Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:46:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081038.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_SRR3081038 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081038.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:46:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081038.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,064,609
Mapped reads	1,567,670 / 75.93%
Unmapped reads	496,939 / 24.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,742 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	43,862 / 2.12%
Duplication rate	2.22%
Clipped reads	868,316 / 42.06%

2.2. ACGT Content

Number/percentage of A's	28,623,770 / 29%
Number/percentage of C's	18,759,936 / 19%
Number/percentage of T's	29,630,759 / 30.02%
Number/percentage of G's	21,699,440 / 21.98%
Number/percentage of N's	1,256 / 0%
GC Percentage	40.99%

2.3. Coverage

Mean	0.0319

Standard Deviation	0.2551

2.4. Mapping Quality

Mean Mapping Quality	46.22

2.5. Mismatches and indels

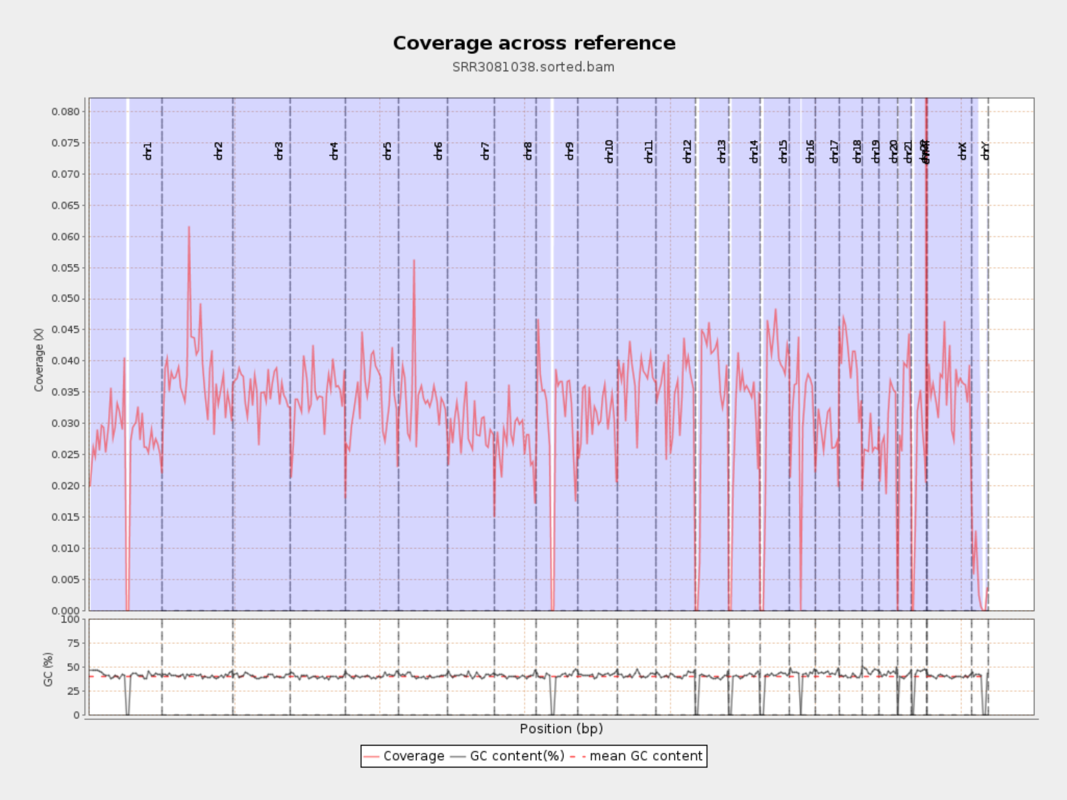
General error rate	0.79%
Mismatches	766,624
Insertions	6,572
Mapped reads with at least one insertion	0.41%
Deletions	19,206
Mapped reads with at least one deletion	1.21%
Homopolymer indels	47.33%

2.6. Chromosome stats

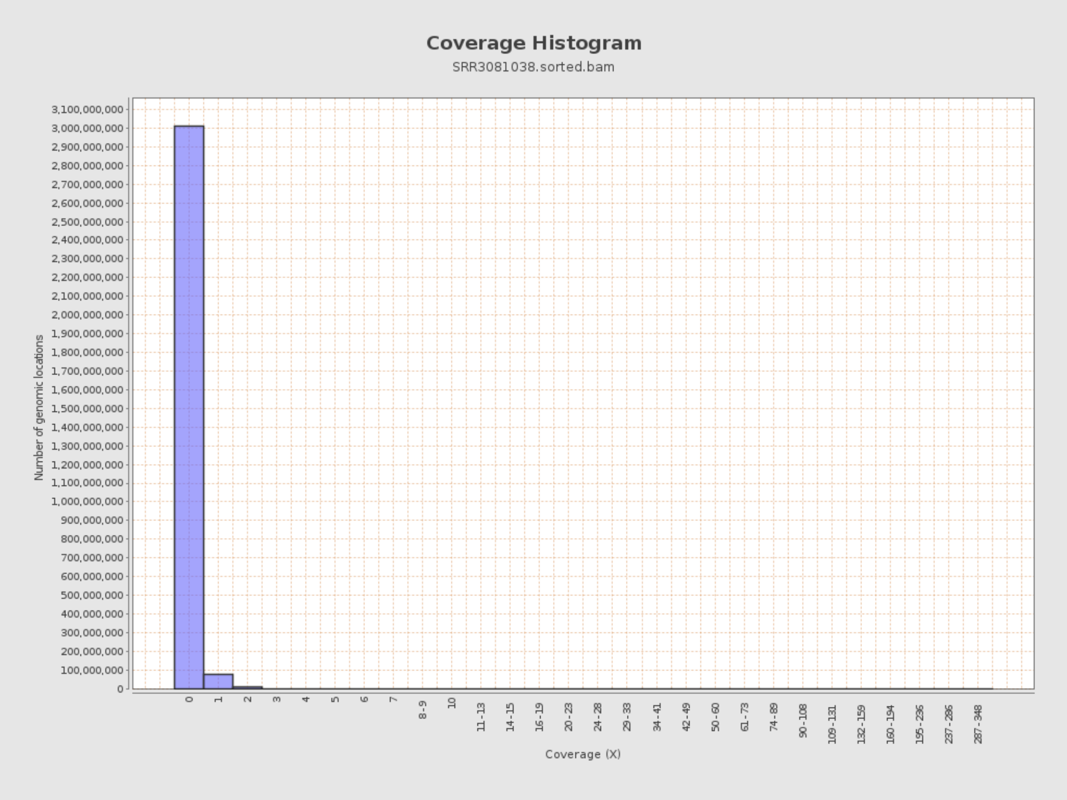
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6679292	0.0268	0.3164
chr2	243199373	9191649	0.0378	0.3042
chr3	198022430	6992094	0.0353	0.2073
chr4	191154276	6590663	0.0345	0.2108
chr5	180915260	6205504	0.0343	0.2047
chr6	171115067	5832123	0.0341	0.2787
chr7	159138663	4663027	0.0293	0.2725

chr8	146364022	3960448	0.0271	0.2602
chr9	141213431	4267472	0.0302	0.259
chr10	135534747	4219529	0.0311	0.2321
chr11	135006516	5002179	0.0371	0.2858
chr12	133851895	4625322	0.0346	0.2075
chr13	115169878	3892776	0.0338	0.2026
chr14	107349540	3126672	0.0291	0.2008
chr15	102531392	3522483	0.0344	0.2123
chr16	90354753	2842410	0.0315	0.2157
chr17	81195210	2272877	0.028	0.2015
chr18	78077248	3141977	0.0402	0.5106
chr19	59128983	1558843	0.0264	0.2786
chr20	63025520	1811909	0.0287	0.1908
chr21	48129895	1496442	0.0311	0.2075
chr22	51304566	1080464	0.0211	0.1591
chrMT	16571	15052	0.9083	1.0613
chrX	155270560	5512458	0.0355	0.2318
chrY	59373566	244047	0.0041	0.098

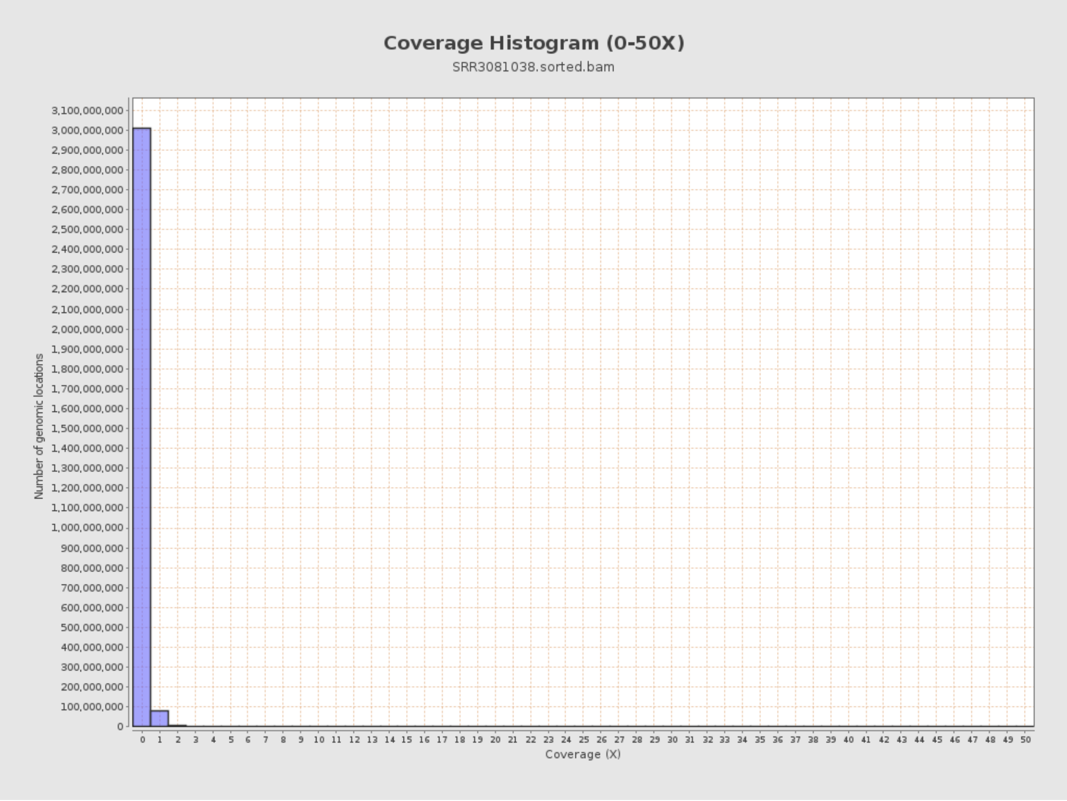
3. Results : Coverage across reference



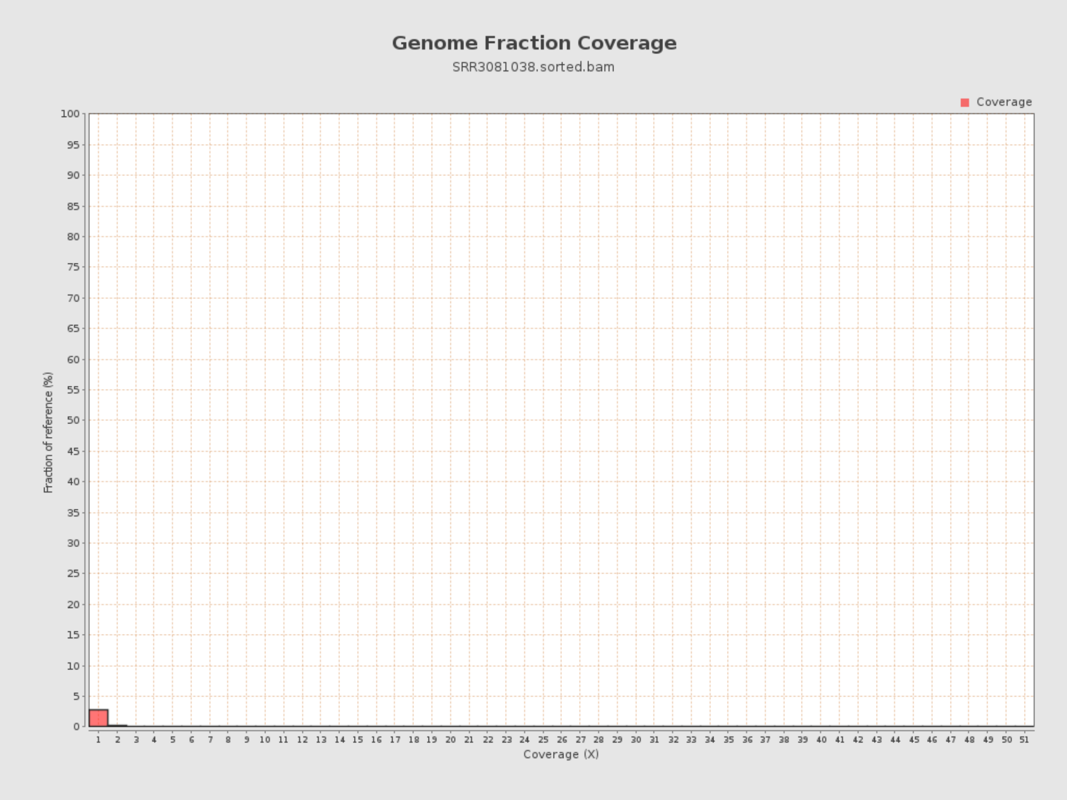
4. Results : Coverage Histogram



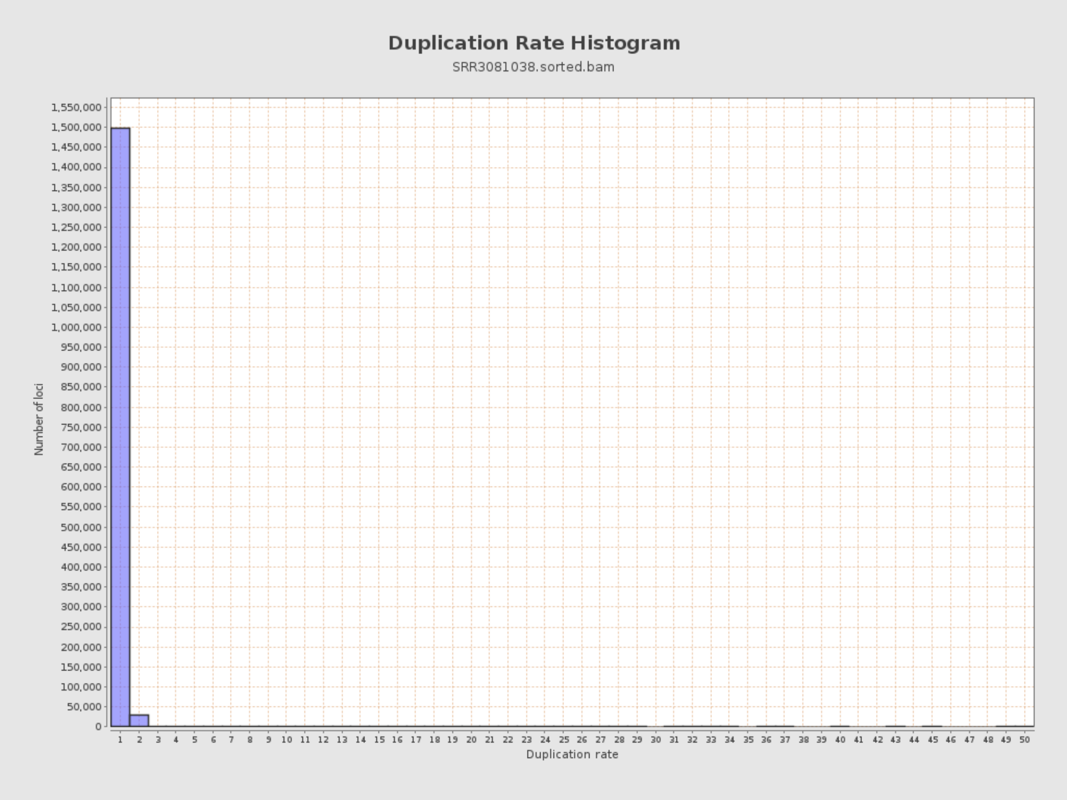
5. Results : Coverage Histogram (0-50X)



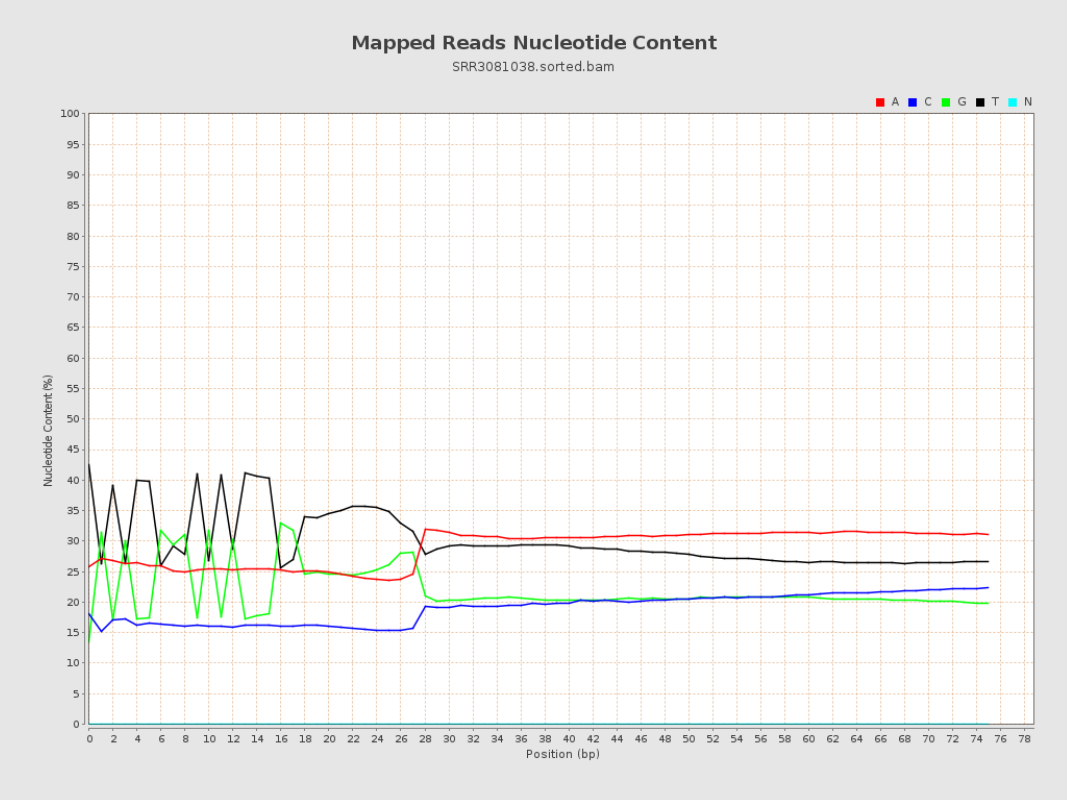
6. Results : Genome Fraction Coverage



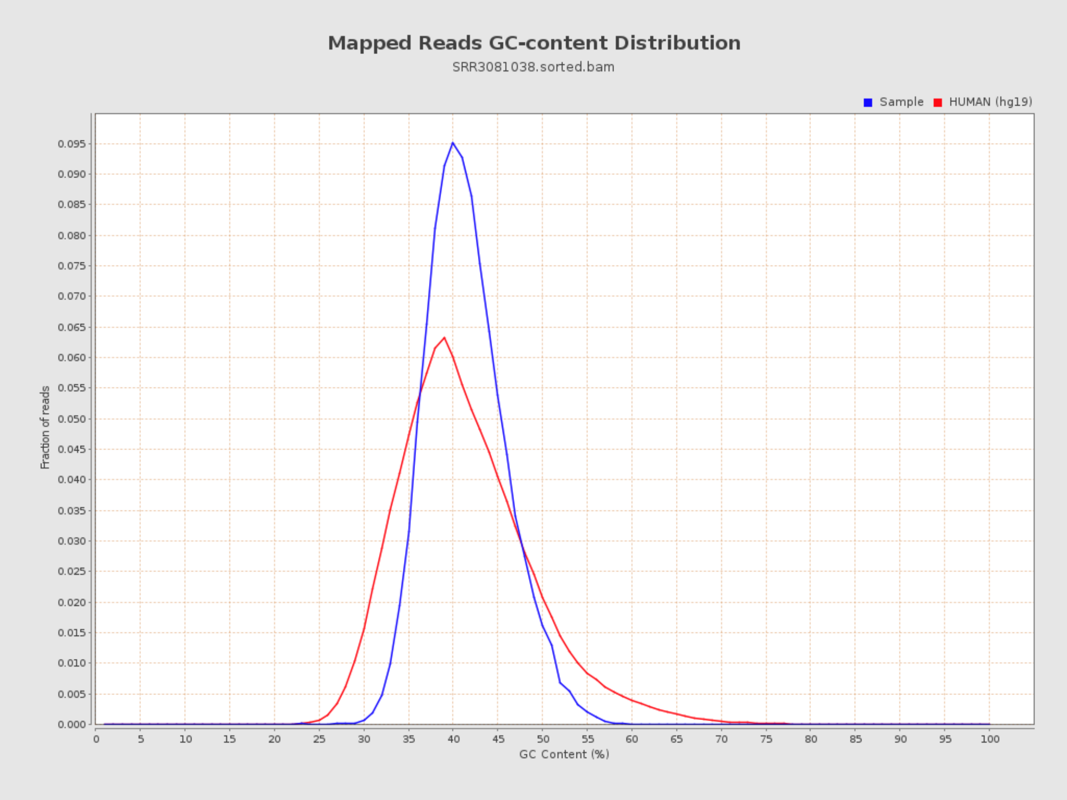
7. Results : Duplication Rate Histogram



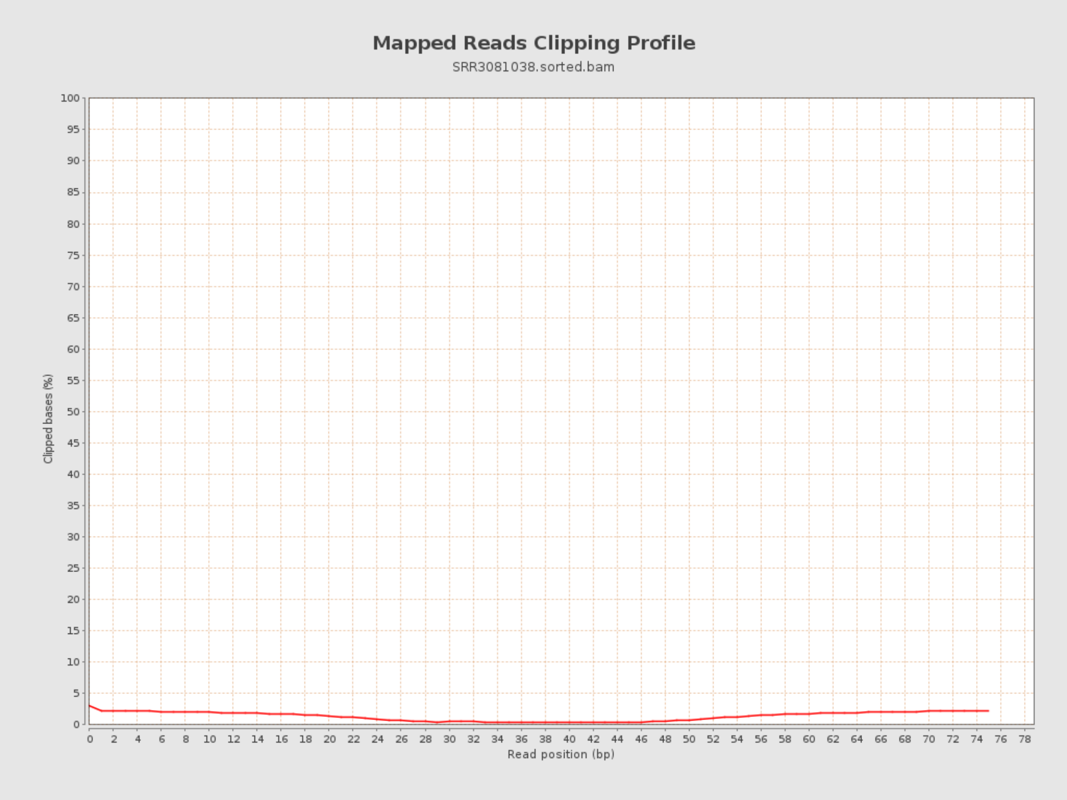
8. Results : Mapped Reads Nucleotide Content



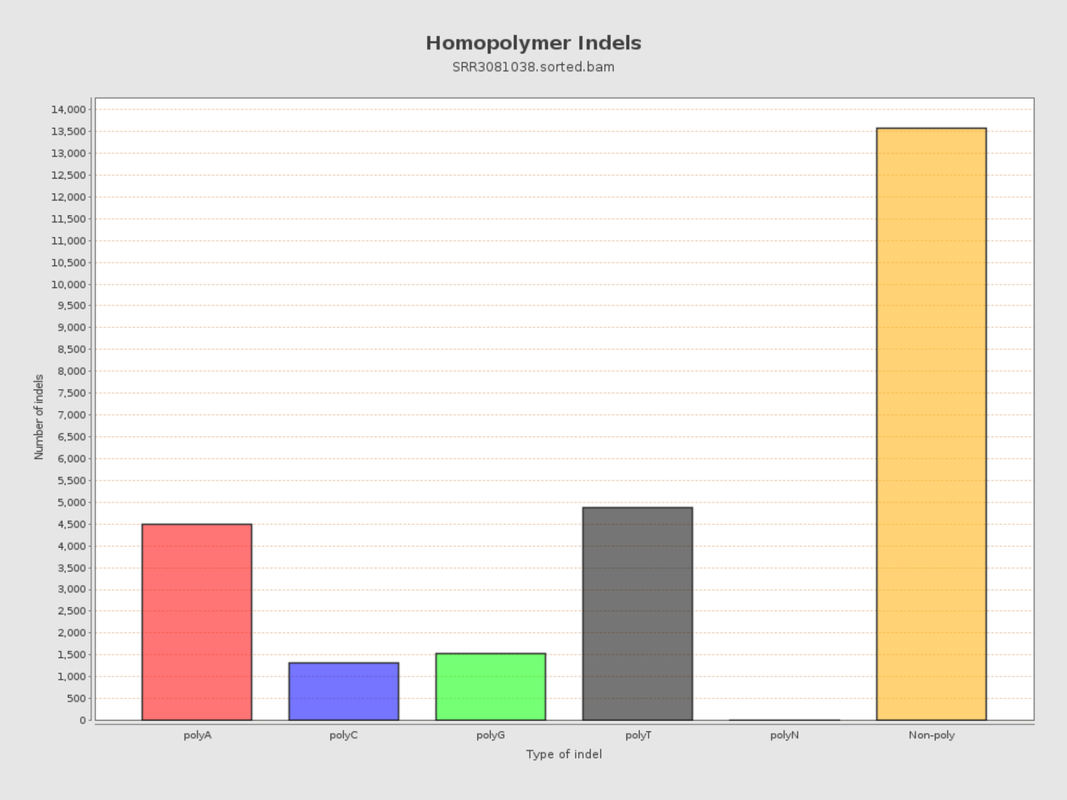
9. Results : Mapped Reads GC-content Distribution



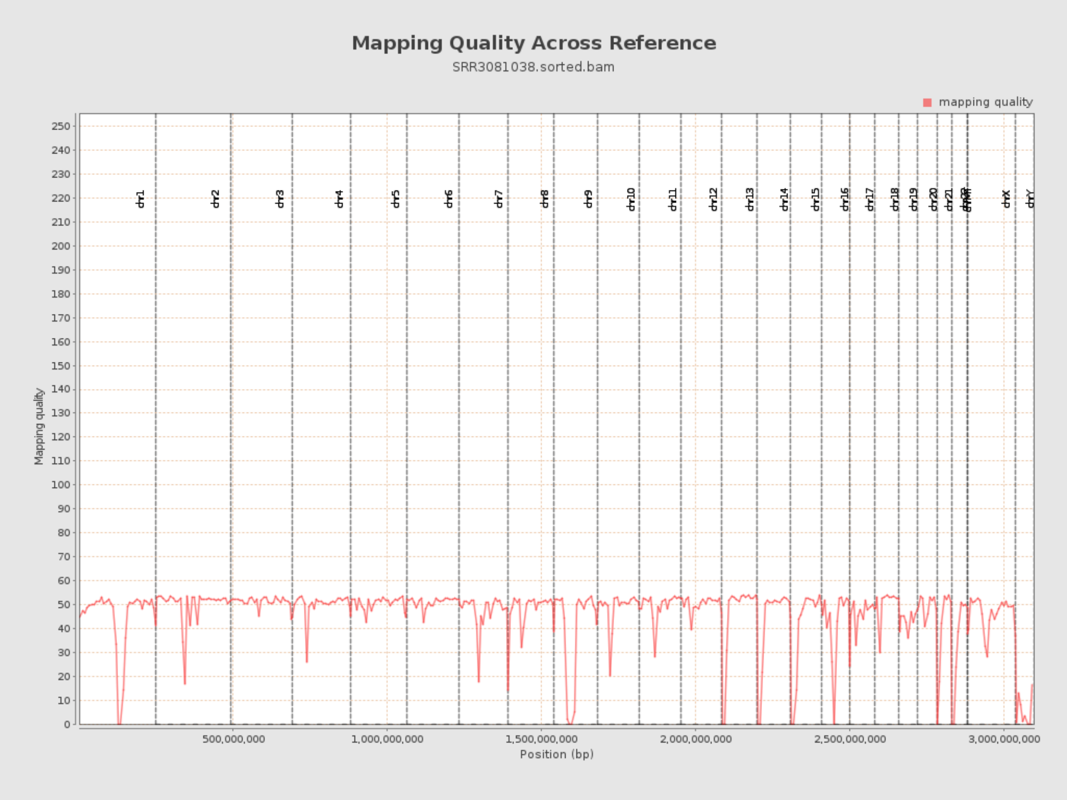
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram