Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 11:17:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975208.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_SRR975208 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975208_1.fastq.gz SRR975208_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 11:17:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975208.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	33,099,416
Mapped reads	33,028,764 / 99.79%
Unmapped reads	70,652 / 0.21%
Mapped paired reads	33,028,764 / 99.79%
Mapped reads, first in pair	16,516,707 / 49.9%
Mapped reads, second in pair	16,512,057 / 49.89%
Mapped reads, both in pair	32,981,992 / 99.65%
Mapped reads, singletons	46,772 / 0.14%
Secondary alignments	0
Supplementary alignments	59,386 / 0.18%
Read min/max/mean length	30 / 101 / 101.07
Duplicated reads (estimated)	20,286,002 / 61.29%
Duplication rate	45.64%
Clipped reads	19,301,839 / 58.31%

2.2. ACGT Content

Number/percentage of A's	865,894,841 / 27.74%
Number/percentage of C's	660,838,759 / 21.17%
Number/percentage of T's	901,354,448 / 28.88%
Number/percentage of G's	692,861,494 / 22.2%
Number/percentage of N's	145,755 / 0%

GC Percentage	43.37%

2.3. Coverage

Mean	1.0086
Standard Deviation	17.7167

2.4. Mapping Quality

Mean Mapping Quality	55.99

2.5. Insert size

Mean	121,215.57
Standard Deviation	3,375,856.62
P25/Median/P75	194 / 237 / 286

2.6. Mismatches and indels

General error rate	0.72%
Mismatches	21,809,748
Insertions	325,069
Mapped reads with at least one insertion	0.97%
Deletions	721,494
Mapped reads with at least one deletion	2.15%
Homopolymer indels	47.79%

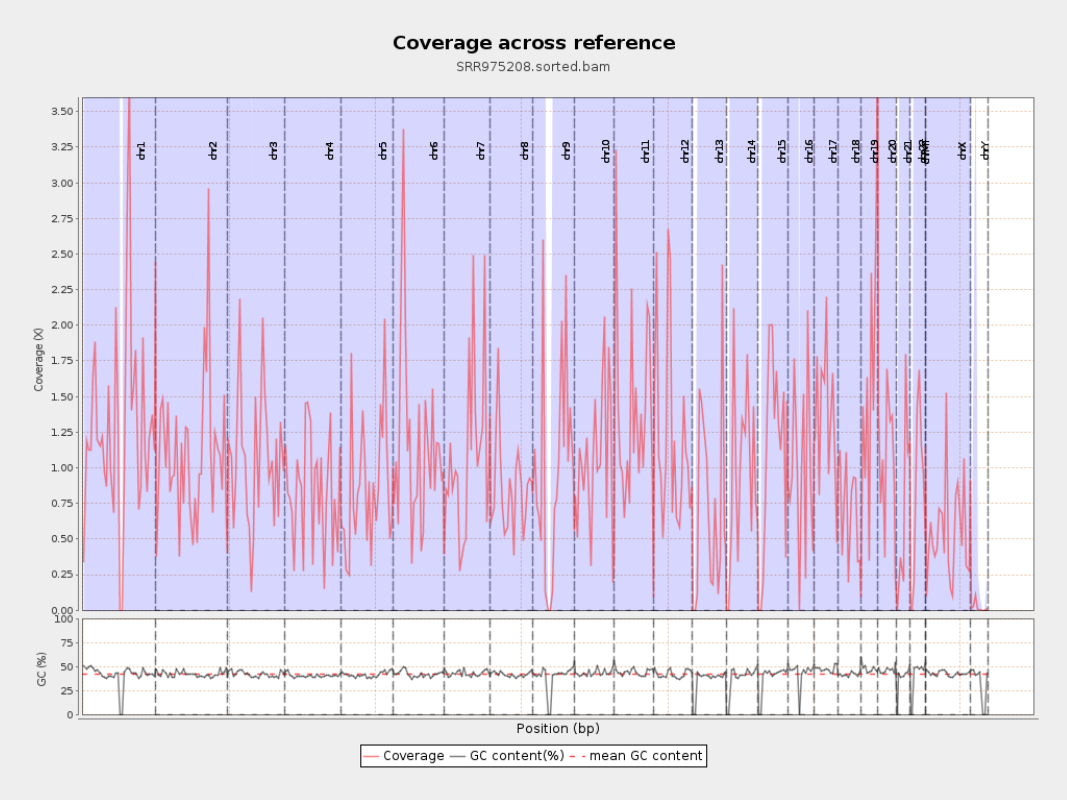
2.7. Chromosome stats

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

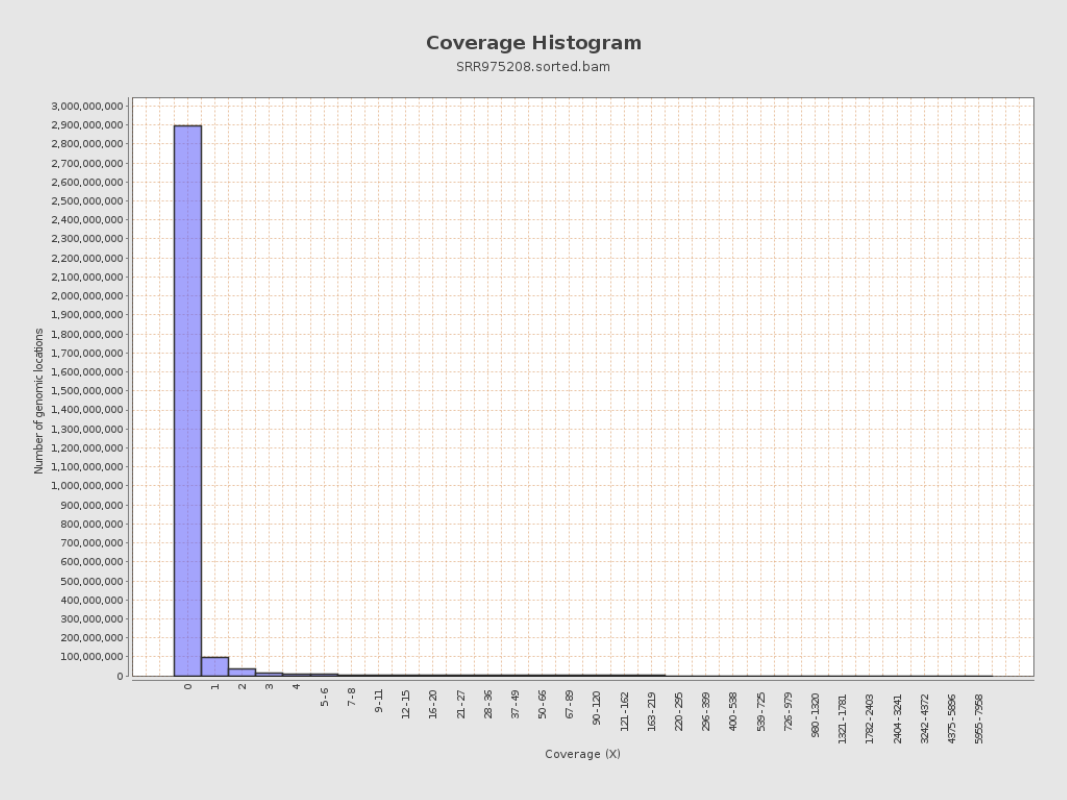
		bases	coverage	deviation
chr1	249250621	321069820	1.2881	20.0187
chr2	243199373	267252390	1.0989	18.3168
chr3	198022430	210272111	1.0619	17.1078
chr4	191154276	161188778	0.8432	14.8428
chr5	180915260	157114454	0.8684	14.7606
chr6	171115067	198096495	1.1577	19.8422
chr7	159138663	168796919	1.0607	19.6869
chr8	146364022	126635292	0.8652	14.552
chr9	141213431	135957046	0.9628	18.1585
chr10	135534747	146642225	1.082	19.0797
chr11	135006516	185694553	1.3754	21.4367
chr12	133851895	165213898	1.2343	18.7614
chr13	115169878	83852279	0.7281	16.5663
chr14	107349540	104318918	0.9718	17.9873
chr15	102531392	109312716	1.0661	16.9964
chr16	90354753	86143424	0.9534	16.4812
chr17	81195210	112365962	1.3839	19.0667
chr18	78077248	56704470	0.7263	14.8846
chr19	59128983	95492660	1.615	26.6421
chr20	63025520	66489118	1.055	19.5314
chr21	48129895	33741322	0.701	15.7765
chr22	51304566	43061570	0.8393	16.829
chrMT	16571	19077	1.1512	3.2553
chrX	155270560	85518201	0.5508	12.7966

chrY	59373566	1214145	0.0204	1.5067

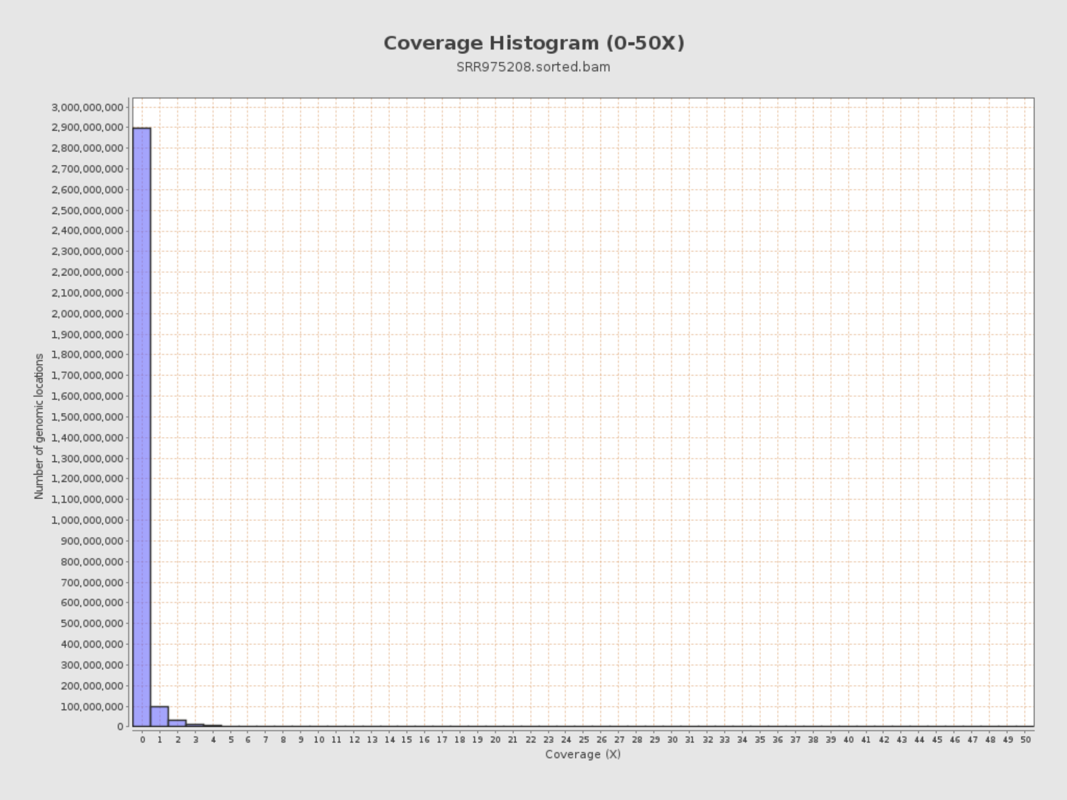
3. Results : Coverage across reference



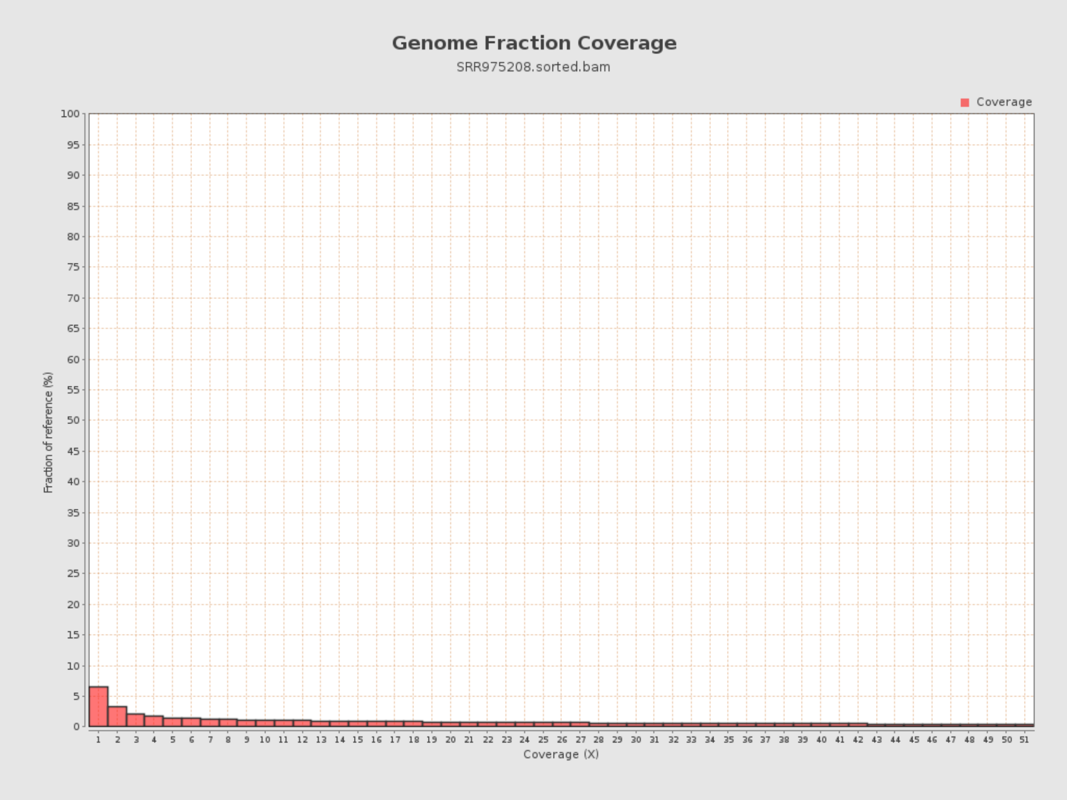
4. Results : Coverage Histogram



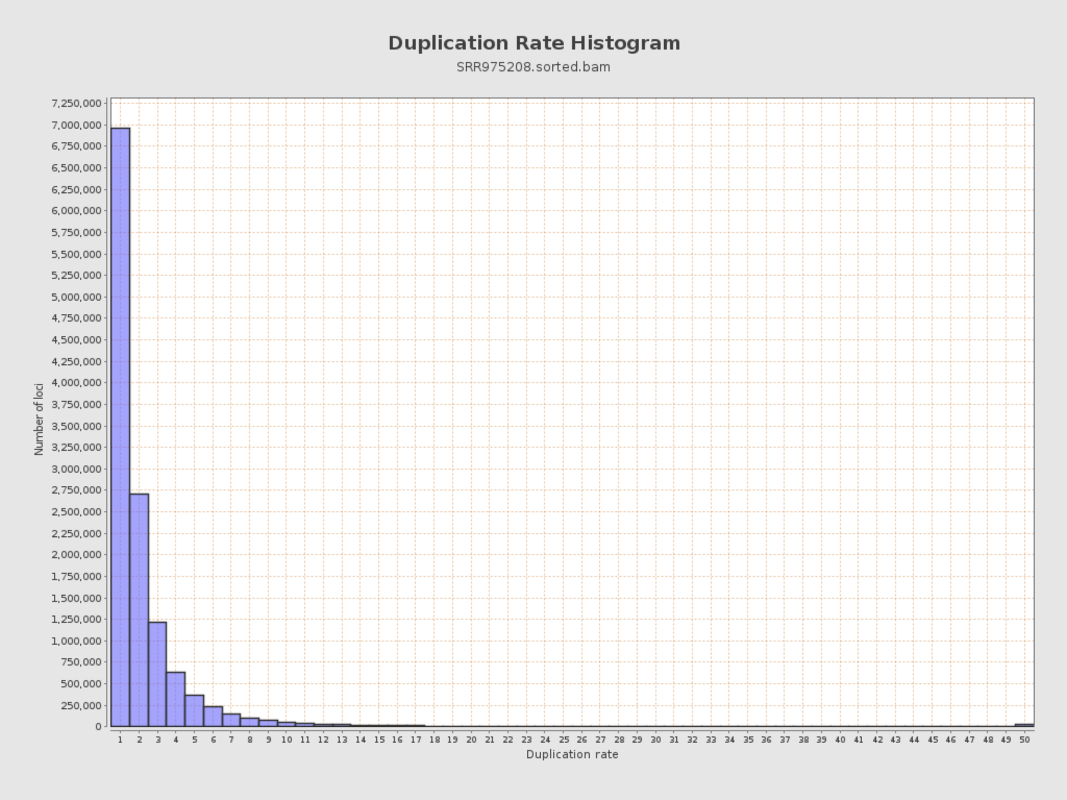
5. Results : Coverage Histogram (0-50X)



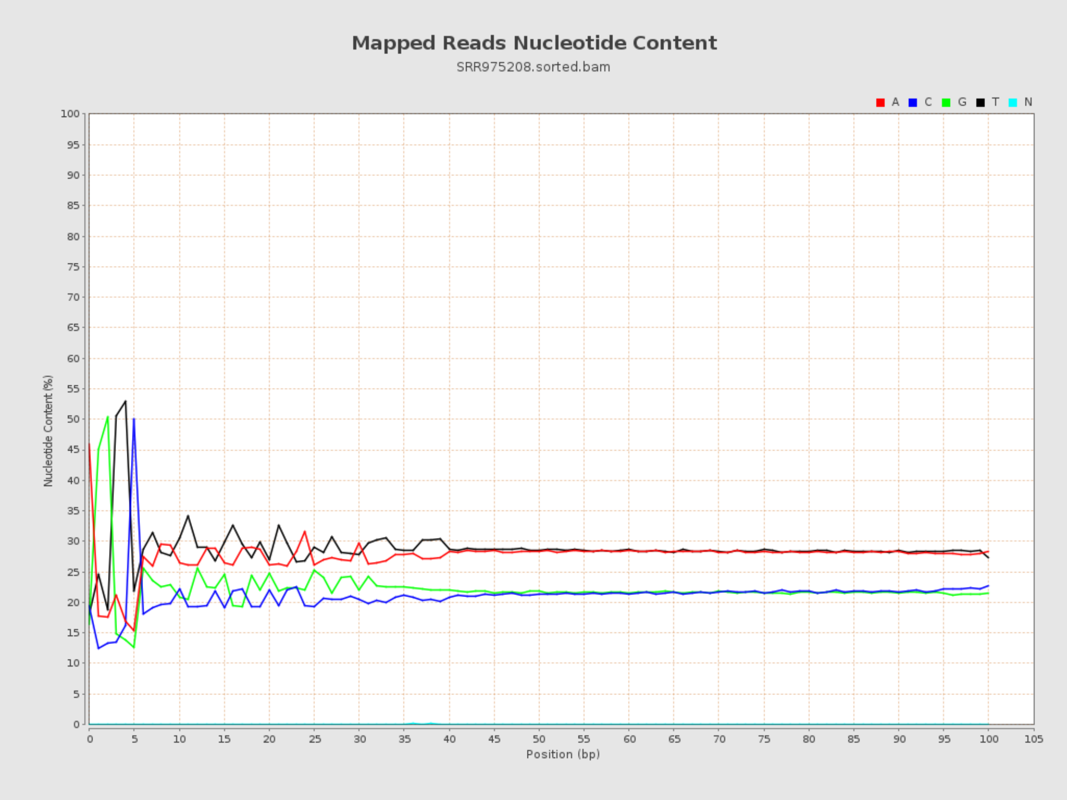
6. Results : Genome Fraction Coverage



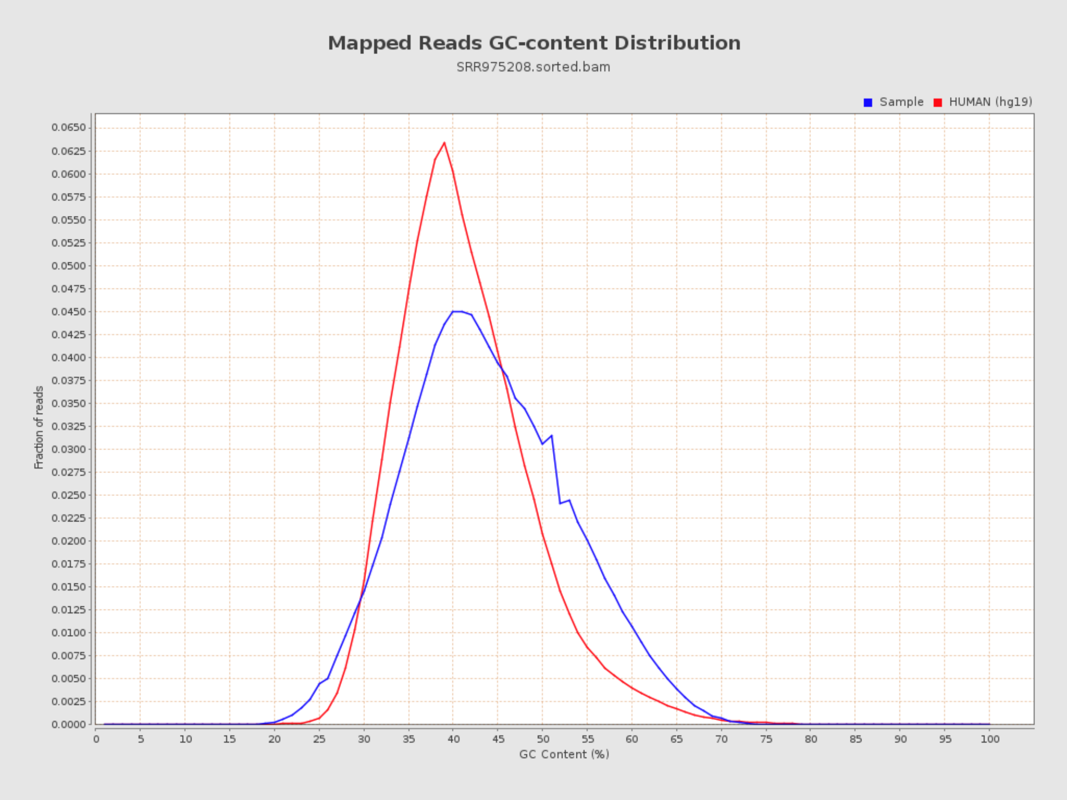
7. Results : Duplication Rate Histogram



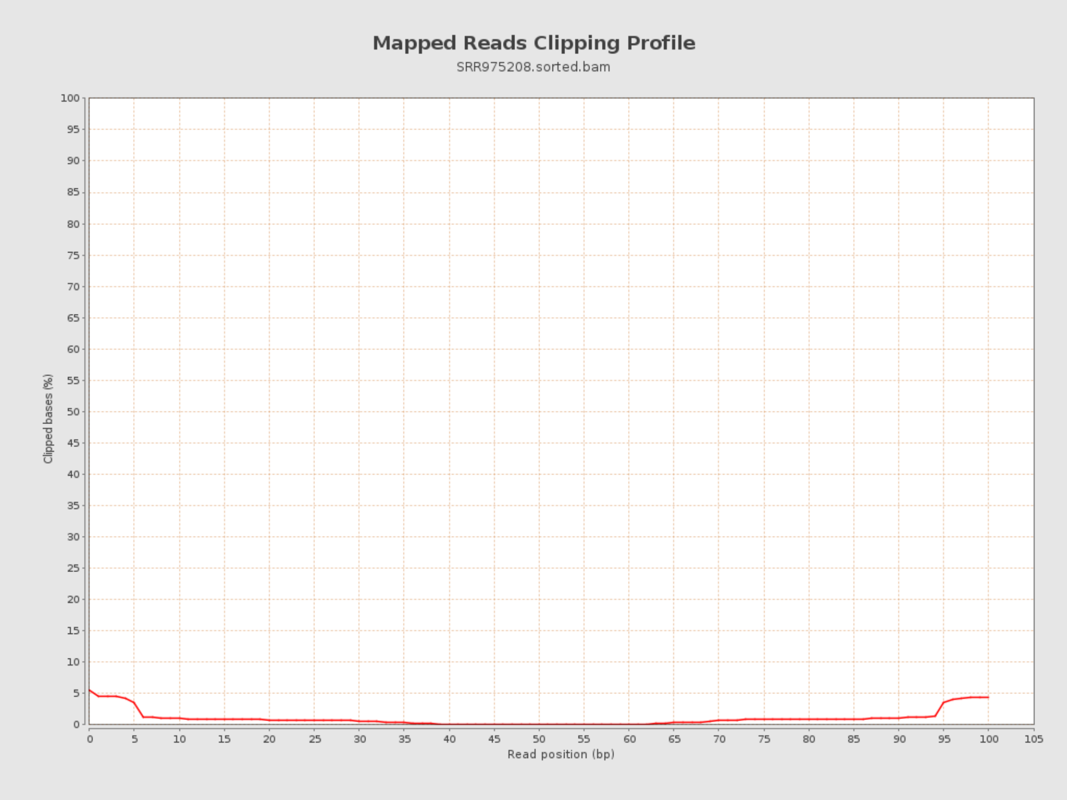
8. Results : Mapped Reads Nucleotide Content



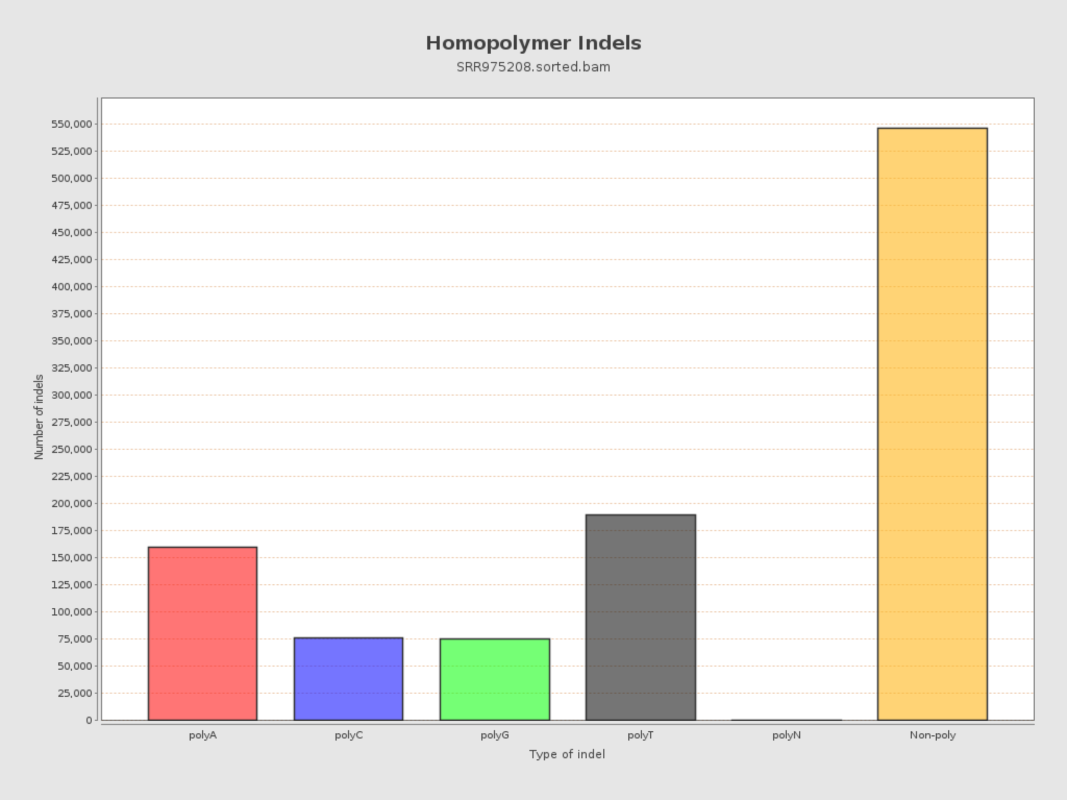
9. Results : Mapped Reads GC-content Distribution



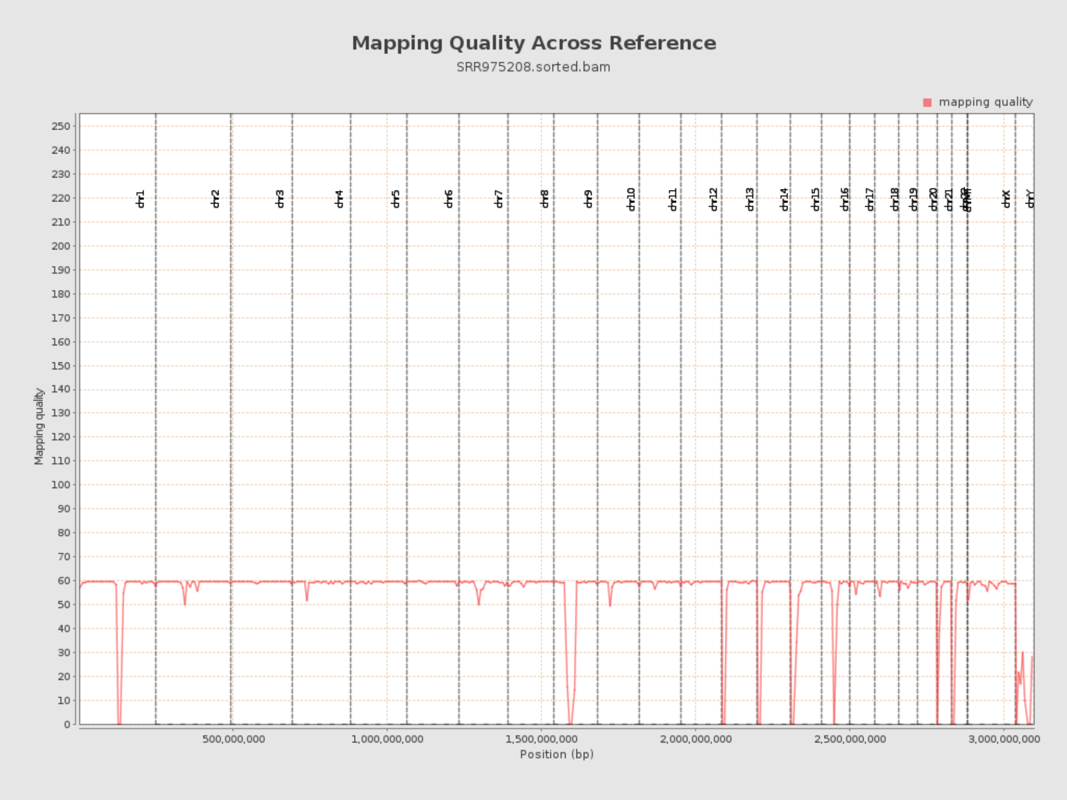
10. Results : Mapped Reads Clipping Profile



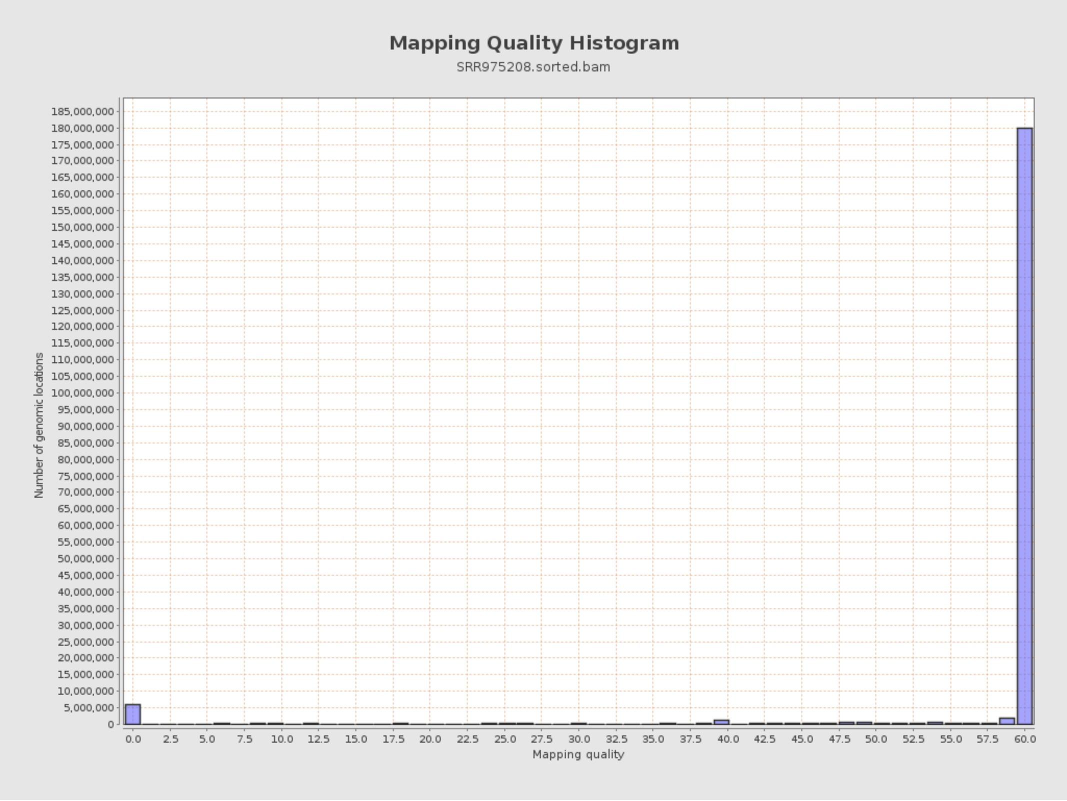
11. Results : Homopolymer Indels



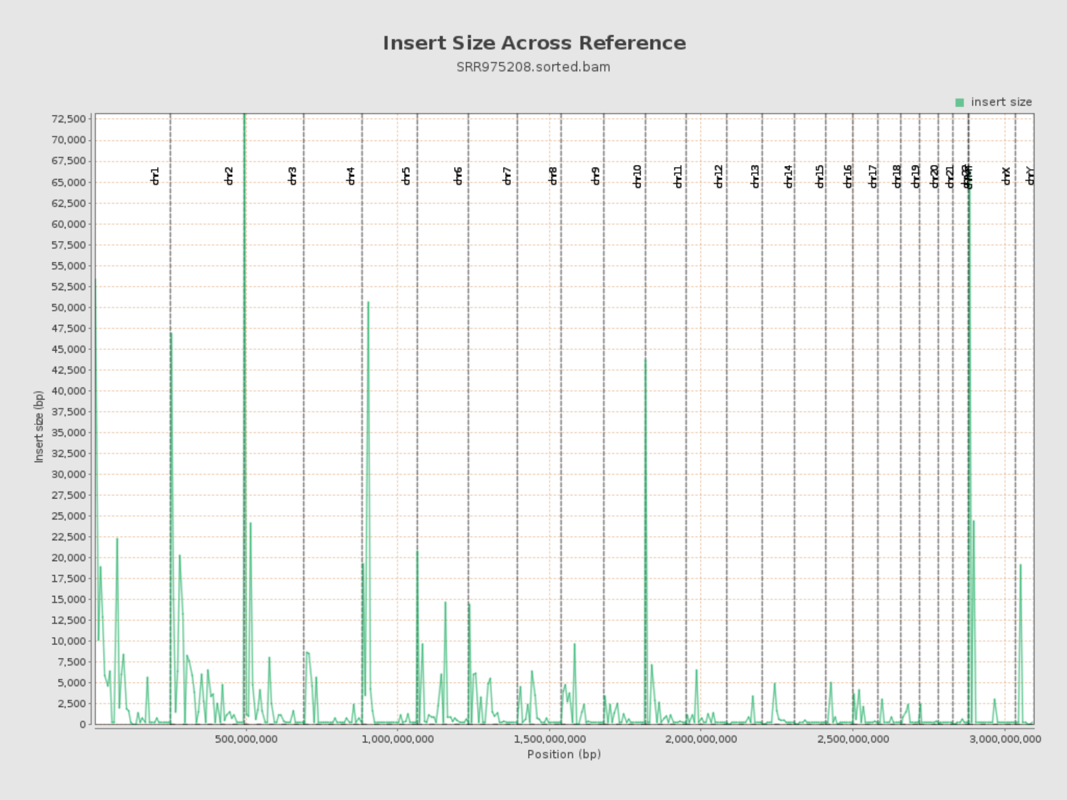
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram