Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/04 15:19:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960891.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_SRR960891 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960891_1.fastq.gz SRR960891_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 04 15:19:39 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960891.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	222,129,622
Mapped reads	218,676,956 / 98.45%
Unmapped reads	3,452,666 / 1.55%
Mapped paired reads	218,676,956 / 98.45%
Mapped reads, first in pair	109,612,832 / 49.35%
Mapped reads, second in pair	109,064,124 / 49.1%
Mapped reads, both in pair	217,421,790 / 97.88%
Mapped reads, singletons	1,255,166 / 0.57%
Secondary alignments	0
Supplementary alignments	387,977 / 0.17%
Read min/max/mean length	30 / 101 / 101.07
Duplicated reads (estimated)	31,347,880 / 14.11%
Duplication rate	9.64%
Clipped reads	29,647,101 / 13.35%

2.2. ACGT Content

Number/percentage of A's	6,573,687,099 / 30.56%
Number/percentage of C's	4,189,259,793 / 19.47%
Number/percentage of T's	6,561,835,702 / 30.5%
Number/percentage of G's	4,185,691,904 / 19.46%
Number/percentage of N's	2,592,947 / 0.01%

GC Percentage	38.93%

2.3. Coverage

Mean	6.9514
Standard Deviation	94.457

2.4. Mapping Quality

Mean Mapping Quality	53.64

2.5. Insert size

Mean	15,544.7
Standard Deviation	1,174,558.54
P25/Median/P75	136 / 163 / 192

2.6. Mismatches and indels

General error rate	1.21%
Mismatches	254,761,836
Insertions	2,545,616
Mapped reads with at least one insertion	1.13%
Deletions	2,708,058
Mapped reads with at least one deletion	1.2%
Homopolymer indels	40.91%

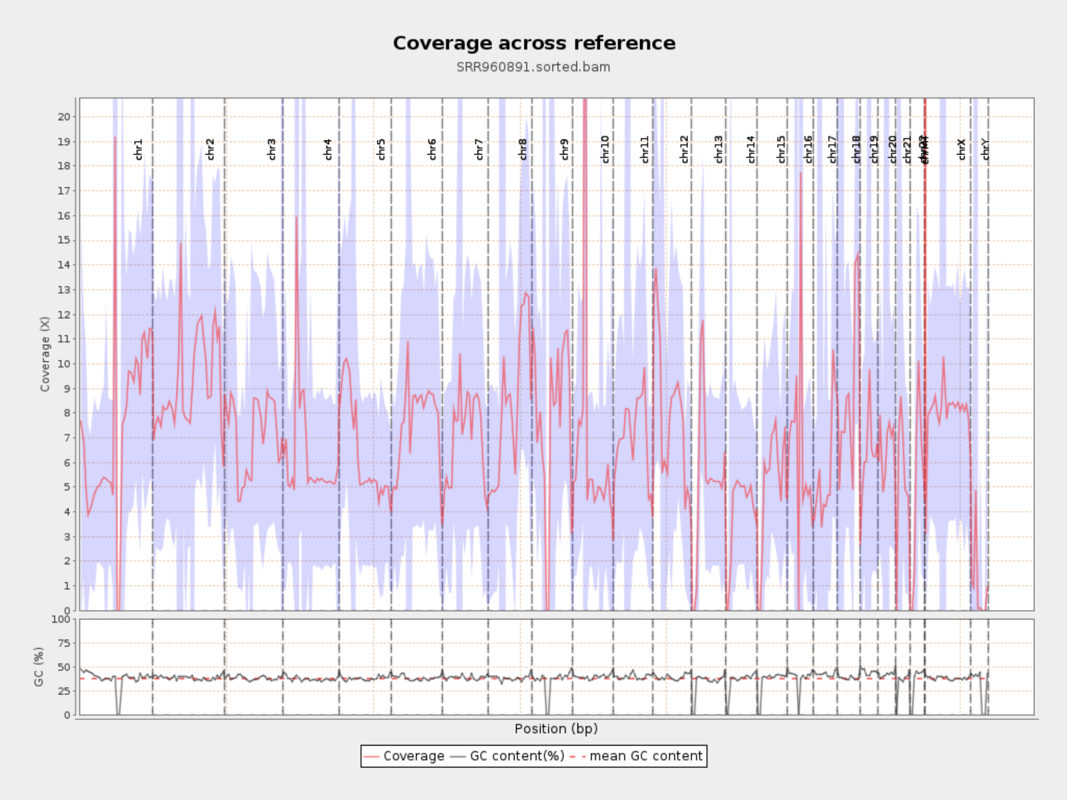
2.7. Chromosome stats

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

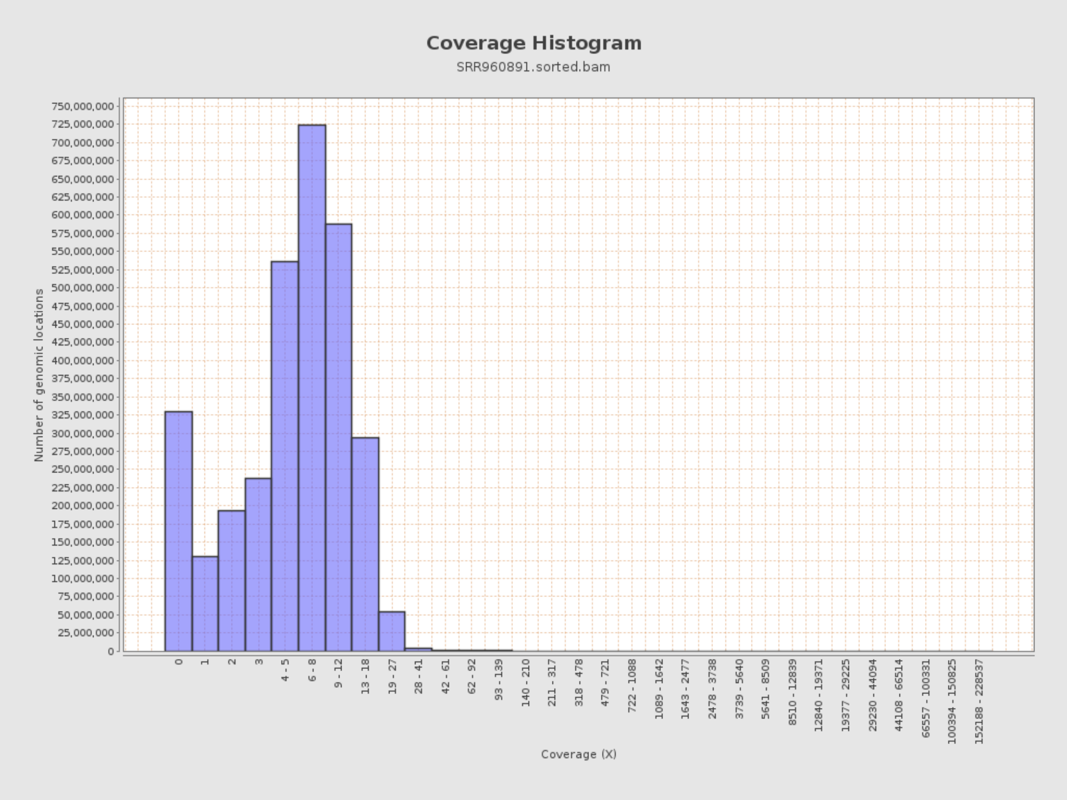
		bases	coverage	deviation
chr1	249250621	1823632632	7.3165	234.7084
chr2	243199373	2261301163	9.2981	50.6924
chr3	198022430	1413739224	7.1393	14.1466
chr4	191154276	1199707553	6.2761	77.0023
chr5	180915260	1162708039	6.4268	8.1443
chr6	171115067	1317878614	7.7017	27.5512
chr7	159138663	1115229930	7.0079	59.0081
chr8	146364022	1229897058	8.403	95.6439
chr9	141213431	1089531712	7.7155	77.2361
chr10	135534747	956723482	7.0589	222.631
chr11	135006516	954100977	7.0671	36.6521
chr12	133851895	1087359471	8.1236	7.8774
chr13	115169878	604589993	5.2495	4.6972
chr14	107349540	427611005	3.9834	6.7977
chr15	102531392	525471528	5.125	4.6043
chr16	90354753	583595371	6.4589	85.6398
chr17	81195210	459544876	5.6598	24.472
chr18	78077248	679449905	8.7023	80.5591
chr19	59128983	374665789	6.3364	102.7823
chr20	63025520	416730682	6.6121	22.5077
chr21	48129895	269201414	5.5932	30.9957
chr22	51304566	247565965	4.8254	6.158
chrMT	16571	8498108	512.8301	109.5576
chrX	155270560	1250605409	8.0544	25.7066

chrY	59373566	60034804	1.0111	66.2234

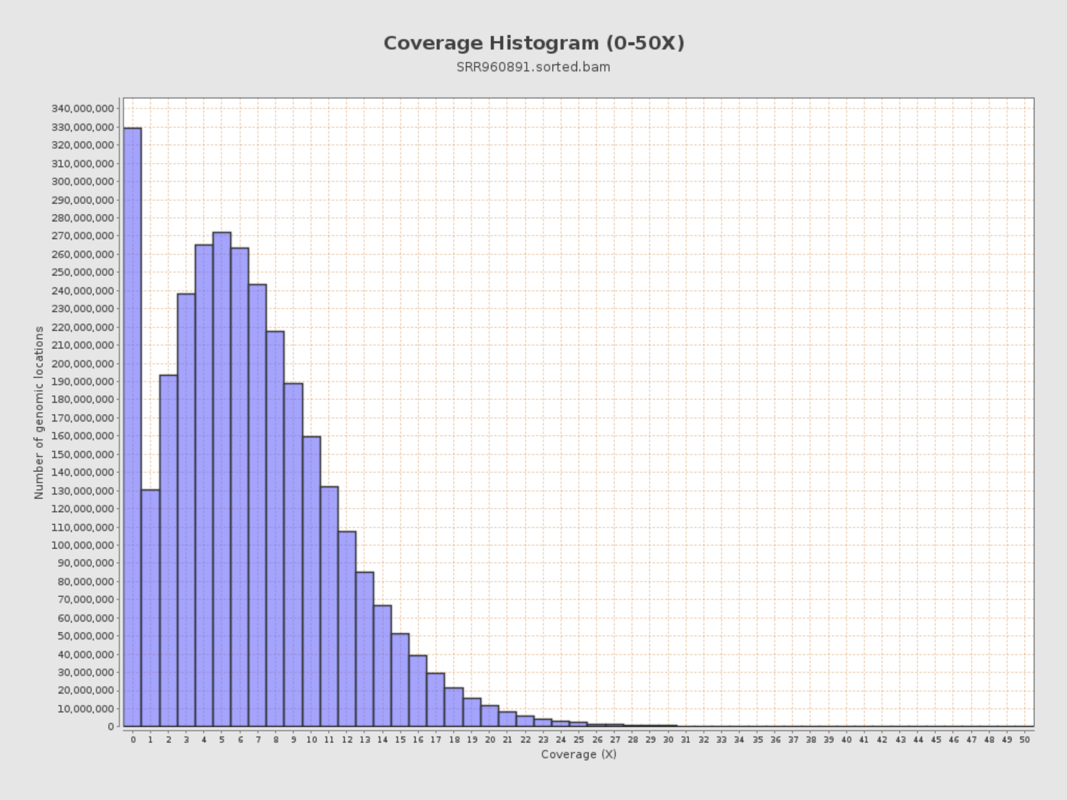
3. Results : Coverage across reference



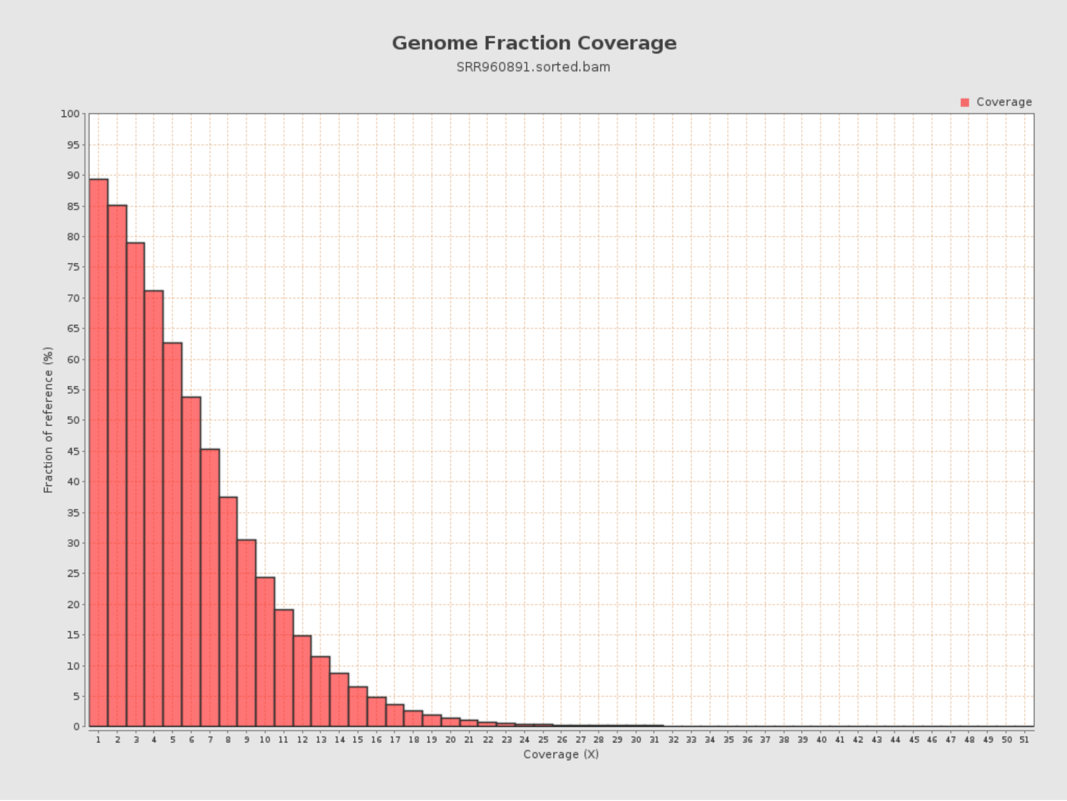
4. Results : Coverage Histogram



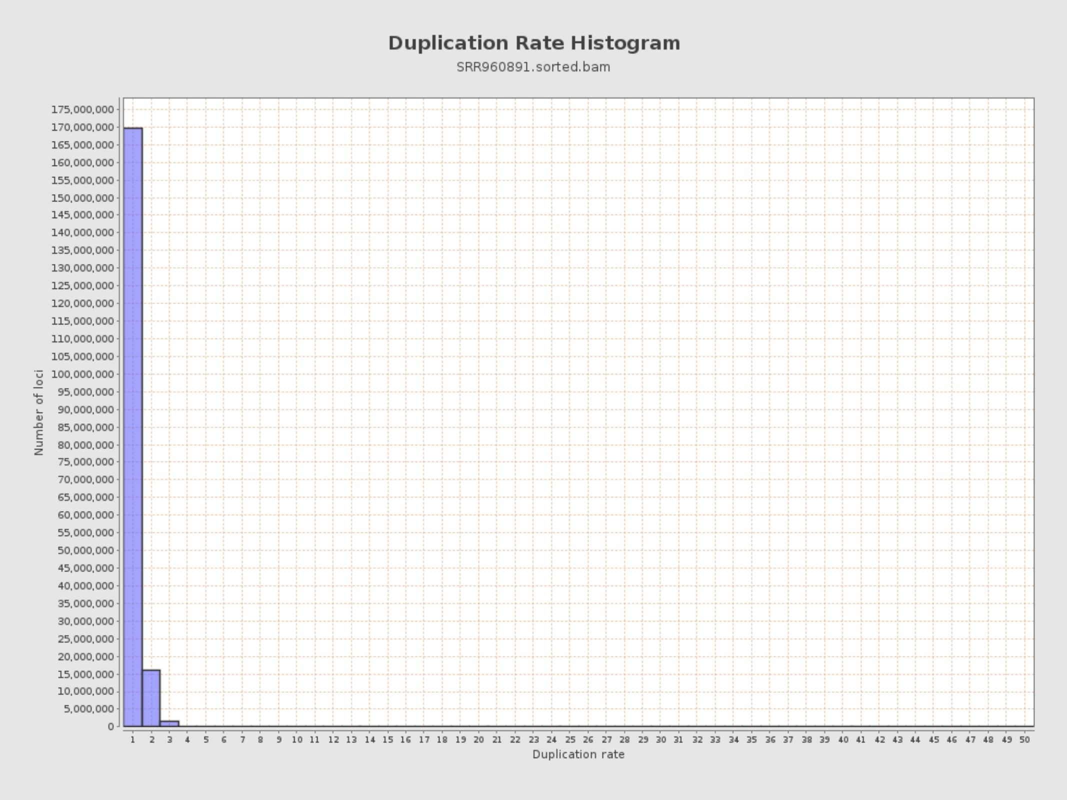
5. Results : Coverage Histogram (0-50X)



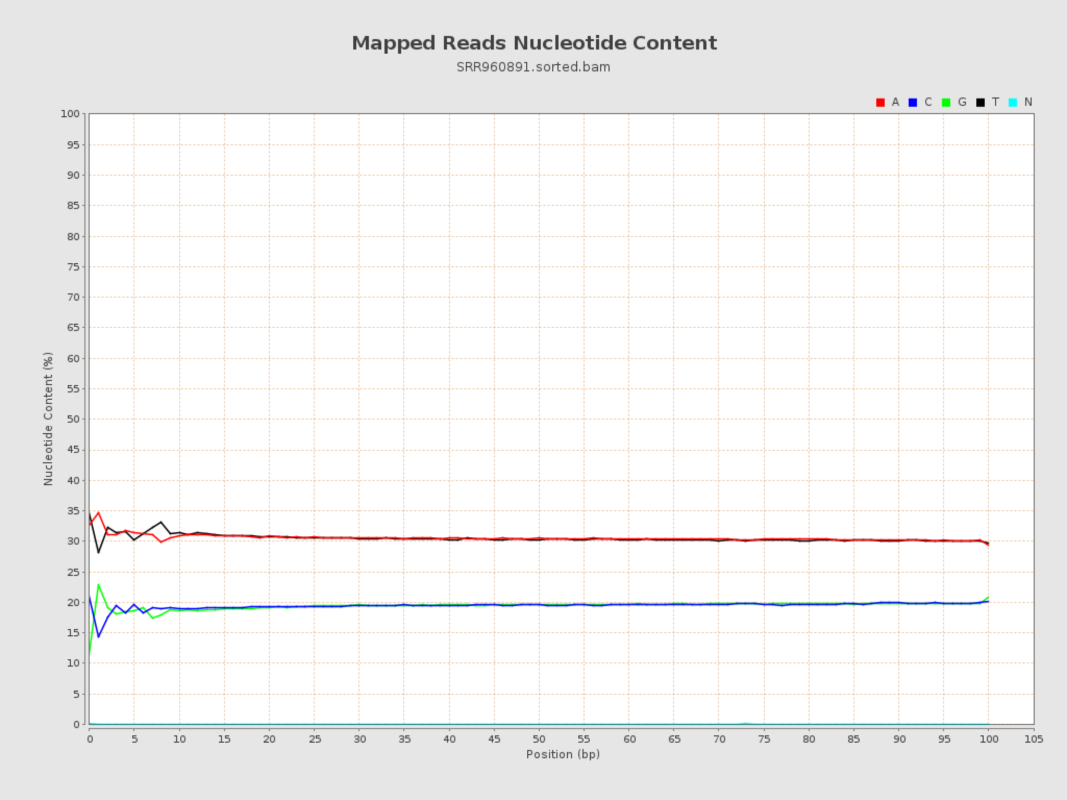
6. Results : Genome Fraction Coverage



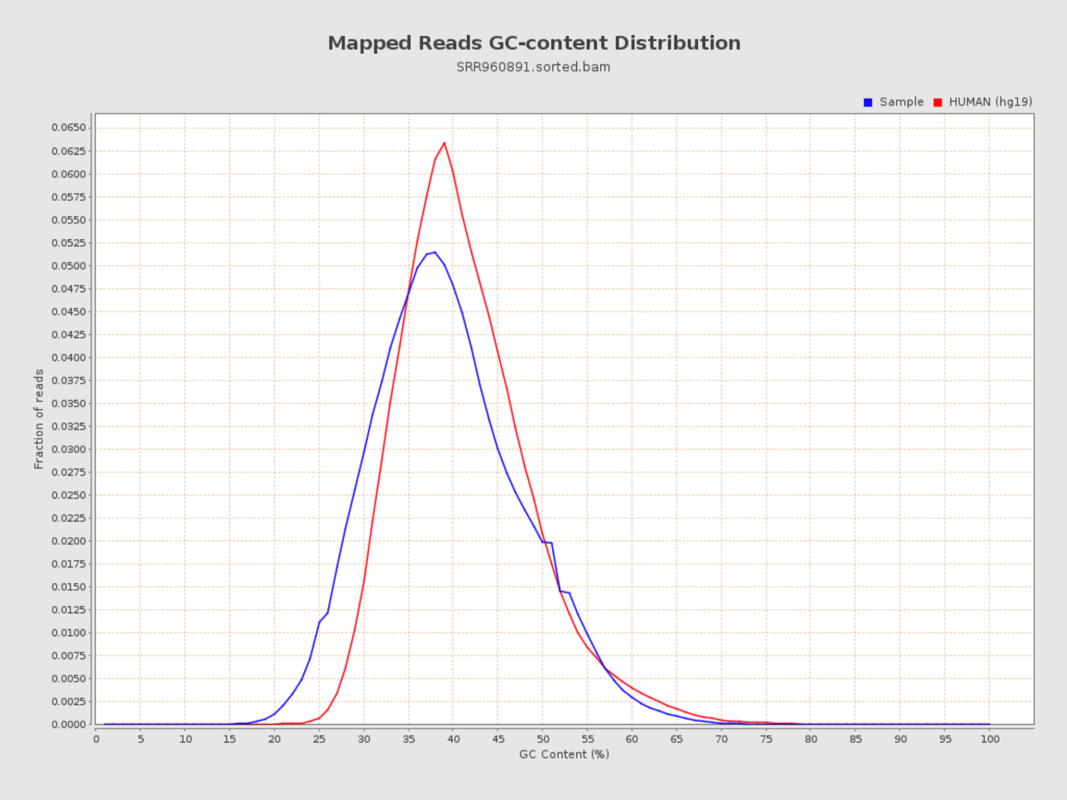
7. Results : Duplication Rate Histogram



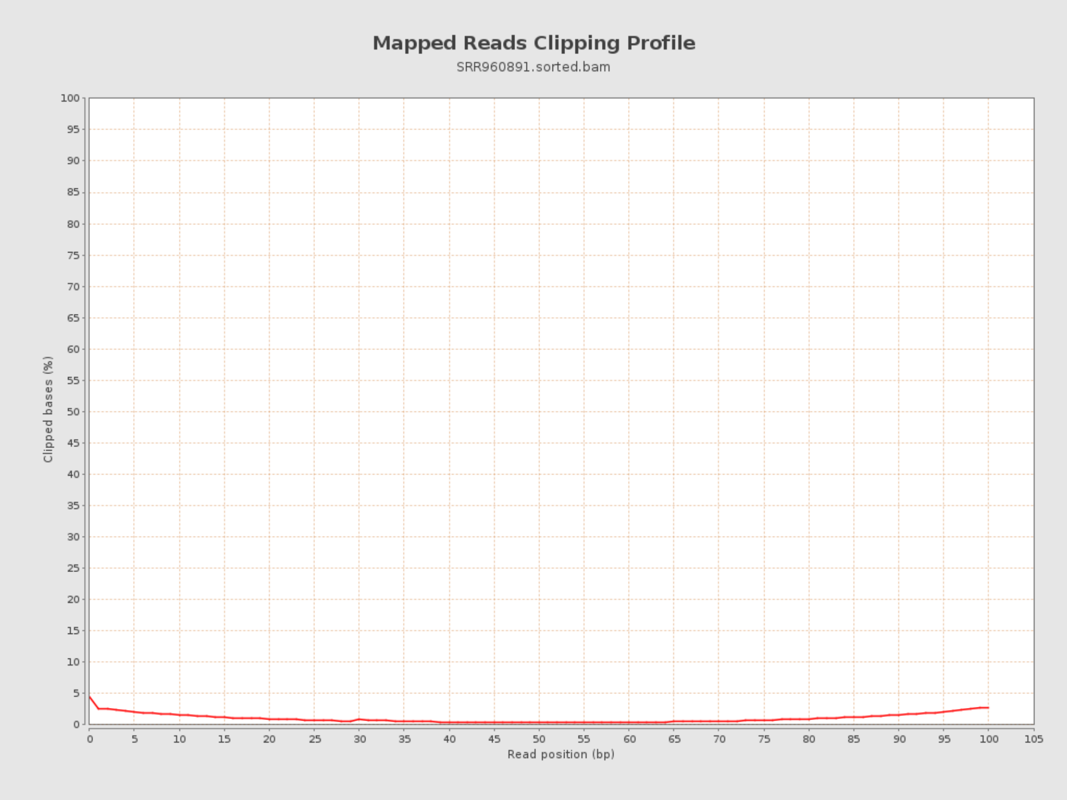
8. Results : Mapped Reads Nucleotide Content



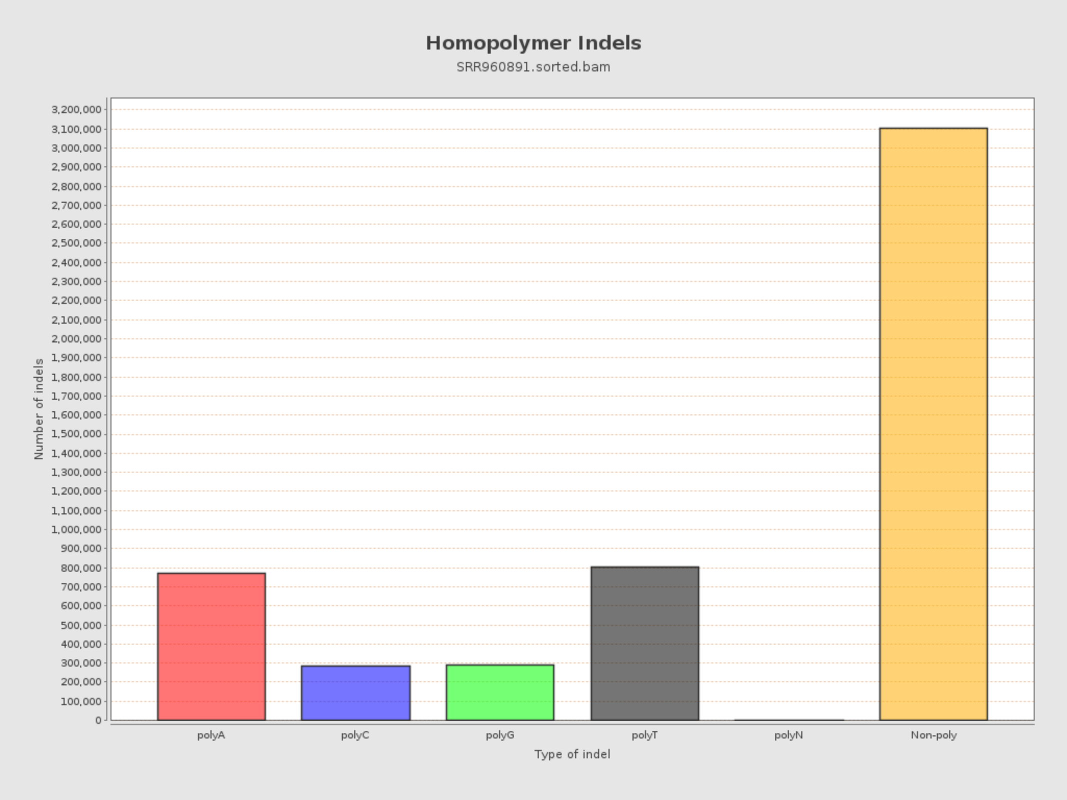
9. Results : Mapped Reads GC-content Distribution



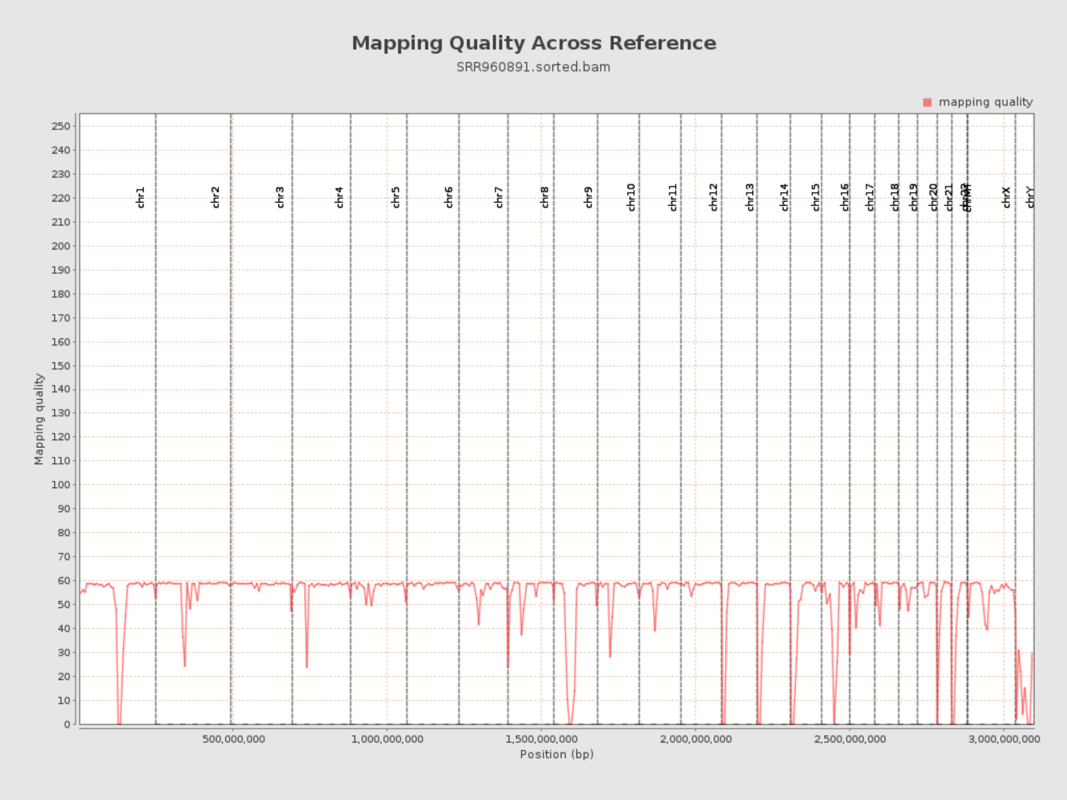
10. Results : Mapped Reads Clipping Profile



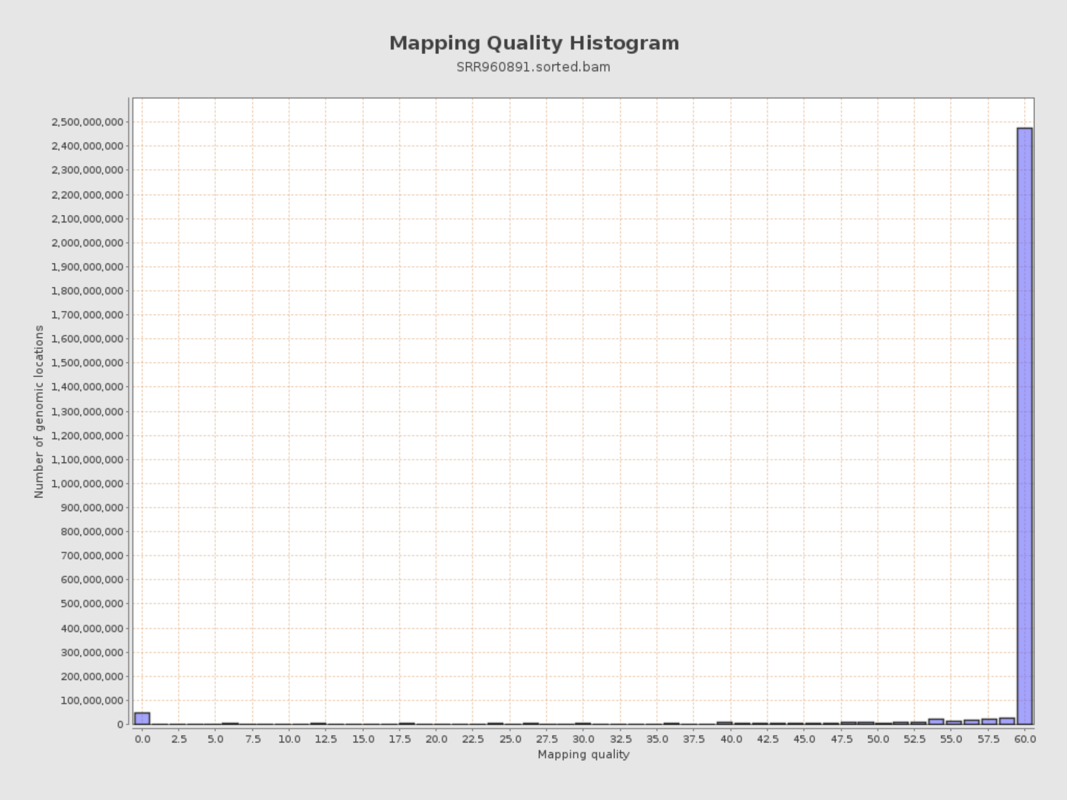
11. Results : Homopolymer Indels



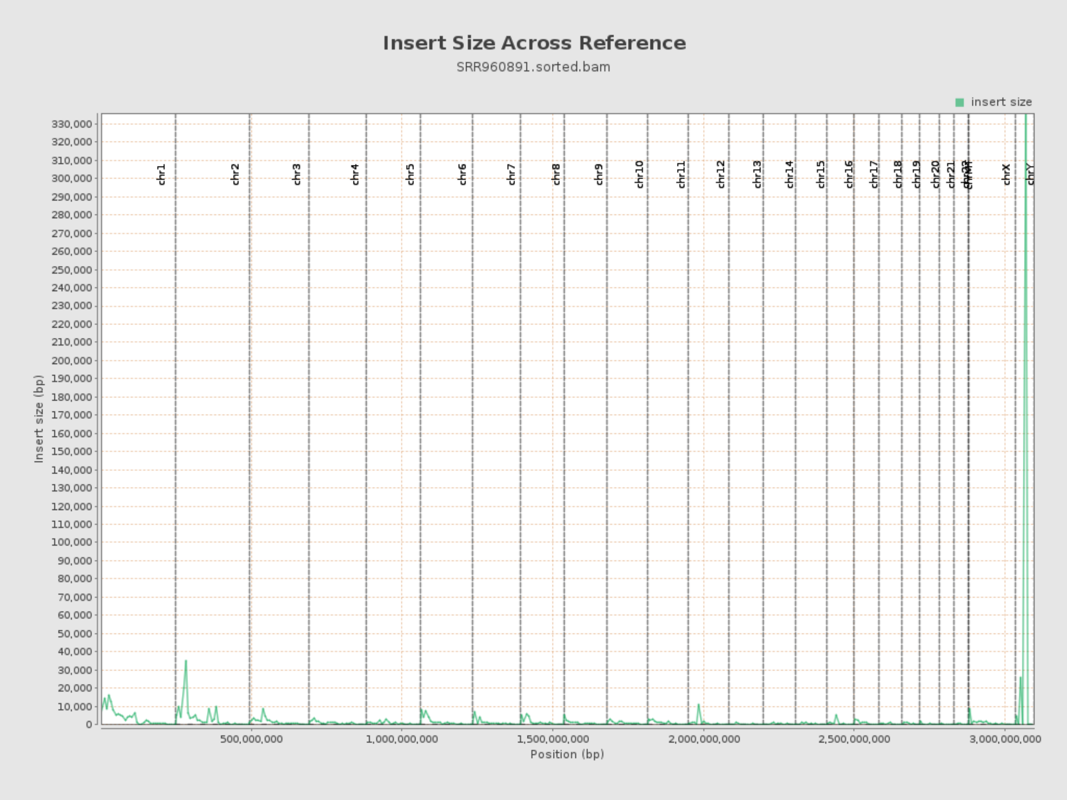
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram