Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 12:12:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524594.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_SRR10524594 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524594.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 12:12:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524594.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,840,227
Mapped reads	1,711,331 / 93%
Unmapped reads	128,896 / 7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,869 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	84,777 / 4.61%
Duplication rate	3.84%
Clipped reads	1,710,634 / 92.96%

2.2. ACGT Content

Number/percentage of A's	24,702,486 / 24.79%
Number/percentage of C's	18,255,499 / 18.32%
Number/percentage of T's	32,250,004 / 32.37%
Number/percentage of G's	24,422,694 / 24.51%
Number/percentage of N's	627 / 0%
GC Percentage	42.84%

2.3. Coverage

Mean	0.0322

Standard Deviation	0.2804

2.4. Mapping Quality

Mean Mapping Quality	45.42

2.5. Mismatches and indels

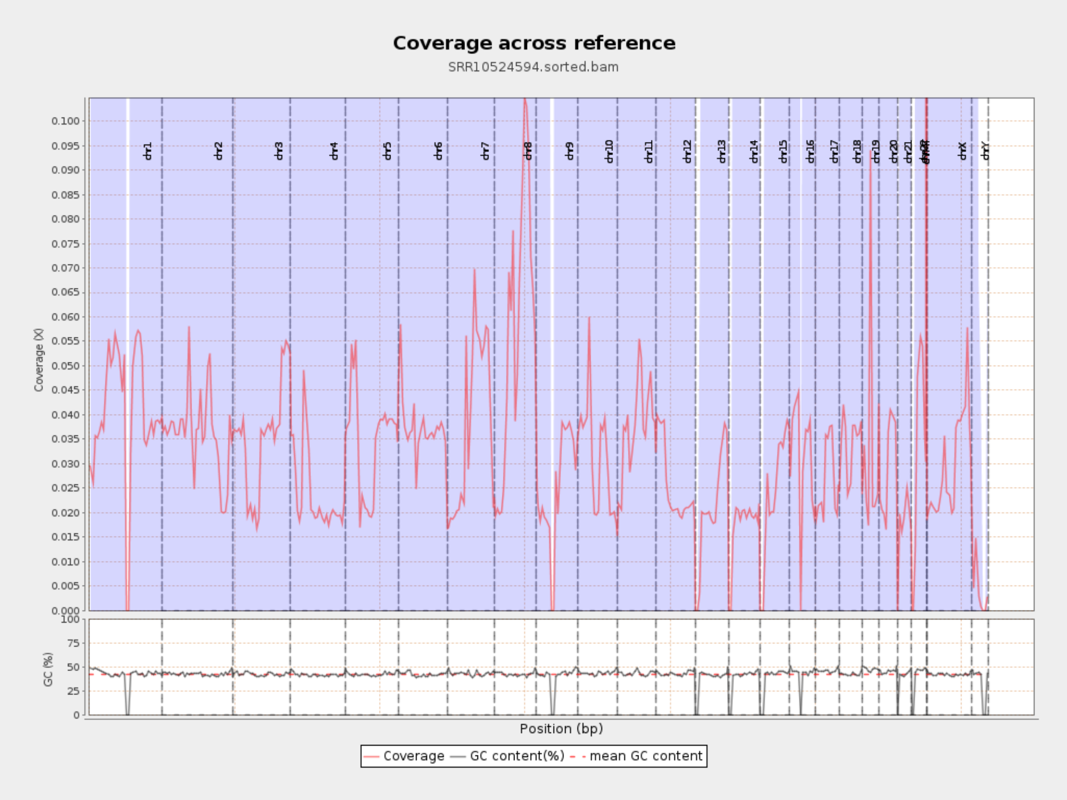
General error rate	0.47%
Mismatches	457,597
Insertions	6,818
Mapped reads with at least one insertion	0.4%
Deletions	17,687
Mapped reads with at least one deletion	1.03%
Homopolymer indels	44.27%

2.6. Chromosome stats

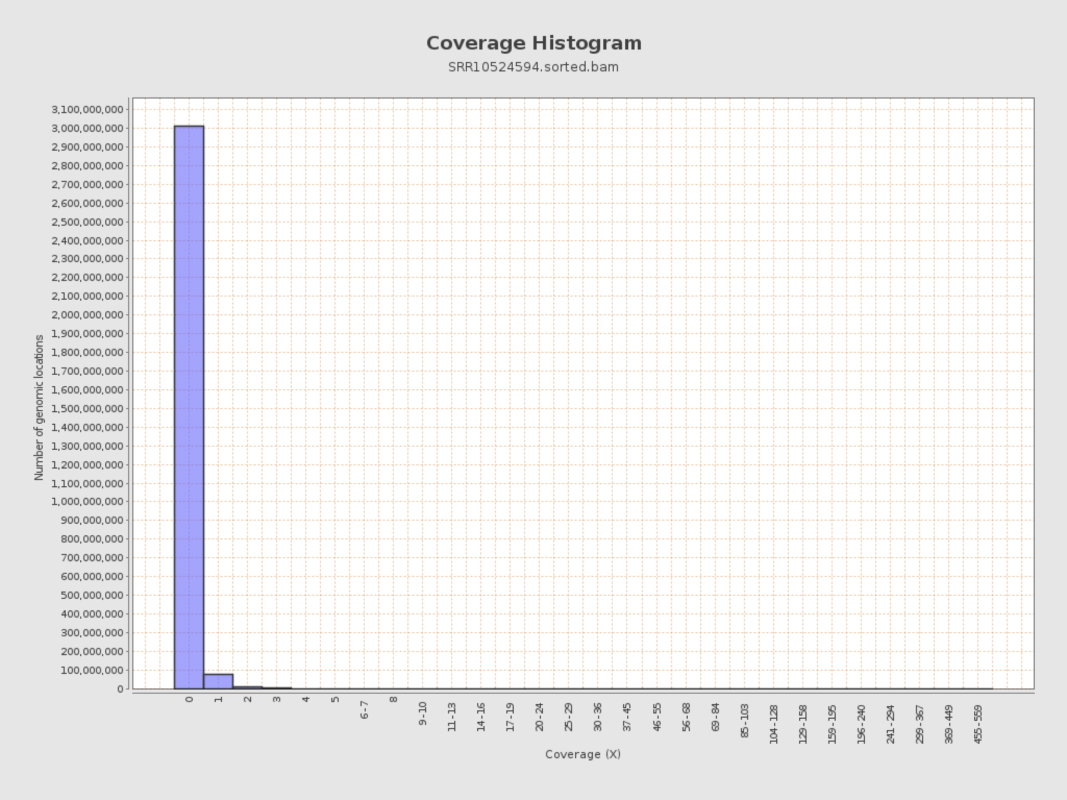
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10135924	0.0407	0.4529
chr2	243199373	8841784	0.0364	0.3312
chr3	198022430	7036503	0.0355	0.2143
chr4	191154276	4520829	0.0237	0.2045
chr5	180915260	6279474	0.0347	0.2105
chr6	171115067	6406626	0.0374	0.234
chr7	159138663	6166087	0.0387	0.4

chr8	146364022	8421029	0.0575	0.3731
chr9	141213431	3493122	0.0247	0.2444
chr10	135534747	4252907	0.0314	0.2884
chr11	135006516	5091361	0.0377	0.2803
chr12	133851895	3375957	0.0252	0.1826
chr13	115169878	2412824	0.021	0.1638
chr14	107349540	1820277	0.017	0.1519
chr15	102531392	2463314	0.024	0.1848
chr16	90354753	2857795	0.0316	0.2105
chr17	81195210	2168442	0.0267	0.1909
chr18	78077248	2689294	0.0344	0.4023
chr19	59128983	1969739	0.0333	0.342
chr20	63025520	1860547	0.0295	0.1989
chr21	48129895	860710	0.0179	0.166
chr22	51304566	1658303	0.0323	0.201
chrMT	16571	10941	0.6602	1.0186
chrX	155270560	4609486	0.0297	0.2253
chrY	59373566	258265	0.0043	0.1249

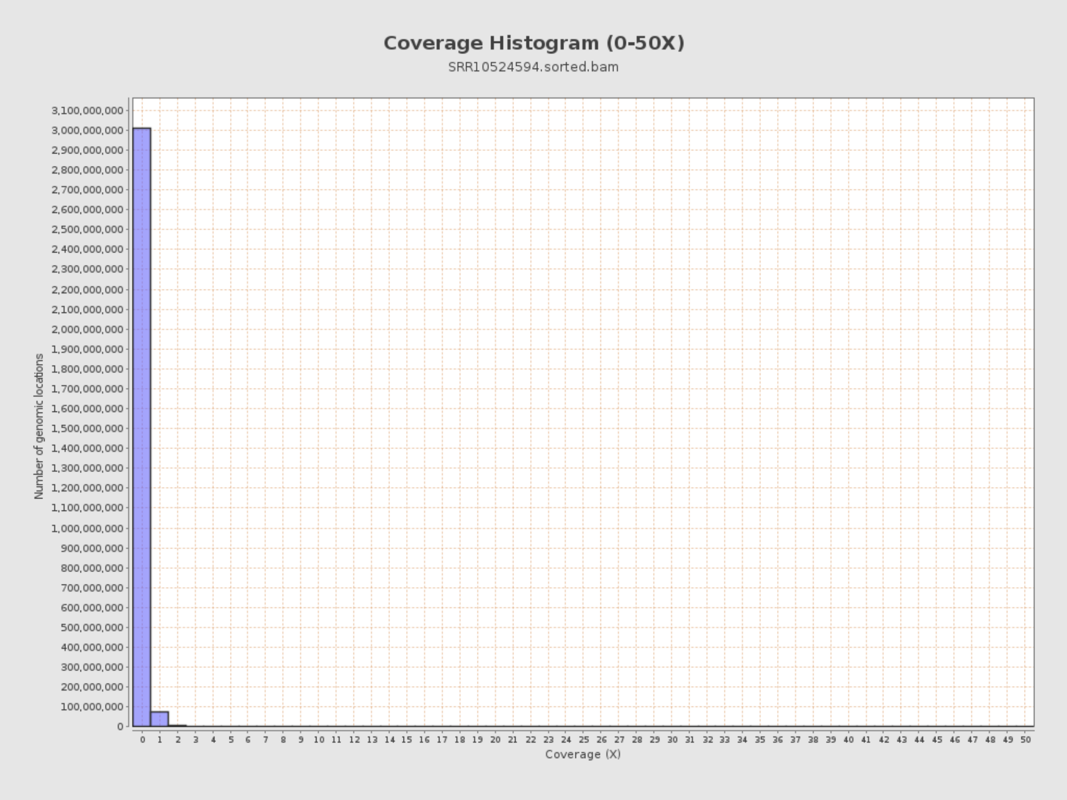
3. Results : Coverage across reference



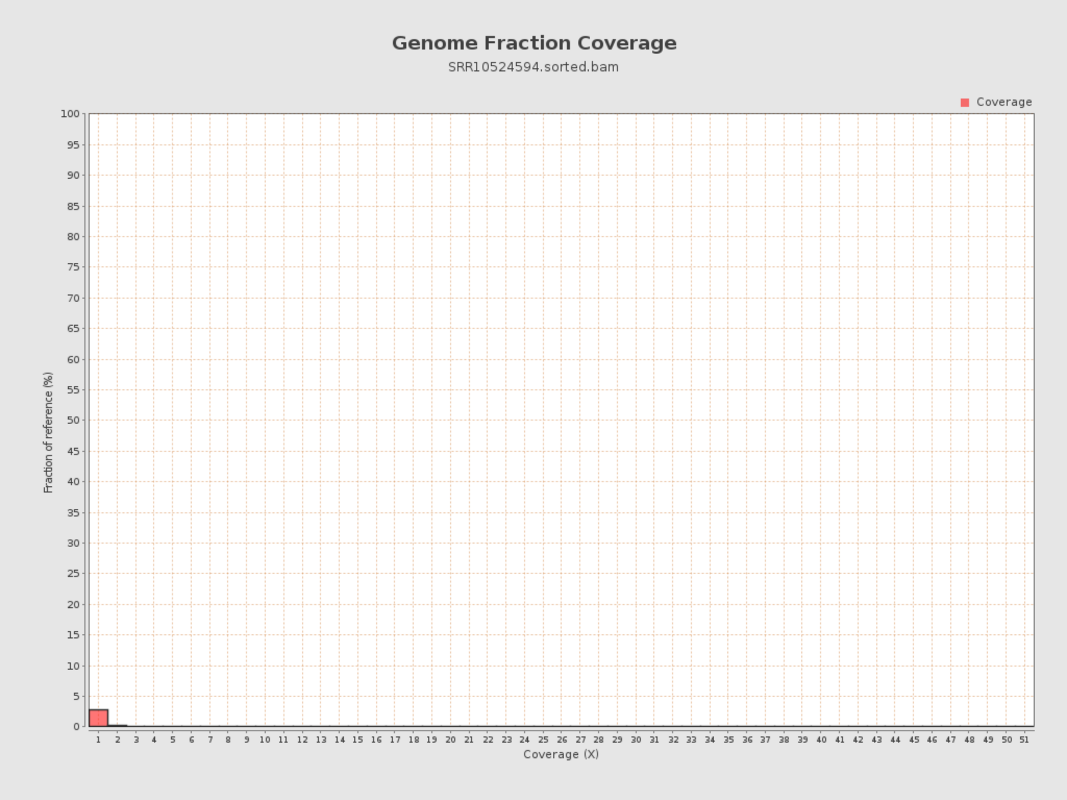
4. Results : Coverage Histogram



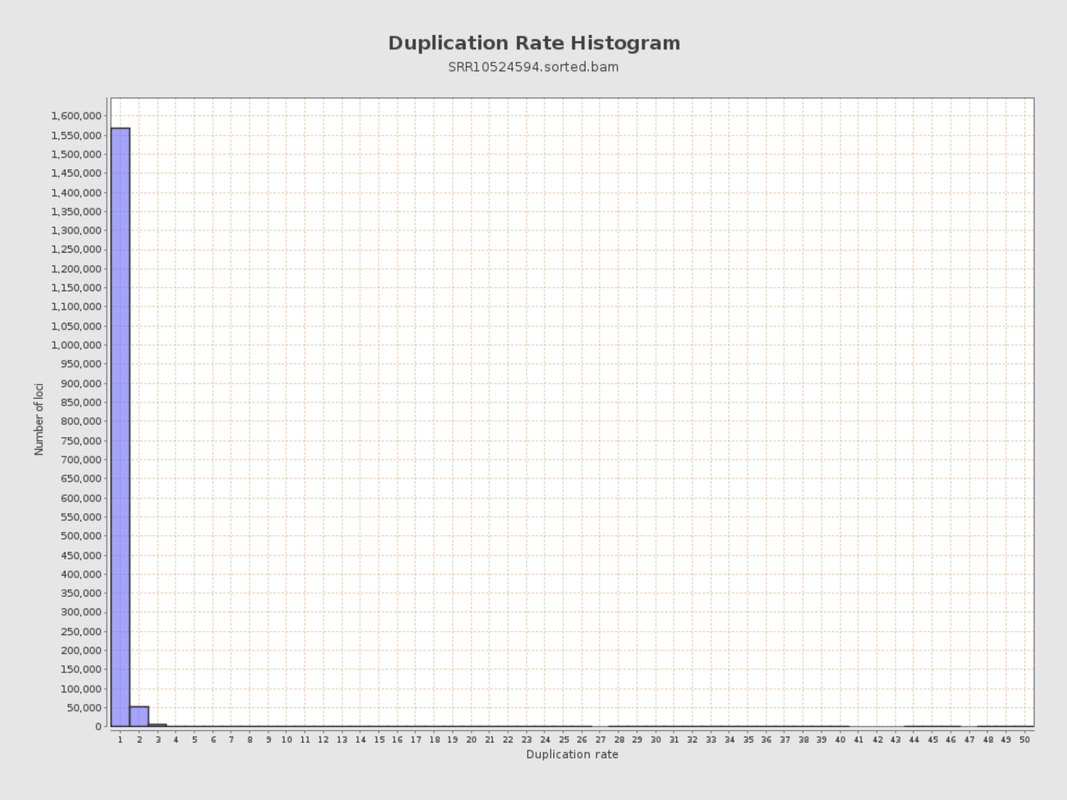
5. Results : Coverage Histogram (0-50X)



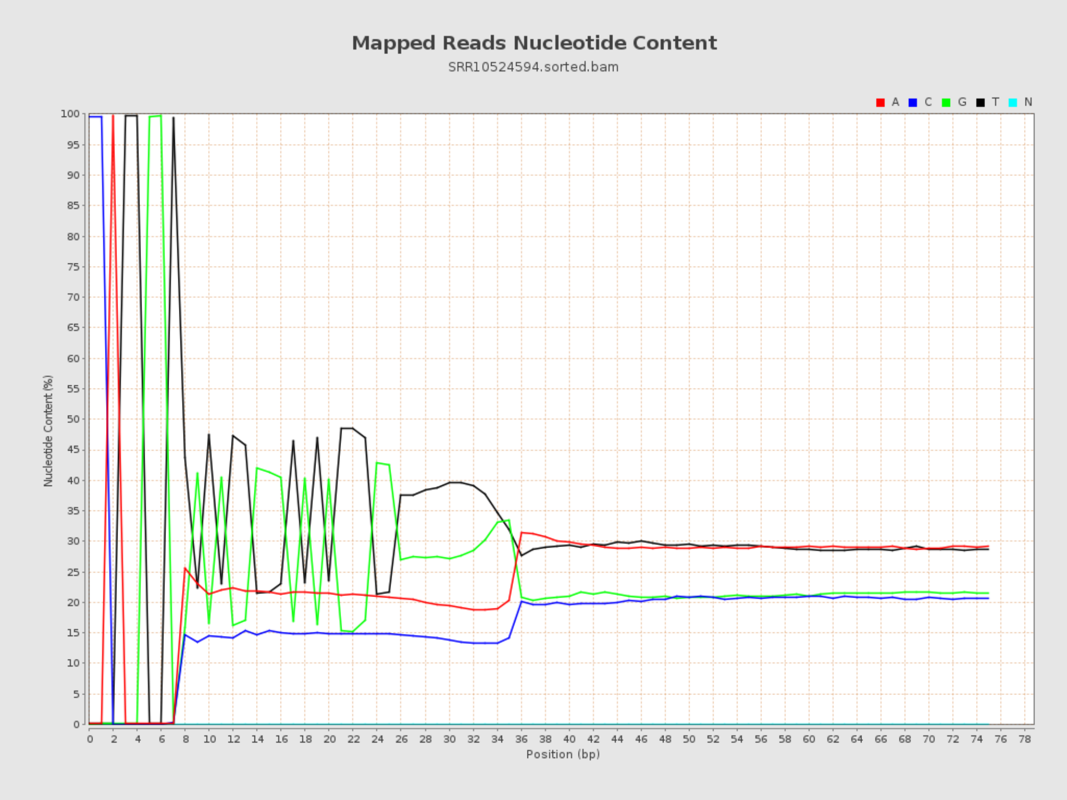
6. Results : Genome Fraction Coverage



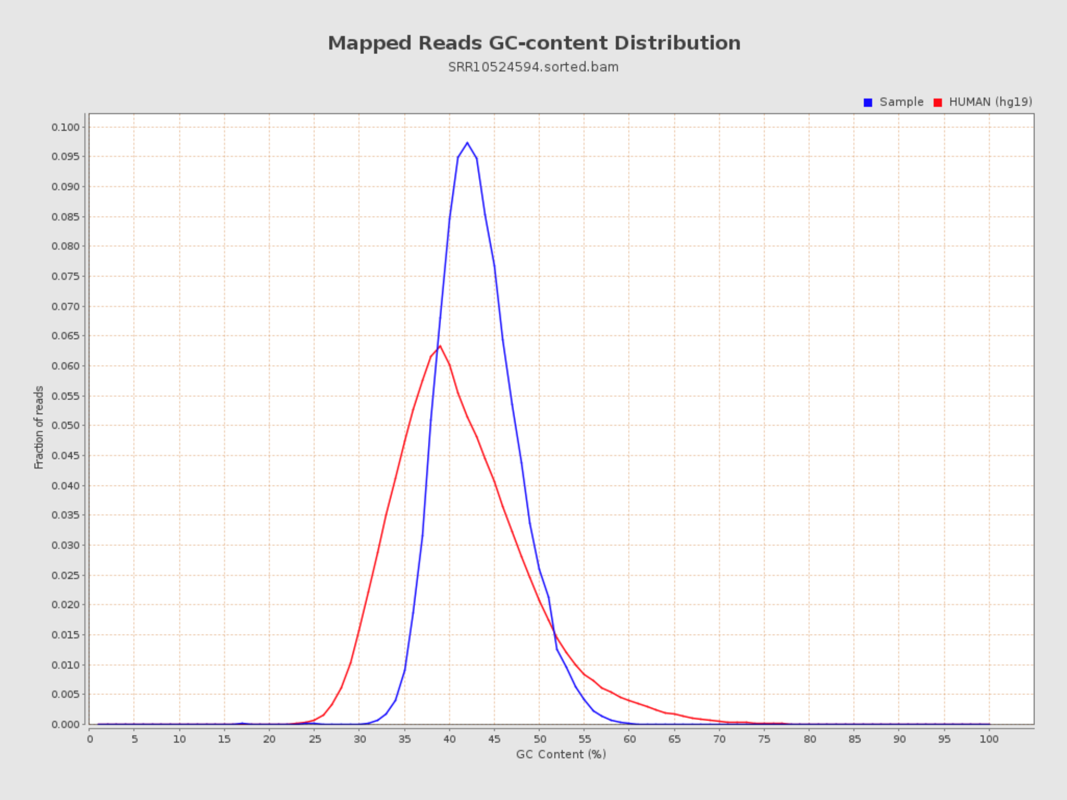
7. Results : Duplication Rate Histogram



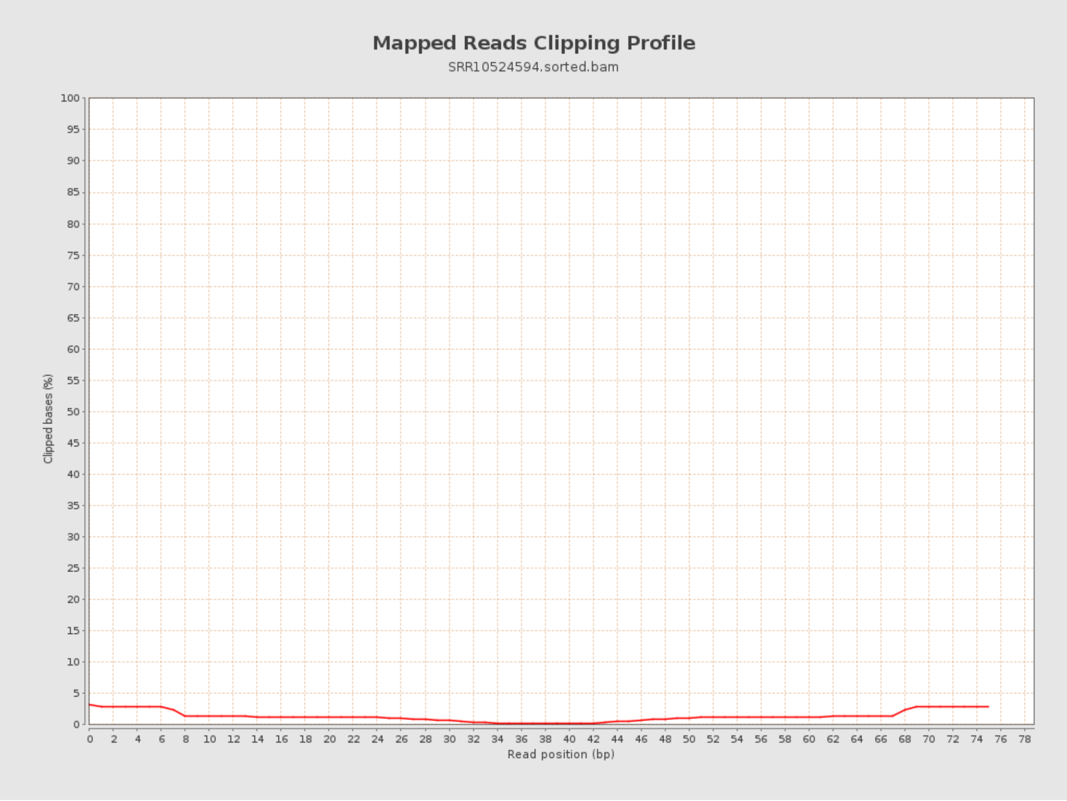
8. Results : Mapped Reads Nucleotide Content



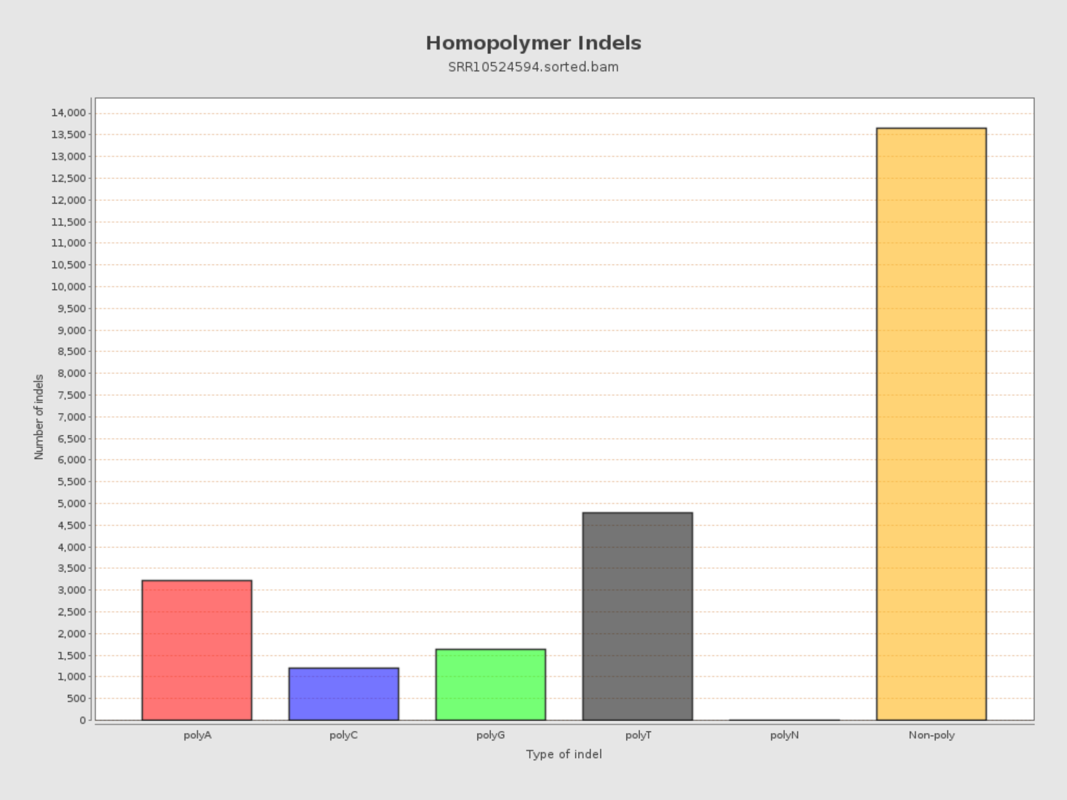
9. Results : Mapped Reads GC-content Distribution



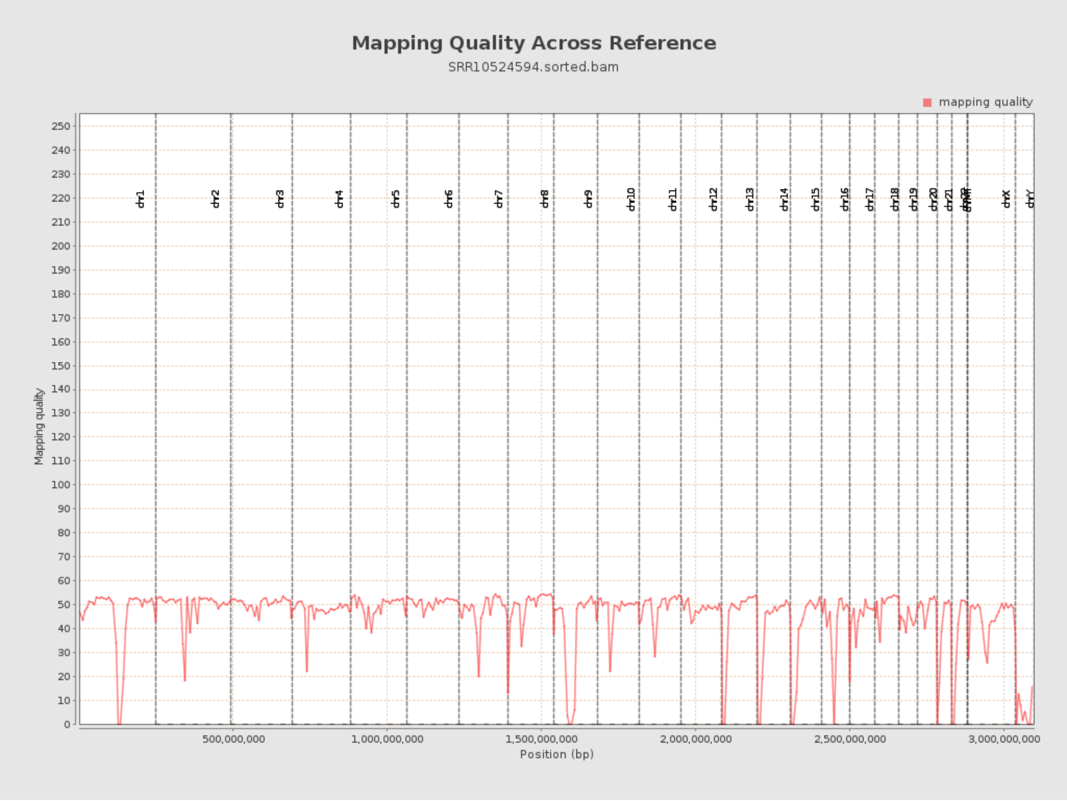
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram