Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 17:45:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716510.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_SRR9716510 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716510.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 17:45:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716510.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,710,854
Mapped reads	1,522,209 / 88.97%
Unmapped reads	188,645 / 11.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,955 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	63,167 / 3.69%
Duplication rate	3.17%
Clipped reads	1,525,202 / 89.15%

2.2. ACGT Content

Number/percentage of A's	22,428,499 / 25.52%
Number/percentage of C's	17,490,608 / 19.9%
Number/percentage of T's	27,202,357 / 30.95%
Number/percentage of G's	20,770,568 / 23.63%
Number/percentage of N's	1,204 / 0%
GC Percentage	43.53%

2.3. Coverage

Mean	0.0284

Standard Deviation	0.2648

2.4. Mapping Quality

Mean Mapping Quality	44.8

2.5. Mismatches and indels

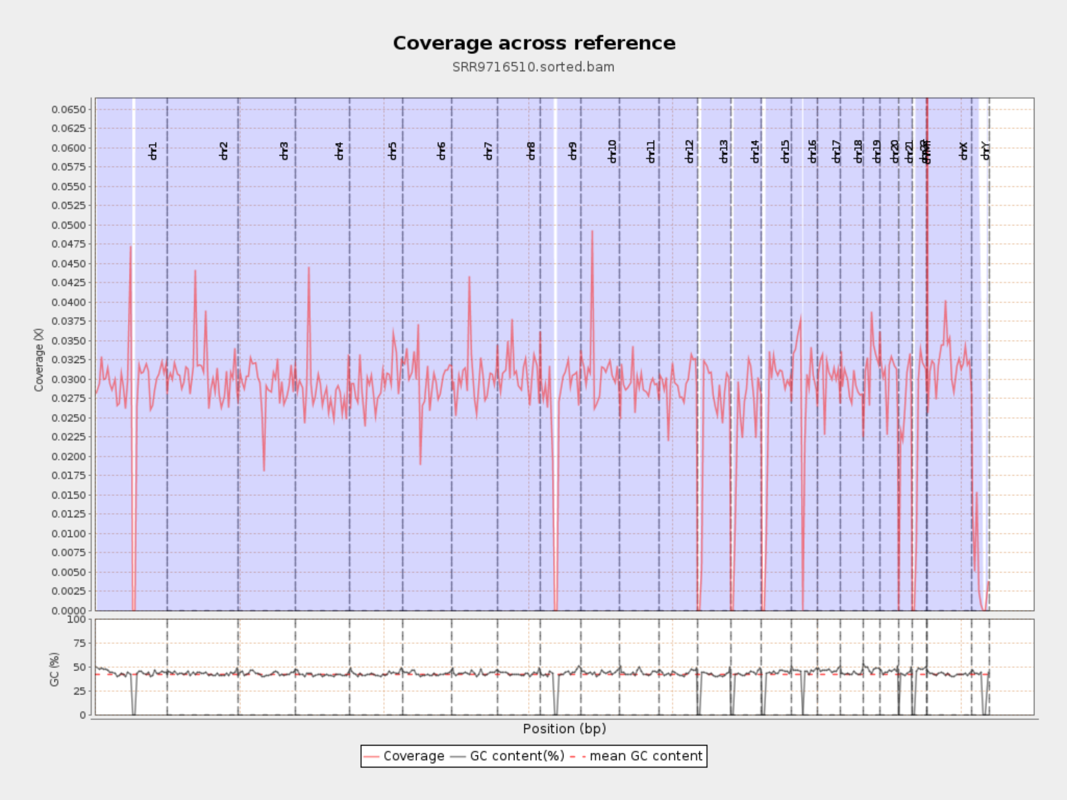
General error rate	0.51%
Mismatches	440,314
Insertions	5,773
Mapped reads with at least one insertion	0.38%
Deletions	16,112
Mapped reads with at least one deletion	1.05%
Homopolymer indels	42.06%

2.6. Chromosome stats

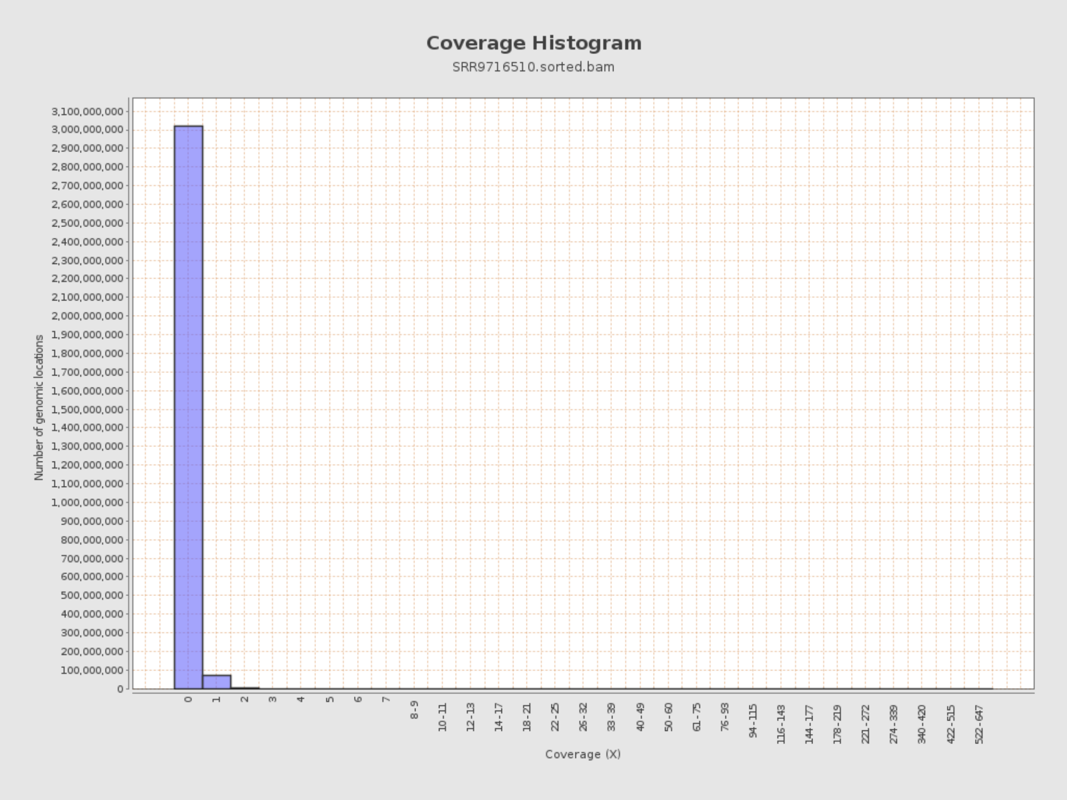
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7058270	0.0283	0.4851
chr2	243199373	7464819	0.0307	0.3425
chr3	198022430	5782865	0.0292	0.1885
chr4	191154276	5494082	0.0287	0.203
chr5	180915260	5333438	0.0295	0.1907
chr6	171115067	5128110	0.03	0.2202
chr7	159138663	4804647	0.0302	0.3073

chr8	146364022	4513188	0.0308	0.2471
chr9	141213431	3635262	0.0257	0.2198
chr10	135534747	4248546	0.0313	0.2543
chr11	135006516	3966927	0.0294	0.2385
chr12	133851895	3946193	0.0295	0.1924
chr13	115169878	2790633	0.0242	0.1716
chr14	107349540	2477755	0.0231	0.1759
chr15	102531392	2550564	0.0249	0.1814
chr16	90354753	2581414	0.0286	0.1977
chr17	81195210	2462609	0.0303	0.2008
chr18	78077248	2277764	0.0292	0.3618
chr19	59128983	1910849	0.0323	0.3441
chr20	63025520	1907329	0.0303	0.1955
chr21	48129895	1189749	0.0247	0.1956
chr22	51304566	1109543	0.0216	0.1633
chrMT	16571	4996	0.3015	0.5919
chrX	155270560	5000306	0.0322	0.2172
chrY	59373566	278628	0.0047	0.1207

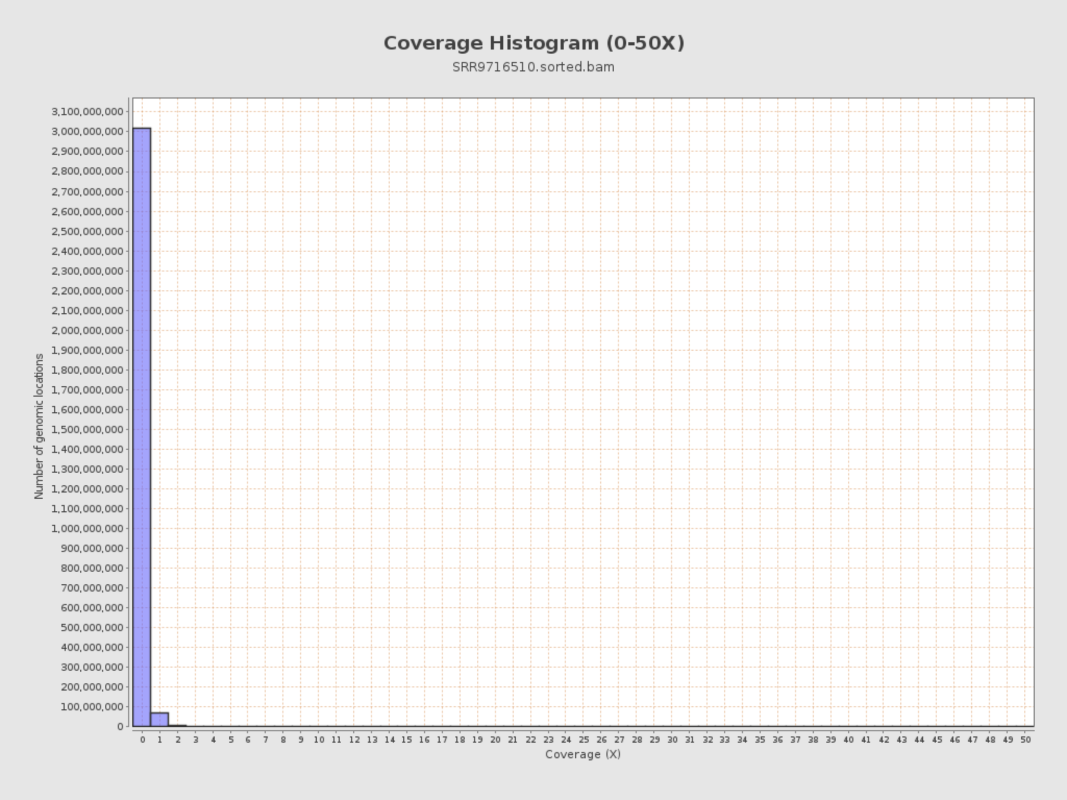
3. Results : Coverage across reference



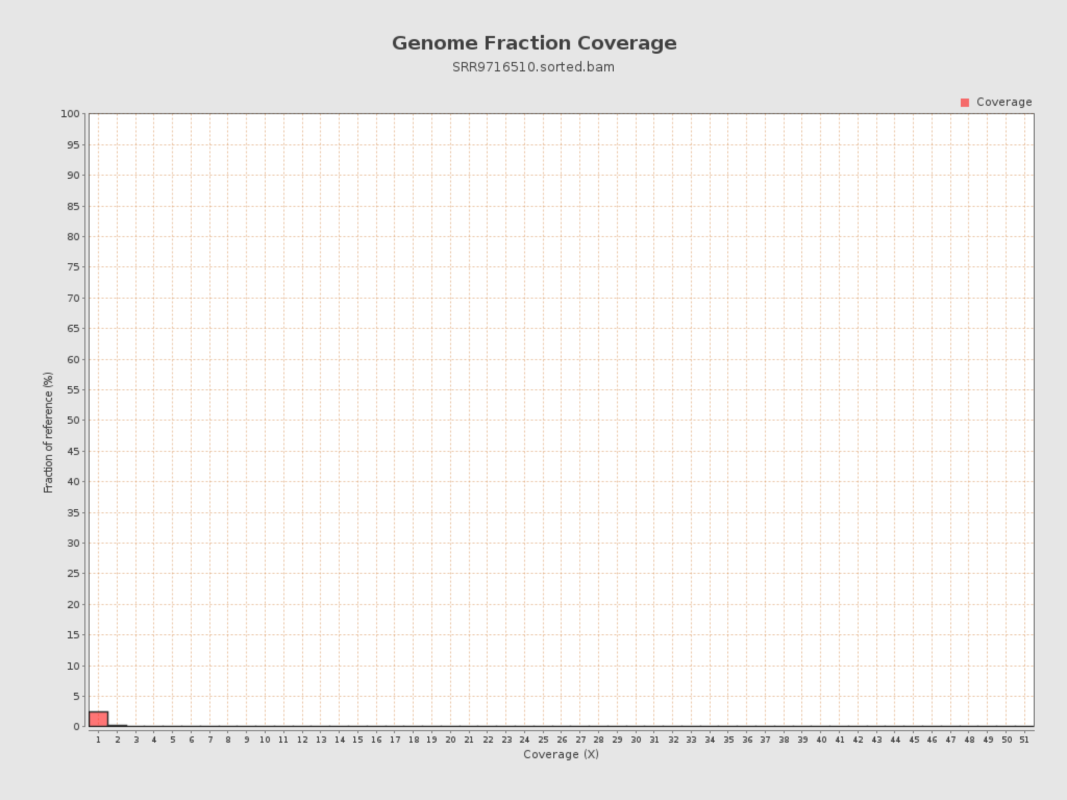
4. Results : Coverage Histogram



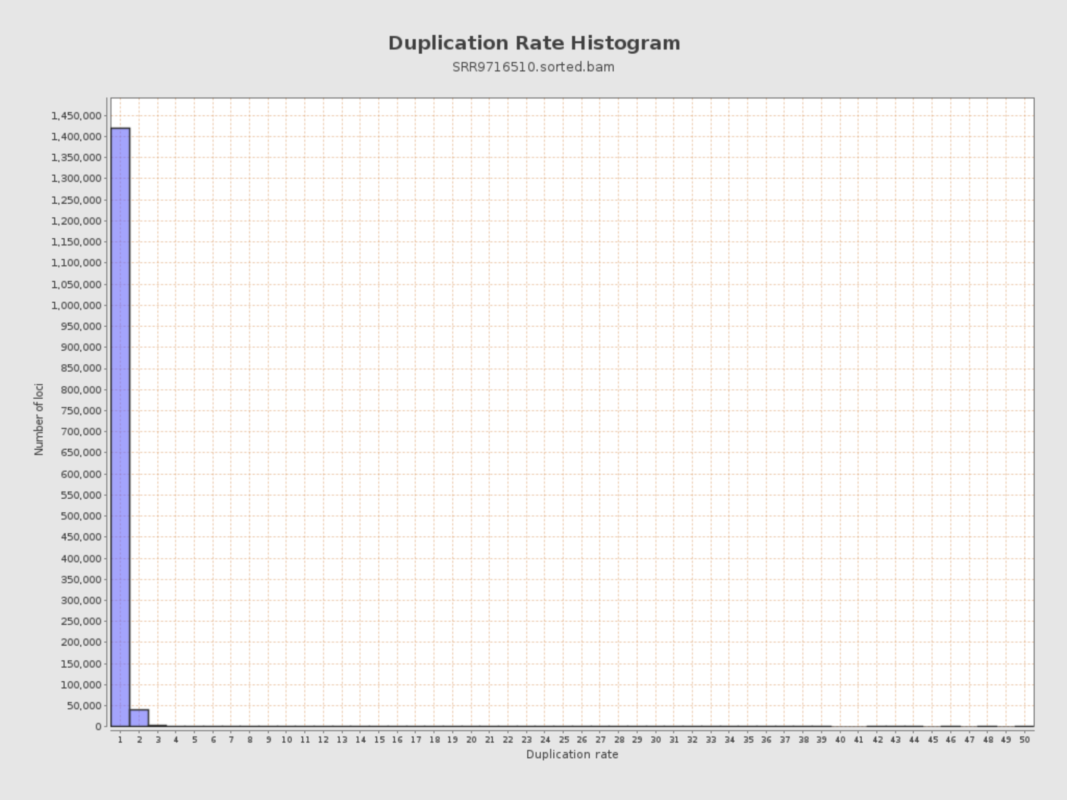
5. Results : Coverage Histogram (0-50X)



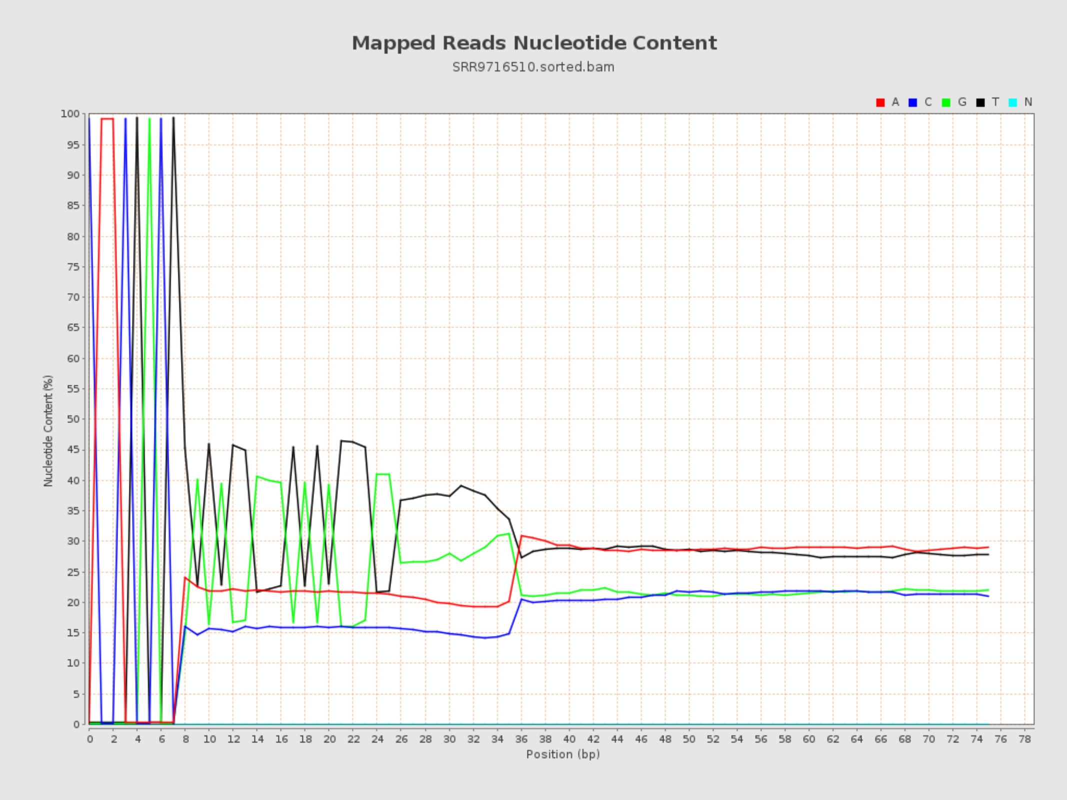
6. Results : Genome Fraction Coverage



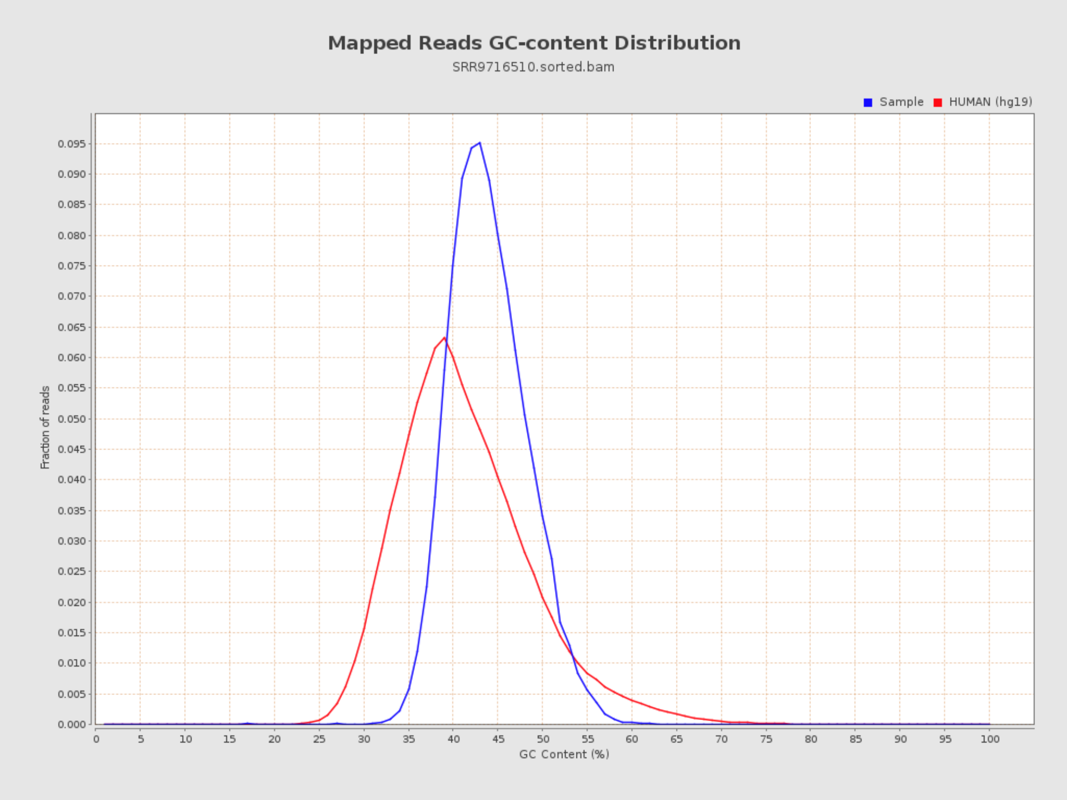
7. Results : Duplication Rate Histogram



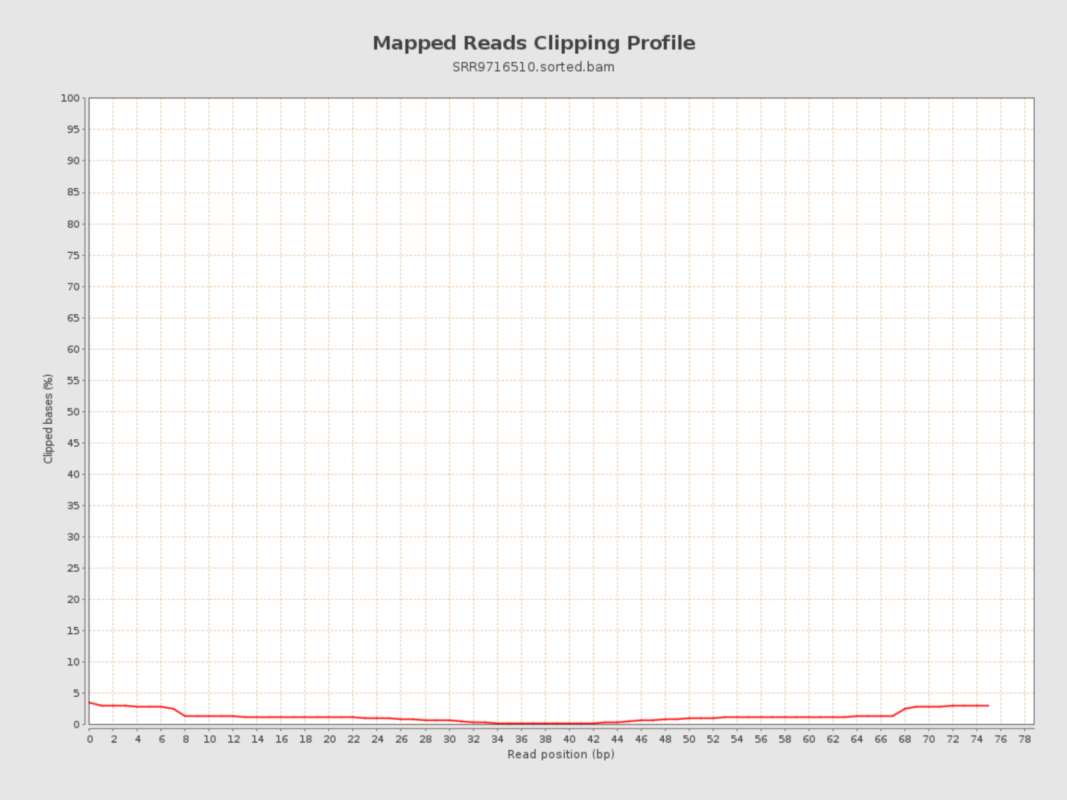
8. Results : Mapped Reads Nucleotide Content



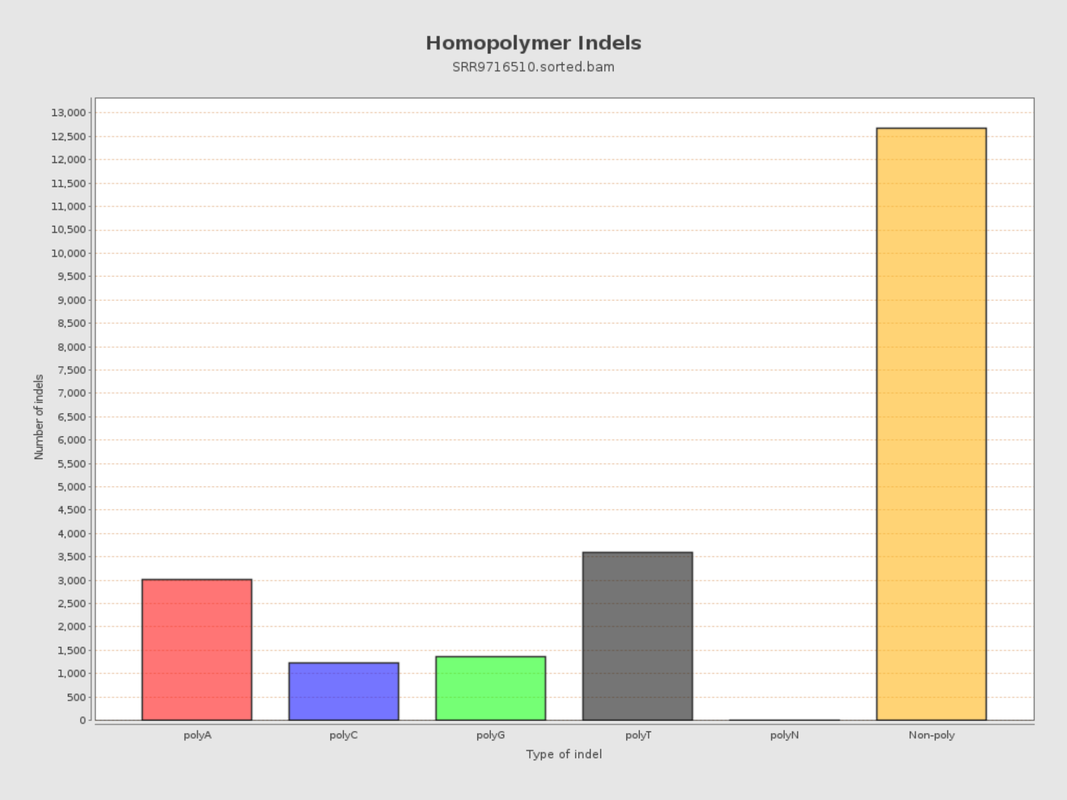
9. Results : Mapped Reads GC-content Distribution



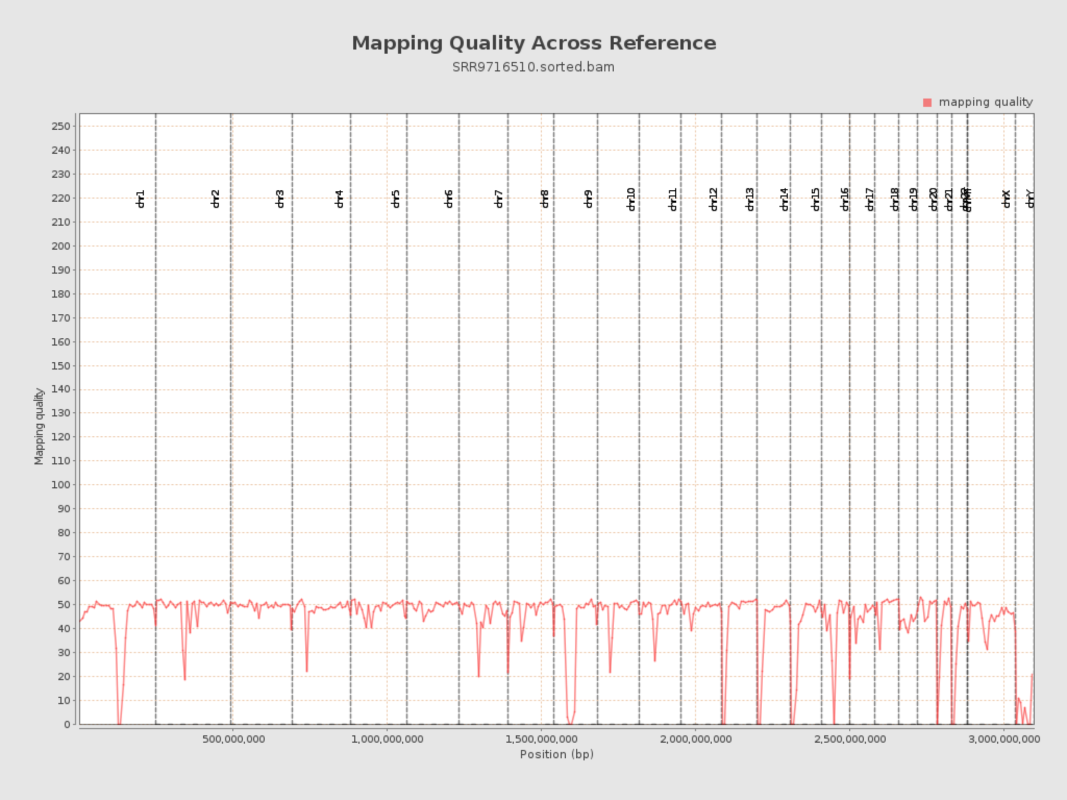
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram