Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 20:46:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524791.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_SRR10524791 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524791.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 20:46:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524791.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,246,774
Mapped reads	1,145,572 / 91.88%
Unmapped reads	101,202 / 8.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,817 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	42,397 / 3.4%
Duplication rate	2.88%
Clipped reads	1,147,309 / 92.02%

2.2. ACGT Content

Number/percentage of A's	16,519,772 / 25.07%
Number/percentage of C's	13,380,696 / 20.31%
Number/percentage of T's	20,173,211 / 30.62%
Number/percentage of G's	15,811,685 / 24%
Number/percentage of N's	7,779 / 0.01%
GC Percentage	44.3%

2.3. Coverage

Mean	0.0213

Standard Deviation	0.2026

2.4. Mapping Quality

Mean Mapping Quality	44.62

2.5. Mismatches and indels

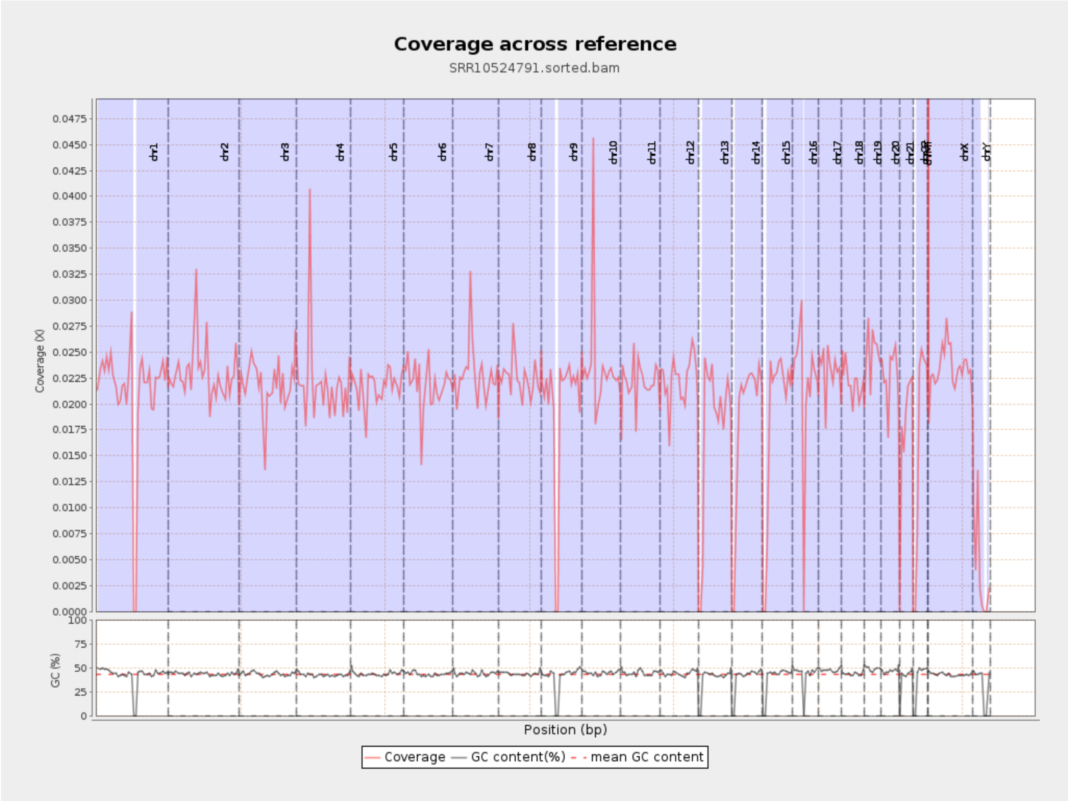
General error rate	0.51%
Mismatches	328,709
Insertions	4,959
Mapped reads with at least one insertion	0.43%
Deletions	13,239
Mapped reads with at least one deletion	1.15%
Homopolymer indels	41.66%

2.6. Chromosome stats

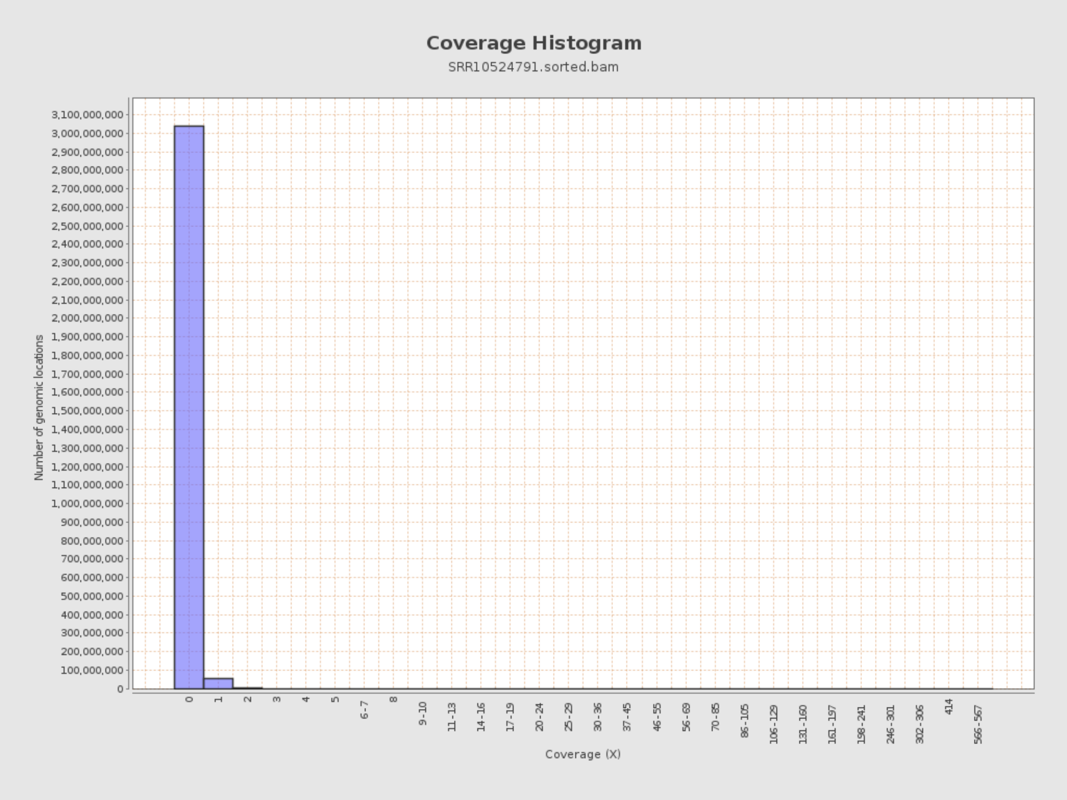
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5275223	0.0212	0.2714
chr2	243199373	5593502	0.023	0.301
chr3	198022430	4312062	0.0218	0.162
chr4	191154276	4225653	0.0221	0.1822
chr5	180915260	3928825	0.0217	0.1595
chr6	171115067	3735833	0.0218	0.1705
chr7	159138663	3638520	0.0229	0.2401

chr8	146364022	3295526	0.0225	0.1871
chr9	141213431	2766112	0.0196	0.1762
chr10	135534747	3196690	0.0236	0.2396
chr11	135006516	3003096	0.0222	0.1827
chr12	133851895	2990956	0.0223	0.1643
chr13	115169878	2023867	0.0176	0.1442
chr14	107349540	1972328	0.0184	0.151
chr15	102531392	1894882	0.0185	0.1473
chr16	90354753	1959282	0.0217	0.1719
chr17	81195210	1884198	0.0232	0.1717
chr18	78077248	1718341	0.022	0.278
chr19	59128983	1474273	0.0249	0.23
chr20	63025520	1422144	0.0226	0.1727
chr21	48129895	858906	0.0178	0.1566
chr22	51304566	849001	0.0165	0.1411
chrMT	16571	17854	1.0774	1.1876
chrX	155270560	3649374	0.0235	0.1756
chrY	59373566	227763	0.0038	0.112

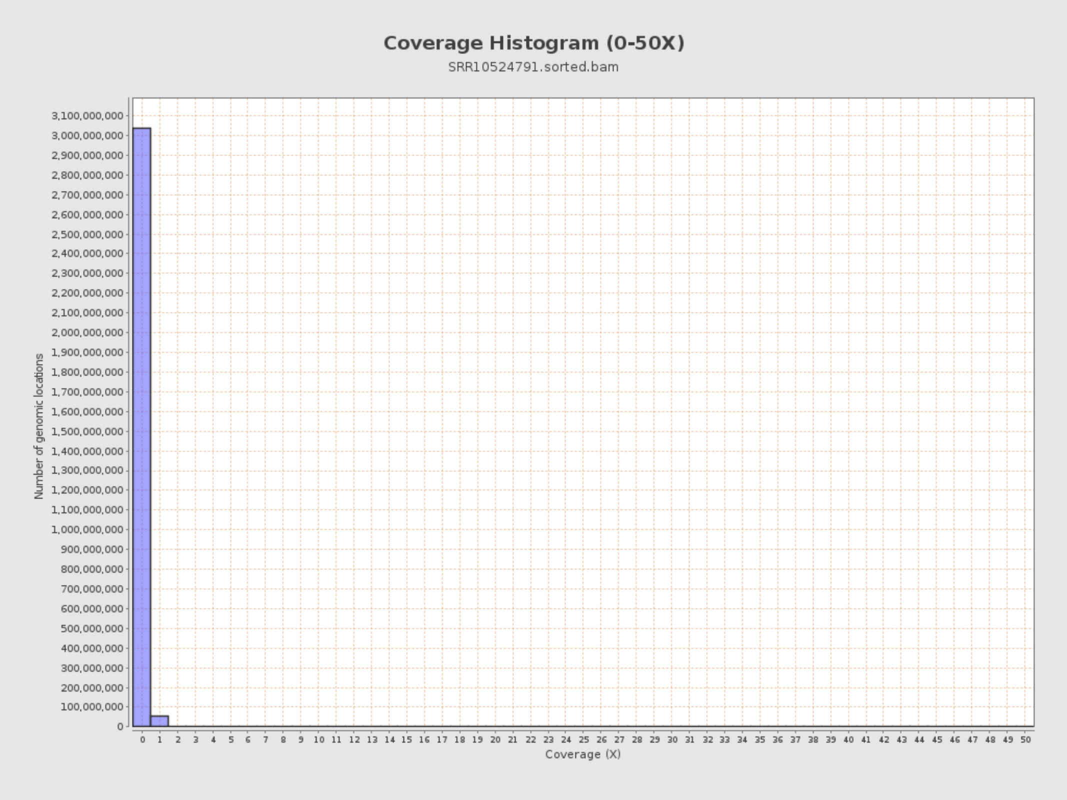
3. Results : Coverage across reference



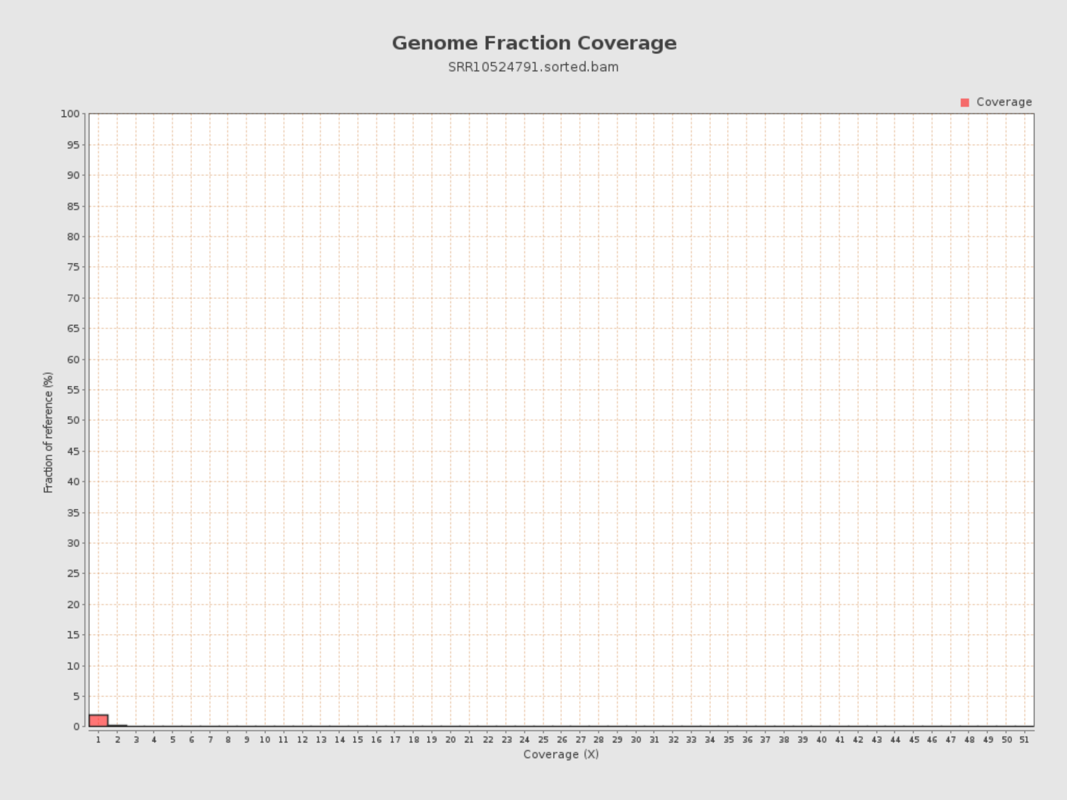
4. Results : Coverage Histogram



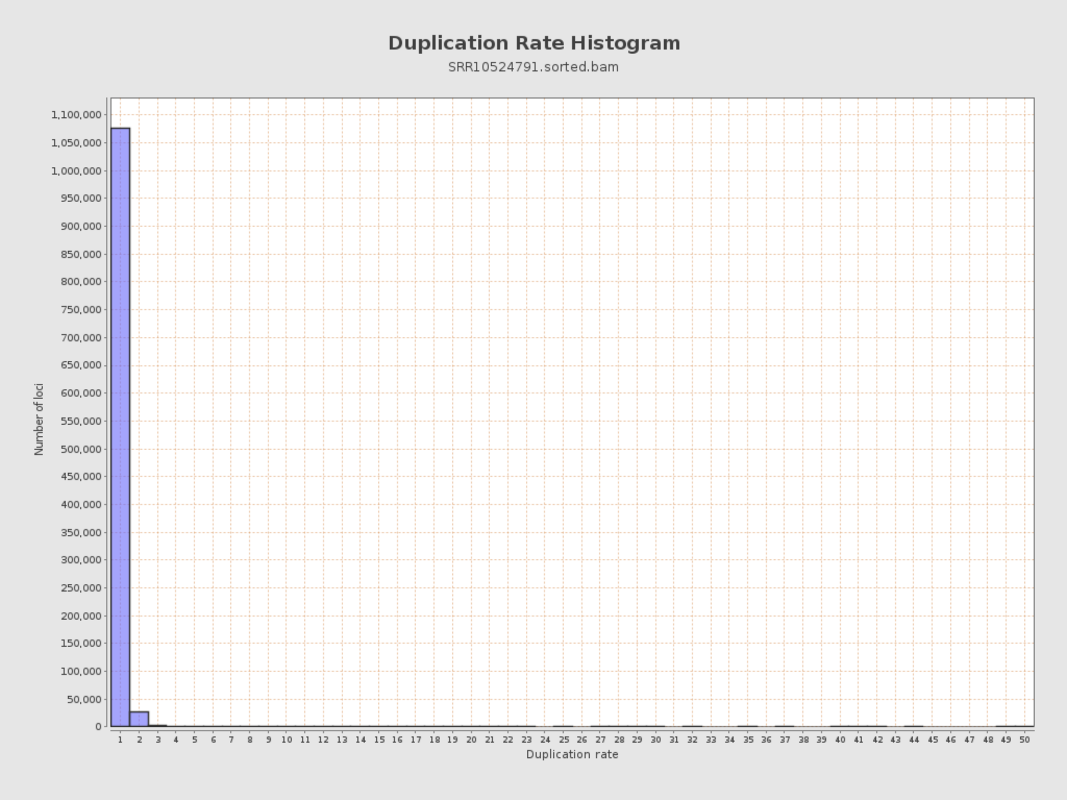
5. Results : Coverage Histogram (0-50X)



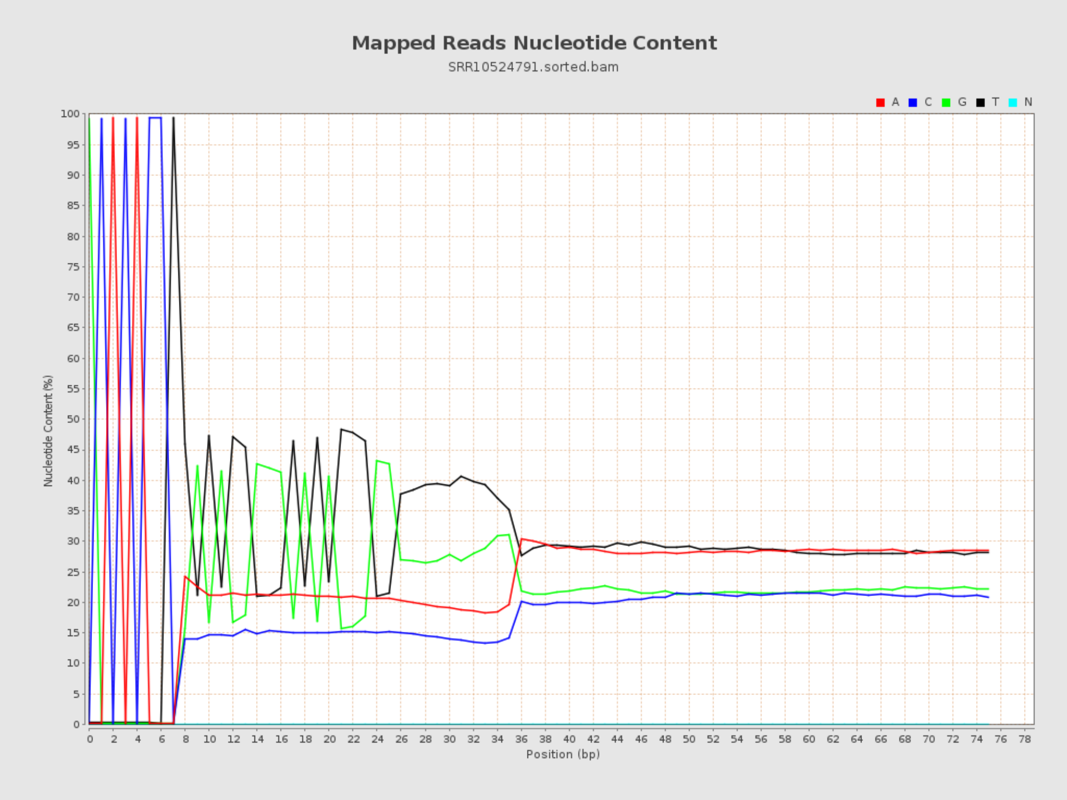
6. Results : Genome Fraction Coverage



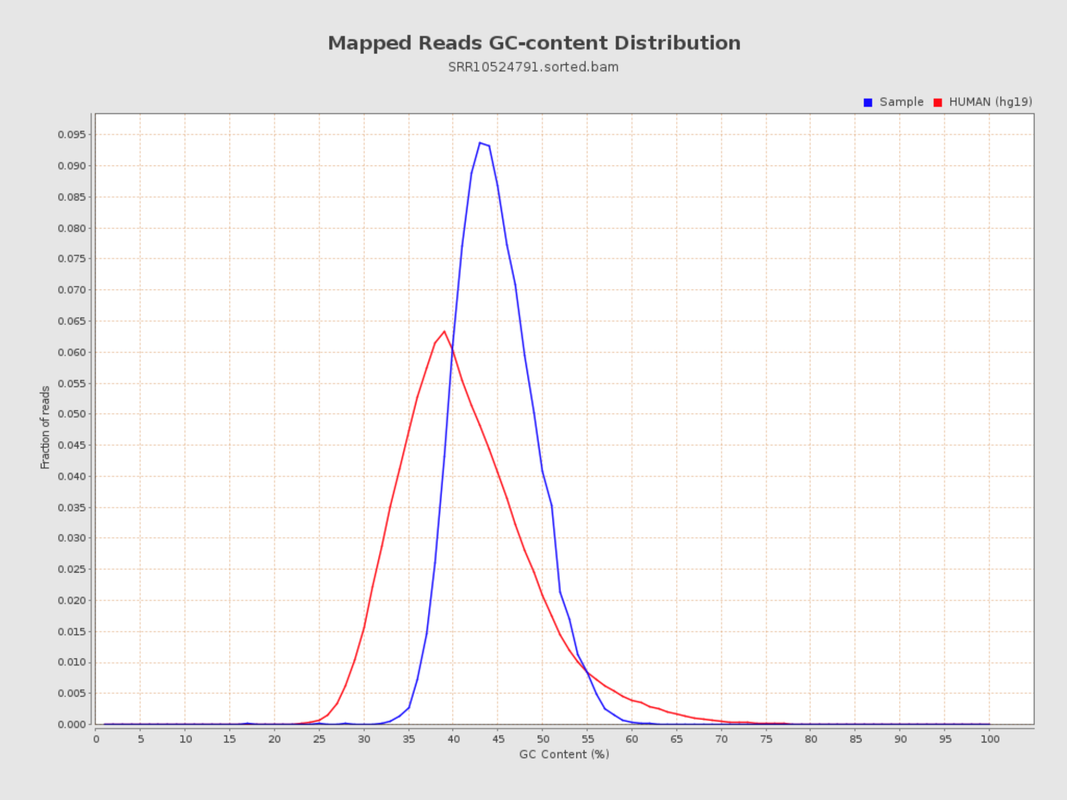
7. Results : Duplication Rate Histogram



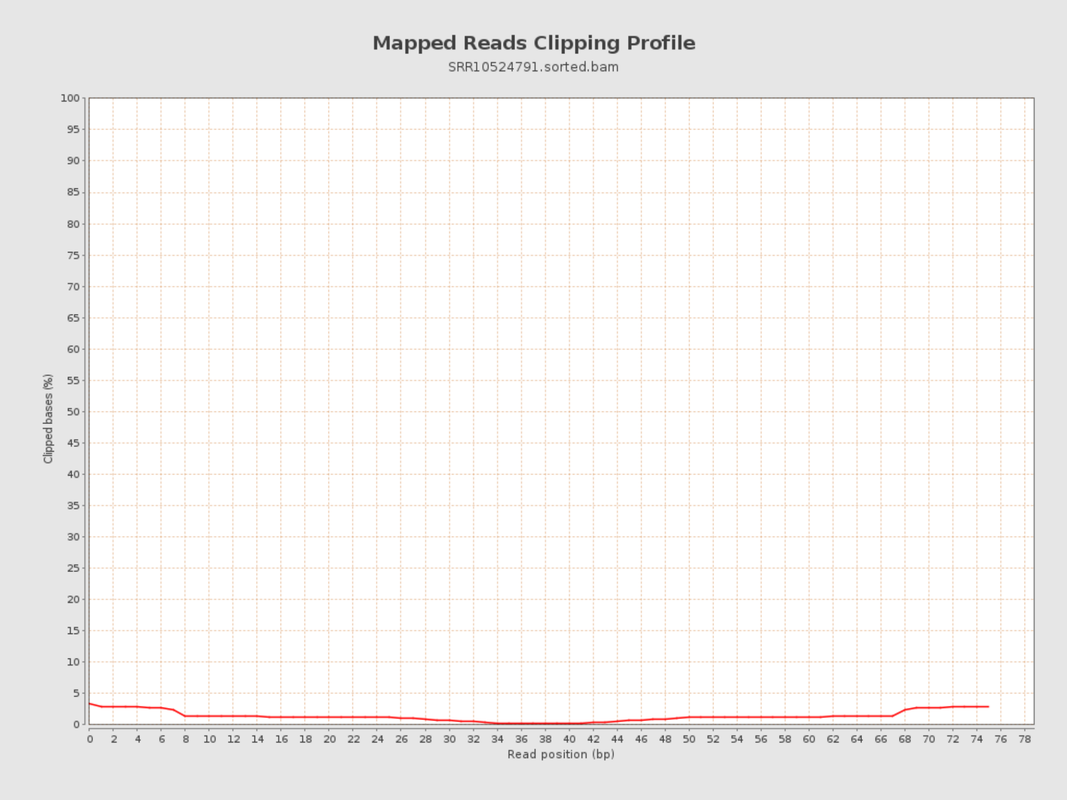
8. Results : Mapped Reads Nucleotide Content



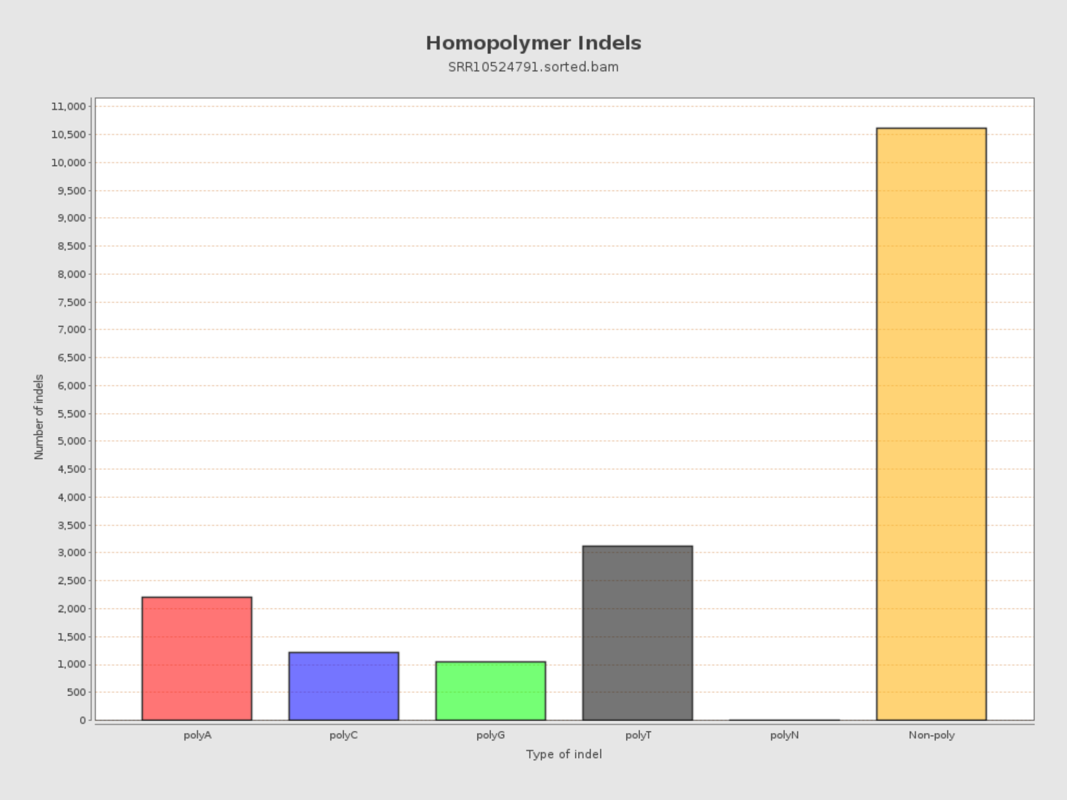
9. Results : Mapped Reads GC-content Distribution



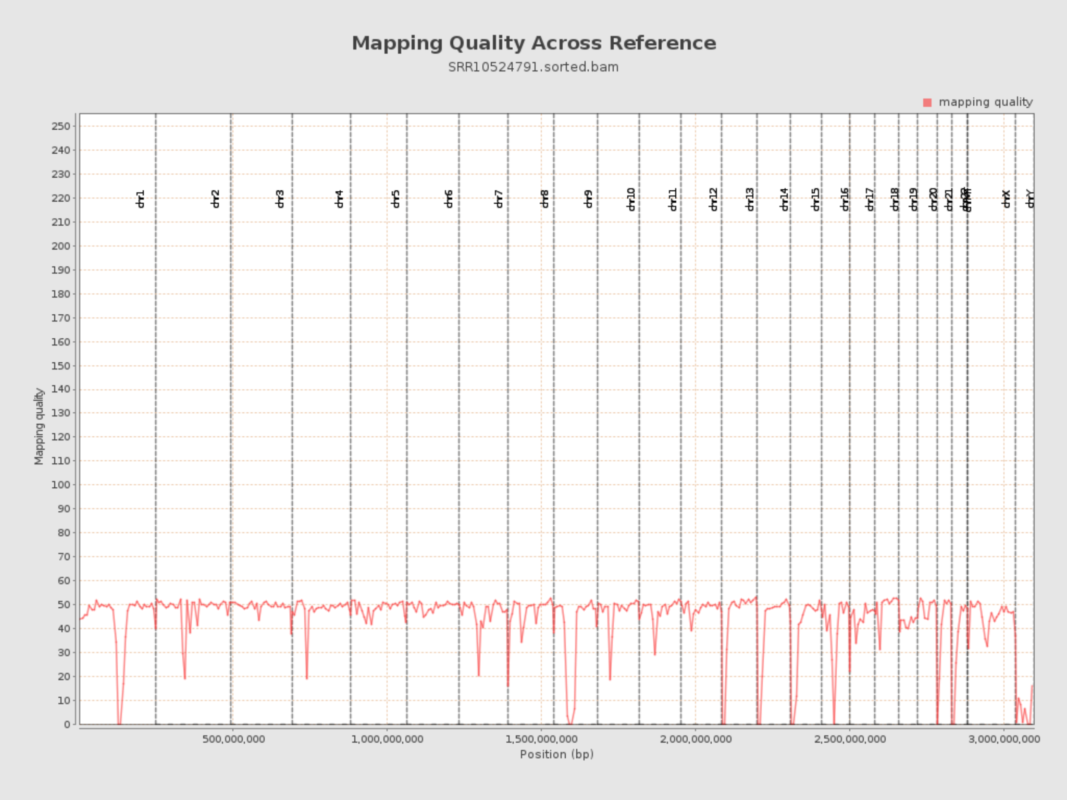
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram