Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 17:45:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975219.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_SRR975219 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975219_1.fastq.gz SRR975219_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 17:45:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975219.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,116,172
Mapped reads	4,072,849 / 98.95%
Unmapped reads	43,323 / 1.05%
Mapped paired reads	4,072,849 / 98.95%
Mapped reads, first in pair	2,045,208 / 49.69%
Mapped reads, second in pair	2,027,641 / 49.26%
Mapped reads, both in pair	4,052,432 / 98.45%
Mapped reads, singletons	20,417 / 0.5%
Secondary alignments	0
Supplementary alignments	48,247 / 1.17%
Read min/max/mean length	30 / 151 / 151.59
Duplicated reads (estimated)	519,958 / 12.63%
Duplication rate	11.34%
Clipped reads	1,558,389 / 37.86%

2.2. ACGT Content

Number/percentage of A's	171,364,335 / 29.42%
Number/percentage of C's	118,725,242 / 20.38%
Number/percentage of T's	169,734,003 / 29.14%
Number/percentage of G's	122,582,018 / 21.05%
Number/percentage of N's	53,502 / 0.01%

GC Percentage	41.43%

2.3. Coverage

Mean	0.1883
Standard Deviation	1.9598

2.4. Mapping Quality

Mean Mapping Quality	53.95

2.5. Insert size

Mean	97,260.01
Standard Deviation	3,085,770.43
P25/Median/P75	148 / 179 / 224

2.6. Mismatches and indels

General error rate	0.96%
Mismatches	5,378,753
Insertions	101,656
Mapped reads with at least one insertion	2.38%
Deletions	226,968
Mapped reads with at least one deletion	5.36%
Homopolymer indels	48.85%

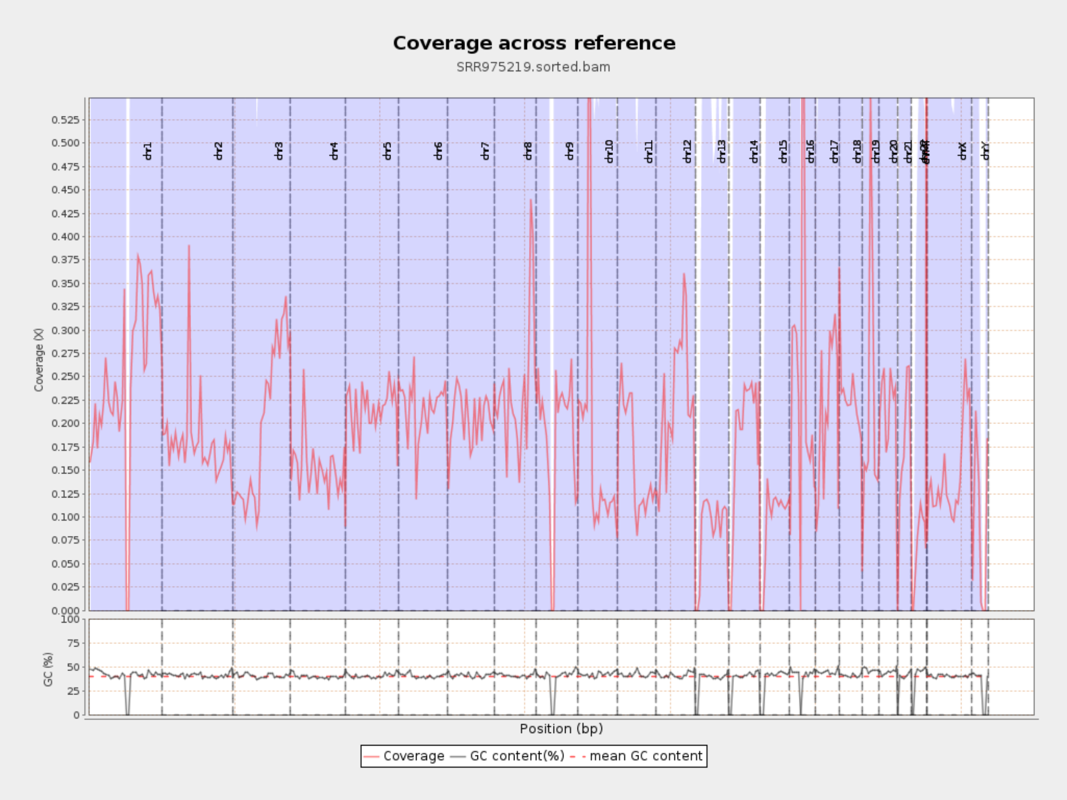
2.7. Chromosome stats

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

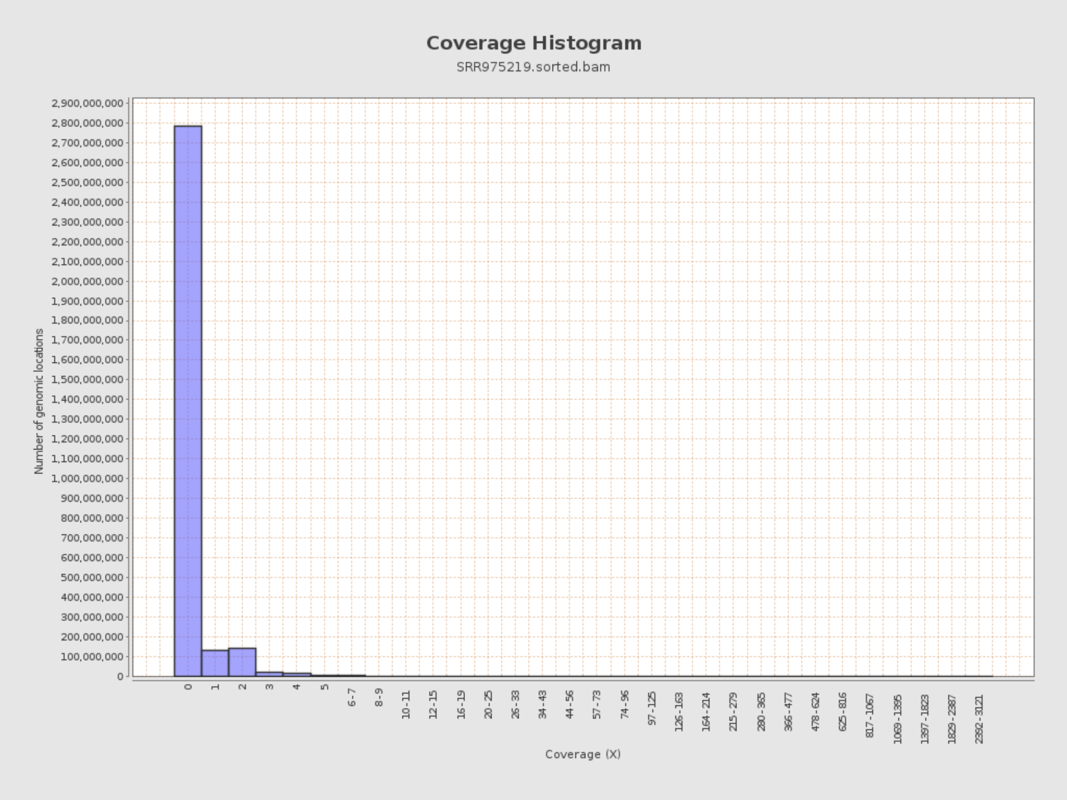
		bases	coverage	deviation
chr1	249250621	62572722	0.251	2.2308
chr2	243199373	44113562	0.1814	1.7178
chr3	198022430	38858667	0.1962	0.6816
chr4	191154276	29001874	0.1517	1.0772
chr5	180915260	39064245	0.2159	0.6764
chr6	171115067	37150352	0.2171	0.9668
chr7	159138663	32892110	0.2067	1.759
chr8	146364022	34786429	0.2377	0.842
chr9	141213431	26253620	0.1859	2.2668
chr10	135534747	24401224	0.18	5.8254
chr11	135006516	21417700	0.1586	1.7502
chr12	133851895	30004910	0.2242	0.6914
chr13	115169878	9822592	0.0853	0.4044
chr14	107349540	19348750	0.1802	0.6265
chr15	102531392	9738796	0.095	0.4339
chr16	90354753	22057290	0.2441	4.2094
chr17	81195210	17259841	0.2126	2.513
chr18	78077248	17869254	0.2289	2.1256
chr19	59128983	13504674	0.2284	1.4145
chr20	63025520	13733882	0.2179	0.7499
chr21	48129895	7988069	0.166	0.8039
chr22	51304566	3434033	0.0669	0.3767
chrMT	16571	41465	2.5023	2.6975
chrX	155270560	22441172	0.1445	0.7646

chrY	59373566	5120113	0.0862	1.5379

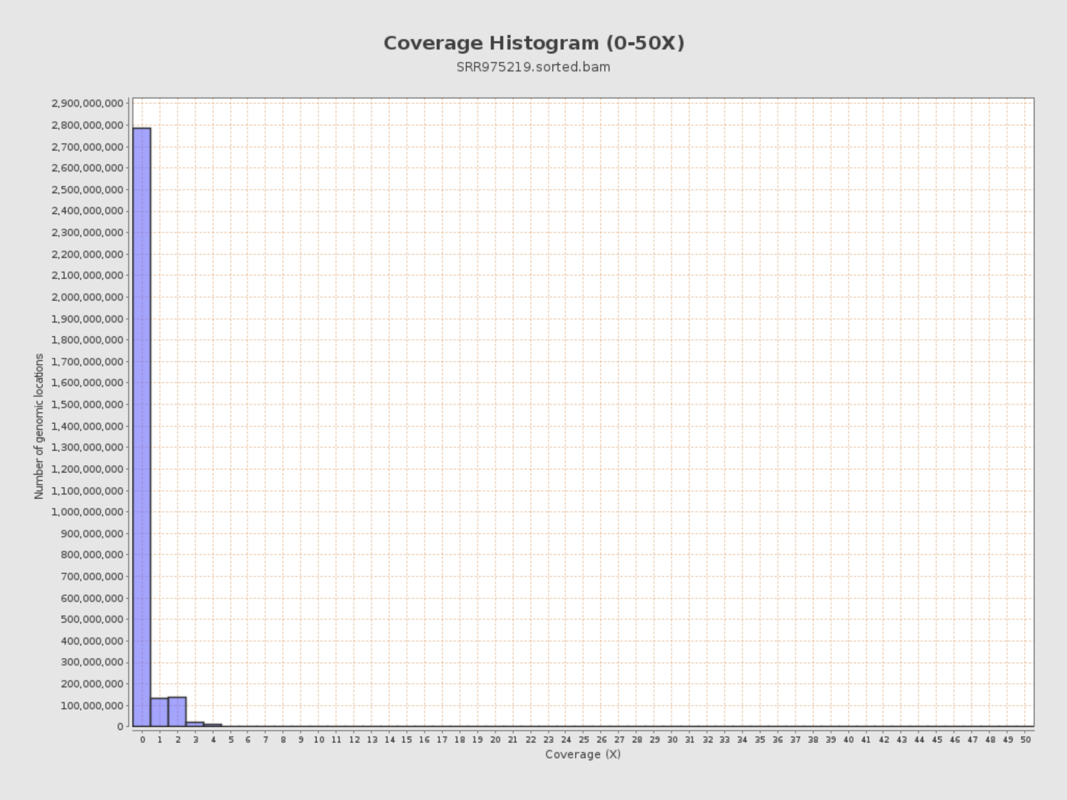
3. Results : Coverage across reference



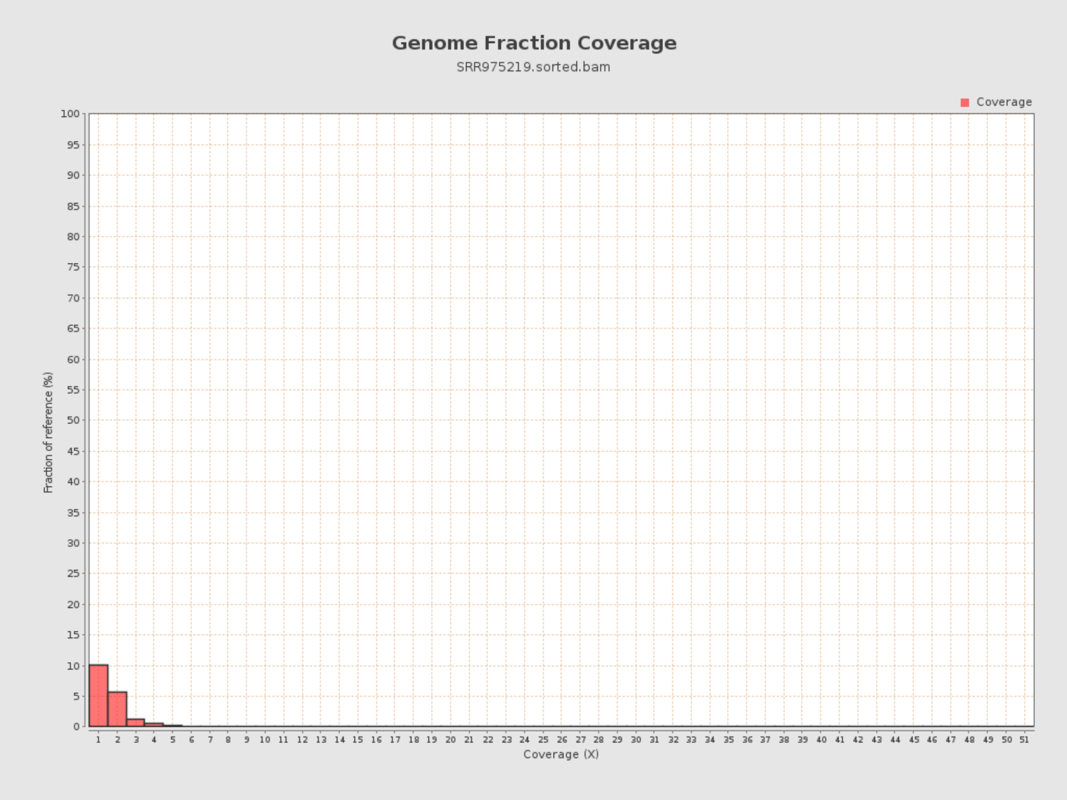
4. Results : Coverage Histogram



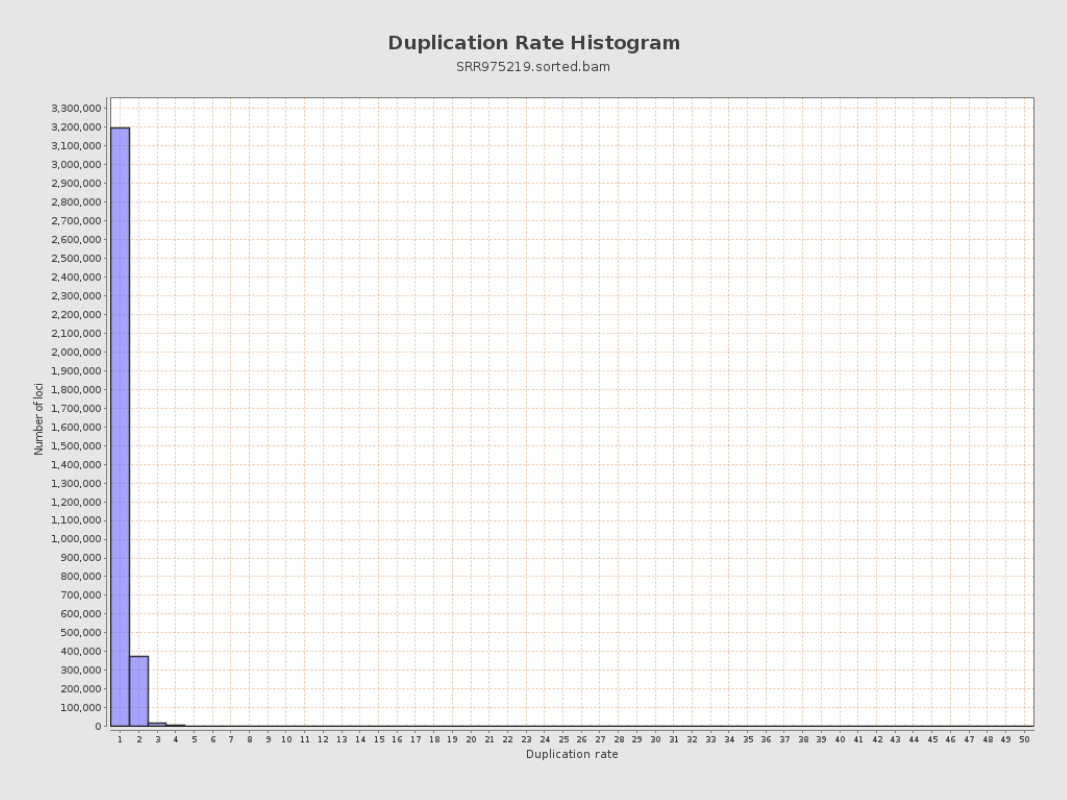
5. Results : Coverage Histogram (0-50X)



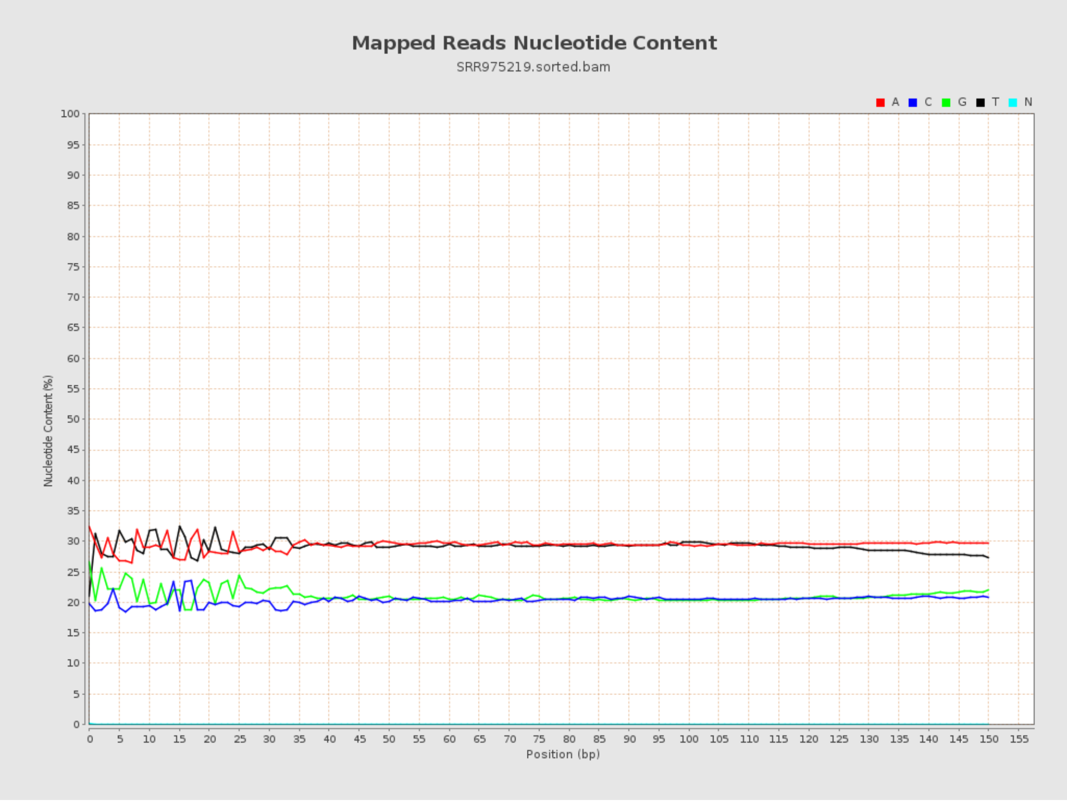
6. Results : Genome Fraction Coverage



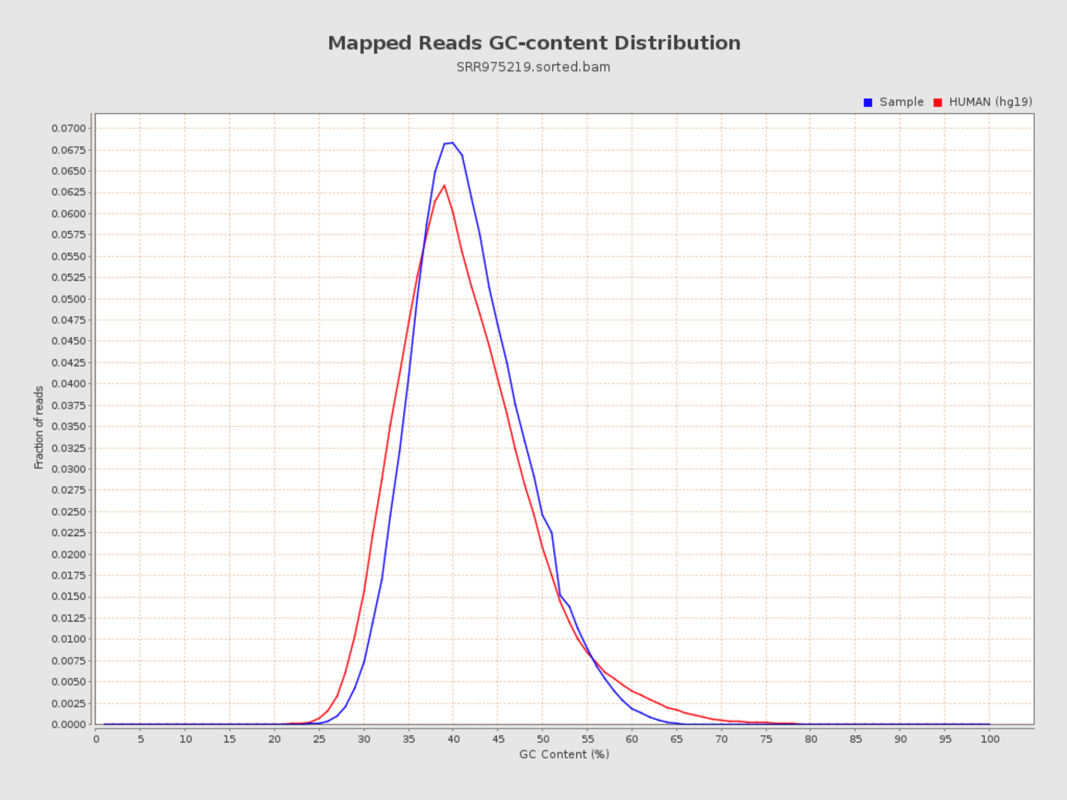
7. Results : Duplication Rate Histogram



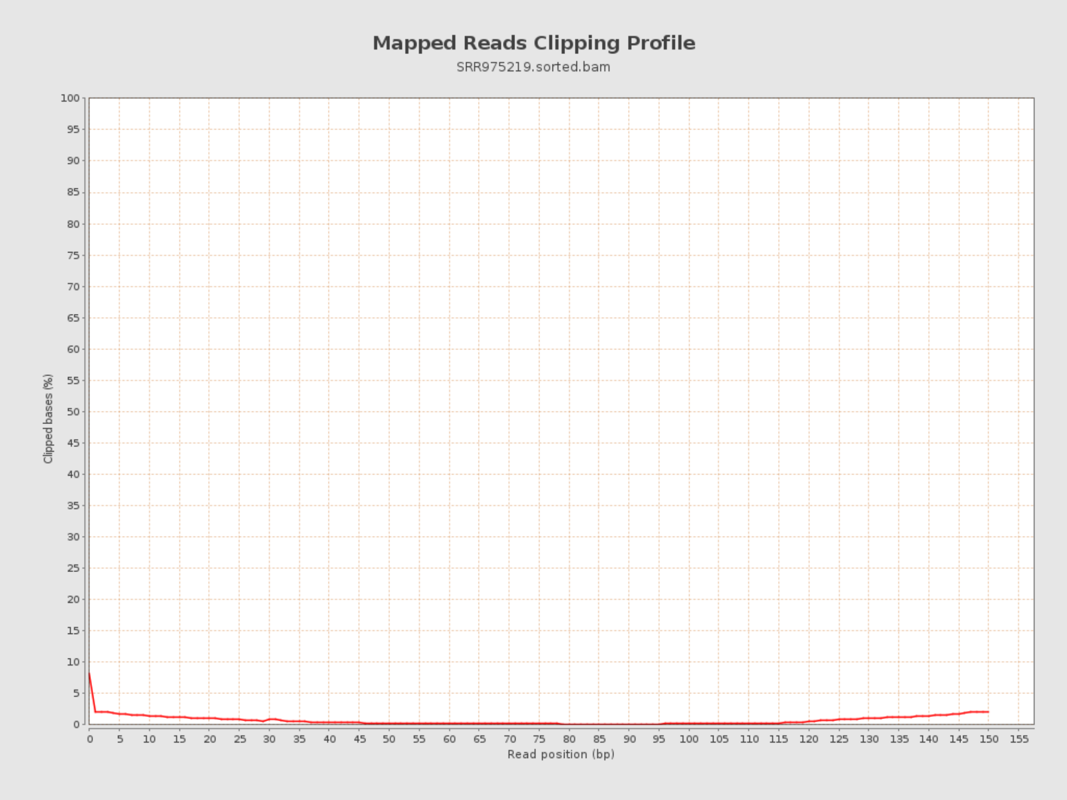
8. Results : Mapped Reads Nucleotide Content



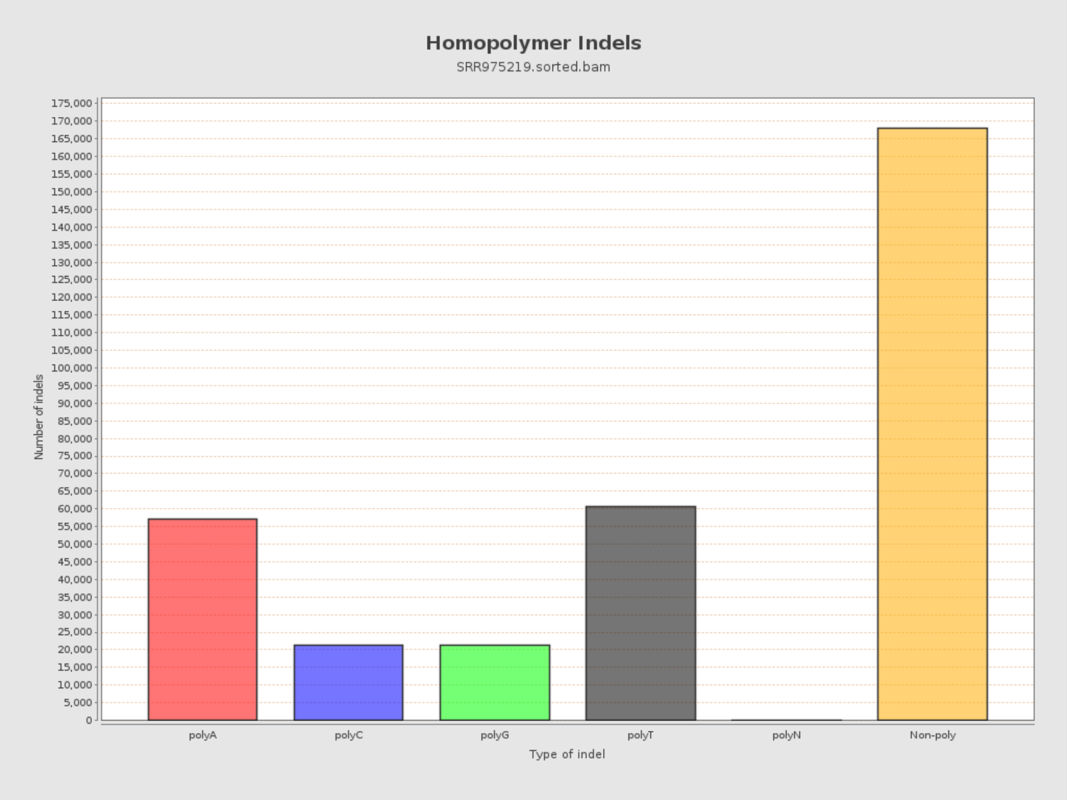
9. Results : Mapped Reads GC-content Distribution



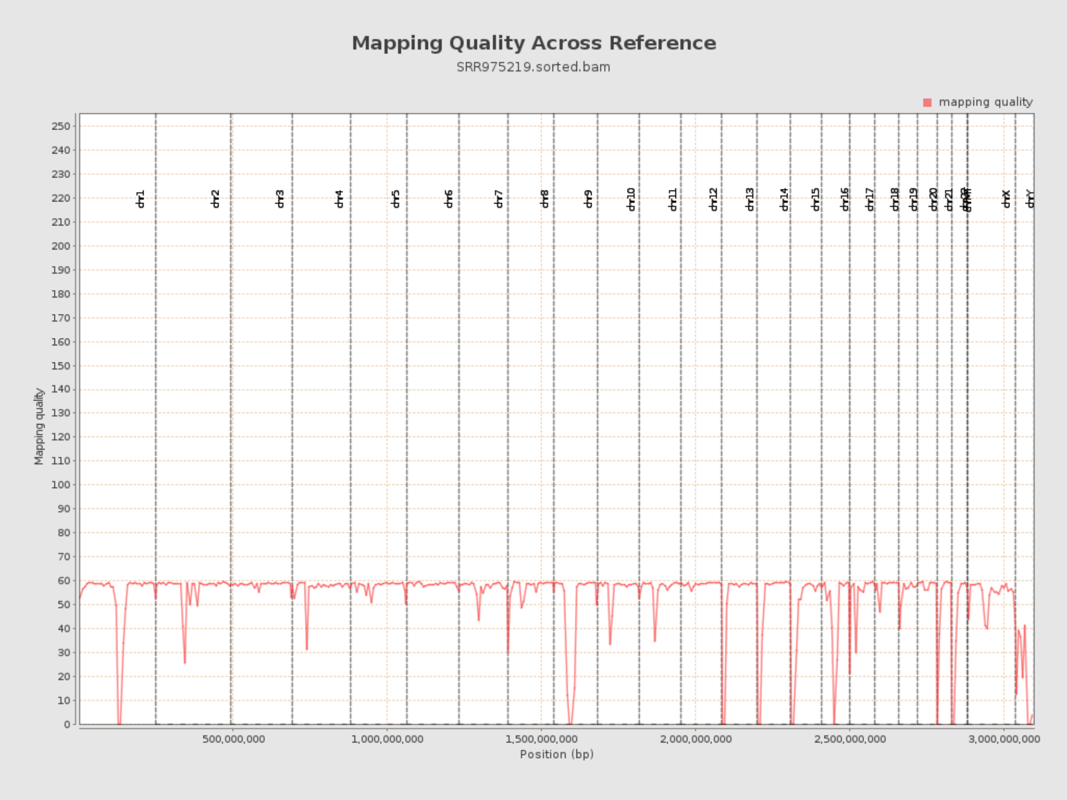
10. Results : Mapped Reads Clipping Profile



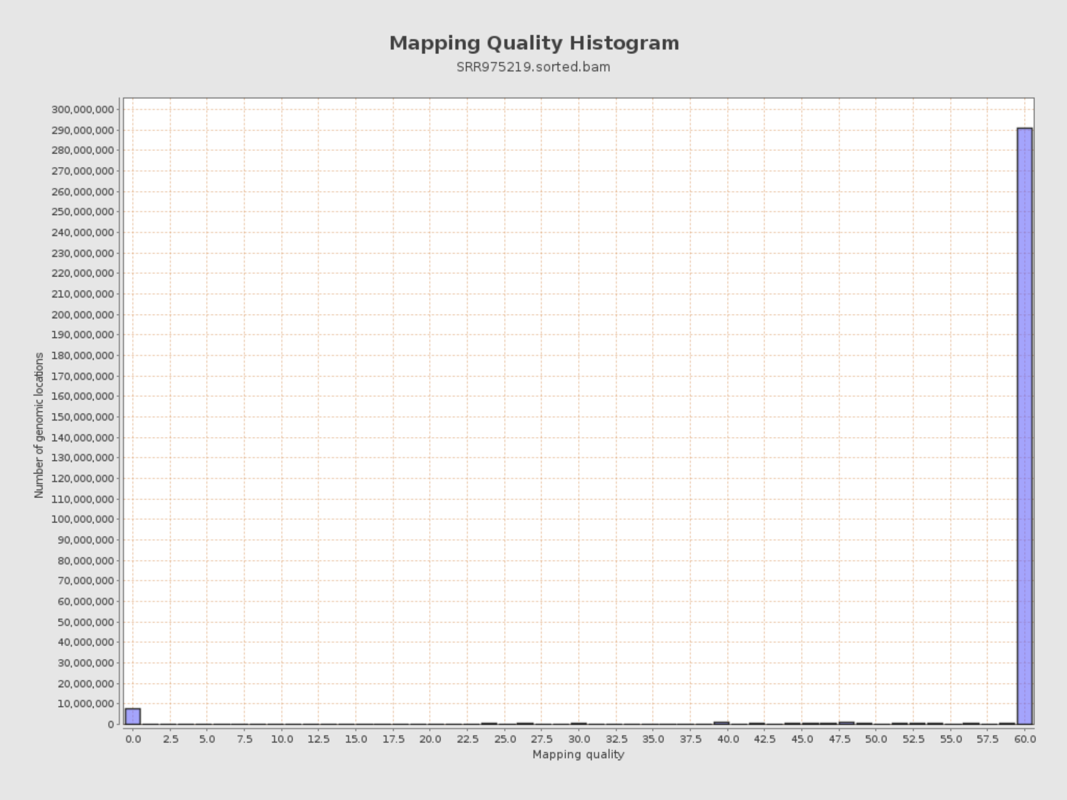
11. Results : Homopolymer Indels



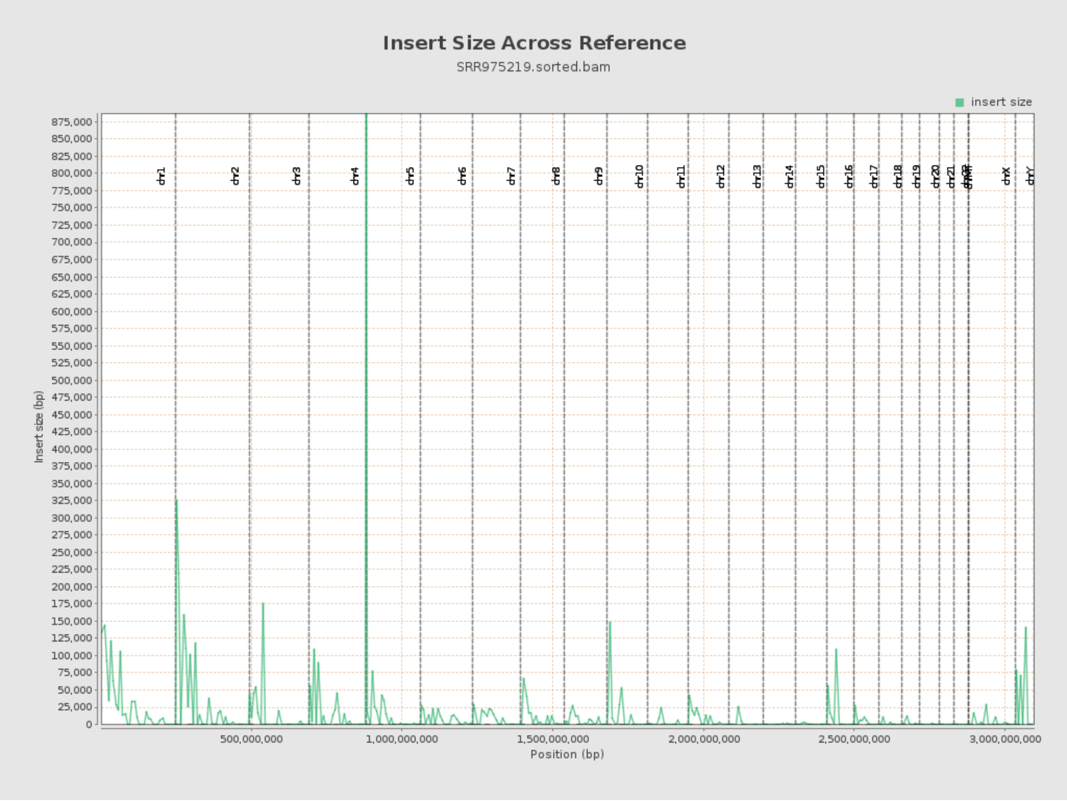
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram