Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 05:47:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231828.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_SRR6231828 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231828.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 05:47:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231828.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,612,731
Mapped reads	4,770,447 / 84.99%
Unmapped reads	842,284 / 15.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,009 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	460,046 / 8.2%
Duplication rate	7.77%
Clipped reads	2,665,145 / 47.48%

2.2. ACGT Content

Number/percentage of A's	77,400,127 / 25.56%
Number/percentage of C's	54,100,634 / 17.86%
Number/percentage of T's	99,110,010 / 32.72%
Number/percentage of G's	72,140,305 / 23.82%
Number/percentage of N's	114,098 / 0.04%
GC Percentage	41.68%

2.3. Coverage

Mean	0.0979

Standard Deviation	0.9359

2.4. Mapping Quality

Mean Mapping Quality	42.52

2.5. Mismatches and indels

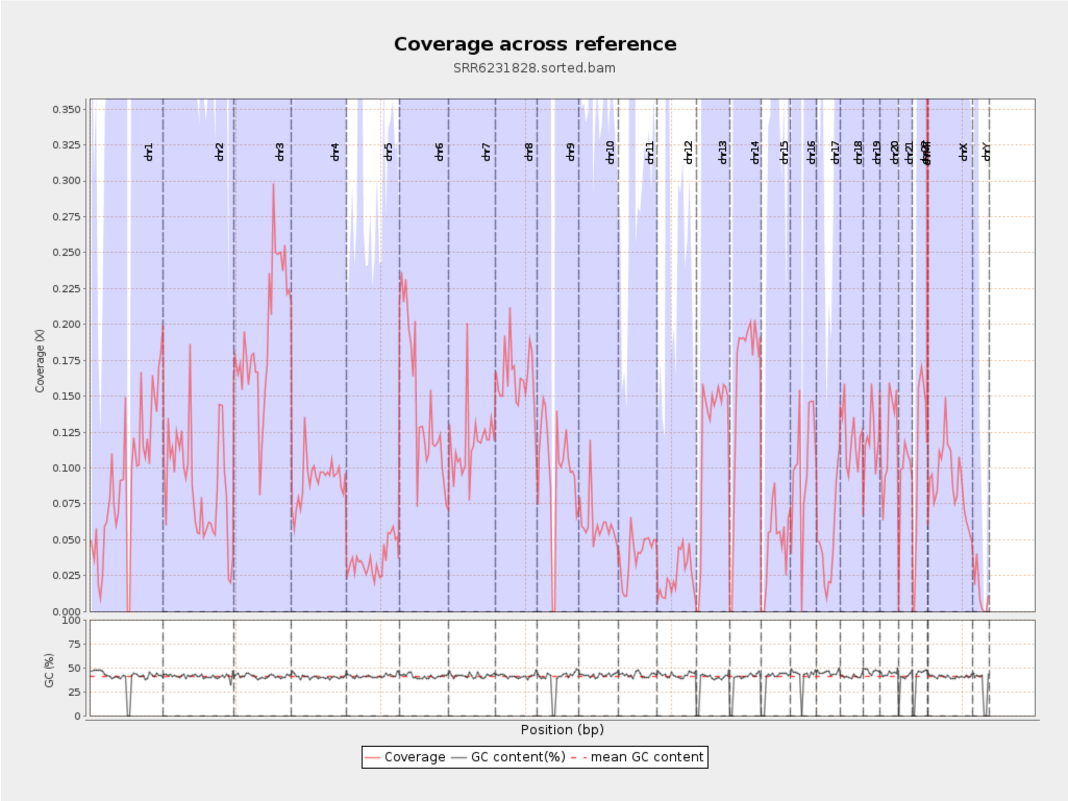
General error rate	0.64%
Mismatches	1,916,020
Insertions	19,671
Mapped reads with at least one insertion	0.41%
Deletions	68,412
Mapped reads with at least one deletion	1.42%
Homopolymer indels	44.08%

2.6. Chromosome stats

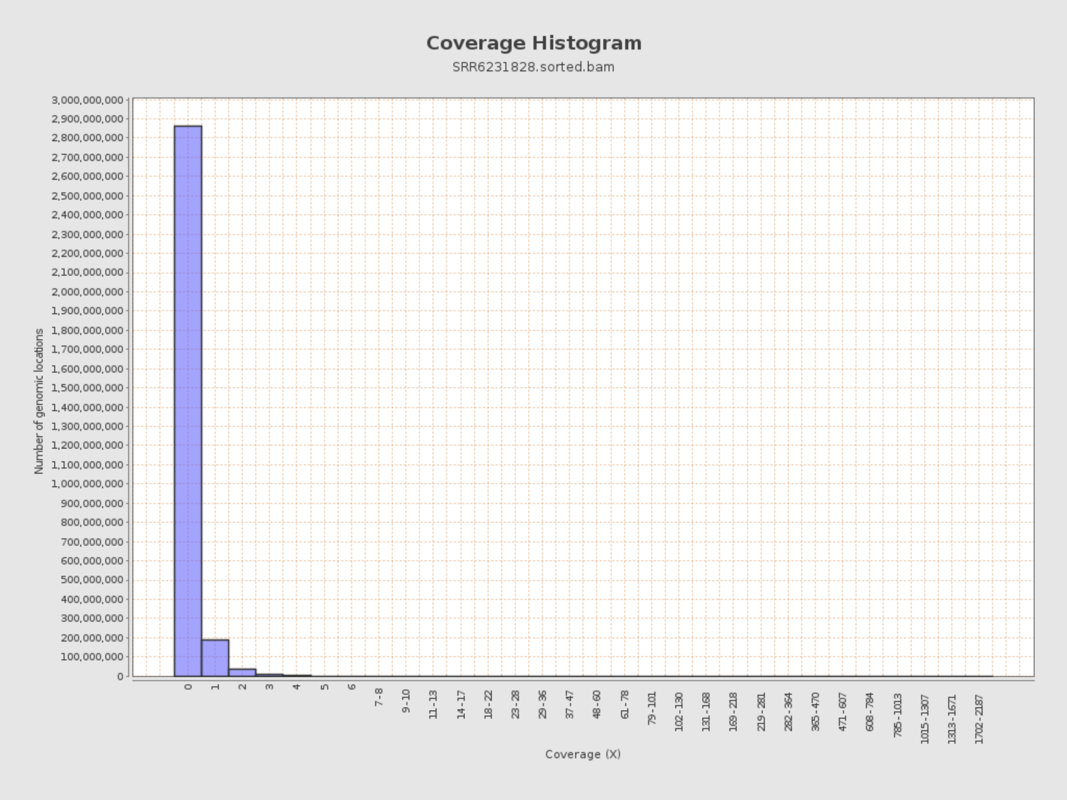
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22623329	0.0908	1.6357
chr2	243199373	21232816	0.0873	1.2771
chr3	198022430	38339586	0.1936	0.5473
chr4	191154276	17449512	0.0913	0.4187
chr5	180915260	6611029	0.0365	0.2677
chr6	171115067	24516937	0.1433	0.7494
chr7	159138663	18603395	0.1169	1.5025

chr8	146364022	23801452	0.1626	1.0408
chr9	141213431	13932433	0.0987	0.9012
chr10	135534747	8248465	0.0609	0.5804
chr11	135006516	5364176	0.0397	0.8023
chr12	133851895	3320216	0.0248	0.2806
chr13	115169878	14257670	0.1238	0.4507
chr14	107349540	16897315	0.1574	0.5768
chr15	102531392	4862715	0.0474	0.3355
chr16	90354753	9376070	0.1038	0.5664
chr17	81195210	3889715	0.0479	0.2993
chr18	78077248	9448312	0.121	2.2081
chr19	59128983	7214438	0.122	1.0327
chr20	63025520	7606340	0.1207	0.4828
chr21	48129895	4552810	0.0946	0.4424
chr22	51304566	5528149	0.1078	0.4086
chrMT	16571	494325	29.8307	16.168
chrX	155270560	14023314	0.0903	0.6098
chrY	59373566	792500	0.0133	0.2658

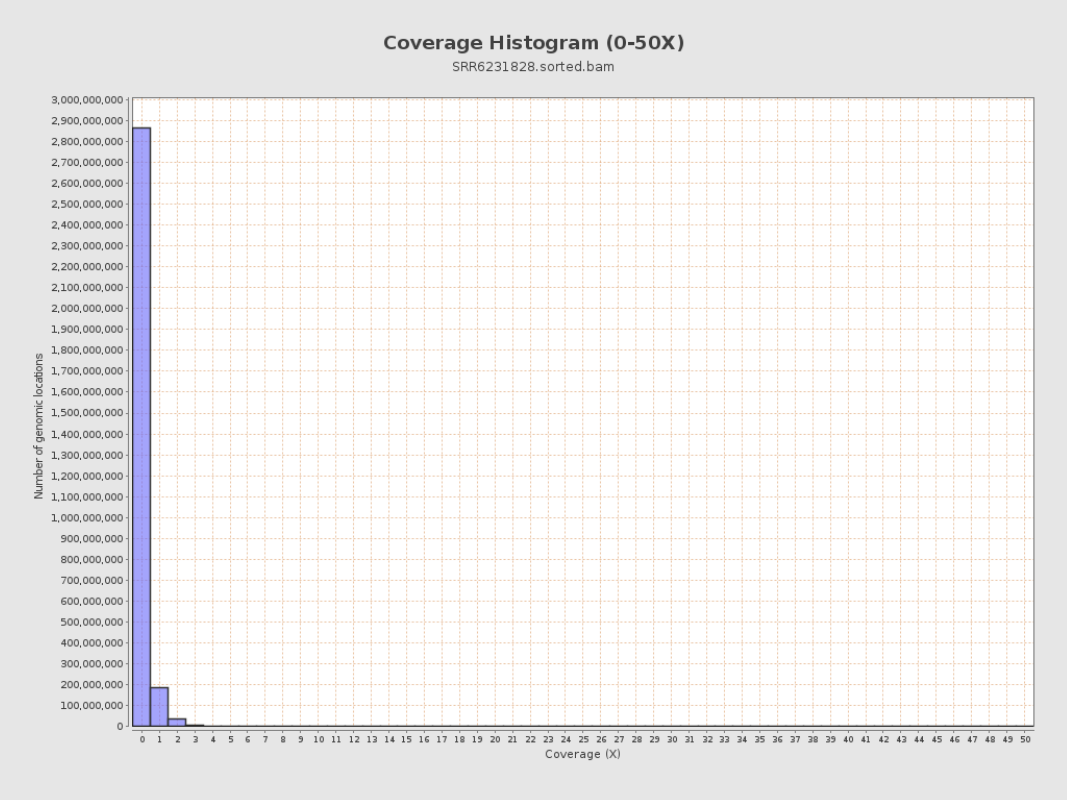
3. Results : Coverage across reference



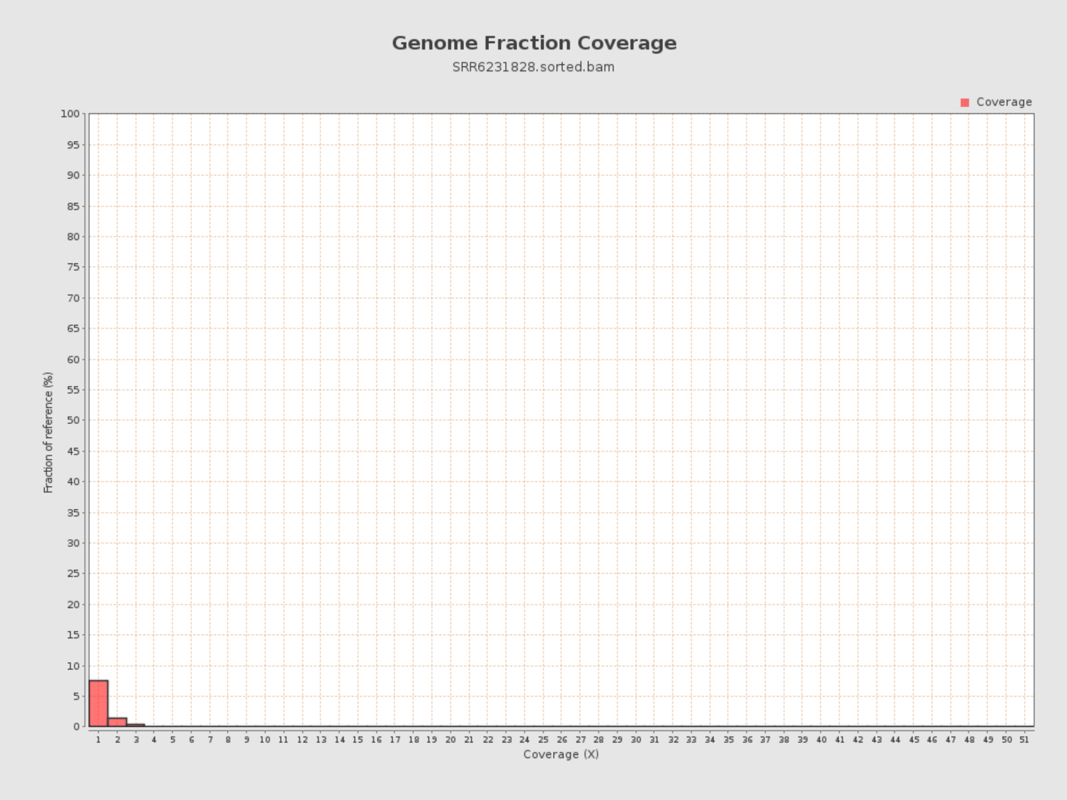
4. Results : Coverage Histogram



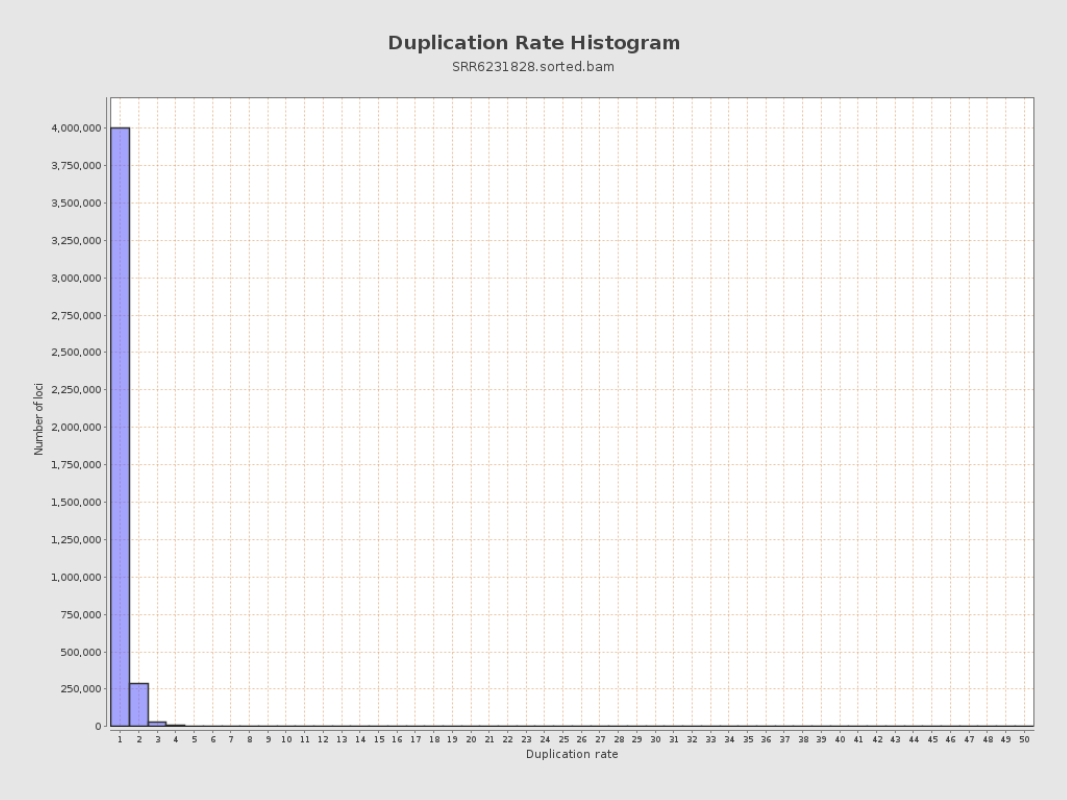
5. Results : Coverage Histogram (0-50X)



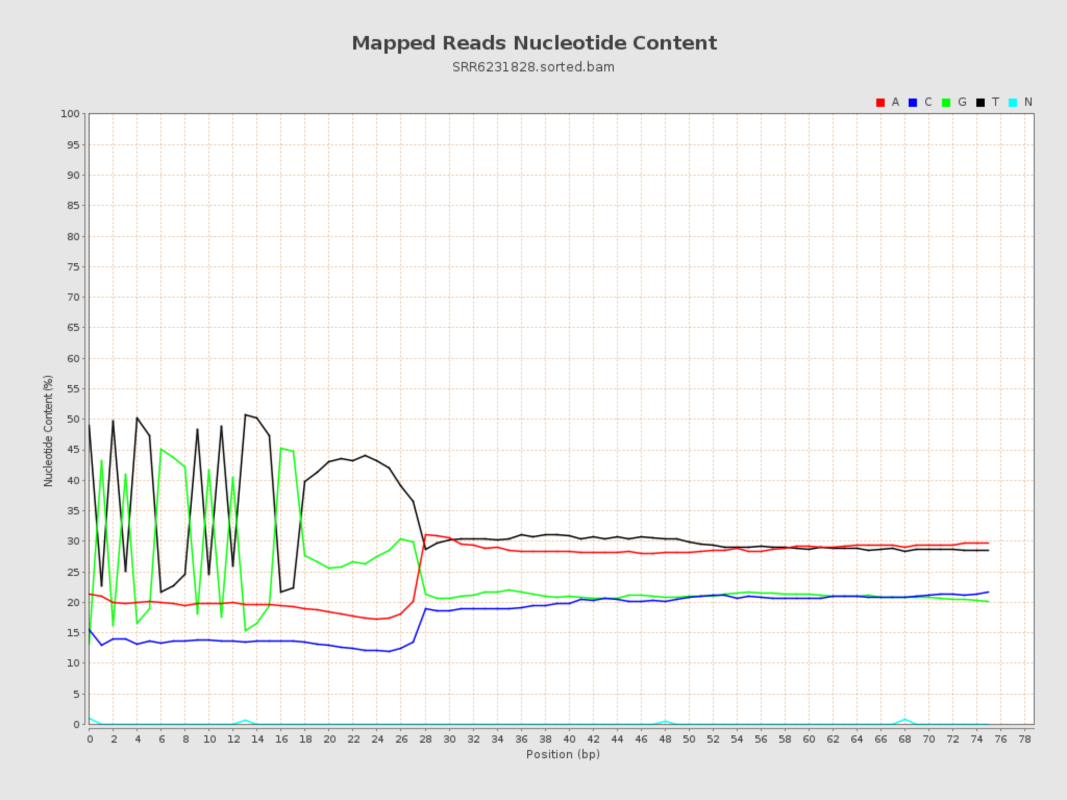
6. Results : Genome Fraction Coverage



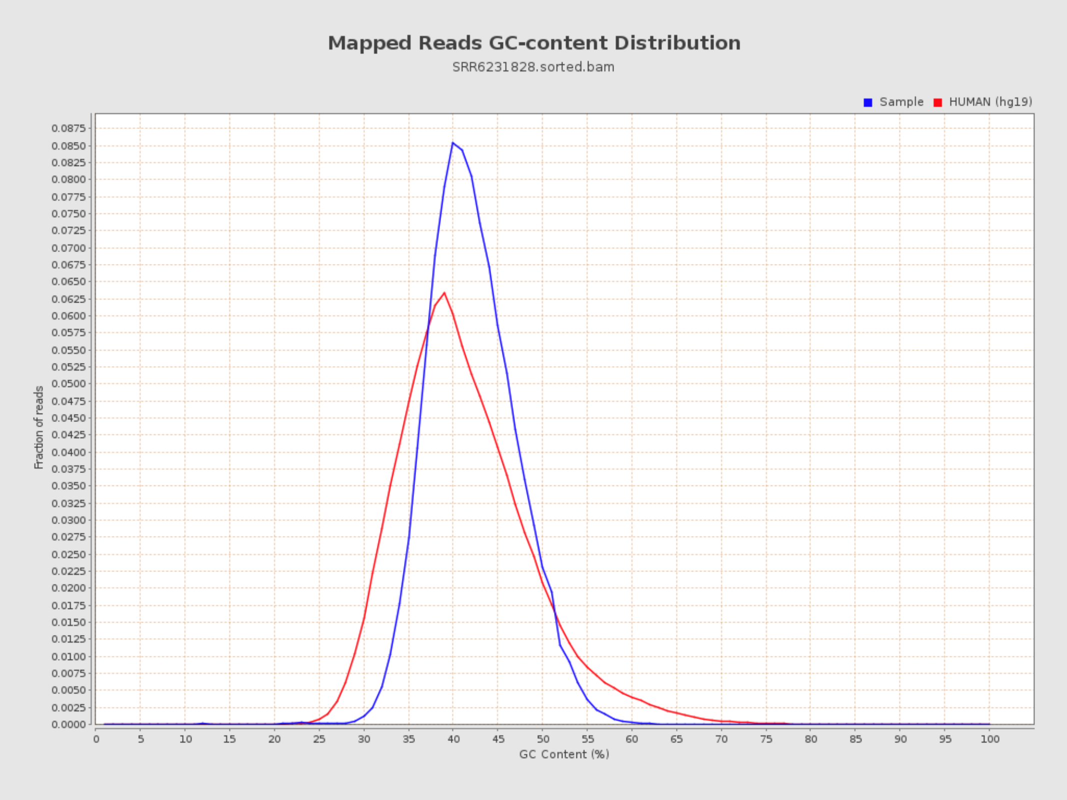
7. Results : Duplication Rate Histogram



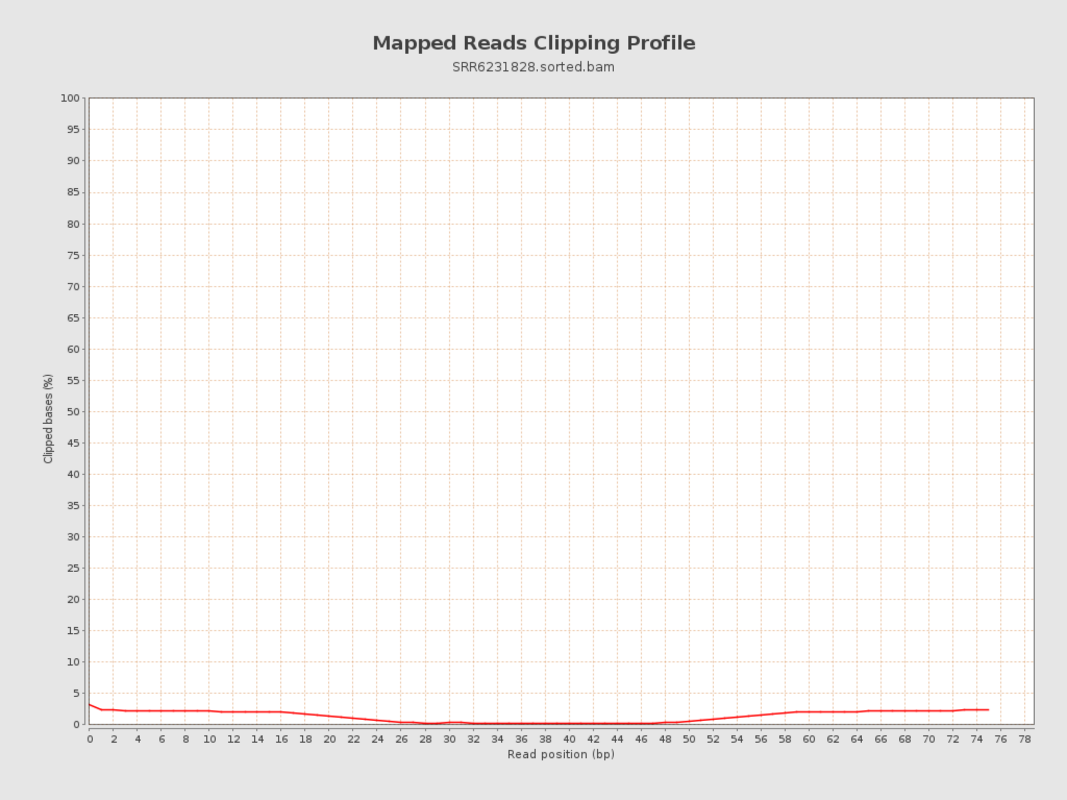
8. Results : Mapped Reads Nucleotide Content



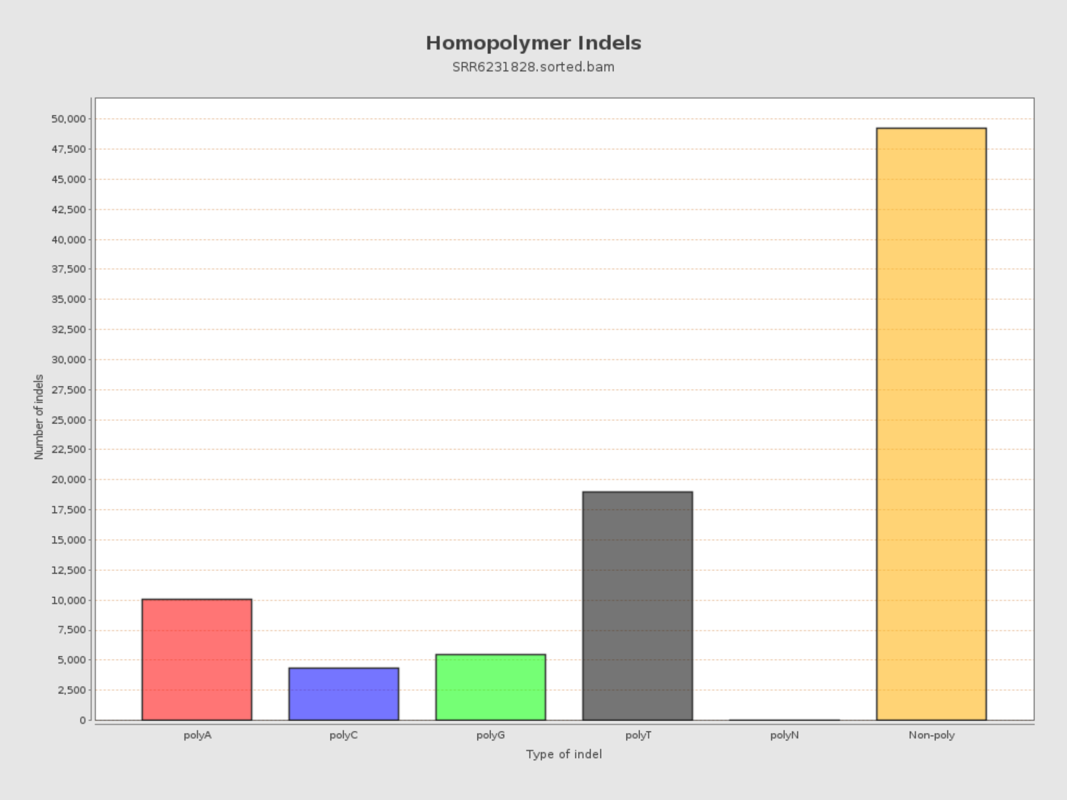
9. Results : Mapped Reads GC-content Distribution



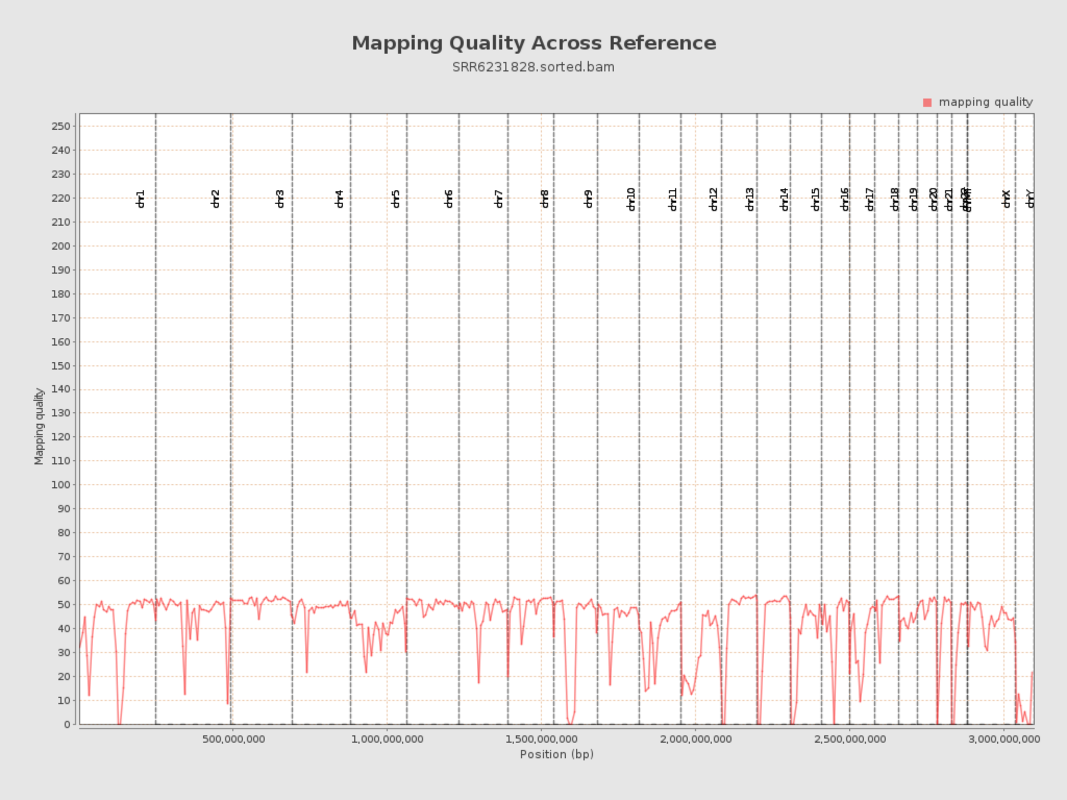
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram