Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 13:52:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716441.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_SRR9716441 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716441.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 13:52:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716441.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,656,359
Mapped reads	1,478,524 / 89.26%
Unmapped reads	177,835 / 10.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,512 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	42,779 / 2.58%
Duplication rate	2.13%
Clipped reads	1,479,038 / 89.29%

2.2. ACGT Content

Number/percentage of A's	22,701,376 / 26.45%
Number/percentage of C's	16,696,749 / 19.45%
Number/percentage of T's	25,588,086 / 29.81%
Number/percentage of G's	20,839,896 / 24.28%
Number/percentage of N's	642 / 0%
GC Percentage	43.74%

2.3. Coverage

Mean	0.0277

Standard Deviation	0.2332

2.4. Mapping Quality

Mean Mapping Quality	44.19

2.5. Mismatches and indels

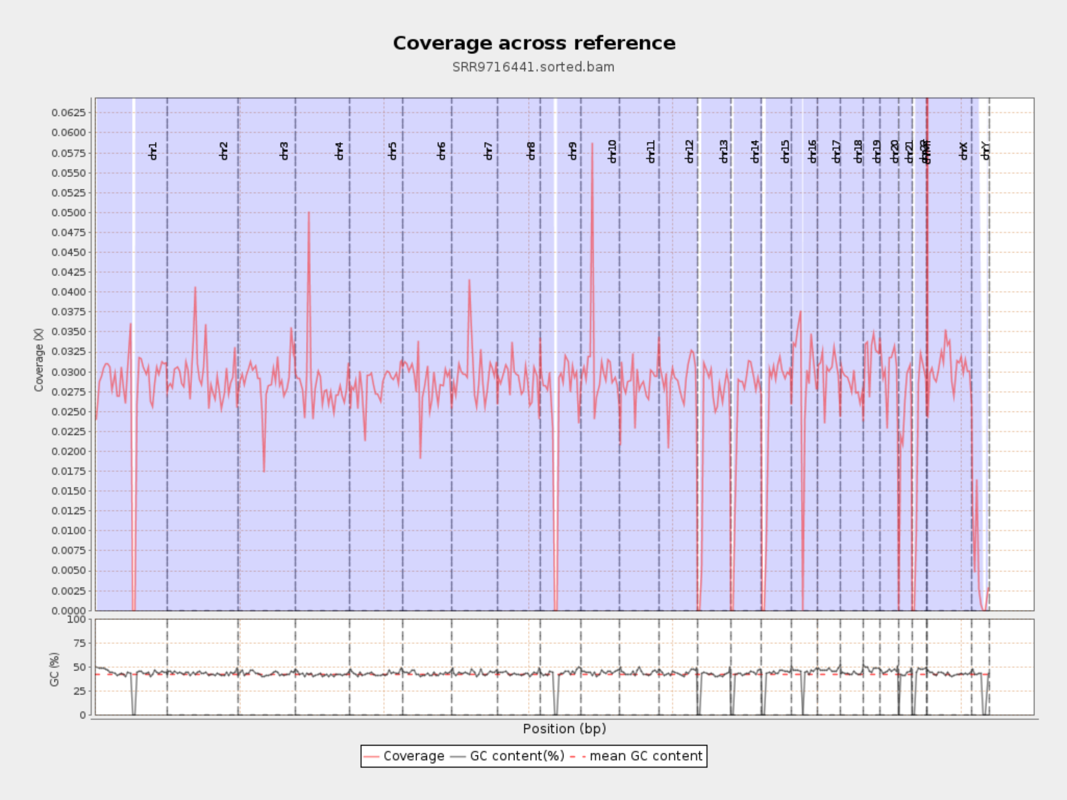
General error rate	0.53%
Mismatches	443,405
Insertions	7,185
Mapped reads with at least one insertion	0.48%
Deletions	17,002
Mapped reads with at least one deletion	1.14%
Homopolymer indels	40.77%

2.6. Chromosome stats

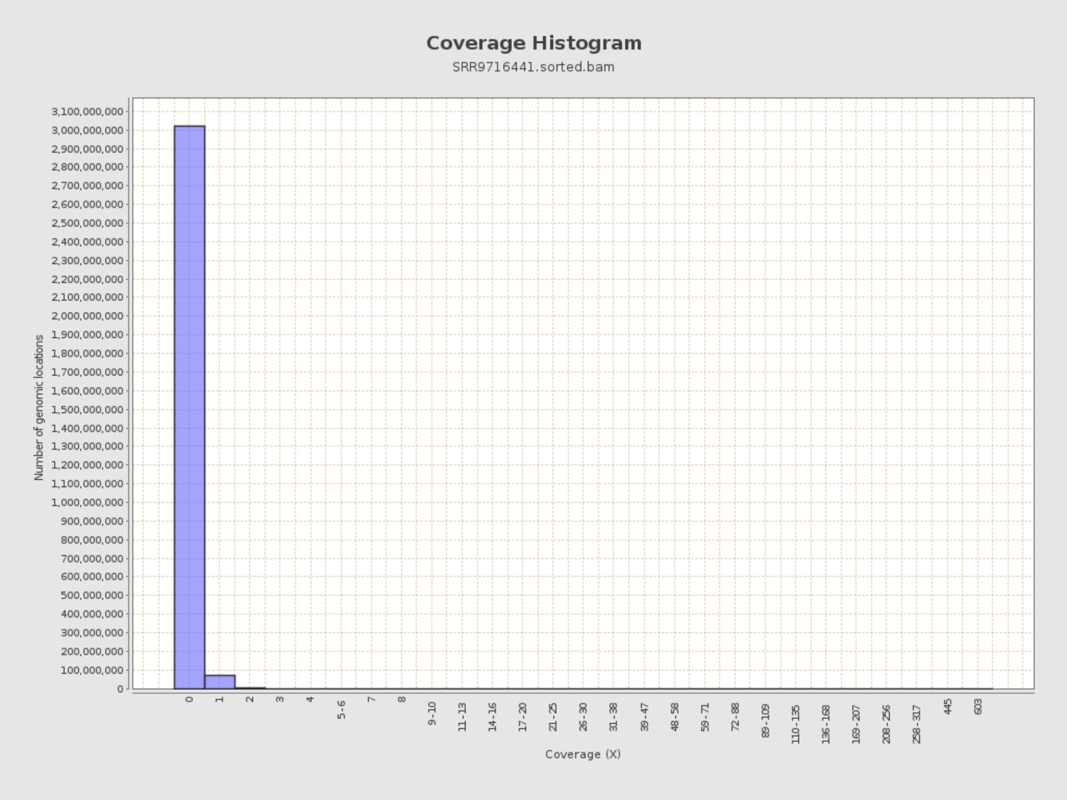
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6871893	0.0276	0.2873
chr2	243199373	7166386	0.0295	0.3298
chr3	198022430	5735586	0.029	0.1891
chr4	191154276	5456092	0.0285	0.2091
chr5	180915260	5147203	0.0285	0.1831
chr6	171115067	4895480	0.0286	0.2039
chr7	159138663	4760359	0.0299	0.2899

chr8	146364022	4232564	0.0289	0.2404
chr9	141213431	3612236	0.0256	0.2045
chr10	135534747	4197309	0.031	0.3001
chr11	135006516	3852077	0.0285	0.217
chr12	133851895	3853766	0.0288	0.1862
chr13	115169878	2713214	0.0236	0.1676
chr14	107349540	2610236	0.0243	0.1775
chr15	102531392	2484363	0.0242	0.1714
chr16	90354753	2590329	0.0287	0.1998
chr17	81195210	2437066	0.03	0.196
chr18	78077248	2225888	0.0285	0.3096
chr19	59128983	1897935	0.0321	0.2805
chr20	63025520	1880492	0.0298	0.1972
chr21	48129895	1135786	0.0236	0.195
chr22	51304566	1065198	0.0208	0.1592
chrMT	16571	11843	0.7147	0.9412
chrX	155270560	4742131	0.0305	0.2025
chrY	59373566	278660	0.0047	0.1486

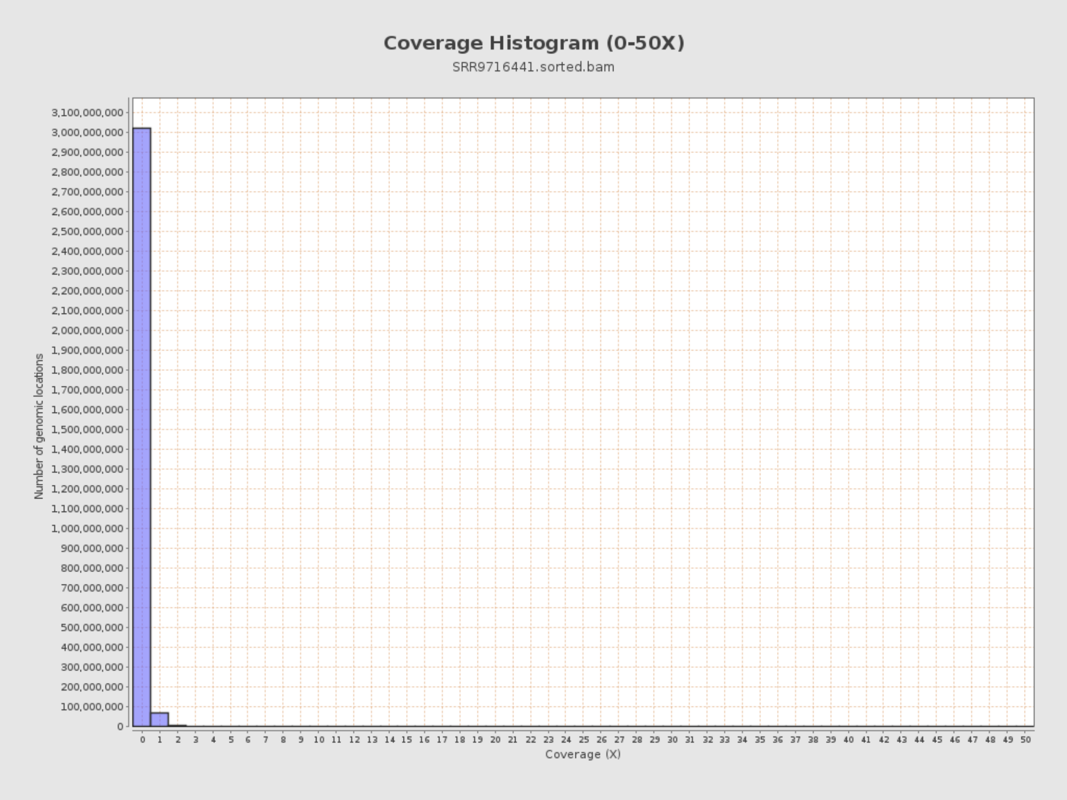
3. Results : Coverage across reference



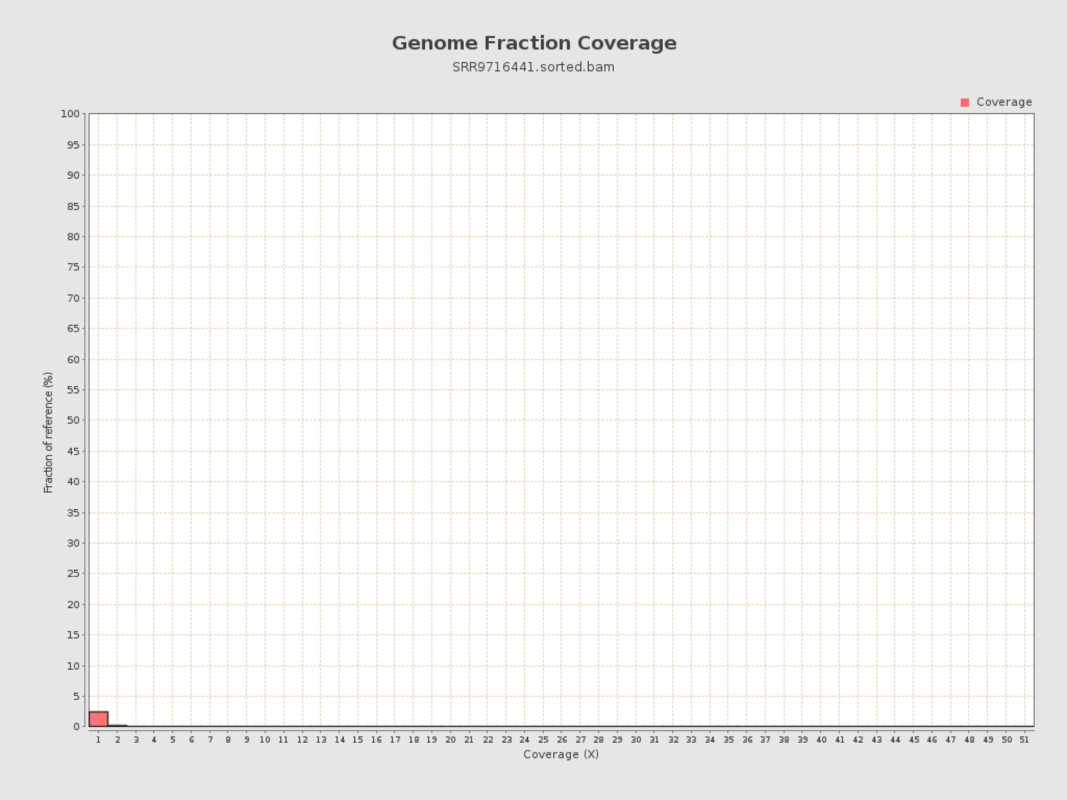
4. Results : Coverage Histogram



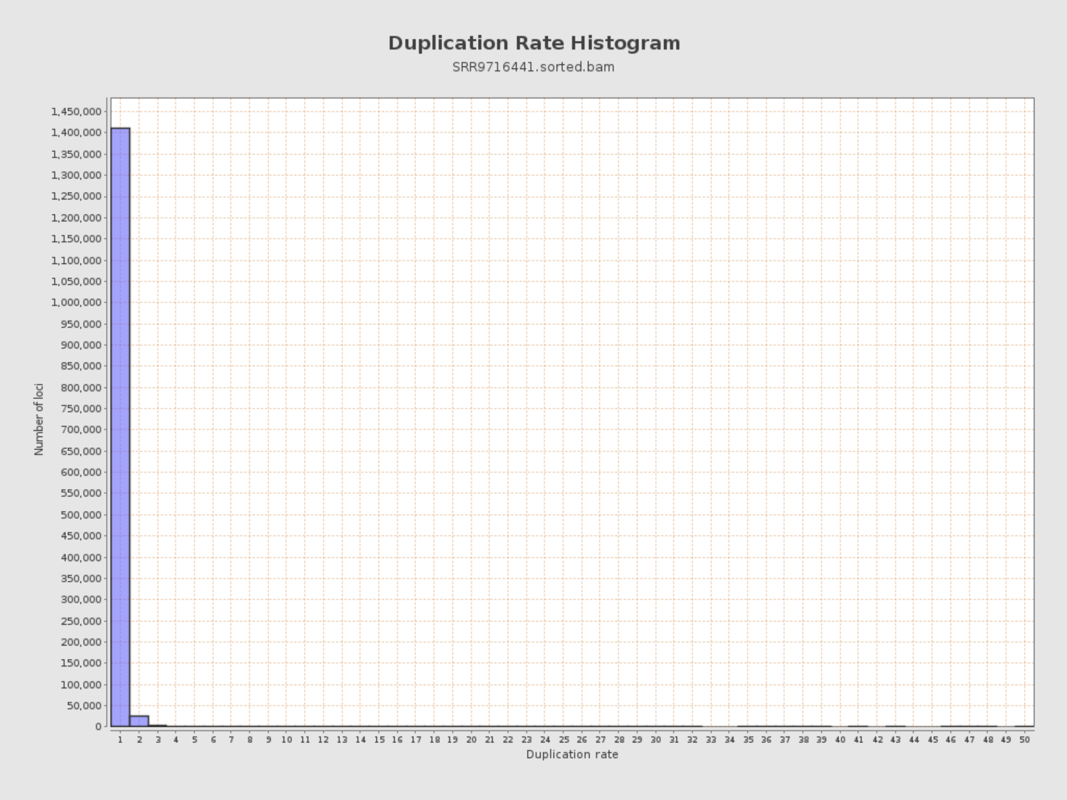
5. Results : Coverage Histogram (0-50X)



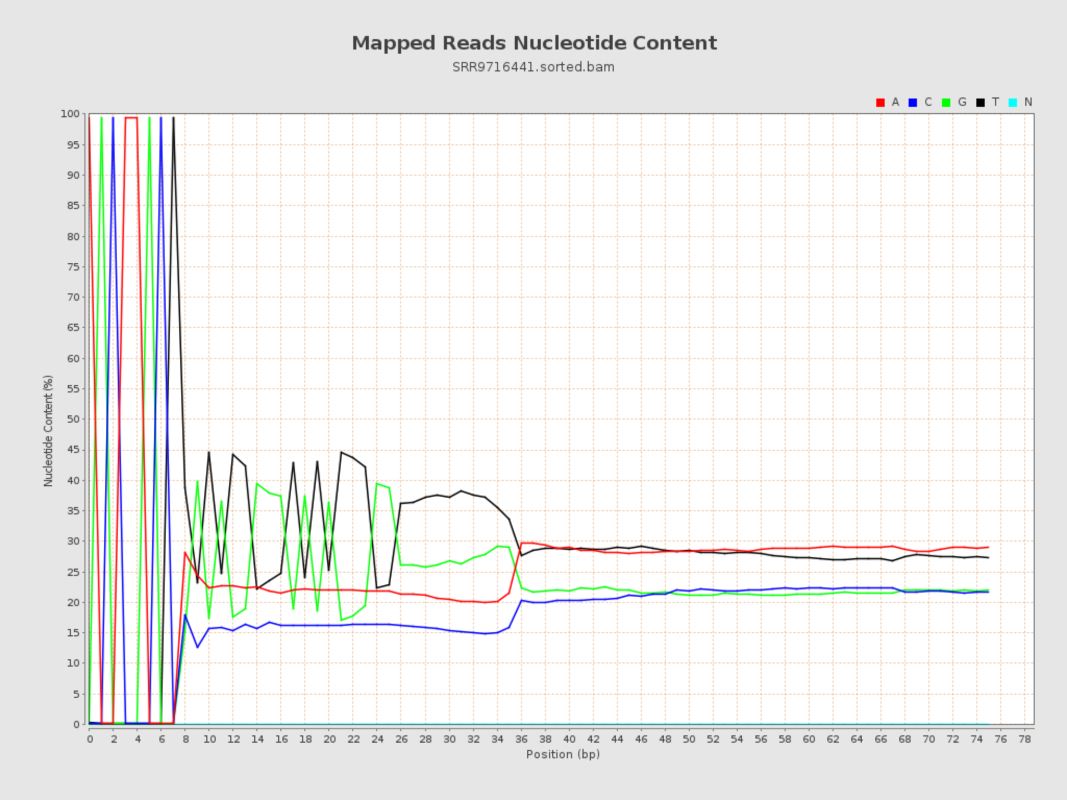
6. Results : Genome Fraction Coverage



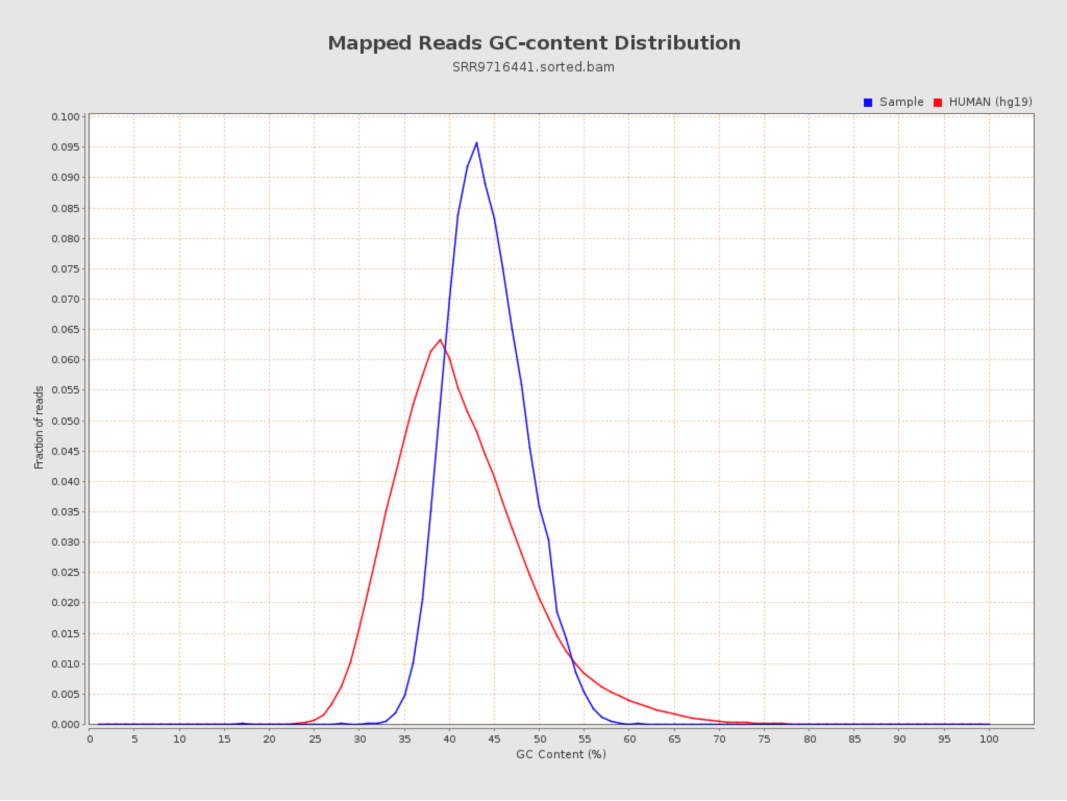
7. Results : Duplication Rate Histogram



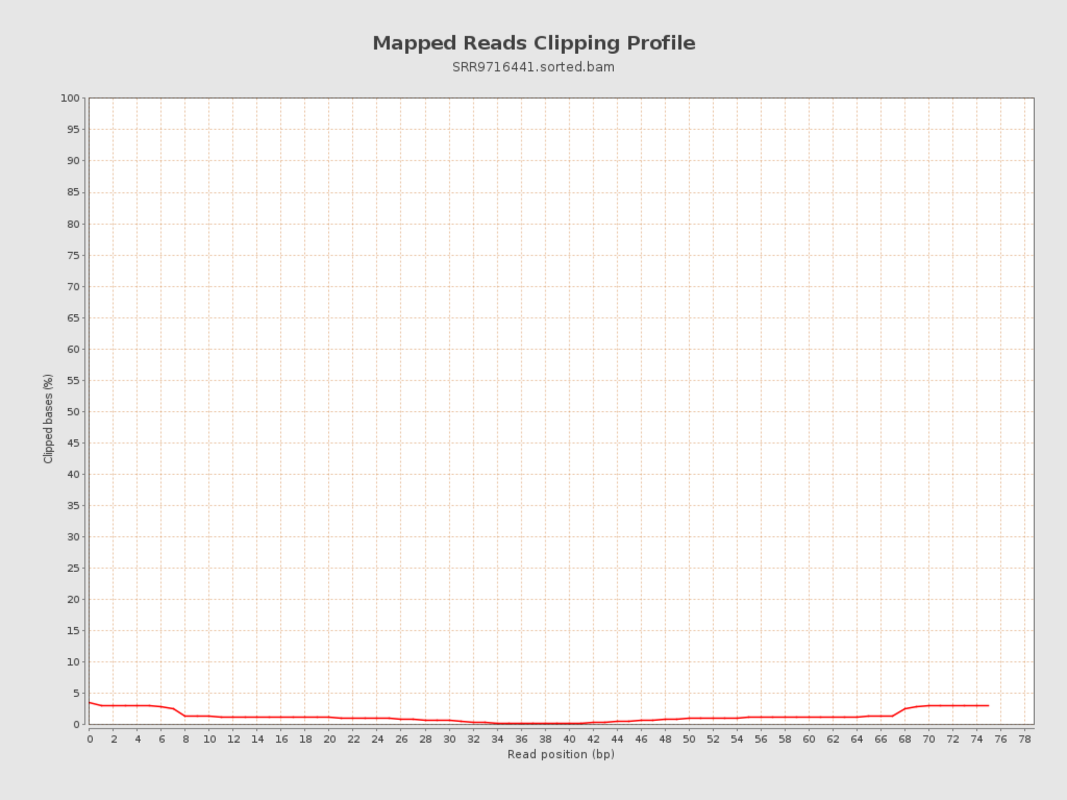
8. Results : Mapped Reads Nucleotide Content



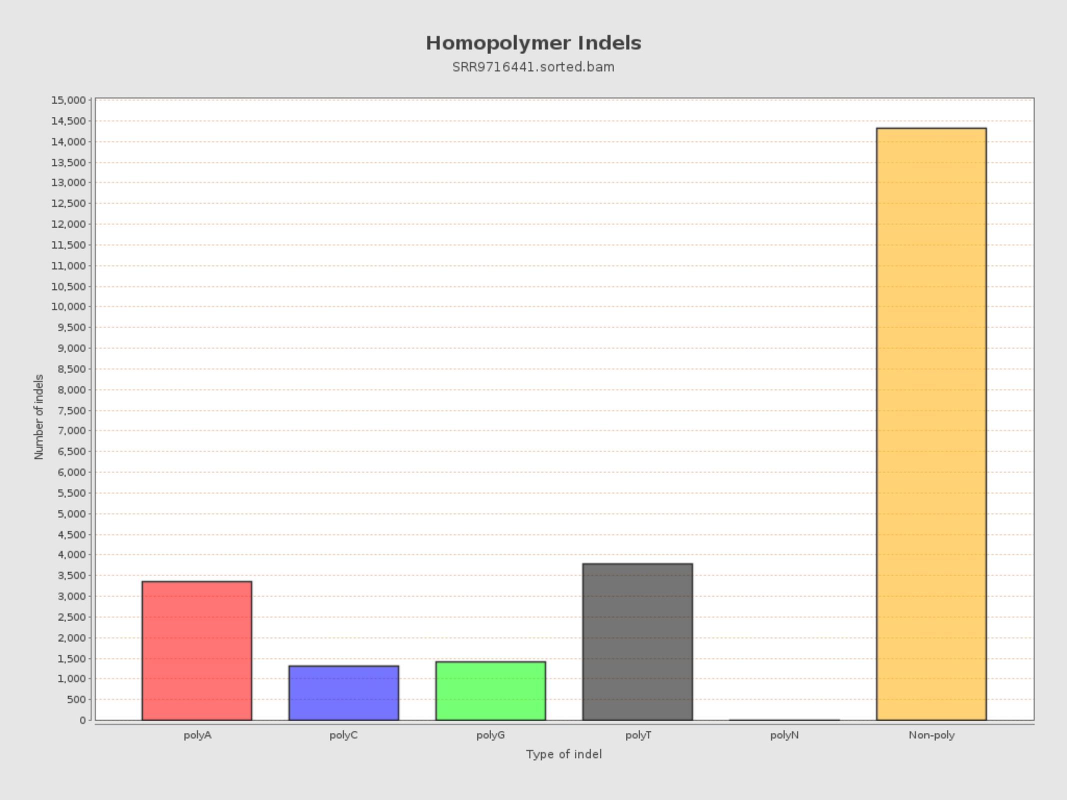
9. Results : Mapped Reads GC-content Distribution



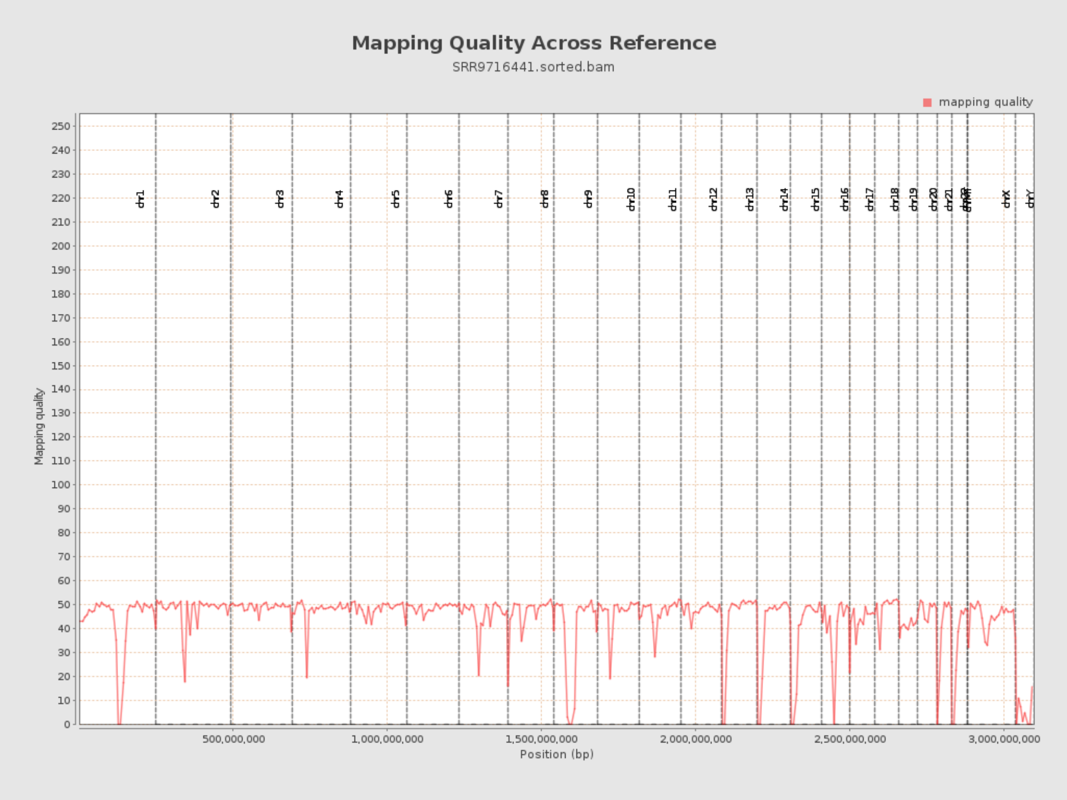
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram