Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 03:22:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716258.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_SRR9716258 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716258.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 03:22:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716258.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,834,381
Mapped reads	2,606,959 / 91.98%
Unmapped reads	227,422 / 8.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,415 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	195,646 / 6.9%
Duplication rate	5.83%
Clipped reads	2,622,025 / 92.51%

2.2. ACGT Content

Number/percentage of A's	38,806,826 / 25.52%
Number/percentage of C's	30,933,824 / 20.35%
Number/percentage of T's	46,161,357 / 30.36%
Number/percentage of G's	36,136,537 / 23.77%
Number/percentage of N's	1,977 / 0%
GC Percentage	44.11%

2.3. Coverage

Mean	0.0491

Standard Deviation	0.3897

2.4. Mapping Quality

Mean Mapping Quality	44.81

2.5. Mismatches and indels

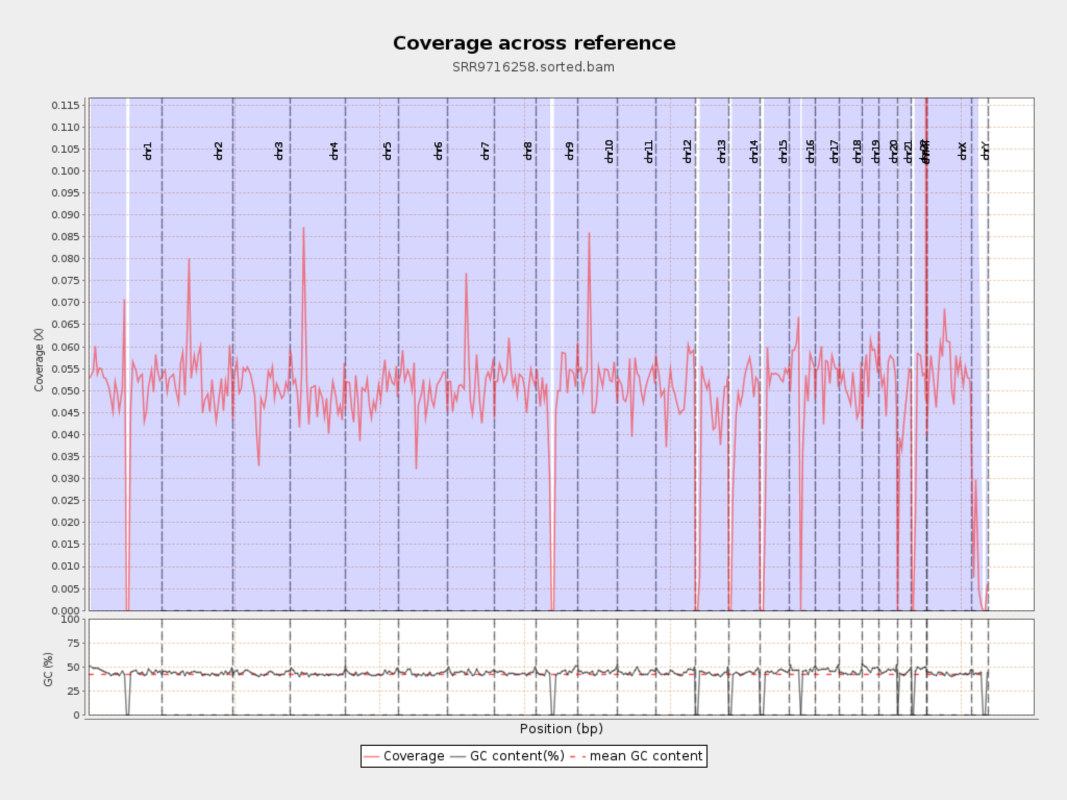
General error rate	0.51%
Mismatches	750,545
Insertions	9,227
Mapped reads with at least one insertion	0.35%
Deletions	27,176
Mapped reads with at least one deletion	1.03%
Homopolymer indels	42.35%

2.6. Chromosome stats

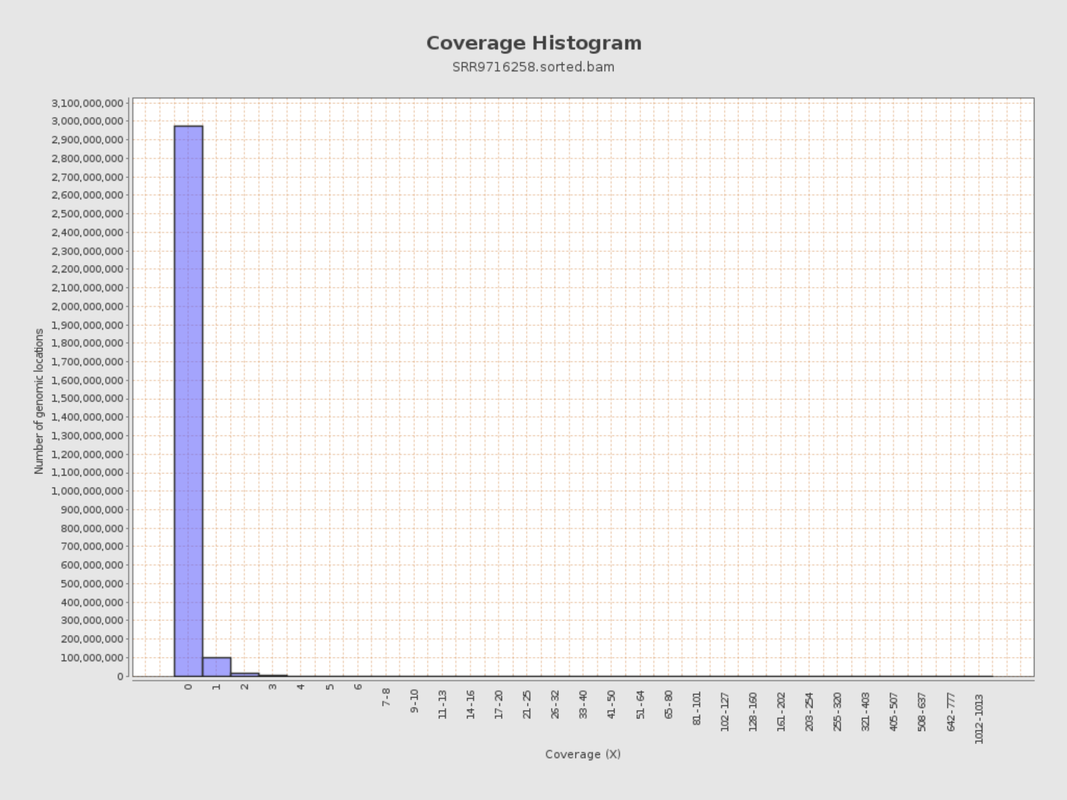
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12279120	0.0493	0.6062
chr2	243199373	12888349	0.053	0.5399
chr3	198022430	9946258	0.0502	0.2728
chr4	191154276	9581555	0.0501	0.3387
chr5	180915260	8983421	0.0497	0.2718
chr6	171115067	8638572	0.0505	0.3011
chr7	159138663	8279672	0.052	0.5195

chr8	146364022	7722468	0.0528	0.4153
chr9	141213431	6362378	0.0451	0.3207
chr10	135534747	7319992	0.054	0.4325
chr11	135006516	6923822	0.0513	0.3432
chr12	133851895	6806180	0.0508	0.2813
chr13	115169878	4604314	0.04	0.2461
chr14	107349540	4629806	0.0431	0.2703
chr15	102531392	4510343	0.044	0.2638
chr16	90354753	4549307	0.0503	0.2917
chr17	81195210	4414113	0.0544	0.3154
chr18	78077248	3919036	0.0502	0.5558
chr19	59128983	3304743	0.0559	0.4762
chr20	63025520	3352457	0.0532	0.294
chr21	48129895	1994202	0.0414	0.3004
chr22	51304566	1987671	0.0387	0.2416
chrMT	16571	98621	5.9514	4.5012
chrX	155270560	8491781	0.0547	0.3125
chrY	59373566	495543	0.0083	0.233

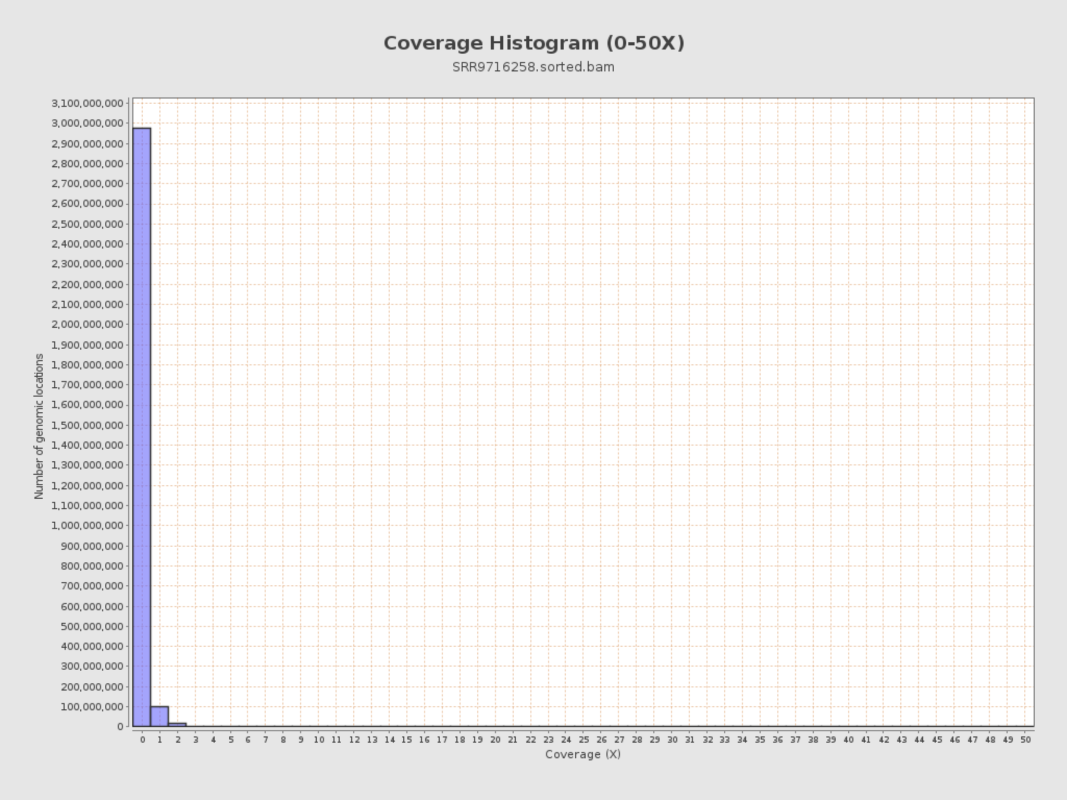
3. Results : Coverage across reference



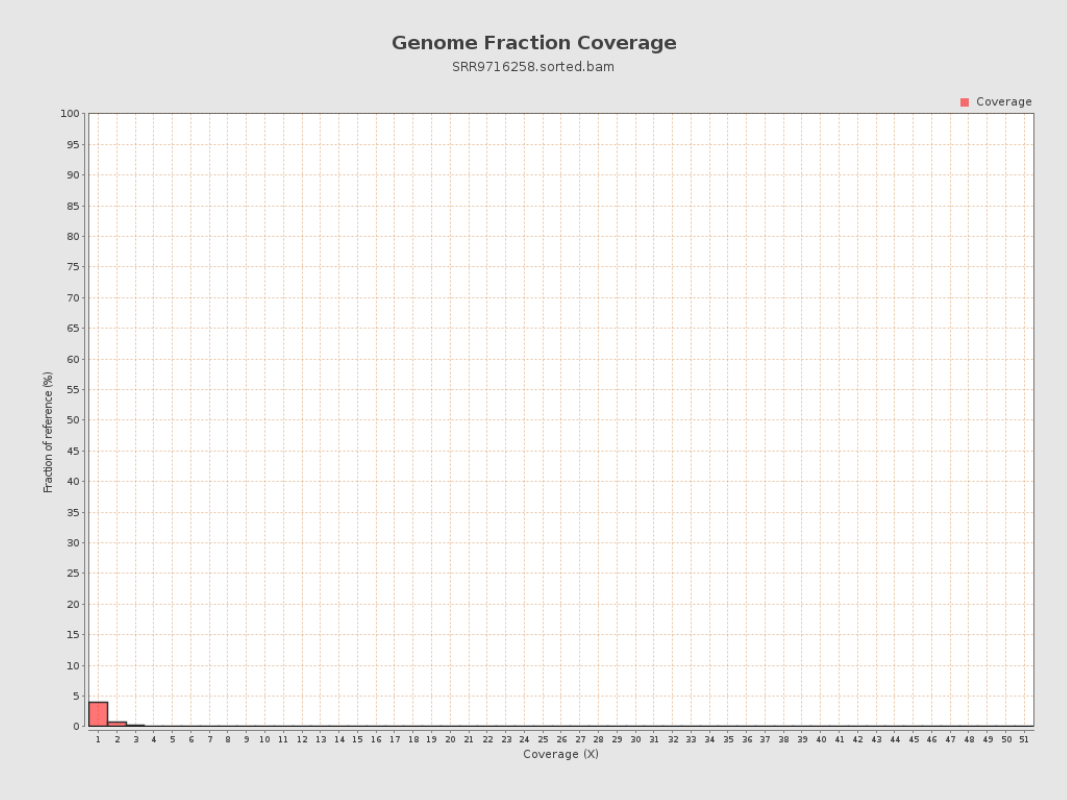
4. Results : Coverage Histogram



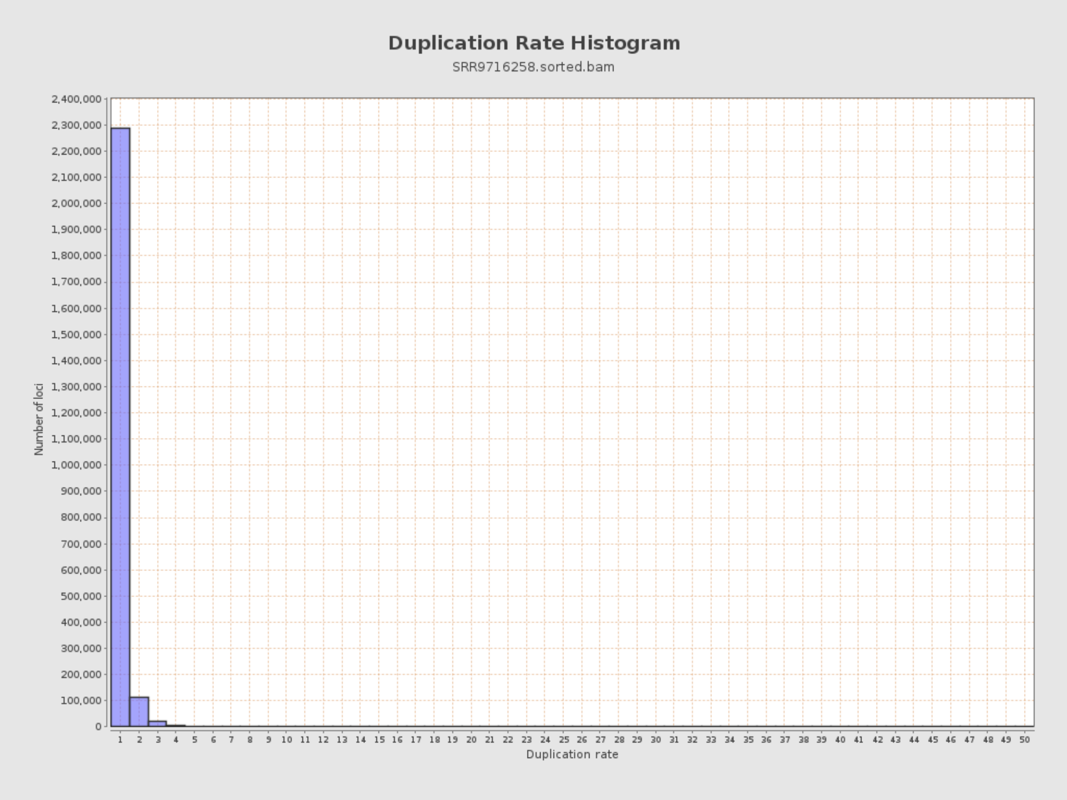
5. Results : Coverage Histogram (0-50X)



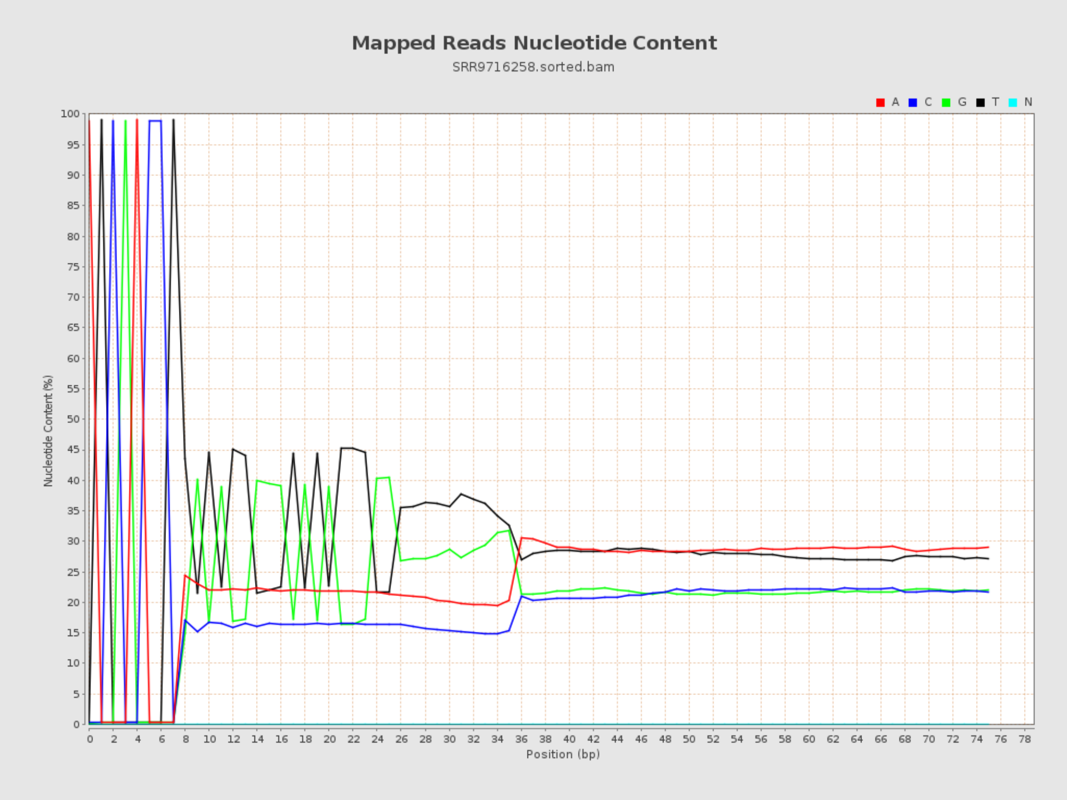
6. Results : Genome Fraction Coverage



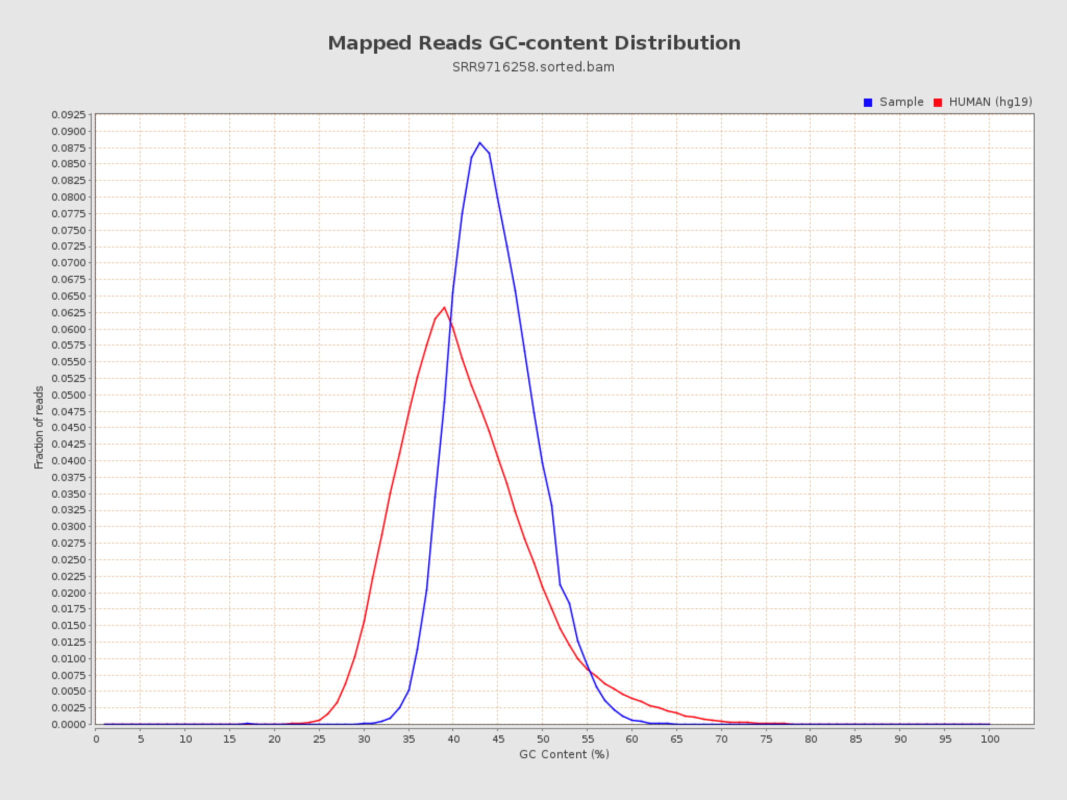
7. Results : Duplication Rate Histogram



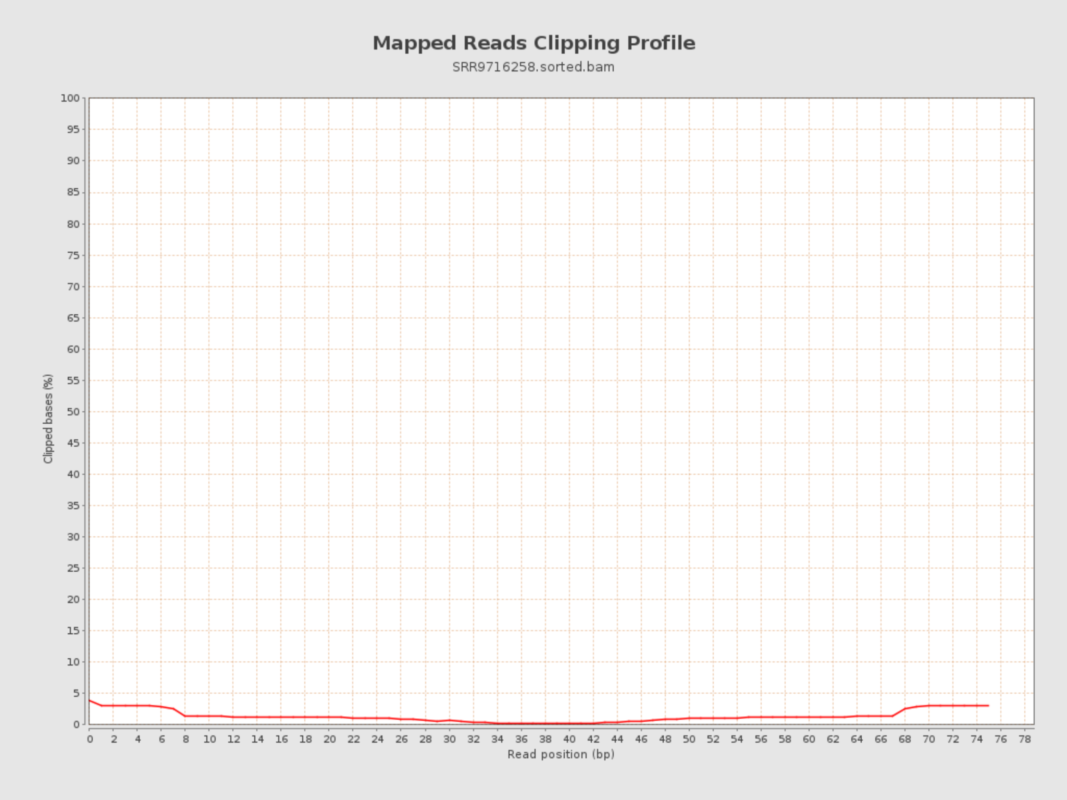
8. Results : Mapped Reads Nucleotide Content



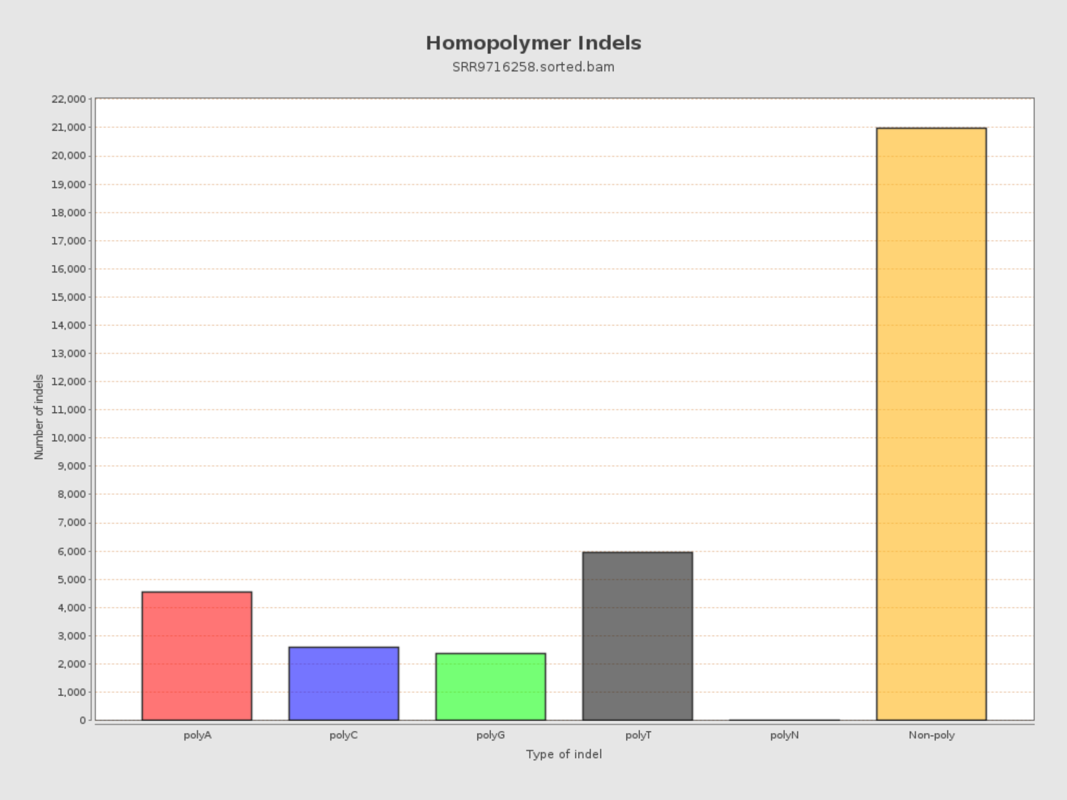
9. Results : Mapped Reads GC-content Distribution



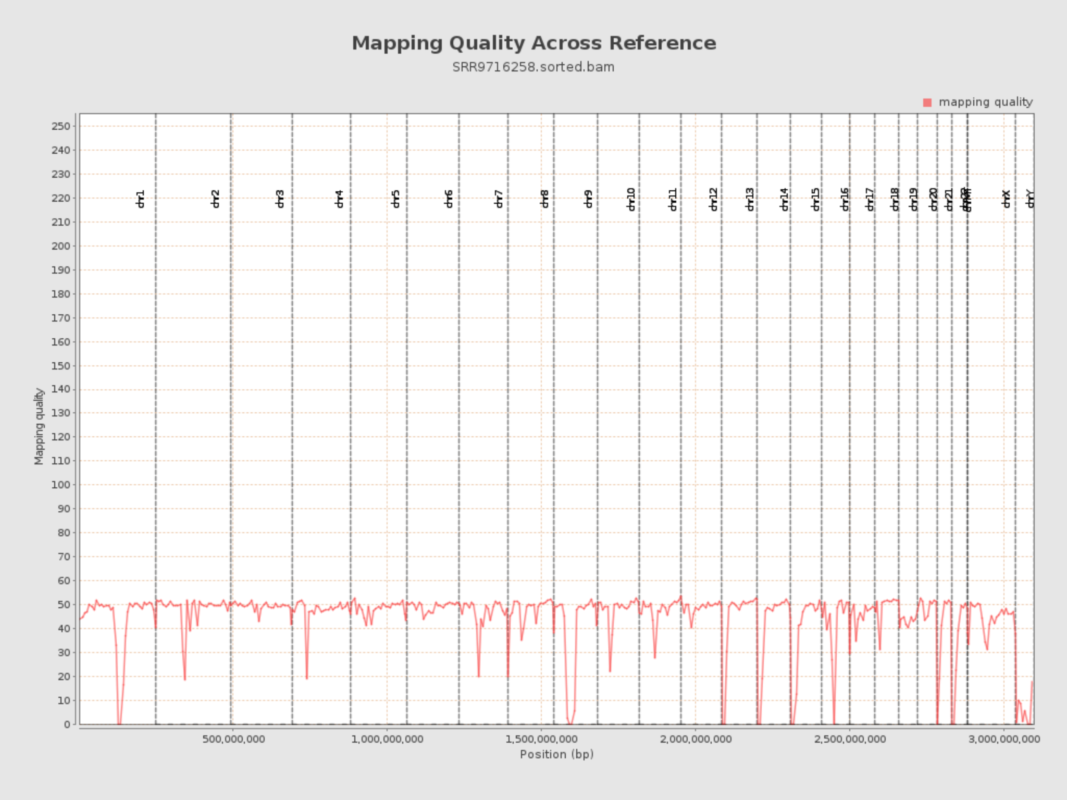
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram