Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 19:31:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081110.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_SRR3081110 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081110.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 19:31:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081110.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,460,553
Mapped reads	2,248,839 / 91.4%
Unmapped reads	211,714 / 8.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,180 / 0.94%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	118,506 / 4.82%
Duplication rate	3.57%
Clipped reads	947,786 / 38.52%

2.2. ACGT Content

Number/percentage of A's	43,150,087 / 28.3%
Number/percentage of C's	28,823,563 / 18.9%
Number/percentage of T's	47,703,358 / 31.29%
Number/percentage of G's	32,790,514 / 21.51%
Number/percentage of N's	1,626 / 0%
GC Percentage	40.41%

2.3. Coverage

Mean	0.0493

Standard Deviation	0.5803

2.4. Mapping Quality

Mean Mapping Quality	46.69

2.5. Mismatches and indels

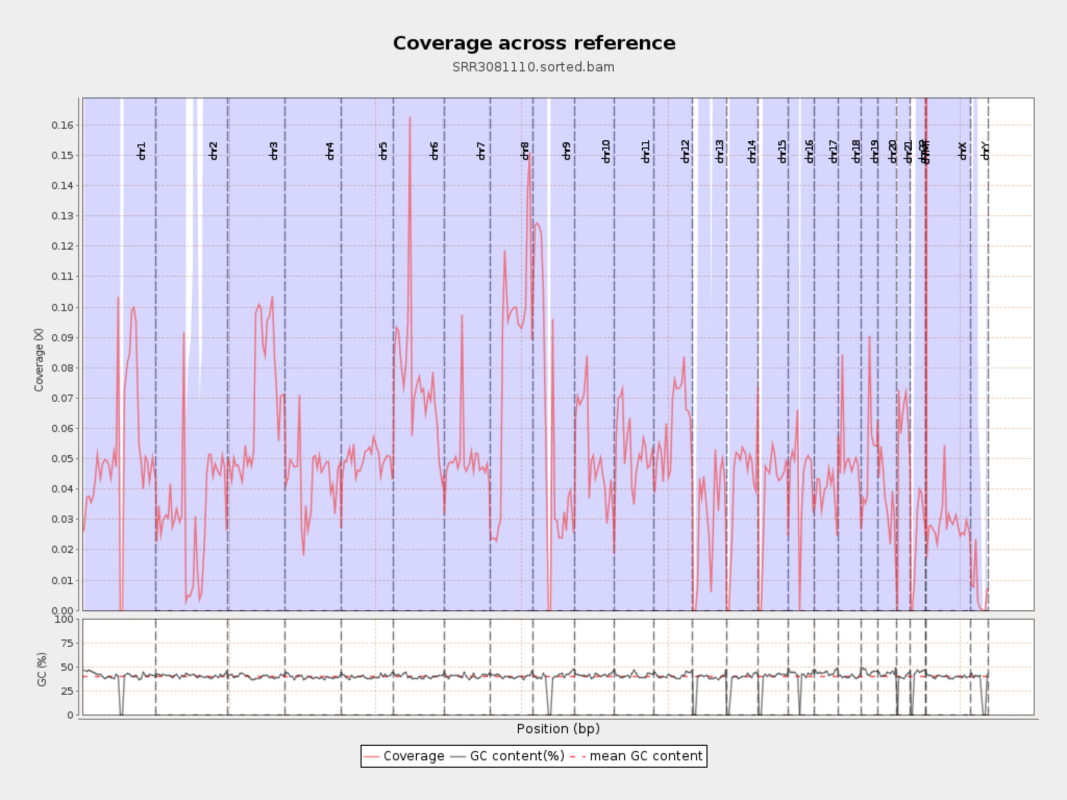
General error rate	0.92%
Mismatches	1,372,908
Insertions	11,912
Mapped reads with at least one insertion	0.53%
Deletions	31,639
Mapped reads with at least one deletion	1.39%
Homopolymer indels	46.07%

2.6. Chromosome stats

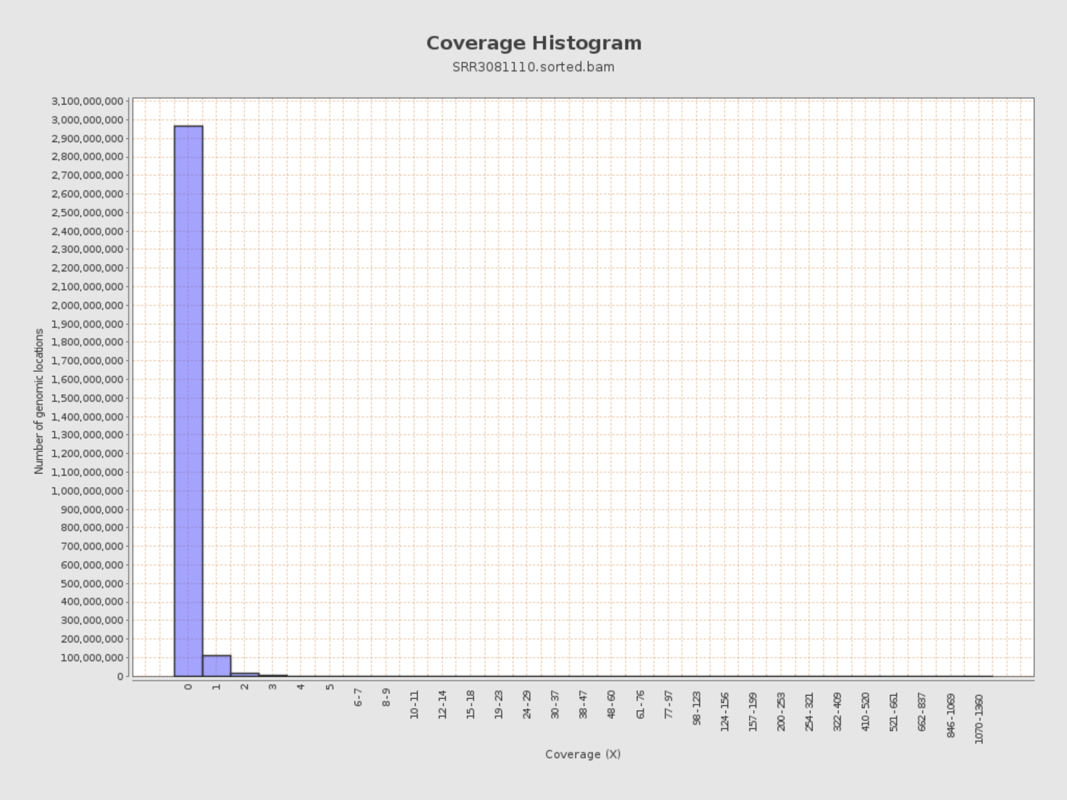
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12994763	0.0521	1.0962
chr2	243199373	7725437	0.0318	0.5571
chr3	198022430	13392070	0.0676	0.2953
chr4	191154276	8305392	0.0434	0.2666
chr5	180915260	8984527	0.0497	0.2601
chr6	171115067	13070993	0.0764	0.7307
chr7	159138663	7952466	0.05	0.6149

chr8	146364022	12262732	0.0838	0.8003
chr9	141213431	8176309	0.0579	0.7095
chr10	135534747	7042595	0.052	0.4446
chr11	135006516	7223674	0.0535	0.4864
chr12	133851895	8120757	0.0607	0.3305
chr13	115169878	3537971	0.0307	0.1985
chr14	107349540	4388850	0.0409	0.3583
chr15	102531392	3968204	0.0387	0.2213
chr16	90354753	3839510	0.0425	0.4154
chr17	81195210	3224383	0.0397	0.2644
chr18	78077248	4002100	0.0513	1.2778
chr19	59128983	3052338	0.0516	0.7607
chr20	63025520	2334689	0.037	0.2567
chr21	48129895	2818825	0.0586	0.359
chr22	51304566	1236090	0.0241	0.1717
chrMT	16571	66520	4.0142	3.1057
chrX	155270560	4429296	0.0285	0.2954
chrY	59373566	371008	0.0062	0.1652

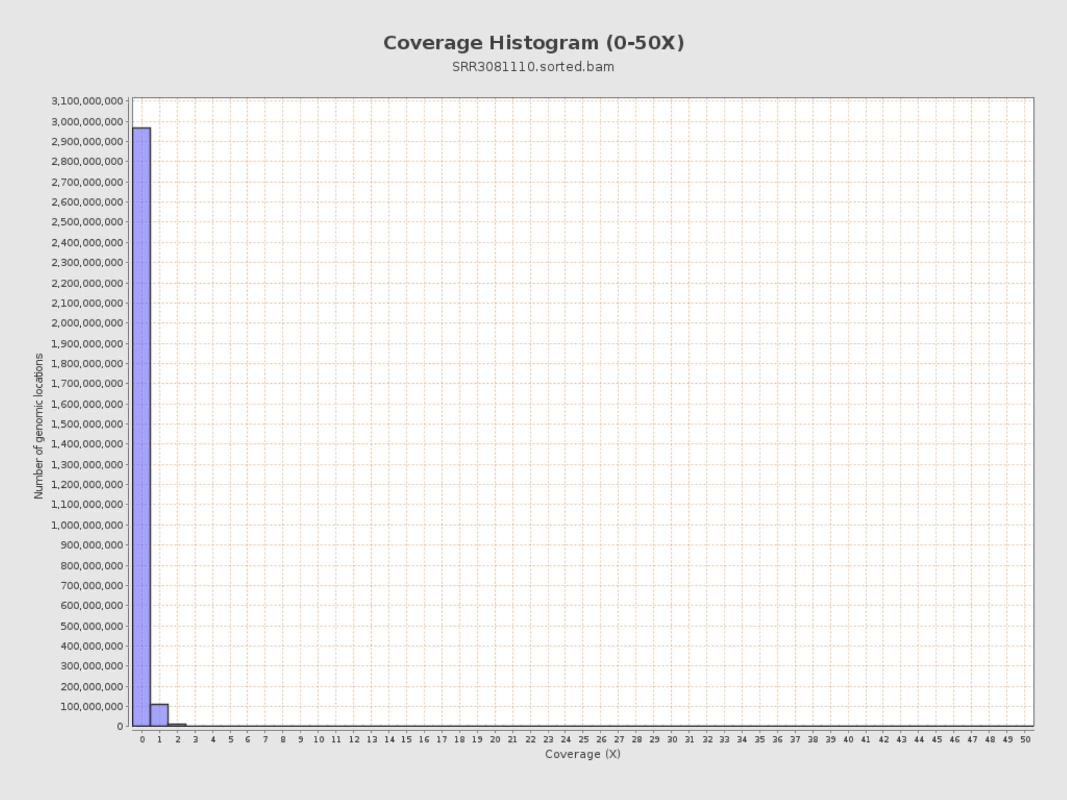
3. Results : Coverage across reference



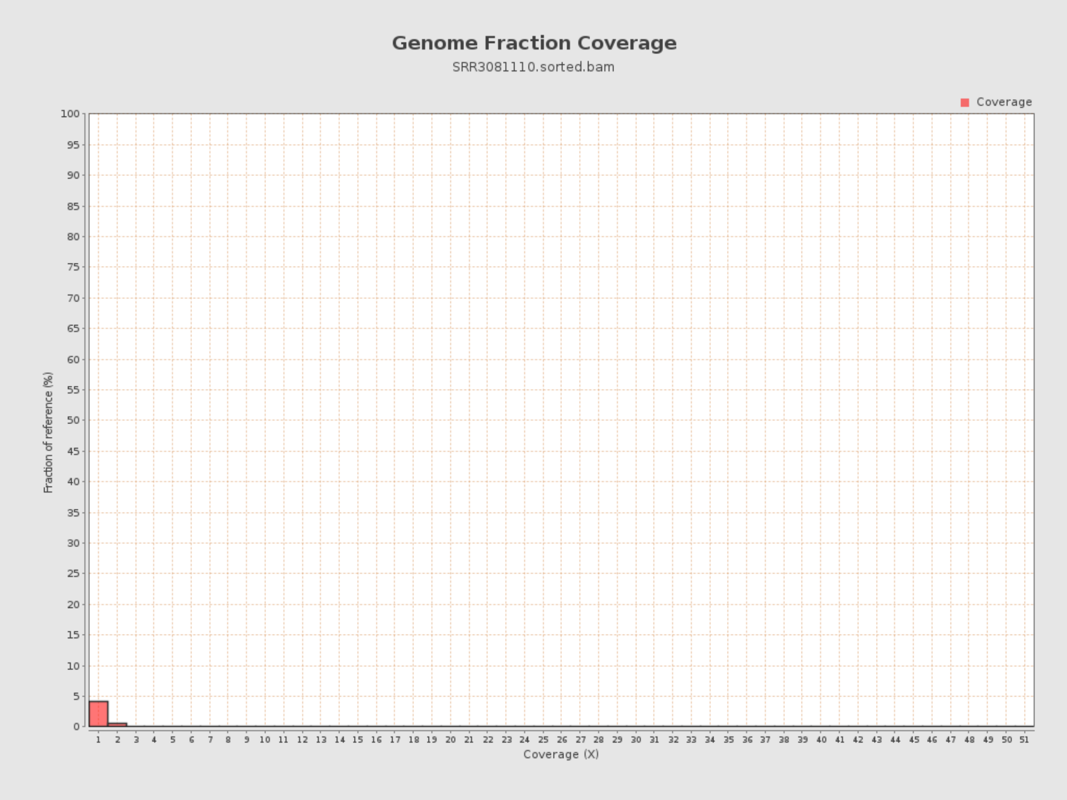
4. Results : Coverage Histogram



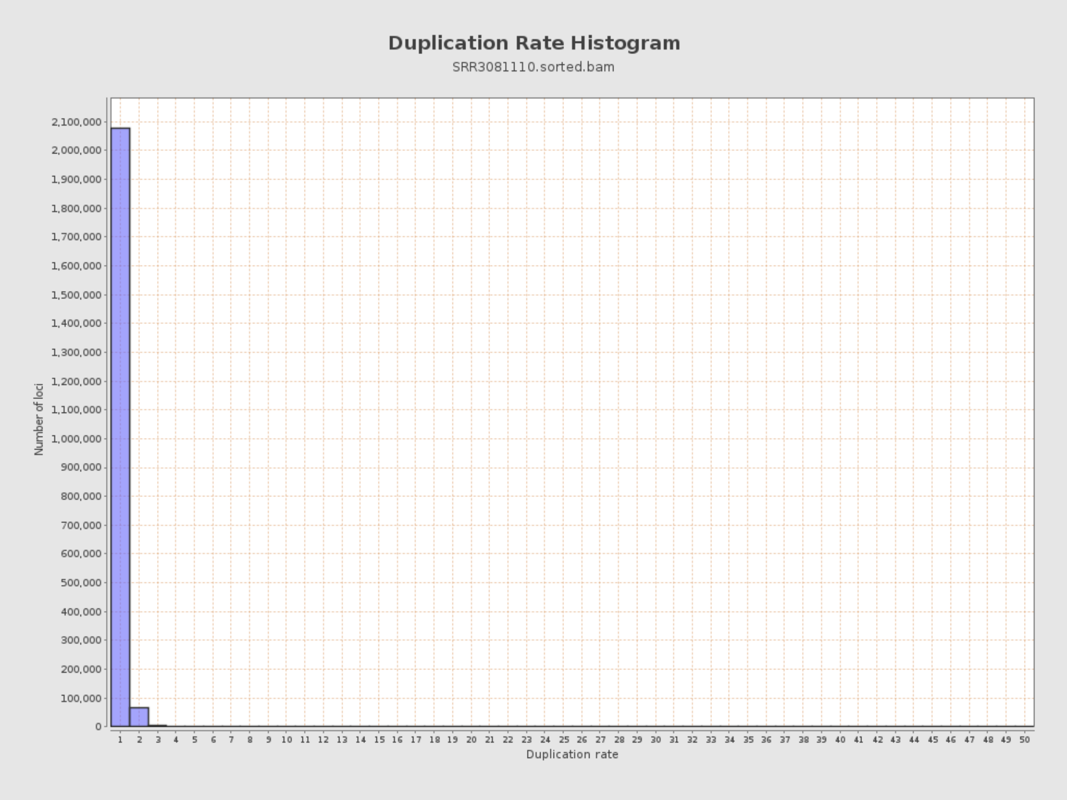
5. Results : Coverage Histogram (0-50X)



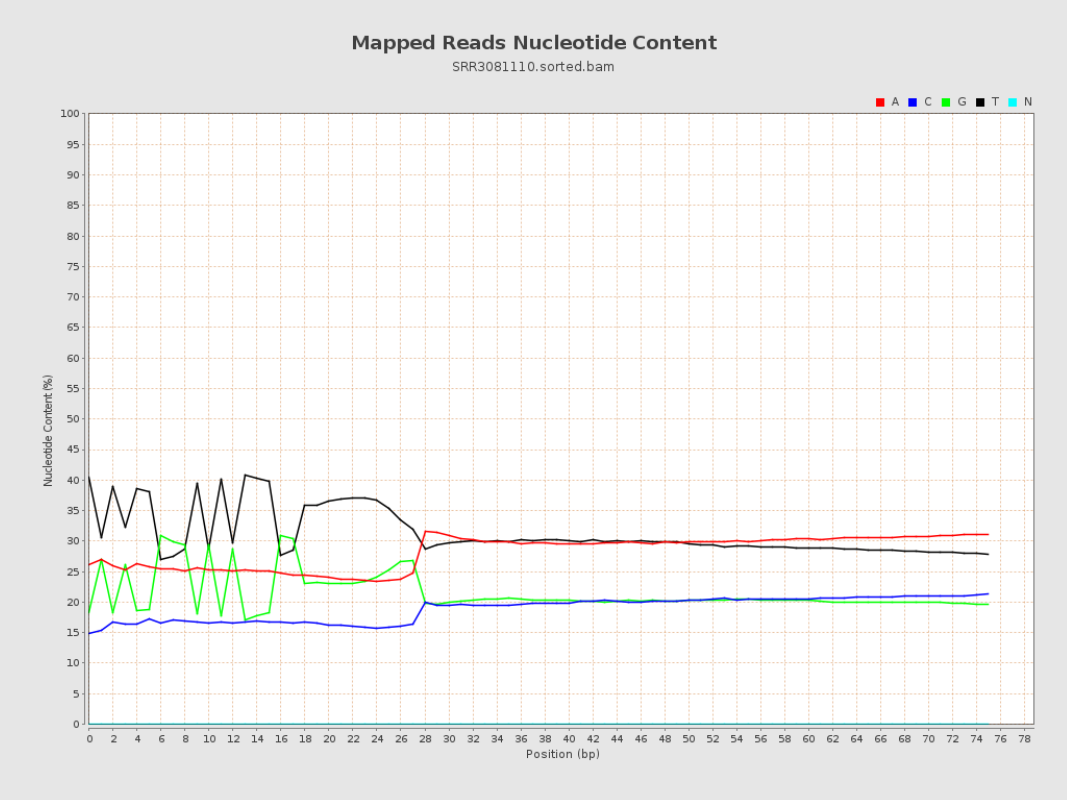
6. Results : Genome Fraction Coverage



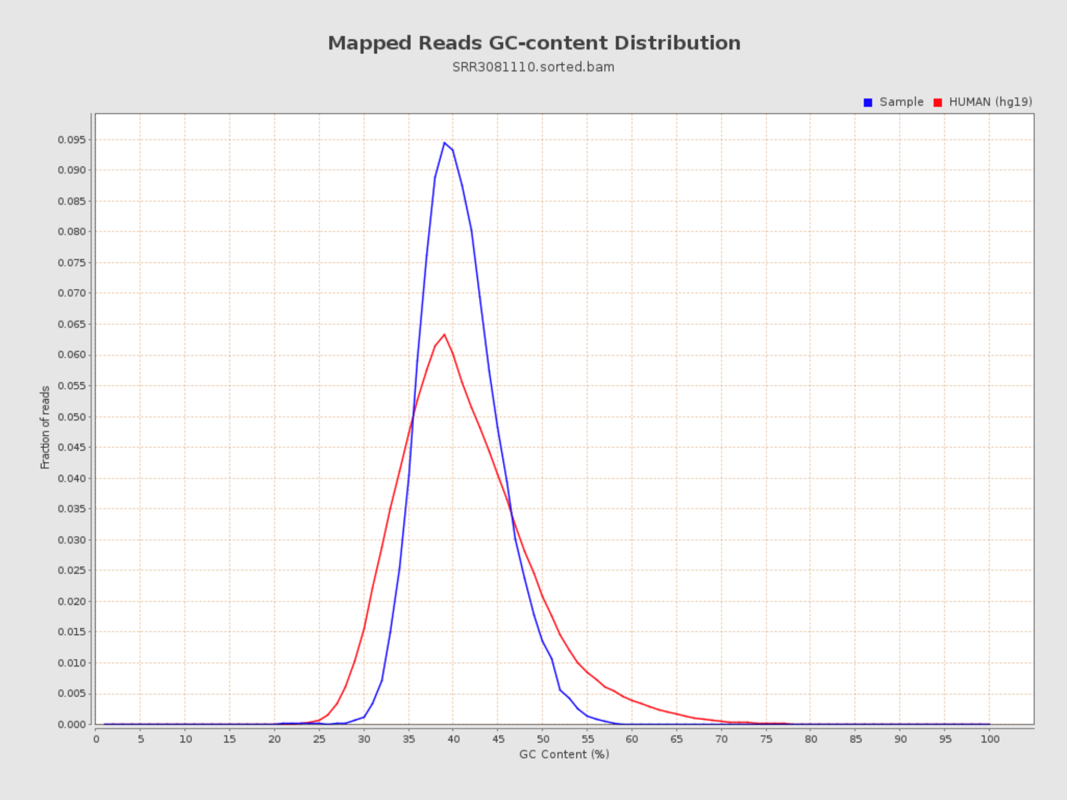
7. Results : Duplication Rate Histogram



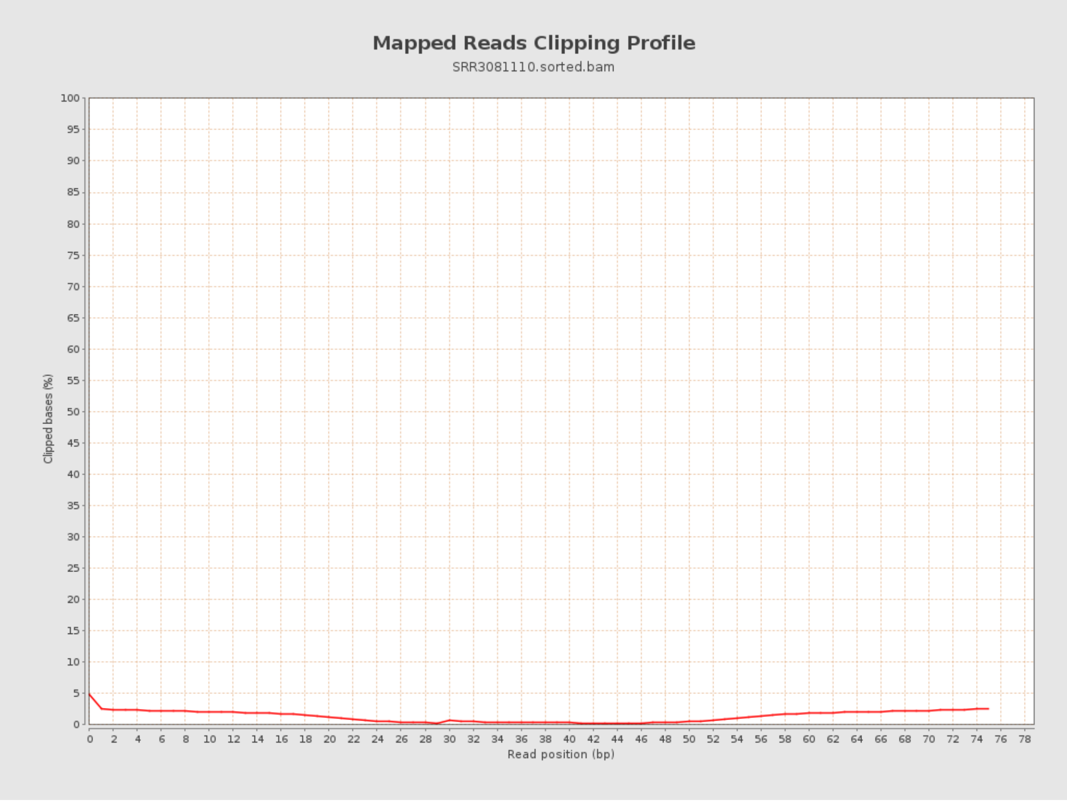
8. Results : Mapped Reads Nucleotide Content



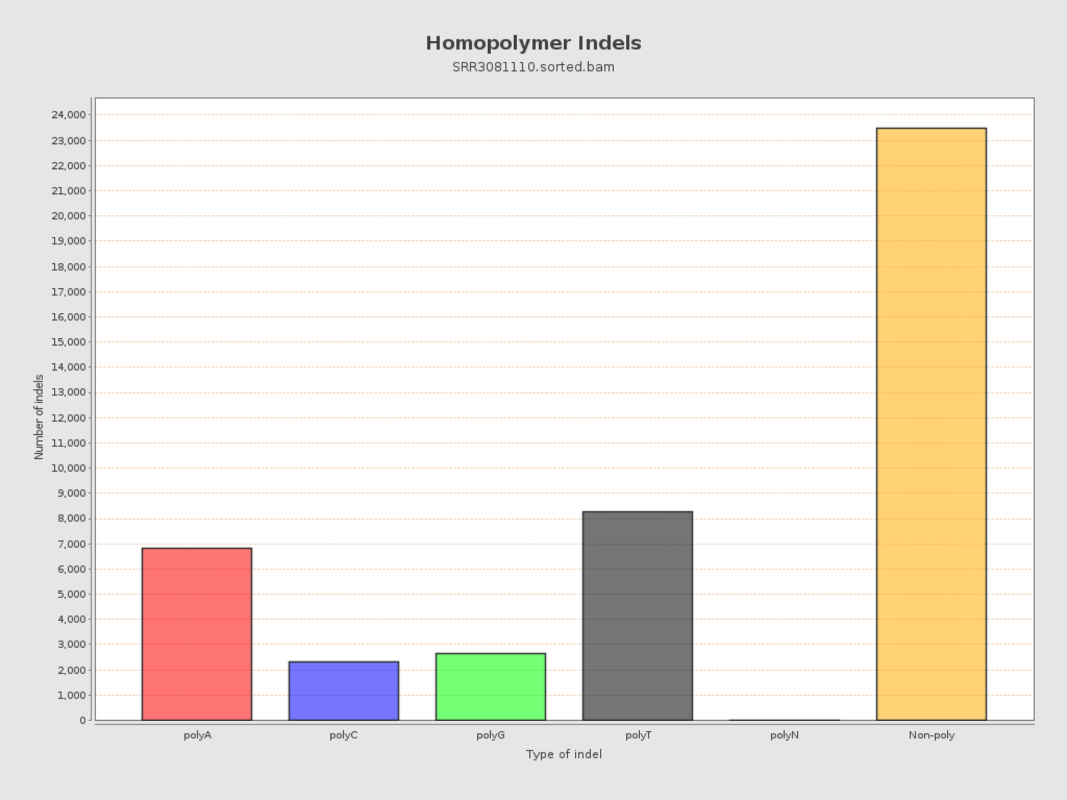
9. Results : Mapped Reads GC-content Distribution



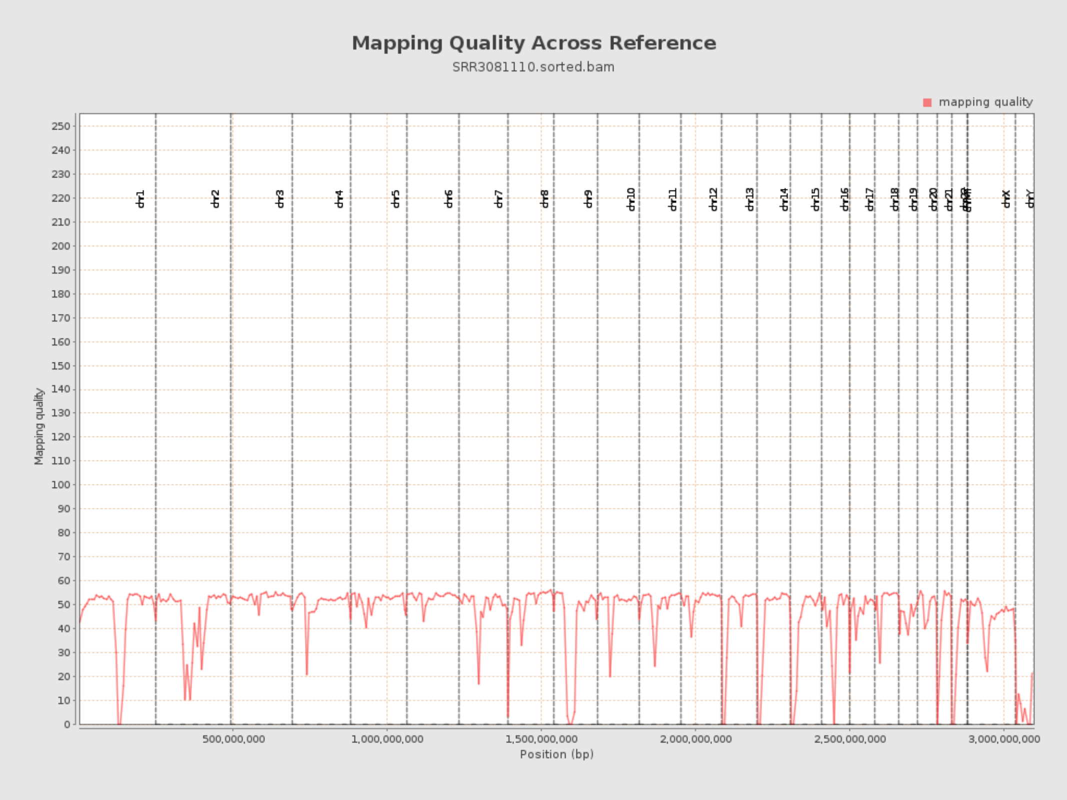
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram