Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 10:39:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716382.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_SRR9716382 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716382.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 10:39:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716382.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,654,455
Mapped reads	2,319,658 / 87.39%
Unmapped reads	334,797 / 12.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,154 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	72,254 / 2.72%
Duplication rate	2.13%
Clipped reads	2,320,856 / 87.43%

2.2. ACGT Content

Number/percentage of A's	31,202,158 / 23.71%
Number/percentage of C's	26,702,245 / 20.29%
Number/percentage of T's	42,177,988 / 32.05%
Number/percentage of G's	31,512,553 / 23.95%
Number/percentage of N's	998 / 0%
GC Percentage	44.24%

2.3. Coverage

Mean	0.0425

Standard Deviation	0.3295

2.4. Mapping Quality

Mean Mapping Quality	42.2

2.5. Mismatches and indels

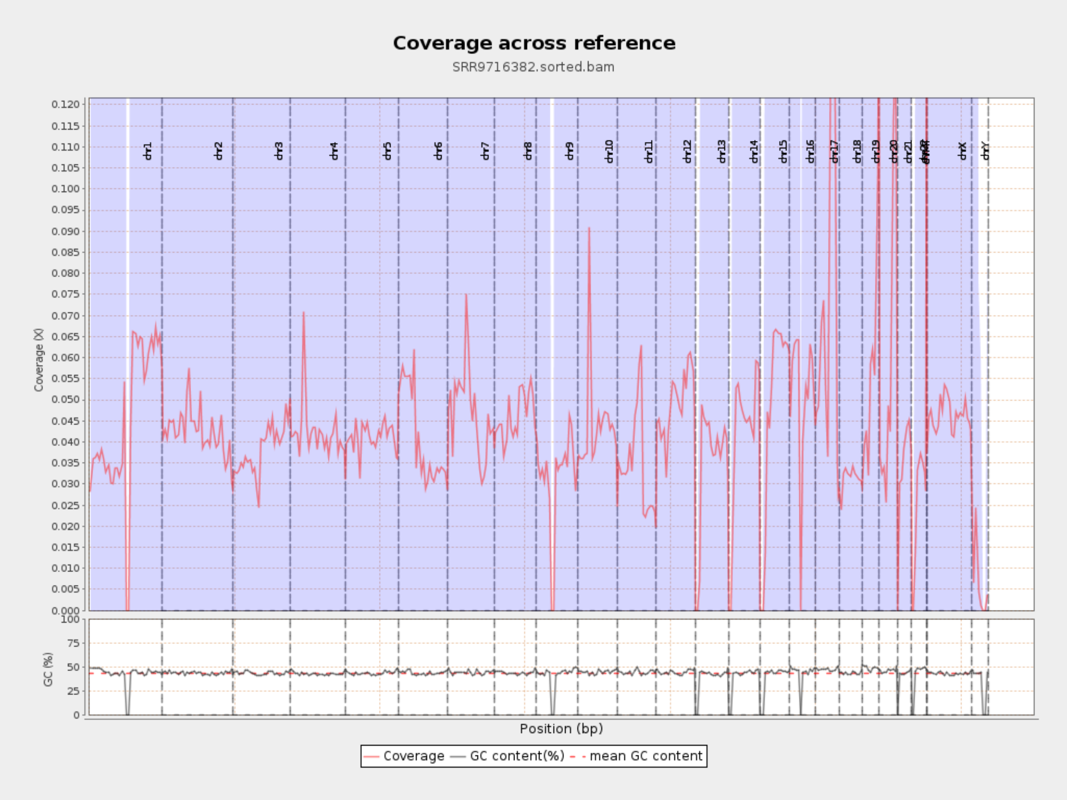
General error rate	0.55%
Mismatches	702,485
Insertions	10,332
Mapped reads with at least one insertion	0.44%
Deletions	25,247
Mapped reads with at least one deletion	1.08%
Homopolymer indels	39.73%

2.6. Chromosome stats

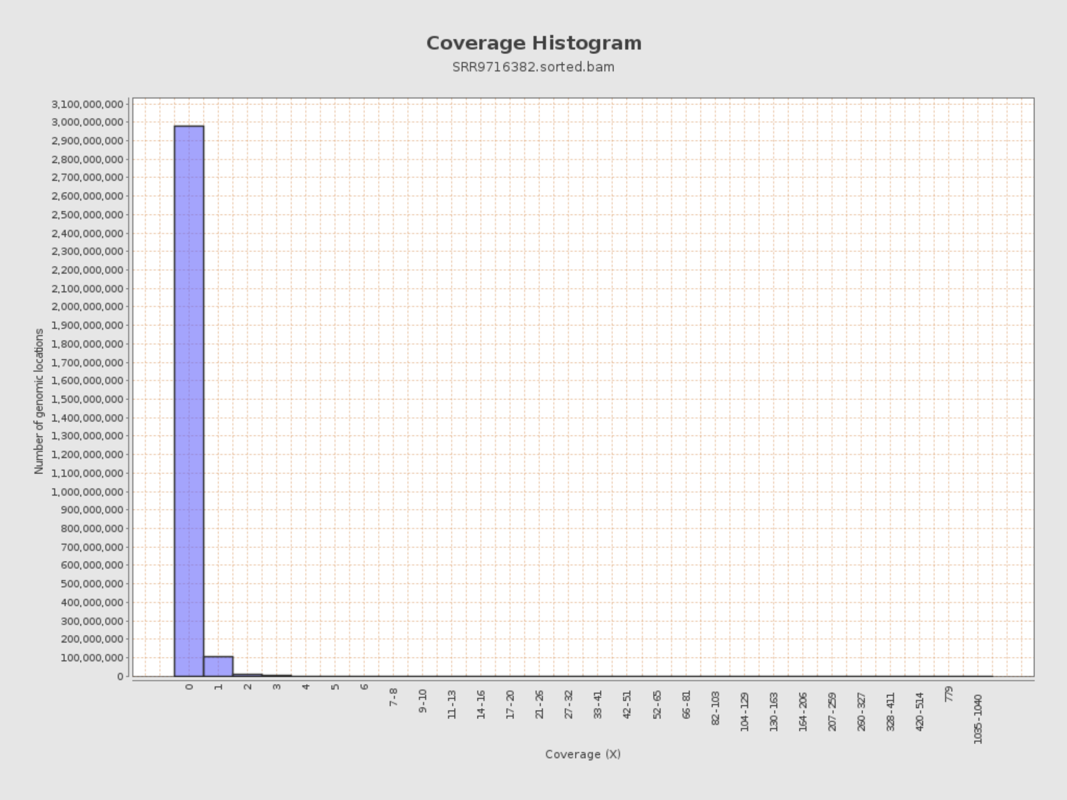
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11136032	0.0447	0.424
chr2	243199373	10363451	0.0426	0.494
chr3	198022430	7515127	0.038	0.2246
chr4	191154276	8059591	0.0422	0.2664
chr5	180915260	7443440	0.0411	0.2245
chr6	171115067	7027911	0.0411	0.2818
chr7	159138663	7524893	0.0473	0.4834

chr8	146364022	6754345	0.0461	0.3118
chr9	141213431	4390430	0.0311	0.2428
chr10	135534747	5936871	0.0438	0.4604
chr11	135006516	4711486	0.0349	0.2664
chr12	133851895	6586236	0.0492	0.2488
chr13	115169878	3971794	0.0345	0.2066
chr14	107349540	4423521	0.0412	0.2427
chr15	102531392	4902166	0.0478	0.2517
chr16	90354753	4631167	0.0513	0.2847
chr17	81195210	5989079	0.0738	0.326
chr18	78077248	2454626	0.0314	0.3997
chr19	59128983	3461428	0.0585	0.4092
chr20	63025520	3869608	0.0614	0.2967
chr21	48129895	1647421	0.0342	0.2321
chr22	51304566	1238450	0.0241	0.1761
chrMT	16571	3379	0.2039	0.6357
chrX	155270560	7183688	0.0463	0.2643
chrY	59373566	409587	0.0069	0.2001

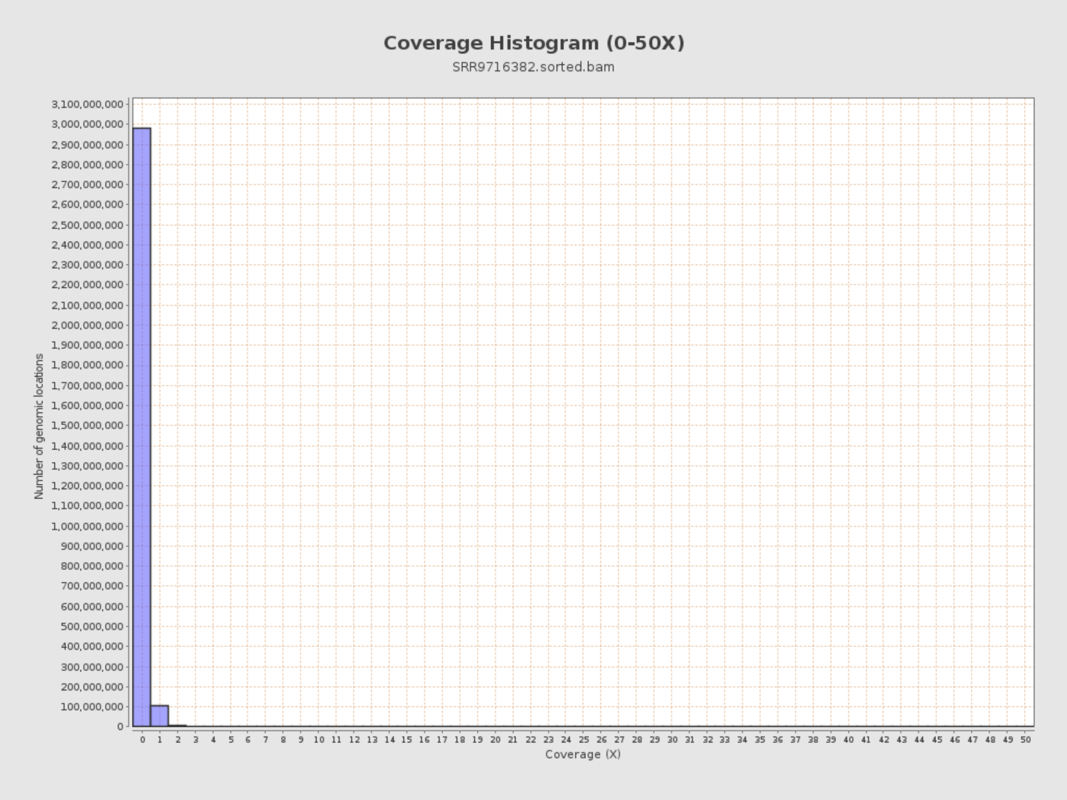
3. Results : Coverage across reference



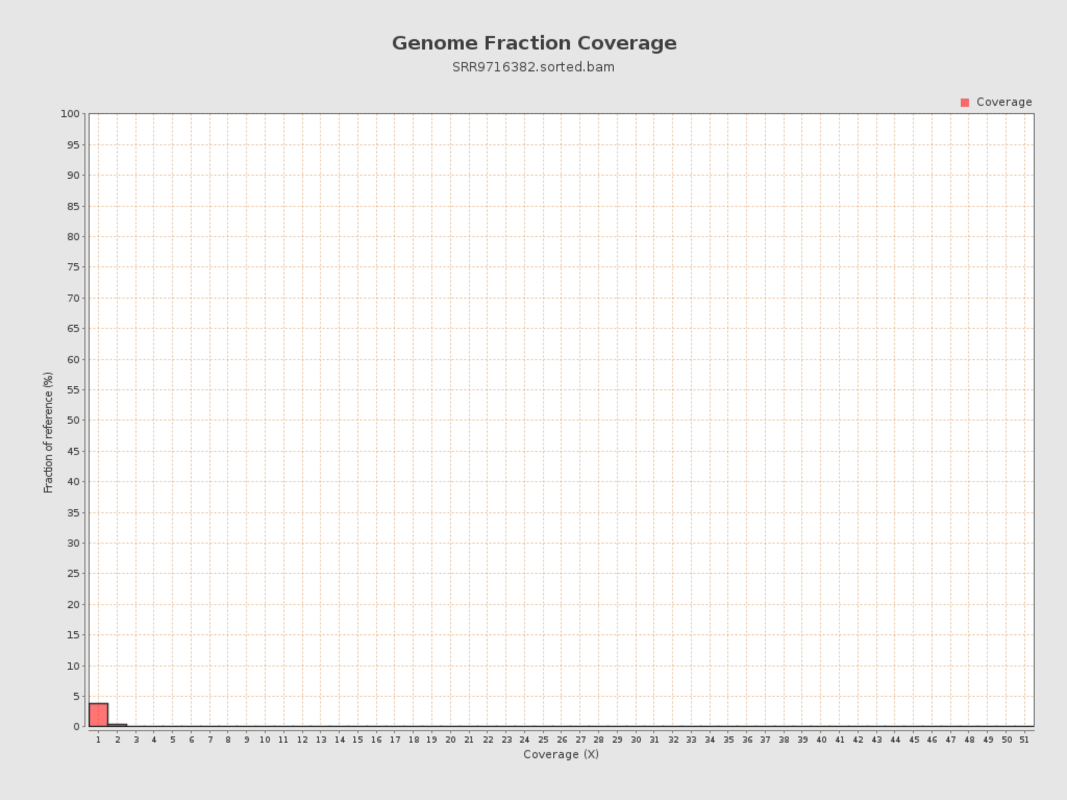
4. Results : Coverage Histogram



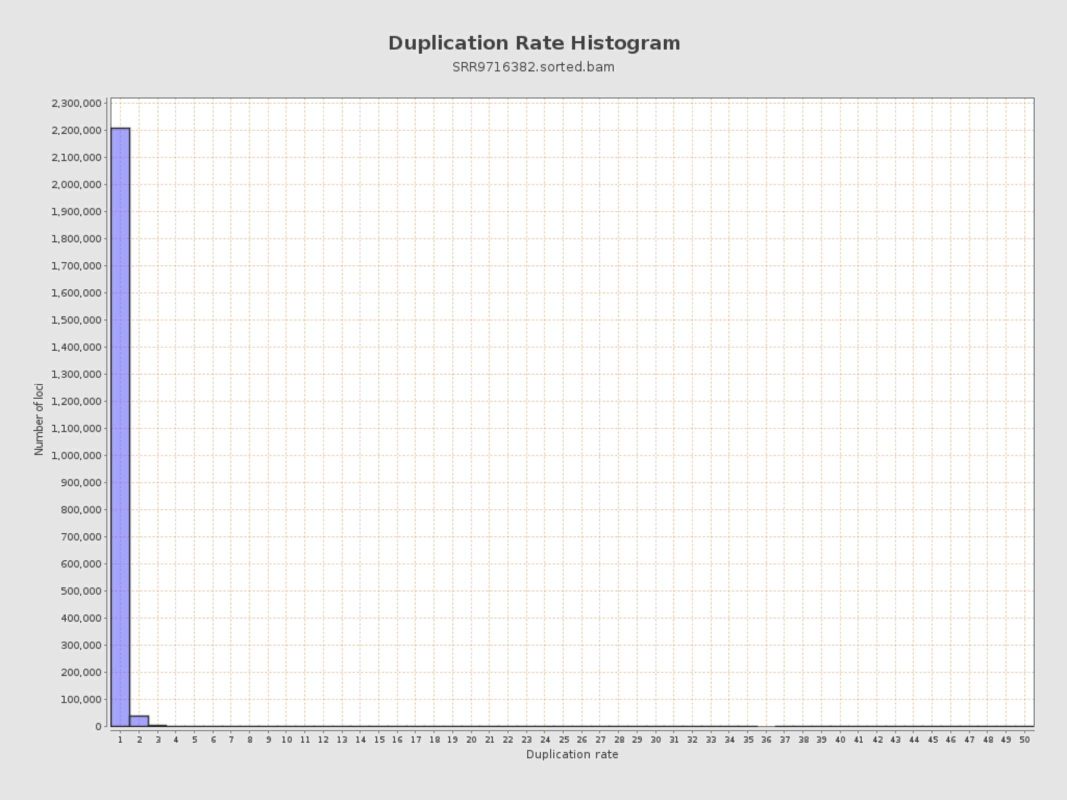
5. Results : Coverage Histogram (0-50X)



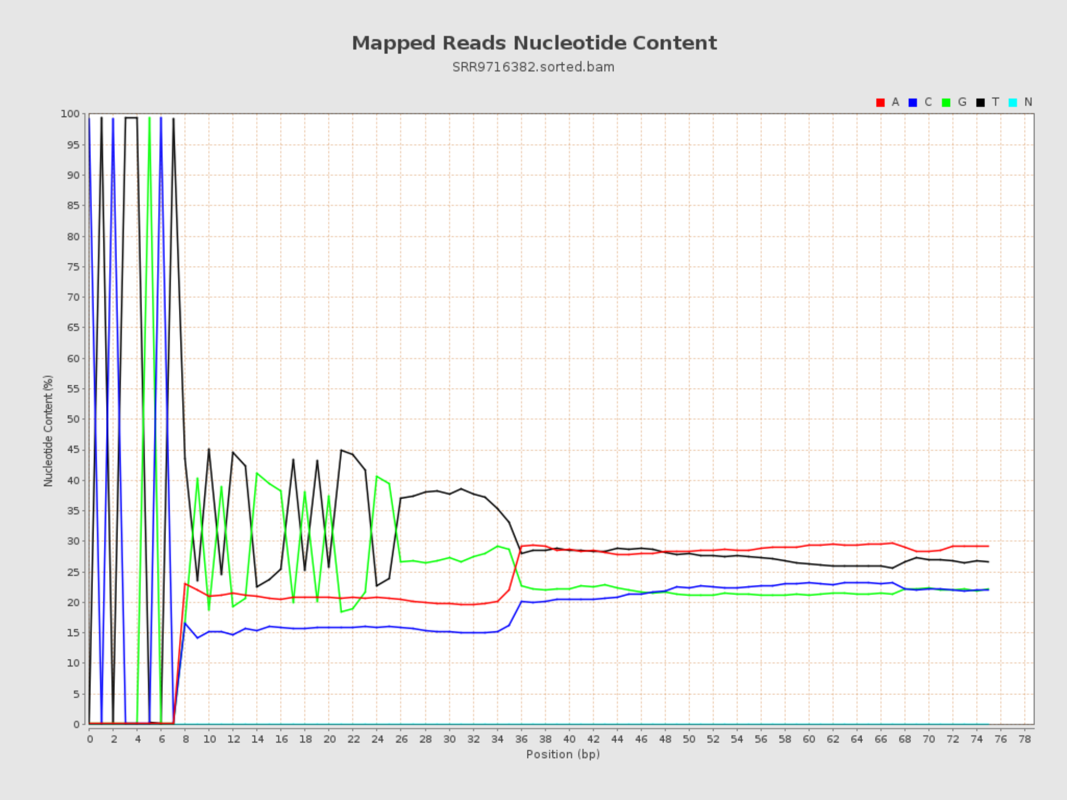
6. Results : Genome Fraction Coverage



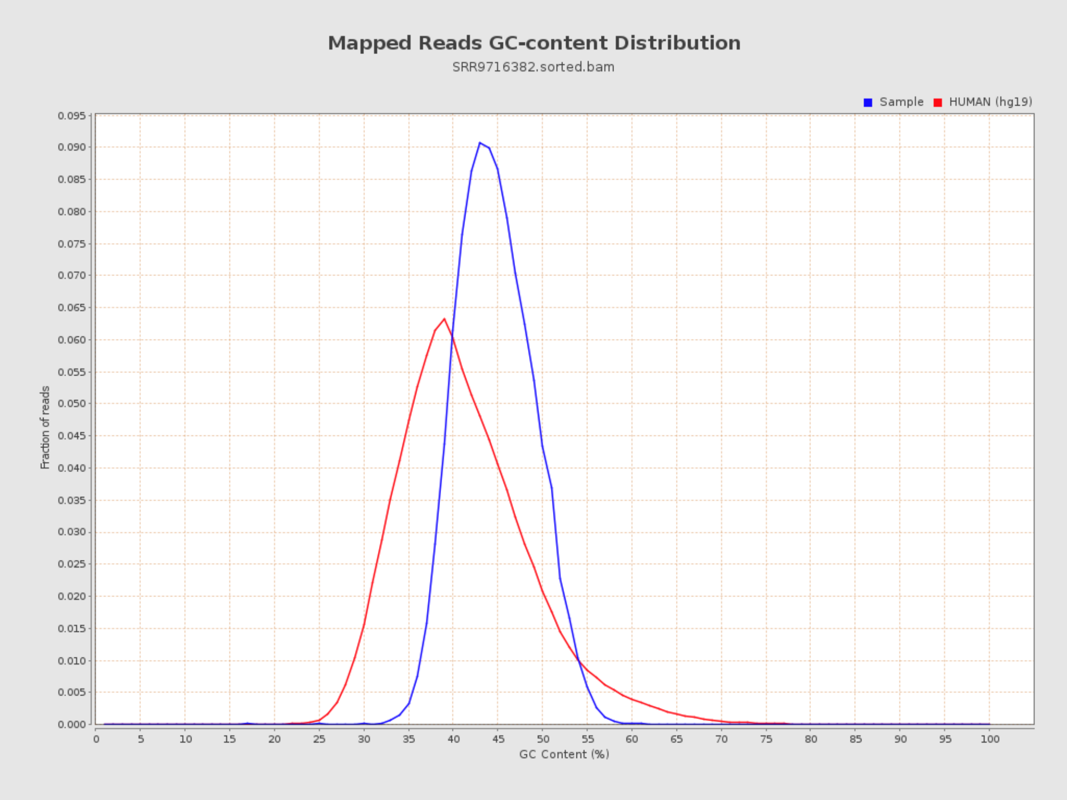
7. Results : Duplication Rate Histogram



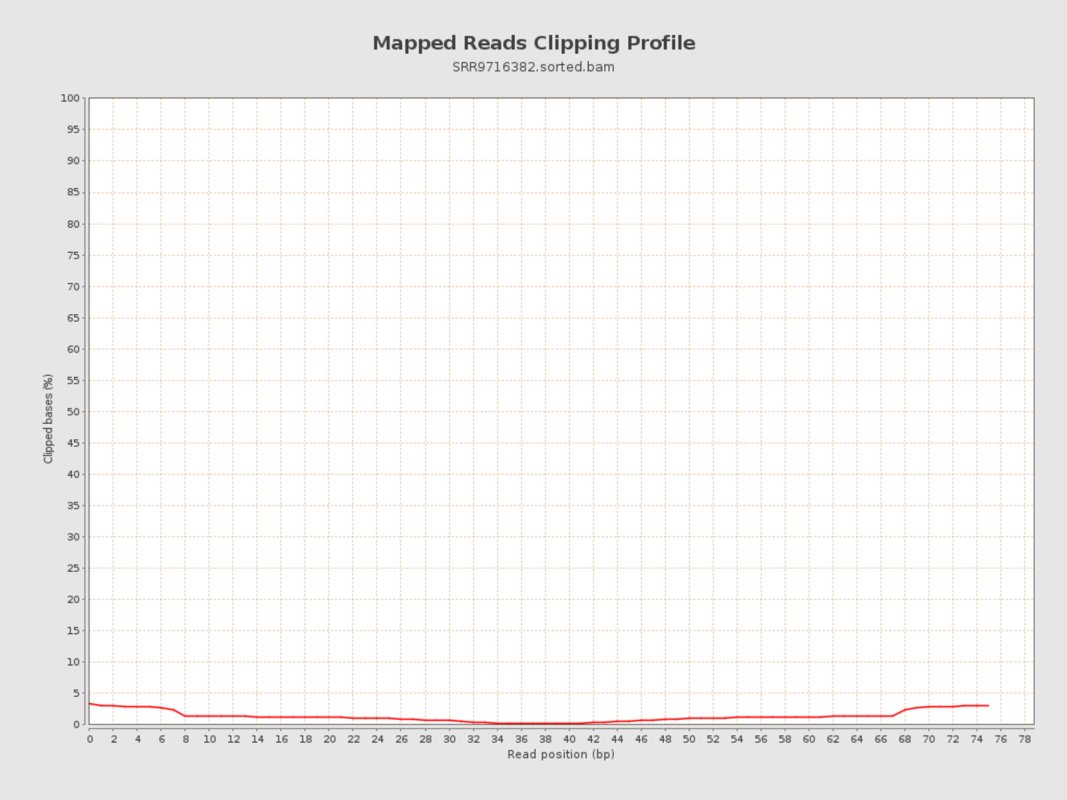
8. Results : Mapped Reads Nucleotide Content



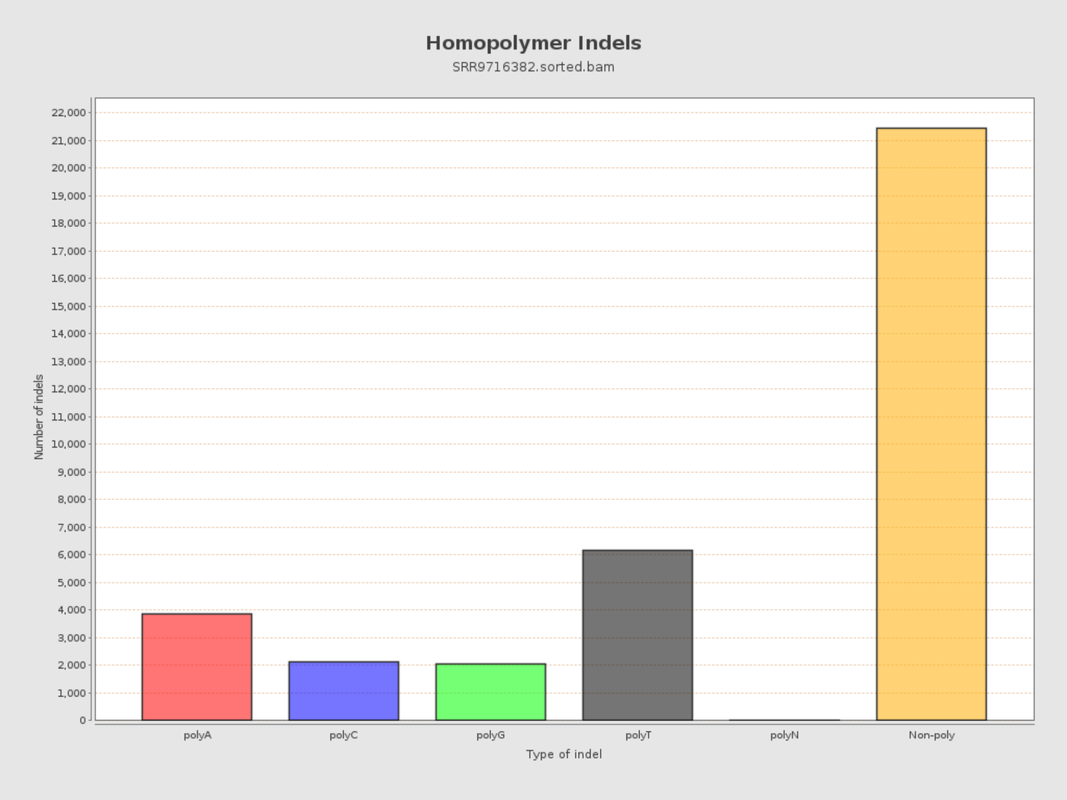
9. Results : Mapped Reads GC-content Distribution



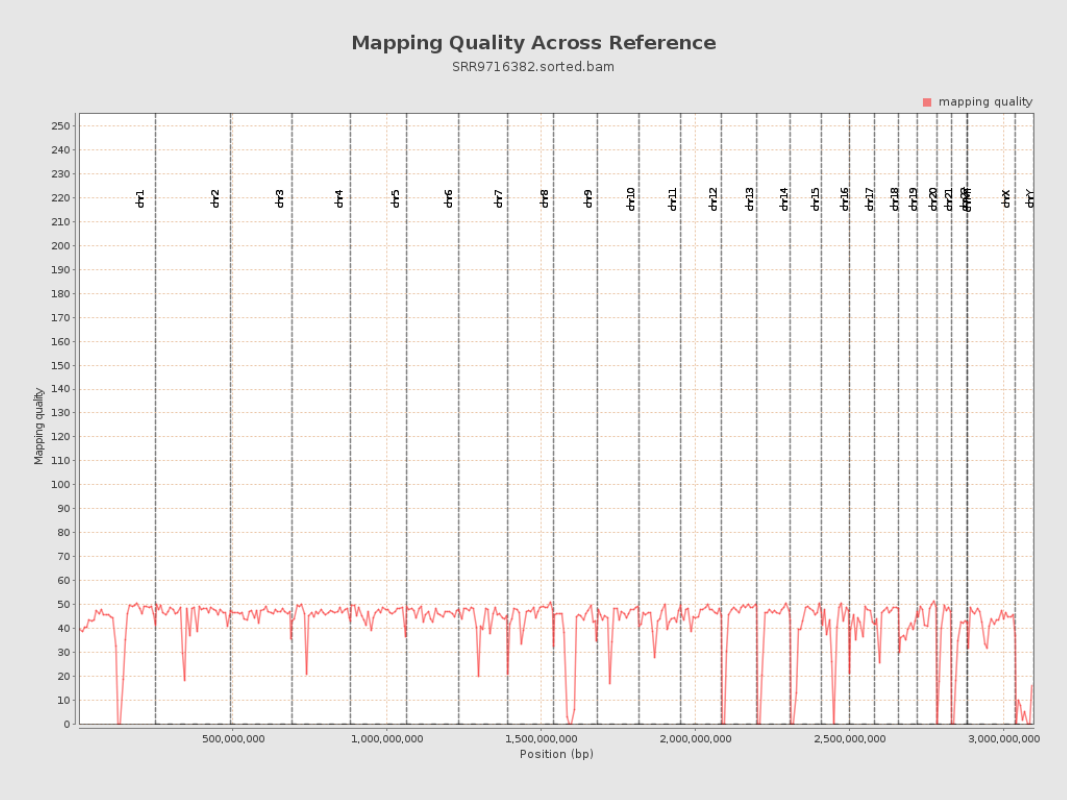
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram