Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 20:40:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716966.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_SRR9716966 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716966.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 20:40:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716966.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	986,330
Mapped reads	822,764 / 83.42%
Unmapped reads	163,566 / 16.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,169 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	15,401 / 1.56%
Duplication rate	1.41%
Clipped reads	824,938 / 83.64%

2.2. ACGT Content

Number/percentage of A's	10,834,309 / 24.2%
Number/percentage of C's	10,177,102 / 22.73%
Number/percentage of T's	12,648,724 / 28.25%
Number/percentage of G's	11,112,455 / 24.82%
Number/percentage of N's	1,178 / 0%
GC Percentage	47.55%

2.3. Coverage

Mean	0.0145

Standard Deviation	0.1432

2.4. Mapping Quality

Mean Mapping Quality	39.98

2.5. Mismatches and indels

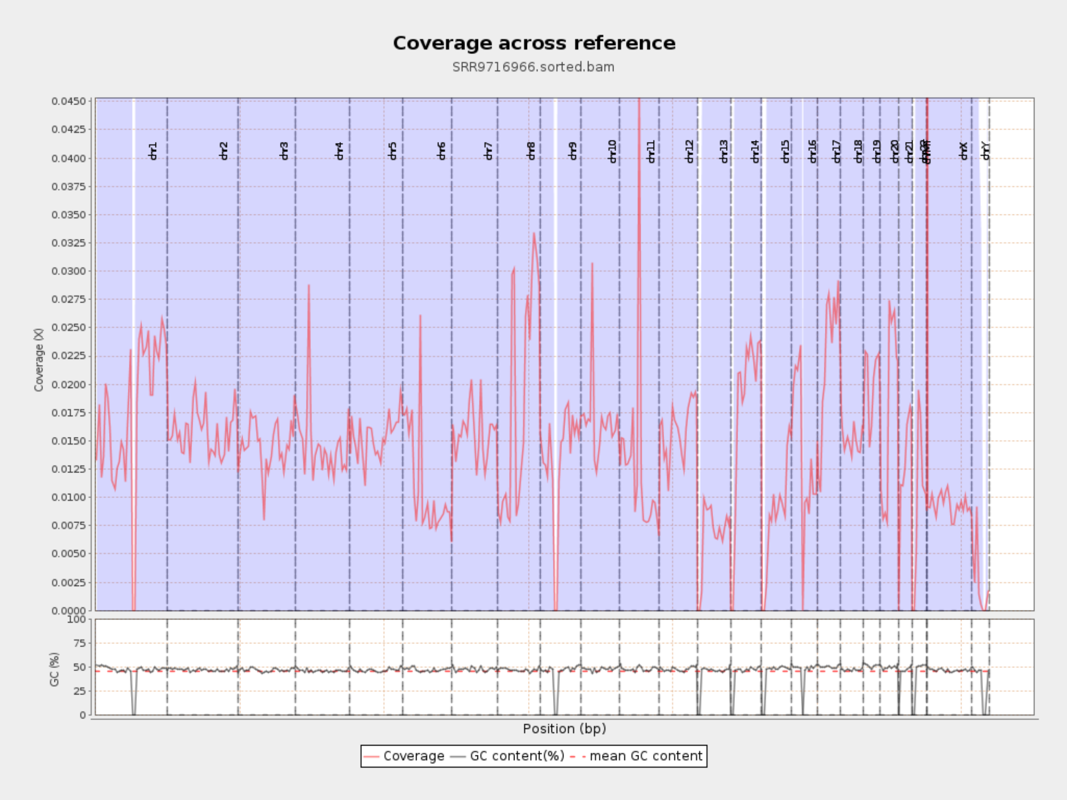
General error rate	0.53%
Mismatches	233,431
Insertions	3,156
Mapped reads with at least one insertion	0.38%
Deletions	7,104
Mapped reads with at least one deletion	0.86%
Homopolymer indels	34.04%

2.6. Chromosome stats

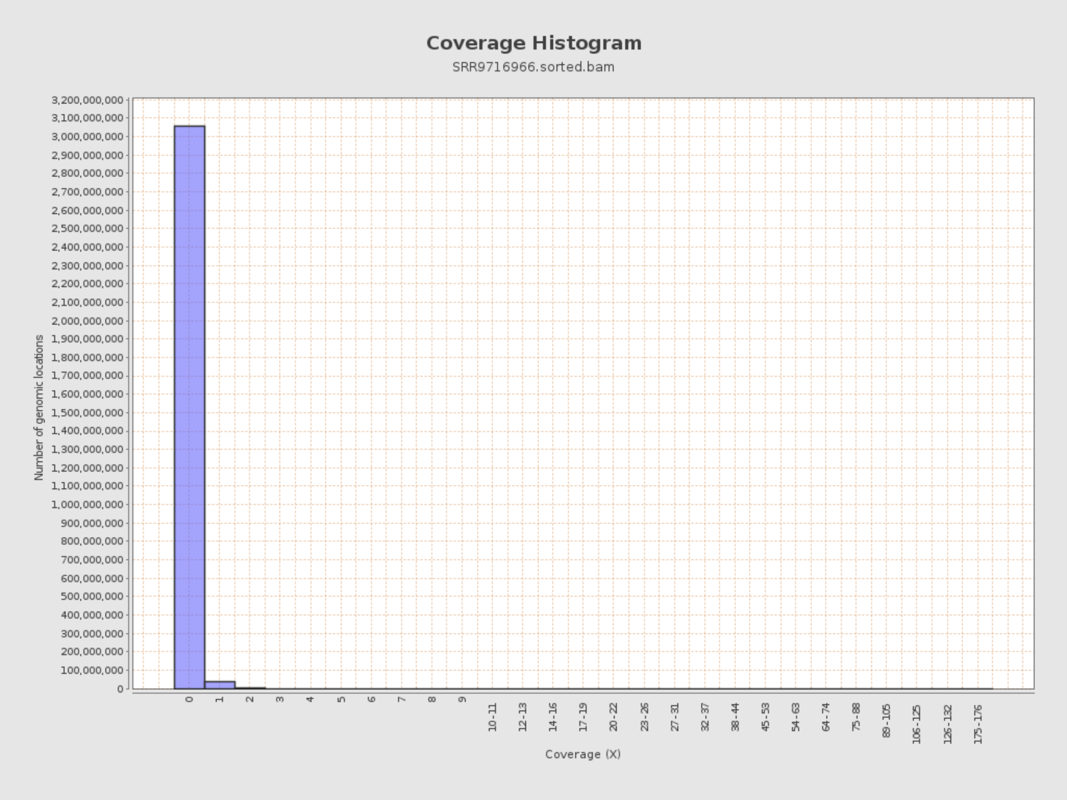
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4372019	0.0175	0.1721
chr2	243199373	3846820	0.0158	0.1647
chr3	198022430	2875490	0.0145	0.1302
chr4	191154276	2835787	0.0148	0.1442
chr5	180915260	2801036	0.0155	0.1324
chr6	171115067	1903822	0.0111	0.1149
chr7	159138663	2507327	0.0158	0.1534

chr8	146364022	2749205	0.0188	0.1522
chr9	141213431	1866445	0.0132	0.1287
chr10	135534747	2286315	0.0169	0.1937
chr11	135006516	1795849	0.0133	0.1409
chr12	133851895	2131729	0.0159	0.1354
chr13	115169878	757312	0.0066	0.0877
chr14	107349540	1930584	0.018	0.1455
chr15	102531392	855770	0.0083	0.1
chr16	90354753	1227111	0.0136	0.1326
chr17	81195210	1809074	0.0223	0.1644
chr18	78077248	1175810	0.0151	0.1627
chr19	59128983	1184935	0.02	0.1723
chr20	63025520	1108787	0.0176	0.1463
chr21	48129895	620669	0.0129	0.1313
chr22	51304566	508717	0.0099	0.1075
chrMT	16571	37293	2.2505	2.436
chrX	155270560	1450779	0.0093	0.1089
chrY	59373566	146971	0.0025	0.0819

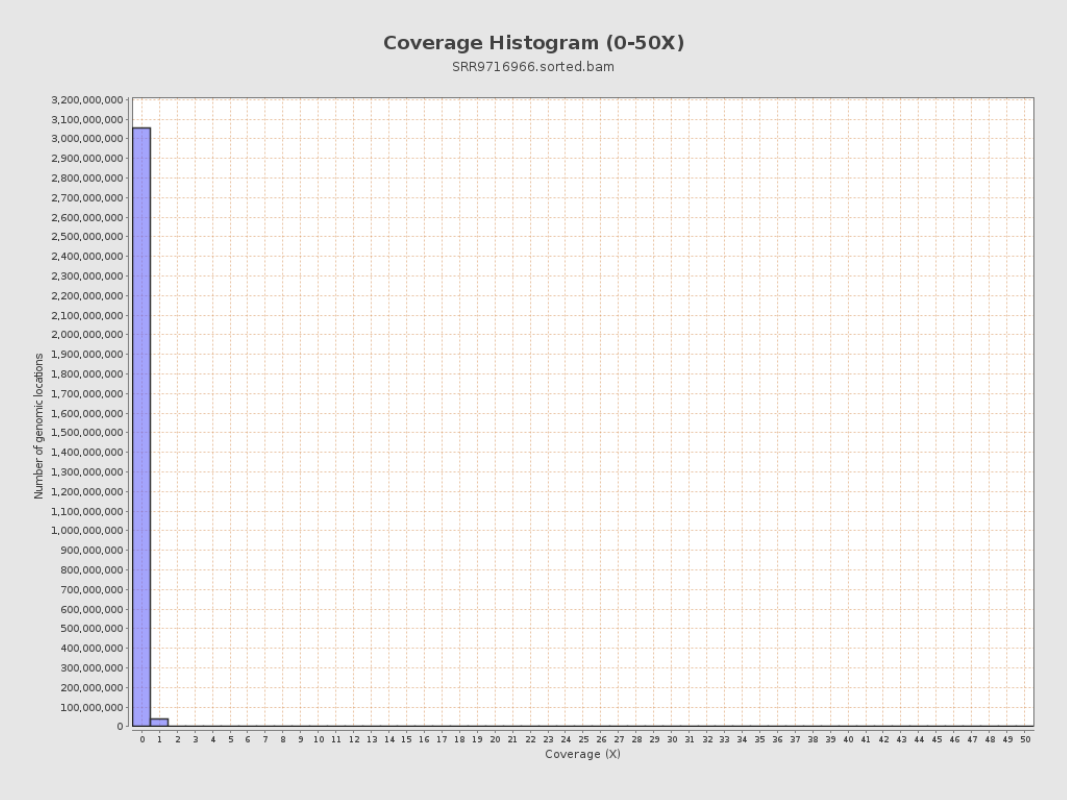
3. Results : Coverage across reference



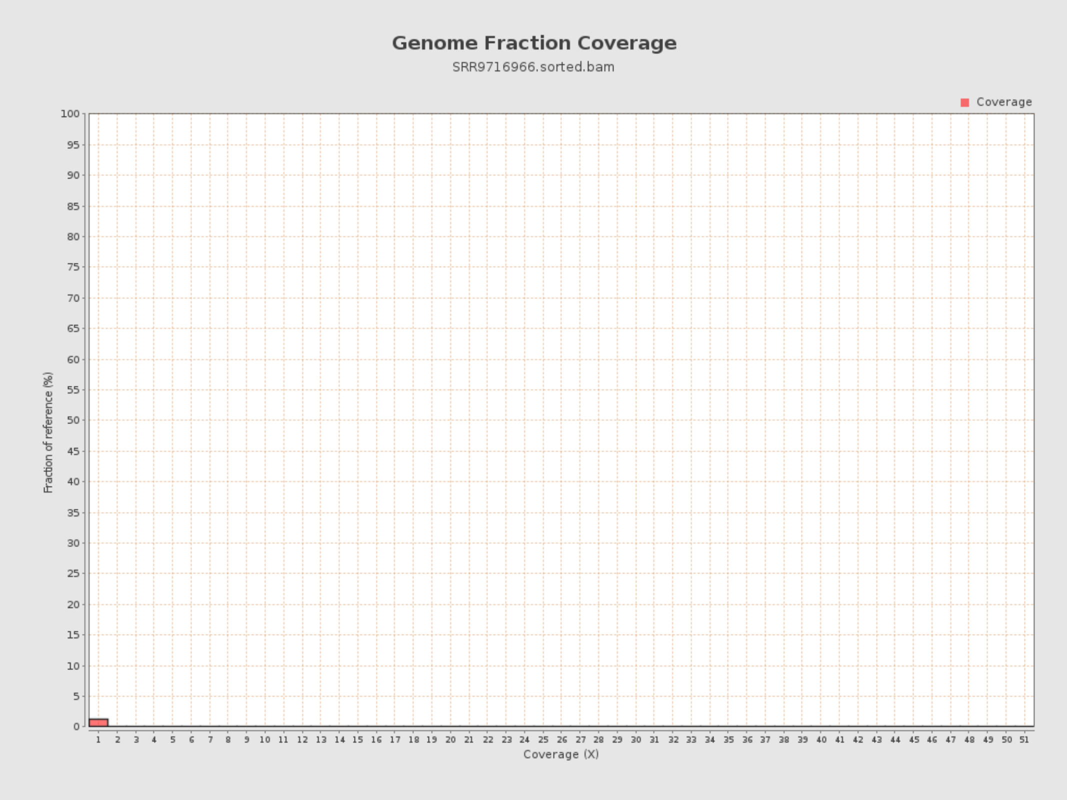
4. Results : Coverage Histogram



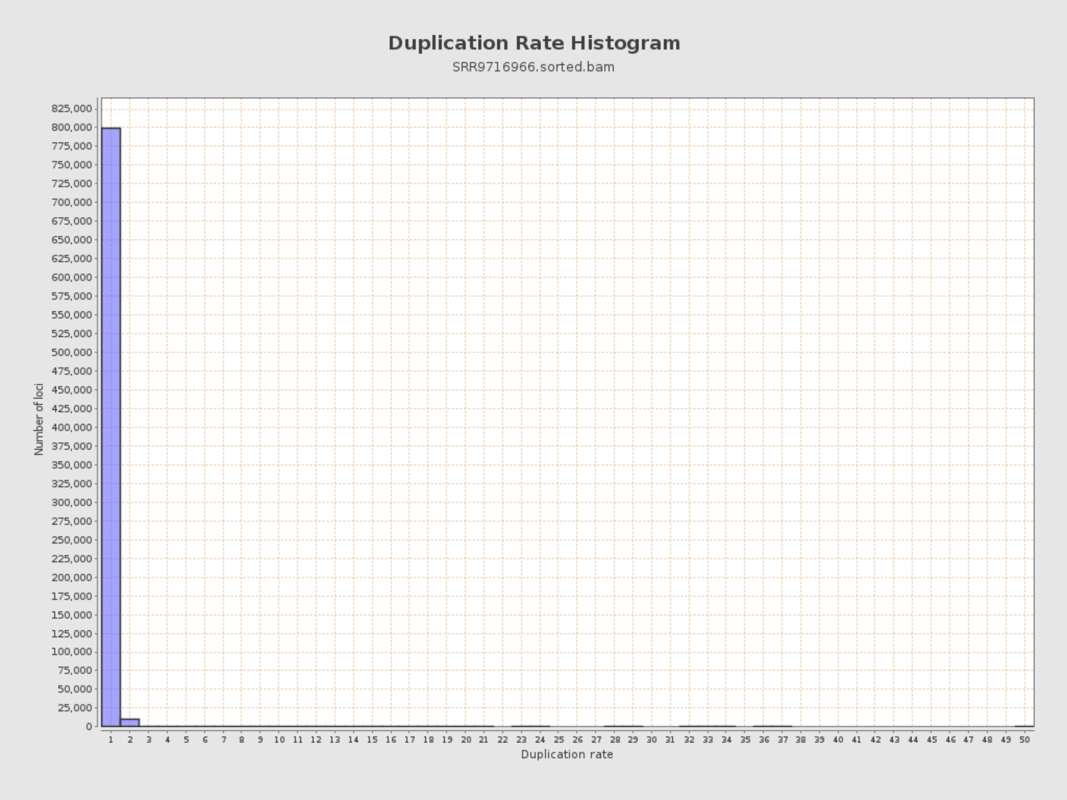
5. Results : Coverage Histogram (0-50X)



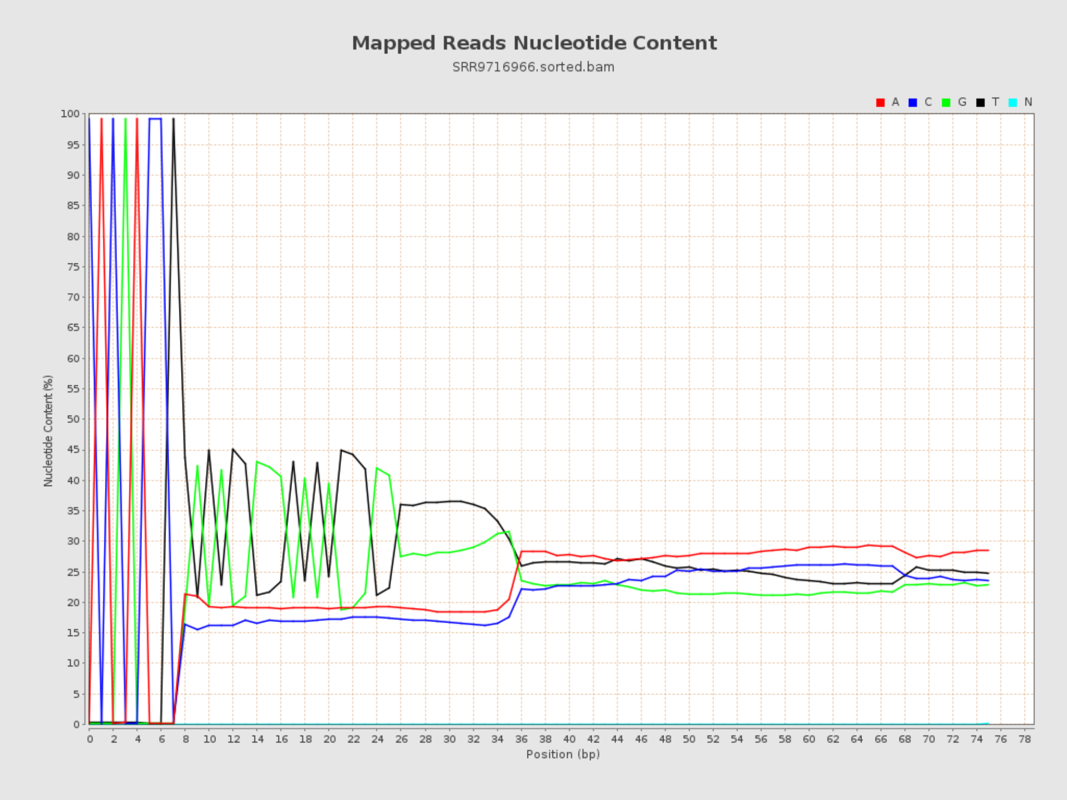
6. Results : Genome Fraction Coverage



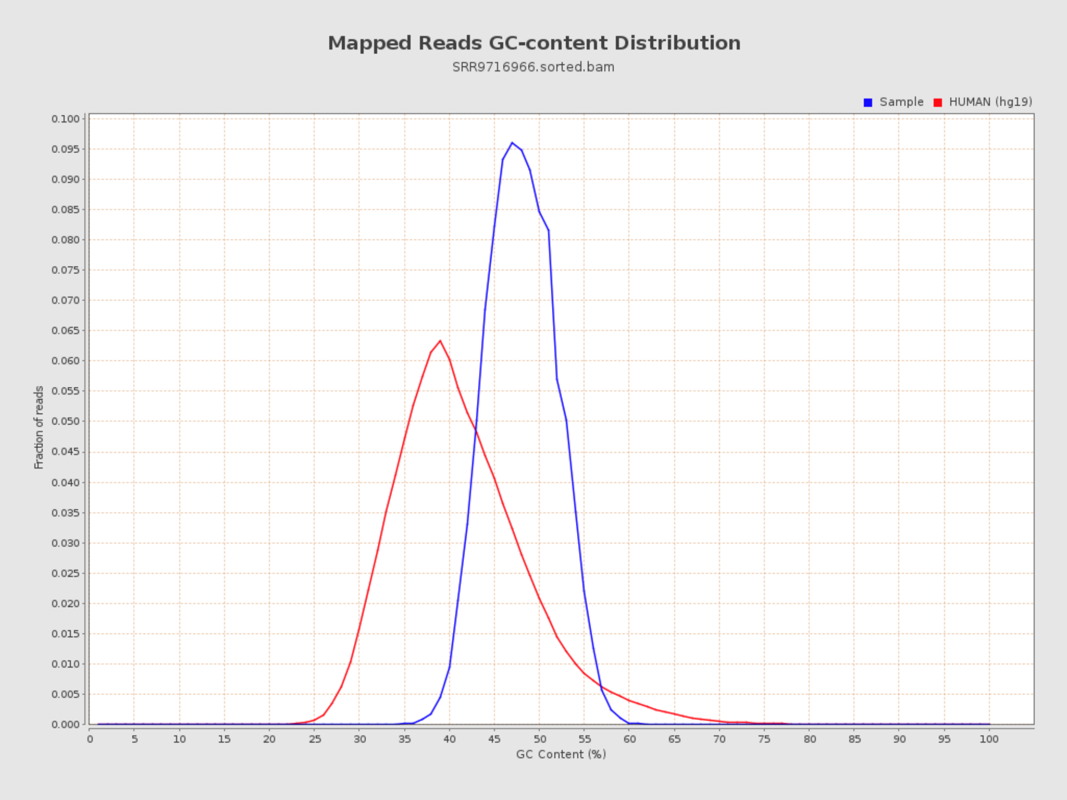
7. Results : Duplication Rate Histogram



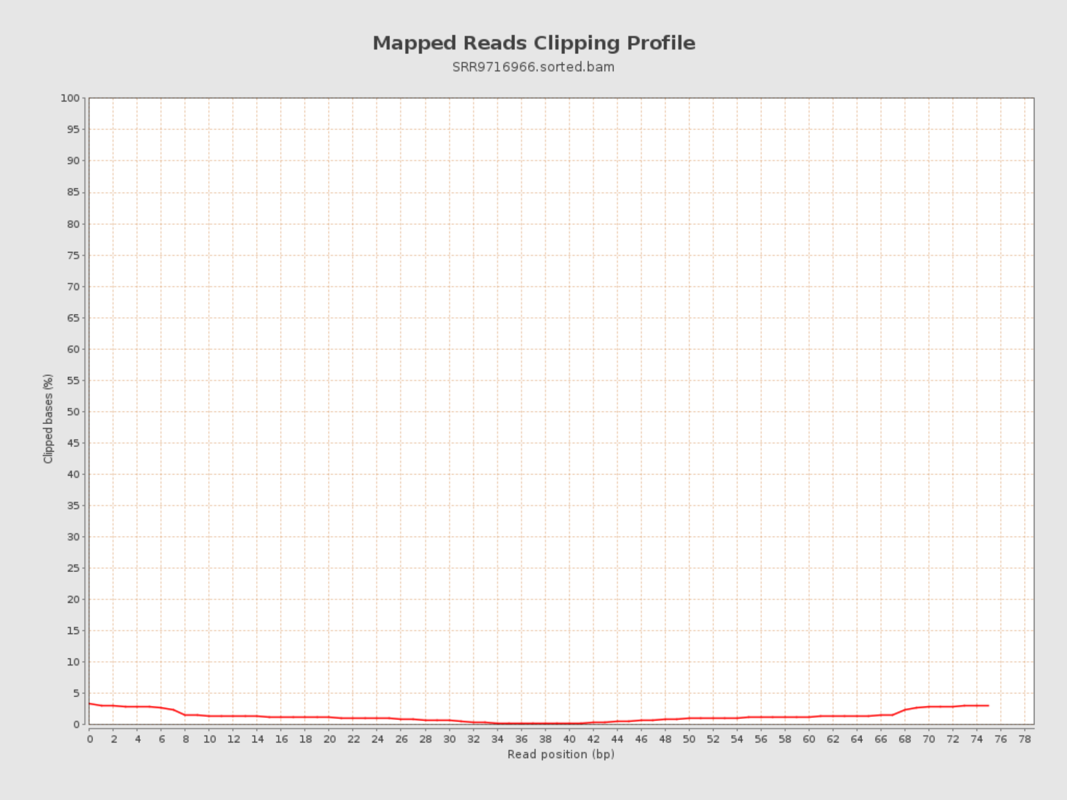
8. Results : Mapped Reads Nucleotide Content



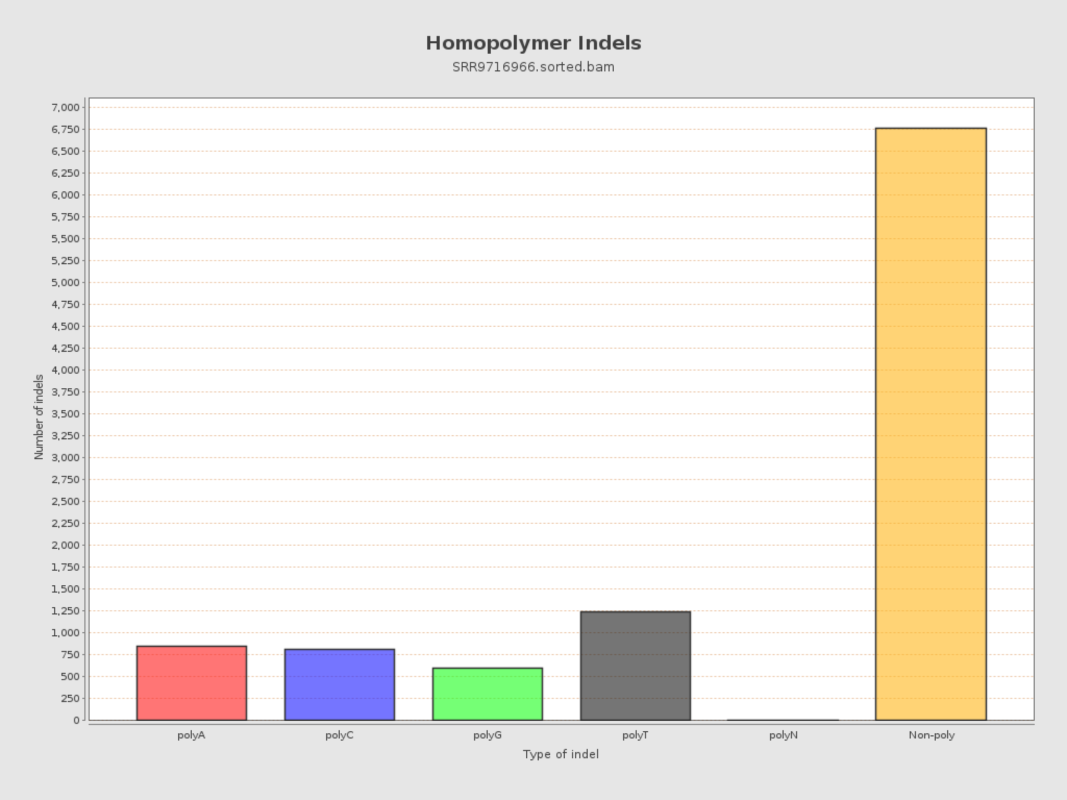
9. Results : Mapped Reads GC-content Distribution



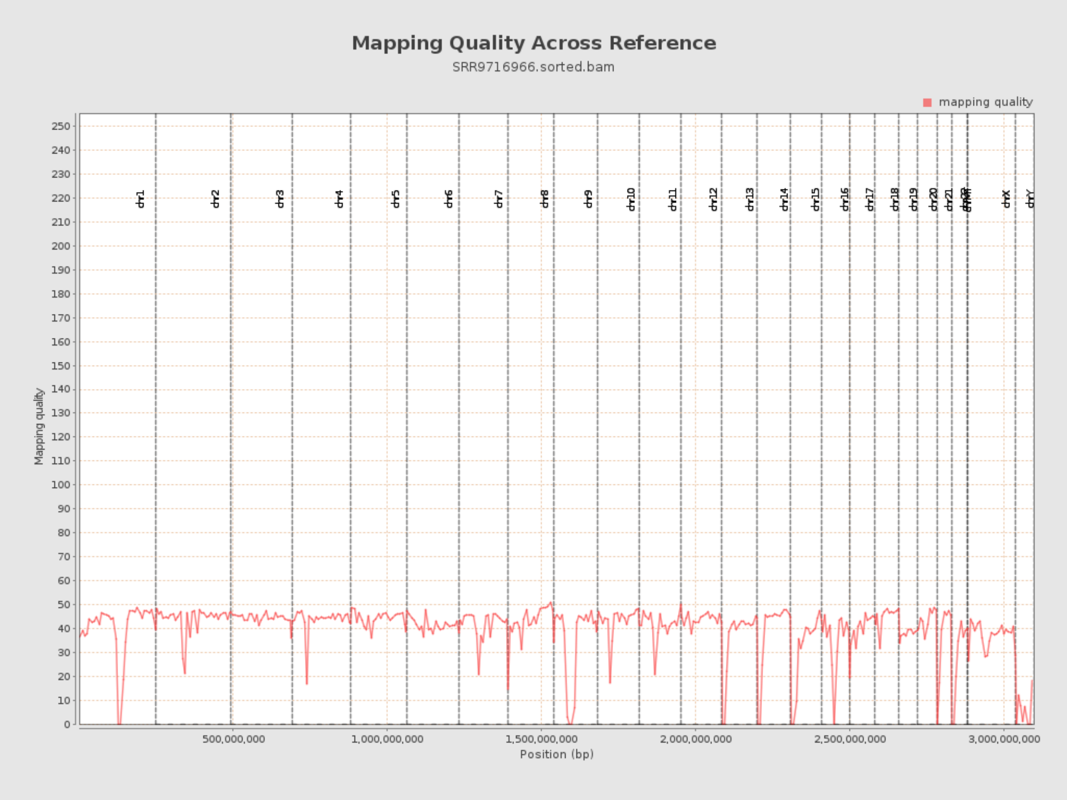
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram