Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 16:02:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716477.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_SRR9716477 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716477.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 16:02:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716477.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	913,531
Mapped reads	827,553 / 90.59%
Unmapped reads	85,978 / 9.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,717 / 0.52%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	25,787 / 2.82%
Duplication rate	2.54%
Clipped reads	829,770 / 90.83%

2.2. ACGT Content

Number/percentage of A's	12,008,469 / 25.18%
Number/percentage of C's	9,876,794 / 20.71%
Number/percentage of T's	14,978,816 / 31.41%
Number/percentage of G's	10,817,852 / 22.69%
Number/percentage of N's	276 / 0%
GC Percentage	43.4%

2.3. Coverage

Mean	0.0154

Standard Deviation	0.1598

2.4. Mapping Quality

Mean Mapping Quality	44.71

2.5. Mismatches and indels

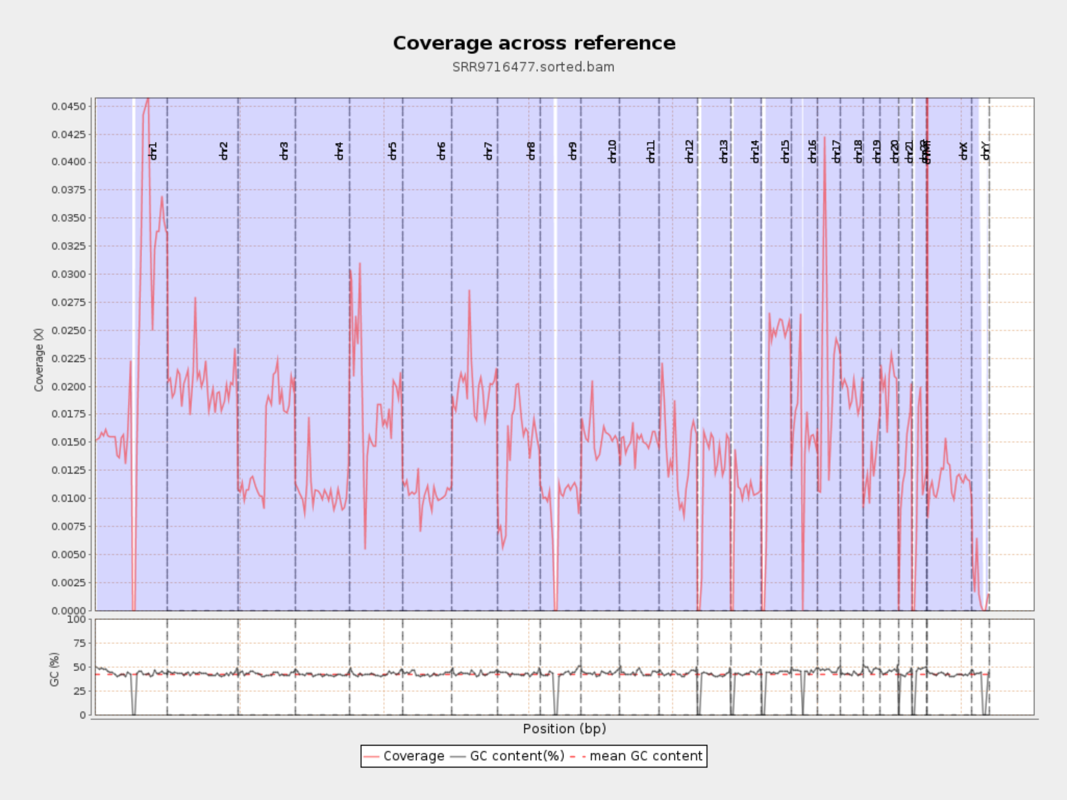
General error rate	0.5%
Mismatches	231,626
Insertions	3,743
Mapped reads with at least one insertion	0.45%
Deletions	8,333
Mapped reads with at least one deletion	1%
Homopolymer indels	41.3%

2.6. Chromosome stats

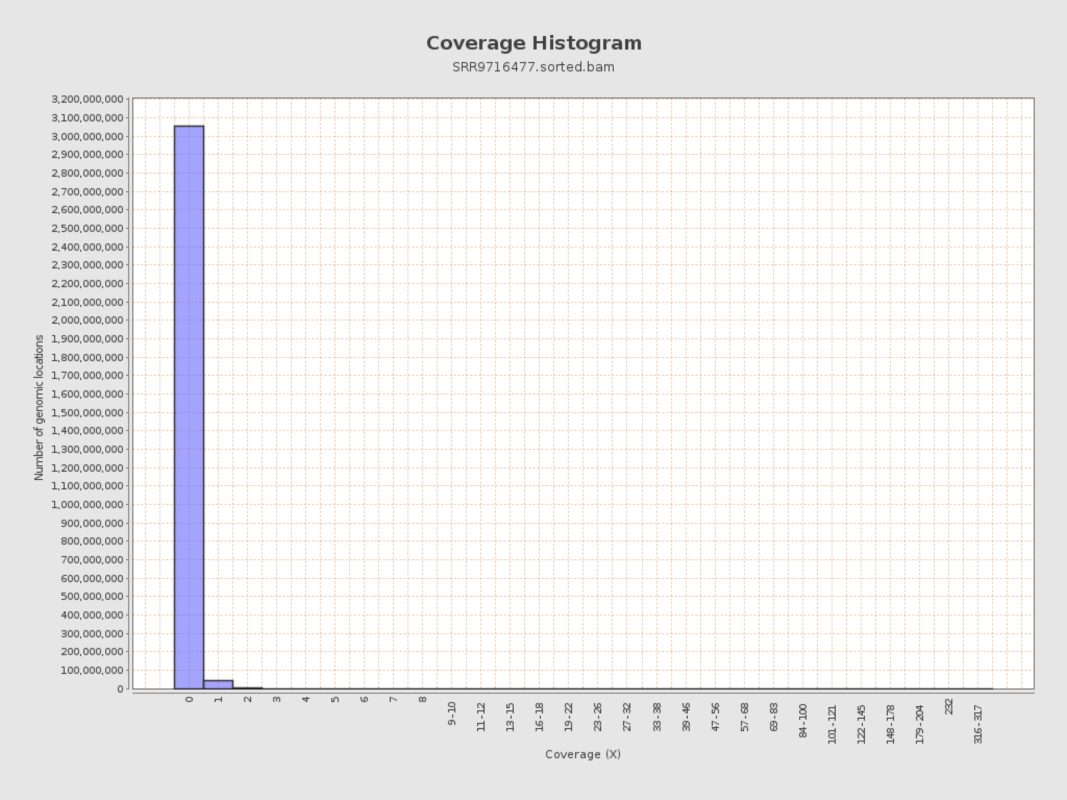
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5628066	0.0226	0.2346
chr2	243199373	4912186	0.0202	0.2121
chr3	198022430	3017377	0.0152	0.1319
chr4	191154276	2022483	0.0106	0.1188
chr5	180915260	3401218	0.0188	0.1468
chr6	171115067	1778955	0.0104	0.1148
chr7	159138663	3185853	0.02	0.2191

chr8	146364022	2101143	0.0144	0.1509
chr9	141213431	1296418	0.0092	0.1203
chr10	135534747	2127916	0.0157	0.1497
chr11	135006516	2037179	0.0151	0.1514
chr12	133851895	1877616	0.014	0.1272
chr13	115169878	1381042	0.012	0.1178
chr14	107349540	1032975	0.0096	0.1081
chr15	102531392	2076383	0.0203	0.1522
chr16	90354753	1387957	0.0154	0.1363
chr17	81195210	1790612	0.0221	0.166
chr18	78077248	1510154	0.0193	0.2392
chr19	59128983	761476	0.0129	0.1702
chr20	63025520	1274478	0.0202	0.1531
chr21	48129895	612093	0.0127	0.1243
chr22	51304566	543127	0.0106	0.1095
chrMT	16571	24930	1.5044	1.5288
chrX	155270560	1803200	0.0116	0.122
chrY	59373566	110403	0.0019	0.0582

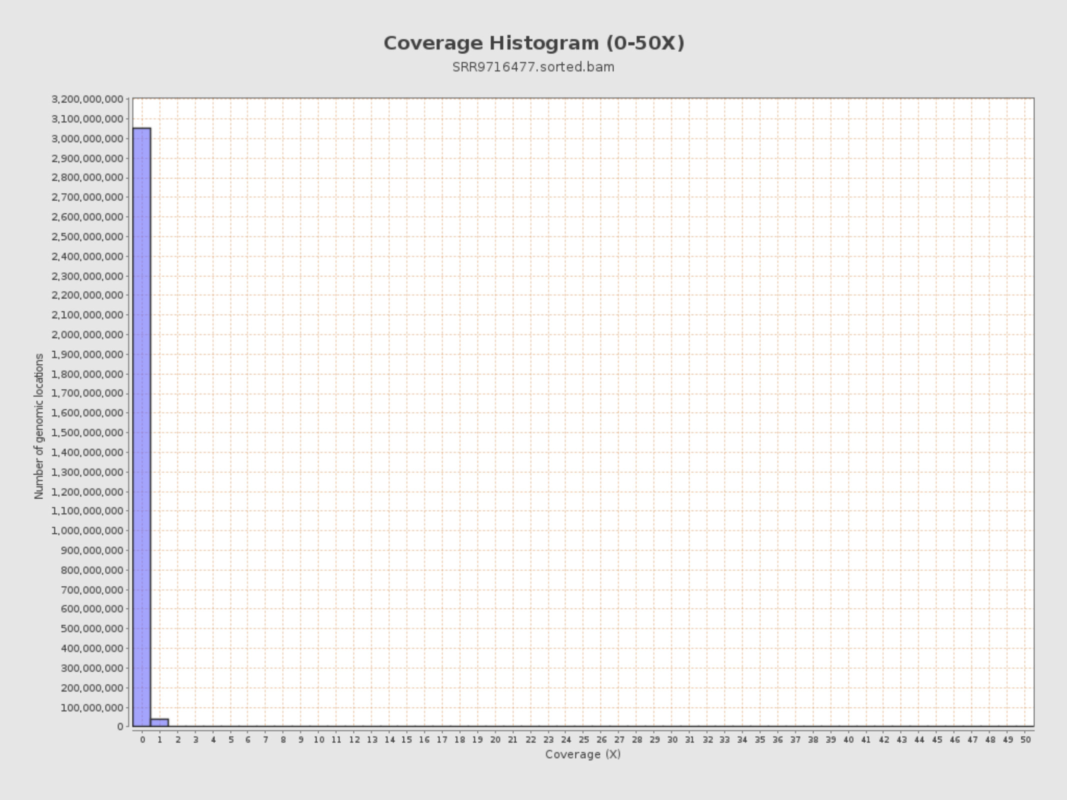
3. Results : Coverage across reference



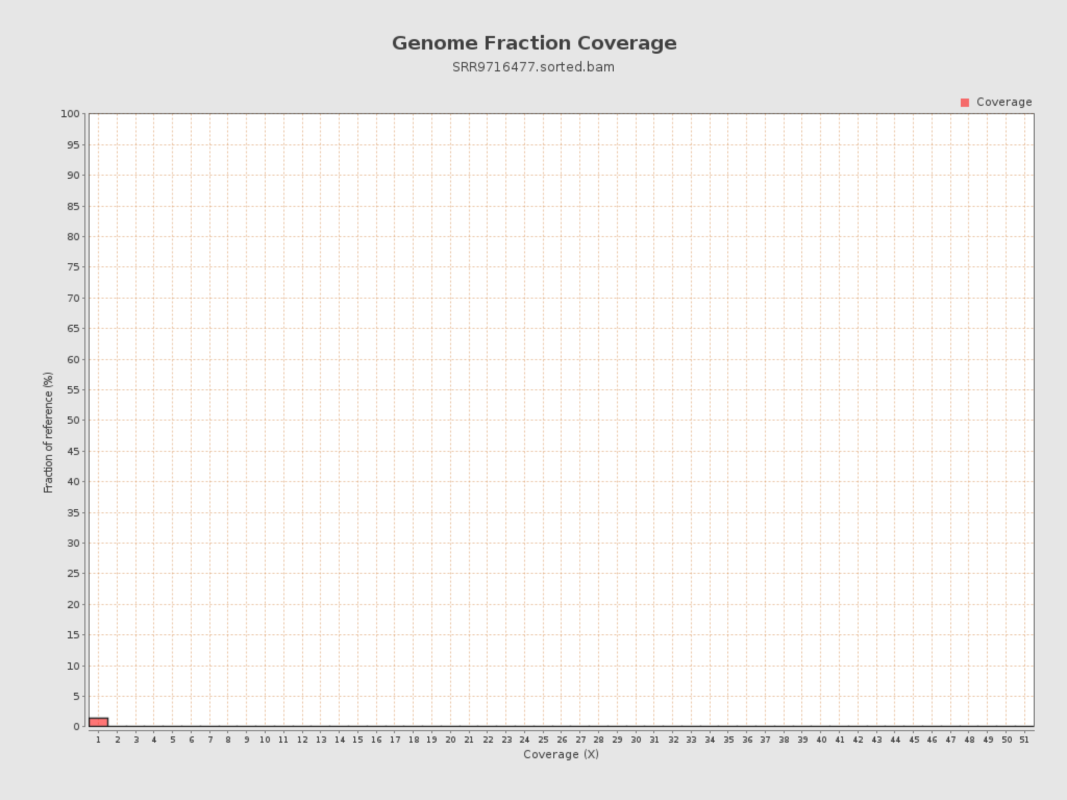
4. Results : Coverage Histogram



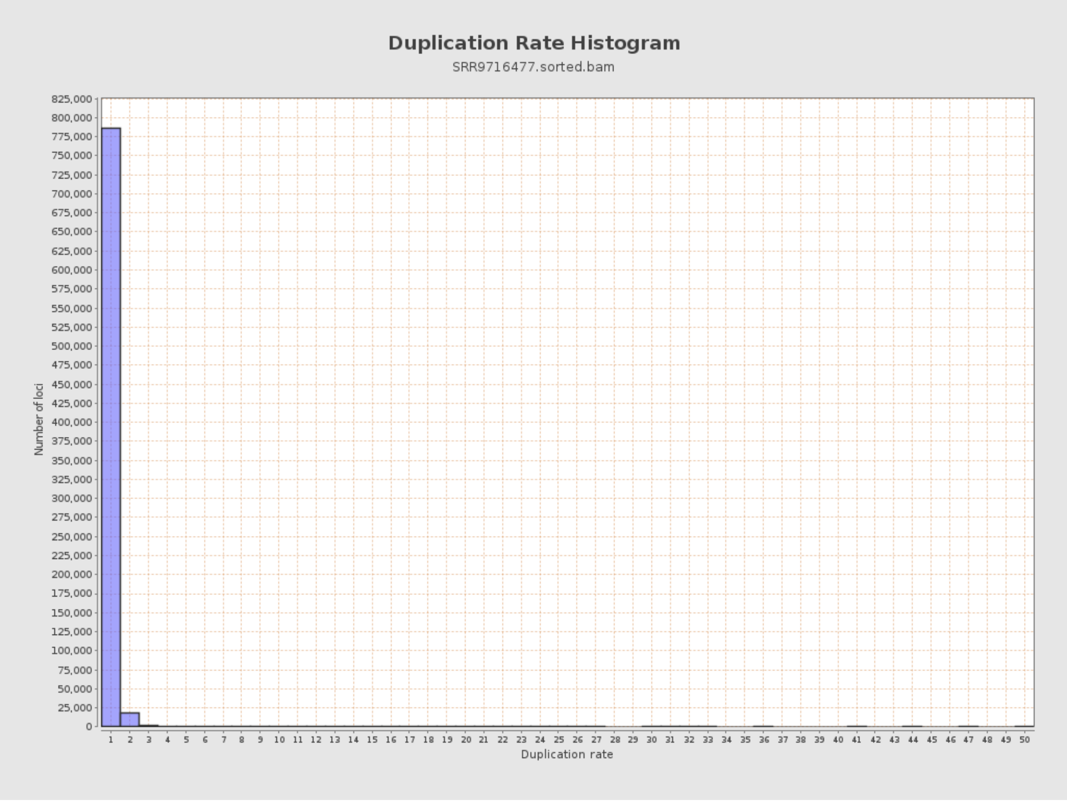
5. Results : Coverage Histogram (0-50X)



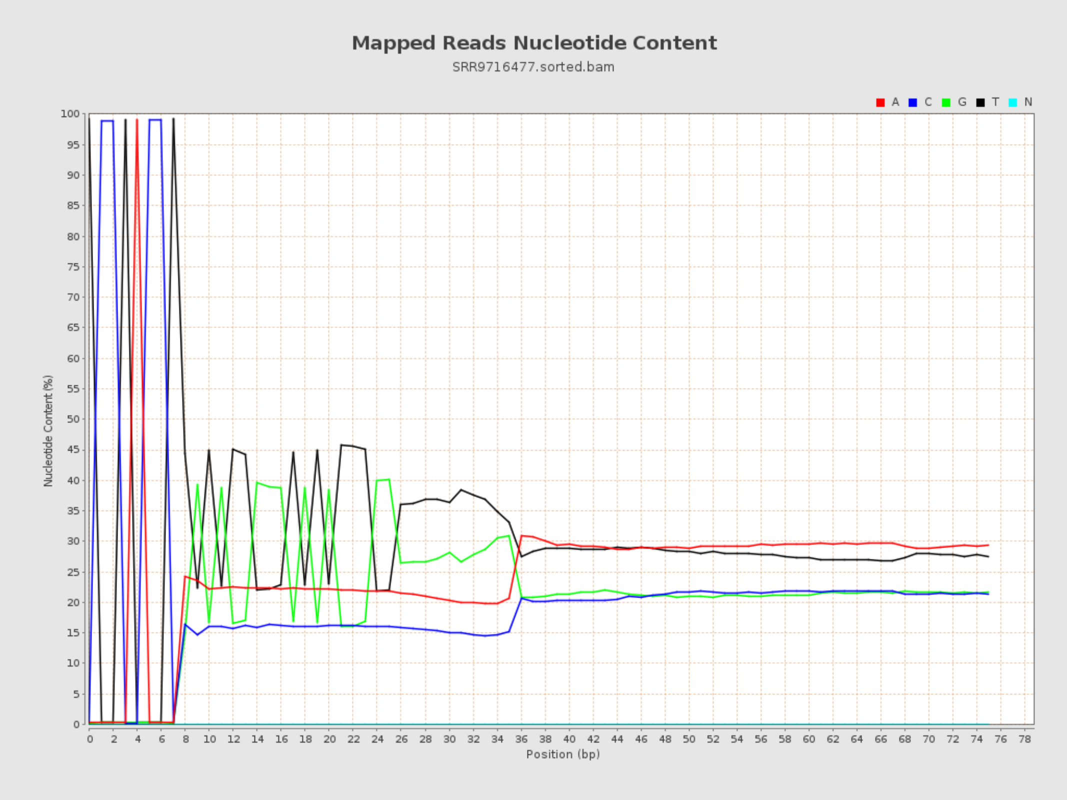
6. Results : Genome Fraction Coverage



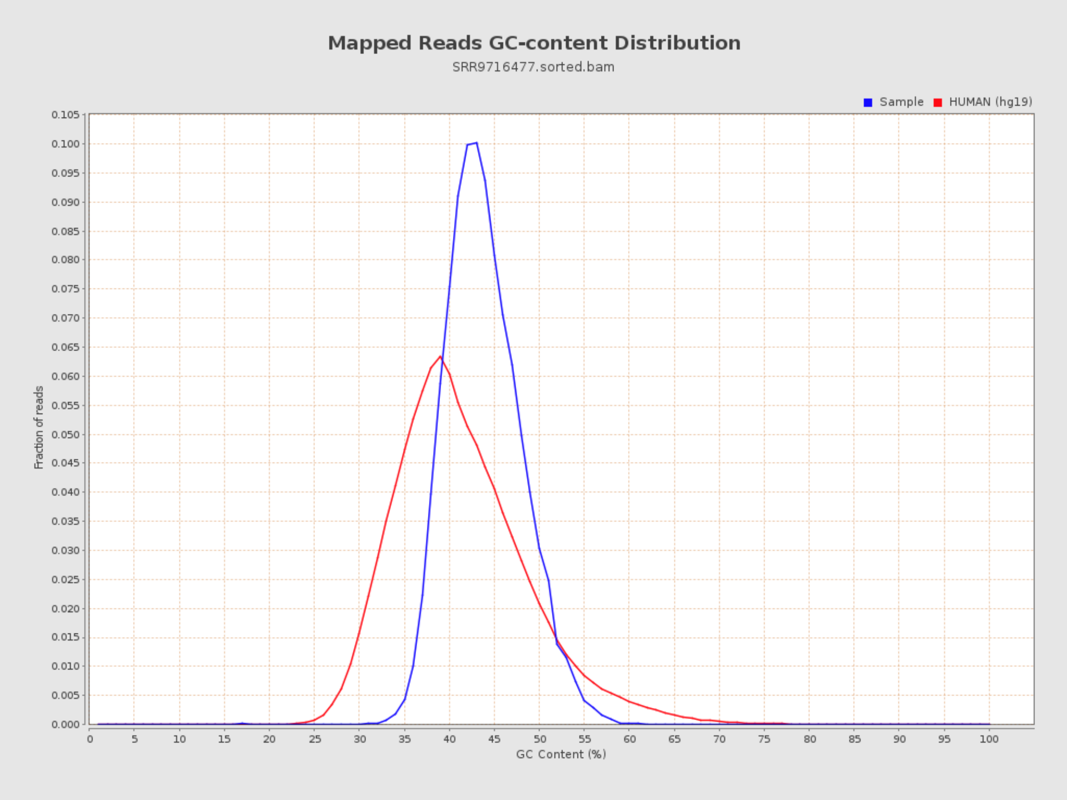
7. Results : Duplication Rate Histogram



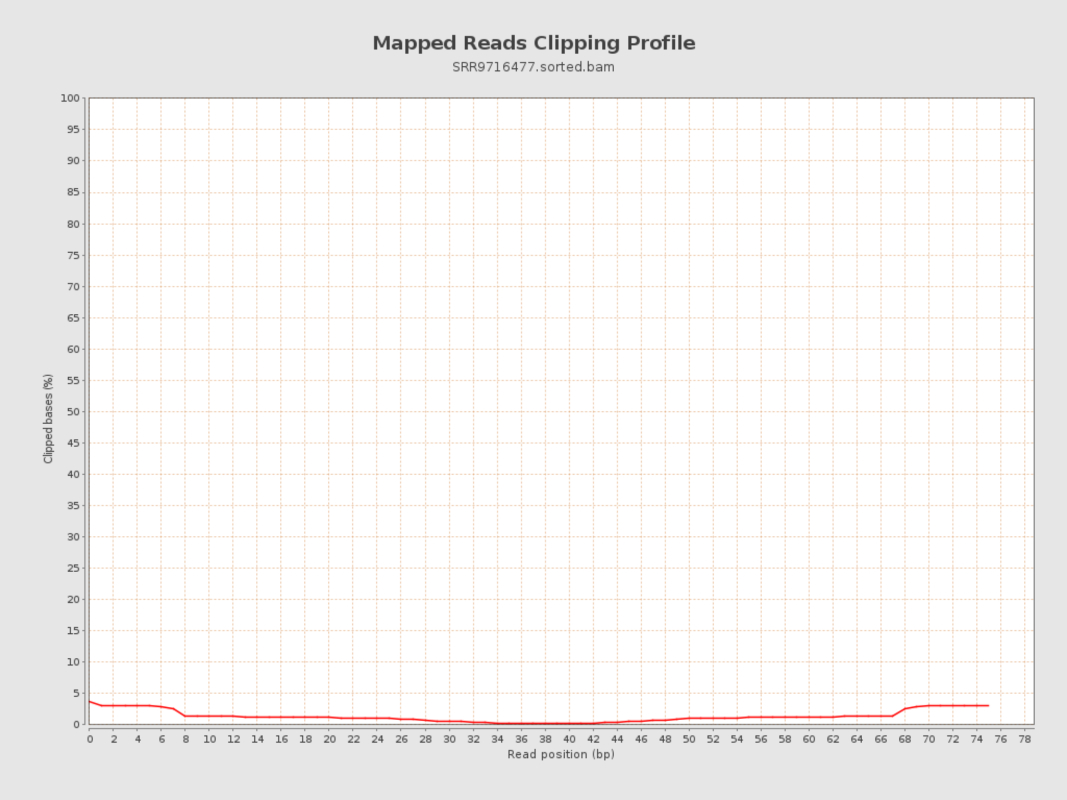
8. Results : Mapped Reads Nucleotide Content



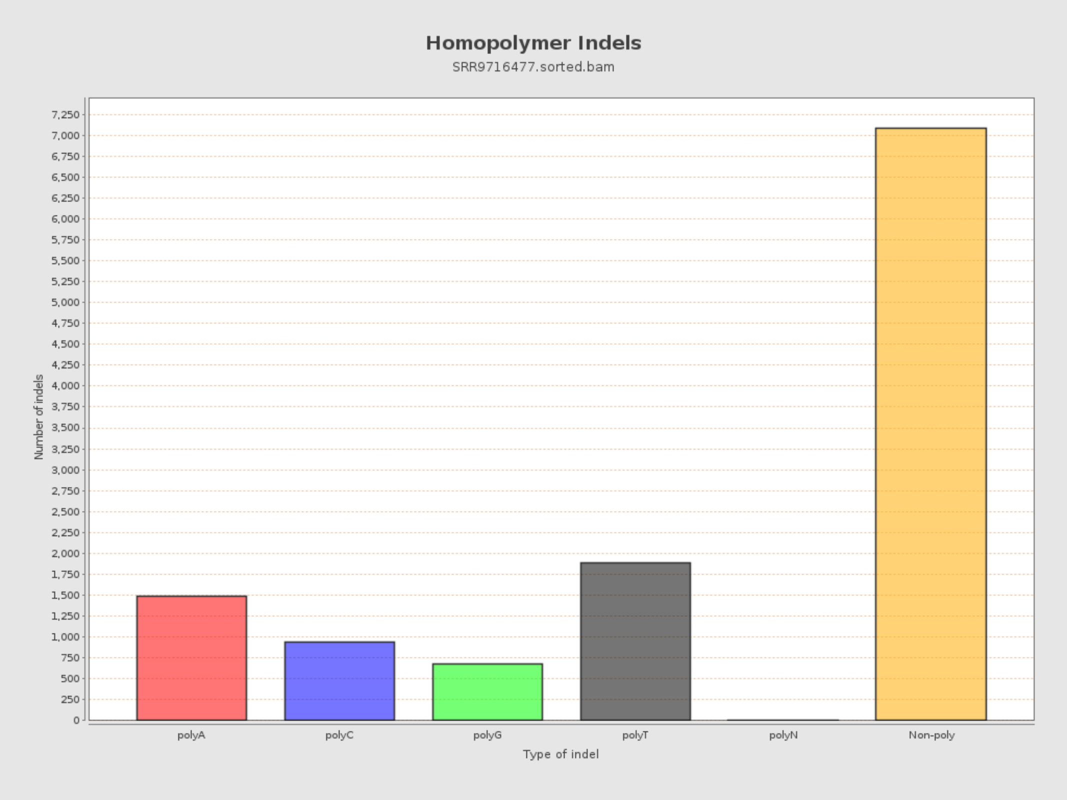
9. Results : Mapped Reads GC-content Distribution



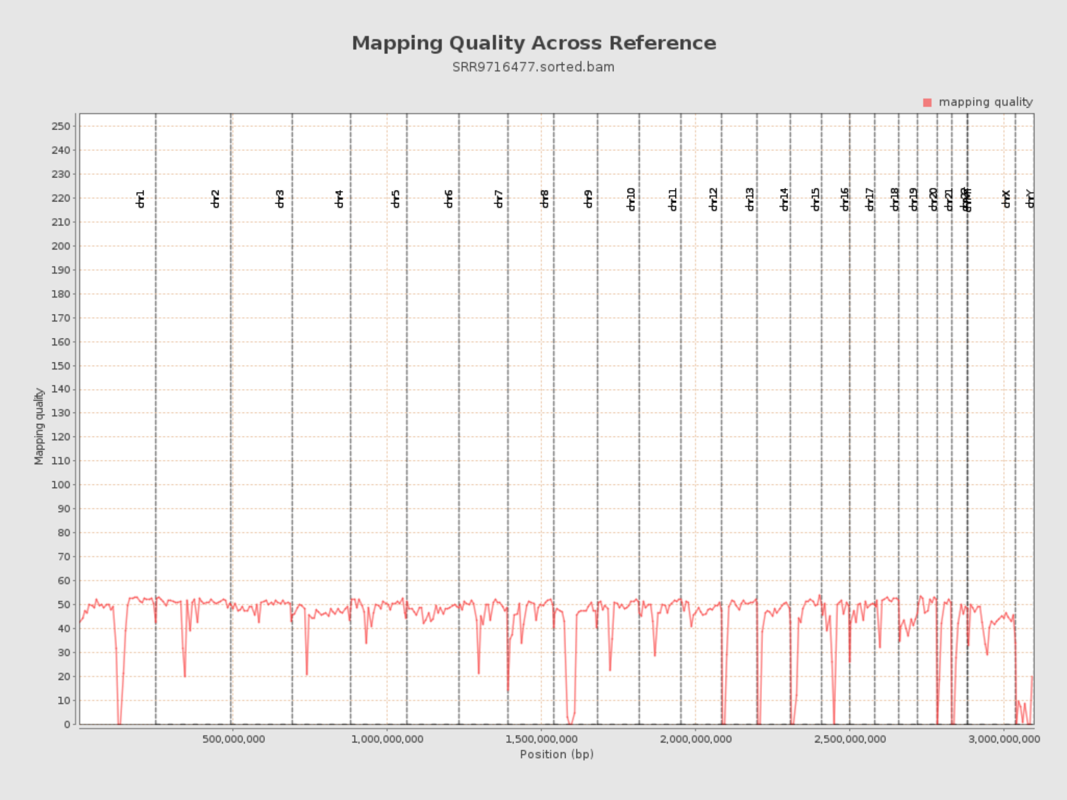
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram