Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 17:49:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716511.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_SRR9716511 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716511.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 17:49:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716511.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,131,496
Mapped reads	1,911,340 / 89.67%
Unmapped reads	220,156 / 10.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,930 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	72,264 / 3.39%
Duplication rate	2.64%
Clipped reads	1,916,397 / 89.91%

2.2. ACGT Content

Number/percentage of A's	28,272,612 / 25.54%
Number/percentage of C's	20,409,174 / 18.44%
Number/percentage of T's	34,119,411 / 30.83%
Number/percentage of G's	27,881,213 / 25.19%
Number/percentage of N's	1,359 / 0%
GC Percentage	43.63%

2.3. Coverage

Mean	0.0358

Standard Deviation	0.3409

2.4. Mapping Quality

Mean Mapping Quality	44.21

2.5. Mismatches and indels

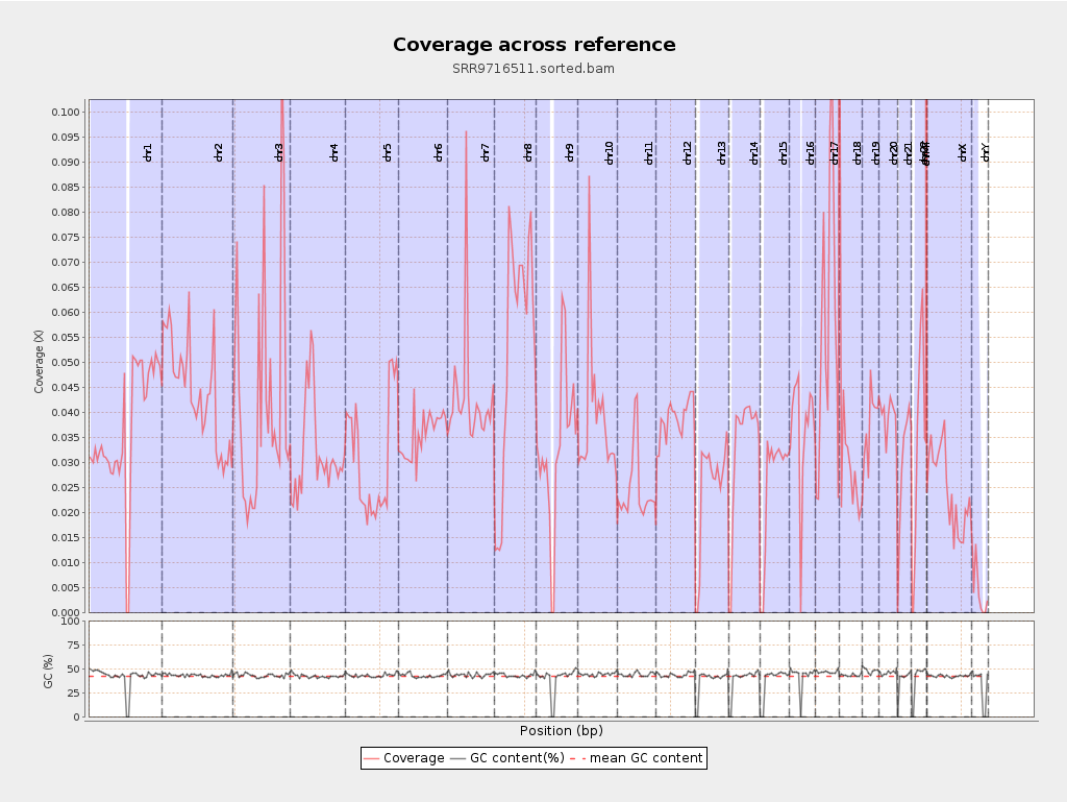
General error rate	0.52%
Mismatches	559,520
Insertions	7,472
Mapped reads with at least one insertion	0.39%
Deletions	21,443
Mapped reads with at least one deletion	1.11%
Homopolymer indels	40.1%

2.6. Chromosome stats

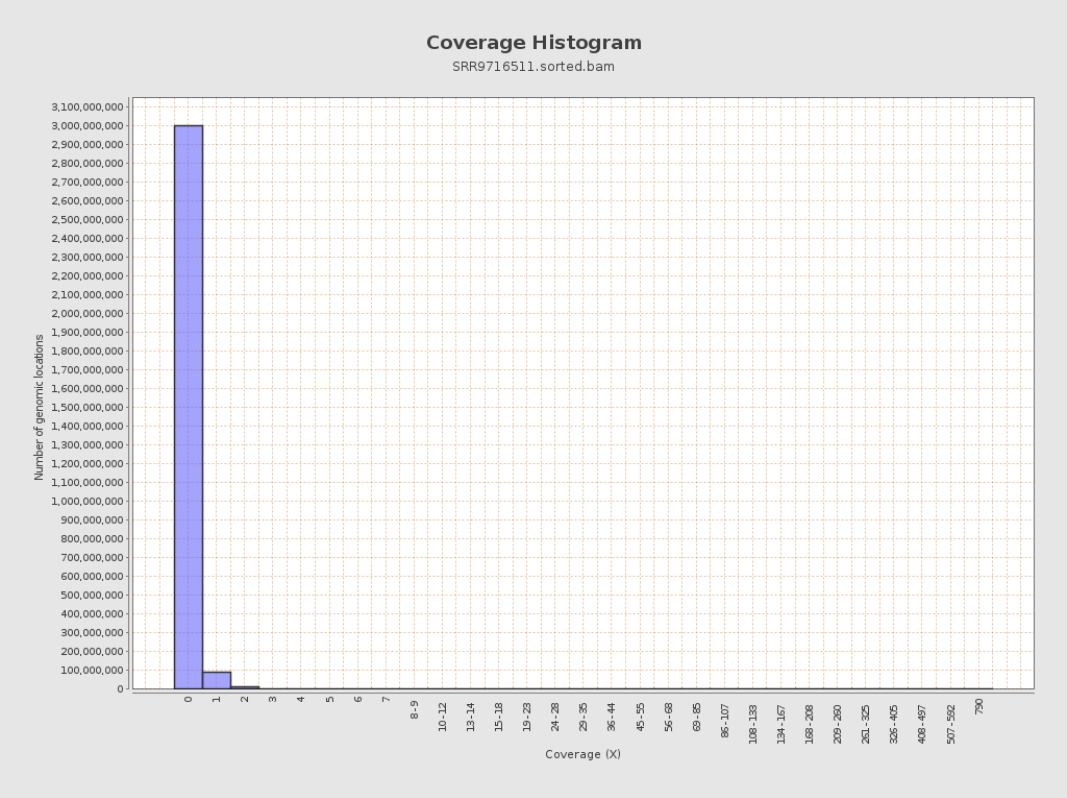
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9129441	0.0366	0.4634
chr2	243199373	10784881	0.0443	0.4088
chr3	198022430	8356238	0.0422	0.2447
chr4	191154276	6106134	0.0319	0.2164
chr5	180915260	5550572	0.0307	0.1951
chr6	171115067	6096584	0.0356	0.2278
chr7	159138663	6848143	0.043	0.7785

chr8	146364022	7805422	0.0533	0.3663
chr9	141213431	4589274	0.0325	0.2341
chr10	135534747	5200255	0.0384	0.4388
chr11	135006516	3297894	0.0244	0.2183
chr12	133851895	5164356	0.0386	0.2426
chr13	115169878	2872471	0.0249	0.1749
chr14	107349540	3535364	0.0329	0.2052
chr15	102531392	2642497	0.0258	0.1852
chr16	90354753	3340141	0.037	0.2257
chr17	81195210	4629517	0.057	0.2768
chr18	78077248	2590362	0.0332	0.379
chr19	59128983	2216239	0.0375	0.4093
chr20	63025520	2469137	0.0392	0.232
chr21	48129895	1426802	0.0296	0.1994
chr22	51304566	1686523	0.0329	0.1997
chrMT	16571	284686	17.1798	10.2782
chrX	155270560	3849872	0.0248	0.2018
chrY	59373566	244913	0.0041	0.117

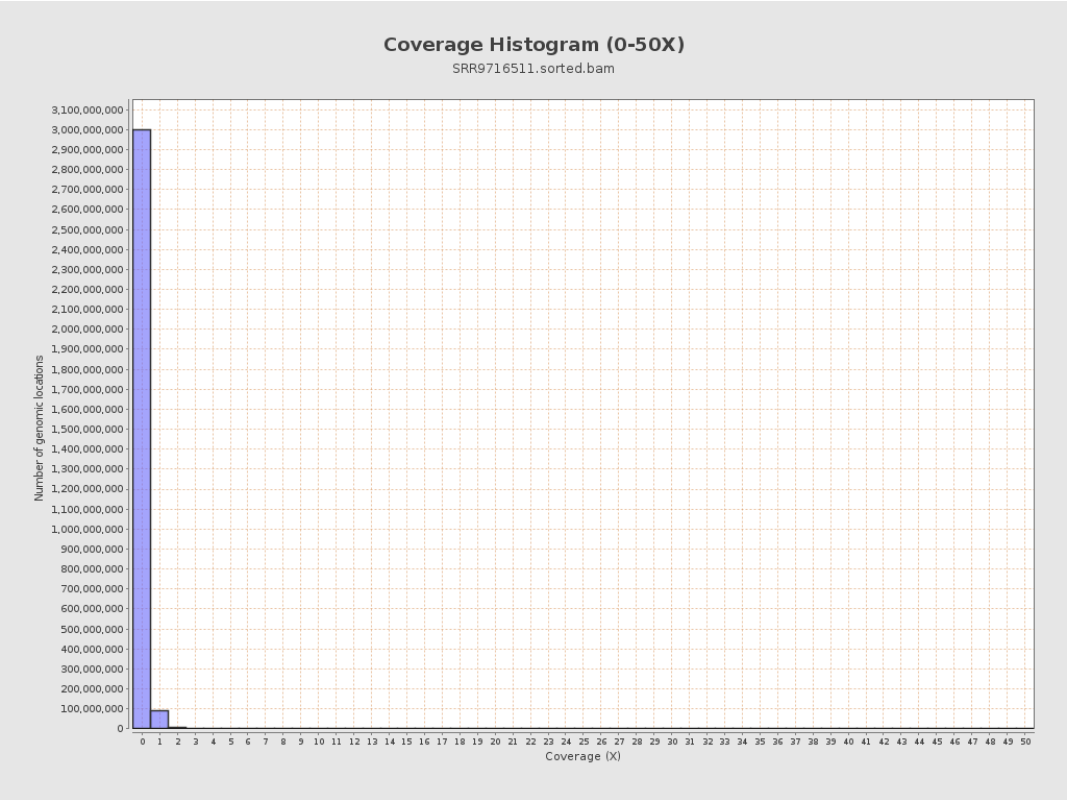
3. Results : Coverage across reference



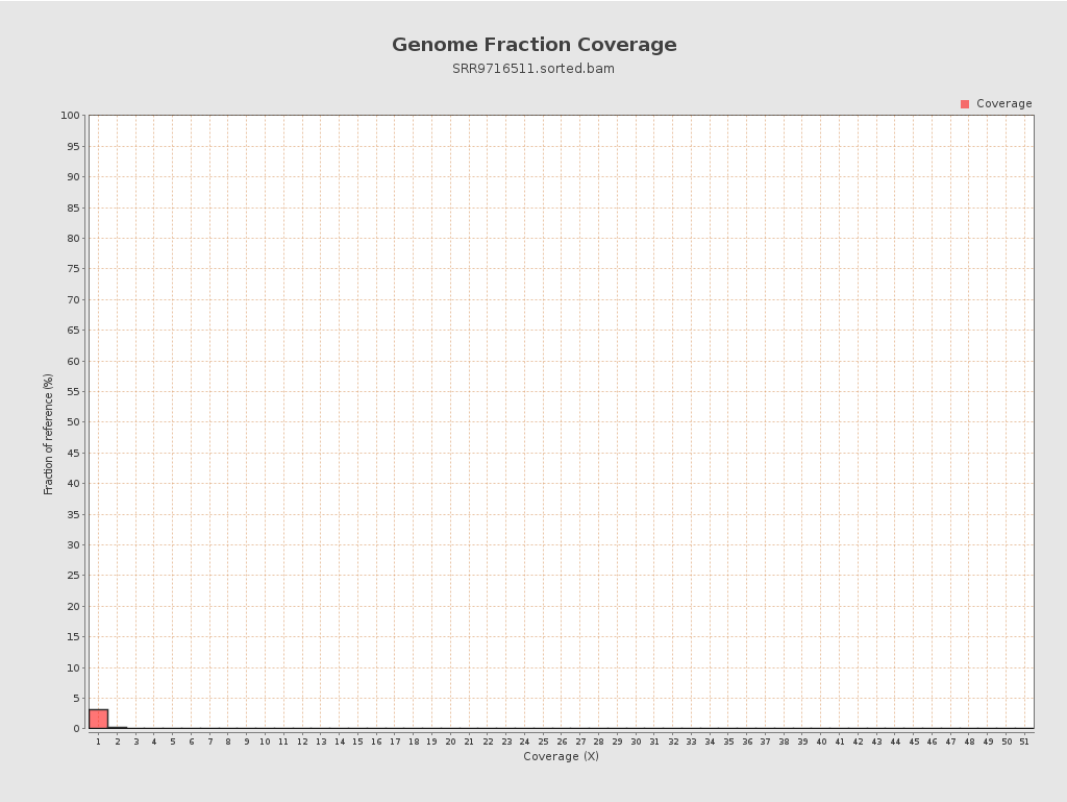
4. Results : Coverage Histogram



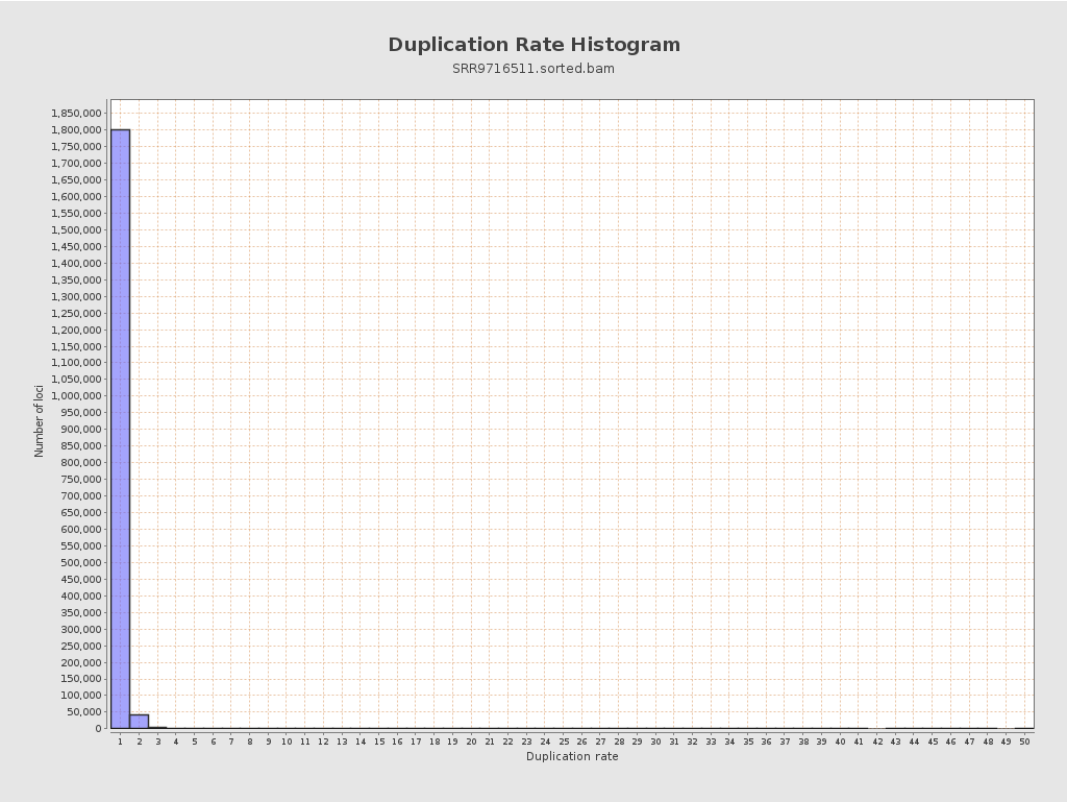
5. Results : Coverage Histogram (0-50X)



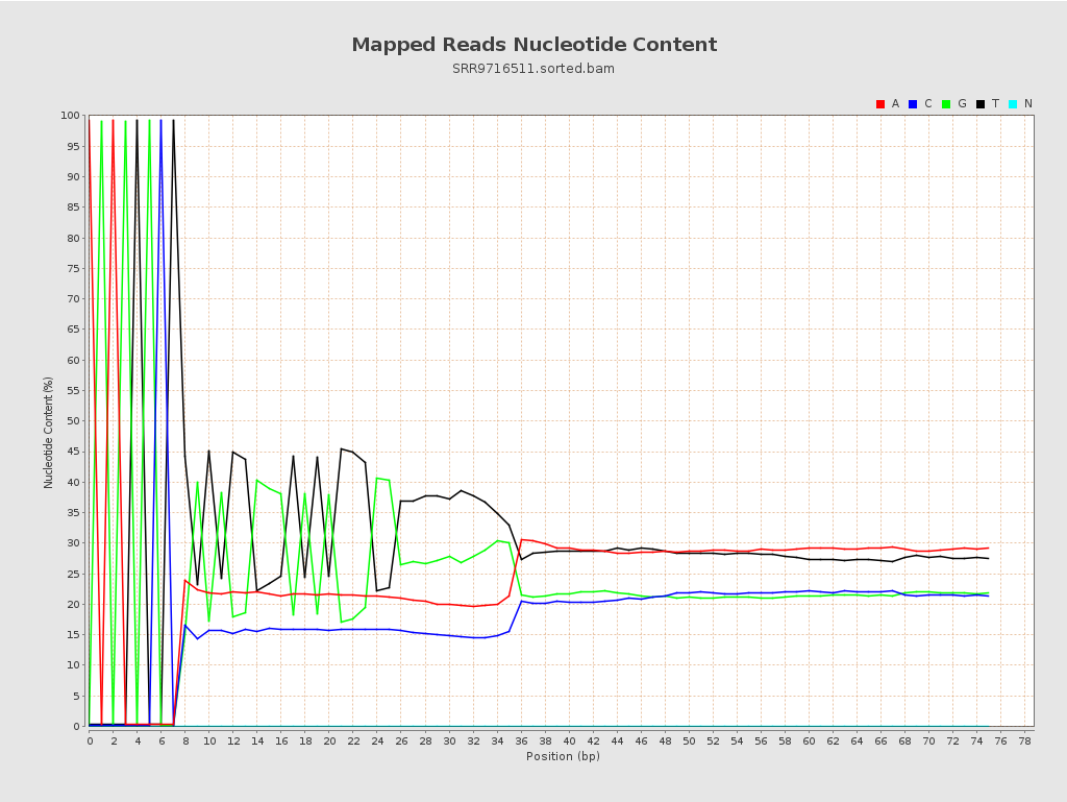
6. Results : Genome Fraction Coverage



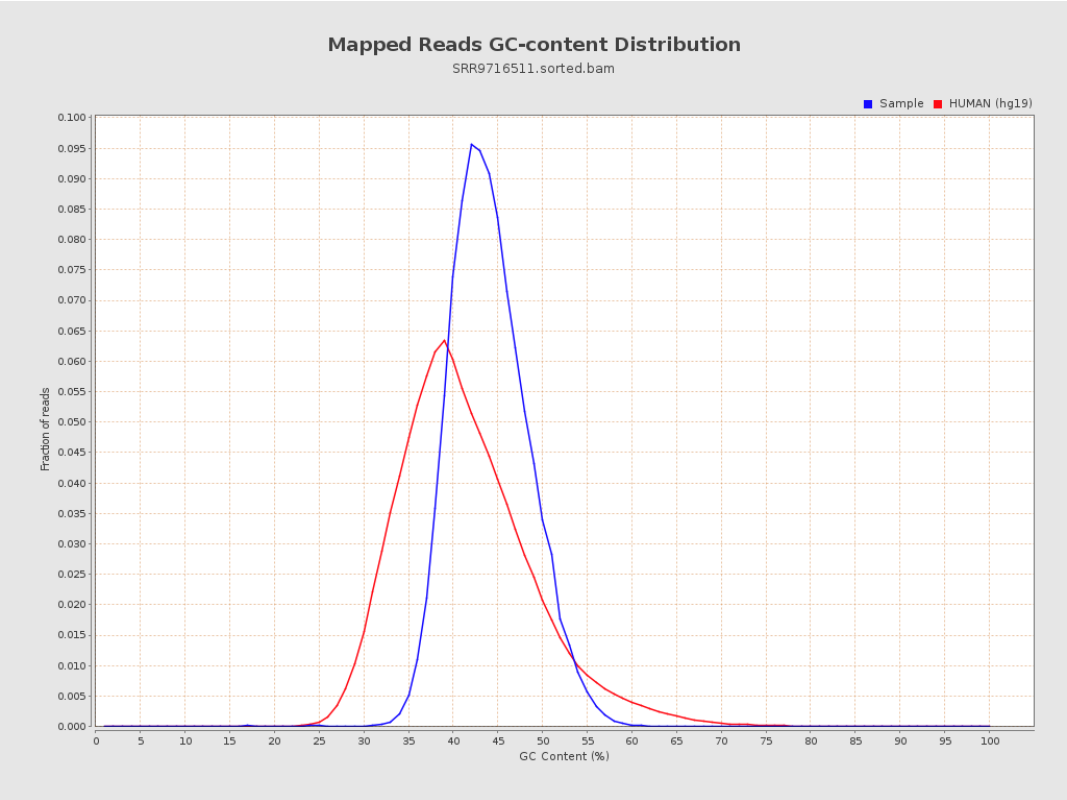
7. Results : Duplication Rate Histogram



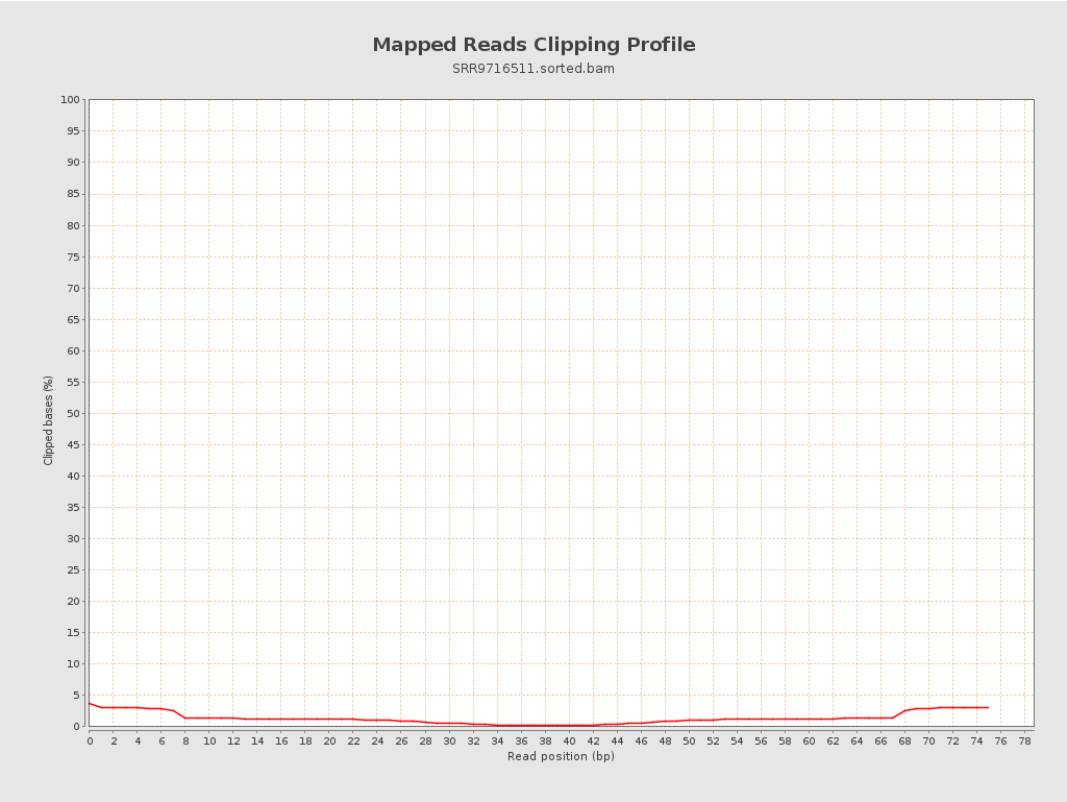
8. Results : Mapped Reads Nucleotide Content



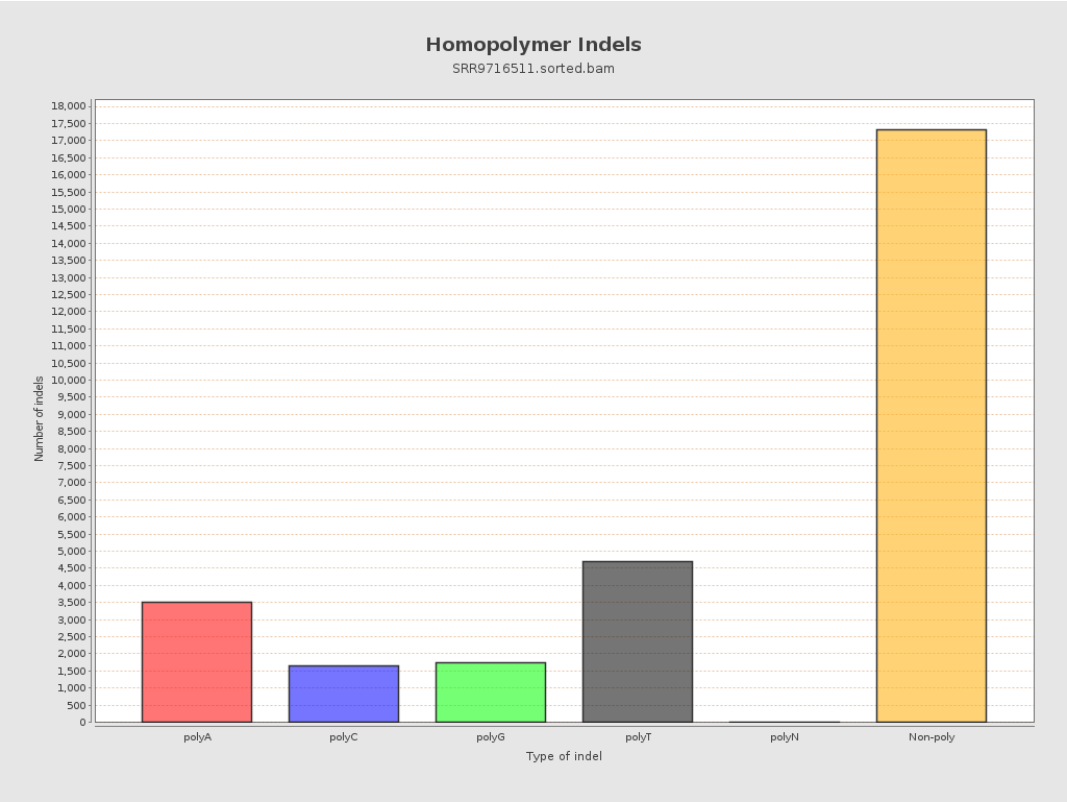
9. Results : Mapped Reads GC-content Distribution



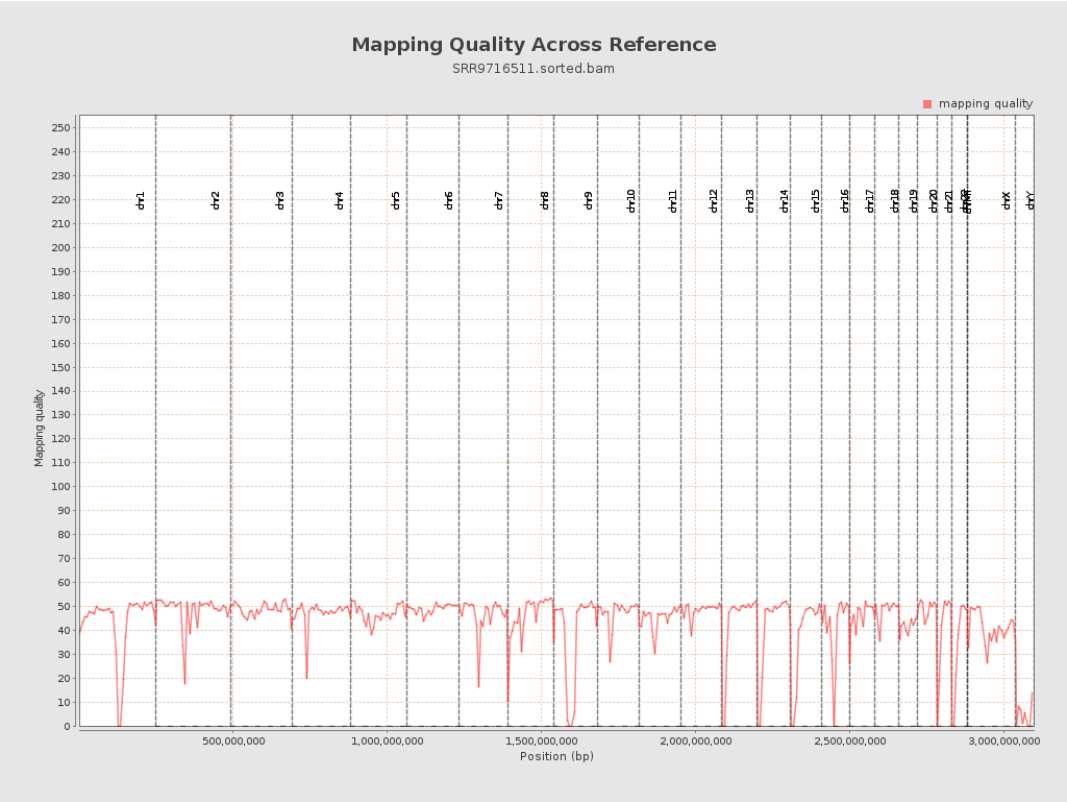
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram