Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 05:14:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975327.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_SRR975327 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975327_1.fastq.gz SRR975327_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 05:14:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975327.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,037,040
Mapped reads	3,966,416 / 98.25%
Unmapped reads	70,624 / 1.75%
Mapped paired reads	3,966,416 / 98.25%
Mapped reads, first in pair	1,981,869 / 49.09%
Mapped reads, second in pair	1,984,547 / 49.16%
Mapped reads, both in pair	3,944,046 / 97.7%
Mapped reads, singletons	22,370 / 0.55%
Secondary alignments	0
Supplementary alignments	20,634 / 0.51%
Read min/max/mean length	30 / 101 / 101.21
Duplicated reads (estimated)	355,722 / 8.81%
Duplication rate	3.46%
Clipped reads	2,449,411 / 60.67%

2.2. ACGT Content

Number/percentage of A's	105,658,439 / 29.19%
Number/percentage of C's	70,273,360 / 19.41%
Number/percentage of T's	107,776,351 / 29.77%
Number/percentage of G's	78,283,977 / 21.63%
Number/percentage of N's	7,022 / 0%

GC Percentage	41.04%

2.3. Coverage

Mean	0.117
Standard Deviation	2.6497

2.4. Mapping Quality

Mean Mapping Quality	52.36

2.5. Insert size

Mean	44,884.33
Standard Deviation	1,970,946.83
P25/Median/P75	137 / 170 / 214

2.6. Mismatches and indels

General error rate	0.92%
Mismatches	3,155,847
Insertions	67,621
Mapped reads with at least one insertion	1.66%
Deletions	117,467
Mapped reads with at least one deletion	2.9%
Homopolymer indels	44.72%

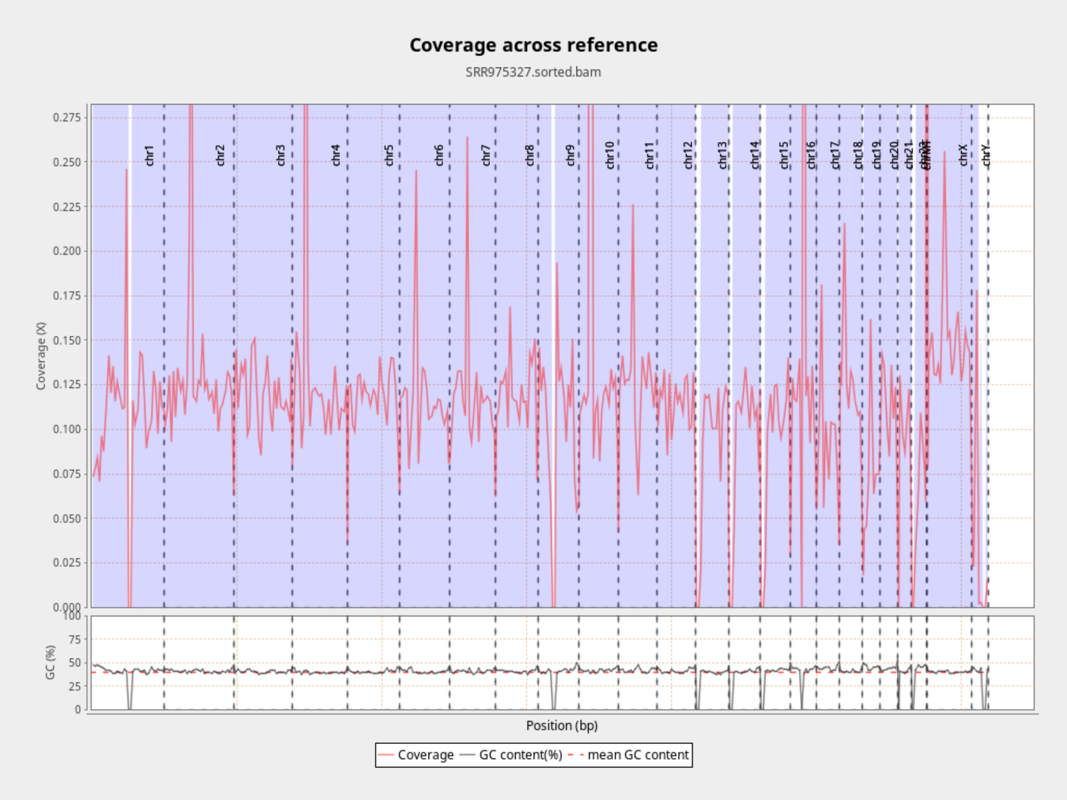
2.7. Chromosome stats

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

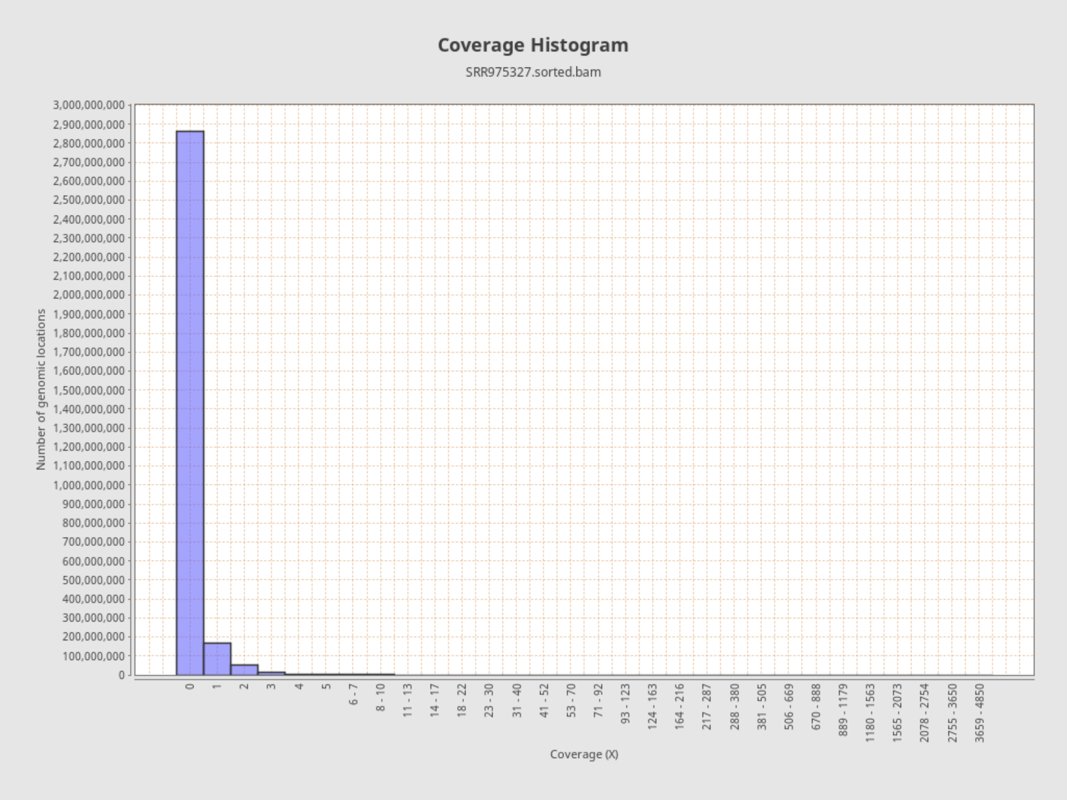
		bases	coverage	deviation
chr1	249250621	26858928	0.1078	2.1061
chr2	243199373	31827015	0.1309	1.8988
chr3	198022430	23651337	0.1194	0.7268
chr4	191154276	25435837	0.1331	2.4968
chr5	180915260	21707776	0.12	0.4639
chr6	171115067	20085441	0.1174	1.4785
chr7	159138663	19018755	0.1195	2.4699
chr8	146364022	17634220	0.1205	0.6798
chr9	141213431	14451684	0.1023	2.1263
chr10	135534747	24654116	0.1819	9.8859
chr11	135006516	17112259	0.1268	1.8895
chr12	133851895	15277823	0.1141	0.4488
chr13	115169878	10293105	0.0894	0.3828
chr14	107349540	9987293	0.093	0.5012
chr15	102531392	9242320	0.0901	0.3894
chr16	90354753	13741698	0.1521	3.5272
chr17	81195210	7732342	0.0952	1.4797
chr18	78077248	9950392	0.1274	2.6588
chr19	59128983	4348422	0.0735	1.2117
chr20	63025520	7048000	0.1118	0.7236
chr21	48129895	4490983	0.0933	1.0361
chr22	51304566	3027332	0.059	0.3208
chrMT	16571	60862	3.6728	2.864
chrX	155270560	22740391	0.1465	0.9778

chrY	59373566	1836699	0.0309	2.4951

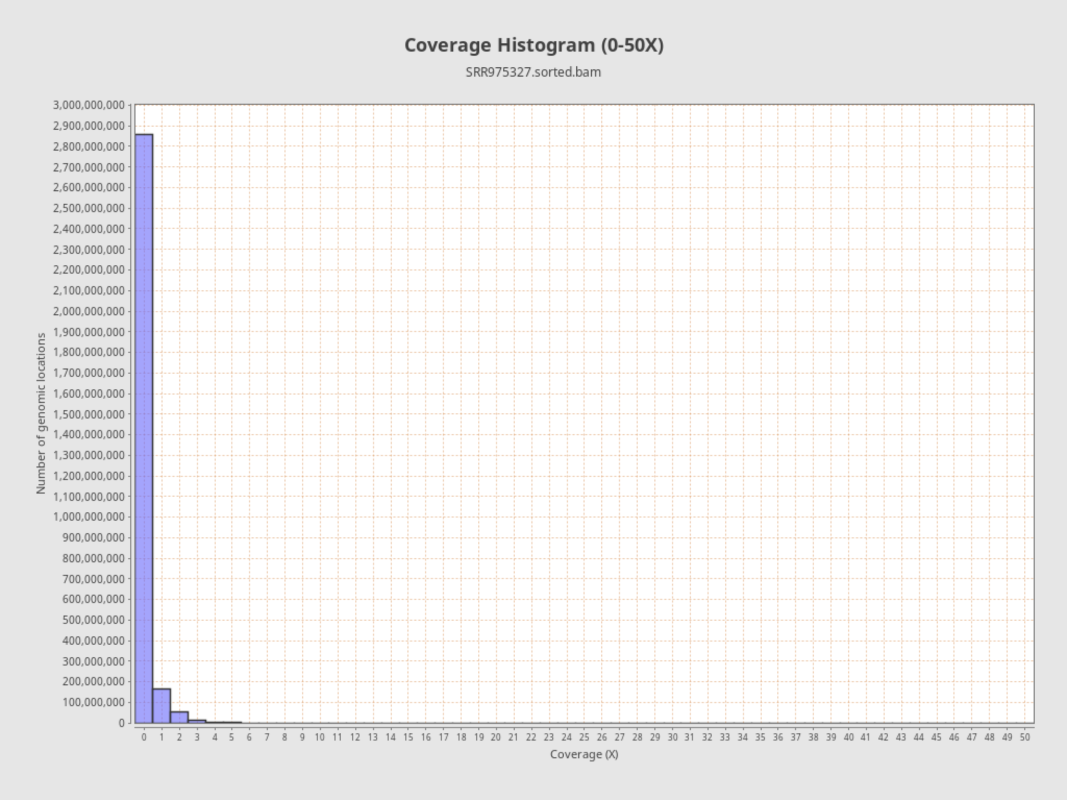
3. Results : Coverage across reference



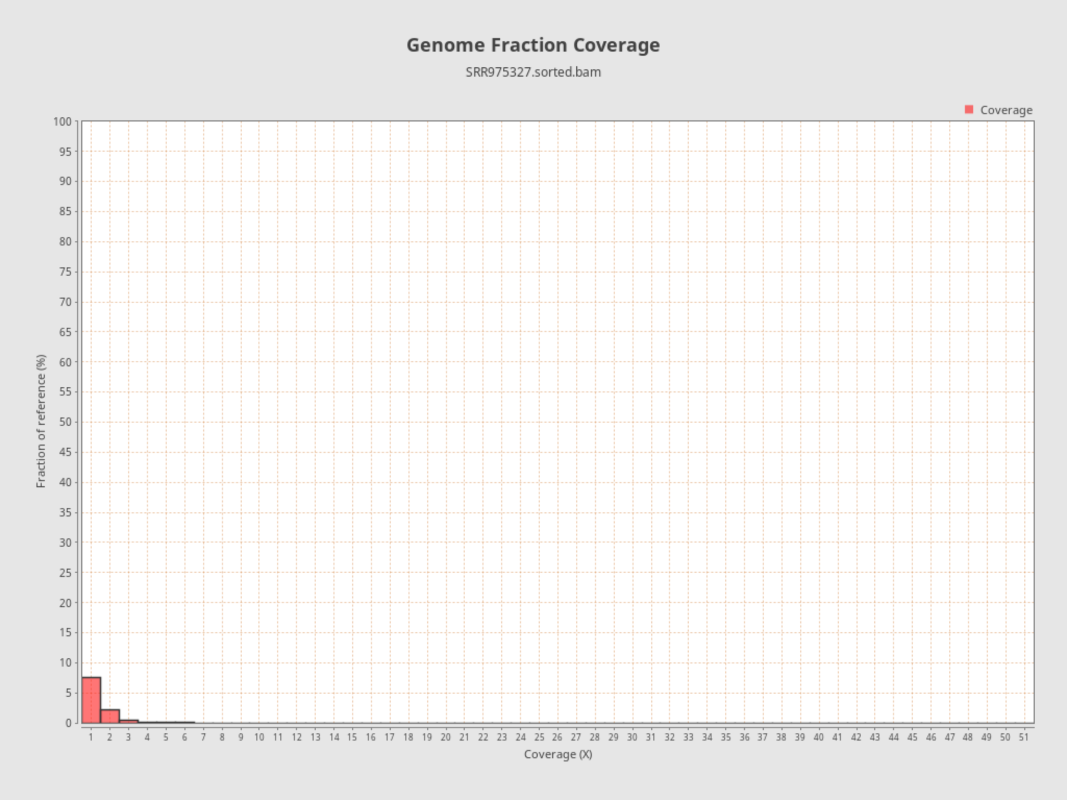
4. Results : Coverage Histogram



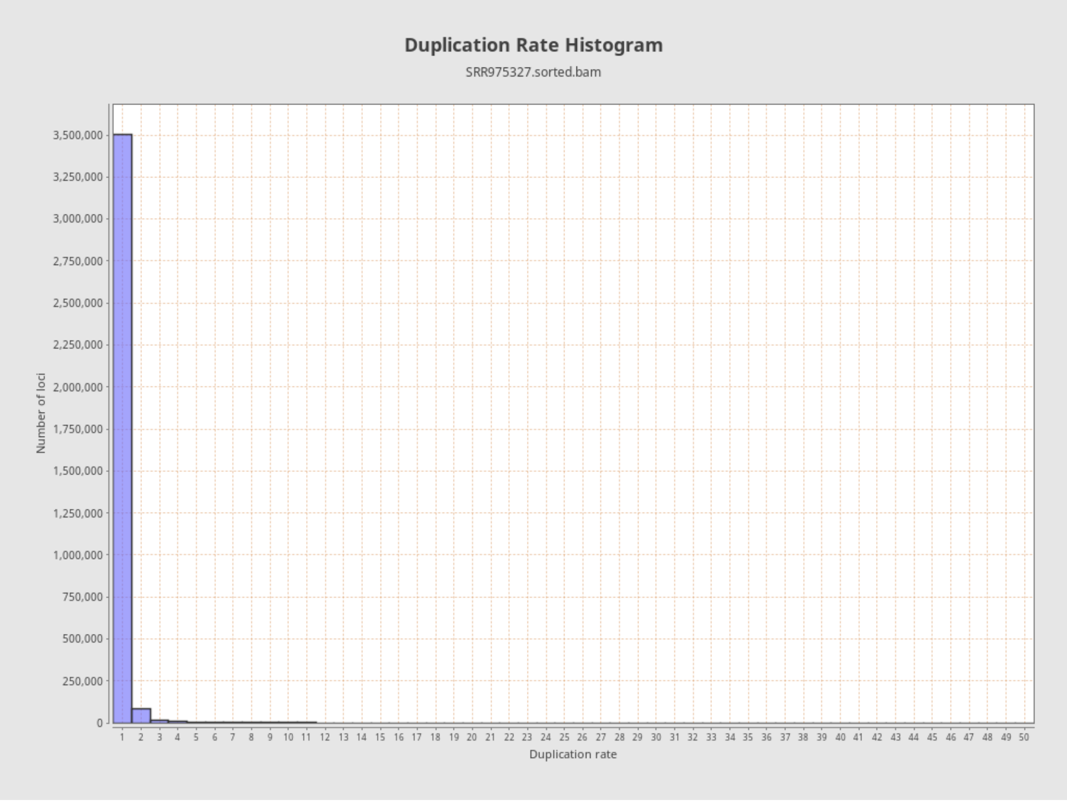
5. Results : Coverage Histogram (0-50X)



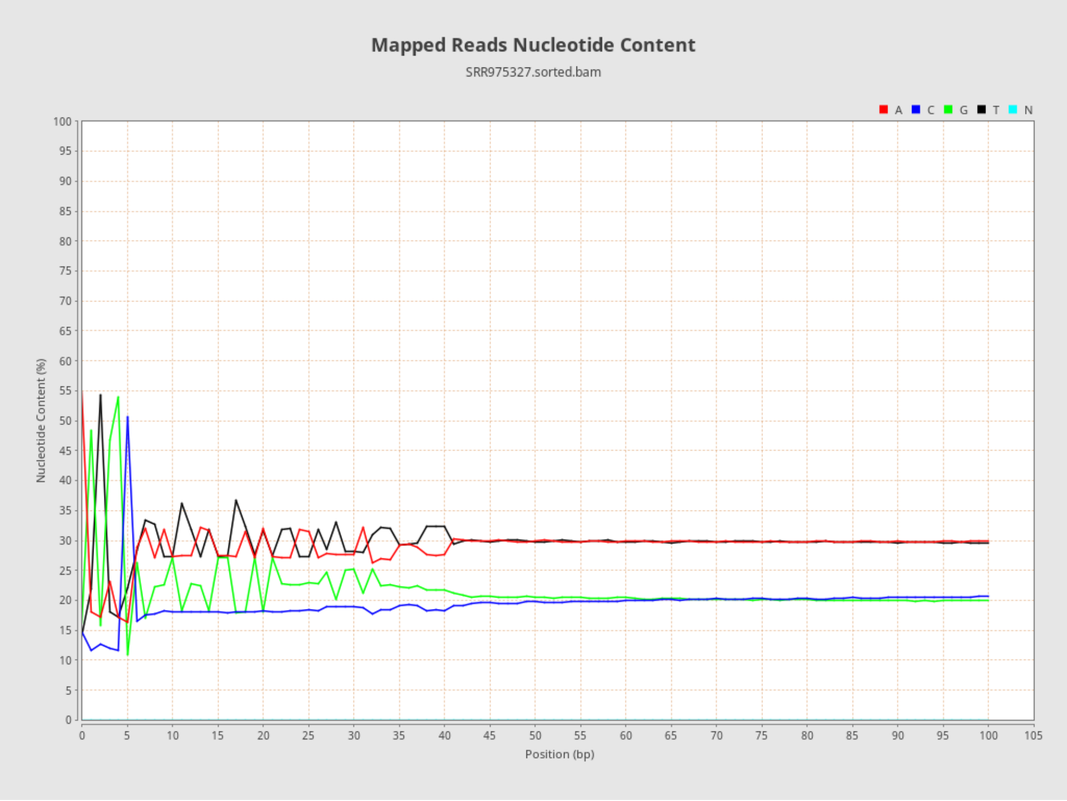
6. Results : Genome Fraction Coverage



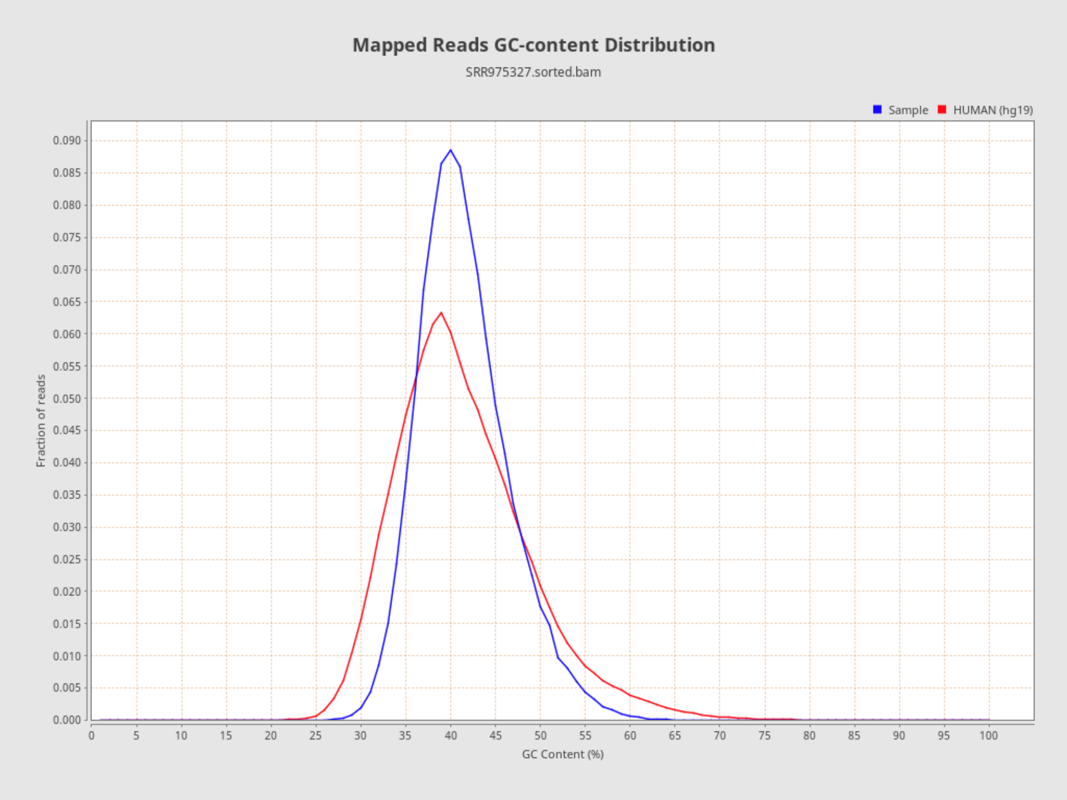
7. Results : Duplication Rate Histogram



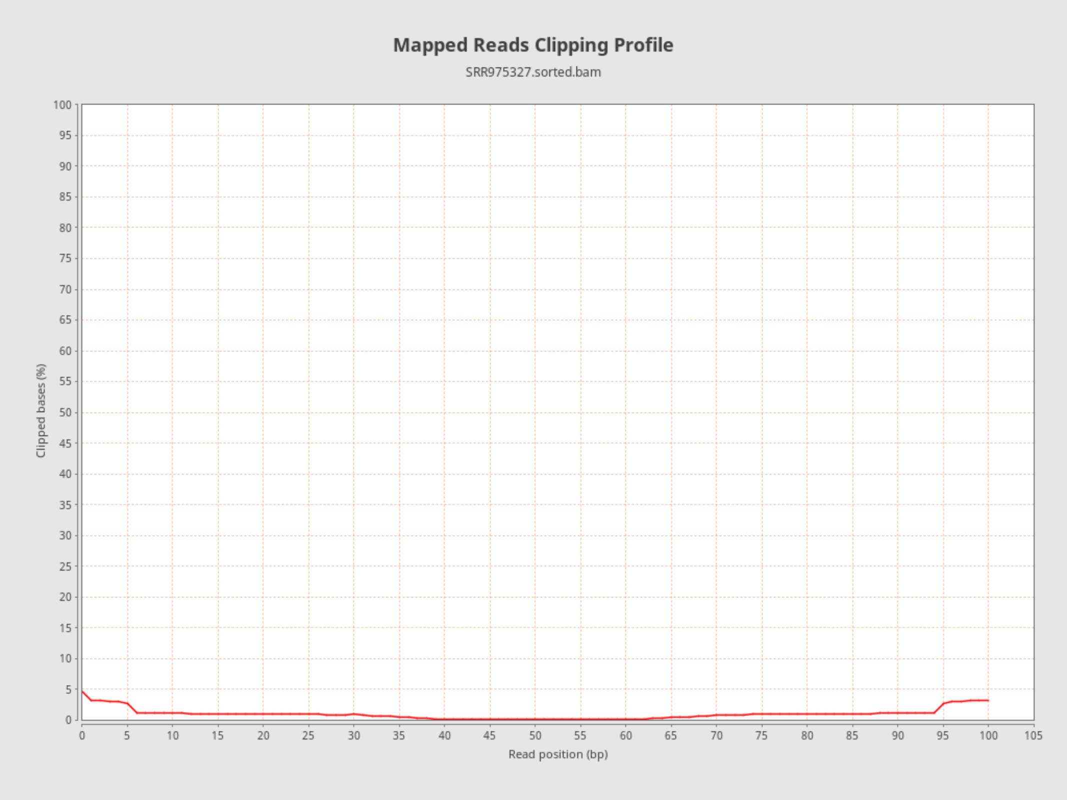
8. Results : Mapped Reads Nucleotide Content



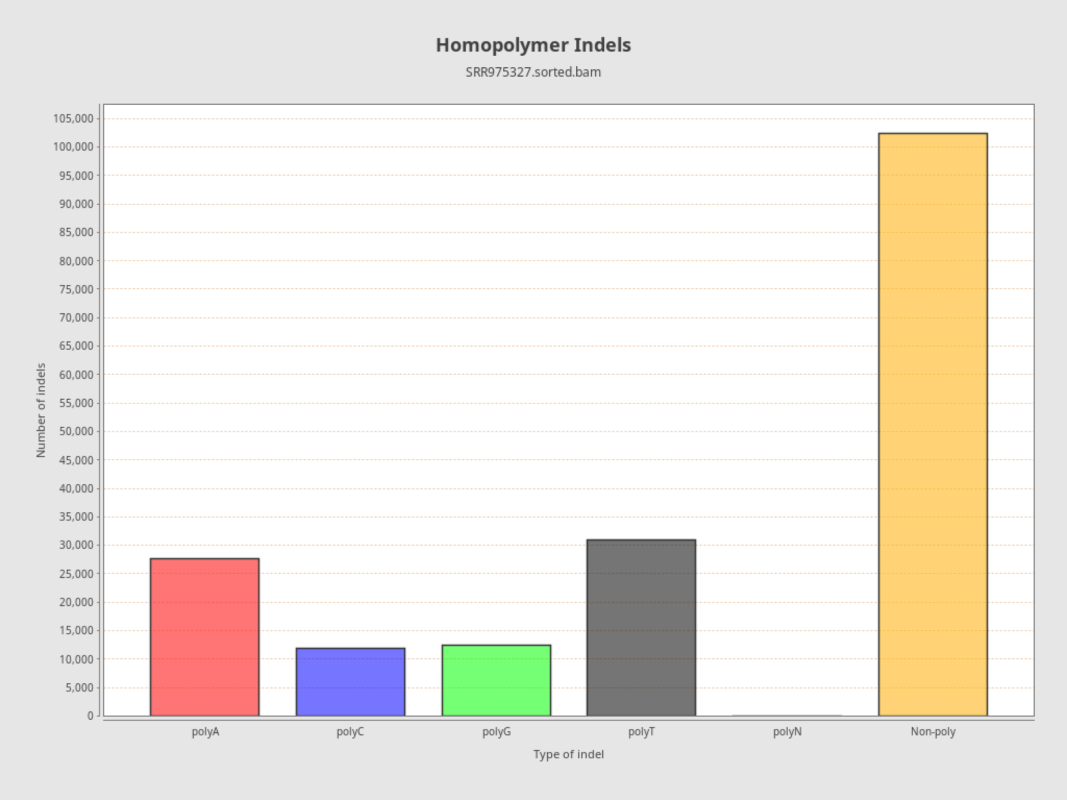
9. Results : Mapped Reads GC-content Distribution



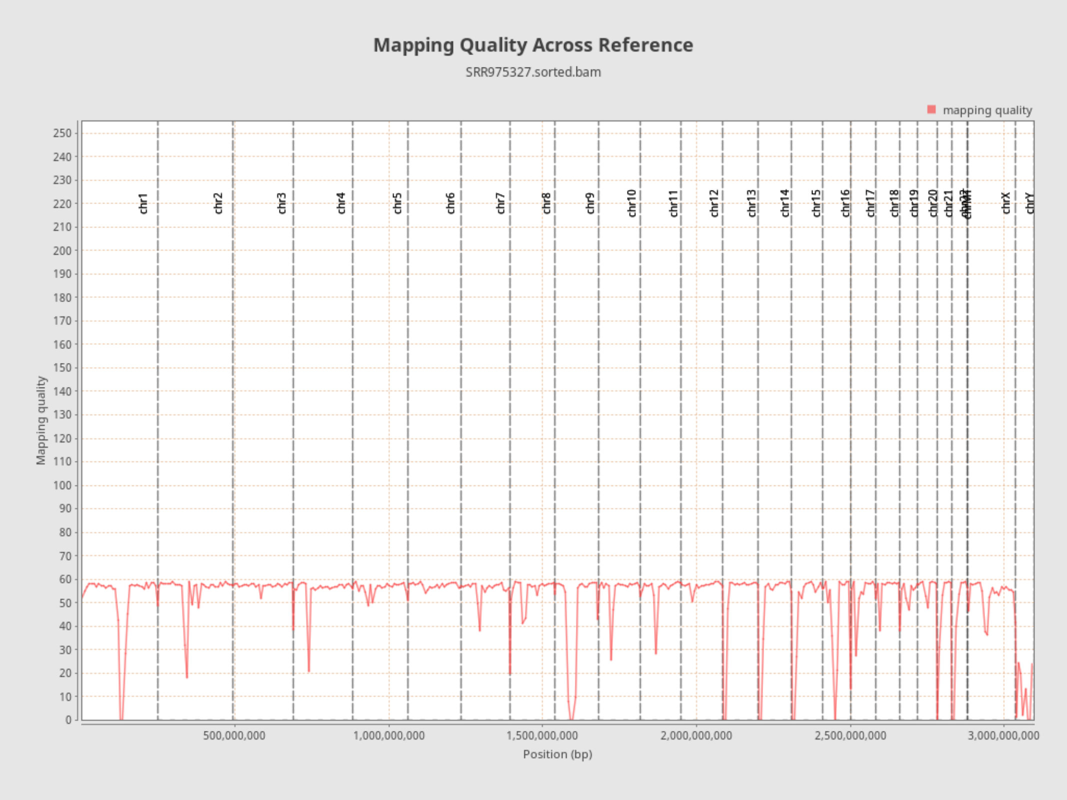
10. Results : Mapped Reads Clipping Profile



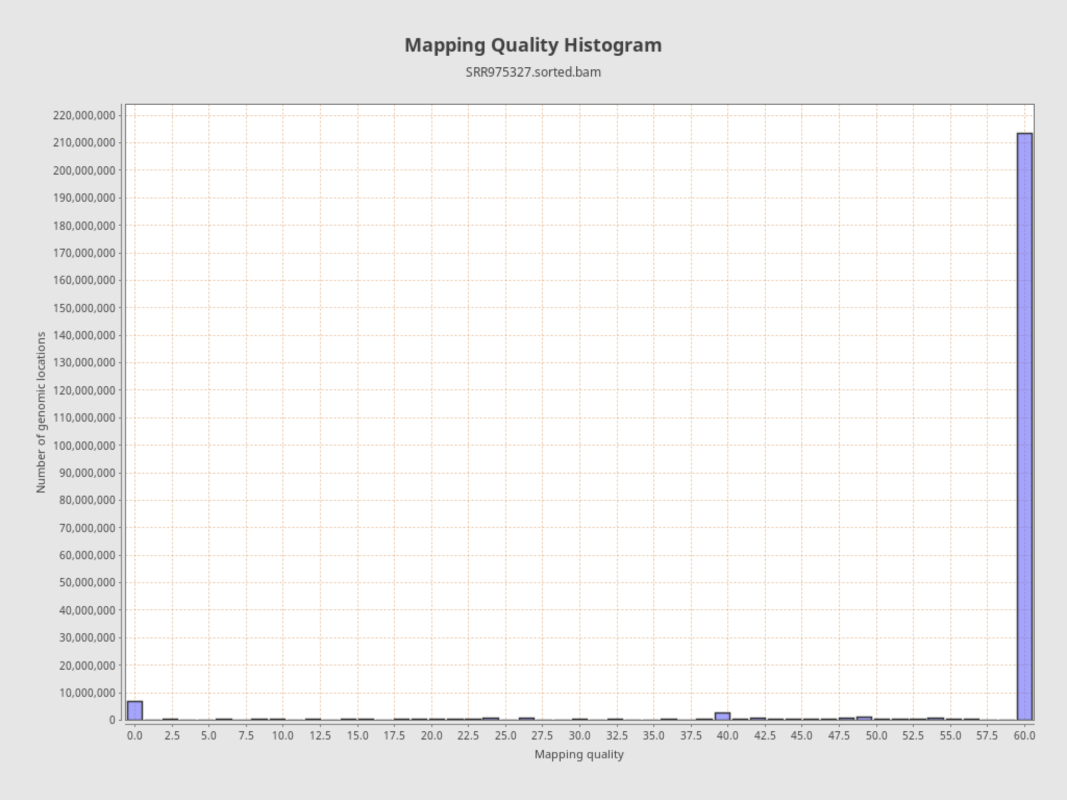
11. Results : Homopolymer Indels



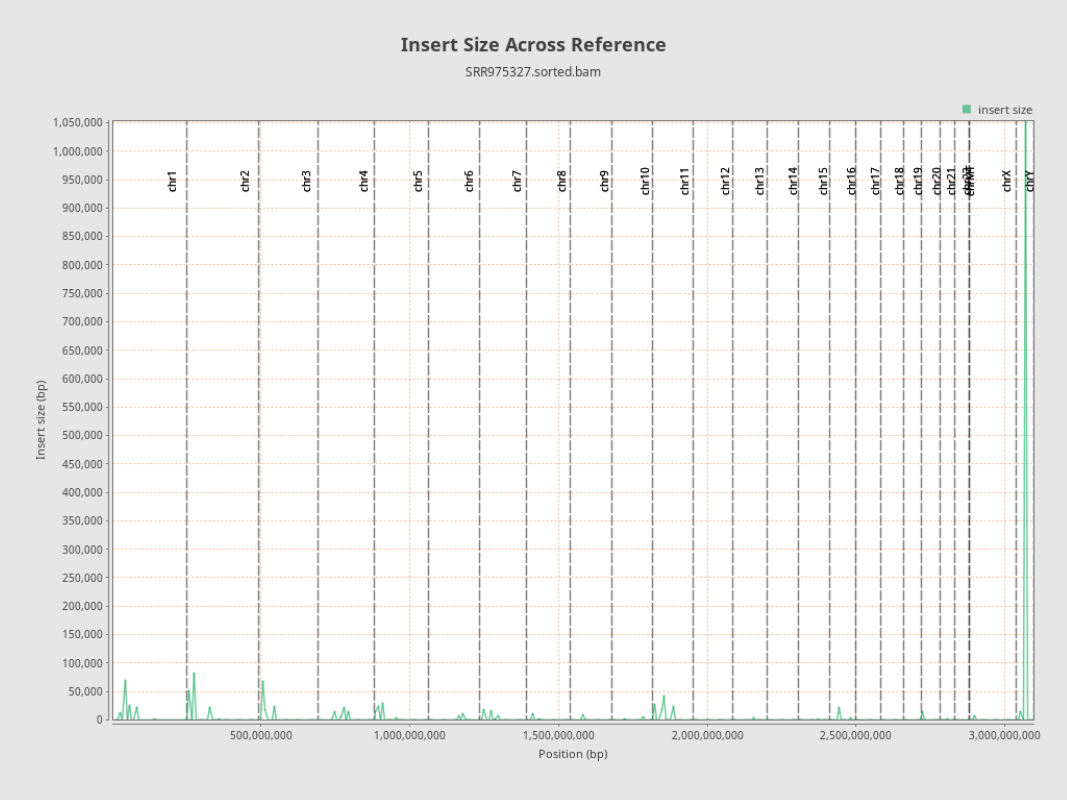
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram