Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 08:43:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716351.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_SRR9716351 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716351.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 08:43:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716351.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	817,674
Mapped reads	736,352 / 90.05%
Unmapped reads	81,322 / 9.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,343 / 1.75%
Read min/max/mean length	30 / 101 / 101.63
Duplicated reads (estimated)	14,154 / 1.73%
Duplication rate	1.3%
Clipped reads	748,883 / 91.59%

2.2. ACGT Content

Number/percentage of A's	14,679,258 / 25.58%
Number/percentage of C's	11,366,363 / 19.81%
Number/percentage of T's	18,108,511 / 31.56%
Number/percentage of G's	13,228,160 / 23.05%
Number/percentage of N's	4,060 / 0.01%
GC Percentage	42.86%

2.3. Coverage

Mean	0.0185

Standard Deviation	0.1848

2.4. Mapping Quality

Mean Mapping Quality	47.28

2.5. Mismatches and indels

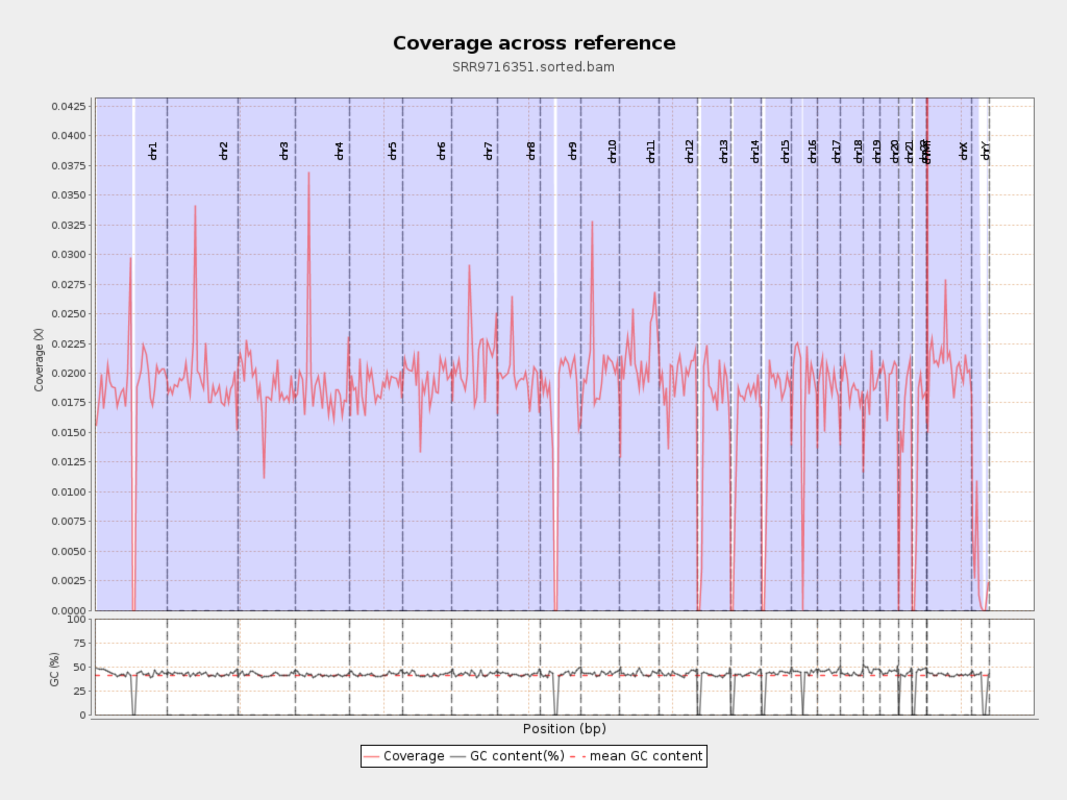
General error rate	0.73%
Mismatches	405,354
Insertions	4,827
Mapped reads with at least one insertion	0.65%
Deletions	13,778
Mapped reads with at least one deletion	1.84%
Homopolymer indels	43.05%

2.6. Chromosome stats

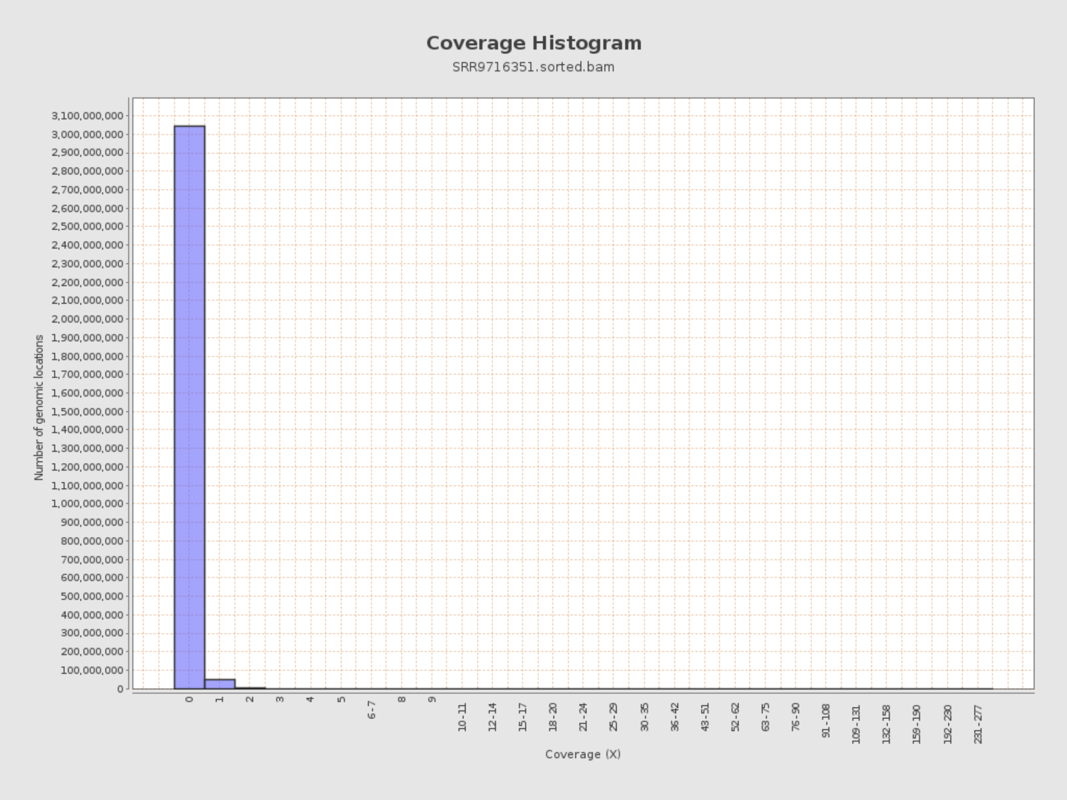
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4547801	0.0182	0.2824
chr2	243199373	4732850	0.0195	0.2122
chr3	198022430	3756126	0.019	0.1427
chr4	191154276	3667086	0.0192	0.1657
chr5	180915260	3433366	0.019	0.1437
chr6	171115067	3329330	0.0195	0.1521
chr7	159138663	3376929	0.0212	0.2469

chr8	146364022	2894931	0.0198	0.2031
chr9	141213431	2428348	0.0172	0.1705
chr10	135534747	2774136	0.0205	0.1928
chr11	135006516	2921862	0.0216	0.1973
chr12	133851895	2613156	0.0195	0.1452
chr13	115169878	1832508	0.0159	0.1307
chr14	107349540	1647101	0.0153	0.1342
chr15	102531392	1622560	0.0158	0.1308
chr16	90354753	1648317	0.0182	0.1439
chr17	81195210	1536538	0.0189	0.1527
chr18	78077248	1476790	0.0189	0.2387
chr19	59128983	1095780	0.0185	0.2322
chr20	63025520	1226639	0.0195	0.1493
chr21	48129895	759567	0.0158	0.1428
chr22	51304566	660771	0.0129	0.1177
chrMT	16571	21865	1.3195	1.3065
chrX	155270560	3238853	0.0209	0.1634
chrY	59373566	169100	0.0028	0.0991

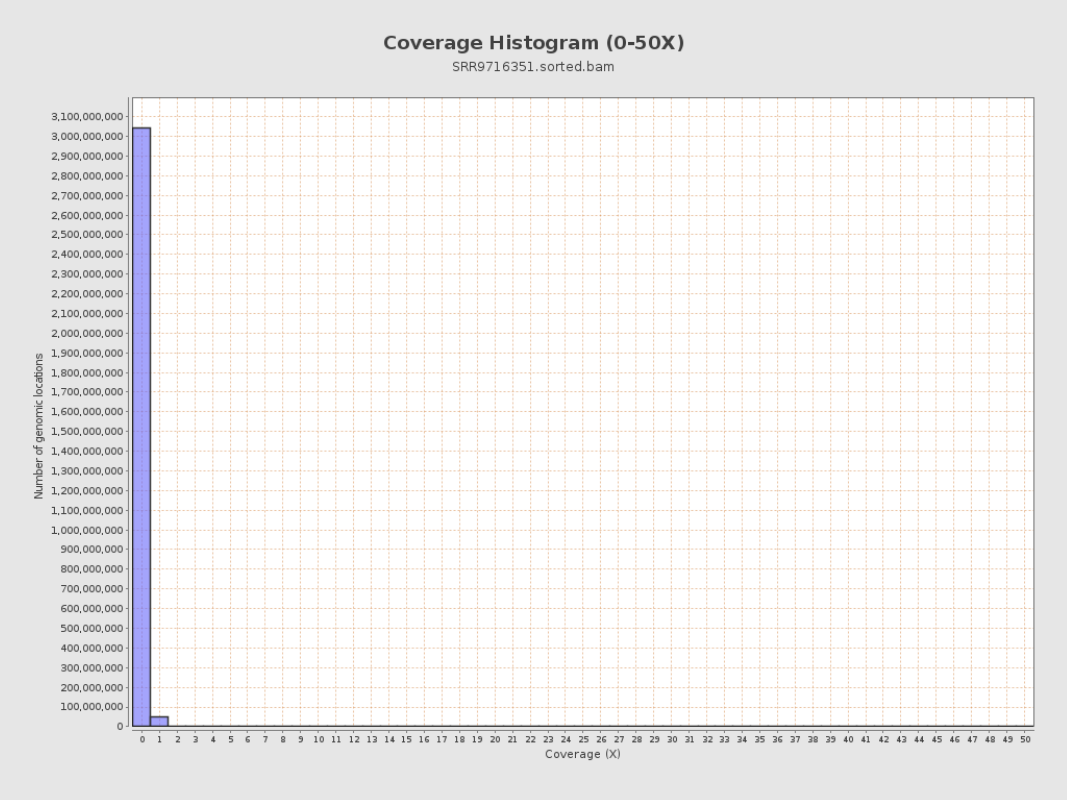
3. Results : Coverage across reference



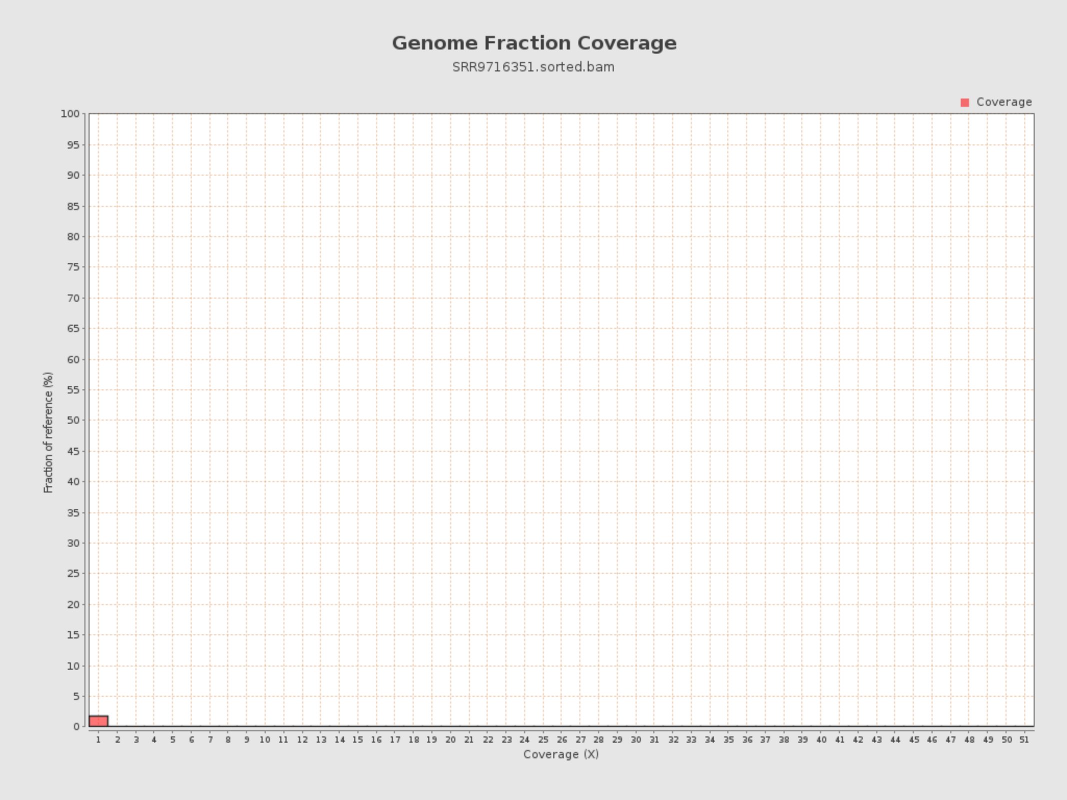
4. Results : Coverage Histogram



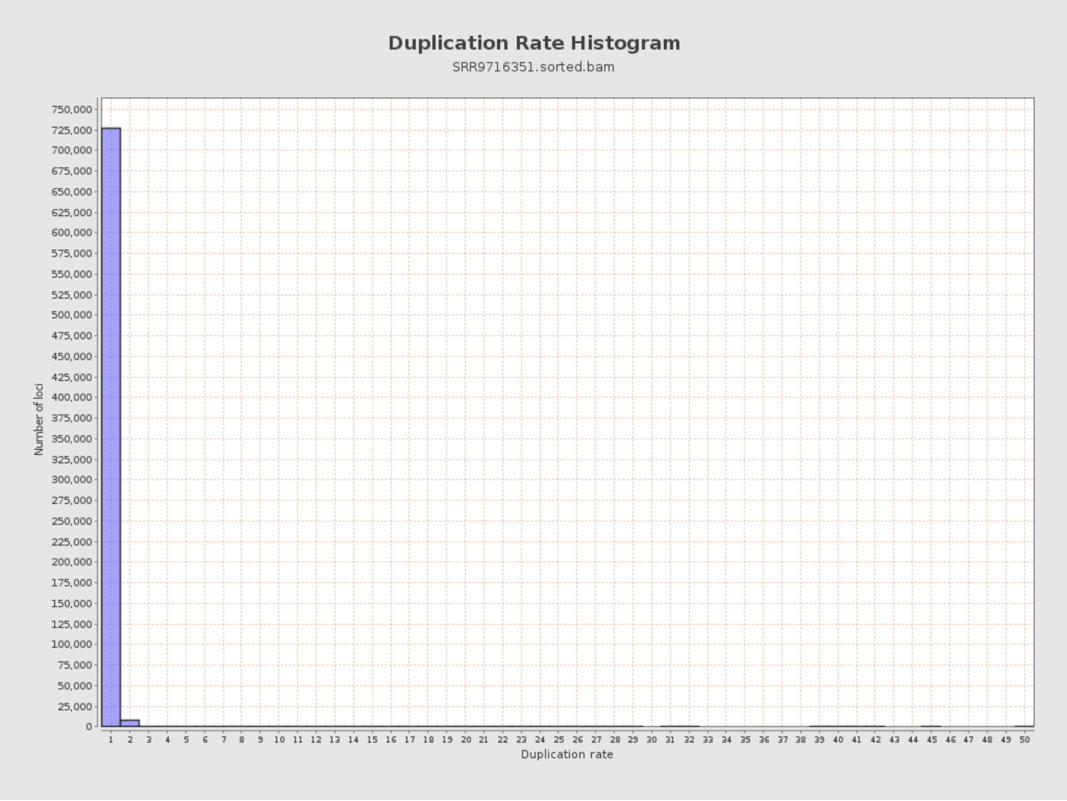
5. Results : Coverage Histogram (0-50X)



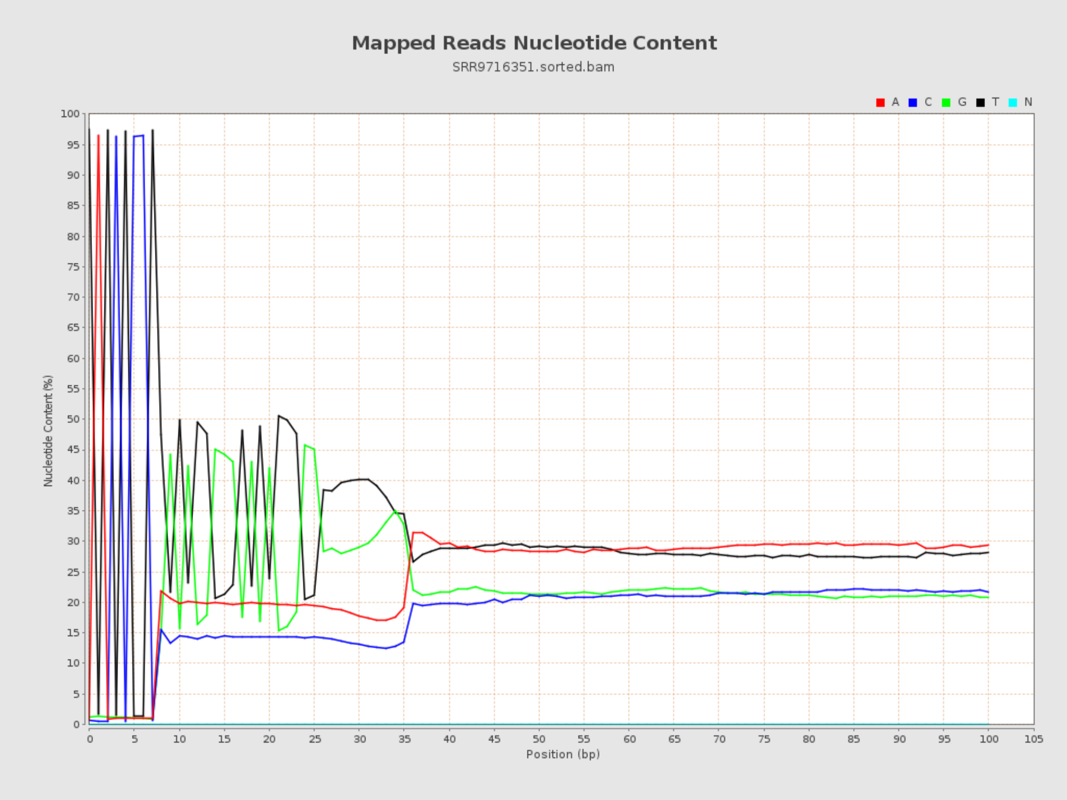
6. Results : Genome Fraction Coverage



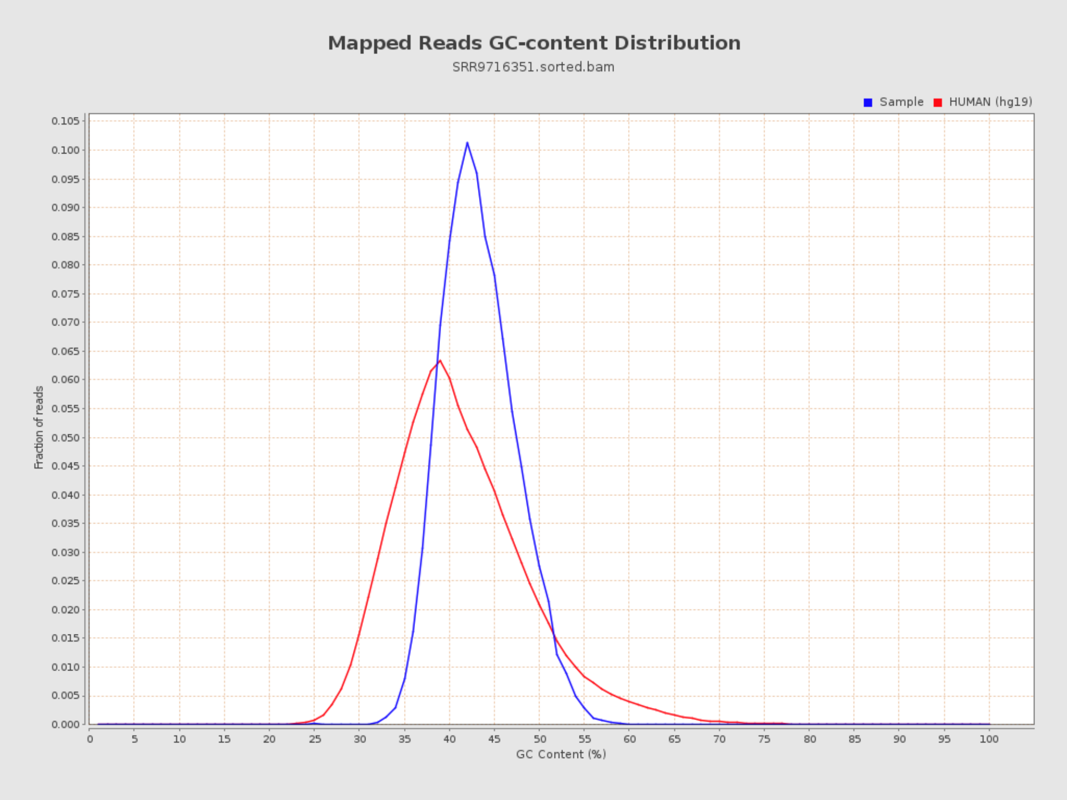
7. Results : Duplication Rate Histogram



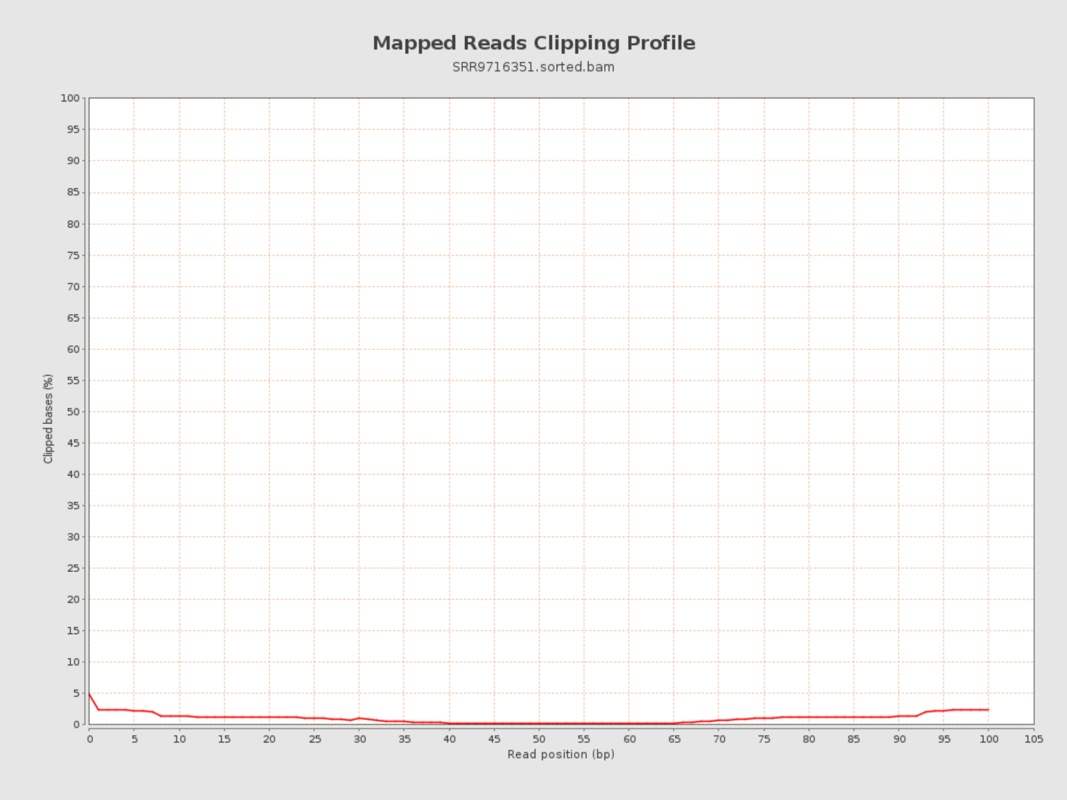
8. Results : Mapped Reads Nucleotide Content



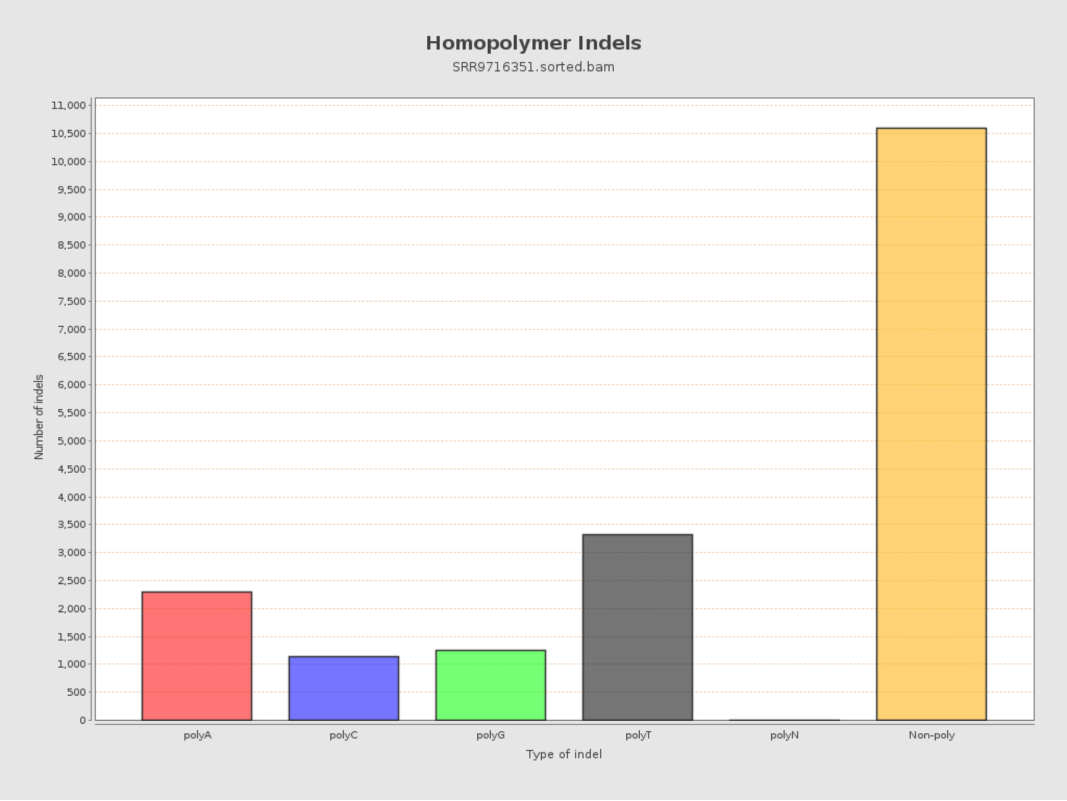
9. Results : Mapped Reads GC-content Distribution



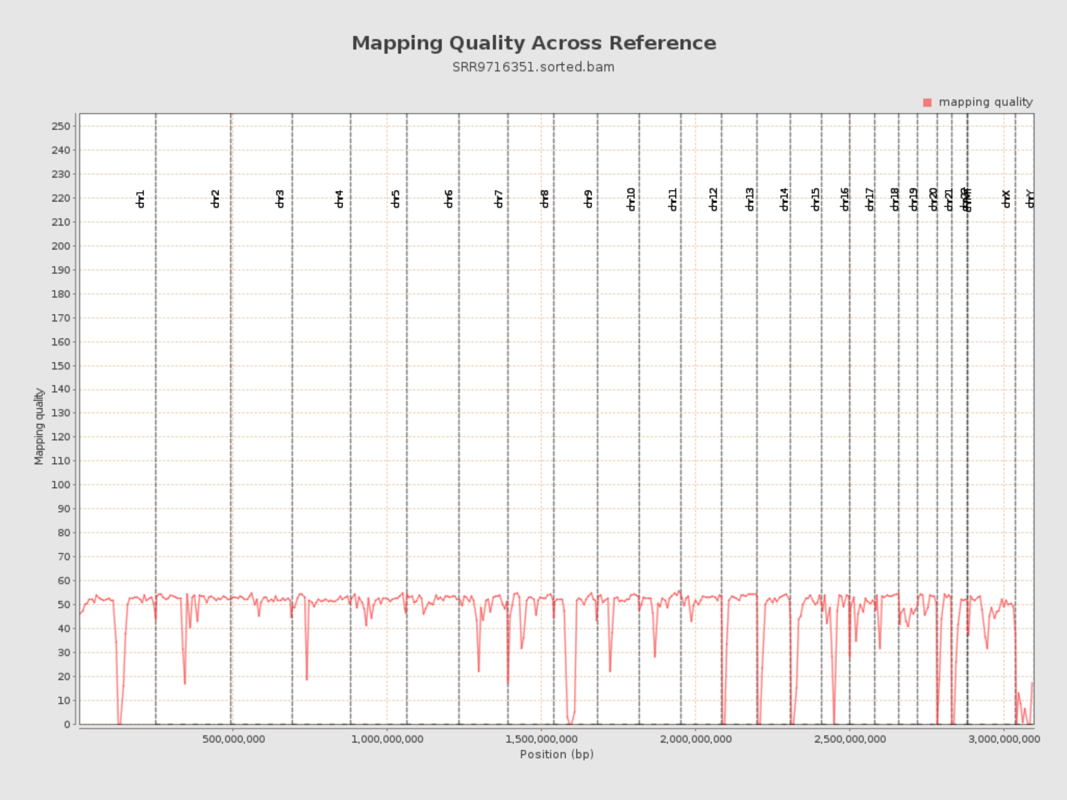
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram