Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 15:31:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716467.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_SRR9716467 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716467.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 15:31:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716467.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	675,869
Mapped reads	606,204 / 89.69%
Unmapped reads	69,665 / 10.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,979 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	13,189 / 1.95%
Duplication rate	1.48%
Clipped reads	606,567 / 89.75%

2.2. ACGT Content

Number/percentage of A's	8,512,308 / 24.78%
Number/percentage of C's	6,260,460 / 18.23%
Number/percentage of T's	11,257,899 / 32.78%
Number/percentage of G's	8,314,723 / 24.21%
Number/percentage of N's	653 / 0%
GC Percentage	42.44%

2.3. Coverage

Mean	0.0111

Standard Deviation	0.1366

2.4. Mapping Quality

Mean Mapping Quality	42.42

2.5. Mismatches and indels

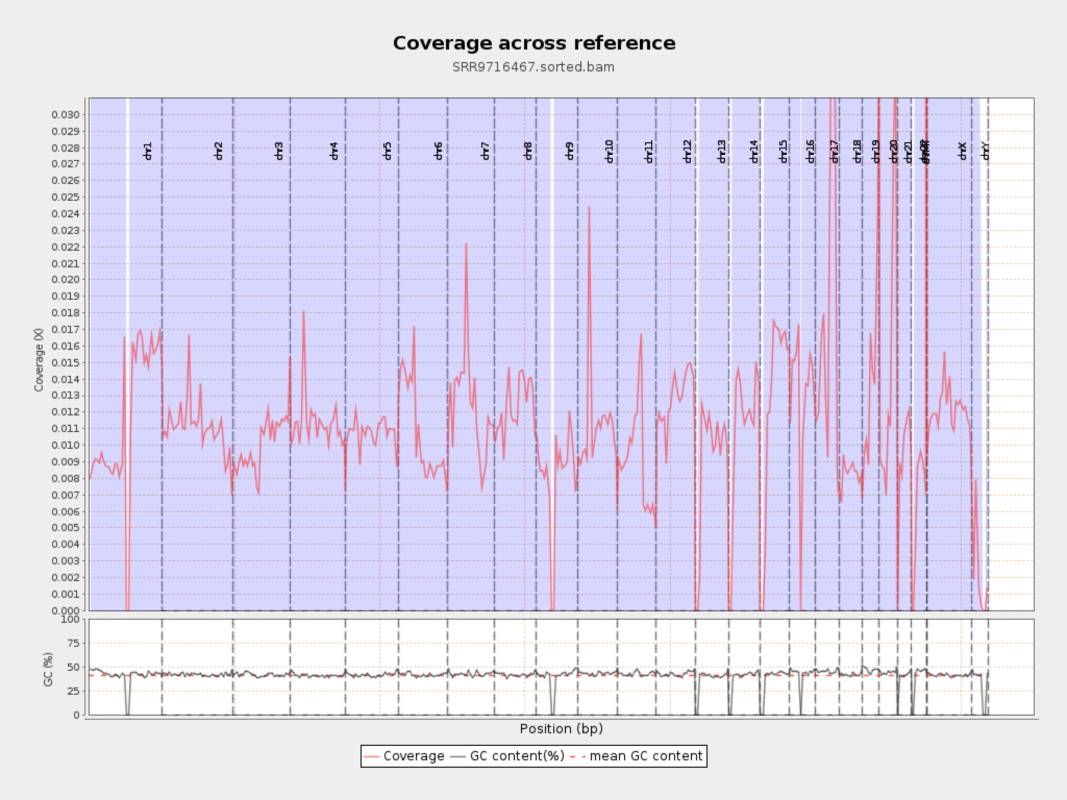
General error rate	0.55%
Mismatches	183,226
Insertions	2,458
Mapped reads with at least one insertion	0.4%
Deletions	6,523
Mapped reads with at least one deletion	1.07%
Homopolymer indels	40.69%

2.6. Chromosome stats

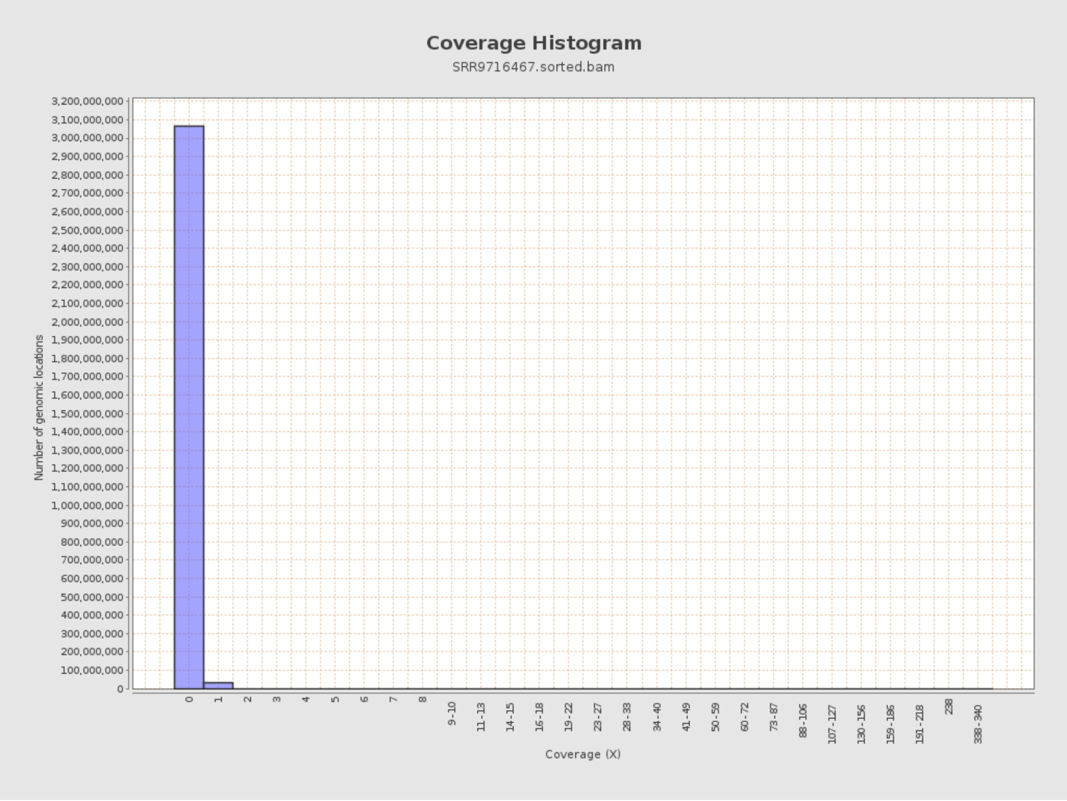
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2864615	0.0115	0.1848
chr2	243199373	2700729	0.0111	0.1756
chr3	198022430	1984224	0.01	0.1051
chr4	191154276	2163872	0.0113	0.1161
chr5	180915260	1947386	0.0108	0.1081
chr6	171115067	1847672	0.0108	0.1193
chr7	159138663	1983867	0.0125	0.1764

chr8	146364022	1809338	0.0124	0.1584
chr9	141213431	1139897	0.0081	0.1056
chr10	135534747	1528489	0.0113	0.1505
chr11	135006516	1240057	0.0092	0.1165
chr12	133851895	1717746	0.0128	0.1184
chr13	115169878	1044017	0.0091	0.099
chr14	107349540	1156949	0.0108	0.109
chr15	102531392	1273150	0.0124	0.1205
chr16	90354753	1177848	0.013	0.1236
chr17	81195210	1474119	0.0182	0.1424
chr18	78077248	647307	0.0083	0.1476
chr19	59128983	856804	0.0145	0.1736
chr20	63025520	963460	0.0153	0.13
chr21	48129895	444651	0.0092	0.1067
chr22	51304566	316905	0.0062	0.0815
chrMT	16571	66332	4.0029	2.7864
chrX	155270560	1882648	0.0121	0.1207
chrY	59373566	124551	0.0021	0.0814

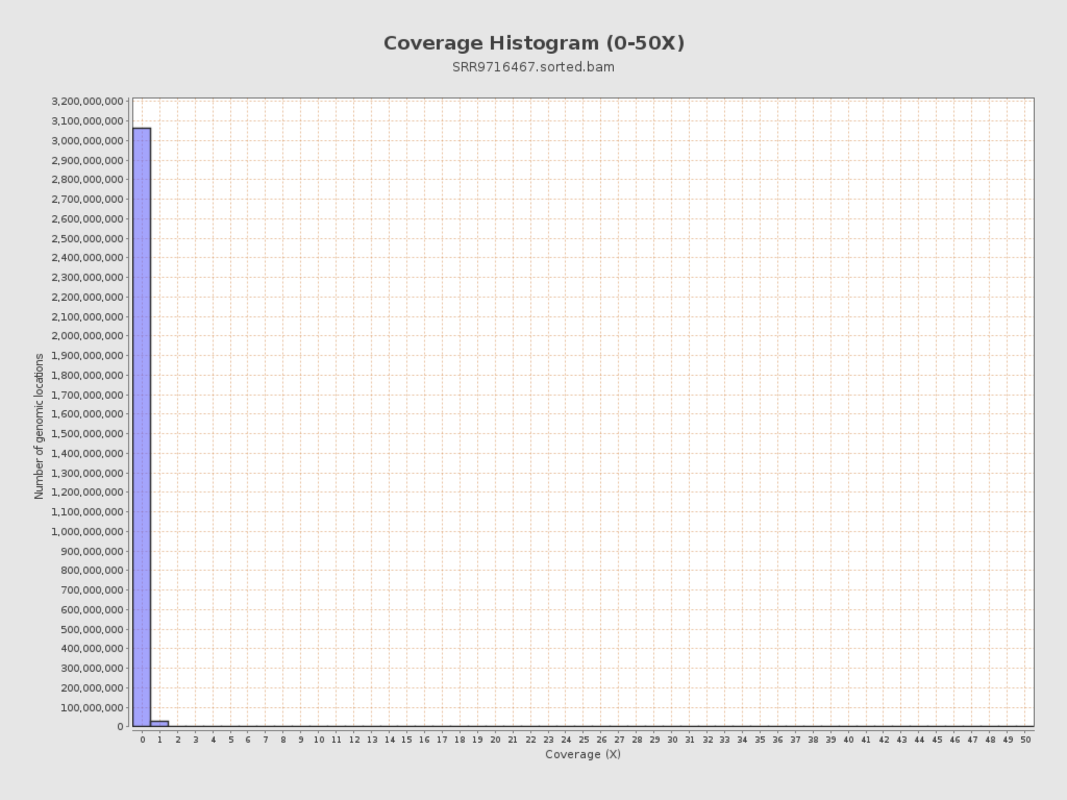
3. Results : Coverage across reference



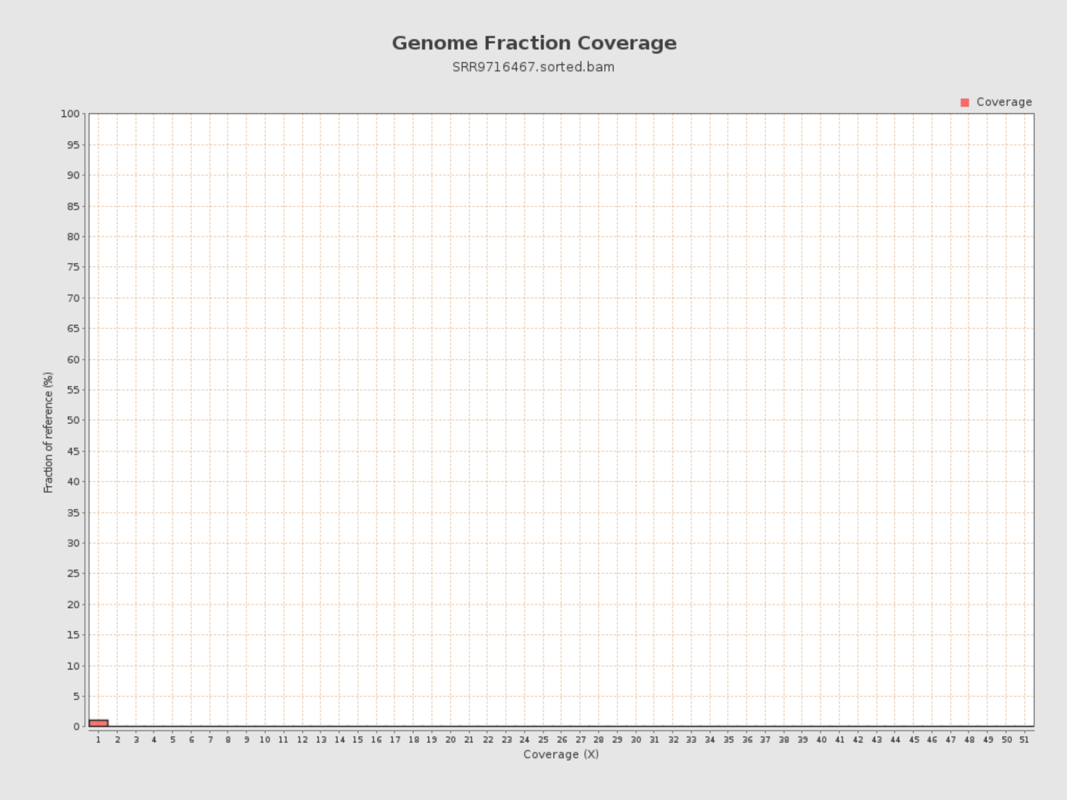
4. Results : Coverage Histogram



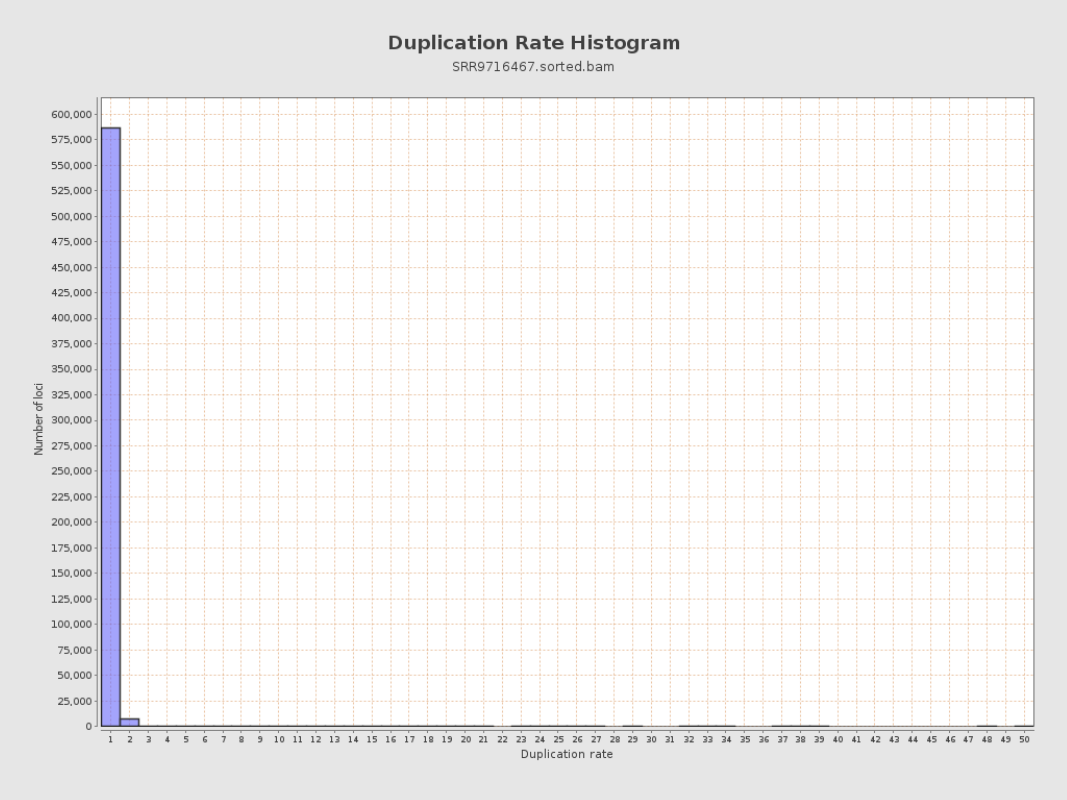
5. Results : Coverage Histogram (0-50X)



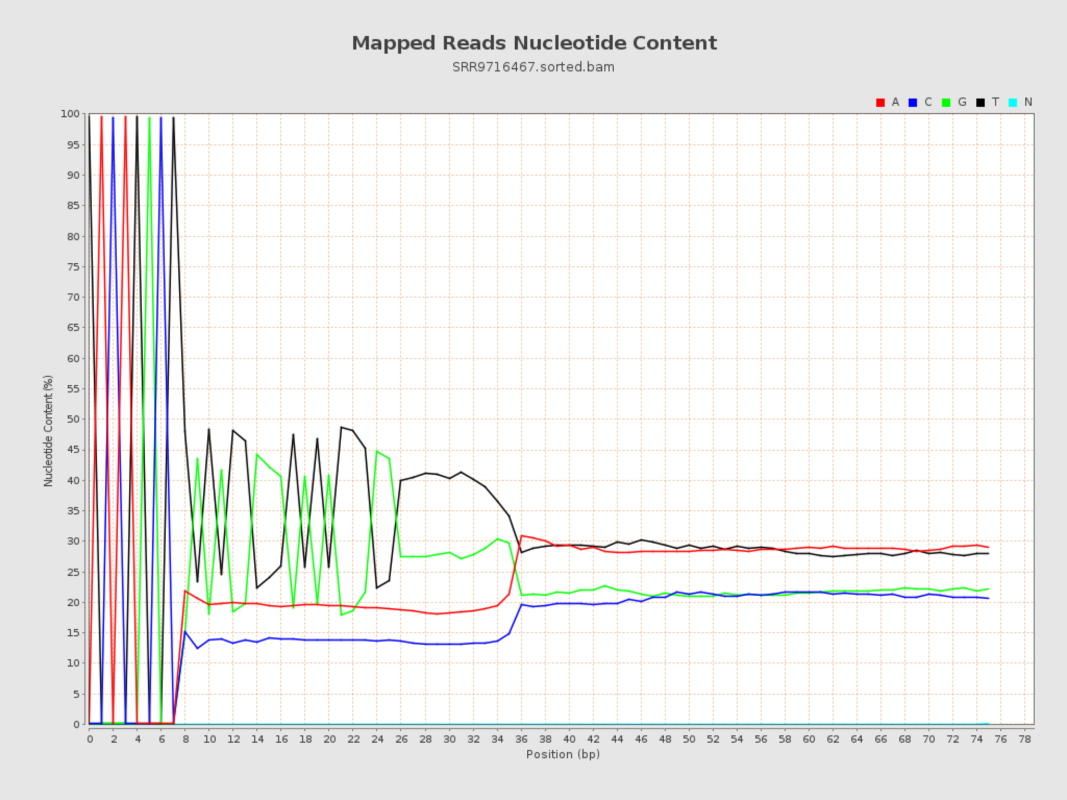
6. Results : Genome Fraction Coverage



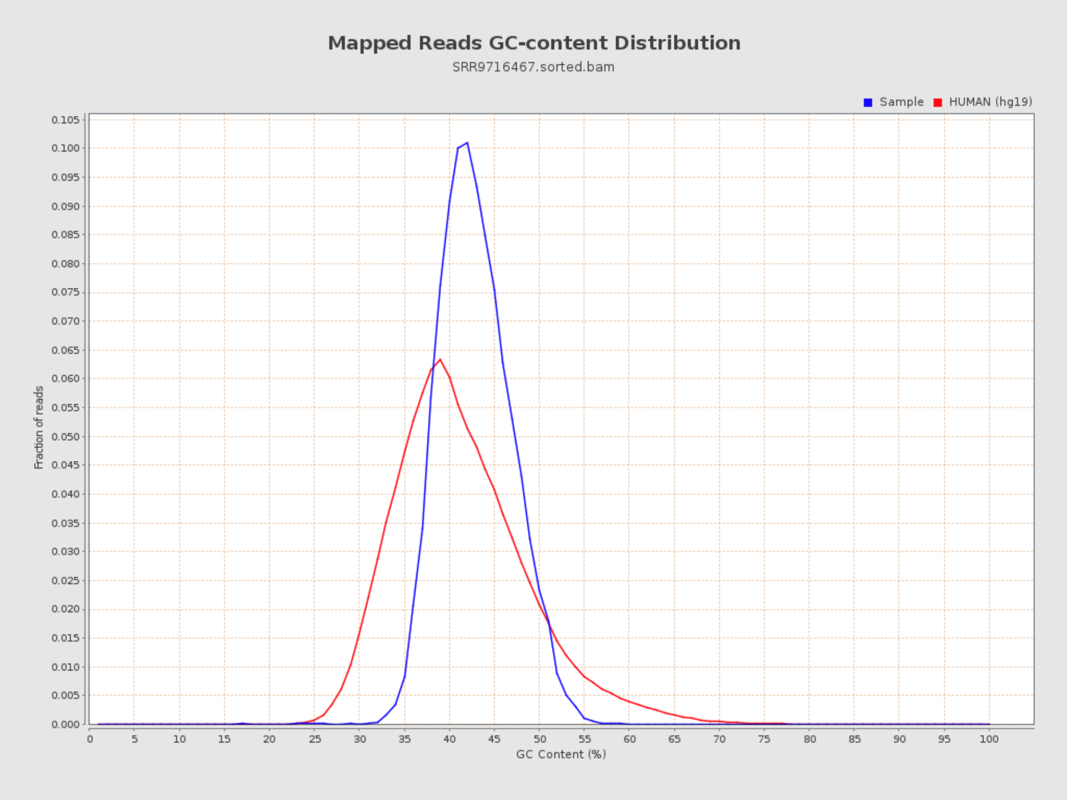
7. Results : Duplication Rate Histogram



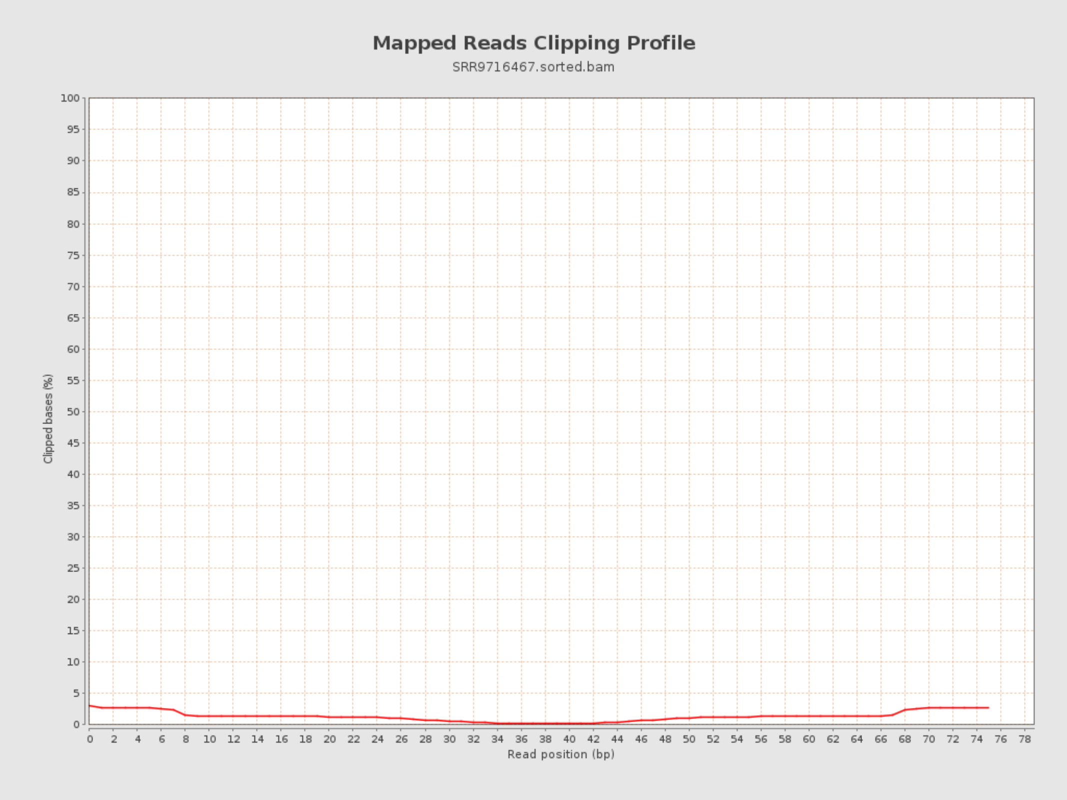
8. Results : Mapped Reads Nucleotide Content



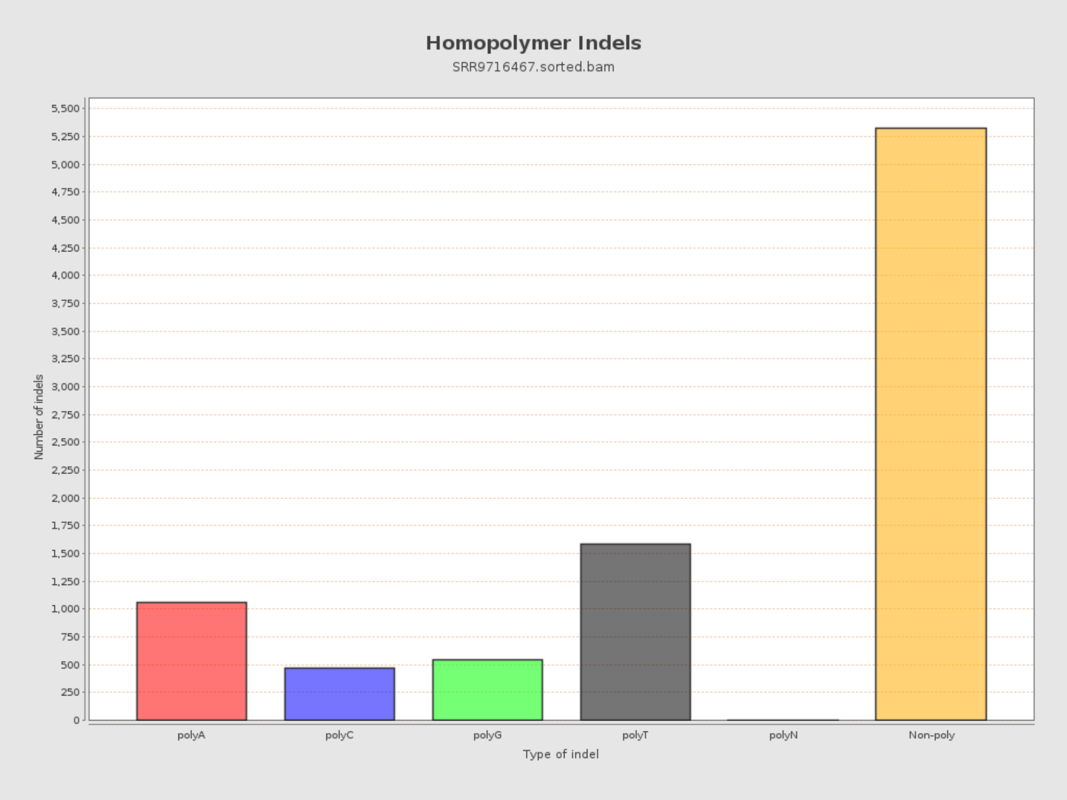
9. Results : Mapped Reads GC-content Distribution



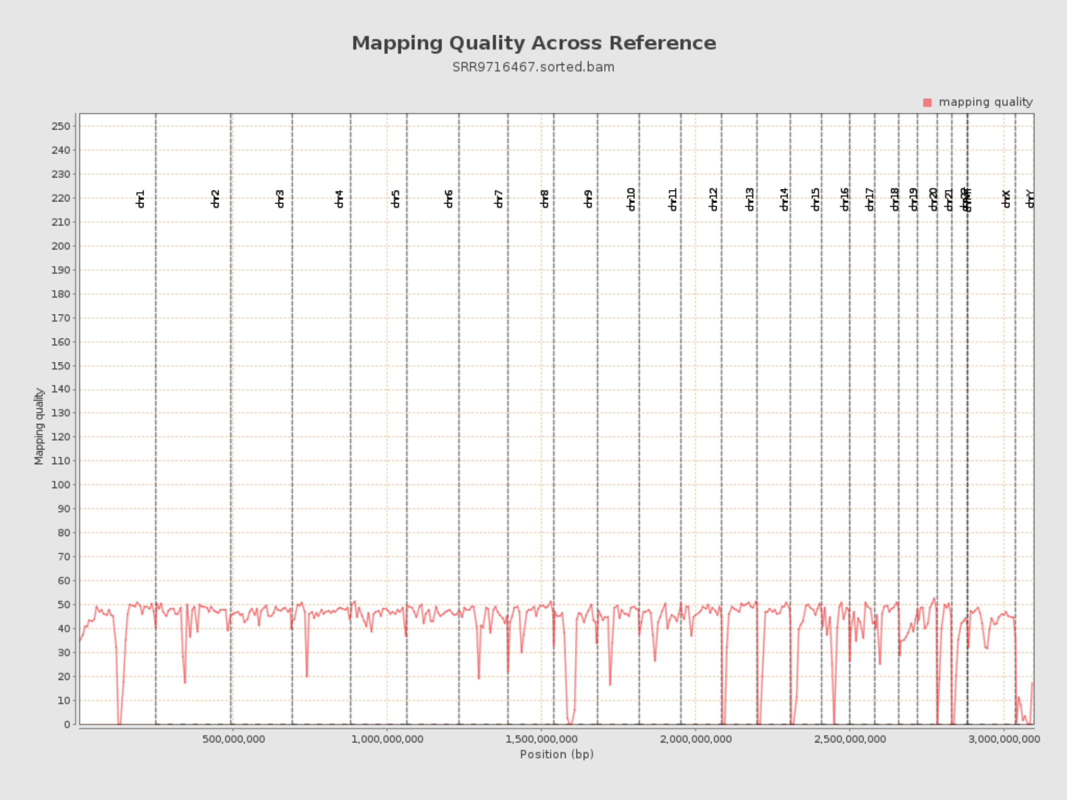
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram