Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 06:30:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231836.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_SRR6231836 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231836.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 06:30:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231836.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,464,576
Mapped reads	5,082,685 / 93.01%
Unmapped reads	381,891 / 6.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,847 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	530,790 / 9.71%
Duplication rate	8.08%
Clipped reads	2,791,603 / 51.09%

2.2. ACGT Content

Number/percentage of A's	85,307,720 / 26.32%
Number/percentage of C's	57,234,597 / 17.66%
Number/percentage of T's	105,411,578 / 32.52%
Number/percentage of G's	76,032,400 / 23.46%
Number/percentage of N's	121,967 / 0.04%
GC Percentage	41.12%

2.3. Coverage

Mean	0.1047

Standard Deviation	1.357

2.4. Mapping Quality

Mean Mapping Quality	44.68

2.5. Mismatches and indels

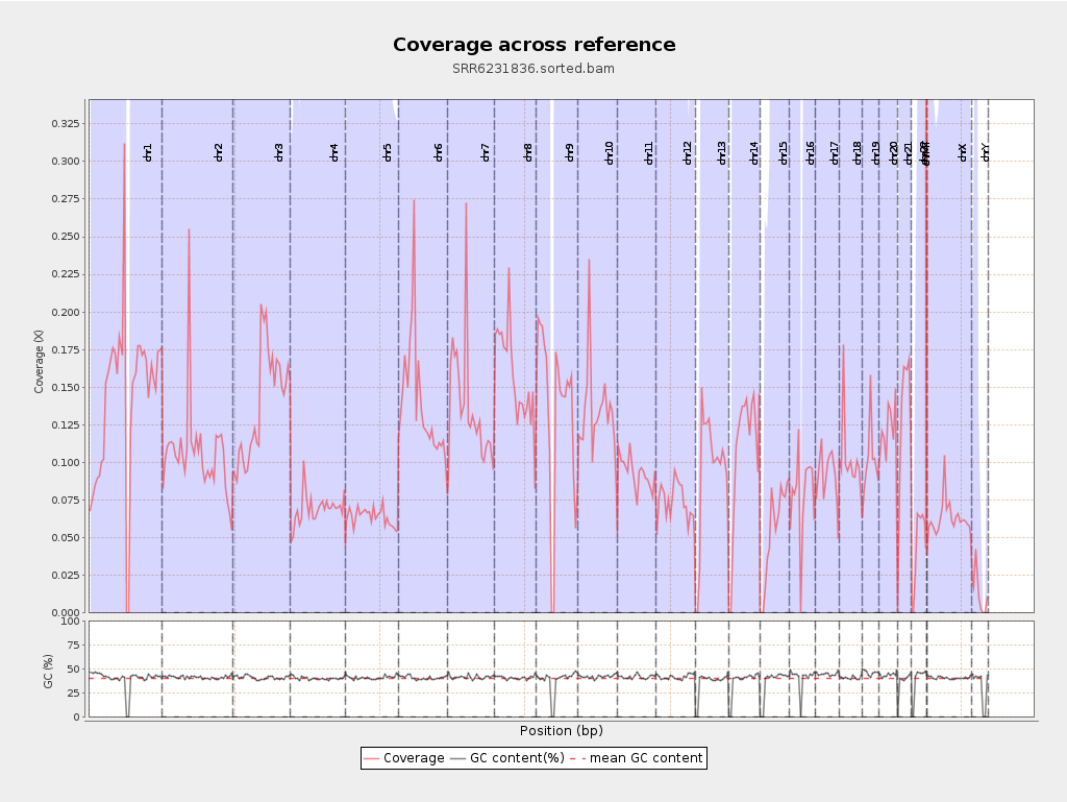
General error rate	0.63%
Mismatches	1,995,515
Insertions	19,692
Mapped reads with at least one insertion	0.38%
Deletions	61,852
Mapped reads with at least one deletion	1.21%
Homopolymer indels	44.83%

2.6. Chromosome stats

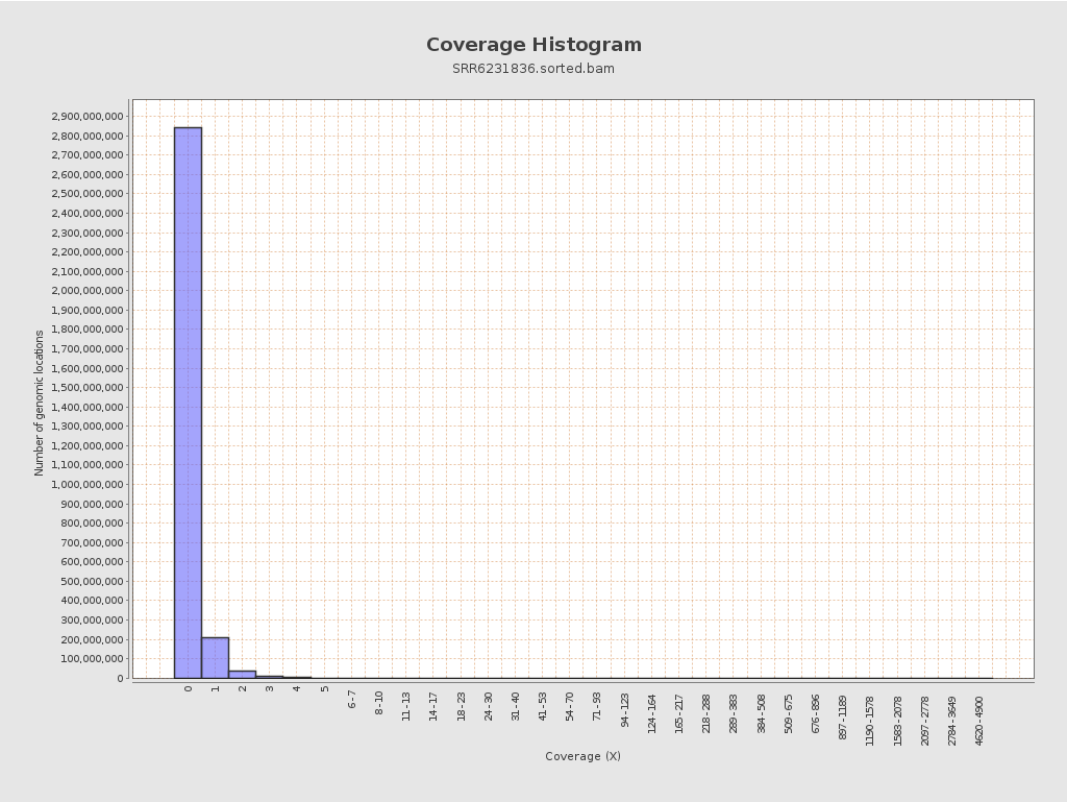
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	35370592	0.1419	3.3553
chr2	243199373	25758065	0.1059	1.2505
chr3	198022430	27305851	0.1379	0.468
chr4	191154276	13128483	0.0687	0.3798
chr5	180915260	11501078	0.0636	0.3605
chr6	171115067	23695218	0.1385	0.9482
chr7	159138663	21908143	0.1377	1.9759

chr8	146364022	22968195	0.1569	1.2825
chr9	141213431	18942629	0.1341	1.1493
chr10	135534747	18094876	0.1335	1.1496
chr11	135006516	12452880	0.0922	0.7023
chr12	133851895	9794696	0.0732	0.4345
chr13	115169878	10770103	0.0935	0.3732
chr14	107349540	11334020	0.1056	0.5497
chr15	102531392	5631220	0.0549	0.3368
chr16	90354753	7090590	0.0785	0.6268
chr17	81195210	7316075	0.0901	0.5061
chr18	78077248	8035272	0.1029	2.4985
chr19	59128983	6063337	0.1025	1.8607
chr20	63025520	7577669	0.1202	0.5996
chr21	48129895	6087294	0.1265	0.5146
chr22	51304566	2251995	0.0439	0.2448
chrMT	16571	738601	44.5719	26.1386
chrX	155270560	9684461	0.0624	0.5545
chrY	59373566	716767	0.0121	0.2565

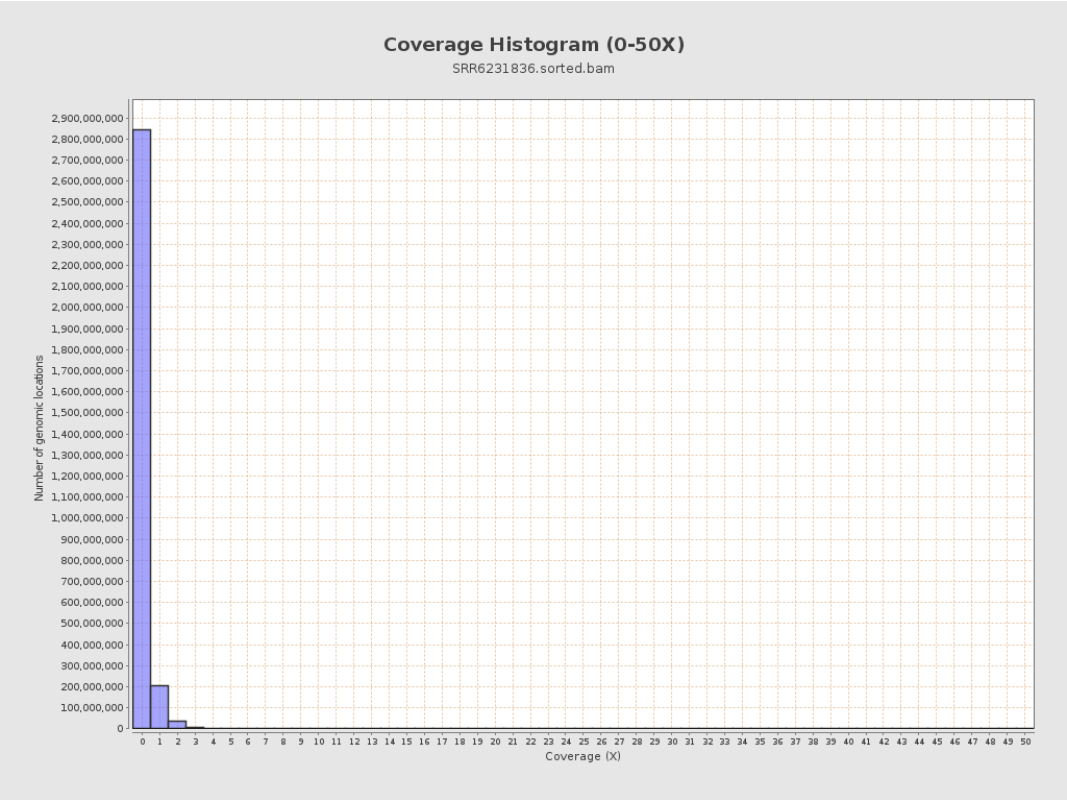
3. Results : Coverage across reference



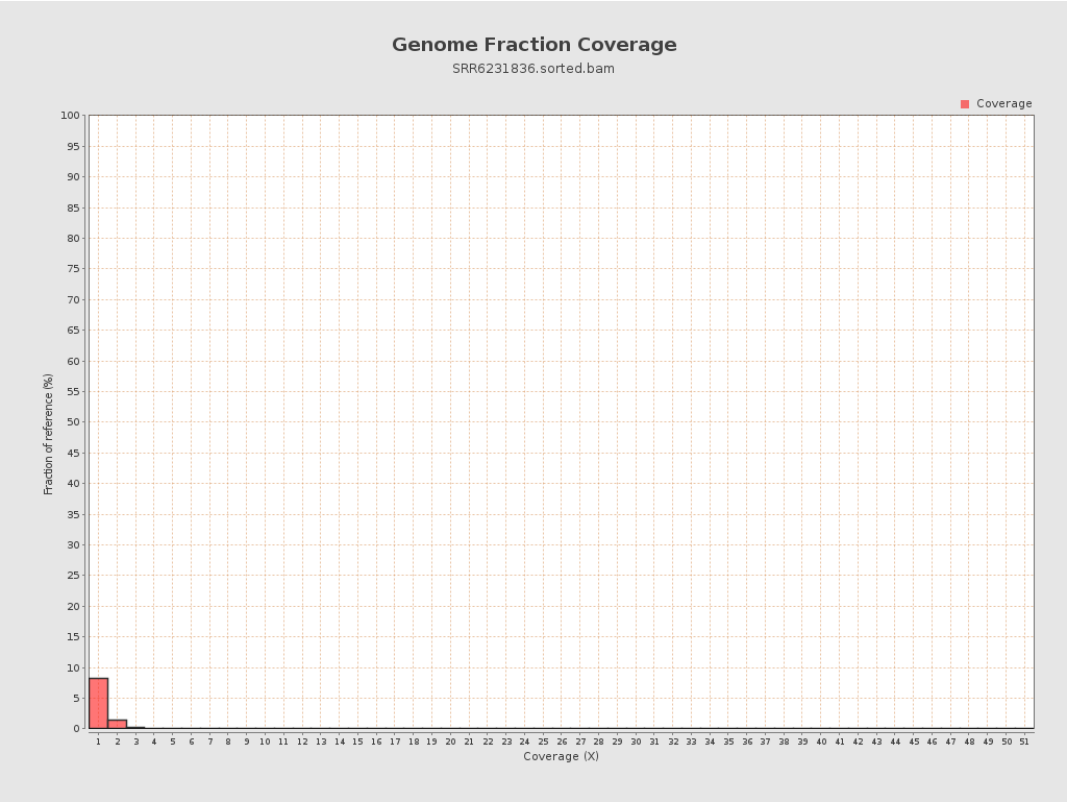
4. Results : Coverage Histogram



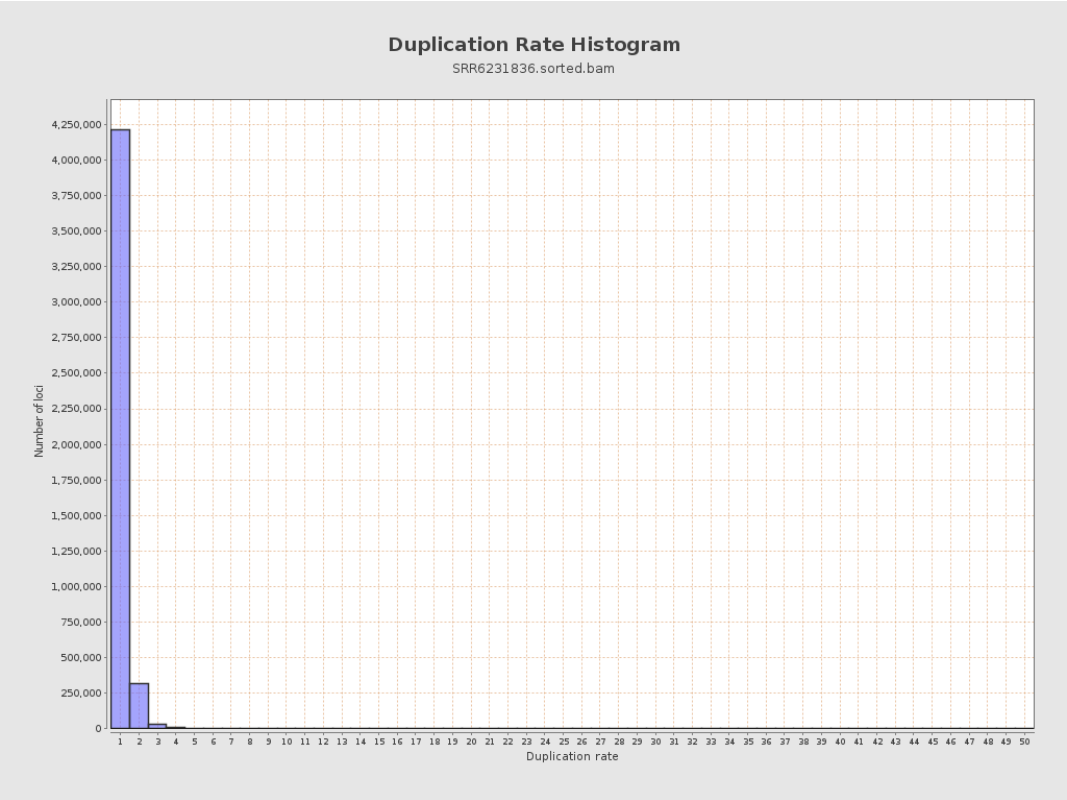
5. Results : Coverage Histogram (0-50X)



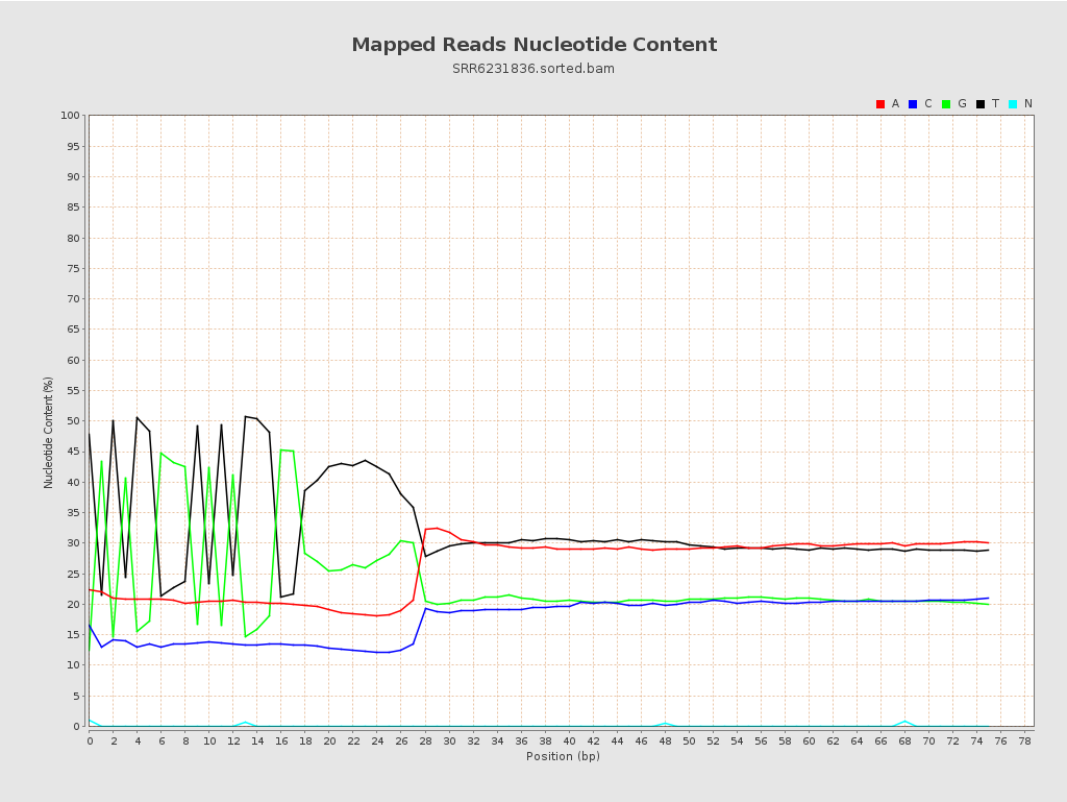
6. Results : Genome Fraction Coverage



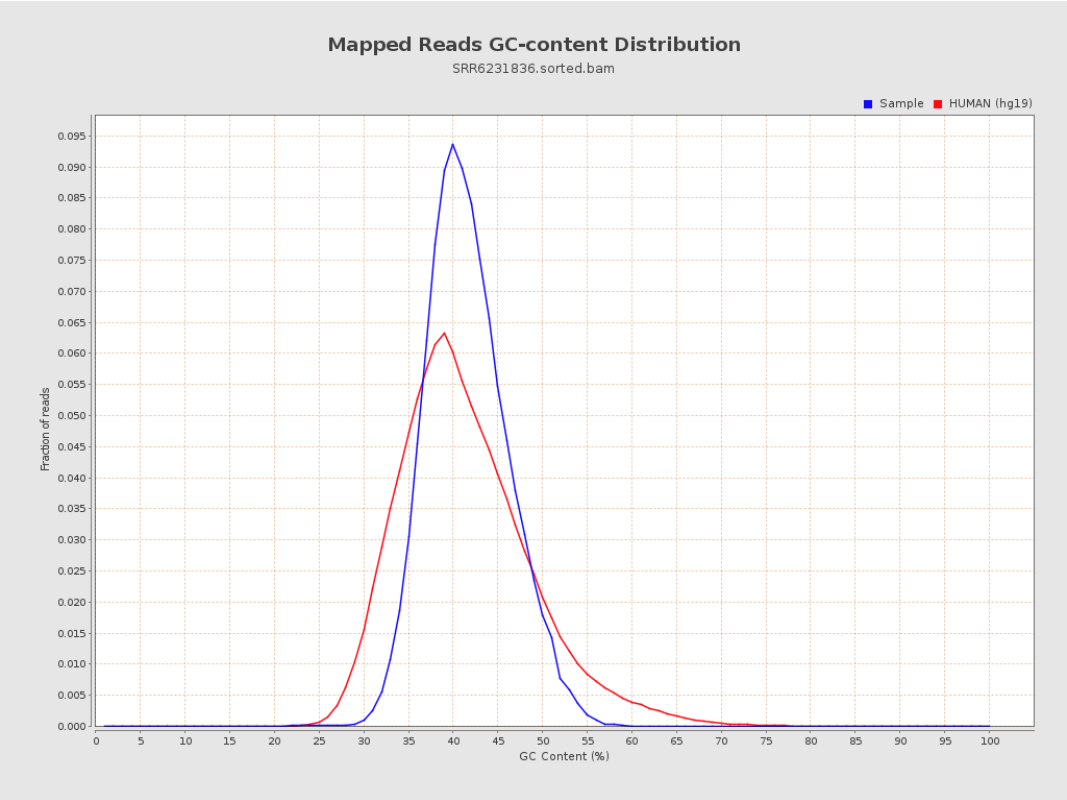
7. Results : Duplication Rate Histogram



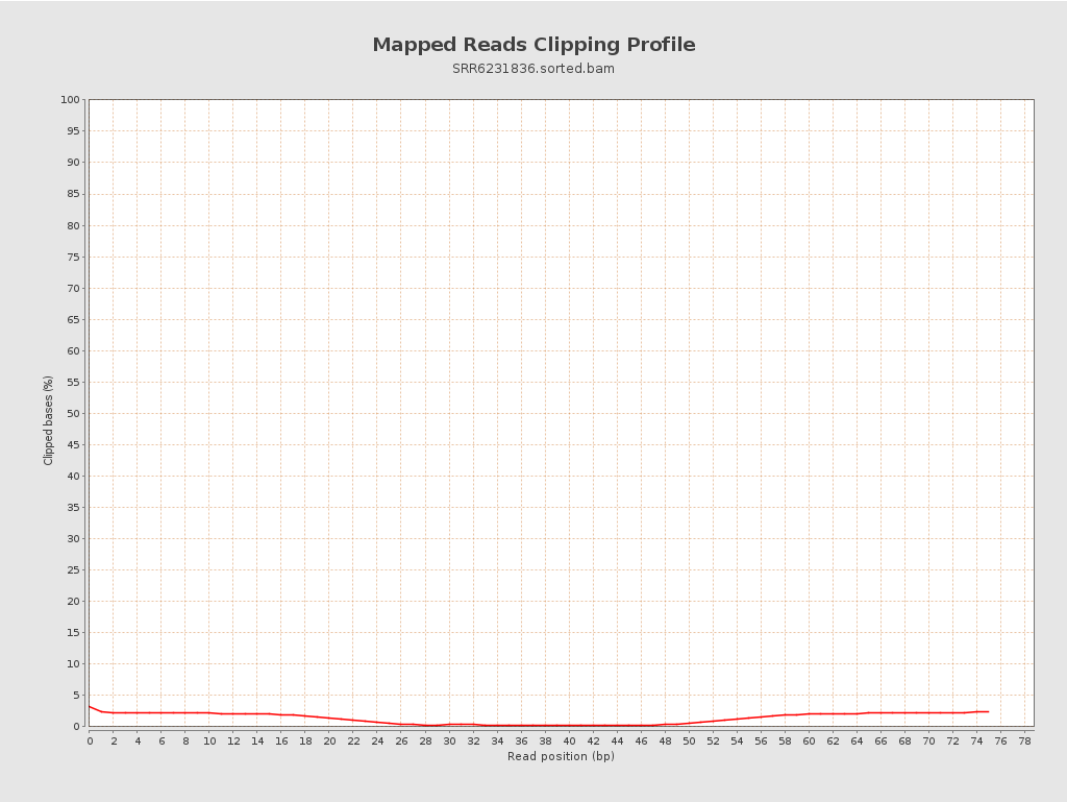
8. Results : Mapped Reads Nucleotide Content



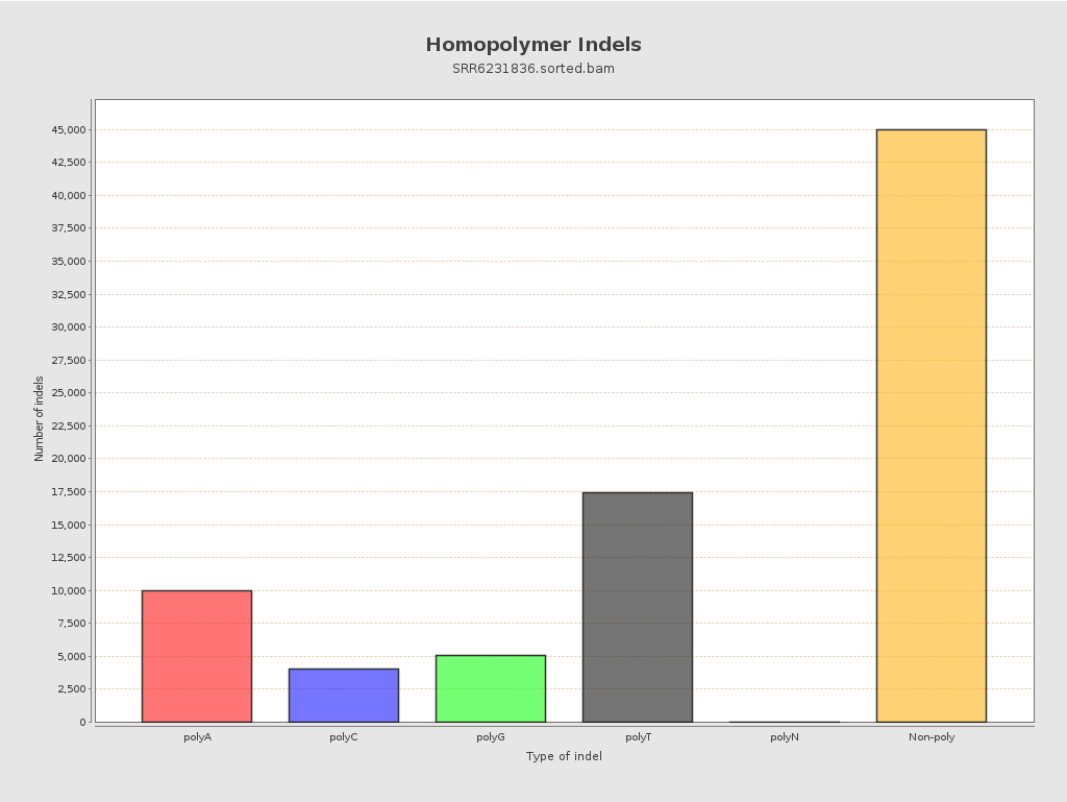
9. Results : Mapped Reads GC-content Distribution



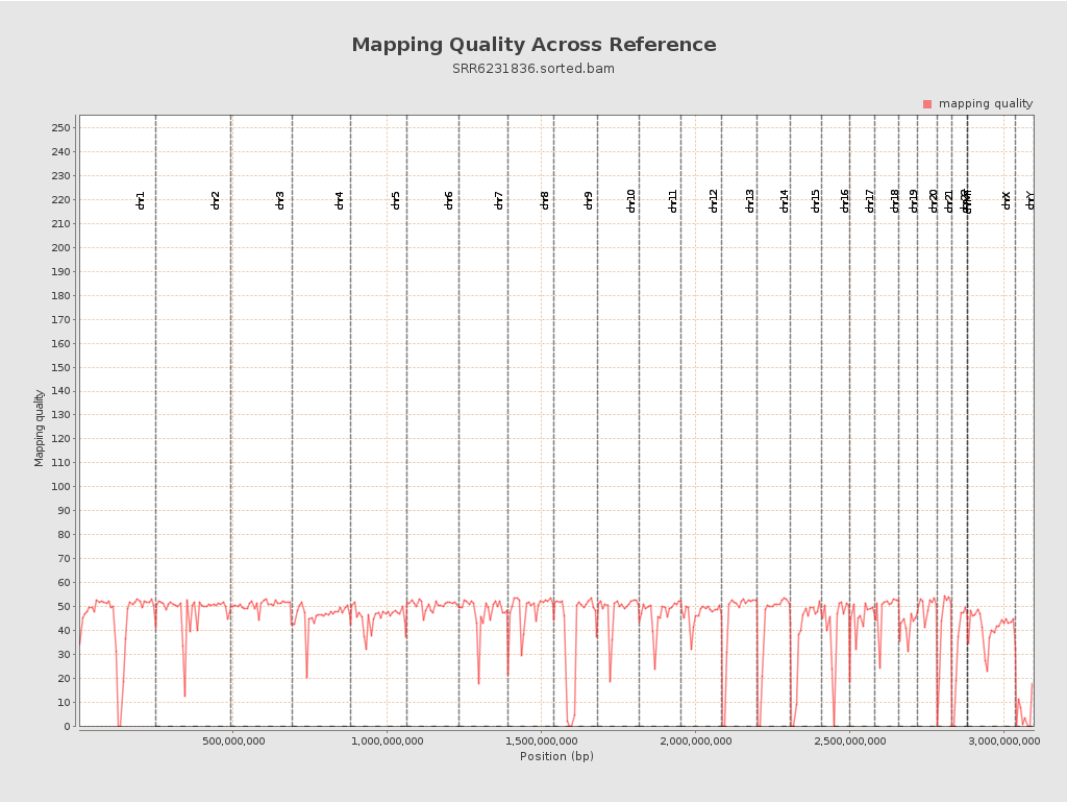
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram