Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 16:54:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234111.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_SRR6234111 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234111.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 16:54:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234111.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,900,017
Mapped reads	3,608,383 / 92.52%
Unmapped reads	291,634 / 7.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,734 / 0.97%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	755,218 / 19.36%
Duplication rate	9.92%
Clipped reads	1,268,094 / 32.52%

2.2. ACGT Content

Number/percentage of A's	62,685,370 / 25.22%
Number/percentage of C's	44,160,461 / 17.77%
Number/percentage of T's	68,146,373 / 27.41%
Number/percentage of G's	73,533,578 / 29.58%
Number/percentage of N's	53,061 / 0.02%
GC Percentage	47.35%

2.3. Coverage

Mean	0.0803

Standard Deviation	47.4348

2.4. Mapping Quality

Mean Mapping Quality	41.99

2.5. Mismatches and indels

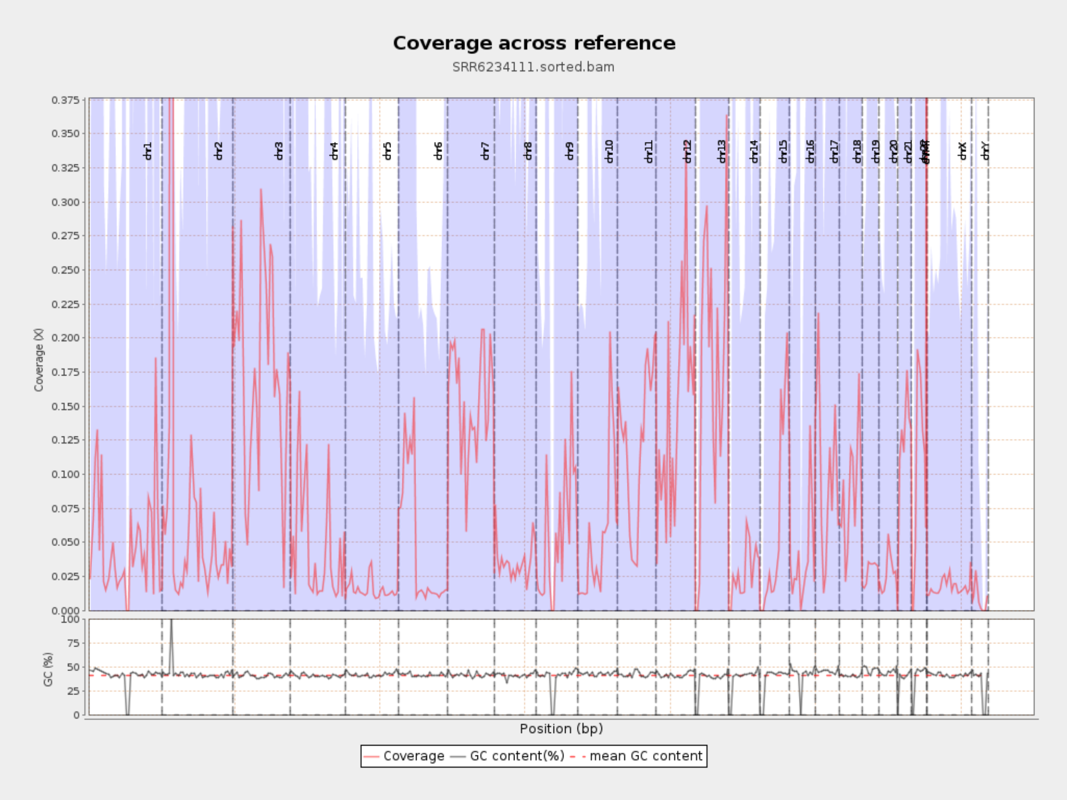
General error rate	0.64%
Mismatches	1,551,658
Insertions	16,054
Mapped reads with at least one insertion	0.44%
Deletions	52,719
Mapped reads with at least one deletion	1.45%
Homopolymer indels	47.15%

2.6. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12164694	0.0488	0.525
chr2	243199373	34842882	0.1433	169.2202
chr3	198022430	34532018	0.1744	0.8814
chr4	191154276	8944854	0.0468	0.4836
chr5	180915260	2848785	0.0157	0.2493
chr6	171115067	8114661	0.0474	0.4954
chr7	159138663	24660867	0.155	1.0322

chr8	146364022	5353203	0.0366	0.6674
chr9	141213431	8025325	0.0568	0.6264
chr10	135534747	7376982	0.0544	0.6429
chr11	135006516	16468374	0.122	0.8906
chr12	133851895	19918257	0.1488	0.8283
chr13	115169878	19926960	0.173	0.8851
chr14	107349540	2913377	0.0271	0.4887
chr15	102531392	6639331	0.0648	0.5415
chr16	90354753	3436086	0.038	0.4958
chr17	81195210	7860520	0.0968	0.6624
chr18	78077248	6867714	0.088	1.5962
chr19	59128983	1691476	0.0286	0.3817
chr20	63025520	1766864	0.028	0.3767
chr21	48129895	5903649	0.1227	0.7844
chr22	51304566	5220695	0.1018	0.6693
chrMT	16571	15784	0.9525	1.8669
chrX	155270560	2681747	0.0173	0.36
chrY	59373566	490593	0.0083	0.1942

3. Results : Coverage across reference



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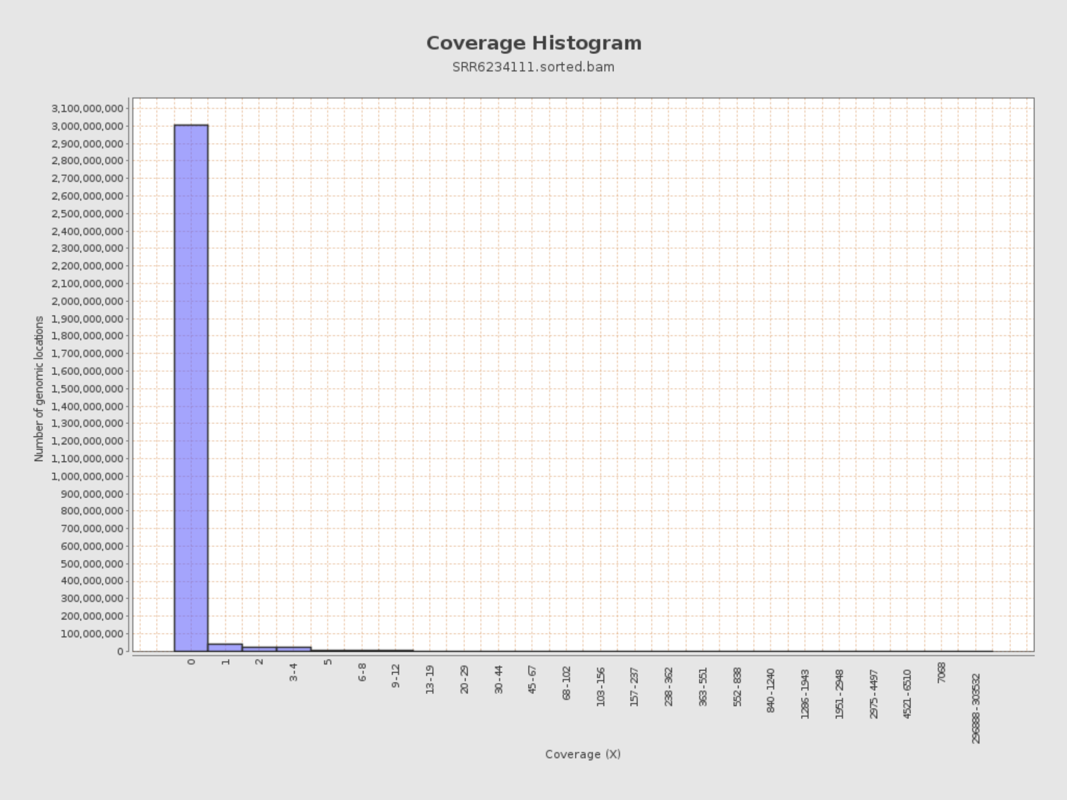
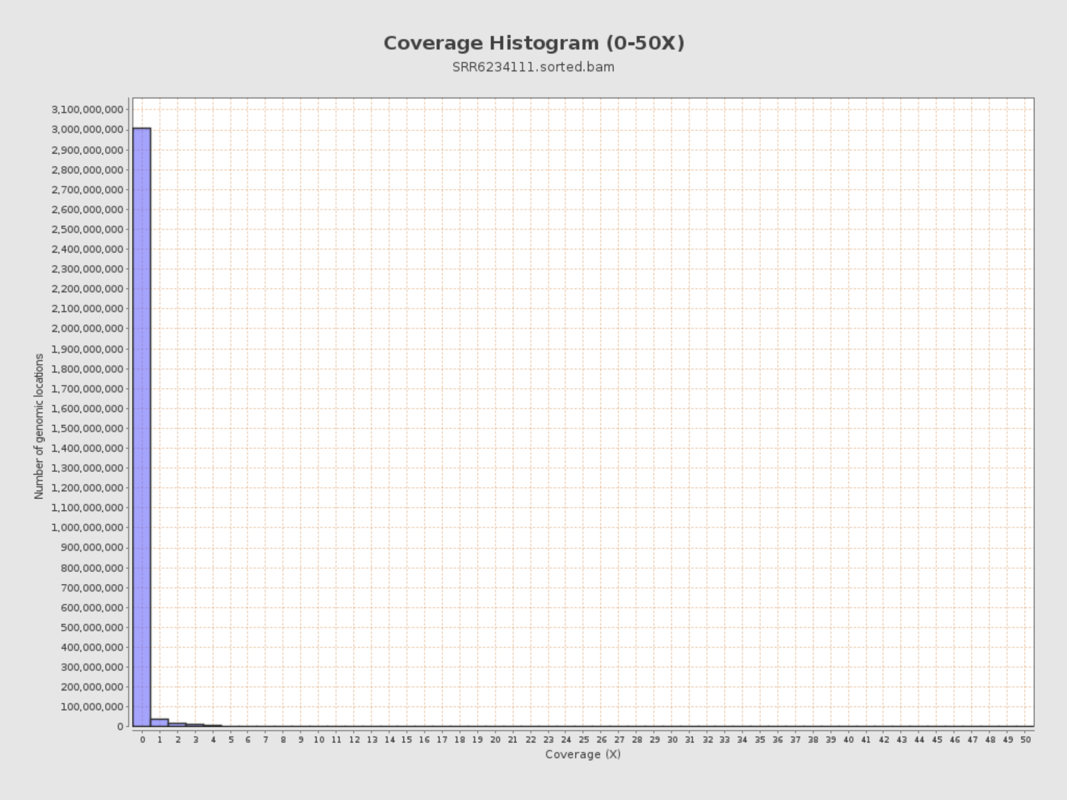
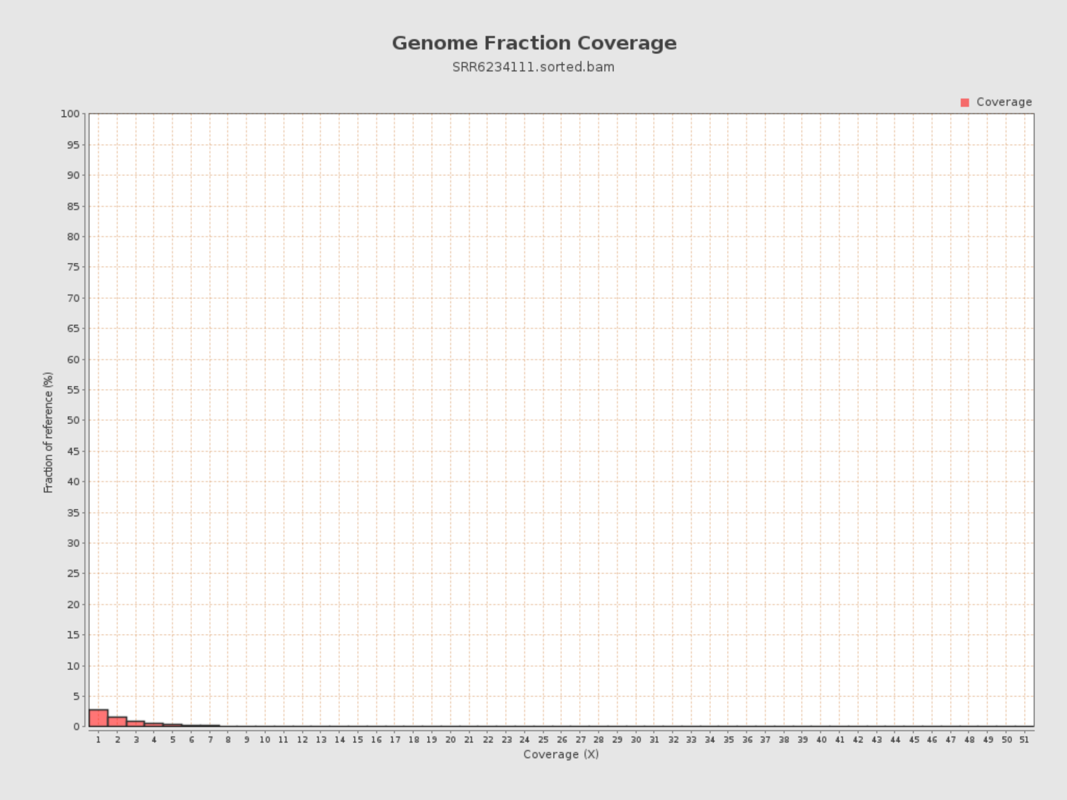
4. Results : Coverage Histogram



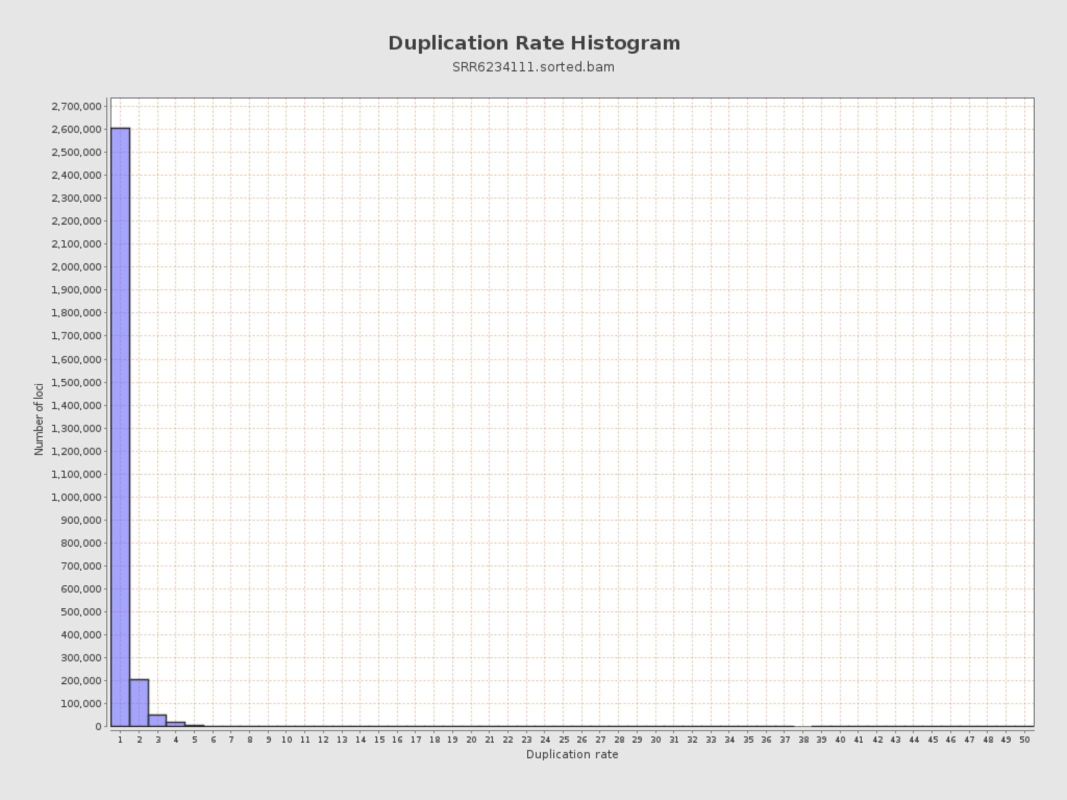
5. Results : Coverage Histogram (0-50X)



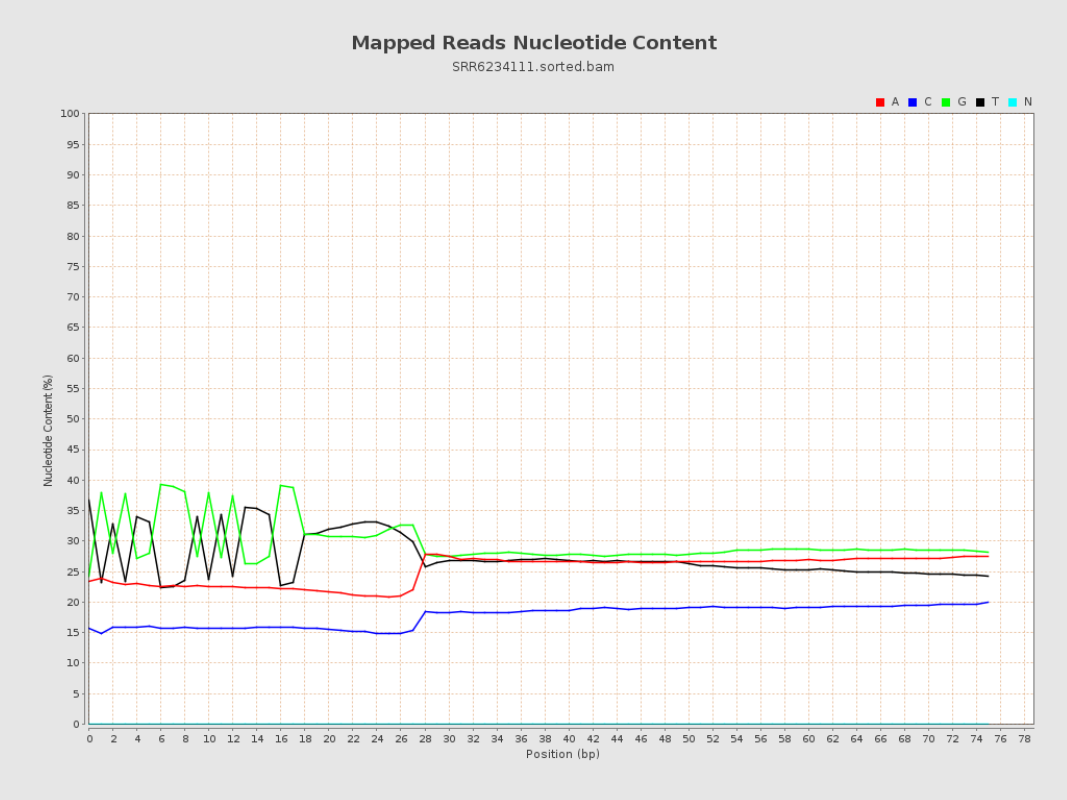
6. Results : Genome Fraction Coverage



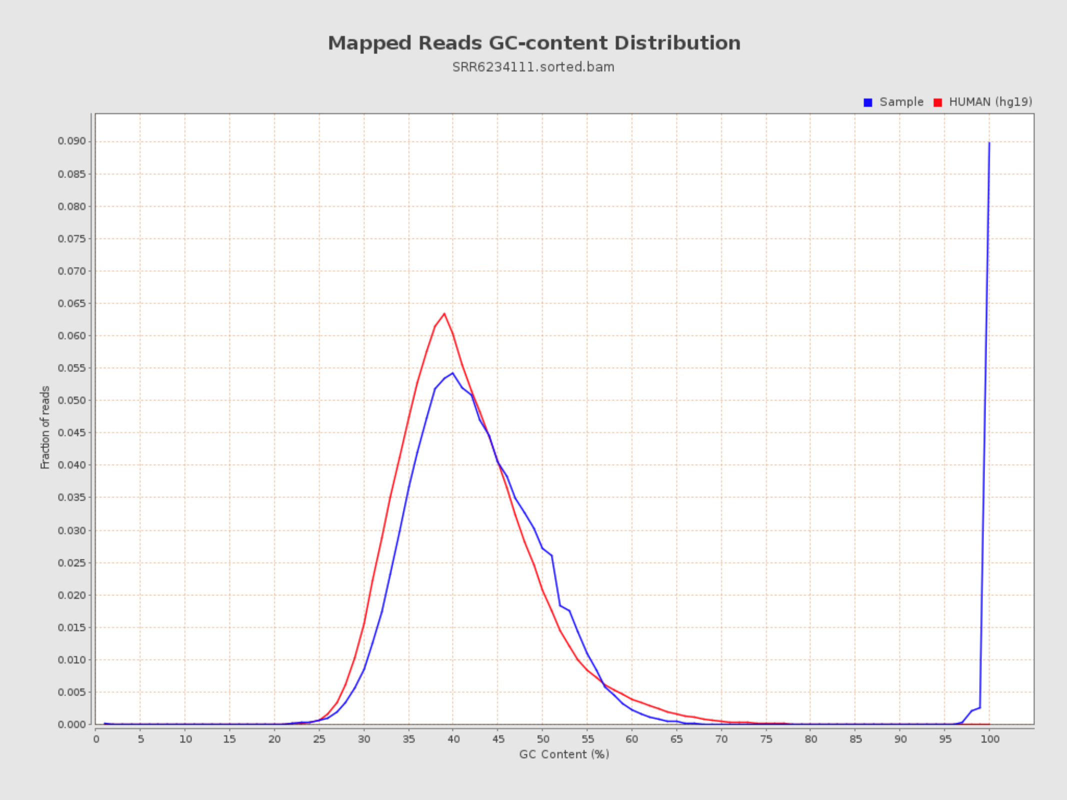
7. Results : Duplication Rate Histogram



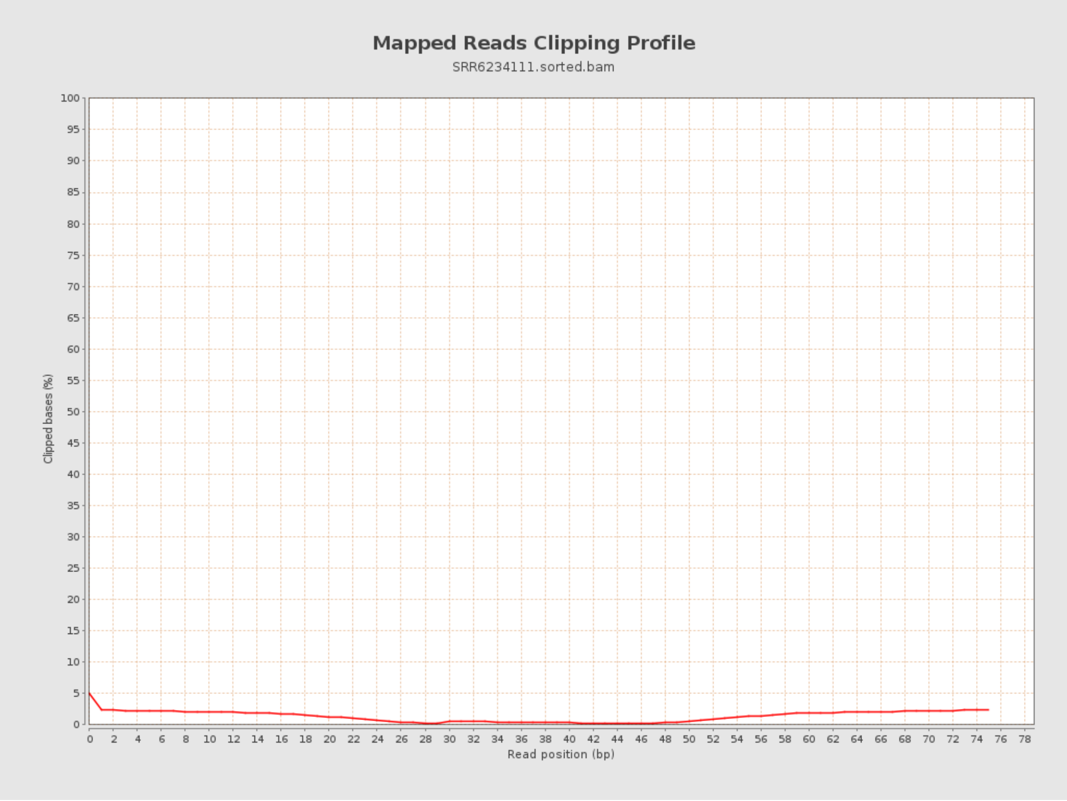
8. Results : Mapped Reads Nucleotide Content



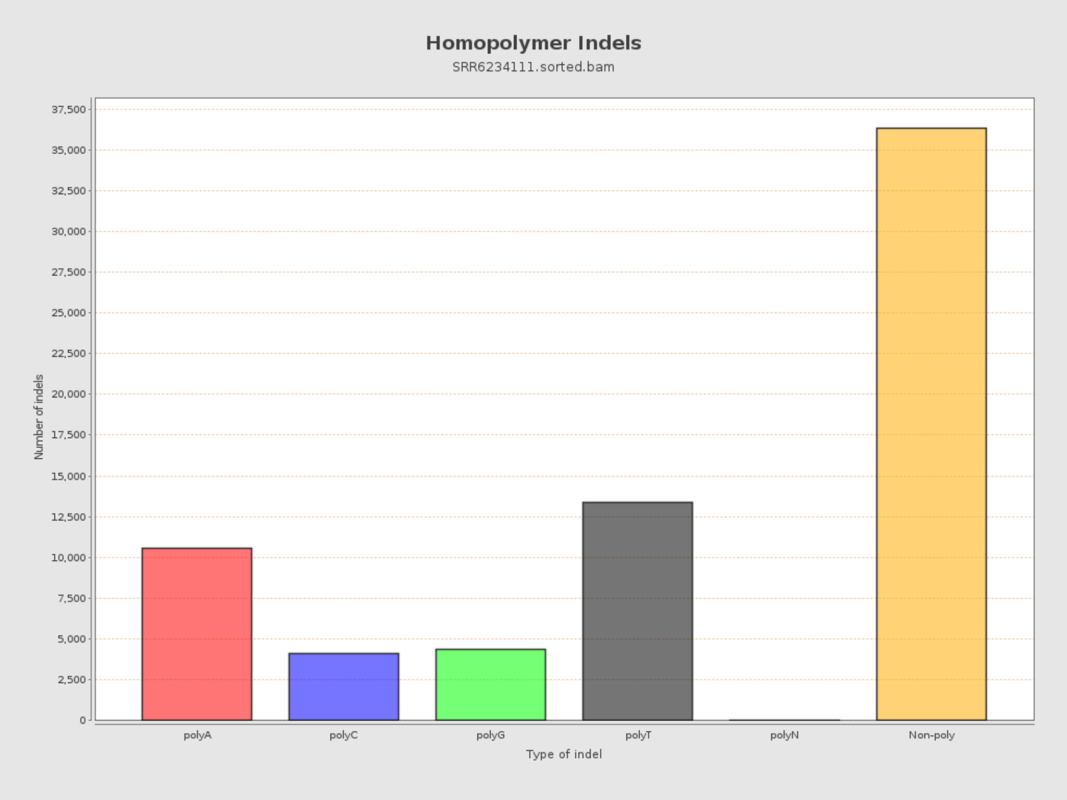
9. Results : Mapped Reads GC-content Distribution



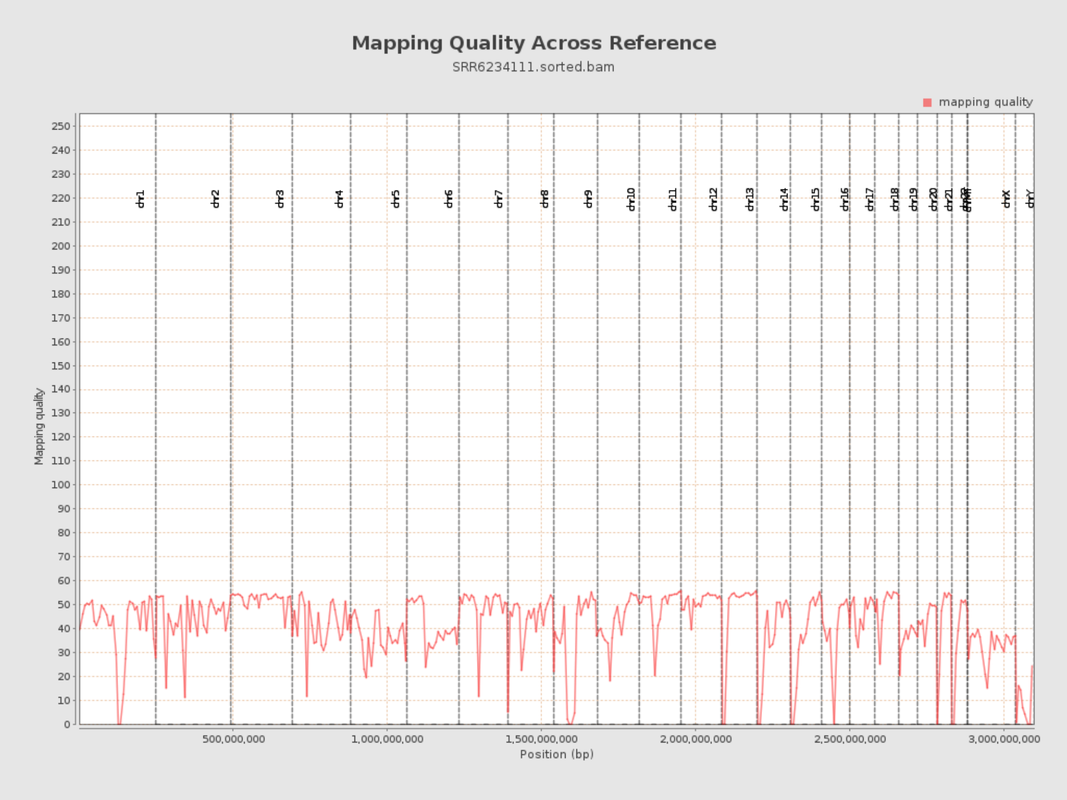
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram