Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 19:33:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716539.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_SRR9716539 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716539.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 19:33:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716539.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,763,574
Mapped reads	1,684,174 / 95.5%
Unmapped reads	79,400 / 4.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,964 / 1.98%
Read min/max/mean length	30 / 101 / 101.72
Duplicated reads (estimated)	95,595 / 5.42%
Duplication rate	4.36%
Clipped reads	1,717,409 / 97.38%

2.2. ACGT Content

Number/percentage of A's	32,788,539 / 24.63%
Number/percentage of C's	27,194,189 / 20.43%
Number/percentage of T's	38,524,101 / 28.94%
Number/percentage of G's	34,618,669 / 26%
Number/percentage of N's	5,148 / 0%
GC Percentage	46.43%

2.3. Coverage

Mean	0.043

Standard Deviation	0.3769

2.4. Mapping Quality

Mean Mapping Quality	47.27

2.5. Mismatches and indels

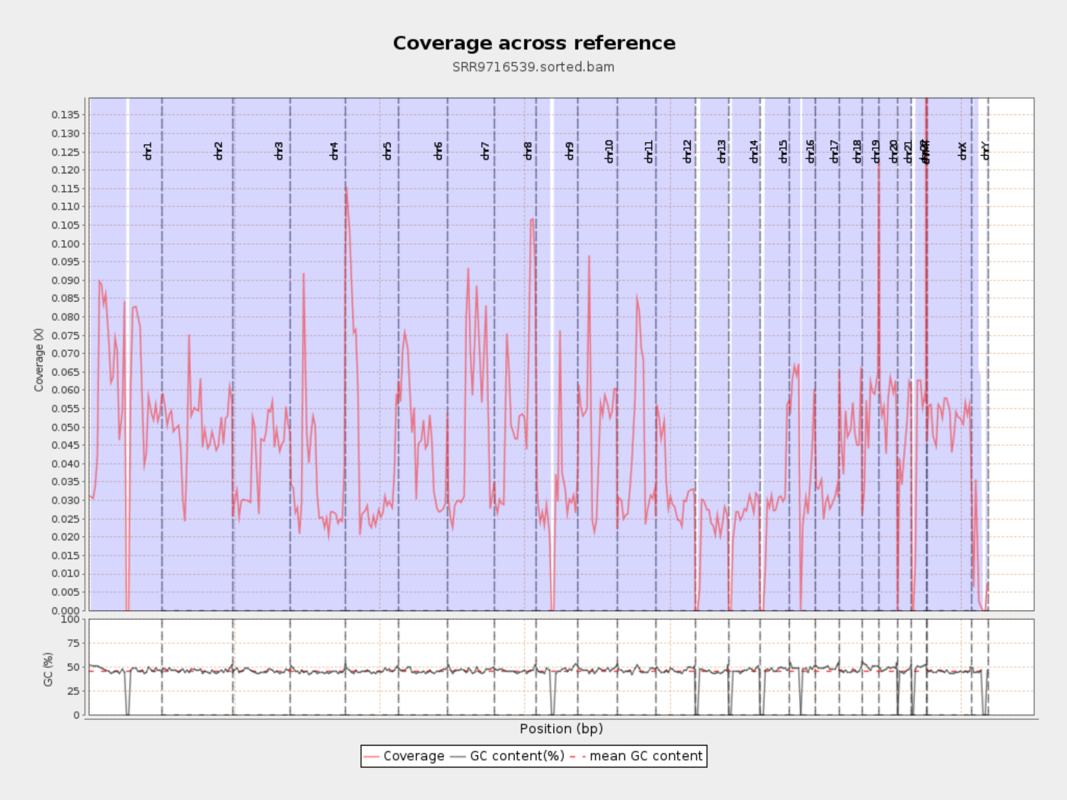
General error rate	0.67%
Mismatches	870,552
Insertions	10,490
Mapped reads with at least one insertion	0.61%
Deletions	24,648
Mapped reads with at least one deletion	1.43%
Homopolymer indels	40.3%

2.6. Chromosome stats

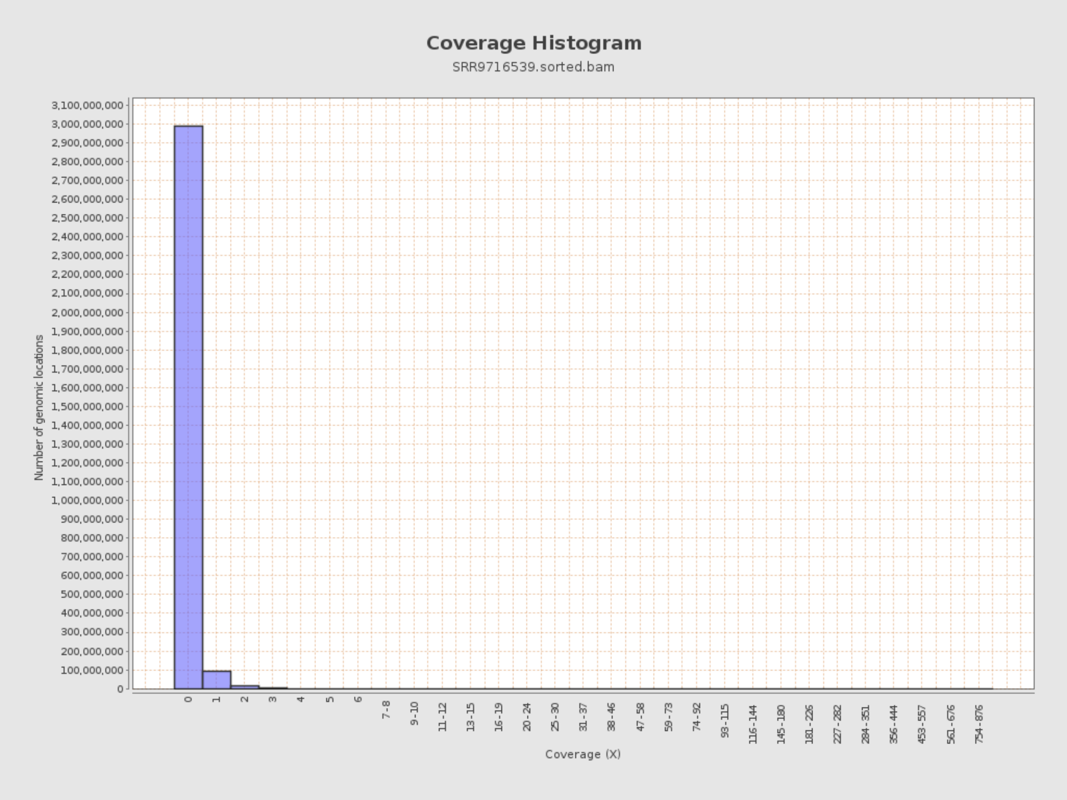
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14534524	0.0583	0.7591
chr2	243199373	12183407	0.0501	0.3787
chr3	198022430	8257635	0.0417	0.2416
chr4	191154276	6470311	0.0338	0.3276
chr5	180915260	8036316	0.0444	0.2539
chr6	171115067	8039678	0.047	0.2693
chr7	159138663	8307732	0.0522	0.4753

chr8	146364022	8124557	0.0555	0.39
chr9	141213431	4024211	0.0285	0.2647
chr10	135534747	7042136	0.052	0.4666
chr11	135006516	5668017	0.042	0.3356
chr12	133851895	4611682	0.0345	0.2186
chr13	115169878	2479774	0.0215	0.1714
chr14	107349540	2571044	0.024	0.2006
chr15	102531392	2753851	0.0269	0.1906
chr16	90354753	3996723	0.0442	0.2666
chr17	81195210	2514018	0.031	0.233
chr18	78077248	3878106	0.0497	0.4364
chr19	59128983	3277197	0.0554	0.5317
chr20	63025520	3561763	0.0565	0.298
chr21	48129895	2081945	0.0433	0.2992
chr22	51304566	2067520	0.0403	0.2467
chrMT	16571	29501	1.7803	1.9327
chrX	155270560	8162514	0.0526	0.2856
chrY	59373566	508294	0.0086	0.3149

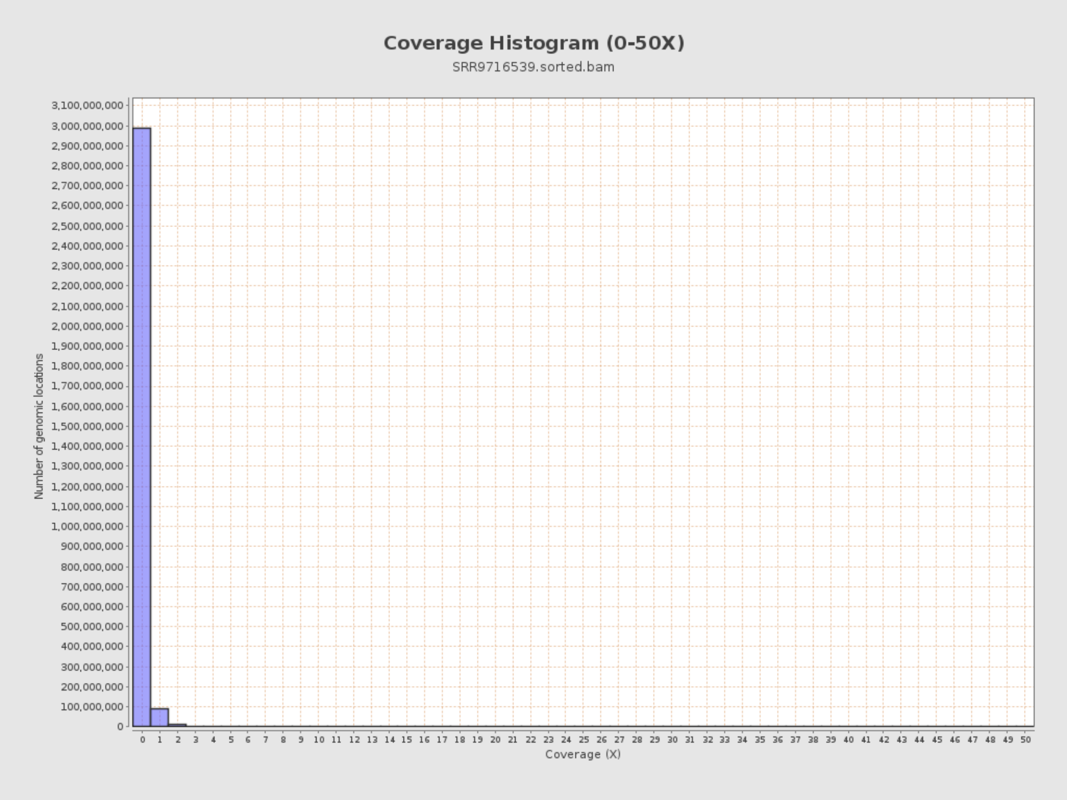
3. Results : Coverage across reference



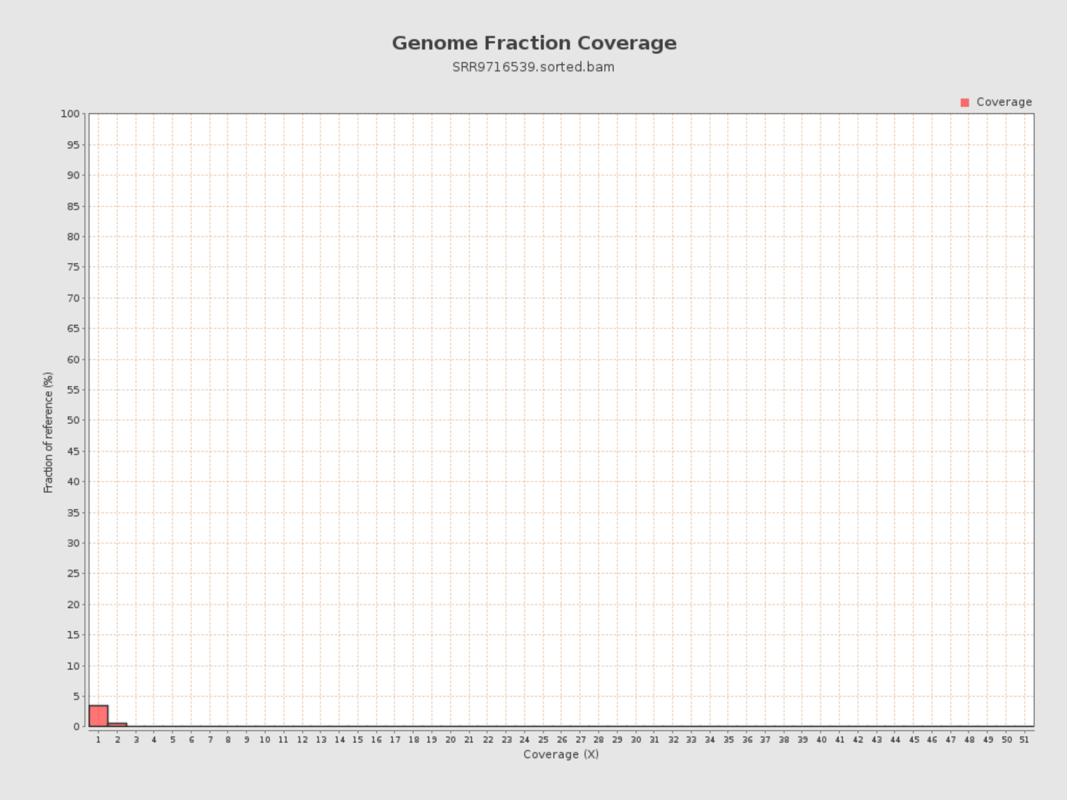
4. Results : Coverage Histogram



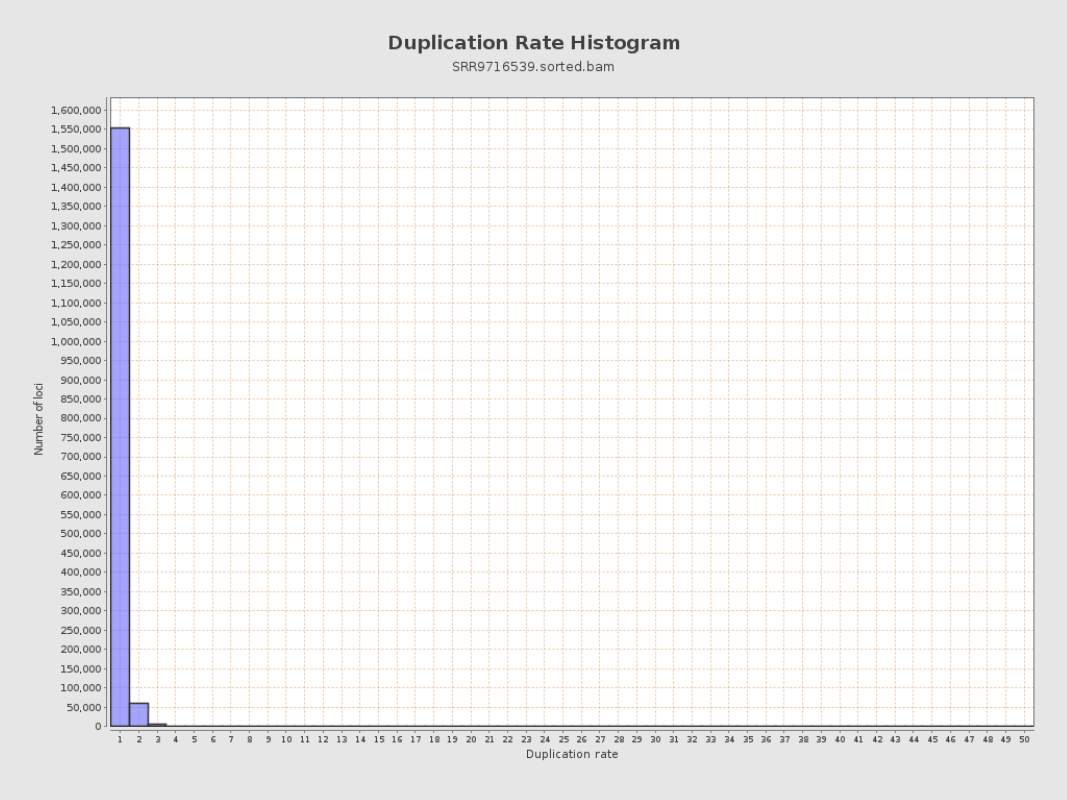
5. Results : Coverage Histogram (0-50X)



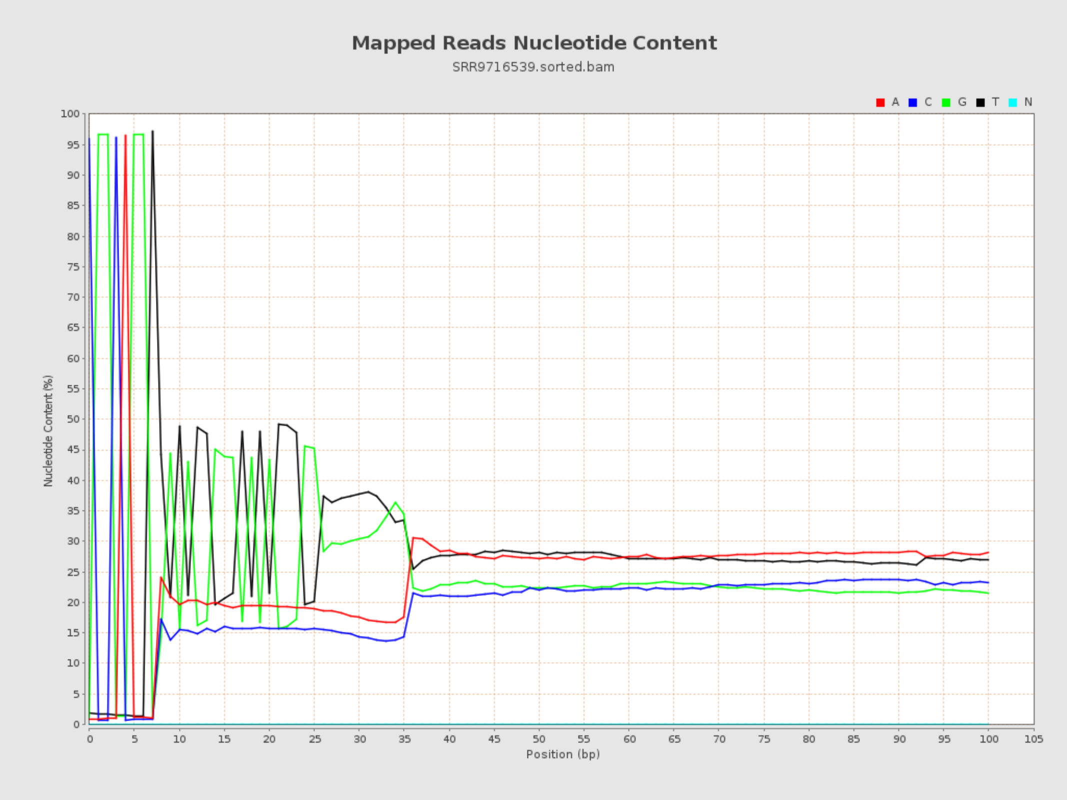
6. Results : Genome Fraction Coverage



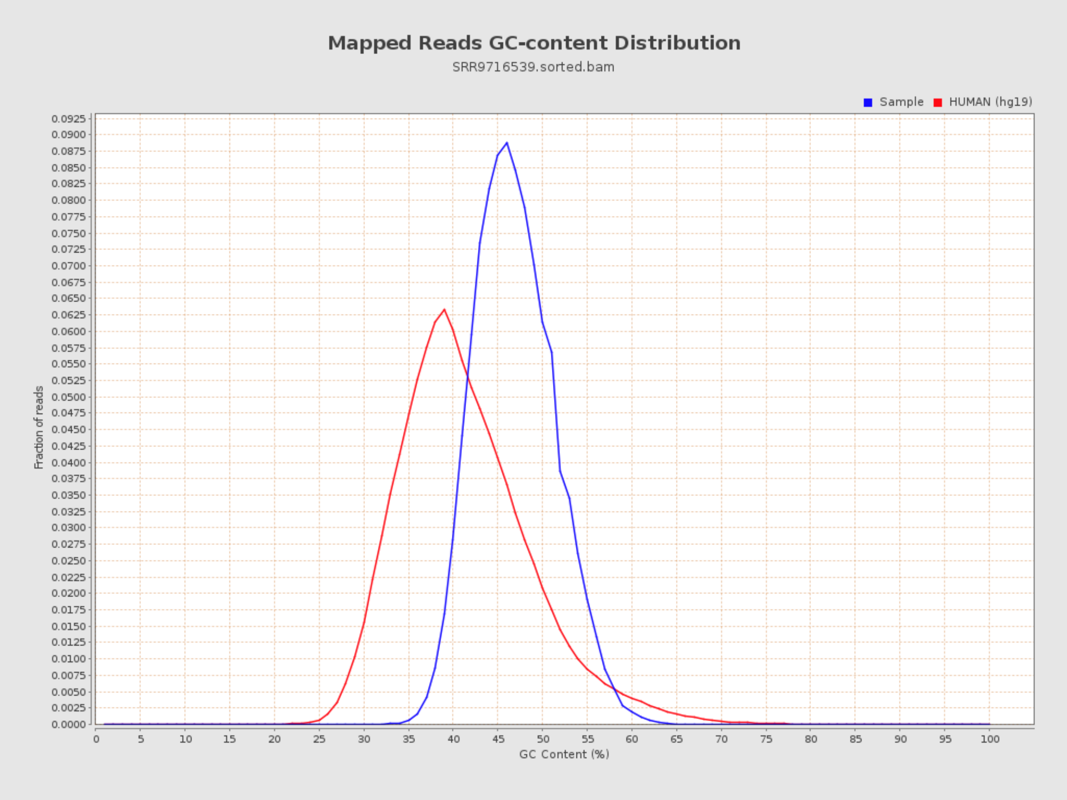
7. Results : Duplication Rate Histogram



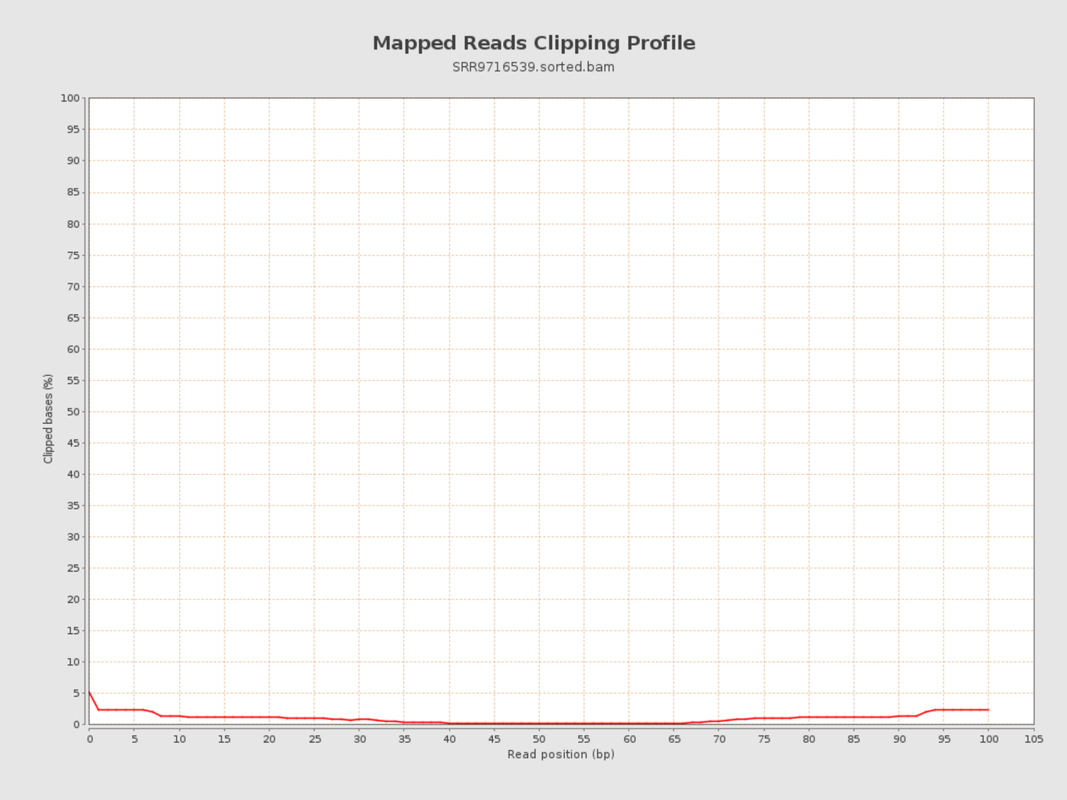
8. Results : Mapped Reads Nucleotide Content



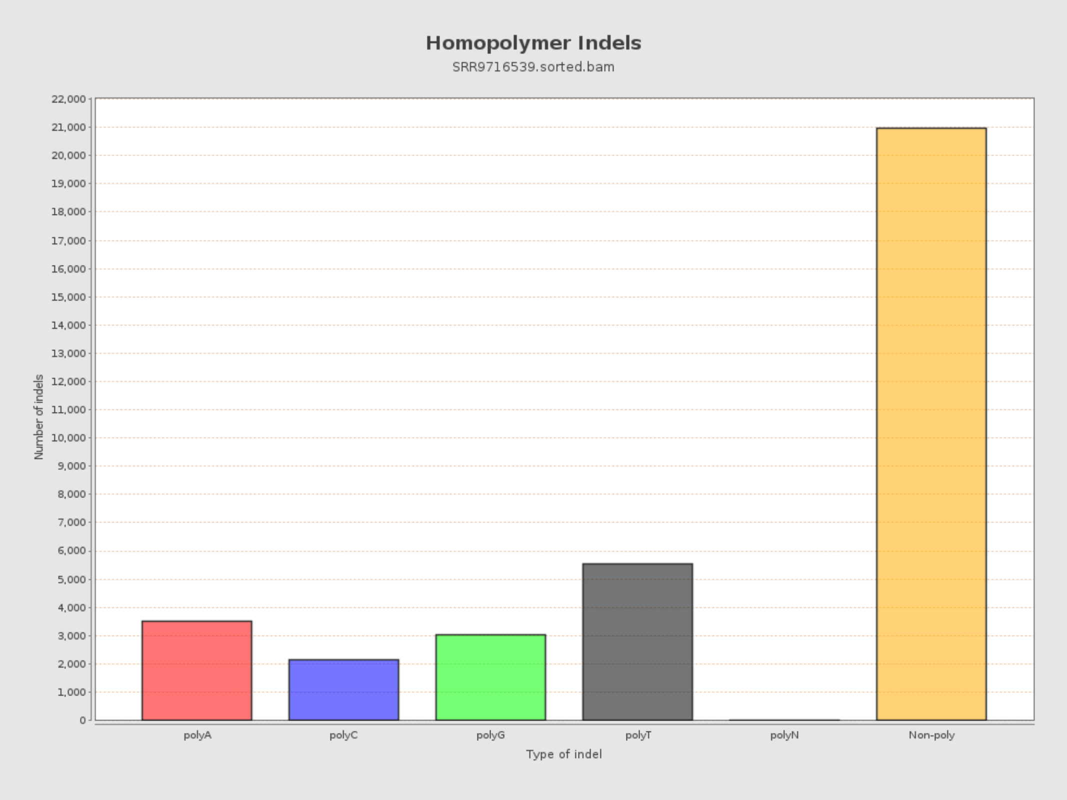
9. Results : Mapped Reads GC-content Distribution



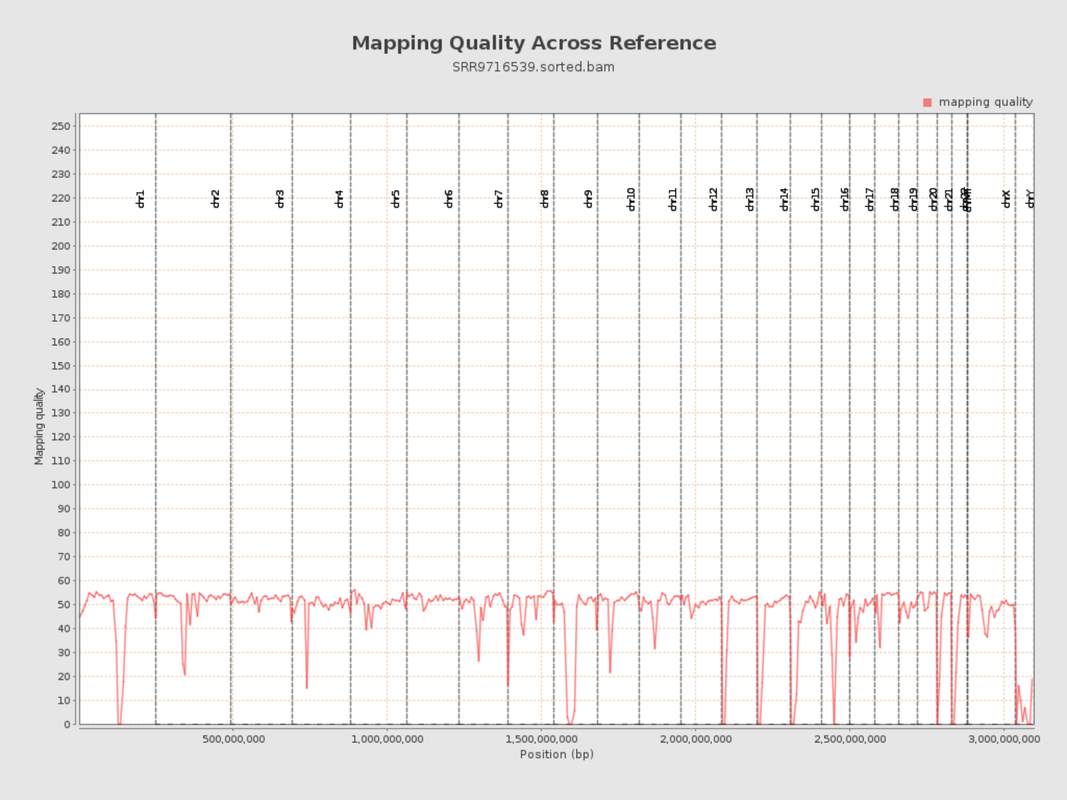
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram