Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/08 16:02:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975291.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_SRR975291 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975291_1.fastq.gz SRR975291_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 08 16:02:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975291.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	51,826,716
Mapped reads	51,520,416 / 99.41%
Unmapped reads	306,300 / 0.59%
Mapped paired reads	51,520,416 / 99.41%
Mapped reads, first in pair	25,843,669 / 49.87%
Mapped reads, second in pair	25,676,747 / 49.54%
Mapped reads, both in pair	51,276,706 / 98.94%
Mapped reads, singletons	243,710 / 0.47%
Secondary alignments	0
Supplementary alignments	112,851 / 0.22%
Read min/max/mean length	30 / 101 / 101.09
Duplicated reads (estimated)	33,716,922 / 65.06%
Duplication rate	57.99%
Clipped reads	31,196,923 / 60.19%

2.2. ACGT Content

Number/percentage of A's	1,292,210,235 / 27.03%
Number/percentage of C's	1,049,011,786 / 21.95%
Number/percentage of T's	1,333,521,886 / 27.9%
Number/percentage of G's	1,104,235,749 / 23.1%
Number/percentage of N's	1,006,236 / 0.02%

GC Percentage	45.05%

2.3. Coverage

Mean	1.5447
Standard Deviation	22.8395

2.4. Mapping Quality

Mean Mapping Quality	55.99

2.5. Insert size

Mean	145,311.4
Standard Deviation	3,753,041.15
P25/Median/P75	190 / 233 / 284

2.6. Mismatches and indels

General error rate	0.88%
Mismatches	41,255,341
Insertions	534,172
Mapped reads with at least one insertion	1.03%
Deletions	1,232,890
Mapped reads with at least one deletion	2.36%
Homopolymer indels	46.24%

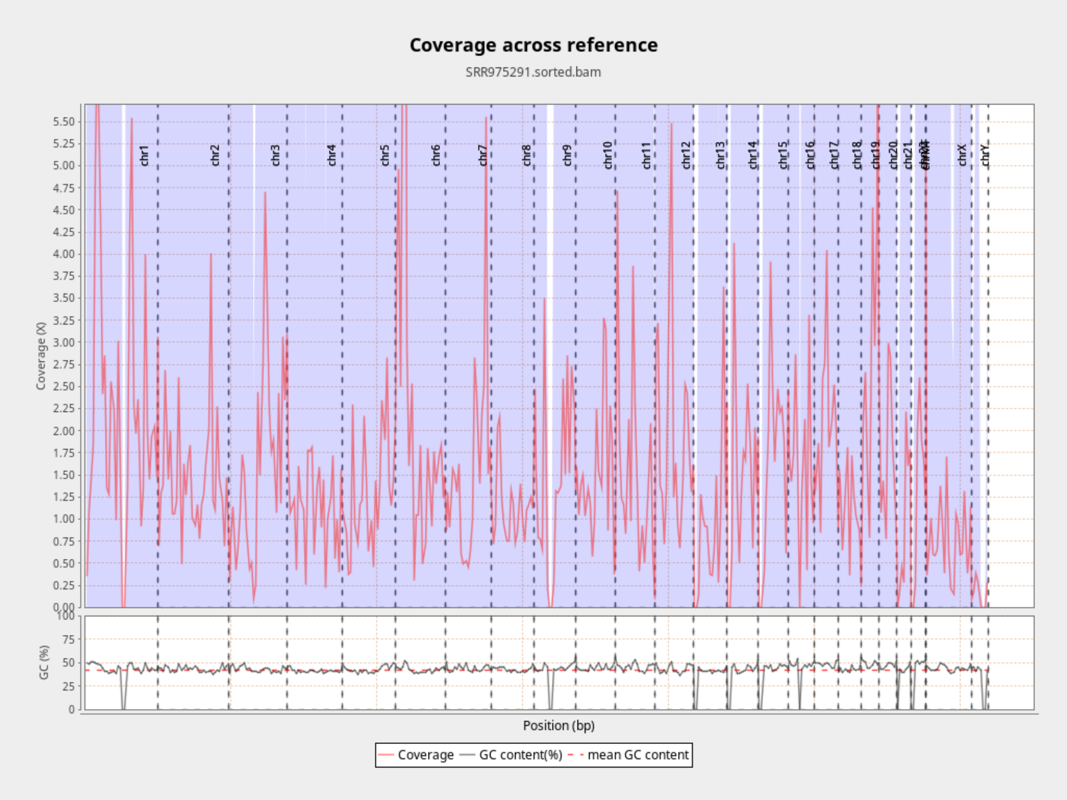
2.7. Chromosome stats

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

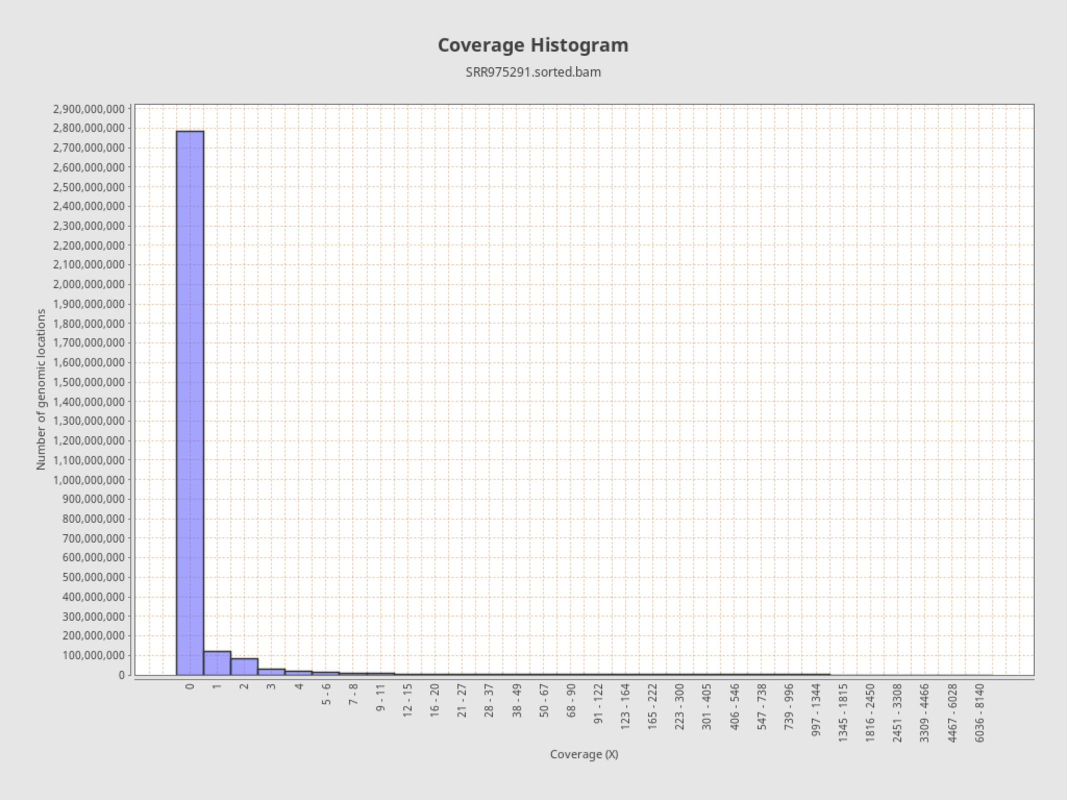
		bases	**coverage**	**deviation**
chr1	249250621	560212566	2.2476	28.9217
chr2	243199373	356286598	1.465	19.723
chr3	198022430	318434497	1.6081	22.4699
chr4	191154276	218487932	1.143	17.7646
chr5	180915260	233201457	1.289	18.4871
chr6	171115067	435395743	2.5445	37.3909
chr7	159138663	252370260	1.5859	23.7445
chr8	146364022	164895455	1.1266	16.9619
chr9	141213431	198438871	1.4052	20.9175
chr10	135534747	211080335	1.5574	22.5757
chr11	135006516	214024526	1.5853	21.8106
chr12	133851895	267603419	1.9993	25.0786
chr13	115169878	107041809	0.9294	17.9932
chr14	107349540	153487632	1.4298	22.4551
chr15	102531392	171403481	1.6717	24.8848
chr16	90354753	141750214	1.5688	21.0319
chr17	81195210	172528003	2.1249	25.3412
chr18	78077248	89913412	1.1516	17.9885
chr19	59128983	161859531	2.7374	33.4276
chr20	63025520	113707880	1.8042	26.0222
chr21	48129895	45600733	0.9475	15.2995
chr22	51304566	67580544	1.3172	17.3775
chrMT	16571	85370	5.1518	10.0926
chrX	155270560	117124833	0.7543	13.8408

chrY	59373566	9270072	0.1561	3.9784

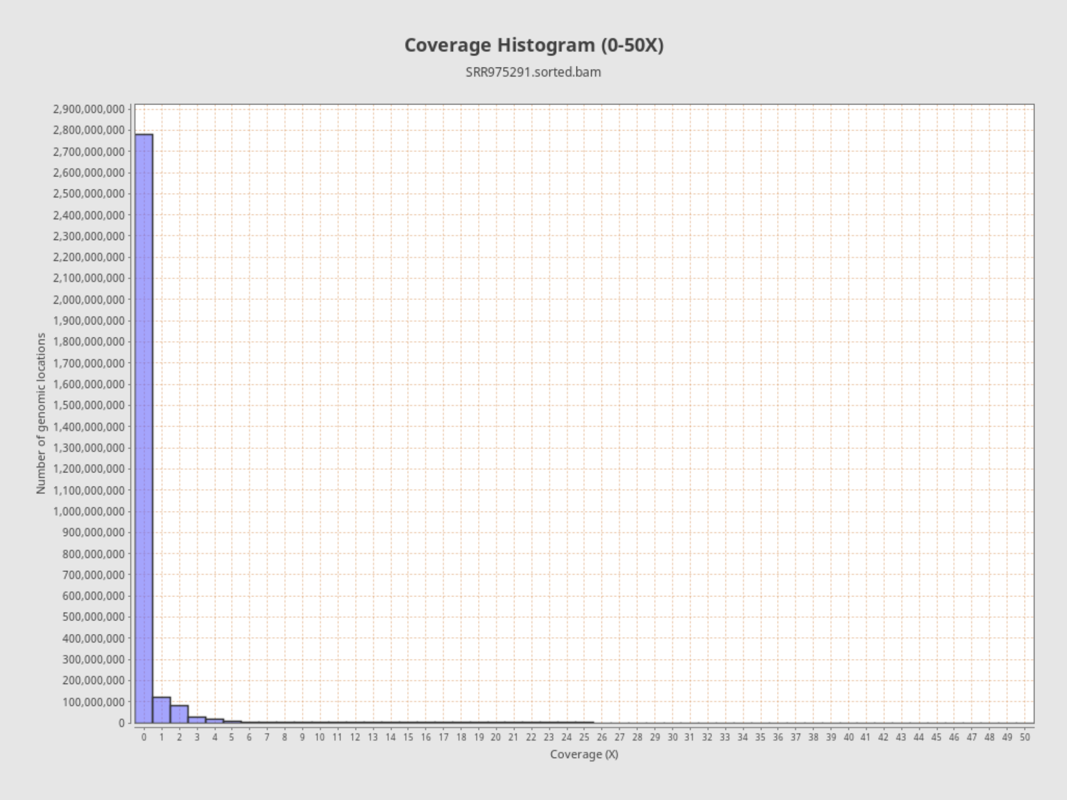
3. Results : Coverage across reference



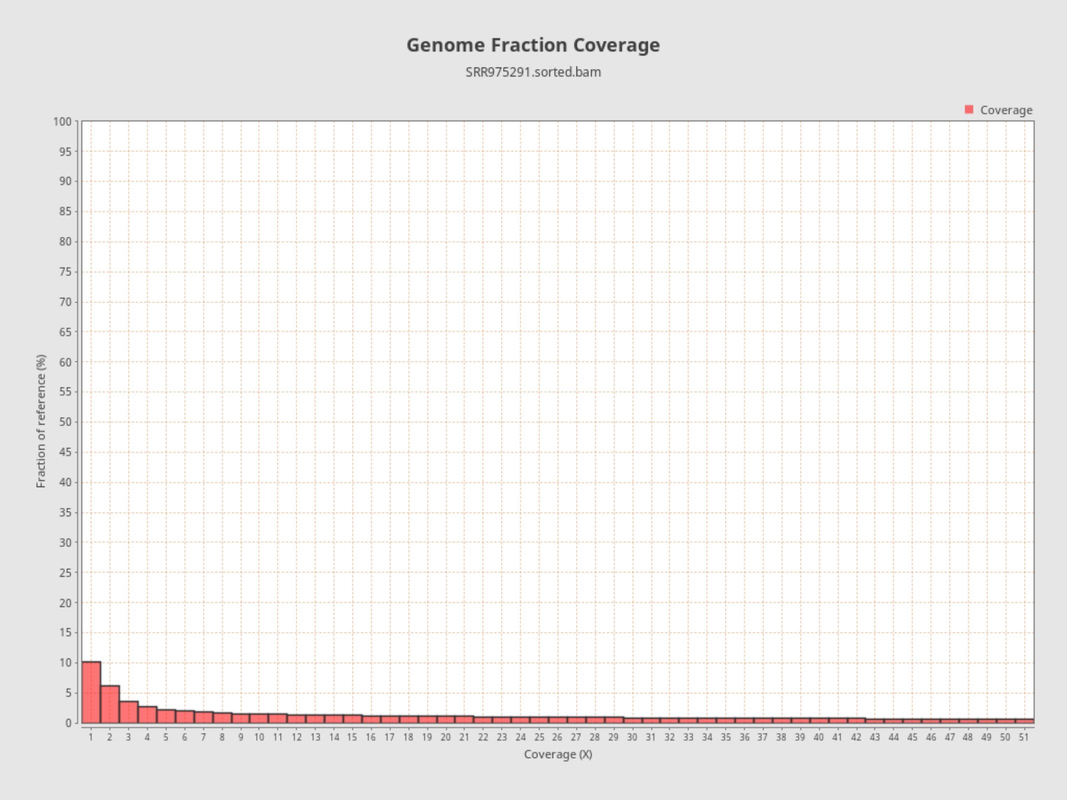
4. Results : Coverage Histogram



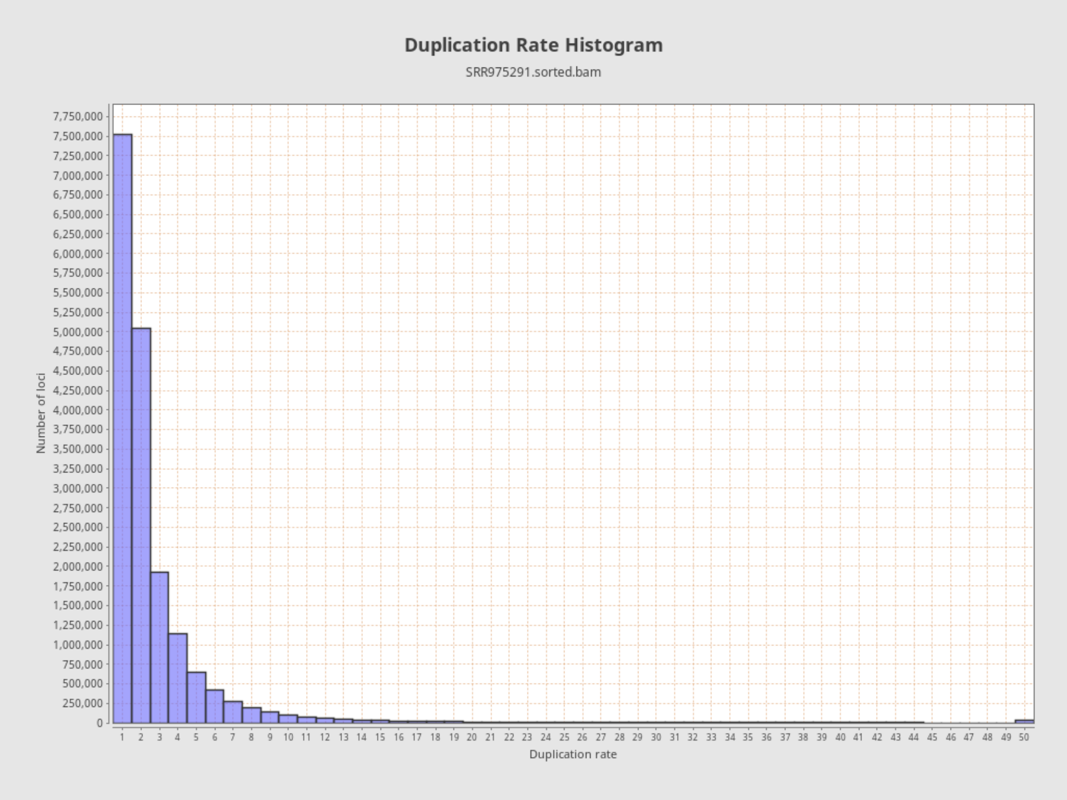
5. Results : Coverage Histogram (0-50X)



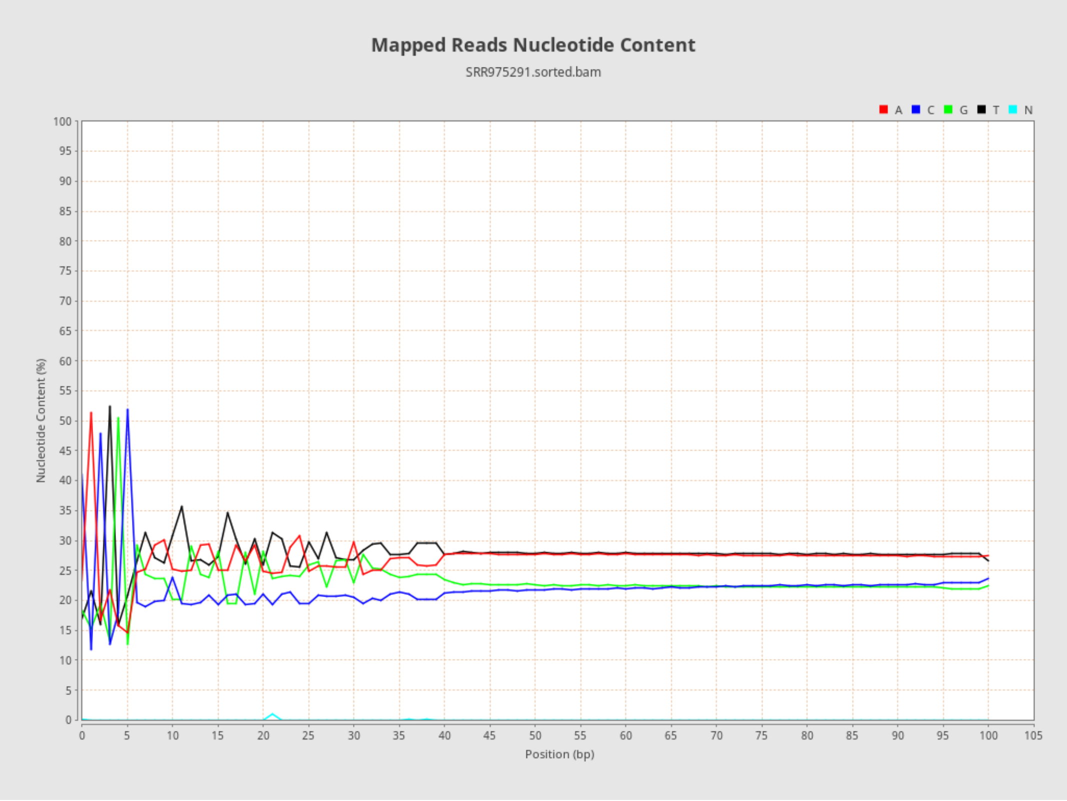
6. Results : Genome Fraction Coverage



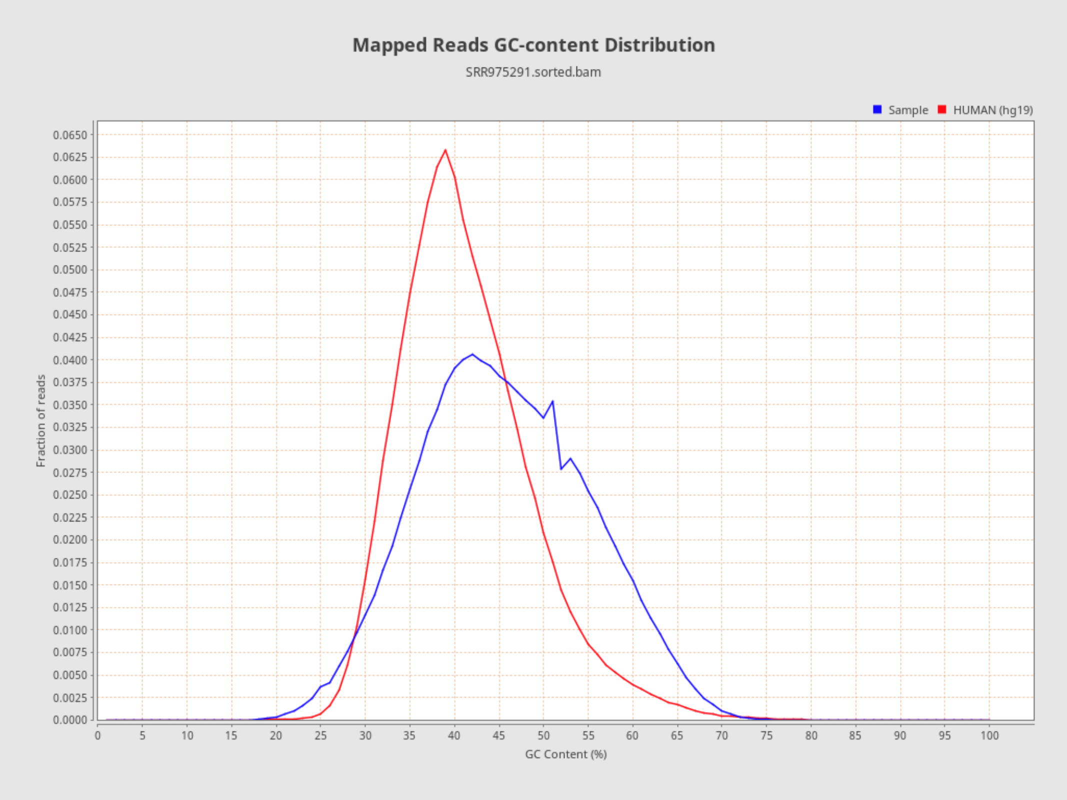
7. Results : Duplication Rate Histogram



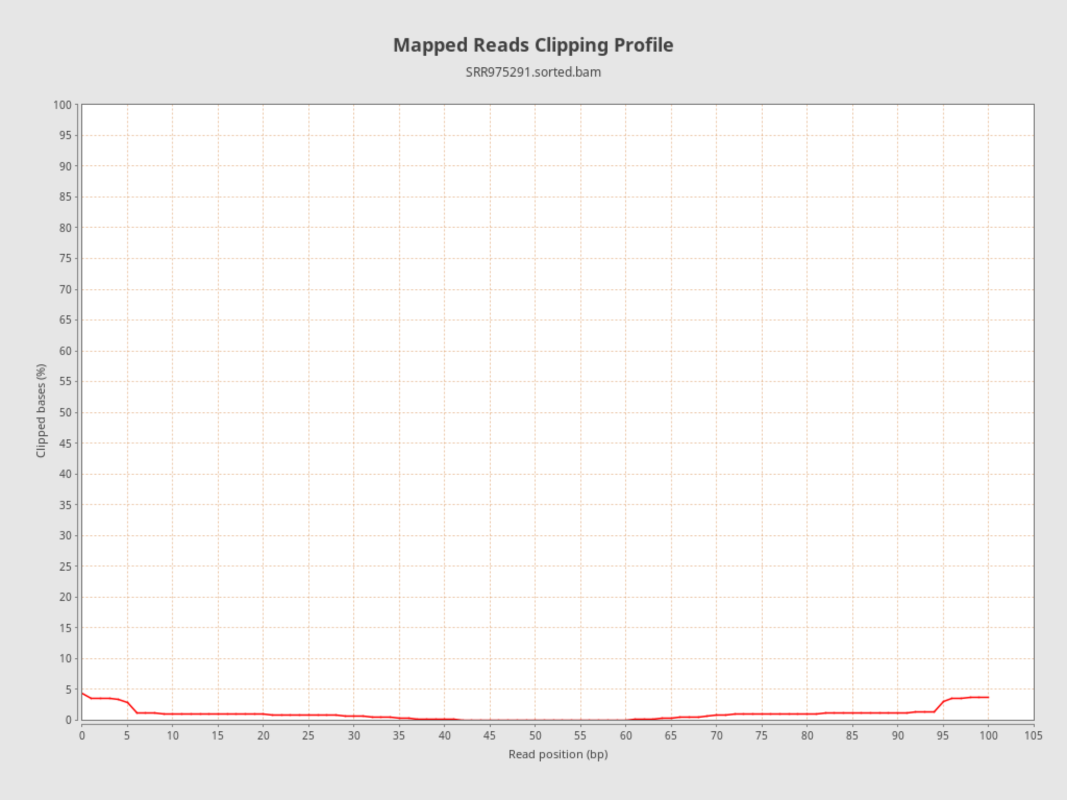
8. Results : Mapped Reads Nucleotide Content



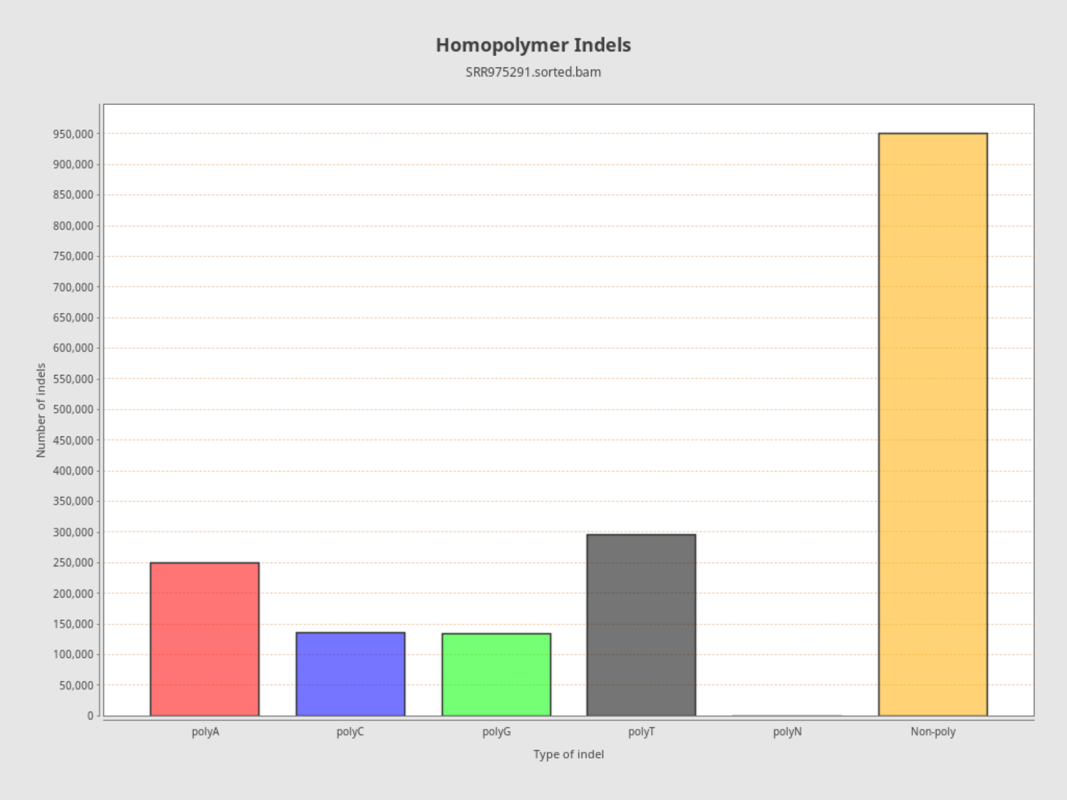
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

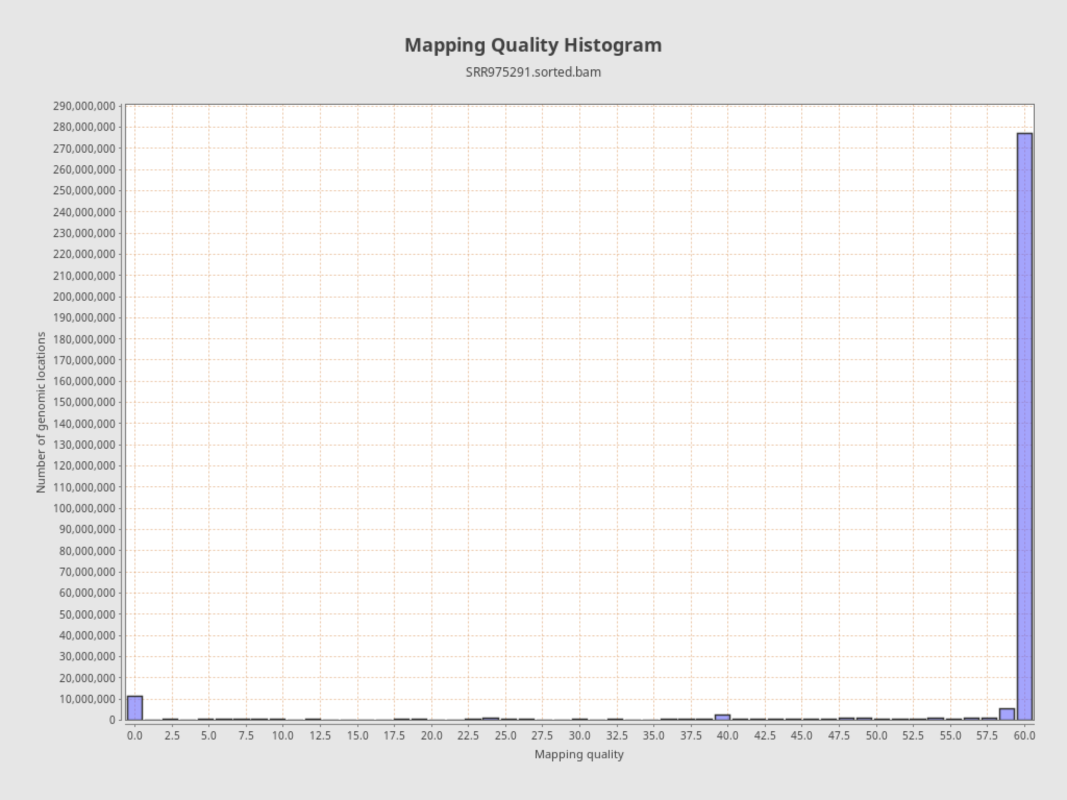


11. Results : Homopolymer Indels

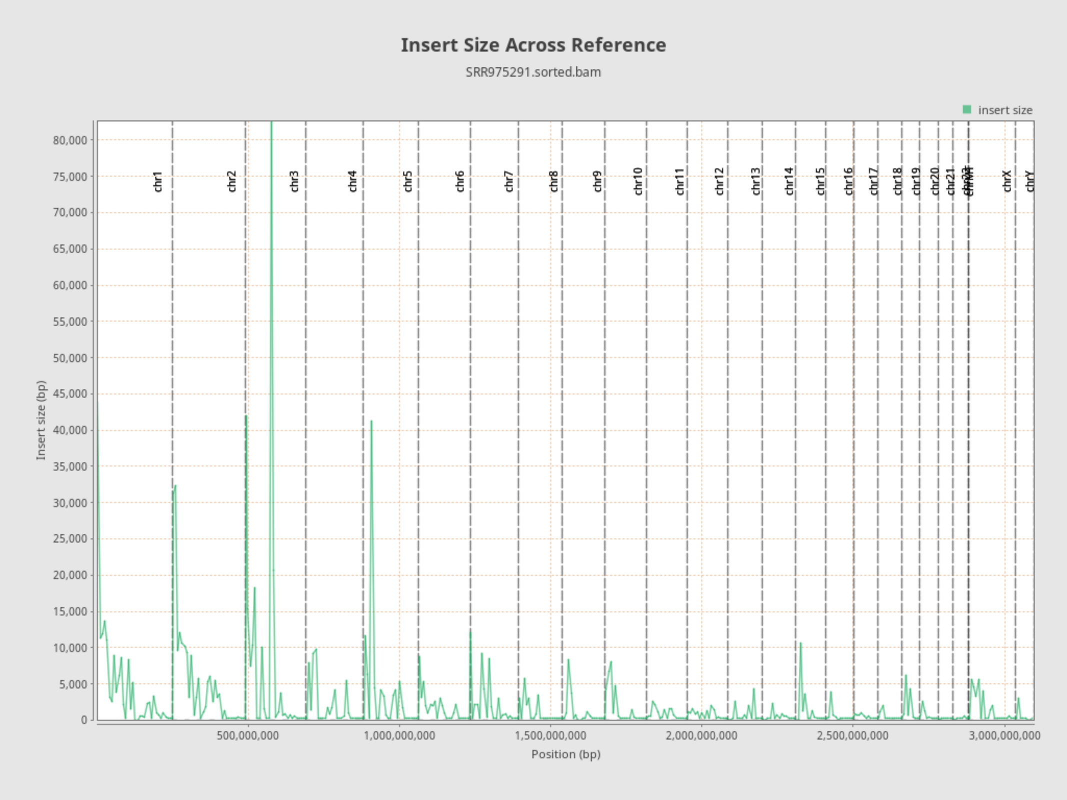


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram