Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 15:07:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524655.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_SRR10524655 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524655.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 15:07:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524655.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,753,014
Mapped reads	1,594,194 / 90.94%
Unmapped reads	158,820 / 9.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,356 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	43,681 / 2.49%
Duplication rate	1.81%
Clipped reads	1,595,150 / 90.99%

2.2. ACGT Content

Number/percentage of A's	23,841,589 / 26.06%
Number/percentage of C's	16,378,695 / 17.9%
Number/percentage of T's	28,599,013 / 31.26%
Number/percentage of G's	22,658,685 / 24.77%
Number/percentage of N's	2,666 / 0%
GC Percentage	42.67%

2.3. Coverage

Mean	0.0296

Standard Deviation	0.2747

2.4. Mapping Quality

Mean Mapping Quality	44.58

2.5. Mismatches and indels

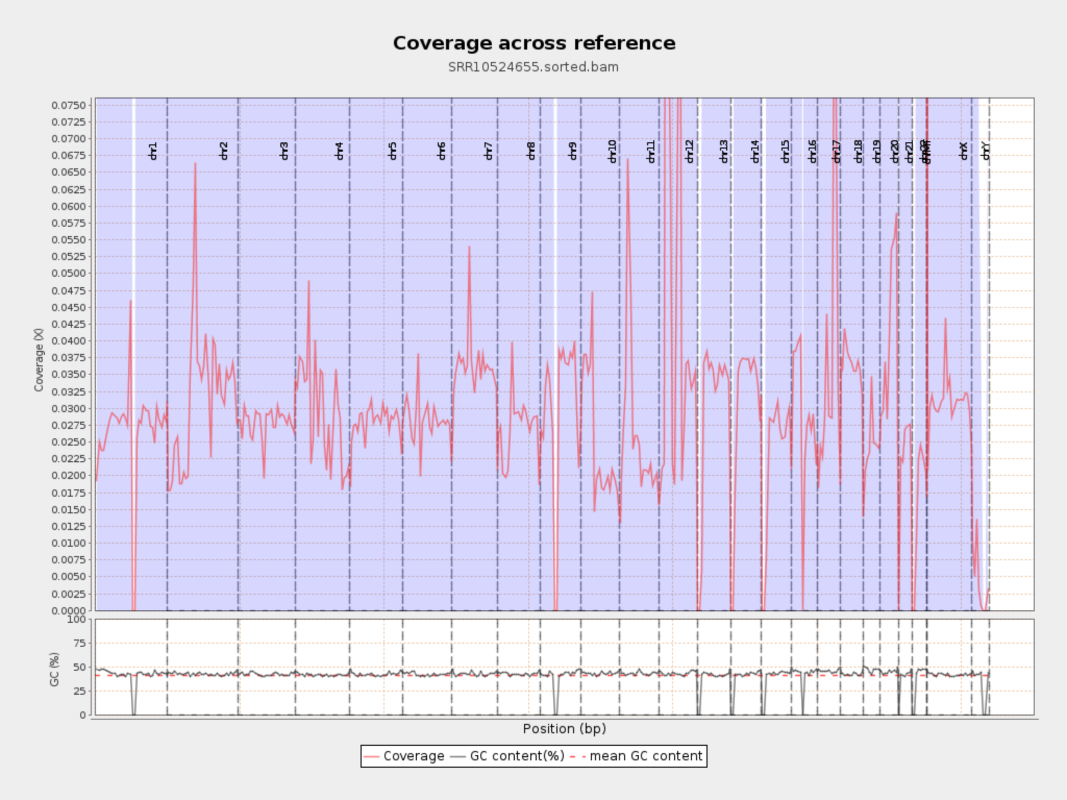
General error rate	0.49%
Mismatches	439,817
Insertions	5,946
Mapped reads with at least one insertion	0.37%
Deletions	14,504
Mapped reads with at least one deletion	0.91%
Homopolymer indels	42.59%

2.6. Chromosome stats

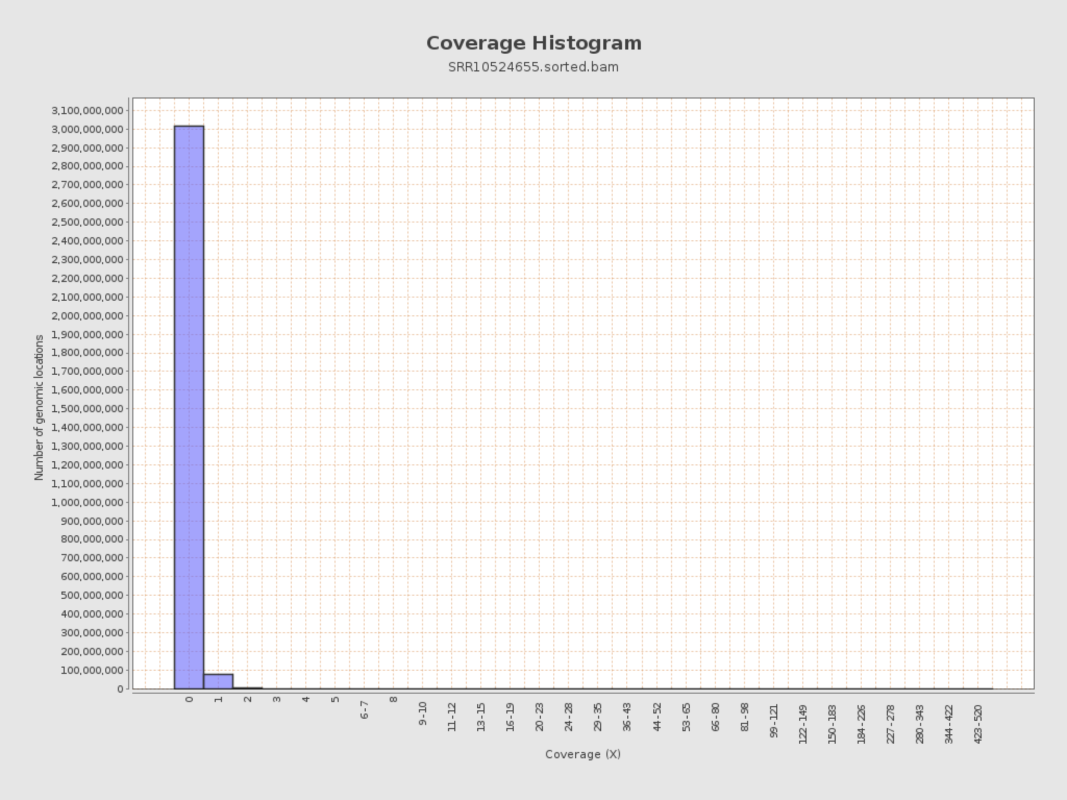
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6556557	0.0263	0.4527
chr2	243199373	7689467	0.0316	0.3205
chr3	198022430	5517271	0.0279	0.1783
chr4	191154276	5644068	0.0295	0.2026
chr5	180915260	5098953	0.0282	0.1835
chr6	171115067	4848450	0.0283	0.1989
chr7	159138663	5786202	0.0364	0.3758

chr8	146364022	3982135	0.0272	0.2594
chr9	141213431	4211185	0.0298	0.289
chr10	135534747	3401902	0.0251	0.2607
chr11	135006516	3573873	0.0265	0.2373
chr12	133851895	6719258	0.0502	0.2712
chr13	115169878	3392249	0.0295	0.1831
chr14	107349540	3200798	0.0298	0.2065
chr15	102531392	2322386	0.0227	0.1635
chr16	90354753	2537318	0.0281	0.1985
chr17	81195210	3123518	0.0385	0.2203
chr18	78077248	2868637	0.0367	0.4956
chr19	59128983	1447415	0.0245	0.3459
chr20	63025520	2592531	0.0411	0.2253
chr21	48129895	1076641	0.0224	0.1805
chr22	51304566	816555	0.0159	0.1342
chrMT	16571	3939	0.2377	0.5095
chrX	155270560	4843524	0.0312	0.2316
chrY	59373566	249453	0.0042	0.1018

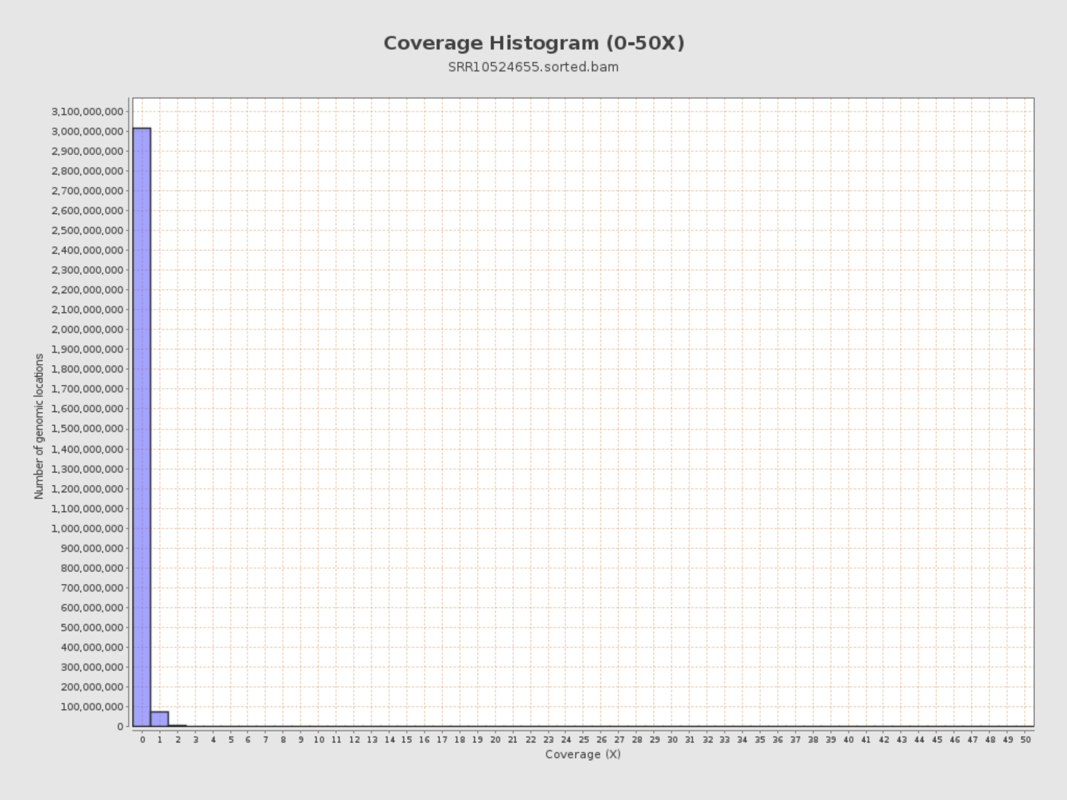
3. Results : Coverage across reference



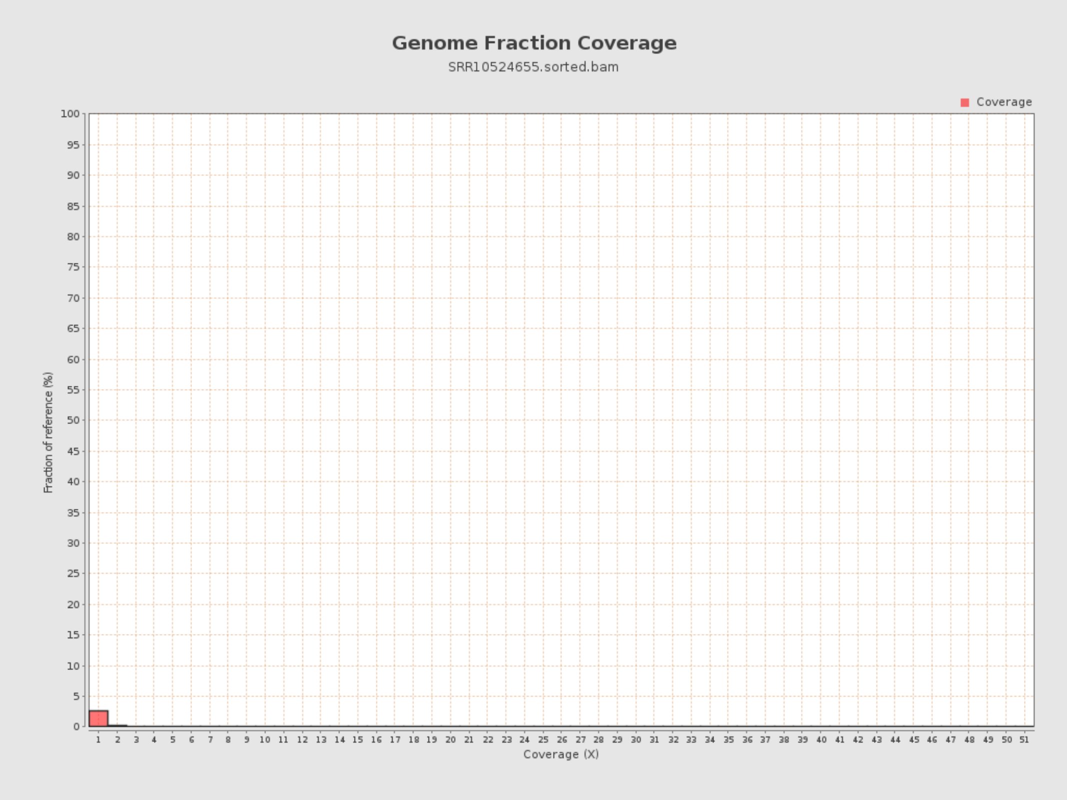
4. Results : Coverage Histogram



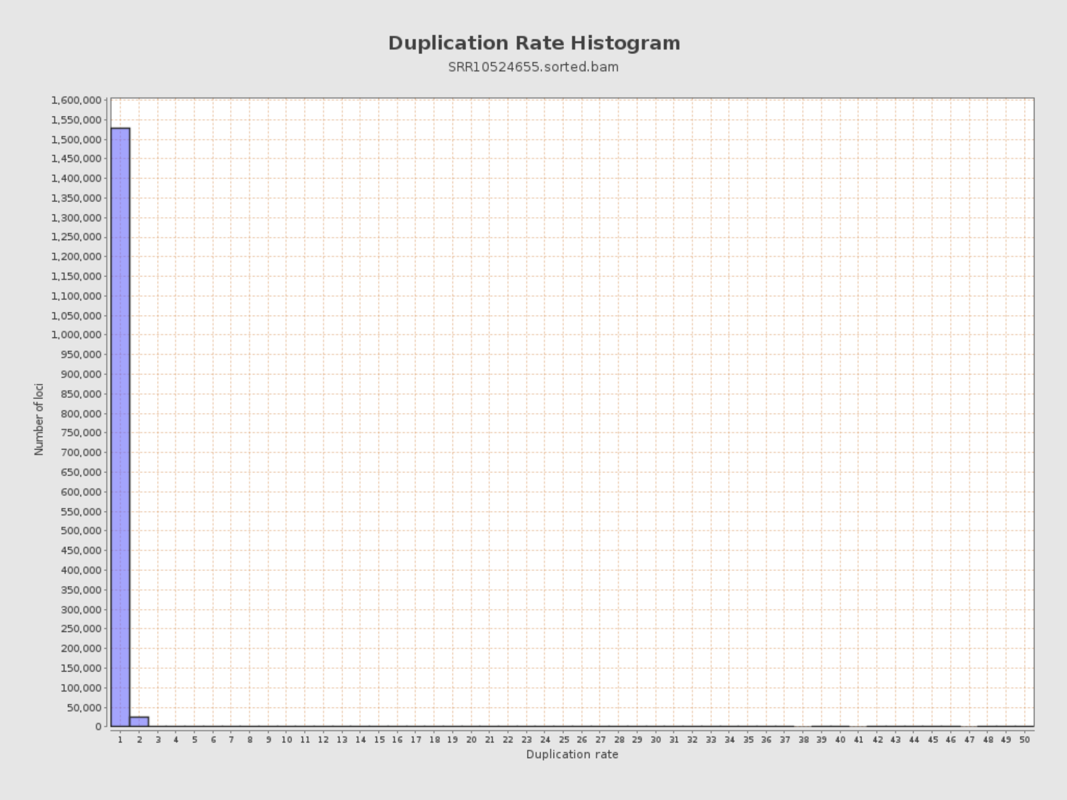
5. Results : Coverage Histogram (0-50X)



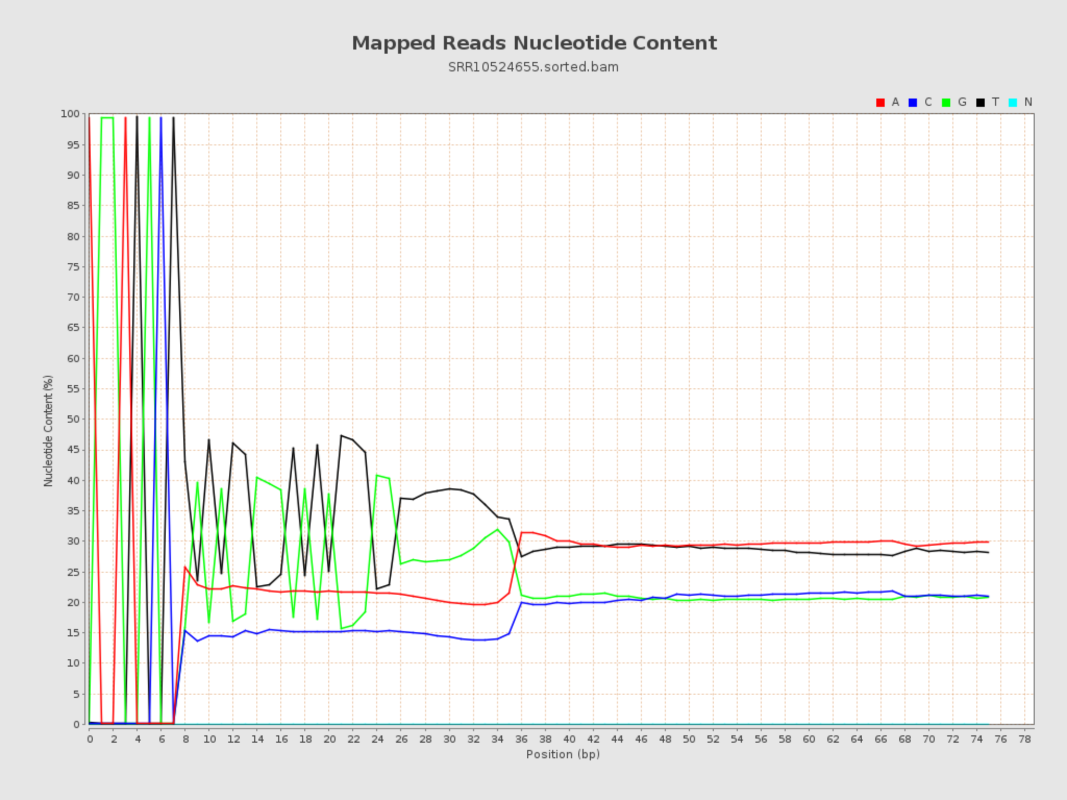
6. Results : Genome Fraction Coverage



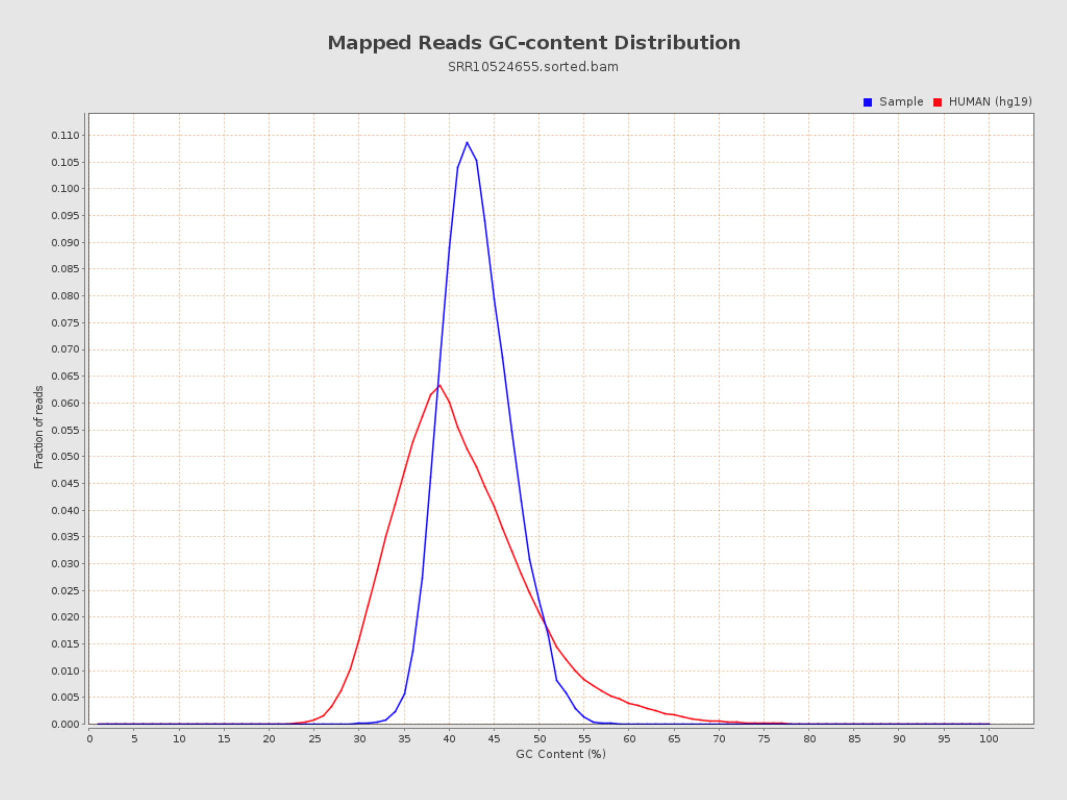
7. Results : Duplication Rate Histogram



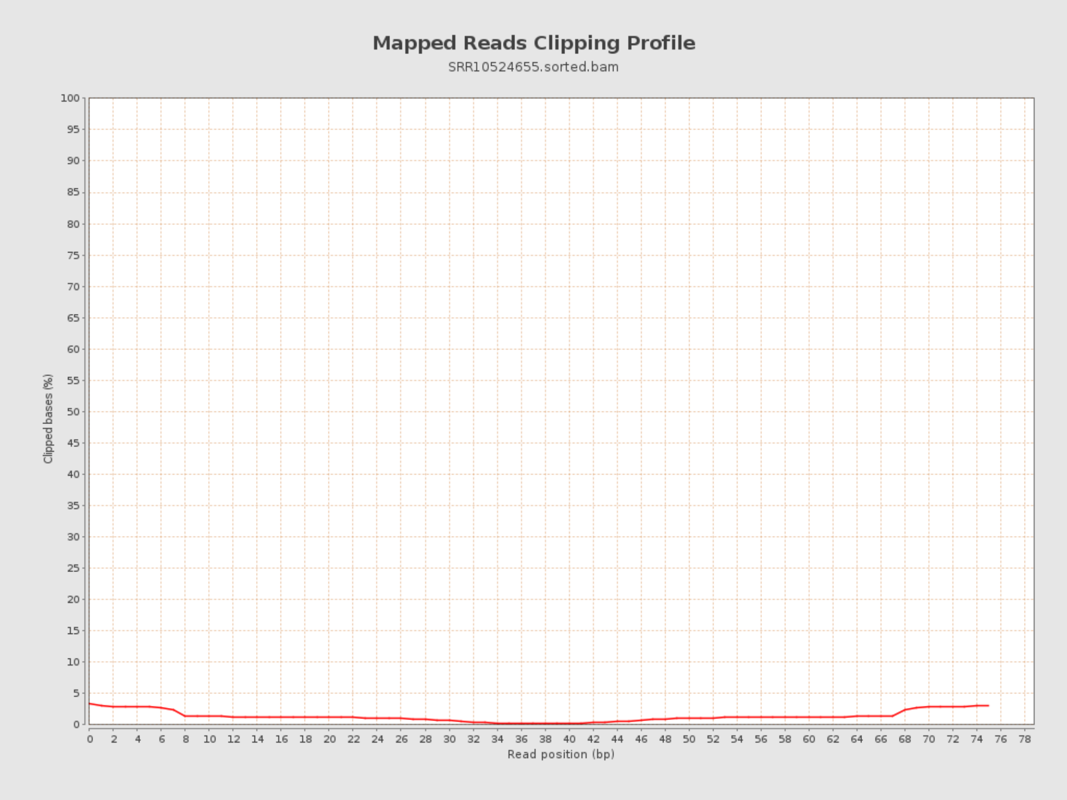
8. Results : Mapped Reads Nucleotide Content



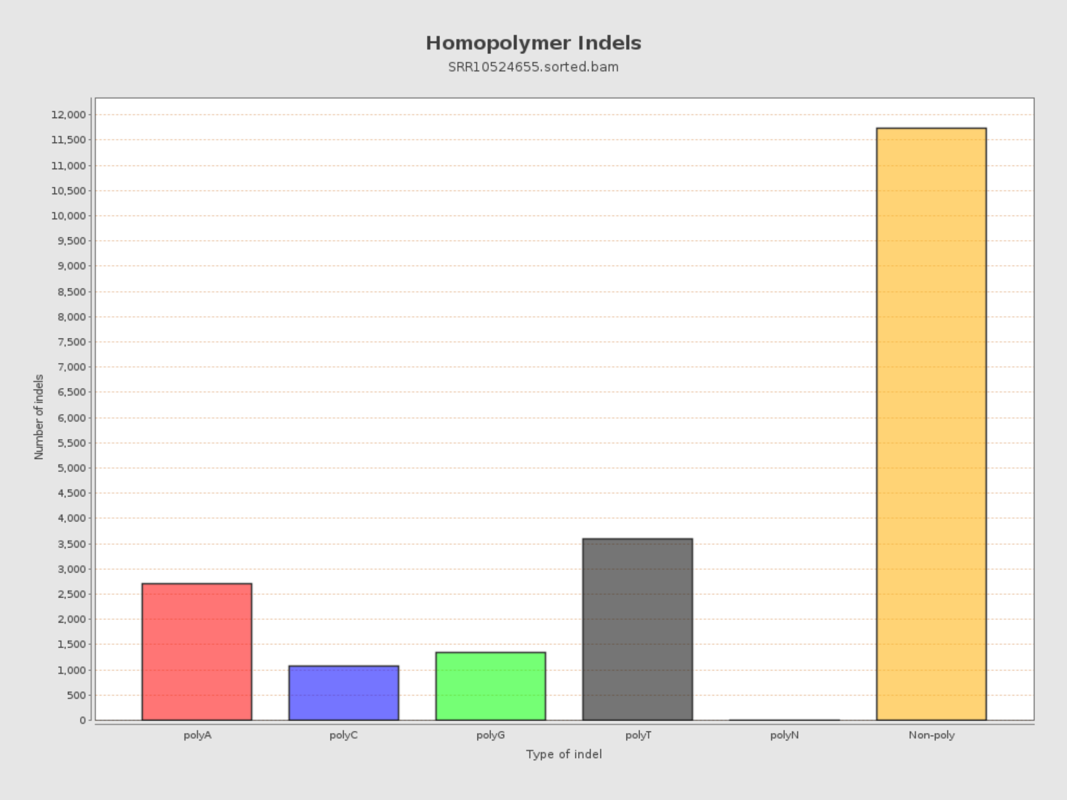
9. Results : Mapped Reads GC-content Distribution



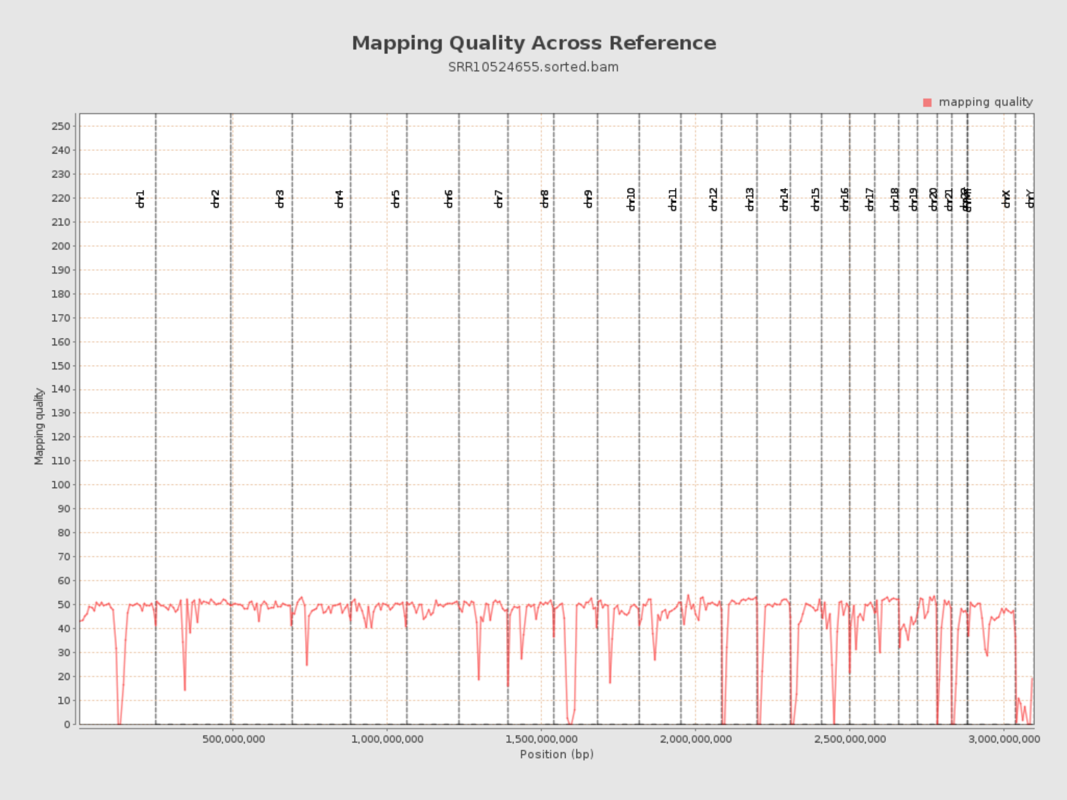
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram