Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 17:08:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524701.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_SRR10524701 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524701.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 17:08:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524701.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,763,606
Mapped reads	1,623,206 / 92.04%
Unmapped reads	140,400 / 7.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,185 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	66,940 / 3.8%
Duplication rate	3%
Clipped reads	1,627,730 / 92.3%

2.2. ACGT Content

Number/percentage of A's	24,928,062 / 26.06%
Number/percentage of C's	18,658,589 / 19.51%
Number/percentage of T's	29,917,972 / 31.28%
Number/percentage of G's	22,122,889 / 23.13%
Number/percentage of N's	12,737 / 0.01%
GC Percentage	42.64%

2.3. Coverage

Mean	0.0309

Standard Deviation	0.3003

2.4. Mapping Quality

Mean Mapping Quality	45.76

2.5. Mismatches and indels

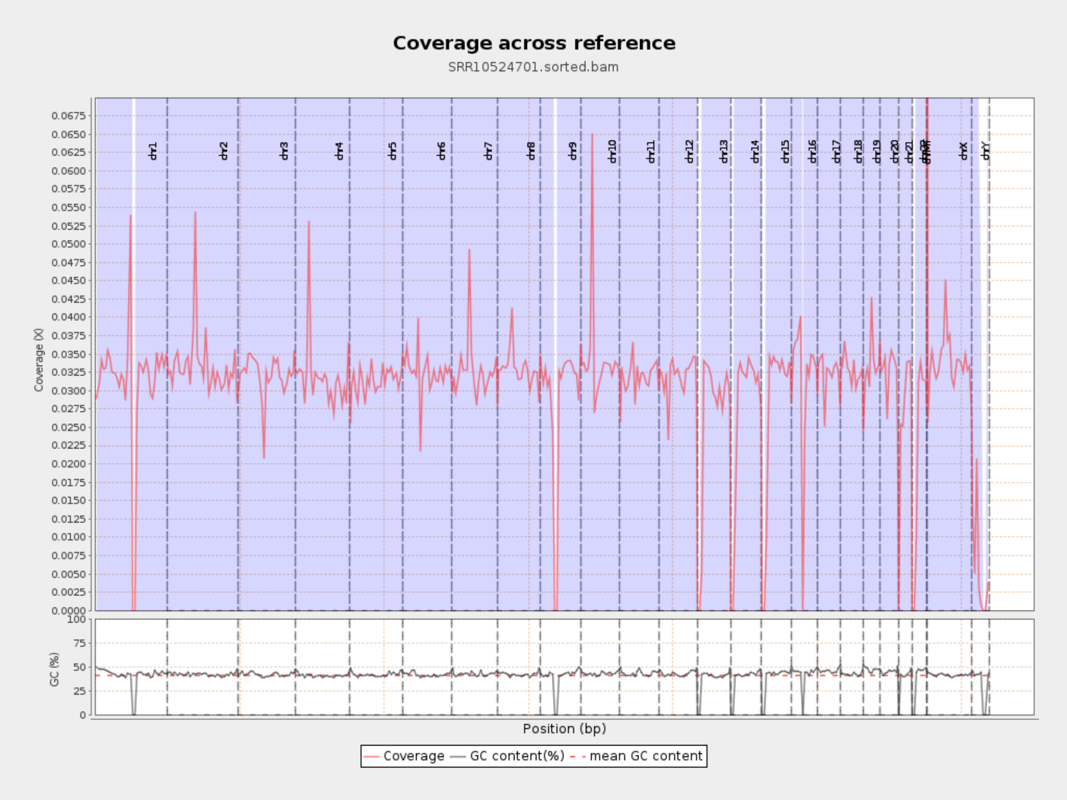
General error rate	0.52%
Mismatches	482,247
Insertions	6,179
Mapped reads with at least one insertion	0.38%
Deletions	18,054
Mapped reads with at least one deletion	1.1%
Homopolymer indels	44.47%

2.6. Chromosome stats

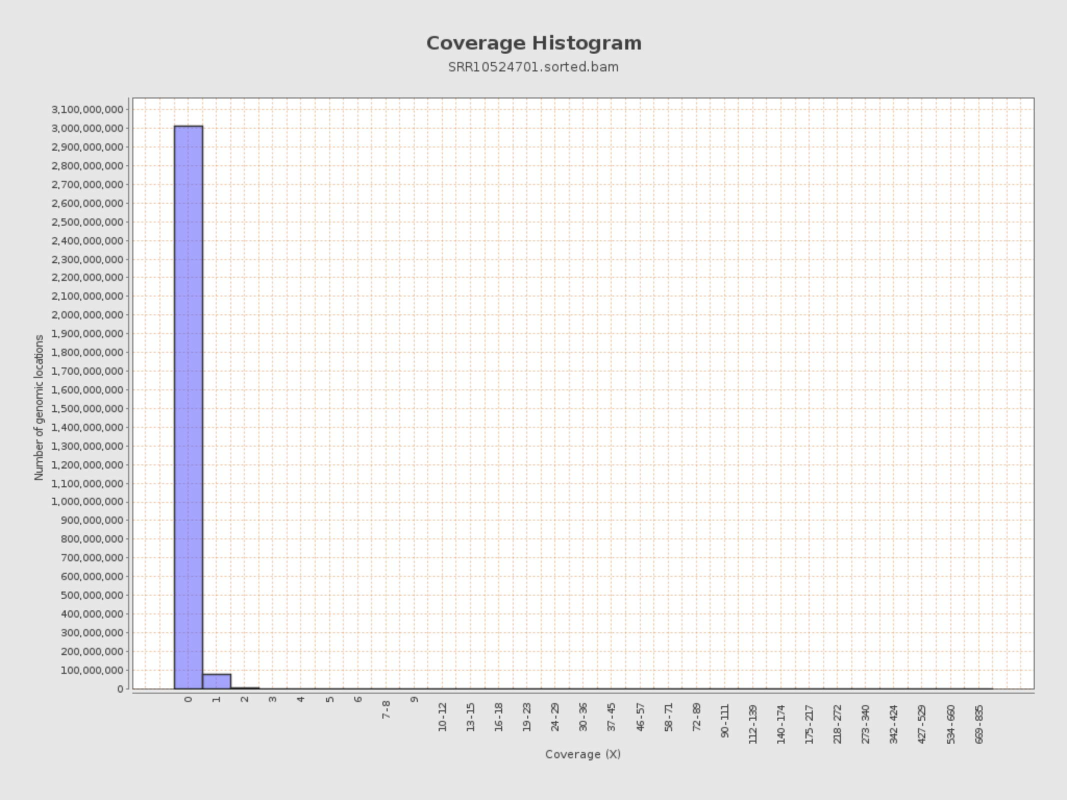
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7744669	0.0311	0.5567
chr2	243199373	8131096	0.0334	0.4153
chr3	198022430	6358475	0.0321	0.1958
chr4	191154276	6117559	0.032	0.2248
chr5	180915260	5689838	0.0315	0.1956
chr6	171115067	5560122	0.0325	0.2214
chr7	159138663	5230571	0.0329	0.3411

chr8	146364022	4844491	0.0331	0.3185
chr9	141213431	4013141	0.0284	0.2415
chr10	135534747	4678516	0.0345	0.3183
chr11	135006516	4330590	0.0321	0.248
chr12	133851895	4277978	0.032	0.1967
chr13	115169878	2966689	0.0258	0.1773
chr14	107349540	2879401	0.0268	0.1846
chr15	102531392	2768065	0.027	0.1797
chr16	90354753	2801159	0.031	0.2127
chr17	81195210	2624654	0.0323	0.2069
chr18	78077248	2560645	0.0328	0.4334
chr19	59128983	1991833	0.0337	0.408
chr20	63025520	2045601	0.0325	0.2003
chr21	48129895	1301235	0.027	0.2028
chr22	51304566	1126163	0.022	0.1609
chrMT	16571	21301	1.2854	1.2726
chrX	155270560	5278854	0.034	0.2209
chrY	59373566	326640	0.0055	0.1981

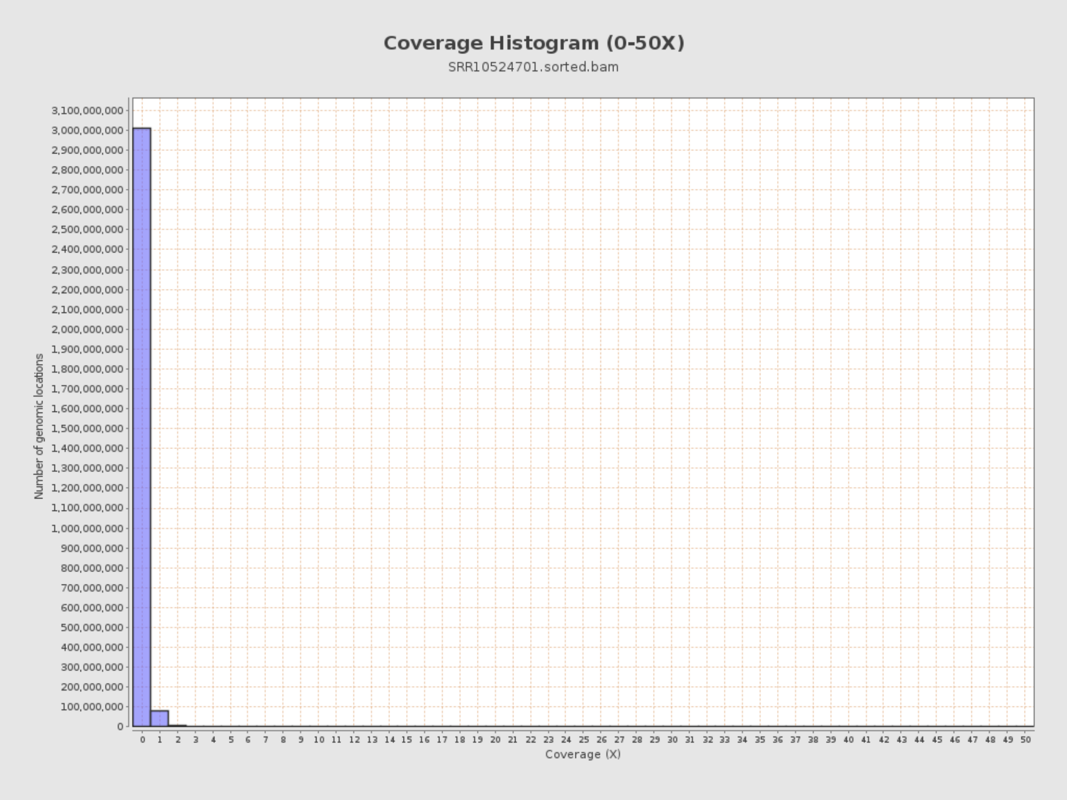
3. Results : Coverage across reference



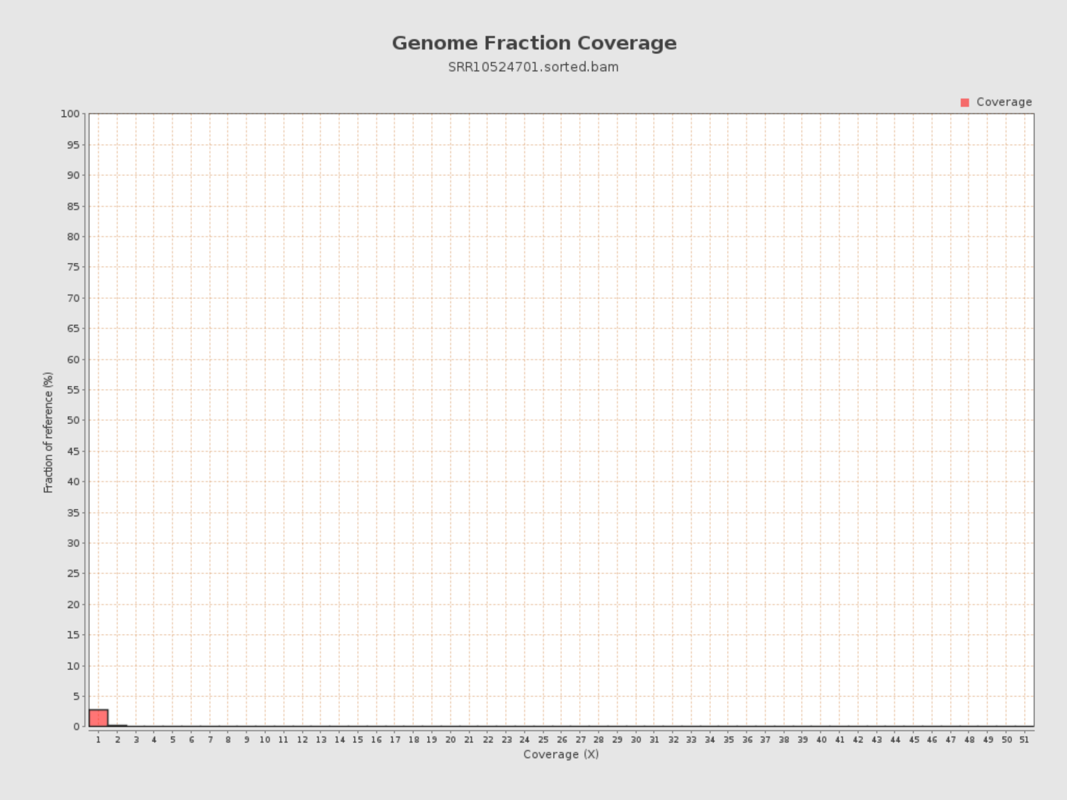
4. Results : Coverage Histogram



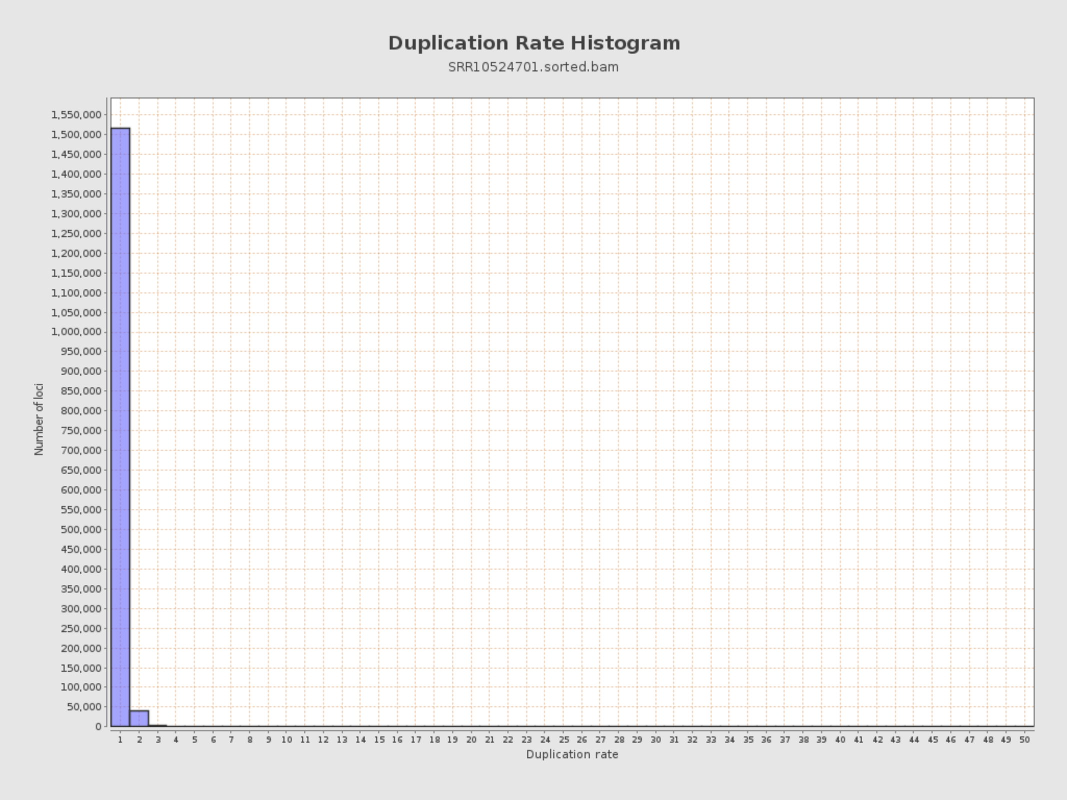
5. Results : Coverage Histogram (0-50X)



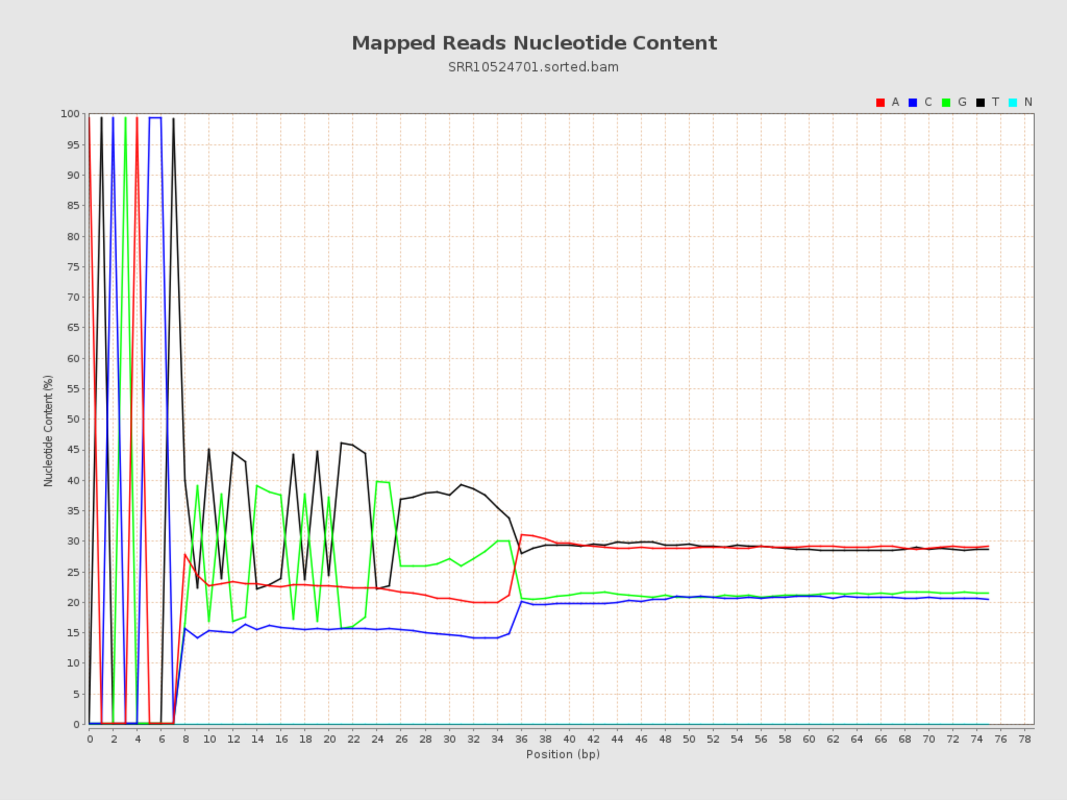
6. Results : Genome Fraction Coverage



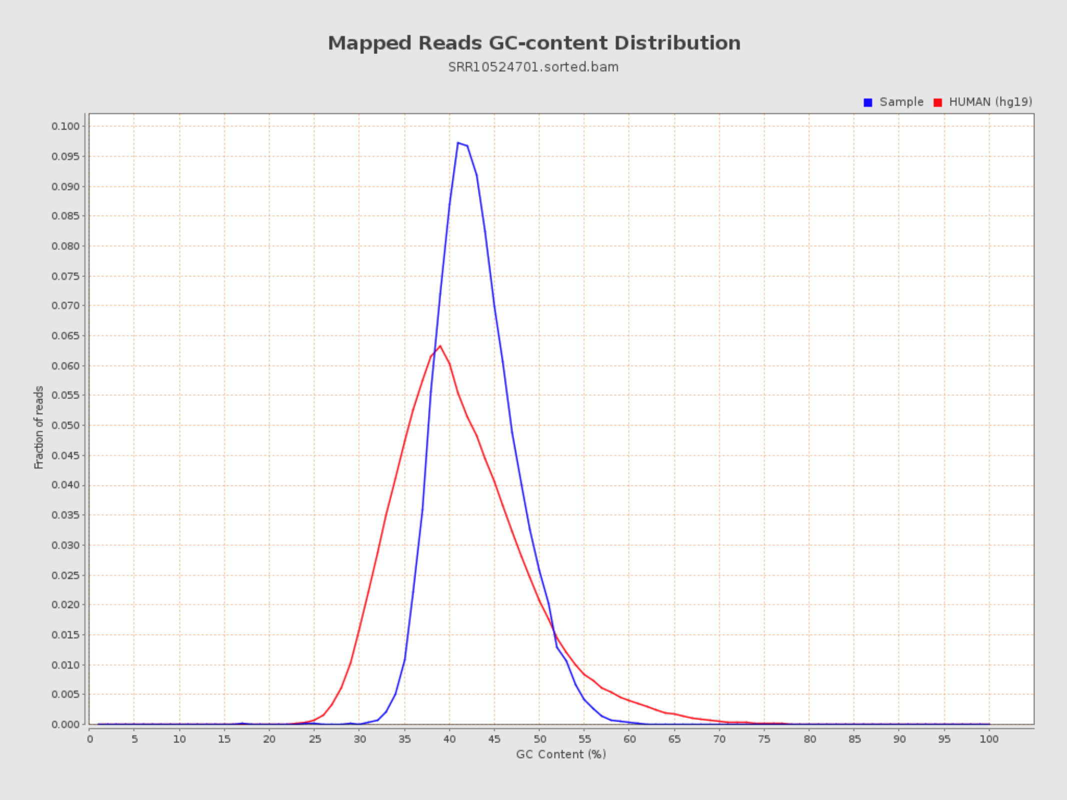
7. Results : Duplication Rate Histogram



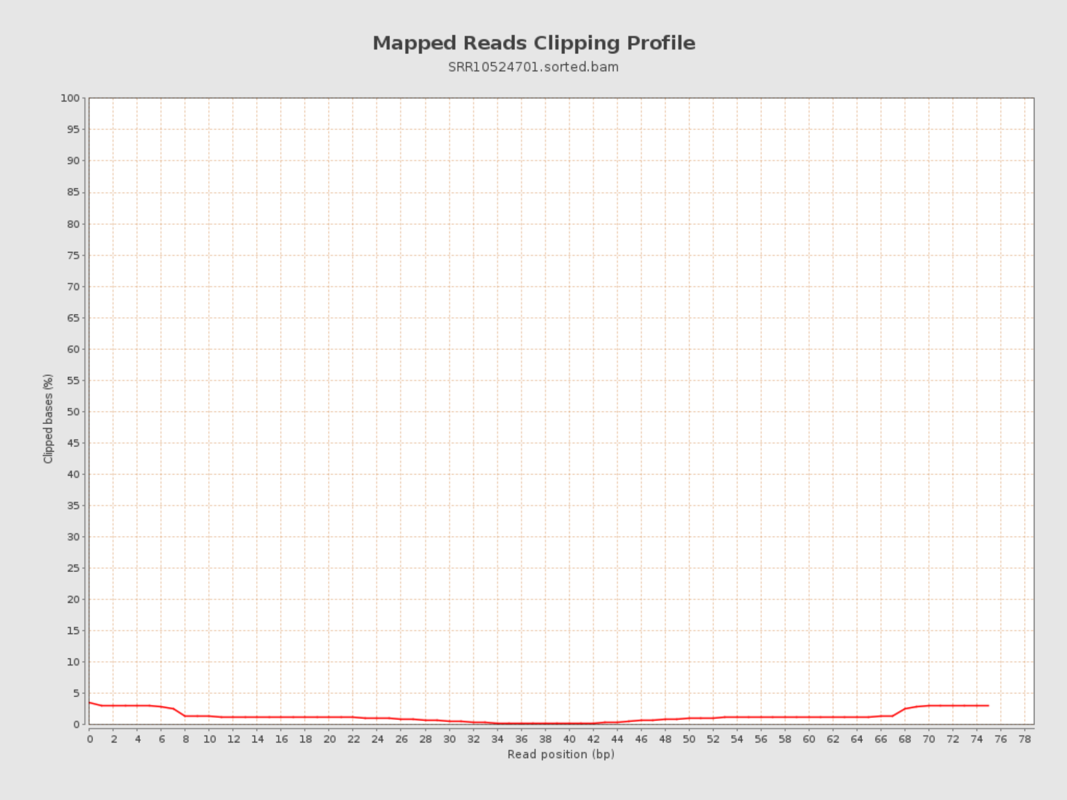
8. Results : Mapped Reads Nucleotide Content



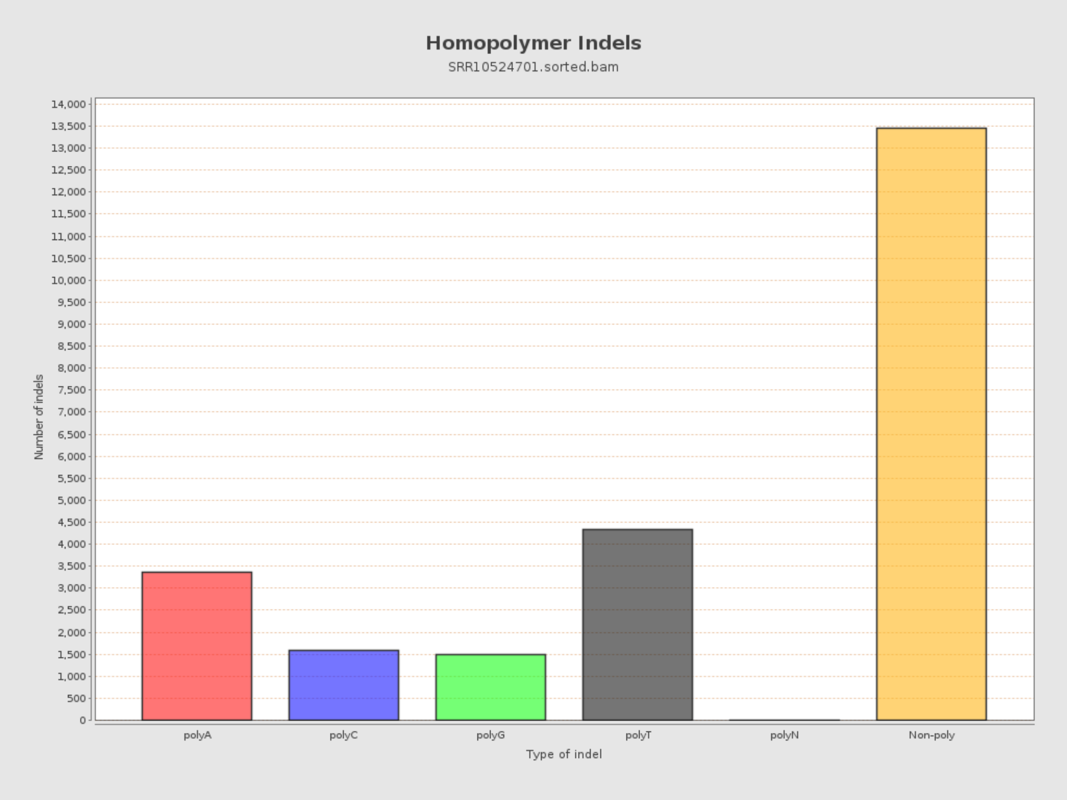
9. Results : Mapped Reads GC-content Distribution



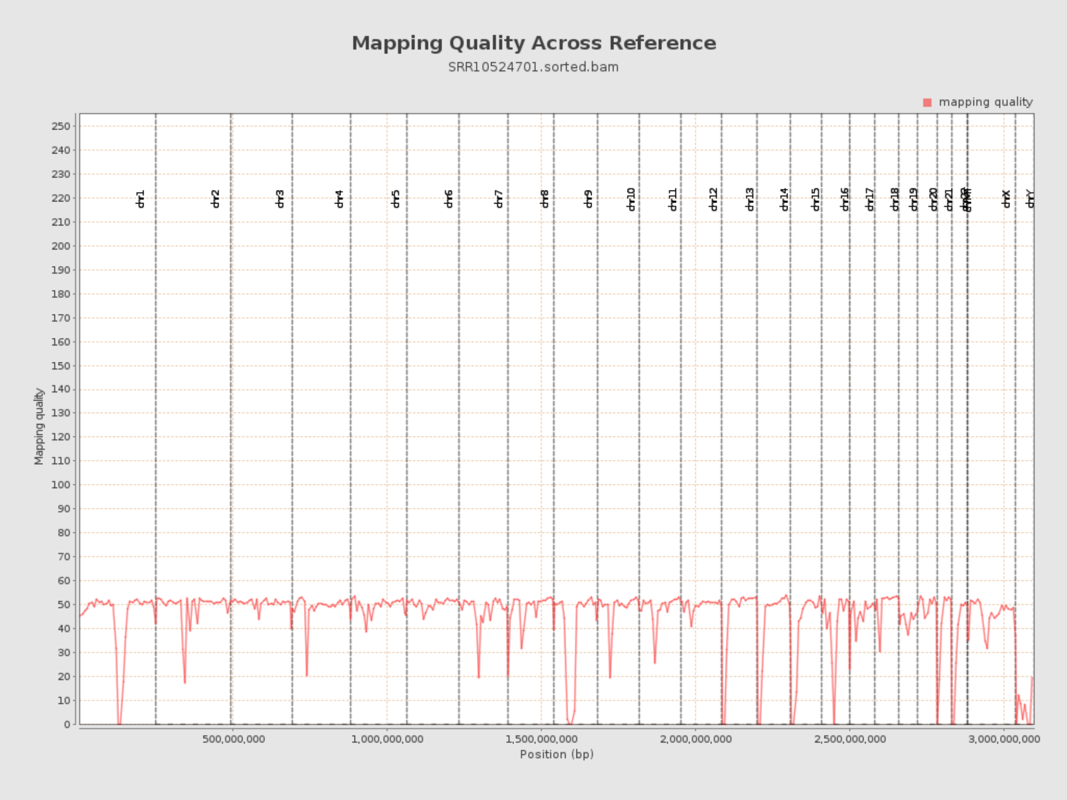
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram