Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 13:01:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716431.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_SRR9716431 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716431.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 13:01:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716431.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,585,101
Mapped reads	1,414,101 / 89.21%
Unmapped reads	171,000 / 10.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,562 / 1.93%
Read min/max/mean length	30 / 101 / 101.69
Duplicated reads (estimated)	38,814 / 2.45%
Duplication rate	1.97%
Clipped reads	1,442,155 / 90.98%

2.2. ACGT Content

Number/percentage of A's	27,351,531 / 26.11%
Number/percentage of C's	22,332,448 / 21.32%
Number/percentage of T's	31,148,205 / 29.74%
Number/percentage of G's	23,901,793 / 22.82%
Number/percentage of N's	12,045 / 0.01%
GC Percentage	44.14%

2.3. Coverage

Mean	0.0338

Standard Deviation	0.2697

2.4. Mapping Quality

Mean Mapping Quality	46.2

2.5. Mismatches and indels

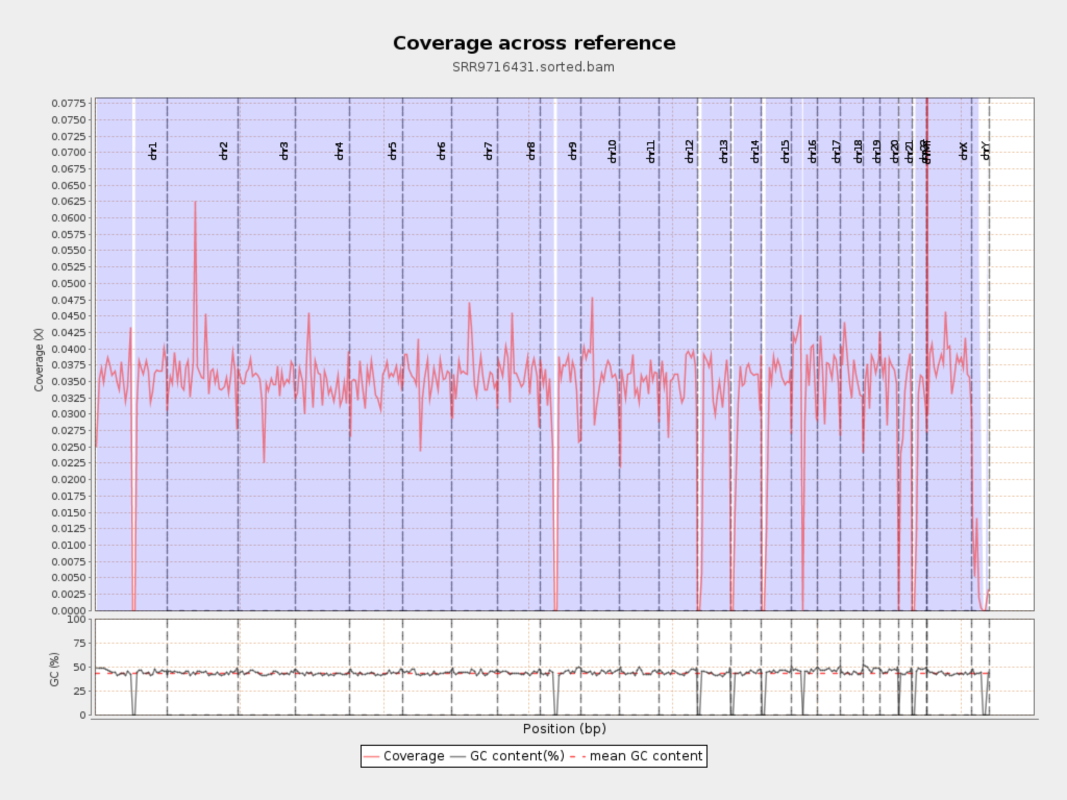
General error rate	0.75%
Mismatches	764,430
Insertions	9,224
Mapped reads with at least one insertion	0.64%
Deletions	21,221
Mapped reads with at least one deletion	1.48%
Homopolymer indels	40.3%

2.6. Chromosome stats

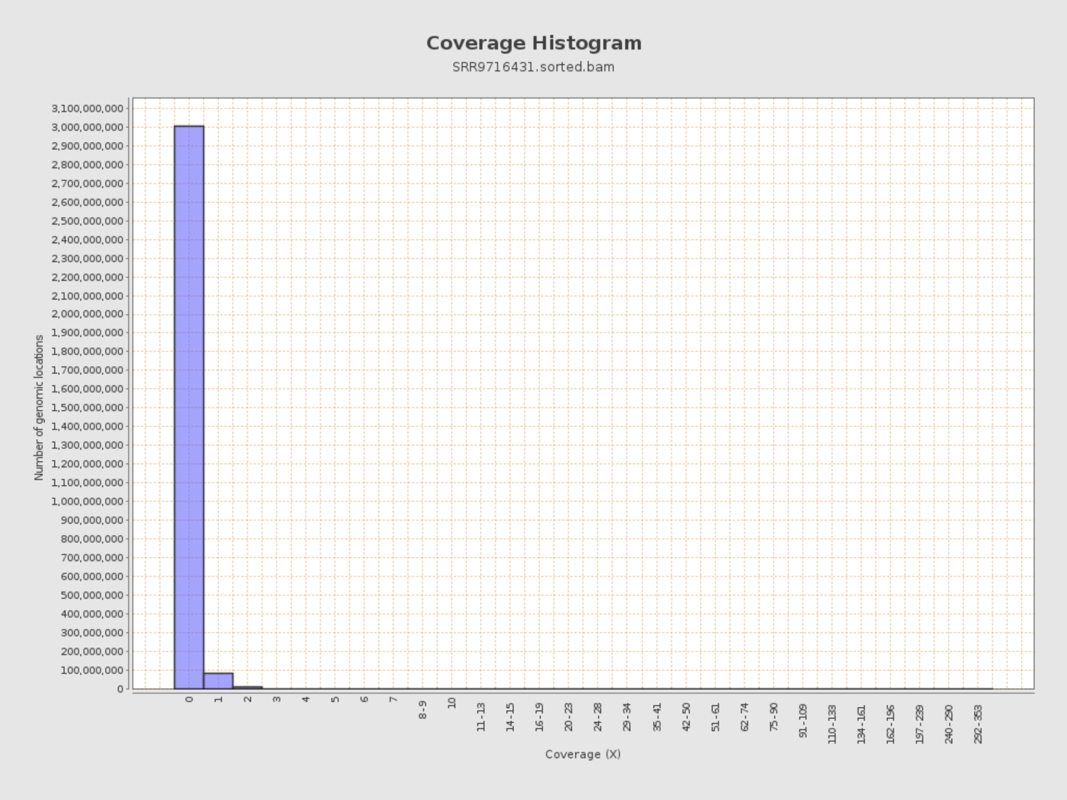
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8380099	0.0336	0.3168
chr2	243199373	8931365	0.0367	0.365
chr3	198022430	6932669	0.035	0.2056
chr4	191154276	6670720	0.0349	0.2188
chr5	180915260	6369155	0.0352	0.2081
chr6	171115067	6069564	0.0355	0.2259
chr7	159138663	5768196	0.0362	0.329

chr8	146364022	5342037	0.0365	0.3228
chr9	141213431	4377552	0.031	0.2776
chr10	135534747	4962102	0.0366	0.2756
chr11	135006516	4726341	0.035	0.2991
chr12	133851895	4750898	0.0355	0.2095
chr13	115169878	3358475	0.0292	0.1874
chr14	107349540	3160256	0.0294	0.2185
chr15	102531392	3005889	0.0293	0.1895
chr16	90354753	3110819	0.0344	0.2204
chr17	81195210	2927678	0.0361	0.2251
chr18	78077248	2849468	0.0365	0.488
chr19	59128983	2137915	0.0362	0.2878
chr20	63025520	2226059	0.0353	0.2154
chr21	48129895	1388605	0.0289	0.1973
chr22	51304566	1192973	0.0233	0.1684
chrMT	16571	4457	0.269	0.5716
chrX	155270560	5876432	0.0378	0.2525
chrY	59373566	262565	0.0044	0.1261

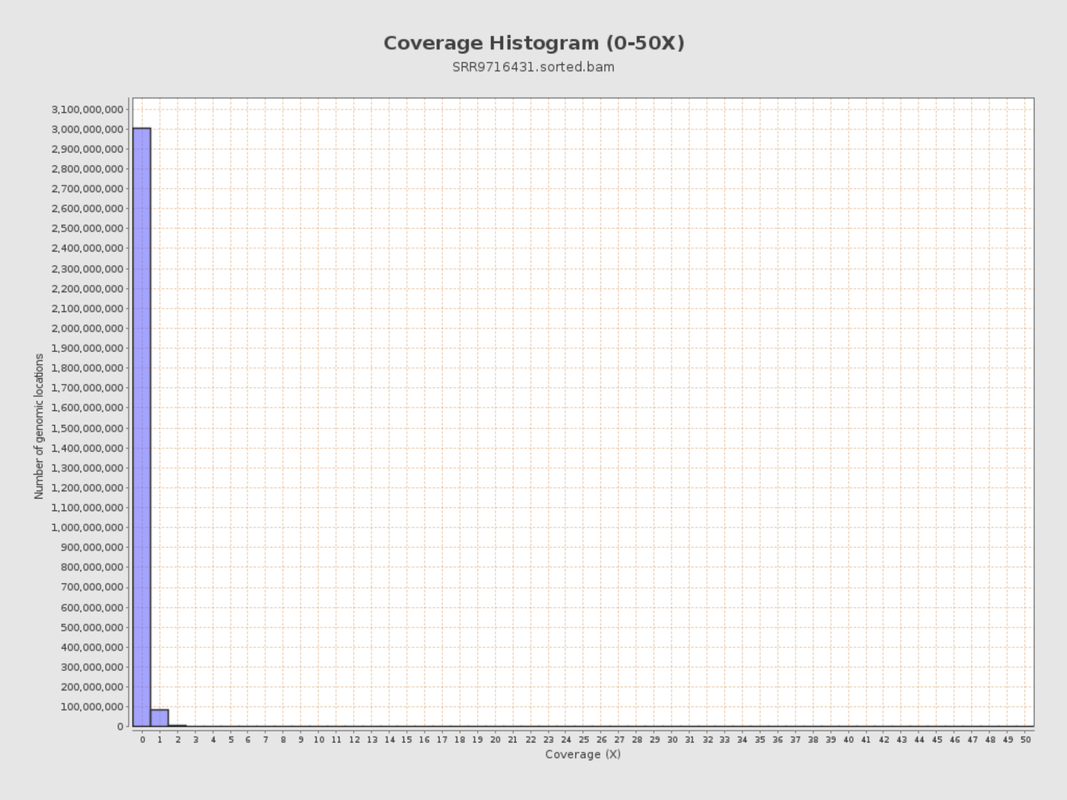
3. Results : Coverage across reference



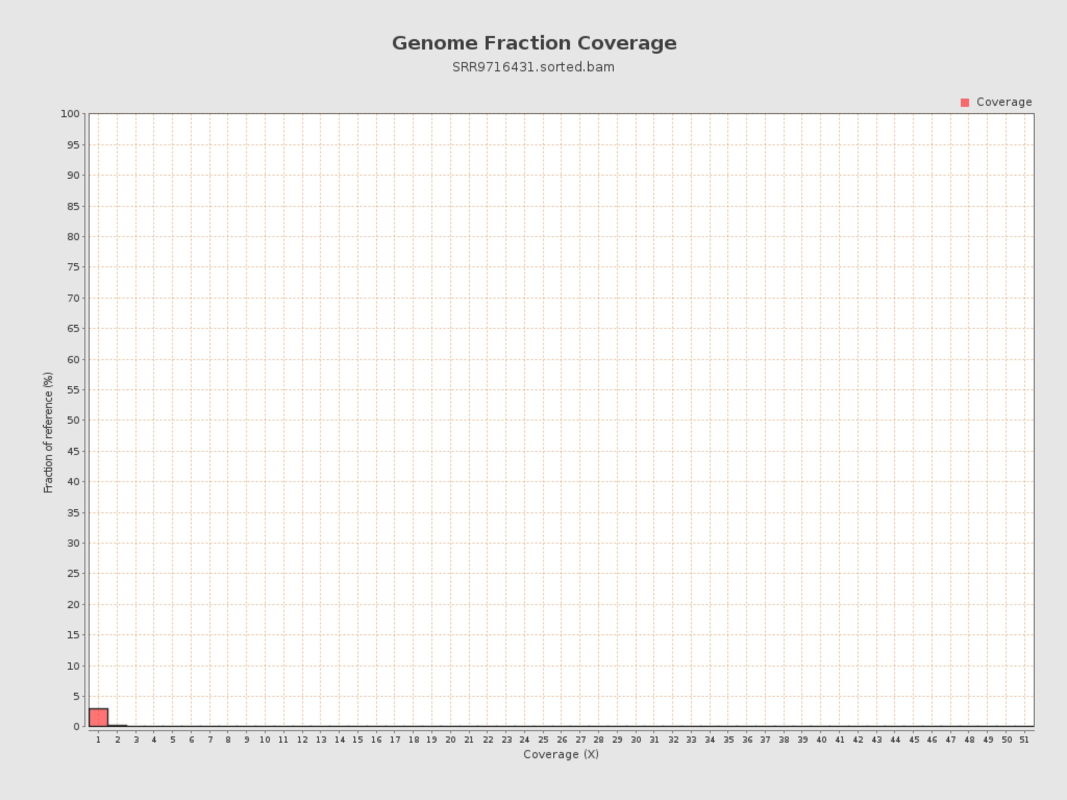
4. Results : Coverage Histogram



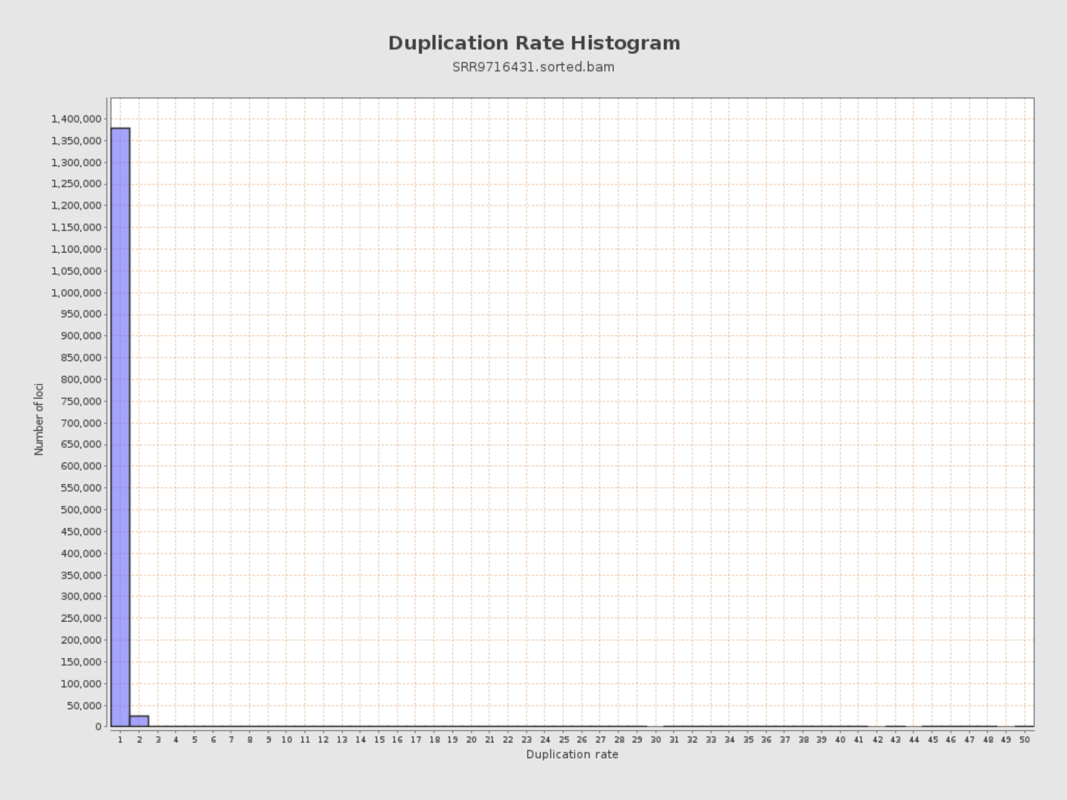
5. Results : Coverage Histogram (0-50X)



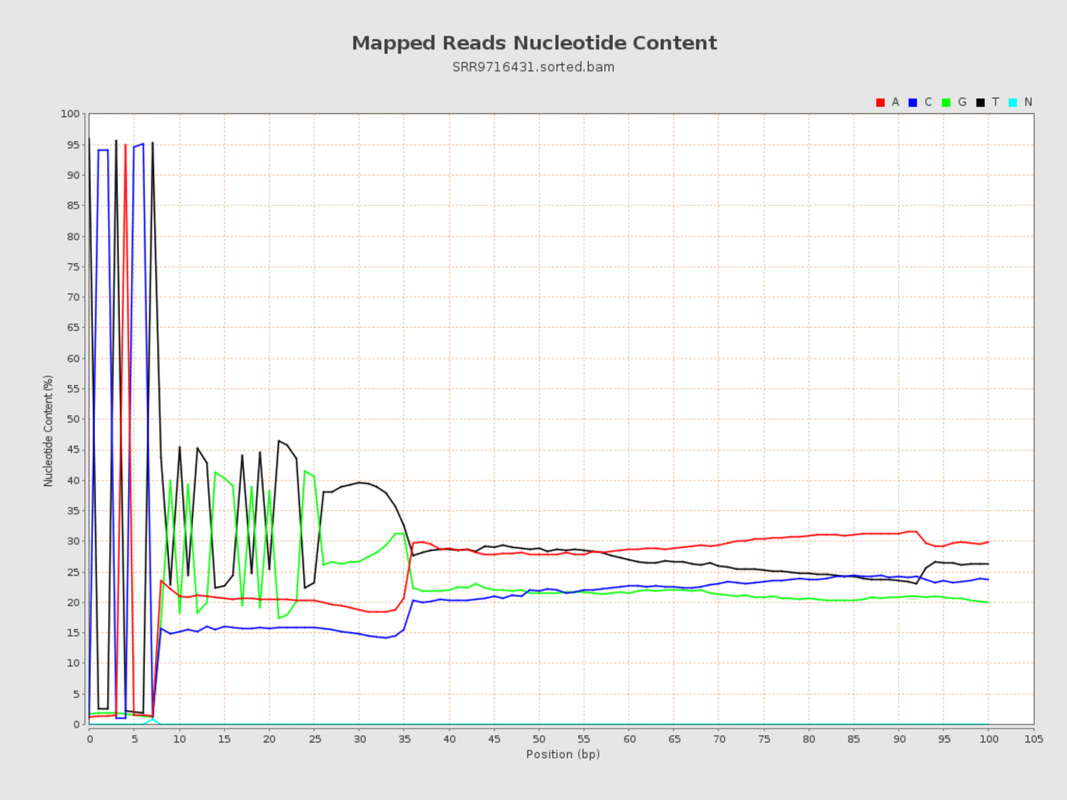
6. Results : Genome Fraction Coverage



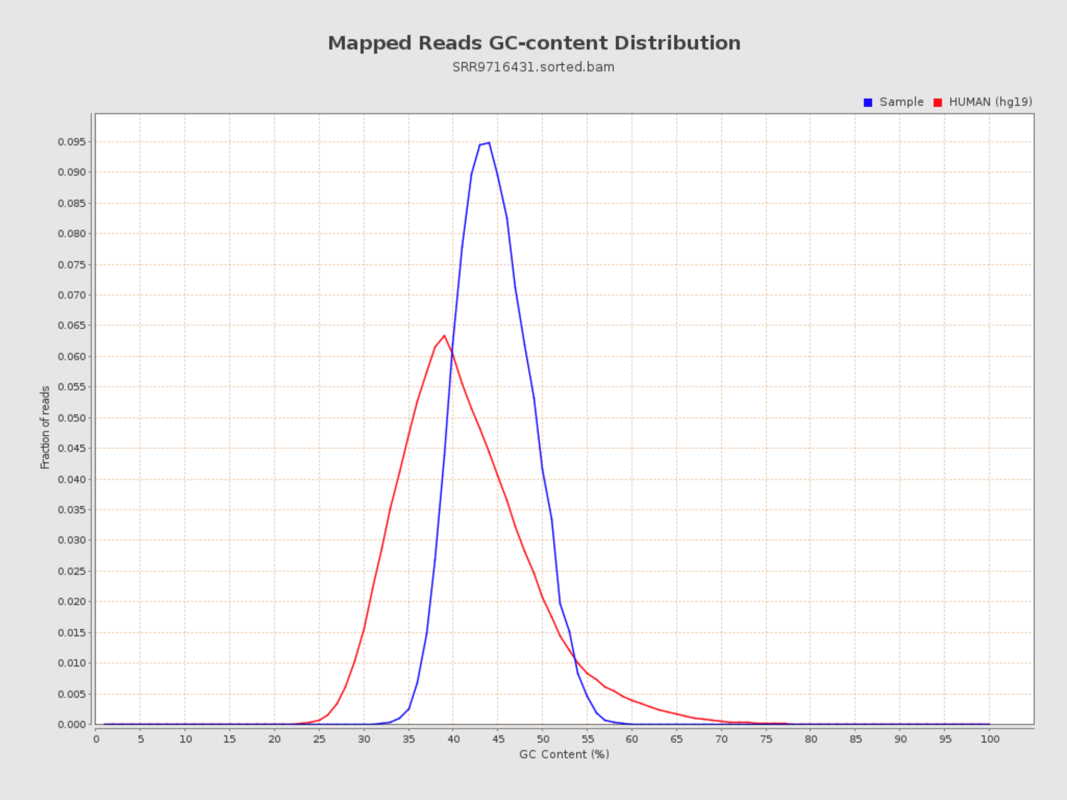
7. Results : Duplication Rate Histogram



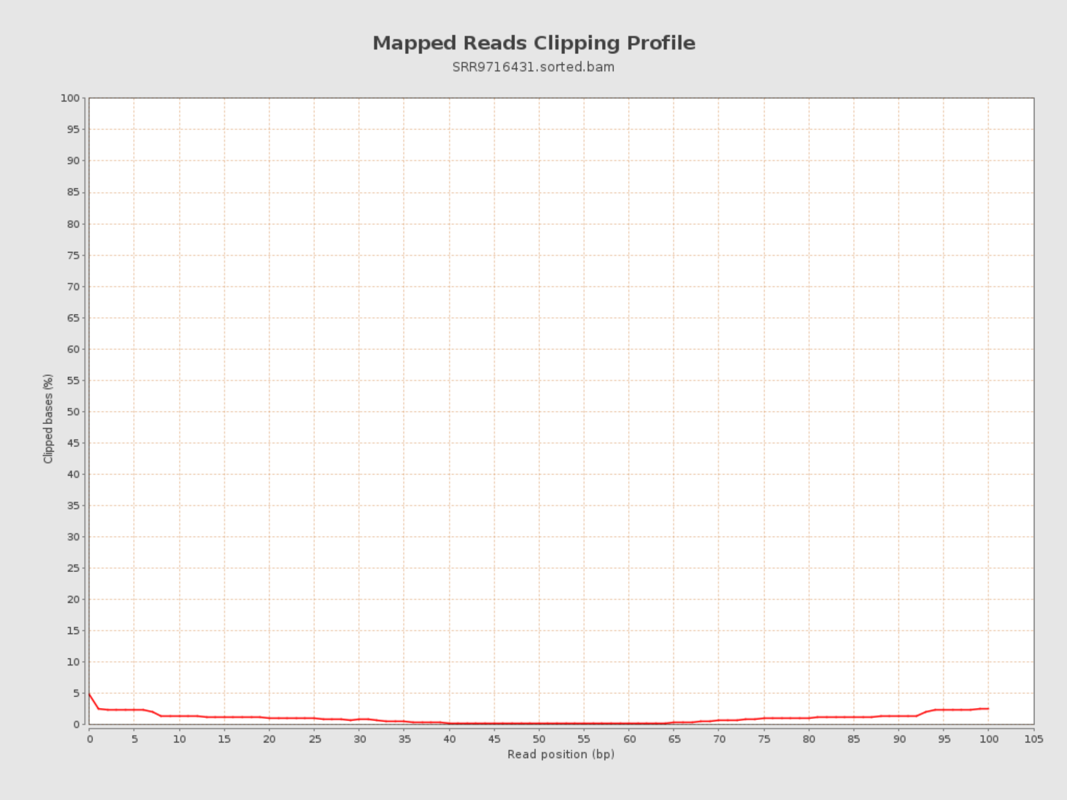
8. Results : Mapped Reads Nucleotide Content



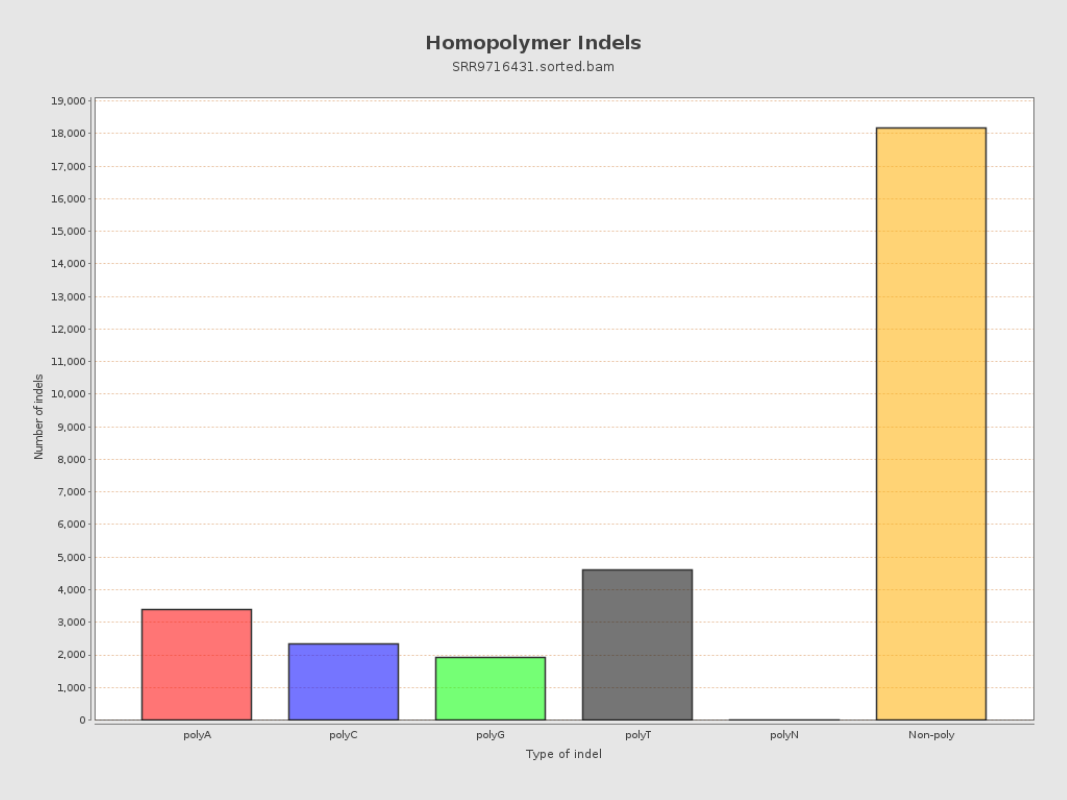
9. Results : Mapped Reads GC-content Distribution



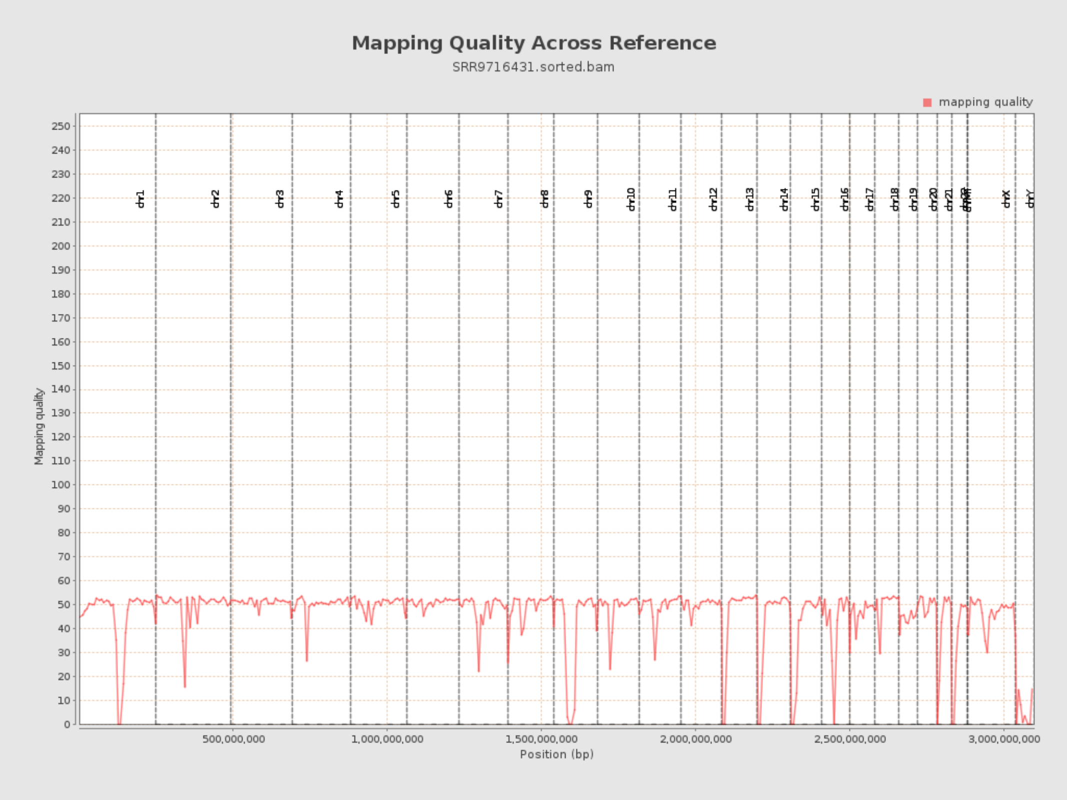
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram