Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 23:52:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975191.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_SRR975191 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975191_1.fastq.gz SRR975191_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 23:52:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975191.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,385,628
Mapped reads	4,345,310 / 99.08%
Unmapped reads	40,318 / 0.92%
Mapped paired reads	4,345,310 / 99.08%
Mapped reads, first in pair	2,181,715 / 49.75%
Mapped reads, second in pair	2,163,595 / 49.33%
Mapped reads, both in pair	4,323,892 / 98.59%
Mapped reads, singletons	21,418 / 0.49%
Secondary alignments	0
Supplementary alignments	61,179 / 1.39%
Read min/max/mean length	30 / 151 / 151.69
Duplicated reads (estimated)	534,730 / 12.19%
Duplication rate	10.31%
Clipped reads	1,640,085 / 37.4%

2.2. ACGT Content

Number/percentage of A's	182,641,087 / 29.53%
Number/percentage of C's	125,226,430 / 20.25%
Number/percentage of T's	181,085,778 / 29.28%
Number/percentage of G's	129,466,259 / 20.93%
Number/percentage of N's	57,078 / 0.01%

GC Percentage	41.18%

2.3. Coverage

Mean	0.1999
Standard Deviation	2.6588

2.4. Mapping Quality

Mean Mapping Quality	53.71

2.5. Insert size

Mean	128,148.76
Standard Deviation	3,509,750.29
P25/Median/P75	148 / 178 / 221

2.6. Mismatches and indels

General error rate	0.94%
Mismatches	5,518,923
Insertions	108,347
Mapped reads with at least one insertion	2.35%
Deletions	231,609
Mapped reads with at least one deletion	5.12%
Homopolymer indels	47.99%

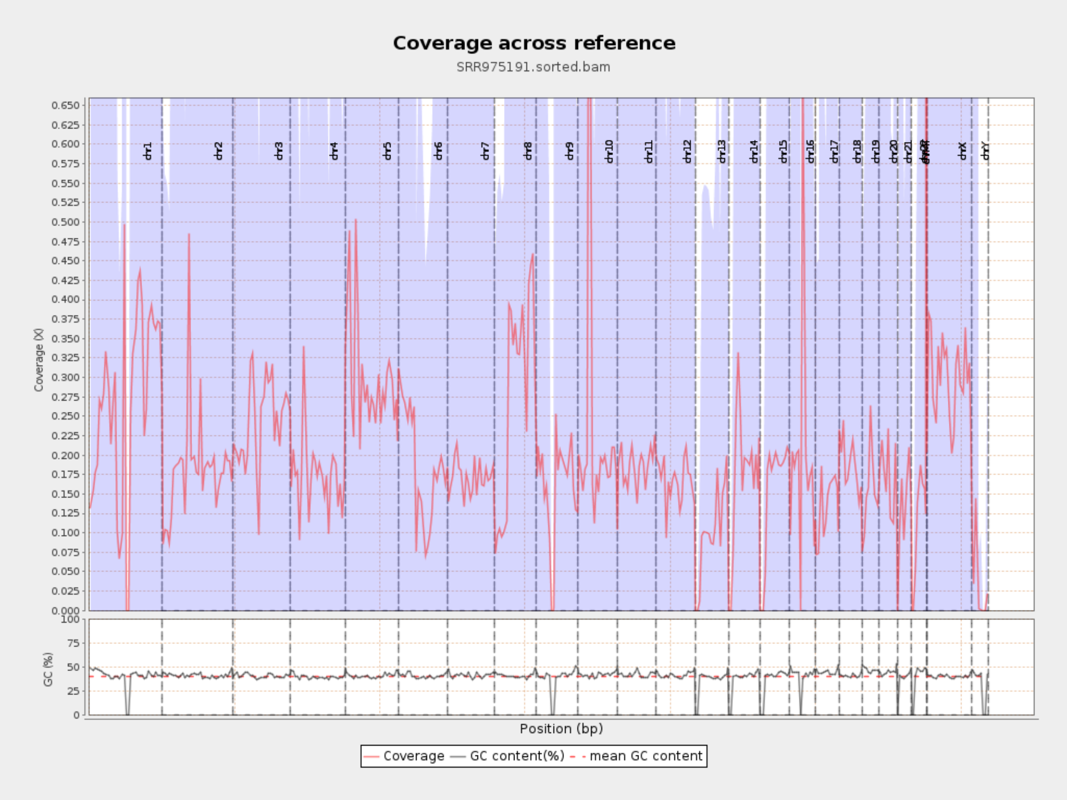
2.7. Chromosome stats

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

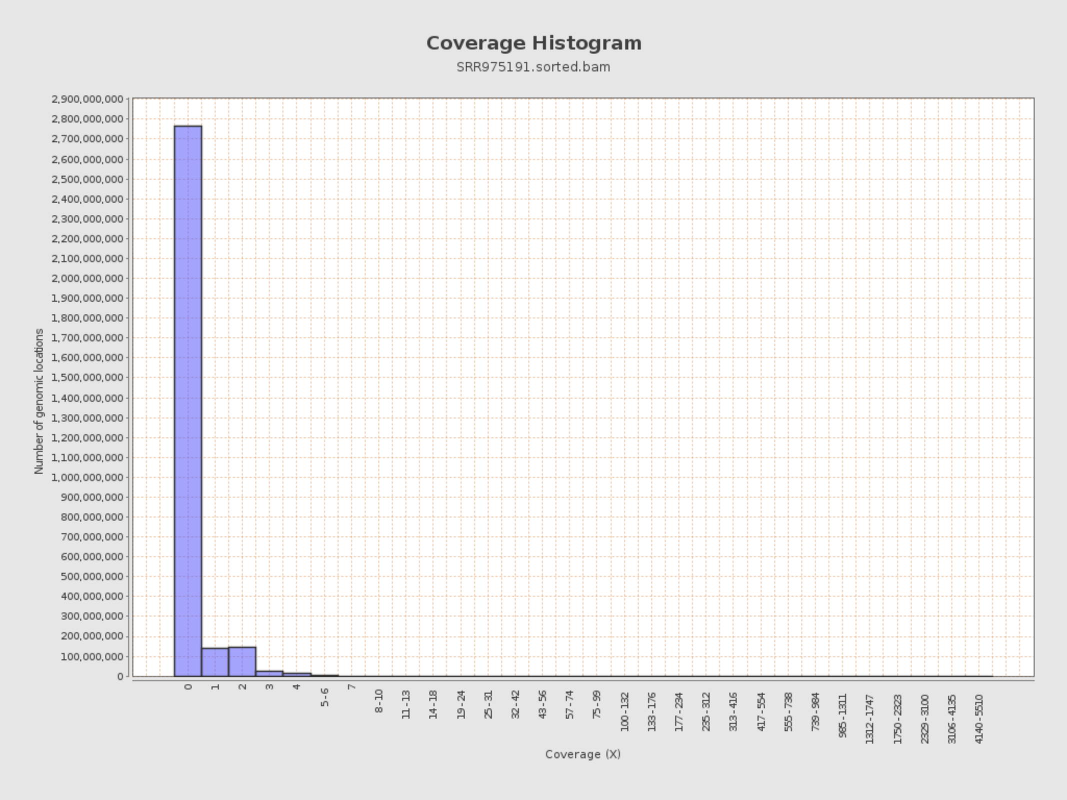
		bases	coverage	deviation
chr1	249250621	66740955	0.2678	3.3829
chr2	243199373	44400756	0.1826	2.287
chr3	198022430	48253633	0.2437	0.7974
chr4	191154276	32942119	0.1723	1.4871
chr5	180915260	54149705	0.2993	0.8119
chr6	171115067	31622745	0.1848	1.1053
chr7	159138663	27414500	0.1723	1.0748
chr8	146364022	40856770	0.2791	1.1539
chr9	141213431	22753983	0.1611	2.7196
chr10	135534747	31512476	0.2325	9.5827
chr11	135006516	24874047	0.1842	1.6286
chr12	133851895	22308237	0.1667	0.5791
chr13	115169878	11637805	0.101	0.4463
chr14	107349540	18540365	0.1727	0.6242
chr15	102531392	15871650	0.1548	0.5591
chr16	90354753	18269796	0.2022	3.4376
chr17	81195210	10868002	0.1339	1.5736
chr18	78077248	14729046	0.1886	2.474
chr19	59128983	9358271	0.1583	1.7086
chr20	63025520	11036069	0.1751	0.7713
chr21	48129895	6459158	0.1342	0.9066
chr22	51304566	5653753	0.1102	0.4917
chrMT	16571	79541	4.8	3.7694
chrX	155270560	46652172	0.3005	1.1392

chrY	59373566	1945162	0.0328	2.216

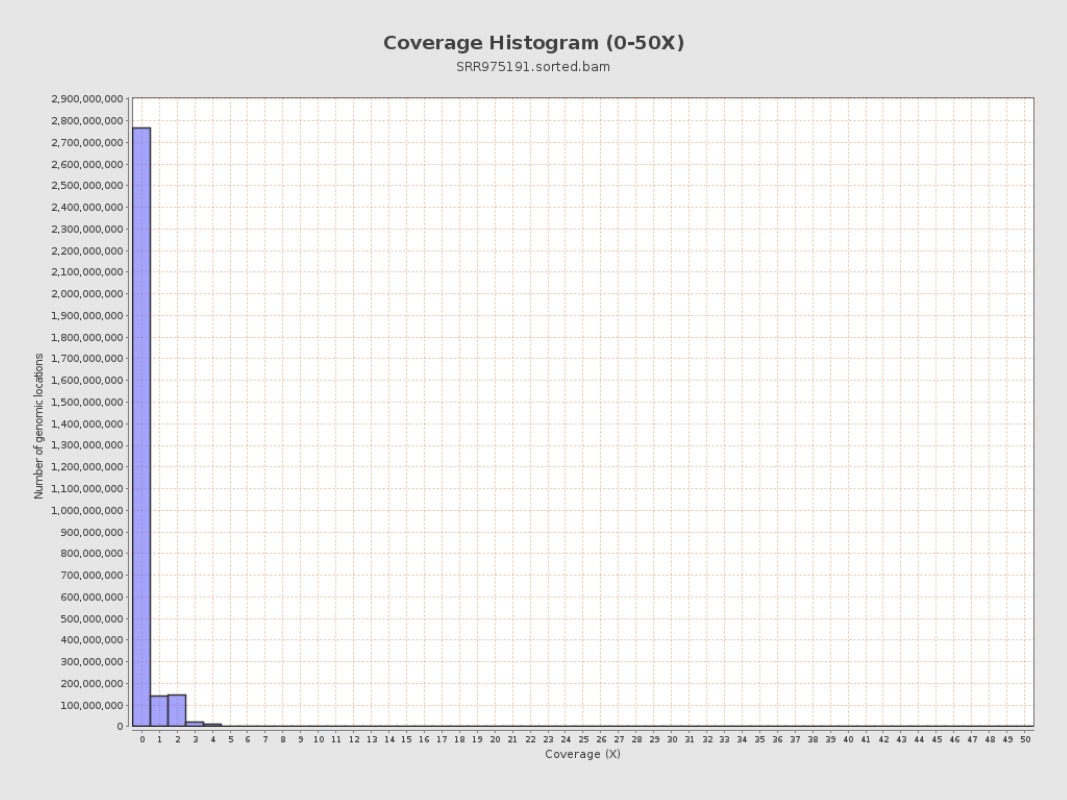
3. Results : Coverage across reference



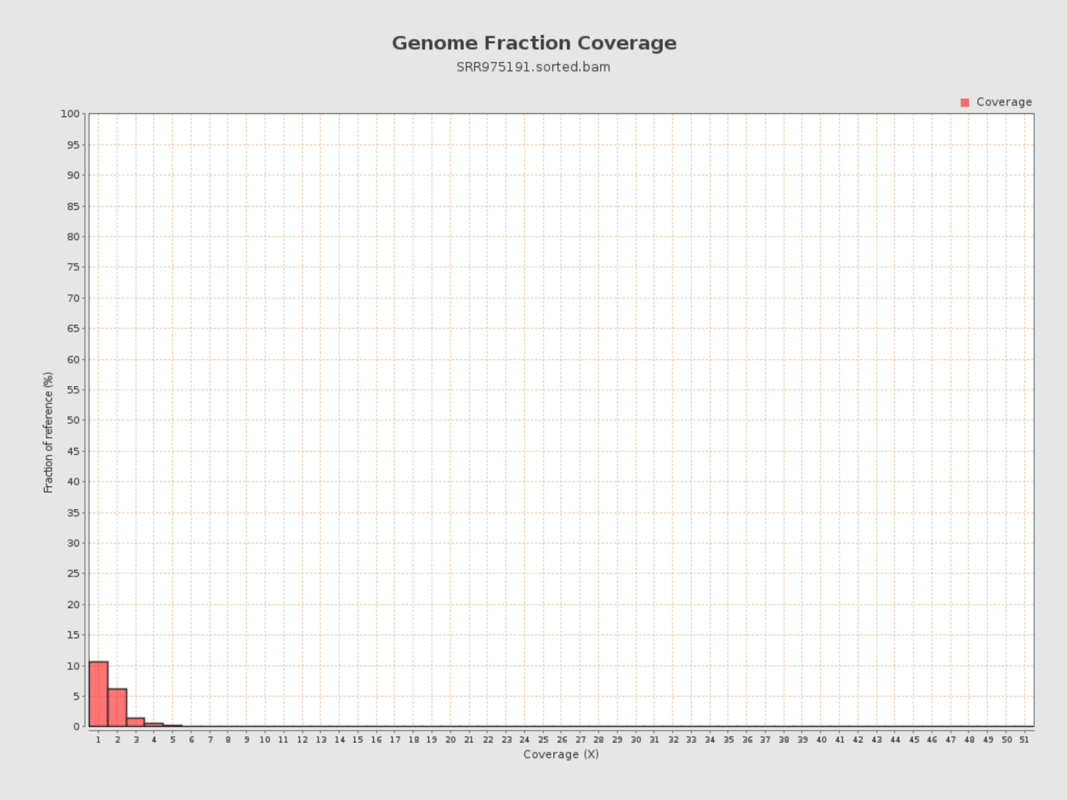
4. Results : Coverage Histogram



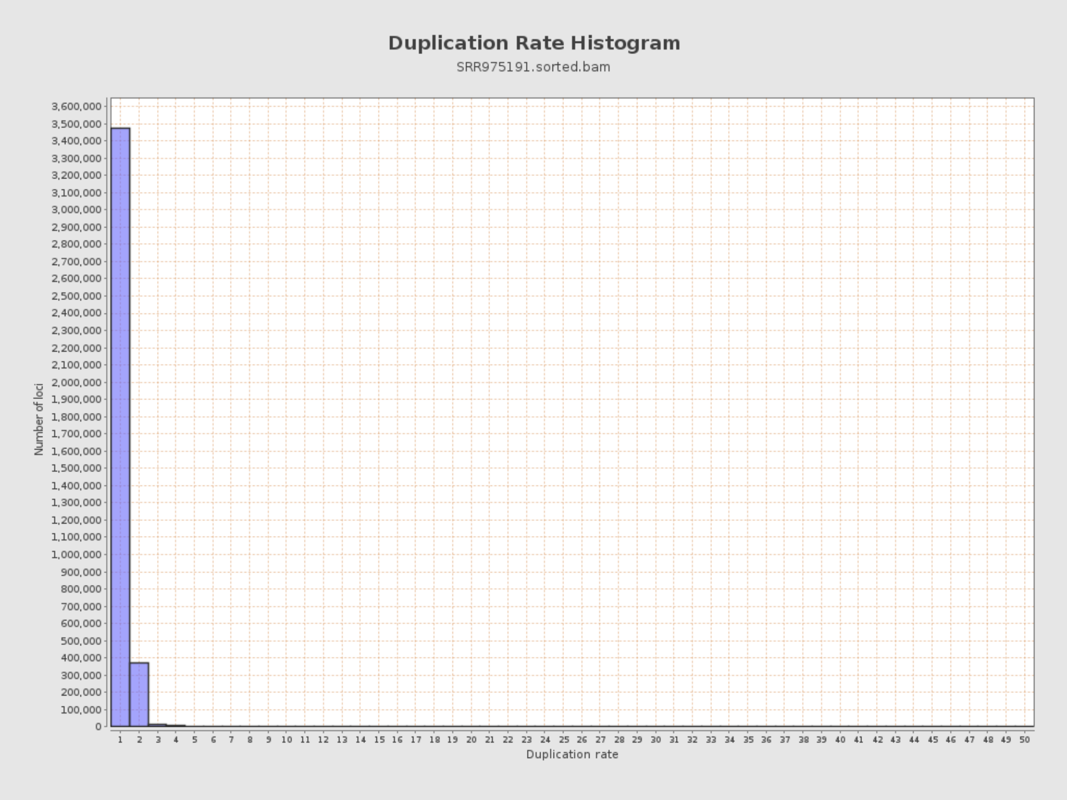
5. Results : Coverage Histogram (0-50X)



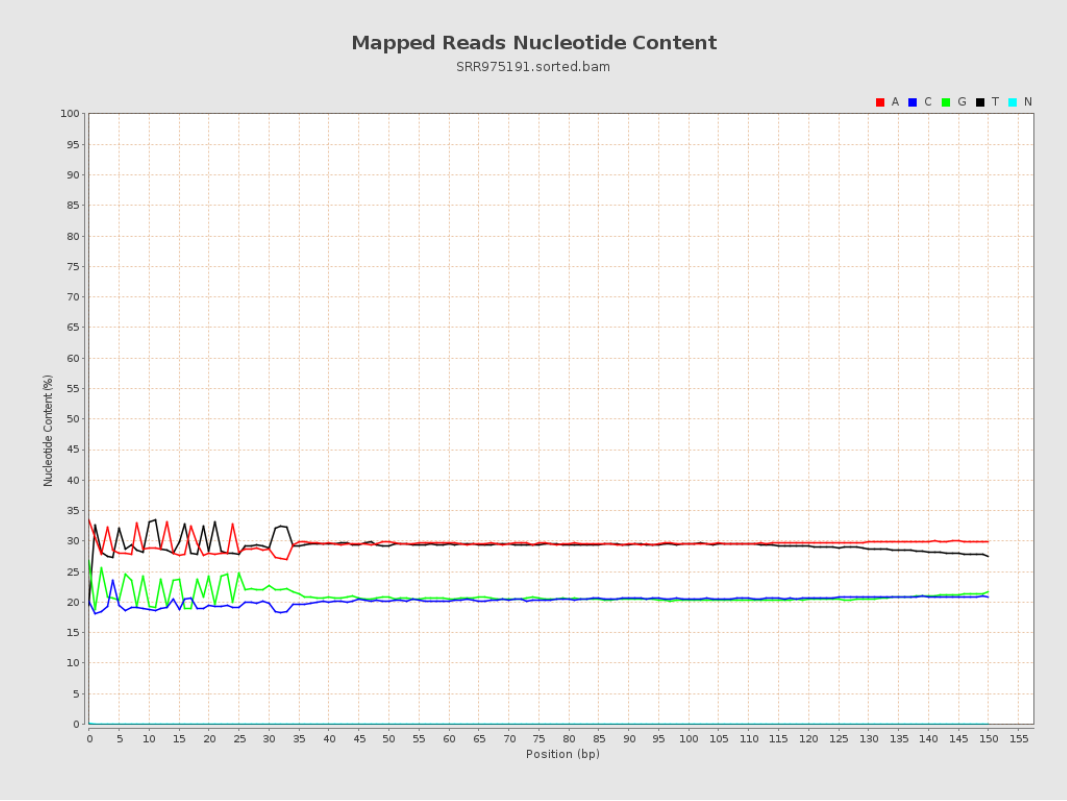
6. Results : Genome Fraction Coverage



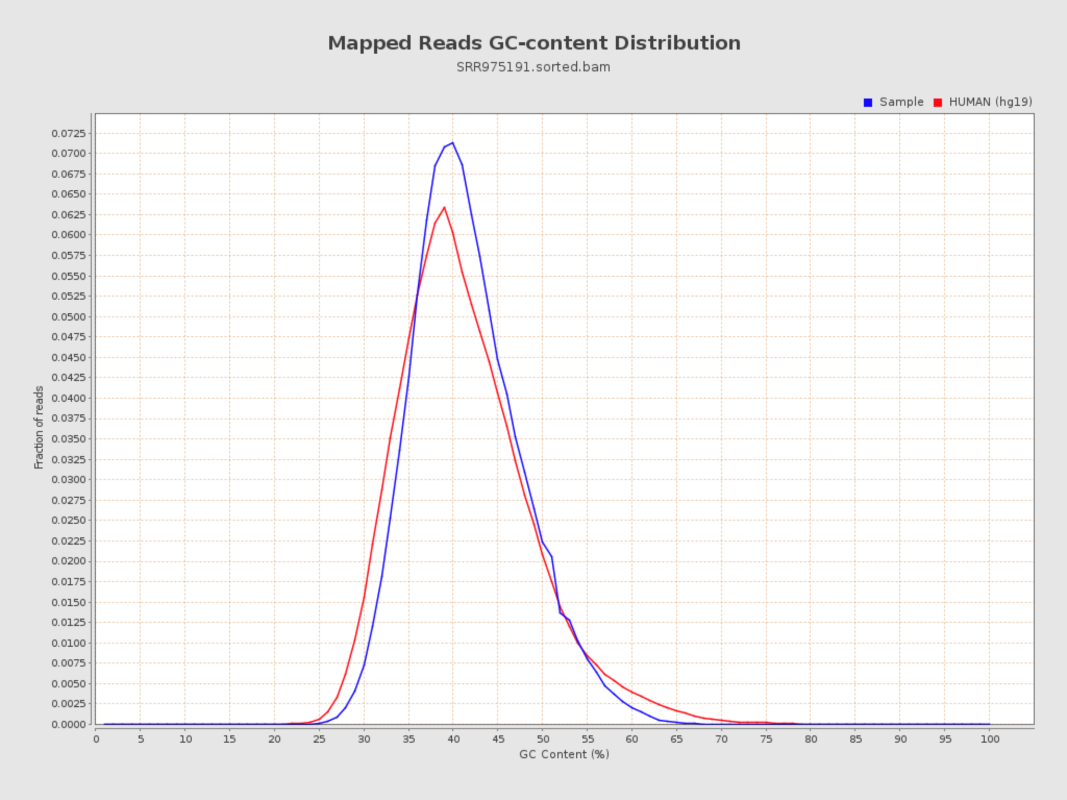
7. Results : Duplication Rate Histogram



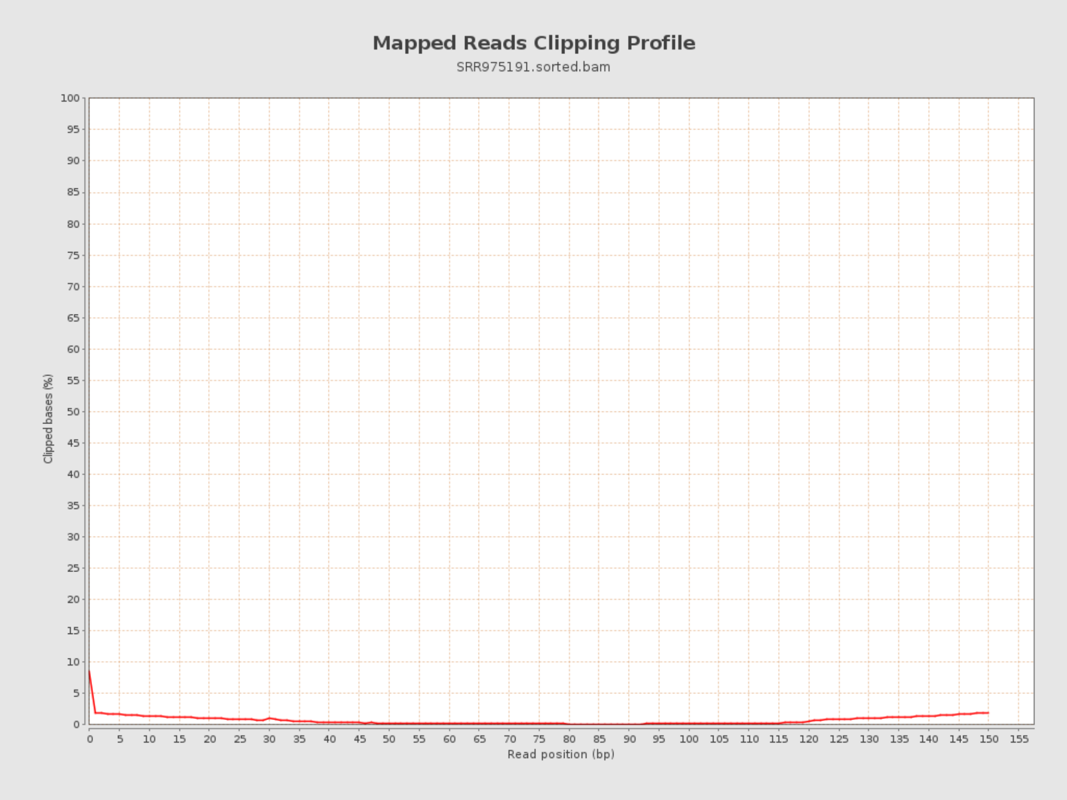
8. Results : Mapped Reads Nucleotide Content



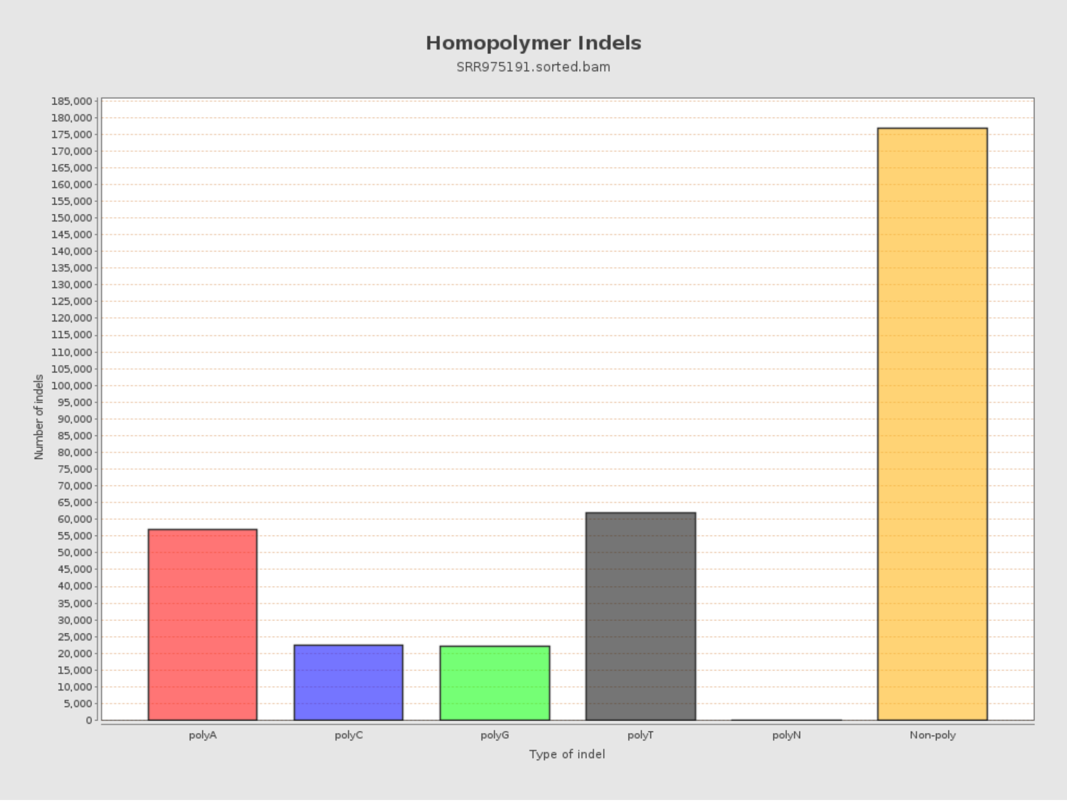
9. Results : Mapped Reads GC-content Distribution



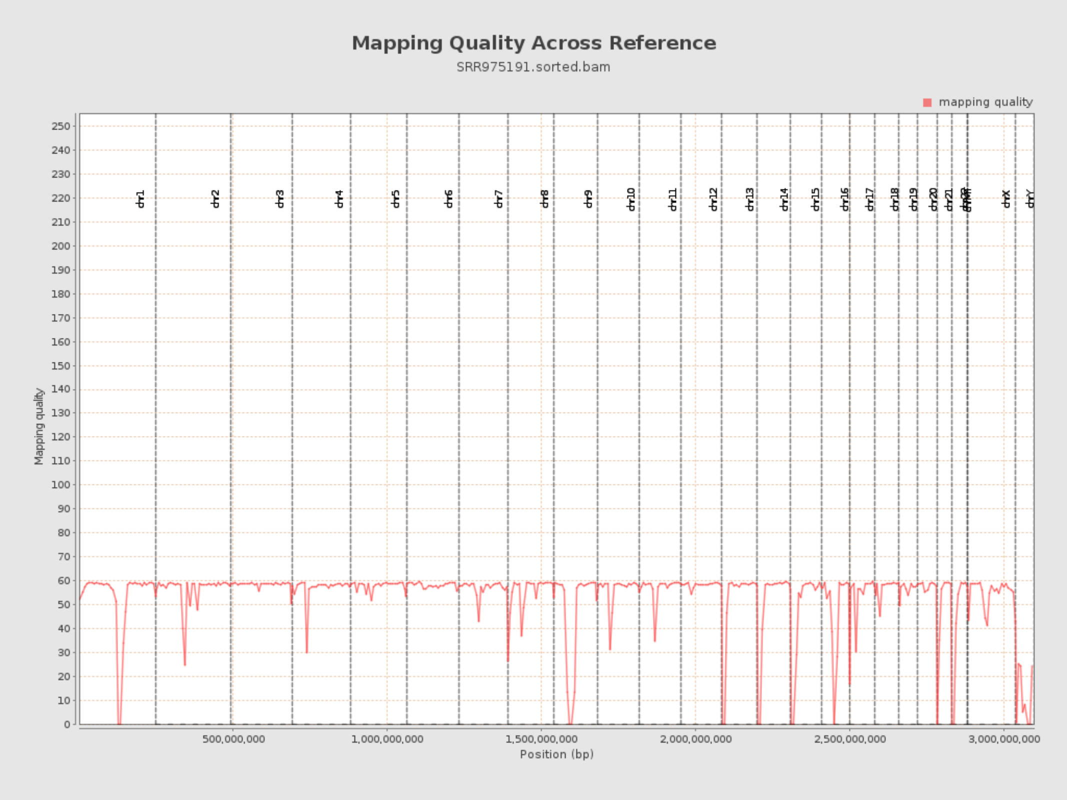
10. Results : Mapped Reads Clipping Profile



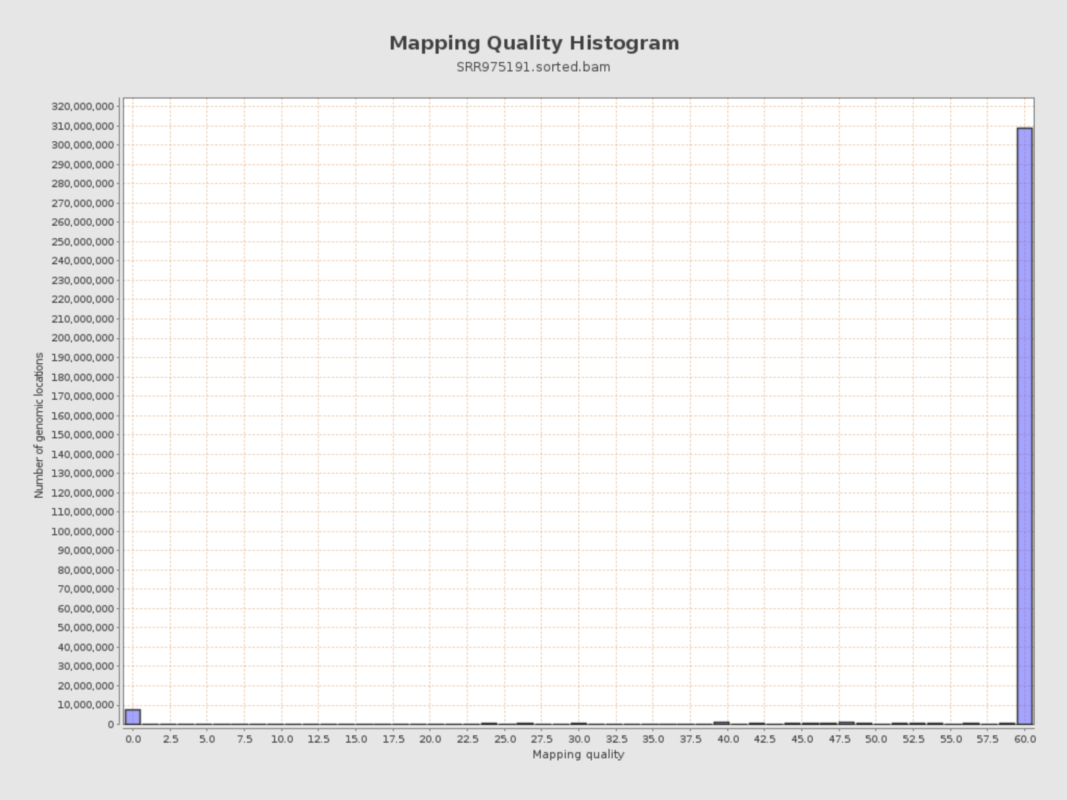
11. Results : Homopolymer Indels



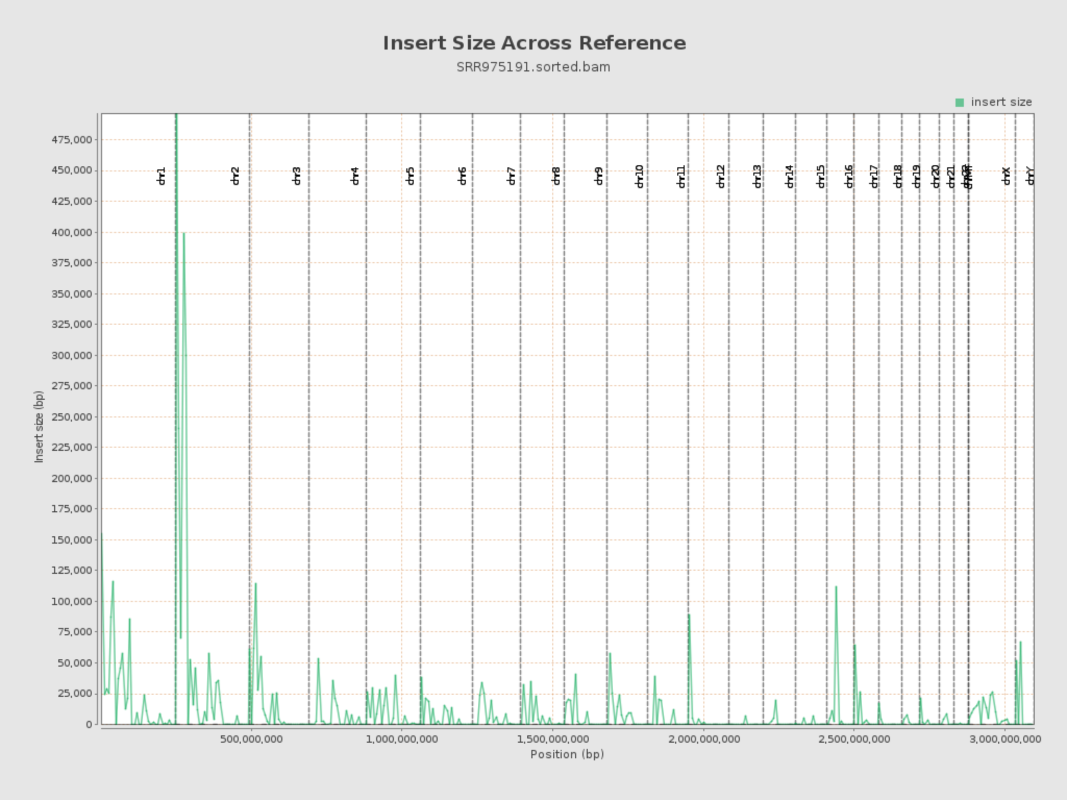
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram