Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 05:26:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716278.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_SRR9716278 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716278.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 05:26:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716278.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,633,801
Mapped reads	1,216,175 / 74.44%
Unmapped reads	417,626 / 25.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,164 / 0.07%
Read min/max/mean length	30 / 76 / 76.02
Duplicated reads (estimated)	96,973 / 5.94%
Duplication rate	6.82%
Clipped reads	1,215,323 / 74.39%

2.2. ACGT Content

Number/percentage of A's	12,064,273 / 19.2%
Number/percentage of C's	10,136,977 / 16.13%
Number/percentage of T's	21,743,920 / 34.6%
Number/percentage of G's	18,902,826 / 30.08%
Number/percentage of N's	990 / 0%
GC Percentage	46.21%

2.3. Coverage

Mean	0.0203

Standard Deviation	0.1901

2.4. Mapping Quality

Mean Mapping Quality	43.01

2.5. Mismatches and indels

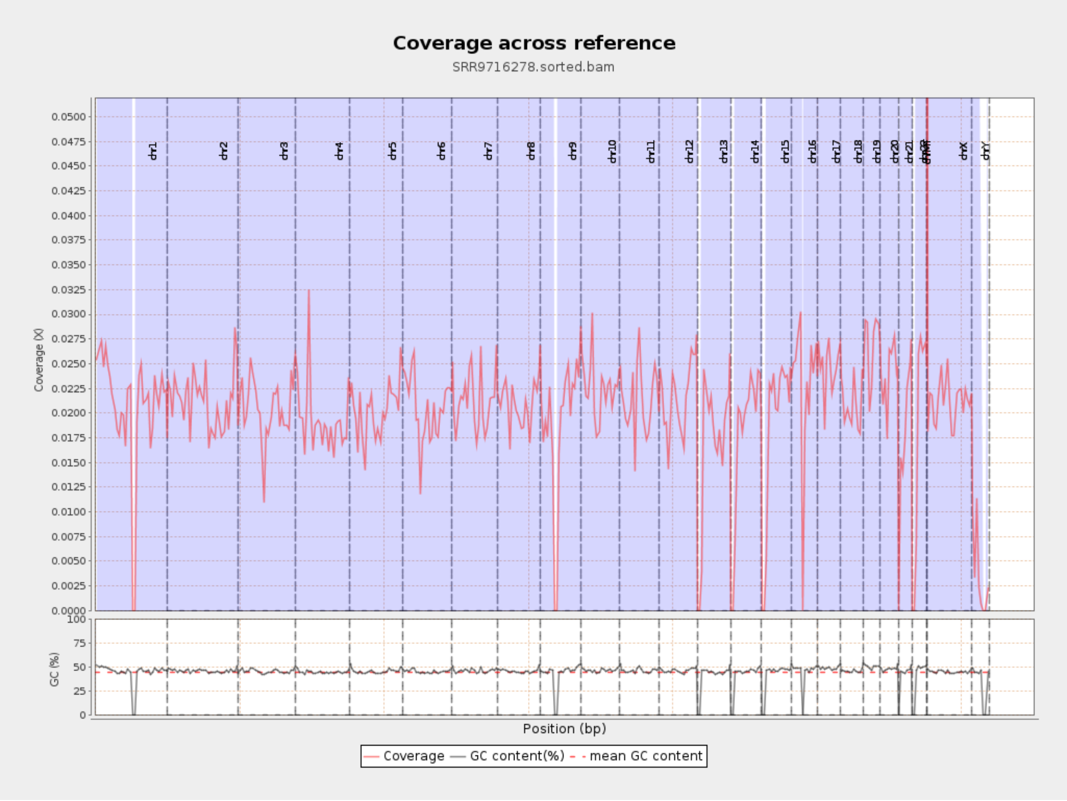
General error rate	0.71%
Mismatches	441,220
Insertions	3,787
Mapped reads with at least one insertion	0.31%
Deletions	9,208
Mapped reads with at least one deletion	0.75%
Homopolymer indels	41%

2.6. Chromosome stats

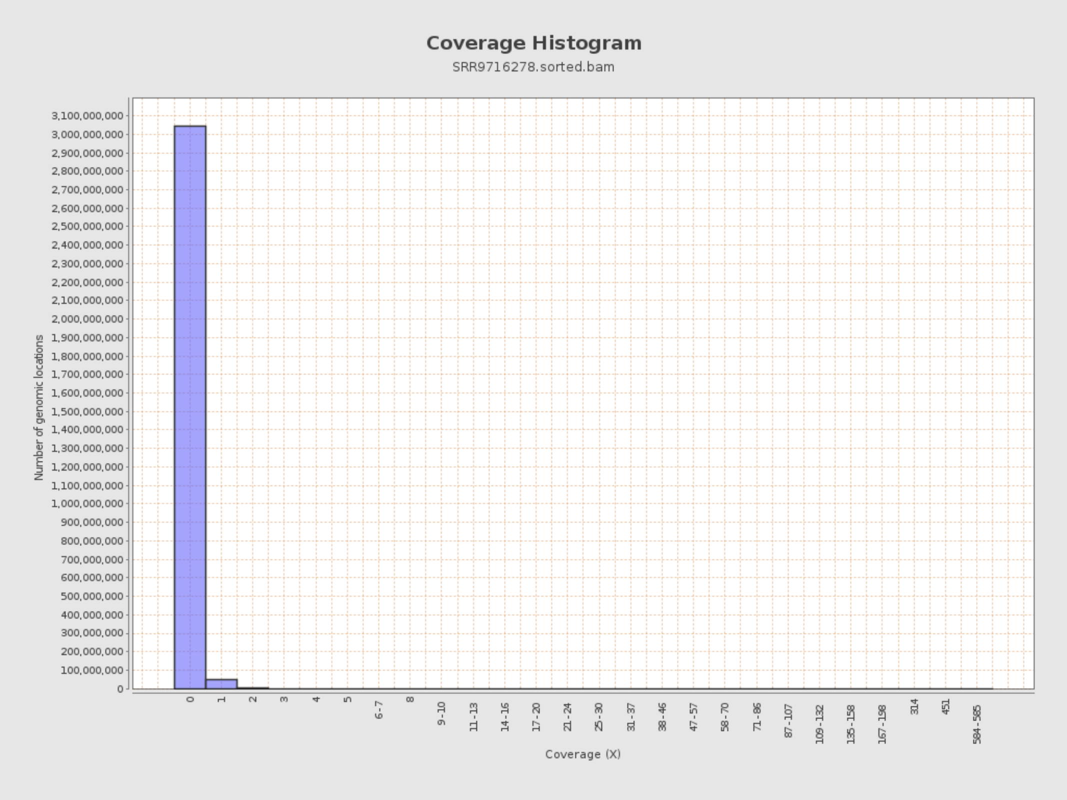
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5144156	0.0206	0.1965
chr2	243199373	5163285	0.0212	0.2888
chr3	198022430	4037832	0.0204	0.1656
chr4	191154276	3723911	0.0195	0.1722
chr5	180915260	3669935	0.0203	0.1637
chr6	171115067	3507852	0.0205	0.1928
chr7	159138663	3389764	0.0213	0.2027

chr8	146364022	3042906	0.0208	0.1747
chr9	141213431	2634694	0.0187	0.1707
chr10	135534747	3063178	0.0226	0.1997
chr11	135006516	2901483	0.0215	0.1865
chr12	133851895	2869050	0.0214	0.1732
chr13	115169878	1900481	0.0165	0.1518
chr14	107349540	1898437	0.0177	0.1554
chr15	102531392	1867583	0.0182	0.1594
chr16	90354753	2037997	0.0226	0.1916
chr17	81195210	1999387	0.0246	0.1911
chr18	78077248	1614671	0.0207	0.1994
chr19	59128983	1578542	0.0267	0.2217
chr20	63025520	1501377	0.0238	0.1876
chr21	48129895	864723	0.018	0.1723
chr22	51304566	934774	0.0182	0.1638
chrMT	16571	21945	1.3243	1.5763
chrX	155270560	3289428	0.0212	0.1726
chrY	59373566	207253	0.0035	0.0954

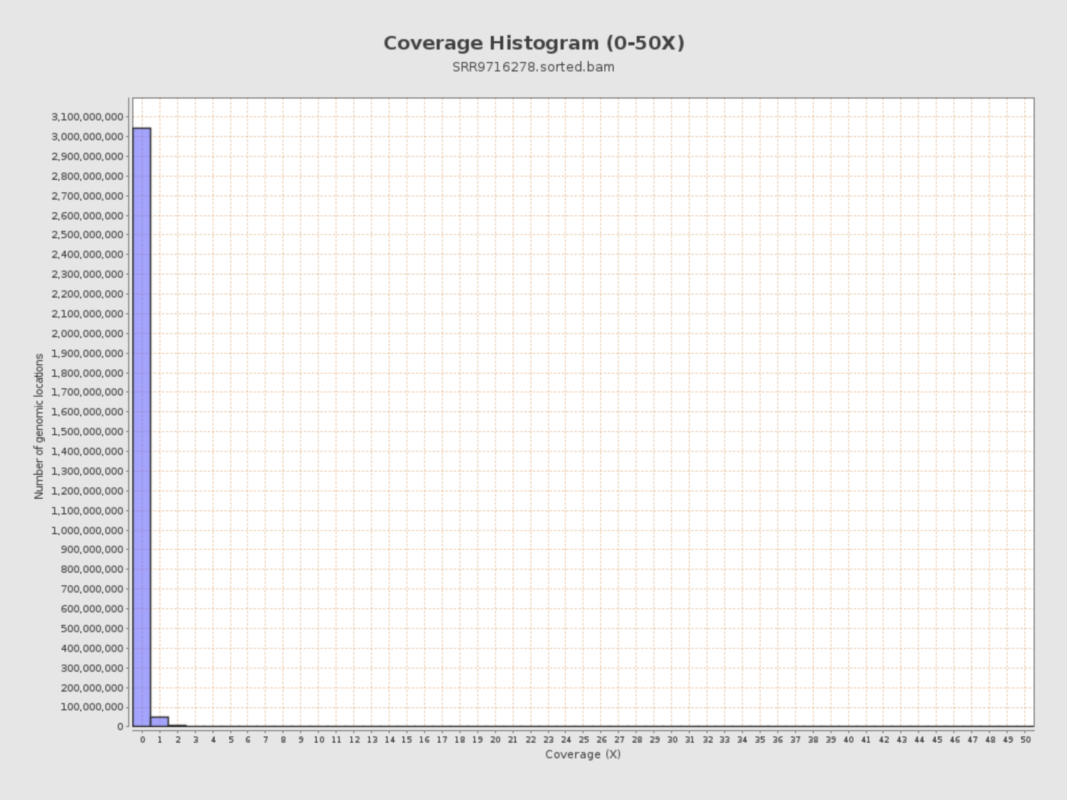
3. Results : Coverage across reference



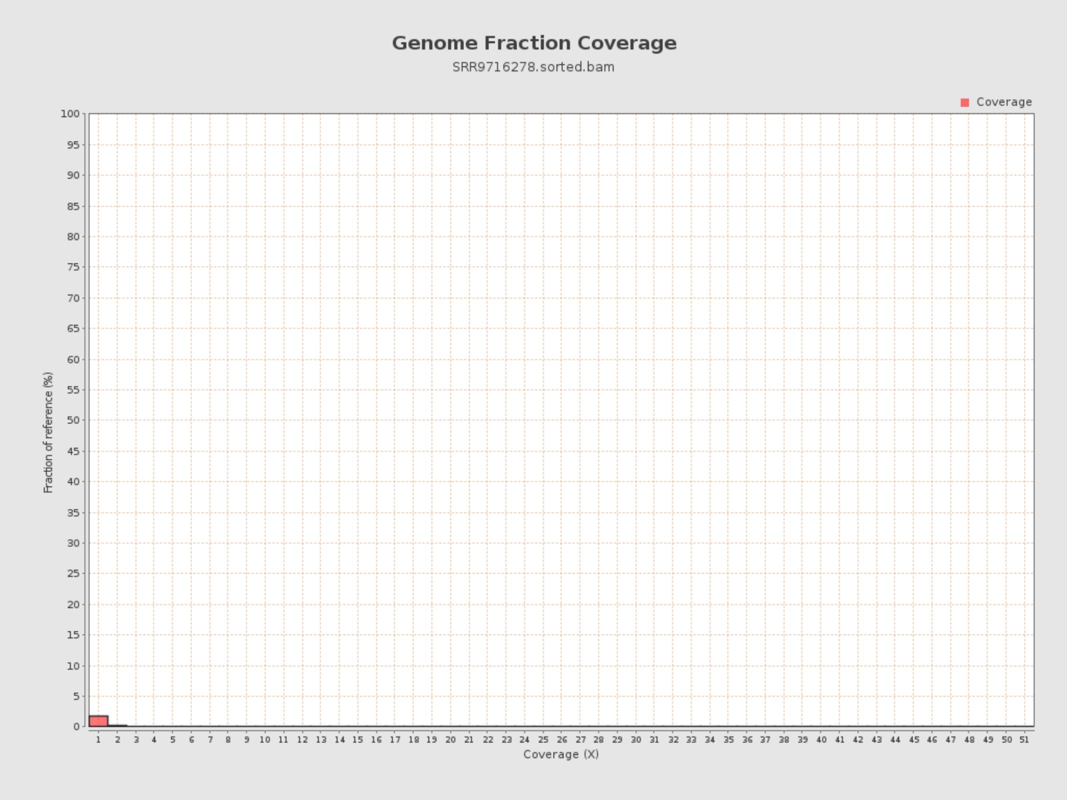
4. Results : Coverage Histogram



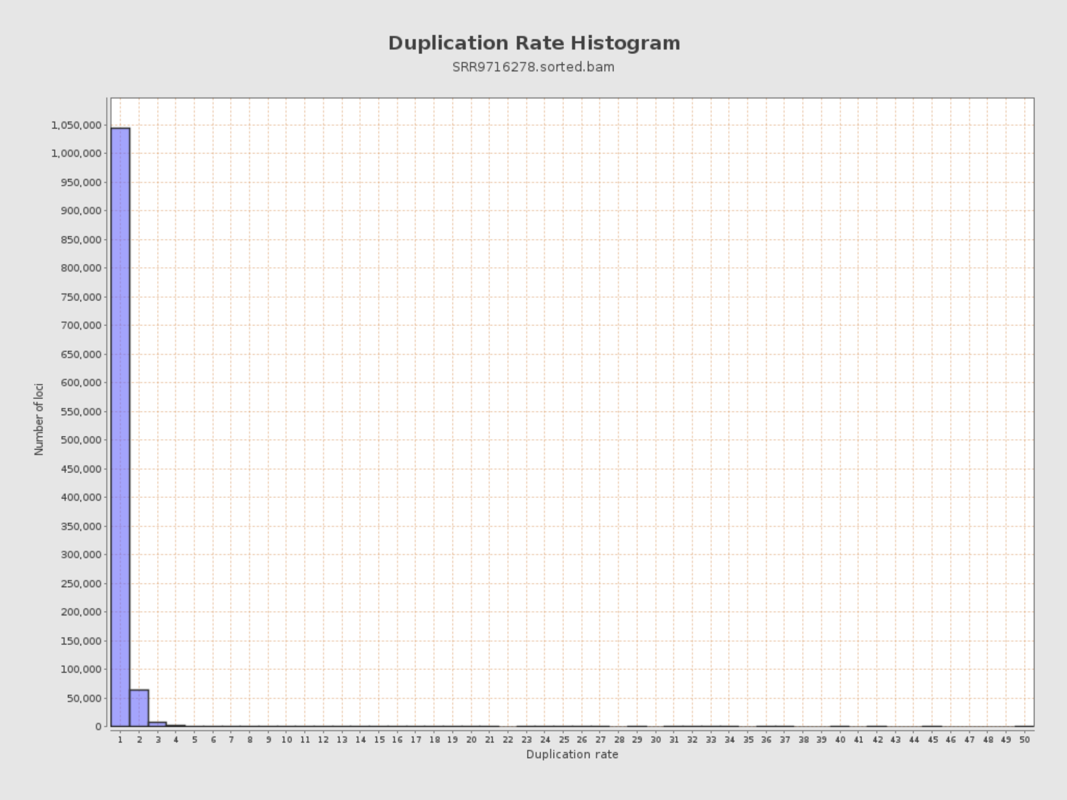
5. Results : Coverage Histogram (0-50X)



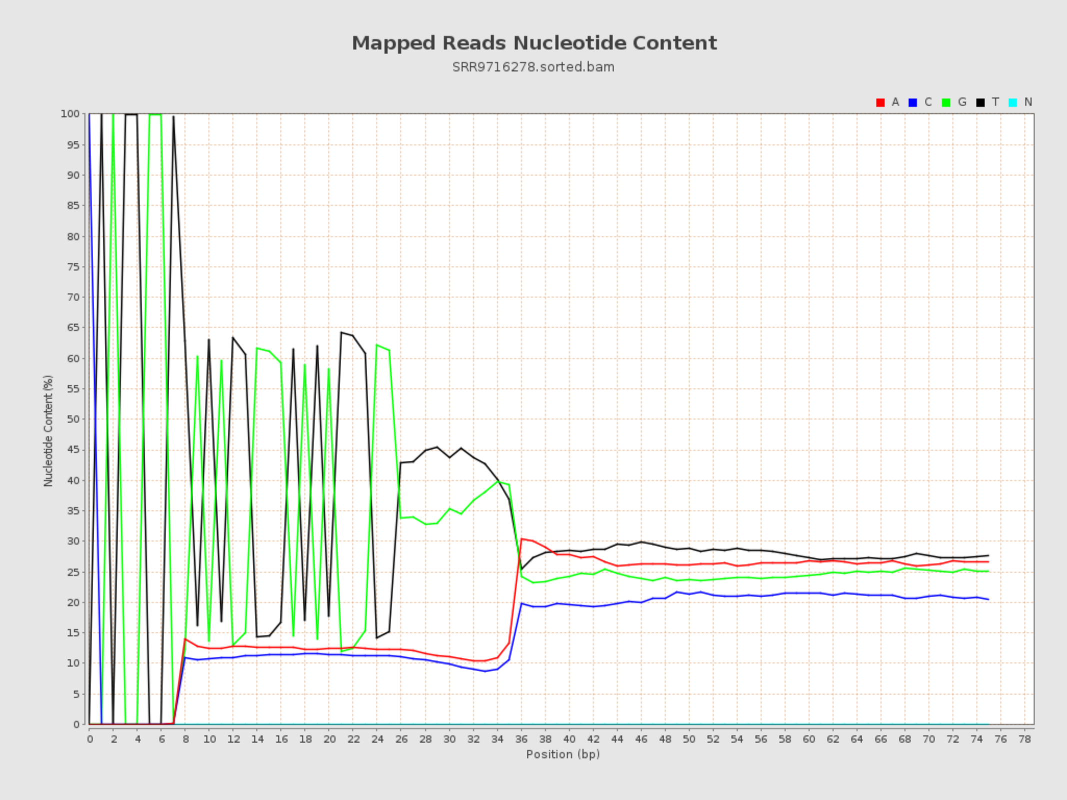
6. Results : Genome Fraction Coverage



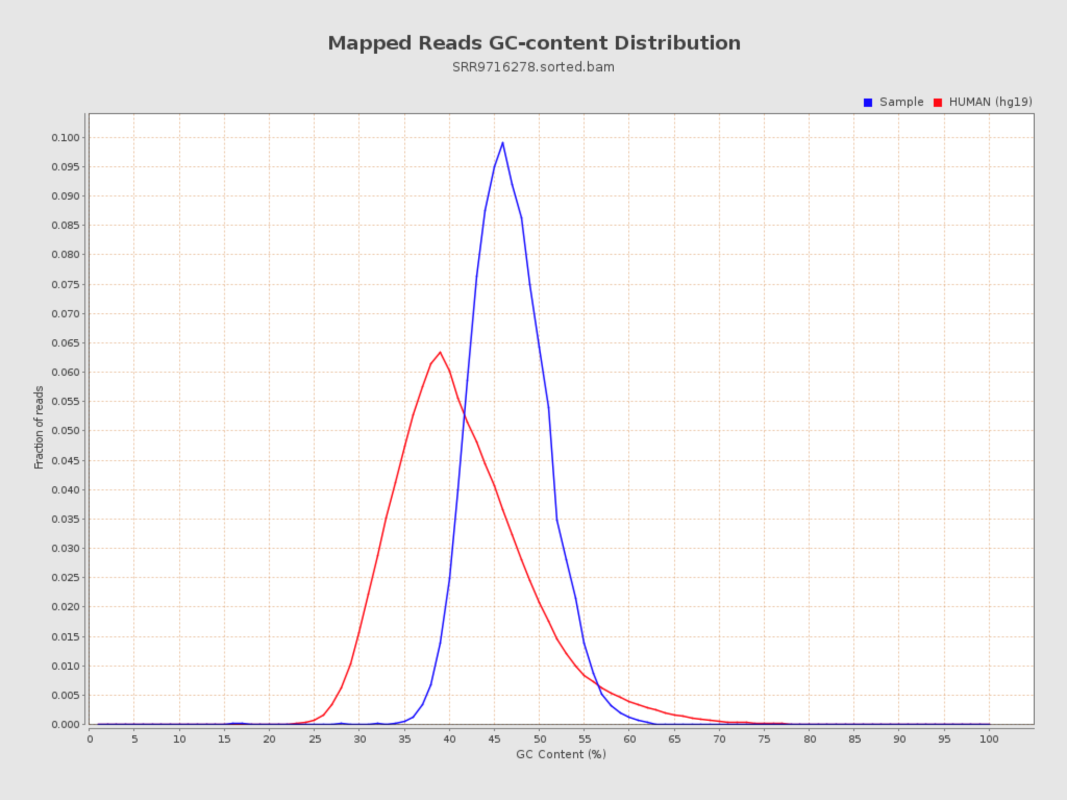
7. Results : Duplication Rate Histogram



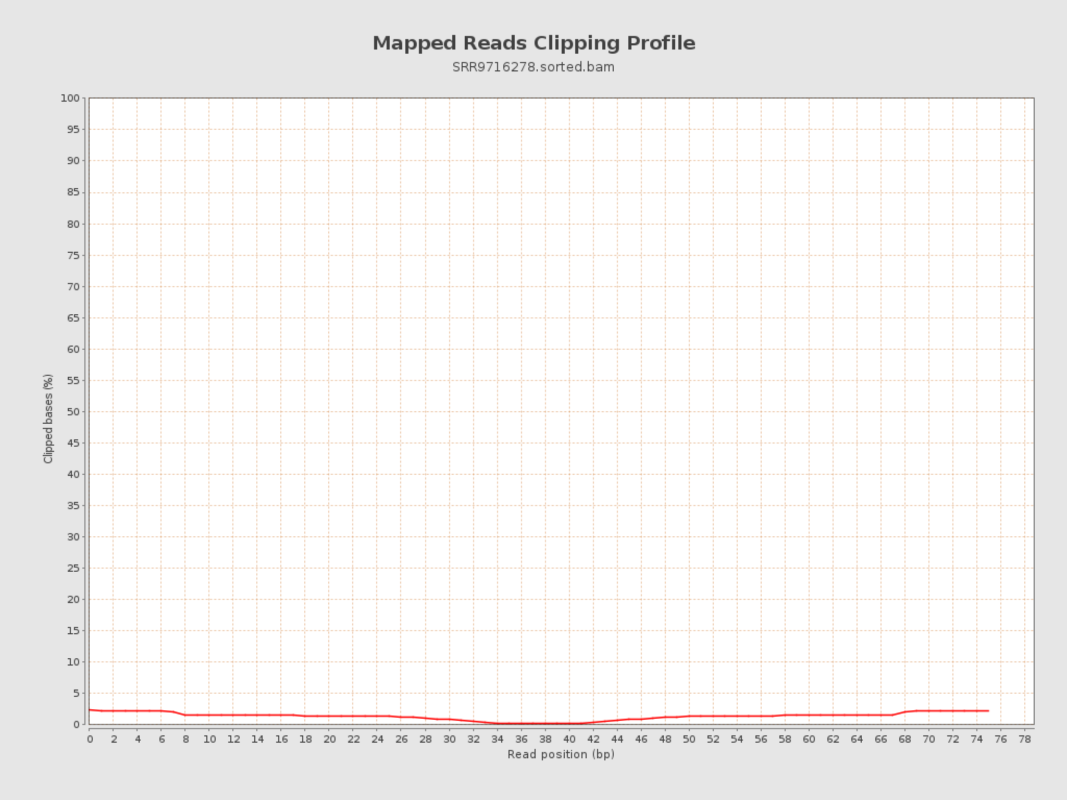
8. Results : Mapped Reads Nucleotide Content



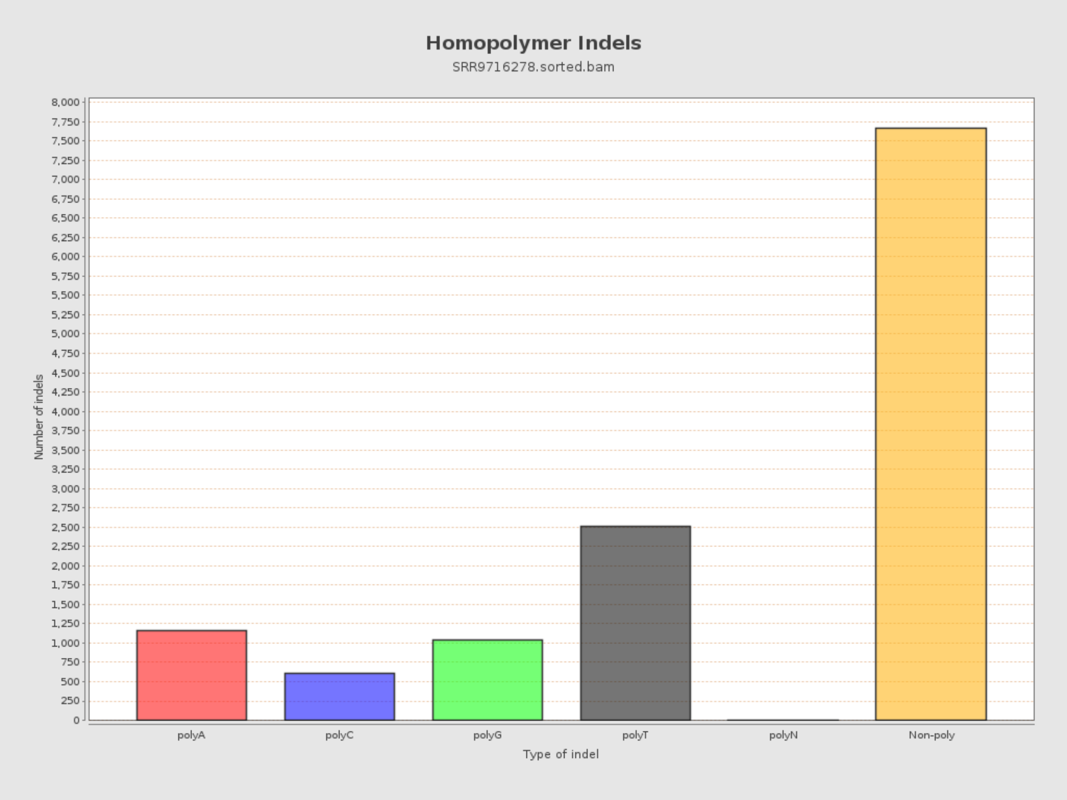
9. Results : Mapped Reads GC-content Distribution



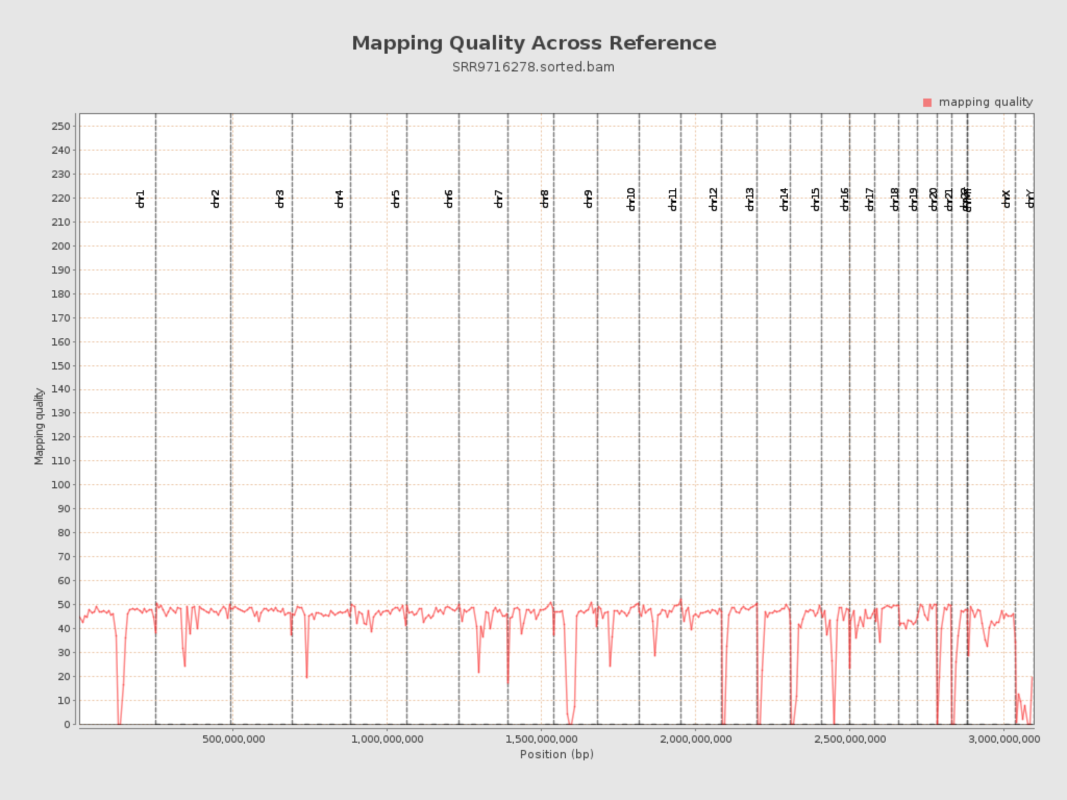
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram