Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 22:21:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716569.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_SRR9716569 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716569.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 22:21:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716569.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,061,586
Mapped reads	989,606 / 93.22%
Unmapped reads	71,980 / 6.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,086 / 2.36%
Read min/max/mean length	30 / 101 / 101.86
Duplicated reads (estimated)	31,901 / 3.01%
Duplication rate	2.47%
Clipped reads	1,012,992 / 95.42%

2.2. ACGT Content

Number/percentage of A's	19,418,142 / 25.4%
Number/percentage of C's	16,072,053 / 21.02%
Number/percentage of T's	22,414,610 / 29.31%
Number/percentage of G's	18,554,919 / 24.27%
Number/percentage of N's	3,292 / 0%
GC Percentage	45.29%

2.3. Coverage

Mean	0.0247

Standard Deviation	0.2316

2.4. Mapping Quality

Mean Mapping Quality	46.03

2.5. Mismatches and indels

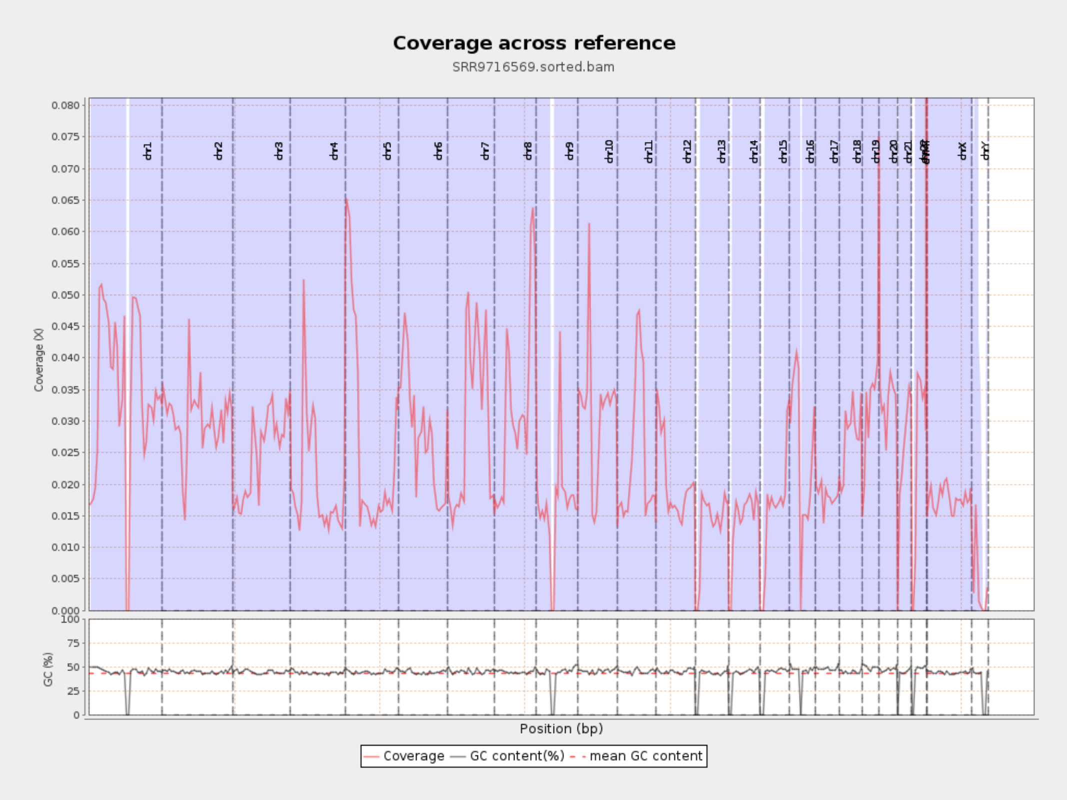
General error rate	0.68%
Mismatches	498,423
Insertions	6,916
Mapped reads with at least one insertion	0.69%
Deletions	14,985
Mapped reads with at least one deletion	1.49%
Homopolymer indels	38.97%

2.6. Chromosome stats

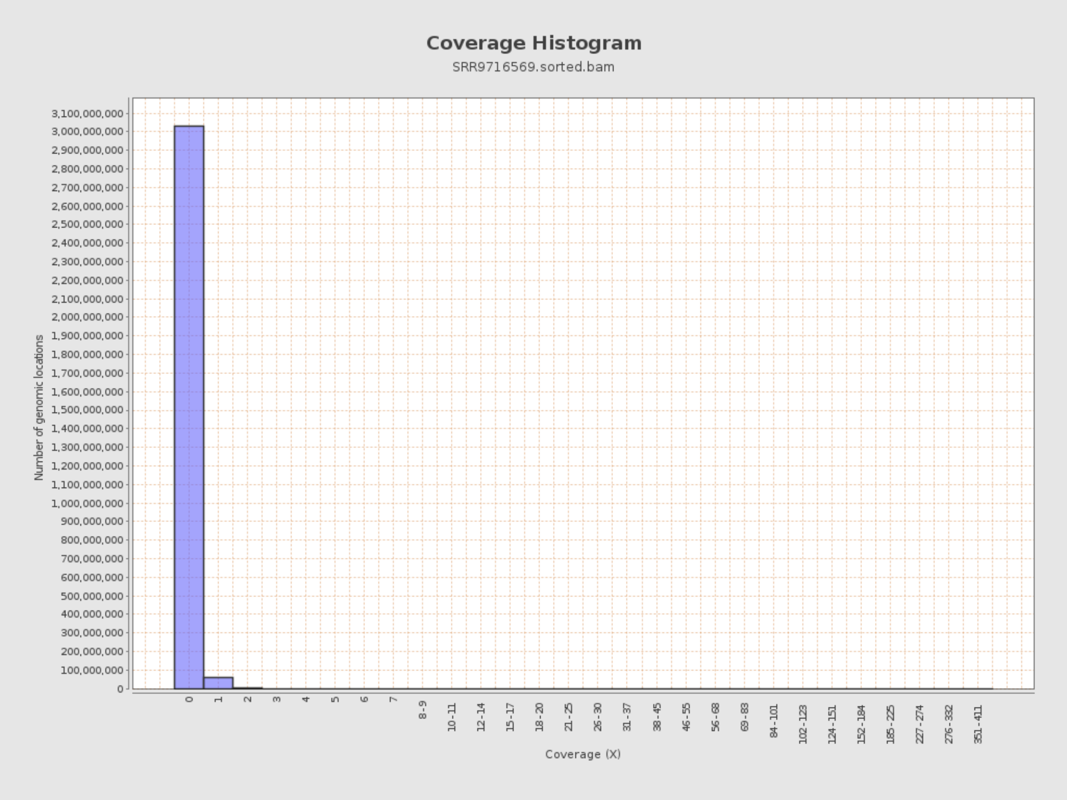
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8617816	0.0346	0.4022
chr2	243199373	7366072	0.0303	0.2593
chr3	198022430	4957819	0.025	0.177
chr4	191154276	3817619	0.02	0.2023
chr5	180915260	4796713	0.0265	0.1809
chr6	171115067	4779880	0.0279	0.1944
chr7	159138663	4788051	0.0301	0.3015

chr8	146364022	4766186	0.0326	0.2515
chr9	141213431	2337070	0.0165	0.1678
chr10	135534747	4266498	0.0315	0.319
chr11	135006516	3291199	0.0244	0.2059
chr12	133851895	2742561	0.0205	0.1571
chr13	115169878	1532882	0.0133	0.1259
chr14	107349540	1507906	0.014	0.1358
chr15	102531392	1593458	0.0155	0.1357
chr16	90354753	2266847	0.0251	0.1832
chr17	81195210	1469633	0.0181	0.1605
chr18	78077248	2154894	0.0276	0.2509
chr19	59128983	1960169	0.0332	0.2995
chr20	63025520	2078308	0.033	0.2063
chr21	48129895	1189898	0.0247	0.1959
chr22	51304566	1224276	0.0239	0.173
chrMT	16571	21339	1.2877	1.5406
chrX	155270560	2734649	0.0176	0.1516
chrY	59373566	232509	0.0039	0.16

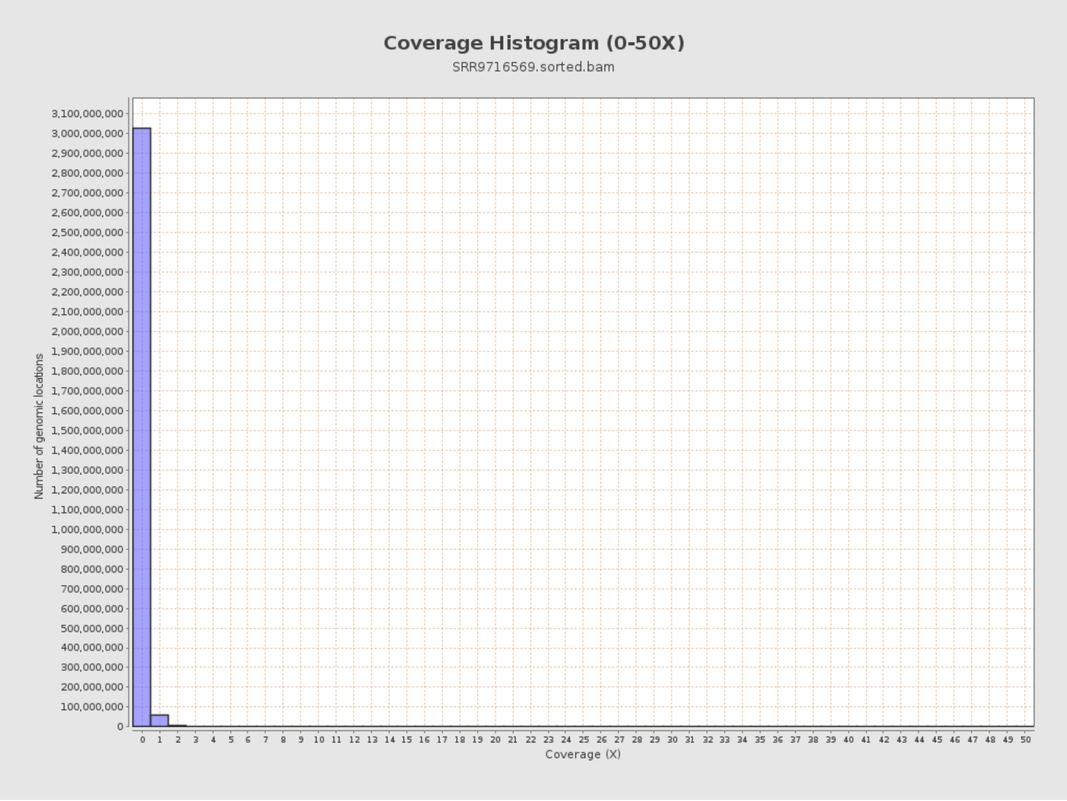
3. Results : Coverage across reference



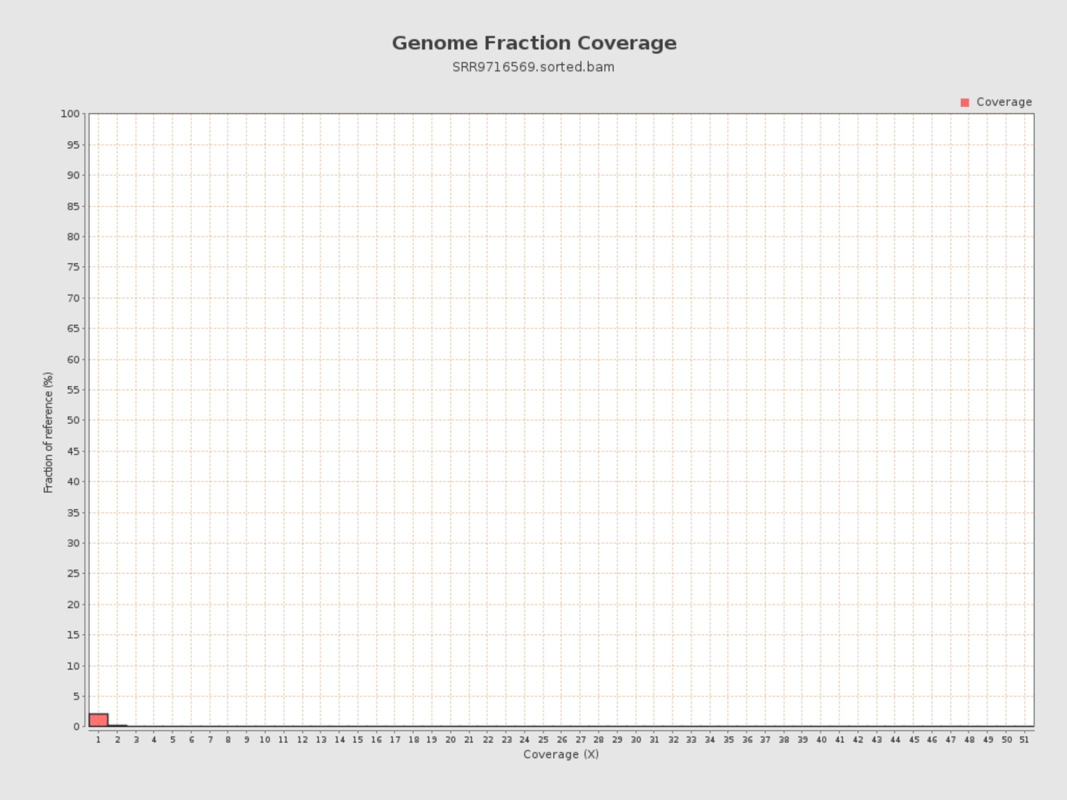
4. Results : Coverage Histogram



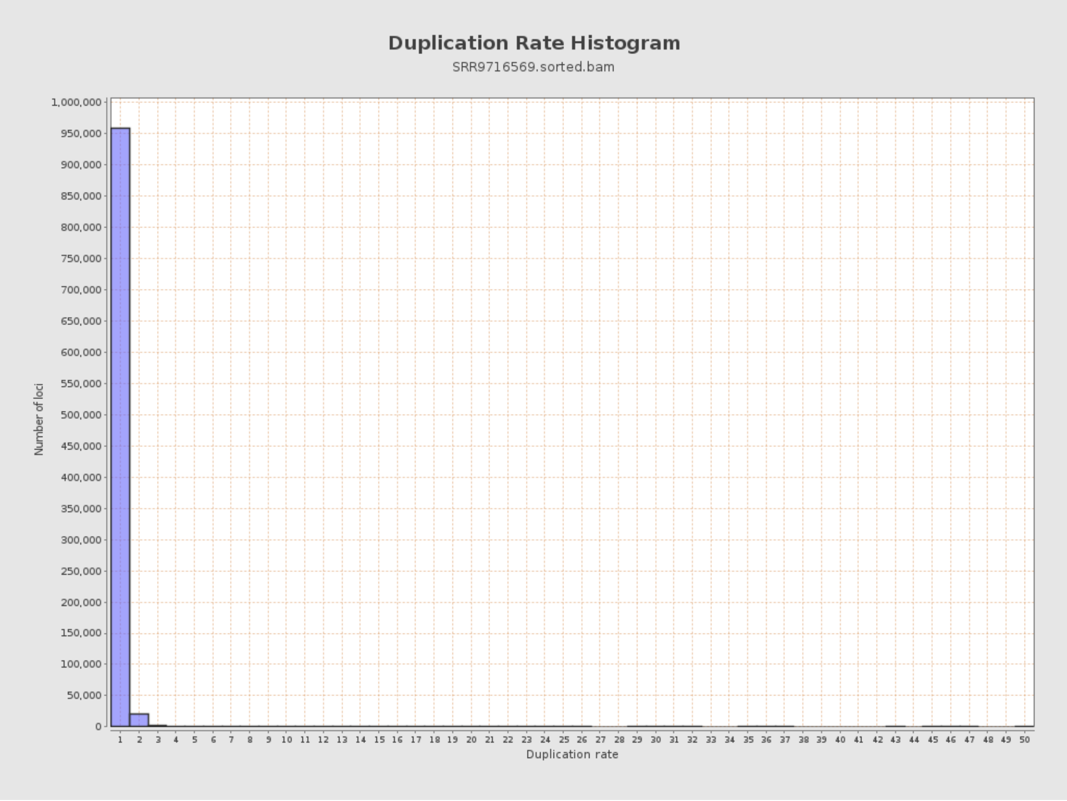
5. Results : Coverage Histogram (0-50X)



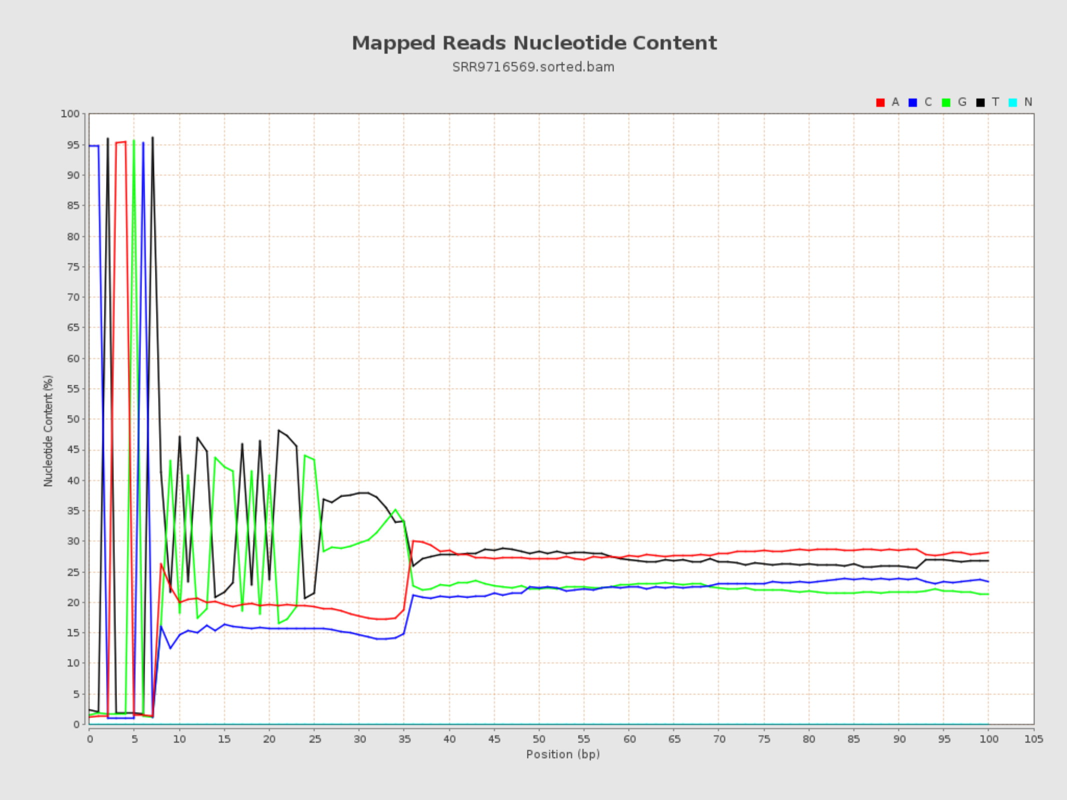
6. Results : Genome Fraction Coverage



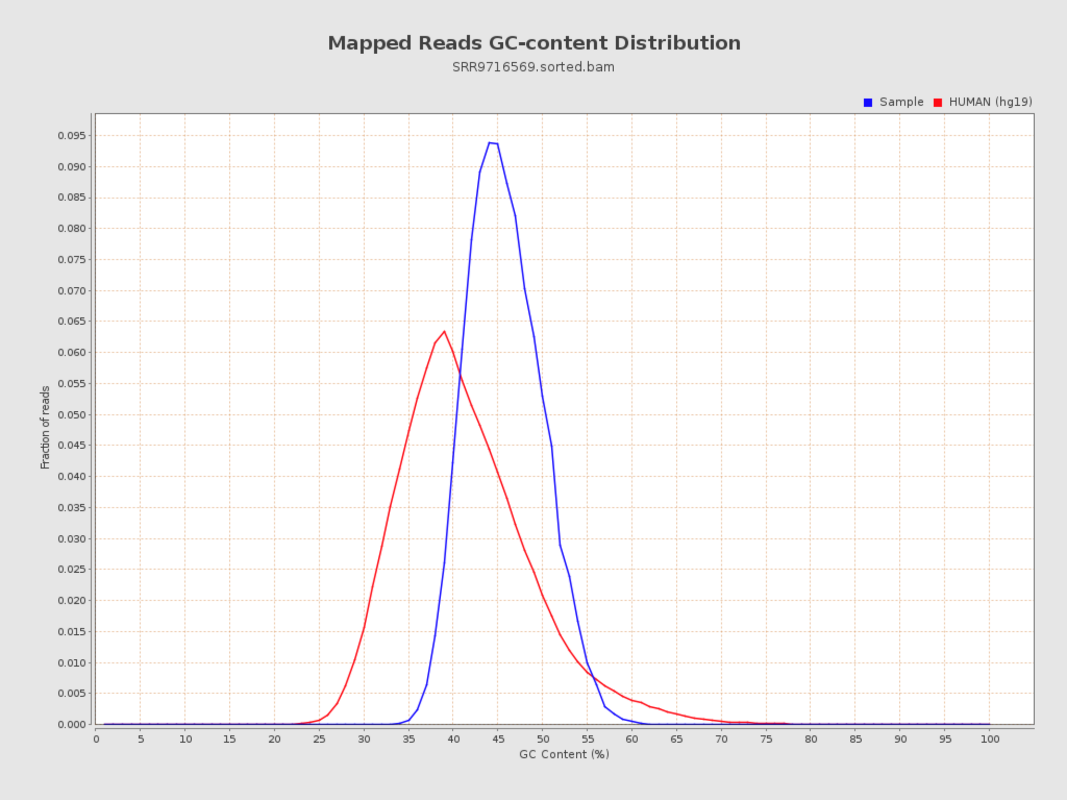
7. Results : Duplication Rate Histogram



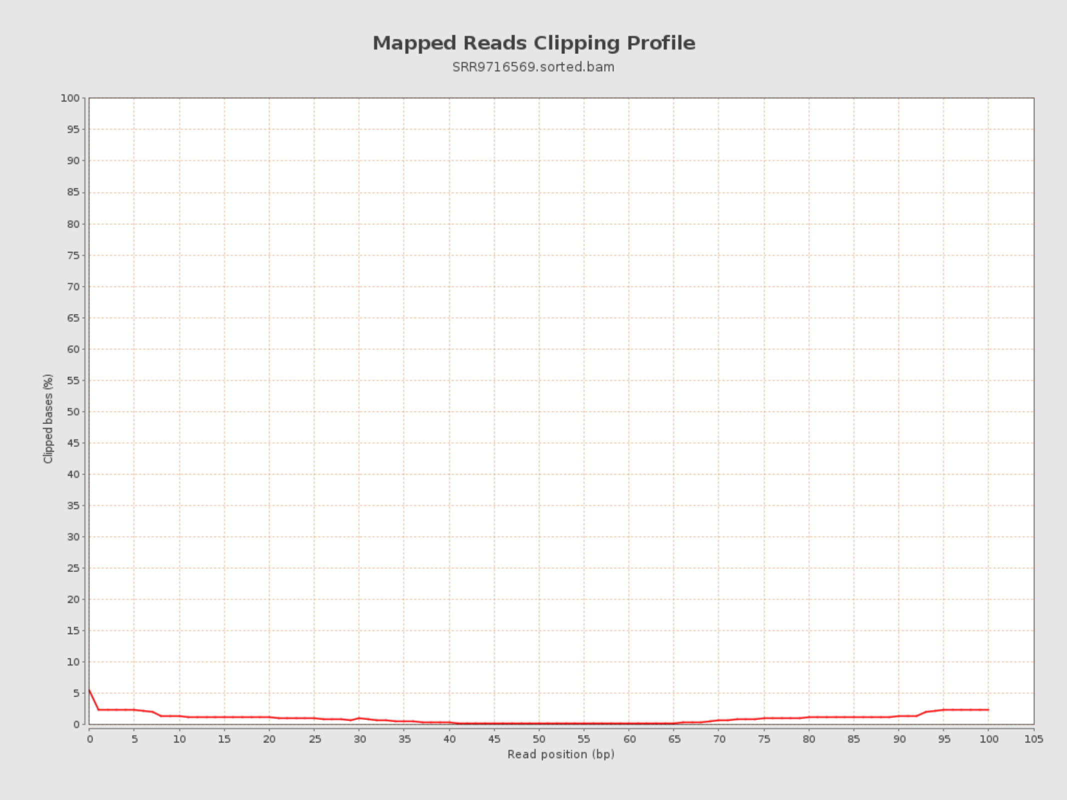
8. Results : Mapped Reads Nucleotide Content



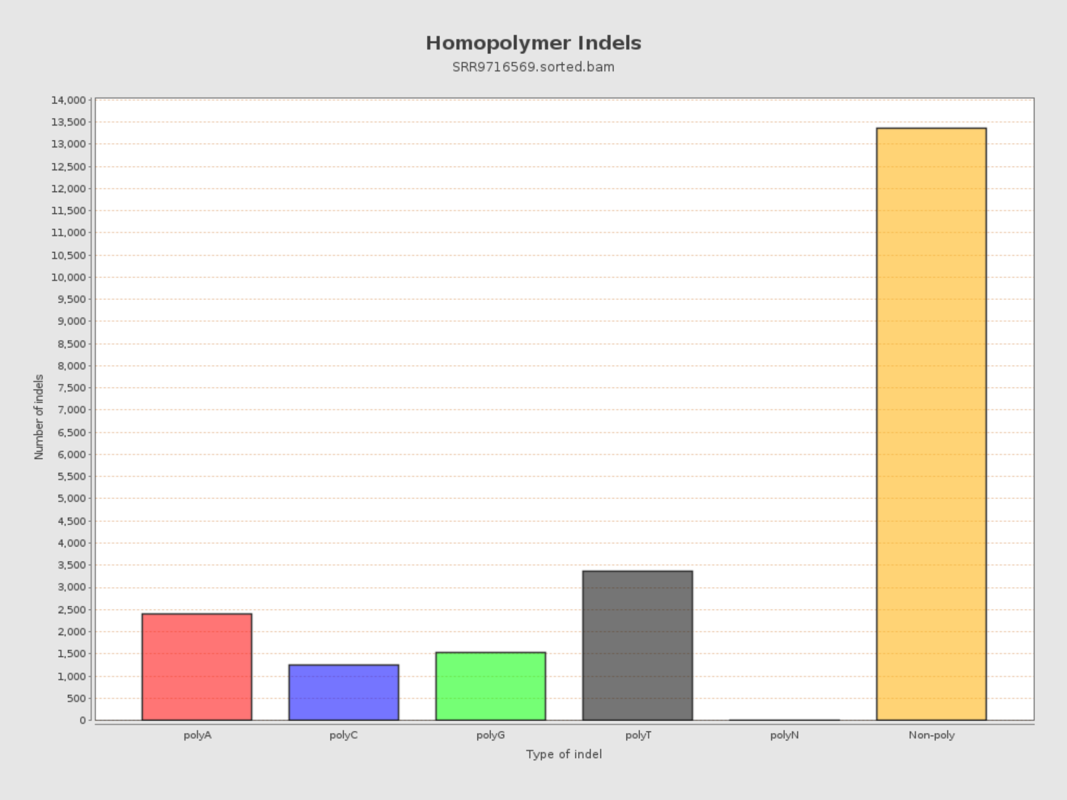
9. Results : Mapped Reads GC-content Distribution



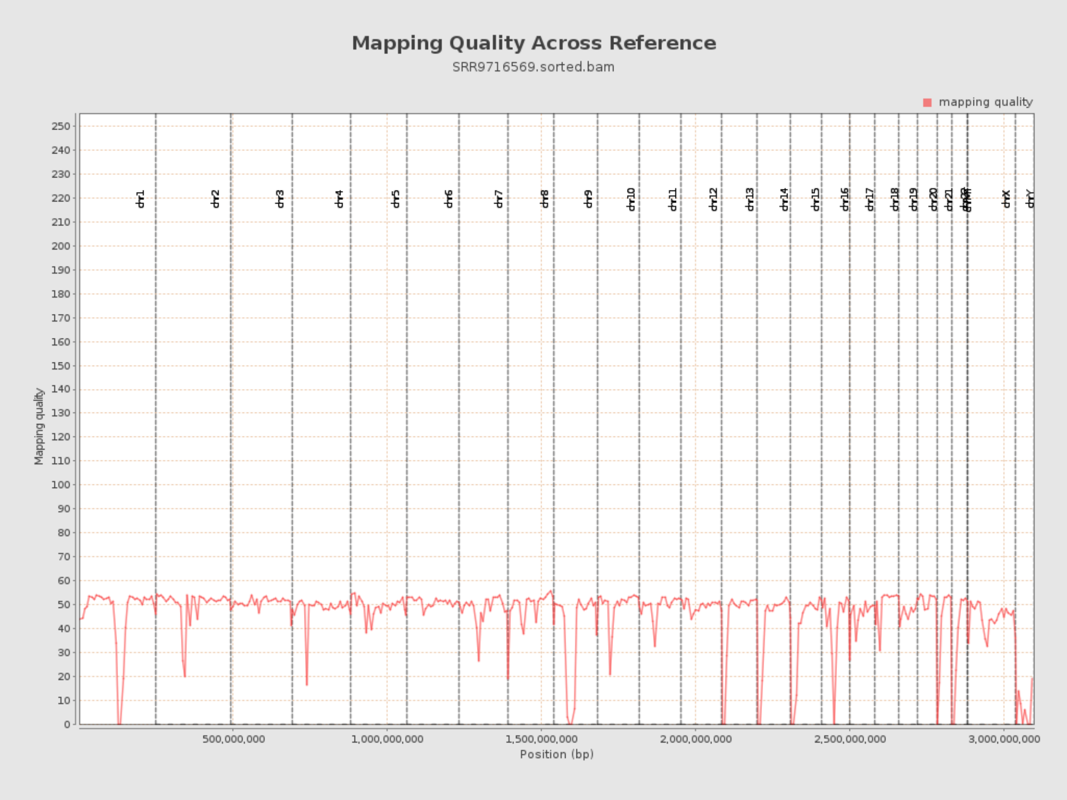
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram