Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 17:52:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716098.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_SRR9716098 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716098.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 17:52:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716098.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	866,646
Mapped reads	774,634 / 89.38%
Unmapped reads	92,012 / 10.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,979 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	21,700 / 2.5%
Duplication rate	2.17%
Clipped reads	775,562 / 89.49%

2.2. ACGT Content

Number/percentage of A's	11,485,660 / 25.69%
Number/percentage of C's	8,309,733 / 18.59%
Number/percentage of T's	14,405,147 / 32.22%
Number/percentage of G's	10,503,485 / 23.49%
Number/percentage of N's	1,308 / 0%
GC Percentage	42.08%

2.3. Coverage

Mean	0.0144

Standard Deviation	0.1614

2.4. Mapping Quality

Mean Mapping Quality	45.12

2.5. Mismatches and indels

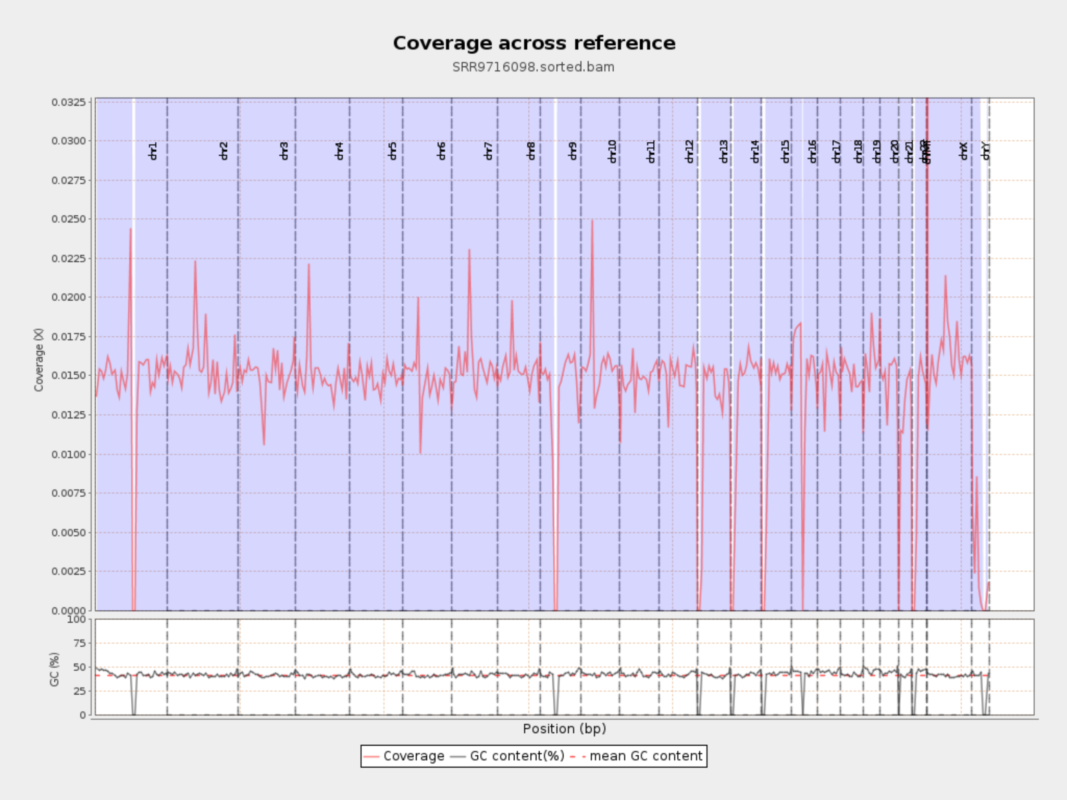
General error rate	0.52%
Mismatches	225,967
Insertions	3,404
Mapped reads with at least one insertion	0.44%
Deletions	8,428
Mapped reads with at least one deletion	1.08%
Homopolymer indels	42.76%

2.6. Chromosome stats

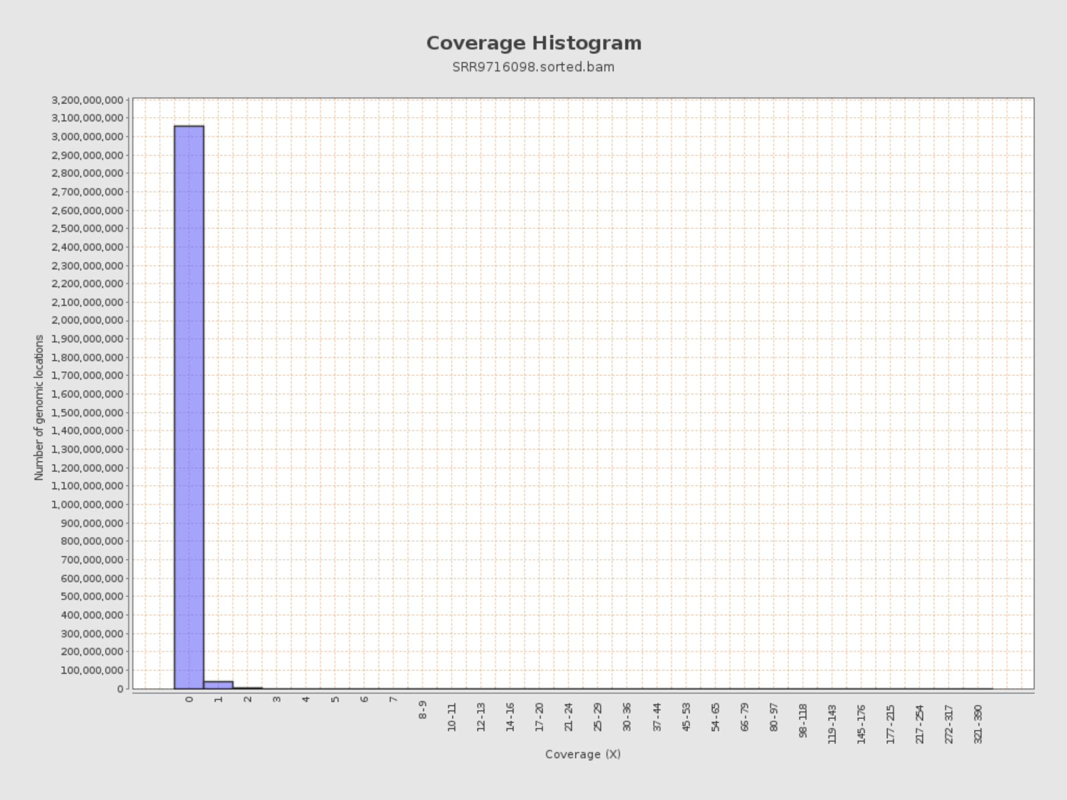
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3607920	0.0145	0.2676
chr2	243199373	3770505	0.0155	0.2083
chr3	198022430	2966711	0.015	0.1295
chr4	191154276	2887227	0.0151	0.1344
chr5	180915260	2690975	0.0149	0.1288
chr6	171115067	2538078	0.0148	0.1412
chr7	159138663	2498628	0.0157	0.1806

chr8	146364022	2259944	0.0154	0.158
chr9	141213431	1858785	0.0132	0.1365
chr10	135534747	2148686	0.0159	0.1588
chr11	135006516	2003912	0.0148	0.1414
chr12	133851895	2035331	0.0152	0.1318
chr13	115169878	1408781	0.0122	0.117
chr14	107349540	1380724	0.0129	0.1241
chr15	102531392	1277475	0.0125	0.1202
chr16	90354753	1316069	0.0146	0.1321
chr17	81195210	1207785	0.0149	0.1314
chr18	78077248	1174872	0.015	0.2046
chr19	59128983	948779	0.016	0.1969
chr20	63025520	937256	0.0149	0.1295
chr21	48129895	580200	0.0121	0.1205
chr22	51304566	532246	0.0104	0.1072
chrMT	16571	18723	1.1299	1.2125
chrX	155270560	2524758	0.0163	0.143
chrY	59373566	144391	0.0024	0.0764

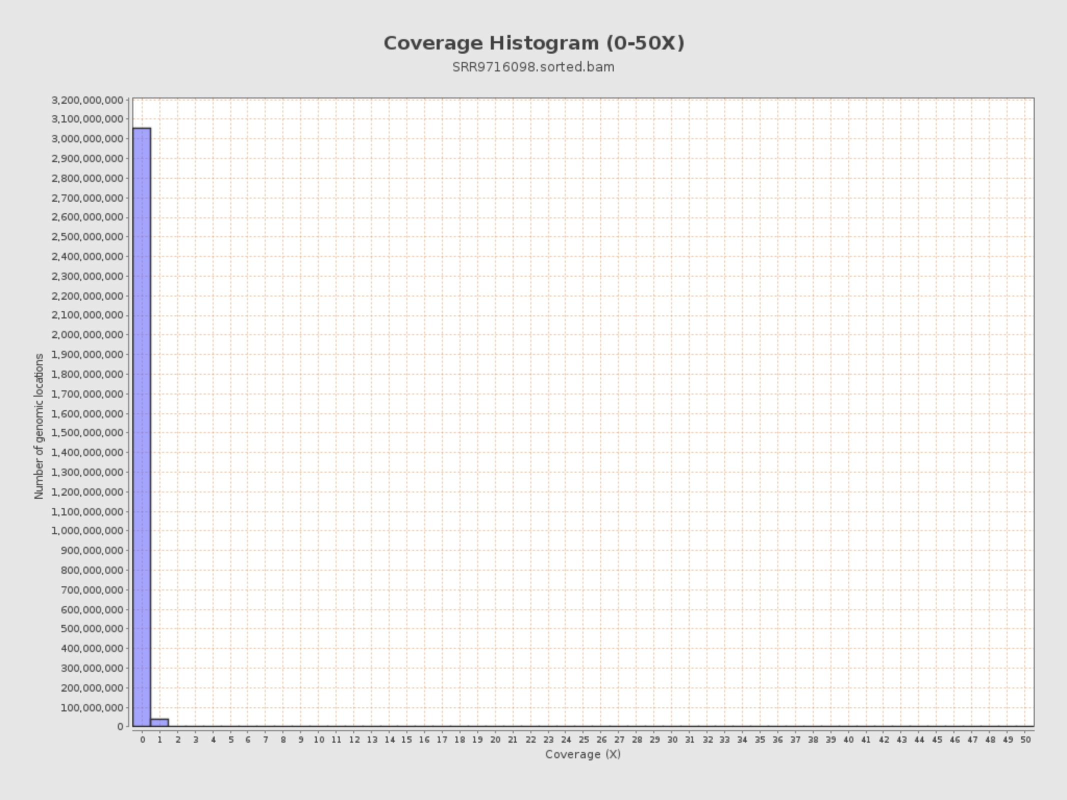
3. Results : Coverage across reference



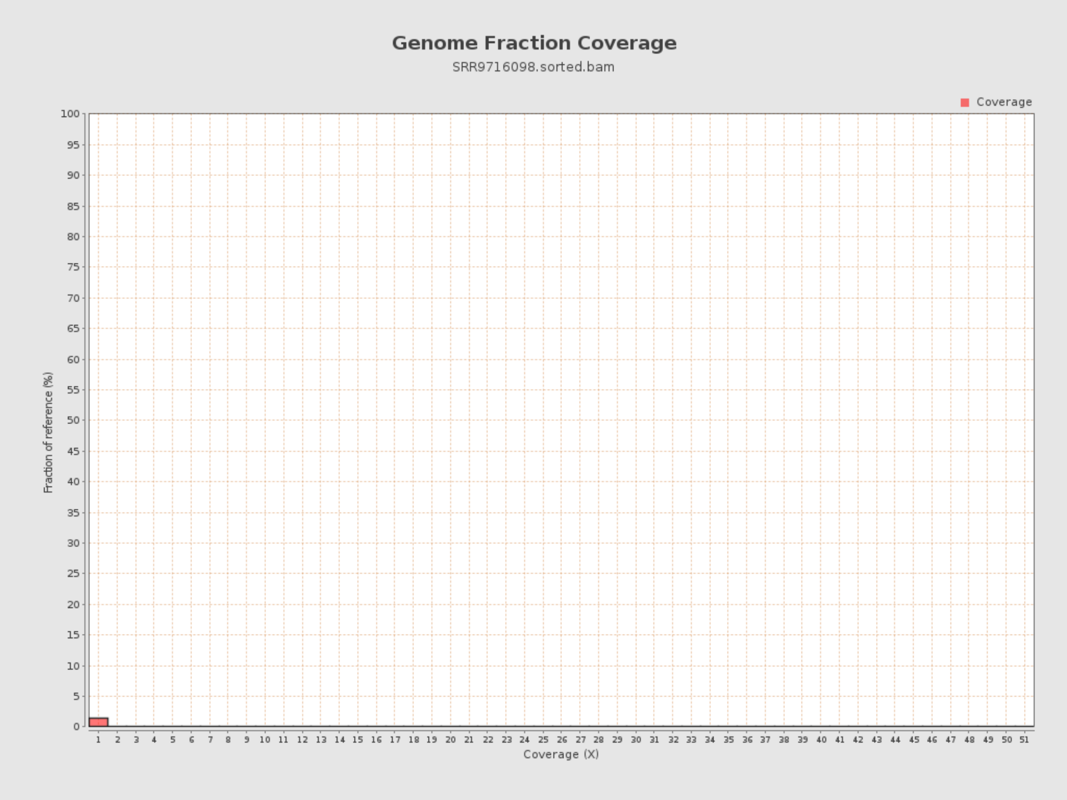
4. Results : Coverage Histogram



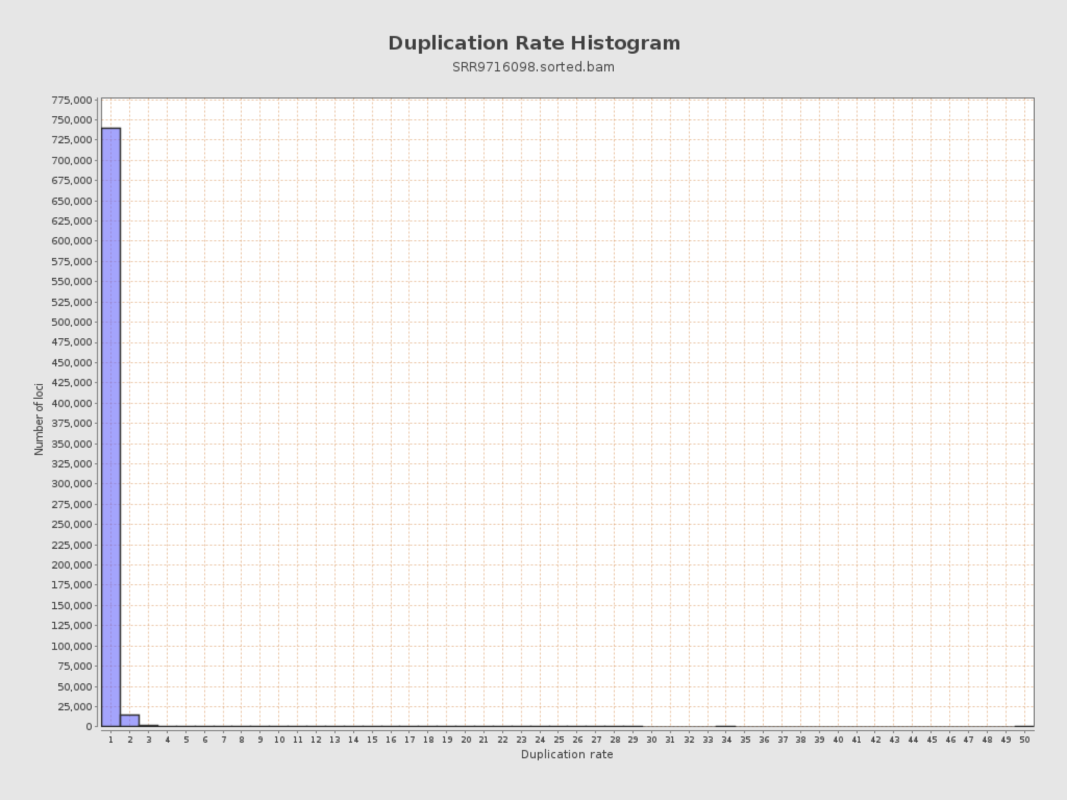
5. Results : Coverage Histogram (0-50X)



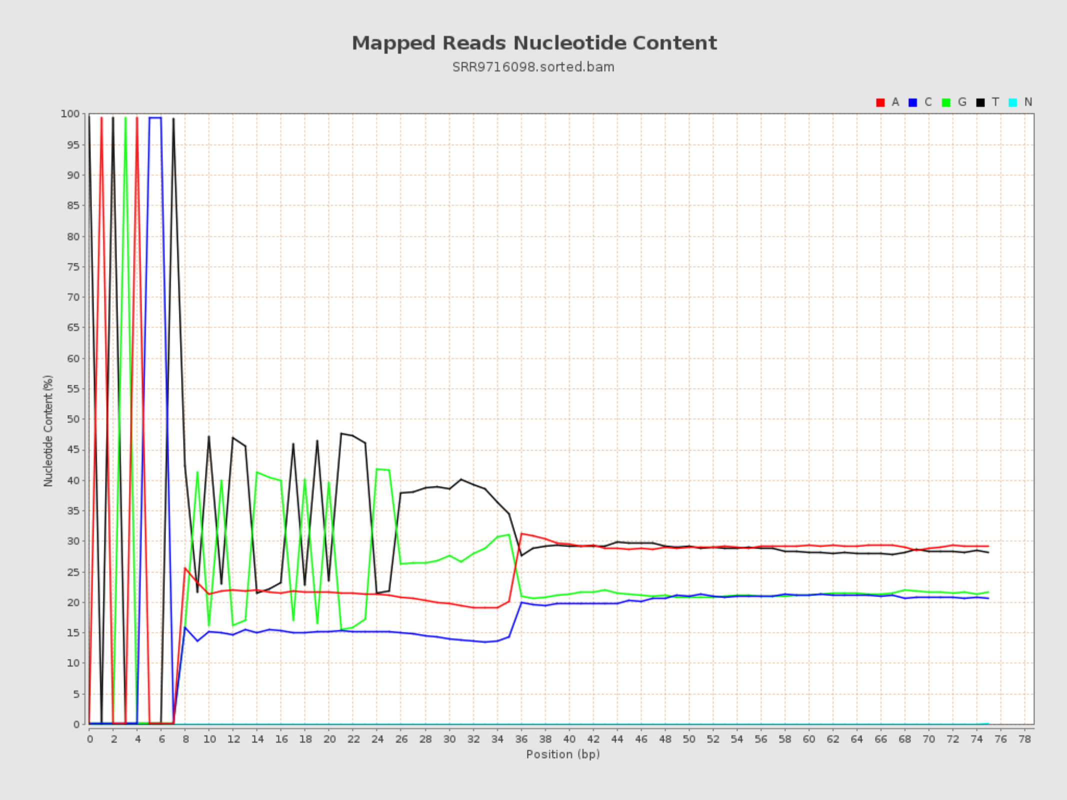
6. Results : Genome Fraction Coverage



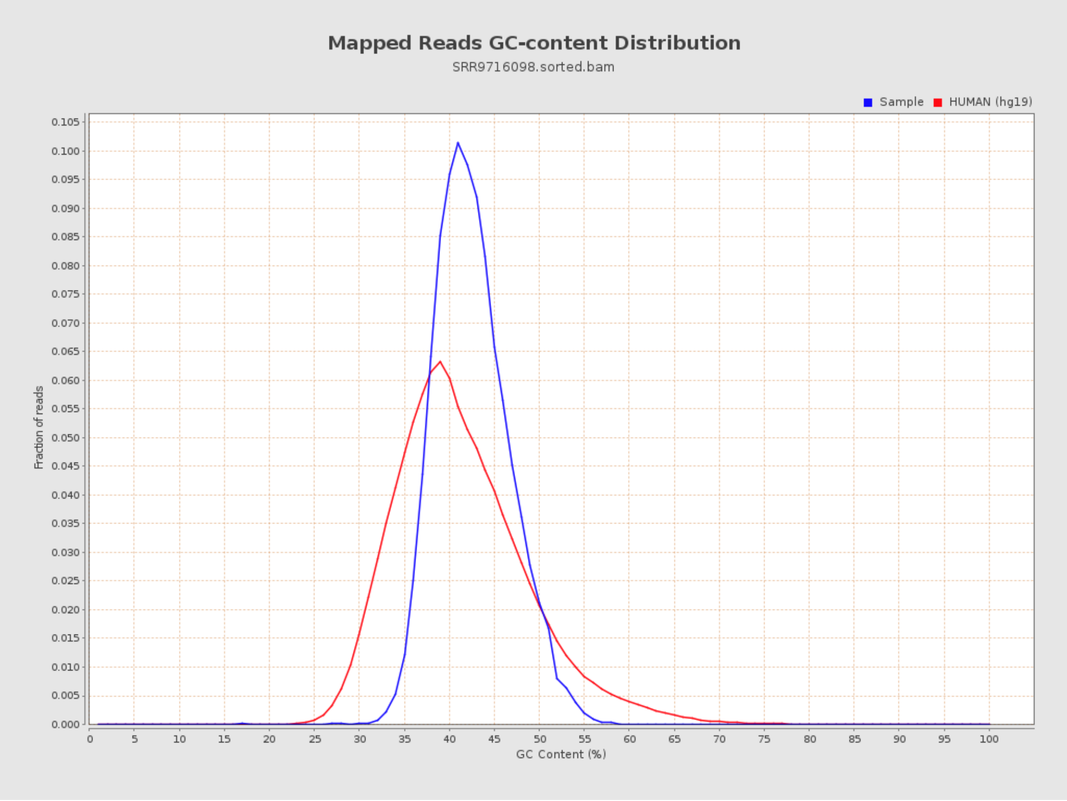
7. Results : Duplication Rate Histogram



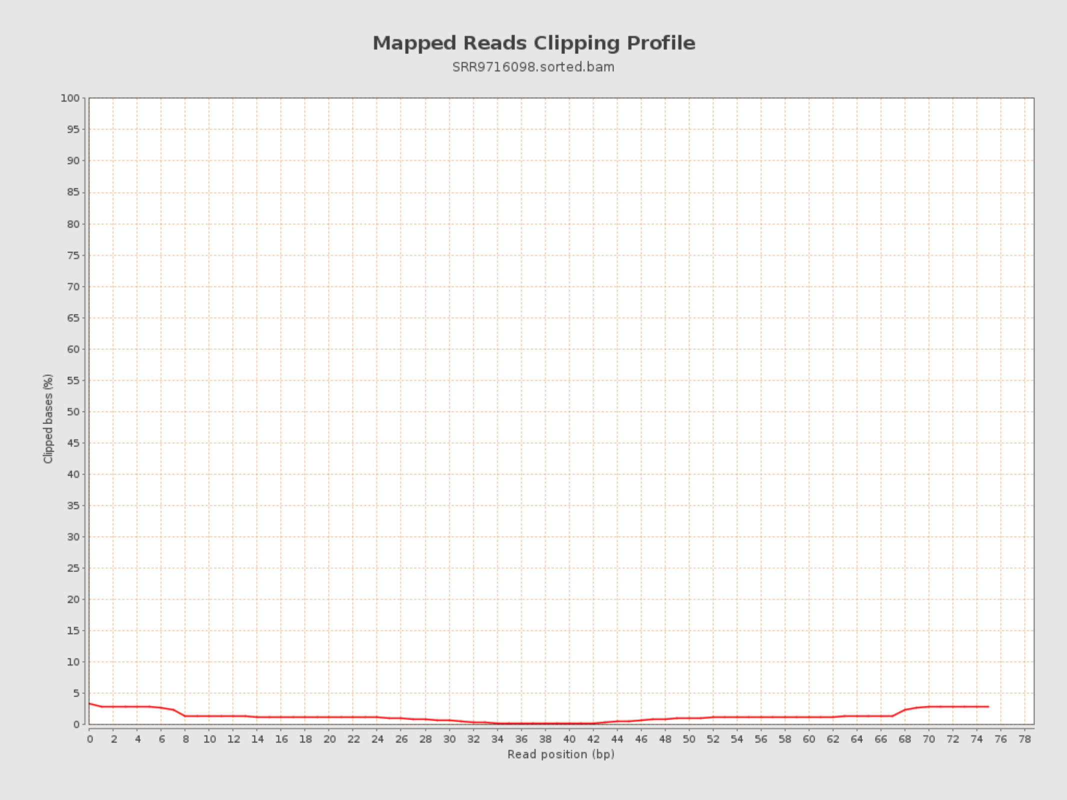
8. Results : Mapped Reads Nucleotide Content



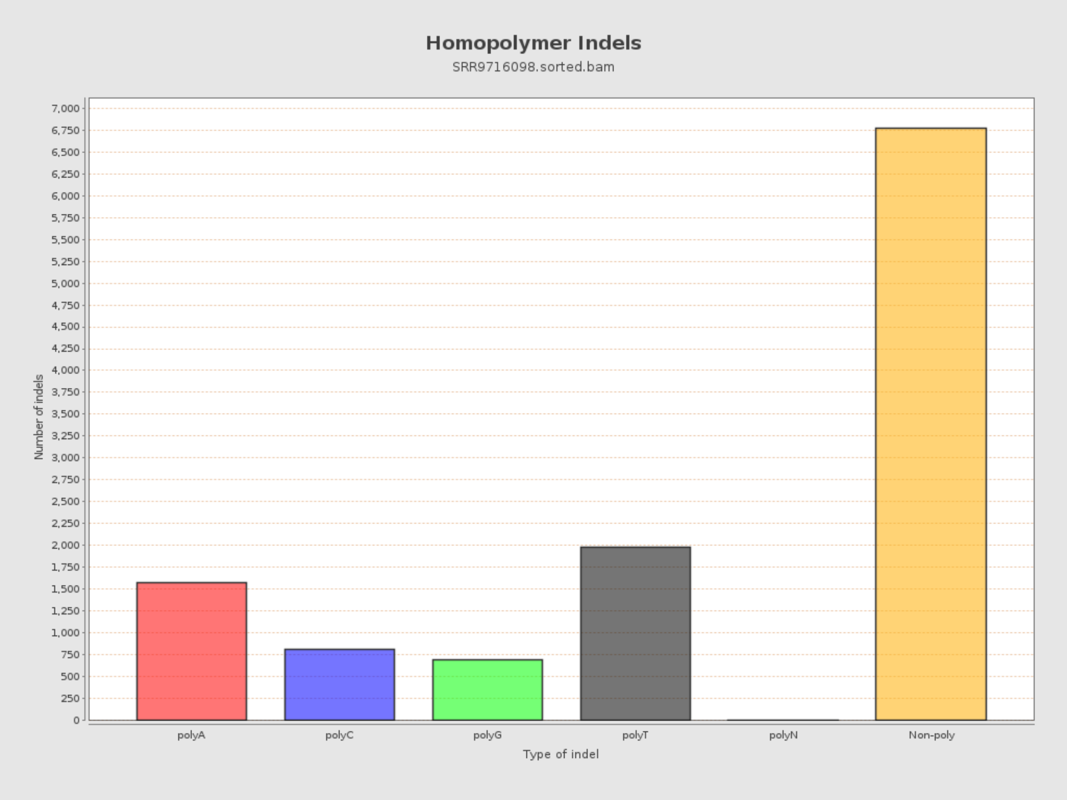
9. Results : Mapped Reads GC-content Distribution



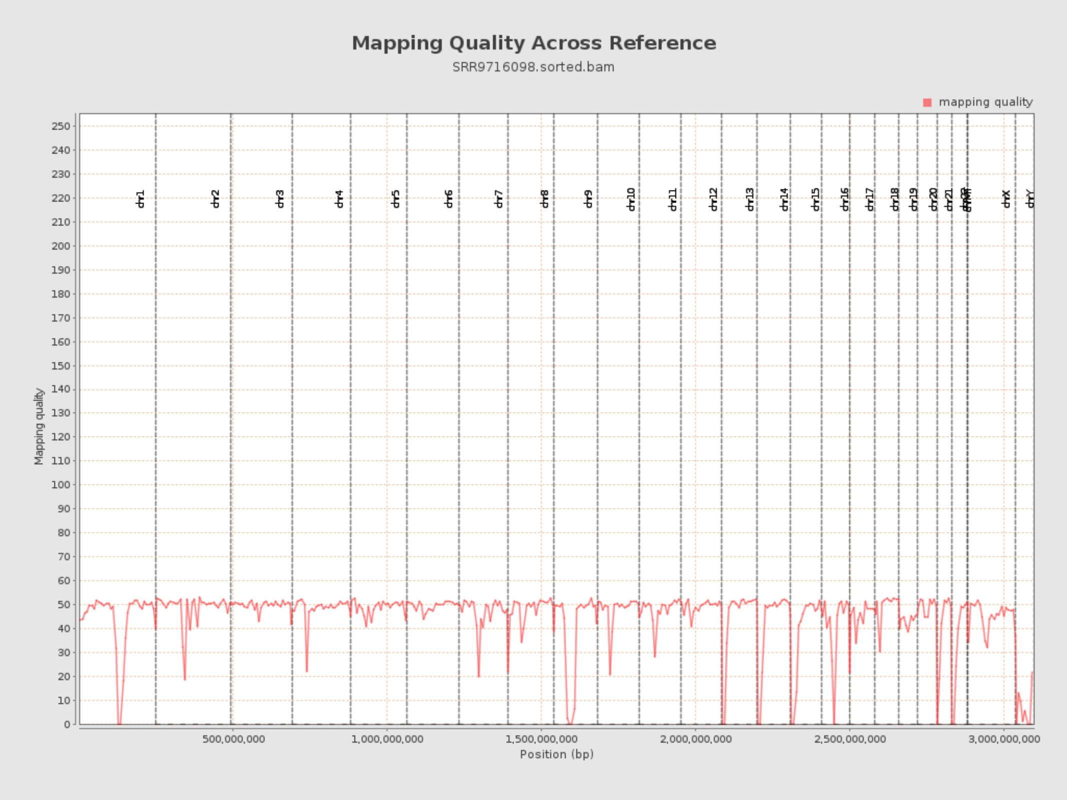
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram