Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 17:13:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716891.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_SRR9716891 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716891.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 17:13:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716891.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,345,528
Mapped reads	1,991,650 / 84.91%
Unmapped reads	353,878 / 15.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	45,129 / 1.92%
Read min/max/mean length	30 / 101 / 101.69
Duplicated reads (estimated)	65,299 / 2.78%
Duplication rate	2.28%
Clipped reads	2,033,434 / 86.69%

2.2. ACGT Content

Number/percentage of A's	39,007,244 / 26.3%
Number/percentage of C's	30,320,782 / 20.44%
Number/percentage of T's	43,375,146 / 29.24%
Number/percentage of G's	35,613,698 / 24.01%
Number/percentage of N's	17,892 / 0.01%
GC Percentage	44.45%

2.3. Coverage

Mean	0.0479

Standard Deviation	0.3671

2.4. Mapping Quality

Mean Mapping Quality	45.93

2.5. Mismatches and indels

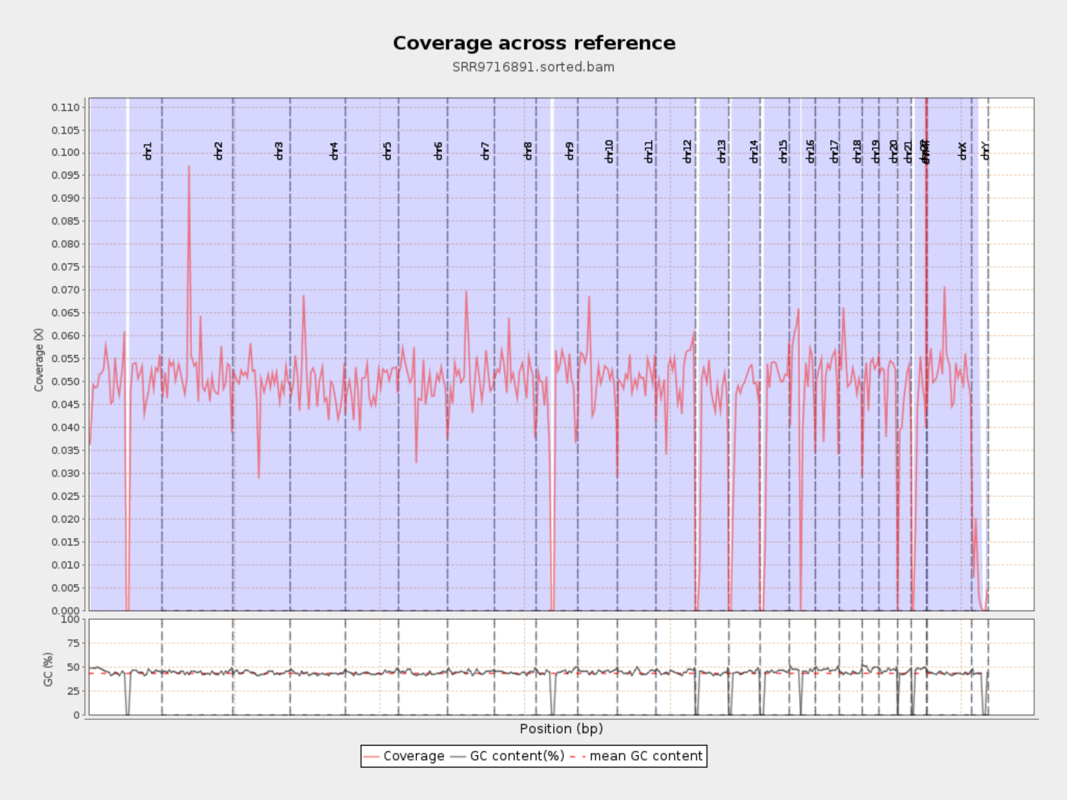
General error rate	0.75%
Mismatches	1,089,721
Insertions	12,115
Mapped reads with at least one insertion	0.6%
Deletions	29,996
Mapped reads with at least one deletion	1.49%
Homopolymer indels	39.97%

2.6. Chromosome stats

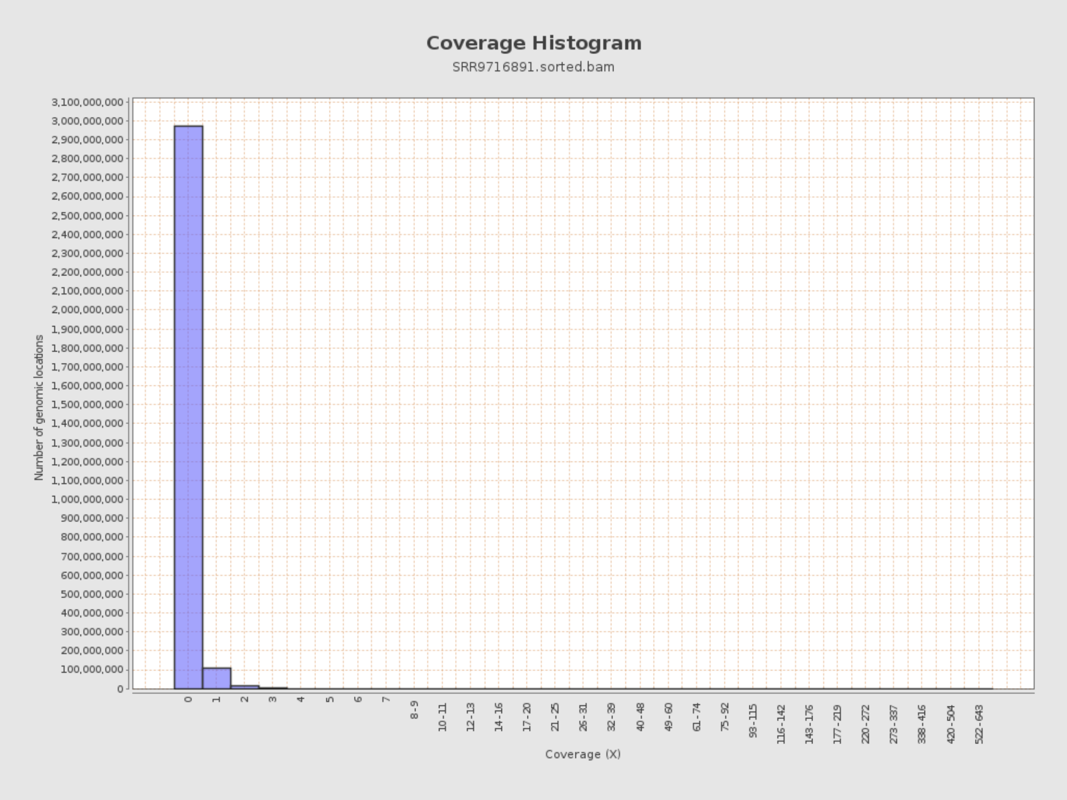
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11823083	0.0474	0.3974
chr2	243199373	12749328	0.0524	0.5462
chr3	198022430	9858470	0.0498	0.254
chr4	191154276	9432009	0.0493	0.2799
chr5	180915260	8907907	0.0492	0.2552
chr6	171115067	8508486	0.0497	0.2916
chr7	159138663	8155320	0.0512	0.4723

chr8	146364022	7536043	0.0515	0.4631
chr9	141213431	6260942	0.0443	0.3927
chr10	135534747	7050186	0.052	0.3571
chr11	135006516	6819008	0.0505	0.4017
chr12	133851895	6791857	0.0507	0.2624
chr13	115169878	4677668	0.0406	0.2285
chr14	107349540	4457978	0.0415	0.2757
chr15	102531392	4312574	0.0421	0.2365
chr16	90354753	4437275	0.0491	0.2831
chr17	81195210	4098548	0.0505	0.2801
chr18	78077248	4124379	0.0528	0.7508
chr19	59128983	3014892	0.051	0.3774
chr20	63025520	3156996	0.0501	0.2673
chr21	48129895	1977688	0.0411	0.2613
chr22	51304566	1711820	0.0334	0.2088
chrMT	16571	19435	1.1728	1.5864
chrX	155270560	8134387	0.0524	0.3241
chrY	59373566	369987	0.0062	0.171

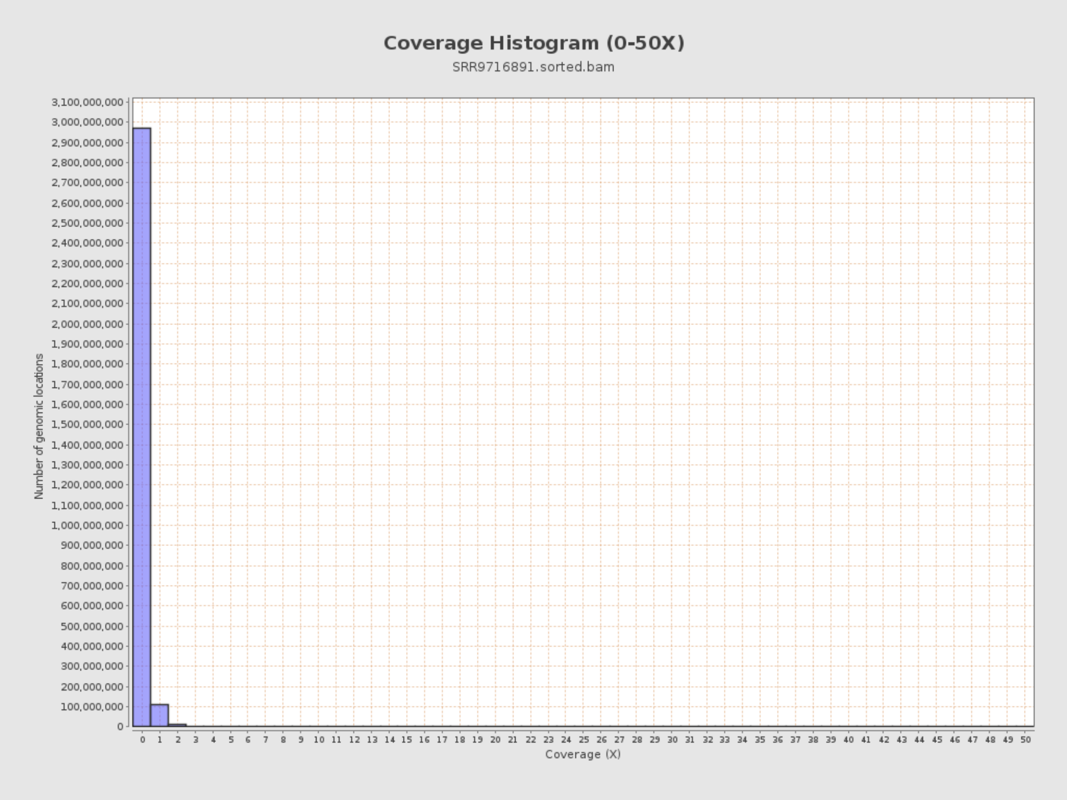
3. Results : Coverage across reference



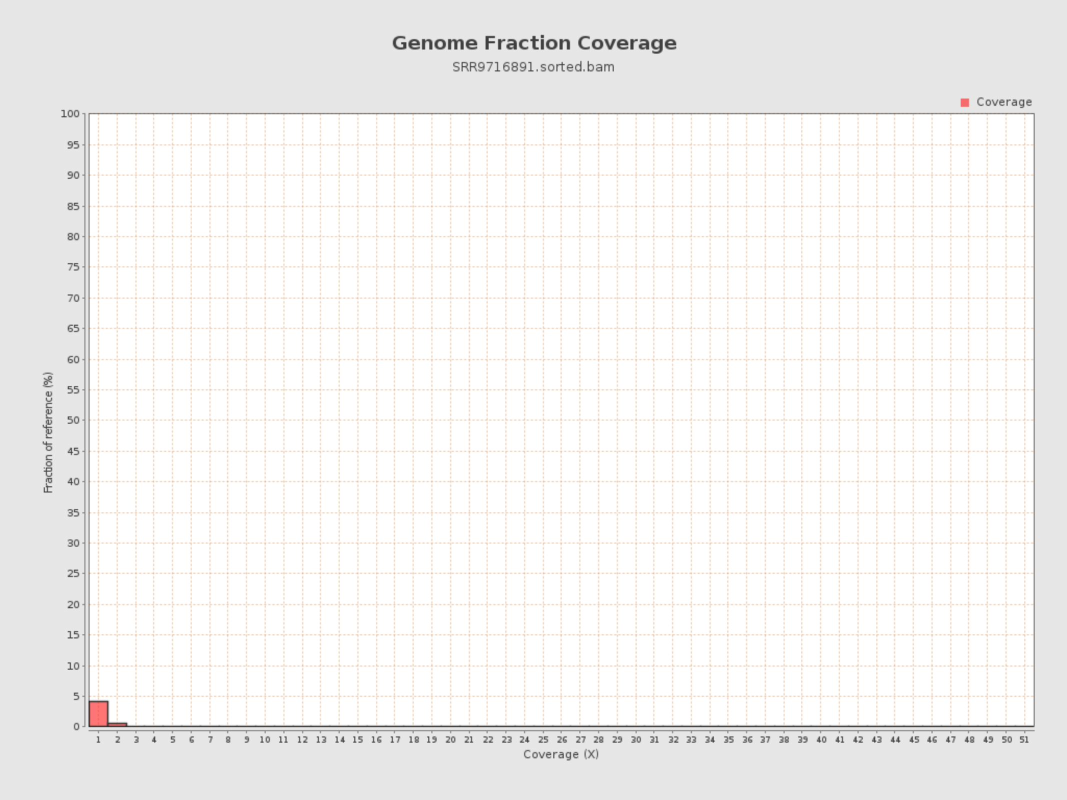
4. Results : Coverage Histogram



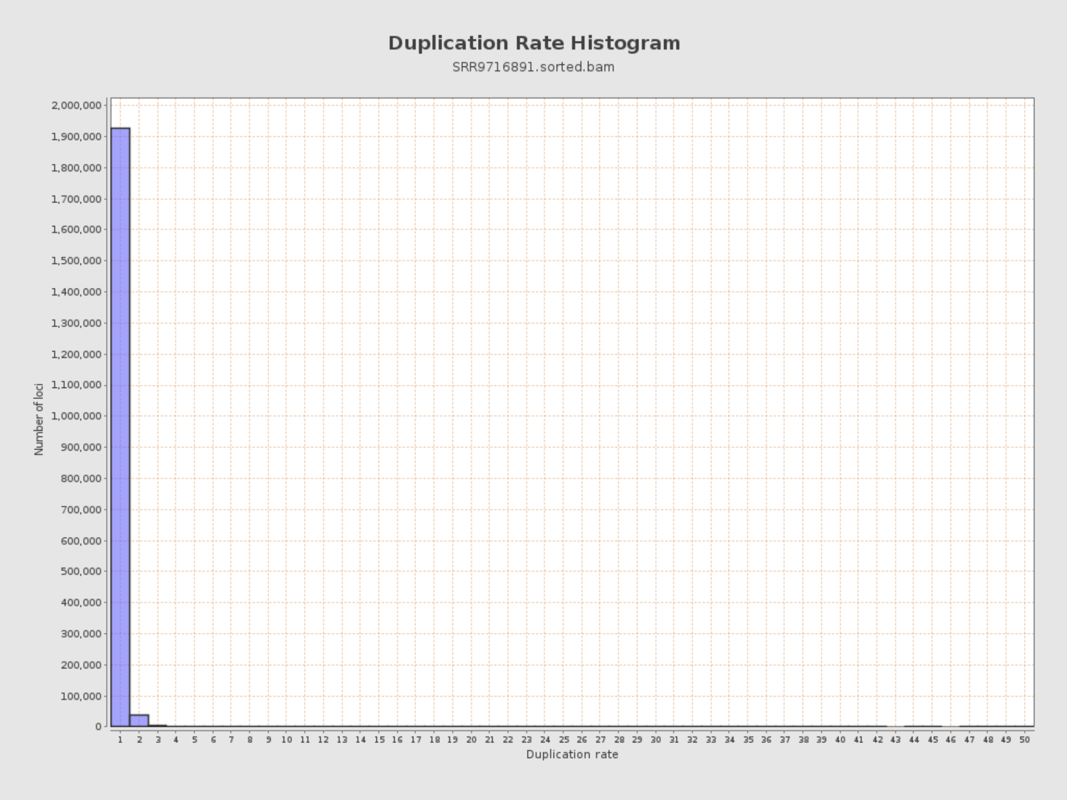
5. Results : Coverage Histogram (0-50X)



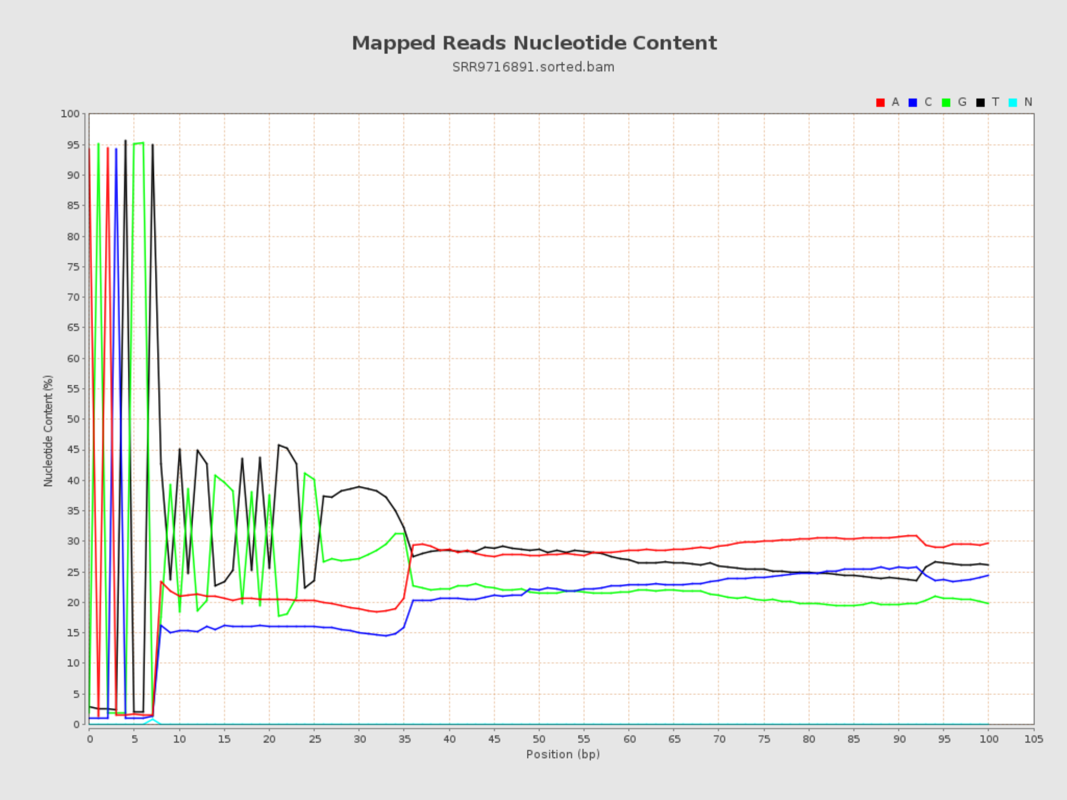
6. Results : Genome Fraction Coverage



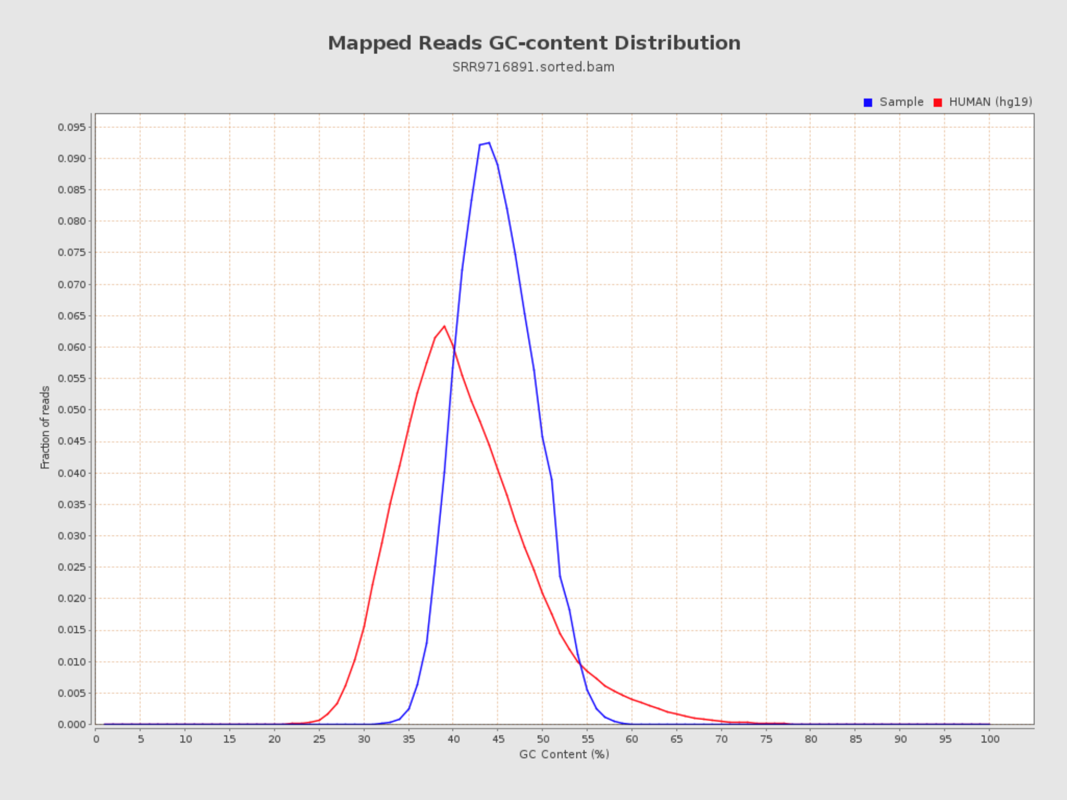
7. Results : Duplication Rate Histogram



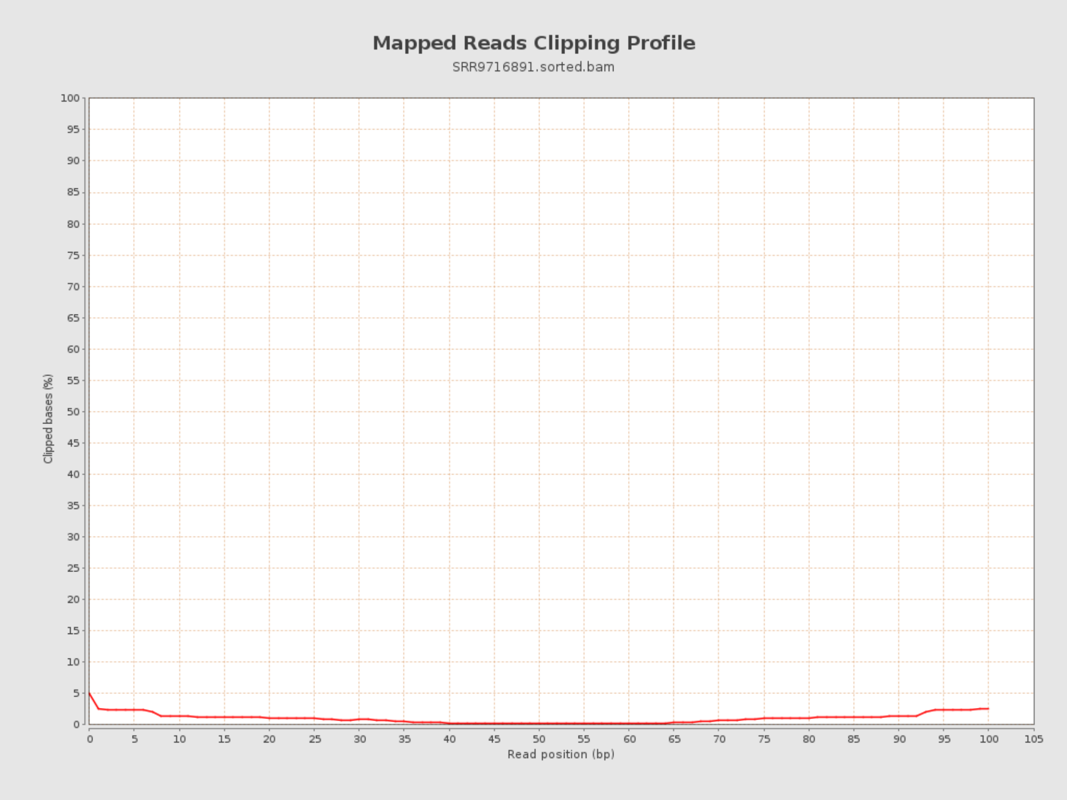
8. Results : Mapped Reads Nucleotide Content



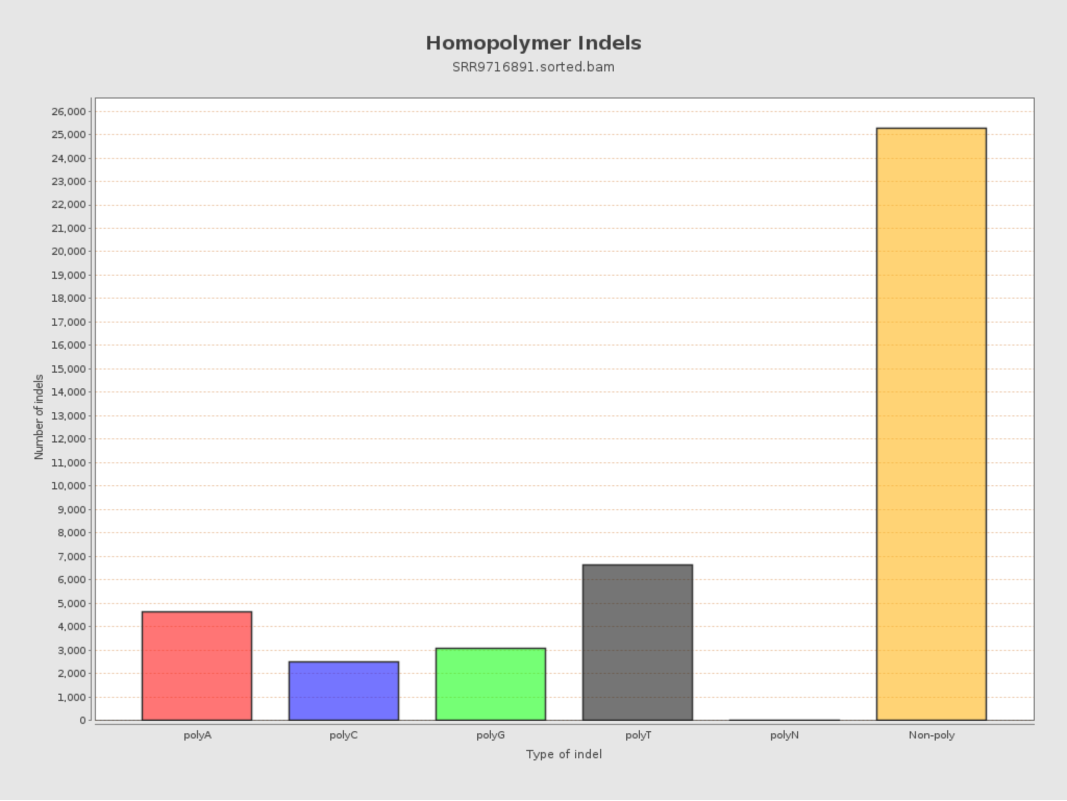
9. Results : Mapped Reads GC-content Distribution



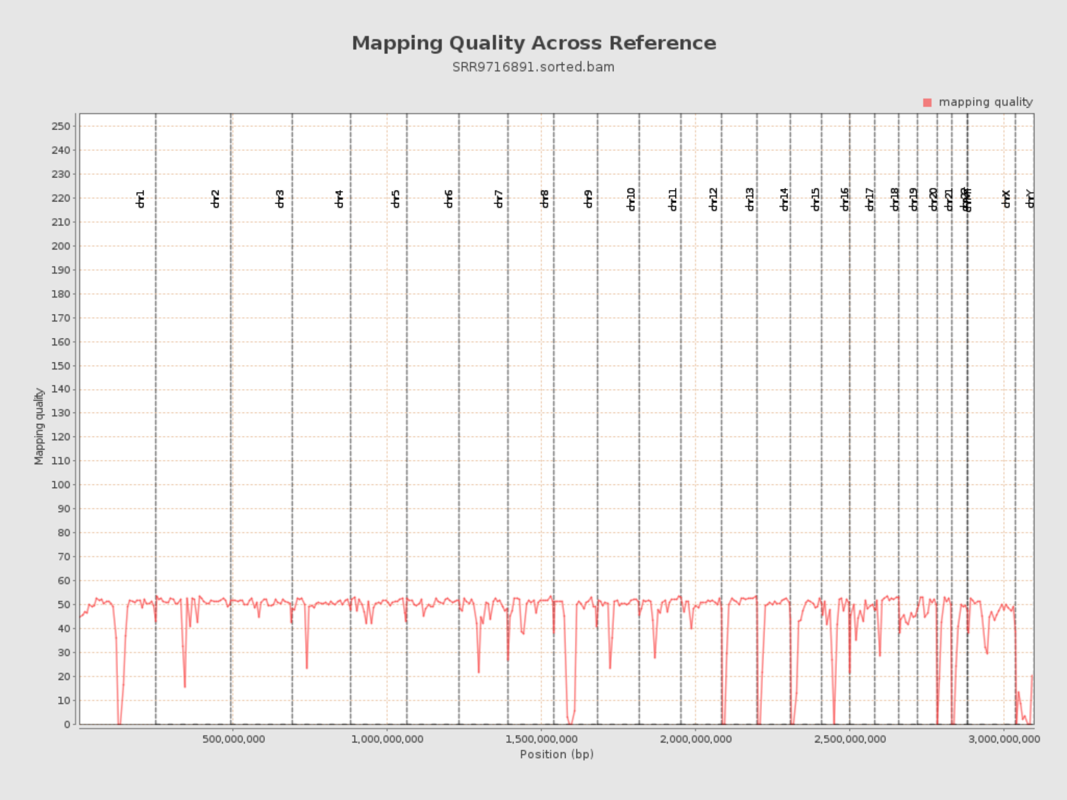
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram