Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 11:02:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716390.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_SRR9716390 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716390.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 11:02:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716390.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,847,365
Mapped reads	1,652,263 / 89.44%
Unmapped reads	195,102 / 10.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,018 / 1.46%
Read min/max/mean length	30 / 101 / 101.54
Duplicated reads (estimated)	75,770 / 4.1%
Duplication rate	2.56%
Clipped reads	1,676,010 / 90.72%

2.2. ACGT Content

Number/percentage of A's	32,662,519 / 25.4%
Number/percentage of C's	24,592,681 / 19.12%
Number/percentage of T's	38,925,652 / 30.27%
Number/percentage of G's	32,423,469 / 25.21%
Number/percentage of N's	7,558 / 0.01%
GC Percentage	44.33%

2.3. Coverage

Mean	0.0416

Standard Deviation	0.5596

2.4. Mapping Quality

Mean Mapping Quality	42.66

2.5. Mismatches and indels

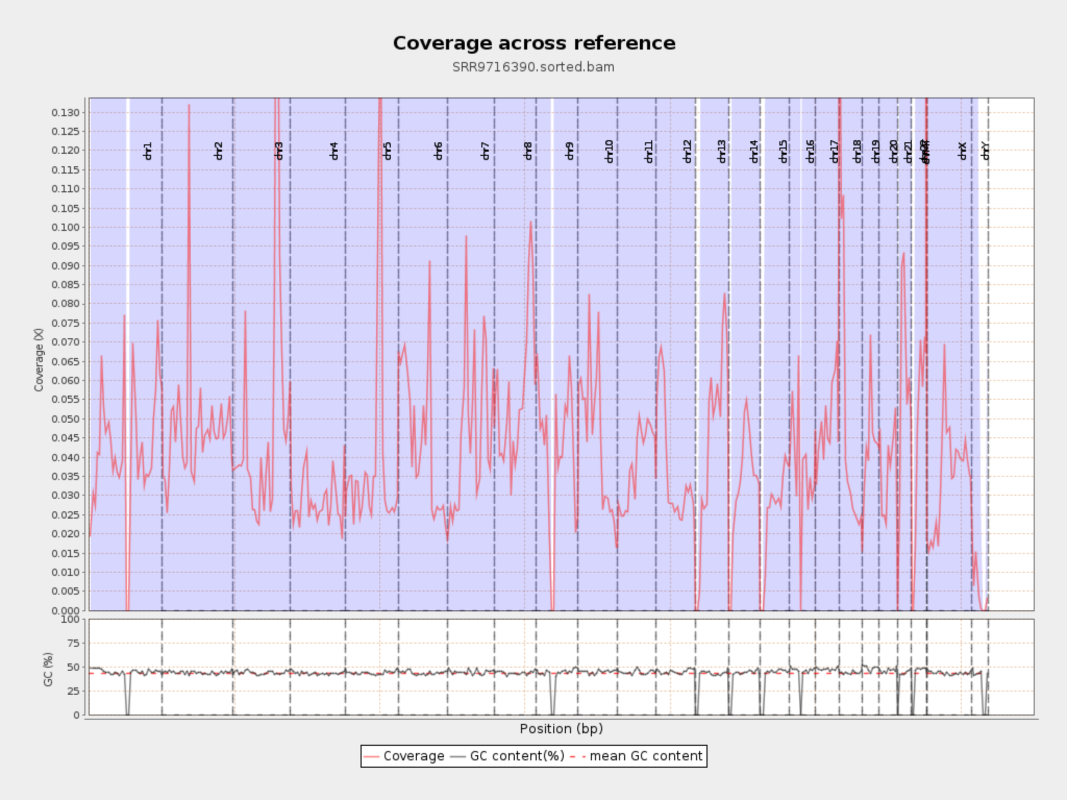
General error rate	0.91%
Mismatches	1,140,745
Insertions	12,727
Mapped reads with at least one insertion	0.76%
Deletions	31,788
Mapped reads with at least one deletion	1.9%
Homopolymer indels	43.89%

2.6. Chromosome stats

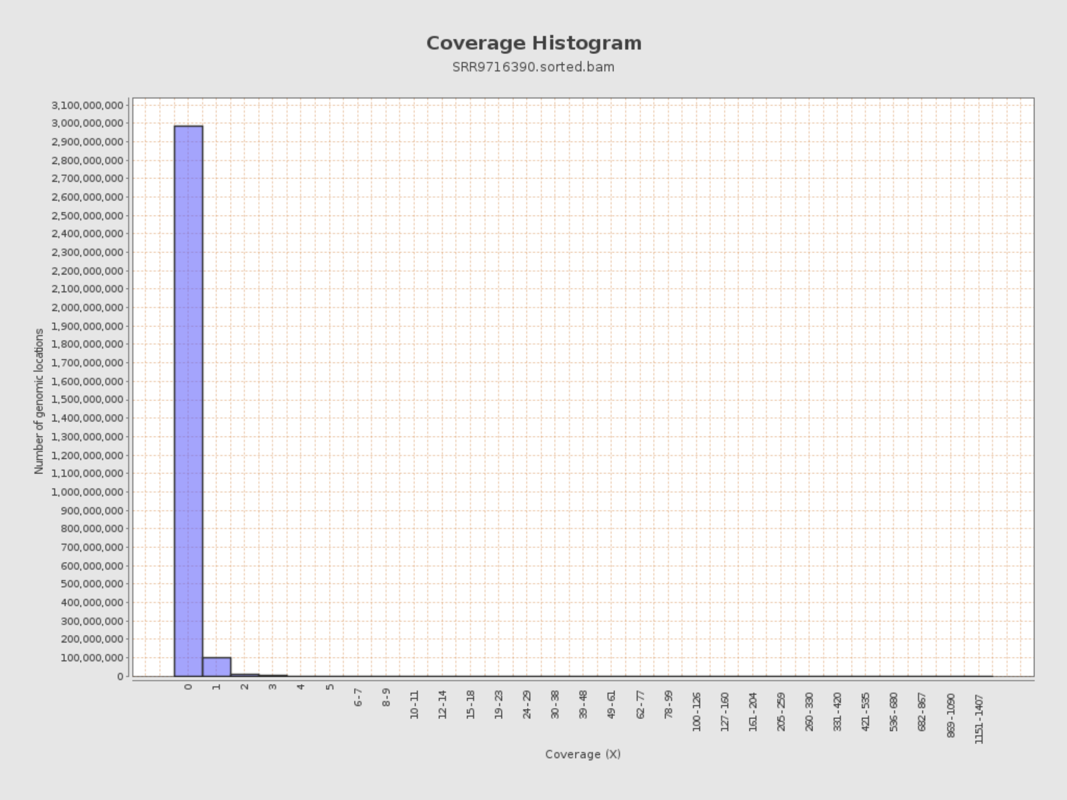
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10479734	0.042	0.8223
chr2	243199373	11598393	0.0477	1.0176
chr3	198022430	9874547	0.0499	0.2626
chr4	191154276	5436156	0.0284	0.2056
chr5	180915260	7209465	0.0398	0.2356
chr6	171115067	7792265	0.0455	0.3127
chr7	159138663	7524586	0.0473	0.8142

chr8	146364022	8329407	0.0569	0.764
chr9	141213431	5774151	0.0409	0.5565
chr10	135534747	6228088	0.046	0.4293
chr11	135006516	5141130	0.0381	0.3797
chr12	133851895	4915097	0.0367	0.2273
chr13	115169878	5139106	0.0446	0.2393
chr14	107349540	3515727	0.0328	0.2756
chr15	102531392	2592013	0.0253	0.1855
chr16	90354753	3321204	0.0368	0.2742
chr17	81195210	4025835	0.0496	0.3078
chr18	78077248	3973724	0.0509	1.2588
chr19	59128983	2609026	0.0441	0.6544
chr20	63025520	2318081	0.0368	0.2787
chr21	48129895	2771976	0.0576	0.2884
chr22	51304566	2188062	0.0426	0.2364
chrMT	16571	125993	7.6032	5.2353
chrX	155270560	5476788	0.0353	0.3431
chrY	59373566	306083	0.0052	0.1409

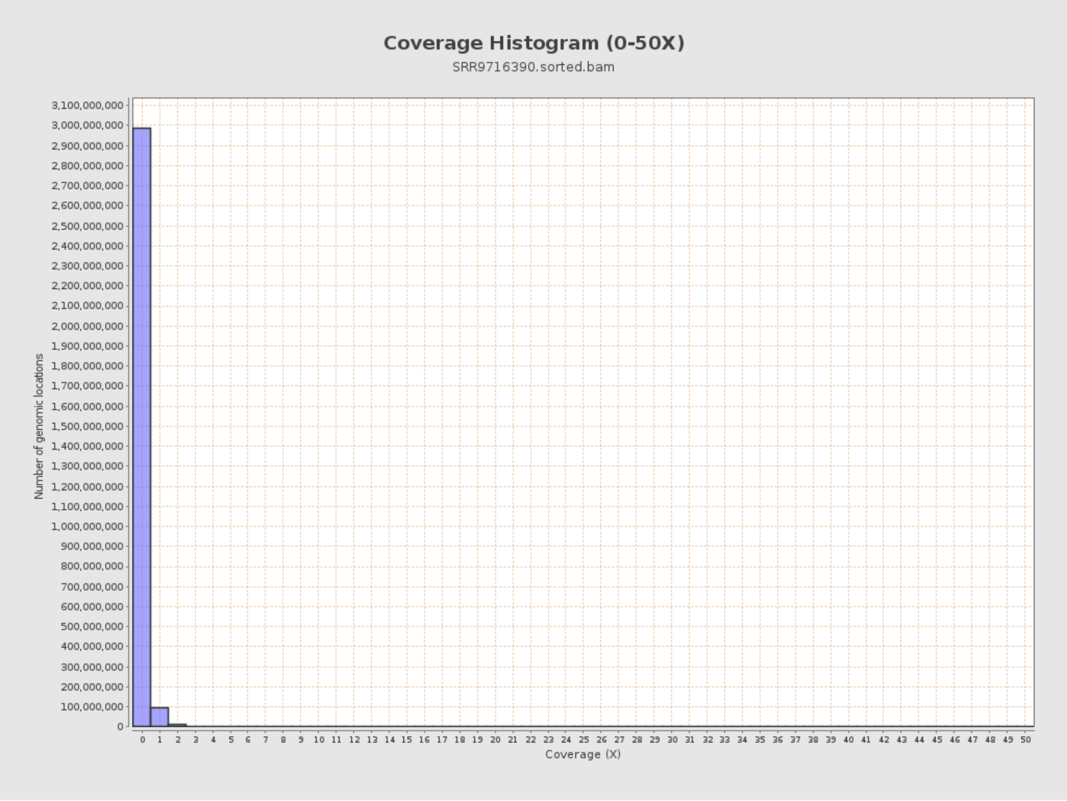
3. Results : Coverage across reference



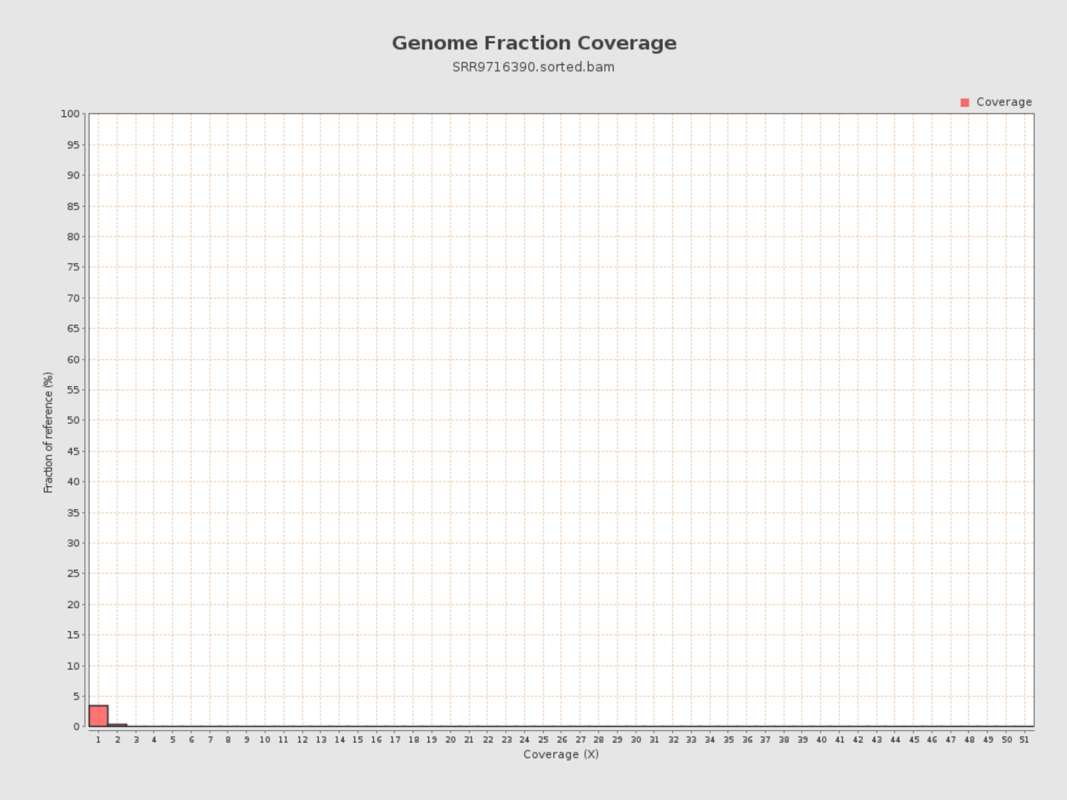
4. Results : Coverage Histogram



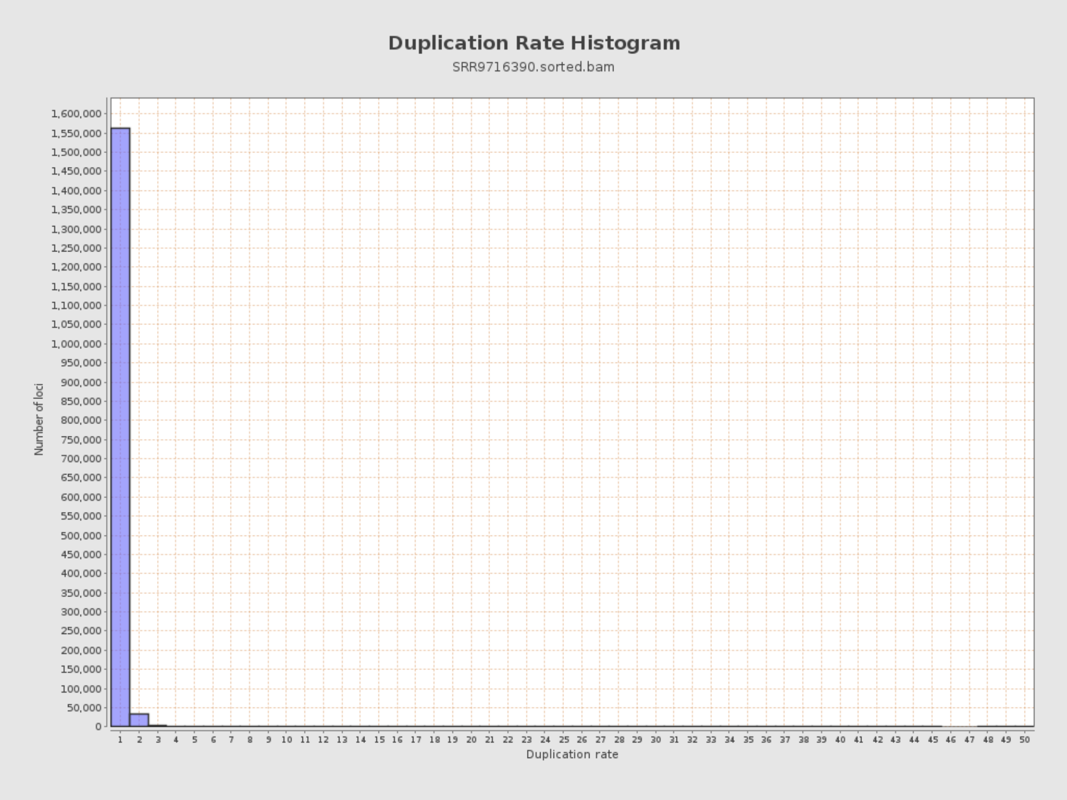
5. Results : Coverage Histogram (0-50X)



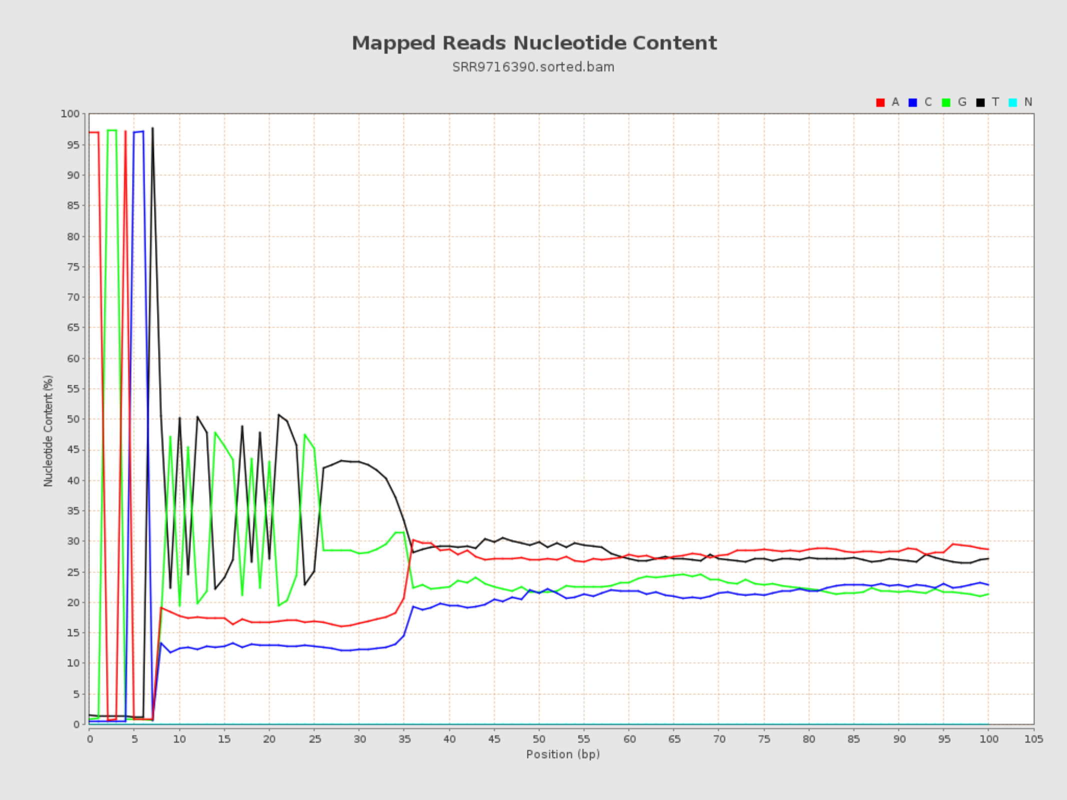
6. Results : Genome Fraction Coverage



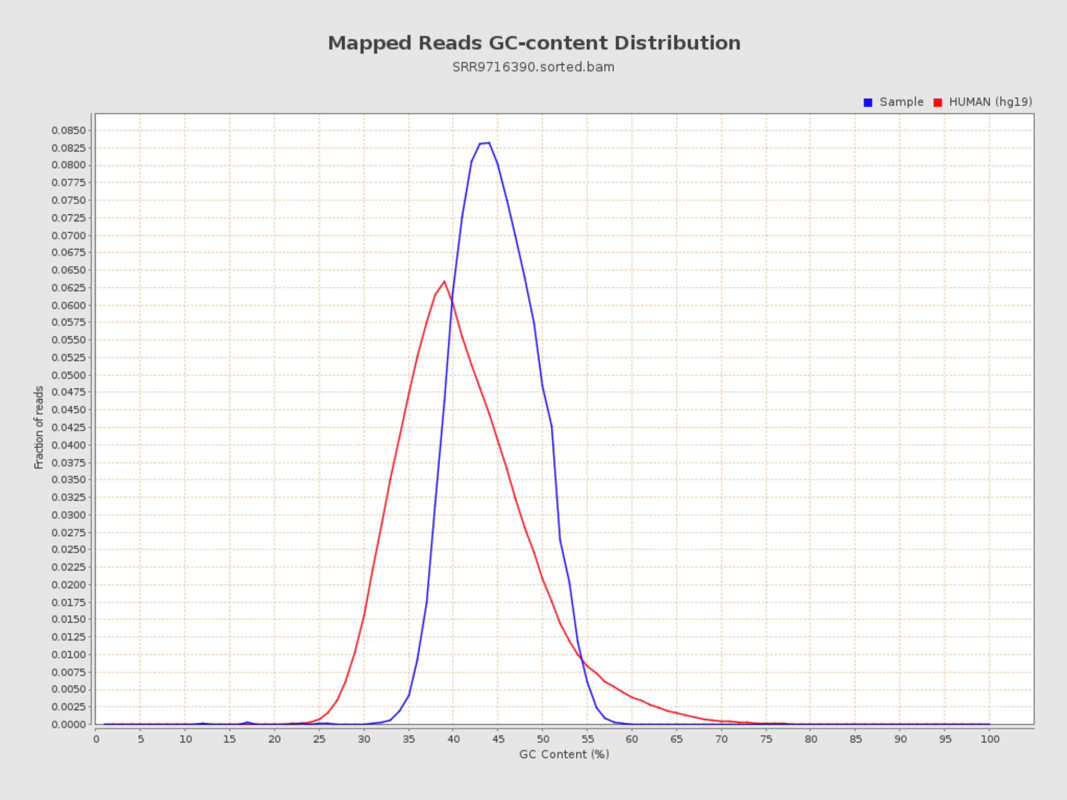
7. Results : Duplication Rate Histogram



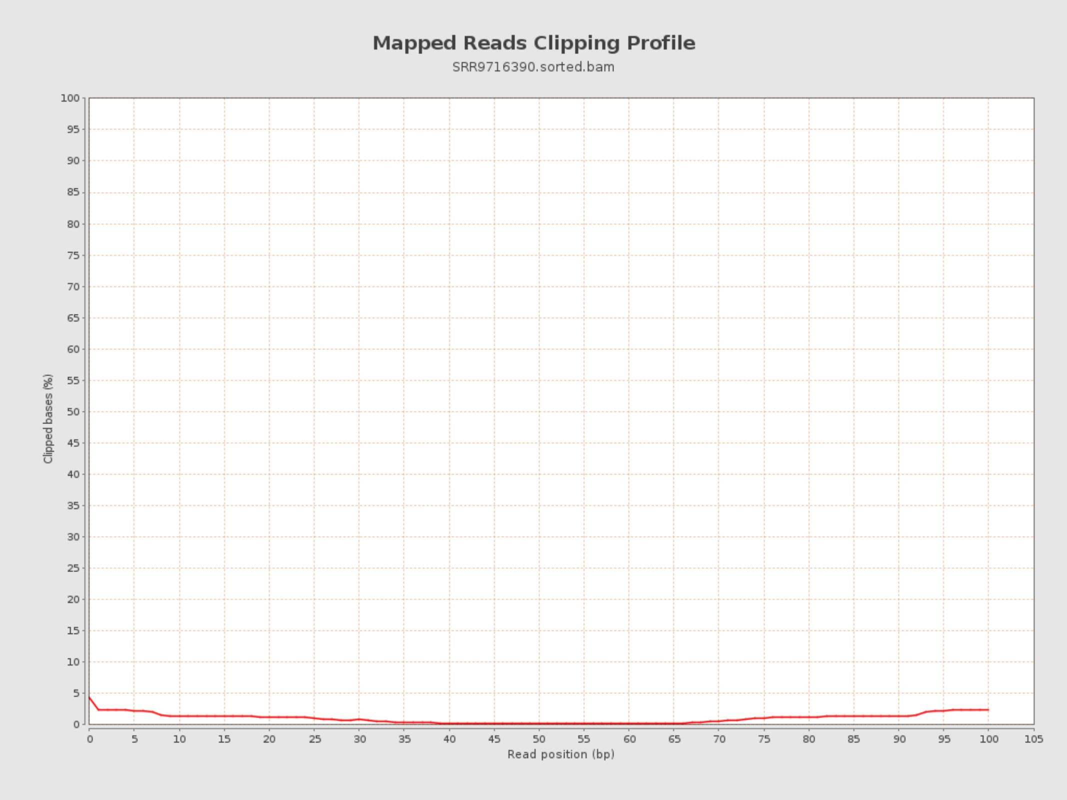
8. Results : Mapped Reads Nucleotide Content



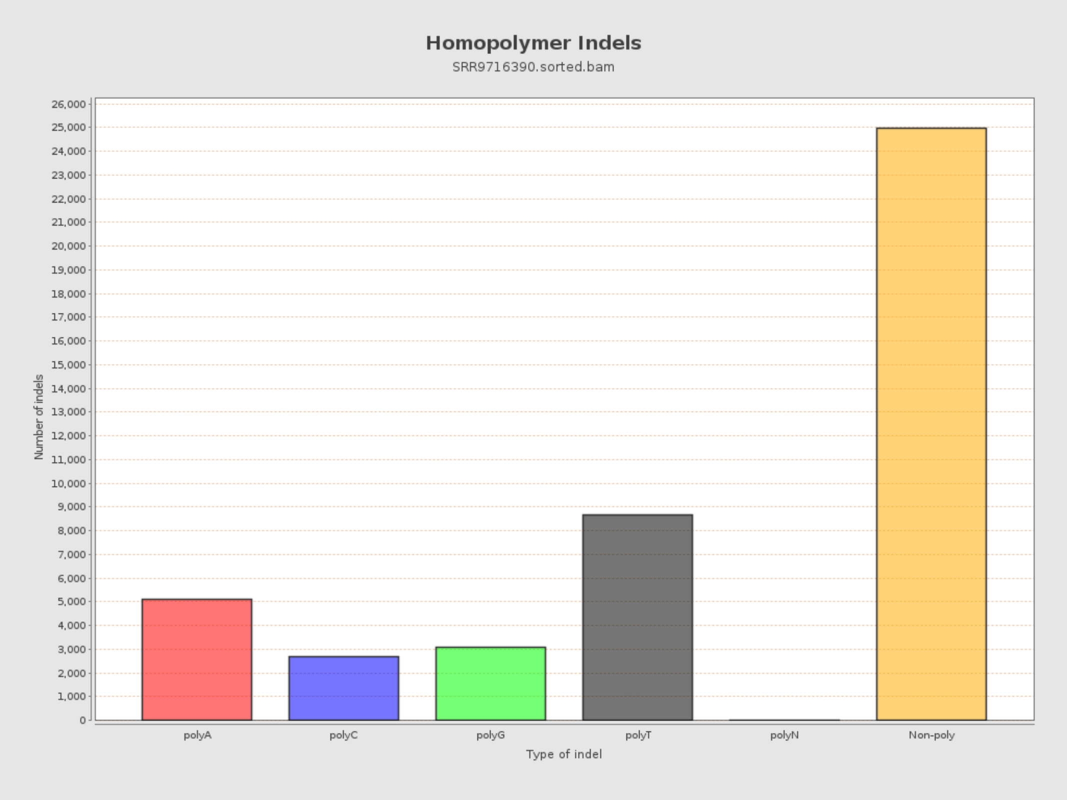
9. Results : Mapped Reads GC-content Distribution



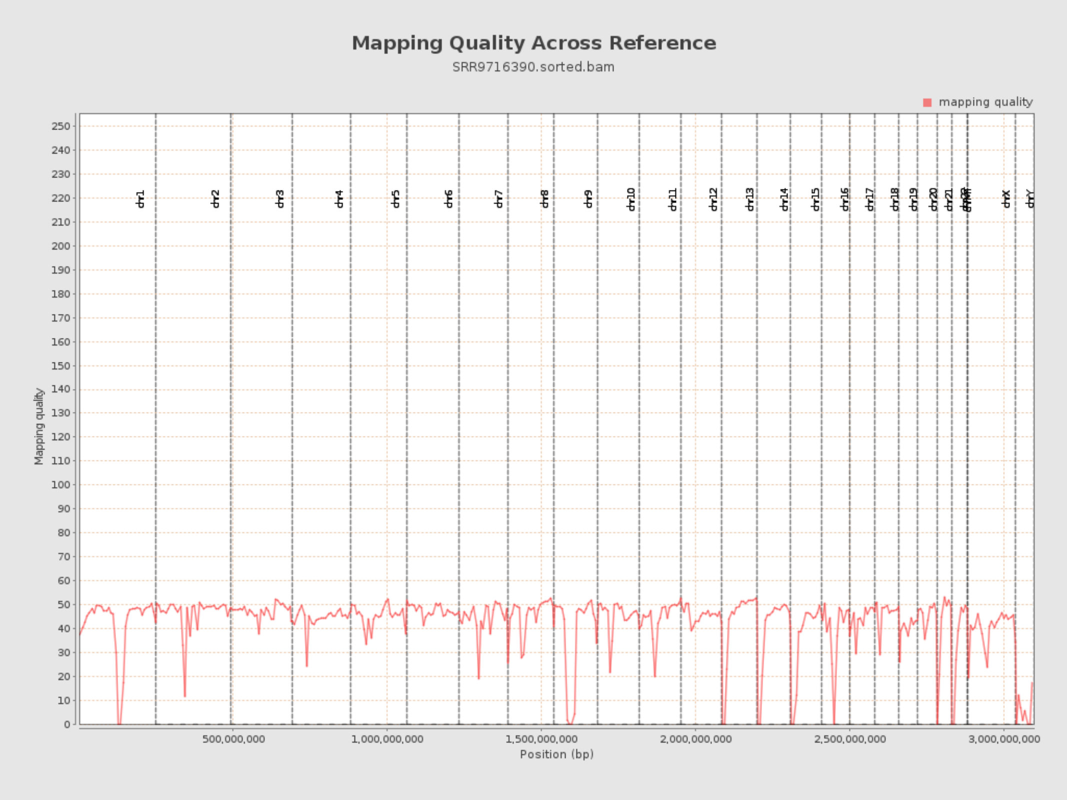
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram