Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 23:18:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975228.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_SRR975228 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975228_1.fastq.gz SRR975228_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 23:17:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975228.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	107,116,602
Mapped reads	106,518,911 / 99.44%
Unmapped reads	597,691 / 0.56%
Mapped paired reads	106,518,911 / 99.44%
Mapped reads, first in pair	53,241,515 / 49.7%
Mapped reads, second in pair	53,277,396 / 49.74%
Mapped reads, both in pair	106,275,236 / 99.21%
Mapped reads, singletons	243,675 / 0.23%
Secondary alignments	0
Supplementary alignments	226,958 / 0.21%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	66,343,252 / 61.94%
Duplication rate	45.14%
Clipped reads	67,273,162 / 62.8%

2.2. ACGT Content

Number/percentage of A's	2,585,340,078 / 26.72%
Number/percentage of C's	2,087,237,094 / 21.58%
Number/percentage of T's	2,715,470,613 / 28.07%
Number/percentage of G's	2,285,675,161 / 23.63%
Number/percentage of N's	274,475 / 0%

GC Percentage	45.2%

2.3. Coverage

Mean	3.126
Standard Deviation	39.0836

2.4. Mapping Quality

Mean Mapping Quality	55.64

2.5. Insert size

Mean	63,123.42
Standard Deviation	2,461,176.33
P25/Median/P75	145 / 182 / 230

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	59,646,712
Insertions	803,334
Mapped reads with at least one insertion	0.74%
Deletions	2,184,291
Mapped reads with at least one deletion	2.02%
Homopolymer indels	48.57%

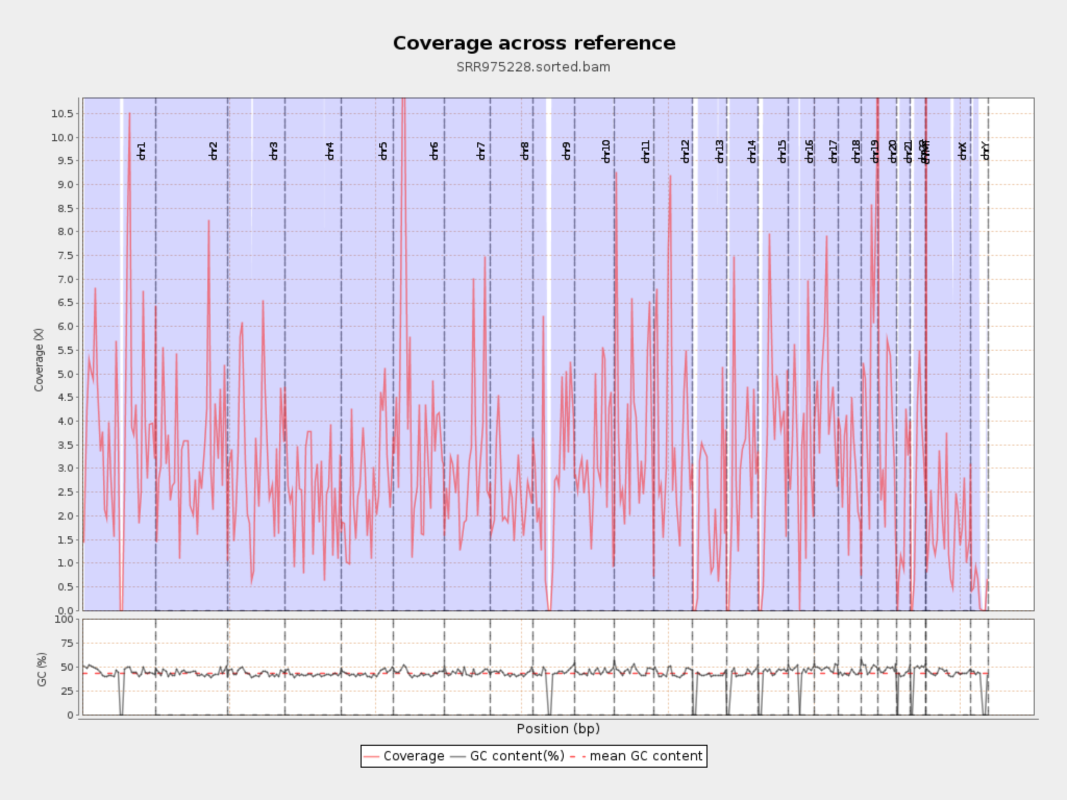
2.7. Chromosome stats

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

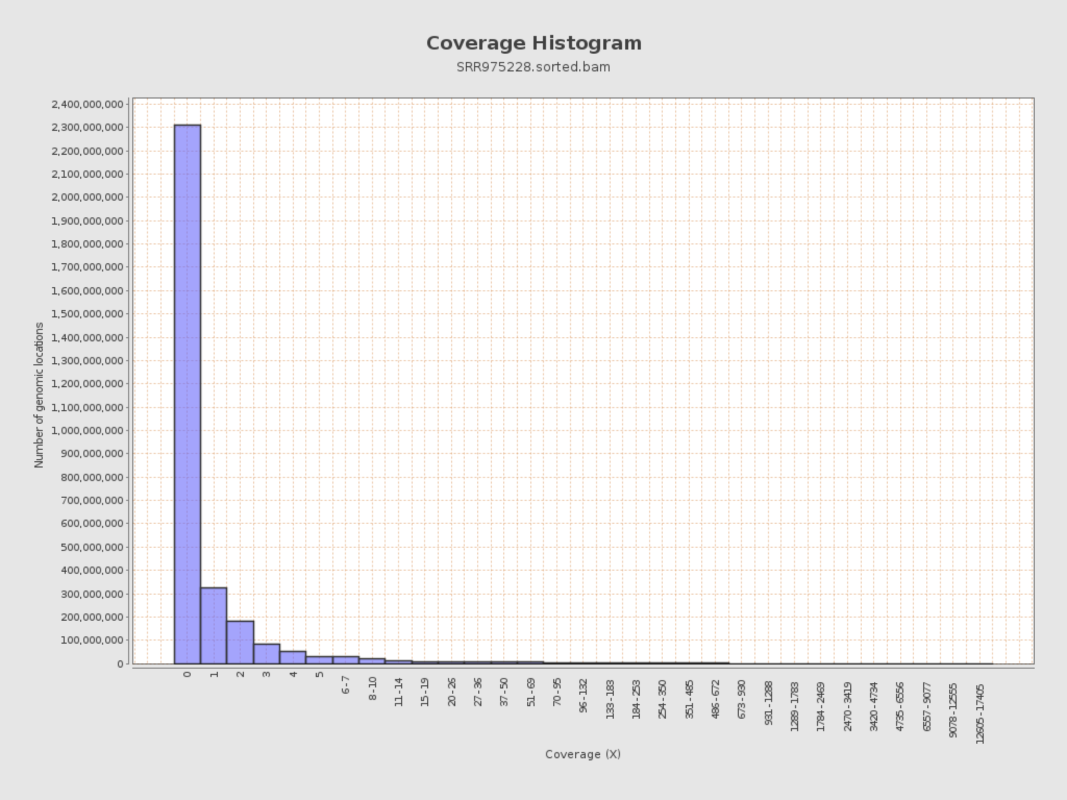
		bases	coverage	deviation
chr1	249250621	968085382	3.884	43.8175
chr2	243199373	811601169	3.3372	40.008
chr3	198022430	611861612	3.0899	38.2017
chr4	191154276	475620105	2.4881	34.7759
chr5	180915260	478428378	2.6445	33.485
chr6	171115067	704936780	4.1197	50.6771
chr7	159138663	485197829	3.0489	39.9541
chr8	146364022	357100541	2.4398	30.5752
chr9	141213431	392297011	2.778	34.8092
chr10	135534747	436215065	3.2185	39.1293
chr11	135006516	521849020	3.8654	43.5204
chr12	133851895	533261383	3.984	43.5347
chr13	115169878	224131803	1.9461	31.2067
chr14	107349540	322111105	3.0006	38.5245
chr15	102531392	340384776	3.3198	38.6707
chr16	90354753	291560394	3.2268	35.9863
chr17	81195210	377846316	4.6536	46.8642
chr18	78077248	241031373	3.0871	42.3767
chr19	59128983	337735354	5.7118	59.1579
chr20	63025520	227948490	3.6168	46.395
chr21	48129895	98433820	2.0452	29.1746
chr22	51304566	141963520	2.7671	37.6067
chrMT	16571	395508	23.8675	31.9257
chrX	155270560	273807248	1.7634	24.9519

chrY	59373566	23445846	0.3949	8.3636

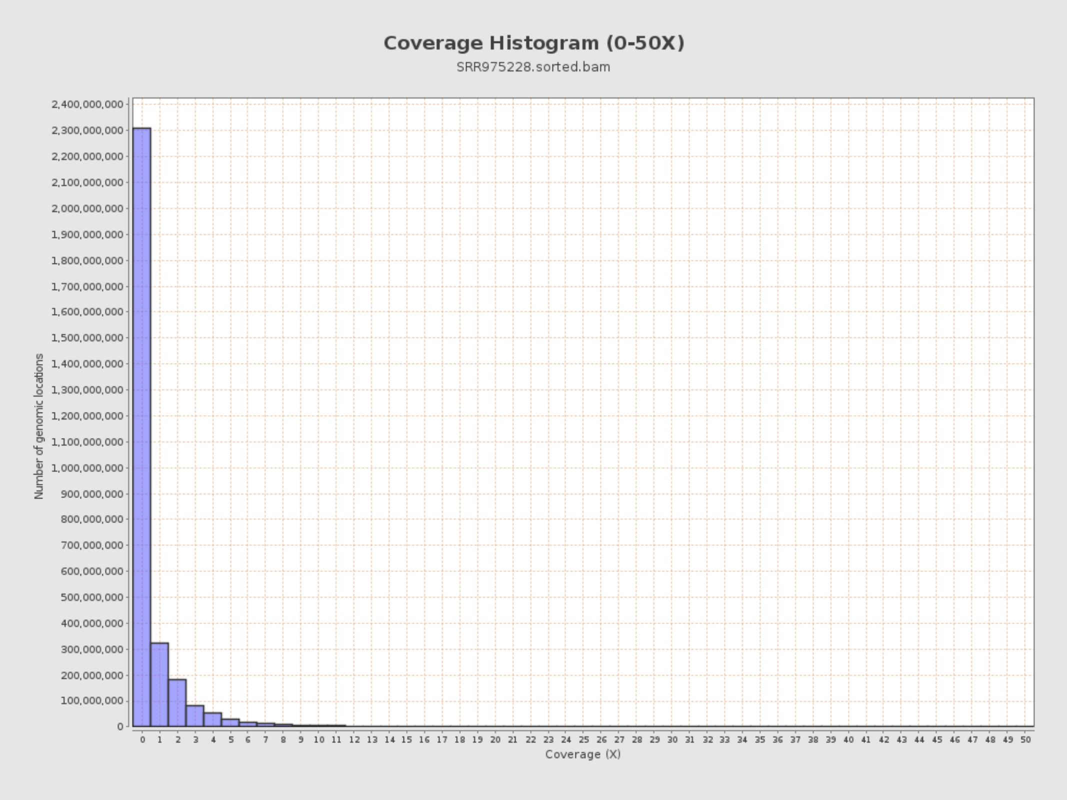
3. Results : Coverage across reference



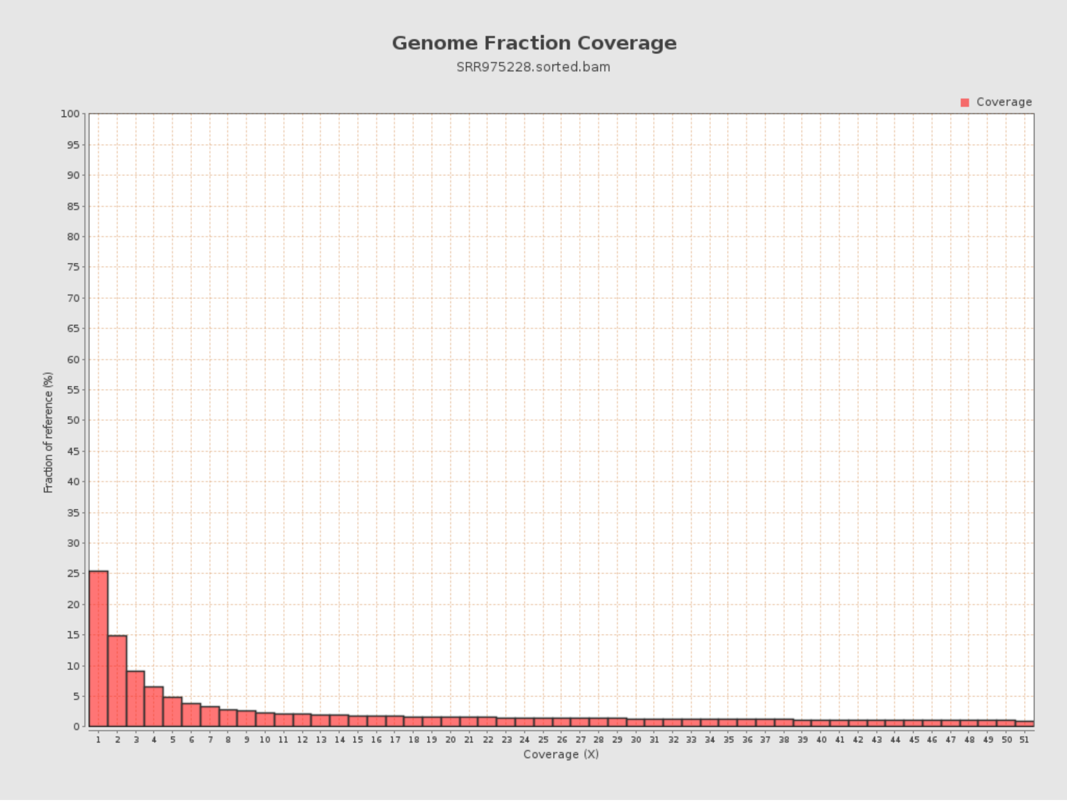
4. Results : Coverage Histogram



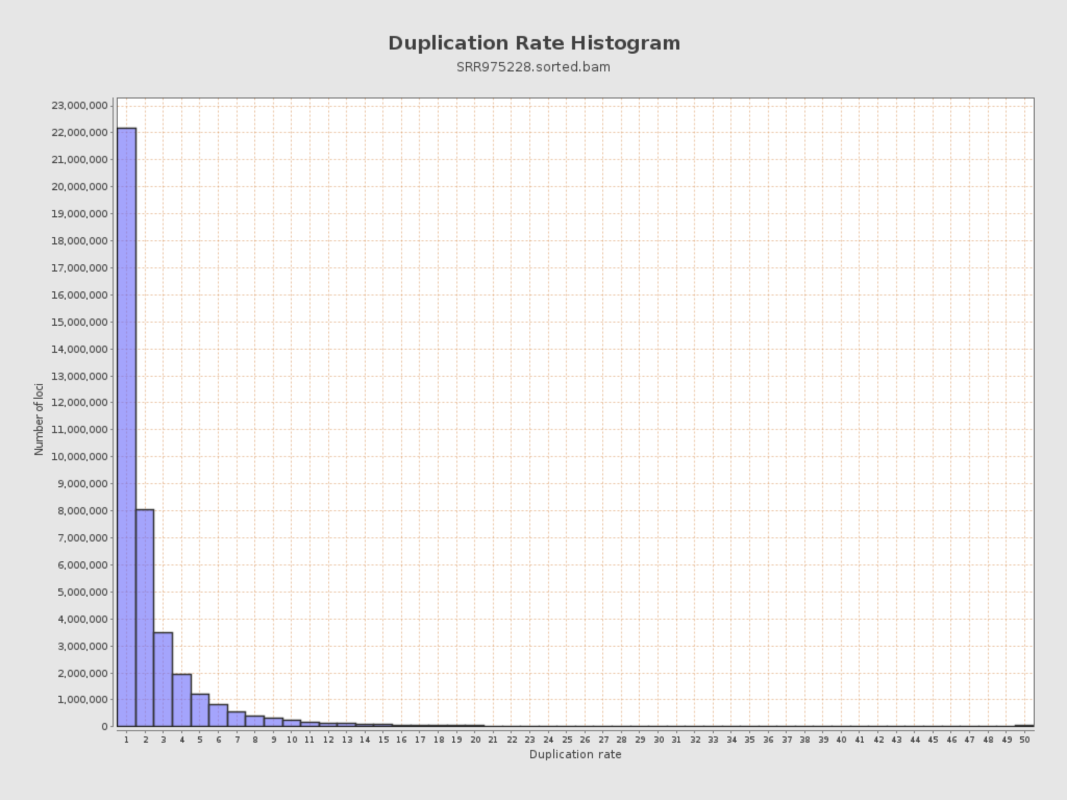
5. Results : Coverage Histogram (0-50X)



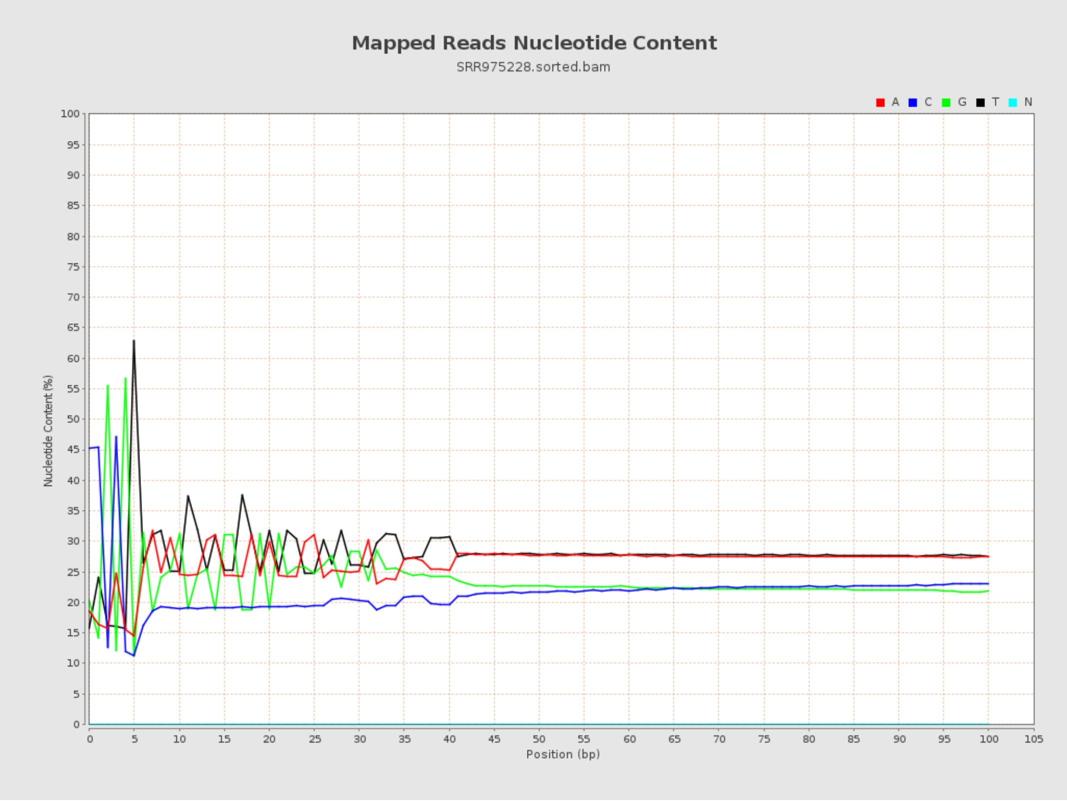
6. Results : Genome Fraction Coverage



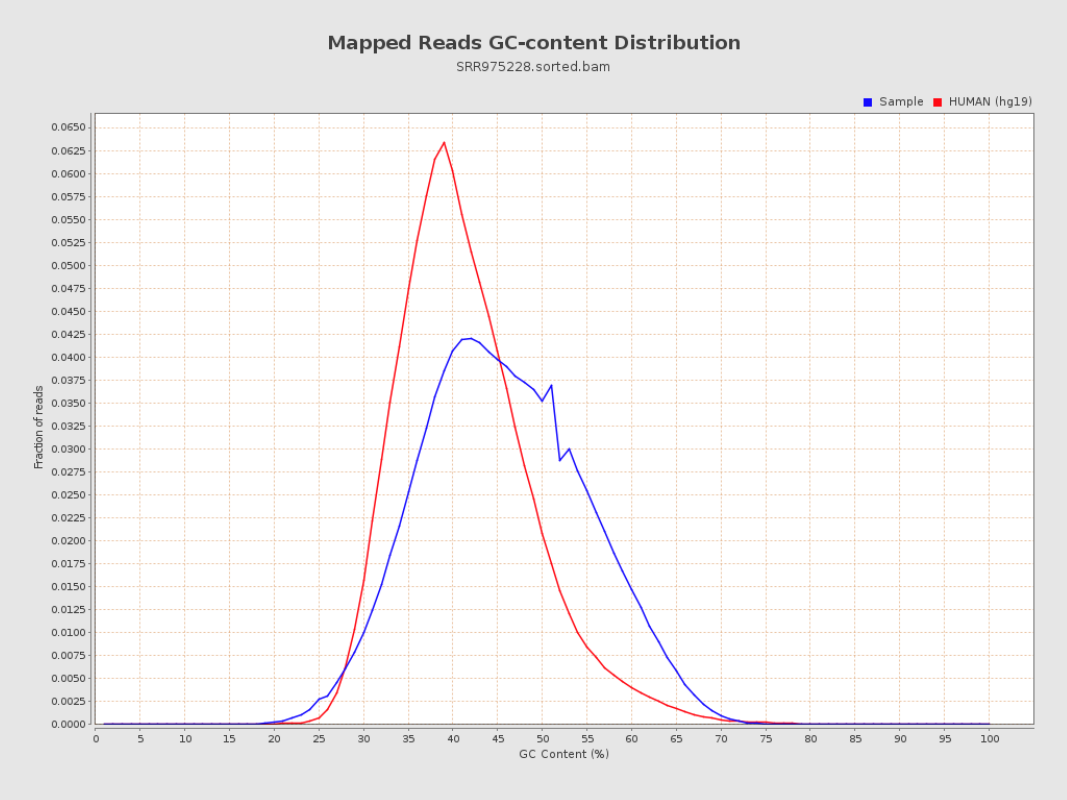
7. Results : Duplication Rate Histogram



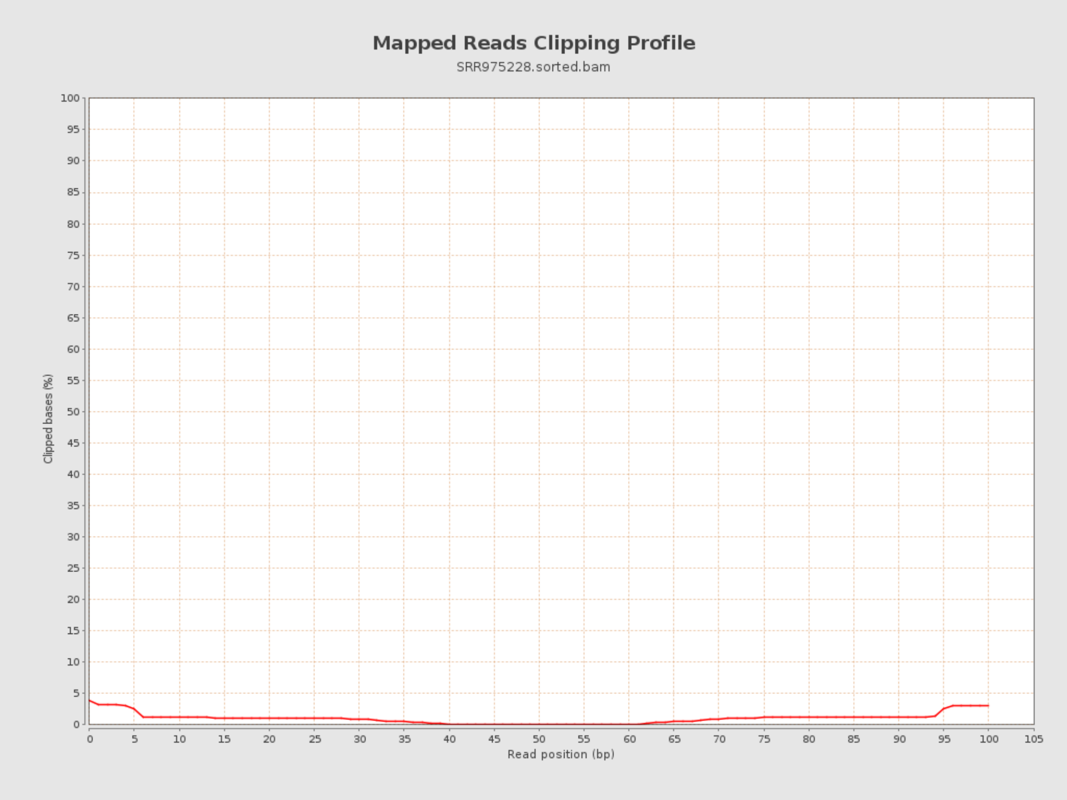
8. Results : Mapped Reads Nucleotide Content



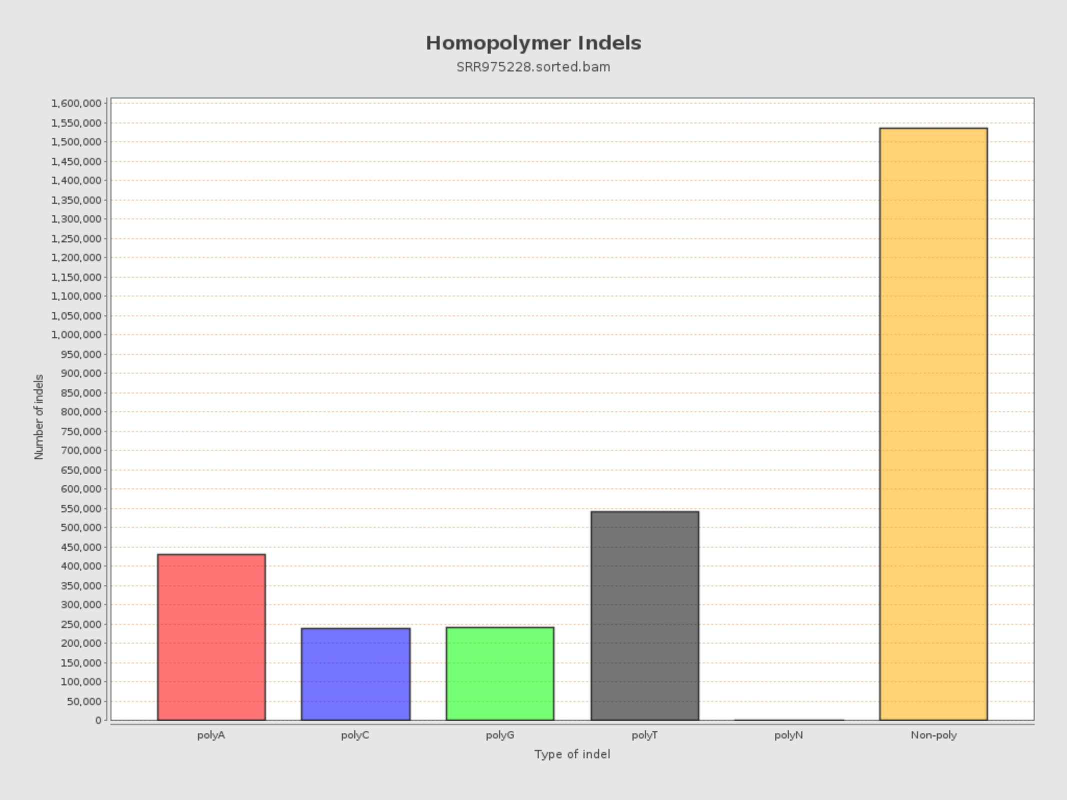
9. Results : Mapped Reads GC-content Distribution



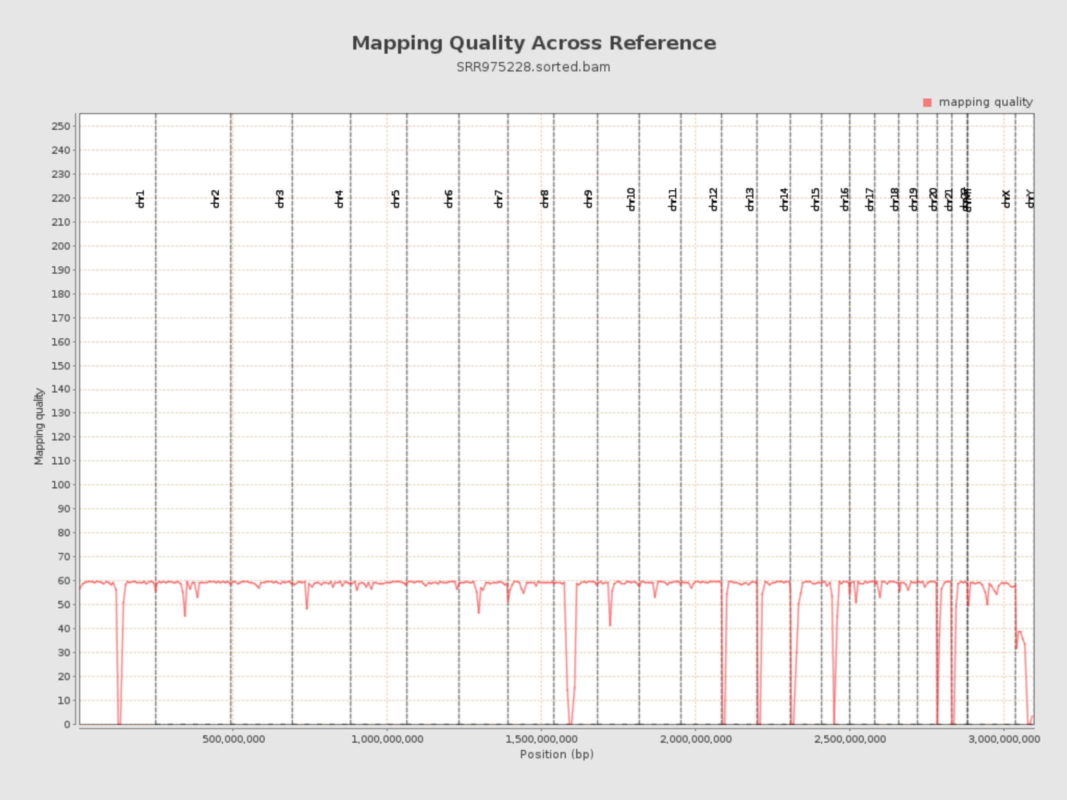
10. Results : Mapped Reads Clipping Profile



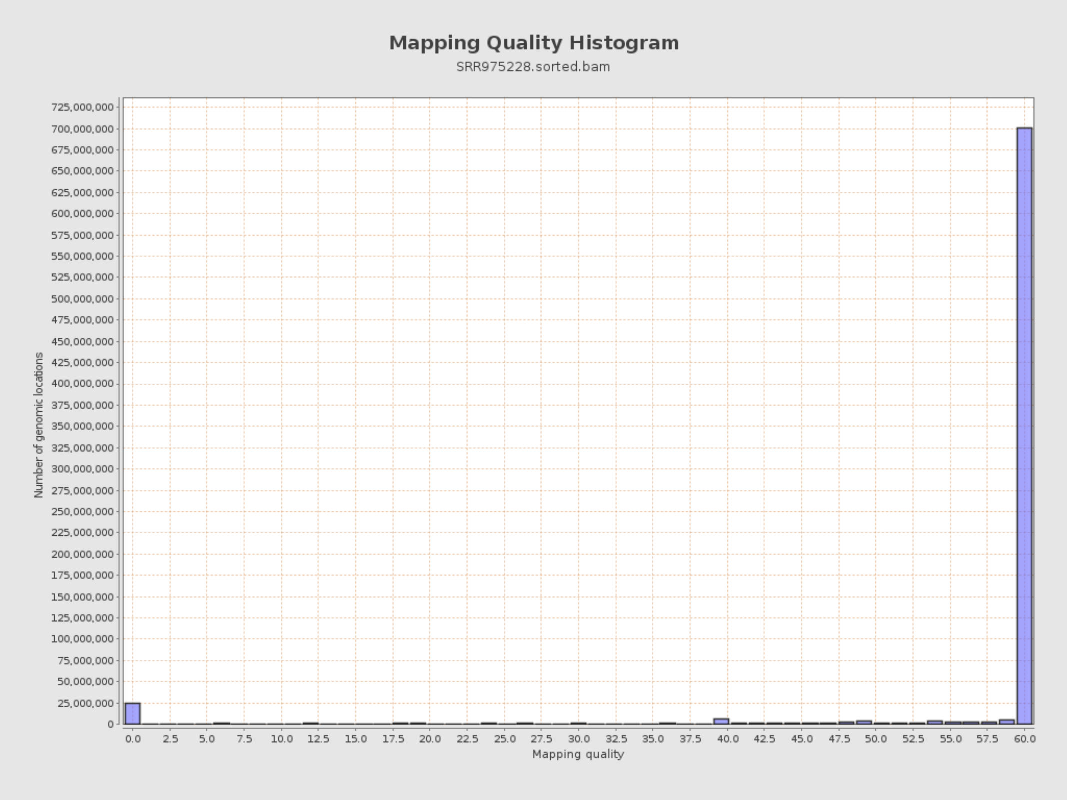
11. Results : Homopolymer Indels



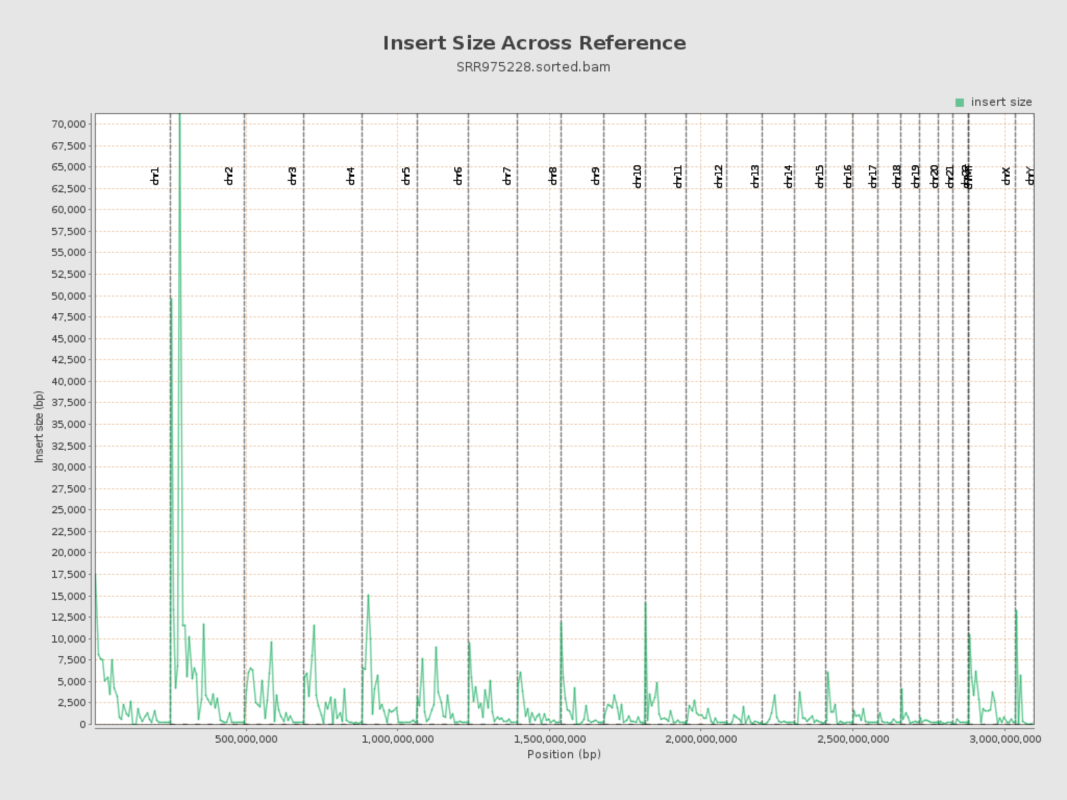
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram