Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 18:39:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716920.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_SRR9716920 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716920.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 18:39:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716920.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,041,351
Mapped reads	835,456 / 80.23%
Unmapped reads	205,895 / 19.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,637 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	15,913 / 1.53%
Duplication rate	1.34%
Clipped reads	837,216 / 80.4%

2.2. ACGT Content

Number/percentage of A's	10,196,298 / 22.13%
Number/percentage of C's	9,486,032 / 20.59%
Number/percentage of T's	13,922,770 / 30.22%
Number/percentage of G's	12,470,700 / 27.06%
Number/percentage of N's	1,178 / 0%
GC Percentage	47.65%

2.3. Coverage

Mean	0.0149

Standard Deviation	0.149

2.4. Mapping Quality

Mean Mapping Quality	37.95

2.5. Mismatches and indels

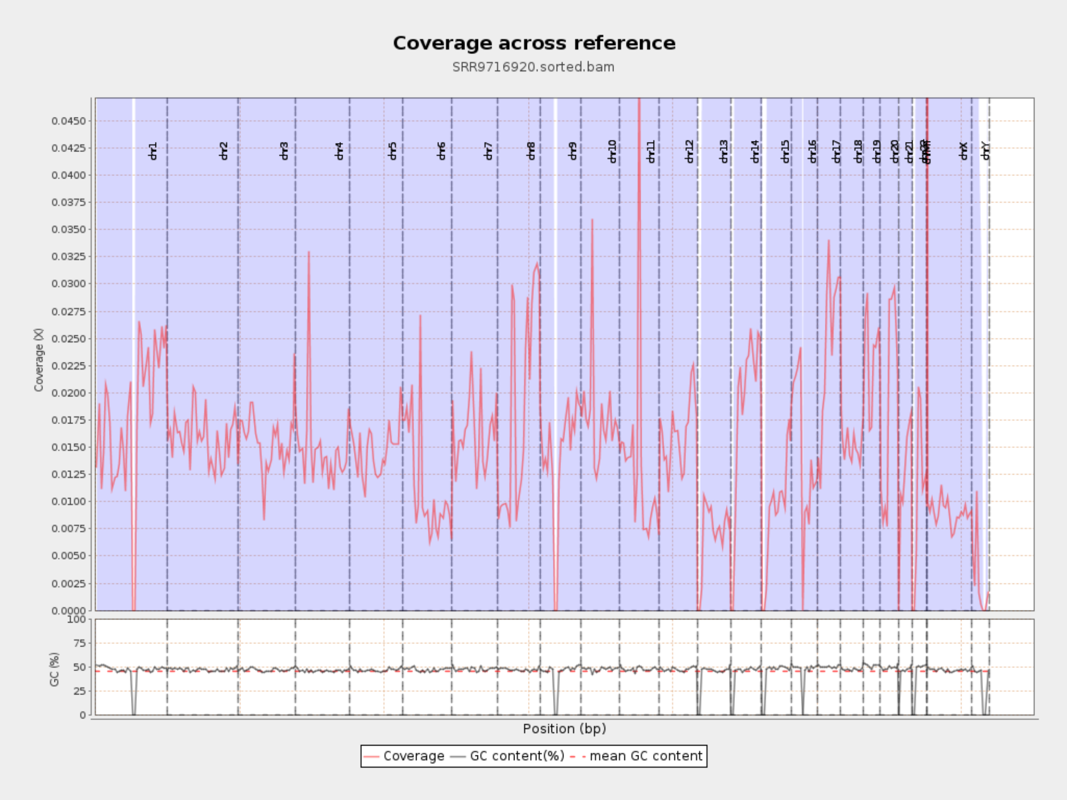
General error rate	0.56%
Mismatches	249,665
Insertions	3,758
Mapped reads with at least one insertion	0.45%
Deletions	7,754
Mapped reads with at least one deletion	0.92%
Homopolymer indels	34.31%

2.6. Chromosome stats

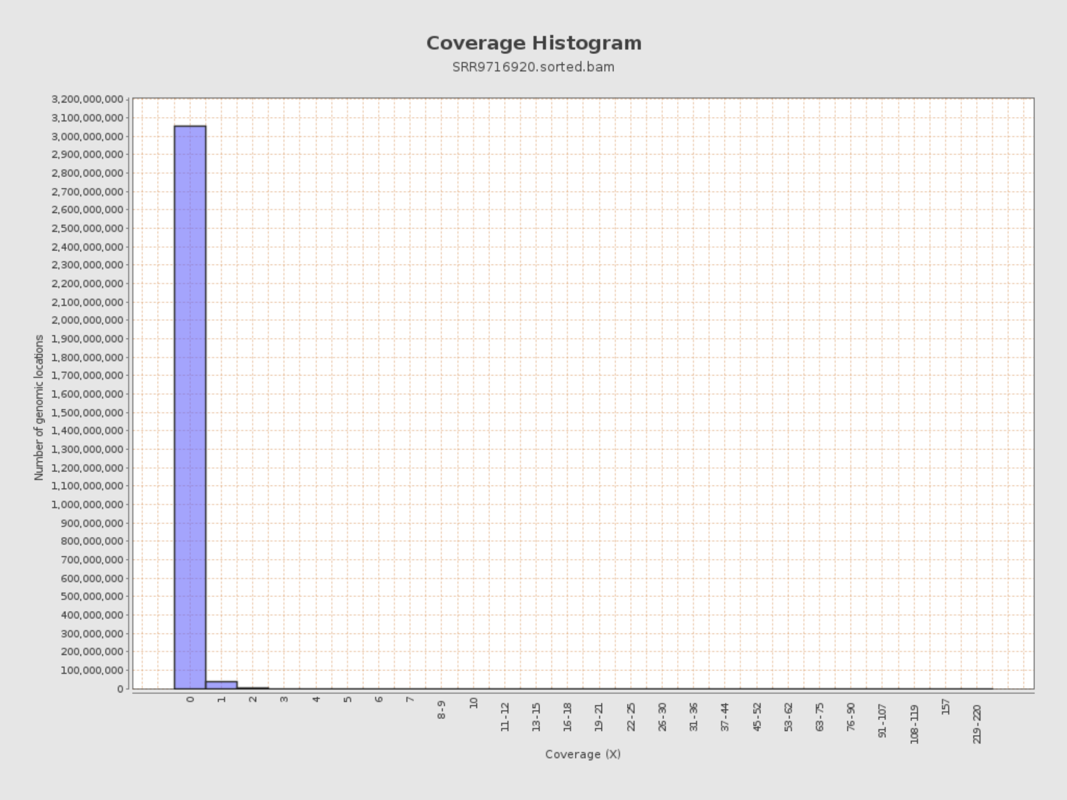
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4412188	0.0177	0.1716
chr2	243199373	3857993	0.0159	0.1803
chr3	198022430	3052479	0.0154	0.1377
chr4	191154276	2865711	0.015	0.1525
chr5	180915260	2669856	0.0148	0.1311
chr6	171115067	1979454	0.0116	0.1175
chr7	159138663	2605322	0.0164	0.1586

chr8	146364022	2714285	0.0185	0.1532
chr9	141213431	2000898	0.0142	0.1361
chr10	135534747	2422087	0.0179	0.2115
chr11	135006516	1881230	0.0139	0.1444
chr12	133851895	2173897	0.0162	0.1365
chr13	115169878	800293	0.0069	0.0922
chr14	107349540	1992331	0.0186	0.1495
chr15	102531392	938359	0.0092	0.1052
chr16	90354753	1277454	0.0141	0.139
chr17	81195210	1974380	0.0243	0.1784
chr18	78077248	1178399	0.0151	0.1571
chr19	59128983	1369499	0.0232	0.181
chr20	63025520	1193154	0.0189	0.1567
chr21	48129895	609265	0.0127	0.1384
chr22	51304566	552544	0.0108	0.1196
chrMT	16571	8305	0.5012	0.8157
chrX	155270560	1399690	0.009	0.1081
chrY	59373566	161132	0.0027	0.0976

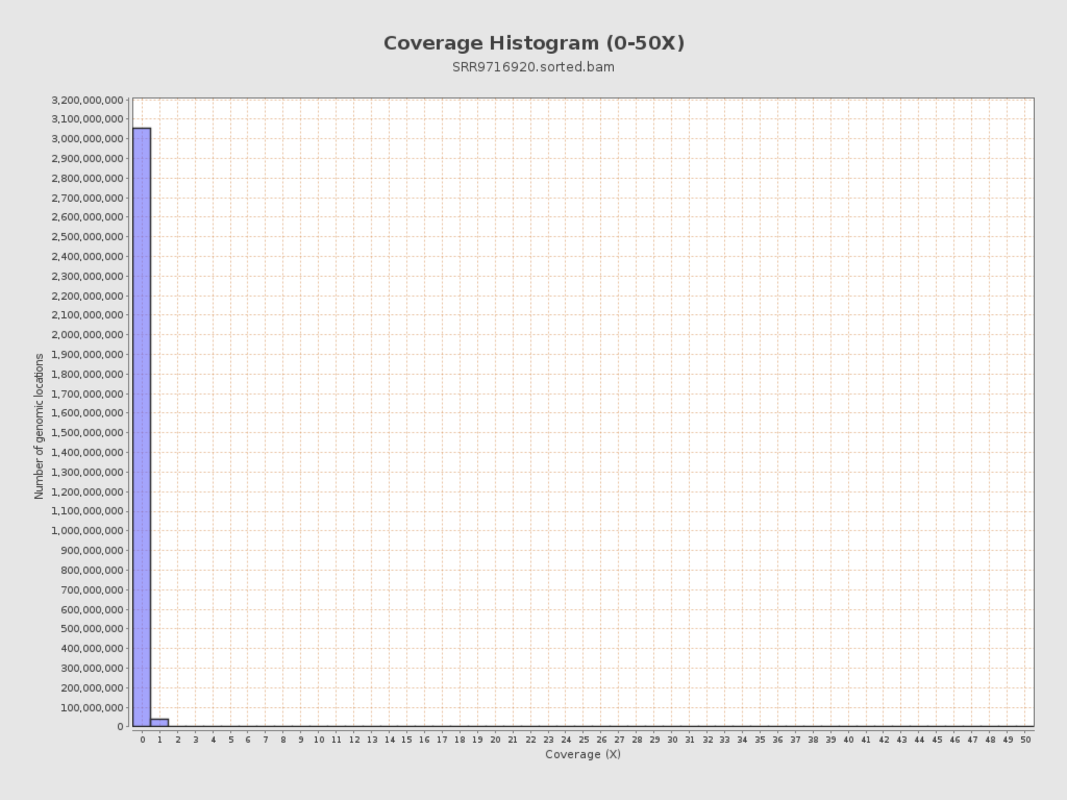
3. Results : Coverage across reference



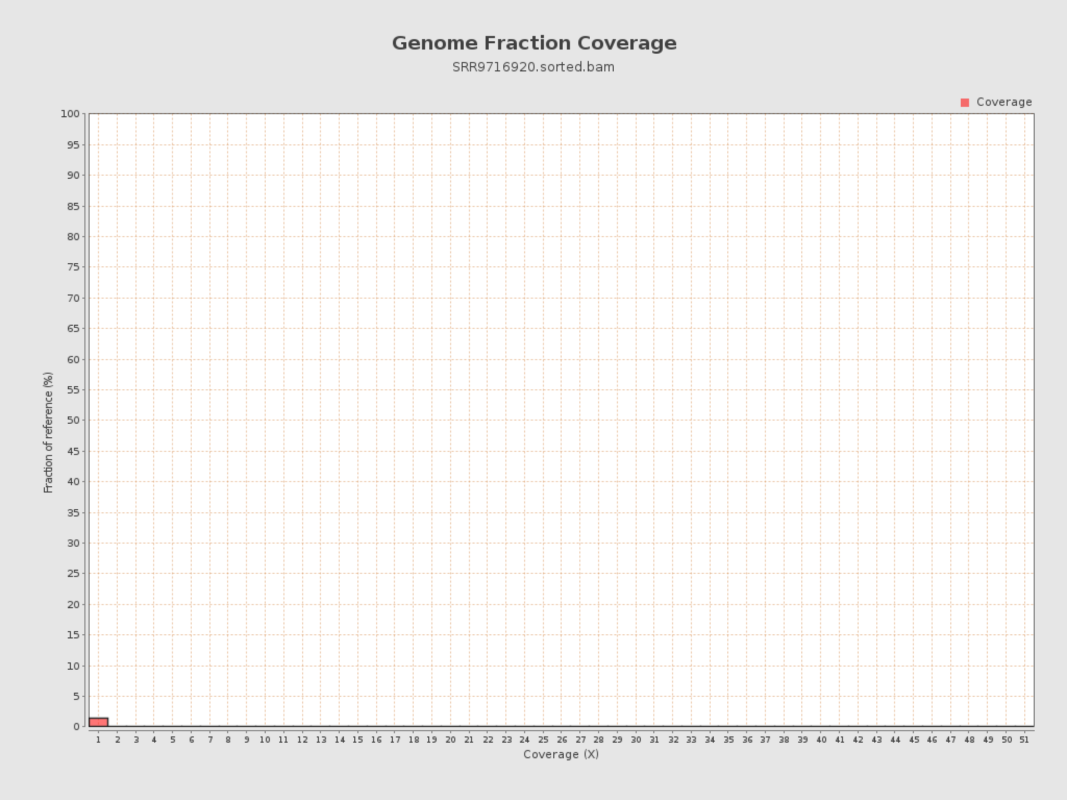
4. Results : Coverage Histogram



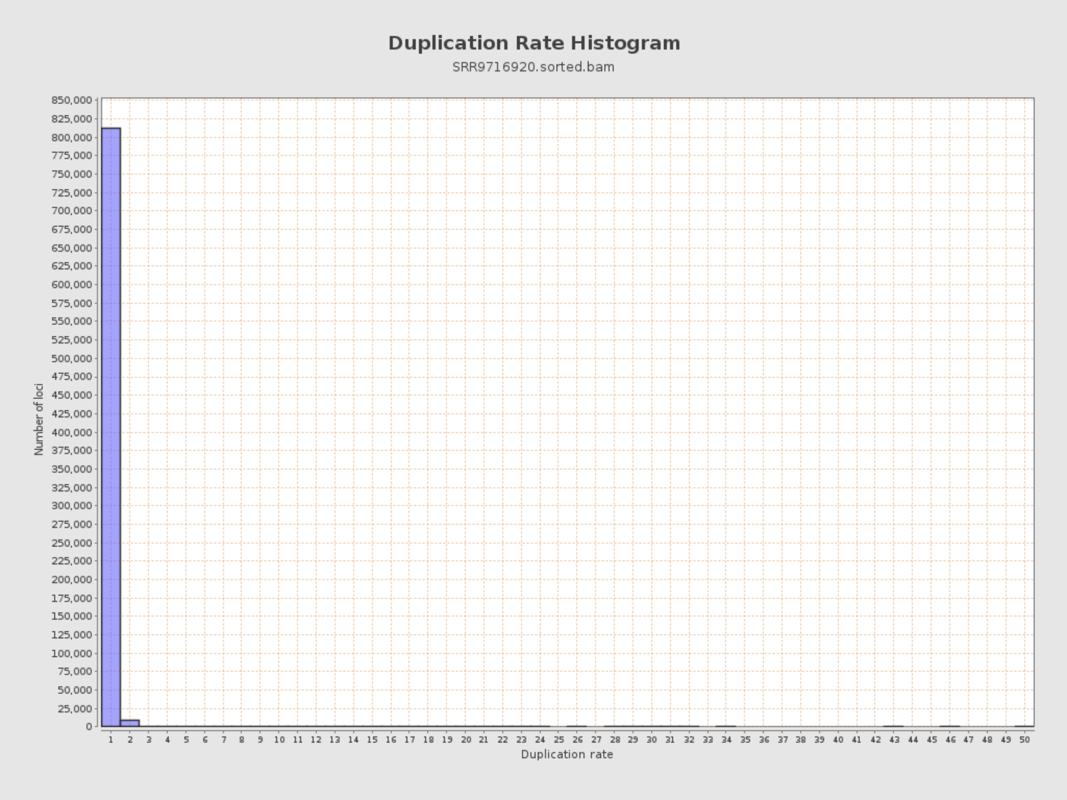
5. Results : Coverage Histogram (0-50X)



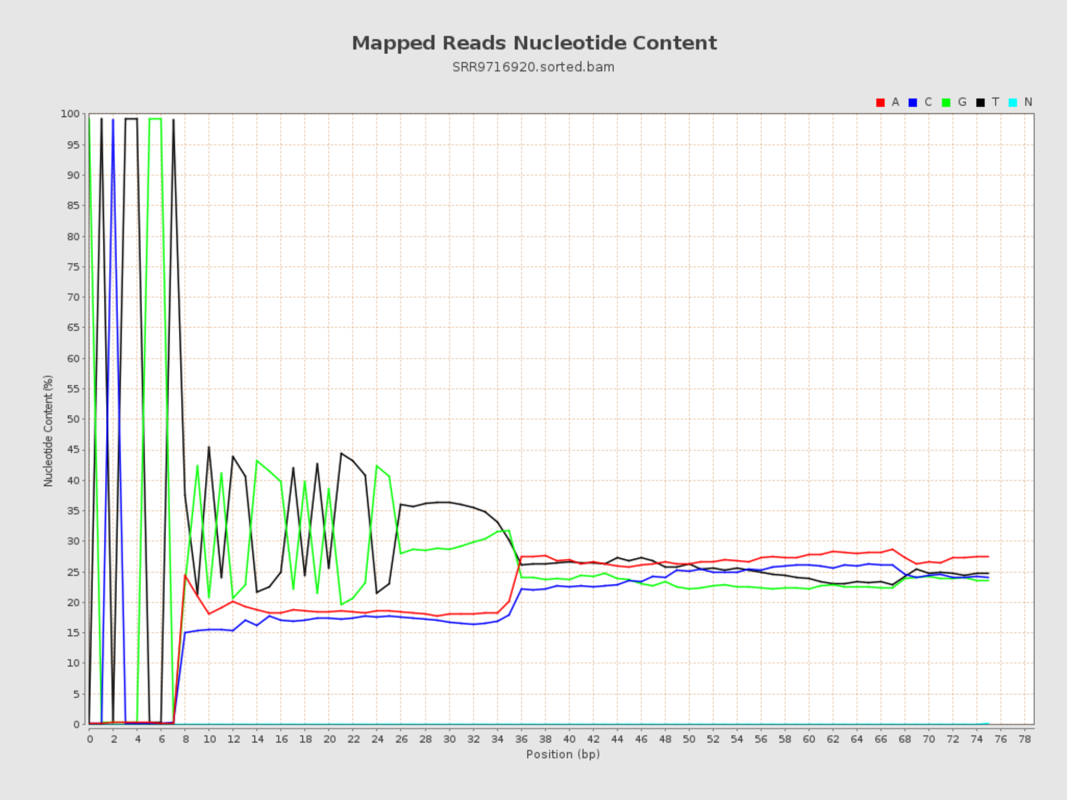
6. Results : Genome Fraction Coverage



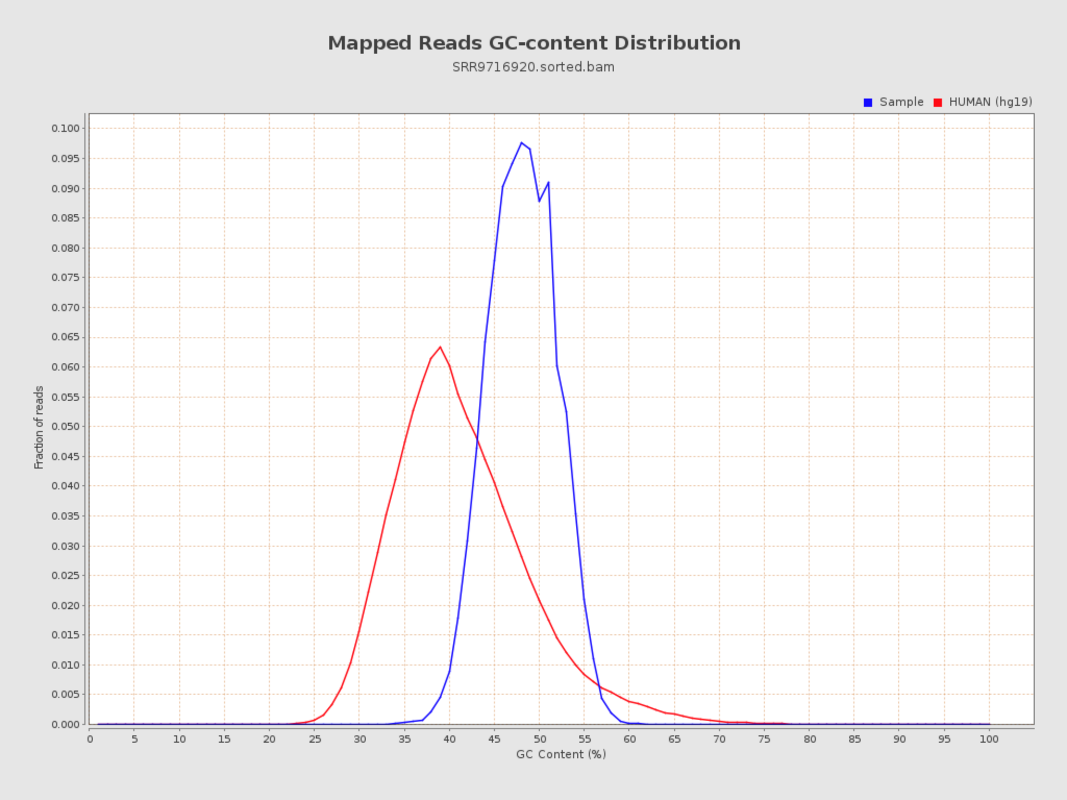
7. Results : Duplication Rate Histogram



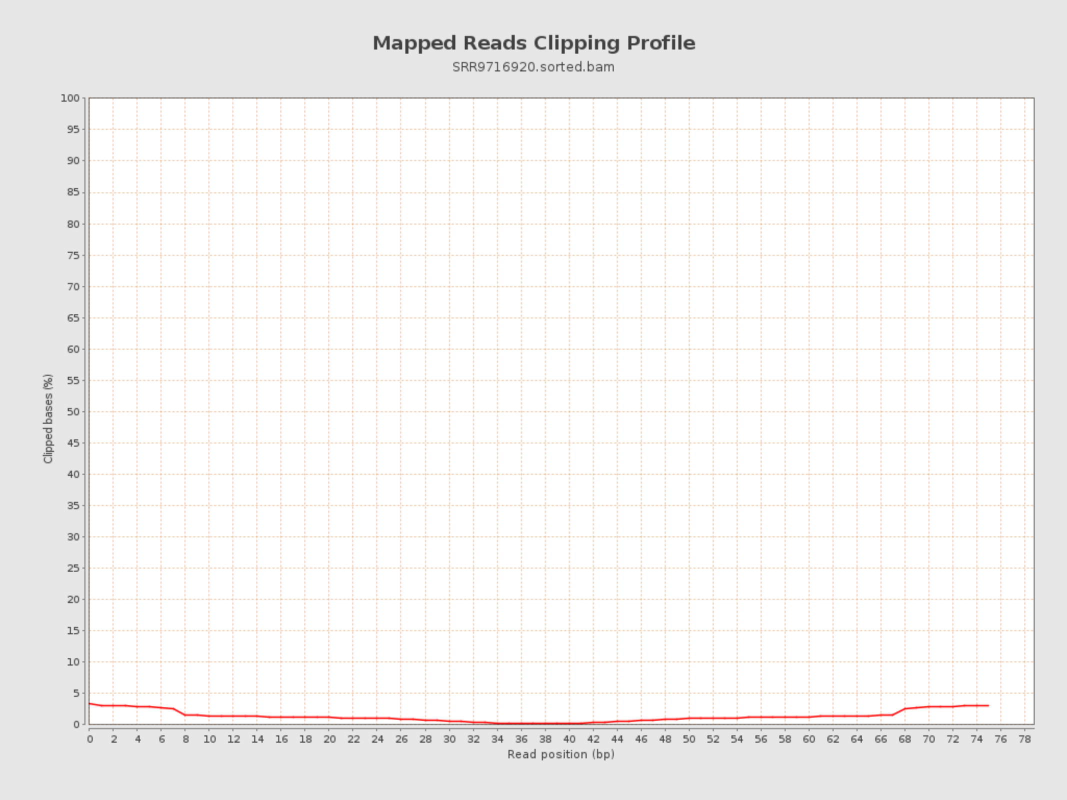
8. Results : Mapped Reads Nucleotide Content



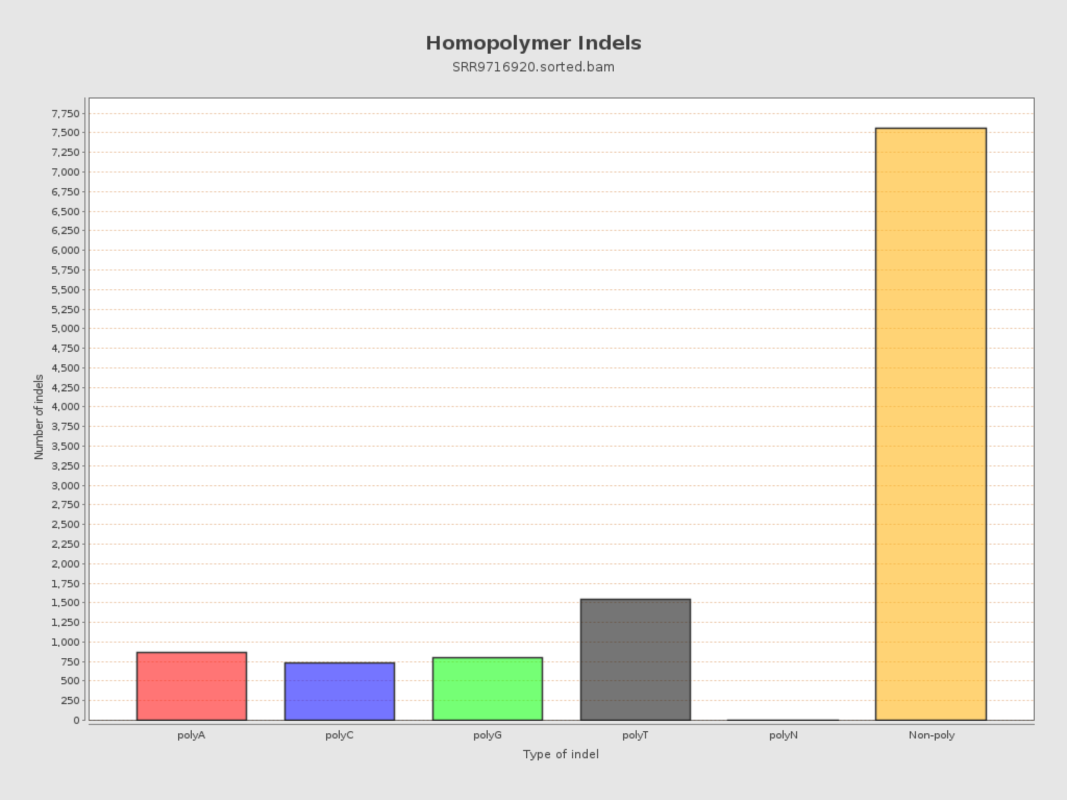
9. Results : Mapped Reads GC-content Distribution



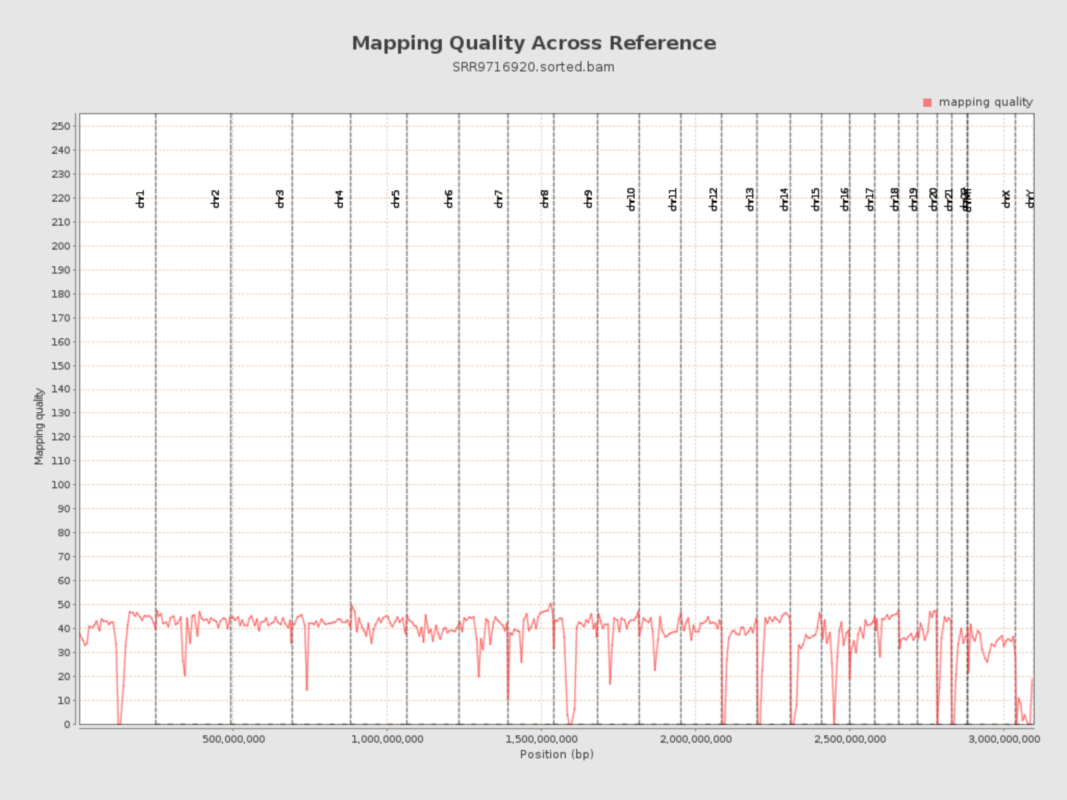
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram