Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 04:53:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524451.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_SRR10524451 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524451.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 04:53:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524451.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,379,349
Mapped reads	1,281,508 / 92.91%
Unmapped reads	97,841 / 7.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,831 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	34,057 / 2.47%
Duplication rate	1.9%
Clipped reads	1,278,450 / 92.69%

2.2. ACGT Content

Number/percentage of A's	21,687,947 / 27.92%
Number/percentage of C's	14,254,682 / 18.35%
Number/percentage of T's	23,421,683 / 30.15%
Number/percentage of G's	18,321,947 / 23.58%
Number/percentage of N's	1,817 / 0%
GC Percentage	41.93%

2.3. Coverage

Mean	0.0251

Standard Deviation	0.2394

2.4. Mapping Quality

Mean Mapping Quality	46.03

2.5. Mismatches and indels

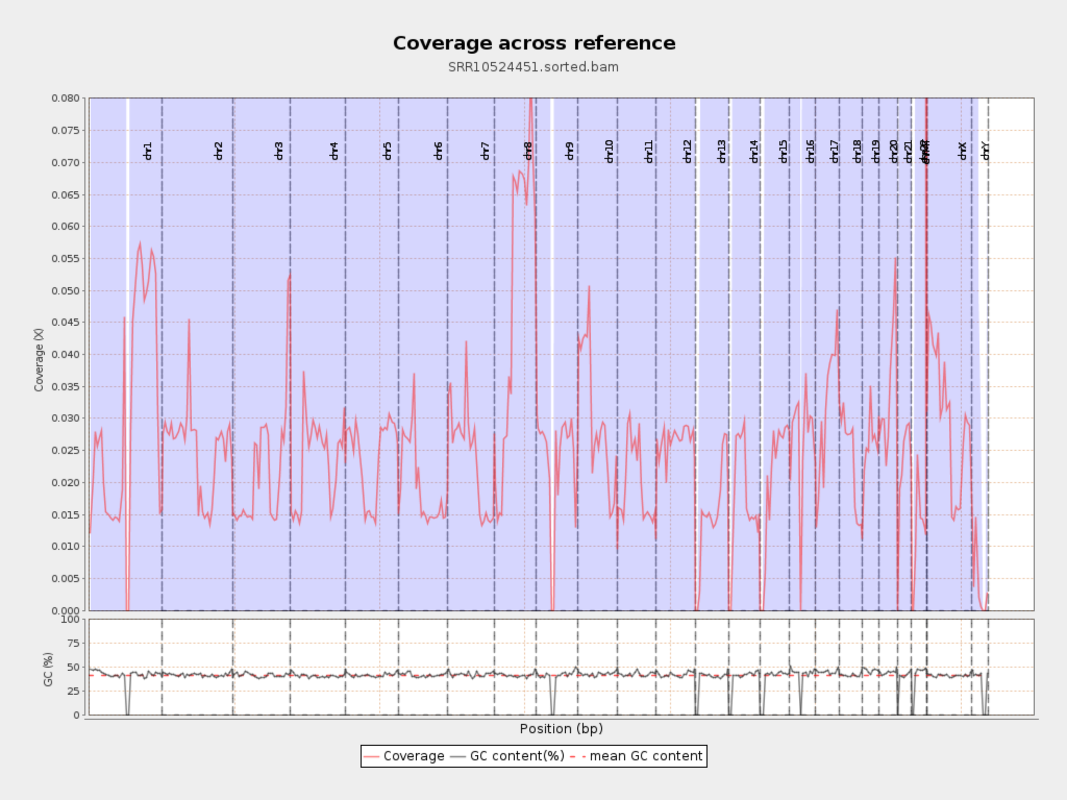
General error rate	0.48%
Mismatches	354,235
Insertions	6,978
Mapped reads with at least one insertion	0.54%
Deletions	14,893
Mapped reads with at least one deletion	1.15%
Homopolymer indels	40.74%

2.6. Chromosome stats

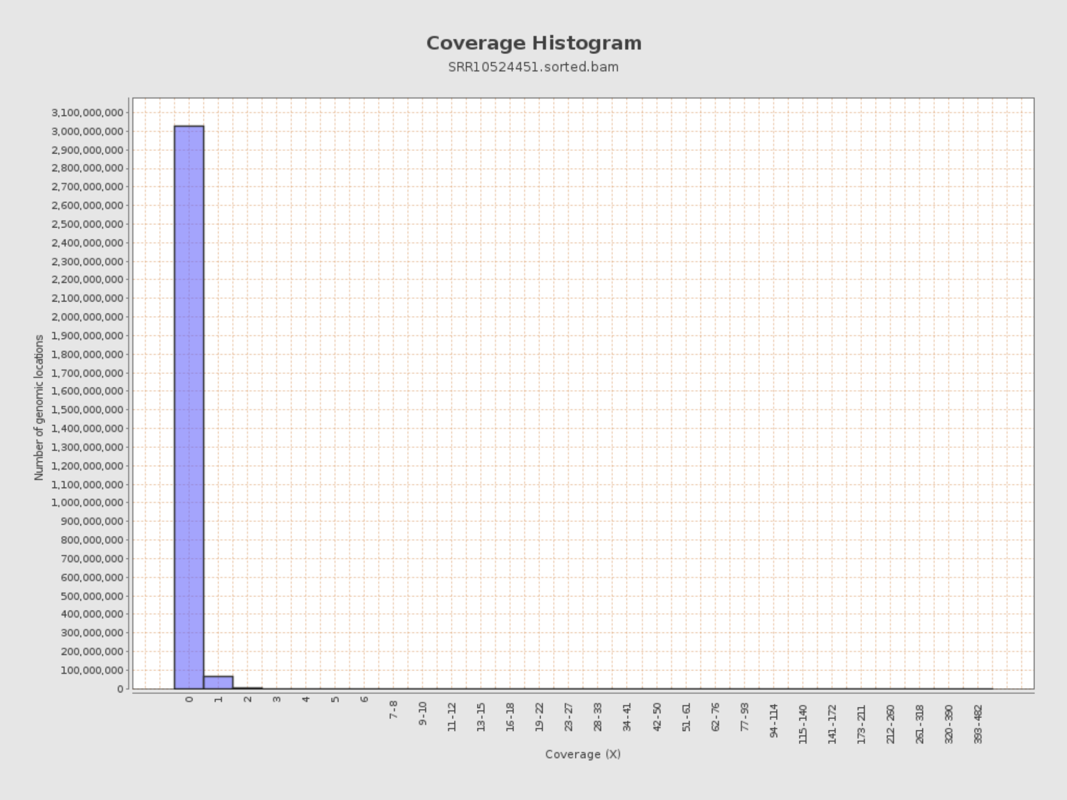
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7616651	0.0306	0.4358
chr2	243199373	6157463	0.0253	0.2455
chr3	198022430	4274530	0.0216	0.1581
chr4	191154276	4481030	0.0234	0.1822
chr5	180915260	4363432	0.0241	0.1665
chr6	171115067	3349936	0.0196	0.1841
chr7	159138663	3839941	0.0241	0.2977

chr8	146364022	7253245	0.0496	0.2732
chr9	141213431	3231763	0.0229	0.2154
chr10	135534747	4080753	0.0301	0.2632
chr11	135006516	2656085	0.0197	0.2082
chr12	133851895	3574623	0.0267	0.1763
chr13	115169878	1734355	0.0151	0.1309
chr14	107349540	1846548	0.0172	0.1441
chr15	102531392	2059683	0.0201	0.1547
chr16	90354753	2414700	0.0267	0.1865
chr17	81195210	2575937	0.0317	0.2009
chr18	78077248	1856237	0.0238	0.3722
chr19	59128983	1539181	0.026	0.3286
chr20	63025520	2203274	0.035	0.2042
chr21	48129895	1077973	0.0224	0.1714
chr22	51304566	600491	0.0117	0.1152
chrMT	16571	14695	0.8868	1.0204
chrX	155270560	4665965	0.0301	0.2006
chrY	59373566	245757	0.0041	0.1201

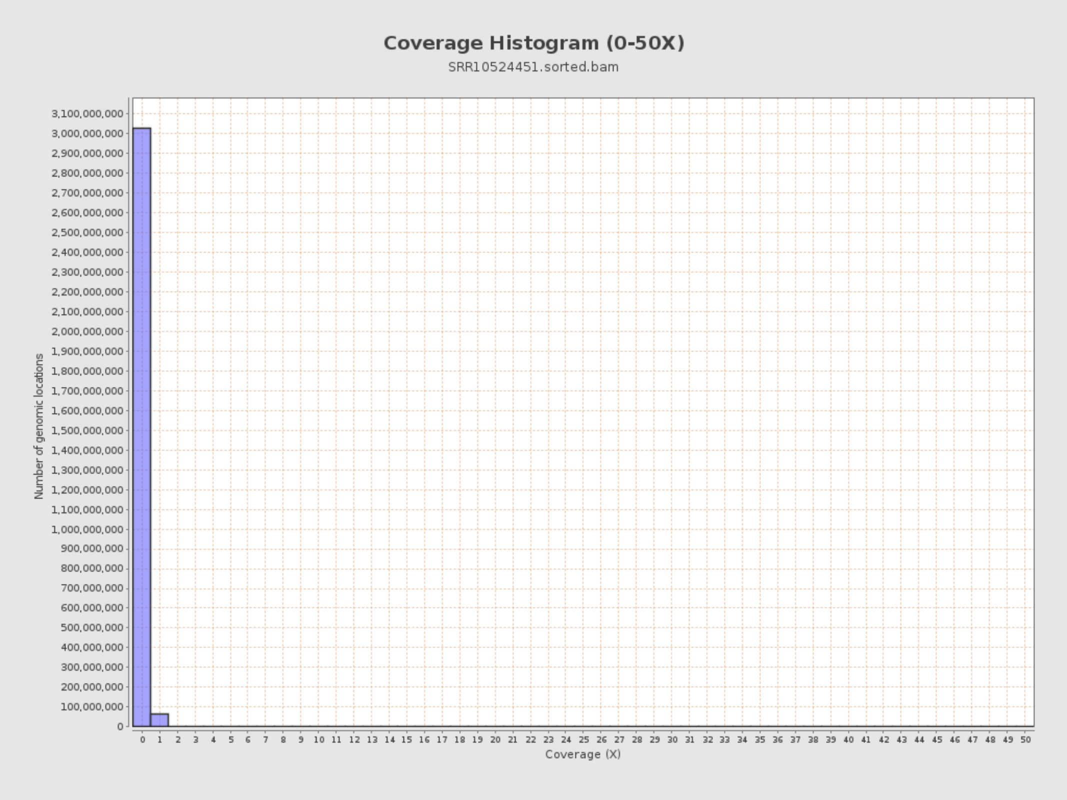
3. Results : Coverage across reference



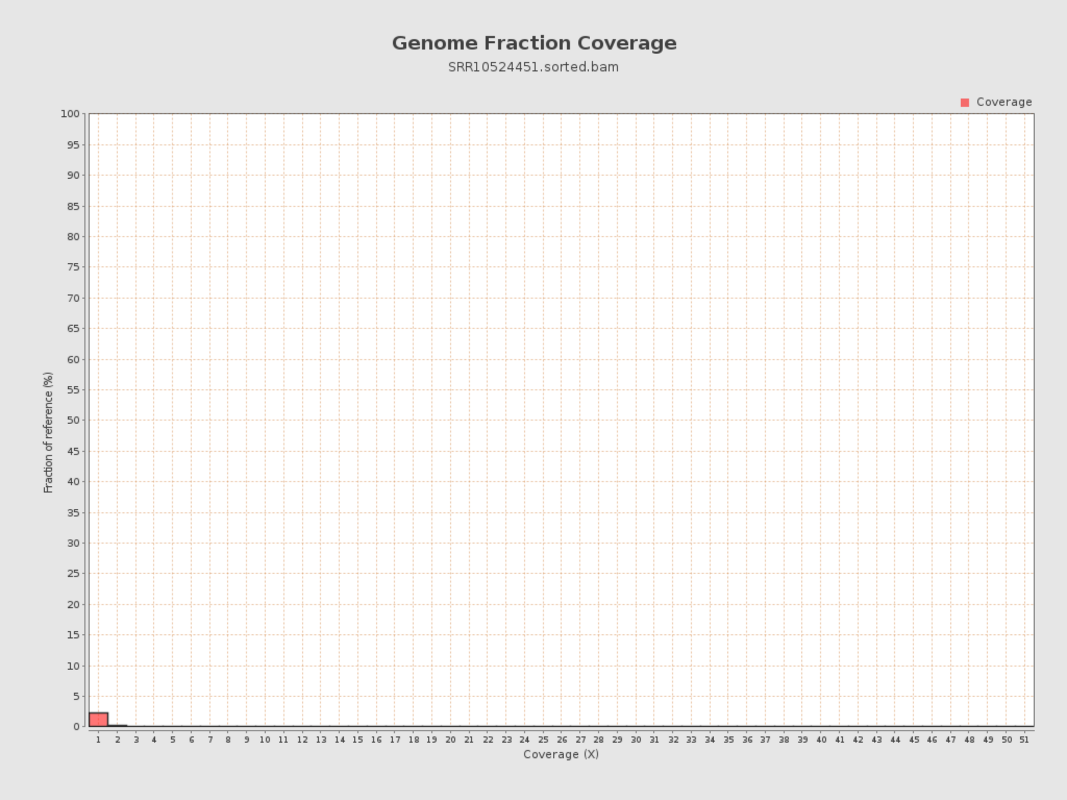
4. Results : Coverage Histogram



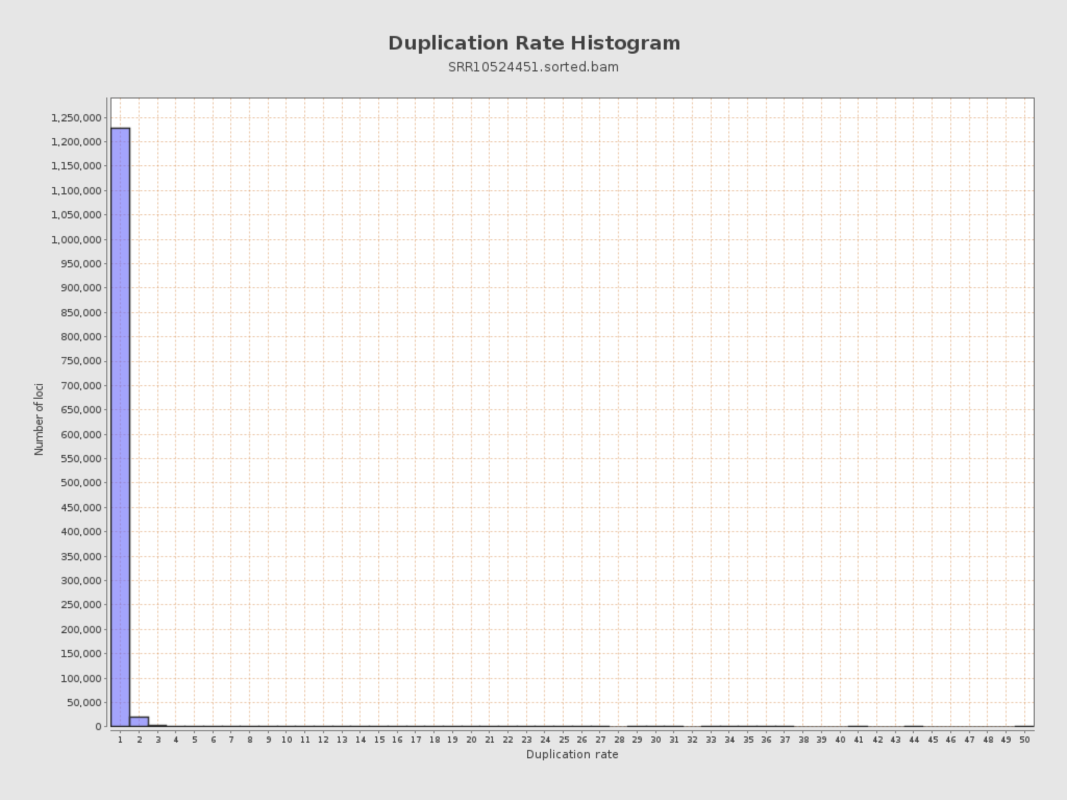
5. Results : Coverage Histogram (0-50X)



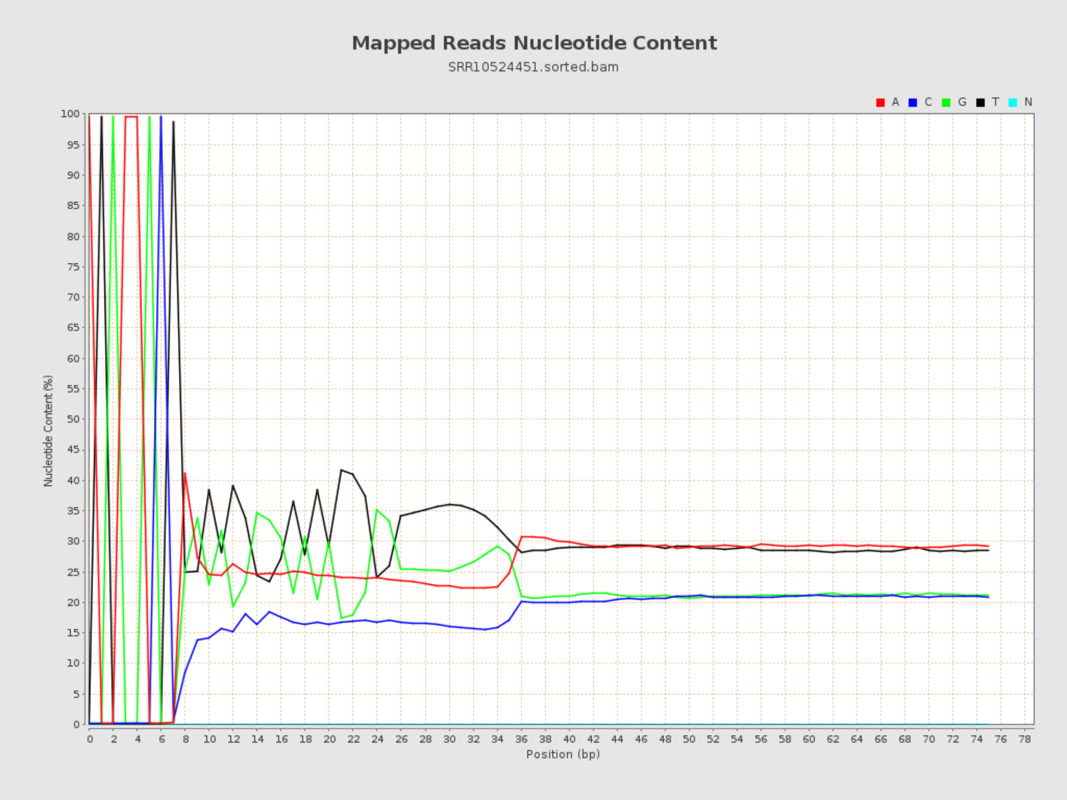
6. Results : Genome Fraction Coverage



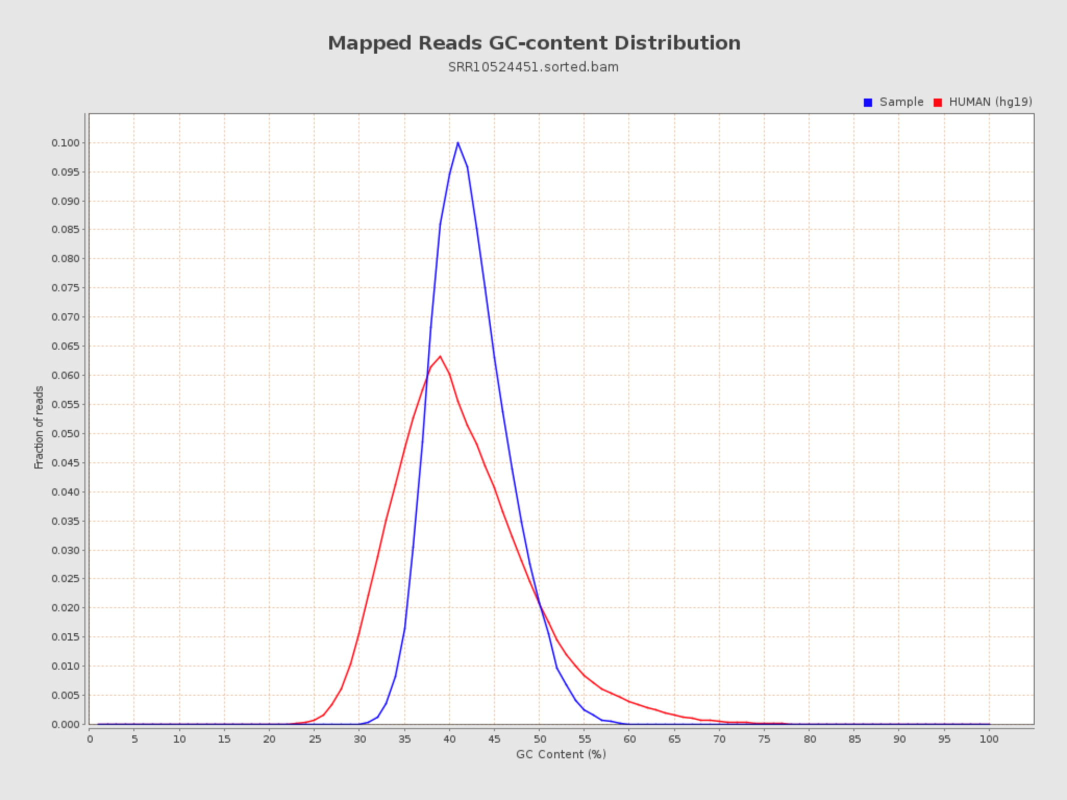
7. Results : Duplication Rate Histogram



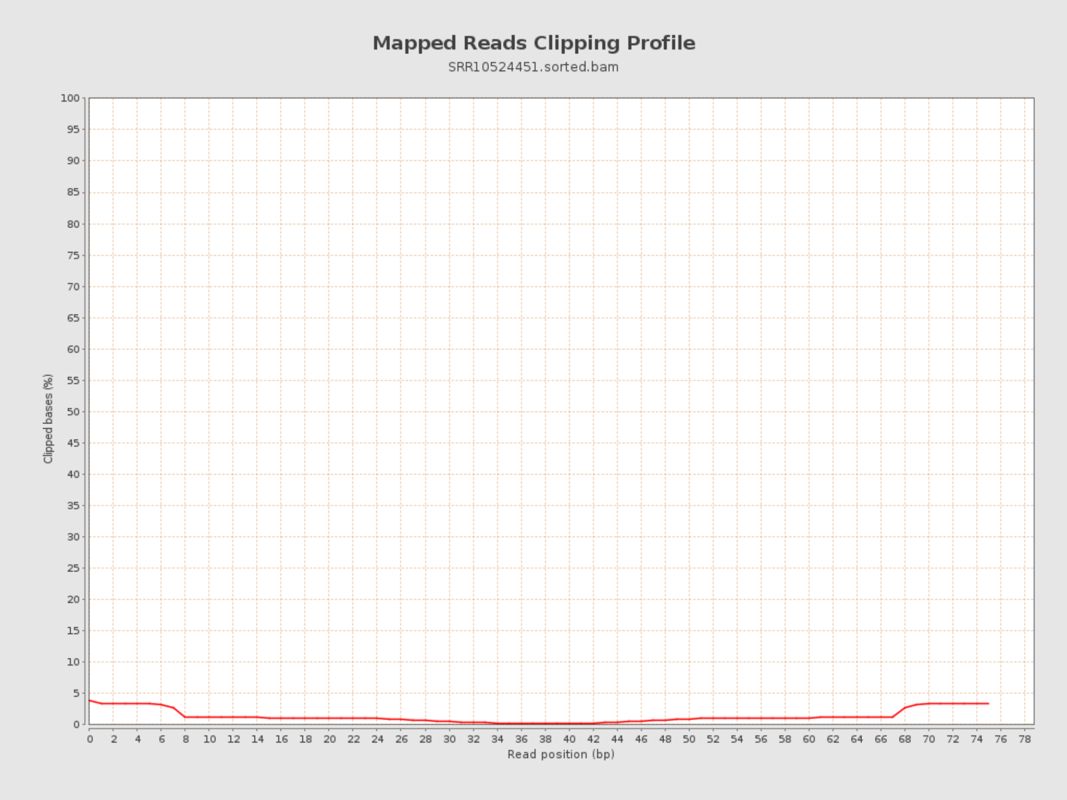
8. Results : Mapped Reads Nucleotide Content



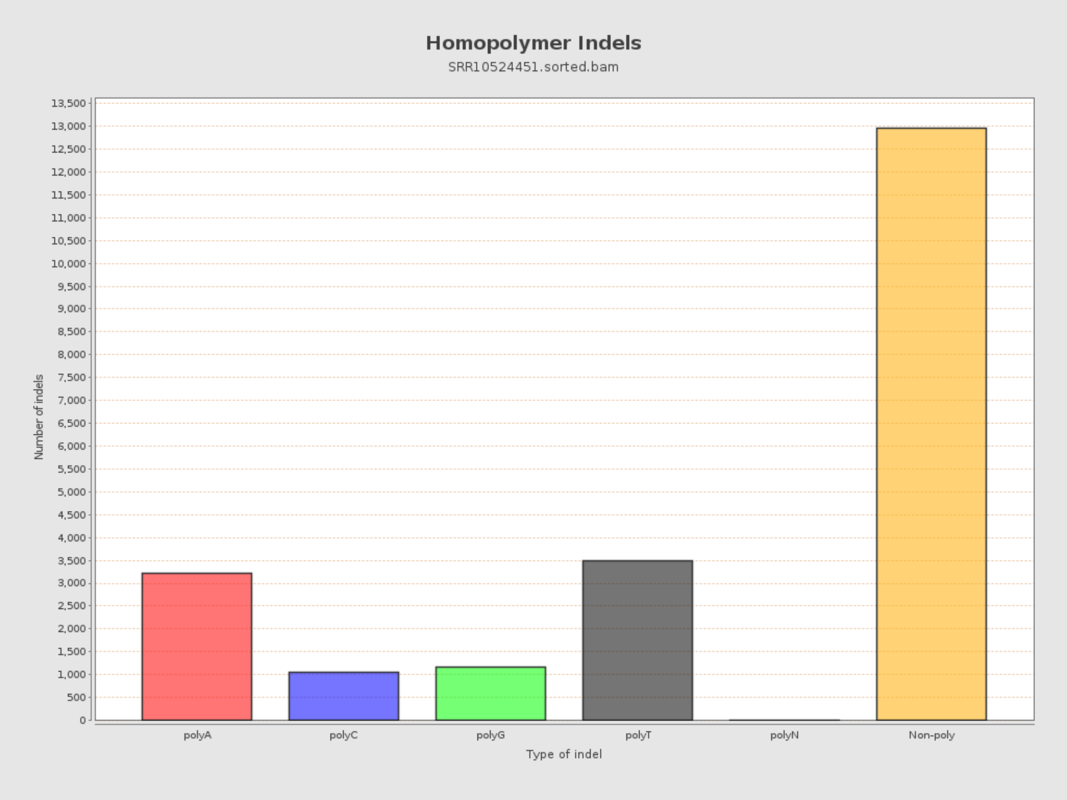
9. Results : Mapped Reads GC-content Distribution



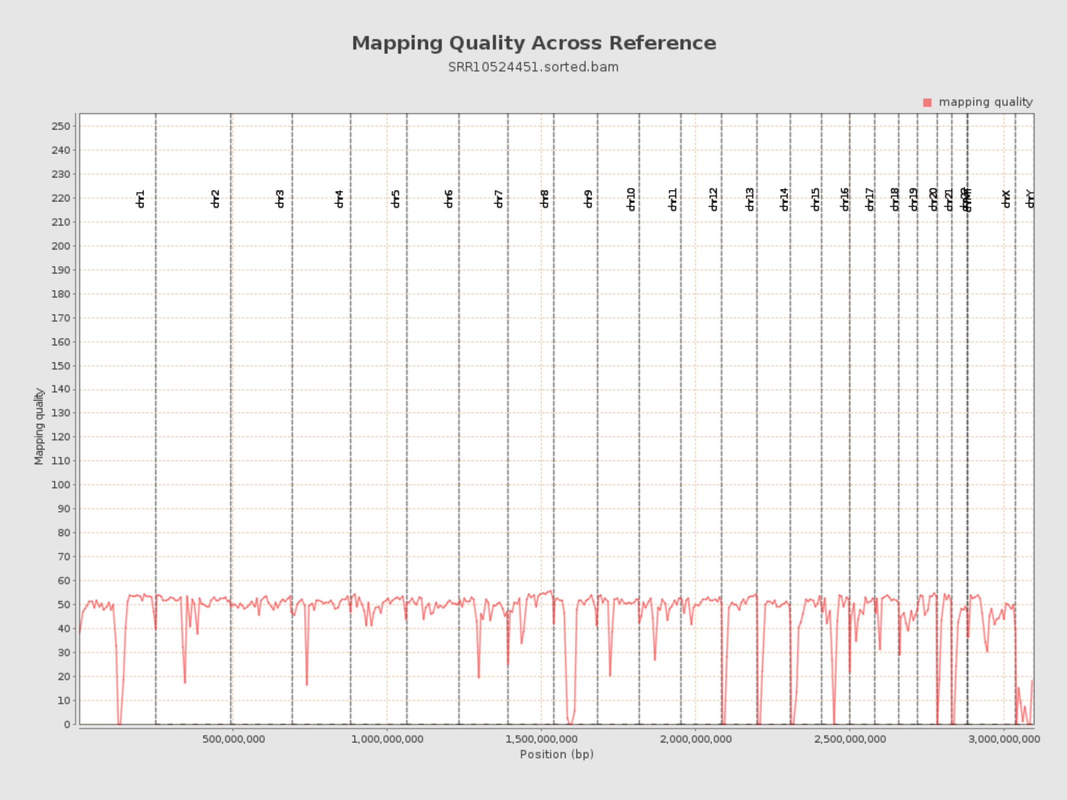
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram