Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 09:07:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231870.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_SRR6231870 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231870.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 09:07:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231870.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,319,117
Mapped reads	5,476,215 / 86.66%
Unmapped reads	842,902 / 13.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	42,893 / 0.68%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	839,634 / 13.29%
Duplication rate	12.67%
Clipped reads	2,914,581 / 46.12%

2.2. ACGT Content

Number/percentage of A's	92,042,295 / 26.08%
Number/percentage of C's	63,745,482 / 18.06%
Number/percentage of T's	114,737,815 / 32.51%
Number/percentage of G's	82,297,185 / 23.32%
Number/percentage of N's	136,294 / 0.04%
GC Percentage	41.38%

2.3. Coverage

Mean	0.1141

Standard Deviation	1.2594

2.4. Mapping Quality

Mean Mapping Quality	41.97

2.5. Mismatches and indels

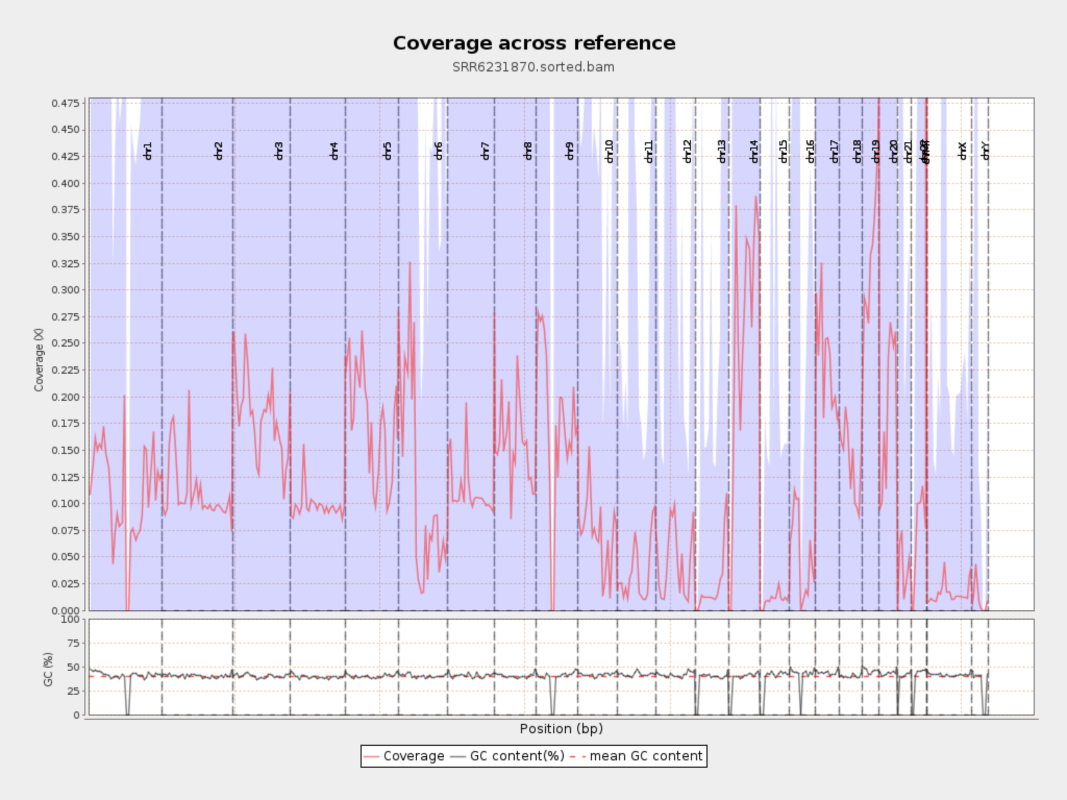
General error rate	0.64%
Mismatches	2,211,865
Insertions	24,565
Mapped reads with at least one insertion	0.44%
Deletions	76,148
Mapped reads with at least one deletion	1.38%
Homopolymer indels	45.32%

2.6. Chromosome stats

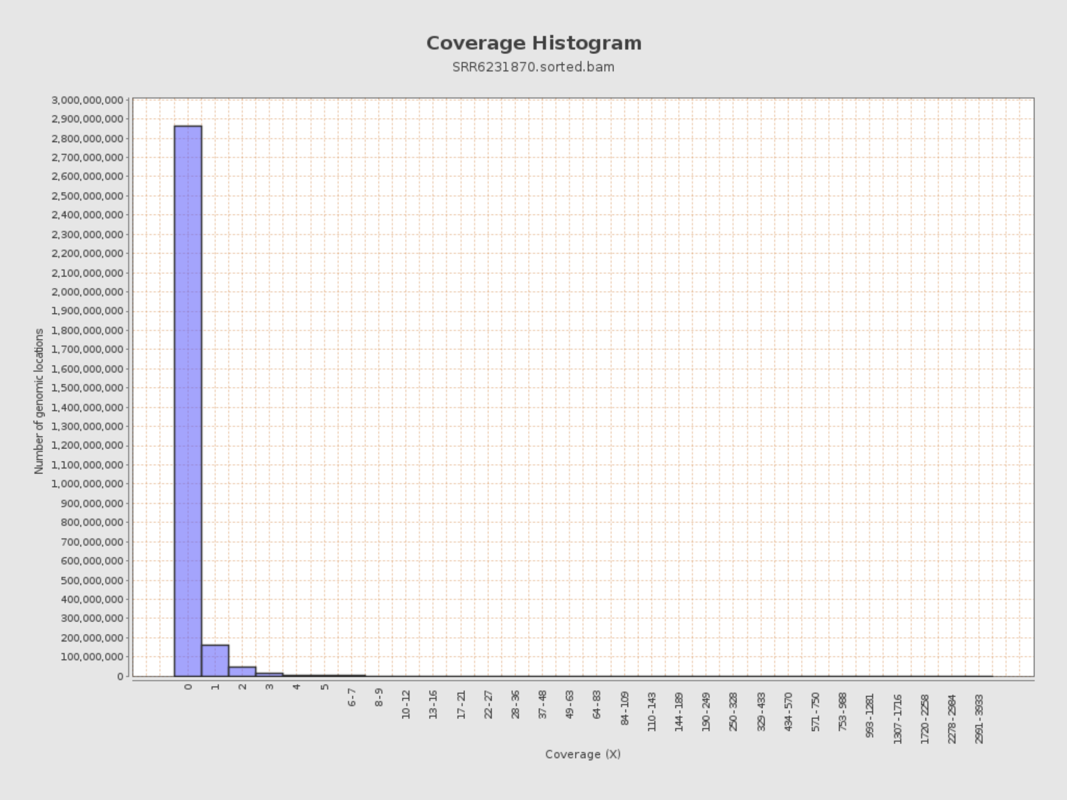
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27343523	0.1097	3.1201
chr2	243199373	27080885	0.1114	1.7896
chr3	198022430	36031880	0.182	0.5963
chr4	191154276	18712445	0.0979	0.5429
chr5	180915260	31942024	0.1766	0.6282
chr6	171115067	19914995	0.1164	0.9242
chr7	159138663	17883198	0.1124	1.0848

chr8	146364022	22641388	0.1547	1.0118
chr9	141213431	24700213	0.1749	1.0412
chr10	135534747	9800238	0.0723	0.703
chr11	135006516	4922882	0.0365	0.5752
chr12	133851895	6055439	0.0452	0.429
chr13	115169878	2981328	0.0259	0.3053
chr14	107349540	27250440	0.2538	0.7884
chr15	102531392	1061436	0.0104	0.2495
chr16	90354753	4826429	0.0534	0.4743
chr17	81195210	18929420	0.2331	0.8799
chr18	78077248	10779621	0.1381	2.0285
chr19	59128983	19570222	0.331	1.636
chr20	63025520	11869436	0.1883	0.6325
chr21	48129895	1900020	0.0395	0.3954
chr22	51304566	3692215	0.072	0.3628
chrMT	16571	95427	5.7587	4.2589
chrX	155270560	2481167	0.016	0.3957
chrY	59373566	627532	0.0106	0.356

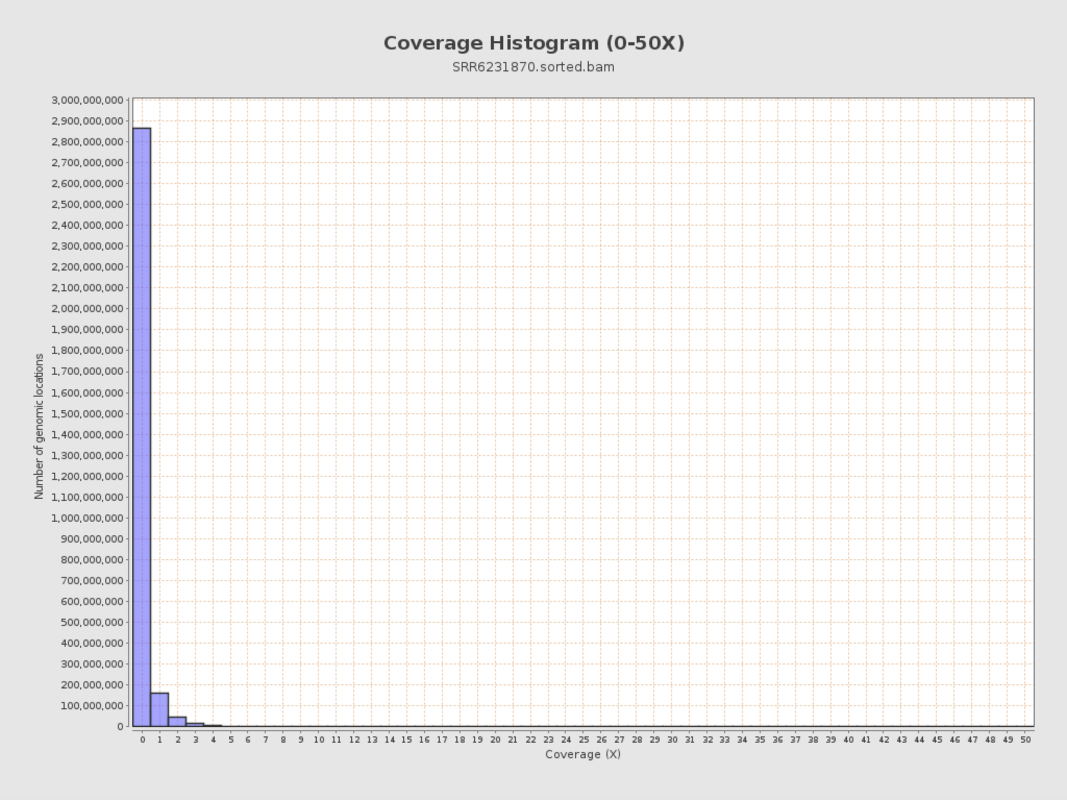
3. Results : Coverage across reference



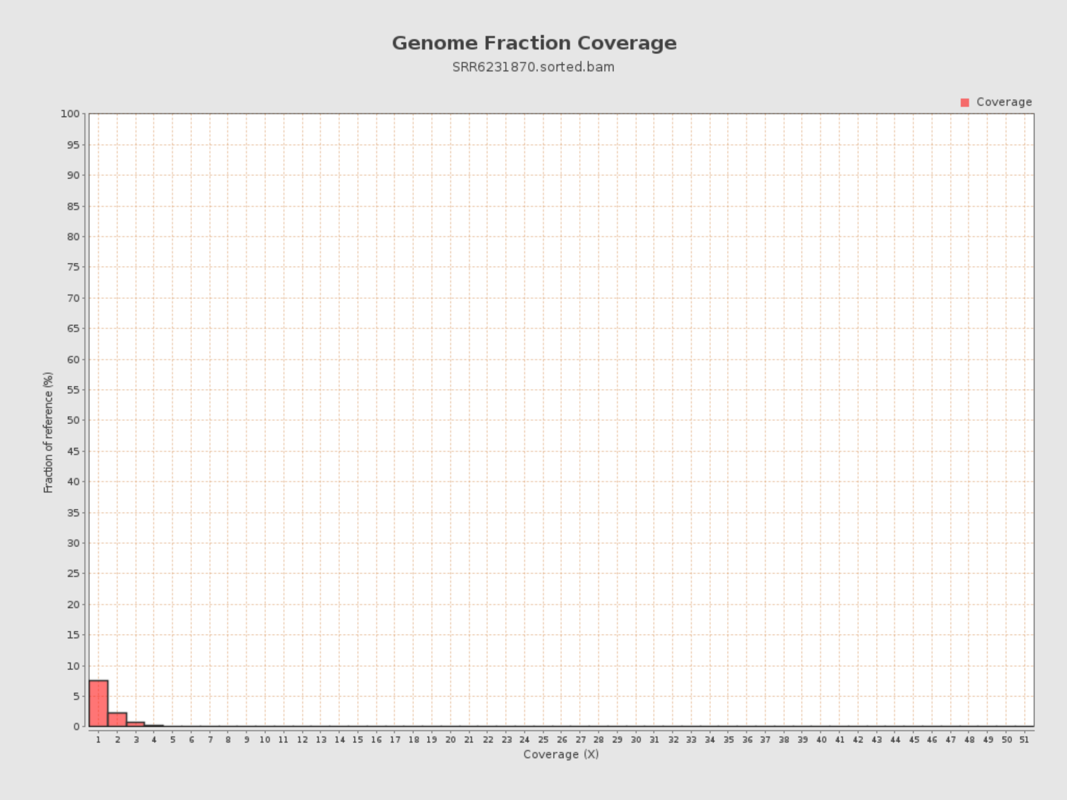
4. Results : Coverage Histogram



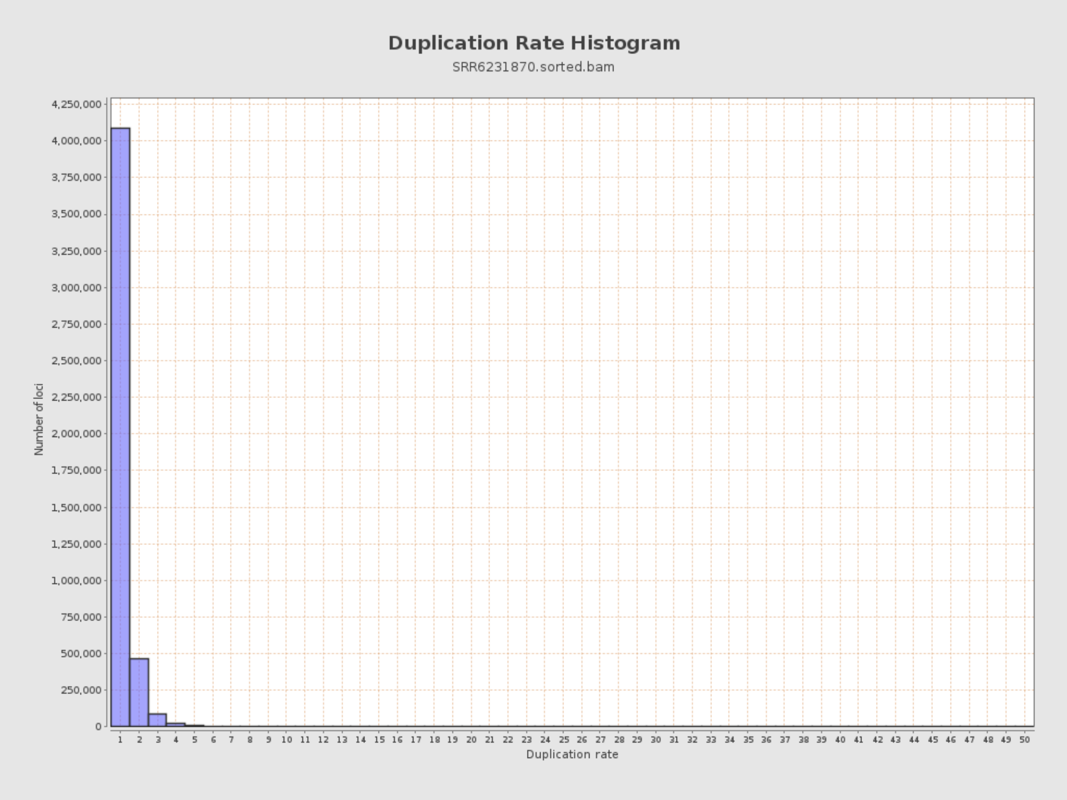
5. Results : Coverage Histogram (0-50X)



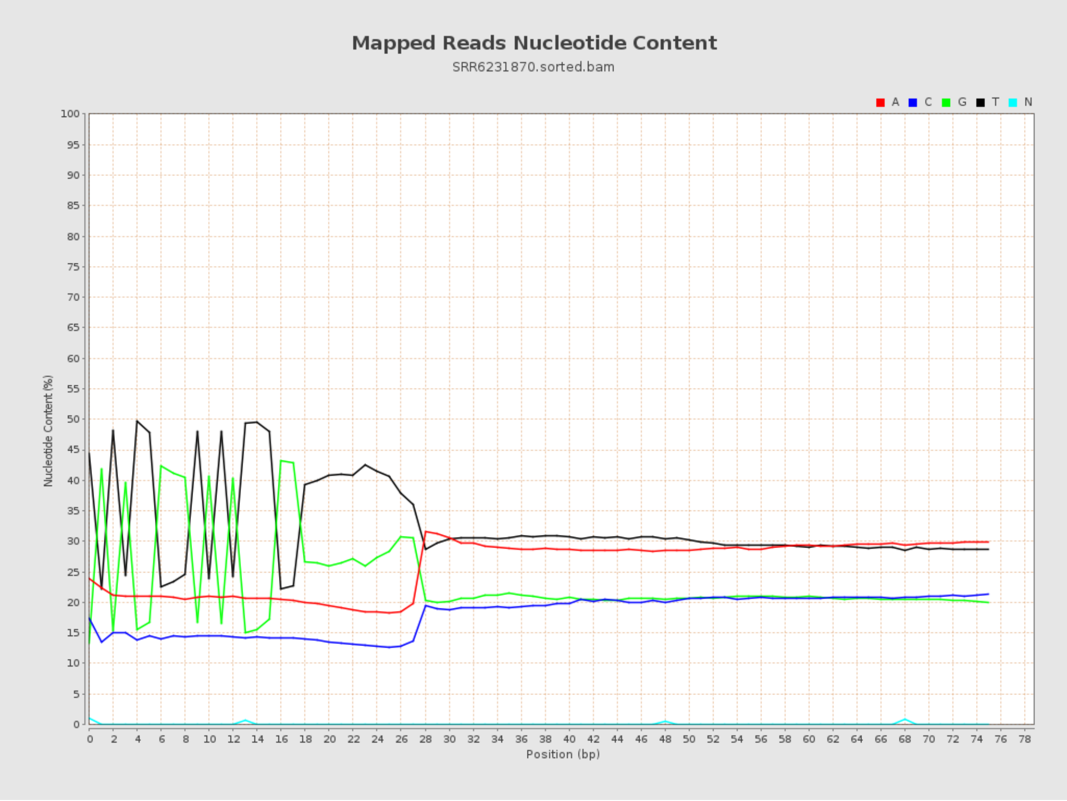
6. Results : Genome Fraction Coverage



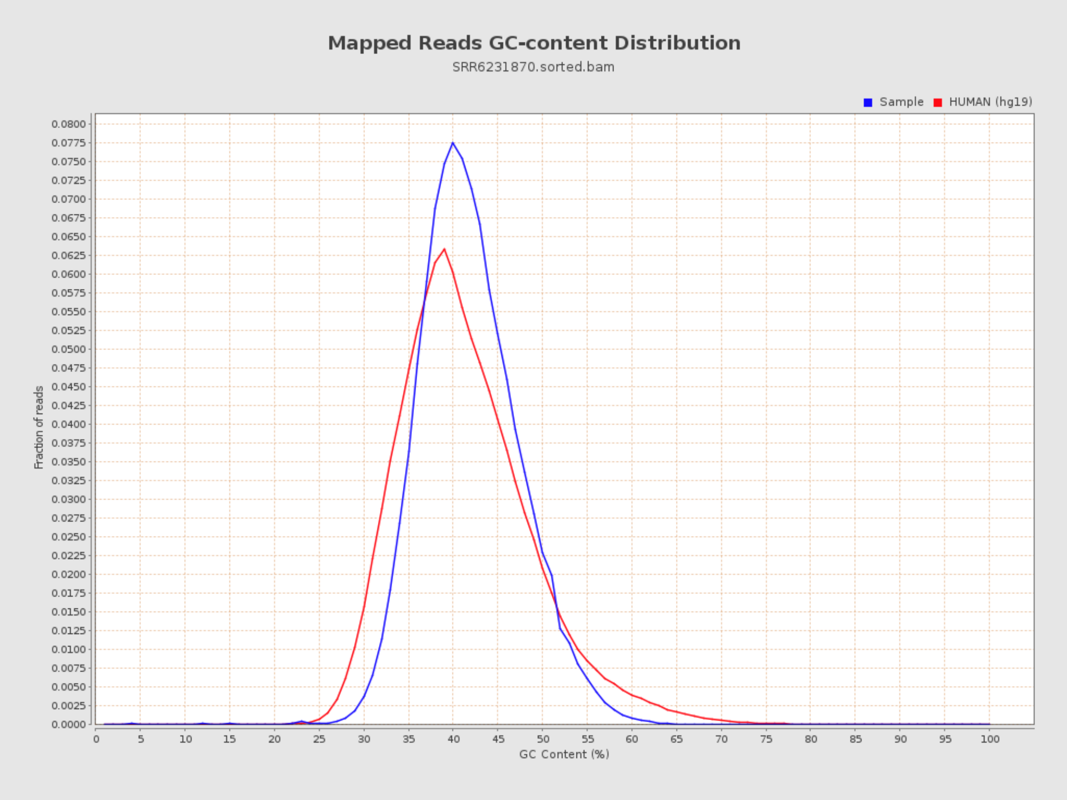
7. Results : Duplication Rate Histogram



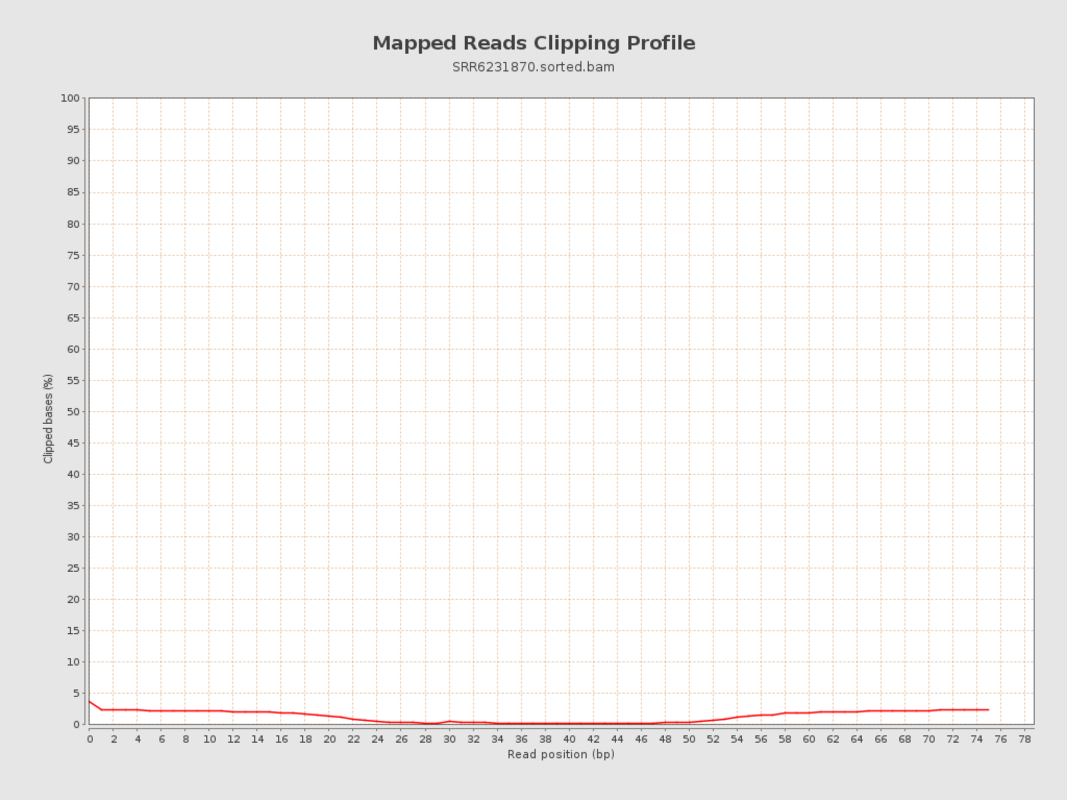
8. Results : Mapped Reads Nucleotide Content



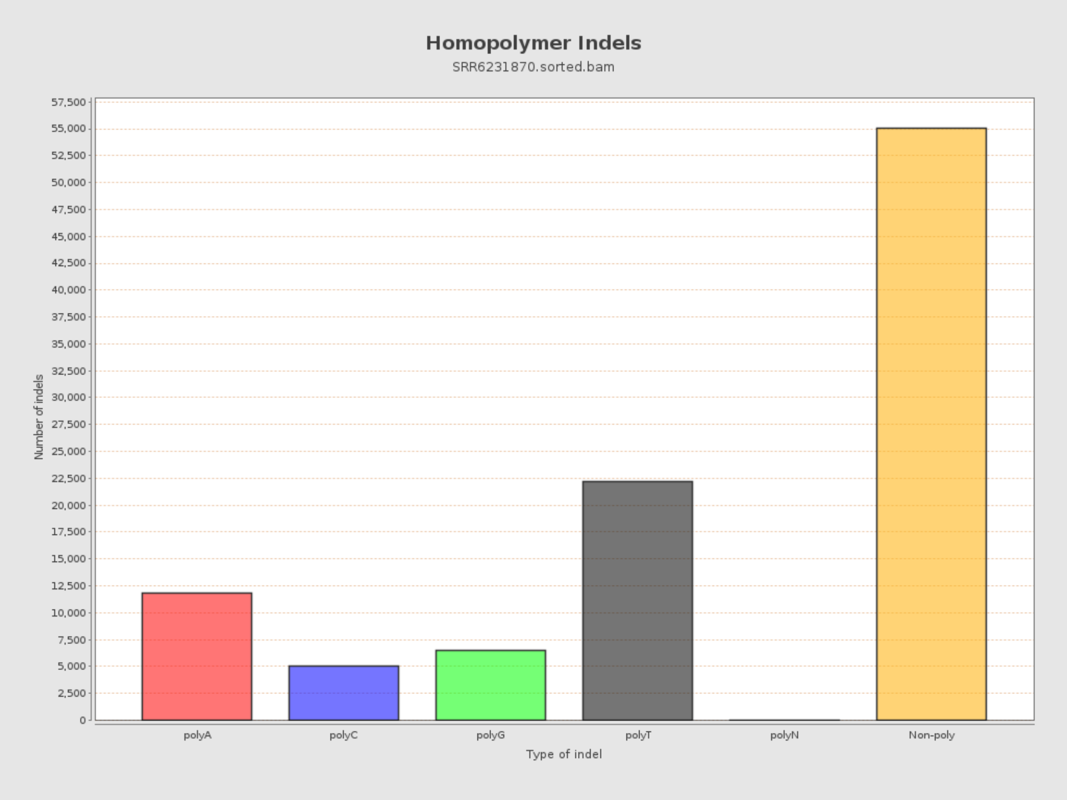
9. Results : Mapped Reads GC-content Distribution



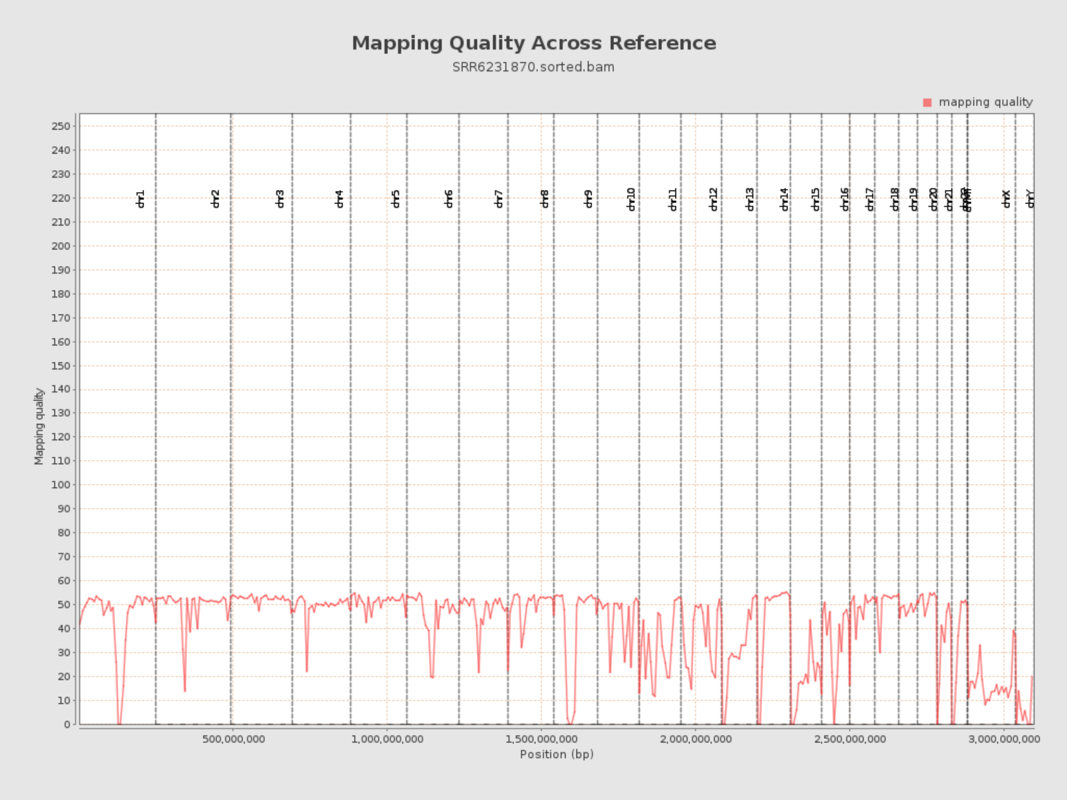
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram