Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 12:09:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524991.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_SRR10524991 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524991.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 12:09:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524991.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,011,048
Mapped reads	942,209 / 93.19%
Unmapped reads	68,839 / 6.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,337 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	26,125 / 2.58%
Duplication rate	2.14%
Clipped reads	941,875 / 93.16%

2.2. ACGT Content

Number/percentage of A's	14,042,107 / 25.33%
Number/percentage of C's	10,311,281 / 18.6%
Number/percentage of T's	17,722,459 / 31.97%
Number/percentage of G's	13,350,909 / 24.09%
Number/percentage of N's	631 / 0%
GC Percentage	42.69%

2.3. Coverage

Mean	0.0179

Standard Deviation	0.1767

2.4. Mapping Quality

Mean Mapping Quality	46.16

2.5. Mismatches and indels

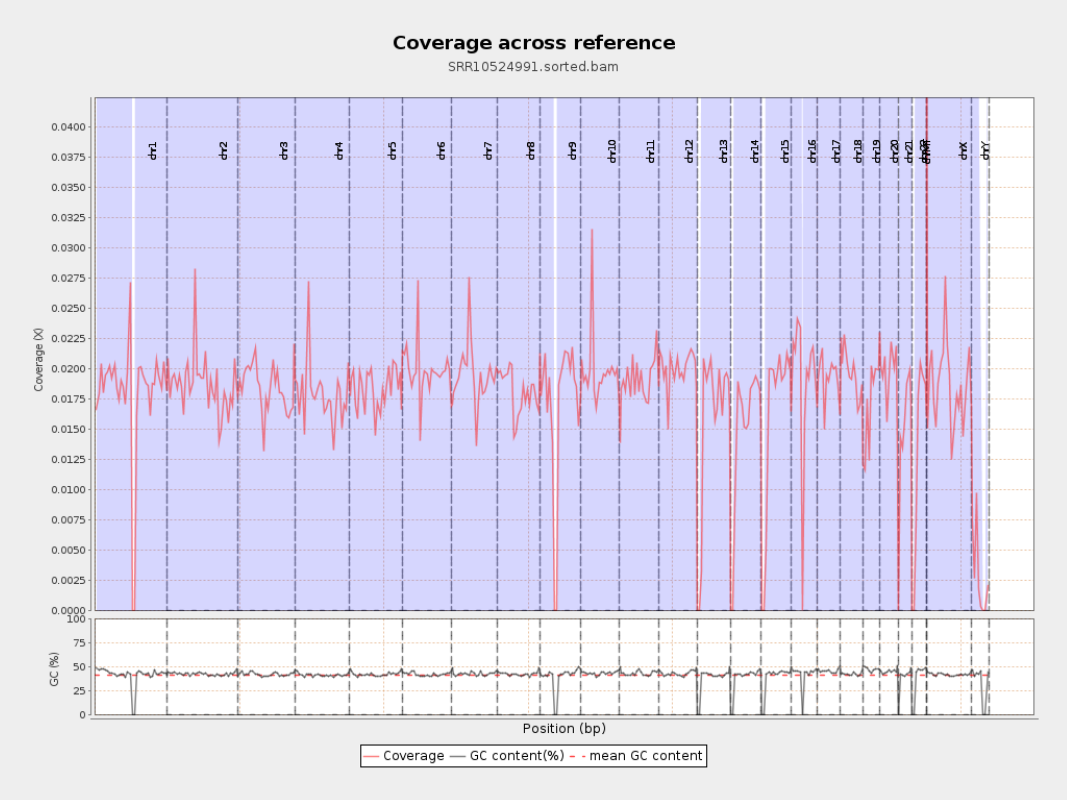
General error rate	0.48%
Mismatches	259,379
Insertions	3,454
Mapped reads with at least one insertion	0.37%
Deletions	9,745
Mapped reads with at least one deletion	1.03%
Homopolymer indels	43.41%

2.6. Chromosome stats

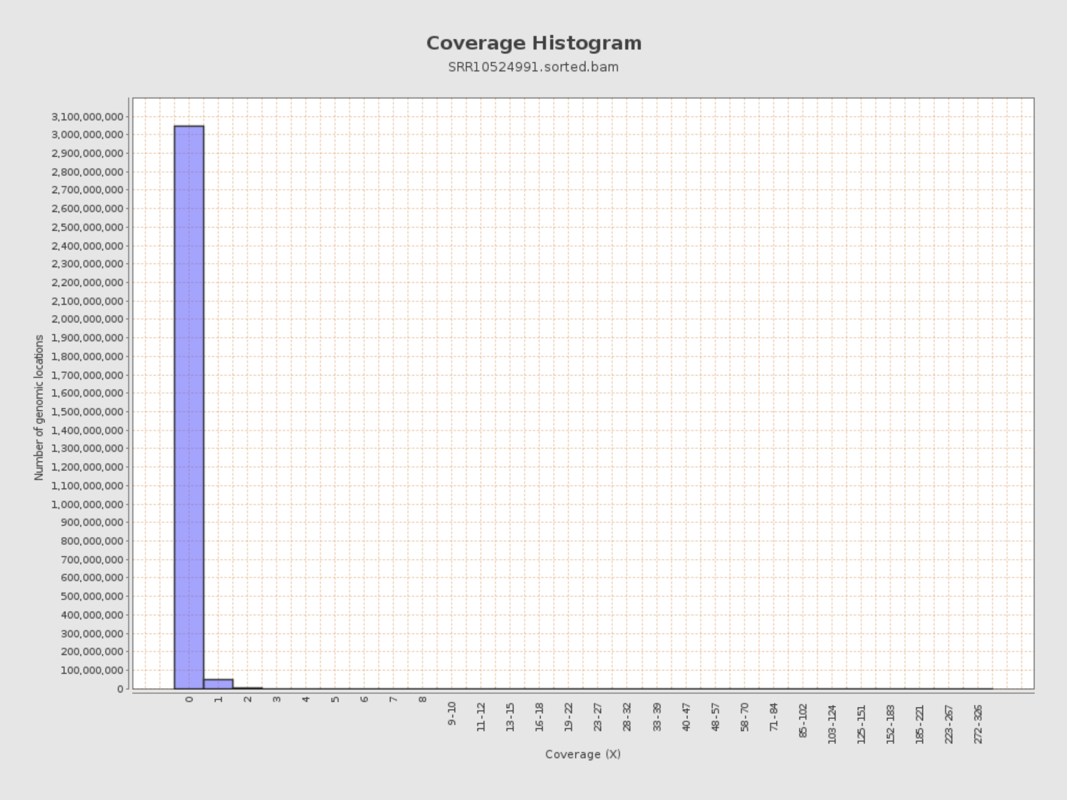
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4474338	0.018	0.2703
chr2	243199373	4553146	0.0187	0.1898
chr3	198022430	3637993	0.0184	0.1437
chr4	191154276	3437058	0.018	0.1549
chr5	180915260	3325879	0.0184	0.1448
chr6	171115067	3399447	0.0199	0.1709
chr7	159138663	3096216	0.0195	0.2011

chr8	146364022	2641047	0.018	0.1906
chr9	141213431	2390189	0.0169	0.1615
chr10	135534747	2694888	0.0199	0.187
chr11	135006516	2586329	0.0192	0.1789
chr12	133851895	2680844	0.02	0.1519
chr13	115169878	1804192	0.0157	0.1331
chr14	107349540	1579110	0.0147	0.132
chr15	102531392	1647274	0.0161	0.1371
chr16	90354753	1691341	0.0187	0.1513
chr17	81195210	1564142	0.0193	0.1576
chr18	78077248	1527871	0.0196	0.2555
chr19	59128983	1016066	0.0172	0.198
chr20	63025520	1235775	0.0196	0.1516
chr21	48129895	720698	0.015	0.1388
chr22	51304566	682607	0.0133	0.1222
chrMT	16571	1018	0.0614	0.2862
chrX	155270560	2891746	0.0186	0.1538
chrY	59373566	165016	0.0028	0.0853

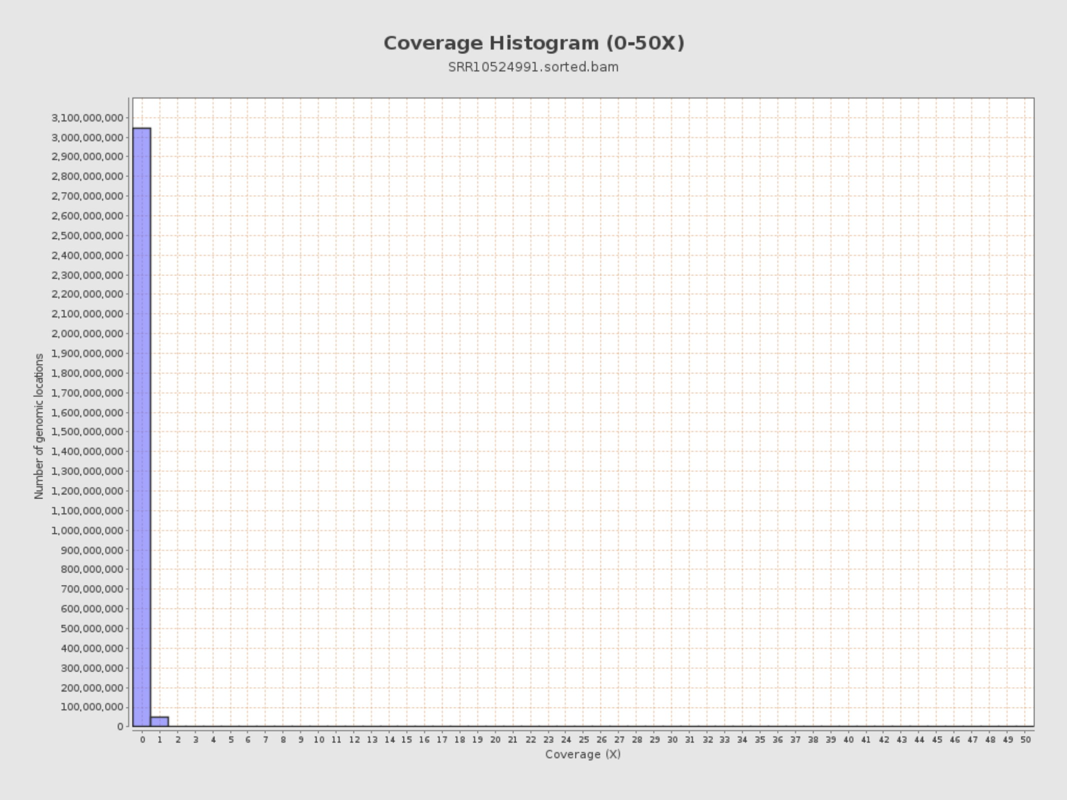
3. Results : Coverage across reference



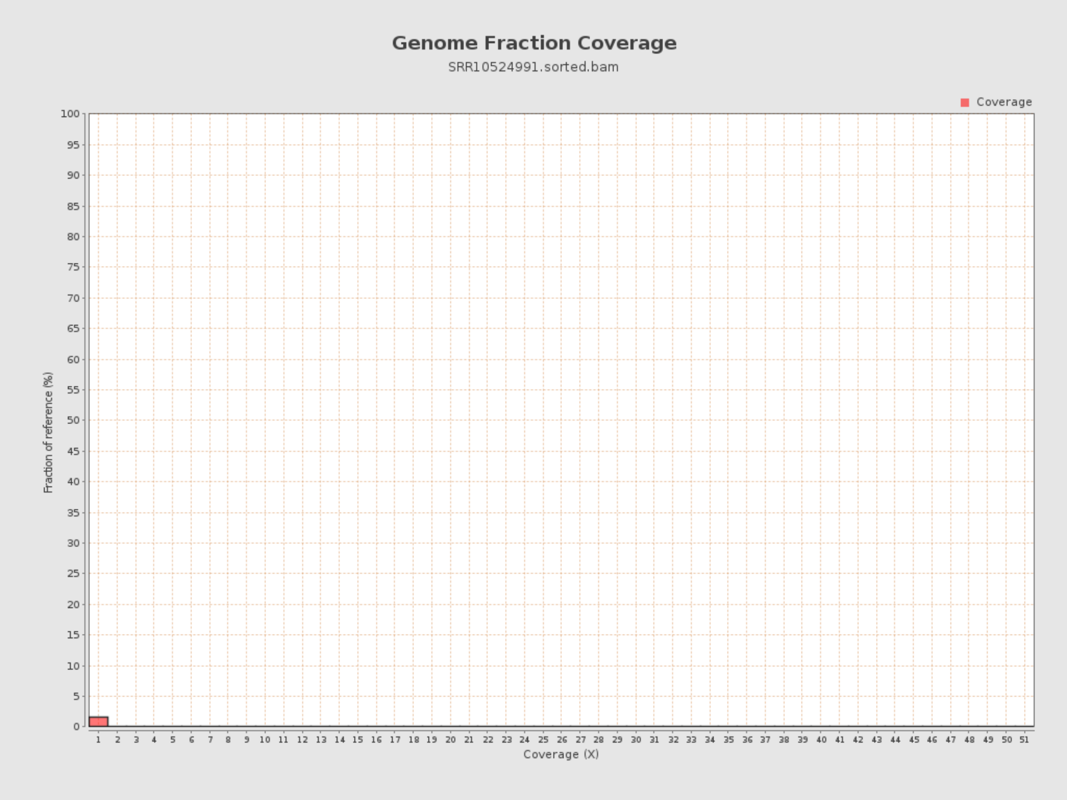
4. Results : Coverage Histogram



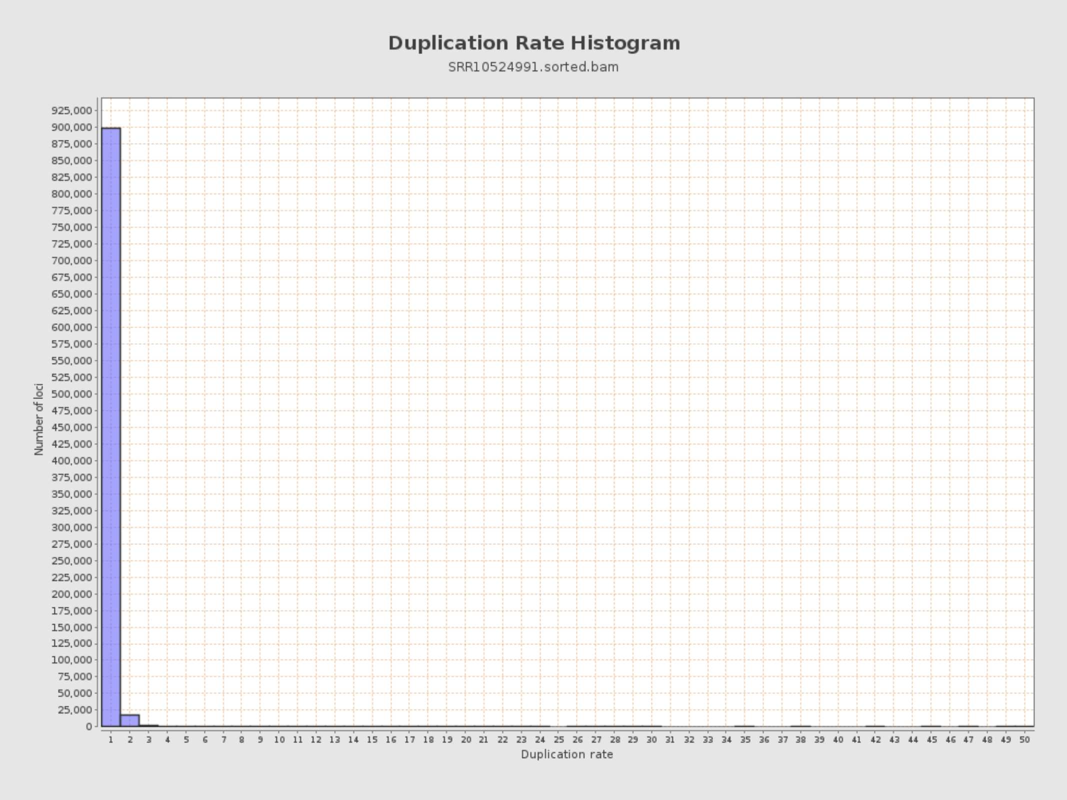
5. Results : Coverage Histogram (0-50X)



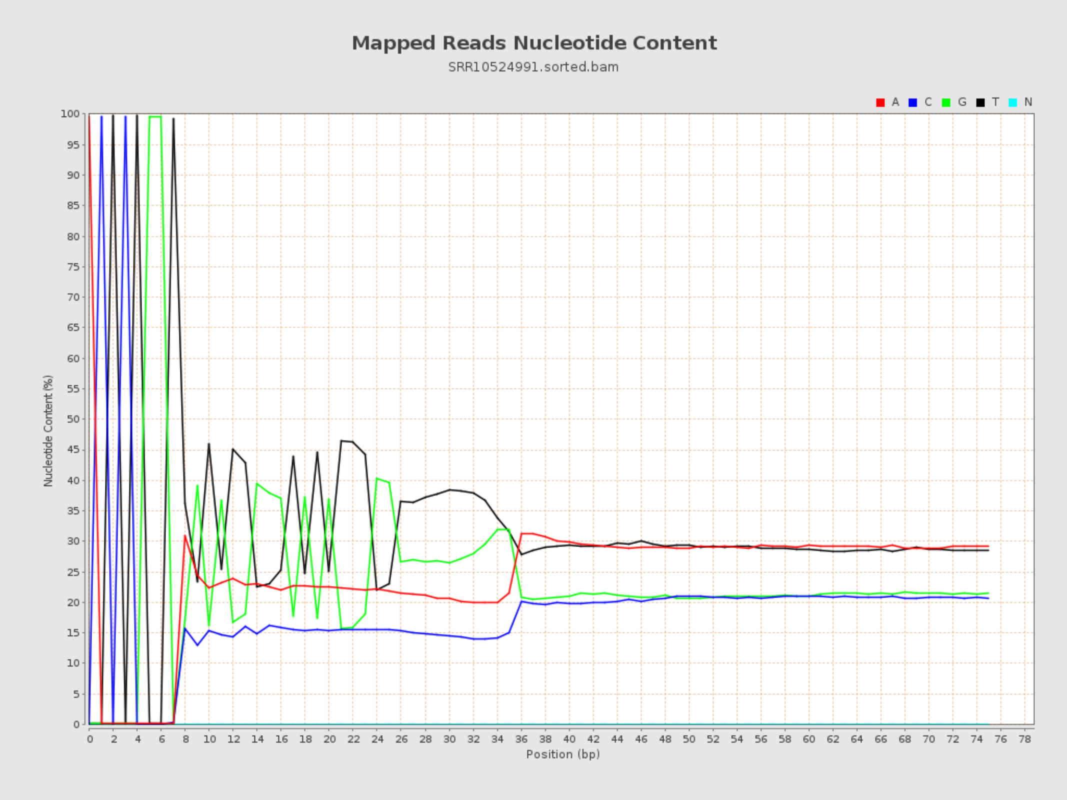
6. Results : Genome Fraction Coverage



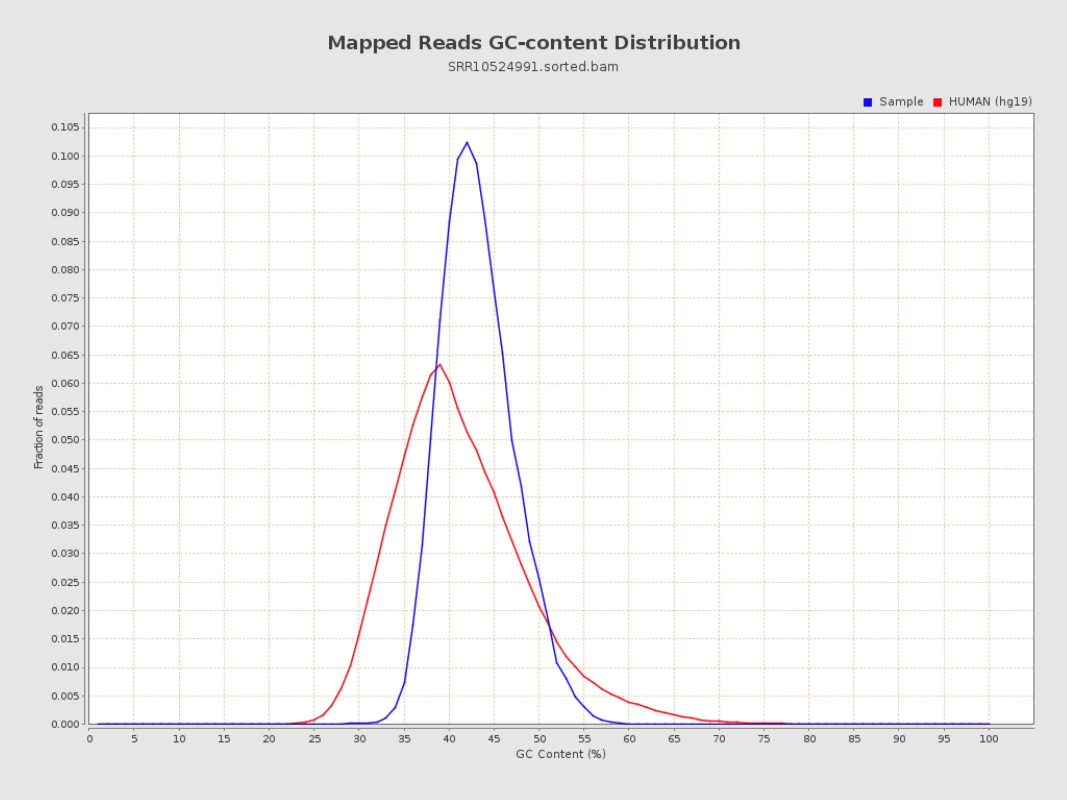
7. Results : Duplication Rate Histogram



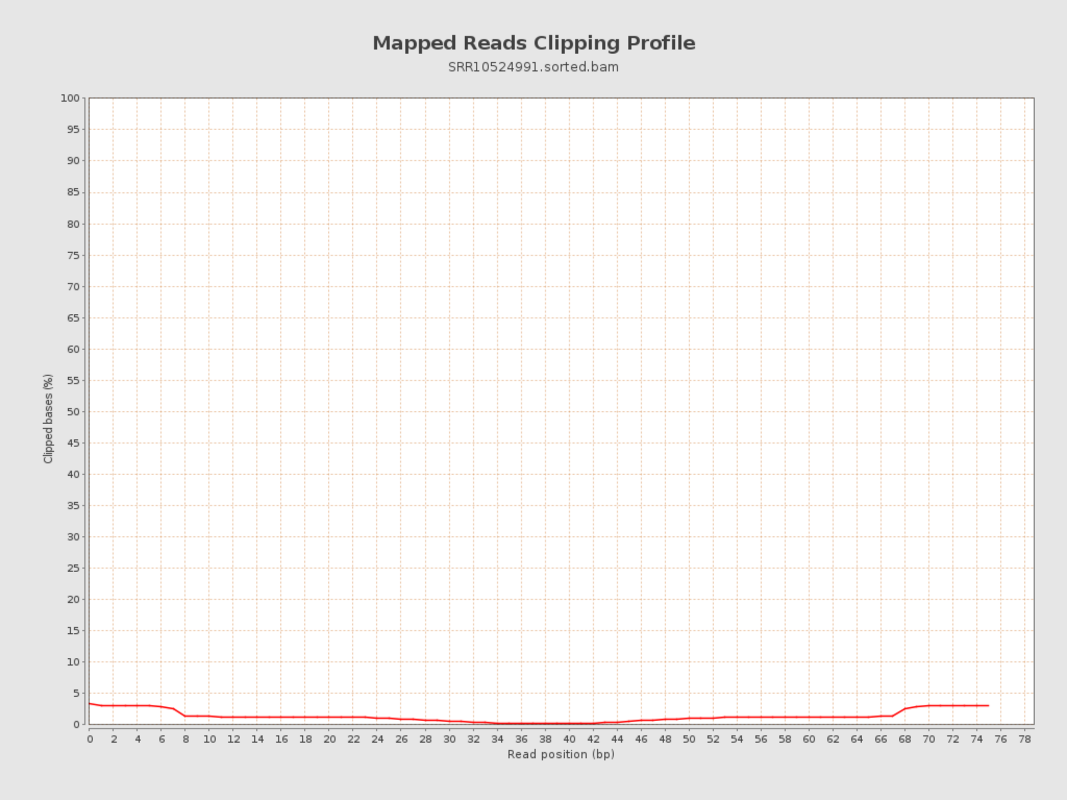
8. Results : Mapped Reads Nucleotide Content



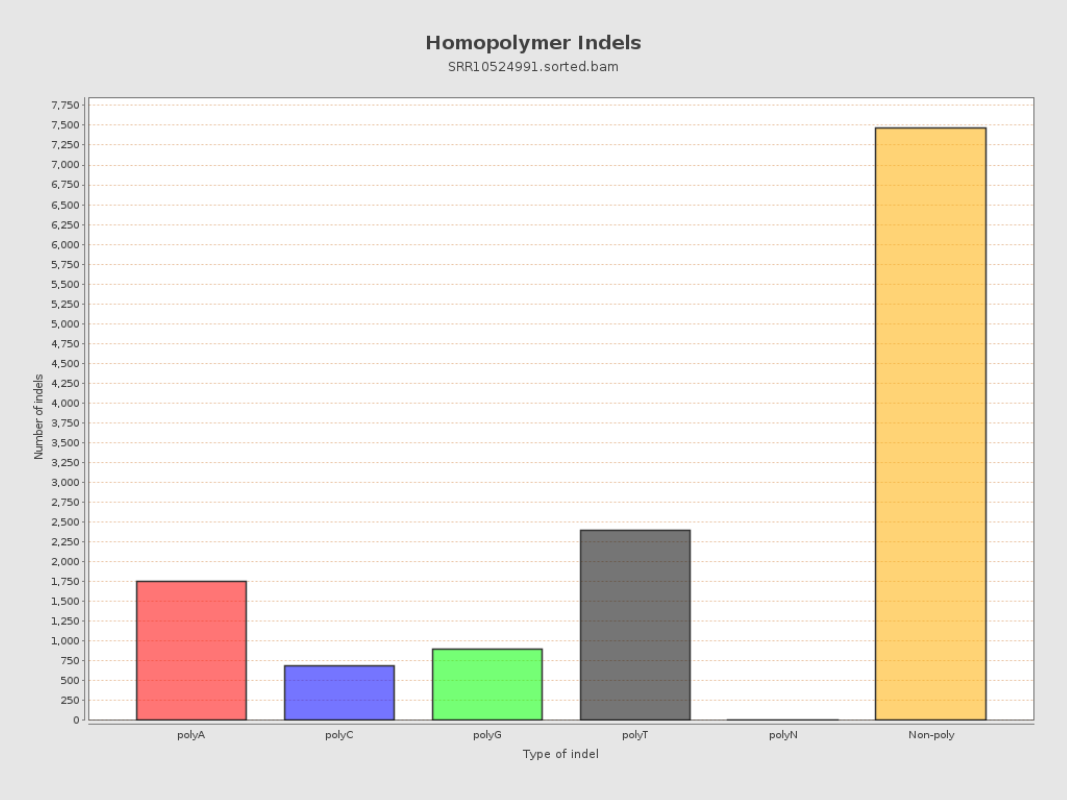
9. Results : Mapped Reads GC-content Distribution



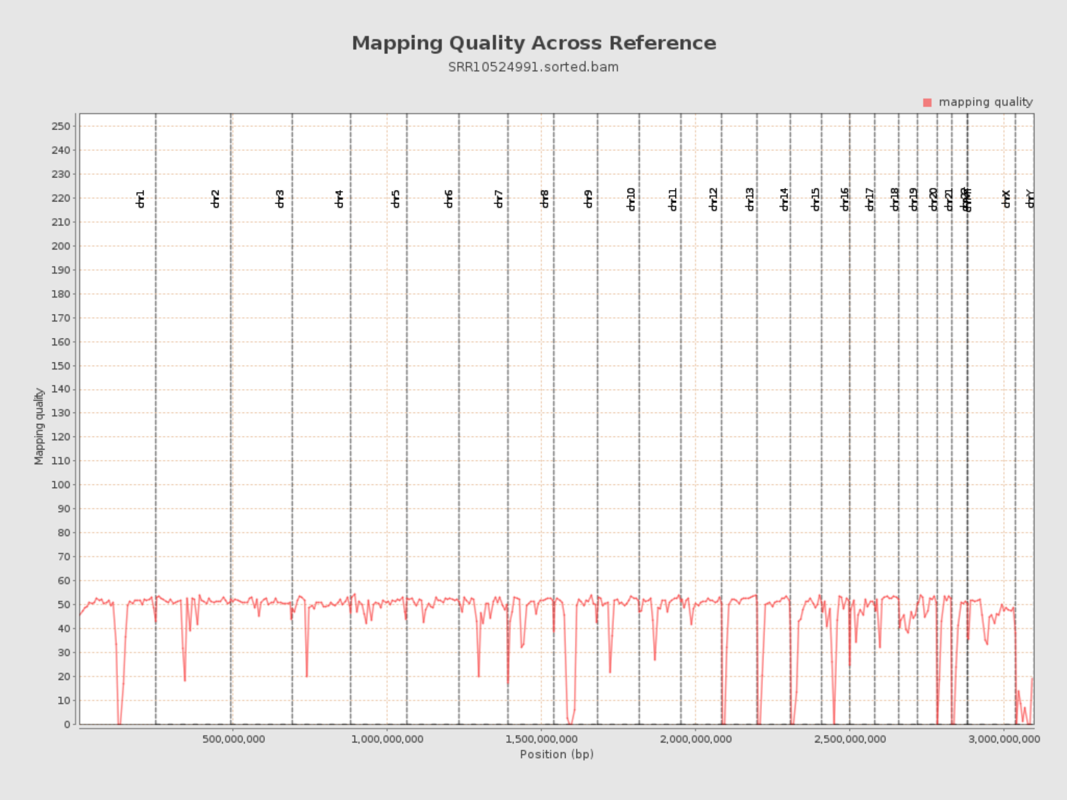
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram