Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 19:17:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716935.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_SRR9716935 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716935.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 19:17:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716935.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	577,521
Mapped reads	390,937 / 67.69%
Unmapped reads	186,584 / 32.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	364 / 0.06%
Read min/max/mean length	30 / 76 / 76.02
Duplicated reads (estimated)	18,279 / 3.17%
Duplication rate	4.18%
Clipped reads	390,786 / 67.67%

2.2. ACGT Content

Number/percentage of A's	4,219,658 / 20.97%
Number/percentage of C's	3,424,934 / 17.02%
Number/percentage of T's	6,901,542 / 34.3%
Number/percentage of G's	5,572,805 / 27.7%
Number/percentage of N's	366 / 0%
GC Percentage	44.72%

2.3. Coverage

Mean	0.0065

Standard Deviation	0.0944

2.4. Mapping Quality

Mean Mapping Quality	41.87

2.5. Mismatches and indels

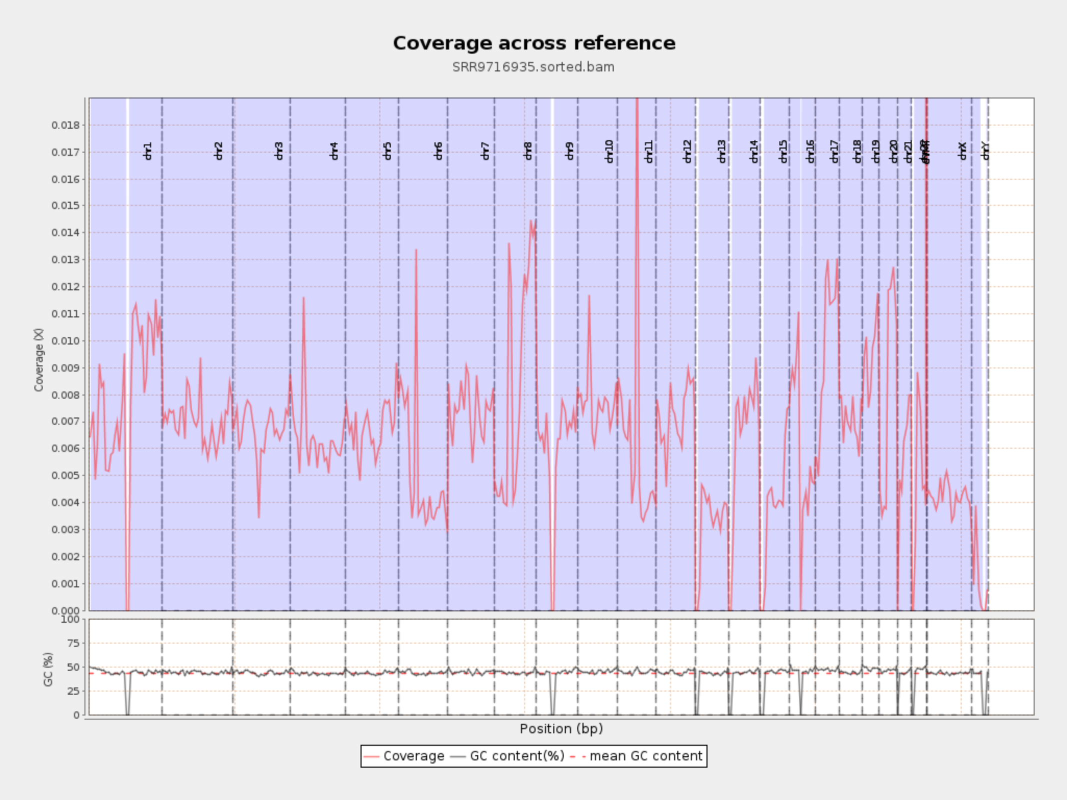
General error rate	0.75%
Mismatches	149,078
Insertions	1,219
Mapped reads with at least one insertion	0.31%
Deletions	3,220
Mapped reads with at least one deletion	0.82%
Homopolymer indels	39.36%

2.6. Chromosome stats

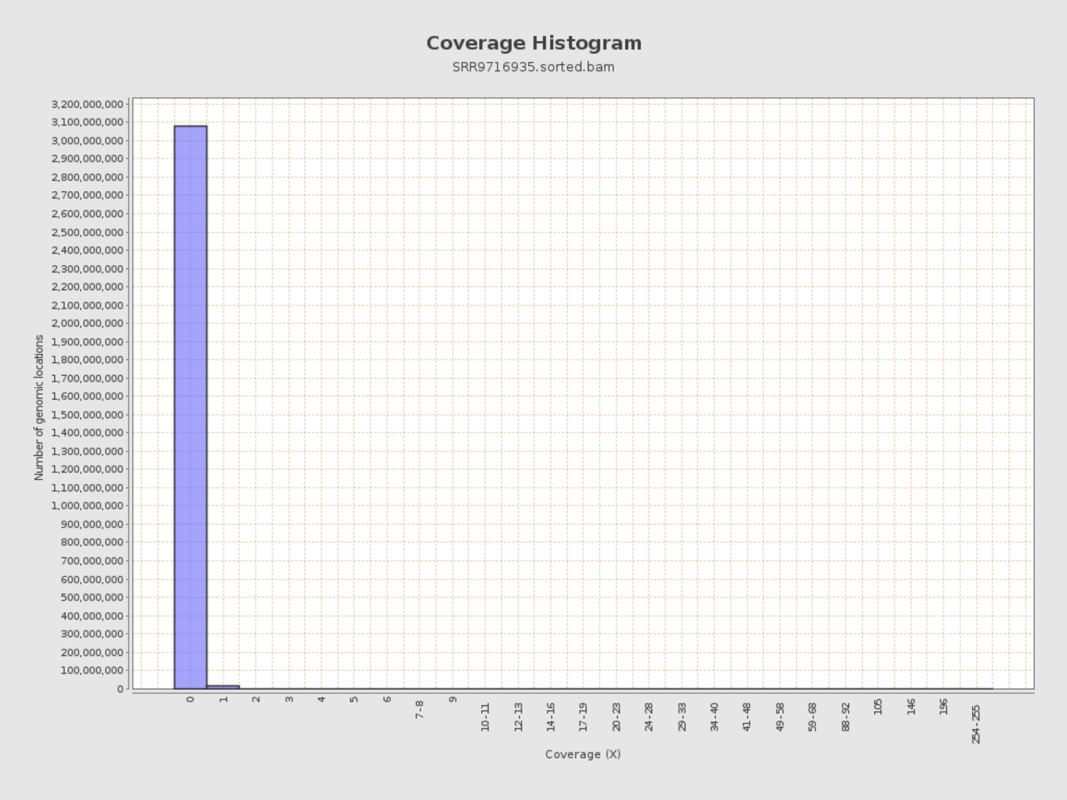
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1956631	0.0079	0.1034
chr2	243199373	1717985	0.0071	0.1343
chr3	198022430	1326422	0.0067	0.0881
chr4	191154276	1220174	0.0064	0.0879
chr5	180915260	1232744	0.0068	0.0883
chr6	171115067	886092	0.0052	0.0919
chr7	159138663	1179824	0.0074	0.0998

chr8	146364022	1257425	0.0086	0.1008
chr9	141213431	829415	0.0059	0.0859
chr10	135534747	1038710	0.0077	0.1007
chr11	135006516	855496	0.0063	0.0886
chr12	133851895	970404	0.0072	0.0914
chr13	115169878	367335	0.0032	0.0612
chr14	107349540	681034	0.0063	0.0865
chr15	102531392	392243	0.0038	0.0666
chr16	90354753	539260	0.006	0.0877
chr17	81195210	819936	0.0101	0.1102
chr18	78077248	547098	0.007	0.0951
chr19	59128983	558154	0.0094	0.1143
chr20	63025520	515890	0.0082	0.0996
chr21	48129895	274528	0.0057	0.0837
chr22	51304566	223558	0.0044	0.0716
chrMT	16571	15532	0.9373	1.2038
chrX	155270560	656280	0.0042	0.0708
chrY	59373566	62496	0.0011	0.0408

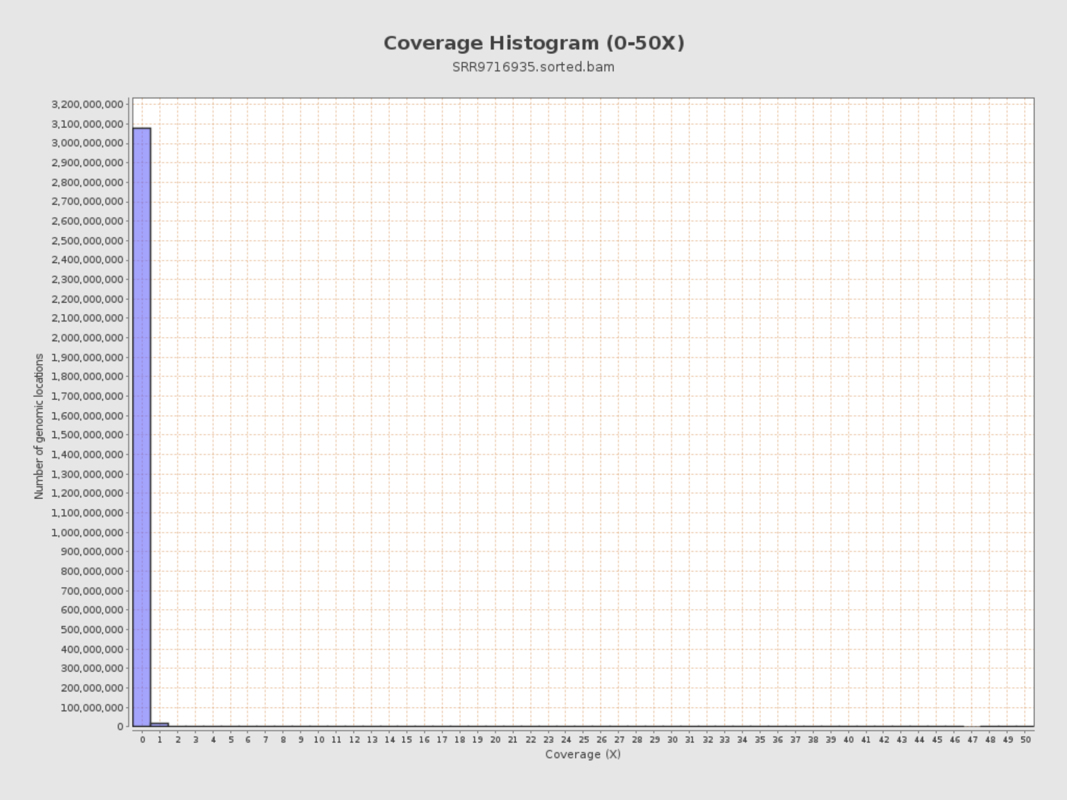
3. Results : Coverage across reference



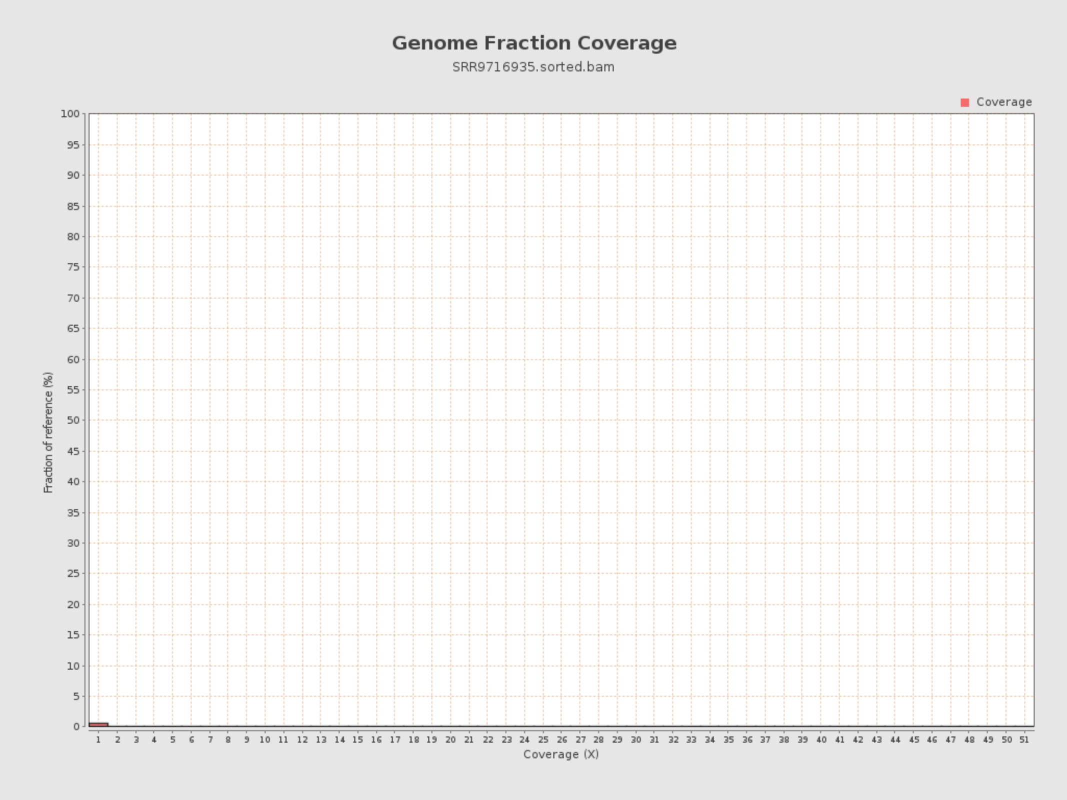
4. Results : Coverage Histogram



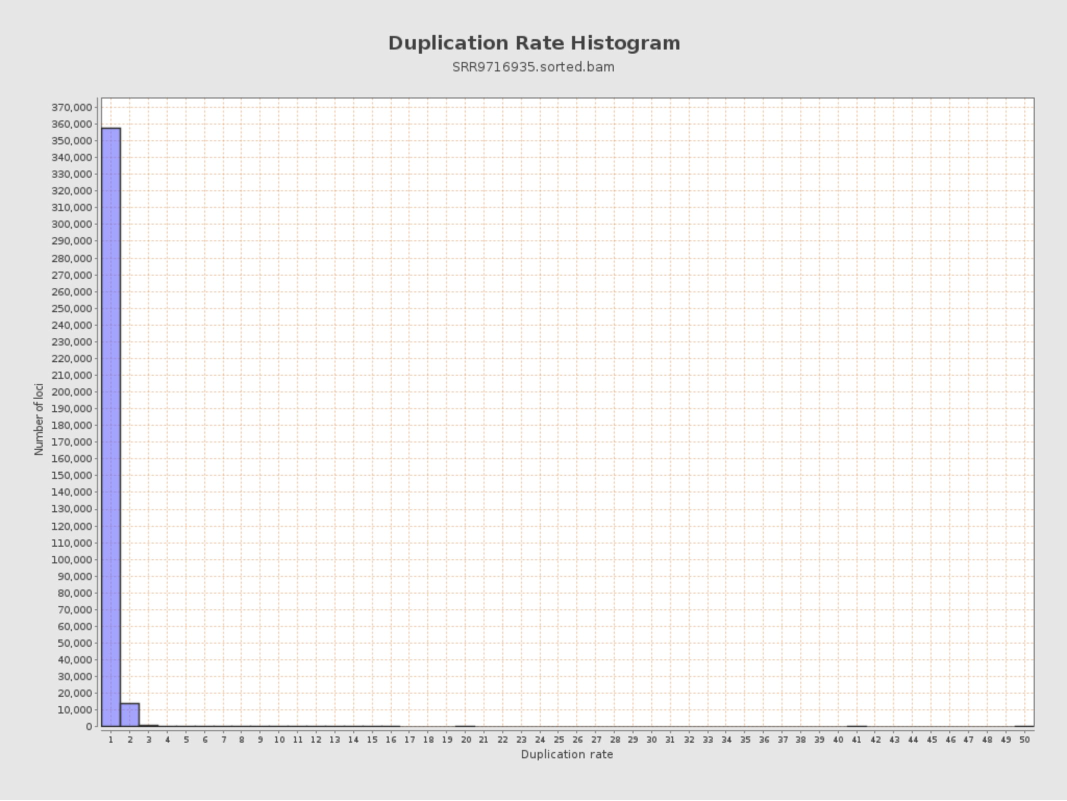
5. Results : Coverage Histogram (0-50X)



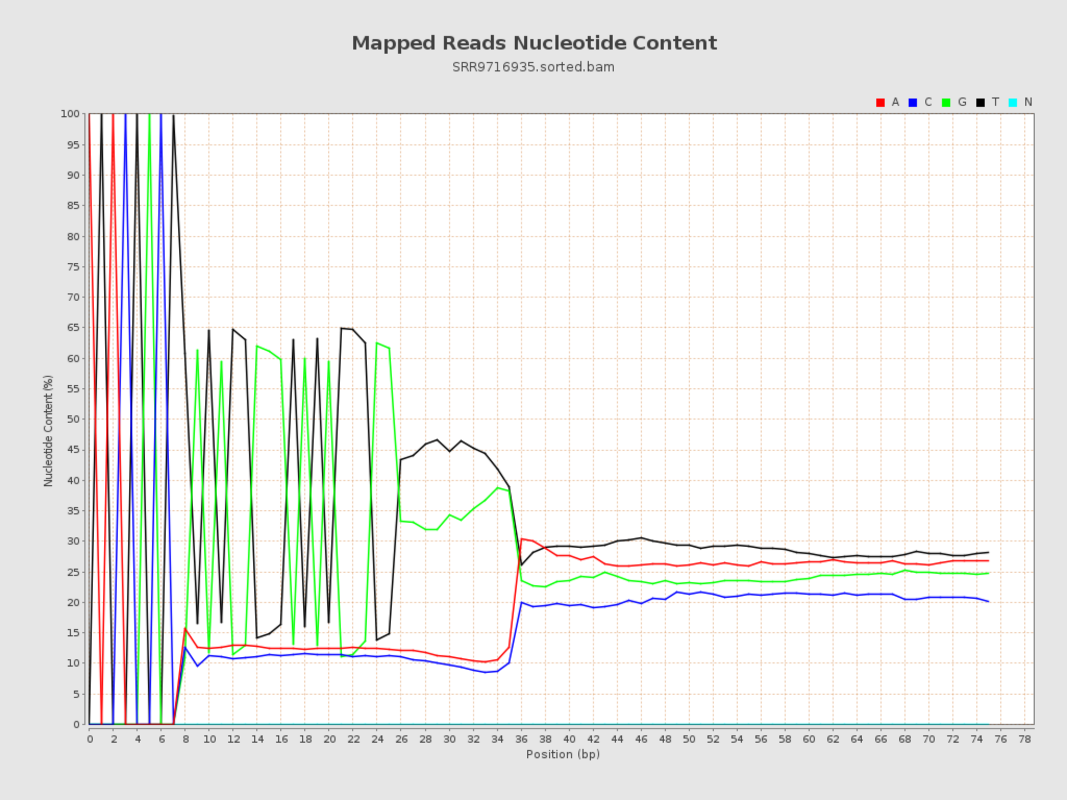
6. Results : Genome Fraction Coverage



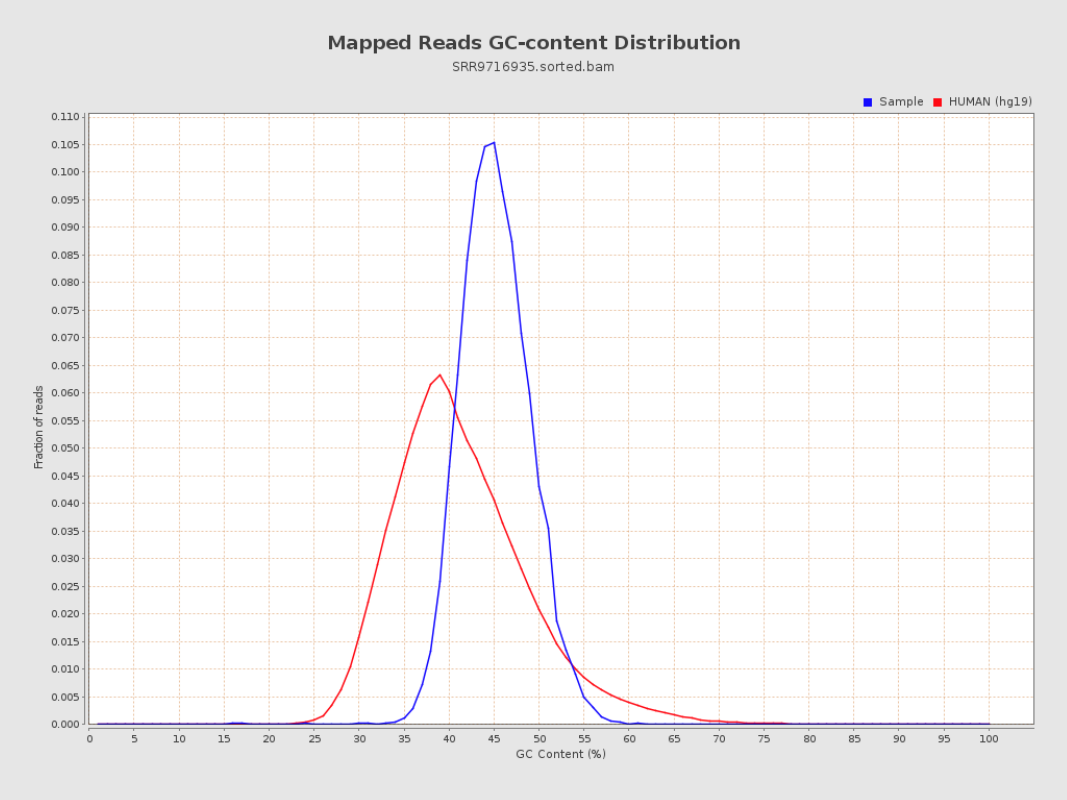
7. Results : Duplication Rate Histogram



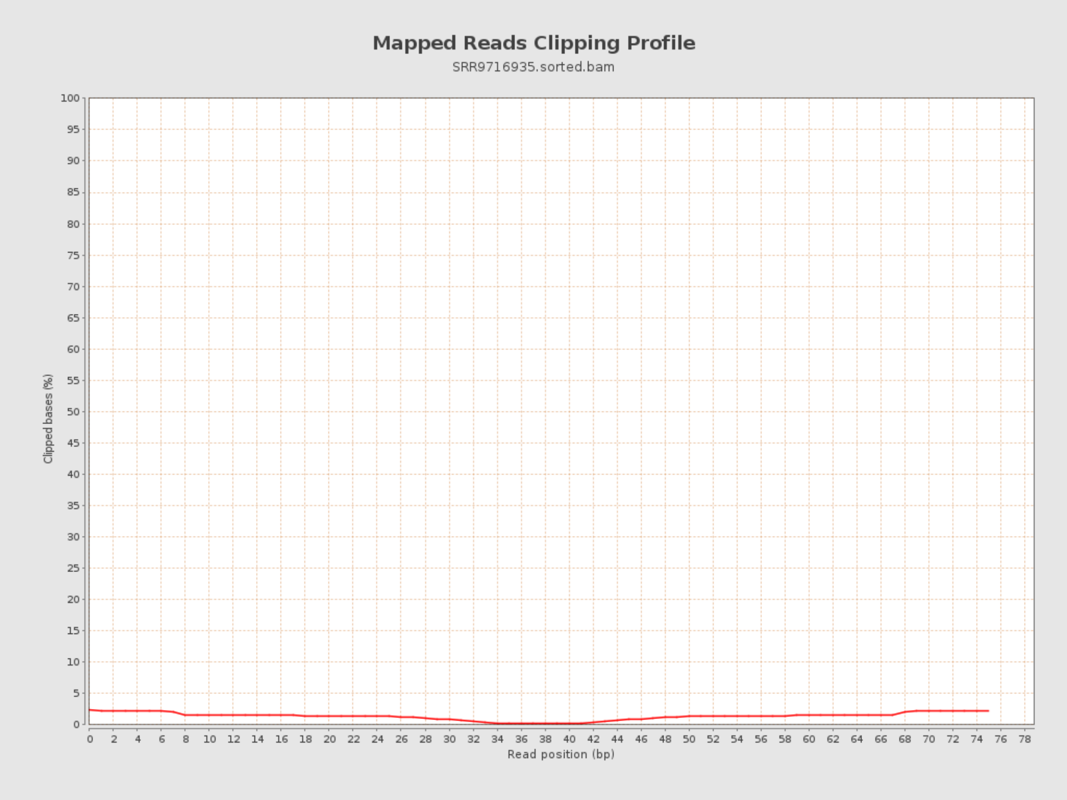
8. Results : Mapped Reads Nucleotide Content



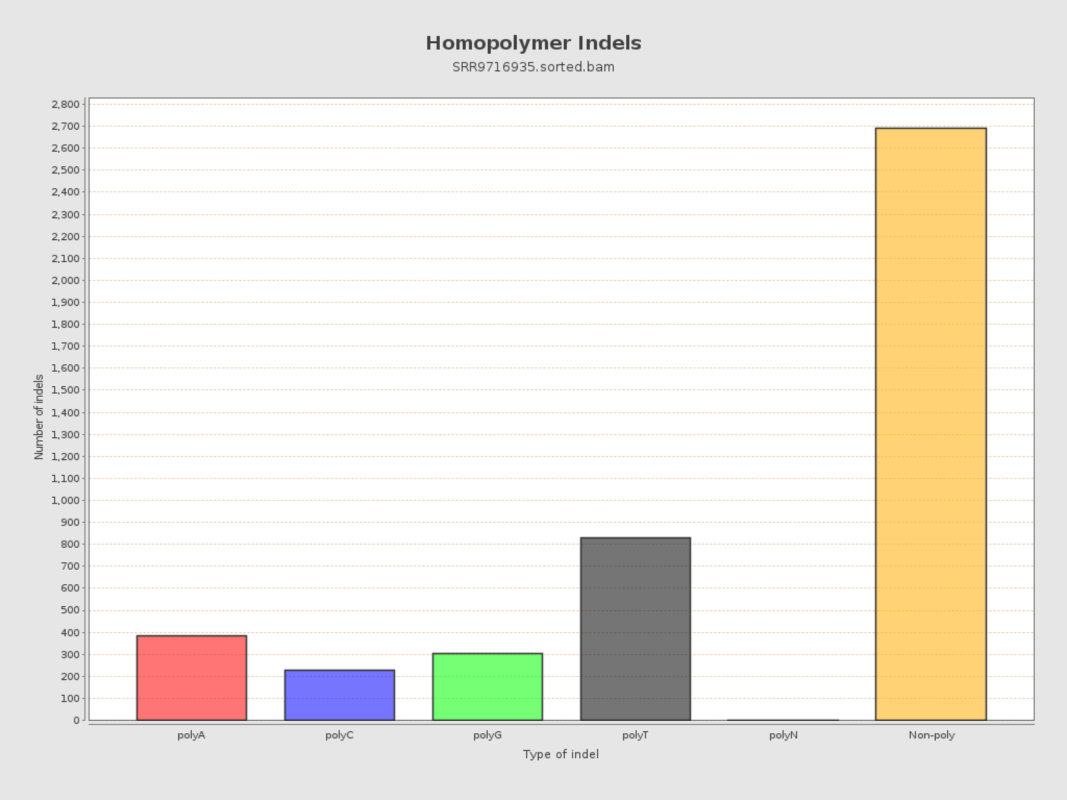
9. Results : Mapped Reads GC-content Distribution



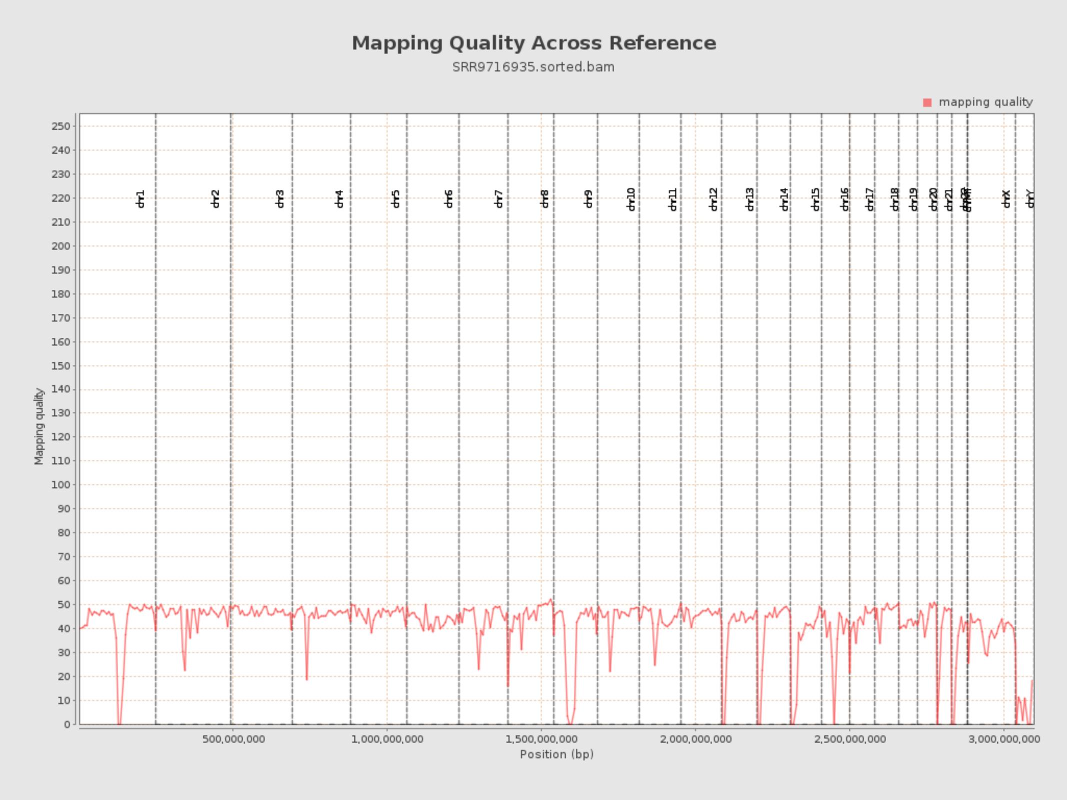
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram