Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 03:35:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231798.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_SRR6231798 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231798.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 03:35:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231798.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,111,684
Mapped reads	1,816,430 / 58.37%
Unmapped reads	1,295,254 / 41.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,948 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	164,429 / 5.28%
Duplication rate	2.17%
Clipped reads	950,850 / 30.56%

2.2. ACGT Content

Number/percentage of A's	34,505,192 / 29.14%
Number/percentage of C's	20,728,292 / 17.51%
Number/percentage of T's	31,266,112 / 26.41%
Number/percentage of G's	31,896,669 / 26.94%
Number/percentage of N's	7,788 / 0.01%
GC Percentage	44.45%

2.3. Coverage

Mean	0.0383

Standard Deviation	16.0424

2.4. Mapping Quality

Mean Mapping Quality	44.77

2.5. Mismatches and indels

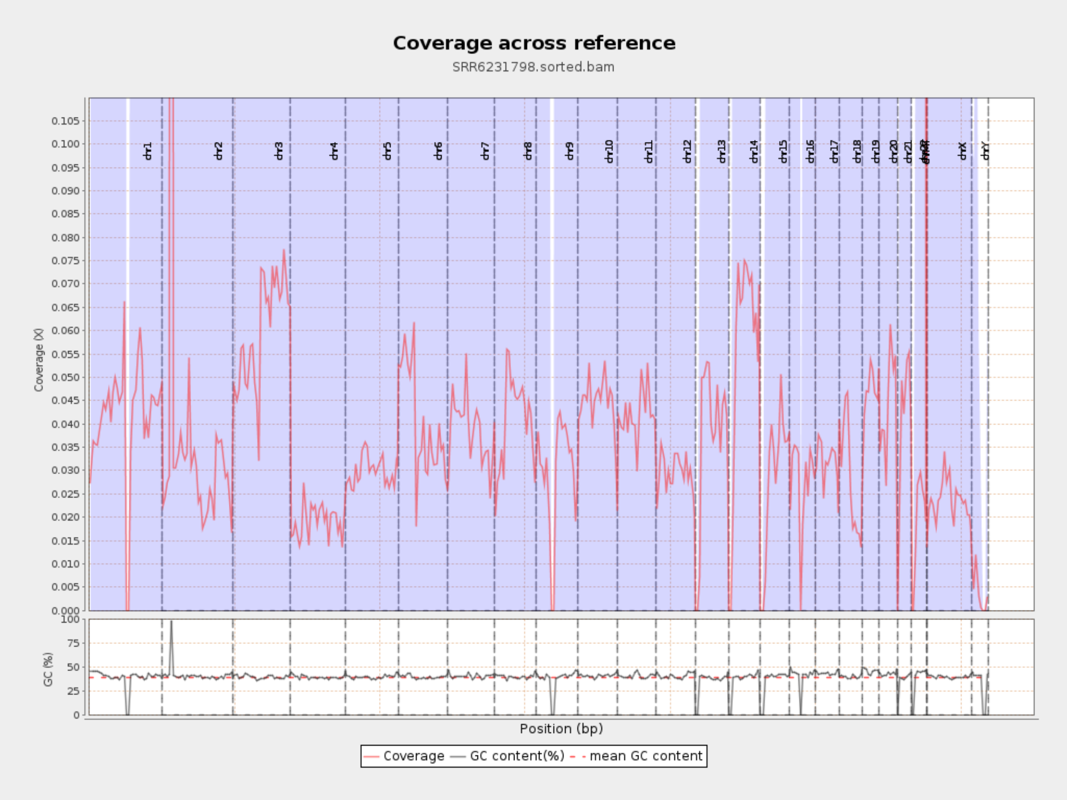
General error rate	0.73%
Mismatches	843,961
Insertions	8,824
Mapped reads with at least one insertion	0.48%
Deletions	26,345
Mapped reads with at least one deletion	1.44%
Homopolymer indels	43.92%

2.6. Chromosome stats

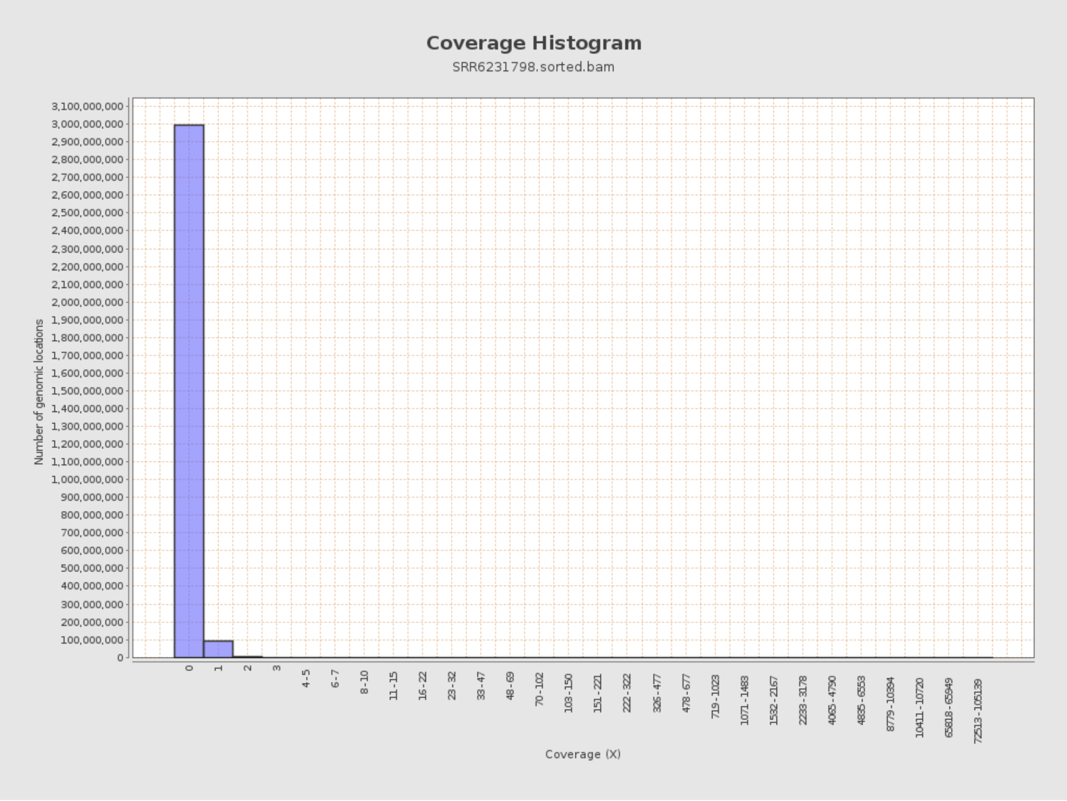
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10375674	0.0416	0.6168
chr2	243199373	15658674	0.0644	57.2248
chr3	198022430	11806232	0.0596	0.2611
chr4	191154276	3629708	0.019	0.1532
chr5	180915260	5405458	0.0299	0.1853
chr6	171115067	6919334	0.0404	0.2516
chr7	159138663	6177041	0.0388	0.3794

chr8	146364022	5909048	0.0404	0.5669
chr9	141213431	4154222	0.0294	0.2343
chr10	135534747	6116796	0.0451	0.2945
chr11	135006516	5636251	0.0417	0.3041
chr12	133851895	3930558	0.0294	0.1854
chr13	115169878	4259174	0.037	0.2049
chr14	107349540	5930664	0.0552	0.3742
chr15	102531392	2914464	0.0284	0.1819
chr16	90354753	2501582	0.0277	0.1927
chr17	81195210	2563029	0.0316	0.2103
chr18	78077248	2206926	0.0283	0.42
chr19	59128983	2766476	0.0468	0.3912
chr20	63025520	2747575	0.0436	0.2274
chr21	48129895	1931735	0.0401	0.2207
chr22	51304566	947617	0.0185	0.144
chrMT	16571	81318	4.9072	3.6642
chrX	155270560	3657970	0.0236	0.1825
chrY	59373566	220180	0.0037	0.0799

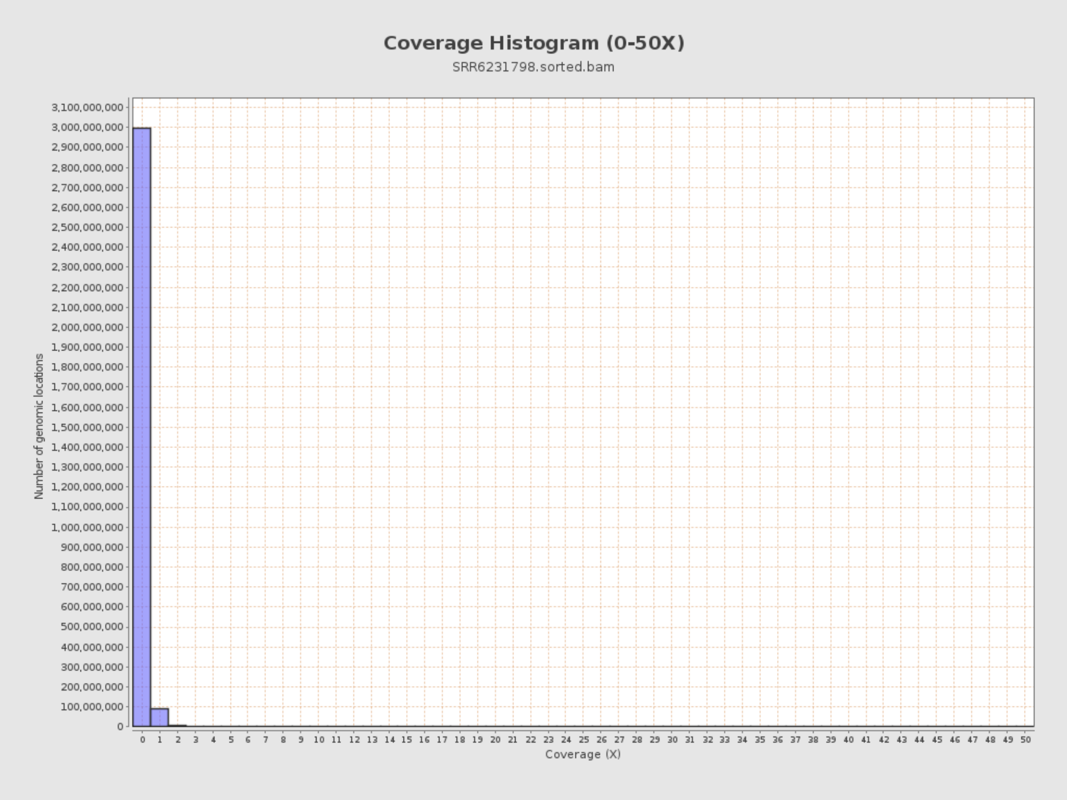
3. Results : Coverage across reference



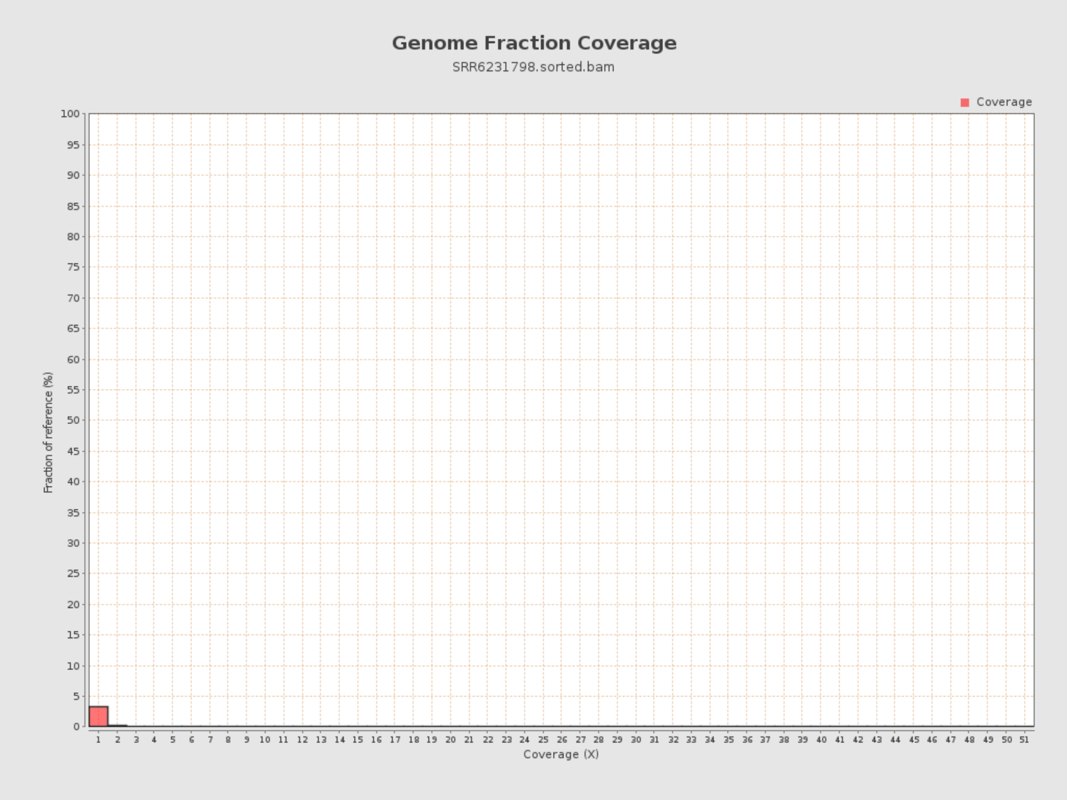
4. Results : Coverage Histogram



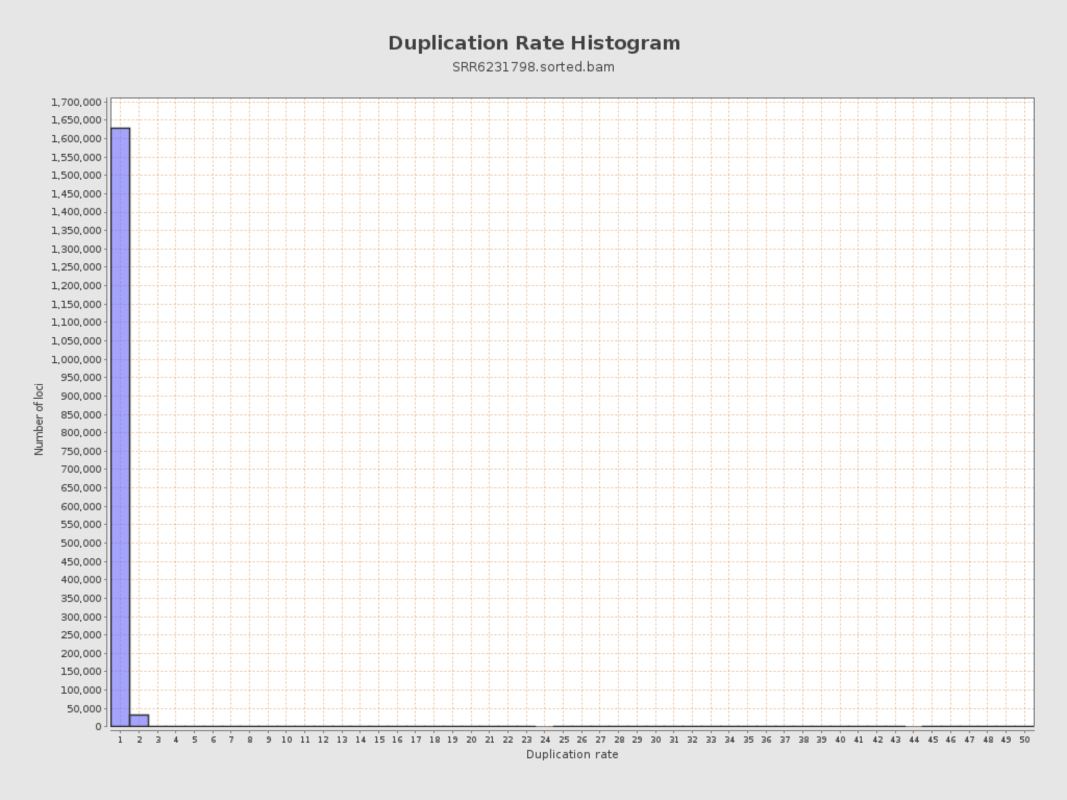
5. Results : Coverage Histogram (0-50X)



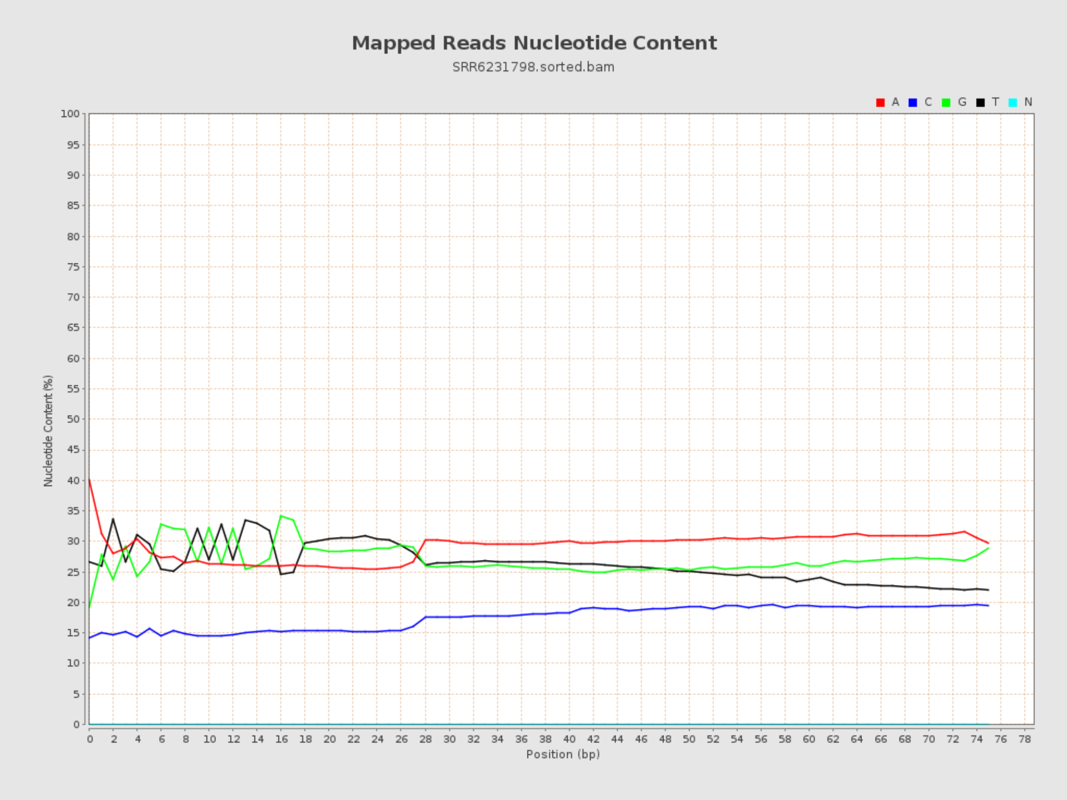
6. Results : Genome Fraction Coverage



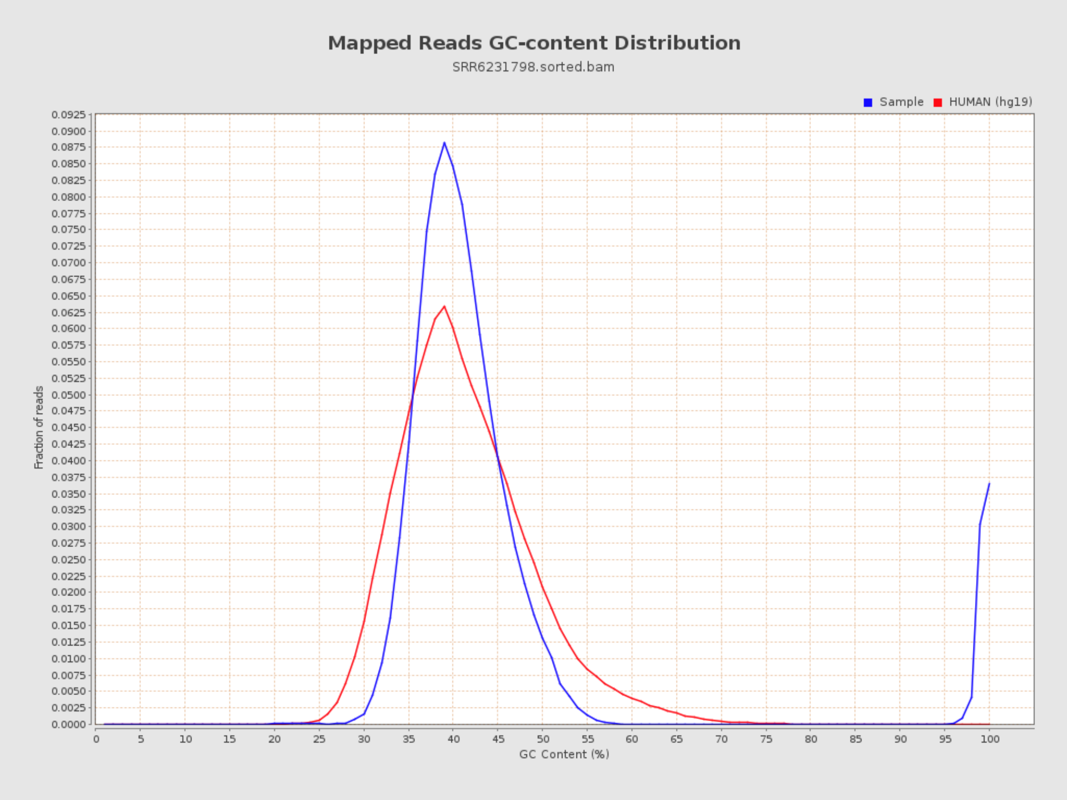
7. Results : Duplication Rate Histogram



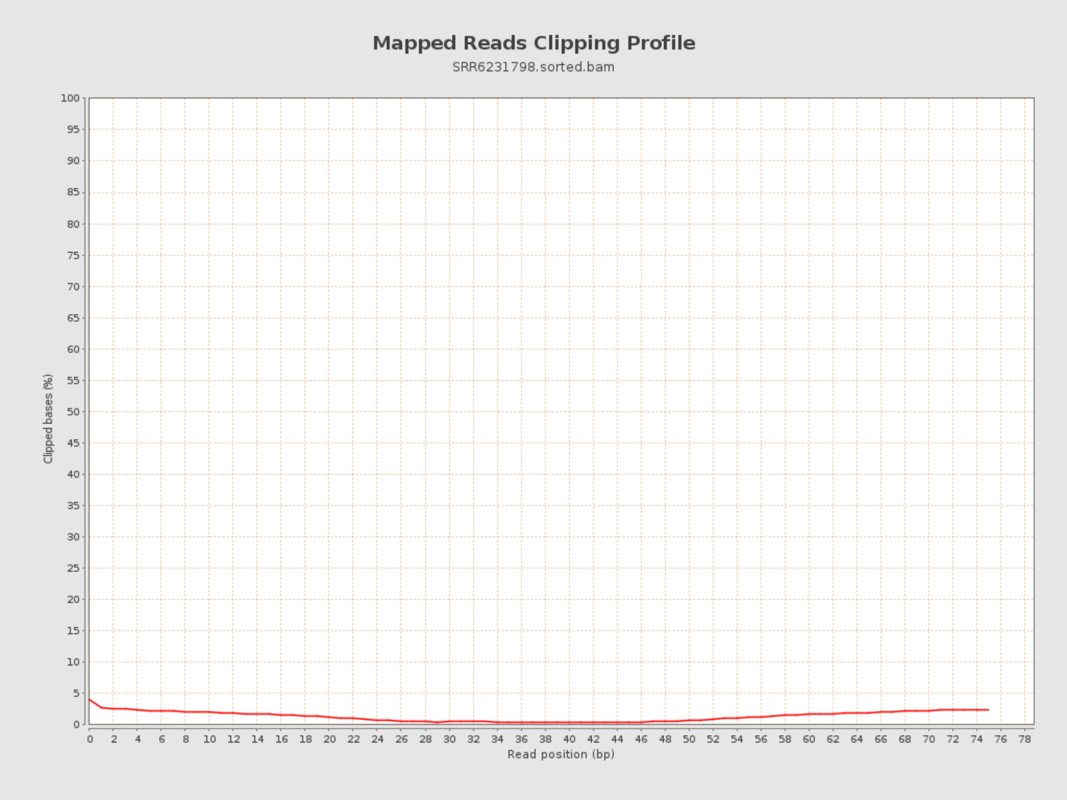
8. Results : Mapped Reads Nucleotide Content



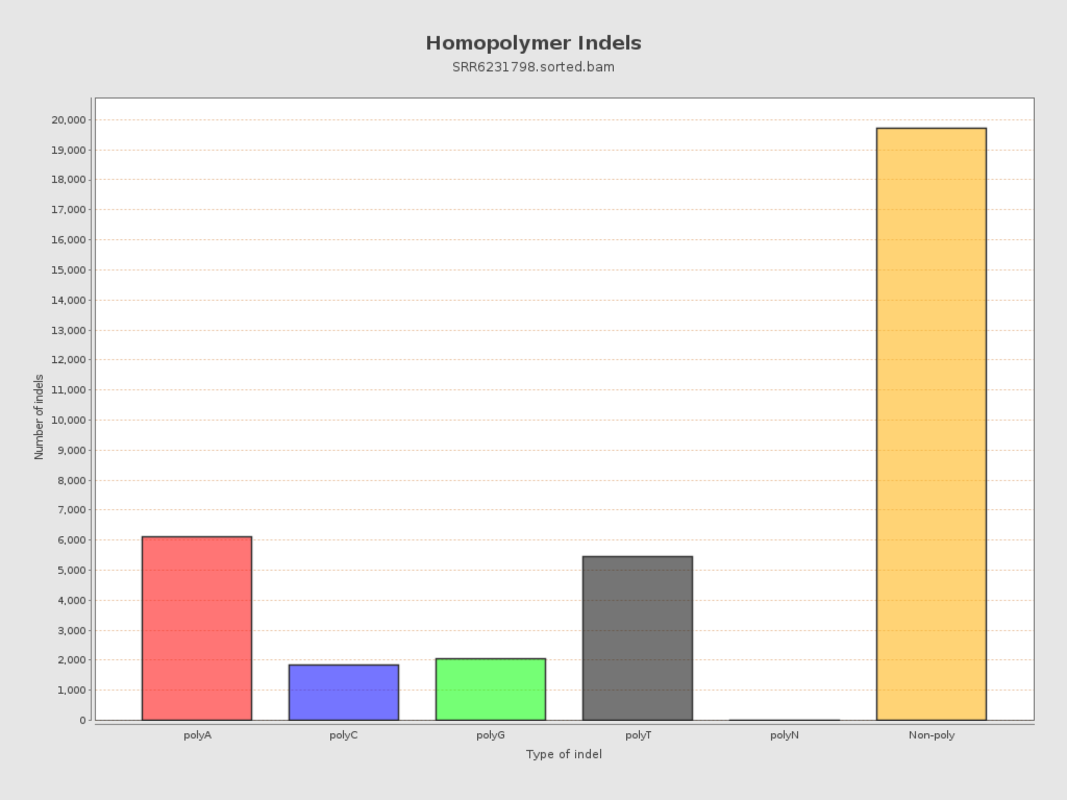
9. Results : Mapped Reads GC-content Distribution



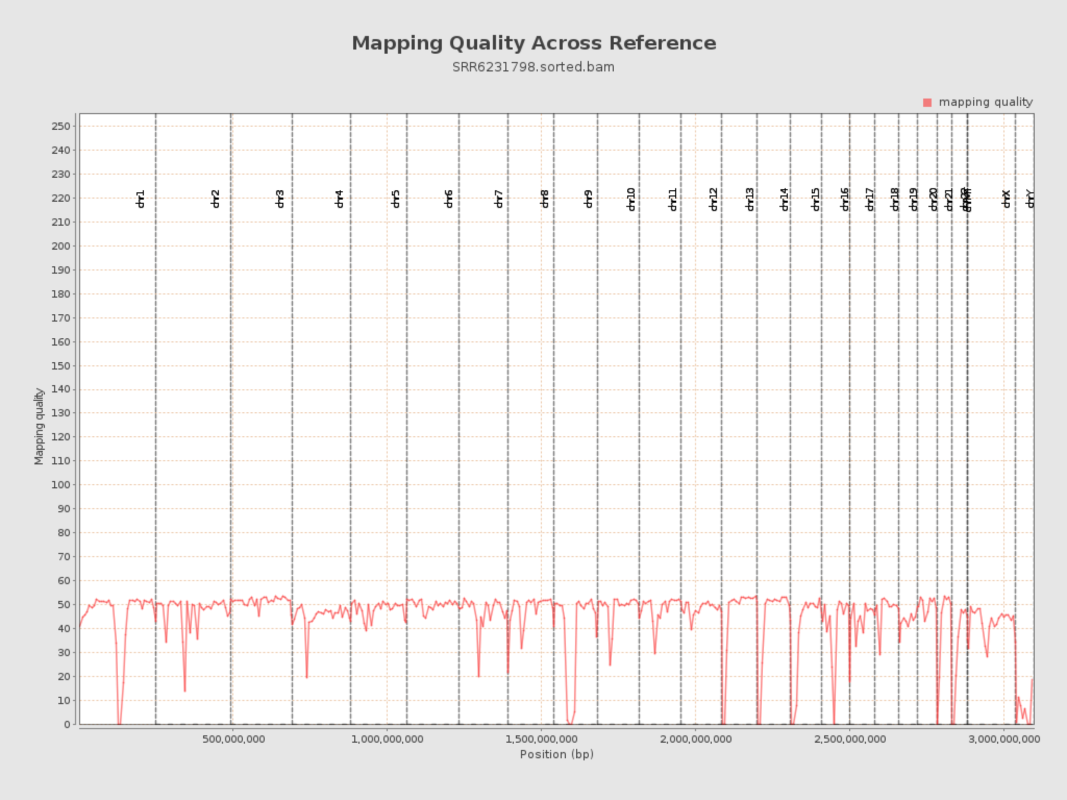
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram