Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 04:46:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716271.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_SRR9716271 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716271.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 04:46:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716271.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	718,725
Mapped reads	638,882 / 88.89%
Unmapped reads	79,843 / 11.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,950 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	10,506 / 1.46%
Duplication rate	1.24%
Clipped reads	640,337 / 89.09%

2.2. ACGT Content

Number/percentage of A's	9,140,304 / 25.19%
Number/percentage of C's	7,276,622 / 20.05%
Number/percentage of T's	11,131,051 / 30.68%
Number/percentage of G's	8,737,626 / 24.08%
Number/percentage of N's	813 / 0%
GC Percentage	44.13%

2.3. Coverage

Mean	0.0117

Standard Deviation	0.1287

2.4. Mapping Quality

Mean Mapping Quality	44.11

2.5. Mismatches and indels

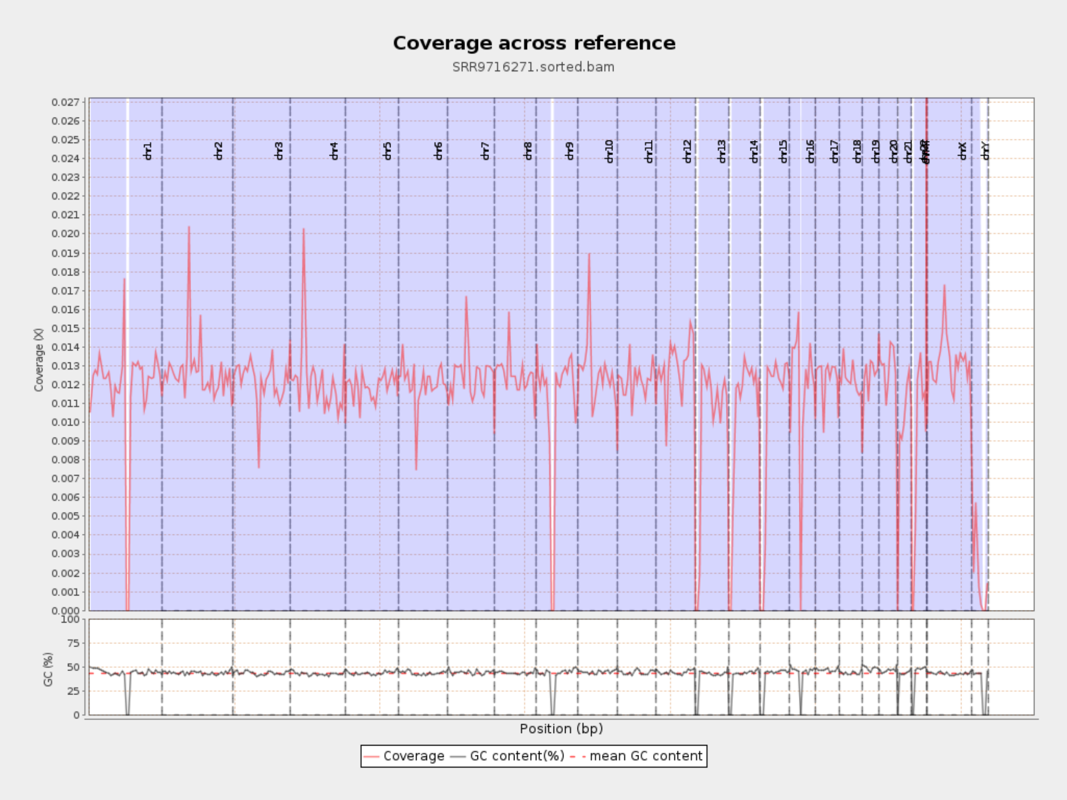
General error rate	0.51%
Mismatches	181,511
Insertions	2,553
Mapped reads with at least one insertion	0.4%
Deletions	5,643
Mapped reads with at least one deletion	0.88%
Homopolymer indels	39.65%

2.6. Chromosome stats

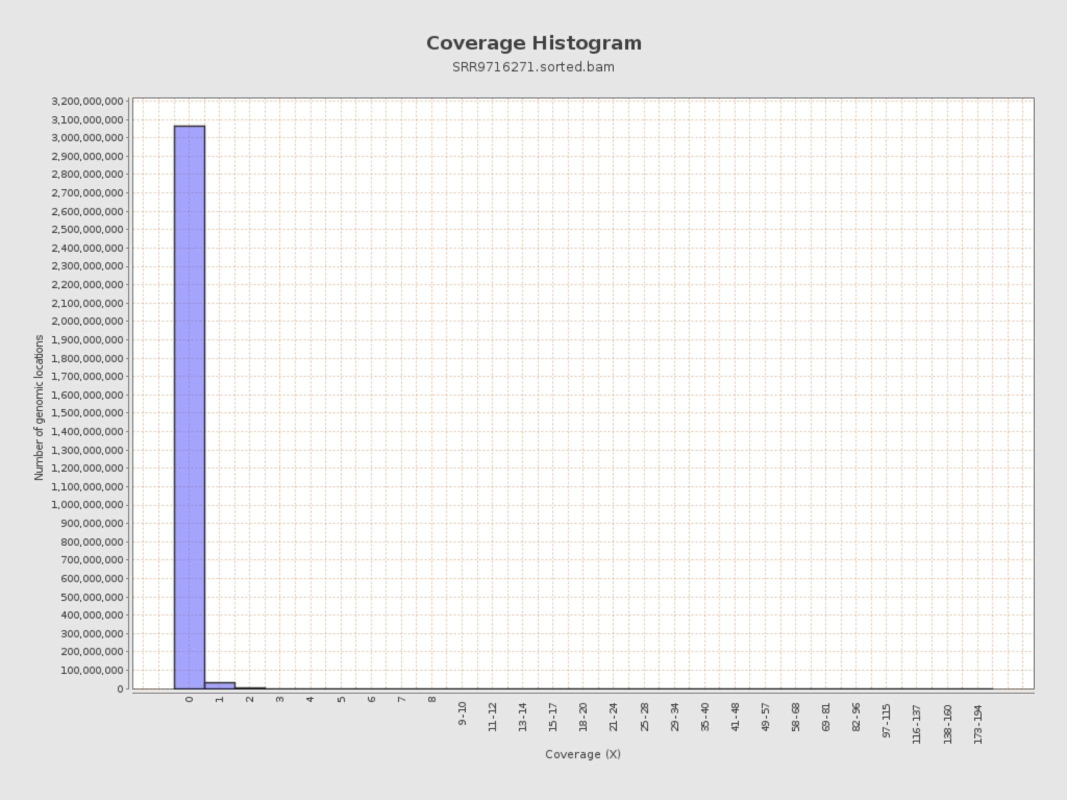
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2919812	0.0117	0.1749
chr2	243199373	3097297	0.0127	0.1416
chr3	198022430	2407585	0.0122	0.1141
chr4	191154276	2327057	0.0122	0.1207
chr5	180915260	2159461	0.0119	0.1137
chr6	171115067	2061186	0.012	0.1163
chr7	159138663	2001954	0.0126	0.1394

chr8	146364022	1831492	0.0125	0.1254
chr9	141213431	1524889	0.0108	0.1293
chr10	135534747	1723046	0.0127	0.1315
chr11	135006516	1644830	0.0122	0.1318
chr12	133851895	1726540	0.0129	0.1191
chr13	115169878	1117168	0.0097	0.1015
chr14	107349540	1092092	0.0102	0.1083
chr15	102531392	1039456	0.0101	0.104
chr16	90354753	1065250	0.0118	0.1171
chr17	81195210	1001190	0.0123	0.1183
chr18	78077248	963434	0.0123	0.1884
chr19	59128983	738635	0.0125	0.137
chr20	63025520	799014	0.0127	0.119
chr21	48129895	464818	0.0097	0.1076
chr22	51304566	430609	0.0084	0.0952
chrMT	16571	738	0.0445	0.2063
chrX	155270560	2048205	0.0132	0.1271
chrY	59373566	110378	0.0019	0.0544

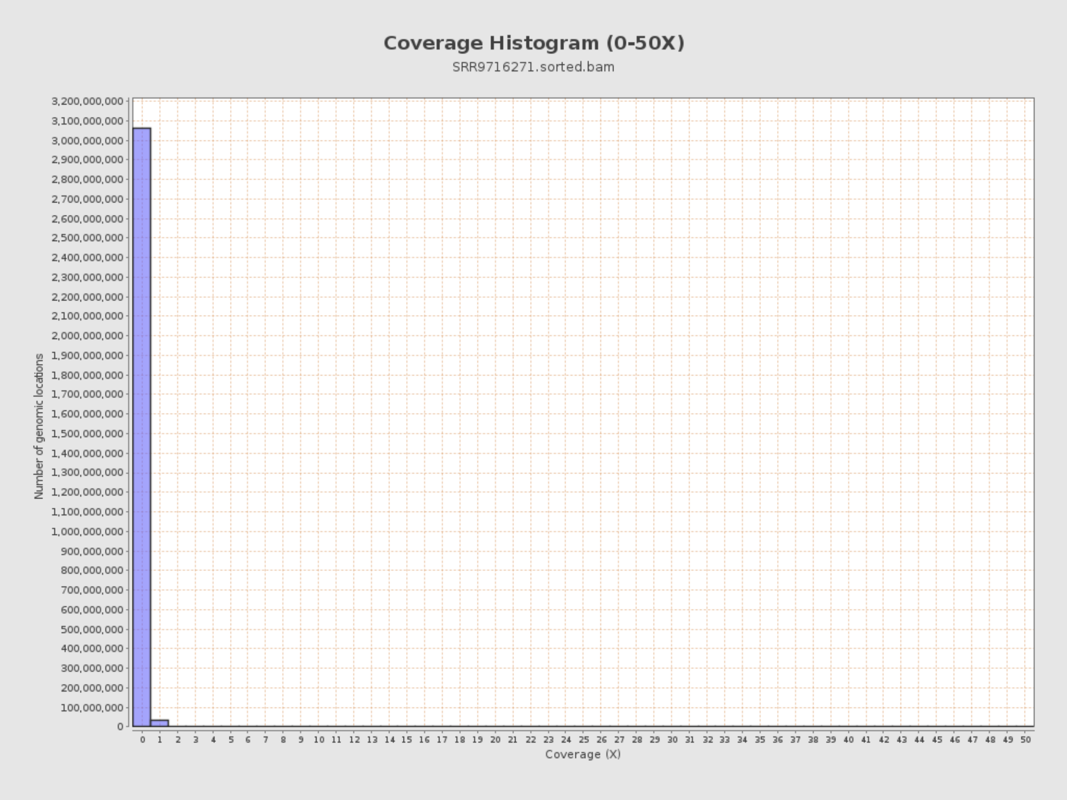
3. Results : Coverage across reference



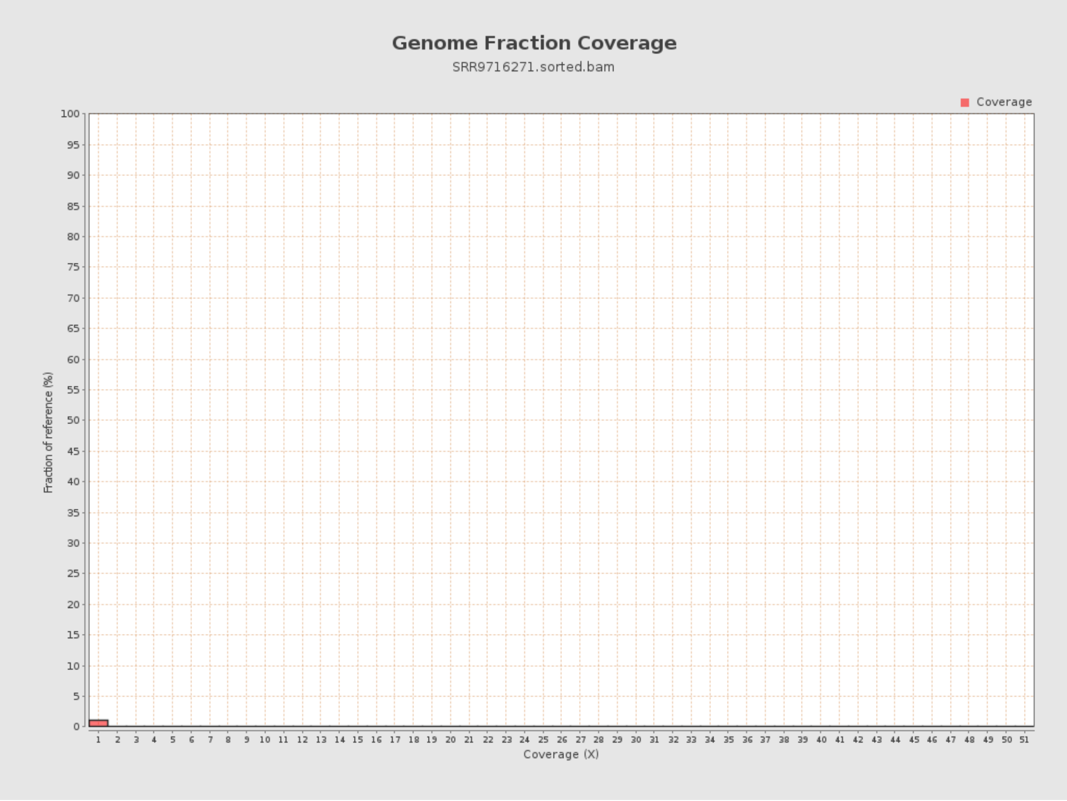
4. Results : Coverage Histogram



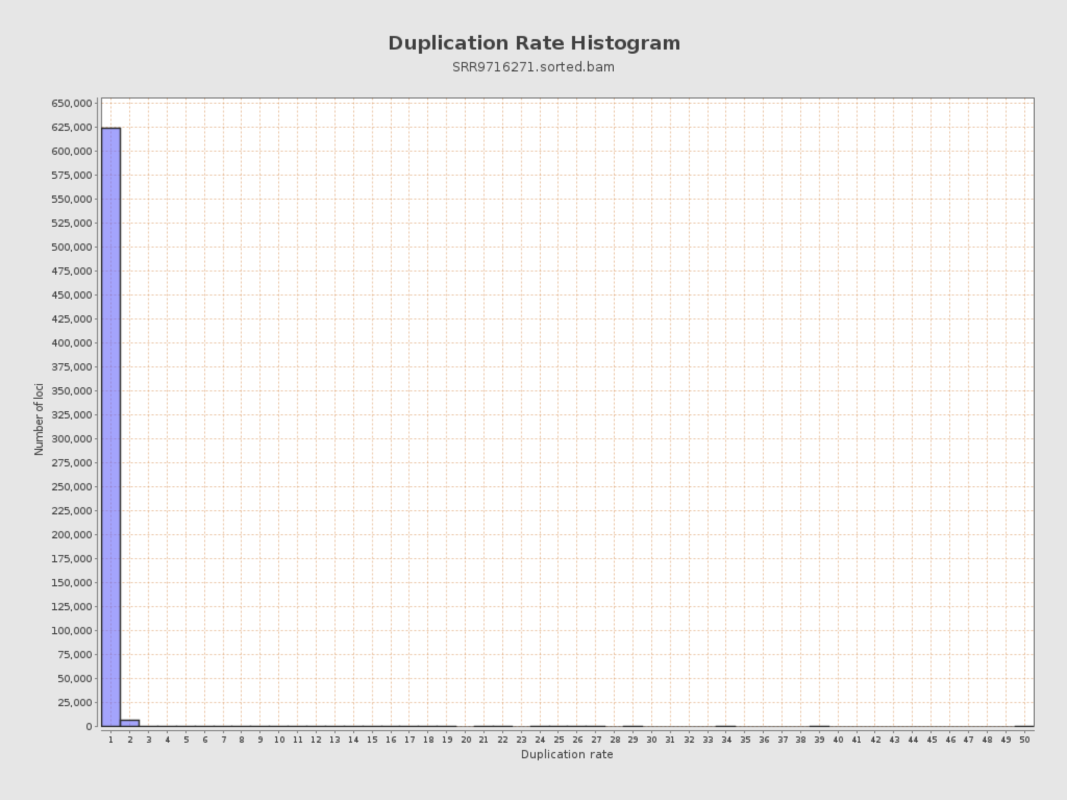
5. Results : Coverage Histogram (0-50X)



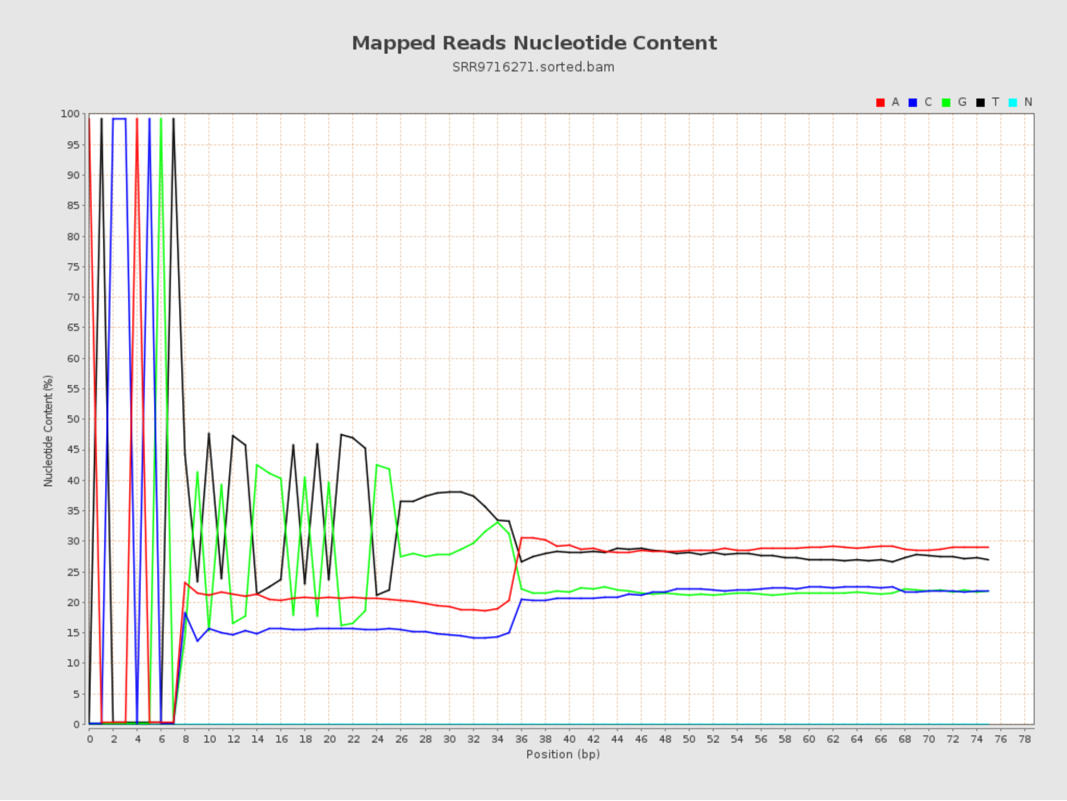
6. Results : Genome Fraction Coverage



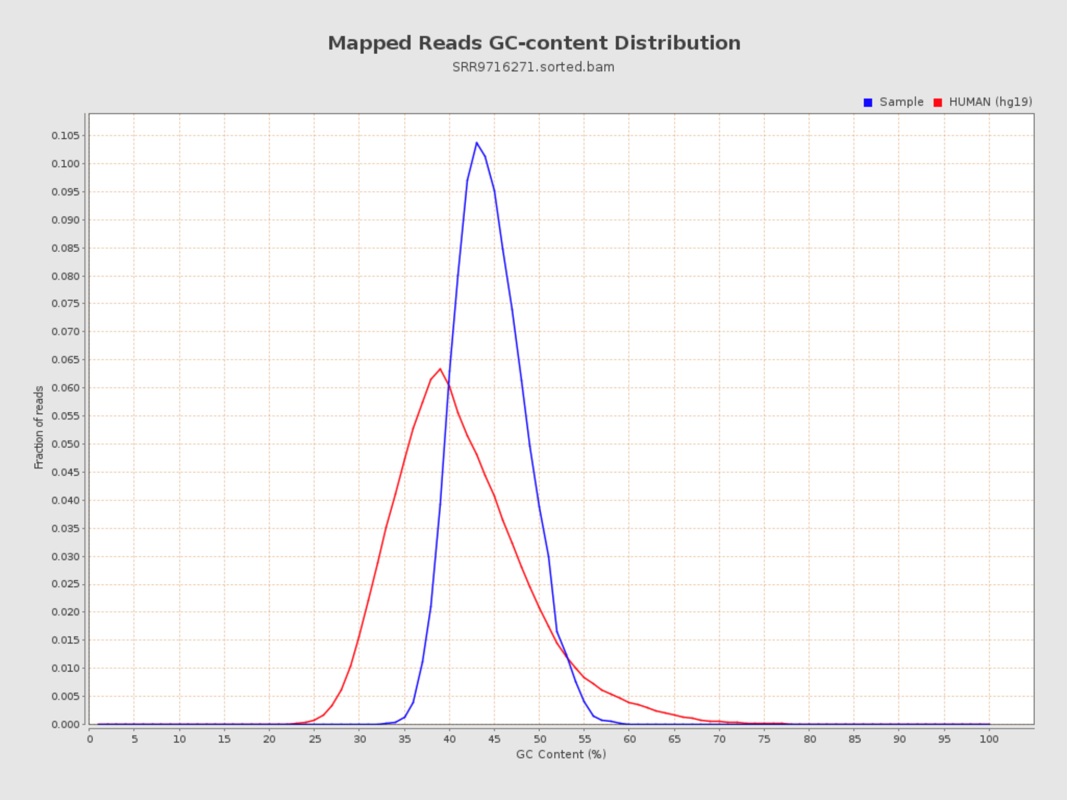
7. Results : Duplication Rate Histogram



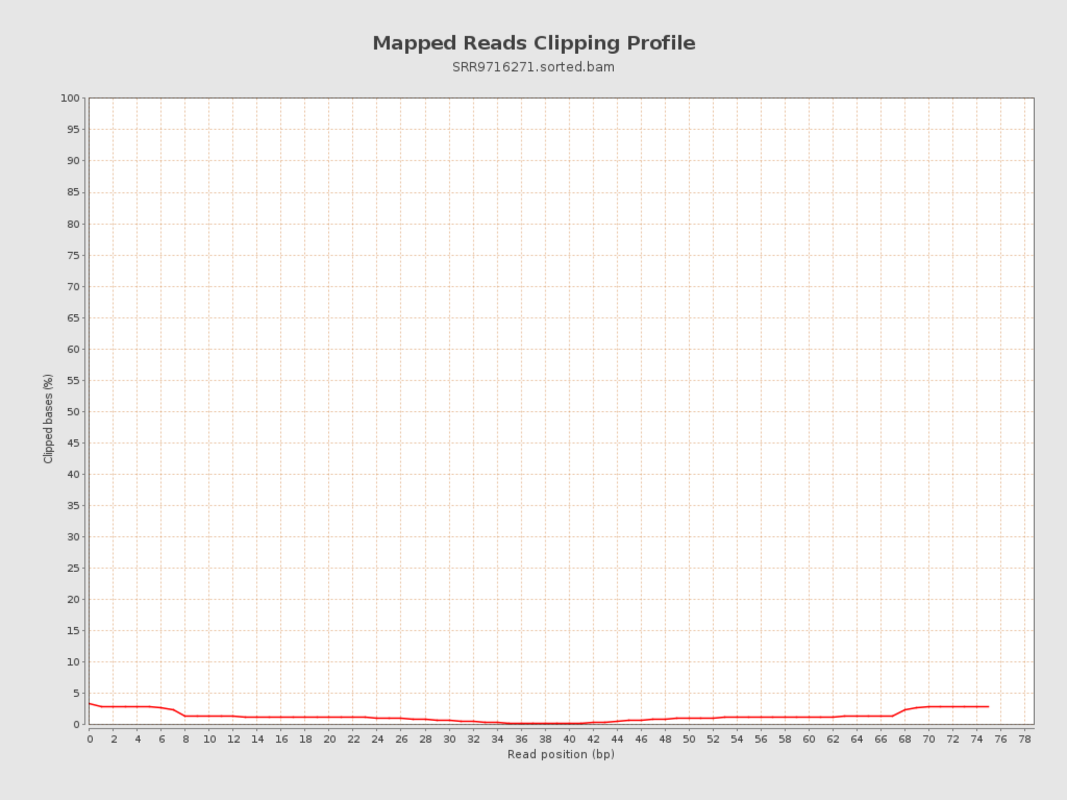
8. Results : Mapped Reads Nucleotide Content



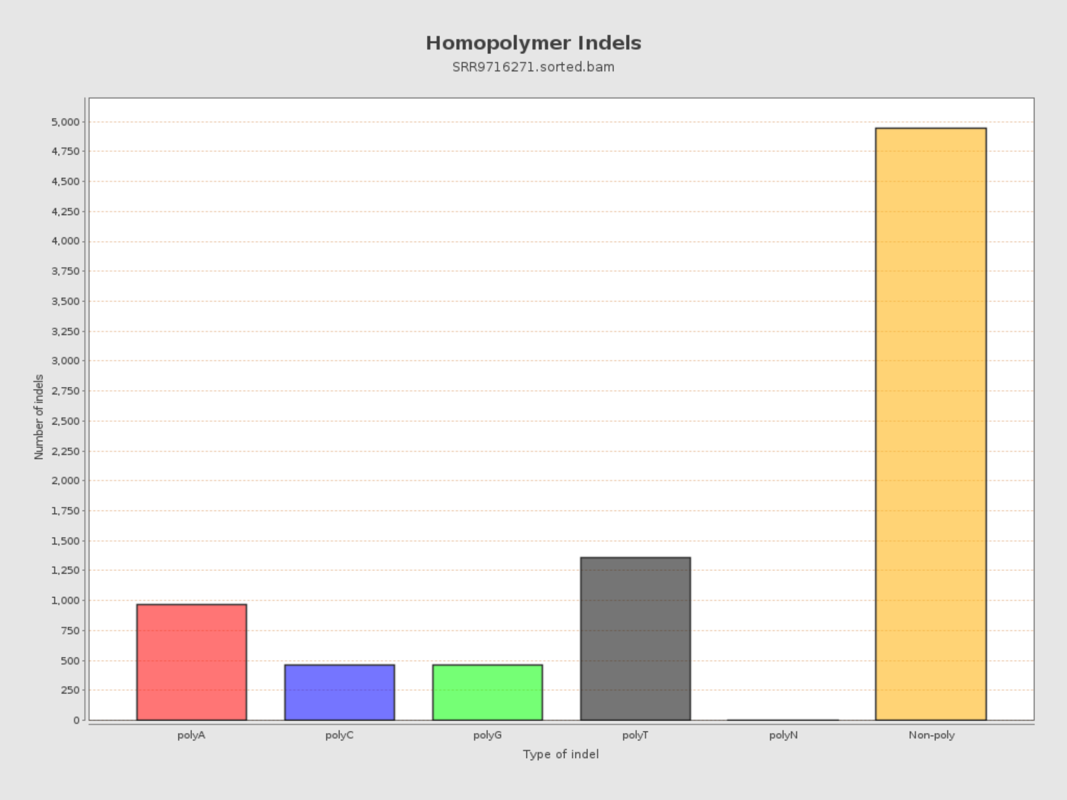
9. Results : Mapped Reads GC-content Distribution



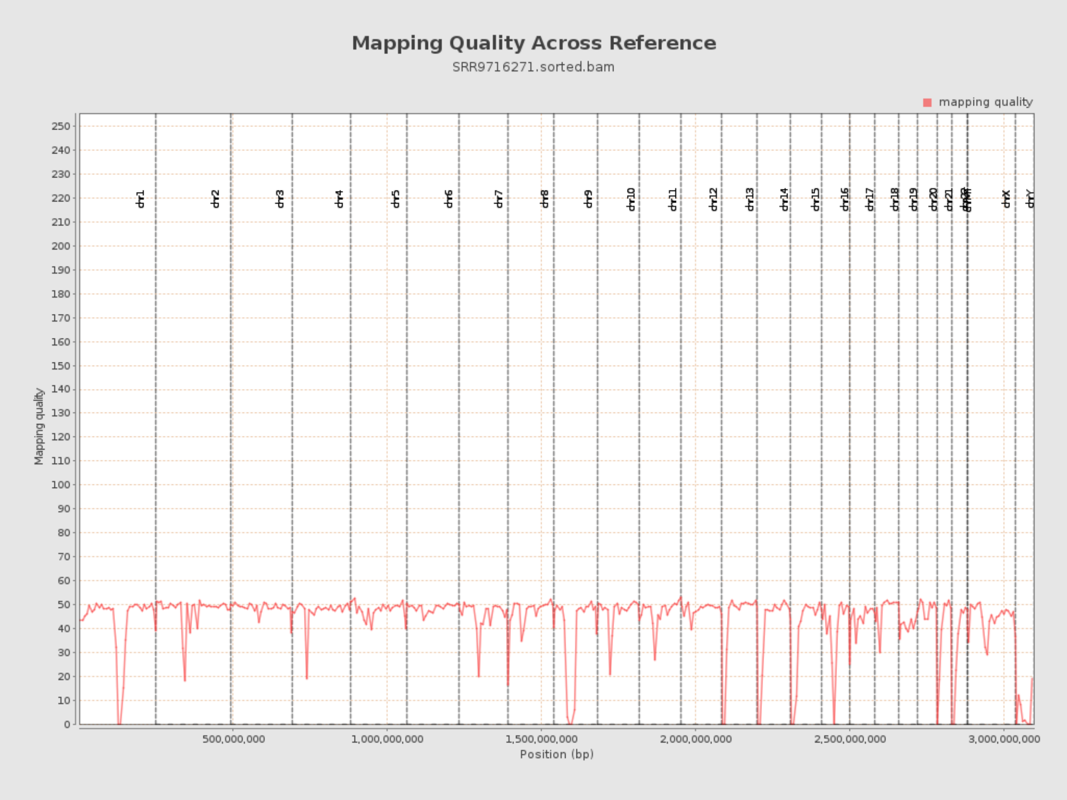
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram