Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 10:59:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716389.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_SRR9716389 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716389.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 10:59:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716389.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	639,446
Mapped reads	531,896 / 83.18%
Unmapped reads	107,550 / 16.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,424 / 0.54%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	14,596 / 2.28%
Duplication rate	2.28%
Clipped reads	533,901 / 83.49%

2.2. ACGT Content

Number/percentage of A's	7,954,596 / 25.29%
Number/percentage of C's	6,173,359 / 19.63%
Number/percentage of T's	9,750,289 / 31%
Number/percentage of G's	7,569,840 / 24.07%
Number/percentage of N's	193 / 0%
GC Percentage	43.7%

2.3. Coverage

Mean	0.0102

Standard Deviation	0.1233

2.4. Mapping Quality

Mean Mapping Quality	45.36

2.5. Mismatches and indels

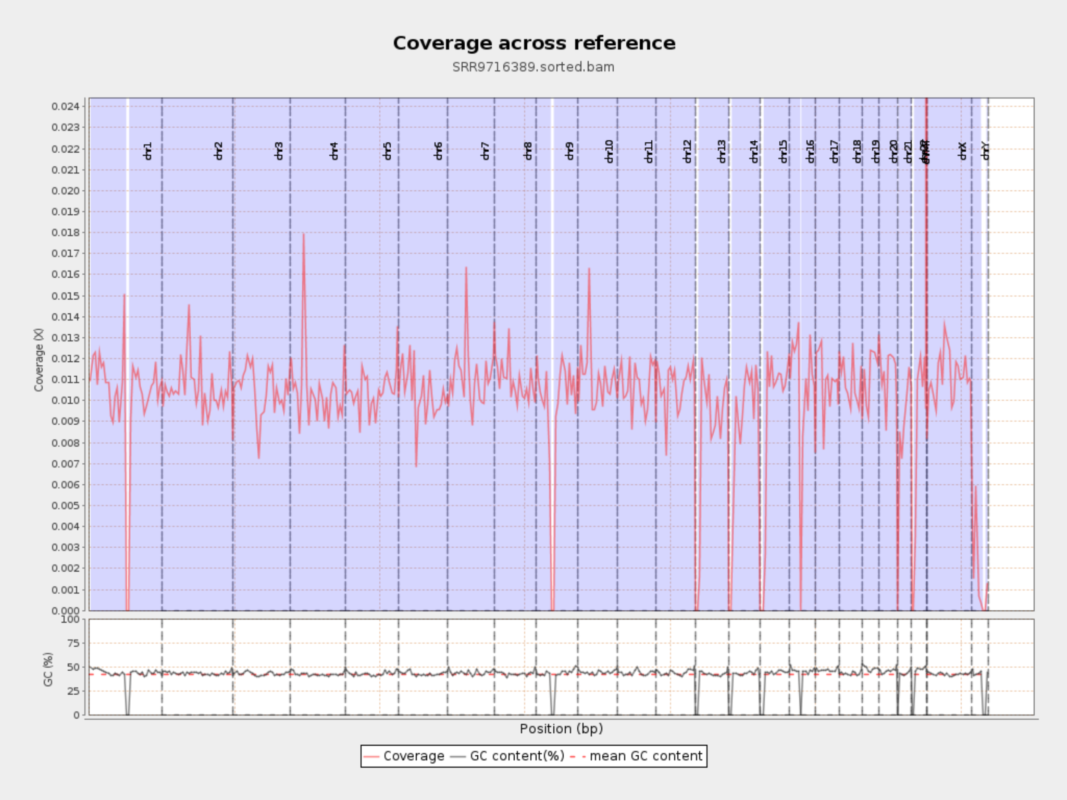
General error rate	0.5%
Mismatches	151,414
Insertions	2,488
Mapped reads with at least one insertion	0.47%
Deletions	5,253
Mapped reads with at least one deletion	0.98%
Homopolymer indels	43.25%

2.6. Chromosome stats

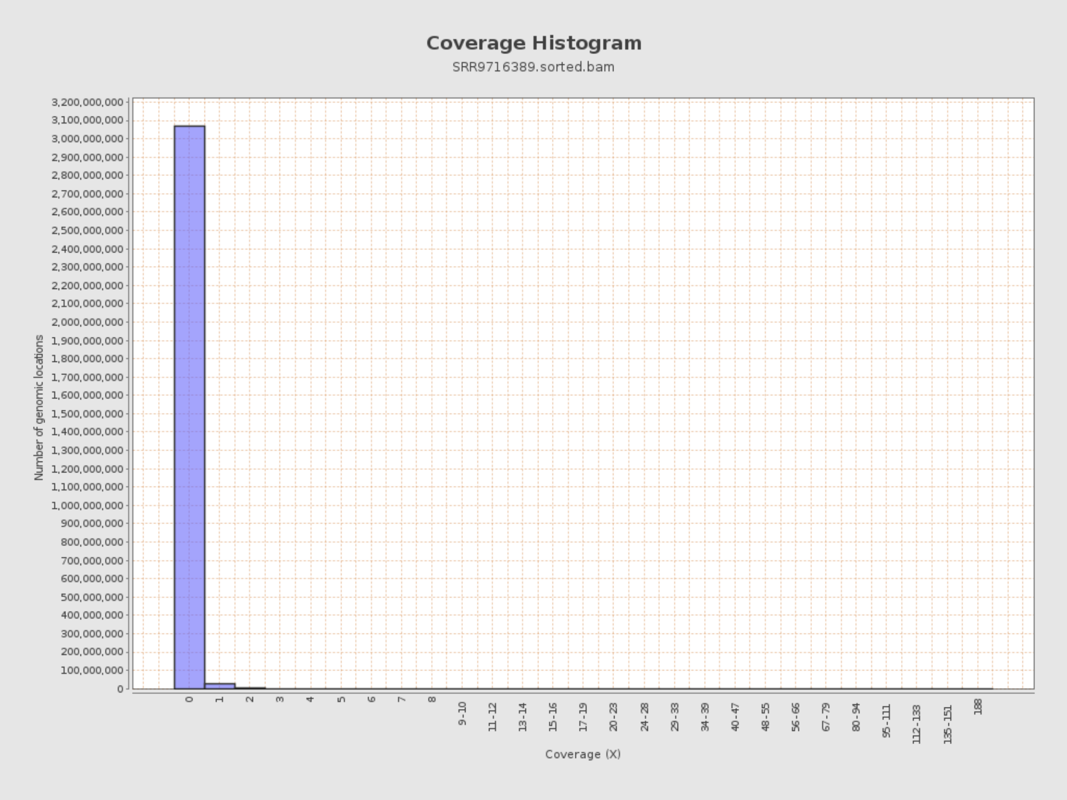
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2533549	0.0102	0.1586
chr2	243199373	2601436	0.0107	0.1419
chr3	198022430	2074437	0.0105	0.1087
chr4	191154276	1998071	0.0105	0.1162
chr5	180915260	1883497	0.0104	0.1088
chr6	171115067	1770644	0.0103	0.1129
chr7	159138663	1780508	0.0112	0.1518

chr8	146364022	1598220	0.0109	0.1414
chr9	141213431	1309262	0.0093	0.1099
chr10	135534747	1505578	0.0111	0.1256
chr11	135006516	1447267	0.0107	0.1208
chr12	133851895	1437601	0.0107	0.1106
chr13	115169878	957011	0.0083	0.0974
chr14	107349540	907288	0.0085	0.0993
chr15	102531392	921938	0.009	0.1012
chr16	90354753	950547	0.0105	0.1114
chr17	81195210	889060	0.0109	0.114
chr18	78077248	849962	0.0109	0.1606
chr19	59128983	667168	0.0113	0.1364
chr20	63025520	712734	0.0113	0.1151
chr21	48129895	412016	0.0086	0.1036
chr22	51304566	400948	0.0078	0.0942
chrMT	16571	17825	1.0757	1.2631
chrX	155270560	1734520	0.0112	0.1153
chrY	59373566	95426	0.0016	0.0589

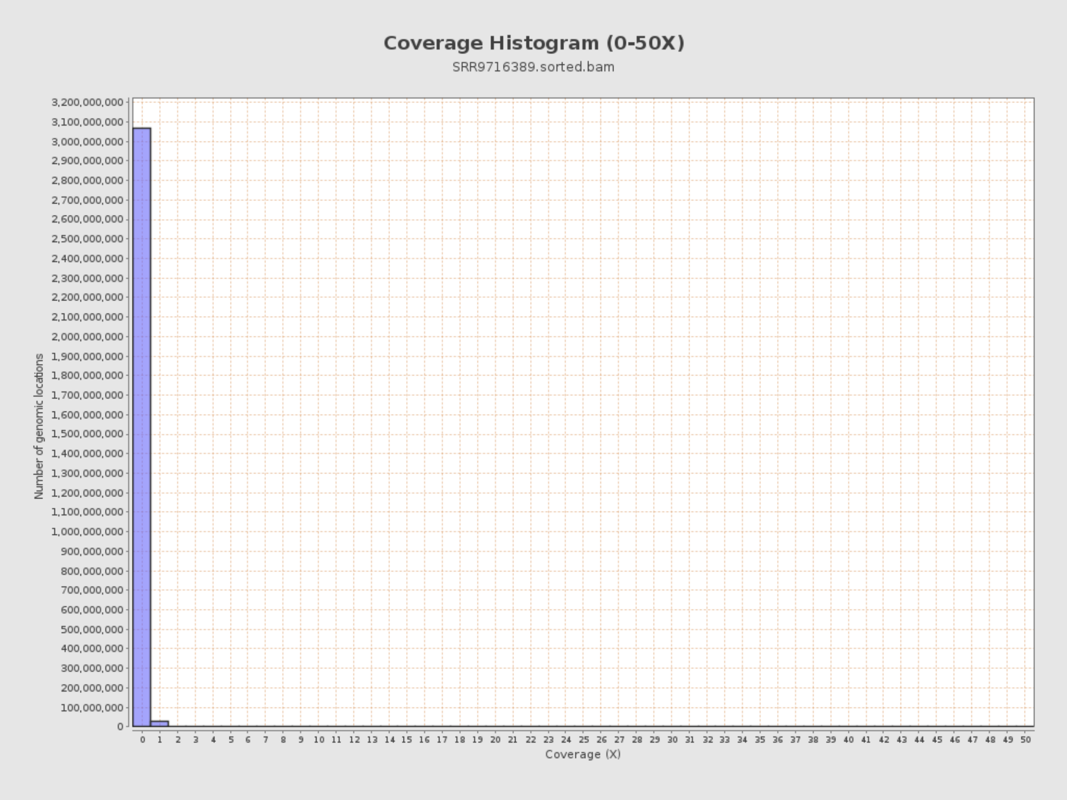
3. Results : Coverage across reference



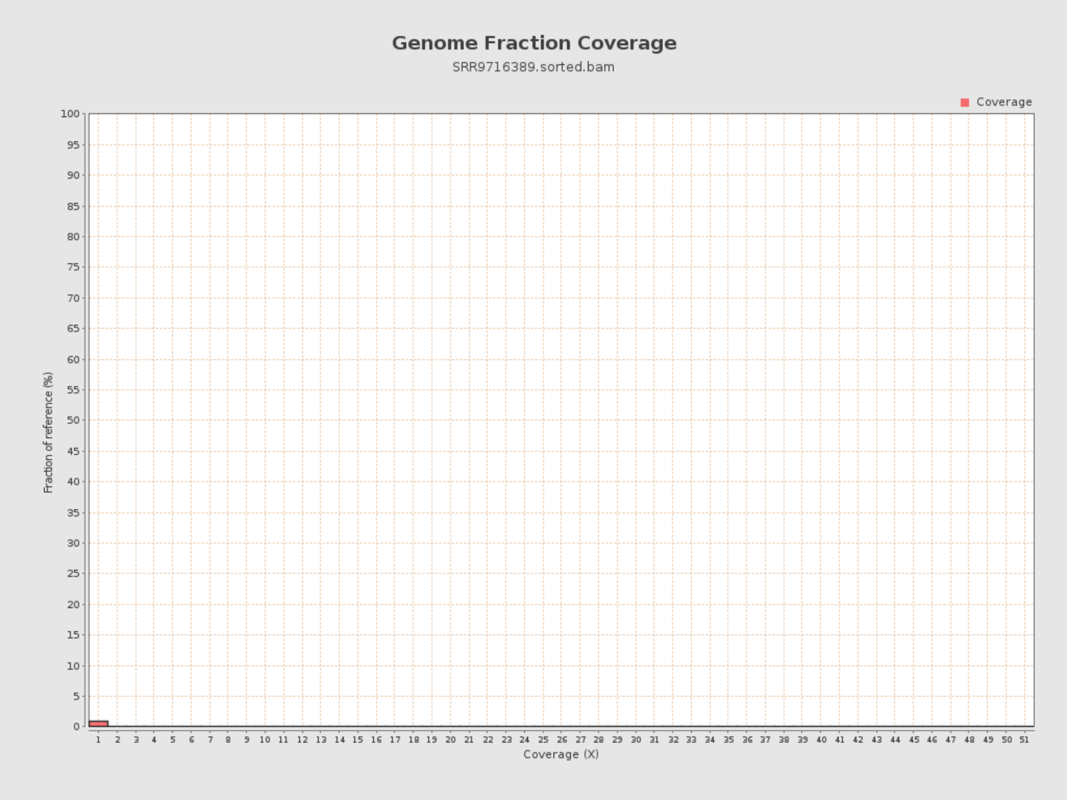
4. Results : Coverage Histogram



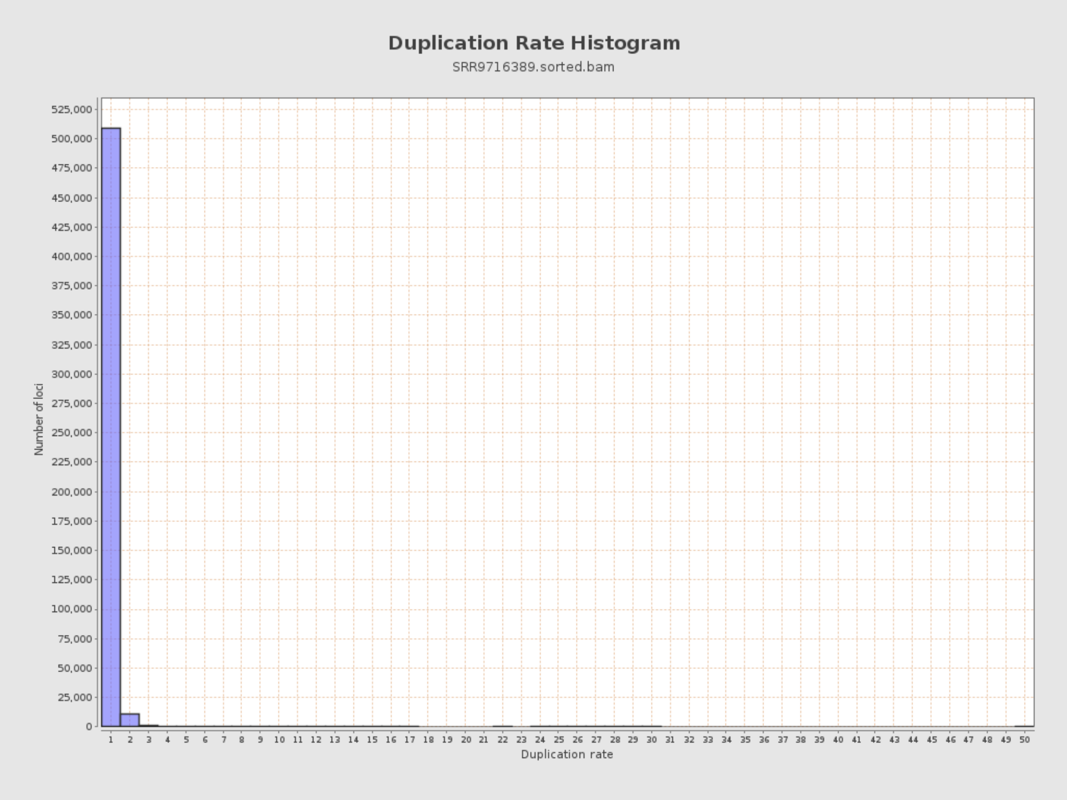
5. Results : Coverage Histogram (0-50X)



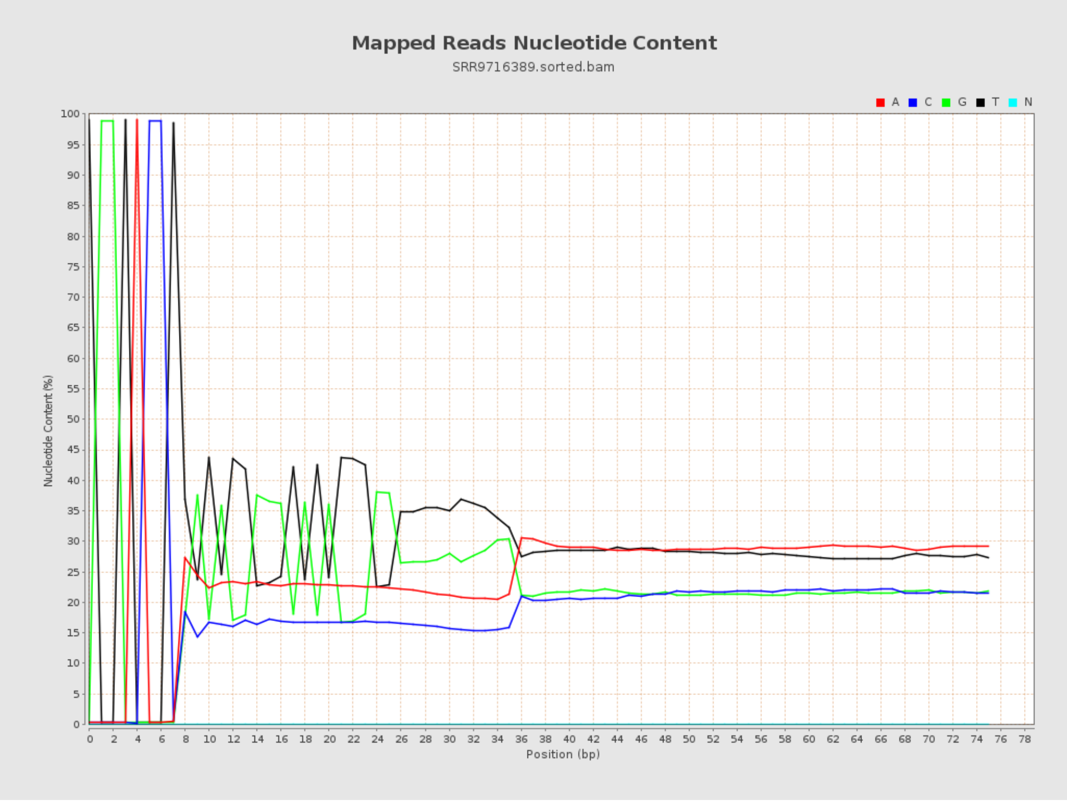
6. Results : Genome Fraction Coverage



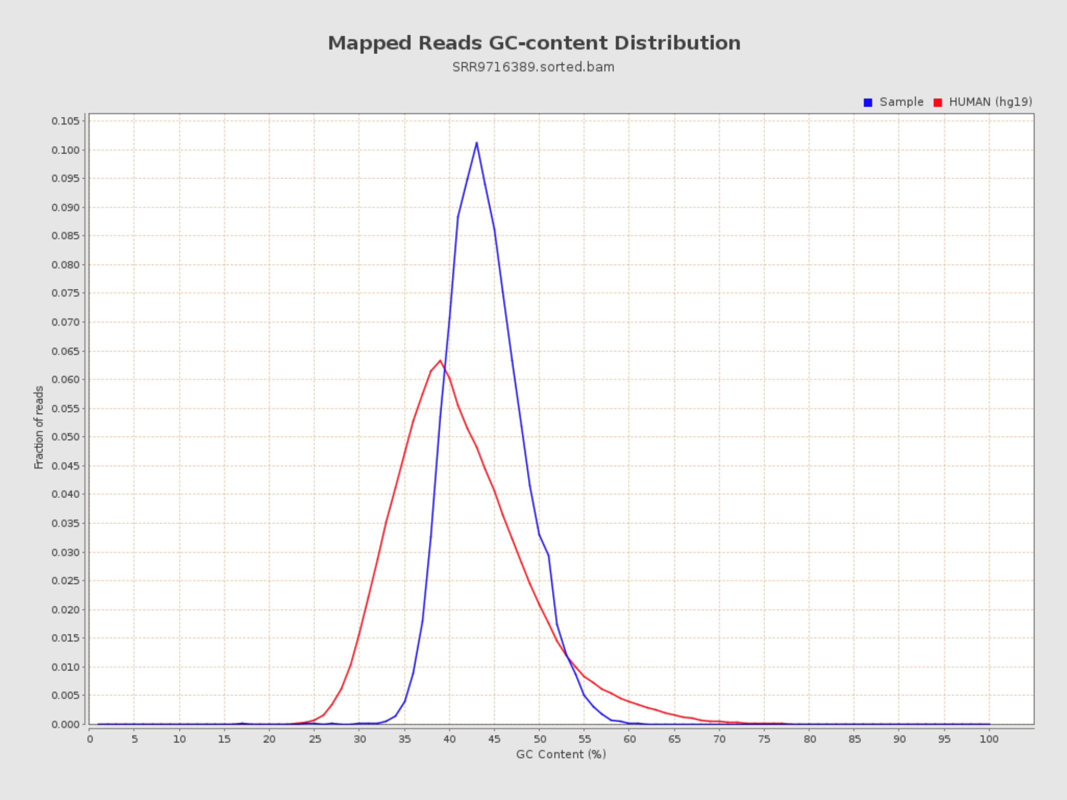
7. Results : Duplication Rate Histogram



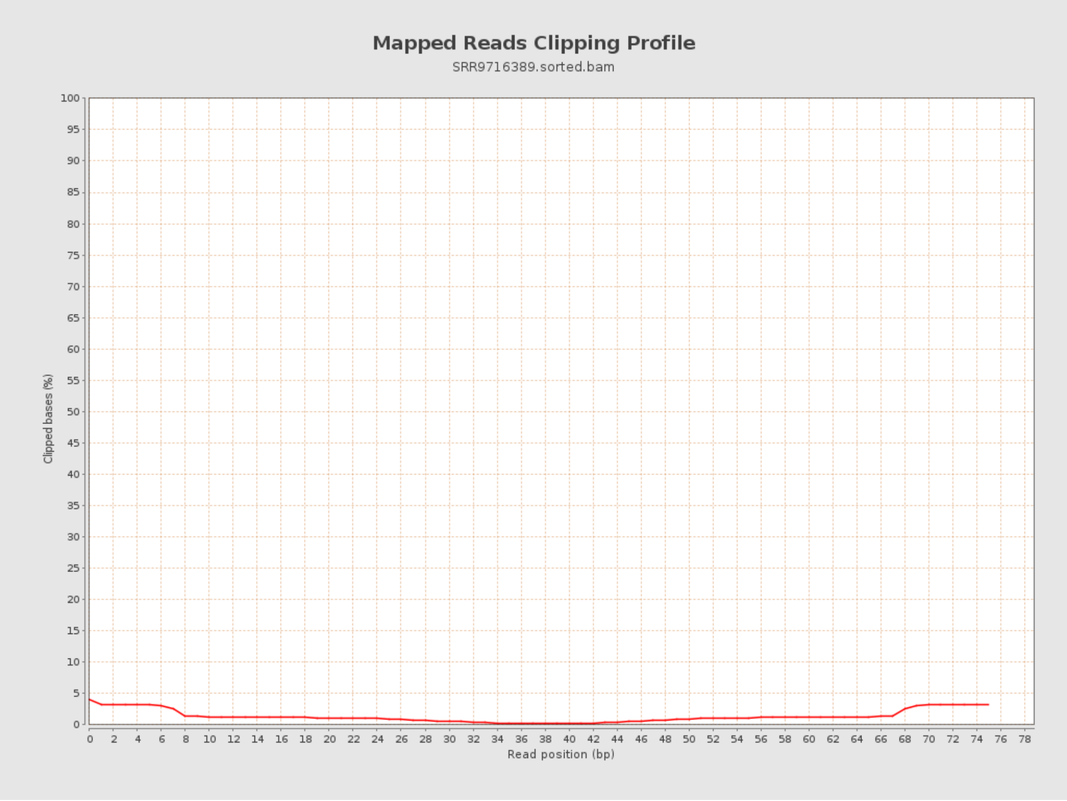
8. Results : Mapped Reads Nucleotide Content



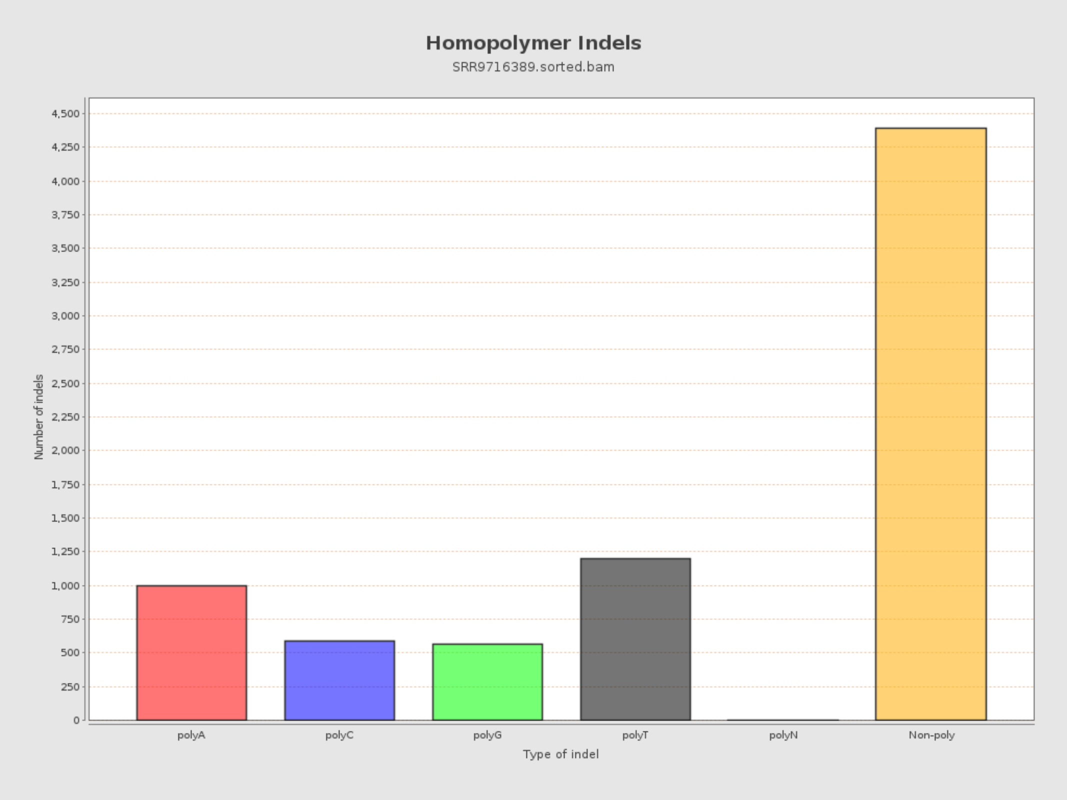
9. Results : Mapped Reads GC-content Distribution



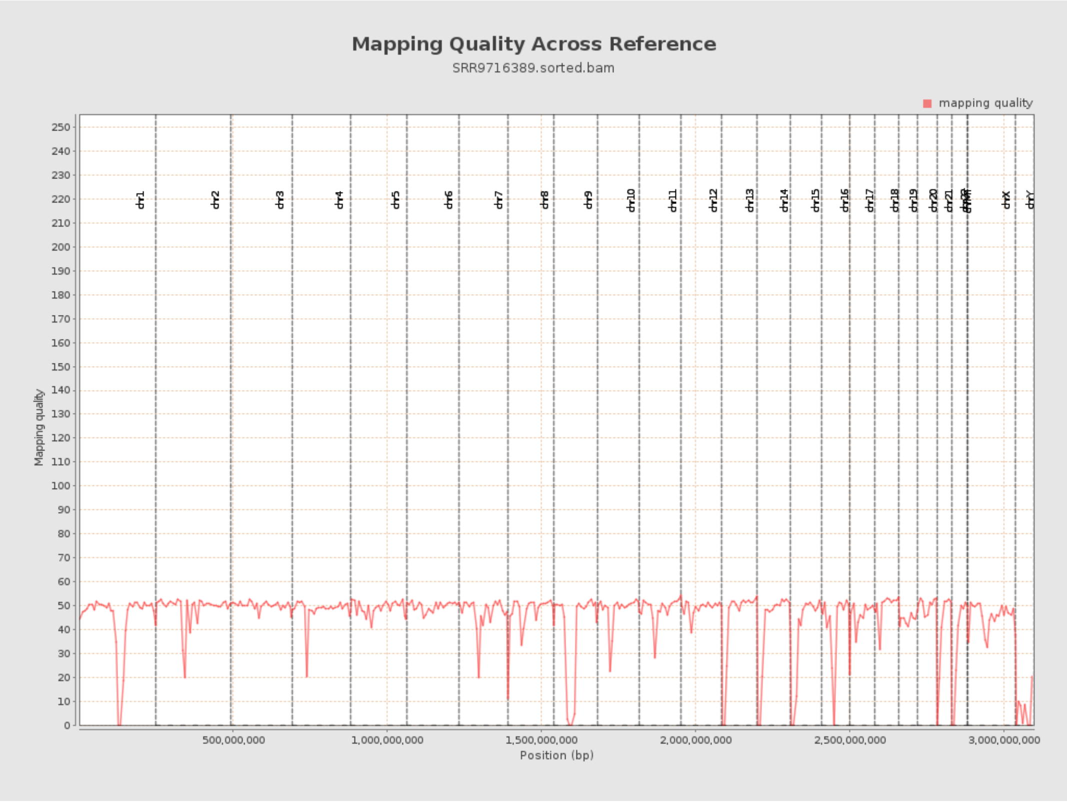
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram