Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 01:36:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716229.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_SRR9716229 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716229.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 01:36:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716229.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,105,361
Mapped reads	991,766 / 89.72%
Unmapped reads	113,595 / 10.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,229 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	28,983 / 2.62%
Duplication rate	2.2%
Clipped reads	993,345 / 89.87%

2.2. ACGT Content

Number/percentage of A's	13,880,350 / 24.44%
Number/percentage of C's	10,082,626 / 17.75%
Number/percentage of T's	18,600,421 / 32.75%
Number/percentage of G's	14,230,323 / 25.06%
Number/percentage of N's	953 / 0%
GC Percentage	42.81%

2.3. Coverage

Mean	0.0184

Standard Deviation	0.1924

2.4. Mapping Quality

Mean Mapping Quality	44.55

2.5. Mismatches and indels

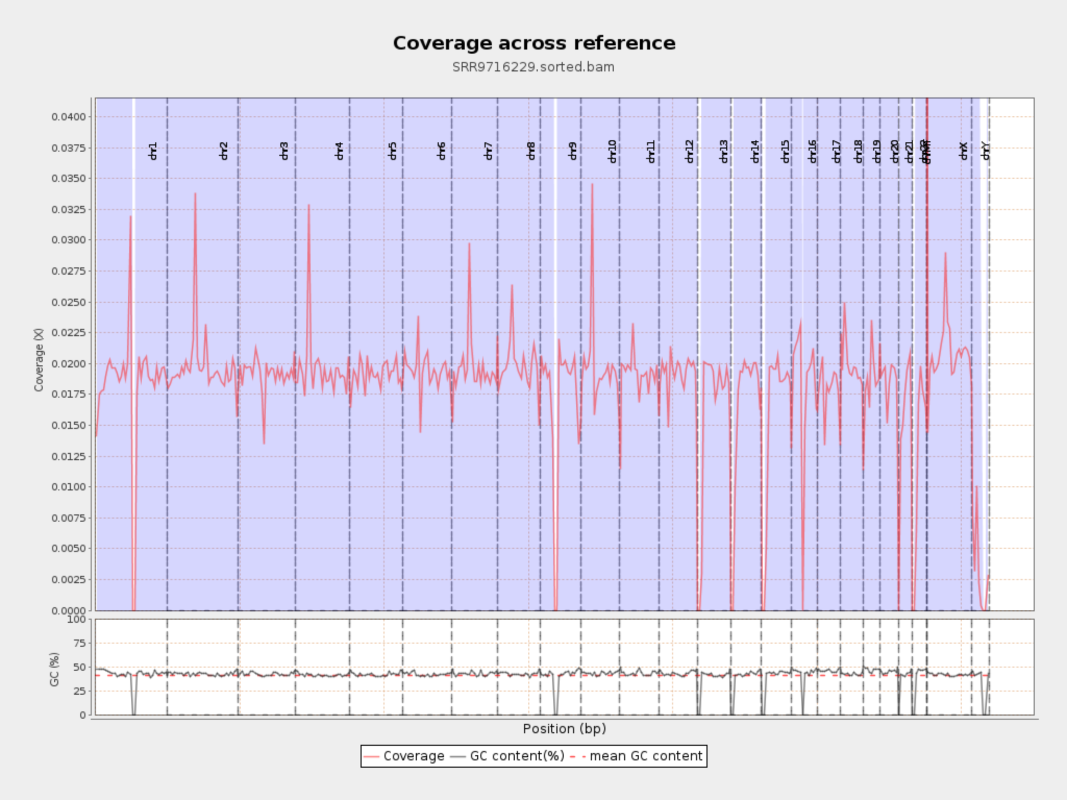
General error rate	0.56%
Mismatches	308,968
Insertions	3,889
Mapped reads with at least one insertion	0.39%
Deletions	9,659
Mapped reads with at least one deletion	0.97%
Homopolymer indels	43.16%

2.6. Chromosome stats

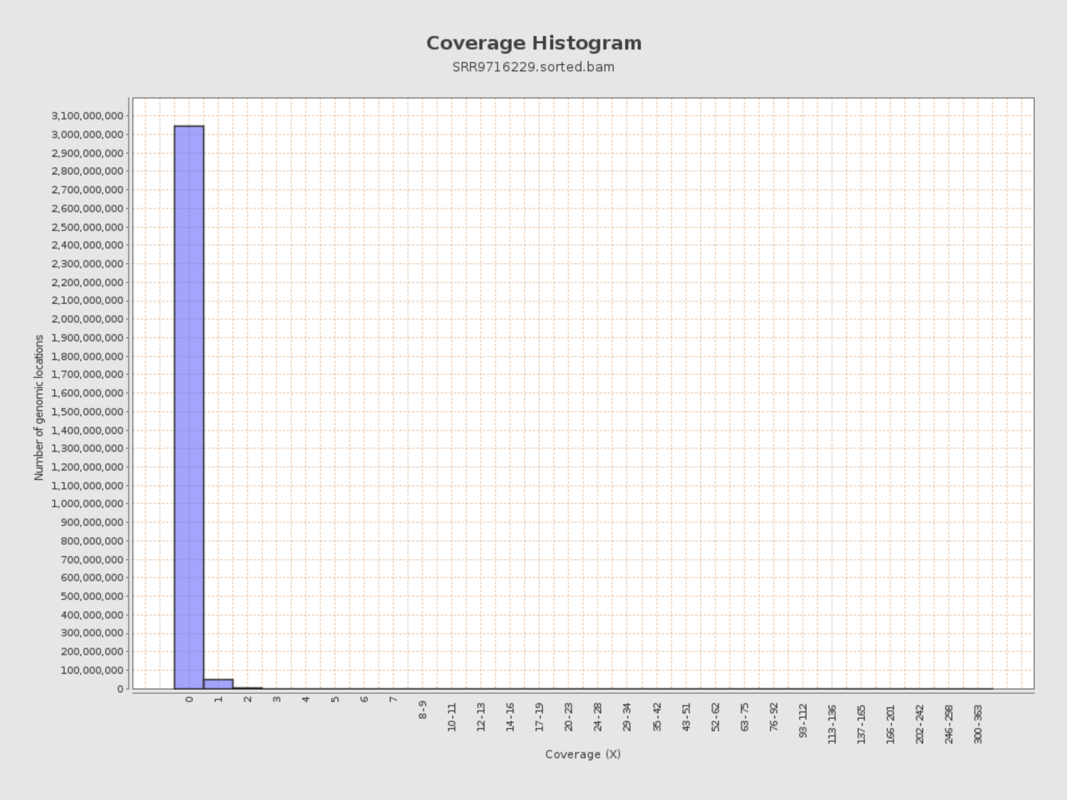
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4533050	0.0182	0.3224
chr2	243199373	4817136	0.0198	0.2065
chr3	198022430	3789072	0.0191	0.146
chr4	191154276	3761831	0.0197	0.1599
chr5	180915260	3472696	0.0192	0.1468
chr6	171115067	3316784	0.0194	0.1573
chr7	159138663	3128691	0.0197	0.2143

chr8	146364022	2901299	0.0198	0.2117
chr9	141213431	2383302	0.0169	0.1916
chr10	135534747	2686107	0.0198	0.1952
chr11	135006516	2598308	0.0192	0.1844
chr12	133851895	2573728	0.0192	0.1494
chr13	115169878	1817464	0.0158	0.1325
chr14	107349540	1725497	0.0161	0.1454
chr15	102531392	1589716	0.0155	0.1323
chr16	90354753	1609117	0.0178	0.1506
chr17	81195210	1454163	0.0179	0.1477
chr18	78077248	1561569	0.02	0.3149
chr19	59128983	1112778	0.0188	0.249
chr20	63025520	1161773	0.0184	0.1478
chr21	48129895	748301	0.0155	0.1409
chr22	51304566	627679	0.0122	0.1162
chrMT	16571	2712	0.1637	0.4336
chrX	155270560	3252739	0.0209	0.1715
chrY	59373566	185407	0.0031	0.0832

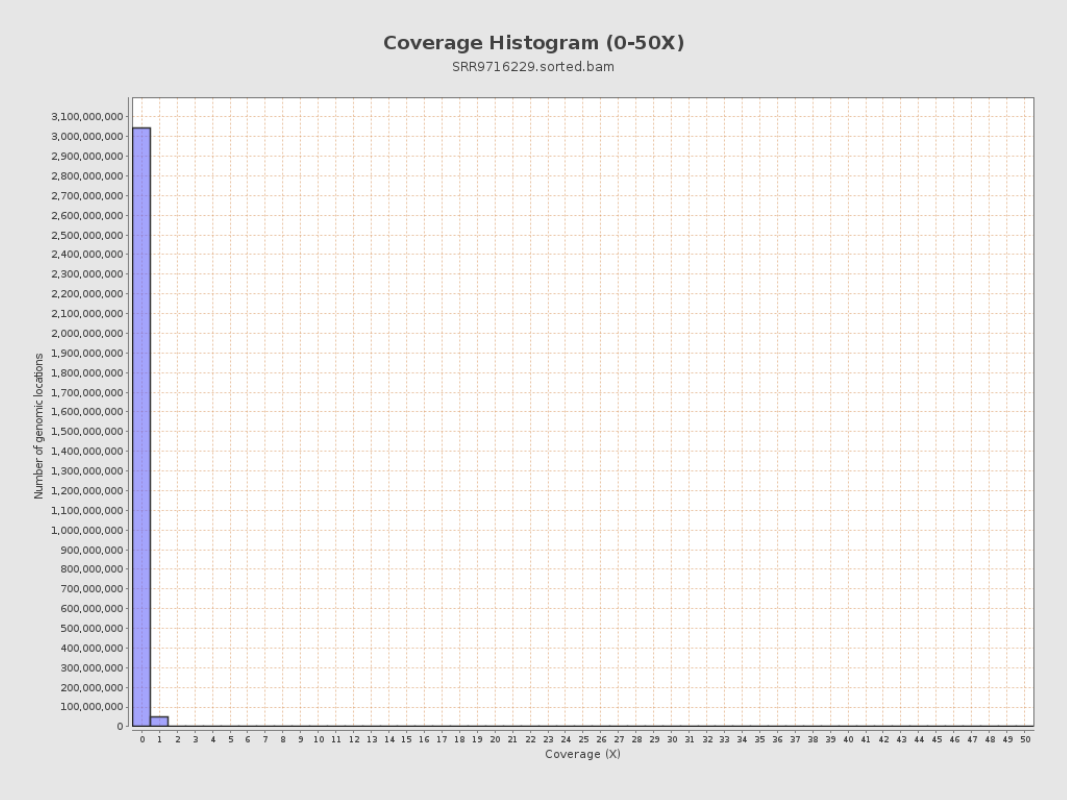
3. Results : Coverage across reference



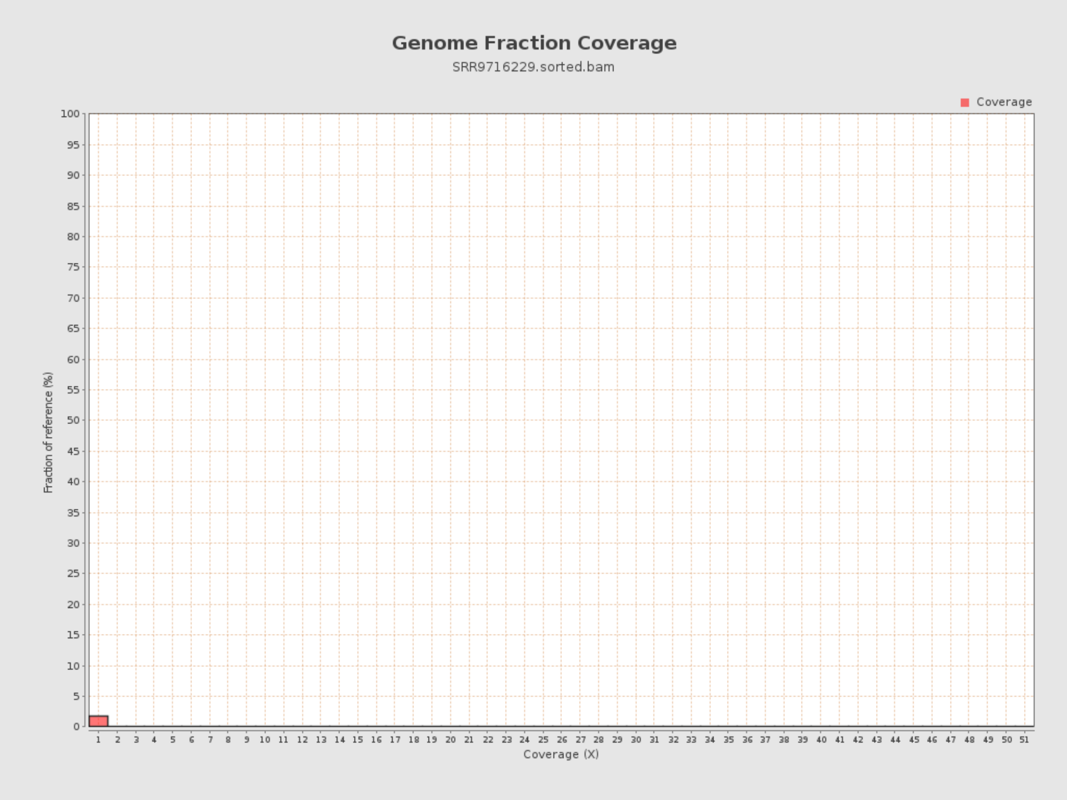
4. Results : Coverage Histogram



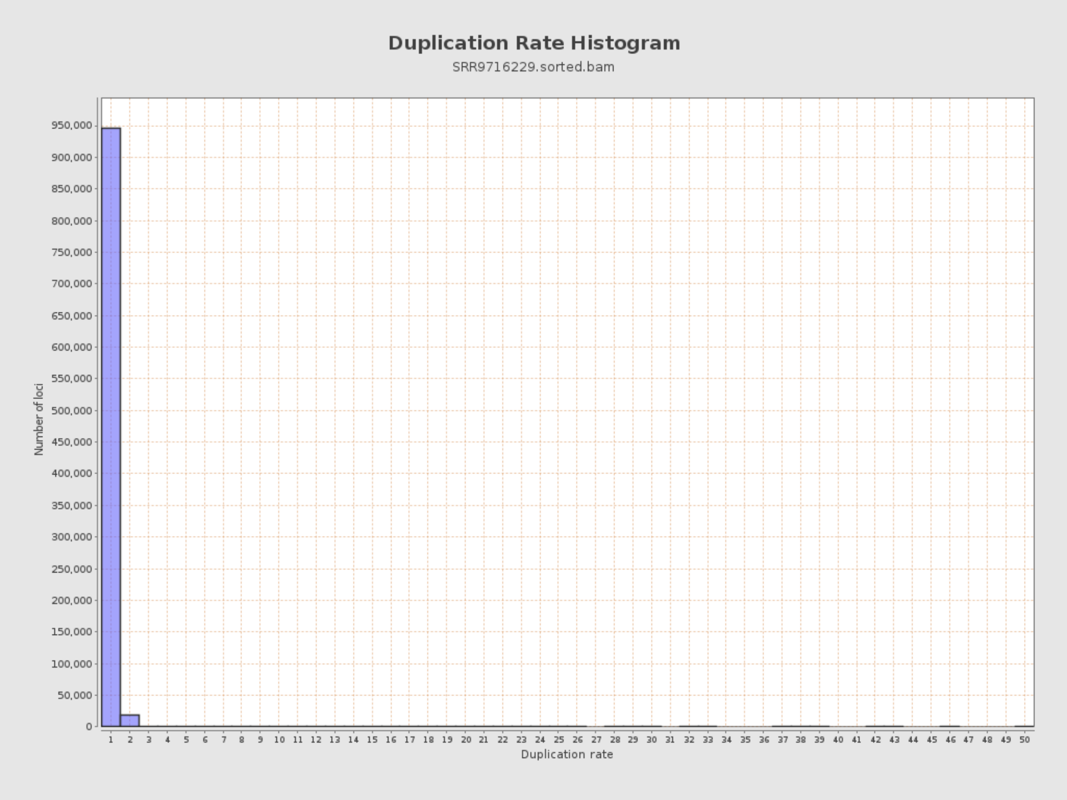
5. Results : Coverage Histogram (0-50X)



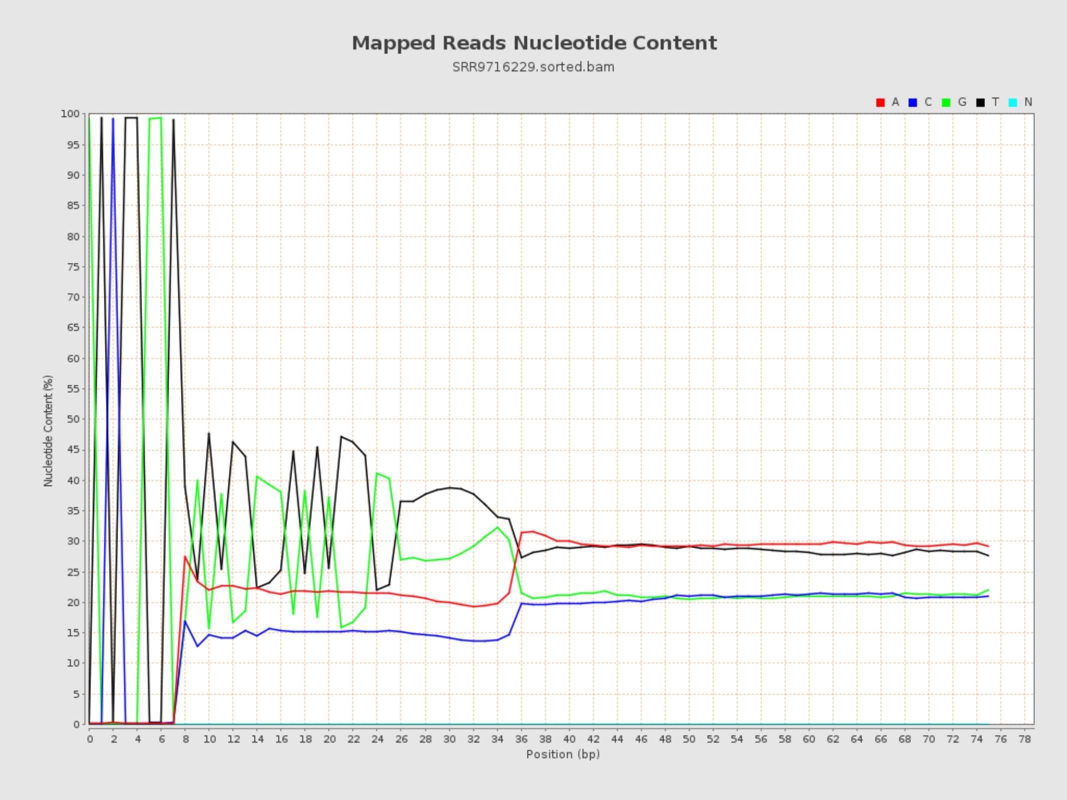
6. Results : Genome Fraction Coverage



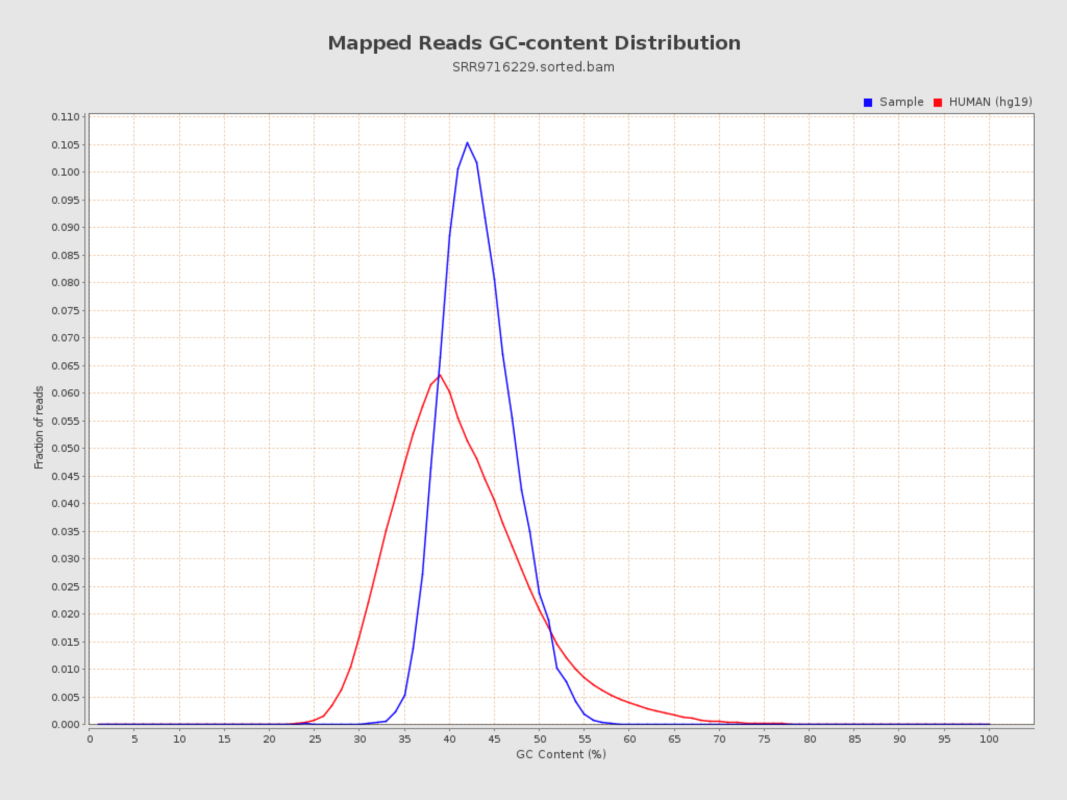
7. Results : Duplication Rate Histogram



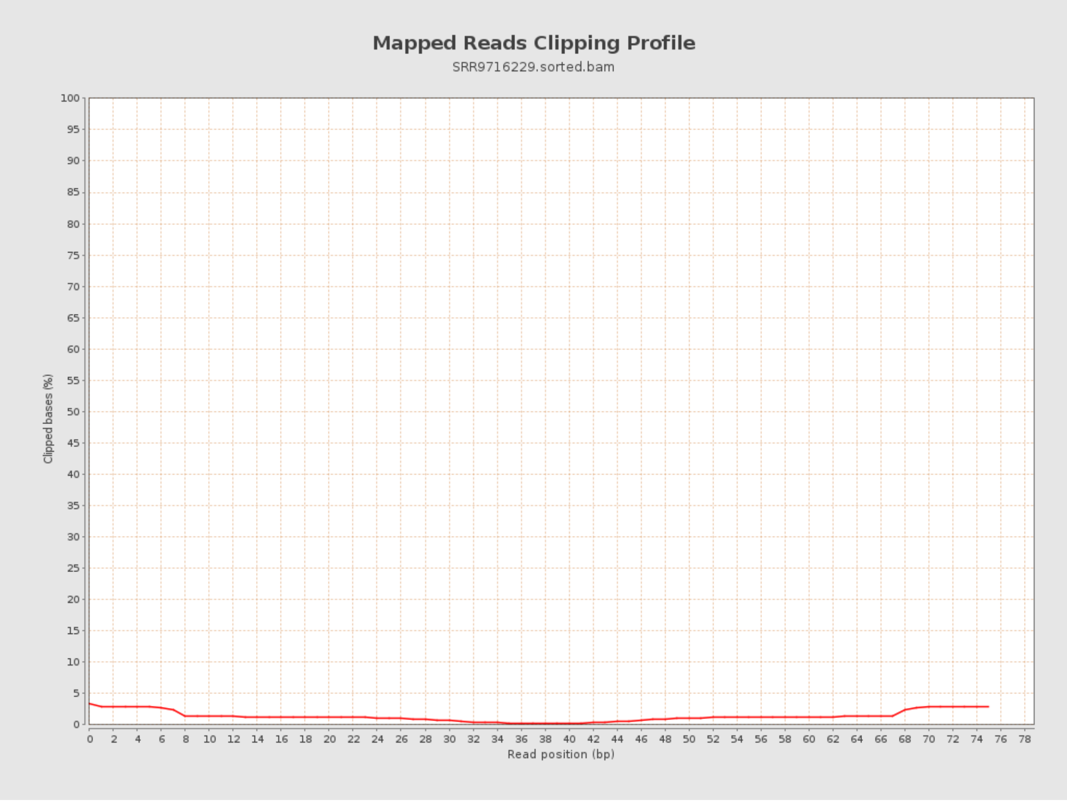
8. Results : Mapped Reads Nucleotide Content



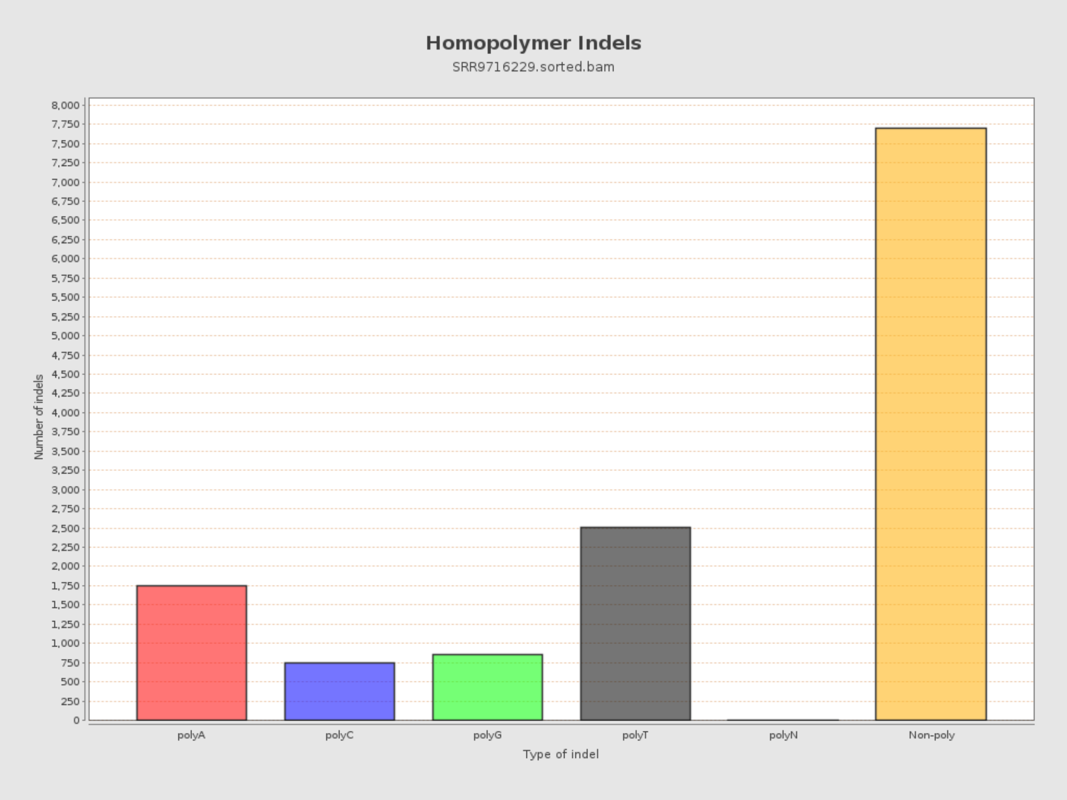
9. Results : Mapped Reads GC-content Distribution



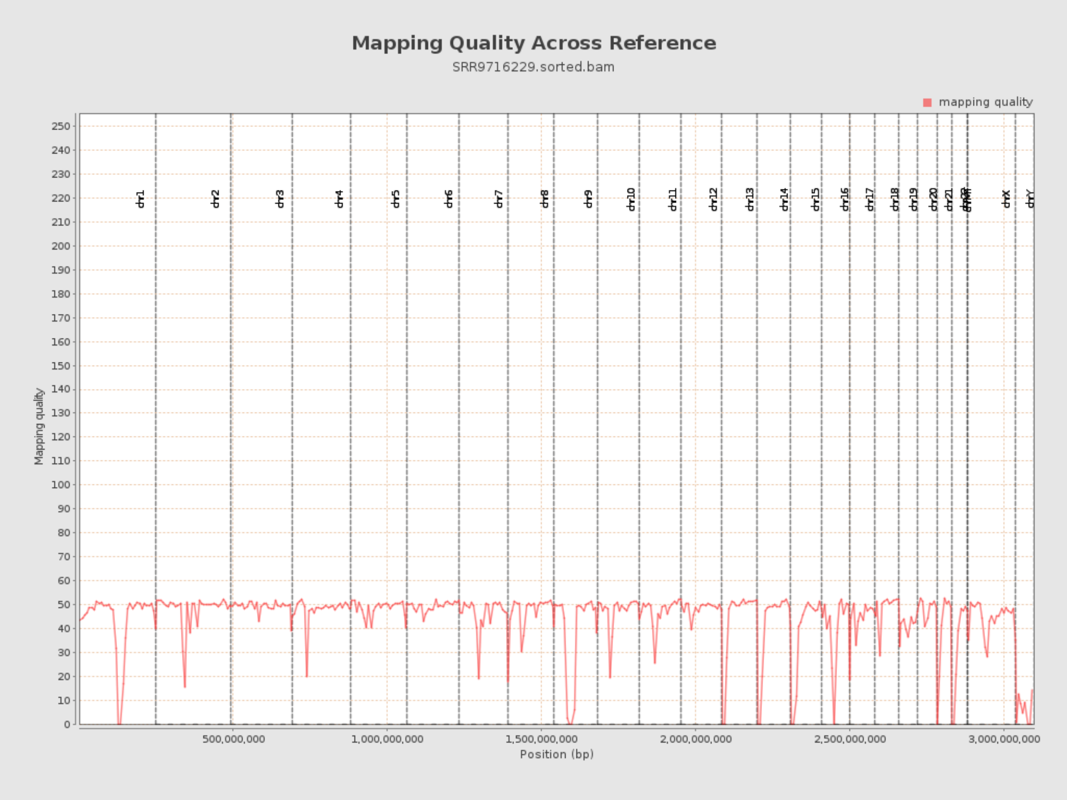
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram