Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 12:29:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716791.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_SRR9716791 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716791.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 12:29:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716791.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,932,139
Mapped reads	1,705,680 / 88.28%
Unmapped reads	226,459 / 11.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,469 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	45,280 / 2.34%
Duplication rate	1.86%
Clipped reads	1,710,808 / 88.54%

2.2. ACGT Content

Number/percentage of A's	24,145,928 / 24.98%
Number/percentage of C's	19,612,563 / 20.29%
Number/percentage of T's	29,740,946 / 30.76%
Number/percentage of G's	23,171,507 / 23.97%
Number/percentage of N's	664 / 0%
GC Percentage	44.26%

2.3. Coverage

Mean	0.0312

Standard Deviation	0.2598

2.4. Mapping Quality

Mean Mapping Quality	42.08

2.5. Mismatches and indels

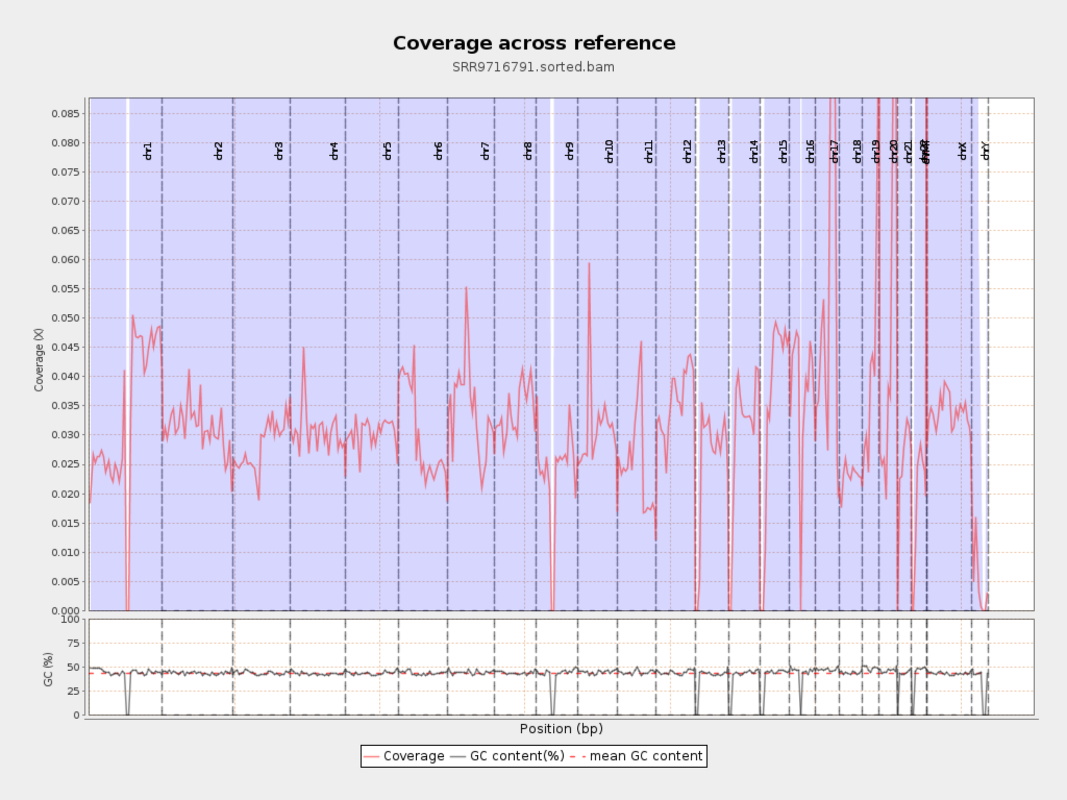
General error rate	0.54%
Mismatches	508,196
Insertions	5,626
Mapped reads with at least one insertion	0.33%
Deletions	17,967
Mapped reads with at least one deletion	1.04%
Homopolymer indels	41.86%

2.6. Chromosome stats

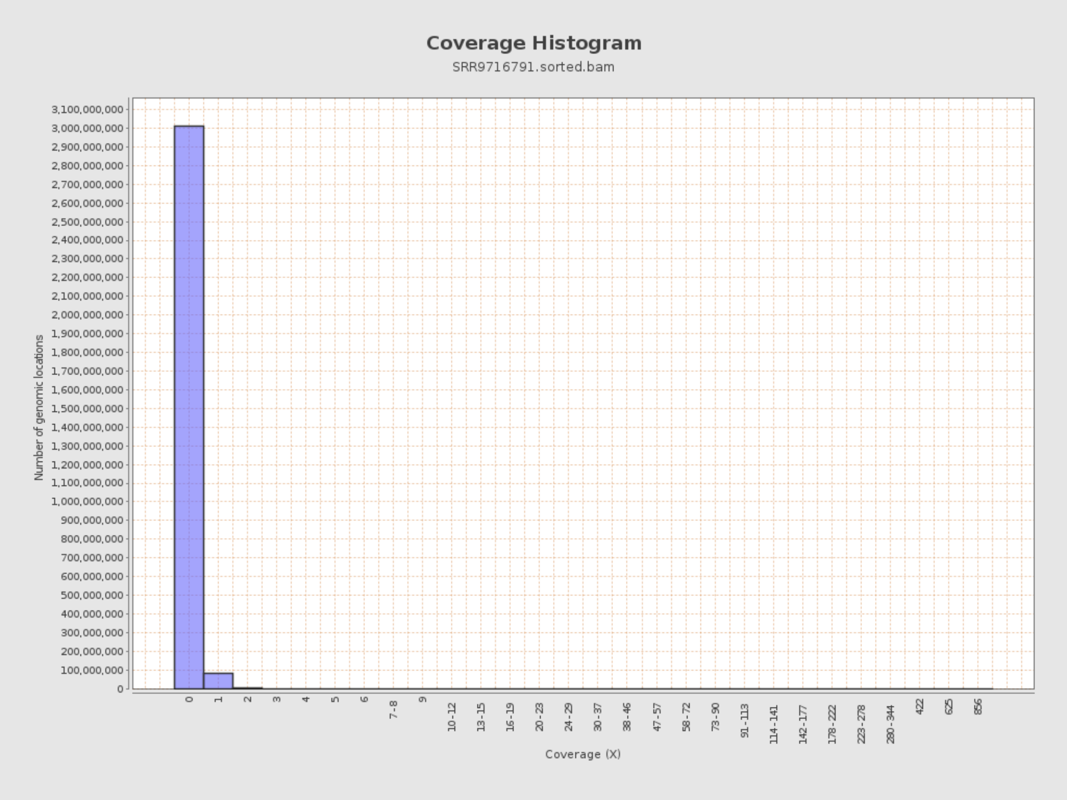
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8155267	0.0327	0.3297
chr2	243199373	7607236	0.0313	0.3973
chr3	198022430	5562835	0.0281	0.1864
chr4	191154276	5862929	0.0307	0.2068
chr5	180915260	5504611	0.0304	0.1901
chr6	171115067	5154303	0.0301	0.2303
chr7	159138663	5500230	0.0346	0.374

chr8	146364022	4997328	0.0341	0.248
chr9	141213431	3231153	0.0229	0.1946
chr10	135534747	4240063	0.0313	0.3139
chr11	135006516	3423814	0.0254	0.216
chr12	133851895	4795828	0.0358	0.2069
chr13	115169878	2903613	0.0252	0.1736
chr14	107349540	3209823	0.0299	0.1944
chr15	102531392	3592849	0.035	0.2116
chr16	90354753	3382639	0.0374	0.2257
chr17	81195210	4379211	0.0539	0.268
chr18	78077248	1790570	0.0229	0.2986
chr19	59128983	2593891	0.0439	0.3172
chr20	63025520	3145423	0.0499	0.2581
chr21	48129895	1203011	0.025	0.1876
chr22	51304566	912688	0.0178	0.1487
chrMT	16571	3338	0.2014	0.4777
chrX	155270560	5261657	0.0339	0.215
chrY	59373566	286040	0.0048	0.1287

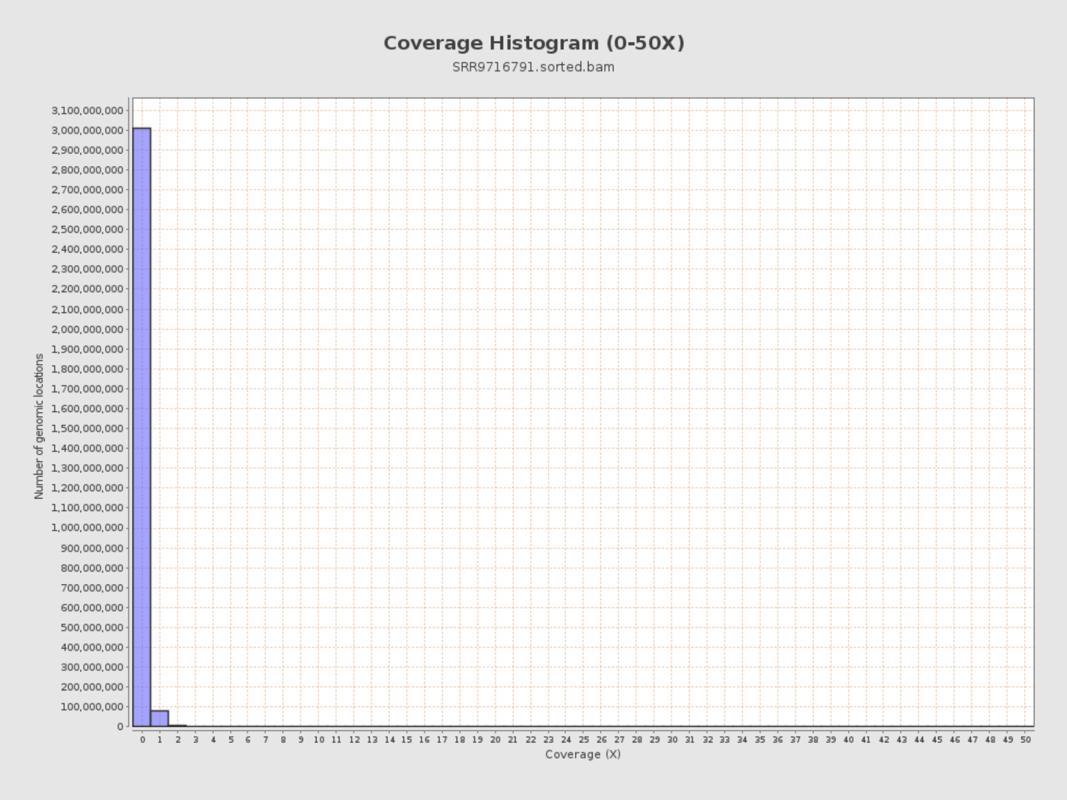
3. Results : Coverage across reference



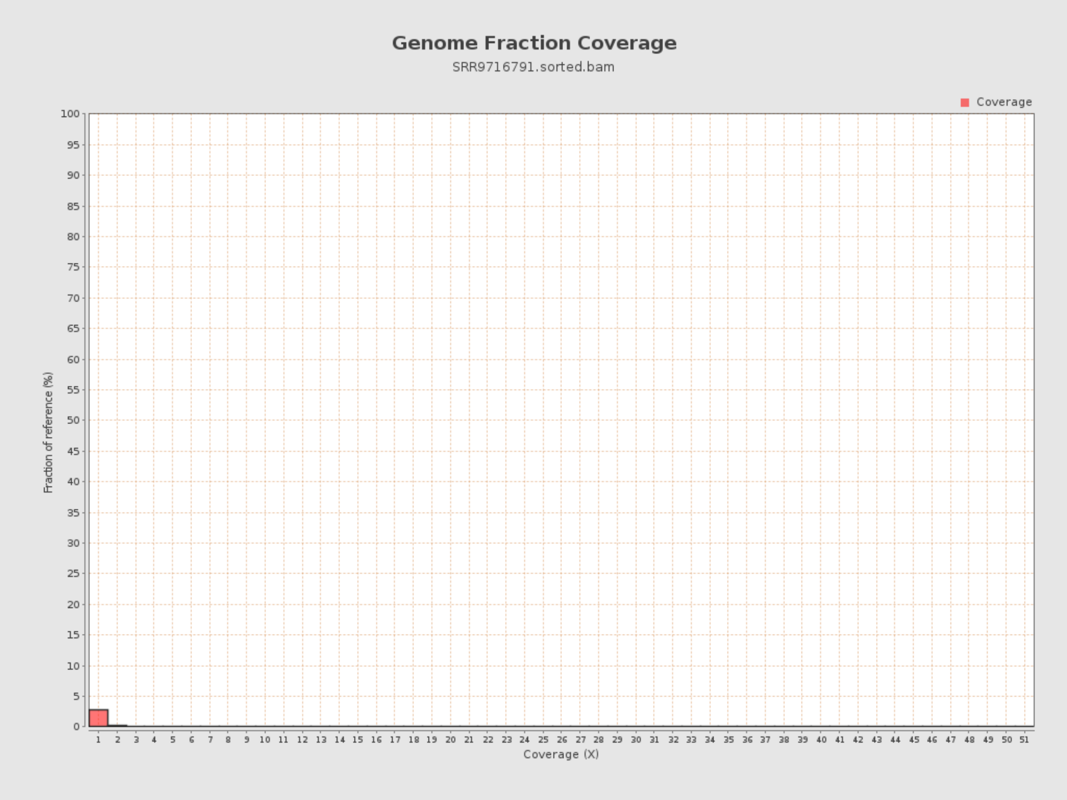
4. Results : Coverage Histogram



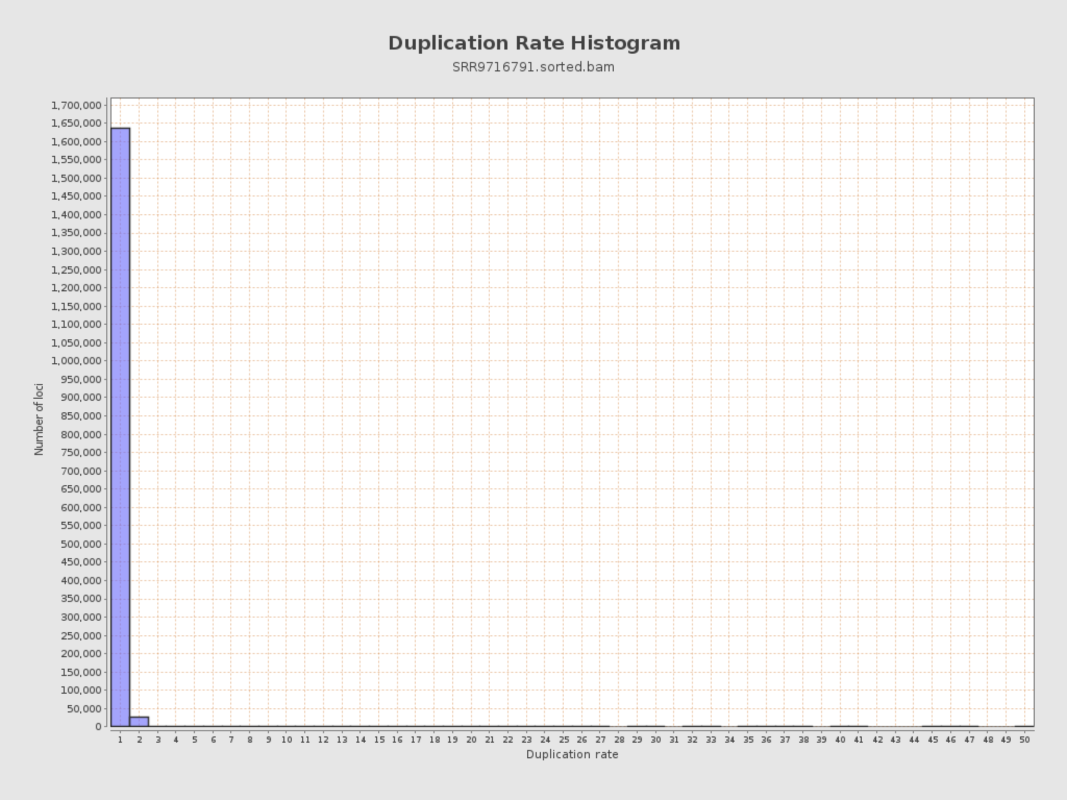
5. Results : Coverage Histogram (0-50X)



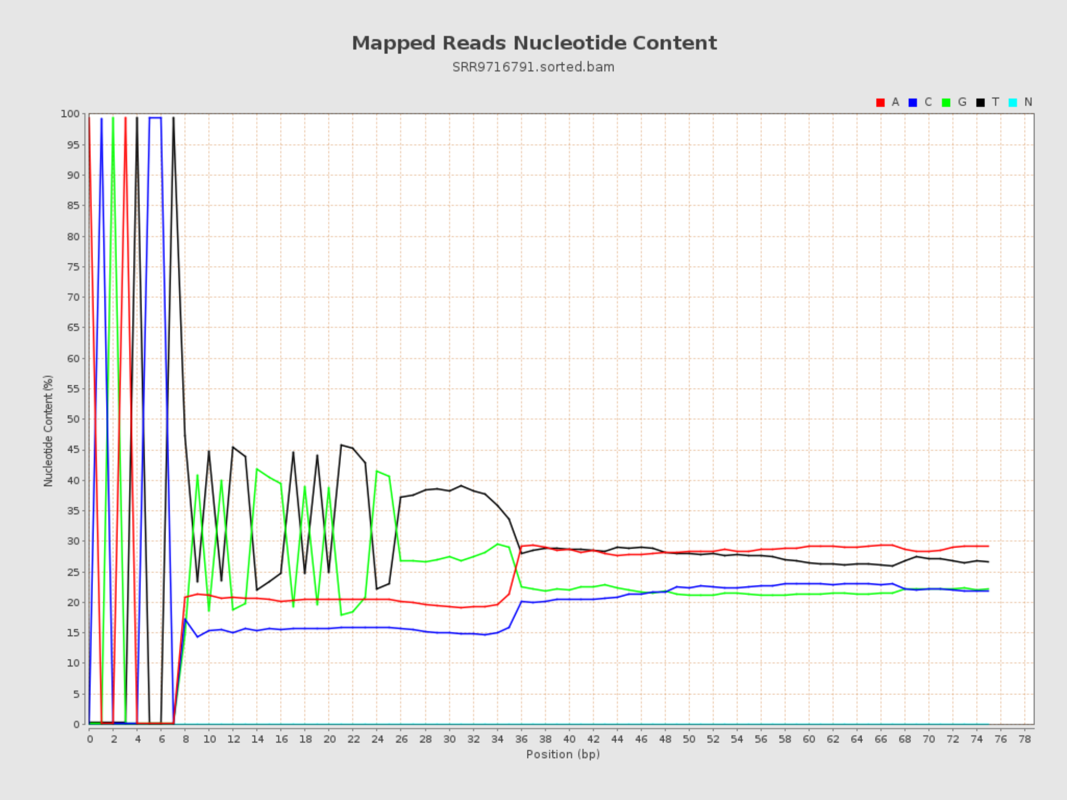
6. Results : Genome Fraction Coverage



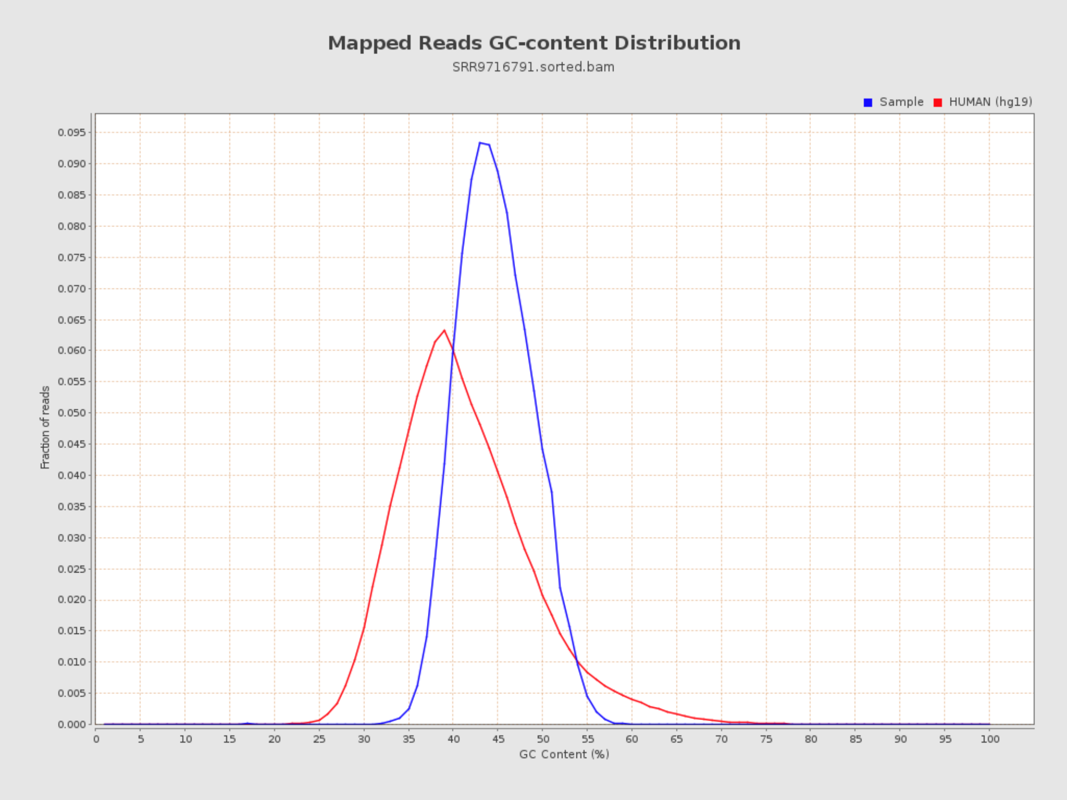
7. Results : Duplication Rate Histogram



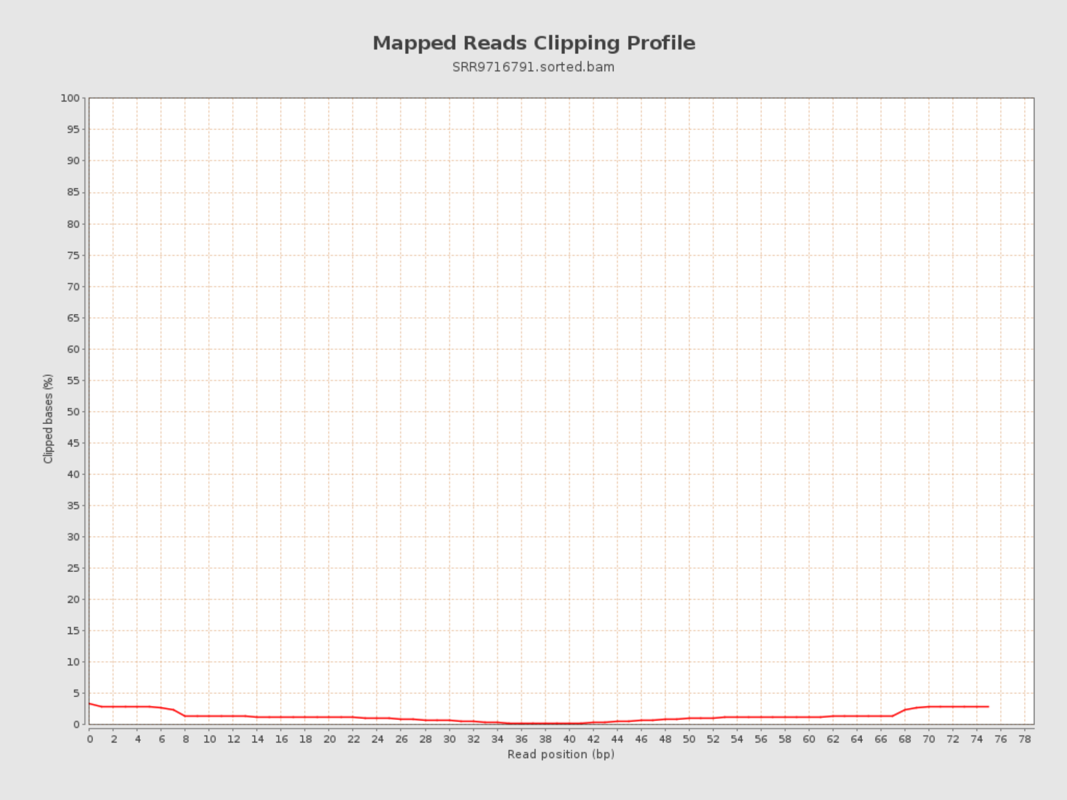
8. Results : Mapped Reads Nucleotide Content



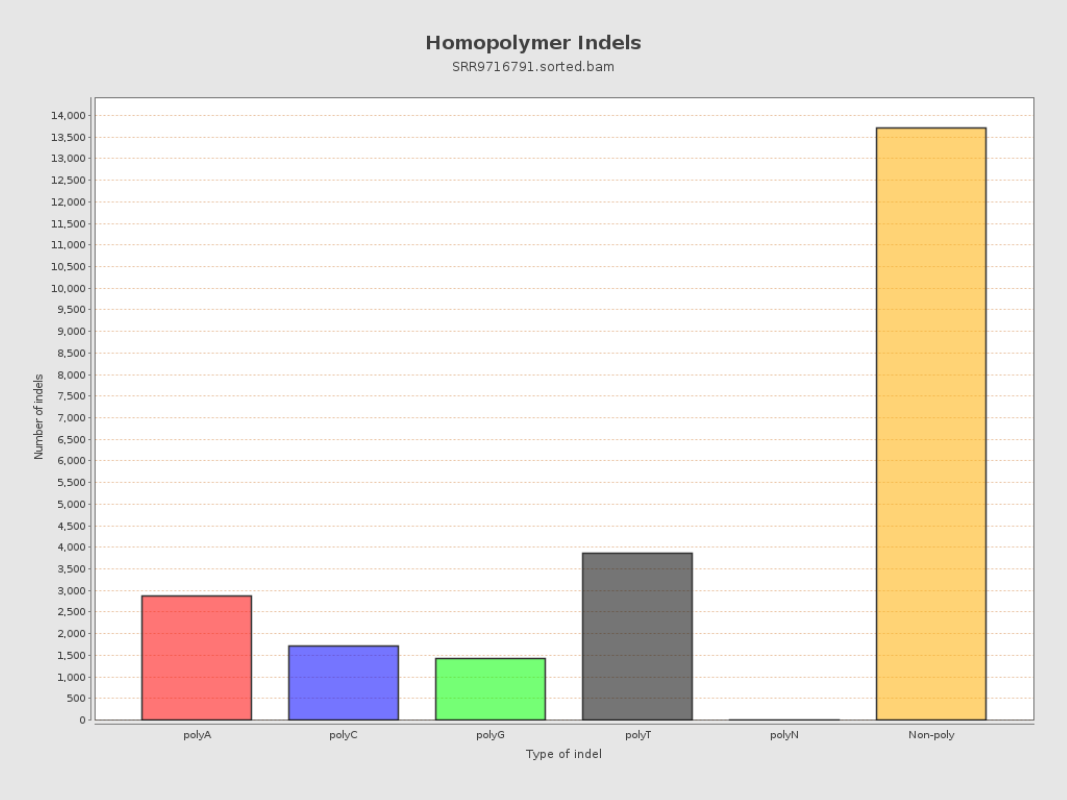
9. Results : Mapped Reads GC-content Distribution



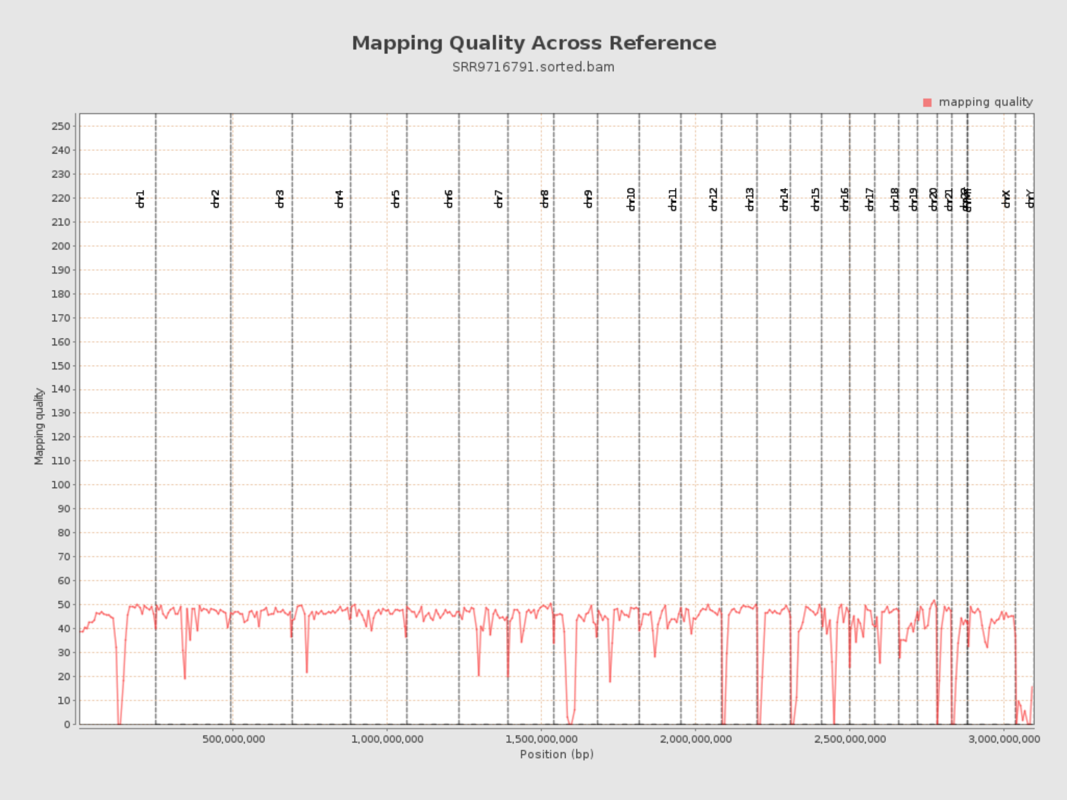
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram