Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:03:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081050.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_SRR3081050 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081050.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:03:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081050.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,690,079
Mapped reads	1,296,798 / 76.73%
Unmapped reads	393,281 / 23.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,040 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	29,013 / 1.72%
Duplication rate	1.78%
Clipped reads	634,176 / 37.52%

2.2. ACGT Content

Number/percentage of A's	24,551,108 / 29.15%
Number/percentage of C's	15,849,267 / 18.82%
Number/percentage of T's	25,267,279 / 30%
Number/percentage of G's	18,556,178 / 22.03%
Number/percentage of N's	1,118 / 0%
GC Percentage	40.85%

2.3. Coverage

Mean	0.0272

Standard Deviation	0.2277

2.4. Mapping Quality

Mean Mapping Quality	46.77

2.5. Mismatches and indels

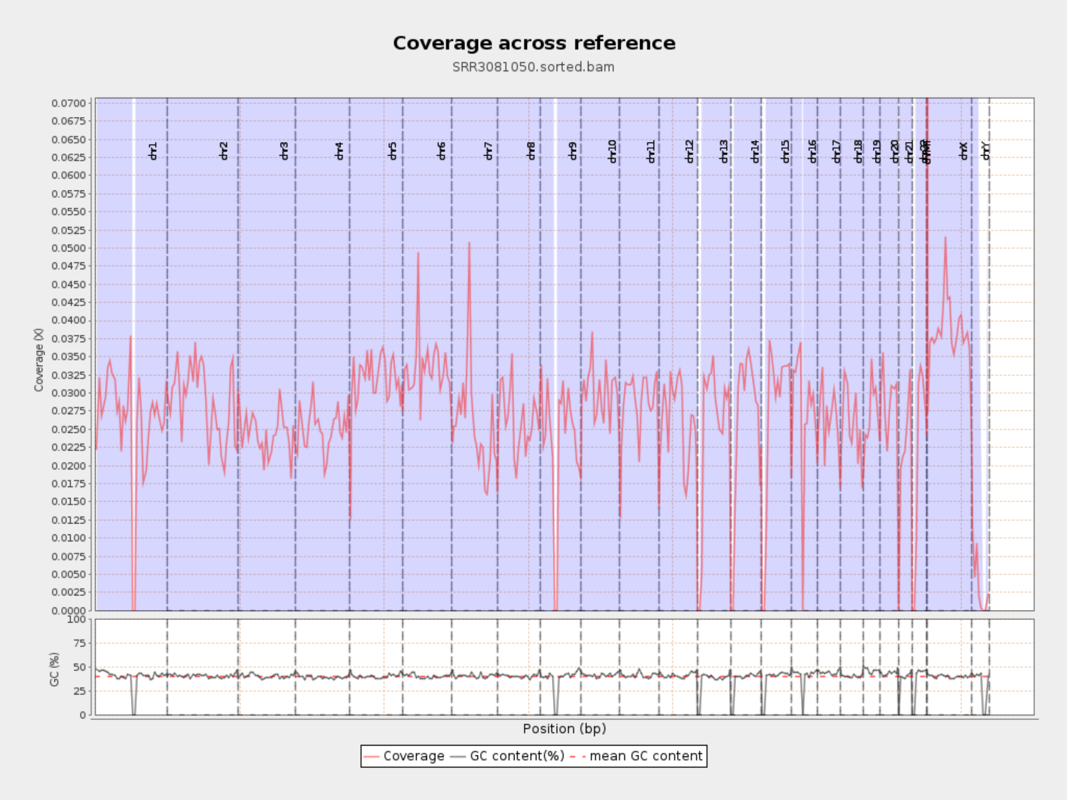
General error rate	0.79%
Mismatches	652,683
Insertions	5,303
Mapped reads with at least one insertion	0.41%
Deletions	17,351
Mapped reads with at least one deletion	1.32%
Homopolymer indels	48.08%

2.6. Chromosome stats

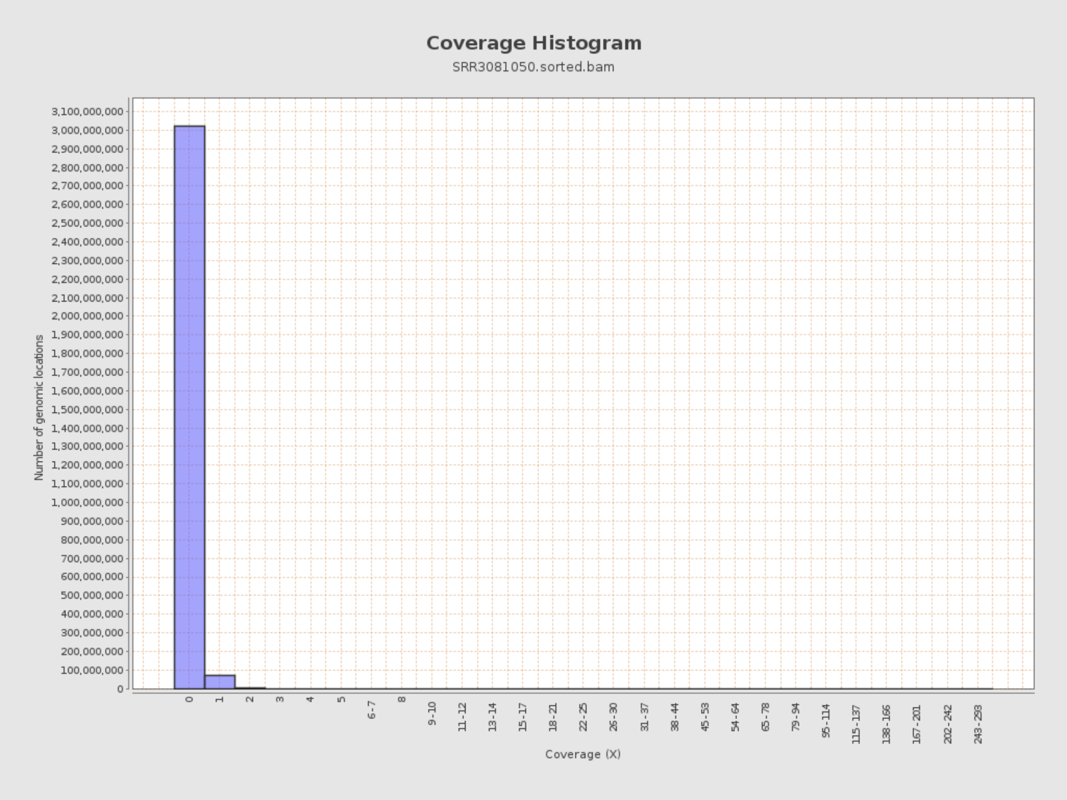
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6525852	0.0262	0.3129
chr2	243199373	7024576	0.0289	0.2313
chr3	198022430	4843382	0.0245	0.1677
chr4	191154276	4796471	0.0251	0.1739
chr5	180915260	5822218	0.0322	0.1936
chr6	171115067	5717514	0.0334	0.2435
chr7	159138663	4124554	0.0259	0.3555

chr8	146364022	3837123	0.0262	0.2309
chr9	141213431	3326608	0.0236	0.2039
chr10	135534747	4076083	0.0301	0.2211
chr11	135006516	3884535	0.0288	0.2093
chr12	133851895	3522655	0.0263	0.1754
chr13	115169878	2865462	0.0249	0.1697
chr14	107349540	2764999	0.0258	0.1801
chr15	102531392	2739991	0.0267	0.1803
chr16	90354753	2445319	0.0271	0.1888
chr17	81195210	2155604	0.0265	0.1965
chr18	78077248	2011814	0.0258	0.3668
chr19	59128983	1601172	0.0271	0.2554
chr20	63025520	1811145	0.0287	0.1835
chr21	48129895	1056658	0.022	0.1671
chr22	51304566	1090091	0.0212	0.1563
chrMT	16571	17142	1.0345	1.2562
chrX	155270560	5994048	0.0386	0.2311
chrY	59373566	199777	0.0034	0.0777

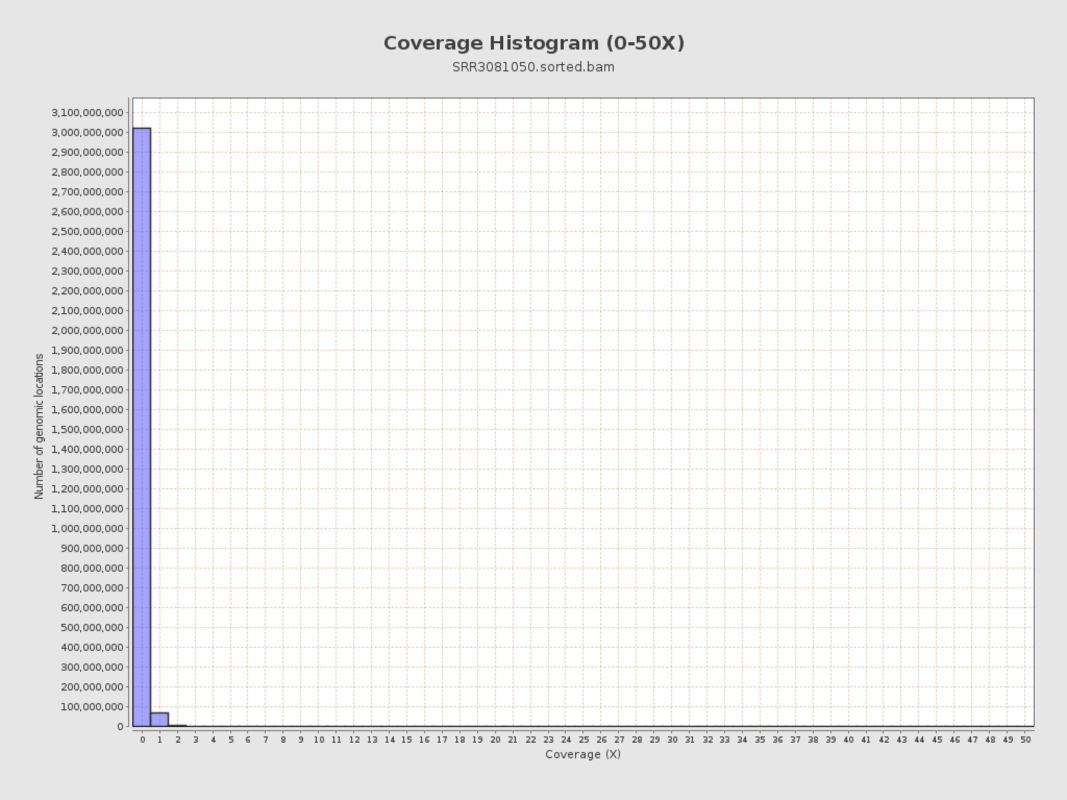
3. Results : Coverage across reference



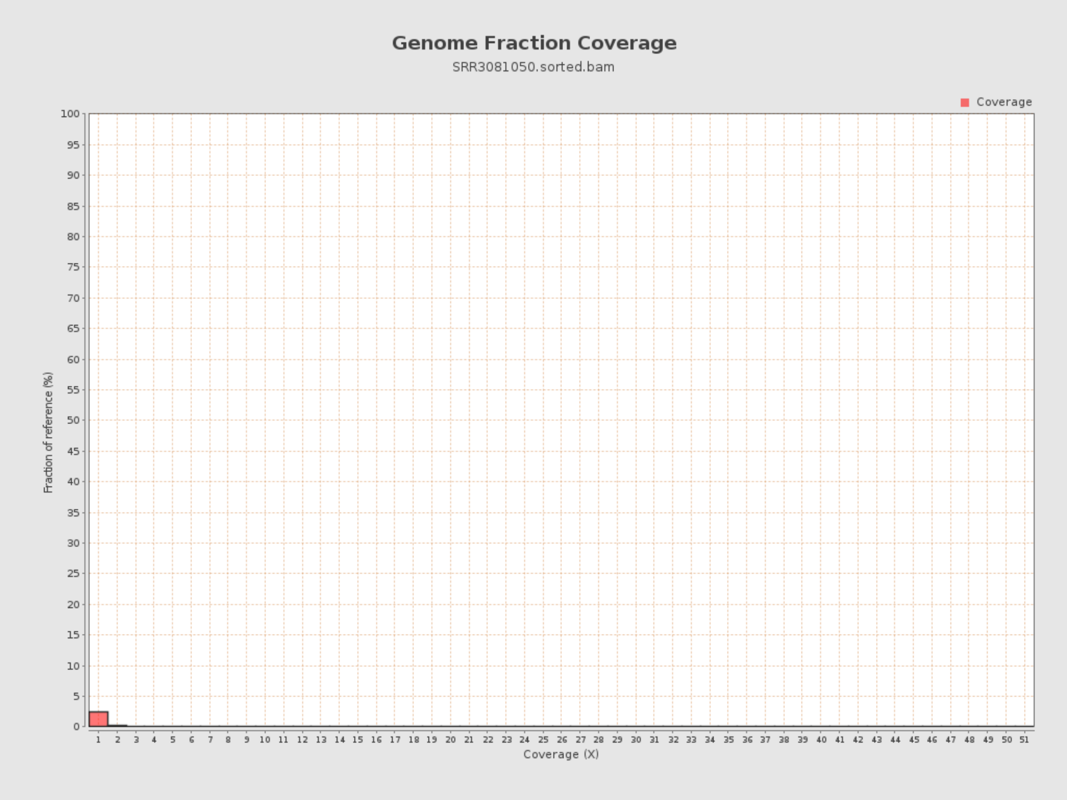
4. Results : Coverage Histogram



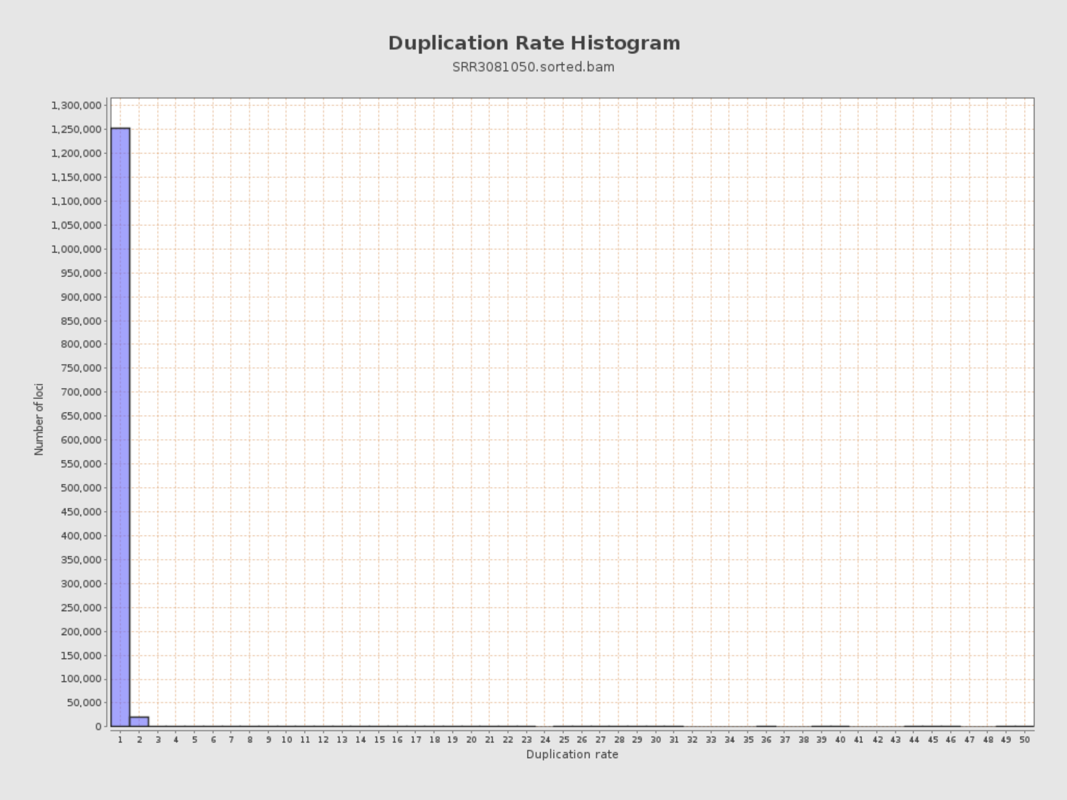
5. Results : Coverage Histogram (0-50X)



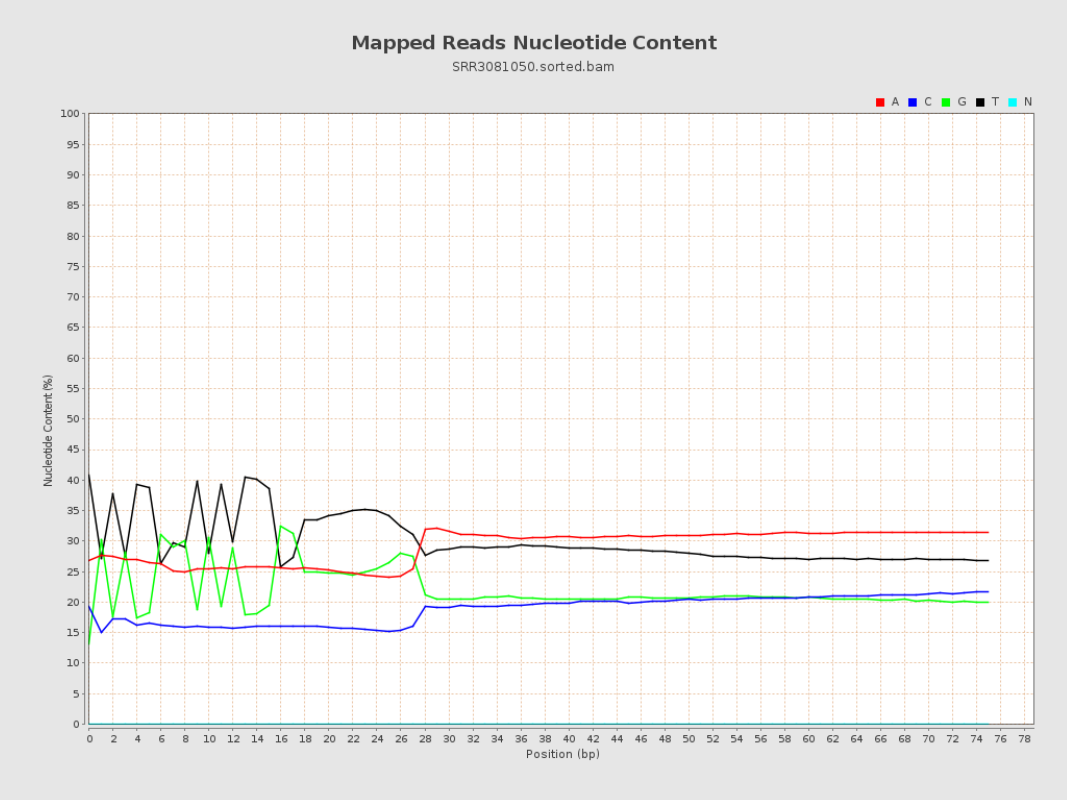
6. Results : Genome Fraction Coverage



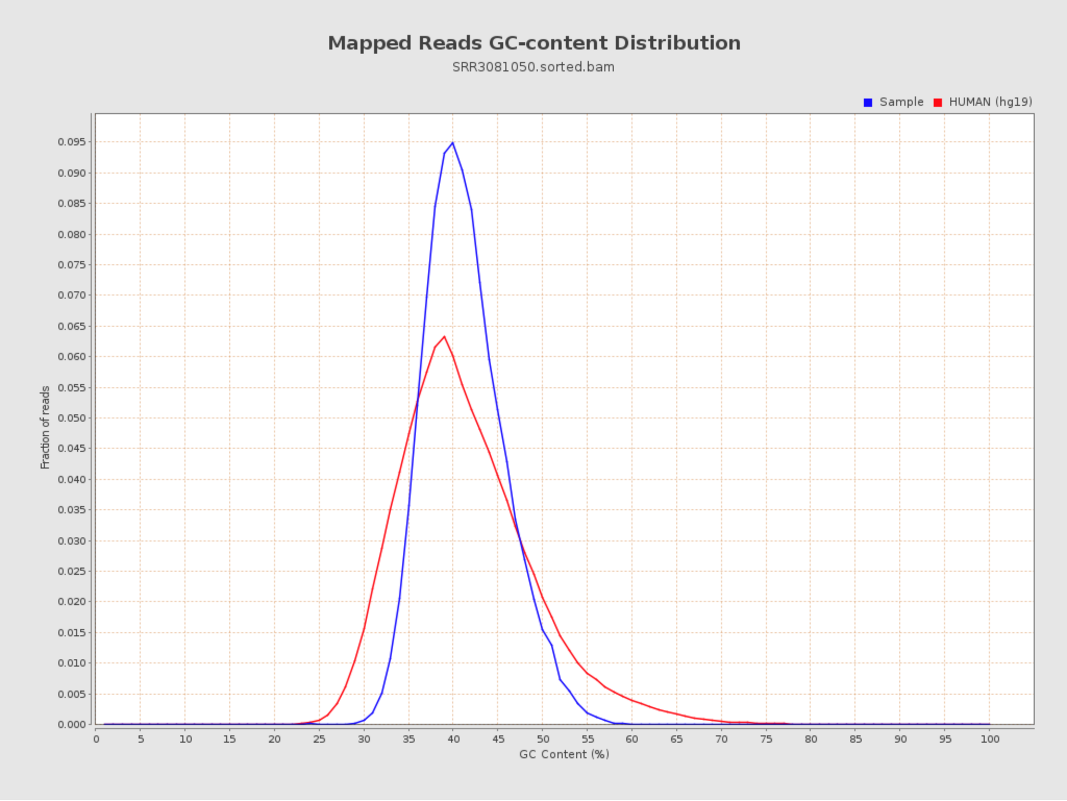
7. Results : Duplication Rate Histogram



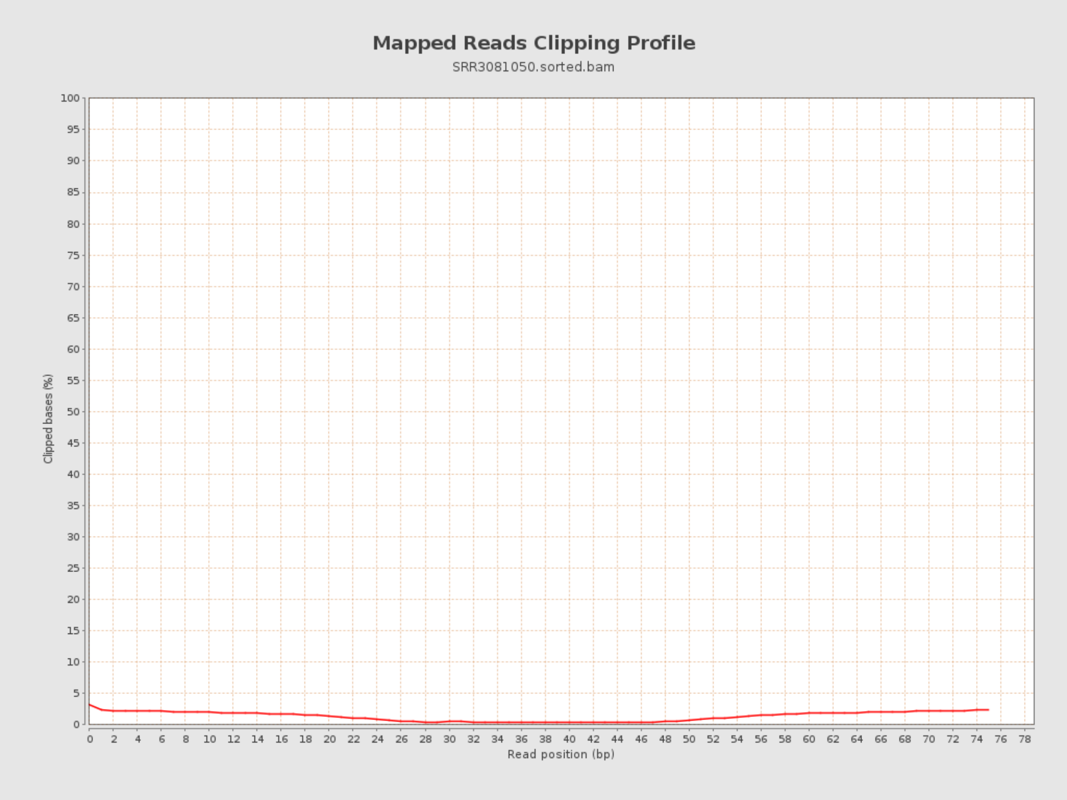
8. Results : Mapped Reads Nucleotide Content



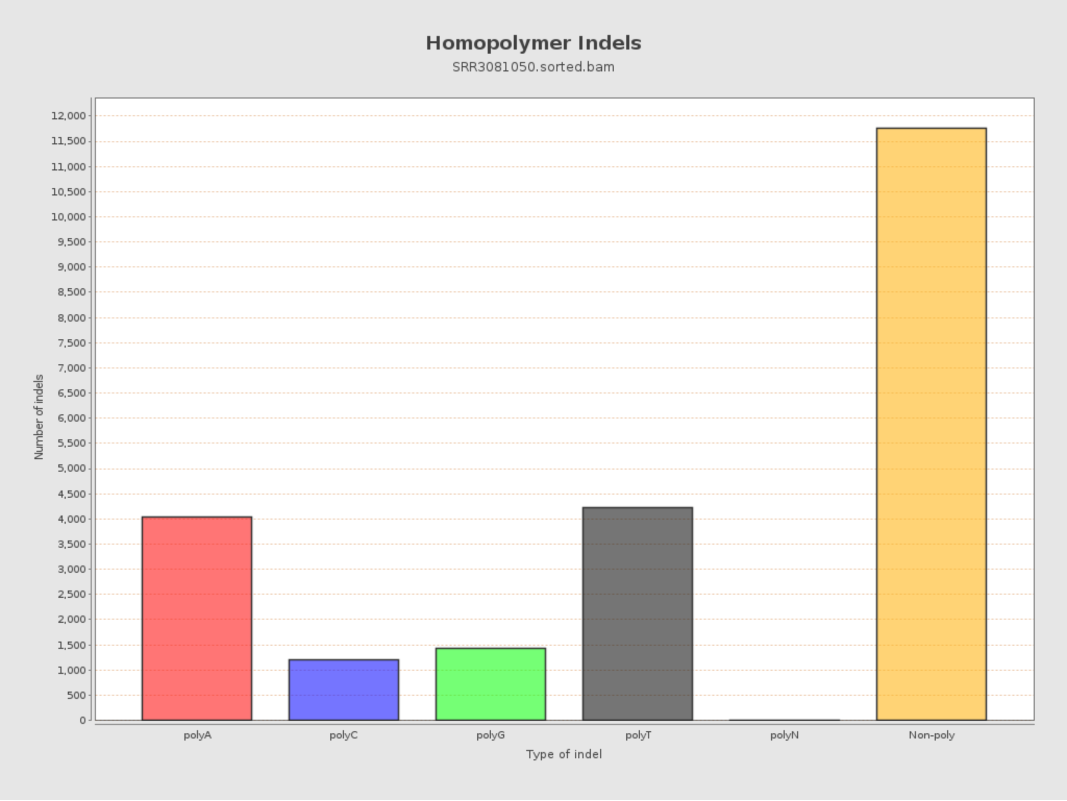
9. Results : Mapped Reads GC-content Distribution



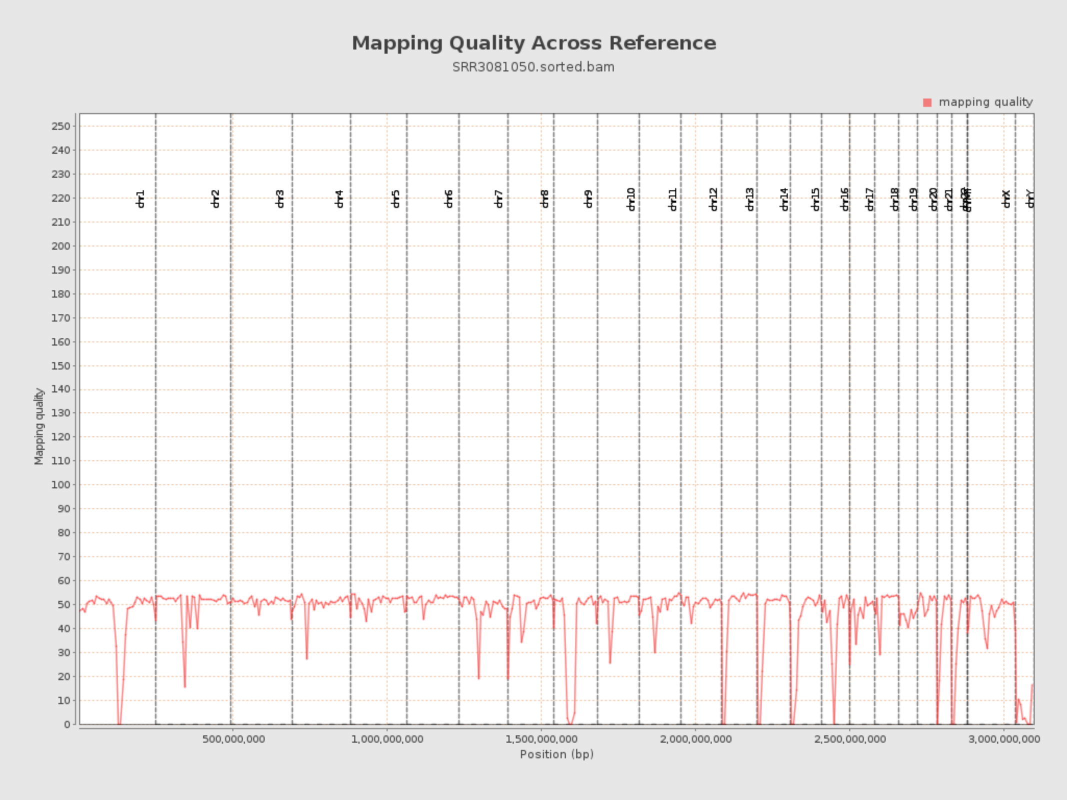
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram