Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:19:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081021.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_SRR3081021 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081021.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:19:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081021.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,885,961
Mapped reads	2,069,214 / 71.7%
Unmapped reads	816,747 / 28.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,735 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	72,857 / 2.52%
Duplication rate	2.89%
Clipped reads	1,339,825 / 46.43%

2.2. ACGT Content

Number/percentage of A's	36,270,386 / 28.81%
Number/percentage of C's	25,347,290 / 20.13%
Number/percentage of T's	36,617,395 / 29.09%
Number/percentage of G's	27,656,593 / 21.97%
Number/percentage of N's	1,738 / 0%
GC Percentage	42.1%

2.3. Coverage

Mean	0.0407

Standard Deviation	0.2982

2.4. Mapping Quality

Mean Mapping Quality	45.06

2.5. Mismatches and indels

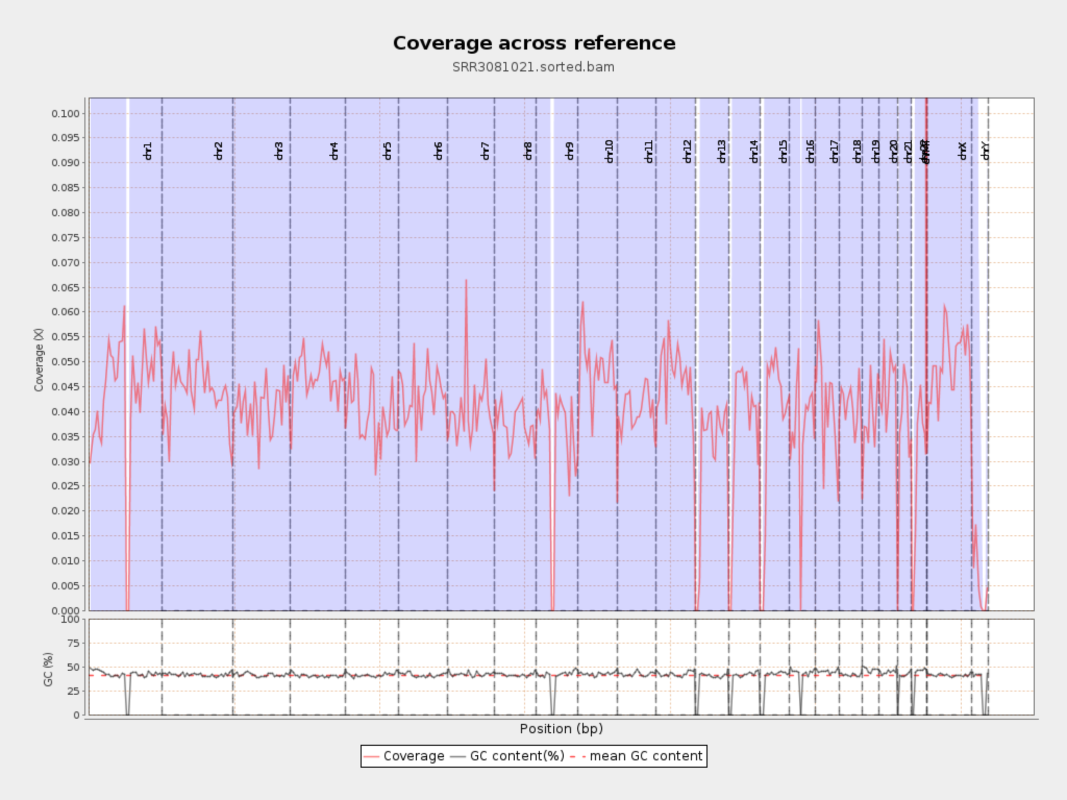
General error rate	0.73%
Mismatches	900,718
Insertions	8,472
Mapped reads with at least one insertion	0.41%
Deletions	24,138
Mapped reads with at least one deletion	1.16%
Homopolymer indels	45.62%

2.6. Chromosome stats

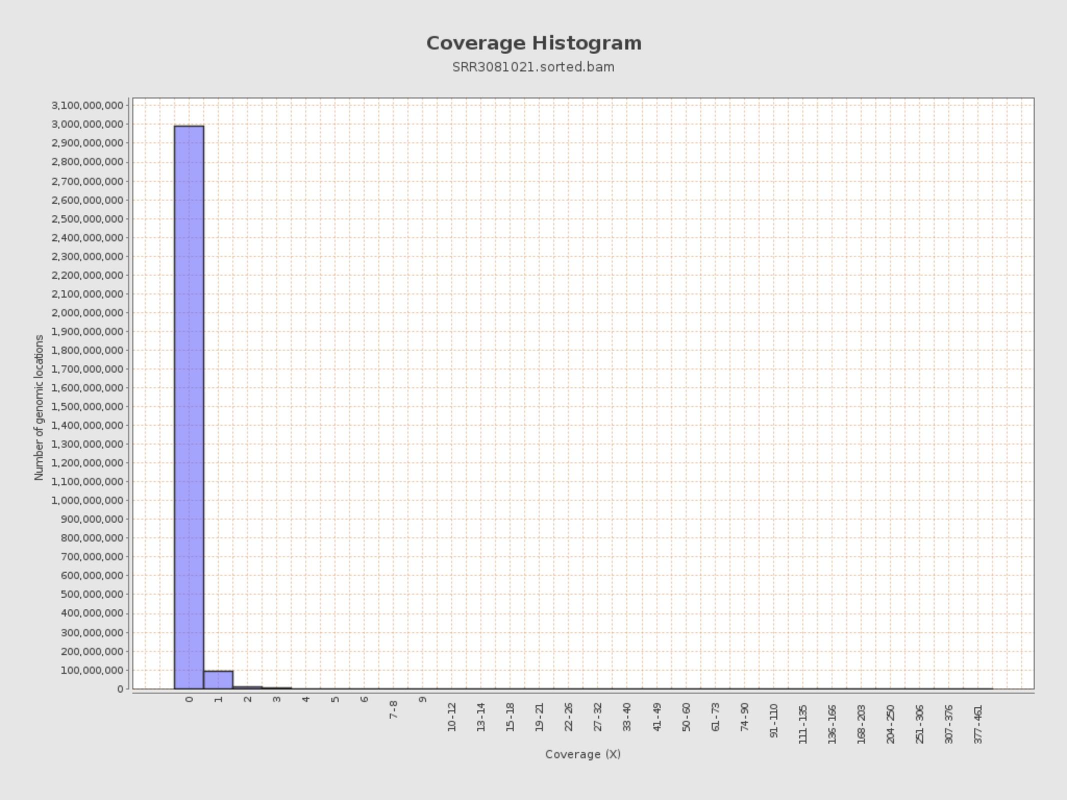
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10898307	0.0437	0.4494
chr2	243199373	10767251	0.0443	0.3145
chr3	198022430	8088954	0.0408	0.2322
chr4	191154276	9012563	0.0471	0.2607
chr5	180915260	7176673	0.0397	0.229
chr6	171115067	7435851	0.0435	0.2671
chr7	159138663	6506334	0.0409	0.4093

chr8	146364022	5477616	0.0374	0.3053
chr9	141213431	4846874	0.0343	0.268
chr10	135534747	6645583	0.049	0.2949
chr11	135006516	5414699	0.0401	0.2794
chr12	133851895	6286766	0.047	0.2527
chr13	115169878	3570655	0.031	0.2012
chr14	107349540	3887636	0.0362	0.2281
chr15	102531392	3801638	0.0371	0.2287
chr16	90354753	3285472	0.0364	0.2386
chr17	81195210	3272744	0.0403	0.247
chr18	78077248	3222433	0.0413	0.5022
chr19	59128983	2312682	0.0391	0.3451
chr20	63025520	2805805	0.0445	0.2467
chr21	48129895	1723227	0.0358	0.2305
chr22	51304566	1386423	0.027	0.1882
chrMT	16571	64774	3.9089	2.9062
chrX	155270560	7684812	0.0495	0.2782
chrY	59373566	359367	0.0061	0.1249

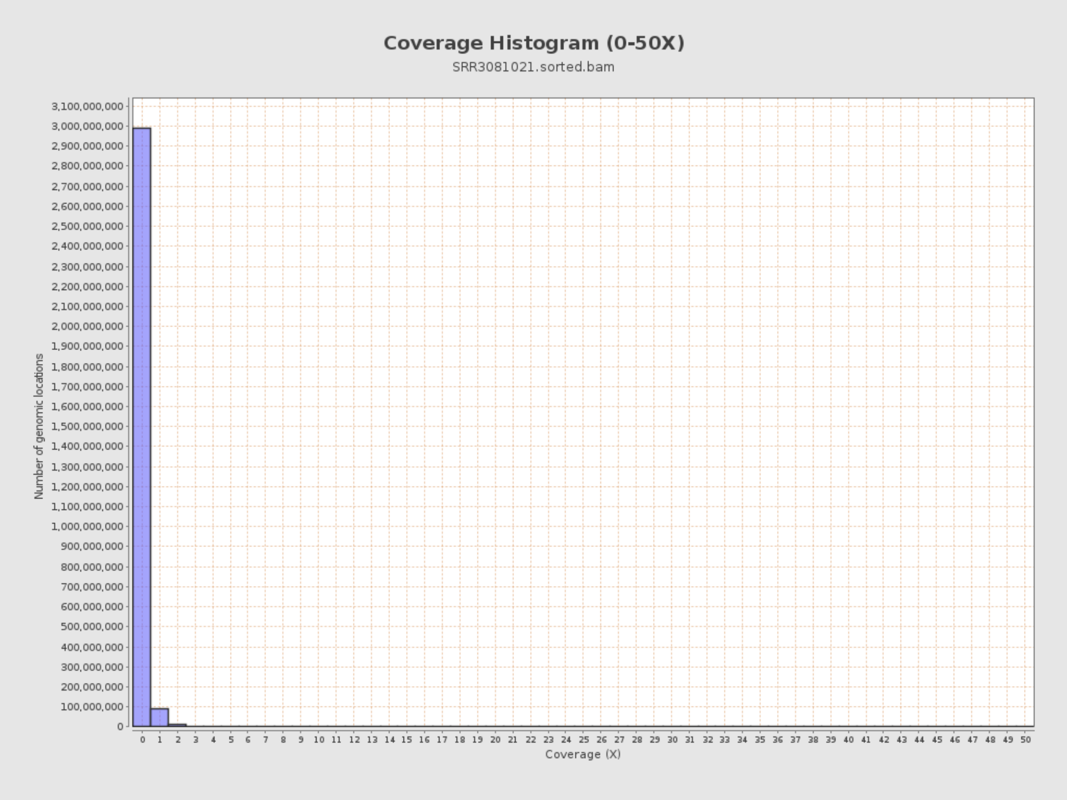
3. Results : Coverage across reference



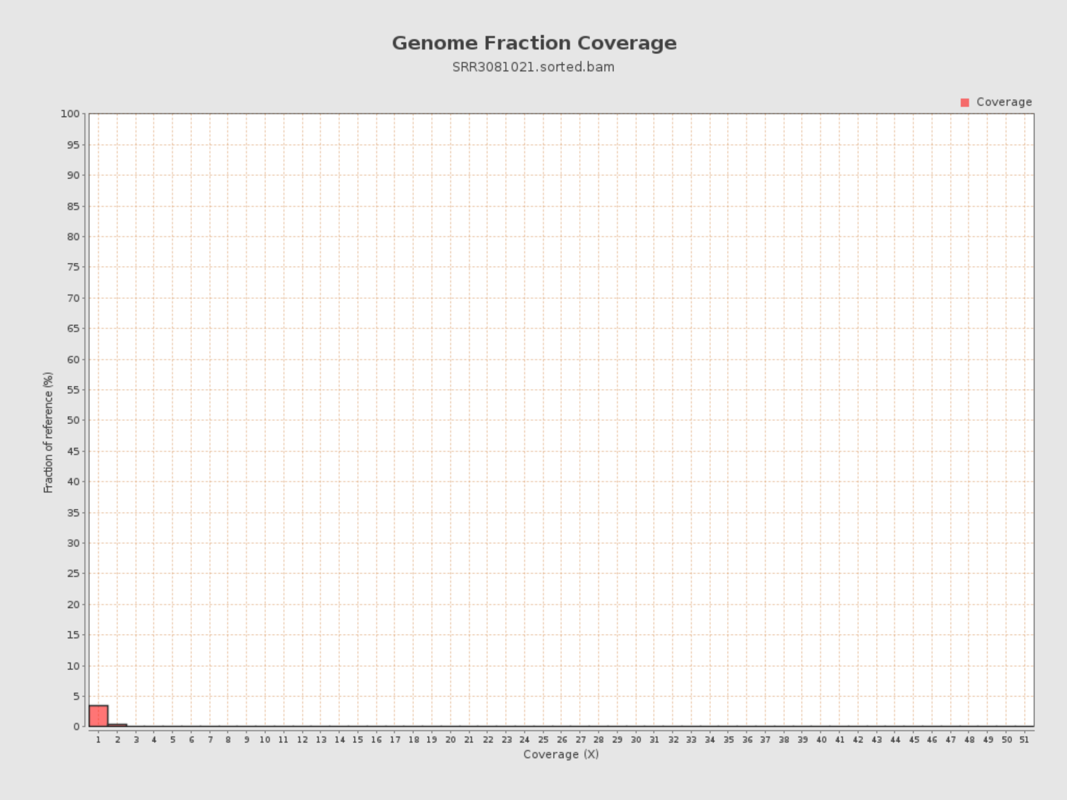
4. Results : Coverage Histogram



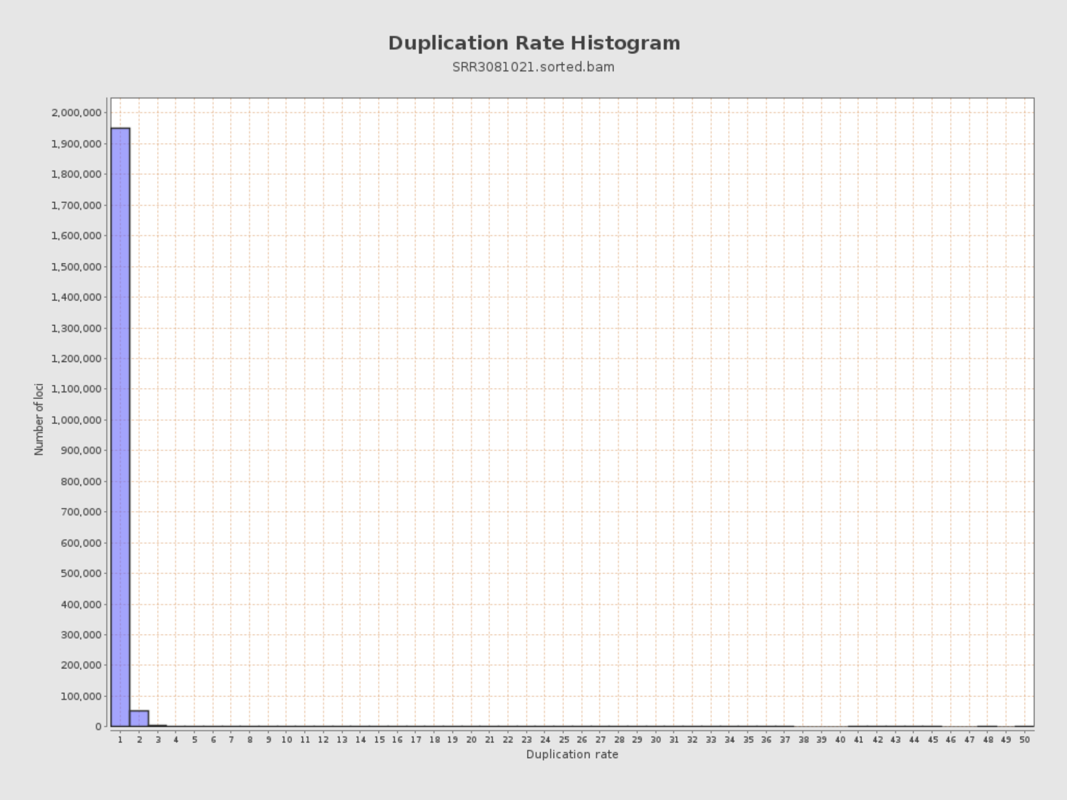
5. Results : Coverage Histogram (0-50X)



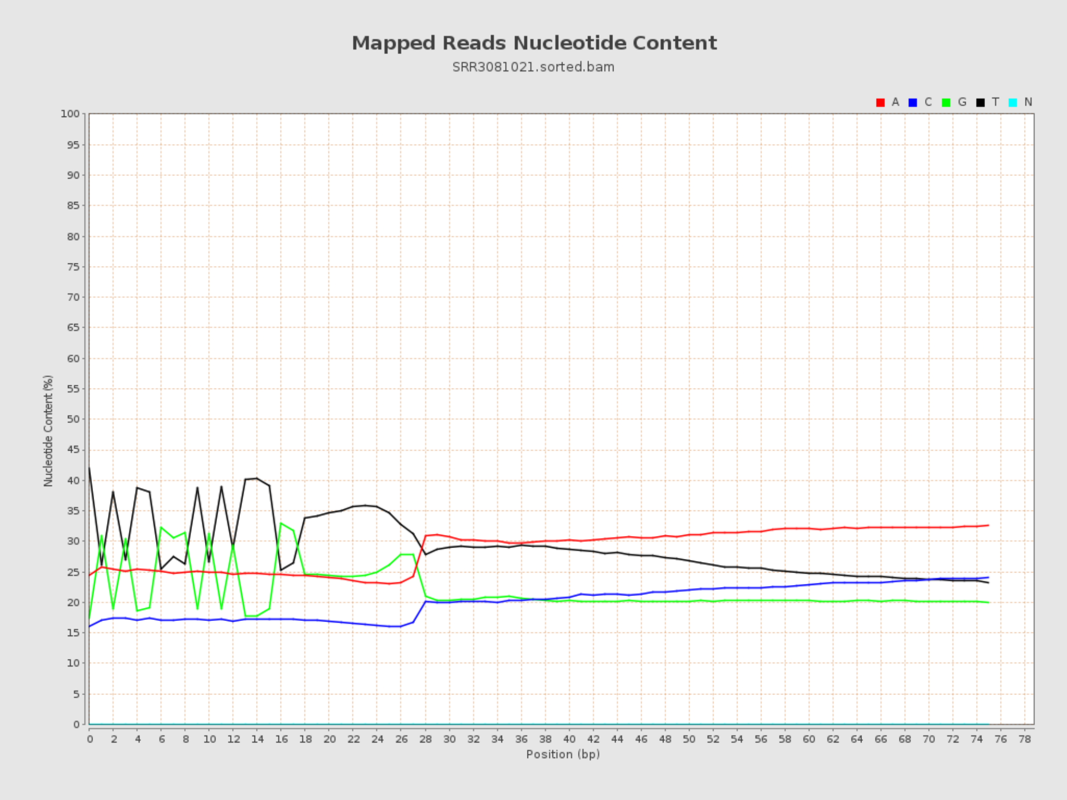
6. Results : Genome Fraction Coverage



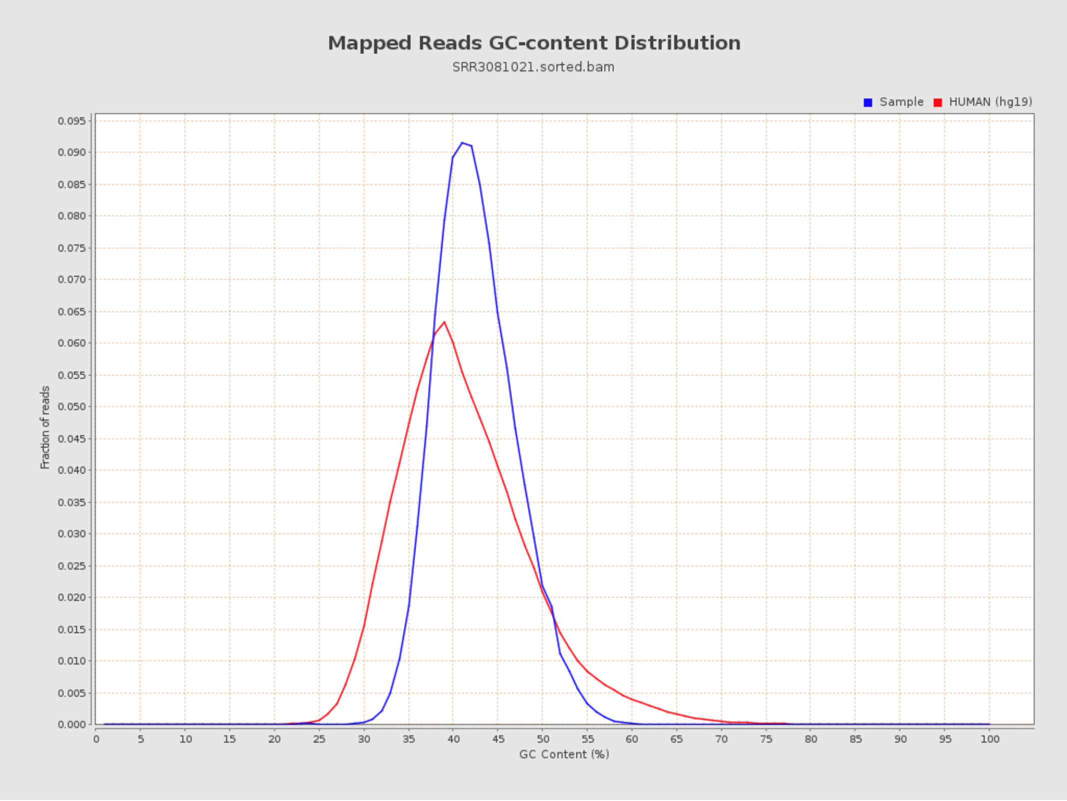
7. Results : Duplication Rate Histogram



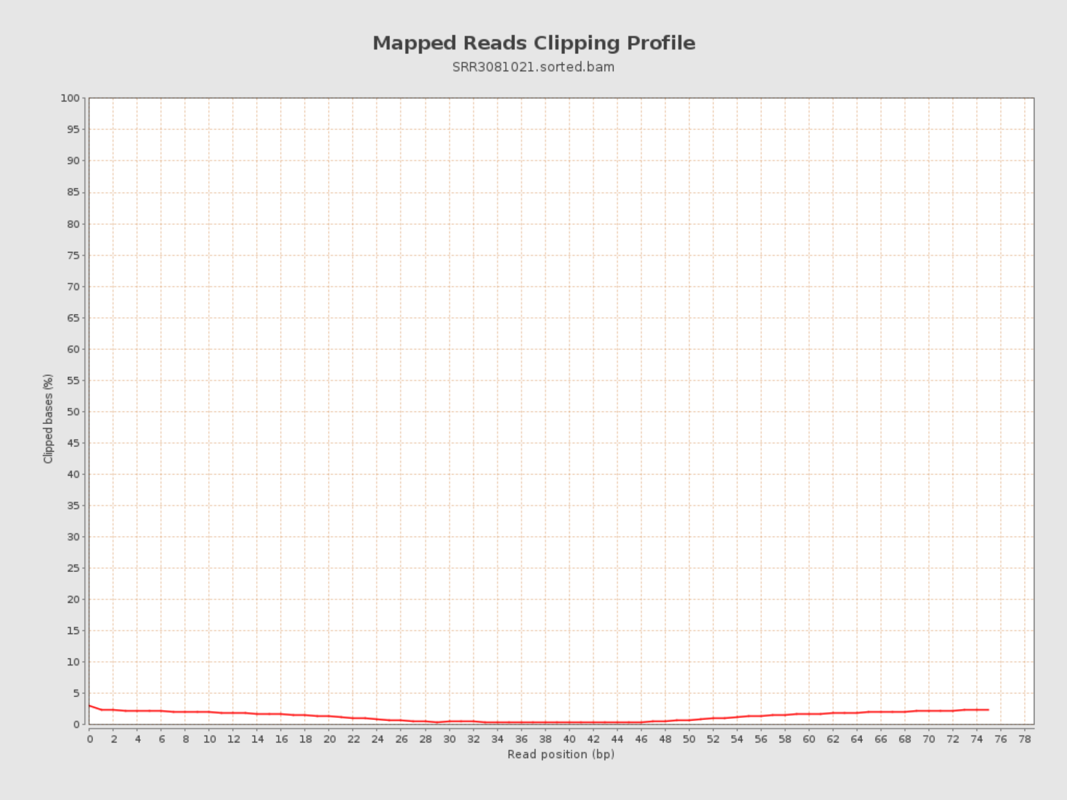
8. Results : Mapped Reads Nucleotide Content



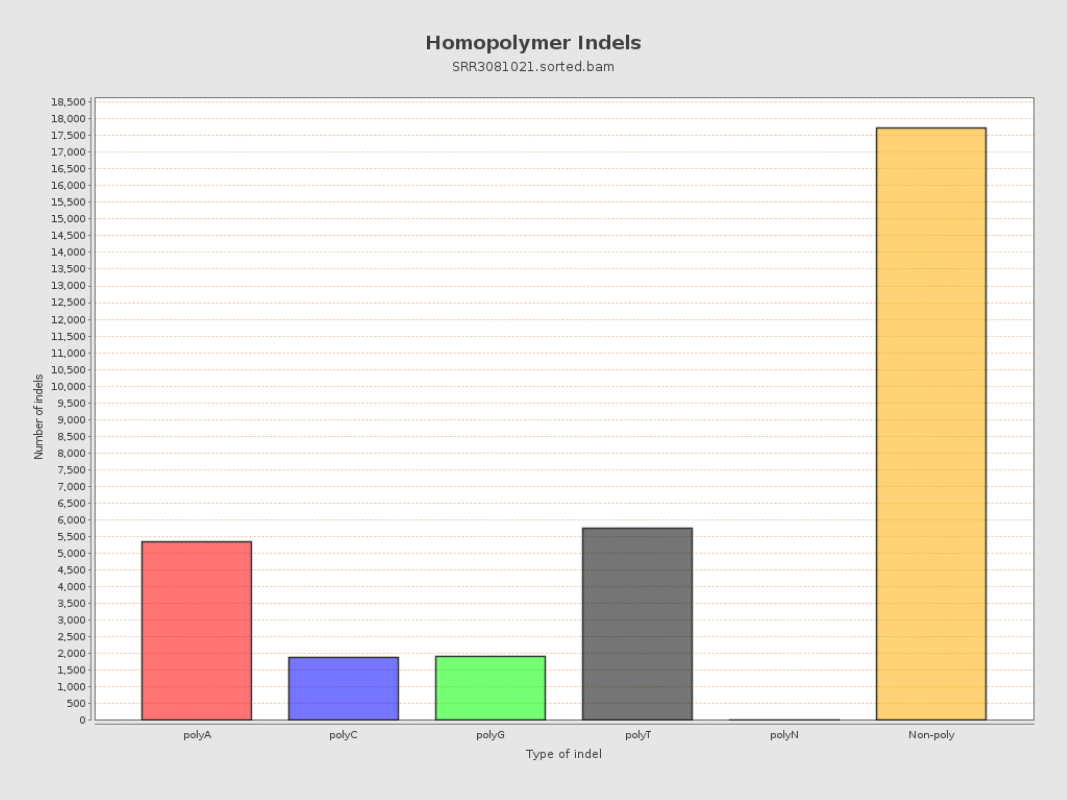
9. Results : Mapped Reads GC-content Distribution



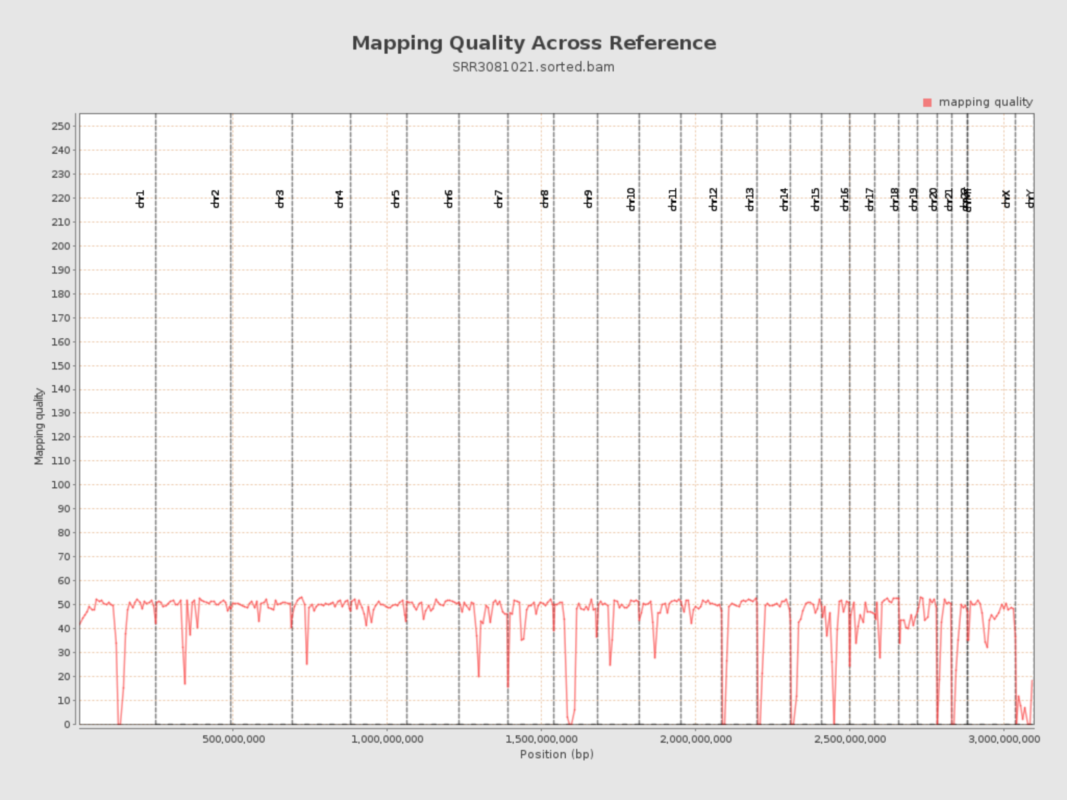
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram