Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 08:39:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231864.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_SRR6231864 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231864.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 08:39:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231864.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,270,516
Mapped reads	925,457 / 72.84%
Unmapped reads	345,059 / 27.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,399 / 0.42%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	55,906 / 4.4%
Duplication rate	5.27%
Clipped reads	535,013 / 42.11%

2.2. ACGT Content

Number/percentage of A's	15,839,982 / 27%
Number/percentage of C's	9,831,017 / 16.76%
Number/percentage of T's	19,630,853 / 33.46%
Number/percentage of G's	13,356,967 / 22.77%
Number/percentage of N's	2,618 / 0%
GC Percentage	39.53%

2.3. Coverage

Mean	0.019

Standard Deviation	0.194

2.4. Mapping Quality

Mean Mapping Quality	46.25

2.5. Mismatches and indels

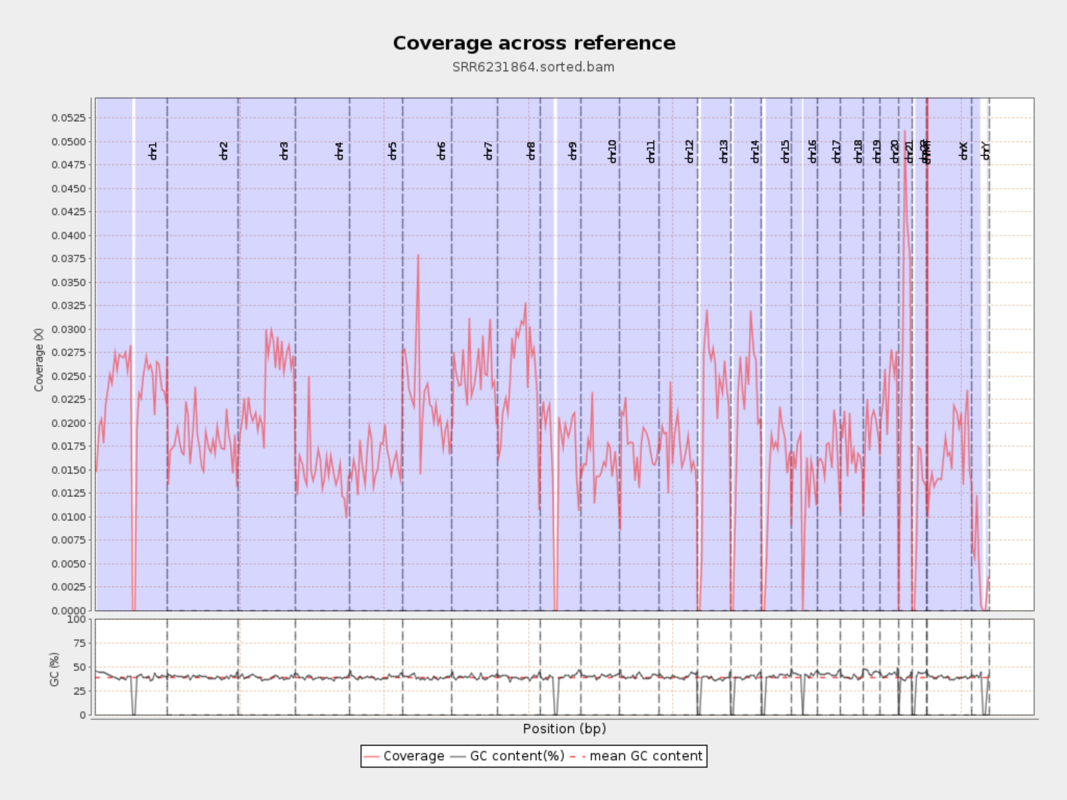
General error rate	0.78%
Mismatches	446,812
Insertions	4,822
Mapped reads with at least one insertion	0.52%
Deletions	18,062
Mapped reads with at least one deletion	1.93%
Homopolymer indels	46.62%

2.6. Chromosome stats

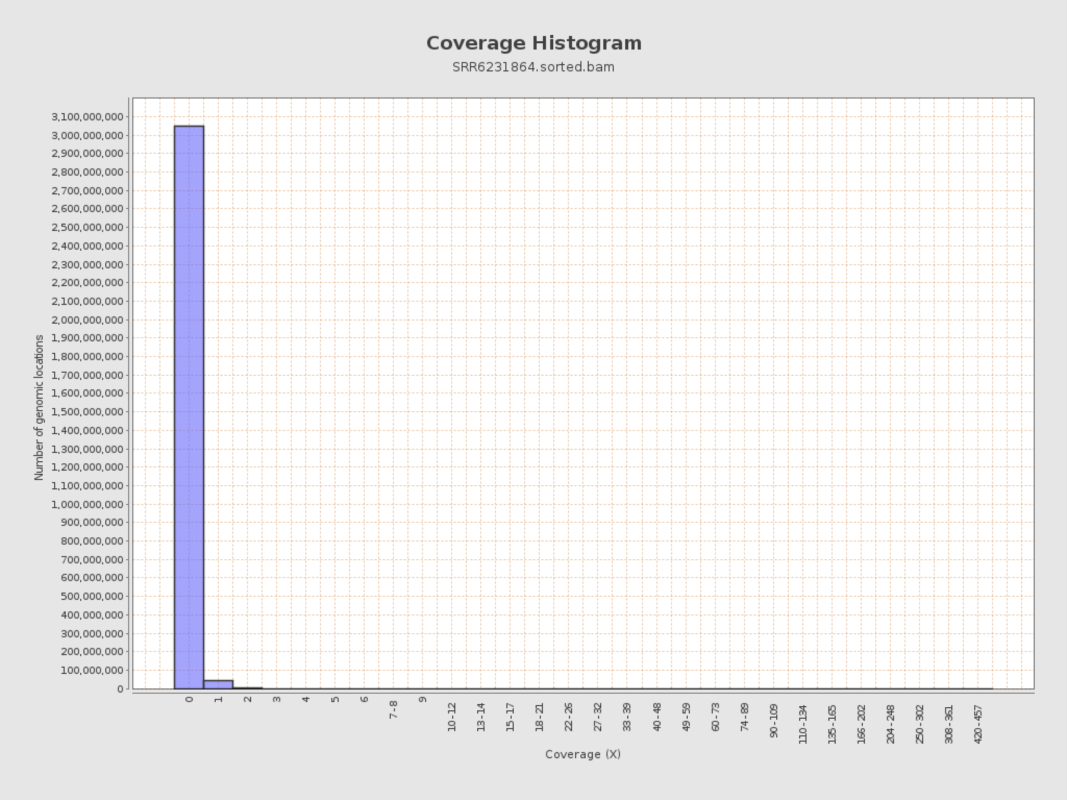
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5626781	0.0226	0.247
chr2	243199373	4354838	0.0179	0.2104
chr3	198022430	4752076	0.024	0.181
chr4	191154276	2823513	0.0148	0.1505
chr5	180915260	2892515	0.016	0.1473
chr6	171115067	3863459	0.0226	0.1983
chr7	159138663	4029508	0.0253	0.2549

chr8	146364022	3673640	0.0251	0.3259
chr9	141213431	2361219	0.0167	0.1672
chr10	135534747	2133516	0.0157	0.17
chr11	135006516	2361573	0.0175	0.1702
chr12	133851895	2330731	0.0174	0.1552
chr13	115169878	2464632	0.0214	0.1724
chr14	107349540	2204710	0.0205	0.1702
chr15	102531392	1458547	0.0142	0.1439
chr16	90354753	1188267	0.0132	0.1371
chr17	81195210	1342632	0.0165	0.1557
chr18	78077248	1346387	0.0172	0.25
chr19	59128983	1135401	0.0192	0.1788
chr20	63025520	1487247	0.0236	0.1821
chr21	48129895	1449383	0.0301	0.2075
chr22	51304566	551921	0.0108	0.1195
chrMT	16571	28641	1.7284	1.7327
chrX	155270560	2587148	0.0167	0.1532
chrY	59373566	245000	0.0041	0.0857

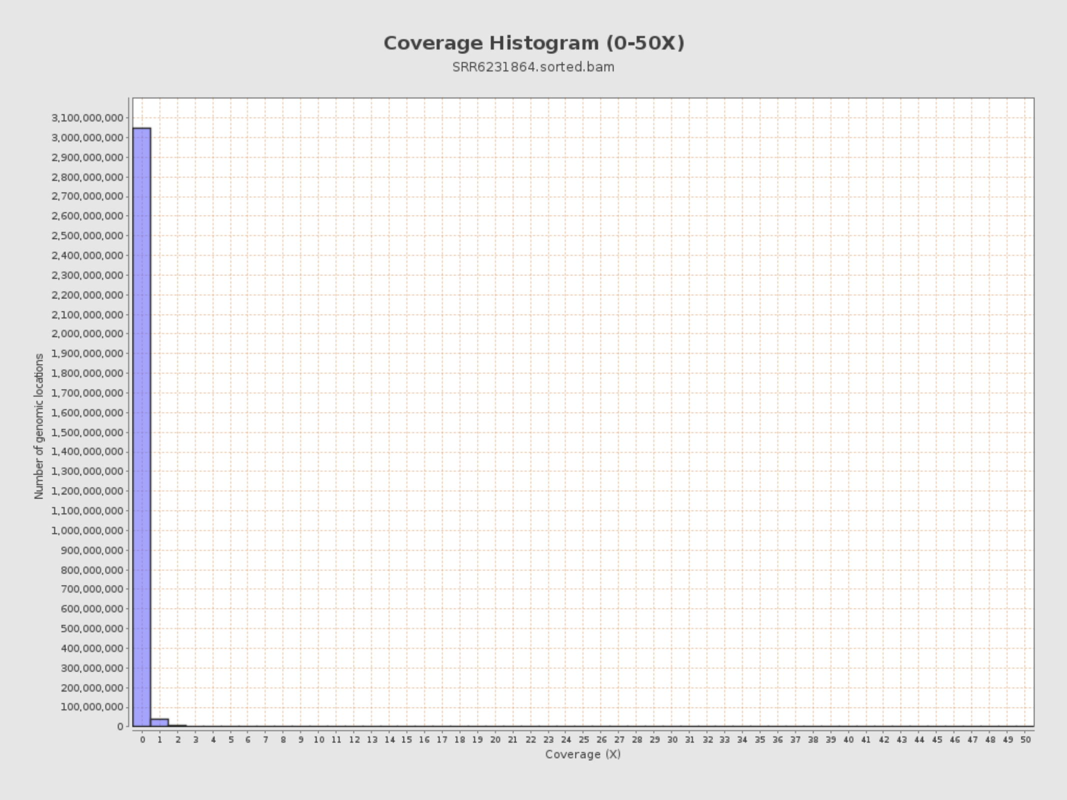
3. Results : Coverage across reference



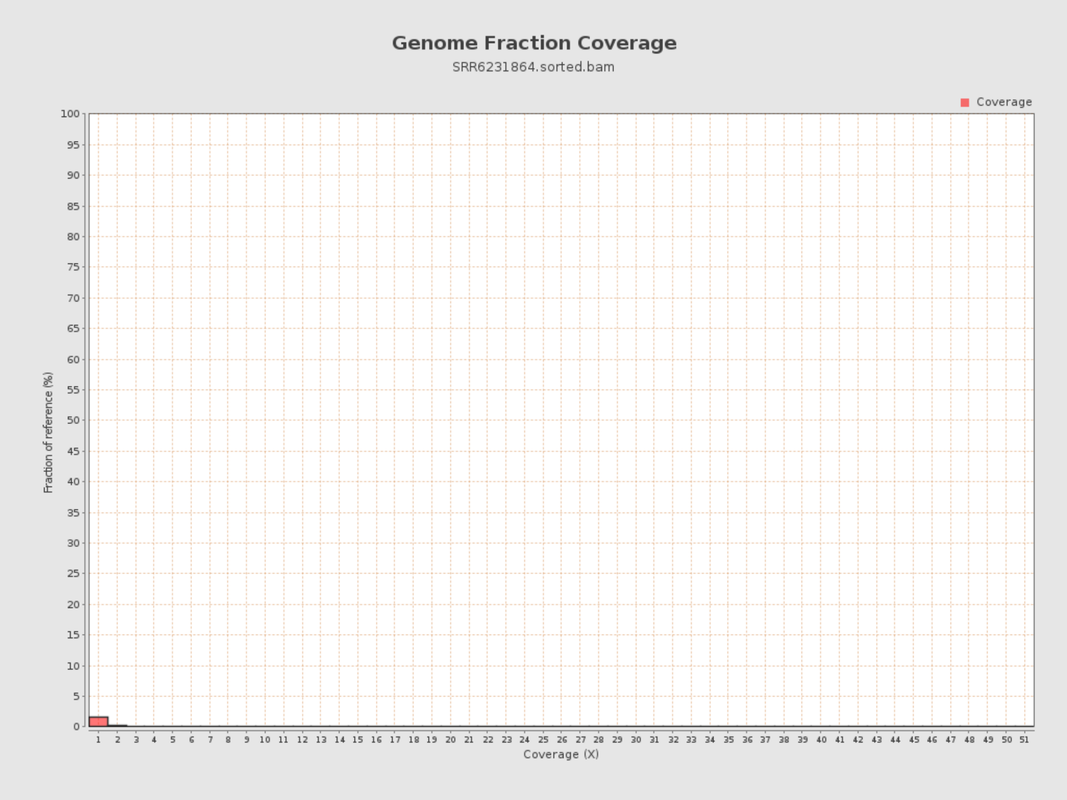
4. Results : Coverage Histogram



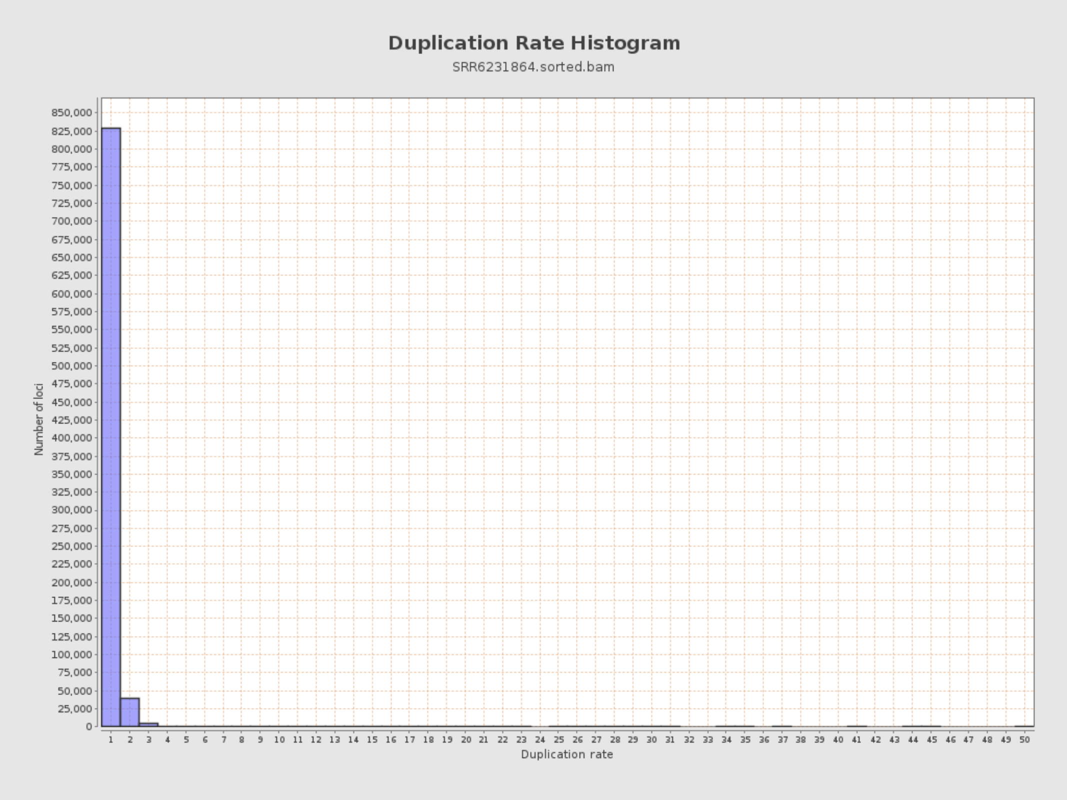
5. Results : Coverage Histogram (0-50X)



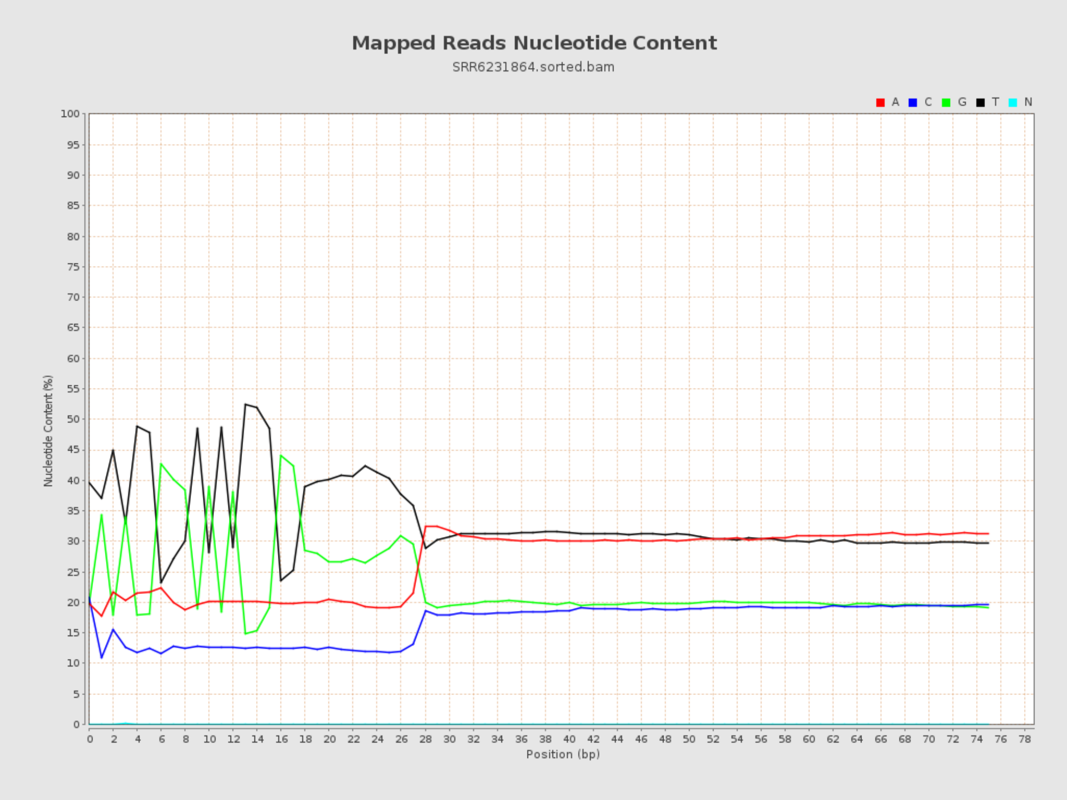
6. Results : Genome Fraction Coverage



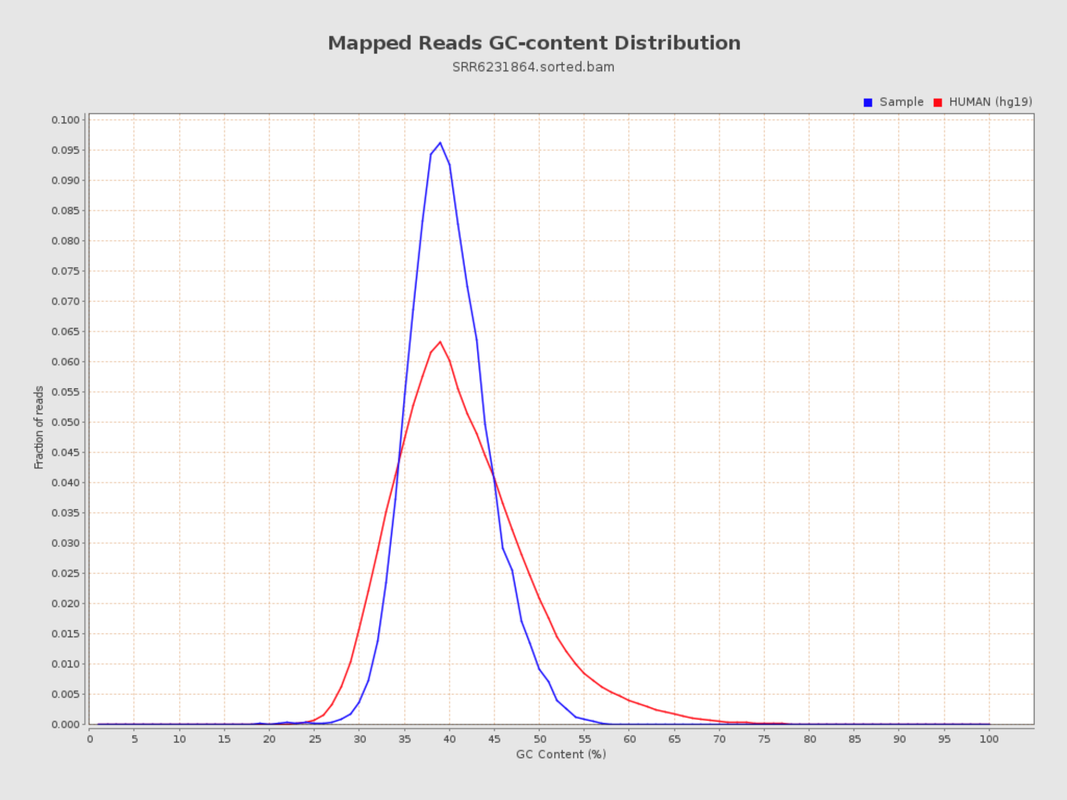
7. Results : Duplication Rate Histogram



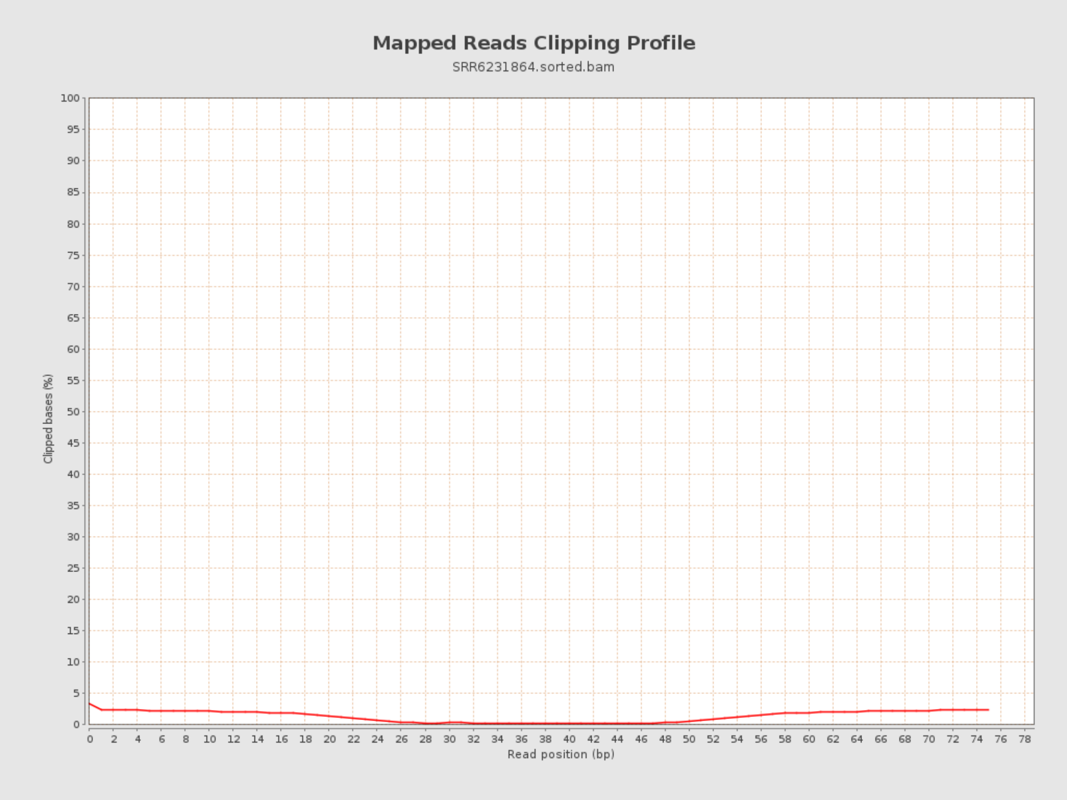
8. Results : Mapped Reads Nucleotide Content



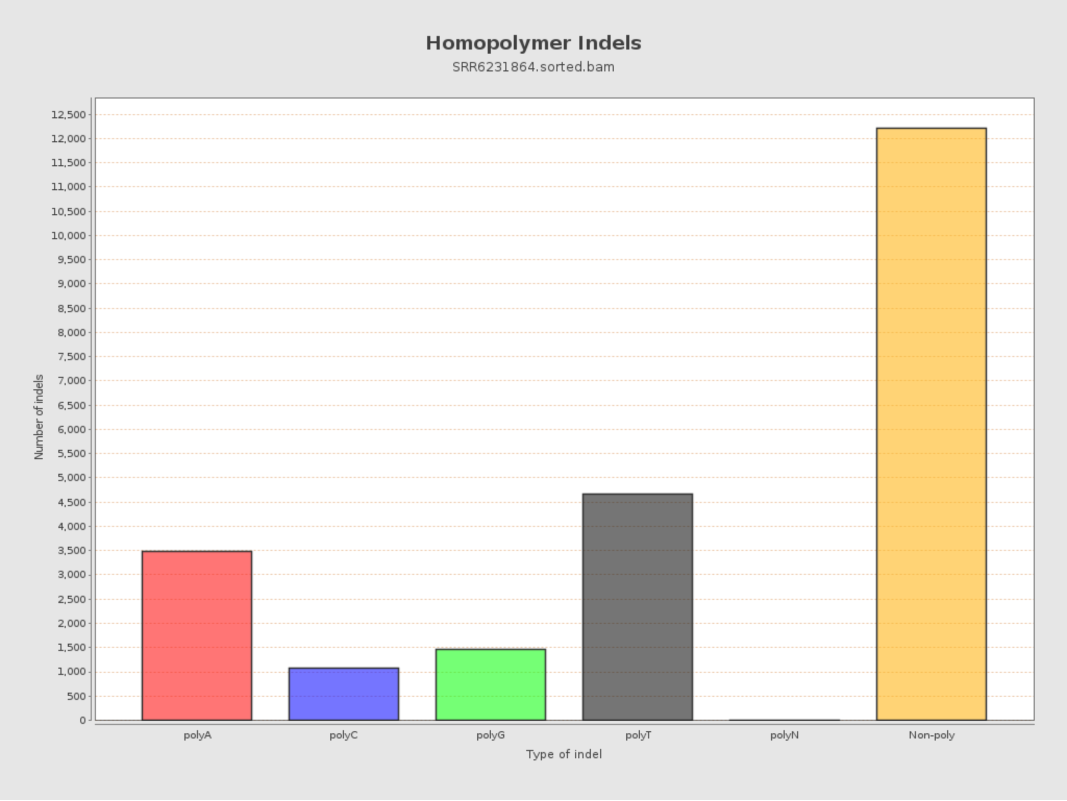
9. Results : Mapped Reads GC-content Distribution



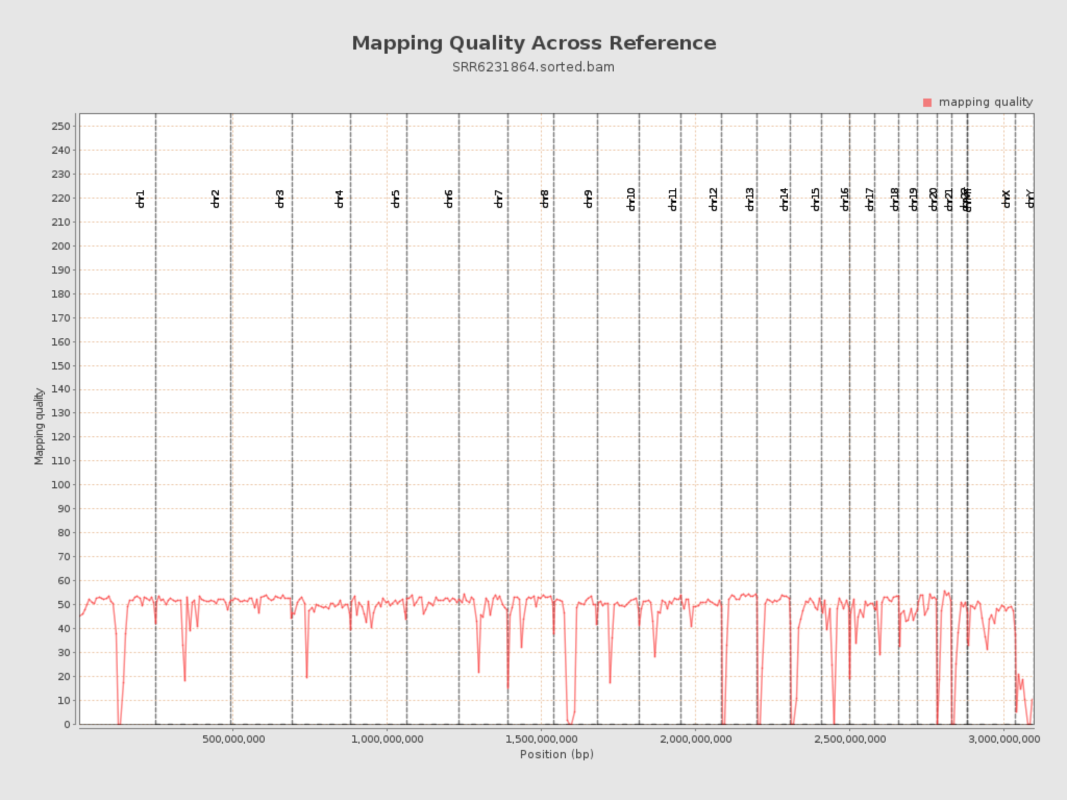
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram