Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 01:52:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231778.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_SRR6231778 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231778.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 01:52:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231778.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,676,015
Mapped reads	2,366,412 / 88.43%
Unmapped reads	309,603 / 11.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,962 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	118,059 / 4.41%
Duplication rate	2.29%
Clipped reads	1,058,212 / 39.54%

2.2. ACGT Content

Number/percentage of A's	44,192,350 / 28.03%
Number/percentage of C's	31,012,885 / 19.67%
Number/percentage of T's	45,370,579 / 28.77%
Number/percentage of G's	37,101,521 / 23.53%
Number/percentage of N's	11,055 / 0.01%
GC Percentage	43.2%

2.3. Coverage

Mean	0.051

Standard Deviation	4.6676

2.4. Mapping Quality

Mean Mapping Quality	42.58

2.5. Mismatches and indels

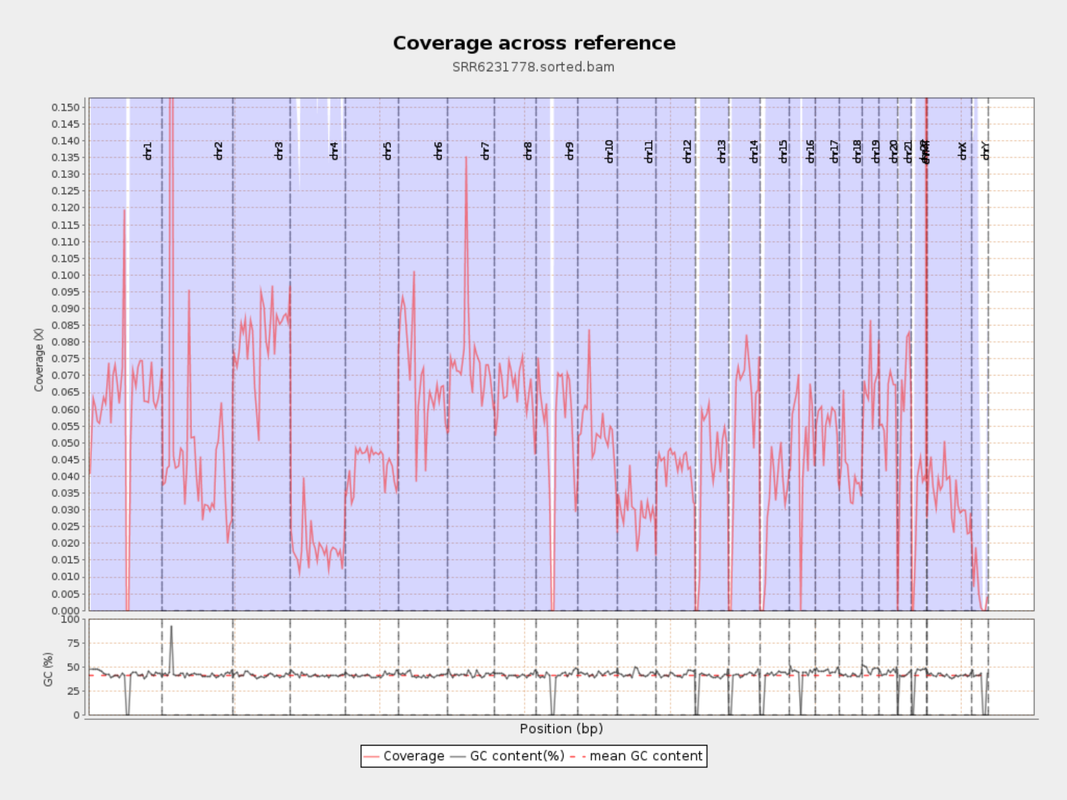
General error rate	0.65%
Mismatches	1,001,587
Insertions	12,977
Mapped reads with at least one insertion	0.54%
Deletions	37,580
Mapped reads with at least one deletion	1.57%
Homopolymer indels	44.64%

2.6. Chromosome stats

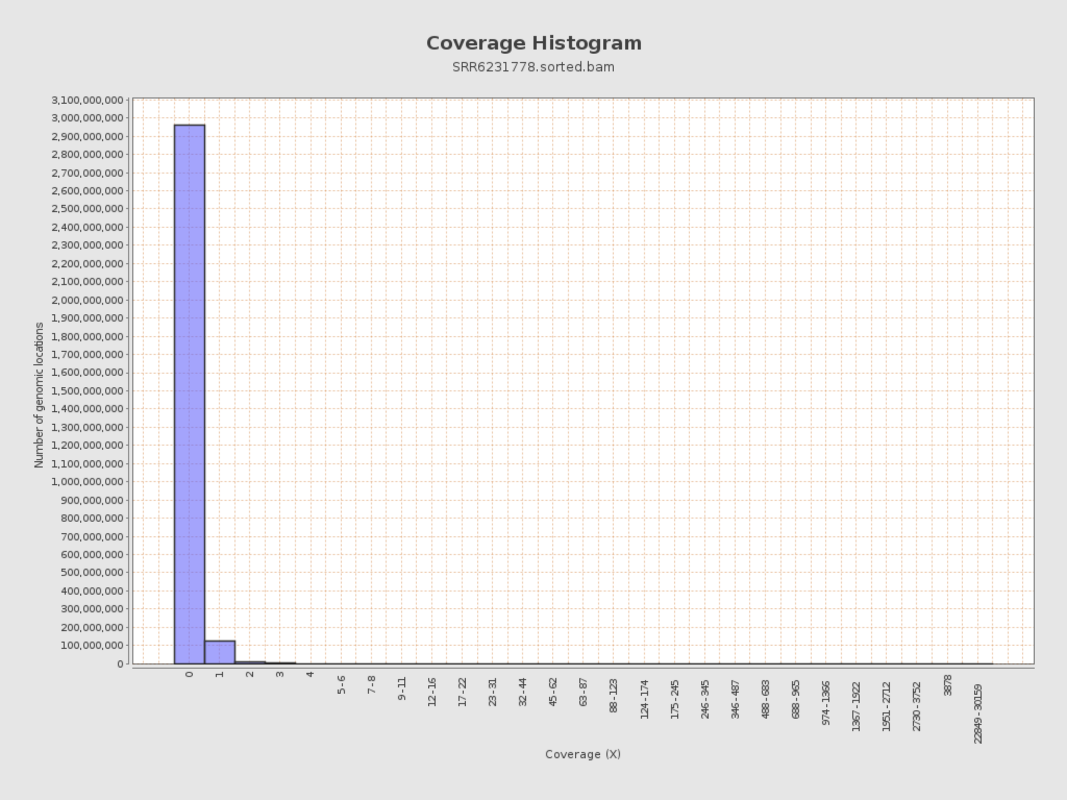
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15446385	0.062	1.2525
chr2	243199373	12771189	0.0525	16.5454
chr3	198022430	16023090	0.0809	0.313
chr4	191154276	3523365	0.0184	0.1712
chr5	180915260	7821483	0.0432	0.2349
chr6	171115067	11851927	0.0693	0.3752
chr7	159138663	11904640	0.0748	0.9206

chr8	146364022	9543273	0.0652	0.5512
chr9	141213431	7476403	0.0529	0.4065
chr10	135534747	7327636	0.0541	0.4548
chr11	135006516	3974960	0.0294	0.4577
chr12	133851895	5831086	0.0436	0.2364
chr13	115169878	4887125	0.0424	0.2238
chr14	107349540	6077284	0.0566	0.3118
chr15	102531392	3178351	0.031	0.1979
chr16	90354753	4584034	0.0507	0.2934
chr17	81195210	4471641	0.0551	0.2855
chr18	78077248	3210179	0.0411	0.8465
chr19	59128983	3980271	0.0673	0.7835
chr20	63025520	3721512	0.059	0.2817
chr21	48129895	2852008	0.0593	0.2877
chr22	51304566	1474057	0.0287	0.1838
chrMT	16571	198402	11.9728	7.1213
chrX	155270560	5274379	0.034	0.2365
chrY	59373566	347162	0.0058	0.1212

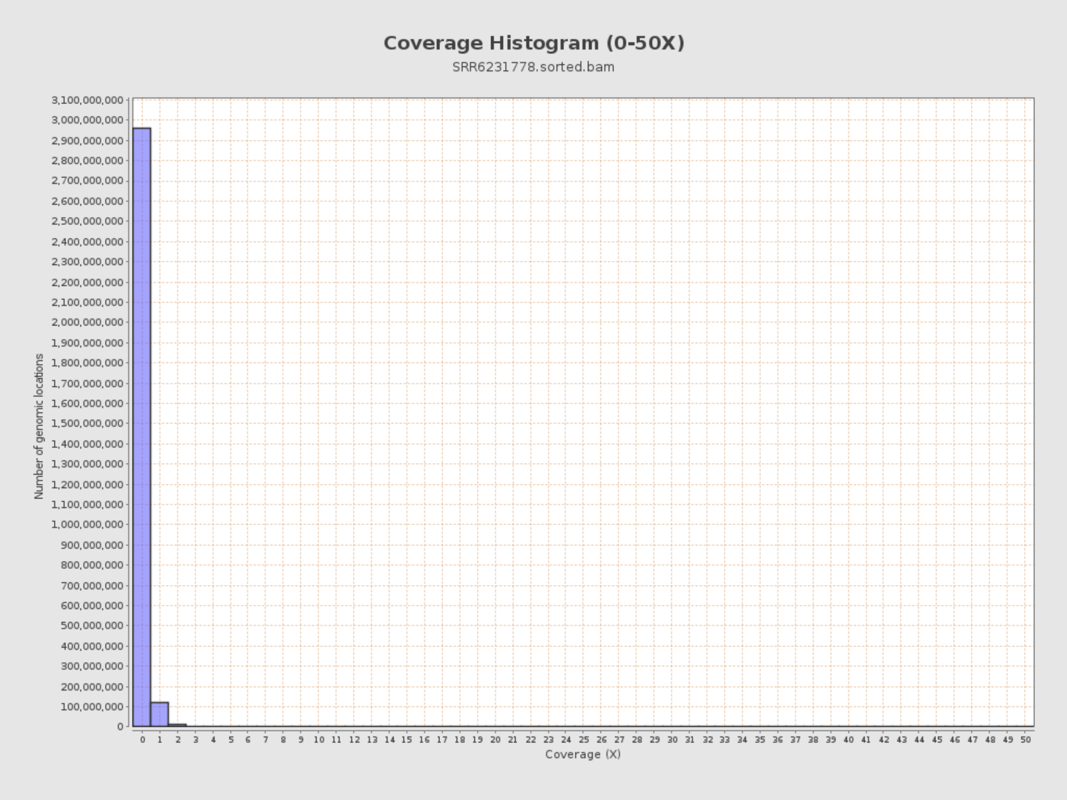
3. Results : Coverage across reference



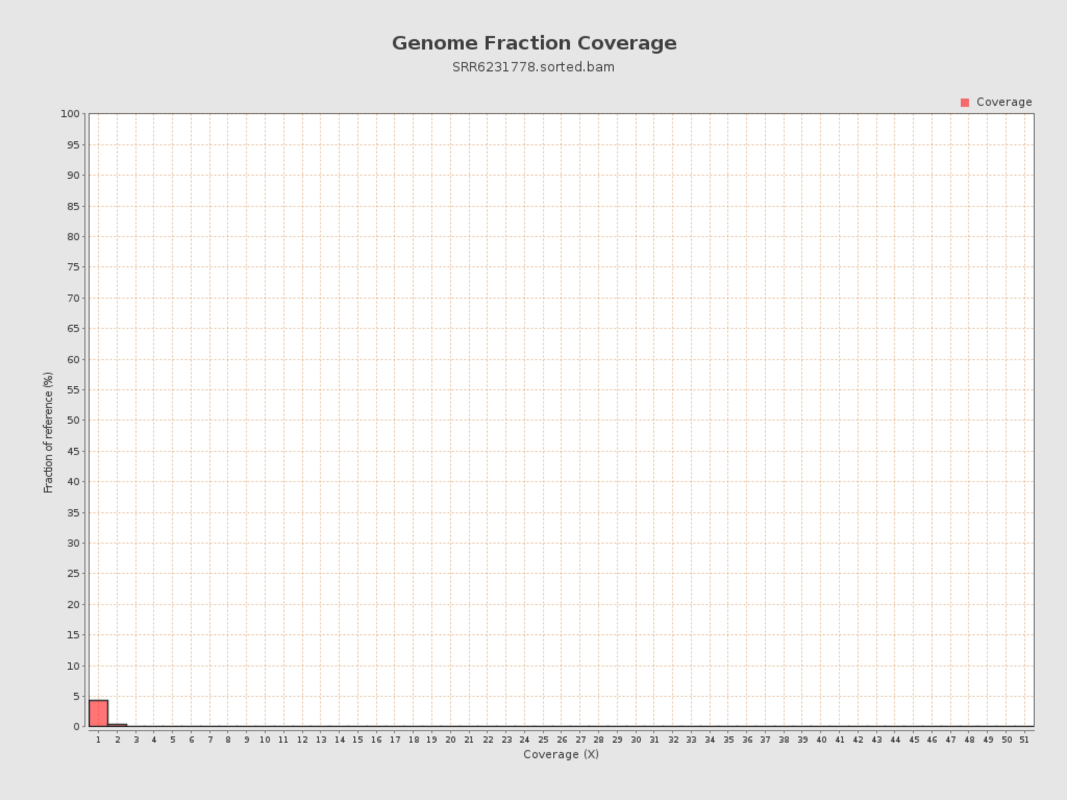
4. Results : Coverage Histogram



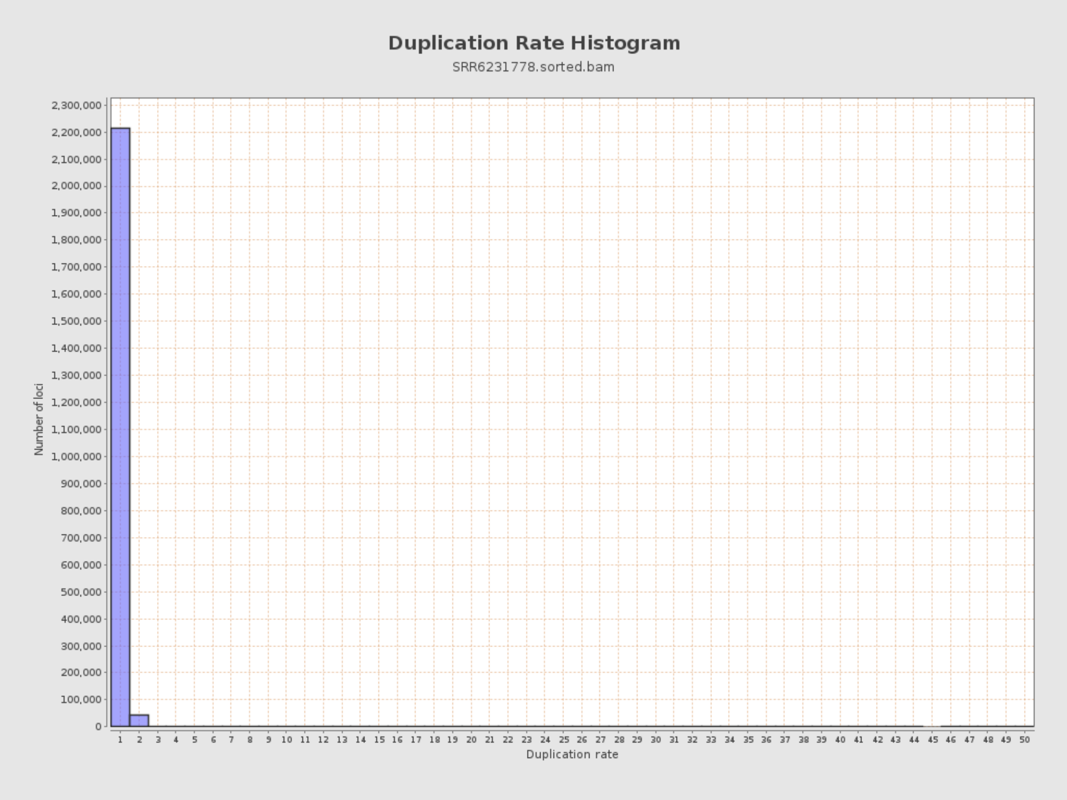
5. Results : Coverage Histogram (0-50X)



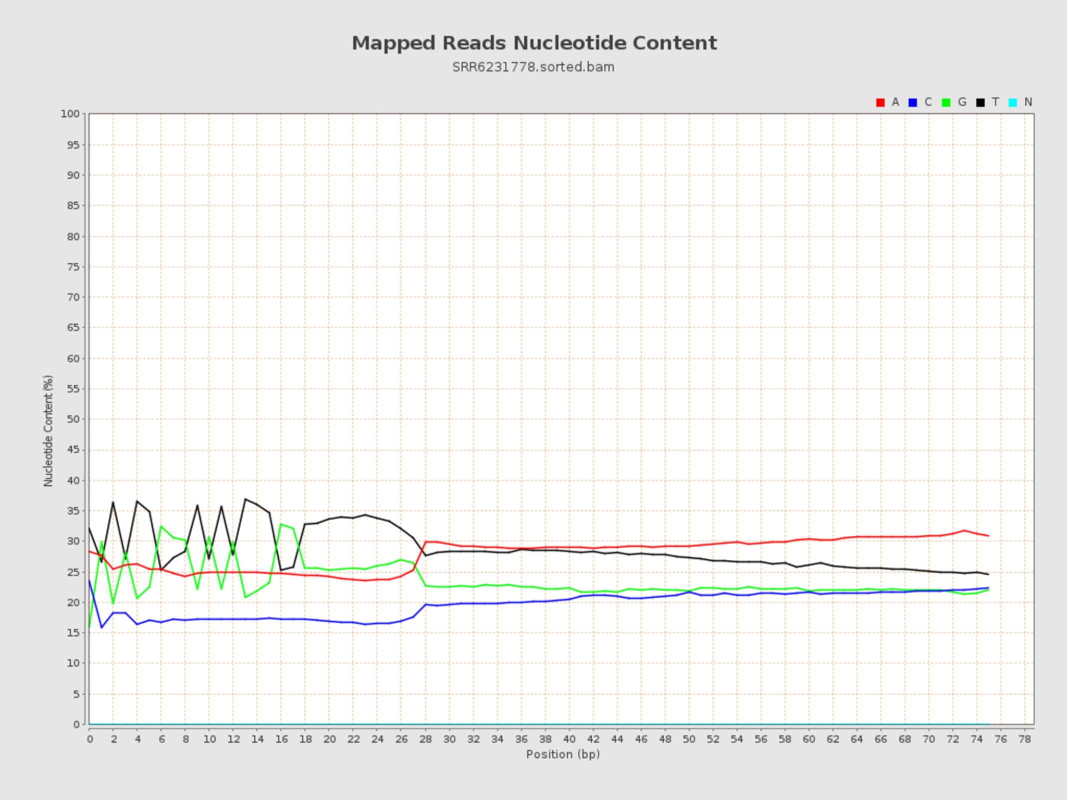
6. Results : Genome Fraction Coverage



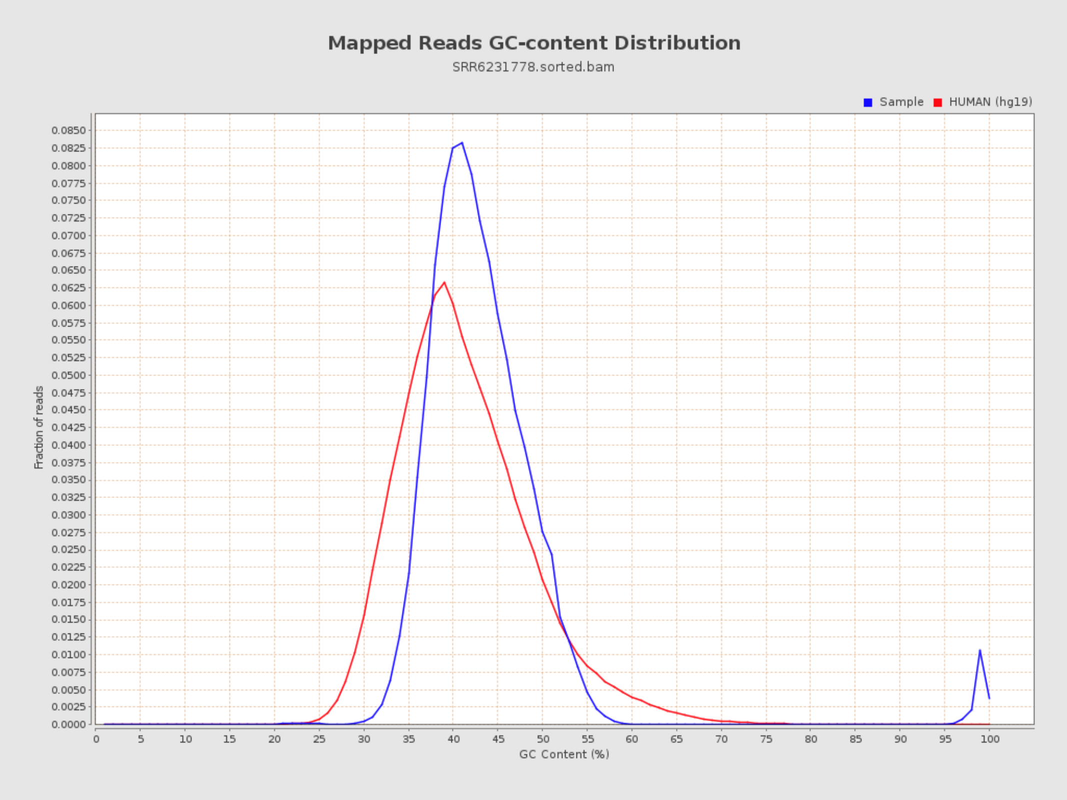
7. Results : Duplication Rate Histogram



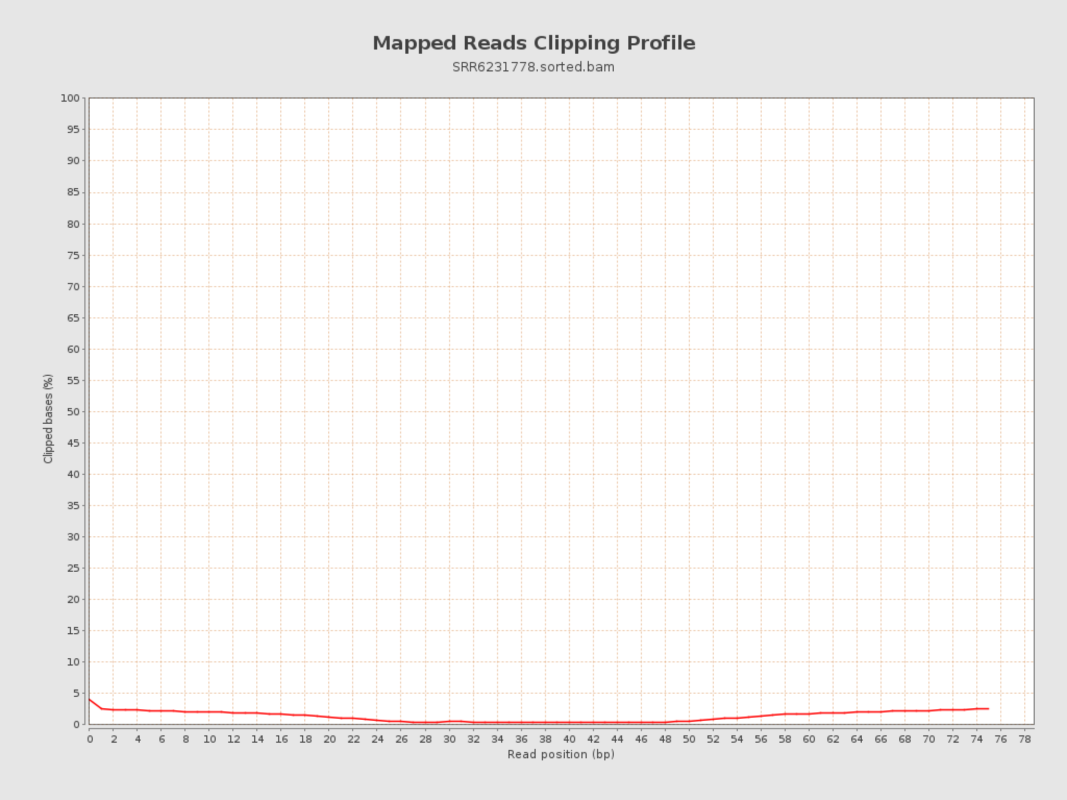
8. Results : Mapped Reads Nucleotide Content



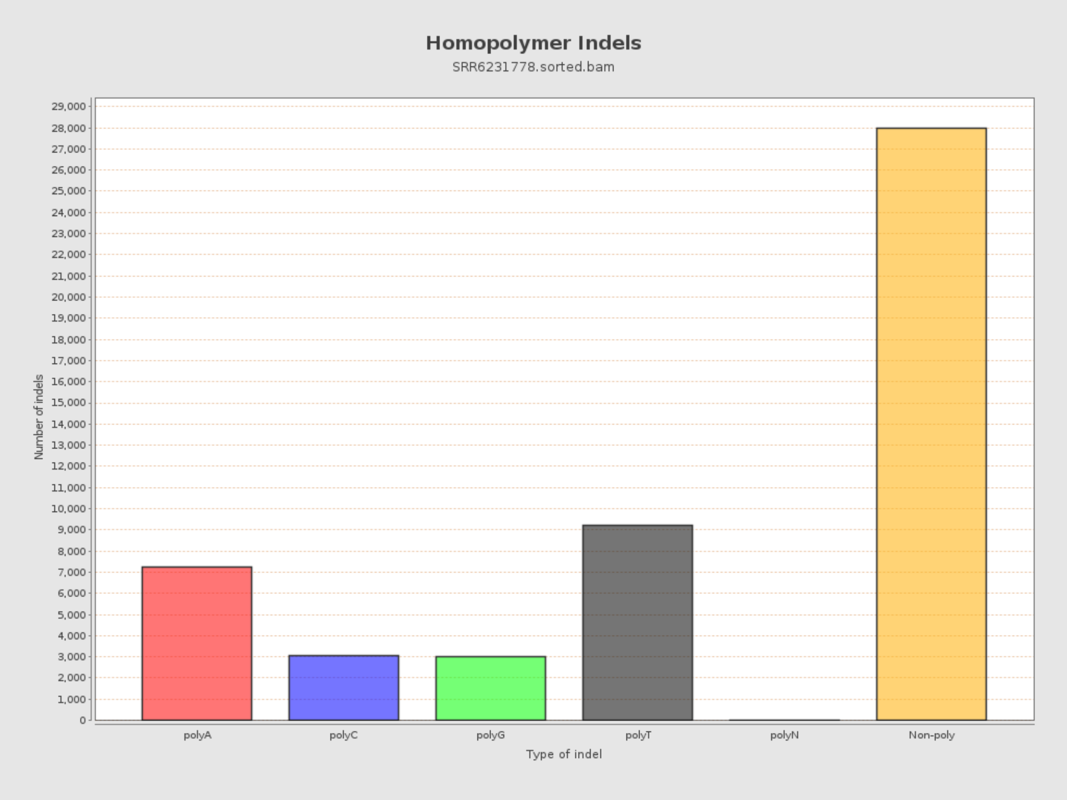
9. Results : Mapped Reads GC-content Distribution



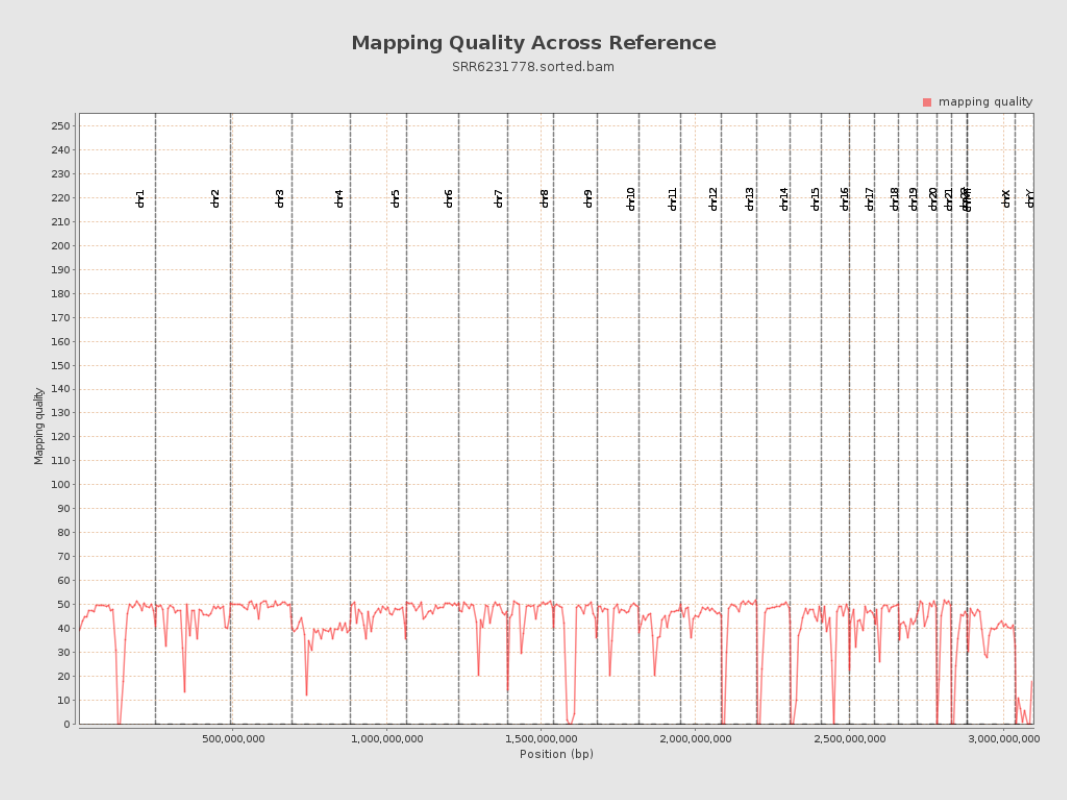
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram