Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 12:10:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716410.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_SRR9716410 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716410.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 12:10:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716410.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	902,920
Mapped reads	760,118 / 84.18%
Unmapped reads	142,802 / 15.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,473 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	18,499 / 2.05%
Duplication rate	1.91%
Clipped reads	762,557 / 84.45%

2.2. ACGT Content

Number/percentage of A's	11,489,958 / 25.94%
Number/percentage of C's	8,684,629 / 19.61%
Number/percentage of T's	13,097,237 / 29.57%
Number/percentage of G's	11,017,597 / 24.88%
Number/percentage of N's	527 / 0%
GC Percentage	44.48%

2.3. Coverage

Mean	0.0143

Standard Deviation	0.1507

2.4. Mapping Quality

Mean Mapping Quality	45.01

2.5. Mismatches and indels

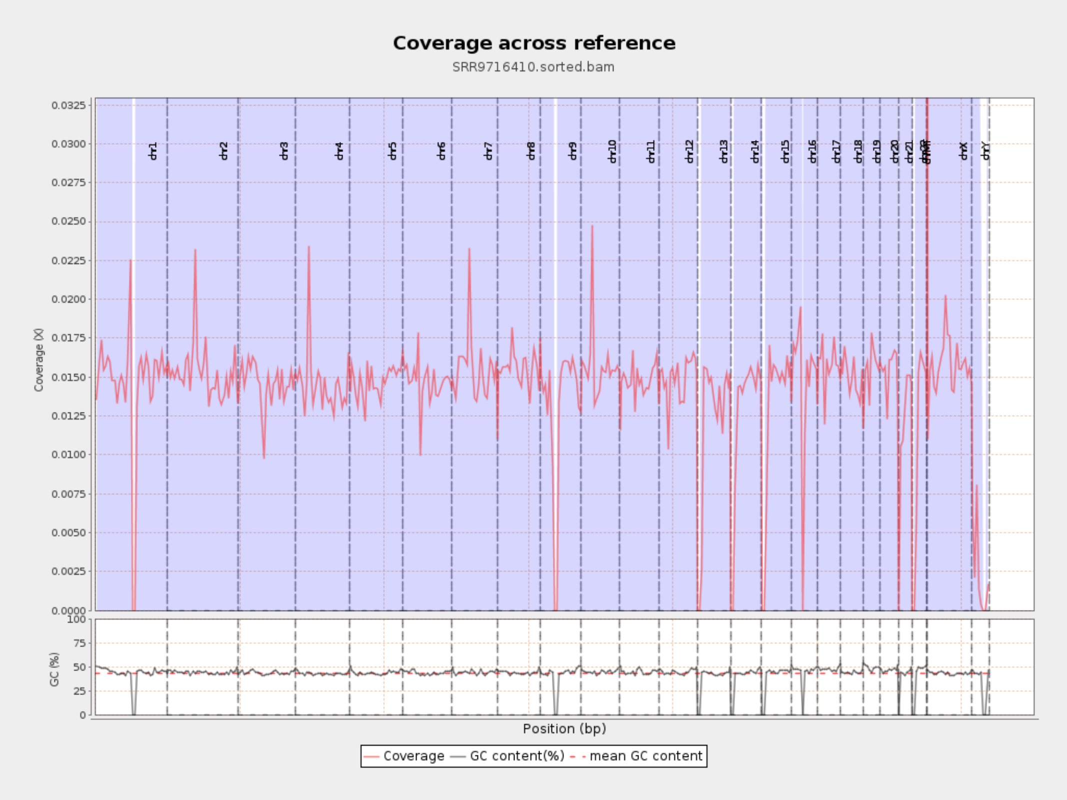
General error rate	0.52%
Mismatches	222,642
Insertions	3,261
Mapped reads with at least one insertion	0.43%
Deletions	8,419
Mapped reads with at least one deletion	1.1%
Homopolymer indels	40.45%

2.6. Chromosome stats

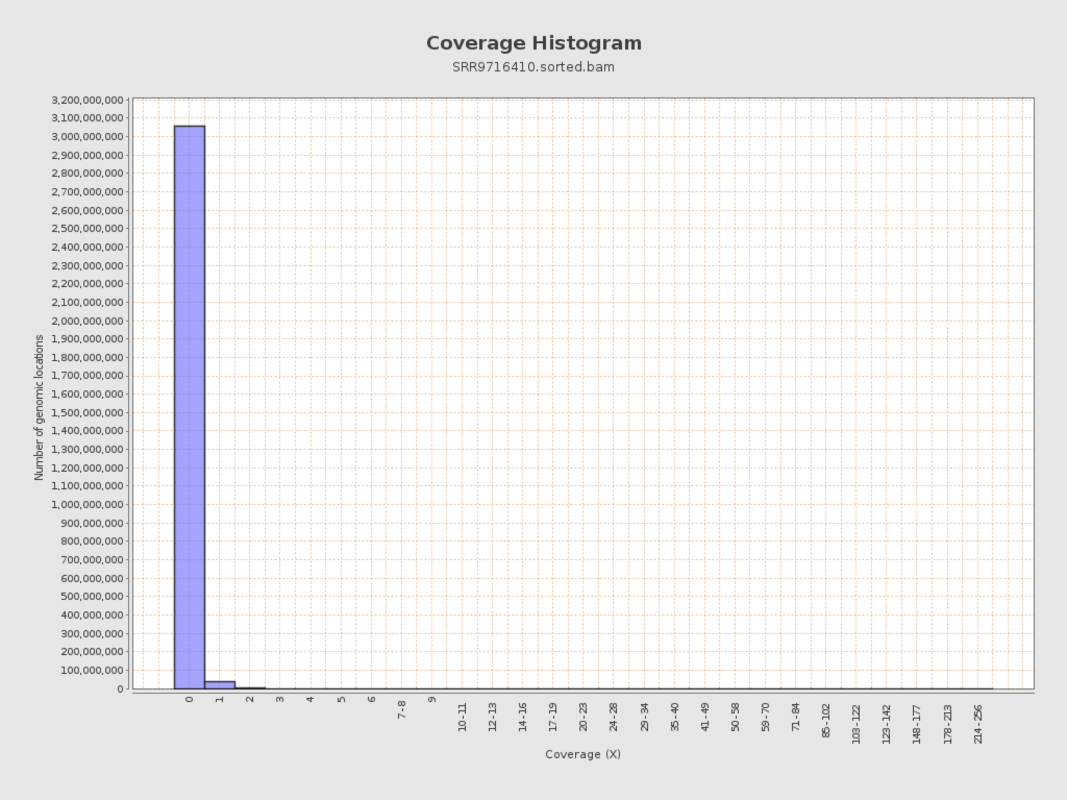
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3610724	0.0145	0.2121
chr2	243199373	3729403	0.0153	0.1773
chr3	198022430	2882110	0.0146	0.127
chr4	191154276	2787030	0.0146	0.1377
chr5	180915260	2666899	0.0147	0.1281
chr6	171115067	2516360	0.0147	0.133
chr7	159138663	2486193	0.0156	0.1839

chr8	146364022	2278257	0.0156	0.1567
chr9	141213431	1831467	0.013	0.1307
chr10	135534747	2139369	0.0158	0.1617
chr11	135006516	2002699	0.0148	0.1428
chr12	133851895	1991904	0.0149	0.1294
chr13	115169878	1363281	0.0118	0.1146
chr14	107349540	1341670	0.0125	0.1198
chr15	102531392	1289494	0.0126	0.1198
chr16	90354753	1311760	0.0145	0.1314
chr17	81195210	1282688	0.0158	0.1386
chr18	78077248	1169314	0.015	0.2082
chr19	59128983	924051	0.0156	0.179
chr20	63025520	974045	0.0155	0.1331
chr21	48129895	572829	0.0119	0.123
chr22	51304566	558933	0.0109	0.1095
chrMT	16571	6265	0.3781	0.7135
chrX	155270560	2449162	0.0158	0.1373
chrY	59373566	137478	0.0023	0.0777

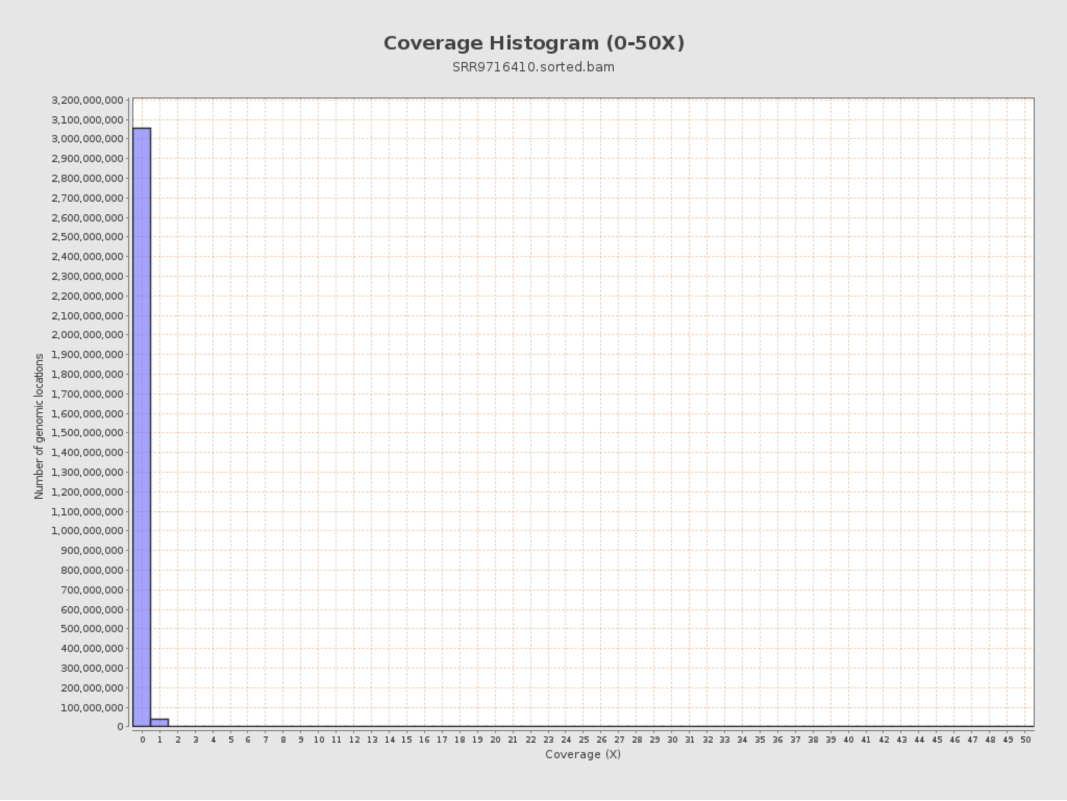
3. Results : Coverage across reference



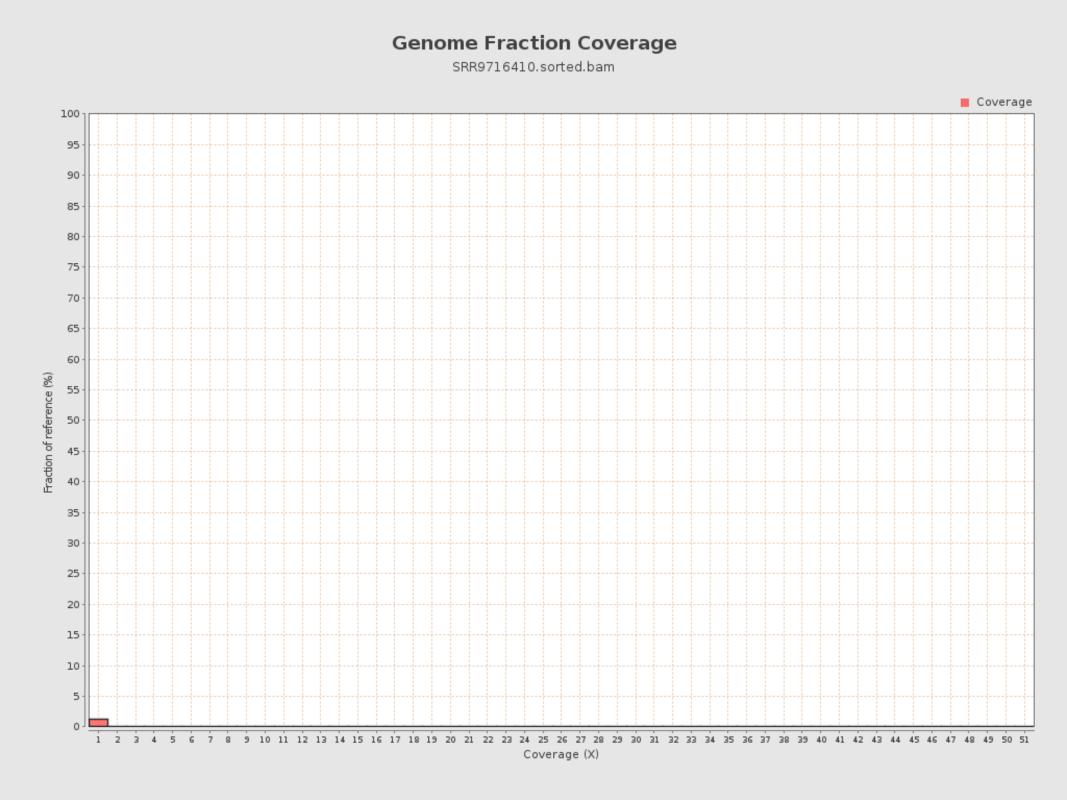
4. Results : Coverage Histogram



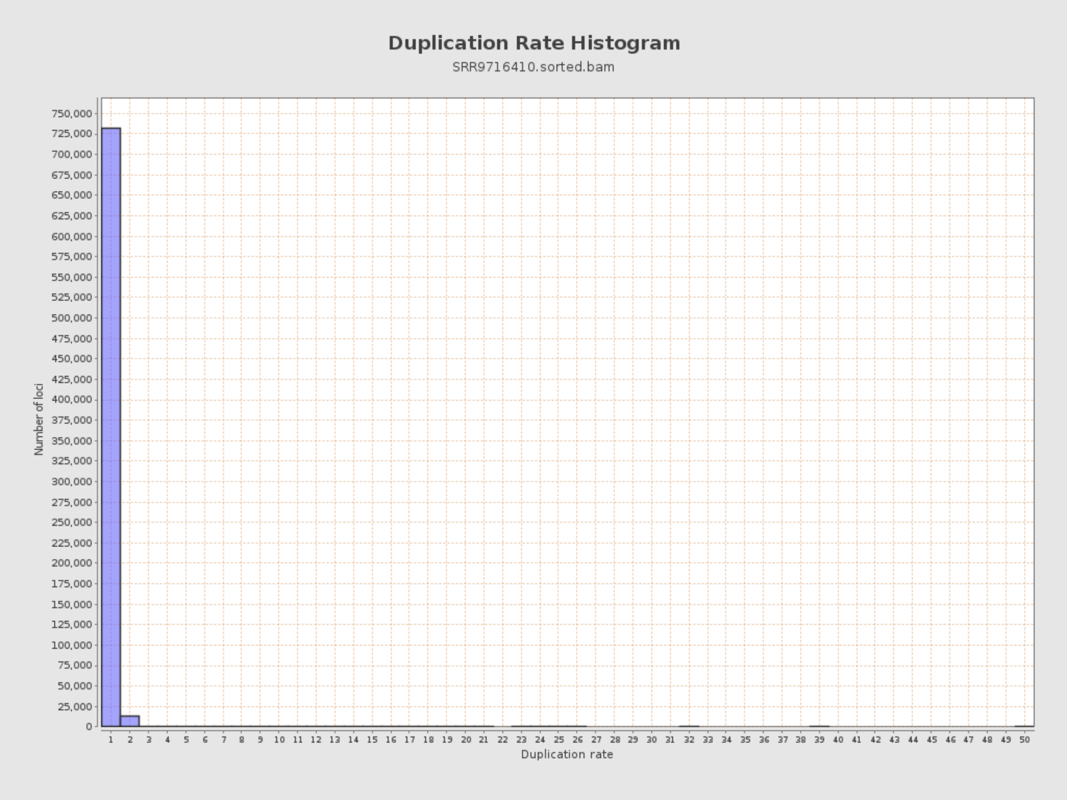
5. Results : Coverage Histogram (0-50X)



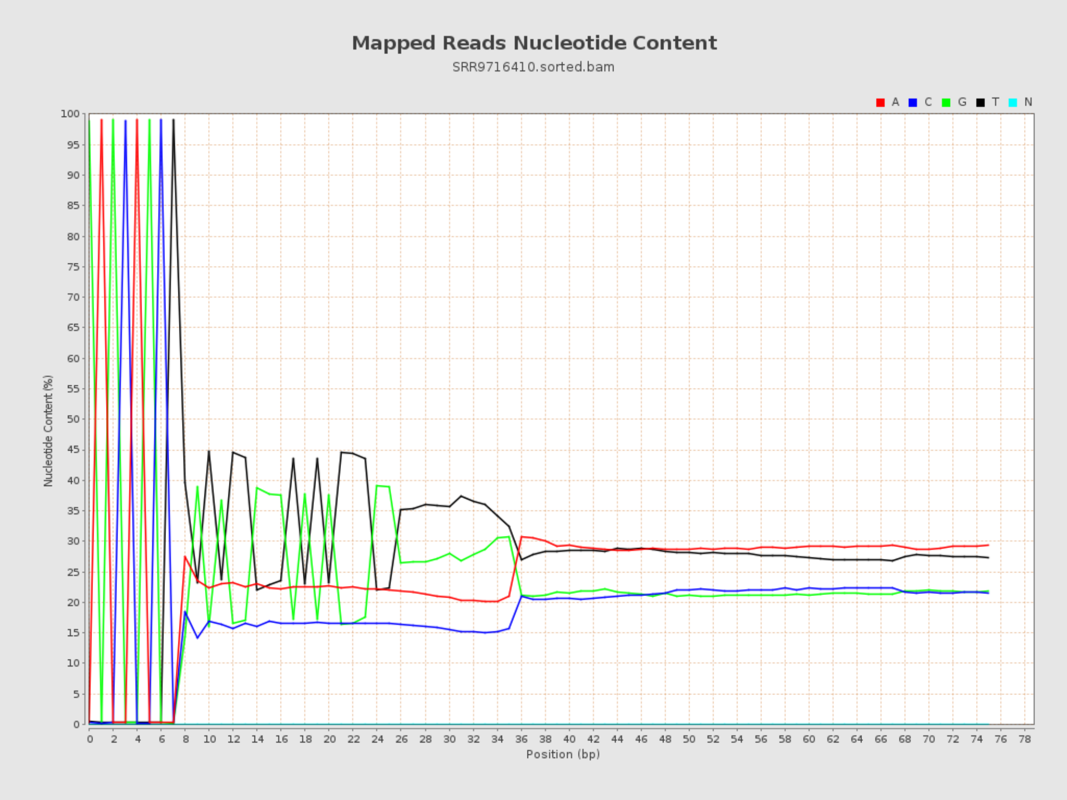
6. Results : Genome Fraction Coverage



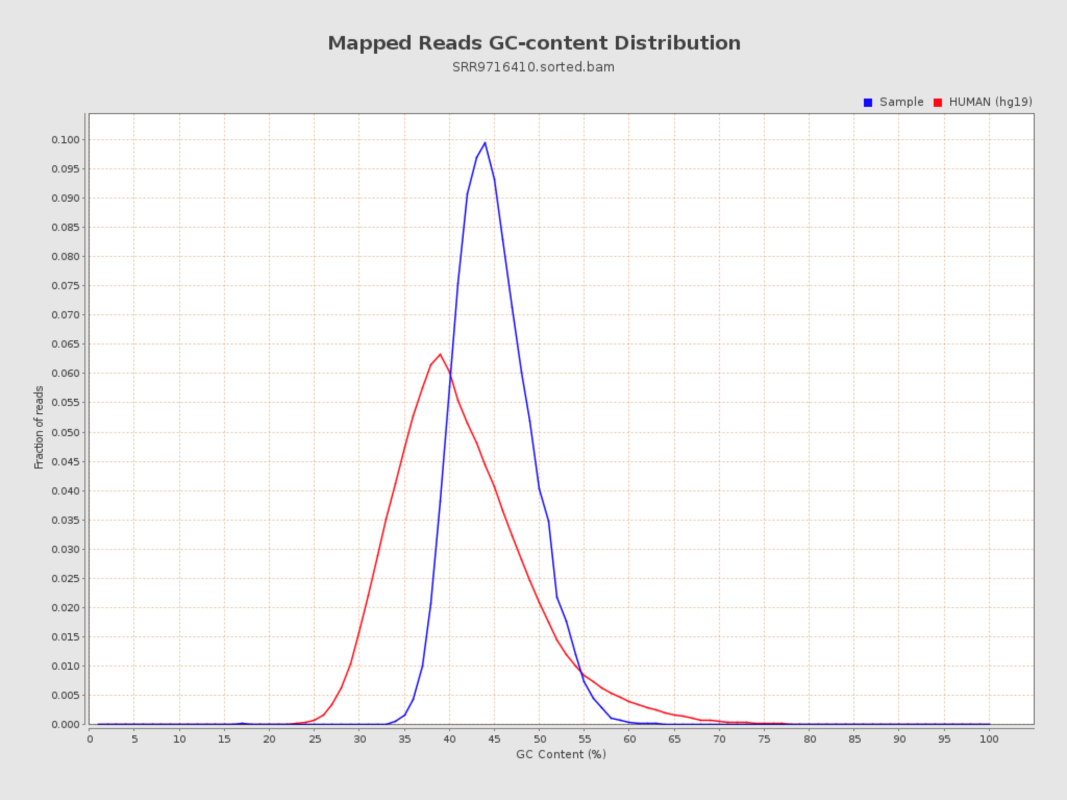
7. Results : Duplication Rate Histogram



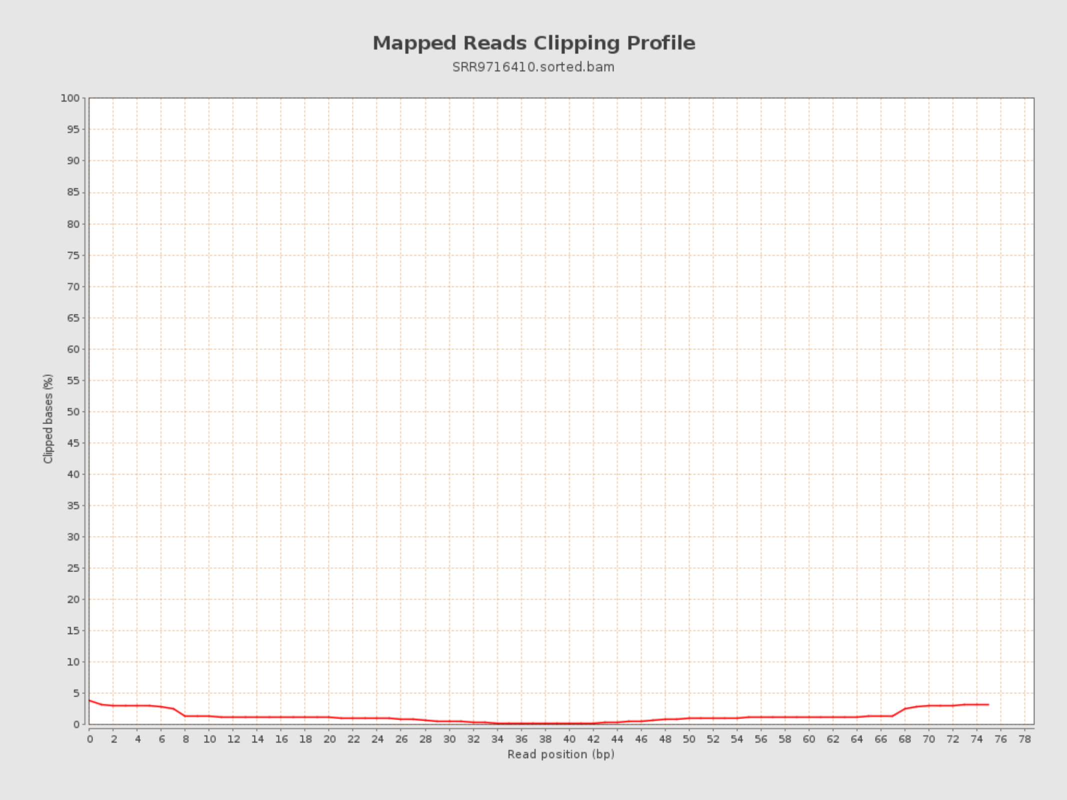
8. Results : Mapped Reads Nucleotide Content



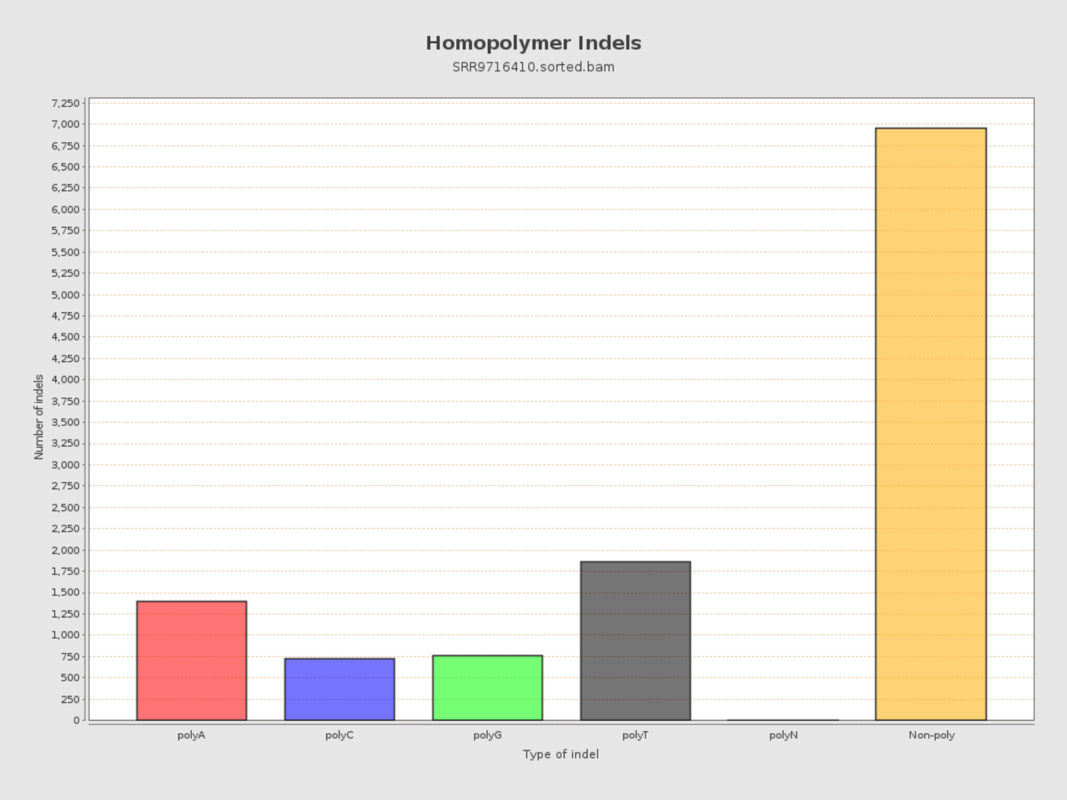
9. Results : Mapped Reads GC-content Distribution



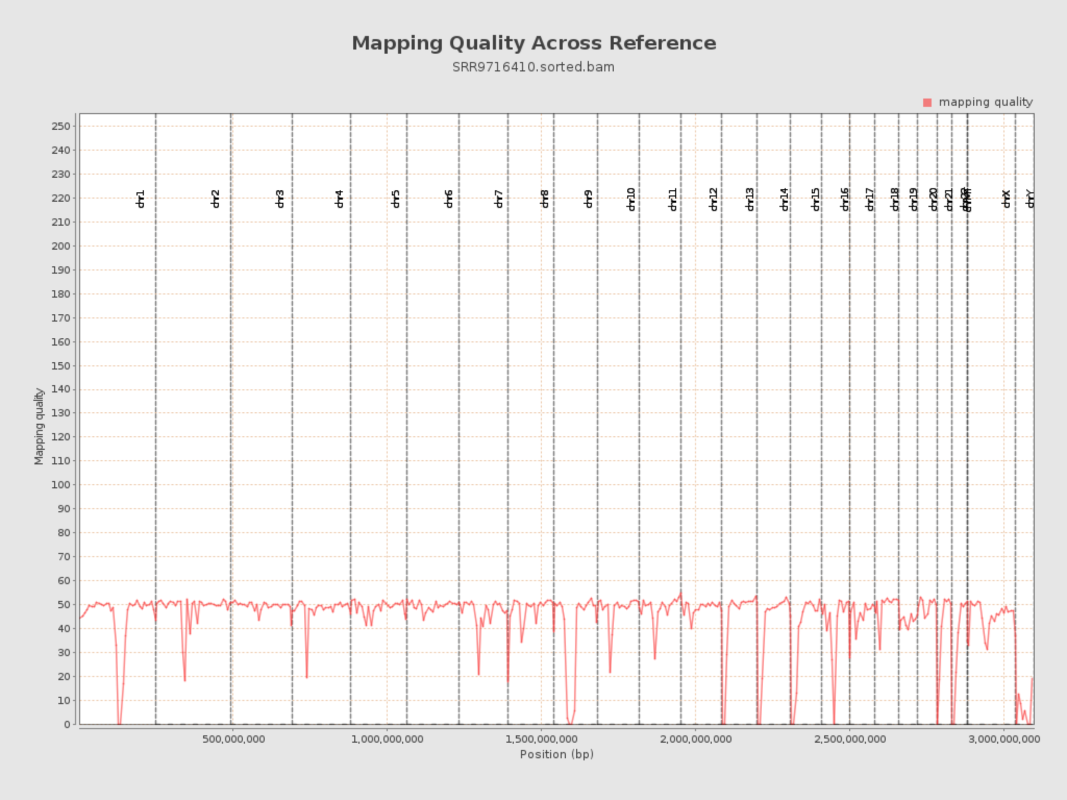
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram