Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 10:45:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081938.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_SRR3081938 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081938.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 10:45:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081938.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,508,881
Mapped reads	2,287,361 / 91.17%
Unmapped reads	221,520 / 8.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,111 / 0.56%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	119,914 / 4.78%
Duplication rate	3.92%
Clipped reads	912,011 / 36.35%

2.2. ACGT Content

Number/percentage of A's	43,252,656 / 28%
Number/percentage of C's	28,298,333 / 18.32%
Number/percentage of T's	49,105,039 / 31.79%
Number/percentage of G's	33,803,722 / 21.88%
Number/percentage of N's	19,322 / 0.01%
GC Percentage	40.2%

2.3. Coverage

Mean	0.0499

Standard Deviation	0.491

2.4. Mapping Quality

Mean Mapping Quality	46.02

2.5. Mismatches and indels

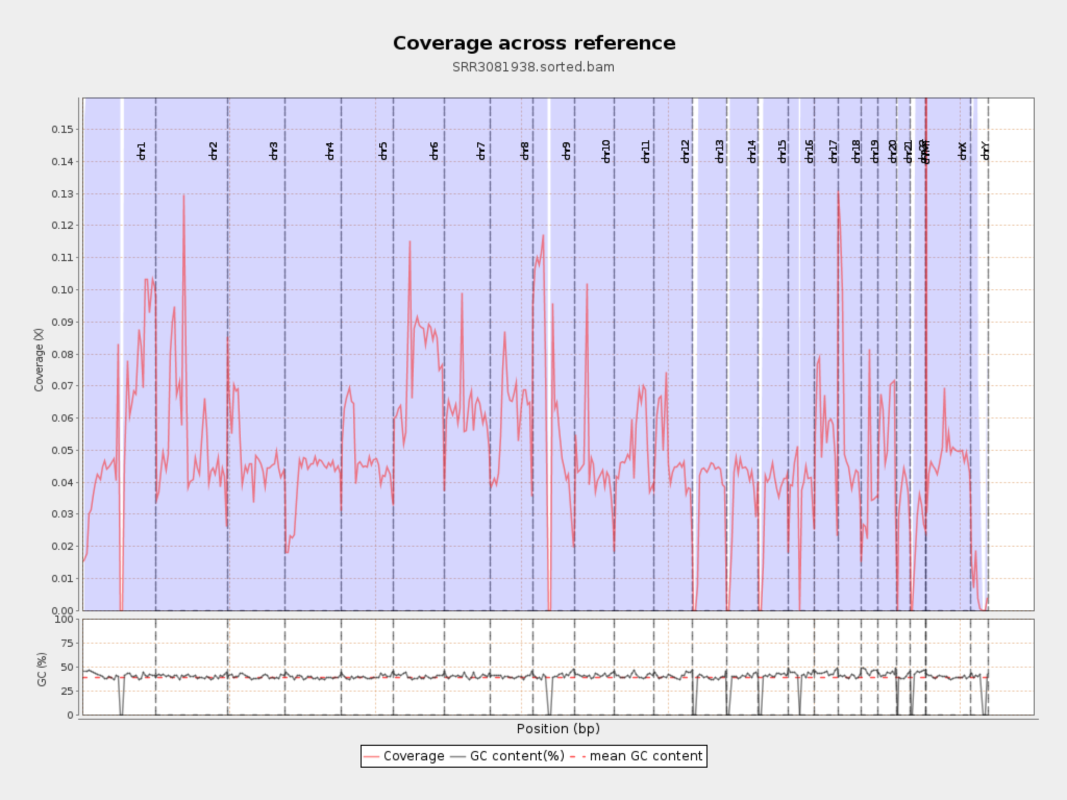
General error rate	0.78%
Mismatches	1,183,425
Insertions	10,801
Mapped reads with at least one insertion	0.47%
Deletions	30,896
Mapped reads with at least one deletion	1.34%
Homopolymer indels	48.02%

2.6. Chromosome stats

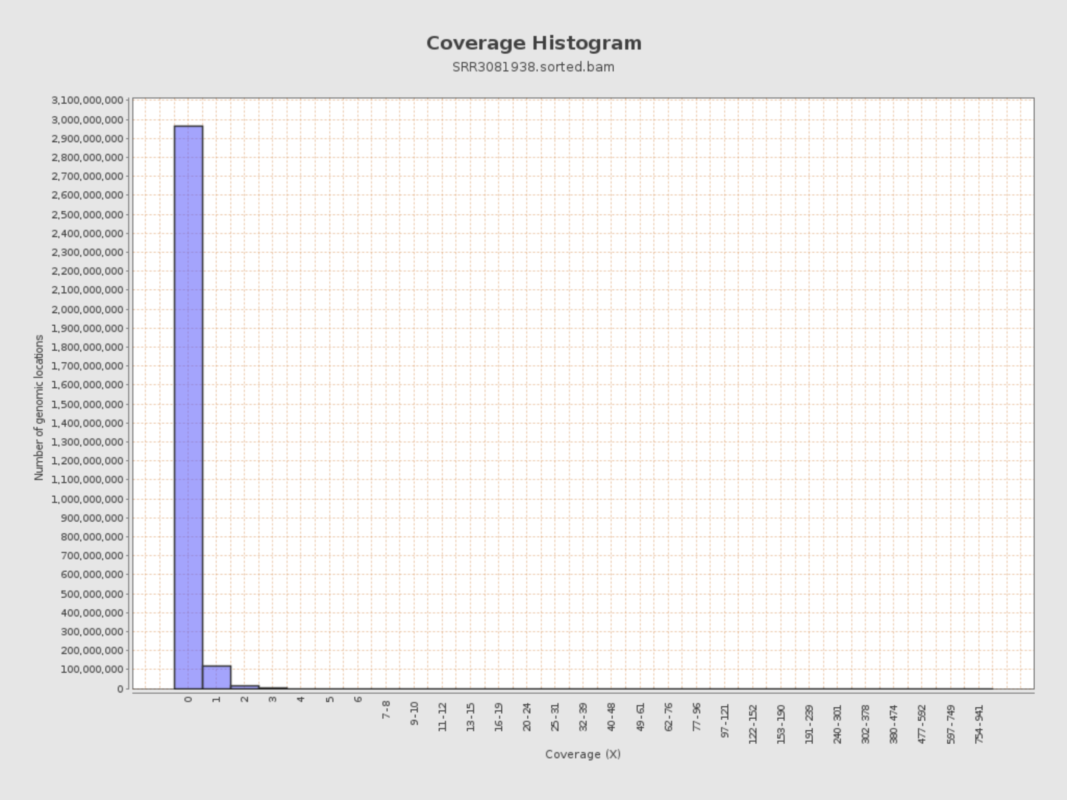
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13917629	0.0558	0.8435
chr2	243199373	13220811	0.0544	0.7065
chr3	198022430	9763186	0.0493	0.2509
chr4	191154276	7780240	0.0407	0.2508
chr5	180915260	8807413	0.0487	0.2502
chr6	171115067	13462418	0.0787	0.4391
chr7	159138663	9903909	0.0622	0.6917

chr8	146364022	8756406	0.0598	0.6038
chr9	141213431	8952058	0.0634	0.5566
chr10	135534747	6190434	0.0457	0.4879
chr11	135006516	6856412	0.0508	0.3639
chr12	133851895	6461503	0.0483	0.2686
chr13	115169878	4132571	0.0359	0.2107
chr14	107349540	3810677	0.0355	0.2552
chr15	102531392	3370842	0.0329	0.2049
chr16	90354753	3273368	0.0362	0.2689
chr17	81195210	4741606	0.0584	0.3235
chr18	78077248	4693906	0.0601	0.8583
chr19	59128983	2139092	0.0362	0.7104
chr20	63025520	3790358	0.0601	0.2851
chr21	48129895	1579867	0.0328	0.247
chr22	51304566	1121571	0.0219	0.1615
chrMT	16571	12679	0.7651	1.0305
chrX	155270560	7451560	0.048	0.3149
chrY	59373566	343028	0.0058	0.1609

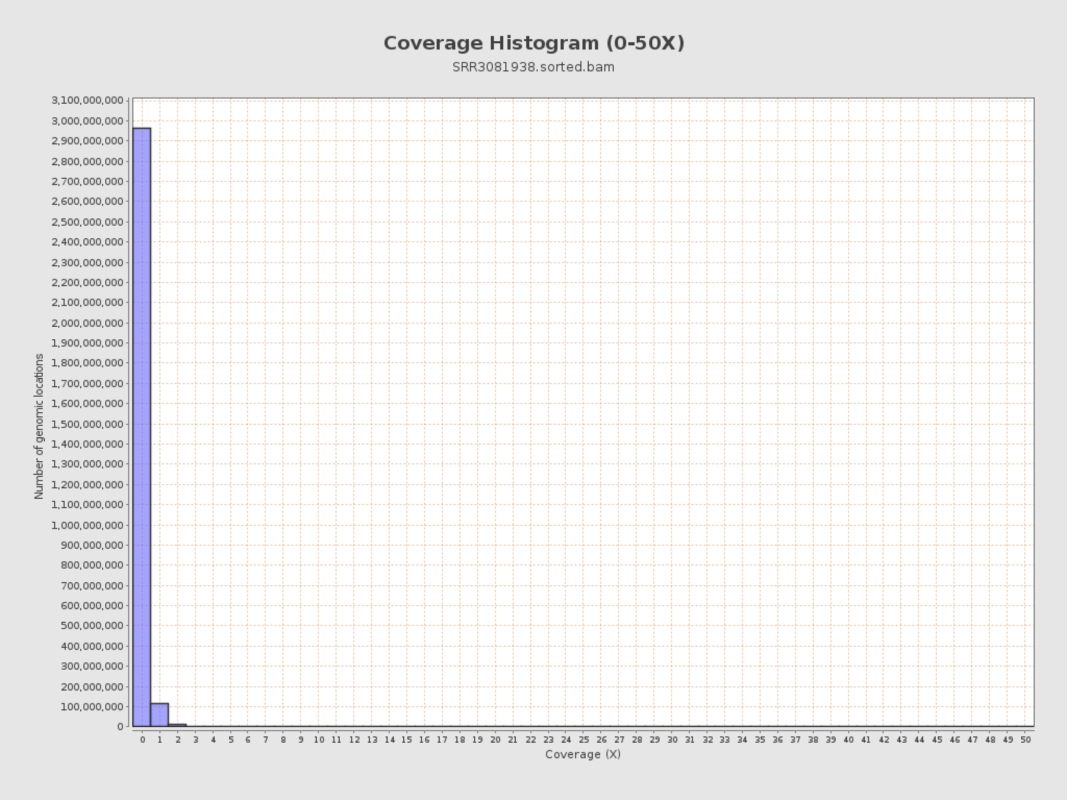
3. Results : Coverage across reference



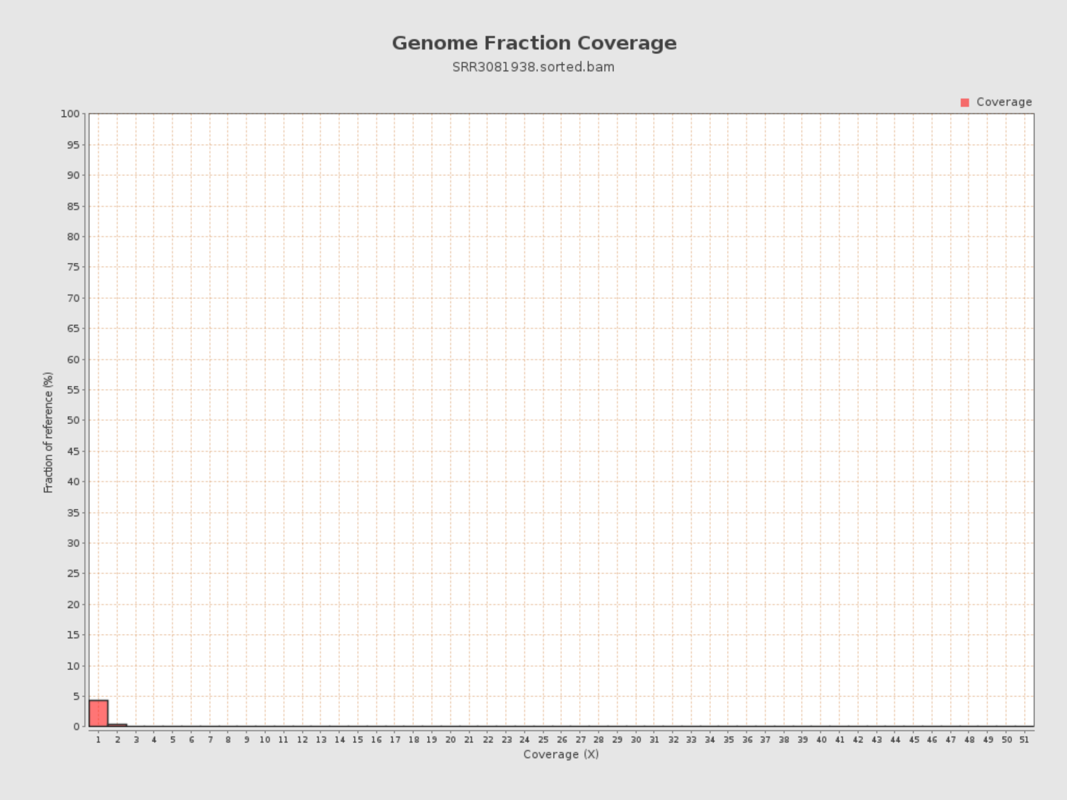
4. Results : Coverage Histogram



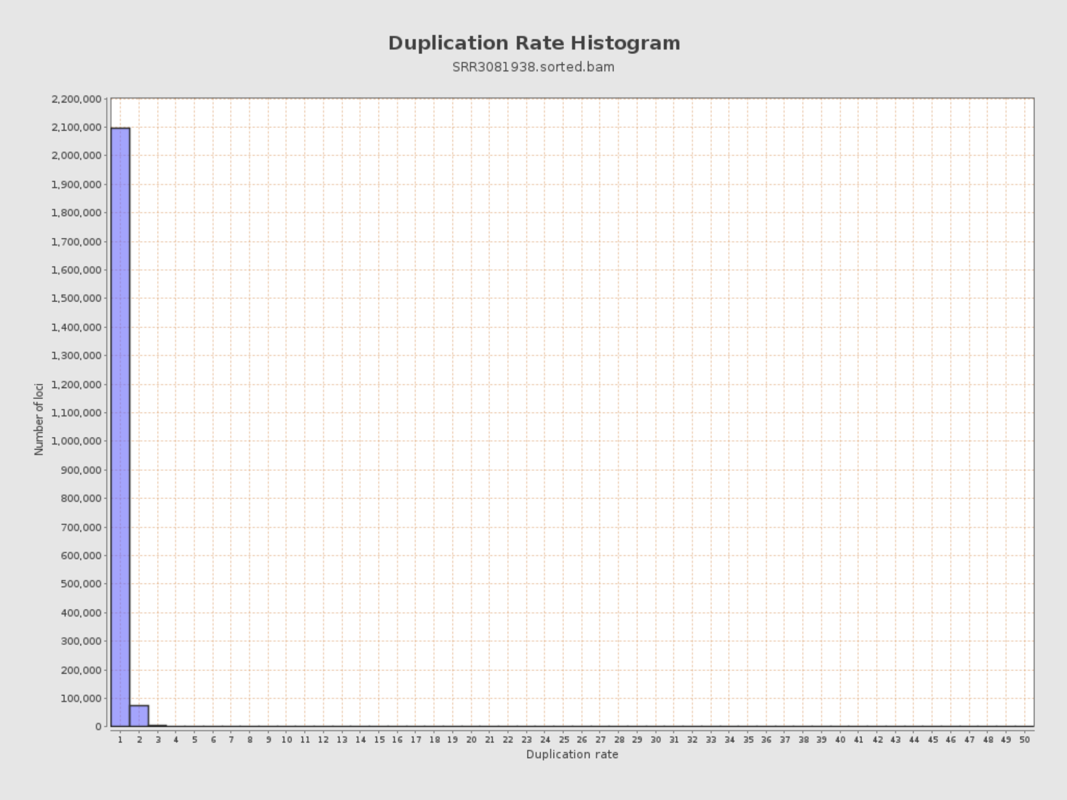
5. Results : Coverage Histogram (0-50X)



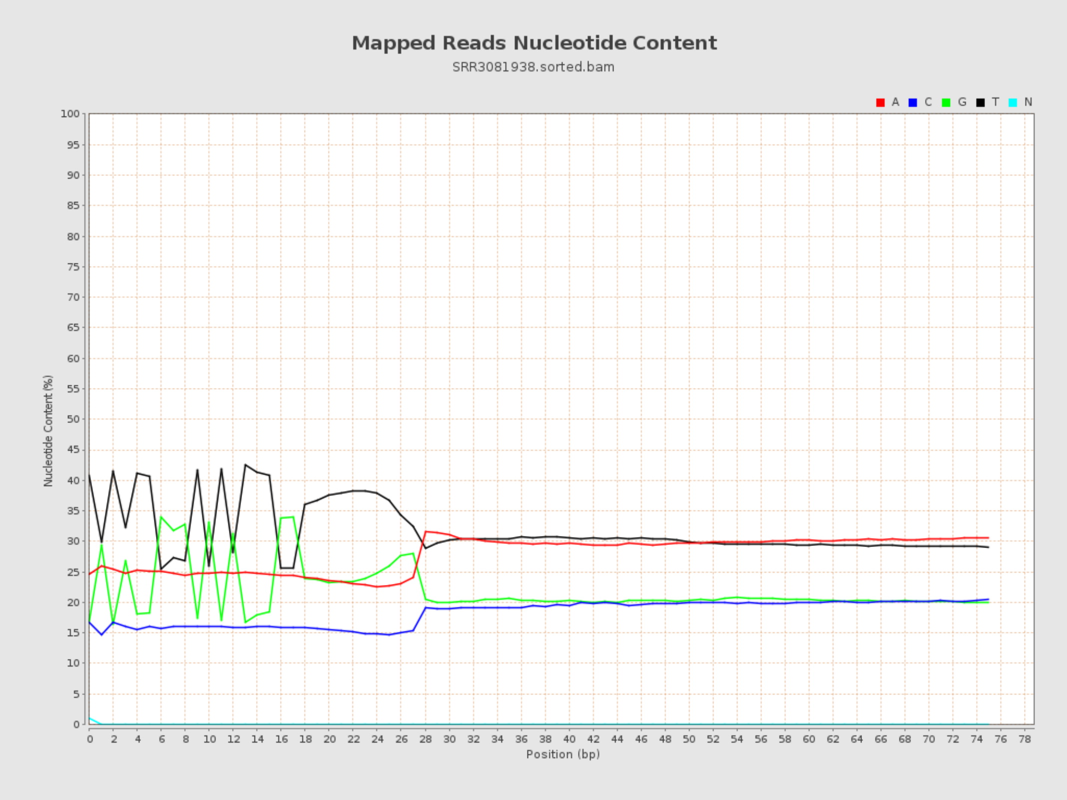
6. Results : Genome Fraction Coverage



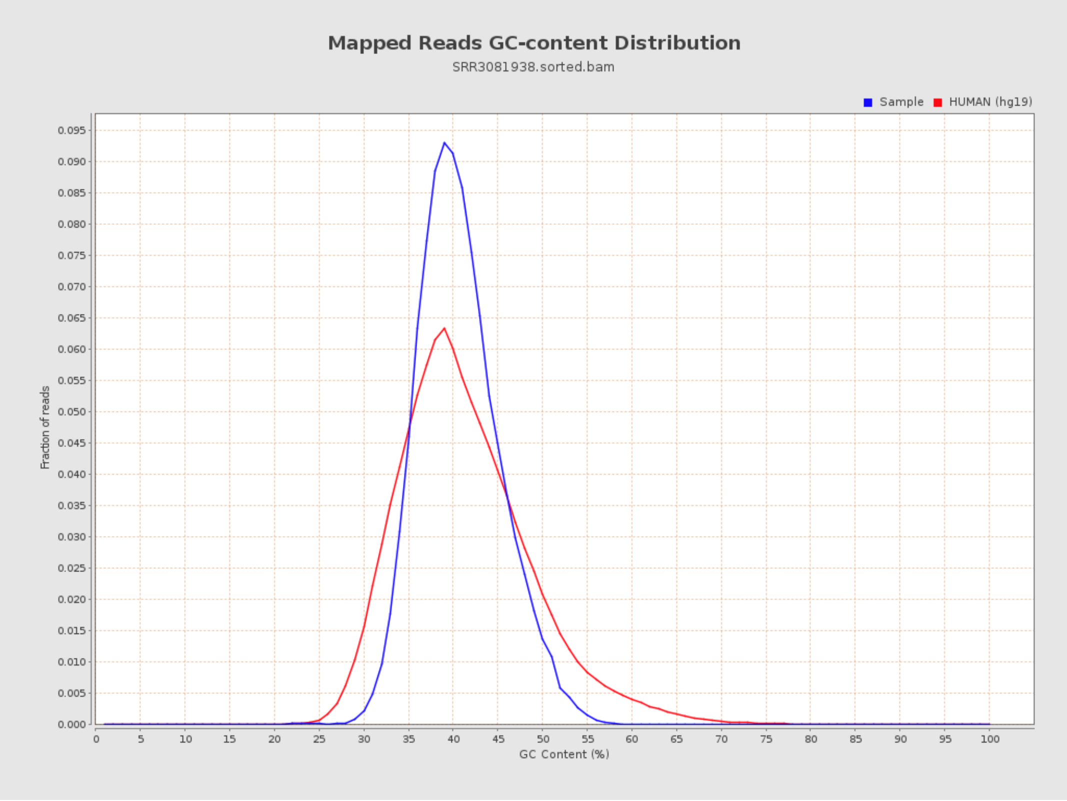
7. Results : Duplication Rate Histogram



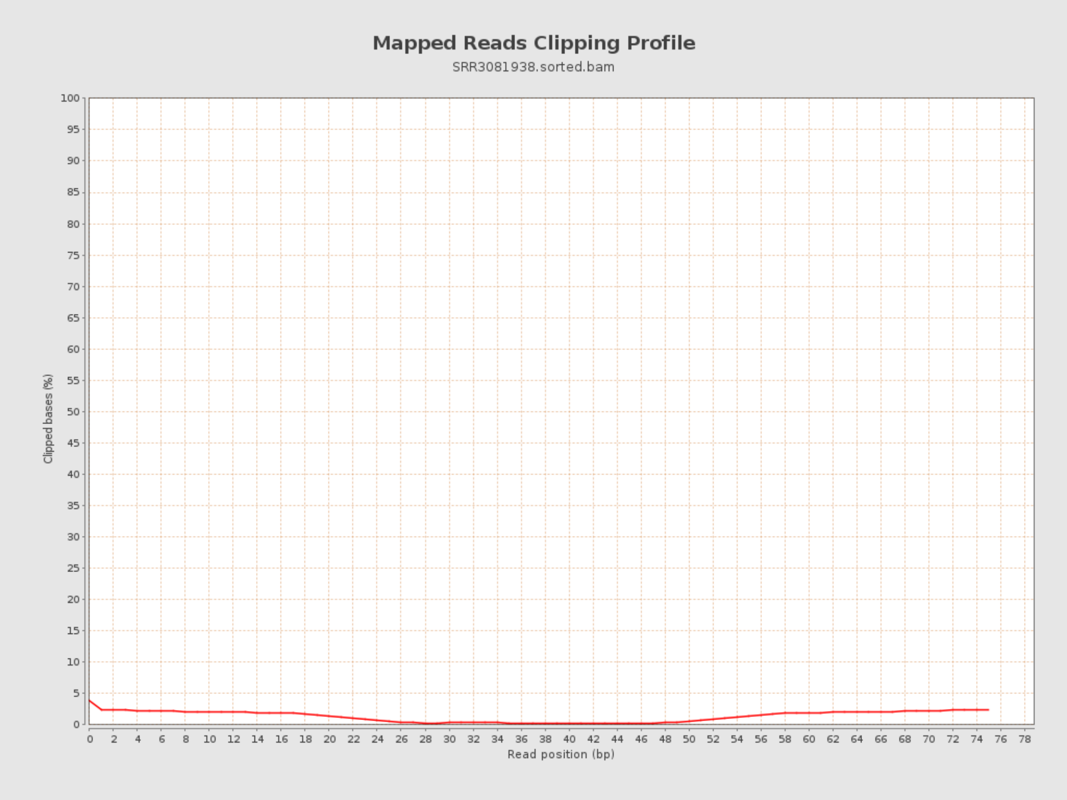
8. Results : Mapped Reads Nucleotide Content



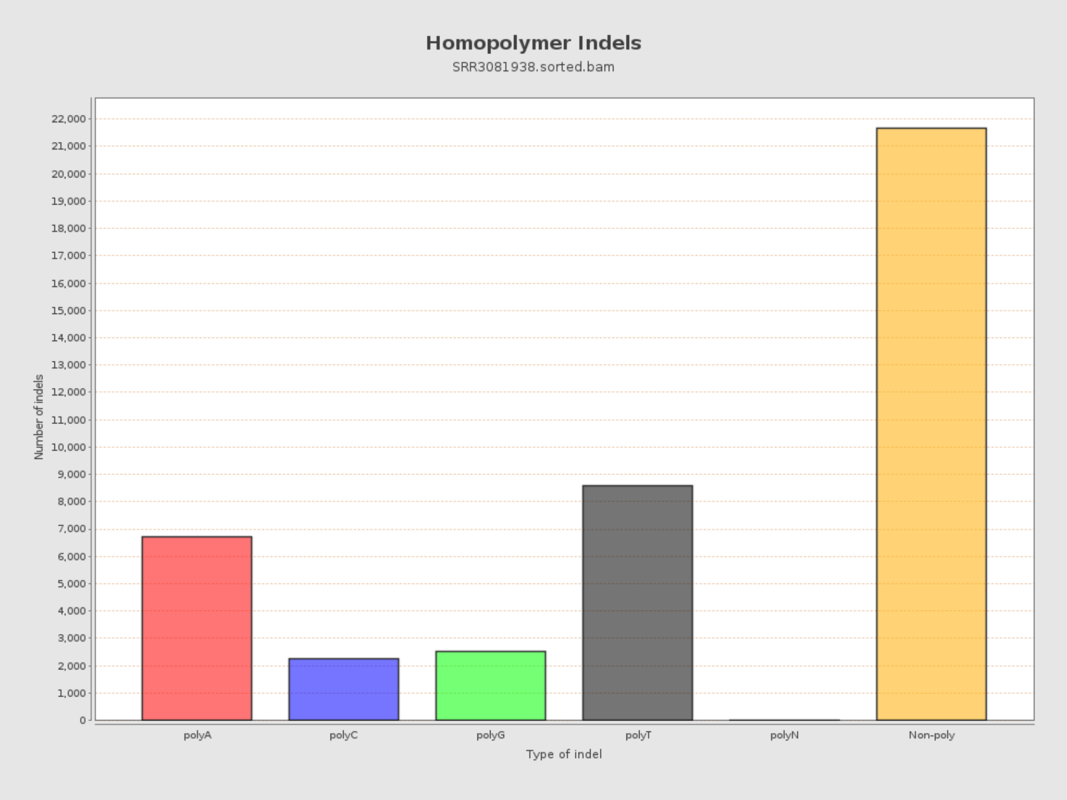
9. Results : Mapped Reads GC-content Distribution



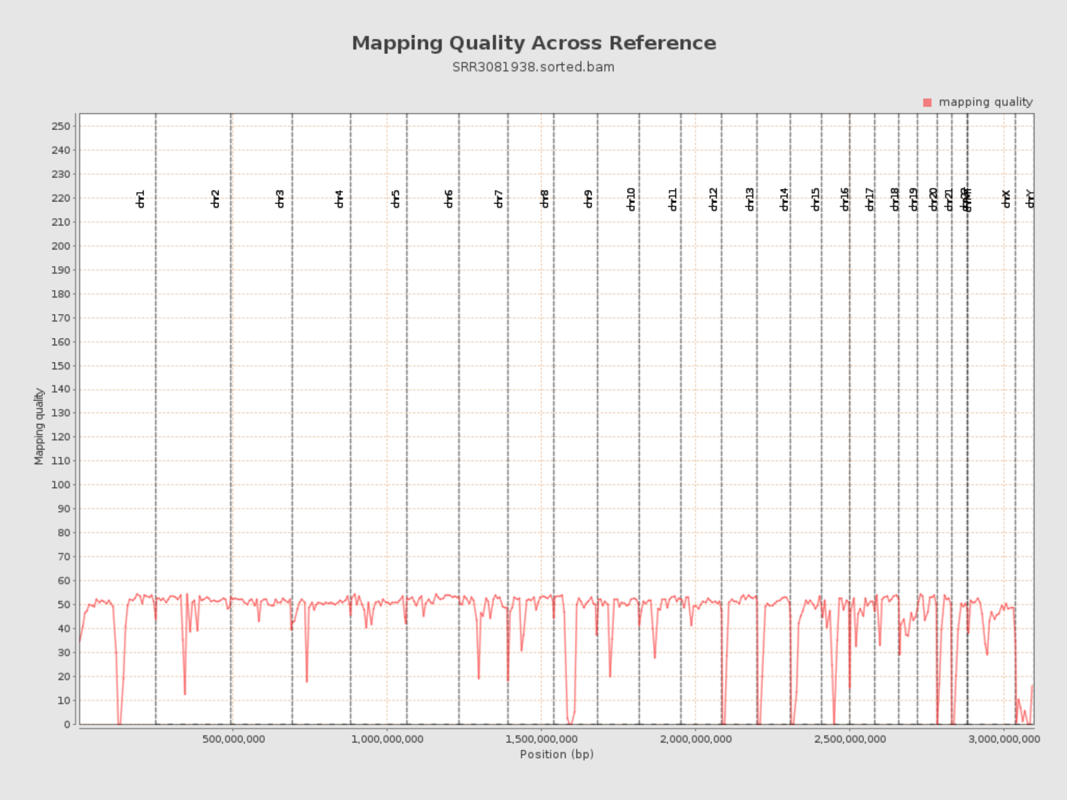
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram