Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 01:43:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716232.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_SRR9716232 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716232.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 01:43:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716232.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	558,577
Mapped reads	488,440 / 87.44%
Unmapped reads	70,137 / 12.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,736 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	13,106 / 2.35%
Duplication rate	1.99%
Clipped reads	488,923 / 87.53%

2.2. ACGT Content

Number/percentage of A's	7,254,929 / 25.87%
Number/percentage of C's	4,948,915 / 17.65%
Number/percentage of T's	8,872,142 / 31.64%
Number/percentage of G's	6,962,897 / 24.83%
Number/percentage of N's	590 / 0%
GC Percentage	42.48%

2.3. Coverage

Mean	0.0091

Standard Deviation	0.1197

2.4. Mapping Quality

Mean Mapping Quality	44.49

2.5. Mismatches and indels

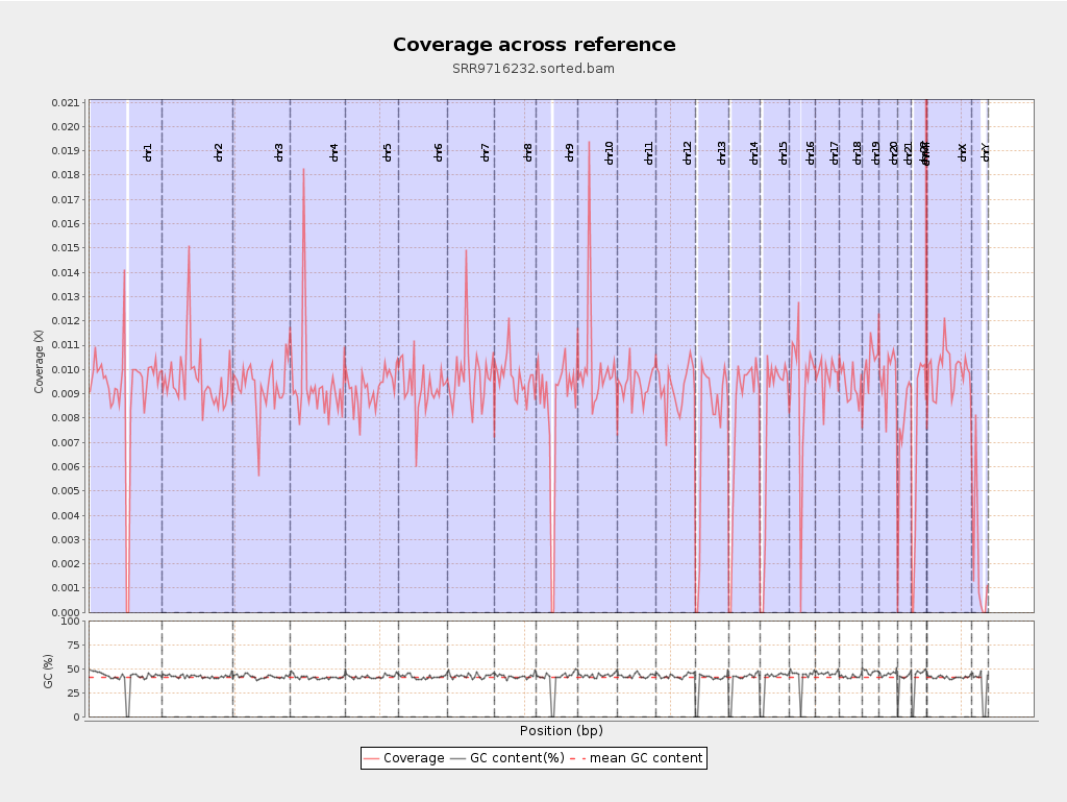
General error rate	0.54%
Mismatches	147,243
Insertions	2,056
Mapped reads with at least one insertion	0.42%
Deletions	5,596
Mapped reads with at least one deletion	1.14%
Homopolymer indels	40.8%

2.6. Chromosome stats

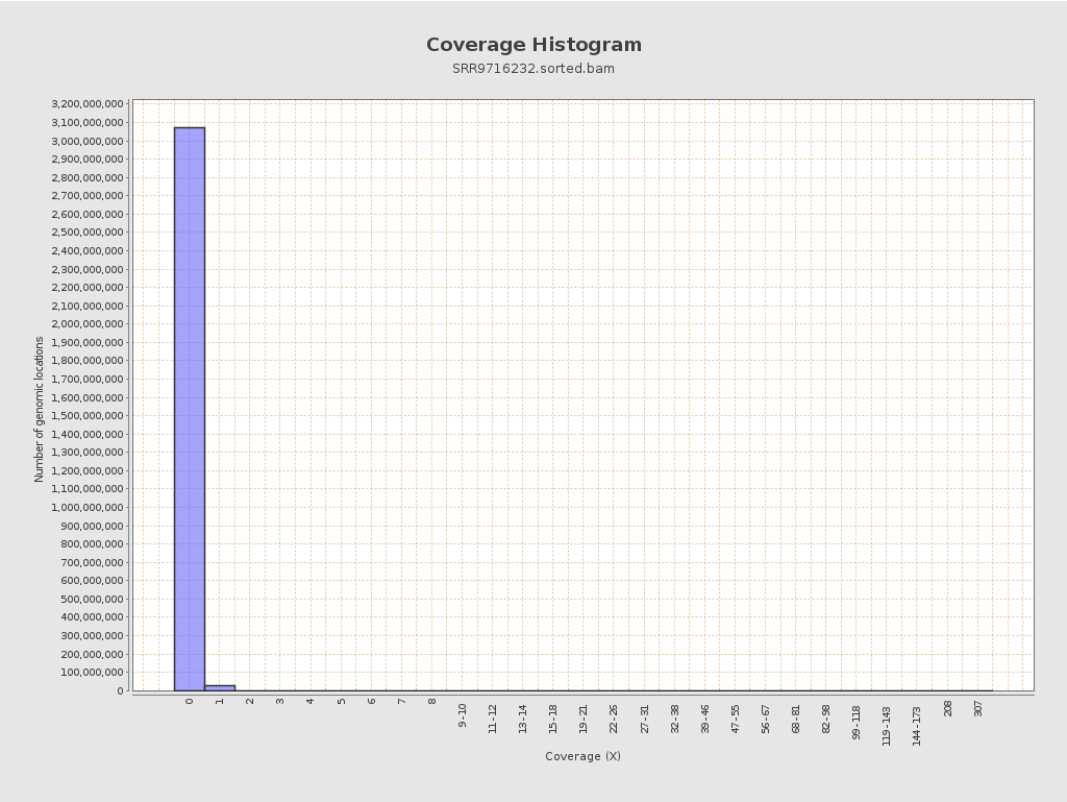
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2272698	0.0091	0.1578
chr2	243199373	2338902	0.0096	0.1658
chr3	198022430	1843567	0.0093	0.1006
chr4	191154276	1788879	0.0094	0.1108
chr5	180915260	1670237	0.0092	0.1006
chr6	171115067	1590117	0.0093	0.1057
chr7	159138663	1551549	0.0097	0.1326

chr8	146364022	1413133	0.0097	0.1347
chr9	141213431	1176735	0.0083	0.1044
chr10	135534747	1368164	0.0101	0.1309
chr11	135006516	1271101	0.0094	0.1104
chr12	133851895	1239761	0.0093	0.1023
chr13	115169878	884816	0.0077	0.0916
chr14	107349540	865712	0.0081	0.0944
chr15	102531392	808099	0.0079	0.0926
chr16	90354753	843125	0.0093	0.1046
chr17	81195210	786763	0.0097	0.1045
chr18	78077248	733166	0.0094	0.133
chr19	59128983	609778	0.0103	0.1356
chr20	63025520	612958	0.0097	0.1041
chr21	48129895	363390	0.0076	0.0997
chr22	51304566	354358	0.0069	0.0872
chrMT	16571	8593	0.5186	0.8015
chrX	155270560	1543074	0.0099	0.1079
chrY	59373566	109766	0.0018	0.094

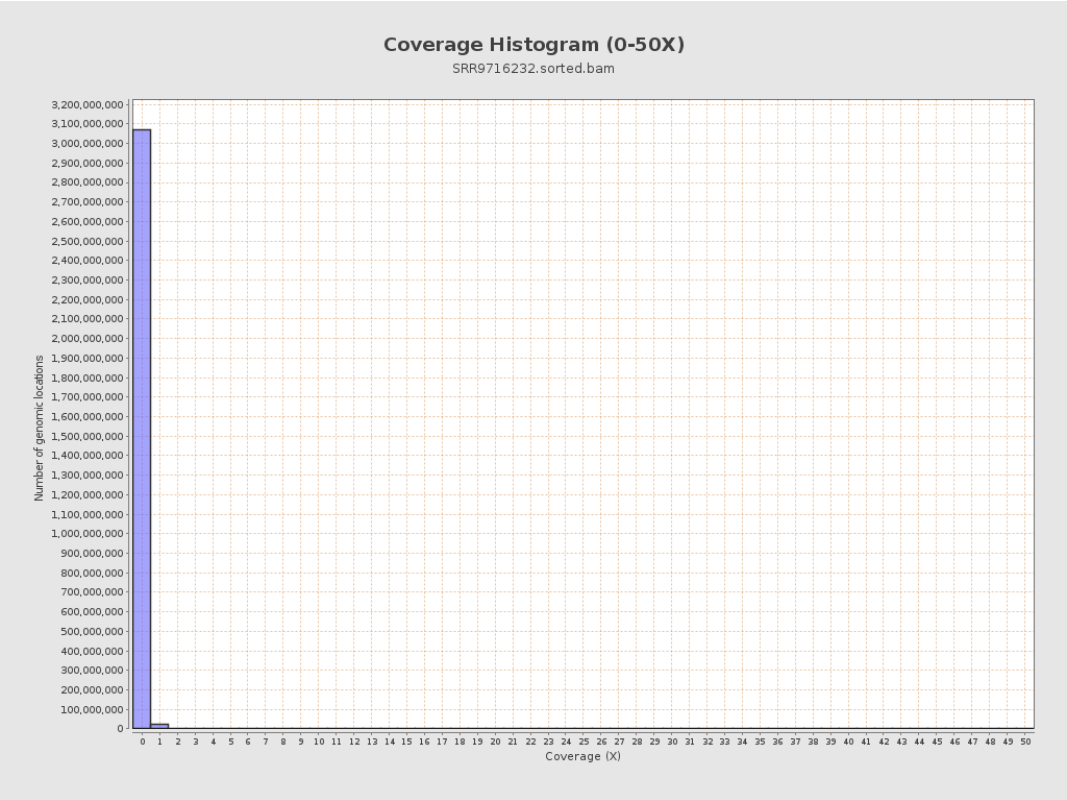
3. Results : Coverage across reference



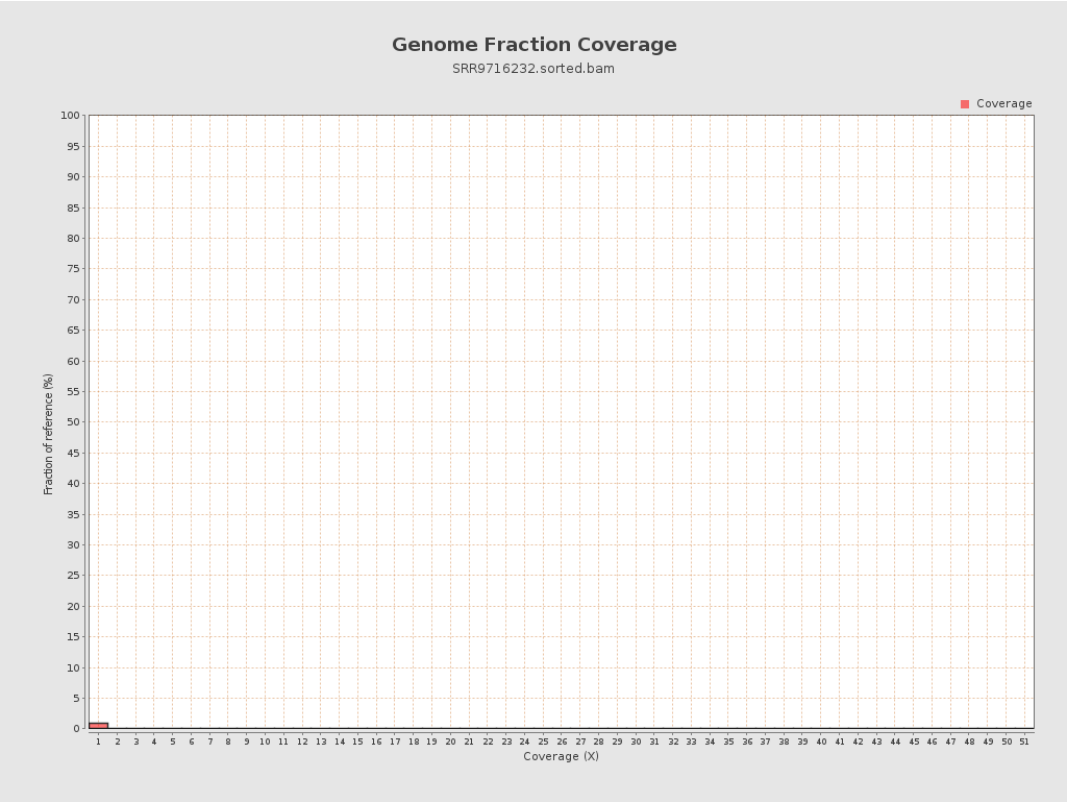
4. Results : Coverage Histogram



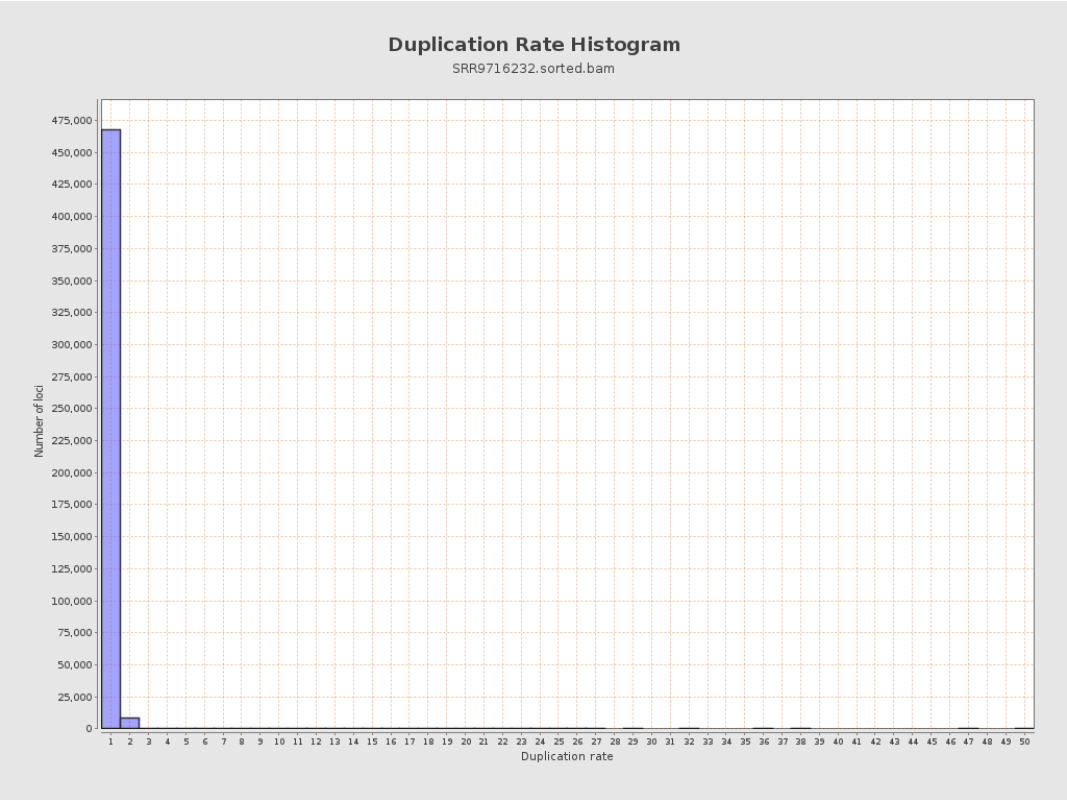
5. Results : Coverage Histogram (0-50X)



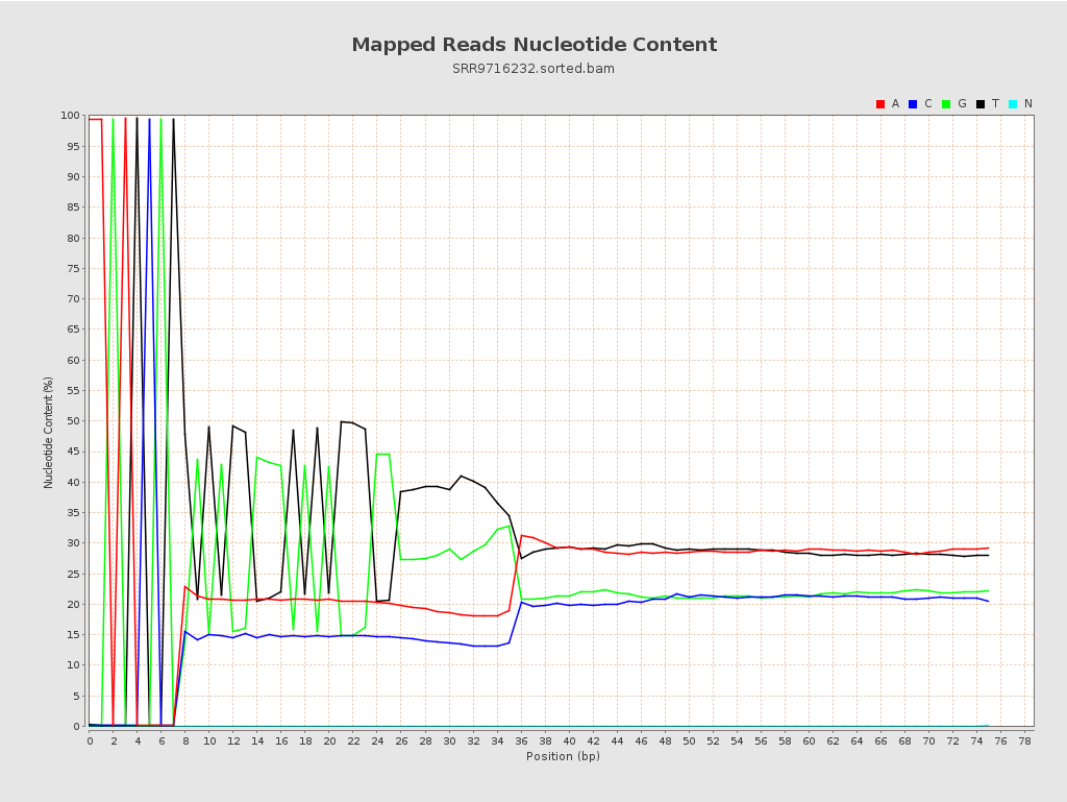
6. Results : Genome Fraction Coverage



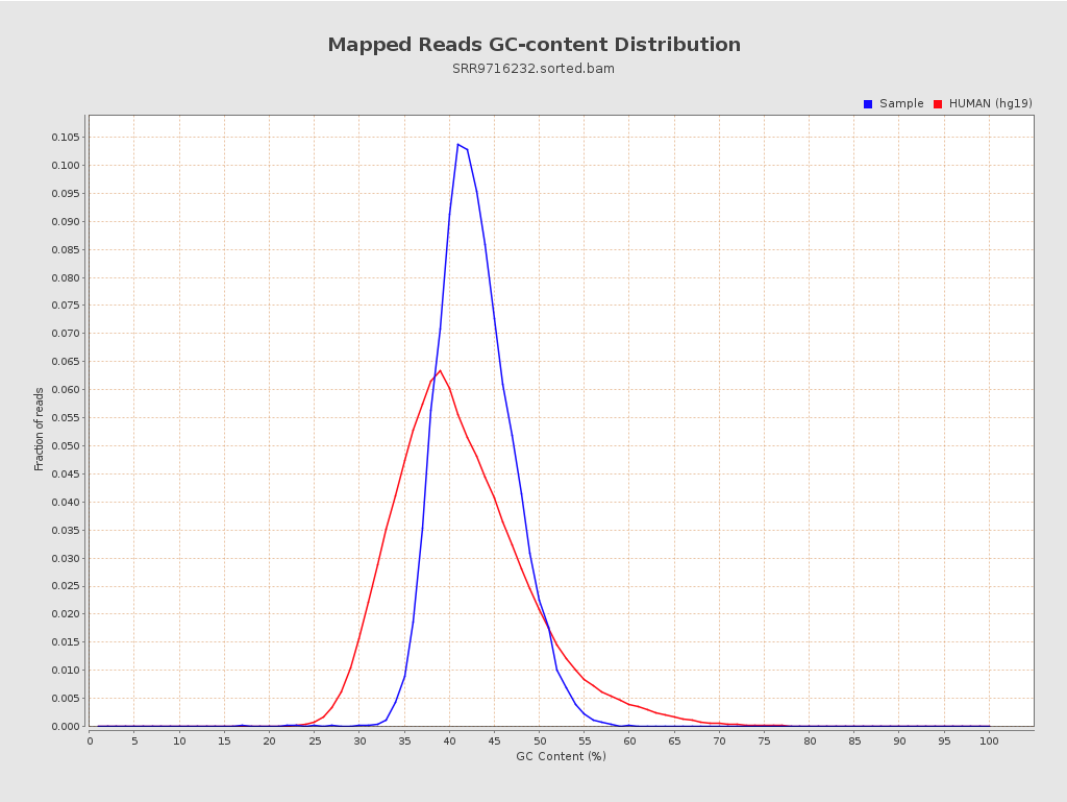
7. Results : Duplication Rate Histogram



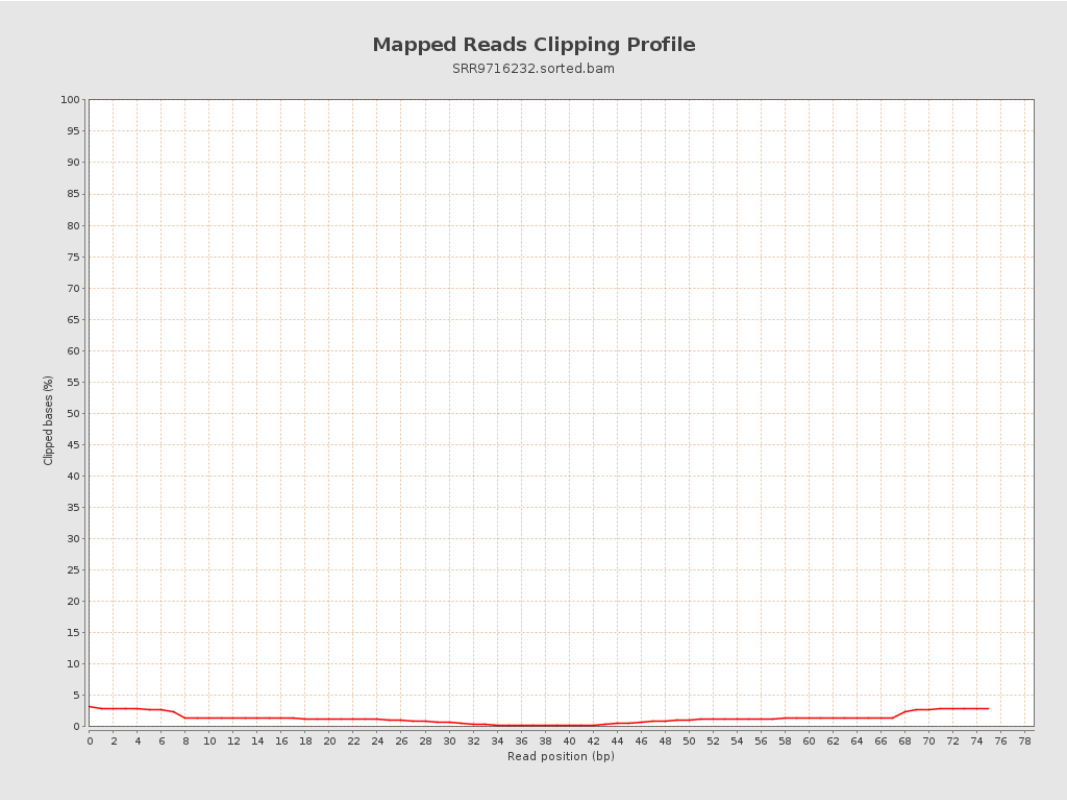
8. Results : Mapped Reads Nucleotide Content



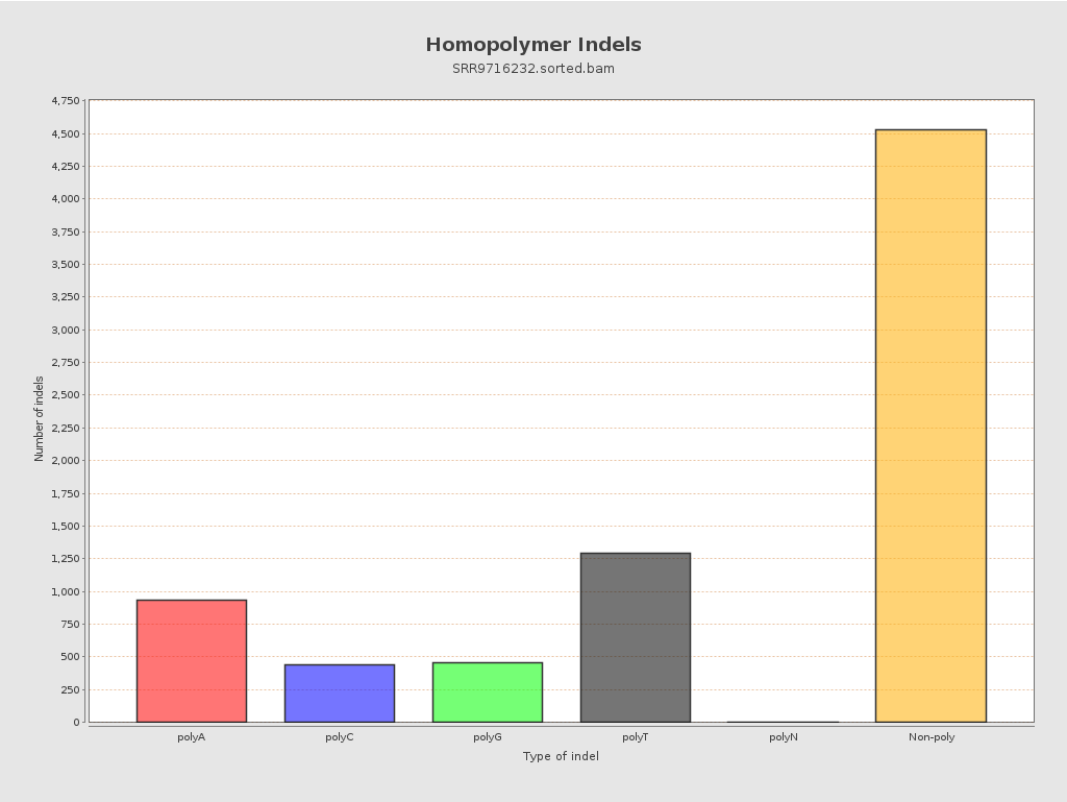
9. Results : Mapped Reads GC-content Distribution



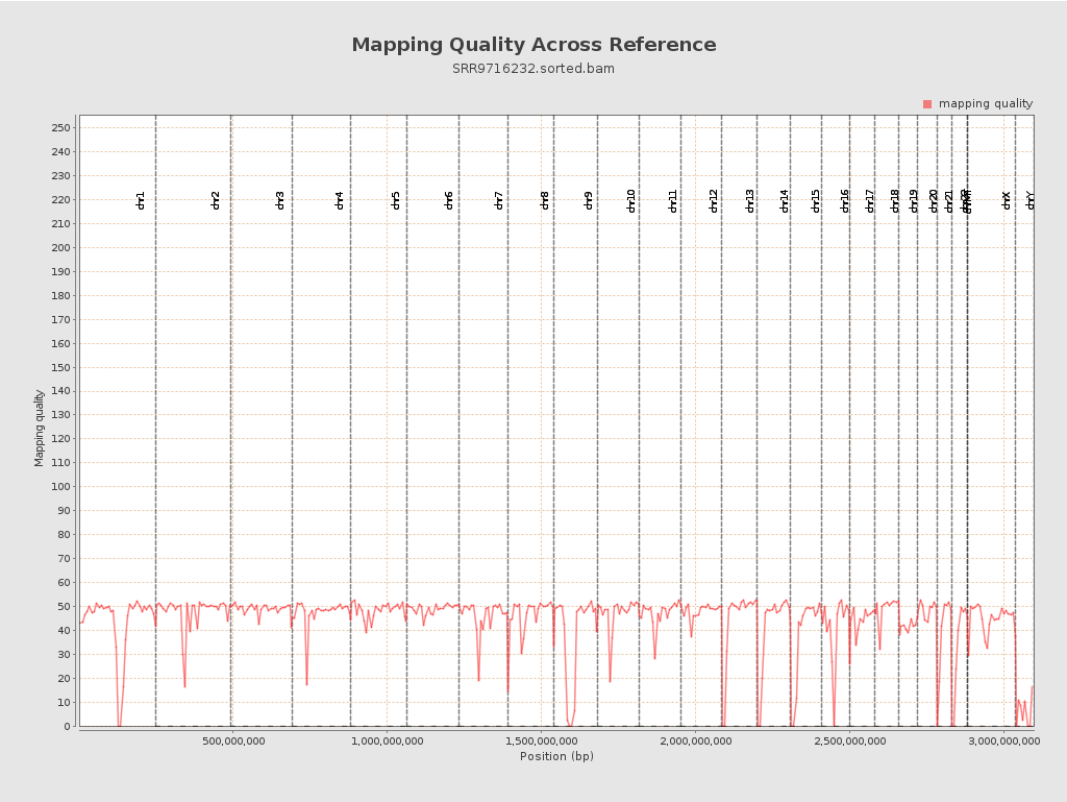
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram