Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 02:03:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716239.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_SRR9716239 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716239.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 02:03:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716239.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,370,124
Mapped reads	1,253,280 / 91.47%
Unmapped reads	116,844 / 8.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,102 / 1.39%
Read min/max/mean length	30 / 101 / 101.51
Duplicated reads (estimated)	47,684 / 3.48%
Duplication rate	2.39%
Clipped reads	1,271,257 / 92.78%

2.2. ACGT Content

Number/percentage of A's	24,466,117 / 24.57%
Number/percentage of C's	18,334,130 / 18.41%
Number/percentage of T's	31,882,905 / 32.02%
Number/percentage of G's	24,898,176 / 25%
Number/percentage of N's	5,960 / 0.01%
GC Percentage	43.41%

2.3. Coverage

Mean	0.0322

Standard Deviation	0.3569

2.4. Mapping Quality

Mean Mapping Quality	45.64

2.5. Mismatches and indels

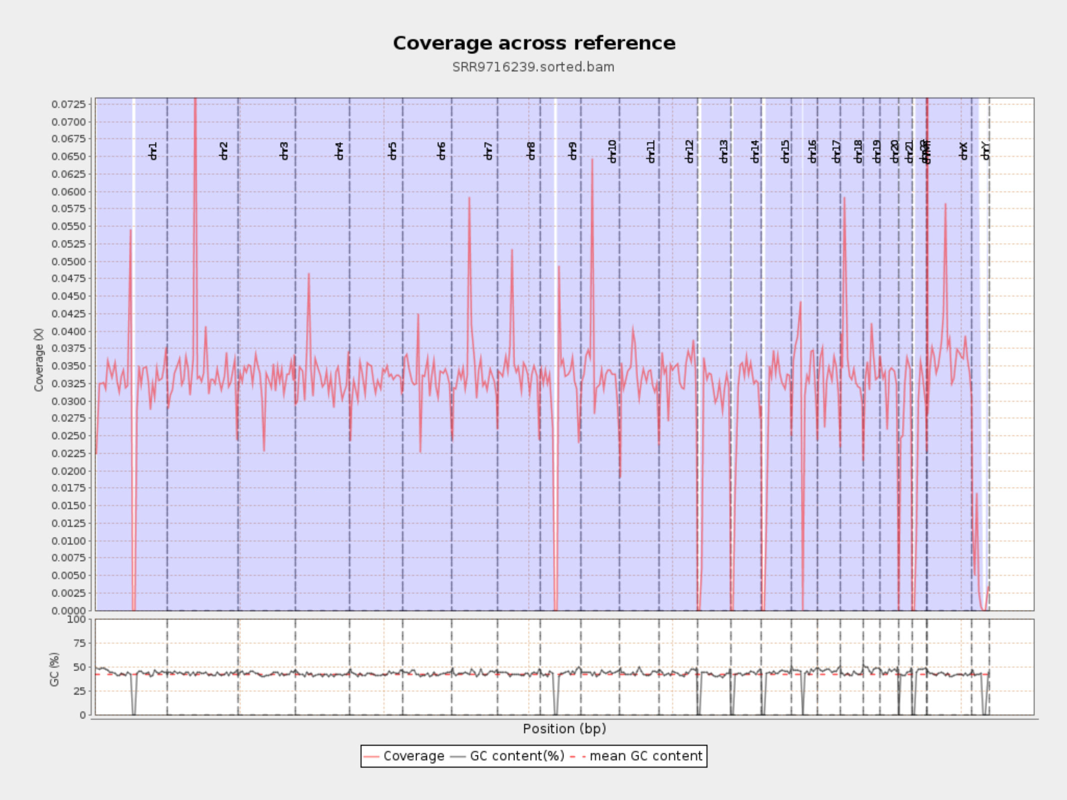
General error rate	0.84%
Mismatches	814,378
Insertions	8,880
Mapped reads with at least one insertion	0.7%
Deletions	24,745
Mapped reads with at least one deletion	1.94%
Homopolymer indels	45.18%

2.6. Chromosome stats

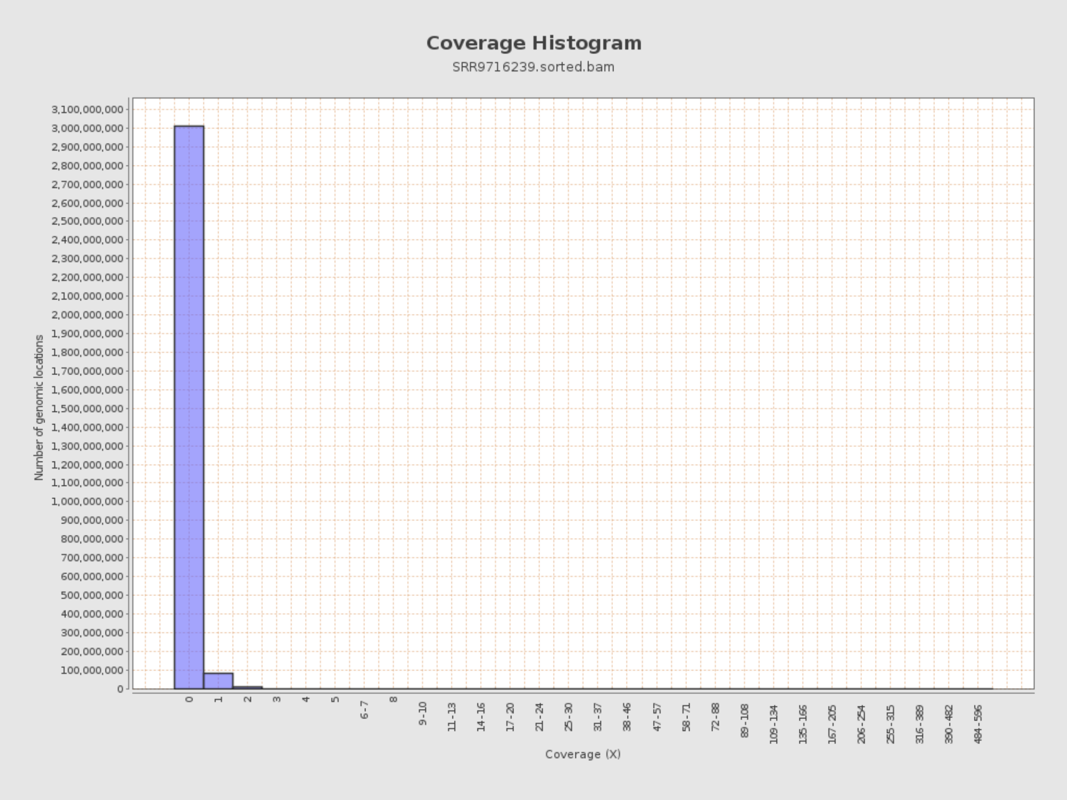
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7835184	0.0314	0.5164
chr2	243199373	8523316	0.035	0.5113
chr3	198022430	6593233	0.0333	0.2025
chr4	191154276	6414168	0.0336	0.2236
chr5	180915260	5996595	0.0331	0.2039
chr6	171115067	5710006	0.0334	0.2427
chr7	159138663	5496389	0.0345	0.4428

chr8	146364022	5093102	0.0348	0.4854
chr9	141213431	4247723	0.0301	0.4031
chr10	135534747	4732000	0.0349	0.3635
chr11	135006516	4529416	0.0335	0.3483
chr12	133851895	4551790	0.034	0.2066
chr13	115169878	3093807	0.0269	0.1789
chr14	107349540	3001147	0.028	0.2407
chr15	102531392	2833315	0.0276	0.1854
chr16	90354753	2899152	0.0321	0.2311
chr17	81195210	2688994	0.0331	0.2272
chr18	78077248	2822109	0.0361	0.7866
chr19	59128983	2030610	0.0343	0.4068
chr20	63025520	2033978	0.0323	0.2085
chr21	48129895	1313209	0.0273	0.1972
chr22	51304566	1128615	0.022	0.1629
chrMT	16571	6765	0.4082	0.6992
chrX	155270560	5774813	0.0372	0.2838
chrY	59373566	281523	0.0047	0.1512

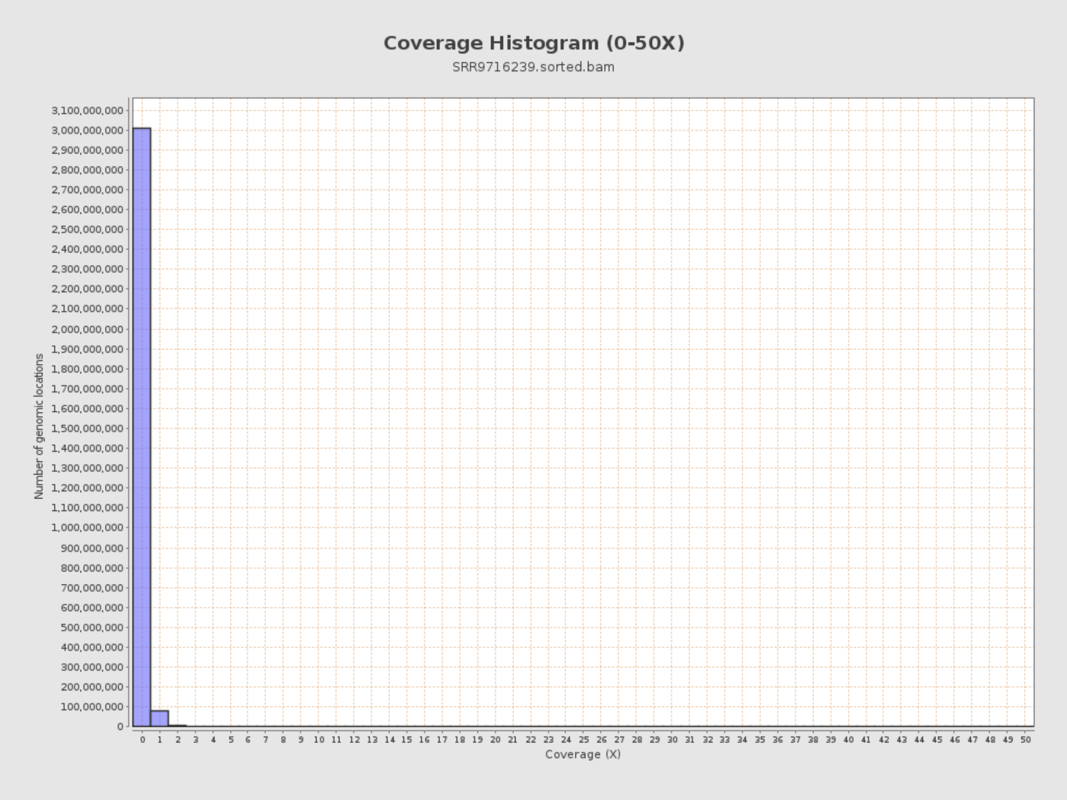
3. Results : Coverage across reference



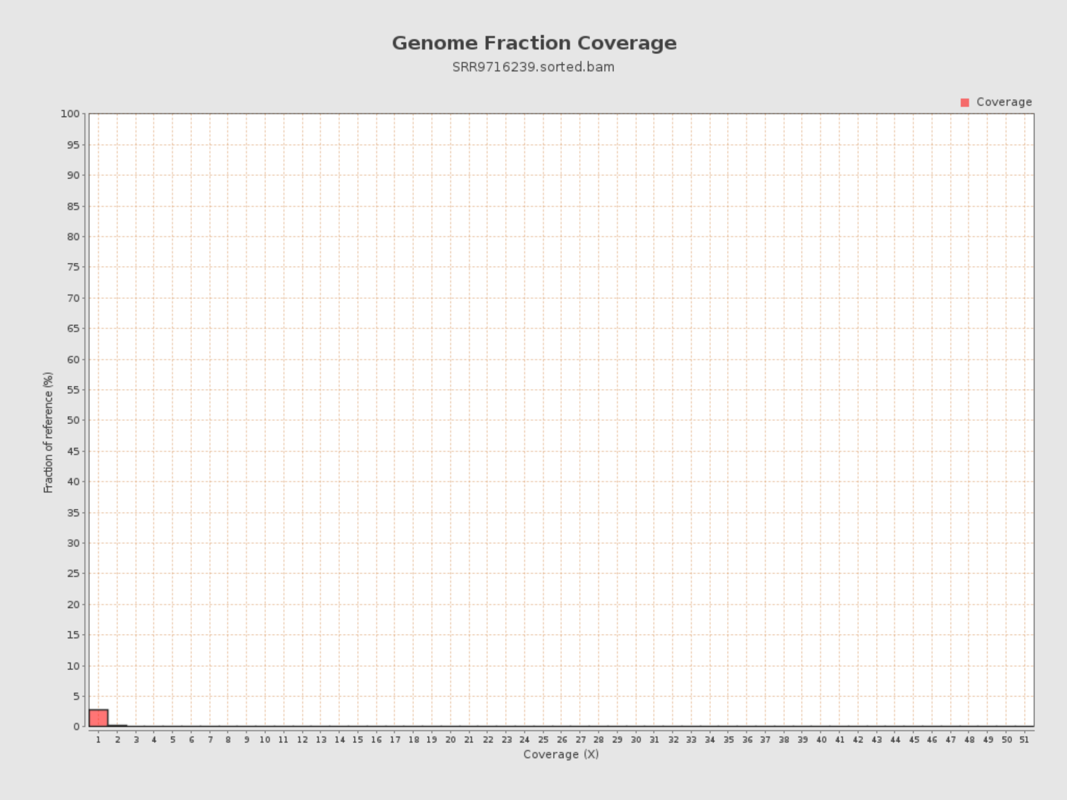
4. Results : Coverage Histogram



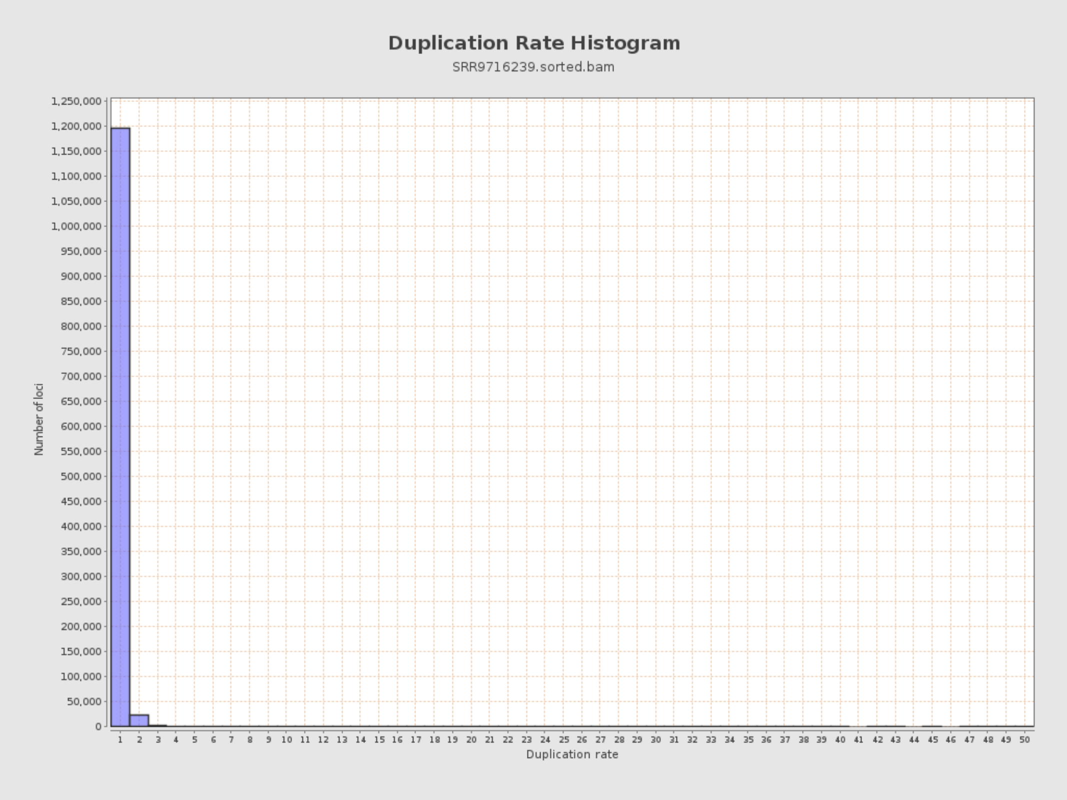
5. Results : Coverage Histogram (0-50X)



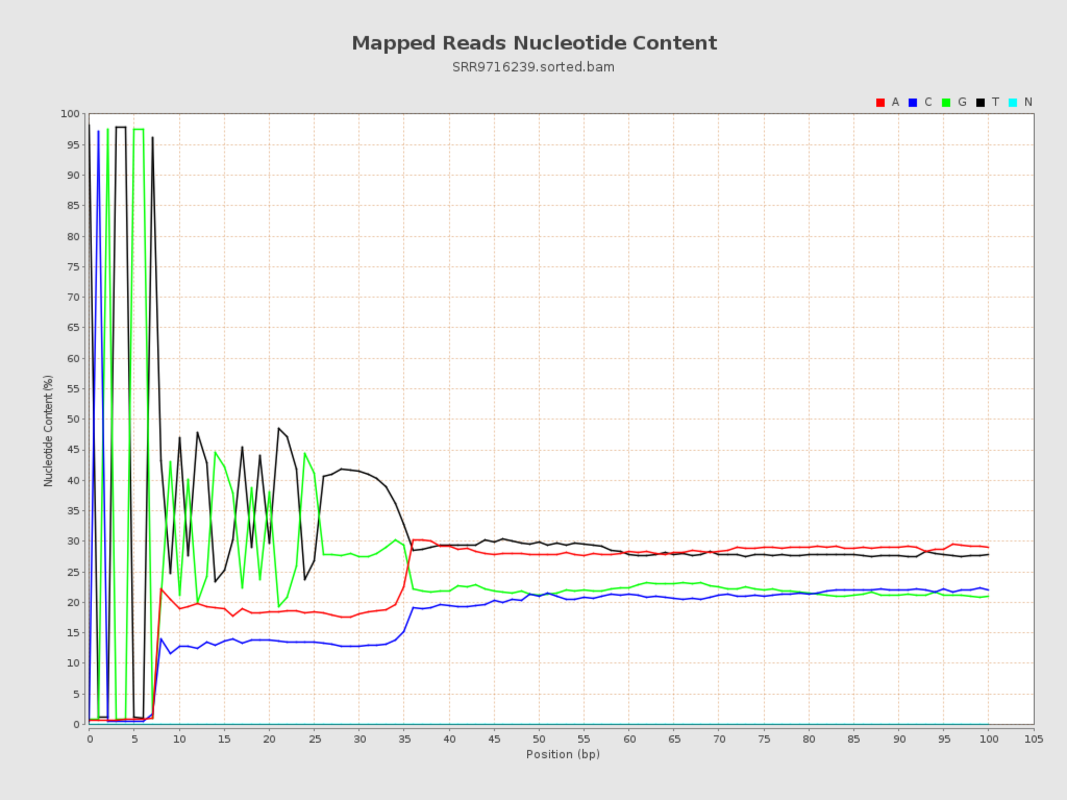
6. Results : Genome Fraction Coverage



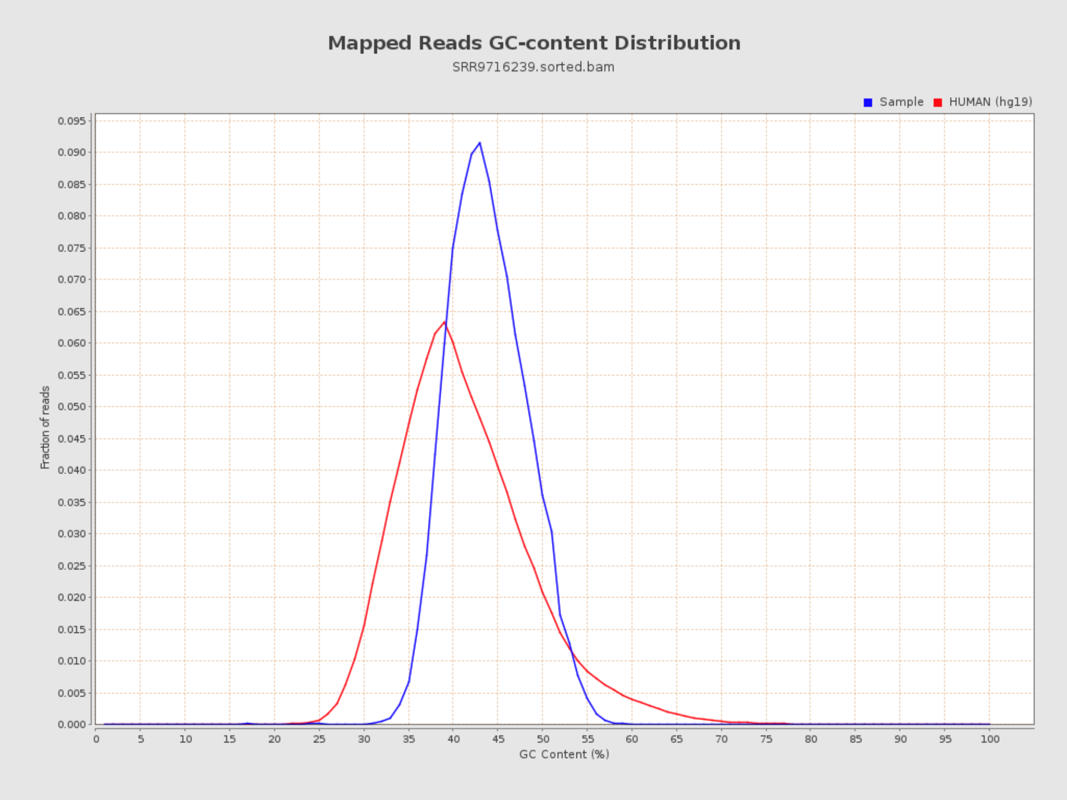
7. Results : Duplication Rate Histogram



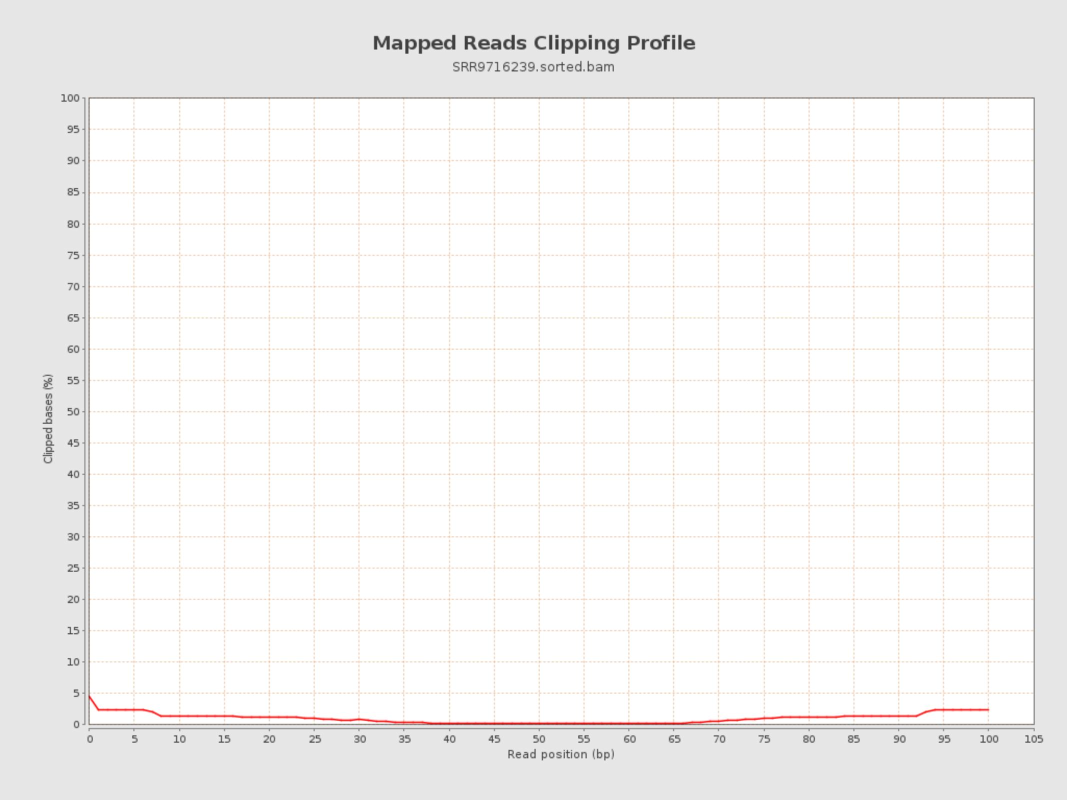
8. Results : Mapped Reads Nucleotide Content



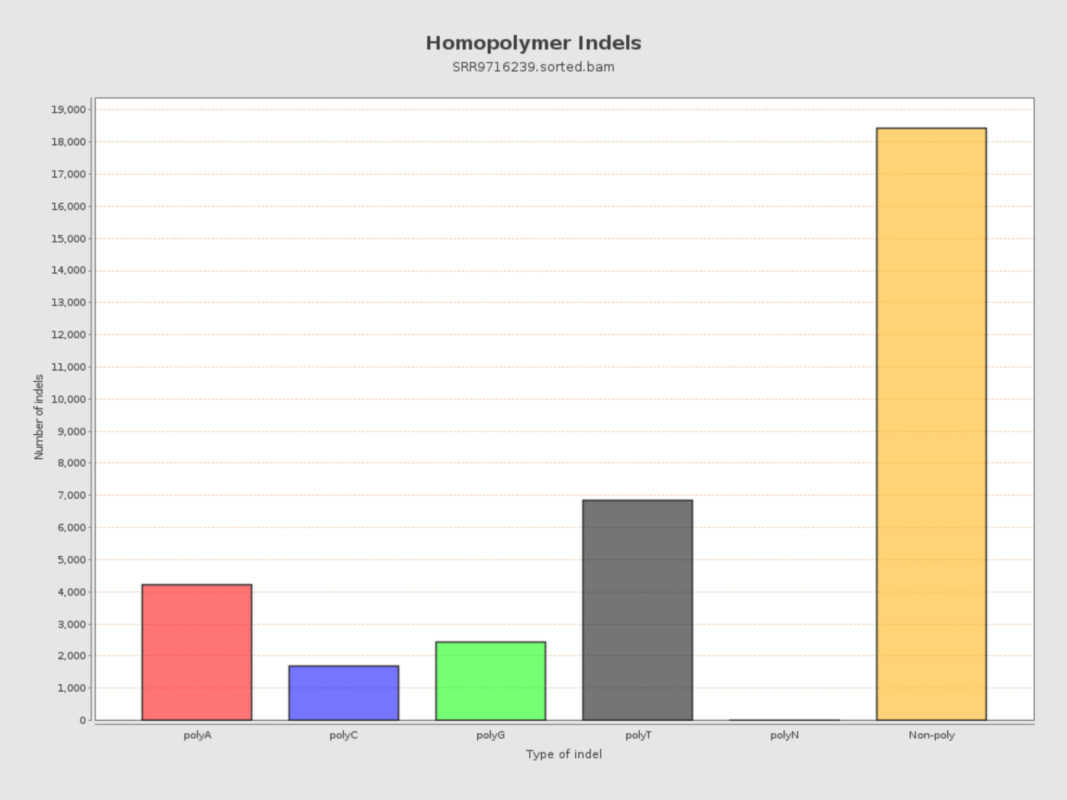
9. Results : Mapped Reads GC-content Distribution



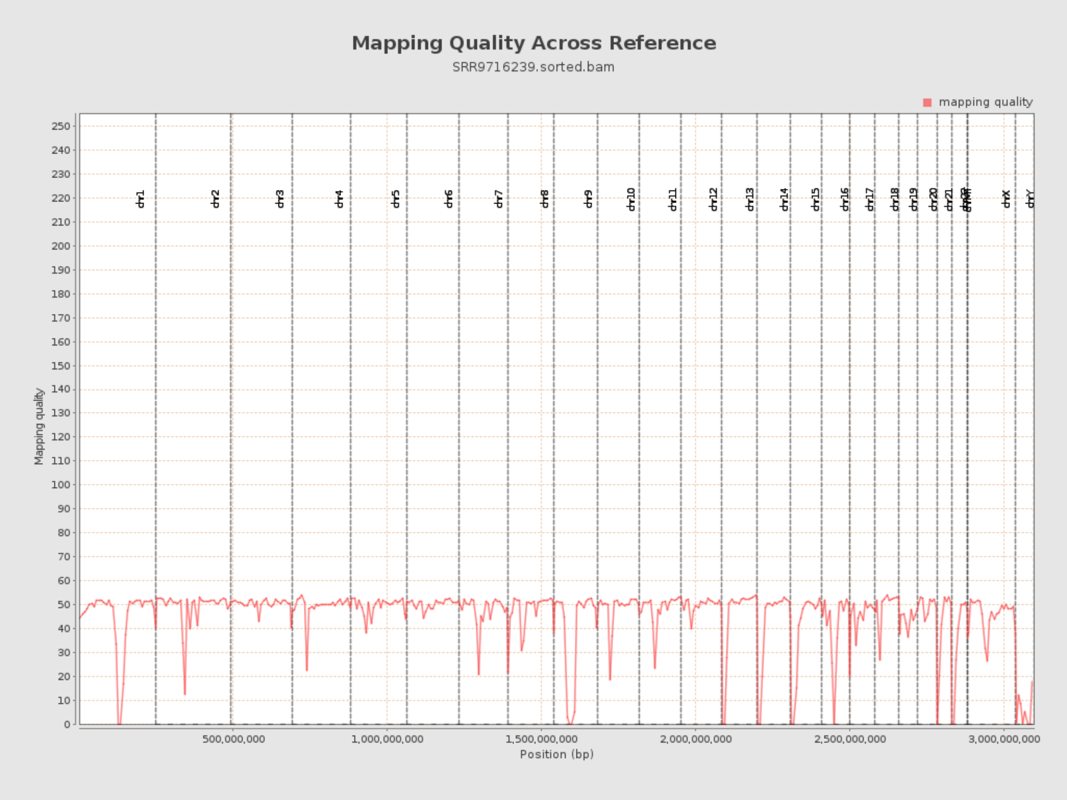
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram