Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/08 05:19:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975260.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_SRR975260 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975260_1.fastq.gz SRR975260_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 08 05:19:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975260.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	141,845,710
Mapped reads	140,818,675 / 99.28%
Unmapped reads	1,027,035 / 0.72%
Mapped paired reads	140,818,675 / 99.28%
Mapped reads, first in pair	70,371,046 / 49.61%
Mapped reads, second in pair	70,447,629 / 49.66%
Mapped reads, both in pair	140,475,850 / 99.03%
Mapped reads, singletons	342,825 / 0.24%
Secondary alignments	0
Supplementary alignments	300,517 / 0.21%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	93,123,641 / 65.65%
Duplication rate	45.23%
Clipped reads	85,014,522 / 59.93%

2.2. ACGT Content

Number/percentage of A's	3,399,700,494 / 26.54%
Number/percentage of C's	2,771,818,518 / 21.64%
Number/percentage of T's	3,525,595,557 / 27.52%
Number/percentage of G's	3,111,799,117 / 24.29%
Number/percentage of N's	331,866 / 0%

GC Percentage	45.93%

2.3. Coverage

Mean	4.1392
Standard Deviation	52.5502

2.4. Mapping Quality

Mean Mapping Quality	55.57

2.5. Insert size

Mean	108,706.89
Standard Deviation	3,264,572.75
P25/Median/P75	144 / 182 / 232

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	79,603,162
Insertions	1,141,050
Mapped reads with at least one insertion	0.8%
Deletions	3,052,749
Mapped reads with at least one deletion	2.13%
Homopolymer indels	47.06%

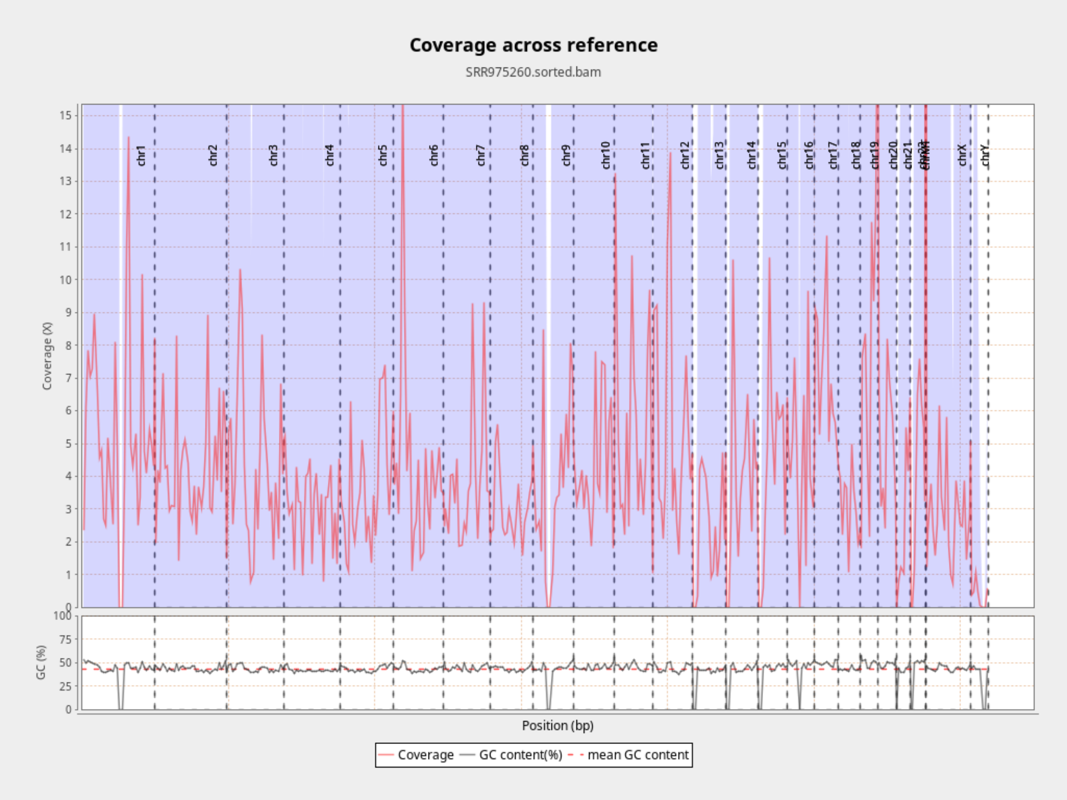
2.7. Chromosome stats

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

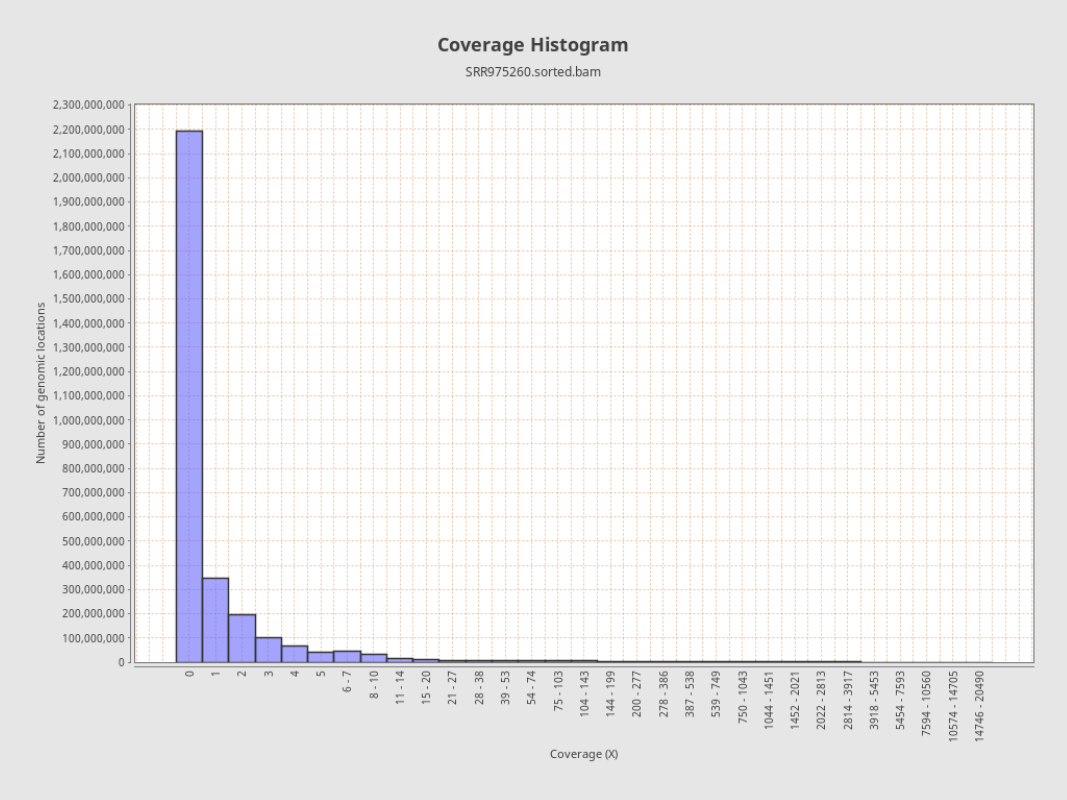
		bases	coverage	deviation
chr1	249250621	1318074249	5.2881	60.5979
chr2	243199373	1034610396	4.2542	51.8406
chr3	198022430	852628120	4.3057	54.0044
chr4	191154276	582900356	3.0494	41.6568
chr5	180915260	658437706	3.6395	48.7416
chr6	171115067	758888023	4.435	55.3981
chr7	159138663	608542867	3.824	50.9347
chr8	146364022	440005552	3.0062	39.0989
chr9	141213431	514089633	3.6405	47.8985
chr10	135534747	592279985	4.3699	56.7137
chr11	135006516	739662315	5.4787	63.614
chr12	133851895	734518886	5.4875	61.5173
chr13	115169878	272926927	2.3698	36.1474
chr14	107349540	417518914	3.8893	49.4819
chr15	102531392	448793910	4.3771	55.1492
chr16	90354753	411861971	4.5583	53.8561
chr17	81195210	582332775	7.172	72.9523
chr18	78077248	243702156	3.1213	44.3829
chr19	59128983	482261475	8.1561	78.5432
chr20	63025520	313845312	4.9797	64.4005
chr21	48129895	129823022	2.6973	41.1032
chr22	51304566	214699358	4.1848	51.7418
chrMT	16571	774881	46.7613	51.536
chrX	155270560	438335773	2.823	39.1023

chrY	59373566	22300249	0.3756	10.1505

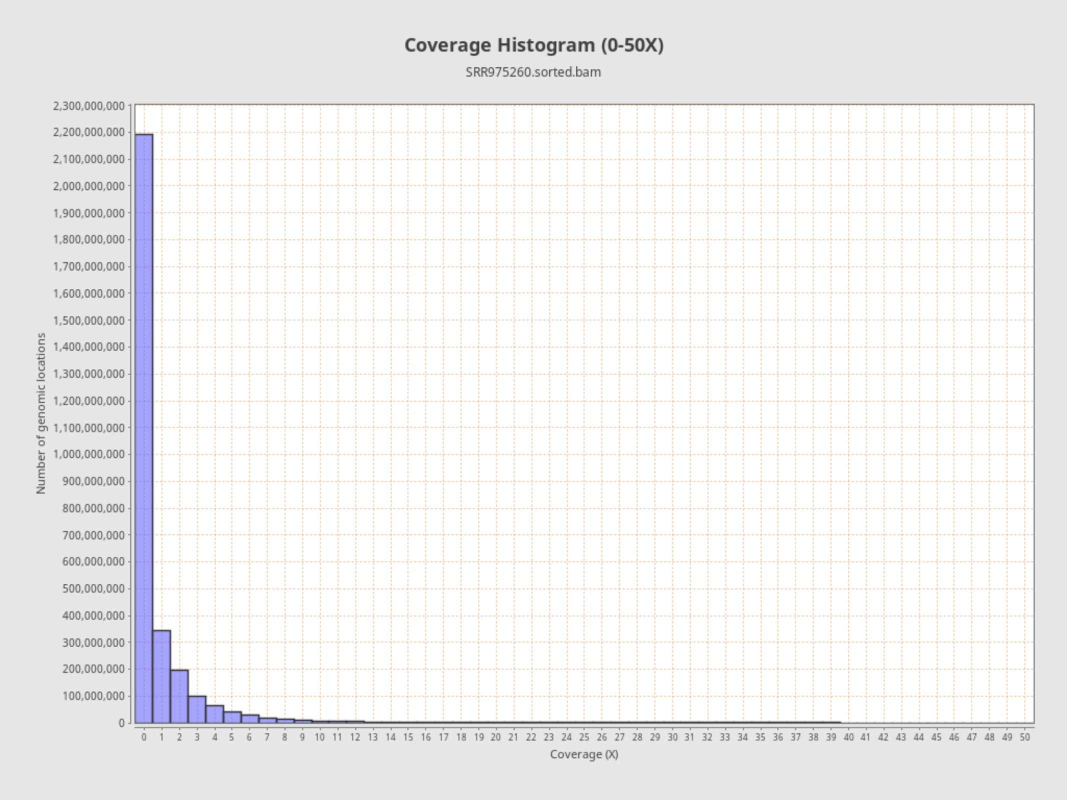
3. Results : Coverage across reference



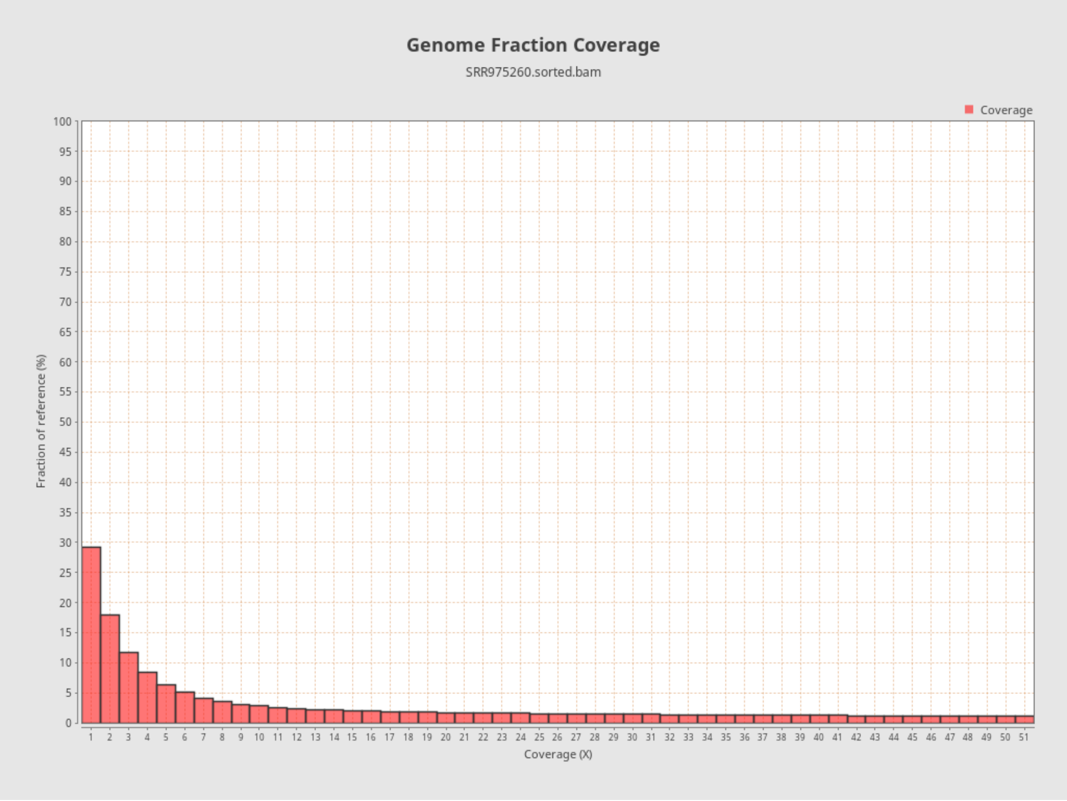
4. Results : Coverage Histogram



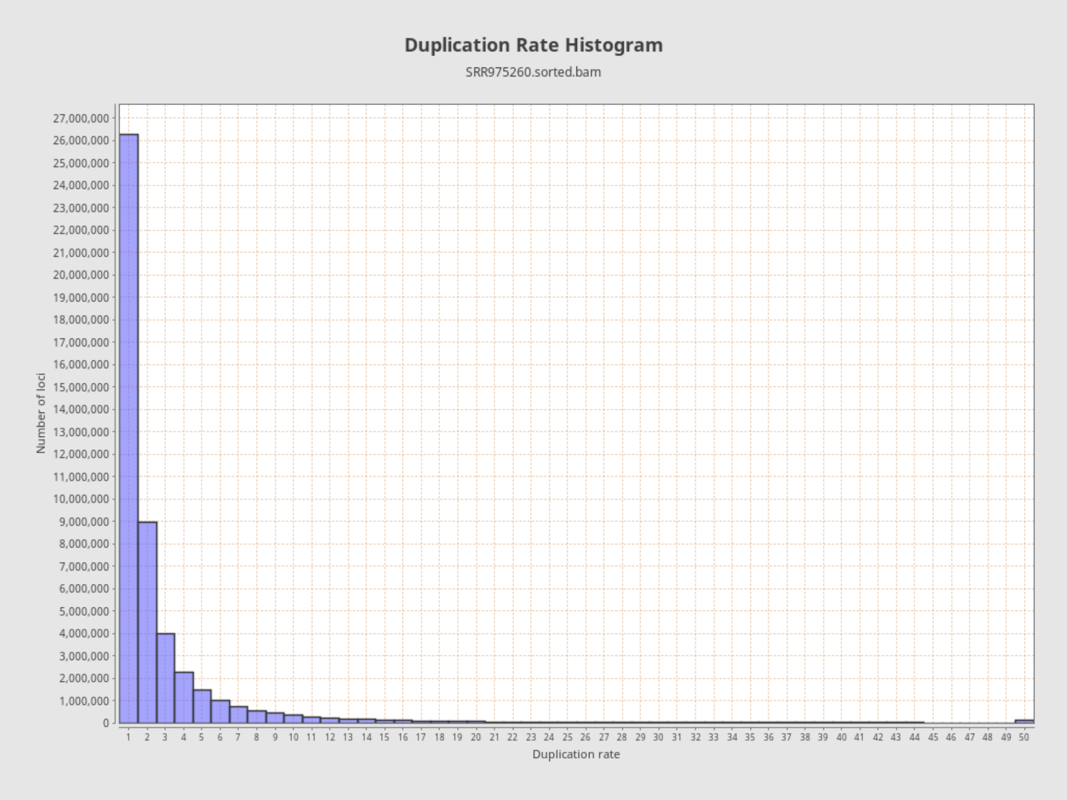
5. Results : Coverage Histogram (0-50X)



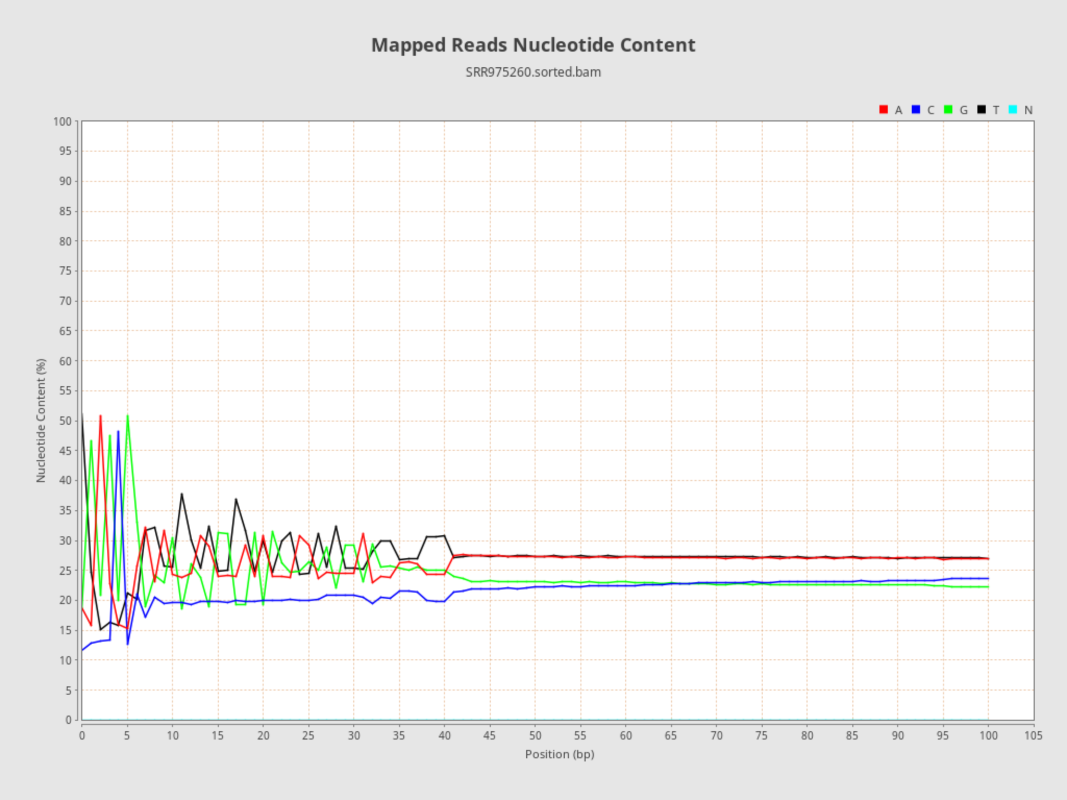
6. Results : Genome Fraction Coverage



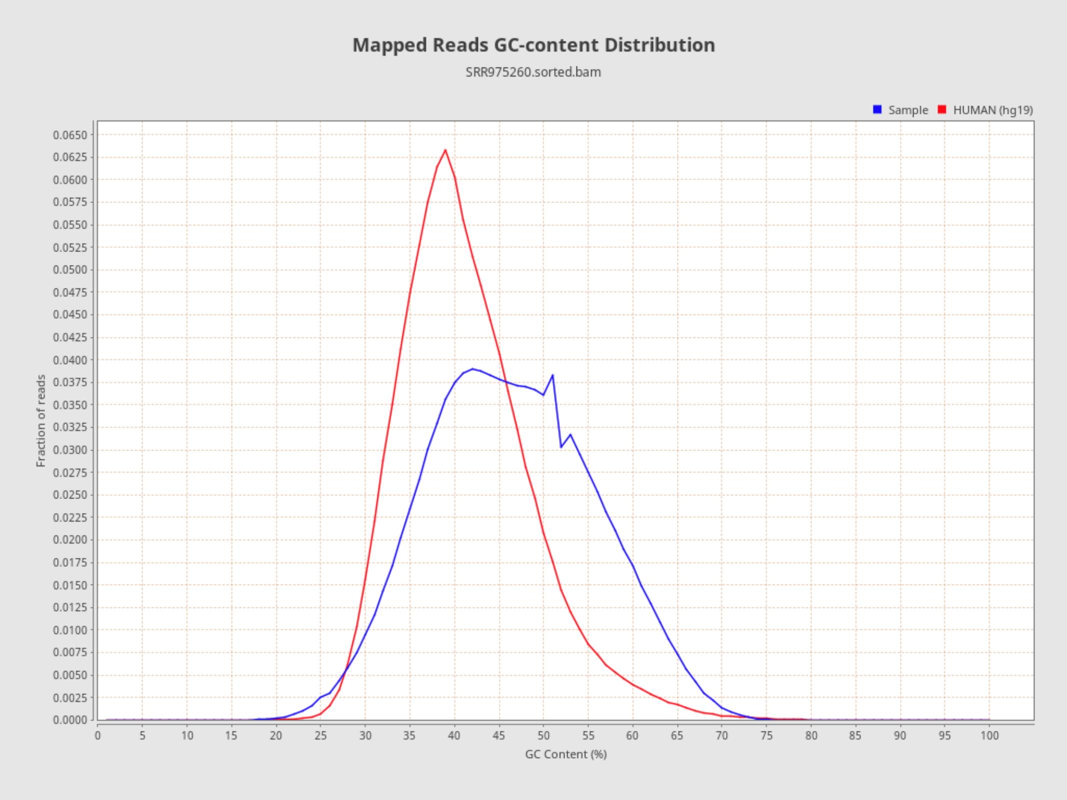
7. Results : Duplication Rate Histogram



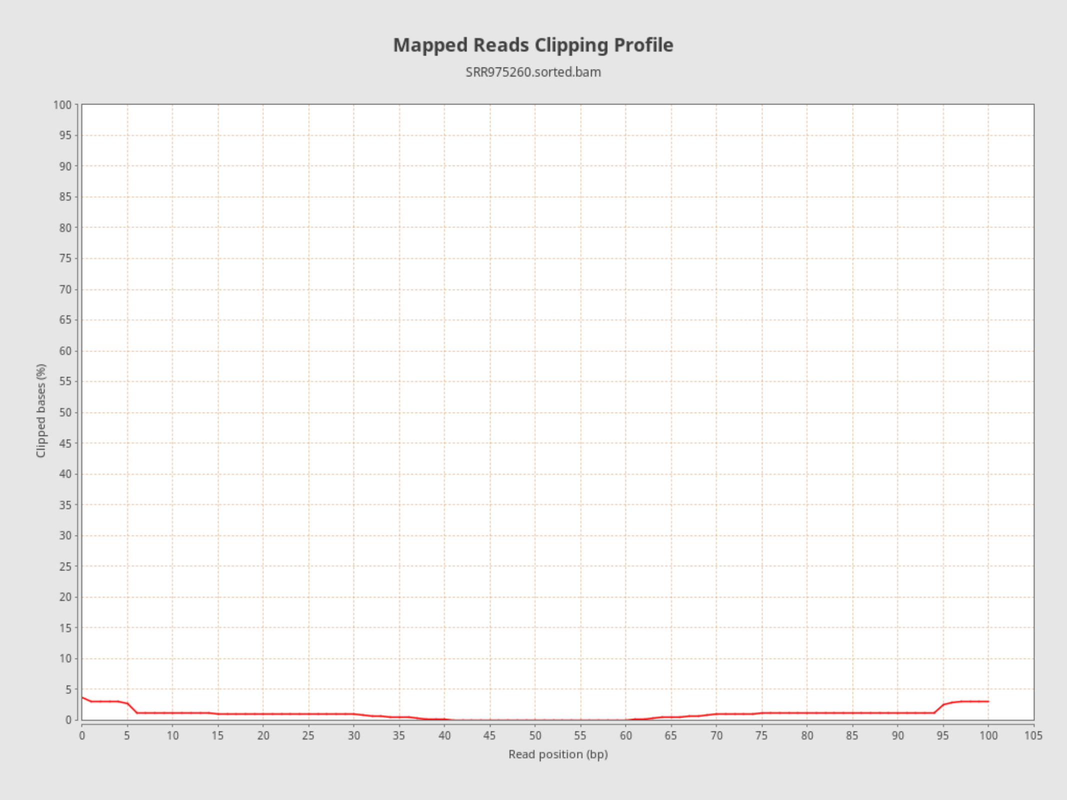
8. Results : Mapped Reads Nucleotide Content



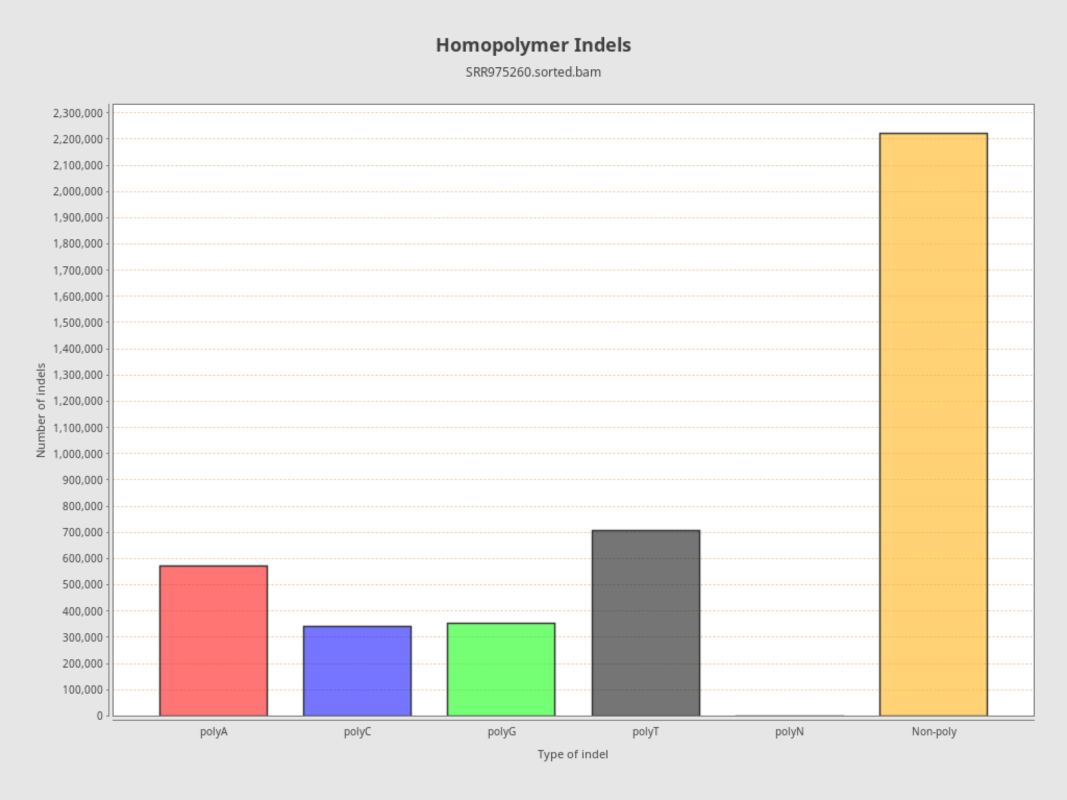
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

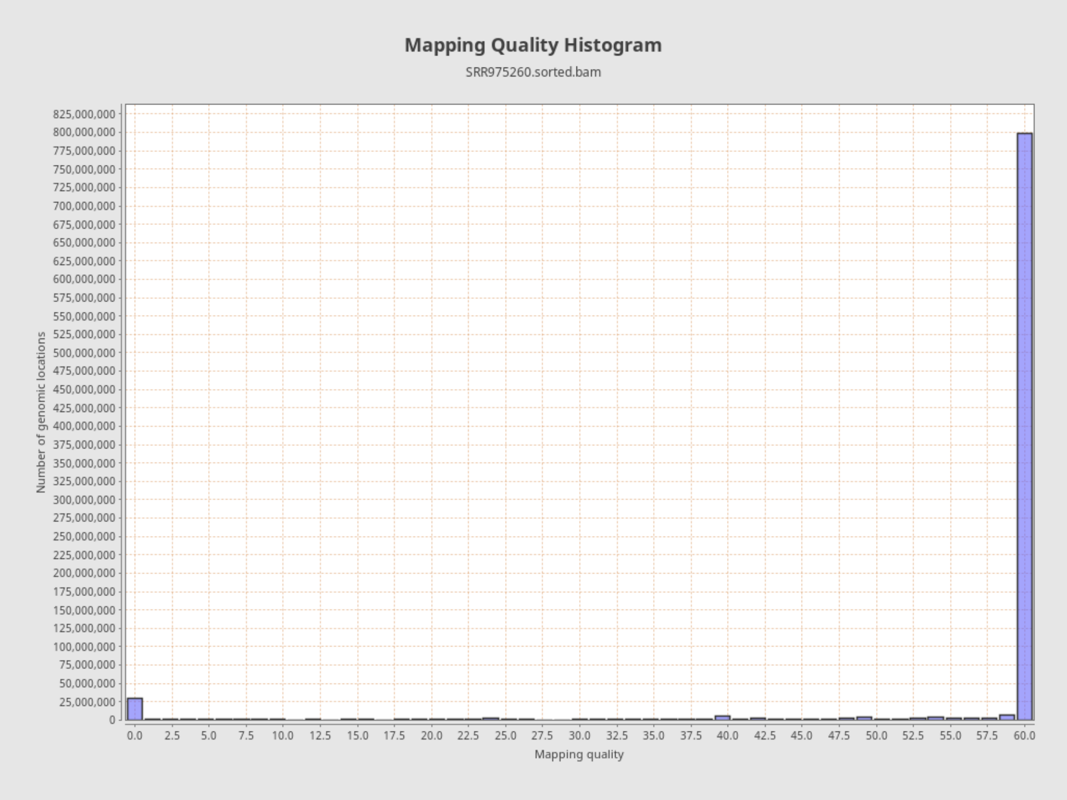


11. Results : Homopolymer Indels

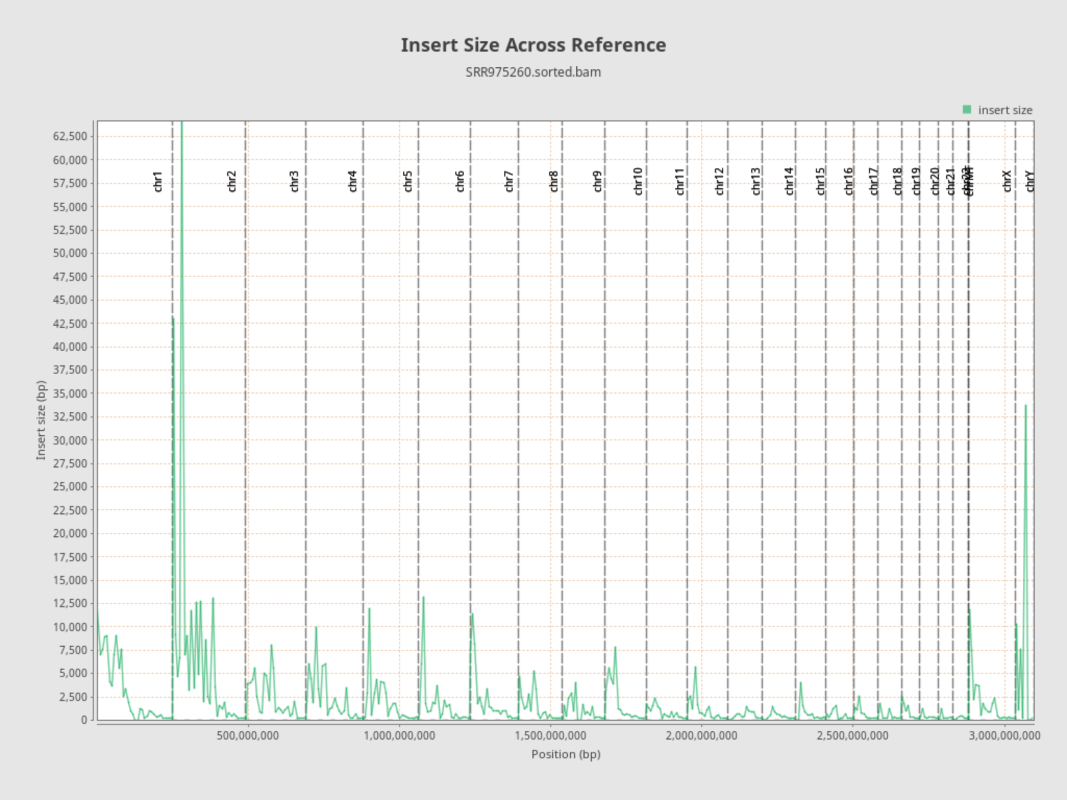


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram