Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 06:33:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716306.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_SRR9716306 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716306.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 06:33:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716306.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,523,752
Mapped reads	1,408,462 / 92.43%
Unmapped reads	115,290 / 7.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,878 / 1.83%
Read min/max/mean length	30 / 101 / 101.66
Duplicated reads (estimated)	49,076 / 3.22%
Duplication rate	2.51%
Clipped reads	1,435,106 / 94.18%

2.2. ACGT Content

Number/percentage of A's	28,688,772 / 25.62%
Number/percentage of C's	21,857,203 / 19.52%
Number/percentage of T's	34,507,622 / 30.82%
Number/percentage of G's	26,921,050 / 24.04%
Number/percentage of N's	8,132 / 0.01%
GC Percentage	43.56%

2.3. Coverage

Mean	0.0362

Standard Deviation	0.322

2.4. Mapping Quality

Mean Mapping Quality	47.65

2.5. Mismatches and indels

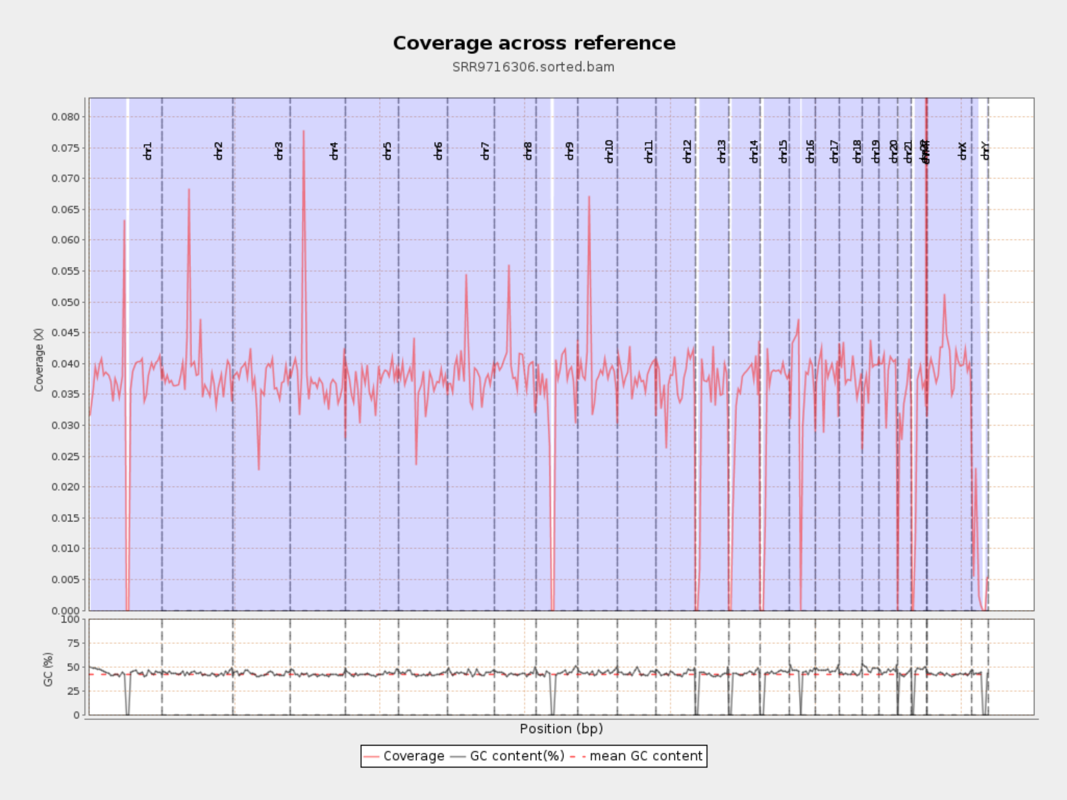
General error rate	0.67%
Mismatches	724,534
Insertions	8,759
Mapped reads with at least one insertion	0.61%
Deletions	26,851
Mapped reads with at least one deletion	1.88%
Homopolymer indels	43.04%

2.6. Chromosome stats

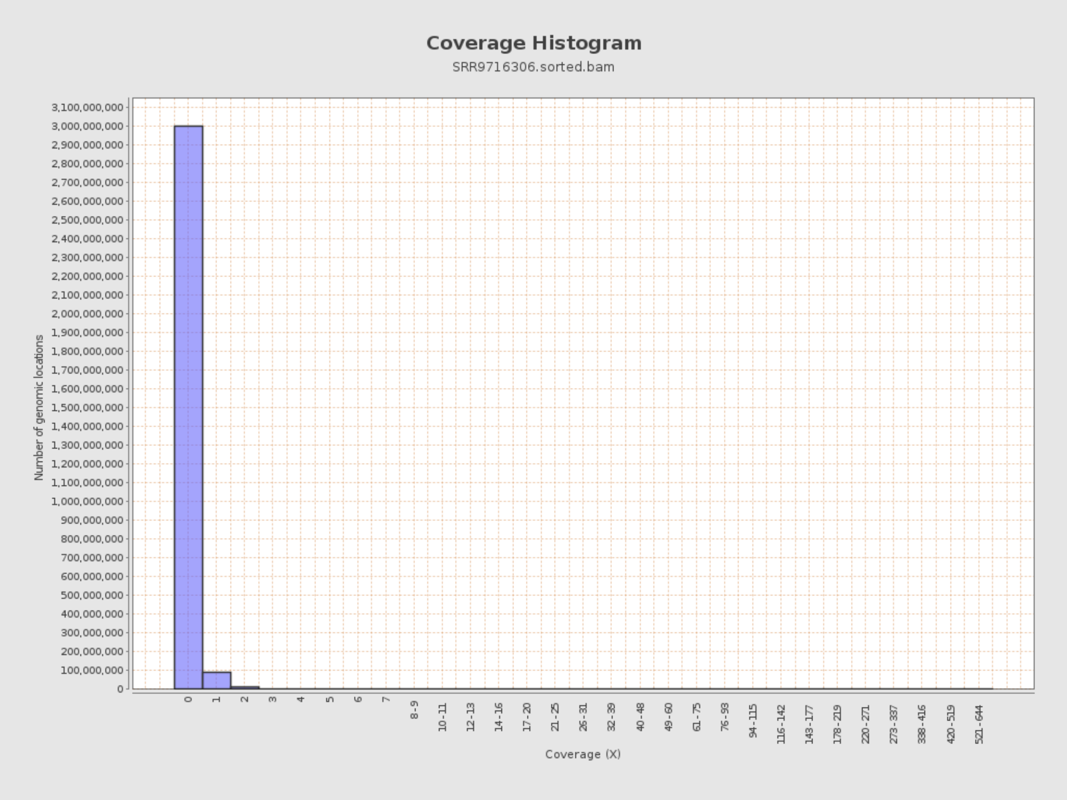
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9079781	0.0364	0.5819
chr2	243199373	9427773	0.0388	0.3705
chr3	198022430	7368365	0.0372	0.2114
chr4	191154276	7330352	0.0383	0.2798
chr5	180915260	6700815	0.037	0.2125
chr6	171115067	6303238	0.0368	0.227
chr7	159138663	6125548	0.0385	0.4

chr8	146364022	5835986	0.0399	0.3962
chr9	141213431	4694871	0.0332	0.284
chr10	135534747	5368088	0.0396	0.3577
chr11	135006516	5143865	0.0381	0.3039
chr12	133851895	4987057	0.0373	0.2134
chr13	115169878	3602325	0.0313	0.1954
chr14	107349540	3367846	0.0314	0.2063
chr15	102531392	3234421	0.0315	0.1952
chr16	90354753	3269331	0.0362	0.2244
chr17	81195210	3080464	0.0379	0.2387
chr18	78077248	3006074	0.0385	0.4548
chr19	59128983	2256632	0.0382	0.3852
chr20	63025520	2428618	0.0385	0.2267
chr21	48129895	1487130	0.0309	0.2265
chr22	51304566	1318521	0.0257	0.1776
chrMT	16571	16841	1.0163	1.1431
chrX	155270560	6245603	0.0402	0.2476
chrY	59373566	355238	0.006	0.2152

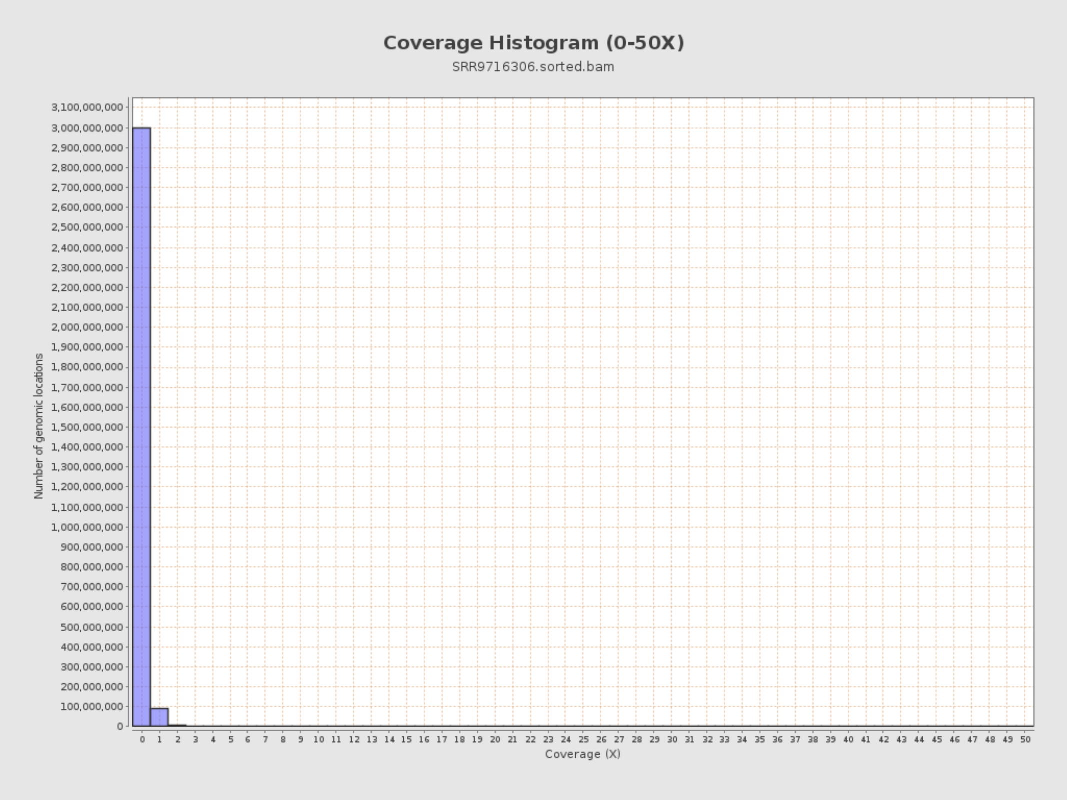
3. Results : Coverage across reference



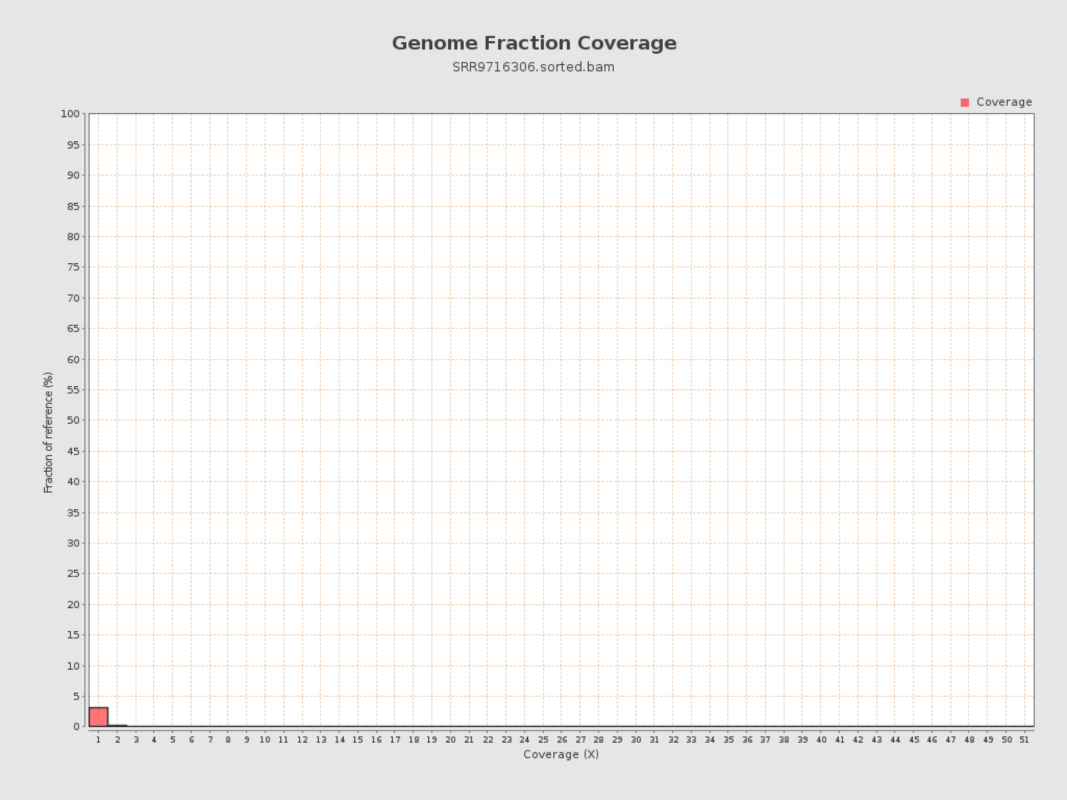
4. Results : Coverage Histogram



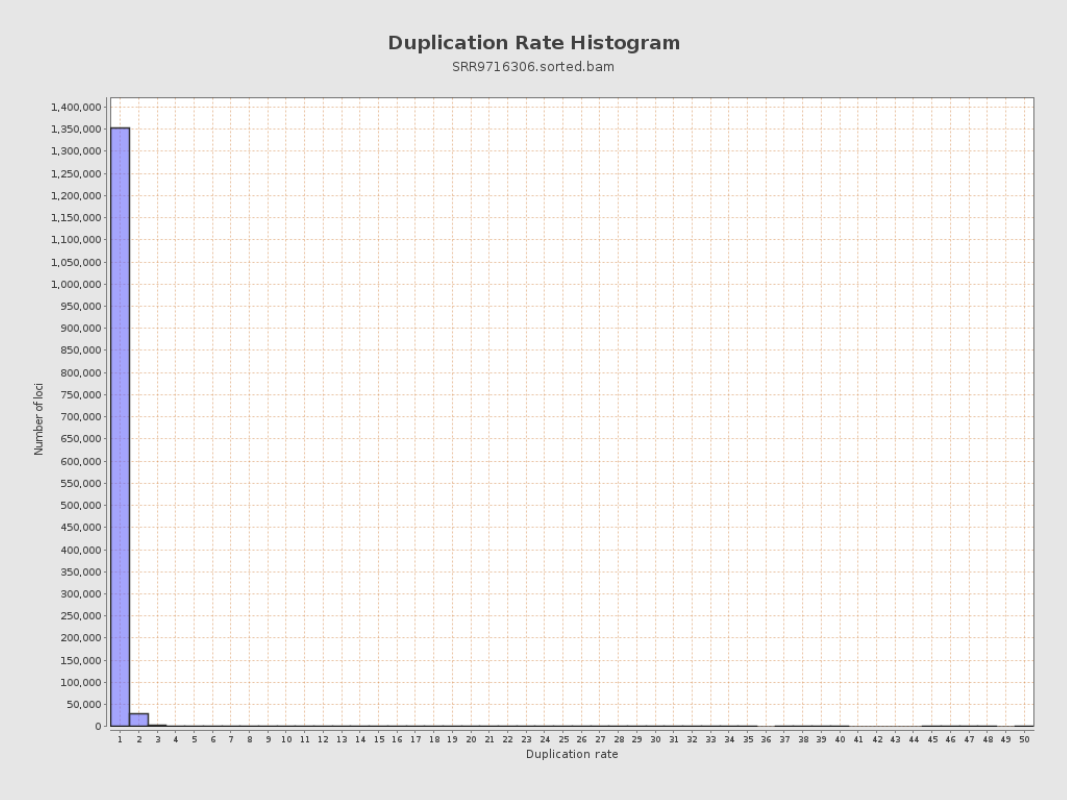
5. Results : Coverage Histogram (0-50X)



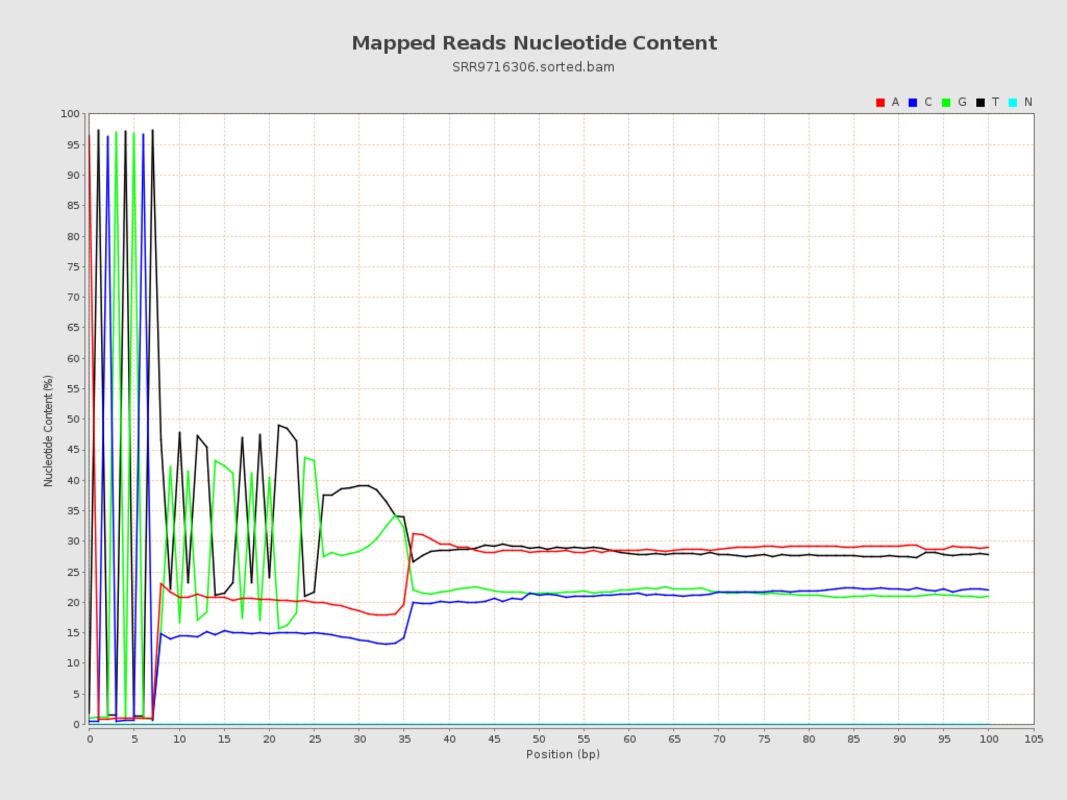
6. Results : Genome Fraction Coverage



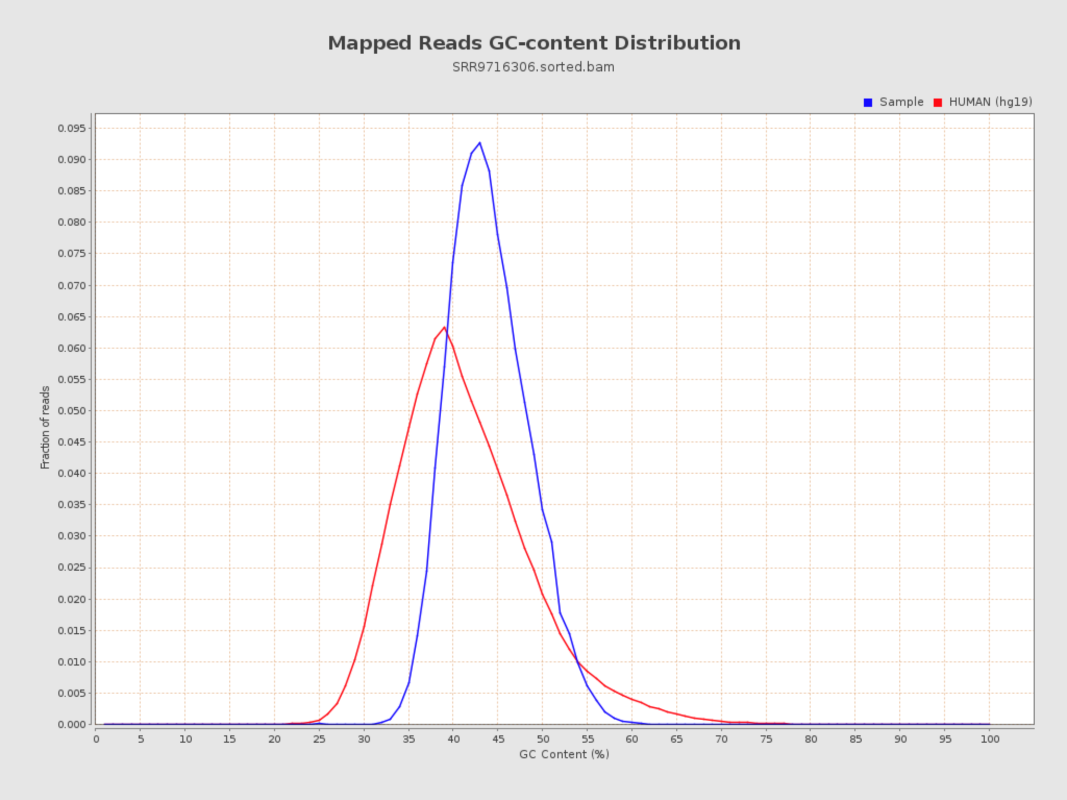
7. Results : Duplication Rate Histogram



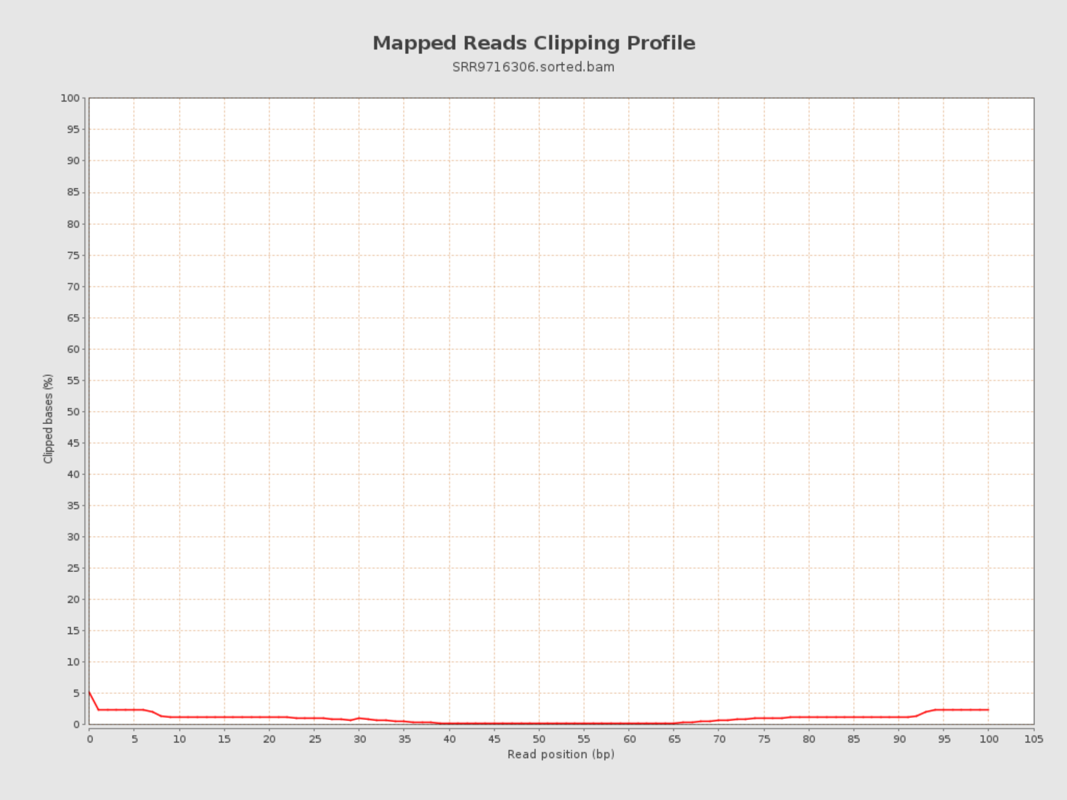
8. Results : Mapped Reads Nucleotide Content



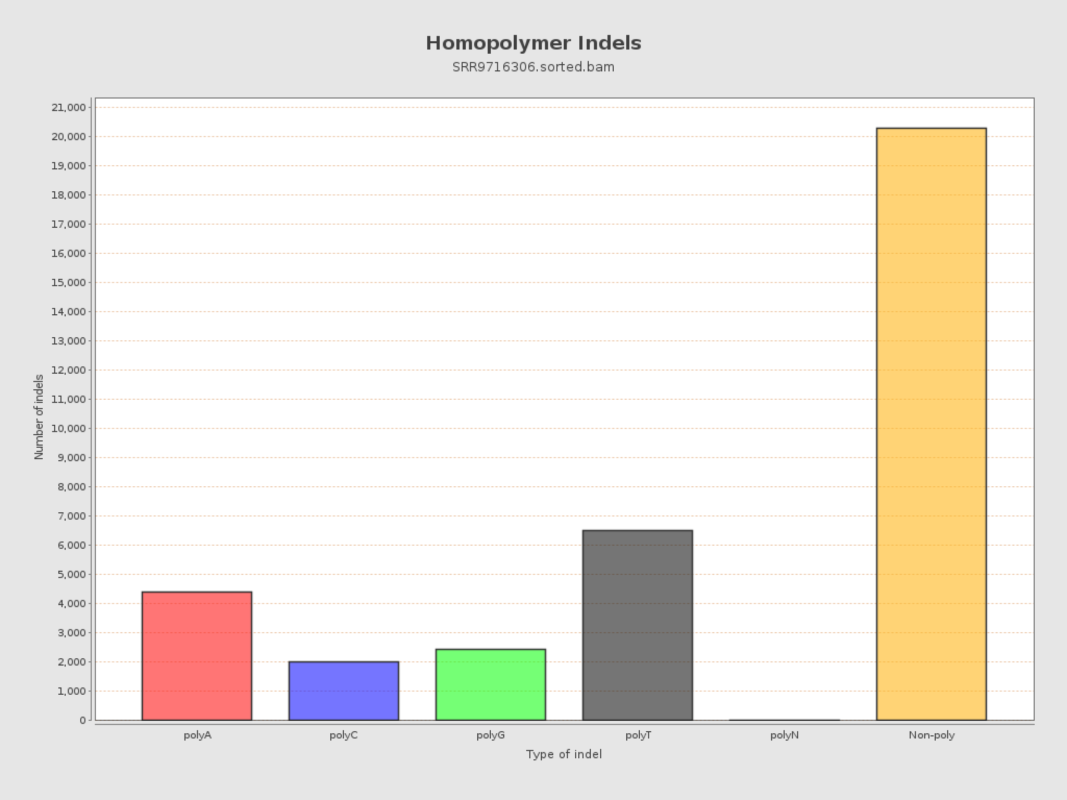
9. Results : Mapped Reads GC-content Distribution



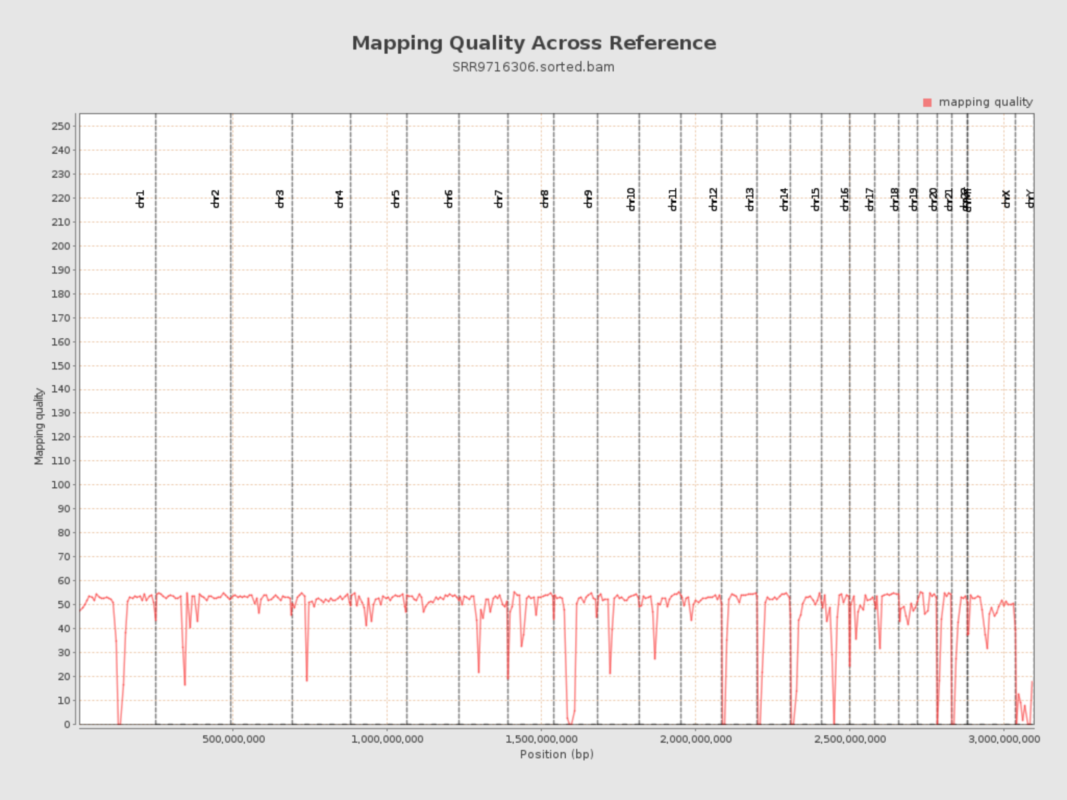
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram