Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 16:19:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716482.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_SRR9716482 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716482.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 16:19:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716482.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	644,510
Mapped reads	561,115 / 87.06%
Unmapped reads	83,395 / 12.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,632 / 0.25%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	9,372 / 1.45%
Duplication rate	1.16%
Clipped reads	562,317 / 87.25%

2.2. ACGT Content

Number/percentage of A's	6,945,201 / 22.03%
Number/percentage of C's	6,505,384 / 20.63%
Number/percentage of T's	9,591,619 / 30.42%
Number/percentage of G's	8,485,249 / 26.91%
Number/percentage of N's	832 / 0%
GC Percentage	47.55%

2.3. Coverage

Mean	0.0102

Standard Deviation	0.119

2.4. Mapping Quality

Mean Mapping Quality	39.99

2.5. Mismatches and indels

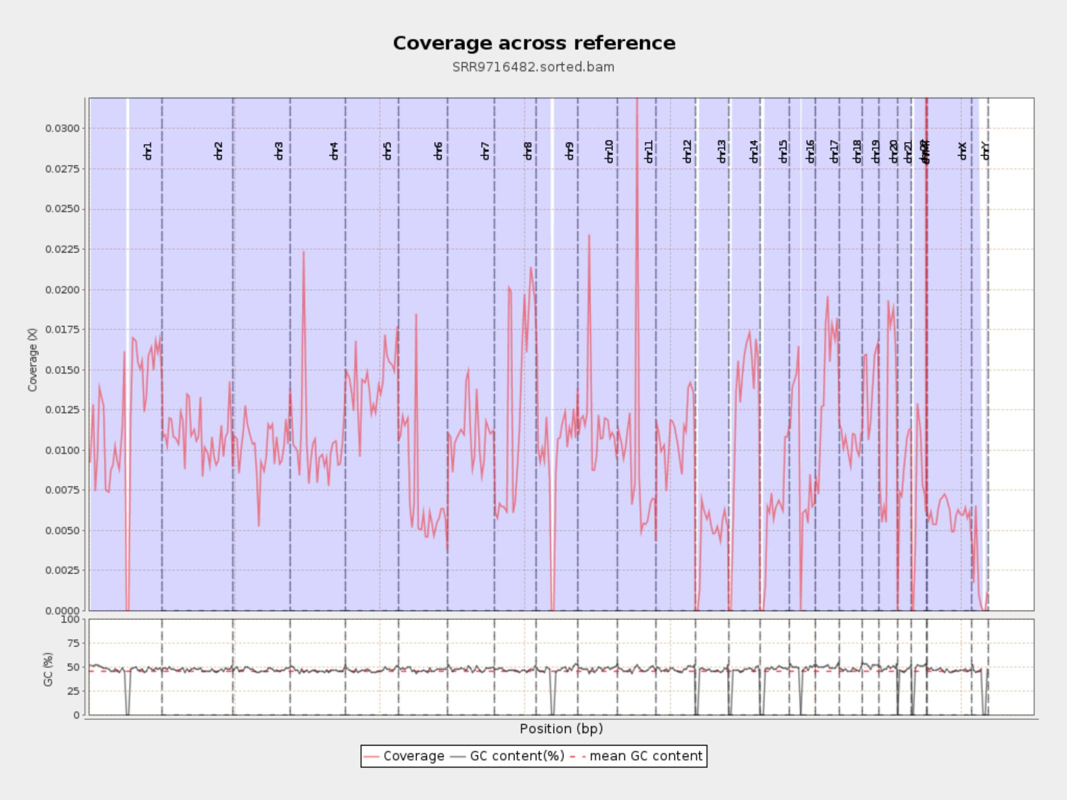
General error rate	0.54%
Mismatches	166,631
Insertions	2,073
Mapped reads with at least one insertion	0.37%
Deletions	5,678
Mapped reads with at least one deletion	1%
Homopolymer indels	39.16%

2.6. Chromosome stats

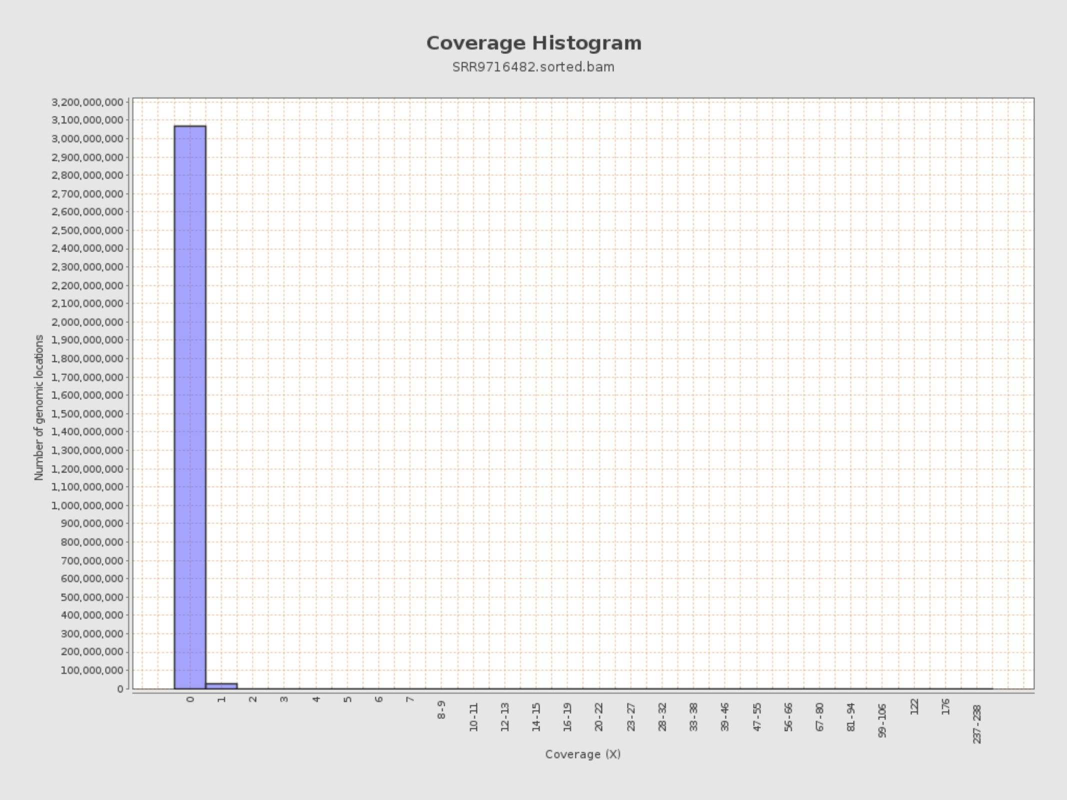
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2980533	0.012	0.1441
chr2	243199373	2648962	0.0109	0.151
chr3	198022430	2014983	0.0102	0.1094
chr4	191154276	1982995	0.0104	0.1176
chr5	180915260	2575396	0.0142	0.1251
chr6	171115067	1267371	0.0074	0.0919
chr7	159138663	1746637	0.011	0.1256

chr8	146364022	1865690	0.0127	0.1218
chr9	141213431	1336049	0.0095	0.1071
chr10	135534747	1581192	0.0117	0.1561
chr11	135006516	1284672	0.0095	0.1132
chr12	133851895	1474086	0.011	0.1098
chr13	115169878	538846	0.0047	0.072
chr14	107349540	1360475	0.0127	0.1194
chr15	102531392	611485	0.006	0.0809
chr16	90354753	823052	0.0091	0.1065
chr17	81195210	1199259	0.0148	0.1302
chr18	78077248	813780	0.0104	0.1253
chr19	59128983	838732	0.0142	0.1424
chr20	63025520	781637	0.0124	0.1194
chr21	48129895	406103	0.0084	0.1022
chr22	51304566	345595	0.0067	0.0871
chrMT	16571	13120	0.7917	1.081
chrX	155270560	944670	0.0061	0.0861
chrY	59373566	102675	0.0017	0.0667

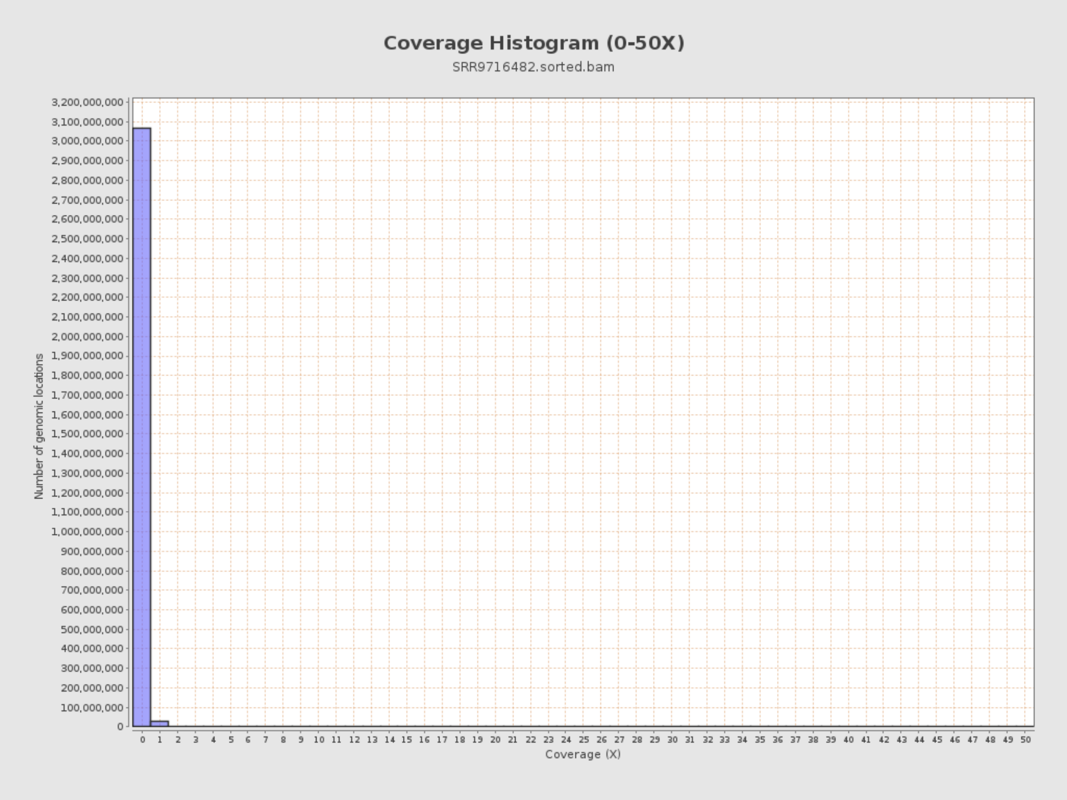
3. Results : Coverage across reference



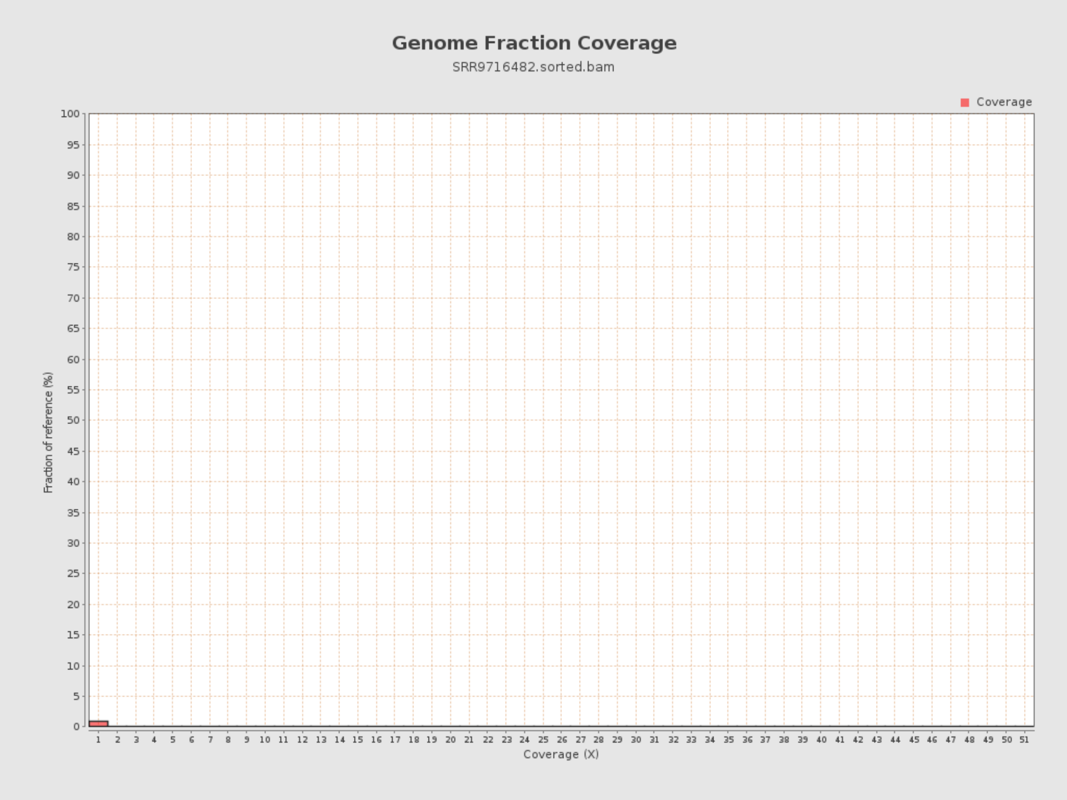
4. Results : Coverage Histogram



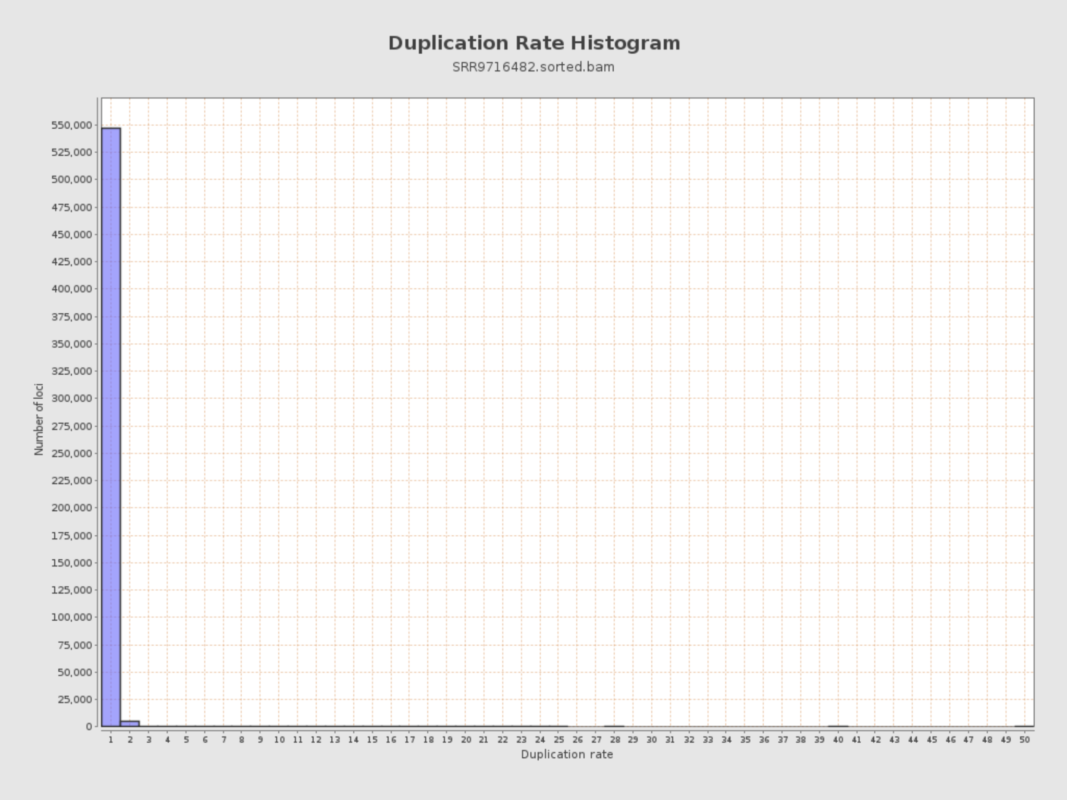
5. Results : Coverage Histogram (0-50X)



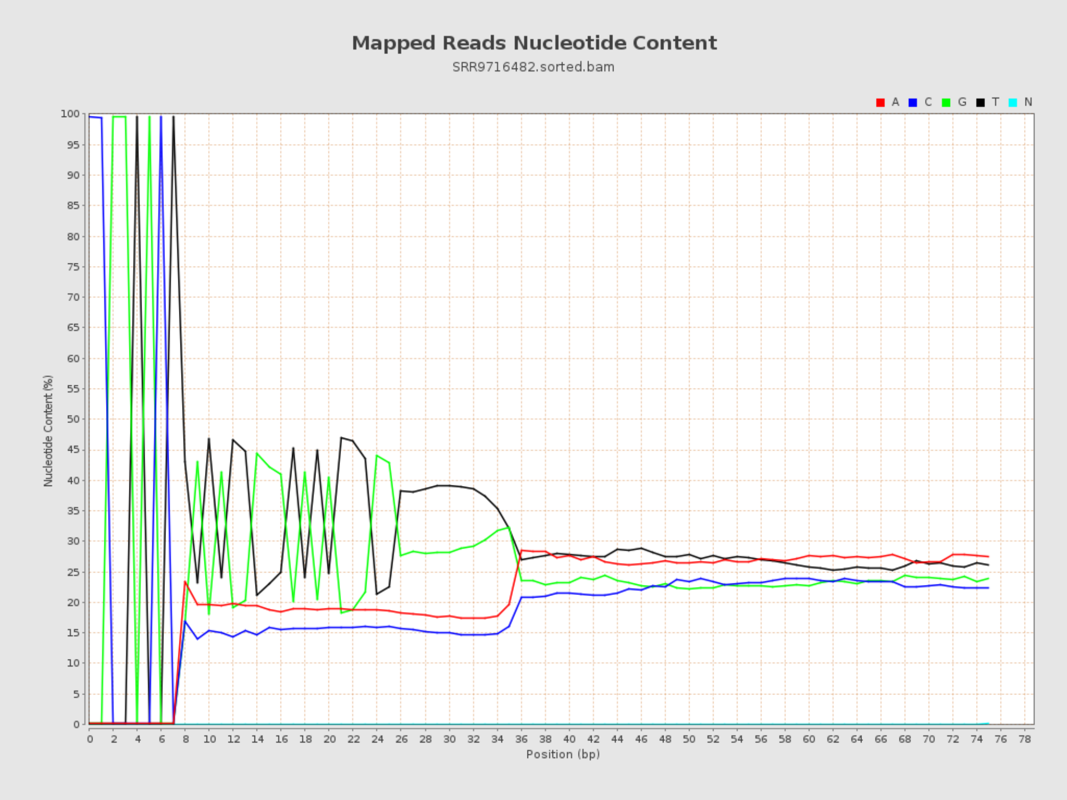
6. Results : Genome Fraction Coverage



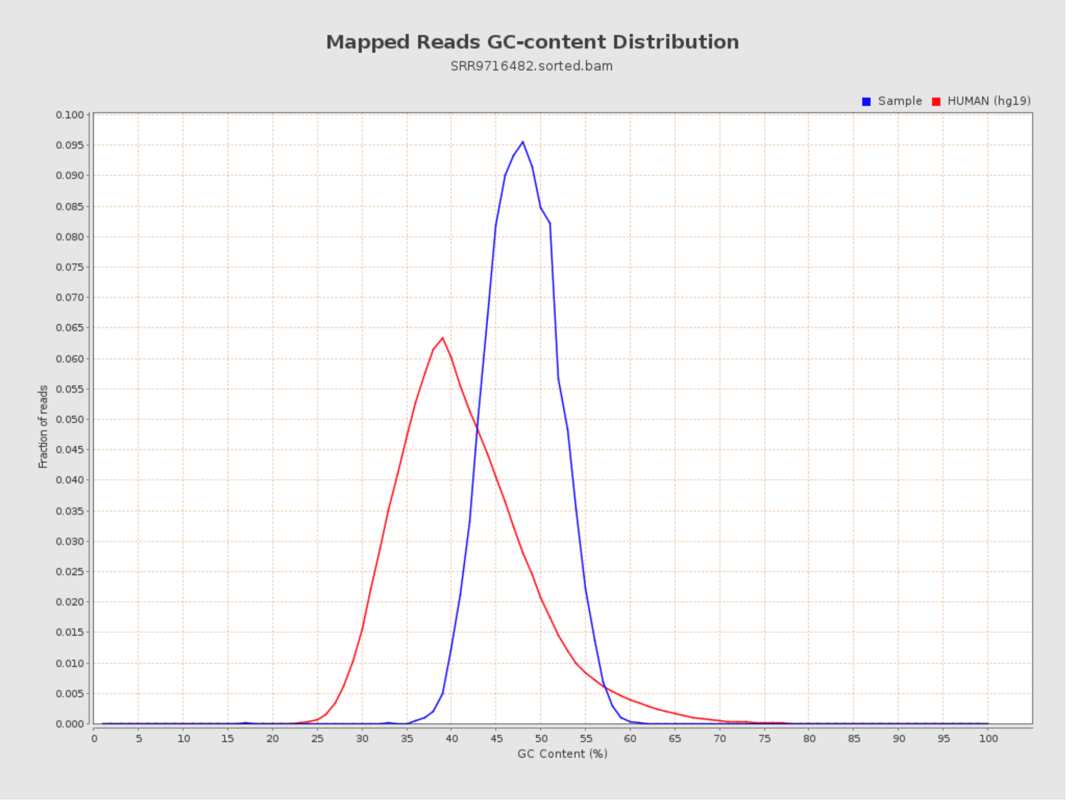
7. Results : Duplication Rate Histogram



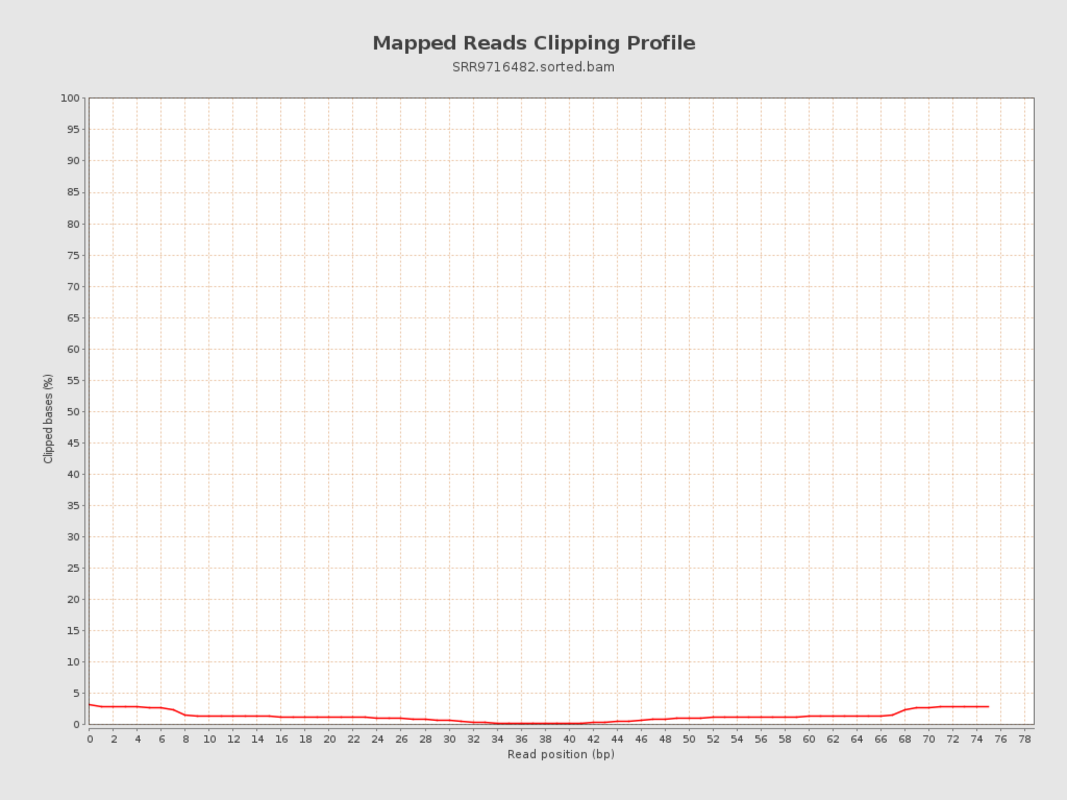
8. Results : Mapped Reads Nucleotide Content



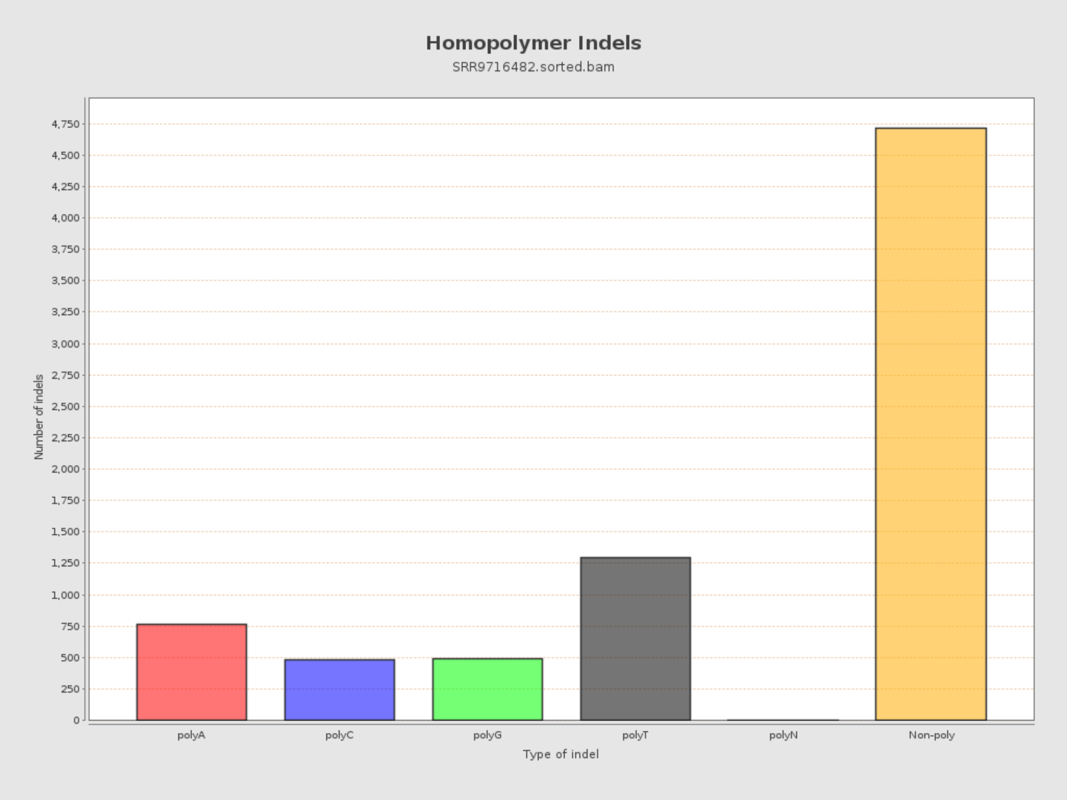
9. Results : Mapped Reads GC-content Distribution



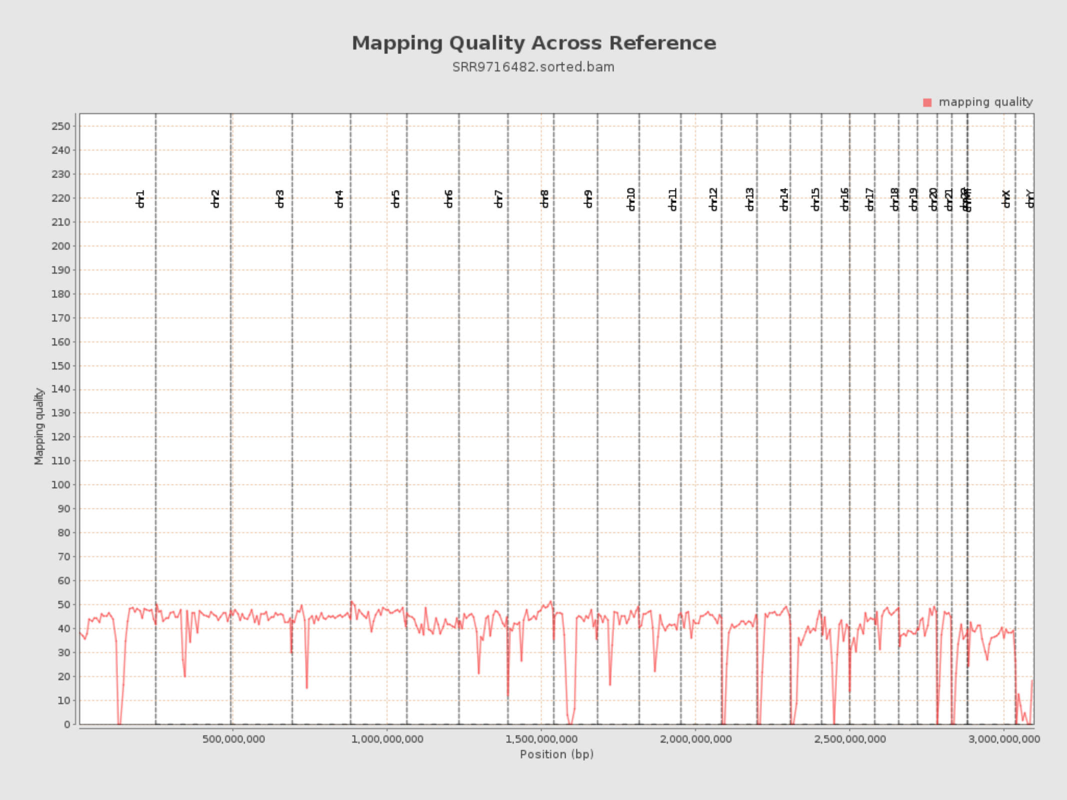
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram