Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 12:26:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975210.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_SRR975210 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975210_1.fastq.gz SRR975210_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 12:26:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975210.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	76,468,628
Mapped reads	76,394,166 / 99.9%
Unmapped reads	74,462 / 0.1%
Mapped paired reads	76,394,166 / 99.9%
Mapped reads, first in pair	38,199,533 / 49.95%
Mapped reads, second in pair	38,194,633 / 49.95%
Mapped reads, both in pair	76,361,418 / 99.86%
Mapped reads, singletons	32,748 / 0.04%
Secondary alignments	0
Supplementary alignments	563,380 / 0.74%
Read min/max/mean length	30 / 101 / 101.3
Duplicated reads (estimated)	47,443,720 / 62.04%
Duplication rate	60.81%
Clipped reads	39,037,809 / 51.05%

2.2. ACGT Content

Number/percentage of A's	1,879,790,352 / 25.16%
Number/percentage of C's	1,835,749,386 / 24.57%
Number/percentage of T's	1,934,886,769 / 25.9%
Number/percentage of G's	1,820,607,807 / 24.37%
Number/percentage of N's	270,087 / 0%

GC Percentage	48.94%

2.3. Coverage

Mean	2.4137
Standard Deviation	21.591

2.4. Mapping Quality

Mean Mapping Quality	56.08

2.5. Insert size

Mean	102,621.39
Standard Deviation	3,218,840.04
P25/Median/P75	158 / 189 / 227

2.6. Mismatches and indels

General error rate	0.41%
Mismatches	29,487,243
Insertions	610,480
Mapped reads with at least one insertion	0.79%
Deletions	406,842
Mapped reads with at least one deletion	0.52%
Homopolymer indels	33.02%

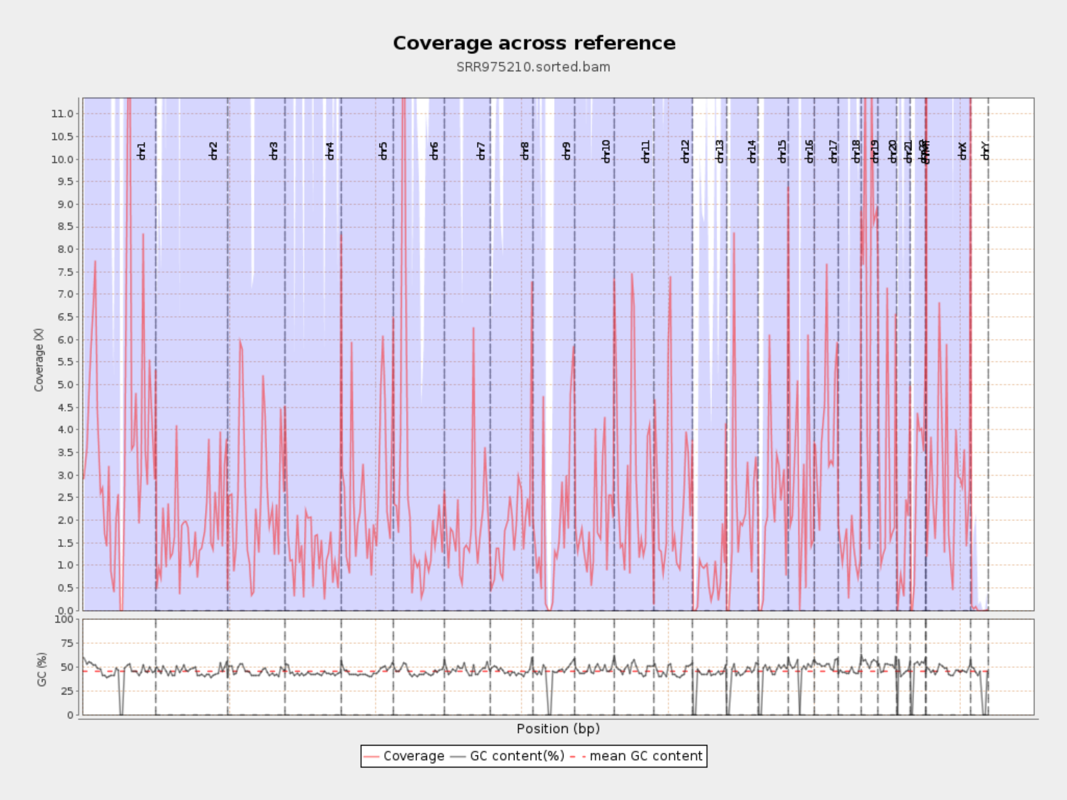
2.7. Chromosome stats

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

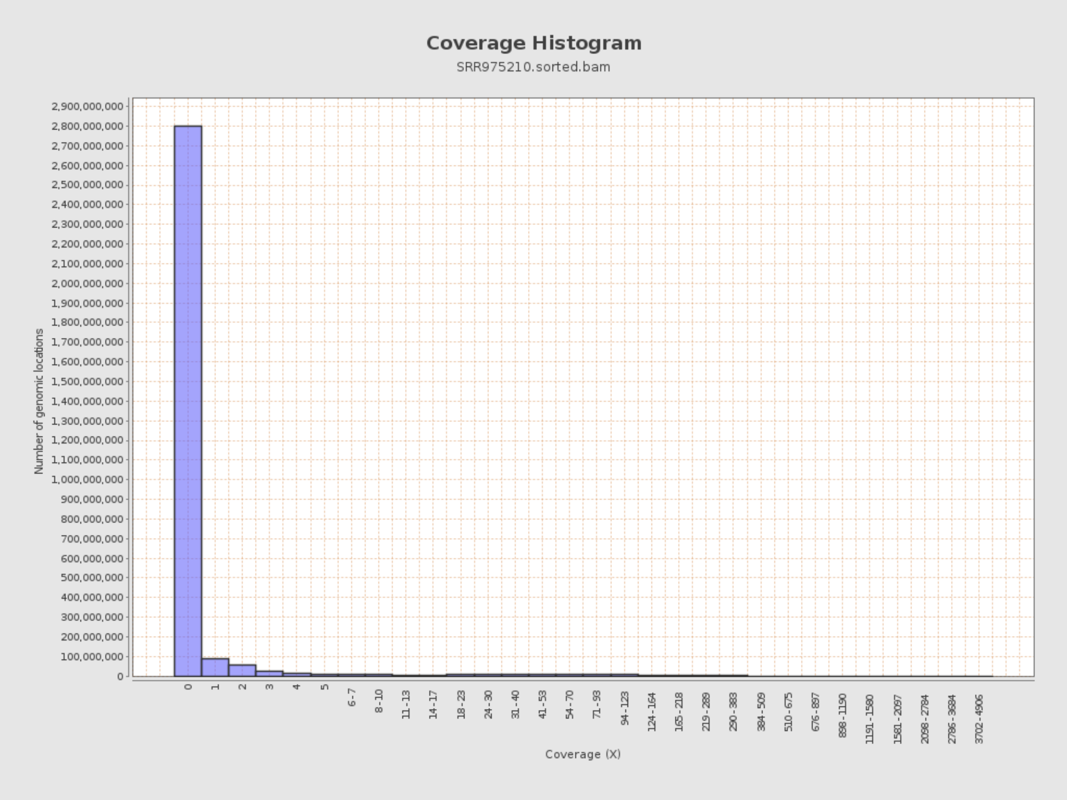
		bases	coverage	deviation
chr1	249250621	974626696	3.9102	32.1209
chr2	243199373	442954413	1.8214	15.5612
chr3	198022430	487643991	2.4626	20.7643
chr4	191154276	255525676	1.3368	13.3131
chr5	180915260	489029546	2.7031	24.774
chr6	171115067	418914984	2.4481	23.6369
chr7	159138663	307208652	1.9304	17.2397
chr8	146364022	286015797	1.9541	19.4655
chr9	141213431	259598689	1.8383	16.2089
chr10	135534747	265246948	1.957	17.3844
chr11	135006516	389505396	2.8851	21.5807
chr12	133851895	356307888	2.662	20.385
chr13	115169878	87881420	0.7631	9.0278
chr14	107349540	252170360	2.3491	21.8025
chr15	102531392	223088249	2.1758	17.6679
chr16	90354753	253283349	2.8032	21.4894
chr17	81195210	326202193	4.0175	24.6656
chr18	78077248	100237570	1.2838	13.2752
chr19	59128983	457793915	7.7423	41.3256
chr20	63025520	165797454	2.6306	21.9569
chr21	48129895	70631467	1.4675	14.912
chr22	51304566	139966441	2.7281	20.1462
chrMT	16571	3452787	208.3632	279.432
chrX	155270560	457441703	2.9461	29.5723

chrY	59373566	1695502	0.0286	1.001

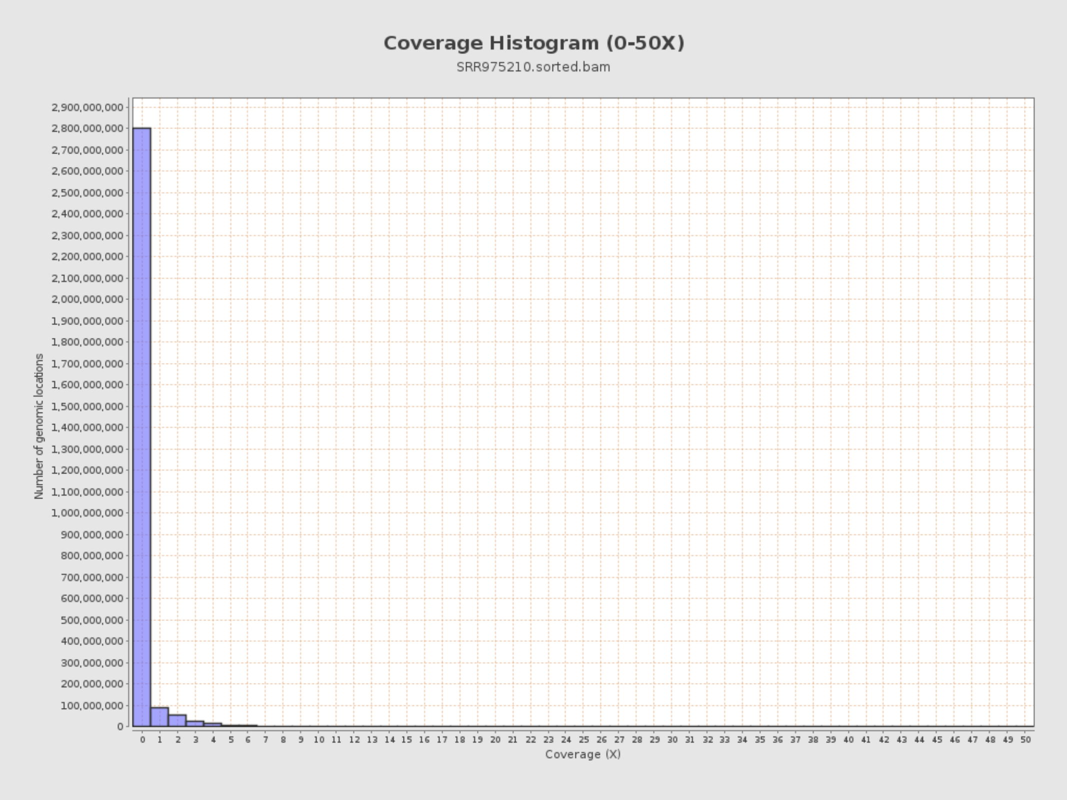
3. Results : Coverage across reference



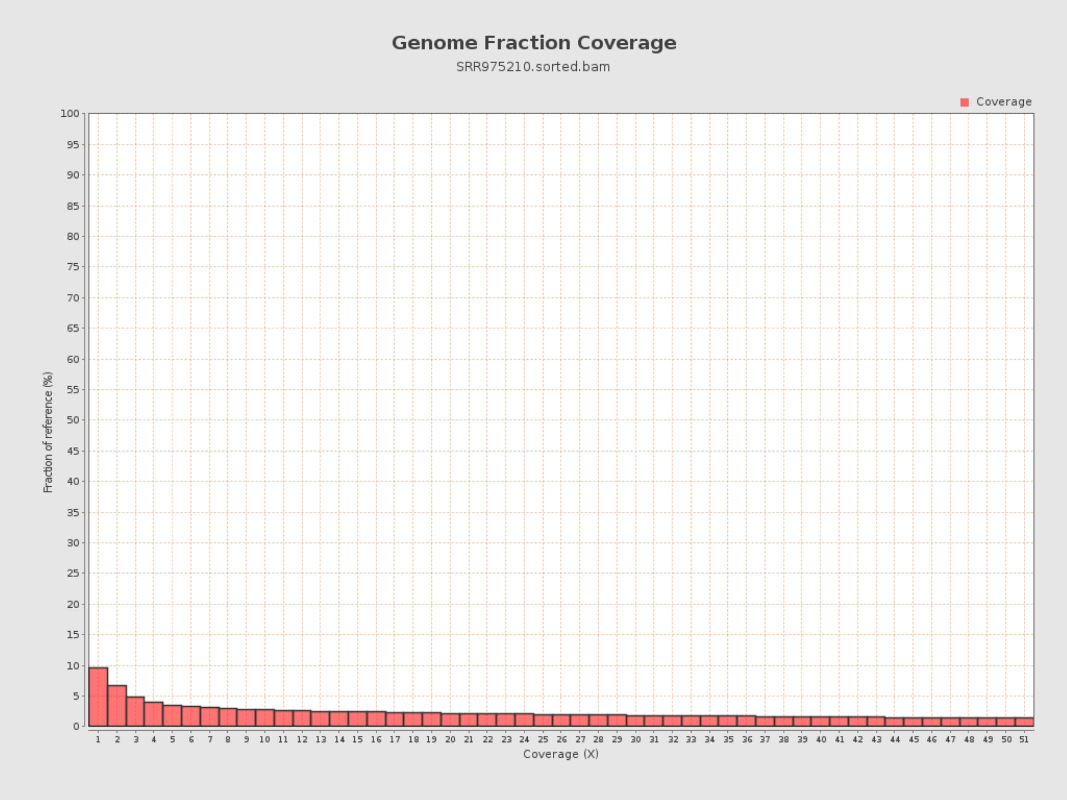
4. Results : Coverage Histogram



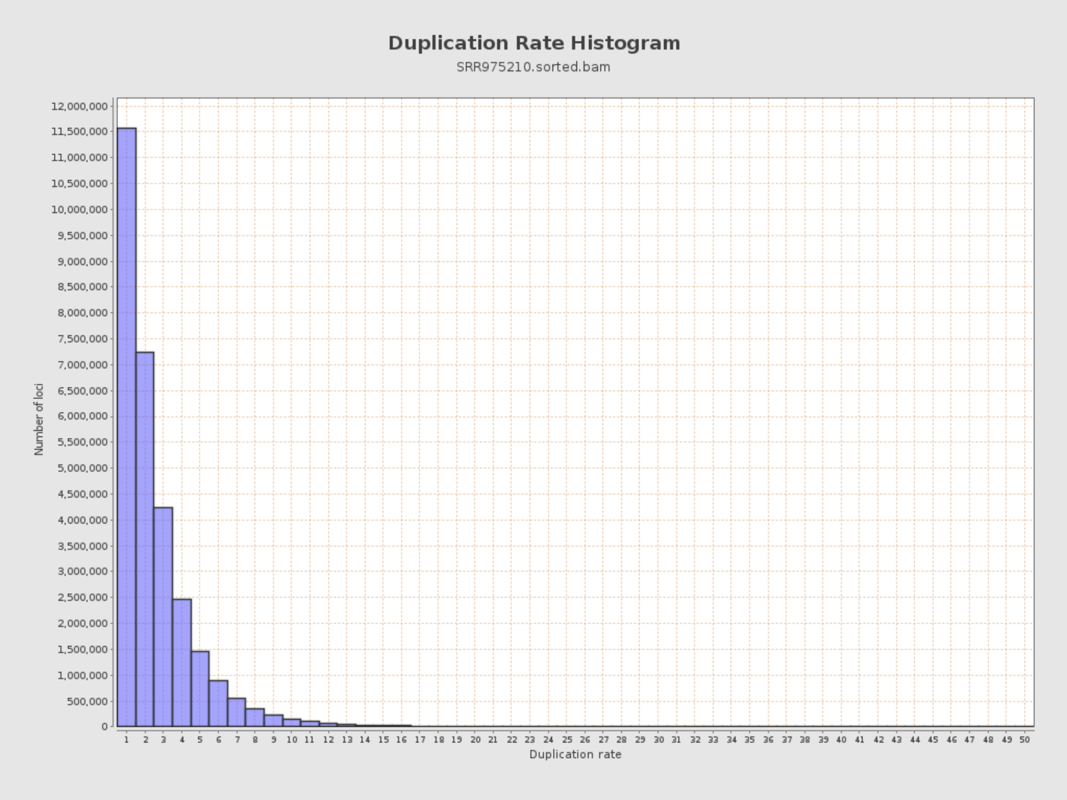
5. Results : Coverage Histogram (0-50X)



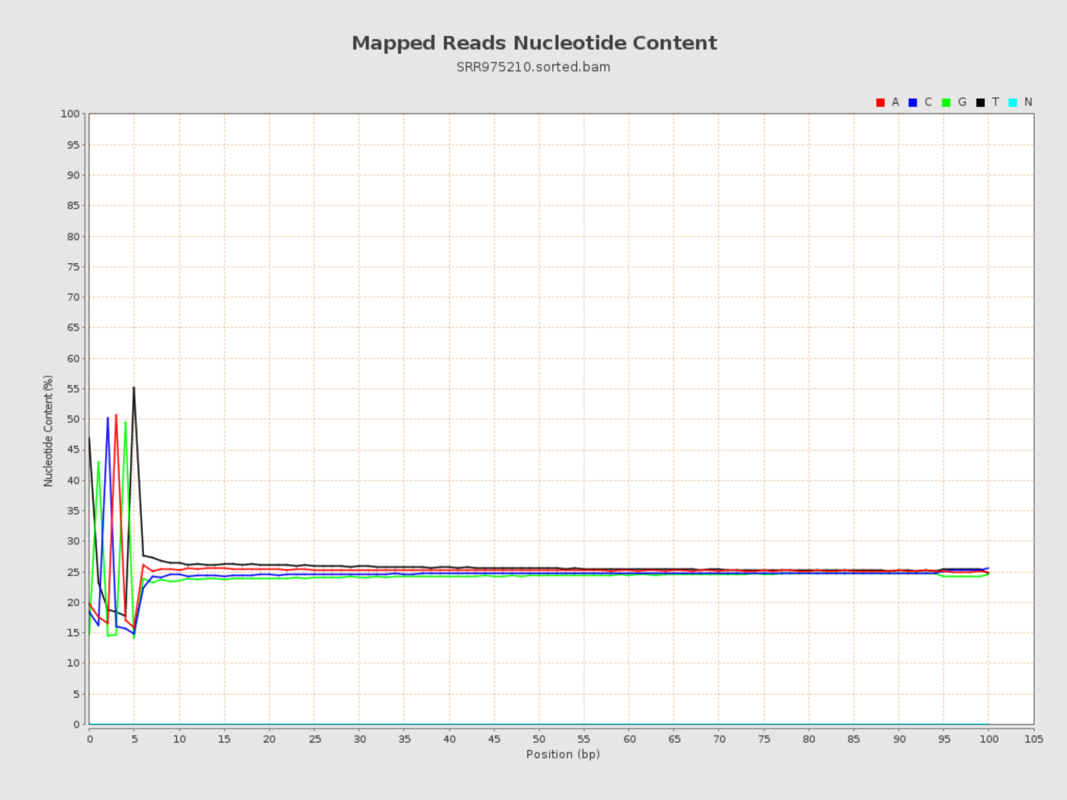
6. Results : Genome Fraction Coverage



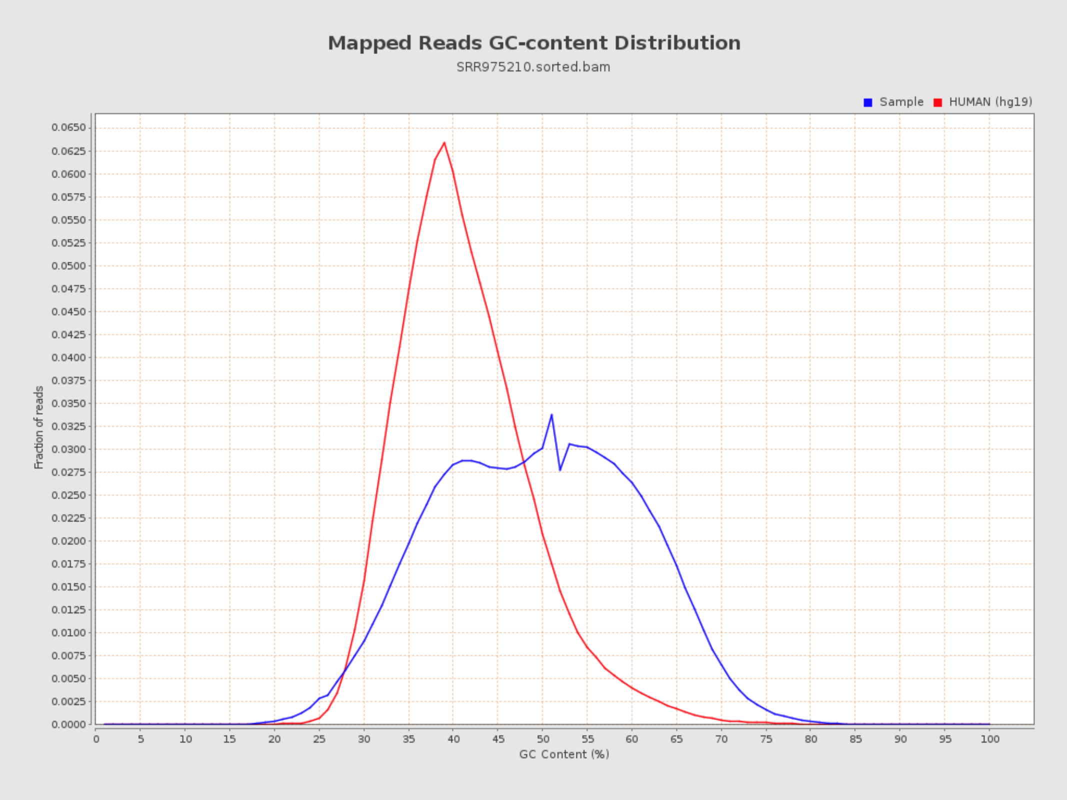
7. Results : Duplication Rate Histogram



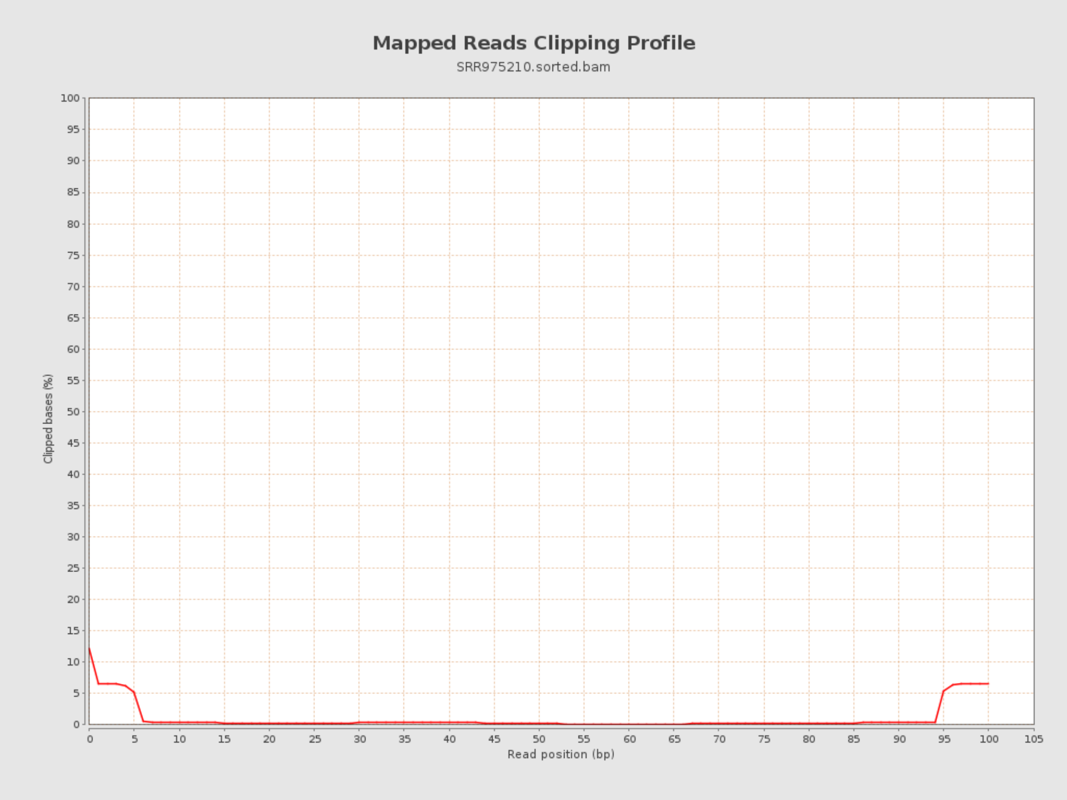
8. Results : Mapped Reads Nucleotide Content



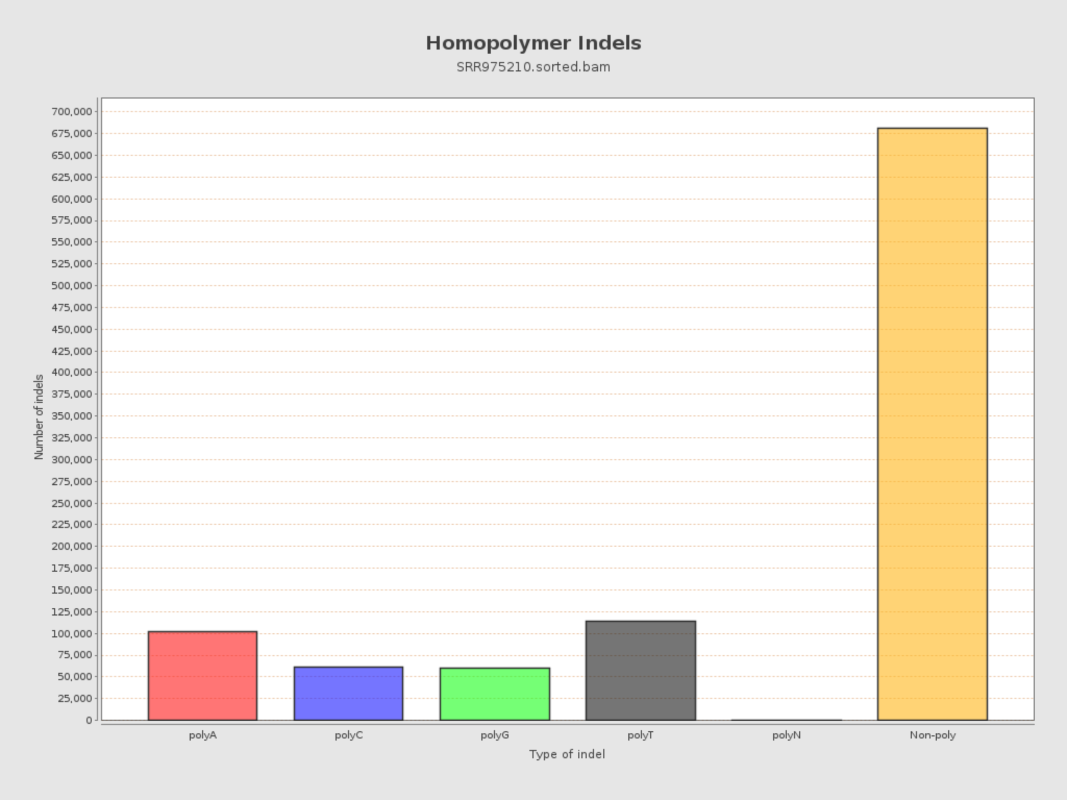
9. Results : Mapped Reads GC-content Distribution



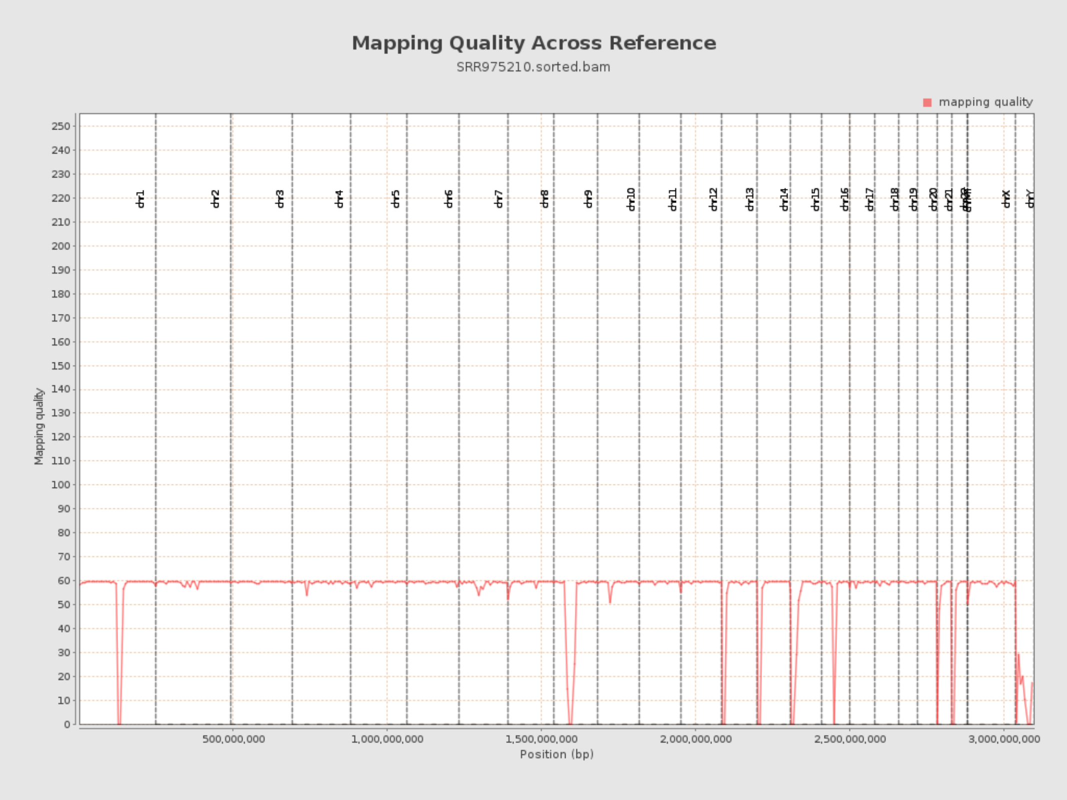
10. Results : Mapped Reads Clipping Profile



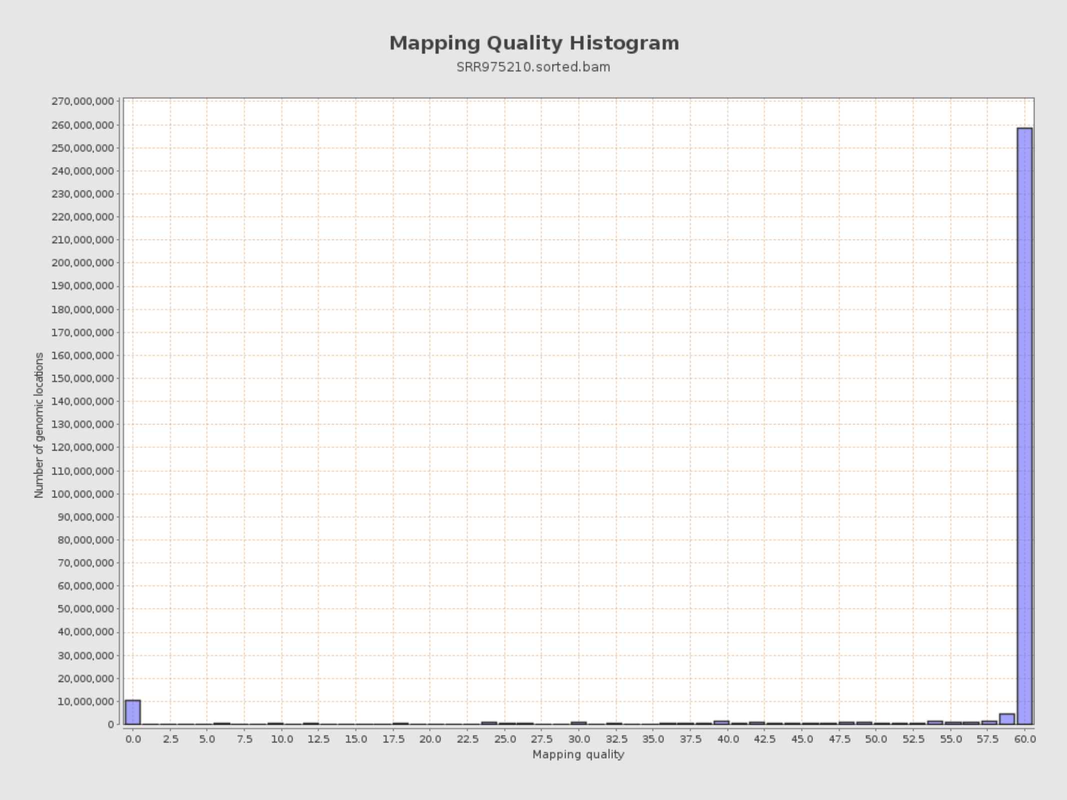
11. Results : Homopolymer Indels



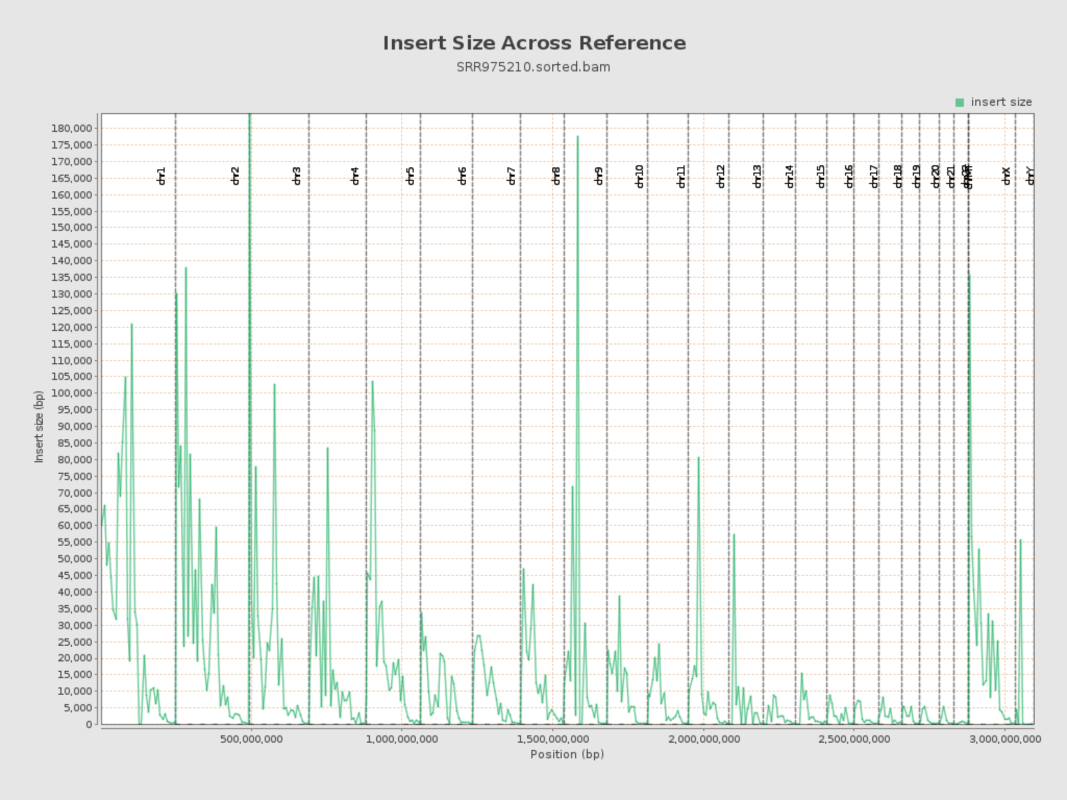
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram