Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 01:54:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524893.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_SRR10524893 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524893.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 01:54:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524893.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	836,023
Mapped reads	767,926 / 91.85%
Unmapped reads	68,097 / 8.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,568 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	20,831 / 2.49%
Duplication rate	1.97%
Clipped reads	767,522 / 91.81%

2.2. ACGT Content

Number/percentage of A's	12,243,580 / 27.3%
Number/percentage of C's	7,693,652 / 17.16%
Number/percentage of T's	14,330,874 / 31.96%
Number/percentage of G's	10,567,268 / 23.57%
Number/percentage of N's	5,446 / 0.01%
GC Percentage	40.72%

2.3. Coverage

Mean	0.0145

Standard Deviation	0.1736

2.4. Mapping Quality

Mean Mapping Quality	46.67

2.5. Mismatches and indels

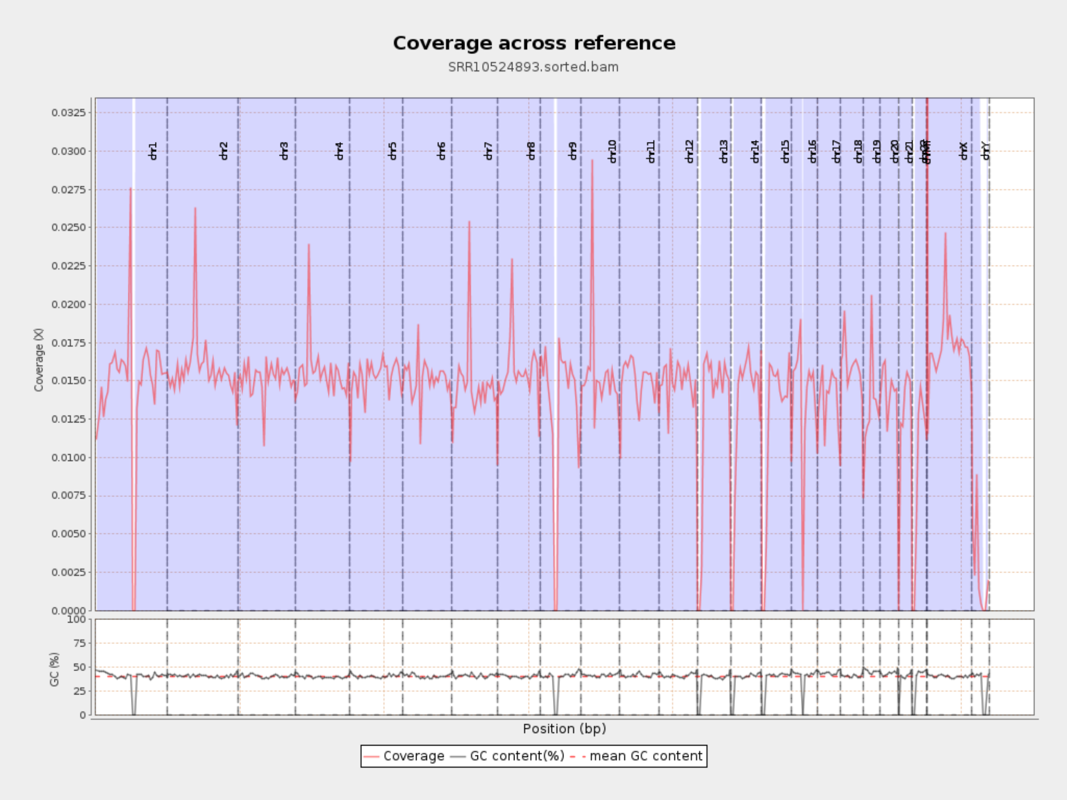
General error rate	0.51%
Mismatches	222,077
Insertions	3,706
Mapped reads with at least one insertion	0.48%
Deletions	8,442
Mapped reads with at least one deletion	1.09%
Homopolymer indels	43.12%

2.6. Chromosome stats

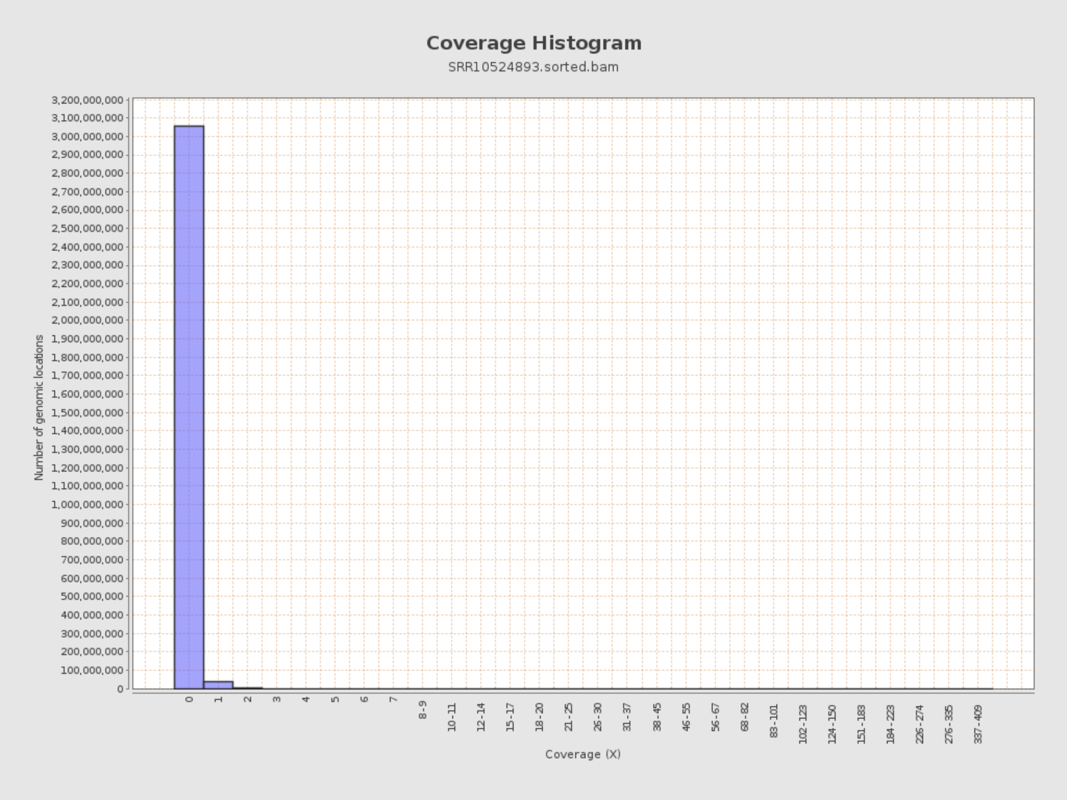
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3646723	0.0146	0.3221
chr2	243199373	3862490	0.0159	0.1826
chr3	198022430	3007727	0.0152	0.1286
chr4	191154276	2980133	0.0156	0.1385
chr5	180915260	2779568	0.0154	0.13
chr6	171115067	2581588	0.0151	0.135
chr7	159138663	2352137	0.0148	0.2081

chr8	146364022	2296419	0.0157	0.1724
chr9	141213431	1884744	0.0133	0.1566
chr10	135534747	2097762	0.0155	0.1678
chr11	135006516	2030845	0.015	0.1606
chr12	133851895	2002614	0.015	0.1296
chr13	115169878	1477789	0.0128	0.1182
chr14	107349540	1380650	0.0129	0.1226
chr15	102531392	1249722	0.0122	0.1152
chr16	90354753	1224673	0.0136	0.1279
chr17	81195210	1123804	0.0138	0.1295
chr18	78077248	1256489	0.0161	0.2726
chr19	59128983	798210	0.0135	0.2093
chr20	63025520	896558	0.0142	0.1269
chr21	48129895	600502	0.0125	0.125
chr22	51304566	474662	0.0093	0.1003
chrMT	16571	8249	0.4978	0.753
chrX	155270560	2696639	0.0174	0.1503
chrY	59373566	143652	0.0024	0.0747

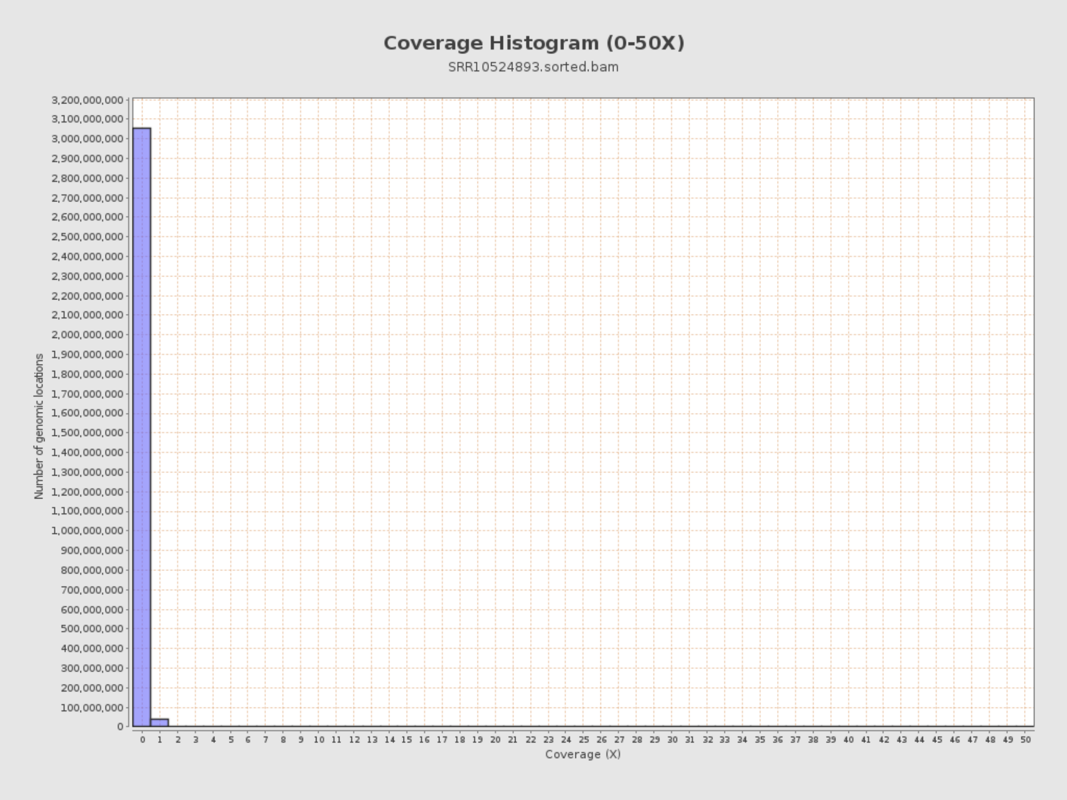
3. Results : Coverage across reference



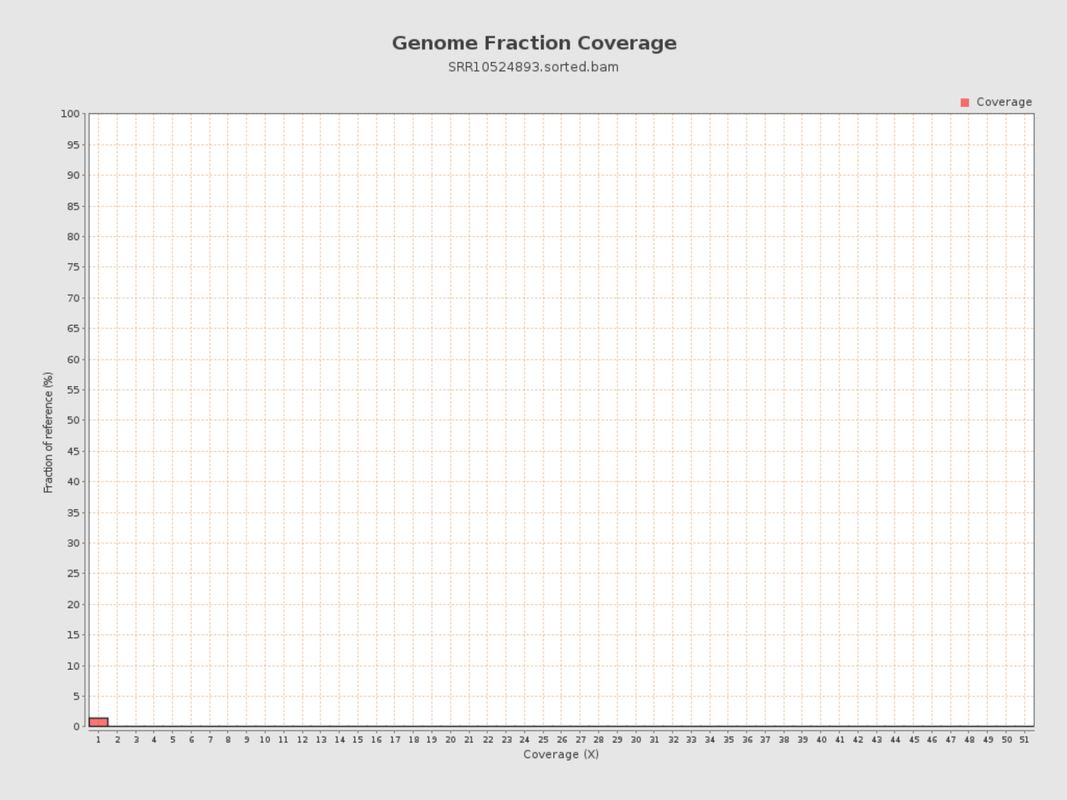
4. Results : Coverage Histogram



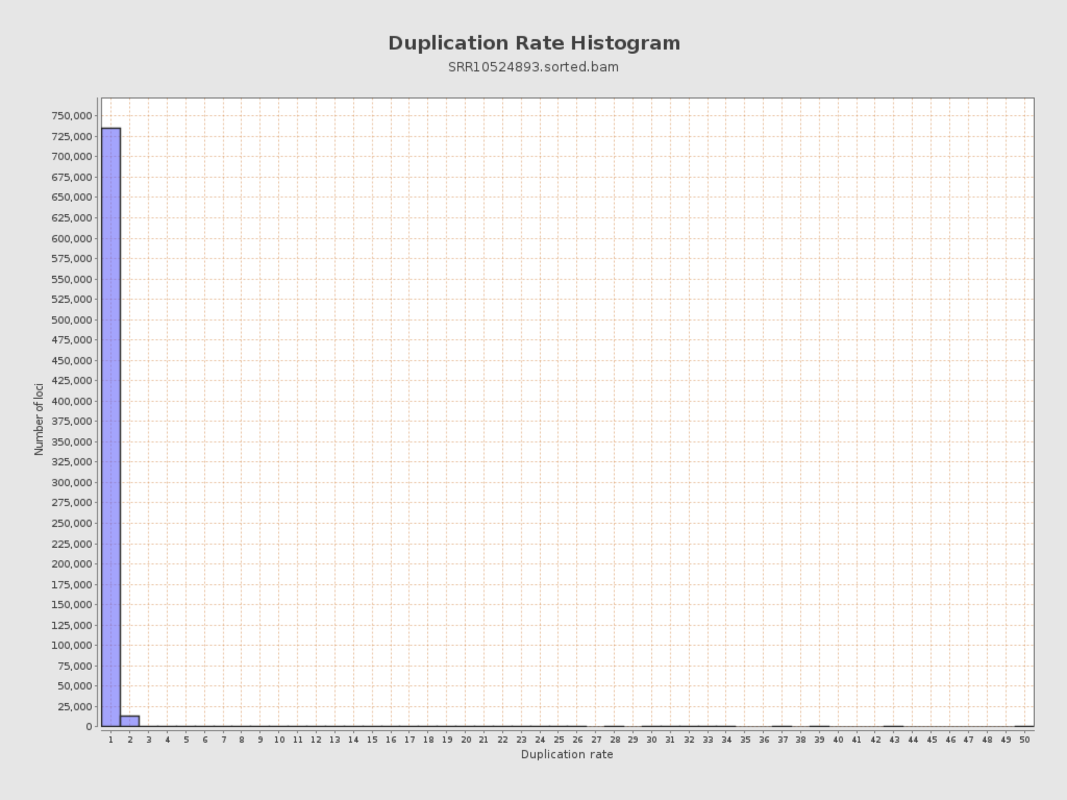
5. Results : Coverage Histogram (0-50X)



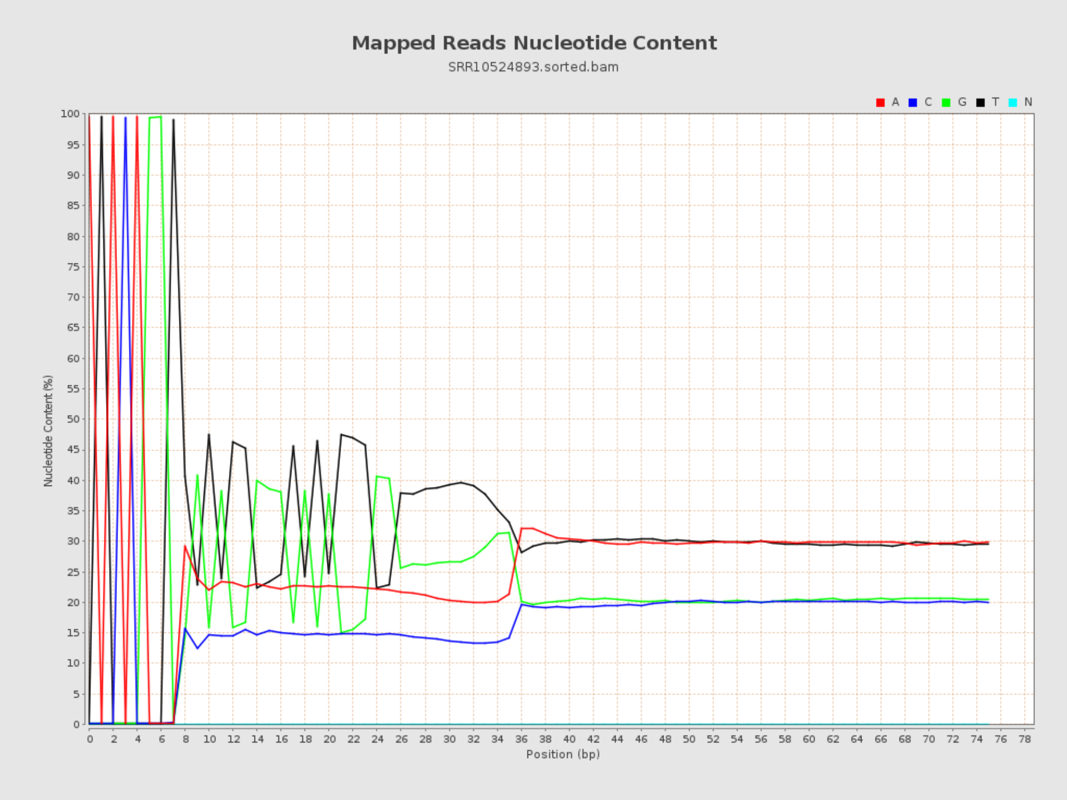
6. Results : Genome Fraction Coverage



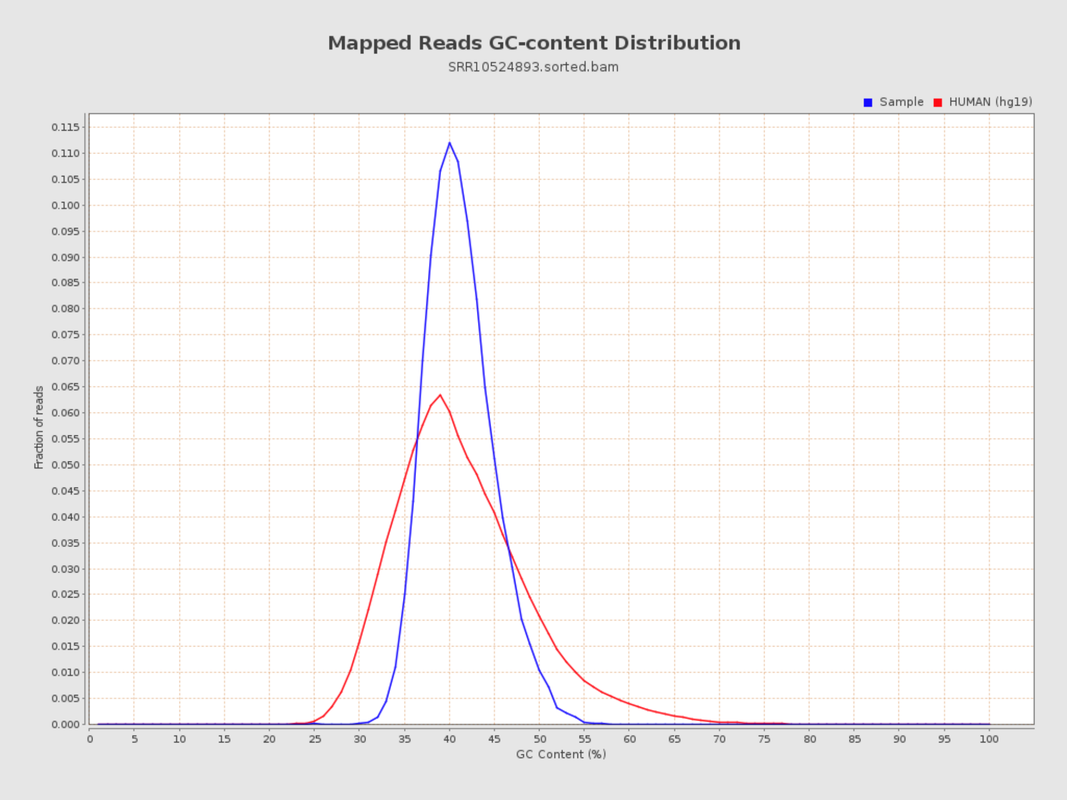
7. Results : Duplication Rate Histogram



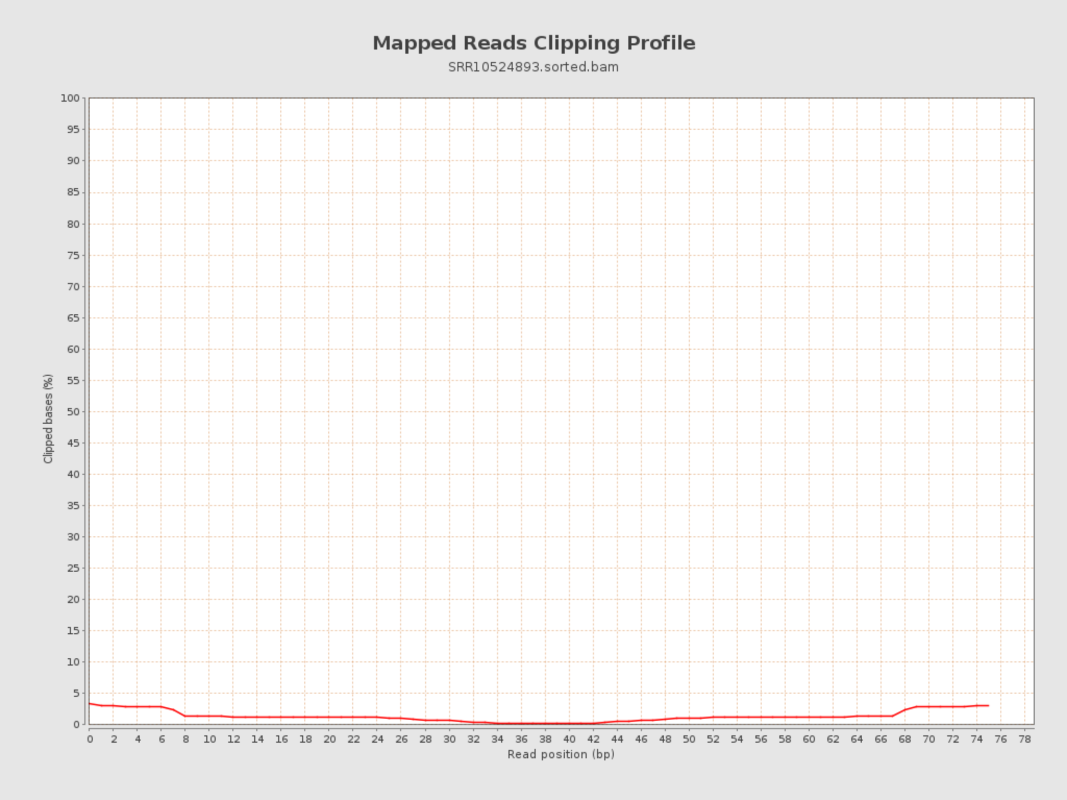
8. Results : Mapped Reads Nucleotide Content



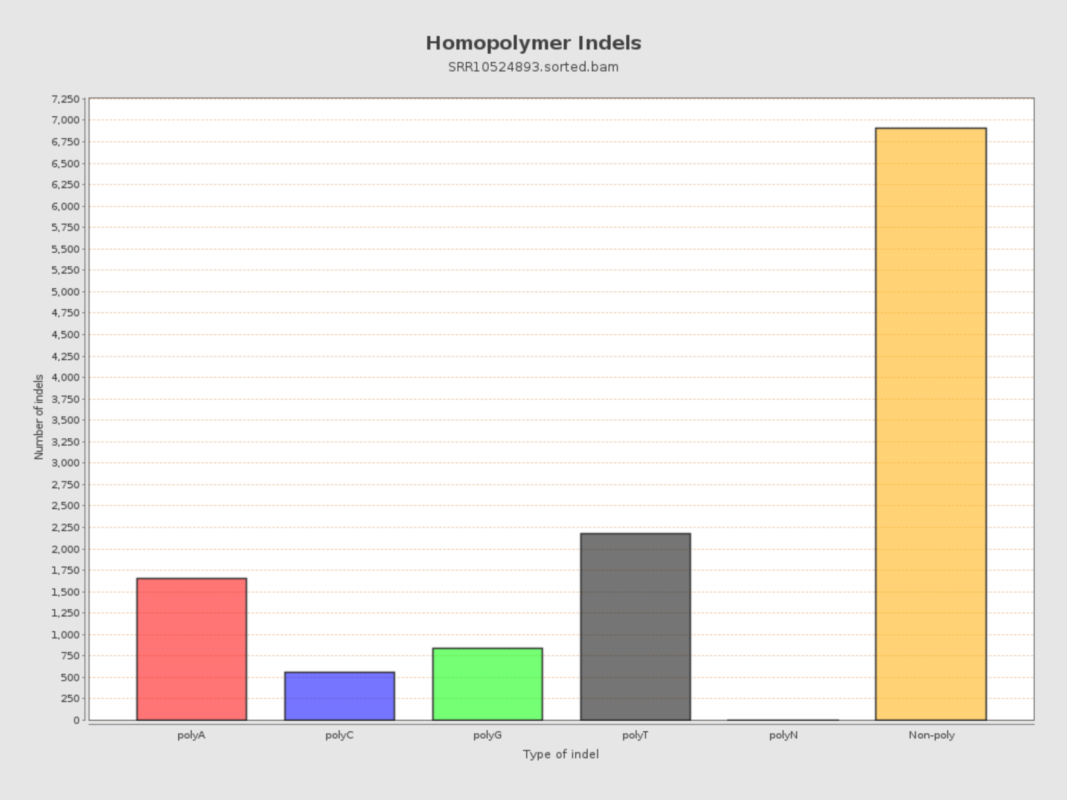
9. Results : Mapped Reads GC-content Distribution



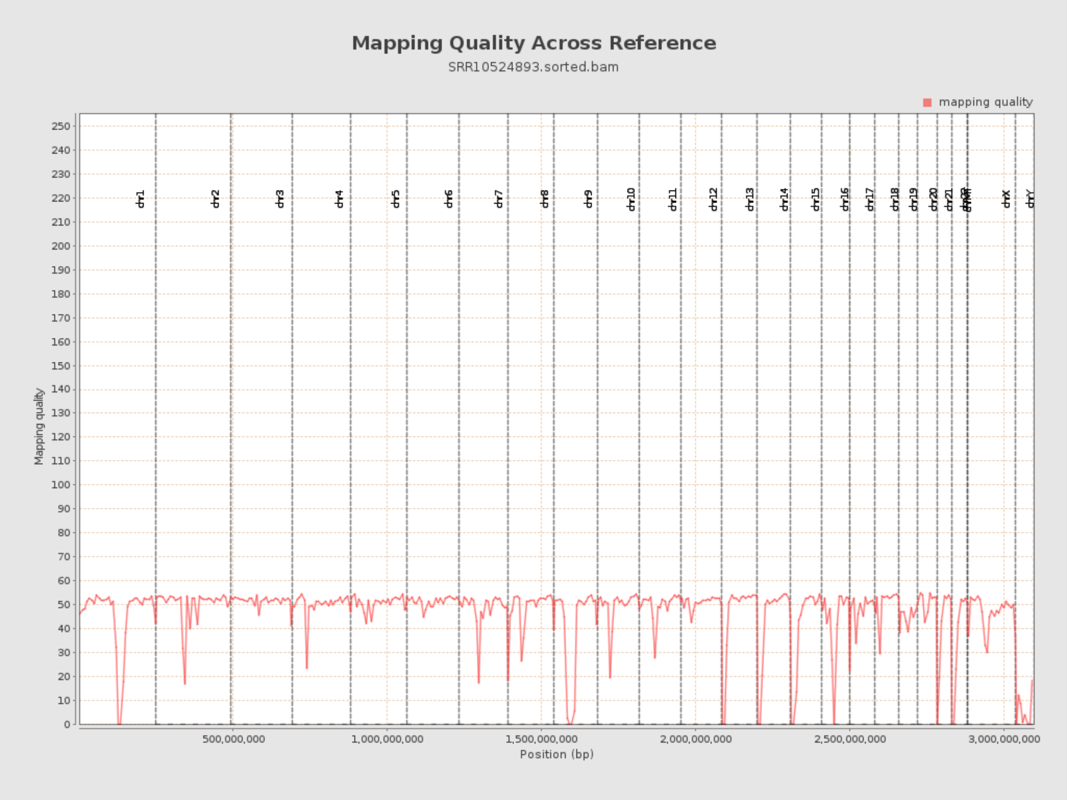
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram