Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 08:24:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716342.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_SRR9716342 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716342.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 08:24:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716342.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,847,495
Mapped reads	1,689,405 / 91.44%
Unmapped reads	158,090 / 8.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,980 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	75,676 / 4.1%
Duplication rate	3.48%
Clipped reads	1,695,267 / 91.76%

2.2. ACGT Content

Number/percentage of A's	24,971,143 / 25.17%
Number/percentage of C's	19,419,990 / 19.57%
Number/percentage of T's	30,862,399 / 31.1%
Number/percentage of G's	23,970,003 / 24.16%
Number/percentage of N's	1,287 / 0%
GC Percentage	43.73%

2.3. Coverage

Mean	0.0321

Standard Deviation	0.2751

2.4. Mapping Quality

Mean Mapping Quality	45.18

2.5. Mismatches and indels

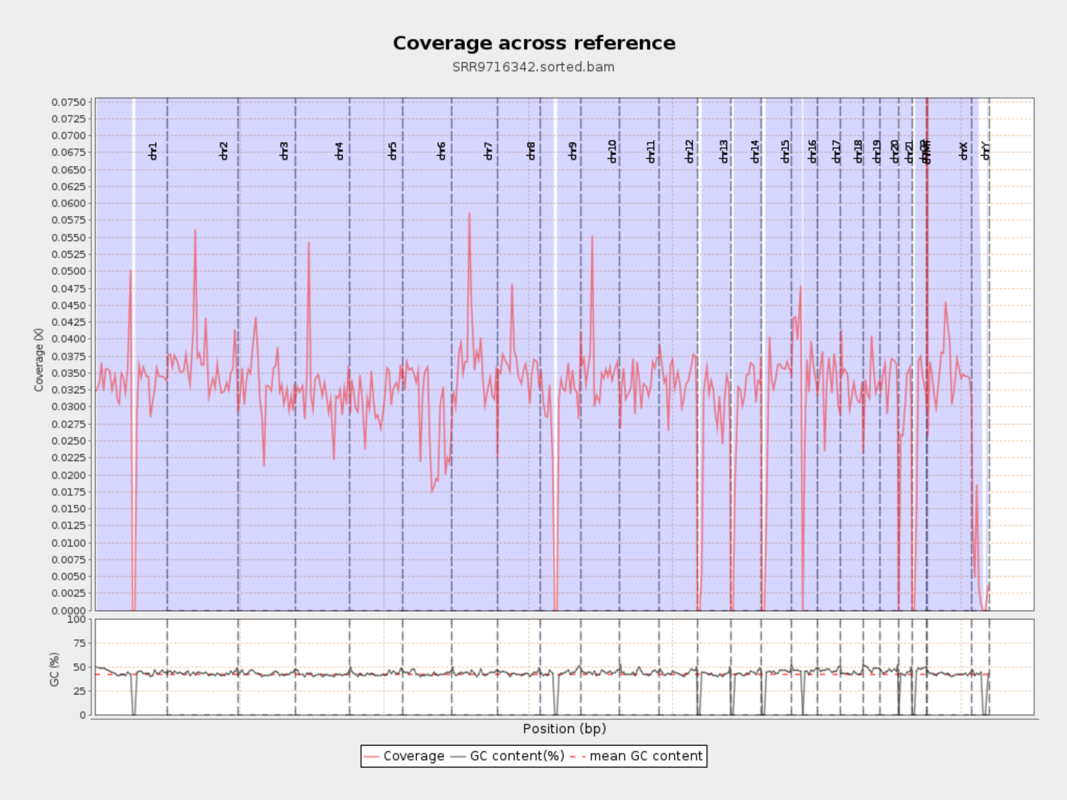
General error rate	0.5%
Mismatches	485,960
Insertions	6,933
Mapped reads with at least one insertion	0.41%
Deletions	17,557
Mapped reads with at least one deletion	1.03%
Homopolymer indels	42.49%

2.6. Chromosome stats

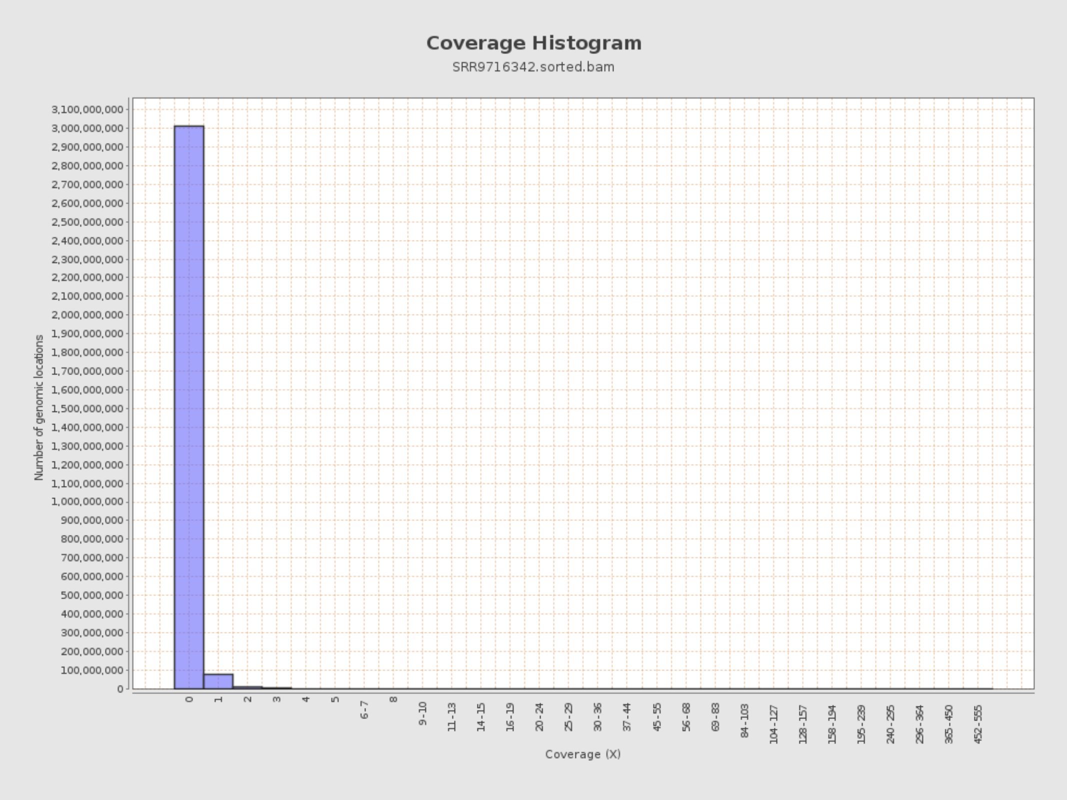
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8001851	0.0321	0.4148
chr2	243199373	8860078	0.0364	0.35
chr3	198022430	6576796	0.0332	0.2043
chr4	191154276	6212305	0.0325	0.2343
chr5	180915260	5701772	0.0315	0.1995
chr6	171115067	4890470	0.0286	0.2065
chr7	159138663	5803800	0.0365	0.4055

chr8	146364022	5284431	0.0361	0.2912
chr9	141213431	3988148	0.0282	0.2277
chr10	135534747	4843185	0.0357	0.2922
chr11	135006516	4521204	0.0335	0.2544
chr12	133851895	4581290	0.0342	0.2108
chr13	115169878	3024223	0.0263	0.1819
chr14	107349540	3027572	0.0282	0.1943
chr15	102531392	2970700	0.029	0.1948
chr16	90354753	3107340	0.0344	0.2236
chr17	81195210	2720357	0.0335	0.226
chr18	78077248	2579307	0.033	0.4004
chr19	59128983	1988435	0.0336	0.3447
chr20	63025520	2174090	0.0345	0.214
chr21	48129895	1330740	0.0276	0.21
chr22	51304566	1253487	0.0244	0.1762
chrMT	16571	35182	2.1231	1.9664
chrX	155270560	5468252	0.0352	0.226
chrY	59373566	307732	0.0052	0.1601

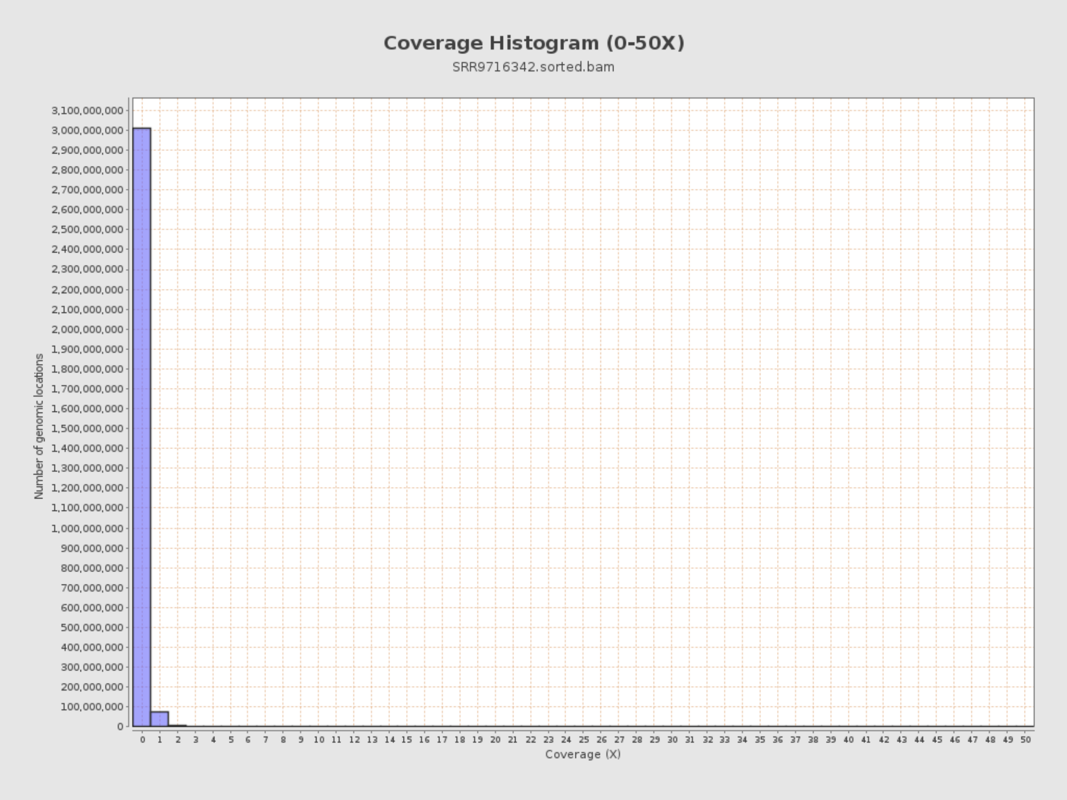
3. Results : Coverage across reference



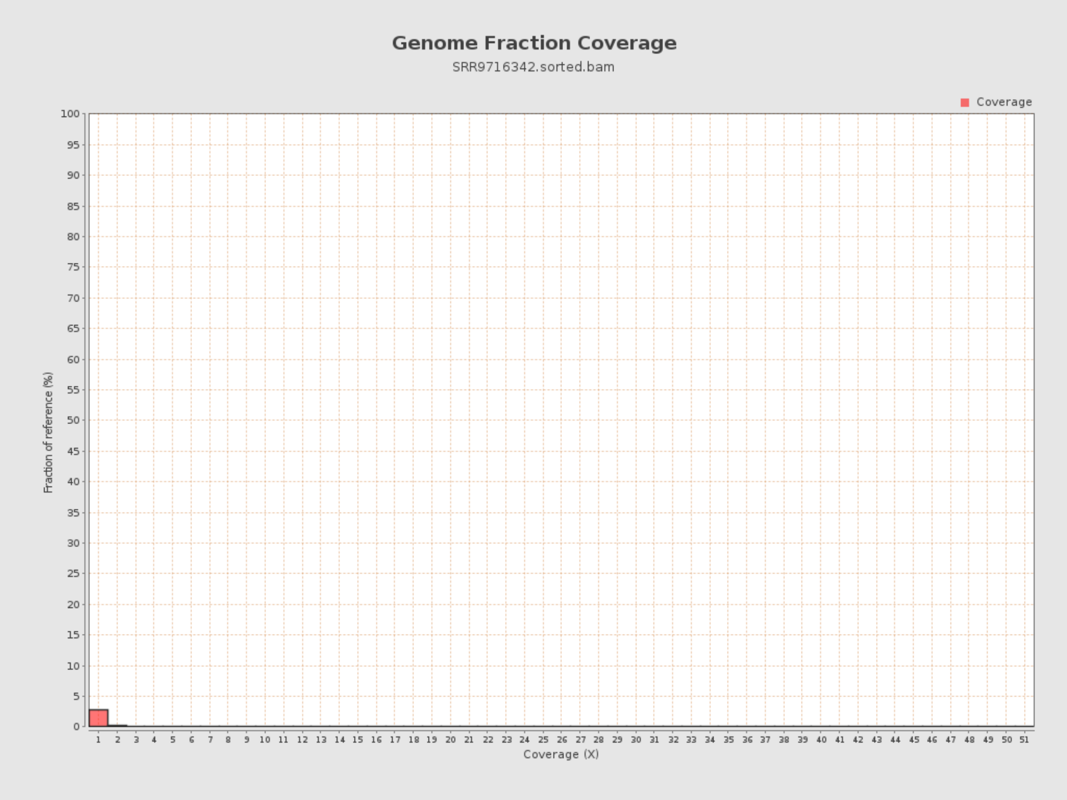
4. Results : Coverage Histogram



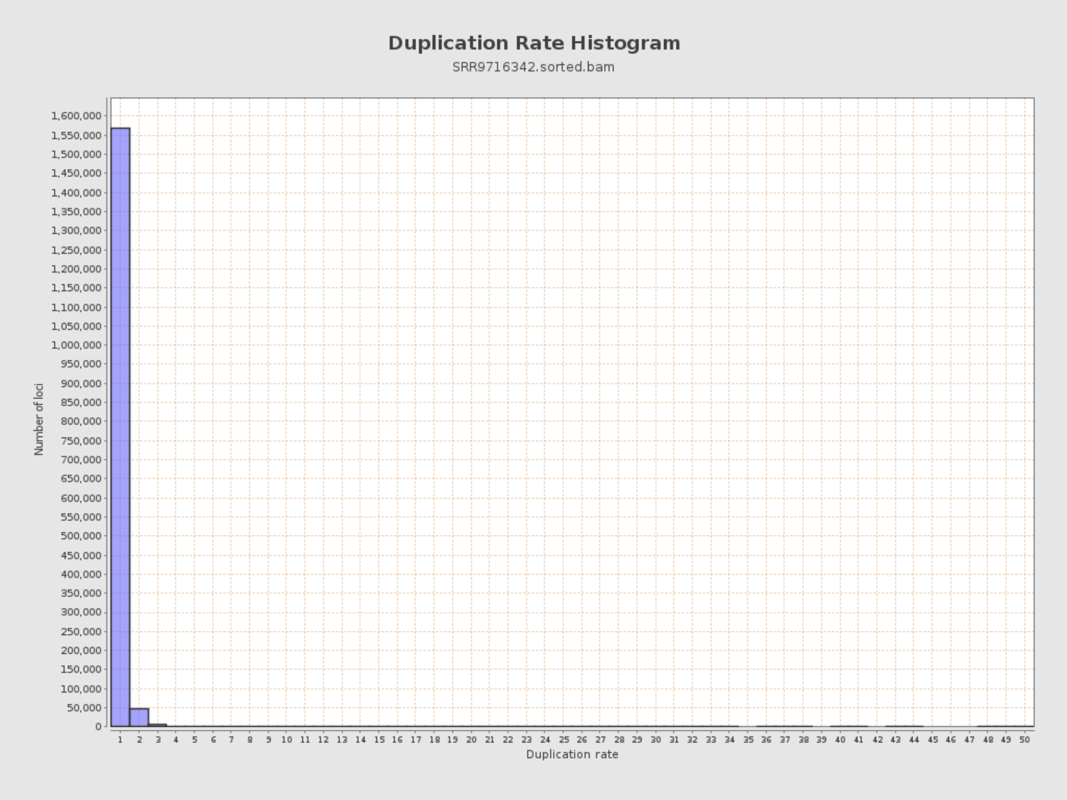
5. Results : Coverage Histogram (0-50X)



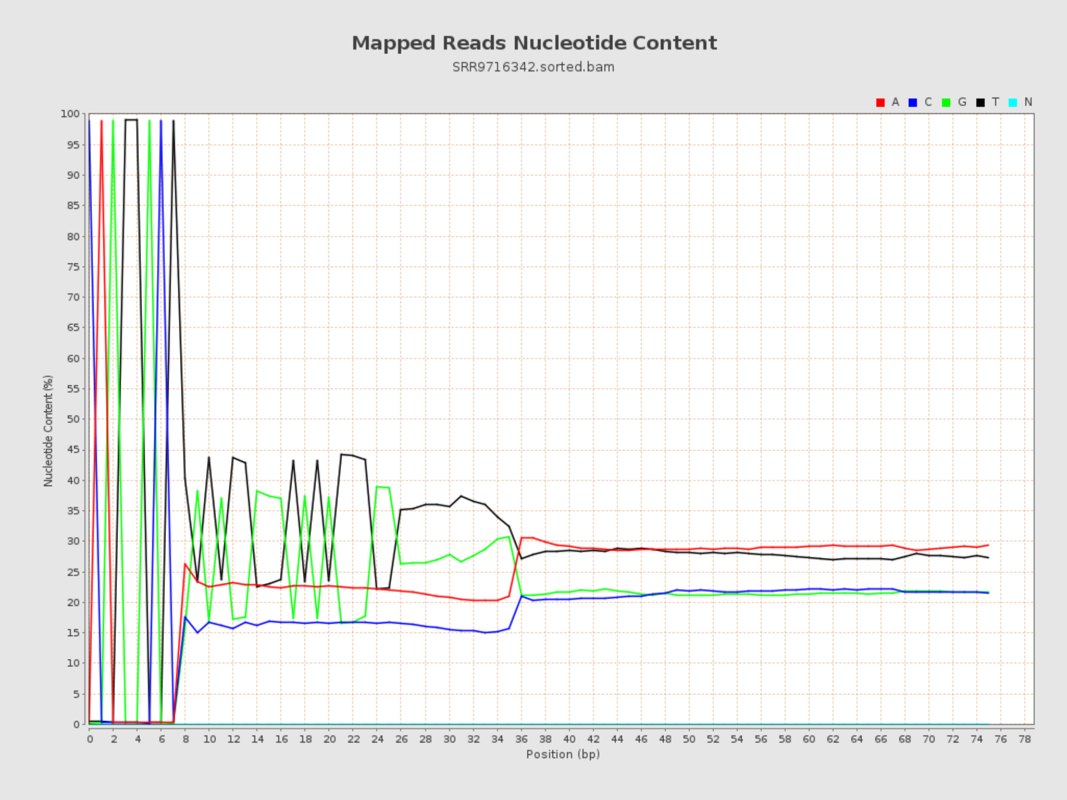
6. Results : Genome Fraction Coverage



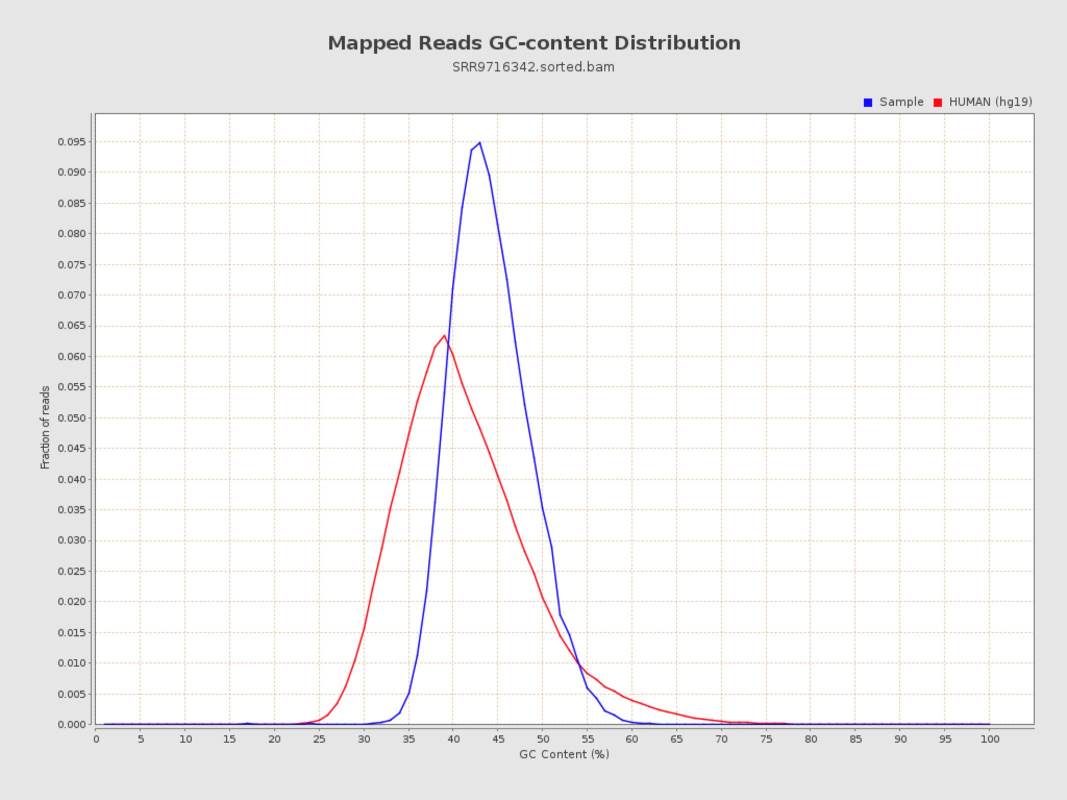
7. Results : Duplication Rate Histogram



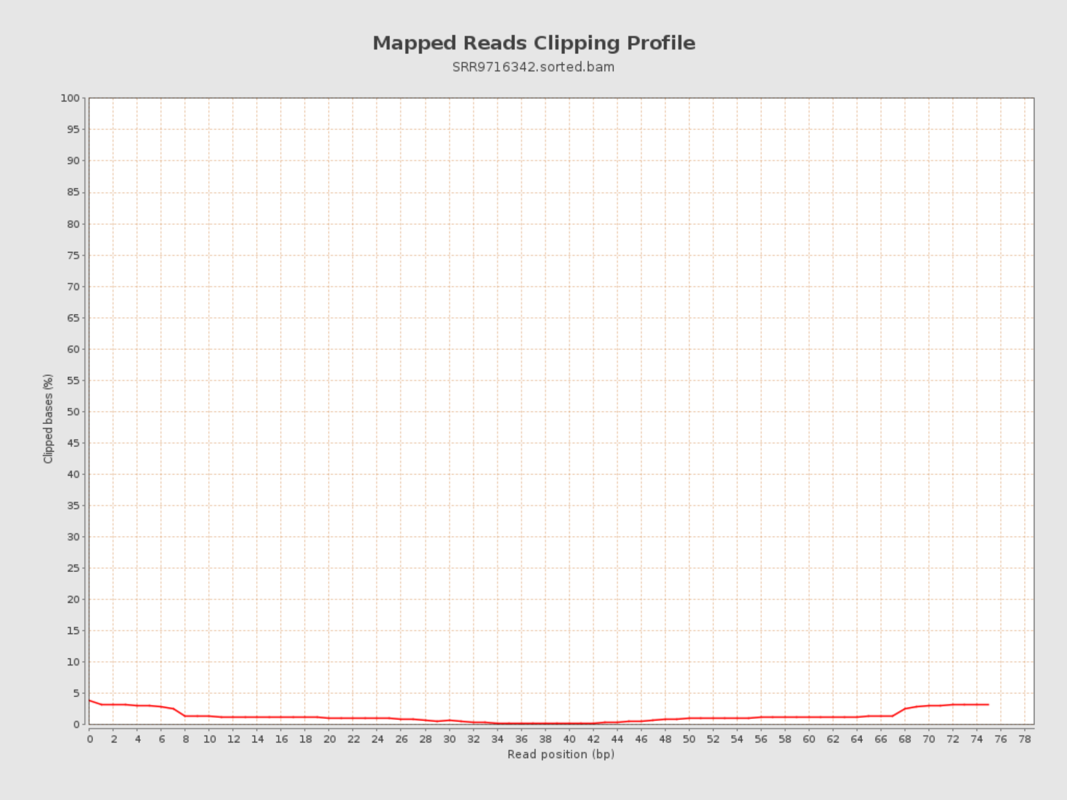
8. Results : Mapped Reads Nucleotide Content



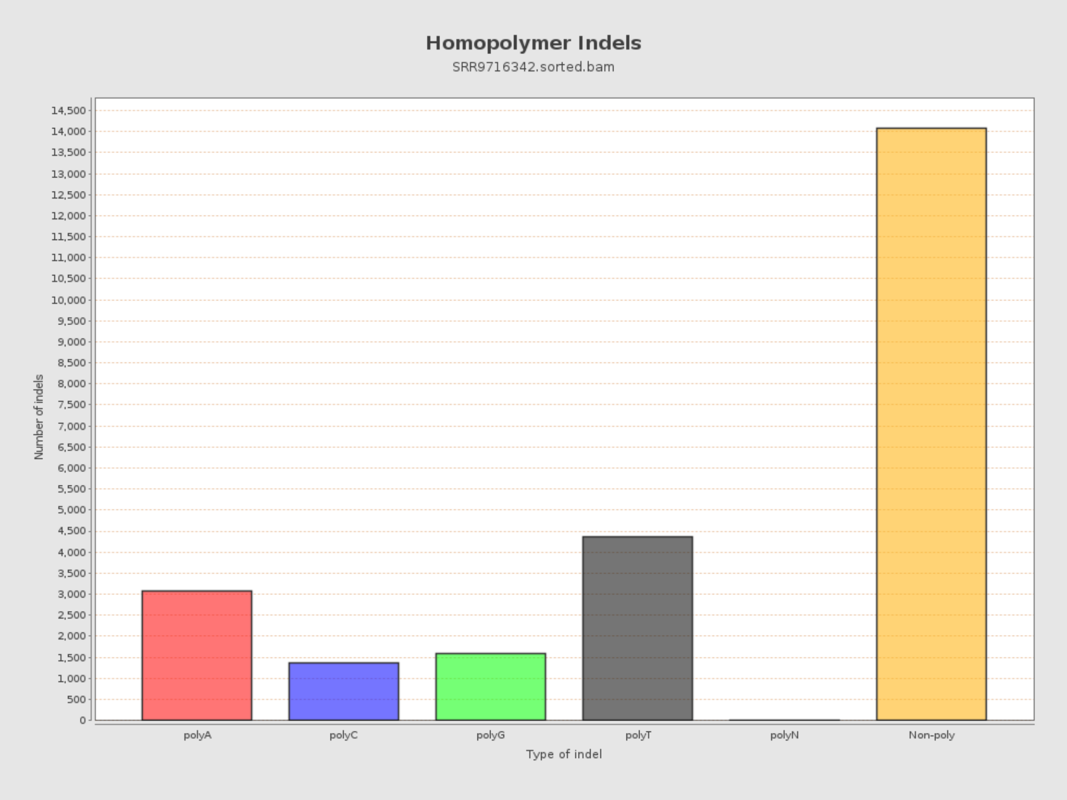
9. Results : Mapped Reads GC-content Distribution



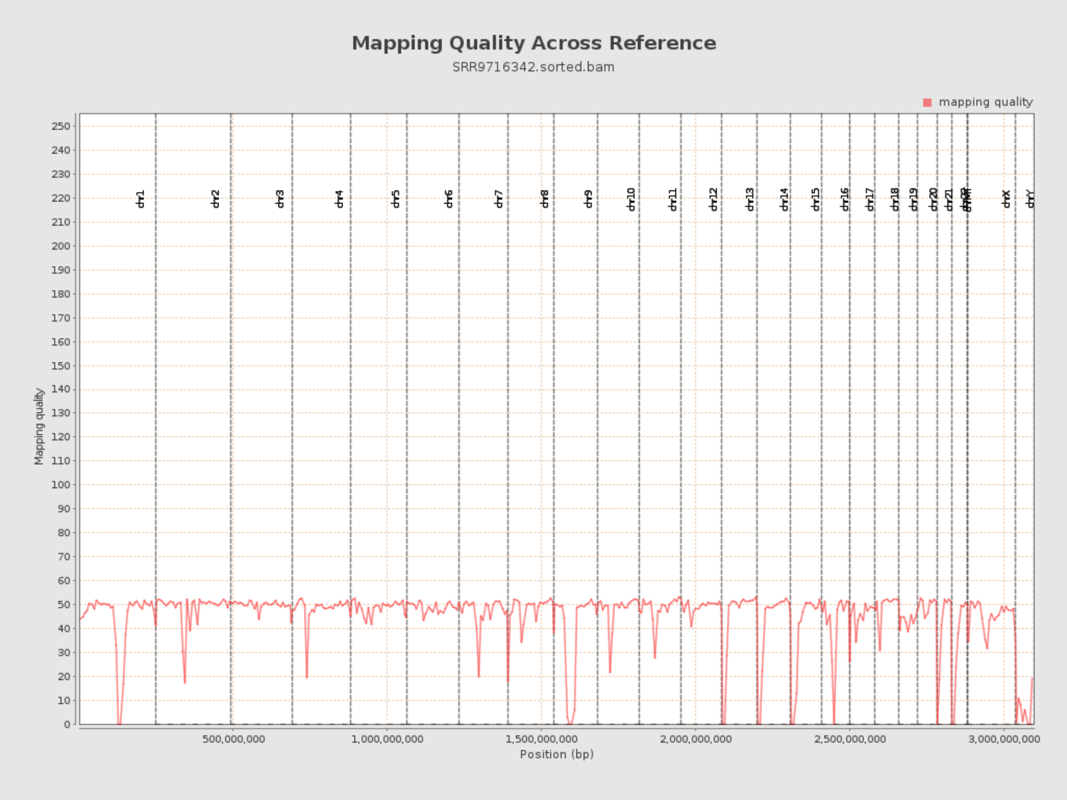
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram