Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 21:38:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975287.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_SRR975287 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975287_1.fastq.gz SRR975287_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 21:38:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975287.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	39,573,016
Mapped reads	39,349,380 / 99.43%
Unmapped reads	223,636 / 0.57%
Mapped paired reads	39,349,380 / 99.43%
Mapped reads, first in pair	19,734,995 / 49.87%
Mapped reads, second in pair	19,614,385 / 49.57%
Mapped reads, both in pair	39,170,564 / 98.98%
Mapped reads, singletons	178,816 / 0.45%
Secondary alignments	0
Supplementary alignments	93,473 / 0.24%
Read min/max/mean length	30 / 101 / 101.09
Duplicated reads (estimated)	24,644,941 / 62.28%
Duplication rate	60.03%
Clipped reads	22,938,027 / 57.96%

2.2. ACGT Content

Number/percentage of A's	1,020,387,599 / 27.74%
Number/percentage of C's	789,595,711 / 21.47%
Number/percentage of T's	1,032,635,966 / 28.08%
Number/percentage of G's	834,756,080 / 22.7%
Number/percentage of N's	751,370 / 0.02%

GC Percentage	44.16%

2.3. Coverage

Mean	1.1886
Standard Deviation	16.7265

2.4. Mapping Quality

Mean Mapping Quality	56.2

2.5. Insert size

Mean	107,499.12
Standard Deviation	3,222,762.74
P25/Median/P75	190 / 232 / 282

2.6. Mismatches and indels

General error rate	0.8%
Mismatches	28,748,643
Insertions	394,353
Mapped reads with at least one insertion	0.99%
Deletions	857,993
Mapped reads with at least one deletion	2.15%
Homopolymer indels	47.62%

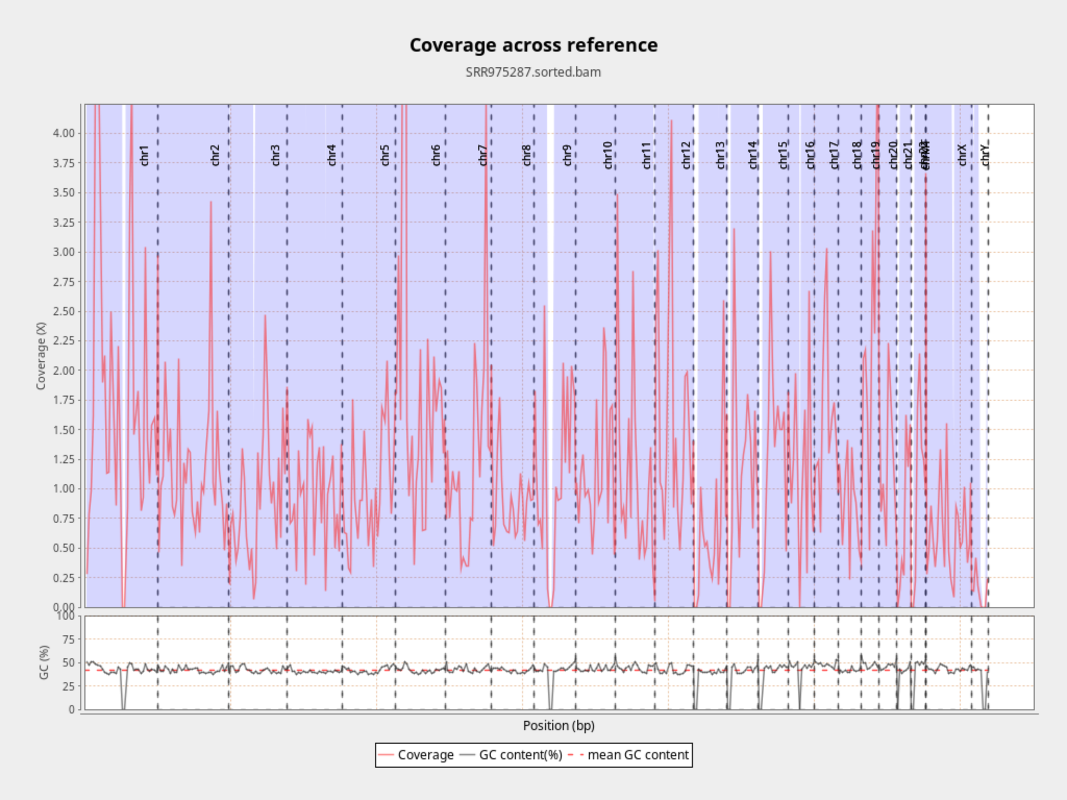
2.7. Chromosome stats

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

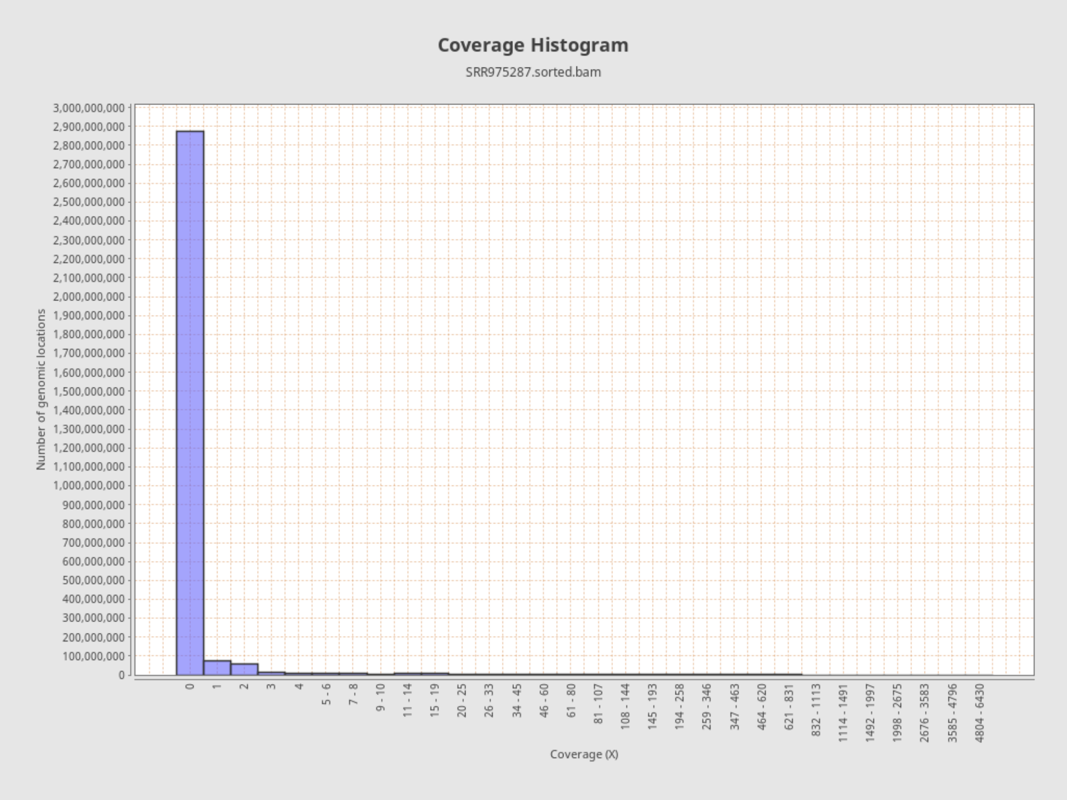
		bases	**coverage**	**deviation**
chr1	249250621	442481522	1.7752	21.715
chr2	243199373	277542738	1.1412	14.8796
chr3	198022430	184820251	0.9333	13.1924
chr4	191154276	181551946	0.9498	14.067
chr5	180915260	177201767	0.9795	12.9056
chr6	171115067	363065997	2.1218	29.1426
chr7	159138663	198096989	1.2448	18.5857
chr8	146364022	129800979	0.8868	12.7277
chr9	141213431	150114823	1.063	14.3811
chr10	135534747	159151261	1.1742	14.8205
chr11	135006516	153796701	1.1392	14.681
chr12	133851895	214432642	1.602	19.2864
chr13	115169878	73625234	0.6393	11.8061
chr14	107349540	122084919	1.1373	15.9429
chr15	102531392	129606748	1.2641	16.6597
chr16	90354753	103054914	1.1406	14.3785
chr17	81195210	132466181	1.6315	17.9317
chr18	78077248	69090862	0.8849	12.812
chr19	59128983	139237777	2.3548	25.9747
chr20	63025520	82370248	1.3069	19.3
chr21	48129895	35532353	0.7383	12.4712
chr22	51304566	53418437	1.0412	14.7118
chrMT	16571	60788	3.6683	10.9351
chrX	155270560	98423752	0.6339	10.4574

chrY	59373566	8382381	0.1412	5.0573

3. Results : Coverage across reference



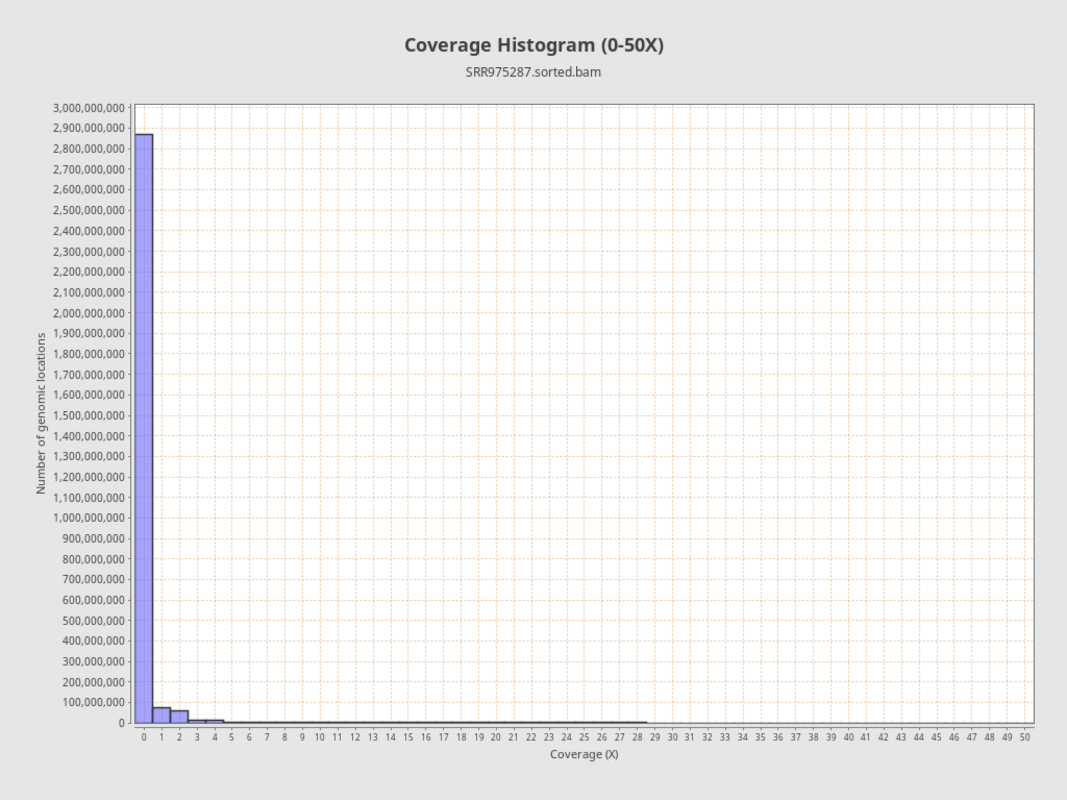
4. Results : Coverage Histogram



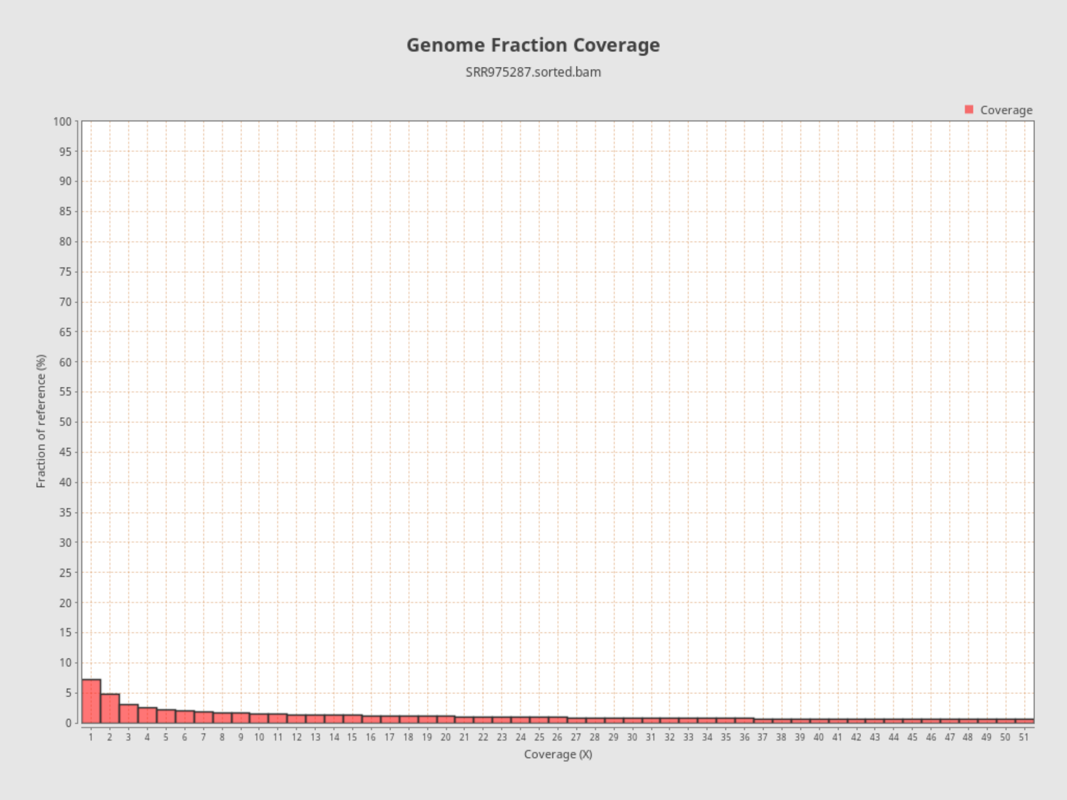
Coverage Histogram

SRR975287.sorted.bam

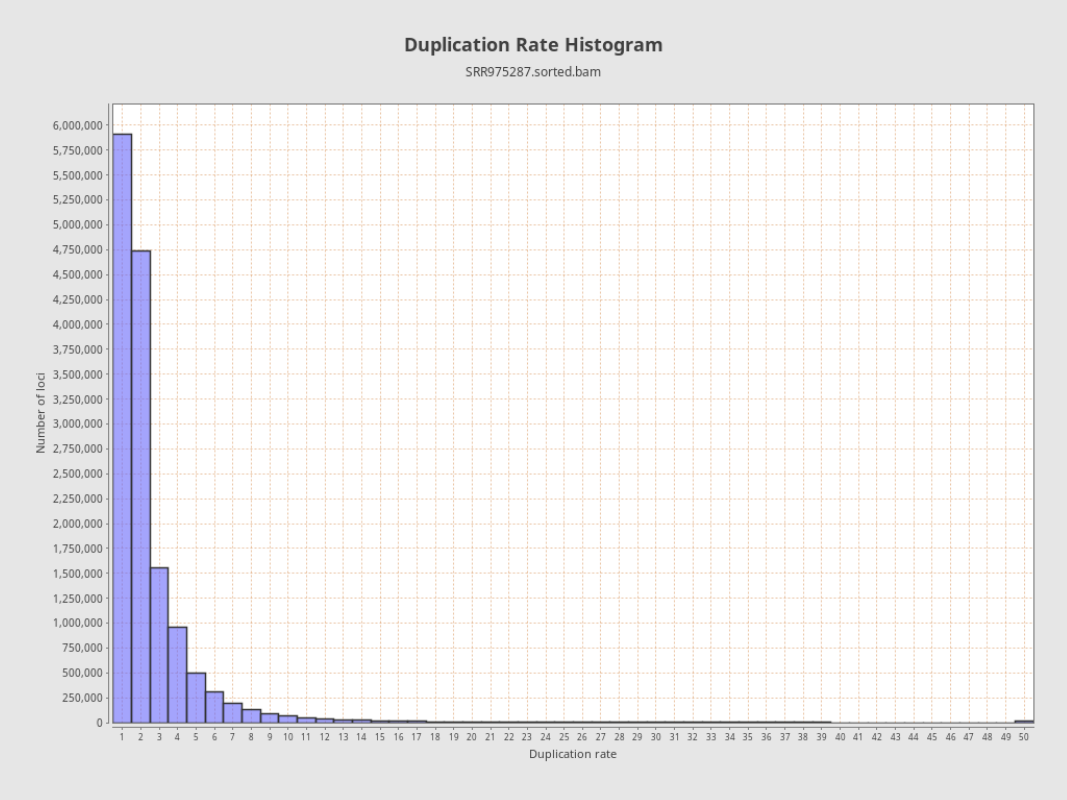
5. Results : Coverage Histogram (0-50X)



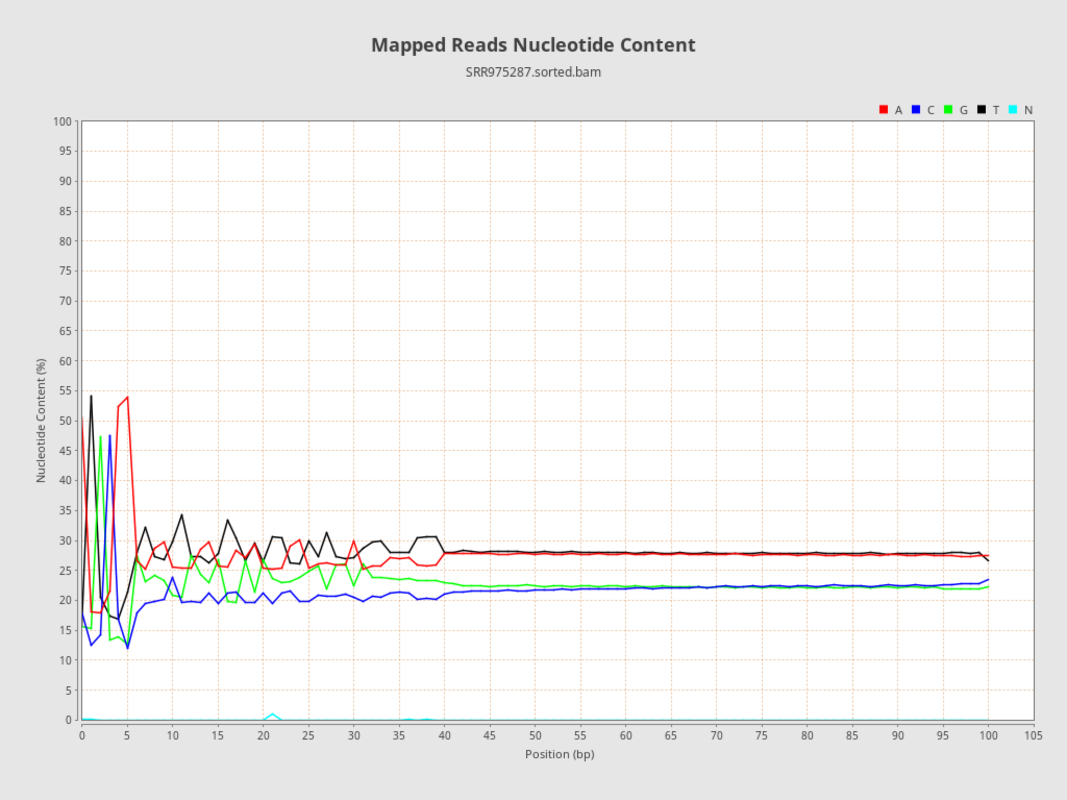
6. Results : Genome Fraction Coverage



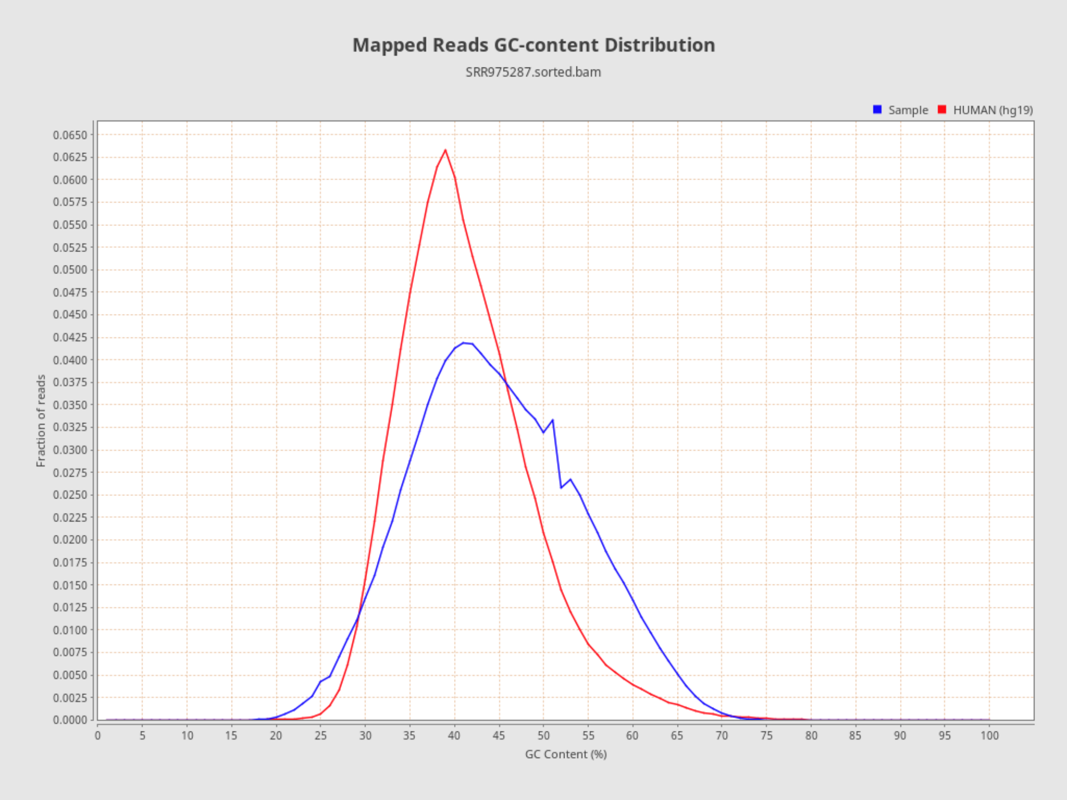
7. Results : Duplication Rate Histogram



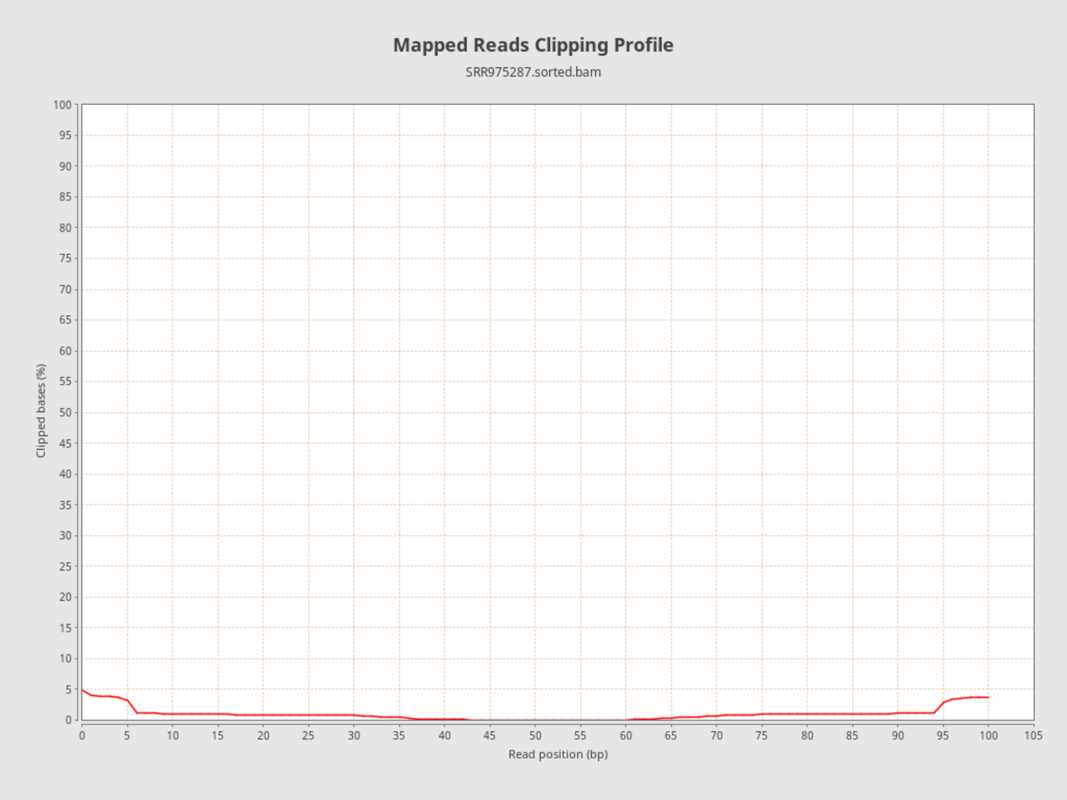
8. Results : Mapped Reads Nucleotide Content



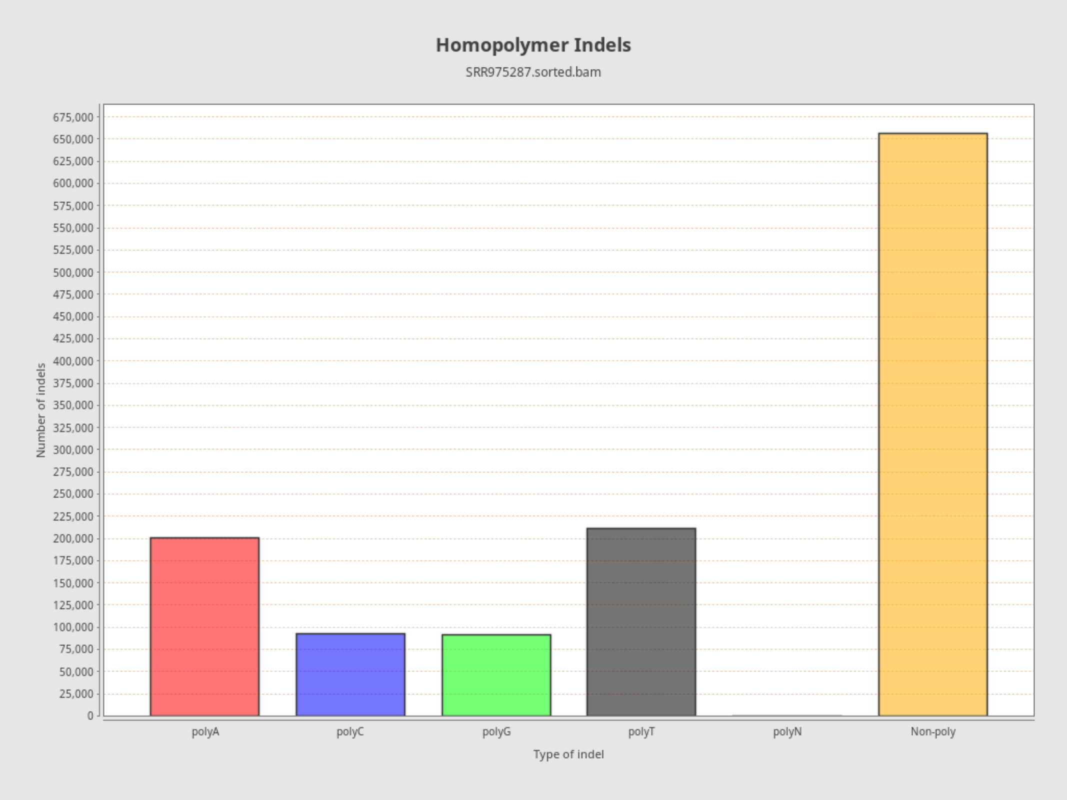
9. Results : Mapped Reads GC-content Distribution



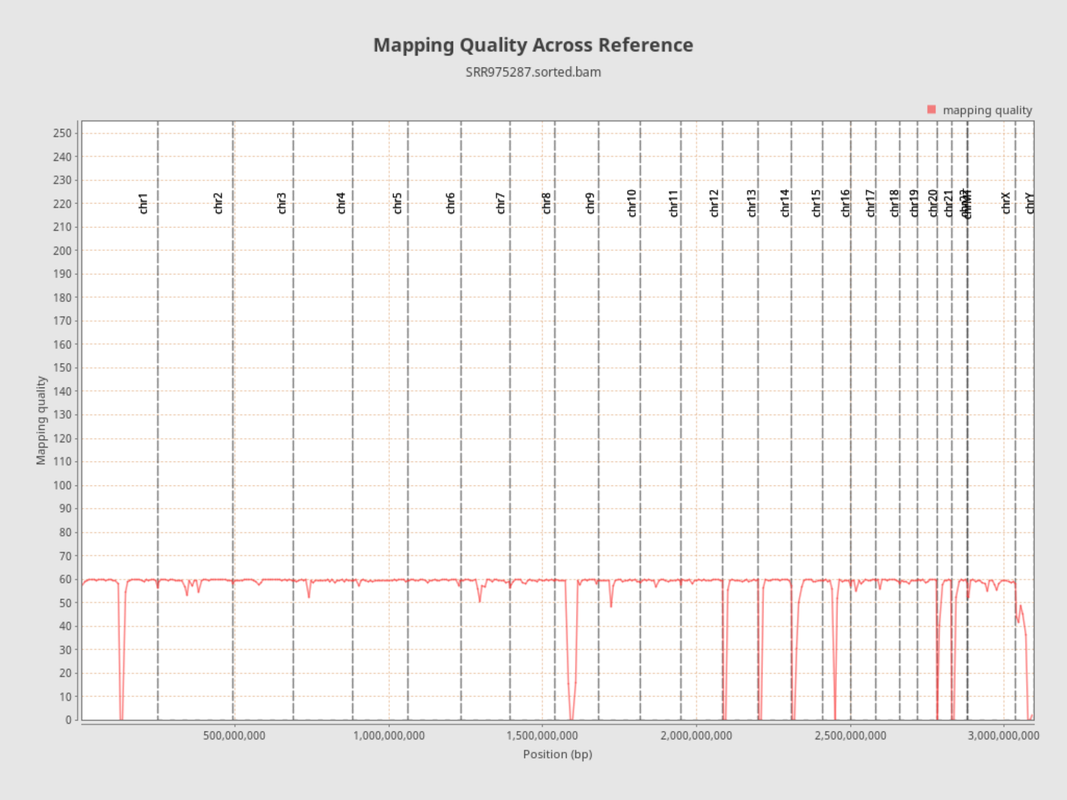
10. Results : Mapped Reads Clipping Profile



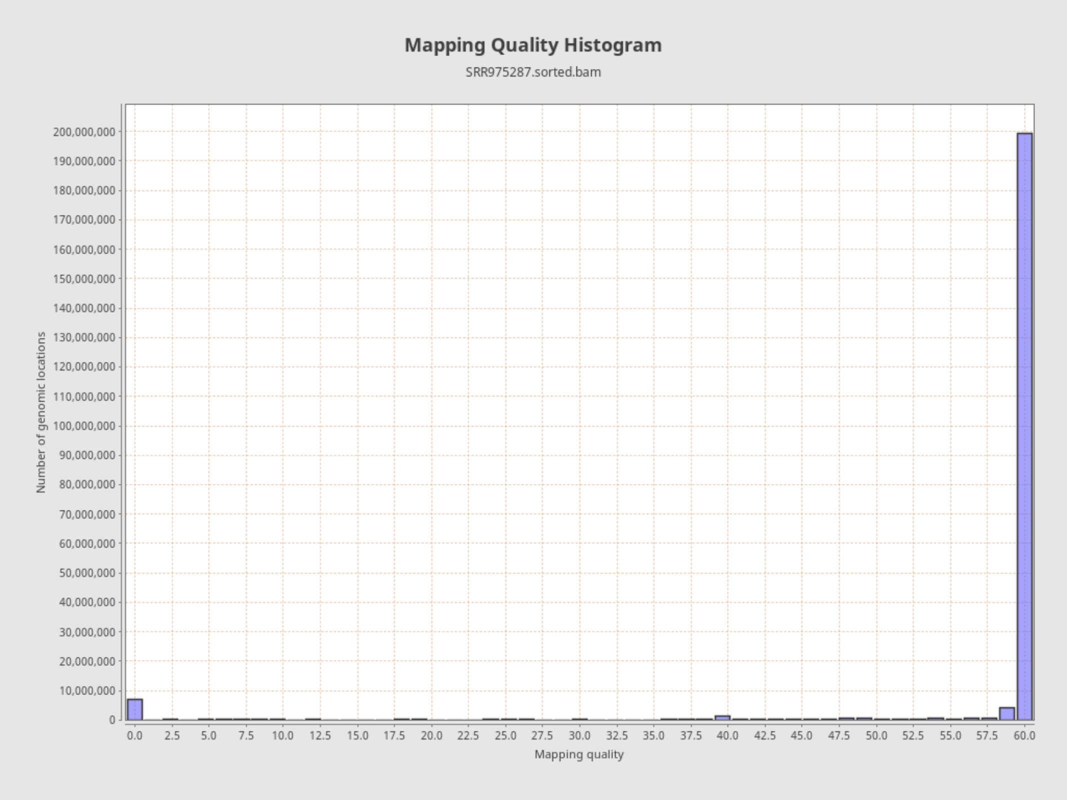
11. Results : Homopolymer Indels



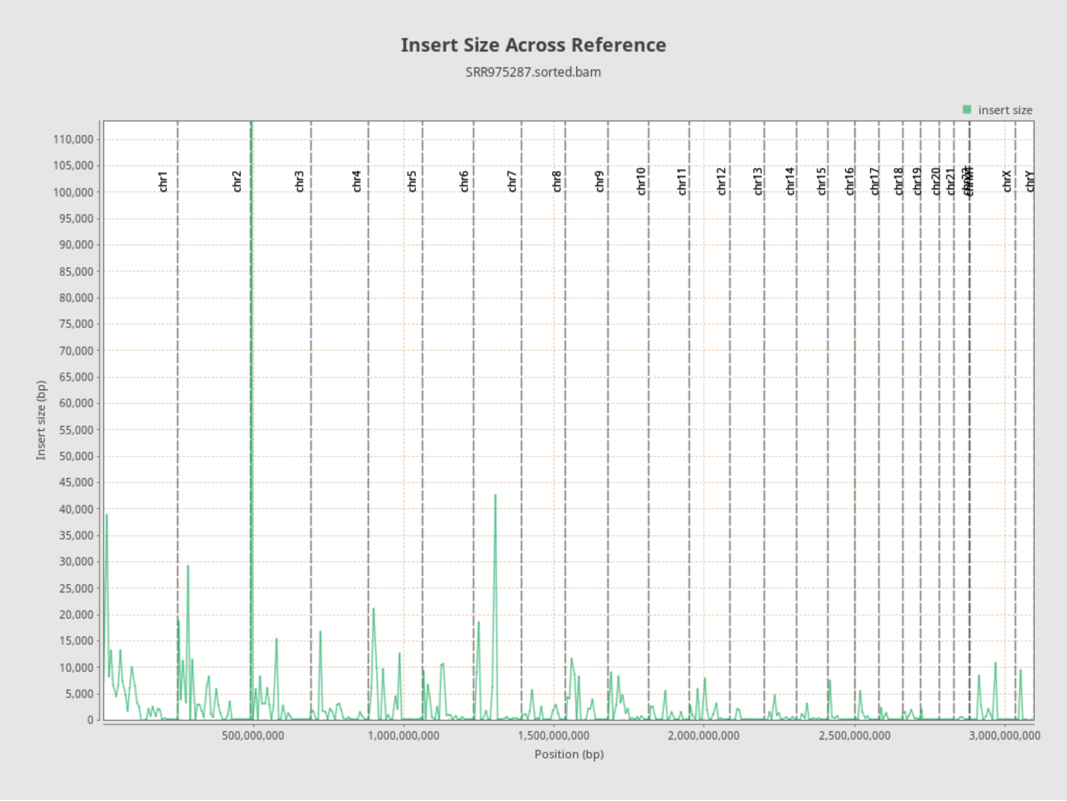
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram