Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 17:05:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716497.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_SRR9716497 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716497.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 17:05:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716497.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,261,388
Mapped reads	1,149,845 / 91.16%
Unmapped reads	111,543 / 8.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,606 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	49,183 / 3.9%
Duplication rate	3.3%
Clipped reads	1,151,910 / 91.32%

2.2. ACGT Content

Number/percentage of A's	17,823,573 / 26.57%
Number/percentage of C's	12,587,799 / 18.76%
Number/percentage of T's	20,434,007 / 30.46%
Number/percentage of G's	16,234,610 / 24.2%
Number/percentage of N's	1,701 / 0%
GC Percentage	42.97%

2.3. Coverage

Mean	0.0217

Standard Deviation	0.2418

2.4. Mapping Quality

Mean Mapping Quality	45.04

2.5. Mismatches and indels

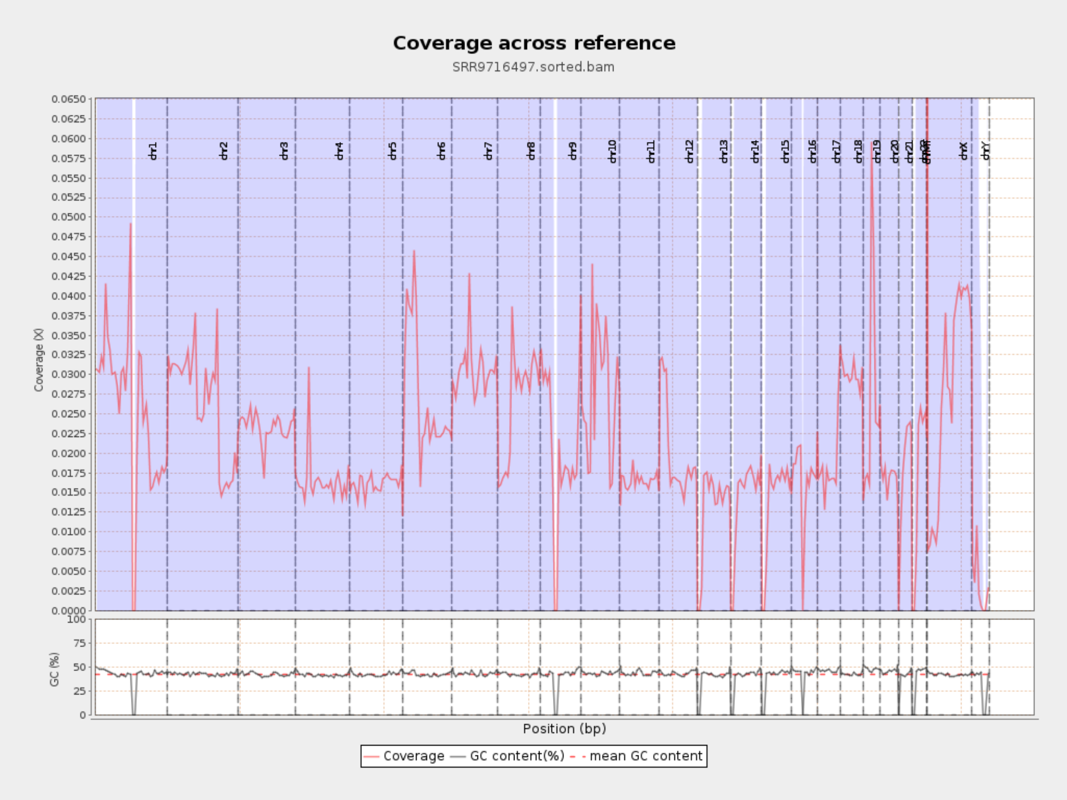
General error rate	0.52%
Mismatches	336,783
Insertions	5,615
Mapped reads with at least one insertion	0.49%
Deletions	12,352
Mapped reads with at least one deletion	1.07%
Homopolymer indels	41.34%

2.6. Chromosome stats

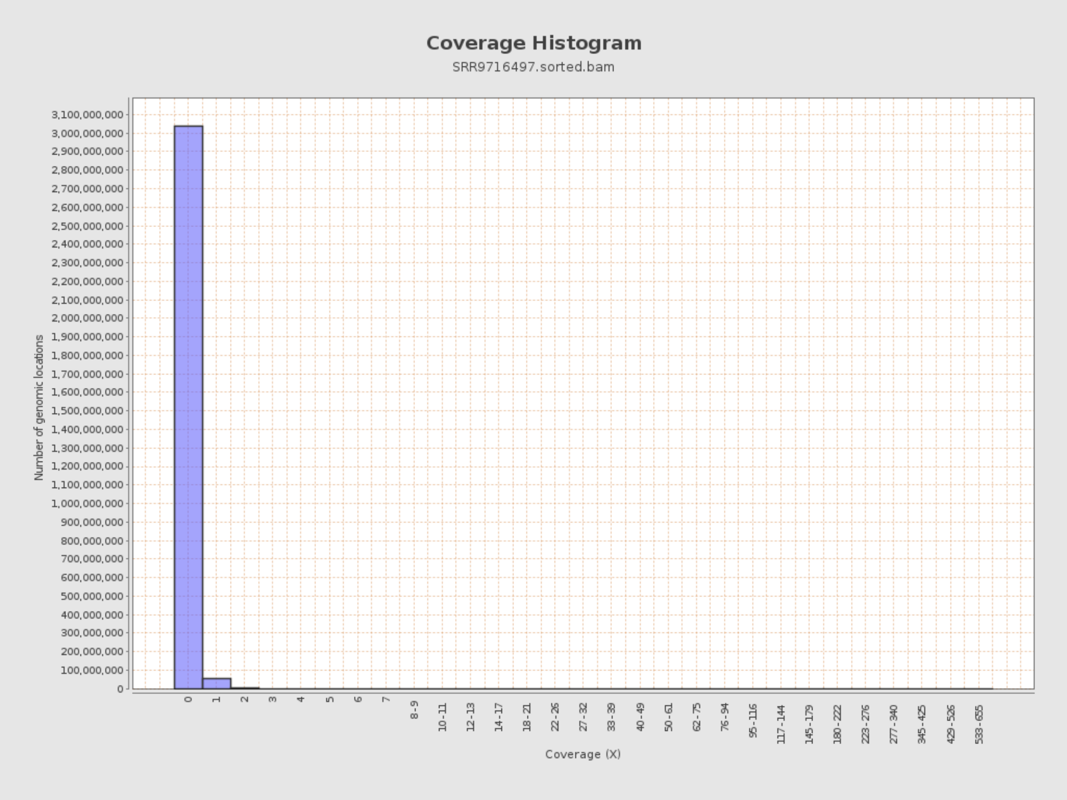
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6317875	0.0253	0.5055
chr2	243199373	6416850	0.0264	0.2862
chr3	198022430	4615821	0.0233	0.1661
chr4	191154276	3161052	0.0165	0.1611
chr5	180915260	2927129	0.0162	0.1405
chr6	171115067	4586263	0.0268	0.1937
chr7	159138663	4888000	0.0307	0.3094

chr8	146364022	3869166	0.0264	0.2154
chr9	141213431	2819225	0.02	0.1896
chr10	135534747	3772517	0.0278	0.2317
chr11	135006516	2235361	0.0166	0.1782
chr12	133851895	2706113	0.0202	0.1587
chr13	115169878	1493022	0.013	0.125
chr14	107349540	1499105	0.014	0.1367
chr15	102531392	1400246	0.0137	0.1286
chr16	90354753	1442625	0.016	0.1445
chr17	81195210	1507476	0.0186	0.1538
chr18	78077248	2342173	0.03	0.3248
chr19	59128983	1668185	0.0282	0.3108
chr20	63025520	1068075	0.0169	0.1441
chr21	48129895	859673	0.0179	0.1606
chr22	51304566	865052	0.0169	0.1417
chrMT	16571	112864	6.8109	4.5147
chrX	155270560	4341983	0.028	0.2026
chrY	59373566	185306	0.0031	0.0955

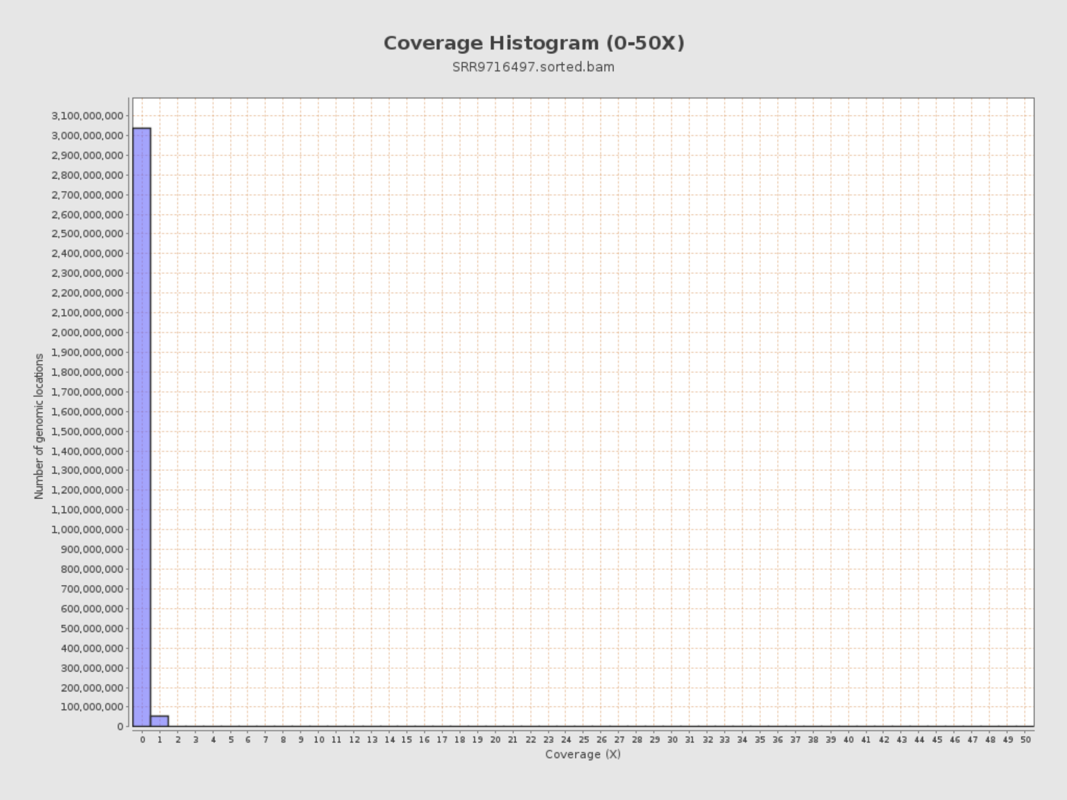
3. Results : Coverage across reference



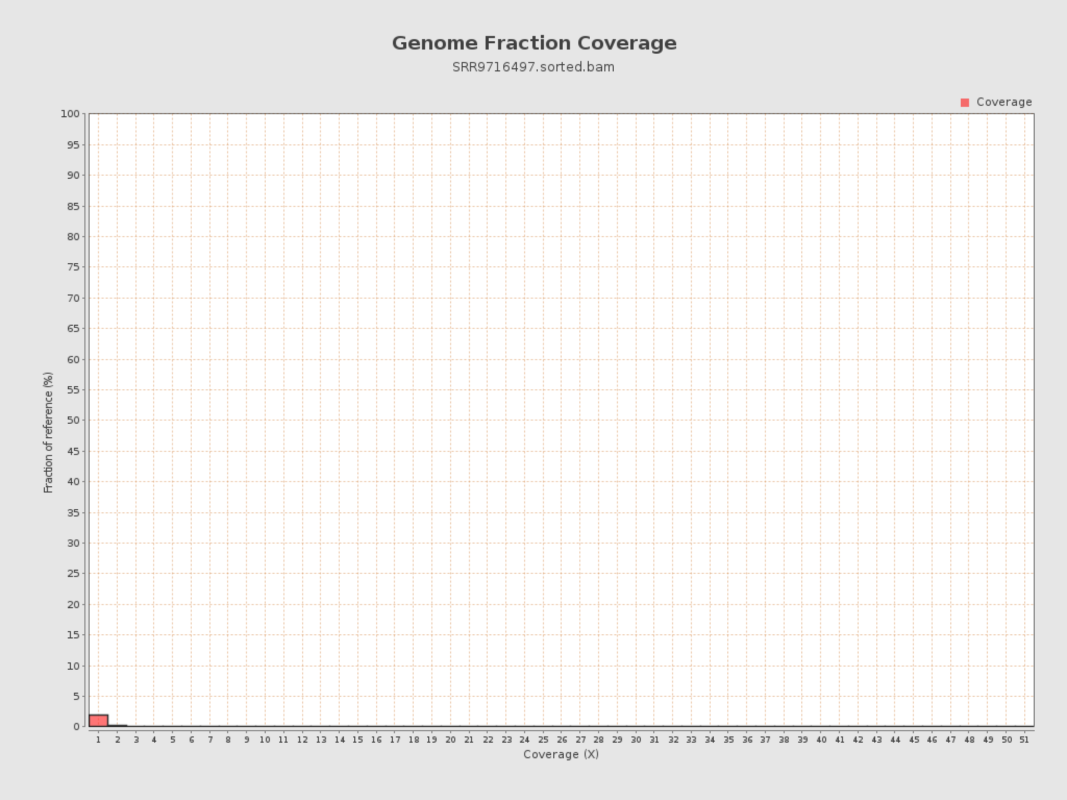
4. Results : Coverage Histogram



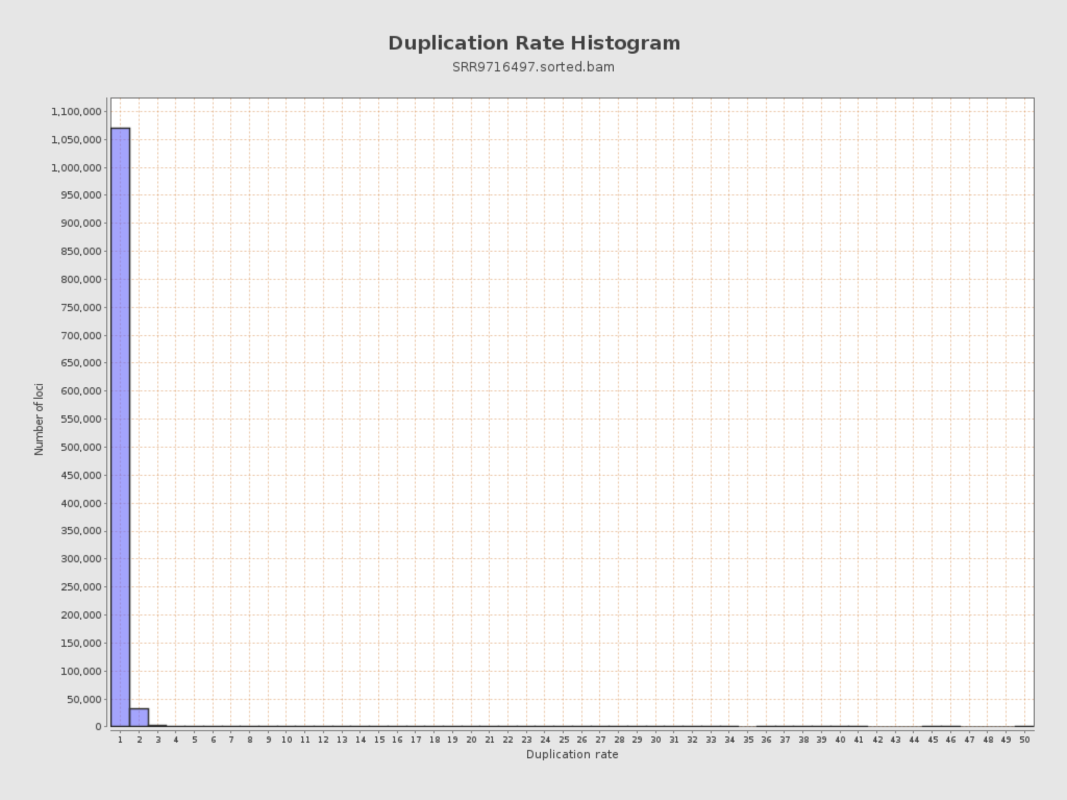
5. Results : Coverage Histogram (0-50X)



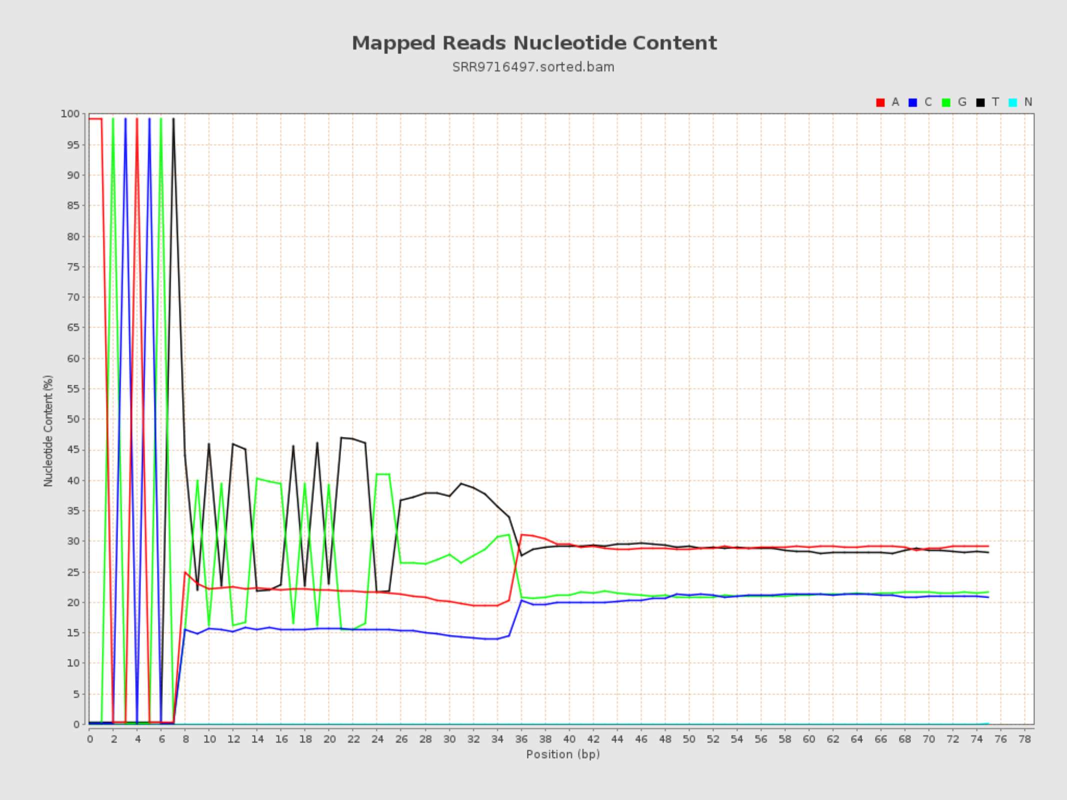
6. Results : Genome Fraction Coverage



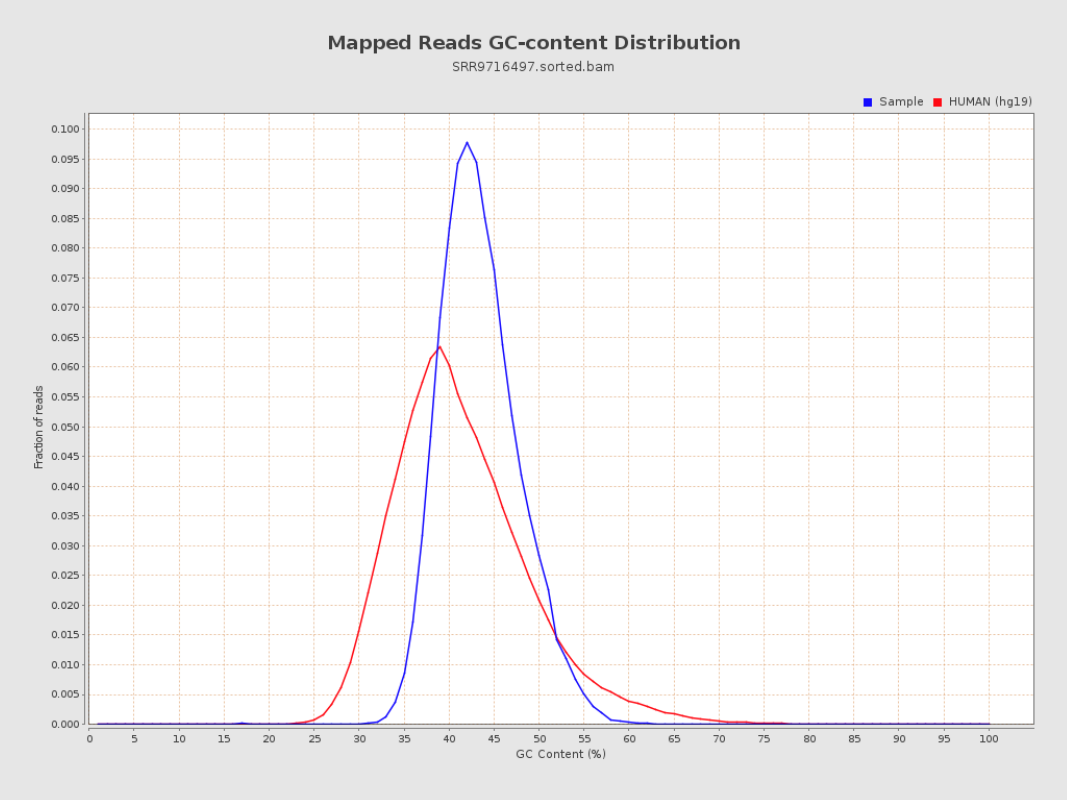
7. Results : Duplication Rate Histogram



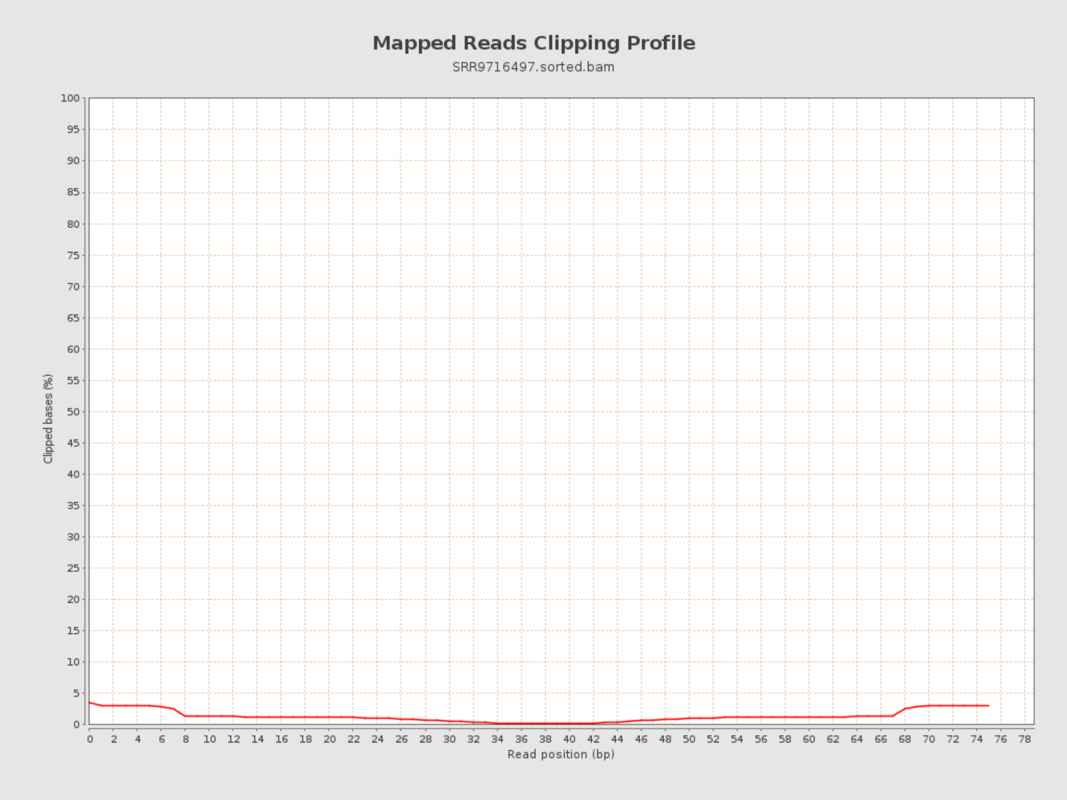
8. Results : Mapped Reads Nucleotide Content



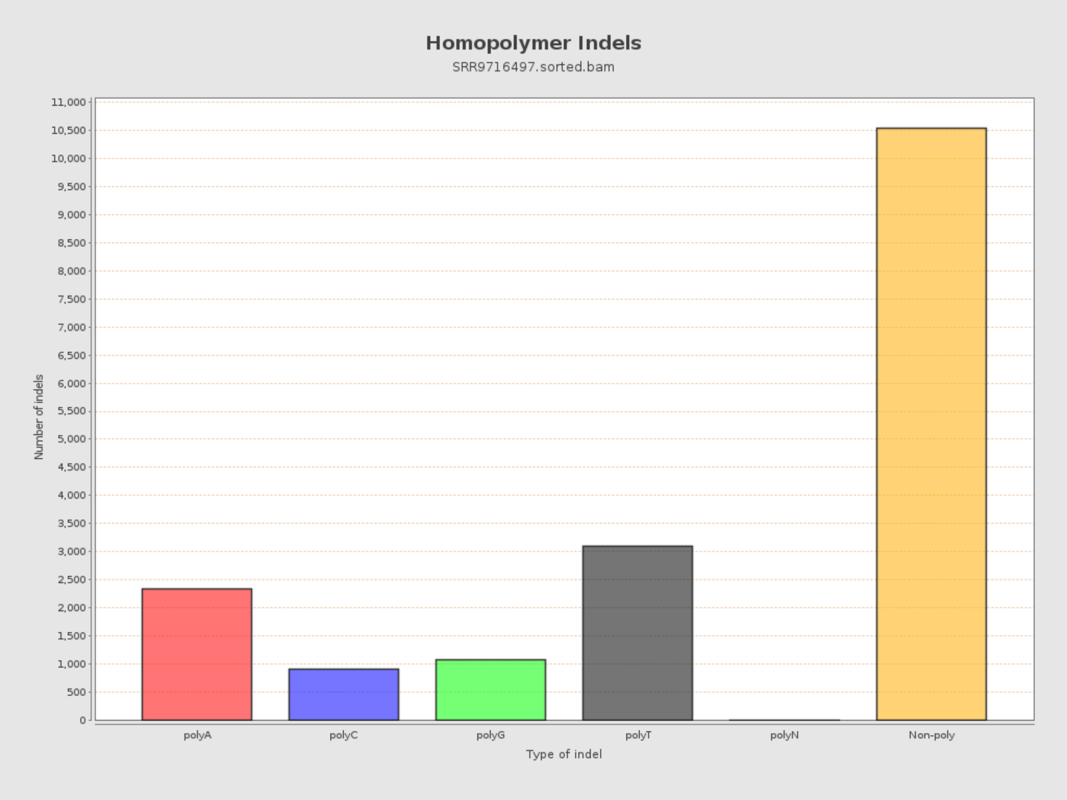
9. Results : Mapped Reads GC-content Distribution



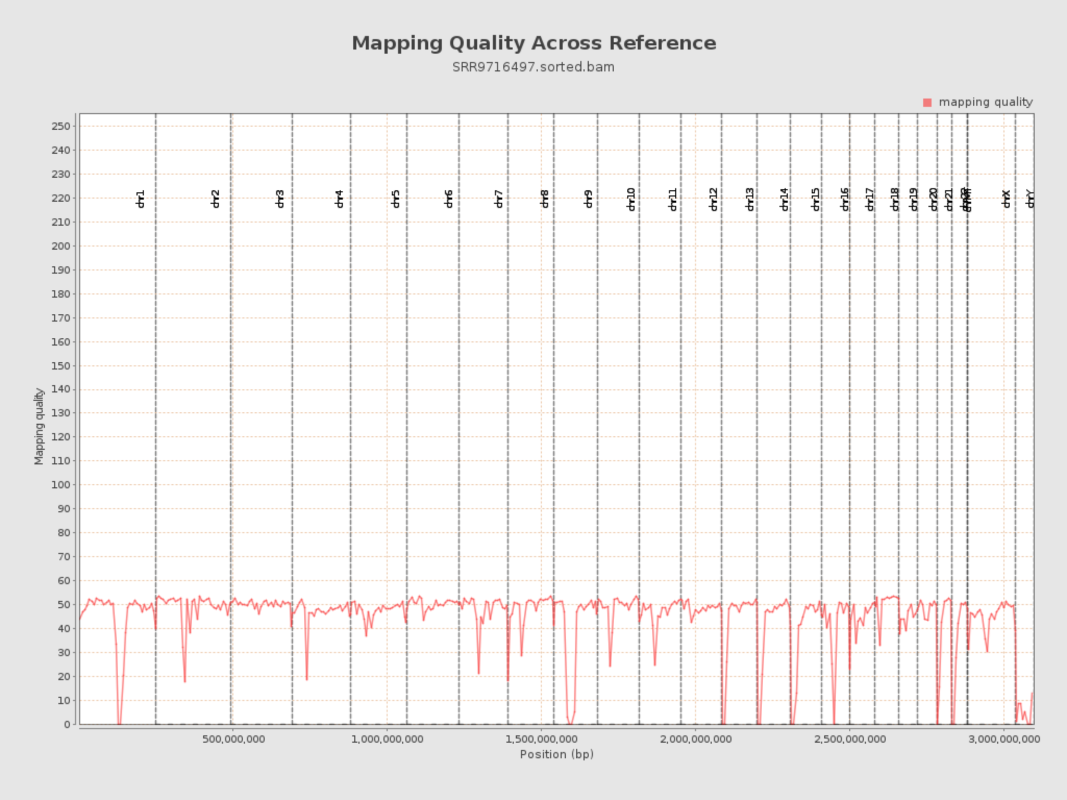
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram