Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 23:51:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081161.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_SRR3081161 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081161.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 23:51:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081161.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,336,075
Mapped reads	2,111,037 / 90.37%
Unmapped reads	225,038 / 9.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,282 / 1.04%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	82,216 / 3.52%
Duplication rate	3.09%
Clipped reads	885,866 / 37.92%

2.2. ACGT Content

Number/percentage of A's	40,764,115 / 28.49%
Number/percentage of C's	26,828,531 / 18.75%
Number/percentage of T's	44,569,890 / 31.15%
Number/percentage of G's	30,868,964 / 21.58%
Number/percentage of N's	43,406 / 0.03%
GC Percentage	40.33%

2.3. Coverage

Mean	0.0462

Standard Deviation	0.3662

2.4. Mapping Quality

Mean Mapping Quality	47.09

2.5. Mismatches and indels

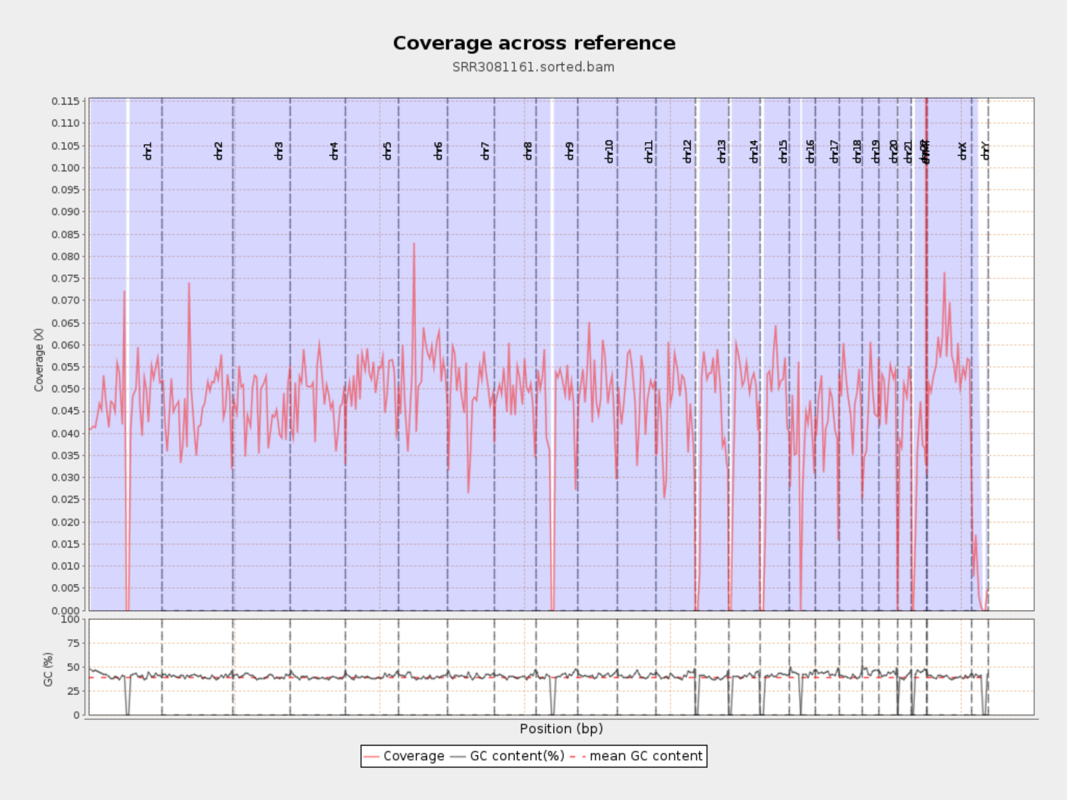
General error rate	0.83%
Mismatches	1,165,863
Insertions	10,888
Mapped reads with at least one insertion	0.51%
Deletions	32,243
Mapped reads with at least one deletion	1.51%
Homopolymer indels	47.01%

2.6. Chromosome stats

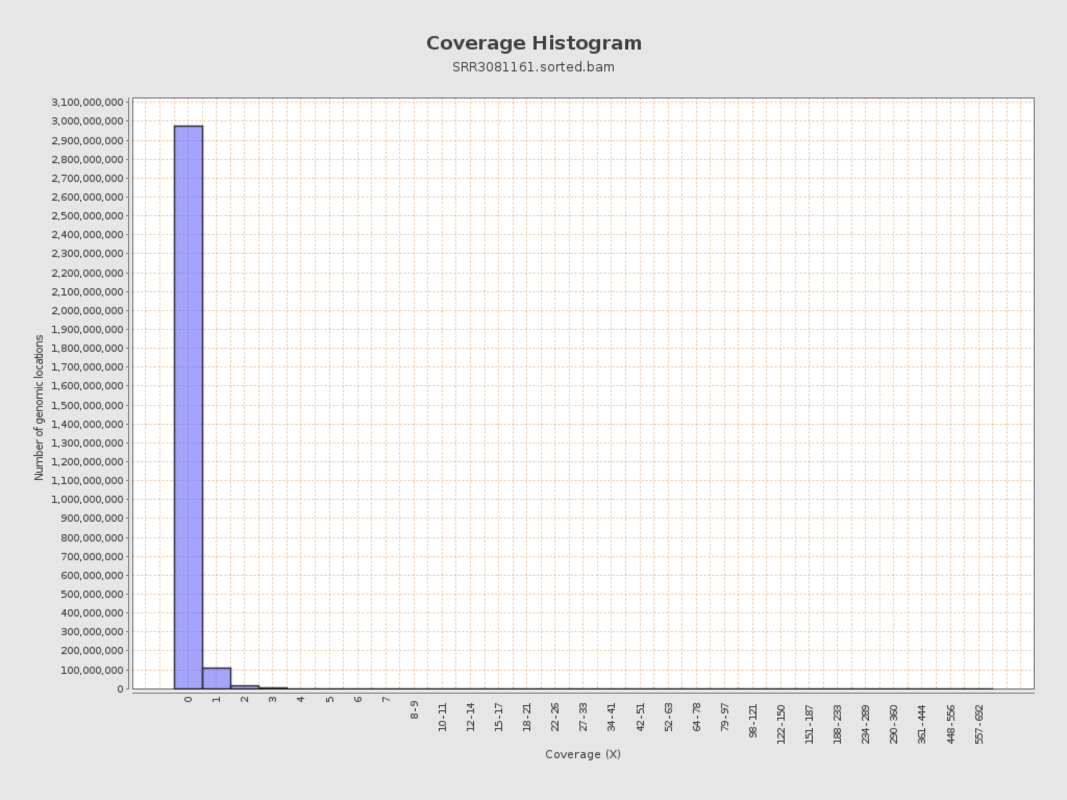
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11426986	0.0458	0.6477
chr2	243199373	11339982	0.0466	0.4145
chr3	198022430	9067312	0.0458	0.2401
chr4	191154276	9213443	0.0482	0.2557
chr5	180915260	9389614	0.0519	0.2581
chr6	171115067	9329622	0.0545	0.3454
chr7	159138663	7818903	0.0491	0.4392

chr8	146364022	7243813	0.0495	0.4682
chr9	141213431	6143891	0.0435	0.3378
chr10	135534747	6832217	0.0504	0.3186
chr11	135006516	6607159	0.0489	0.3609
chr12	133851895	6069088	0.0453	0.2428
chr13	115169878	4729646	0.0411	0.2279
chr14	107349540	4733592	0.0441	0.2565
chr15	102531392	4370324	0.0426	0.2344
chr16	90354753	3320791	0.0368	0.2421
chr17	81195210	3402592	0.0419	0.269
chr18	78077248	3833031	0.0491	0.5993
chr19	59128983	2636141	0.0446	0.4628
chr20	63025520	3114168	0.0494	0.2561
chr21	48129895	2025820	0.0421	0.2423
chr22	51304566	1407729	0.0274	0.1843
chrMT	16571	24248	1.4633	1.4084
chrX	155270560	8708822	0.0561	0.3005
chrY	59373566	338660	0.0057	0.1151

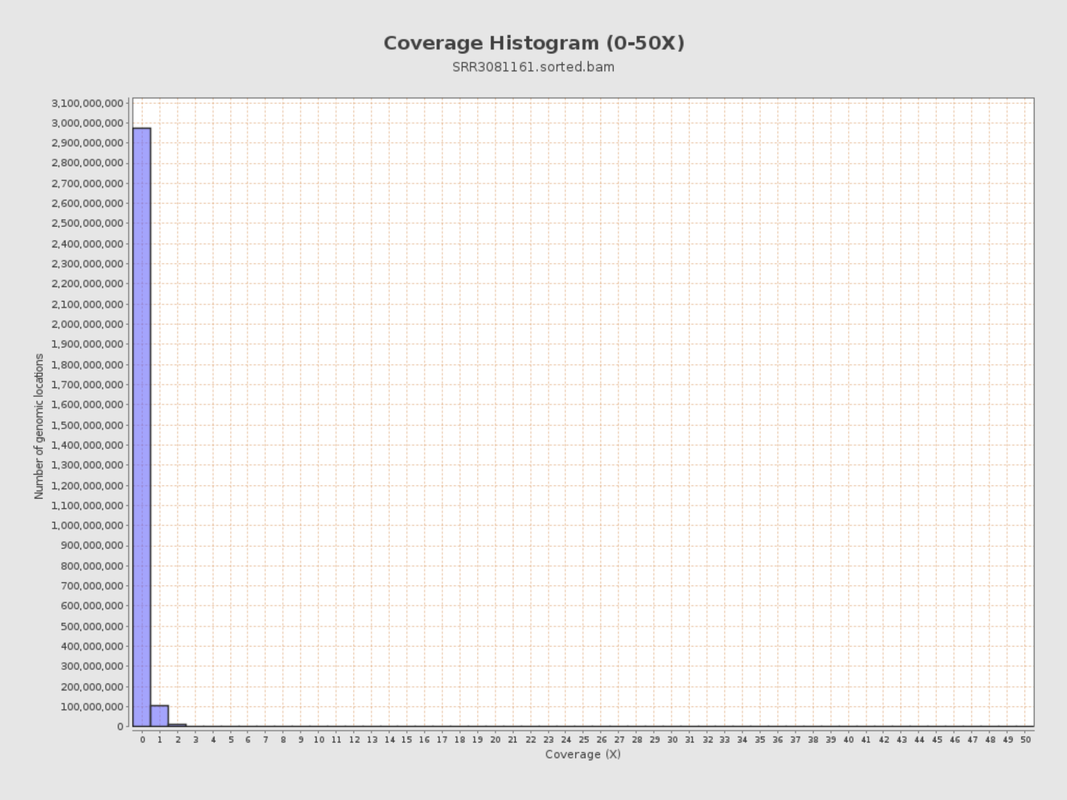
3. Results : Coverage across reference



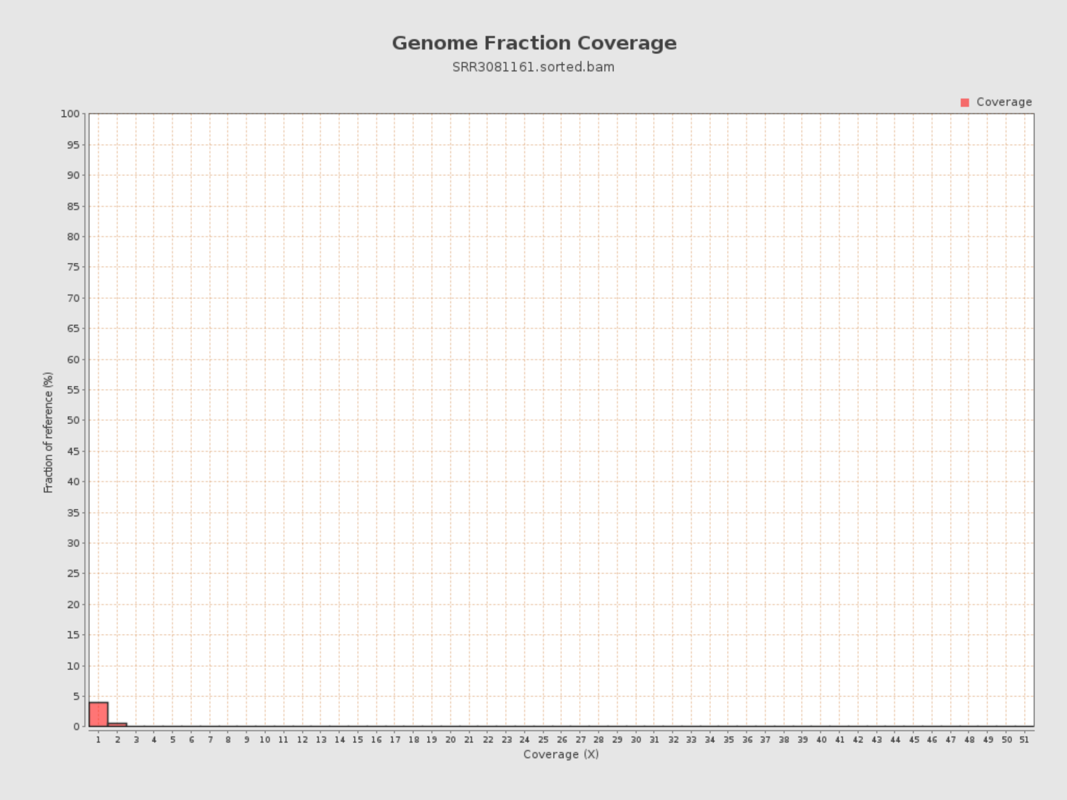
4. Results : Coverage Histogram



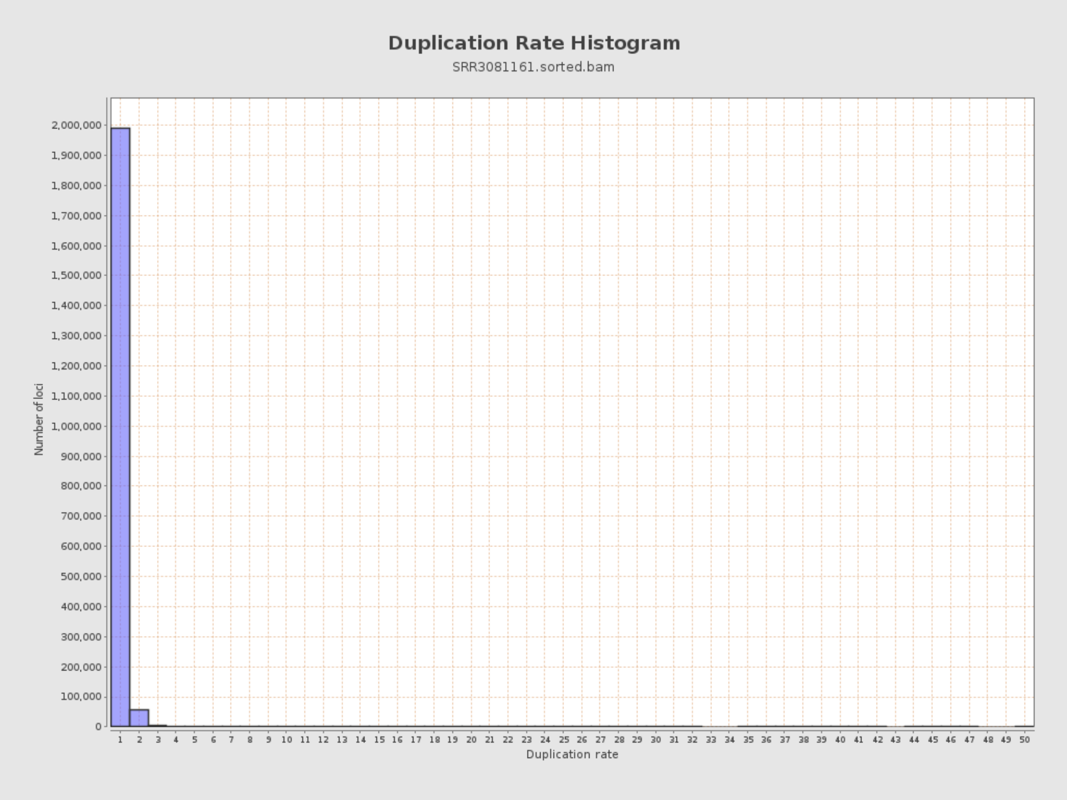
5. Results : Coverage Histogram (0-50X)



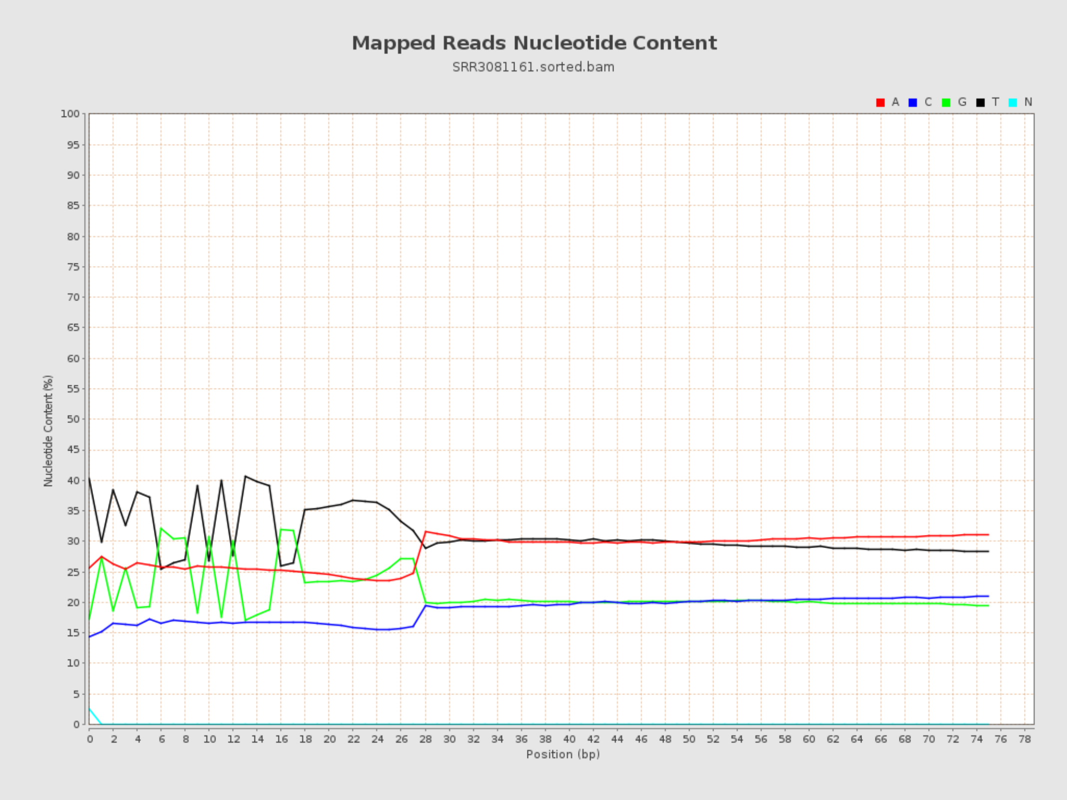
6. Results : Genome Fraction Coverage



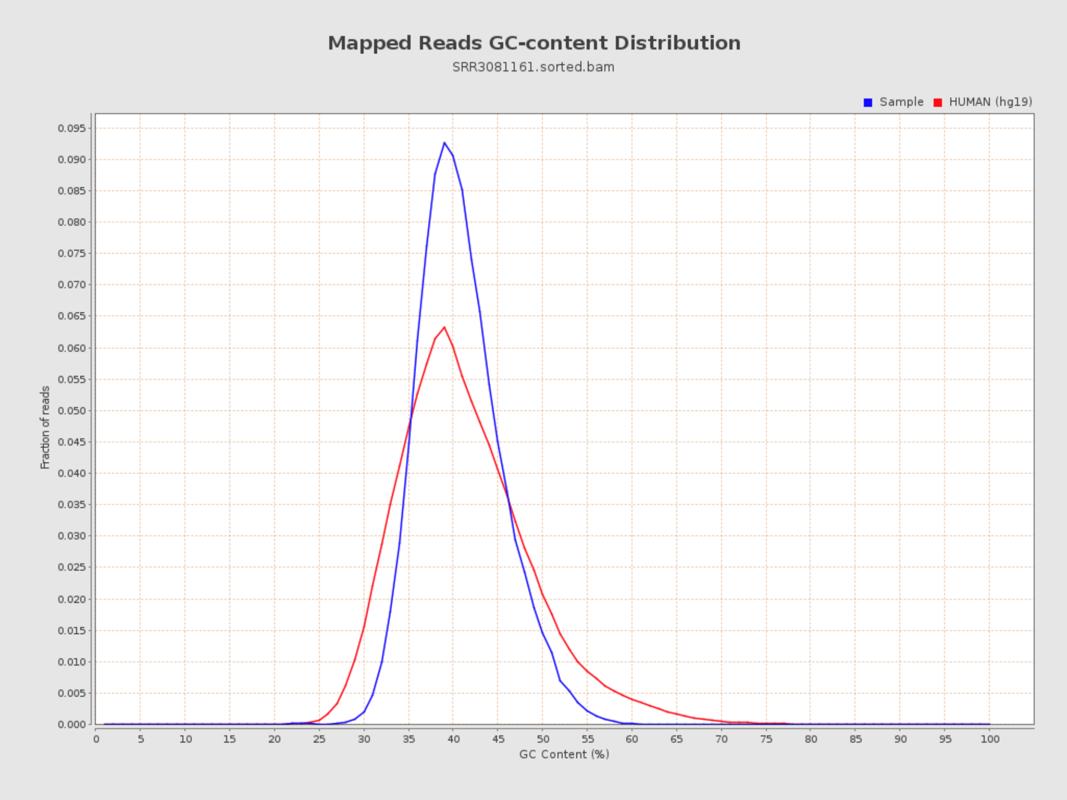
7. Results : Duplication Rate Histogram



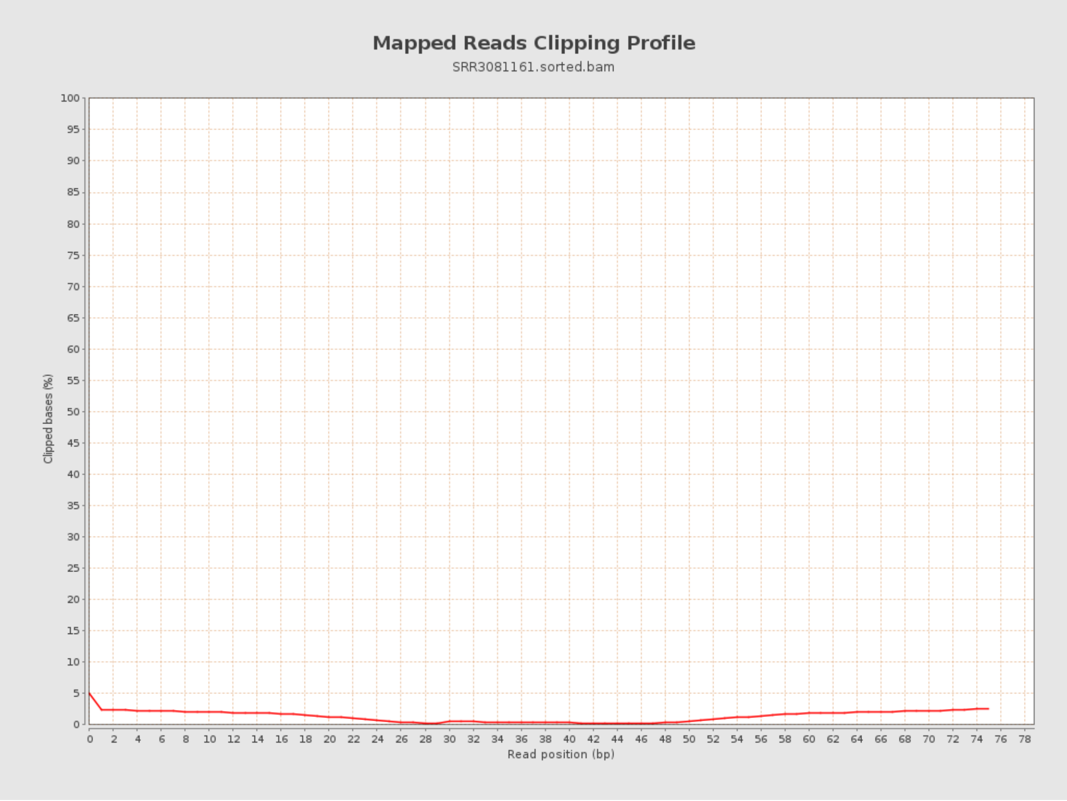
8. Results : Mapped Reads Nucleotide Content



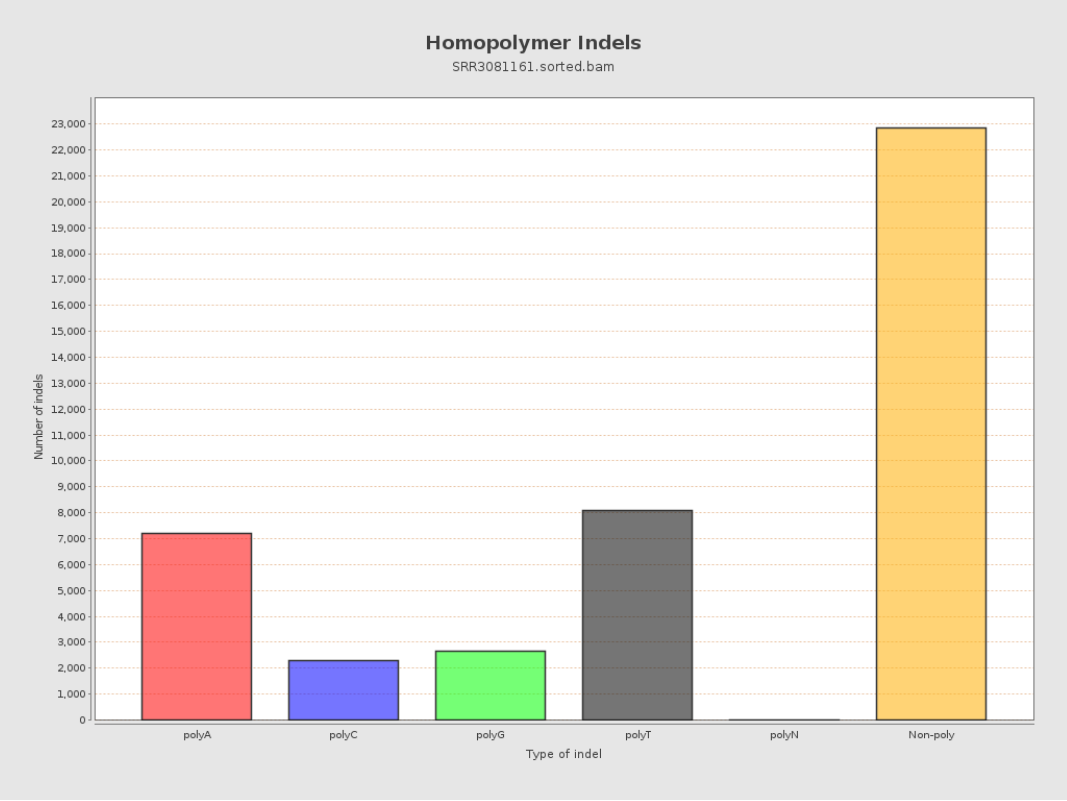
9. Results : Mapped Reads GC-content Distribution



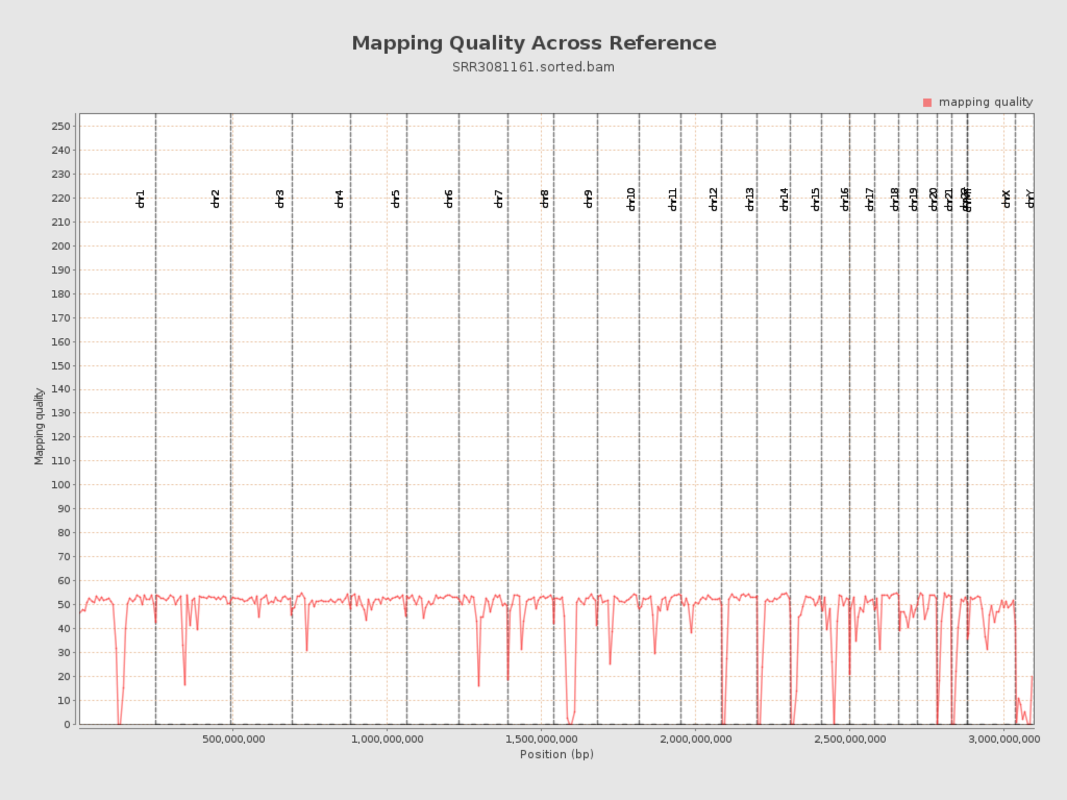
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram