Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 11:31:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716396.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_SRR9716396 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716396.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 11:31:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716396.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,989,213
Mapped reads	1,827,070 / 91.85%
Unmapped reads	162,143 / 8.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,747 / 1.39%
Read min/max/mean length	30 / 101 / 101.51
Duplicated reads (estimated)	87,336 / 4.39%
Duplication rate	3.08%
Clipped reads	1,852,604 / 93.13%

2.2. ACGT Content

Number/percentage of A's	35,866,931 / 24.92%
Number/percentage of C's	27,183,691 / 18.88%
Number/percentage of T's	45,651,059 / 31.71%
Number/percentage of G's	35,240,777 / 24.48%
Number/percentage of N's	8,021 / 0.01%
GC Percentage	43.37%

2.3. Coverage

Mean	0.0465

Standard Deviation	0.5002

2.4. Mapping Quality

Mean Mapping Quality	45.32

2.5. Mismatches and indels

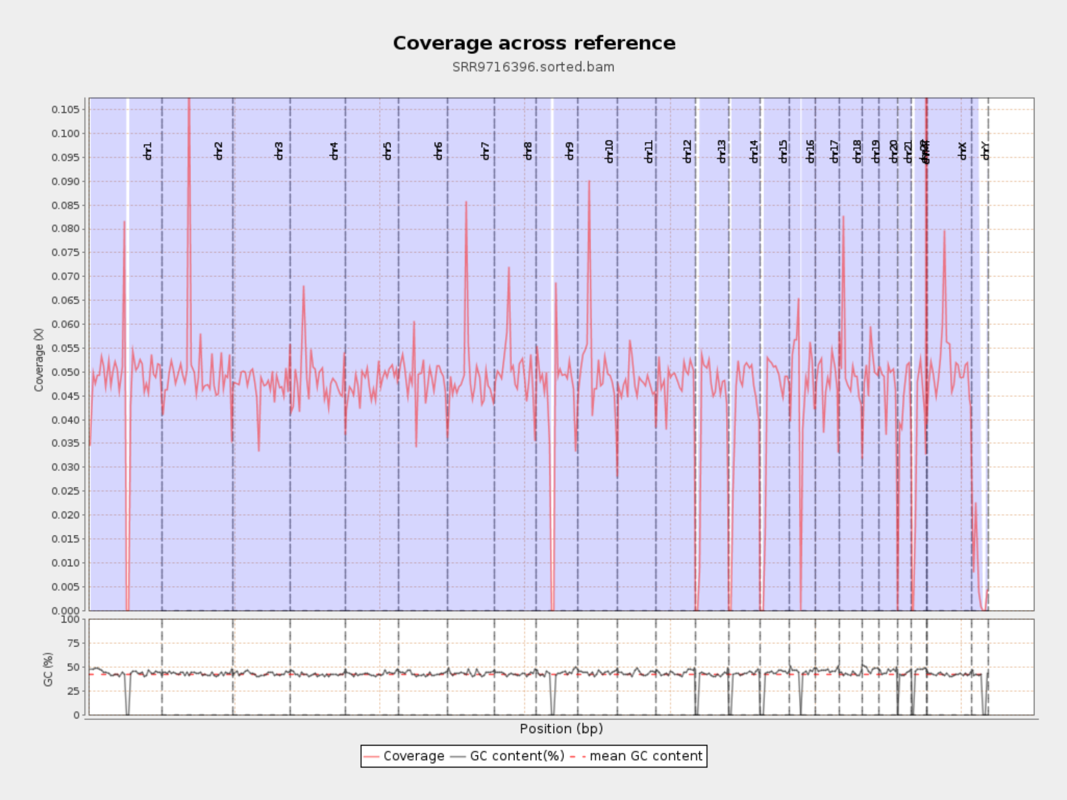
General error rate	0.86%
Mismatches	1,214,302
Insertions	13,198
Mapped reads with at least one insertion	0.71%
Deletions	37,010
Mapped reads with at least one deletion	1.99%
Homopolymer indels	43.99%

2.6. Chromosome stats

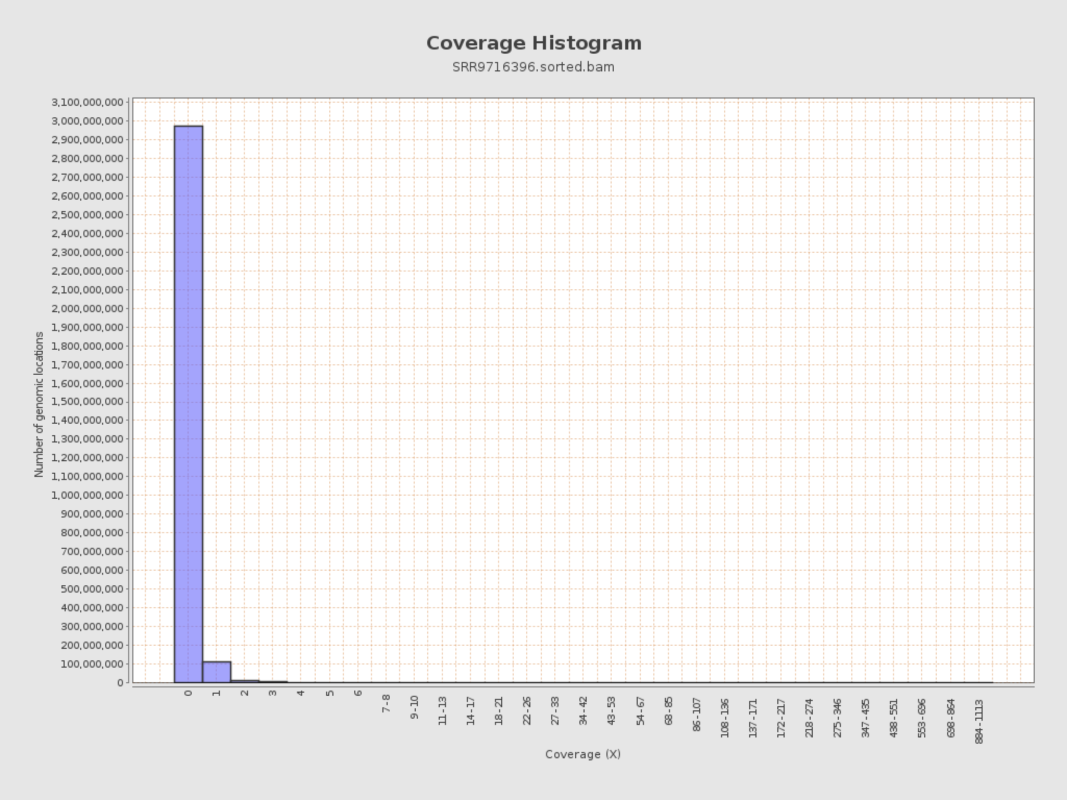
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11761906	0.0472	0.7858
chr2	243199373	12378471	0.0509	0.7668
chr3	198022430	9379015	0.0474	0.2515
chr4	191154276	9275443	0.0485	0.2864
chr5	180915260	8642742	0.0478	0.2555
chr6	171115067	8335626	0.0487	0.3095
chr7	159138663	7808924	0.0491	0.6105

chr8	146364022	7369691	0.0504	0.6806
chr9	141213431	6121575	0.0433	0.5644
chr10	135534747	6931058	0.0511	0.4805
chr11	135006516	6404383	0.0474	0.4831
chr12	133851895	6456183	0.0482	0.2578
chr13	115169878	4629312	0.0402	0.2275
chr14	107349540	4358384	0.0406	0.313
chr15	102531392	4129870	0.0403	0.2372
chr16	90354753	4208807	0.0466	0.2979
chr17	81195210	3854558	0.0475	0.2746
chr18	78077248	4050582	0.0519	1.0552
chr19	59128983	2960925	0.0501	0.5742
chr20	63025520	2970871	0.0471	0.2647
chr21	48129895	1930645	0.0401	0.2609
chr22	51304566	1662407	0.0324	0.2059
chrMT	16571	11530	0.6958	1.042
chrX	155270560	7986950	0.0514	0.3787
chrY	59373566	395518	0.0067	0.1924

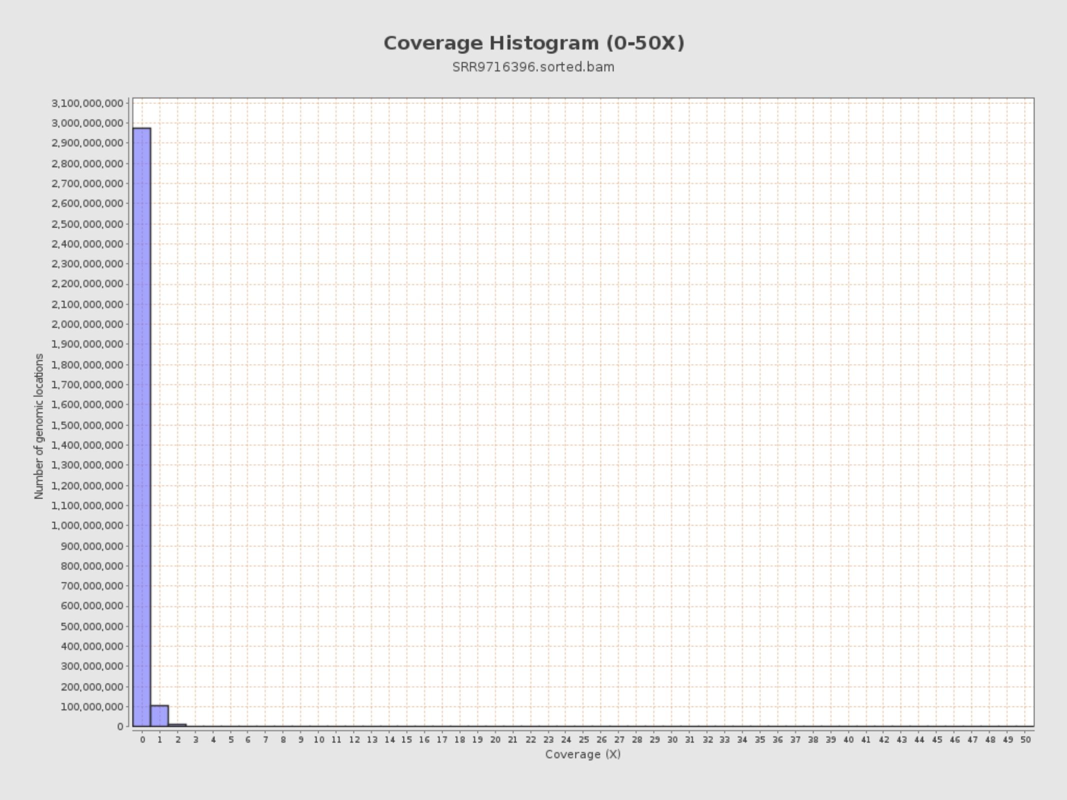
3. Results : Coverage across reference



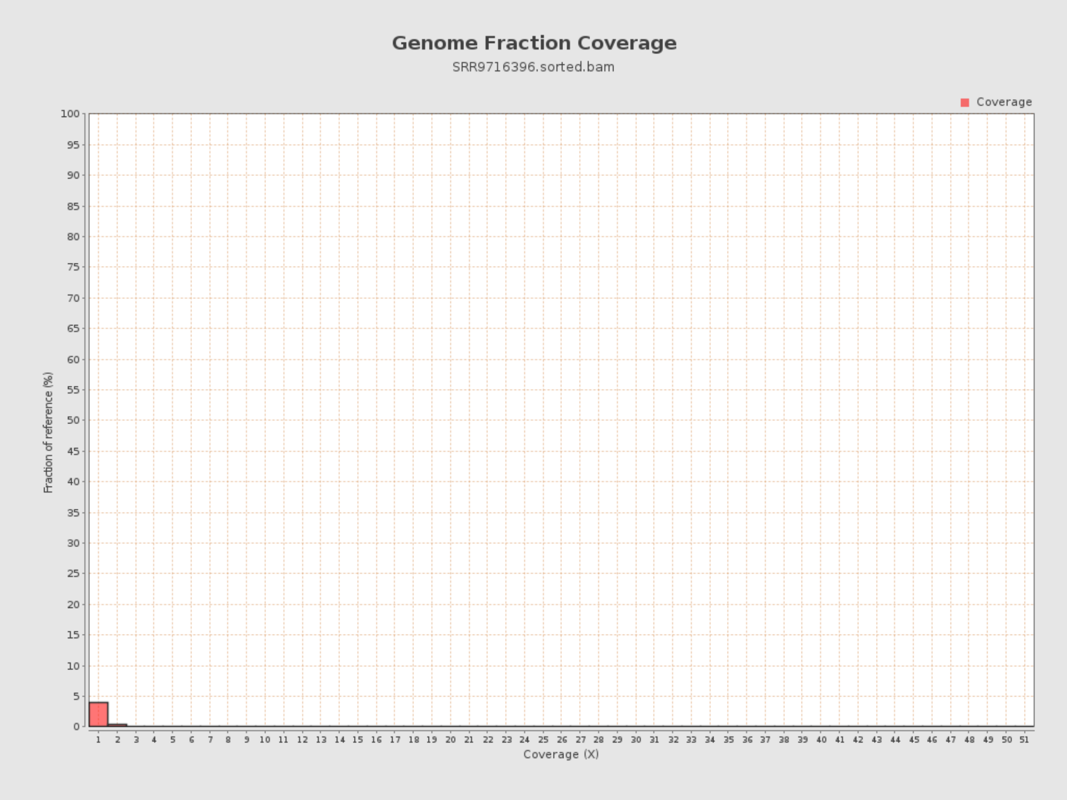
4. Results : Coverage Histogram



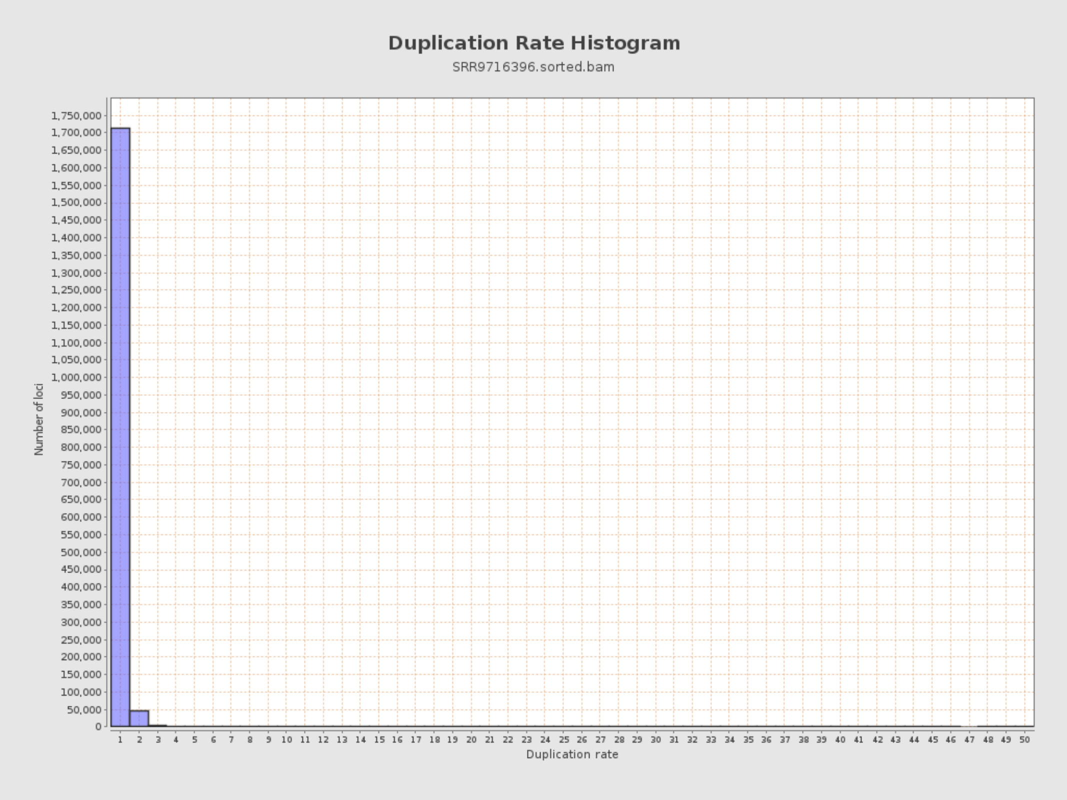
5. Results : Coverage Histogram (0-50X)



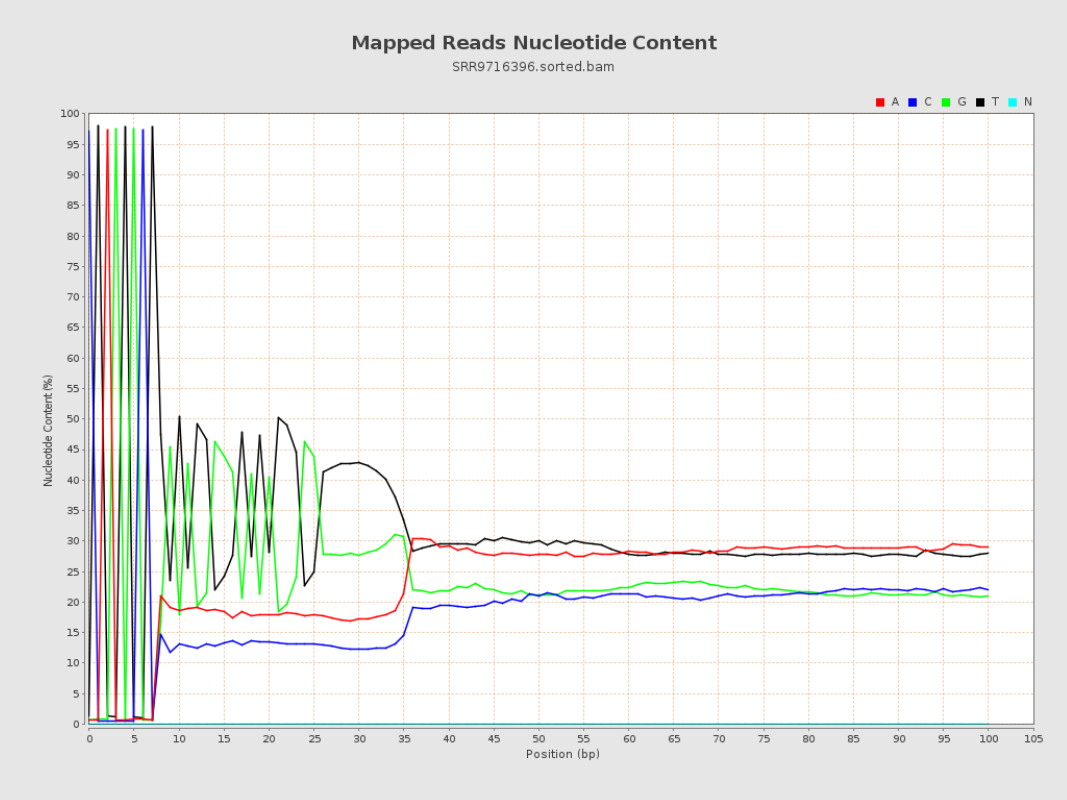
6. Results : Genome Fraction Coverage



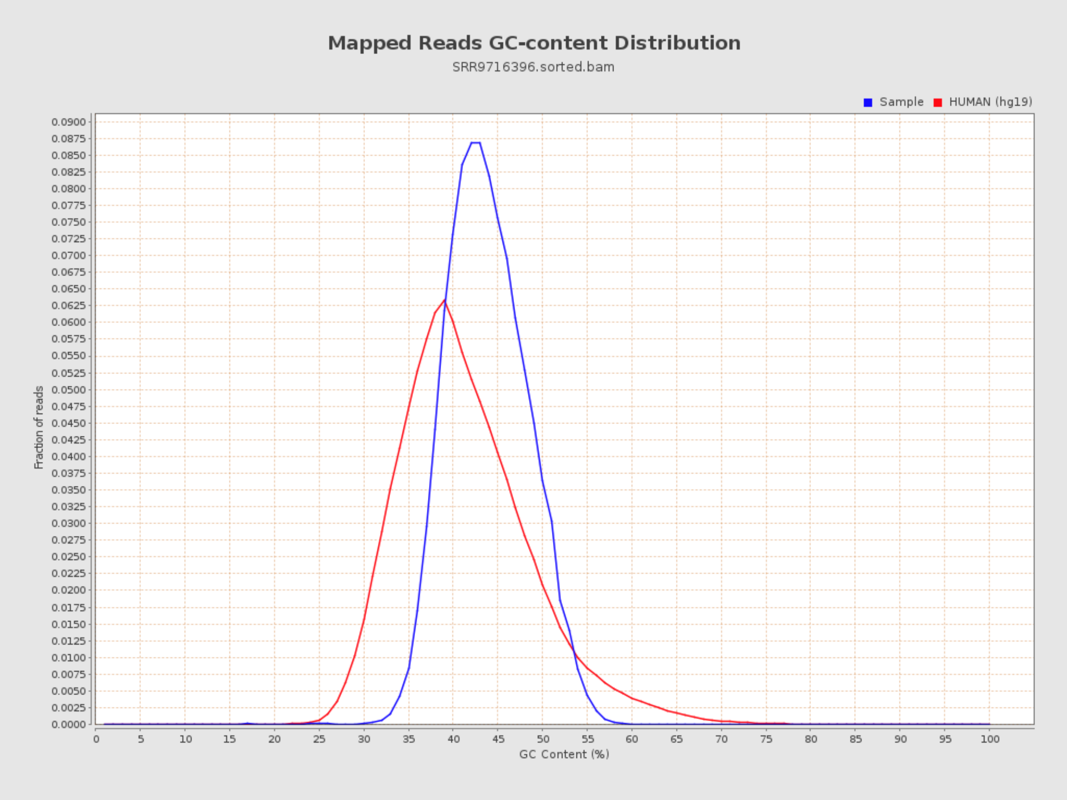
7. Results : Duplication Rate Histogram



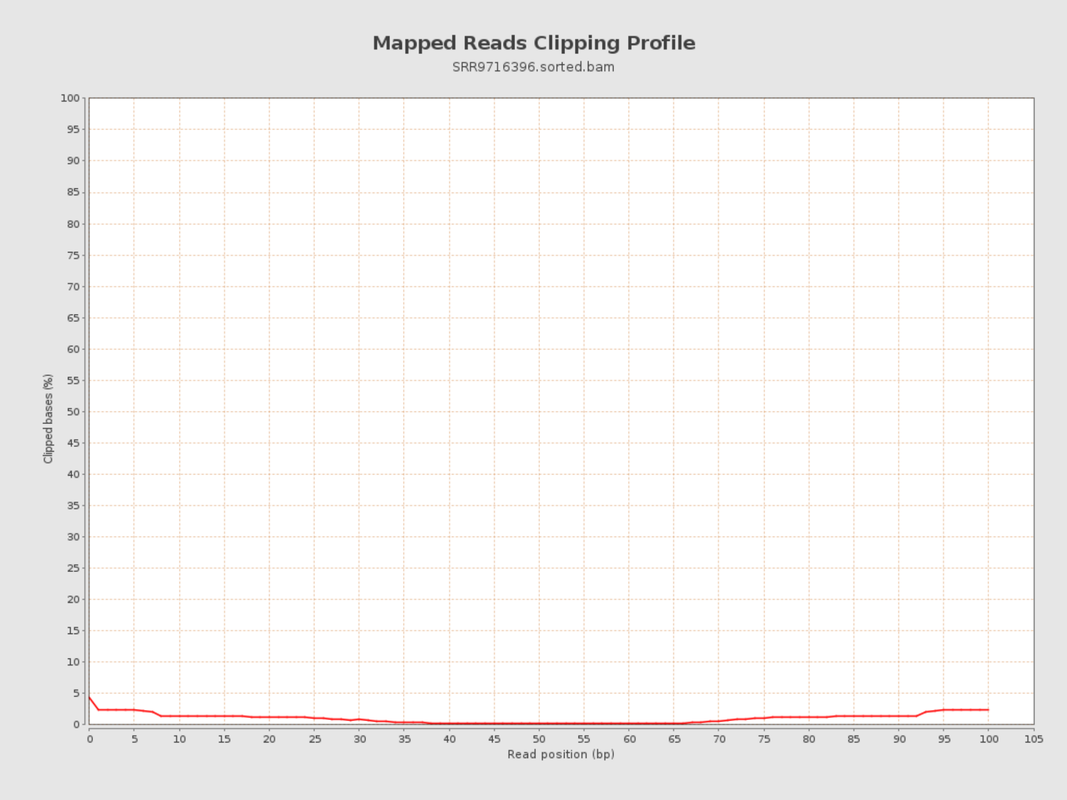
8. Results : Mapped Reads Nucleotide Content



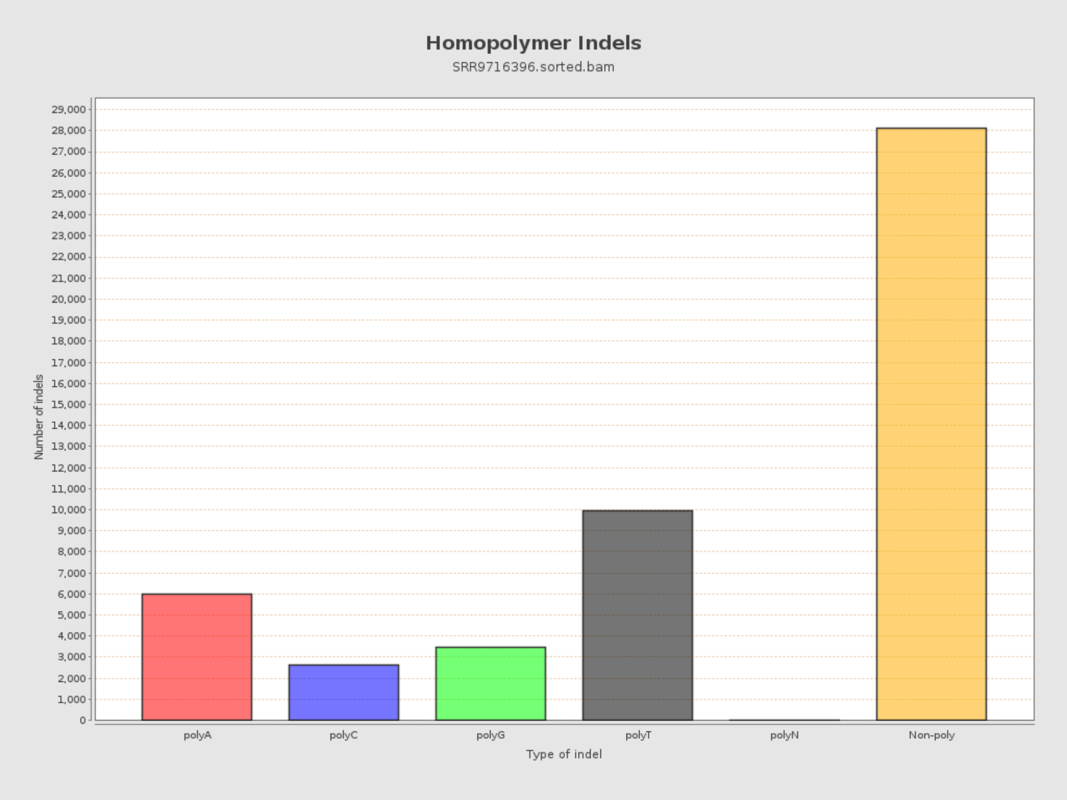
9. Results : Mapped Reads GC-content Distribution



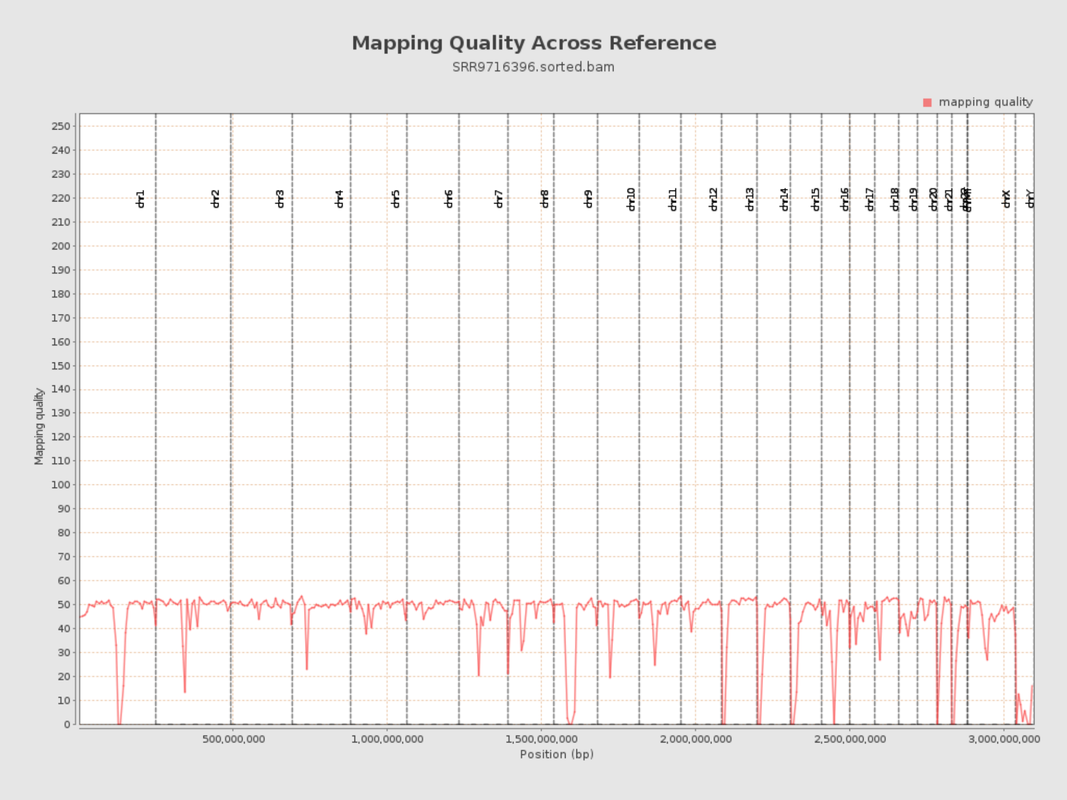
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram