Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 01:52:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524395.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_SRR10524395 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524395.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 01:52:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524395.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,179,436
Mapped reads	2,021,687 / 92.76%
Unmapped reads	157,749 / 7.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,104 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	102,287 / 4.69%
Duplication rate	3.81%
Clipped reads	2,023,977 / 92.87%

2.2. ACGT Content

Number/percentage of A's	30,618,802 / 25.78%
Number/percentage of C's	22,203,890 / 18.7%
Number/percentage of T's	37,973,114 / 31.98%
Number/percentage of G's	27,936,458 / 23.53%
Number/percentage of N's	16,217 / 0.01%
GC Percentage	42.22%

2.3. Coverage

Mean	0.0384

Standard Deviation	0.3751

2.4. Mapping Quality

Mean Mapping Quality	45.99

2.5. Mismatches and indels

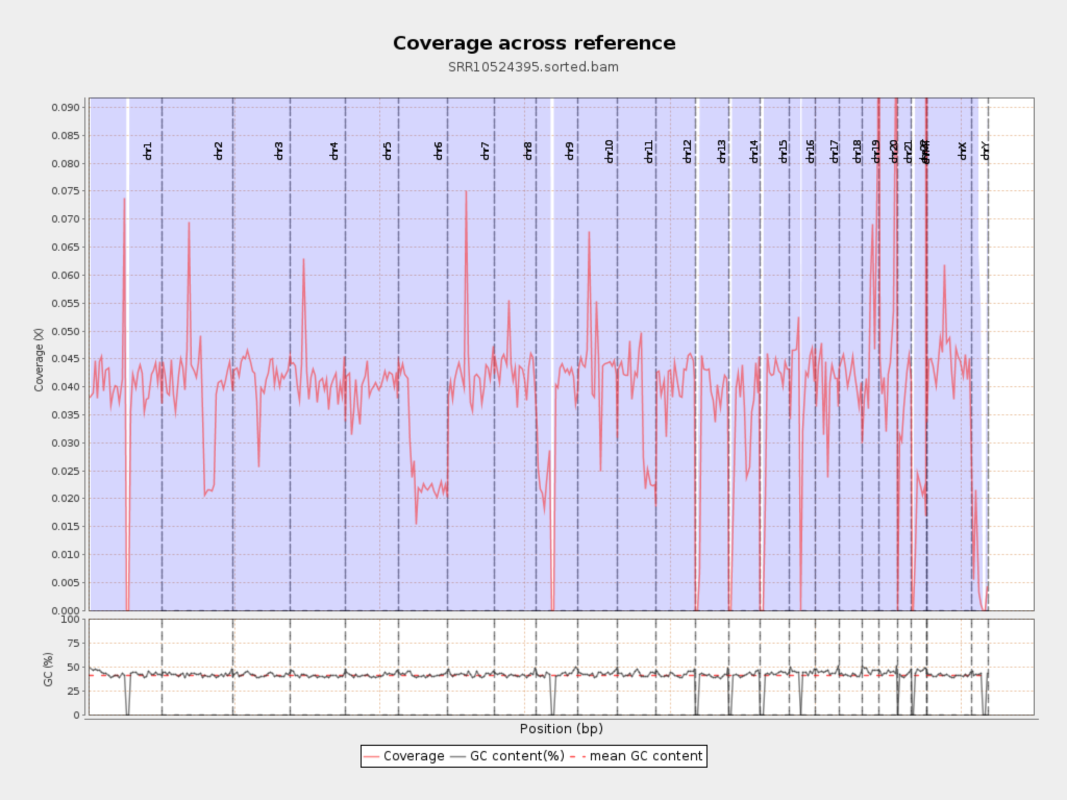
General error rate	0.5%
Mismatches	574,079
Insertions	8,999
Mapped reads with at least one insertion	0.44%
Deletions	21,631
Mapped reads with at least one deletion	1.06%
Homopolymer indels	42.98%

2.6. Chromosome stats

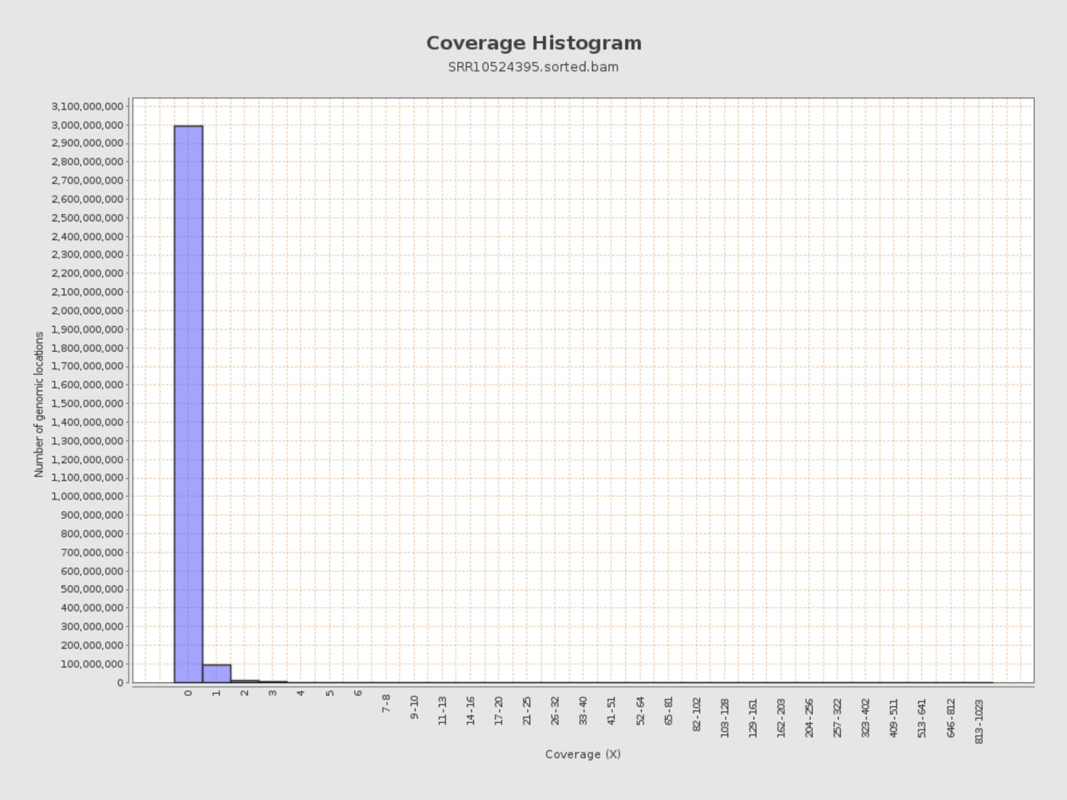
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9783447	0.0393	0.8126
chr2	243199373	9598717	0.0395	0.3966
chr3	198022430	8299914	0.0419	0.2266
chr4	191154276	7987178	0.0418	0.2577
chr5	180915260	7228417	0.04	0.2239
chr6	171115067	4568644	0.0267	0.2011
chr7	159138663	6838864	0.043	0.5631

chr8	146364022	6354013	0.0434	0.3398
chr9	141213431	4372094	0.031	0.2647
chr10	135534747	6034054	0.0445	0.33
chr11	135006516	4921820	0.0365	0.2877
chr12	133851895	5541084	0.0414	0.2407
chr13	115169878	3887086	0.0338	0.2064
chr14	107349540	3316566	0.0309	0.2023
chr15	102531392	3611274	0.0352	0.2095
chr16	90354753	3608923	0.0399	0.235
chr17	81195210	3202139	0.0394	0.2527
chr18	78077248	3295758	0.0422	0.4954
chr19	59128983	3278244	0.0554	0.5621
chr20	63025520	3262490	0.0518	0.2635
chr21	48129895	1647641	0.0342	0.2359
chr22	51304566	804519	0.0157	0.1374
chrMT	16571	13191	0.796	1.0172
chrX	155270560	6965505	0.0449	0.267
chrY	59373566	361402	0.0061	0.1742

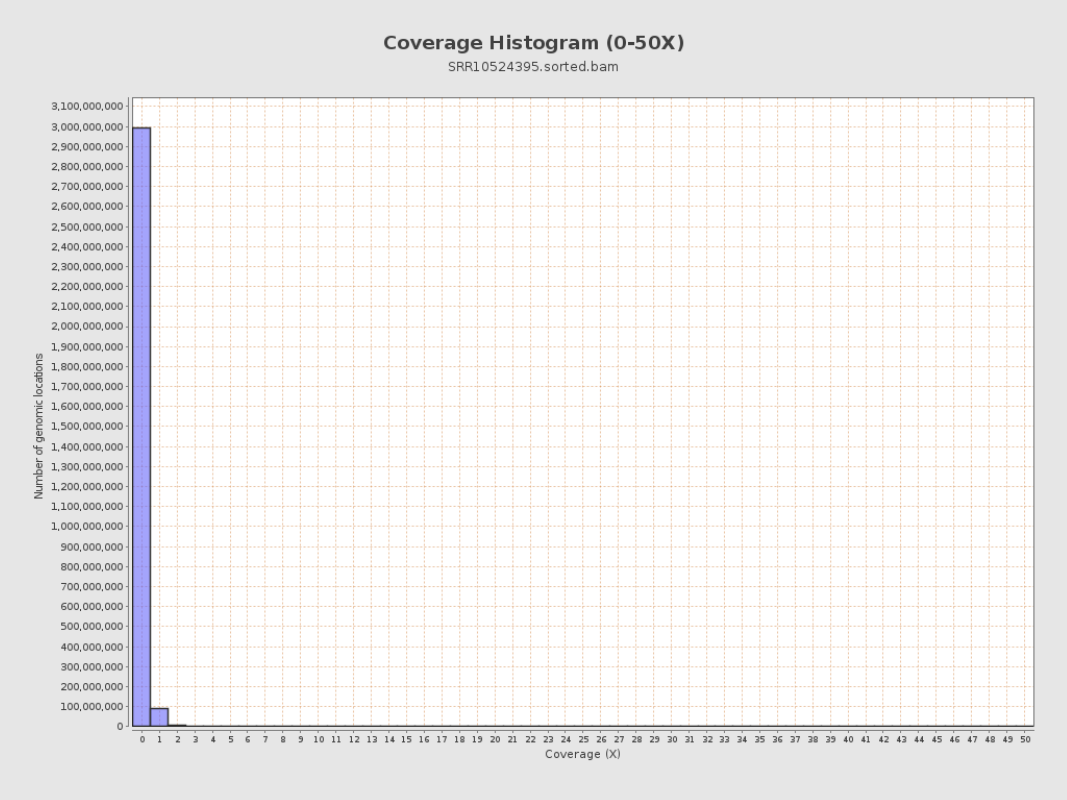
3. Results : Coverage across reference



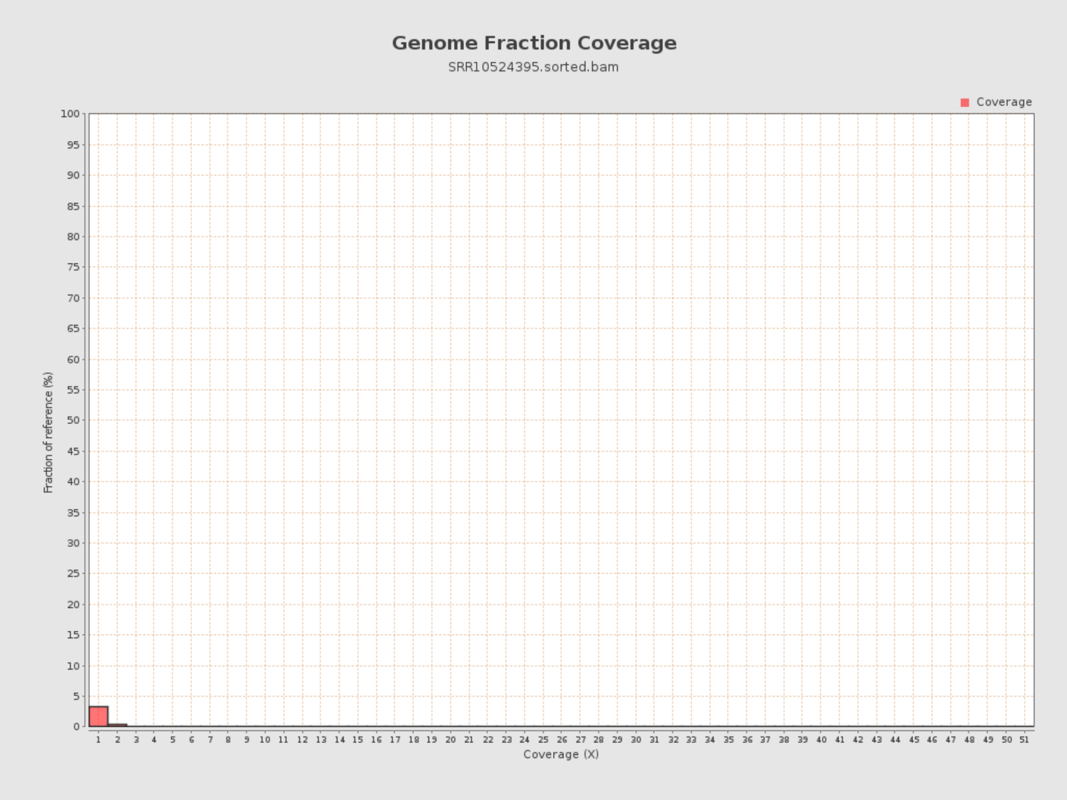
4. Results : Coverage Histogram



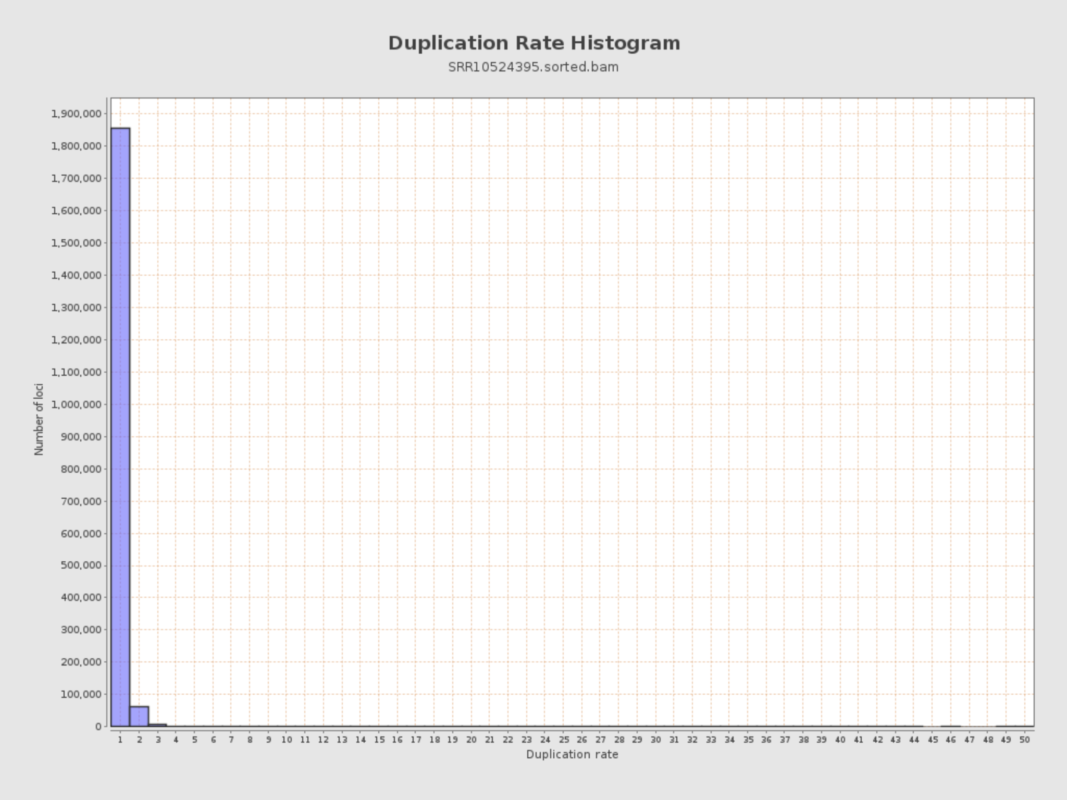
5. Results : Coverage Histogram (0-50X)



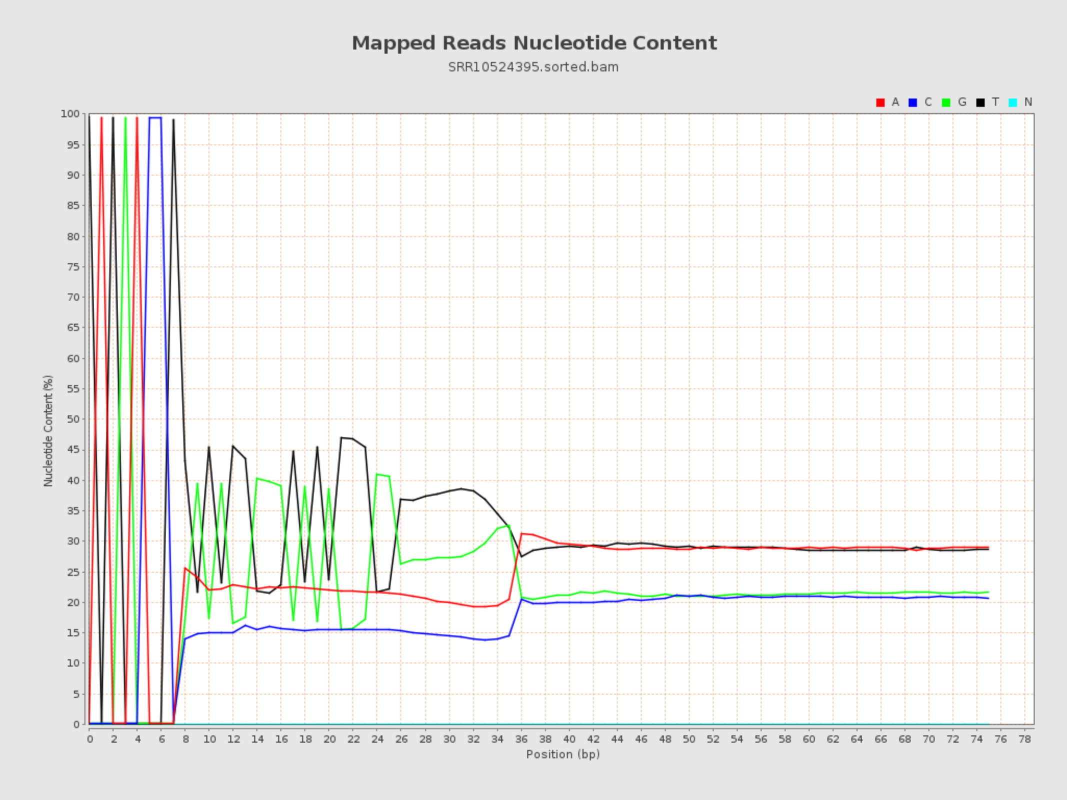
6. Results : Genome Fraction Coverage



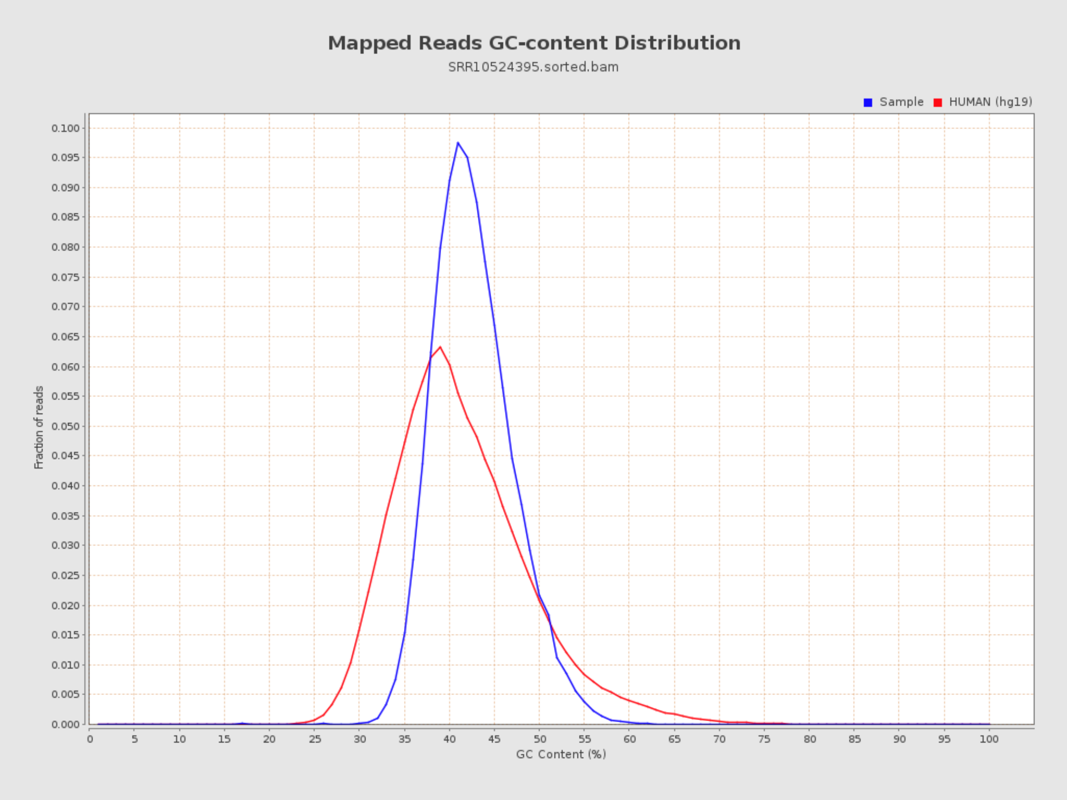
7. Results : Duplication Rate Histogram



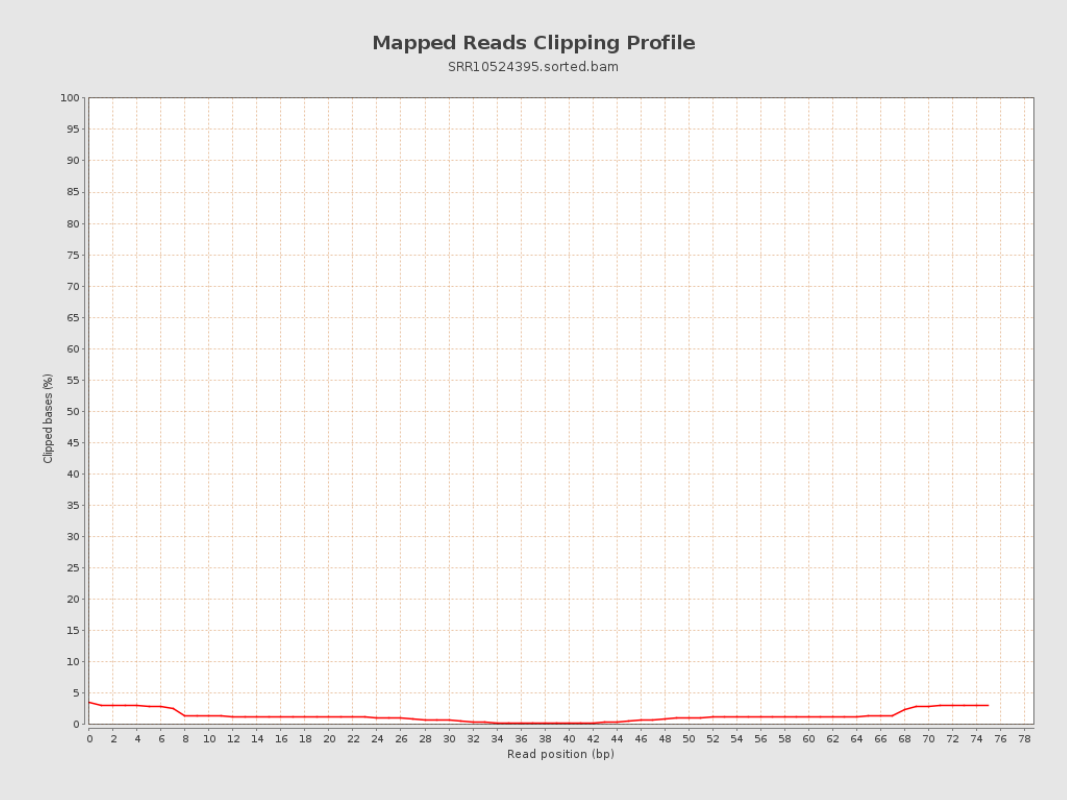
8. Results : Mapped Reads Nucleotide Content



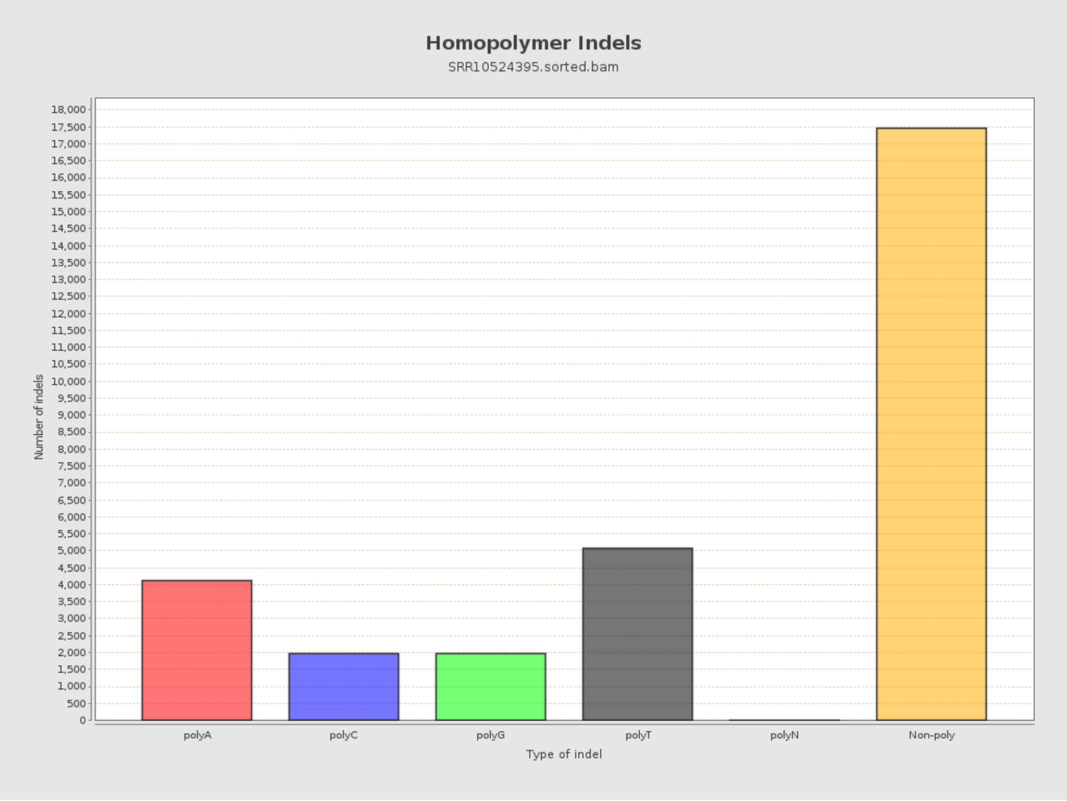
9. Results : Mapped Reads GC-content Distribution



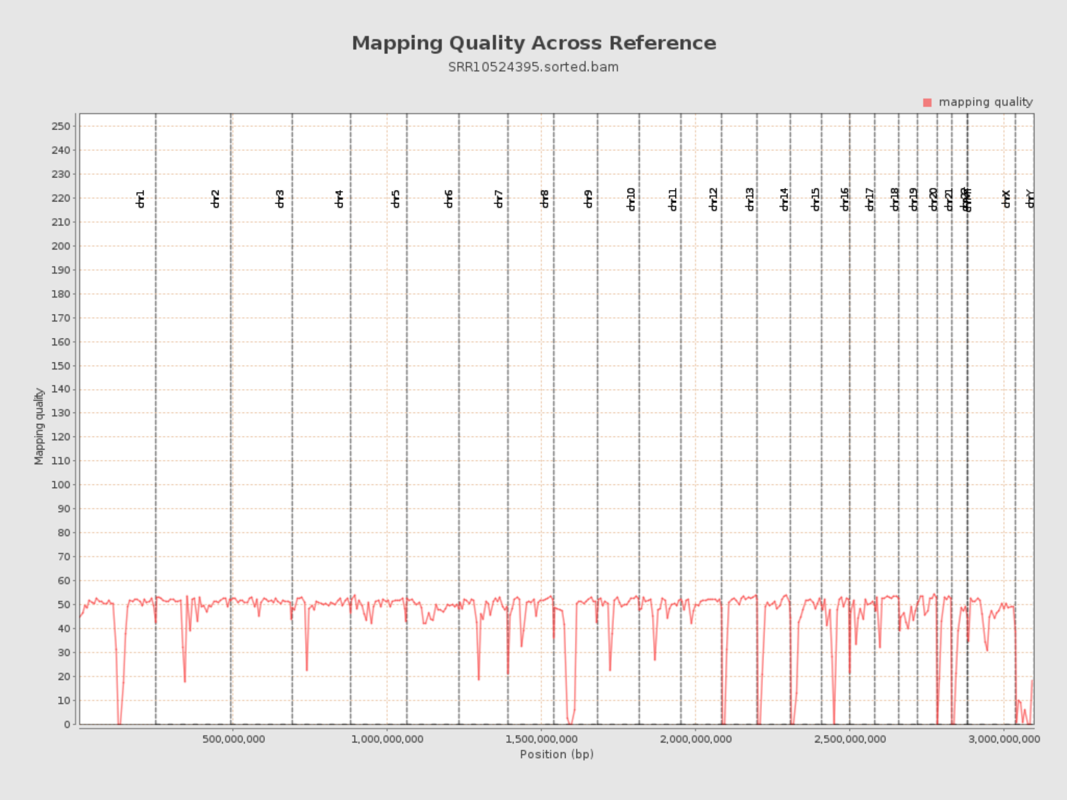
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram