Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 21:08:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524801.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_SRR10524801 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524801.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 21:08:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524801.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,069,256
Mapped reads	959,328 / 89.72%
Unmapped reads	109,928 / 10.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,509 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	31,742 / 2.97%
Duplication rate	2.55%
Clipped reads	960,596 / 89.84%

2.2. ACGT Content

Number/percentage of A's	13,429,325 / 24.67%
Number/percentage of C's	9,977,645 / 18.33%
Number/percentage of T's	17,761,849 / 32.63%
Number/percentage of G's	13,256,979 / 24.36%
Number/percentage of N's	6,468 / 0.01%
GC Percentage	42.69%

2.3. Coverage

Mean	0.0176

Standard Deviation	0.1807

2.4. Mapping Quality

Mean Mapping Quality	44.38

2.5. Mismatches and indels

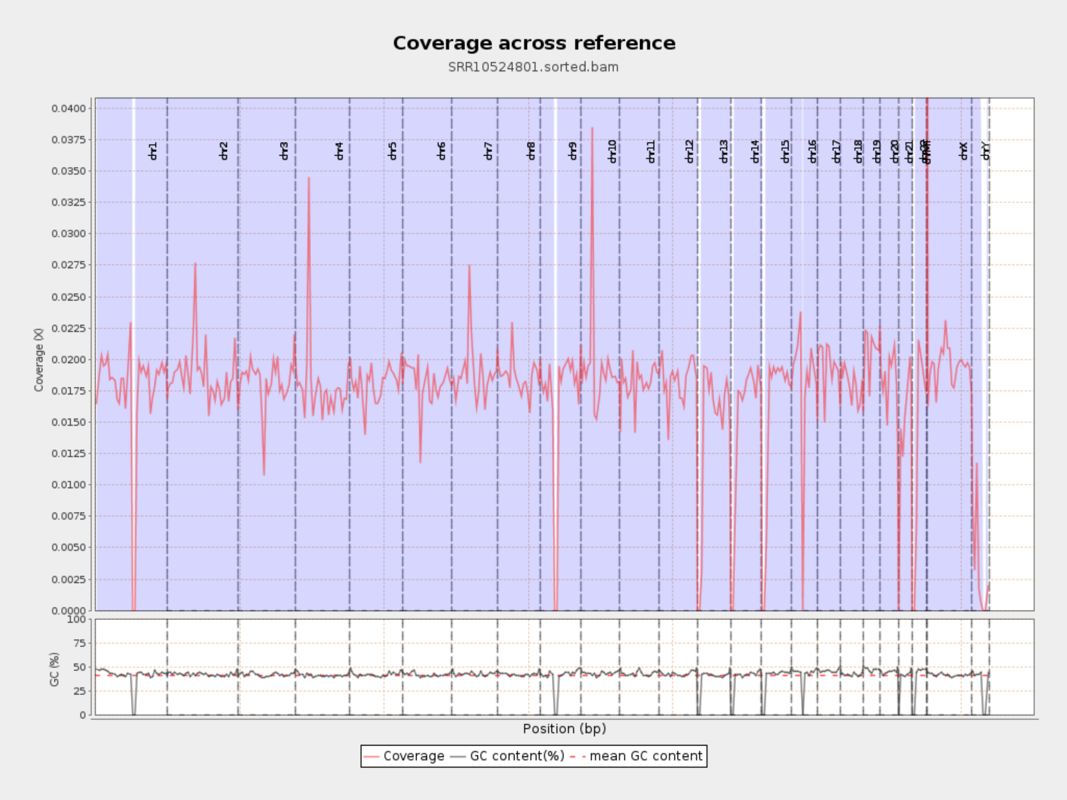
General error rate	0.53%
Mismatches	281,970
Insertions	3,772
Mapped reads with at least one insertion	0.39%
Deletions	10,627
Mapped reads with at least one deletion	1.1%
Homopolymer indels	41.55%

2.6. Chromosome stats

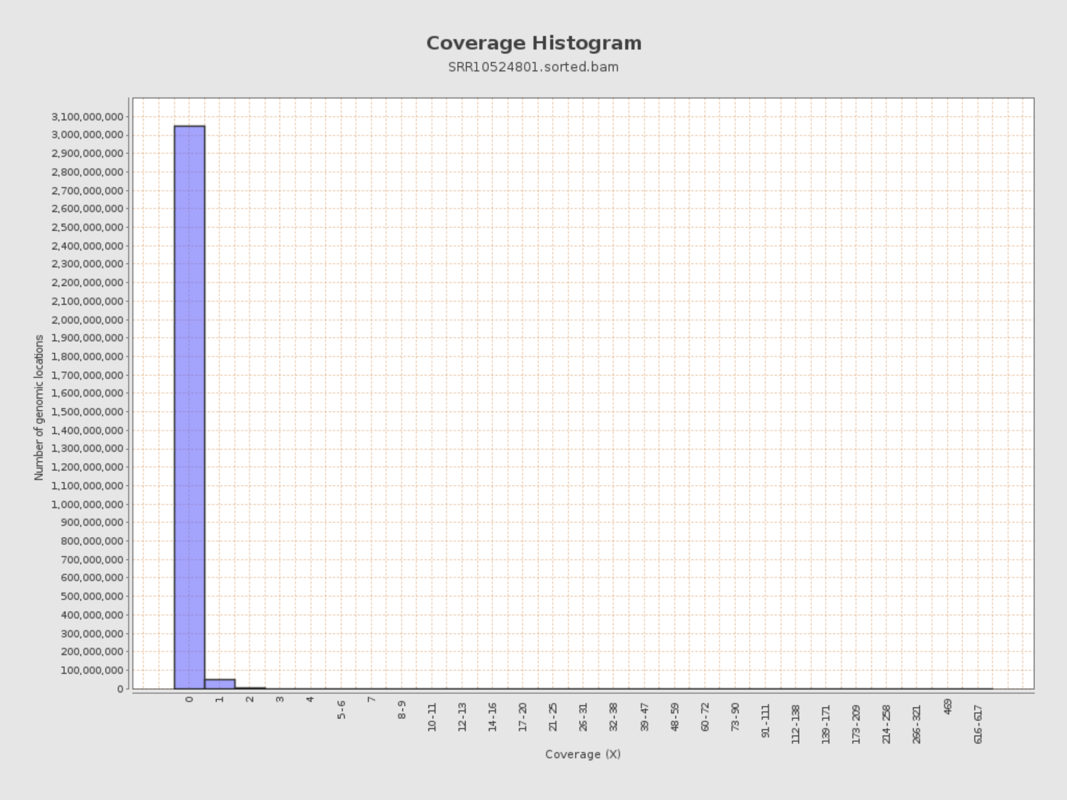
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4343402	0.0174	0.2255
chr2	243199373	4571325	0.0188	0.2934
chr3	198022430	3605514	0.0182	0.1468
chr4	191154276	3444406	0.018	0.1613
chr5	180915260	3283965	0.0182	0.1448
chr6	171115067	3104310	0.0181	0.1566
chr7	159138663	3014367	0.0189	0.2031

chr8	146364022	2722827	0.0186	0.169
chr9	141213431	2325274	0.0165	0.156
chr10	135534747	2655652	0.0196	0.2113
chr11	135006516	2472674	0.0183	0.1632
chr12	133851895	2458186	0.0184	0.1467
chr13	115169878	1658906	0.0144	0.1295
chr14	107349540	1610914	0.015	0.1336
chr15	102531392	1560327	0.0152	0.1336
chr16	90354753	1617856	0.0179	0.1535
chr17	81195210	1584831	0.0195	0.1549
chr18	78077248	1401301	0.0179	0.215
chr19	59128983	1224435	0.0207	0.1994
chr20	63025520	1160672	0.0184	0.1515
chr21	48129895	706050	0.0147	0.1419
chr22	51304566	696155	0.0136	0.1264
chrMT	16571	5844	0.3527	0.6659
chrX	155270560	3027314	0.0195	0.16
chrY	59373566	192819	0.0032	0.1017

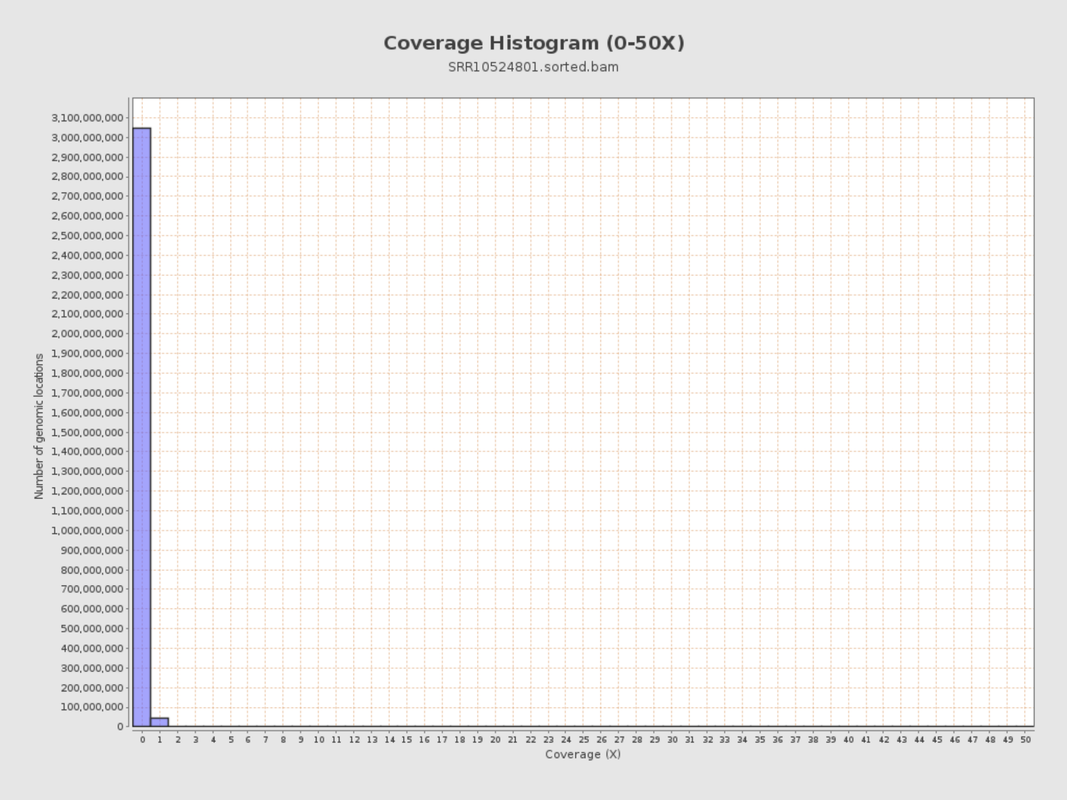
3. Results : Coverage across reference



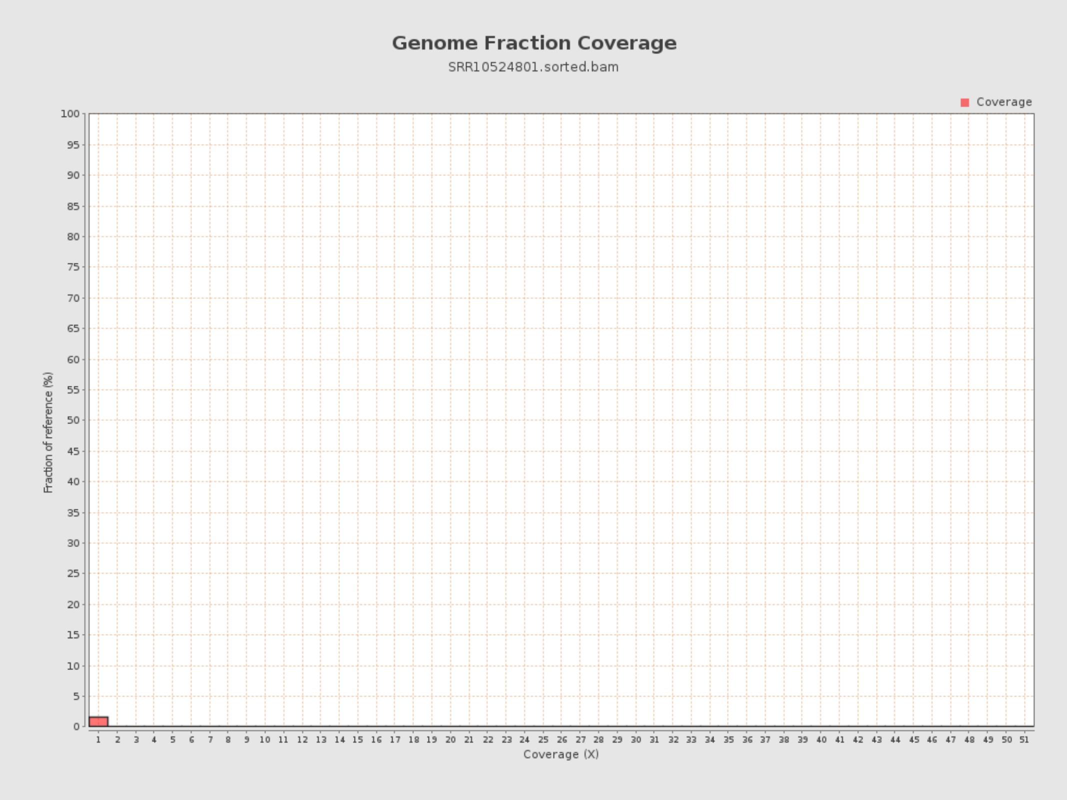
4. Results : Coverage Histogram



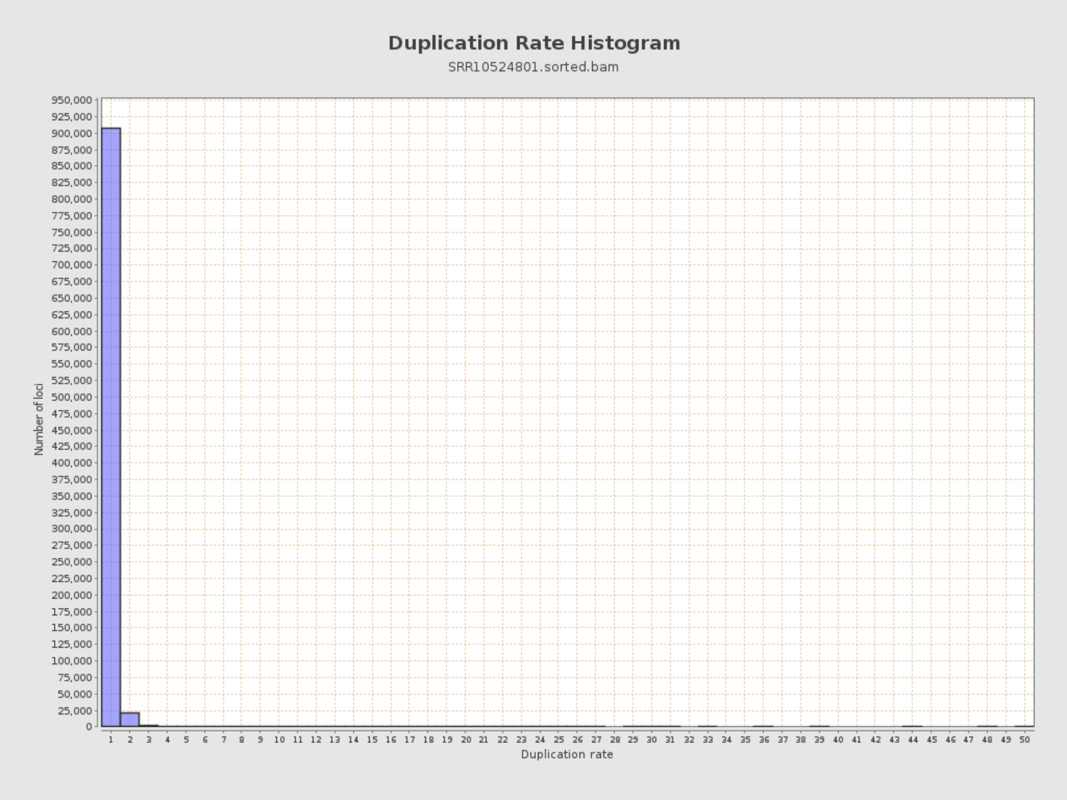
5. Results : Coverage Histogram (0-50X)



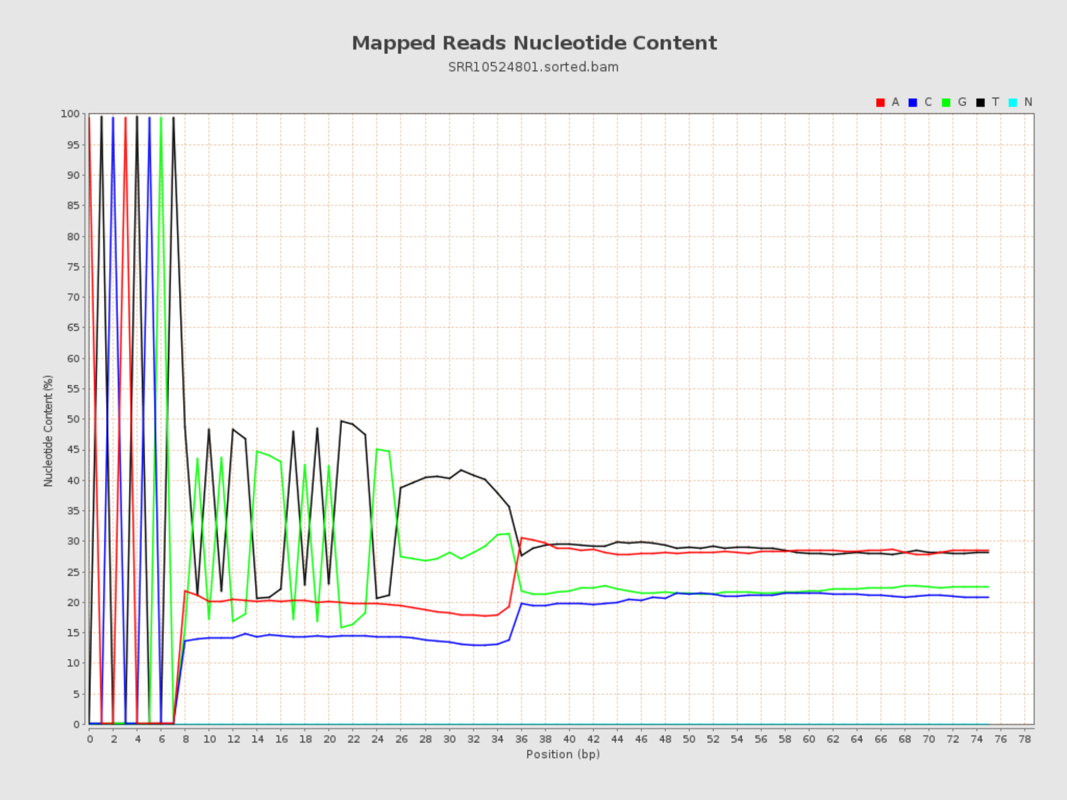
6. Results : Genome Fraction Coverage



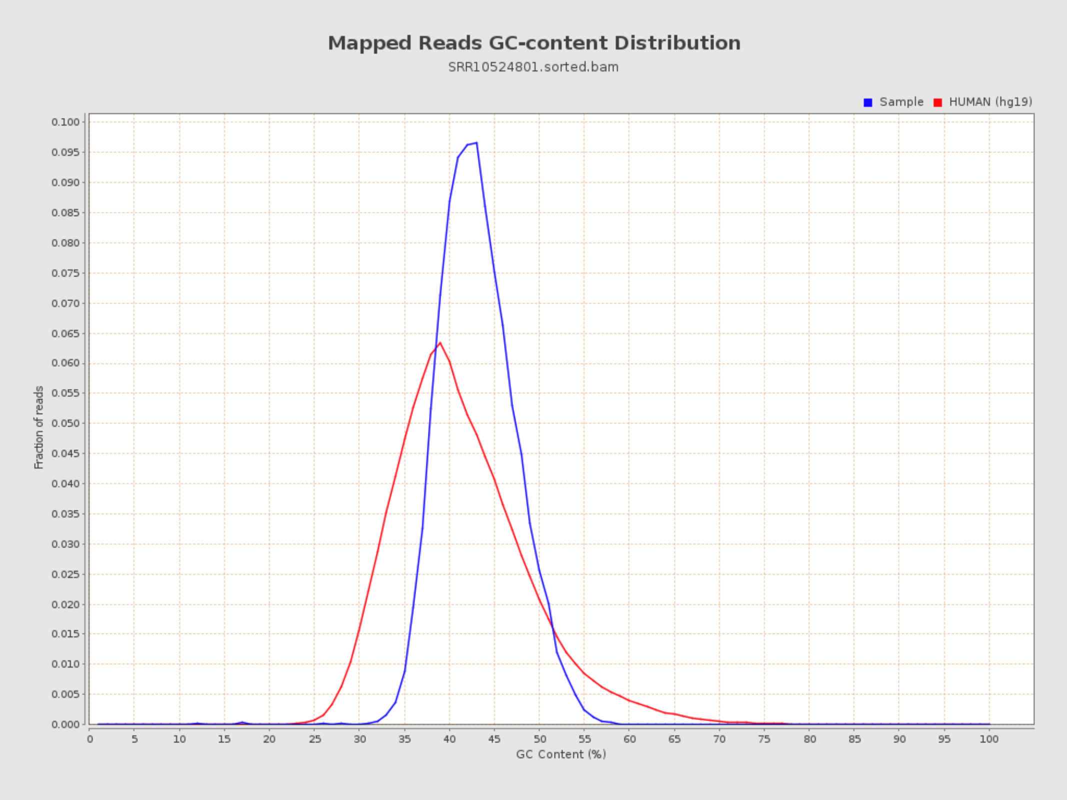
7. Results : Duplication Rate Histogram



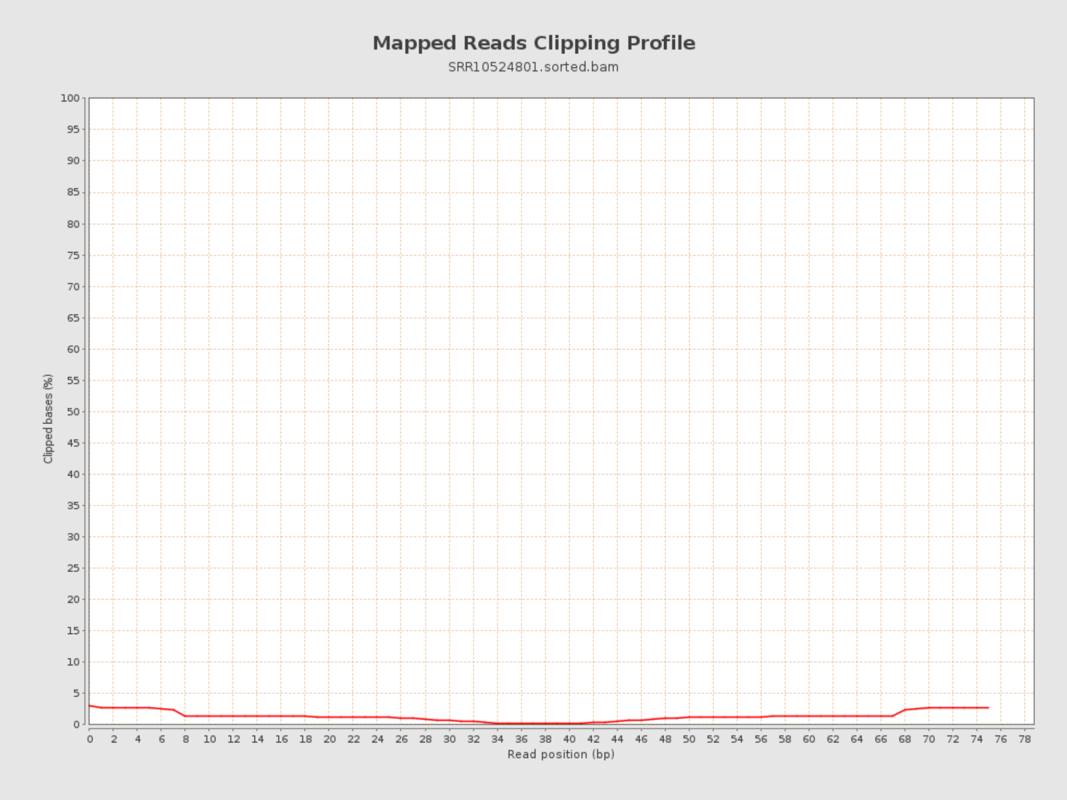
8. Results : Mapped Reads Nucleotide Content



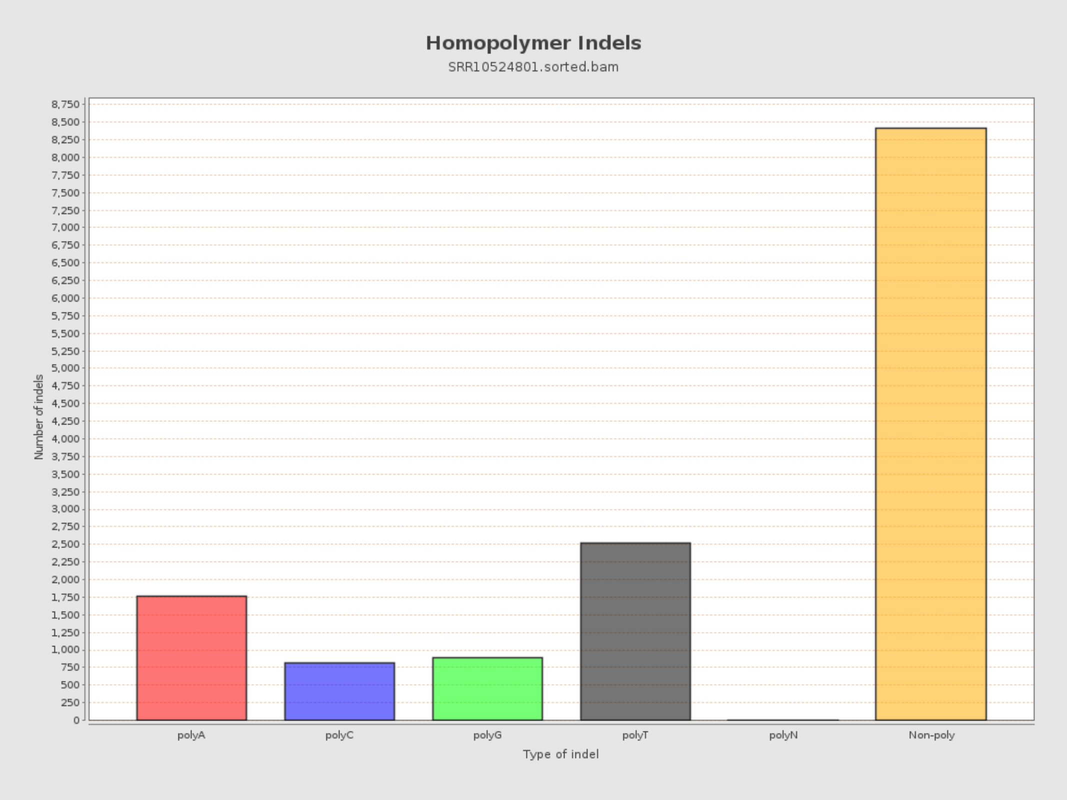
9. Results : Mapped Reads GC-content Distribution



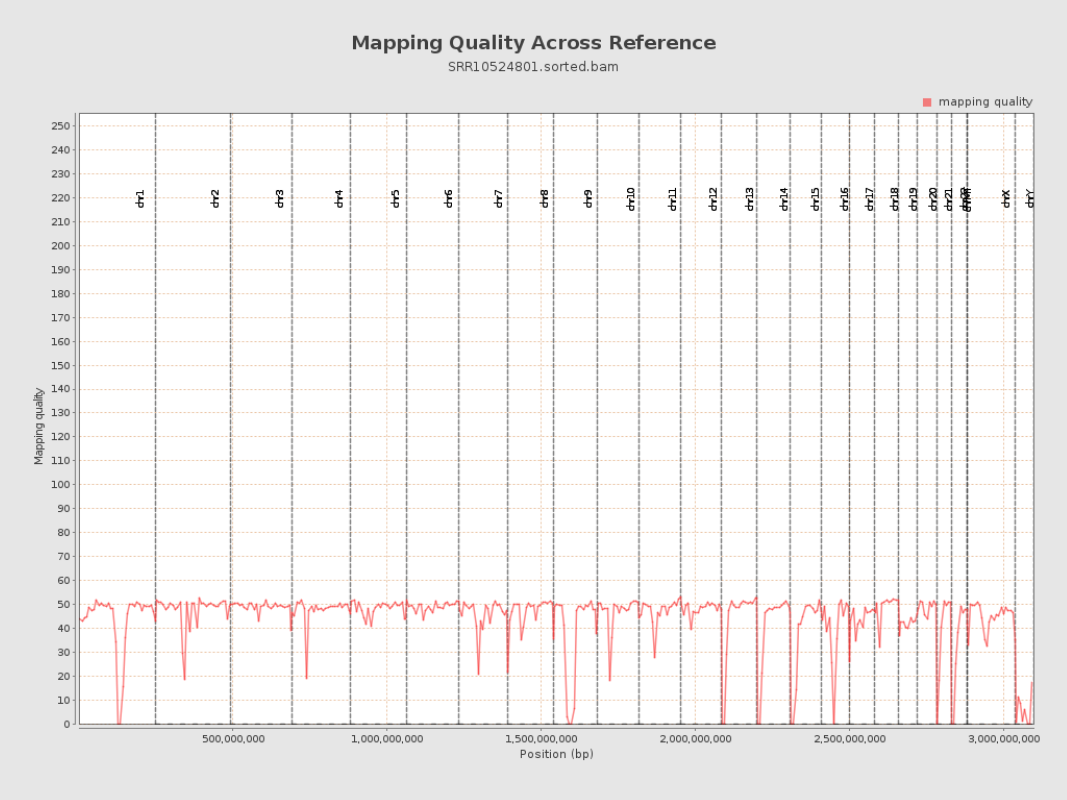
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram