Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 17:23:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716503.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_SRR9716503 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716503.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 17:23:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716503.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	878,343
Mapped reads	801,909 / 91.3%
Unmapped reads	76,434 / 8.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,138 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	23,508 / 2.68%
Duplication rate	2.28%
Clipped reads	802,448 / 91.36%

2.2. ACGT Content

Number/percentage of A's	11,042,423 / 23.88%
Number/percentage of C's	9,396,358 / 20.32%
Number/percentage of T's	14,840,156 / 32.1%
Number/percentage of G's	10,954,194 / 23.69%
Number/percentage of N's	1,336 / 0%
GC Percentage	44.02%

2.3. Coverage

Mean	0.0149

Standard Deviation	0.1655

2.4. Mapping Quality

Mean Mapping Quality	45.11

2.5. Mismatches and indels

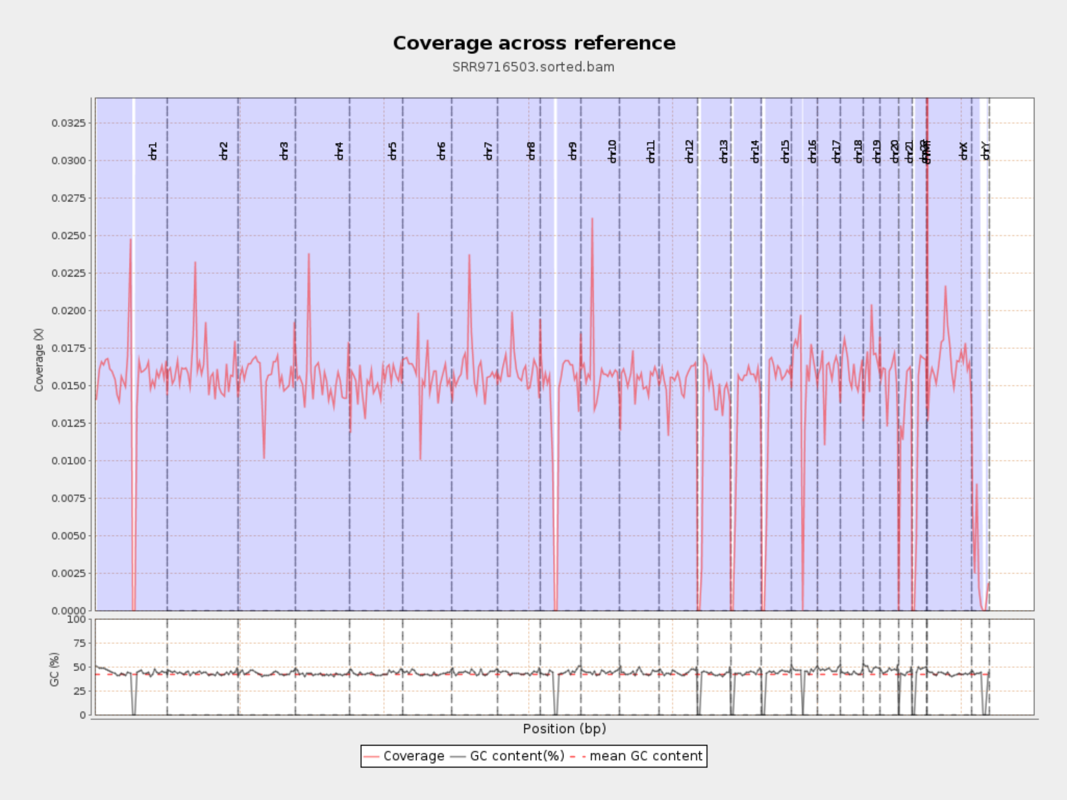
General error rate	0.52%
Mismatches	236,371
Insertions	3,333
Mapped reads with at least one insertion	0.41%
Deletions	9,009
Mapped reads with at least one deletion	1.12%
Homopolymer indels	42.38%

2.6. Chromosome stats

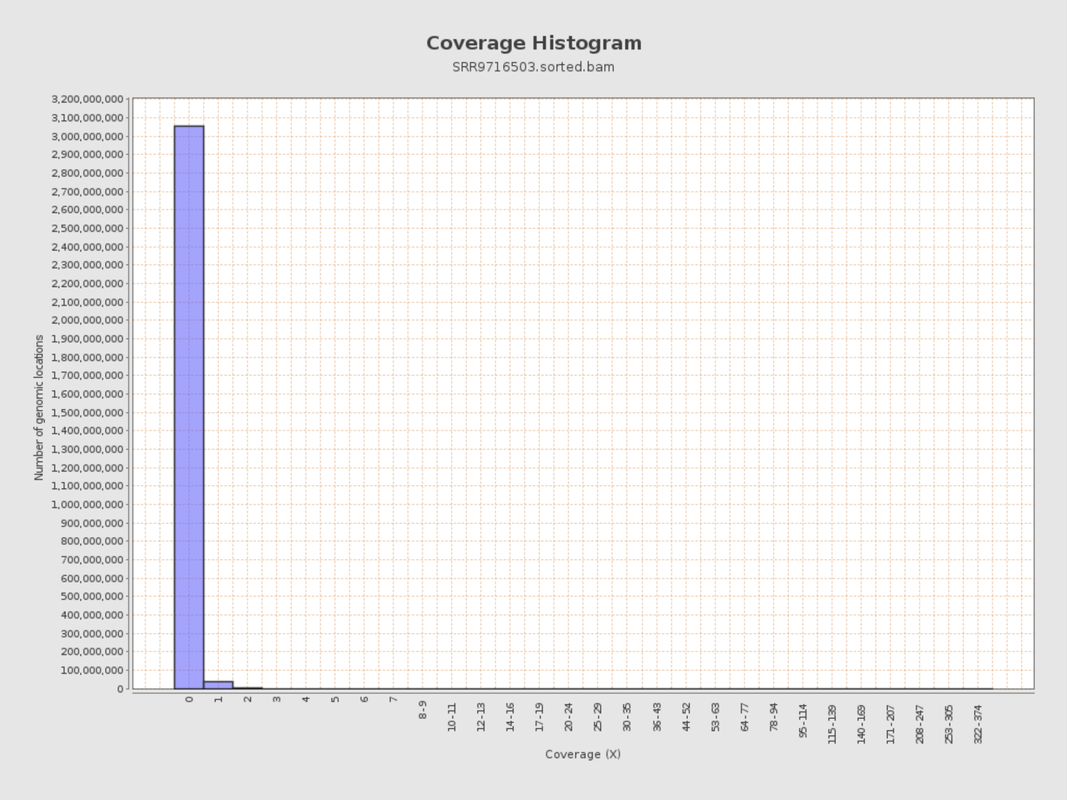
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3735916	0.015	0.2777
chr2	243199373	3908798	0.0161	0.2074
chr3	198022430	3092559	0.0156	0.1324
chr4	191154276	2974431	0.0156	0.138
chr5	180915260	2766635	0.0153	0.131
chr6	171115067	2689972	0.0157	0.1451
chr7	159138663	2562887	0.0161	0.1857

chr8	146364022	2345217	0.016	0.1586
chr9	141213431	1935025	0.0137	0.1476
chr10	135534747	2175044	0.016	0.1598
chr11	135006516	2084341	0.0154	0.1494
chr12	133851895	2042985	0.0153	0.132
chr13	115169878	1426867	0.0124	0.1176
chr14	107349540	1382590	0.0129	0.1222
chr15	102531392	1332974	0.013	0.1211
chr16	90354753	1366680	0.0151	0.1354
chr17	81195210	1276790	0.0157	0.1372
chr18	78077248	1254039	0.0161	0.2172
chr19	59128983	988653	0.0167	0.2099
chr20	63025520	972671	0.0154	0.1333
chr21	48129895	614313	0.0128	0.1262
chr22	51304566	576695	0.0112	0.1124
chrMT	16571	4392	0.265	0.5516
chrX	155270560	2591130	0.0167	0.1432
chrY	59373566	147035	0.0025	0.0736

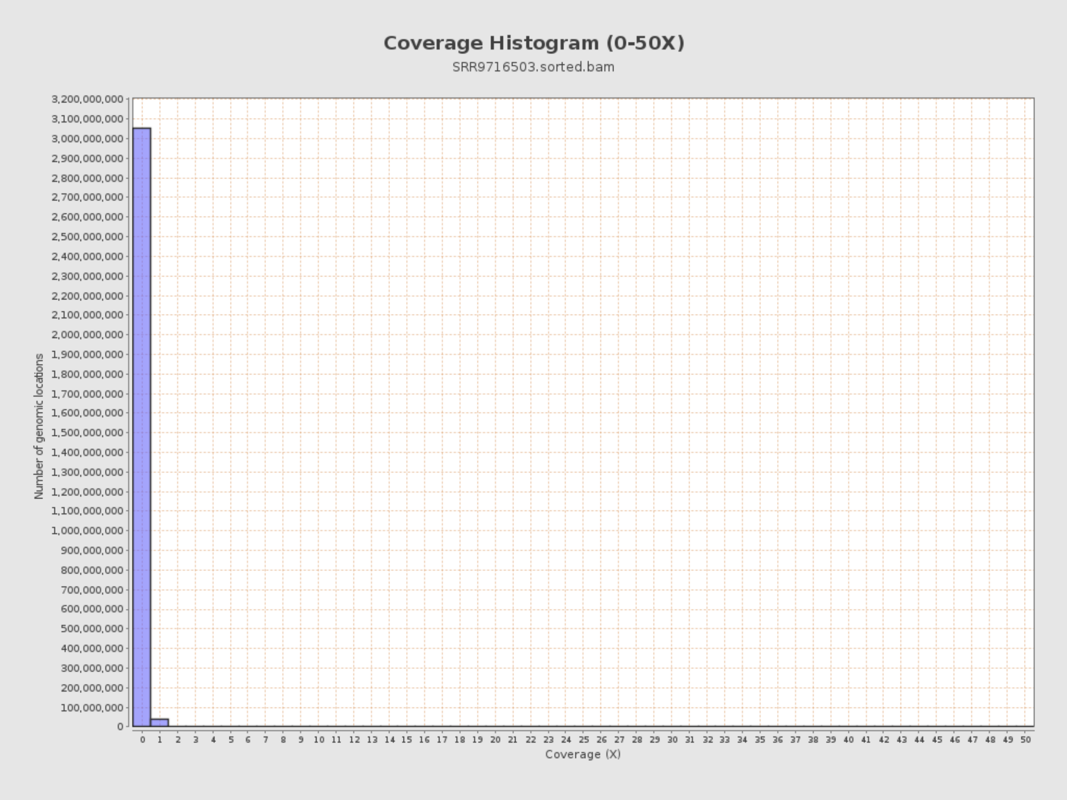
3. Results : Coverage across reference



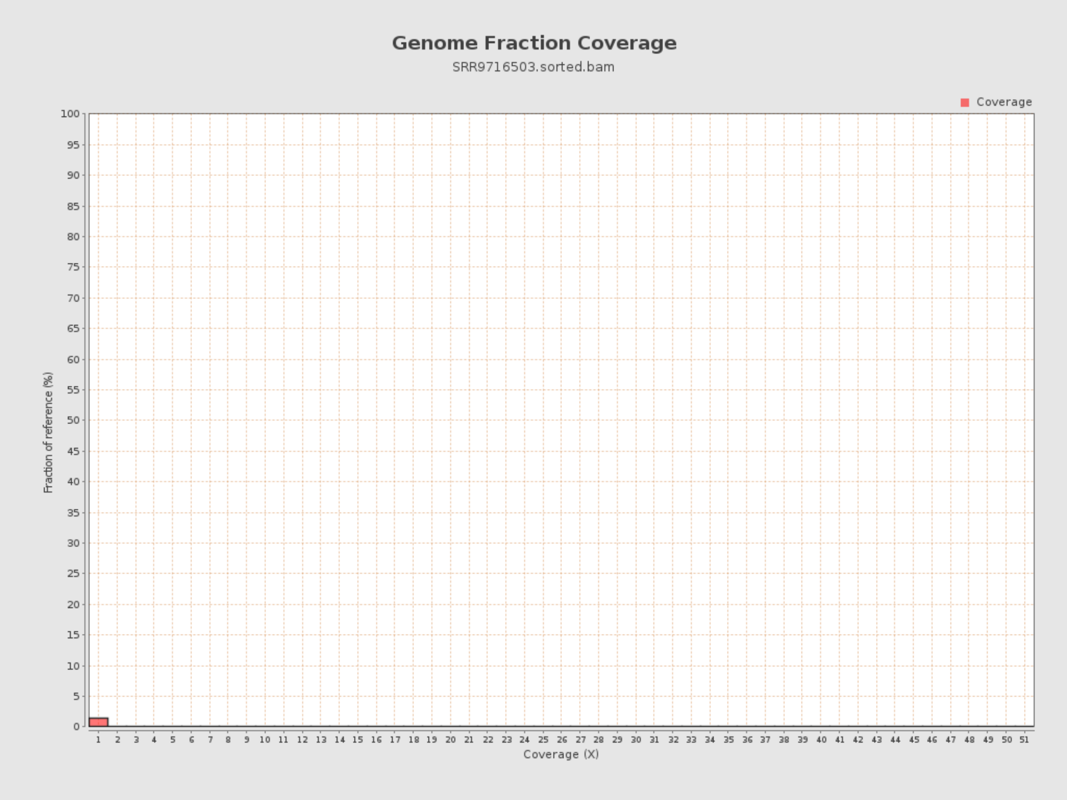
4. Results : Coverage Histogram



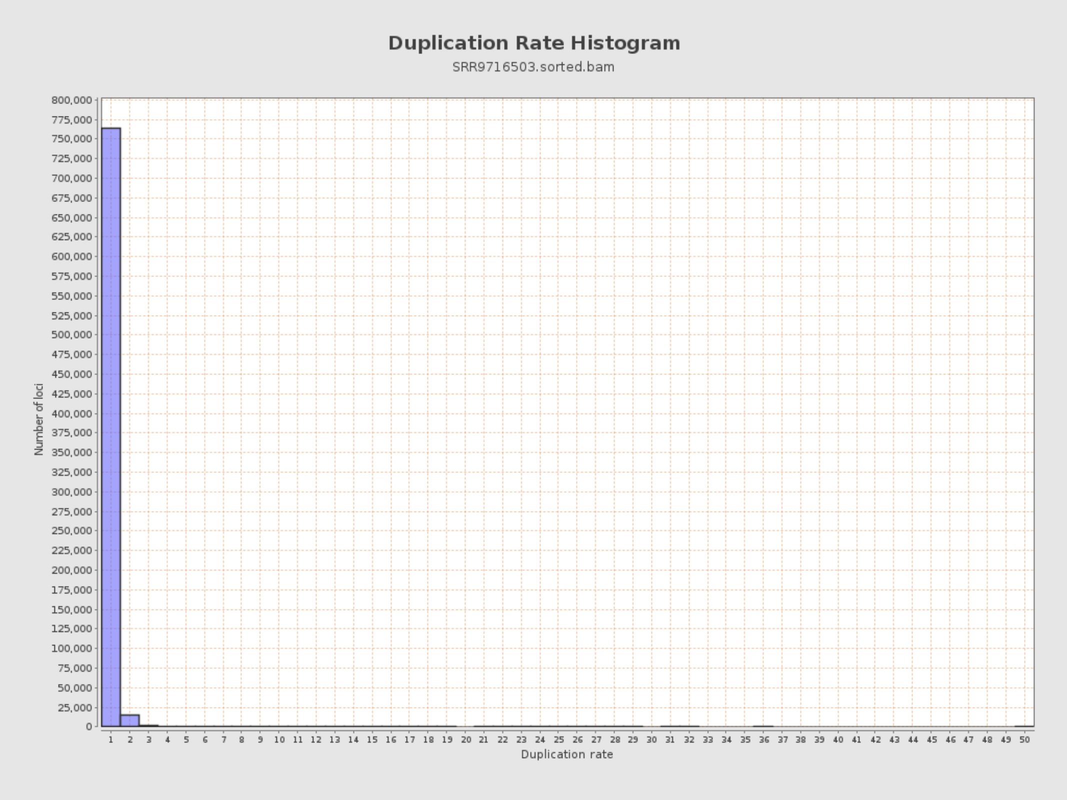
5. Results : Coverage Histogram (0-50X)



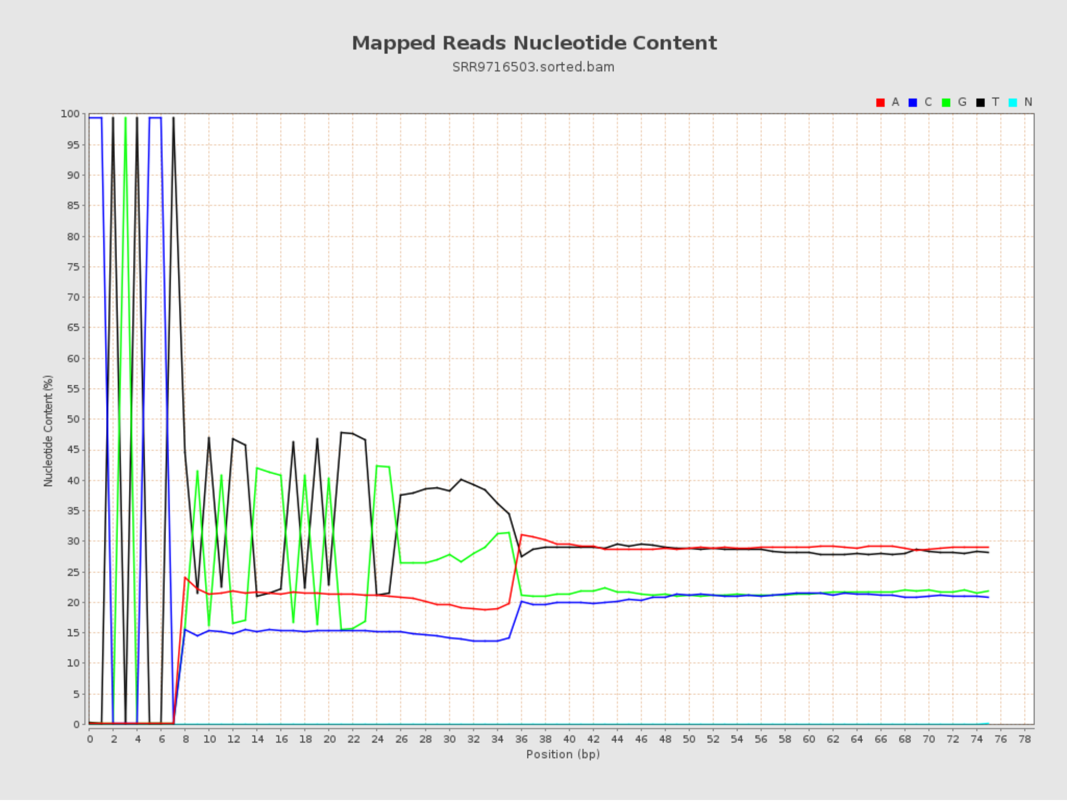
6. Results : Genome Fraction Coverage



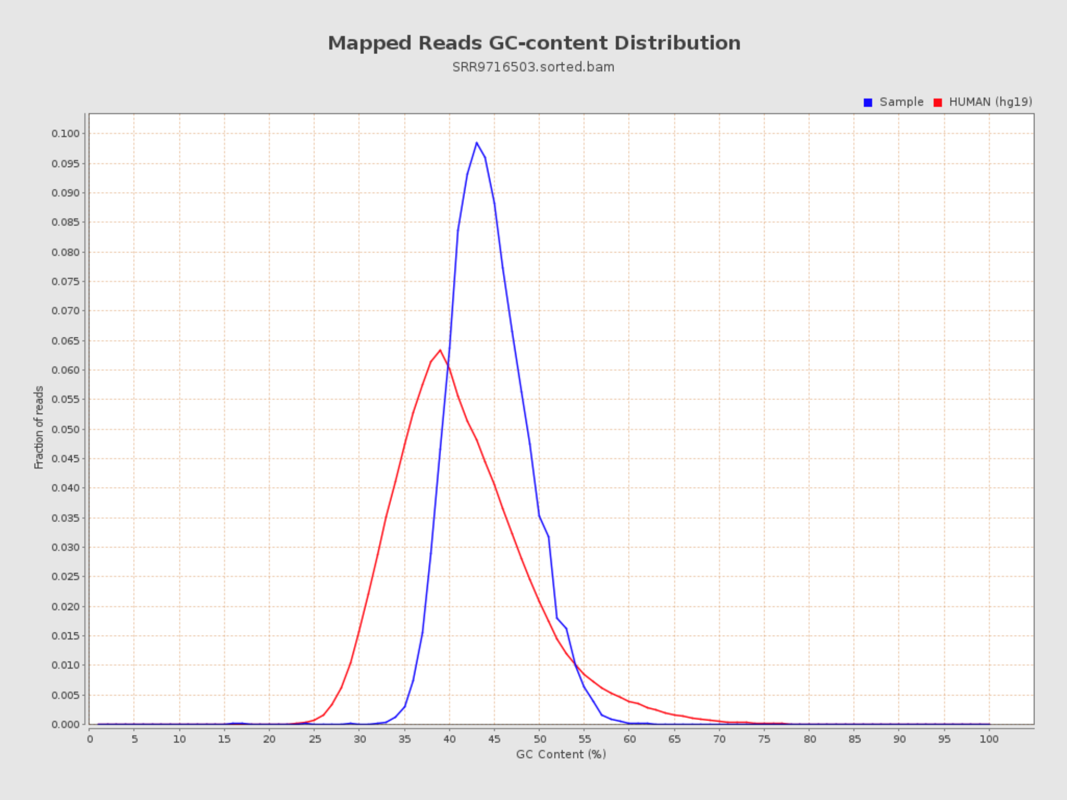
7. Results : Duplication Rate Histogram



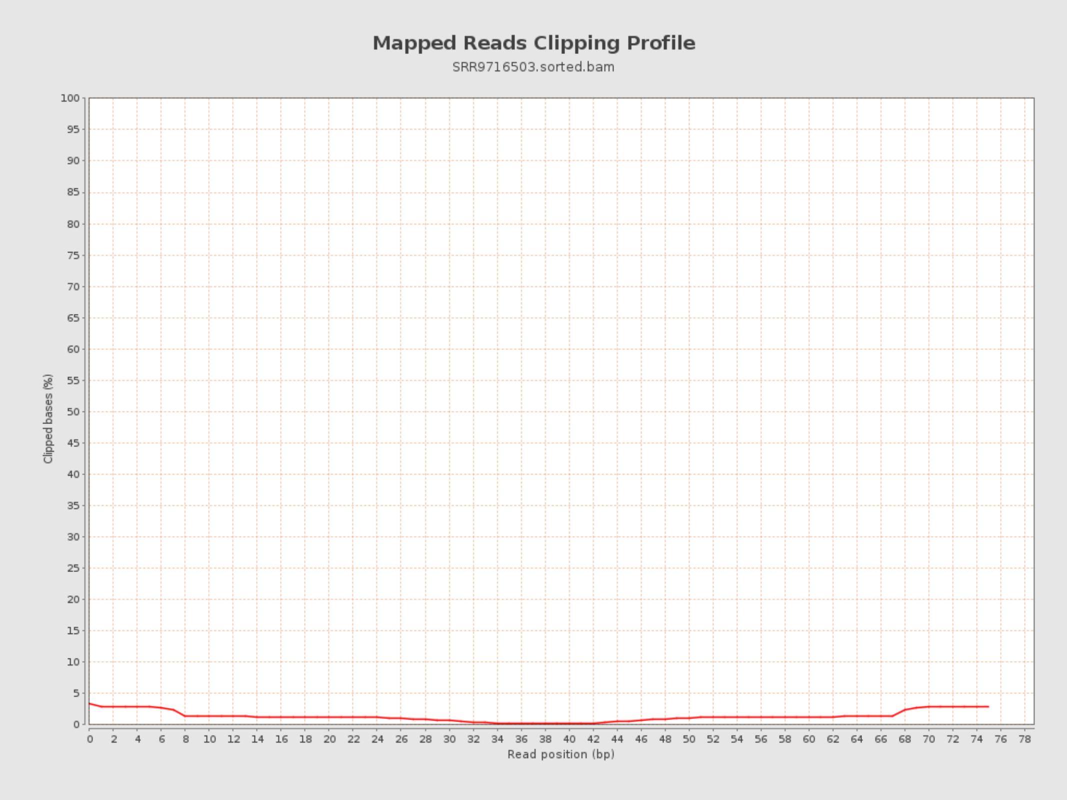
8. Results : Mapped Reads Nucleotide Content



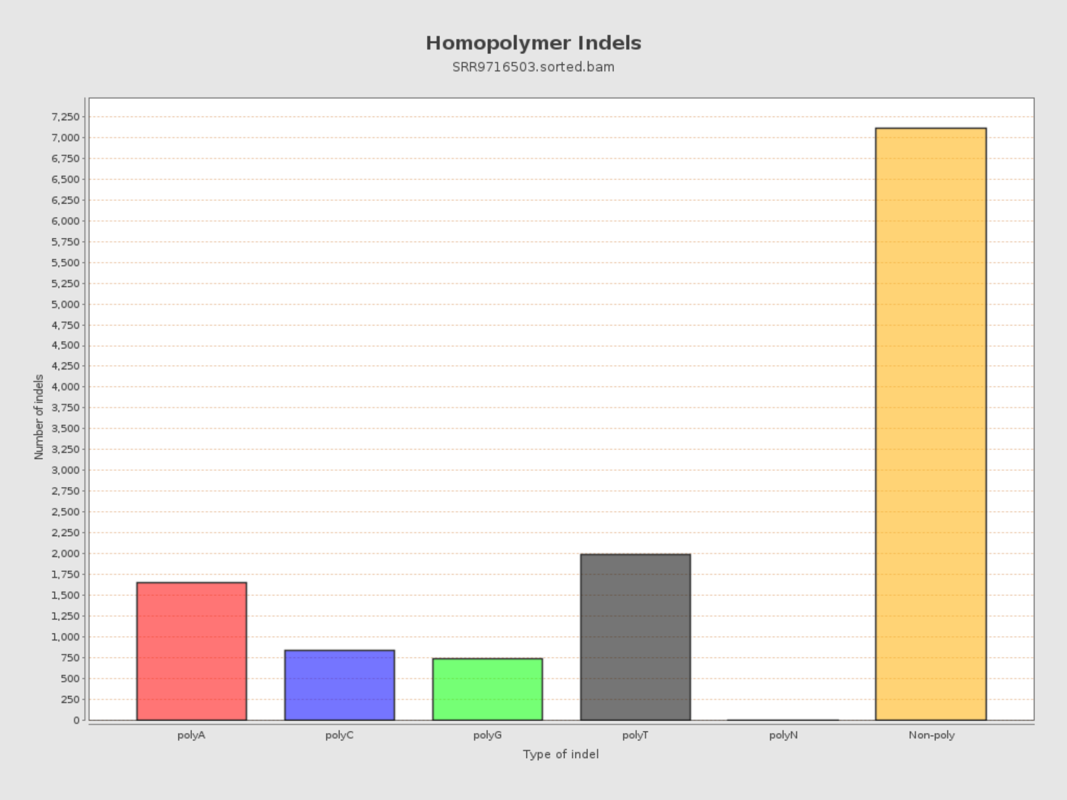
9. Results : Mapped Reads GC-content Distribution



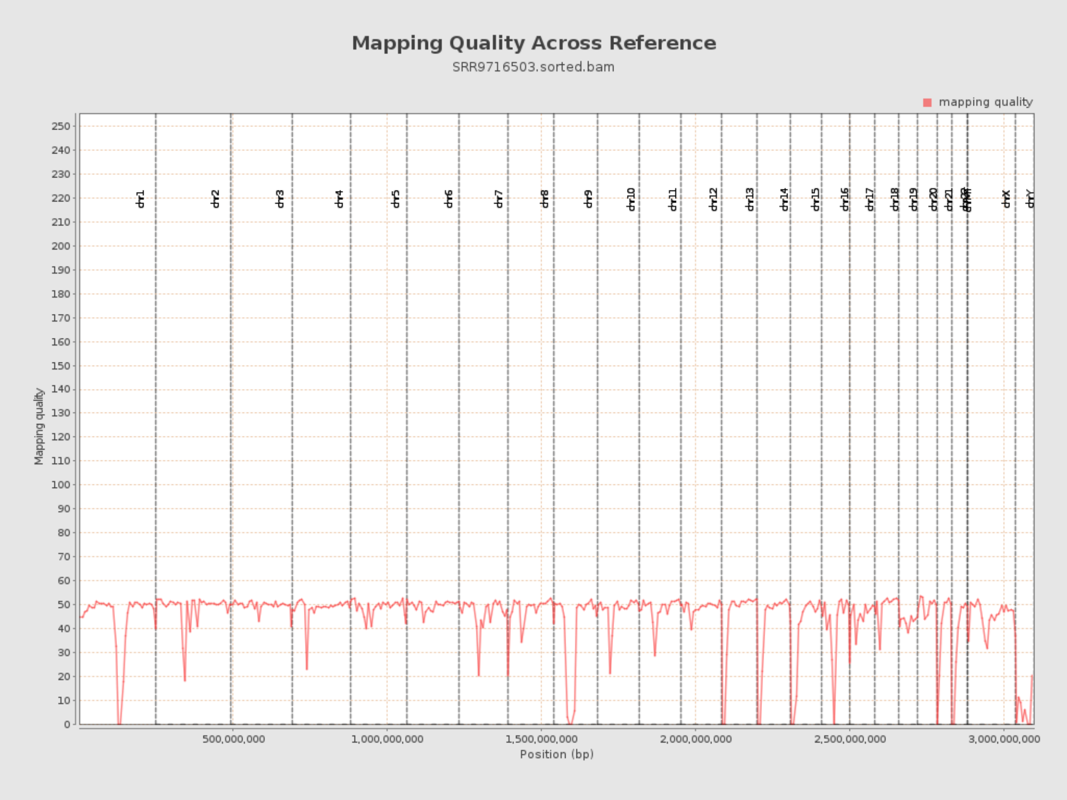
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram