Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 08:58:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716358.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_SRR9716358 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716358.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 08:58:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716358.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,121,296
Mapped reads	1,908,346 / 89.96%
Unmapped reads	212,950 / 10.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,896 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	75,460 / 3.56%
Duplication rate	2.9%
Clipped reads	1,915,577 / 90.3%

2.2. ACGT Content

Number/percentage of A's	28,393,322 / 25.9%
Number/percentage of C's	21,211,239 / 19.35%
Number/percentage of T's	34,196,837 / 31.2%
Number/percentage of G's	25,807,273 / 23.54%
Number/percentage of N's	1,802 / 0%
GC Percentage	42.9%

2.3. Coverage

Mean	0.0354

Standard Deviation	0.3233

2.4. Mapping Quality

Mean Mapping Quality	44.44

2.5. Mismatches and indels

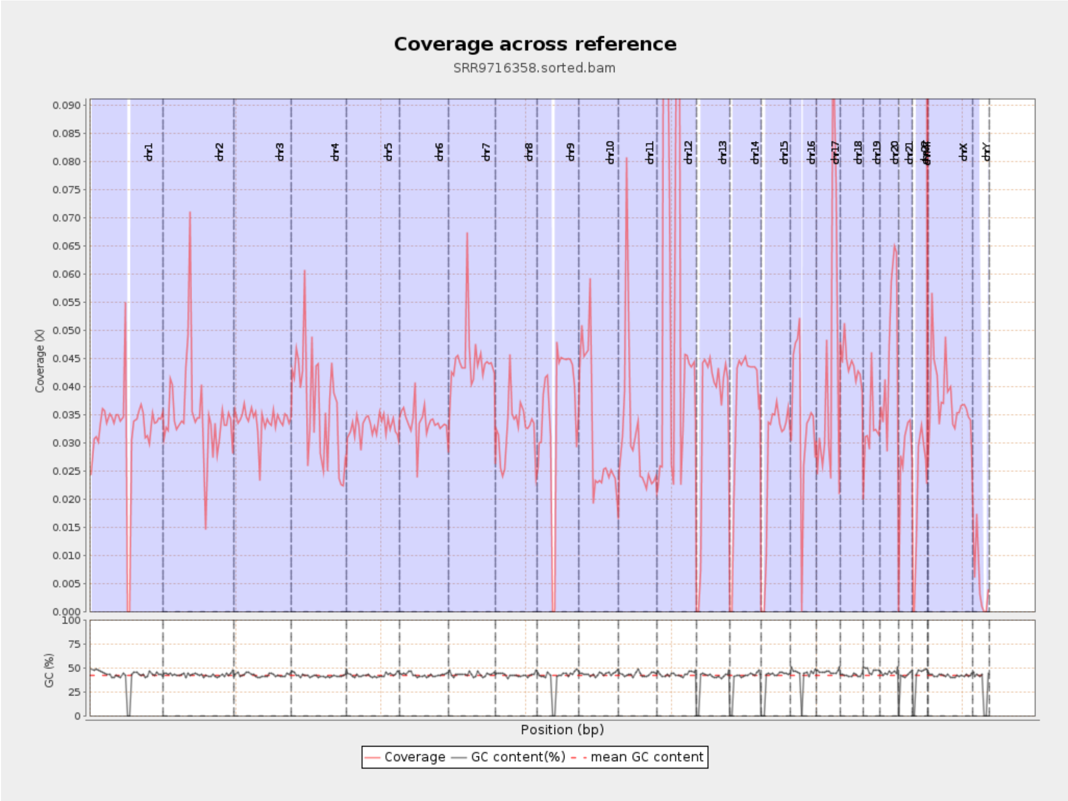
General error rate	0.54%
Mismatches	585,794
Insertions	6,000
Mapped reads with at least one insertion	0.31%
Deletions	18,518
Mapped reads with at least one deletion	0.96%
Homopolymer indels	44.28%

2.6. Chromosome stats

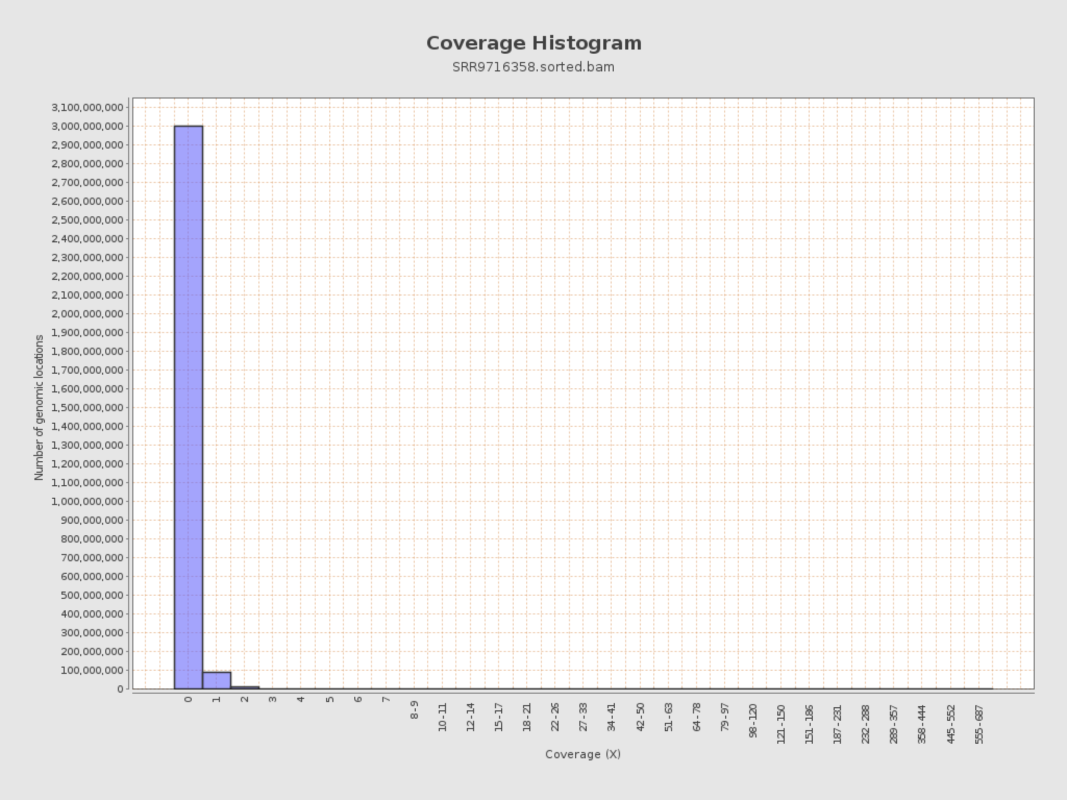
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7967537	0.032	0.5482
chr2	243199373	8520239	0.035	0.3595
chr3	198022430	6728416	0.034	0.2005
chr4	191154276	6981547	0.0365	0.2361
chr5	180915260	5955138	0.0329	0.2018
chr6	171115067	5753957	0.0336	0.2266
chr7	159138663	7121522	0.0448	0.4533

chr8	146364022	4775037	0.0326	0.314
chr9	141213431	5044738	0.0357	0.3543
chr10	135534747	4321292	0.0319	0.3199
chr11	135006516	4228338	0.0313	0.2709
chr12	133851895	8094683	0.0605	0.3071
chr13	115169878	4046635	0.0351	0.2034
chr14	107349540	3875851	0.0361	0.2321
chr15	102531392	2817866	0.0275	0.182
chr16	90354753	3146043	0.0348	0.2283
chr17	81195210	3380663	0.0416	0.2338
chr18	78077248	3440479	0.0441	0.5969
chr19	59128983	1934317	0.0327	0.4479
chr20	63025520	2958057	0.0469	0.246
chr21	48129895	1312986	0.0273	0.2076
chr22	51304566	1064537	0.0207	0.1556
chrMT	16571	13679	0.8255	1.0534
chrX	155270560	5855537	0.0377	0.2548
chrY	59373566	302873	0.0051	0.123

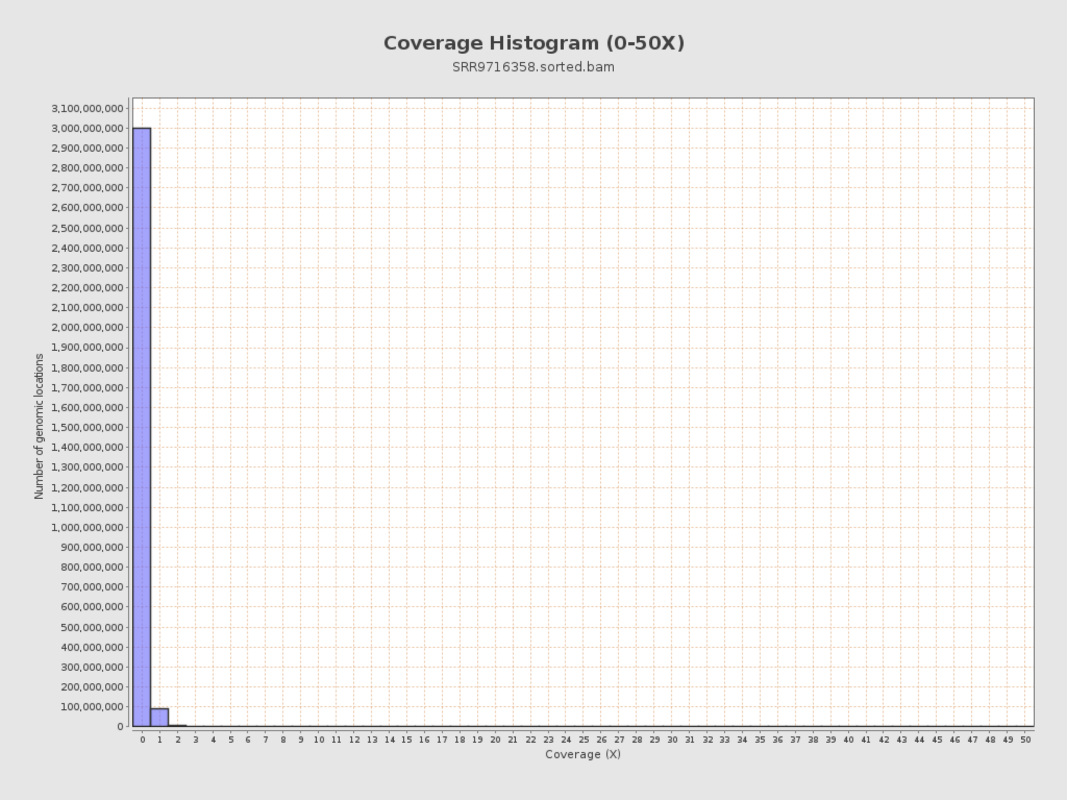
3. Results : Coverage across reference



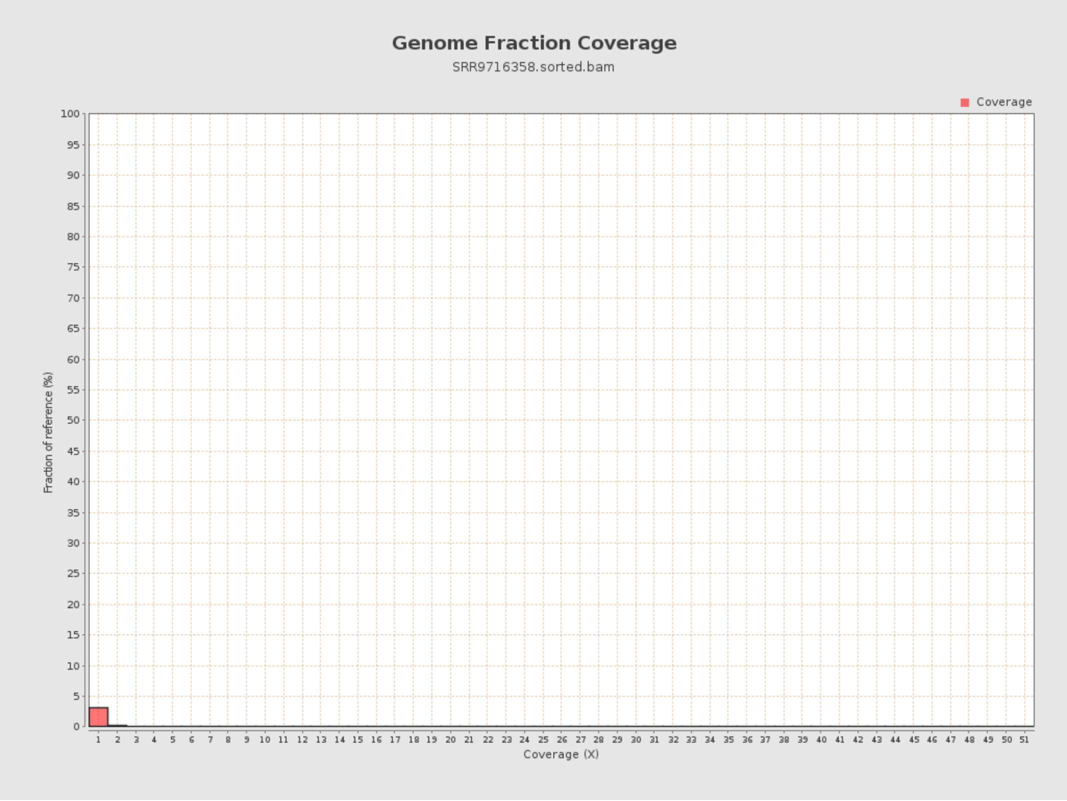
4. Results : Coverage Histogram



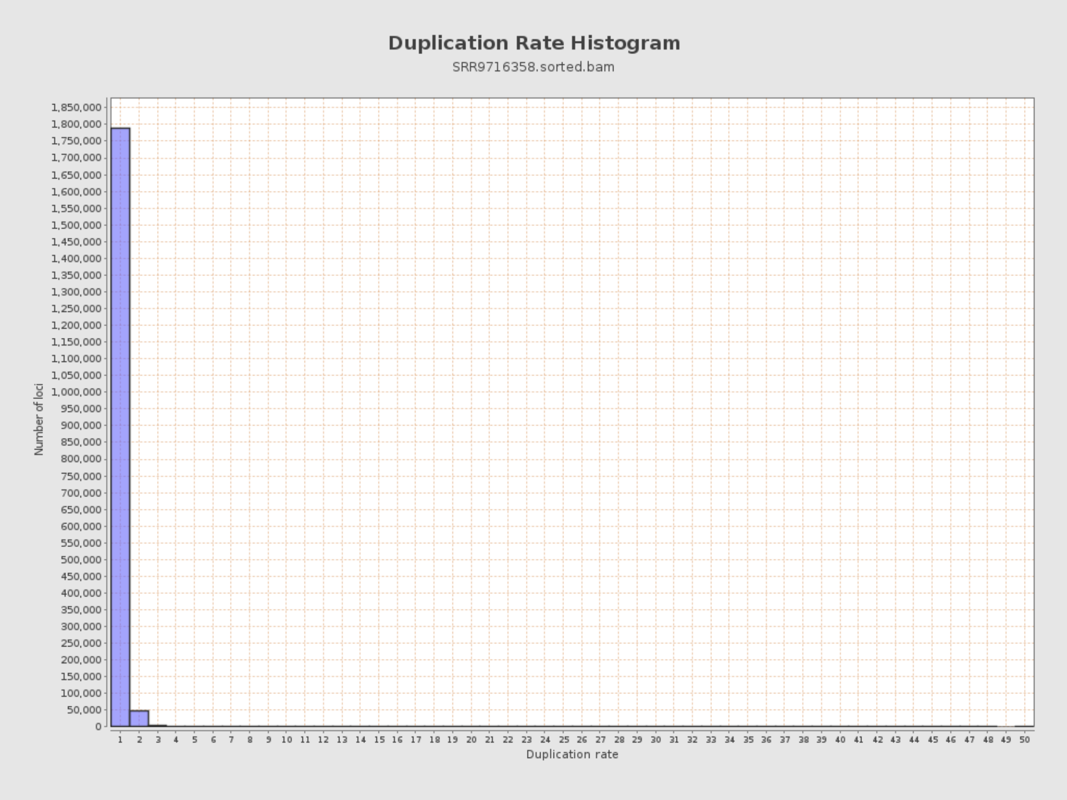
5. Results : Coverage Histogram (0-50X)



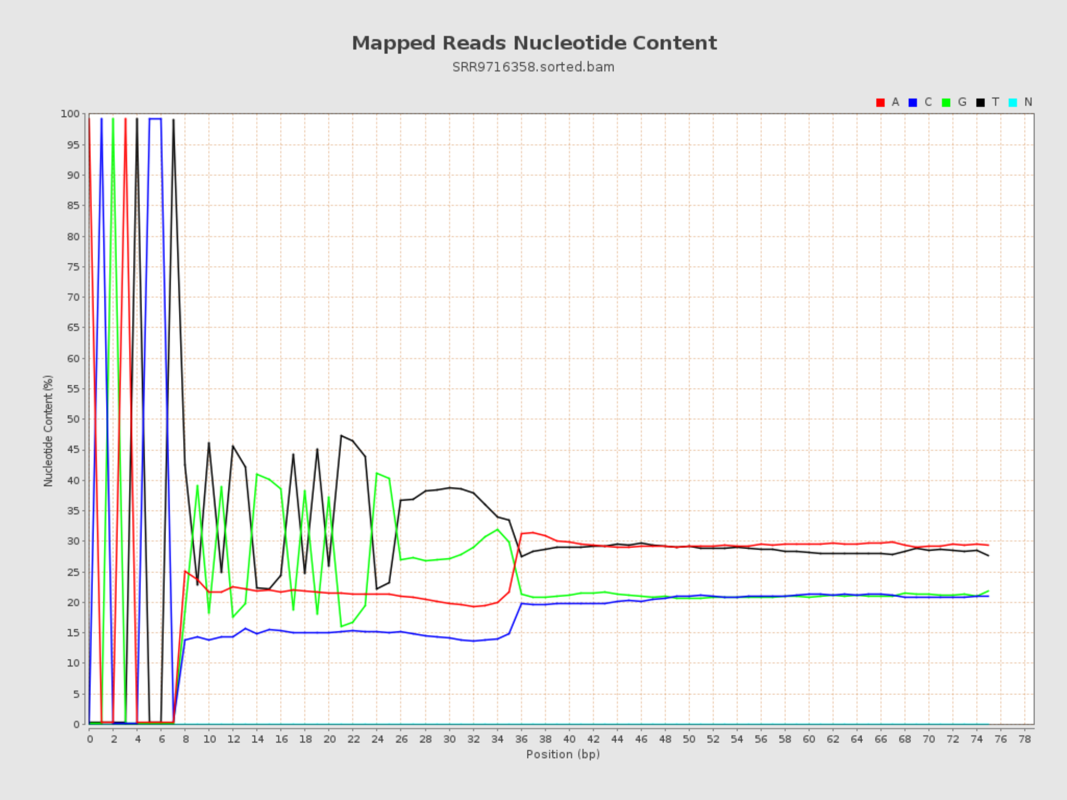
6. Results : Genome Fraction Coverage



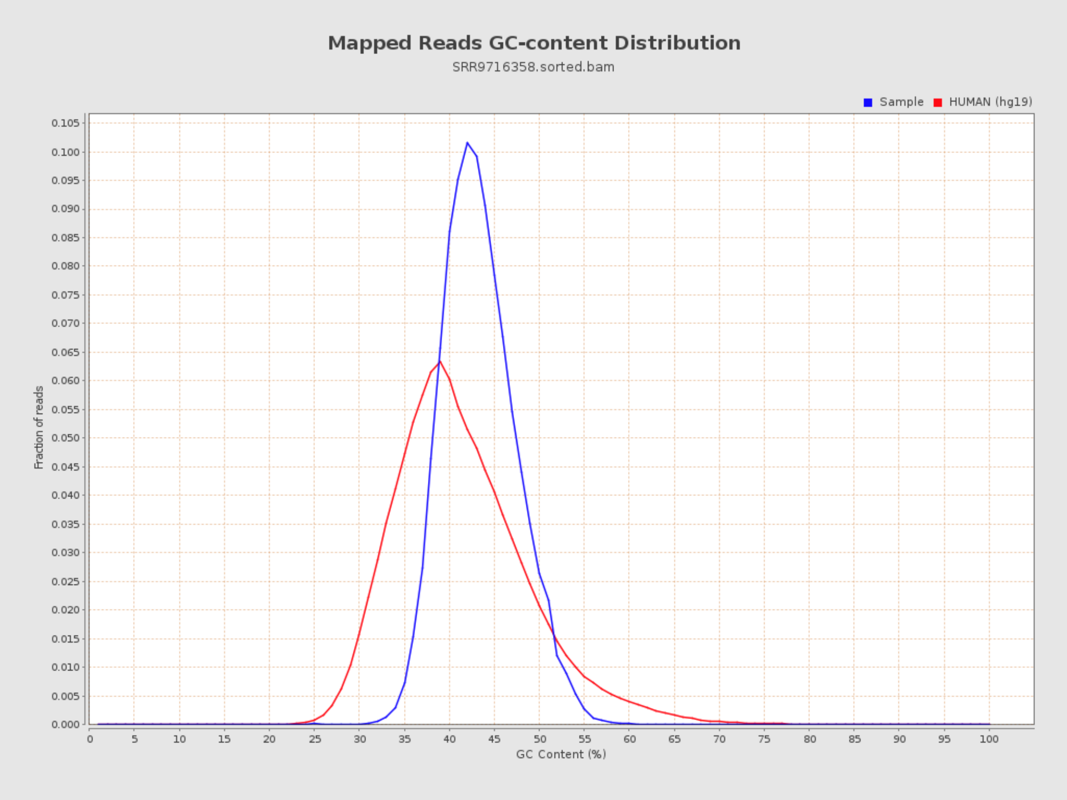
7. Results : Duplication Rate Histogram



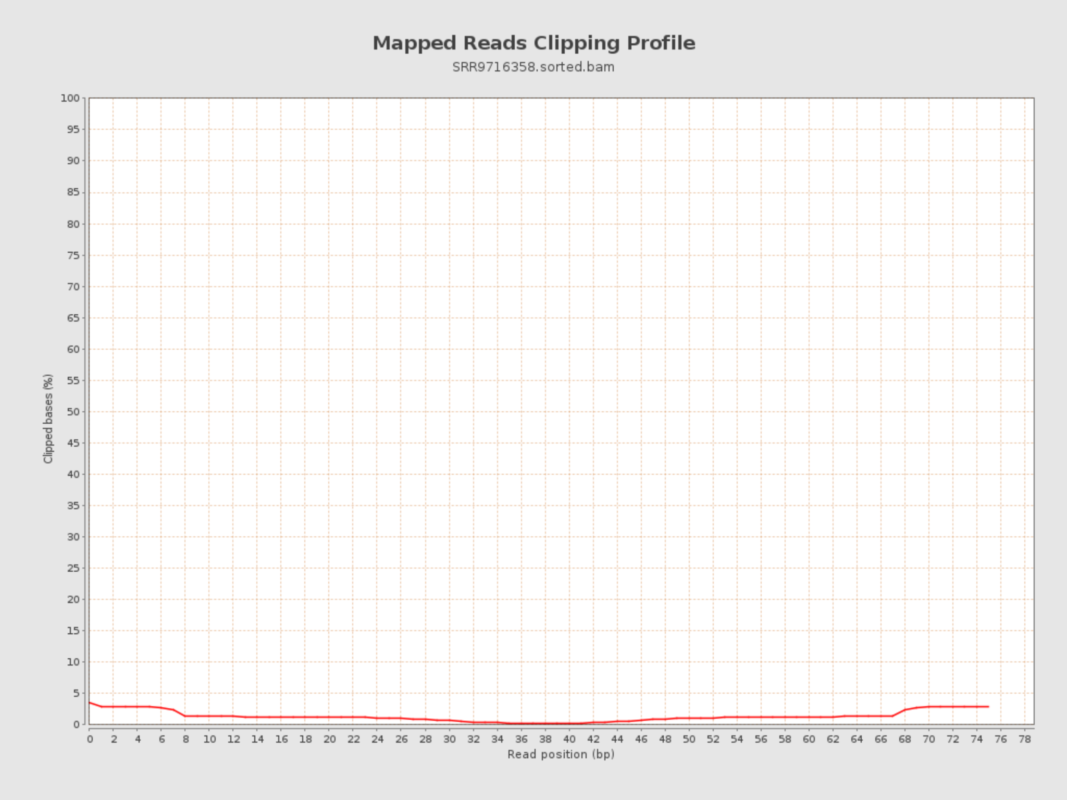
8. Results : Mapped Reads Nucleotide Content



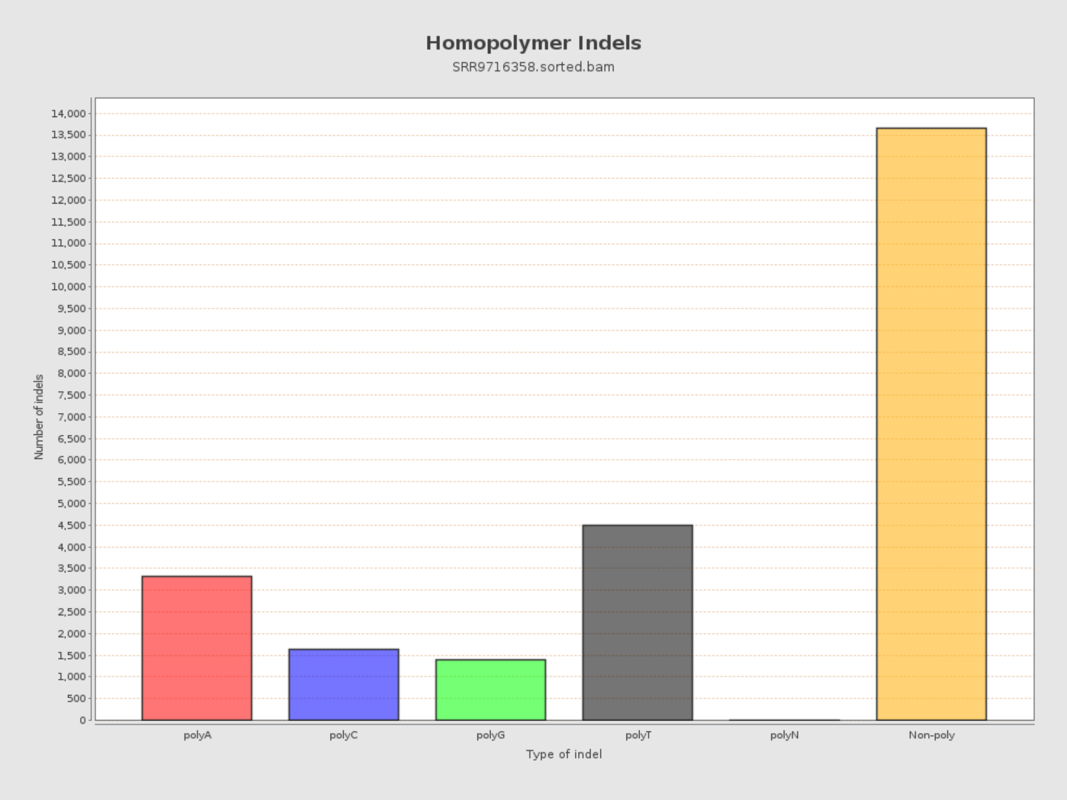
9. Results : Mapped Reads GC-content Distribution



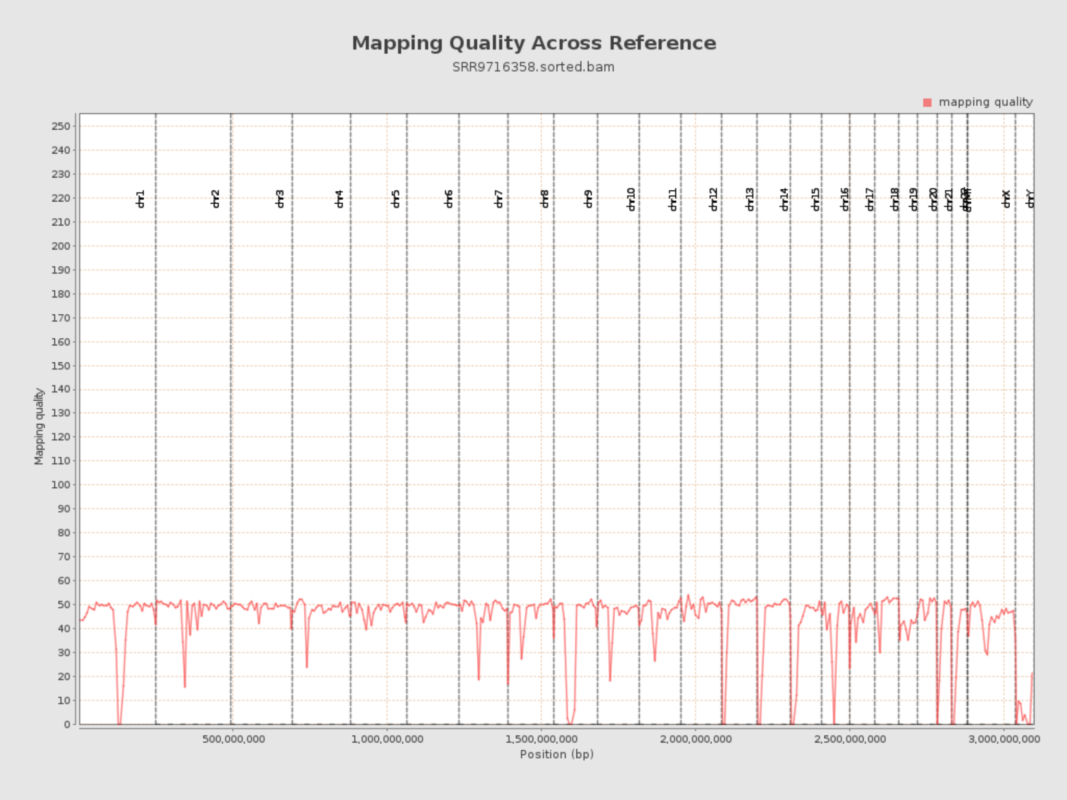
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram