Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 22:17:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716173.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_SRR9716173 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716173.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 22:17:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716173.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,250,550
Mapped reads	1,960,466 / 87.11%
Unmapped reads	290,084 / 12.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	59,126 / 2.63%
Read min/max/mean length	30 / 101 / 101.94
Duplicated reads (estimated)	47,919 / 2.13%
Duplication rate	1.66%
Clipped reads	2,016,750 / 89.61%

2.2. ACGT Content

Number/percentage of A's	37,214,750 / 25.33%
Number/percentage of C's	29,957,595 / 20.39%
Number/percentage of T's	44,046,140 / 29.98%
Number/percentage of G's	35,666,004 / 24.28%
Number/percentage of N's	16,911 / 0.01%
GC Percentage	44.67%

2.3. Coverage

Mean	0.0475

Standard Deviation	0.3457

2.4. Mapping Quality

Mean Mapping Quality	44.81

2.5. Mismatches and indels

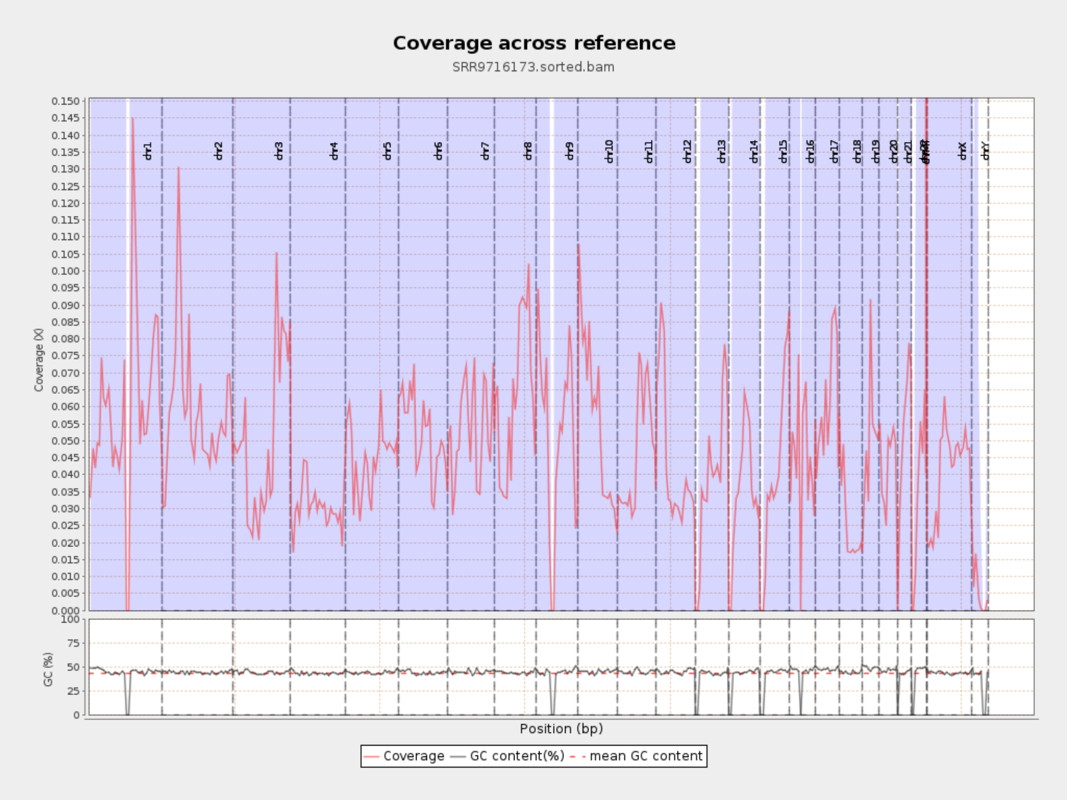
General error rate	0.74%
Mismatches	1,066,273
Insertions	12,026
Mapped reads with at least one insertion	0.61%
Deletions	29,703
Mapped reads with at least one deletion	1.49%
Homopolymer indels	41.76%

2.6. Chromosome stats

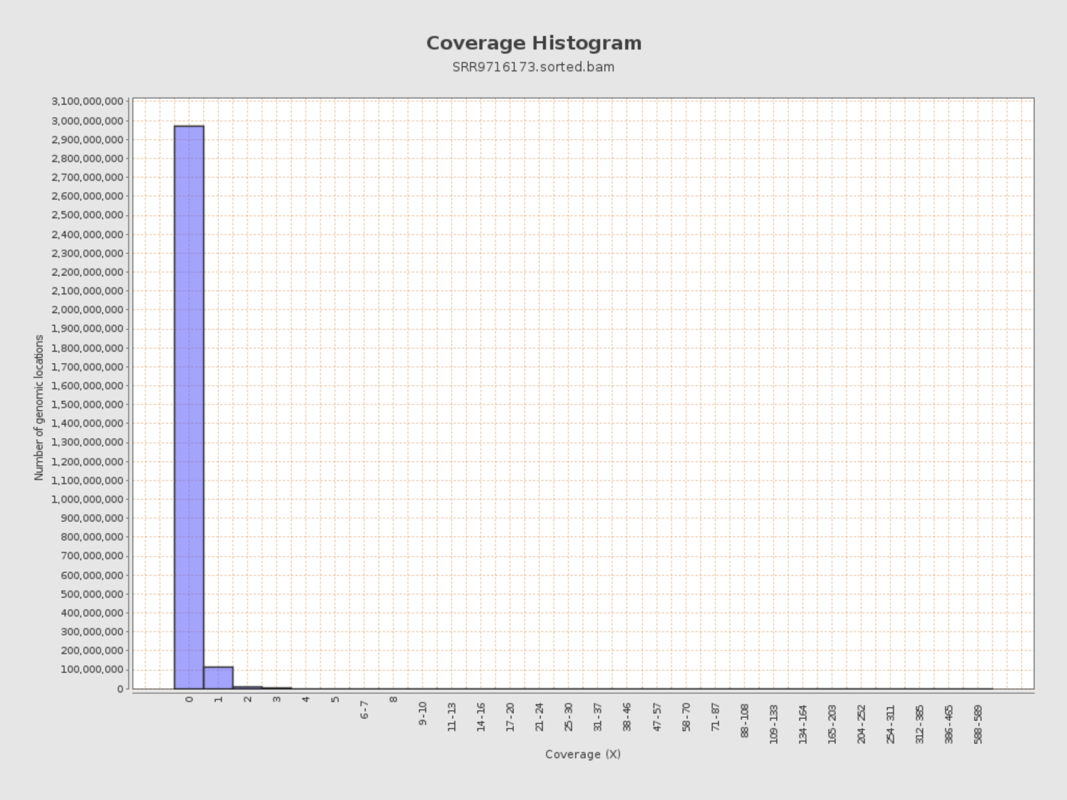
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14697910	0.059	0.5017
chr2	243199373	14297470	0.0588	0.483
chr3	198022430	9867998	0.0498	0.2516
chr4	191154276	5790096	0.0303	0.2084
chr5	180915260	8088385	0.0447	0.236
chr6	171115067	9031063	0.0528	0.3071
chr7	159138663	8534474	0.0536	0.4733

chr8	146364022	9251403	0.0632	0.4035
chr9	141213431	7394974	0.0524	0.3355
chr10	135534747	7876564	0.0581	0.4065
chr11	135006516	6353170	0.0471	0.3057
chr12	133851895	5764512	0.0431	0.2326
chr13	115169878	4596780	0.0399	0.2234
chr14	107349540	3762756	0.0351	0.2297
chr15	102531392	4108856	0.0401	0.2249
chr16	90354753	3931127	0.0435	0.2567
chr17	81195210	4984438	0.0614	0.3236
chr18	78077248	2021645	0.0259	0.5291
chr19	59128983	2968504	0.0502	0.4252
chr20	63025520	2676287	0.0425	0.2429
chr21	48129895	2477977	0.0515	0.2656
chr22	51304566	1711450	0.0334	0.2068
chrMT	16571	23466	1.4161	1.8675
chrX	155270560	6410573	0.0413	0.2663
chrY	59373566	331325	0.0056	0.1565

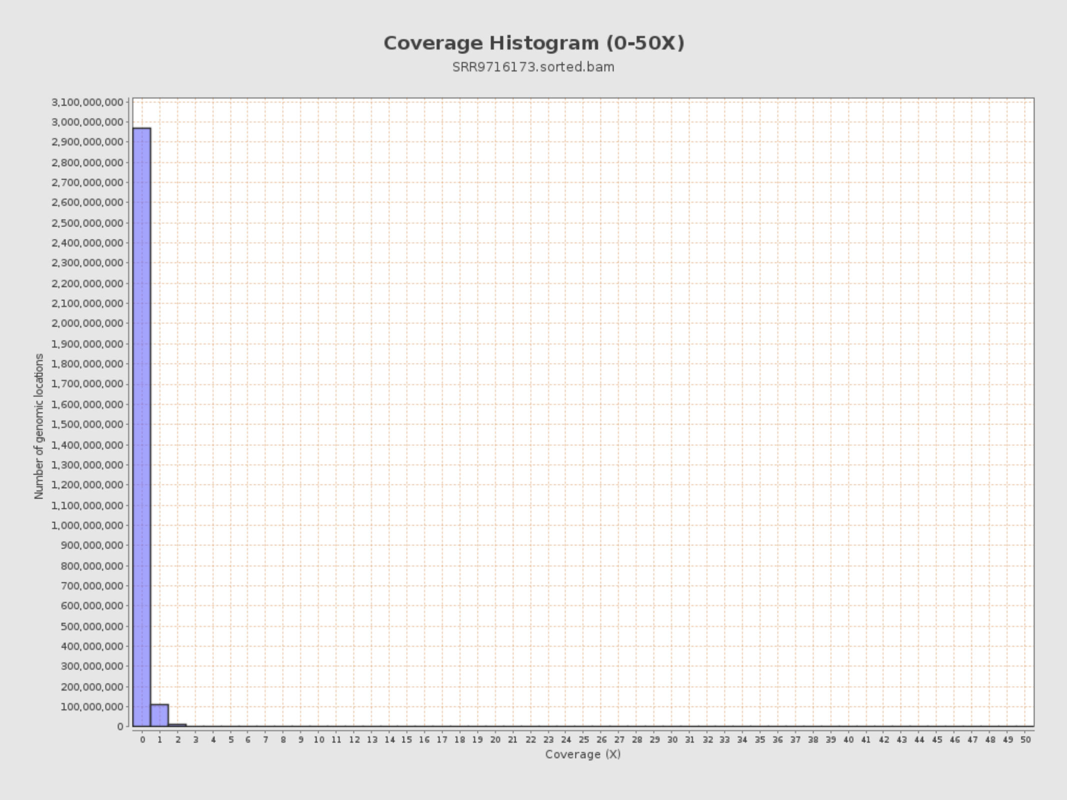
3. Results : Coverage across reference



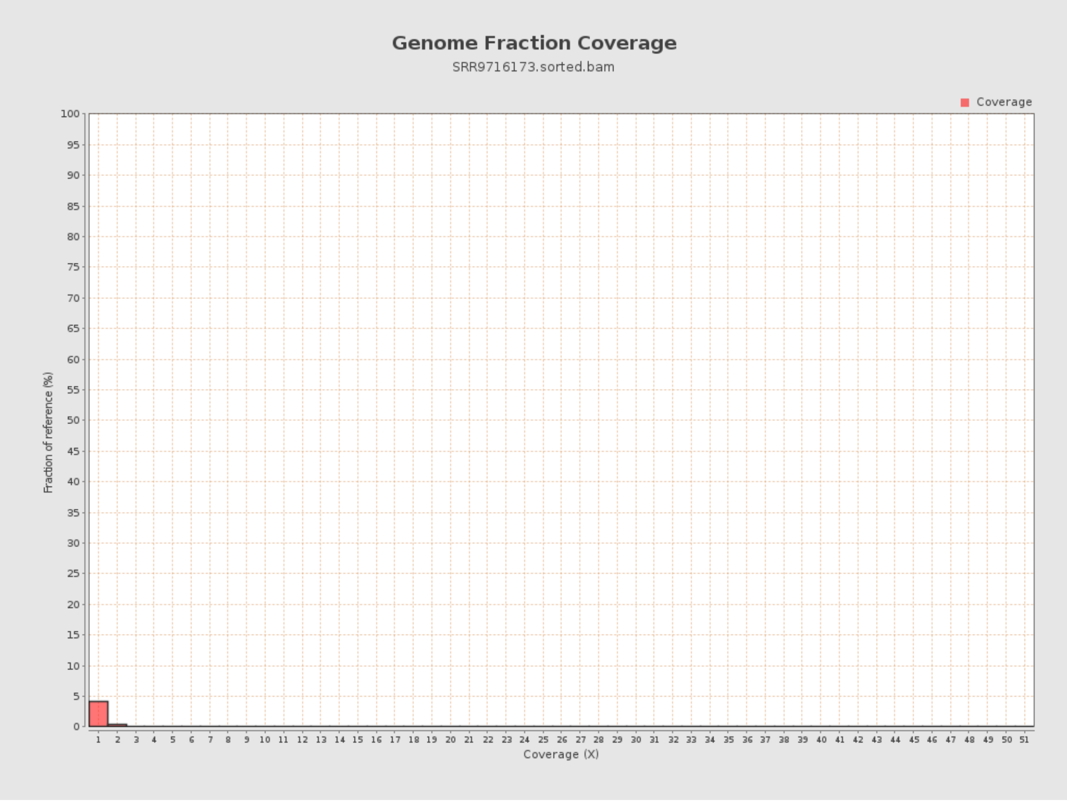
4. Results : Coverage Histogram



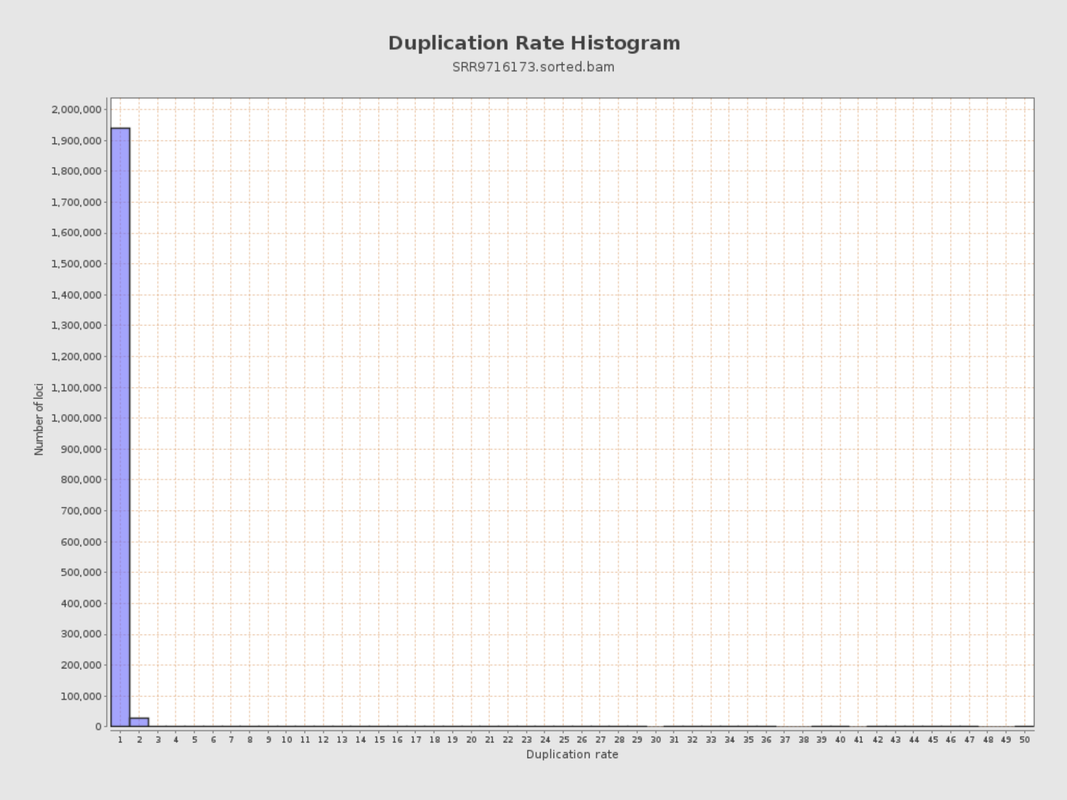
5. Results : Coverage Histogram (0-50X)



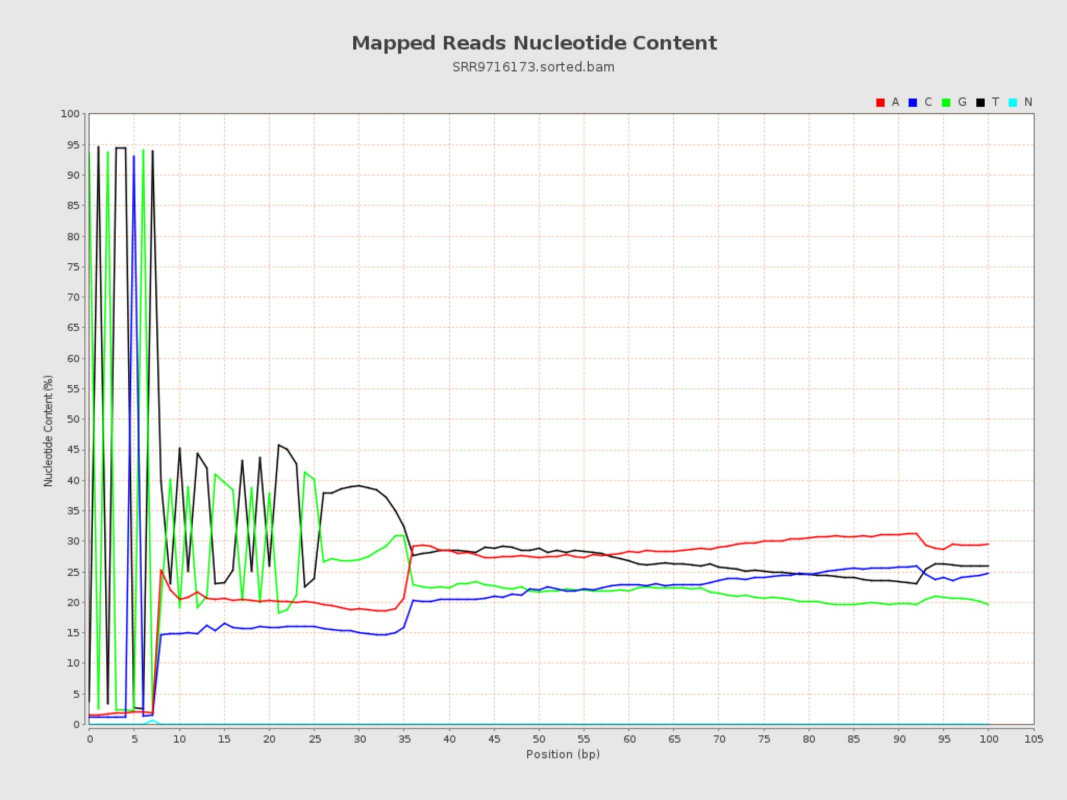
6. Results : Genome Fraction Coverage



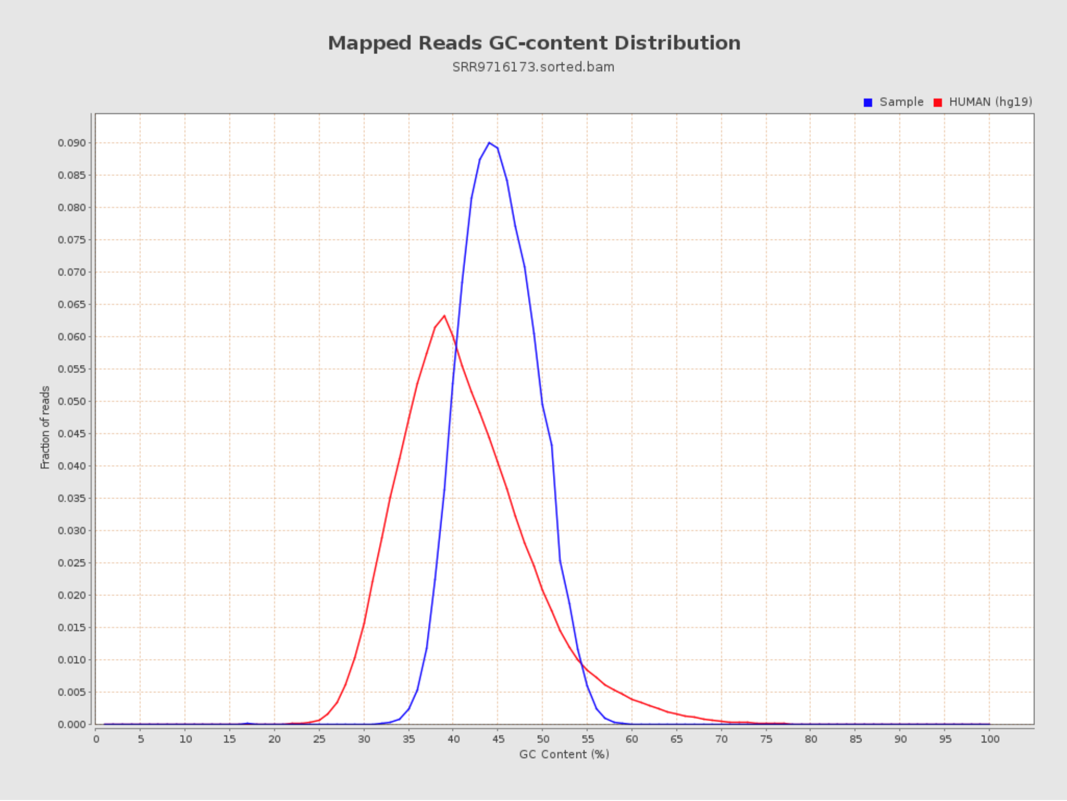
7. Results : Duplication Rate Histogram



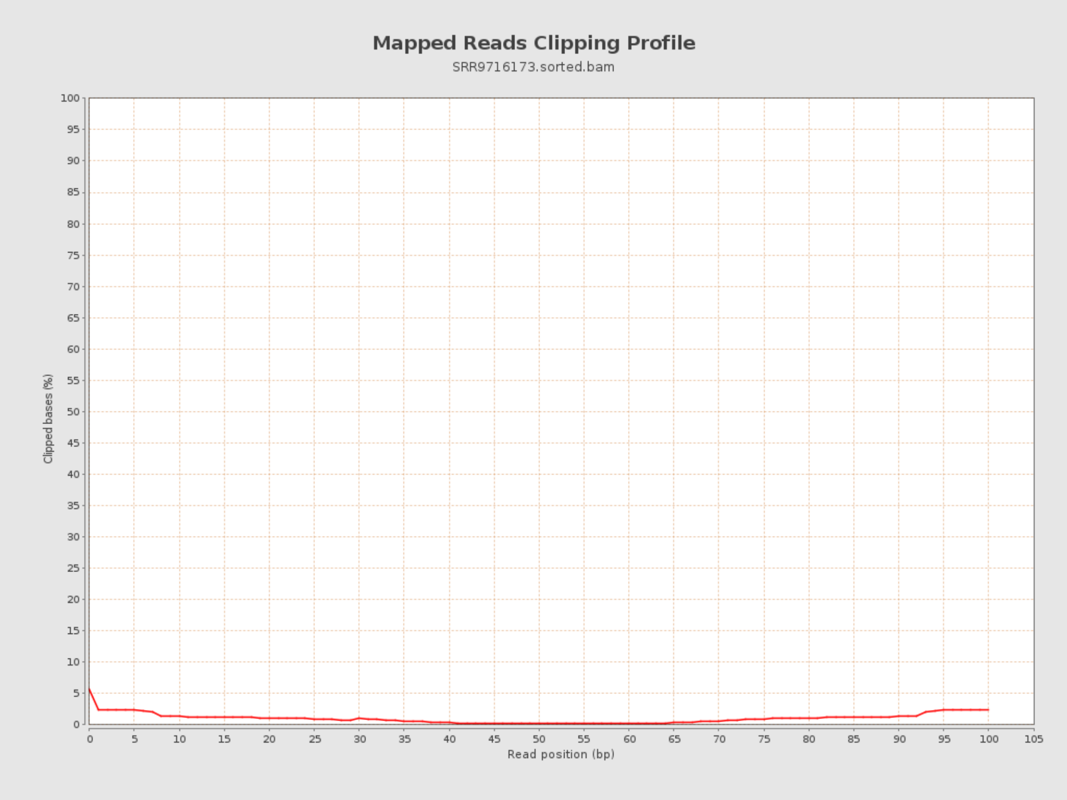
8. Results : Mapped Reads Nucleotide Content



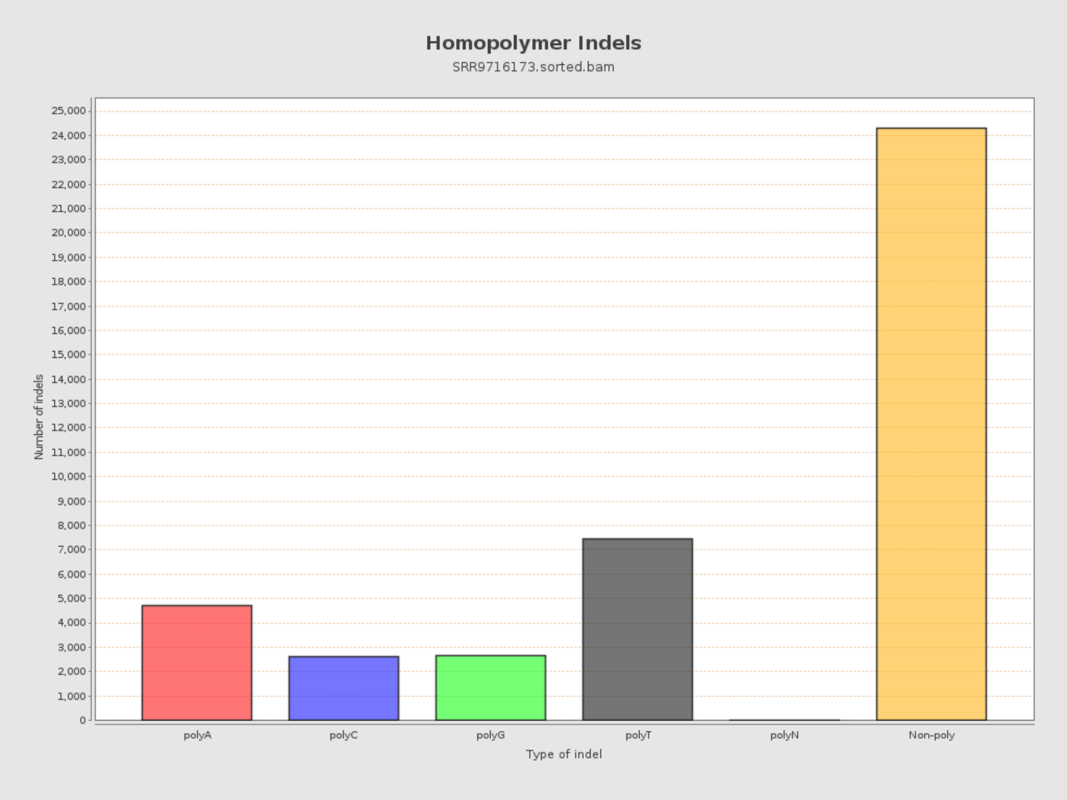
9. Results : Mapped Reads GC-content Distribution



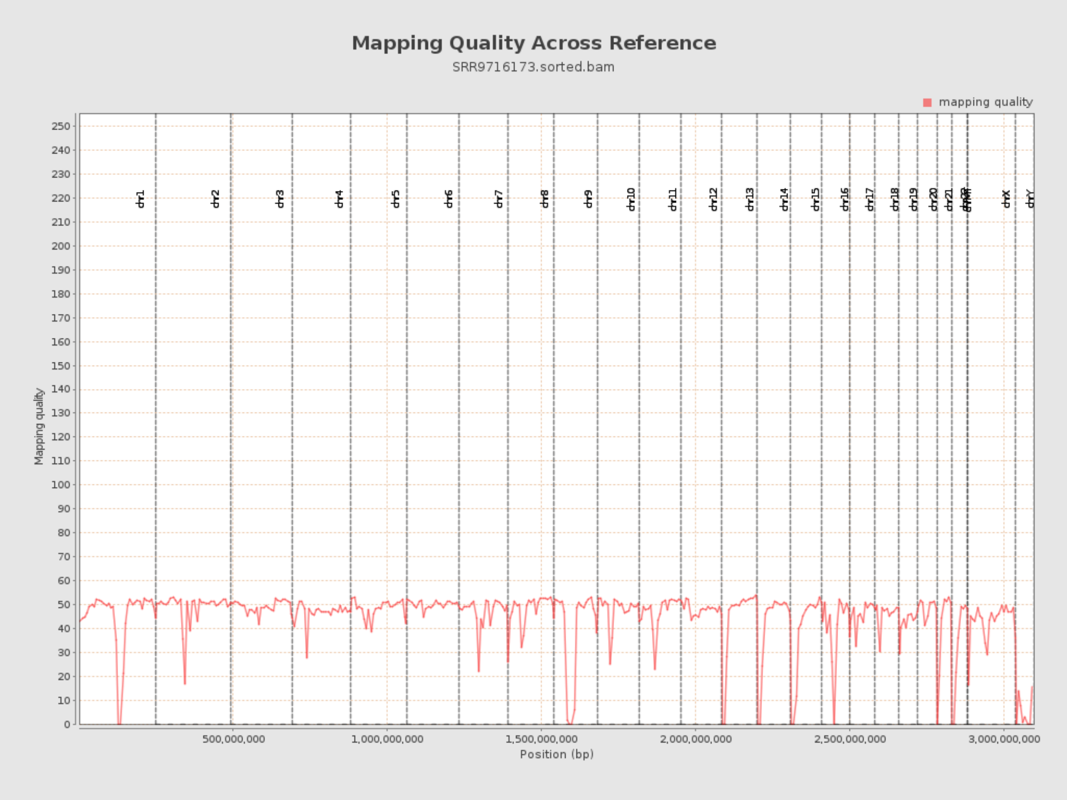
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram