Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 05:53:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716290.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_SRR9716290 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716290.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 05:53:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716290.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	715,583
Mapped reads	622,643 / 87.01%
Unmapped reads	92,940 / 12.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,767 / 0.25%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	10,676 / 1.49%
Duplication rate	1.2%
Clipped reads	623,044 / 87.07%

2.2. ACGT Content

Number/percentage of A's	7,999,973 / 22.84%
Number/percentage of C's	7,681,032 / 21.93%
Number/percentage of T's	10,233,930 / 29.21%
Number/percentage of G's	9,117,084 / 26.02%
Number/percentage of N's	980 / 0%
GC Percentage	47.95%

2.3. Coverage

Mean	0.0113

Standard Deviation	0.1261

2.4. Mapping Quality

Mean Mapping Quality	39.52

2.5. Mismatches and indels

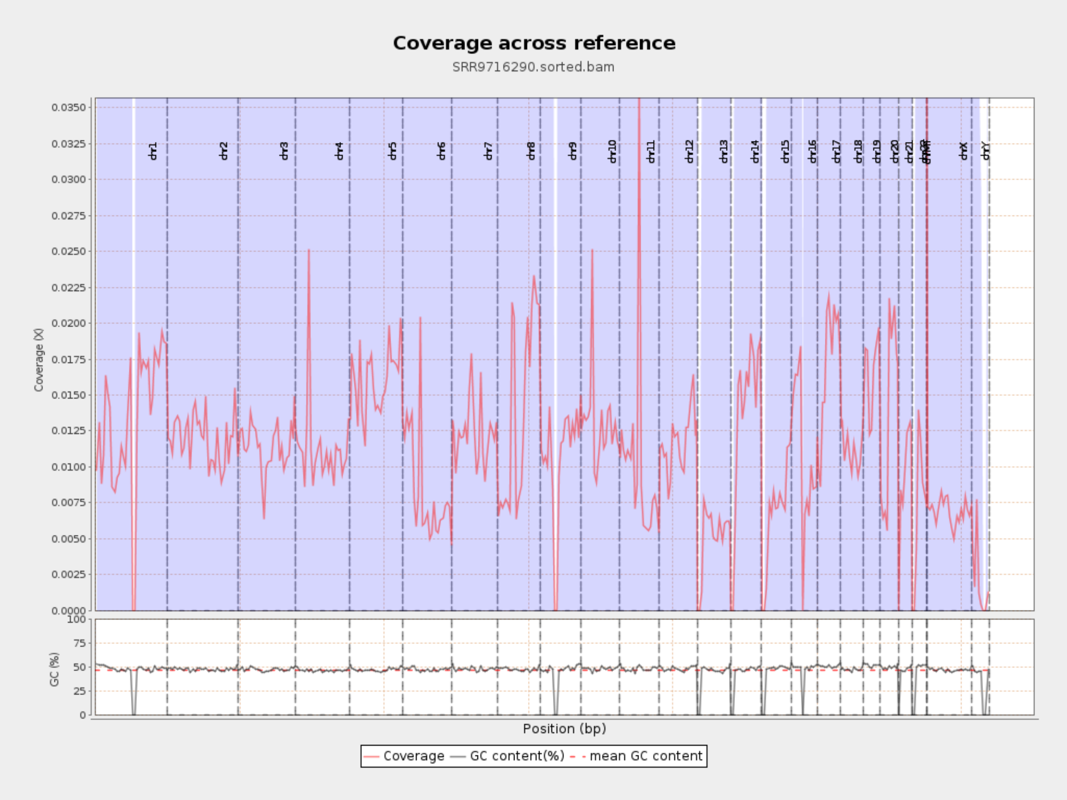
General error rate	0.55%
Mismatches	184,997
Insertions	2,810
Mapped reads with at least one insertion	0.45%
Deletions	6,221
Mapped reads with at least one deletion	0.99%
Homopolymer indels	37.83%

2.6. Chromosome stats

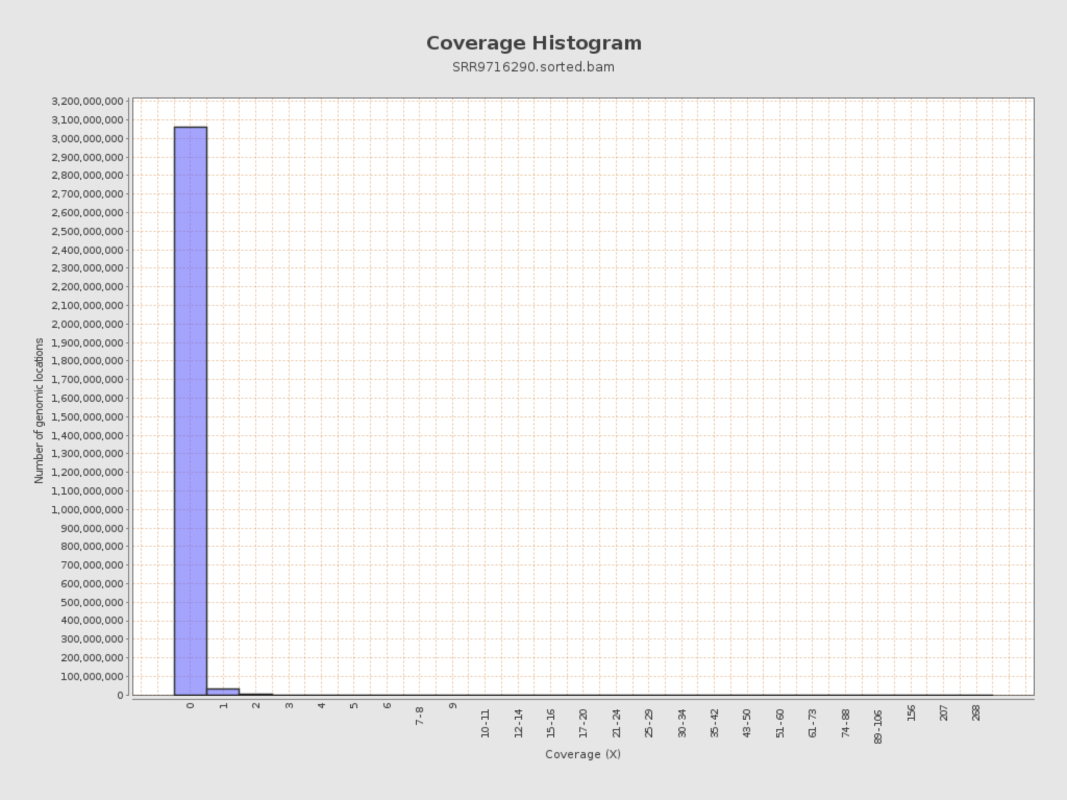
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3318722	0.0133	0.1465
chr2	243199373	2912296	0.012	0.1626
chr3	198022430	2251735	0.0114	0.1154
chr4	191154276	2171044	0.0114	0.1248
chr5	180915260	2928868	0.0162	0.1341
chr6	171115067	1454750	0.0085	0.0987
chr7	159138663	1971111	0.0124	0.1378

chr8	146364022	2022540	0.0138	0.1286
chr9	141213431	1478232	0.0105	0.1142
chr10	135534747	1776982	0.0131	0.1613
chr11	135006516	1405589	0.0104	0.1235
chr12	133851895	1567262	0.0117	0.1146
chr13	115169878	580006	0.005	0.0751
chr14	107349540	1456749	0.0136	0.1242
chr15	102531392	683865	0.0067	0.0865
chr16	90354753	953826	0.0106	0.1173
chr17	81195210	1384592	0.0171	0.142
chr18	78077248	864546	0.0111	0.1302
chr19	59128983	969856	0.0164	0.1482
chr20	63025520	864154	0.0137	0.1267
chr21	48129895	456647	0.0095	0.1102
chr22	51304566	377158	0.0074	0.0915
chrMT	16571	648	0.0391	0.205
chrX	155270560	1073611	0.0069	0.0923
chrY	59373566	118774	0.002	0.071

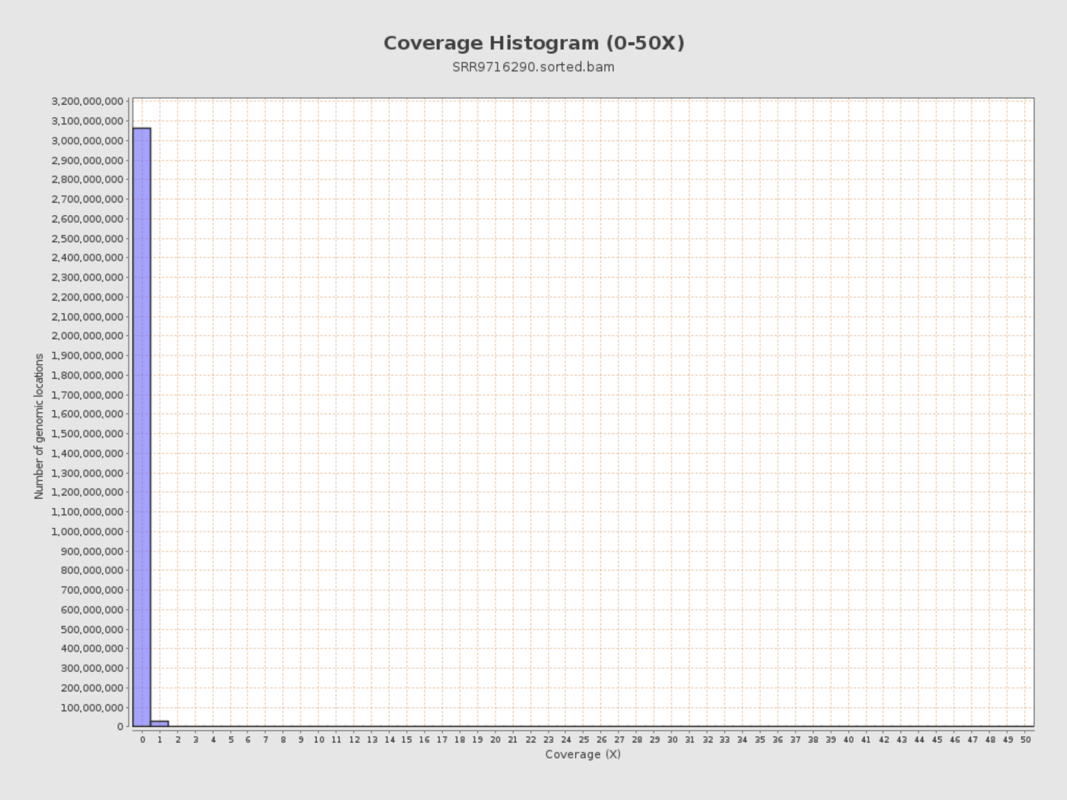
3. Results : Coverage across reference



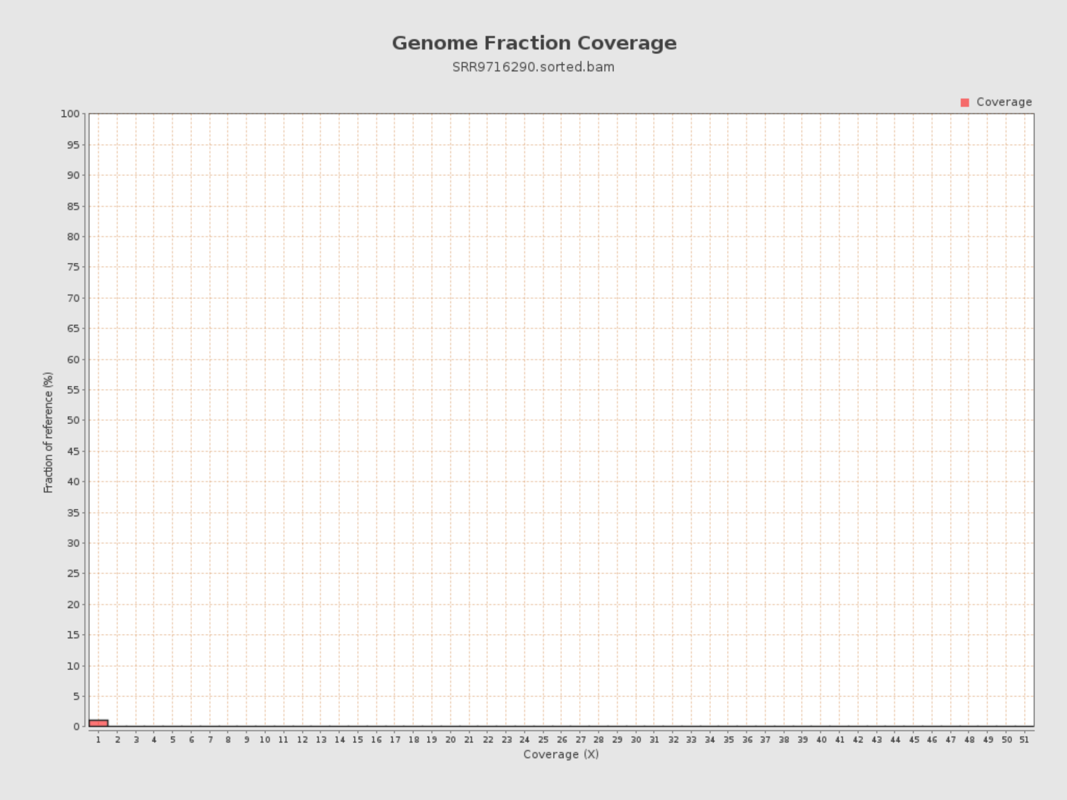
4. Results : Coverage Histogram



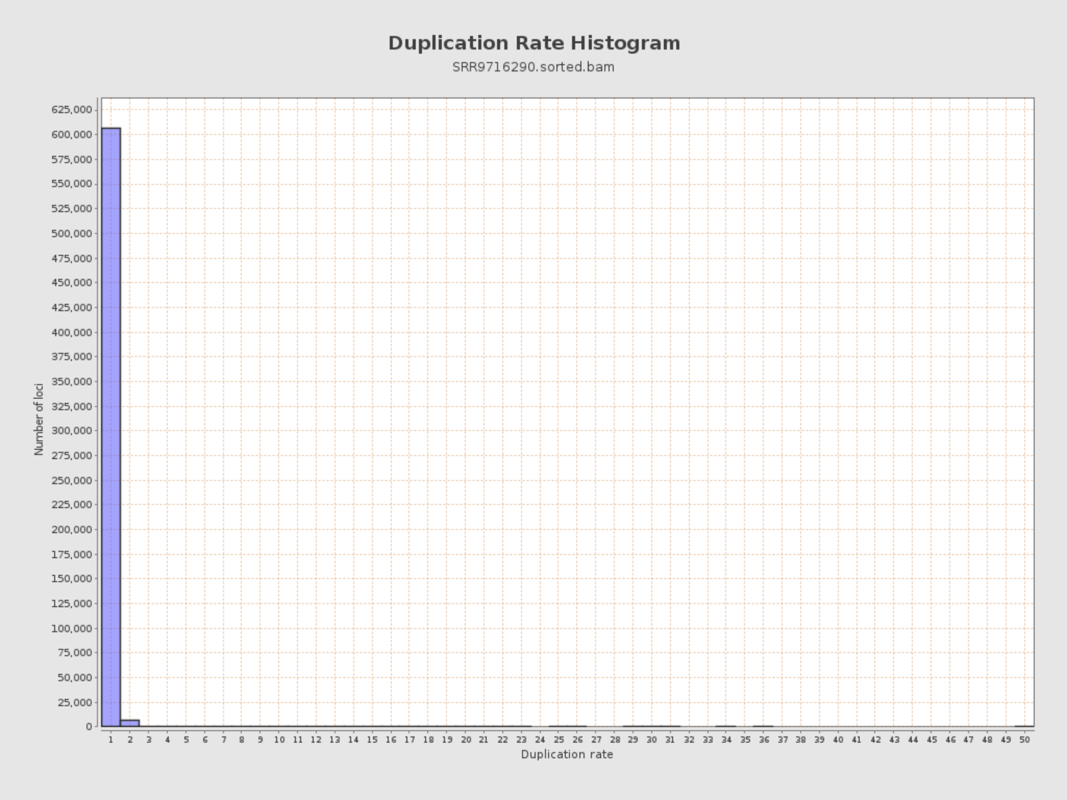
5. Results : Coverage Histogram (0-50X)



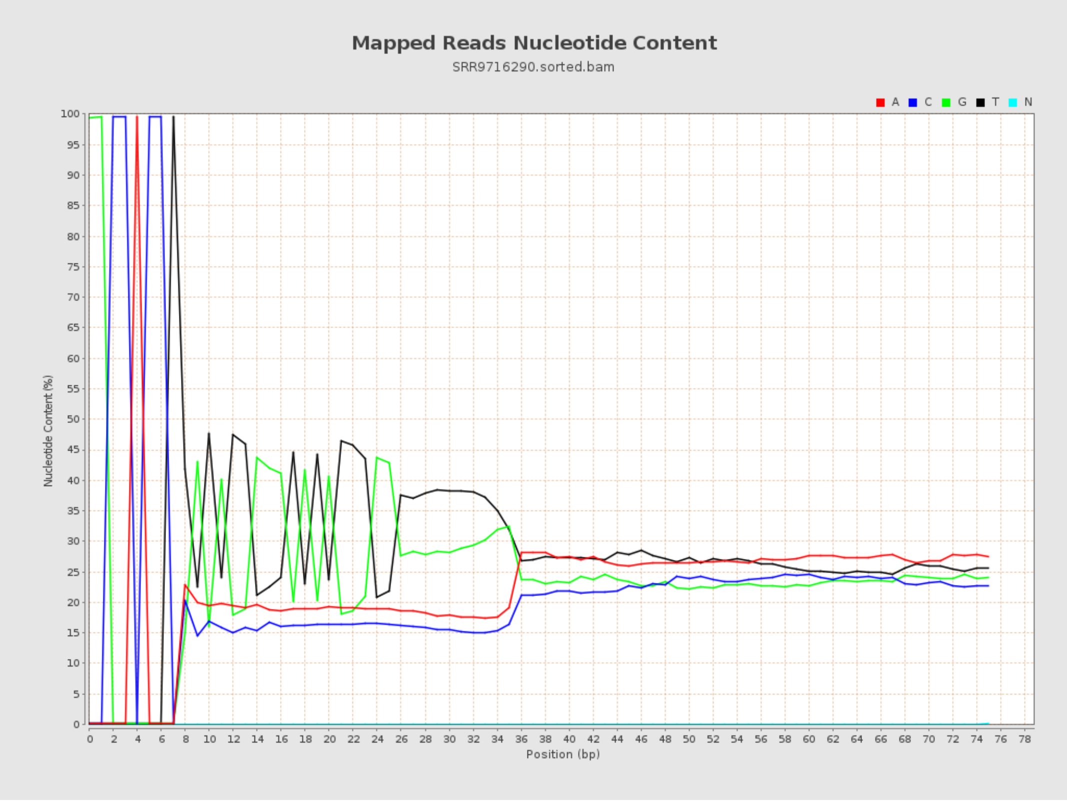
6. Results : Genome Fraction Coverage



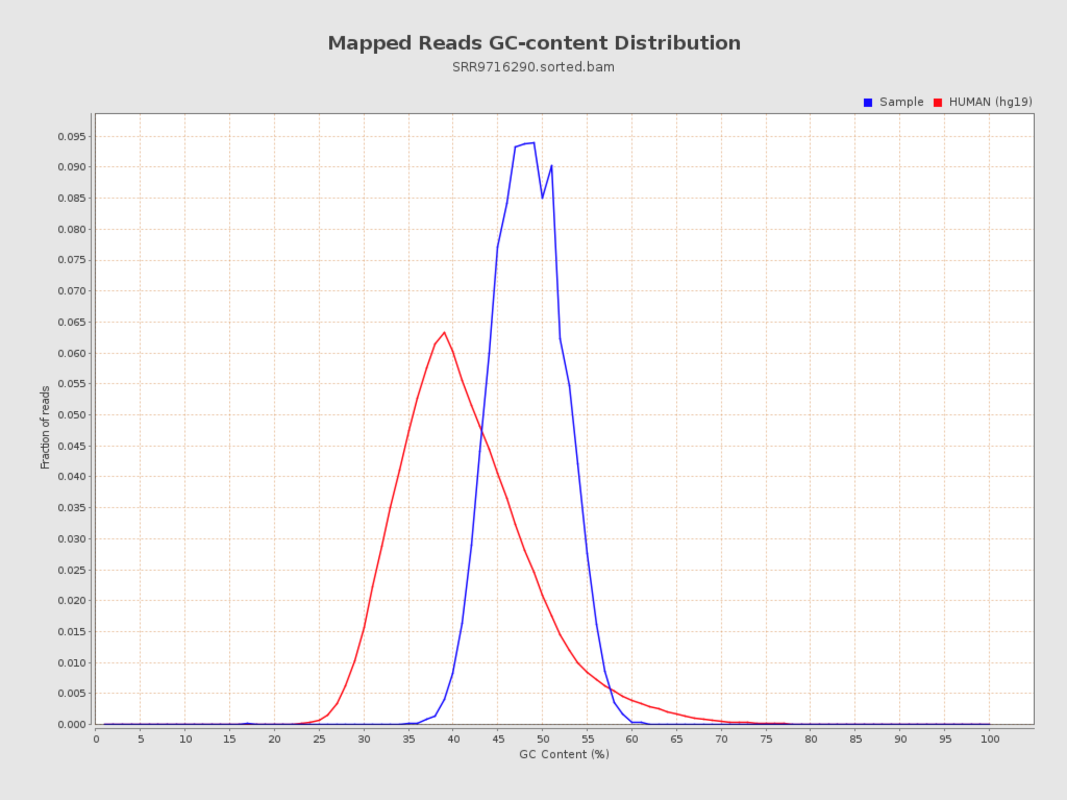
7. Results : Duplication Rate Histogram



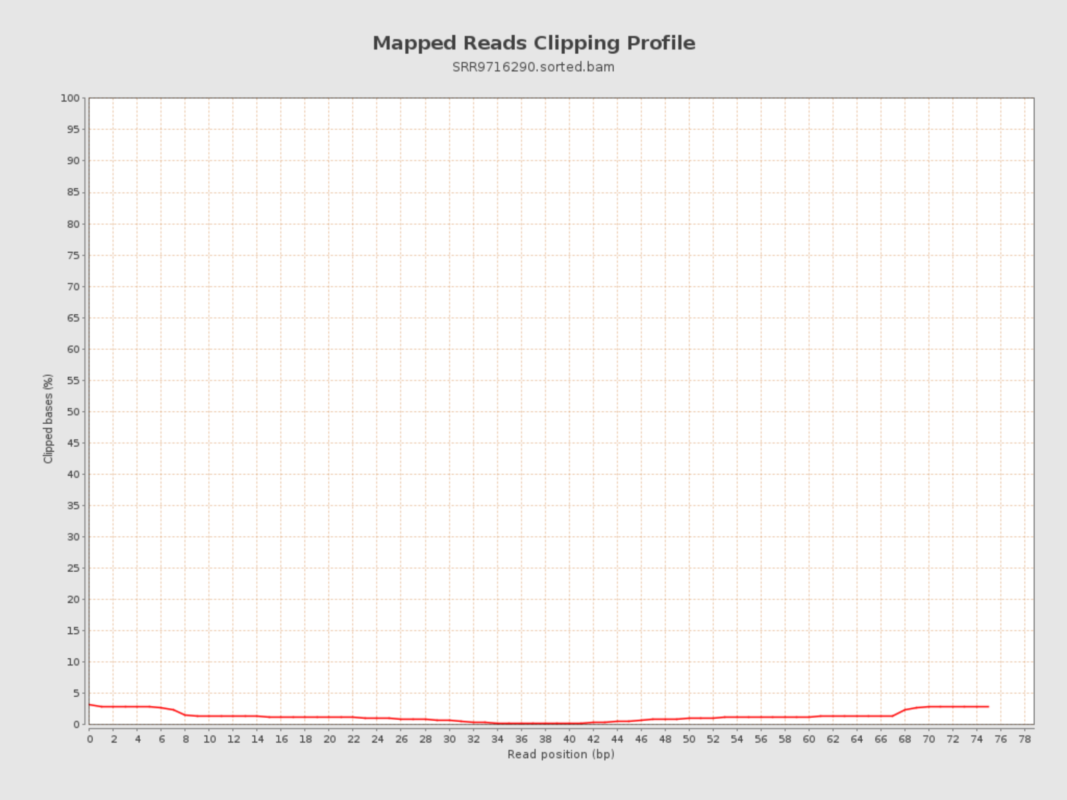
8. Results : Mapped Reads Nucleotide Content



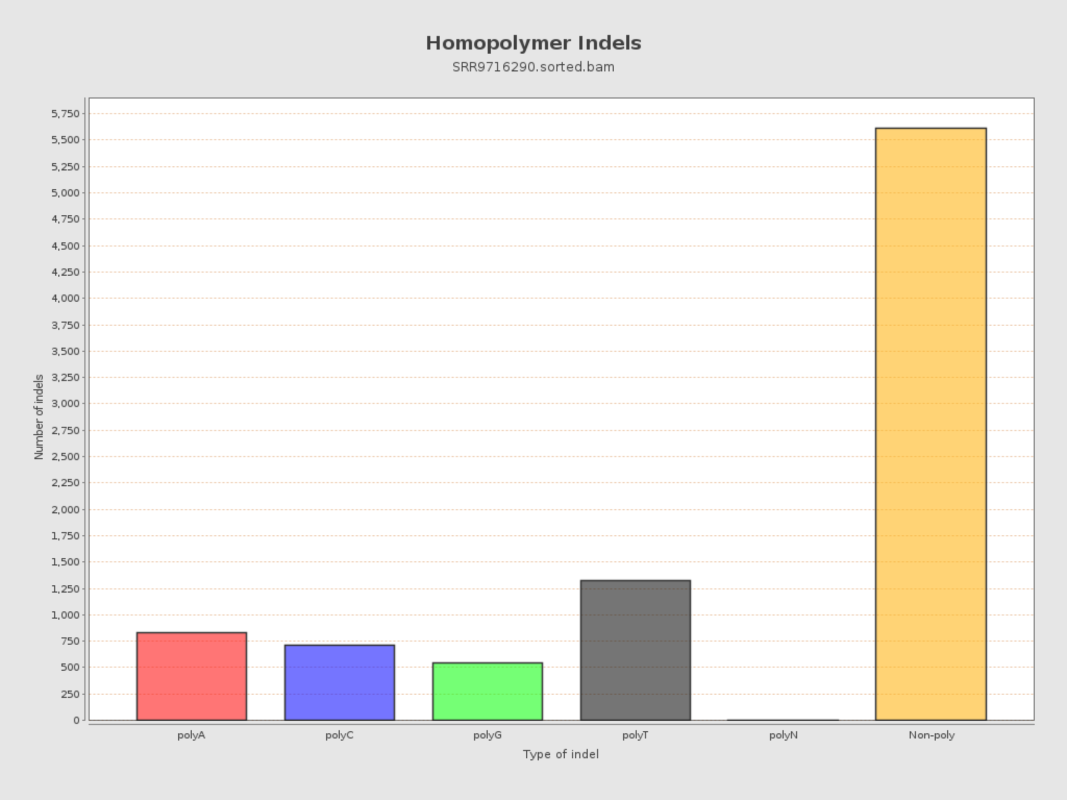
9. Results : Mapped Reads GC-content Distribution



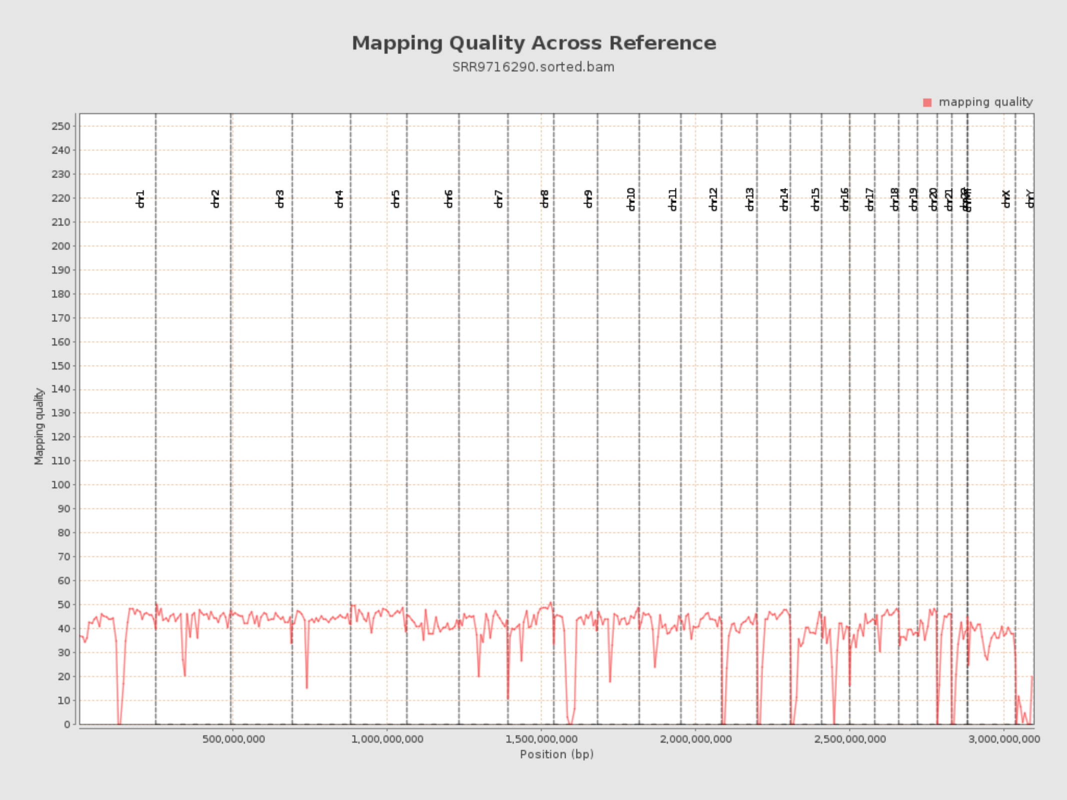
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram