Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 18:12:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975220.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_SRR975220 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975220_1.fastq.gz SRR975220_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 18:12:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975220.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	51,951,140
Mapped reads	51,784,744 / 99.68%
Unmapped reads	166,396 / 0.32%
Mapped paired reads	51,784,744 / 99.68%
Mapped reads, first in pair	25,887,827 / 49.83%
Mapped reads, second in pair	25,896,917 / 49.85%
Mapped reads, both in pair	51,717,784 / 99.55%
Mapped reads, singletons	66,960 / 0.13%
Secondary alignments	0
Supplementary alignments	107,582 / 0.21%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	28,922,611 / 55.67%
Duplication rate	40.49%
Clipped reads	31,726,537 / 61.07%

2.2. ACGT Content

Number/percentage of A's	1,259,382,349 / 26.55%
Number/percentage of C's	1,065,921,313 / 22.47%
Number/percentage of T's	1,270,352,468 / 26.78%
Number/percentage of G's	1,147,615,014 / 24.19%
Number/percentage of N's	190,182 / 0%

GC Percentage	46.67%

2.3. Coverage

Mean	1.5328
Standard Deviation	22.1459

2.4. Mapping Quality

Mean Mapping Quality	55.8

2.5. Insert size

Mean	54,458.89
Standard Deviation	2,395,004.69
P25/Median/P75	147 / 184 / 233

2.6. Mismatches and indels

General error rate	0.72%
Mismatches	33,531,950
Insertions	506,237
Mapped reads with at least one insertion	0.97%
Deletions	1,249,504
Mapped reads with at least one deletion	2.38%
Homopolymer indels	47.38%

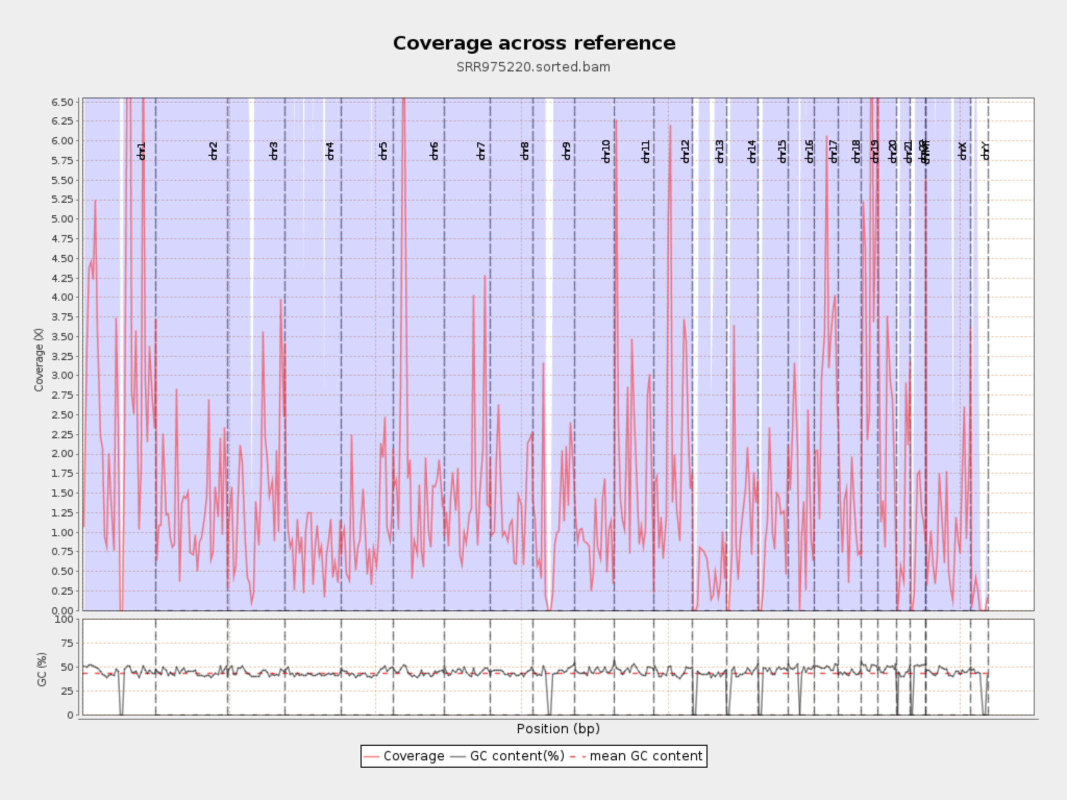
2.7. Chromosome stats

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

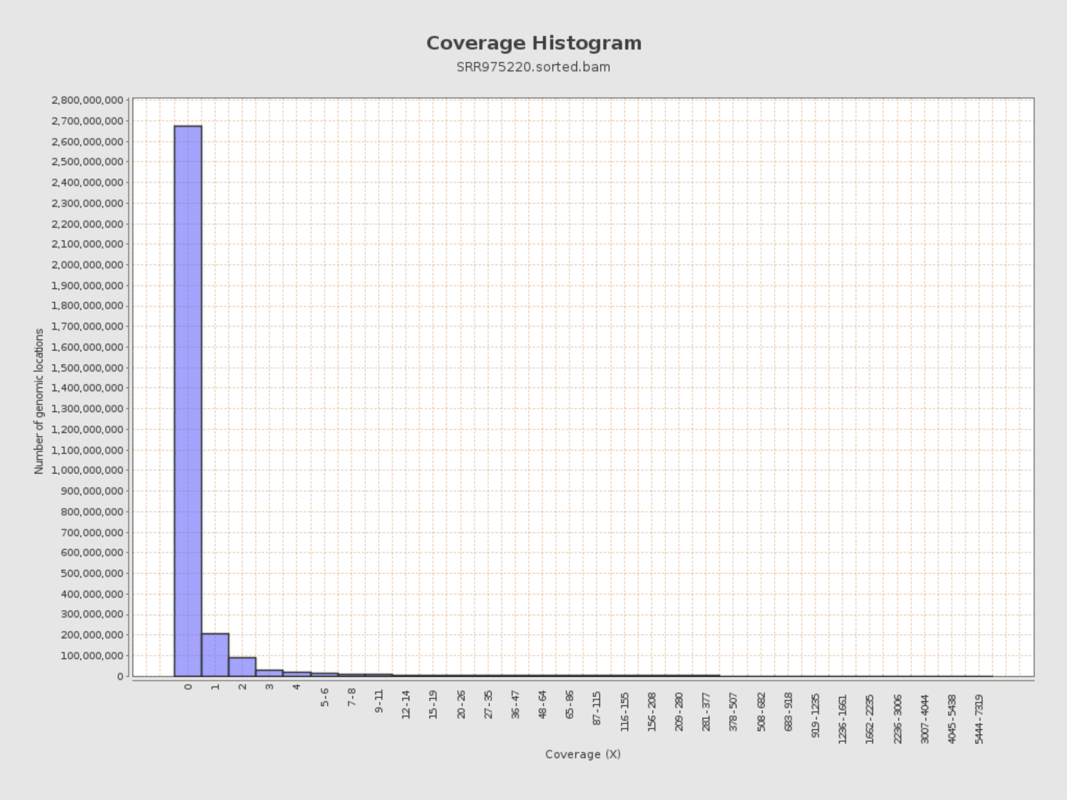
		bases	coverage	deviation
chr1	249250621	741764177	2.976	36.2199
chr2	243199373	307135217	1.2629	16.8678
chr3	198022430	286497004	1.4468	20.6596
chr4	191154276	155544575	0.8137	12.3882
chr5	180915260	194918575	1.0774	15.5807
chr6	171115067	311745400	1.8218	25.7335
chr7	159138663	243874317	1.5325	21.4628
chr8	146364022	198474922	1.356	19.83
chr9	141213431	158123781	1.1198	15.8802
chr10	135534747	125696919	0.9274	13.1794
chr11	135006516	269389867	1.9954	25.5636
chr12	133851895	292941595	2.1886	26.8161
chr13	115169878	50250289	0.4363	7.5998
chr14	107349540	130983159	1.2202	17.0629
chr15	102531392	99983272	0.9751	14.2009
chr16	90354753	132750482	1.4692	20.5624
chr17	81195210	260003017	3.2022	34.3637
chr18	78077248	94256506	1.2072	18.1189
chr19	59128983	272861371	4.6147	46.5634
chr20	63025520	134824479	2.1392	26.8639
chr21	48129895	63165421	1.3124	20.9901
chr22	51304566	49356166	0.962	14.1417
chrMT	16571	91524	5.5231	7.266
chrX	155270560	162167833	1.0444	17.9869

chrY	59373566	8425006	0.1419	3.6211

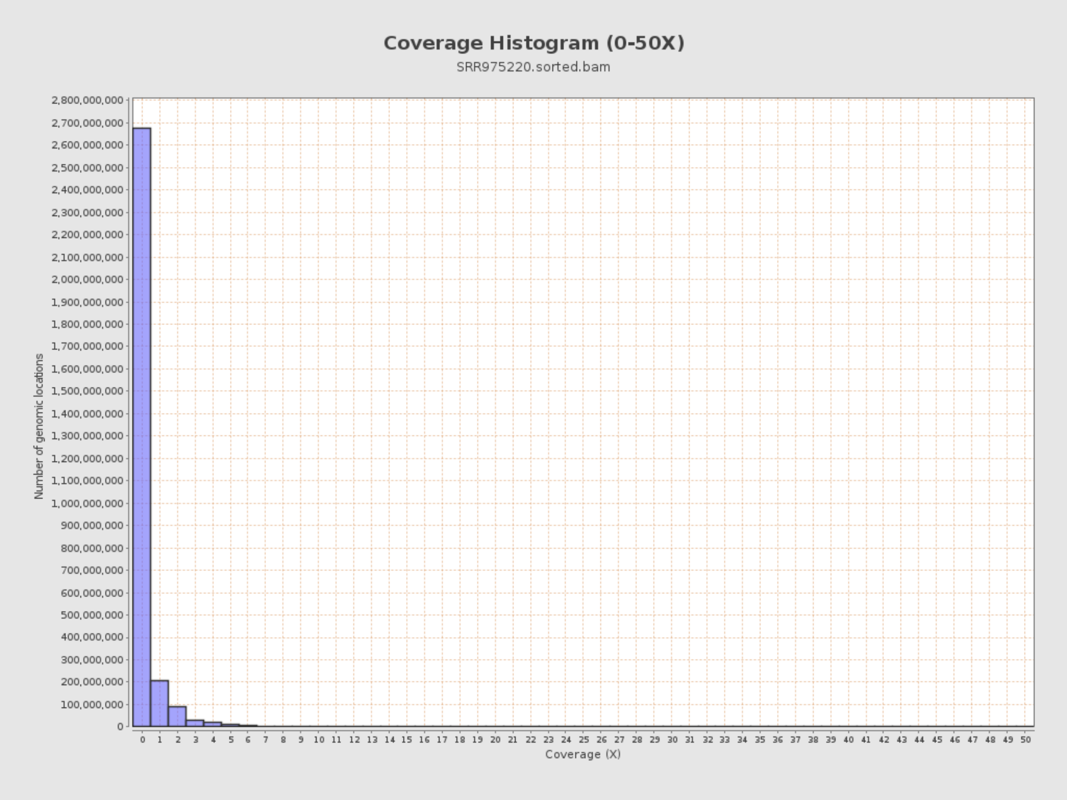
3. Results : Coverage across reference



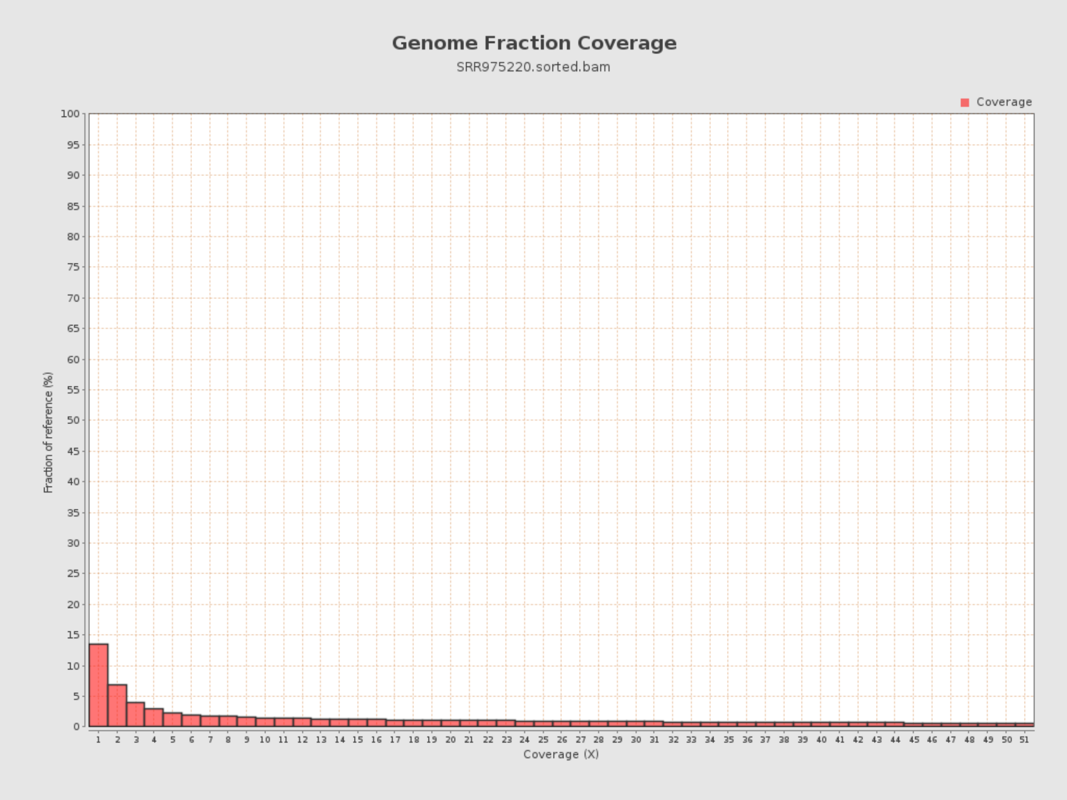
4. Results : Coverage Histogram



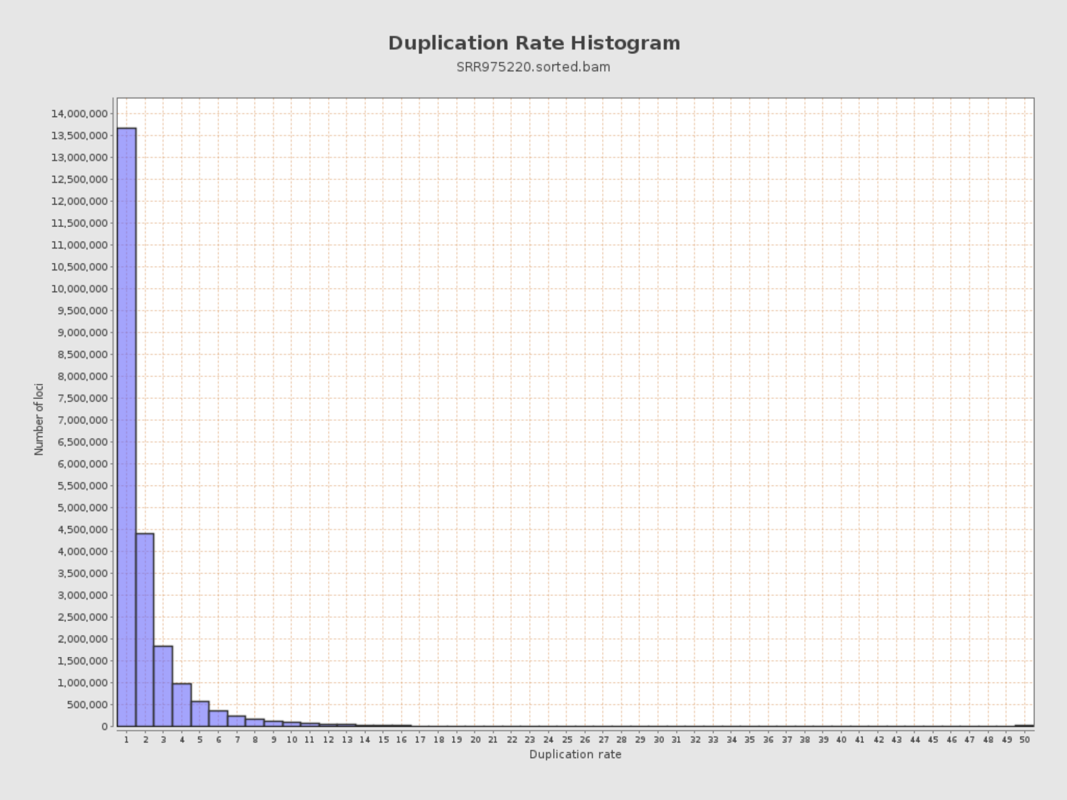
5. Results : Coverage Histogram (0-50X)



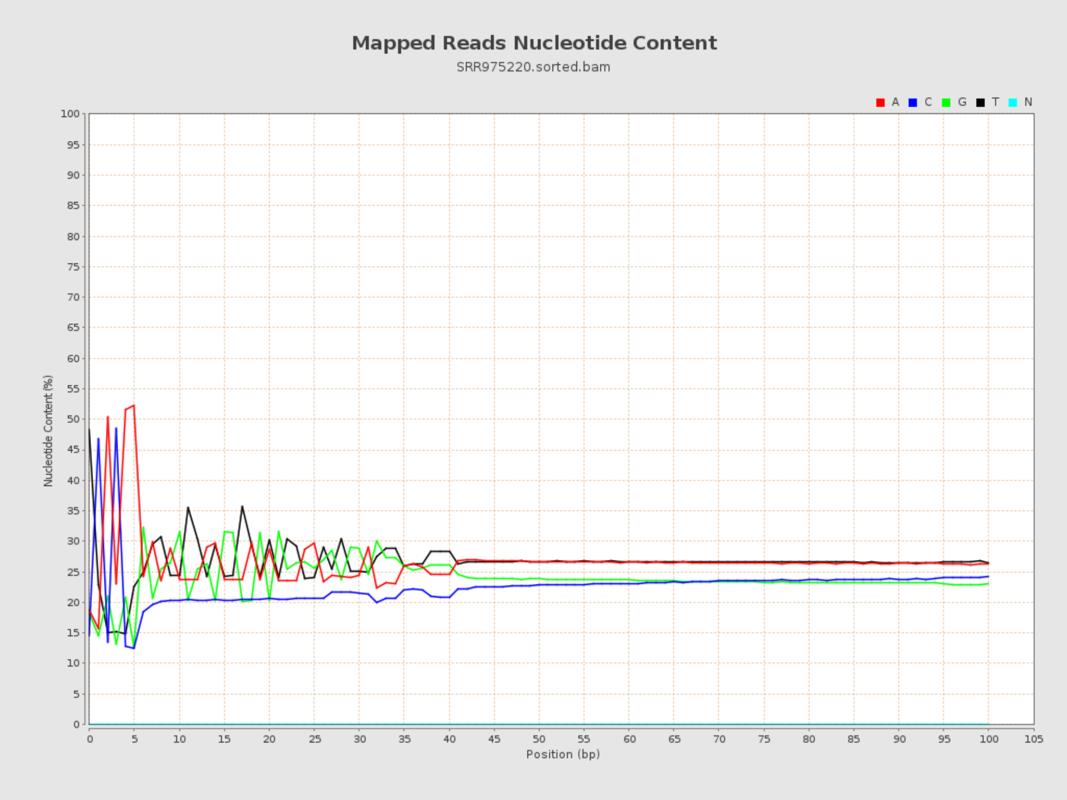
6. Results : Genome Fraction Coverage



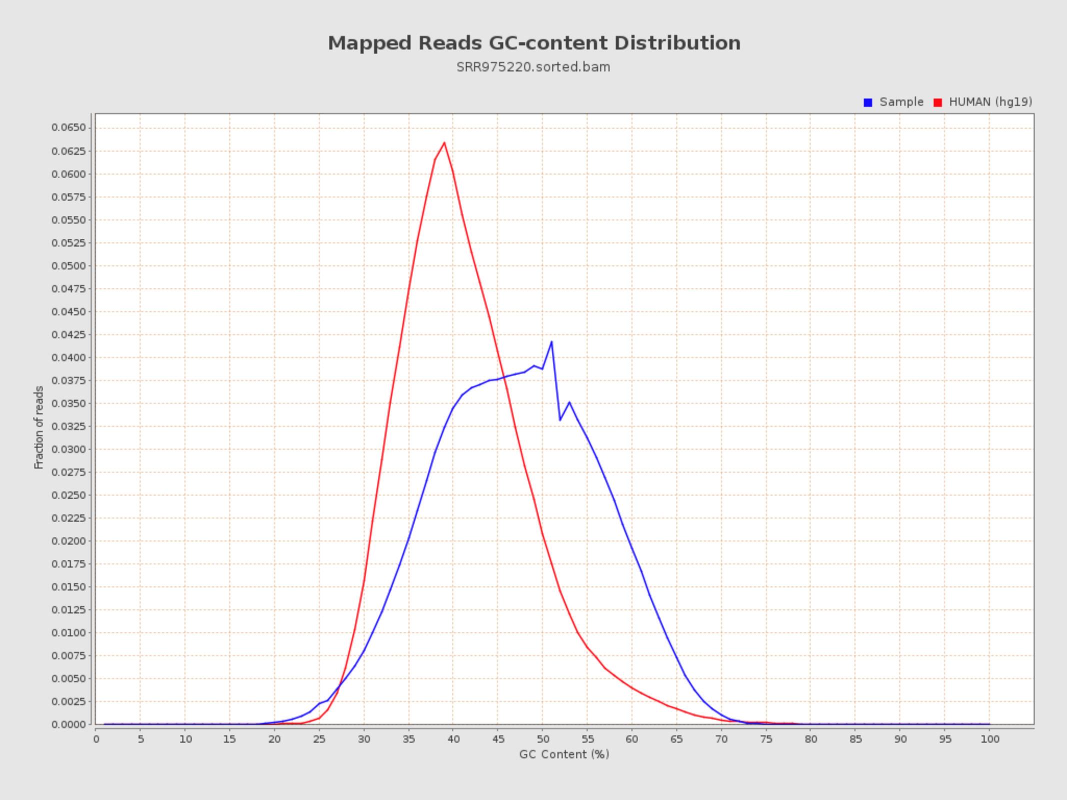
7. Results : Duplication Rate Histogram



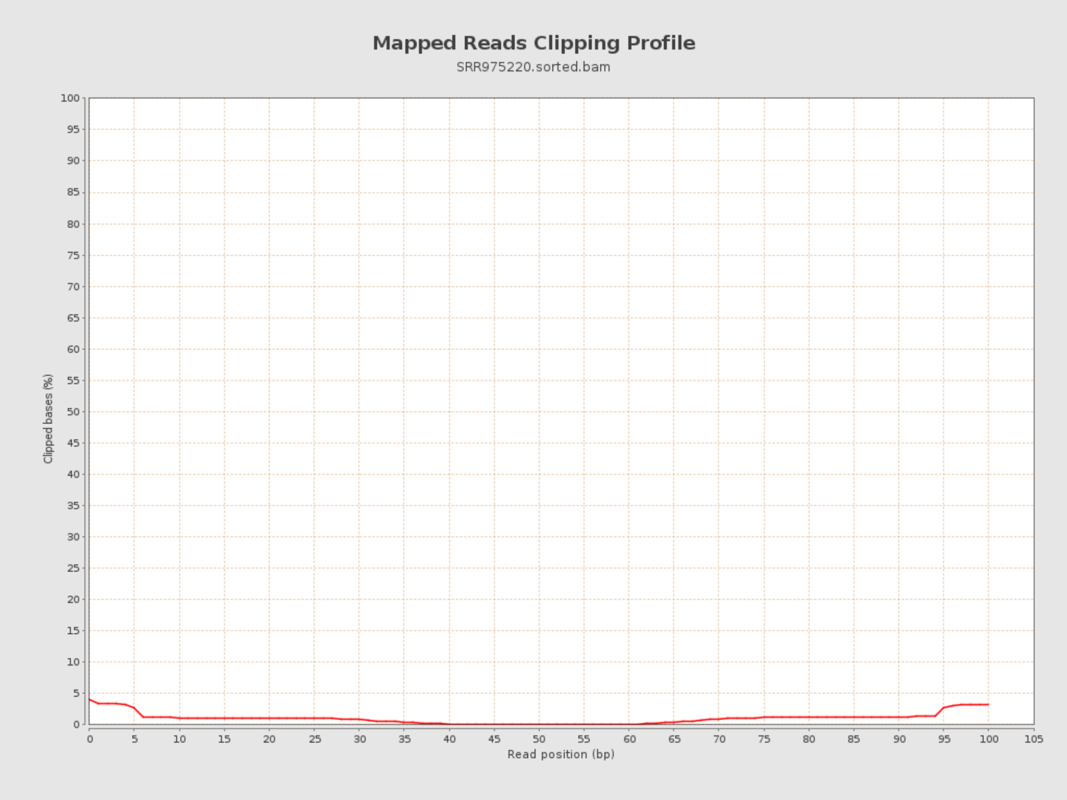
8. Results : Mapped Reads Nucleotide Content



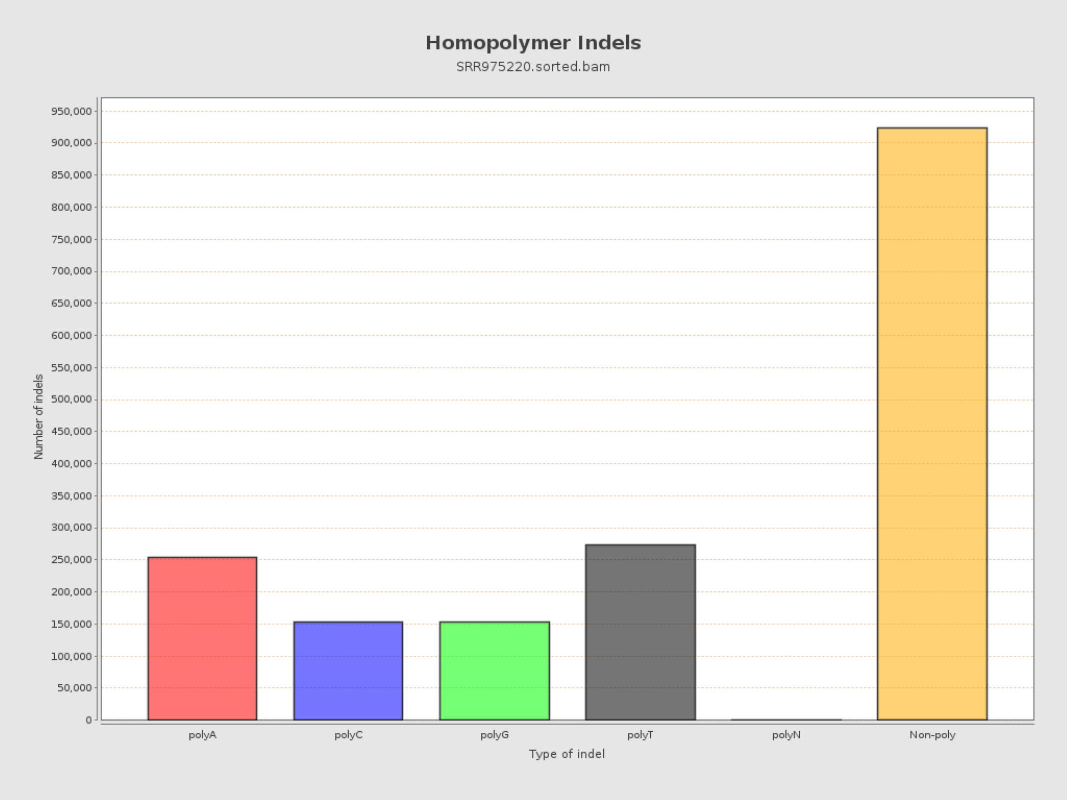
9. Results : Mapped Reads GC-content Distribution



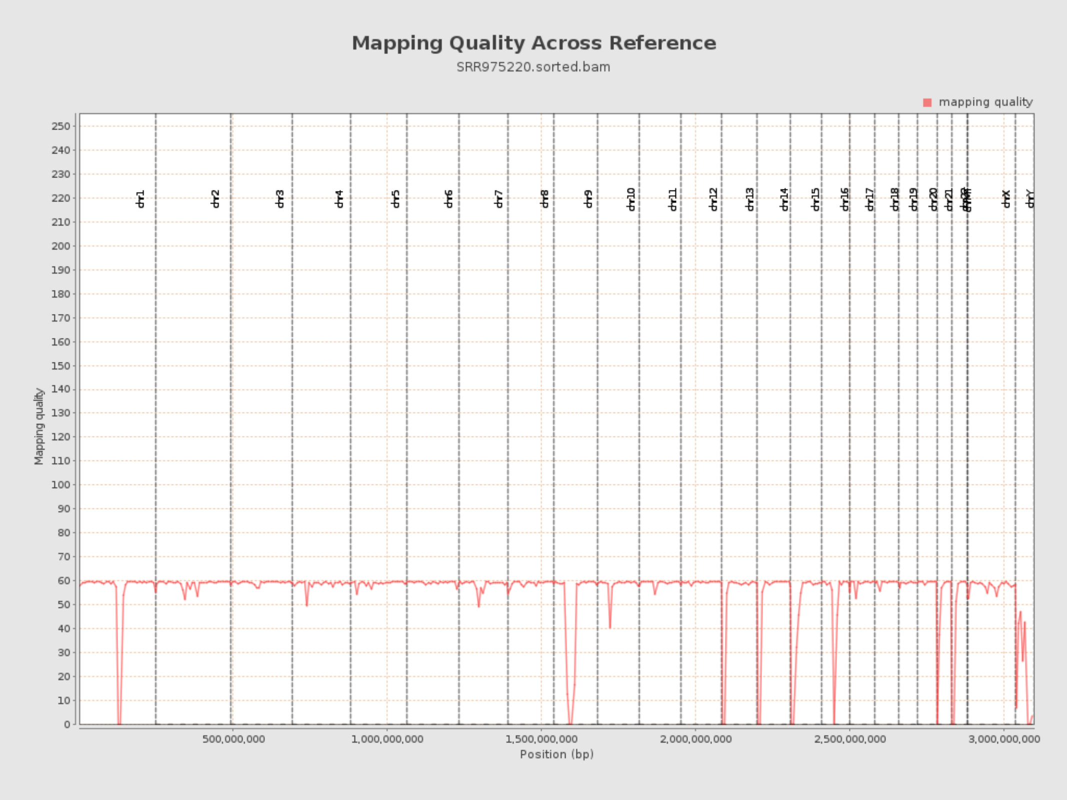
10. Results : Mapped Reads Clipping Profile



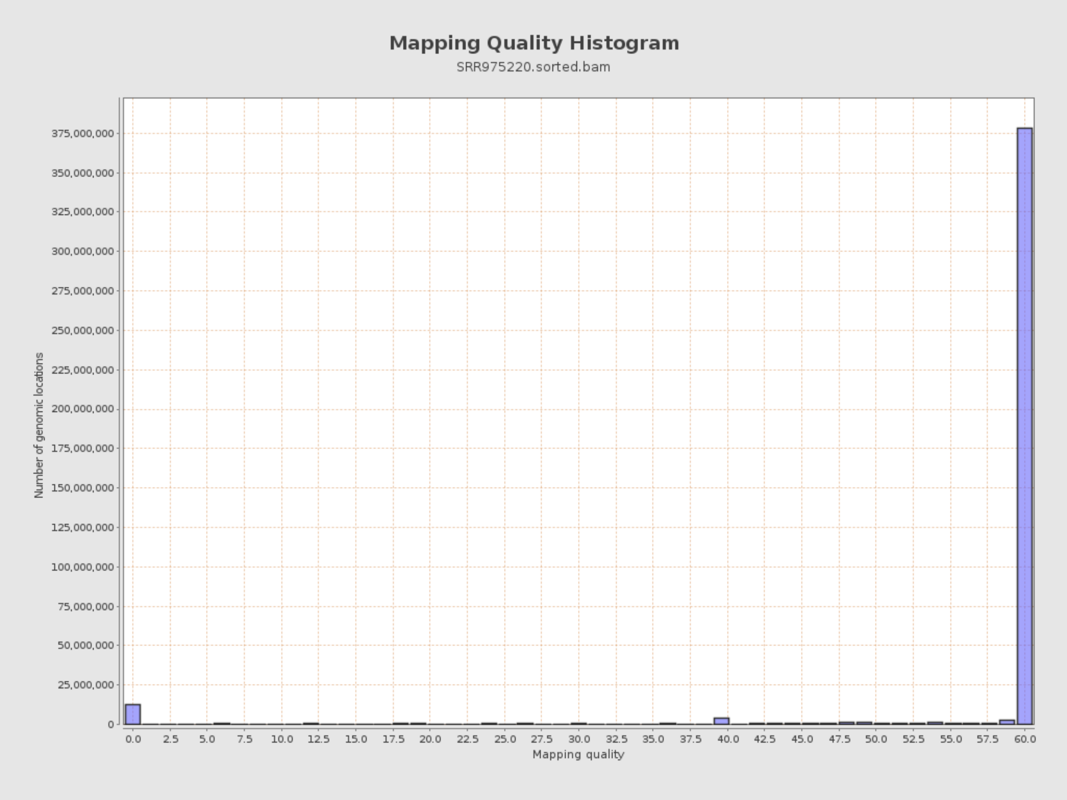
11. Results : Homopolymer Indels



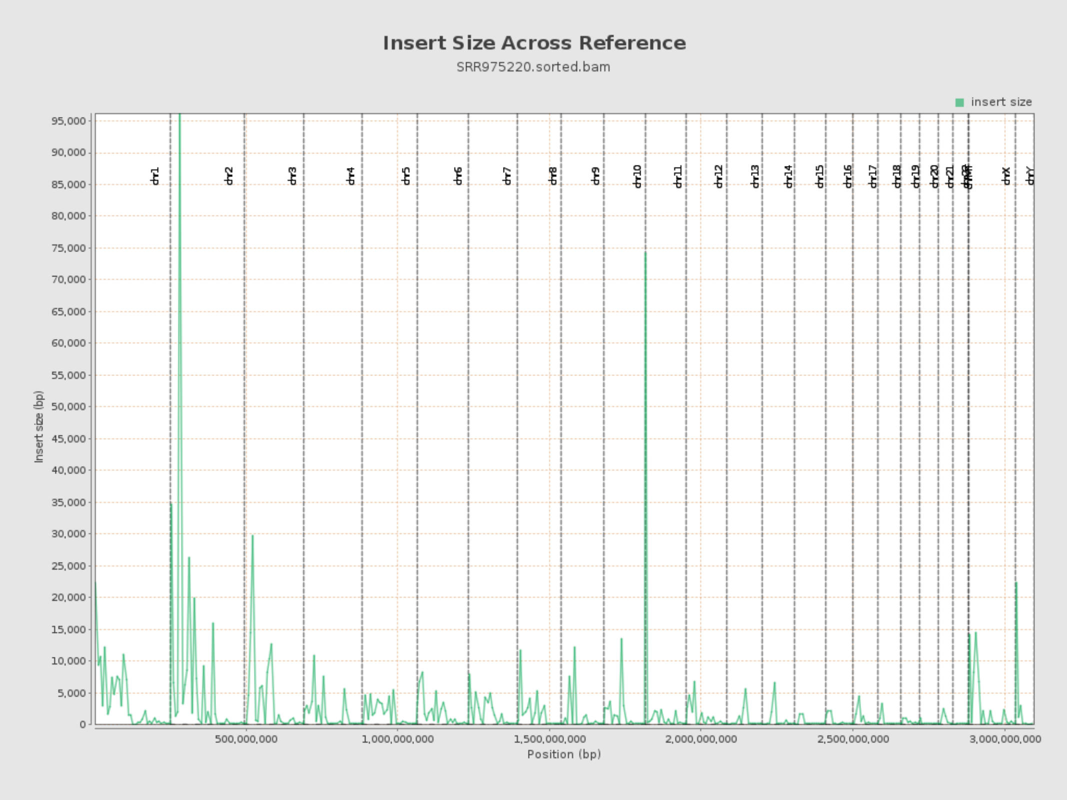
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram