Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 12:03:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716407.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_SRR9716407 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716407.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 12:03:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716407.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,450,504
Mapped reads	2,125,666 / 86.74%
Unmapped reads	324,838 / 13.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,175 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	81,797 / 3.34%
Duplication rate	2.85%
Clipped reads	2,126,570 / 86.78%

2.2. ACGT Content

Number/percentage of A's	28,095,619 / 23.38%
Number/percentage of C's	24,804,888 / 20.64%
Number/percentage of T's	38,239,253 / 31.82%
Number/percentage of G's	29,038,311 / 24.16%
Number/percentage of N's	1,657 / 0%
GC Percentage	44.8%

2.3. Coverage

Mean	0.0388

Standard Deviation	0.3073

2.4. Mapping Quality

Mean Mapping Quality	43.16

2.5. Mismatches and indels

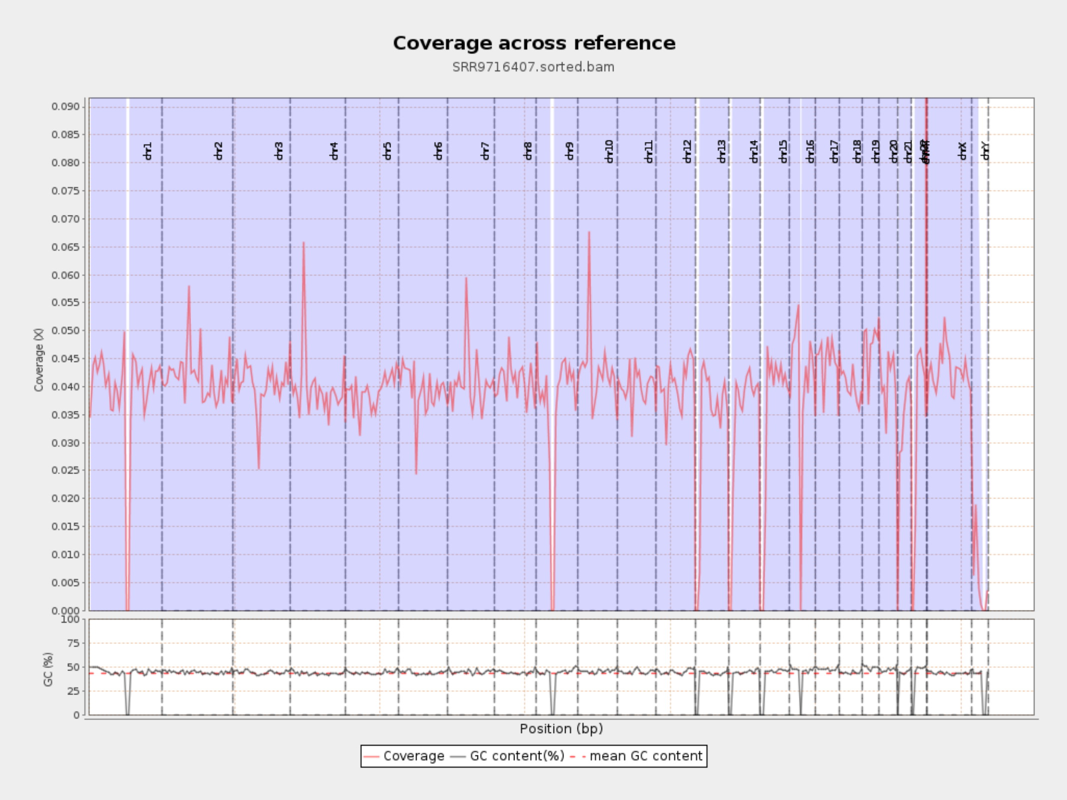
General error rate	0.54%
Mismatches	631,443
Insertions	9,062
Mapped reads with at least one insertion	0.42%
Deletions	23,613
Mapped reads with at least one deletion	1.1%
Homopolymer indels	40.35%

2.6. Chromosome stats

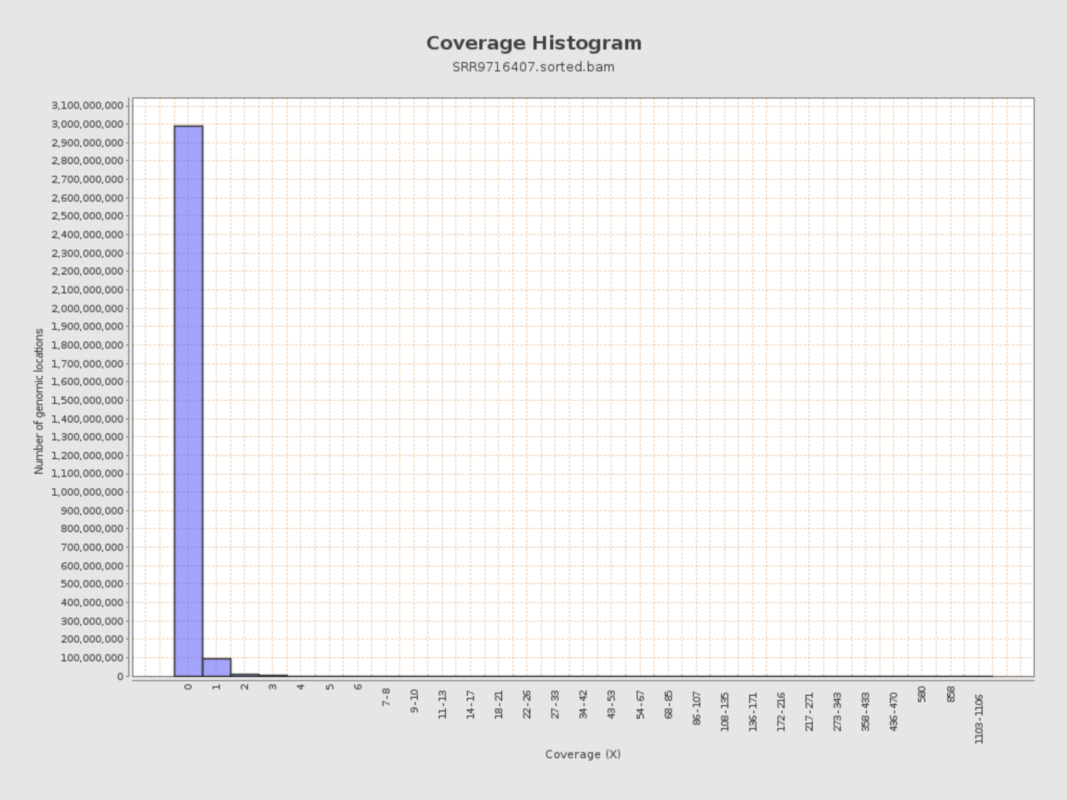
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9642071	0.0387	0.401
chr2	243199373	10197689	0.0419	0.515
chr3	198022430	7983332	0.0403	0.2294
chr4	191154276	7607424	0.0398	0.253
chr5	180915260	7074316	0.0391	0.2217
chr6	171115067	6756819	0.0395	0.2608
chr7	159138663	6517632	0.041	0.4025

chr8	146364022	6000668	0.041	0.2764
chr9	141213431	4979211	0.0353	0.2511
chr10	135534747	5834891	0.0431	0.3324
chr11	135006516	5392809	0.0399	0.2774
chr12	133851895	5456513	0.0408	0.2304
chr13	115169878	3705786	0.0322	0.2039
chr14	107349540	3574531	0.0333	0.2138
chr15	102531392	3537615	0.0345	0.2176
chr16	90354753	3729047	0.0413	0.2493
chr17	81195210	3599834	0.0443	0.2554
chr18	78077248	3150947	0.0404	0.4177
chr19	59128983	2780803	0.047	0.3521
chr20	63025520	2568632	0.0408	0.2347
chr21	48129895	1534738	0.0319	0.2259
chr22	51304566	1566159	0.0305	0.1979
chrMT	16571	16257	0.9811	1.3255
chrX	155270560	6648751	0.0428	0.2592
chrY	59373566	360909	0.0061	0.1459

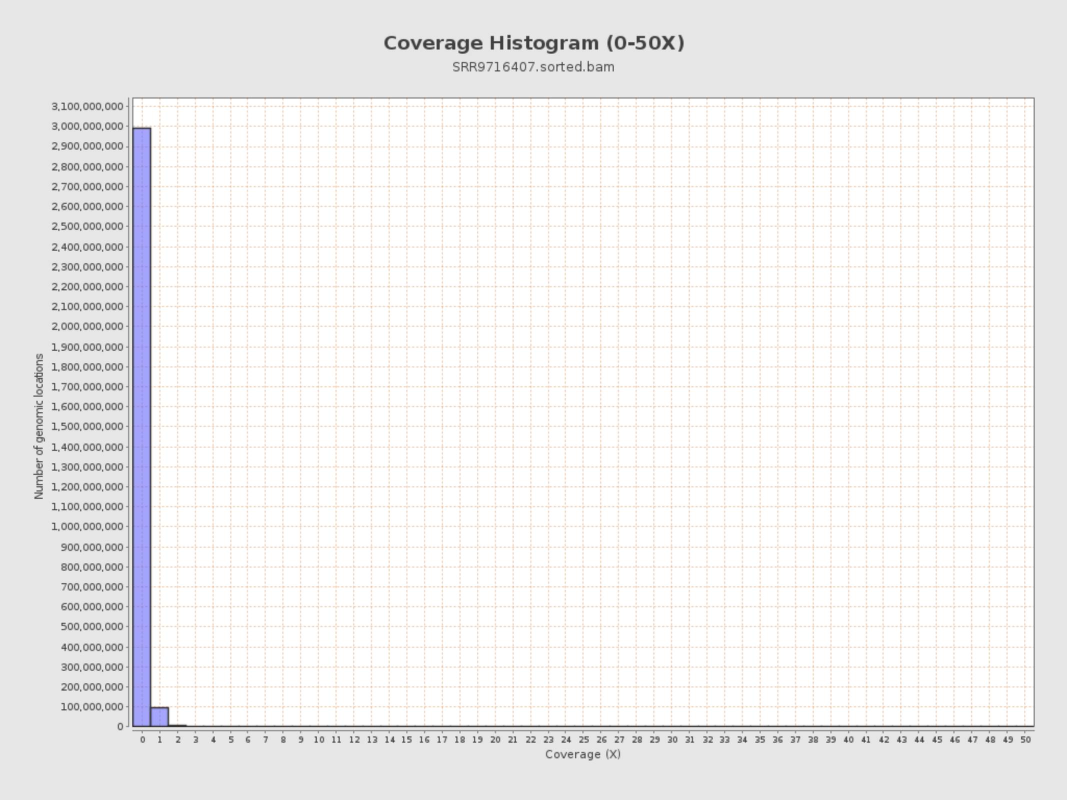
3. Results : Coverage across reference



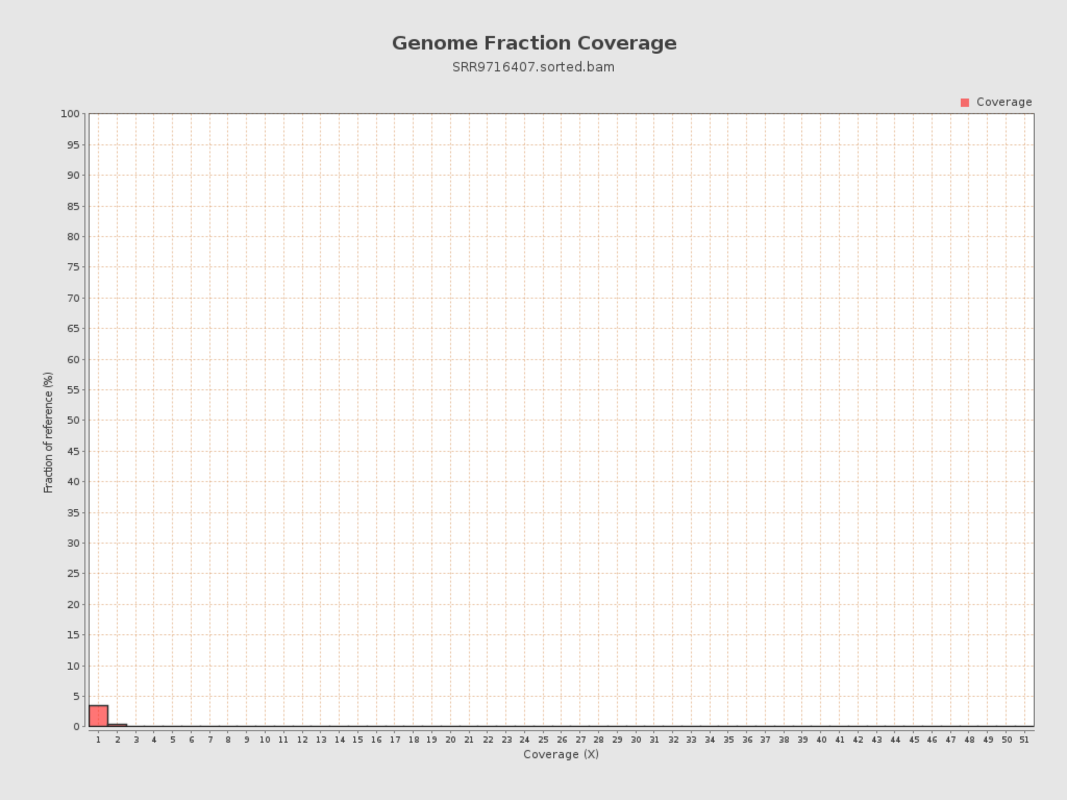
4. Results : Coverage Histogram



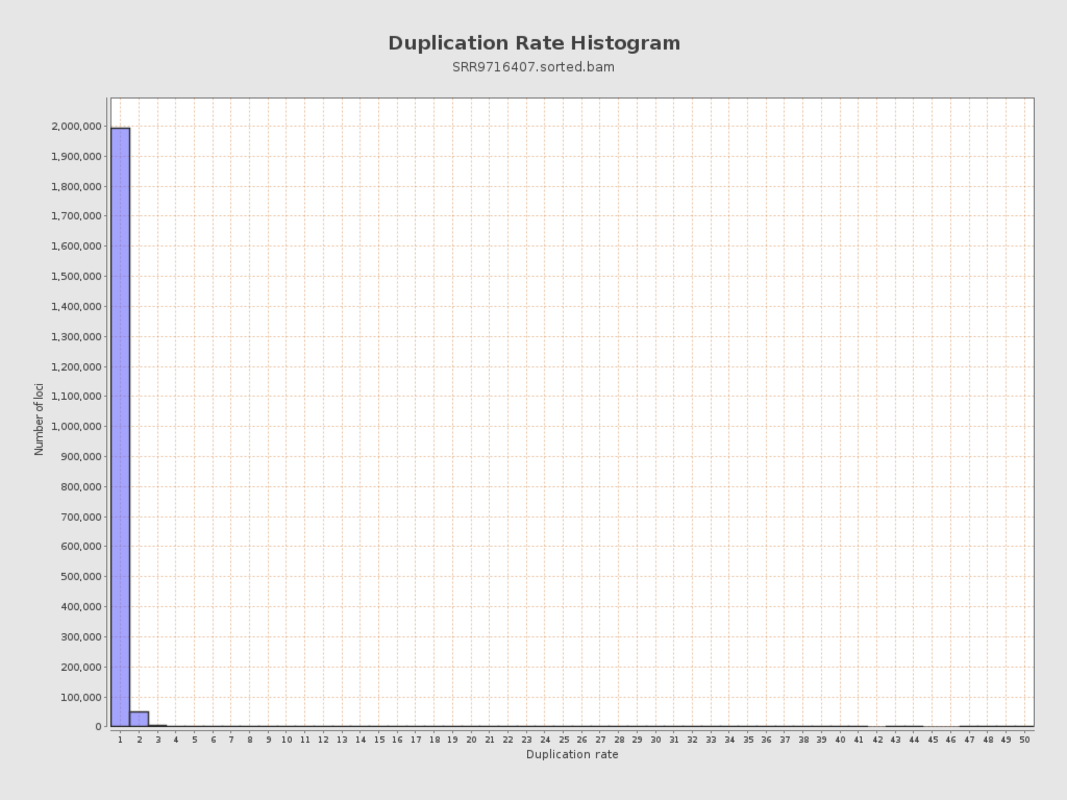
5. Results : Coverage Histogram (0-50X)



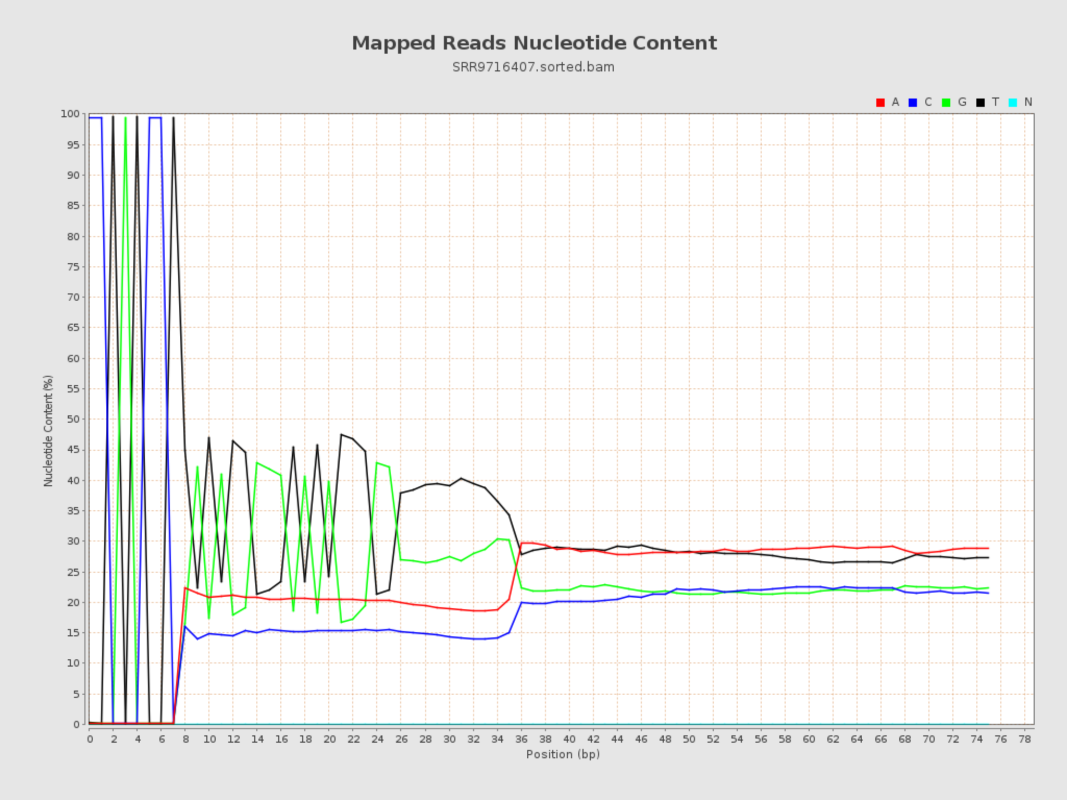
6. Results : Genome Fraction Coverage



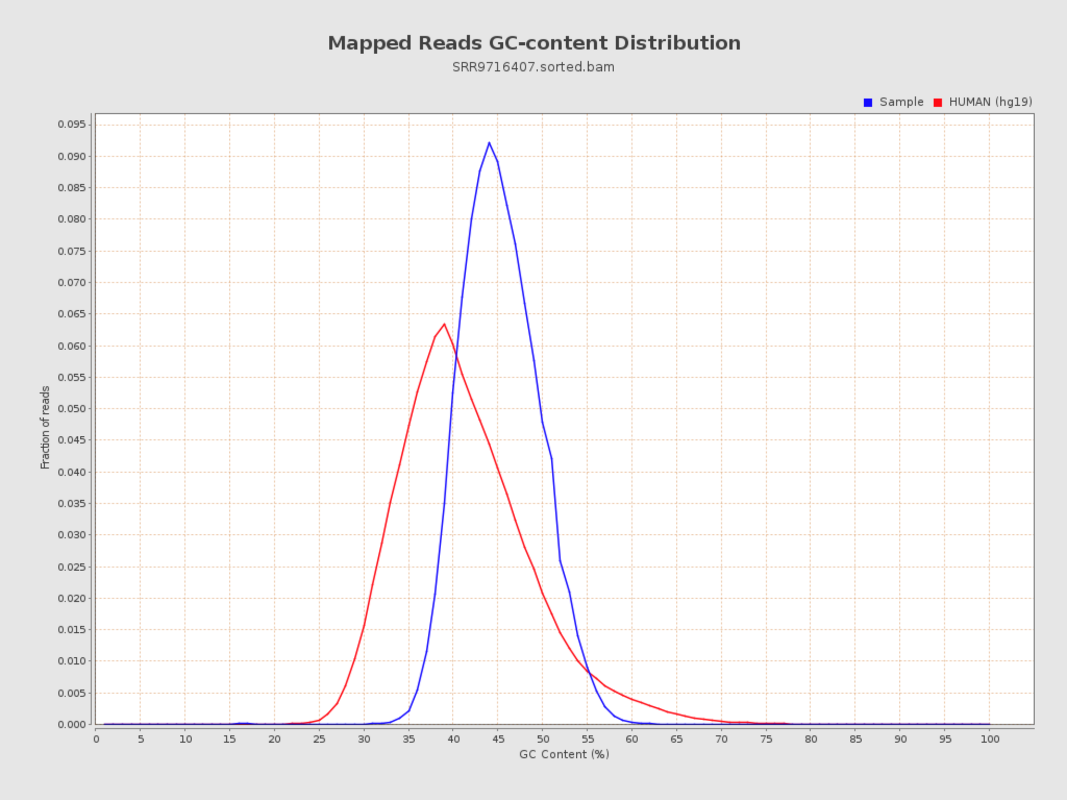
7. Results : Duplication Rate Histogram



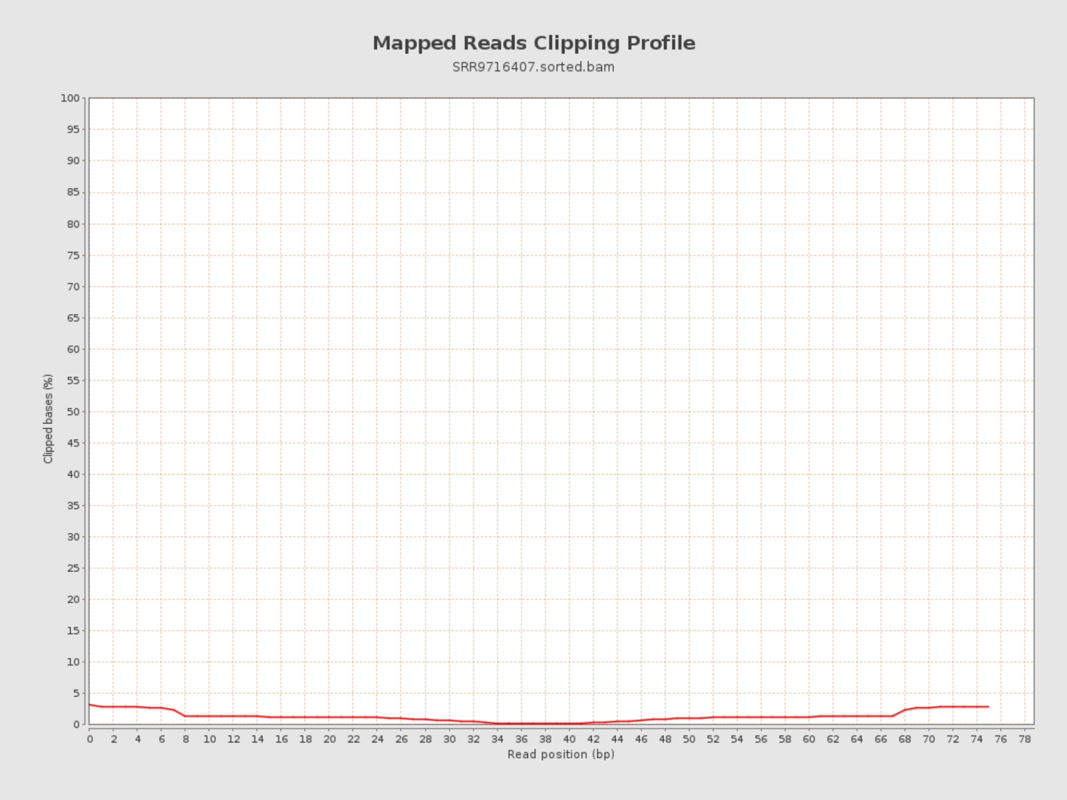
8. Results : Mapped Reads Nucleotide Content



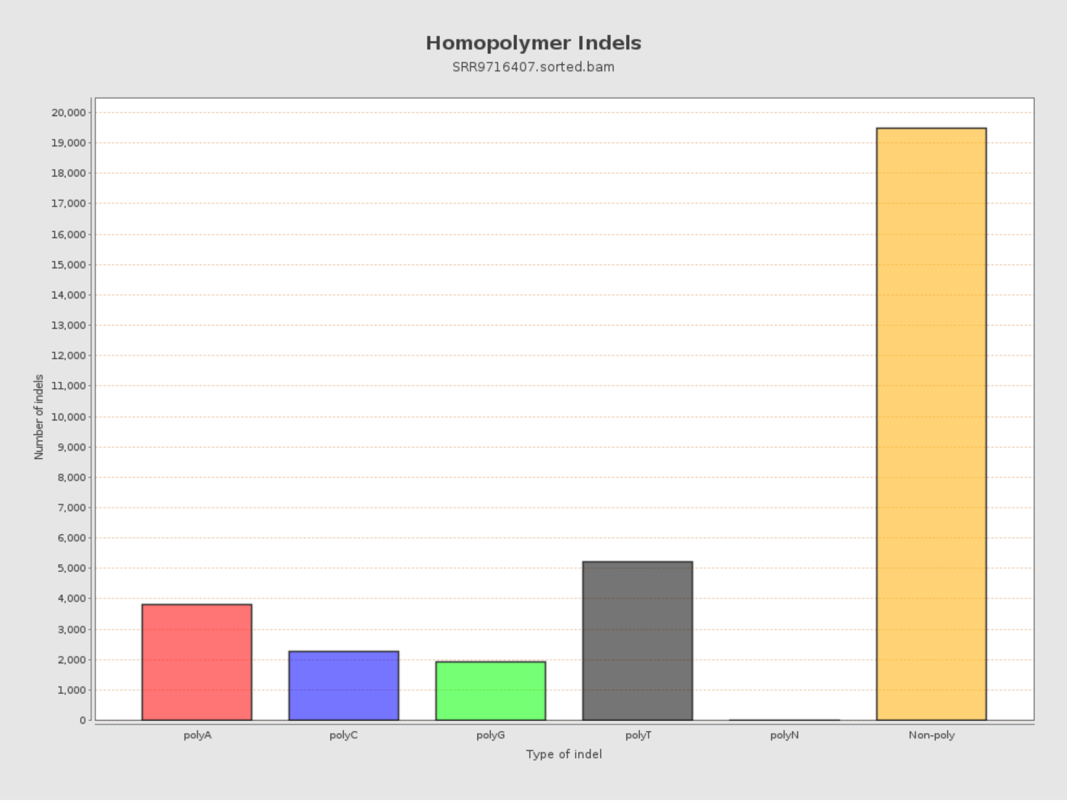
9. Results : Mapped Reads GC-content Distribution



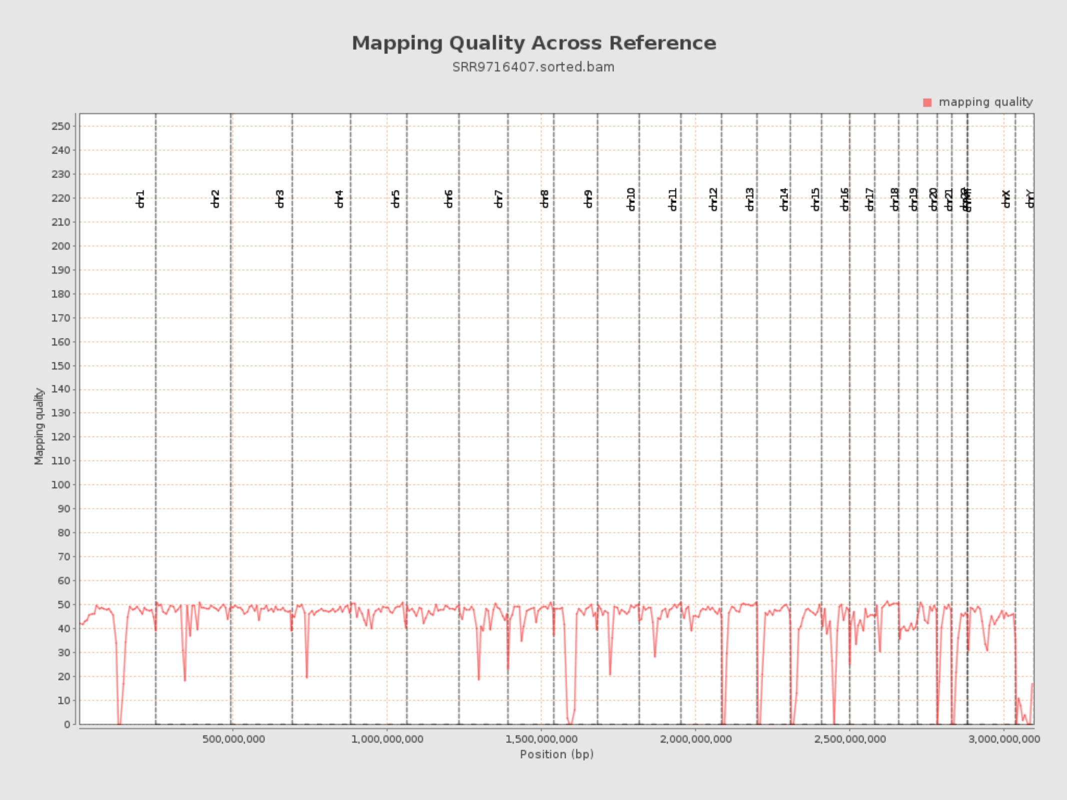
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram