Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 19:27:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716538.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_SRR9716538 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716538.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 19:27:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716538.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	436,039
Mapped reads	399,983 / 91.73%
Unmapped reads	36,056 / 8.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,593 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	7,797 / 1.79%
Duplication rate	1.54%
Clipped reads	400,394 / 91.83%

2.2. ACGT Content

Number/percentage of A's	5,984,953 / 25.79%
Number/percentage of C's	4,733,505 / 20.4%
Number/percentage of T's	7,064,352 / 30.44%
Number/percentage of G's	5,421,843 / 23.36%
Number/percentage of N's	693 / 0%
GC Percentage	43.76%

2.3. Coverage

Mean	0.0075

Standard Deviation	0.1031

2.4. Mapping Quality

Mean Mapping Quality	45.24

2.5. Mismatches and indels

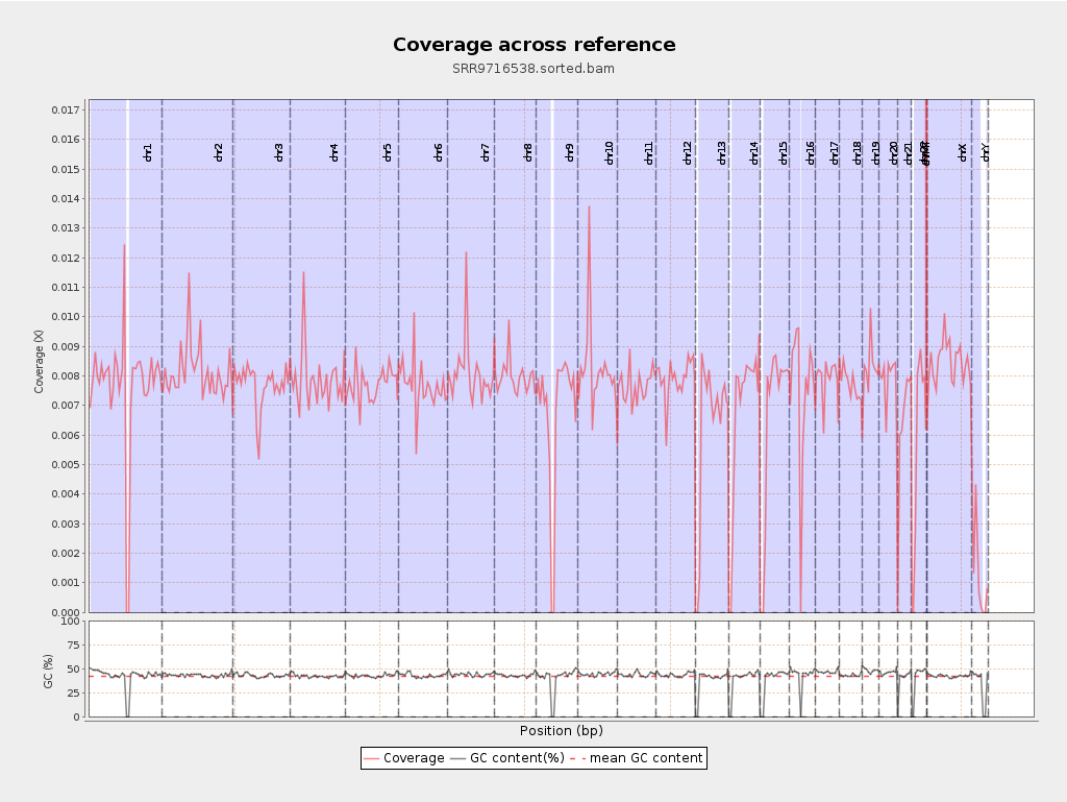
General error rate	0.52%
Mismatches	117,517
Insertions	1,852
Mapped reads with at least one insertion	0.46%
Deletions	4,480
Mapped reads with at least one deletion	1.11%
Homopolymer indels	41.17%

2.6. Chromosome stats

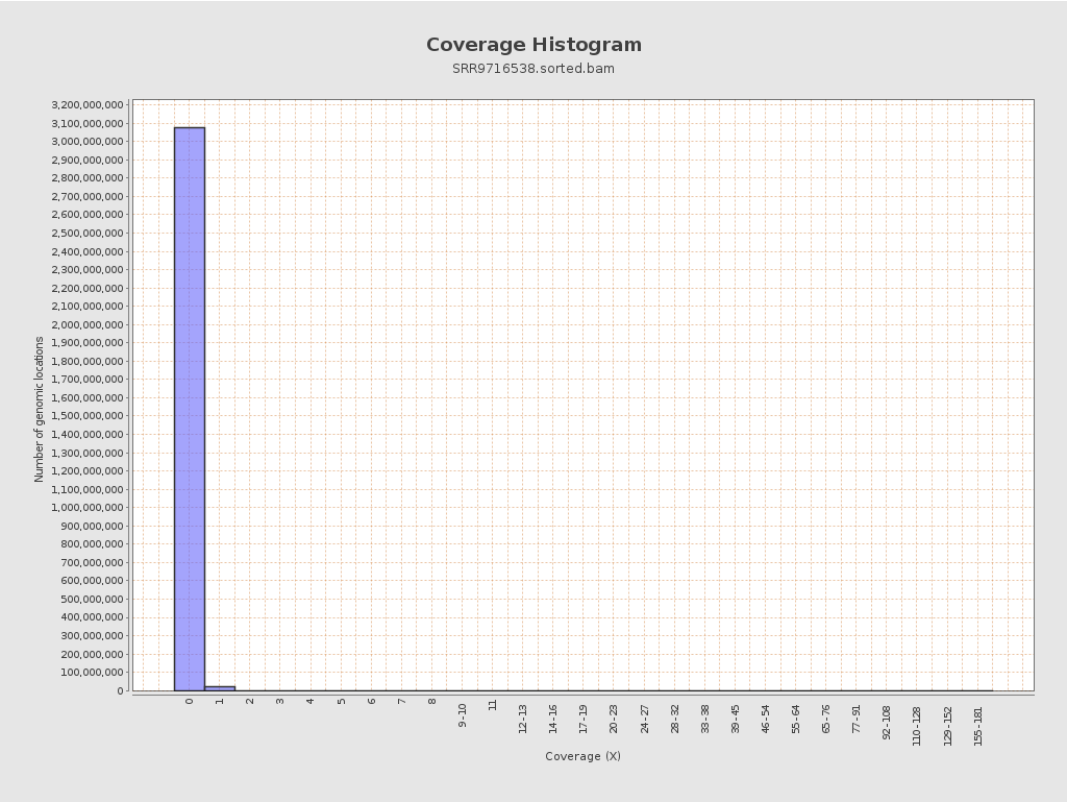
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1898300	0.0076	0.1511
chr2	243199373	1984072	0.0082	0.1212
chr3	198022430	1521440	0.0077	0.0904
chr4	191154276	1499160	0.0078	0.0934
chr5	180915260	1395423	0.0077	0.0906
chr6	171115067	1314354	0.0077	0.0952
chr7	159138663	1286978	0.0081	0.1137

chr8	146364022	1164169	0.008	0.1021
chr9	141213431	948268	0.0067	0.0905
chr10	135534747	1114258	0.0082	0.1044
chr11	135006516	1030761	0.0076	0.0977
chr12	133851895	1058502	0.0079	0.0919
chr13	115169878	715635	0.0062	0.0812
chr14	107349540	712030	0.0066	0.0845
chr15	102531392	671796	0.0066	0.0835
chr16	90354753	678355	0.0075	0.0909
chr17	81195210	639164	0.0079	0.0921
chr18	78077248	606921	0.0078	0.1281
chr19	59128983	491470	0.0083	0.1241
chr20	63025520	497045	0.0079	0.0927
chr21	48129895	307957	0.0064	0.084
chr22	51304566	286674	0.0056	0.0771
chrMT	16571	7590	0.458	0.6968
chrX	155270560	1308246	0.0084	0.0974
chrY	59373566	73829	0.0012	0.047

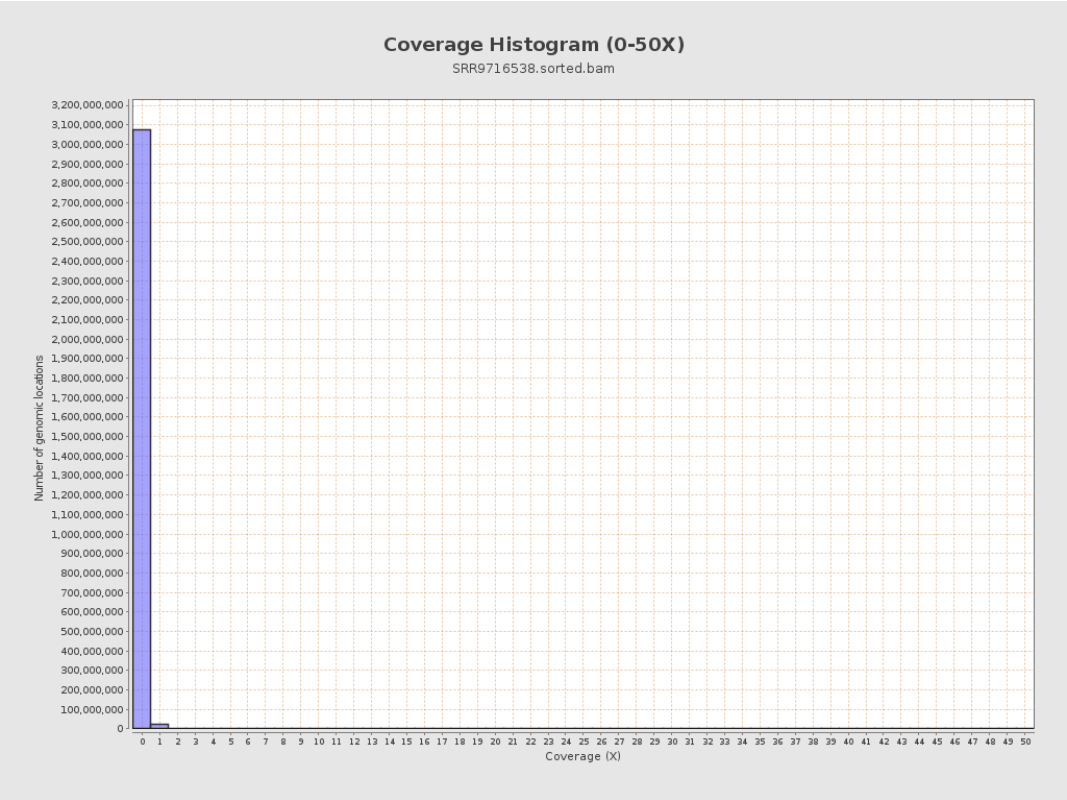
3. Results : Coverage across reference



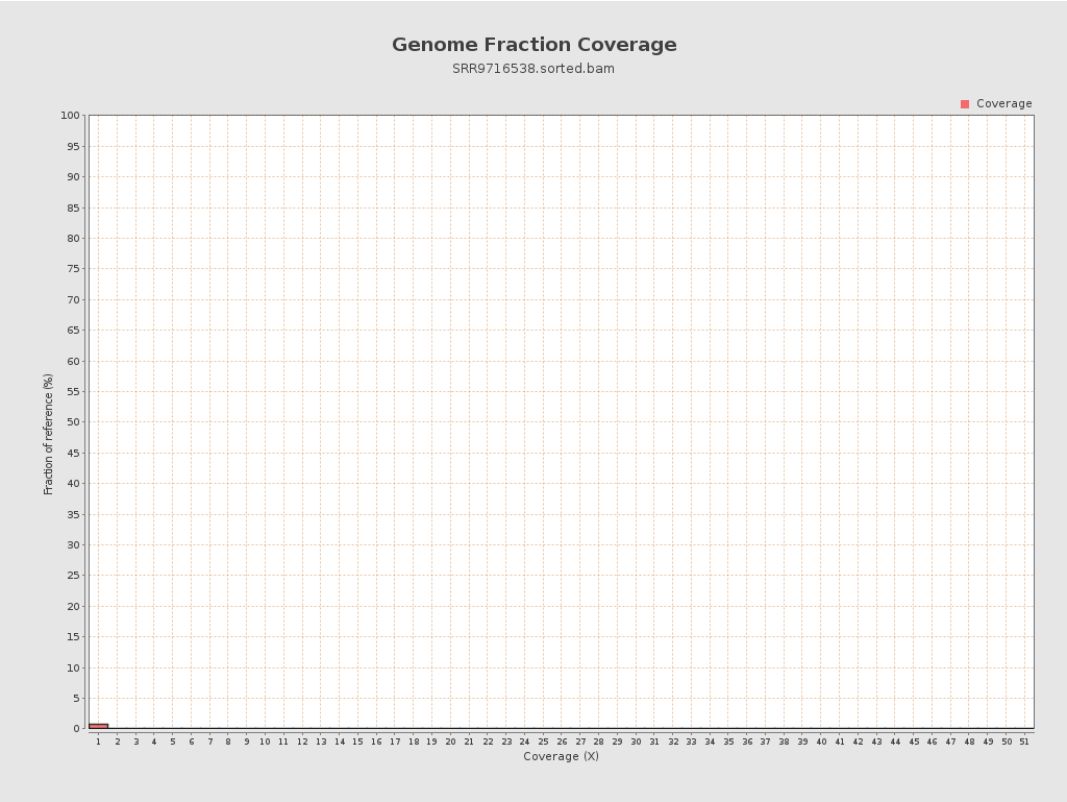
4. Results : Coverage Histogram



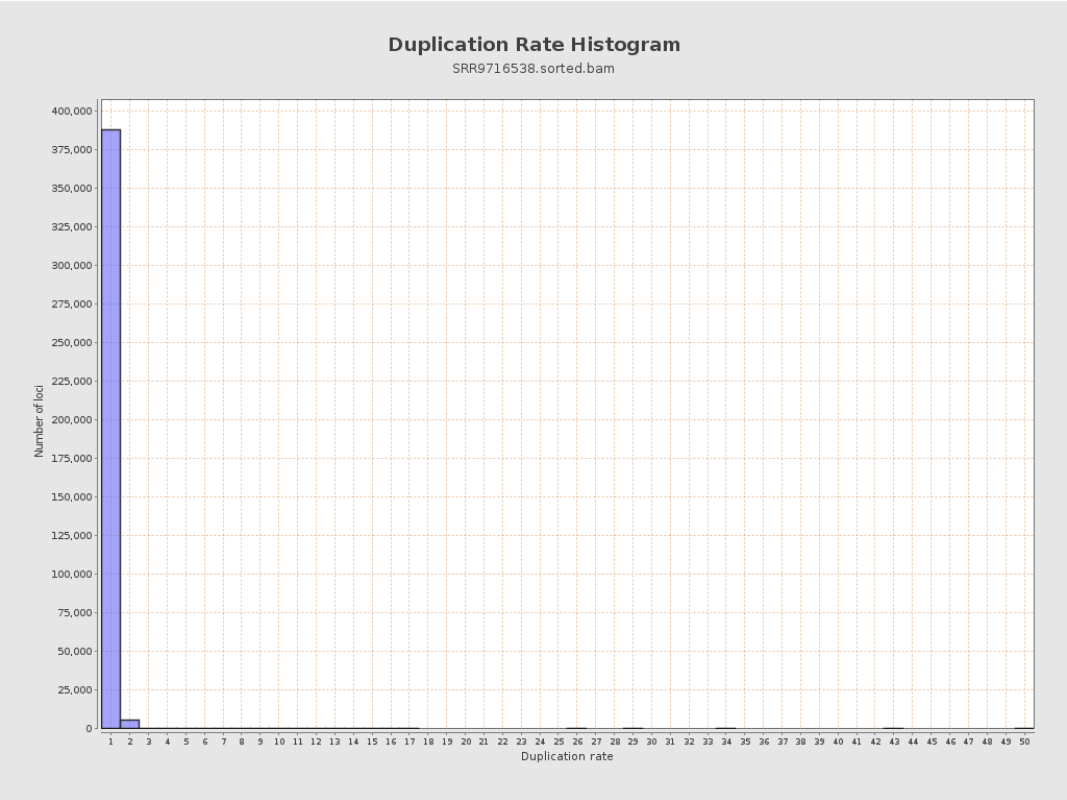
5. Results : Coverage Histogram (0-50X)



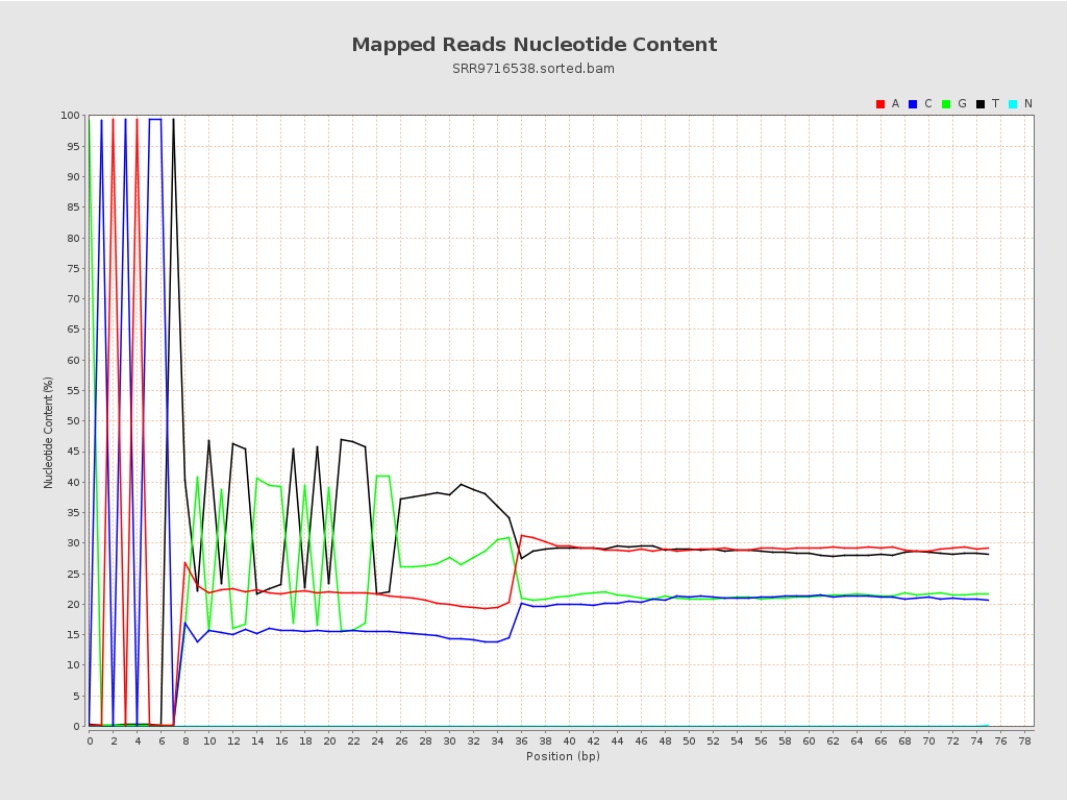
6. Results : Genome Fraction Coverage



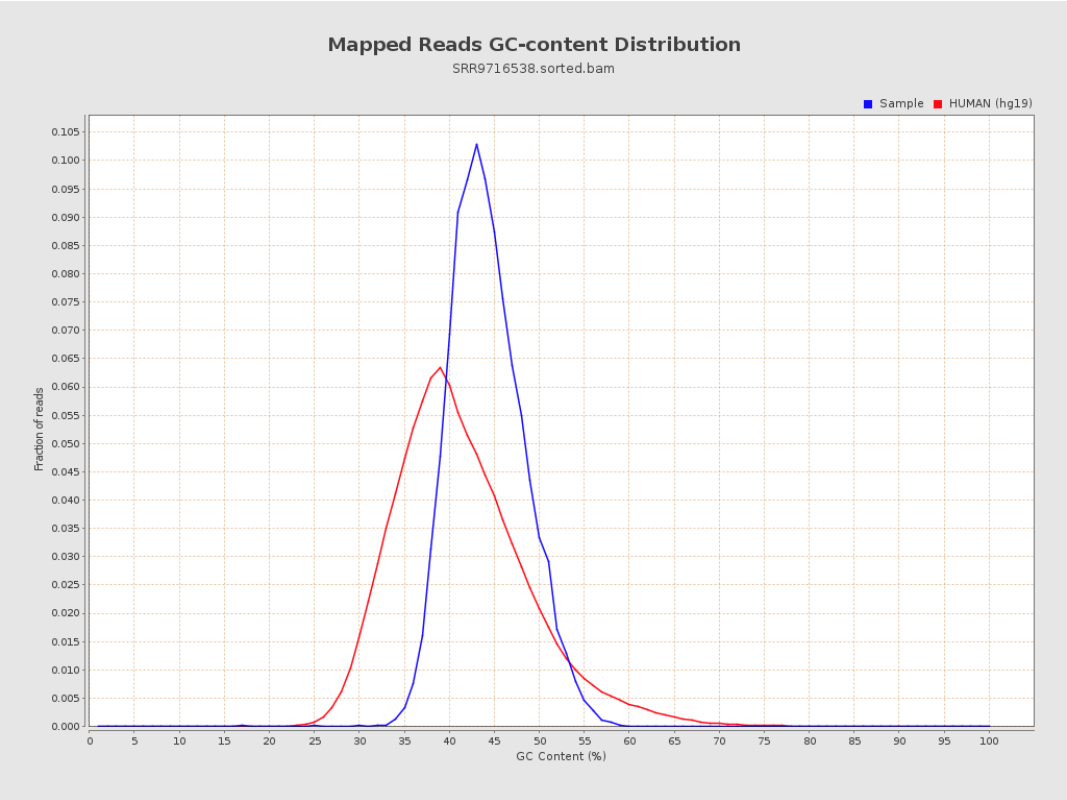
7. Results : Duplication Rate Histogram



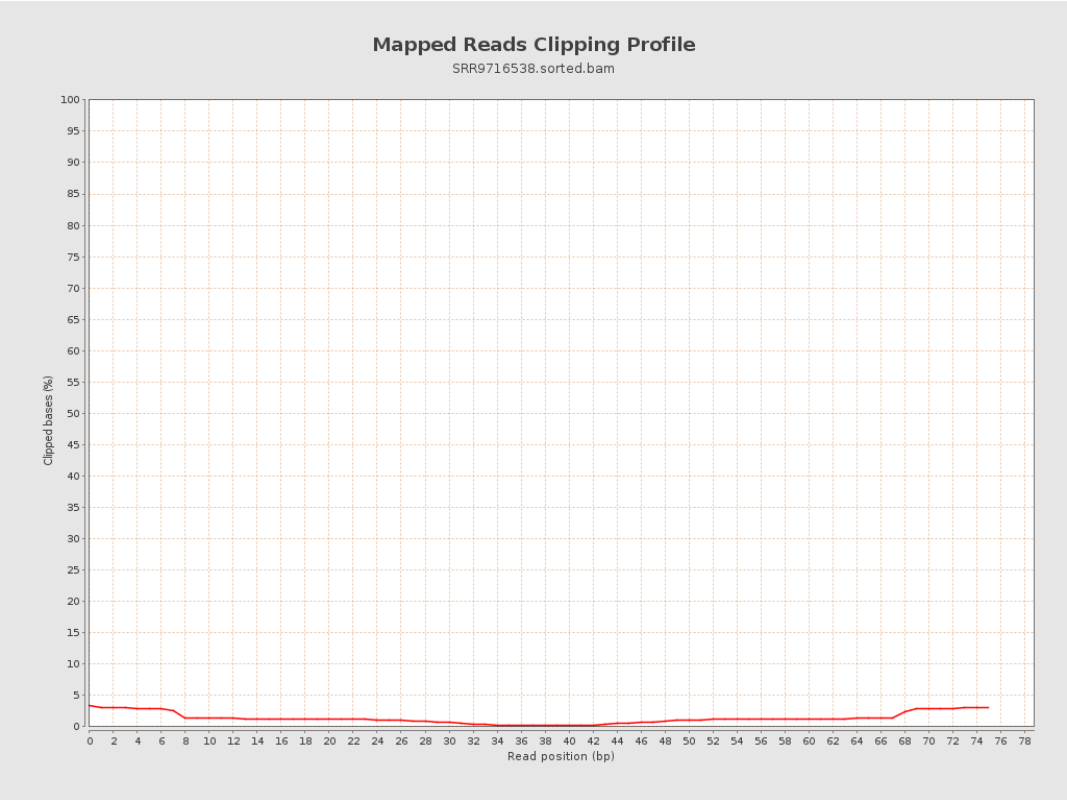
8. Results : Mapped Reads Nucleotide Content



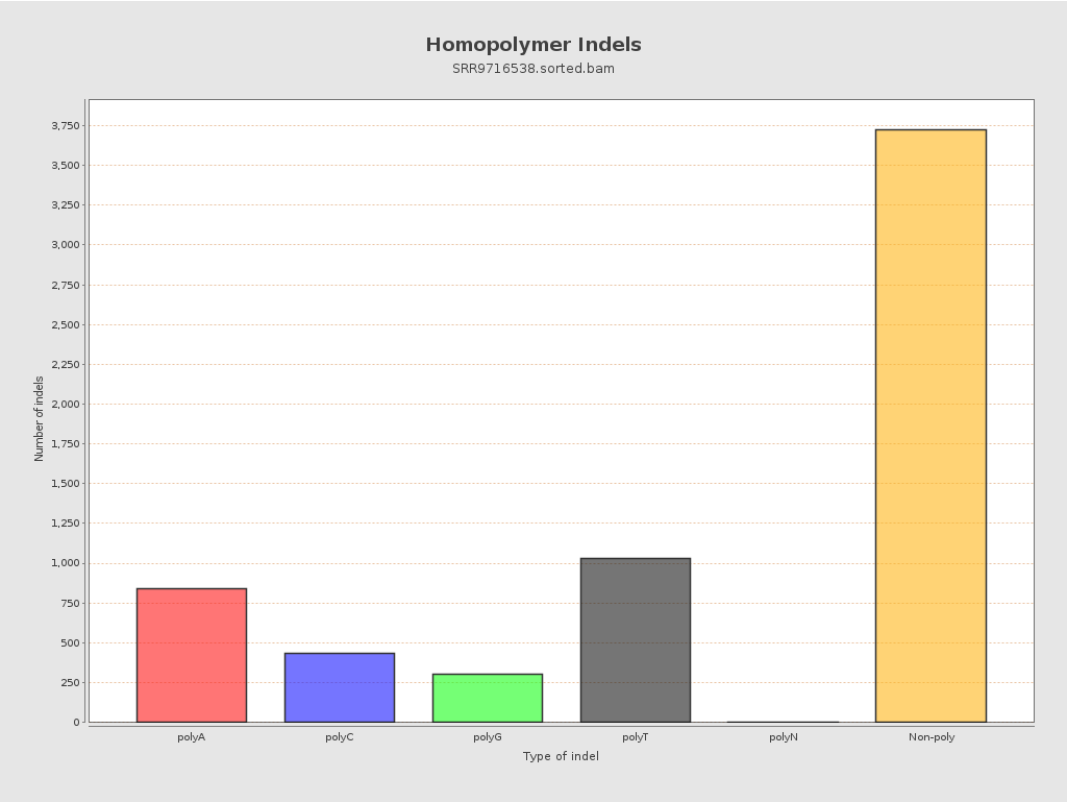
9. Results : Mapped Reads GC-content Distribution



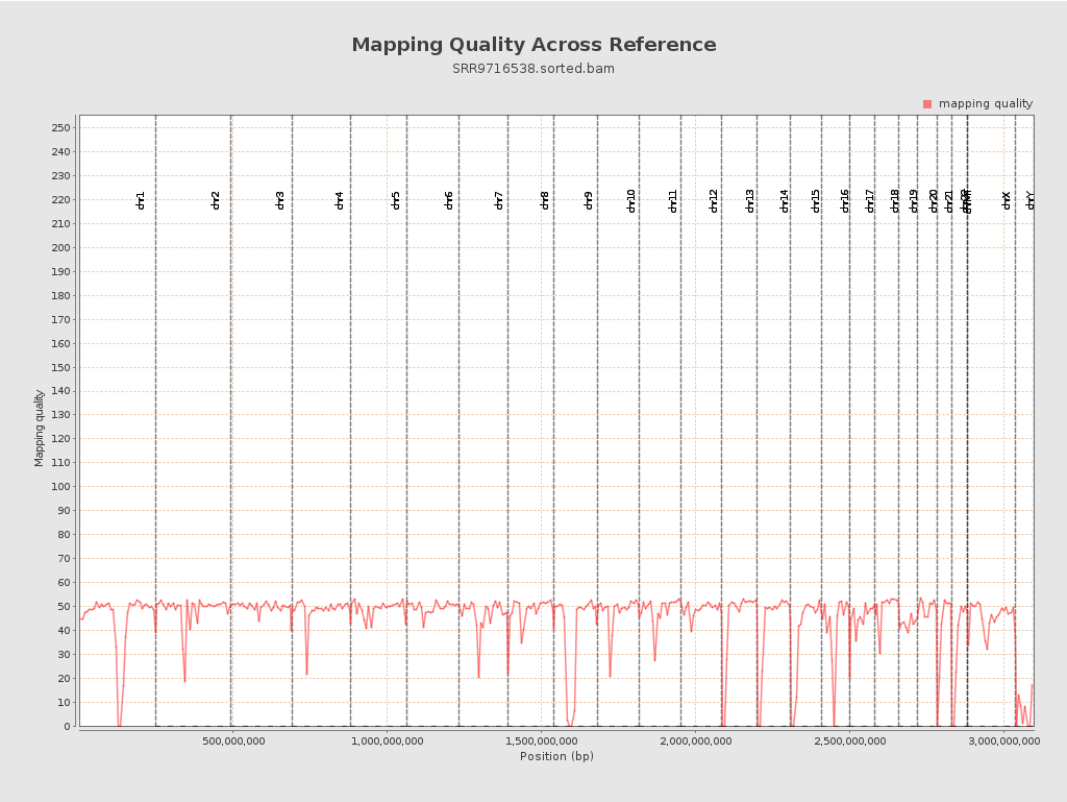
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram