Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 17:44:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716095.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_SRR9716095 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716095.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 17:44:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716095.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	935,465
Mapped reads	838,604 / 89.65%
Unmapped reads	96,861 / 10.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,547 / 0.49%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	25,638 / 2.74%
Duplication rate	2.37%
Clipped reads	841,011 / 89.9%

2.2. ACGT Content

Number/percentage of A's	12,636,613 / 25.84%
Number/percentage of C's	9,805,502 / 20.05%
Number/percentage of T's	14,993,028 / 30.66%
Number/percentage of G's	11,466,310 / 23.45%
Number/percentage of N's	316 / 0%
GC Percentage	43.5%

2.3. Coverage

Mean	0.0158

Standard Deviation	0.1687

2.4. Mapping Quality

Mean Mapping Quality	44.83

2.5. Mismatches and indels

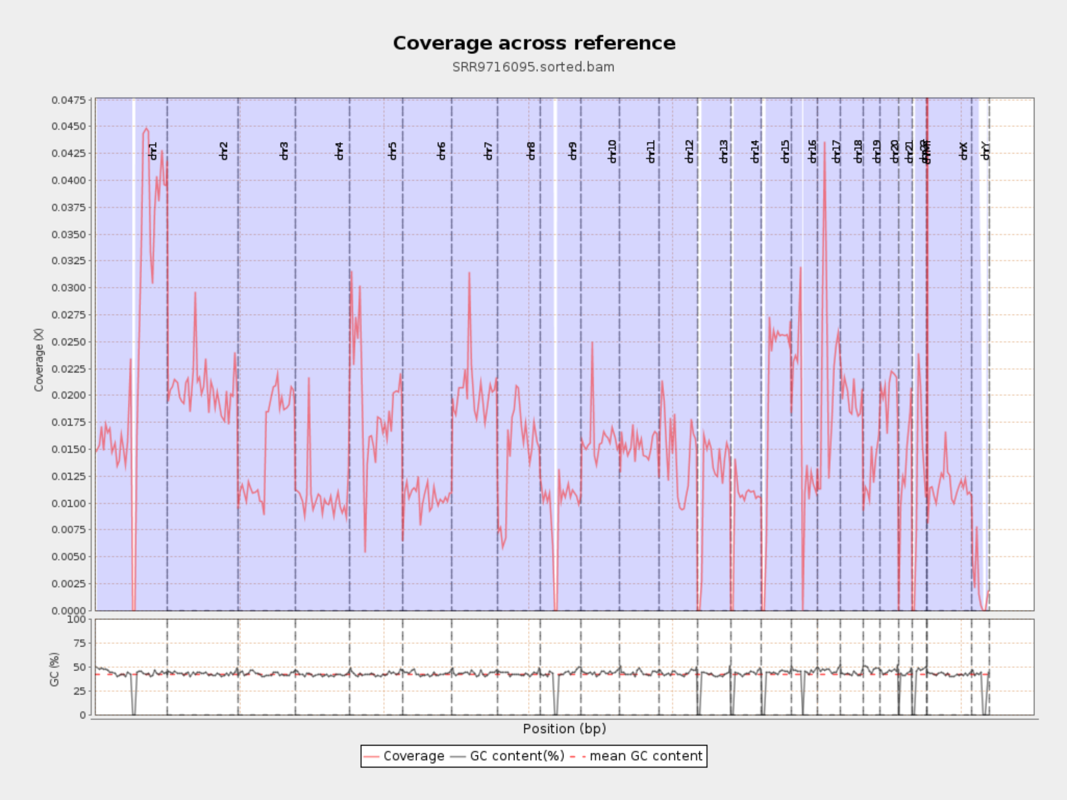
General error rate	0.52%
Mismatches	247,069
Insertions	3,797
Mapped reads with at least one insertion	0.45%
Deletions	9,046
Mapped reads with at least one deletion	1.07%
Homopolymer indels	40.77%

2.6. Chromosome stats

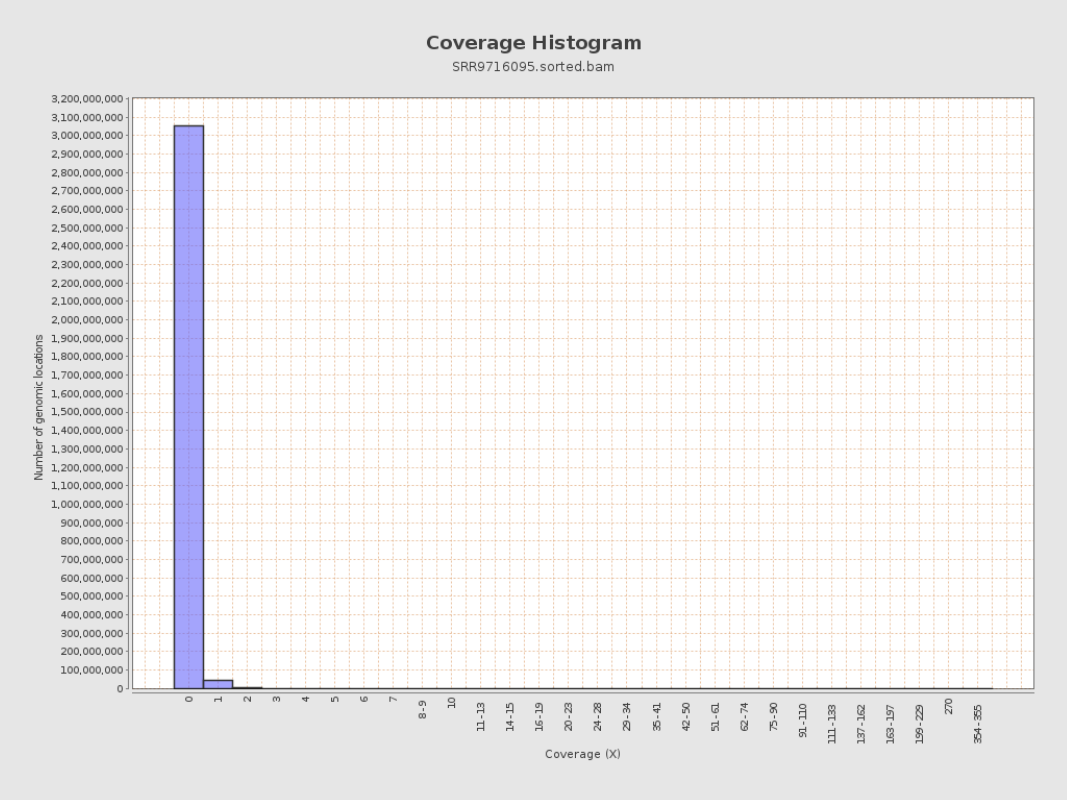
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5980761	0.024	0.2473
chr2	243199373	5012967	0.0206	0.2306
chr3	198022430	3054499	0.0154	0.1324
chr4	191154276	2034800	0.0106	0.1255
chr5	180915260	3484892	0.0193	0.1485
chr6	171115067	1792575	0.0105	0.1147
chr7	159138663	3271866	0.0206	0.2428

chr8	146364022	2155447	0.0147	0.1575
chr9	141213431	1338255	0.0095	0.1301
chr10	135534747	2178764	0.0161	0.1608
chr11	135006516	2073016	0.0154	0.1669
chr12	133851895	1946965	0.0145	0.1297
chr13	115169878	1380360	0.012	0.1163
chr14	107349540	1036468	0.0097	0.1083
chr15	102531392	2106411	0.0205	0.1542
chr16	90354753	1427875	0.0158	0.1408
chr17	81195210	1856072	0.0229	0.1694
chr18	78077248	1537379	0.0197	0.2585
chr19	59128983	767789	0.013	0.1794
chr20	63025520	1291416	0.0205	0.1546
chr21	48129895	626768	0.013	0.128
chr22	51304566	626150	0.0122	0.1172
chrMT	16571	8199	0.4948	0.7541
chrX	155270560	1796506	0.0116	0.1228
chrY	59373566	130252	0.0022	0.0739

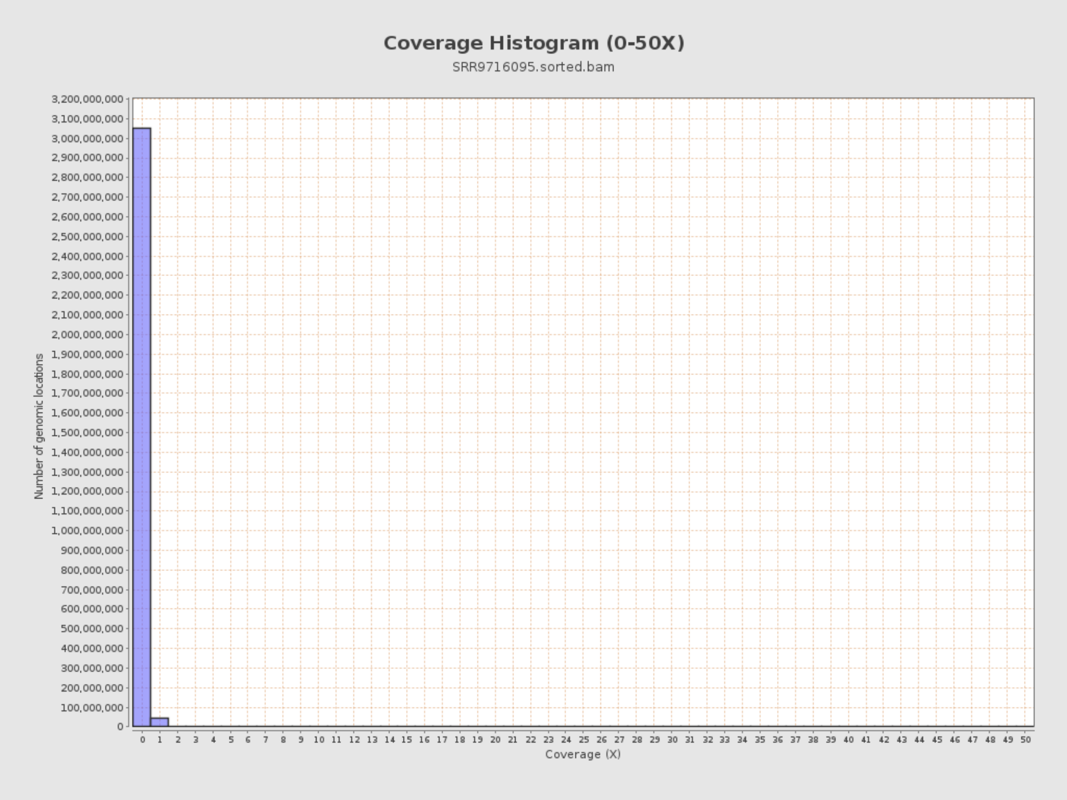
3. Results : Coverage across reference



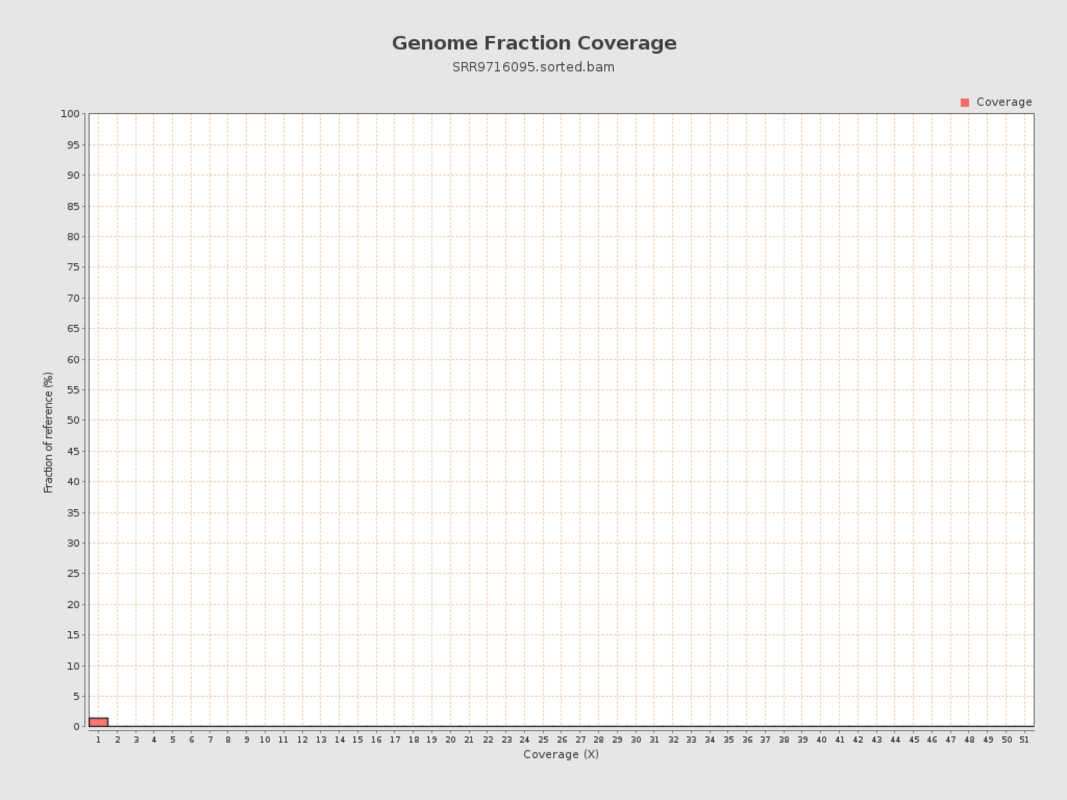
4. Results : Coverage Histogram



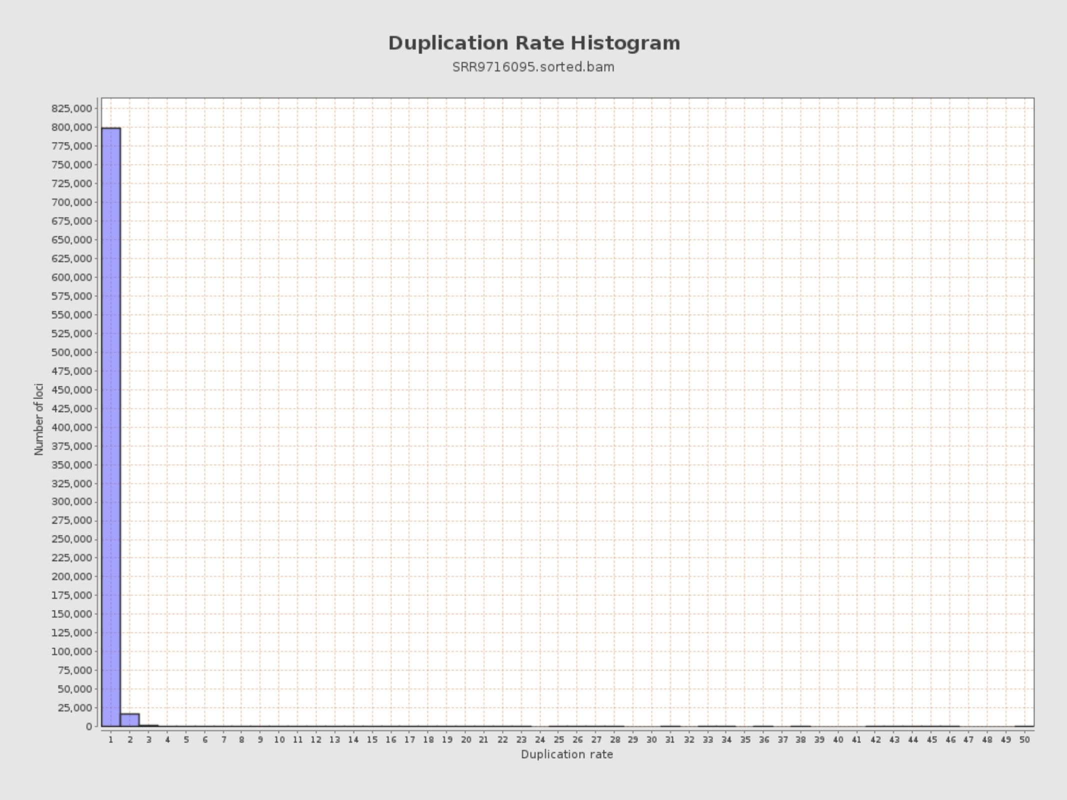
5. Results : Coverage Histogram (0-50X)



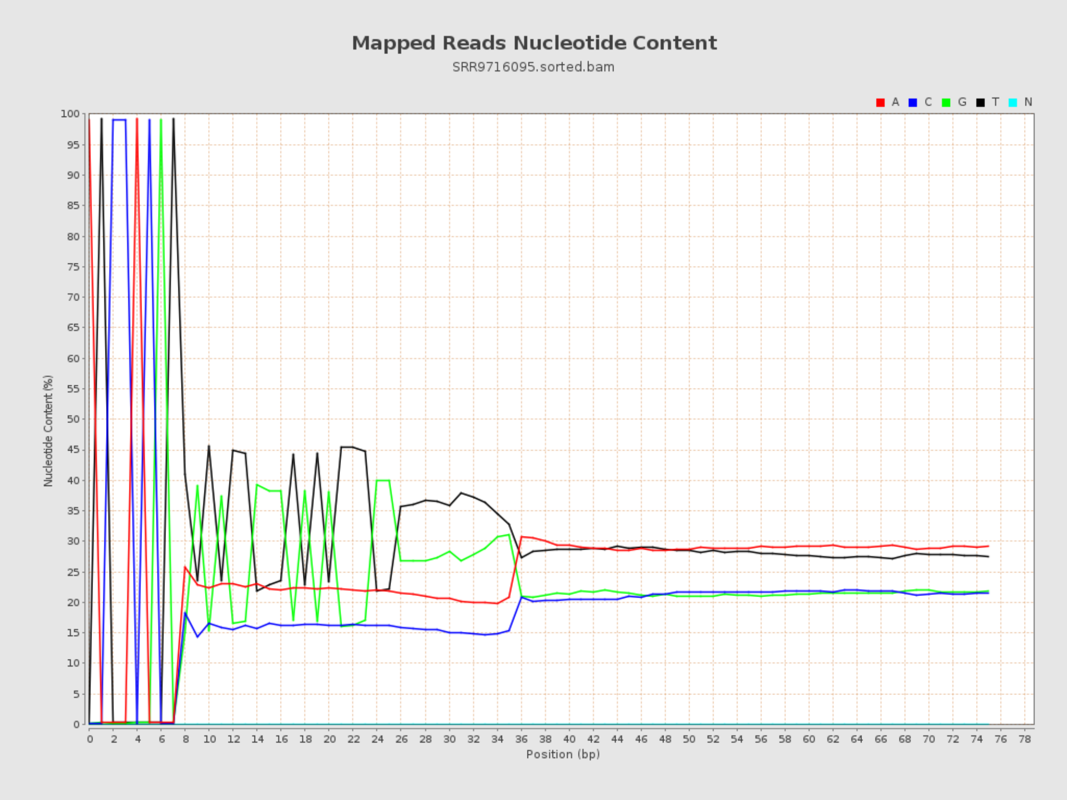
6. Results : Genome Fraction Coverage



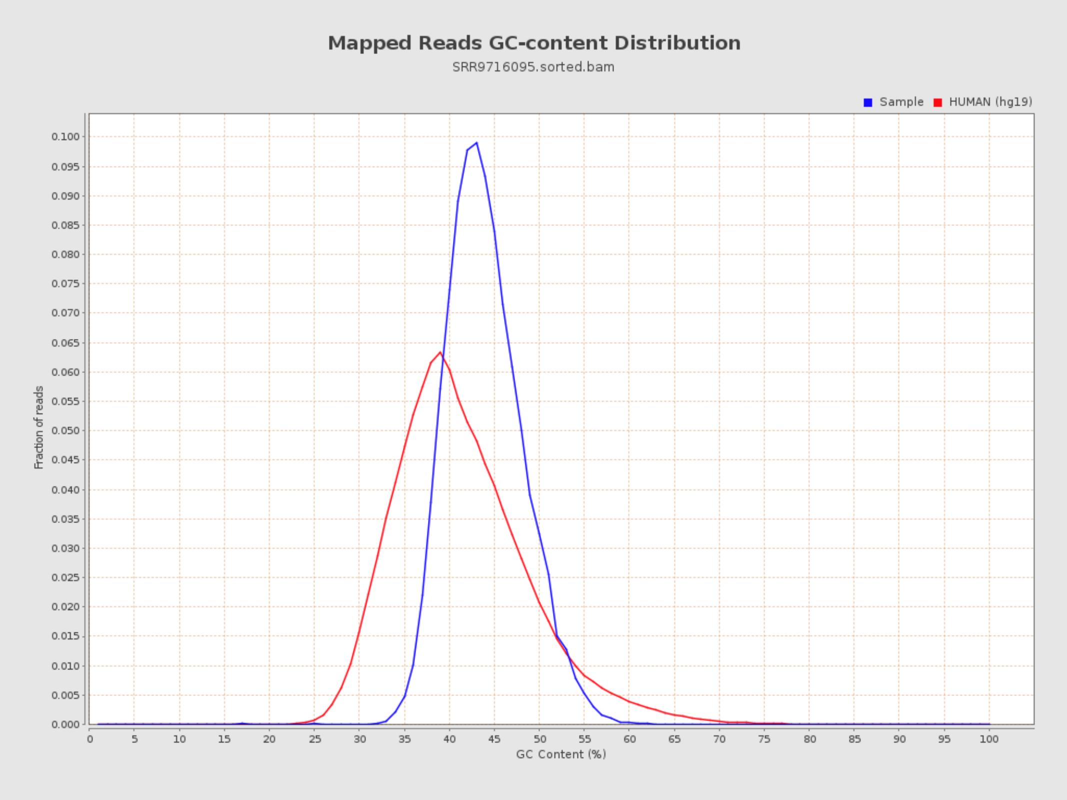
7. Results : Duplication Rate Histogram



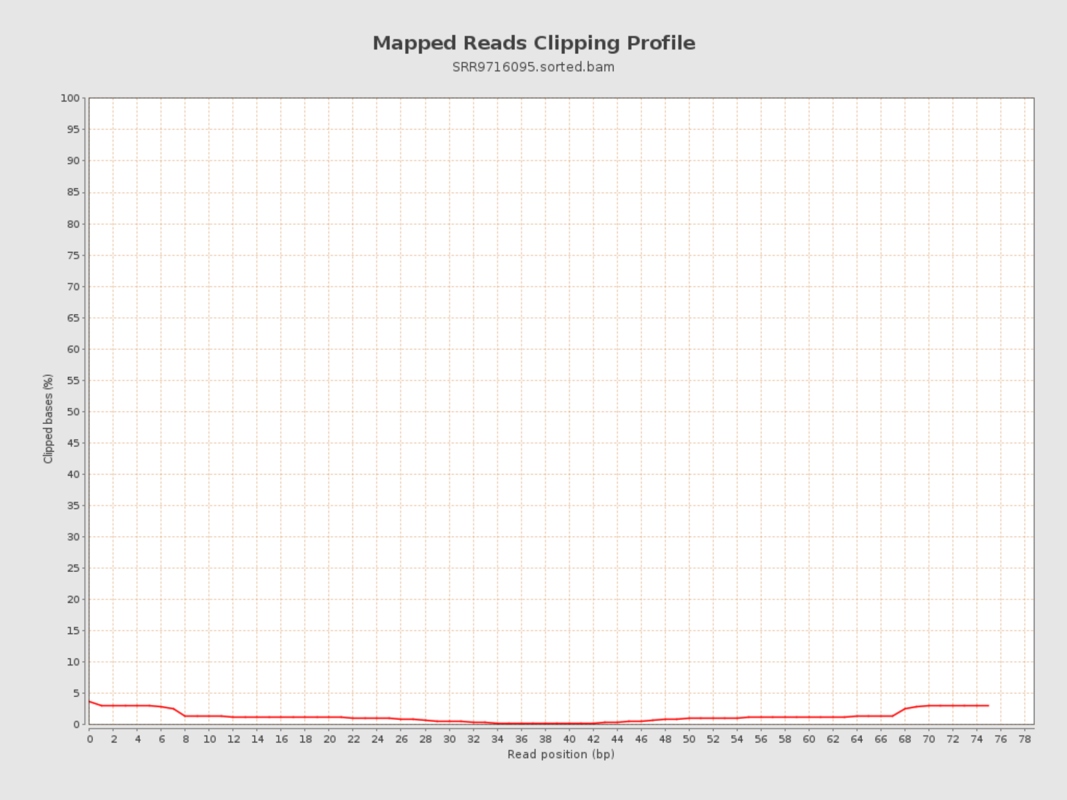
8. Results : Mapped Reads Nucleotide Content



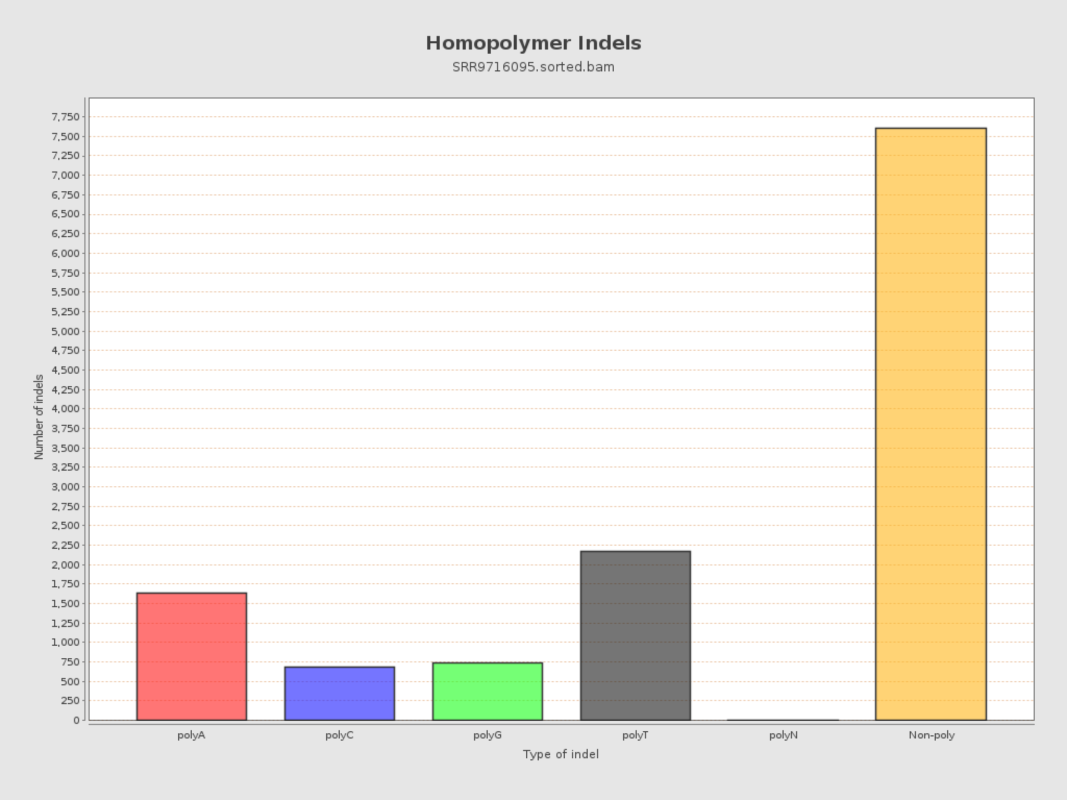
9. Results : Mapped Reads GC-content Distribution



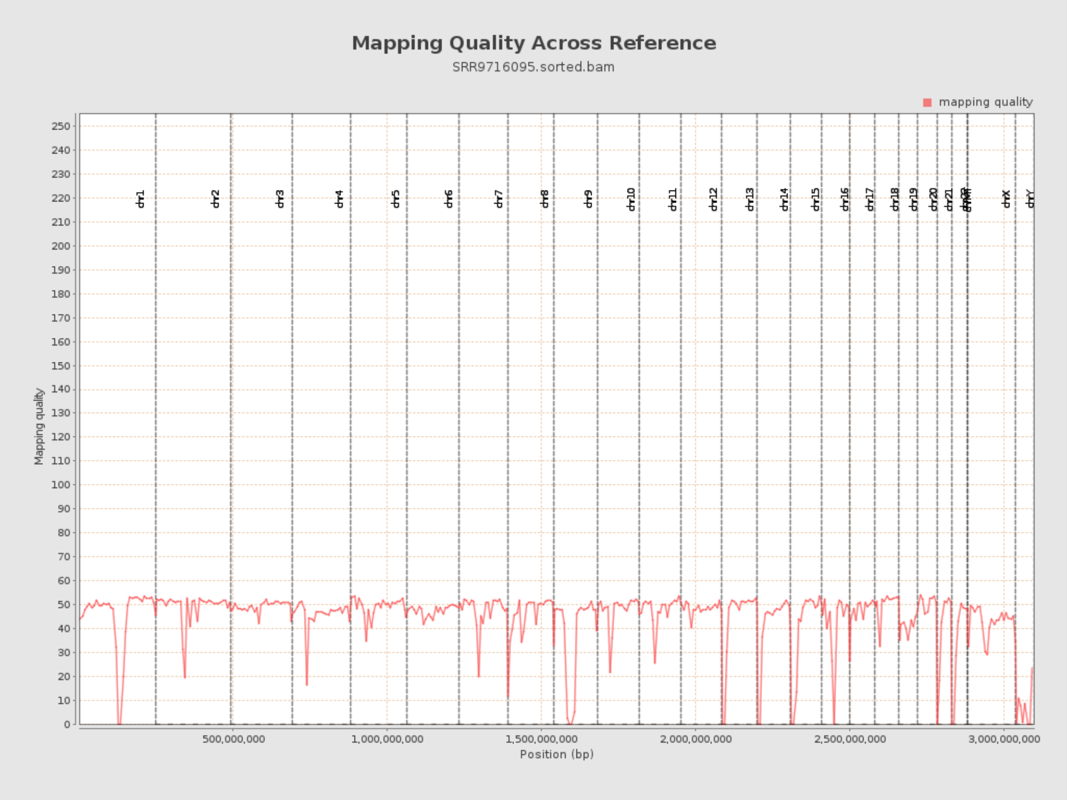
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram