Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 22:15:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081141.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_SRR3081141 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081141.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 22:15:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081141.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,709,122
Mapped reads	2,412,135 / 89.04%
Unmapped reads	296,987 / 10.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,137 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	101,390 / 3.74%
Duplication rate	3.39%
Clipped reads	1,085,448 / 40.07%

2.2. ACGT Content

Number/percentage of A's	45,468,803 / 28.16%
Number/percentage of C's	30,190,696 / 18.7%
Number/percentage of T's	50,372,403 / 31.19%
Number/percentage of G's	35,398,534 / 21.92%
Number/percentage of N's	47,983 / 0.03%
GC Percentage	40.62%

2.3. Coverage

Mean	0.0522

Standard Deviation	0.3904

2.4. Mapping Quality

Mean Mapping Quality	46.75

2.5. Mismatches and indels

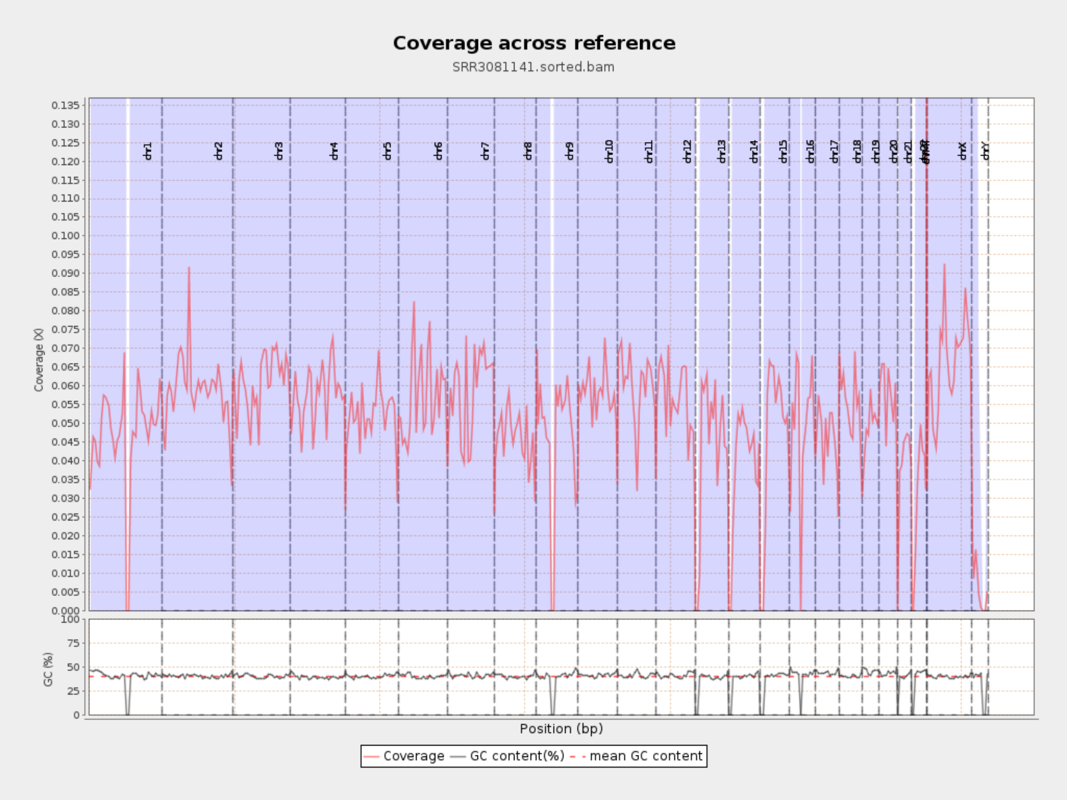
General error rate	0.84%
Mismatches	1,335,251
Insertions	11,951
Mapped reads with at least one insertion	0.49%
Deletions	36,362
Mapped reads with at least one deletion	1.49%
Homopolymer indels	47.17%

2.6. Chromosome stats

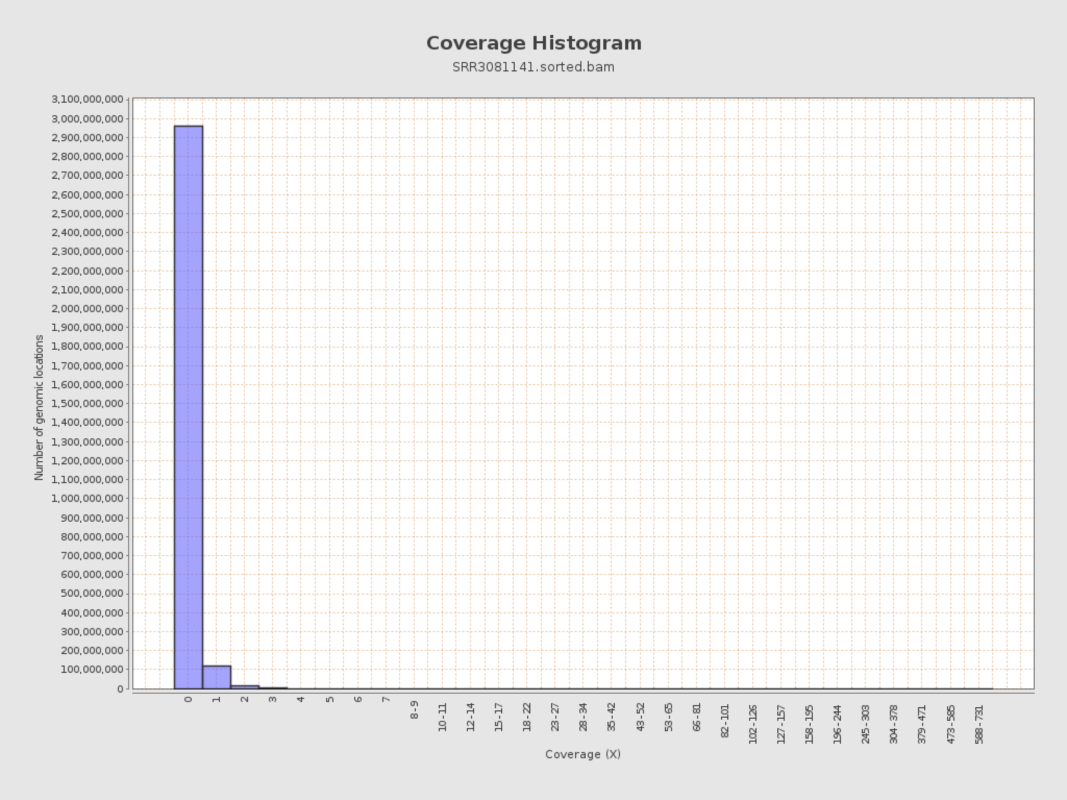
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11667045	0.0468	0.6514
chr2	243199373	14331273	0.0589	0.4835
chr3	198022430	12111715	0.0612	0.2789
chr4	191154276	11018441	0.0576	0.2795
chr5	180915260	9476645	0.0524	0.2606
chr6	171115067	9794094	0.0572	0.3323
chr7	159138663	9427067	0.0592	0.4893

chr8	146364022	6768922	0.0462	0.4795
chr9	141213431	6509235	0.0461	0.3718
chr10	135534747	7923085	0.0585	0.3489
chr11	135006516	8014415	0.0594	0.4094
chr12	133851895	7584442	0.0567	0.2751
chr13	115169878	4980210	0.0432	0.2356
chr14	107349540	4103991	0.0382	0.2417
chr15	102531392	4797992	0.0468	0.2522
chr16	90354753	4468185	0.0495	0.2748
chr17	81195210	3685773	0.0454	0.2795
chr18	78077248	4355734	0.0558	0.6538
chr19	59128983	2884013	0.0488	0.4761
chr20	63025520	3657009	0.058	0.2816
chr21	48129895	1854833	0.0385	0.2411
chr22	51304566	1474782	0.0287	0.1897
chrMT	16571	2481	0.1497	0.4042
chrX	155270560	10292409	0.0663	0.3332
chrY	59373566	352729	0.0059	0.1146

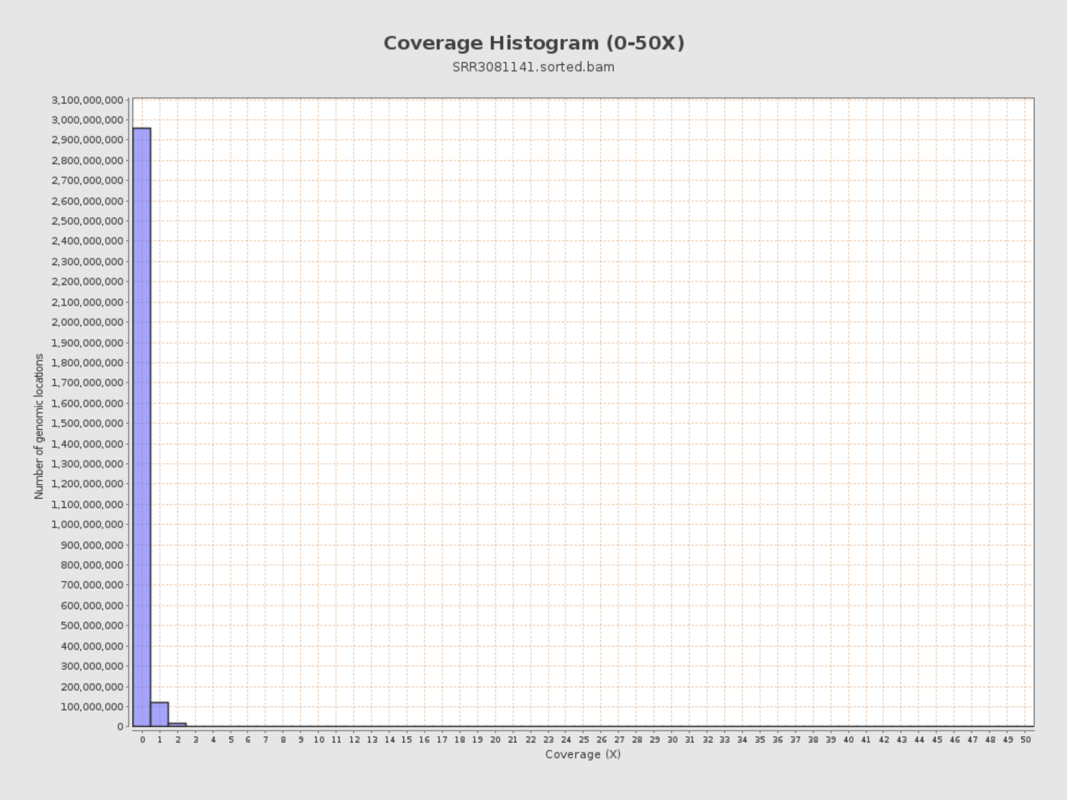
3. Results : Coverage across reference



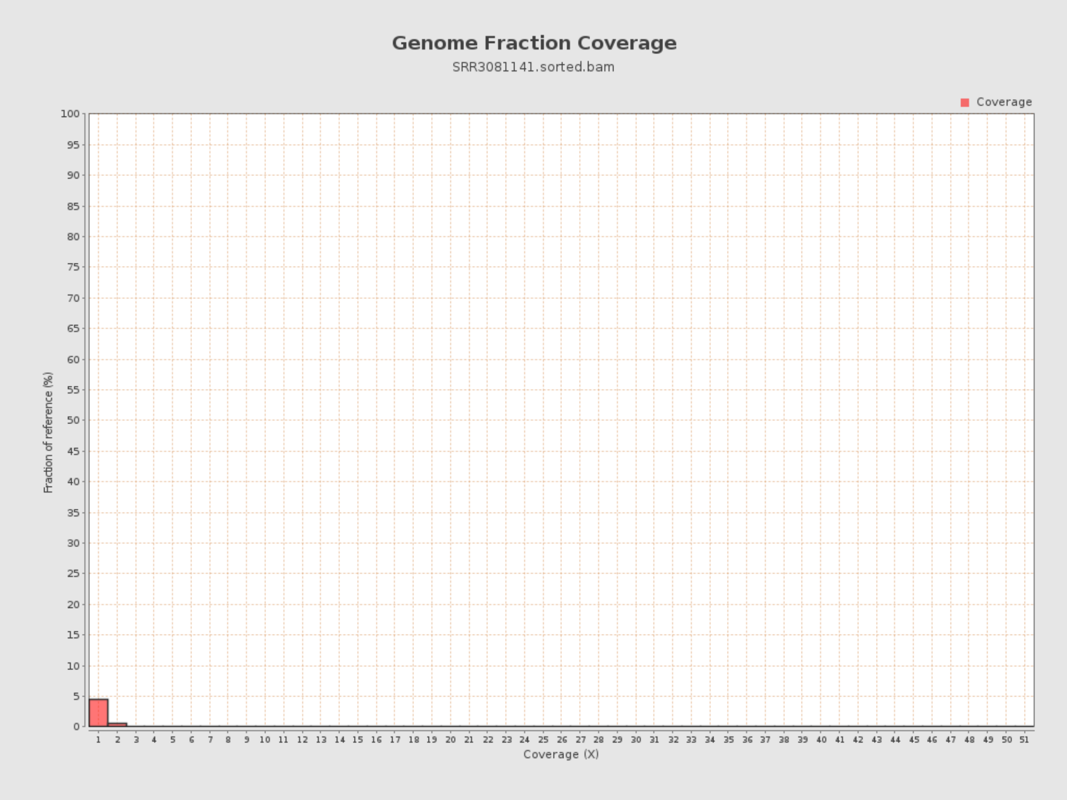
4. Results : Coverage Histogram



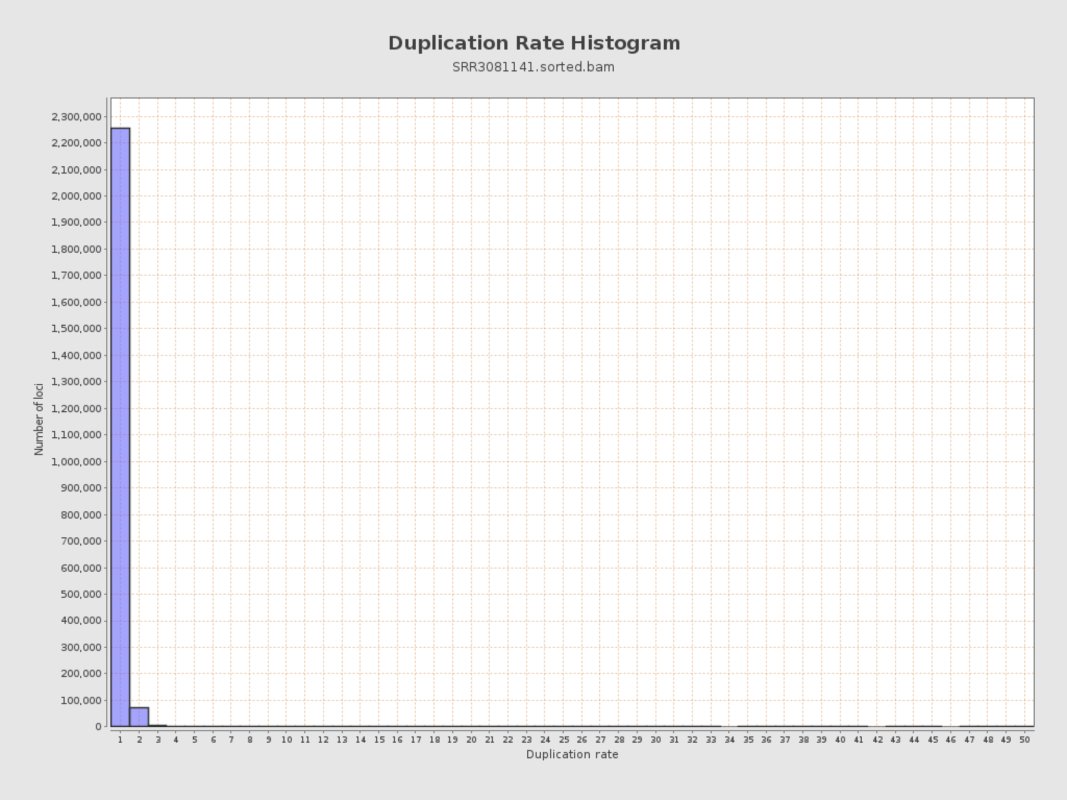
5. Results : Coverage Histogram (0-50X)



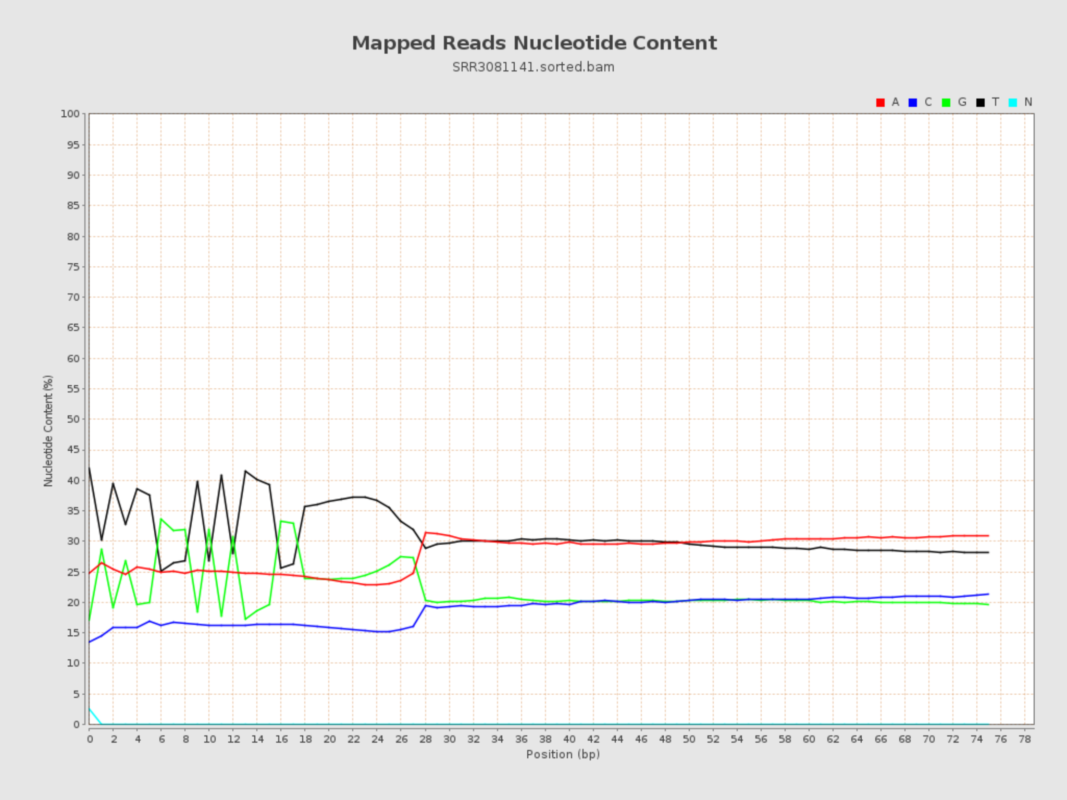
6. Results : Genome Fraction Coverage



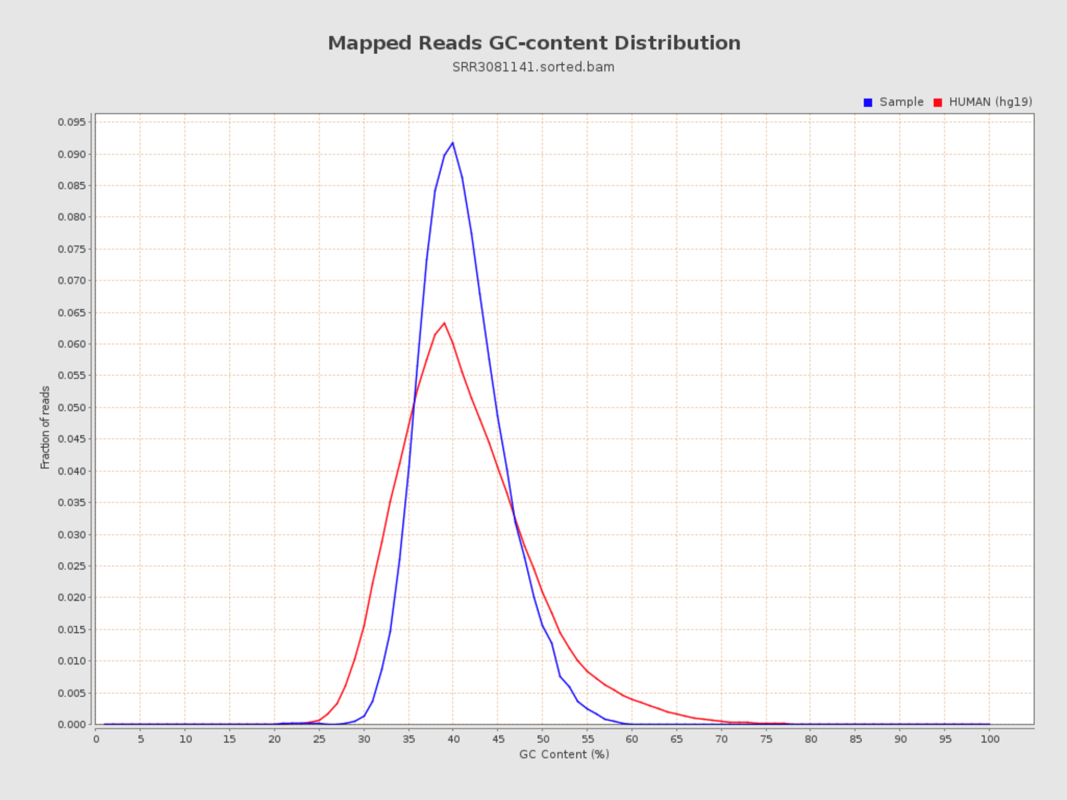
7. Results : Duplication Rate Histogram



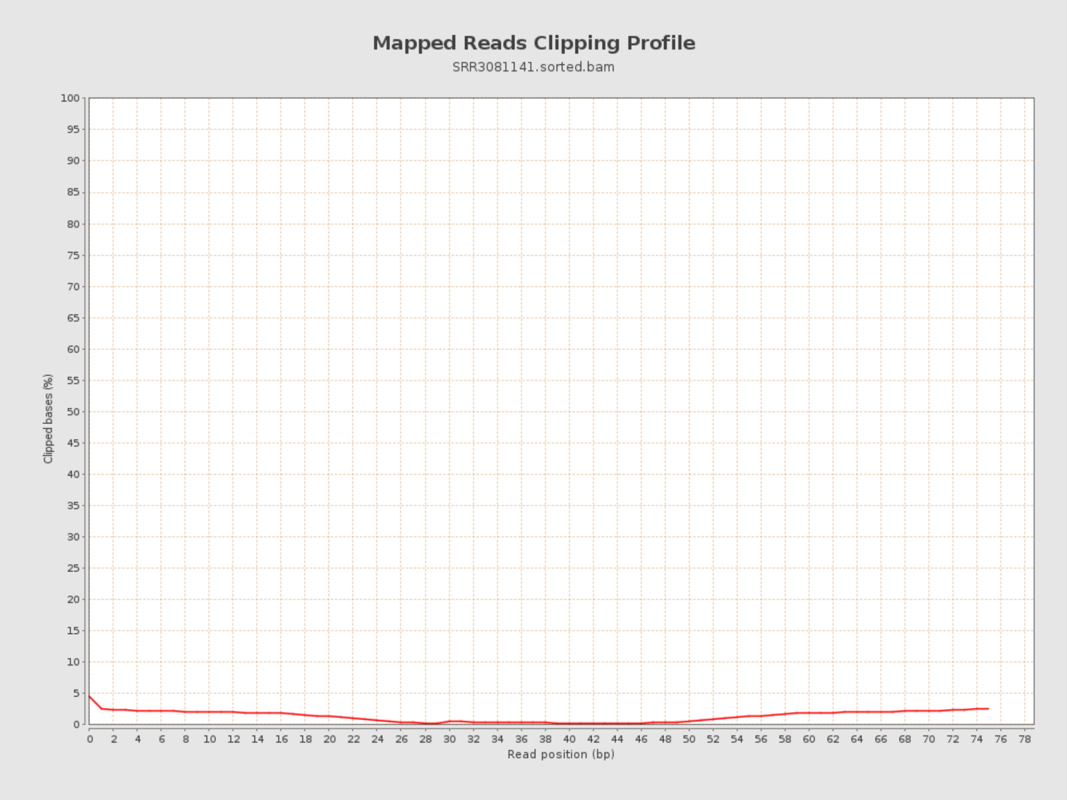
8. Results : Mapped Reads Nucleotide Content



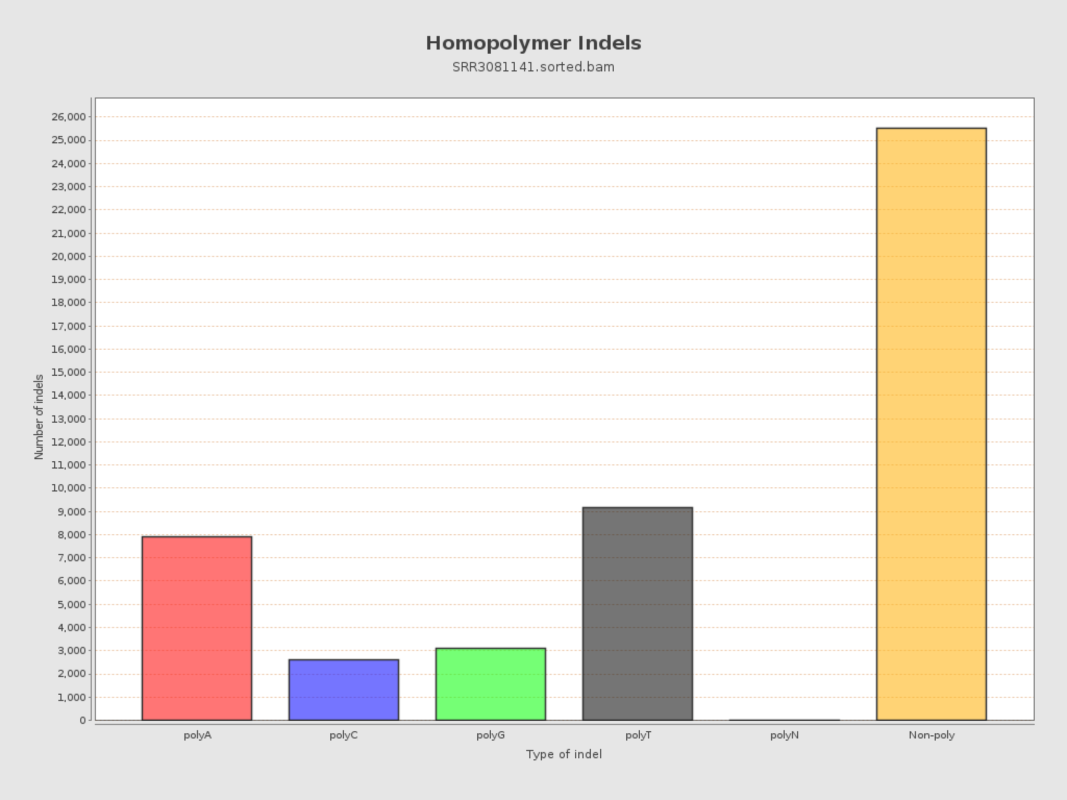
9. Results : Mapped Reads GC-content Distribution



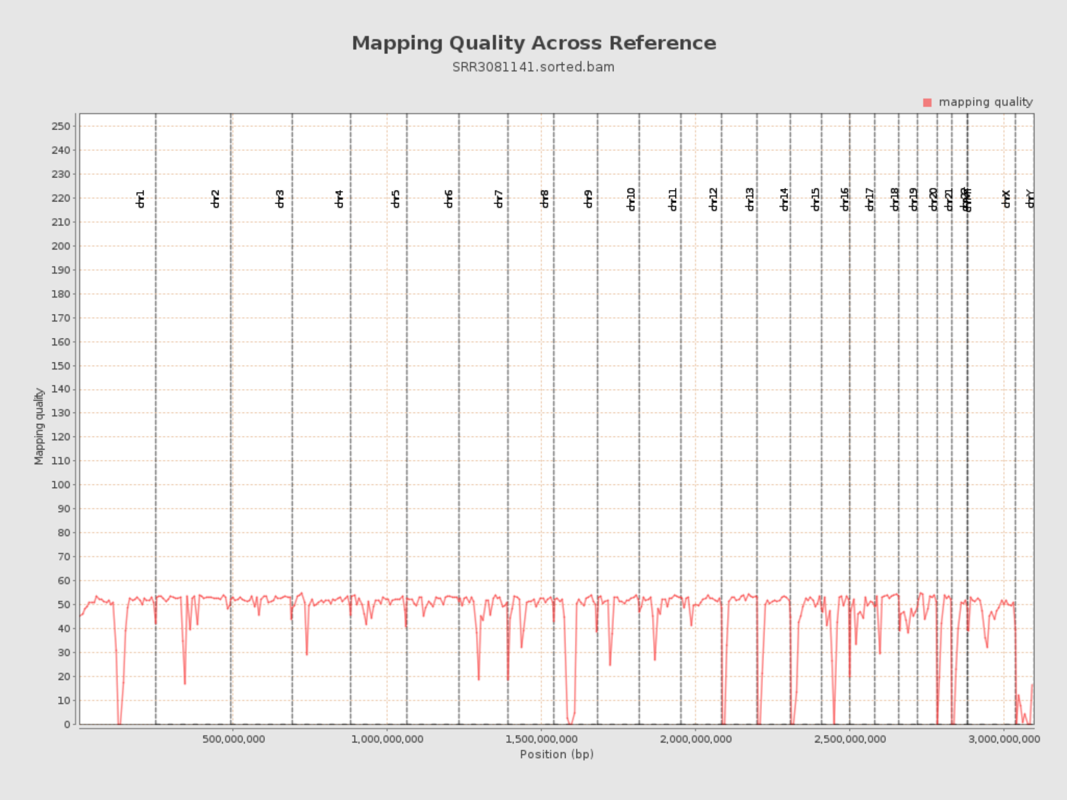
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram