Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 23:25:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716591.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_SRR9716591 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716591.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 23:25:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716591.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	578,673
Mapped reads	499,214 / 86.27%
Unmapped reads	79,459 / 13.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,356 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	9,586 / 1.66%
Duplication rate	1.49%
Clipped reads	500,399 / 86.47%

2.2. ACGT Content

Number/percentage of A's	7,349,437 / 25.65%
Number/percentage of C's	5,720,440 / 19.96%
Number/percentage of T's	8,833,902 / 30.83%
Number/percentage of G's	6,753,994 / 23.57%
Number/percentage of N's	377 / 0%
GC Percentage	43.53%

2.3. Coverage

Mean	0.0093

Standard Deviation	0.1153

2.4. Mapping Quality

Mean Mapping Quality	44.63

2.5. Mismatches and indels

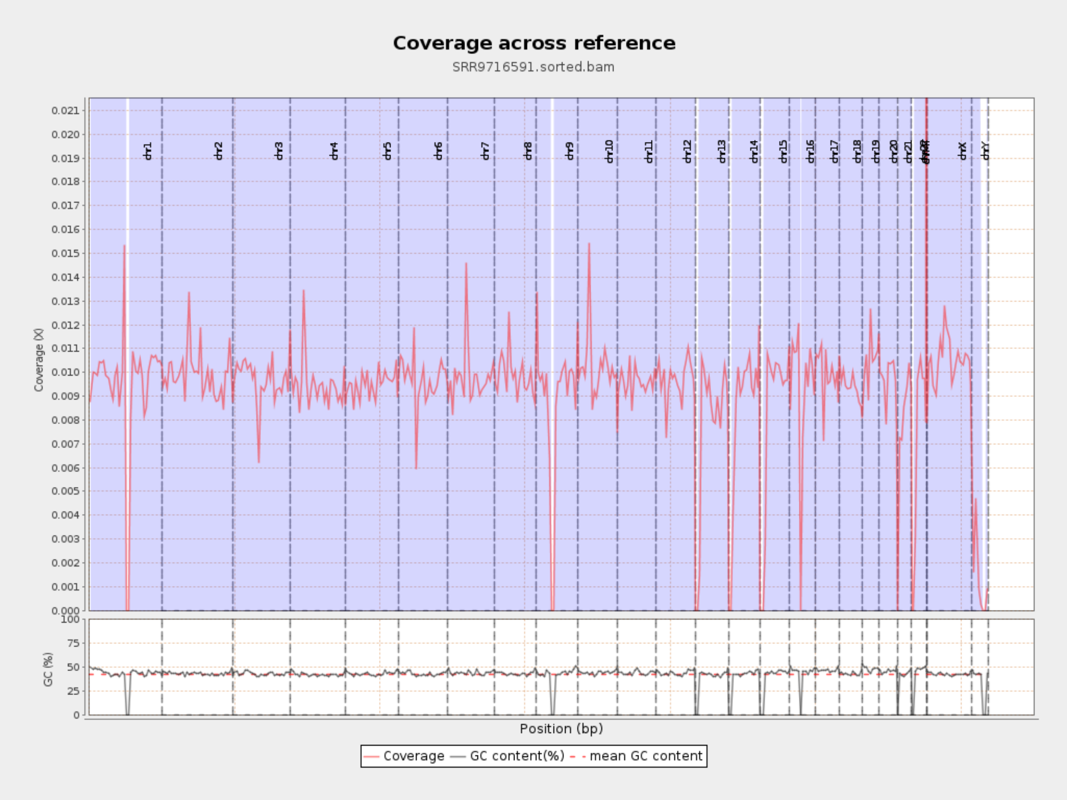
General error rate	0.52%
Mismatches	144,348
Insertions	1,893
Mapped reads with at least one insertion	0.38%
Deletions	5,348
Mapped reads with at least one deletion	1.06%
Homopolymer indels	41.47%

2.6. Chromosome stats

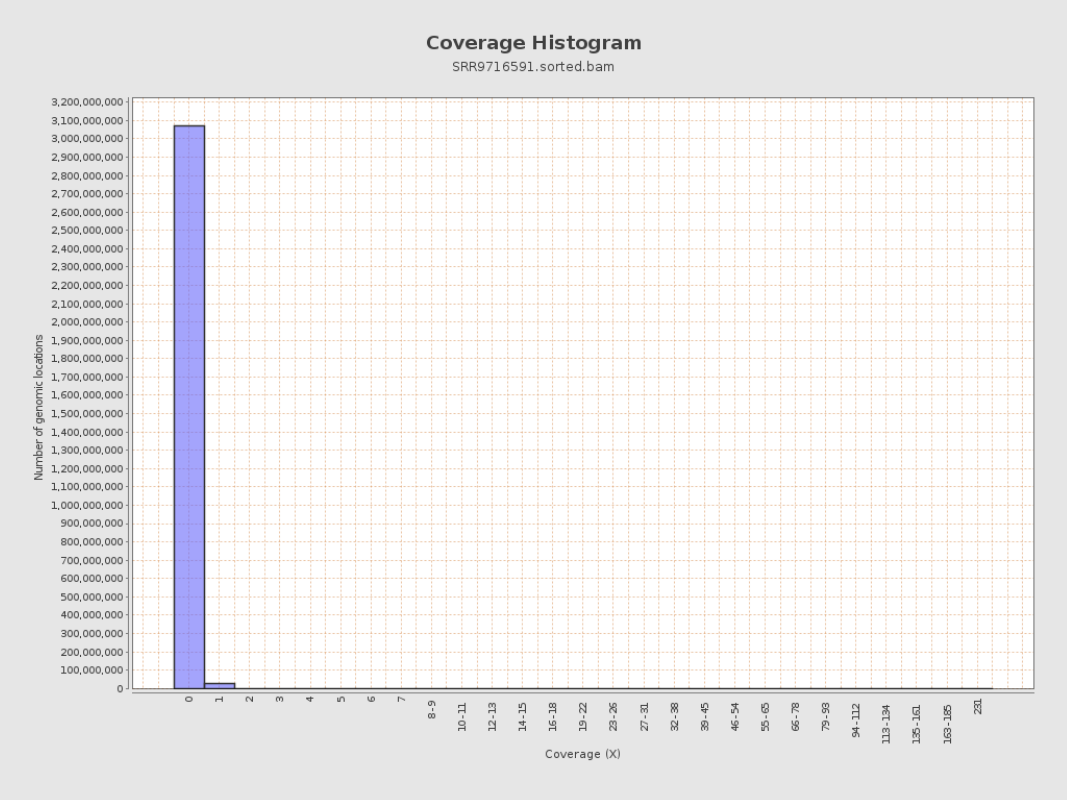
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2345432	0.0094	0.1666
chr2	243199373	2417502	0.0099	0.1411
chr3	198022430	1908322	0.0096	0.1019
chr4	191154276	1805906	0.0094	0.1032
chr5	180915260	1721958	0.0095	0.1013
chr6	171115067	1656504	0.0097	0.1081
chr7	159138663	1564210	0.0098	0.1286

chr8	146364022	1442450	0.0099	0.1099
chr9	141213431	1191646	0.0084	0.1021
chr10	135534747	1389185	0.0102	0.1163
chr11	135006516	1292589	0.0096	0.1094
chr12	133851895	1297853	0.0097	0.1028
chr13	115169878	880118	0.0076	0.091
chr14	107349540	867228	0.0081	0.0943
chr15	102531392	831664	0.0081	0.0934
chr16	90354753	838683	0.0093	0.1015
chr17	81195210	802928	0.0099	0.1055
chr18	78077248	739417	0.0095	0.1333
chr19	59128983	621277	0.0105	0.1414
chr20	63025520	609441	0.0097	0.1023
chr21	48129895	377519	0.0078	0.0952
chr22	51304566	347461	0.0068	0.0856
chrMT	16571	1476	0.0891	0.2893
chrX	155270560	1629482	0.0105	0.1106
chrY	59373566	86283	0.0015	0.0488

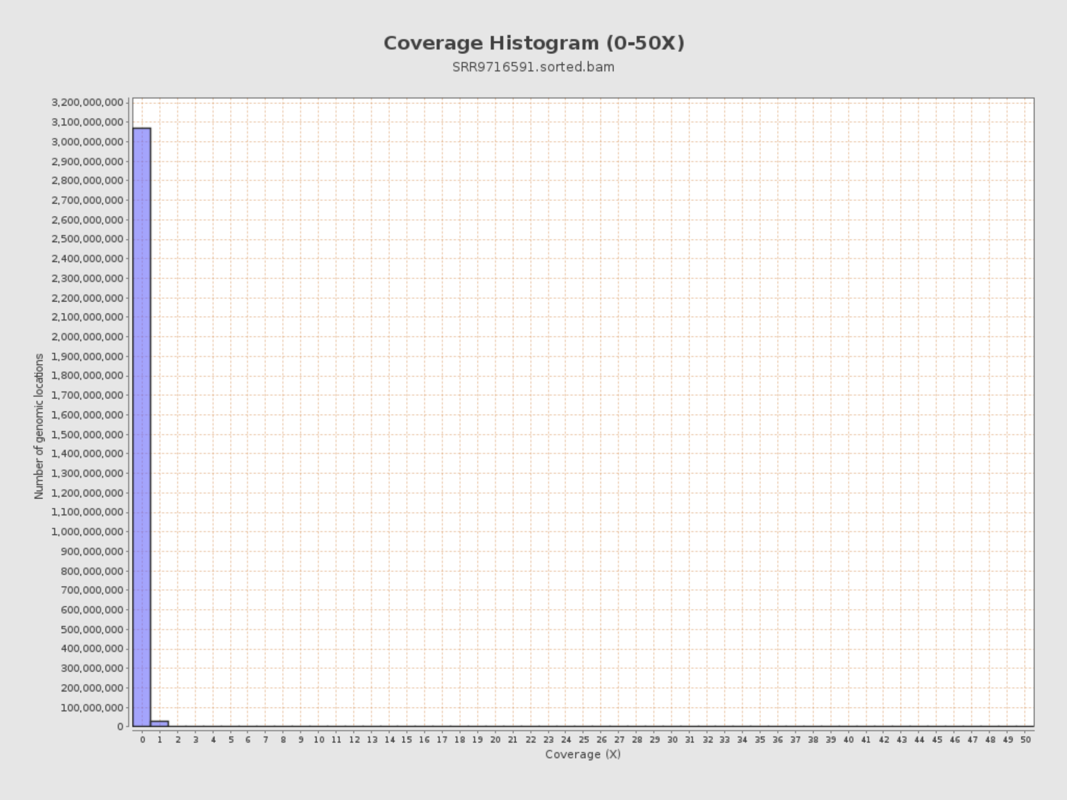
3. Results : Coverage across reference



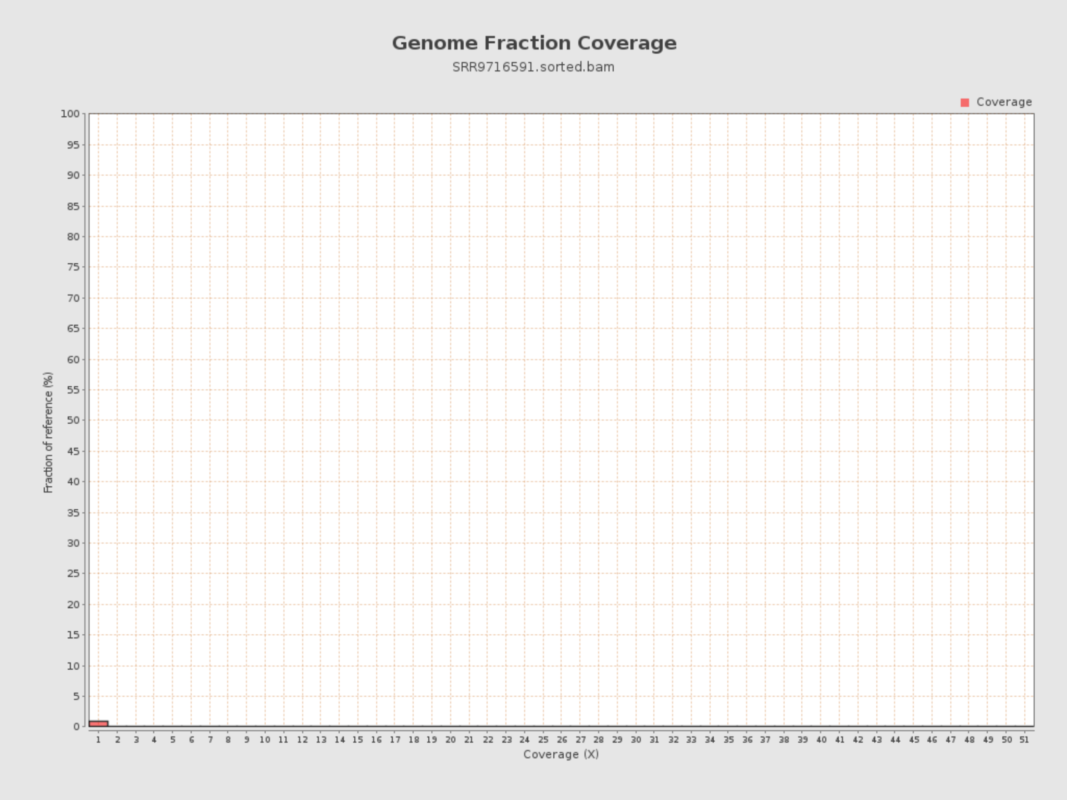
4. Results : Coverage Histogram



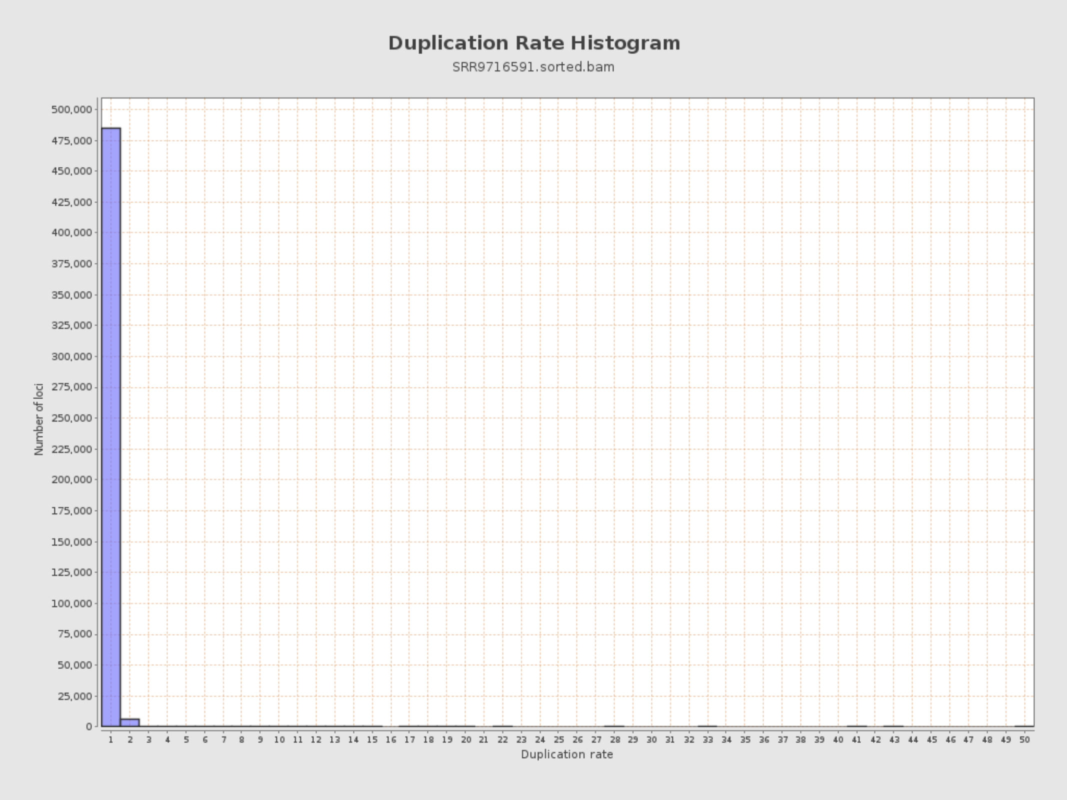
5. Results : Coverage Histogram (0-50X)



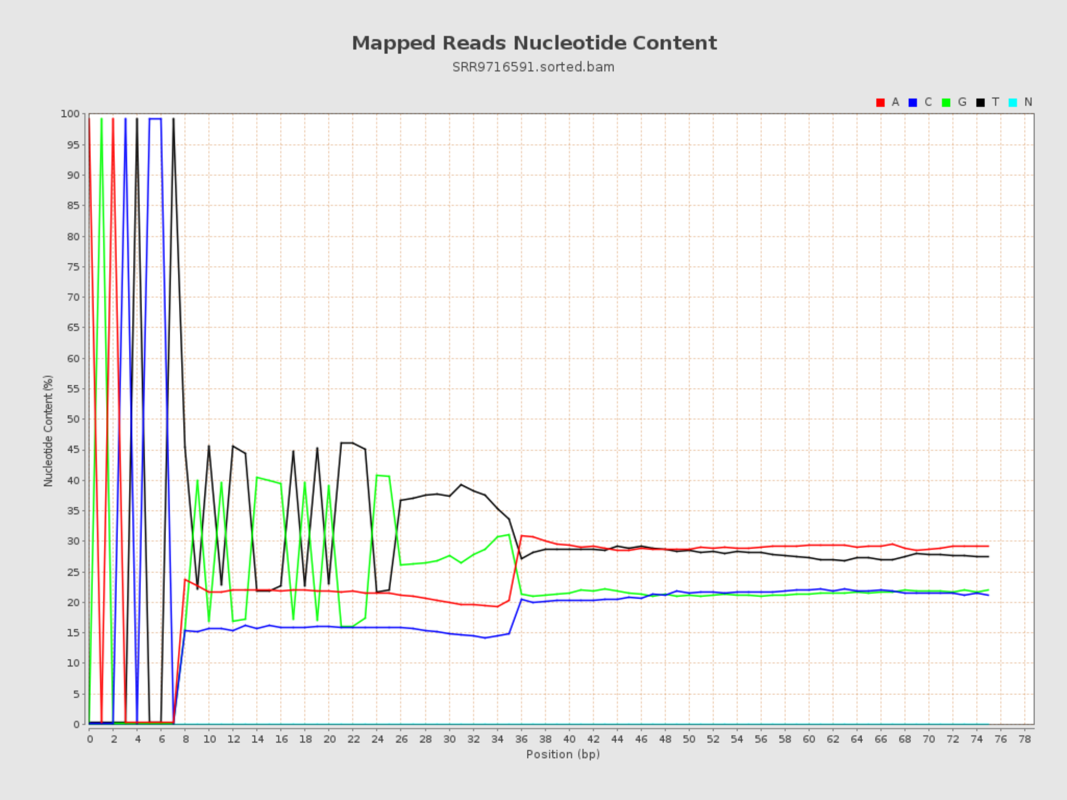
6. Results : Genome Fraction Coverage



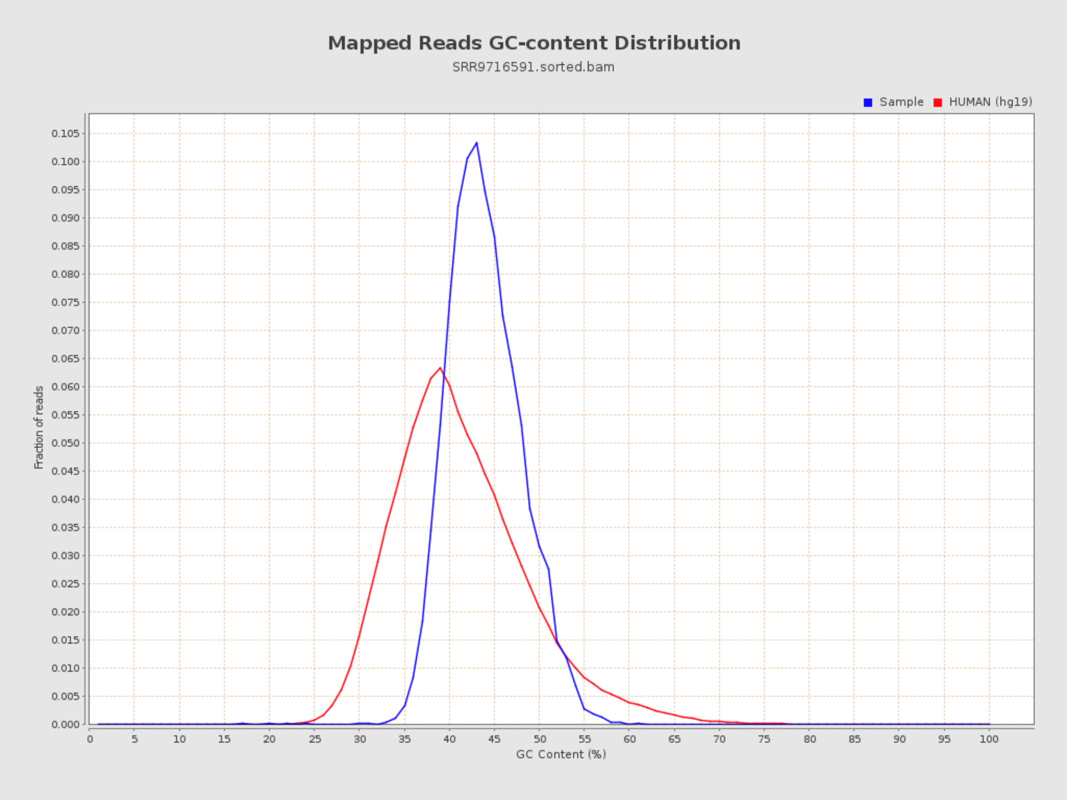
7. Results : Duplication Rate Histogram



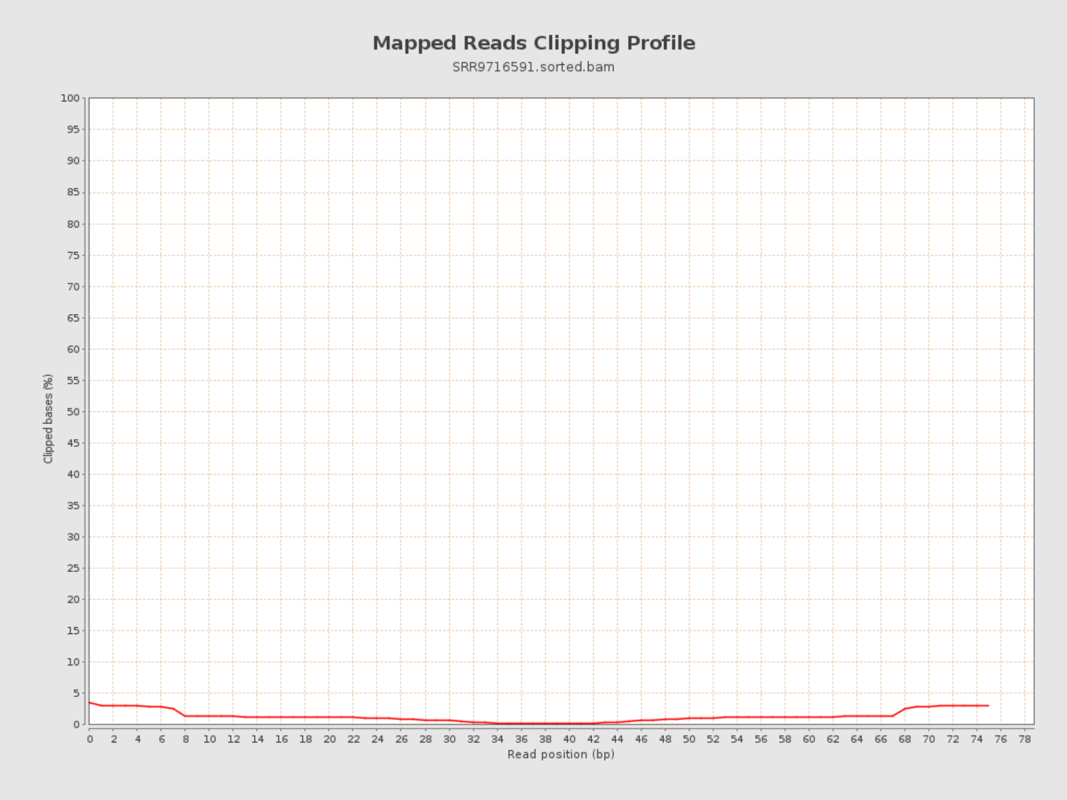
8. Results : Mapped Reads Nucleotide Content



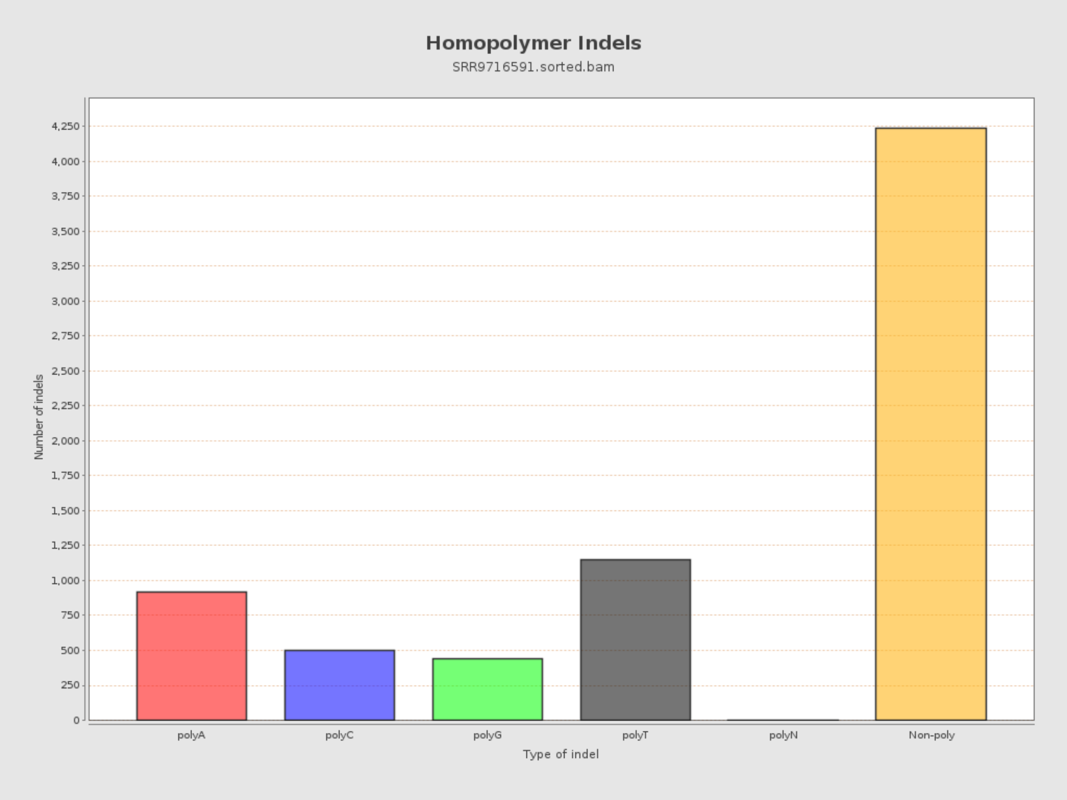
9. Results : Mapped Reads GC-content Distribution



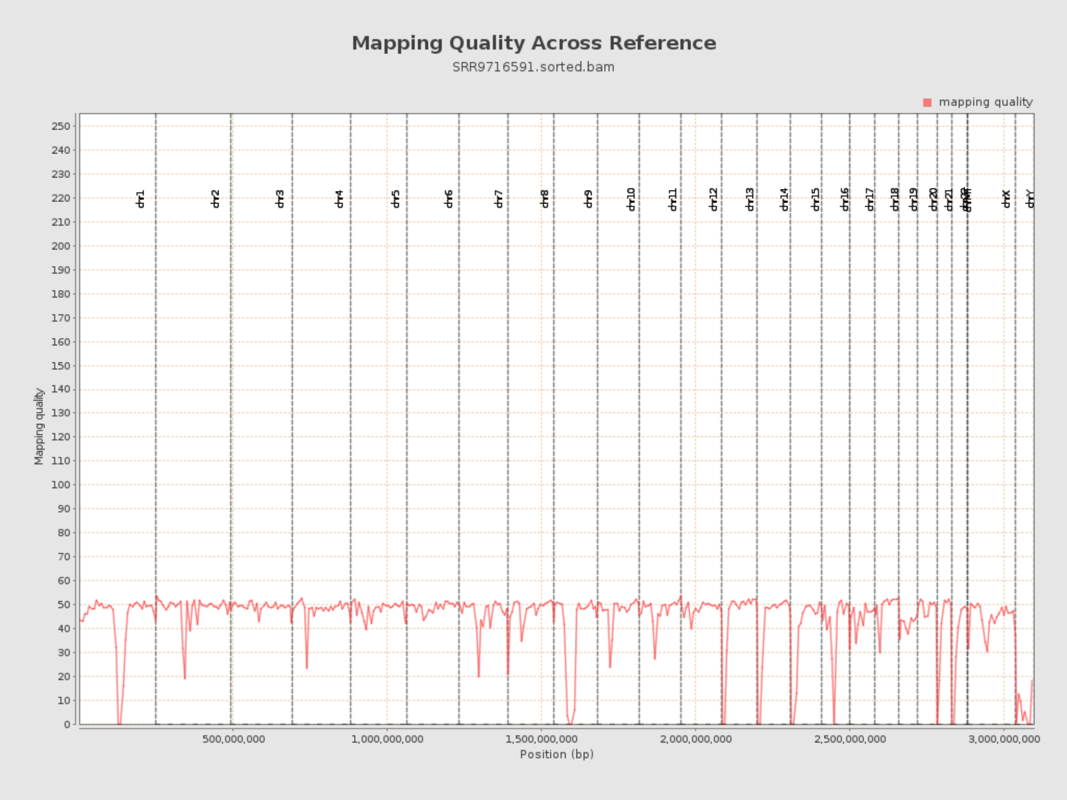
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram