Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/08 19:17:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975299.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_SRR975299 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975299_1.fastq.gz SRR975299_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 08 19:17:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975299.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	54,716,628
Mapped reads	54,527,324 / 99.65%
Unmapped reads	189,304 / 0.35%
Mapped paired reads	54,527,324 / 99.65%
Mapped reads, first in pair	27,286,812 / 49.87%
Mapped reads, second in pair	27,240,512 / 49.78%
Mapped reads, both in pair	54,432,548 / 99.48%
Mapped reads, singletons	94,776 / 0.17%
Secondary alignments	0
Supplementary alignments	126,806 / 0.23%
Read min/max/mean length	30 / 101 / 101.09
Duplicated reads (estimated)	34,447,220 / 62.96%
Duplication rate	45.18%
Clipped reads	30,781,607 / 56.26%

2.2. ACGT Content

Number/percentage of A's	1,332,726,815 / 26.97%
Number/percentage of C's	1,037,844,832 / 21%
Number/percentage of T's	1,390,484,079 / 28.14%
Number/percentage of G's	1,179,913,303 / 23.88%
Number/percentage of N's	211,274 / 0%

GC Percentage	44.88%

2.3. Coverage

Mean	1.5967
Standard Deviation	25.7736

2.4. Mapping Quality

Mean Mapping Quality	55.76

2.5. Insert size

Mean	97,939.49
Standard Deviation	3,076,286.99
P25/Median/P75	149 / 187 / 238

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	26,117,784
Insertions	454,734
Mapped reads with at least one insertion	0.82%
Deletions	1,000,403
Mapped reads with at least one deletion	1.81%
Homopolymer indels	47.25%

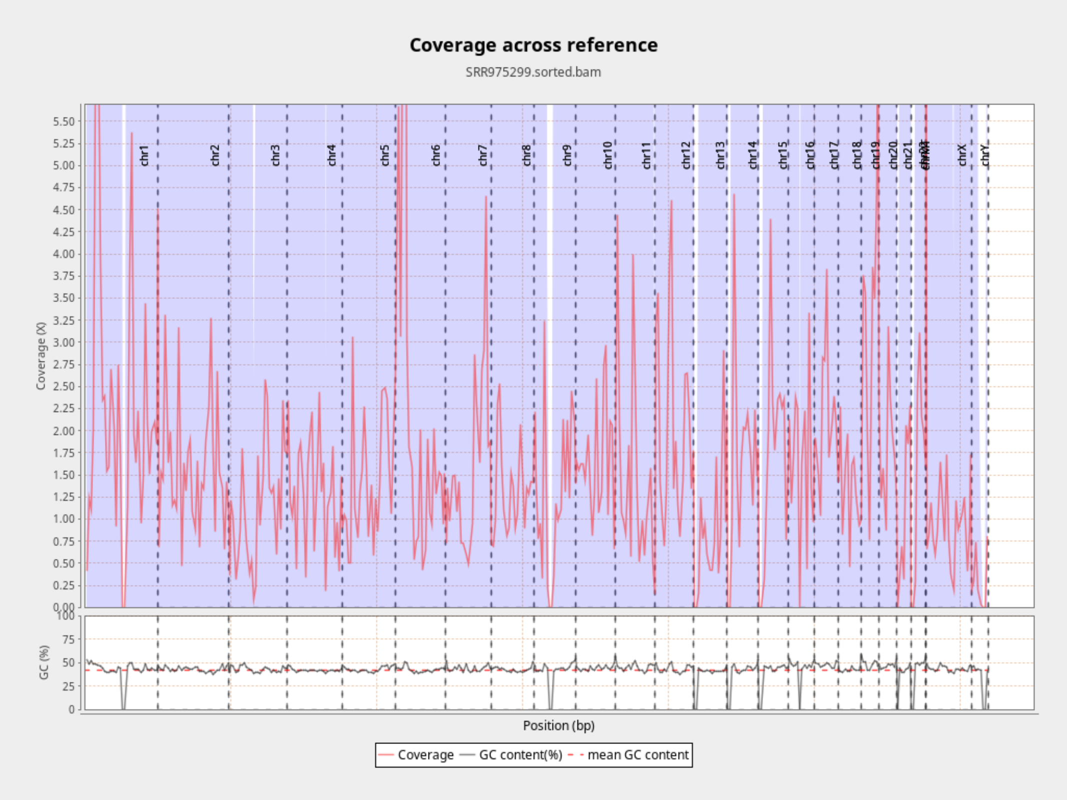
2.7. Chromosome stats

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

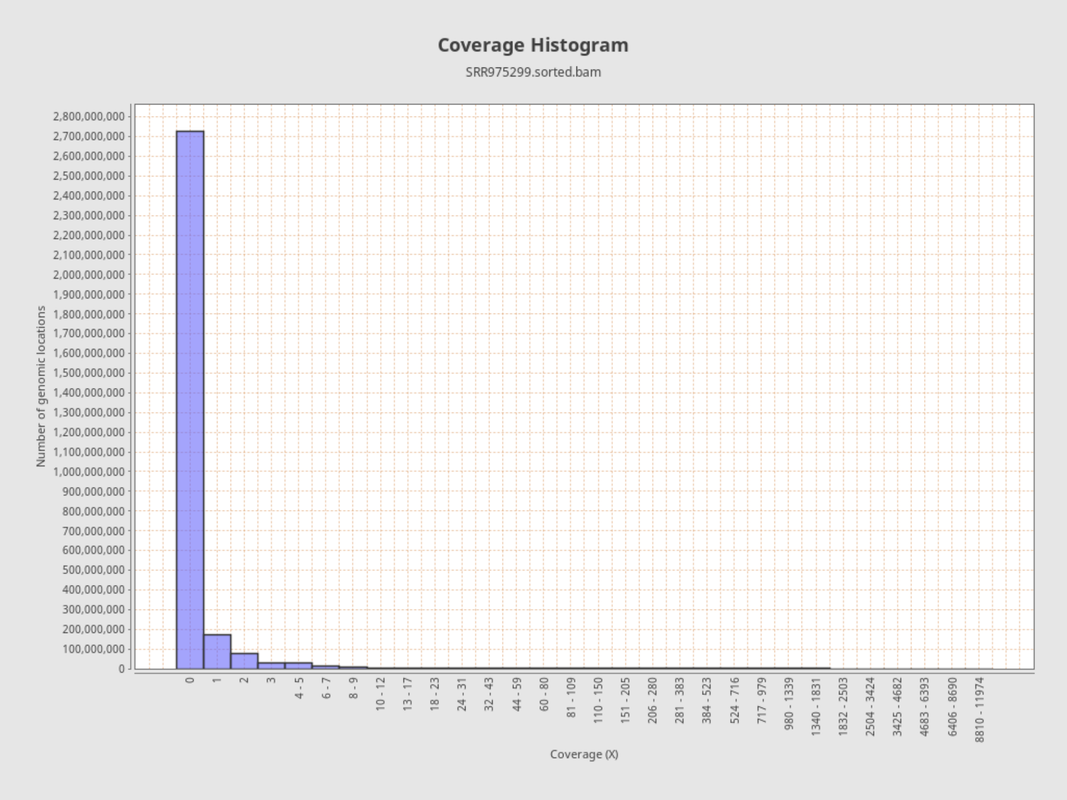
		bases	coverage	deviation
chr1	249250621	563984897	2.2627	31.4791
chr2	243199373	384051454	1.5792	24.561
chr3	198022430	228583303	1.1543	19.854
chr4	191154276	248859381	1.3019	22.7414
chr5	180915260	261217430	1.4439	23.2847
chr6	171115067	440862340	2.5764	41.0982
chr7	159138663	256089166	1.6092	26.5849
chr8	146364022	197798902	1.3514	22.4519
chr9	141213431	172766990	1.2234	20.7217
chr10	135534747	227494850	1.6785	26.0769
chr11	135006516	206471374	1.5293	23.2581
chr12	133851895	275007442	2.0546	27.7281
chr13	115169878	97358954	0.8454	17.1077
chr14	107349540	174084136	1.6217	26.3366
chr15	102531392	176033340	1.7169	27.5432
chr16	90354753	146068781	1.6166	23.8443
chr17	81195210	176465057	2.1733	27.1535
chr18	78077248	108559918	1.3904	27.707
chr19	59128983	190599908	3.2235	33.1982
chr20	63025520	116651487	1.8509	27.6875
chr21	48129895	52141704	1.0834	20.6895
chr22	51304566	80574308	1.5705	25.0742
chrMT	16571	226955	13.6959	23.066
chrX	155270560	143805365	0.9262	19.0959

chrY	59373566	17023157	0.2867	6.8106

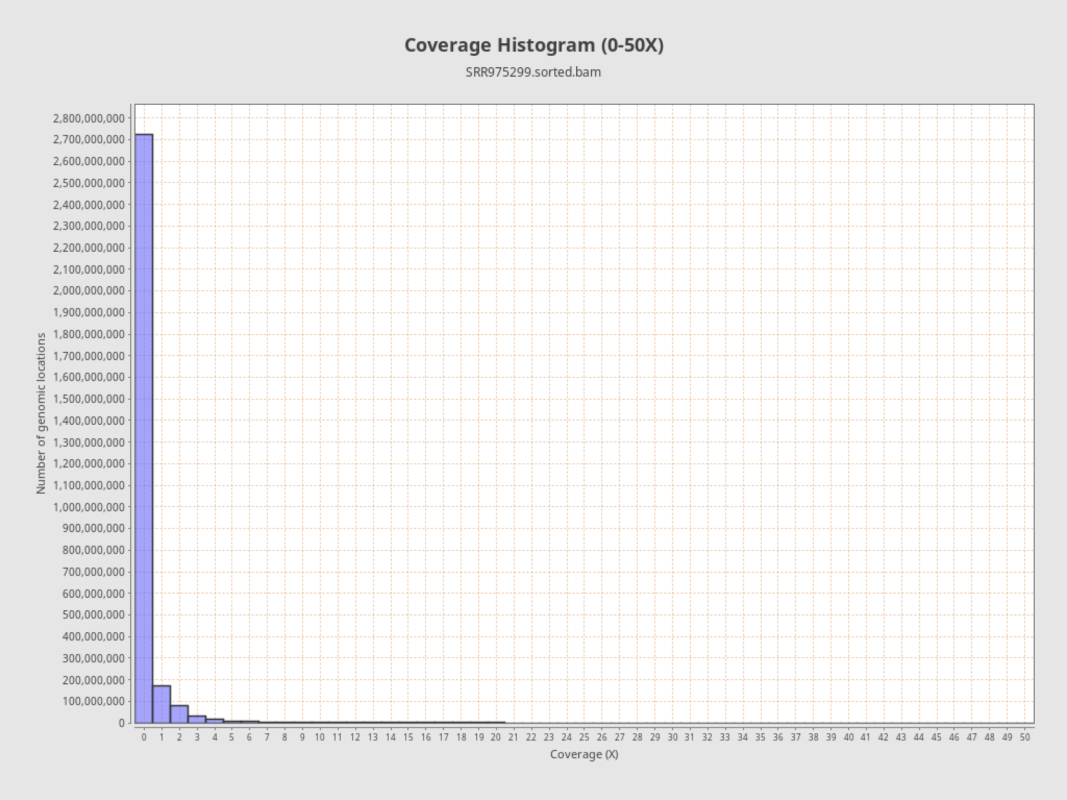
3. Results : Coverage across reference



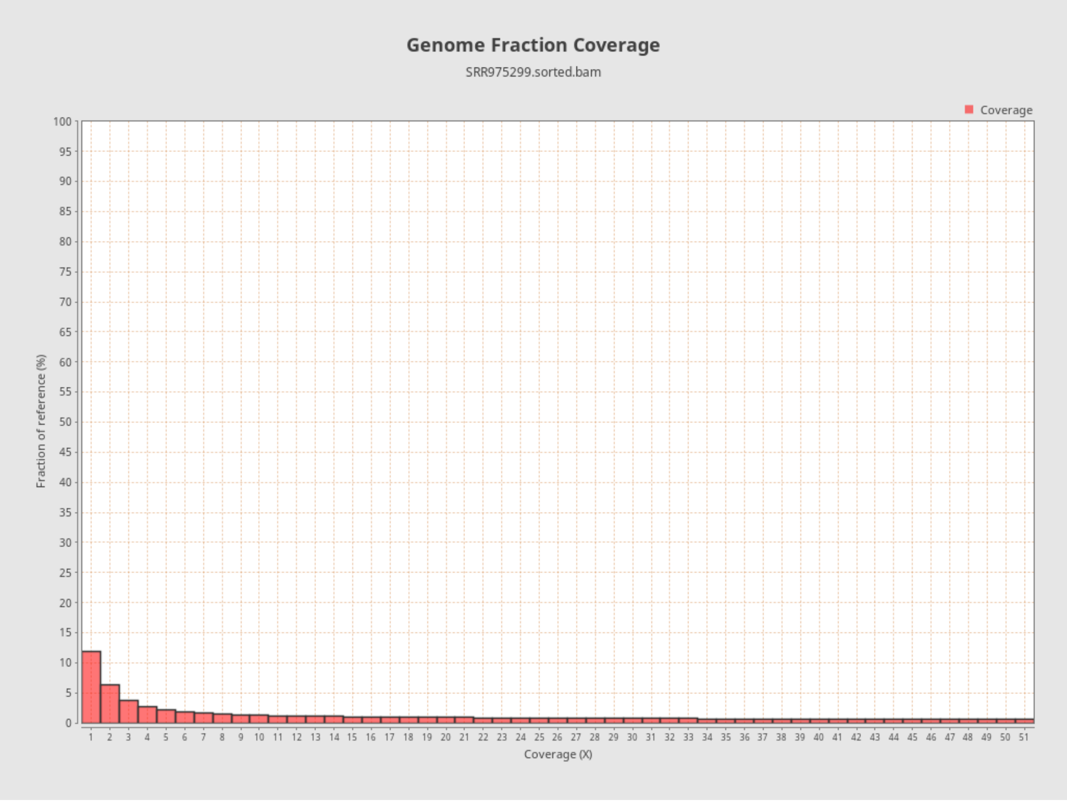
4. Results : Coverage Histogram



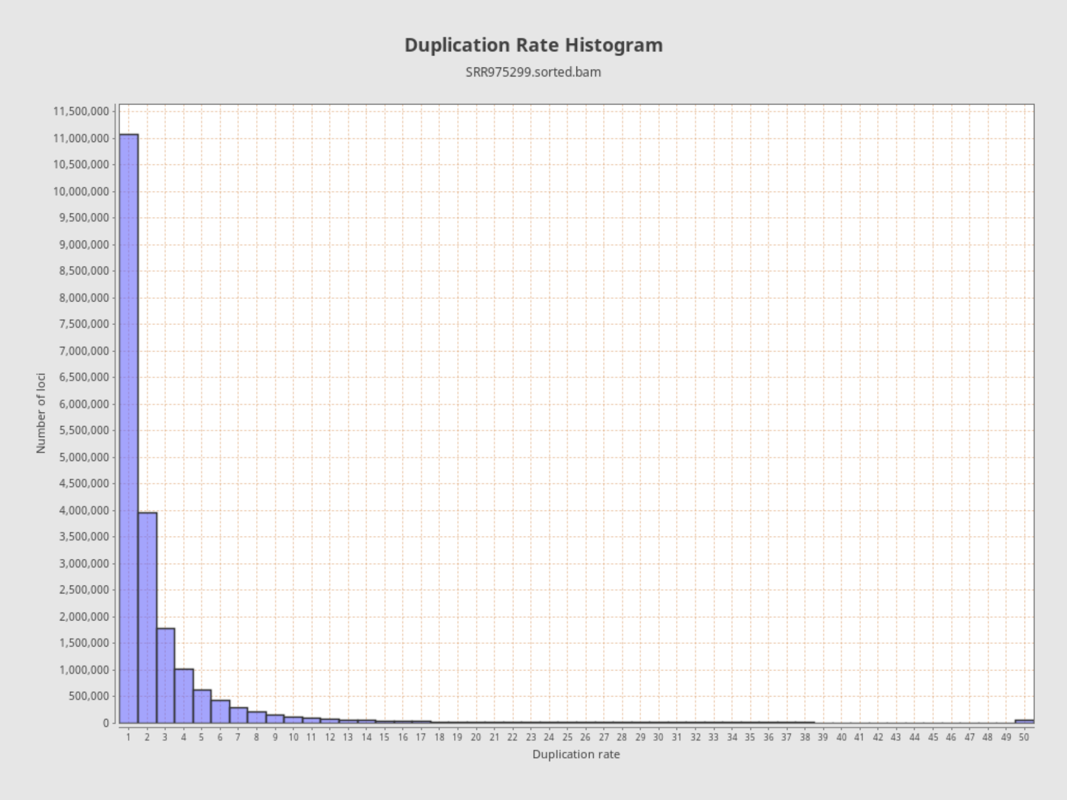
5. Results : Coverage Histogram (0-50X)



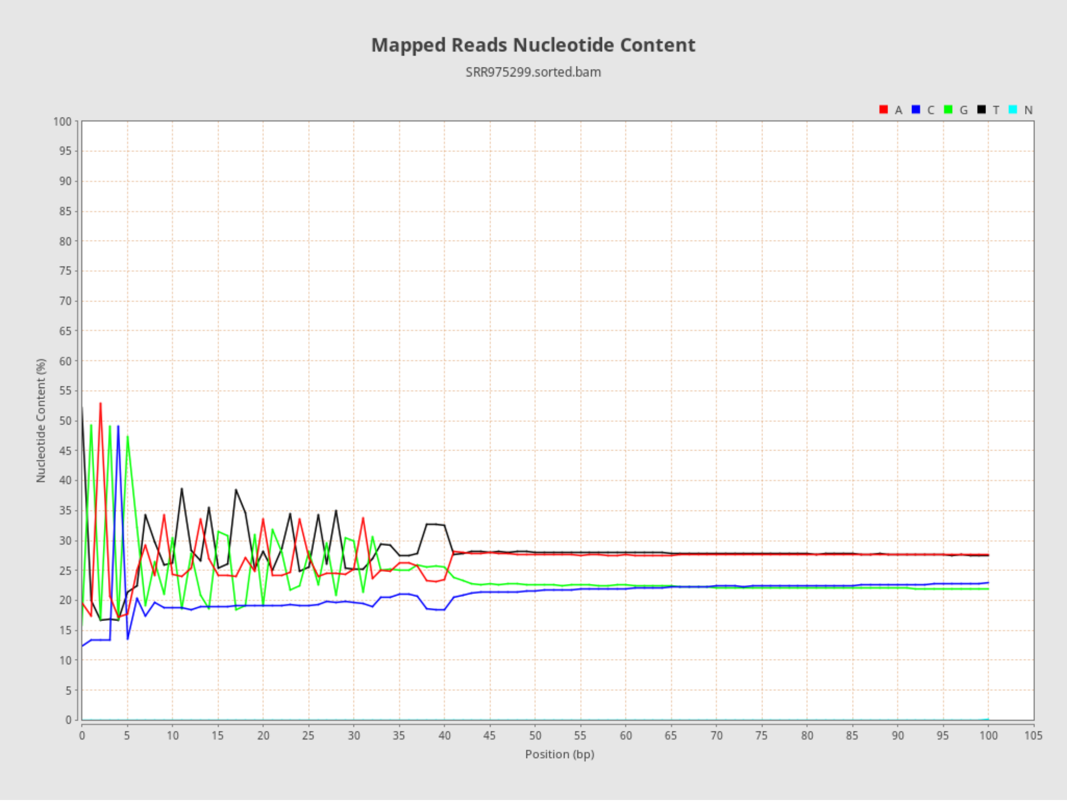
6. Results : Genome Fraction Coverage



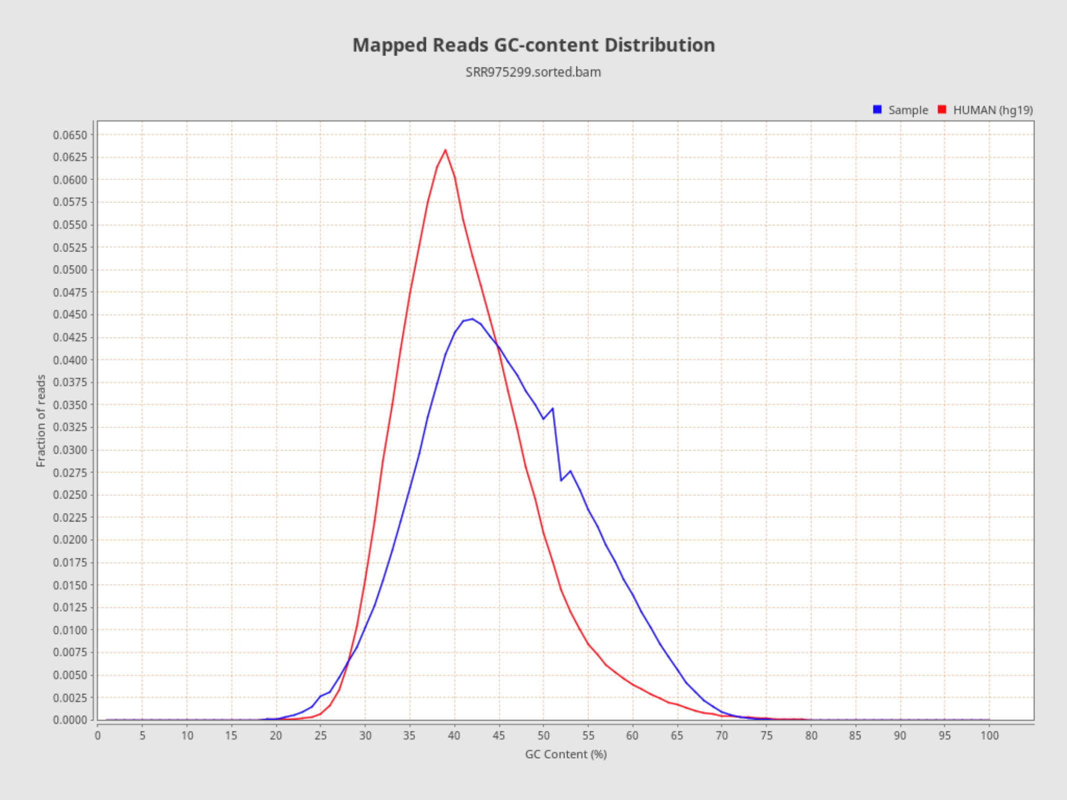
7. Results : Duplication Rate Histogram



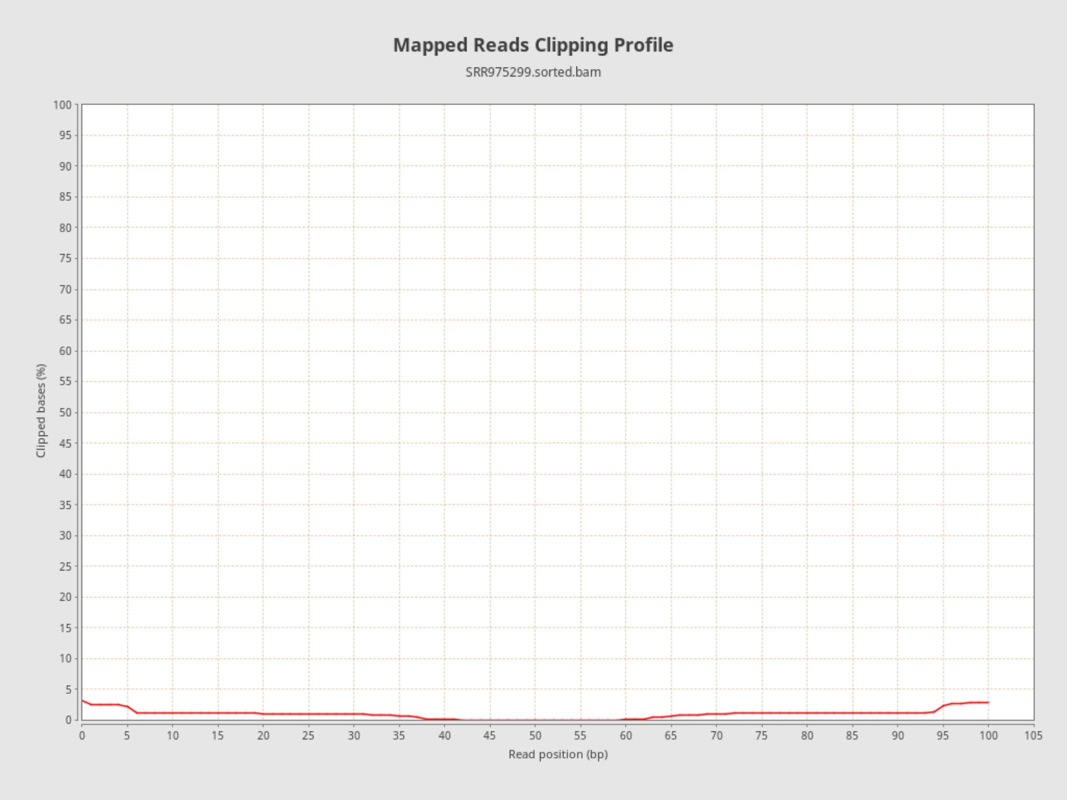
8. Results : Mapped Reads Nucleotide Content



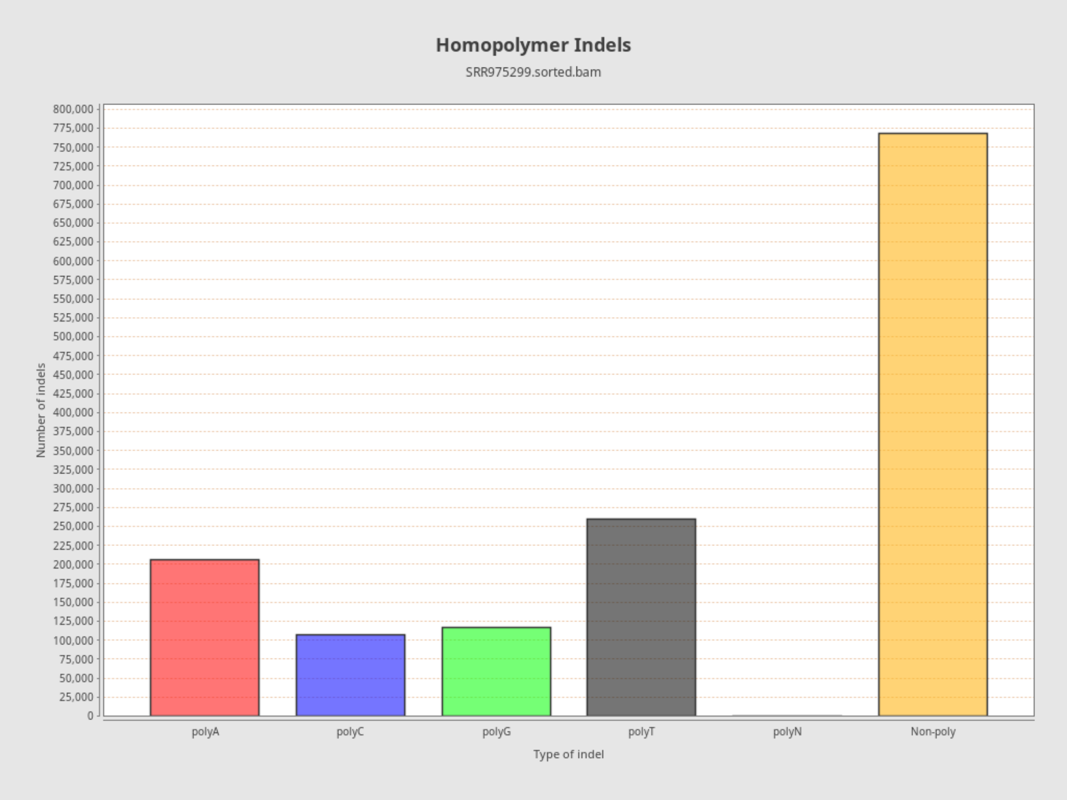
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

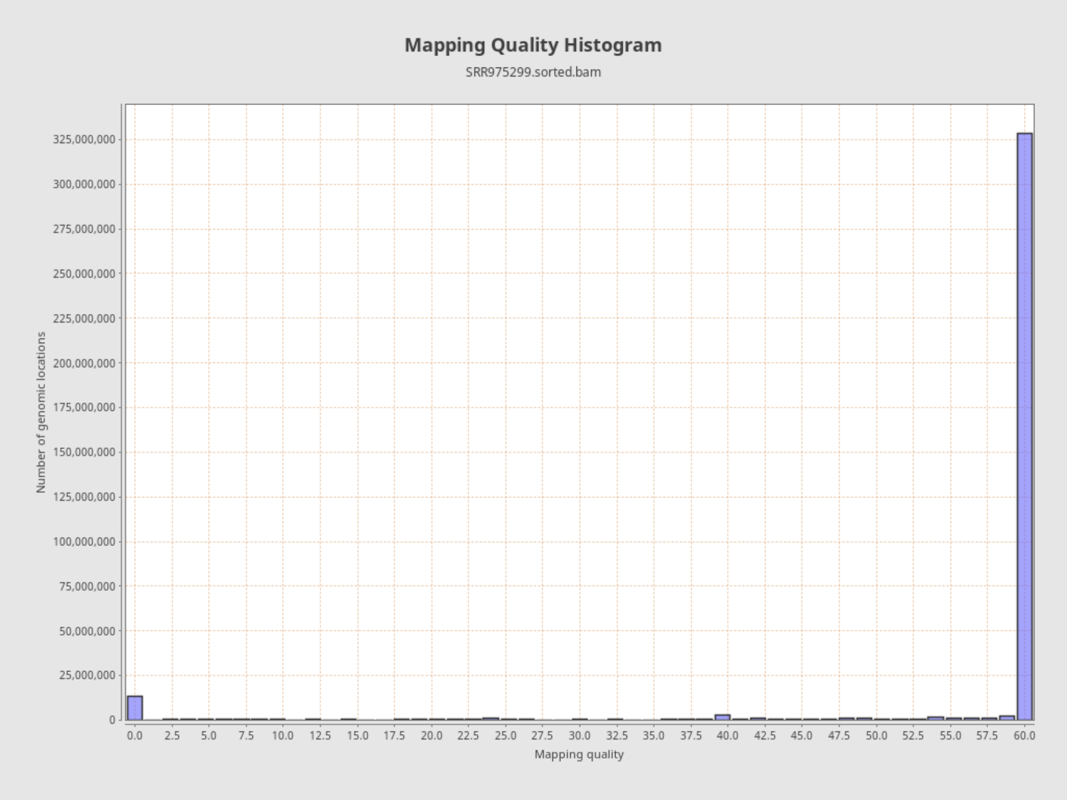


11. Results : Homopolymer Indels

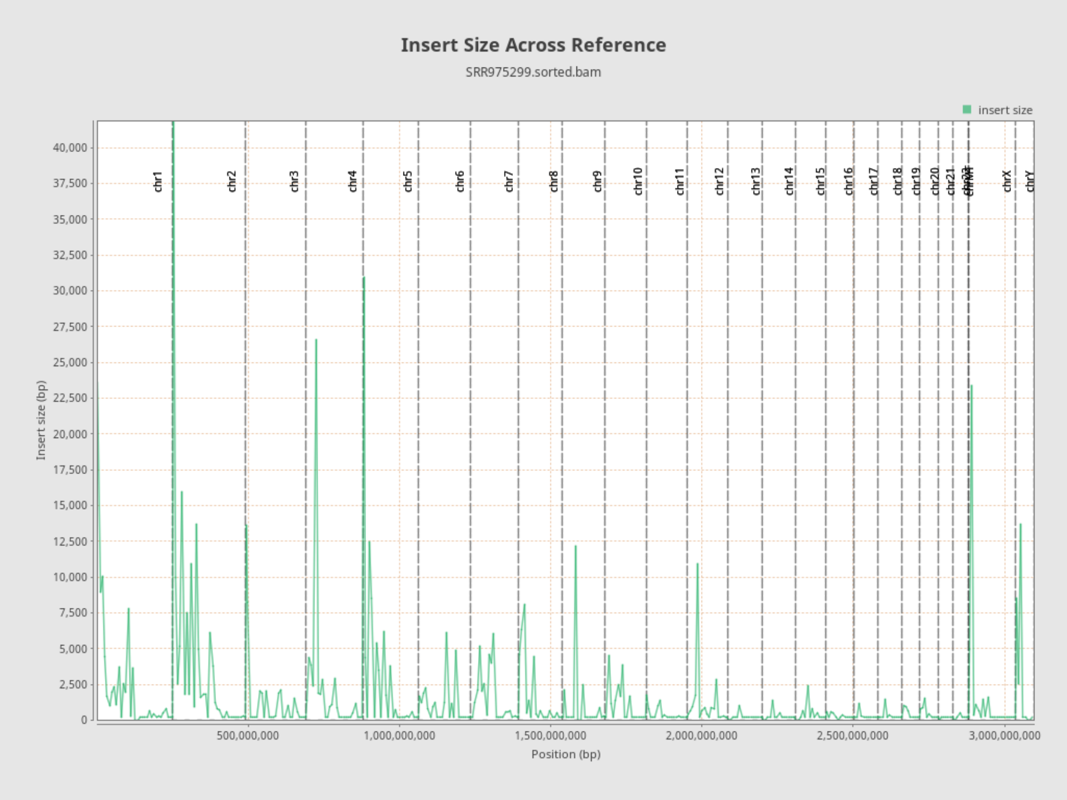


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram