Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:13:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081030.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_SRR3081030 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081030.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:13:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081030.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,131,038
Mapped reads	2,487,720 / 79.45%
Unmapped reads	643,318 / 20.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,114 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	104,451 / 3.34%
Duplication rate	3.5%
Clipped reads	1,553,364 / 49.61%

2.2. ACGT Content

Number/percentage of A's	43,851,605 / 28.63%
Number/percentage of C's	30,906,887 / 20.18%
Number/percentage of T's	44,724,803 / 29.2%
Number/percentage of G's	33,675,132 / 21.99%
Number/percentage of N's	1,960 / 0%
GC Percentage	42.17%

2.3. Coverage

Mean	0.0495

Standard Deviation	0.3319

2.4. Mapping Quality

Mean Mapping Quality	45.63

2.5. Mismatches and indels

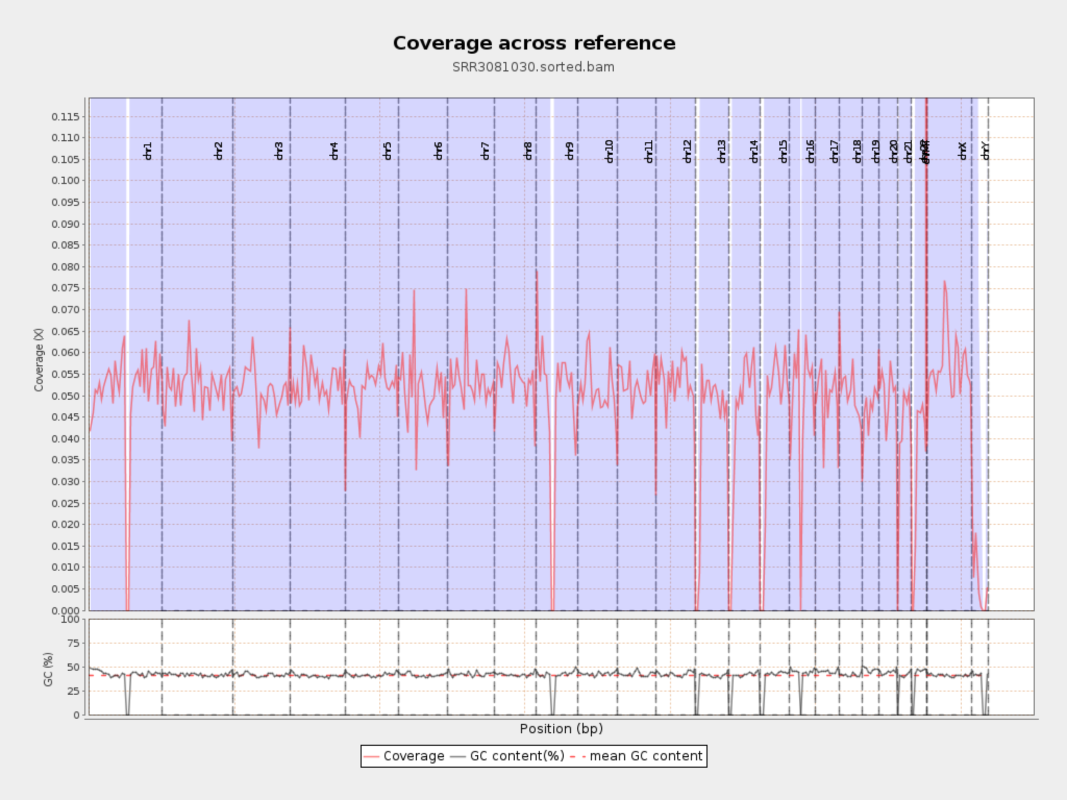
General error rate	0.74%
Mismatches	1,117,174
Insertions	10,194
Mapped reads with at least one insertion	0.41%
Deletions	29,635
Mapped reads with at least one deletion	1.18%
Homopolymer indels	45.94%

2.6. Chromosome stats

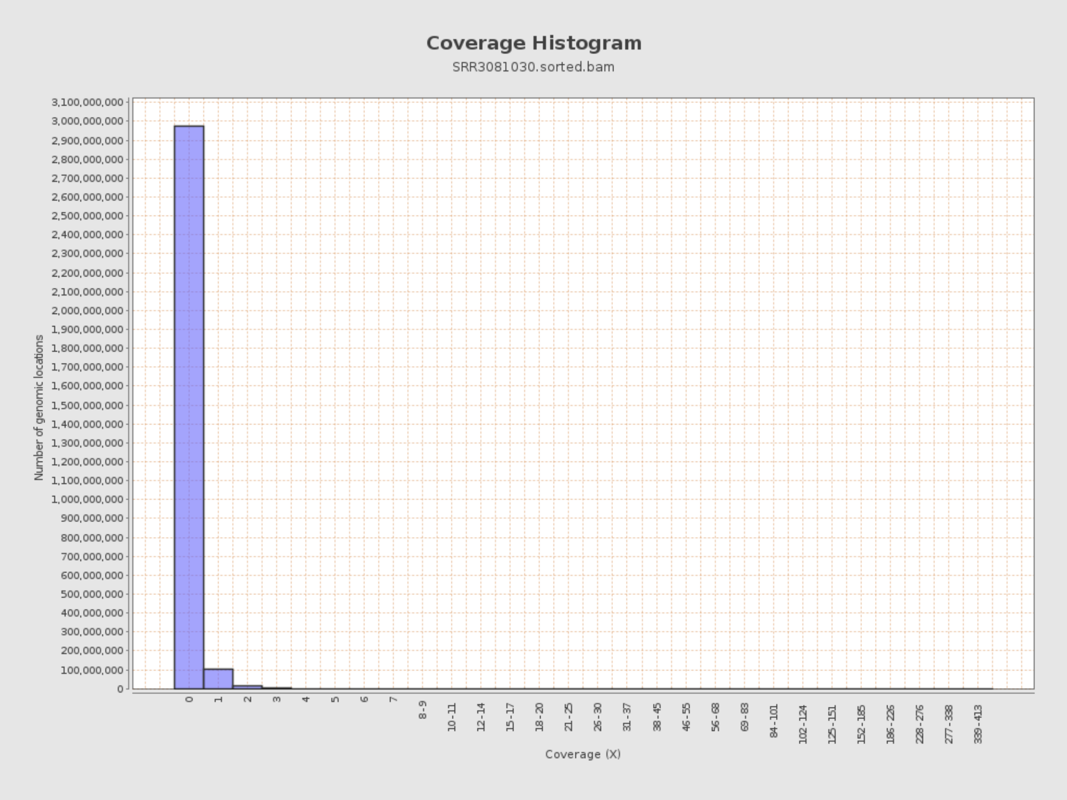
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12550284	0.0504	0.4282
chr2	243199373	12744249	0.0524	0.3815
chr3	198022430	10174075	0.0514	0.2724
chr4	191154276	10101311	0.0528	0.2887
chr5	180915260	9508645	0.0526	0.2768
chr6	171115067	8783814	0.0513	0.3365
chr7	159138663	8482606	0.0533	0.4768

chr8	146364022	7842557	0.0536	0.3549
chr9	141213431	6668401	0.0472	0.3152
chr10	135534747	7009769	0.0517	0.317
chr11	135006516	7045484	0.0522	0.3279
chr12	133851895	7179861	0.0536	0.283
chr13	115169878	4822424	0.0419	0.246
chr14	107349540	4626122	0.0431	0.2649
chr15	102531392	4511115	0.044	0.2633
chr16	90354753	4363282	0.0483	0.2792
chr17	81195210	3997364	0.0492	0.2845
chr18	78077248	3998263	0.0512	0.493
chr19	59128983	2795418	0.0473	0.3483
chr20	63025520	3172348	0.0503	0.2762
chr21	48129895	1956922	0.0407	0.2585
chr22	51304566	1612228	0.0314	0.2309
chrMT	16571	58856	3.5517	2.7816
chrX	155270560	8823856	0.0568	0.3094
chrY	59373566	382284	0.0064	0.1299

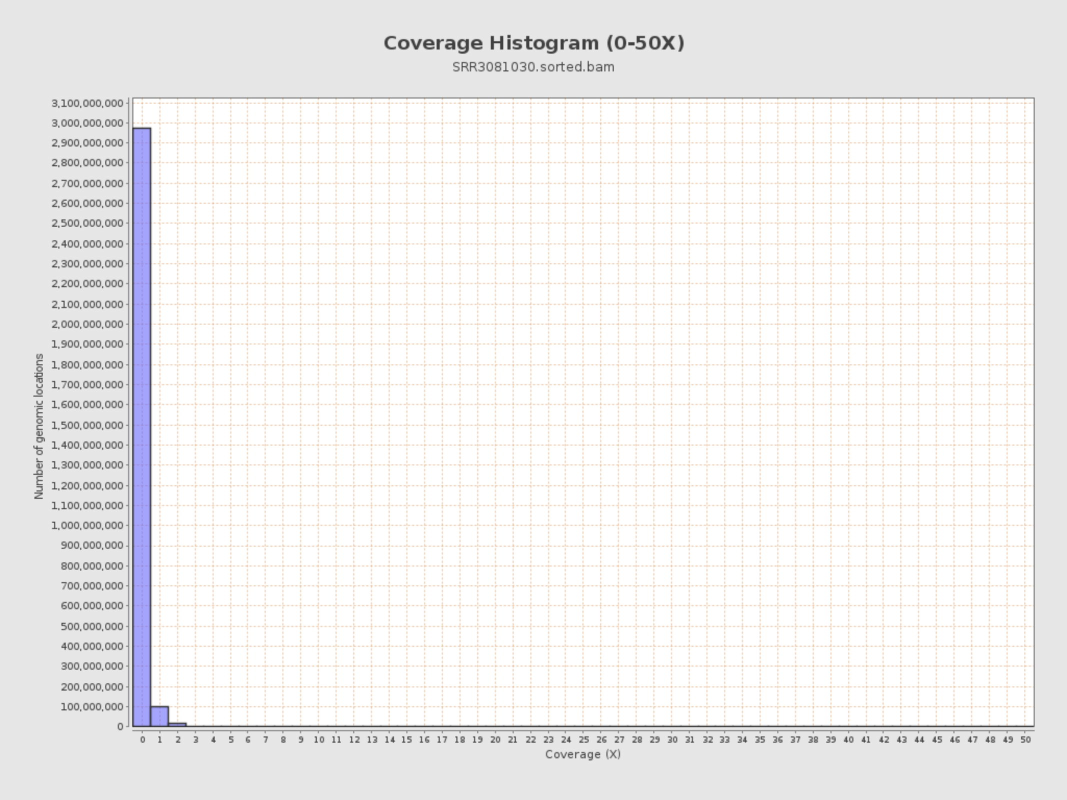
3. Results : Coverage across reference



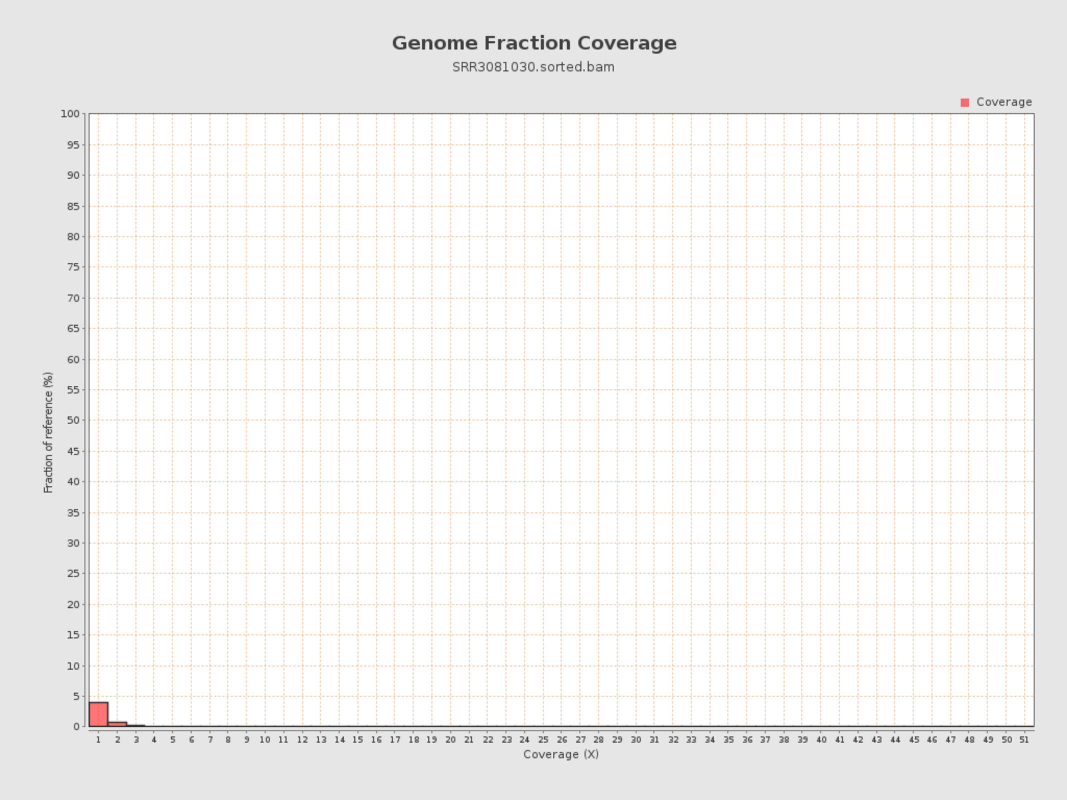
4. Results : Coverage Histogram



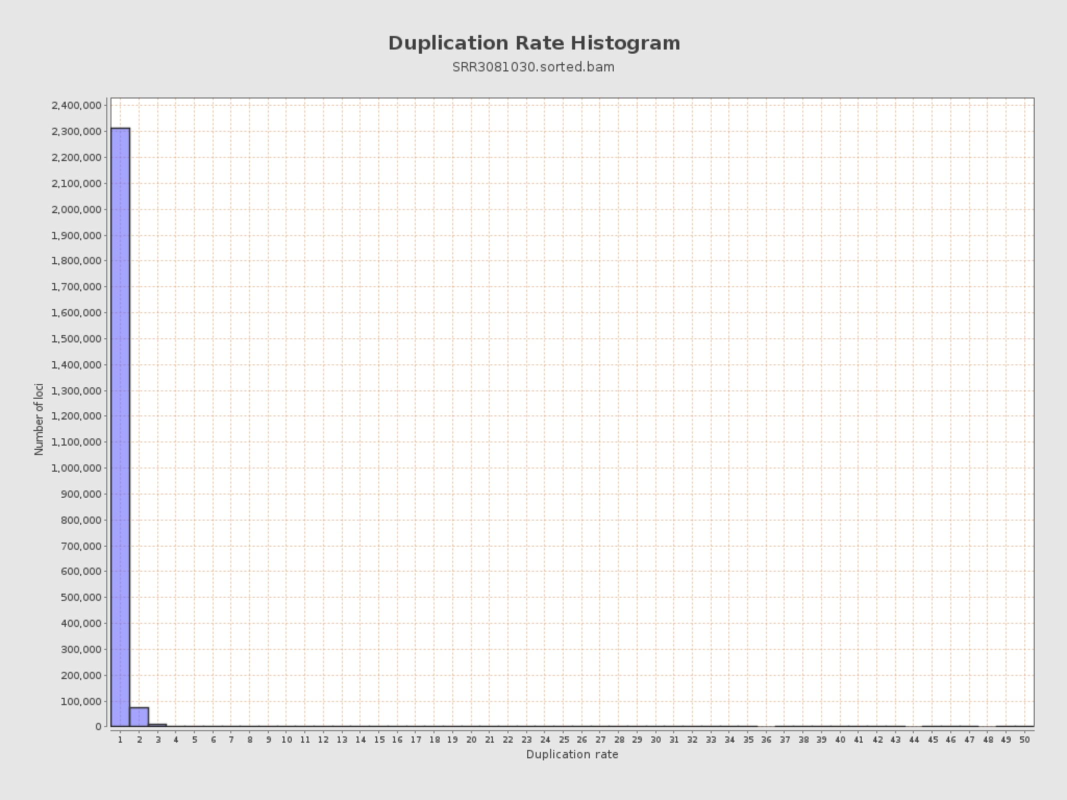
5. Results : Coverage Histogram (0-50X)



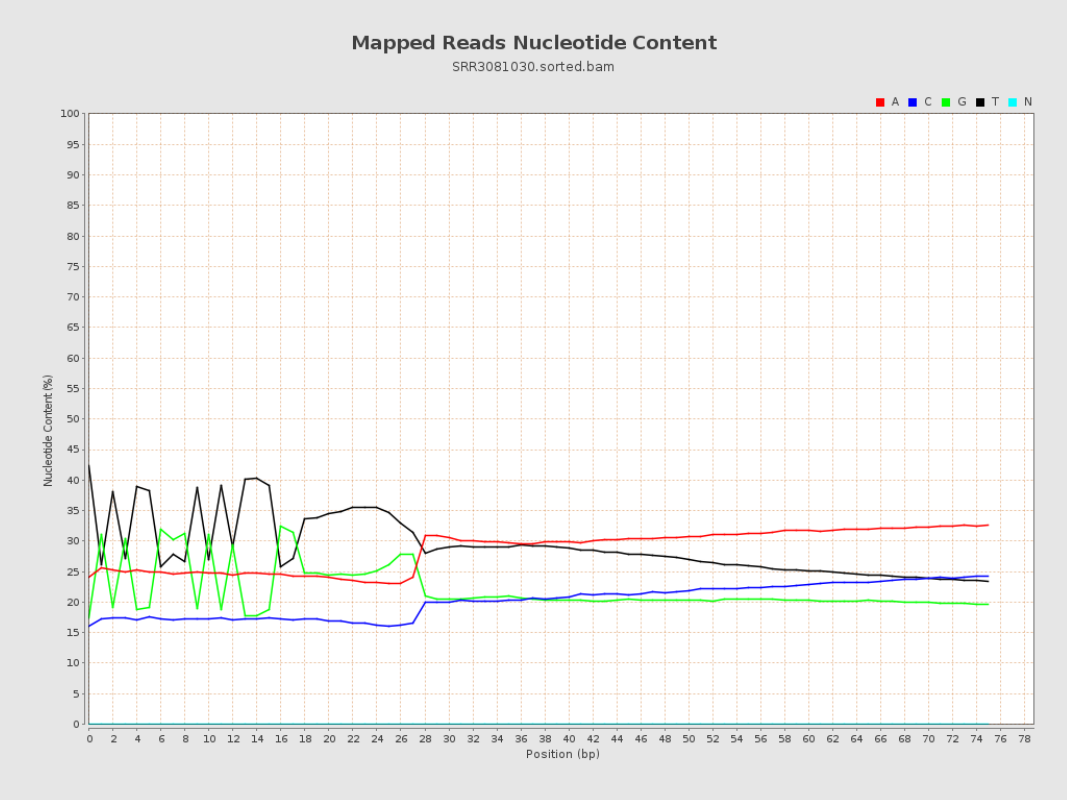
6. Results : Genome Fraction Coverage



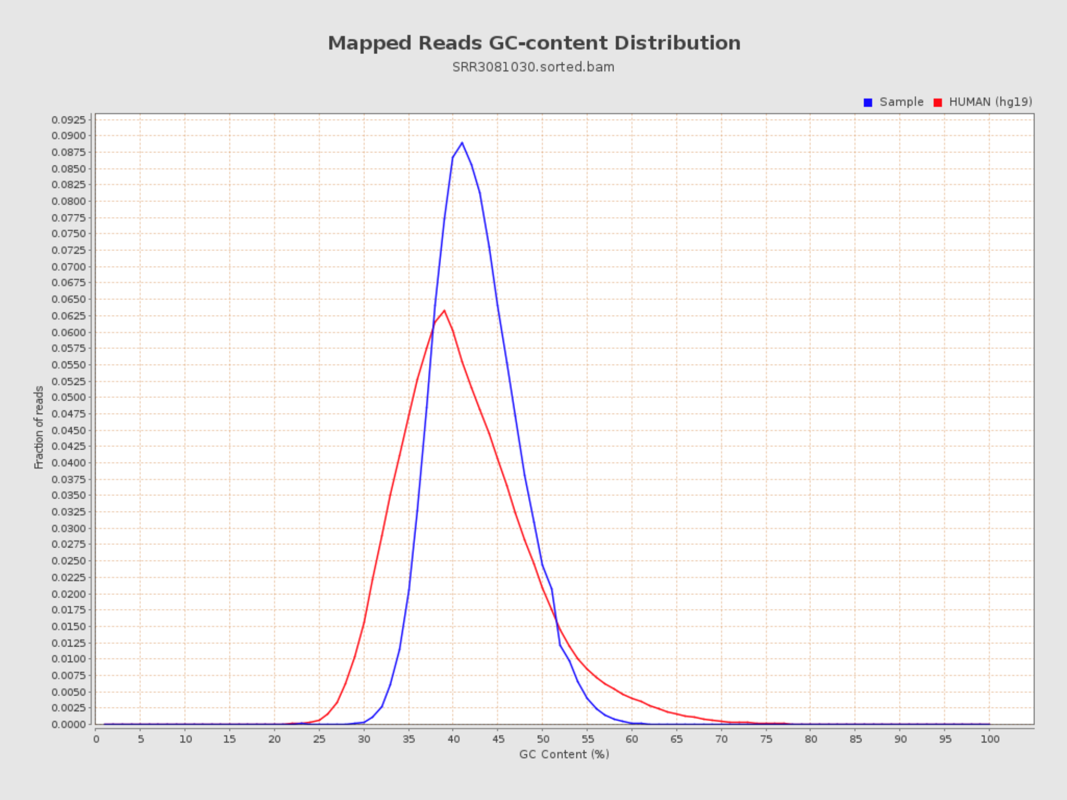
7. Results : Duplication Rate Histogram



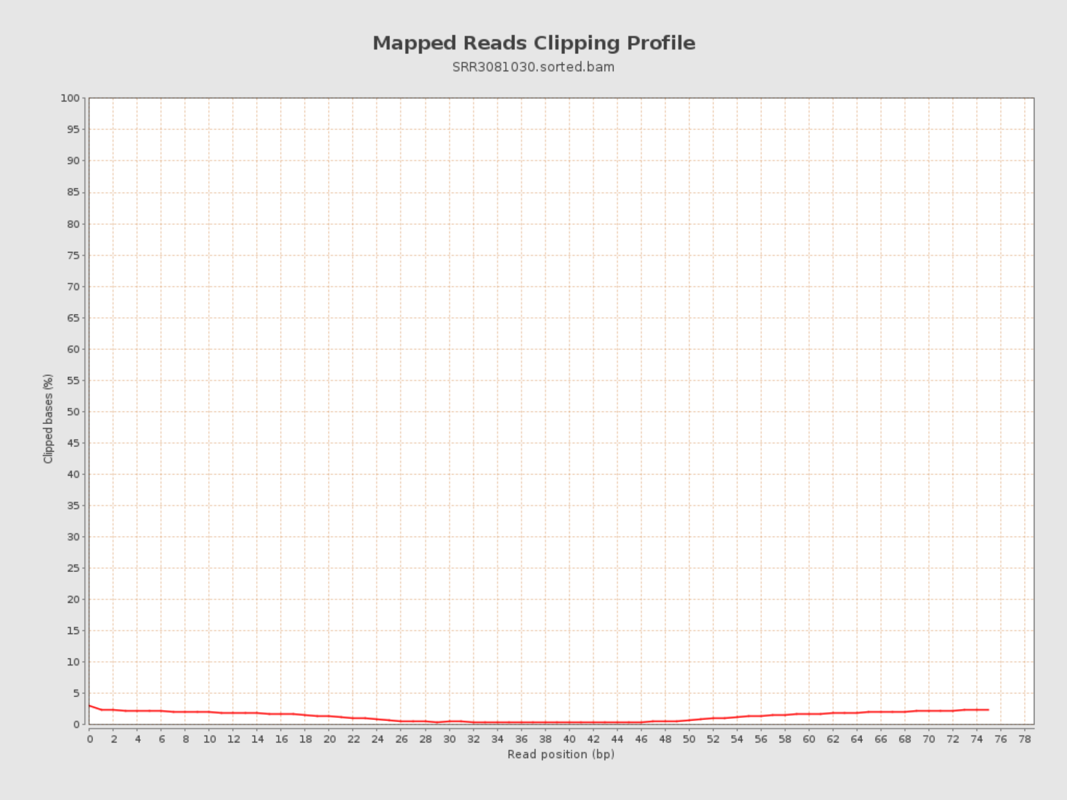
8. Results : Mapped Reads Nucleotide Content



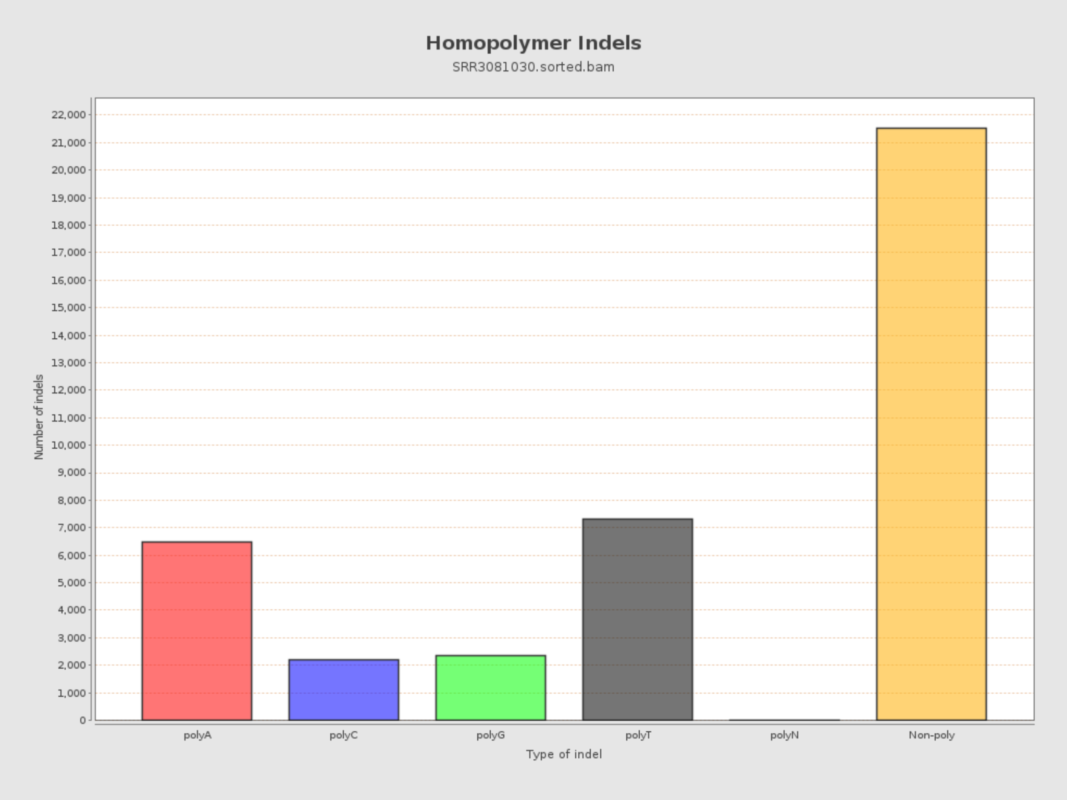
9. Results : Mapped Reads GC-content Distribution



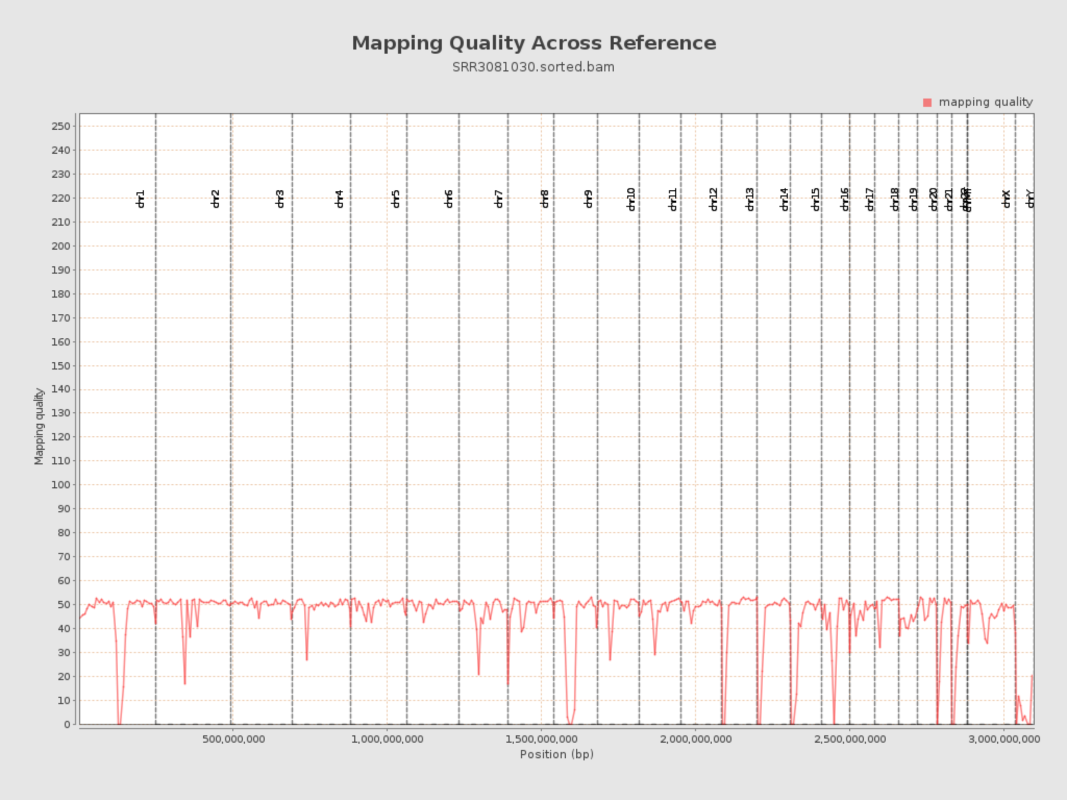
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram