Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 11:29:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524976.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_SRR10524976 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524976.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 11:29:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524976.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,795,044
Mapped reads	1,631,740 / 90.9%
Unmapped reads	163,304 / 9.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,736 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	62,591 / 3.49%
Duplication rate	2.9%
Clipped reads	1,631,129 / 90.87%

2.2. ACGT Content

Number/percentage of A's	24,539,324 / 25.76%
Number/percentage of C's	17,623,740 / 18.5%
Number/percentage of T's	30,545,530 / 32.06%
Number/percentage of G's	22,553,423 / 23.67%
Number/percentage of N's	973 / 0%
GC Percentage	42.17%

2.3. Coverage

Mean	0.0308

Standard Deviation	0.2651

2.4. Mapping Quality

Mean Mapping Quality	45.75

2.5. Mismatches and indels

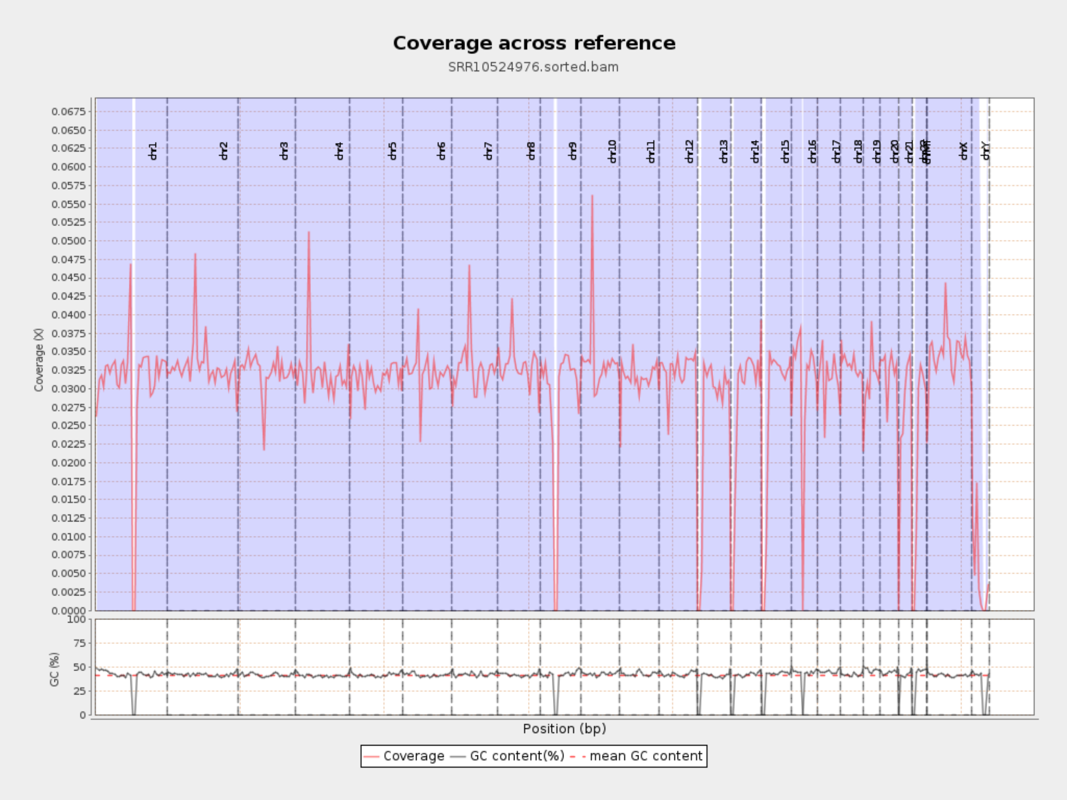
General error rate	0.5%
Mismatches	462,897
Insertions	6,214
Mapped reads with at least one insertion	0.38%
Deletions	17,655
Mapped reads with at least one deletion	1.07%
Homopolymer indels	42.13%

2.6. Chromosome stats

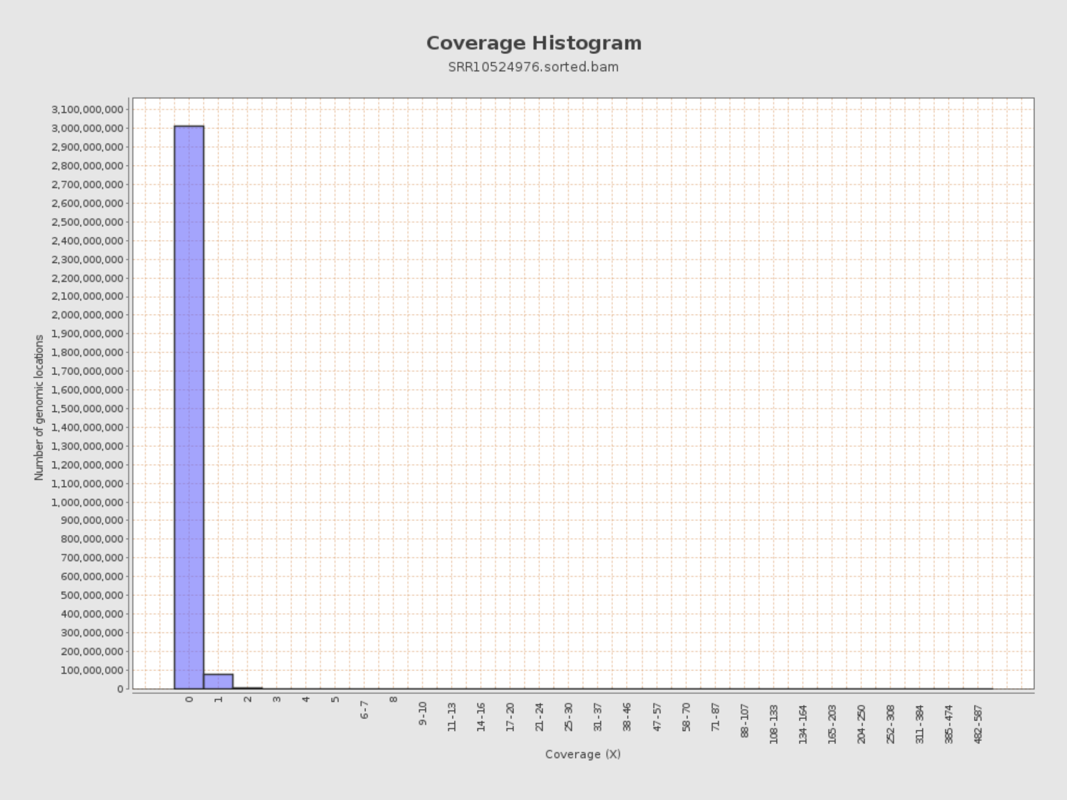
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7612072	0.0305	0.4464
chr2	243199373	8066689	0.0332	0.304
chr3	198022430	6389562	0.0323	0.197
chr4	191154276	6190599	0.0324	0.2228
chr5	180915260	5726840	0.0317	0.1966
chr6	171115067	5524938	0.0323	0.2344
chr7	159138663	5247294	0.033	0.3191

chr8	146364022	4862814	0.0332	0.2767
chr9	141213431	3975417	0.0282	0.2434
chr10	135534747	4611747	0.034	0.2898
chr11	135006516	4280883	0.0317	0.2634
chr12	133851895	4332008	0.0324	0.1987
chr13	115169878	2976227	0.0258	0.1765
chr14	107349540	2917924	0.0272	0.1854
chr15	102531392	2732500	0.0267	0.1916
chr16	90354753	2743052	0.0304	0.202
chr17	81195210	2559025	0.0315	0.2176
chr18	78077248	2594943	0.0332	0.3677
chr19	59128983	1858427	0.0314	0.3264
chr20	63025520	2023083	0.0321	0.2021
chr21	48129895	1261649	0.0262	0.1968
chr22	51304566	1106444	0.0216	0.1604
chrMT	16571	375	0.0226	0.1487
chrX	155270560	5410471	0.0348	0.2236
chrY	59373566	288258	0.0049	0.1335

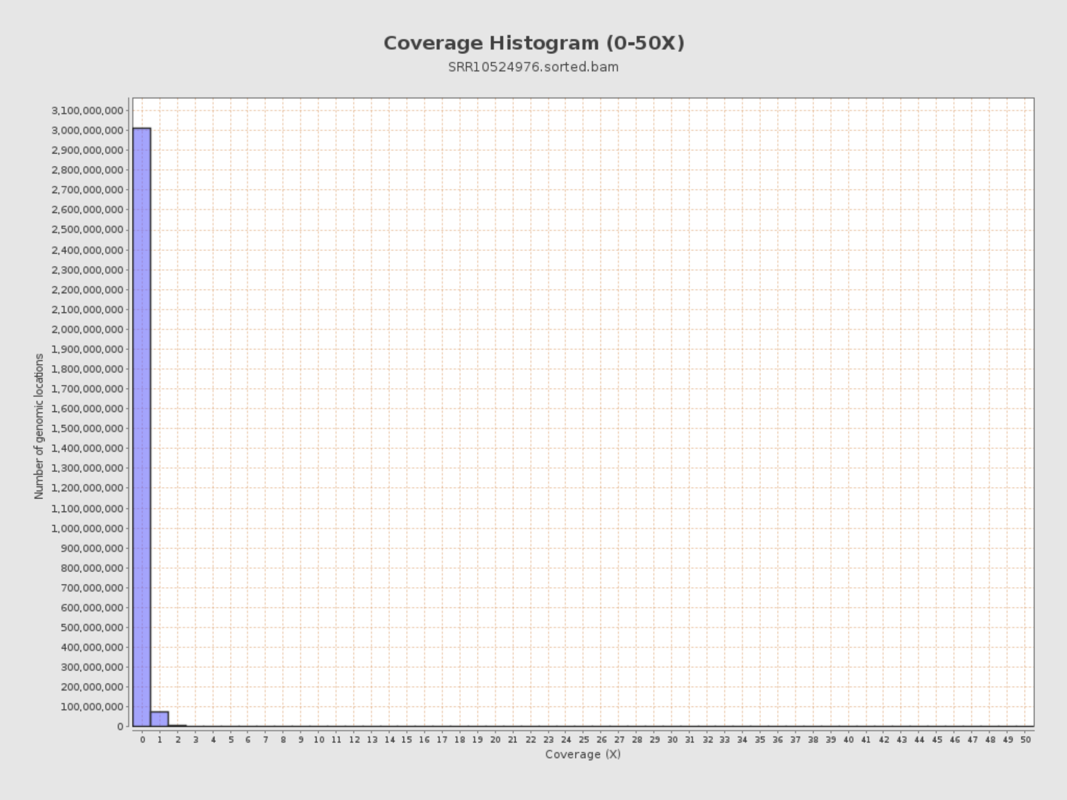
3. Results : Coverage across reference



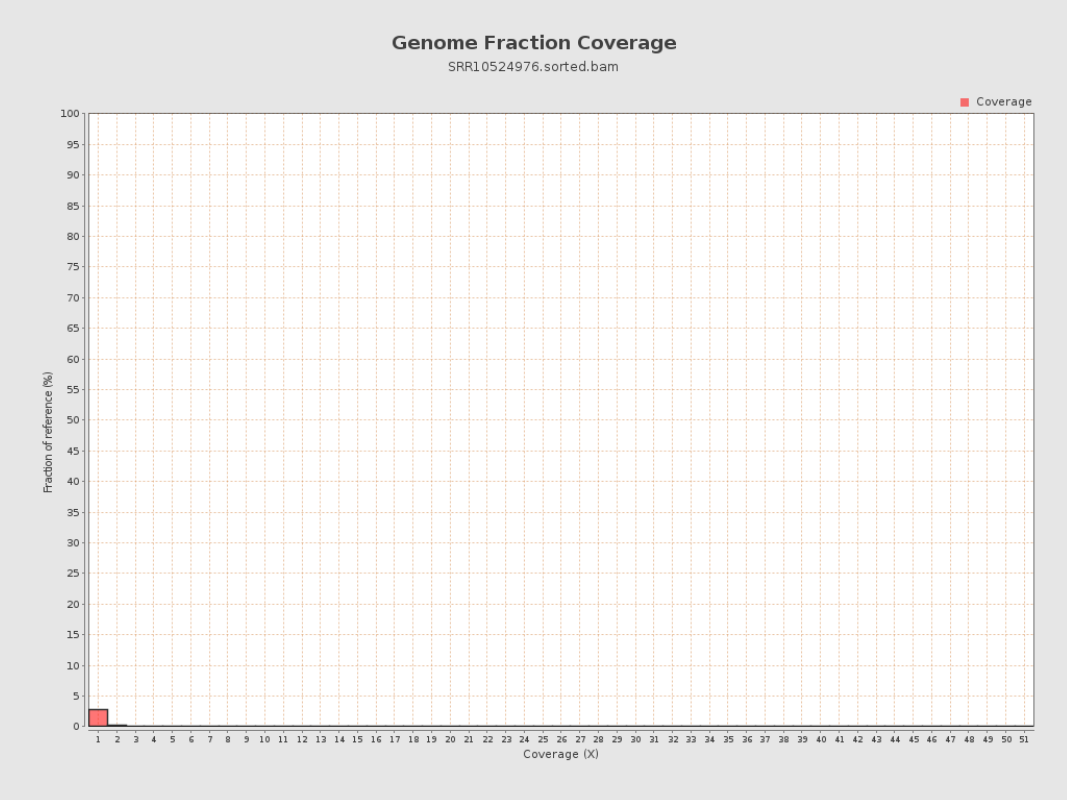
4. Results : Coverage Histogram



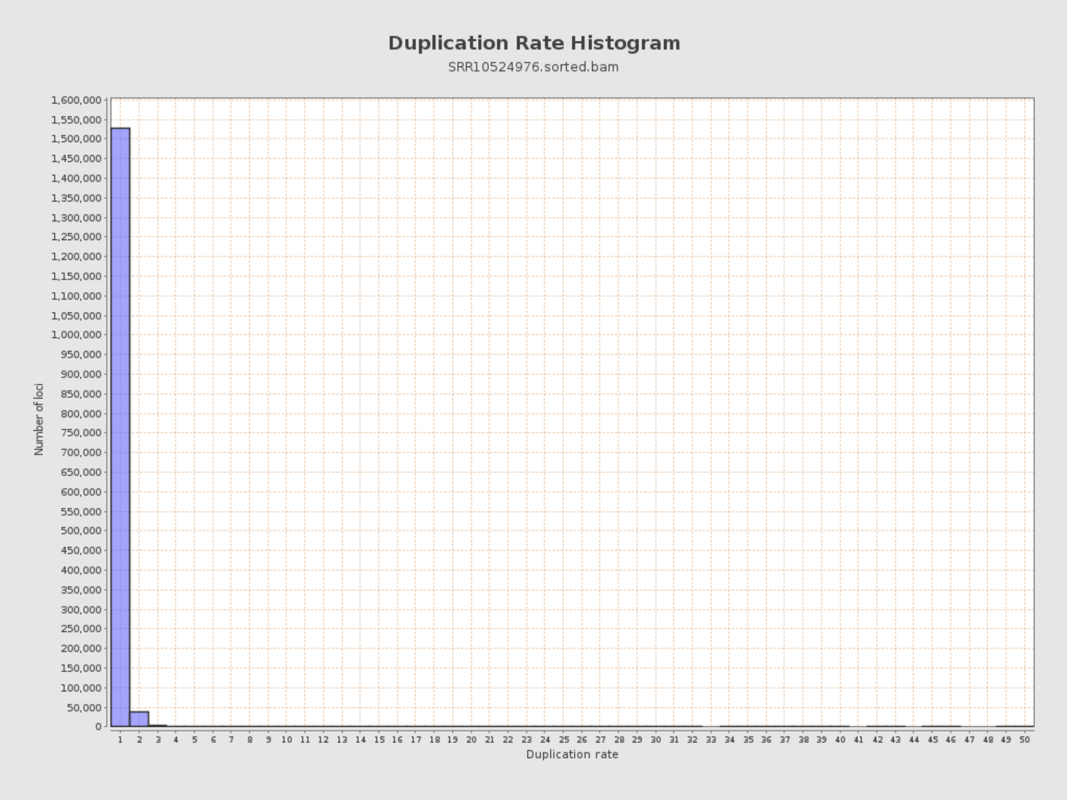
5. Results : Coverage Histogram (0-50X)



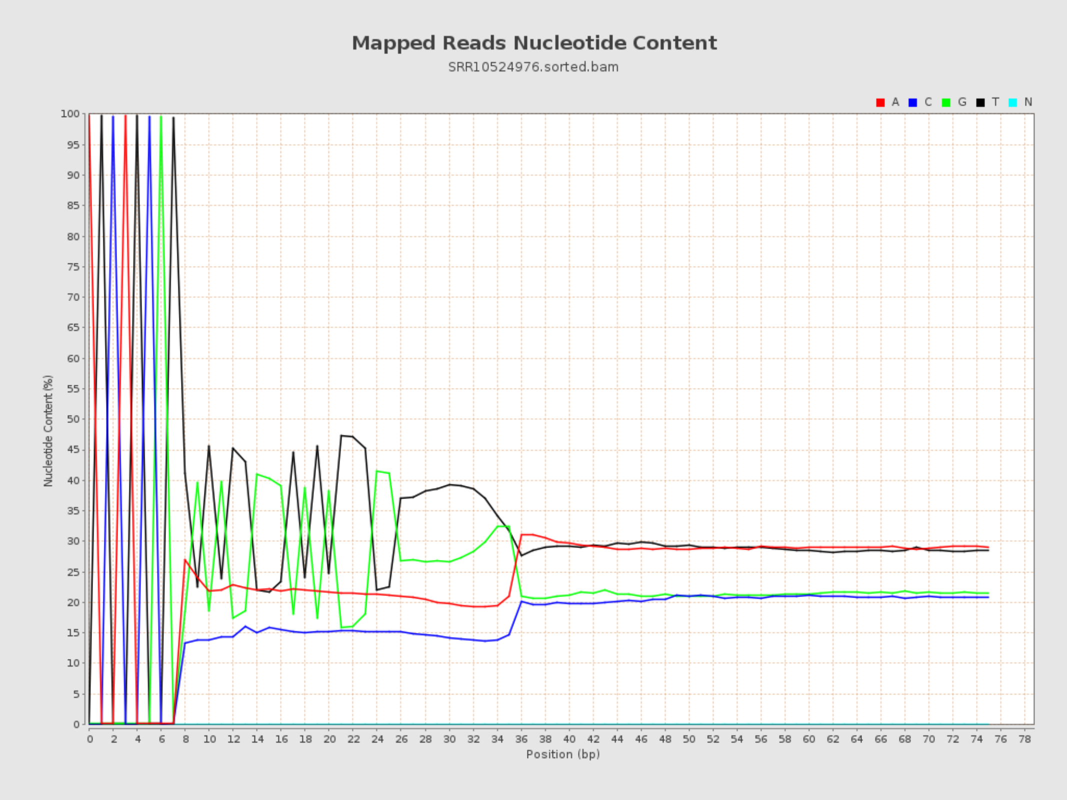
6. Results : Genome Fraction Coverage



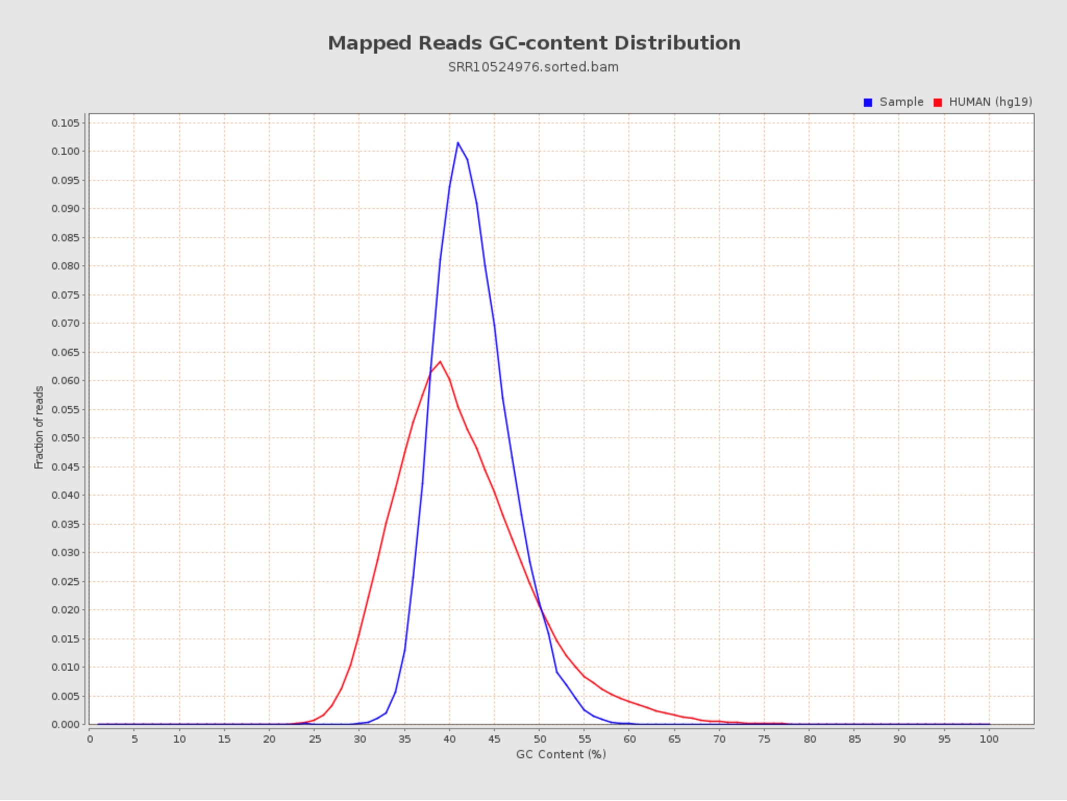
7. Results : Duplication Rate Histogram



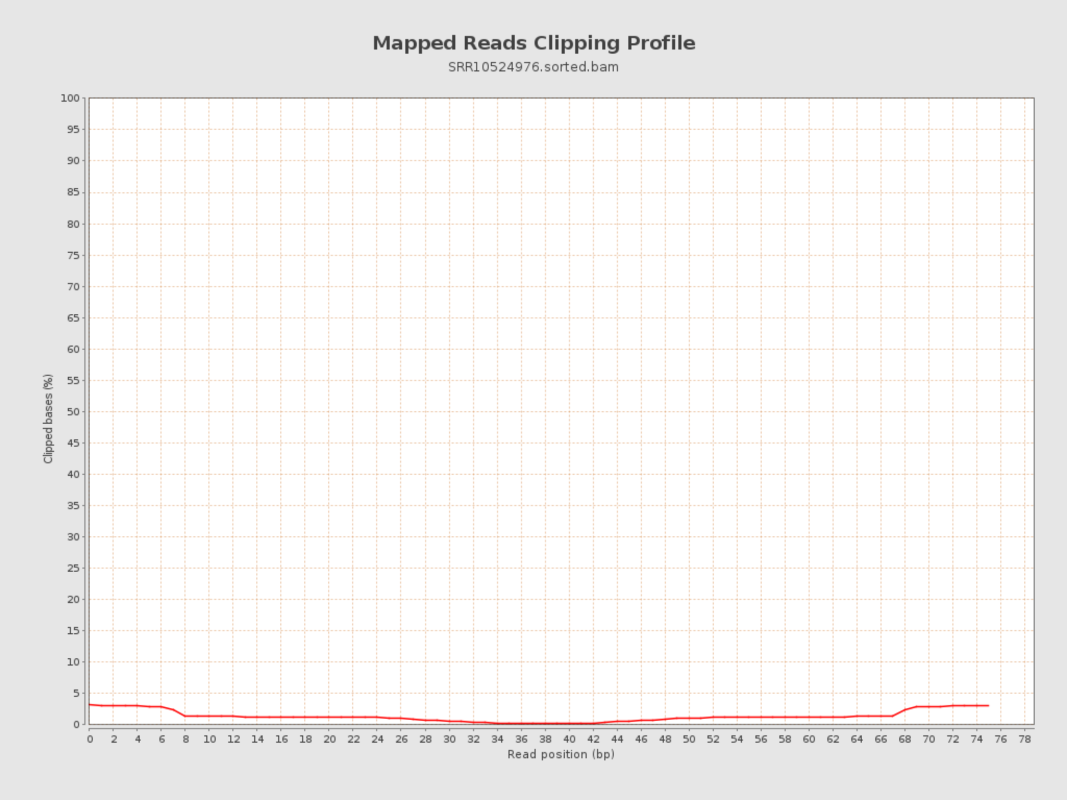
8. Results : Mapped Reads Nucleotide Content



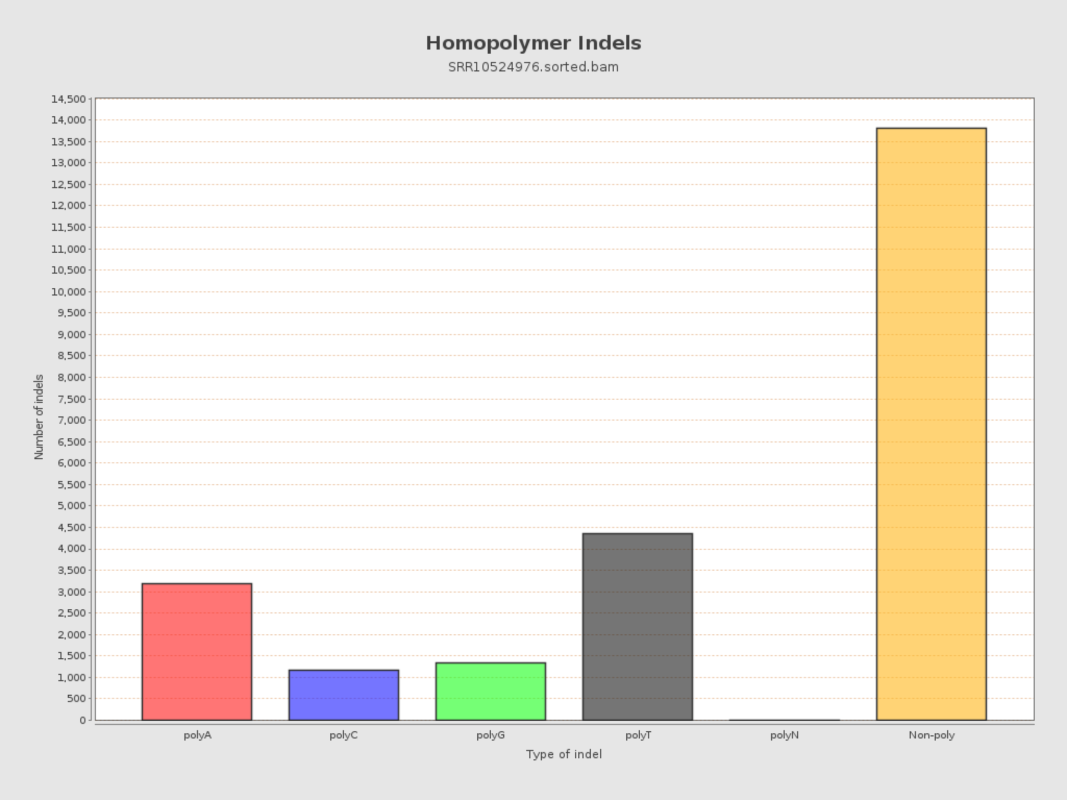
9. Results : Mapped Reads GC-content Distribution



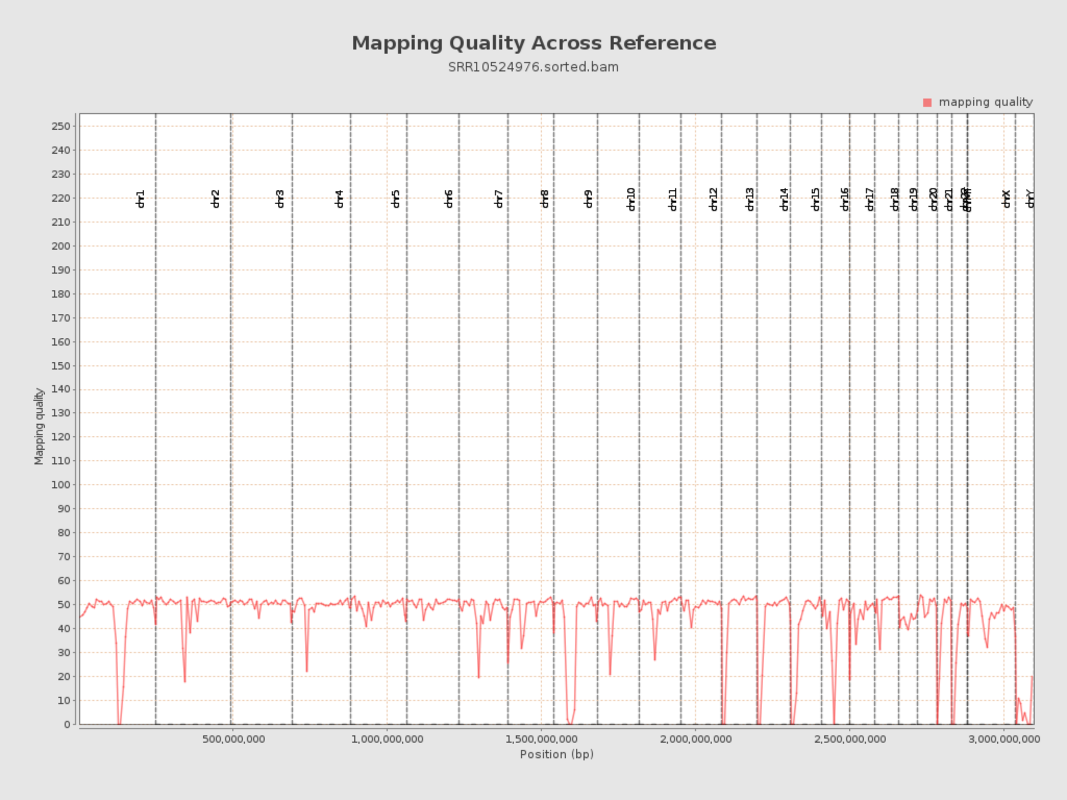
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram