Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 17:28:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975250.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_SRR975250 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975250_1.fastq.gz SRR975250_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 17:28:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975250.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	116,022,292
Mapped reads	115,473,156 / 99.53%
Unmapped reads	549,136 / 0.47%
Mapped paired reads	115,473,156 / 99.53%
Mapped reads, first in pair	57,725,168 / 49.75%
Mapped reads, second in pair	57,747,988 / 49.77%
Mapped reads, both in pair	115,207,452 / 99.3%
Mapped reads, singletons	265,704 / 0.23%
Secondary alignments	0
Supplementary alignments	235,508 / 0.2%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	76,248,053 / 65.72%
Duplication rate	49.68%
Clipped reads	69,170,978 / 59.62%

2.2. ACGT Content

Number/percentage of A's	2,855,245,259 / 26.83%
Number/percentage of C's	2,304,529,788 / 21.65%
Number/percentage of T's	2,995,440,056 / 28.15%
Number/percentage of G's	2,486,873,677 / 23.37%
Number/percentage of N's	310,415 / 0%

GC Percentage	45.02%

2.3. Coverage

Mean	3.439
Standard Deviation	45.5712

2.4. Mapping Quality

Mean Mapping Quality	55.94

2.5. Insert size

Mean	58,677.33
Standard Deviation	2,376,816.09
P25/Median/P75	148 / 184 / 233

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	62,675,177
Insertions	1,182,918
Mapped reads with at least one insertion	1.01%
Deletions	2,437,326
Mapped reads with at least one deletion	2.08%
Homopolymer indels	45.28%

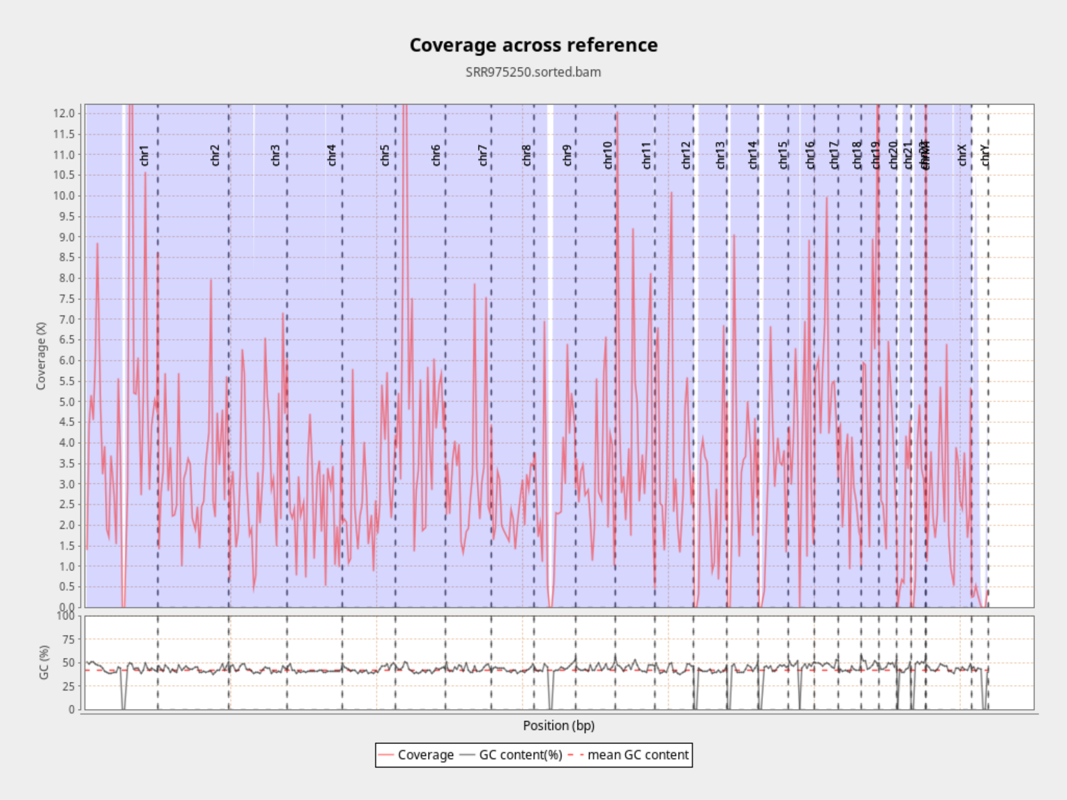
2.7. Chromosome stats

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

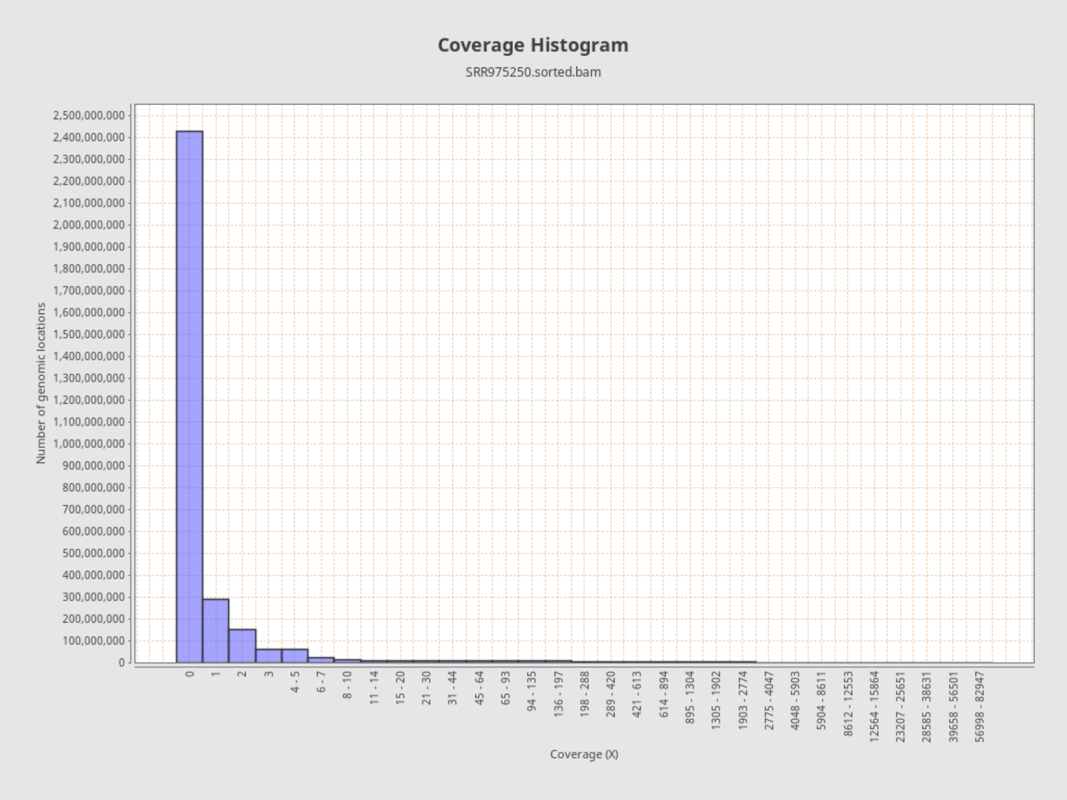
		bases	coverage	deviation
chr1	249250621	1181764669	4.7413	54.0133
chr2	243199373	801244519	3.2946	40.7793
chr3	198022430	665483009	3.3606	41.7964
chr4	191154276	480404325	2.5132	60.5361
chr5	180915260	497991470	2.7526	36.5454
chr6	171115067	926712998	5.4157	66.807
chr7	159138663	516961502	3.2485	43.6561
chr8	146364022	354090855	2.4192	32.0109
chr9	141213431	393983097	2.79	34.8801
chr10	135534747	443484629	3.2721	41.9192
chr11	135006516	623918543	4.6214	52.4874
chr12	133851895	531826572	3.9732	42.9143
chr13	115169878	272709355	2.3679	37.4613
chr14	107349540	342123662	3.187	40.3573
chr15	102531392	293763511	2.8651	34.7765
chr16	90354753	356935126	3.9504	46.7403
chr17	81195210	462090912	5.6911	57.5457
chr18	78077248	230821175	2.9563	42.3498
chr19	59128983	360070828	6.0896	59.276
chr20	63025520	245650735	3.8976	49.2011
chr21	48129895	93882998	1.9506	30.9579
chr22	51304566	128240008	2.4996	31.8927
chrMT	16571	214946	12.9712	23.6979
chrX	155270560	428424185	2.7592	38.7418

chrY	59373566	13207068	0.2224	5.3801

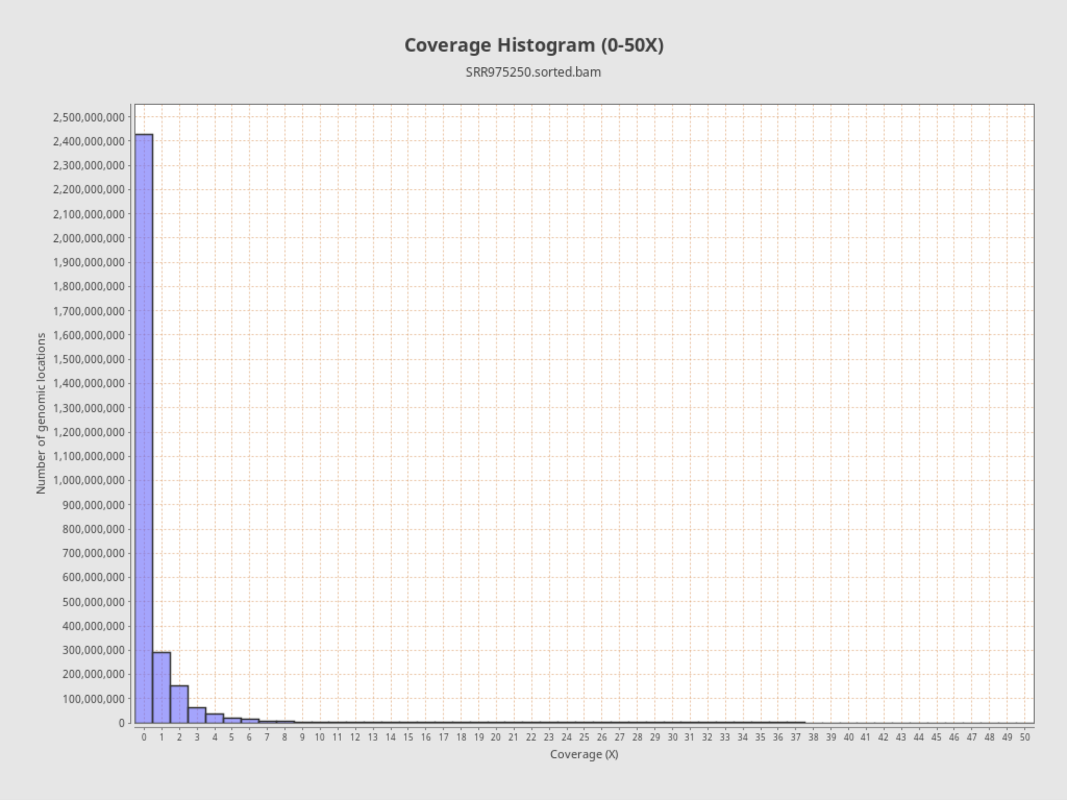
3. Results : Coverage across reference



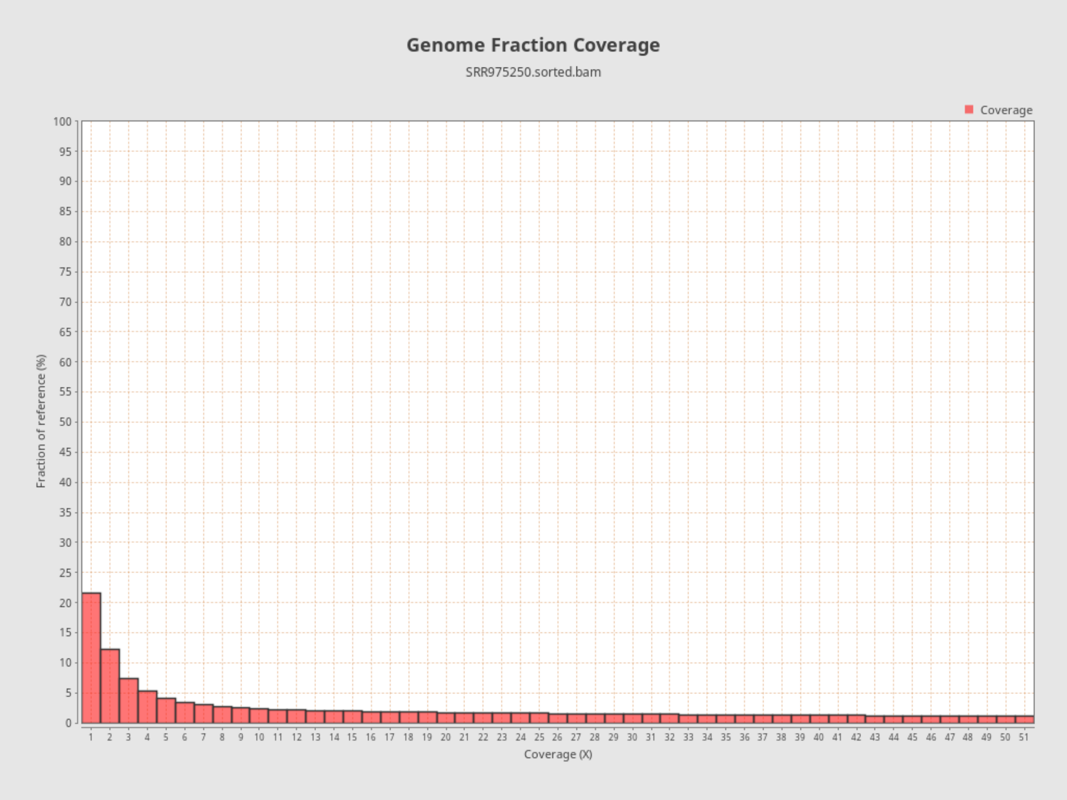
4. Results : Coverage Histogram



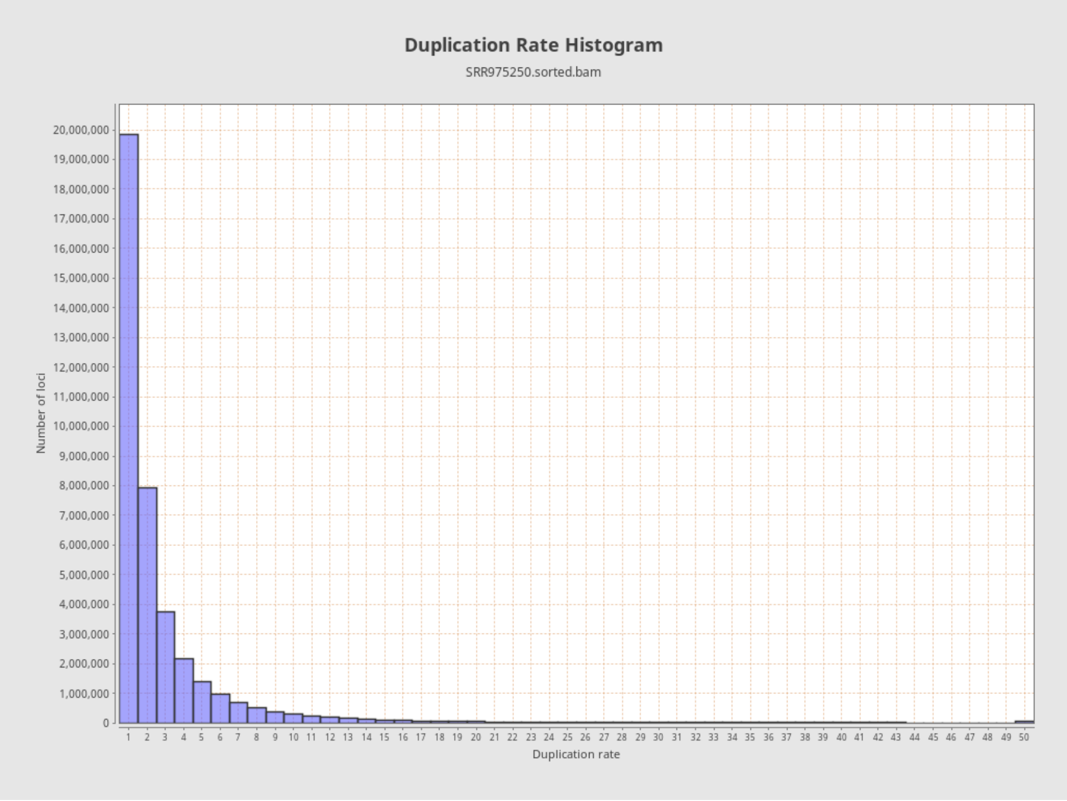
5. Results : Coverage Histogram (0-50X)



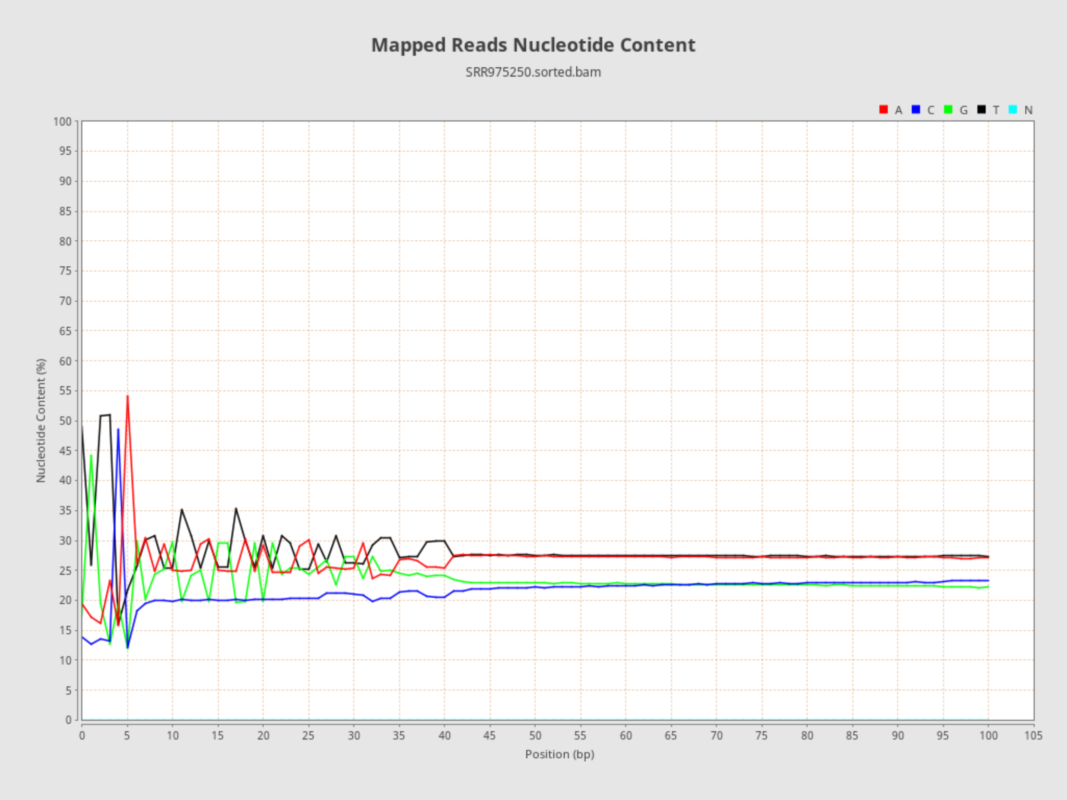
6. Results : Genome Fraction Coverage



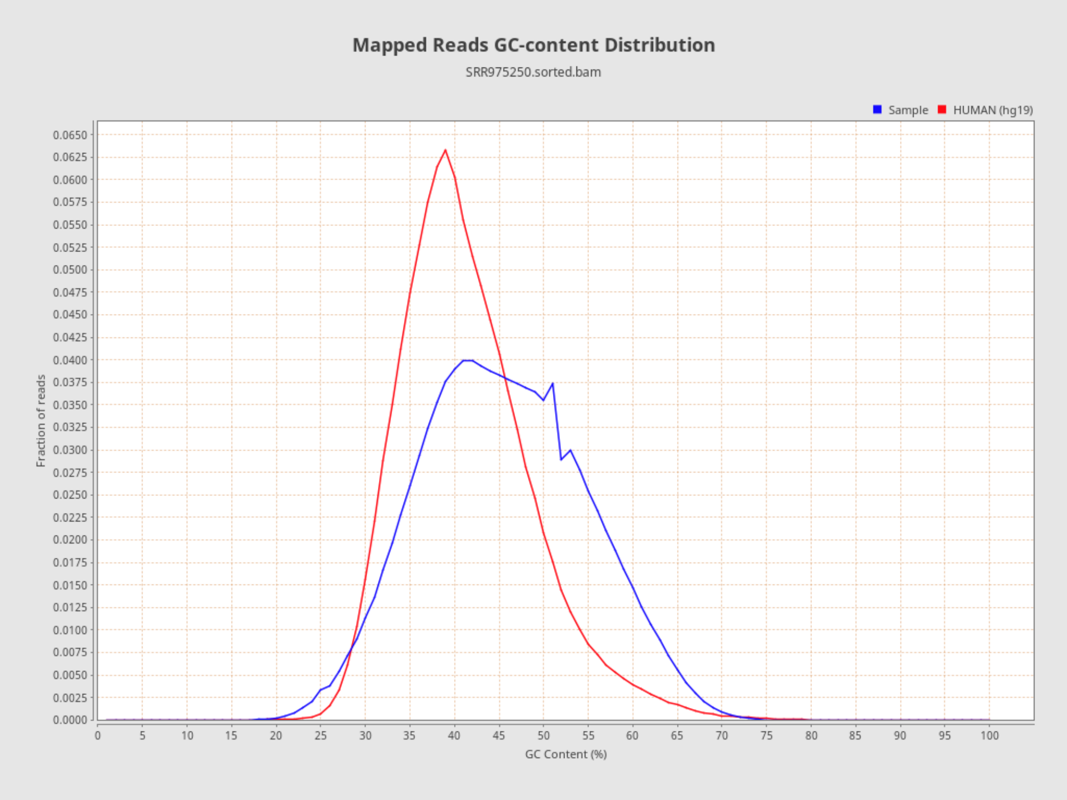
7. Results : Duplication Rate Histogram



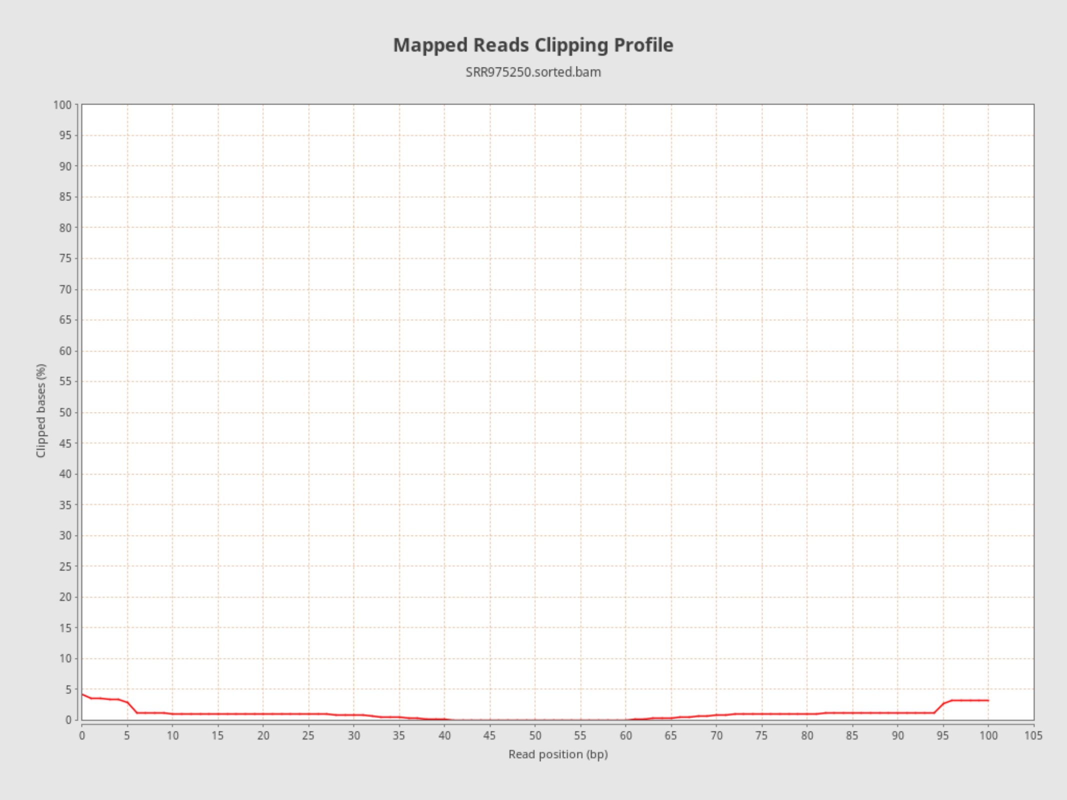
8. Results : Mapped Reads Nucleotide Content



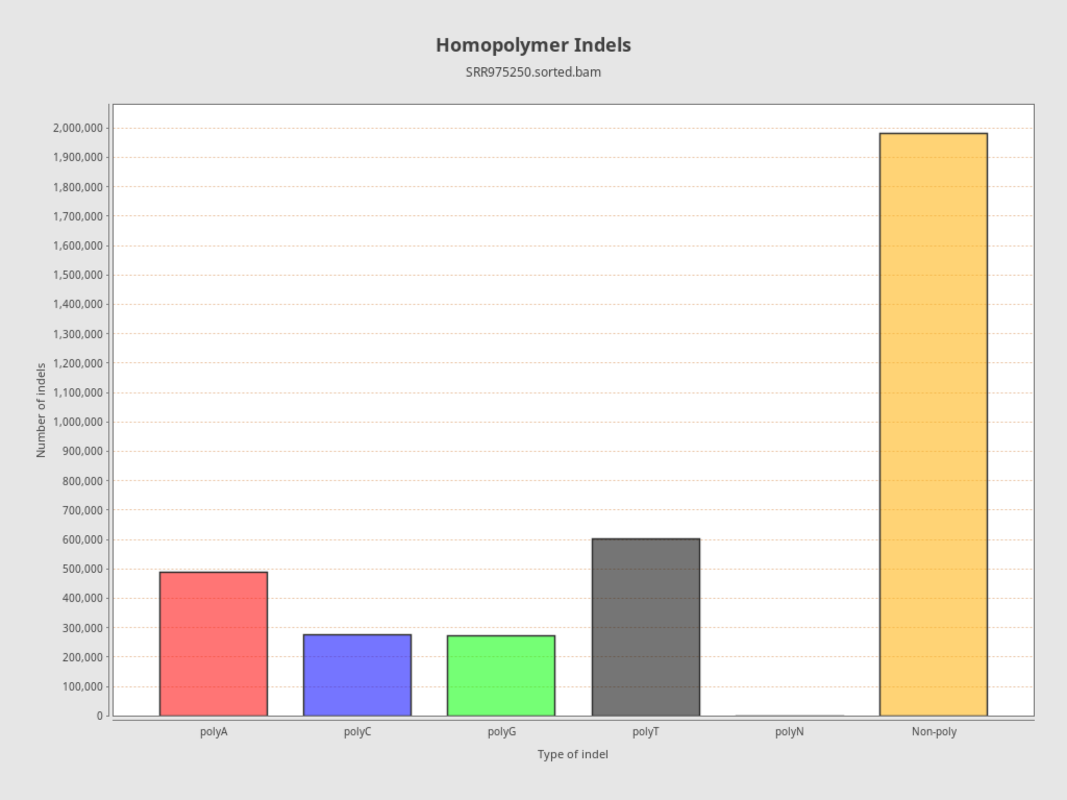
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

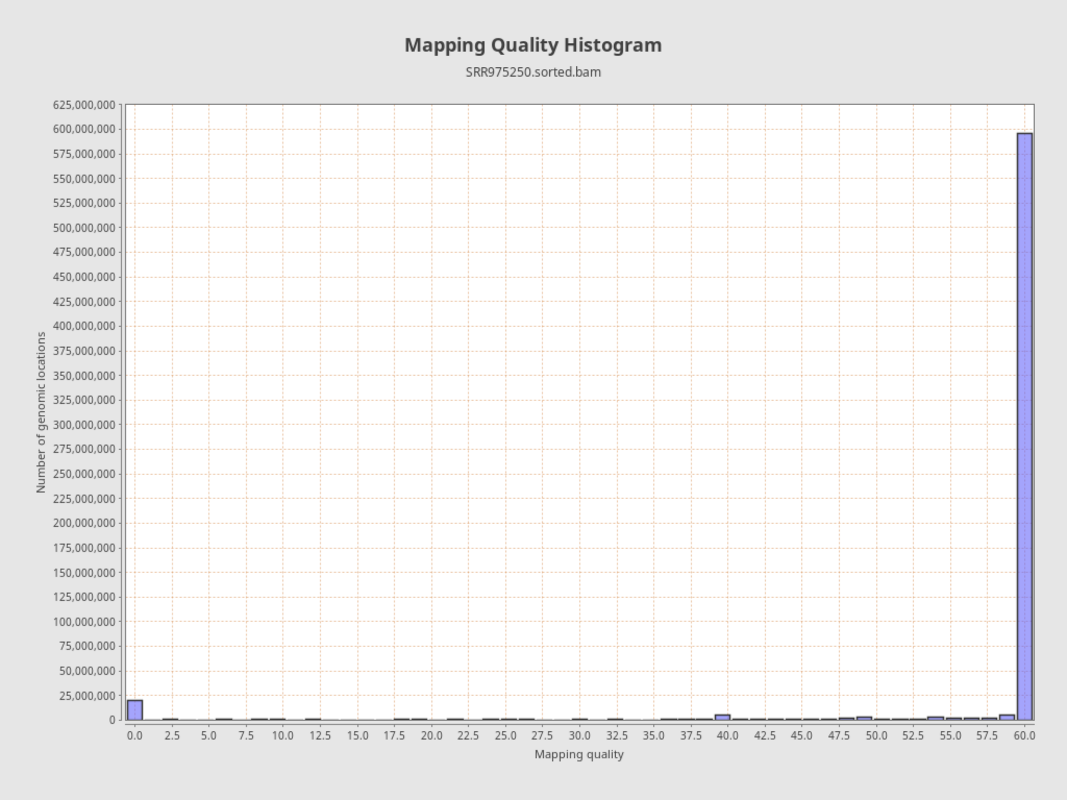


11. Results : Homopolymer Indels

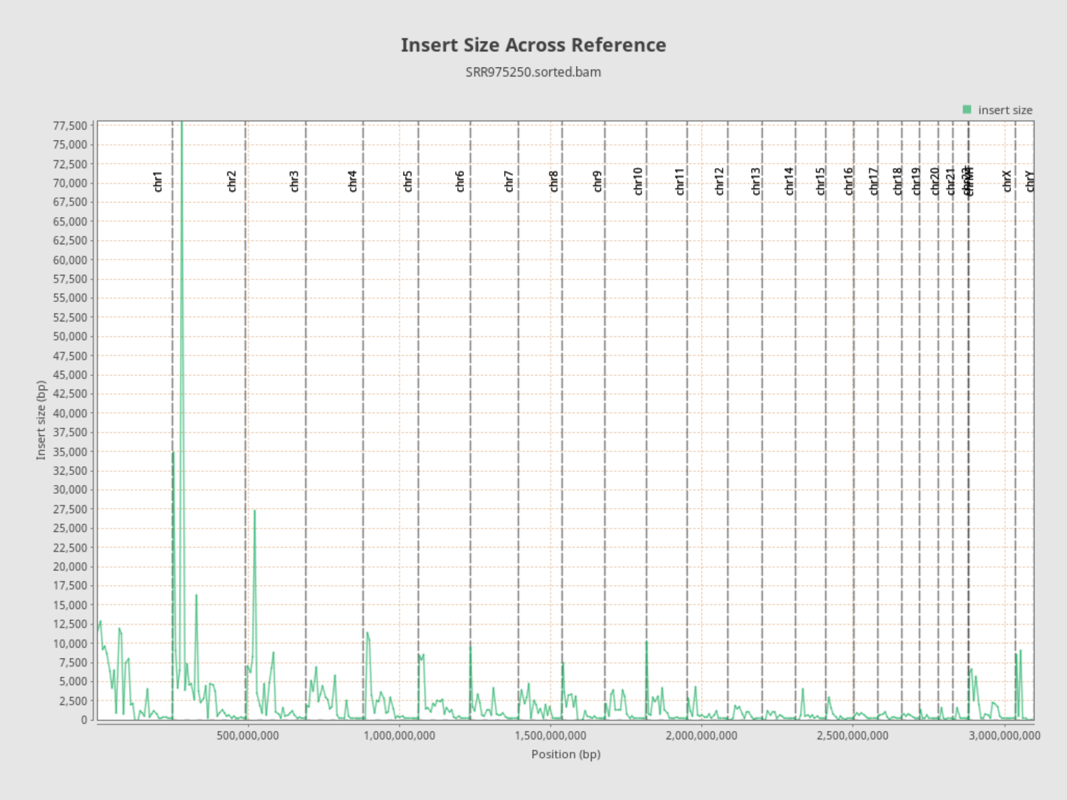


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram