Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 03:03:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081216.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_SRR3081216 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081216.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 03:03:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081216.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,739,945
Mapped reads	2,384,153 / 87.01%
Unmapped reads	355,792 / 12.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,606 / 0.97%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	99,637 / 3.64%
Duplication rate	3.43%
Clipped reads	1,427,542 / 52.1%

2.2. ACGT Content

Number/percentage of A's	43,629,985 / 28.88%
Number/percentage of C's	29,712,734 / 19.66%
Number/percentage of T's	45,345,744 / 30.01%
Number/percentage of G's	32,387,986 / 21.44%
Number/percentage of N's	19,311 / 0.01%
GC Percentage	41.1%

2.3. Coverage

Mean	0.0488

Standard Deviation	0.3562

2.4. Mapping Quality

Mean Mapping Quality	44.31

2.5. Mismatches and indels

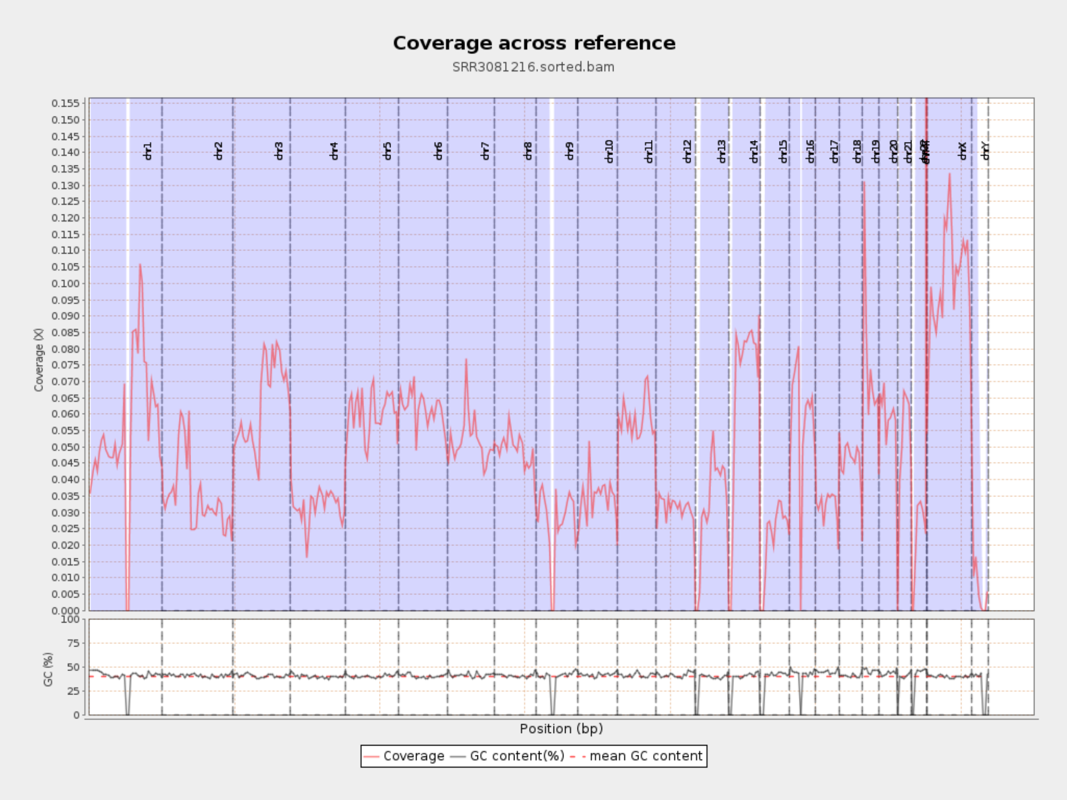
General error rate	0.91%
Mismatches	1,363,666
Insertions	11,179
Mapped reads with at least one insertion	0.46%
Deletions	32,741
Mapped reads with at least one deletion	1.36%
Homopolymer indels	46.73%

2.6. Chromosome stats

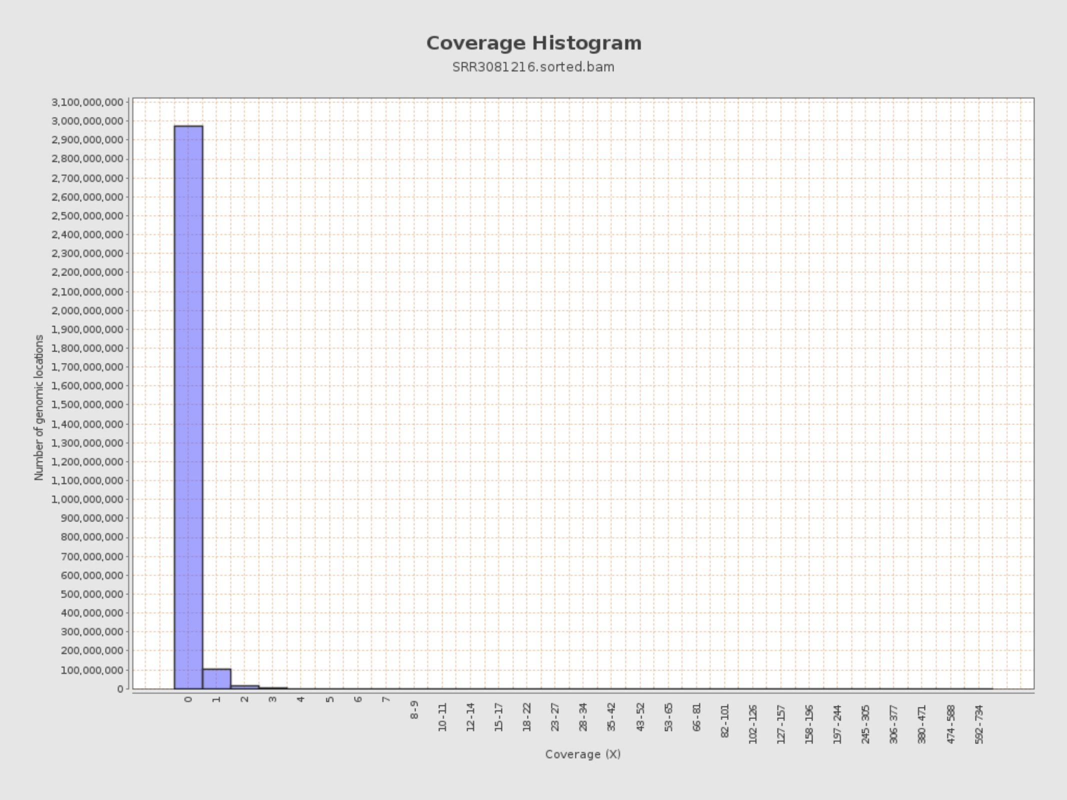
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13992591	0.0561	0.6332
chr2	243199373	8597038	0.0353	0.3783
chr3	198022430	12432079	0.0628	0.2973
chr4	191154276	6099430	0.0319	0.213
chr5	180915260	10940860	0.0605	0.2906
chr6	171115067	10542252	0.0616	0.3294
chr7	159138663	8308871	0.0522	0.4412

chr8	146364022	7181953	0.0491	0.3656
chr9	141213431	3830544	0.0271	0.2591
chr10	135534747	4724615	0.0349	0.3121
chr11	135006516	7808044	0.0578	0.3635
chr12	133851895	4189369	0.0313	0.2095
chr13	115169878	3711672	0.0322	0.2105
chr14	107349540	7200866	0.0671	0.3101
chr15	102531392	2302428	0.0225	0.1914
chr16	90354753	5330876	0.059	0.2994
chr17	81195210	2581480	0.0318	0.2248
chr18	78077248	3643327	0.0467	0.4394
chr19	59128983	4359545	0.0737	0.5433
chr20	63025520	3738833	0.0593	0.2874
chr21	48129895	2412350	0.0501	0.2733
chr22	51304566	1118625	0.0218	0.1708
chrMT	16571	33331	2.0114	2.0707
chrX	155270560	15617934	0.1006	0.3986
chrY	59373566	449783	0.0076	0.1189

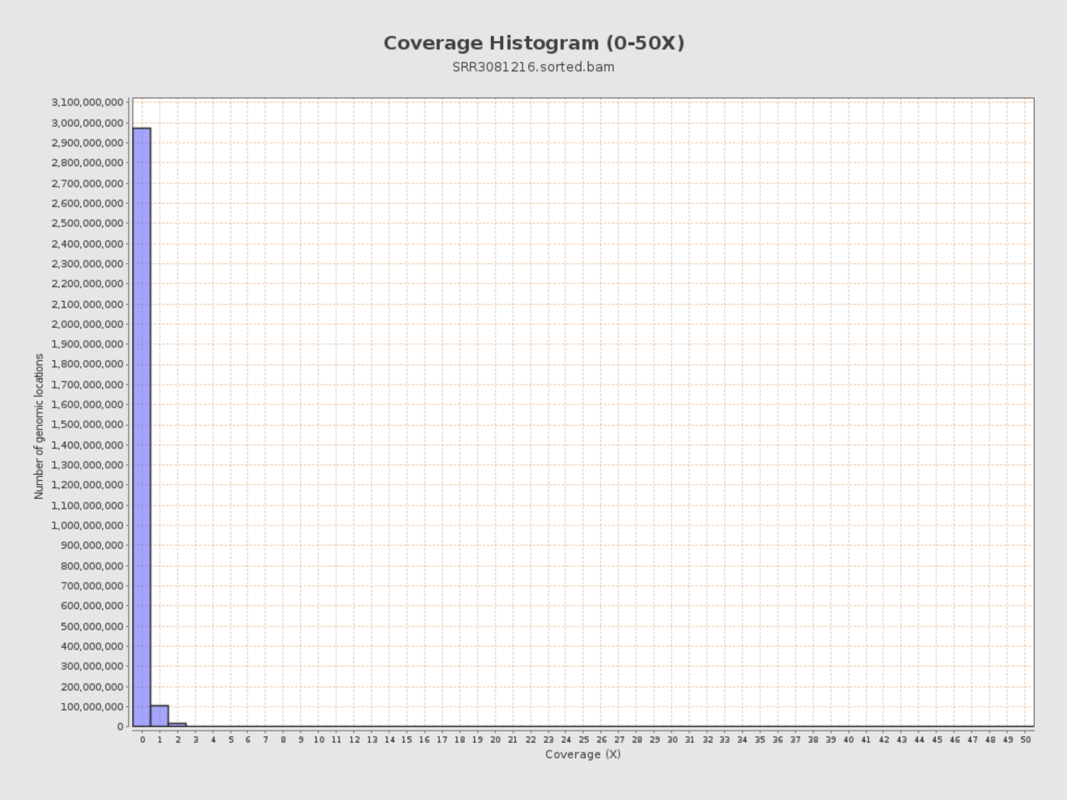
3. Results : Coverage across reference



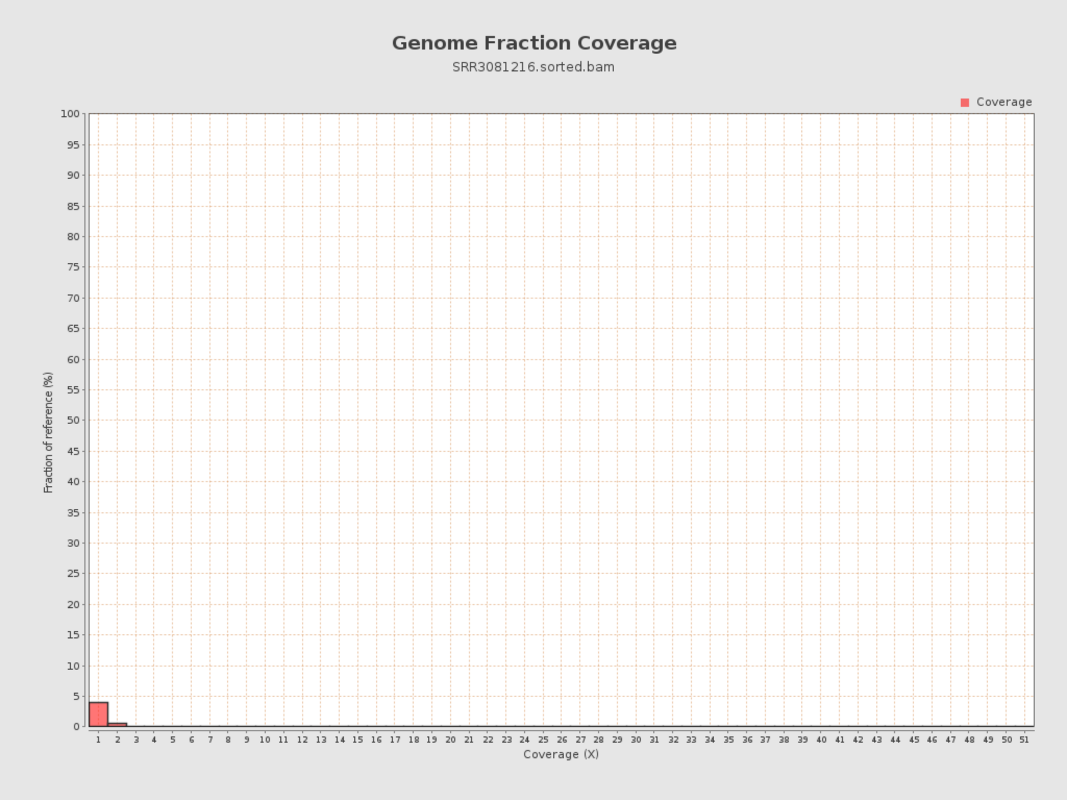
4. Results : Coverage Histogram



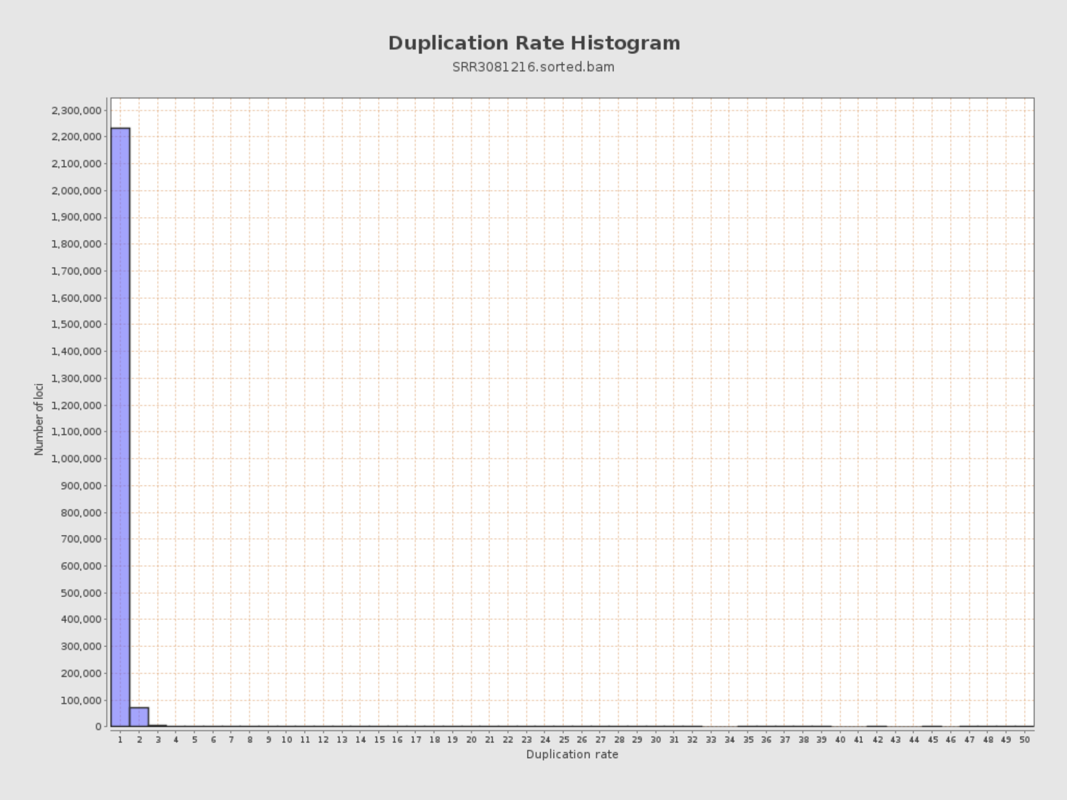
5. Results : Coverage Histogram (0-50X)



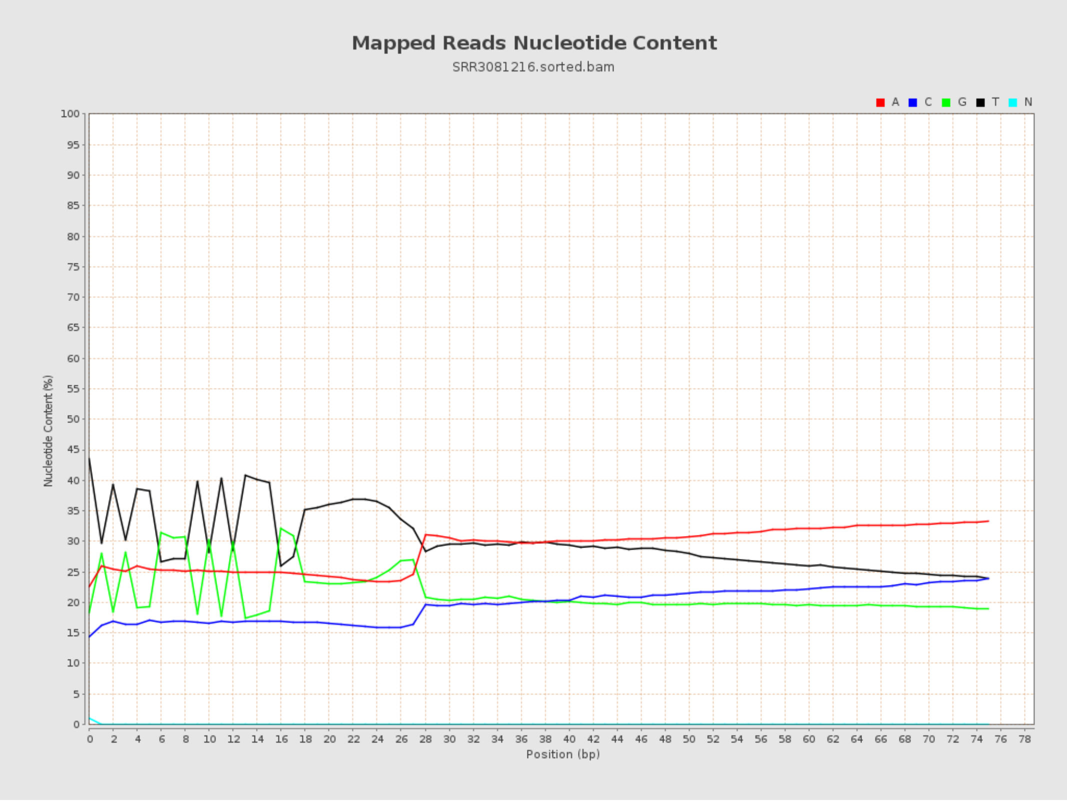
6. Results : Genome Fraction Coverage



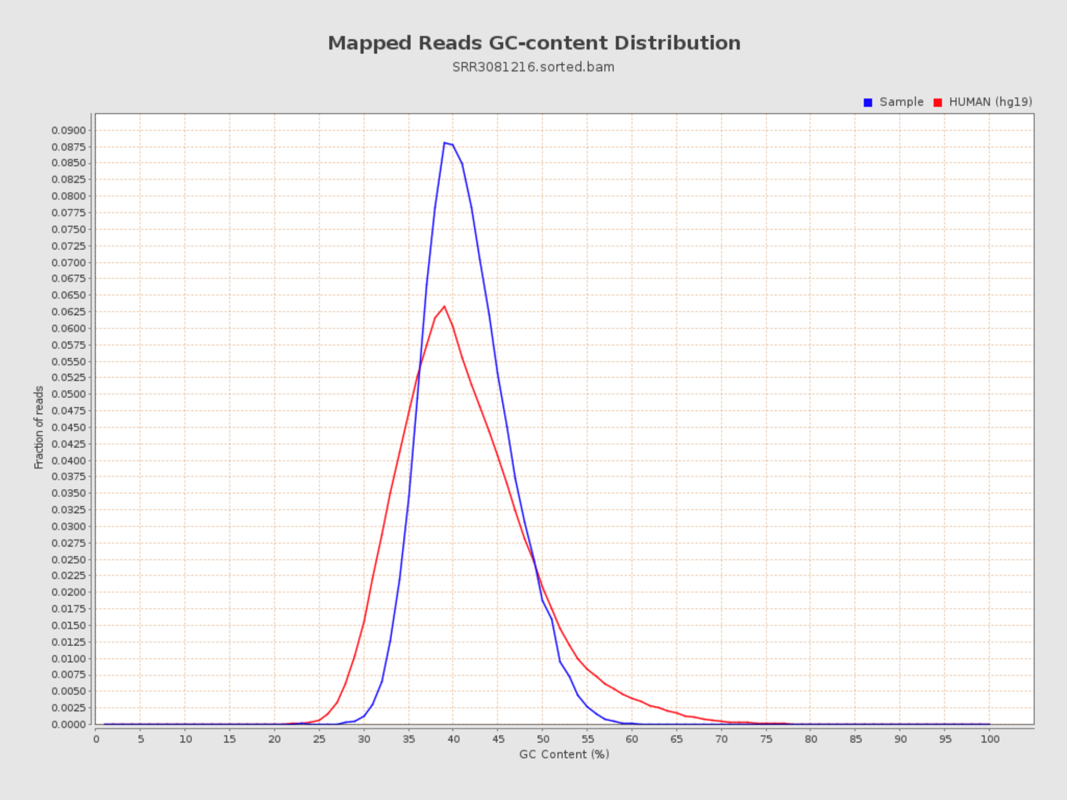
7. Results : Duplication Rate Histogram



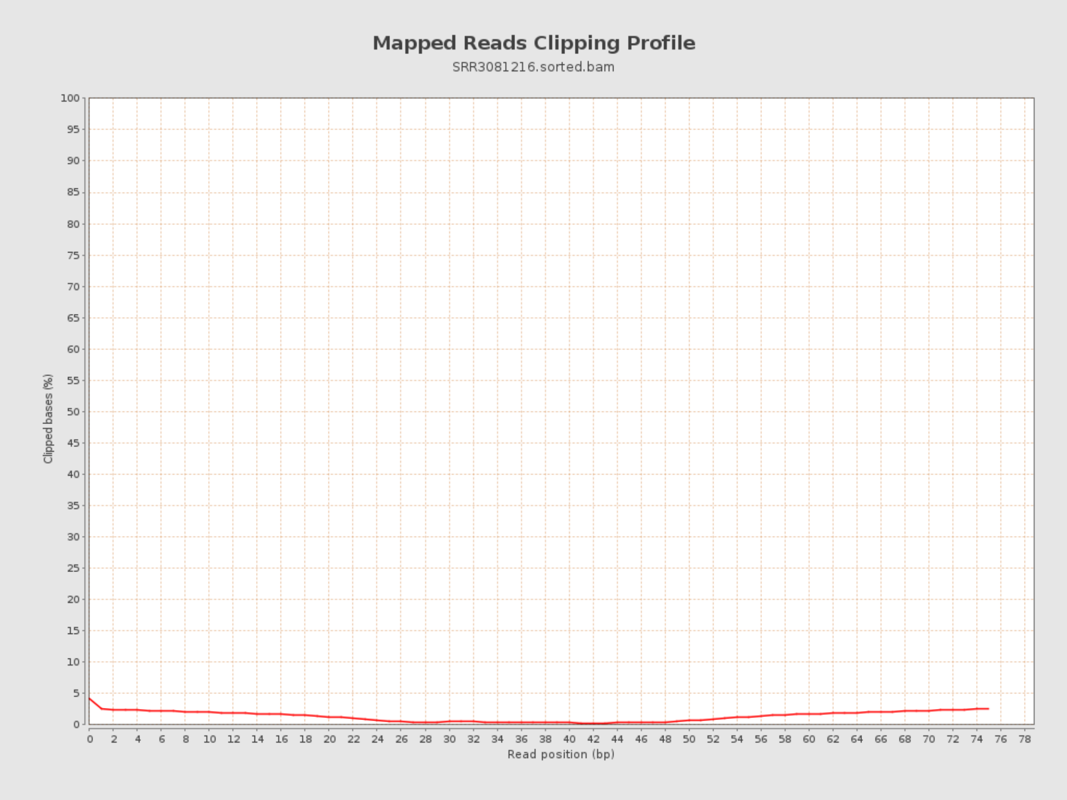
8. Results : Mapped Reads Nucleotide Content



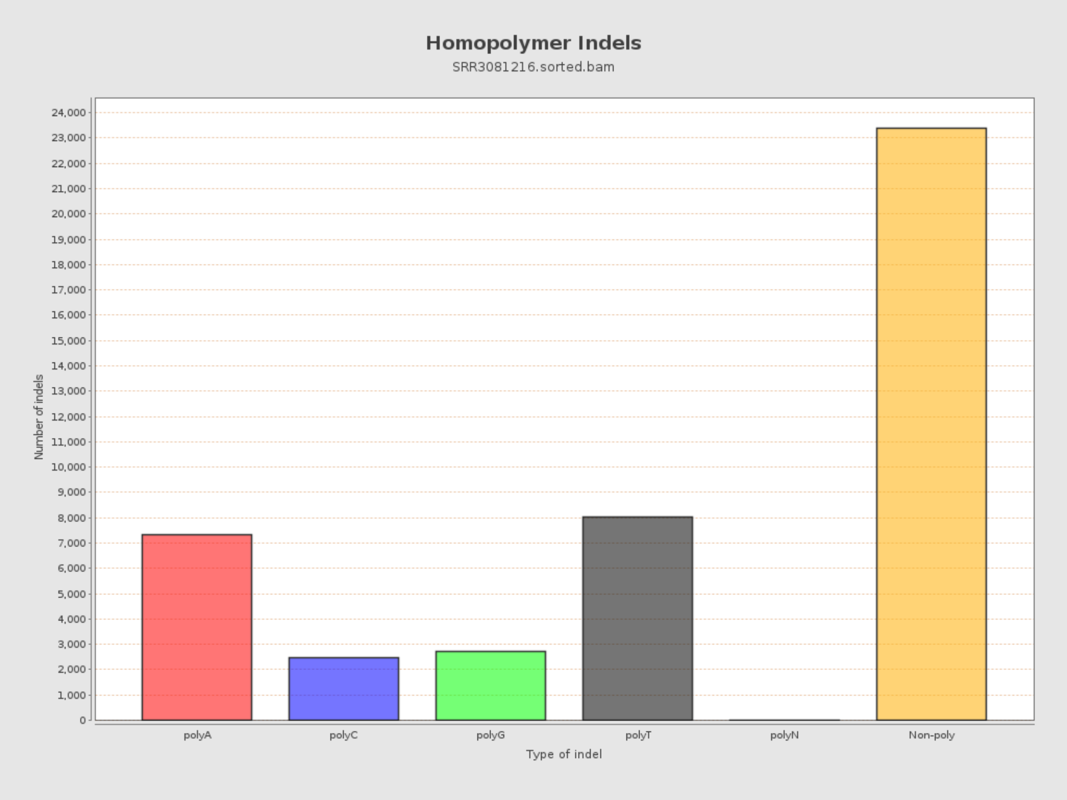
9. Results : Mapped Reads GC-content Distribution



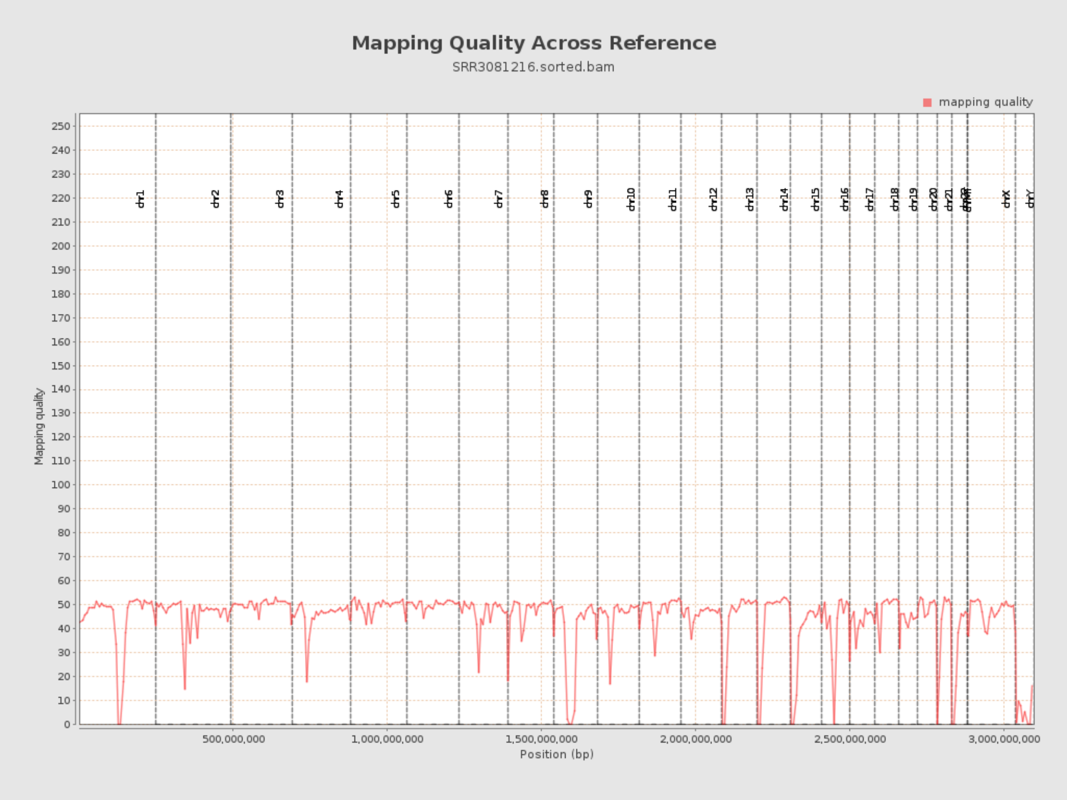
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram