Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 18:46:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716528.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_SRR9716528 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716528.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 18:46:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716528.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	559,870
Mapped reads	503,010 / 89.84%
Unmapped reads	56,860 / 10.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,864 / 0.51%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	7,450 / 1.33%
Duplication rate	1.12%
Clipped reads	504,693 / 90.14%

2.2. ACGT Content

Number/percentage of A's	7,262,392 / 25.37%
Number/percentage of C's	5,497,477 / 19.2%
Number/percentage of T's	9,055,275 / 31.63%
Number/percentage of G's	6,814,998 / 23.8%
Number/percentage of N's	585 / 0%
GC Percentage	43%

2.3. Coverage

Mean	0.0093

Standard Deviation	0.1119

2.4. Mapping Quality

Mean Mapping Quality	43.87

2.5. Mismatches and indels

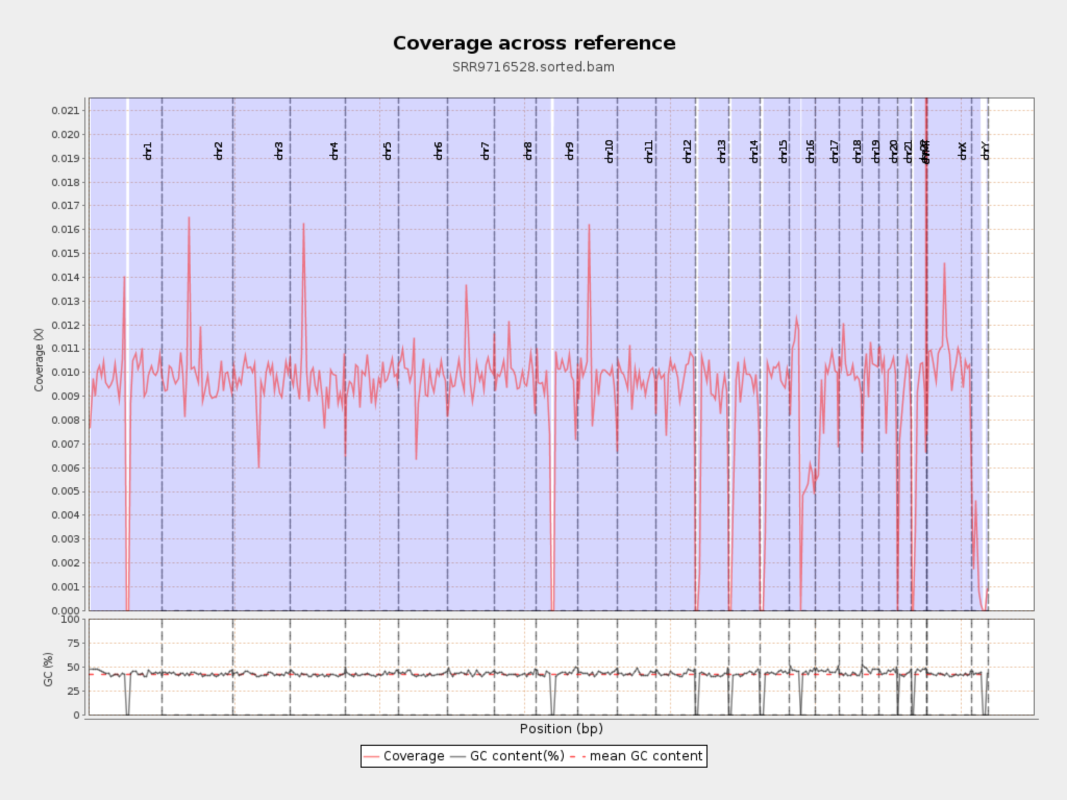
General error rate	0.52%
Mismatches	145,777
Insertions	1,813
Mapped reads with at least one insertion	0.36%
Deletions	4,998
Mapped reads with at least one deletion	0.99%
Homopolymer indels	40.92%

2.6. Chromosome stats

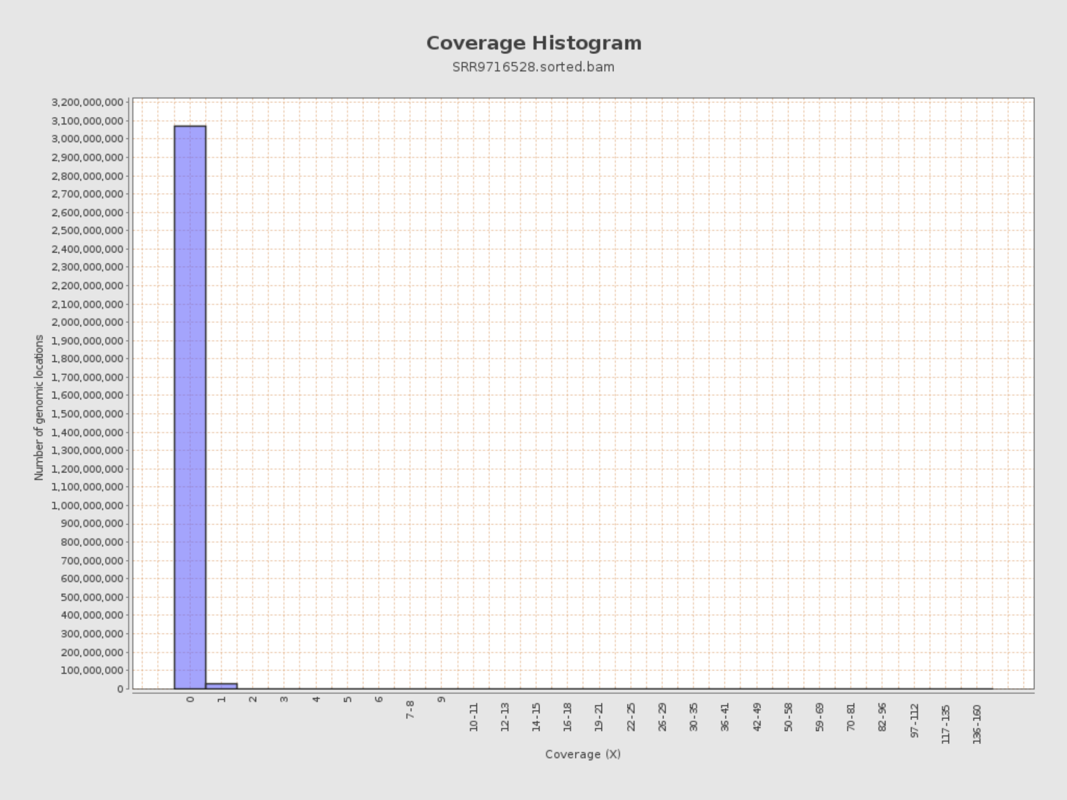
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2331624	0.0094	0.1477
chr2	243199373	2409726	0.0099	0.1206
chr3	198022430	1914176	0.0097	0.1012
chr4	191154276	1865690	0.0098	0.1054
chr5	180915260	1753558	0.0097	0.1017
chr6	171115067	1670944	0.0098	0.1042
chr7	159138663	1599486	0.0101	0.1215

chr8	146364022	1449837	0.0099	0.1096
chr9	141213431	1217726	0.0086	0.1129
chr10	135534747	1358336	0.01	0.1138
chr11	135006516	1311257	0.0097	0.1142
chr12	133851895	1313598	0.0098	0.1027
chr13	115169878	912977	0.0079	0.0914
chr14	107349540	862452	0.008	0.0947
chr15	102531392	824086	0.008	0.0921
chr16	90354753	649831	0.0072	0.0913
chr17	81195210	722205	0.0089	0.0992
chr18	78077248	794493	0.0102	0.1702
chr19	59128983	597909	0.0101	0.1197
chr20	63025520	617697	0.0098	0.1046
chr21	48129895	392404	0.0082	0.098
chr22	51304566	341534	0.0067	0.0841
chrMT	16571	10091	0.609	0.8321
chrX	155270560	1635943	0.0105	0.1123
chrY	59373566	81614	0.0014	0.0464

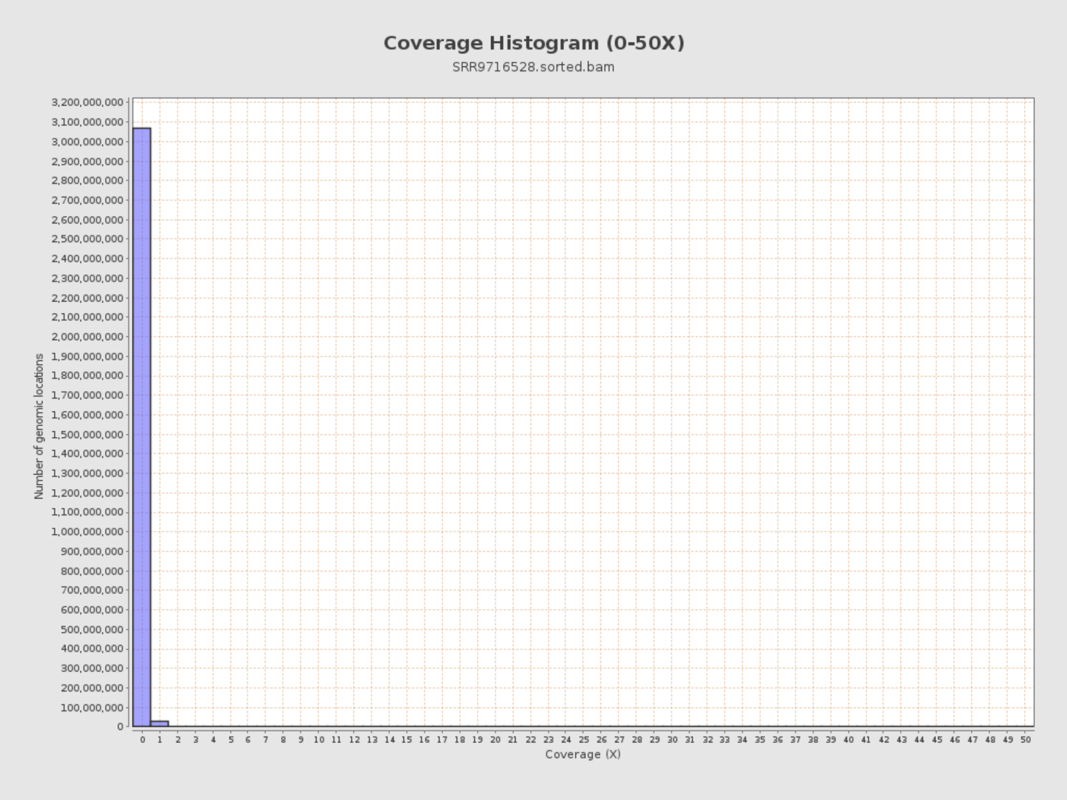
3. Results : Coverage across reference



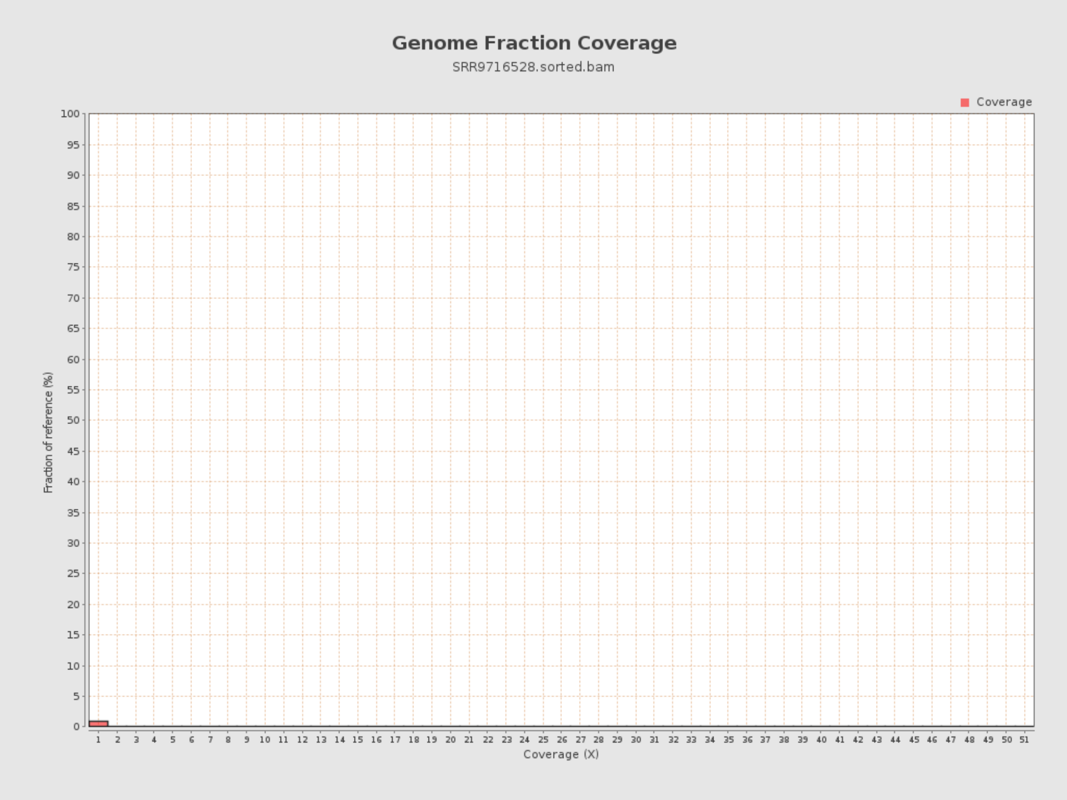
4. Results : Coverage Histogram



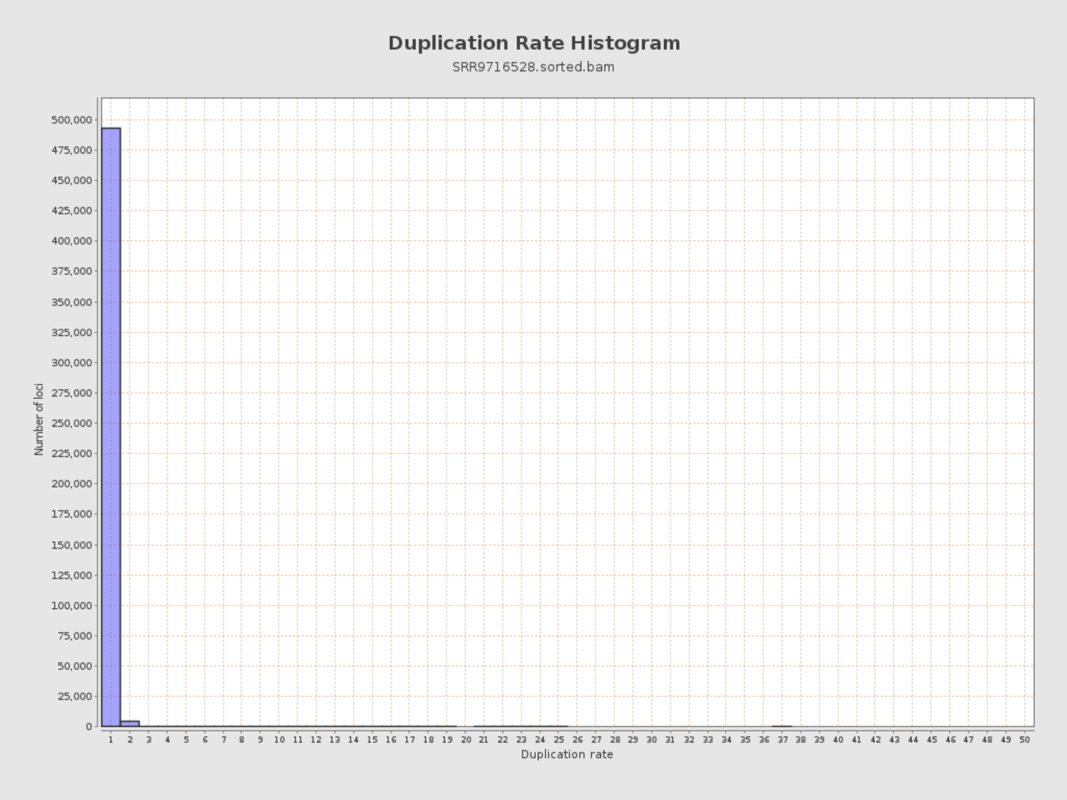
5. Results : Coverage Histogram (0-50X)



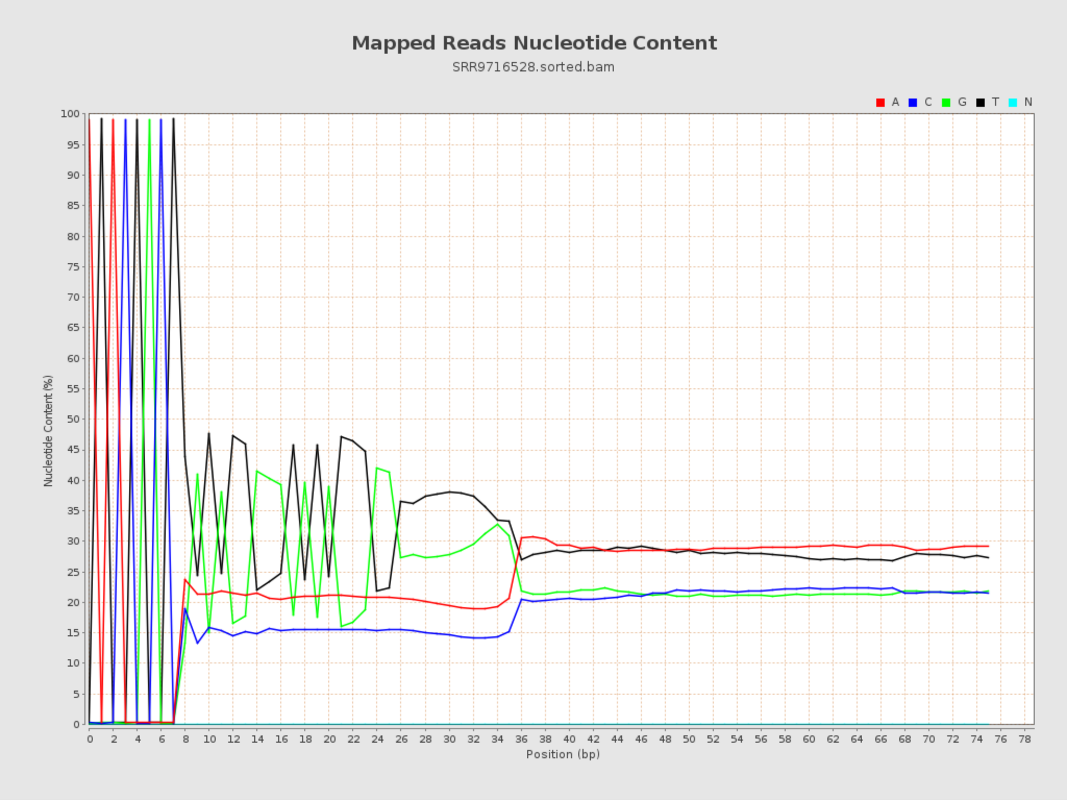
6. Results : Genome Fraction Coverage



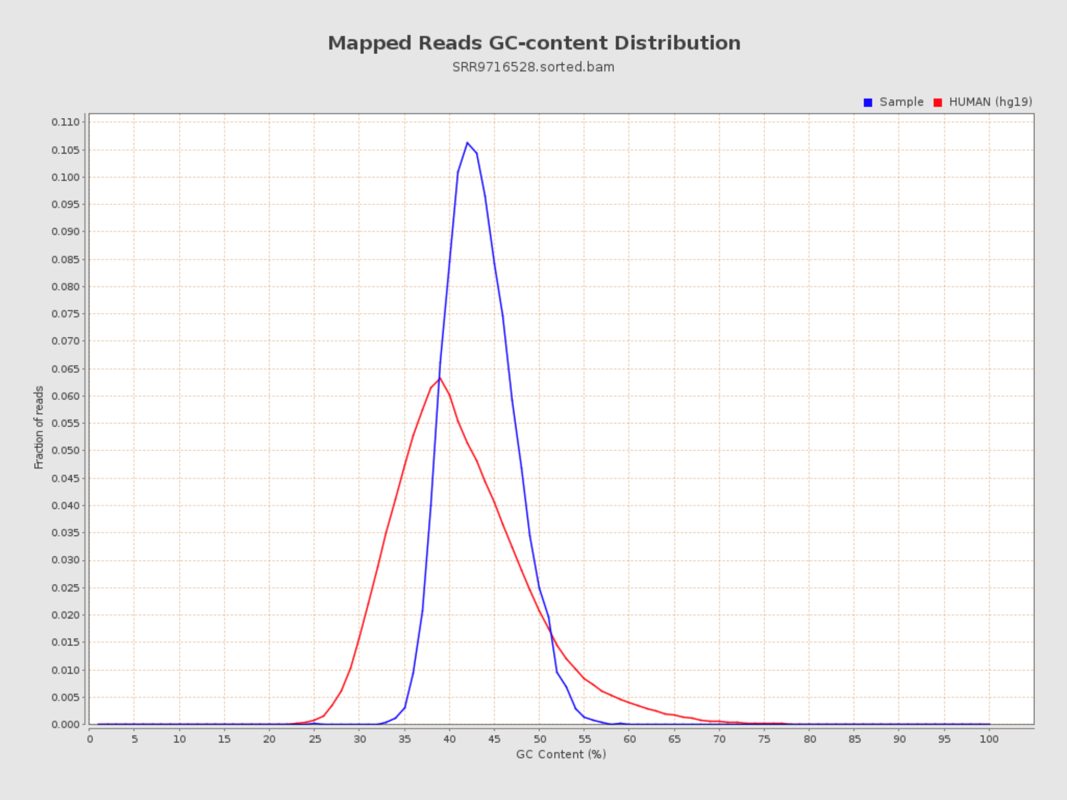
7. Results : Duplication Rate Histogram



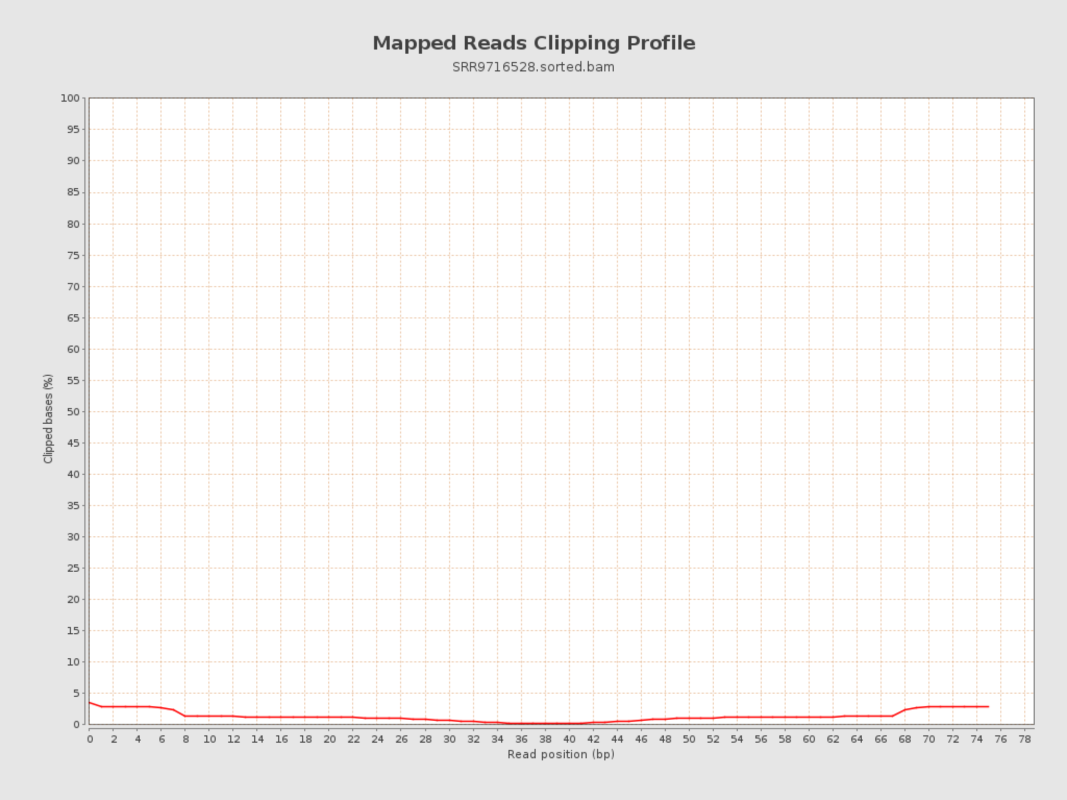
8. Results : Mapped Reads Nucleotide Content



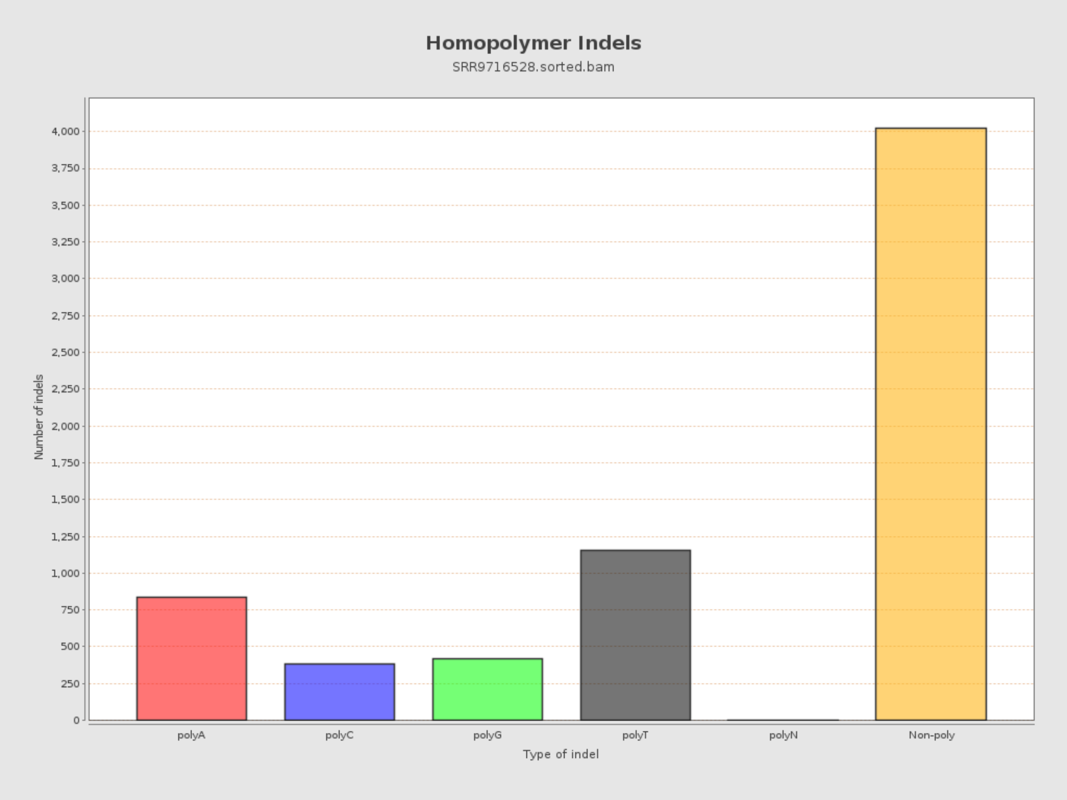
9. Results : Mapped Reads GC-content Distribution



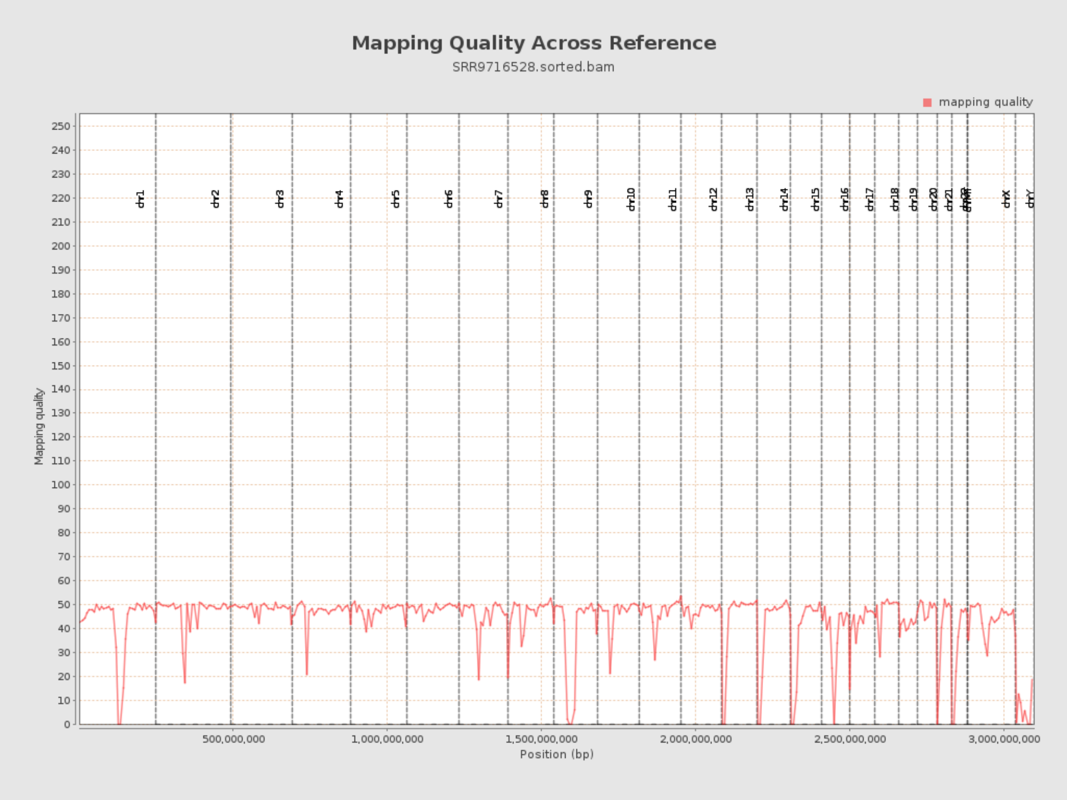
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram