Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 03:55:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975319.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_SRR975319 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975319_1.fastq.gz SRR975319_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 03:55:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975319.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	34,466,882
Mapped reads	34,259,917 / 99.4%
Unmapped reads	206,965 / 0.6%
Mapped paired reads	34,259,917 / 99.4%
Mapped reads, first in pair	17,177,969 / 49.84%
Mapped reads, second in pair	17,081,948 / 49.56%
Mapped reads, both in pair	34,095,808 / 98.92%
Mapped reads, singletons	164,109 / 0.48%
Secondary alignments	0
Supplementary alignments	81,570 / 0.24%
Read min/max/mean length	30 / 101 / 101.09
Duplicated reads (estimated)	21,392,781 / 62.07%
Duplication rate	56.89%
Clipped reads	20,741,216 / 60.18%

2.2. ACGT Content

Number/percentage of A's	881,656,518 / 27.81%
Number/percentage of C's	652,855,969 / 20.59%
Number/percentage of T's	916,368,282 / 28.9%
Number/percentage of G's	718,843,279 / 22.67%
Number/percentage of N's	687,897 / 0.02%

GC Percentage	43.27%

2.3. Coverage

Mean	1.0245
Standard Deviation	15.4489

2.4. Mapping Quality

Mean Mapping Quality	55.91

2.5. Insert size

Mean	178,810.08
Standard Deviation	4,135,292.88
P25/Median/P75	191 / 234 / 286

2.6. Mismatches and indels

General error rate	0.77%
Mismatches	23,752,990
Insertions	301,038
Mapped reads with at least one insertion	0.87%
Deletions	801,739
Mapped reads with at least one deletion	2.29%
Homopolymer indels	48.62%

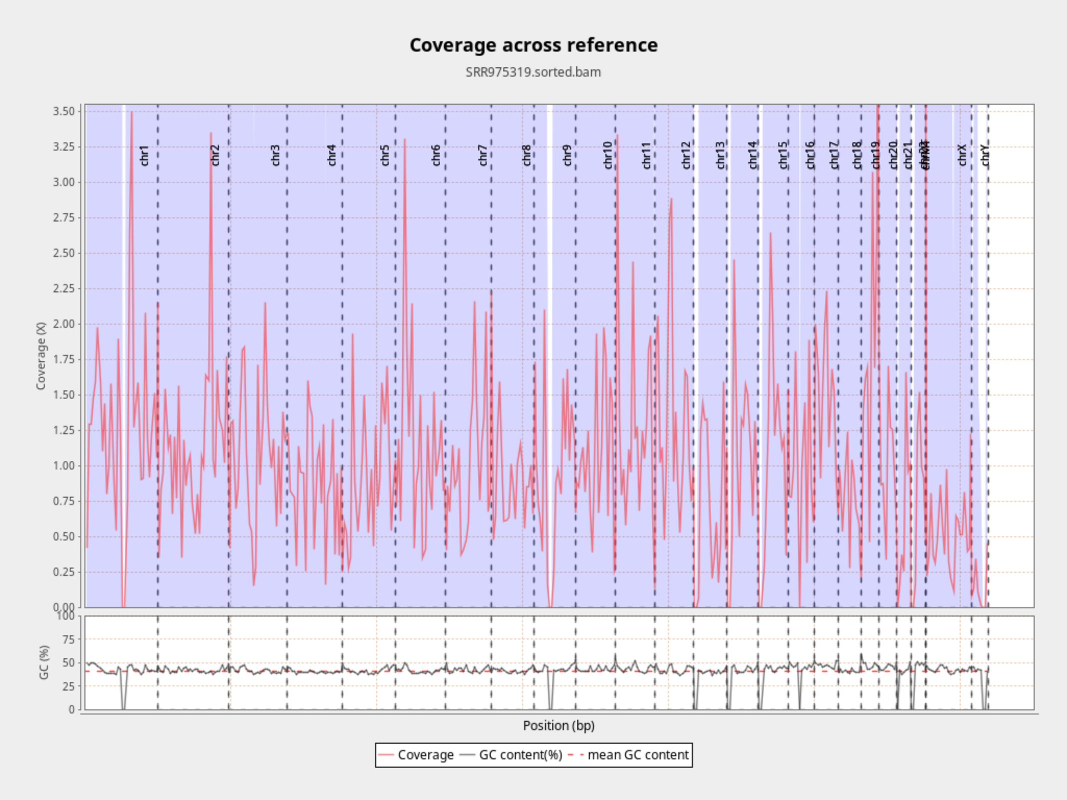
2.7. Chromosome stats

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

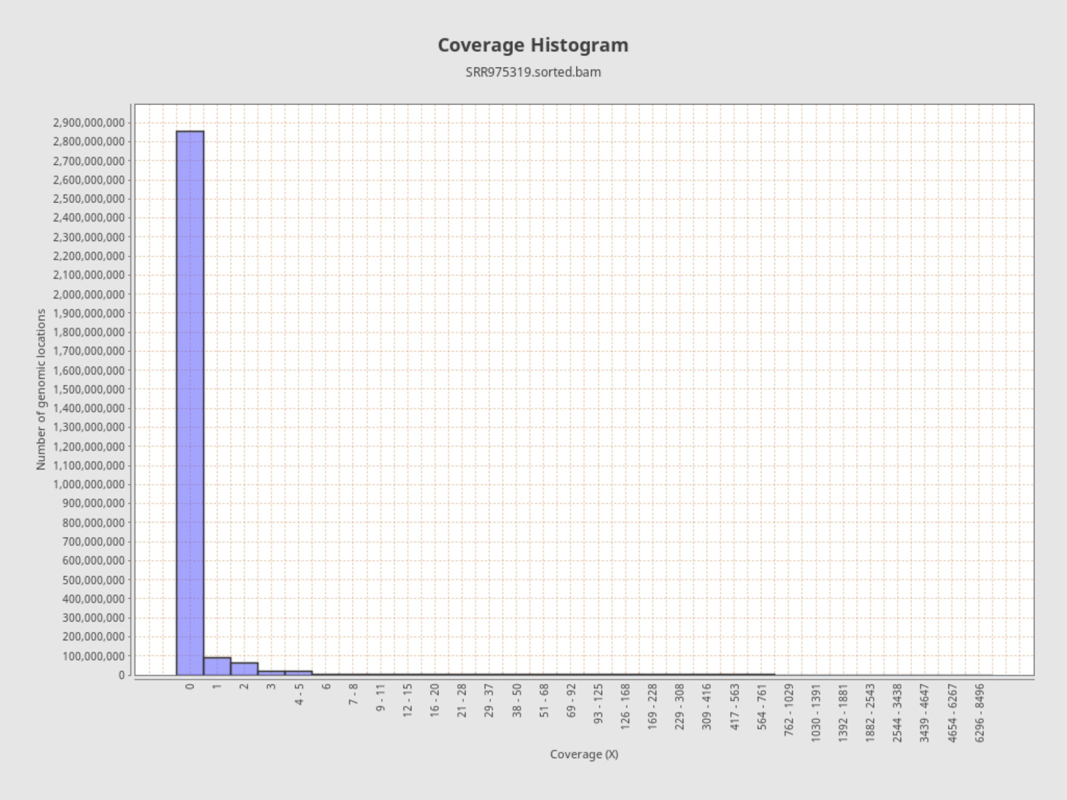
		bases	coverage	deviation
chr1	249250621	322183590	1.2926	17.0969
chr2	243199373	274330933	1.128	15.6258
chr3	198022430	216888105	1.0953	15.6113
chr4	191154276	167879328	0.8782	13.6894
chr5	180915260	167935604	0.9283	15.1097
chr6	171115067	199384552	1.1652	18.3612
chr7	159138663	160985877	1.0116	15.5077
chr8	146364022	127379575	0.8703	13.0547
chr9	141213431	126168408	0.8935	13.6402
chr10	135534747	149073755	1.0999	15.9366
chr11	135006516	176228316	1.3053	17.0164
chr12	133851895	179405394	1.3403	17.0991
chr13	115169878	78030197	0.6775	12.637
chr14	107349540	109982924	1.0245	15.4709
chr15	102531392	111993921	1.0923	15.4313
chr16	90354753	86701637	0.9596	13.4152
chr17	81195210	122276556	1.506	19.5678
chr18	78077248	60574000	0.7758	11.9407
chr19	59128983	108484727	1.8347	28.2117
chr20	63025520	68070710	1.08	16.9429
chr21	48129895	31350977	0.6514	12.0164
chr22	51304566	38641110	0.7532	12.0031
chrMT	16571	58765	3.5463	9.0565
chrX	155270560	79123384	0.5096	9.4945

chrY	59373566	8505917	0.1433	3.3833

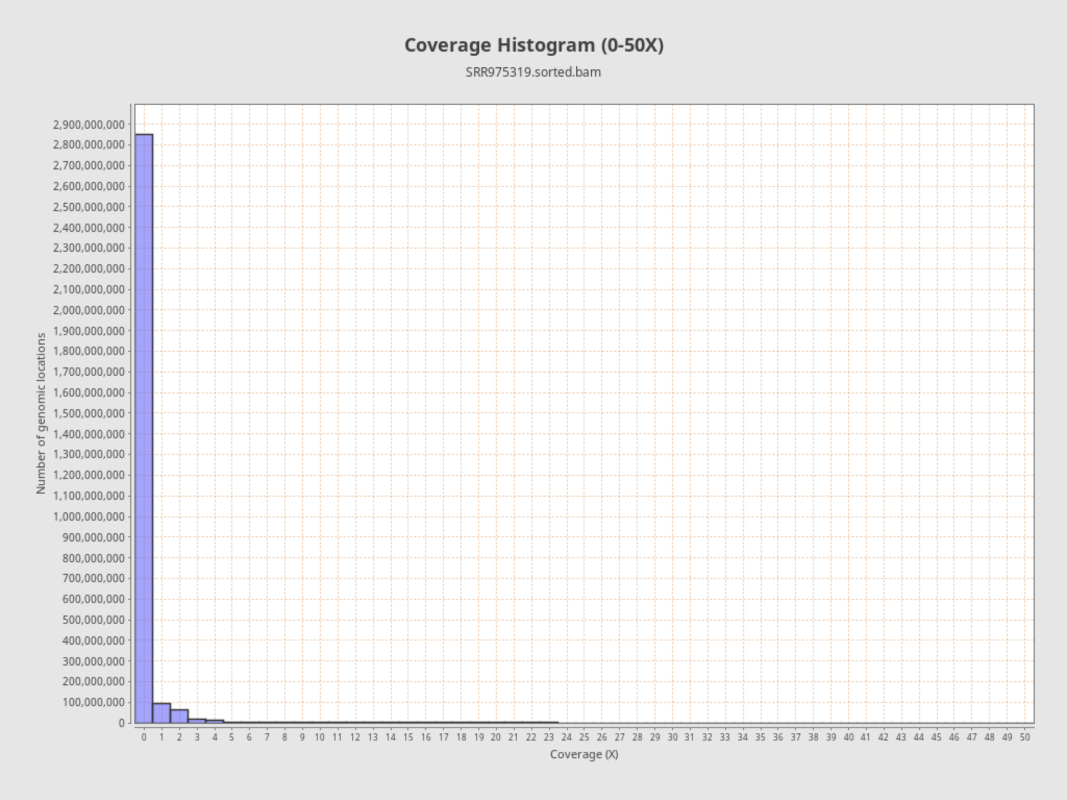
3. Results : Coverage across reference



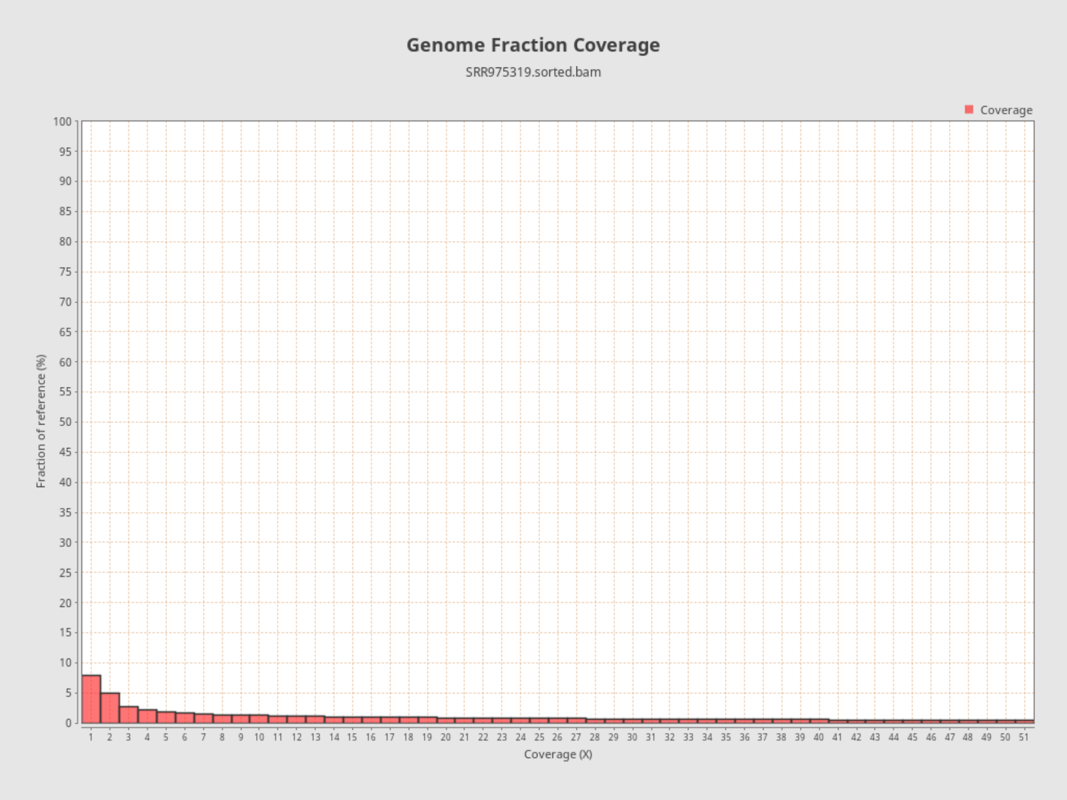
4. Results : Coverage Histogram



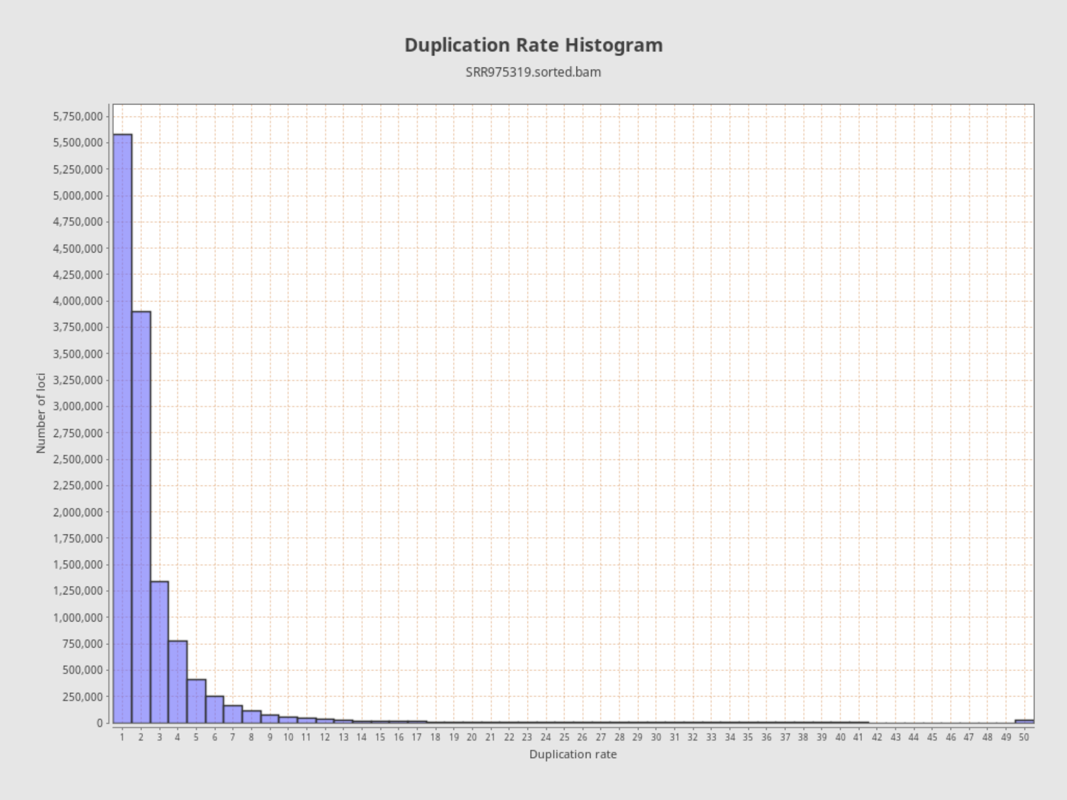
5. Results : Coverage Histogram (0-50X)



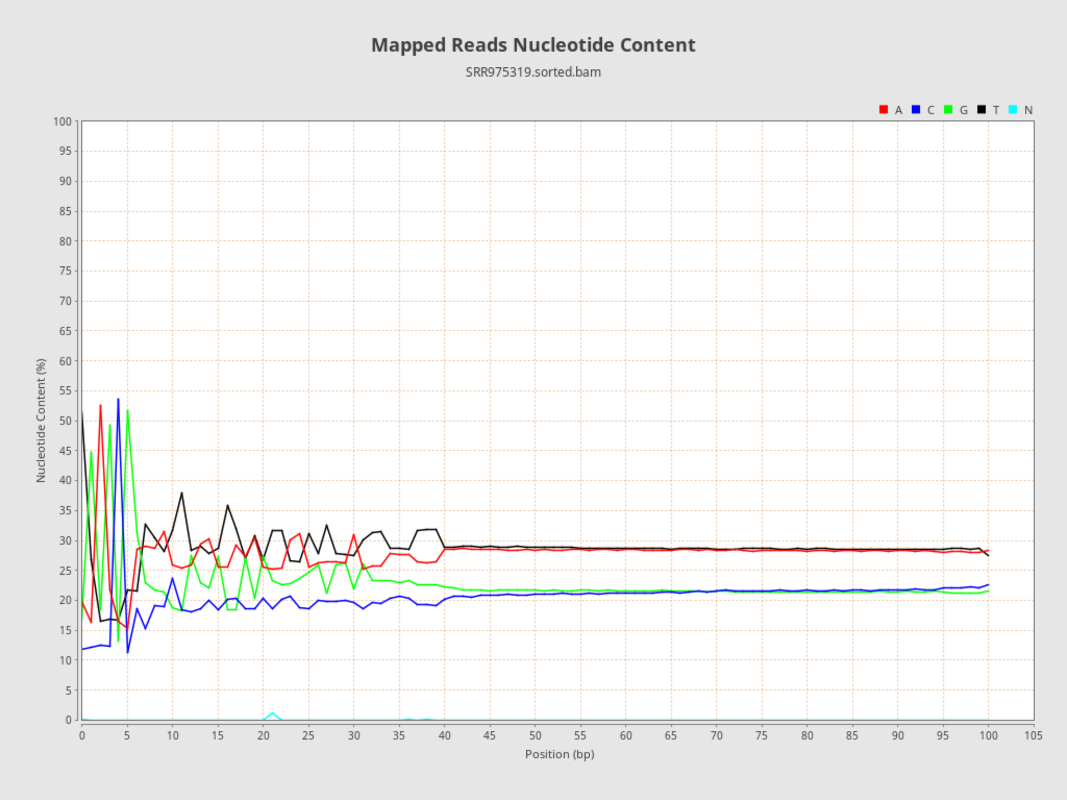
6. Results : Genome Fraction Coverage



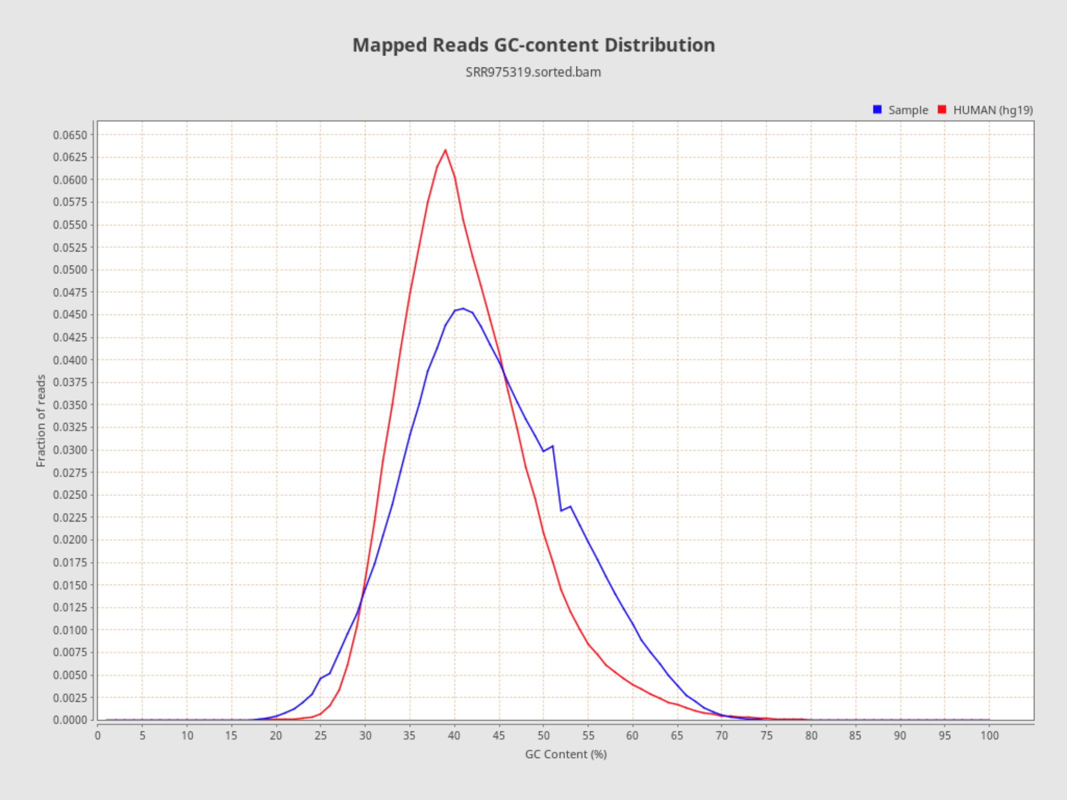
7. Results : Duplication Rate Histogram



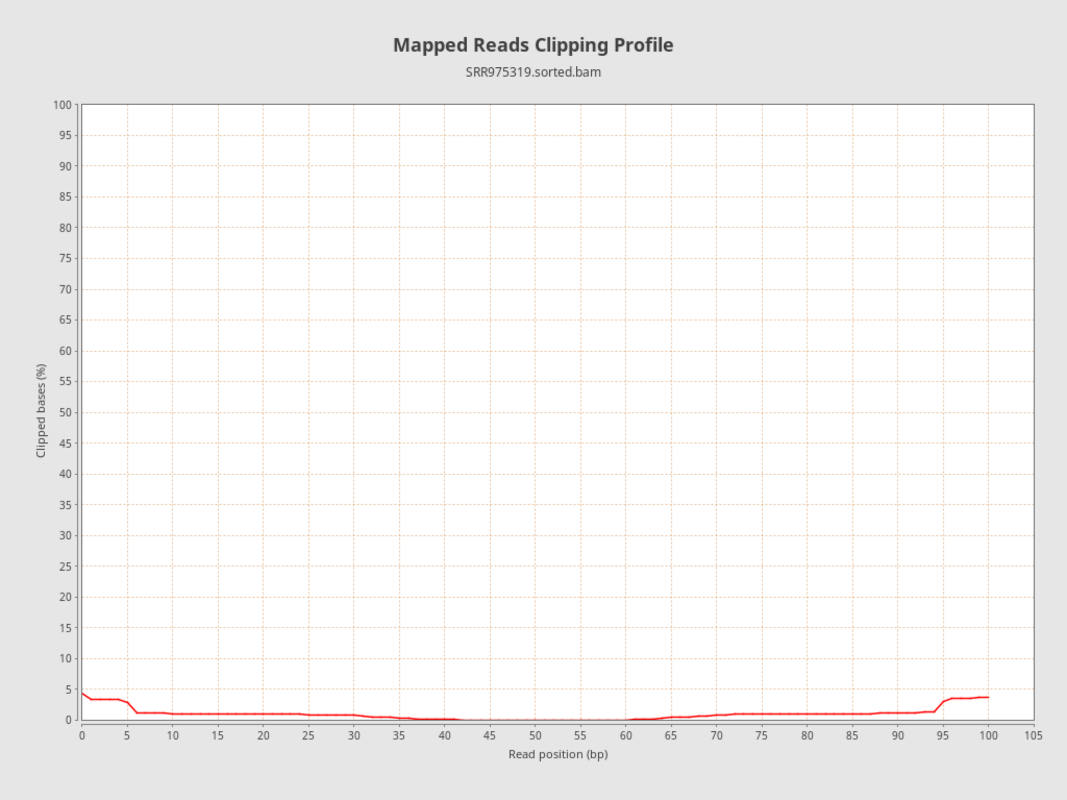
8. Results : Mapped Reads Nucleotide Content



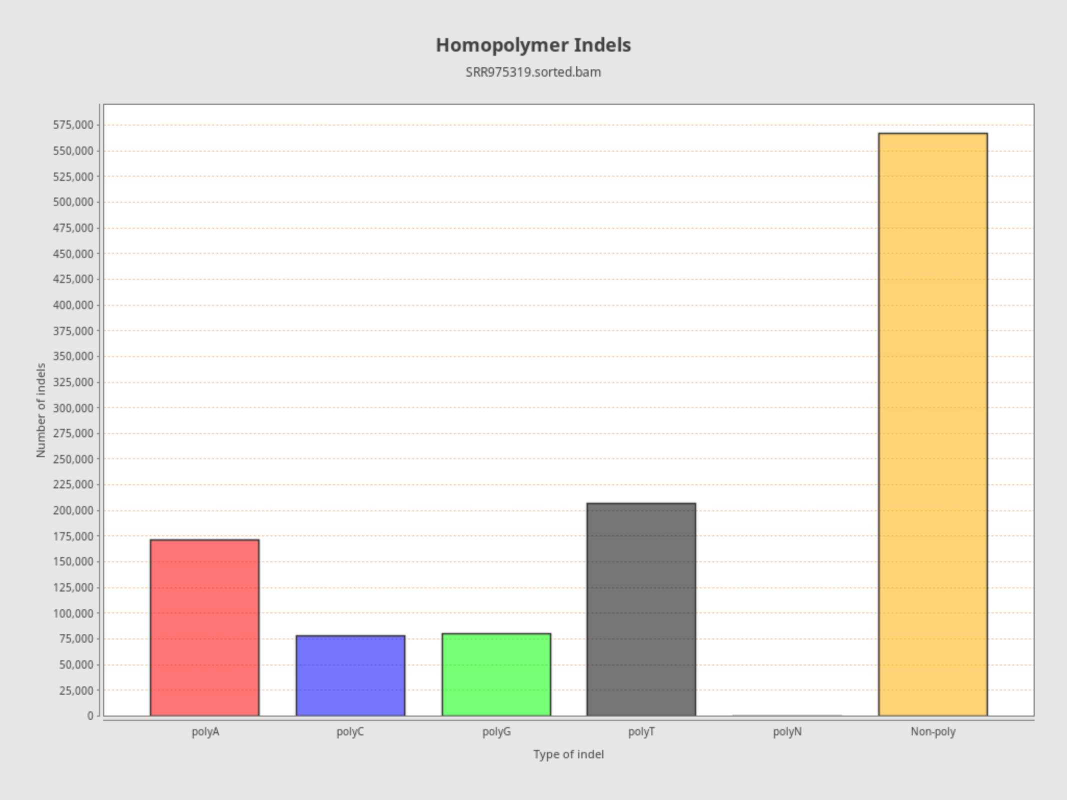
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

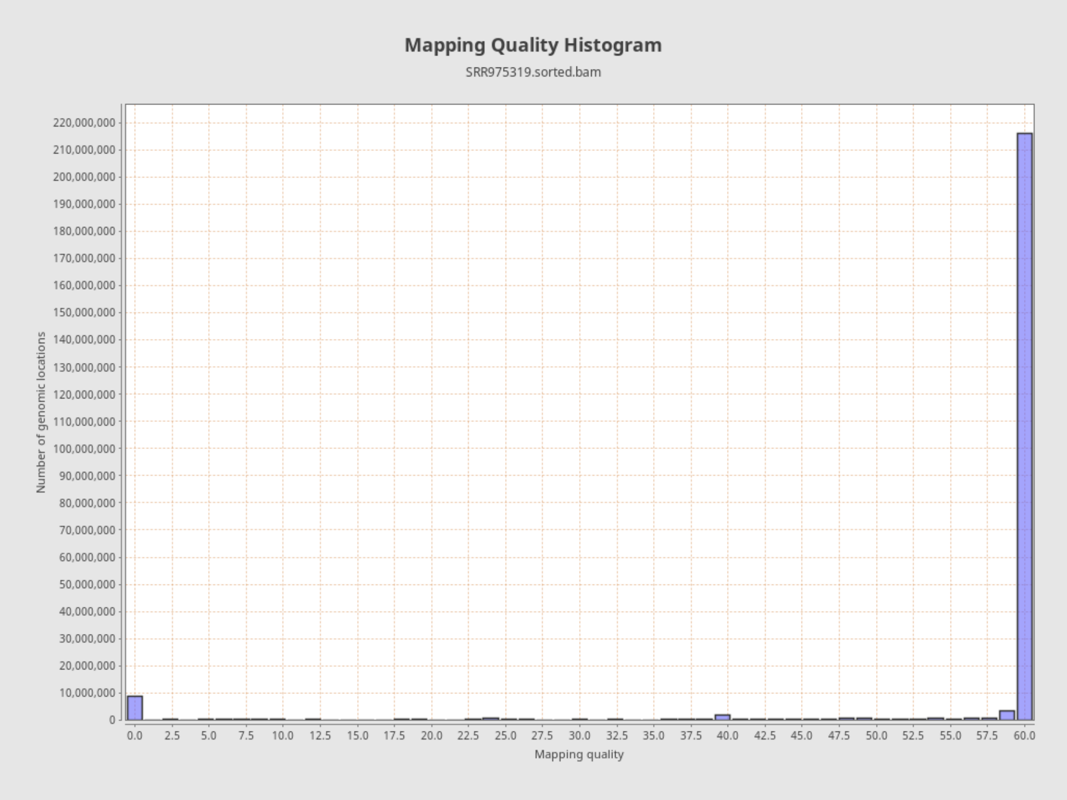


11. Results : Homopolymer Indels

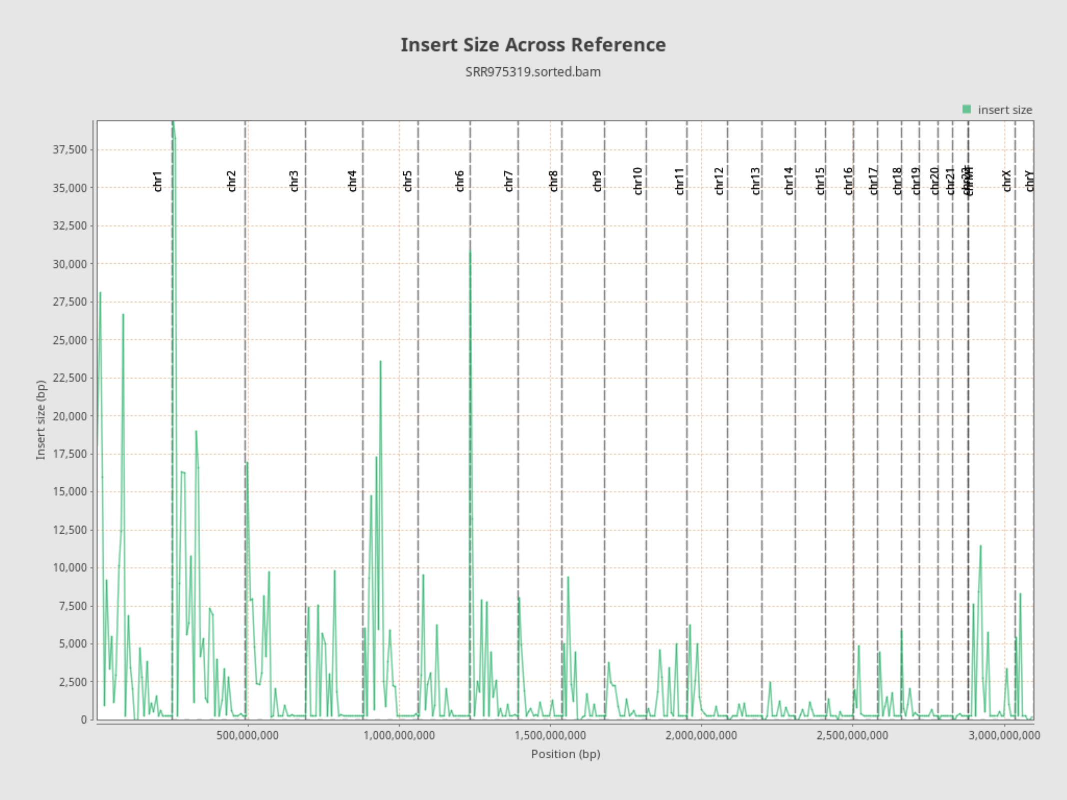


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram