Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 15:45:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716472.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_SRR9716472 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716472.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 15:45:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716472.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,062,525
Mapped reads	958,053 / 90.17%
Unmapped reads	104,472 / 9.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,010 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	24,536 / 2.31%
Duplication rate	1.78%
Clipped reads	960,608 / 90.41%

2.2. ACGT Content

Number/percentage of A's	13,662,643 / 24.77%
Number/percentage of C's	10,505,448 / 19.04%
Number/percentage of T's	17,550,528 / 31.81%
Number/percentage of G's	13,449,009 / 24.38%
Number/percentage of N's	637 / 0%
GC Percentage	43.42%

2.3. Coverage

Mean	0.0178

Standard Deviation	0.1952

2.4. Mapping Quality

Mean Mapping Quality	44.14

2.5. Mismatches and indels

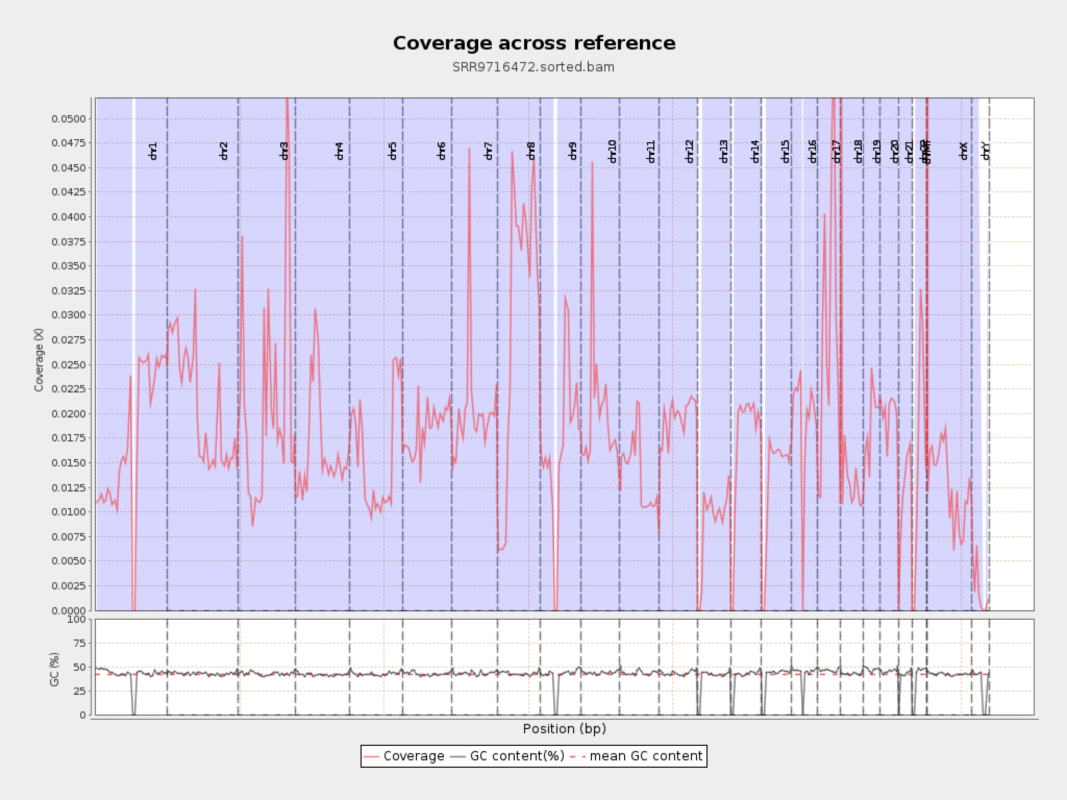
General error rate	0.52%
Mismatches	276,391
Insertions	4,324
Mapped reads with at least one insertion	0.45%
Deletions	10,186
Mapped reads with at least one deletion	1.06%
Homopolymer indels	39.21%

2.6. Chromosome stats

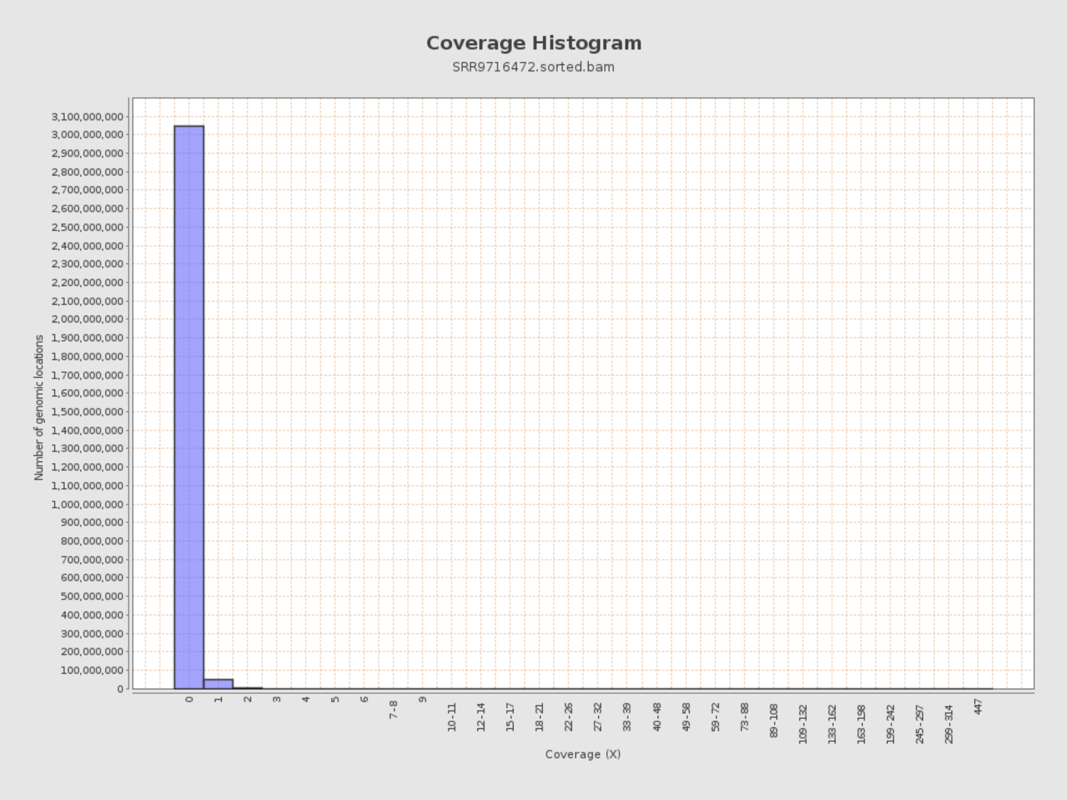
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4301645	0.0173	0.246
chr2	243199373	5045866	0.0207	0.2402
chr3	198022430	4124591	0.0208	0.1591
chr4	191154276	3137180	0.0164	0.1444
chr5	180915260	2822683	0.0156	0.1316
chr6	171115067	3149157	0.0184	0.1511
chr7	159138663	3259296	0.0205	0.404

chr8	146364022	4440802	0.0303	0.22
chr9	141213431	2332671	0.0165	0.1497
chr10	135534747	2702217	0.0199	0.2469
chr11	135006516	1896673	0.014	0.1419
chr12	133851895	2627405	0.0196	0.1576
chr13	115169878	1032601	0.009	0.1001
chr14	107349540	1823250	0.017	0.1393
chr15	102531392	1341695	0.0131	0.1224
chr16	90354753	1708329	0.0189	0.1505
chr17	81195210	2338274	0.0288	0.1838
chr18	78077248	1162933	0.0149	0.2037
chr19	59128983	1127131	0.0191	0.2287
chr20	63025520	1249863	0.0198	0.1545
chr21	48129895	576205	0.012	0.1185
chr22	51304566	824074	0.0161	0.1337
chrMT	16571	55041	3.3215	2.5629
chrX	155270560	1982703	0.0128	0.1306
chrY	59373566	121993	0.0021	0.0615

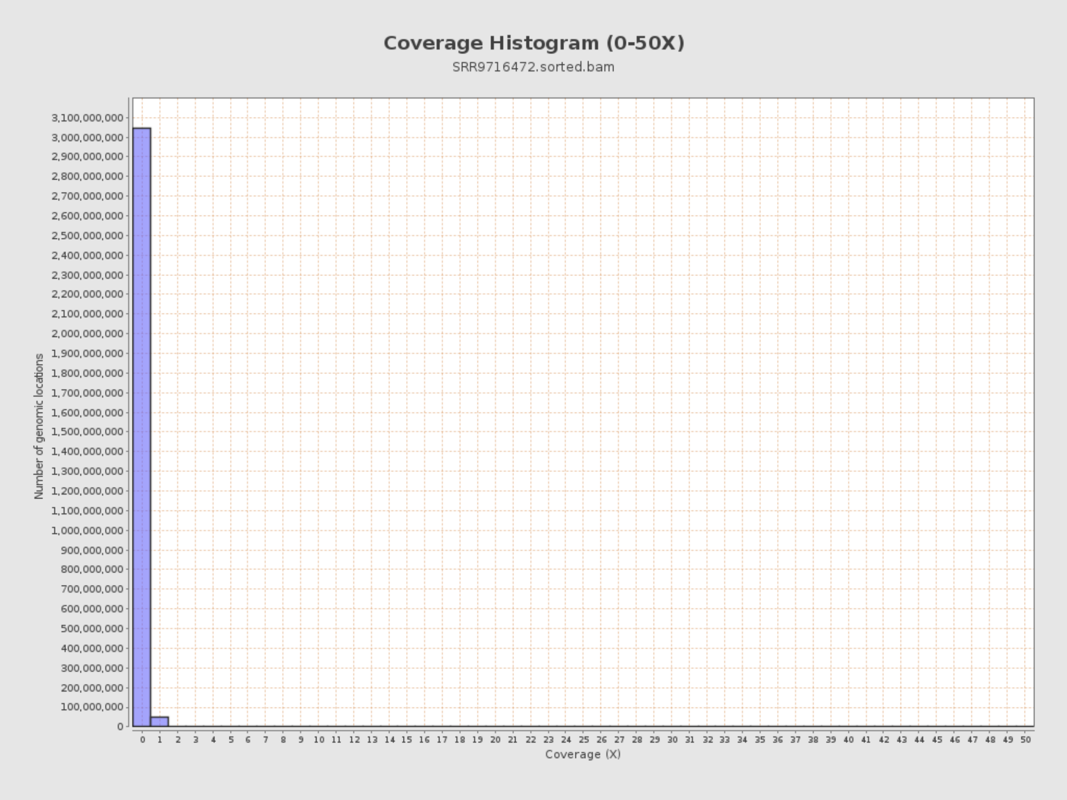
3. Results : Coverage across reference



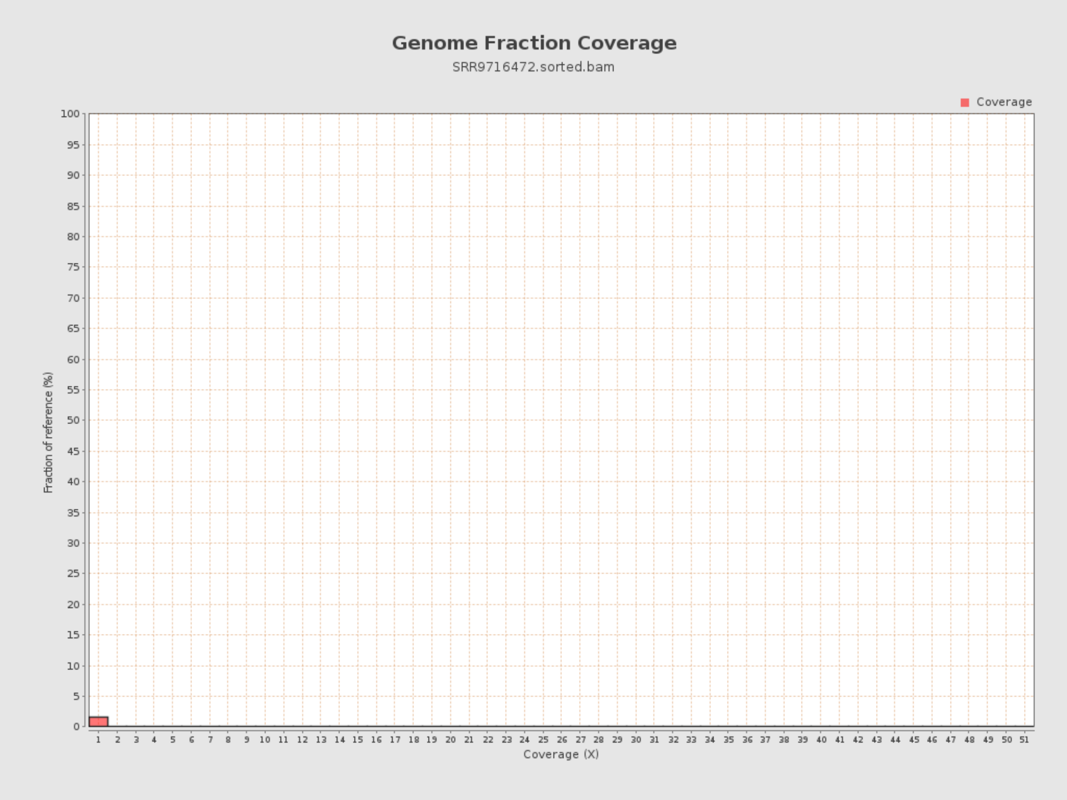
4. Results : Coverage Histogram



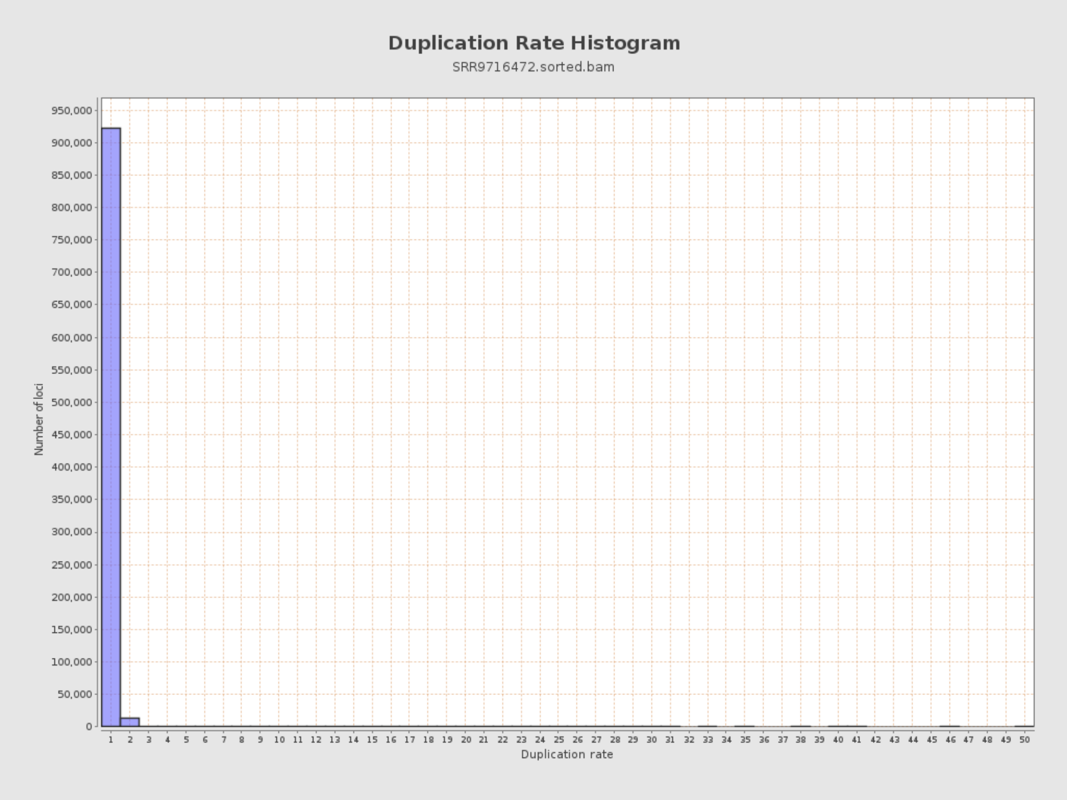
5. Results : Coverage Histogram (0-50X)



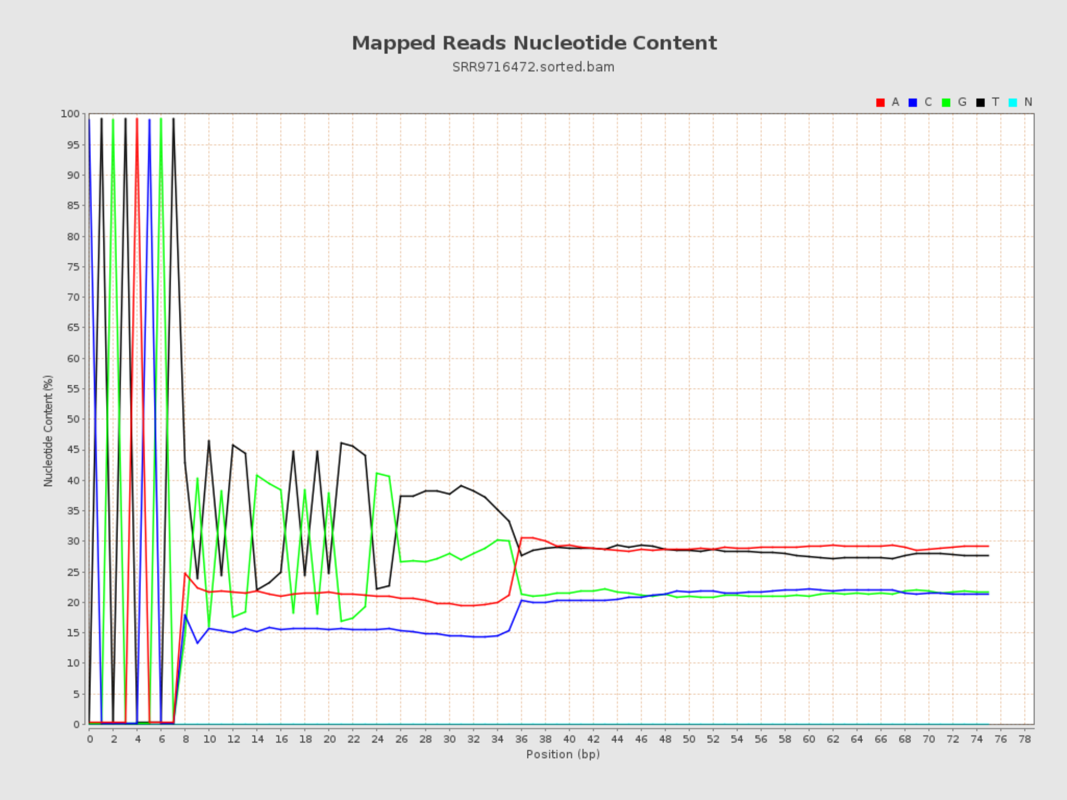
6. Results : Genome Fraction Coverage



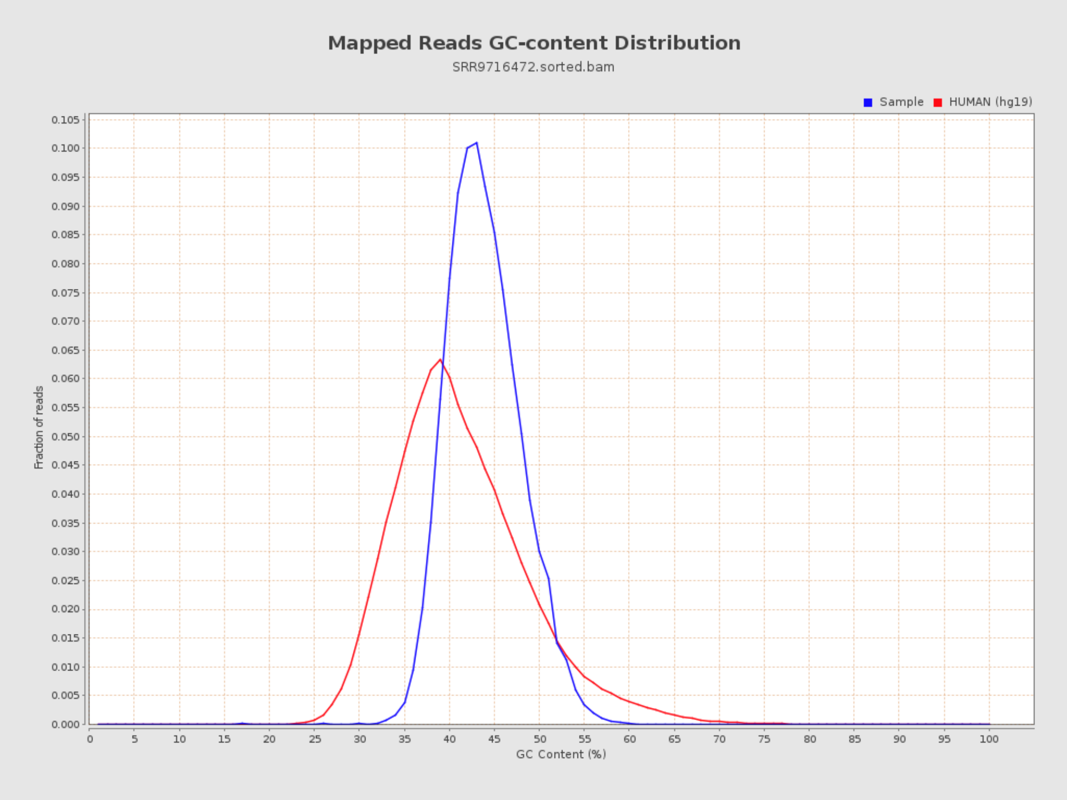
7. Results : Duplication Rate Histogram



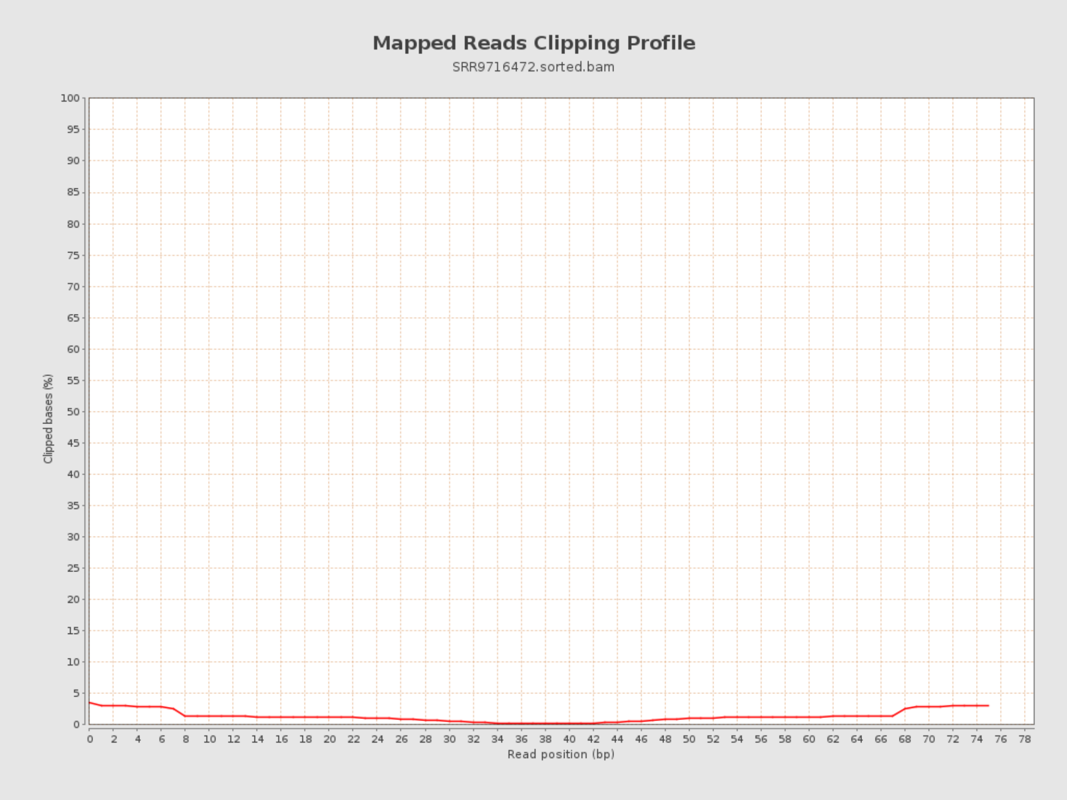
8. Results : Mapped Reads Nucleotide Content



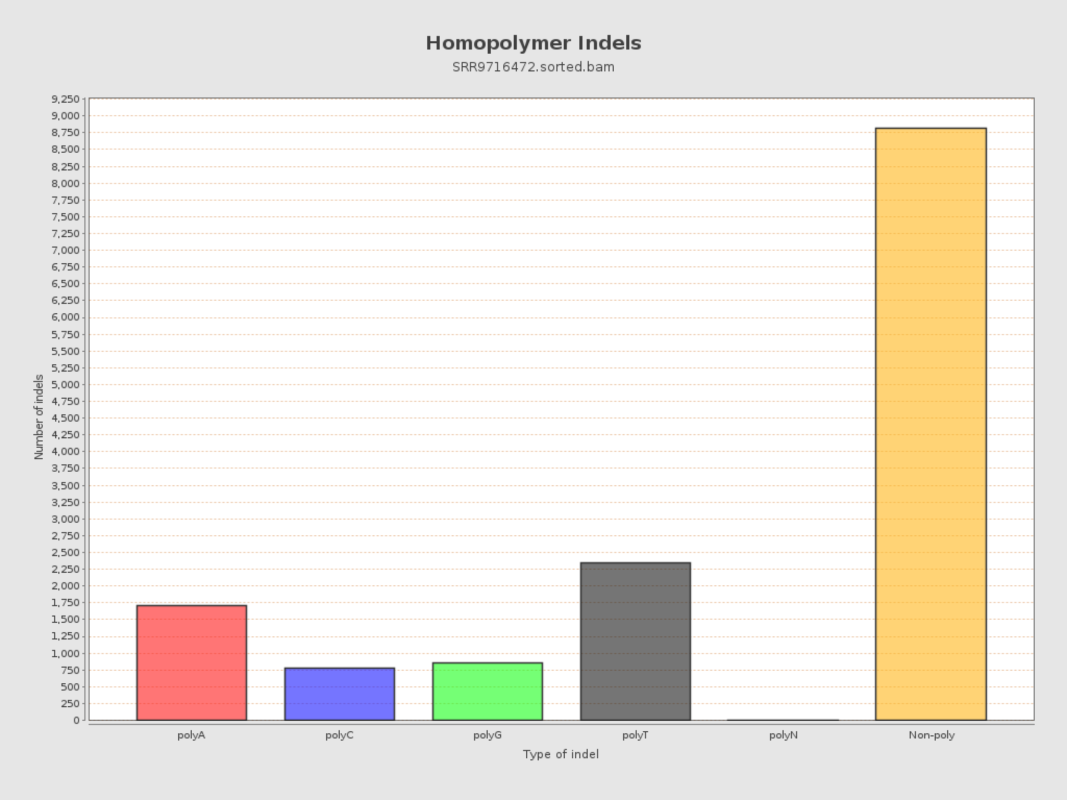
9. Results : Mapped Reads GC-content Distribution



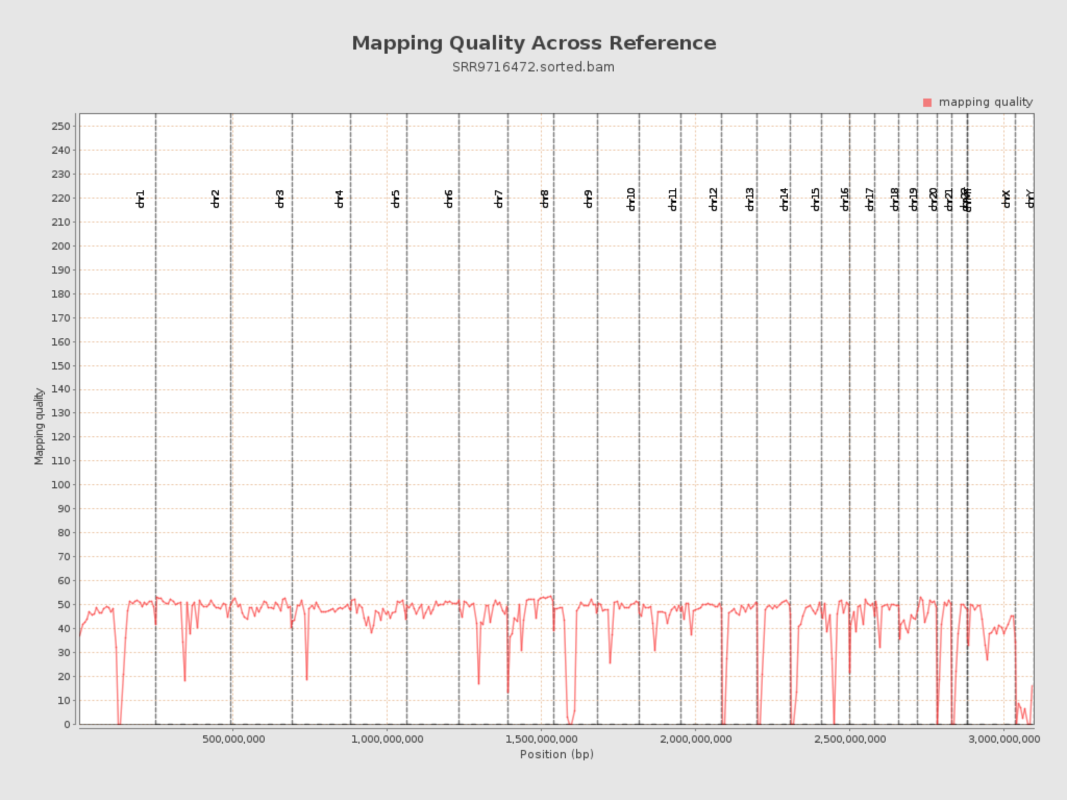
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram