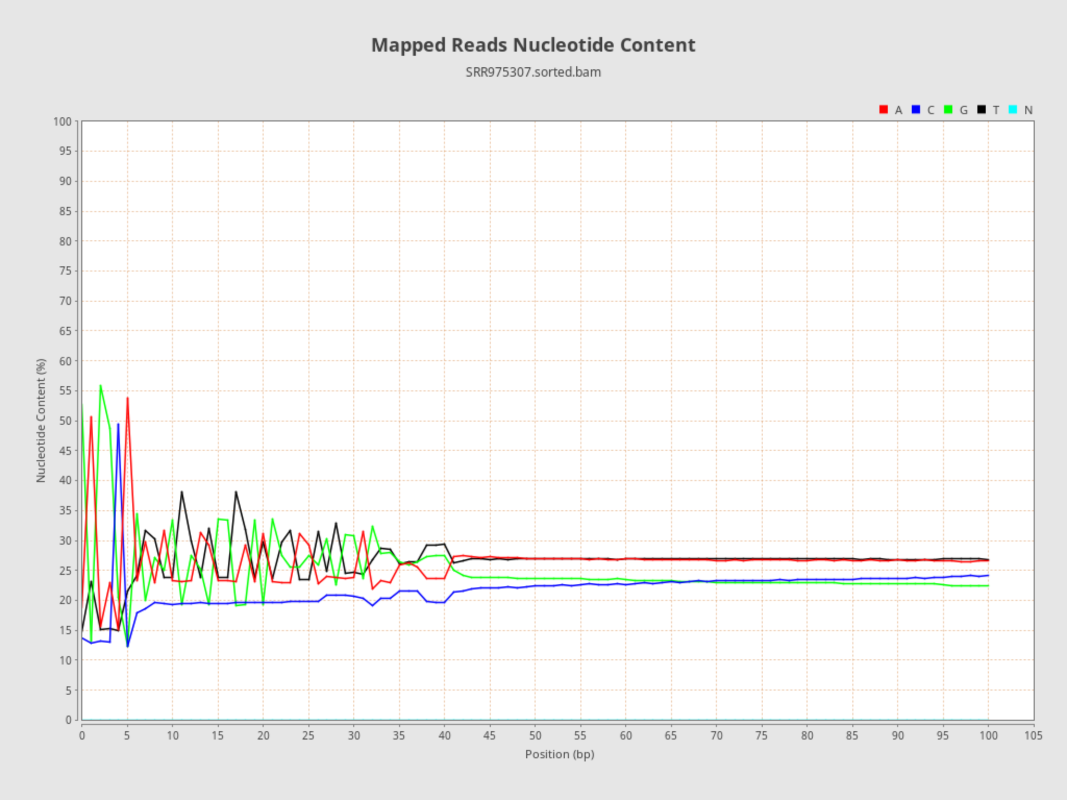
6. Results : Genome Fraction Coverage



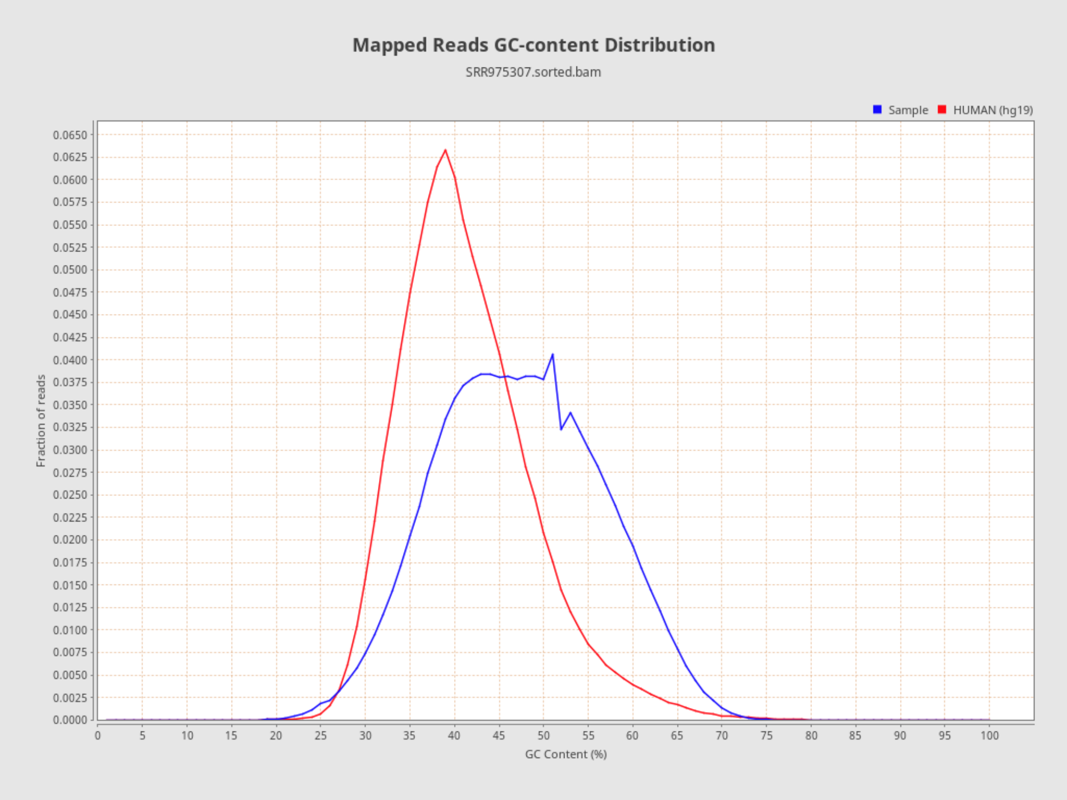
7. Results : Duplication Rate Histogram



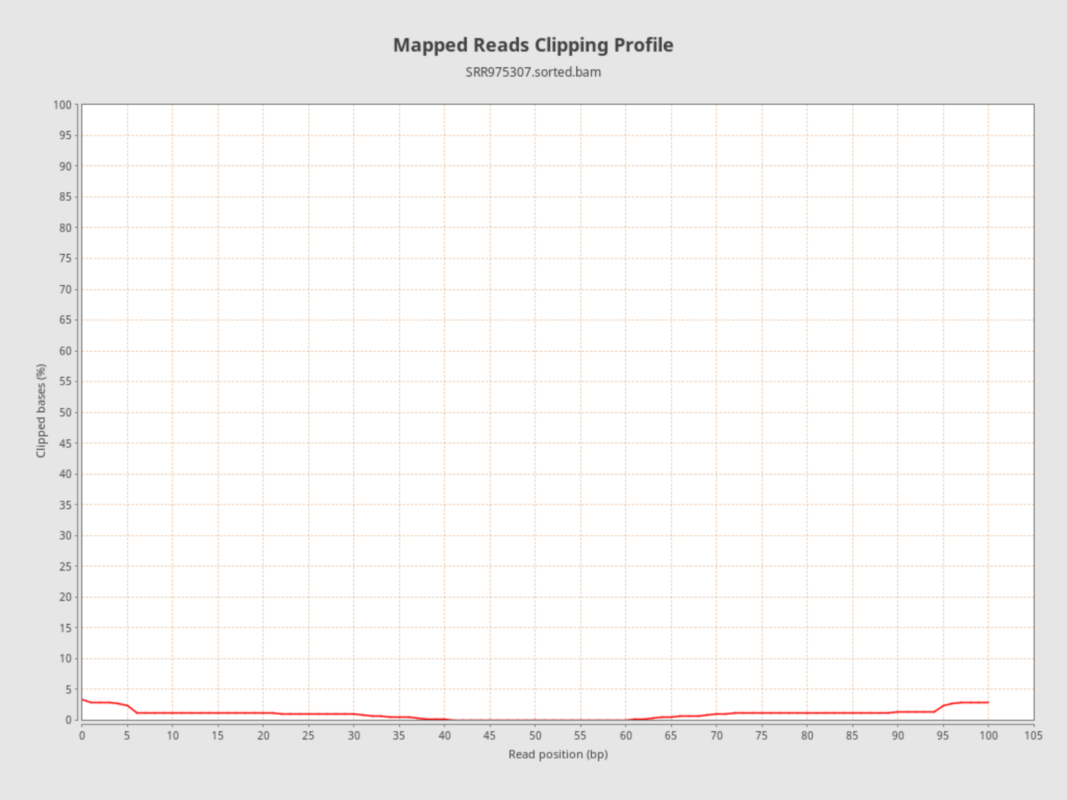
8. Results : Mapped Reads Nucleotide Content



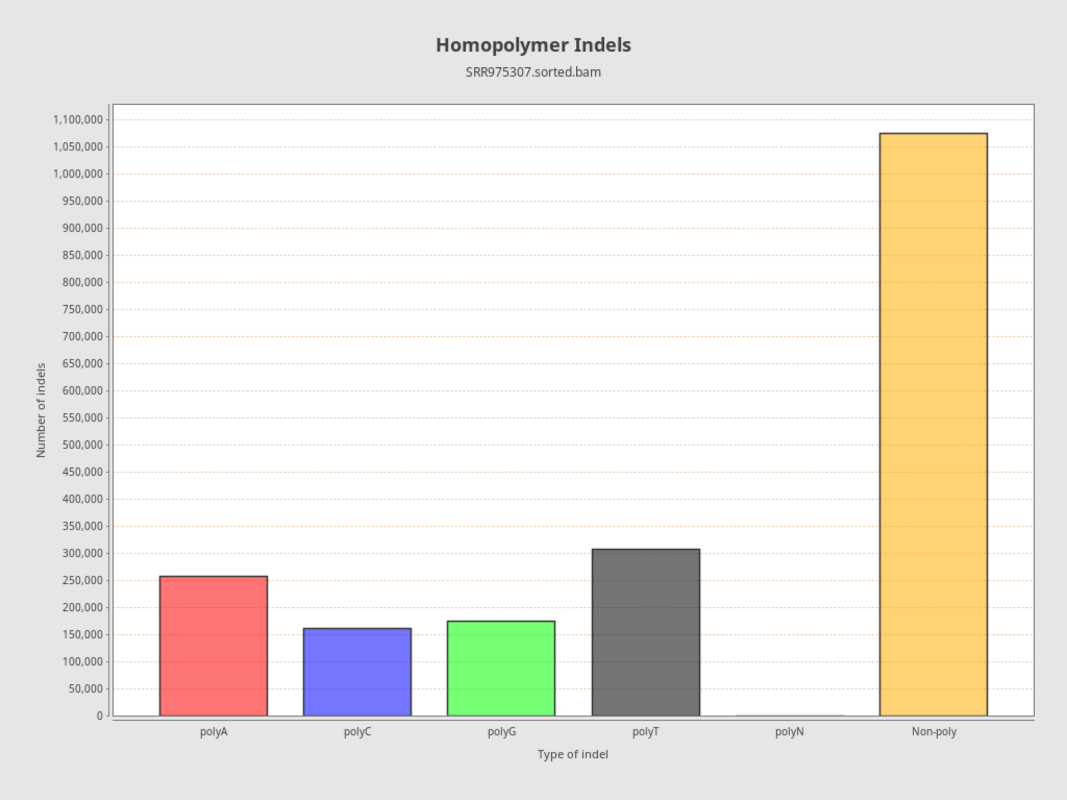
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

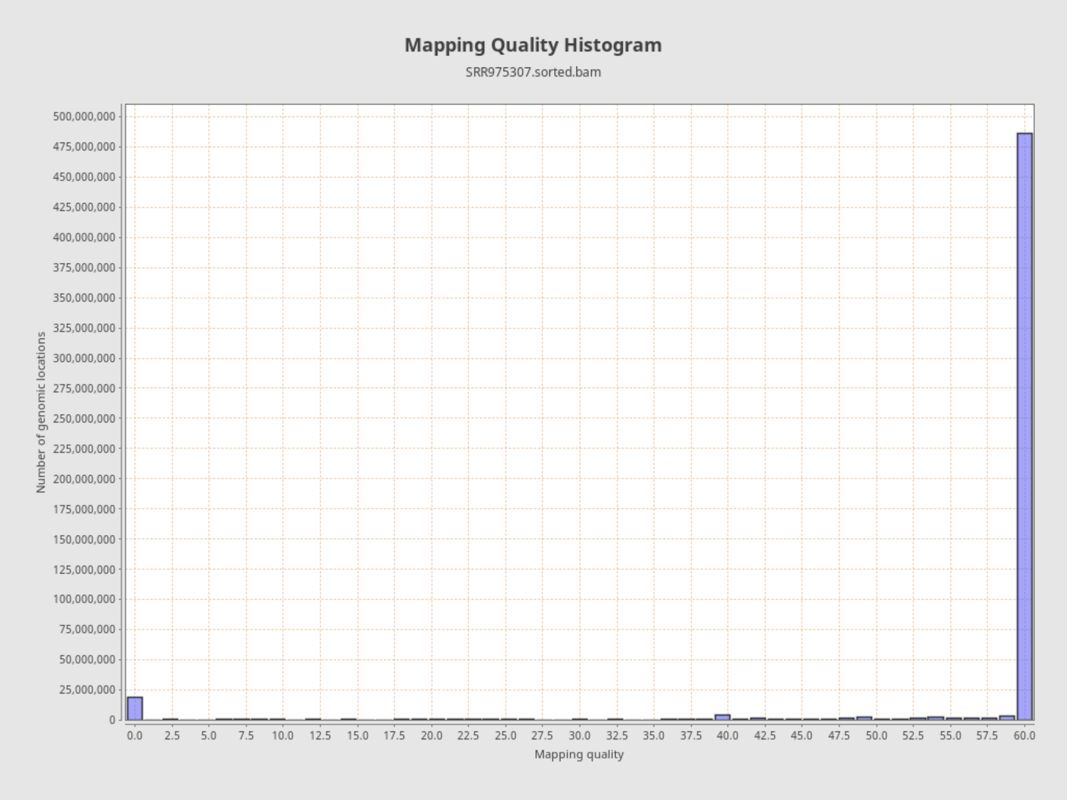


11. Results : Homopolymer Indels

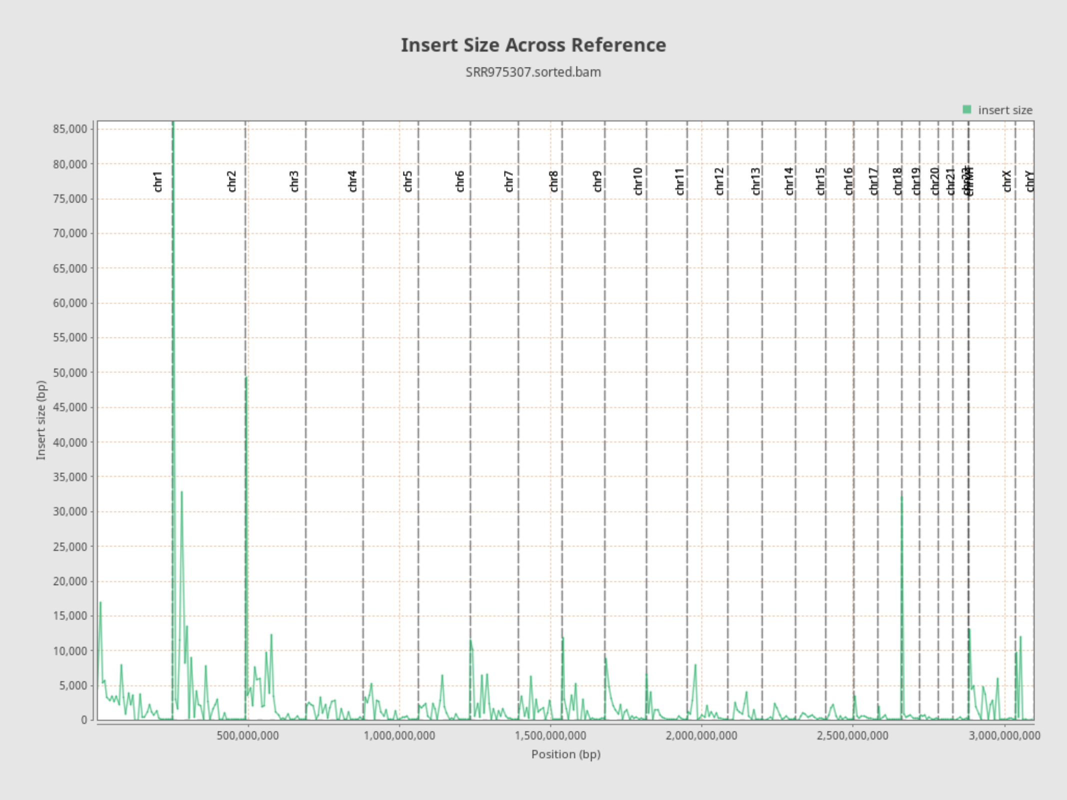


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram