Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 05:34:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716282.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_SRR9716282 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716282.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 05:34:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716282.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	879,800
Mapped reads	796,360 / 90.52%
Unmapped reads	83,440 / 9.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,794 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	14,561 / 1.66%
Duplication rate	1.36%
Clipped reads	797,726 / 90.67%

2.2. ACGT Content

Number/percentage of A's	11,504,748 / 25.33%
Number/percentage of C's	8,702,708 / 19.16%
Number/percentage of T's	14,377,177 / 31.65%
Number/percentage of G's	10,842,594 / 23.87%
Number/percentage of N's	979 / 0%
GC Percentage	43.02%

2.3. Coverage

Mean	0.0147

Standard Deviation	0.1474

2.4. Mapping Quality

Mean Mapping Quality	43.84

2.5. Mismatches and indels

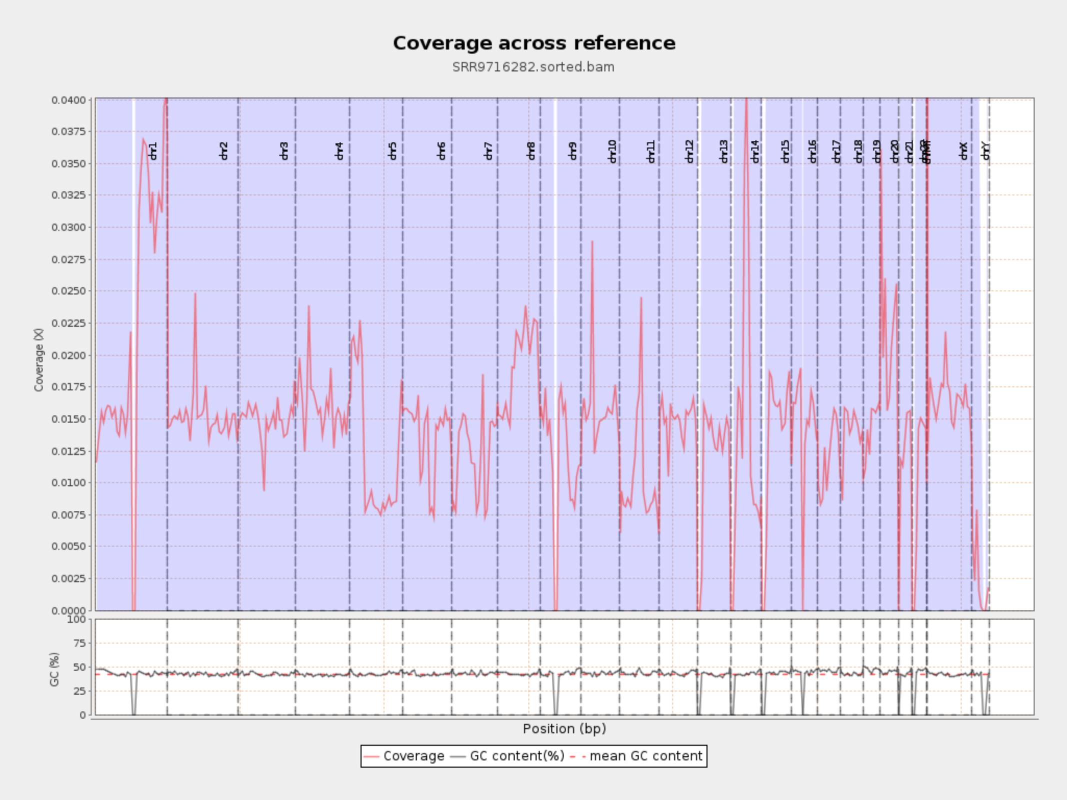
General error rate	0.5%
Mismatches	223,432
Insertions	3,000
Mapped reads with at least one insertion	0.38%
Deletions	7,229
Mapped reads with at least one deletion	0.9%
Homopolymer indels	41.43%

2.6. Chromosome stats

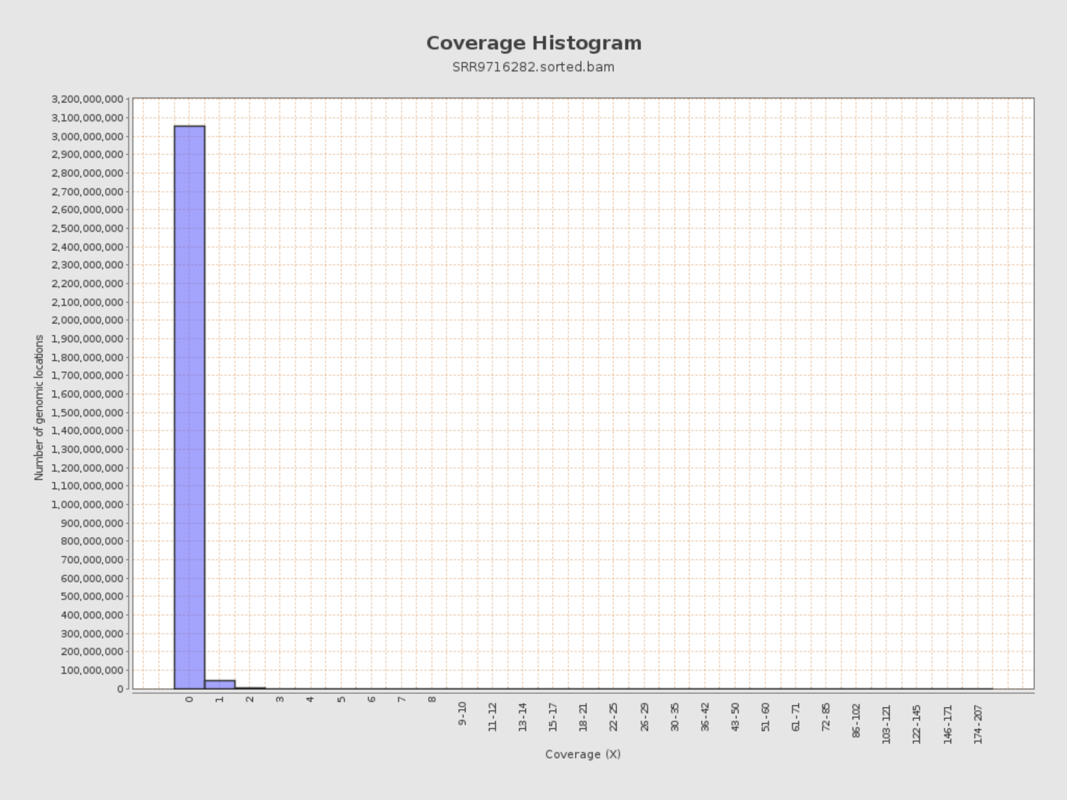
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5505897	0.0221	0.2151
chr2	243199373	3704760	0.0152	0.1601
chr3	198022430	2932037	0.0148	0.1282
chr4	191154276	3070816	0.0161	0.1381
chr5	180915260	2207560	0.0122	0.1159
chr6	171115067	2351318	0.0137	0.1261
chr7	159138663	1937876	0.0122	0.1287

chr8	146364022	2810337	0.0192	0.1565
chr9	141213431	1661342	0.0118	0.1494
chr10	135534747	2157962	0.0159	0.1768
chr11	135006516	1427108	0.0106	0.1306
chr12	133851895	1993737	0.0149	0.1287
chr13	115169878	1350255	0.0117	0.1123
chr14	107349540	1558087	0.0145	0.1307
chr15	102531392	1377932	0.0134	0.1209
chr16	90354753	1289867	0.0143	0.1317
chr17	81195210	970415	0.012	0.1164
chr18	78077248	1082642	0.0139	0.2231
chr19	59128983	842499	0.0142	0.1578
chr20	63025520	1395542	0.0221	0.1573
chr21	48129895	583222	0.0121	0.1257
chr22	51304566	509922	0.0099	0.1034
chrMT	16571	8703	0.5252	0.7956
chrX	155270560	2574431	0.0166	0.1451
chrY	59373566	136134	0.0023	0.0693

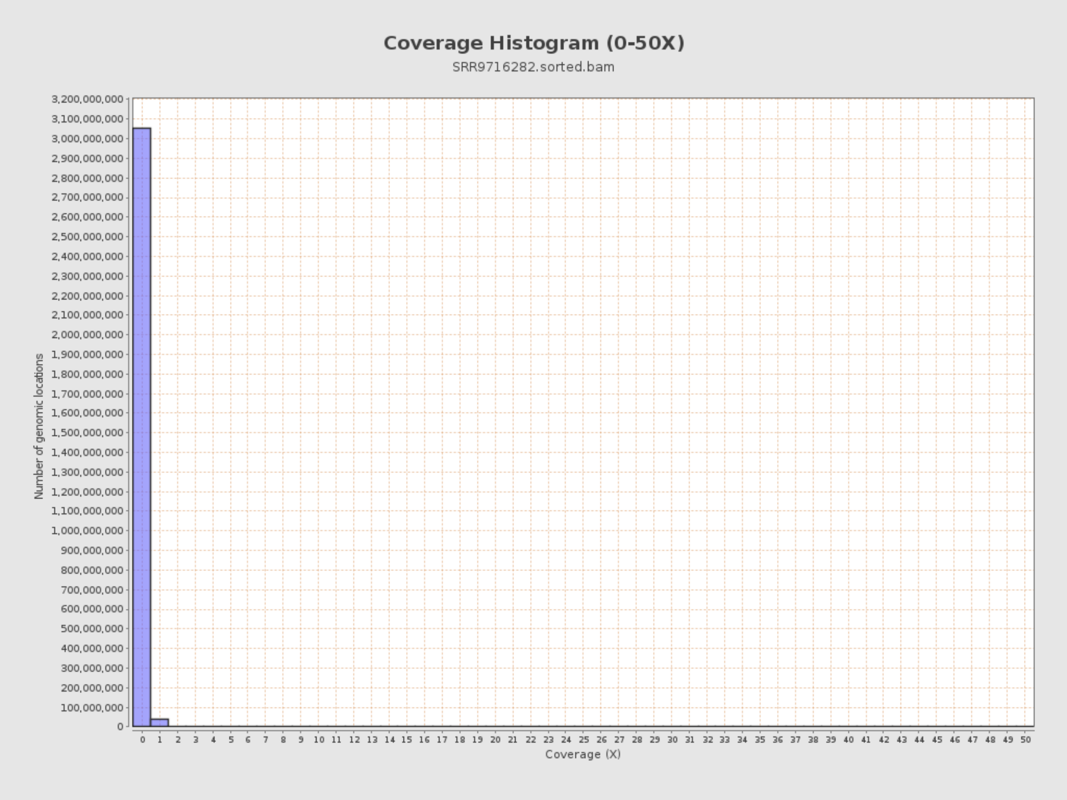
3. Results : Coverage across reference



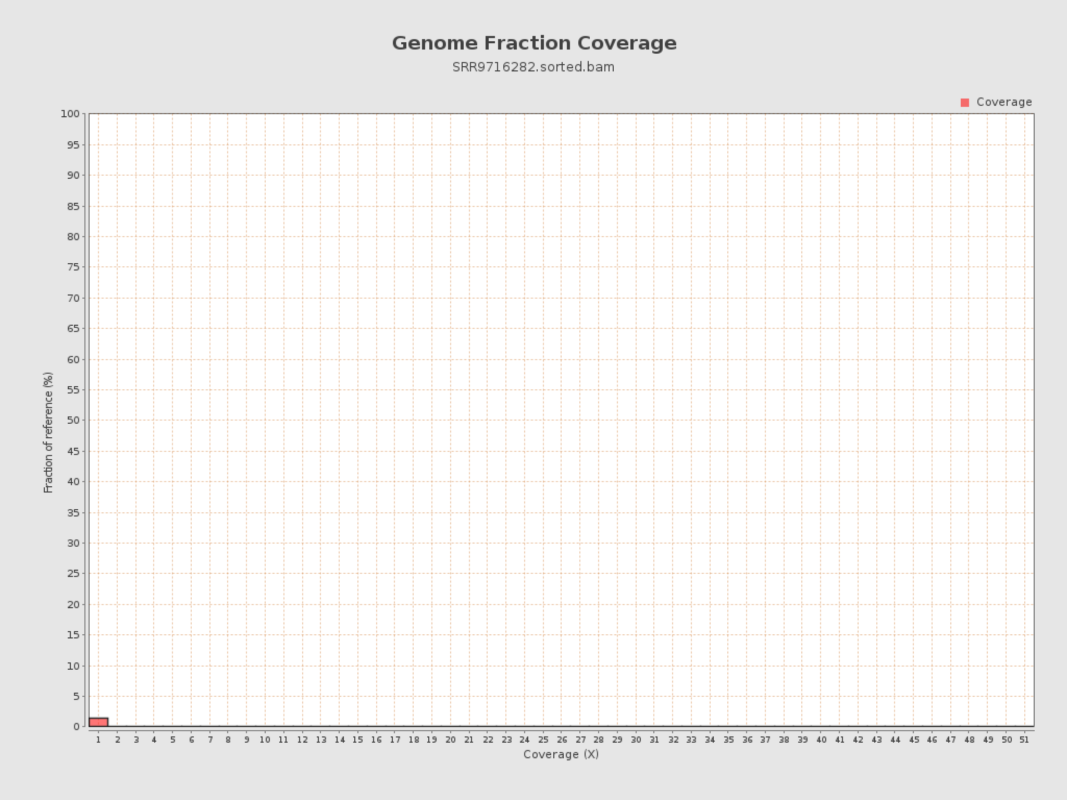
4. Results : Coverage Histogram



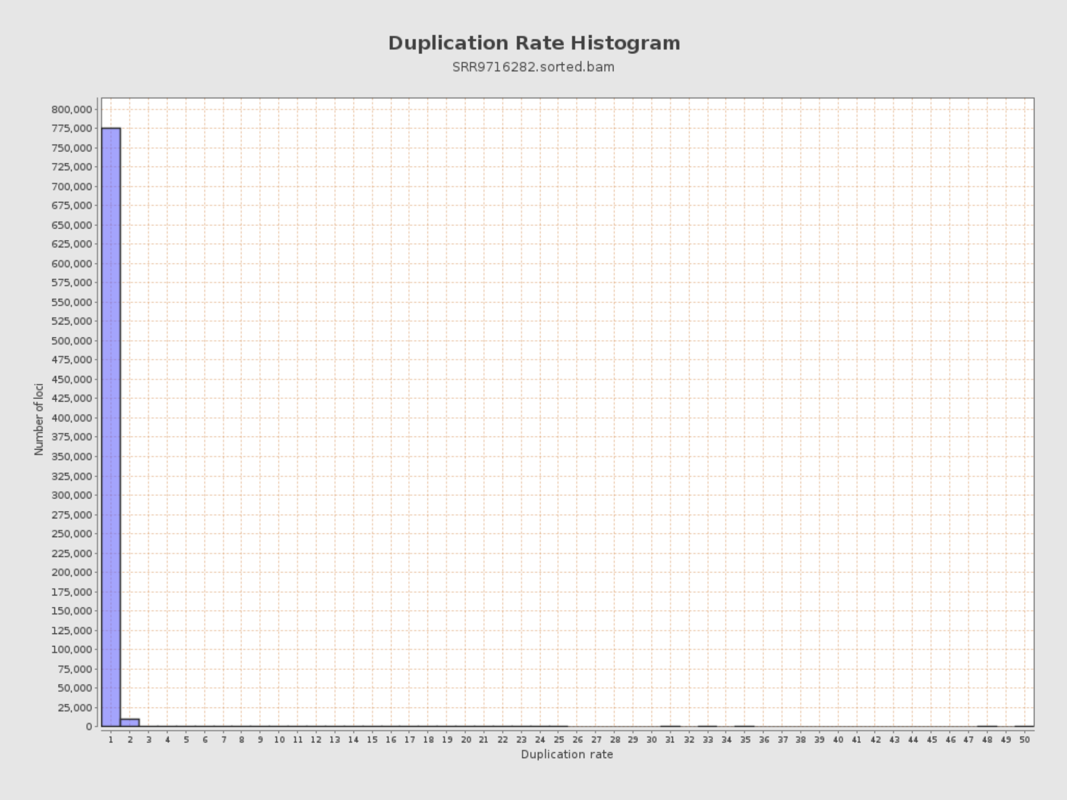
5. Results : Coverage Histogram (0-50X)



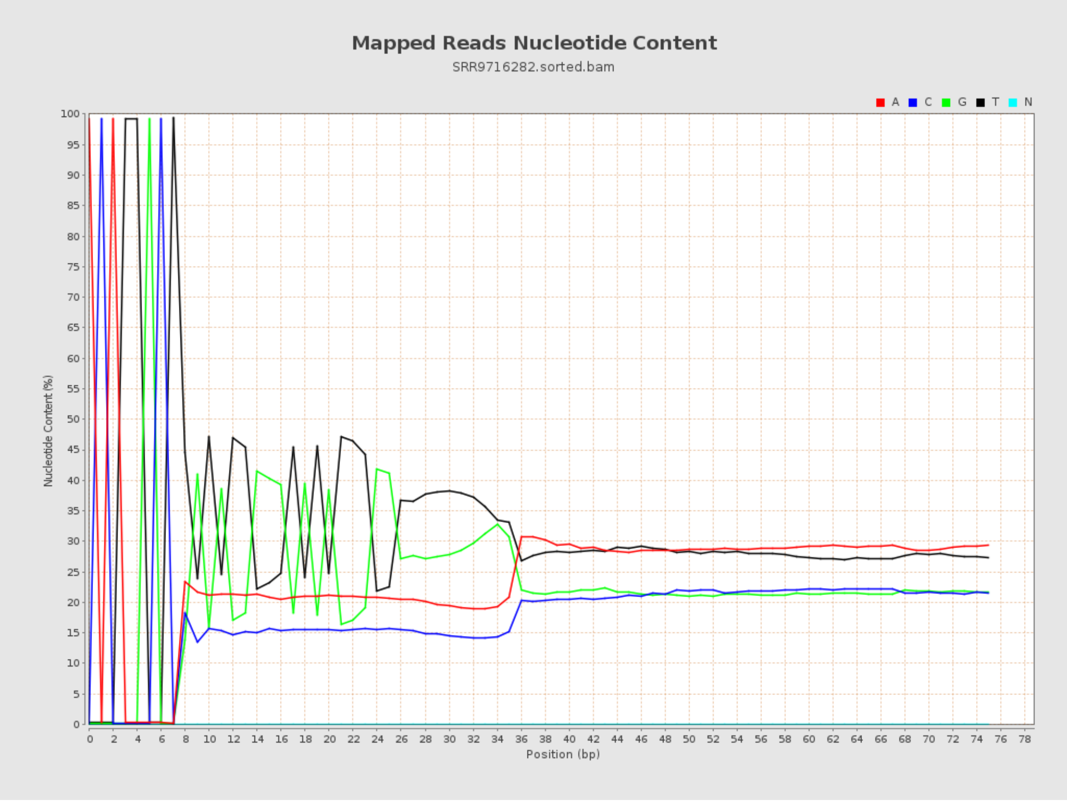
6. Results : Genome Fraction Coverage



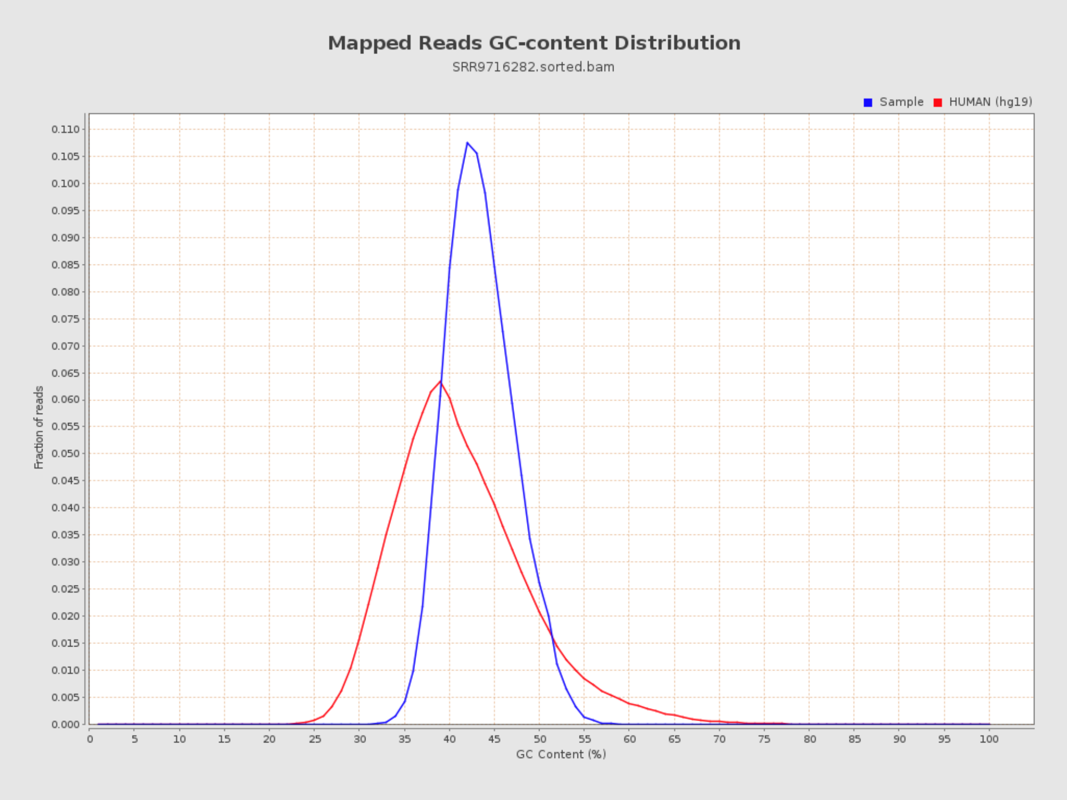
7. Results : Duplication Rate Histogram



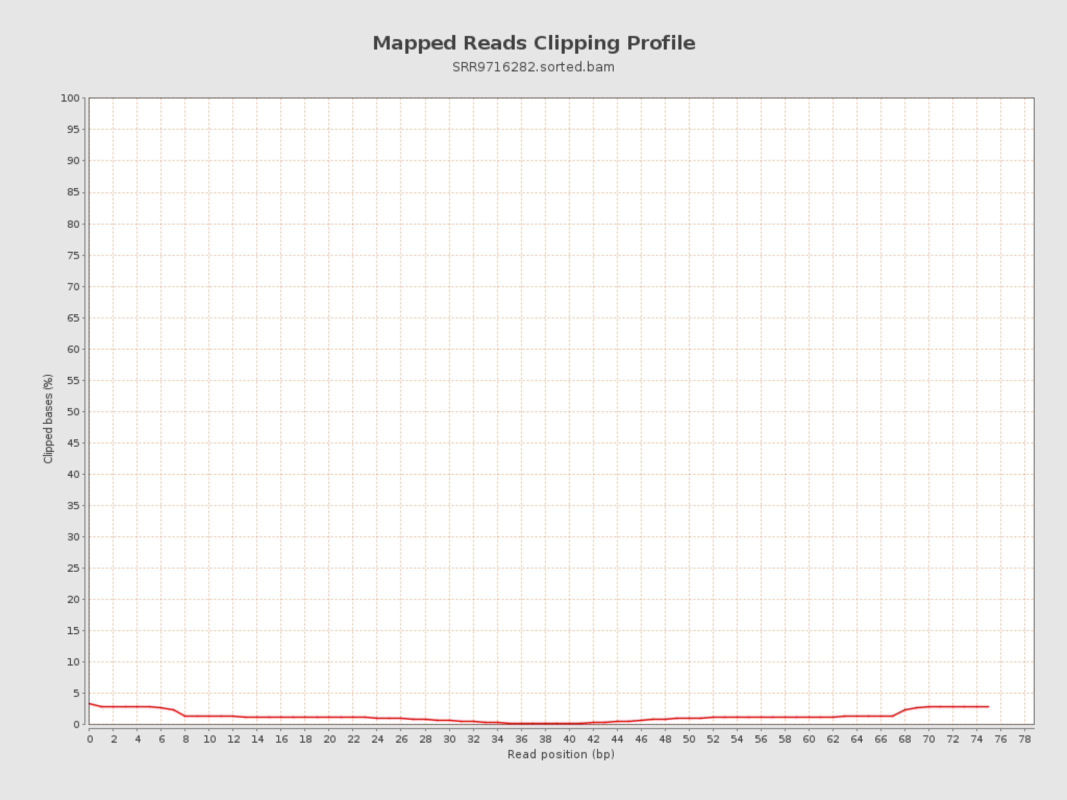
8. Results : Mapped Reads Nucleotide Content



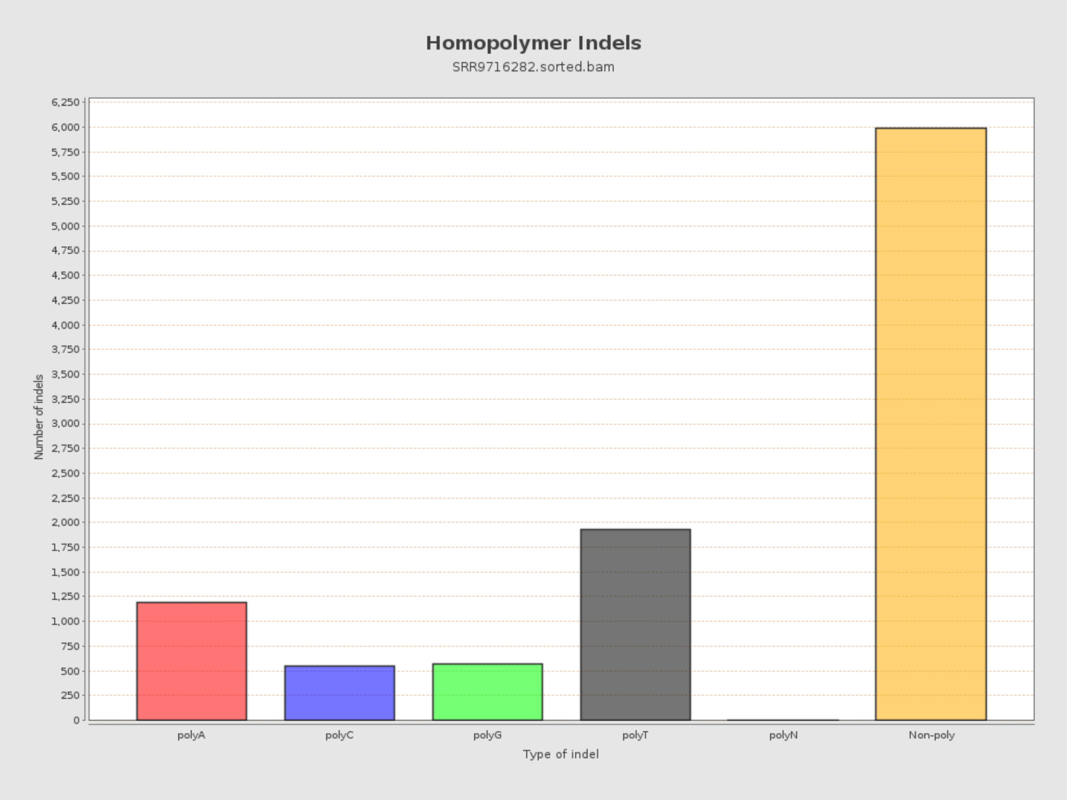
9. Results : Mapped Reads GC-content Distribution



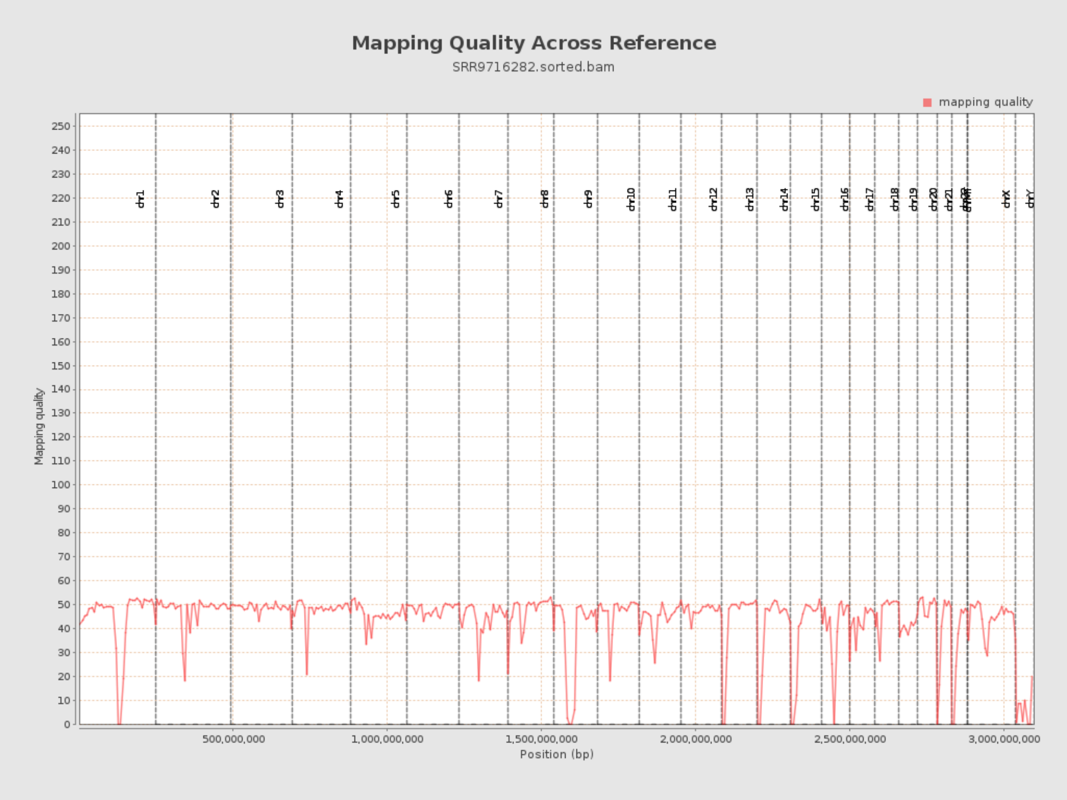
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram