Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 09:44:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716371.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_SRR9716371 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716371.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 09:44:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716371.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,072,502
Mapped reads	2,802,455 / 91.21%
Unmapped reads	270,047 / 8.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	51,726 / 1.68%
Read min/max/mean length	30 / 101 / 101.61
Duplicated reads (estimated)	172,443 / 5.61%
Duplication rate	4.58%
Clipped reads	2,847,198 / 92.67%

2.2. ACGT Content

Number/percentage of A's	56,331,206 / 25.46%
Number/percentage of C's	45,357,513 / 20.5%
Number/percentage of T's	68,419,042 / 30.92%
Number/percentage of G's	51,151,893 / 23.12%
Number/percentage of N's	15,090 / 0.01%
GC Percentage	43.62%

2.3. Coverage

Mean	0.0715

Standard Deviation	0.5828

2.4. Mapping Quality

Mean Mapping Quality	47.51

2.5. Mismatches and indels

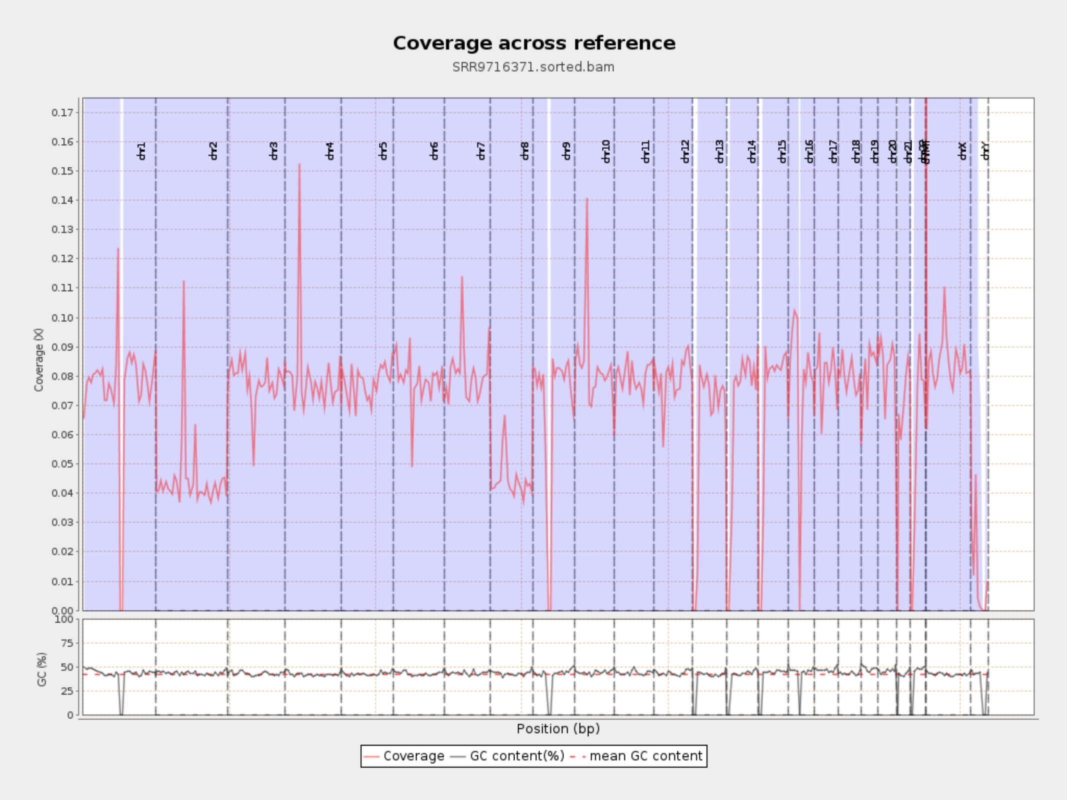
General error rate	0.71%
Mismatches	1,526,913
Insertions	18,770
Mapped reads with at least one insertion	0.66%
Deletions	52,195
Mapped reads with at least one deletion	1.83%
Homopolymer indels	43.18%

2.6. Chromosome stats

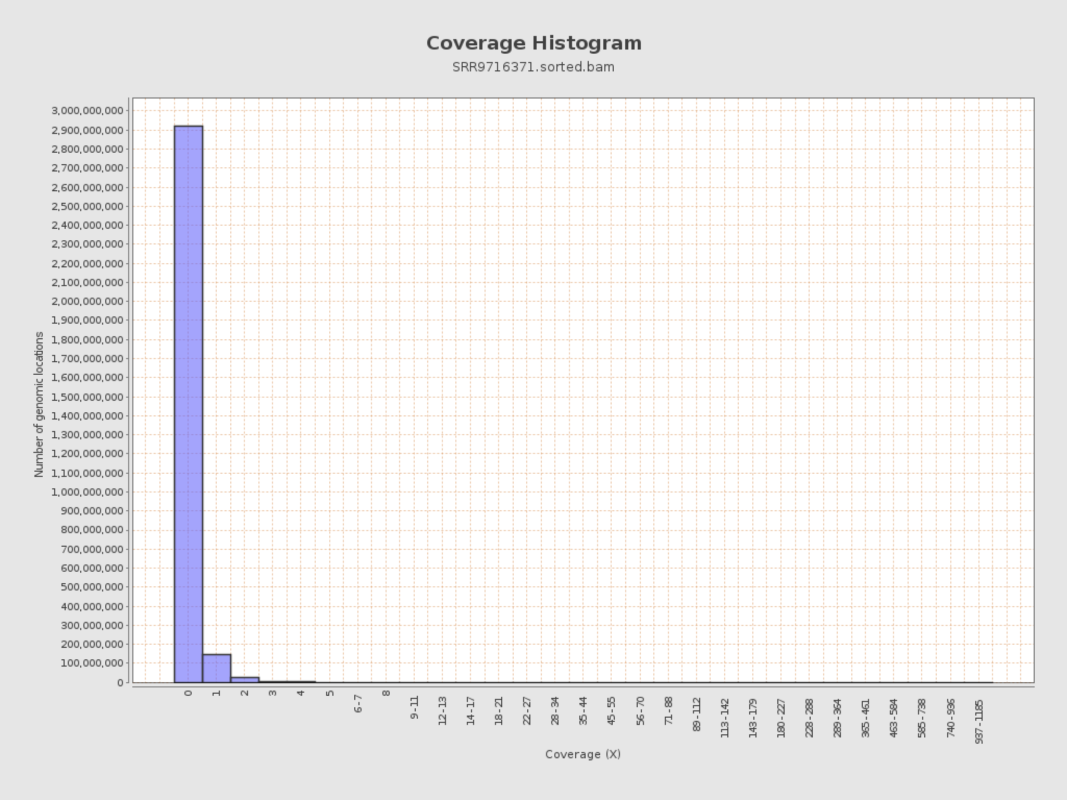
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18846212	0.0756	1.0562
chr2	243199373	10969447	0.0451	0.6566
chr3	198022430	15423936	0.0779	0.3334
chr4	191154276	15273658	0.0799	0.4752
chr5	180915260	14118252	0.078	0.3401
chr6	171115067	13451568	0.0786	0.3865
chr7	159138663	12921187	0.0812	0.8212

chr8	146364022	6526886	0.0446	0.7077
chr9	141213431	9871238	0.0699	0.5432
chr10	135534747	11323064	0.0835	0.6543
chr11	135006516	10738739	0.0795	0.5644
chr12	133851895	10671647	0.0797	0.3451
chr13	115169878	7248929	0.0629	0.2998
chr14	107349540	7208812	0.0672	0.3516
chr15	102531392	6980616	0.0681	0.3178
chr16	90354753	6914682	0.0765	0.3736
chr17	81195210	6607002	0.0814	0.4181
chr18	78077248	6241687	0.0799	0.919
chr19	59128983	4851910	0.0821	0.7202
chr20	63025520	5272260	0.0837	0.3743
chr21	48129895	3203059	0.0666	0.3913
chr22	51304566	2864524	0.0558	0.2961
chrMT	16571	7108	0.4289	0.6819
chrX	155270560	13119332	0.0845	0.4279
chrY	59373566	719635	0.0121	0.4164

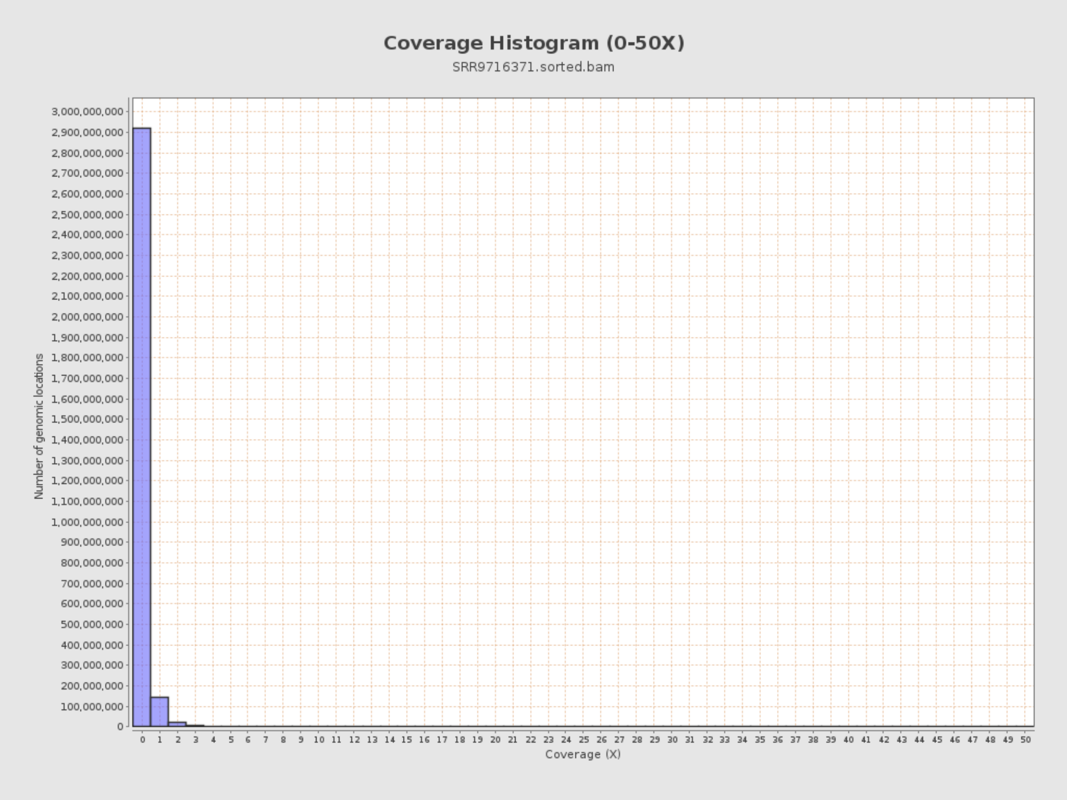
3. Results : Coverage across reference



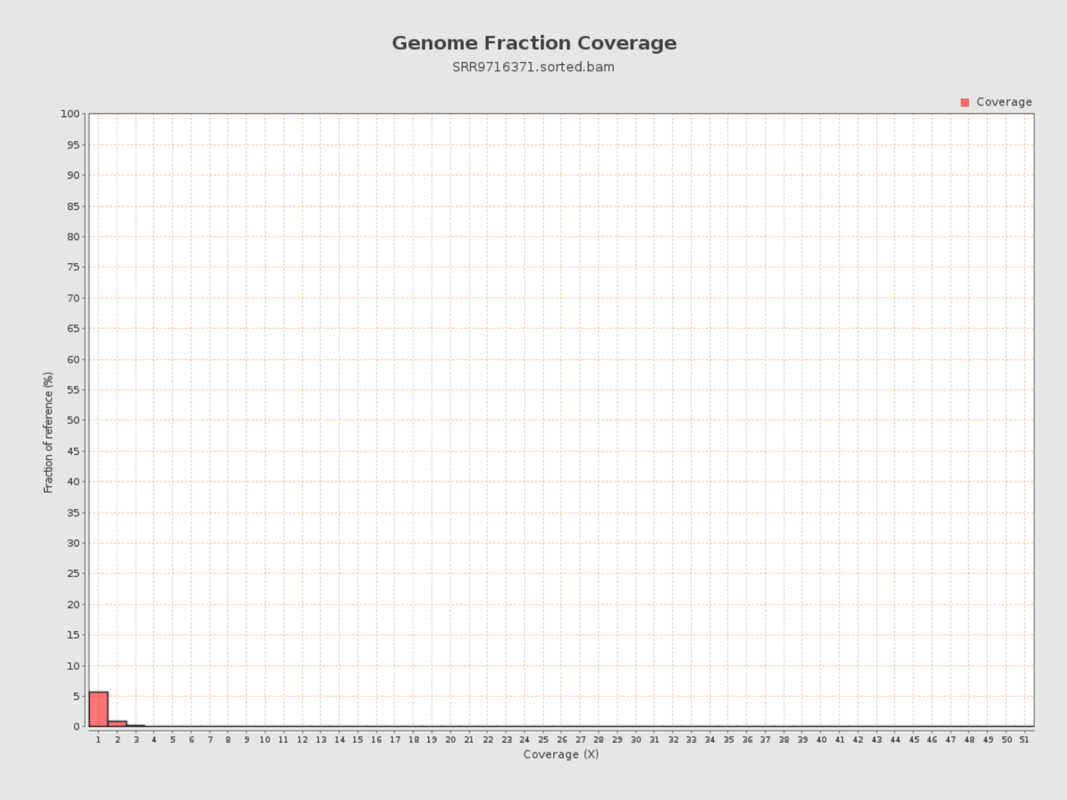
4. Results : Coverage Histogram



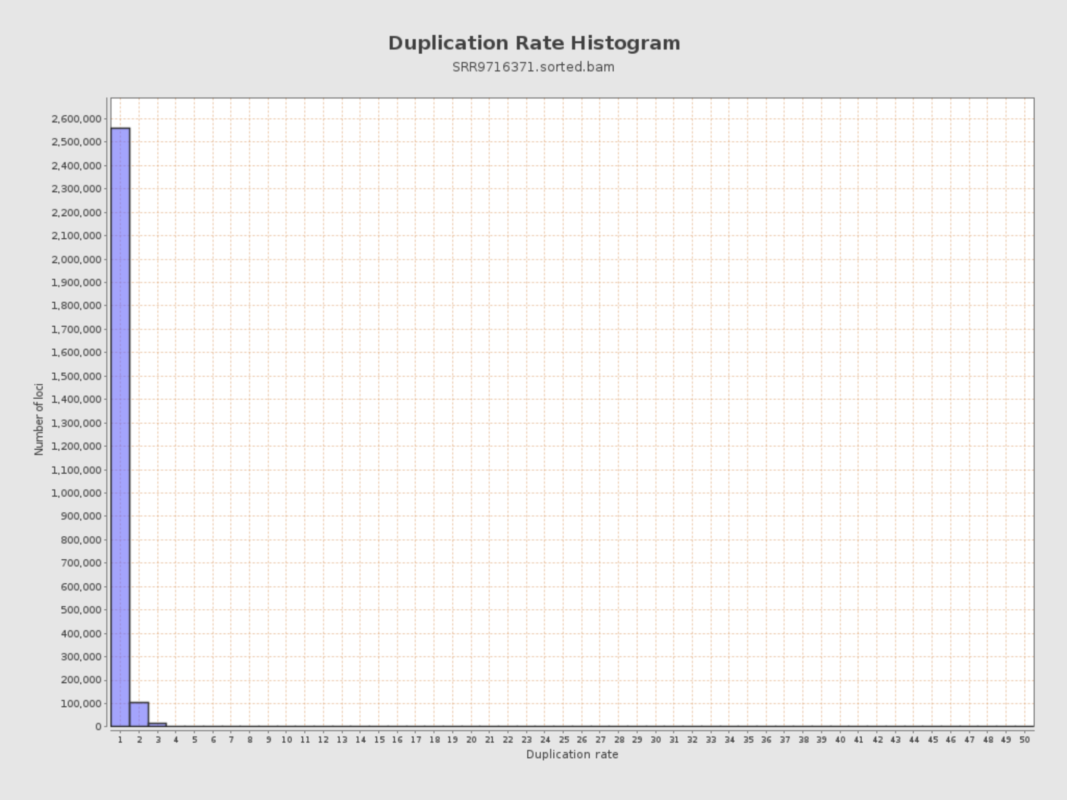
5. Results : Coverage Histogram (0-50X)



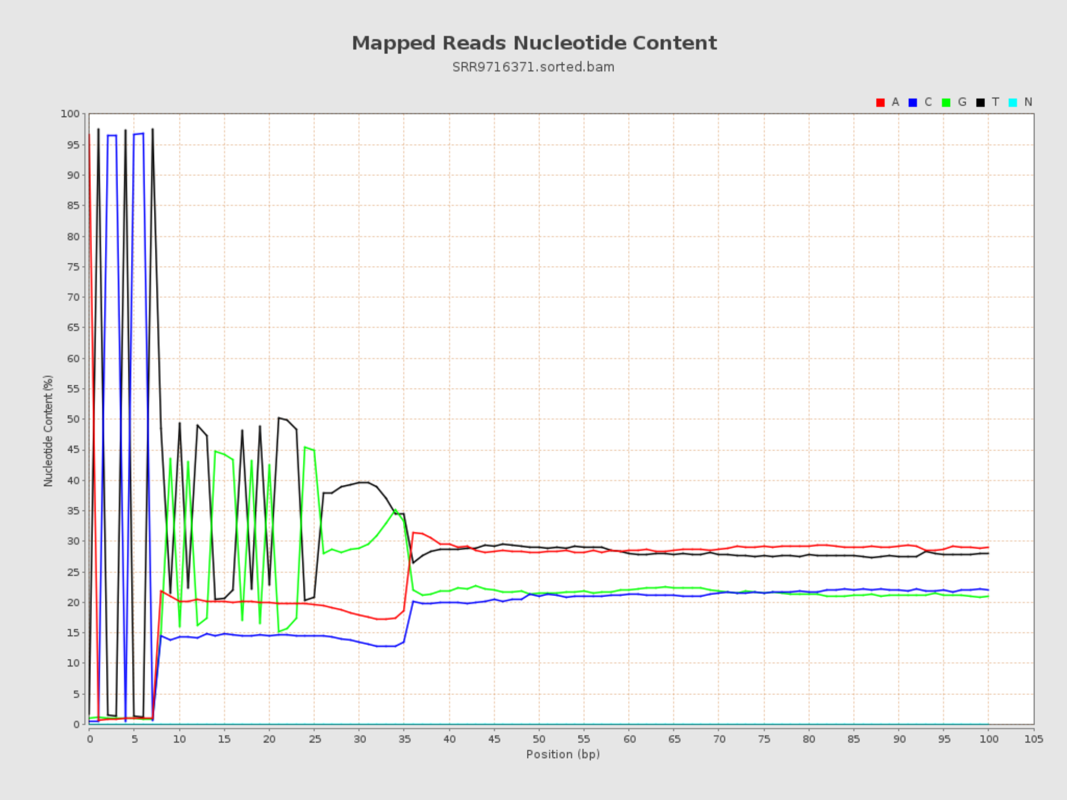
6. Results : Genome Fraction Coverage



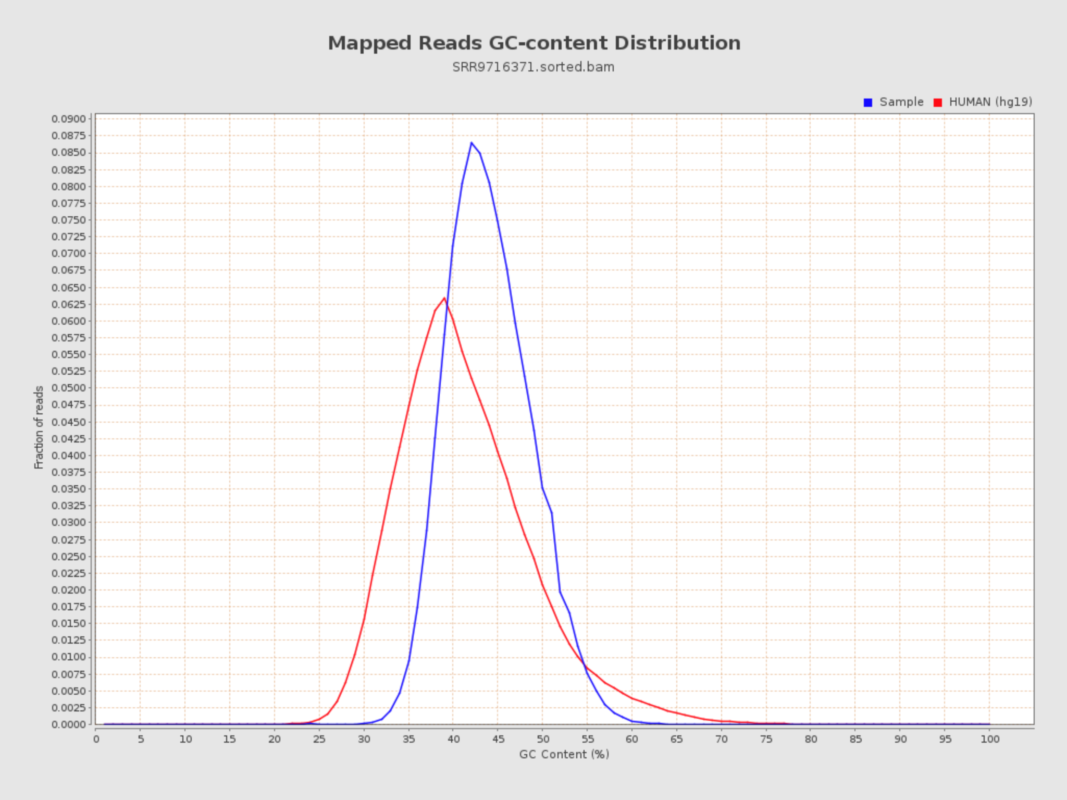
7. Results : Duplication Rate Histogram



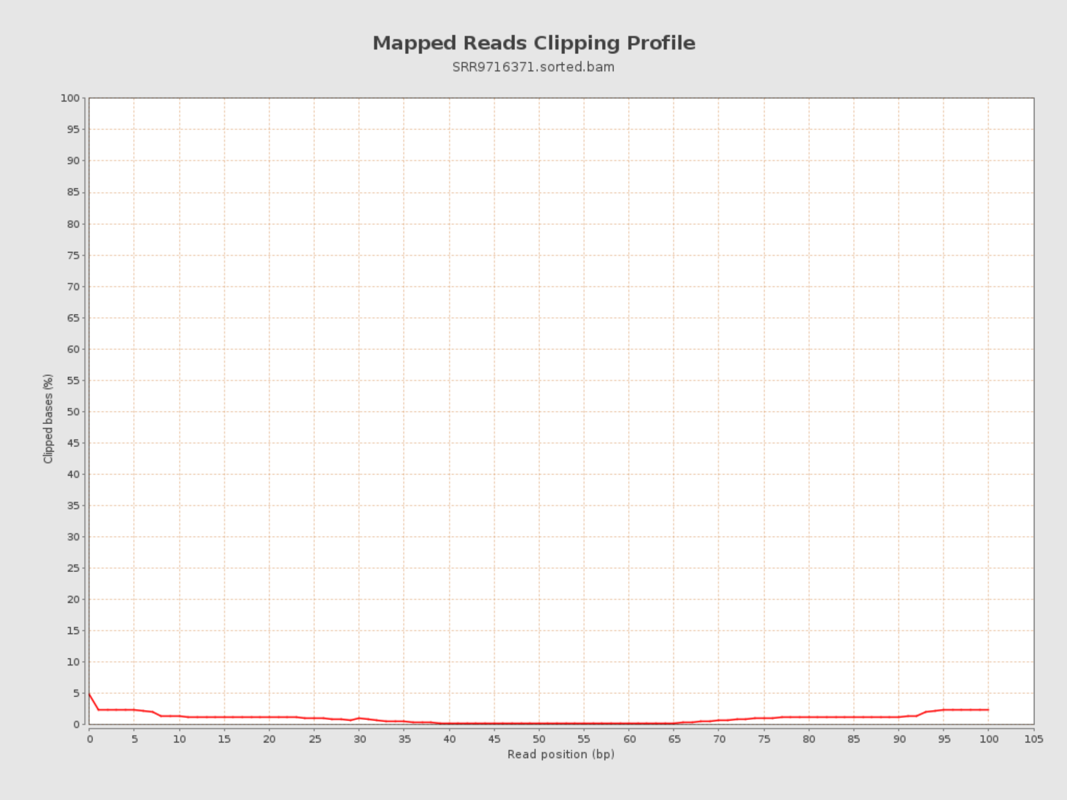
8. Results : Mapped Reads Nucleotide Content



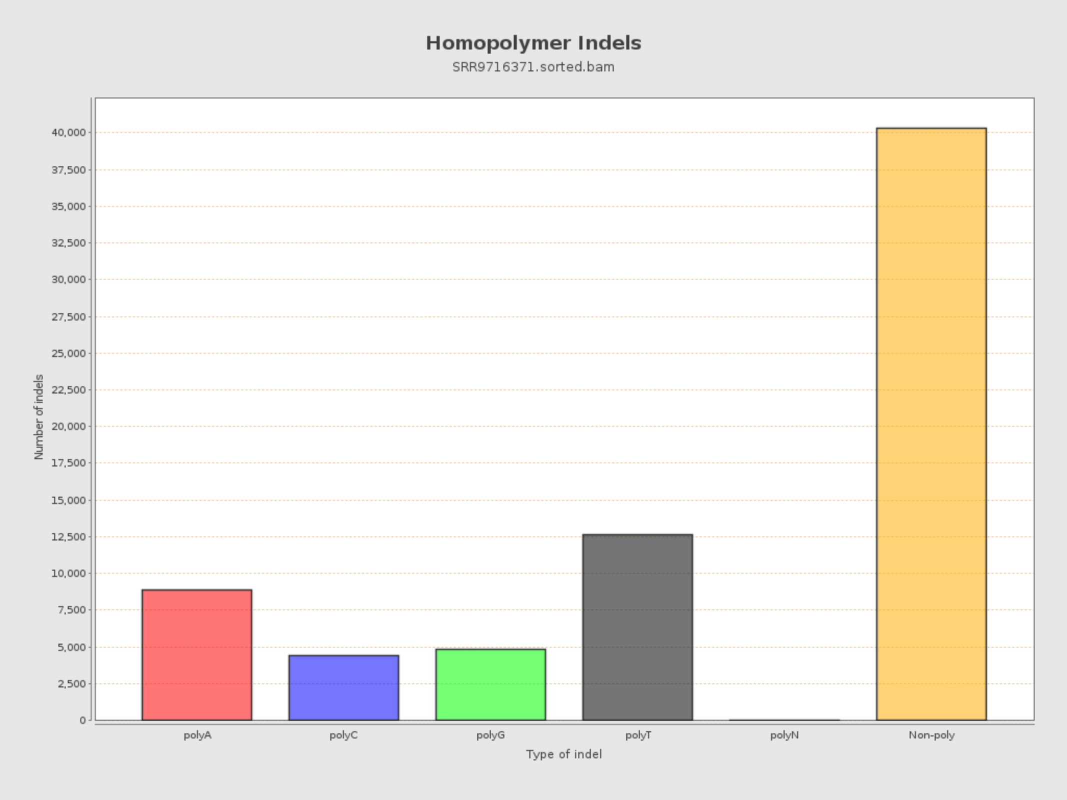
9. Results : Mapped Reads GC-content Distribution



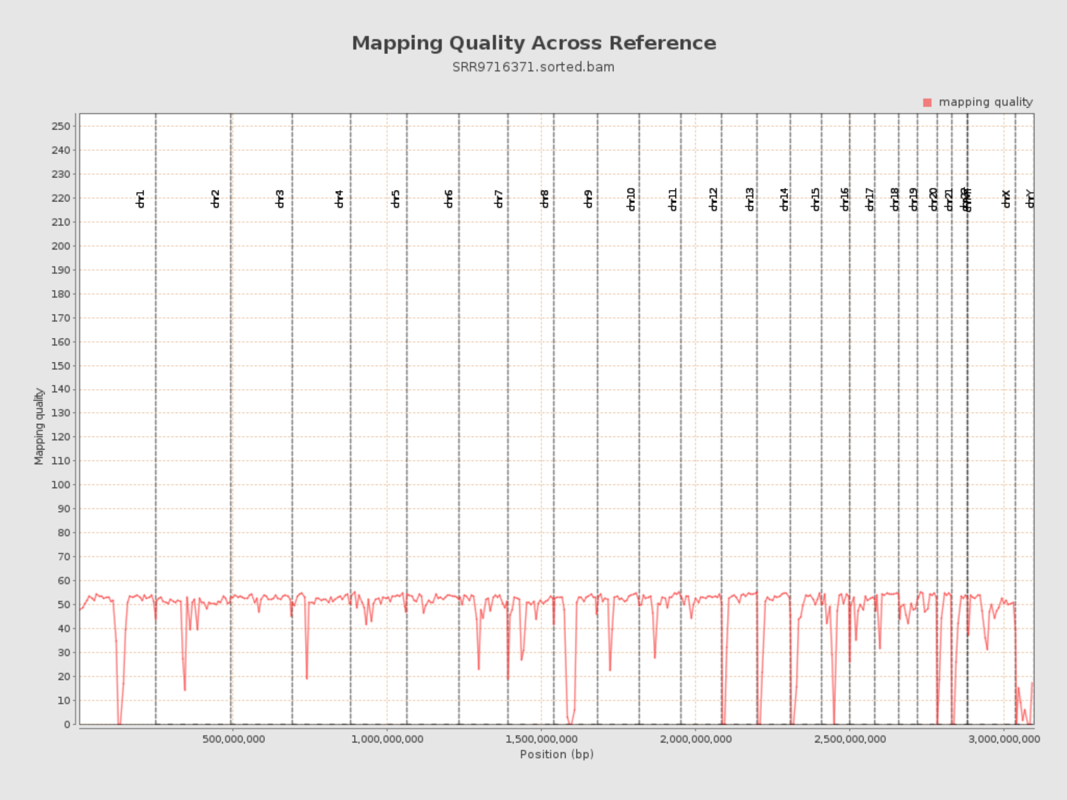
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram