Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 08:49:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716354.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_SRR9716354 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716354.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 08:49:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716354.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,257,310
Mapped reads	1,168,989 / 92.98%
Unmapped reads	88,321 / 7.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,454 / 1.87%
Read min/max/mean length	30 / 101 / 101.67
Duplicated reads (estimated)	36,200 / 2.88%
Duplication rate	2.2%
Clipped reads	1,189,494 / 94.61%

2.2. ACGT Content

Number/percentage of A's	22,799,547 / 24.86%
Number/percentage of C's	18,824,253 / 20.53%
Number/percentage of T's	28,308,124 / 30.87%
Number/percentage of G's	21,768,408 / 23.74%
Number/percentage of N's	6,681 / 0.01%
GC Percentage	44.26%

2.3. Coverage

Mean	0.0296

Standard Deviation	0.2768

2.4. Mapping Quality

Mean Mapping Quality	47.32

2.5. Mismatches and indels

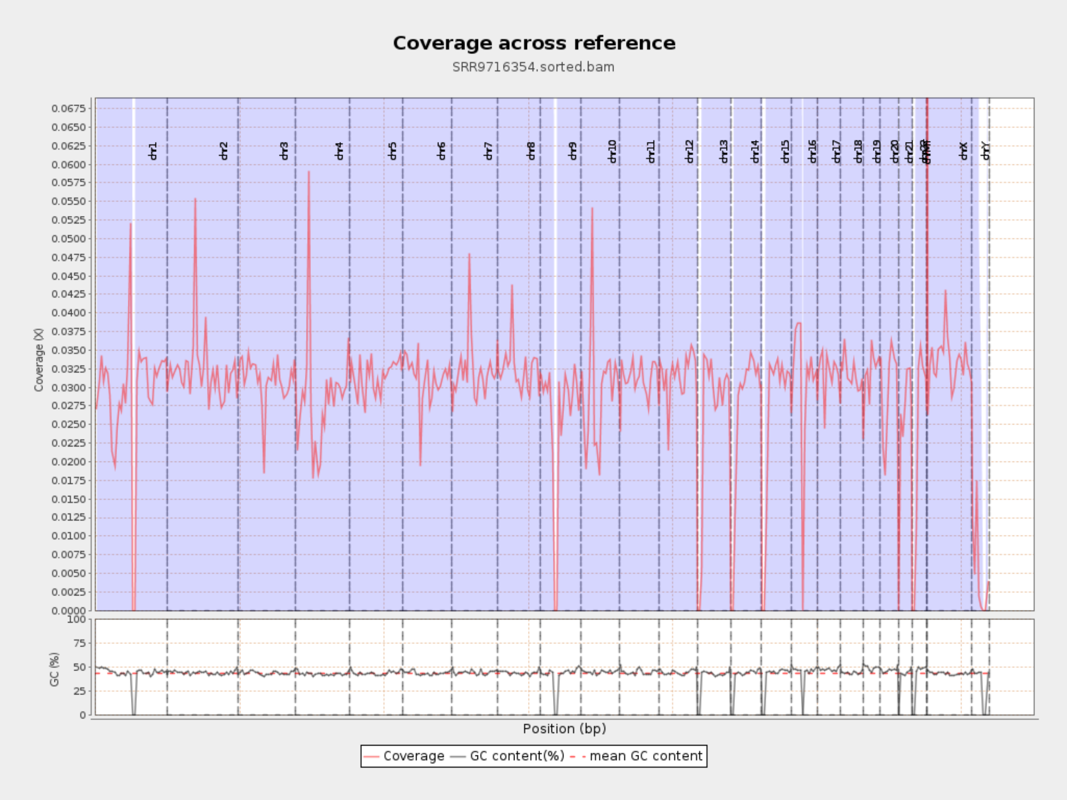
General error rate	0.7%
Mismatches	624,878
Insertions	8,200
Mapped reads with at least one insertion	0.69%
Deletions	23,045
Mapped reads with at least one deletion	1.94%
Homopolymer indels	42.85%

2.6. Chromosome stats

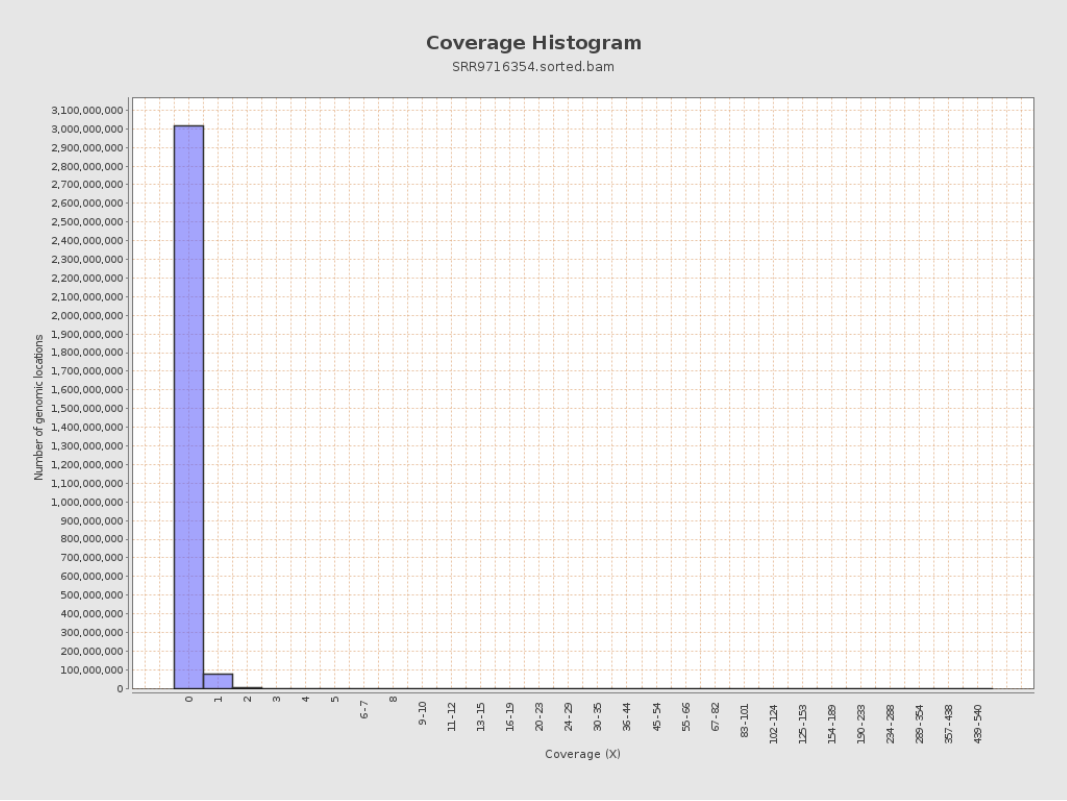
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7235414	0.029	0.4884
chr2	243199373	7892570	0.0325	0.3076
chr3	198022430	6135889	0.031	0.1897
chr4	191154276	5490314	0.0287	0.2237
chr5	180915260	5713846	0.0316	0.1925
chr6	171115067	5327576	0.0311	0.2036
chr7	159138663	5119288	0.0322	0.3689

chr8	146364022	4765421	0.0326	0.3368
chr9	141213431	3642503	0.0258	0.2501
chr10	135534747	4040256	0.0298	0.2879
chr11	135006516	4242366	0.0314	0.2567
chr12	133851895	4238140	0.0317	0.1931
chr13	115169878	2952781	0.0256	0.1715
chr14	107349540	2820897	0.0263	0.1865
chr15	102531392	2678184	0.0261	0.1751
chr16	90354753	2724809	0.0302	0.1996
chr17	81195210	2594080	0.0319	0.2073
chr18	78077248	2479108	0.0318	0.4002
chr19	59128983	1907648	0.0323	0.3546
chr20	63025520	1833673	0.0291	0.1917
chr21	48129895	1238615	0.0257	0.1979
chr22	51304566	1164167	0.0227	0.1641
chrMT	16571	12526	0.7559	1.0201
chrX	155270560	5217232	0.0336	0.2213
chrY	59373566	283268	0.0048	0.1571

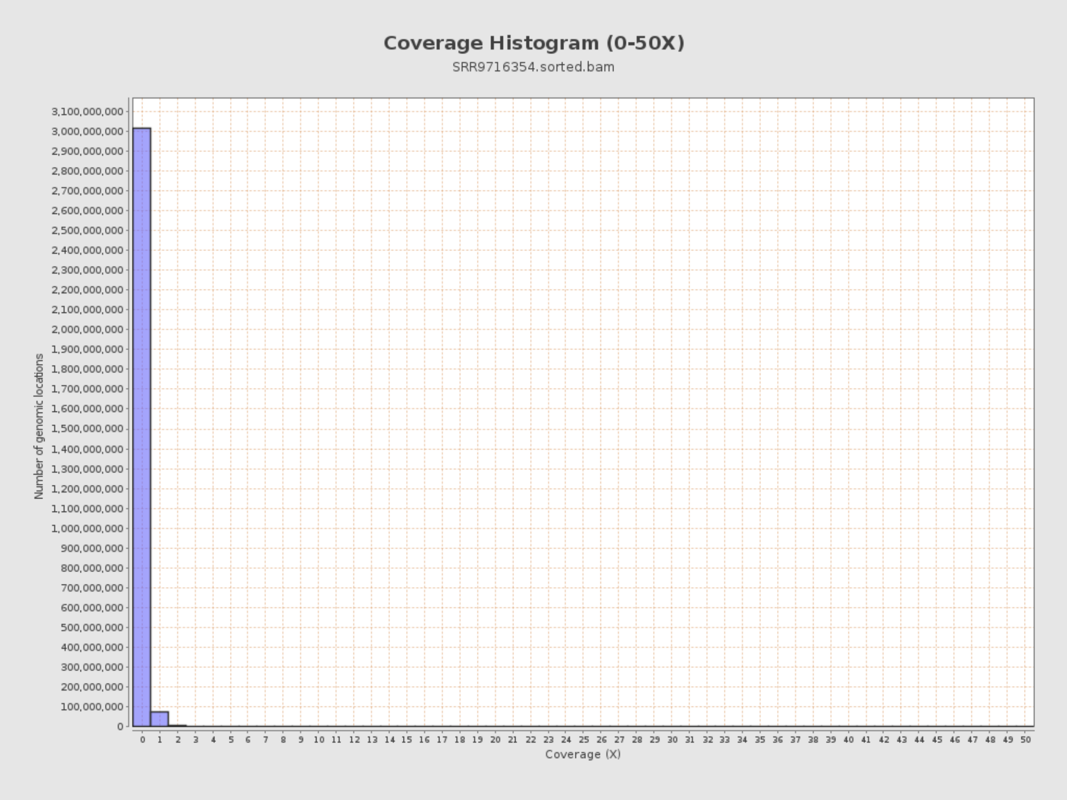
3. Results : Coverage across reference



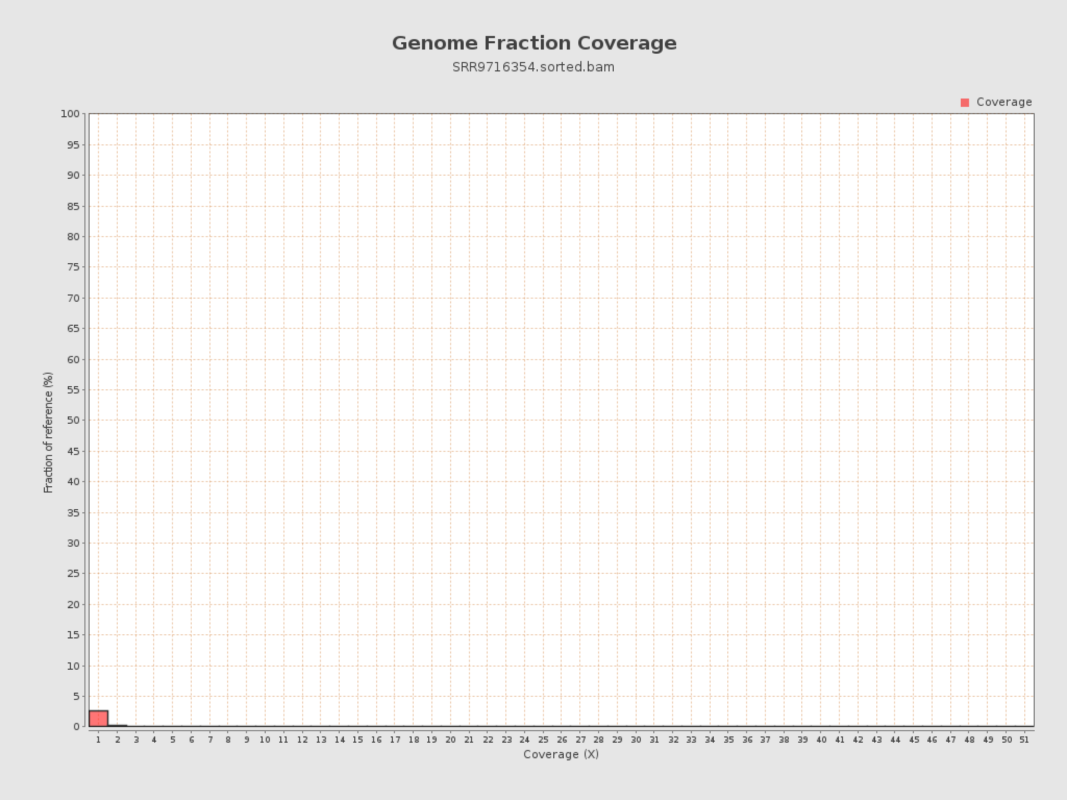
4. Results : Coverage Histogram



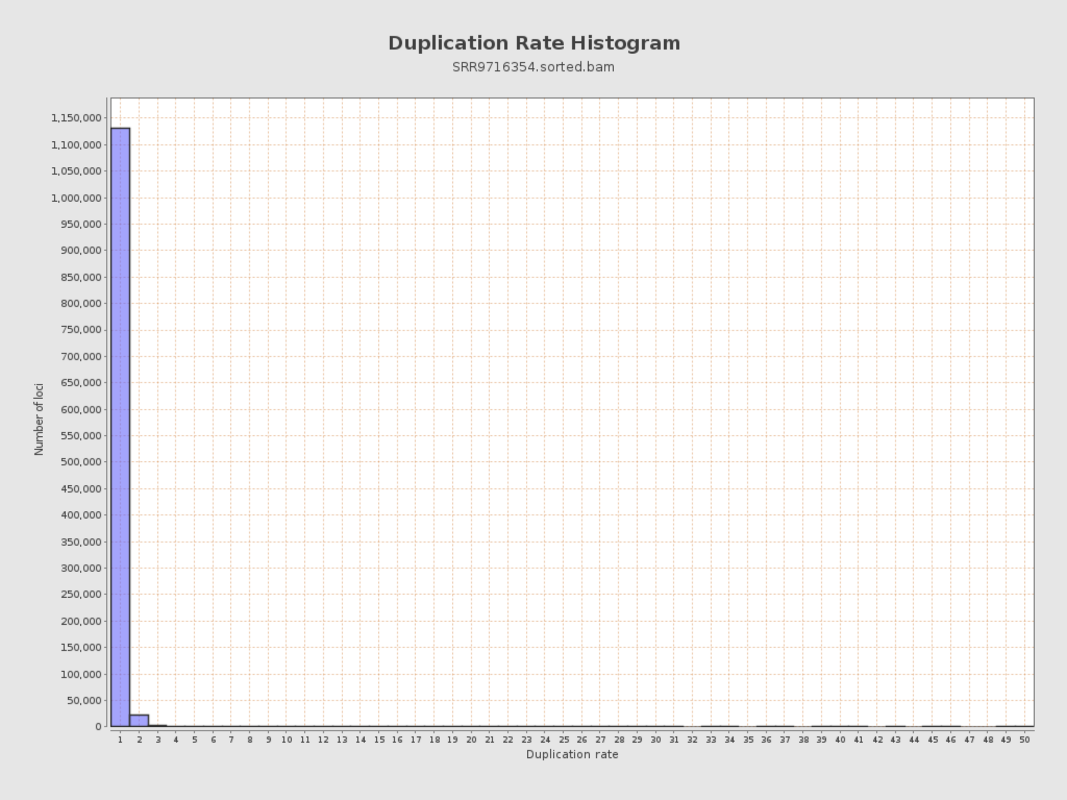
5. Results : Coverage Histogram (0-50X)



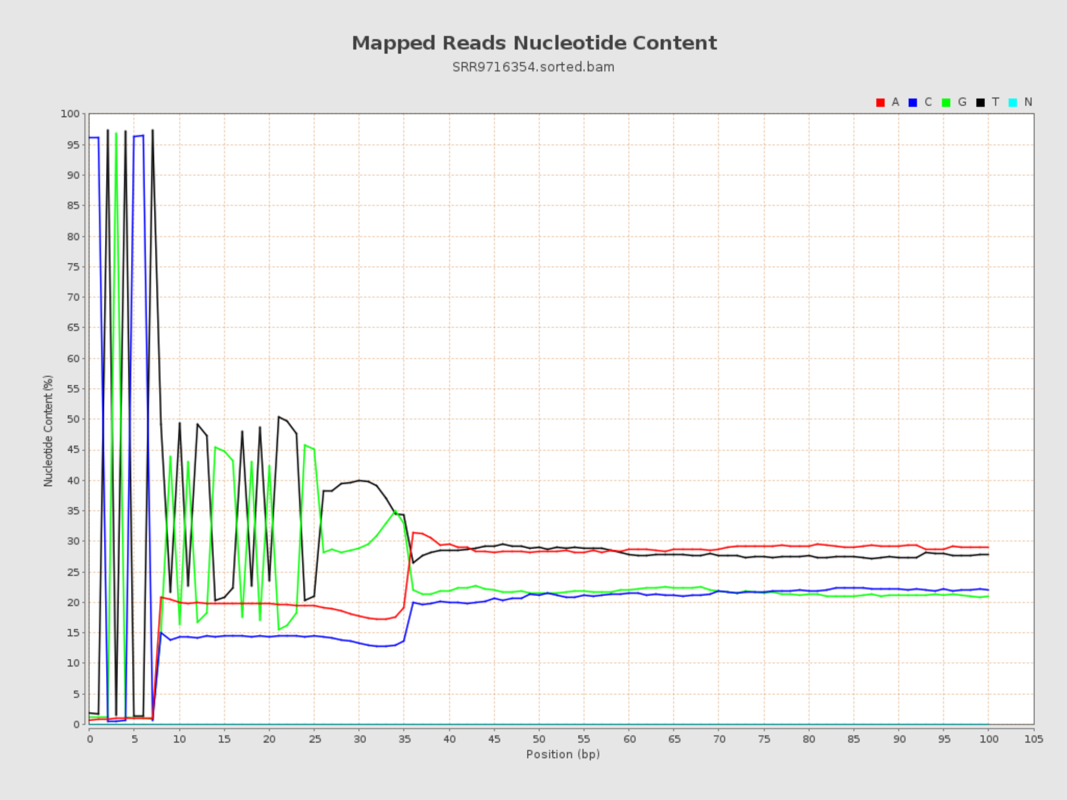
6. Results : Genome Fraction Coverage



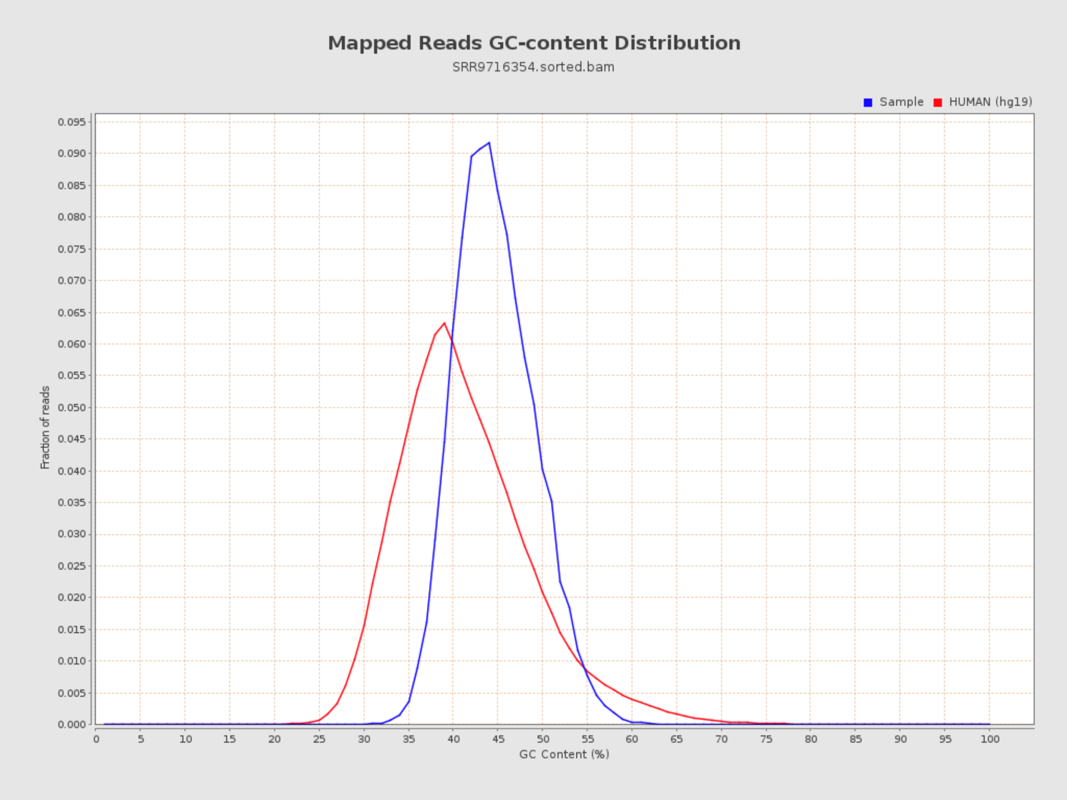
7. Results : Duplication Rate Histogram



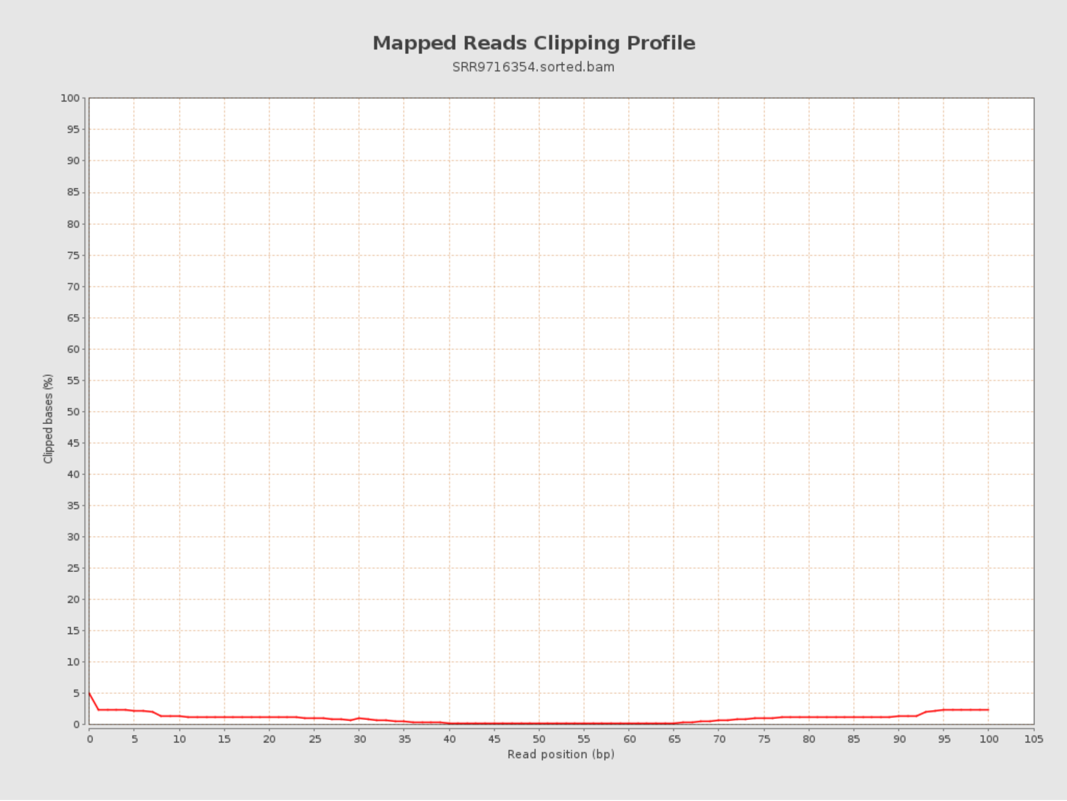
8. Results : Mapped Reads Nucleotide Content



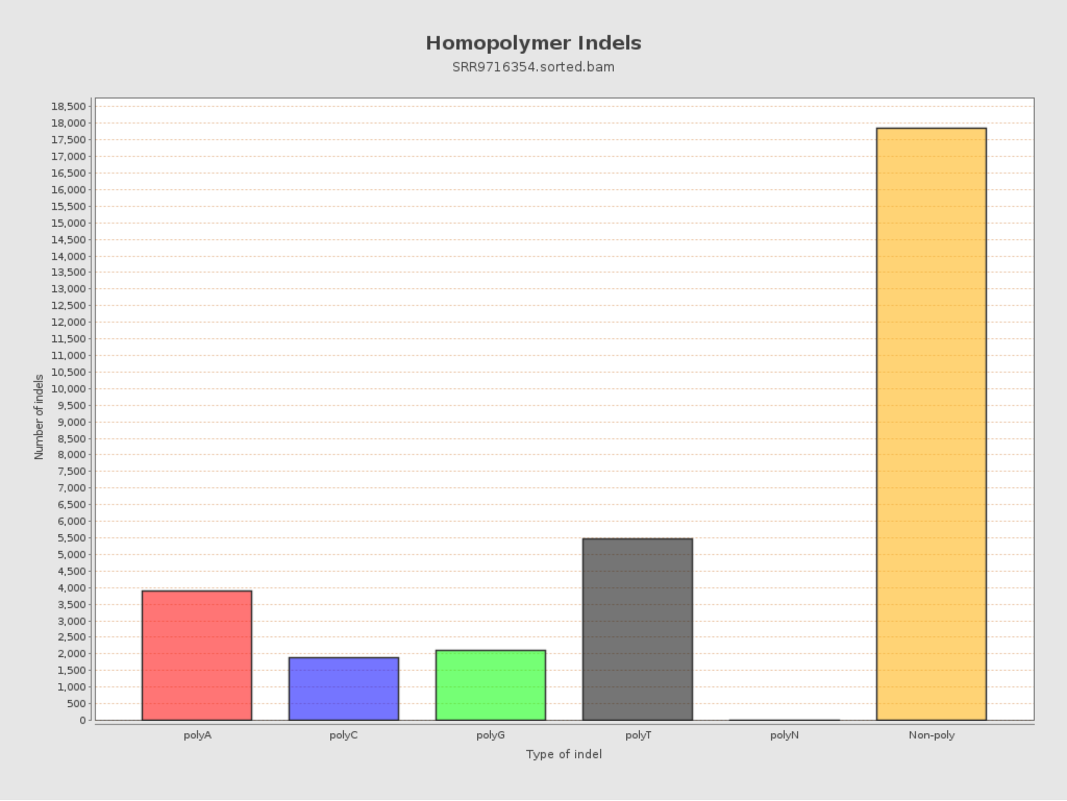
9. Results : Mapped Reads GC-content Distribution



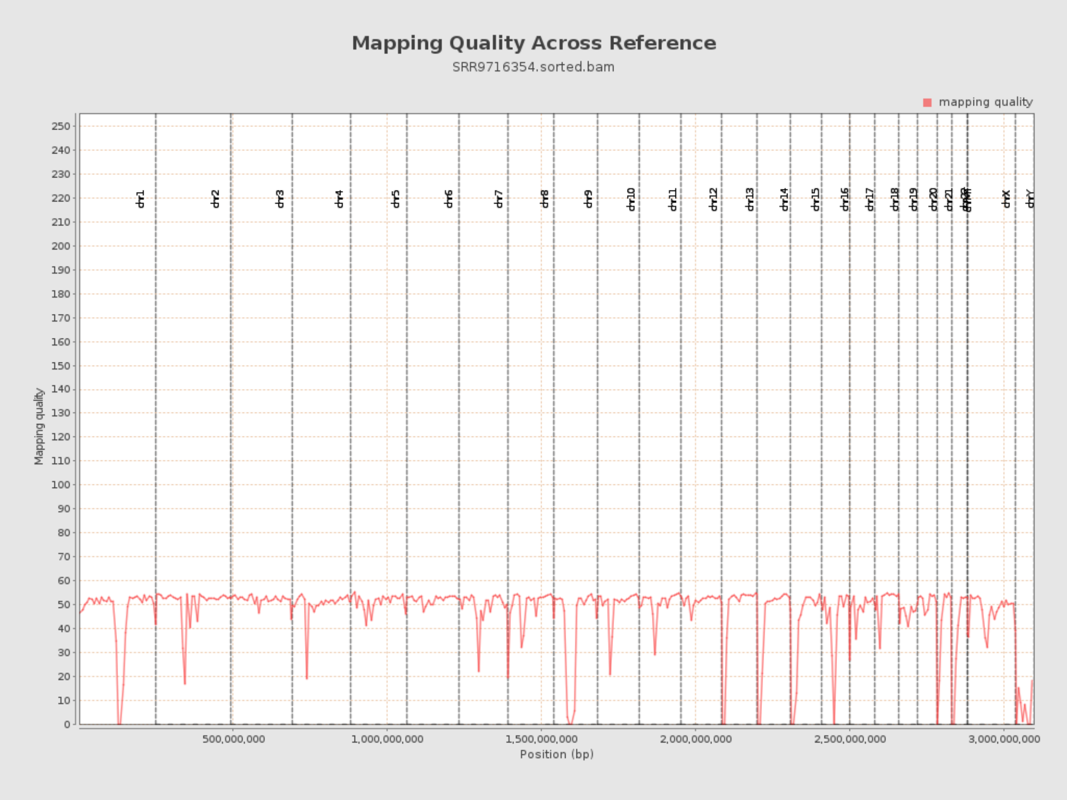
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram