Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 06:20:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716301.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_SRR9716301 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716301.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 06:20:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716301.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	471,191
Mapped reads	418,406 / 88.8%
Unmapped reads	52,785 / 11.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,590 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	7,597 / 1.61%
Duplication rate	1.43%
Clipped reads	419,895 / 89.11%

2.2. ACGT Content

Number/percentage of A's	5,899,847 / 24.15%
Number/percentage of C's	4,813,394 / 19.7%
Number/percentage of T's	7,578,634 / 31.02%
Number/percentage of G's	6,138,785 / 25.13%
Number/percentage of N's	677 / 0%
GC Percentage	44.83%

2.3. Coverage

Mean	0.0079

Standard Deviation	0.1054

2.4. Mapping Quality

Mean Mapping Quality	45.56

2.5. Mismatches and indels

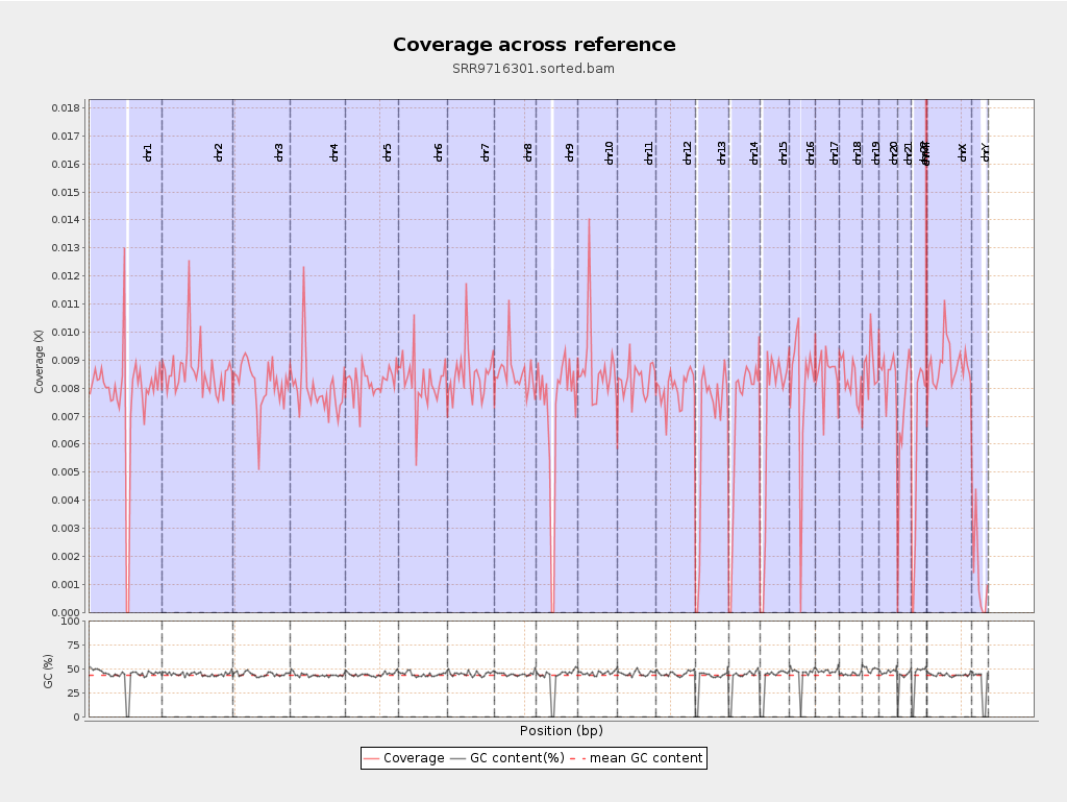
General error rate	0.51%
Mismatches	120,982
Insertions	1,384
Mapped reads with at least one insertion	0.33%
Deletions	4,339
Mapped reads with at least one deletion	1.03%
Homopolymer indels	44.52%

2.6. Chromosome stats

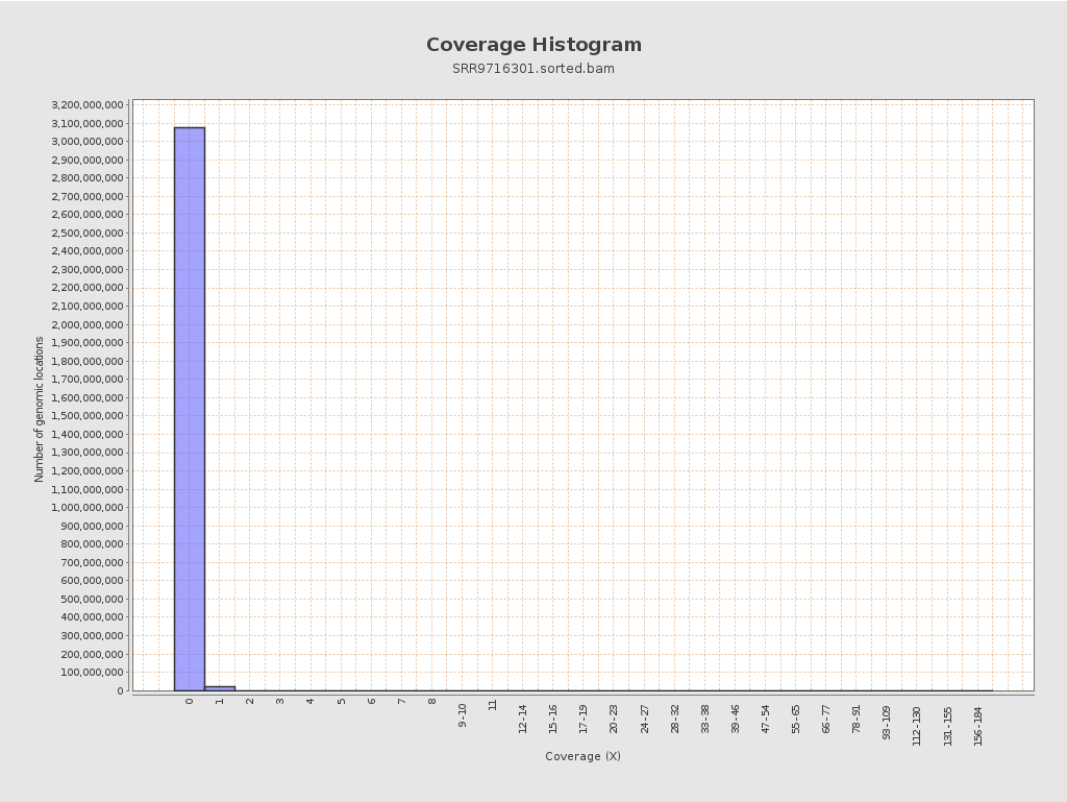
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1924596	0.0077	0.1507
chr2	243199373	2093906	0.0086	0.1238
chr3	198022430	1614950	0.0082	0.0931
chr4	191154276	1520728	0.008	0.0944
chr5	180915260	1485769	0.0082	0.0937
chr6	171115067	1408077	0.0082	0.0987
chr7	159138663	1355977	0.0085	0.1161

chr8	146364022	1248846	0.0085	0.1067
chr9	141213431	1010690	0.0072	0.0935
chr10	135534747	1176978	0.0087	0.107
chr11	135006516	1115933	0.0083	0.1011
chr12	133851895	1068662	0.008	0.0927
chr13	115169878	763593	0.0066	0.0839
chr14	107349540	738826	0.0069	0.0864
chr15	102531392	712558	0.0069	0.0861
chr16	90354753	725021	0.008	0.0943
chr17	81195210	686676	0.0085	0.0967
chr18	78077248	652123	0.0084	0.1334
chr19	59128983	518786	0.0088	0.1243
chr20	63025520	535091	0.0085	0.0956
chr21	48129895	333745	0.0069	0.0883
chr22	51304566	295827	0.0058	0.0784
chrMT	16571	4519	0.2727	0.5872
chrX	155270560	1369003	0.0088	0.0994
chrY	59373566	77463	0.0013	0.045

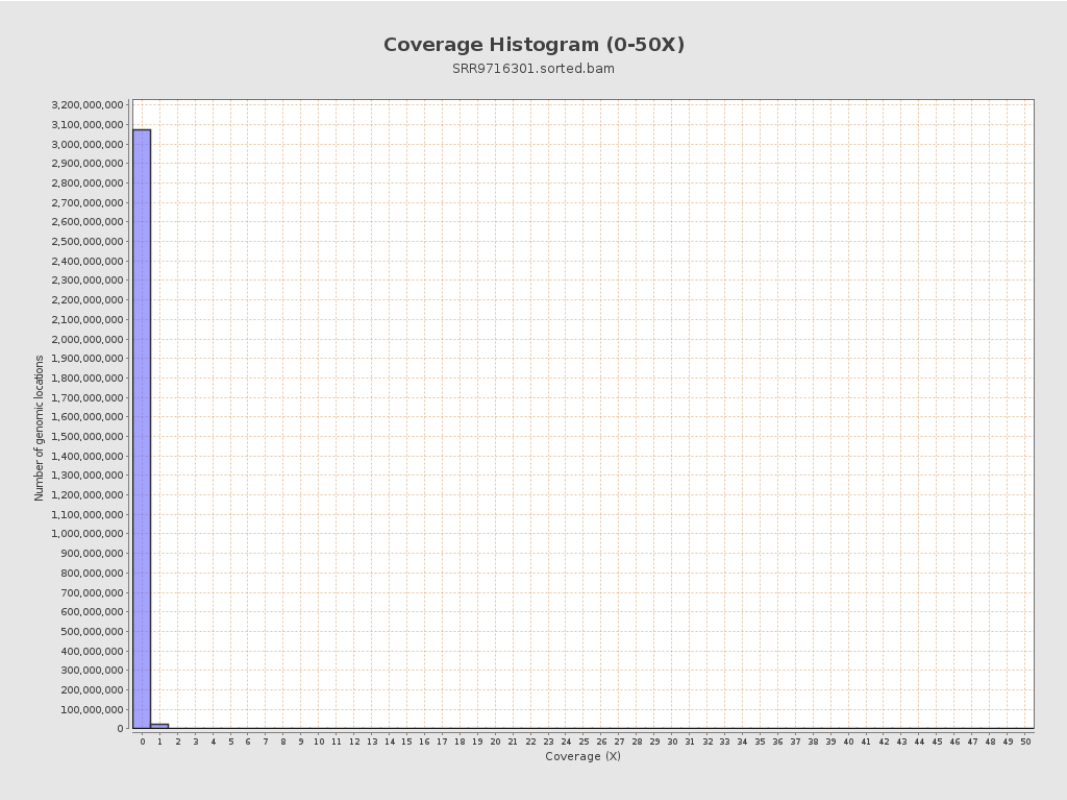
3. Results : Coverage across reference



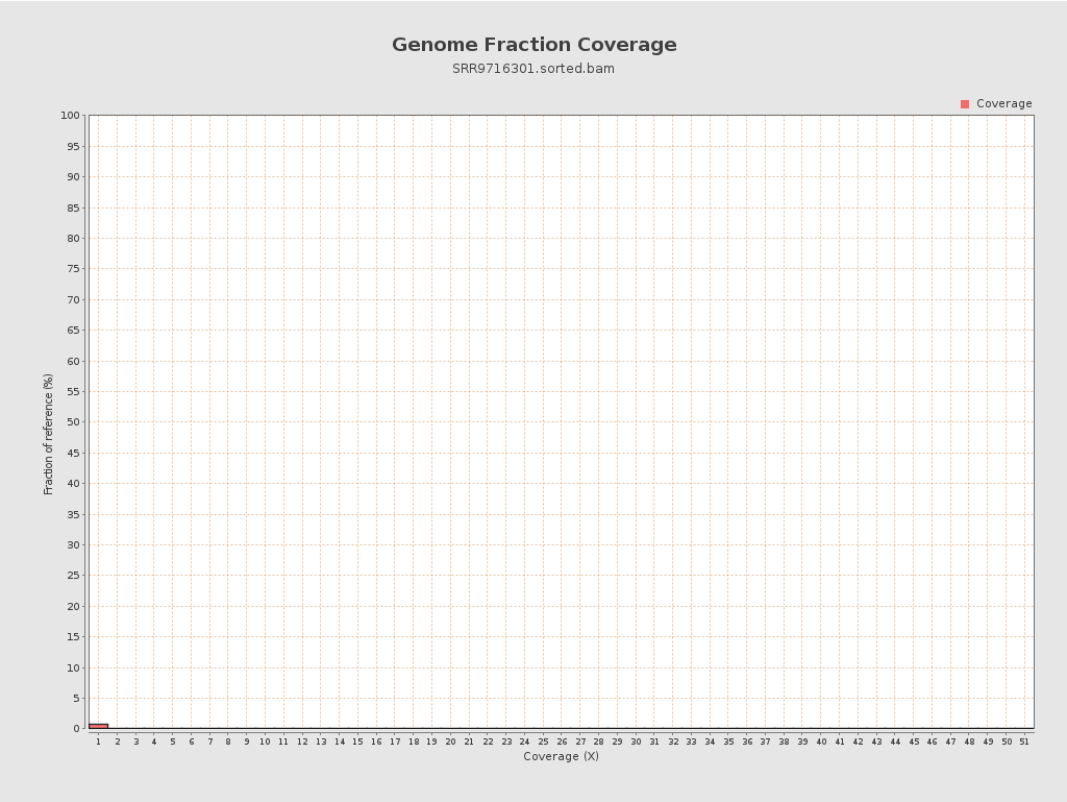
4. Results : Coverage Histogram



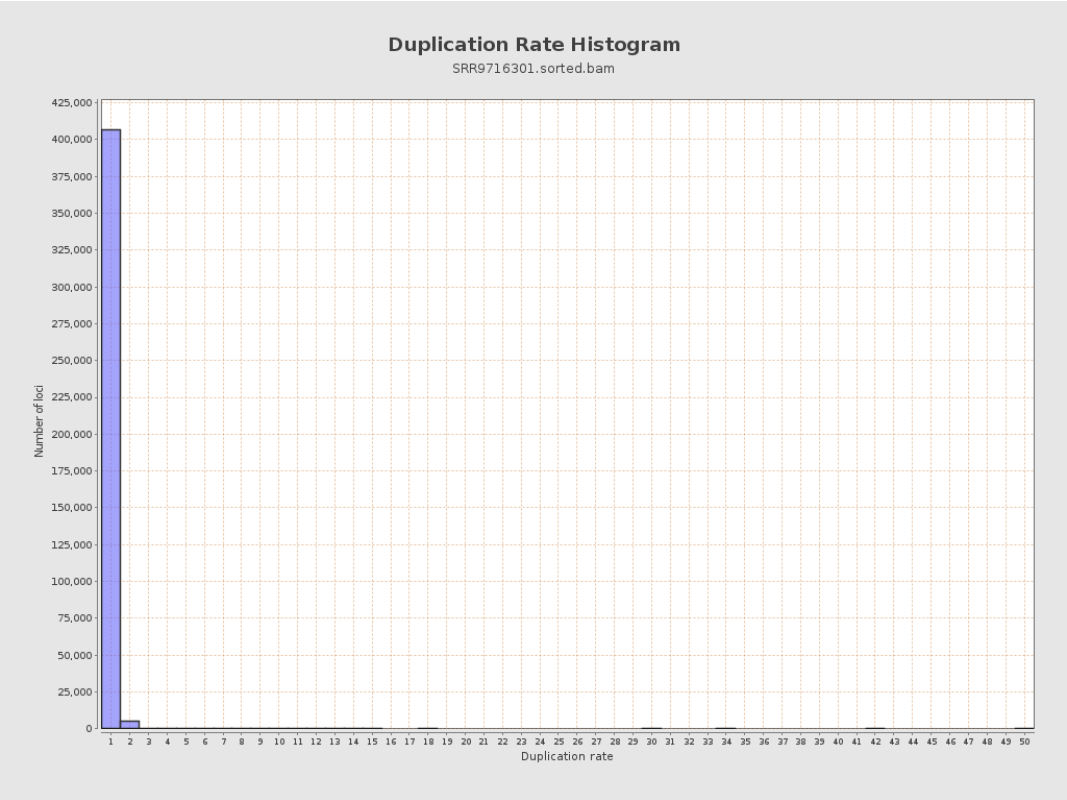
5. Results : Coverage Histogram (0-50X)



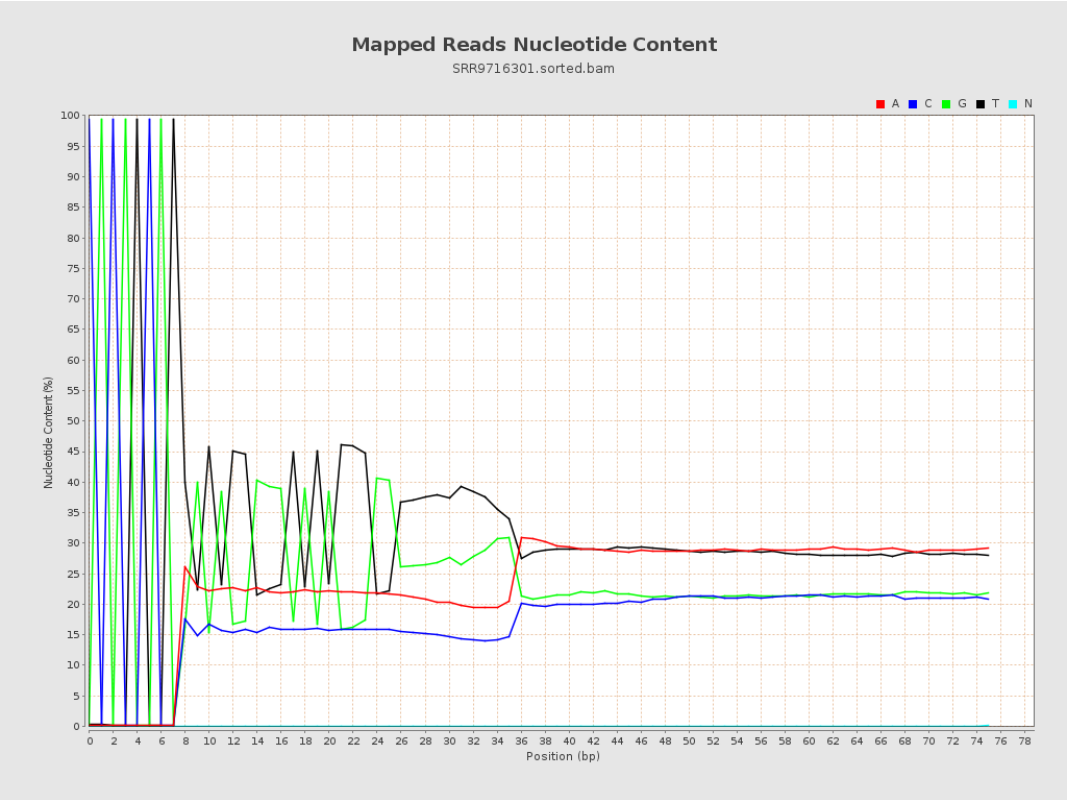
6. Results : Genome Fraction Coverage



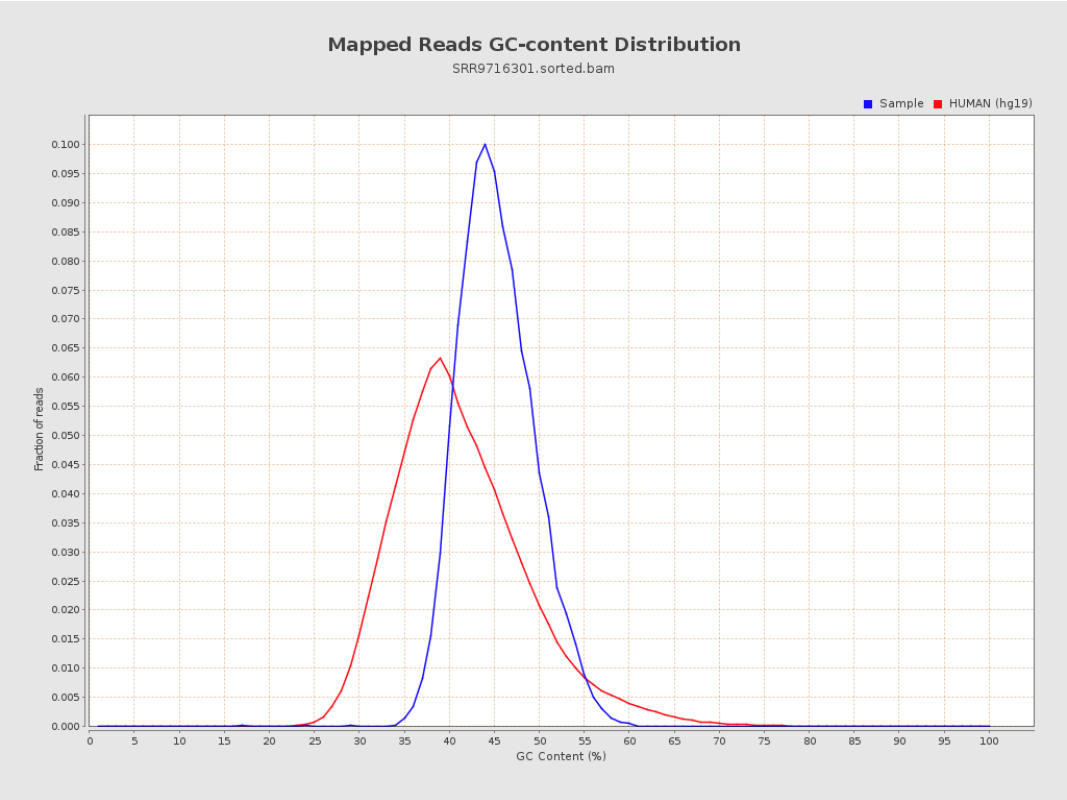
7. Results : Duplication Rate Histogram



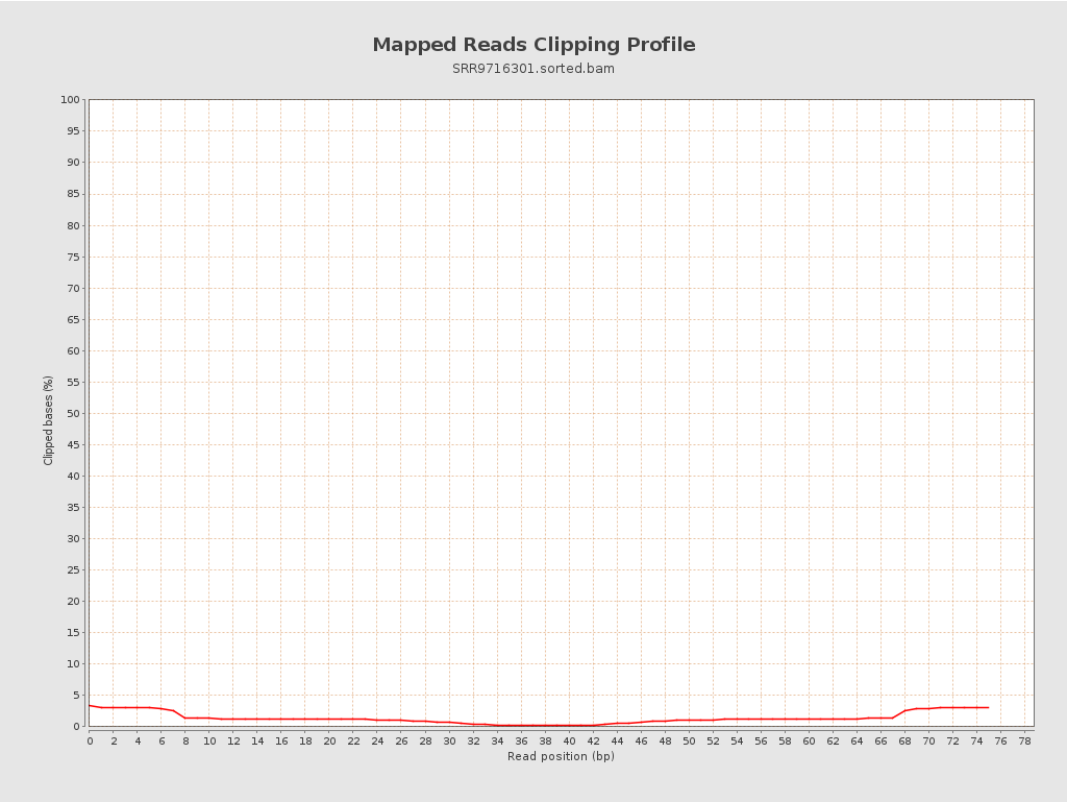
8. Results : Mapped Reads Nucleotide Content



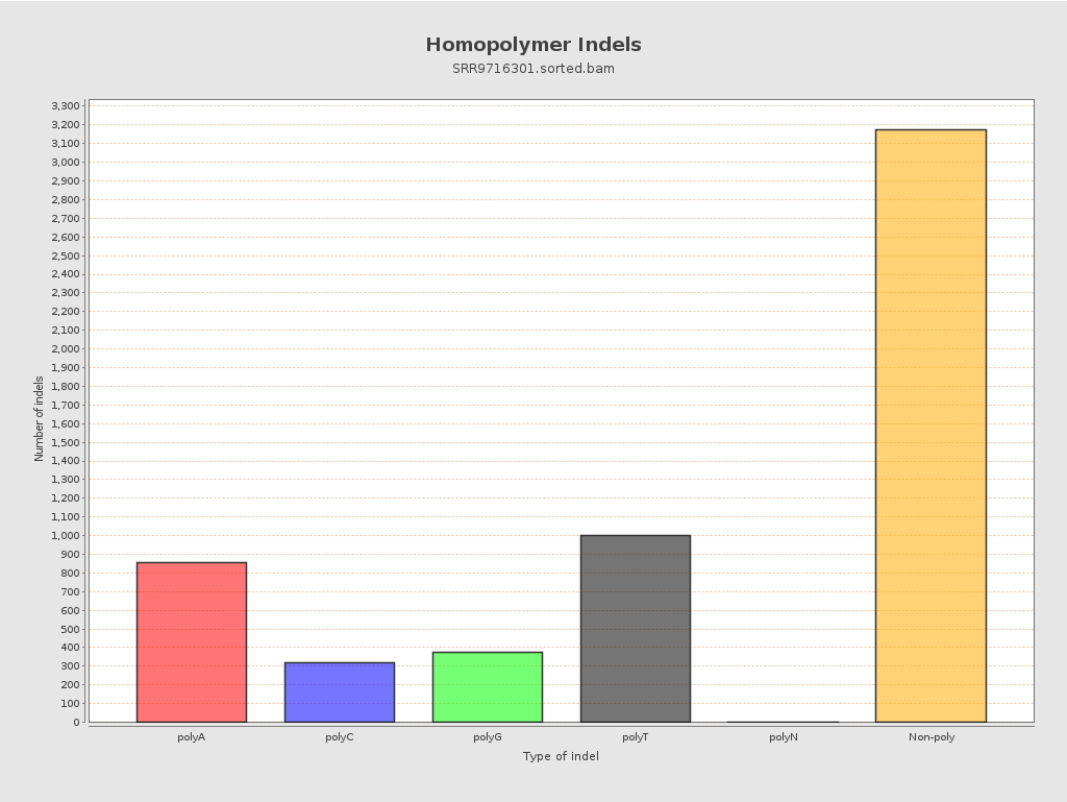
9. Results : Mapped Reads GC-content Distribution



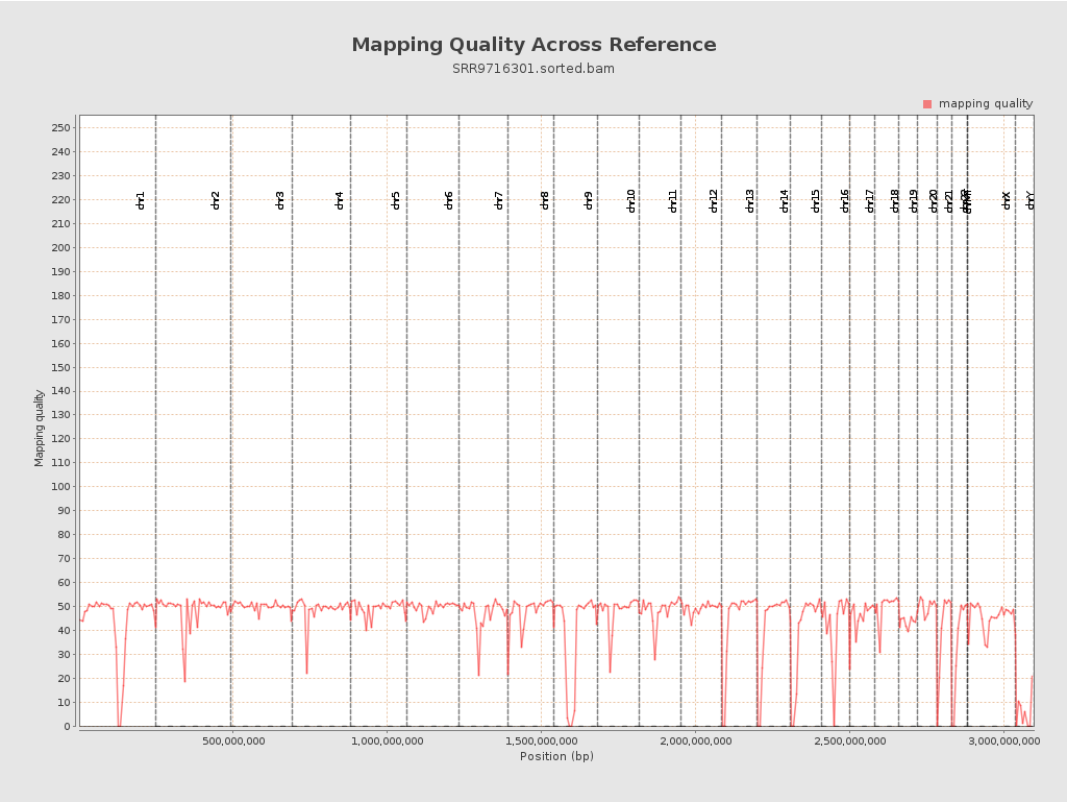
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram