Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 21:00:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081121.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_SRR3081121 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081121.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 21:00:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081121.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,637
Mapped reads	887 / 24.39%
Unmapped reads	2,750 / 75.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2 / 0.05%
Read min/max/mean length	30 / 76 / 76.02
Duplicated reads (estimated)	0 / 0%
Duplication rate	0%
Clipped reads	349 / 9.6%

2.2. ACGT Content

Number/percentage of A's	16,625 / 27.78%
Number/percentage of C's	11,148 / 18.63%
Number/percentage of T's	19,054 / 31.84%
Number/percentage of G's	13,014 / 21.75%
Number/percentage of N's	0 / 0%
GC Percentage	40.38%

2.3. Coverage

Mean	0

Standard Deviation	0.0044

2.4. Mapping Quality

Mean Mapping Quality	38.01

2.5. Mismatches and indels

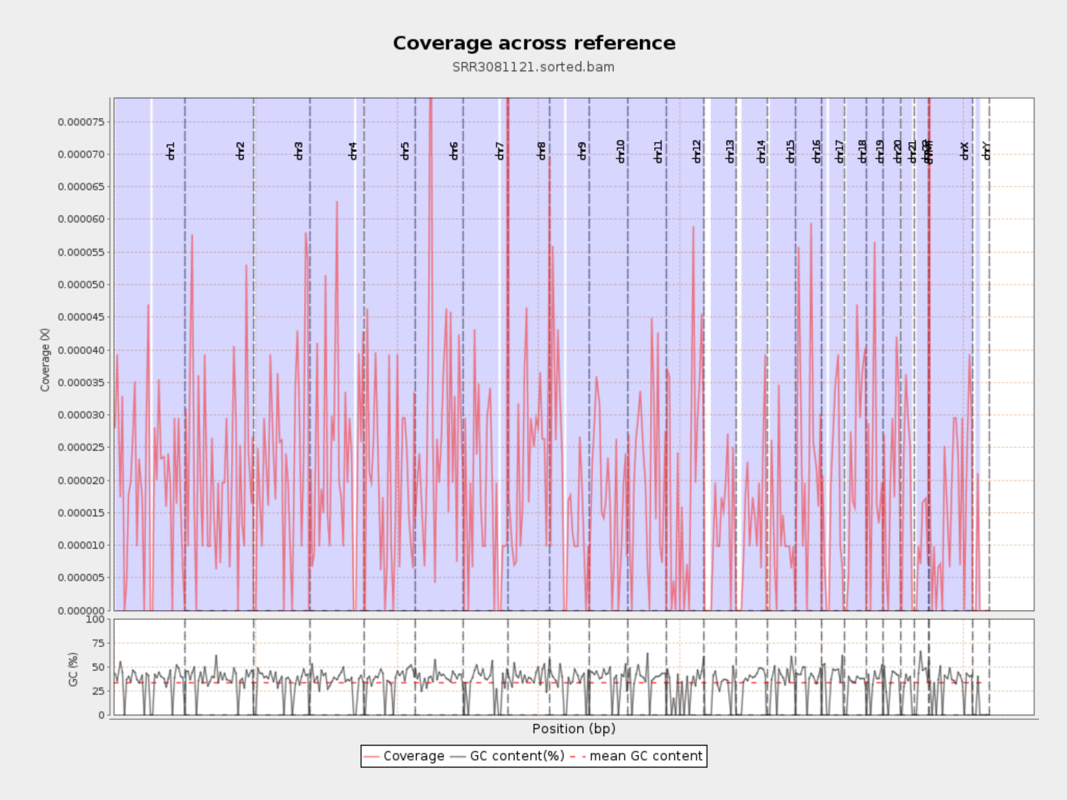
General error rate	0.71%
Mismatches	425
Insertions	1
Mapped reads with at least one insertion	0.11%
Deletions	8
Mapped reads with at least one deletion	0.9%
Homopolymer indels	66.67%

2.6. Chromosome stats

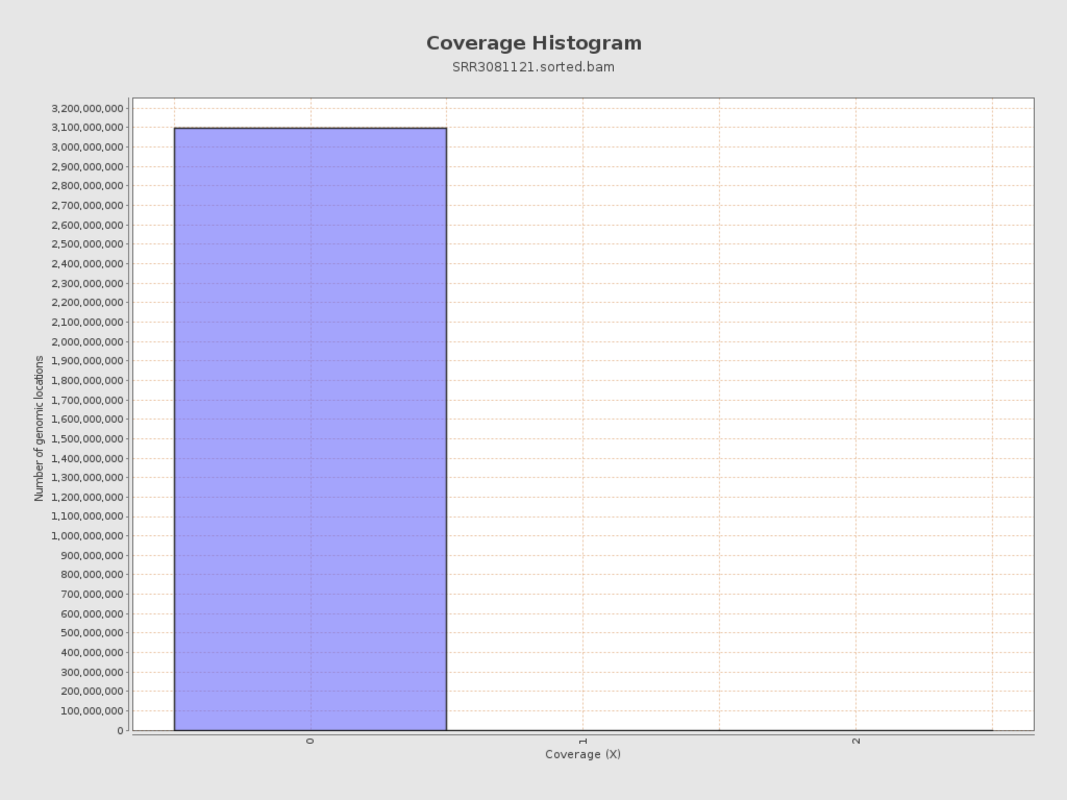
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4917	0	0.0044
chr2	243199373	5175	0	0.0046
chr3	198022430	4593	0	0.0048
chr4	191154276	4405	0	0.0048
chr5	180915260	3429	0	0.0044
chr6	171115067	4875	0	0.0054
chr7	159138663	2523	0	0.004

chr8	146364022	3521	0	0.0049
chr9	141213431	2573	0	0.0043
chr10	135534747	2385	0	0.0042
chr11	135006516	2784	0	0.0045
chr12	133851895	2705	0	0.0045
chr13	115169878	1265	0	0.0033
chr14	107349540	1483	0	0.0037
chr15	102531392	1068	0	0.0032
chr16	90354753	2339	0	0.0051
chr17	81195210	1258	0	0.0039
chr18	78077248	1882	0	0.0049
chr19	59128983	1238	0	0.0046
chr20	63025520	1301	0	0.0045
chr21	48129895	894	0	0.0043
chr22	51304566	599	0	0.0034
chrMT	16571	76	0.0046	0.0676
chrX	155270560	2402	0	0.0039
chrY	59373566	163	0	0.0017

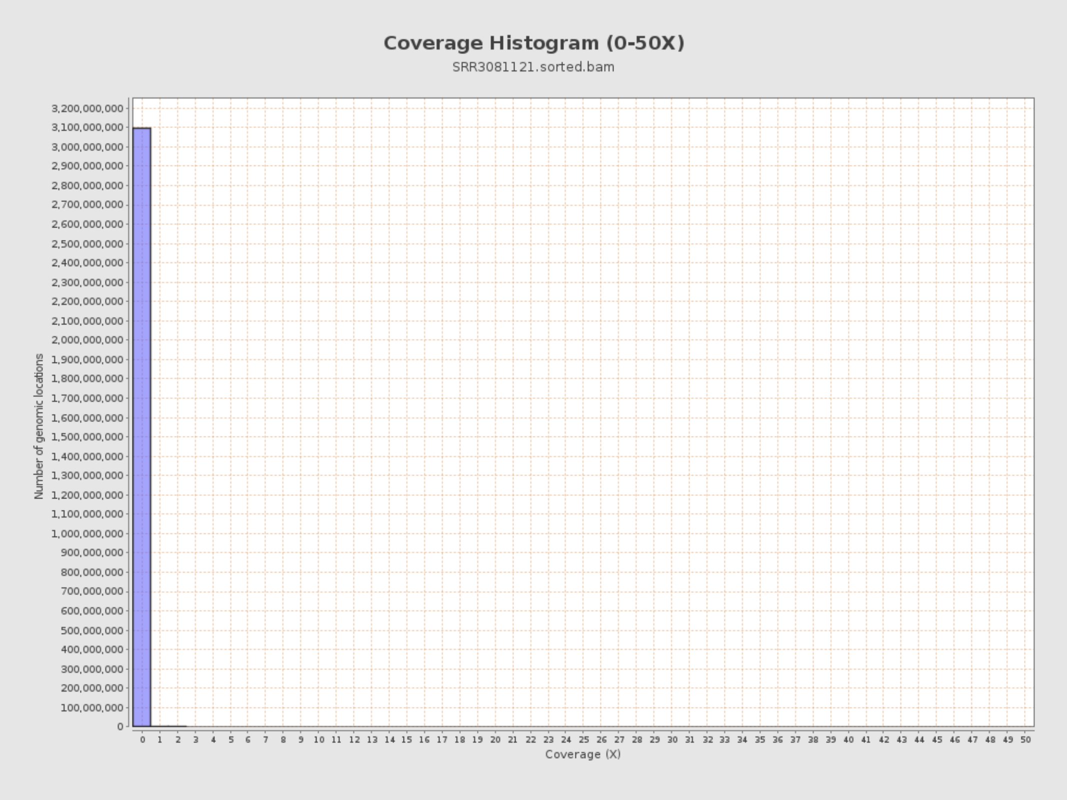
3. Results : Coverage across reference



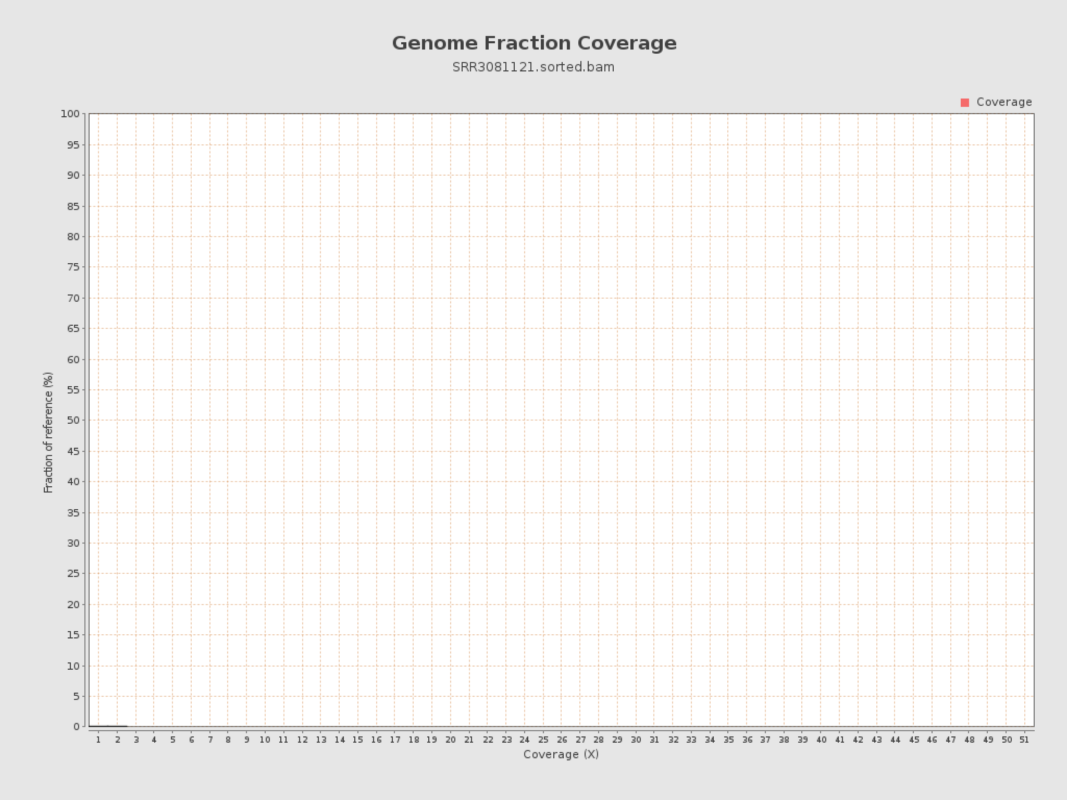
4. Results : Coverage Histogram



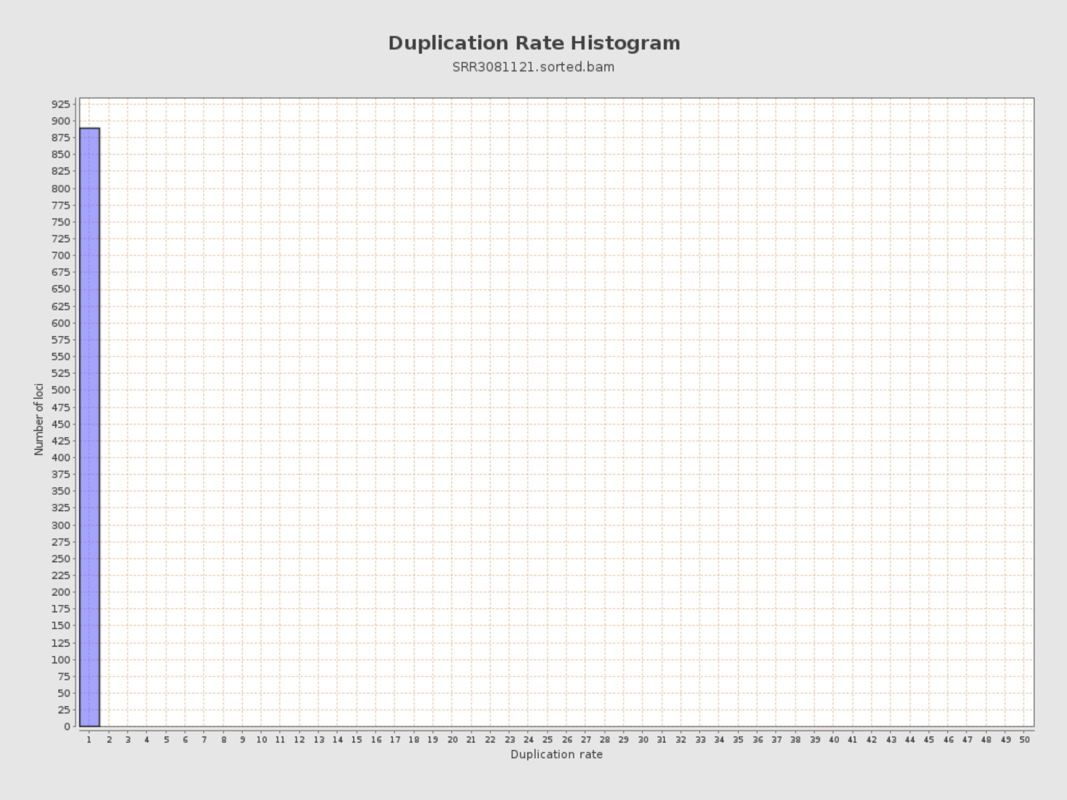
5. Results : Coverage Histogram (0-50X)



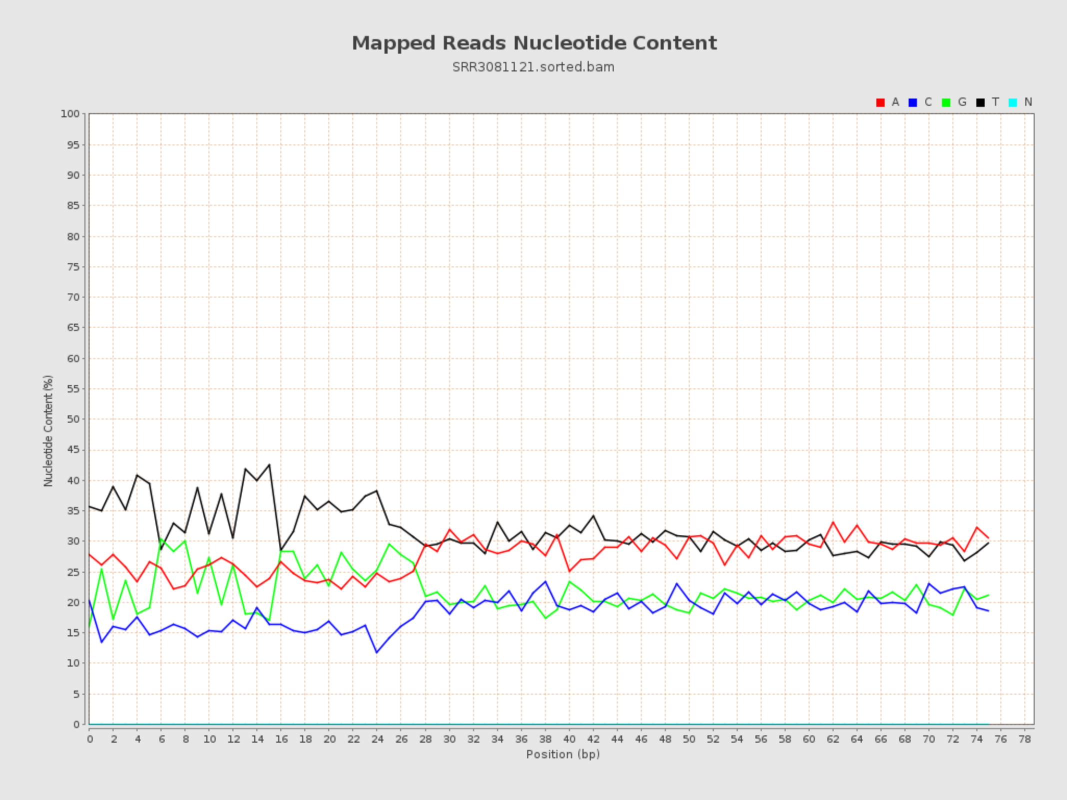
6. Results : Genome Fraction Coverage



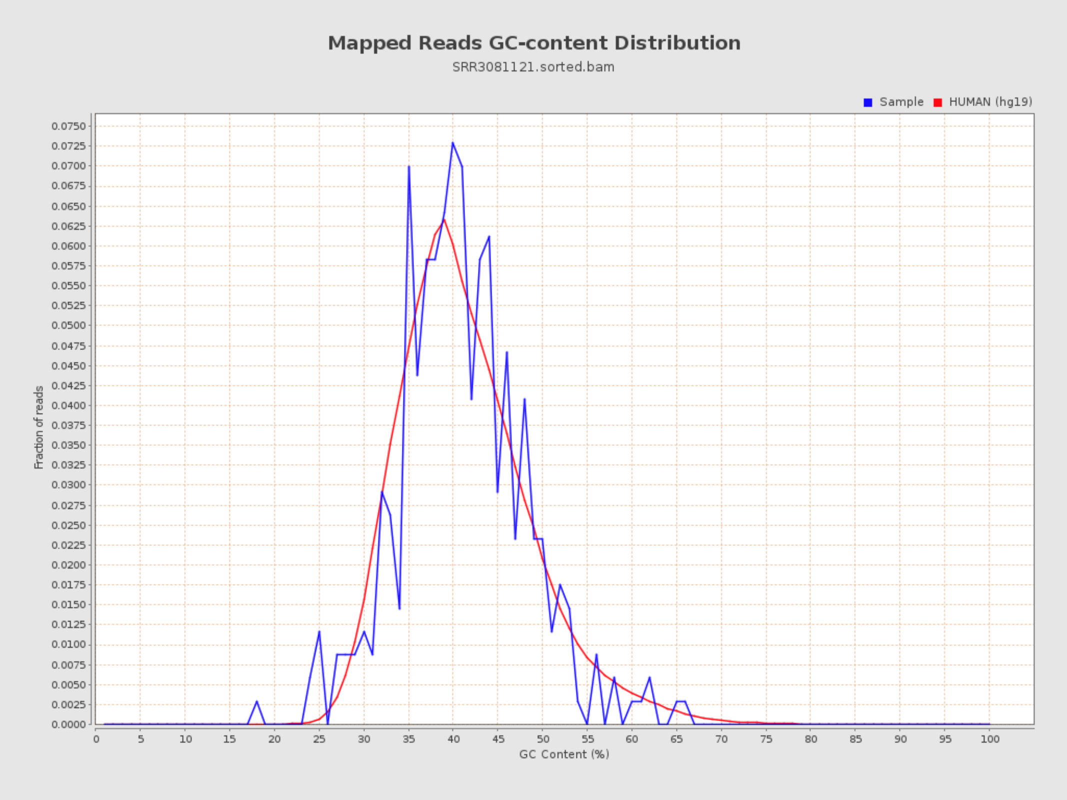
7. Results : Duplication Rate Histogram



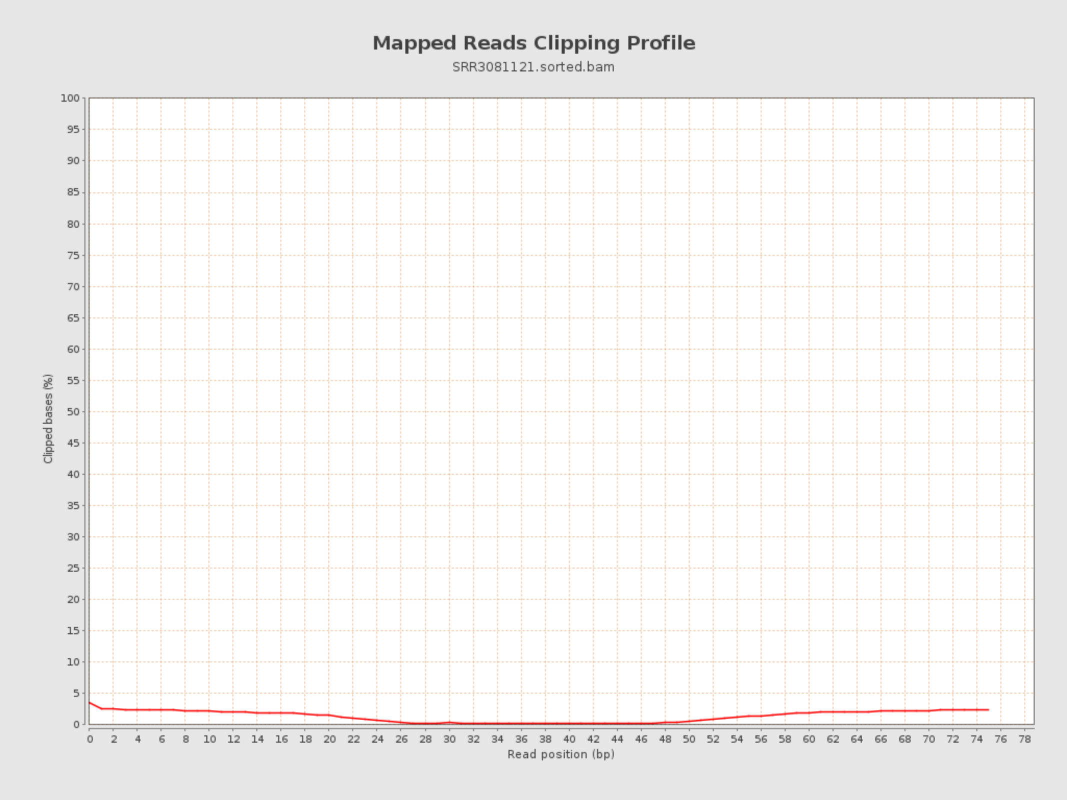
8. Results : Mapped Reads Nucleotide Content



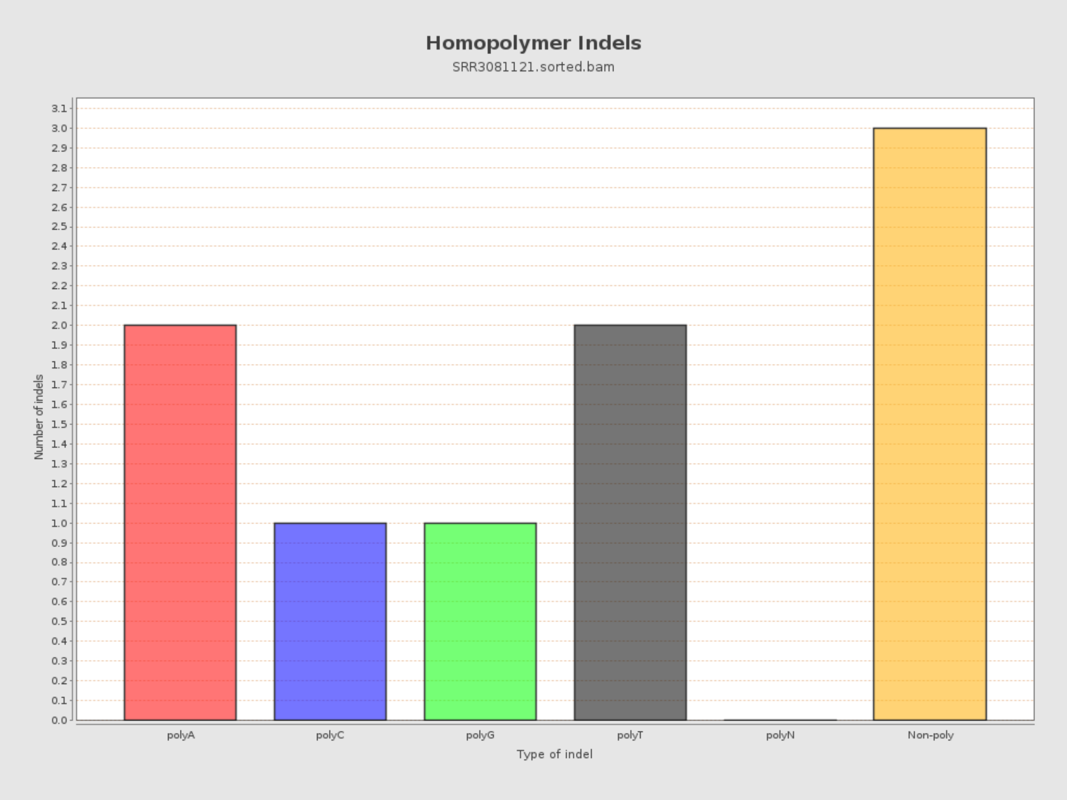
9. Results : Mapped Reads GC-content Distribution



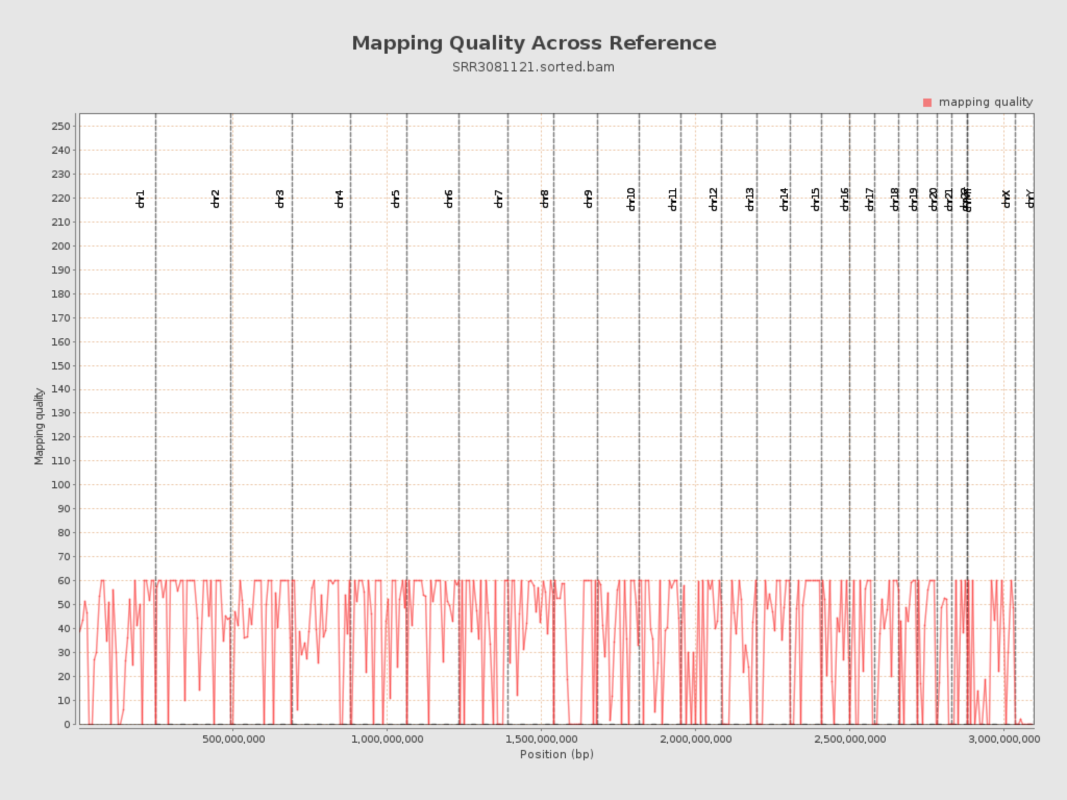
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram