Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 15:55:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975255.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_SRR975255 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975255_1.fastq.gz SRR975255_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 15:55:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975255.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,522,864
Mapped reads	5,481,136 / 99.24%
Unmapped reads	41,728 / 0.76%
Mapped paired reads	5,481,136 / 99.24%
Mapped reads, first in pair	2,740,174 / 49.62%
Mapped reads, second in pair	2,740,962 / 49.63%
Mapped reads, both in pair	5,469,844 / 99.04%
Mapped reads, singletons	11,292 / 0.2%
Secondary alignments	0
Supplementary alignments	13,941 / 0.25%
Read min/max/mean length	30 / 101 / 101.1
Duplicated reads (estimated)	208,064 / 3.77%
Duplication rate	2.65%
Clipped reads	3,245,571 / 58.77%

2.2. ACGT Content

Number/percentage of A's	146,475,752 / 28.95%
Number/percentage of C's	101,908,849 / 20.14%
Number/percentage of T's	149,104,508 / 29.47%
Number/percentage of G's	108,429,676 / 21.43%
Number/percentage of N's	7,165 / 0%

GC Percentage	41.57%

2.3. Coverage

Mean	0.1635
Standard Deviation	1.1199

2.4. Mapping Quality

Mean Mapping Quality	52.91

2.5. Insert size

Mean	69,799.55
Standard Deviation	2,565,101.22
P25/Median/P75	139 / 172 / 220

2.6. Mismatches and indels

General error rate	0.68%
Mismatches	3,289,009
Insertions	78,246
Mapped reads with at least one insertion	1.41%
Deletions	146,766
Mapped reads with at least one deletion	2.63%
Homopolymer indels	46%

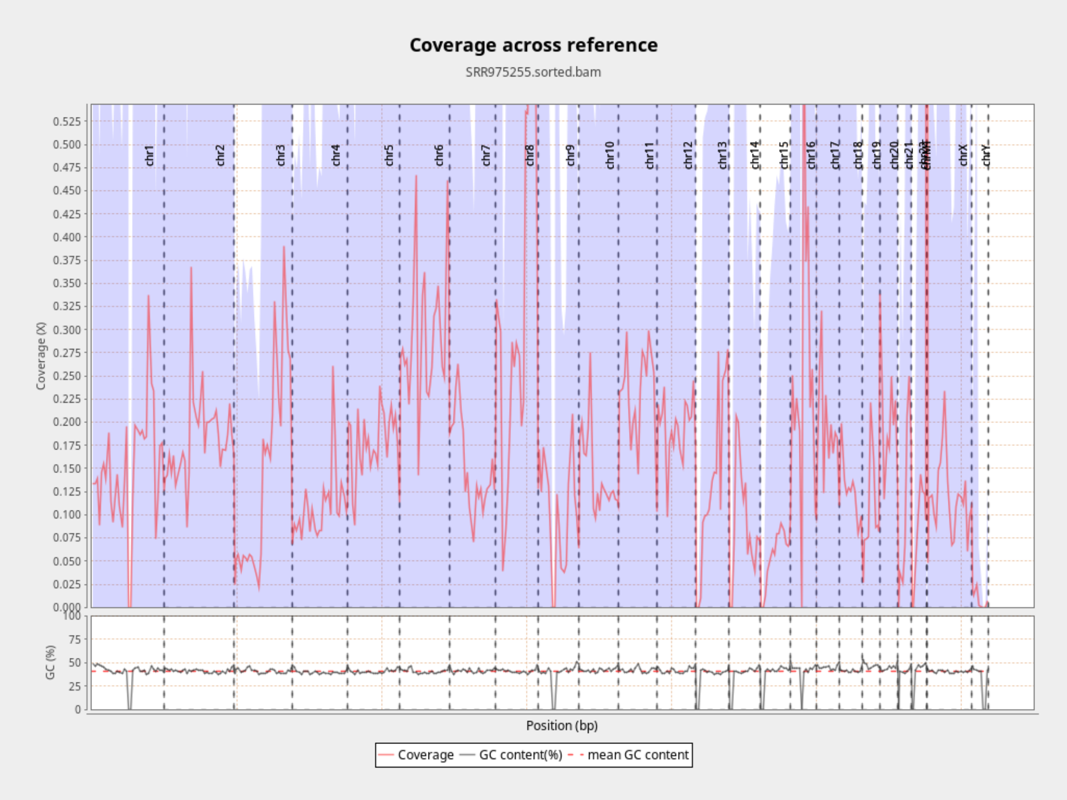
2.7. Chromosome stats

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

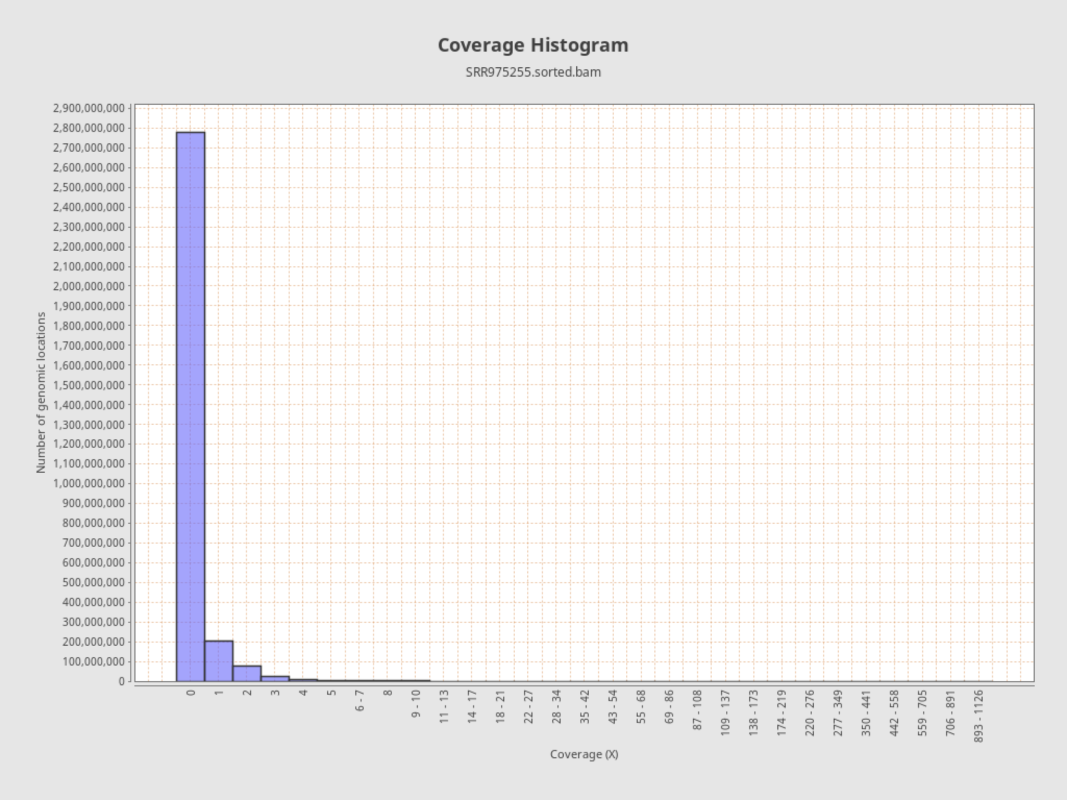
		bases	coverage	deviation
chr1	249250621	36815922	0.1477	1.1686
chr2	243199373	44486607	0.1829	1.3541
chr3	198022430	29532990	0.1491	0.552
chr4	191154276	21061345	0.1102	0.5633
chr5	180915260	32414207	0.1792	0.583
chr6	171115067	50334312	0.2942	1.9603
chr7	159138663	23921037	0.1503	1.0958
chr8	146364022	48074104	0.3285	0.93
chr9	141213431	14899815	0.1055	1.0078
chr10	135534747	19573945	0.1444	1.2489
chr11	135006516	31072467	0.2302	1.5057
chr12	133851895	26108124	0.1951	0.6144
chr13	115169878	15854194	0.1377	0.5222
chr14	107349540	9694747	0.0903	0.4178
chr15	102531392	5565543	0.0543	0.3103
chr16	90354753	23044041	0.255	2.5814
chr17	81195210	15815145	0.1948	1.9652
chr18	78077248	9963082	0.1276	0.9499
chr19	59128983	6291408	0.1064	0.6893
chr20	63025520	13063934	0.2073	0.6473
chr21	48129895	5422768	0.1127	0.4837
chr22	51304566	4363085	0.085	0.3932
chrMT	16571	114956	6.9372	5.37
chrX	155270560	18200789	0.1172	0.7529

chrY	59373566	471929	0.0079	0.2452

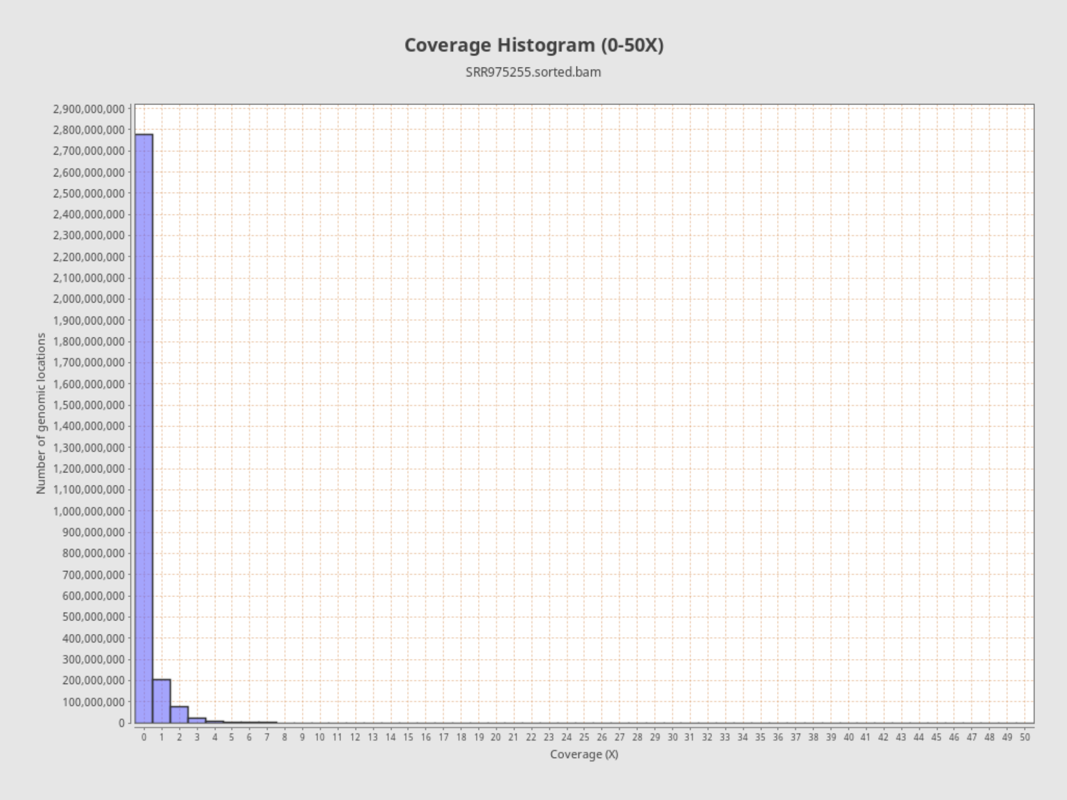
3. Results : Coverage across reference



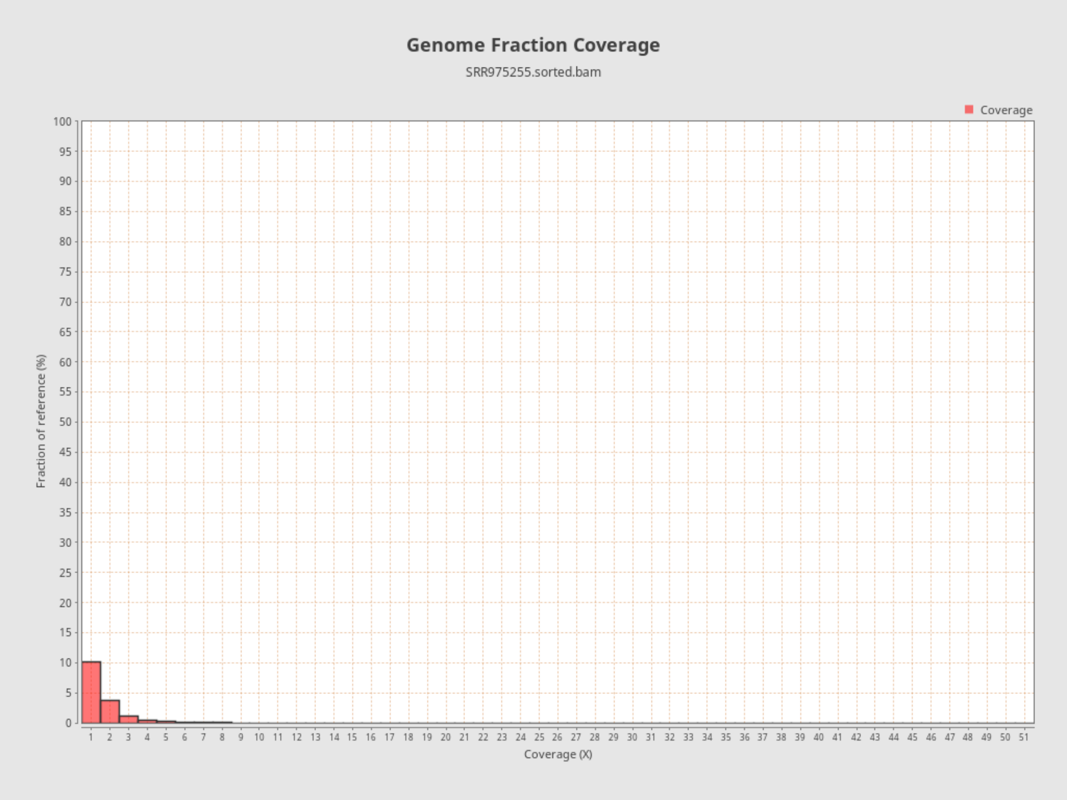
4. Results : Coverage Histogram



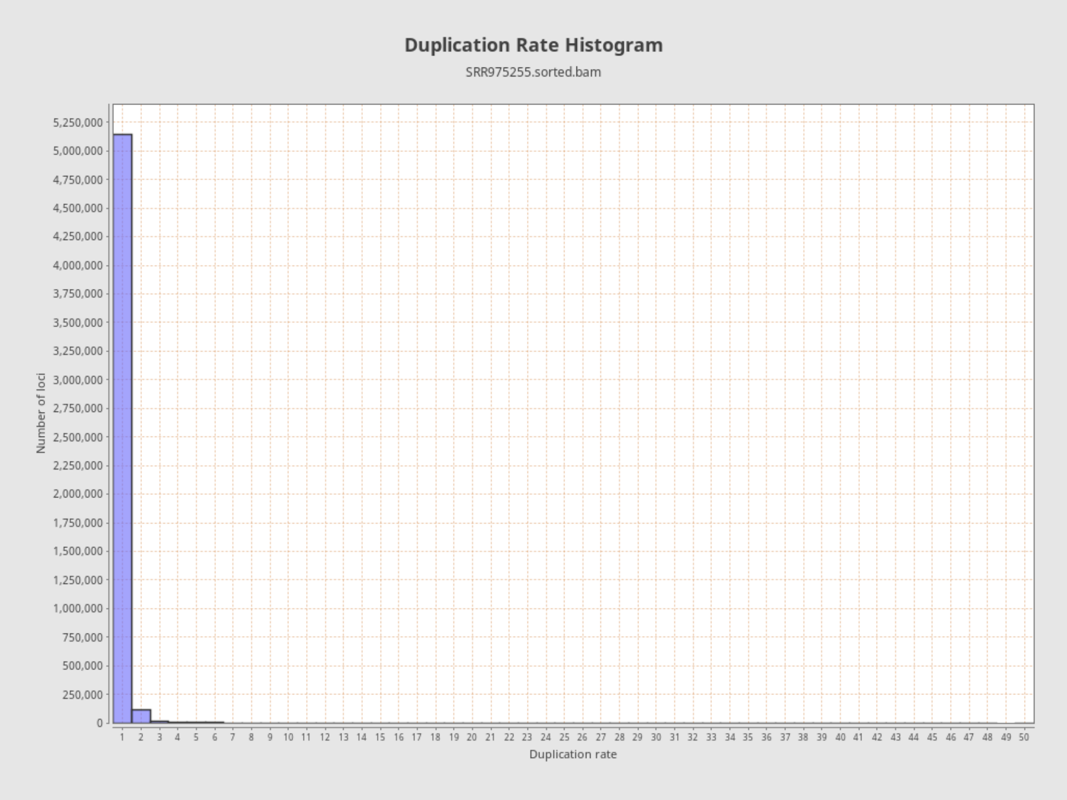
5. Results : Coverage Histogram (0-50X)



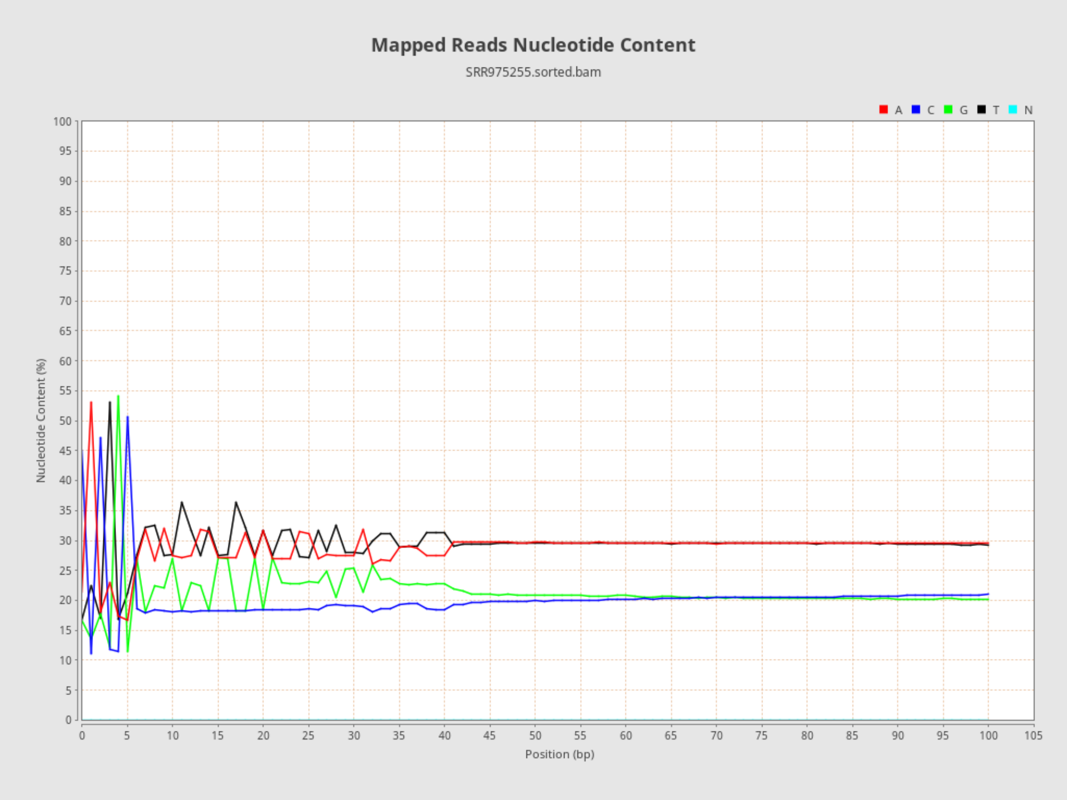
6. Results : Genome Fraction Coverage



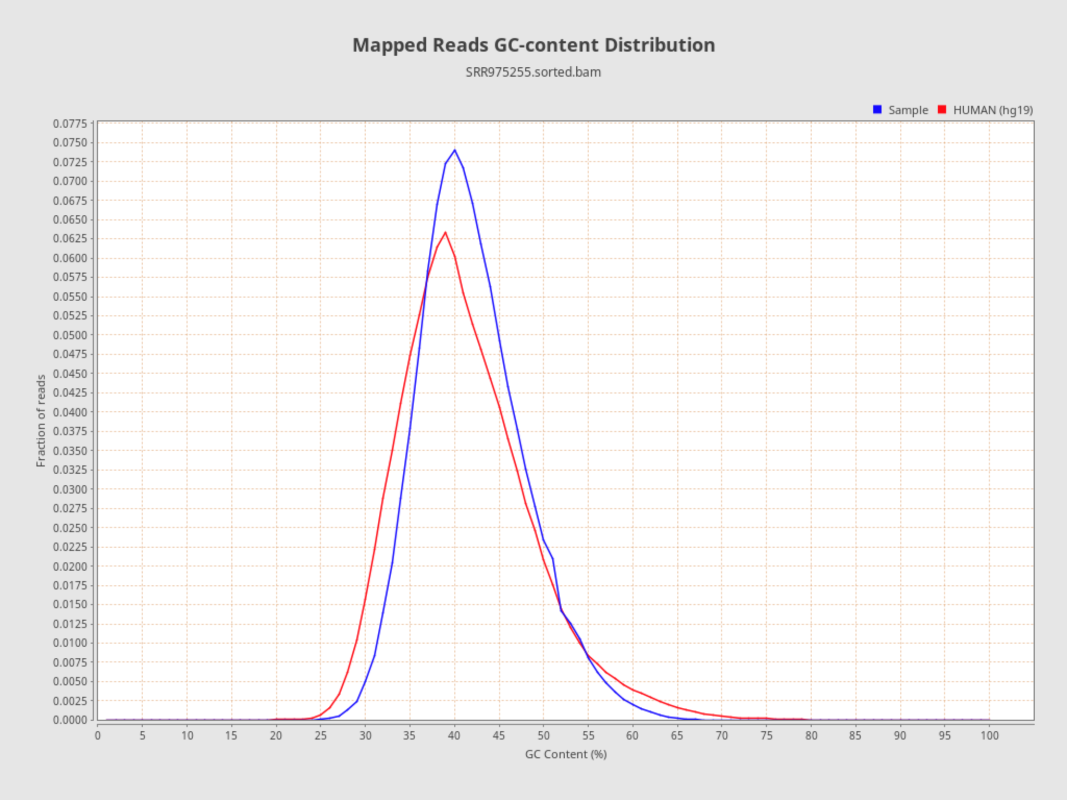
7. Results : Duplication Rate Histogram



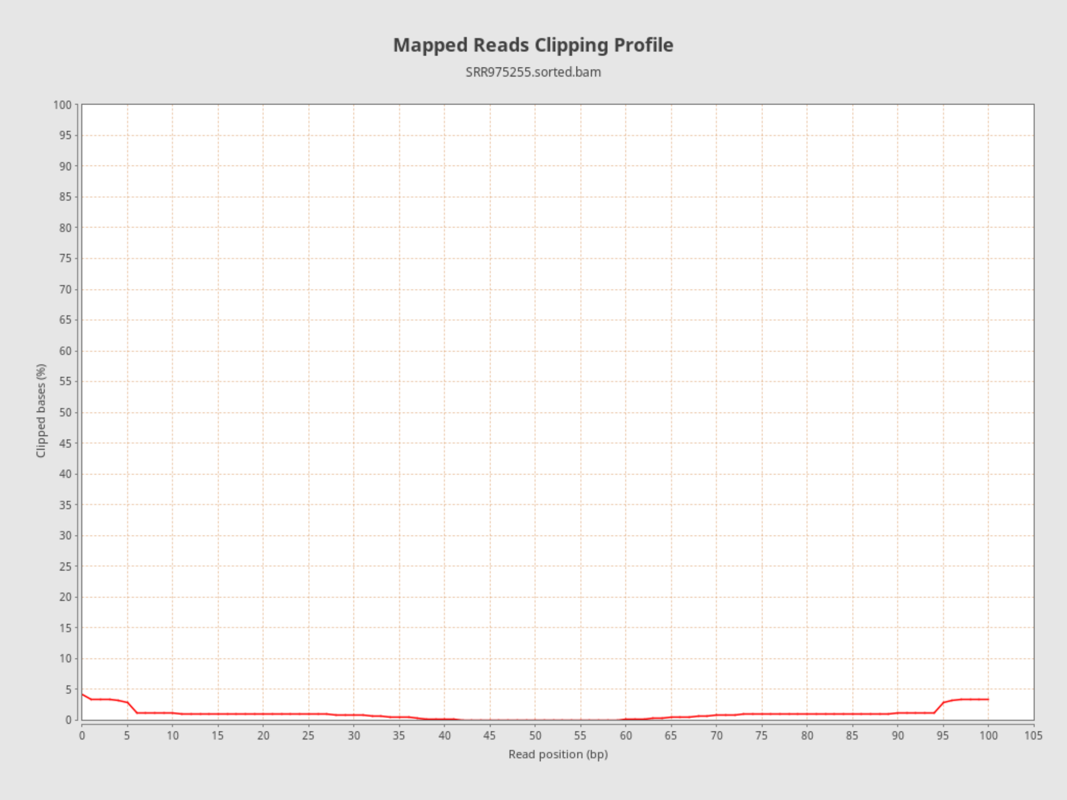
8. Results : Mapped Reads Nucleotide Content



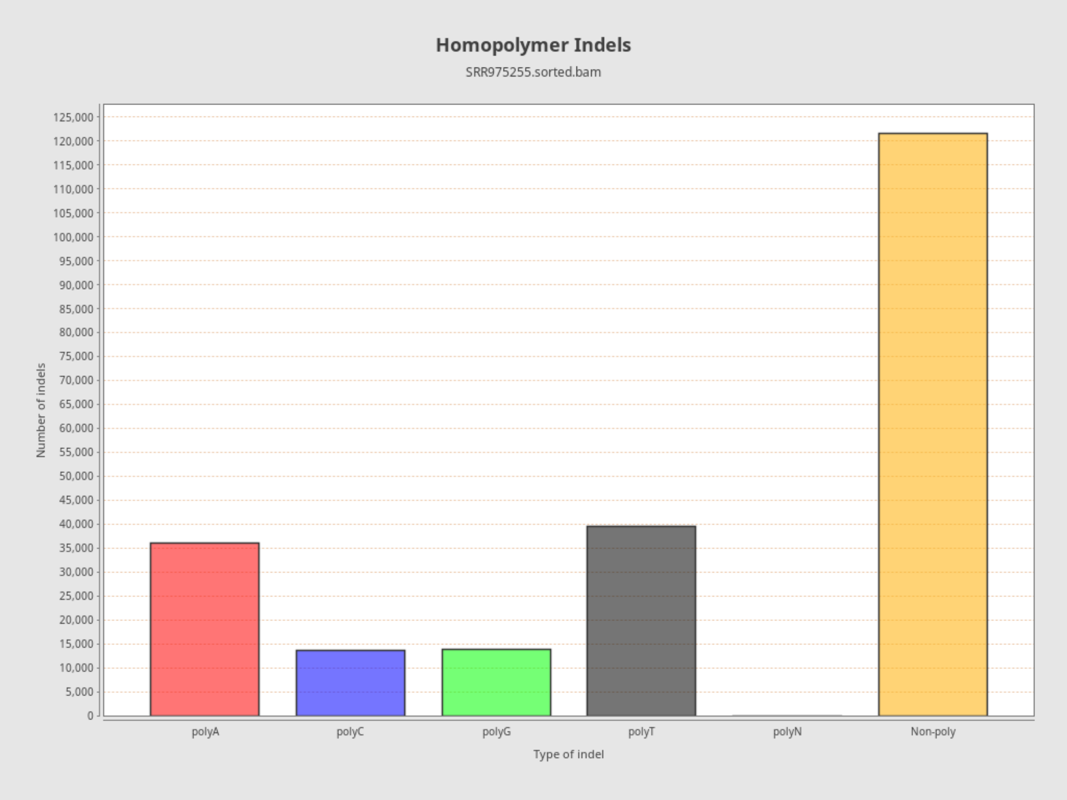
9. Results : Mapped Reads GC-content Distribution



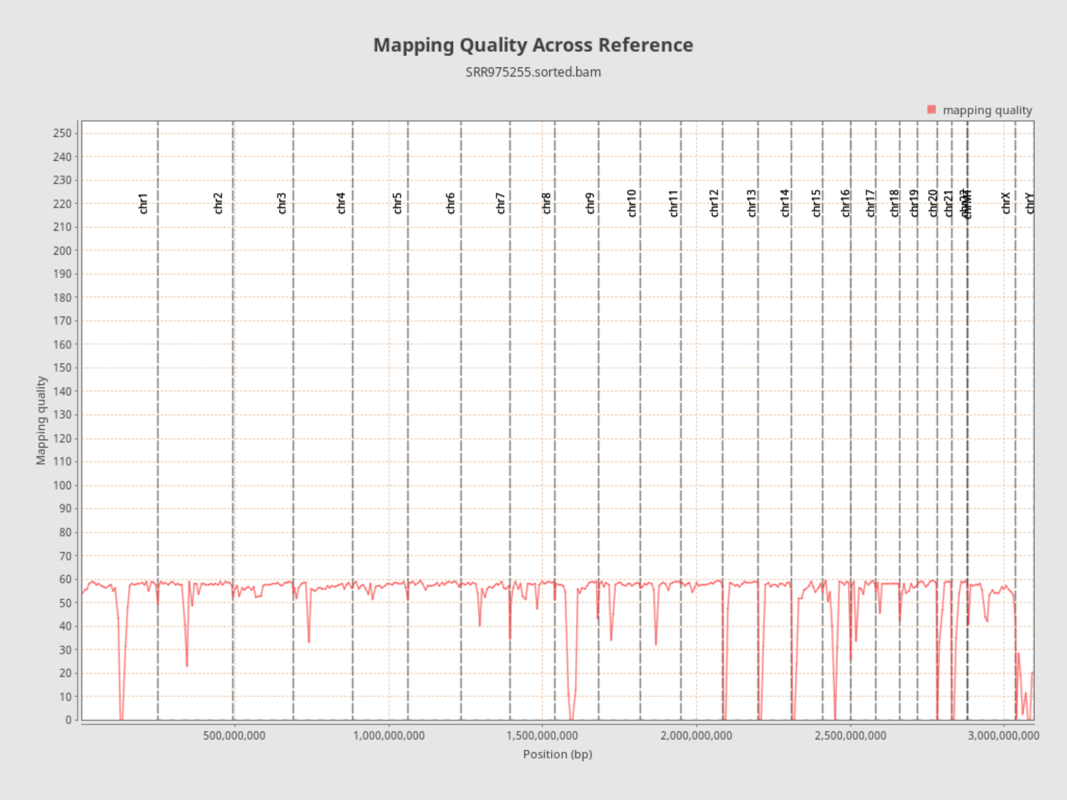
10. Results : Mapped Reads Clipping Profile



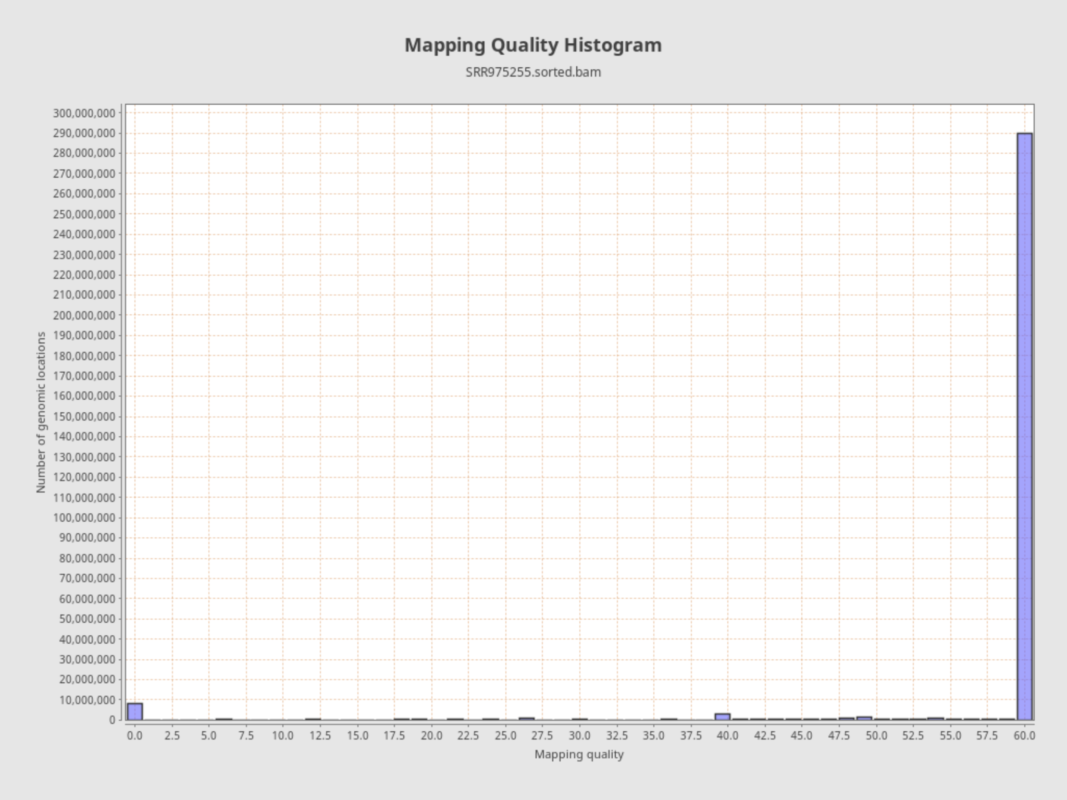
11. Results : Homopolymer Indels



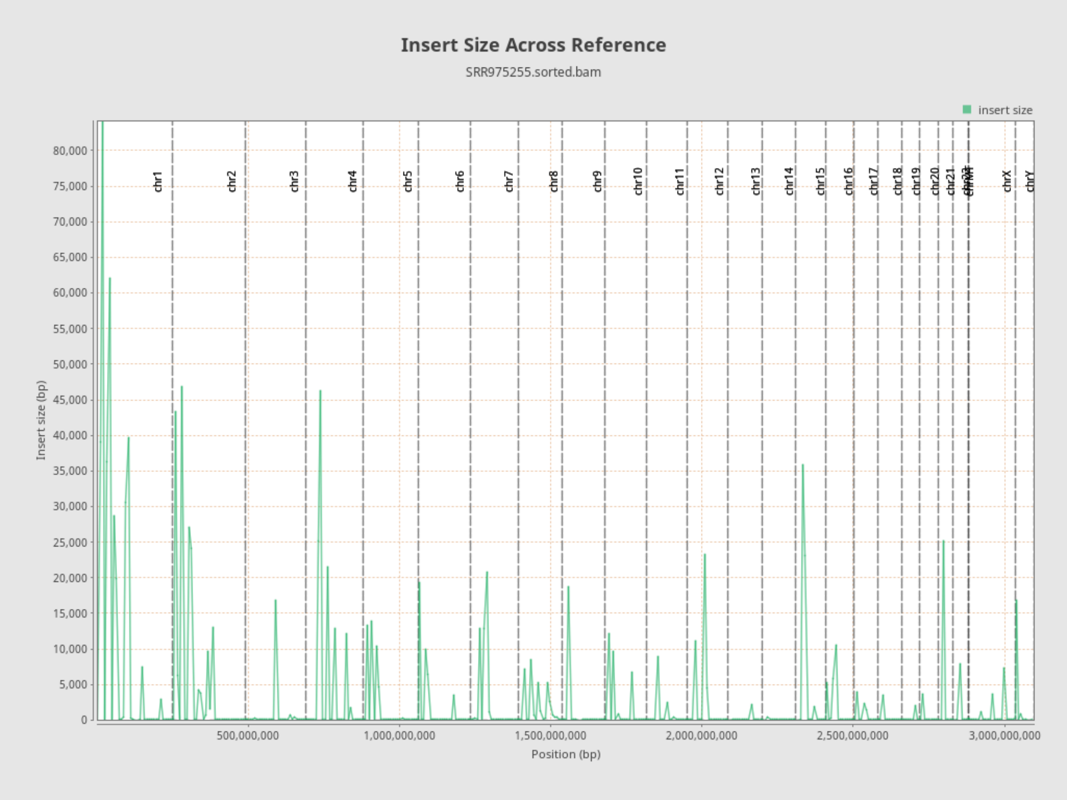
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram