Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 17:22:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975265.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_SRR975265 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975265_1.fastq.gz SRR975265_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 17:22:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975265.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,211,316
Mapped reads	5,112,677 / 98.11%
Unmapped reads	98,639 / 1.89%
Mapped paired reads	5,112,677 / 98.11%
Mapped reads, first in pair	2,565,379 / 49.23%
Mapped reads, second in pair	2,547,298 / 48.88%
Mapped reads, both in pair	5,077,658 / 97.44%
Mapped reads, singletons	35,019 / 0.67%
Secondary alignments	0
Supplementary alignments	70,957 / 1.36%
Read min/max/mean length	30 / 151 / 151.68
Duplicated reads (estimated)	628,250 / 12.06%
Duplication rate	9.58%
Clipped reads	2,294,632 / 44.03%

2.2. ACGT Content

Number/percentage of A's	204,609,555 / 29.04%
Number/percentage of C's	141,872,376 / 20.14%
Number/percentage of T's	206,073,251 / 29.25%
Number/percentage of G's	151,954,790 / 21.57%
Number/percentage of N's	56,943 / 0.01%

GC Percentage	41.7%

2.3. Coverage

Mean	0.2278
Standard Deviation	3.1212

2.4. Mapping Quality

Mean Mapping Quality	53.52

2.5. Insert size

Mean	51,743
Standard Deviation	2,146,121.75
P25/Median/P75	152 / 194 / 255

2.6. Mismatches and indels

General error rate	1.14%
Mismatches	7,721,867
Insertions	119,865
Mapped reads with at least one insertion	2.21%
Deletions	244,753
Mapped reads with at least one deletion	4.6%
Homopolymer indels	47.29%

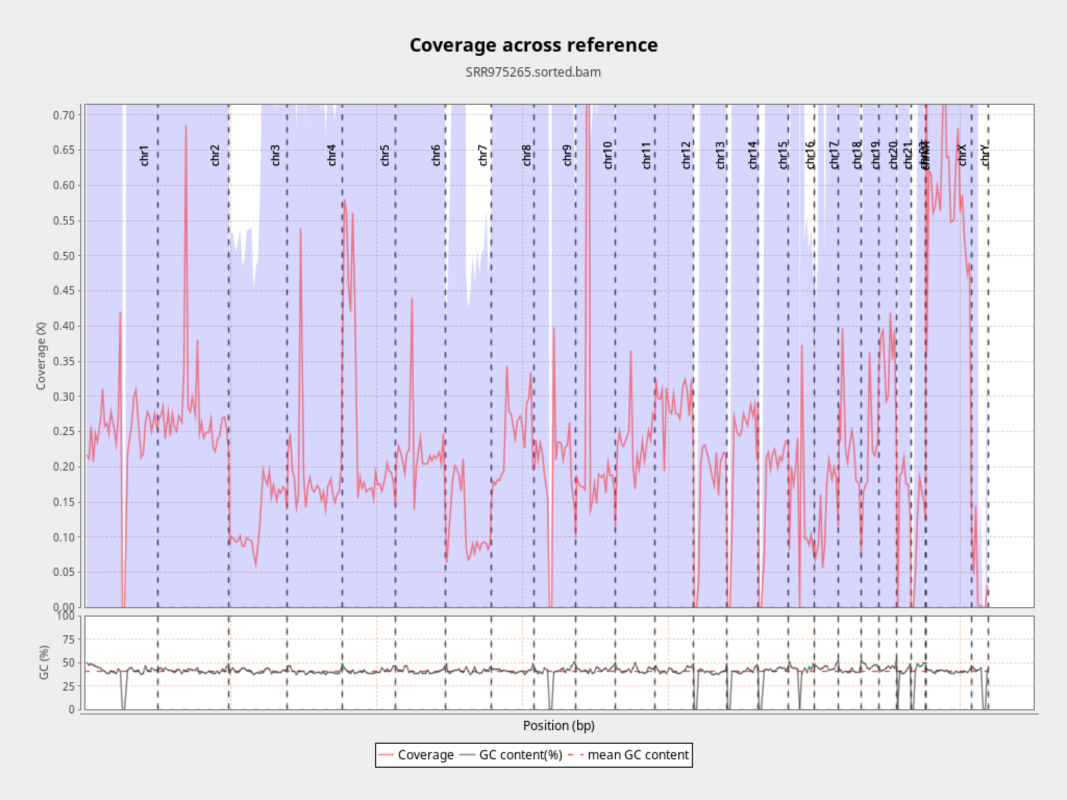
2.7. Chromosome stats

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

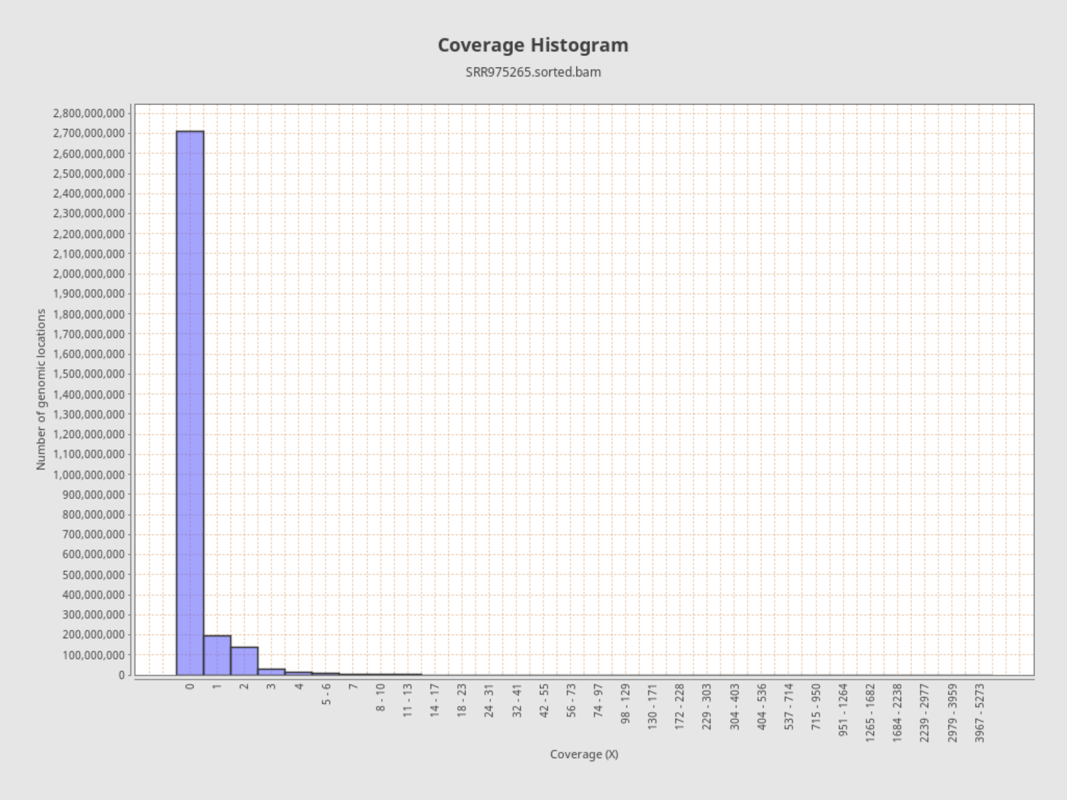
		bases	coverage	deviation
chr1	249250621	60754465	0.2437	3.4478
chr2	243199373	67868383	0.2791	2.7872
chr3	198022430	25217647	0.1273	0.5736
chr4	191154276	35813061	0.1874	2.3724
chr5	180915260	47189239	0.2608	0.765
chr6	171115067	37879563	0.2214	2.7056
chr7	159138663	18530311	0.1164	1.5486
chr8	146364022	35706569	0.244	1.0203
chr9	141213431	27924327	0.1977	4.0307
chr10	135534747	32480861	0.2396	10.5428
chr11	135006516	31528440	0.2335	3.1543
chr12	133851895	38799502	0.2899	0.7722
chr13	115169878	19632498	0.1705	0.5737
chr14	107349540	23315629	0.2172	0.6986
chr15	102531392	17966607	0.1752	0.5893
chr16	90354753	13207854	0.1462	1.9819
chr17	81195210	11446303	0.141	1.3362
chr18	78077248	18139399	0.2323	4.3381
chr19	59128983	12674948	0.2144	1.8108
chr20	63025520	22287100	0.3536	1.1763
chr21	48129895	7935867	0.1649	1.2456
chr22	51304566	5486986	0.1069	0.4821
chrMT	16571	141877	8.5618	5.7622
chrX	155270560	90776087	0.5846	2.1309

chrY	59373566	2345853	0.0395	2.2067

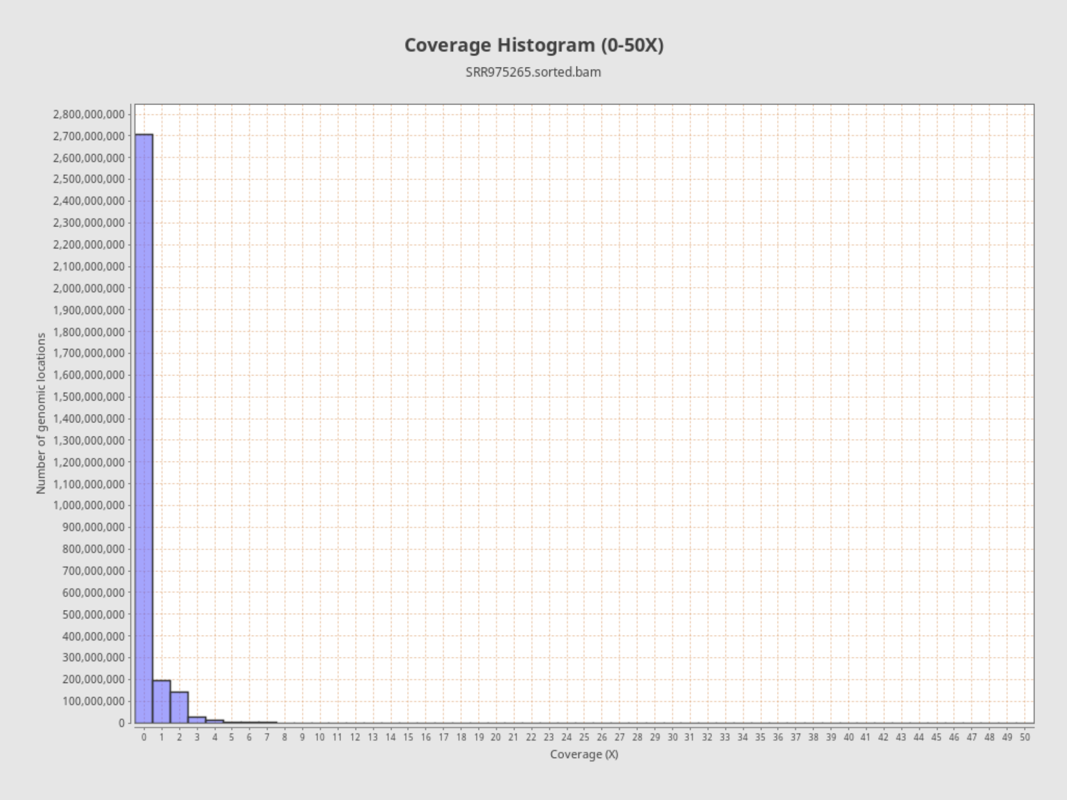
3. Results : Coverage across reference



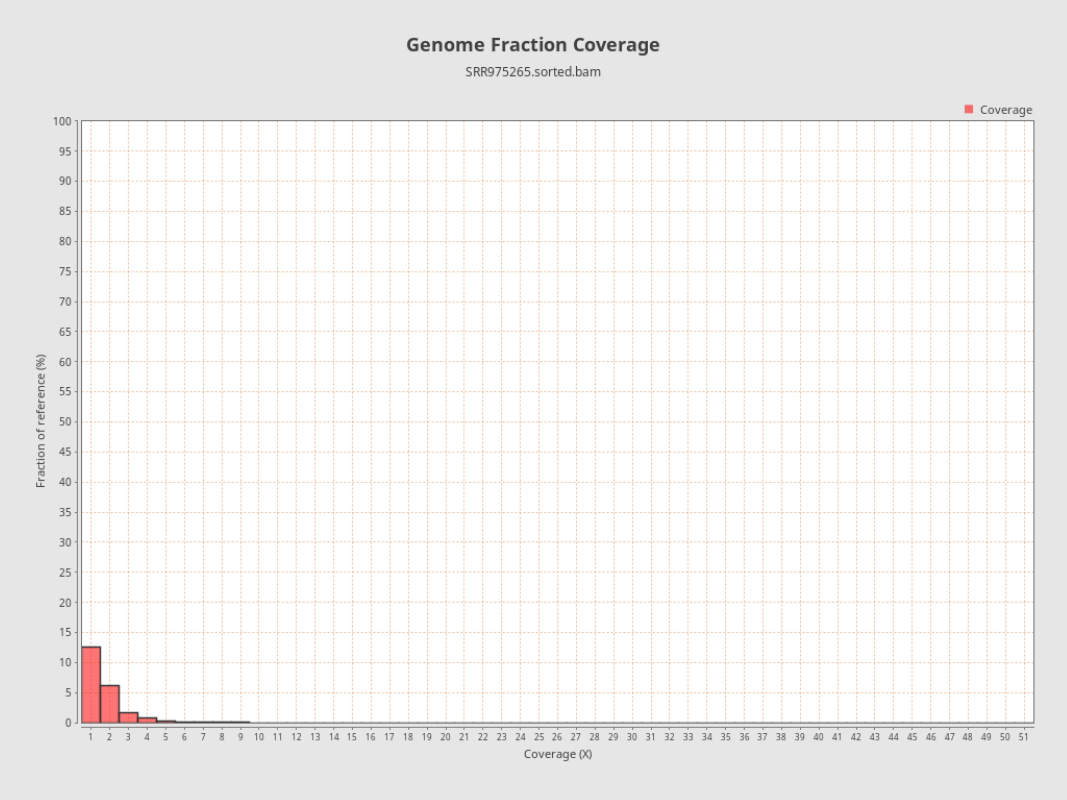
4. Results : Coverage Histogram



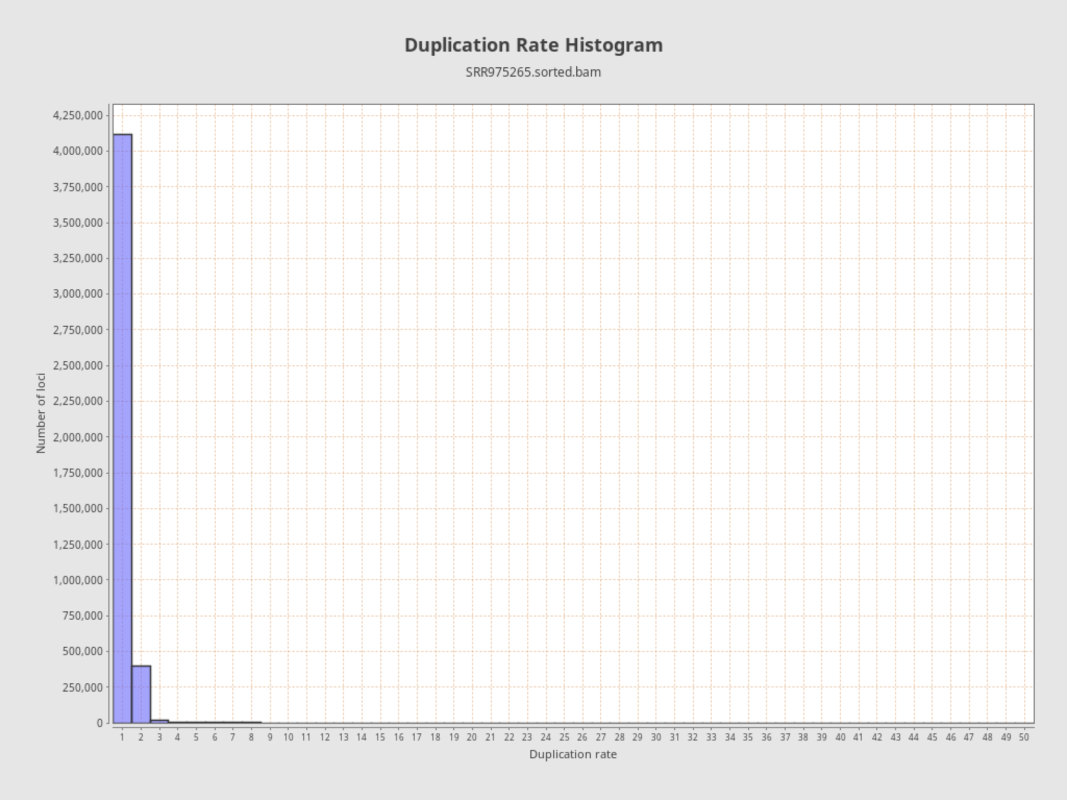
5. Results : Coverage Histogram (0-50X)



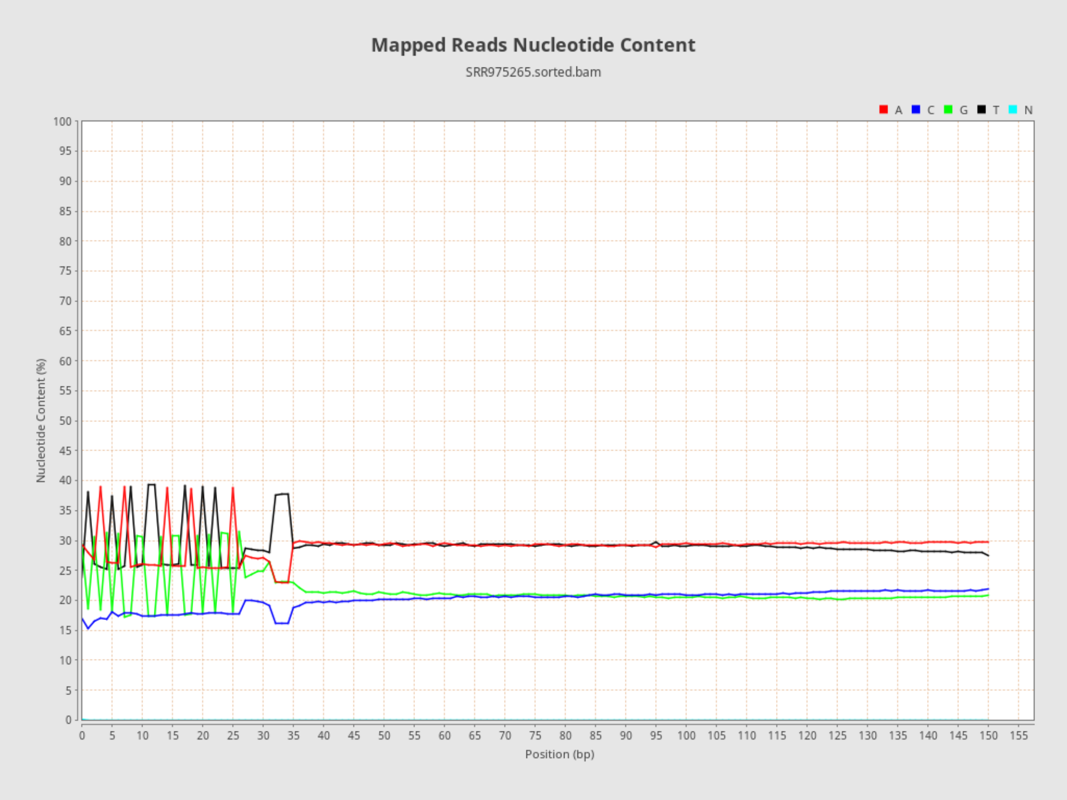
6. Results : Genome Fraction Coverage



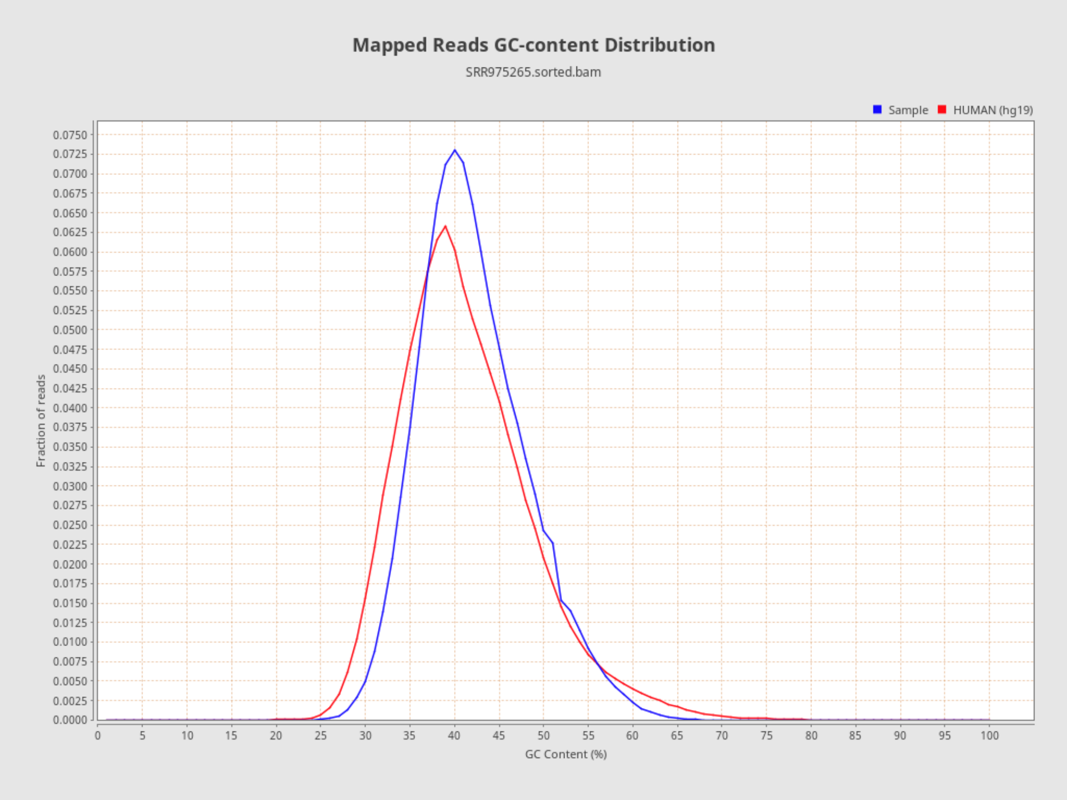
7. Results : Duplication Rate Histogram



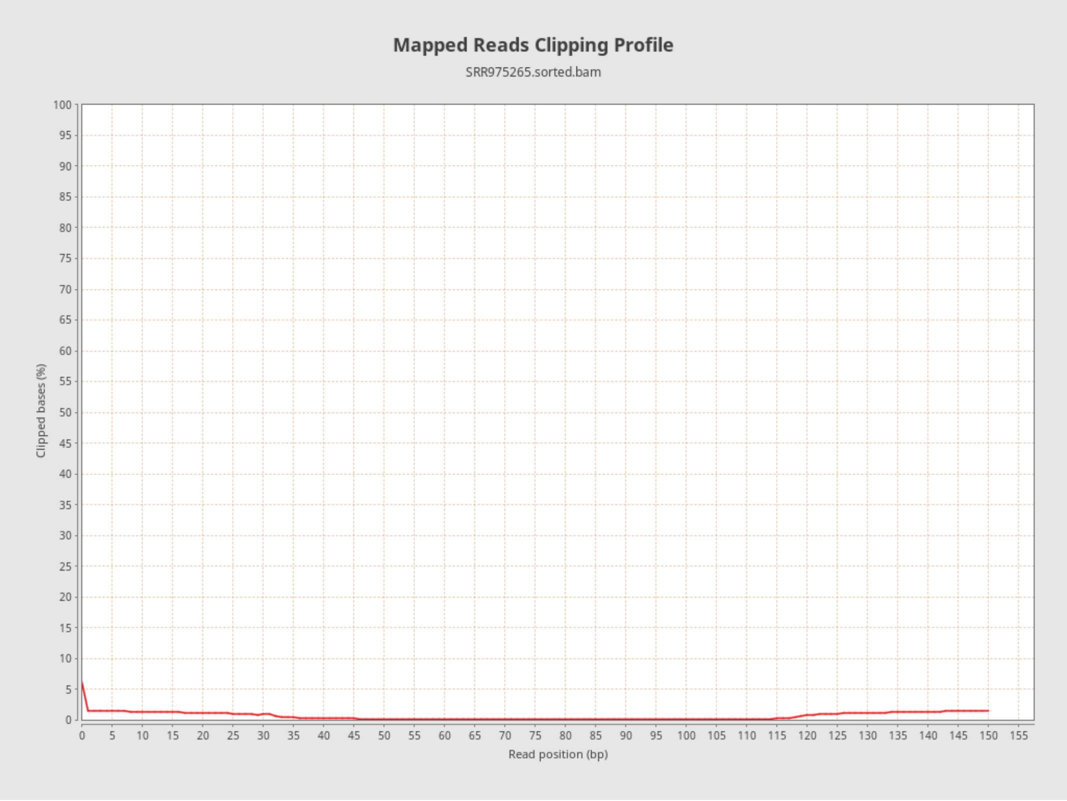
8. Results : Mapped Reads Nucleotide Content



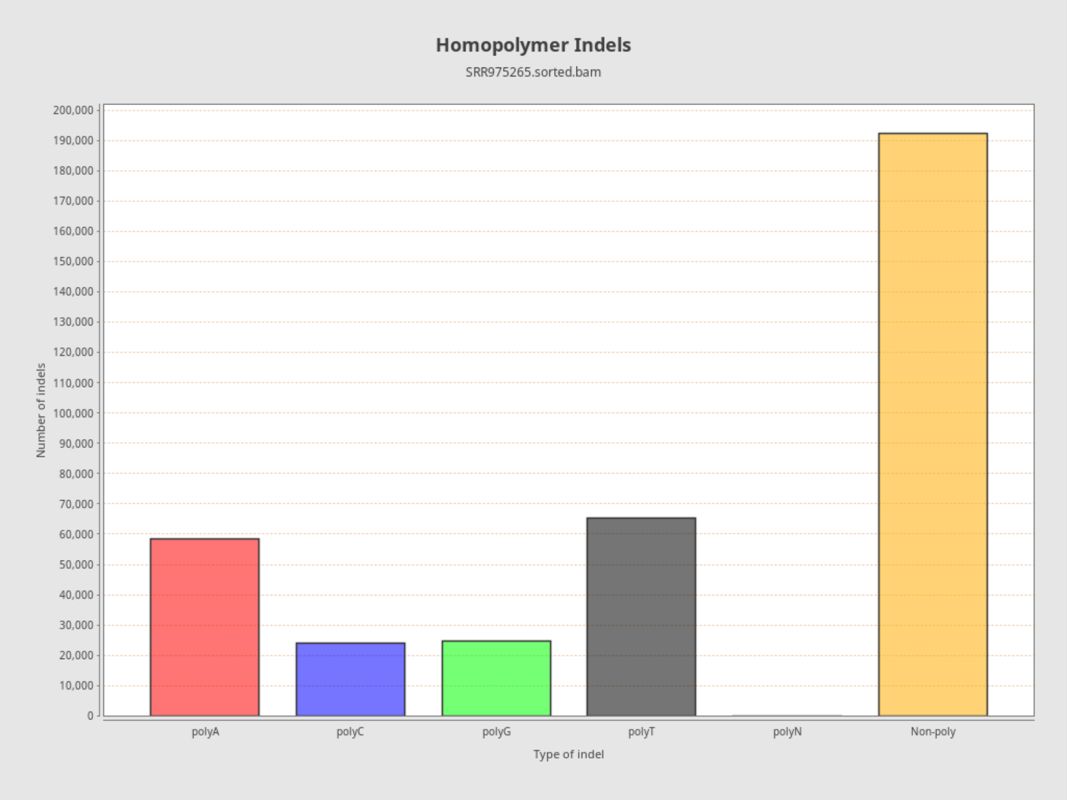
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

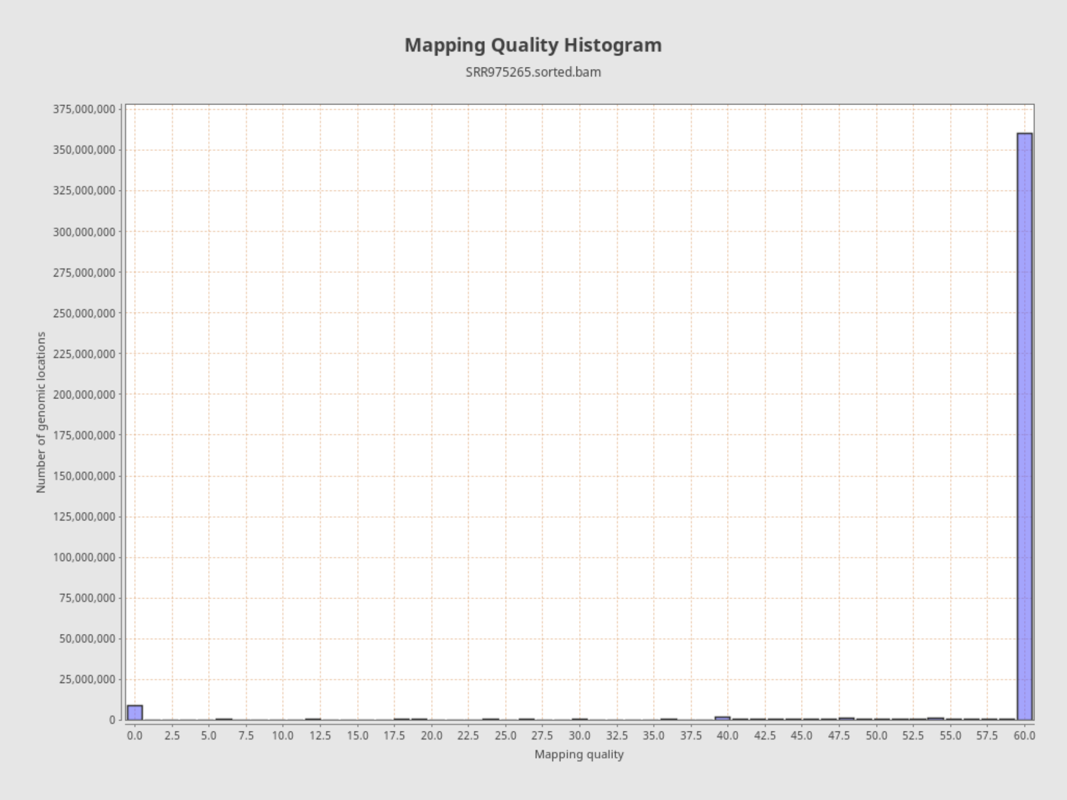


11. Results : Homopolymer Indels

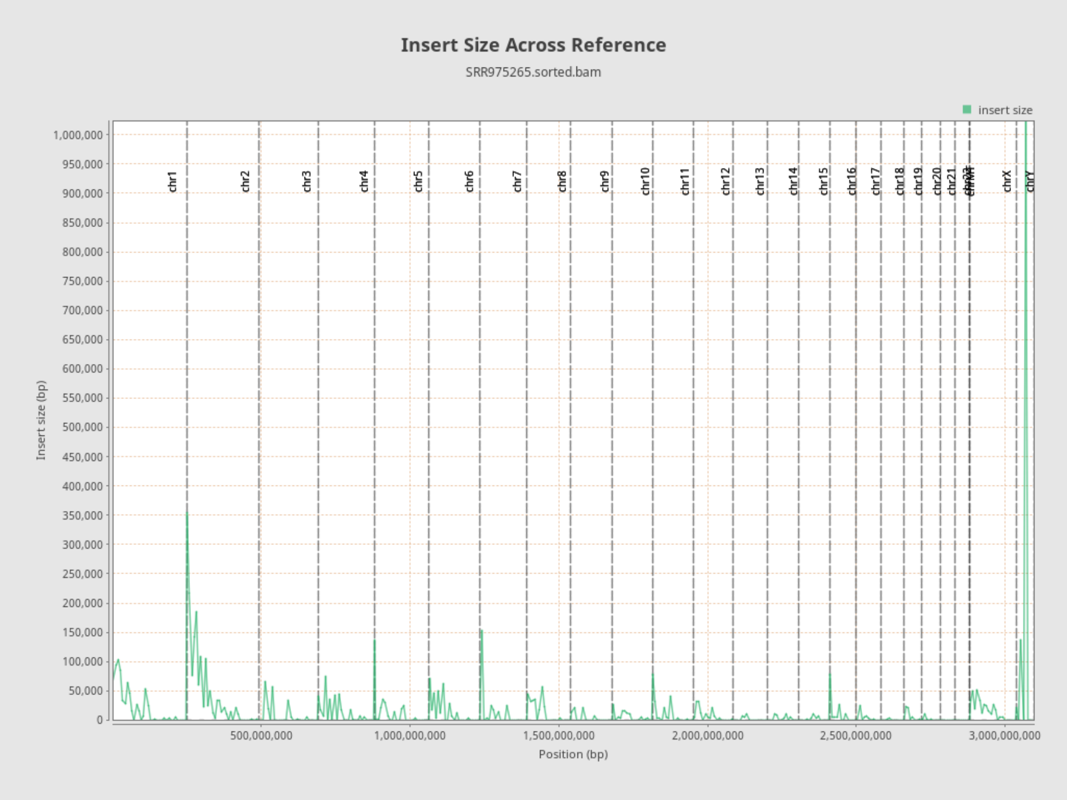


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram