Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 14:06:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716447.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_SRR9716447 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716447.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 14:06:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716447.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	456,465
Mapped reads	384,517 / 84.24%
Unmapped reads	71,948 / 15.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,846 / 1.28%
Read min/max/mean length	30 / 101 / 101.47
Duplicated reads (estimated)	9,219 / 2.02%
Duplication rate	1.41%
Clipped reads	389,775 / 85.39%

2.2. ACGT Content

Number/percentage of A's	7,507,703 / 25.17%
Number/percentage of C's	5,818,714 / 19.51%
Number/percentage of T's	9,247,564 / 31.01%
Number/percentage of G's	7,247,212 / 24.3%
Number/percentage of N's	1,479 / 0%
GC Percentage	43.81%

2.3. Coverage

Mean	0.0096

Standard Deviation	0.1467

2.4. Mapping Quality

Mean Mapping Quality	44.31

2.5. Mismatches and indels

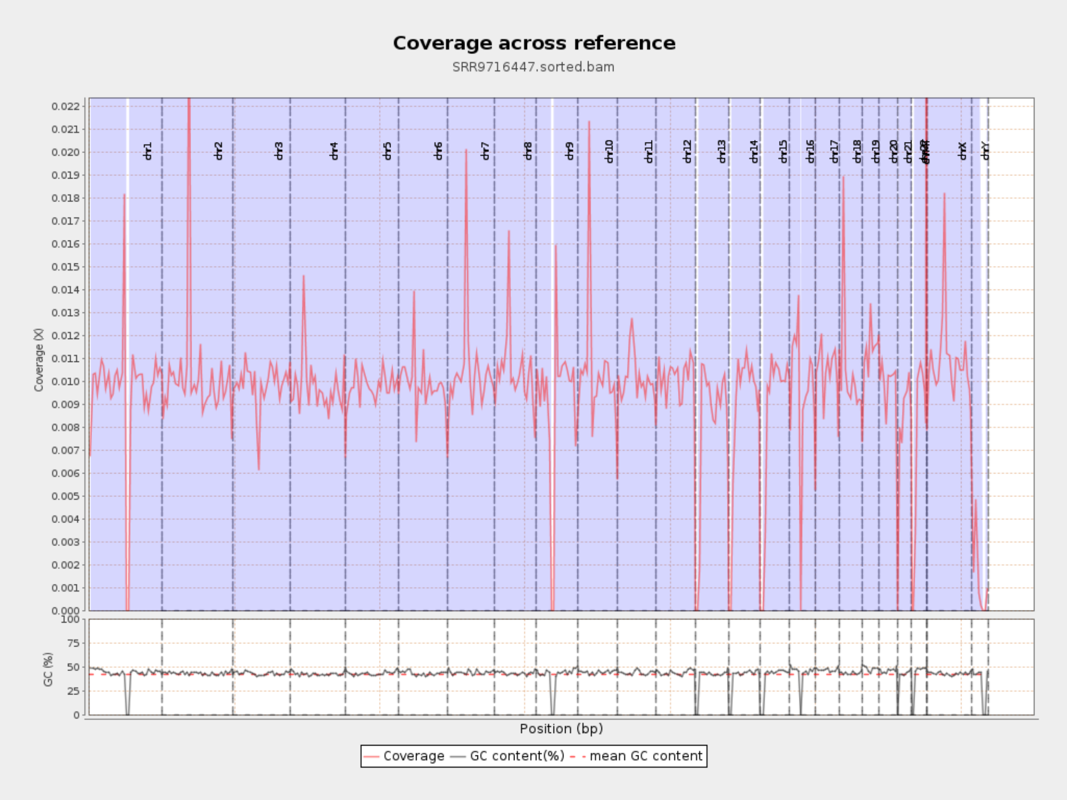
General error rate	0.89%
Mismatches	258,594
Insertions	2,886
Mapped reads with at least one insertion	0.74%
Deletions	7,447
Mapped reads with at least one deletion	1.91%
Homopolymer indels	43.99%

2.6. Chromosome stats

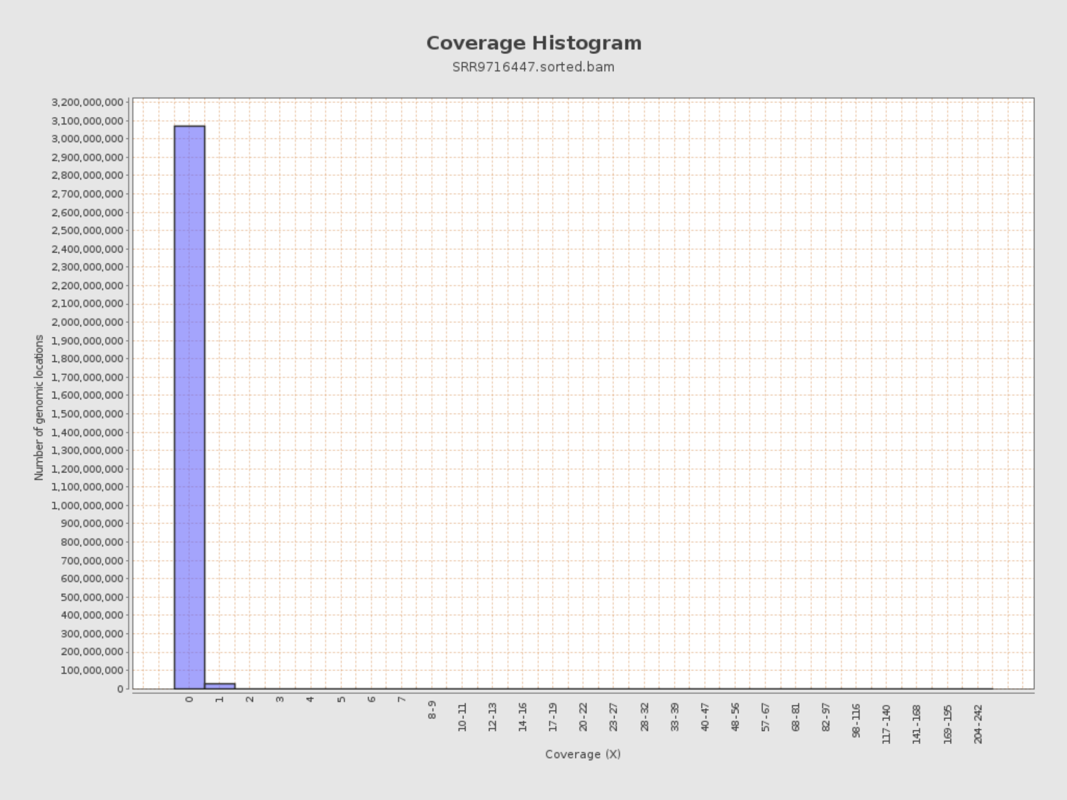
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2385125	0.0096	0.205
chr2	243199373	2513833	0.0103	0.2026
chr3	198022430	1947710	0.0098	0.1025
chr4	191154276	1865401	0.0098	0.1066
chr5	180915260	1776272	0.0098	0.1028
chr6	171115067	1691882	0.0099	0.1123
chr7	159138663	1675523	0.0105	0.1821

chr8	146364022	1527061	0.0104	0.1845
chr9	141213431	1275552	0.009	0.1605
chr10	135534747	1417906	0.0105	0.1497
chr11	135006516	1359446	0.0101	0.1494
chr12	133851895	1357629	0.0101	0.1061
chr13	115169878	913196	0.0079	0.0914
chr14	107349540	919903	0.0086	0.1165
chr15	102531392	852169	0.0083	0.0946
chr16	90354753	867616	0.0096	0.1093
chr17	81195210	843952	0.0104	0.1102
chr18	78077248	829965	0.0106	0.2599
chr19	59128983	669281	0.0113	0.1644
chr20	63025520	620196	0.0098	0.1057
chr21	48129895	386625	0.008	0.0962
chr22	51304566	358169	0.007	0.0859
chrMT	16571	1080	0.0652	0.2684
chrX	155270560	1695793	0.0109	0.1251
chrY	59373566	84300	0.0014	0.0528

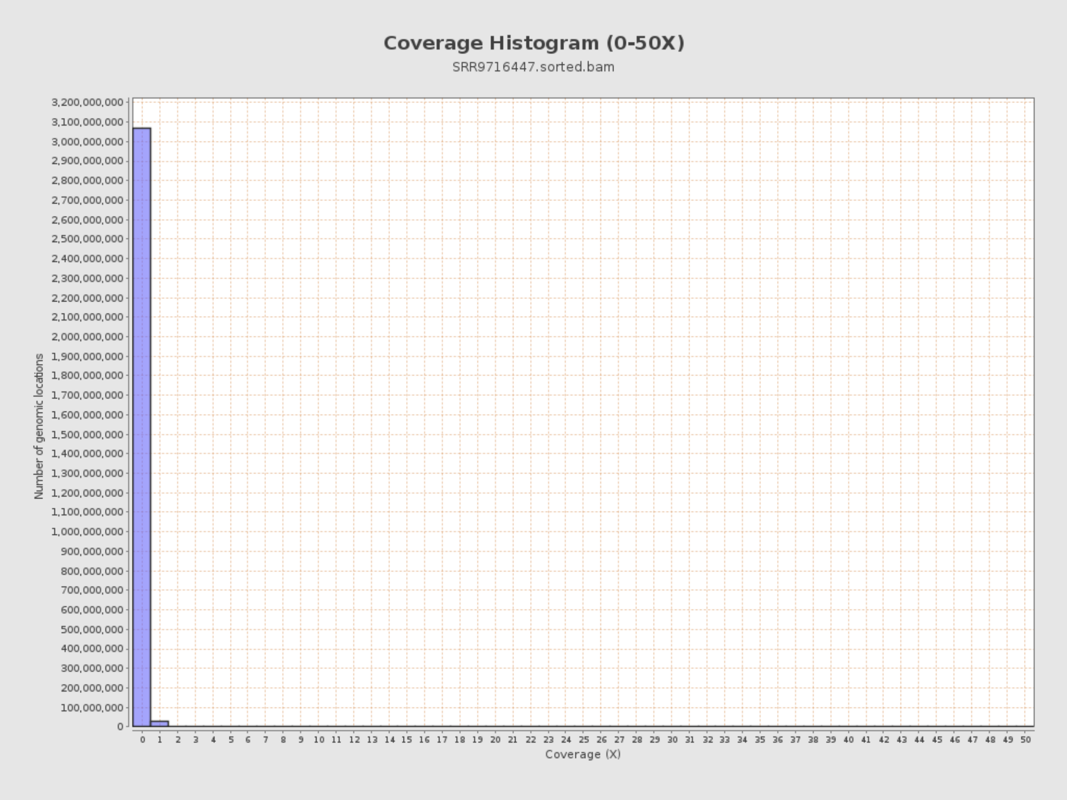
3. Results : Coverage across reference



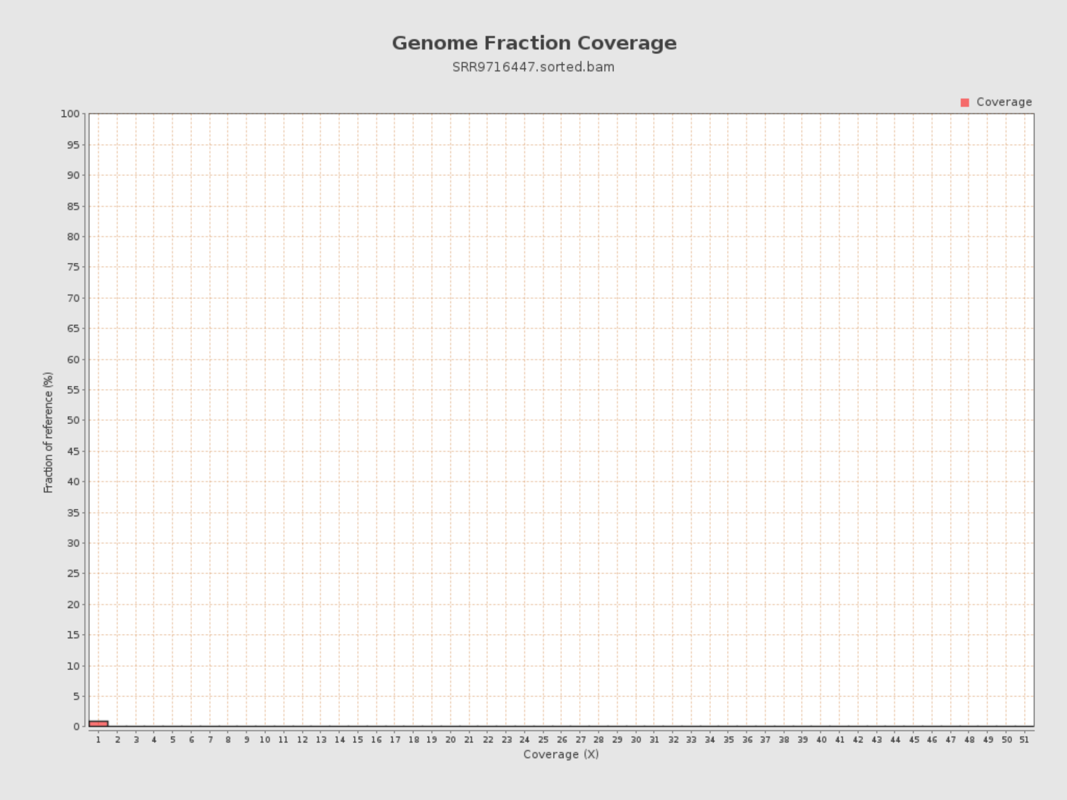
4. Results : Coverage Histogram



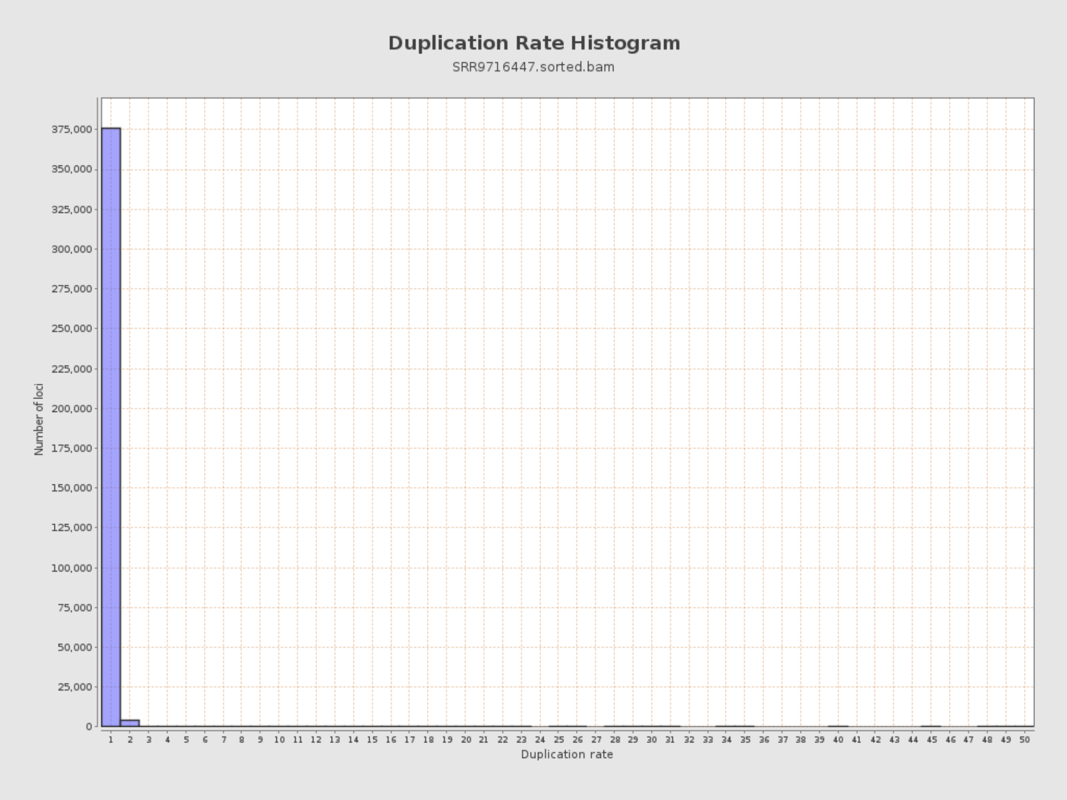
5. Results : Coverage Histogram (0-50X)



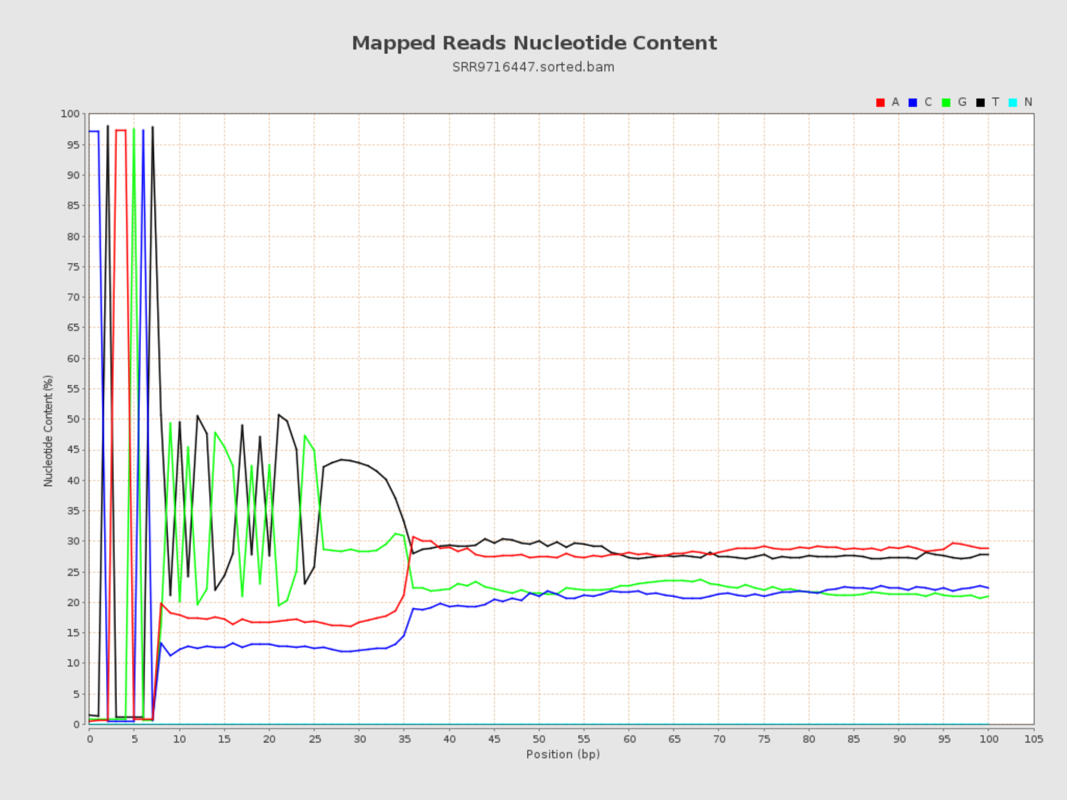
6. Results : Genome Fraction Coverage



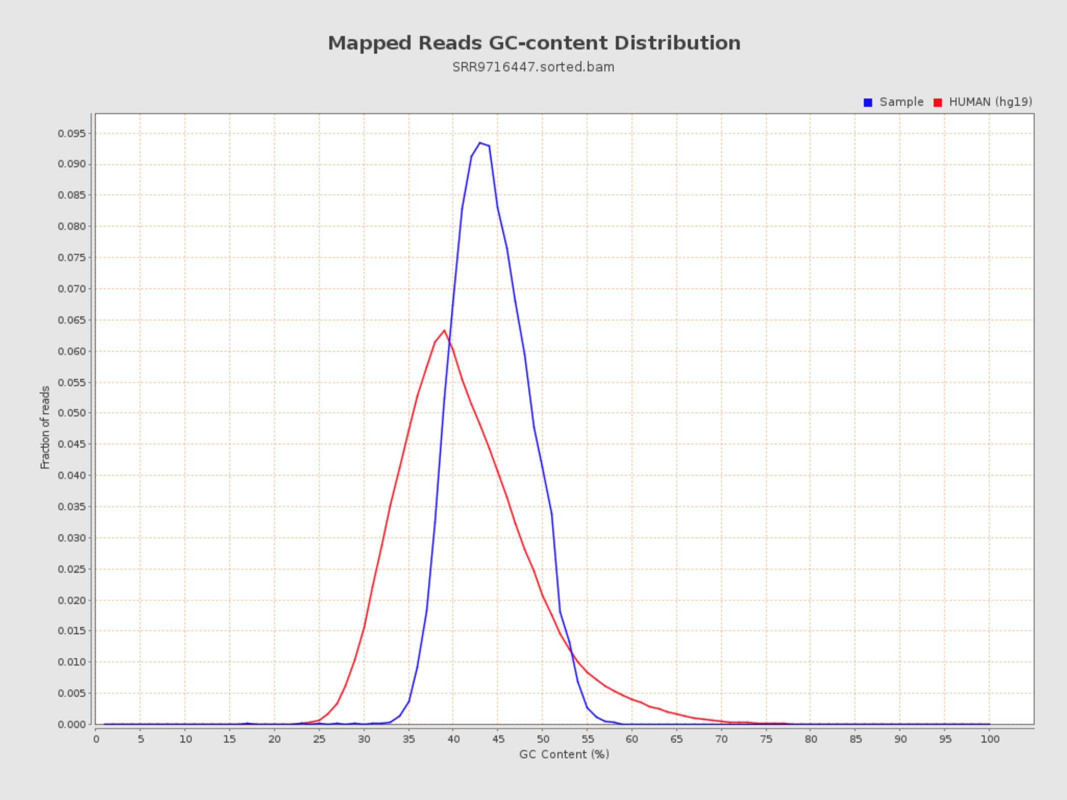
7. Results : Duplication Rate Histogram



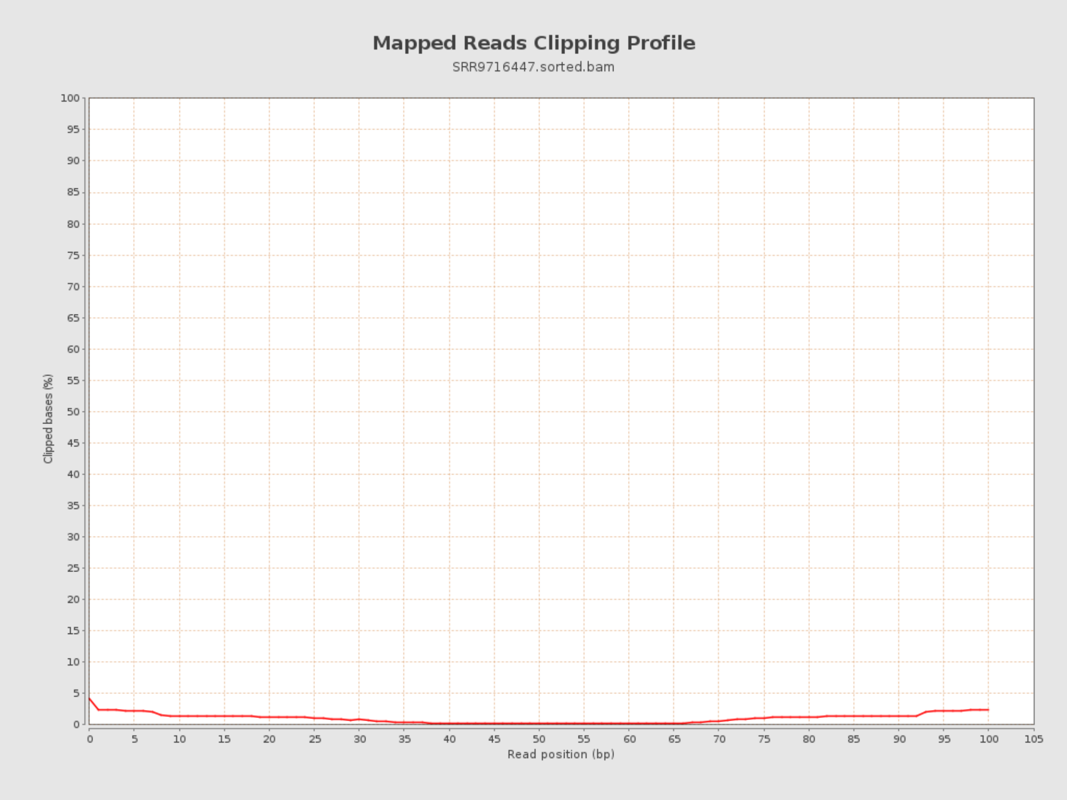
8. Results : Mapped Reads Nucleotide Content



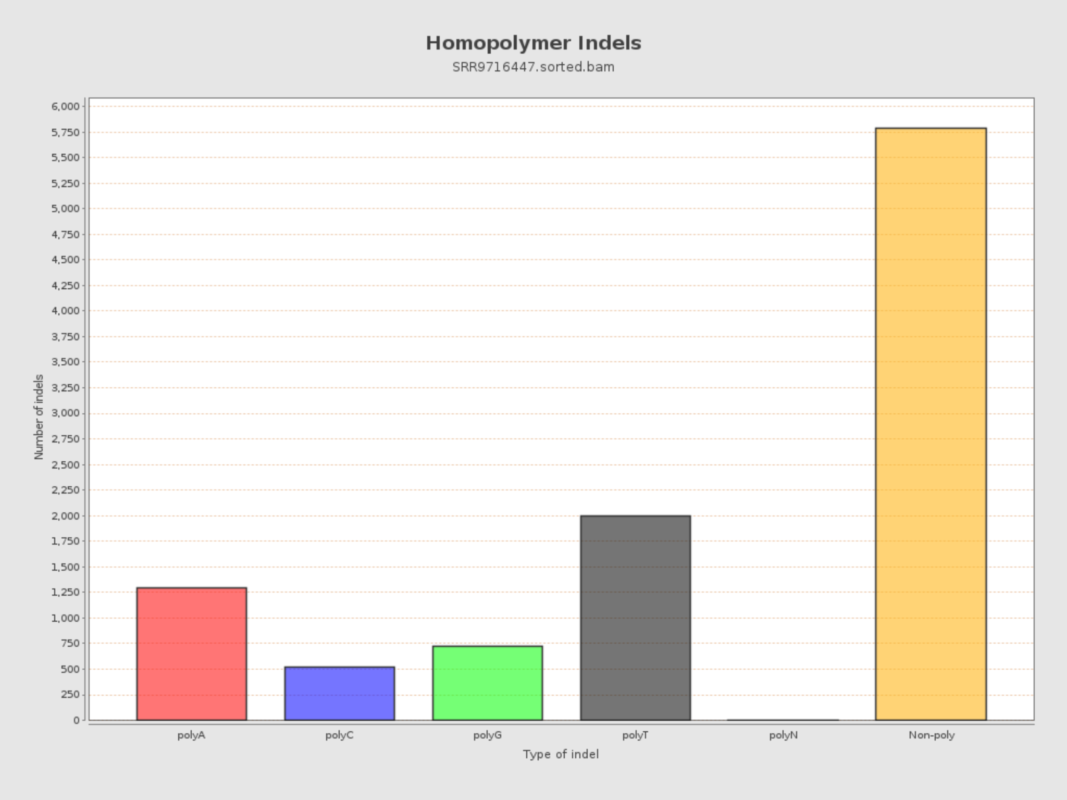
9. Results : Mapped Reads GC-content Distribution



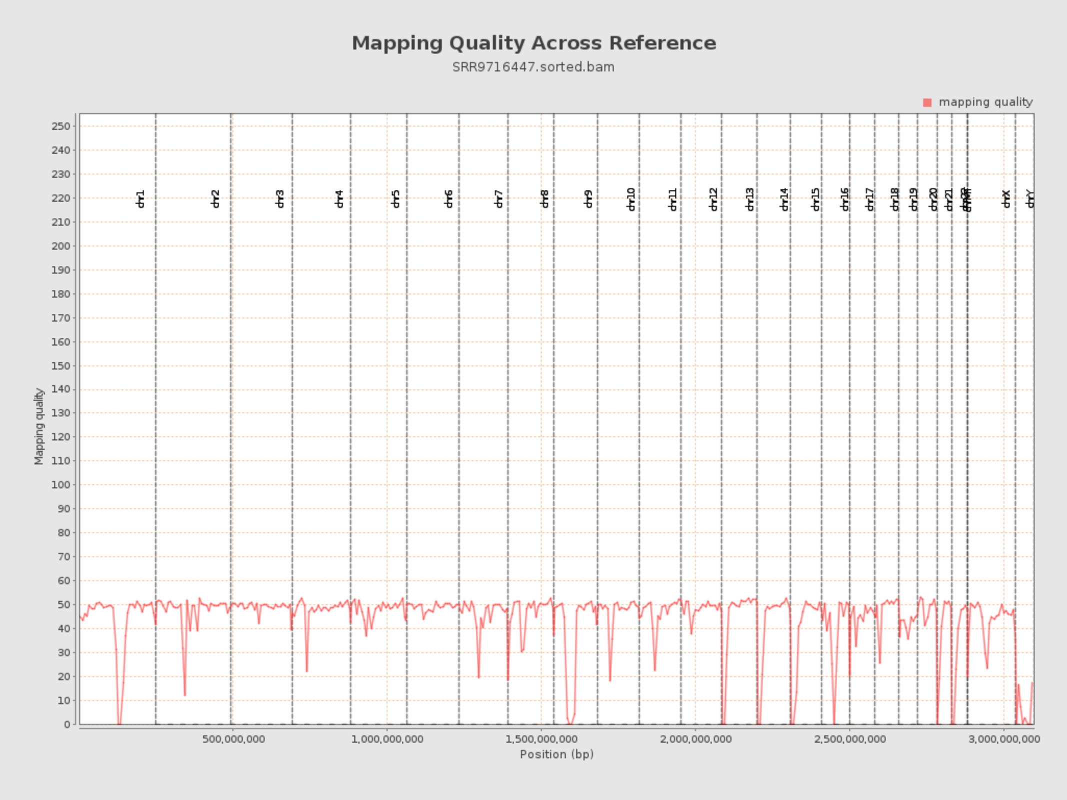
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram