Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 16:05:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716478.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_SRR9716478 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716478.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 16:05:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716478.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,160,820
Mapped reads	1,005,344 / 86.61%
Unmapped reads	155,476 / 13.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,193 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	32,136 / 2.77%
Duplication rate	2.45%
Clipped reads	1,007,917 / 86.83%

2.2. ACGT Content

Number/percentage of A's	15,090,689 / 25.81%
Number/percentage of C's	11,177,914 / 19.12%
Number/percentage of T's	18,475,572 / 31.6%
Number/percentage of G's	13,724,299 / 23.47%
Number/percentage of N's	413 / 0%
GC Percentage	42.59%

2.3. Coverage

Mean	0.0189

Standard Deviation	0.193

2.4. Mapping Quality

Mean Mapping Quality	44.71

2.5. Mismatches and indels

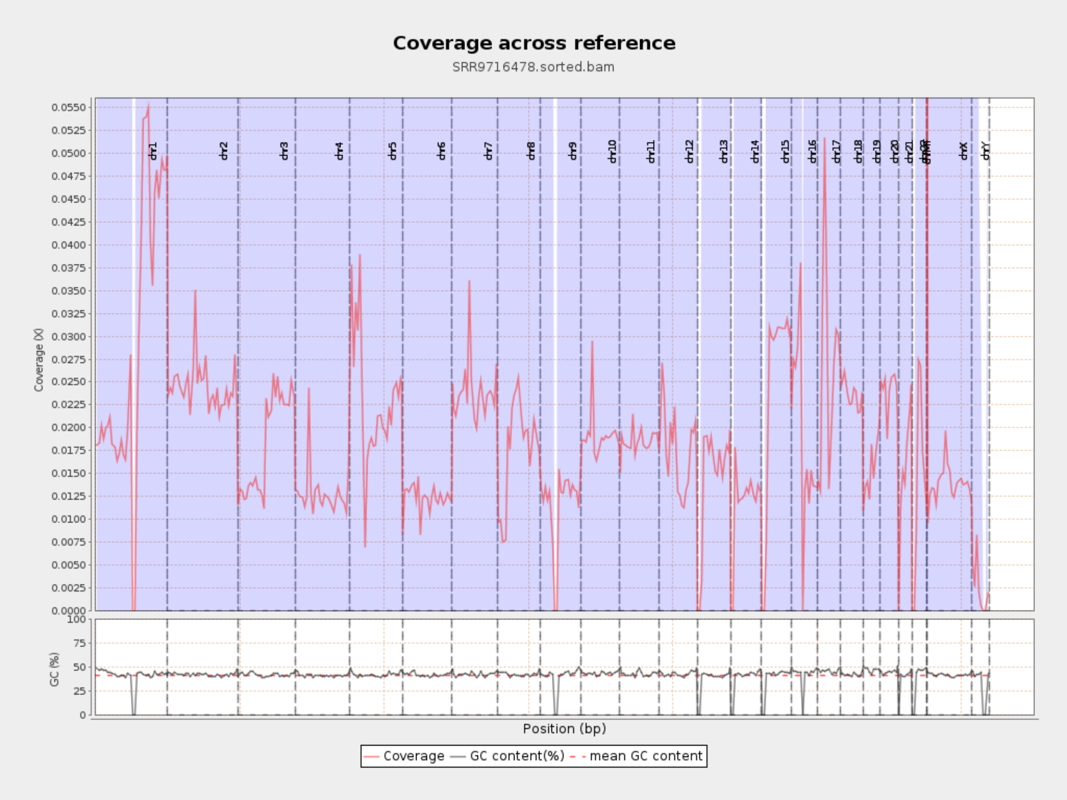
General error rate	0.51%
Mismatches	290,858
Insertions	4,659
Mapped reads with at least one insertion	0.46%
Deletions	10,631
Mapped reads with at least one deletion	1.05%
Homopolymer indels	41.51%

2.6. Chromosome stats

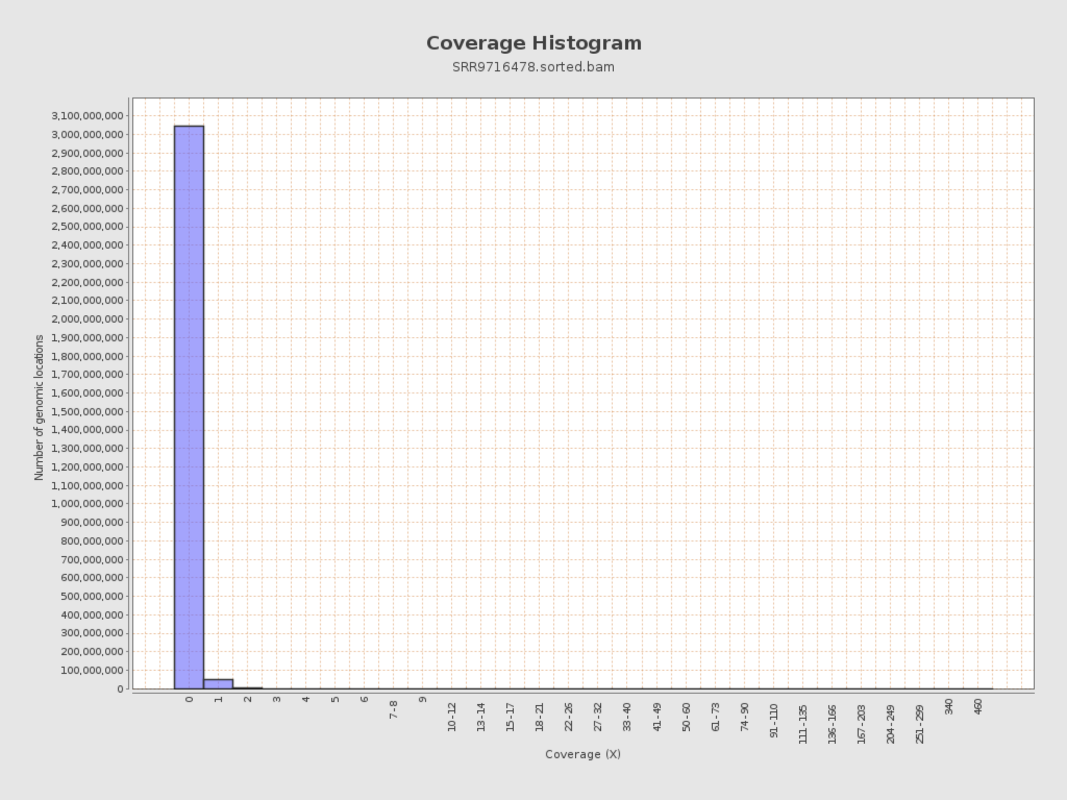
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7206581	0.0289	0.3025
chr2	243199373	5965146	0.0245	0.2676
chr3	198022430	3641872	0.0184	0.1452
chr4	191154276	2455193	0.0128	0.1356
chr5	180915260	4182421	0.0231	0.1632
chr6	171115067	2107534	0.0123	0.1283
chr7	159138663	3819001	0.024	0.2669

chr8	146364022	2609966	0.0178	0.1876
chr9	141213431	1619805	0.0115	0.1466
chr10	135534747	2606200	0.0192	0.1772
chr11	135006516	2510106	0.0186	0.189
chr12	133851895	2347498	0.0175	0.1425
chr13	115169878	1657652	0.0144	0.1294
chr14	107349540	1239533	0.0115	0.1186
chr15	102531392	2520183	0.0246	0.1683
chr16	90354753	1691232	0.0187	0.153
chr17	81195210	2212484	0.0272	0.1867
chr18	78077248	1842444	0.0236	0.3105
chr19	59128983	925393	0.0157	0.2103
chr20	63025520	1510849	0.024	0.1688
chr21	48129895	754984	0.0157	0.1435
chr22	51304566	741773	0.0145	0.1284
chrMT	16571	3978	0.2401	0.5101
chrX	155270560	2167056	0.014	0.139
chrY	59373566	147052	0.0025	0.0734

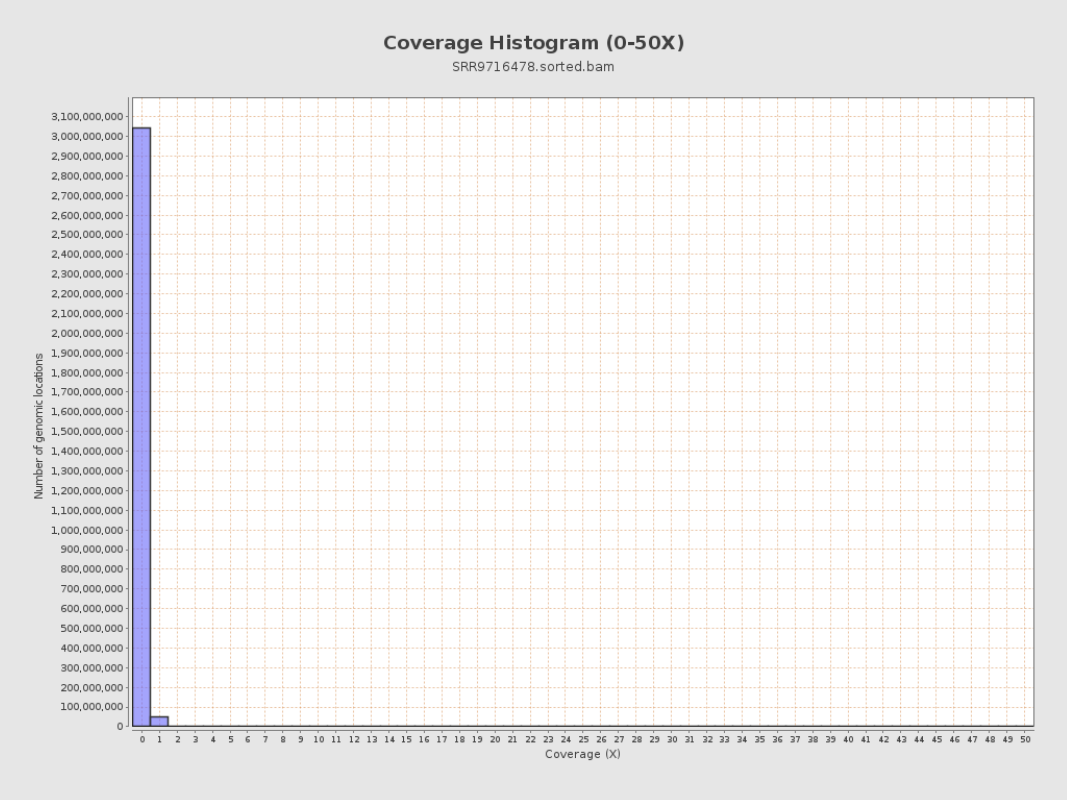
3. Results : Coverage across reference



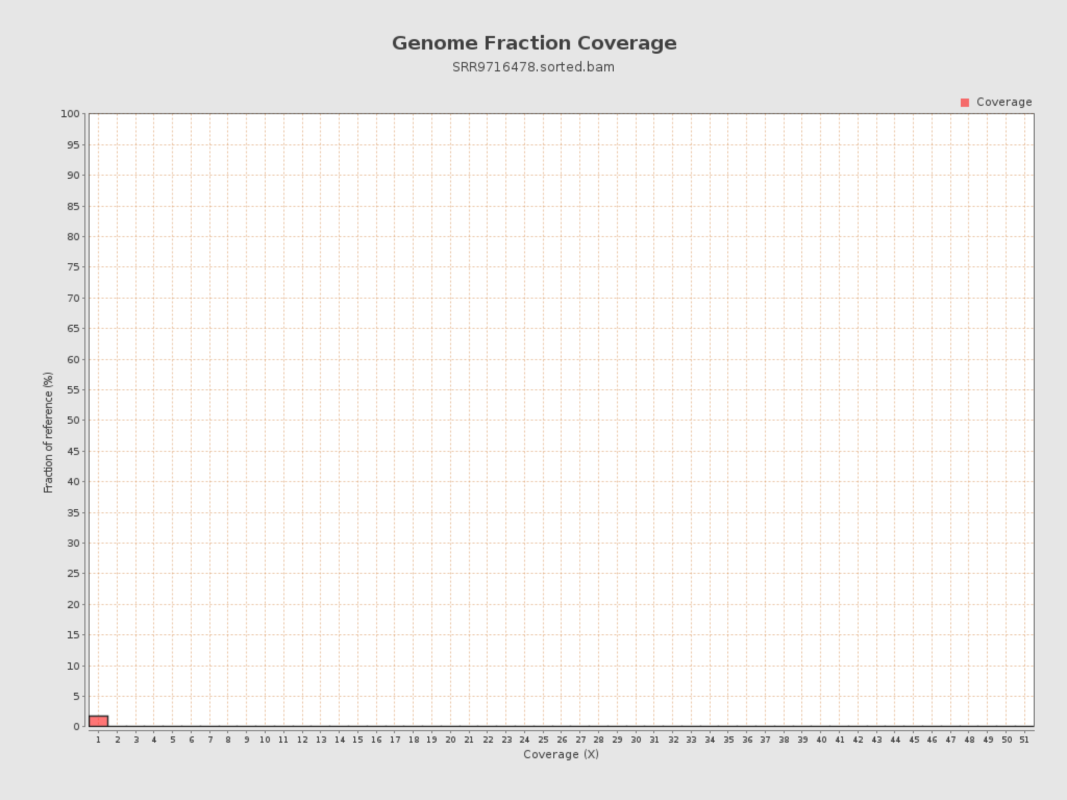
4. Results : Coverage Histogram



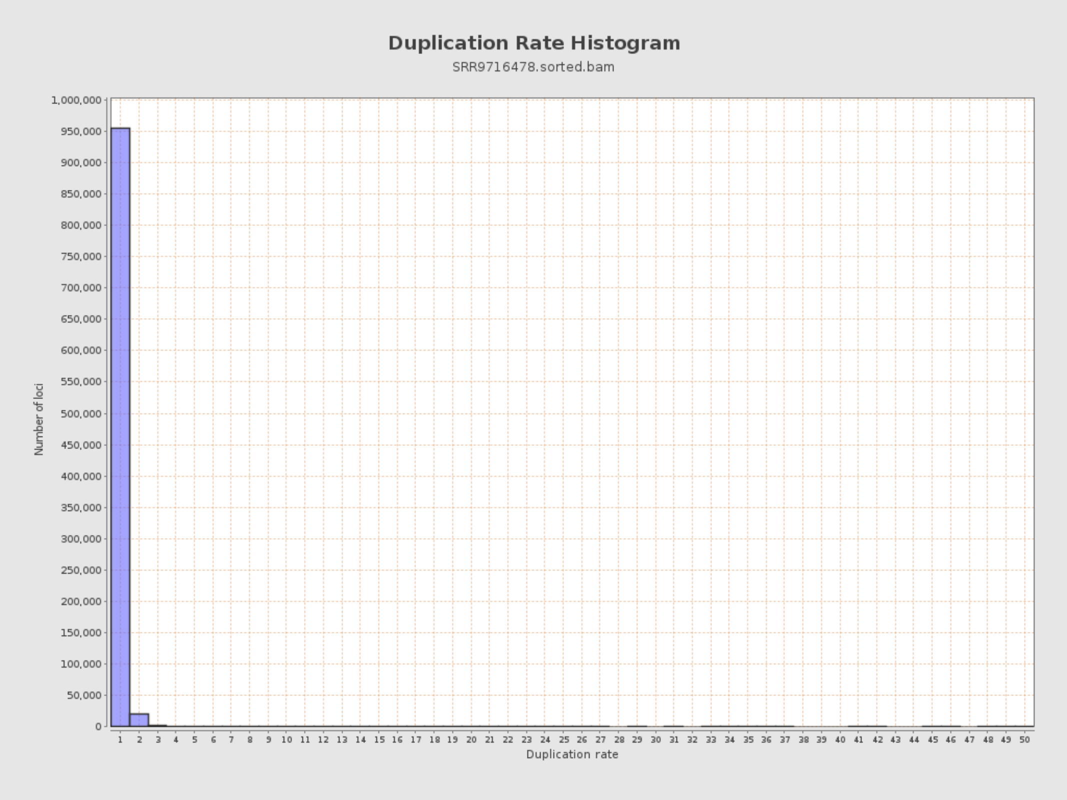
5. Results : Coverage Histogram (0-50X)



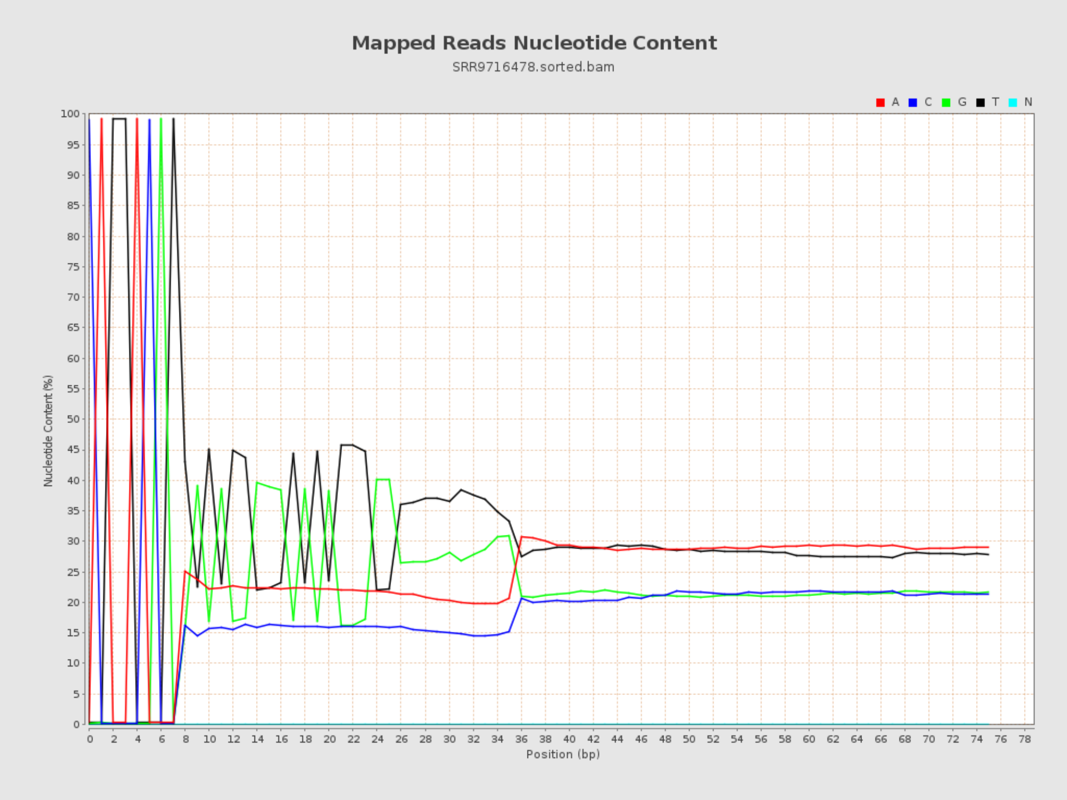
6. Results : Genome Fraction Coverage



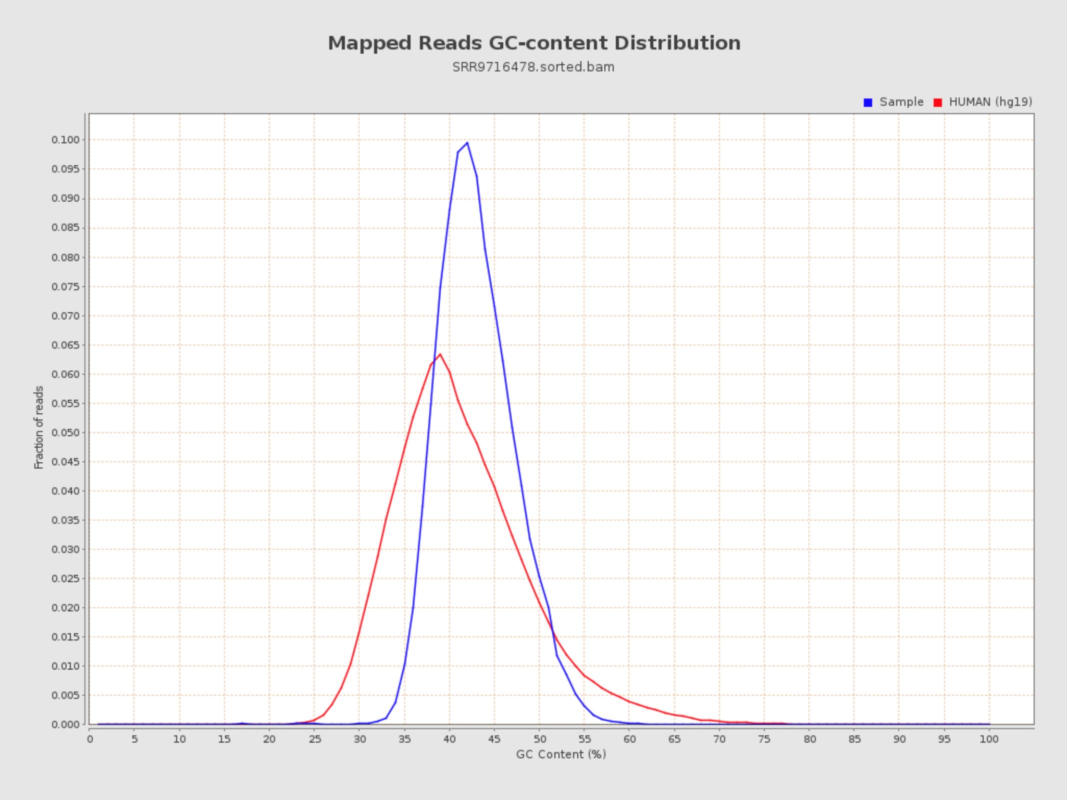
7. Results : Duplication Rate Histogram



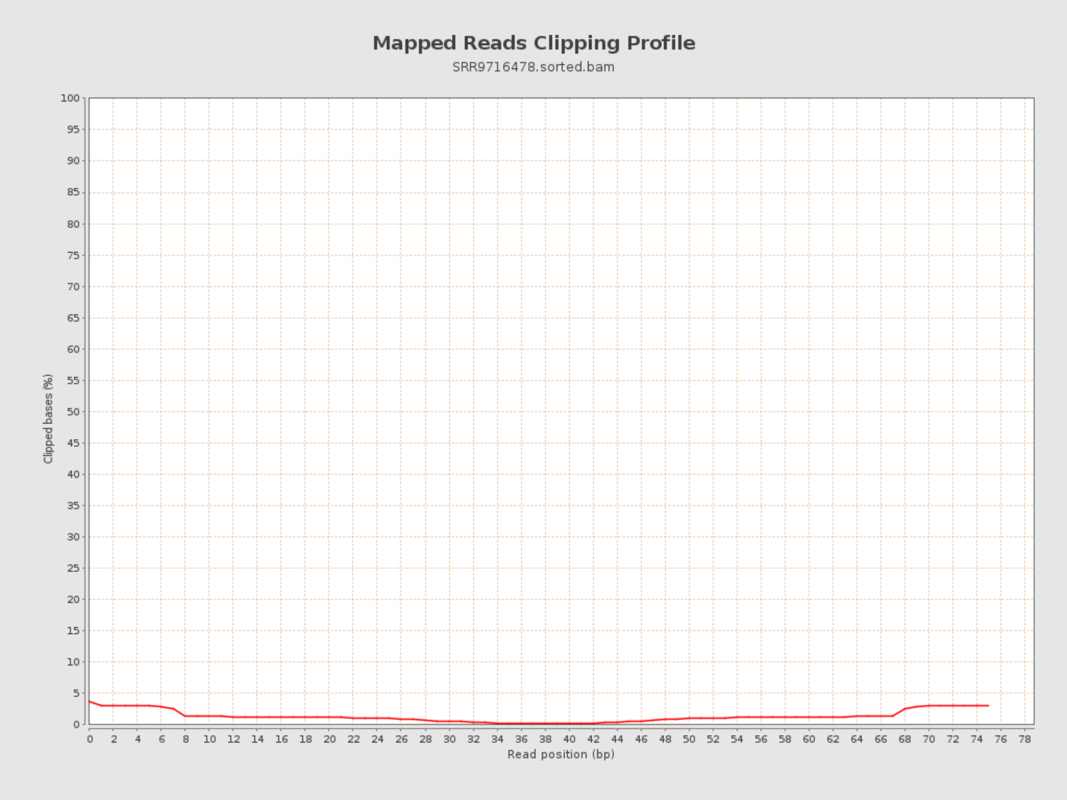
8. Results : Mapped Reads Nucleotide Content



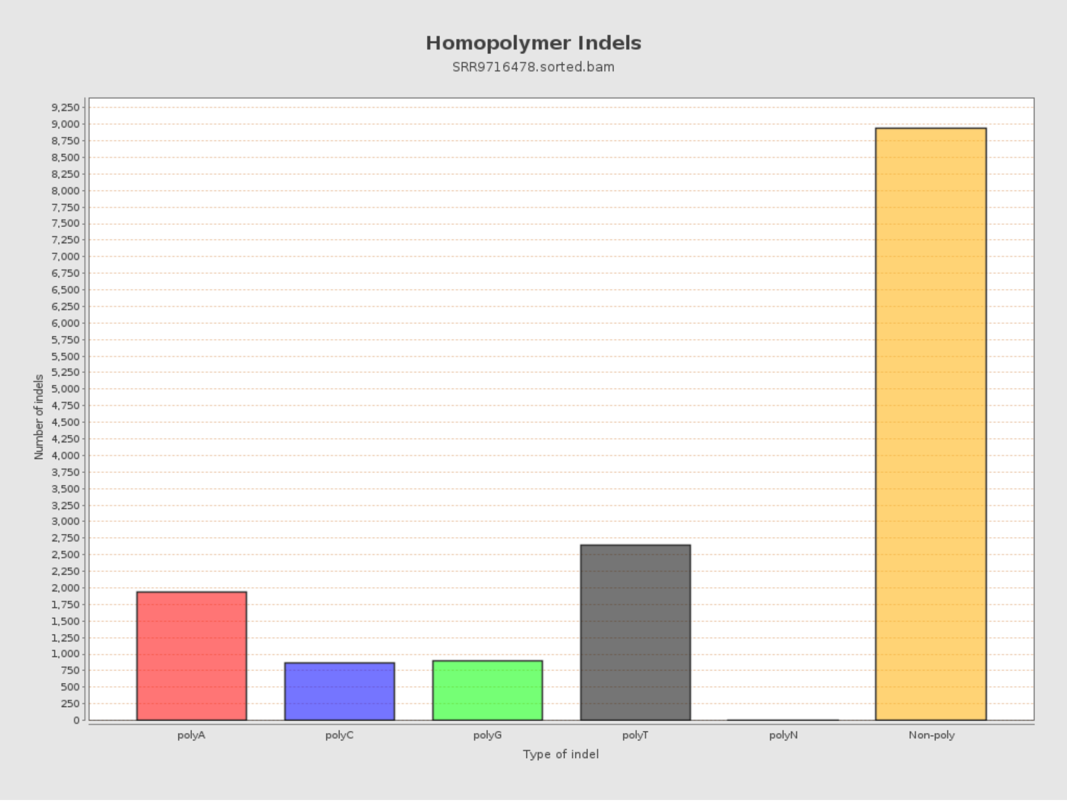
9. Results : Mapped Reads GC-content Distribution



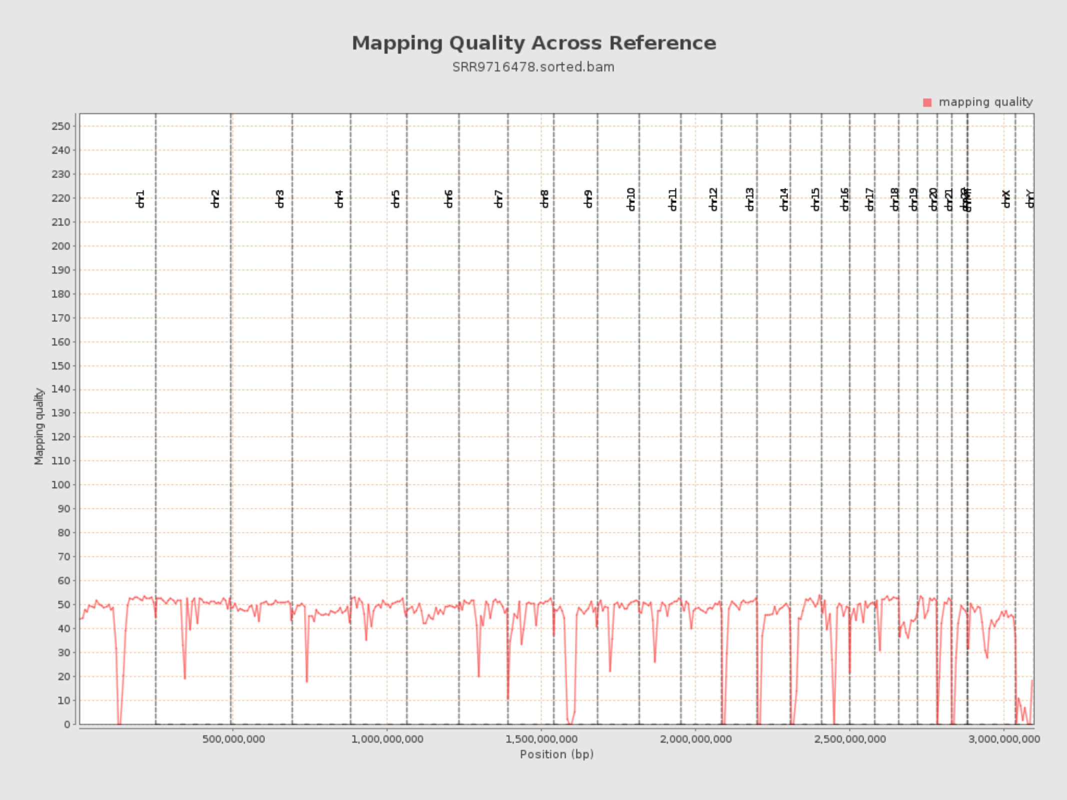
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram