Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 09:20:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716365.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_SRR9716365 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716365.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 09:20:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716365.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	746,071
Mapped reads	627,803 / 84.15%
Unmapped reads	118,268 / 15.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,626 / 0.22%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	11,171 / 1.5%
Duplication rate	1.23%
Clipped reads	628,448 / 84.23%

2.2. ACGT Content

Number/percentage of A's	8,324,253 / 23.87%
Number/percentage of C's	6,932,302 / 19.88%
Number/percentage of T's	10,833,670 / 31.06%
Number/percentage of G's	8,786,375 / 25.19%
Number/percentage of N's	919 / 0%
GC Percentage	45.07%

2.3. Coverage

Mean	0.0113

Standard Deviation	0.1261

2.4. Mapping Quality

Mean Mapping Quality	39.95

2.5. Mismatches and indels

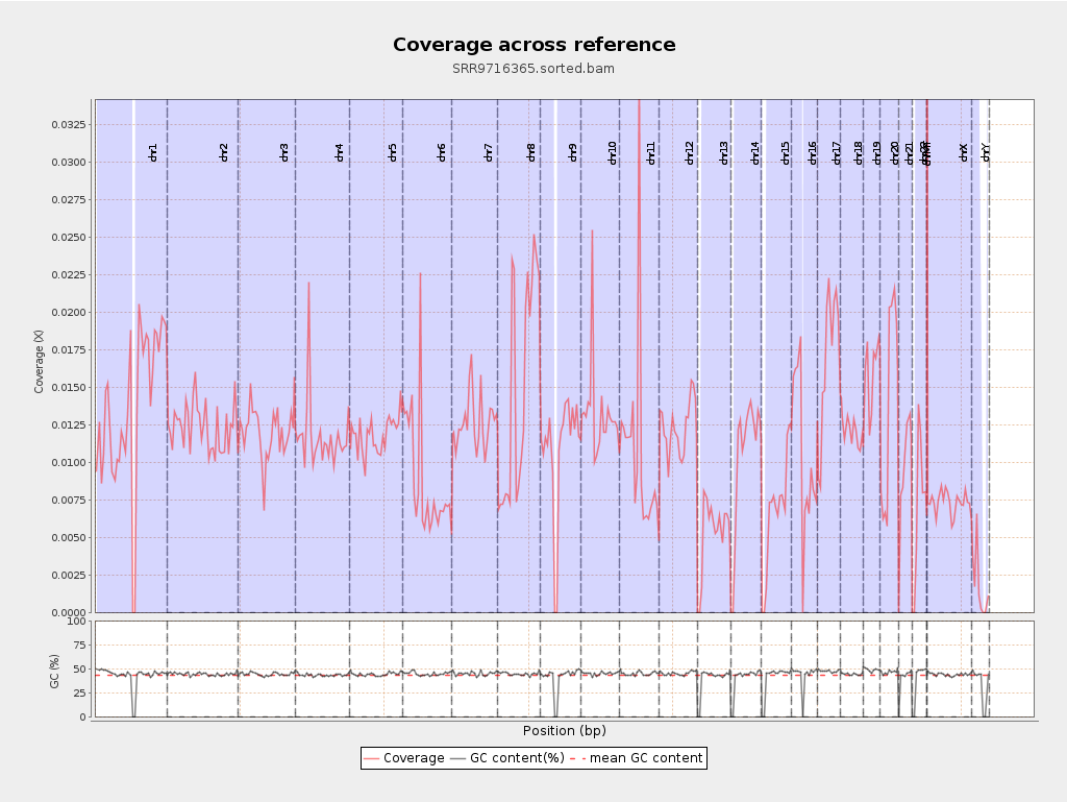
General error rate	0.54%
Mismatches	185,077
Insertions	2,349
Mapped reads with at least one insertion	0.37%
Deletions	5,908
Mapped reads with at least one deletion	0.93%
Homopolymer indels	37.88%

2.6. Chromosome stats

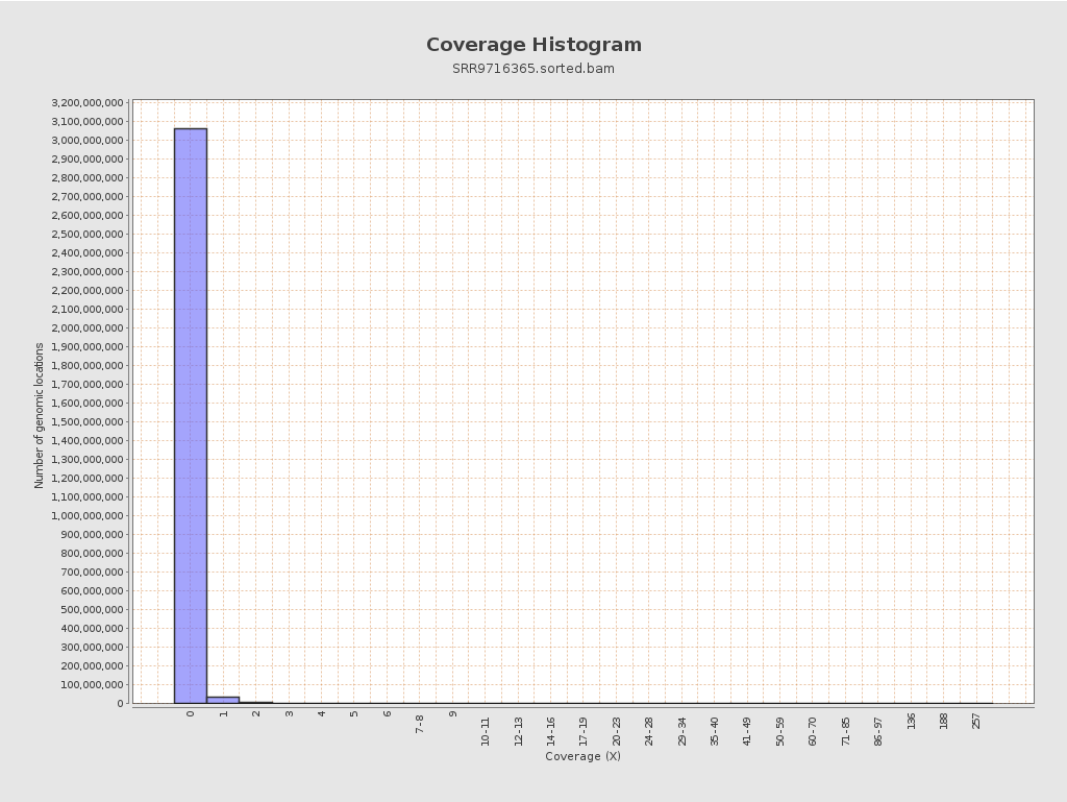
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3413714	0.0137	0.1487
chr2	243199373	3007946	0.0124	0.1628
chr3	198022430	2367970	0.012	0.119
chr4	191154276	2246848	0.0118	0.1226
chr5	180915260	2153944	0.0119	0.115
chr6	171115067	1512839	0.0088	0.1019
chr7	159138663	2014607	0.0127	0.1371

chr8	146364022	2183293	0.0149	0.1353
chr9	141213431	1526616	0.0108	0.1166
chr10	135534747	1797667	0.0133	0.1679
chr11	135006516	1467204	0.0109	0.1265
chr12	133851895	1645901	0.0123	0.1174
chr13	115169878	611337	0.0053	0.0771
chr14	107349540	1113610	0.0104	0.1101
chr15	102531392	687776	0.0067	0.0865
chr16	90354753	938396	0.0104	0.114
chr17	81195210	1366920	0.0168	0.141
chr18	78077248	943796	0.0121	0.1364
chr19	59128983	934845	0.0158	0.1515
chr20	63025520	872885	0.0138	0.1264
chr21	48129895	464369	0.0096	0.1079
chr22	51304566	369890	0.0072	0.0913
chrMT	16571	1264	0.0763	0.2702
chrX	155270560	1139344	0.0073	0.0954
chrY	59373566	104154	0.0018	0.0617

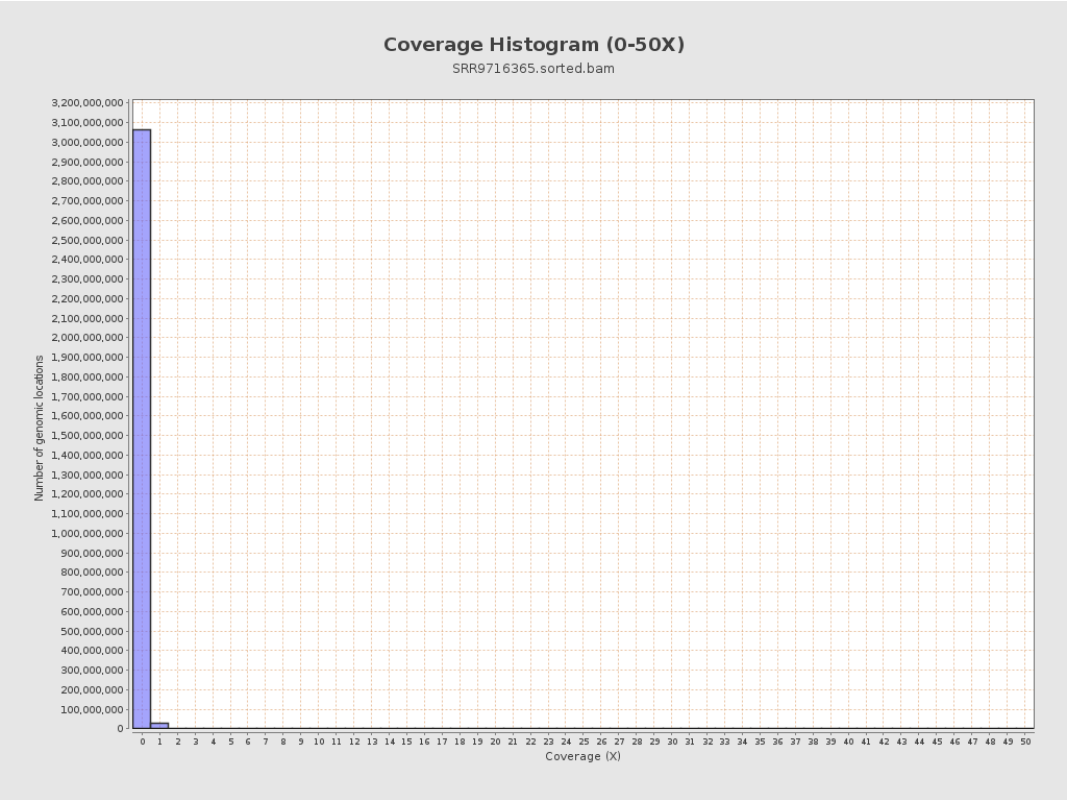
3. Results : Coverage across reference



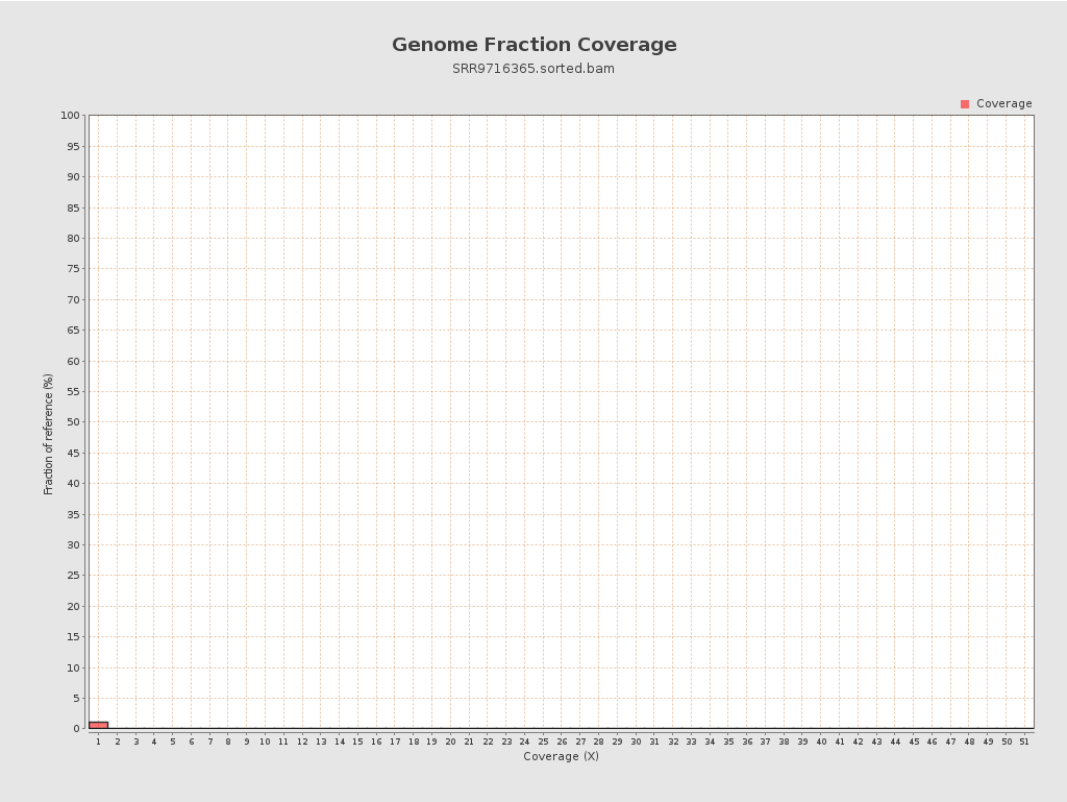
4. Results : Coverage Histogram



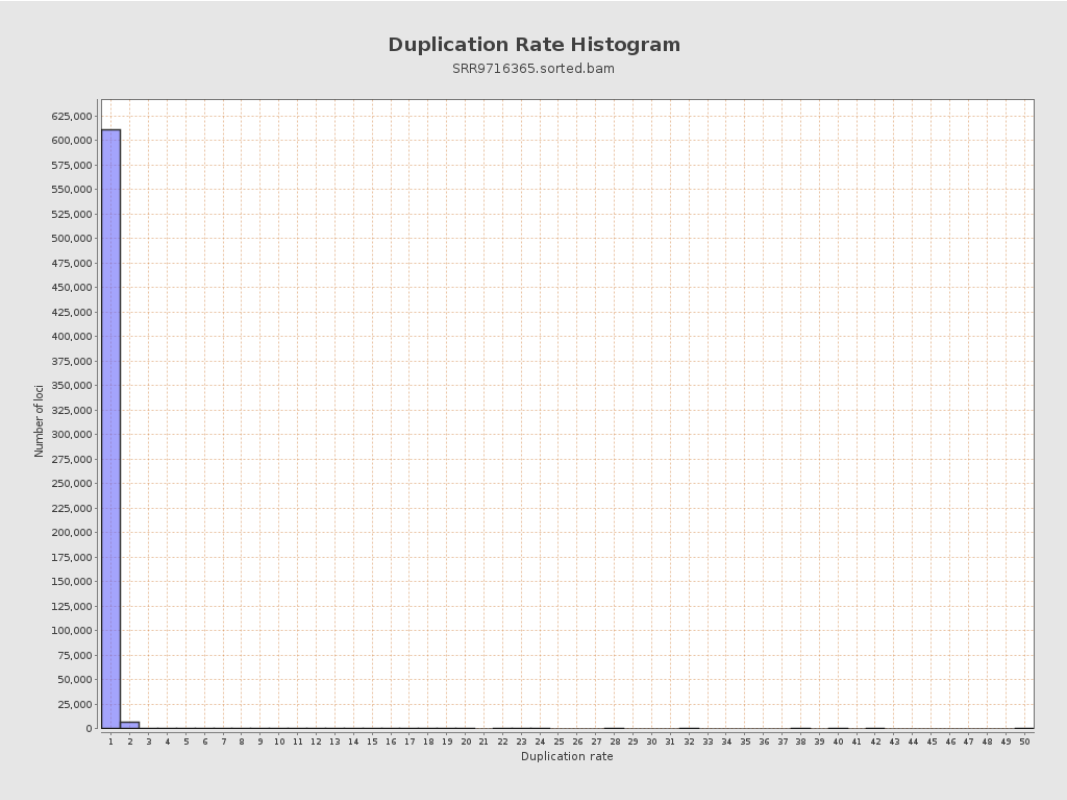
5. Results : Coverage Histogram (0-50X)



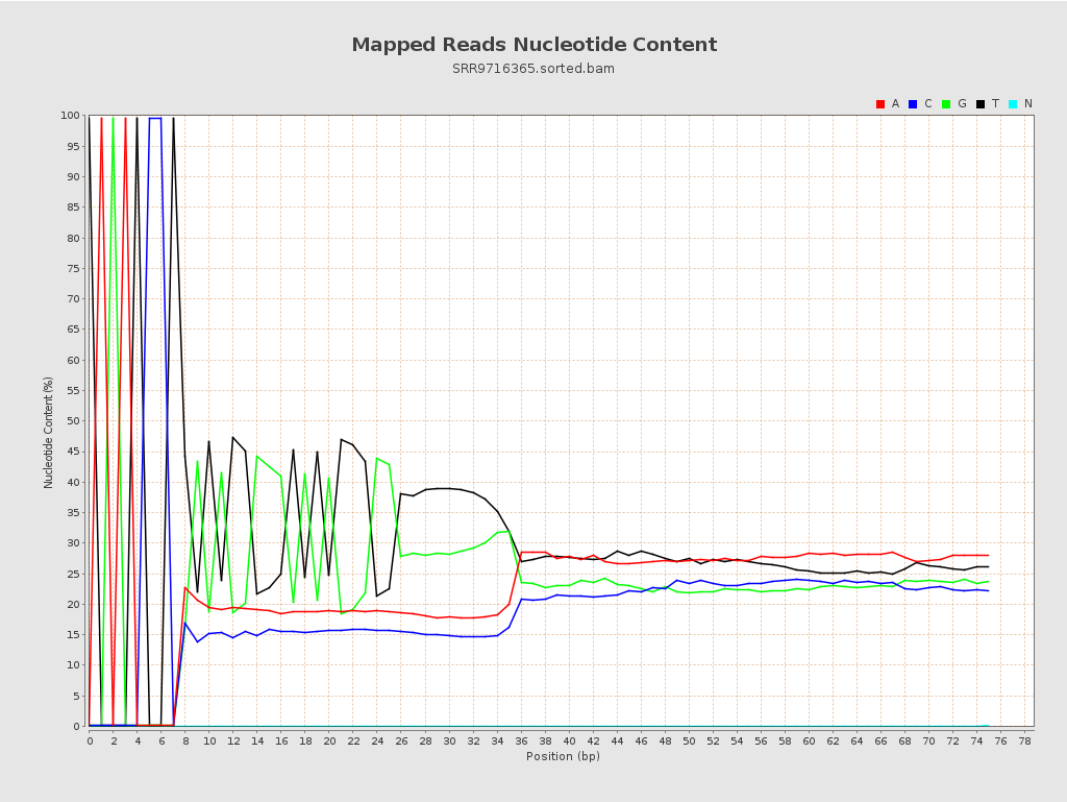
6. Results : Genome Fraction Coverage



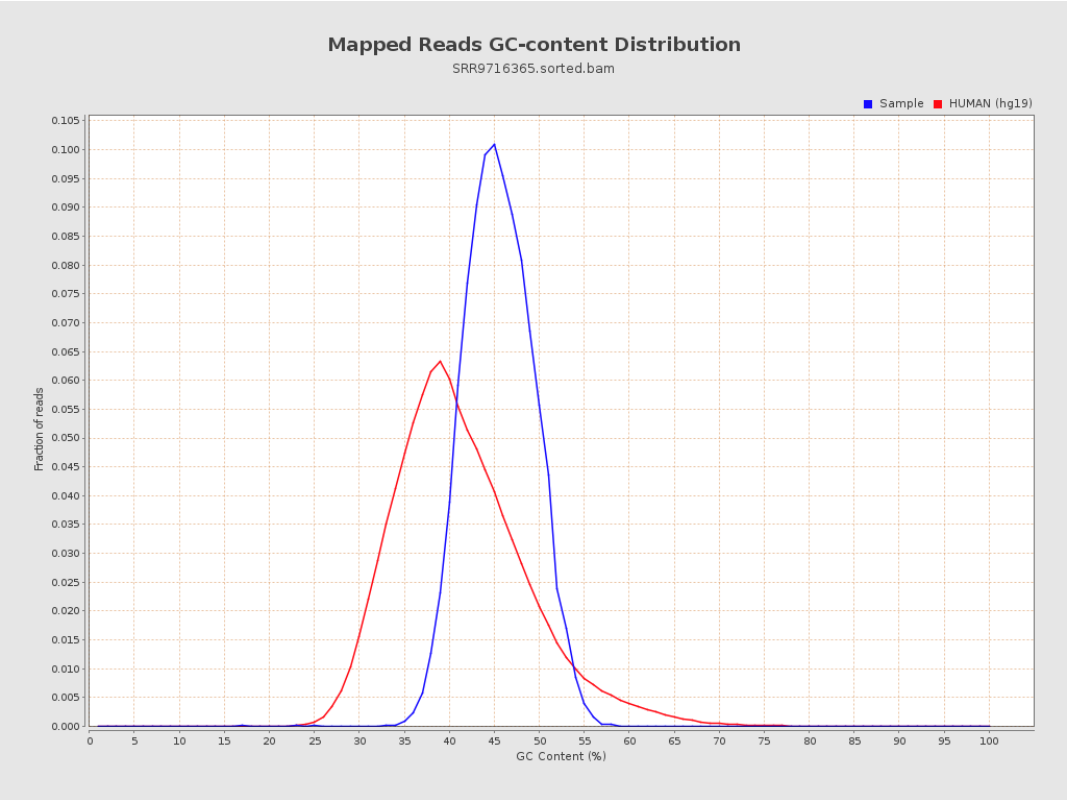
7. Results : Duplication Rate Histogram



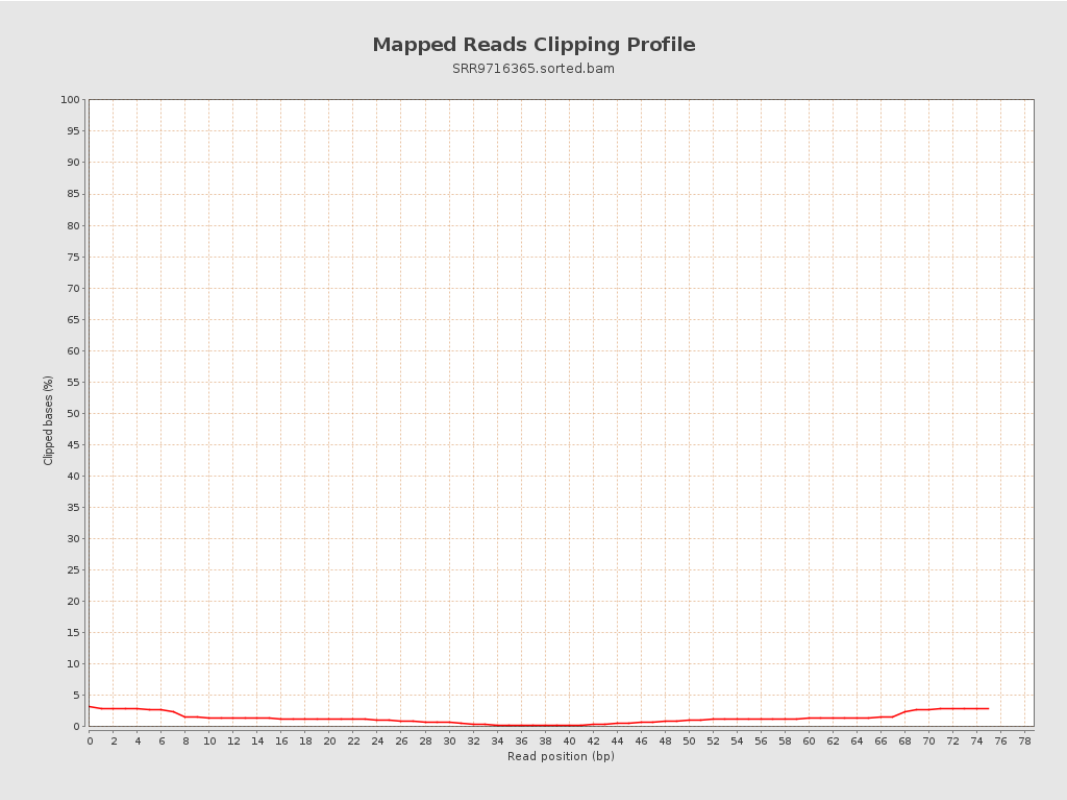
8. Results : Mapped Reads Nucleotide Content



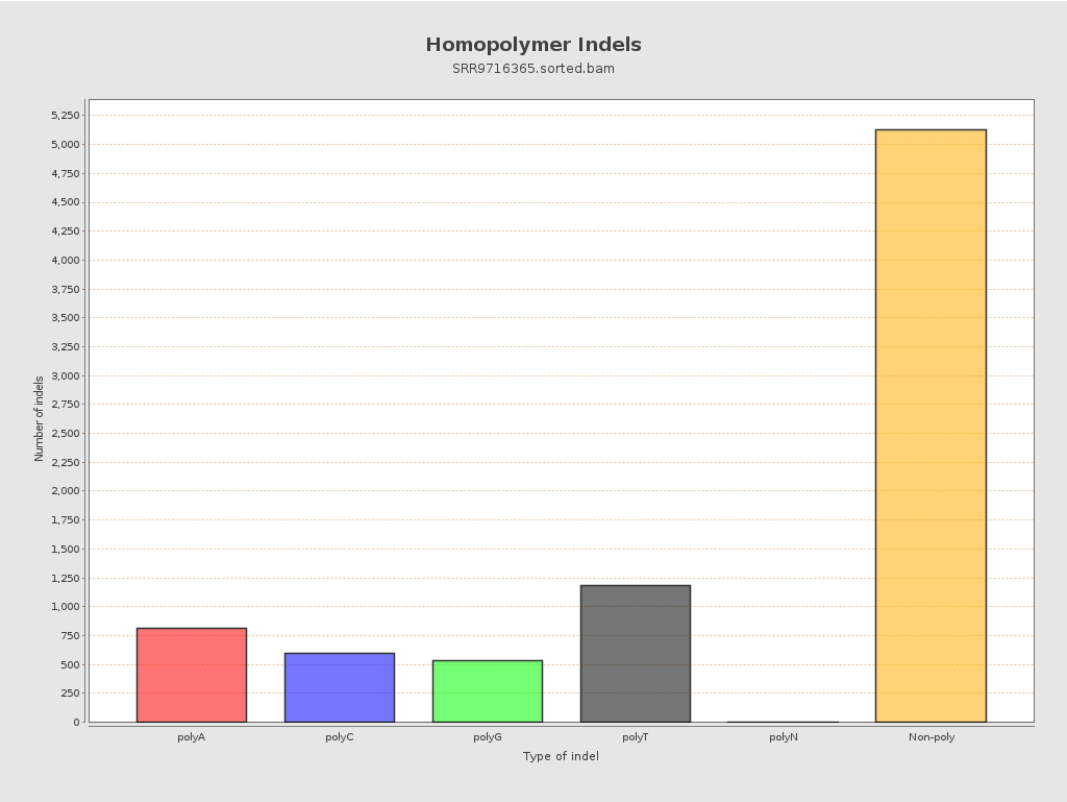
9. Results : Mapped Reads GC-content Distribution



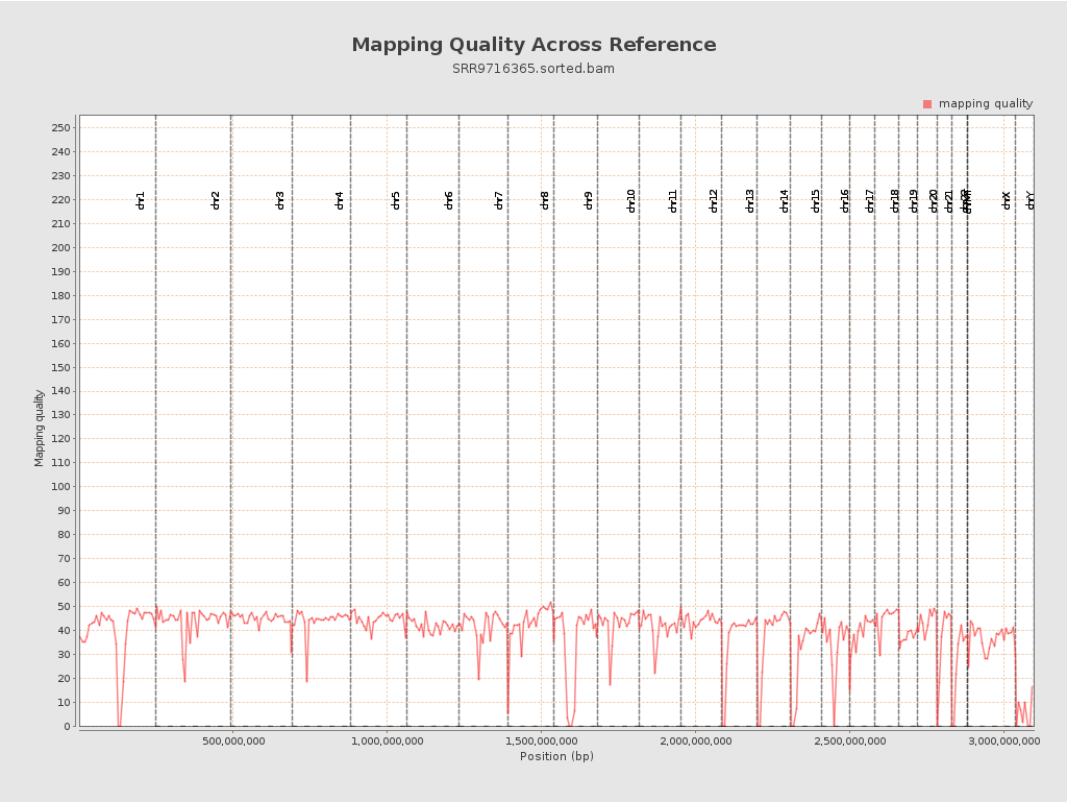
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram