Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 13:32:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524631.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_SRR10524631 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524631.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 13:32:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524631.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	511,370
Mapped reads	474,652 / 92.82%
Unmapped reads	36,718 / 7.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,058 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	9,119 / 1.78%
Duplication rate	1.48%
Clipped reads	474,371 / 92.76%

2.2. ACGT Content

Number/percentage of A's	7,132,651 / 25.79%
Number/percentage of C's	5,084,331 / 18.38%
Number/percentage of T's	8,944,246 / 32.33%
Number/percentage of G's	6,499,981 / 23.5%
Number/percentage of N's	149 / 0%
GC Percentage	41.88%

2.3. Coverage

Mean	0.0089

Standard Deviation	0.1129

2.4. Mapping Quality

Mean Mapping Quality	45.25

2.5. Mismatches and indels

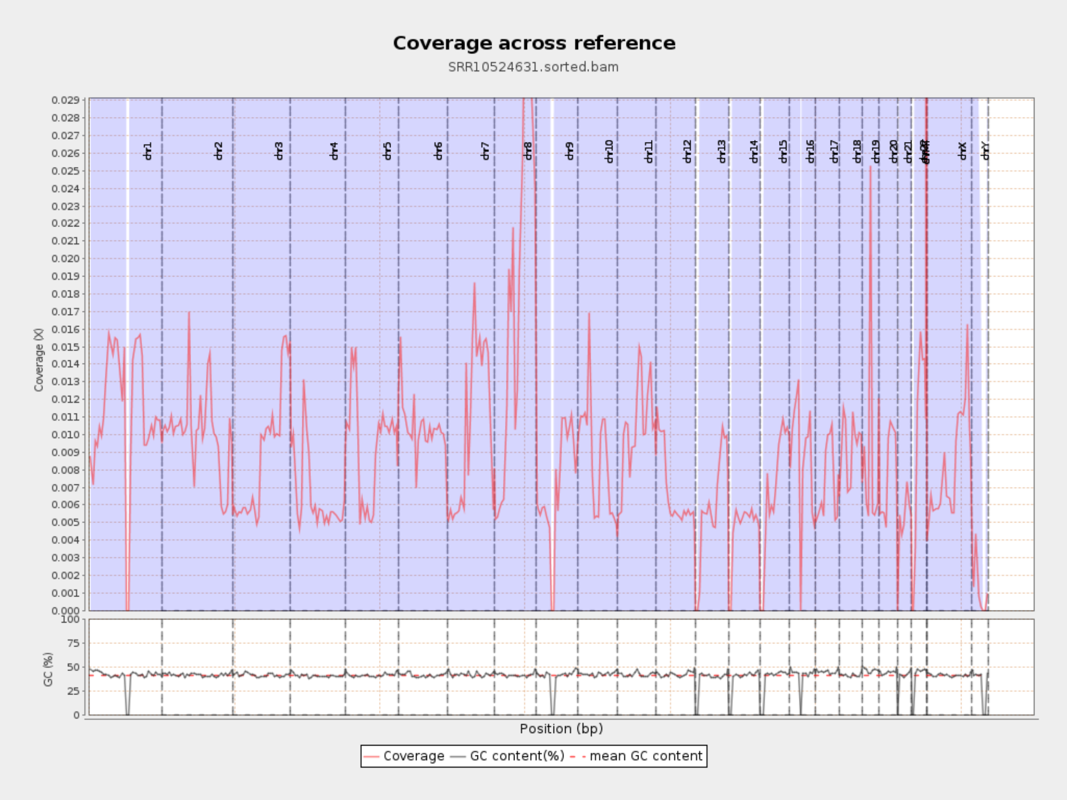
General error rate	0.49%
Mismatches	131,275
Insertions	2,001
Mapped reads with at least one insertion	0.42%
Deletions	5,214
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.43%

2.6. Chromosome stats

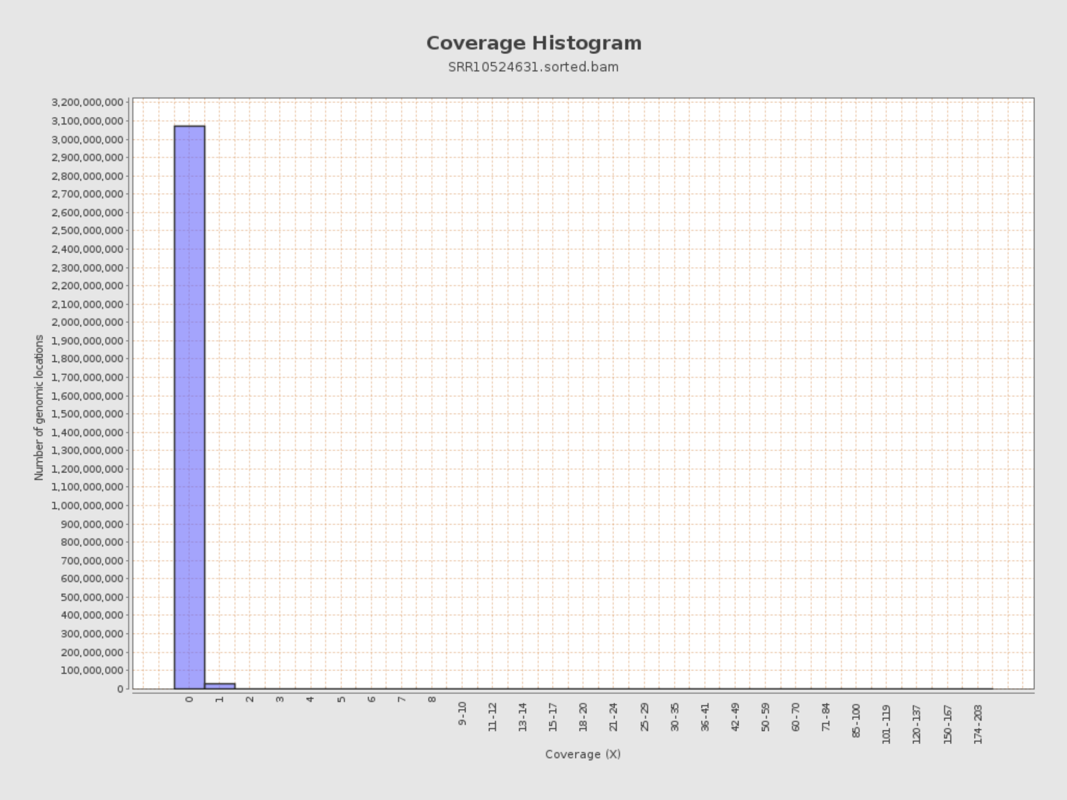
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2819254	0.0113	0.1684
chr2	243199373	2470309	0.0102	0.1271
chr3	198022430	1744497	0.0088	0.0973
chr4	191154276	1243464	0.0065	0.0875
chr5	180915260	1701433	0.0094	0.1005
chr6	171115067	1780548	0.0104	0.1089
chr7	159138663	1668354	0.0105	0.1311

chr8	146364022	2687700	0.0184	0.1589
chr9	141213431	985726	0.007	0.098
chr10	135534747	1178866	0.0087	0.1108
chr11	135006516	1394110	0.0103	0.1147
chr12	133851895	903860	0.0068	0.0858
chr13	115169878	676744	0.0059	0.0793
chr14	107349540	496708	0.0046	0.0718
chr15	102531392	699482	0.0068	0.0875
chr16	90354753	789299	0.0087	0.0994
chr17	81195210	590449	0.0073	0.0888
chr18	78077248	737495	0.0094	0.1381
chr19	59128983	535587	0.0091	0.128
chr20	63025520	496169	0.0079	0.0926
chr21	48129895	243425	0.0051	0.0761
chr22	51304566	485849	0.0095	0.1011
chrMT	16571	5853	0.3532	0.5806
chrX	155270560	1263039	0.0081	0.0983
chrY	59373566	71955	0.0012	0.046

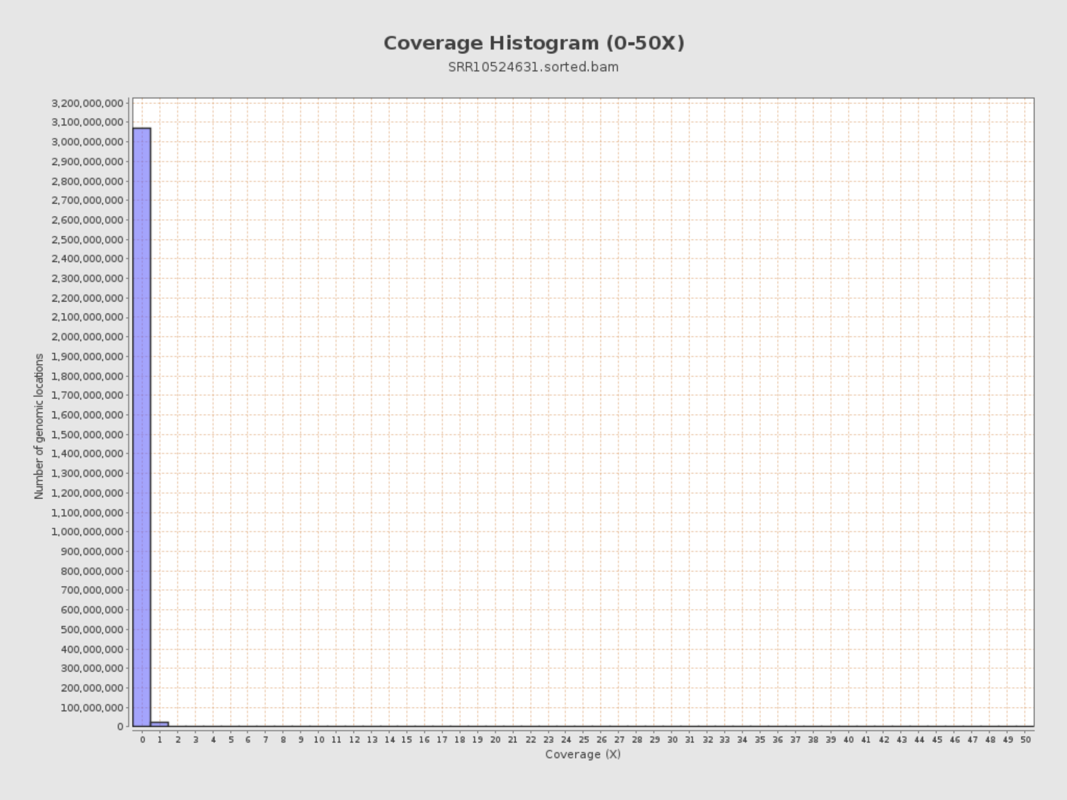
3. Results : Coverage across reference



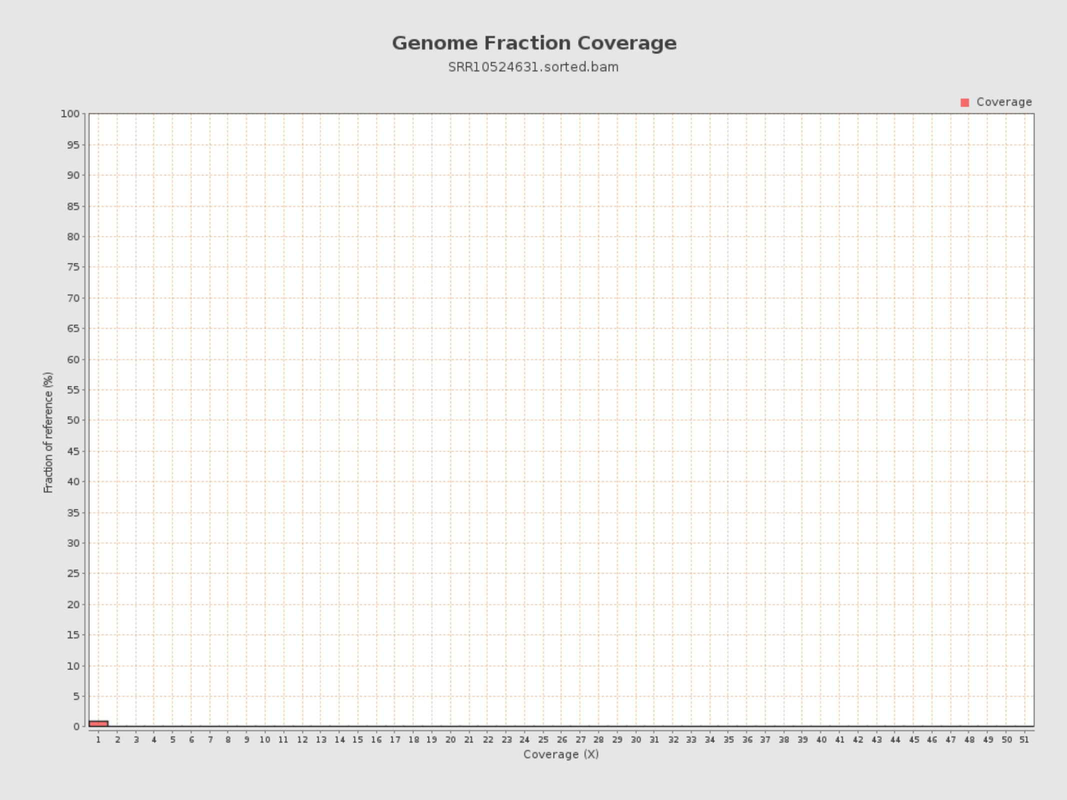
4. Results : Coverage Histogram



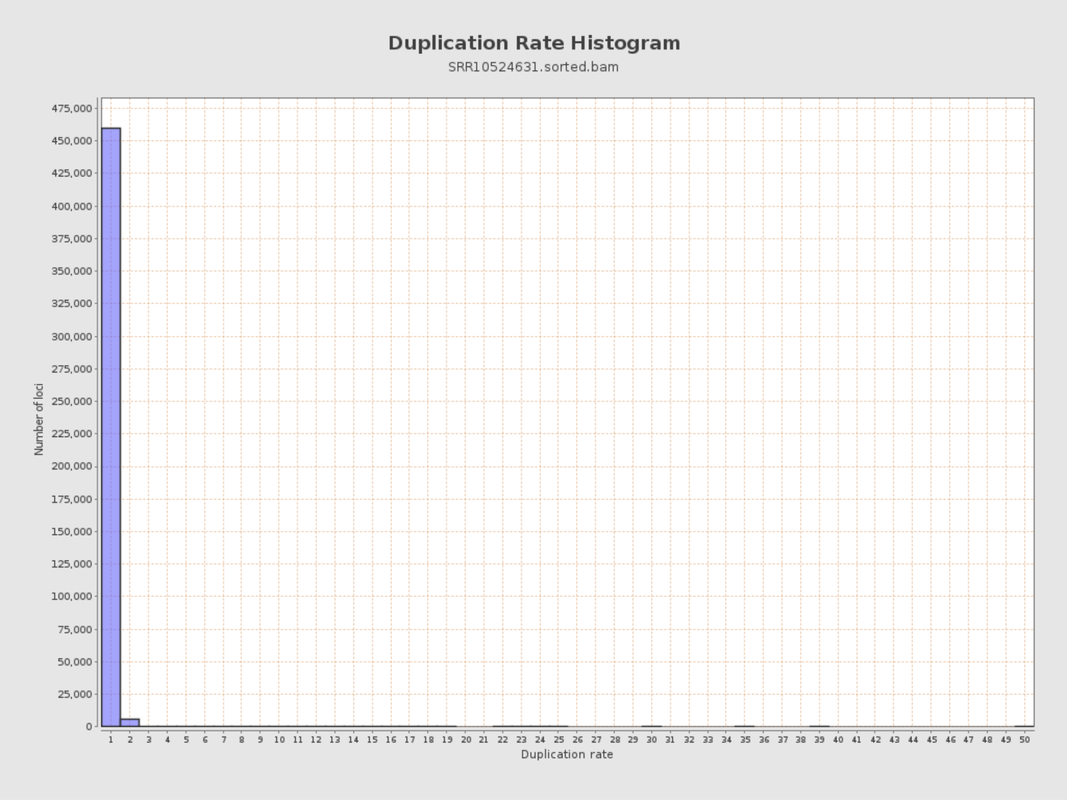
5. Results : Coverage Histogram (0-50X)



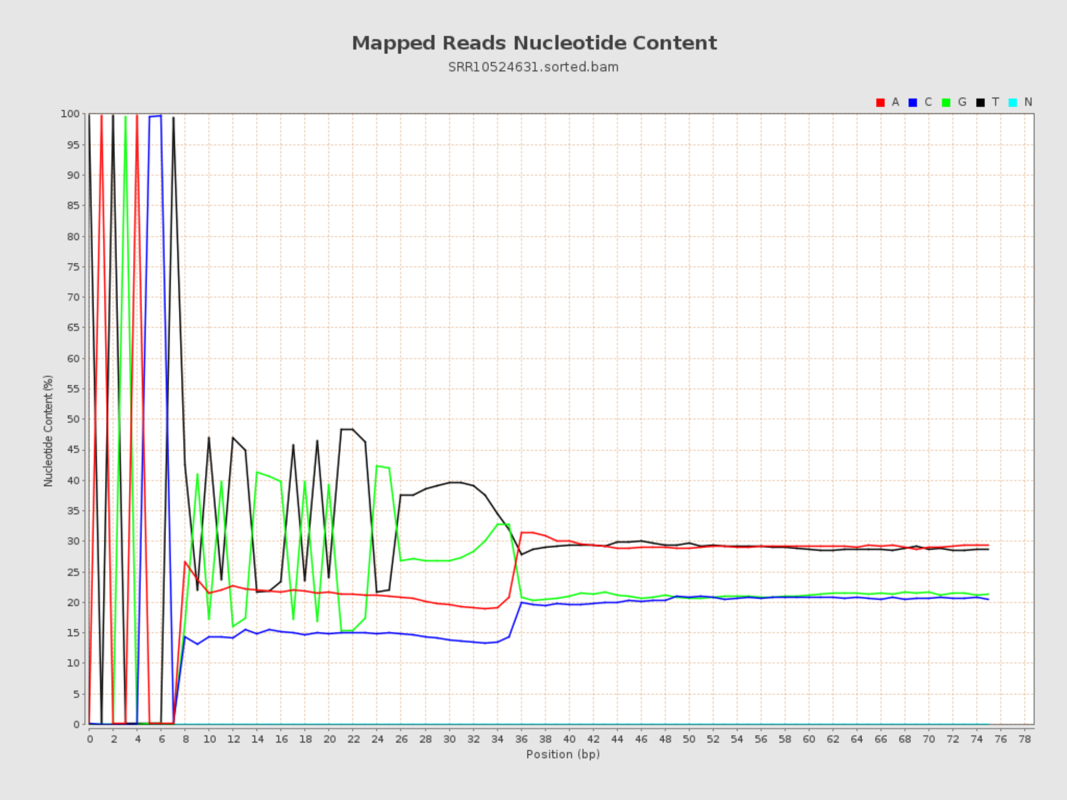
6. Results : Genome Fraction Coverage



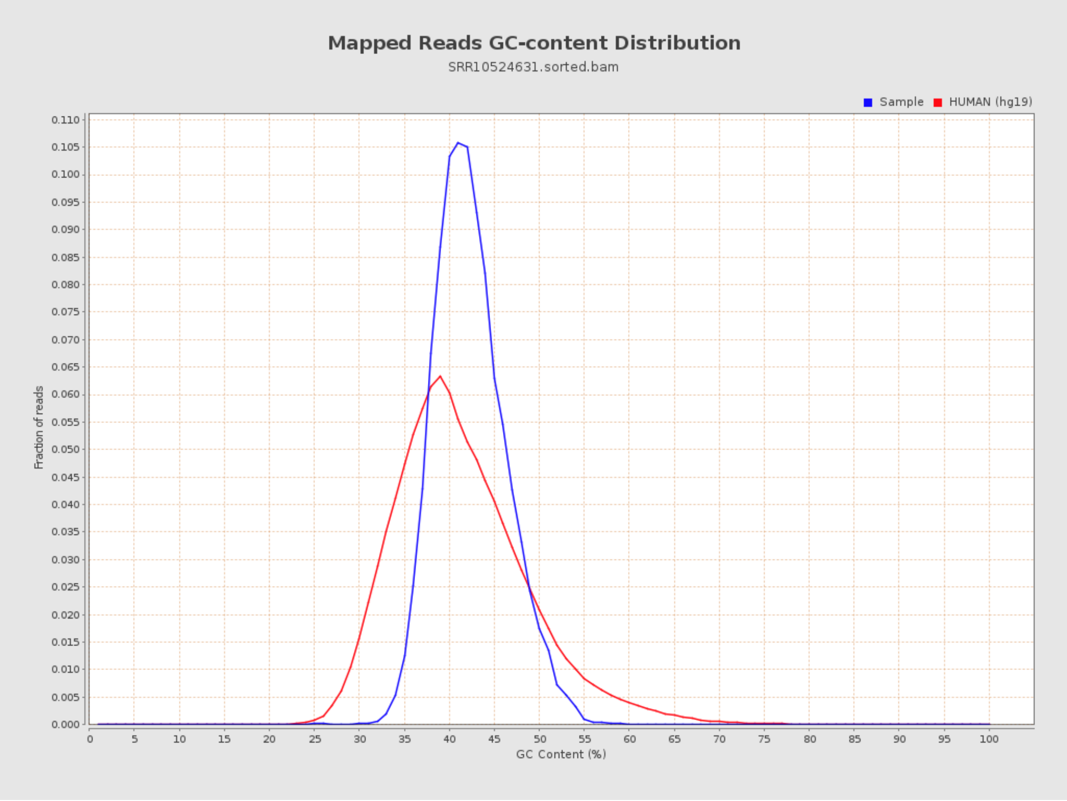
7. Results : Duplication Rate Histogram



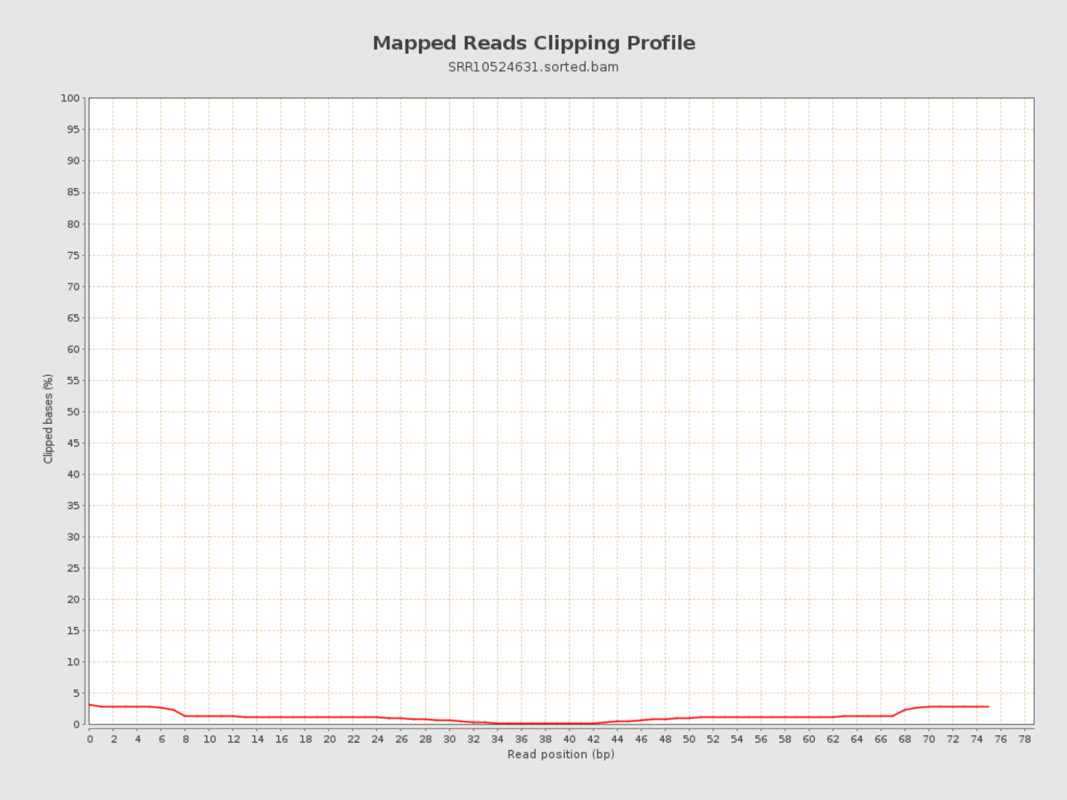
8. Results : Mapped Reads Nucleotide Content



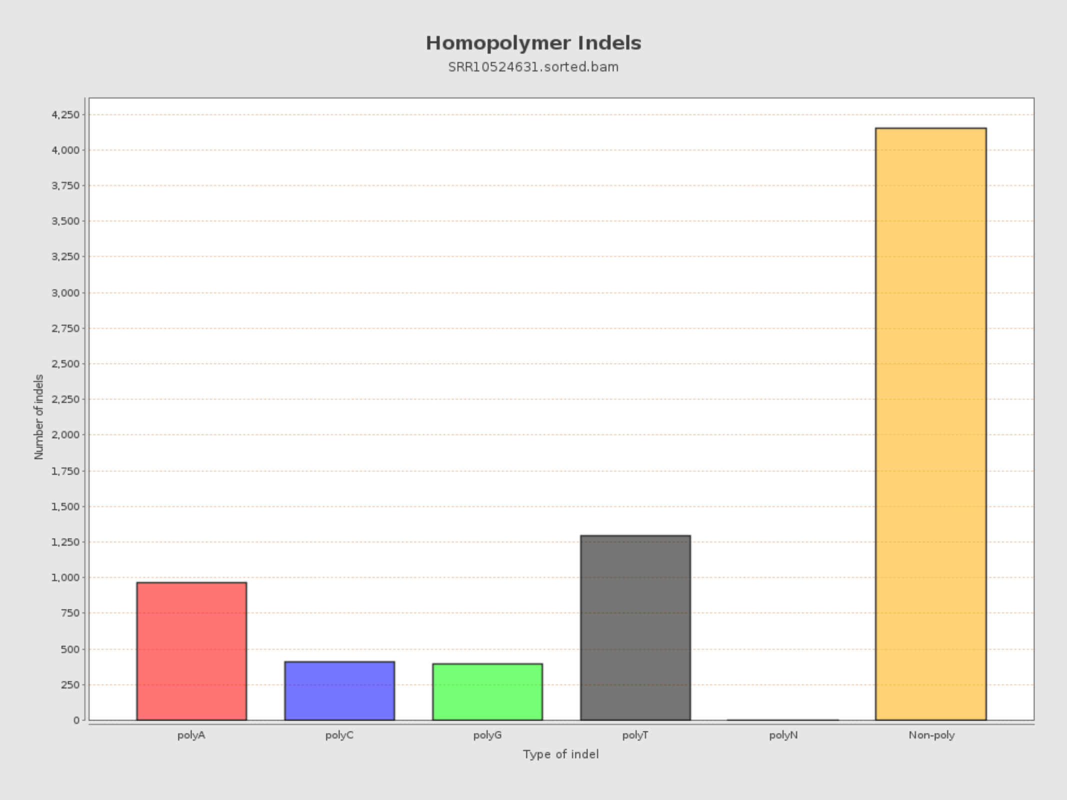
9. Results : Mapped Reads GC-content Distribution



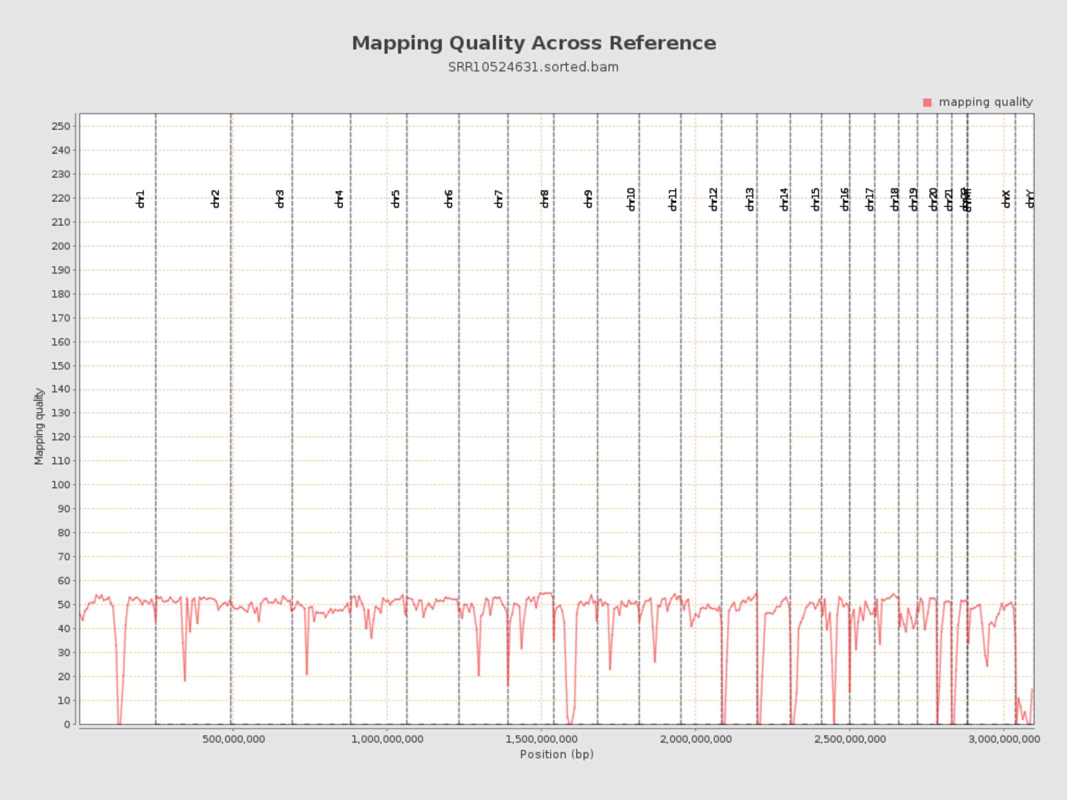
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram