Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 17:49:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716897.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_SRR9716897 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716897.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 17:49:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716897.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,996,505
Mapped reads	3,692,397 / 92.39%
Unmapped reads	304,108 / 7.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	76,754 / 1.92%
Read min/max/mean length	30 / 101 / 101.69
Duplicated reads (estimated)	194,919 / 4.88%
Duplication rate	3.81%
Clipped reads	3,765,316 / 94.22%

2.2. ACGT Content

Number/percentage of A's	71,922,390 / 25.8%
Number/percentage of C's	57,307,749 / 20.56%
Number/percentage of T's	83,415,198 / 29.92%
Number/percentage of G's	66,094,420 / 23.71%
Number/percentage of N's	34,137 / 0.01%
GC Percentage	44.27%

2.3. Coverage

Mean	0.0901

Standard Deviation	0.6322

2.4. Mapping Quality

Mean Mapping Quality	46.42

2.5. Mismatches and indels

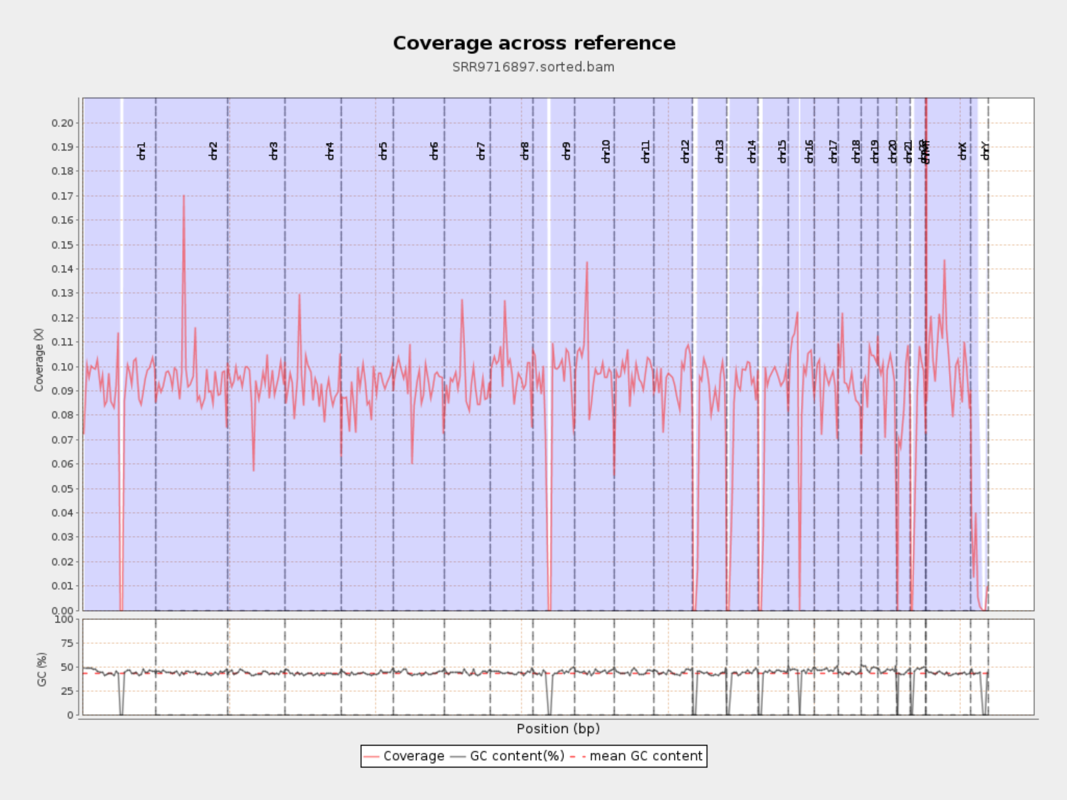
General error rate	0.74%
Mismatches	2,025,417
Insertions	21,954
Mapped reads with at least one insertion	0.59%
Deletions	58,284
Mapped reads with at least one deletion	1.56%
Homopolymer indels	40.06%

2.6. Chromosome stats

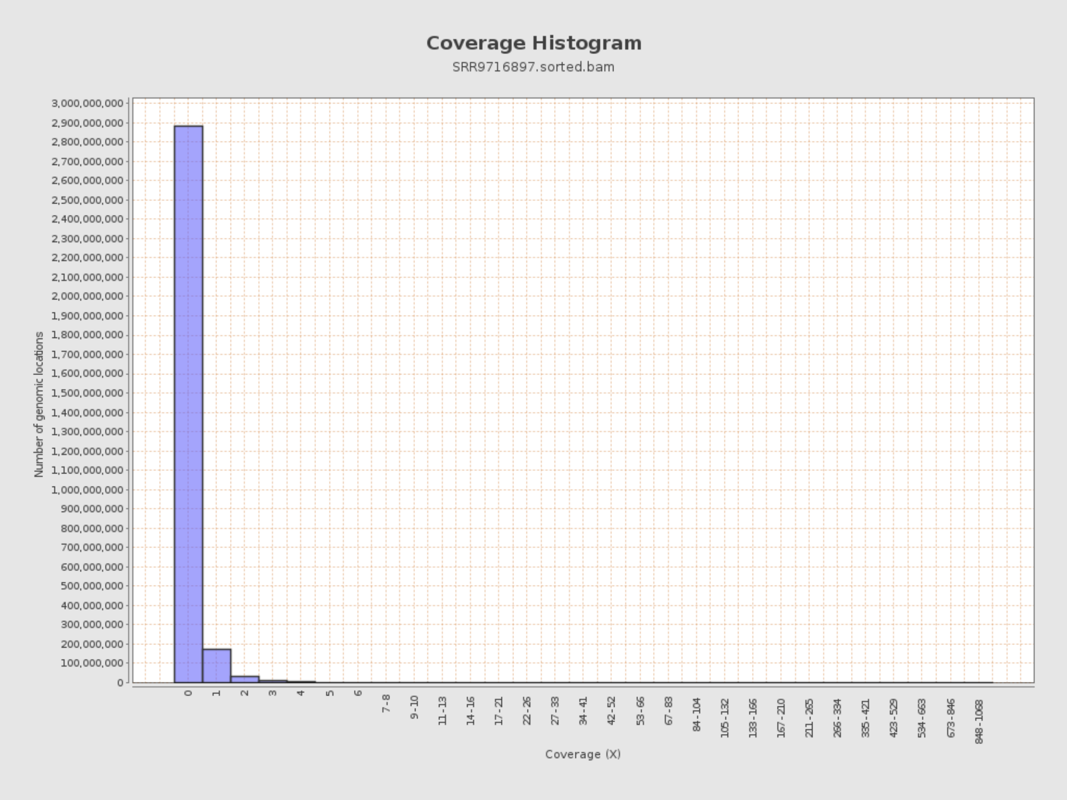
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22110696	0.0887	0.7692
chr2	243199373	23232938	0.0955	0.9346
chr3	198022430	18501088	0.0934	0.382
chr4	191154276	17752229	0.0929	0.447
chr5	180915260	16337794	0.0903	0.3865
chr6	171115067	15955850	0.0932	0.4541
chr7	159138663	14817288	0.0931	0.7814

chr8	146364022	14378978	0.0982	0.8267
chr9	141213431	12131354	0.0859	0.6857
chr10	135534747	13503419	0.0996	0.6584
chr11	135006516	12965734	0.096	0.7078
chr12	133851895	12705958	0.0949	0.3984
chr13	115169878	8905895	0.0773	0.3485
chr14	107349540	8493150	0.0791	0.4593
chr15	102531392	7956306	0.0776	0.3523
chr16	90354753	8424903	0.0932	0.4575
chr17	81195210	7546713	0.0929	0.4423
chr18	78077248	7436543	0.0952	1.3538
chr19	59128983	5766242	0.0975	0.7182
chr20	63025520	5916820	0.0939	0.413
chr21	48129895	3742839	0.0778	0.4018
chr22	51304566	3497600	0.0682	0.3324
chrMT	16571	34048	2.0547	2.186
chrX	155270560	16026648	0.1032	0.5561
chrY	59373566	733592	0.0124	0.3197

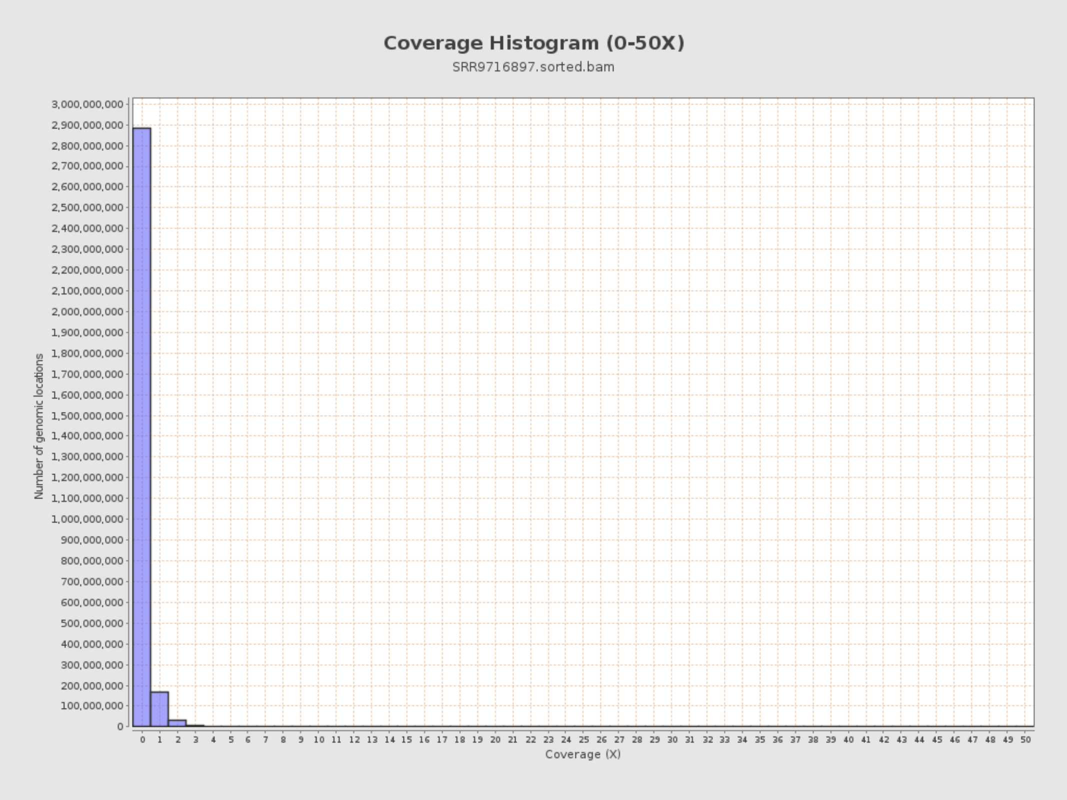
3. Results : Coverage across reference



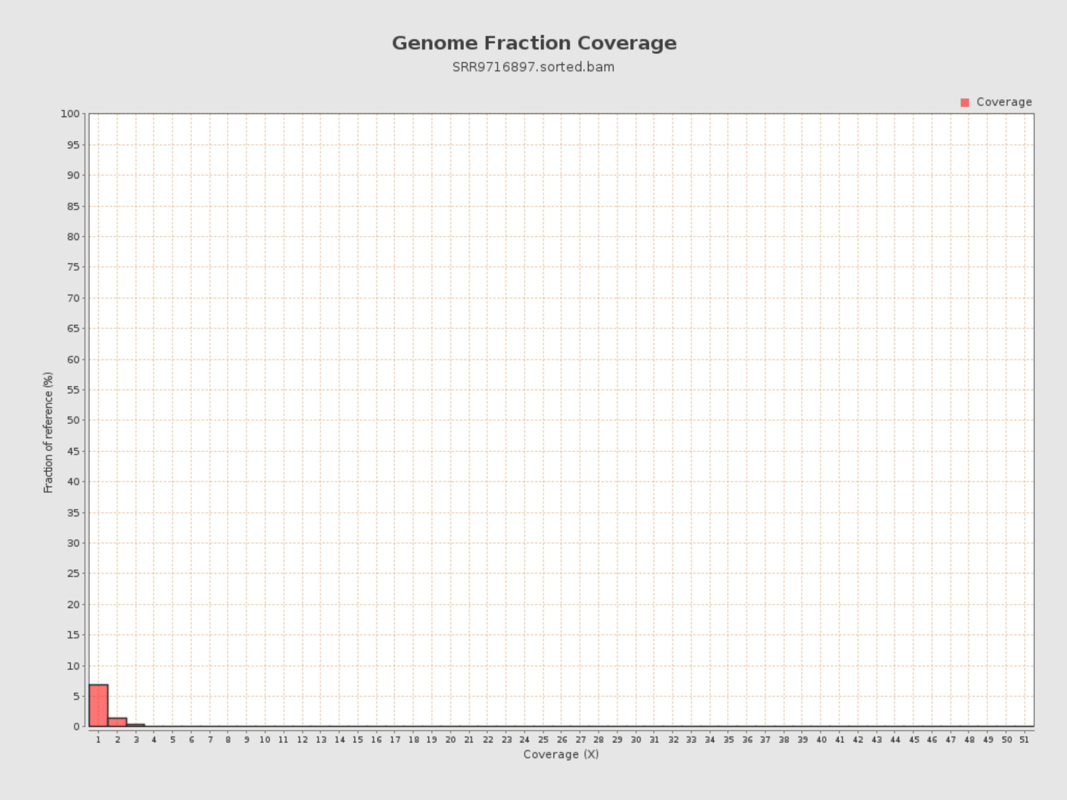
4. Results : Coverage Histogram



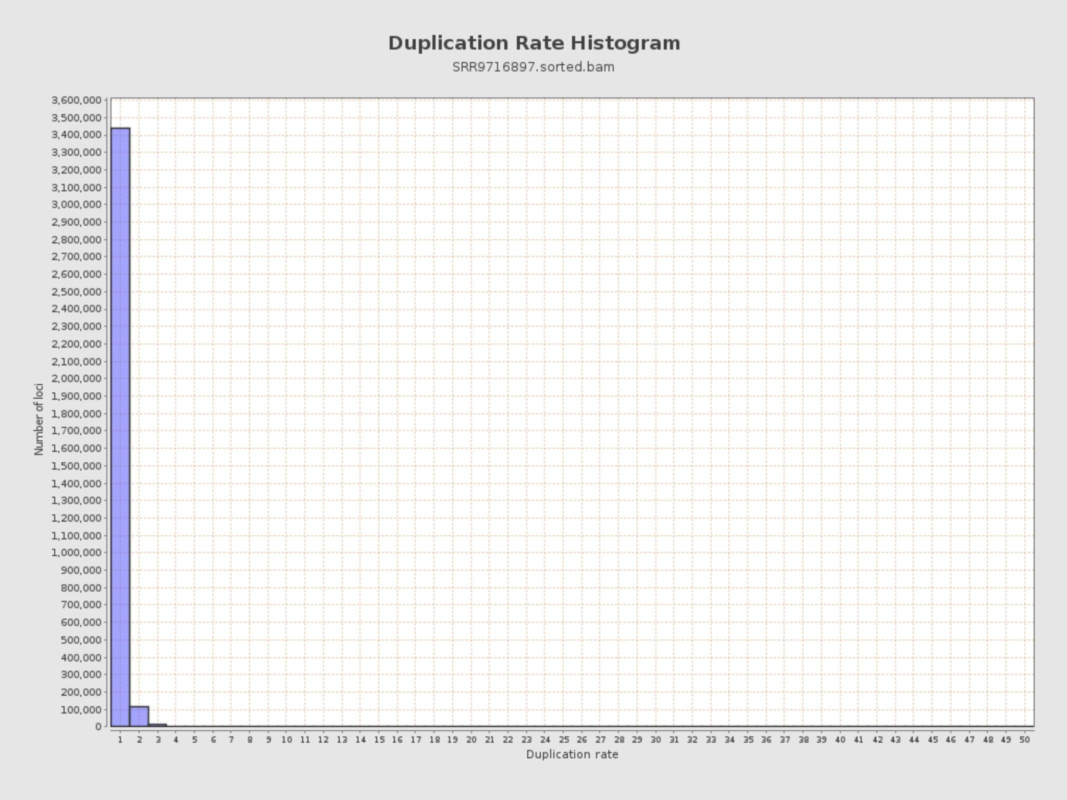
5. Results : Coverage Histogram (0-50X)



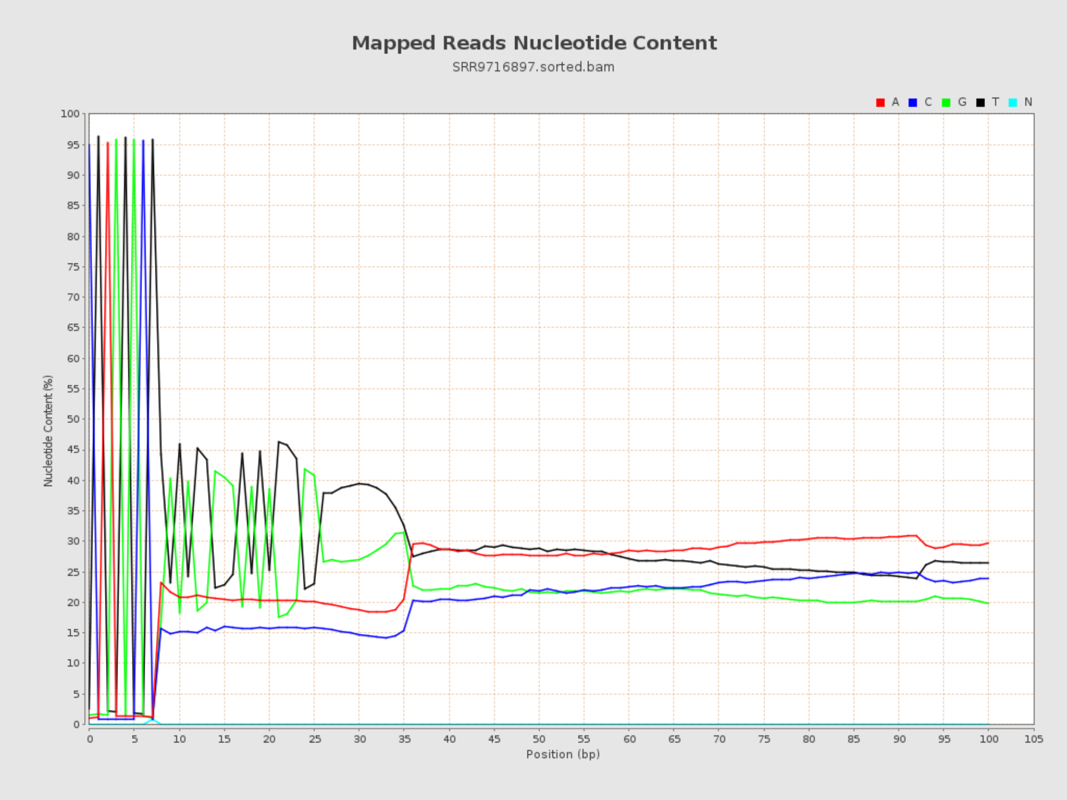
6. Results : Genome Fraction Coverage



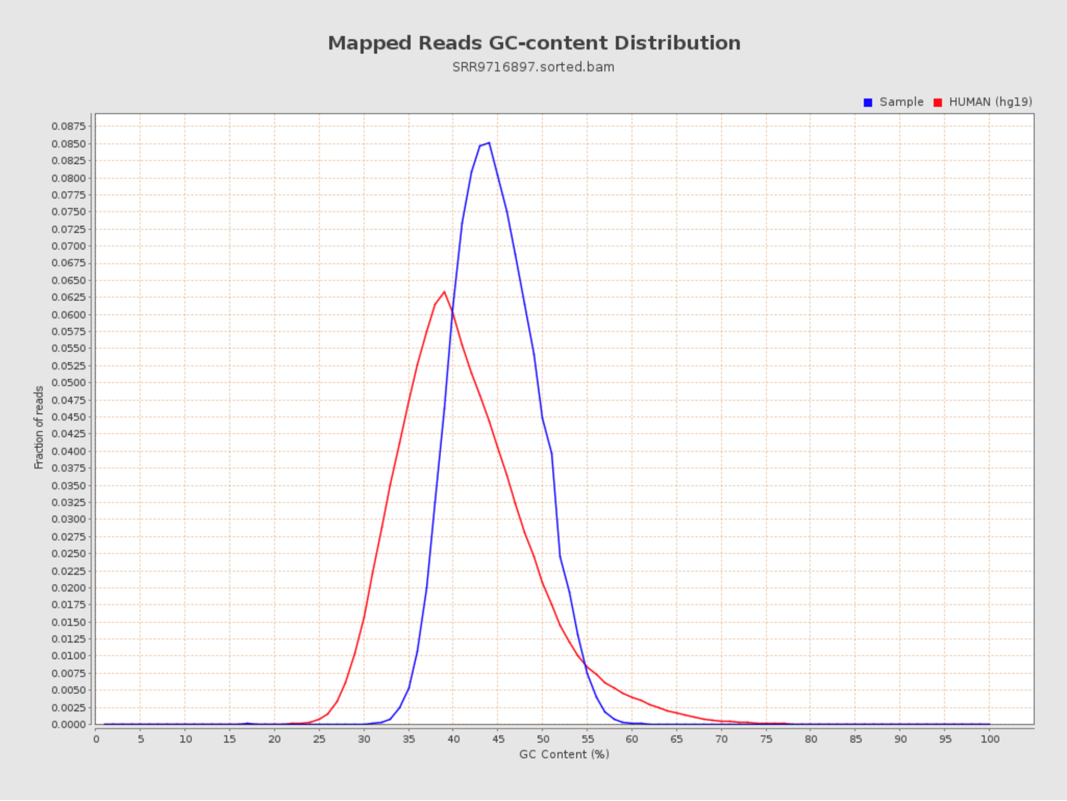
7. Results : Duplication Rate Histogram



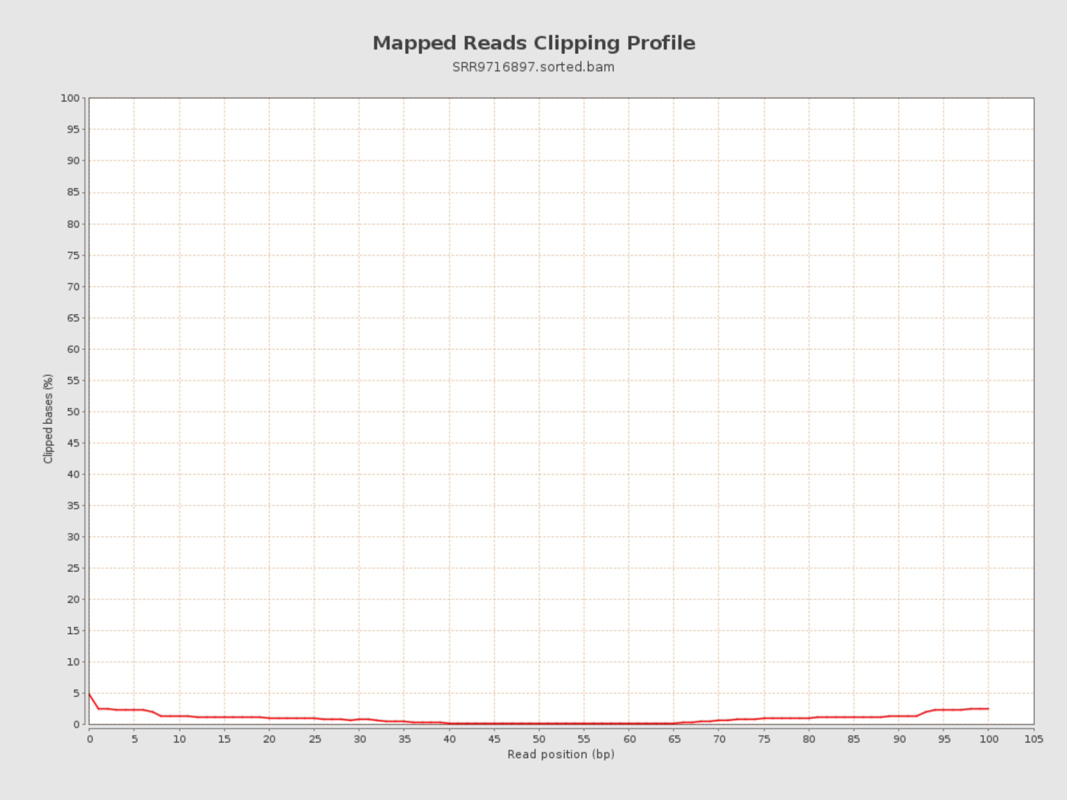
8. Results : Mapped Reads Nucleotide Content



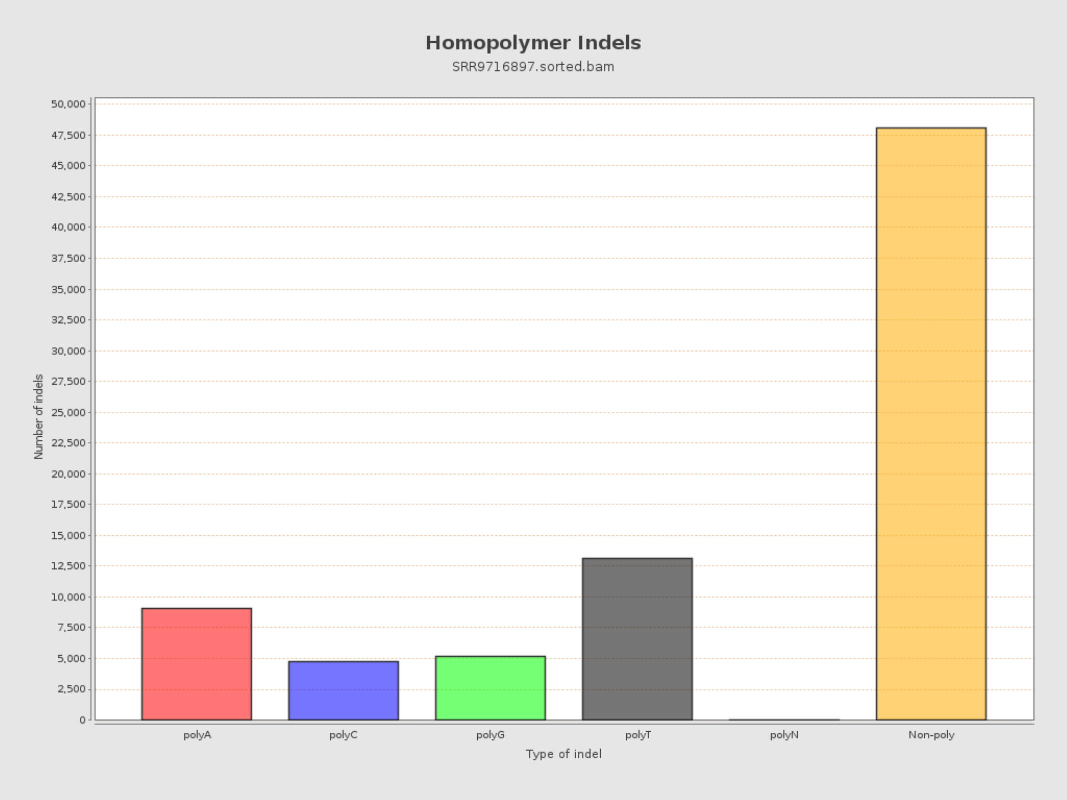
9. Results : Mapped Reads GC-content Distribution



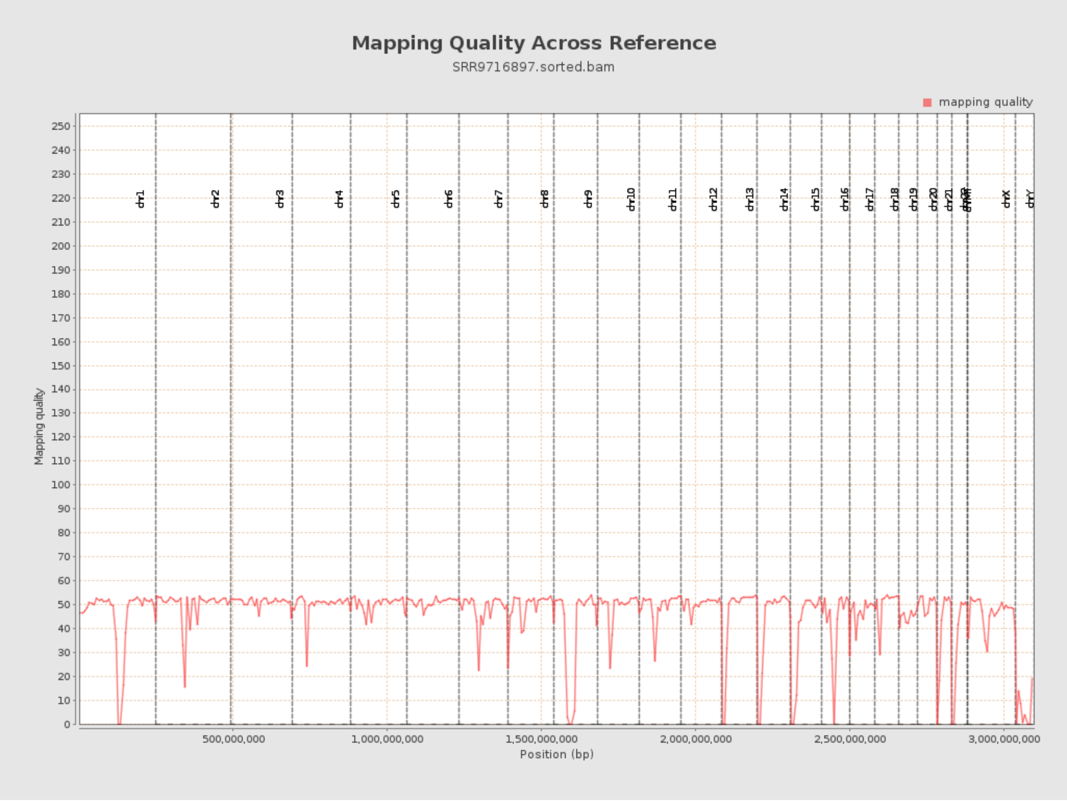
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram