Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 13:48:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975212.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_SRR975212 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975212_1.fastq.gz SRR975212_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 13:48:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975212.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	92,240,876
Mapped reads	92,123,141 / 99.87%
Unmapped reads	117,735 / 0.13%
Mapped paired reads	92,123,141 / 99.87%
Mapped reads, first in pair	46,063,051 / 49.94%
Mapped reads, second in pair	46,060,090 / 49.93%
Mapped reads, both in pair	92,059,848 / 99.8%
Mapped reads, singletons	63,293 / 0.07%
Secondary alignments	0
Supplementary alignments	838,345 / 0.91%
Read min/max/mean length	30 / 101 / 101.37
Duplicated reads (estimated)	58,158,246 / 63.05%
Duplication rate	60.85%
Clipped reads	47,460,268 / 51.45%

2.2. ACGT Content

Number/percentage of A's	2,193,272,597 / 24.34%
Number/percentage of C's	2,317,690,764 / 25.72%
Number/percentage of T's	2,177,702,653 / 24.17%
Number/percentage of G's	2,322,051,921 / 25.77%
Number/percentage of N's	337,805 / 0%

GC Percentage	51.49%

2.3. Coverage

Mean	2.9112
Standard Deviation	25.8343

2.4. Mapping Quality

Mean Mapping Quality	55.86

2.5. Insert size

Mean	136,265.07
Standard Deviation	3,660,814.06
P25/Median/P75	163 / 196 / 235

2.6. Mismatches and indels

General error rate	0.44%
Mismatches	37,980,384
Insertions	820,568
Mapped reads with at least one insertion	0.88%
Deletions	522,007
Mapped reads with at least one deletion	0.56%
Homopolymer indels	32.01%

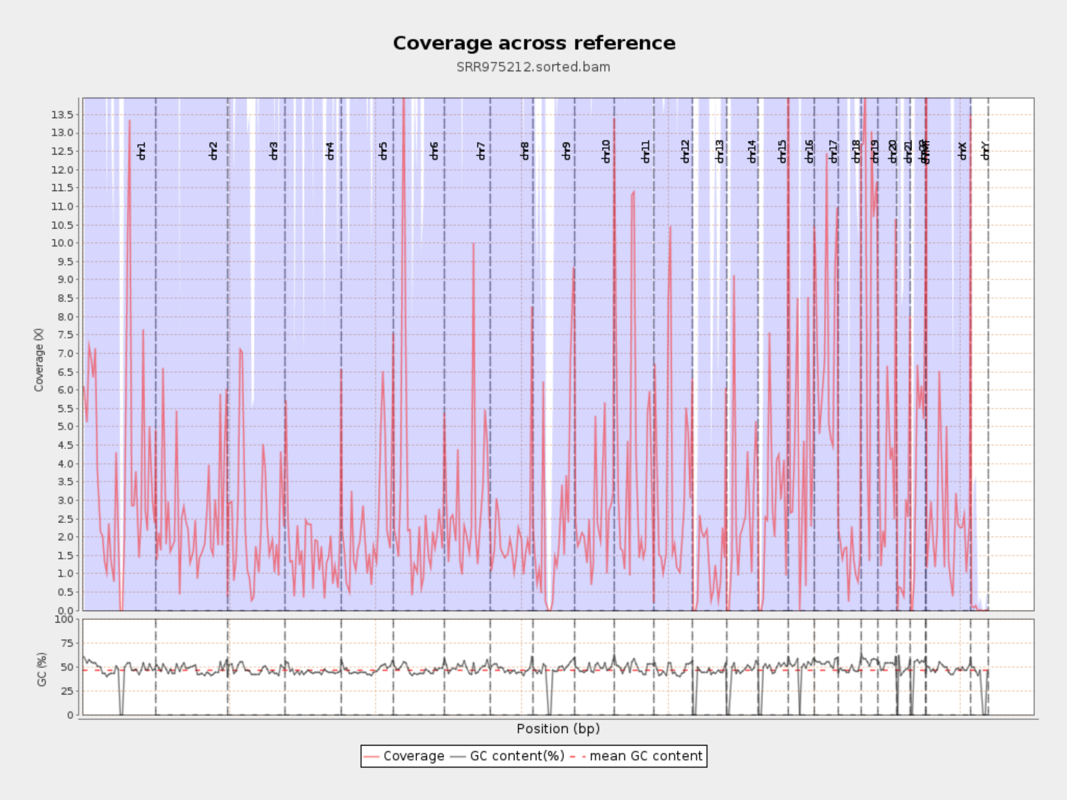
2.7. Chromosome stats

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

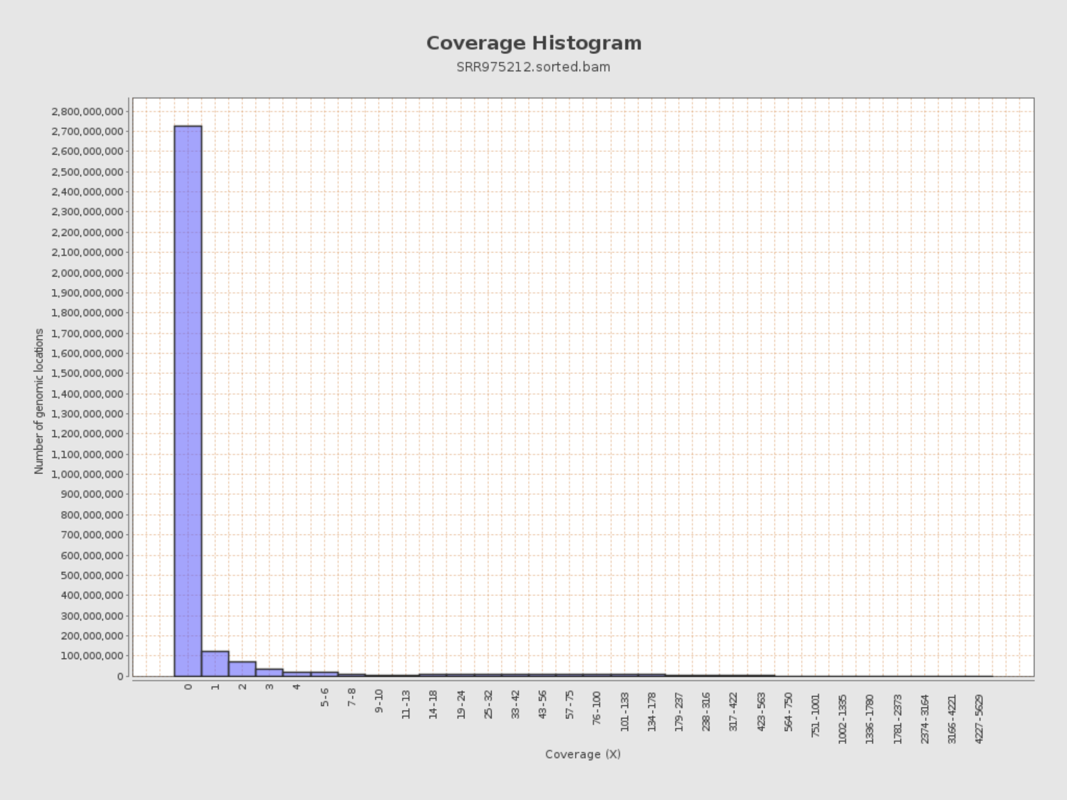
		bases	coverage	deviation
chr1	249250621	952306407	3.8207	31.448
chr2	243199373	611129423	2.5129	22.0766
chr3	198022430	467771281	2.3622	20.5157
chr4	191154276	306861779	1.6053	16.7125
chr5	180915260	436743861	2.4141	22.8109
chr6	171115067	450722046	2.634	24.8794
chr7	159138663	471889256	2.9653	26.878
chr8	146364022	296395912	2.0251	19.6091
chr9	141213431	336615612	2.3837	21.8325
chr10	135534747	336450147	2.4824	22.8348
chr11	135006516	558327505	4.1356	31.7886
chr12	133851895	469870232	3.5104	28.0557
chr13	115169878	145209752	1.2608	14.463
chr14	107349540	290086269	2.7023	24.7699
chr15	102531392	272975442	2.6624	22.4969
chr16	90354753	396045820	4.3832	33.2687
chr17	81195210	583931704	7.1917	44.0689
chr18	78077248	110485612	1.4151	15.0121
chr19	59128983	578606997	9.7855	50.9549
chr20	63025520	237663071	3.7709	28.9184
chr21	48129895	95319568	1.9805	22.2161
chr22	51304566	209726632	4.0879	30.0777
chrMT	16571	5264788	317.7109	443.8387
chrX	155270560	389190445	2.5065	26.3563

chrY	59373566	2645280	0.0446	1.8028

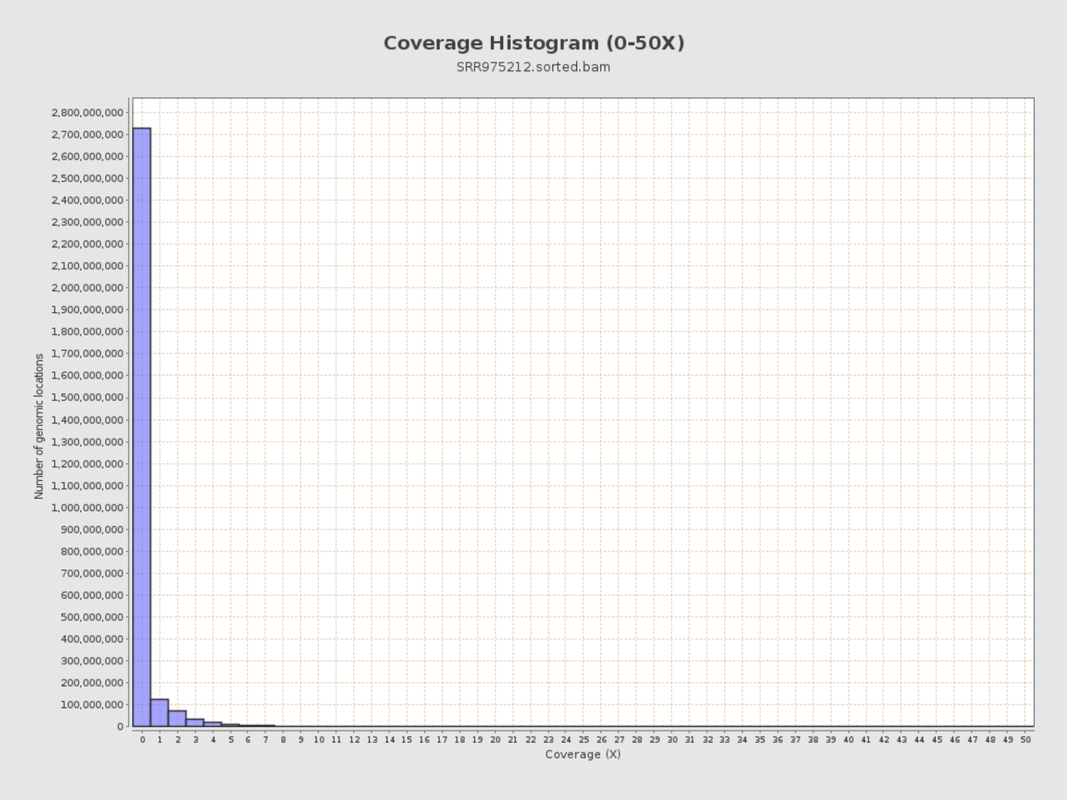
3. Results : Coverage across reference



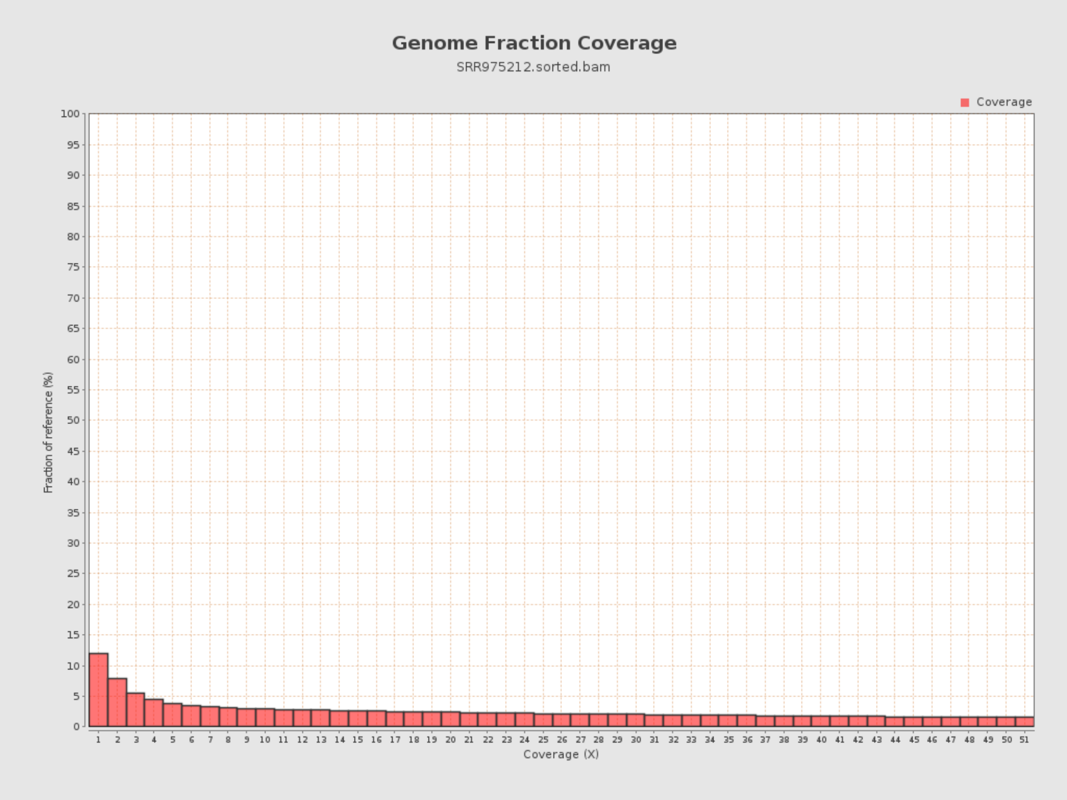
4. Results : Coverage Histogram



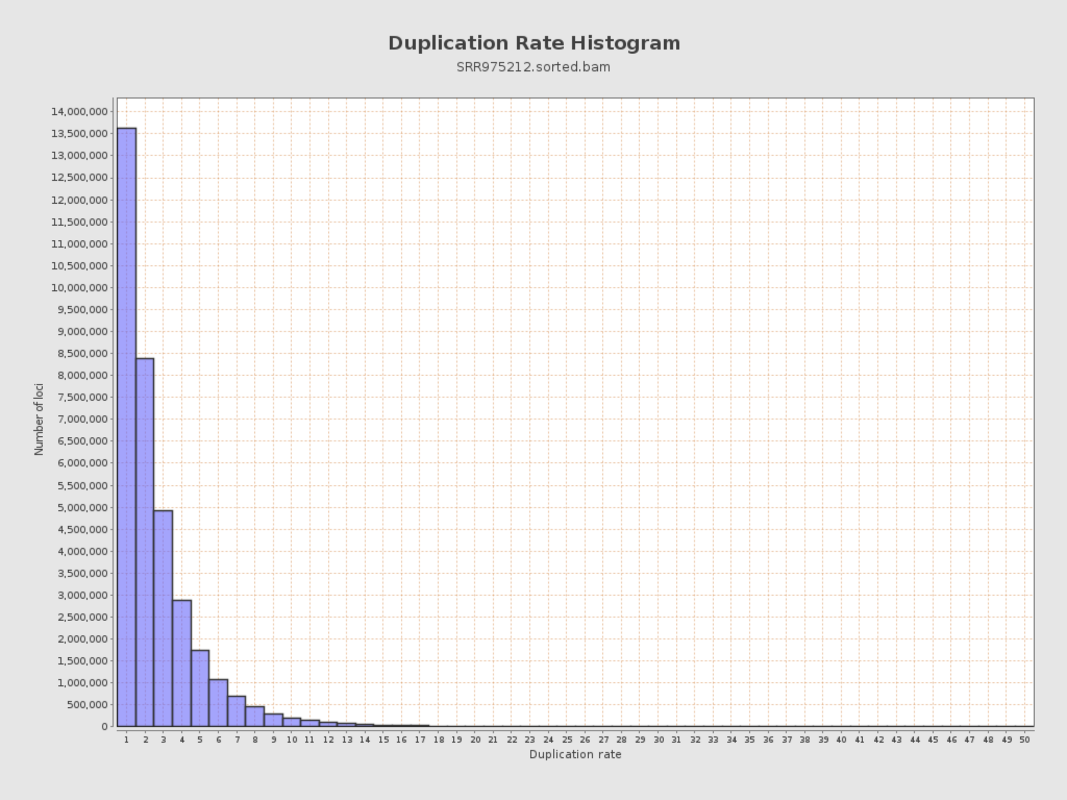
5. Results : Coverage Histogram (0-50X)



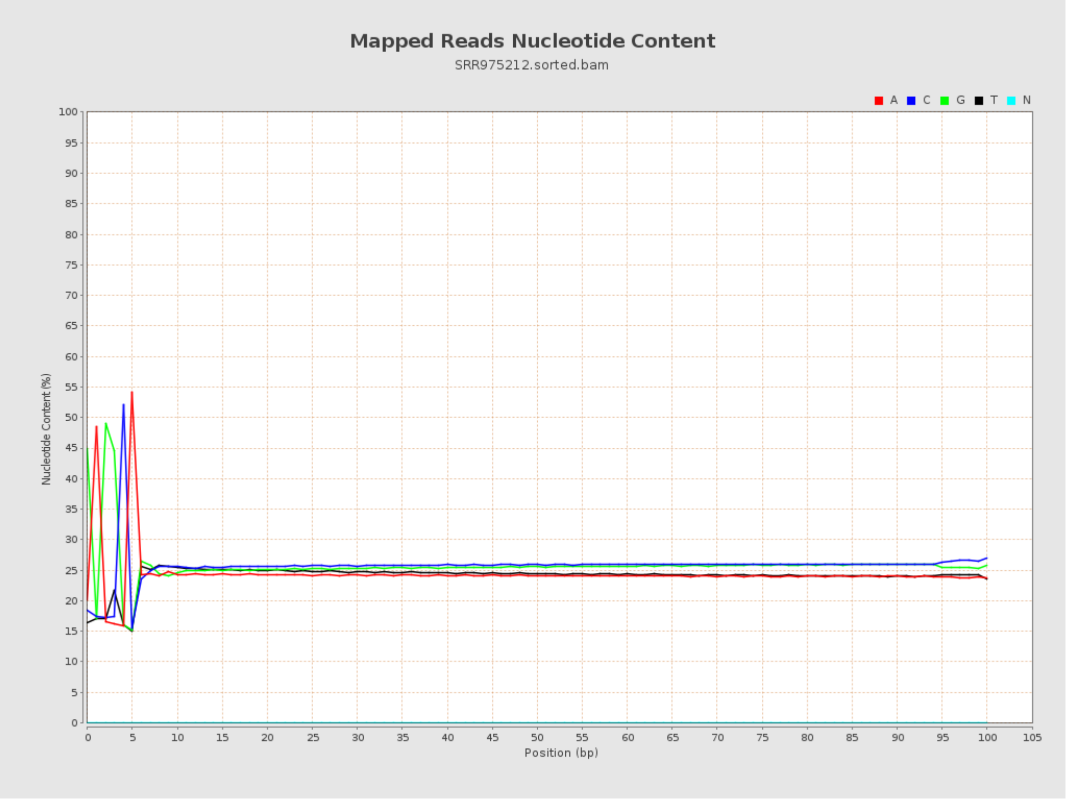
6. Results : Genome Fraction Coverage



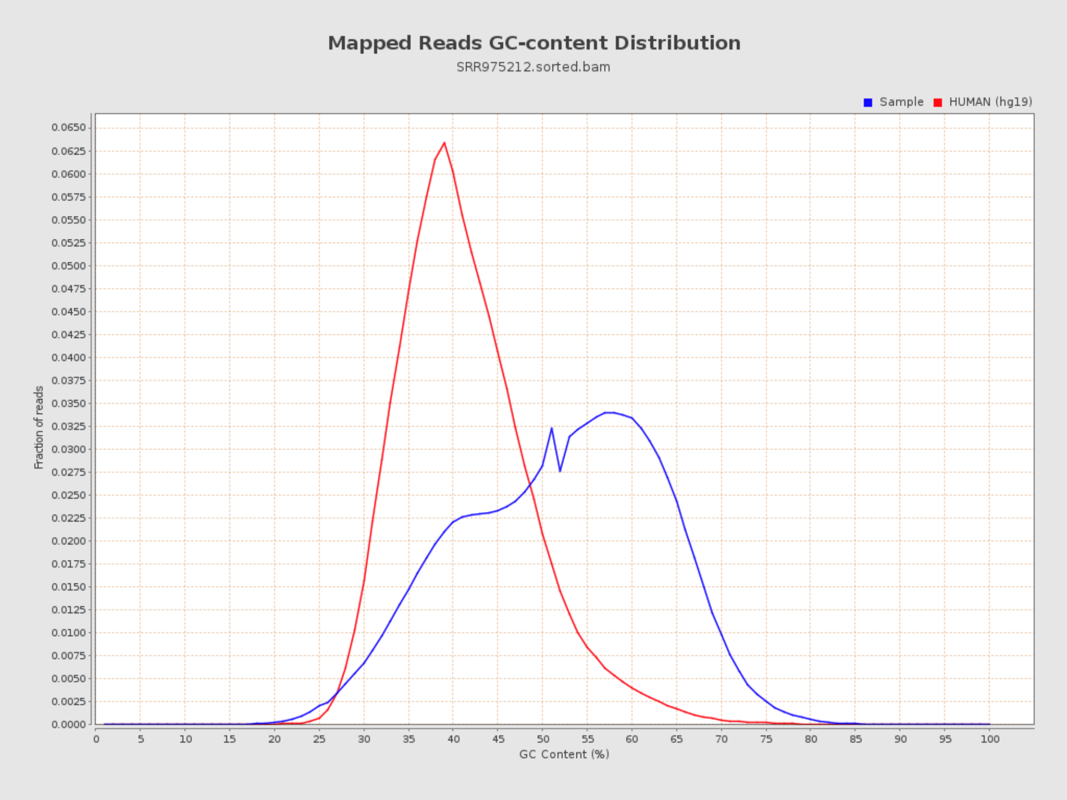
7. Results : Duplication Rate Histogram



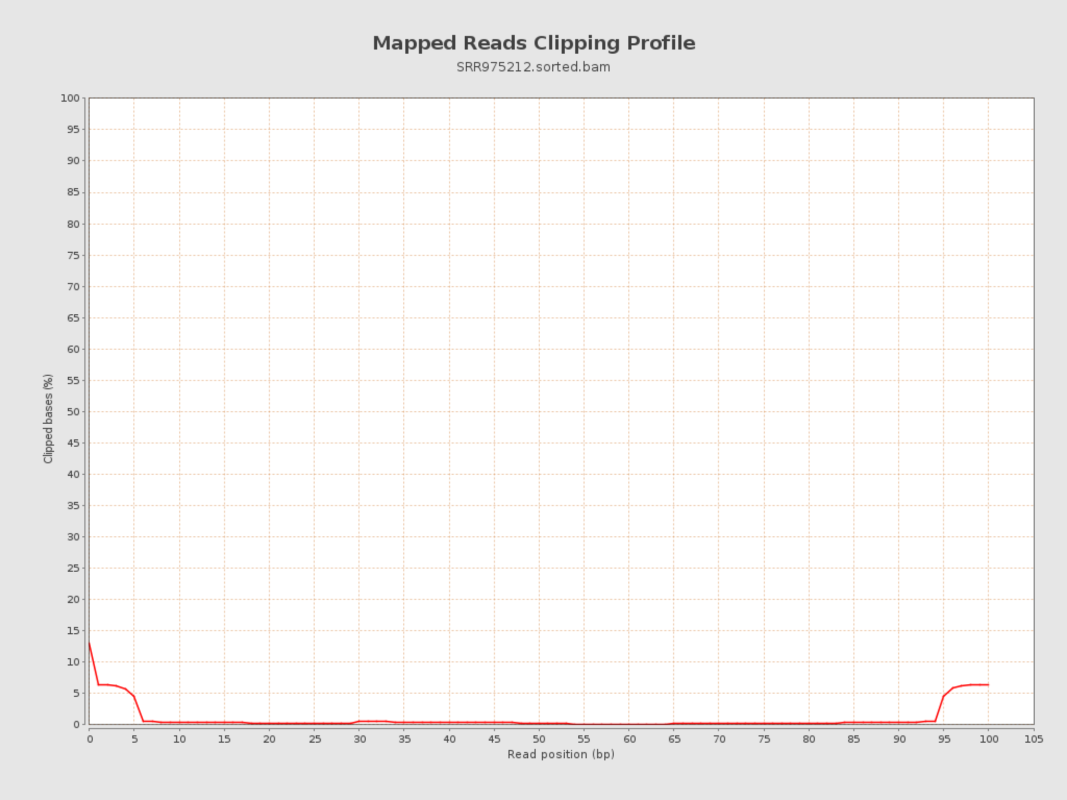
8. Results : Mapped Reads Nucleotide Content



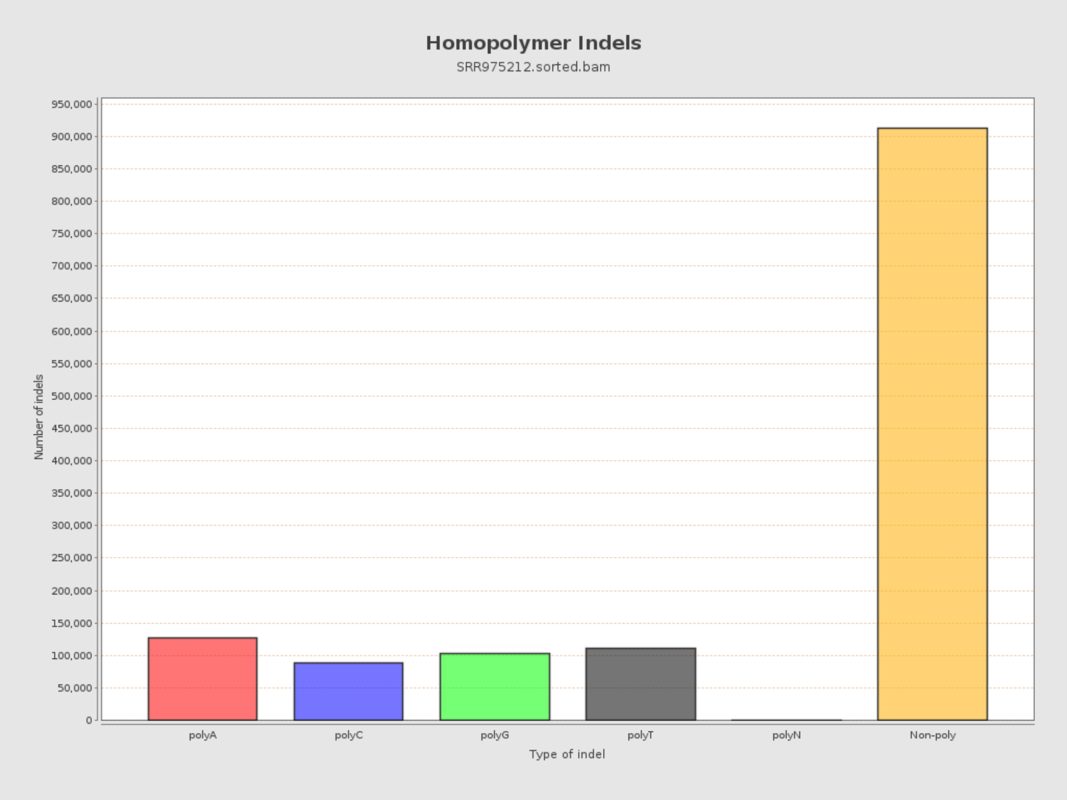
9. Results : Mapped Reads GC-content Distribution



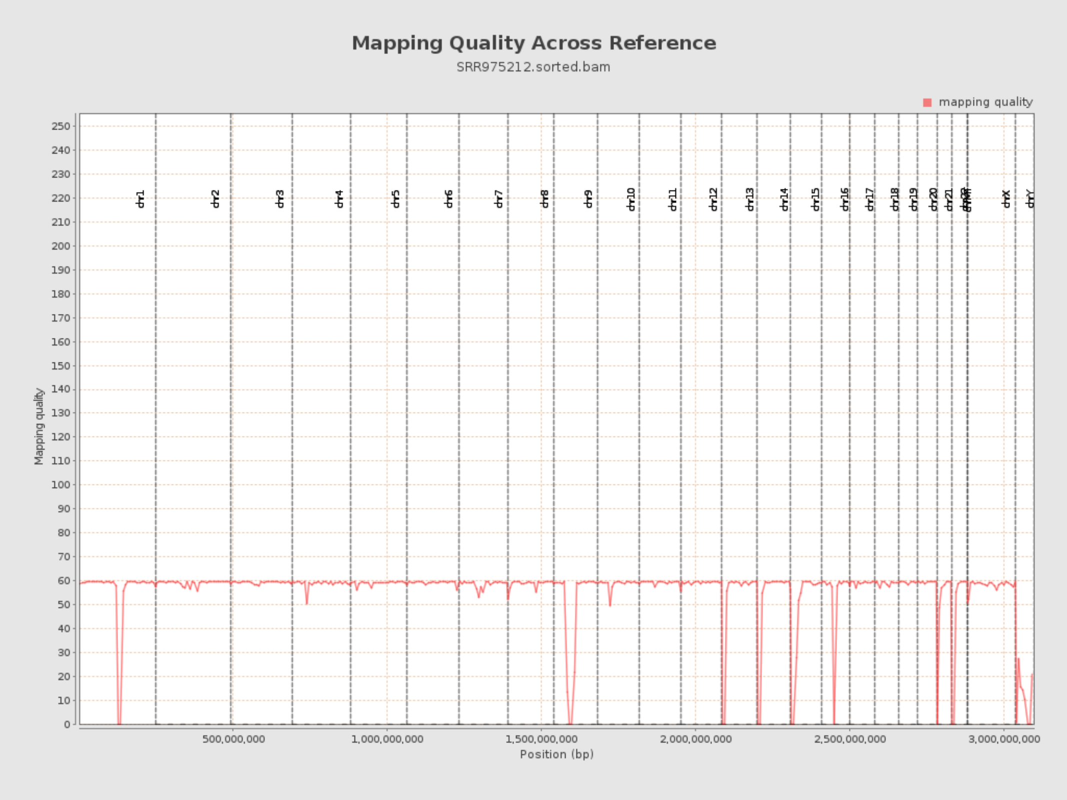
10. Results : Mapped Reads Clipping Profile



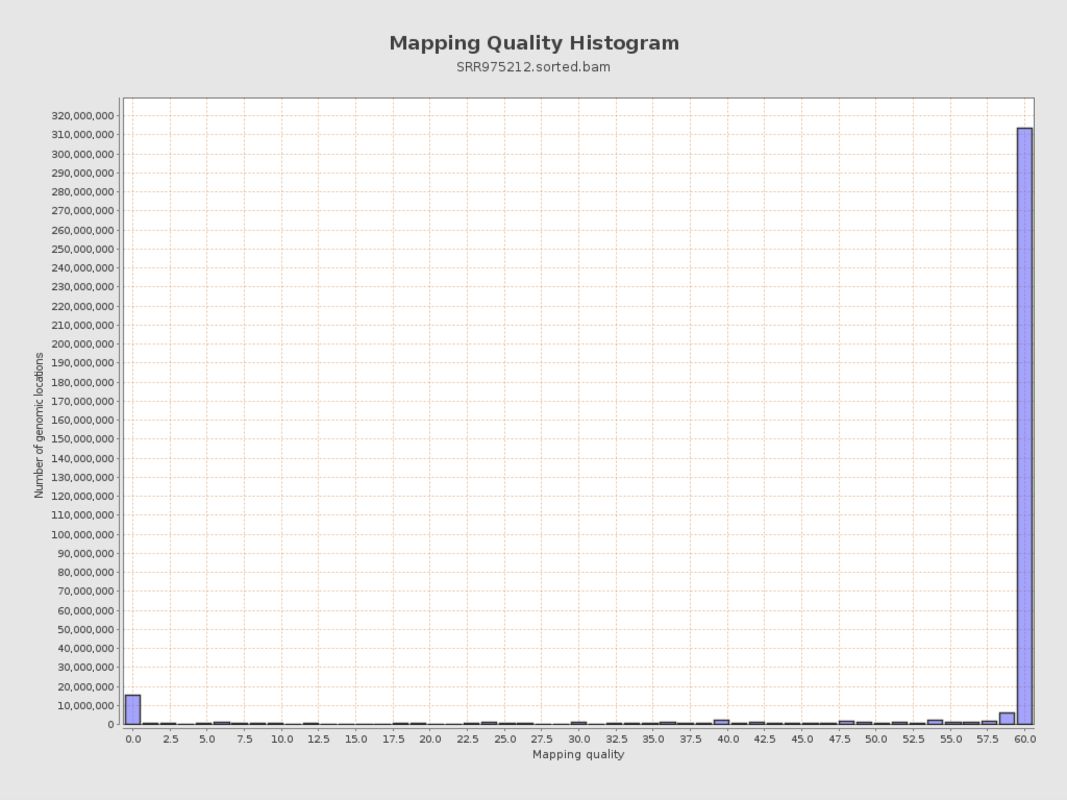
11. Results : Homopolymer Indels



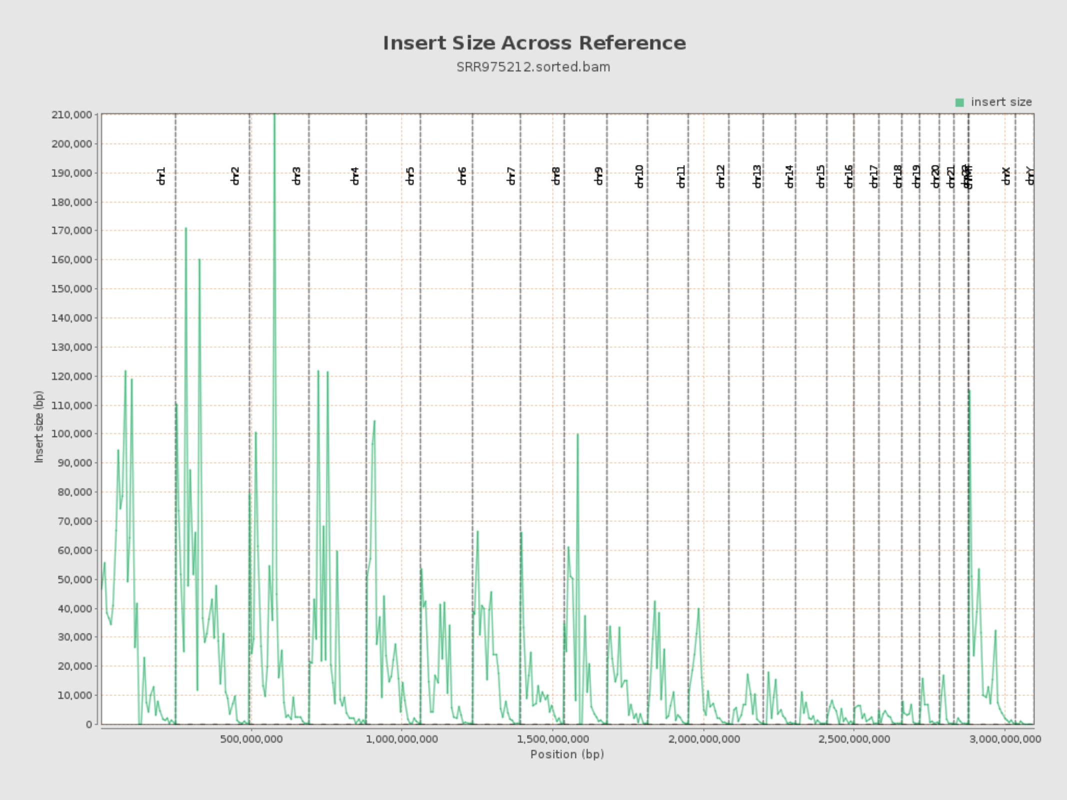
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram