Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 12:31:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716419.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_SRR9716419 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716419.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 12:31:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716419.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,865,955
Mapped reads	2,565,314 / 89.51%
Unmapped reads	300,641 / 10.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,177 / 0.46%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	132,791 / 4.63%
Duplication rate	3.97%
Clipped reads	2,570,430 / 89.69%

2.2. ACGT Content

Number/percentage of A's	38,089,449 / 25.7%
Number/percentage of C's	29,750,085 / 20.08%
Number/percentage of T's	45,498,073 / 30.7%
Number/percentage of G's	34,844,748 / 23.51%
Number/percentage of N's	2,148 / 0%
GC Percentage	43.59%

2.3. Coverage

Mean	0.0479

Standard Deviation	0.3914

2.4. Mapping Quality

Mean Mapping Quality	44.27

2.5. Mismatches and indels

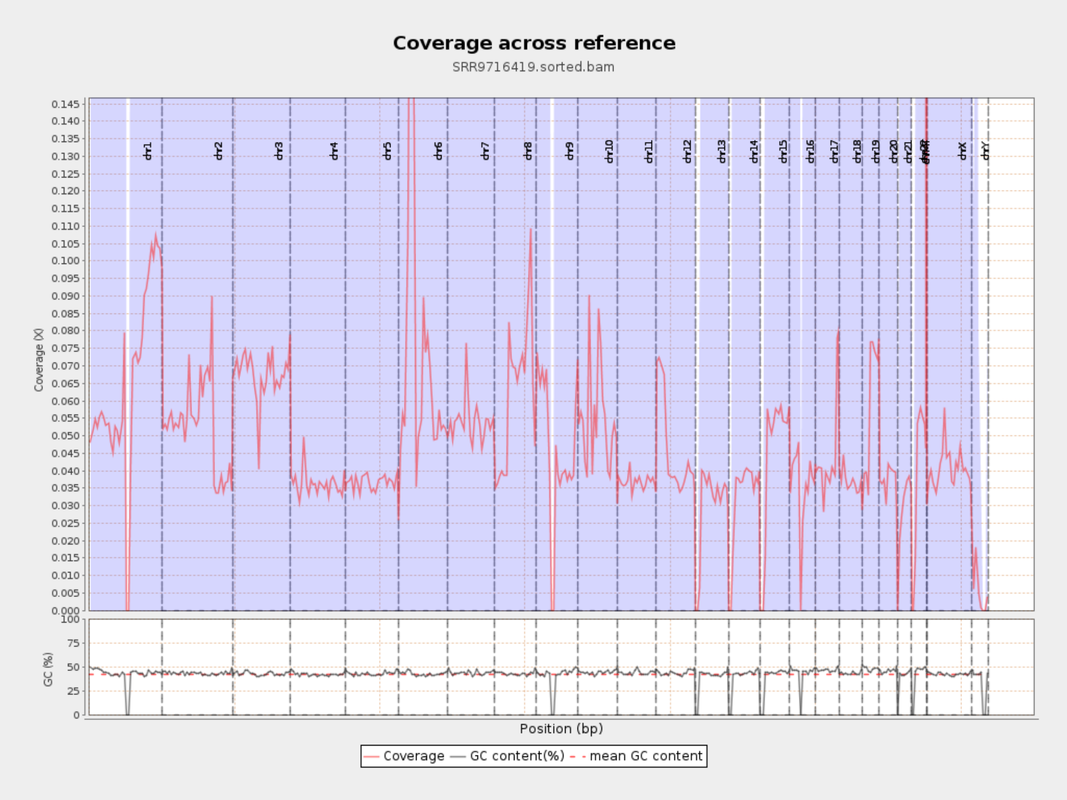
General error rate	0.5%
Mismatches	722,932
Insertions	12,048
Mapped reads with at least one insertion	0.47%
Deletions	25,750
Mapped reads with at least one deletion	1%
Homopolymer indels	40.07%

2.6. Chromosome stats

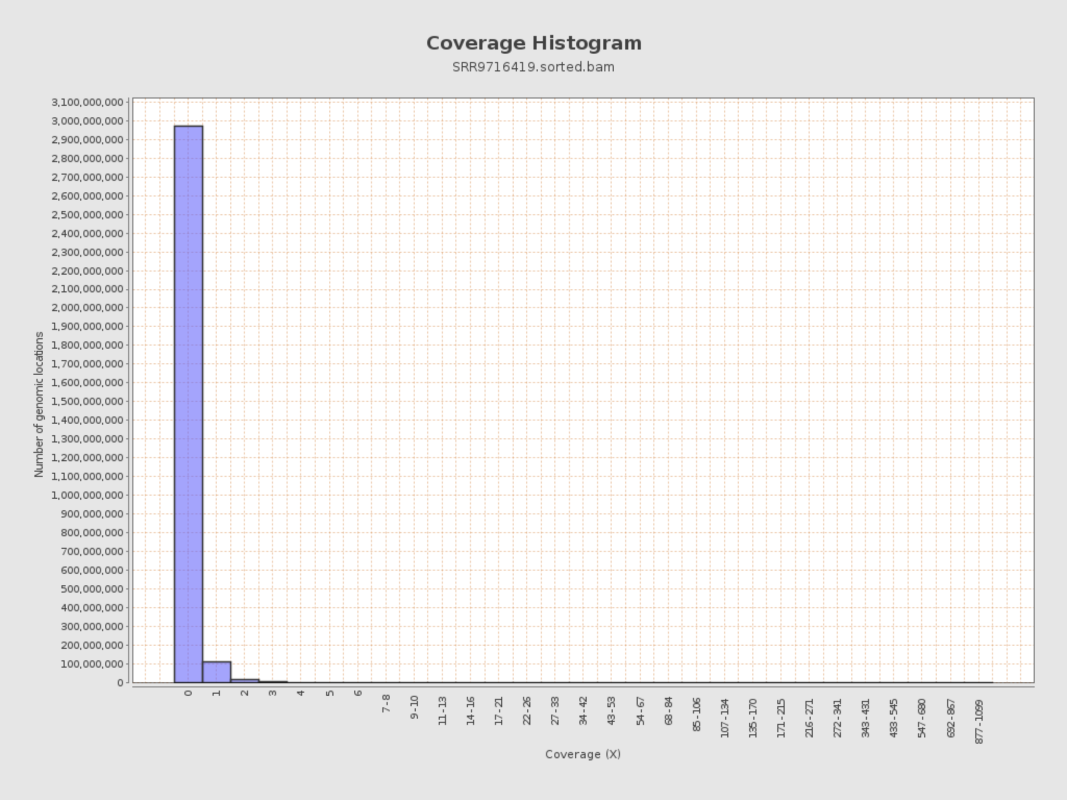
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16177346	0.0649	0.695
chr2	243199373	12851201	0.0528	0.5286
chr3	198022430	13331401	0.0673	0.3005
chr4	191154276	6921389	0.0362	0.24
chr5	180915260	6657242	0.0368	0.2252
chr6	171115067	12778100	0.0747	0.4789
chr7	159138663	8636085	0.0543	0.5024

chr8	146364022	9190395	0.0628	0.3431
chr9	141213431	6247645	0.0442	0.344
chr10	135534747	7492413	0.0553	0.3784
chr11	135006516	4964620	0.0368	0.3086
chr12	133851895	6152469	0.046	0.2614
chr13	115169878	3406595	0.0296	0.1993
chr14	107349540	3405271	0.0317	0.2533
chr15	102531392	4541611	0.0443	0.2477
chr16	90354753	3211485	0.0355	0.2447
chr17	81195210	3584792	0.0442	0.2571
chr18	78077248	2897643	0.0371	0.5807
chr19	59128983	3431877	0.058	0.5128
chr20	63025520	2362190	0.0375	0.2273
chr21	48129895	1379554	0.0287	0.2223
chr22	51304566	1915681	0.0373	0.2263
chrMT	16571	37312	2.2516	2.0255
chrX	155270560	6306095	0.0406	0.2833
chrY	59373566	343710	0.0058	0.1342

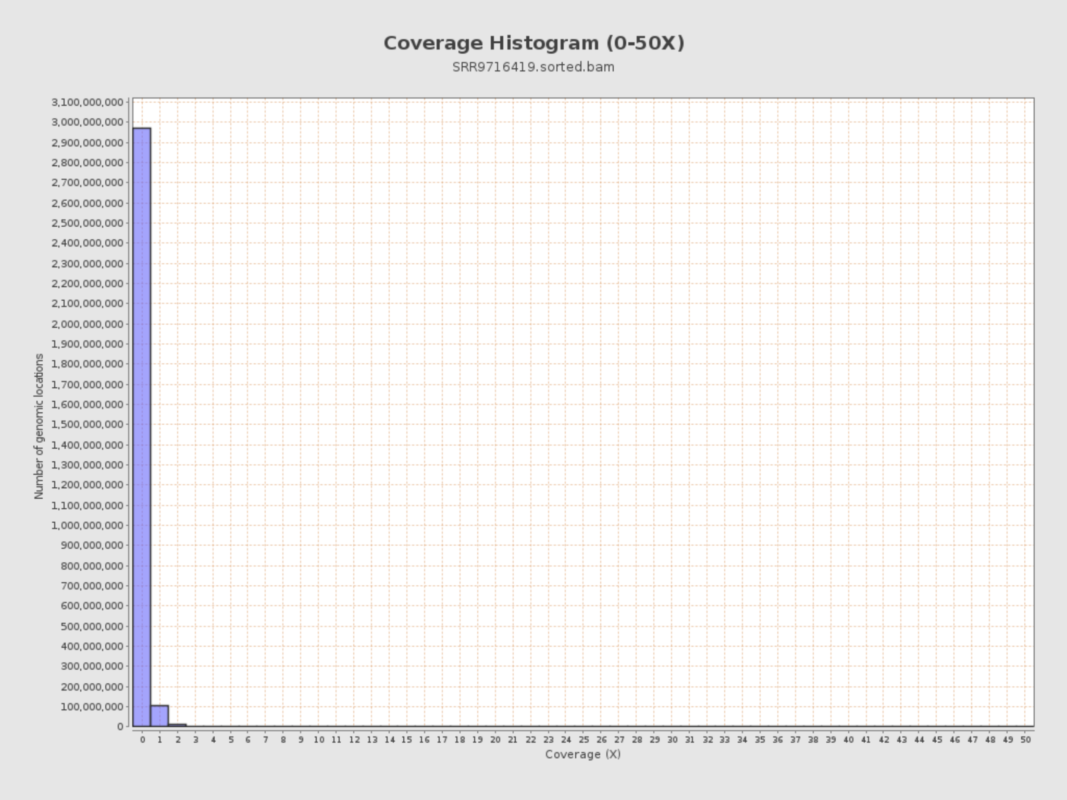
3. Results : Coverage across reference



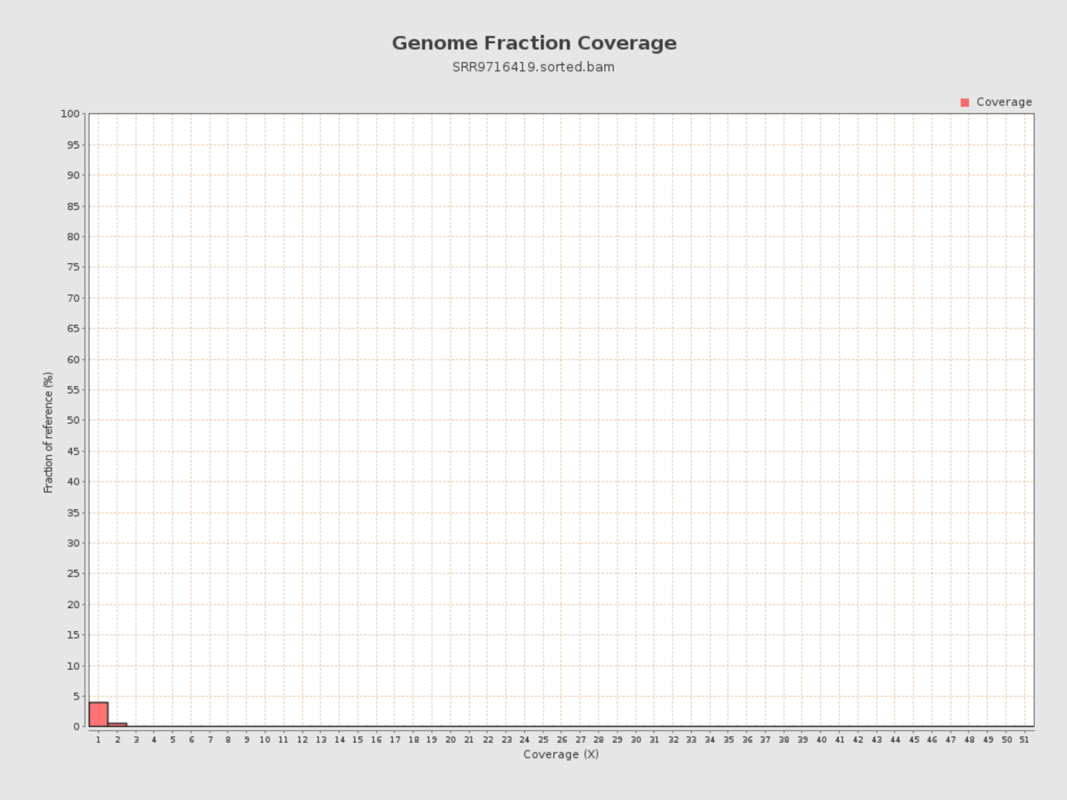
4. Results : Coverage Histogram



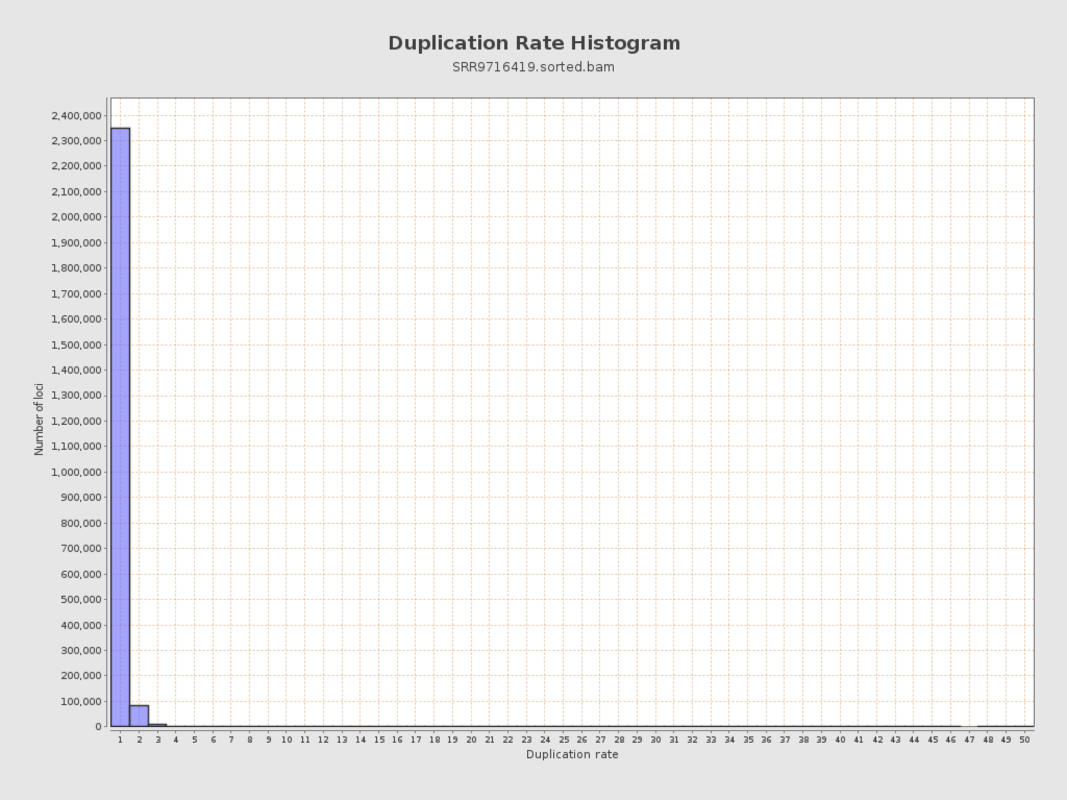
5. Results : Coverage Histogram (0-50X)



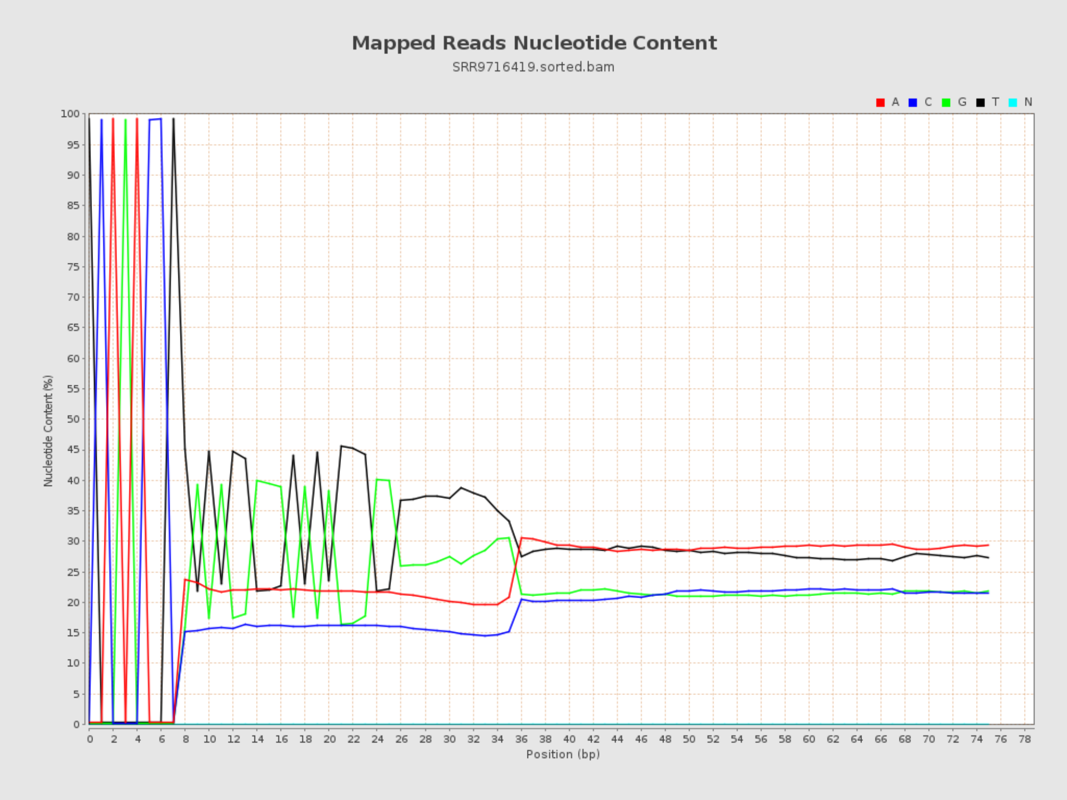
6. Results : Genome Fraction Coverage



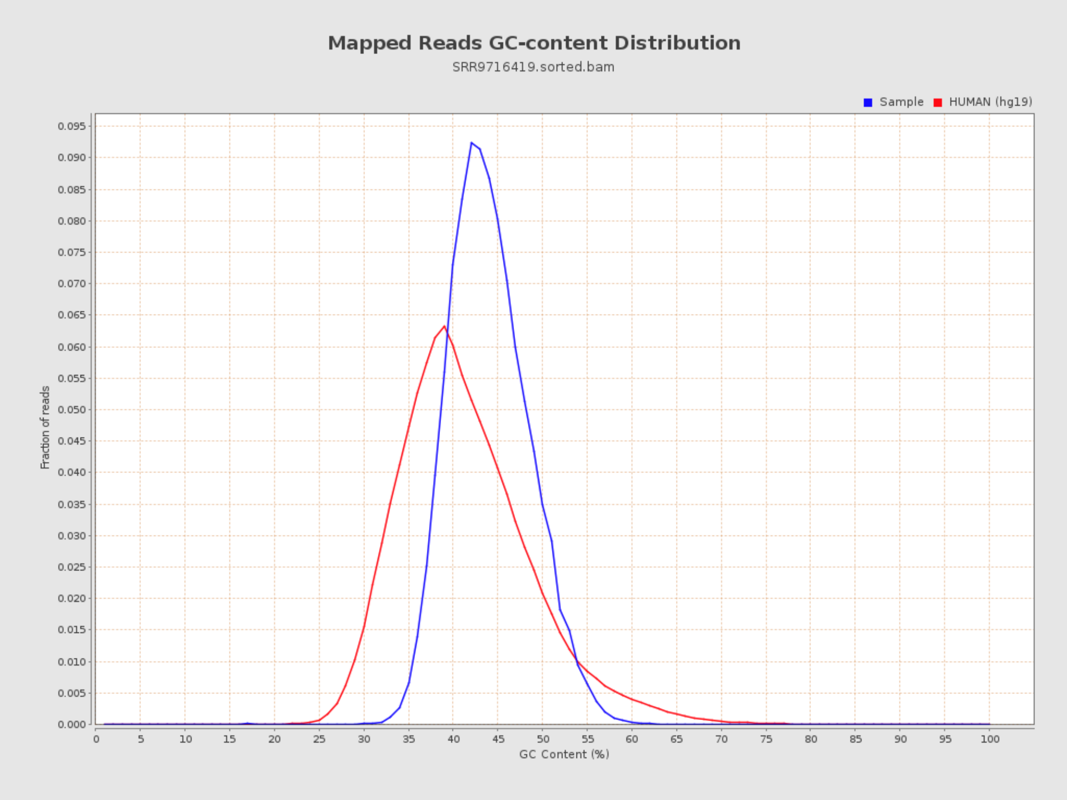
7. Results : Duplication Rate Histogram



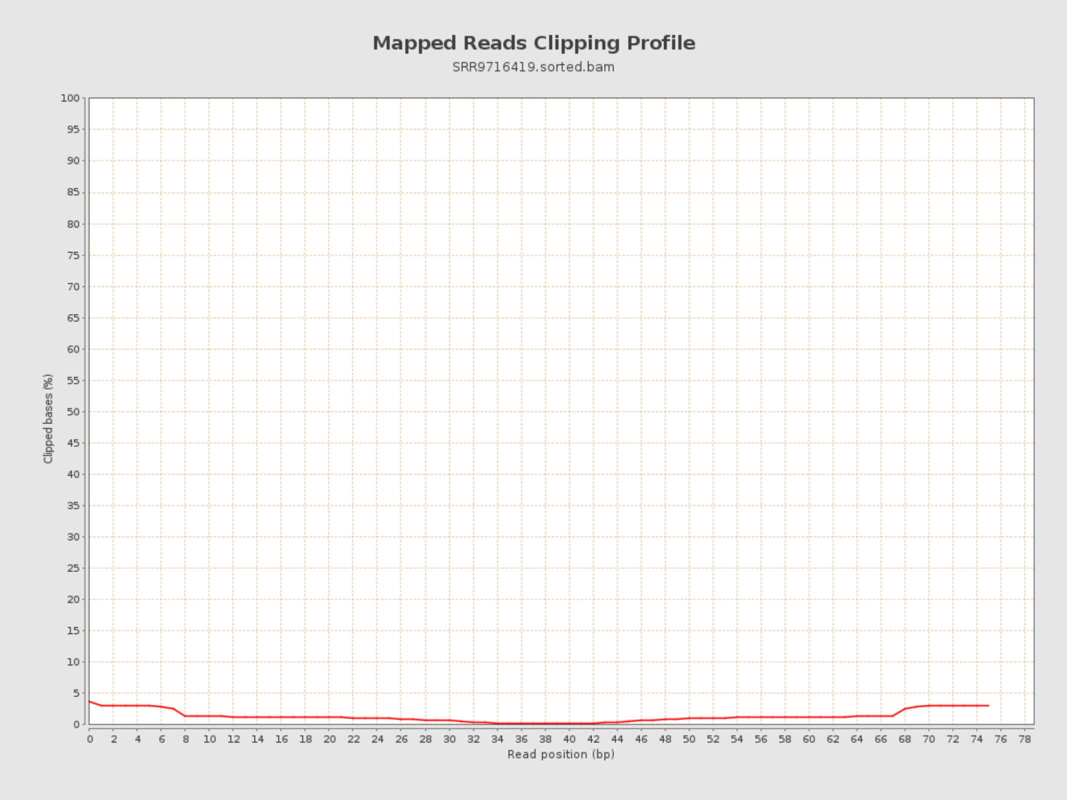
8. Results : Mapped Reads Nucleotide Content



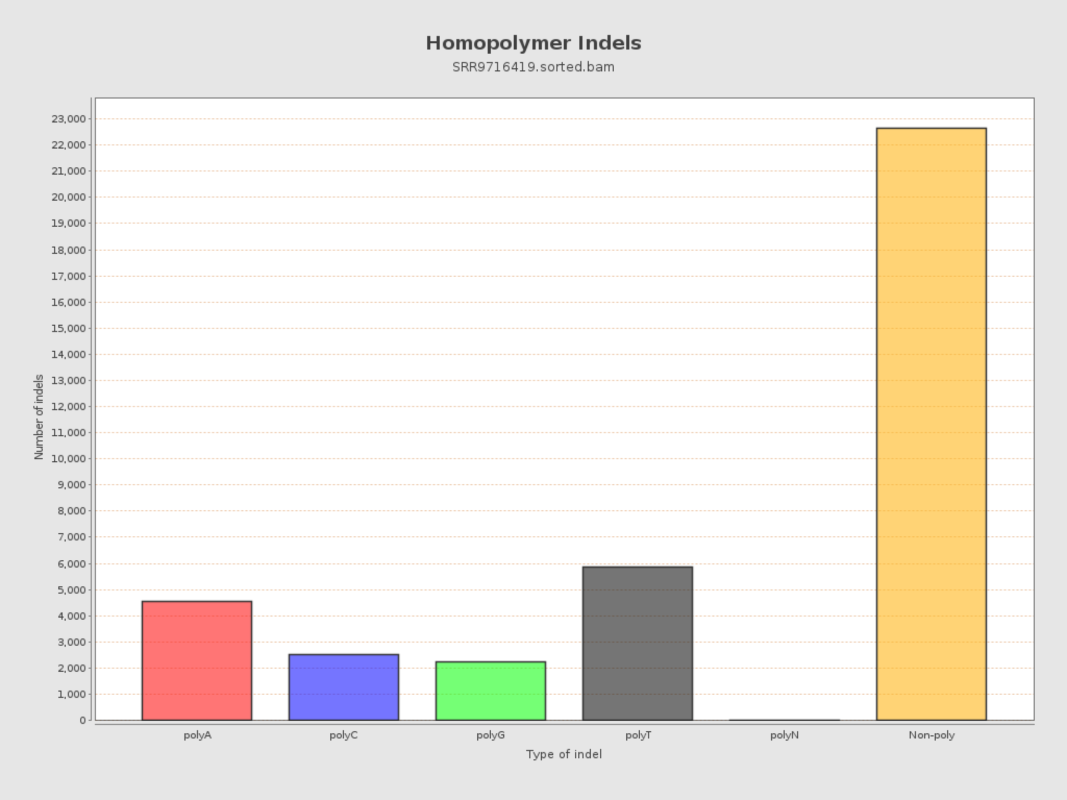
9. Results : Mapped Reads GC-content Distribution



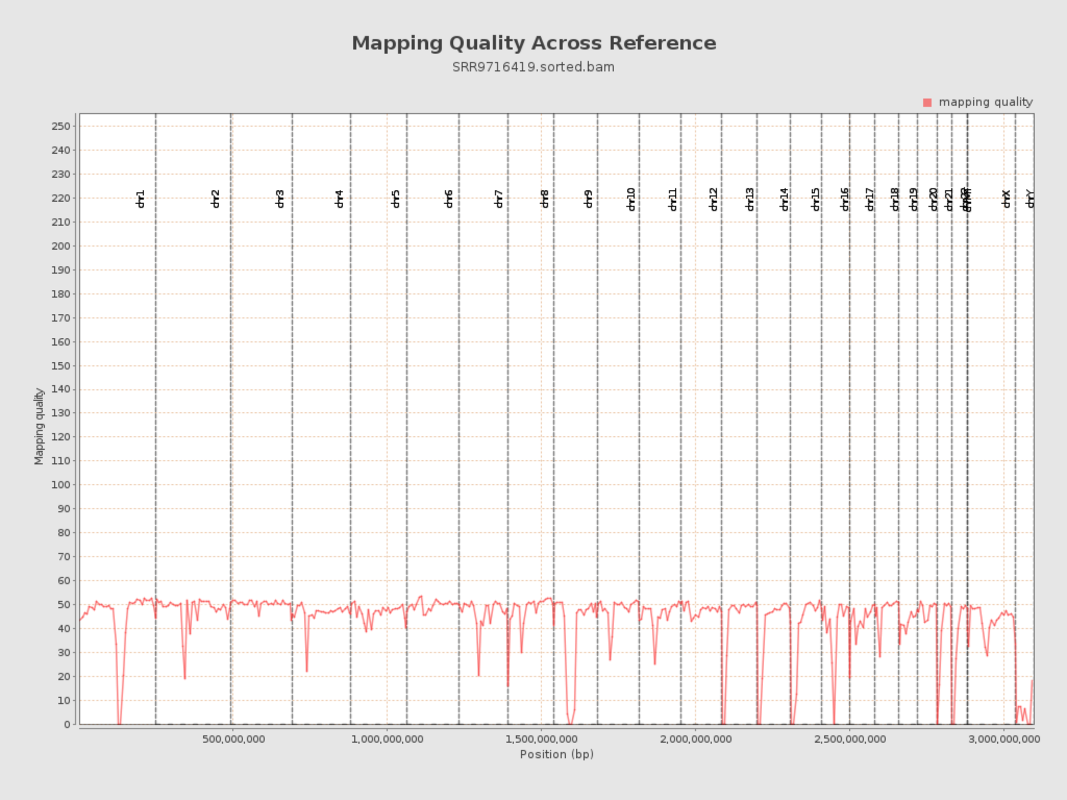
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram