Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 09:18:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081910.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_SRR3081910 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081910.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 09:18:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081910.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,366,156
Mapped reads	2,198,729 / 92.92%
Unmapped reads	167,427 / 7.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,938 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	75,352 / 3.18%
Duplication rate	2.77%
Clipped reads	813,454 / 34.38%

2.2. ACGT Content

Number/percentage of A's	42,370,685 / 28.12%
Number/percentage of C's	28,458,906 / 18.89%
Number/percentage of T's	46,950,789 / 31.16%
Number/percentage of G's	32,896,235 / 21.83%
Number/percentage of N's	1,748 / 0%
GC Percentage	40.72%

2.3. Coverage

Mean	0.0487

Standard Deviation	0.3429

2.4. Mapping Quality

Mean Mapping Quality	46.66

2.5. Mismatches and indels

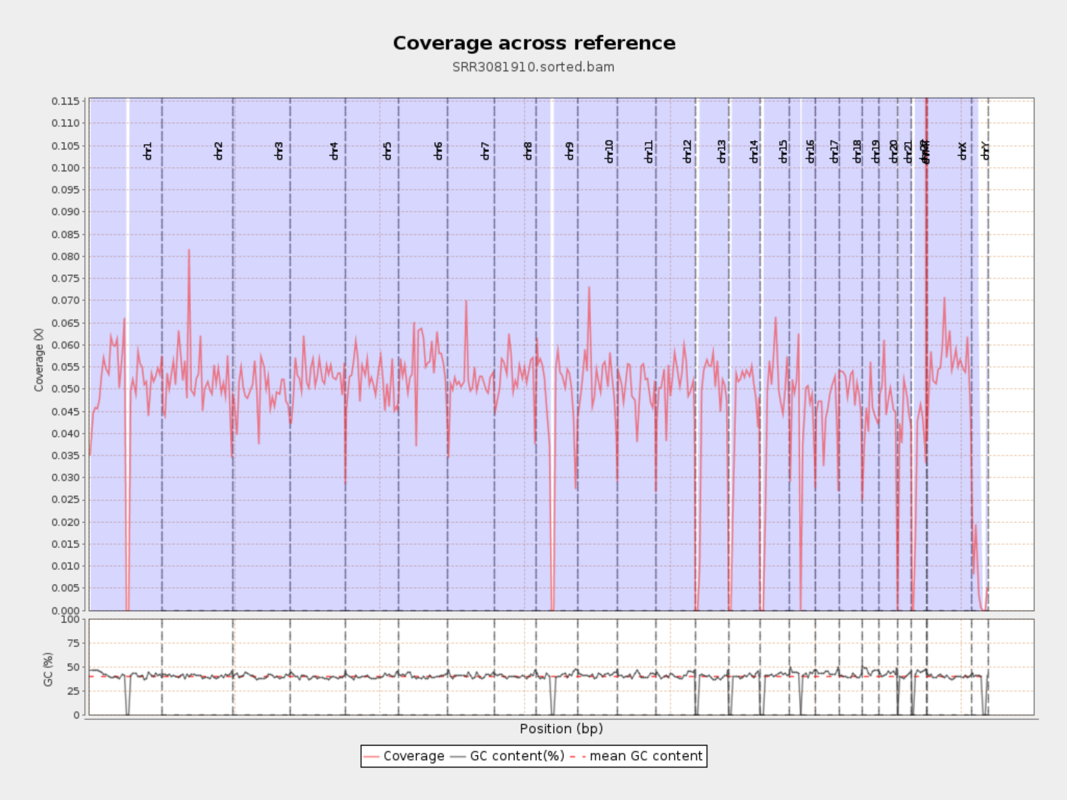
General error rate	0.82%
Mismatches	1,218,231
Insertions	11,702
Mapped reads with at least one insertion	0.53%
Deletions	32,464
Mapped reads with at least one deletion	1.46%
Homopolymer indels	47.32%

2.6. Chromosome stats

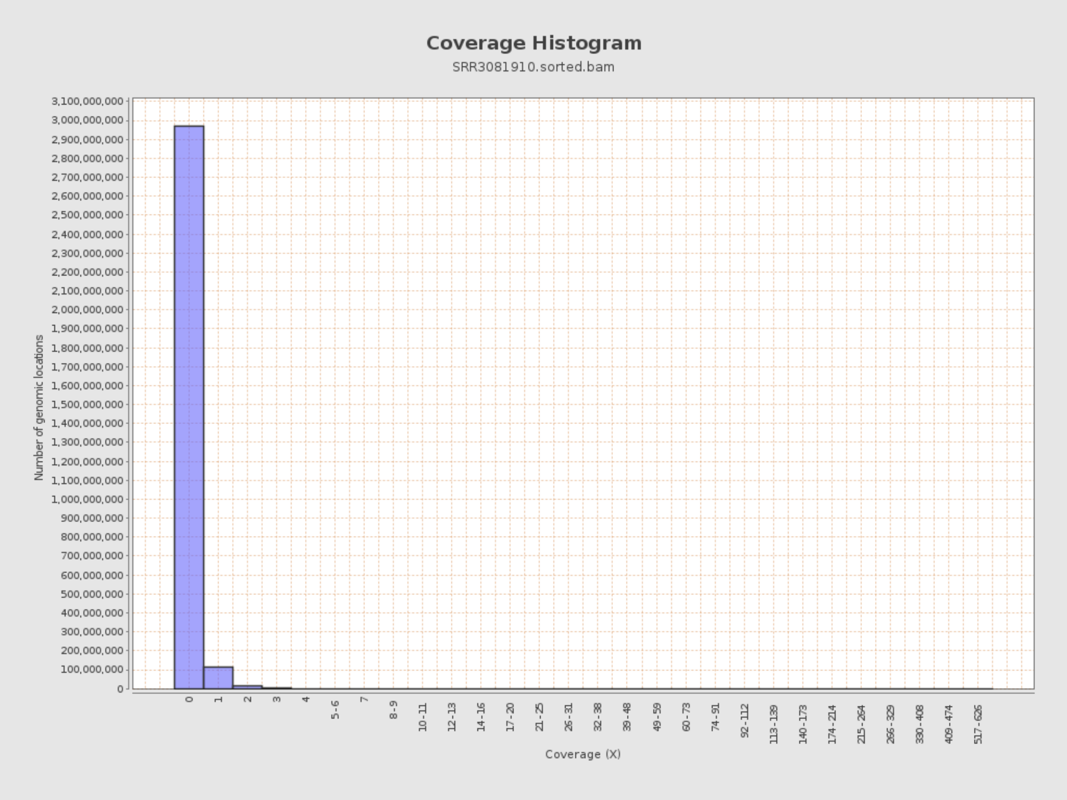
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12384680	0.0497	0.4721
chr2	243199373	12791160	0.0526	0.4227
chr3	198022430	9789935	0.0494	0.2541
chr4	191154276	10133151	0.053	0.2753
chr5	180915260	9384520	0.0519	0.2607
chr6	171115067	9526818	0.0557	0.3021
chr7	159138663	8260896	0.0519	0.4177

chr8	146364022	7731621	0.0528	0.4704
chr9	141213431	6333556	0.0449	0.3416
chr10	135534747	7154849	0.0528	0.3574
chr11	135006516	6721534	0.0498	0.3166
chr12	133851895	6880402	0.0514	0.2603
chr13	115169878	5016284	0.0436	0.2381
chr14	107349540	4620315	0.043	0.2493
chr15	102531392	4382515	0.0427	0.2391
chr16	90354753	3911697	0.0433	0.2652
chr17	81195210	3602521	0.0444	0.2573
chr18	78077248	3991775	0.0511	0.598
chr19	59128983	2576545	0.0436	0.4246
chr20	63025520	3013806	0.0478	0.2571
chr21	48129895	1944378	0.0404	0.2466
chr22	51304566	1512327	0.0295	0.1936
chrMT	16571	49867	3.0093	2.5131
chrX	155270560	8641578	0.0557	0.2917
chrY	59373566	375649	0.0063	0.1378

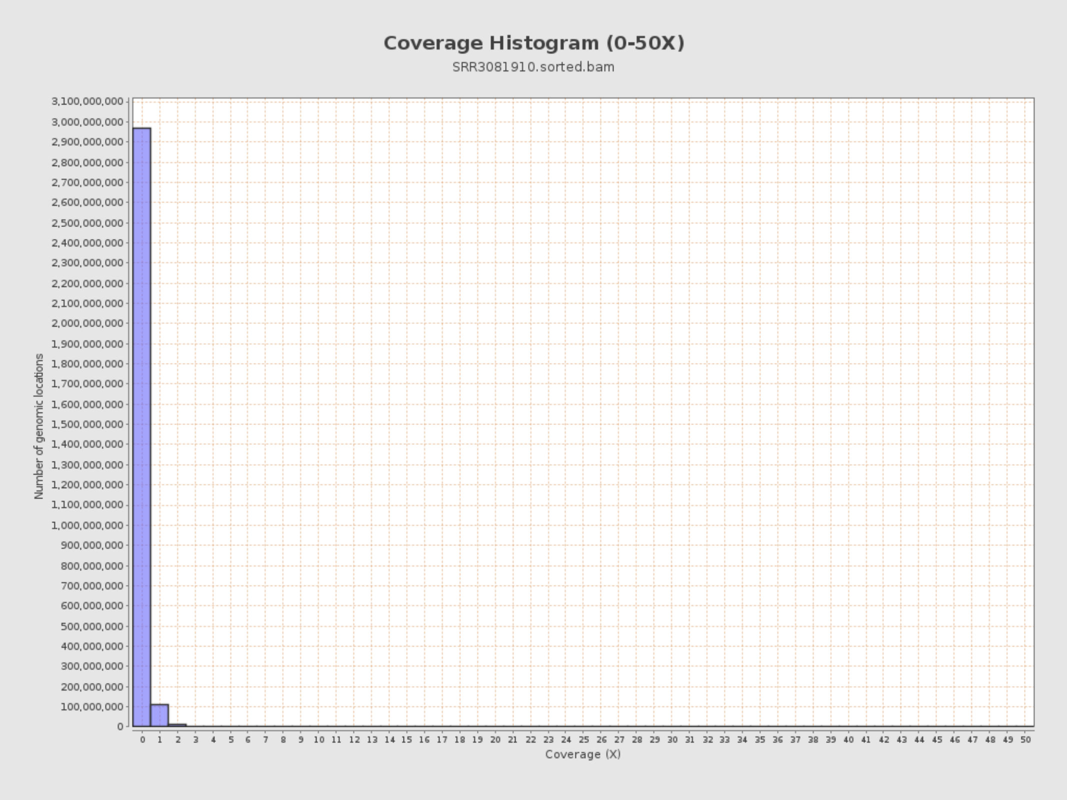
3. Results : Coverage across reference



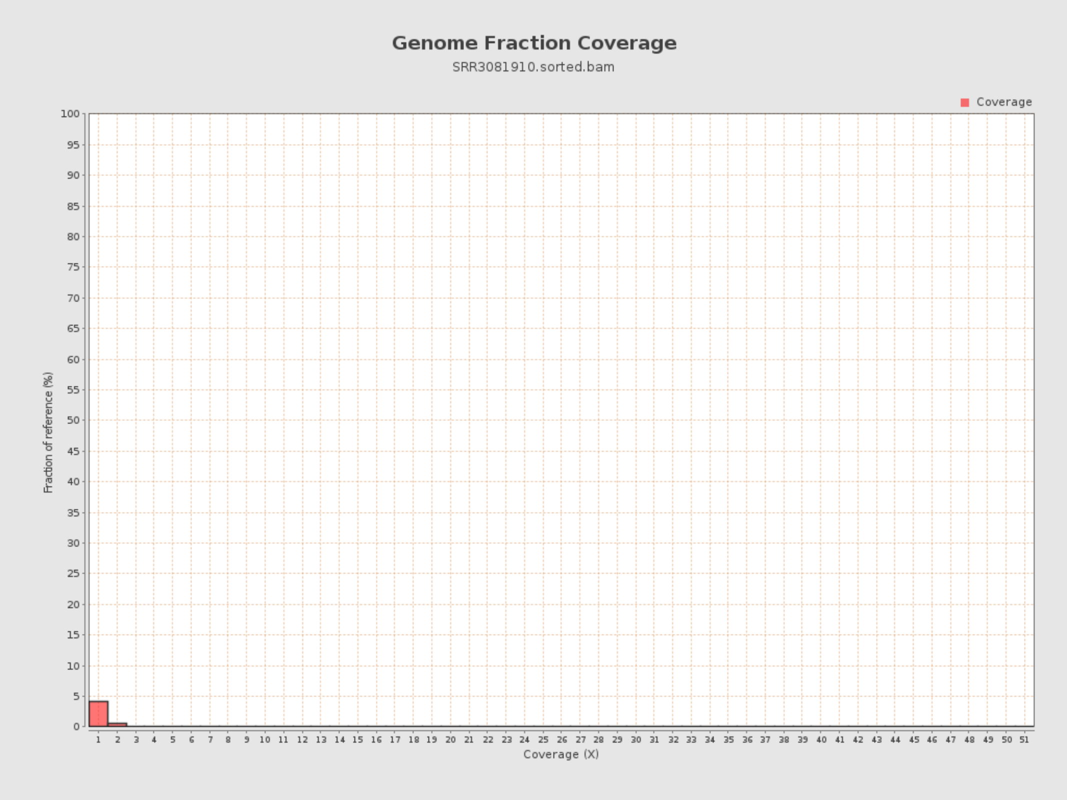
4. Results : Coverage Histogram



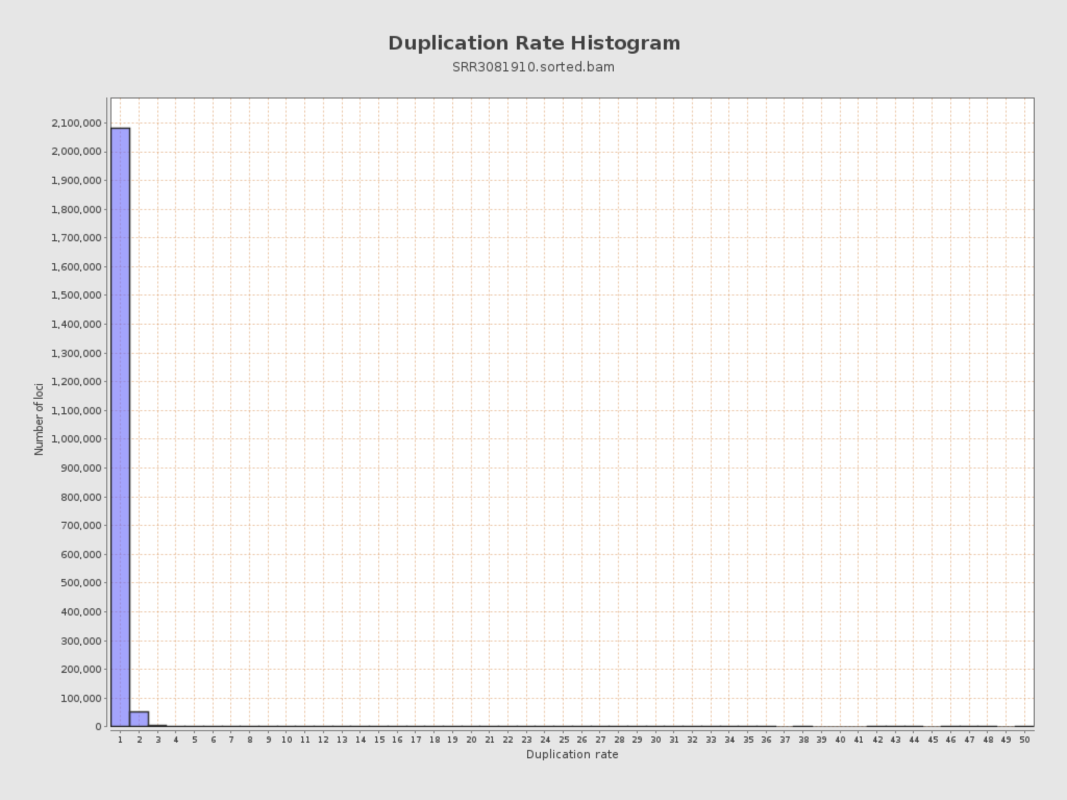
5. Results : Coverage Histogram (0-50X)



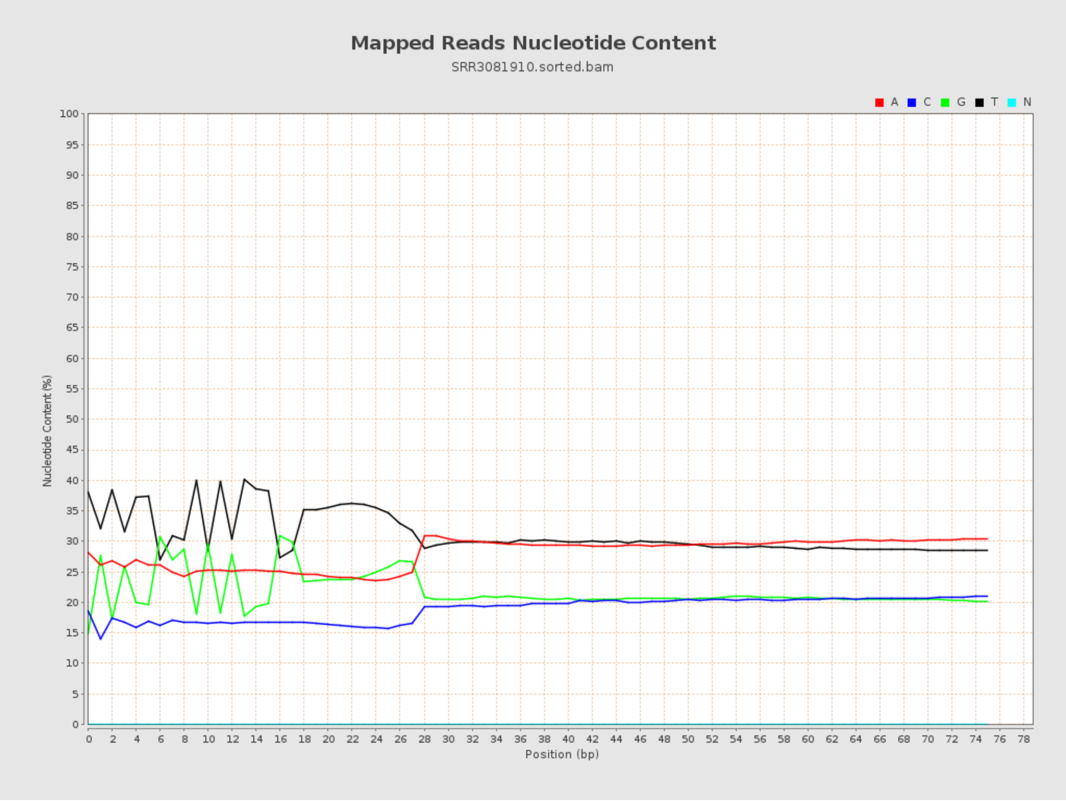
6. Results : Genome Fraction Coverage



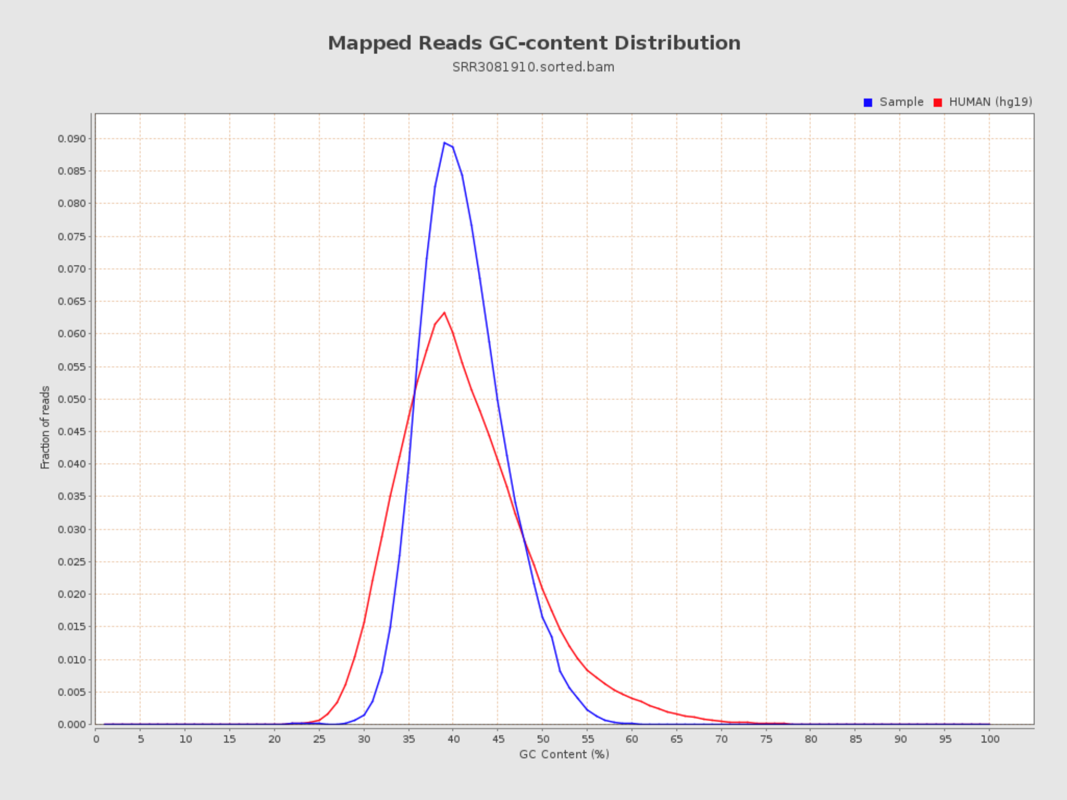
7. Results : Duplication Rate Histogram



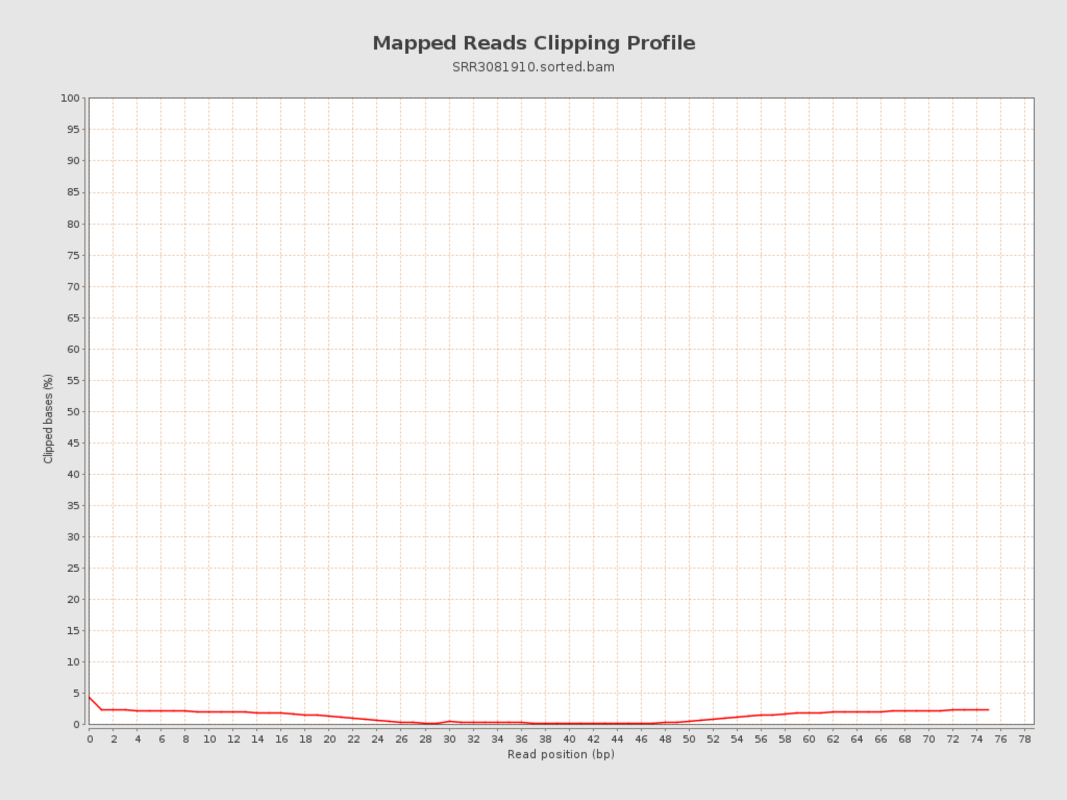
8. Results : Mapped Reads Nucleotide Content



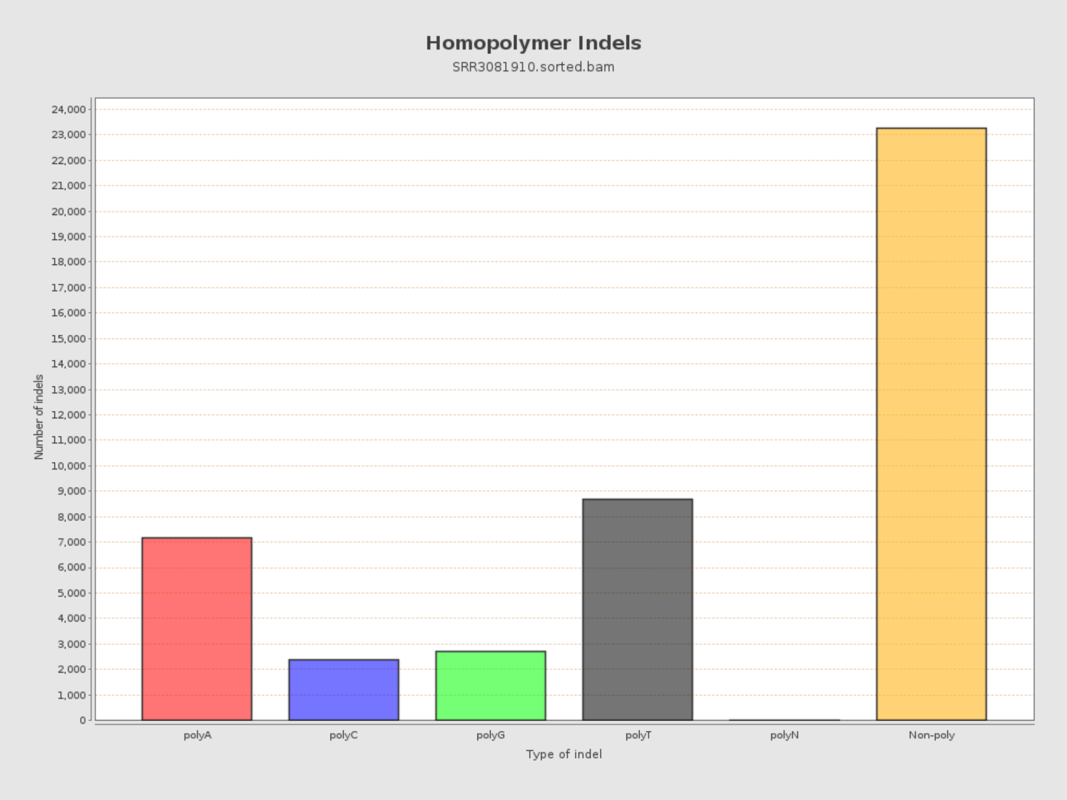
9. Results : Mapped Reads GC-content Distribution



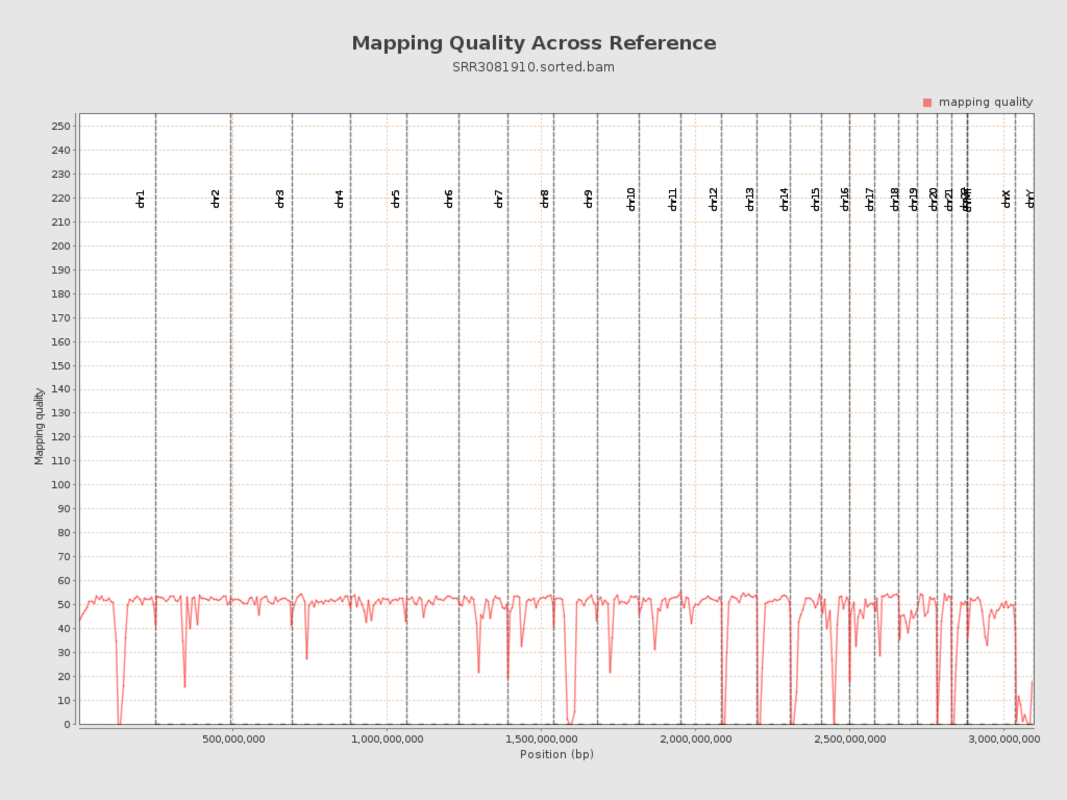
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram