Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 10:11:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081922.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_SRR3081922 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081922.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 10:11:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081922.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,238,709
Mapped reads	2,070,615 / 92.49%
Unmapped reads	168,094 / 7.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,439 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	98,346 / 4.39%
Duplication rate	3.72%
Clipped reads	776,977 / 34.71%

2.2. ACGT Content

Number/percentage of A's	39,952,111 / 28.32%
Number/percentage of C's	25,888,752 / 18.35%
Number/percentage of T's	44,855,666 / 31.8%
Number/percentage of G's	30,349,121 / 21.51%
Number/percentage of N's	18,078 / 0.01%
GC Percentage	39.87%

2.3. Coverage

Mean	0.0456

Standard Deviation	0.4345

2.4. Mapping Quality

Mean Mapping Quality	46.45

2.5. Mismatches and indels

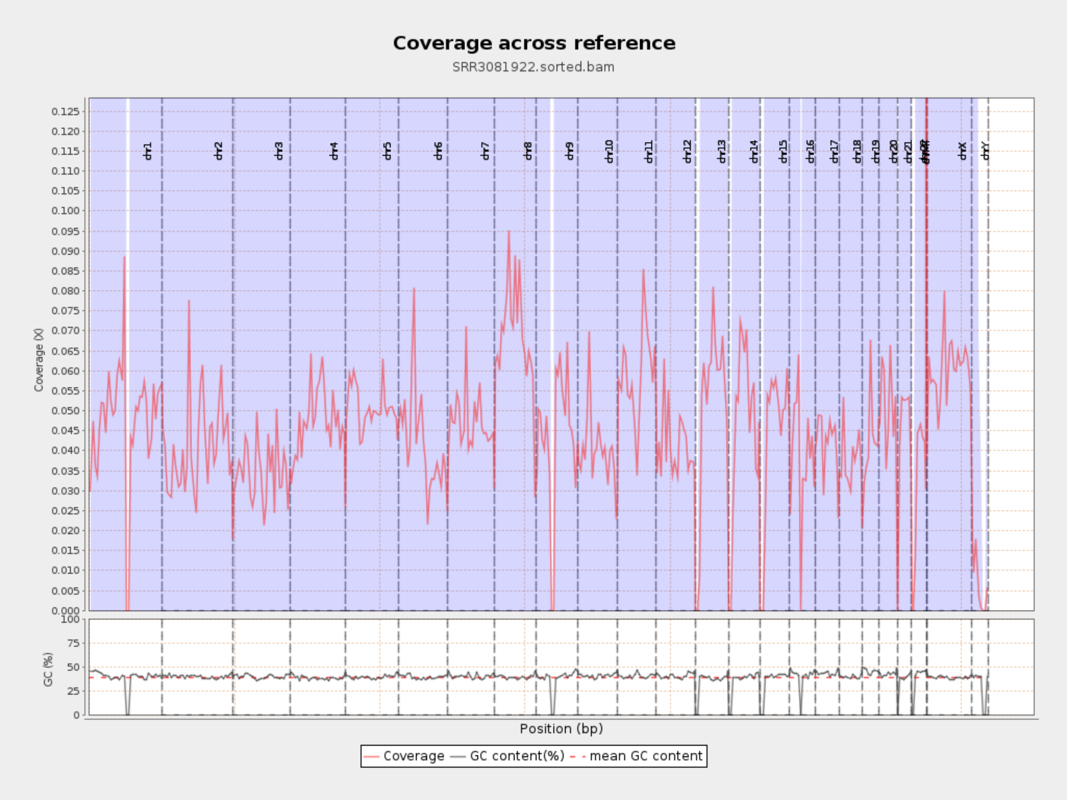
General error rate	0.77%
Mismatches	1,072,769
Insertions	10,269
Mapped reads with at least one insertion	0.49%
Deletions	29,643
Mapped reads with at least one deletion	1.42%
Homopolymer indels	47.95%

2.6. Chromosome stats

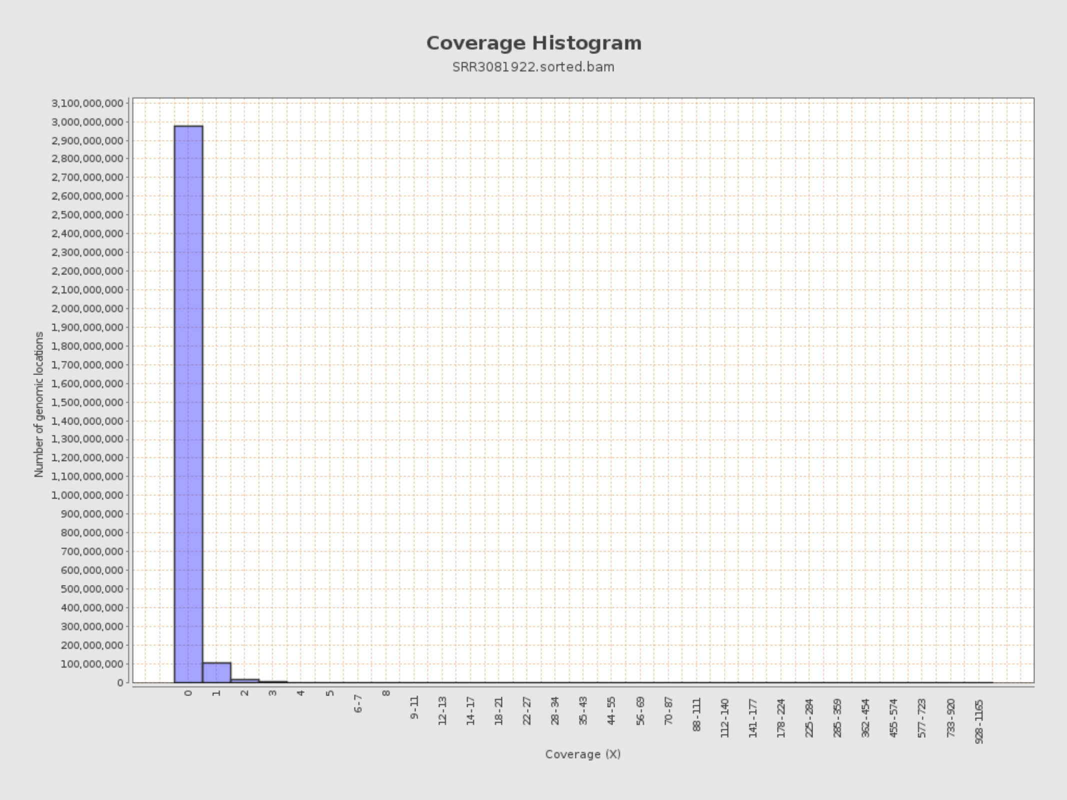
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11840026	0.0475	0.8304
chr2	243199373	10031992	0.0413	0.425
chr3	198022430	6837200	0.0345	0.2134
chr4	191154276	9048120	0.0473	0.2587
chr5	180915260	9227320	0.051	0.2546
chr6	171115067	7206828	0.0421	0.3009
chr7	159138663	7569536	0.0476	0.4359

chr8	146364022	10042080	0.0686	0.7622
chr9	141213431	6159567	0.0436	0.4028
chr10	135534747	5490234	0.0405	0.3964
chr11	135006516	7955735	0.0589	0.3906
chr12	133851895	5538195	0.0414	0.2353
chr13	115169878	5799980	0.0504	0.2529
chr14	107349540	4943349	0.046	0.2621
chr15	102531392	4447002	0.0434	0.2372
chr16	90354753	3509779	0.0388	0.2671
chr17	81195210	3390910	0.0418	0.2603
chr18	78077248	2996709	0.0384	0.8167
chr19	59128983	2492516	0.0422	0.5996
chr20	63025520	3203344	0.0508	0.2649
chr21	48129895	2130098	0.0443	0.2591
chr22	51304566	1532471	0.0299	0.1929
chrMT	16571	12529	0.7561	1.0567
chrX	155270560	9332179	0.0601	0.3154
chrY	59373566	377883	0.0064	0.1379

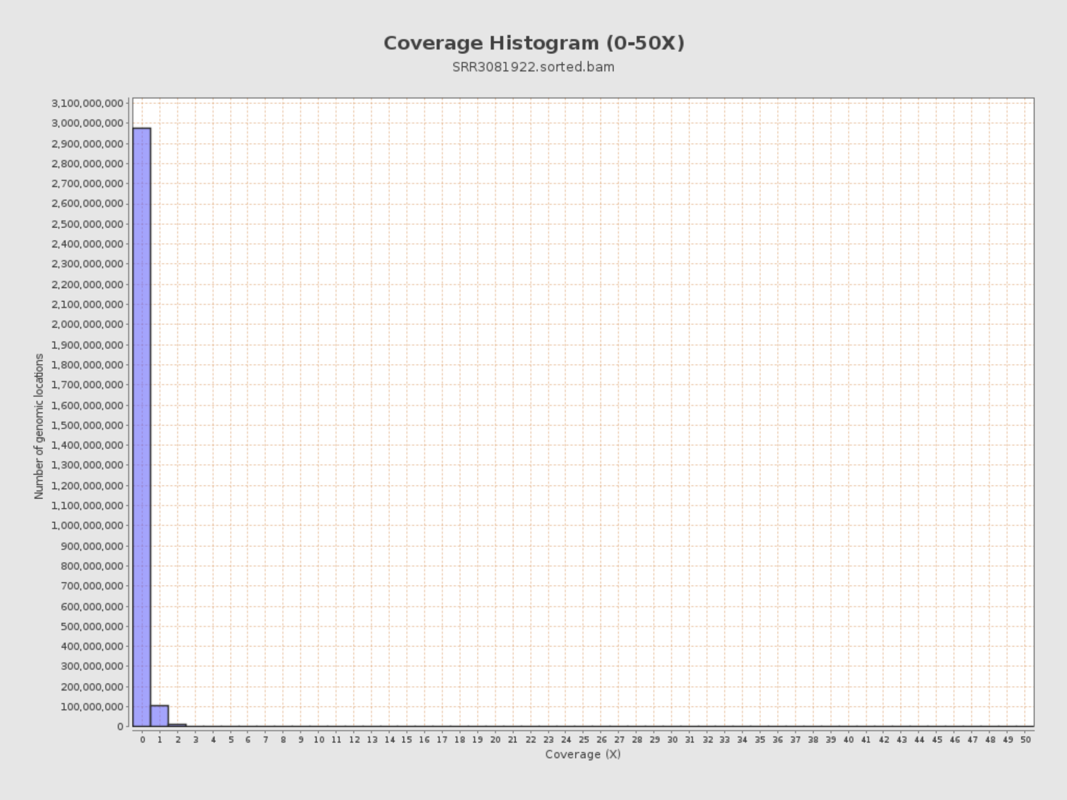
3. Results : Coverage across reference



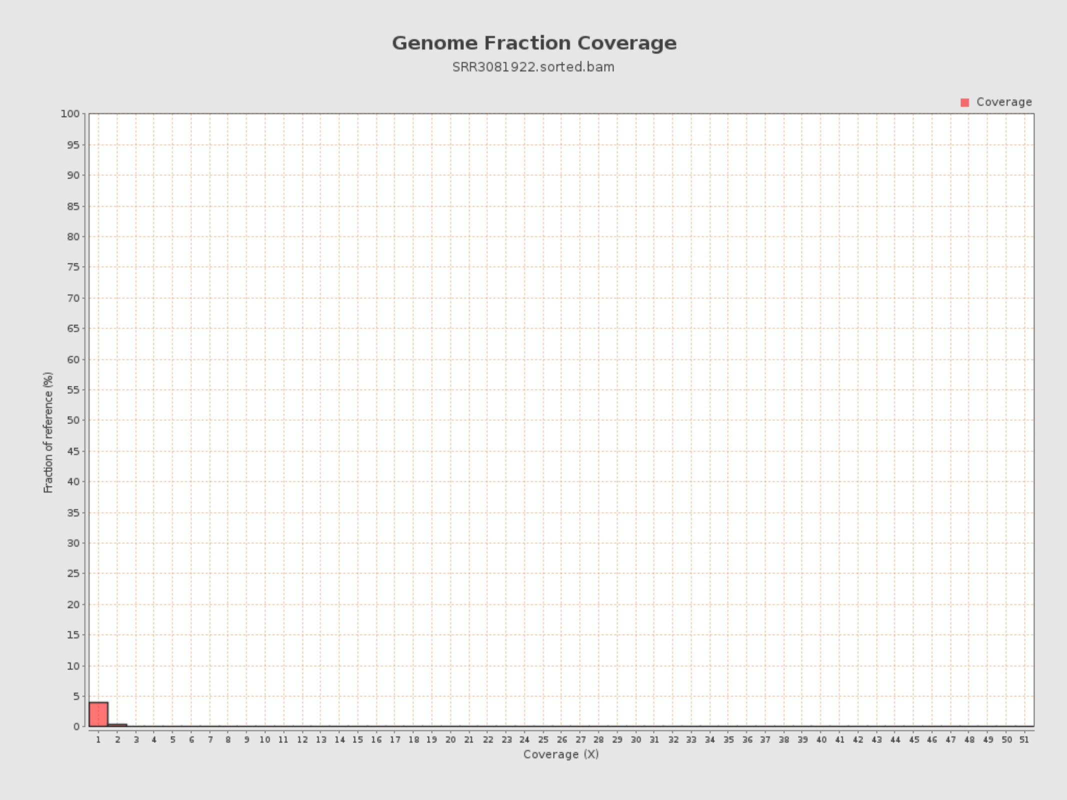
4. Results : Coverage Histogram



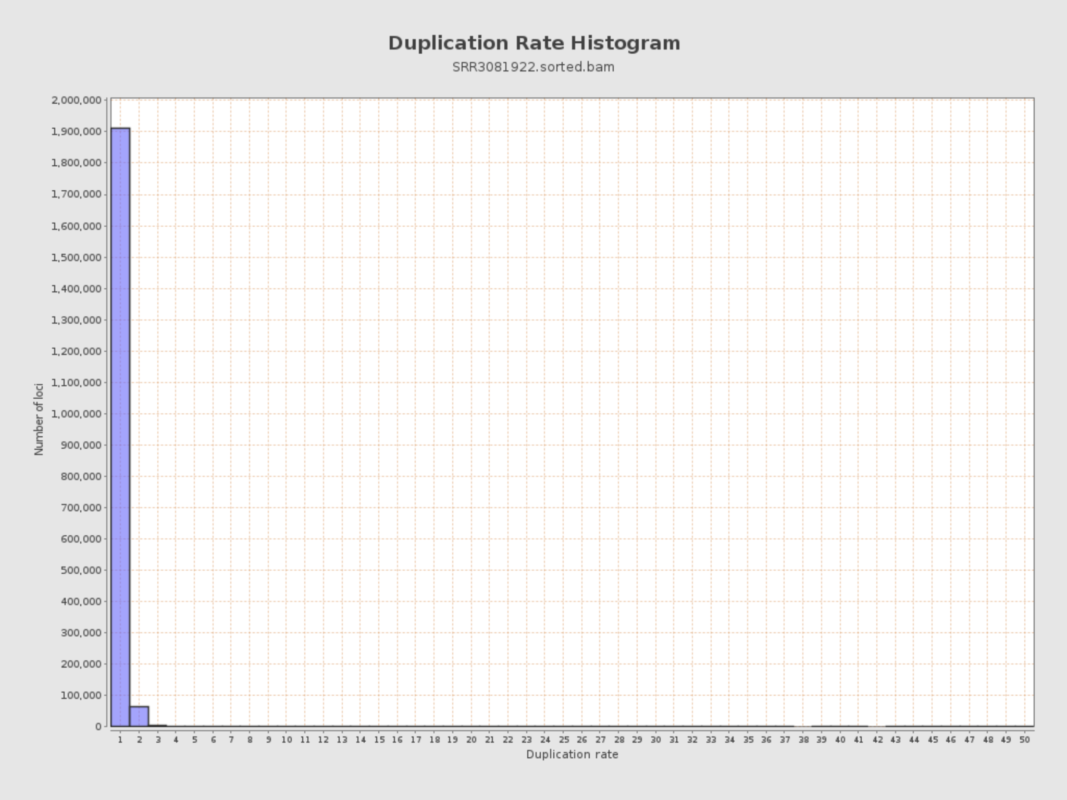
5. Results : Coverage Histogram (0-50X)



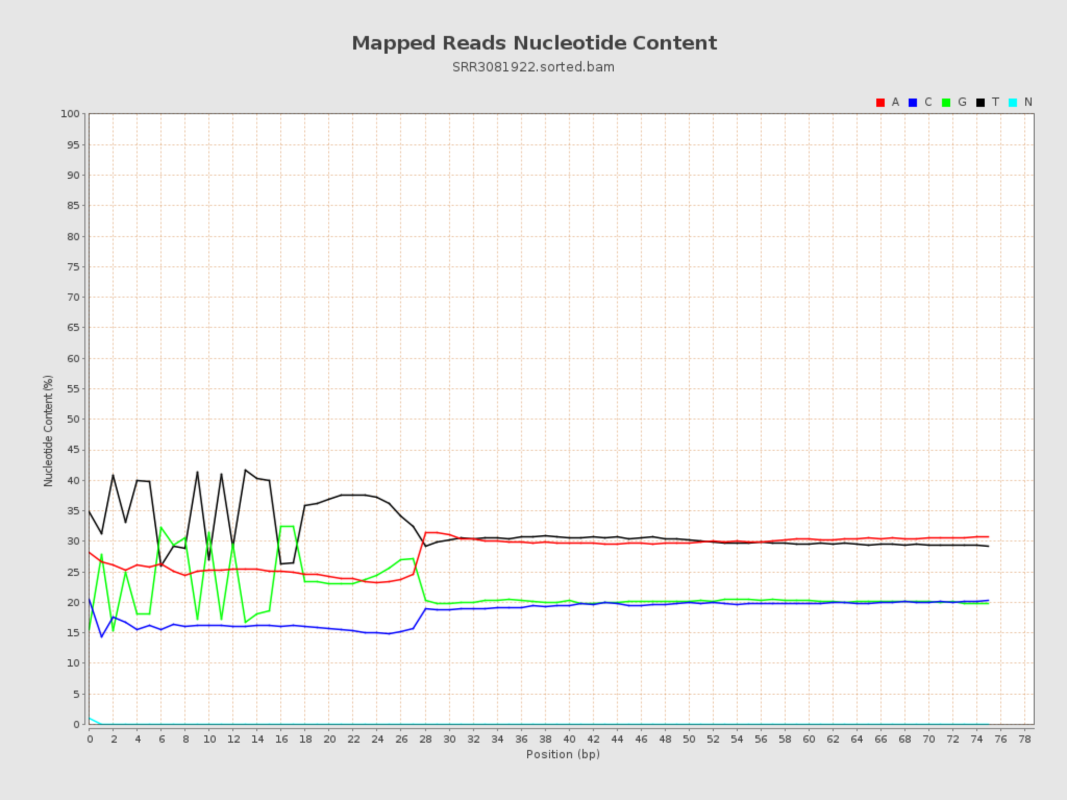
6. Results : Genome Fraction Coverage



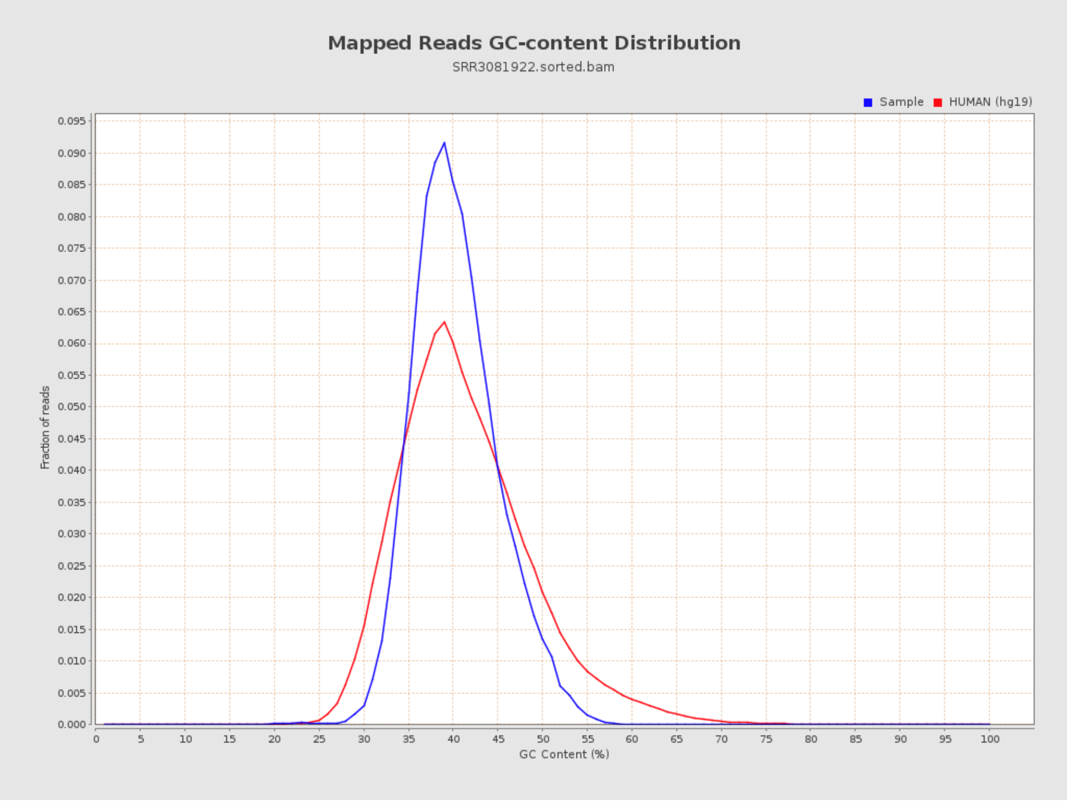
7. Results : Duplication Rate Histogram



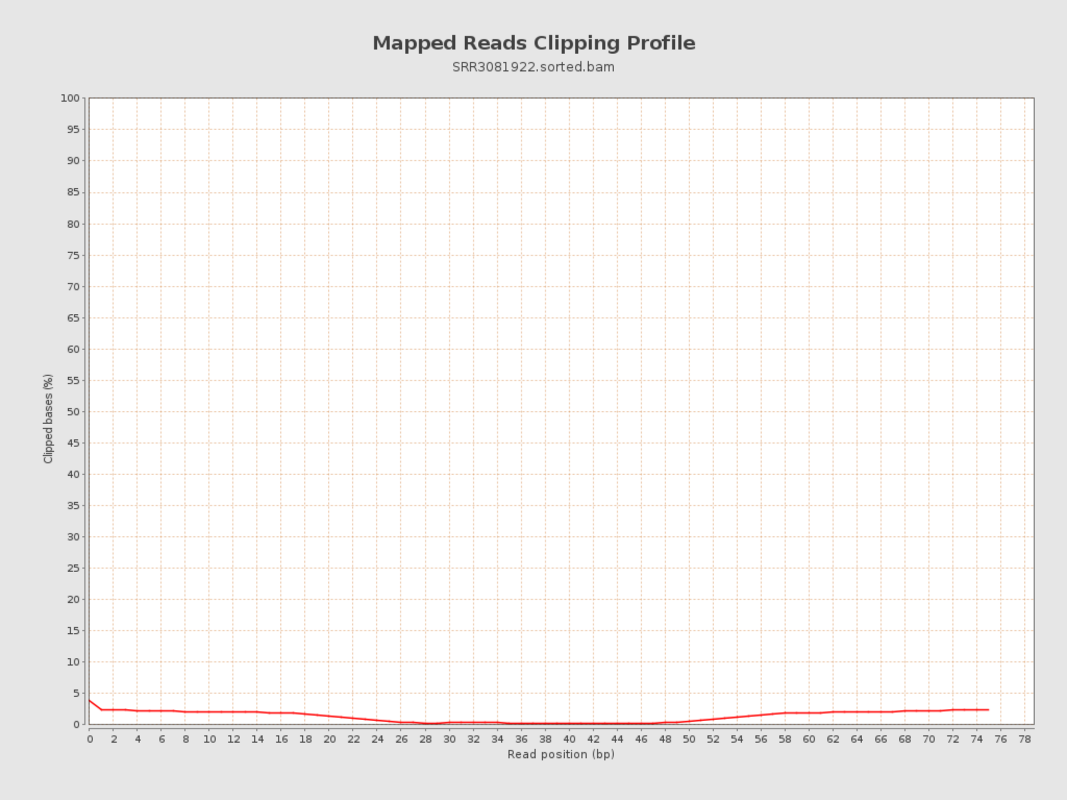
8. Results : Mapped Reads Nucleotide Content



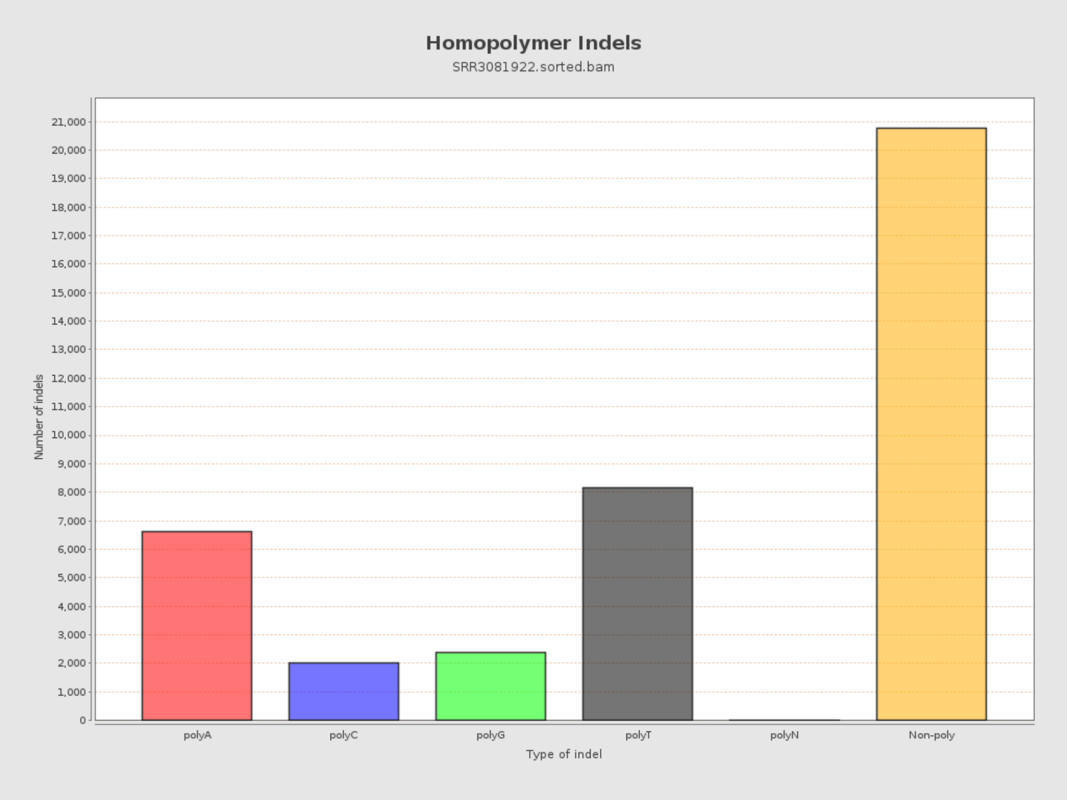
9. Results : Mapped Reads GC-content Distribution



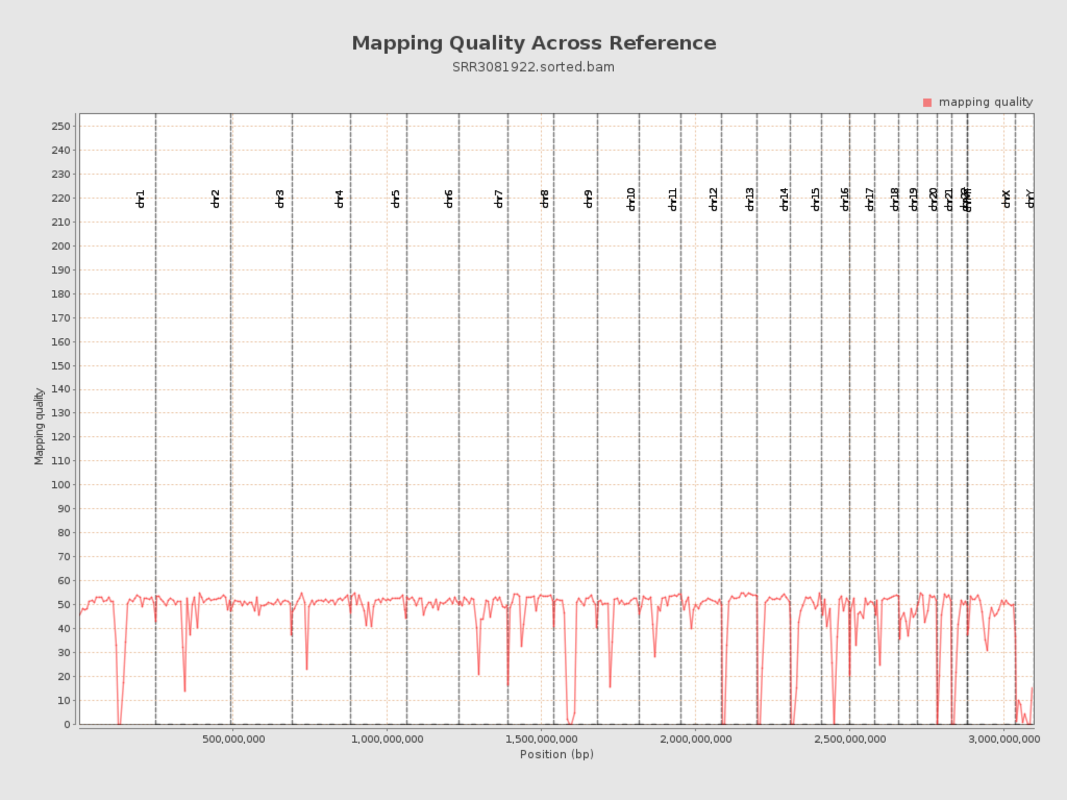
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram