Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 01:52:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716235.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_SRR9716235 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716235.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 01:52:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716235.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,659,650
Mapped reads	1,559,494 / 93.97%
Unmapped reads	100,156 / 6.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,172 / 1.46%
Read min/max/mean length	30 / 101 / 101.54
Duplicated reads (estimated)	67,053 / 4.04%
Duplication rate	2.74%
Clipped reads	1,582,465 / 95.35%

2.2. ACGT Content

Number/percentage of A's	31,500,865 / 25.41%
Number/percentage of C's	23,699,393 / 19.12%
Number/percentage of T's	37,546,299 / 30.29%
Number/percentage of G's	31,193,638 / 25.17%
Number/percentage of N's	7,156 / 0.01%
GC Percentage	44.29%

2.3. Coverage

Mean	0.0401

Standard Deviation	0.4339

2.4. Mapping Quality

Mean Mapping Quality	45.26

2.5. Mismatches and indels

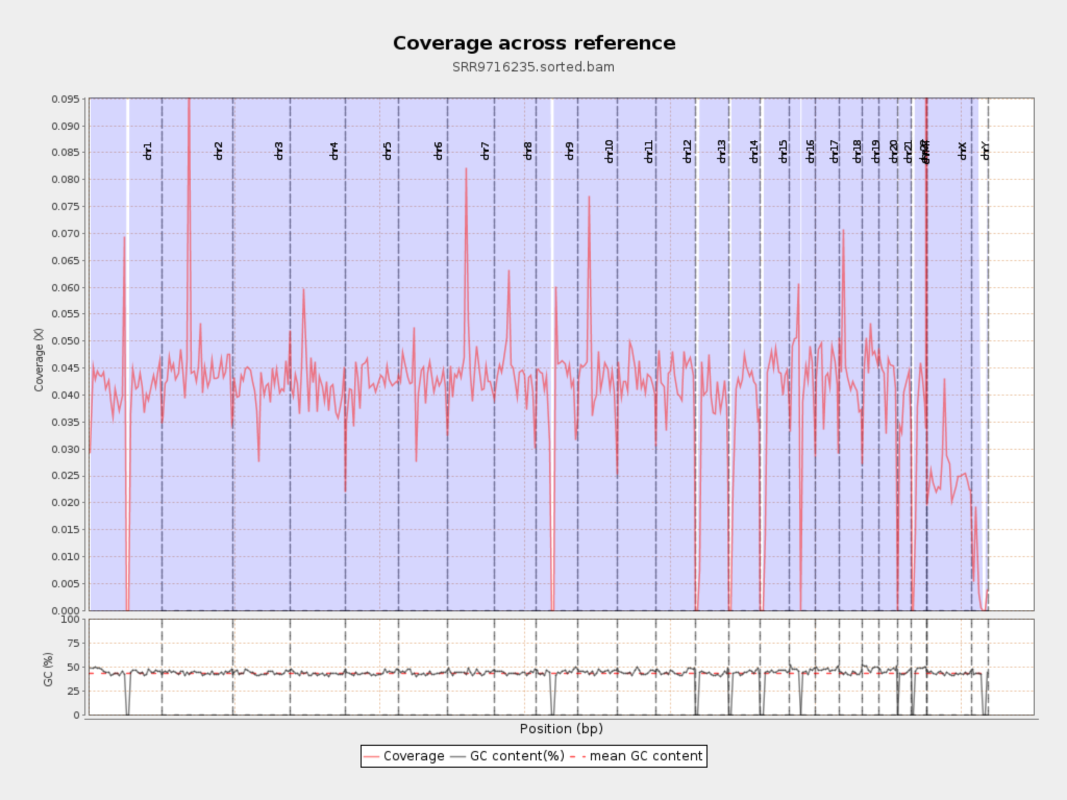
General error rate	0.8%
Mismatches	974,365
Insertions	11,206
Mapped reads with at least one insertion	0.71%
Deletions	29,973
Mapped reads with at least one deletion	1.89%
Homopolymer indels	44.13%

2.6. Chromosome stats

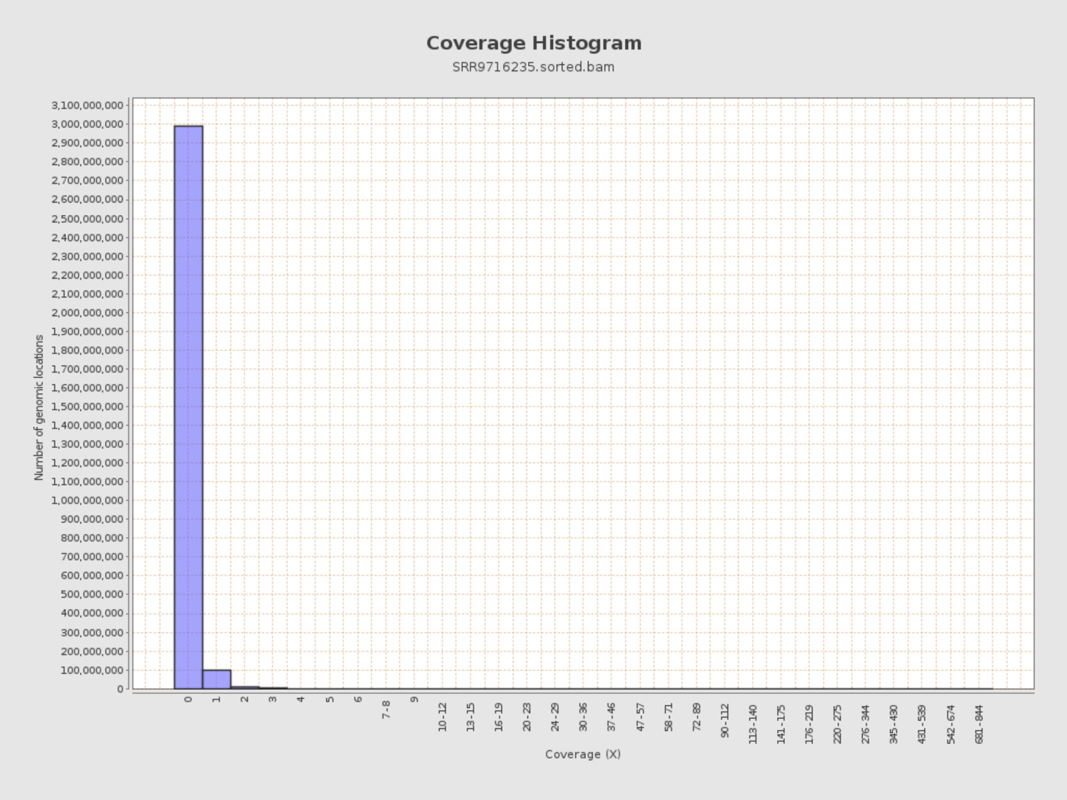
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9822305	0.0394	0.687
chr2	243199373	11208278	0.0461	0.6316
chr3	198022430	8244794	0.0416	0.2304
chr4	191154276	7987587	0.0418	0.2575
chr5	180915260	7604698	0.042	0.2357
chr6	171115067	7313846	0.0427	0.2759
chr7	159138663	7251048	0.0456	0.6067

chr8	146364022	6447964	0.0441	0.5817
chr9	141213431	5480886	0.0388	0.4726
chr10	135534747	6052636	0.0447	0.4198
chr11	135006516	5788808	0.0429	0.4231
chr12	133851895	5775851	0.0432	0.2409
chr13	115169878	3876239	0.0337	0.2048
chr14	107349540	3837503	0.0357	0.2702
chr15	102531392	3691351	0.036	0.2151
chr16	90354753	3800883	0.0421	0.2683
chr17	81195210	3521320	0.0434	0.2612
chr18	78077248	3505425	0.0449	0.8843
chr19	59128983	2769336	0.0468	0.5001
chr20	63025520	2669847	0.0424	0.2479
chr21	48129895	1677265	0.0348	0.2354
chr22	51304566	1456128	0.0284	0.1891
chrMT	16571	32875	1.9839	1.8719
chrX	155270560	3883718	0.025	0.2632
chrY	59373566	299272	0.005	0.1691

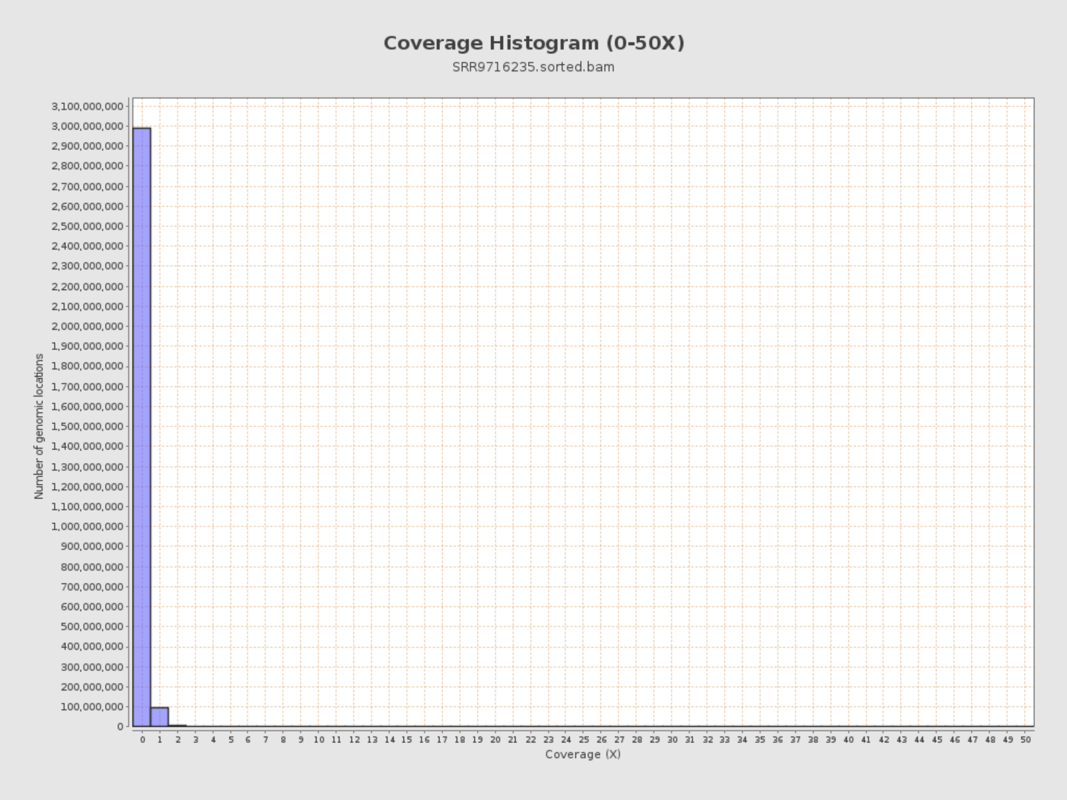
3. Results : Coverage across reference



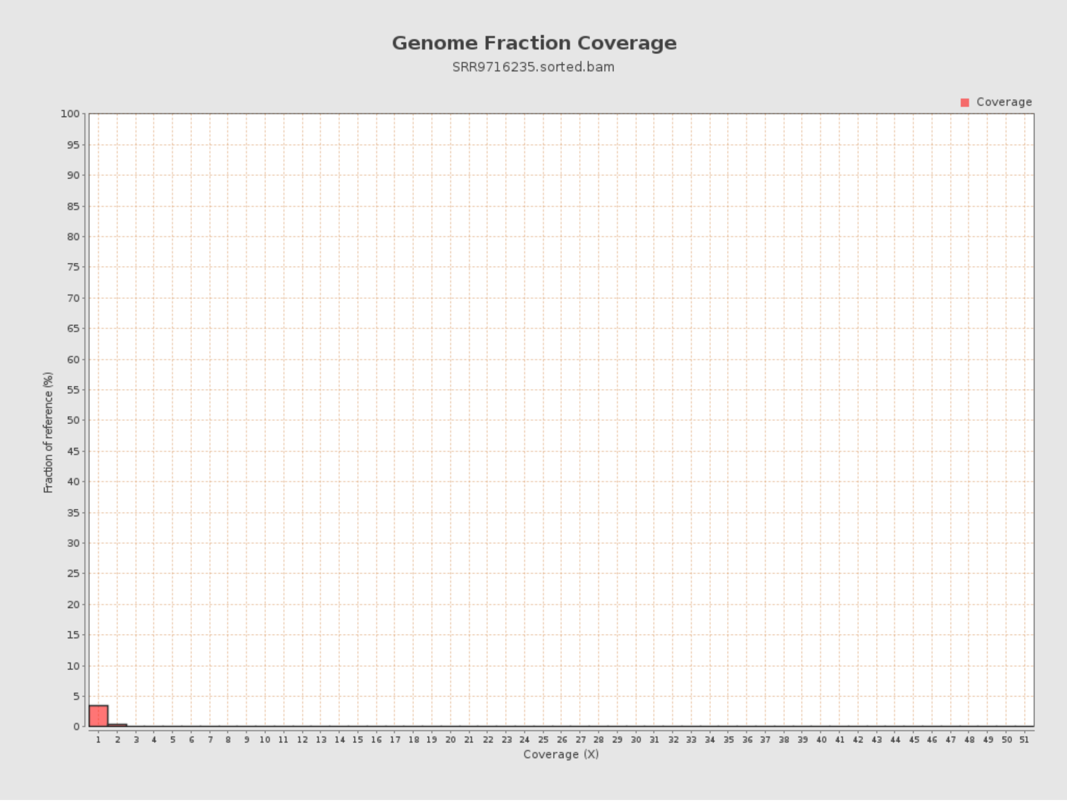
4. Results : Coverage Histogram



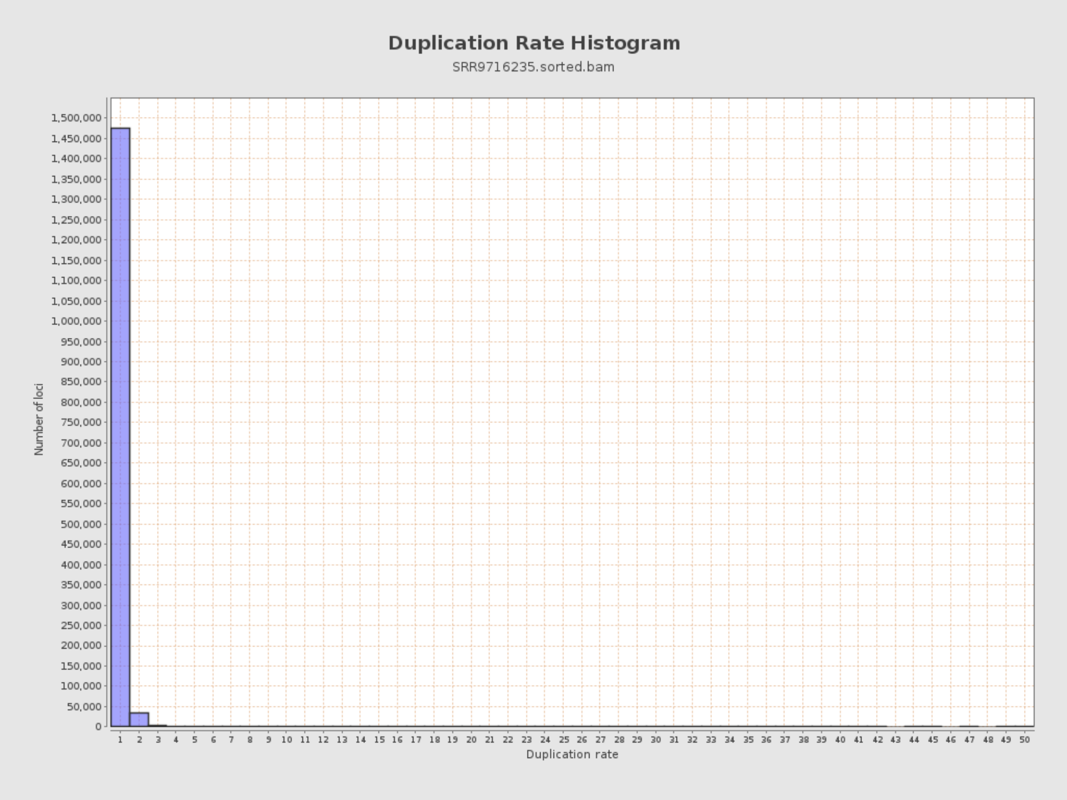
5. Results : Coverage Histogram (0-50X)



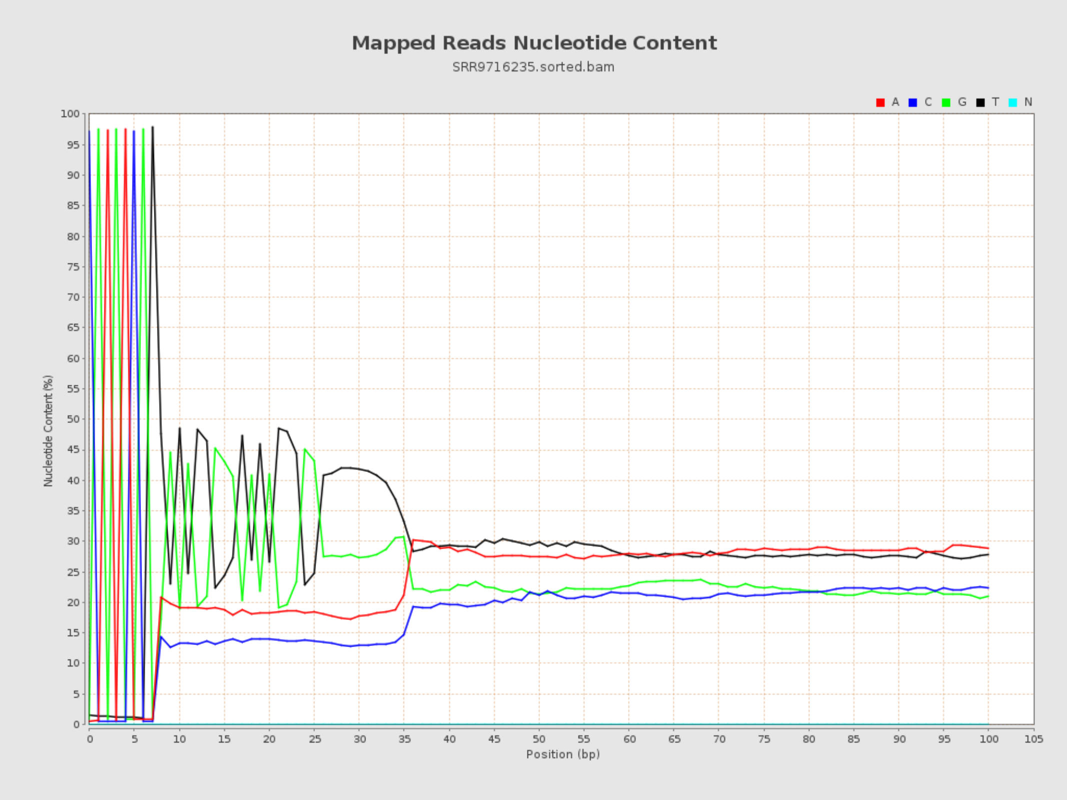
6. Results : Genome Fraction Coverage



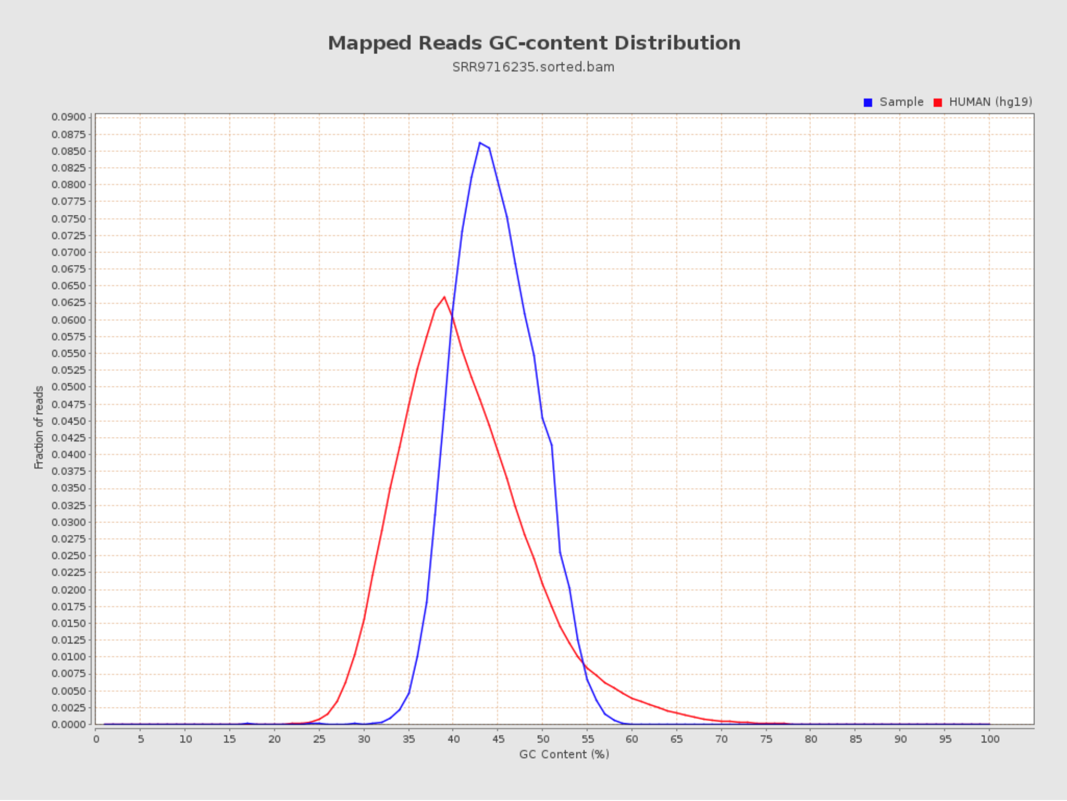
7. Results : Duplication Rate Histogram



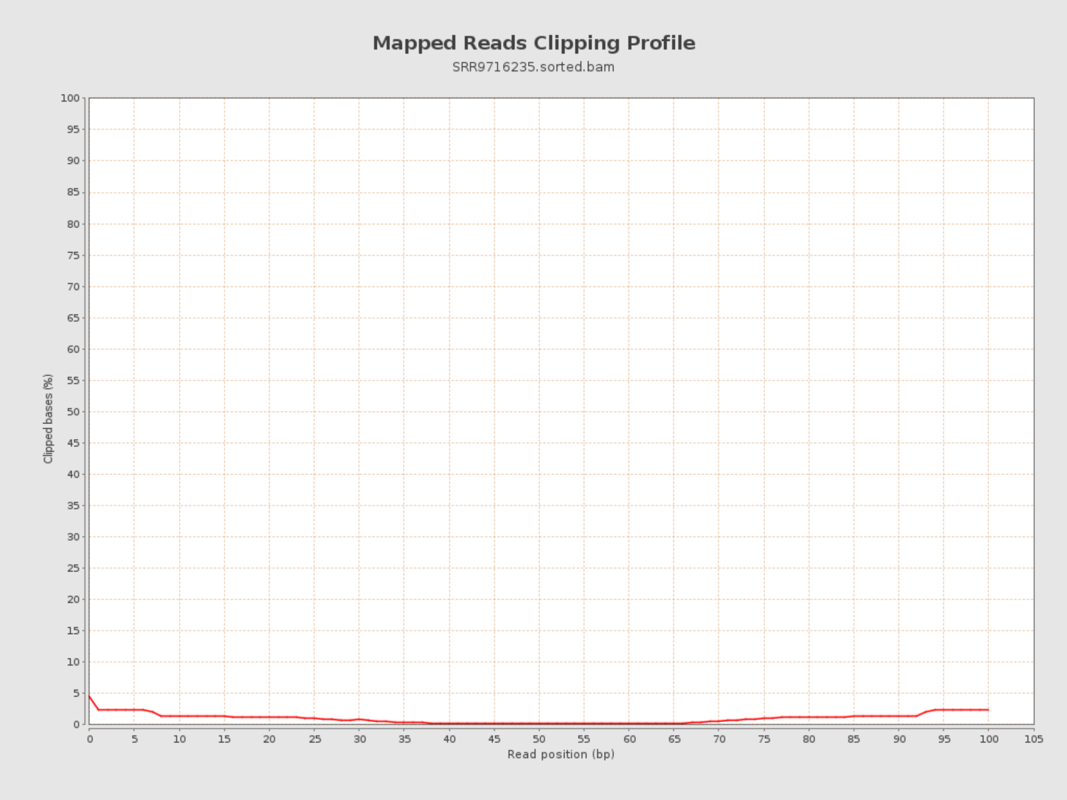
8. Results : Mapped Reads Nucleotide Content



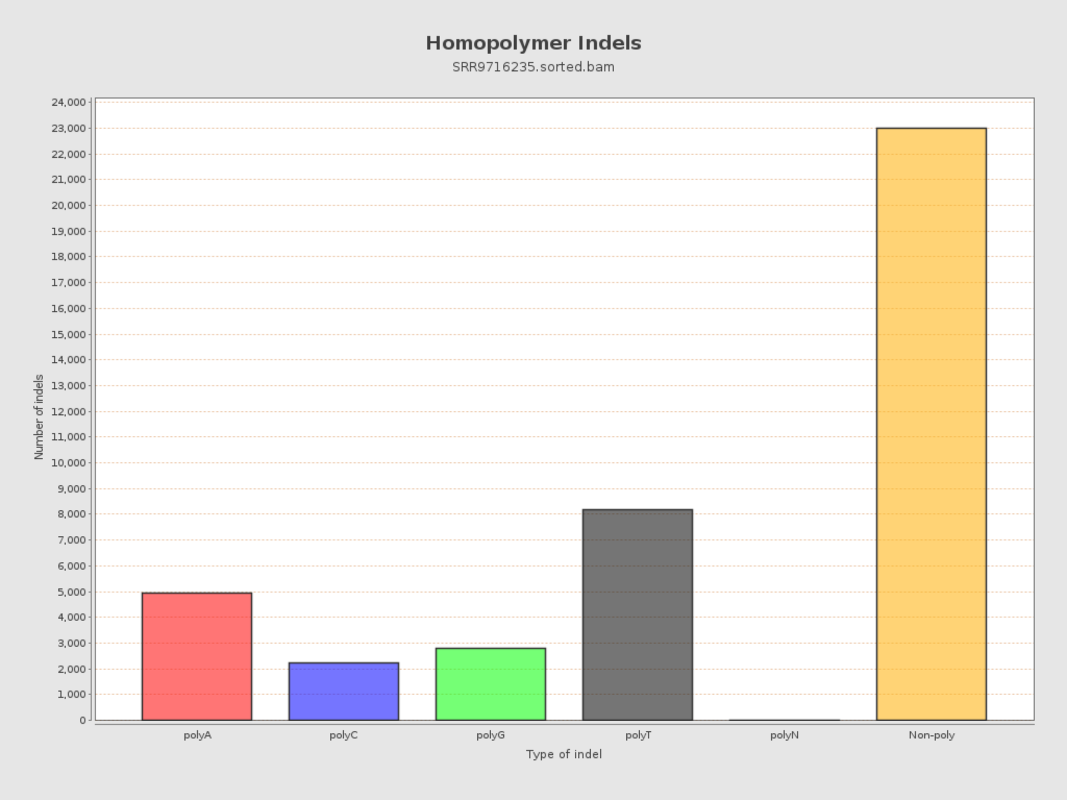
9. Results : Mapped Reads GC-content Distribution



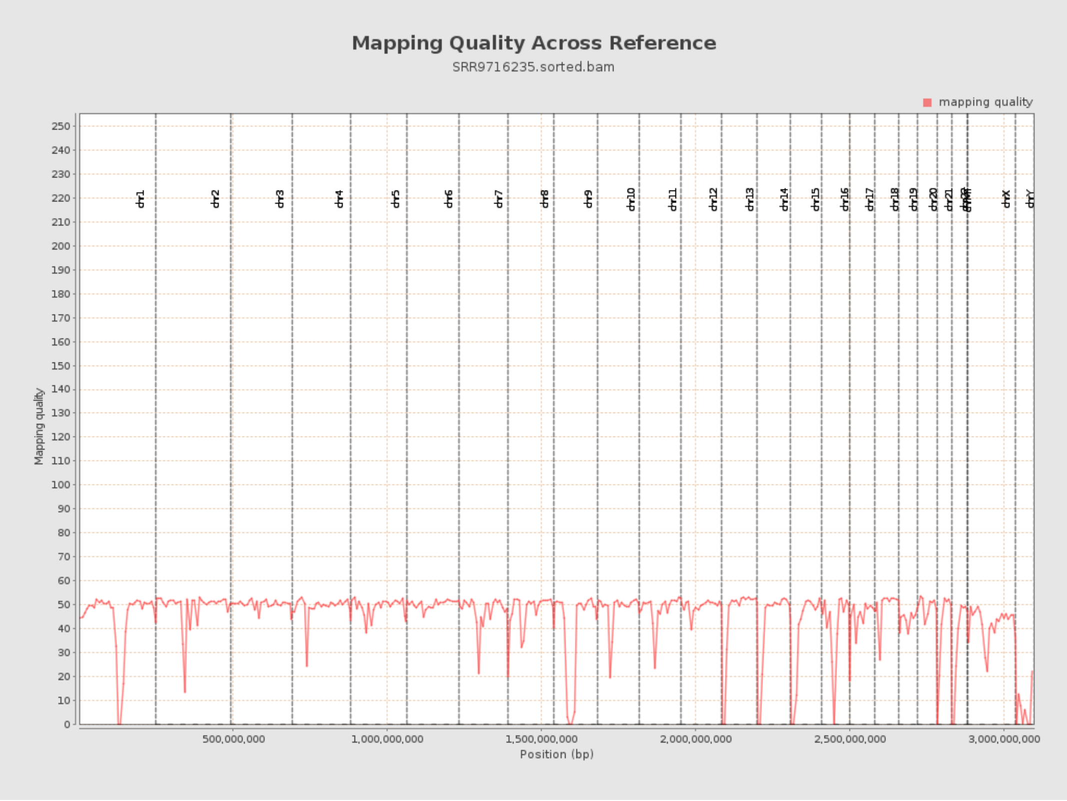
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram