Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 18:37:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716919.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_SRR9716919 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716919.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 18:37:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716919.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	831,386
Mapped reads	697,884 / 83.94%
Unmapped reads	133,502 / 16.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,824 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	11,947 / 1.44%
Duplication rate	1.25%
Clipped reads	700,195 / 84.22%

2.2. ACGT Content

Number/percentage of A's	9,192,103 / 23.85%
Number/percentage of C's	8,471,772 / 21.98%
Number/percentage of T's	11,114,109 / 28.83%
Number/percentage of G's	9,769,329 / 25.34%
Number/percentage of N's	964 / 0%
GC Percentage	47.32%

2.3. Coverage

Mean	0.0125

Standard Deviation	0.1317

2.4. Mapping Quality

Mean Mapping Quality	38.58

2.5. Mismatches and indels

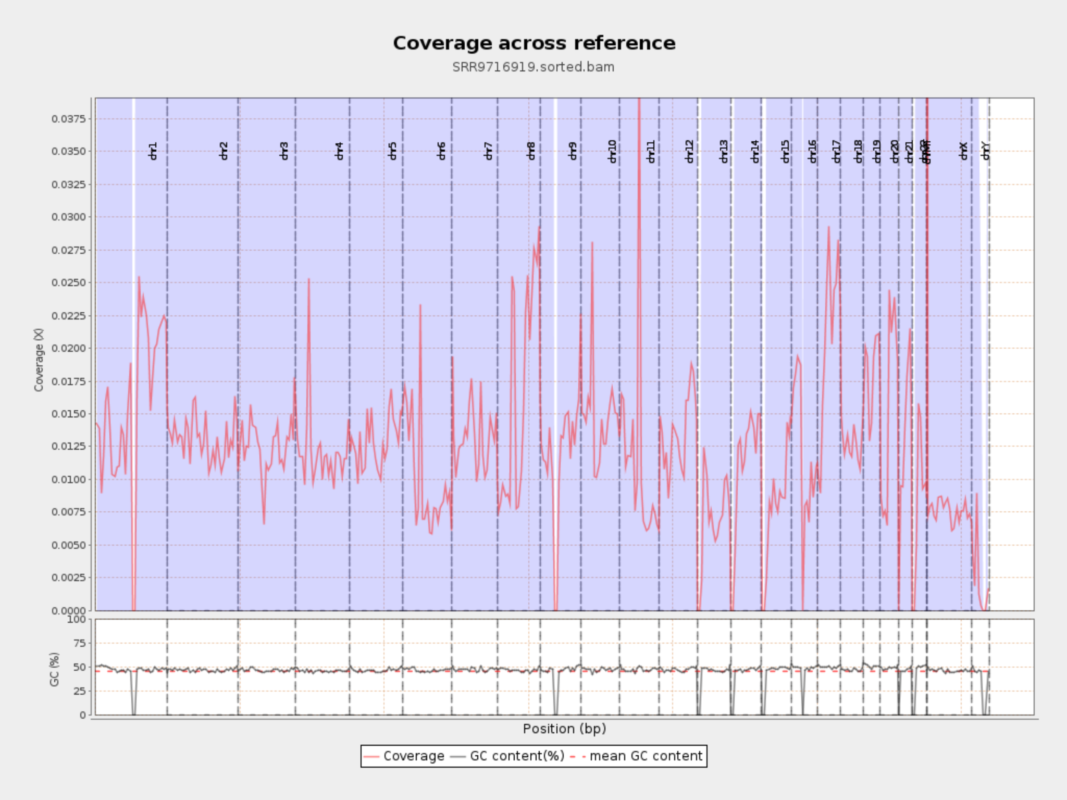
General error rate	0.55%
Mismatches	206,264
Insertions	2,667
Mapped reads with at least one insertion	0.38%
Deletions	6,201
Mapped reads with at least one deletion	0.88%
Homopolymer indels	34.48%

2.6. Chromosome stats

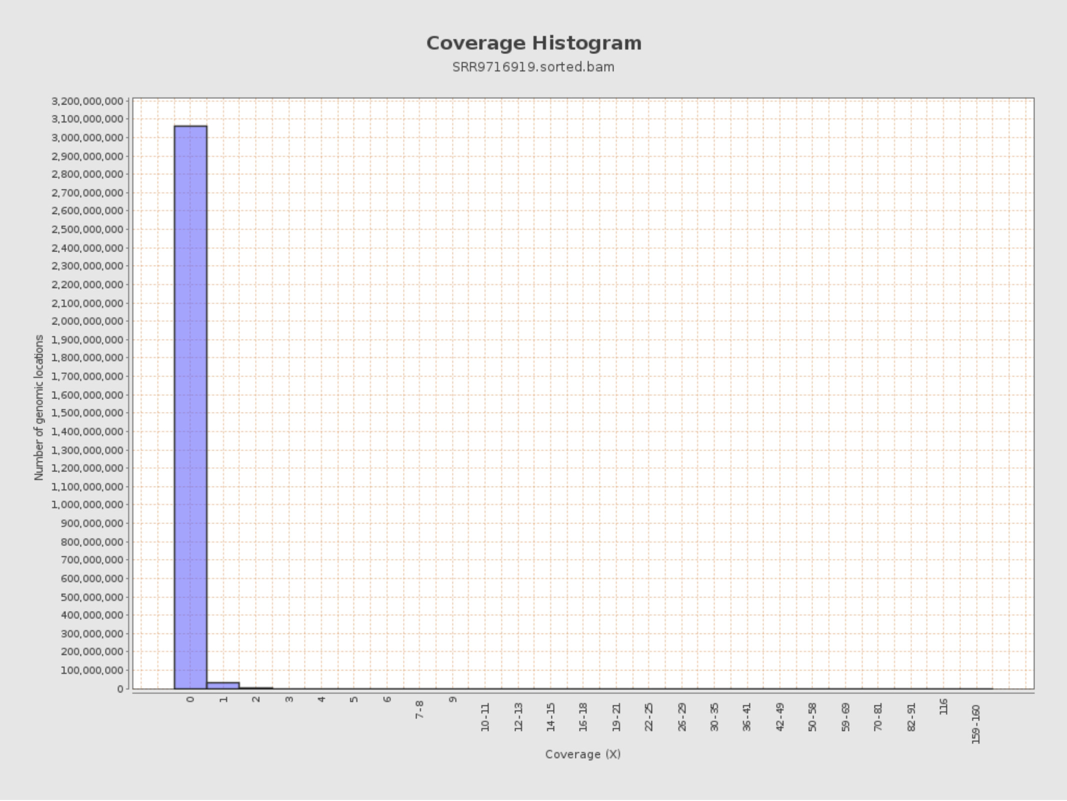
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3916122	0.0157	0.1563
chr2	243199373	3180160	0.0131	0.1506
chr3	198022430	2462479	0.0124	0.1215
chr4	191154276	2349095	0.0123	0.1305
chr5	180915260	2336187	0.0129	0.121
chr6	171115067	1733102	0.0101	0.1084
chr7	159138663	2120255	0.0133	0.1384

chr8	146364022	2444569	0.0167	0.1434
chr9	141213431	1629185	0.0115	0.1212
chr10	135534747	2010761	0.0148	0.1823
chr11	135006516	1601771	0.0119	0.132
chr12	133851895	1810630	0.0135	0.1243
chr13	115169878	782986	0.0068	0.0893
chr14	107349540	1177574	0.011	0.1129
chr15	102531392	800386	0.0078	0.0951
chr16	90354753	1058980	0.0117	0.1218
chr17	81195210	1693693	0.0209	0.1595
chr18	78077248	989167	0.0127	0.1387
chr19	59128983	1073453	0.0182	0.16
chr20	63025520	972253	0.0154	0.1378
chr21	48129895	638362	0.0133	0.1348
chr22	51304566	437593	0.0085	0.1003
chrMT	16571	30630	1.8484	1.9005
chrX	155270560	1177977	0.0076	0.0972
chrY	59373566	131476	0.0022	0.0761

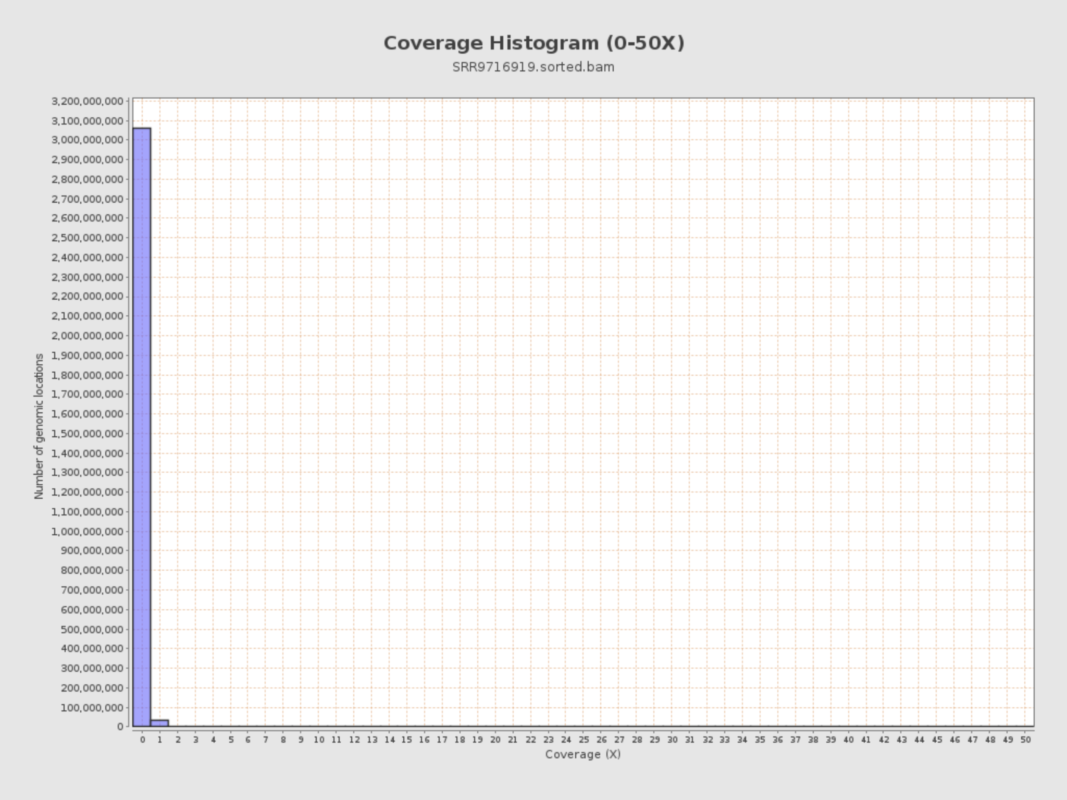
3. Results : Coverage across reference



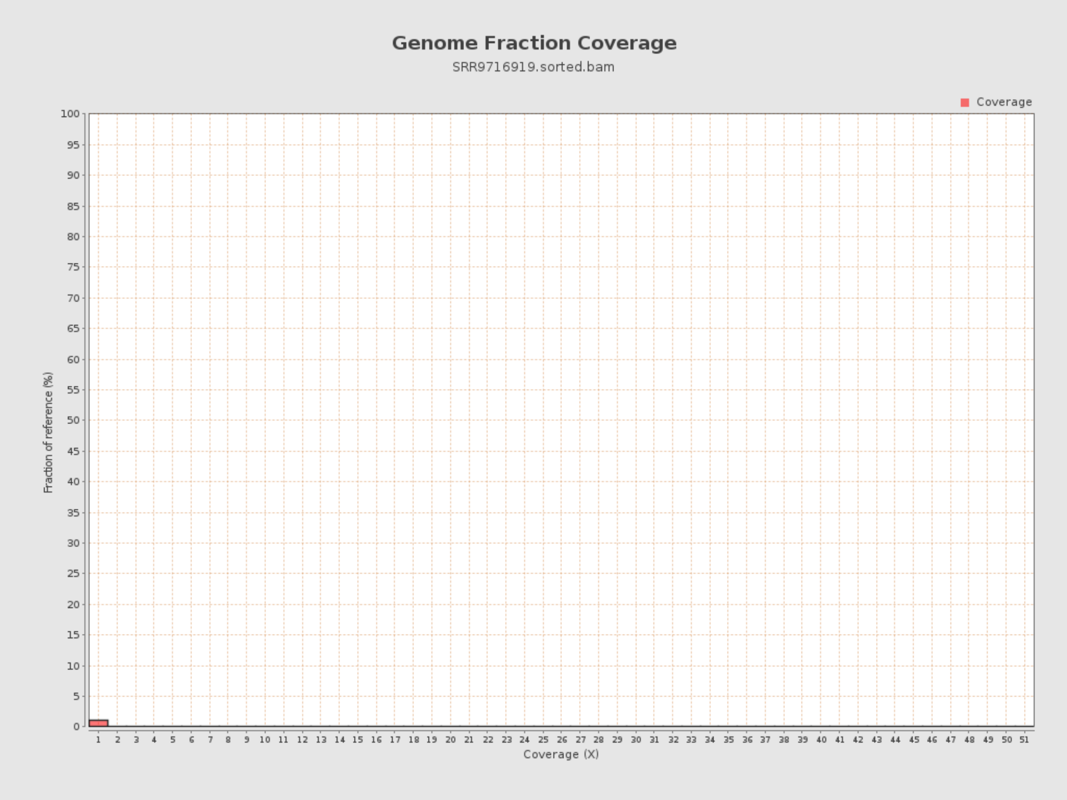
4. Results : Coverage Histogram



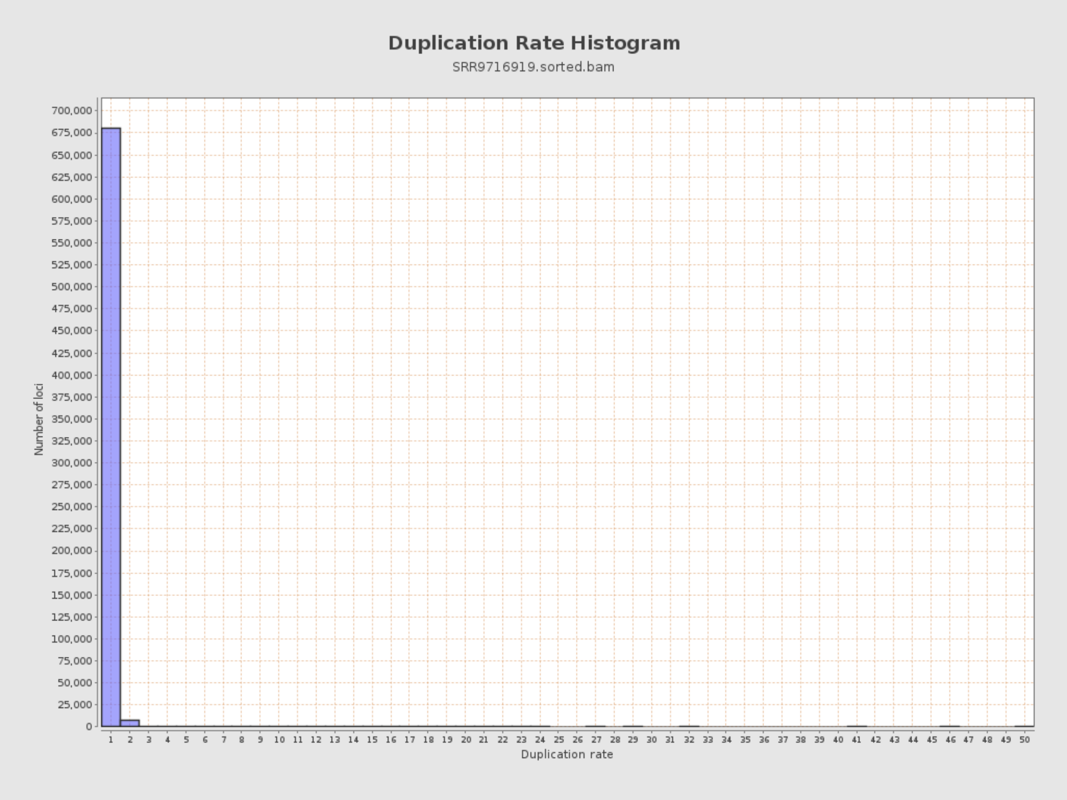
5. Results : Coverage Histogram (0-50X)



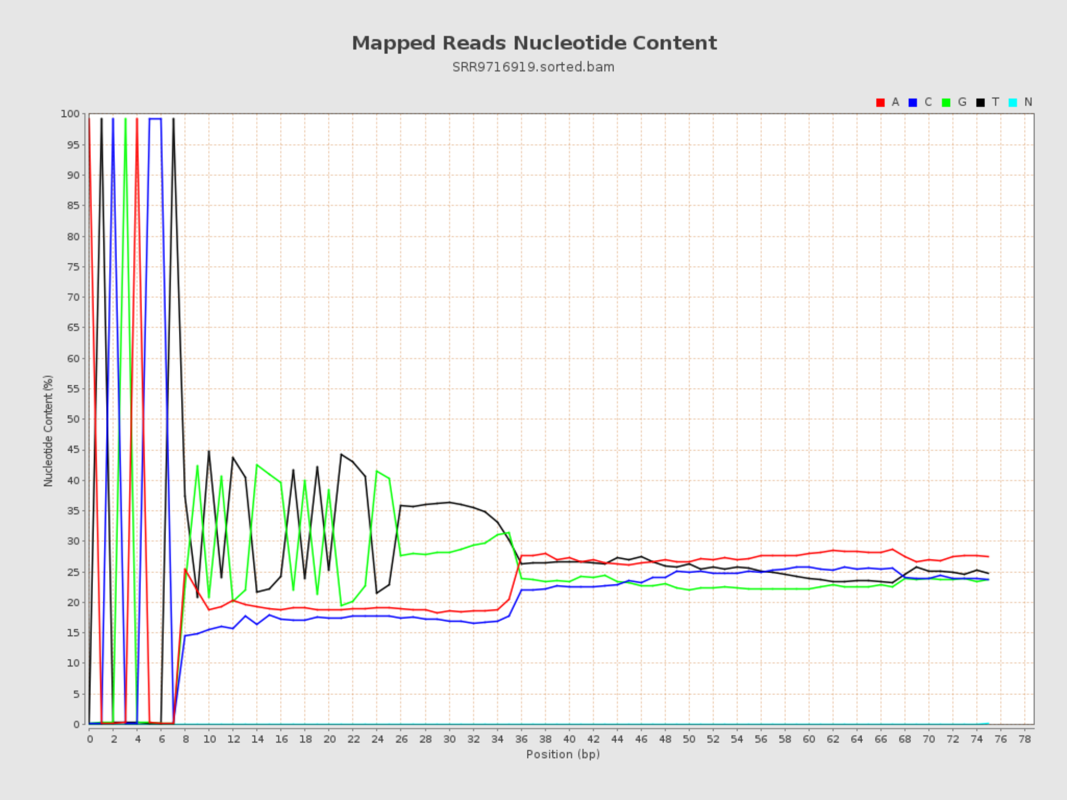
6. Results : Genome Fraction Coverage



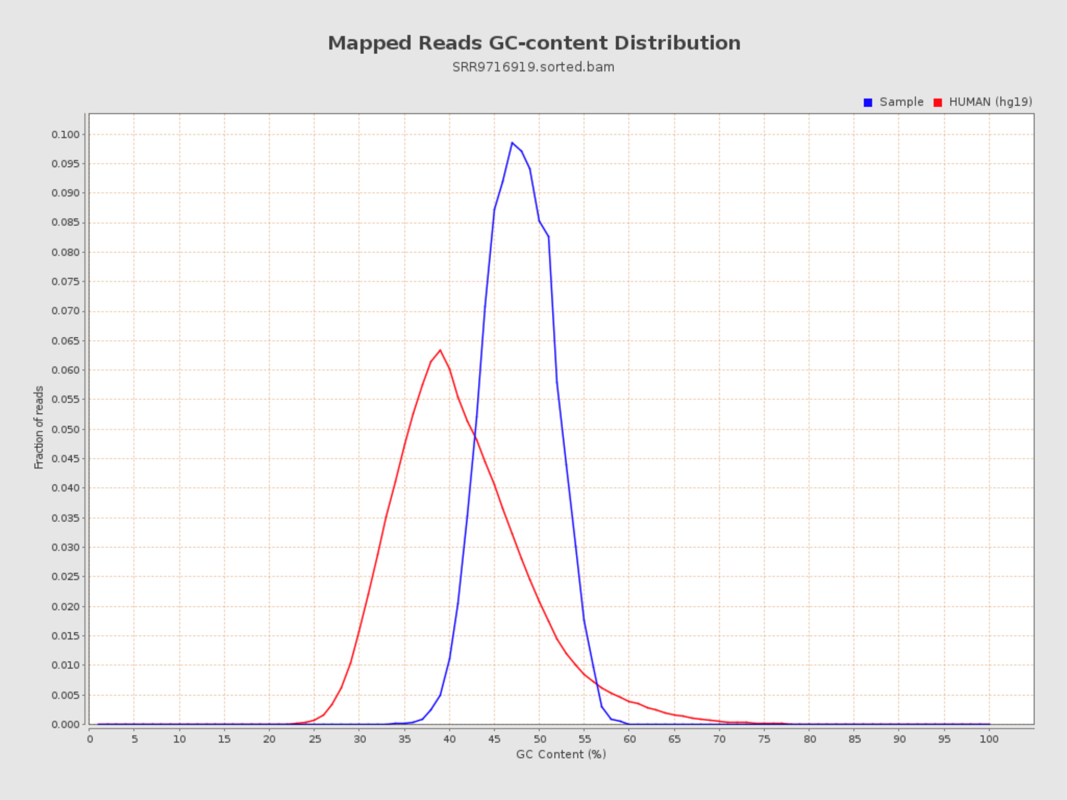
7. Results : Duplication Rate Histogram



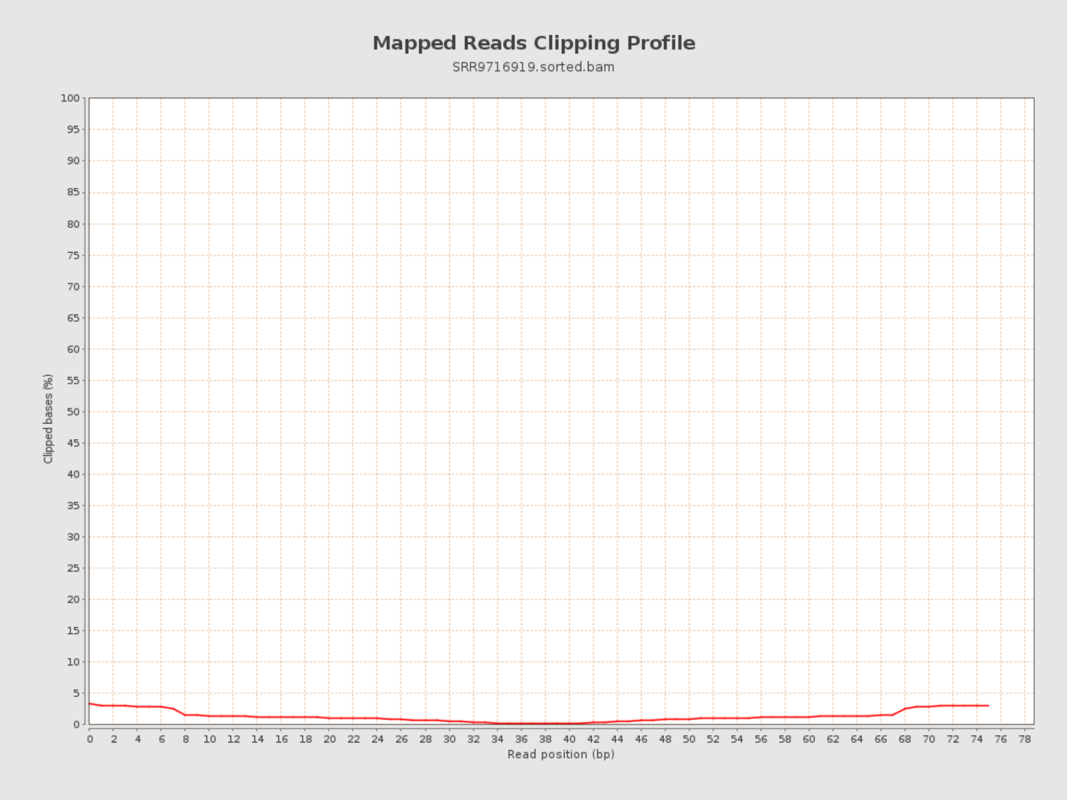
8. Results : Mapped Reads Nucleotide Content



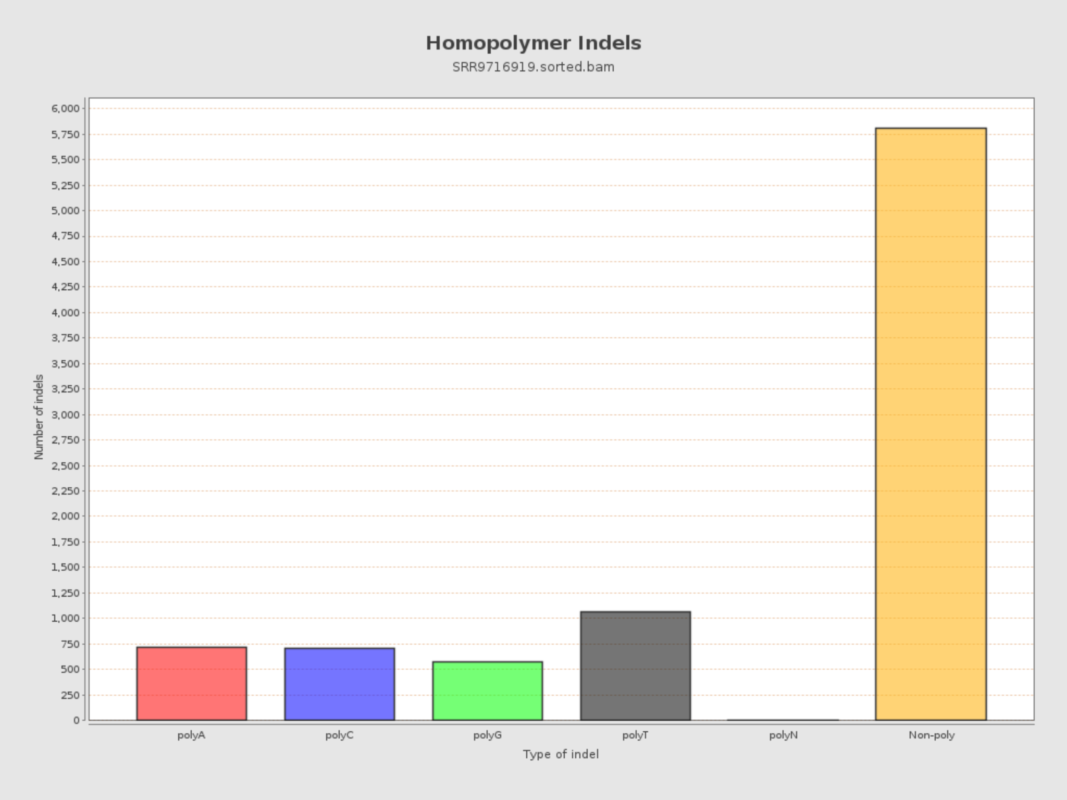
9. Results : Mapped Reads GC-content Distribution



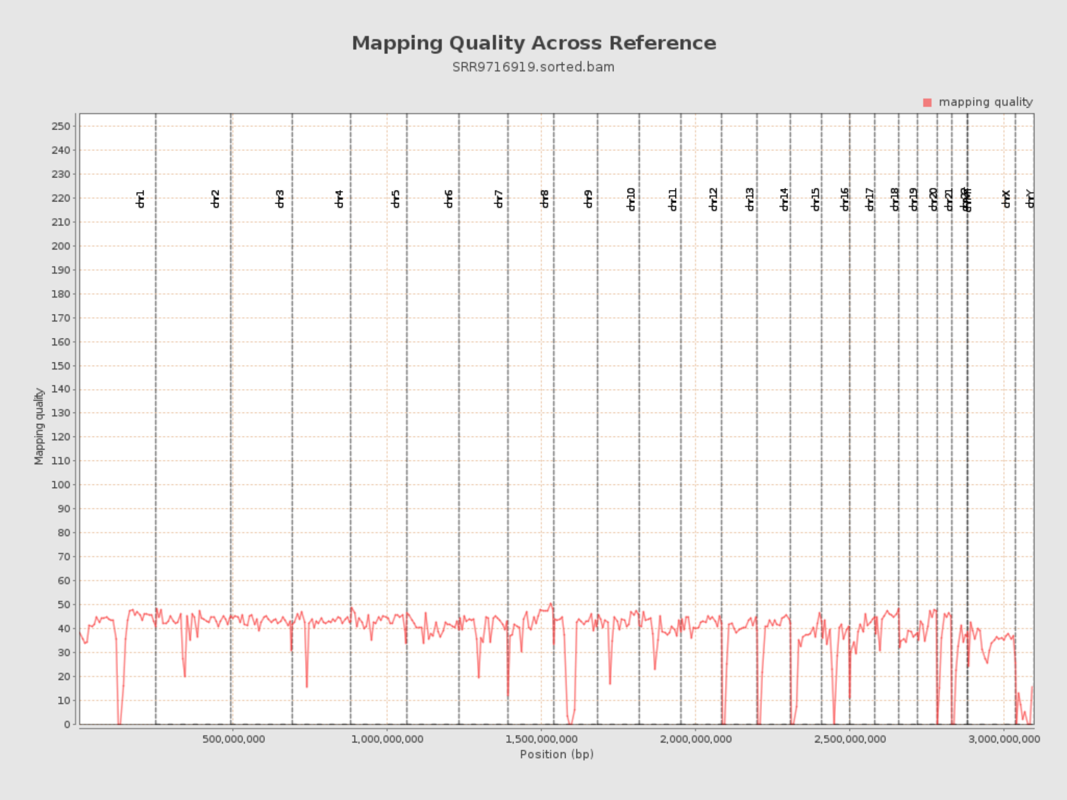
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram