Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 02:55:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716656.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_SRR9716656 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716656.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 02:55:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716656.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,652,067
Mapped reads	1,535,150 / 92.92%
Unmapped reads	116,917 / 7.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,078 / 0.61%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	49,513 / 3%
Duplication rate	2.26%
Clipped reads	1,541,062 / 93.28%

2.2. ACGT Content

Number/percentage of A's	22,811,392 / 25.18%
Number/percentage of C's	17,721,366 / 19.56%
Number/percentage of T's	28,381,368 / 31.33%
Number/percentage of G's	21,662,683 / 23.92%
Number/percentage of N's	1,085 / 0%
GC Percentage	43.48%

2.3. Coverage

Mean	0.0293

Standard Deviation	0.292

2.4. Mapping Quality

Mean Mapping Quality	44.83

2.5. Mismatches and indels

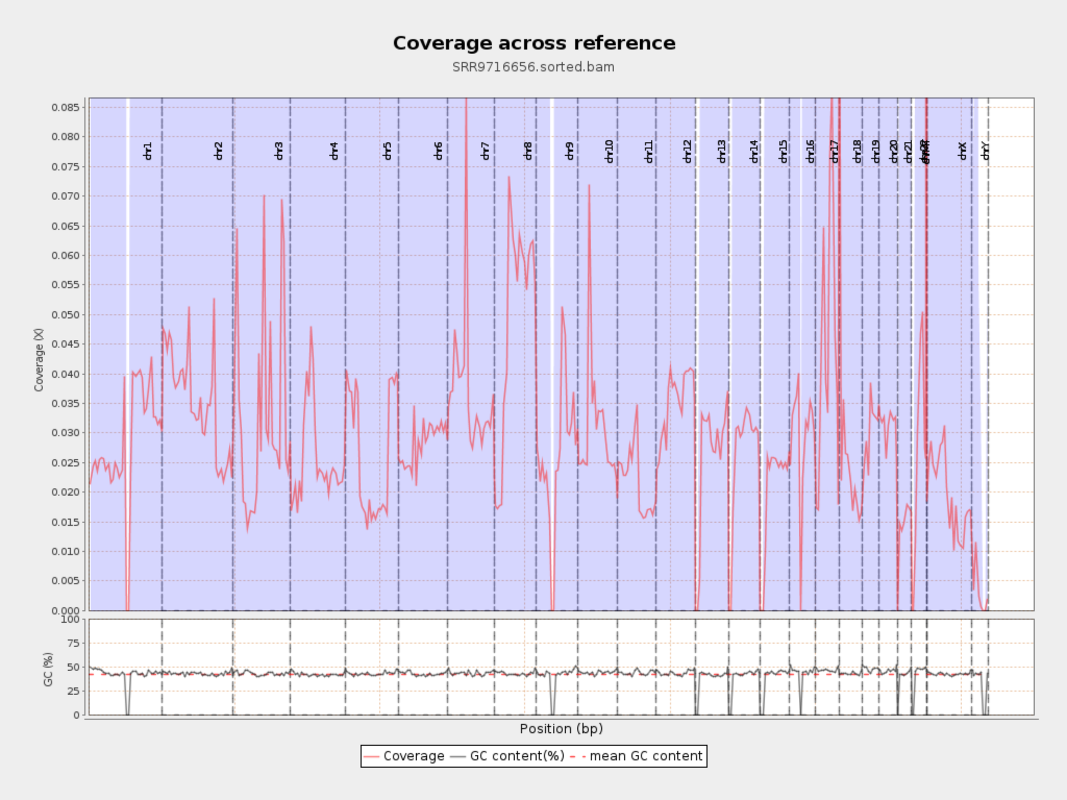
General error rate	0.51%
Mismatches	452,325
Insertions	6,072
Mapped reads with at least one insertion	0.39%
Deletions	17,111
Mapped reads with at least one deletion	1.11%
Homopolymer indels	40.36%

2.6. Chromosome stats

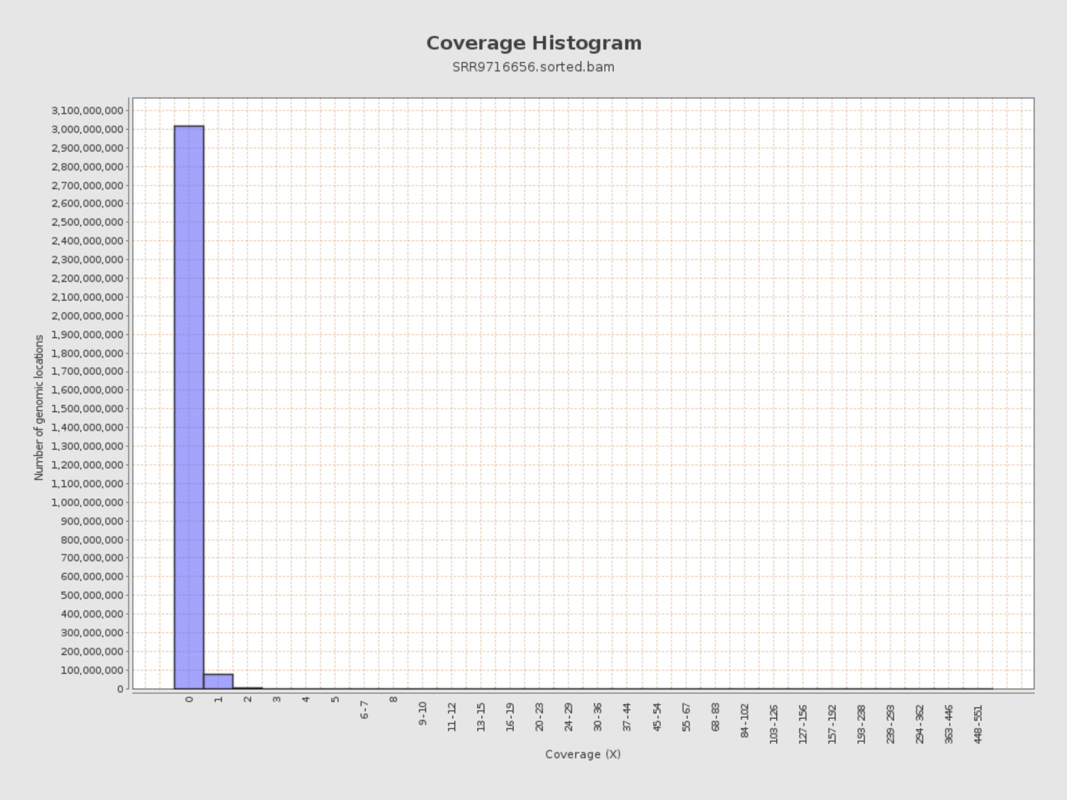
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7010623	0.0281	0.3852
chr2	243199373	8651874	0.0356	0.315
chr3	198022430	6476014	0.0327	0.2018
chr4	191154276	4886216	0.0256	0.1931
chr5	180915260	4735989	0.0262	0.1751
chr6	171115067	4837932	0.0283	0.1955
chr7	159138663	5939334	0.0373	0.7265

chr8	146364022	7246376	0.0495	0.3315
chr9	141213431	3637442	0.0258	0.1983
chr10	135534747	4206281	0.031	0.3472
chr11	135006516	2940633	0.0218	0.2022
chr12	133851895	4716342	0.0352	0.2149
chr13	115169878	2948836	0.0256	0.1736
chr14	107349540	2812202	0.0262	0.1785
chr15	102531392	2086120	0.0203	0.156
chr16	90354753	2669249	0.0295	0.1948
chr17	81195210	3673266	0.0452	0.2419
chr18	78077248	2074414	0.0266	0.3057
chr19	59128983	1777189	0.0301	0.3376
chr20	63025520	1967214	0.0312	0.199
chr21	48129895	687222	0.0143	0.1442
chr22	51304566	1336565	0.0261	0.1748
chrMT	16571	10445	0.6303	0.9005
chrX	155270560	3078347	0.0198	0.1697
chrY	59373566	198965	0.0034	0.101

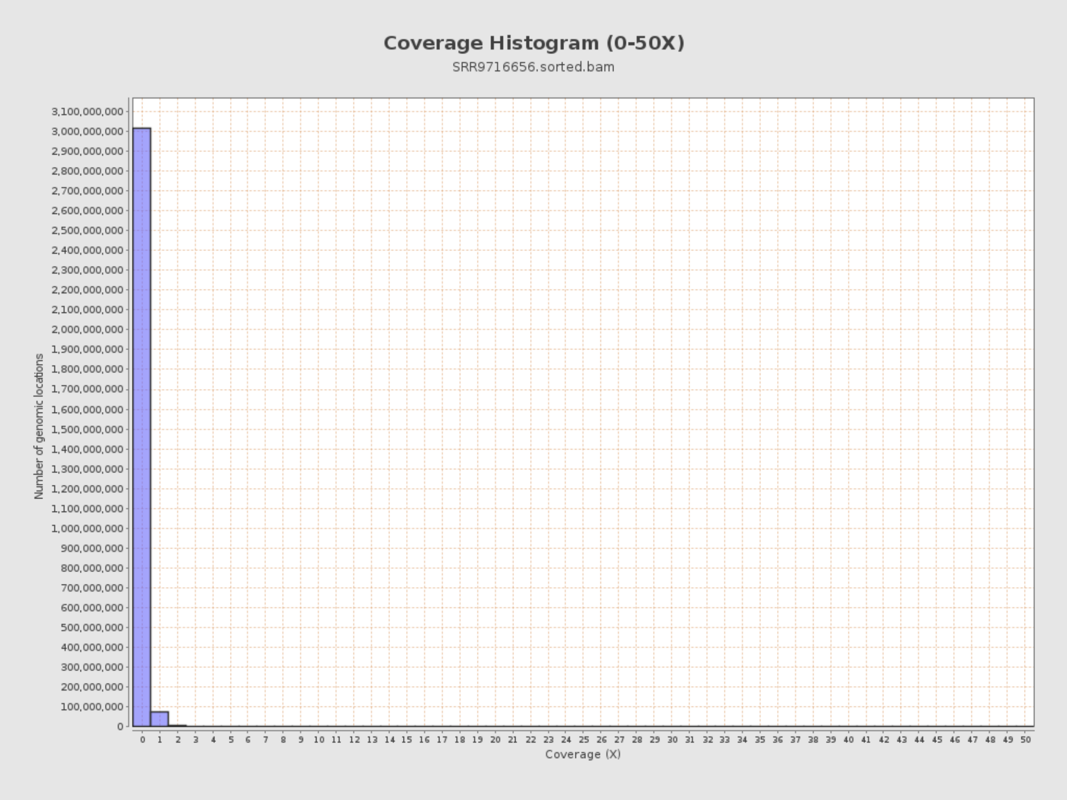
3. Results : Coverage across reference



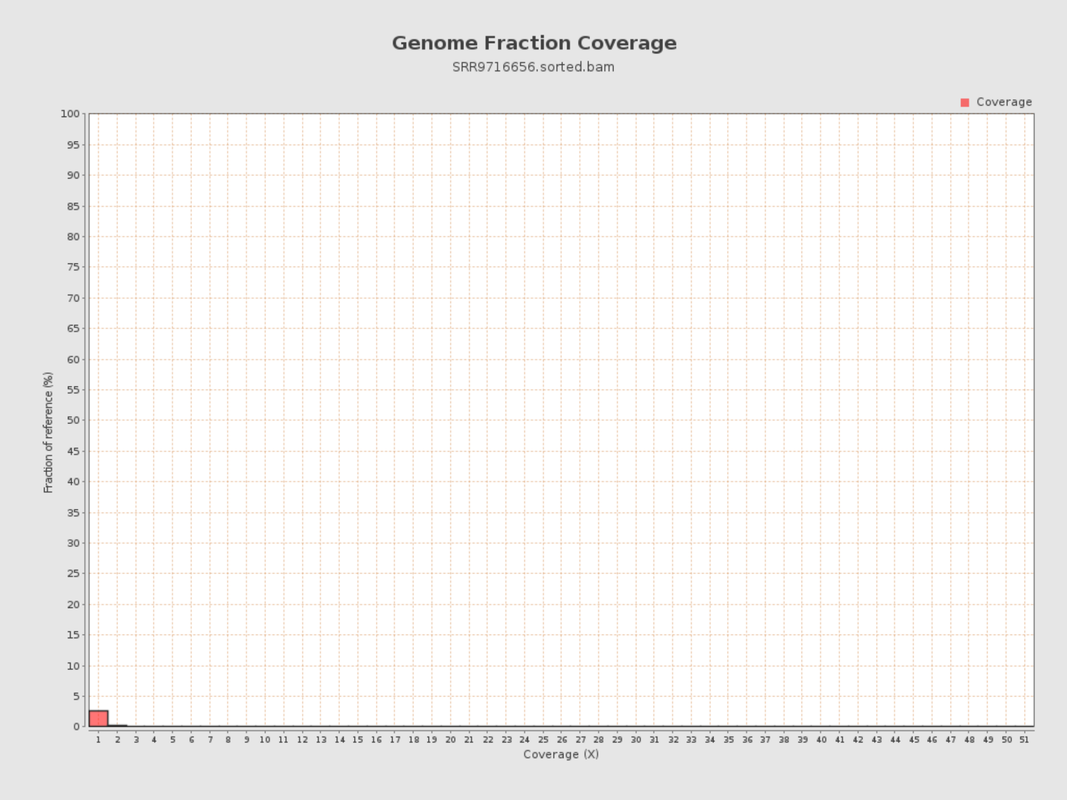
4. Results : Coverage Histogram



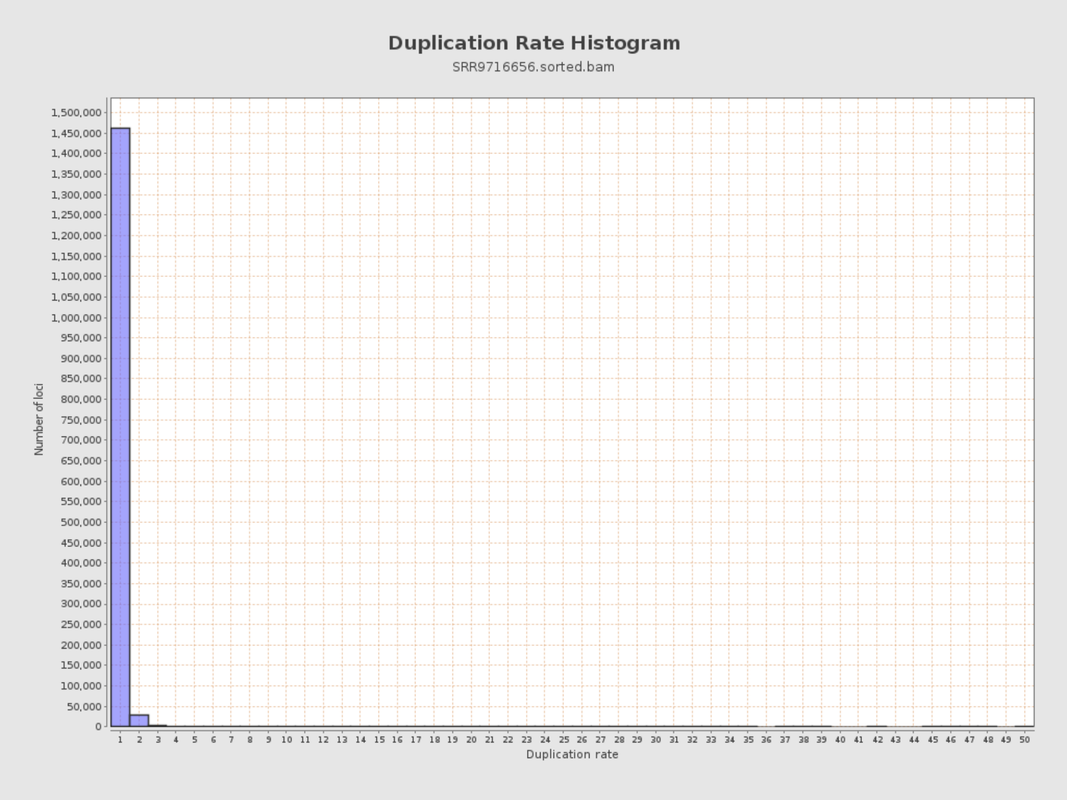
5. Results : Coverage Histogram (0-50X)



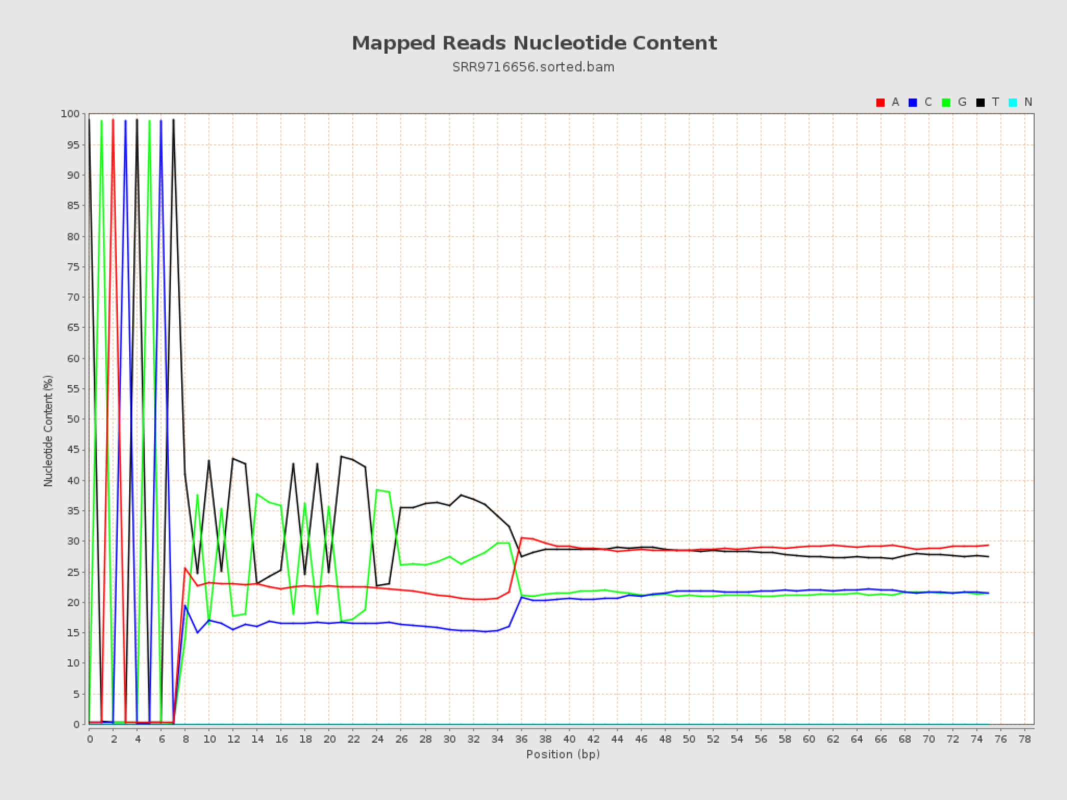
6. Results : Genome Fraction Coverage



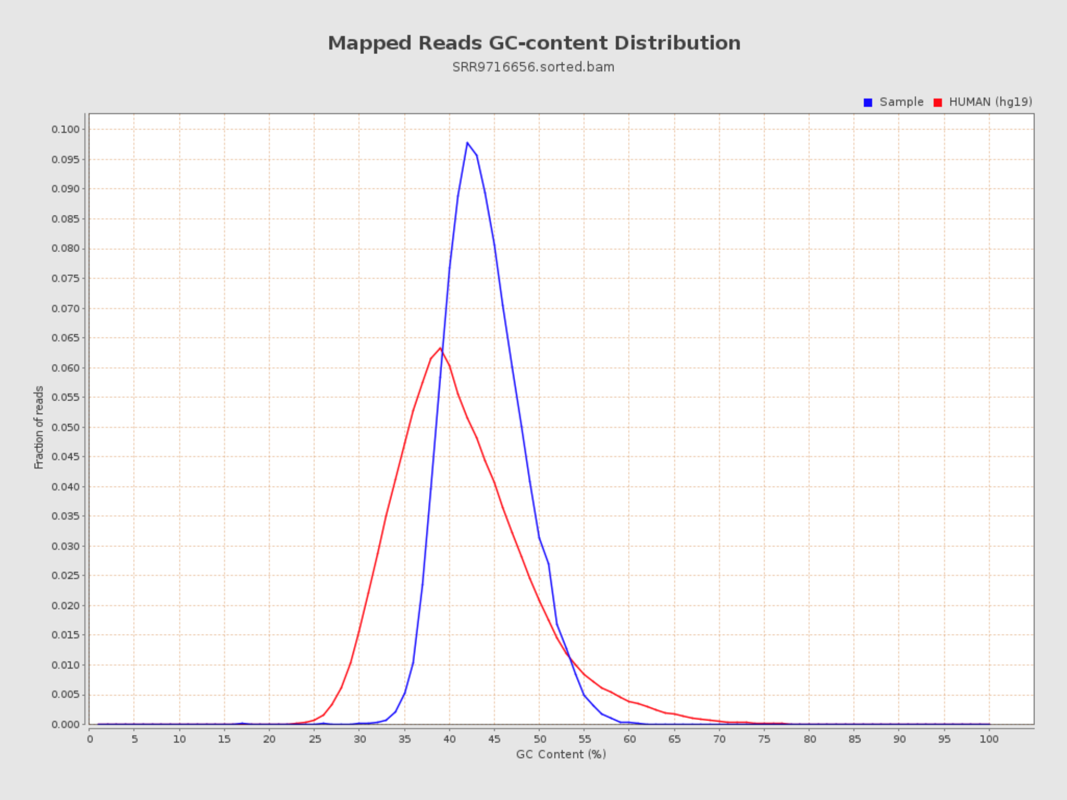
7. Results : Duplication Rate Histogram



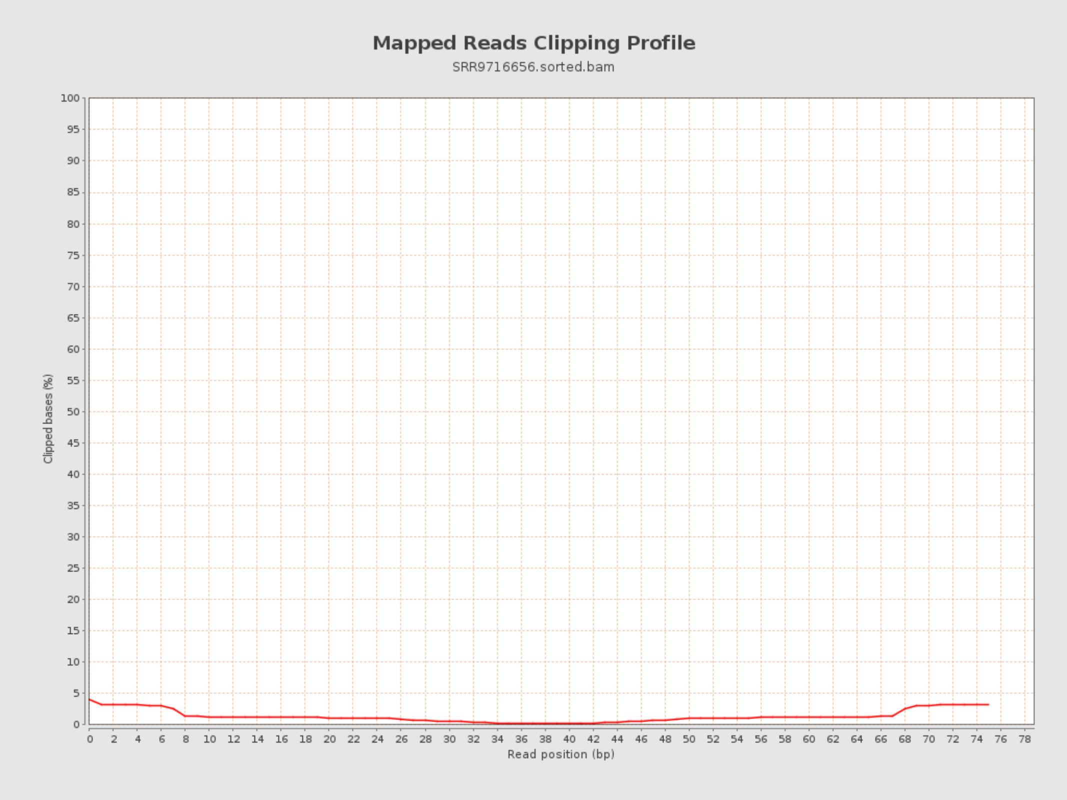
8. Results : Mapped Reads Nucleotide Content



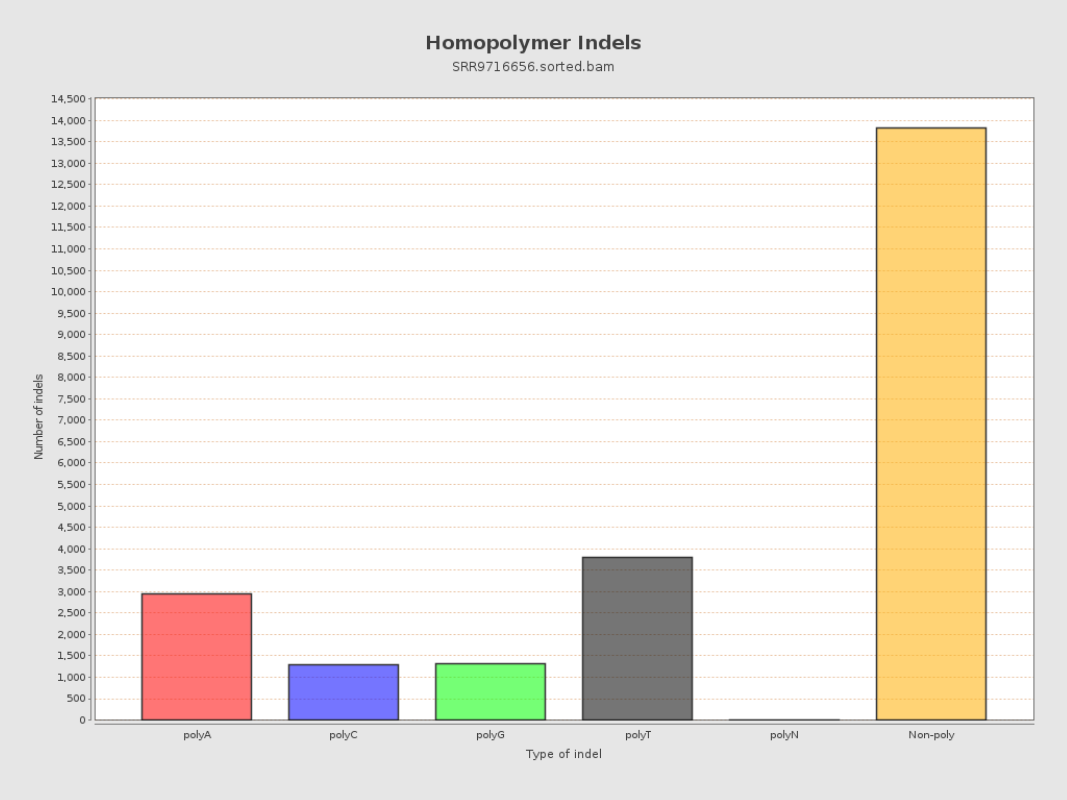
9. Results : Mapped Reads GC-content Distribution



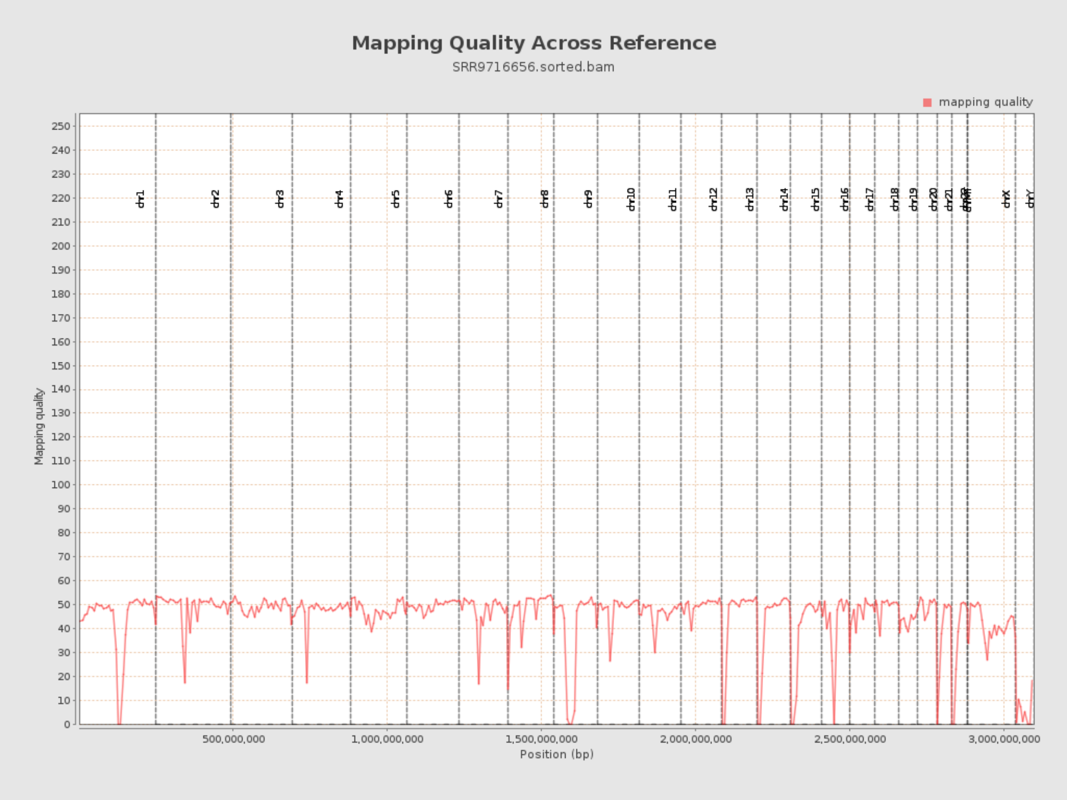
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram