Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 21:18:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524291.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_SRR10524291 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524291.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 21:18:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524291.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	945,623
Mapped reads	880,794 / 93.14%
Unmapped reads	64,829 / 6.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,115 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	22,284 / 2.36%
Duplication rate	1.79%
Clipped reads	882,030 / 93.28%

2.2. ACGT Content

Number/percentage of A's	13,839,649 / 26.46%
Number/percentage of C's	9,768,036 / 18.67%
Number/percentage of T's	15,937,341 / 30.47%
Number/percentage of G's	12,758,145 / 24.39%
Number/percentage of N's	7,087 / 0.01%
GC Percentage	43.06%

2.3. Coverage

Mean	0.0169

Standard Deviation	0.1899

2.4. Mapping Quality

Mean Mapping Quality	46.54

2.5. Mismatches and indels

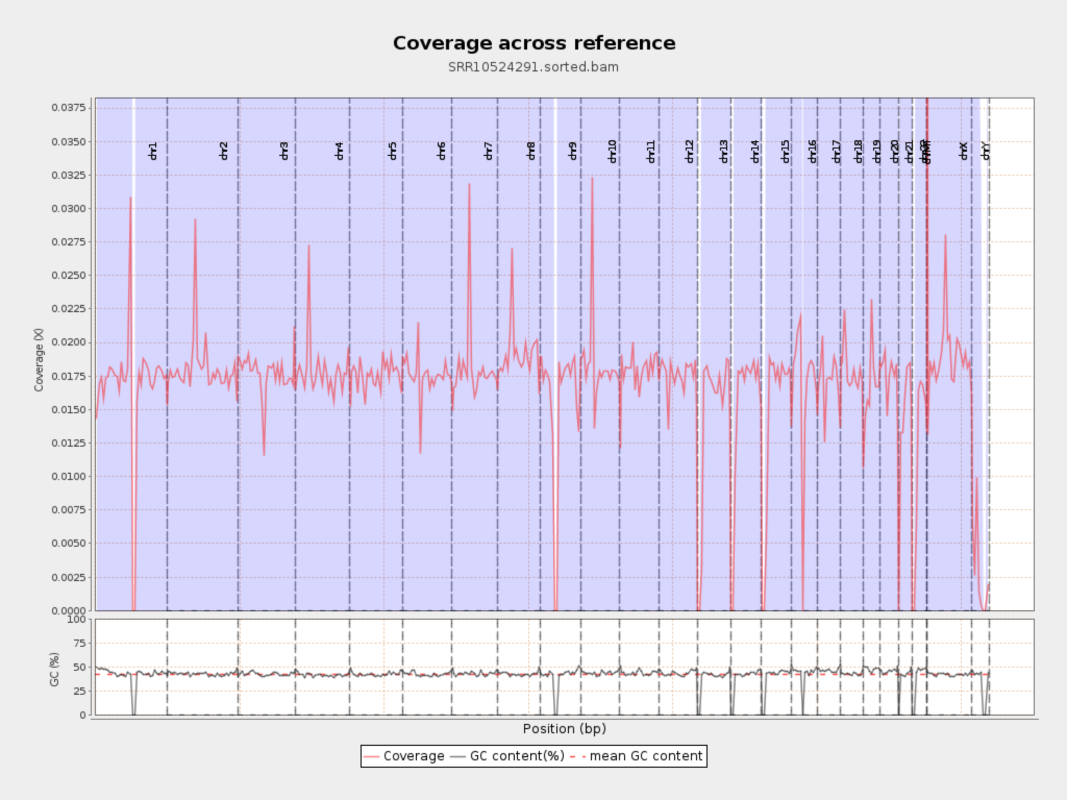
General error rate	0.5%
Mismatches	253,432
Insertions	3,991
Mapped reads with at least one insertion	0.45%
Deletions	10,068
Mapped reads with at least one deletion	1.14%
Homopolymer indels	42.63%

2.6. Chromosome stats

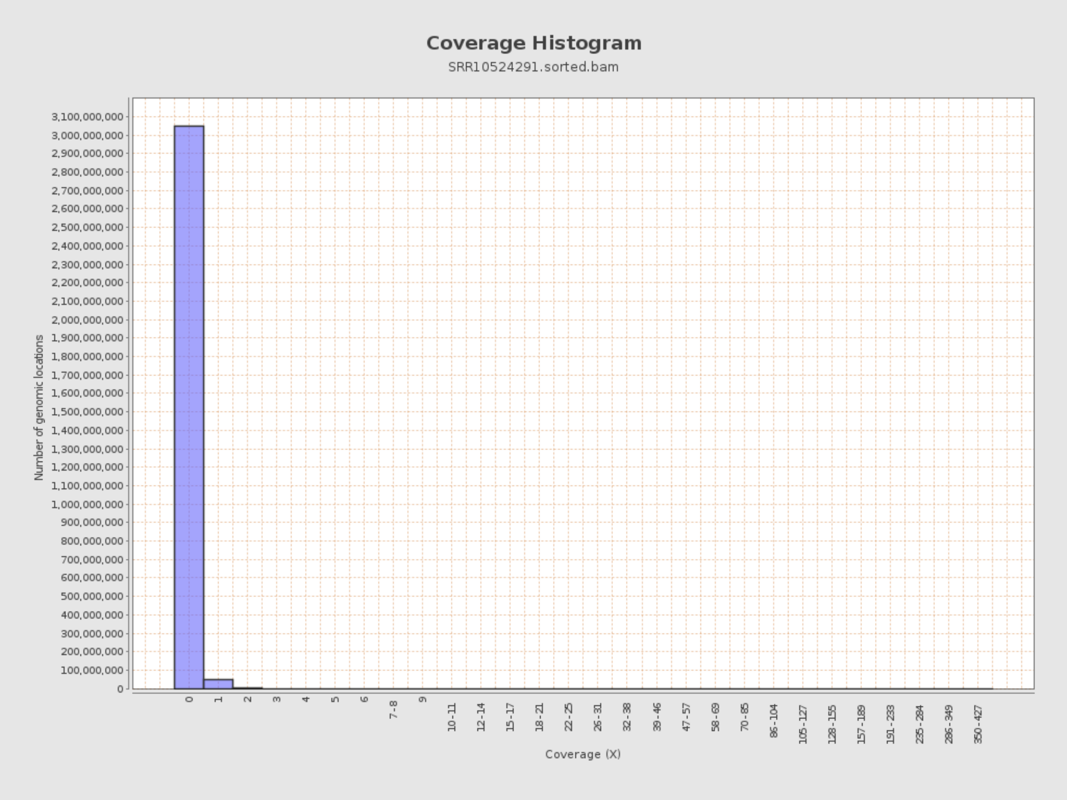
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4154130	0.0167	0.3463
chr2	243199373	4408293	0.0181	0.193
chr3	198022430	3481792	0.0176	0.1389
chr4	191154276	3423844	0.0179	0.1492
chr5	180915260	3189544	0.0176	0.1388
chr6	171115067	3003211	0.0176	0.147
chr7	159138663	2883190	0.0181	0.2569

chr8	146364022	2811999	0.0192	0.1913
chr9	141213431	2164973	0.0153	0.166
chr10	135534747	2497629	0.0184	0.1832
chr11	135006516	2426065	0.018	0.1756
chr12	133851895	2353314	0.0176	0.1405
chr13	115169878	1654759	0.0144	0.1247
chr14	107349540	1602027	0.0149	0.1332
chr15	102531392	1481268	0.0144	0.1253
chr16	90354753	1494095	0.0165	0.1436
chr17	81195210	1393026	0.0172	0.1452
chr18	78077248	1401833	0.018	0.3054
chr19	59128983	999879	0.0169	0.2282
chr20	63025520	1108641	0.0176	0.1398
chr21	48129895	689281	0.0143	0.1354
chr22	51304566	586293	0.0114	0.1123
chrMT	16571	5485	0.331	0.6275
chrX	155270560	2952415	0.019	0.1579
chrY	59373566	159229	0.0027	0.0844

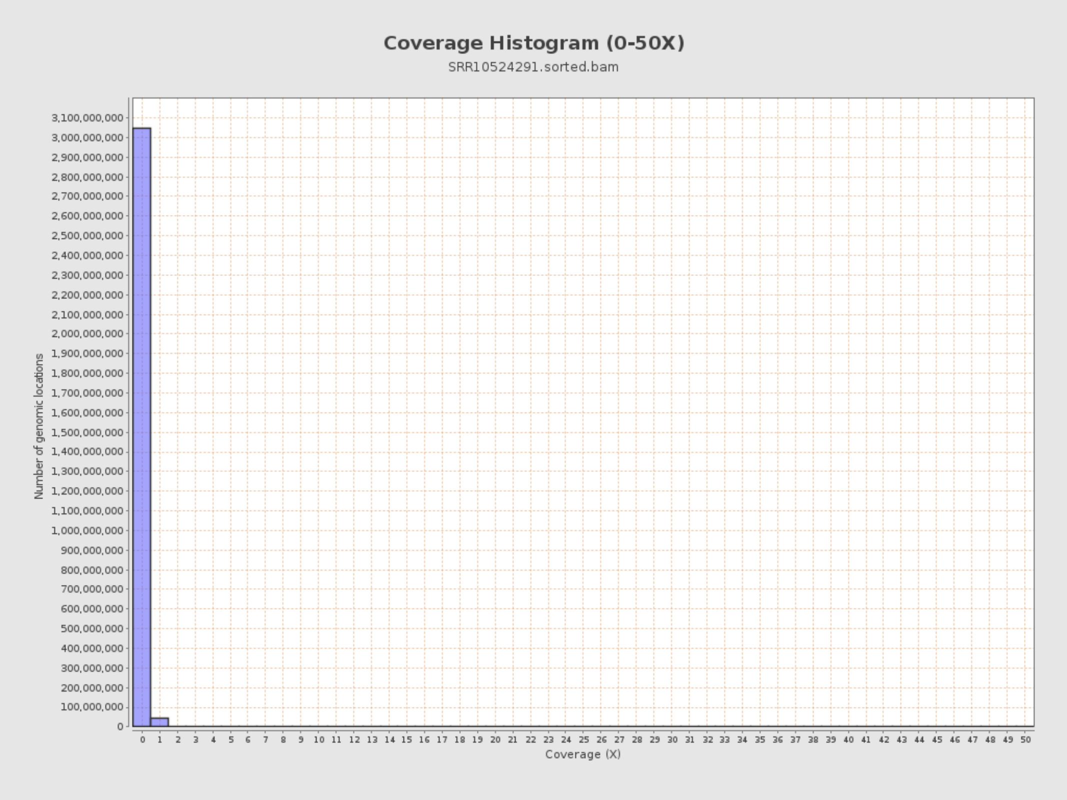
3. Results : Coverage across reference



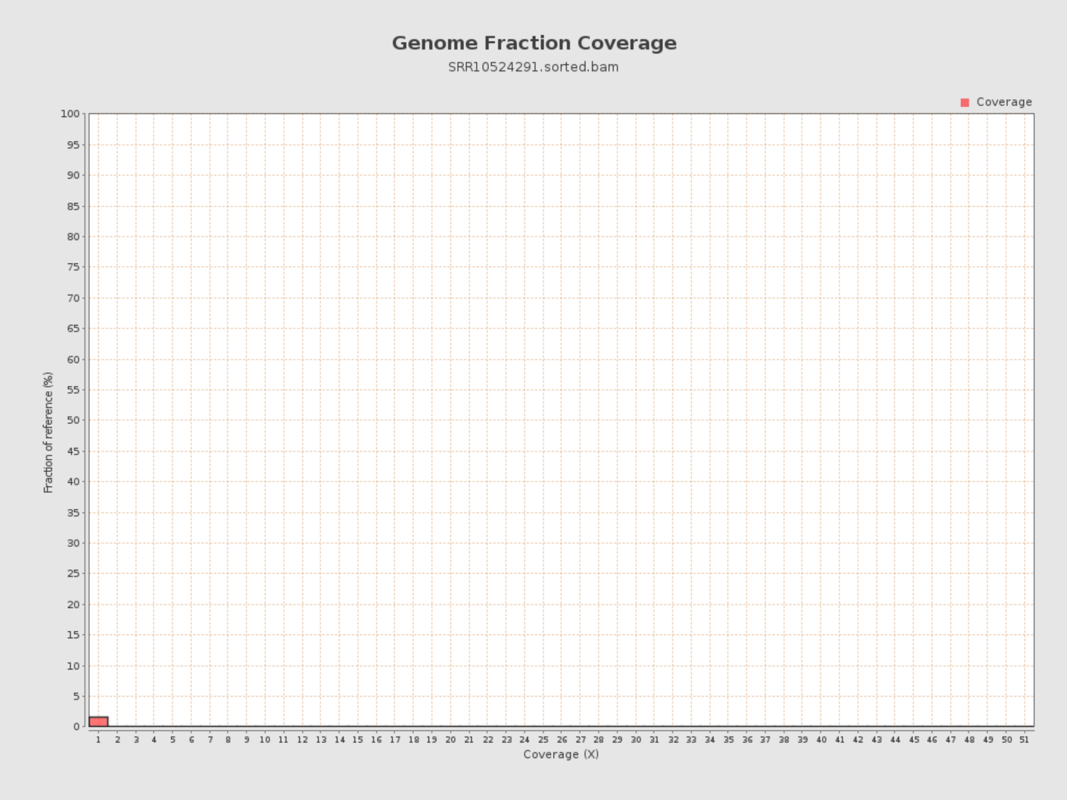
4. Results : Coverage Histogram



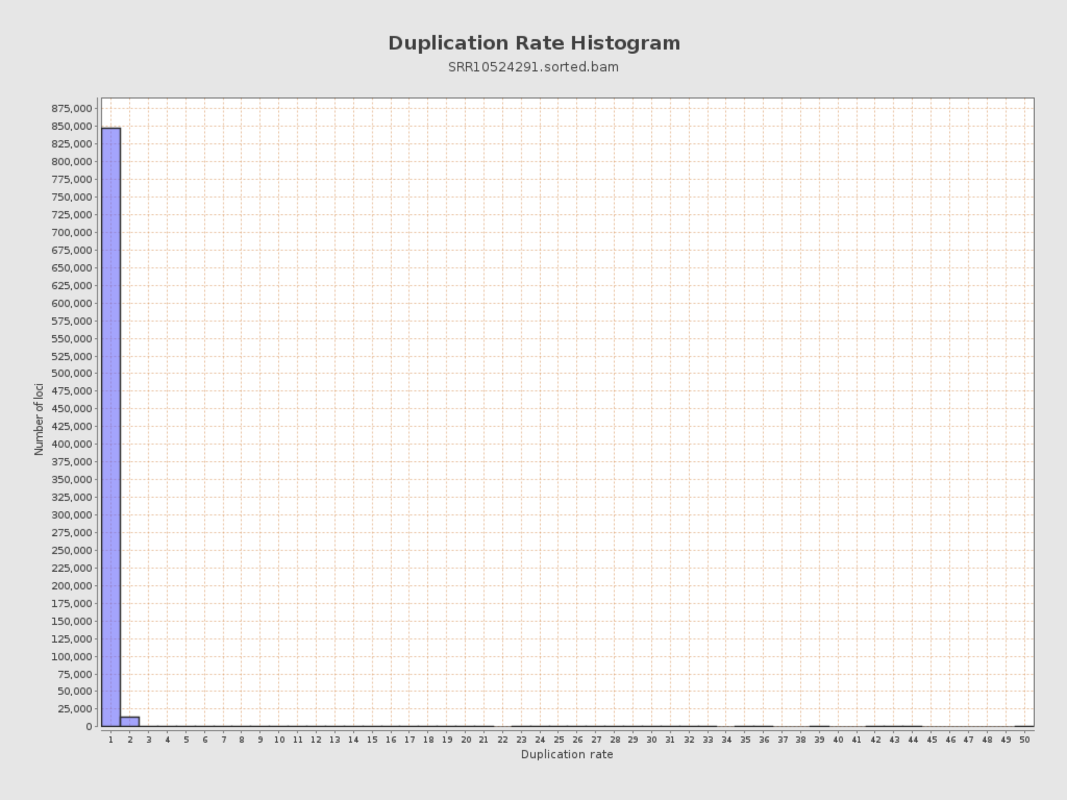
5. Results : Coverage Histogram (0-50X)



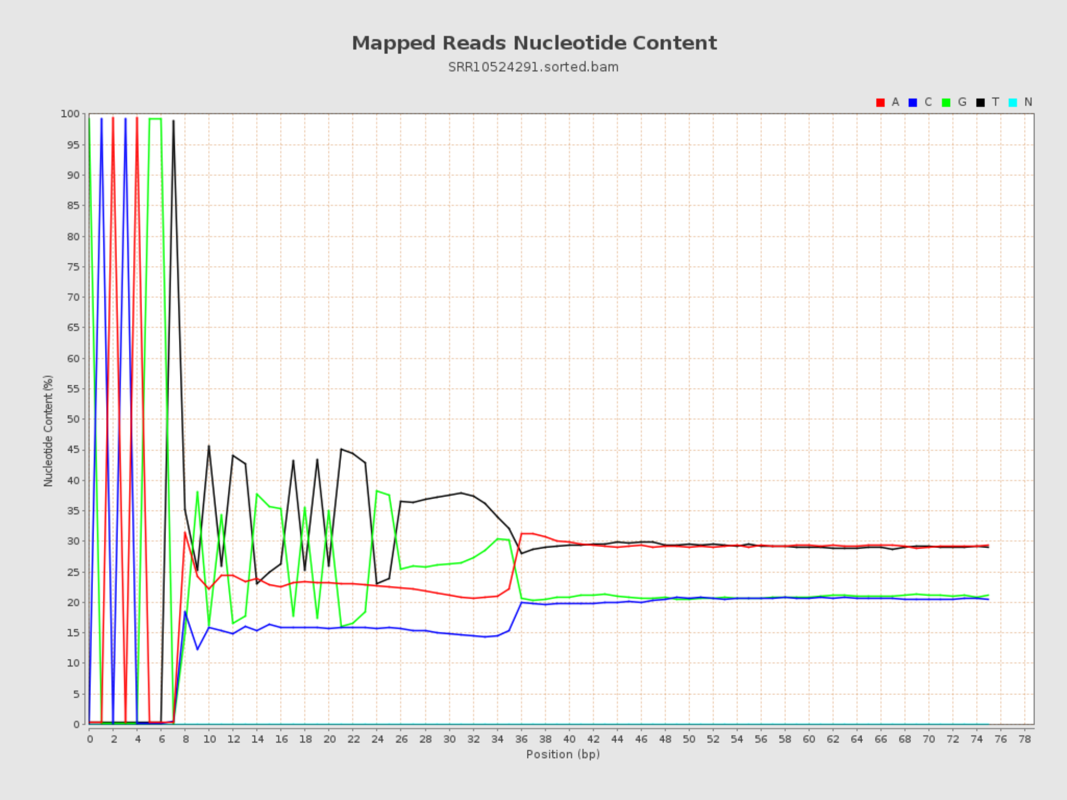
6. Results : Genome Fraction Coverage



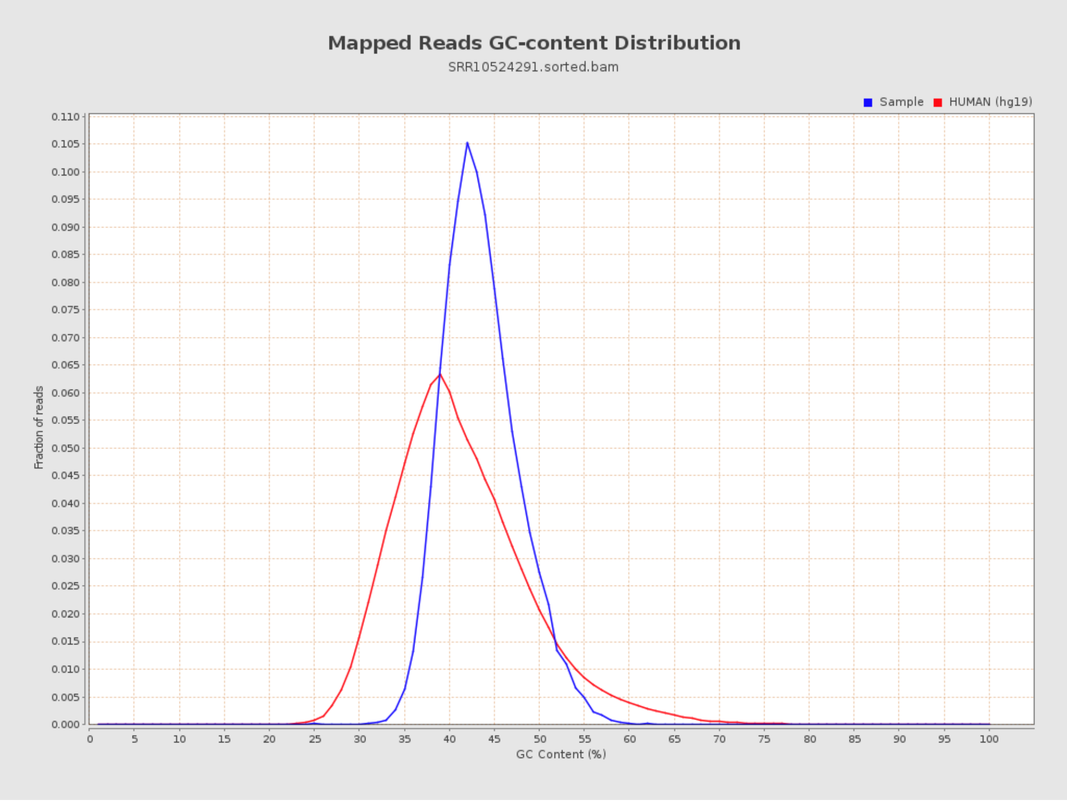
7. Results : Duplication Rate Histogram



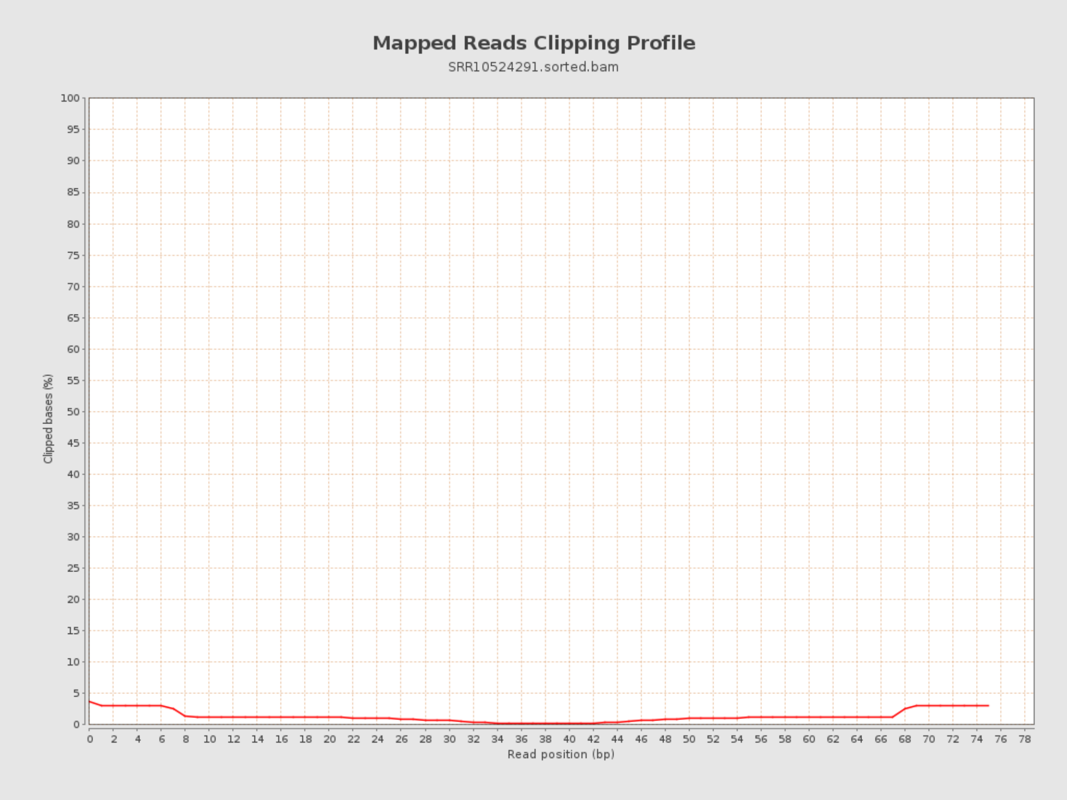
8. Results : Mapped Reads Nucleotide Content



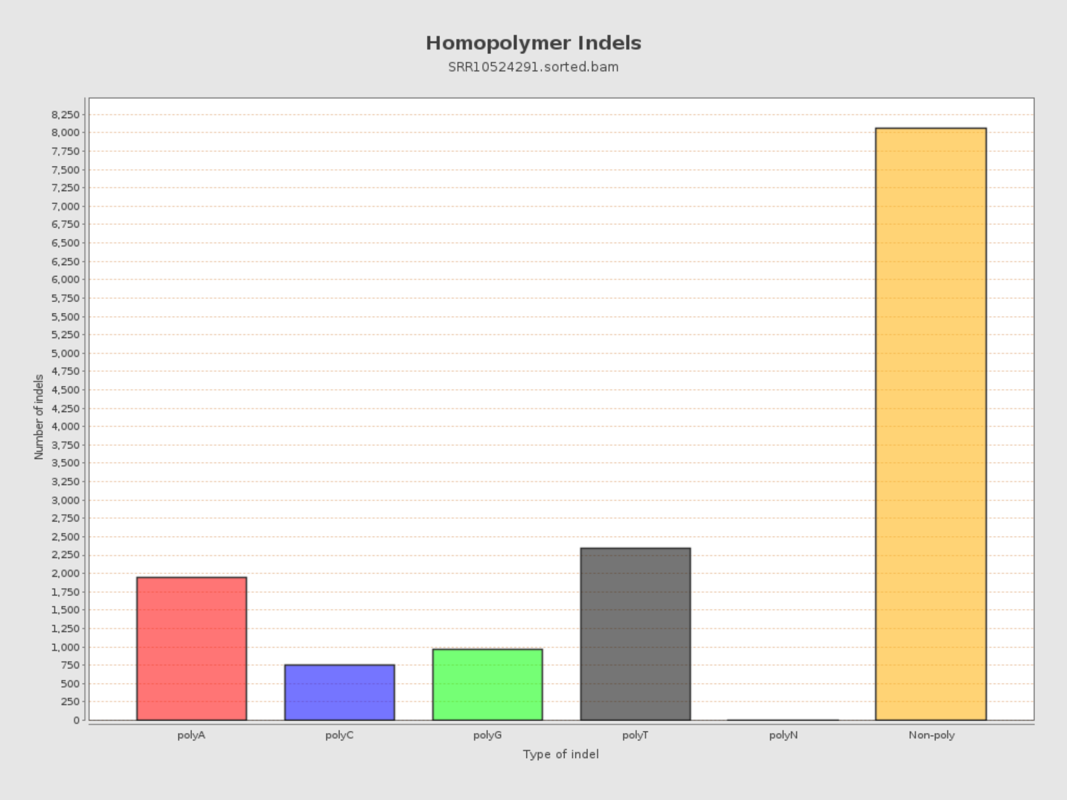
9. Results : Mapped Reads GC-content Distribution



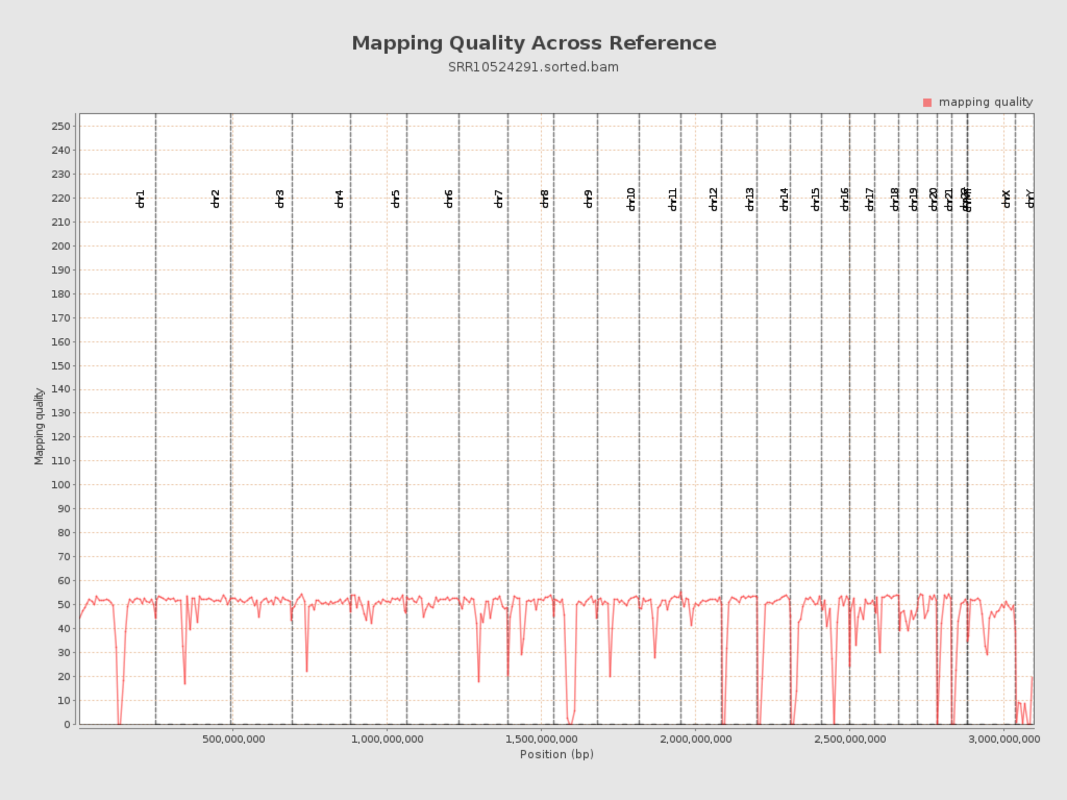
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram