Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 15:27:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975248.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_SRR975248 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975248_1.fastq.gz SRR975248_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 15:27:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975248.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	103,921,590
Mapped reads	103,435,119 / 99.53%
Unmapped reads	486,471 / 0.47%
Mapped paired reads	103,435,119 / 99.53%
Mapped reads, first in pair	51,709,037 / 49.76%
Mapped reads, second in pair	51,726,082 / 49.77%
Mapped reads, both in pair	103,201,312 / 99.31%
Mapped reads, singletons	233,807 / 0.22%
Secondary alignments	0
Supplementary alignments	206,516 / 0.2%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	65,373,087 / 62.91%
Duplication rate	47.04%
Clipped reads	63,537,437 / 61.14%

2.2. ACGT Content

Number/percentage of A's	2,577,222,001 / 27.15%
Number/percentage of C's	2,035,899,354 / 21.45%
Number/percentage of T's	2,640,769,680 / 27.82%
Number/percentage of G's	2,236,943,360 / 23.57%
Number/percentage of N's	295,207 / 0%

GC Percentage	45.02%

2.3. Coverage

Mean	3.0669
Standard Deviation	40.1865

2.4. Mapping Quality

Mean Mapping Quality	55.79

2.5. Insert size

Mean	68,274.62
Standard Deviation	2,564,656.64
P25/Median/P75	149 / 187 / 238

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	55,810,114
Insertions	1,073,363
Mapped reads with at least one insertion	1.03%
Deletions	2,103,812
Mapped reads with at least one deletion	2%
Homopolymer indels	44.37%

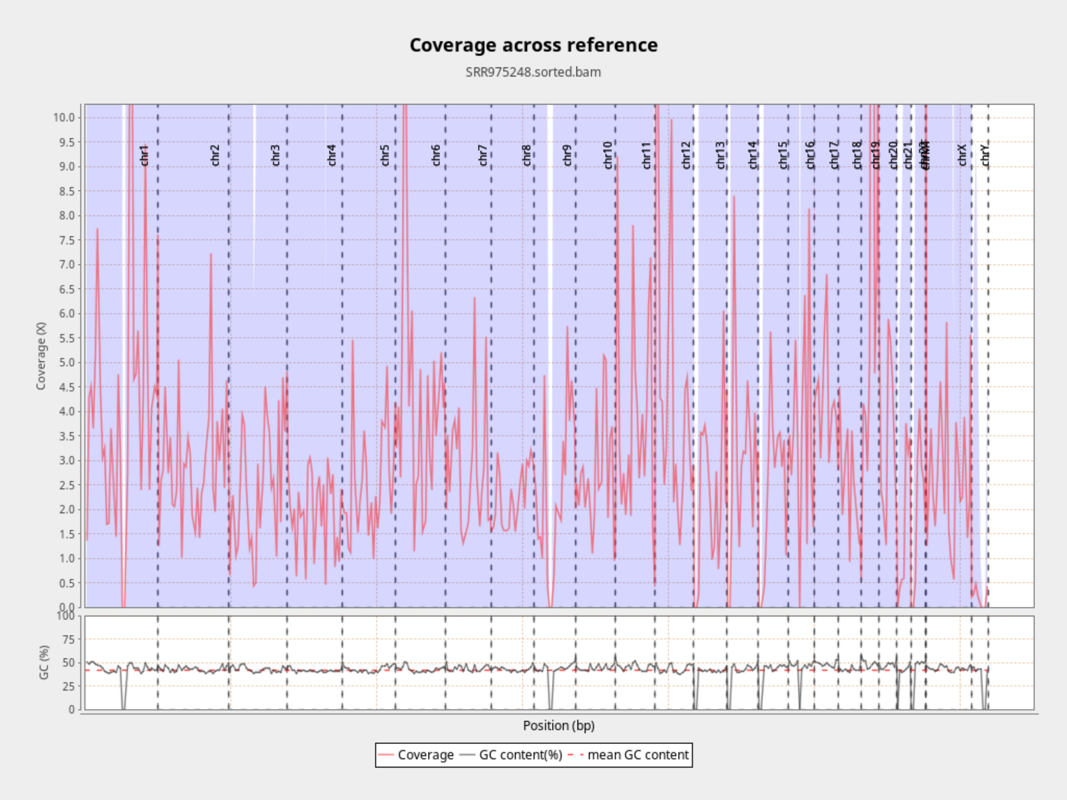
2.7. Chromosome stats

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

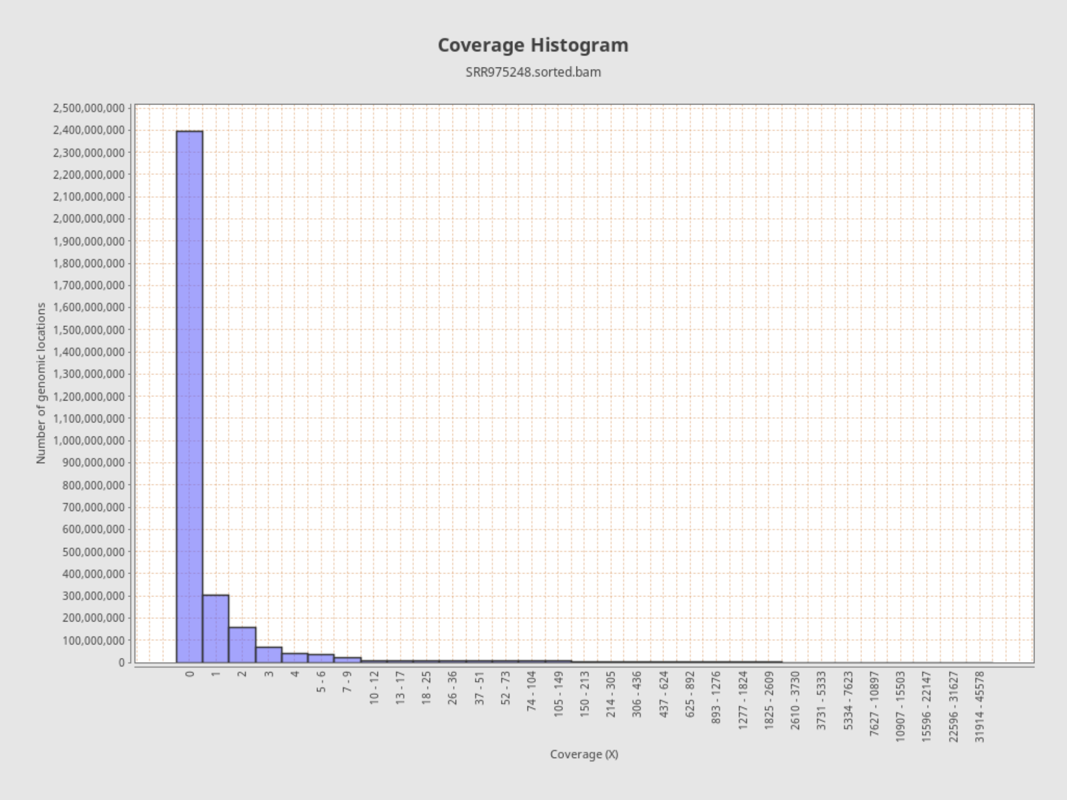
		bases	**coverage**	**deviation**
chr1	249250621	1052770216	4.2237	48.0684
chr2	243199373	717440652	2.95	34.3085
chr3	198022430	490442820	2.4767	31.1894
chr4	191154276	372256607	1.9474	38.9996
chr5	180915260	456753487	2.5247	31.8506
chr6	171115067	756527744	4.4212	52.4271
chr7	159138663	455356468	2.8614	37.2151
chr8	146364022	334664660	2.2865	29.4847
chr9	141213431	327292976	2.3177	29.3906
chr10	135534747	377723999	2.7869	34.7444
chr11	135006516	537734269	3.983	44.9837
chr12	133851895	611310418	4.5671	51.5578
chr13	115169878	258993729	2.2488	31.9929
chr14	107349540	310822203	2.8954	37.3204
chr15	102531392	253892950	2.4762	31.1772
chr16	90354753	322376964	3.5679	40.191
chr17	81195210	350579227	4.3177	43.0538
chr18	78077248	201442669	2.58	34.0001
chr19	59128983	463093924	7.8319	99.0593
chr20	63025520	234915309	3.7273	45.1121
chr21	48129895	82499605	1.7141	28.7561
chr22	51304566	104237319	2.0317	25.7892
chrMT	16571	232940	14.0571	23.3053
chrX	155270560	408869522	2.6333	35.5536

chrY	59373566	12059253	0.2031	4.8044

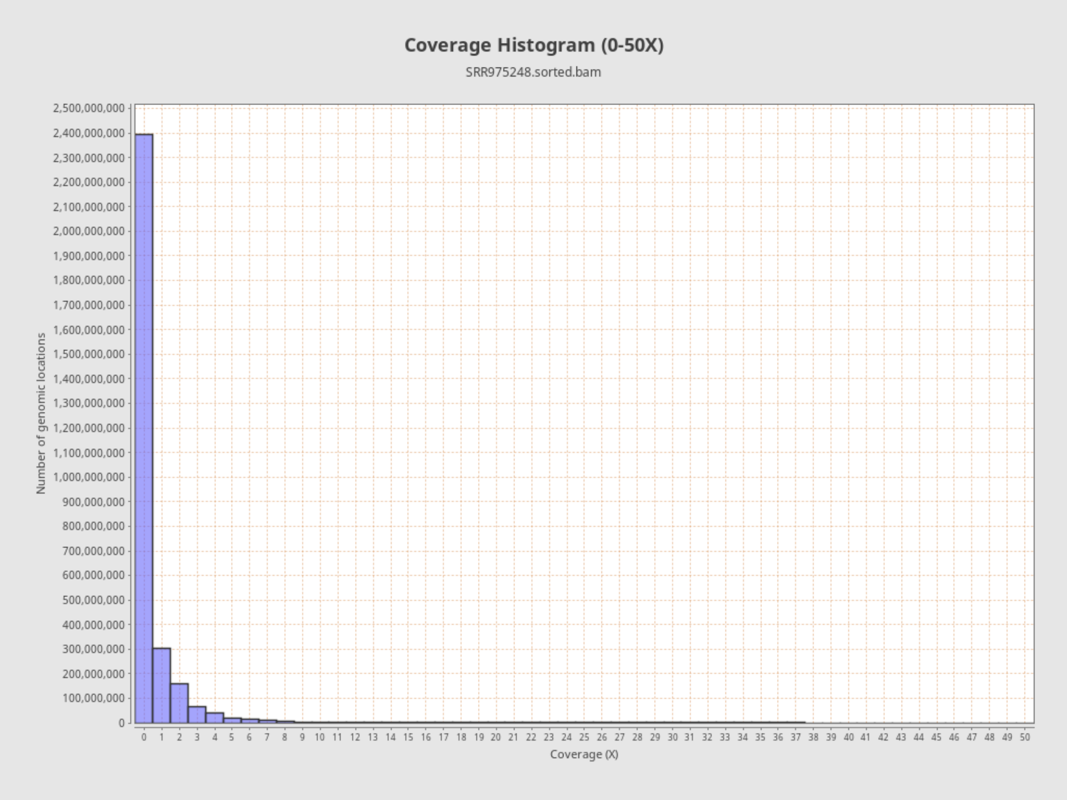
3. Results : Coverage across reference



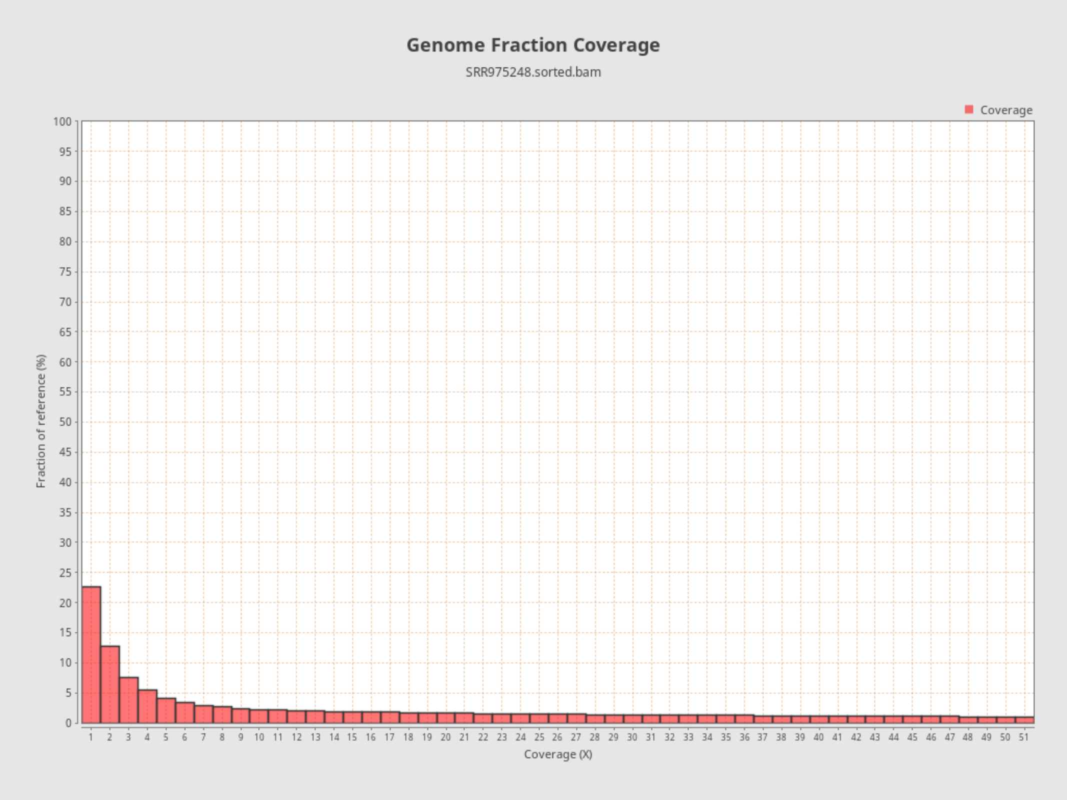
4. Results : Coverage Histogram



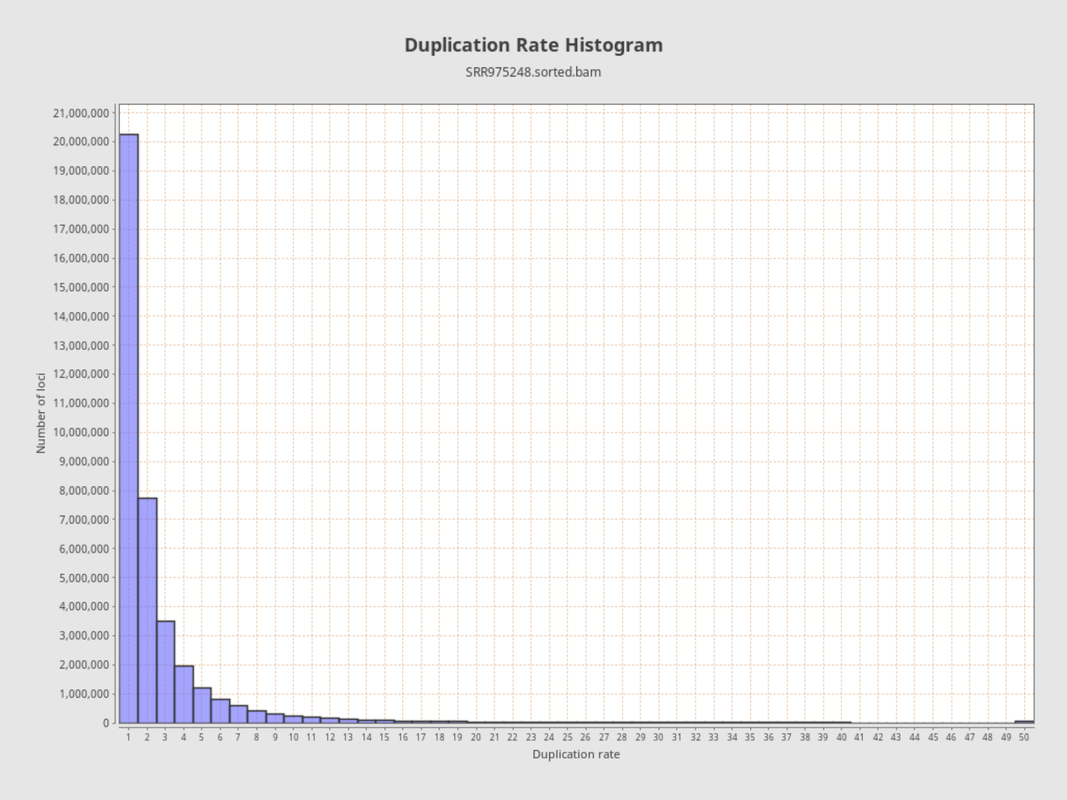
5. Results : Coverage Histogram (0-50X)



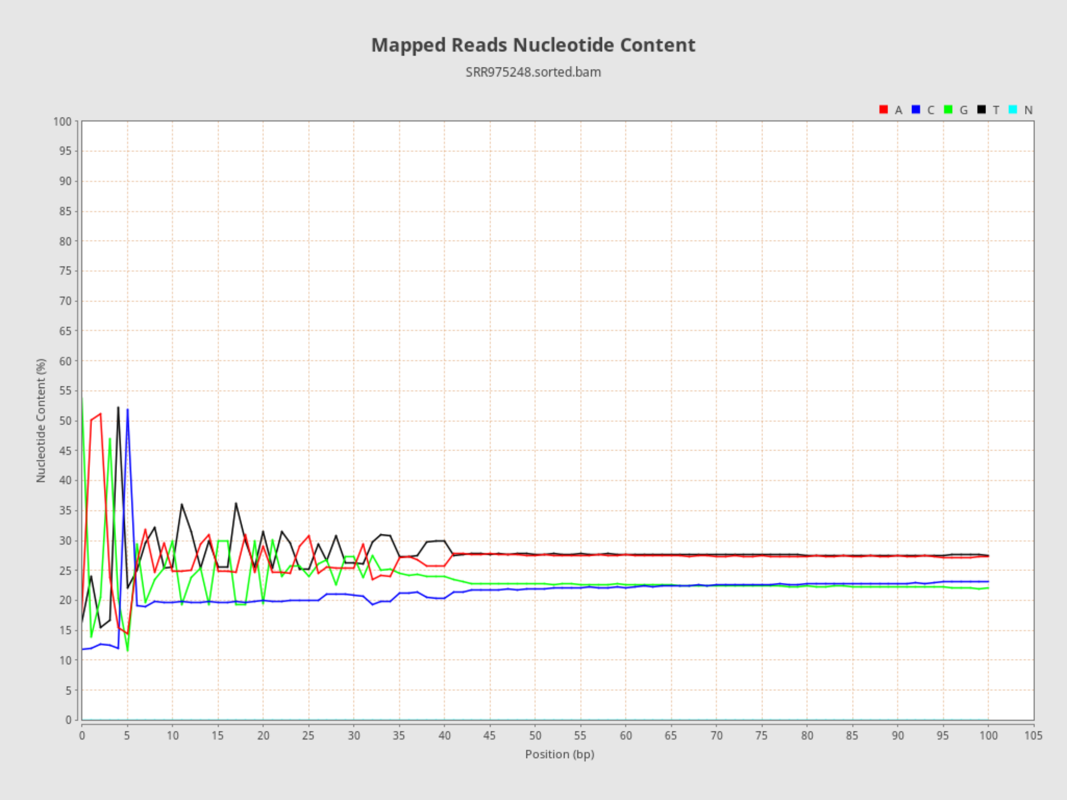
6. Results : Genome Fraction Coverage



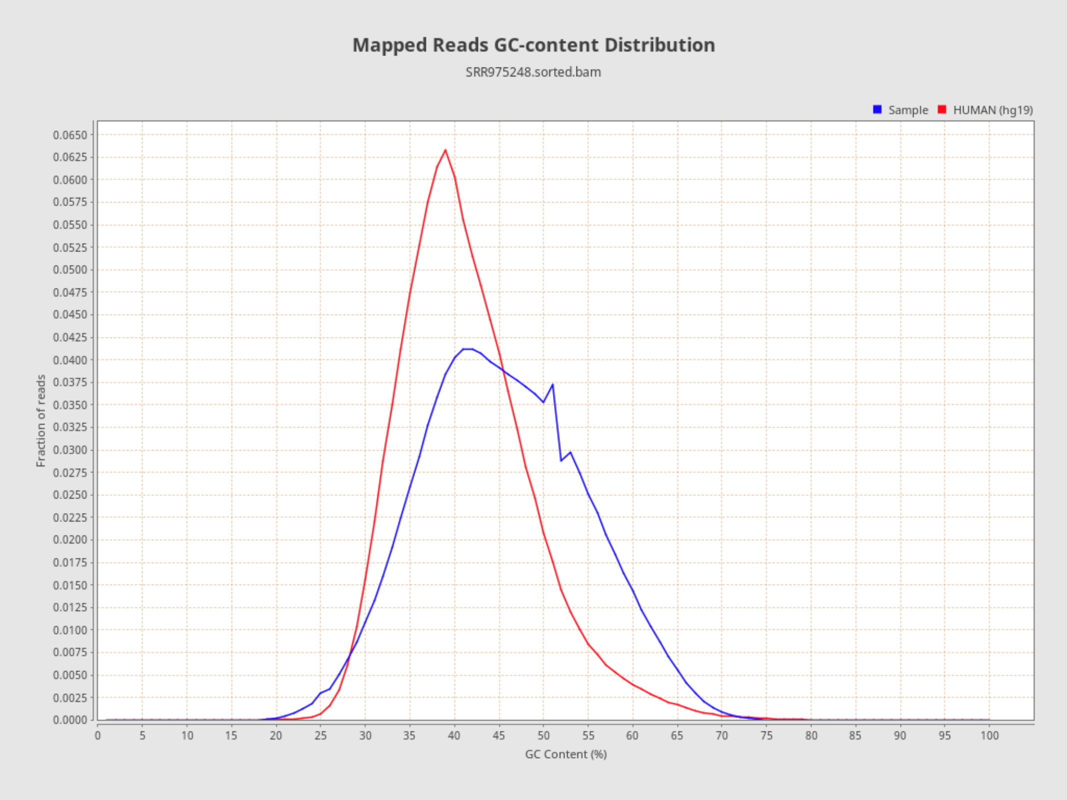
7. Results : Duplication Rate Histogram



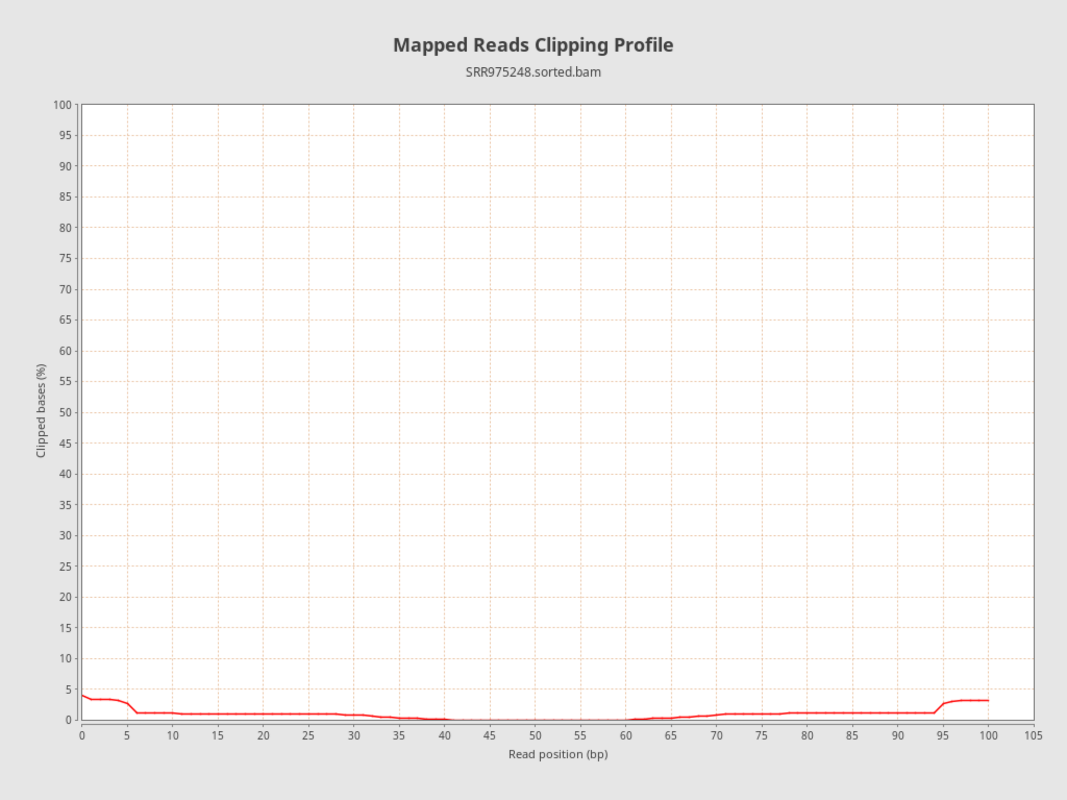
8. Results : Mapped Reads Nucleotide Content



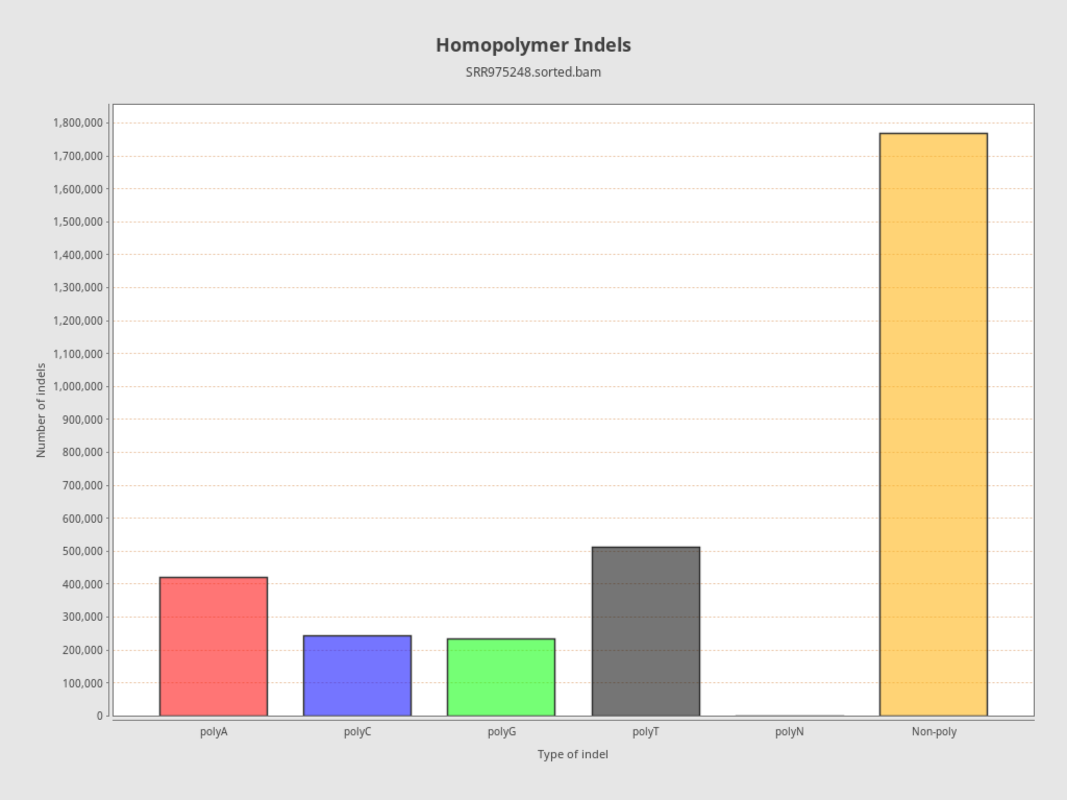
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

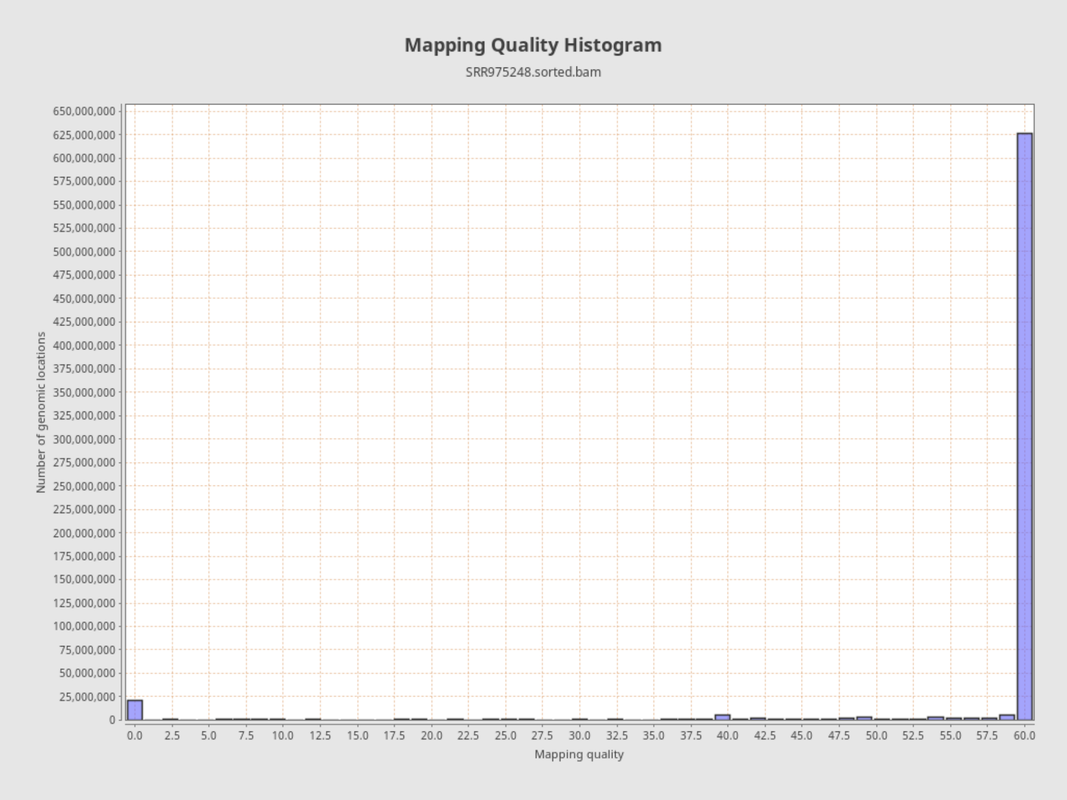


11. Results : Homopolymer Indels

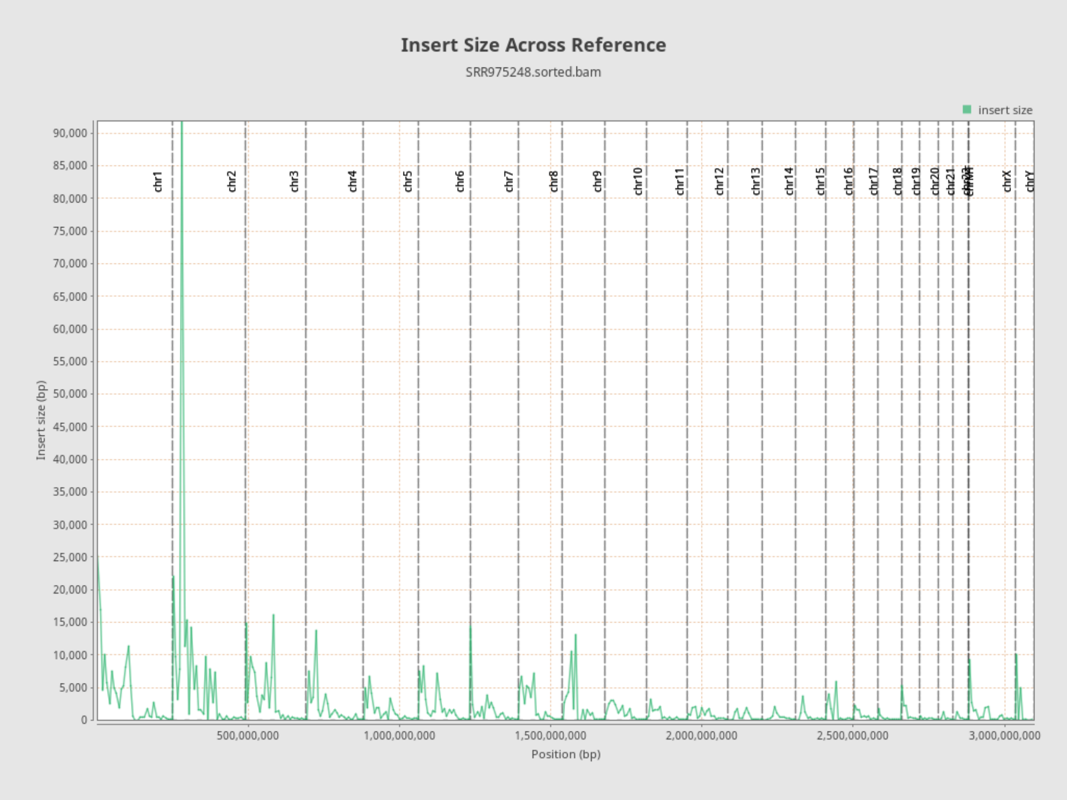


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram