Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 08:37:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716348.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_SRR9716348 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716348.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 08:37:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716348.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	624,099
Mapped reads	584,120 / 93.59%
Unmapped reads	39,979 / 6.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,343 / 1.98%
Read min/max/mean length	30 / 101 / 101.71
Duplicated reads (estimated)	11,892 / 1.91%
Duplication rate	1.44%
Clipped reads	595,929 / 95.49%

2.2. ACGT Content

Number/percentage of A's	11,808,721 / 25.74%
Number/percentage of C's	9,206,991 / 20.07%
Number/percentage of T's	13,866,522 / 30.22%
Number/percentage of G's	10,996,369 / 23.97%
Number/percentage of N's	3,514 / 0.01%
GC Percentage	44.03%

2.3. Coverage

Mean	0.0148

Standard Deviation	0.1648

2.4. Mapping Quality

Mean Mapping Quality	47.33

2.5. Mismatches and indels

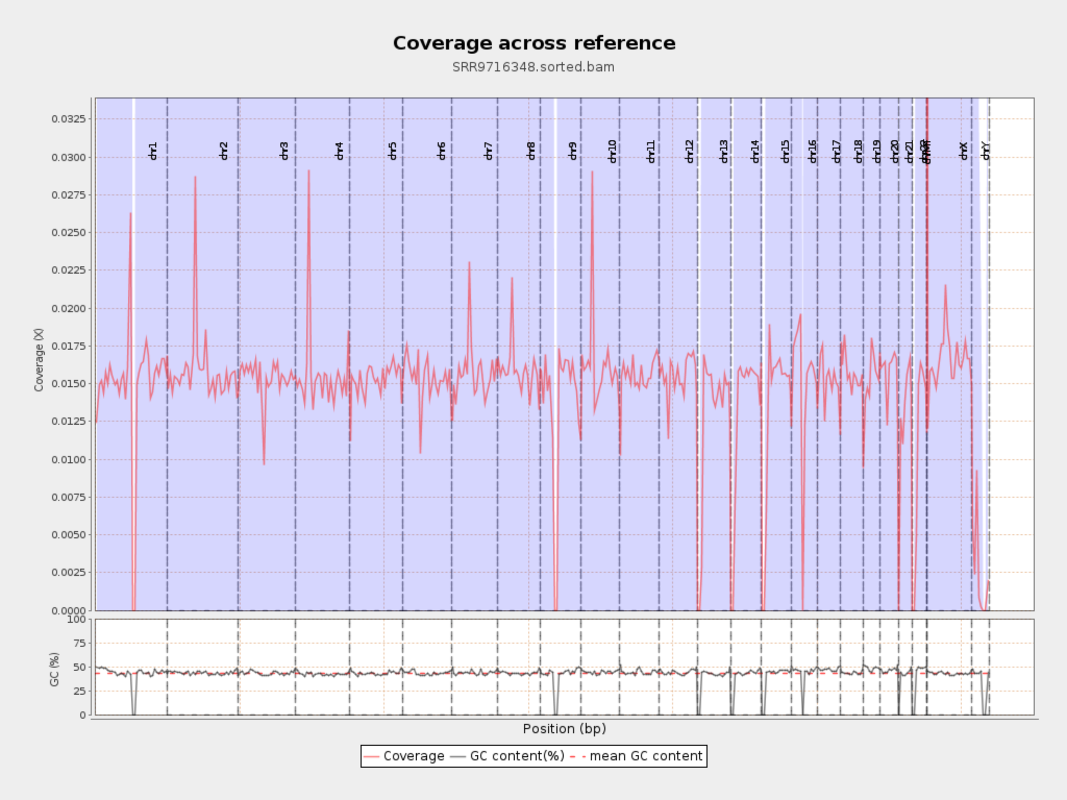
General error rate	0.65%
Mismatches	291,823
Insertions	3,641
Mapped reads with at least one insertion	0.61%
Deletions	11,295
Mapped reads with at least one deletion	1.9%
Homopolymer indels	43.95%

2.6. Chromosome stats

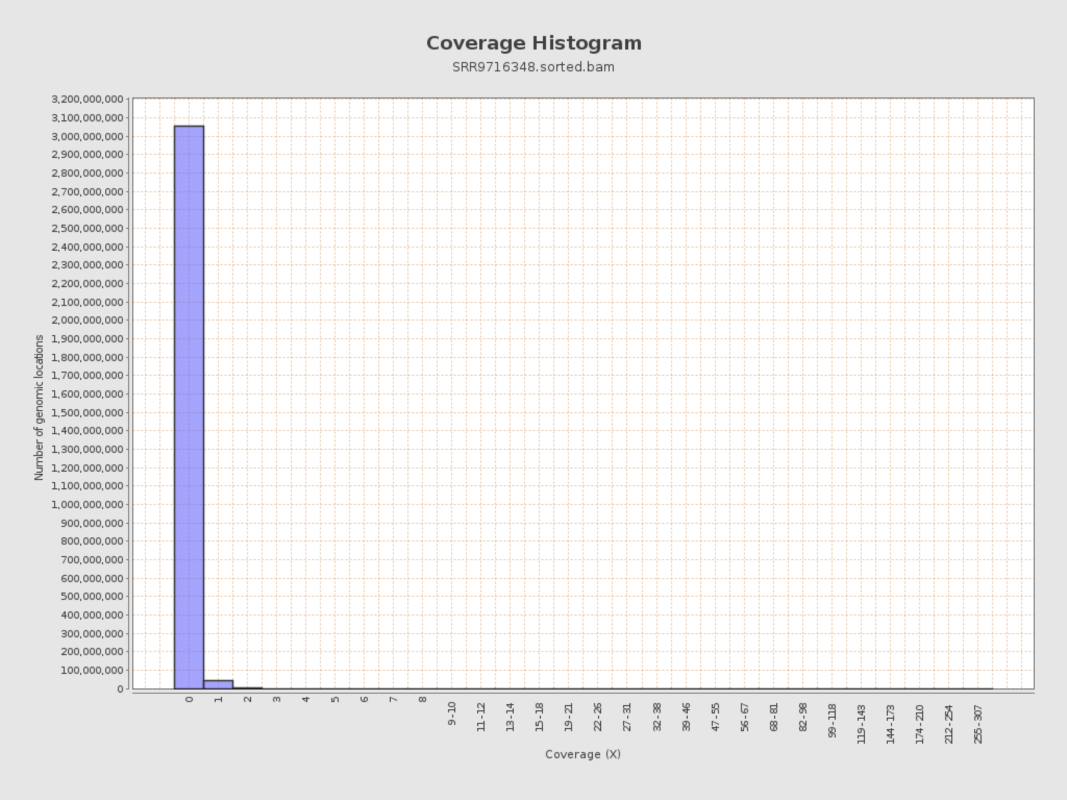
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3701609	0.0149	0.2769
chr2	243199373	3866165	0.0159	0.1817
chr3	198022430	3033148	0.0153	0.1283
chr4	191154276	2987050	0.0156	0.144
chr5	180915260	2788823	0.0154	0.1296
chr6	171115067	2616573	0.0153	0.133
chr7	159138663	2505810	0.0157	0.1977

chr8	146364022	2325742	0.0159	0.1853
chr9	141213431	1916978	0.0136	0.1539
chr10	135534747	2214627	0.0163	0.1776
chr11	135006516	2105499	0.0156	0.1533
chr12	133851895	2084064	0.0156	0.1301
chr13	115169878	1436337	0.0125	0.1158
chr14	107349540	1394659	0.013	0.1238
chr15	102531392	1344444	0.0131	0.119
chr16	90354753	1344022	0.0149	0.1317
chr17	81195210	1231168	0.0152	0.1334
chr18	78077248	1226282	0.0157	0.2091
chr19	59128983	905787	0.0153	0.1904
chr20	63025520	992795	0.0158	0.1332
chr21	48129895	610941	0.0127	0.1265
chr22	51304566	540654	0.0105	0.1066
chrMT	16571	7637	0.4609	0.6924
chrX	155270560	2579356	0.0166	0.1422
chrY	59373566	143578	0.0024	0.0877

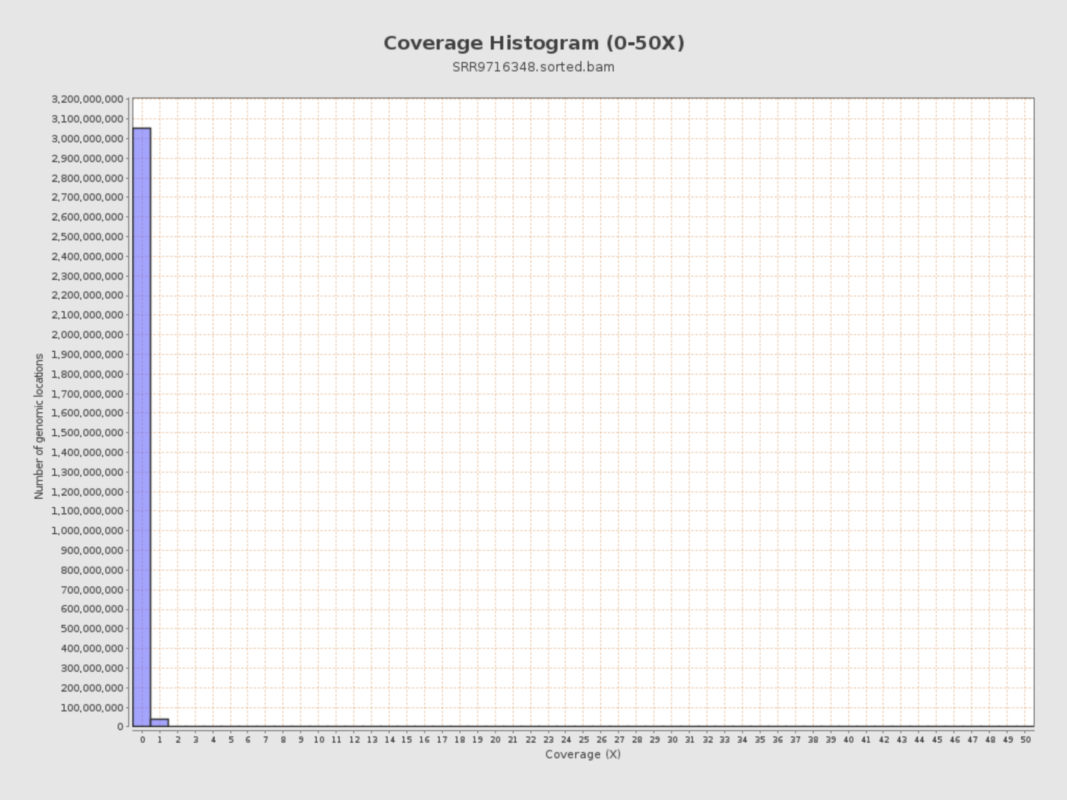
3. Results : Coverage across reference



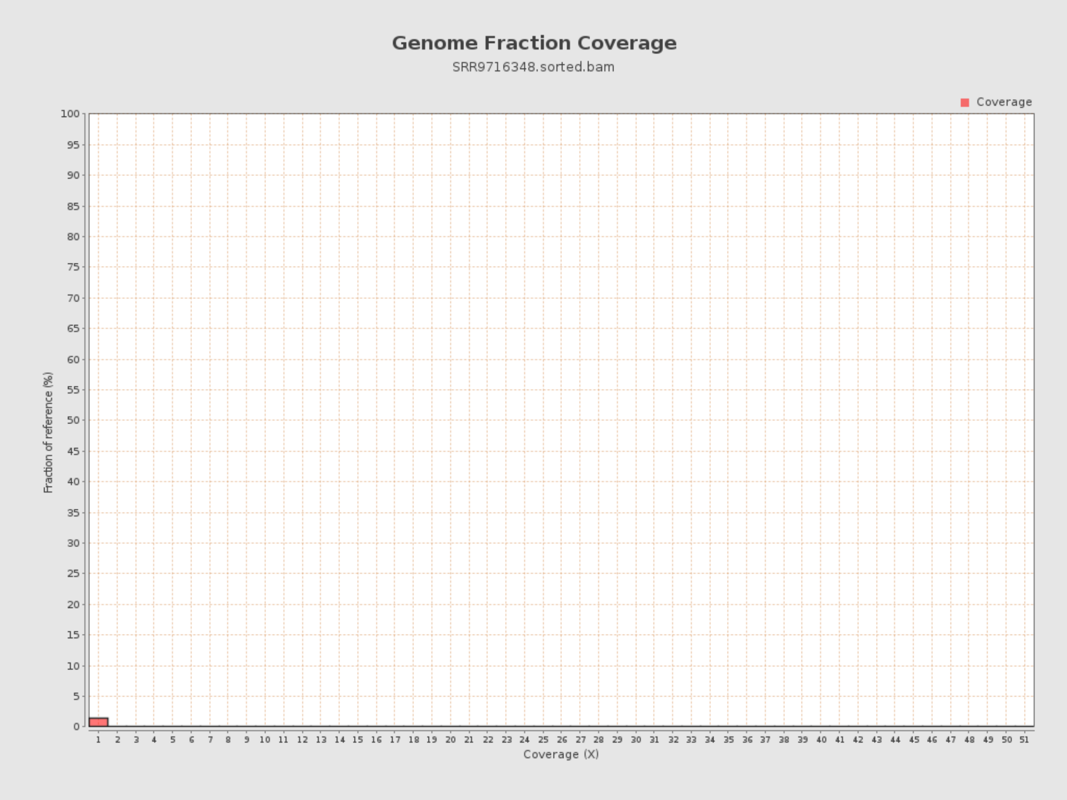
4. Results : Coverage Histogram



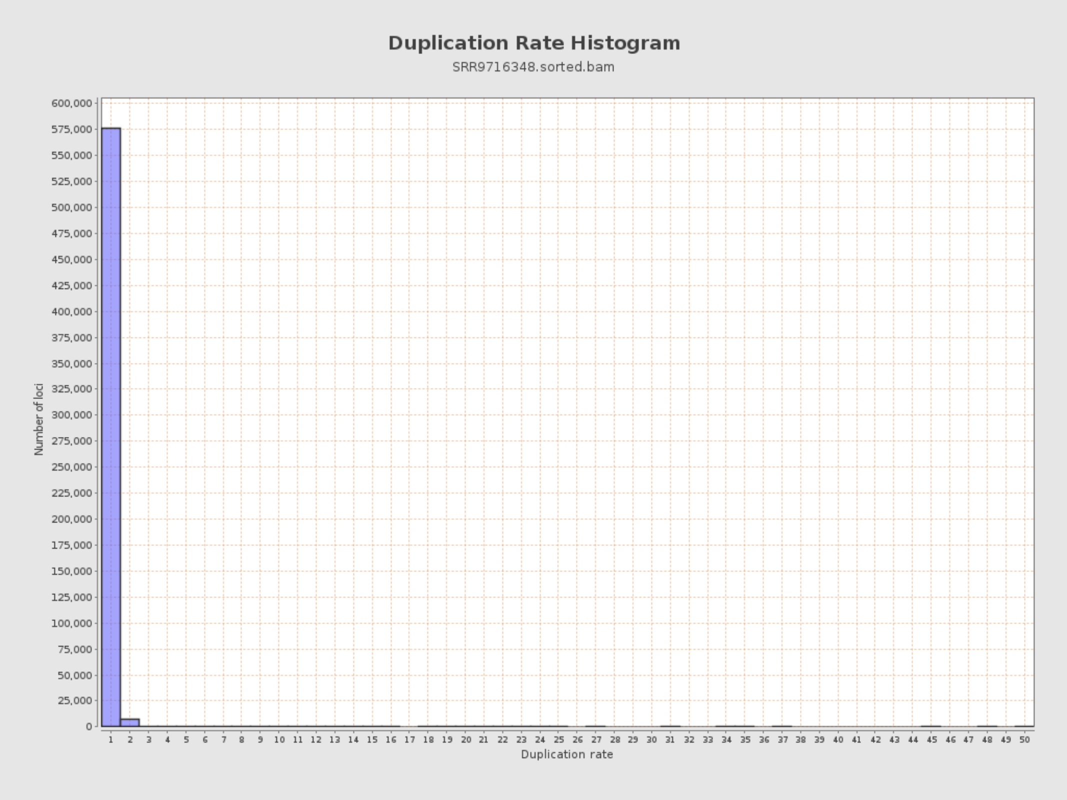
5. Results : Coverage Histogram (0-50X)



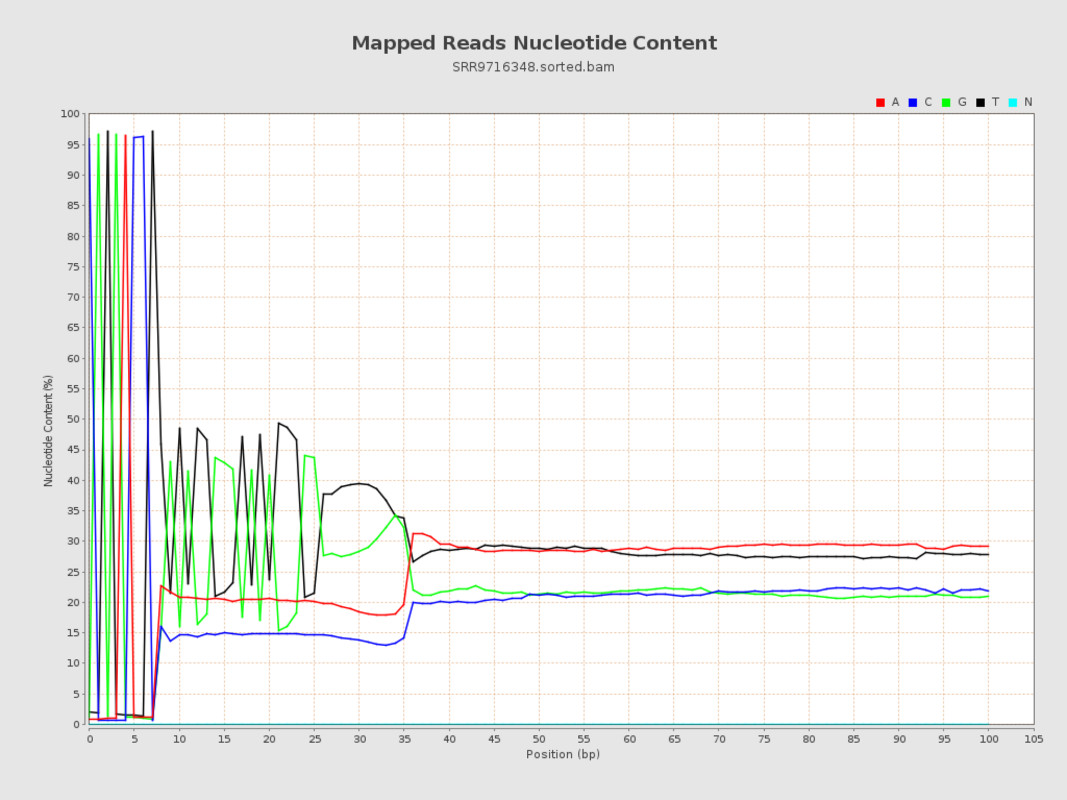
6. Results : Genome Fraction Coverage



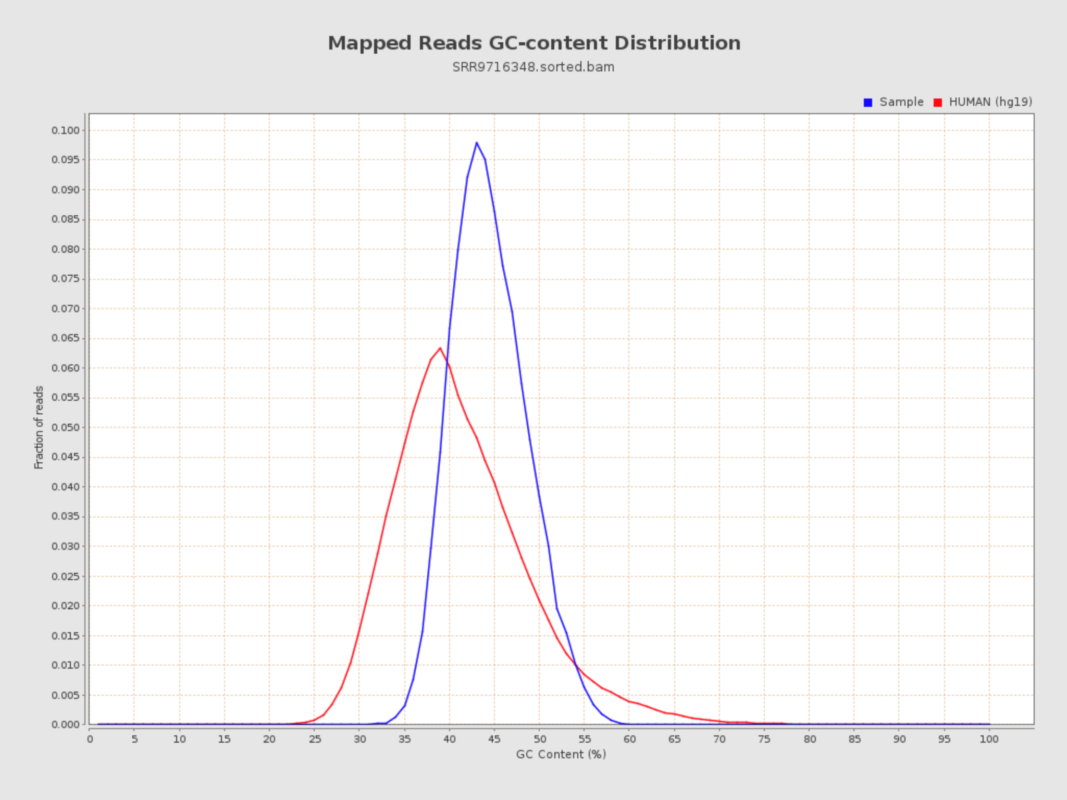
7. Results : Duplication Rate Histogram



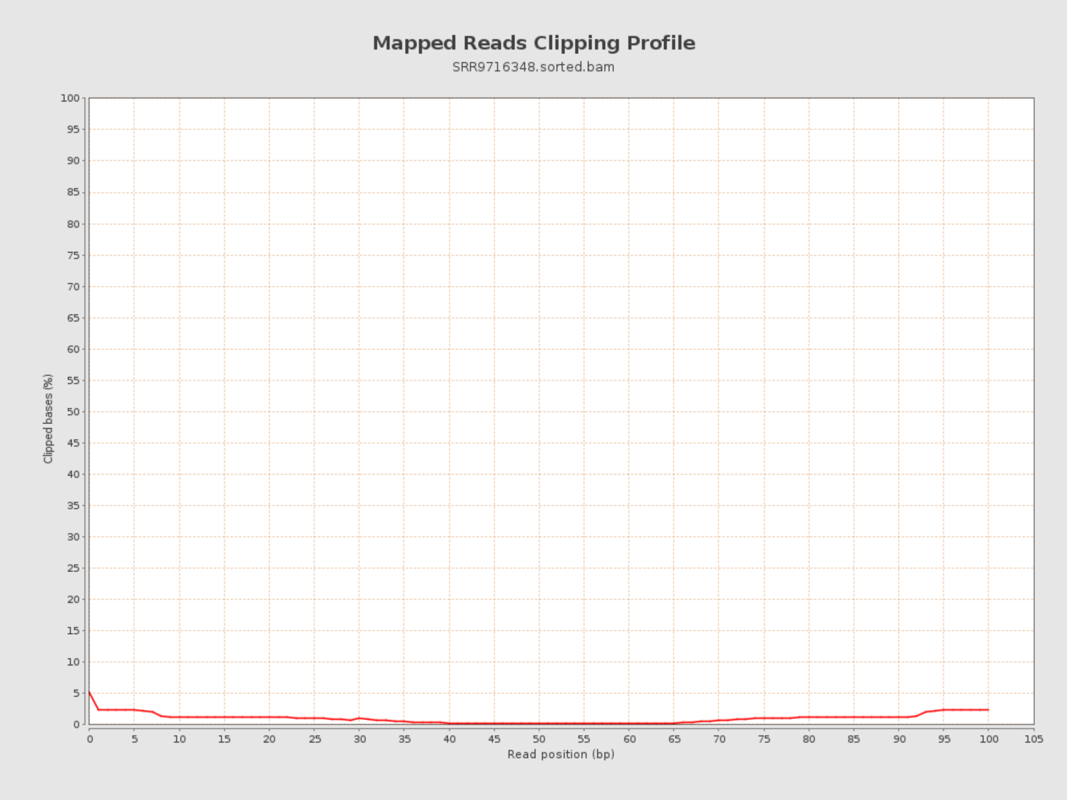
8. Results : Mapped Reads Nucleotide Content



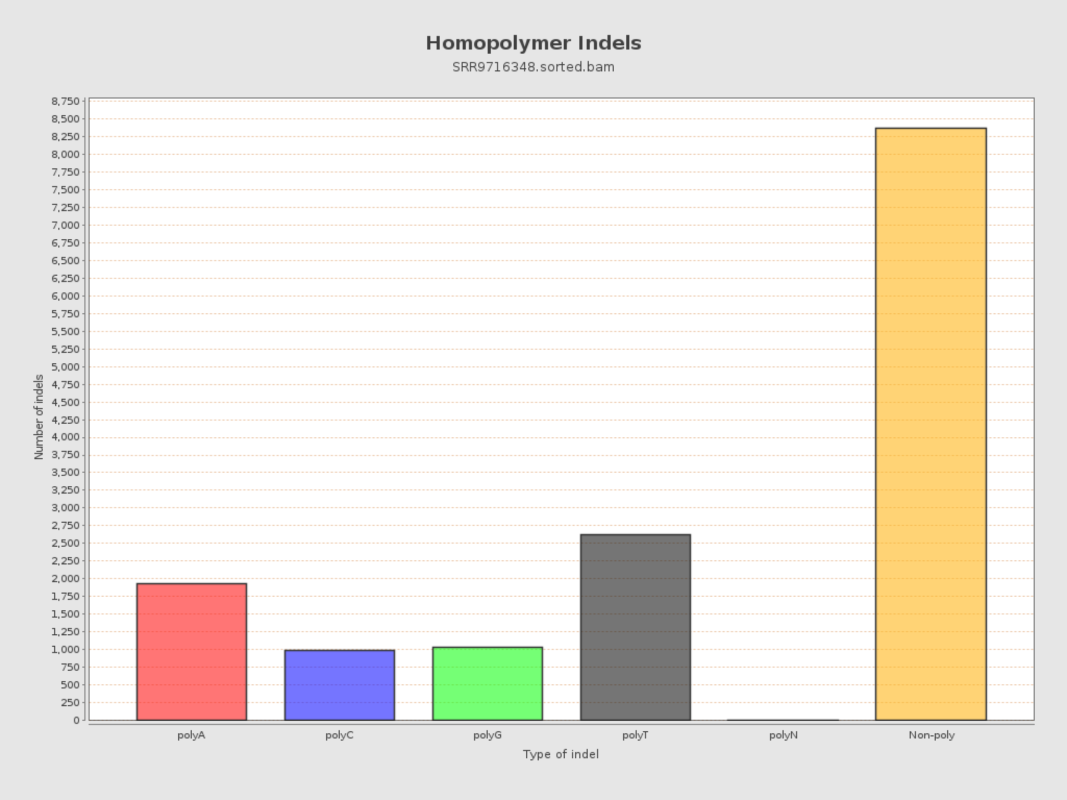
9. Results : Mapped Reads GC-content Distribution



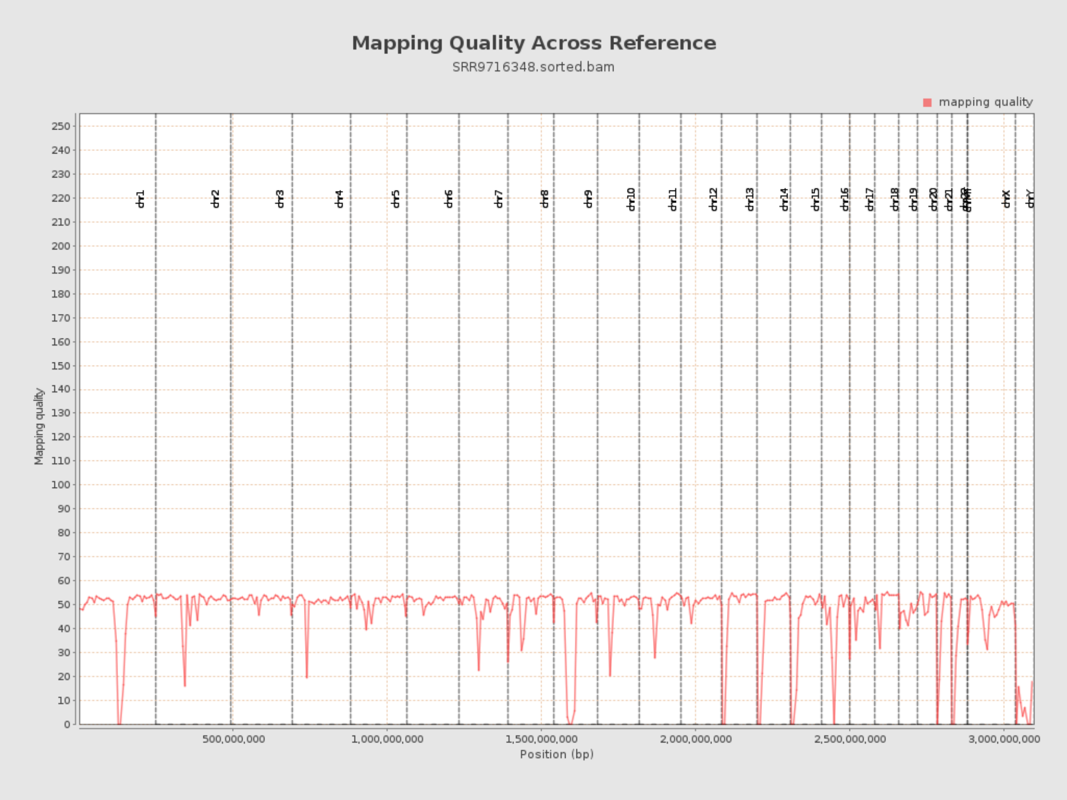
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram