Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 14:22:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716840.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_SRR9716840 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716840.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 14:22:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716840.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,263,115
Mapped reads	2,901,294 / 88.91%
Unmapped reads	361,821 / 11.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,793 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	123,286 / 3.78%
Duplication rate	3.06%
Clipped reads	2,908,385 / 89.13%

2.2. ACGT Content

Number/percentage of A's	42,515,402 / 25.58%
Number/percentage of C's	30,536,611 / 18.37%
Number/percentage of T's	51,285,791 / 30.86%
Number/percentage of G's	41,876,083 / 25.19%
Number/percentage of N's	1,144 / 0%
GC Percentage	43.57%

2.3. Coverage

Mean	0.0537

Standard Deviation	0.4424

2.4. Mapping Quality

Mean Mapping Quality	43.75

2.5. Mismatches and indels

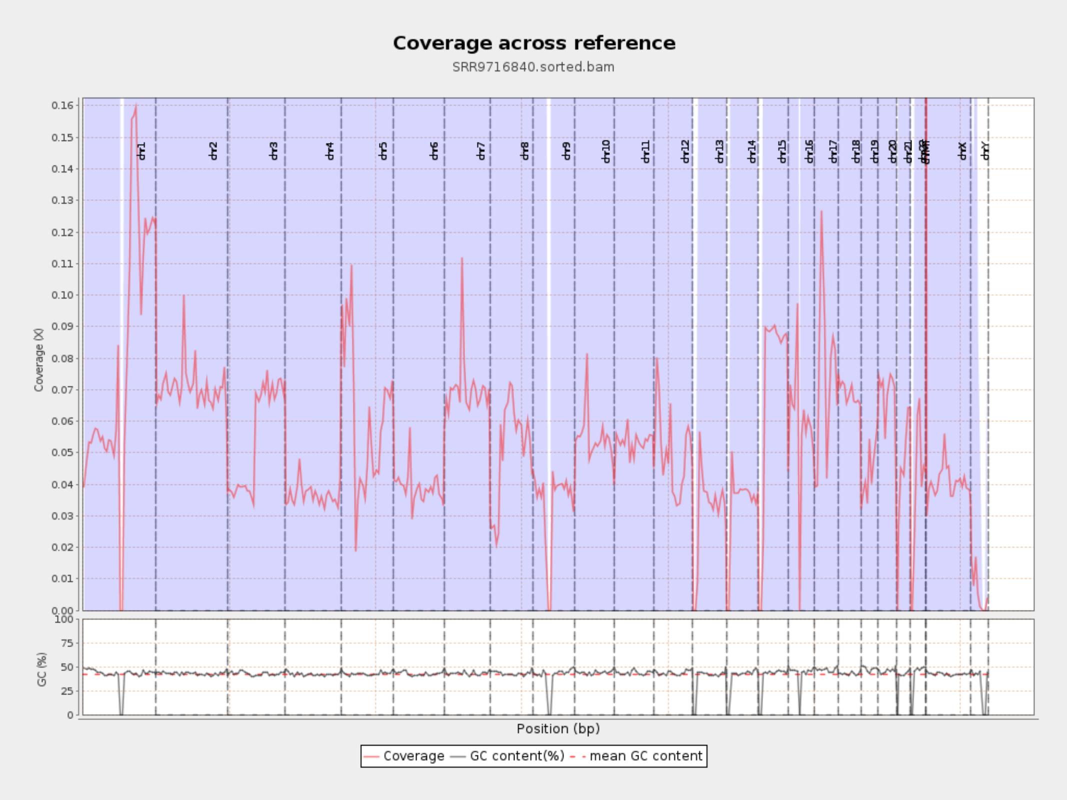
General error rate	0.52%
Mismatches	849,156
Insertions	10,866
Mapped reads with at least one insertion	0.37%
Deletions	29,384
Mapped reads with at least one deletion	1.01%
Homopolymer indels	41.39%

2.6. Chromosome stats

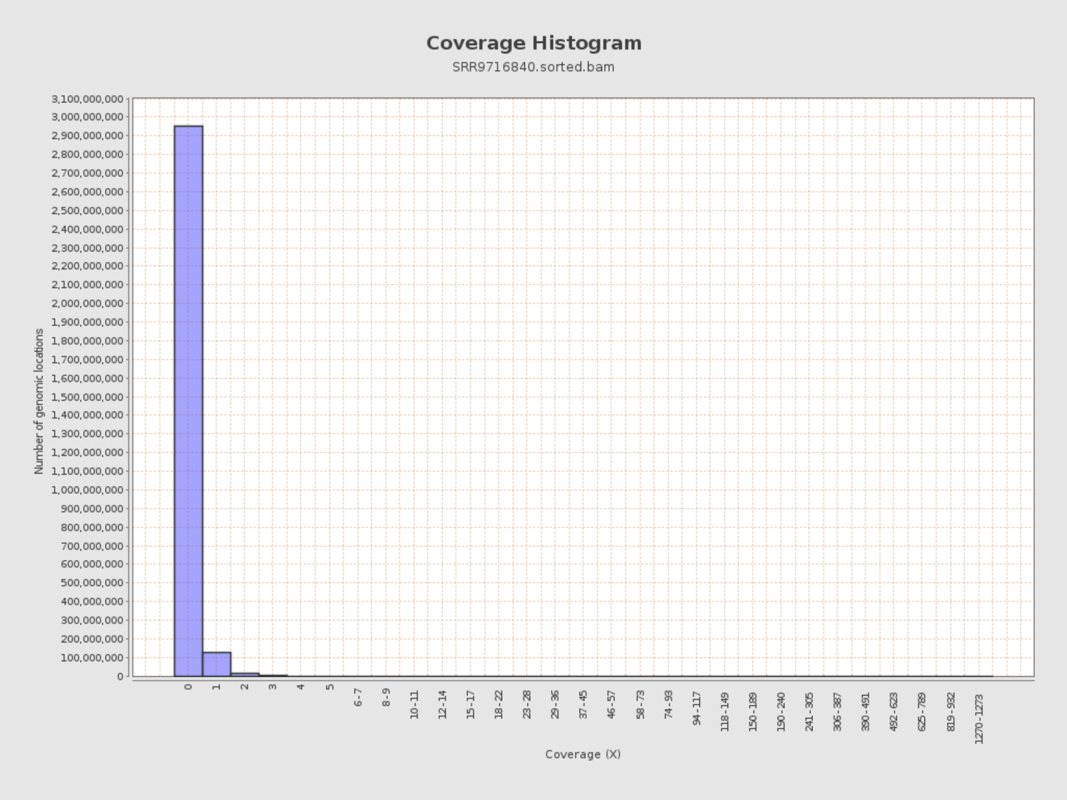
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19794203	0.0794	0.7403
chr2	243199373	17232434	0.0709	0.6404
chr3	198022430	10782130	0.0544	0.2681
chr4	191154276	7027584	0.0368	0.2361
chr5	180915260	11094320	0.0613	0.2846
chr6	171115067	6701792	0.0392	0.2739
chr7	159138663	11251361	0.0707	0.7991

chr8	146364022	7534815	0.0515	0.3516
chr9	141213431	4746301	0.0336	0.3332
chr10	135534747	7459059	0.055	0.381
chr11	135006516	7179697	0.0532	0.4258
chr12	133851895	6736195	0.0503	0.2611
chr13	115169878	3627500	0.0315	0.2036
chr14	107349540	3583483	0.0334	0.2265
chr15	102531392	7234736	0.0706	0.3157
chr16	90354753	5214785	0.0577	0.3049
chr17	81195210	5989785	0.0738	0.3454
chr18	78077248	5378000	0.0689	0.7315
chr19	59128983	2632275	0.0445	0.6064
chr20	63025520	4336690	0.0688	0.3031
chr21	48129895	2126830	0.0442	0.2499
chr22	51304566	1911694	0.0373	0.2189
chrMT	16571	11085	0.6689	0.9003
chrX	155270560	6320543	0.0407	0.2932
chrY	59373566	353350	0.006	0.1179

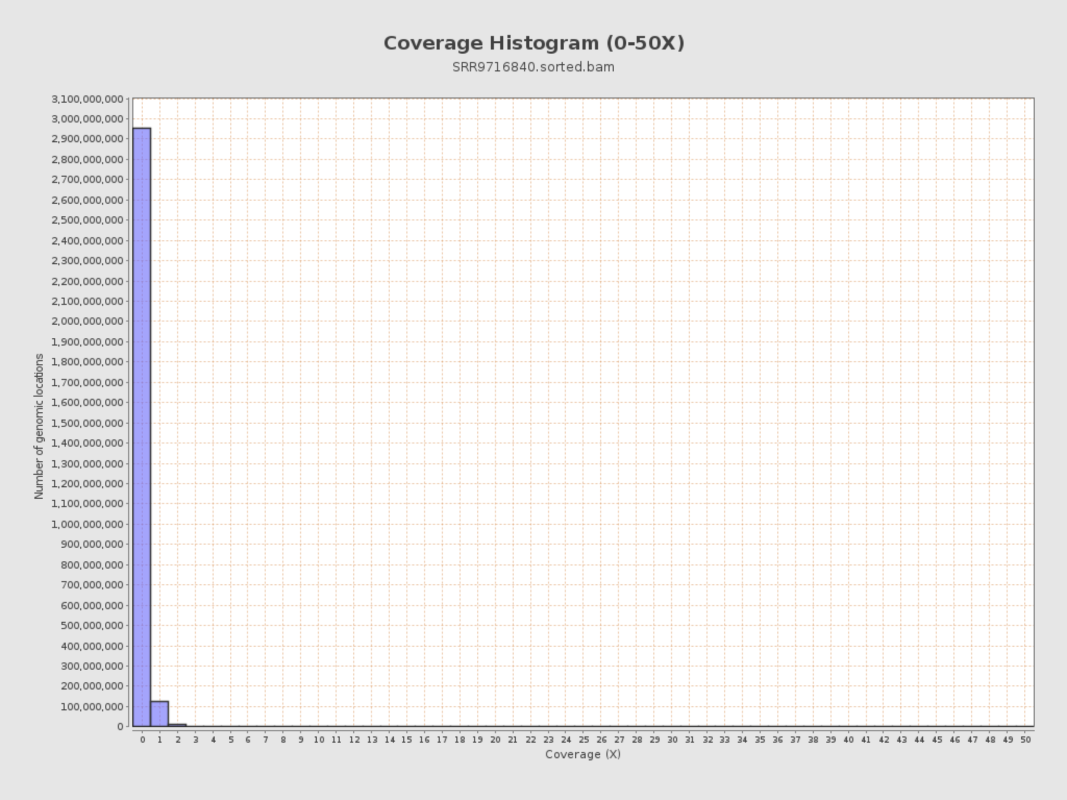
3. Results : Coverage across reference



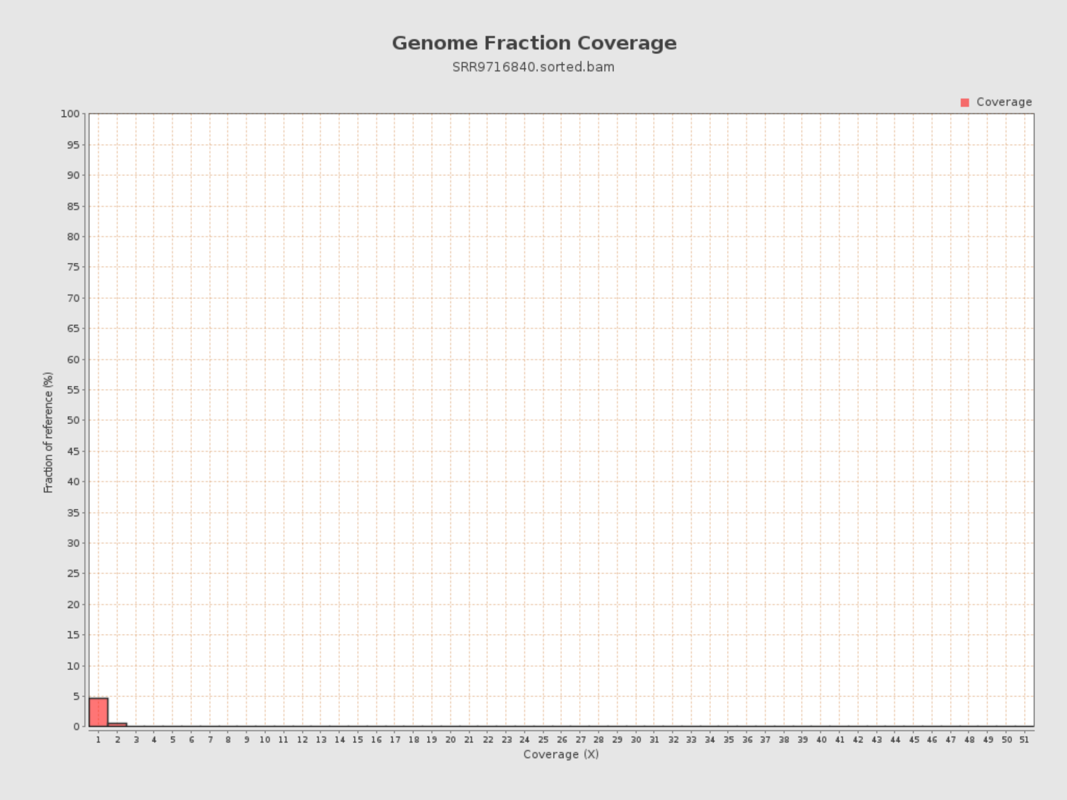
4. Results : Coverage Histogram



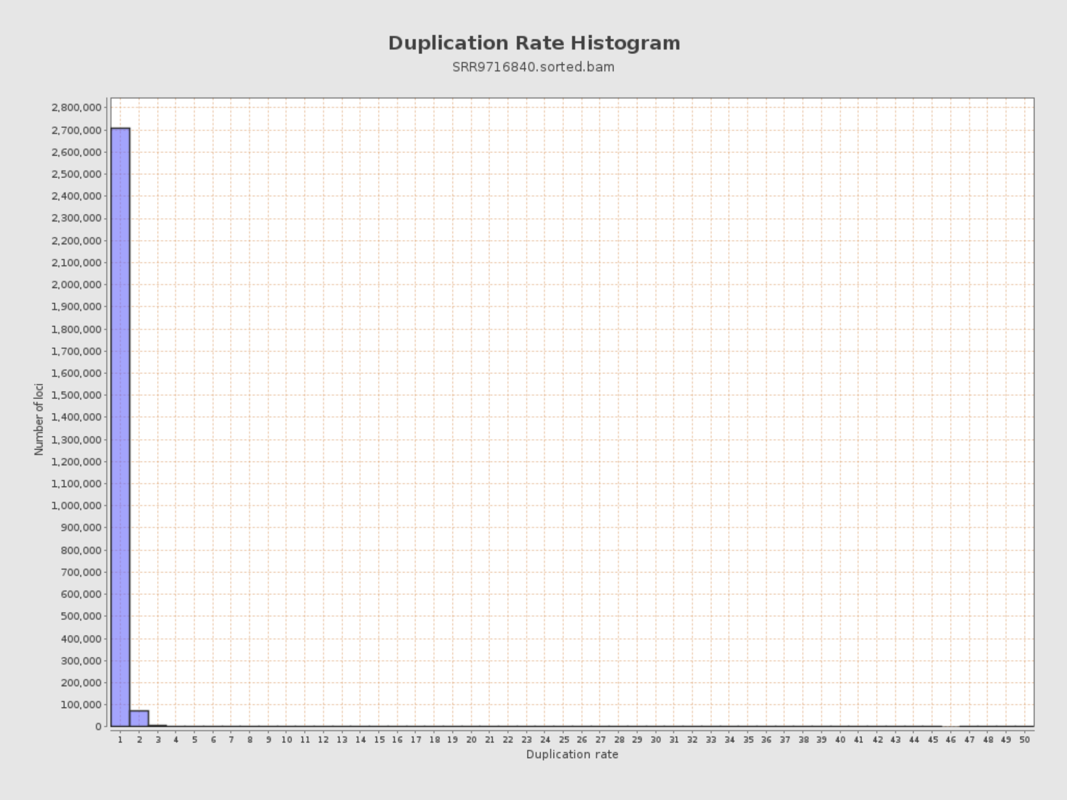
5. Results : Coverage Histogram (0-50X)



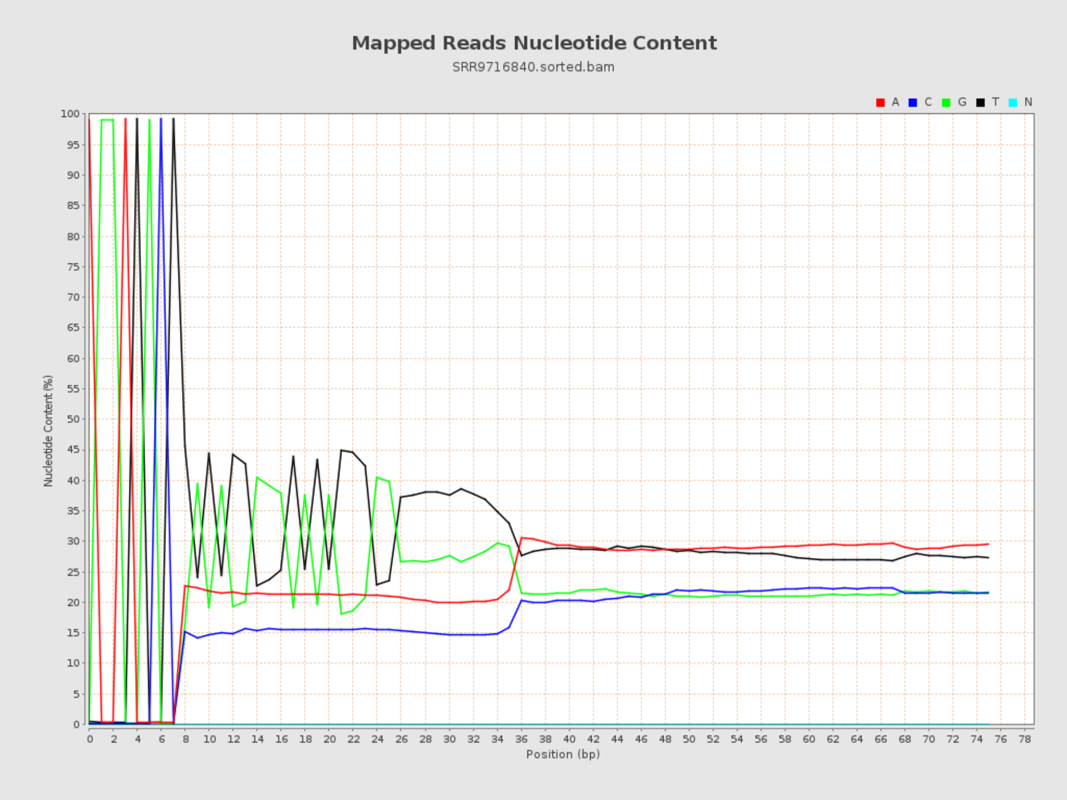
6. Results : Genome Fraction Coverage



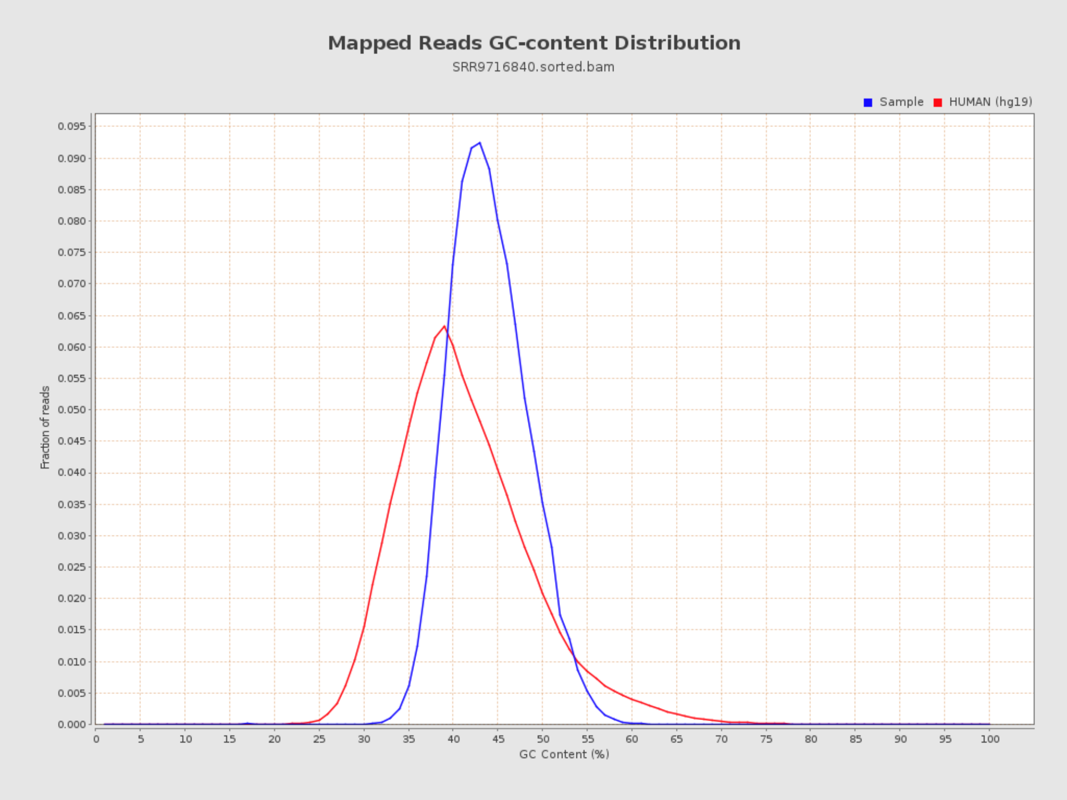
7. Results : Duplication Rate Histogram



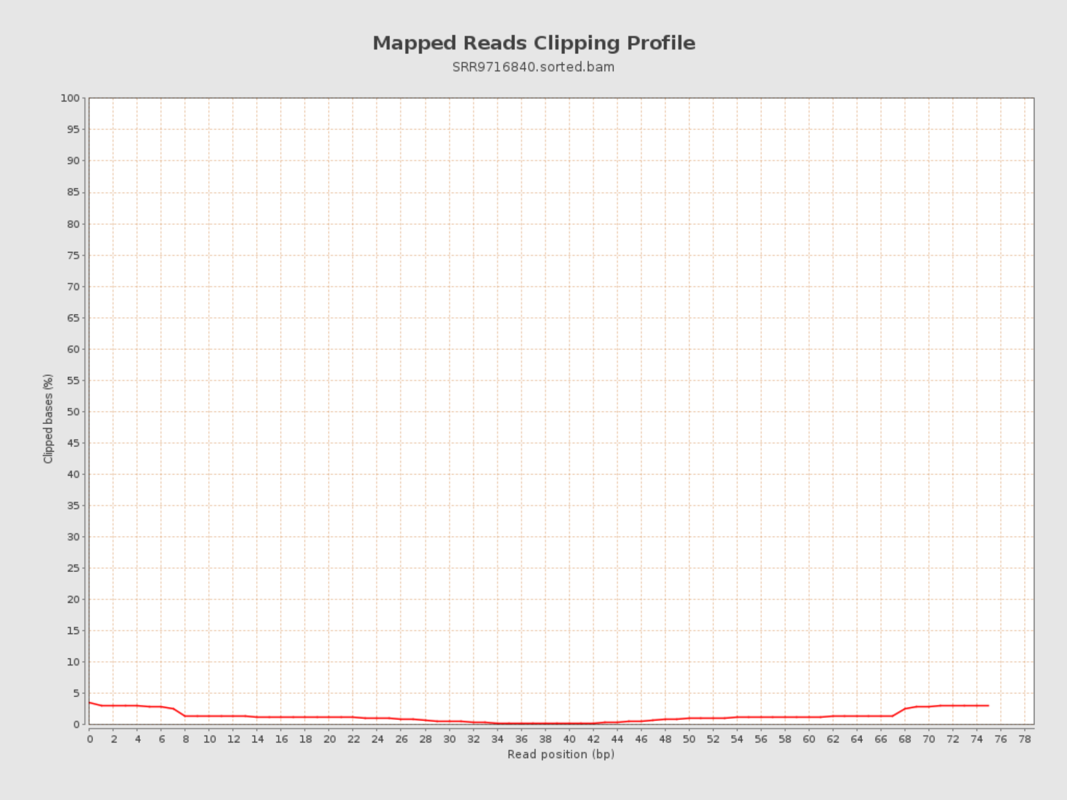
8. Results : Mapped Reads Nucleotide Content



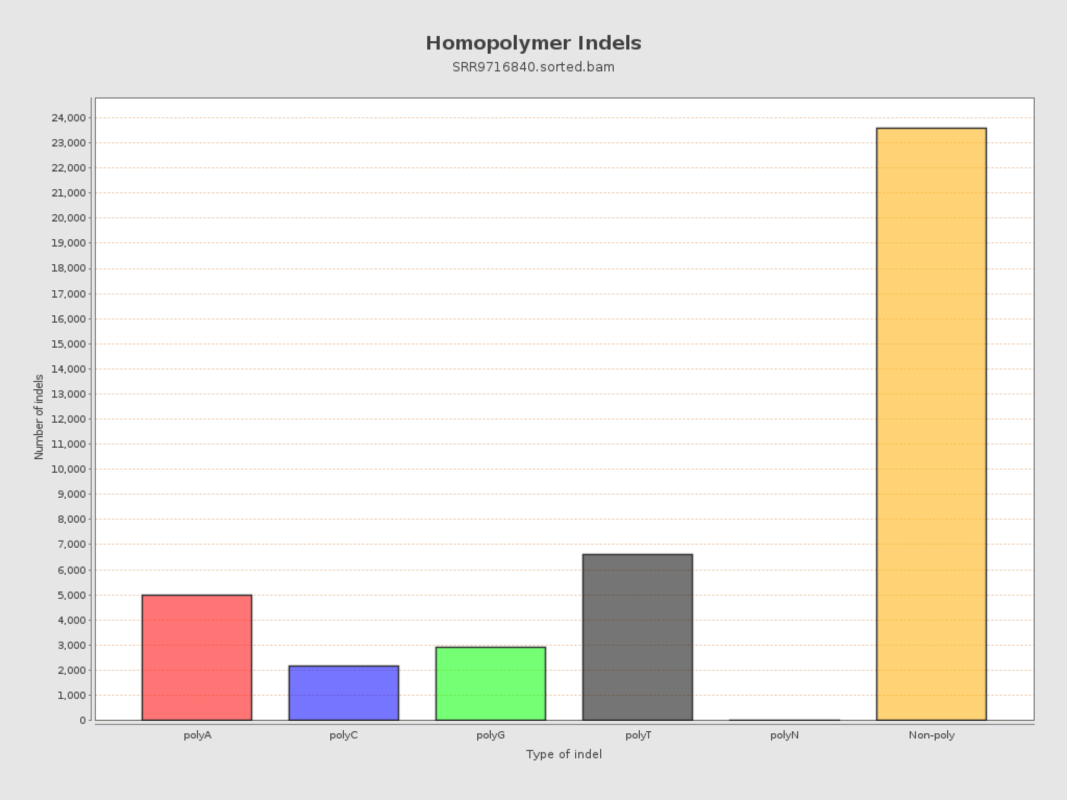
9. Results : Mapped Reads GC-content Distribution



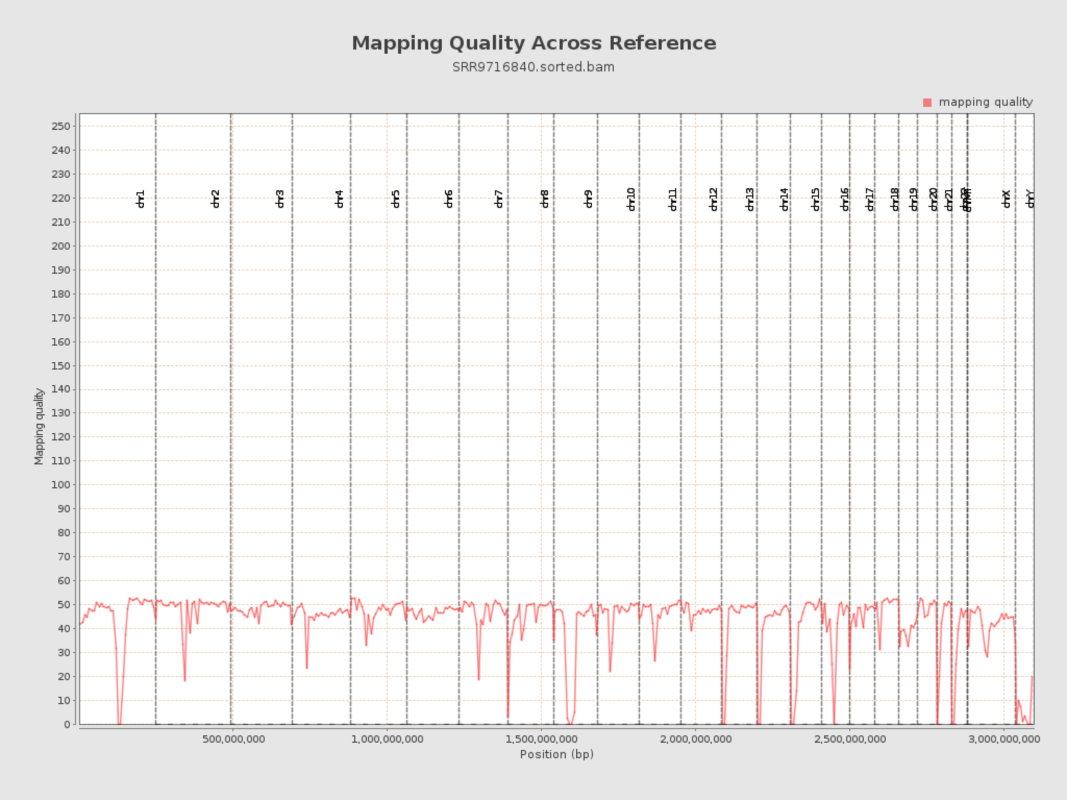
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram