Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 17:05:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524700.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_SRR10524700 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524700.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 17:05:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524700.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,691,402
Mapped reads	1,549,825 / 91.63%
Unmapped reads	141,577 / 8.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,611 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	57,977 / 3.43%
Duplication rate	2.71%
Clipped reads	1,551,397 / 91.72%

2.2. ACGT Content

Number/percentage of A's	22,426,767 / 24.98%
Number/percentage of C's	17,747,012 / 19.77%
Number/percentage of T's	29,514,643 / 32.87%
Number/percentage of G's	20,097,099 / 22.38%
Number/percentage of N's	1,889 / 0%
GC Percentage	42.15%

2.3. Coverage

Mean	0.029

Standard Deviation	0.2929

2.4. Mapping Quality

Mean Mapping Quality	45.27

2.5. Mismatches and indels

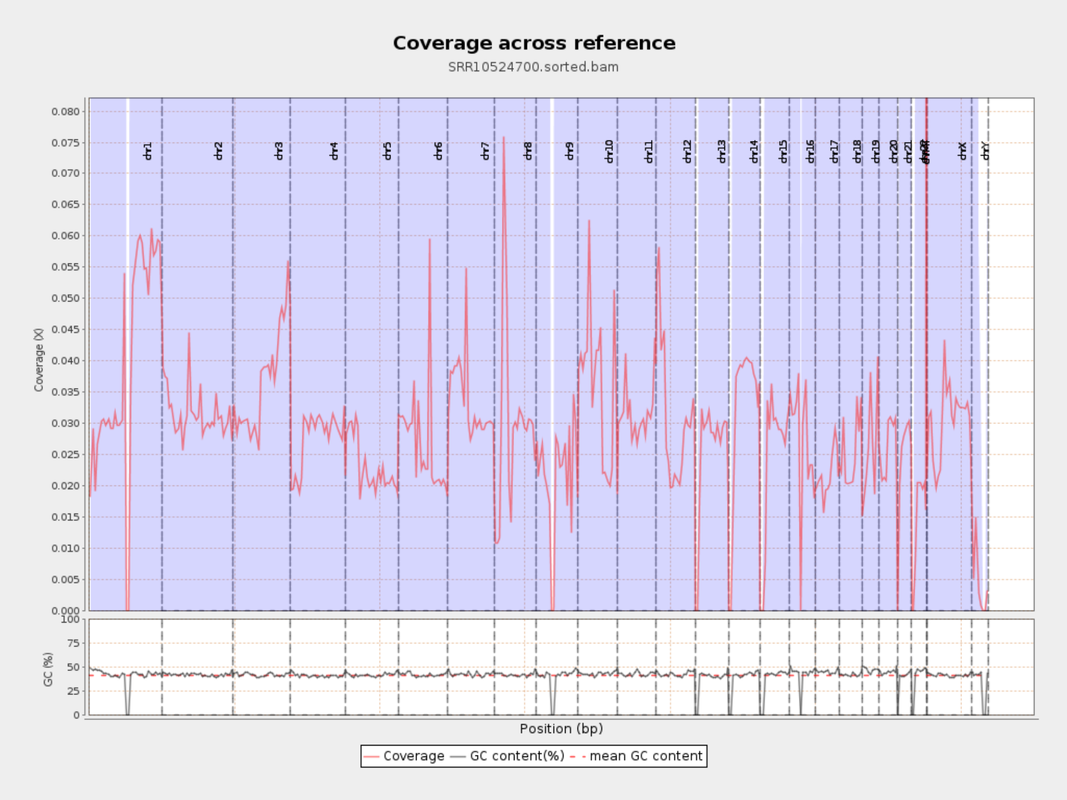
General error rate	0.52%
Mismatches	455,647
Insertions	7,006
Mapped reads with at least one insertion	0.45%
Deletions	19,370
Mapped reads with at least one deletion	1.24%
Homopolymer indels	43.64%

2.6. Chromosome stats

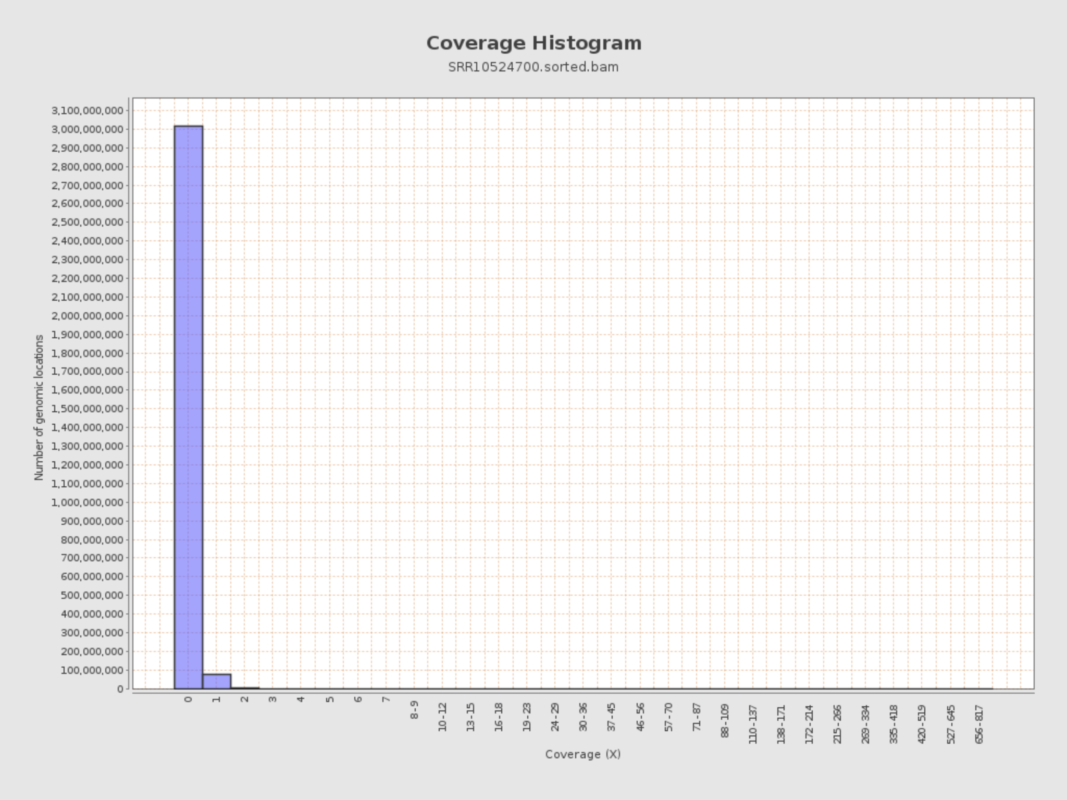
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9776528	0.0392	0.5764
chr2	243199373	7689053	0.0316	0.3833
chr3	198022430	7210704	0.0364	0.2077
chr4	191154276	5274335	0.0276	0.1899
chr5	180915260	4163748	0.023	0.1645
chr6	171115067	4633051	0.0271	0.2039
chr7	159138663	5377779	0.0338	0.4152

chr8	146364022	4273650	0.0292	0.2864
chr9	141213431	3010429	0.0213	0.206
chr10	135534747	4939645	0.0364	0.2954
chr11	135006516	4250691	0.0315	0.2409
chr12	133851895	4134834	0.0309	0.1925
chr13	115169878	2931054	0.0254	0.1742
chr14	107349540	3415797	0.0318	0.1962
chr15	102531392	2504217	0.0244	0.1699
chr16	90354753	2397068	0.0265	0.1939
chr17	81195210	1761199	0.0217	0.1656
chr18	78077248	1965004	0.0252	0.3951
chr19	59128983	1570442	0.0266	0.389
chr20	63025520	1639489	0.026	0.1765
chr21	48129895	1173079	0.0244	0.1791
chr22	51304566	720505	0.014	0.1268
chrMT	16571	5529	0.3337	0.6405
chrX	155270560	4730338	0.0305	0.2055
chrY	59373566	269882	0.0045	0.142

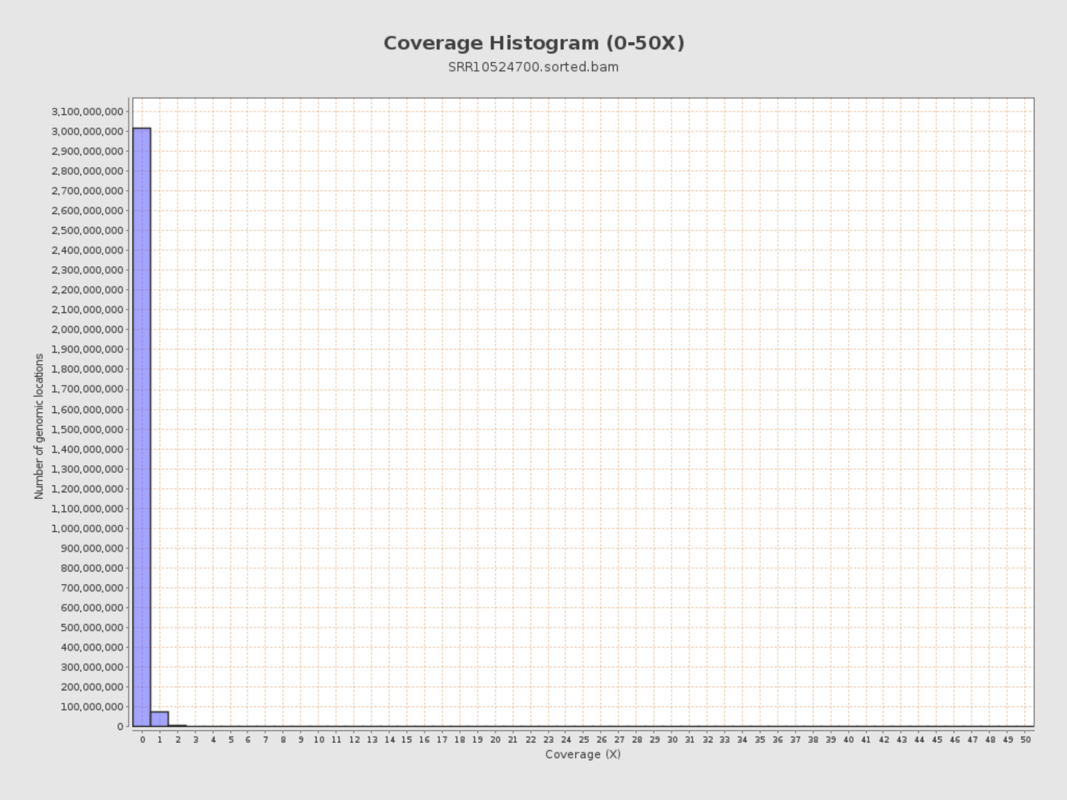
3. Results : Coverage across reference



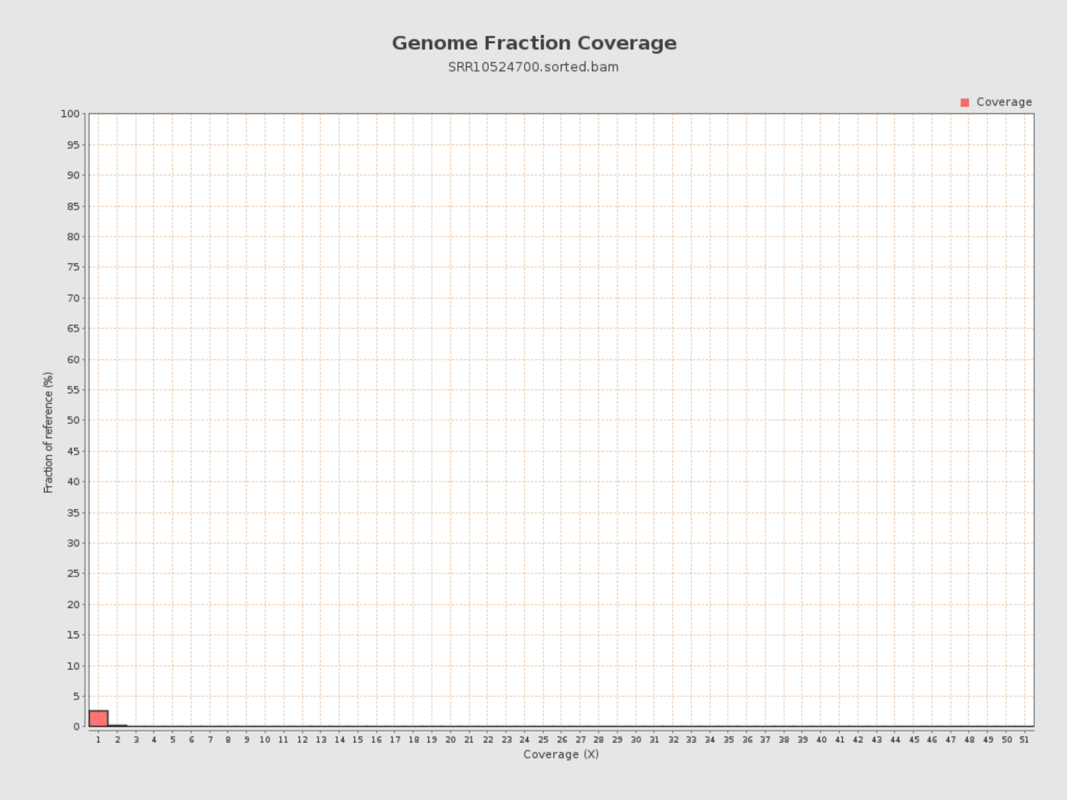
4. Results : Coverage Histogram



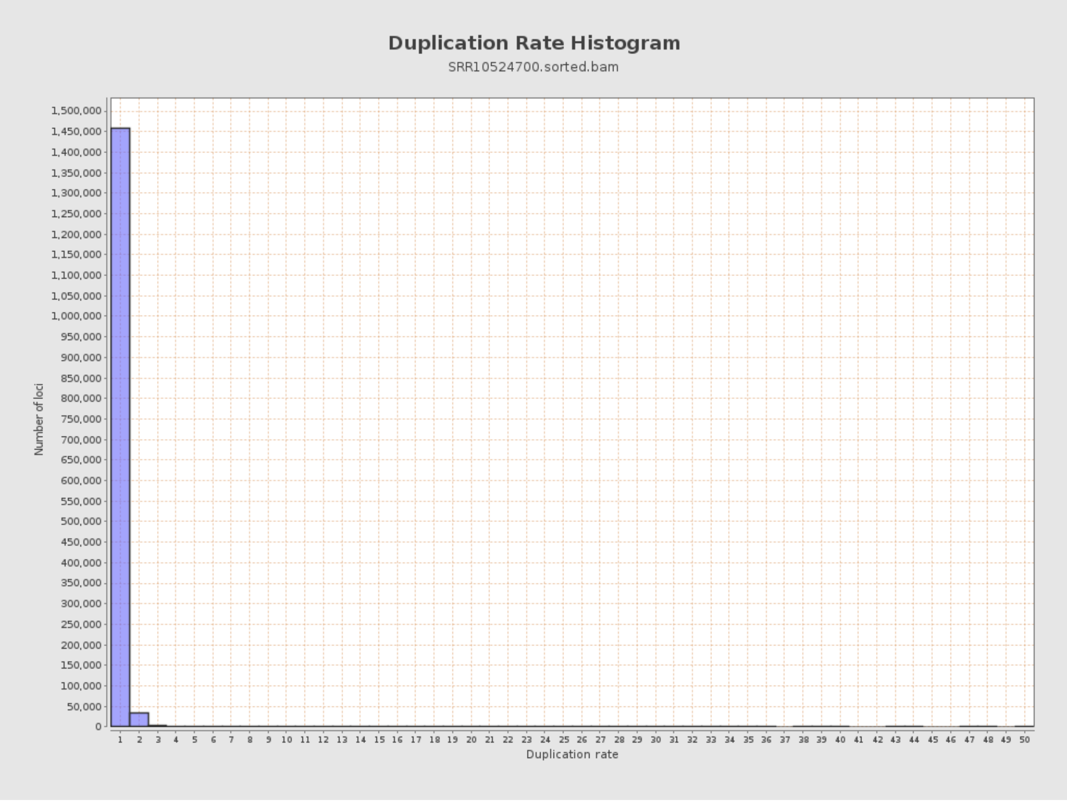
5. Results : Coverage Histogram (0-50X)



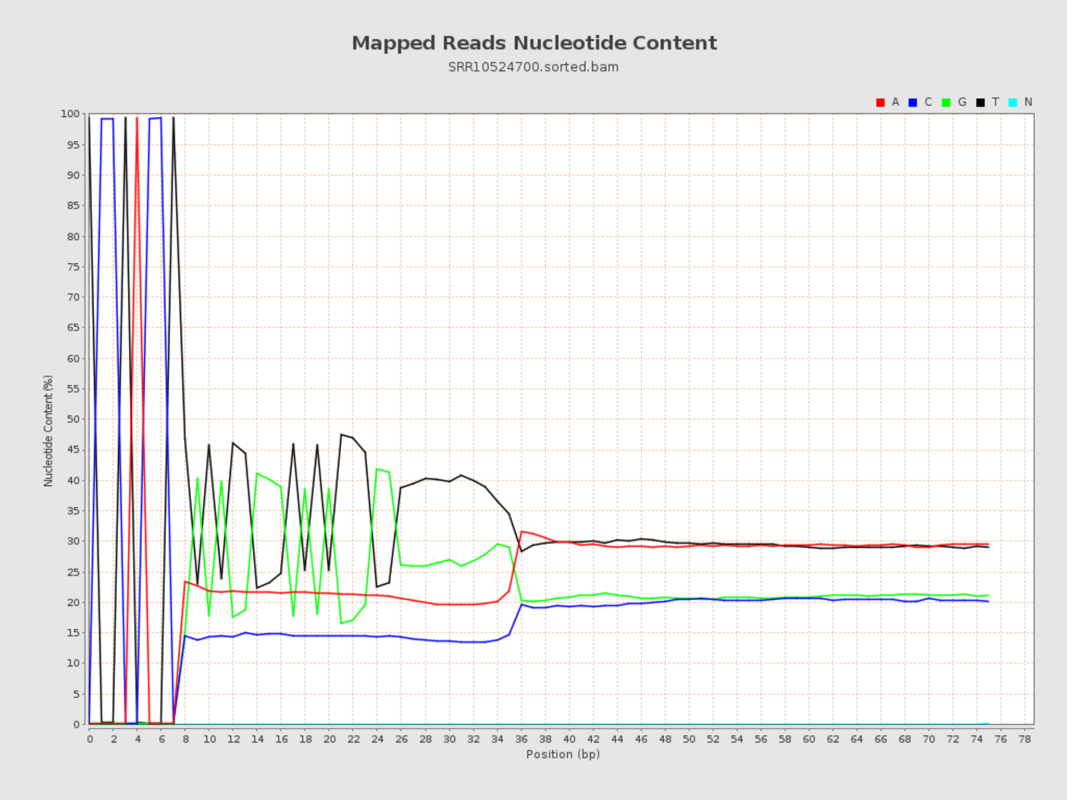
6. Results : Genome Fraction Coverage



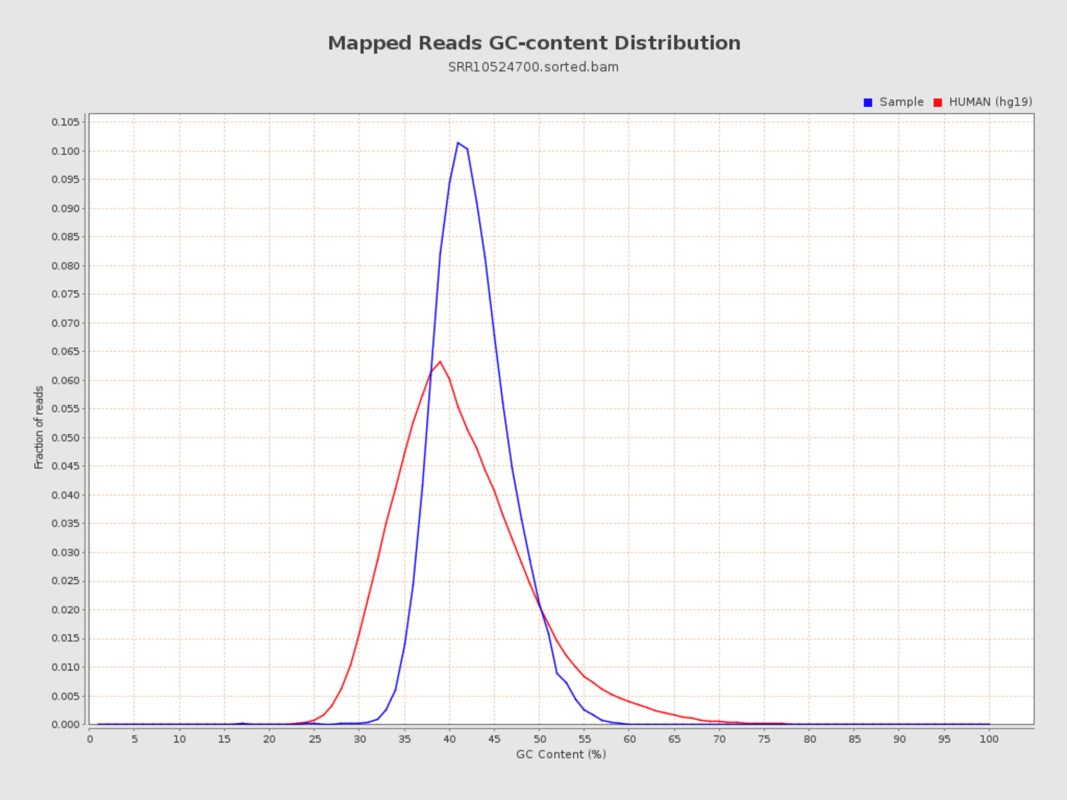
7. Results : Duplication Rate Histogram



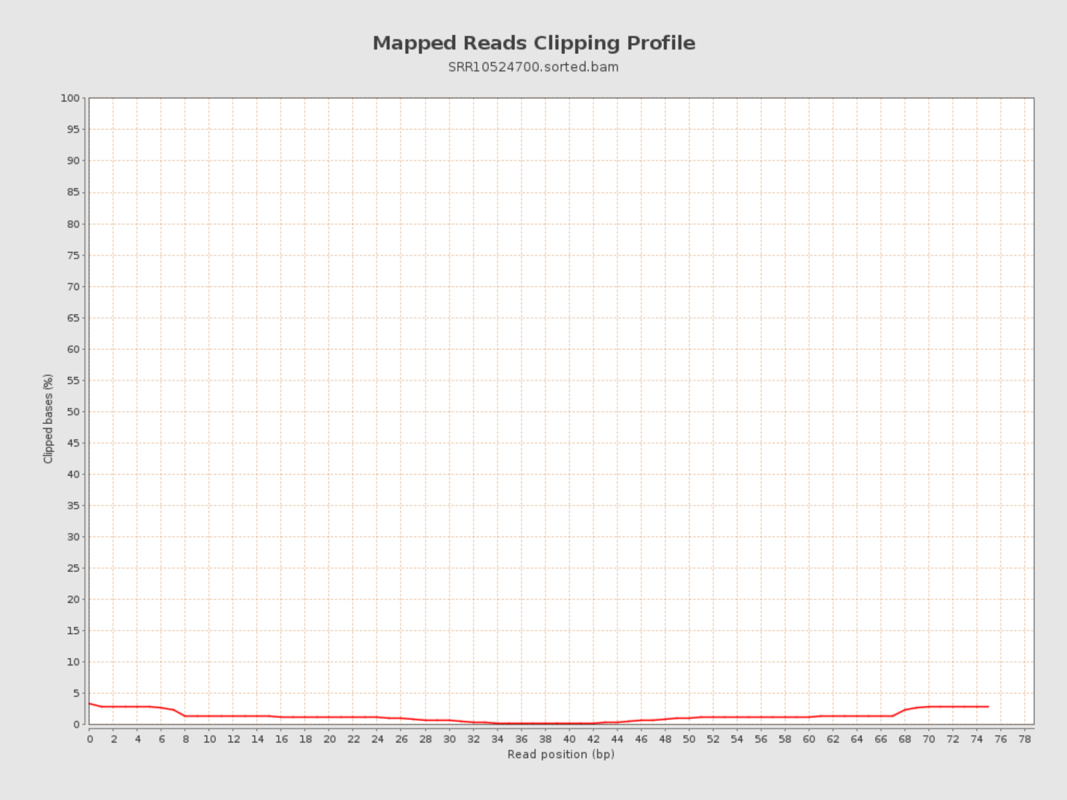
8. Results : Mapped Reads Nucleotide Content



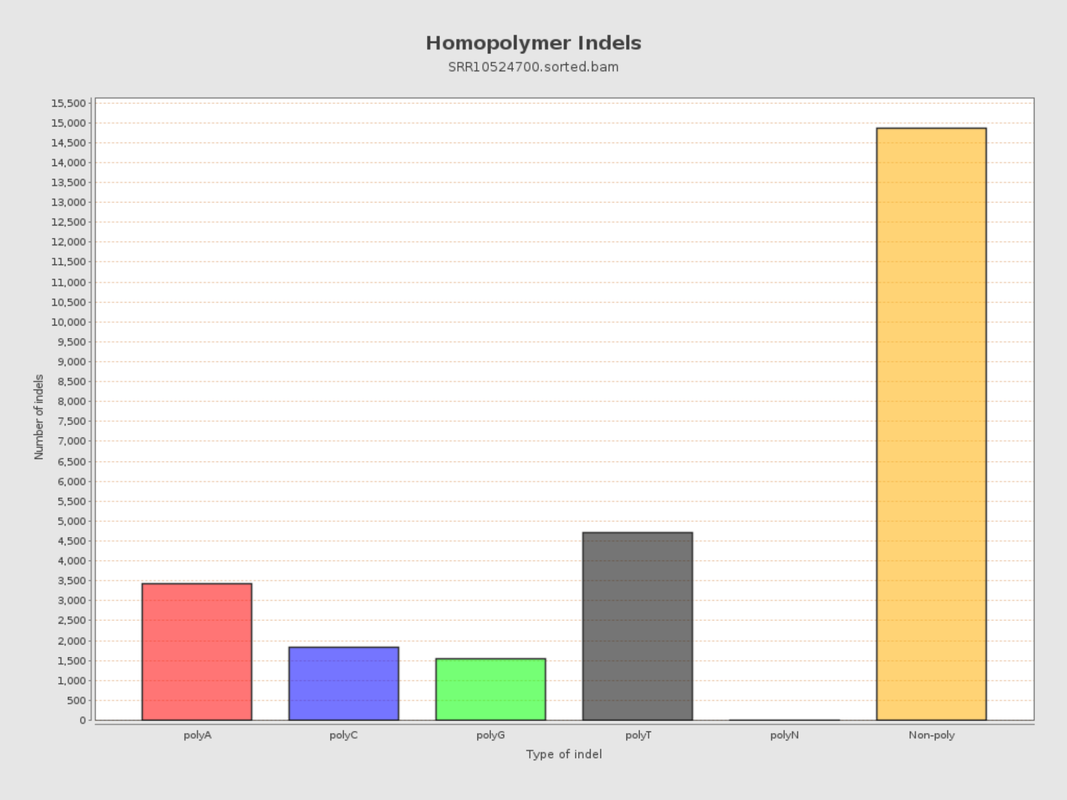
9. Results : Mapped Reads GC-content Distribution



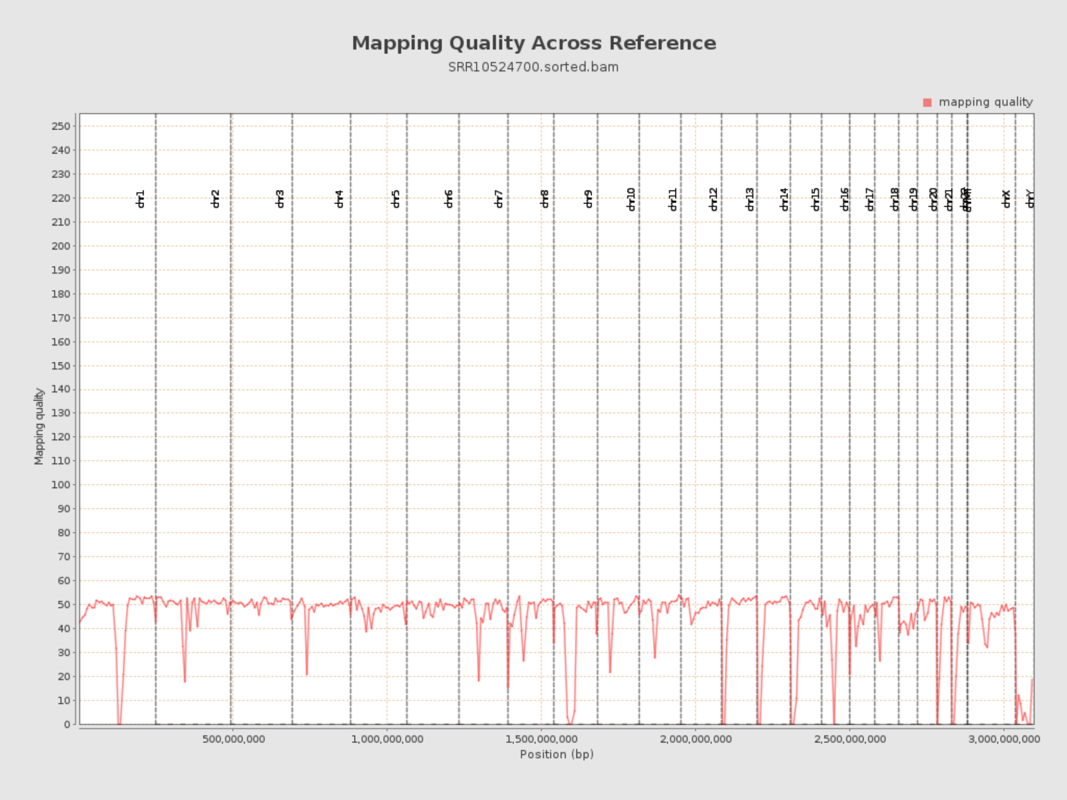
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram