Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 19:05:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975222.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_SRR975222 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975222_1.fastq.gz SRR975222_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 19:05:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975222.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	54,271,510
Mapped reads	54,178,816 / 99.83%
Unmapped reads	92,694 / 0.17%
Mapped paired reads	54,178,816 / 99.83%
Mapped reads, first in pair	27,099,675 / 49.93%
Mapped reads, second in pair	27,079,141 / 49.9%
Mapped reads, both in pair	54,127,846 / 99.74%
Mapped reads, singletons	50,970 / 0.09%
Secondary alignments	0
Supplementary alignments	133,879 / 0.25%
Read min/max/mean length	30 / 101 / 101.1
Duplicated reads (estimated)	28,852,232 / 53.16%
Duplication rate	33.98%
Clipped reads	8,582,683 / 15.81%

2.2. ACGT Content

Number/percentage of A's	1,408,562,400 / 26.6%
Number/percentage of C's	1,200,398,662 / 22.66%
Number/percentage of T's	1,425,276,626 / 26.91%
Number/percentage of G's	1,261,783,816 / 23.82%
Number/percentage of N's	253,593 / 0%

GC Percentage	46.49%

2.3. Coverage

Mean	1.7115
Standard Deviation	22.2799

2.4. Mapping Quality

Mean Mapping Quality	55.75

2.5. Insert size

Mean	135,786.7
Standard Deviation	3,699,494.94
P25/Median/P75	166 / 203 / 250

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	32,443,597
Insertions	449,120
Mapped reads with at least one insertion	0.82%
Deletions	1,404,413
Mapped reads with at least one deletion	2.55%
Homopolymer indels	49.98%

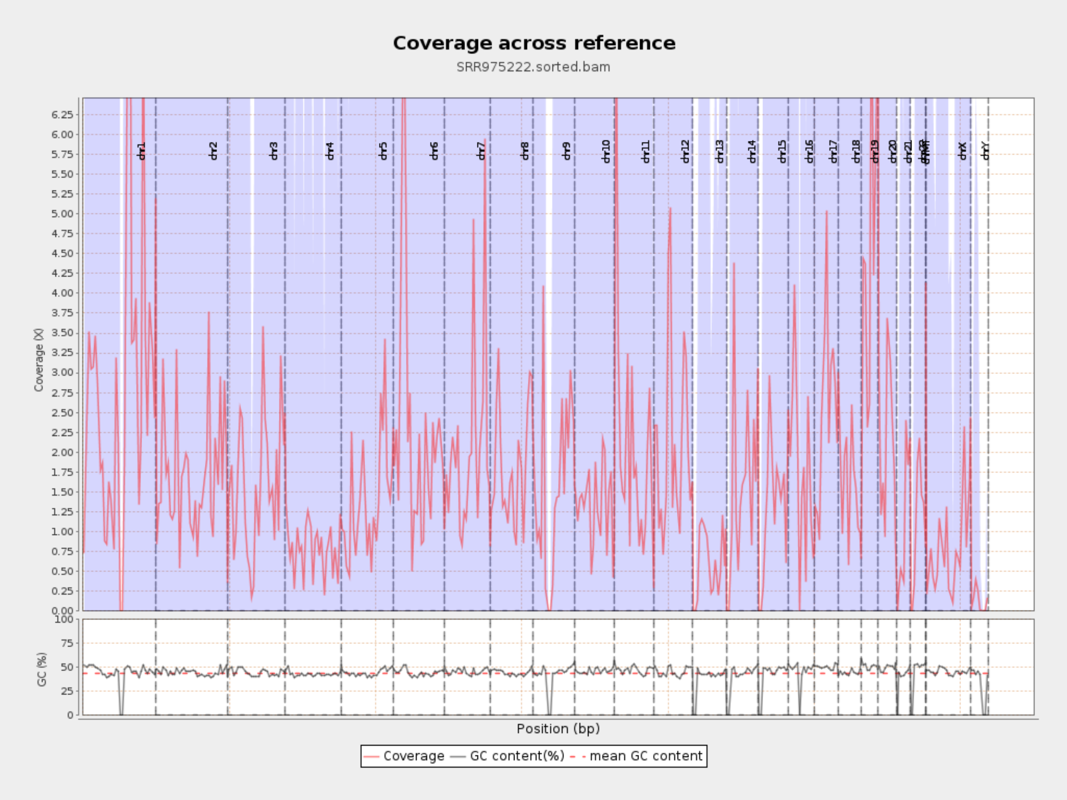
2.7. Chromosome stats

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

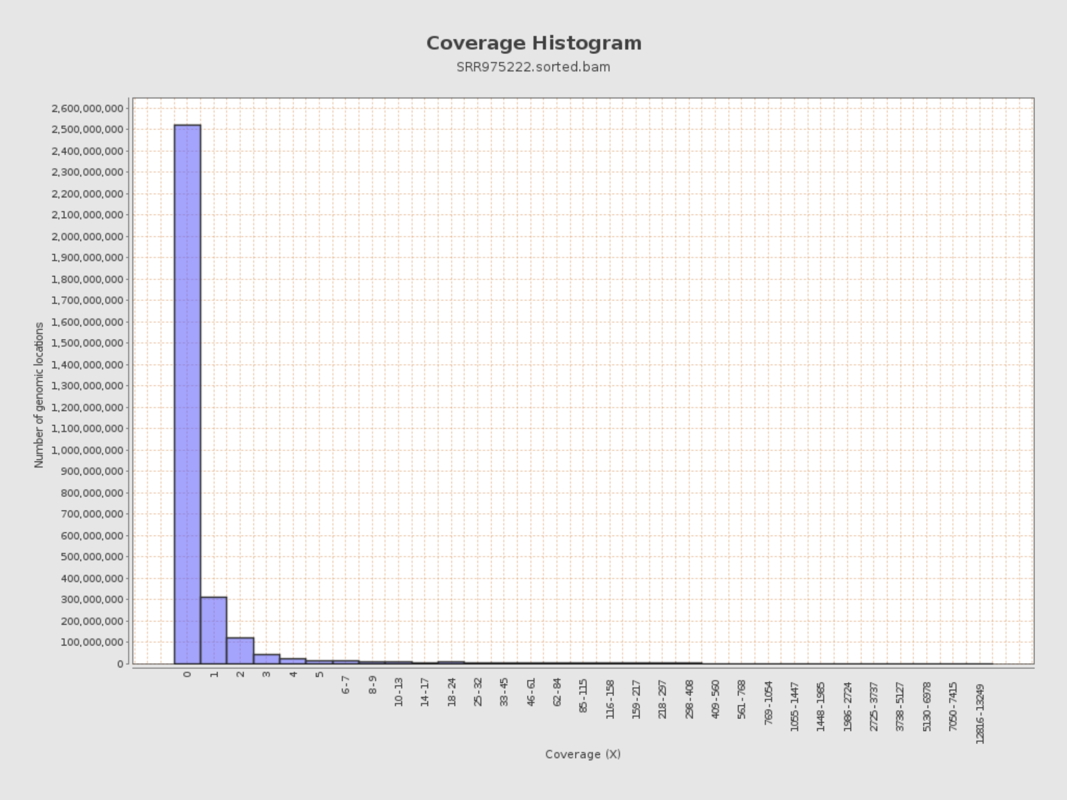
		bases	coverage	deviation
chr1	249250621	710448323	2.8503	32.9602
chr2	243199373	414296512	1.7035	19.576
chr3	198022430	307978135	1.5553	18.3542
chr4	191154276	150360298	0.7866	10.9955
chr5	180915260	253935952	1.4036	17.9858
chr6	171115067	390831045	2.284	27.6801
chr7	159138663	326440401	2.0513	28.3128
chr8	146364022	268049580	1.8314	22.6067
chr9	141213431	213917072	1.5148	19.5279
chr10	135534747	183785922	1.356	16.6221
chr11	135006516	279426556	2.0697	24.7748
chr12	133851895	289229898	2.1608	25.2157
chr13	115169878	68312894	0.5931	8.9318
chr14	107349540	166373721	1.5498	19.7198
chr15	102531392	127771068	1.2462	14.873
chr16	90354753	160079949	1.7717	22.3061
chr17	81195210	208003844	2.5618	28.826
chr18	78077248	129036846	1.6527	21.7015
chr19	59128983	276166430	4.6706	44.1754
chr20	63025520	133481198	2.1179	25.7508
chr21	48129895	52137944	1.0833	16.8095
chr22	51304566	57401532	1.1188	15.0407
chrMT	16571	68608	4.1402	6.2058
chrX	155270560	123045335	0.7925	12.4608

chrY	59373566	7773587	0.1309	3.1419

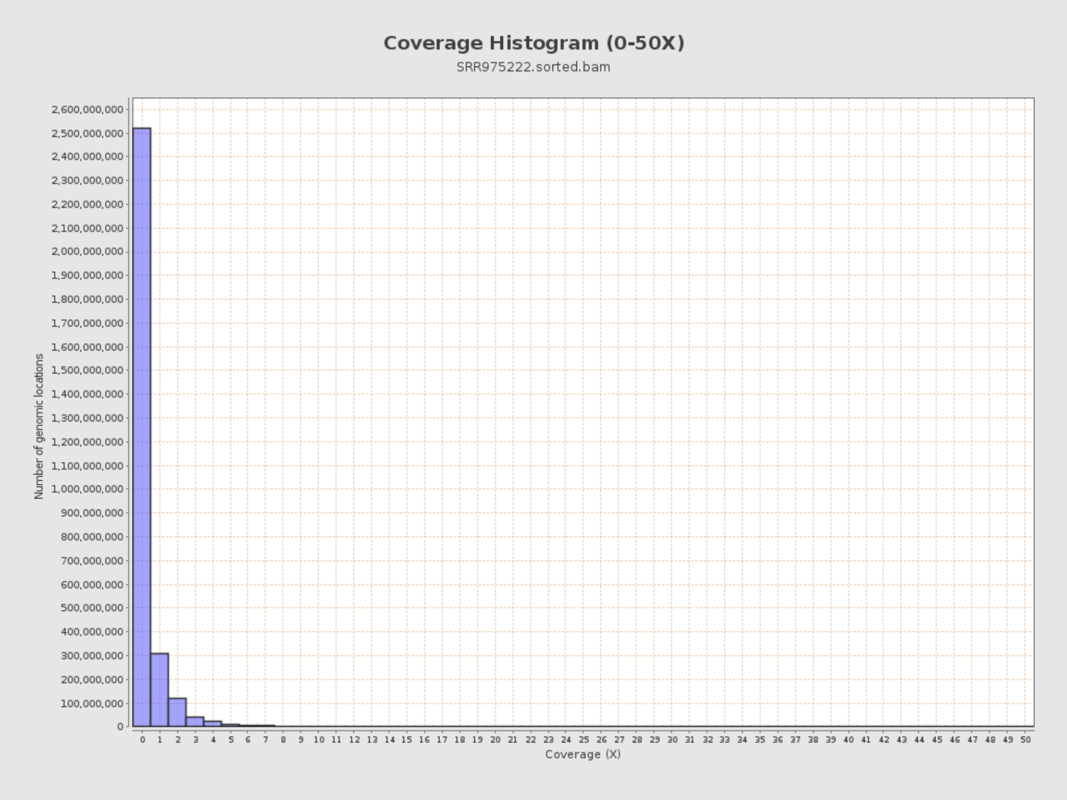
3. Results : Coverage across reference



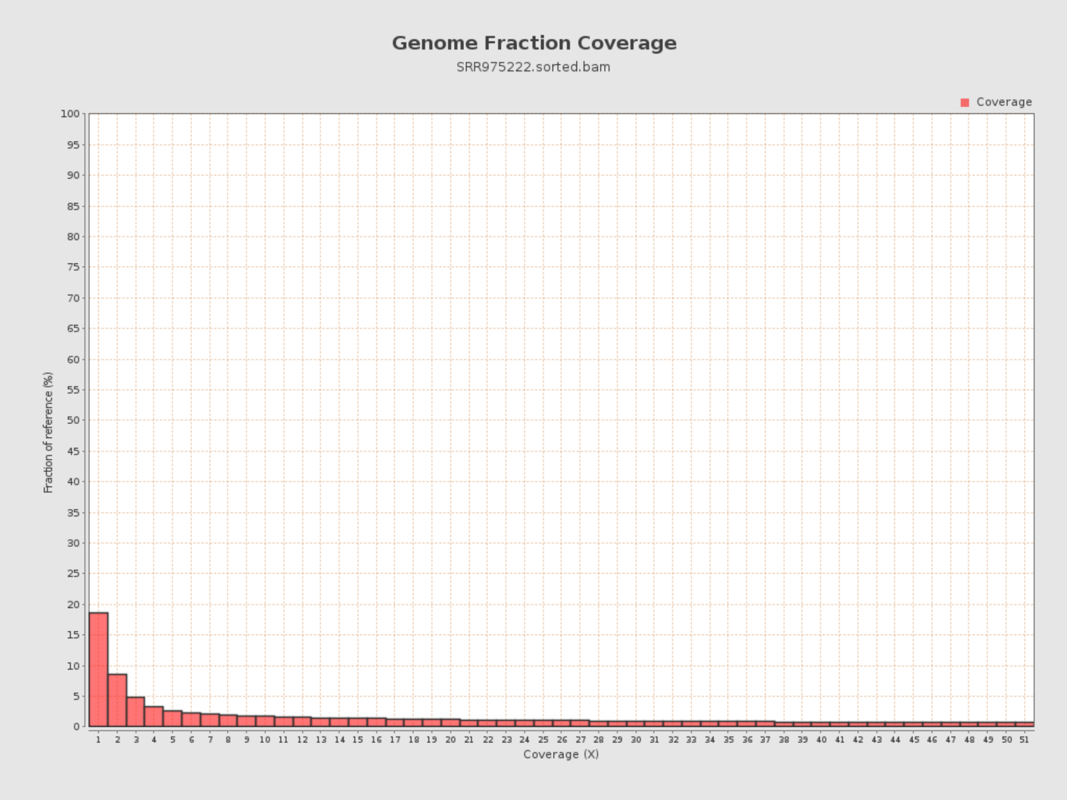
4. Results : Coverage Histogram



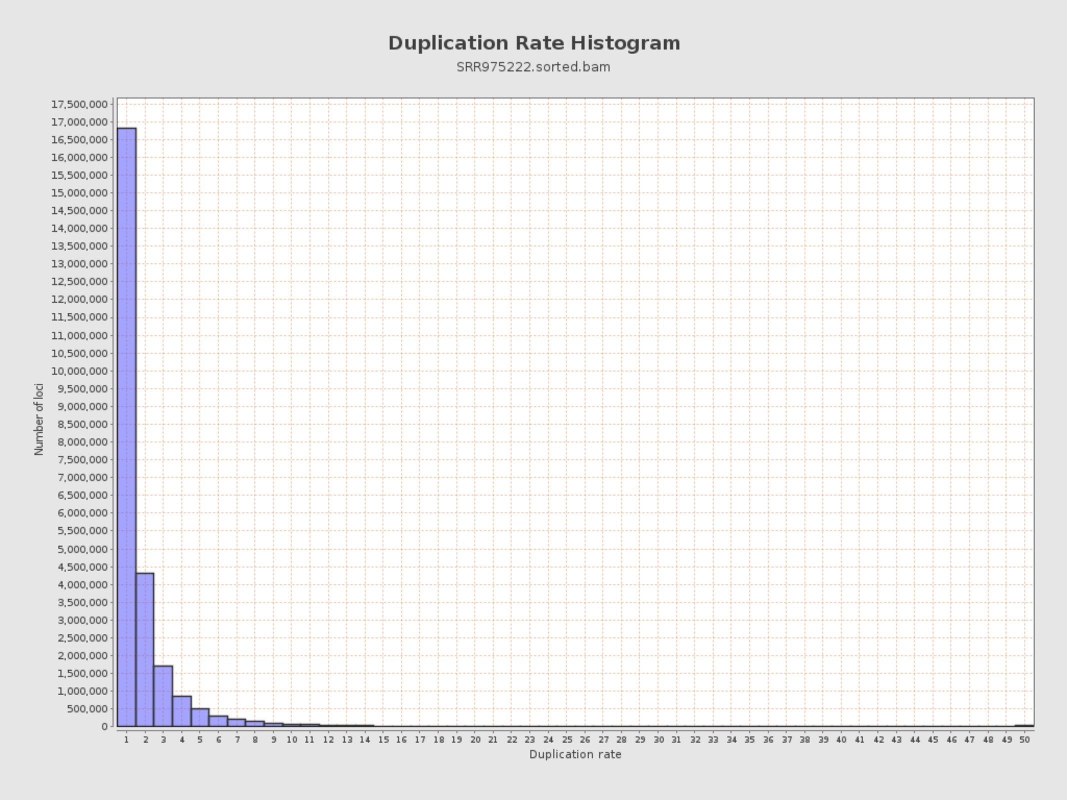
5. Results : Coverage Histogram (0-50X)



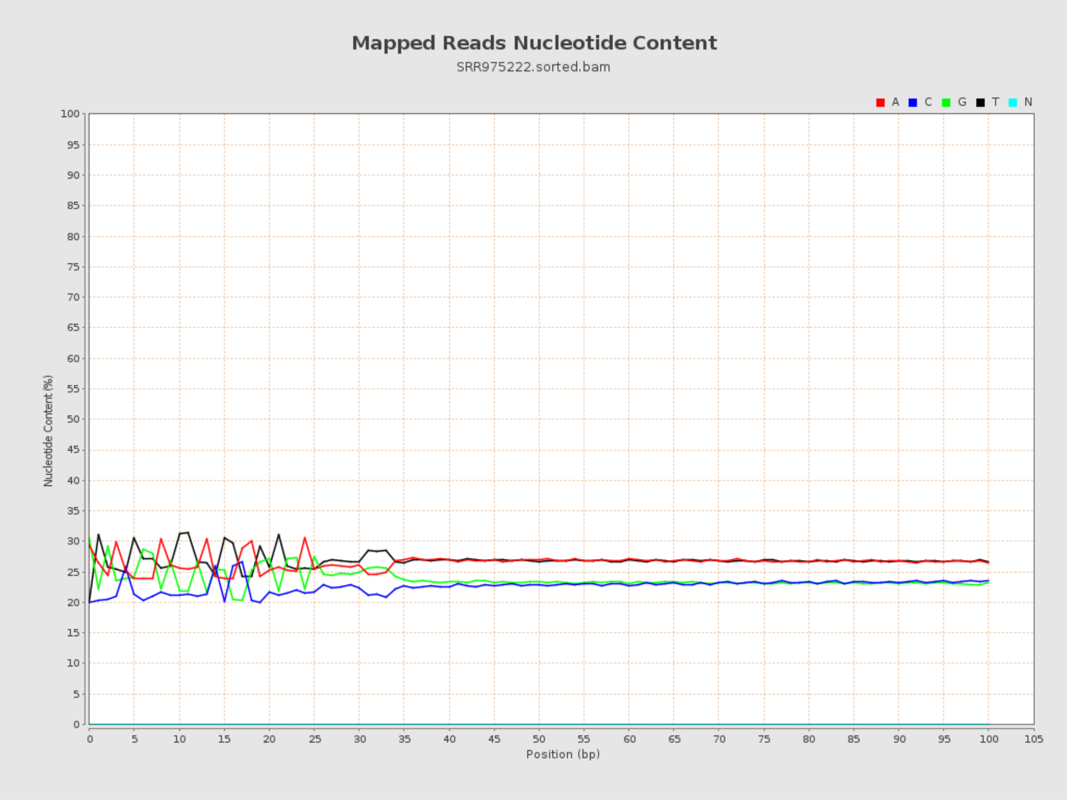
6. Results : Genome Fraction Coverage



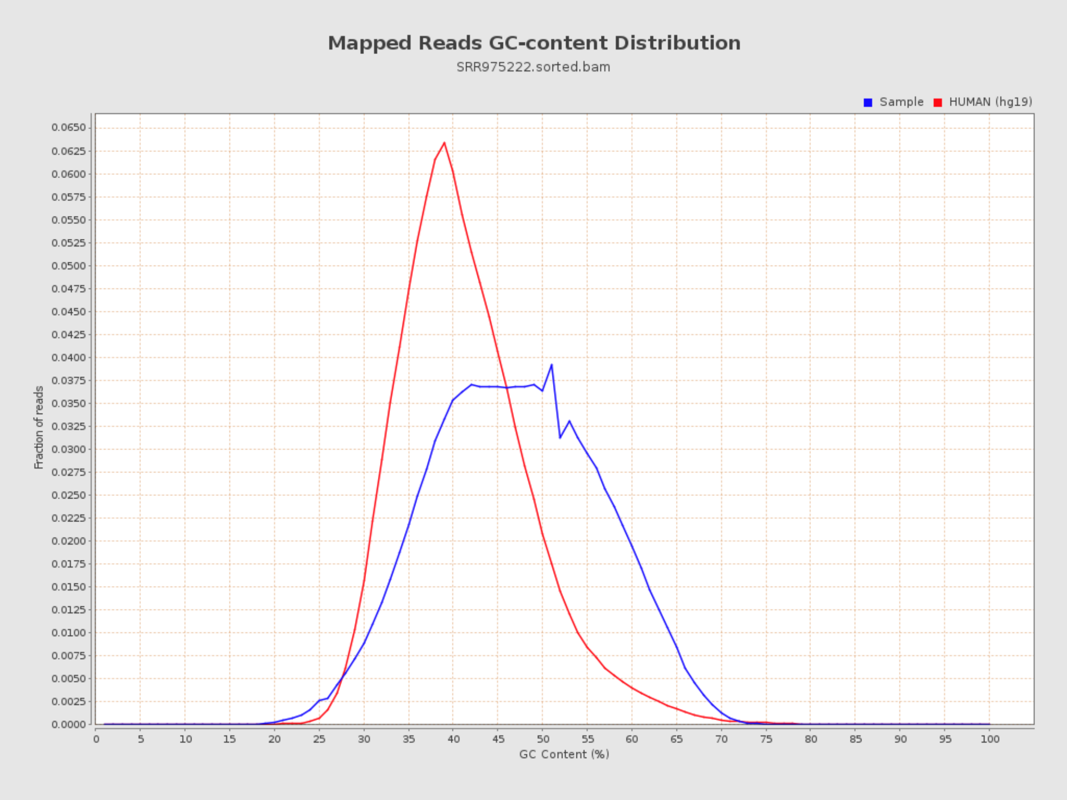
7. Results : Duplication Rate Histogram



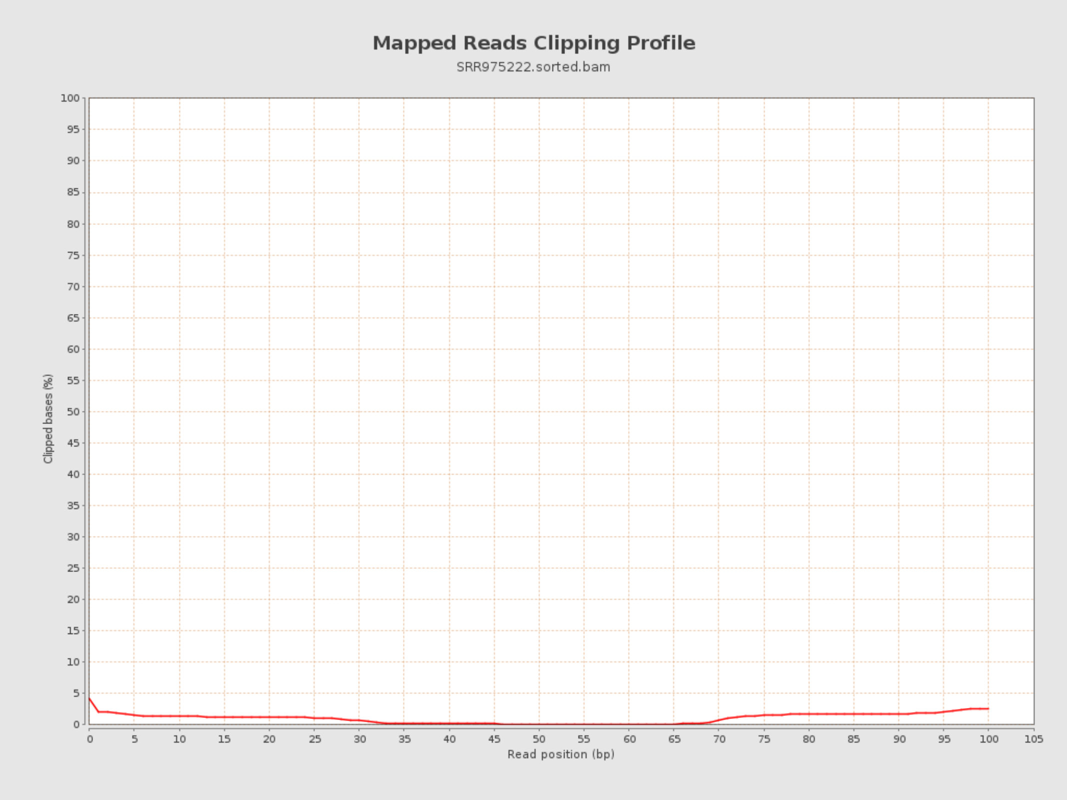
8. Results : Mapped Reads Nucleotide Content



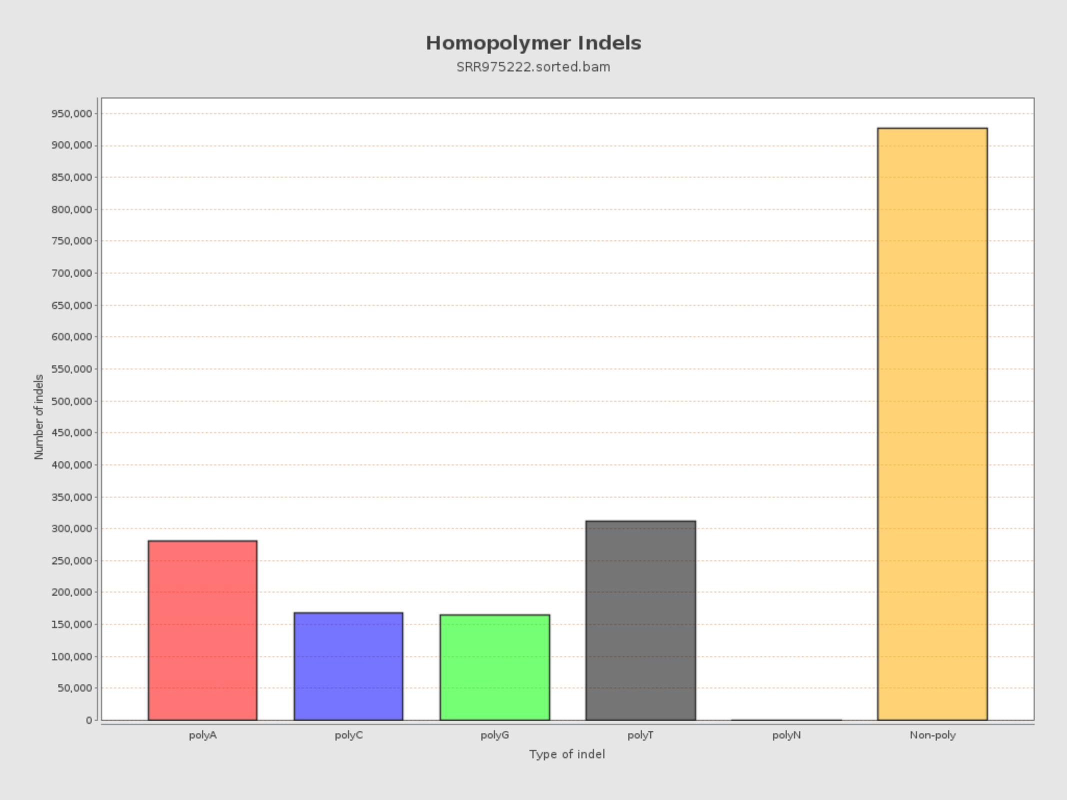
9. Results : Mapped Reads GC-content Distribution



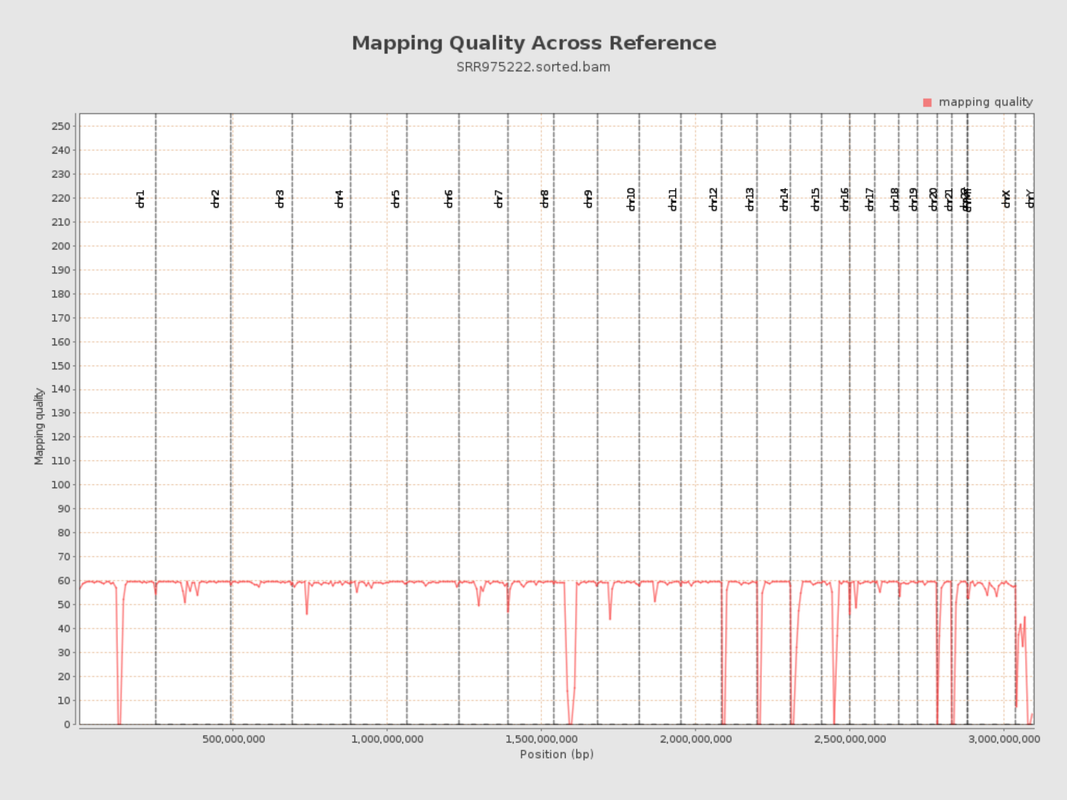
10. Results : Mapped Reads Clipping Profile



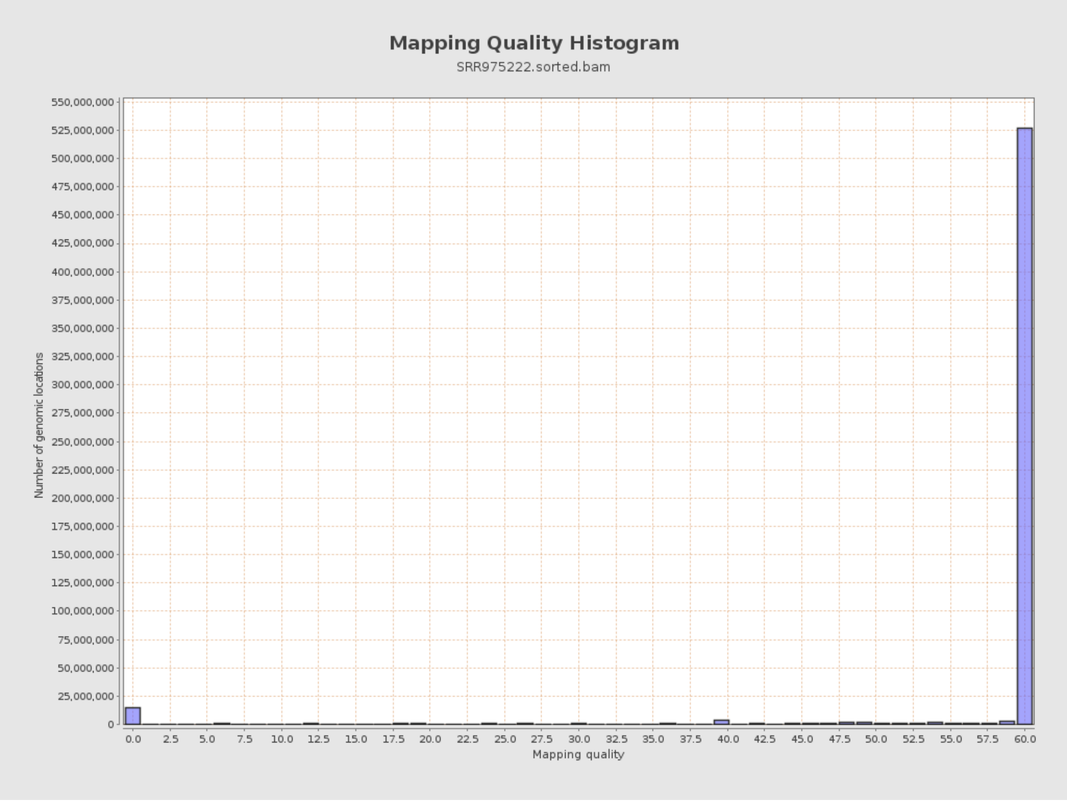
11. Results : Homopolymer Indels



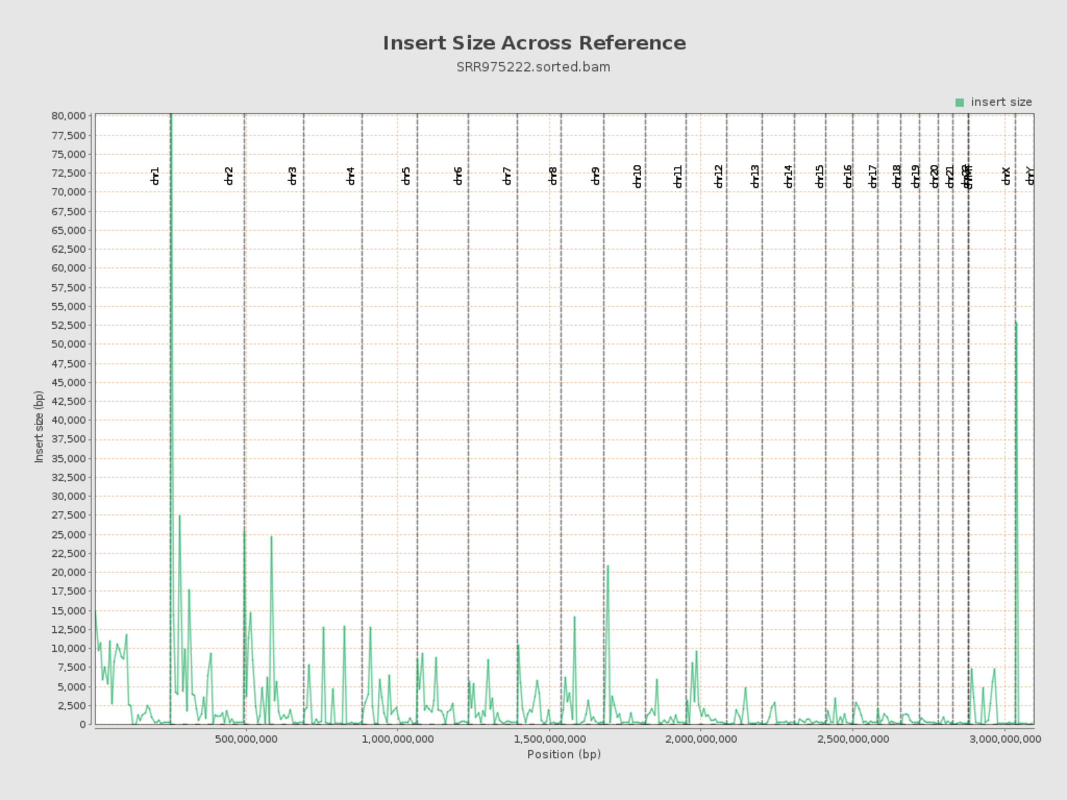
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram