Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 02:02:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524896.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_SRR10524896 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524896.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 02:02:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524896.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	641,247
Mapped reads	593,998 / 92.63%
Unmapped reads	47,249 / 7.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,268 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	12,139 / 1.89%
Duplication rate	1.5%
Clipped reads	594,610 / 92.73%

2.2. ACGT Content

Number/percentage of A's	9,142,200 / 26.22%
Number/percentage of C's	6,448,570 / 18.49%
Number/percentage of T's	10,698,180 / 30.68%
Number/percentage of G's	8,576,640 / 24.6%
Number/percentage of N's	4,789 / 0.01%
GC Percentage	43.09%

2.3. Coverage

Mean	0.0113

Standard Deviation	0.1401

2.4. Mapping Quality

Mean Mapping Quality	46.35

2.5. Mismatches and indels

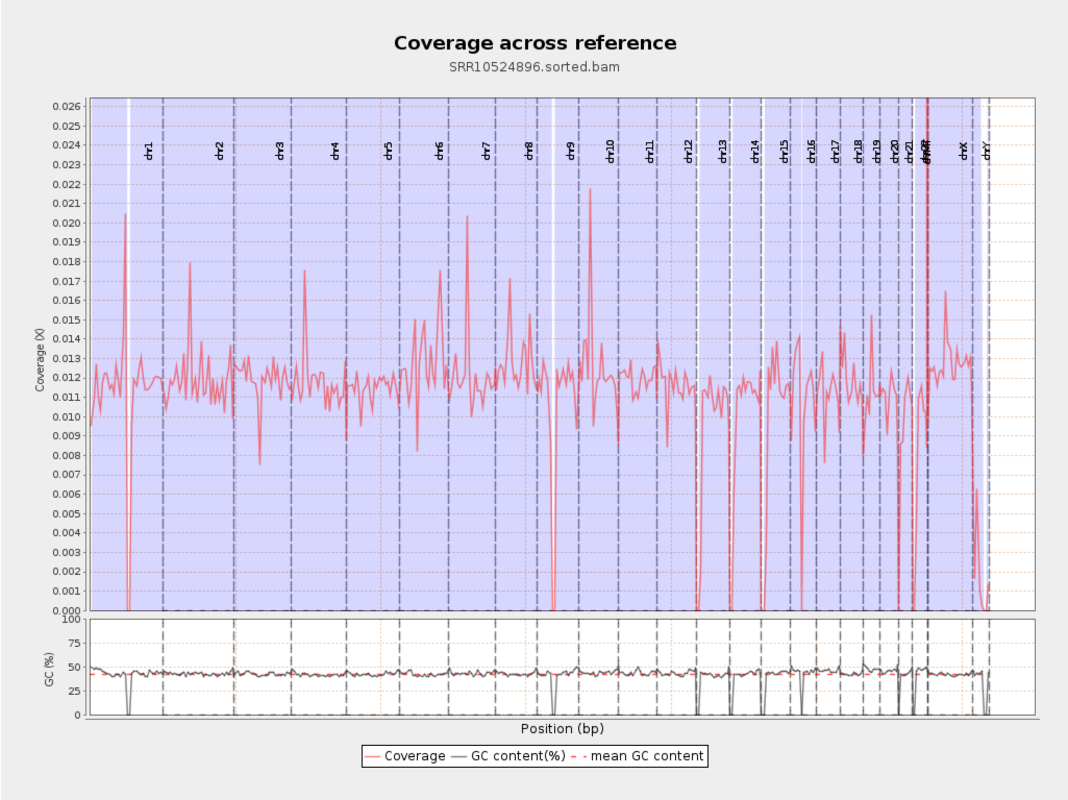
General error rate	0.5%
Mismatches	167,968
Insertions	2,600
Mapped reads with at least one insertion	0.44%
Deletions	6,571
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.49%

2.6. Chromosome stats

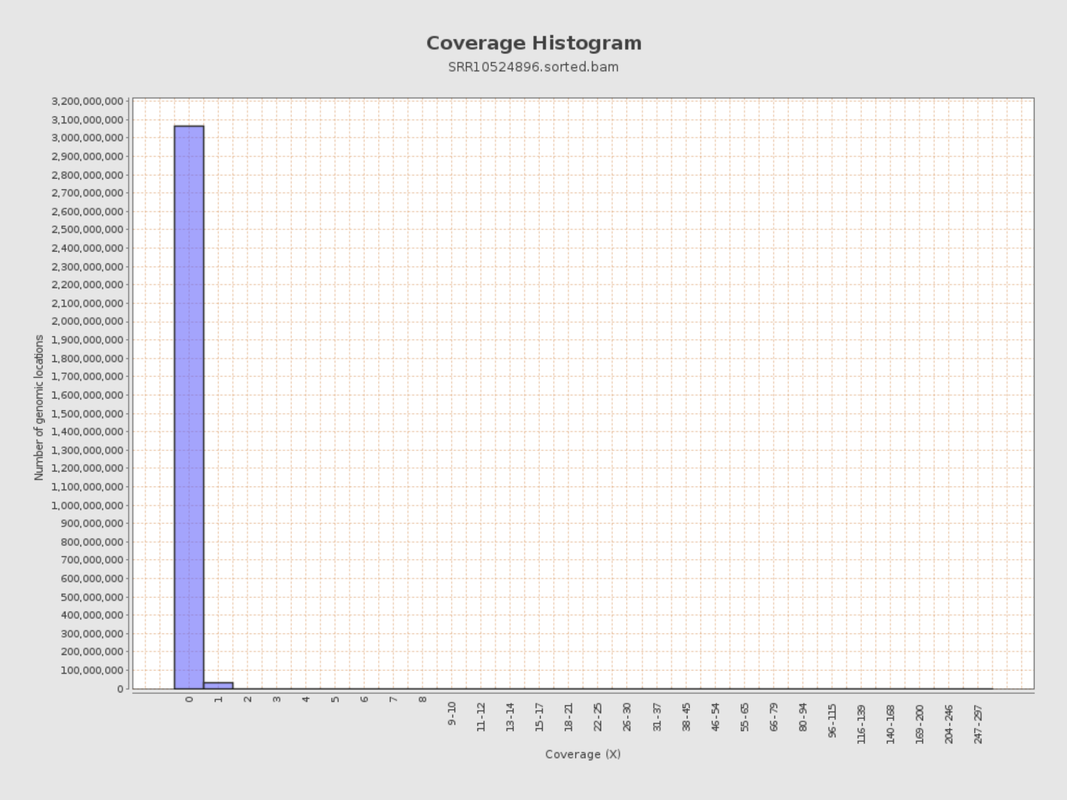
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2804234	0.0113	0.2412
chr2	243199373	2896820	0.0119	0.1415
chr3	198022430	2358692	0.0119	0.1126
chr4	191154276	2249253	0.0118	0.1157
chr5	180915260	2076706	0.0115	0.1115
chr6	171115067	2192932	0.0128	0.1207
chr7	159138663	1920552	0.0121	0.1755

chr8	146364022	1870262	0.0128	0.1487
chr9	141213431	1467181	0.0104	0.1268
chr10	135534747	1707417	0.0126	0.1387
chr11	135006516	1608393	0.0119	0.1294
chr12	133851895	1564033	0.0117	0.1133
chr13	115169878	1062245	0.0092	0.0995
chr14	107349540	1031379	0.0096	0.1025
chr15	102531392	985709	0.0096	0.1013
chr16	90354753	975530	0.0108	0.1127
chr17	81195210	904565	0.0111	0.1131
chr18	78077248	934928	0.012	0.2015
chr19	59128983	664819	0.0112	0.17
chr20	63025520	691457	0.011	0.1095
chr21	48129895	450551	0.0094	0.1042
chr22	51304566	383407	0.0075	0.0889
chrMT	16571	4283	0.2585	0.5298
chrX	155270560	1971952	0.0127	0.1226
chrY	59373566	103774	0.0017	0.0579

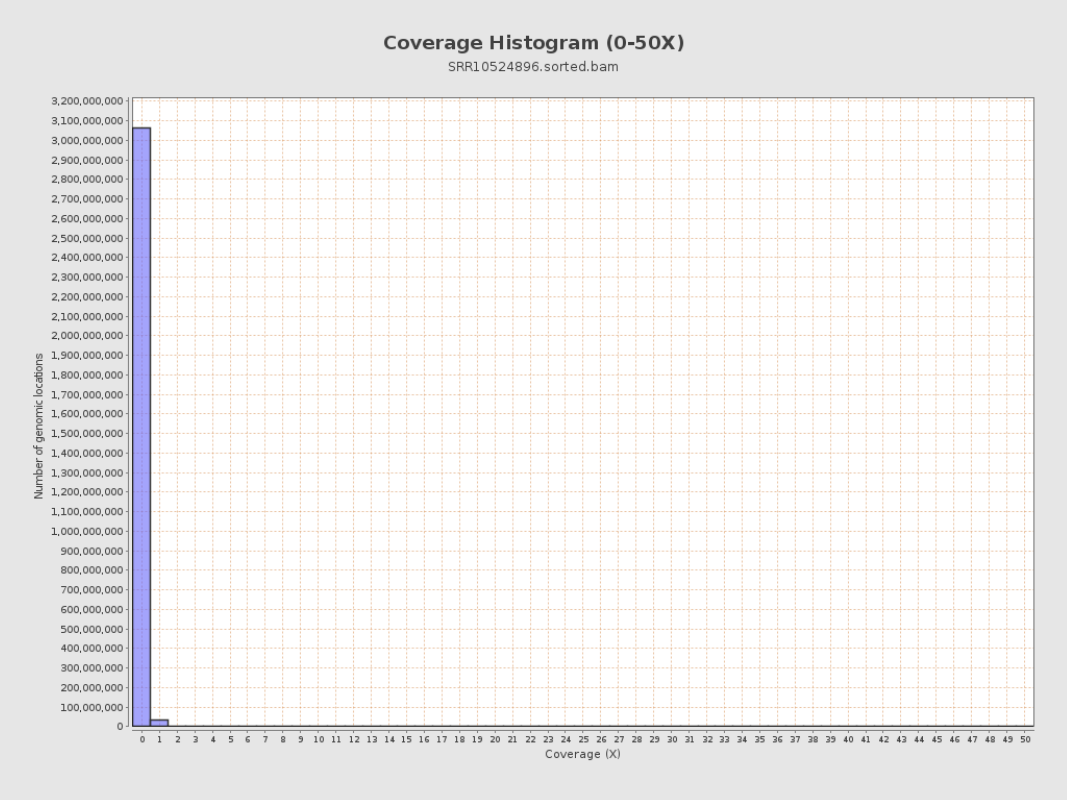
3. Results : Coverage across reference



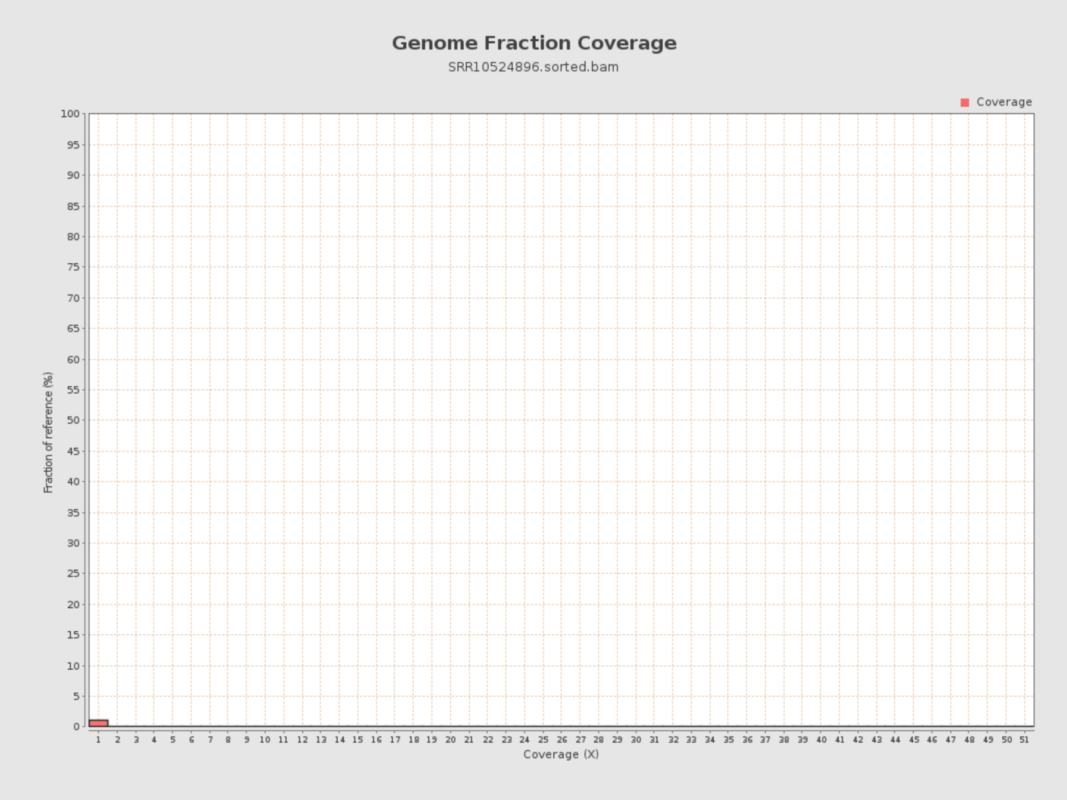
4. Results : Coverage Histogram



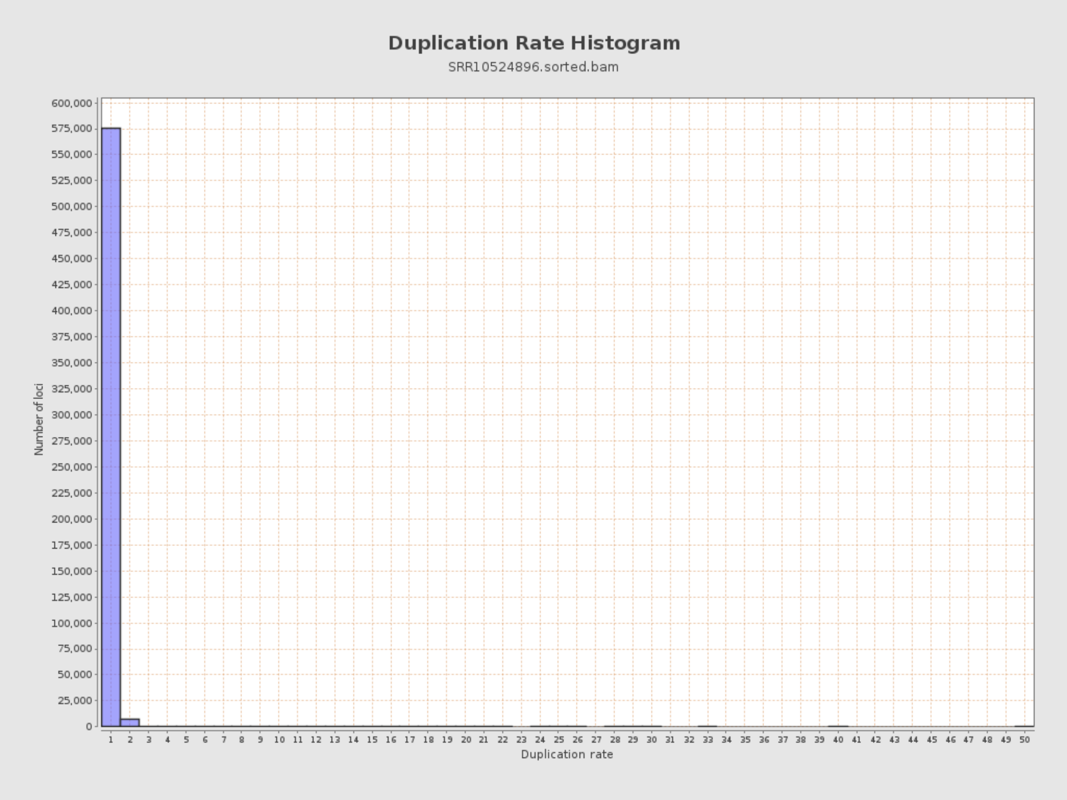
5. Results : Coverage Histogram (0-50X)



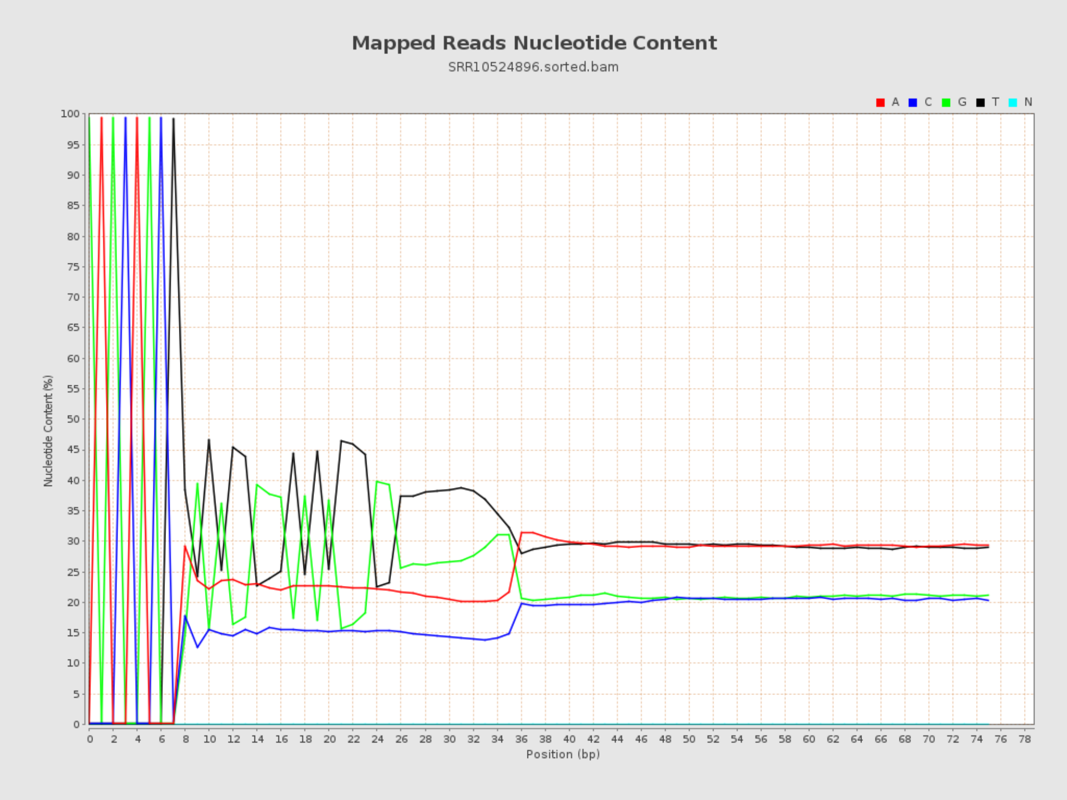
6. Results : Genome Fraction Coverage



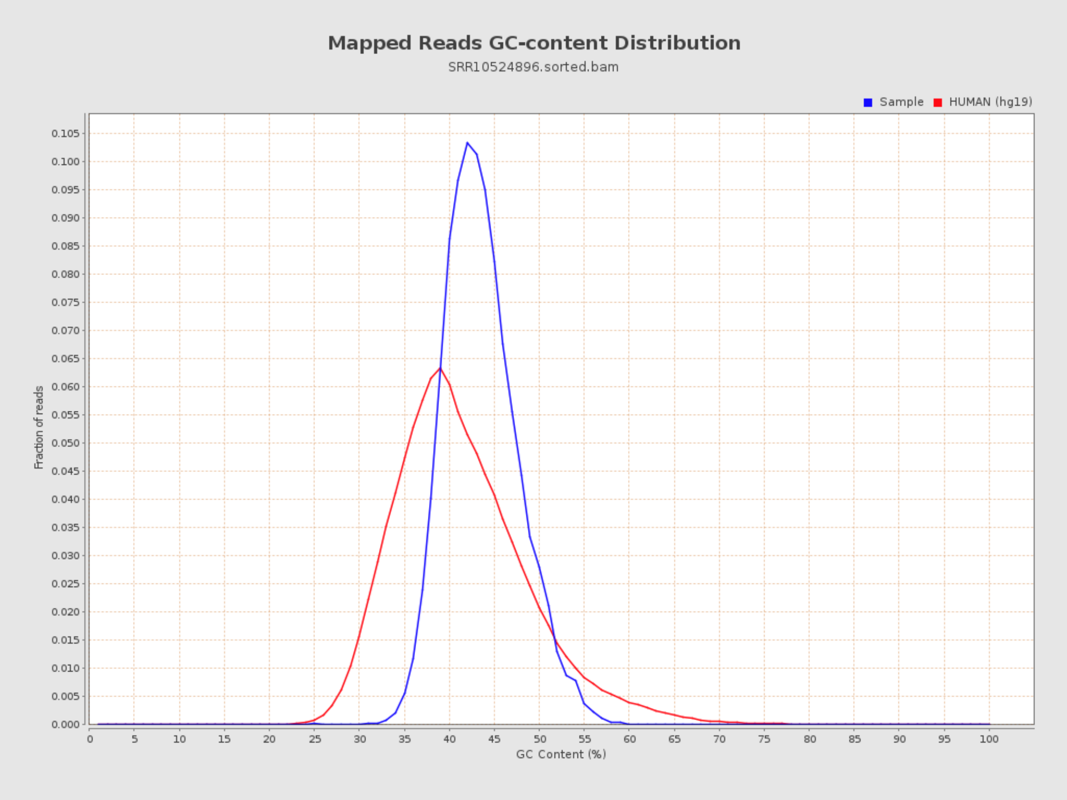
7. Results : Duplication Rate Histogram



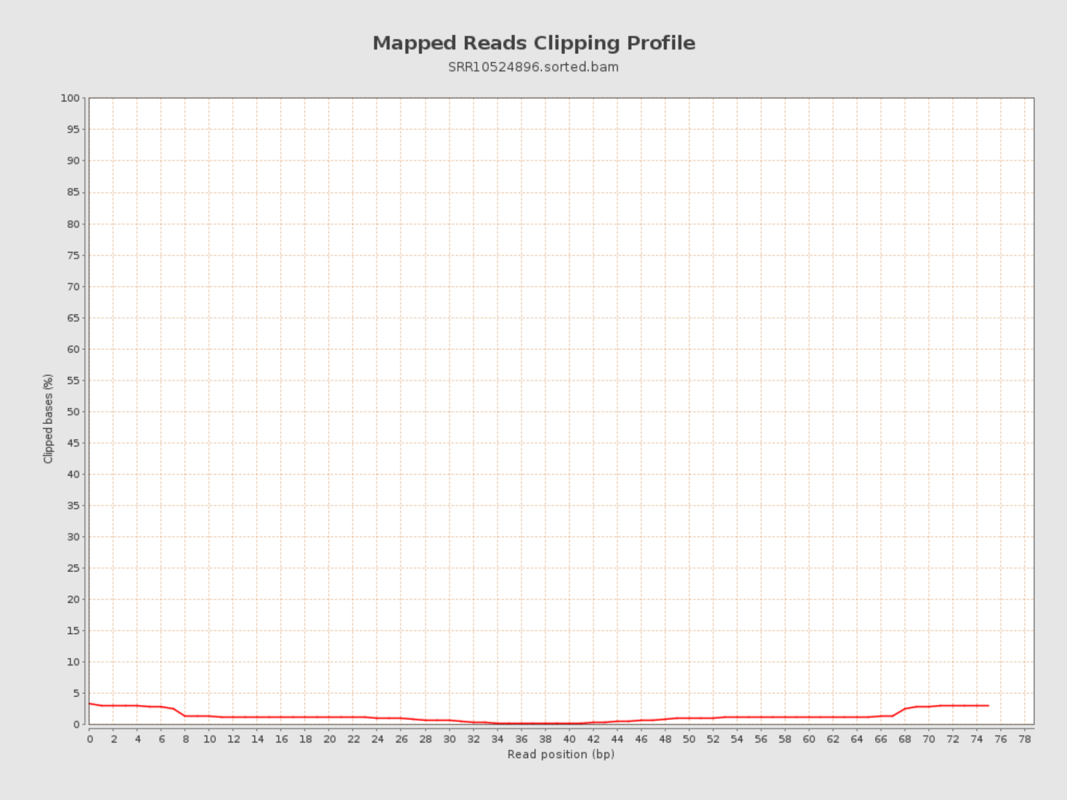
8. Results : Mapped Reads Nucleotide Content



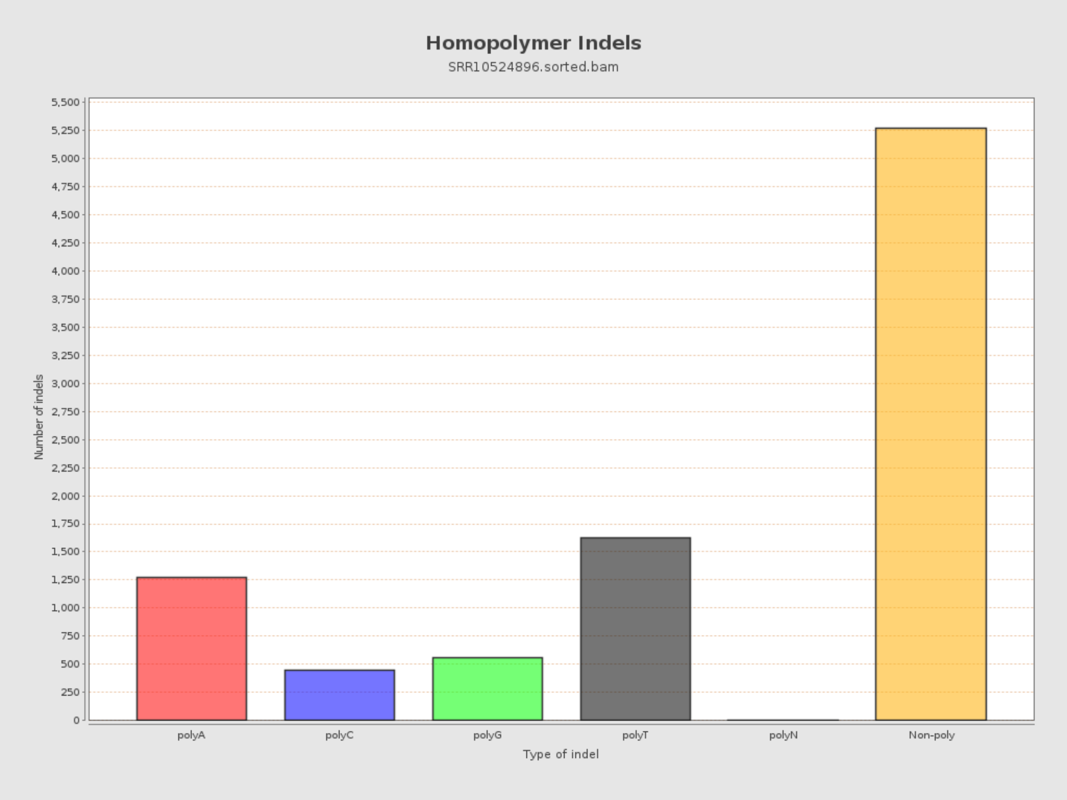
9. Results : Mapped Reads GC-content Distribution



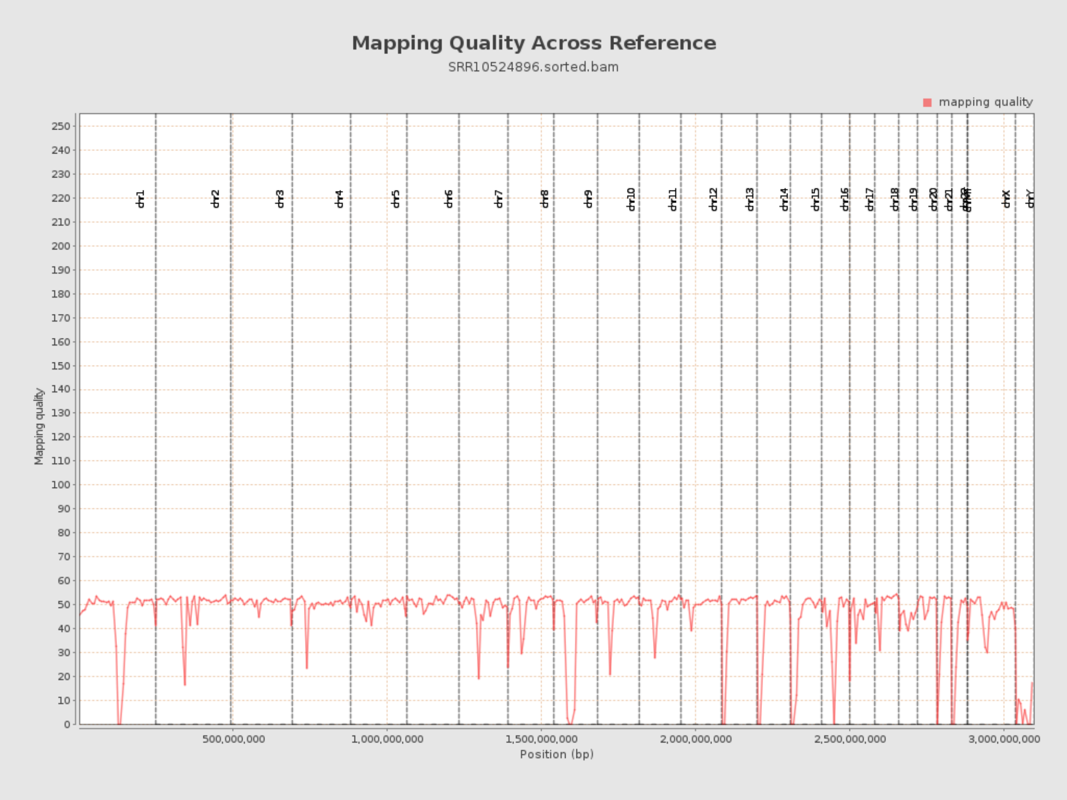
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram