Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 12:50:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716427.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_SRR9716427 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716427.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 12:50:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716427.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,537,164
Mapped reads	1,420,513 / 92.41%
Unmapped reads	116,651 / 7.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,448 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	58,867 / 3.83%
Duplication rate	3.02%
Clipped reads	1,423,037 / 92.58%

2.2. ACGT Content

Number/percentage of A's	20,446,728 / 24.6%
Number/percentage of C's	14,991,917 / 18.04%
Number/percentage of T's	25,948,506 / 31.22%
Number/percentage of G's	21,719,815 / 26.13%
Number/percentage of N's	1,571 / 0%
GC Percentage	44.17%

2.3. Coverage

Mean	0.0269

Standard Deviation	0.266

2.4. Mapping Quality

Mean Mapping Quality	44.91

2.5. Mismatches and indels

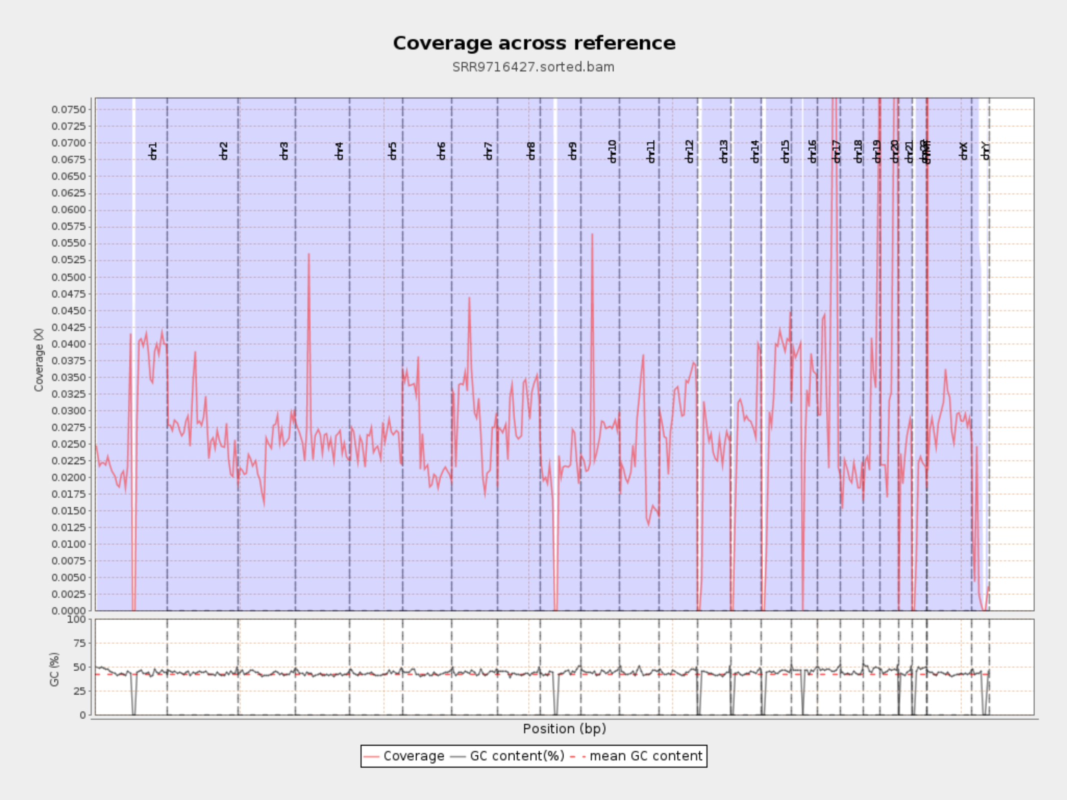
General error rate	0.52%
Mismatches	416,648
Insertions	6,236
Mapped reads with at least one insertion	0.44%
Deletions	15,980
Mapped reads with at least one deletion	1.12%
Homopolymer indels	42.27%

2.6. Chromosome stats

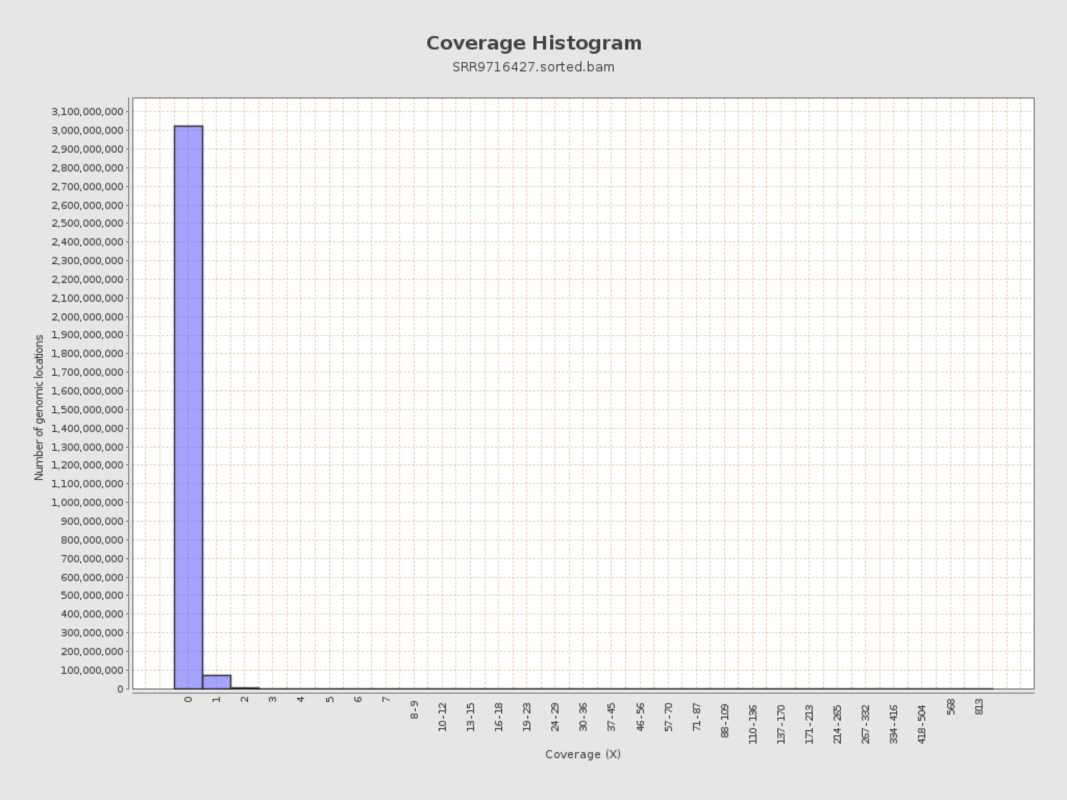
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6992299	0.0281	0.3969
chr2	243199373	6533174	0.0269	0.3808
chr3	198022430	4699386	0.0237	0.1676
chr4	191154276	5067307	0.0265	0.2253
chr5	180915260	4611887	0.0255	0.1736
chr6	171115067	4379413	0.0256	0.1972
chr7	159138663	4694257	0.0295	0.3132

chr8	146364022	4363621	0.0298	0.348
chr9	141213431	2705121	0.0192	0.1821
chr10	135534747	3680721	0.0272	0.3008
chr11	135006516	2930038	0.0217	0.1959
chr12	133851895	4105167	0.0307	0.1913
chr13	115169878	2447247	0.0212	0.1609
chr14	107349540	2775155	0.0259	0.178
chr15	102531392	3072449	0.03	0.1874
chr16	90354753	2897310	0.0321	0.2043
chr17	81195210	3668913	0.0452	0.2429
chr18	78077248	1539217	0.0197	0.3058
chr19	59128983	2221108	0.0376	0.3343
chr20	63025520	2809066	0.0446	0.2405
chr21	48129895	1066425	0.0222	0.2089
chr22	51304566	787476	0.0153	0.1342
chrMT	16571	298494	18.013	10.8986
chrX	155270560	4450555	0.0287	0.1959
chrY	59373566	338747	0.0057	0.2679

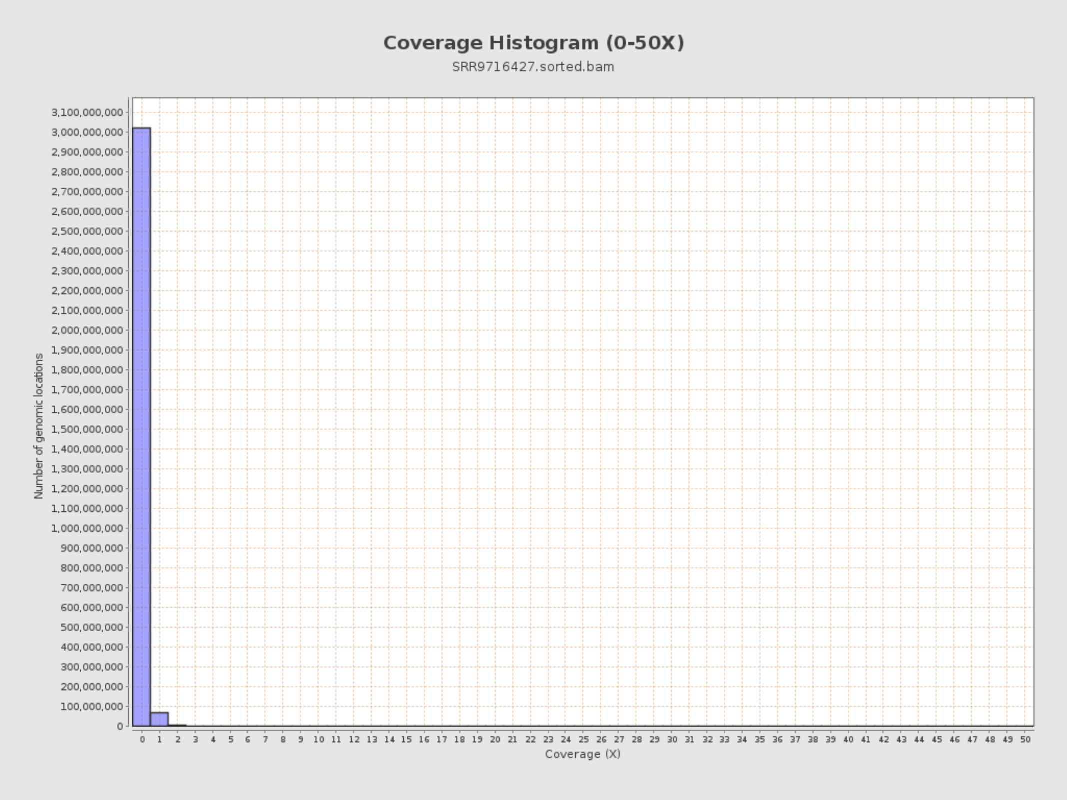
3. Results : Coverage across reference



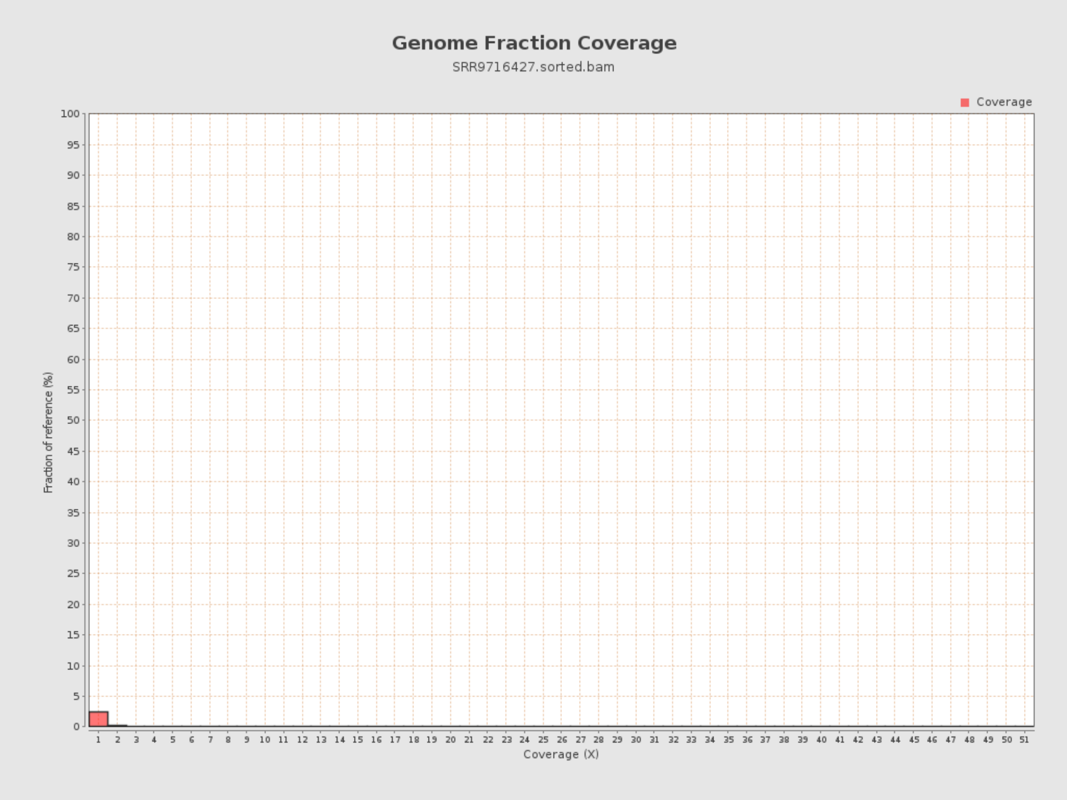
4. Results : Coverage Histogram



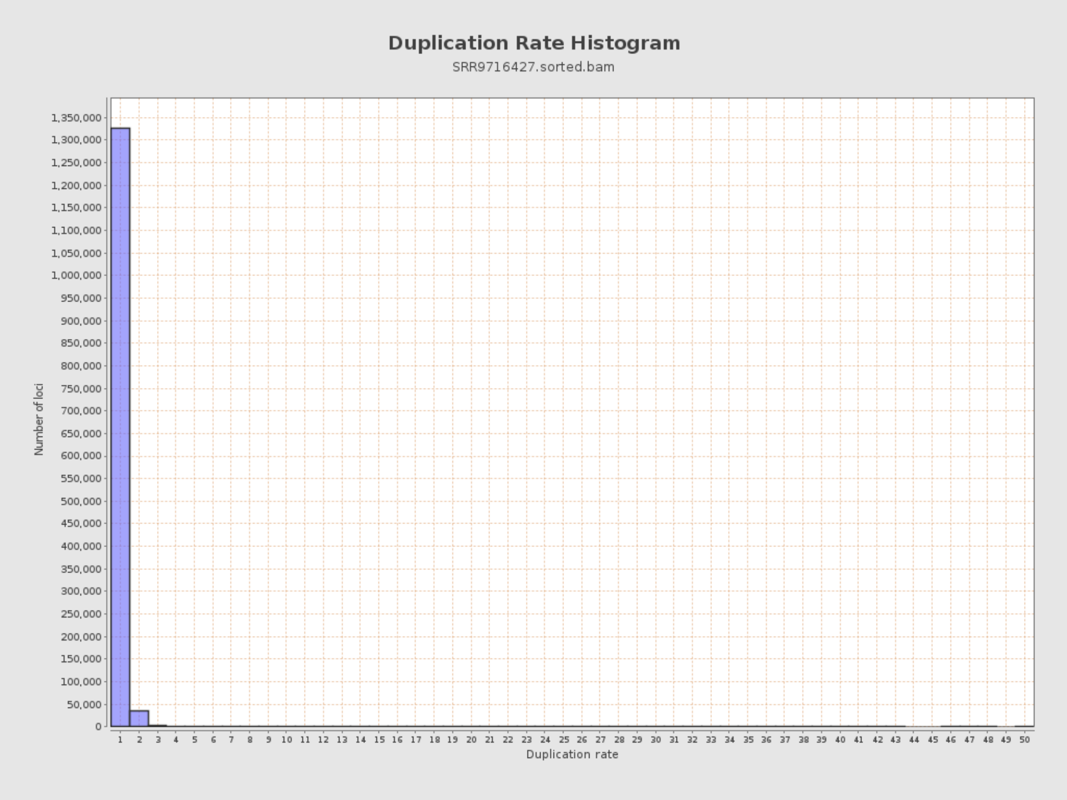
5. Results : Coverage Histogram (0-50X)



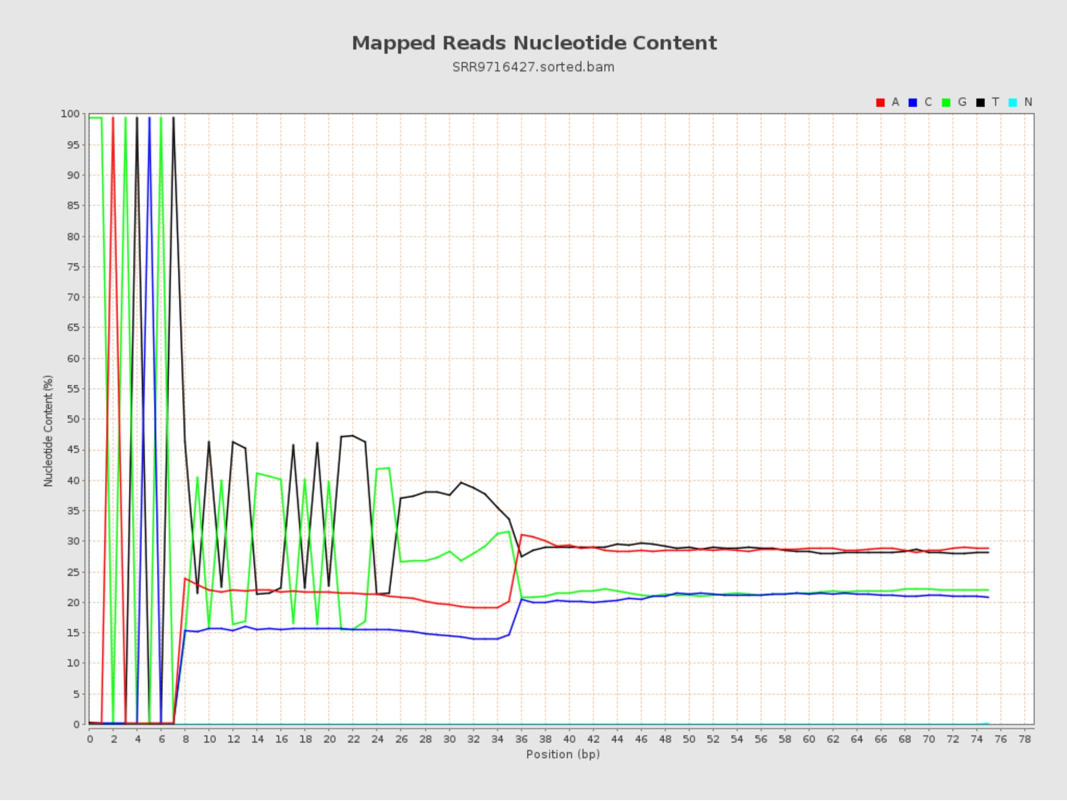
6. Results : Genome Fraction Coverage



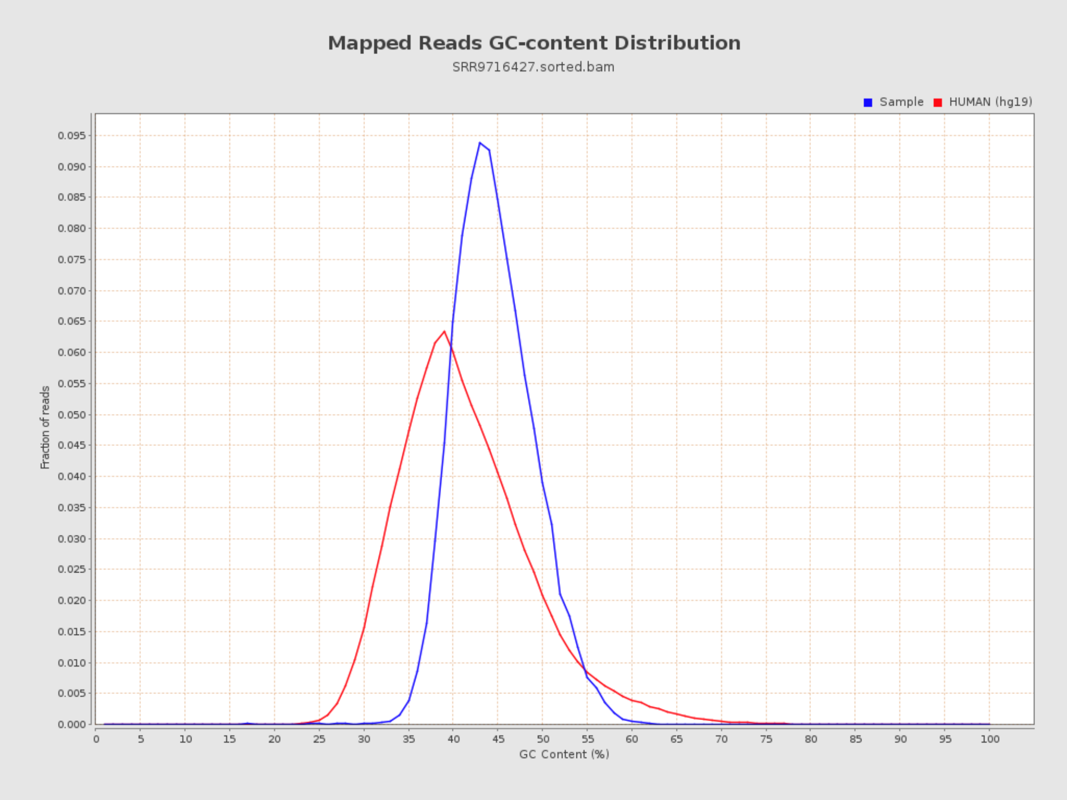
7. Results : Duplication Rate Histogram



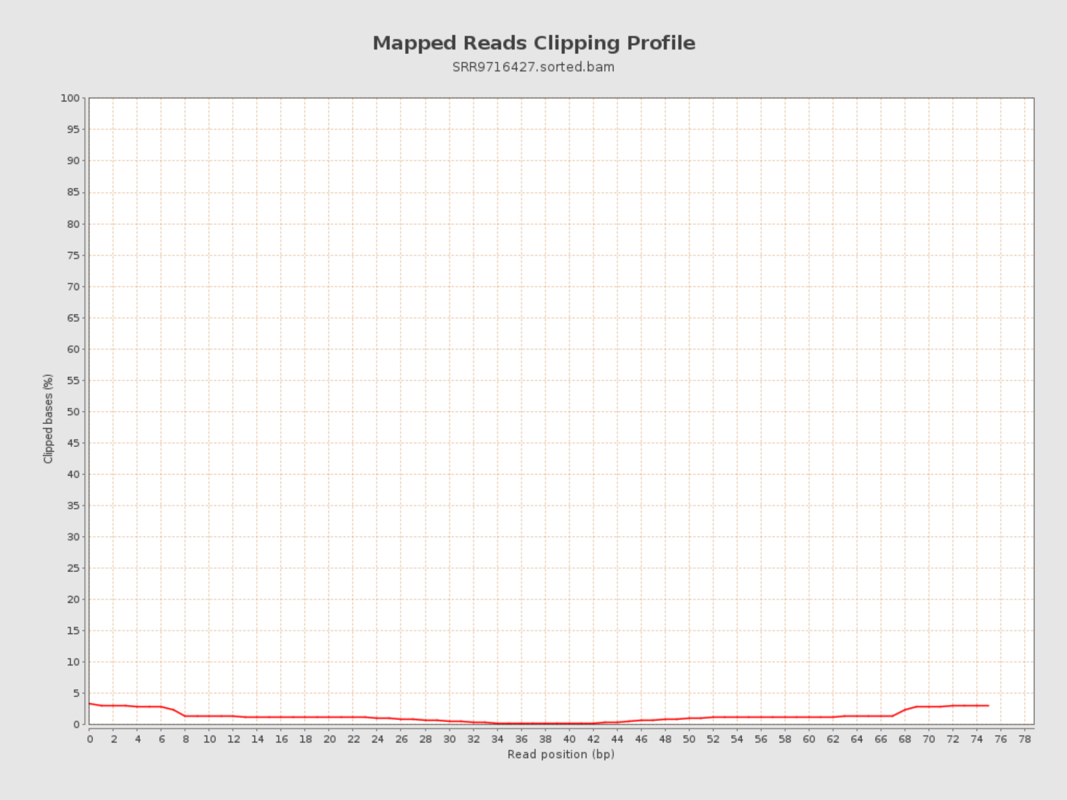
8. Results : Mapped Reads Nucleotide Content



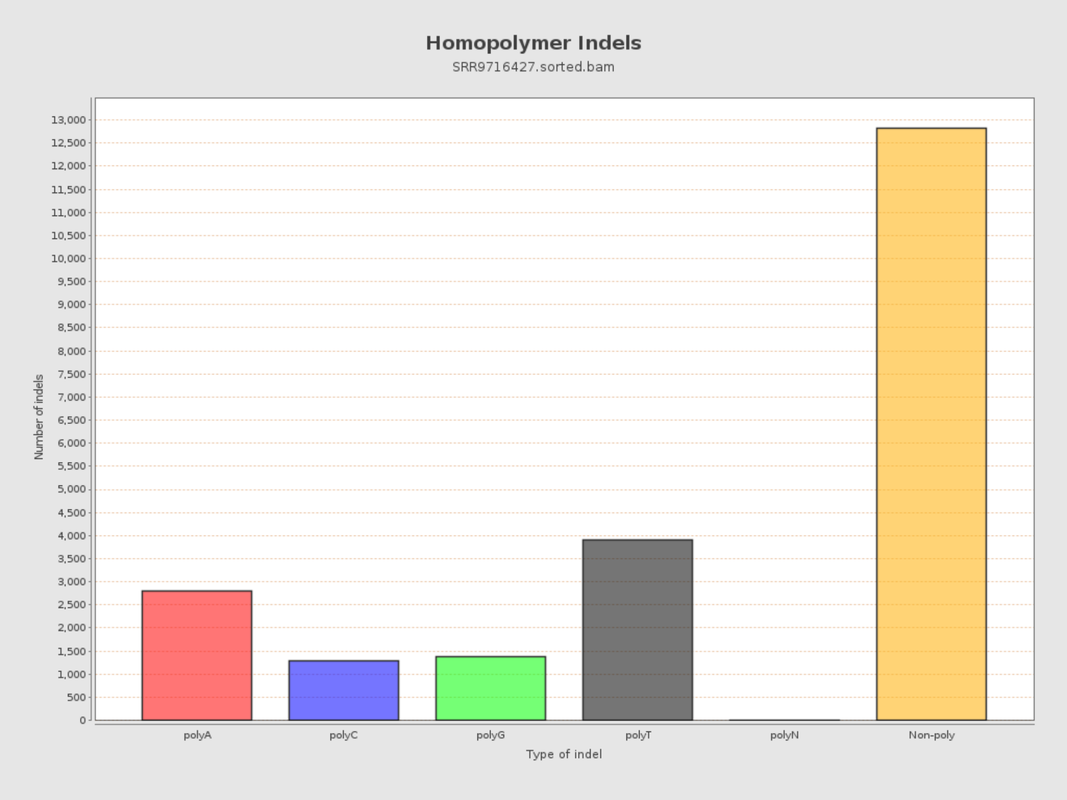
9. Results : Mapped Reads GC-content Distribution



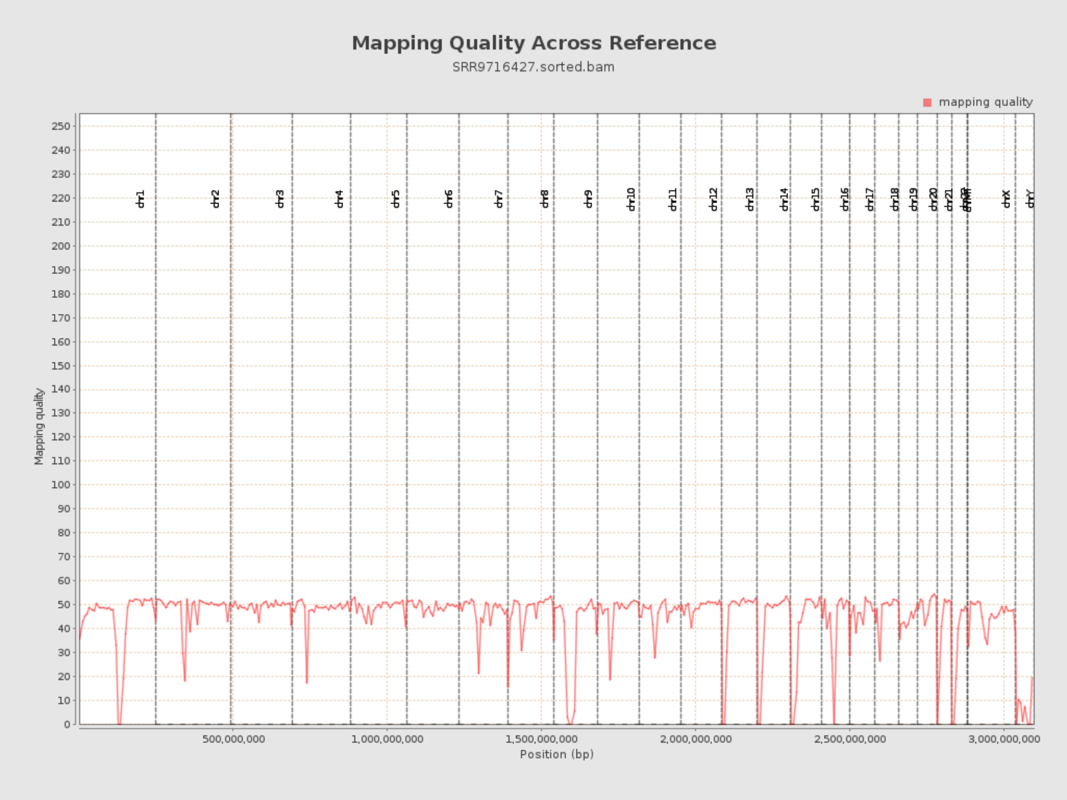
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram