Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 11:00:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975207.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_SRR975207 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975207_1.fastq.gz SRR975207_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 11:00:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975207.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,808,684
Mapped reads	2,786,463 / 99.21%
Unmapped reads	22,221 / 0.79%
Mapped paired reads	2,786,463 / 99.21%
Mapped reads, first in pair	1,394,919 / 49.66%
Mapped reads, second in pair	1,391,544 / 49.54%
Mapped reads, both in pair	2,778,910 / 98.94%
Mapped reads, singletons	7,553 / 0.27%
Secondary alignments	0
Supplementary alignments	126,018 / 4.49%
Read min/max/mean length	30 / 151 / 153.37
Duplicated reads (estimated)	417,674 / 14.87%
Duplication rate	14.5%
Clipped reads	1,992,010 / 70.92%

2.2. ACGT Content

Number/percentage of A's	115,533,813 / 29.32%
Number/percentage of C's	81,680,129 / 20.73%
Number/percentage of T's	114,277,527 / 29%
Number/percentage of G's	82,568,392 / 20.95%
Number/percentage of N's	22,695 / 0.01%

GC Percentage	41.68%

2.3. Coverage

Mean	0.1274
Standard Deviation	1.5782

2.4. Mapping Quality

Mean Mapping Quality	53.91

2.5. Insert size

Mean	216,632.94
Standard Deviation	4,412,478.03
P25/Median/P75	142 / 173 / 215

2.6. Mismatches and indels

General error rate	0.84%
Mismatches	3,147,670
Insertions	58,764
Mapped reads with at least one insertion	2%
Deletions	58,678
Mapped reads with at least one deletion	2.01%
Homopolymer indels	41.69%

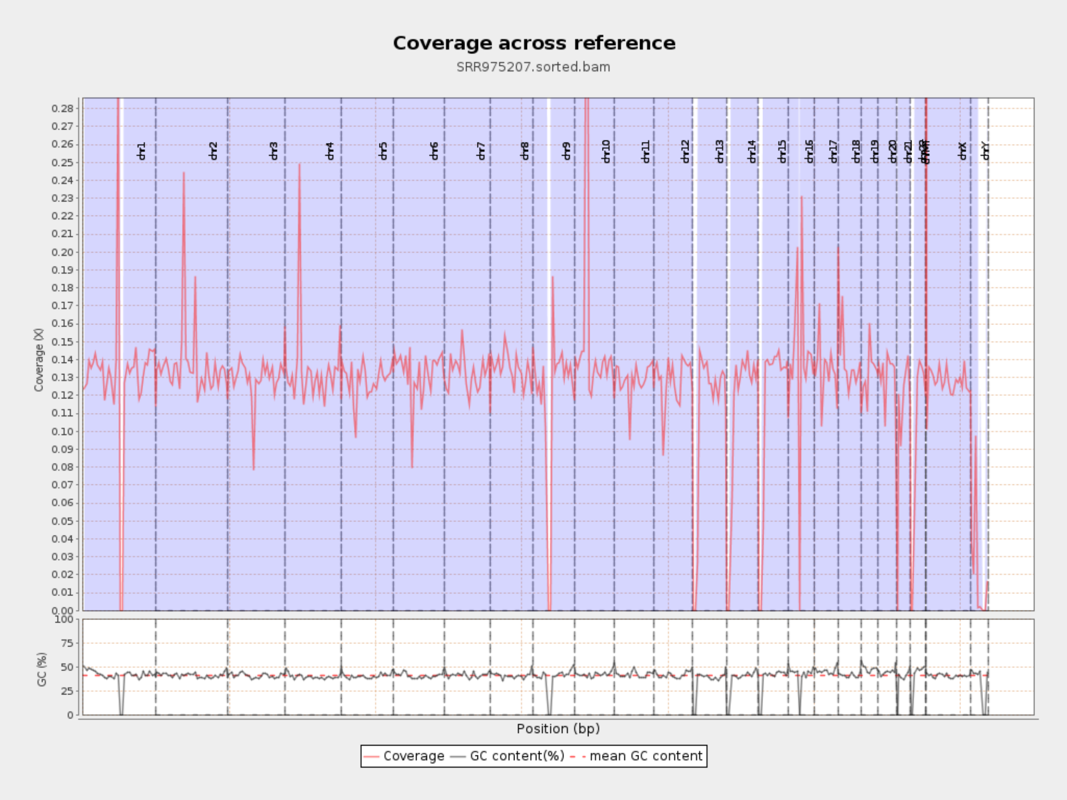
2.7. Chromosome stats

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

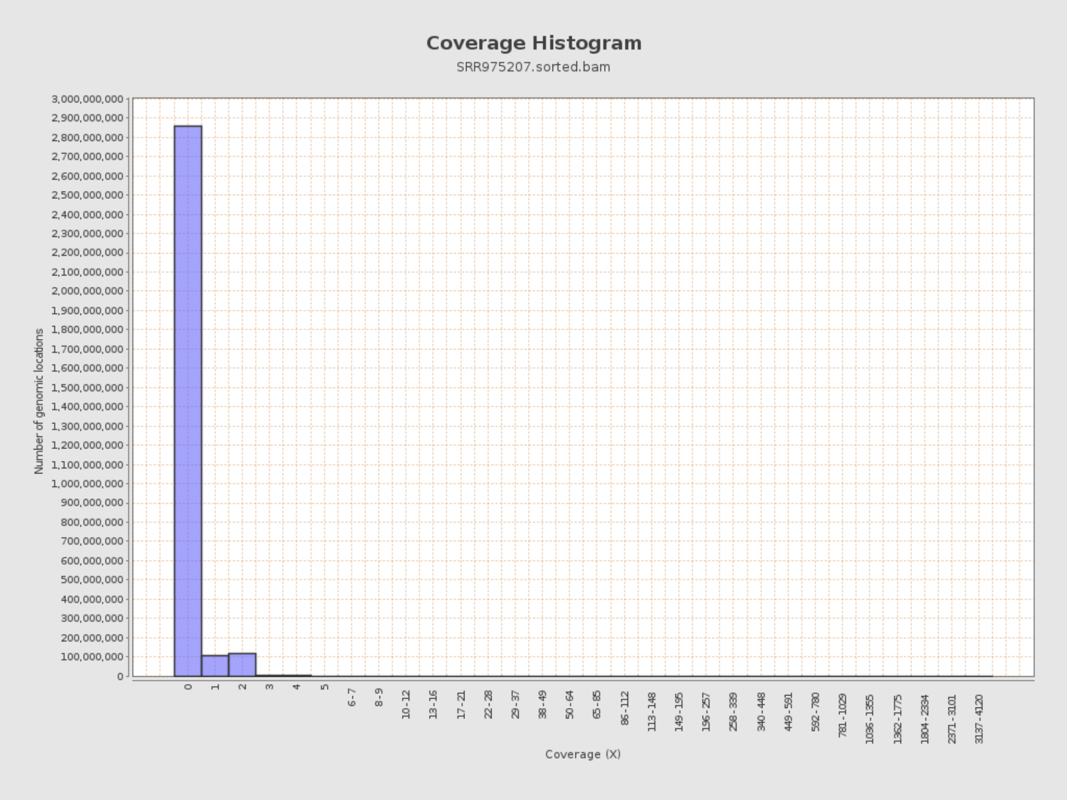
		bases	coverage	deviation
chr1	249250621	32552624	0.1306	4.1394
chr2	243199373	33506196	0.1378	0.967
chr3	198022430	25642284	0.1295	0.5054
chr4	191154276	25712432	0.1345	1.0654
chr5	180915260	23277291	0.1287	0.4755
chr6	171115067	22624340	0.1322	0.5538
chr7	159138663	21142763	0.1329	1.0526
chr8	146364022	19708618	0.1347	1.2135
chr9	141213431	16746259	0.1186	1.611
chr10	135534747	20823610	0.1536	2.9678
chr11	135006516	17325570	0.1283	0.6655
chr12	133851895	17315696	0.1294	0.4763
chr13	115169878	12596245	0.1094	0.4404
chr14	107349540	11858128	0.1105	0.4438
chr15	102531392	11494908	0.1121	0.4421
chr16	90354753	12473143	0.138	0.983
chr17	81195210	10948458	0.1348	0.6971
chr18	78077248	10944539	0.1402	1.6026
chr19	59128983	7822465	0.1323	1.9693
chr20	63025520	8275535	0.1313	0.6199
chr21	48129895	5331039	0.1108	0.6775
chr22	51304566	4787510	0.0933	0.4104
chrMT	16571	270552	16.3268	6.5809
chrX	155270560	19800384	0.1275	0.5468

chrY	59373566	1258978	0.0212	1.171

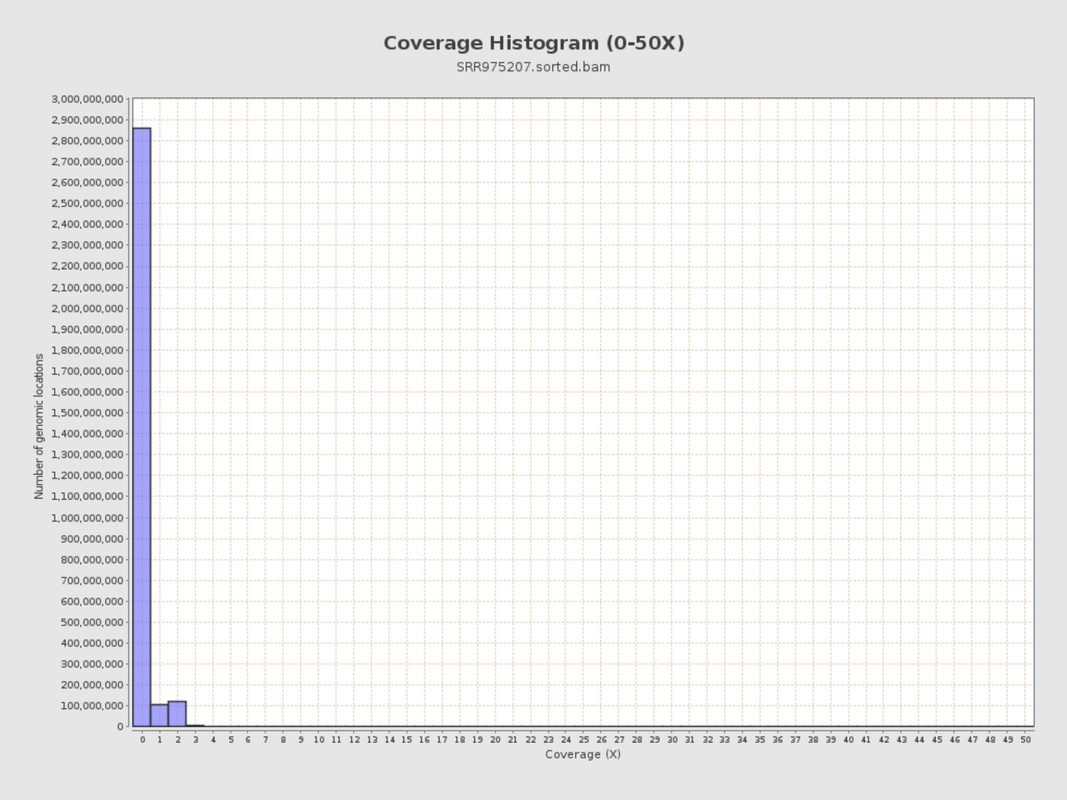
3. Results : Coverage across reference



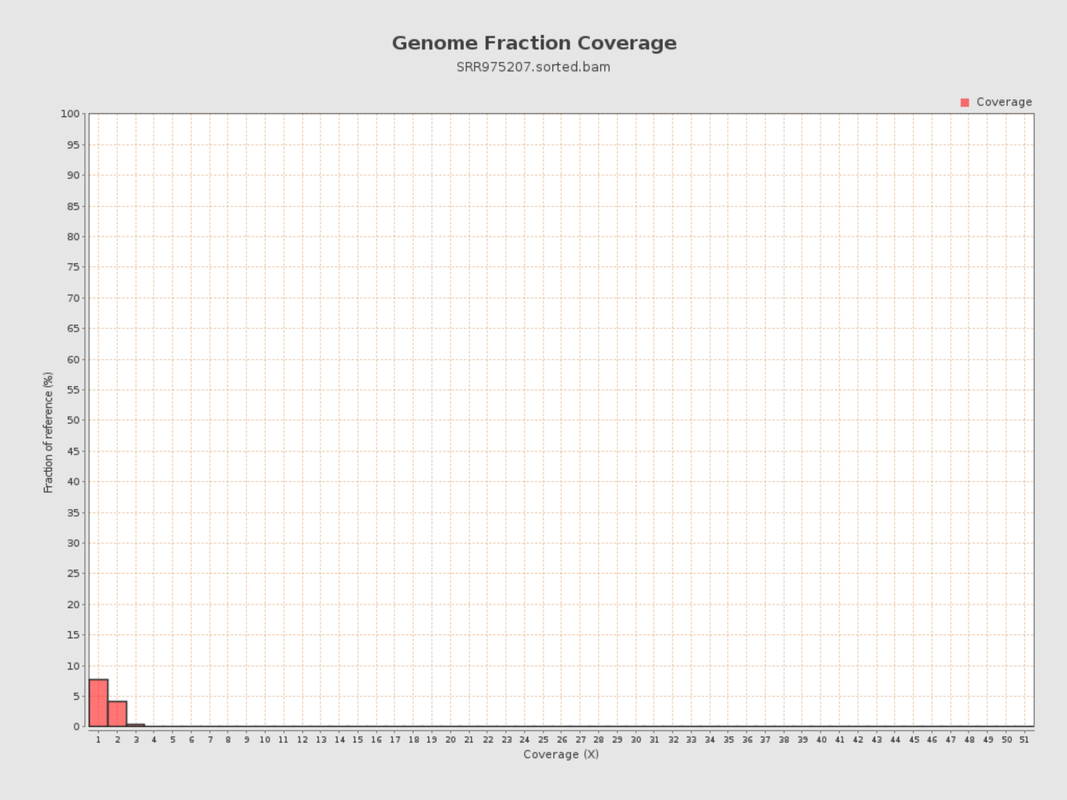
4. Results : Coverage Histogram



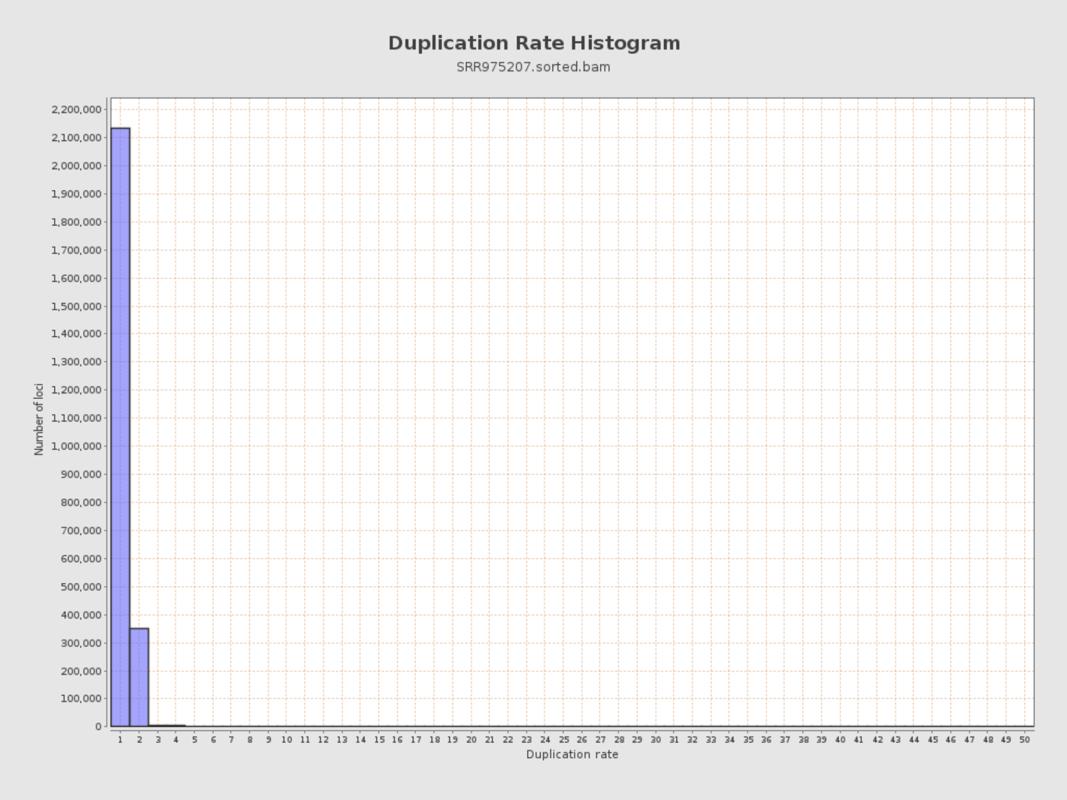
5. Results : Coverage Histogram (0-50X)



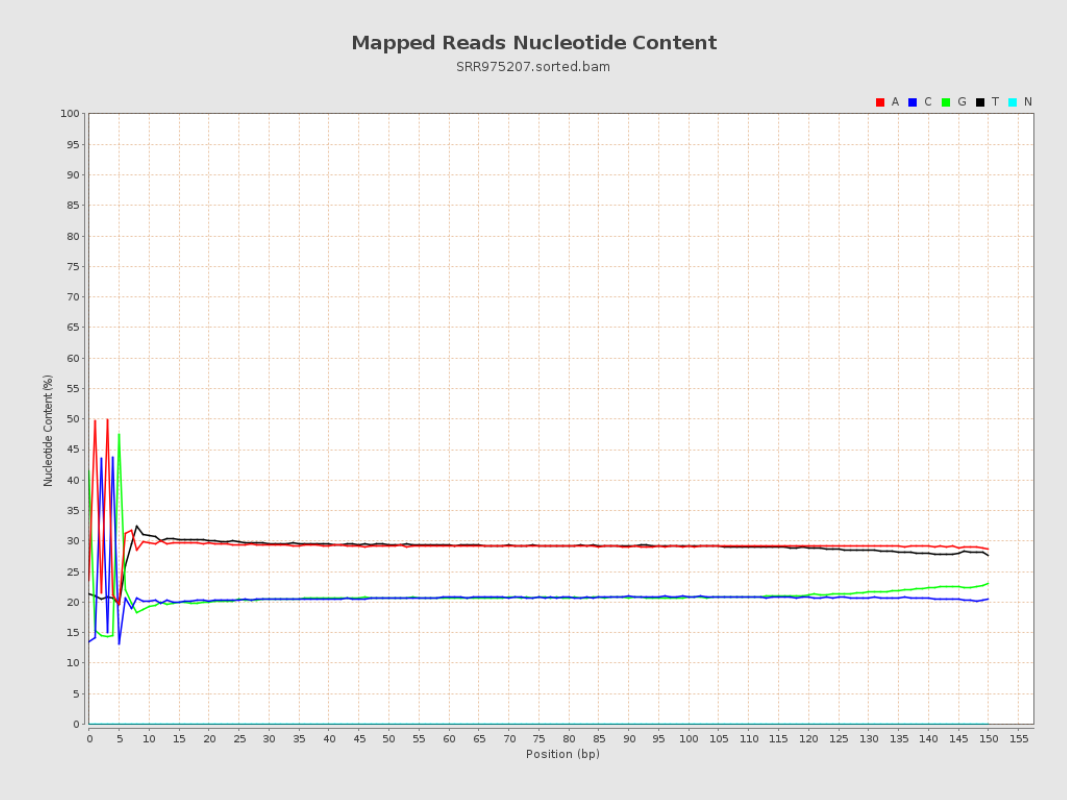
6. Results : Genome Fraction Coverage



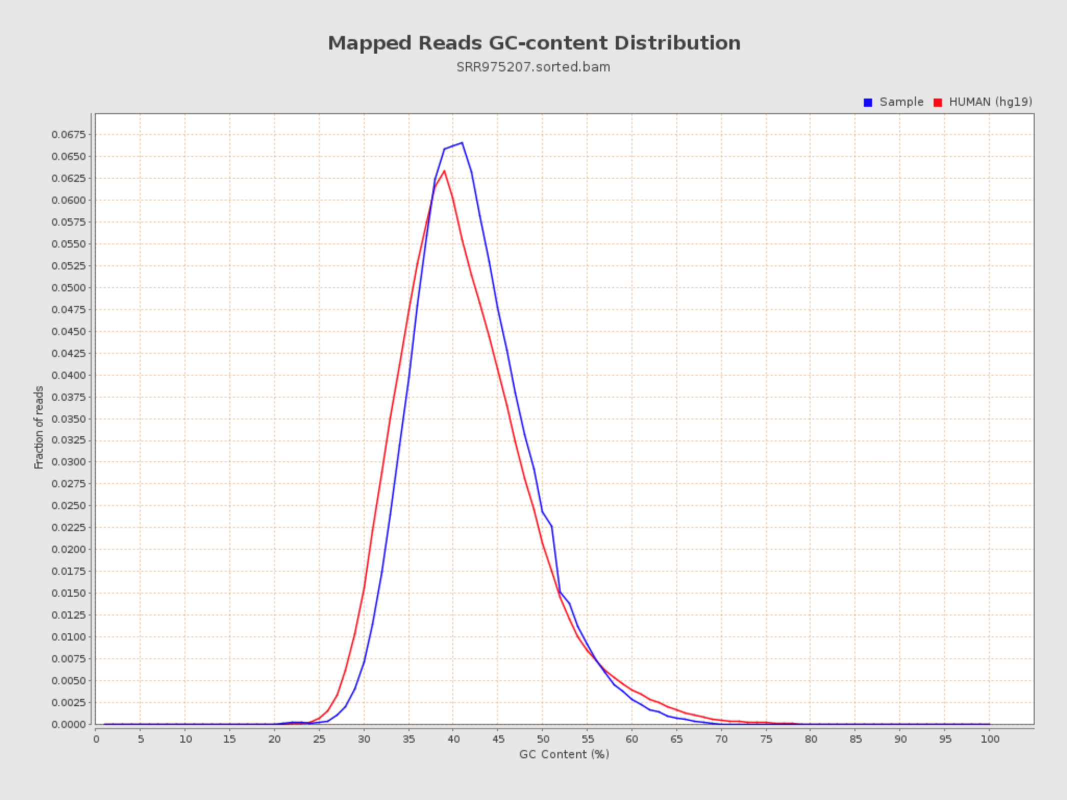
7. Results : Duplication Rate Histogram



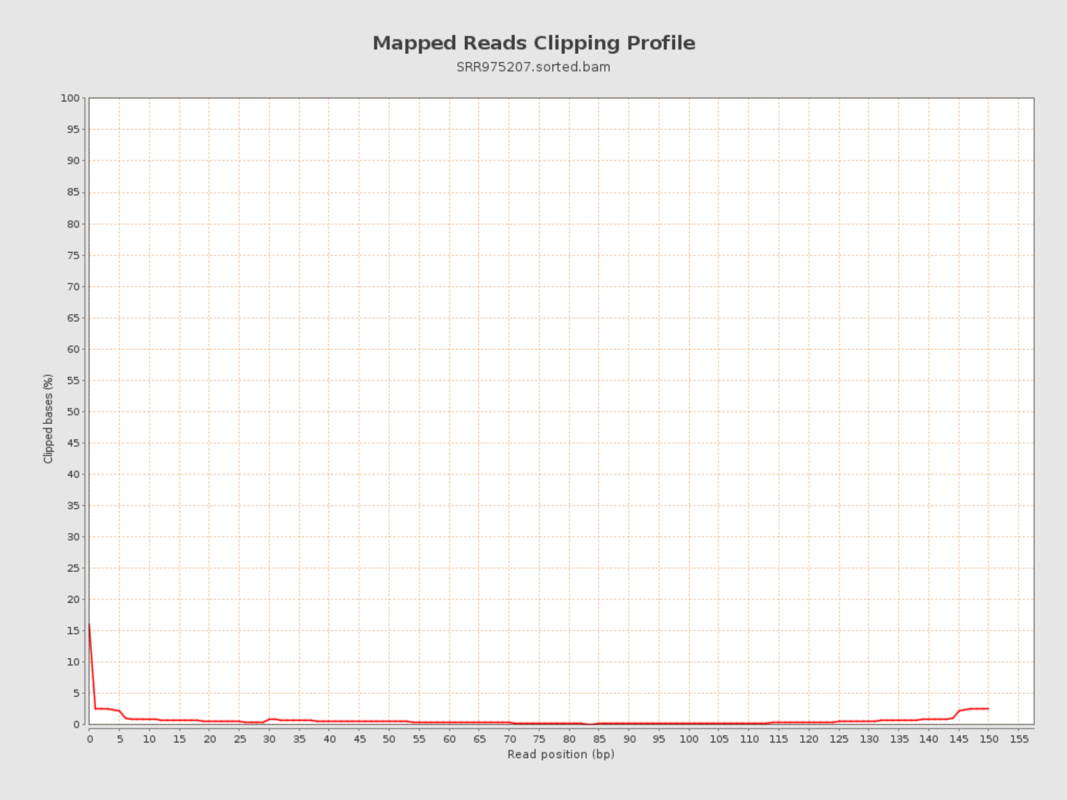
8. Results : Mapped Reads Nucleotide Content



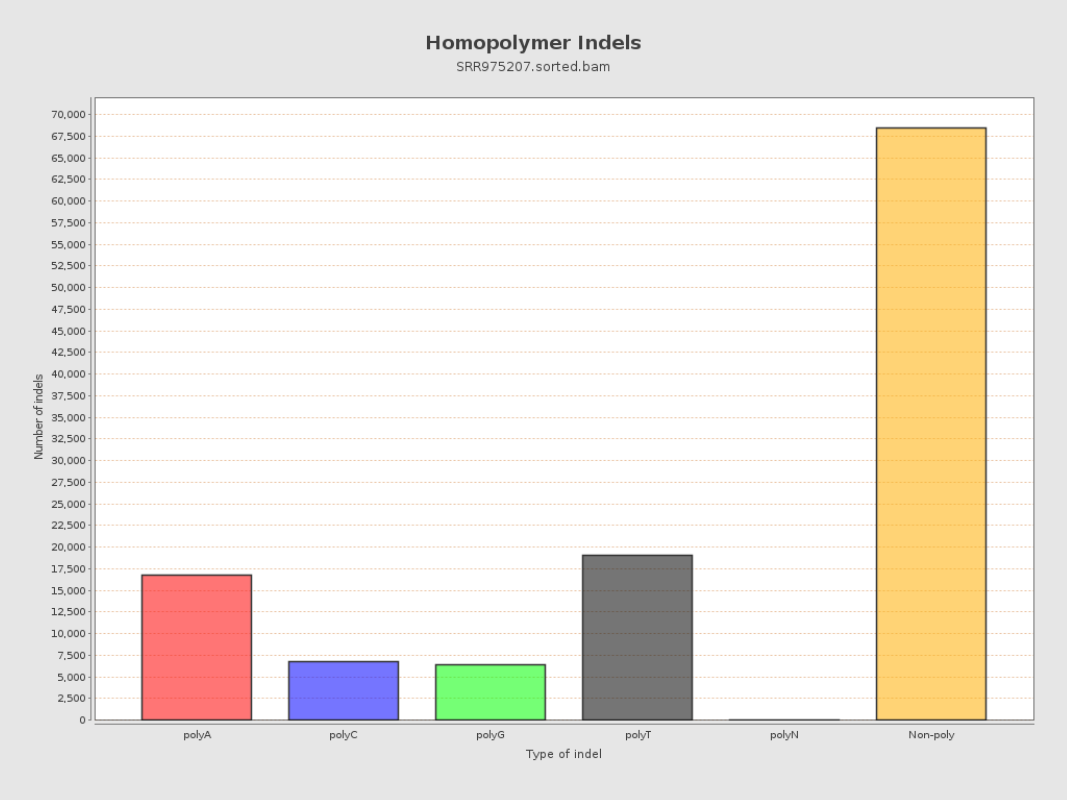
9. Results : Mapped Reads GC-content Distribution



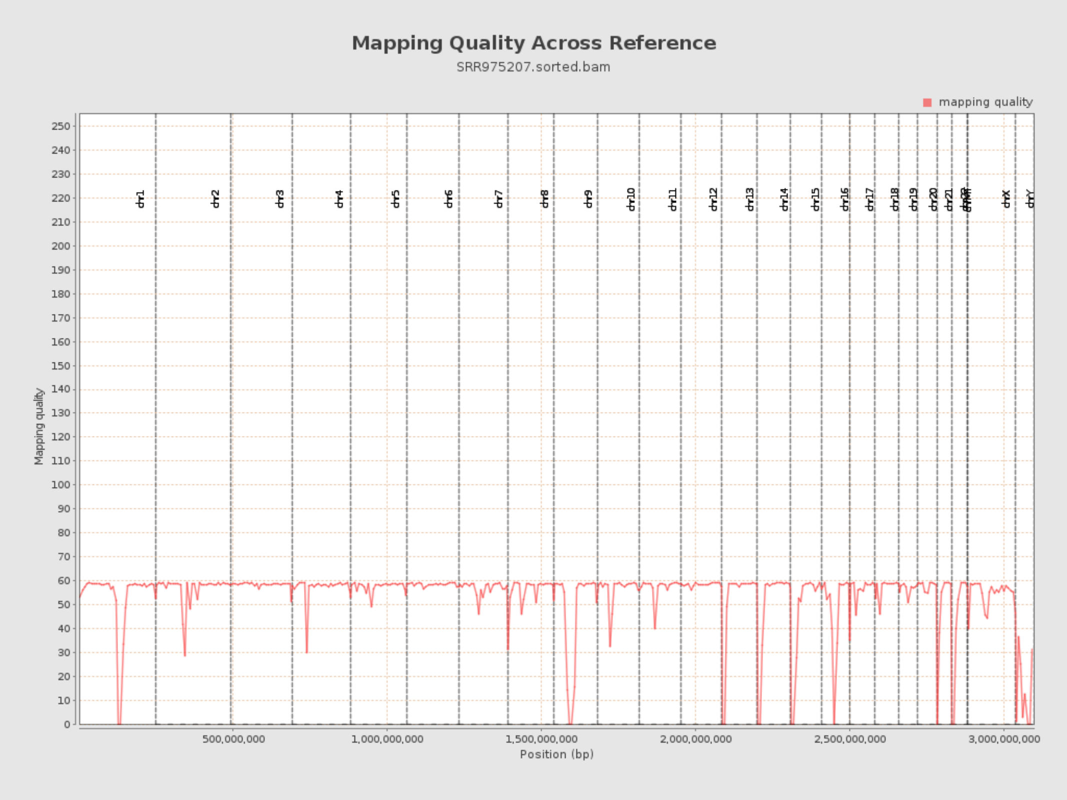
10. Results : Mapped Reads Clipping Profile



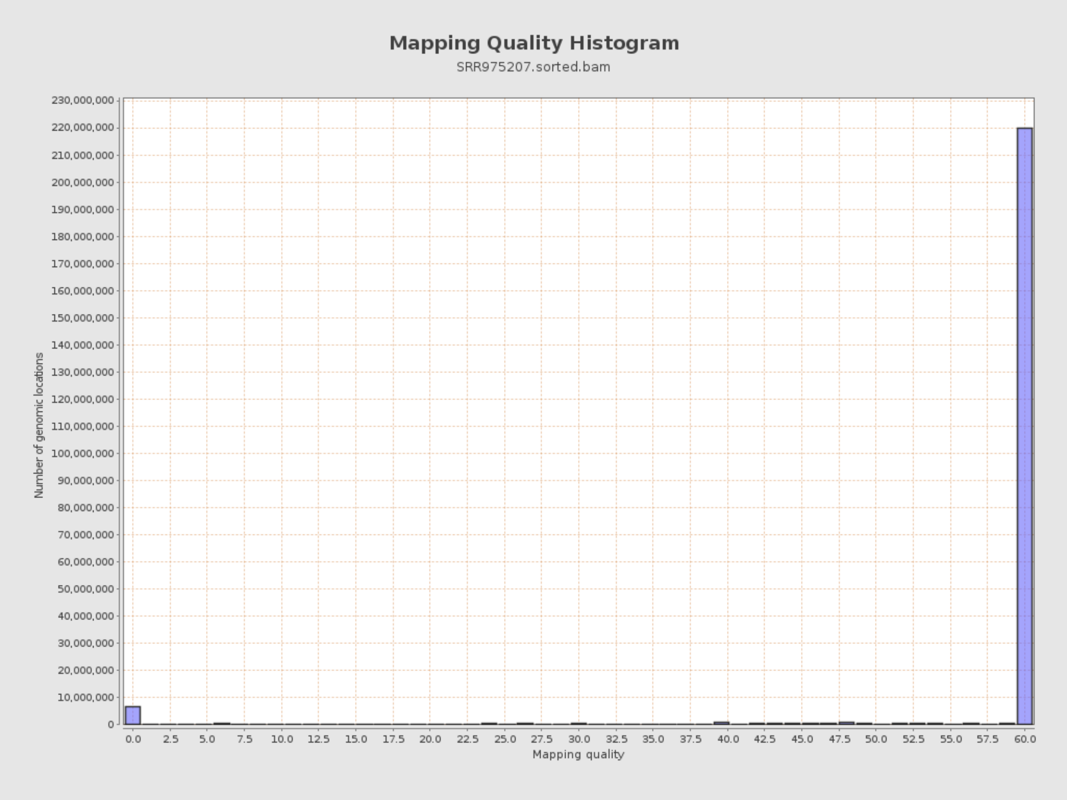
11. Results : Homopolymer Indels



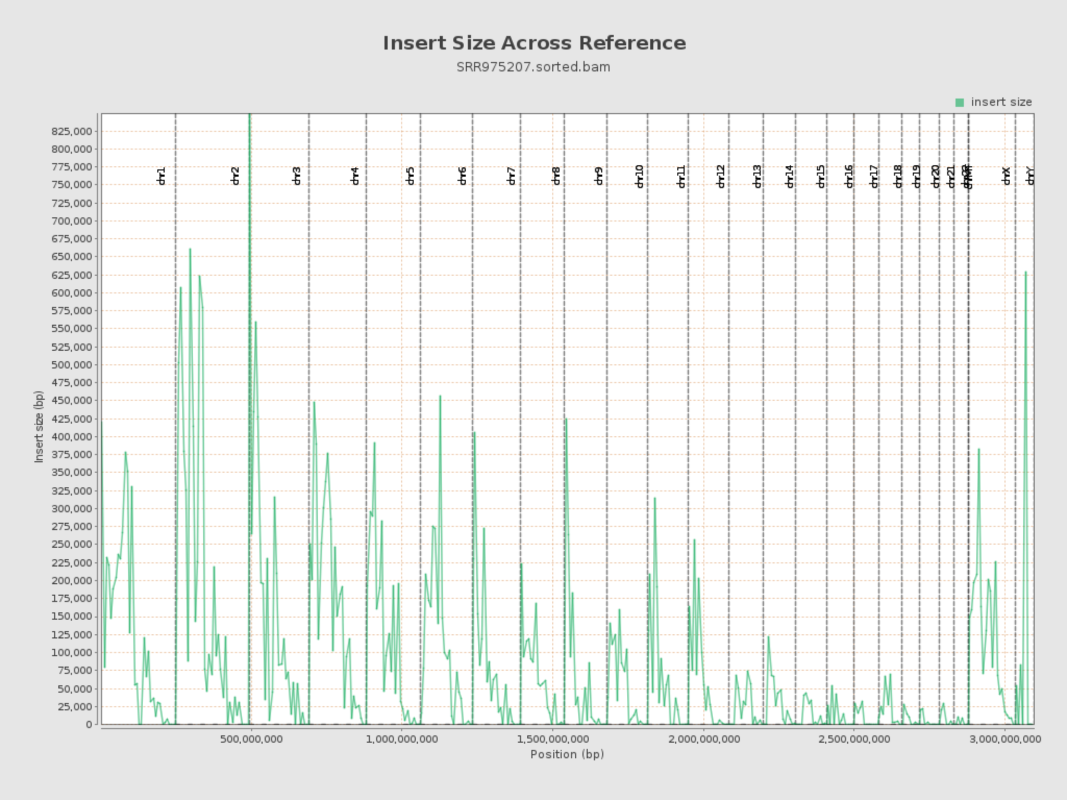
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram