Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 19:19:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716535.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_SRR9716535 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716535.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 19:19:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716535.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,196,373
Mapped reads	1,110,416 / 92.82%
Unmapped reads	85,957 / 7.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,920 / 1.92%
Read min/max/mean length	30 / 101 / 101.69
Duplicated reads (estimated)	32,671 / 2.73%
Duplication rate	2.05%
Clipped reads	1,131,341 / 94.56%

2.2. ACGT Content

Number/percentage of A's	22,923,214 / 26.17%
Number/percentage of C's	17,536,286 / 20.02%
Number/percentage of T's	26,610,706 / 30.38%
Number/percentage of G's	20,524,648 / 23.43%
Number/percentage of N's	6,220 / 0.01%
GC Percentage	43.45%

2.3. Coverage

Mean	0.0283

Standard Deviation	0.2861

2.4. Mapping Quality

Mean Mapping Quality	47.3

2.5. Mismatches and indels

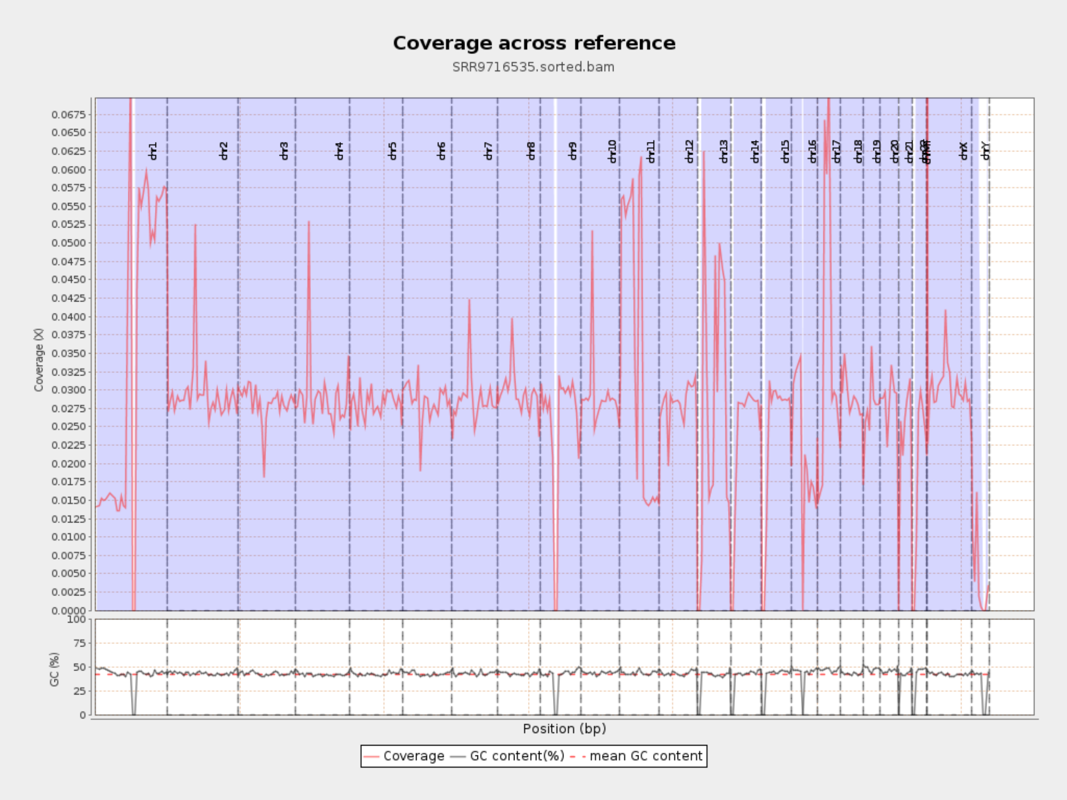
General error rate	0.68%
Mismatches	575,383
Insertions	7,238
Mapped reads with at least one insertion	0.64%
Deletions	20,612
Mapped reads with at least one deletion	1.83%
Homopolymer indels	42.66%

2.6. Chromosome stats

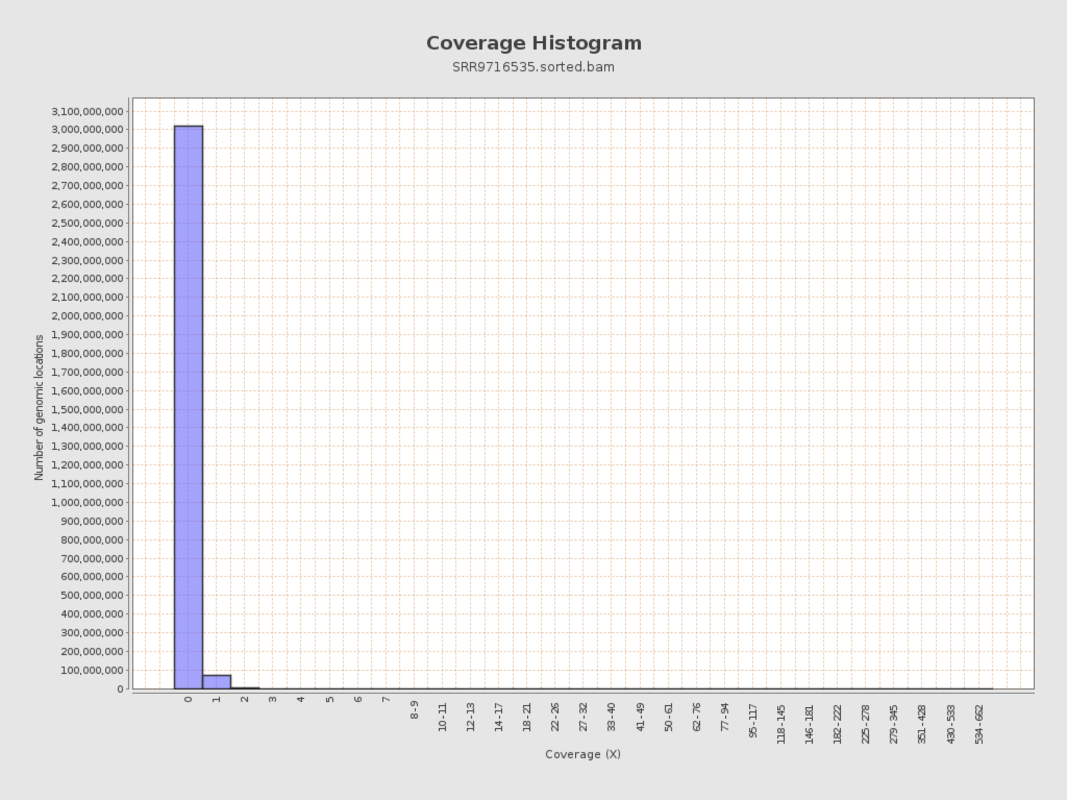
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8512807	0.0342	0.5924
chr2	243199373	7190271	0.0296	0.2956
chr3	198022430	5592021	0.0282	0.1795
chr4	191154276	5591046	0.0292	0.2127
chr5	180915260	5127456	0.0283	0.1821
chr6	171115067	4858999	0.0284	0.1933
chr7	159138663	4584626	0.0288	0.3139

chr8	146364022	4345545	0.0297	0.3162
chr9	141213431	3564964	0.0252	0.2341
chr10	135534747	3990484	0.0294	0.2796
chr11	135006516	4841157	0.0359	0.301
chr12	133851895	3778124	0.0282	0.1818
chr13	115169878	3109391	0.027	0.1777
chr14	107349540	2527452	0.0235	0.1778
chr15	102531392	2427506	0.0237	0.1647
chr16	90354753	1919592	0.0212	0.1711
chr17	81195210	2886589	0.0356	0.2421
chr18	78077248	2274437	0.0291	0.3736
chr19	59128983	1643388	0.0278	0.4212
chr20	63025520	1788540	0.0284	0.1851
chr21	48129895	1141448	0.0237	0.1826
chr22	51304566	954026	0.0186	0.1471
chrMT	16571	44629	2.6932	2.299
chrX	155270560	4691573	0.0302	0.2127
chrY	59373566	254027	0.0043	0.141

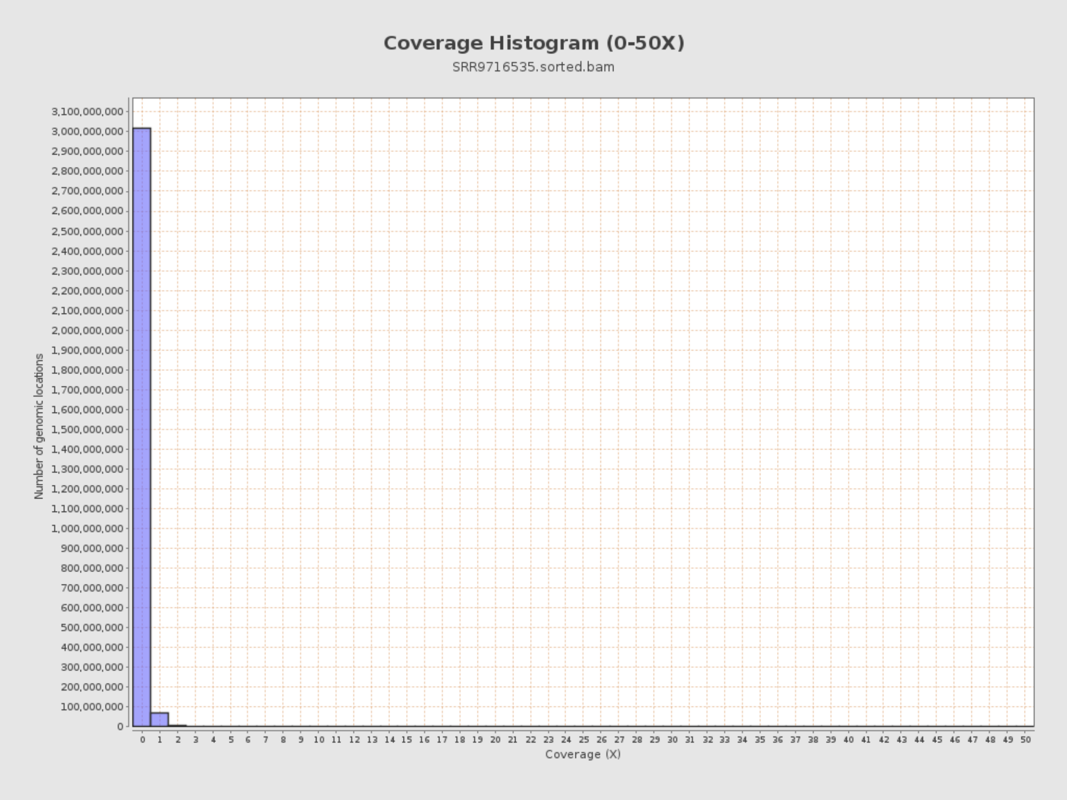
3. Results : Coverage across reference



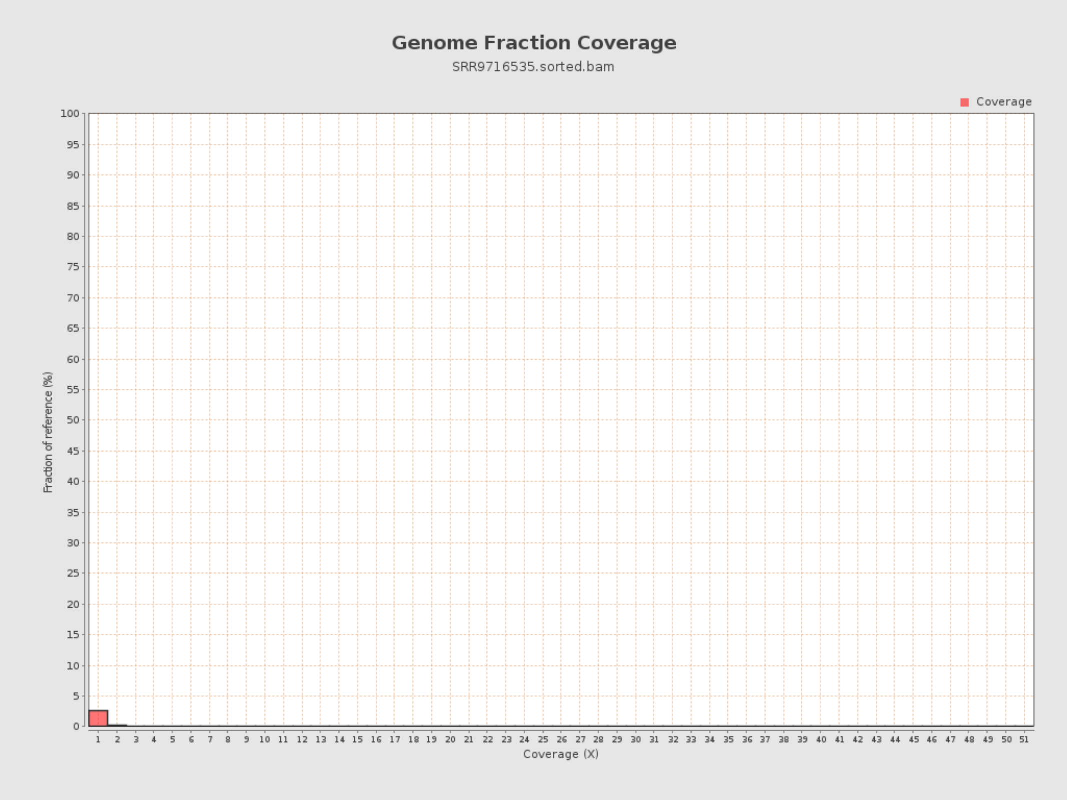
4. Results : Coverage Histogram



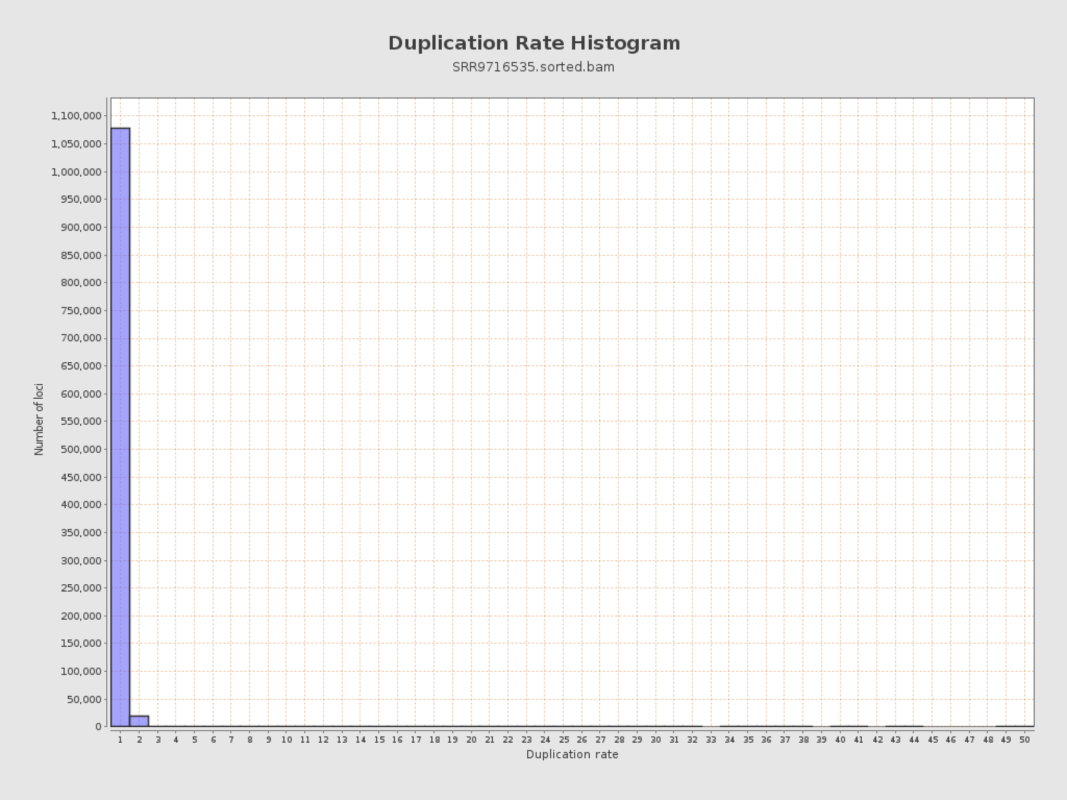
5. Results : Coverage Histogram (0-50X)



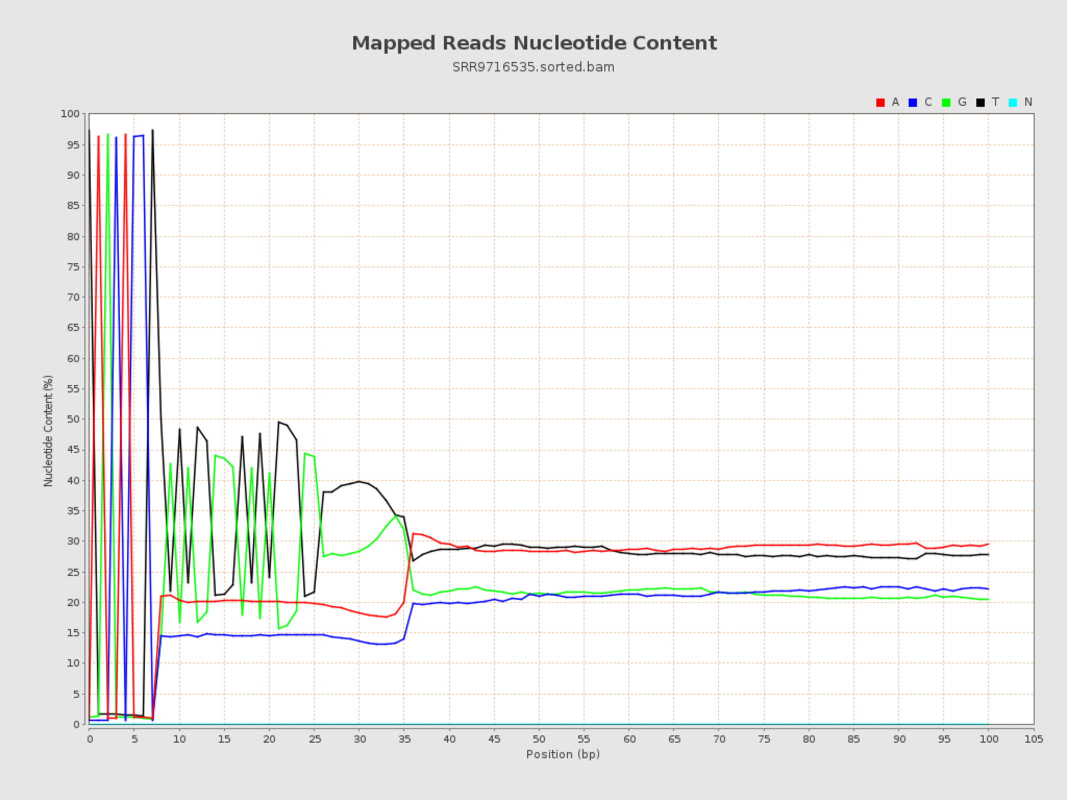
6. Results : Genome Fraction Coverage



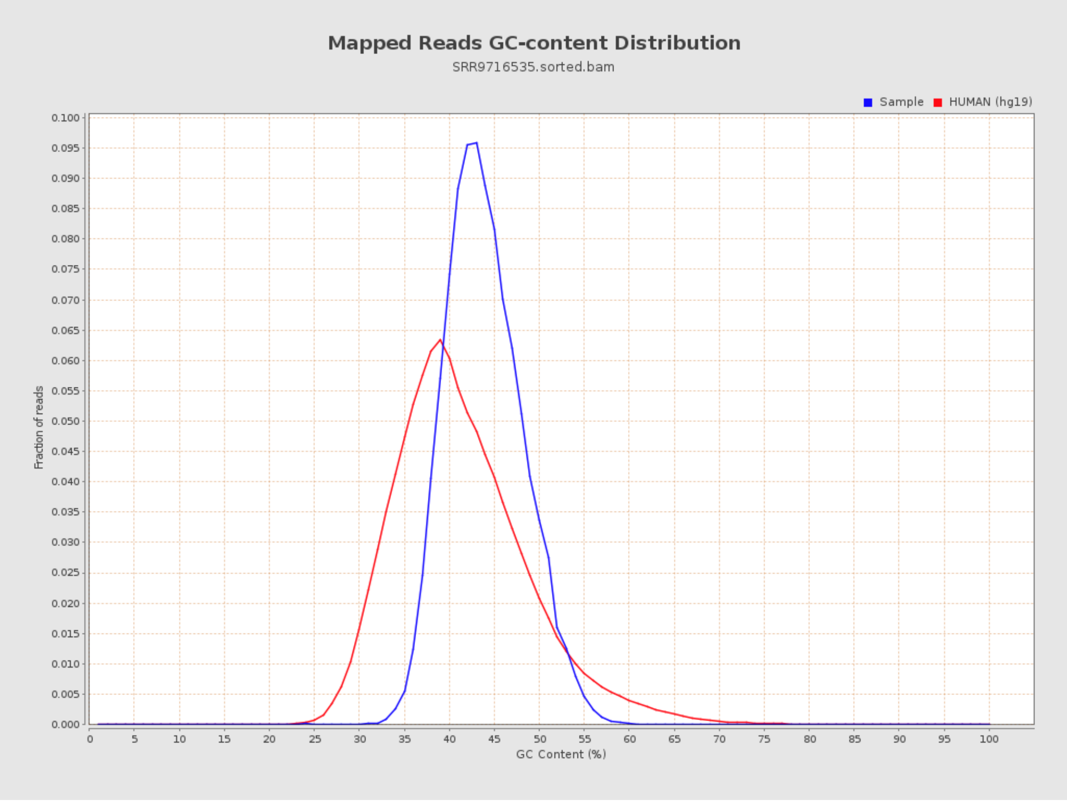
7. Results : Duplication Rate Histogram



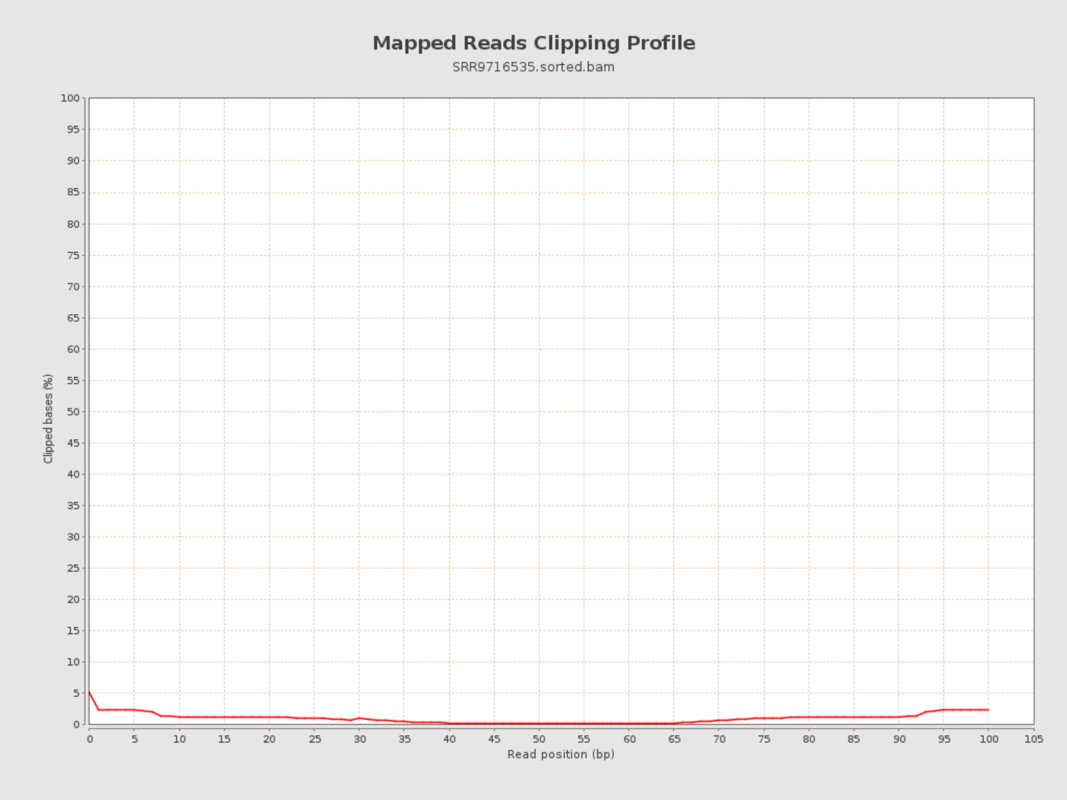
8. Results : Mapped Reads Nucleotide Content



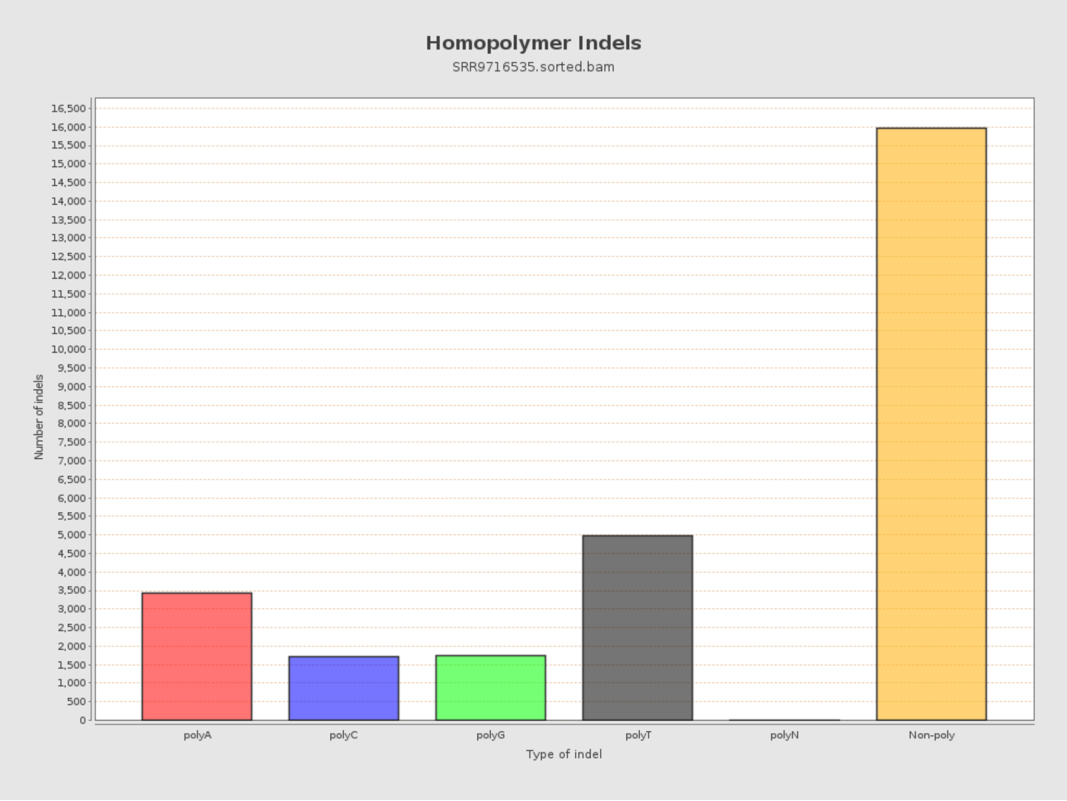
9. Results : Mapped Reads GC-content Distribution



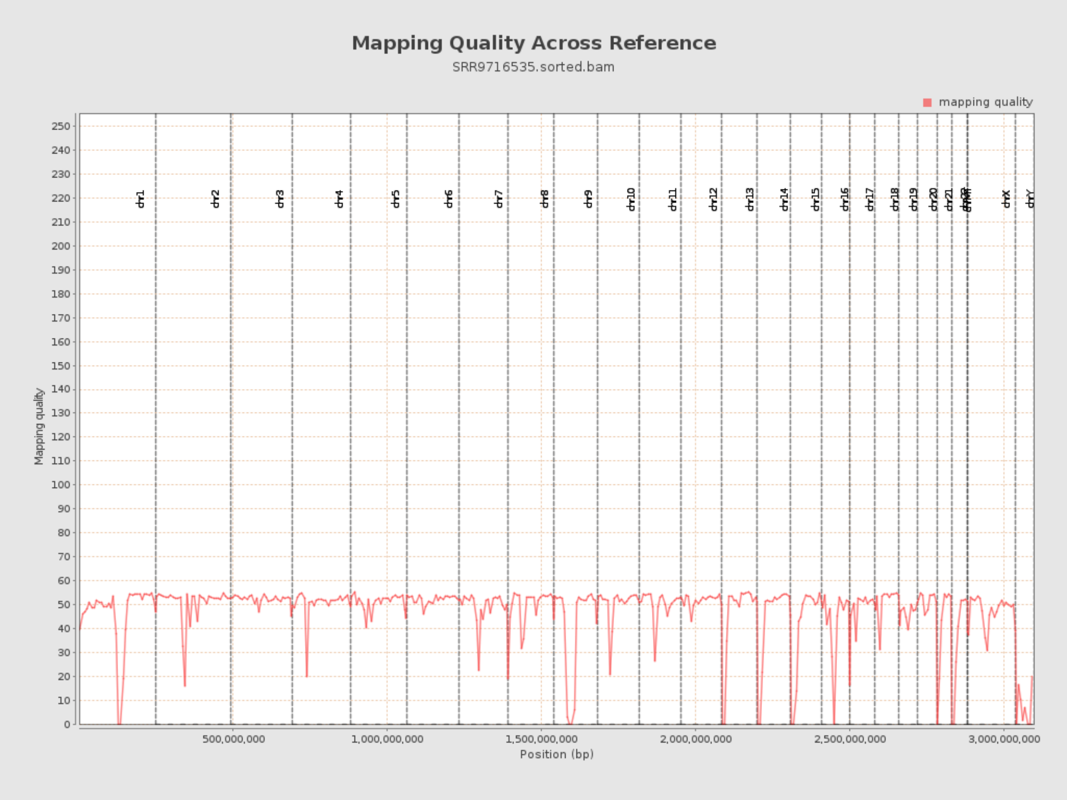
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram