Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 08:20:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231856.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_SRR6231856 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231856.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 08:20:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231856.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,409,648
Mapped reads	954,647 / 67.72%
Unmapped reads	455,001 / 32.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,639 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	31,420 / 2.23%
Duplication rate	2.65%
Clipped reads	467,838 / 33.19%

2.2. ACGT Content

Number/percentage of A's	17,044,776 / 27.43%
Number/percentage of C's	11,301,567 / 18.19%
Number/percentage of T's	19,678,768 / 31.67%
Number/percentage of G's	14,102,350 / 22.7%
Number/percentage of N's	3,089 / 0%
GC Percentage	40.89%

2.3. Coverage

Mean	0.0201

Standard Deviation	0.2149

2.4. Mapping Quality

Mean Mapping Quality	45.32

2.5. Mismatches and indels

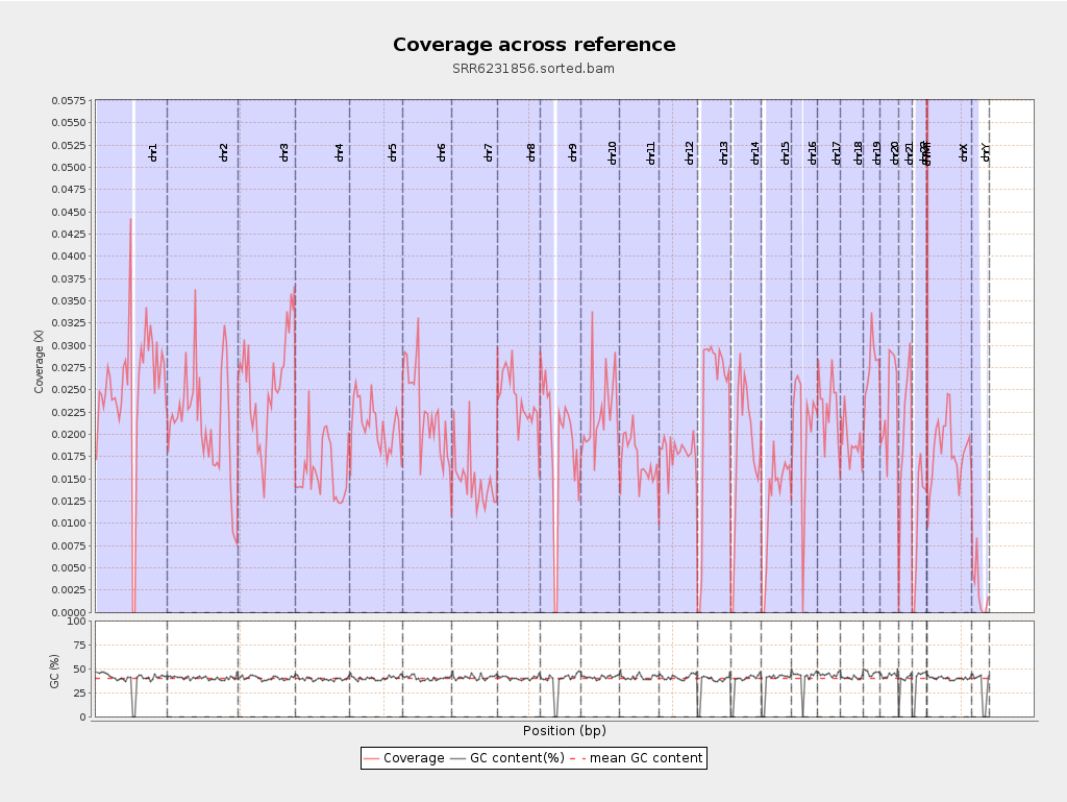
General error rate	0.78%
Mismatches	478,287
Insertions	4,779
Mapped reads with at least one insertion	0.49%
Deletions	19,263
Mapped reads with at least one deletion	2%
Homopolymer indels	45%

2.6. Chromosome stats

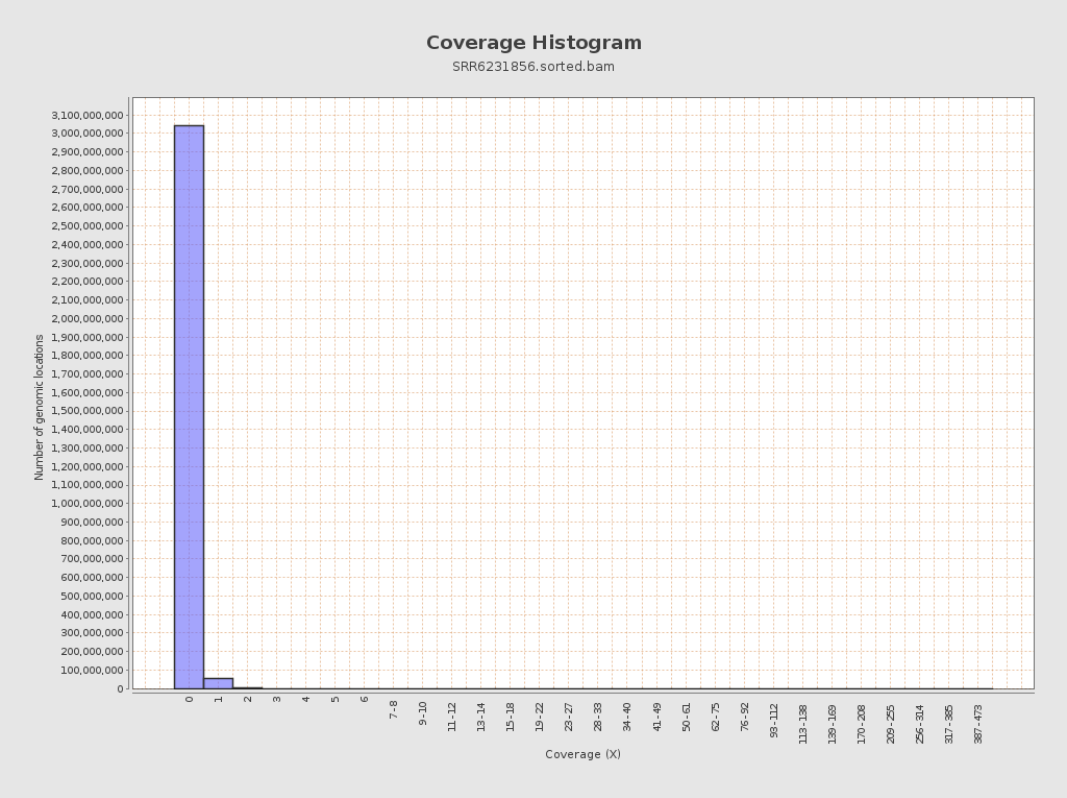
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6253298	0.0251	0.4214
chr2	243199373	5149042	0.0212	0.258
chr3	198022430	5038241	0.0254	0.1717
chr4	191154276	3044789	0.0159	0.142
chr5	180915260	3824638	0.0211	0.1569
chr6	171115067	3841704	0.0225	0.1845
chr7	159138663	2354074	0.0148	0.1817

chr8	146364022	3475900	0.0237	0.2442
chr9	141213431	2684097	0.019	0.1802
chr10	135534747	3009925	0.0222	0.2104
chr11	135006516	2320306	0.0172	0.1656
chr12	133851895	2415833	0.018	0.1453
chr13	115169878	2699997	0.0234	0.1647
chr14	107349540	1940972	0.0181	0.1497
chr15	102531392	1284414	0.0125	0.1212
chr16	90354753	1820502	0.0201	0.165
chr17	81195210	1873036	0.0231	0.1687
chr18	78077248	1490794	0.0191	0.2997
chr19	59128983	1633268	0.0276	0.2895
chr20	63025520	1481634	0.0235	0.1682
chr21	48129895	995559	0.0207	0.1613
chr22	51304566	548322	0.0107	0.111
chrMT	16571	13783	0.8318	1.0296
chrX	155270560	2826963	0.0182	0.1546
chrY	59373566	143418	0.0024	0.0685

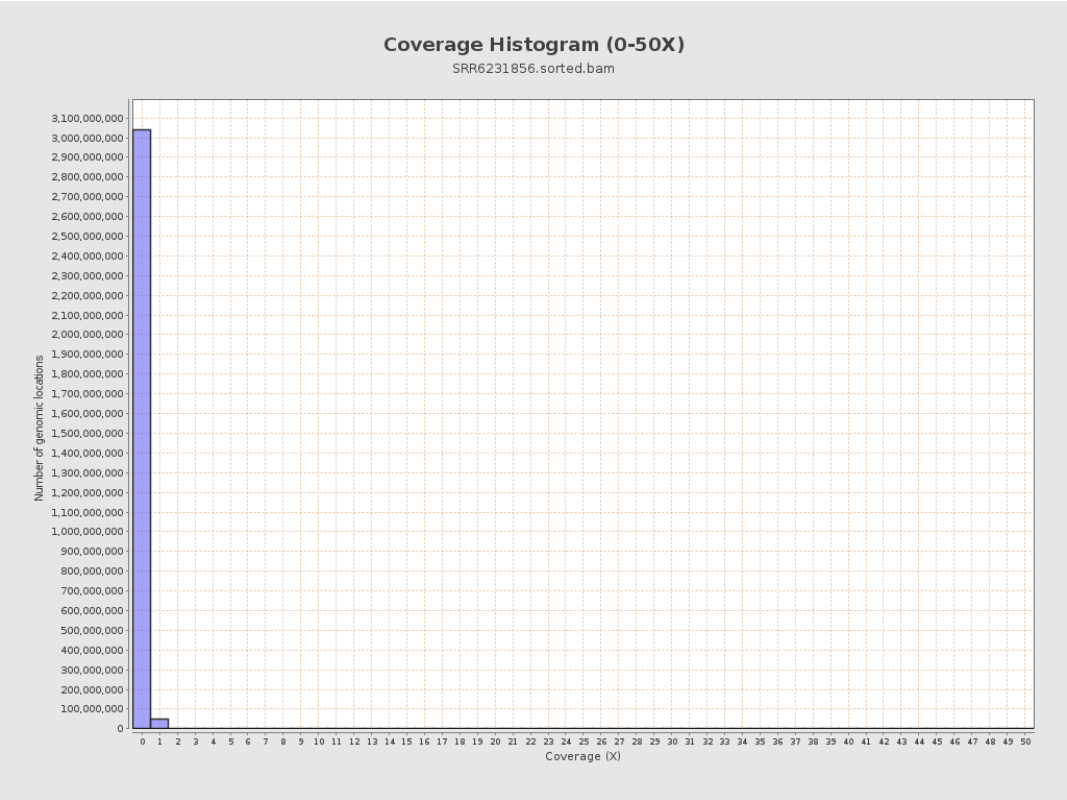
3. Results : Coverage across reference



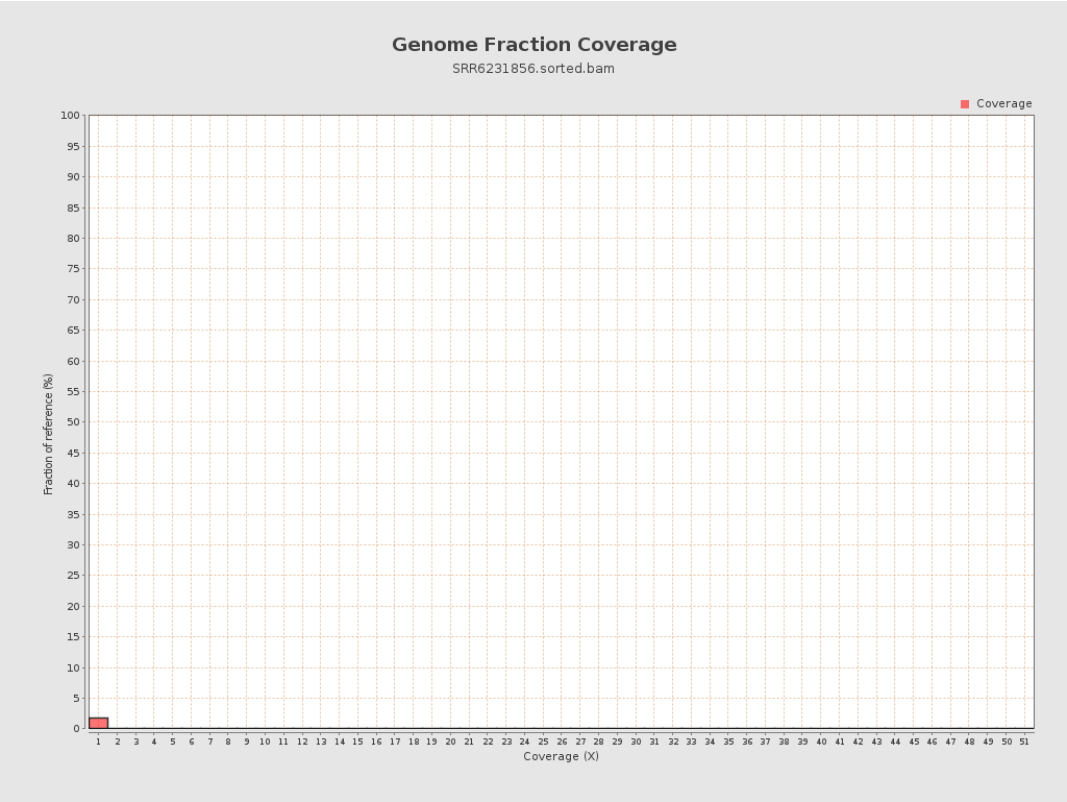
4. Results : Coverage Histogram



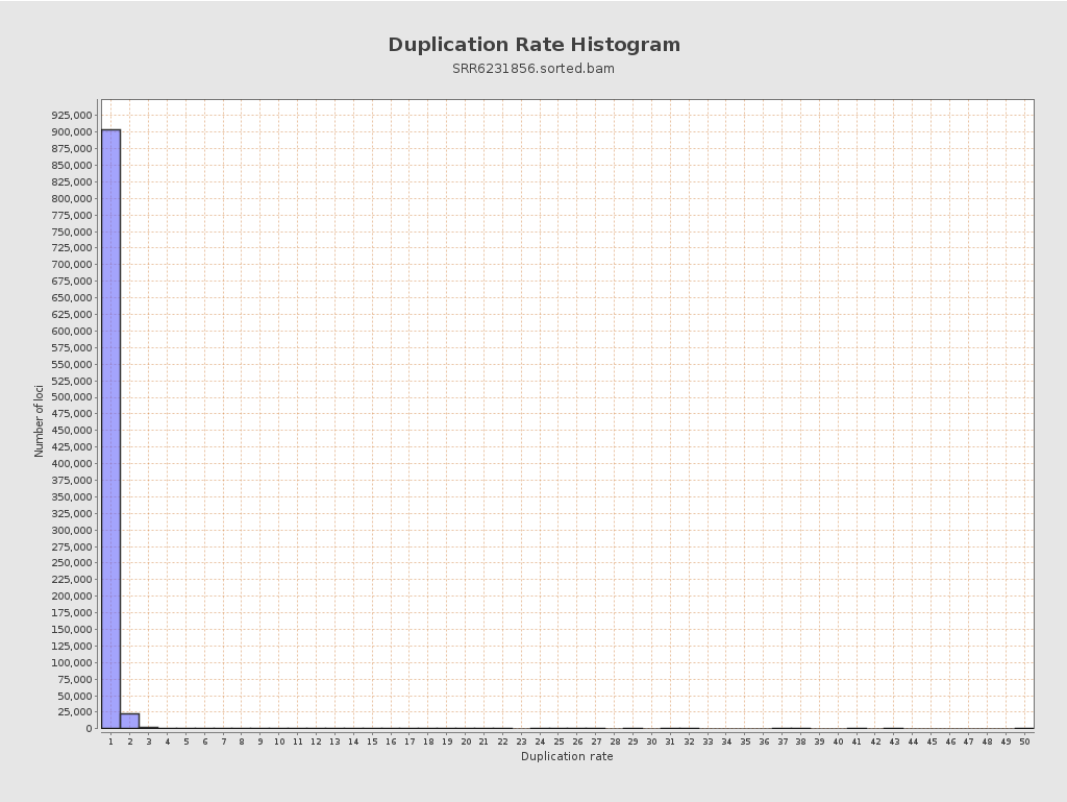
5. Results : Coverage Histogram (0-50X)



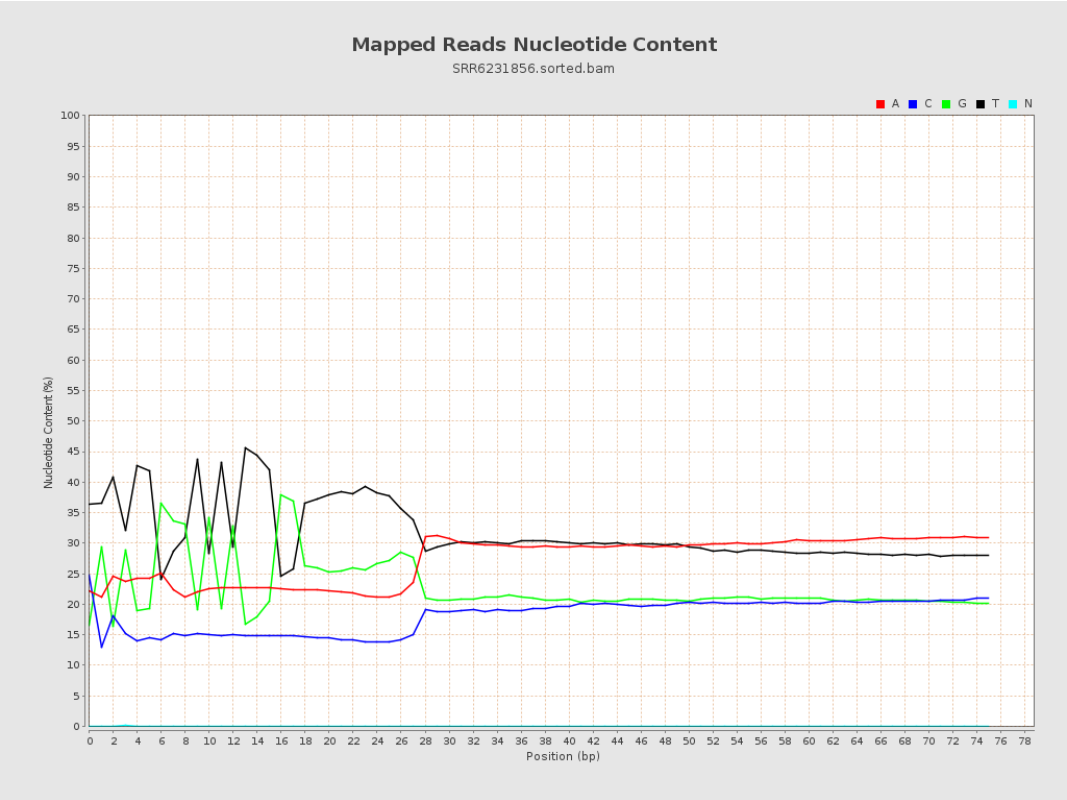
6. Results : Genome Fraction Coverage



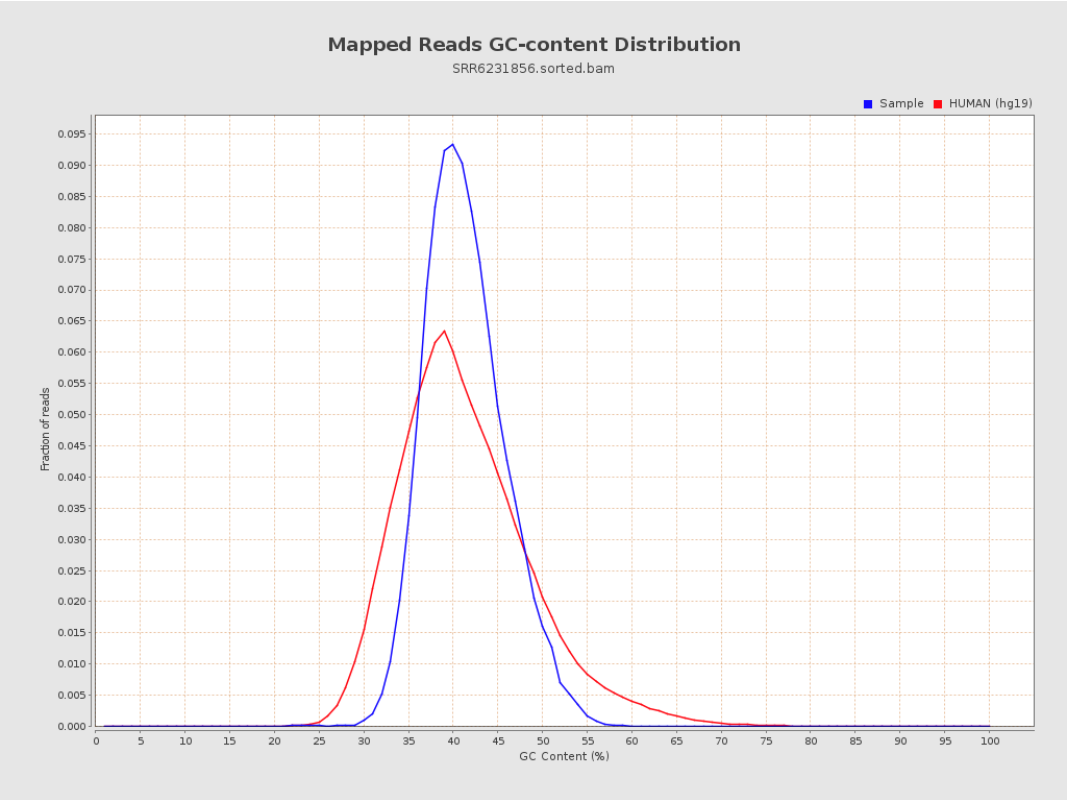
7. Results : Duplication Rate Histogram



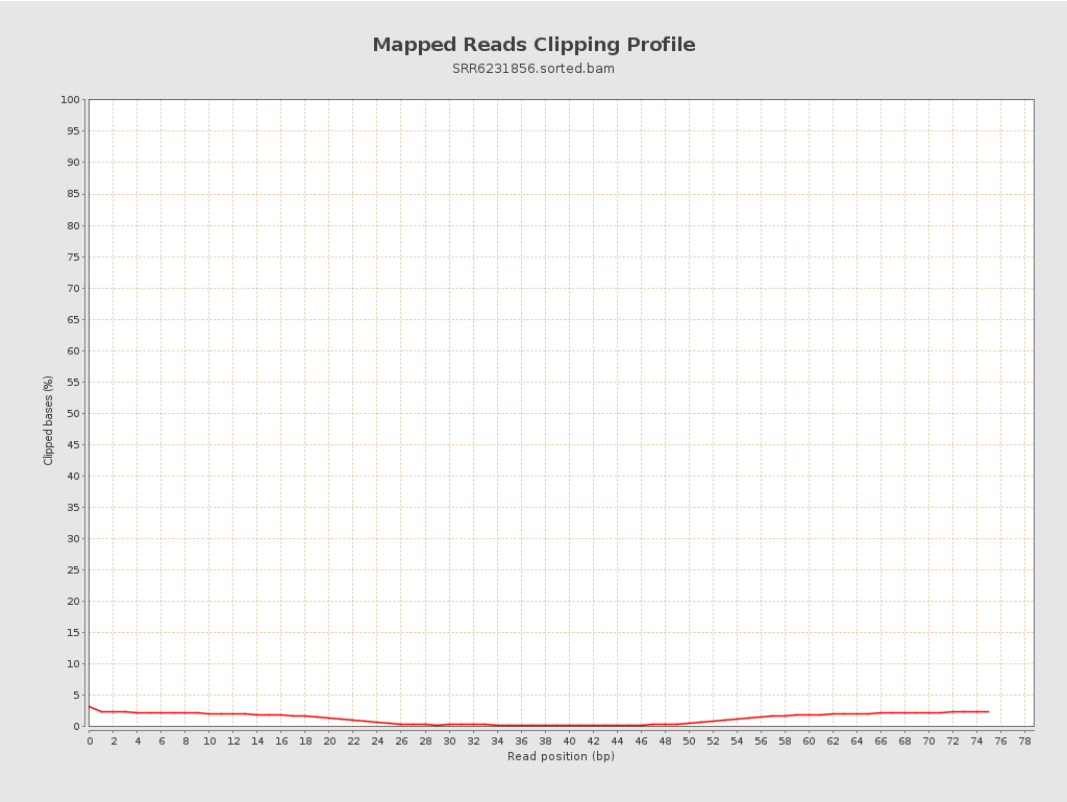
8. Results : Mapped Reads Nucleotide Content



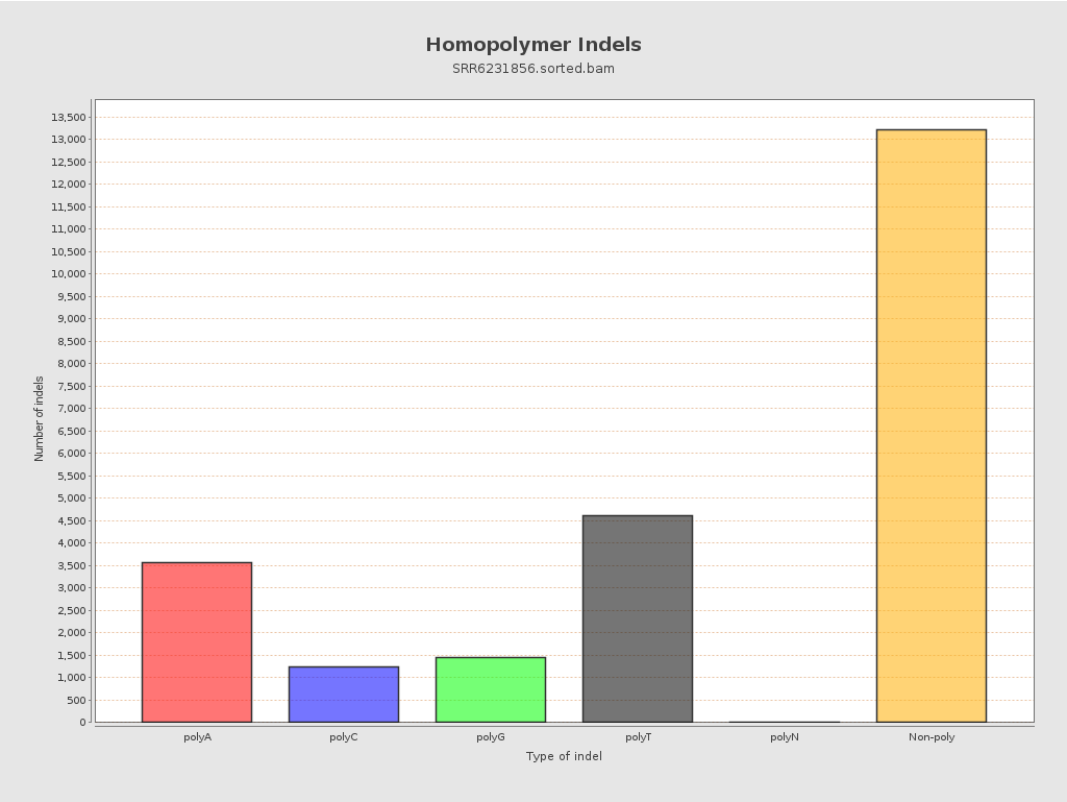
9. Results : Mapped Reads GC-content Distribution



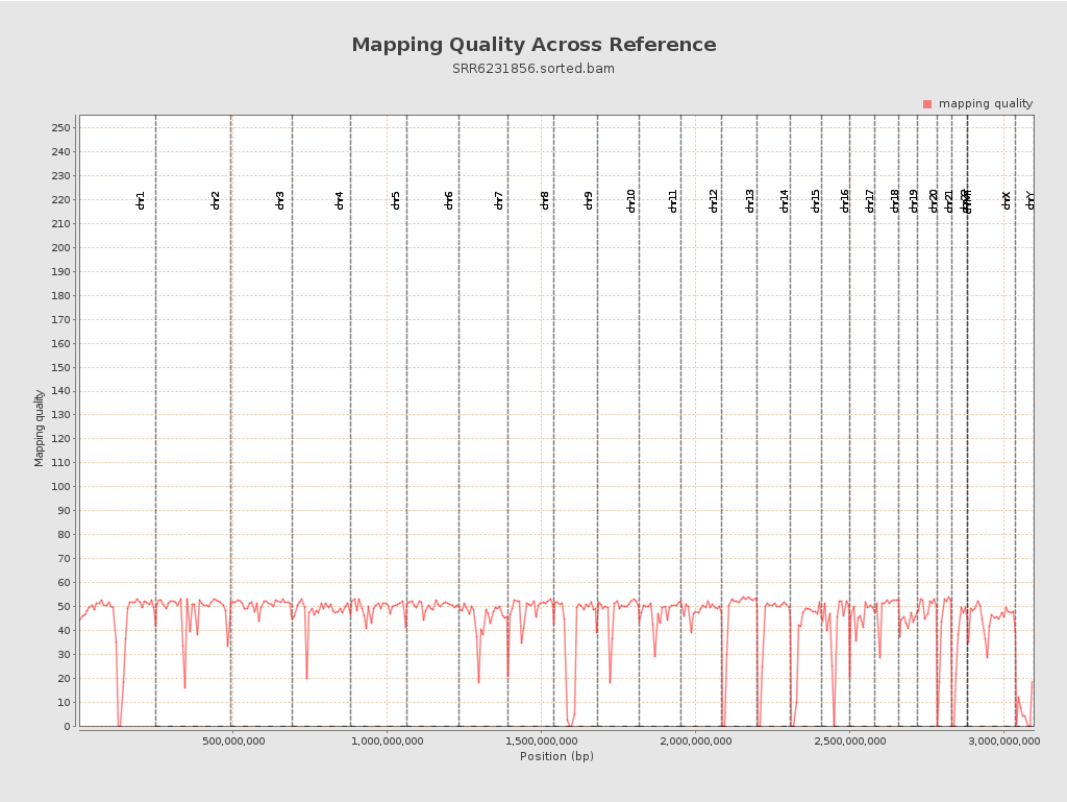
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram