Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 17:39:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716508.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_SRR9716508 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716508.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 17:39:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716508.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	486,711
Mapped reads	444,179 / 91.26%
Unmapped reads	42,532 / 8.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,051 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	8,328 / 1.71%
Duplication rate	1.49%
Clipped reads	444,929 / 91.42%

2.2. ACGT Content

Number/percentage of A's	6,620,606 / 25.62%
Number/percentage of C's	5,388,765 / 20.86%
Number/percentage of T's	7,743,238 / 29.97%
Number/percentage of G's	6,085,995 / 23.55%
Number/percentage of N's	359 / 0%
GC Percentage	44.41%

2.3. Coverage

Mean	0.0083

Standard Deviation	0.1087

2.4. Mapping Quality

Mean Mapping Quality	44.93

2.5. Mismatches and indels

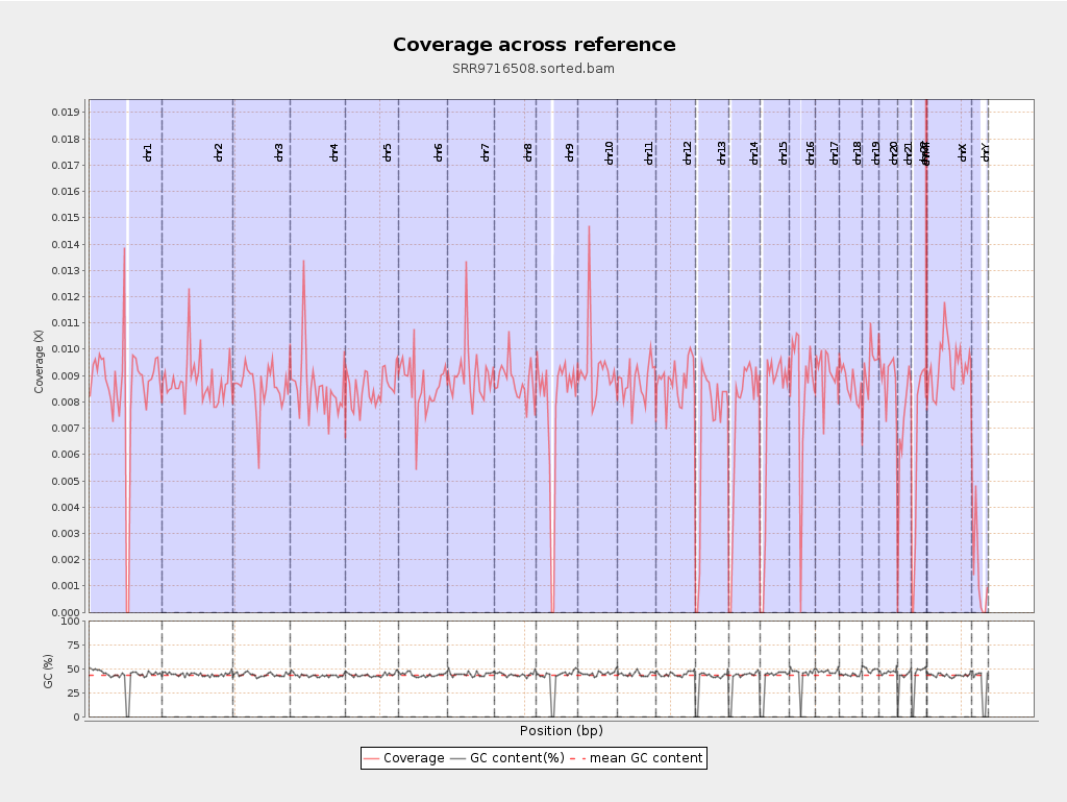
General error rate	0.51%
Mismatches	127,635
Insertions	1,967
Mapped reads with at least one insertion	0.44%
Deletions	4,807
Mapped reads with at least one deletion	1.07%
Homopolymer indels	40.12%

2.6. Chromosome stats

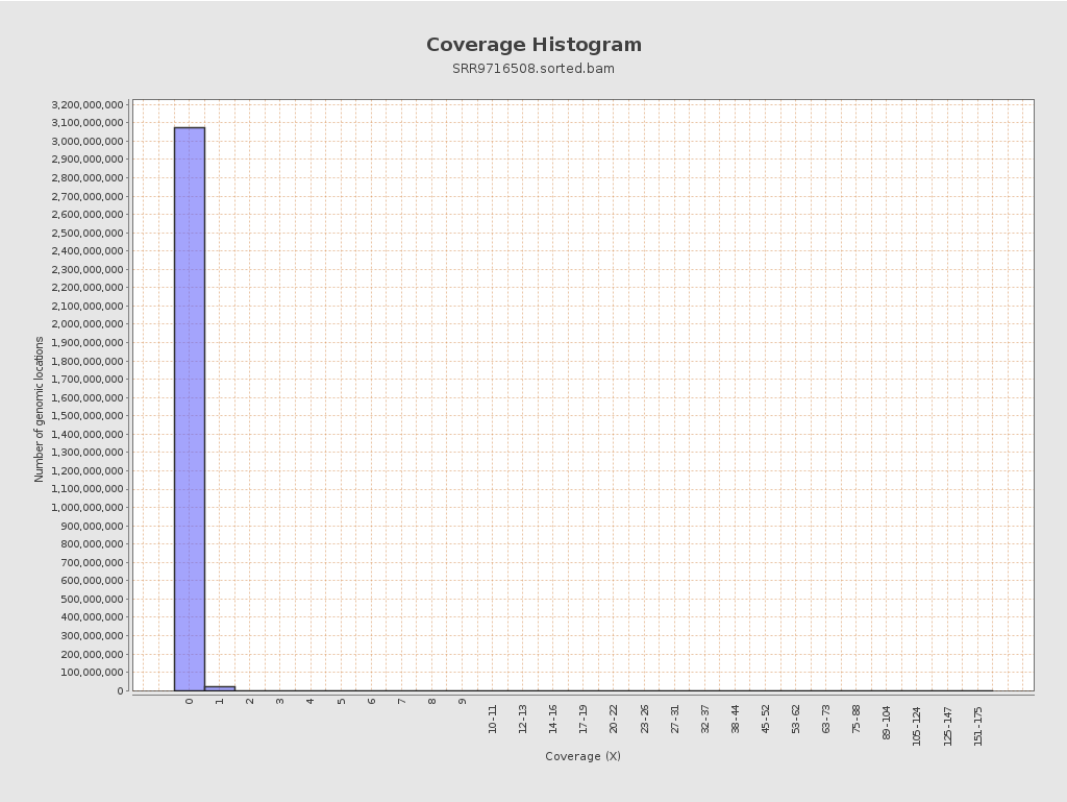
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2113550	0.0085	0.1603
chr2	243199373	2137899	0.0088	0.1235
chr3	198022430	1695490	0.0086	0.0957
chr4	191154276	1631289	0.0085	0.0986
chr5	180915260	1539120	0.0085	0.0955
chr6	171115067	1475326	0.0086	0.1008
chr7	159138663	1439387	0.009	0.1234

chr8	146364022	1283453	0.0088	0.1053
chr9	141213431	1084483	0.0077	0.0983
chr10	135534747	1249228	0.0092	0.1109
chr11	135006516	1182775	0.0088	0.106
chr12	133851895	1175712	0.0088	0.0972
chr13	115169878	801536	0.007	0.0863
chr14	107349540	778427	0.0073	0.0896
chr15	102531392	756560	0.0074	0.0898
chr16	90354753	767568	0.0085	0.0968
chr17	81195210	739860	0.0091	0.1006
chr18	78077248	679934	0.0087	0.1297
chr19	59128983	554084	0.0094	0.1202
chr20	63025520	564538	0.009	0.0983
chr21	48129895	336381	0.007	0.0892
chr22	51304566	312514	0.0061	0.081
chrMT	16571	4594	0.2772	0.5646
chrX	155270560	1460075	0.0094	0.103
chrY	59373566	82622	0.0014	0.0501

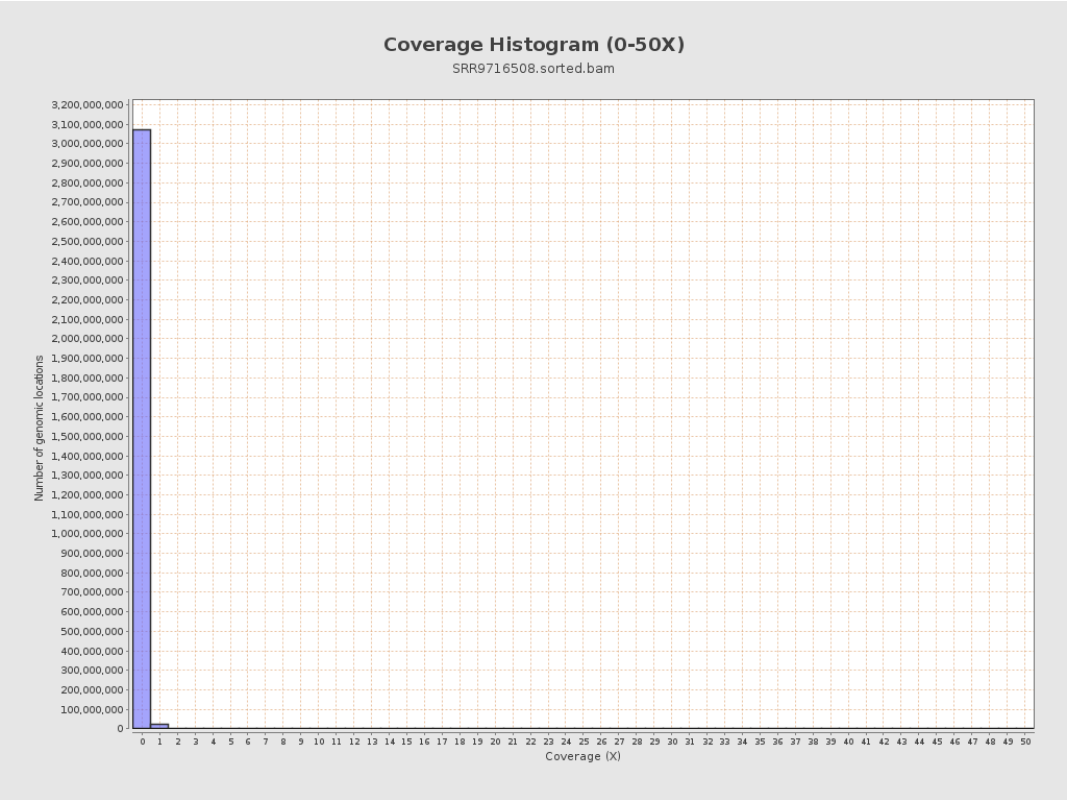
3. Results : Coverage across reference



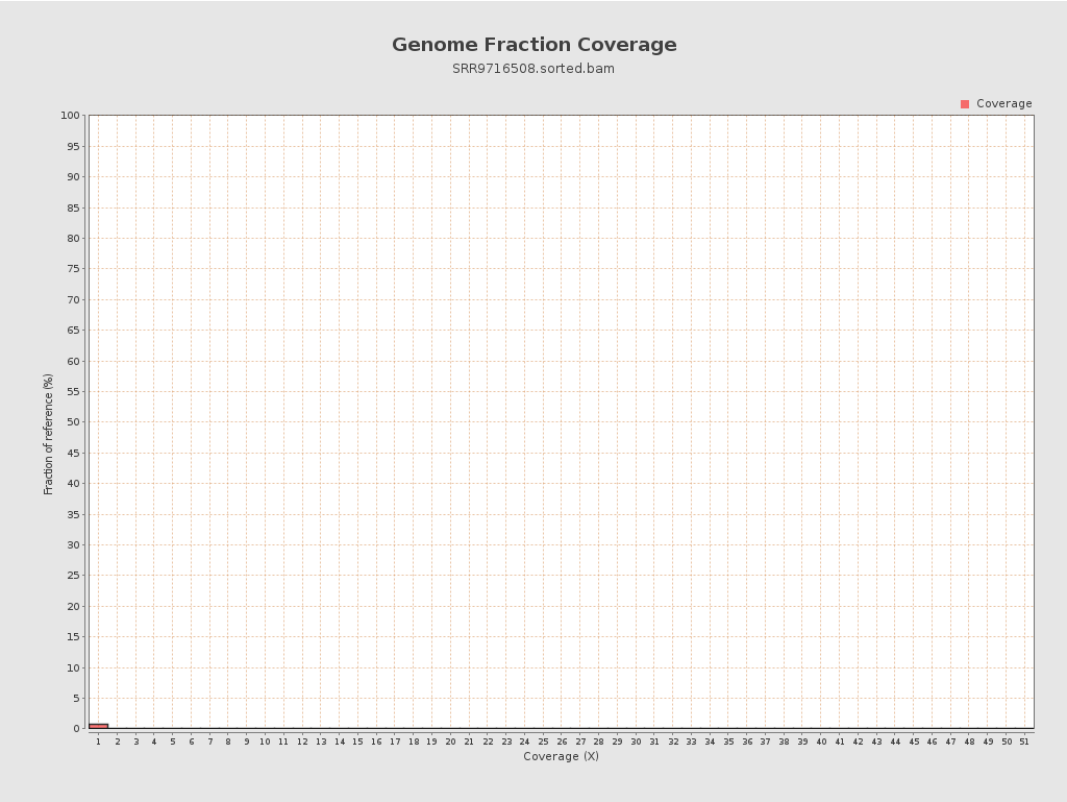
4. Results : Coverage Histogram



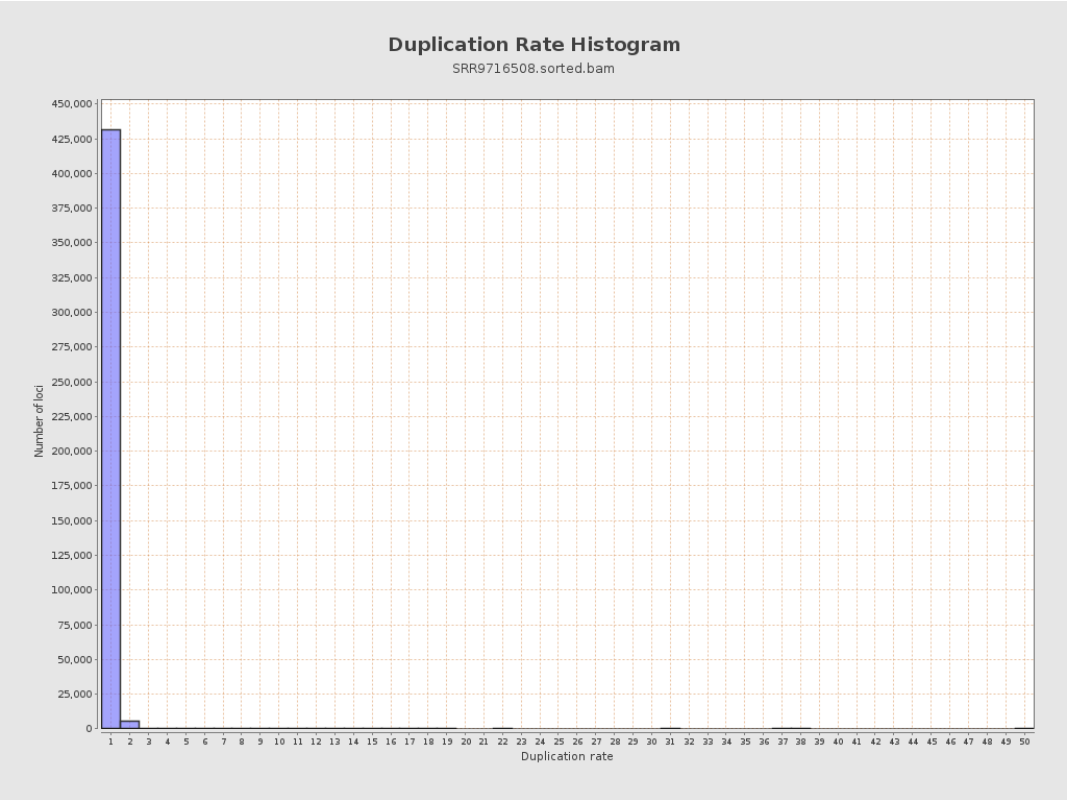
5. Results : Coverage Histogram (0-50X)



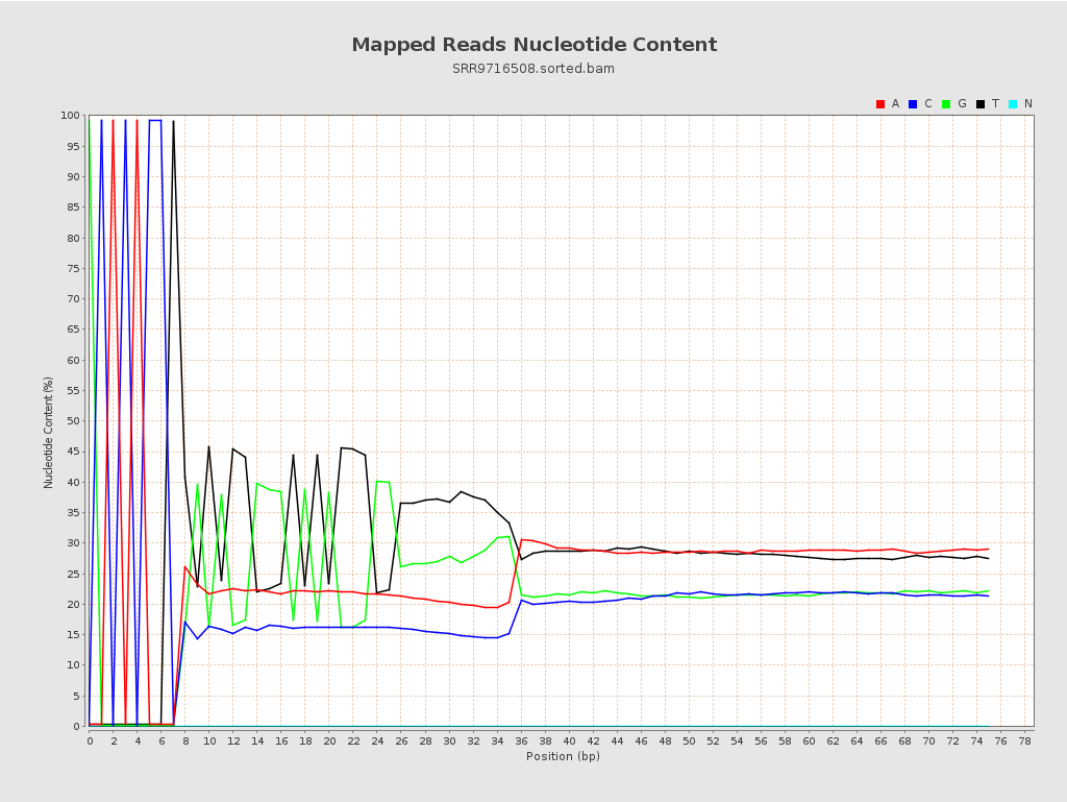
6. Results : Genome Fraction Coverage



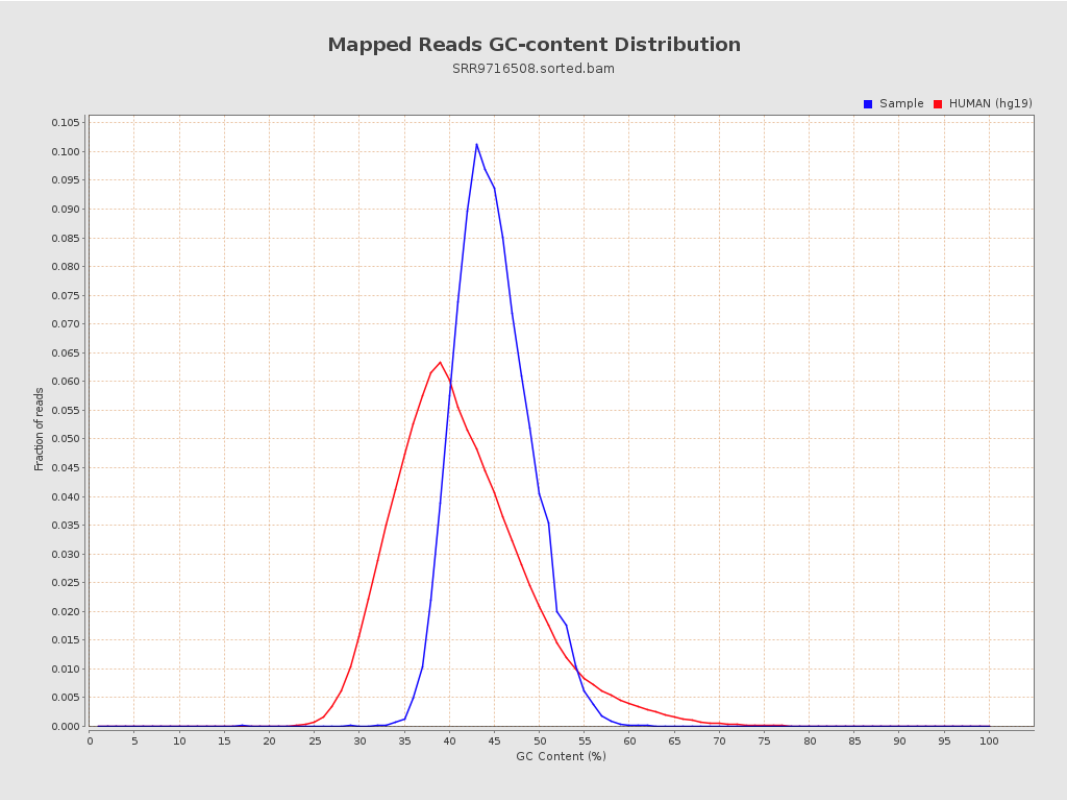
7. Results : Duplication Rate Histogram



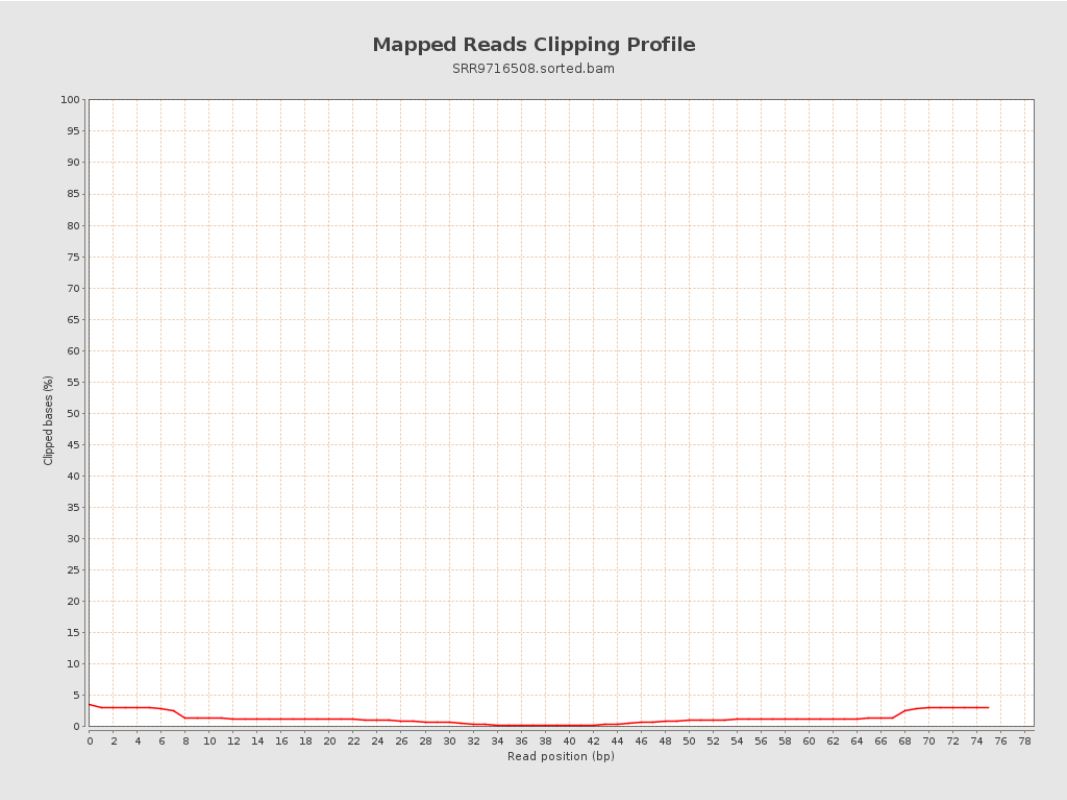
8. Results : Mapped Reads Nucleotide Content



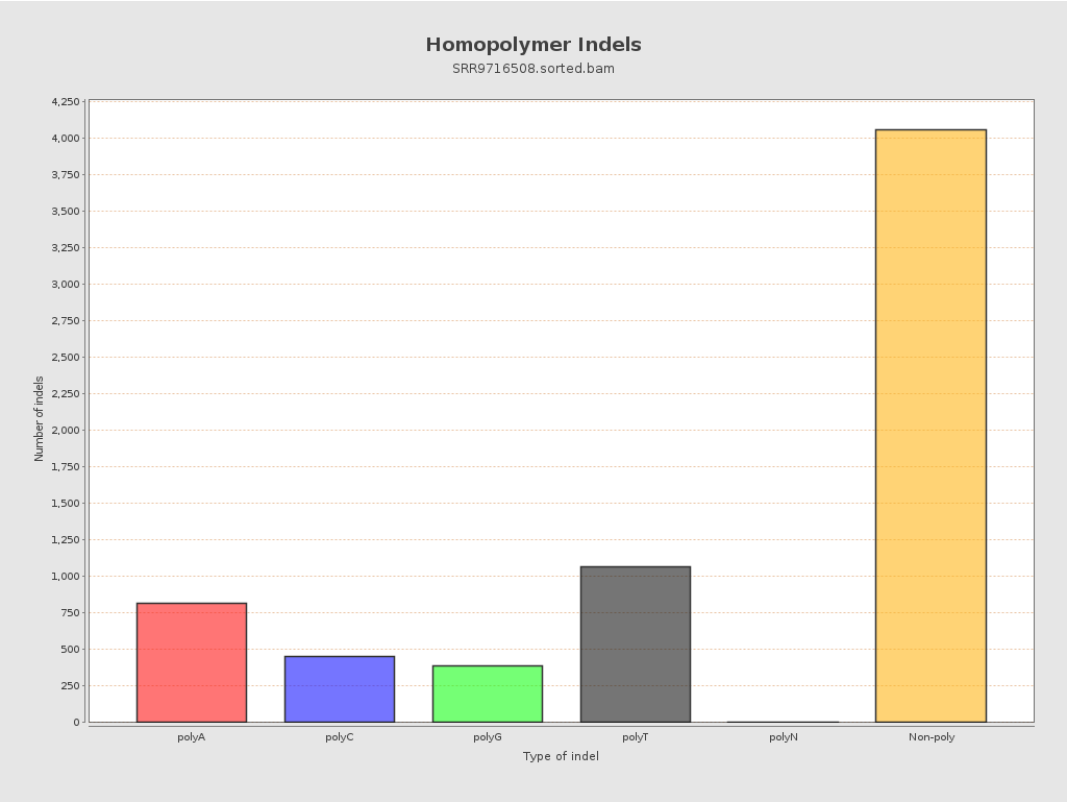
9. Results : Mapped Reads GC-content Distribution



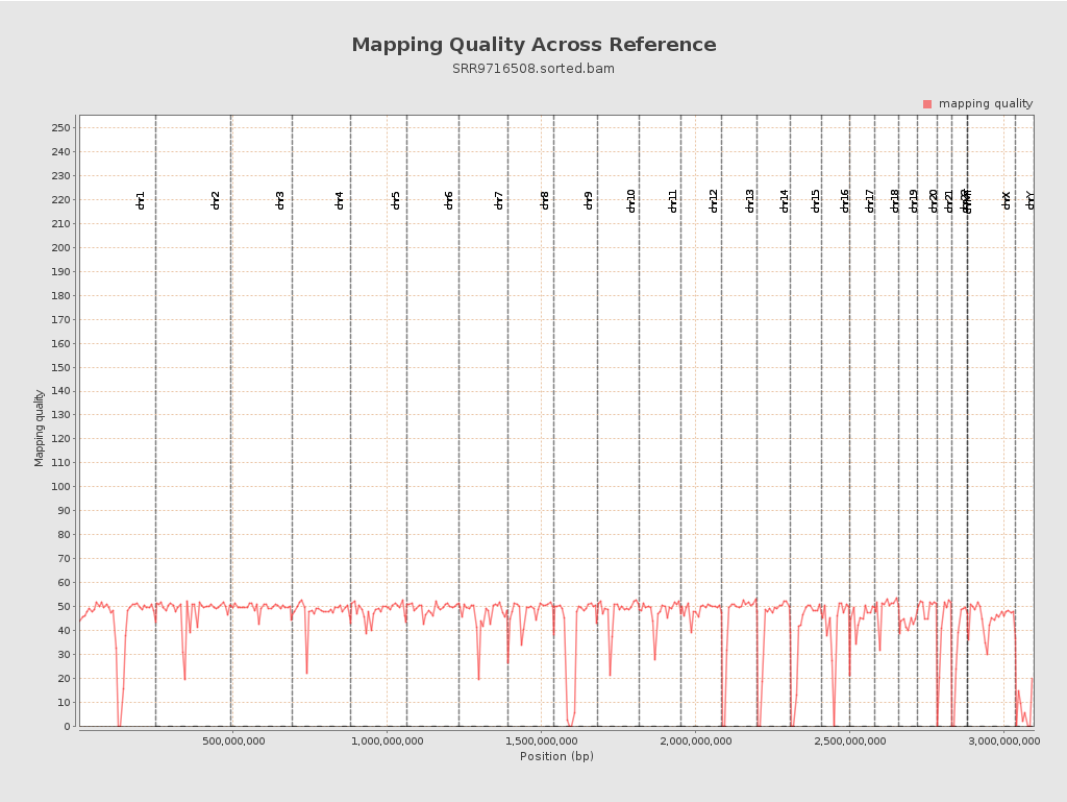
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram