Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 15:48:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716473.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_SRR9716473 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716473.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 15:48:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716473.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,227,931
Mapped reads	2,987,650 / 92.56%
Unmapped reads	240,281 / 7.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,290 / 0.57%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	161,576 / 5.01%
Duplication rate	4.14%
Clipped reads	2,999,309 / 92.92%

2.2. ACGT Content

Number/percentage of A's	43,573,439 / 25.01%
Number/percentage of C's	36,305,605 / 20.84%
Number/percentage of T's	52,063,890 / 29.88%
Number/percentage of G's	42,281,065 / 24.27%
Number/percentage of N's	1,277 / 0%
GC Percentage	45.11%

2.3. Coverage

Mean	0.0563

Standard Deviation	0.44

2.4. Mapping Quality

Mean Mapping Quality	44.66

2.5. Mismatches and indels

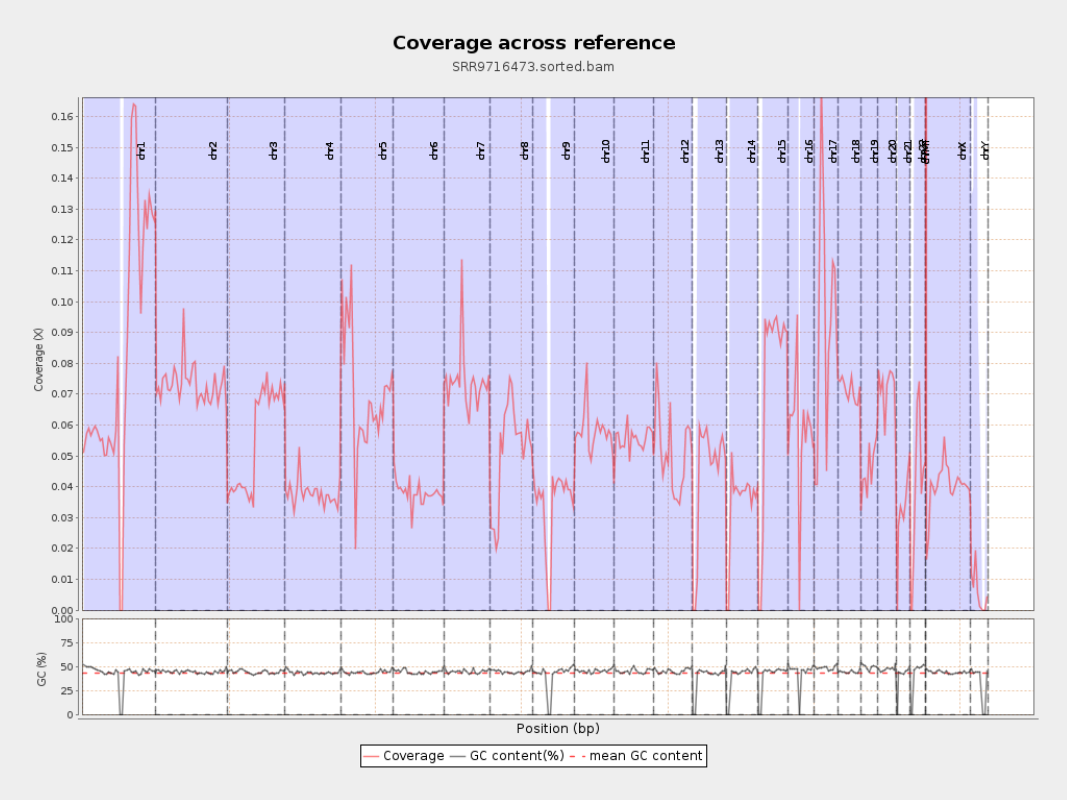
General error rate	0.51%
Mismatches	868,992
Insertions	11,802
Mapped reads with at least one insertion	0.39%
Deletions	30,470
Mapped reads with at least one deletion	1.01%
Homopolymer indels	42.5%

2.6. Chromosome stats

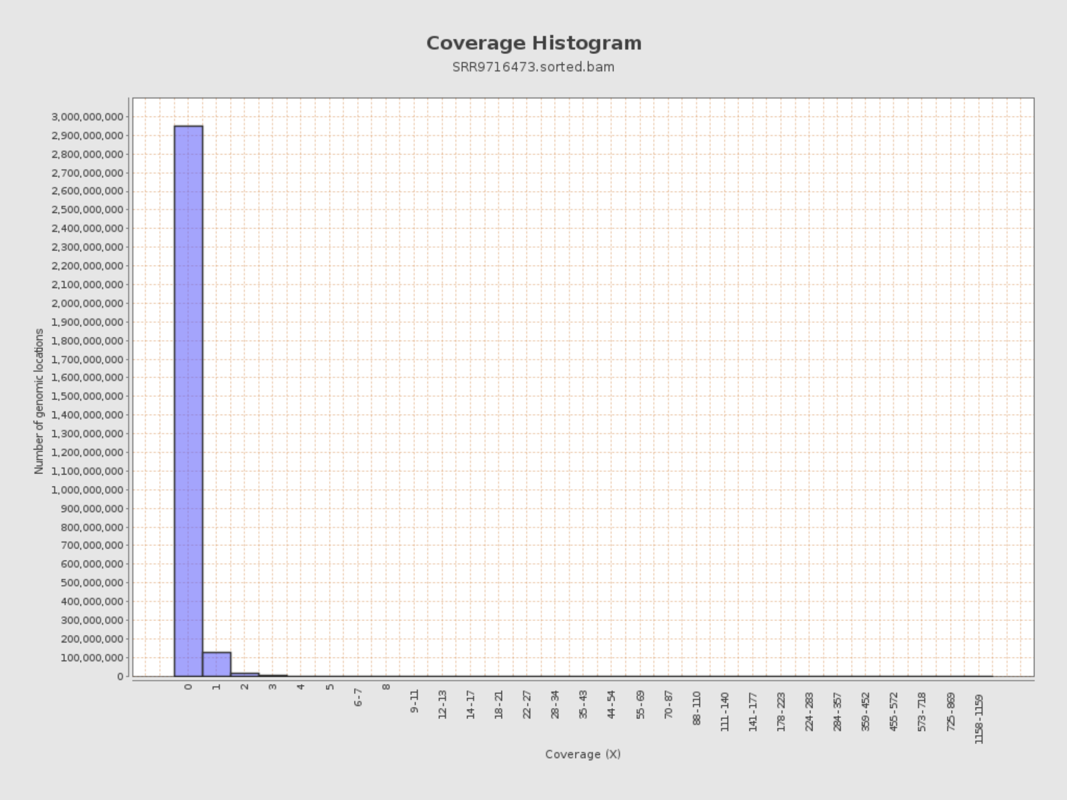
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20627251	0.0828	0.7174
chr2	243199373	17800556	0.0732	0.6184
chr3	198022430	10852716	0.0548	0.2728
chr4	191154276	7254261	0.0379	0.2591
chr5	180915260	12618931	0.0698	0.3083
chr6	171115067	6494949	0.038	0.2586
chr7	159138663	11832922	0.0744	0.7874

chr8	146364022	7647717	0.0523	0.369
chr9	141213431	4802614	0.034	0.3289
chr10	135534747	7860412	0.058	0.3721
chr11	135006516	7470194	0.0553	0.4198
chr12	133851895	6860003	0.0513	0.2681
chr13	115169878	5124065	0.0445	0.2463
chr14	107349540	3713111	0.0346	0.2359
chr15	102531392	7539274	0.0735	0.3241
chr16	90354753	5172157	0.0572	0.3006
chr17	81195210	7508975	0.0925	0.4081
chr18	78077248	5572867	0.0714	0.7584
chr19	59128983	2725839	0.0461	0.5714
chr20	63025520	4535147	0.072	0.3175
chr21	48129895	1570107	0.0326	0.2279
chr22	51304566	2019006	0.0394	0.2294
chrMT	16571	57626	3.4775	2.6584
chrX	155270560	6256828	0.0403	0.2802
chrY	59373566	355201	0.006	0.1365

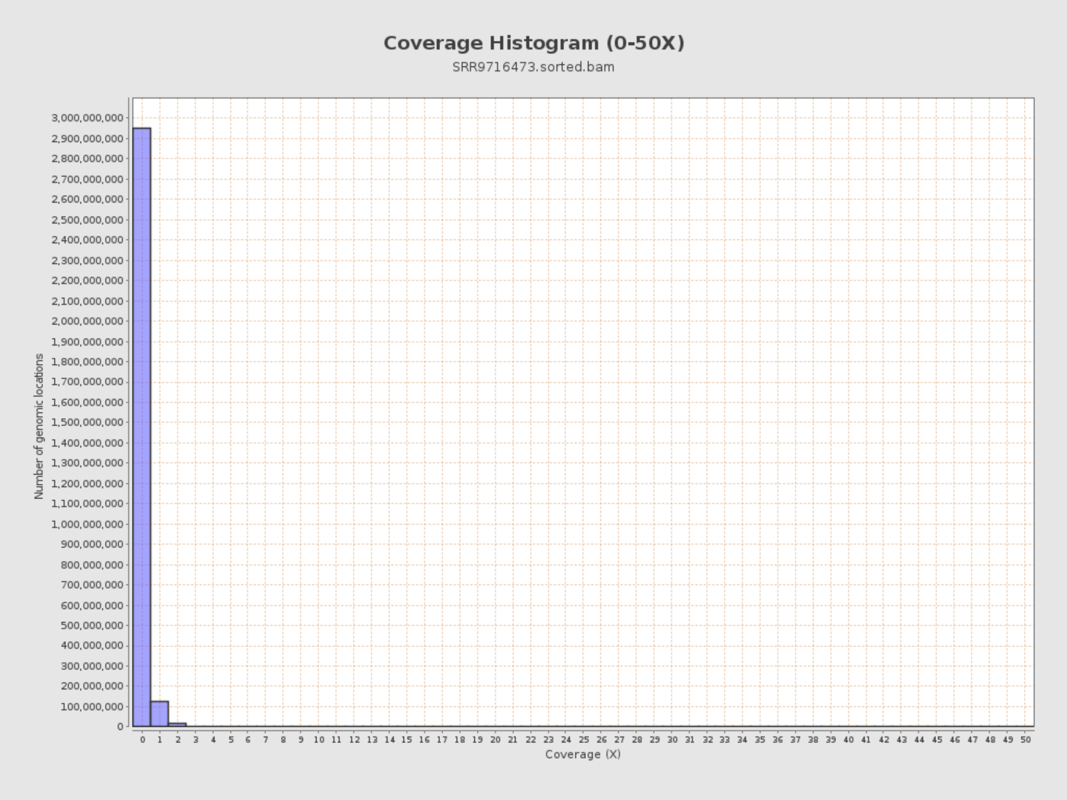
3. Results : Coverage across reference



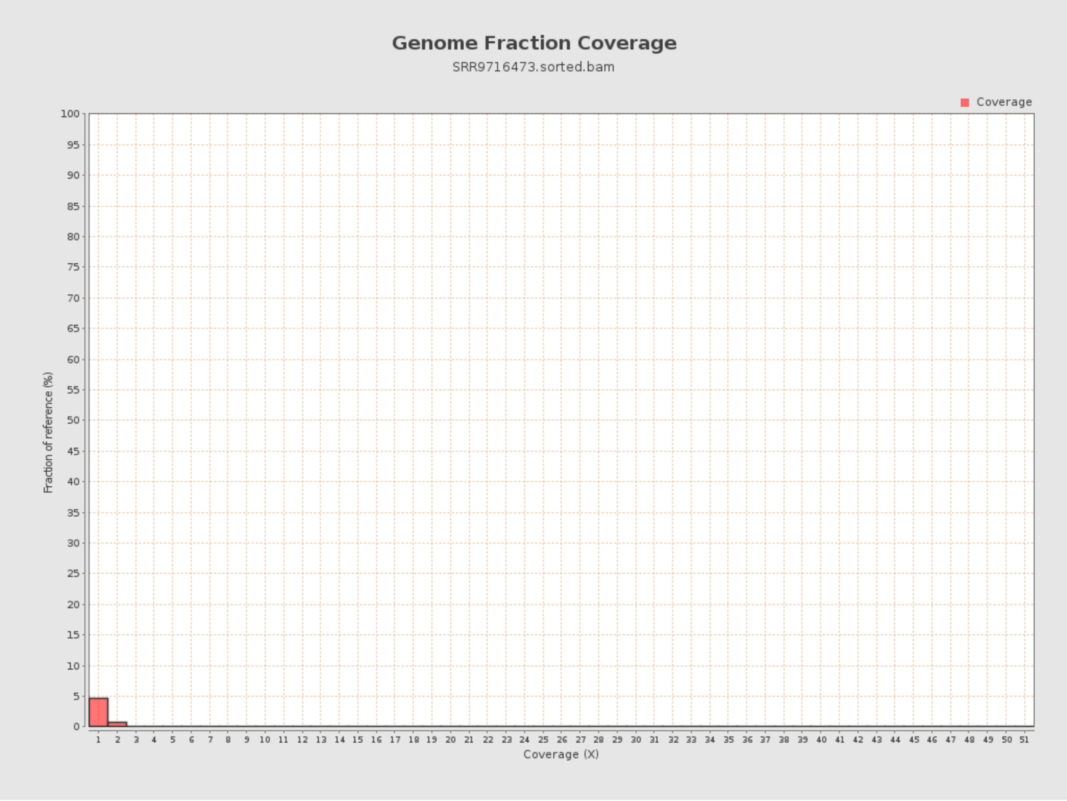
4. Results : Coverage Histogram



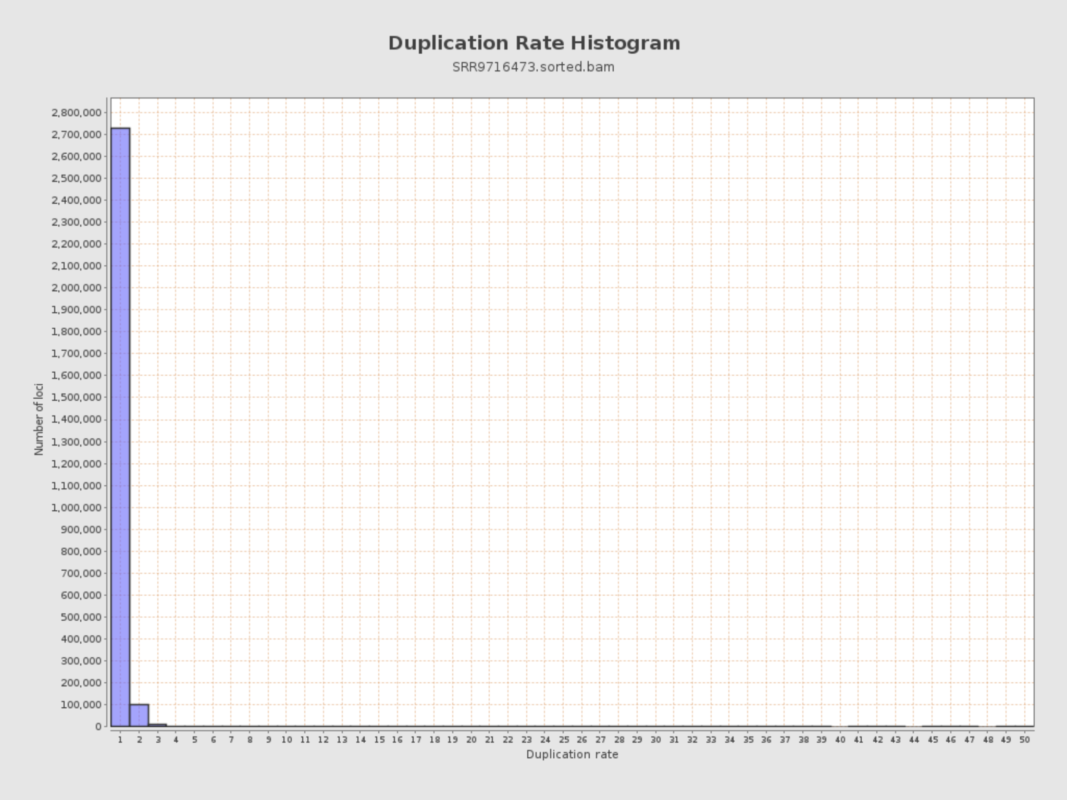
5. Results : Coverage Histogram (0-50X)



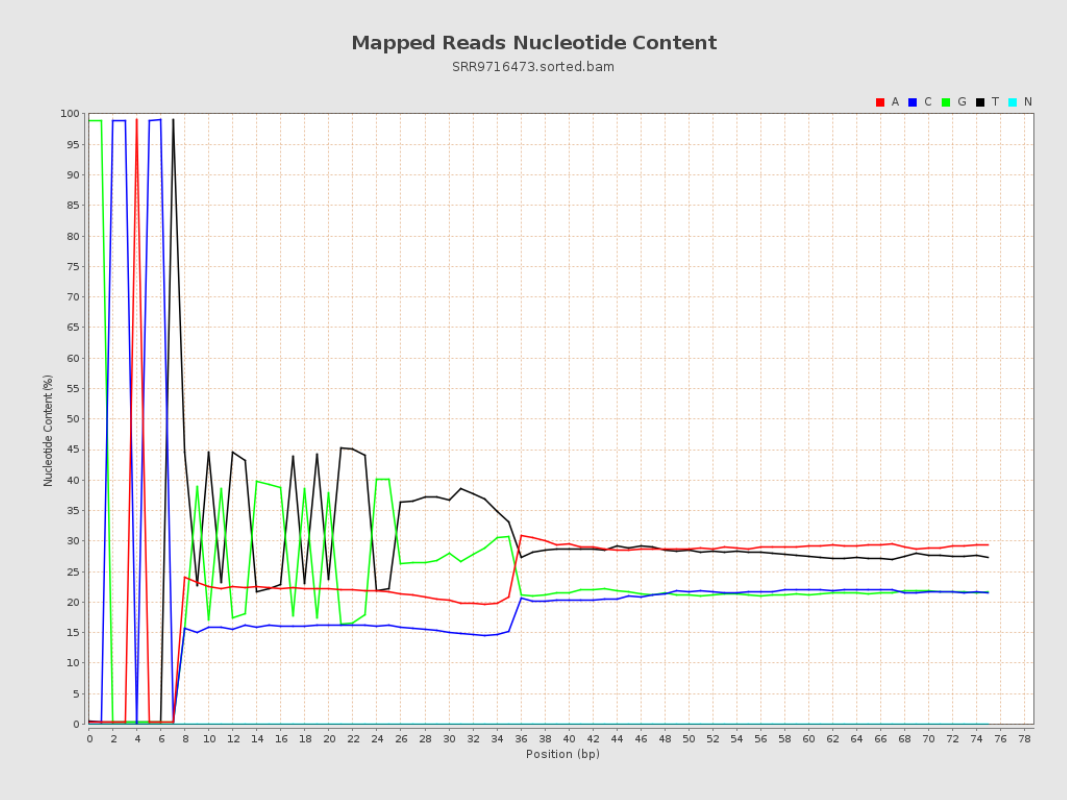
6. Results : Genome Fraction Coverage



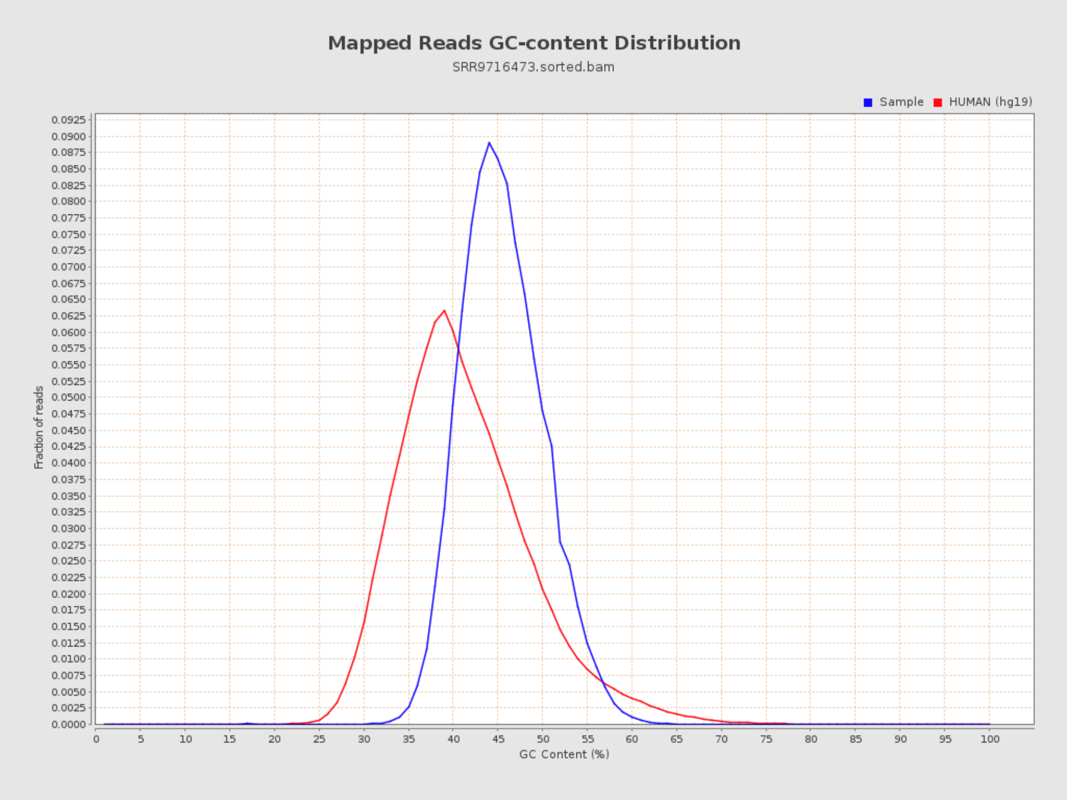
7. Results : Duplication Rate Histogram



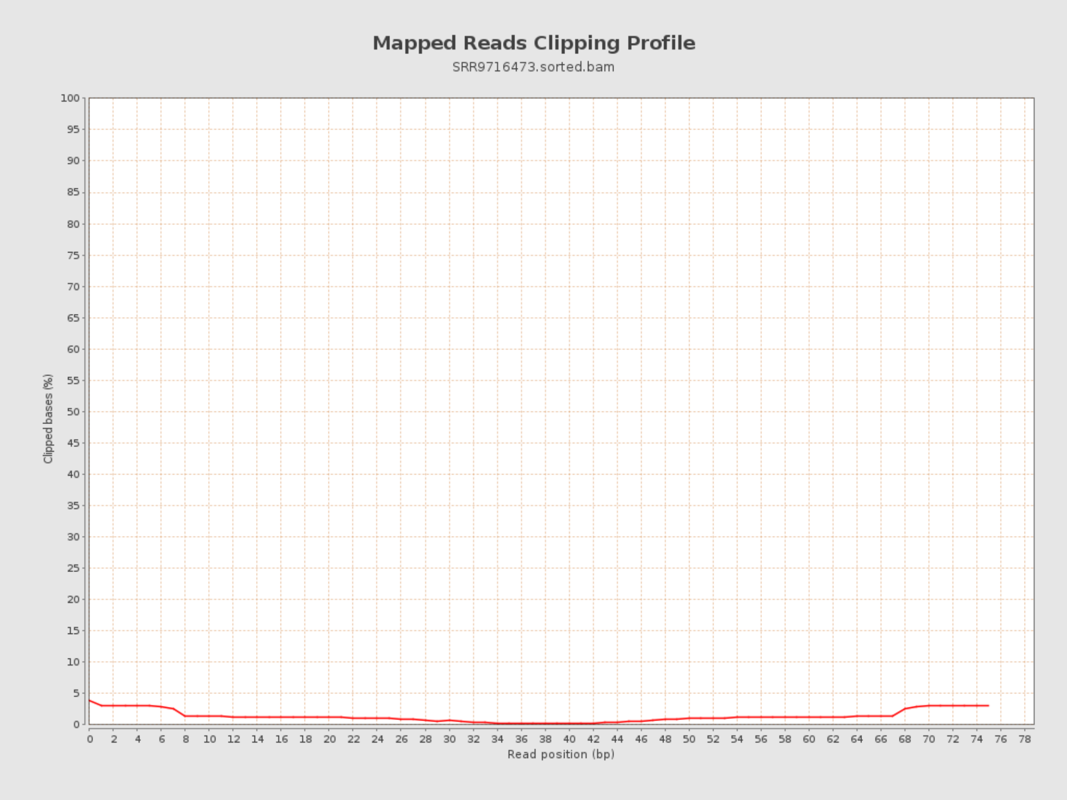
8. Results : Mapped Reads Nucleotide Content



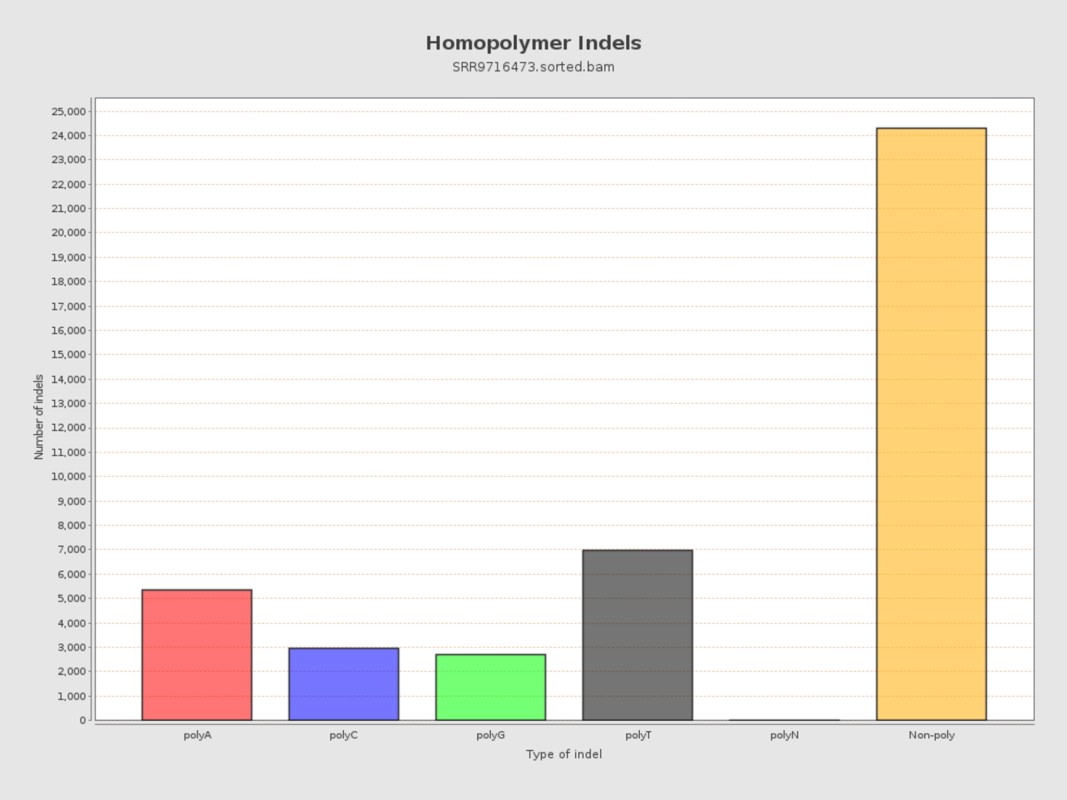
9. Results : Mapped Reads GC-content Distribution



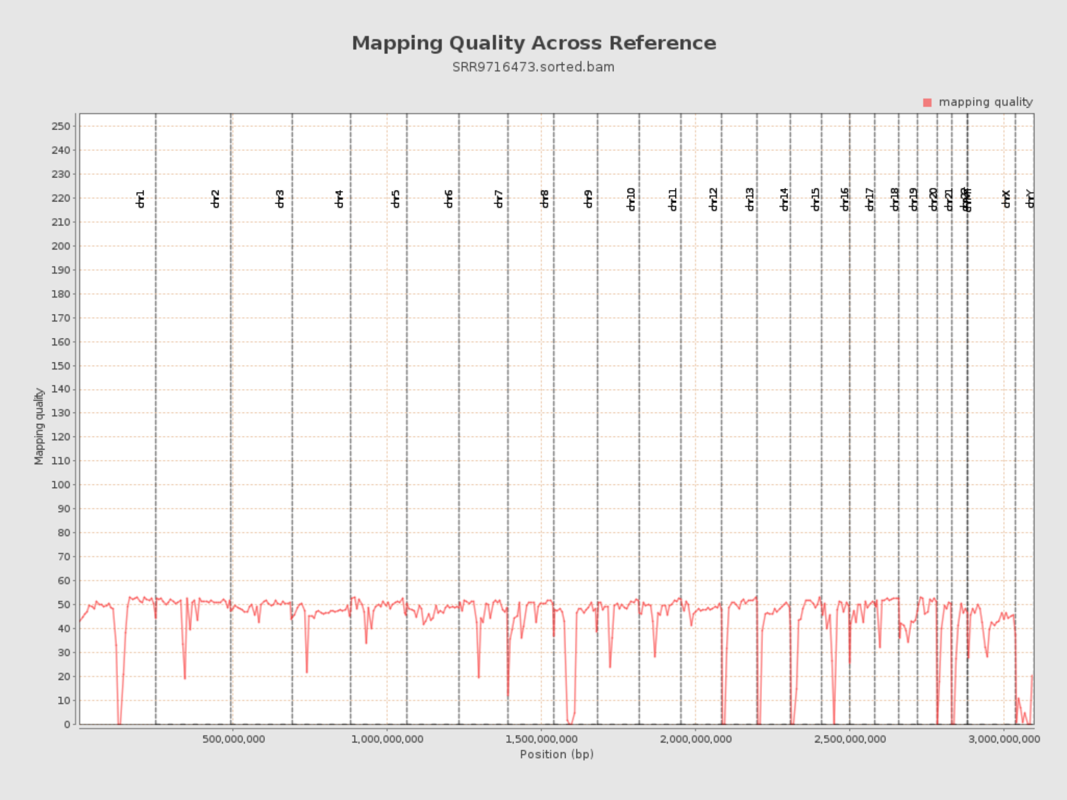
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram