Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 08:13:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716338.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_SRR9716338 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716338.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 08:13:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716338.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,679,452
Mapped reads	1,507,246 / 89.75%
Unmapped reads	172,206 / 10.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,464 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	51,071 / 3.04%
Duplication rate	2.46%
Clipped reads	1,509,285 / 89.87%

2.2. ACGT Content

Number/percentage of A's	21,024,162 / 24.39%
Number/percentage of C's	17,429,032 / 20.22%
Number/percentage of T's	27,412,284 / 31.8%
Number/percentage of G's	20,324,634 / 23.58%
Number/percentage of N's	1,331 / 0%
GC Percentage	43.8%

2.3. Coverage

Mean	0.0279

Standard Deviation	0.2681

2.4. Mapping Quality

Mean Mapping Quality	44.18

2.5. Mismatches and indels

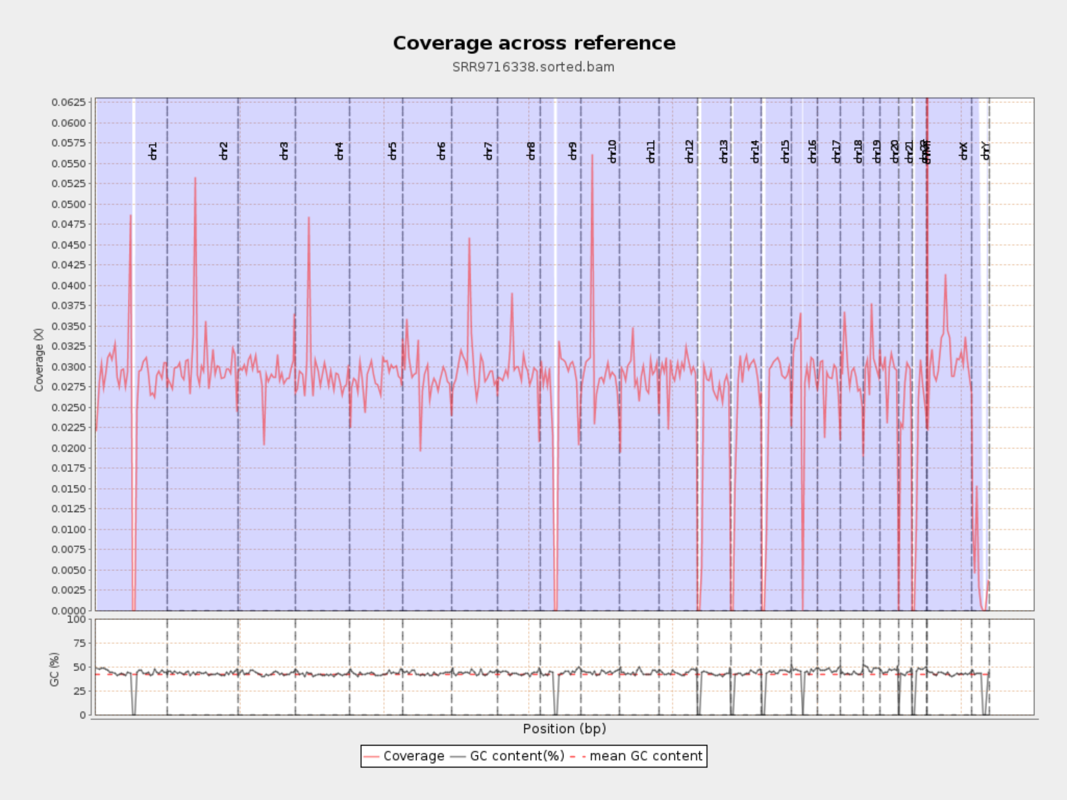
General error rate	0.56%
Mismatches	474,220
Insertions	6,073
Mapped reads with at least one insertion	0.4%
Deletions	15,471
Mapped reads with at least one deletion	1.02%
Homopolymer indels	42.26%

2.6. Chromosome stats

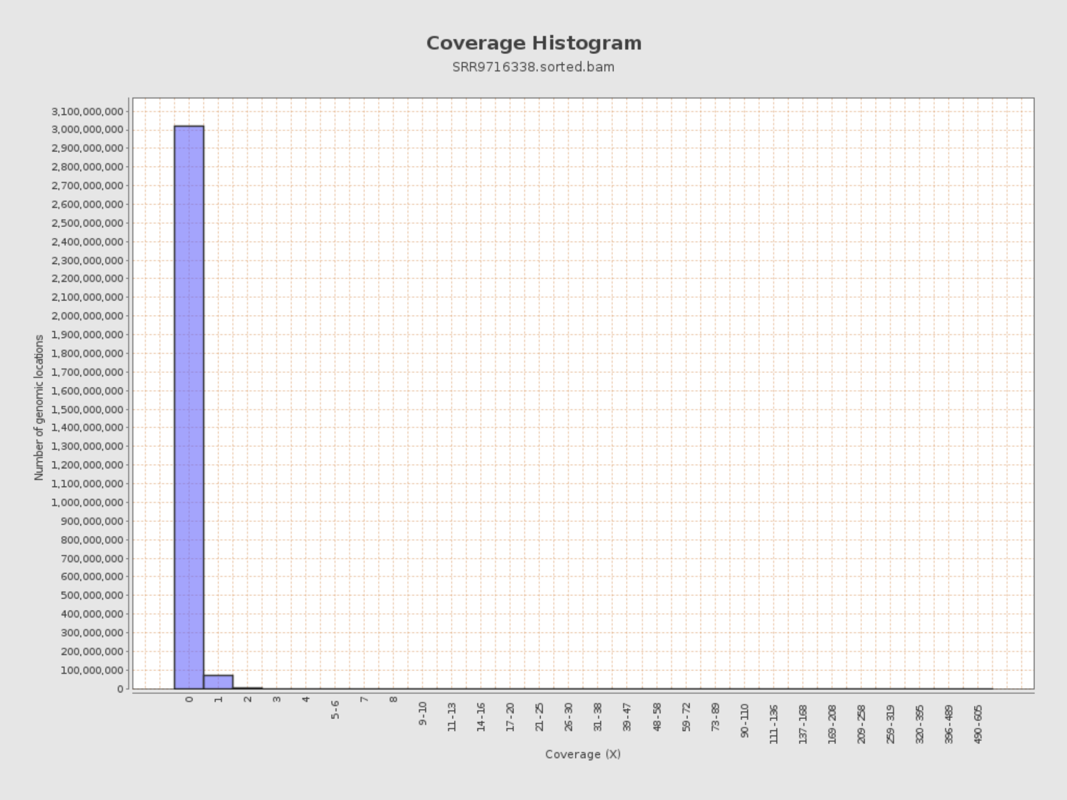
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6905436	0.0277	0.494
chr2	243199373	7393580	0.0304	0.2921
chr3	198022430	5771003	0.0291	0.1845
chr4	191154276	5616511	0.0294	0.2057
chr5	180915260	5223019	0.0289	0.1838
chr6	171115067	4927453	0.0288	0.2012
chr7	159138663	4806821	0.0302	0.3045

chr8	146364022	4321757	0.0295	0.2762
chr9	141213431	3621622	0.0256	0.2598
chr10	135534747	4062392	0.03	0.2818
chr11	135006516	3919960	0.029	0.2451
chr12	133851895	3928990	0.0294	0.1903
chr13	115169878	2662856	0.0231	0.1624
chr14	107349540	2654401	0.0247	0.185
chr15	102531392	2464010	0.024	0.1669
chr16	90354753	2526373	0.028	0.1999
chr17	81195210	2275405	0.028	0.1957
chr18	78077248	2293994	0.0294	0.453
chr19	59128983	1783077	0.0302	0.3691
chr20	63025520	1817878	0.0288	0.1883
chr21	48129895	1153152	0.024	0.1916
chr22	51304566	972045	0.0189	0.1465
chrMT	16571	10772	0.6501	0.8619
chrX	155270560	4838807	0.0312	0.2198
chrY	59373566	266013	0.0045	0.1153

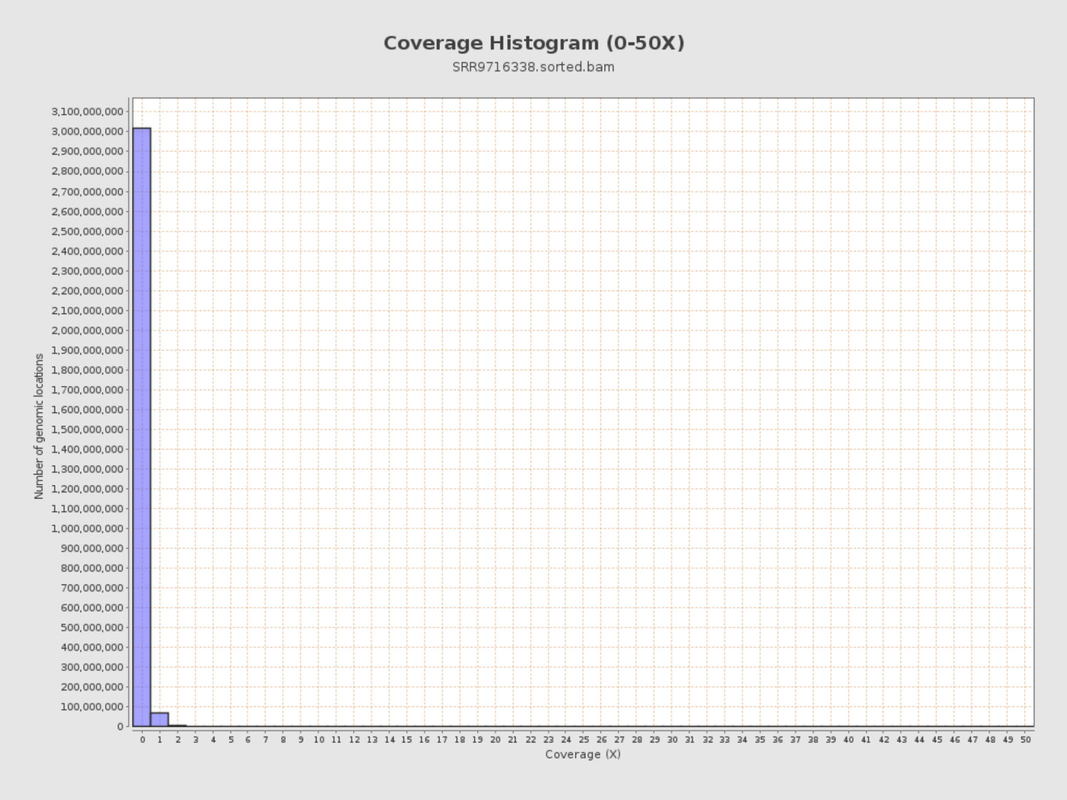
3. Results : Coverage across reference



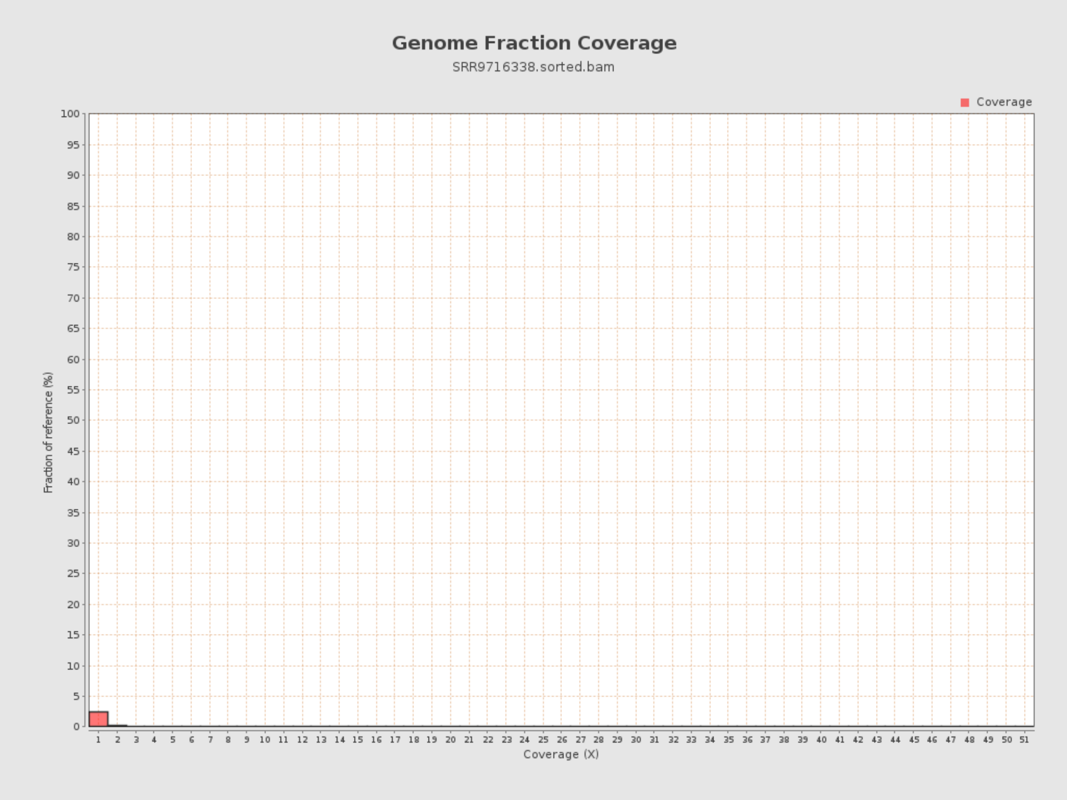
4. Results : Coverage Histogram



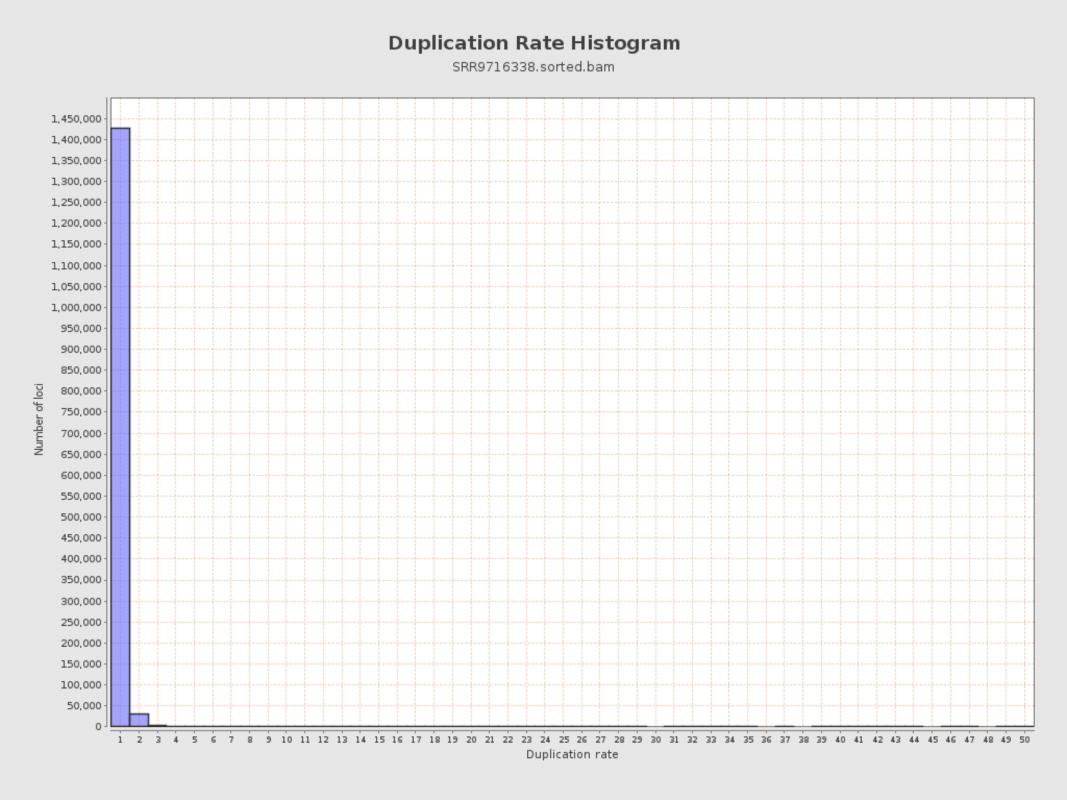
5. Results : Coverage Histogram (0-50X)



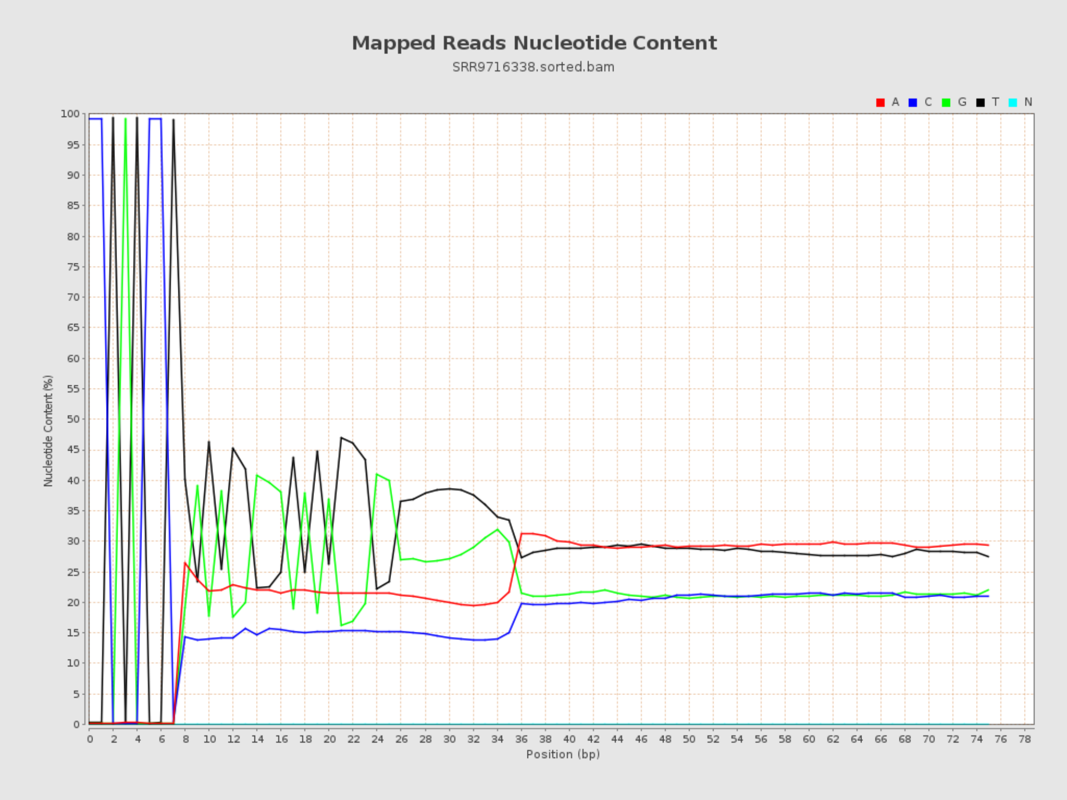
6. Results : Genome Fraction Coverage



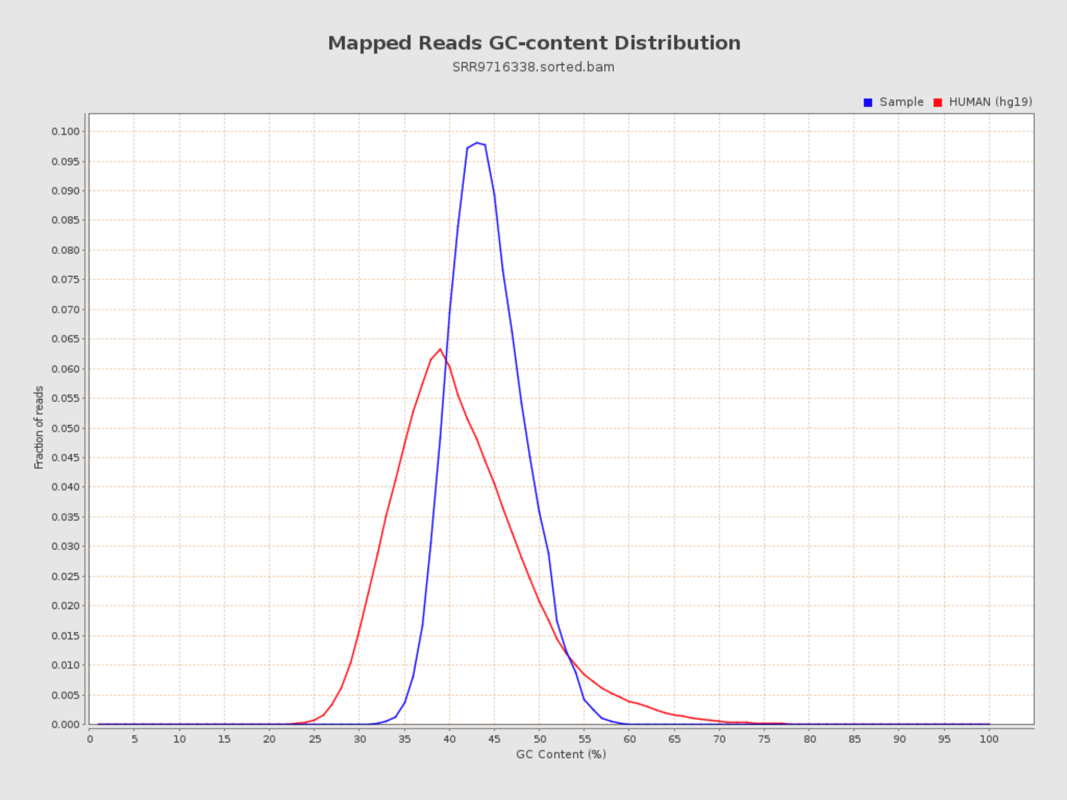
7. Results : Duplication Rate Histogram



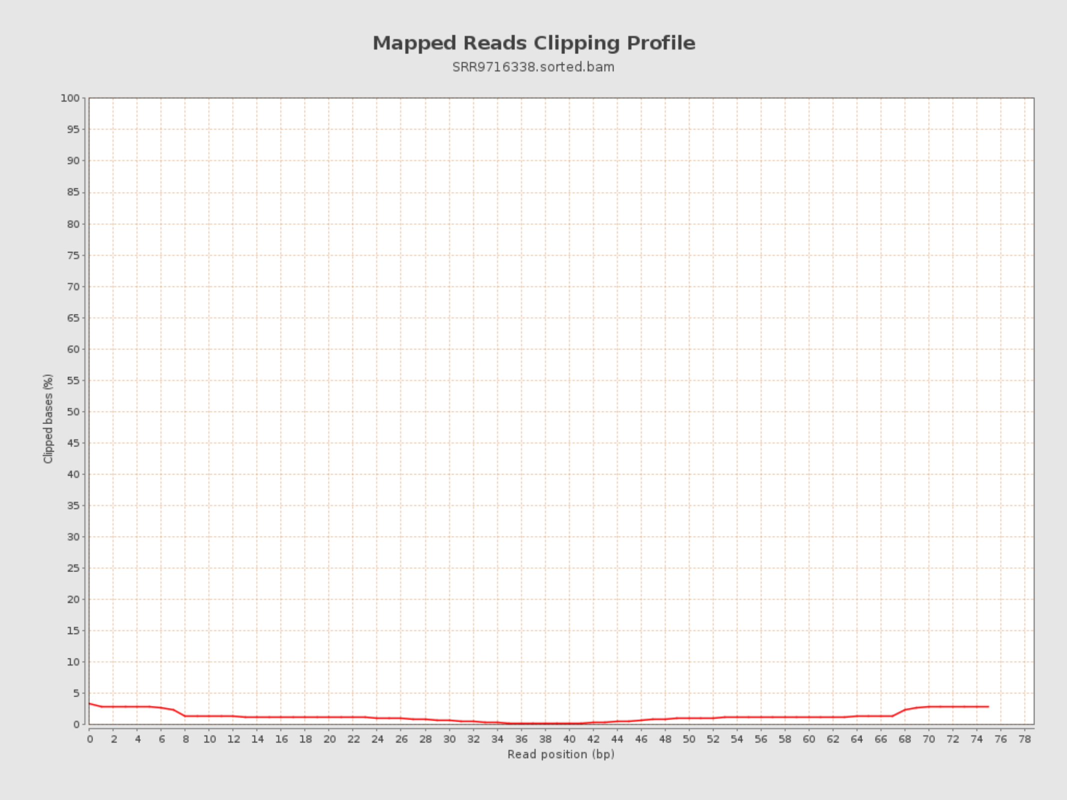
8. Results : Mapped Reads Nucleotide Content



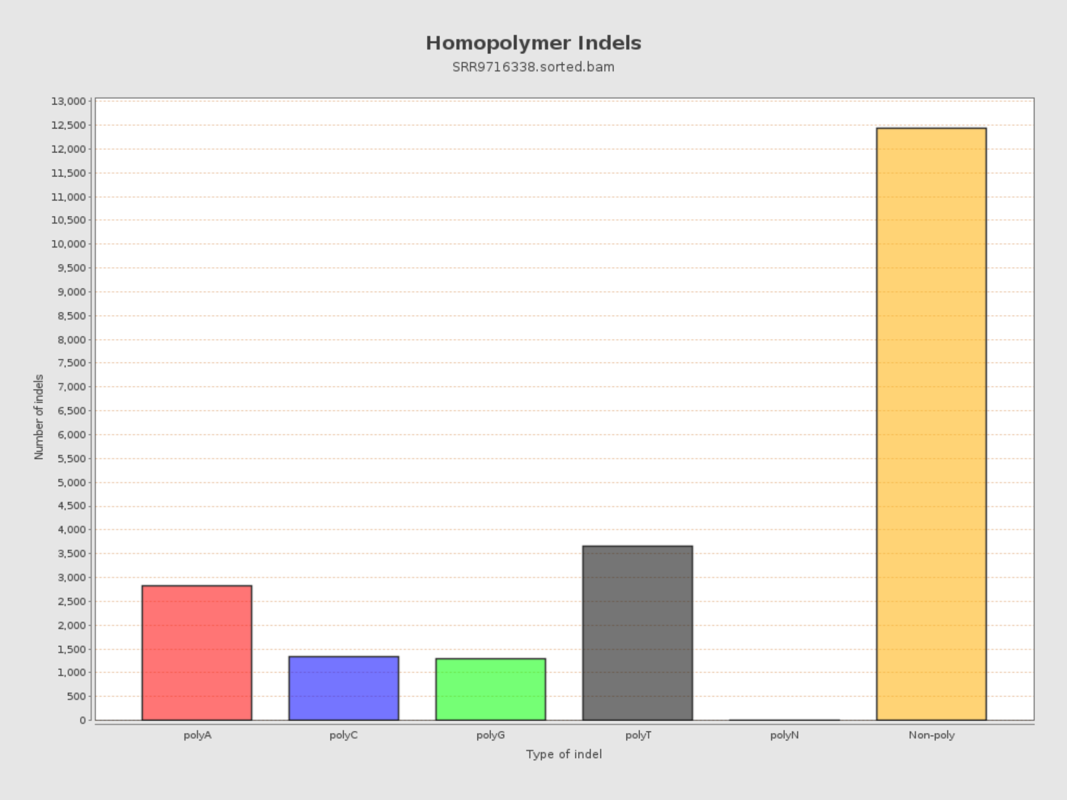
9. Results : Mapped Reads GC-content Distribution



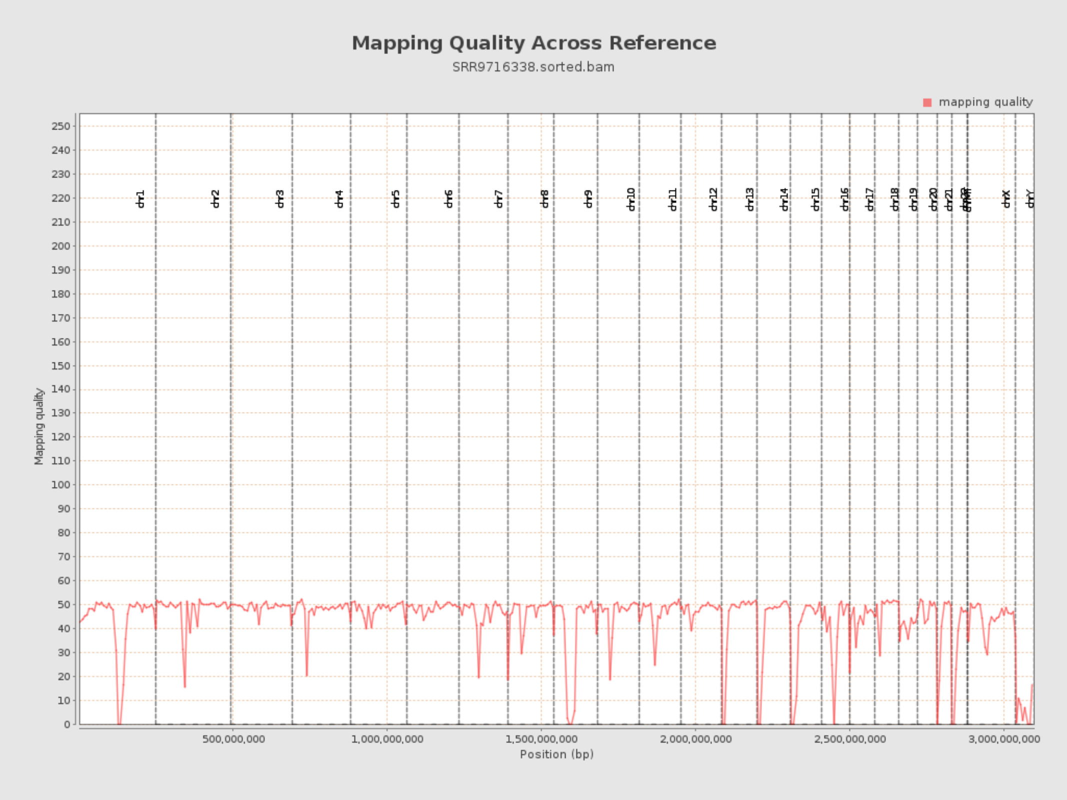
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram