Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 10:27:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716378.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_SRR9716378 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716378.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 10:27:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716378.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,176,694
Mapped reads	1,043,666 / 88.69%
Unmapped reads	133,028 / 11.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,736 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	20,741 / 1.76%
Duplication rate	1.41%
Clipped reads	1,046,400 / 88.93%

2.2. ACGT Content

Number/percentage of A's	15,068,061 / 25.34%
Number/percentage of C's	11,458,515 / 19.27%
Number/percentage of T's	17,929,203 / 30.16%
Number/percentage of G's	14,998,370 / 25.23%
Number/percentage of N's	424 / 0%
GC Percentage	44.5%

2.3. Coverage

Mean	0.0192

Standard Deviation	0.1793

2.4. Mapping Quality

Mean Mapping Quality	42.65

2.5. Mismatches and indels

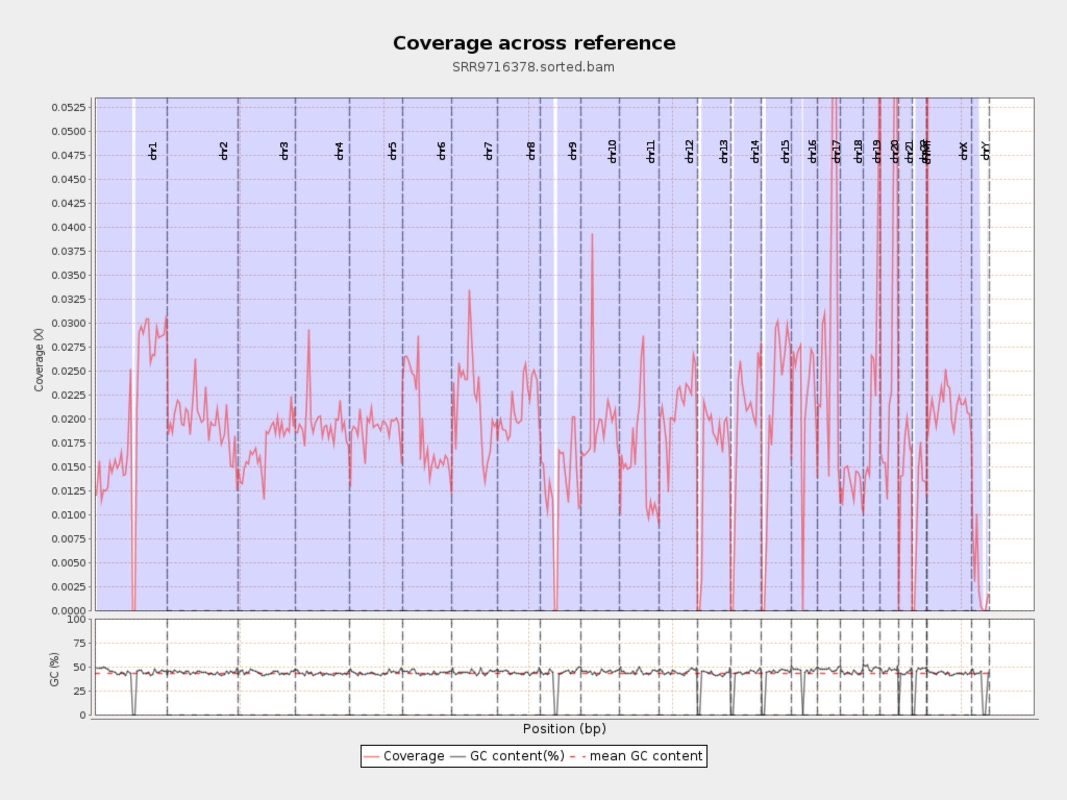
General error rate	0.52%
Mismatches	303,239
Insertions	3,699
Mapped reads with at least one insertion	0.35%
Deletions	10,760
Mapped reads with at least one deletion	1.02%
Homopolymer indels	40.83%

2.6. Chromosome stats

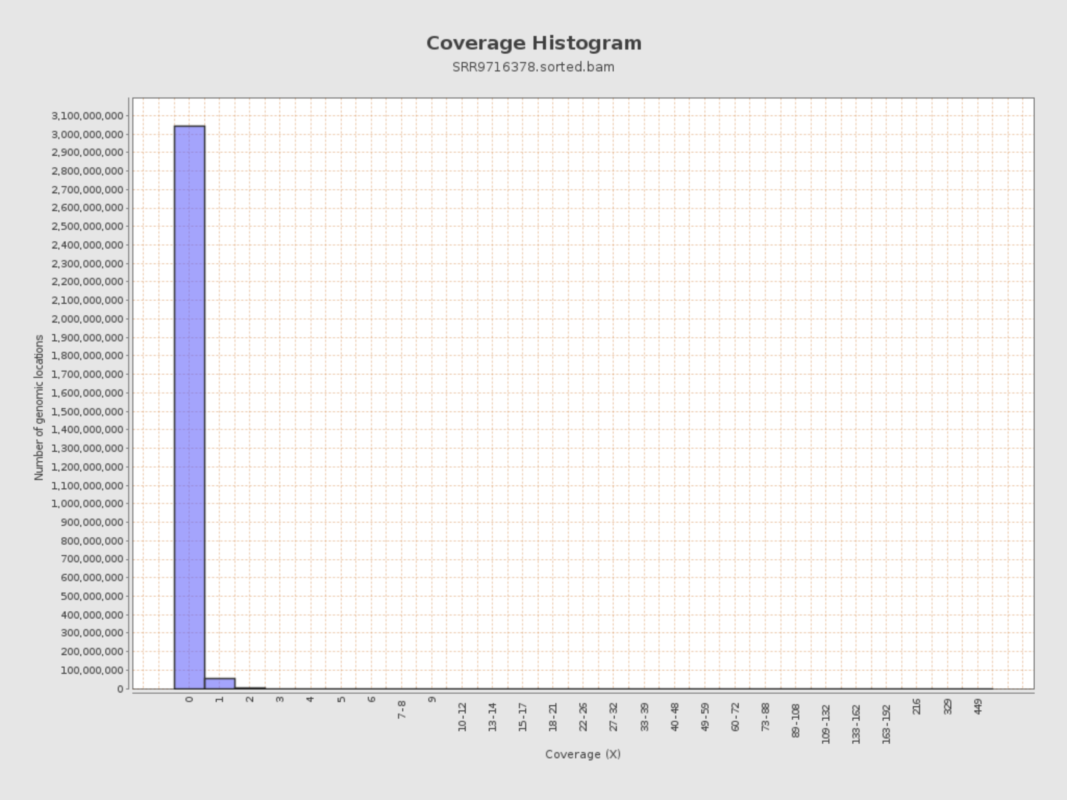
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4946938	0.0198	0.2095
chr2	243199373	4769023	0.0196	0.2393
chr3	198022430	3397493	0.0172	0.1406
chr4	191154276	3737870	0.0196	0.1553
chr5	180915260	3455076	0.0191	0.146
chr6	171115067	3265159	0.0191	0.1644
chr7	159138663	3450147	0.0217	0.2457

chr8	146364022	3113299	0.0213	0.1776
chr9	141213431	1845258	0.0131	0.1381
chr10	135534747	2658137	0.0196	0.2265
chr11	135006516	2122327	0.0157	0.1542
chr12	133851895	2850065	0.0213	0.1543
chr13	115169878	1838332	0.016	0.1338
chr14	107349540	2052179	0.0191	0.15
chr15	102531392	2119566	0.0207	0.1548
chr16	90354753	1986886	0.022	0.1654
chr17	81195210	2619625	0.0323	0.1971
chr18	78077248	1039370	0.0133	0.1958
chr19	59128983	1506898	0.0255	0.2195
chr20	63025520	1877823	0.0298	0.1886
chr21	48129895	725354	0.0151	0.1383
chr22	51304566	533811	0.0104	0.1088
chrMT	16571	70220	4.2375	3.5334
chrX	155270560	3309146	0.0213	0.1627
chrY	59373566	181693	0.0031	0.0914

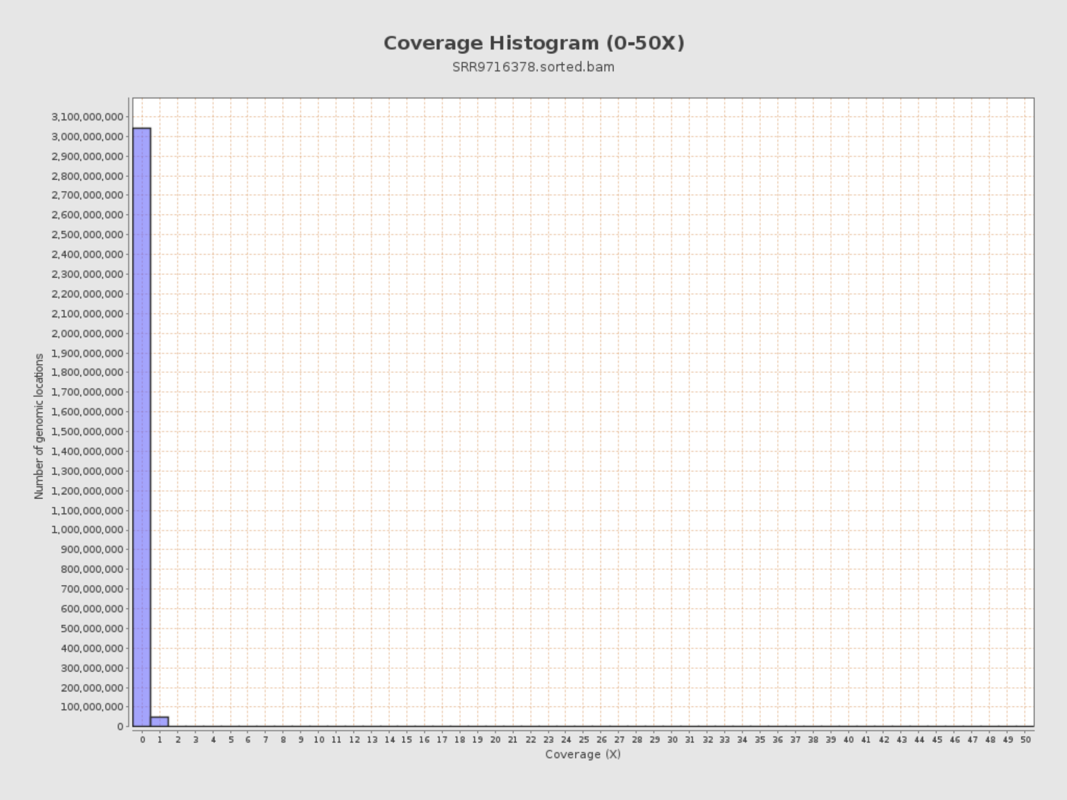
3. Results : Coverage across reference



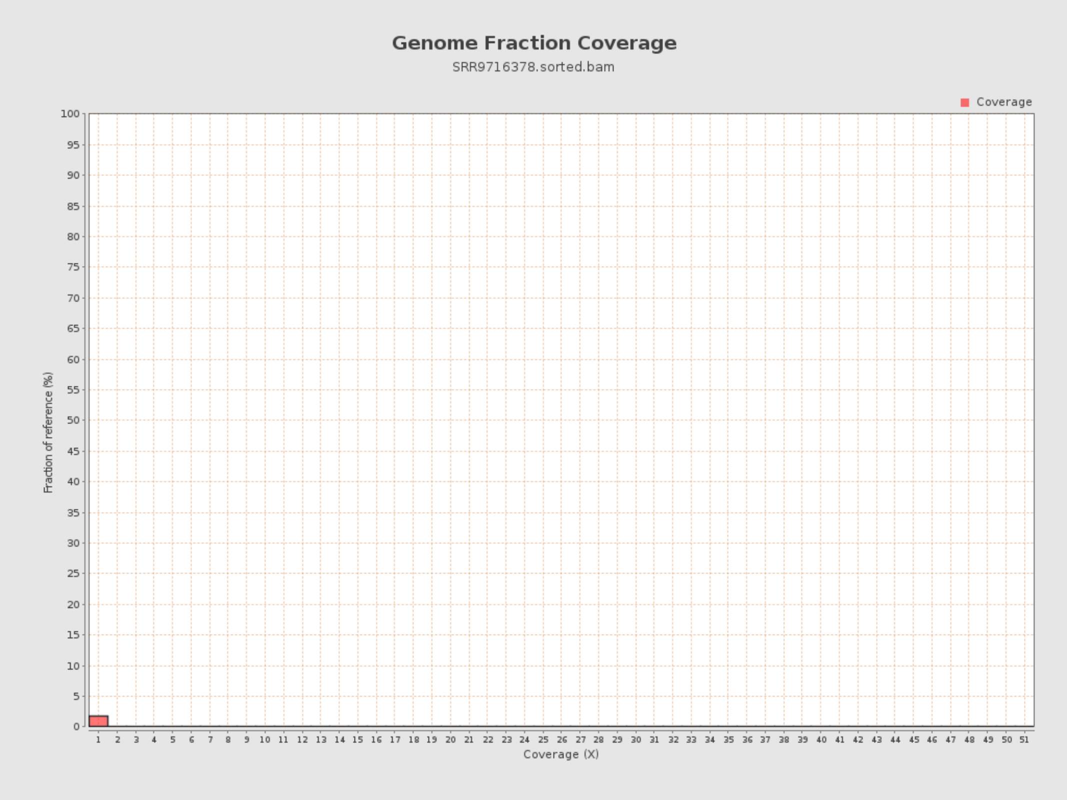
4. Results : Coverage Histogram



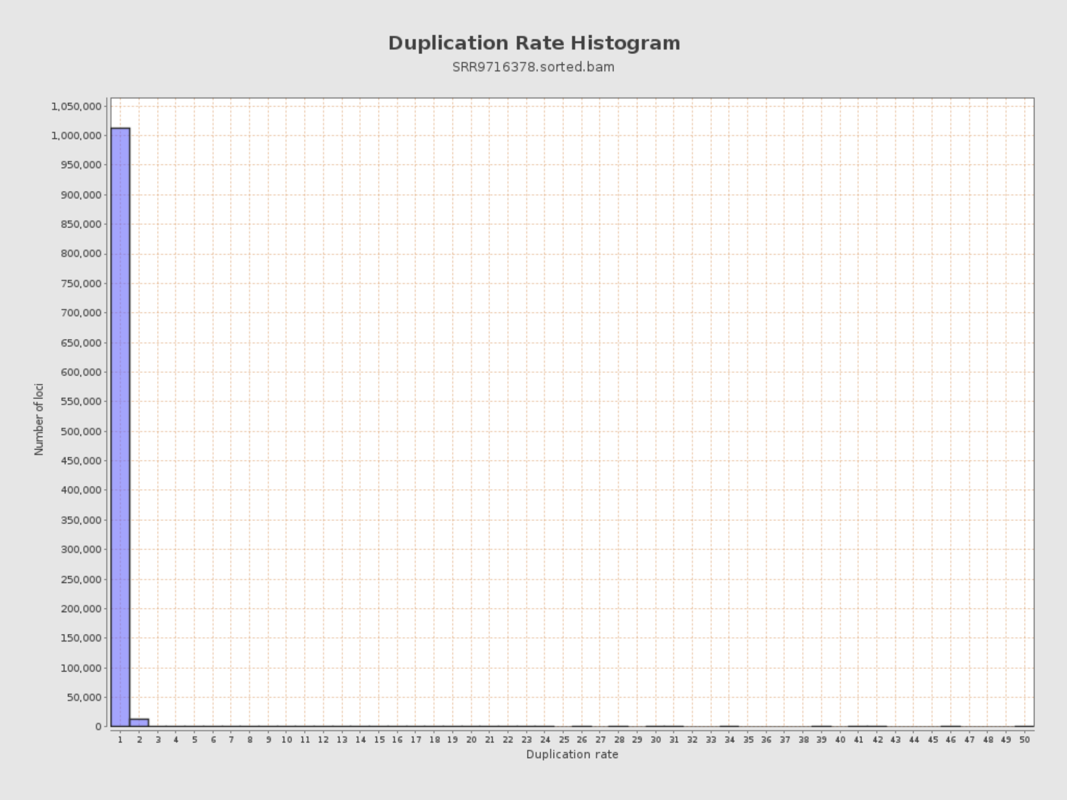
5. Results : Coverage Histogram (0-50X)



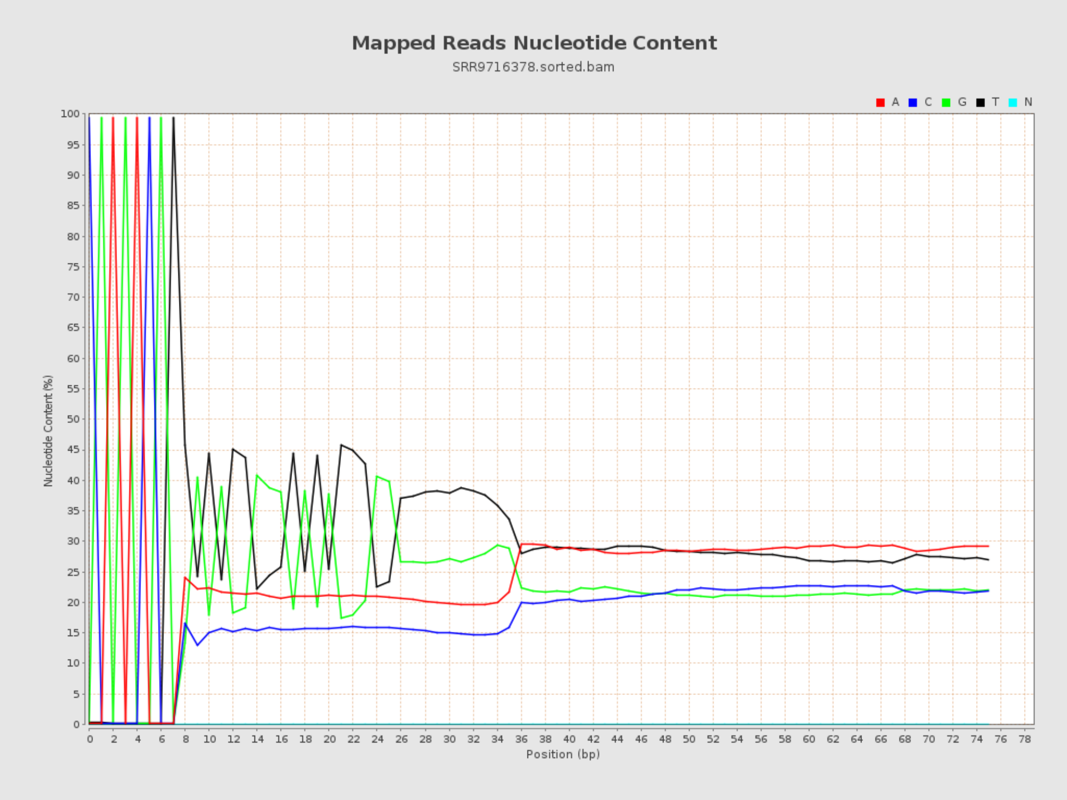
6. Results : Genome Fraction Coverage



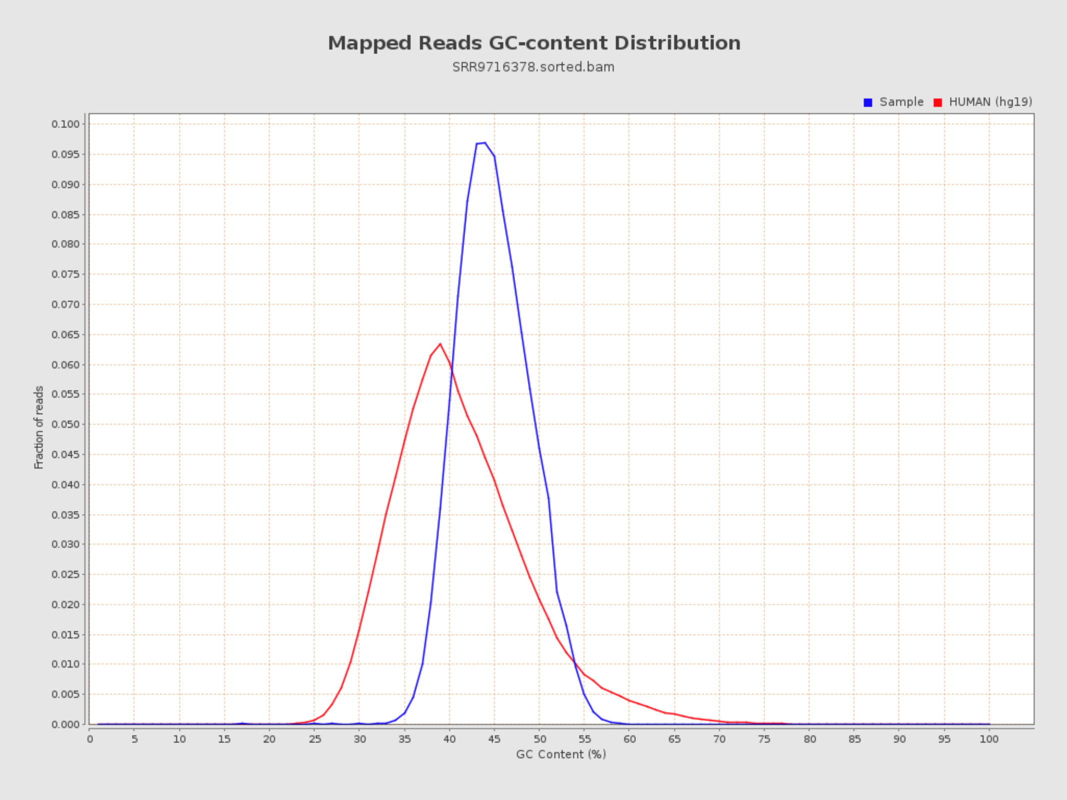
7. Results : Duplication Rate Histogram



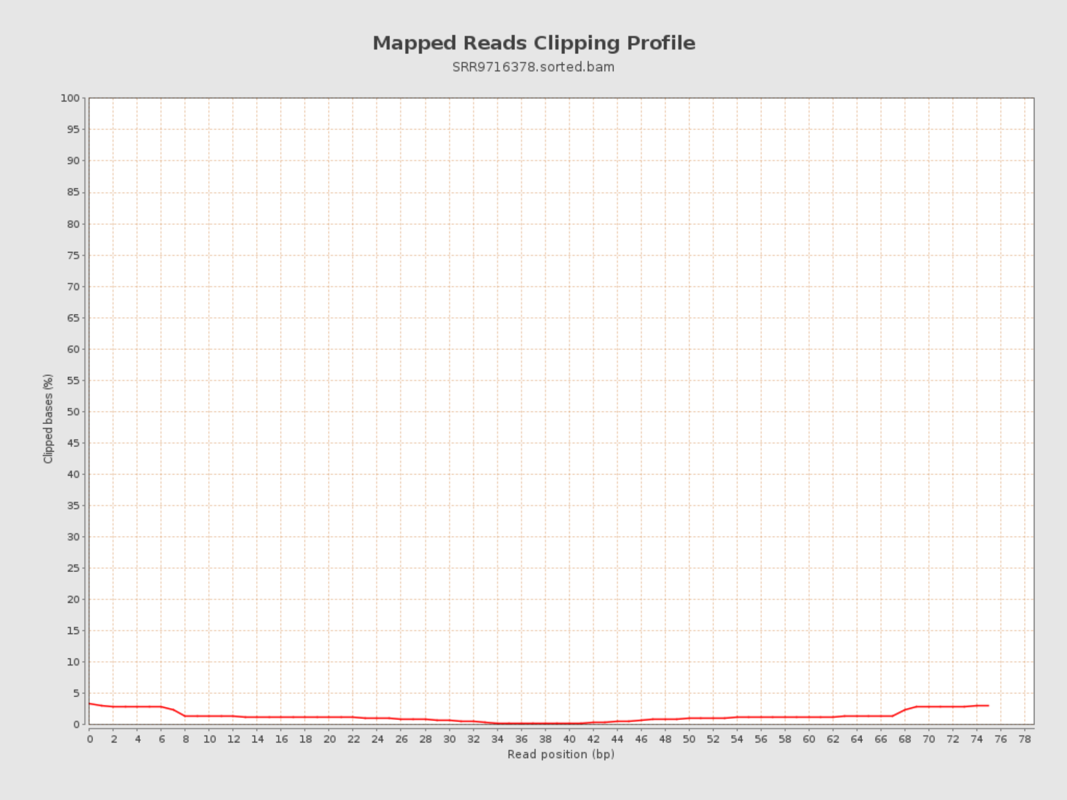
8. Results : Mapped Reads Nucleotide Content



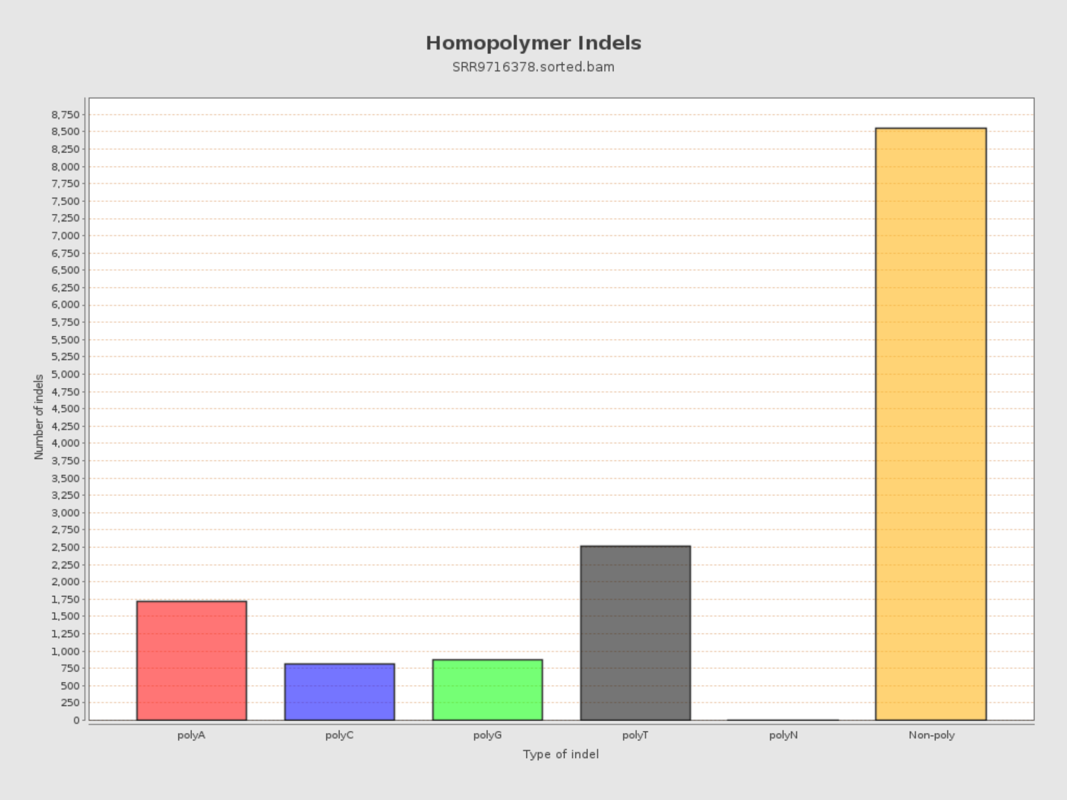
9. Results : Mapped Reads GC-content Distribution



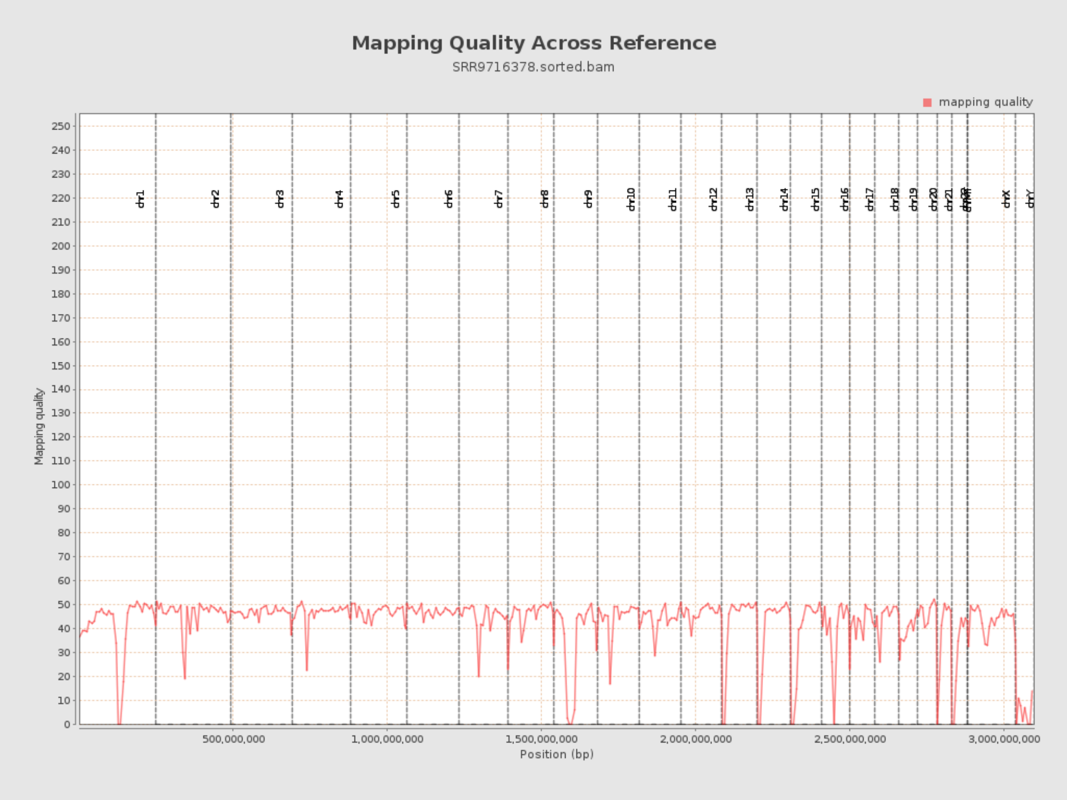
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram