Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 00:10:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975229.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_SRR975229 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975229_1.fastq.gz SRR975229_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 00:10:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975229.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,711,736
Mapped reads	3,666,447 / 98.78%
Unmapped reads	45,289 / 1.22%
Mapped paired reads	3,666,447 / 98.78%
Mapped reads, first in pair	1,832,621 / 49.37%
Mapped reads, second in pair	1,833,826 / 49.41%
Mapped reads, both in pair	3,649,772 / 98.33%
Mapped reads, singletons	16,675 / 0.45%
Secondary alignments	0
Supplementary alignments	14,727 / 0.4%
Read min/max/mean length	30 / 101 / 101.16
Duplicated reads (estimated)	204,923 / 5.52%
Duplication rate	2.82%
Clipped reads	2,334,648 / 62.9%

2.2. ACGT Content

Number/percentage of A's	97,662,168 / 29.41%
Number/percentage of C's	63,245,547 / 19.05%
Number/percentage of T's	101,102,441 / 30.45%
Number/percentage of G's	70,028,735 / 21.09%
Number/percentage of N's	4,625 / 0%

GC Percentage	40.14%

2.3. Coverage

Mean	0.1073
Standard Deviation	1.35

2.4. Mapping Quality

Mean Mapping Quality	52.65

2.5. Insert size

Mean	50,979.86
Standard Deviation	2,100,739.16
P25/Median/P75	138 / 170 / 215

2.6. Mismatches and indels

General error rate	0.86%
Mismatches	2,731,571
Insertions	46,940
Mapped reads with at least one insertion	1.25%
Deletions	102,271
Mapped reads with at least one deletion	2.73%
Homopolymer indels	46.97%

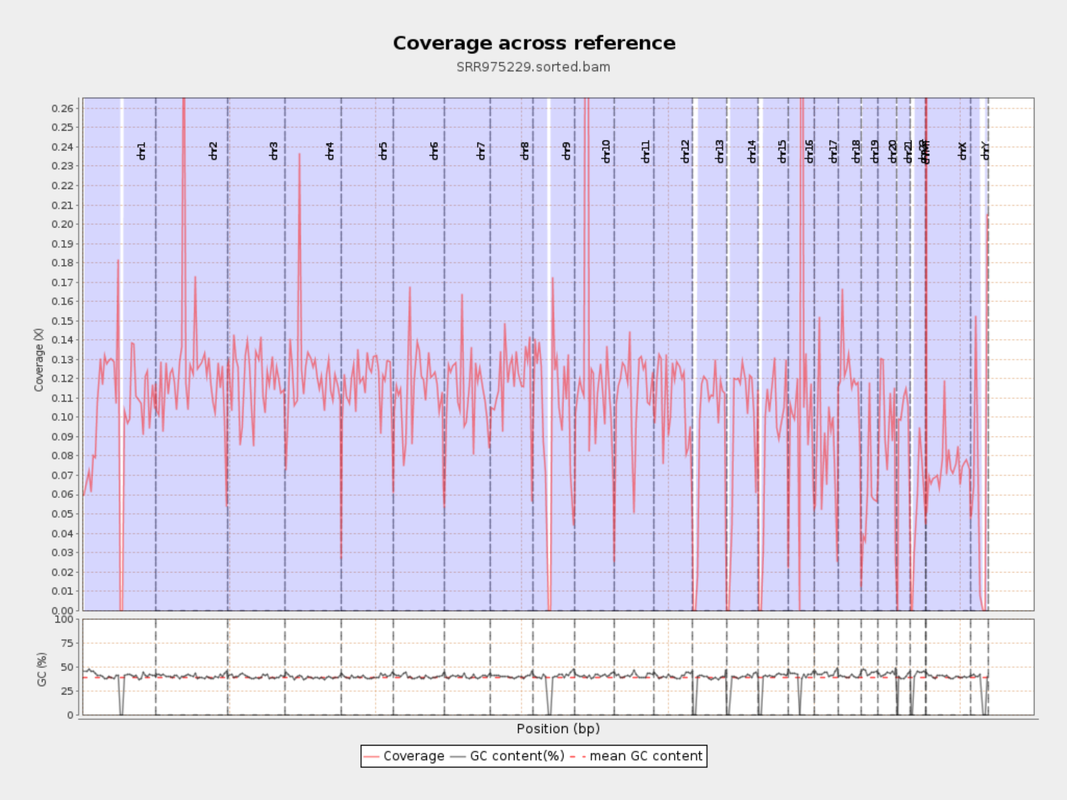
2.7. Chromosome stats

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

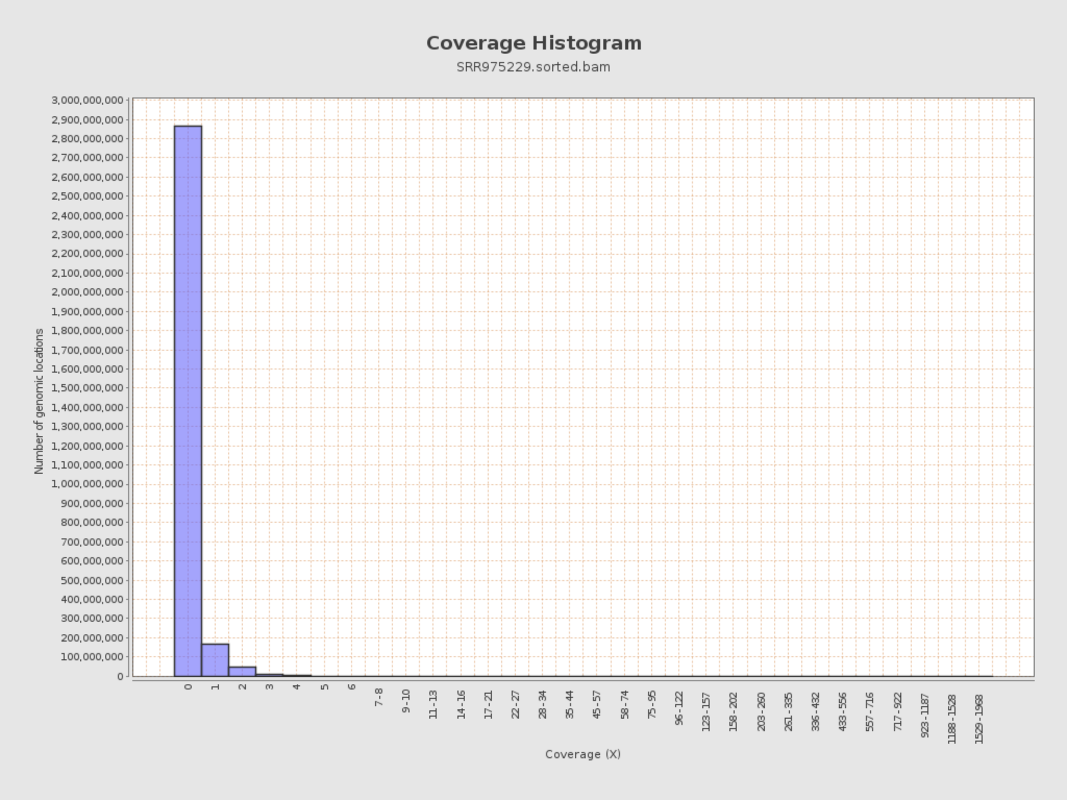
		bases	coverage	deviation
chr1	249250621	25466910	0.1022	1.1963
chr2	243199373	30639861	0.126	1.526
chr3	198022430	23584362	0.1191	0.4893
chr4	191154276	23488080	0.1229	0.939
chr5	180915260	21229016	0.1173	0.4442
chr6	171115067	19806083	0.1157	0.6516
chr7	159138663	17907543	0.1125	1.1481
chr8	146364022	17418164	0.119	0.5693
chr9	141213431	14101931	0.0999	1.6149
chr10	135534747	18717949	0.1381	4.1138
chr11	135006516	15220632	0.1127	0.9345
chr12	133851895	14661942	0.1095	0.4257
chr13	115169878	10745617	0.0933	0.3858
chr14	107349540	9993775	0.0931	0.4283
chr15	102531392	8889837	0.0867	0.3753
chr16	90354753	11494847	0.1272	2.6981
chr17	81195210	6886085	0.0848	1.205
chr18	78077248	9577963	0.1227	1.794
chr19	59128983	3471230	0.0587	0.6868
chr20	63025520	6269919	0.0995	0.4513
chr21	48129895	4291208	0.0892	0.5297
chr22	51304566	2636479	0.0514	0.3153
chrMT	16571	52075	3.1425	2.6452
chrX	155270560	11480851	0.0739	0.5129

chrY	59373566	4190213	0.0706	1.608

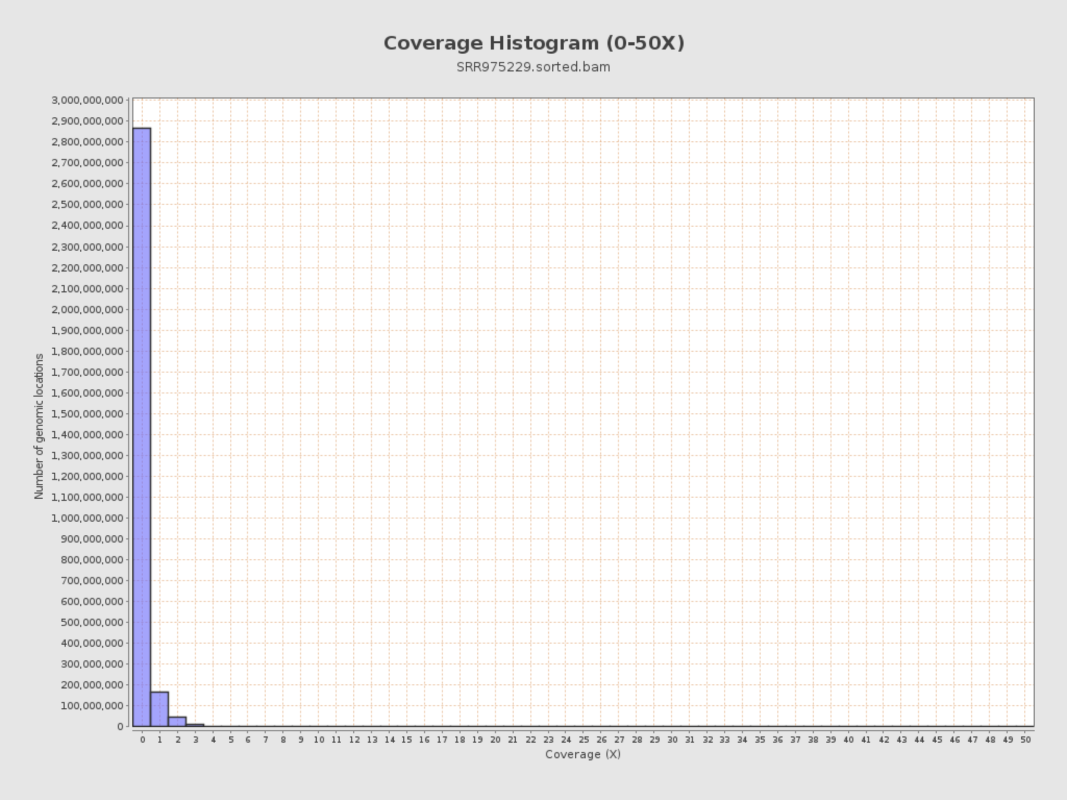
3. Results : Coverage across reference



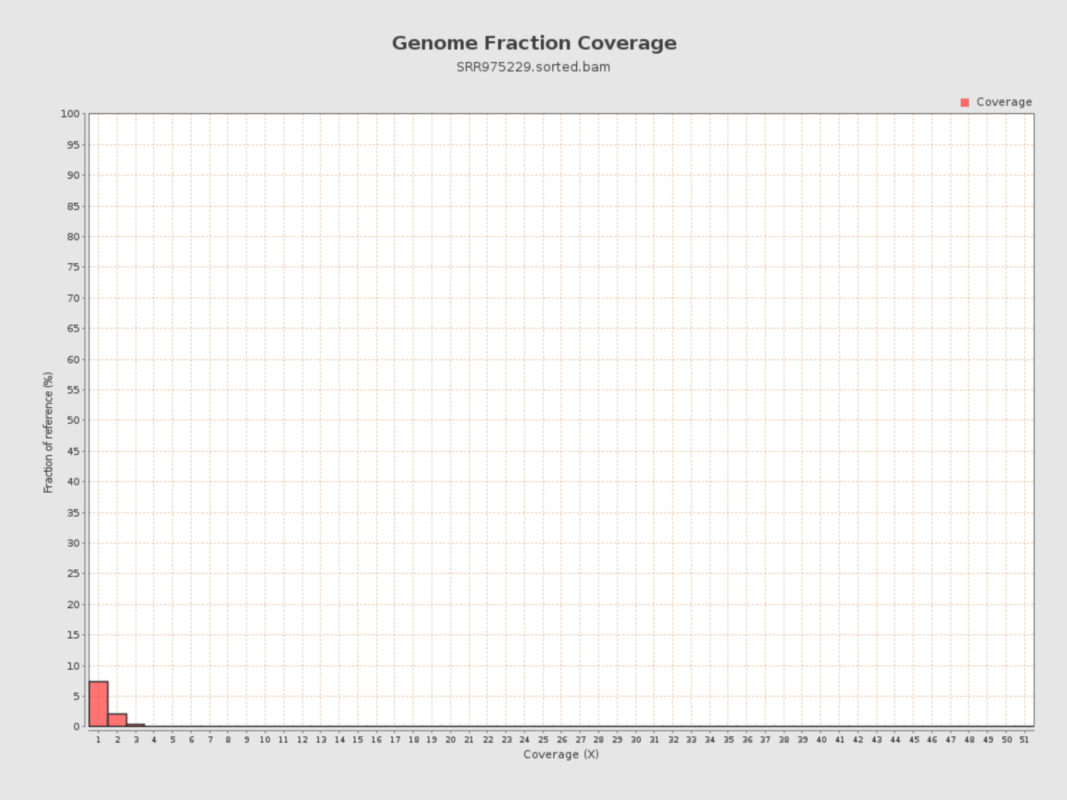
4. Results : Coverage Histogram



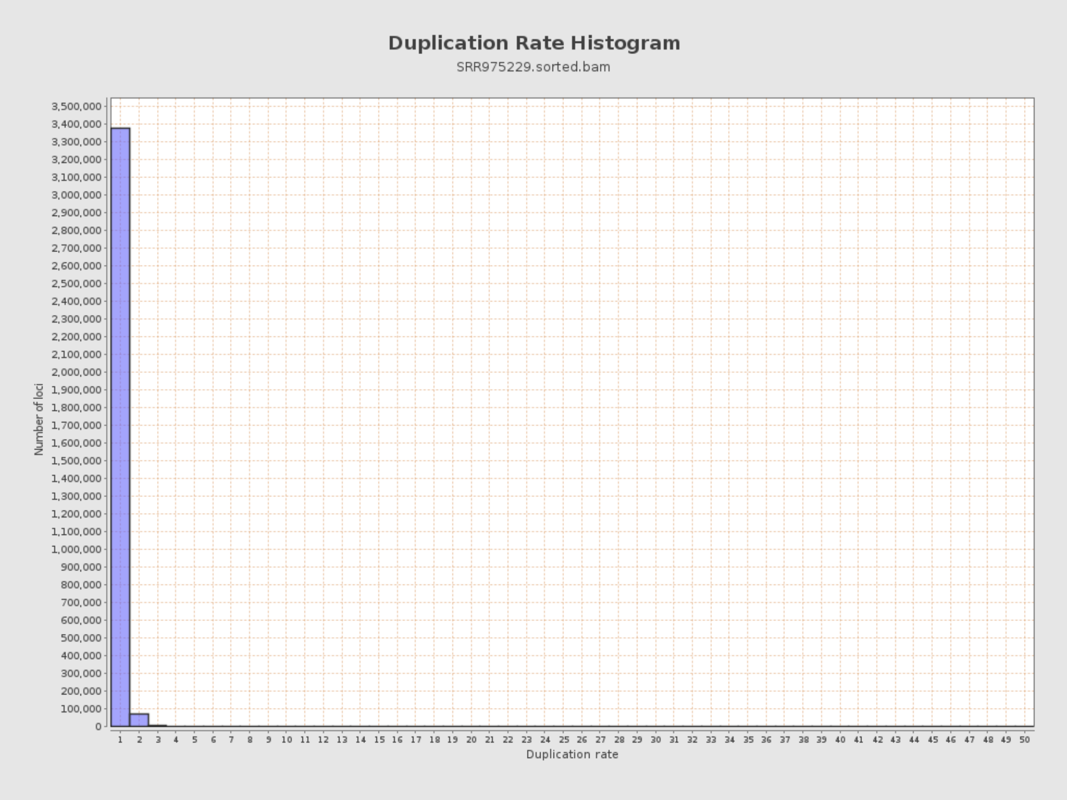
5. Results : Coverage Histogram (0-50X)



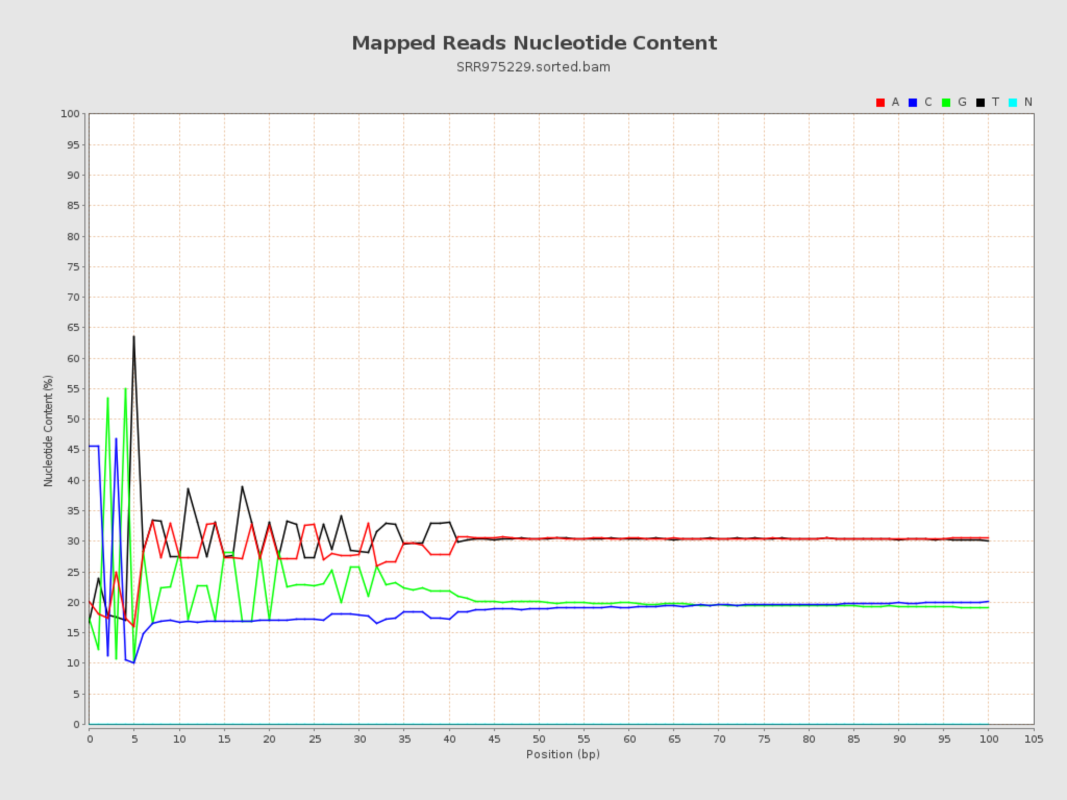
6. Results : Genome Fraction Coverage



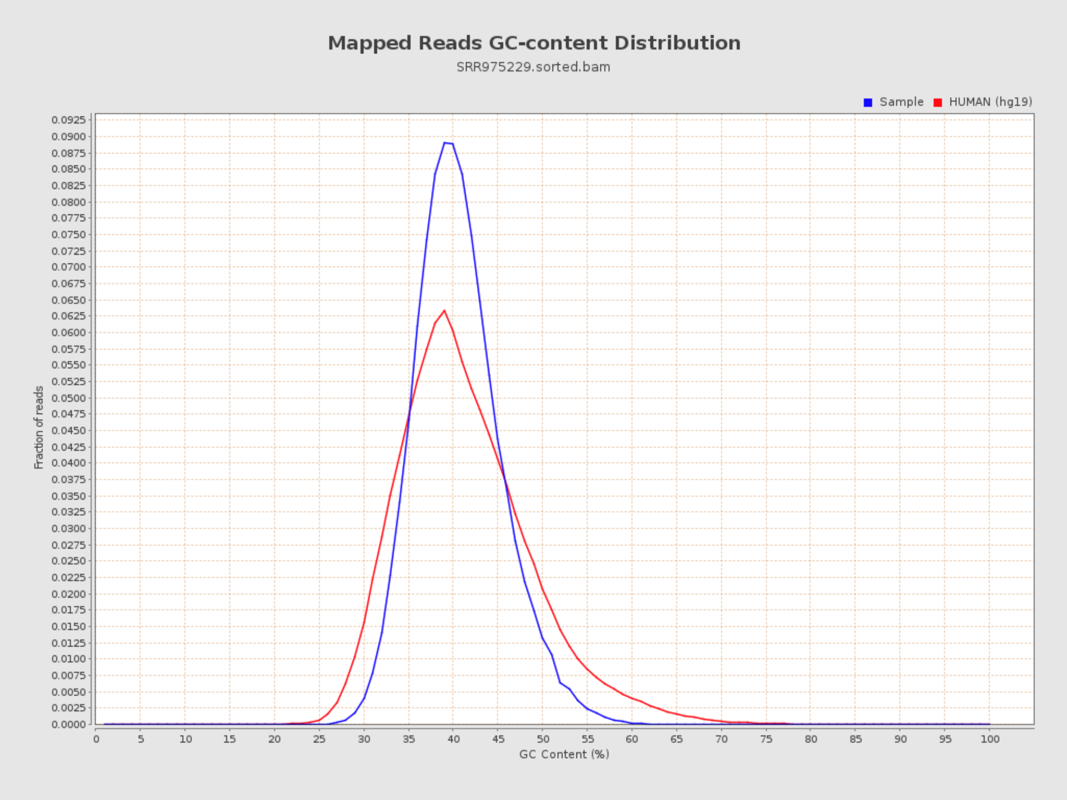
7. Results : Duplication Rate Histogram



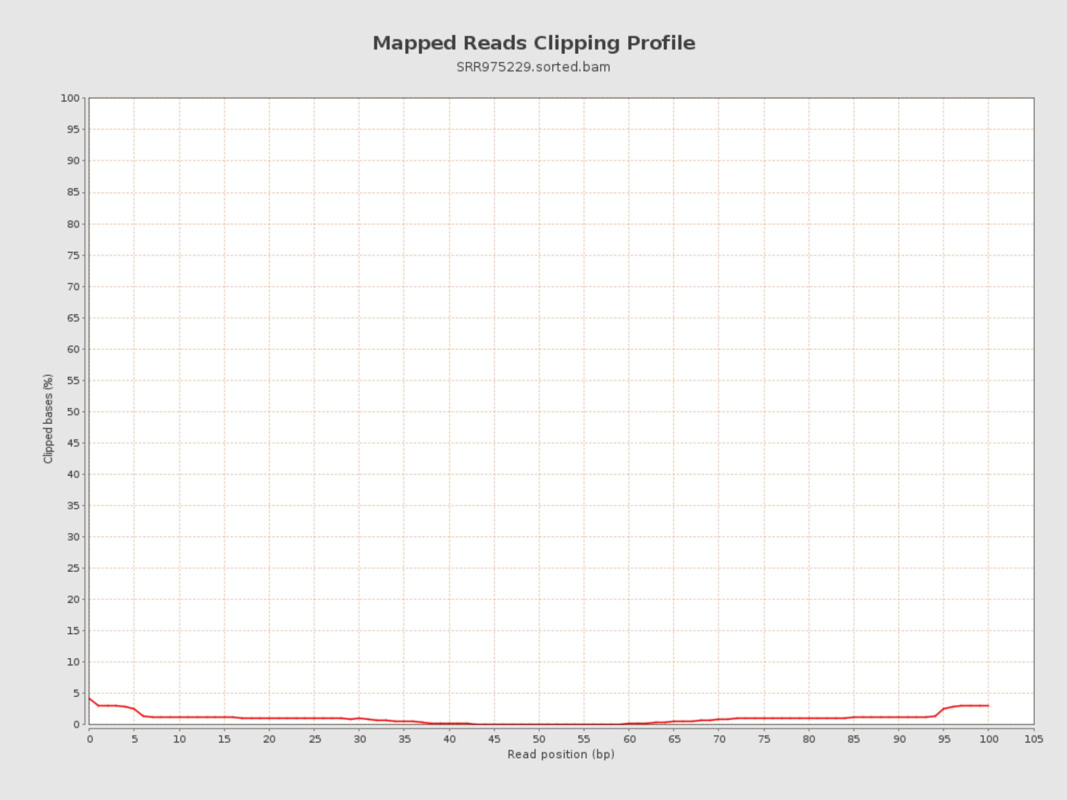
8. Results : Mapped Reads Nucleotide Content



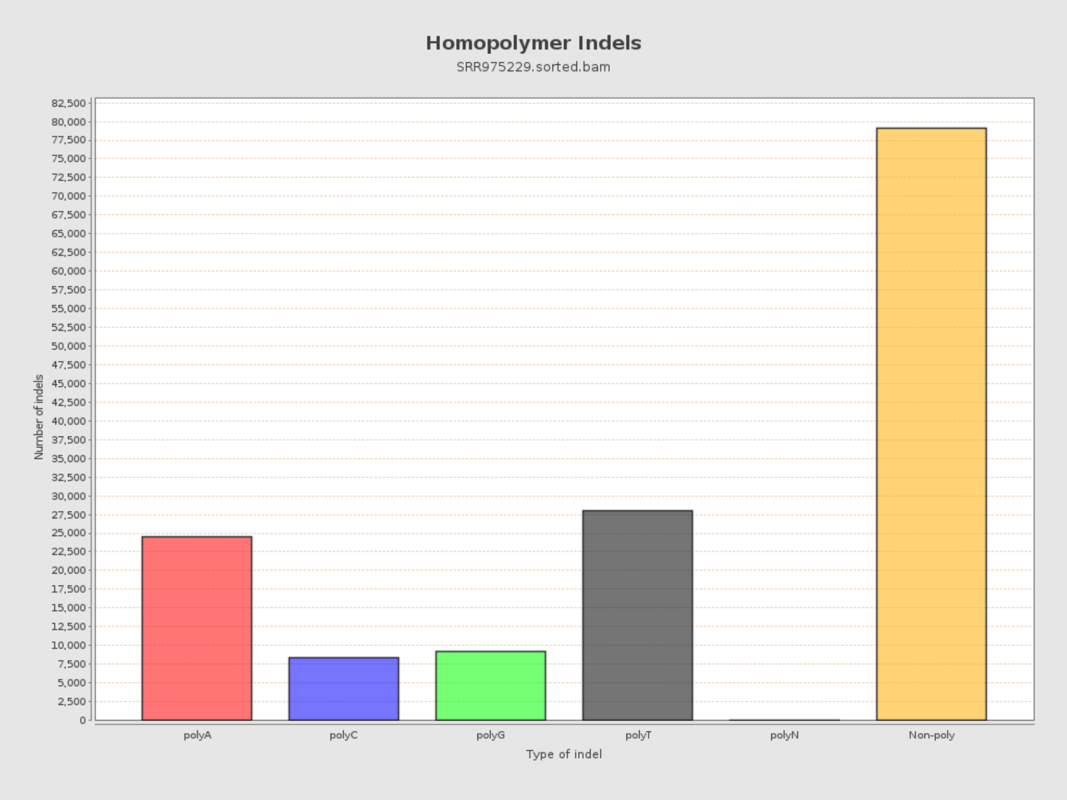
9. Results : Mapped Reads GC-content Distribution



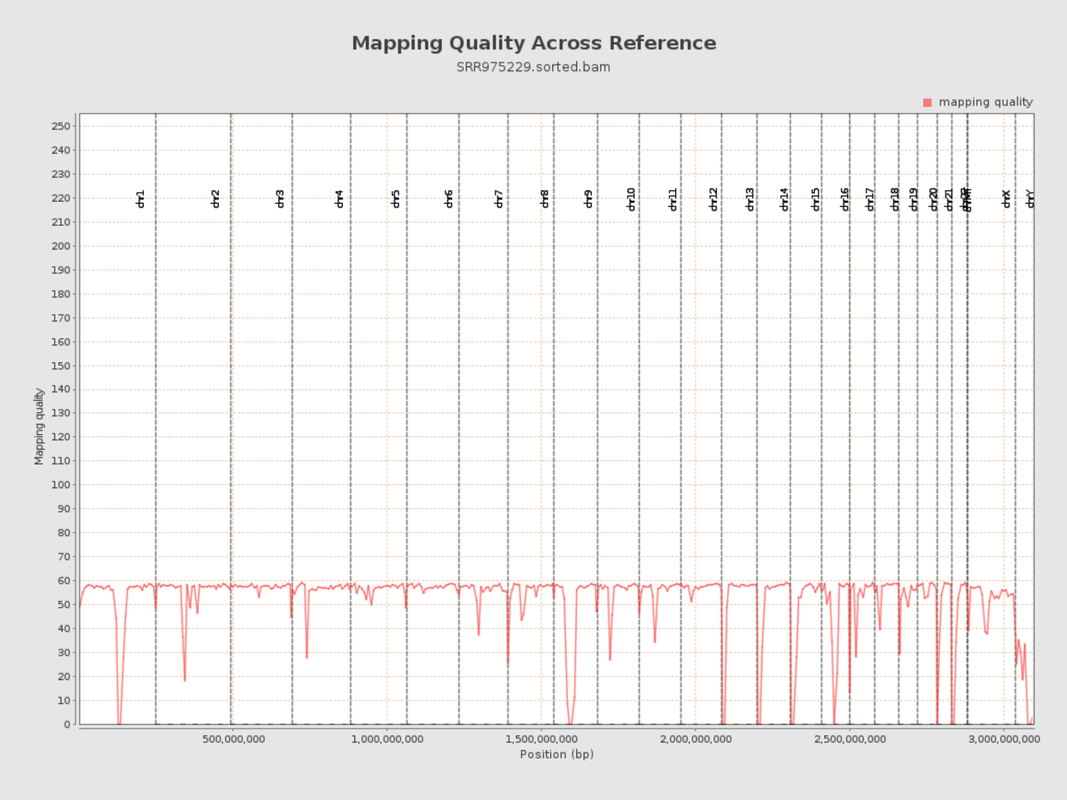
10. Results : Mapped Reads Clipping Profile



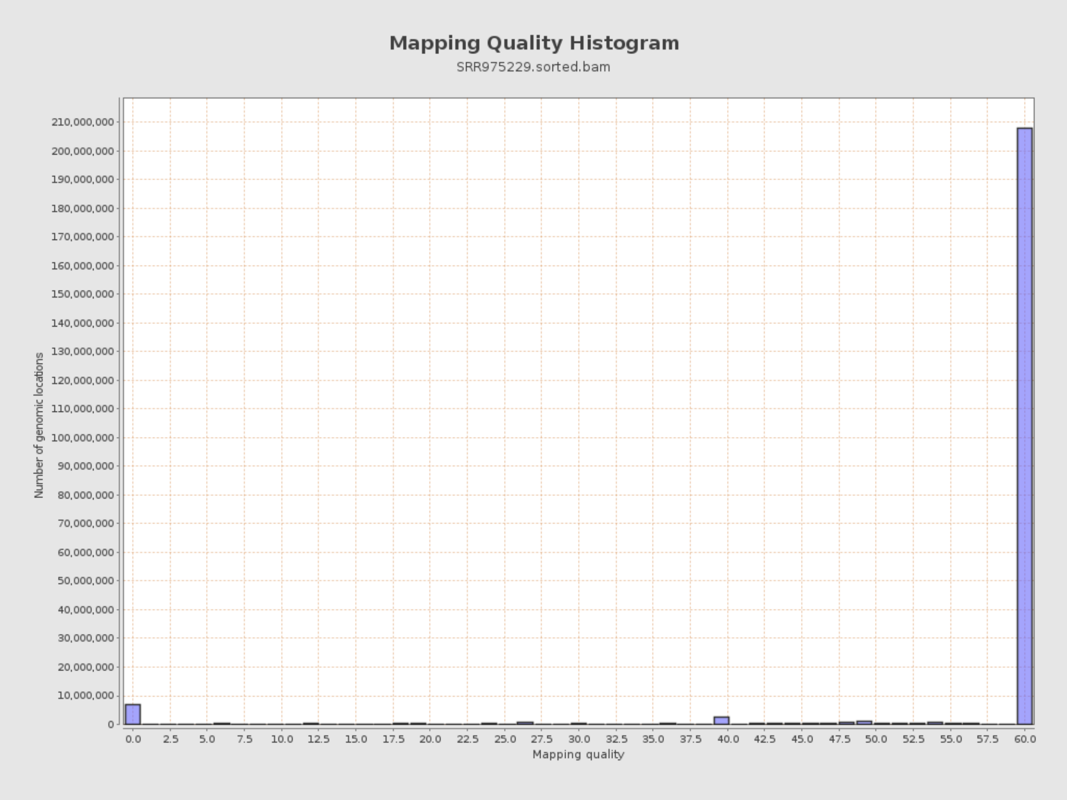
11. Results : Homopolymer Indels



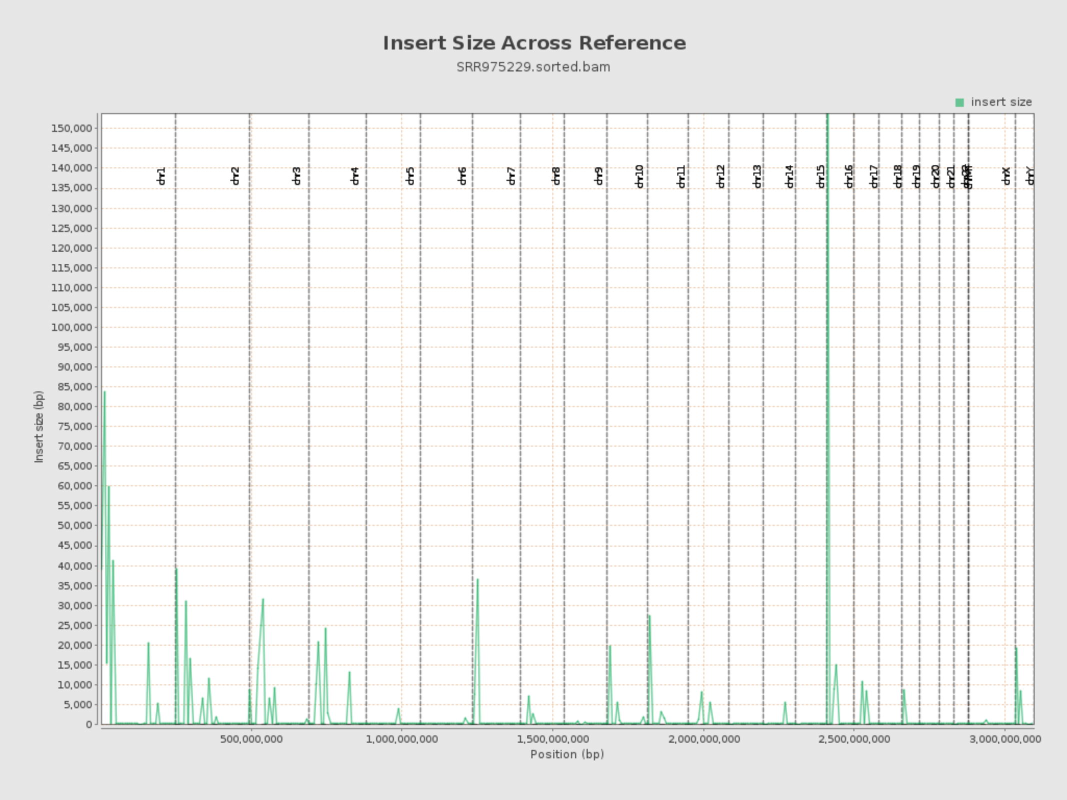
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram