Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:19:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081031.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_SRR3081031 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081031.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:19:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081031.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,196,294
Mapped reads	2,231,976 / 69.83%
Unmapped reads	964,318 / 30.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,567 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	90,291 / 2.82%
Duplication rate	3.39%
Clipped reads	1,359,479 / 42.53%

2.2. ACGT Content

Number/percentage of A's	38,762,436 / 28.08%
Number/percentage of C's	28,085,378 / 20.35%
Number/percentage of T's	40,215,969 / 29.14%
Number/percentage of G's	30,967,625 / 22.43%
Number/percentage of N's	1,716 / 0%
GC Percentage	42.78%

2.3. Coverage

Mean	0.0446

Standard Deviation	0.318

2.4. Mapping Quality

Mean Mapping Quality	46.17

2.5. Mismatches and indels

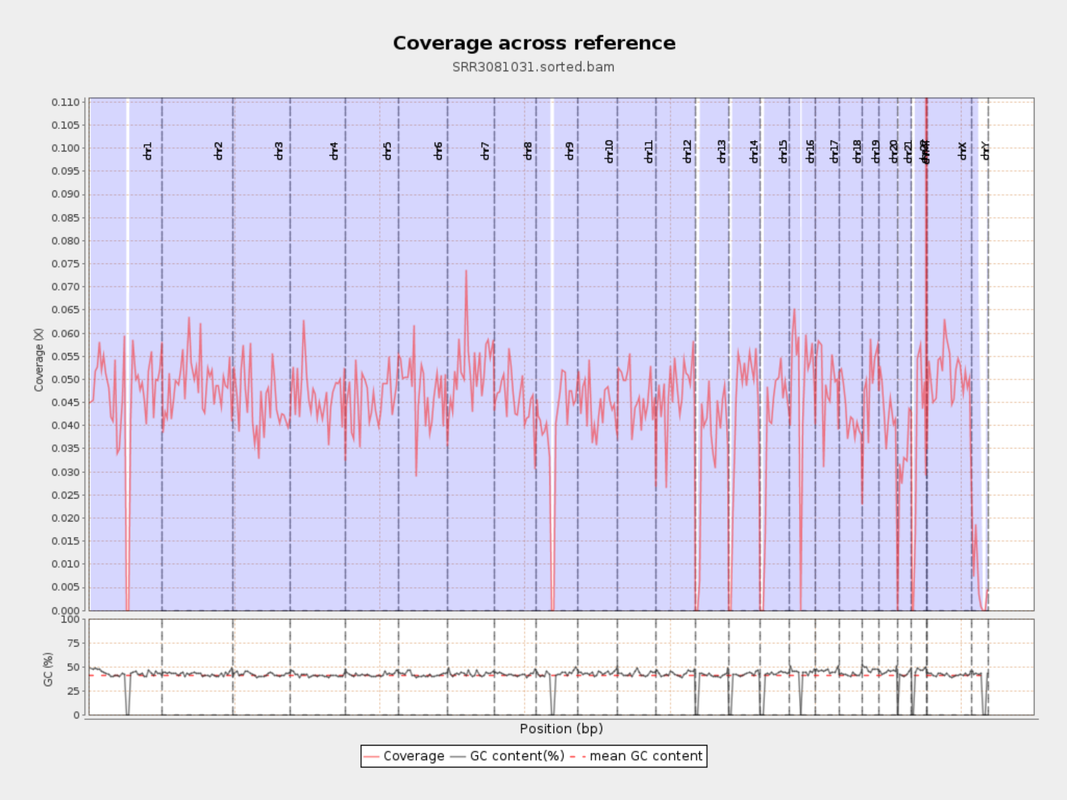
General error rate	0.73%
Mismatches	989,329
Insertions	8,662
Mapped reads with at least one insertion	0.39%
Deletions	25,530
Mapped reads with at least one deletion	1.13%
Homopolymer indels	46.56%

2.6. Chromosome stats

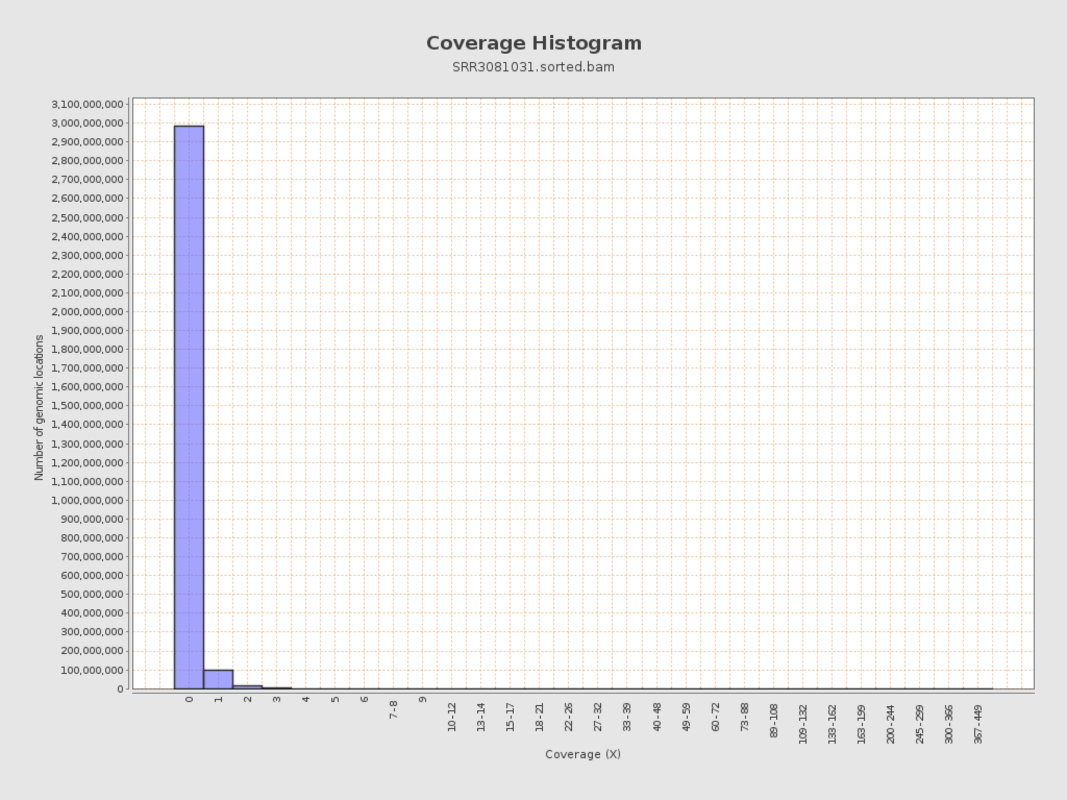
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11368488	0.0456	0.4708
chr2	243199373	11962948	0.0492	0.3214
chr3	198022430	8887424	0.0449	0.2482
chr4	191154276	8943431	0.0468	0.2698
chr5	180915260	8264415	0.0457	0.2514
chr6	171115067	8138752	0.0476	0.2914
chr7	159138663	8363992	0.0526	0.5186

chr8	146364022	6694215	0.0457	0.293
chr9	141213431	5464040	0.0387	0.2801
chr10	135534747	6000799	0.0443	0.3064
chr11	135006516	6273430	0.0465	0.3082
chr12	133851895	6343745	0.0474	0.256
chr13	115169878	3976813	0.0345	0.2186
chr14	107349540	4594261	0.0428	0.2486
chr15	102531392	3903274	0.0381	0.2423
chr16	90354753	4478836	0.0496	0.2725
chr17	81195210	3987491	0.0491	0.2899
chr18	78077248	3338208	0.0428	0.4615
chr19	59128983	2899764	0.049	0.3813
chr20	63025520	2657101	0.0422	0.2488
chr21	48129895	1513712	0.0315	0.2346
chr22	51304566	1774223	0.0346	0.2181
chrMT	16571	27025	1.6309	1.5907
chrX	155270560	7875311	0.0507	0.285
chrY	59373566	347158	0.0058	0.1356

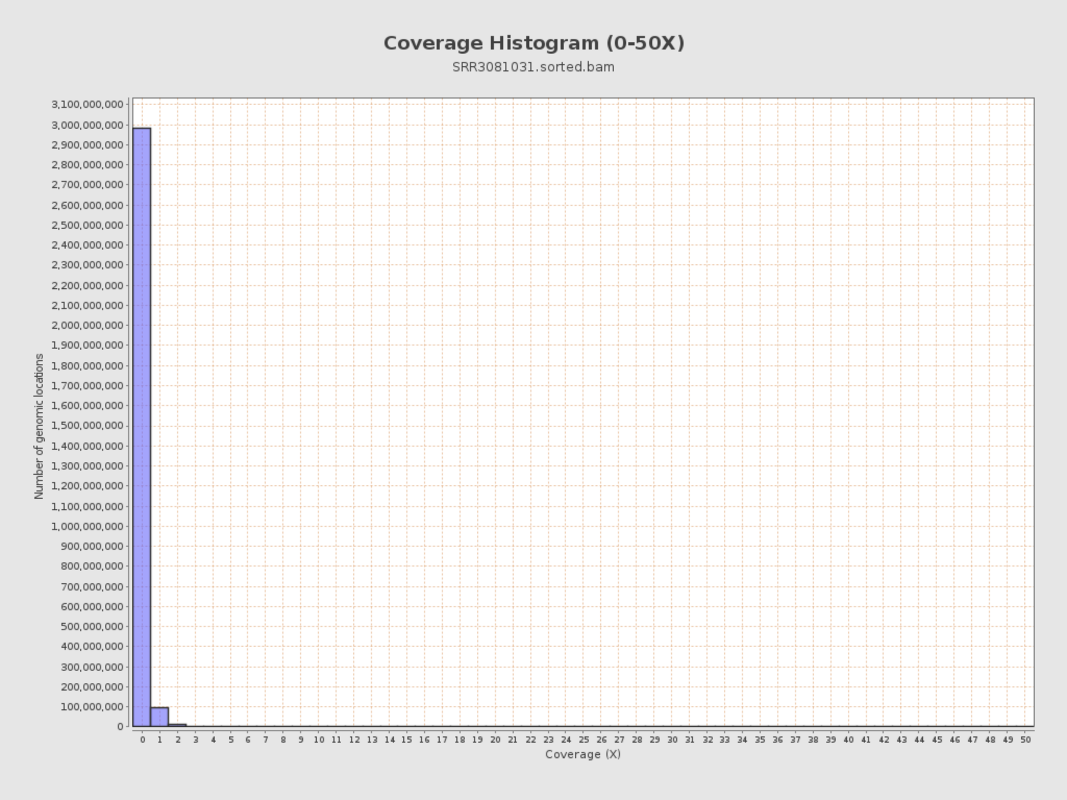
3. Results : Coverage across reference



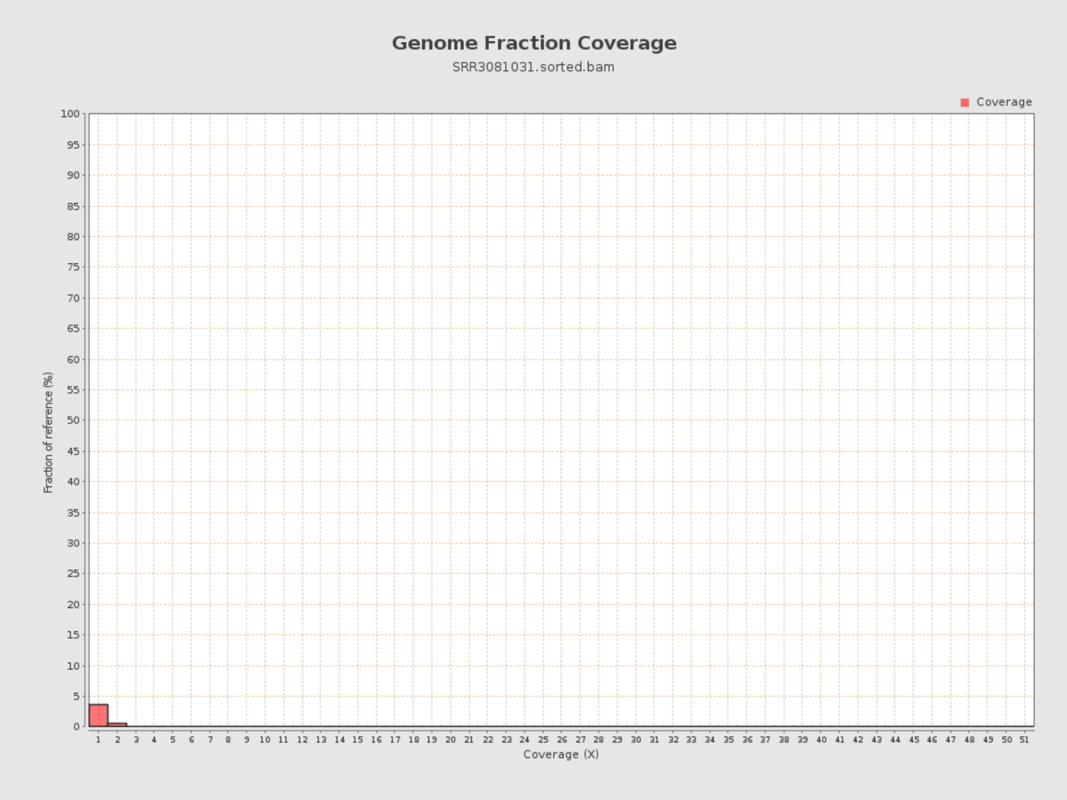
4. Results : Coverage Histogram



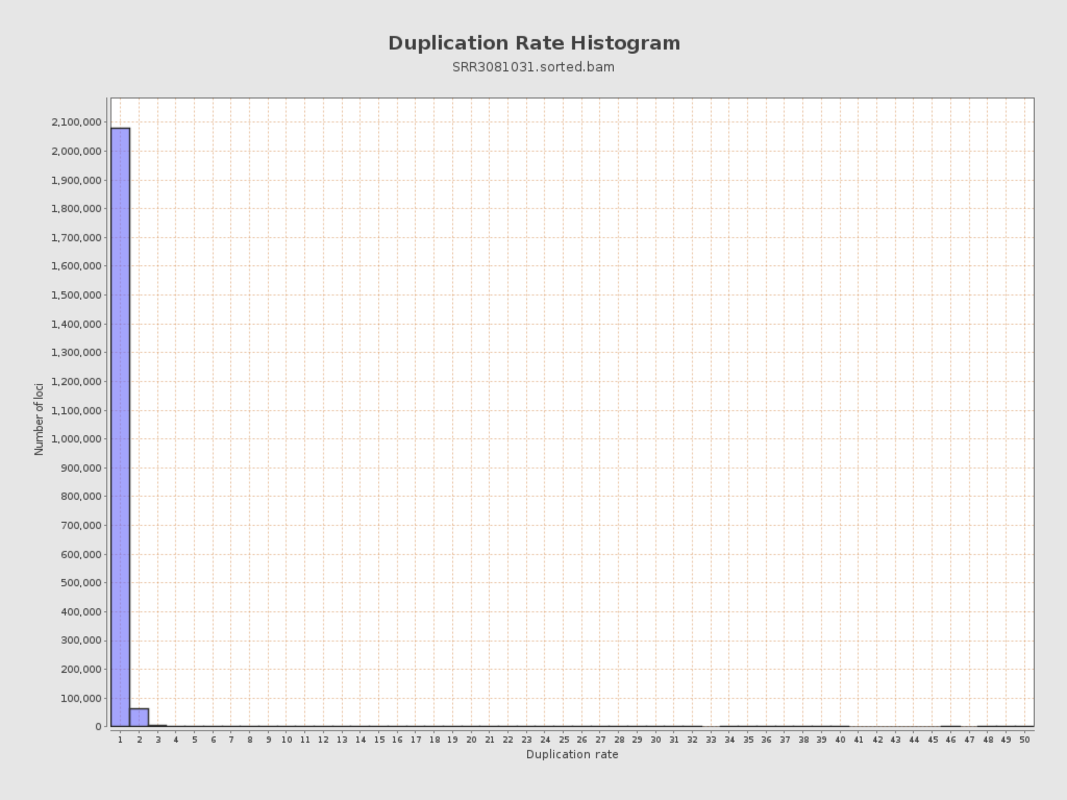
5. Results : Coverage Histogram (0-50X)



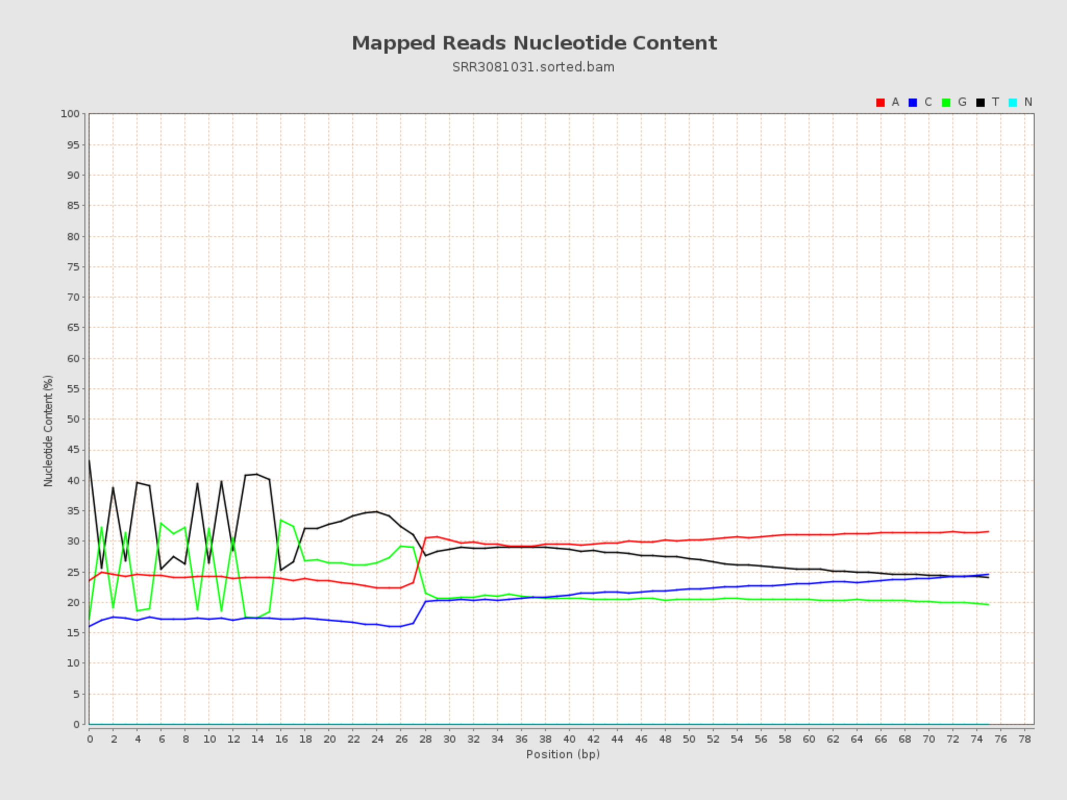
6. Results : Genome Fraction Coverage



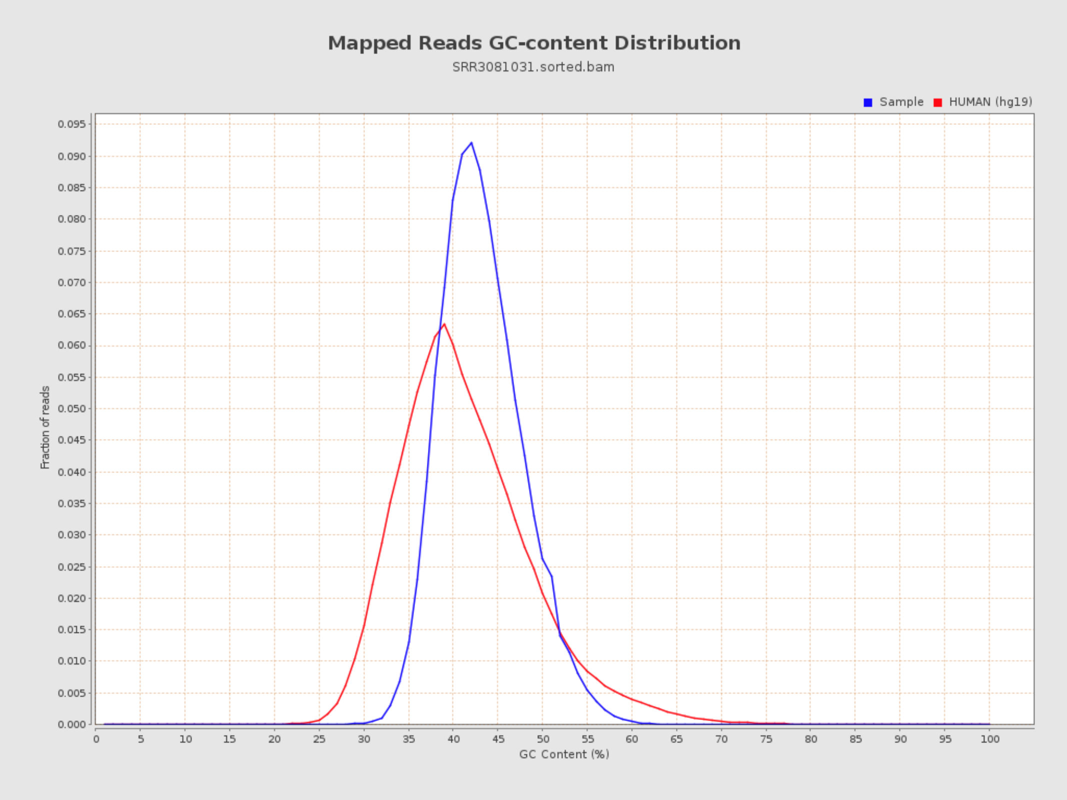
7. Results : Duplication Rate Histogram



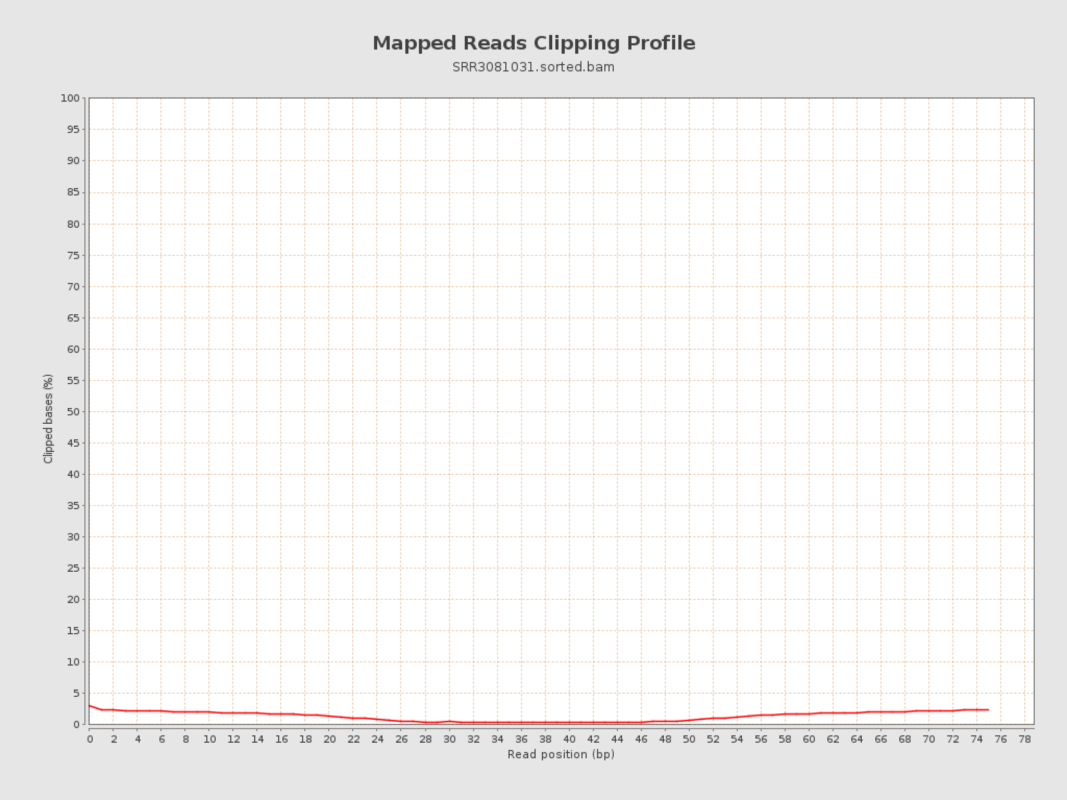
8. Results : Mapped Reads Nucleotide Content



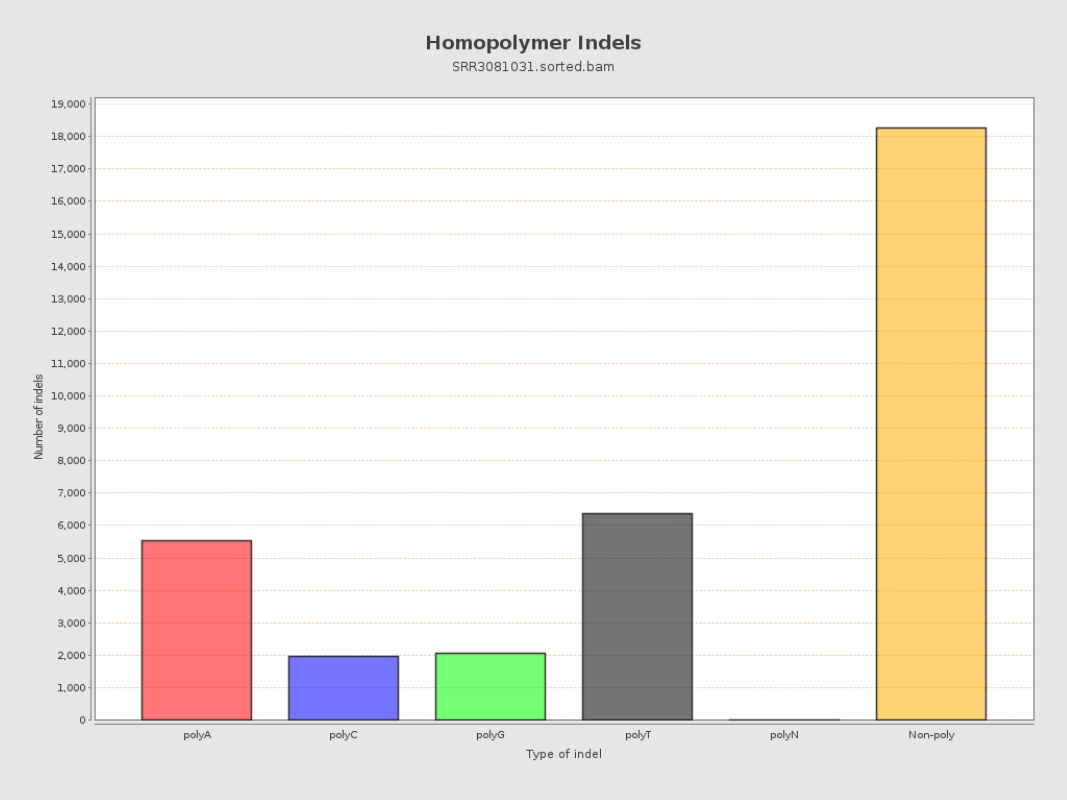
9. Results : Mapped Reads GC-content Distribution



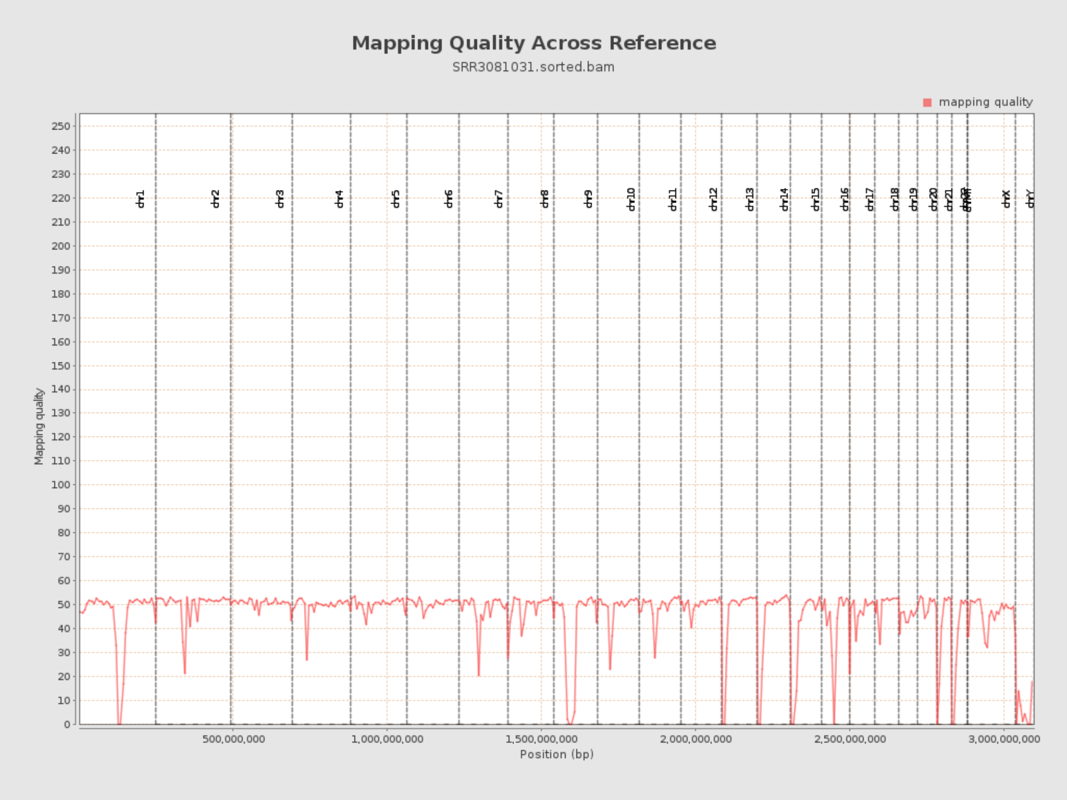
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram