Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 05:39:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231825.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_SRR6231825 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231825.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 05:39:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231825.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,680,554
Mapped reads	668,059 / 39.75%
Unmapped reads	1,012,495 / 60.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,625 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	80,570 / 4.79%
Duplication rate	9.59%
Clipped reads	375,621 / 22.35%

2.2. ACGT Content

Number/percentage of A's	11,524,757 / 27.14%
Number/percentage of C's	8,154,999 / 19.21%
Number/percentage of T's	13,180,737 / 31.04%
Number/percentage of G's	9,594,111 / 22.6%
Number/percentage of N's	4,791 / 0.01%
GC Percentage	41.8%

2.3. Coverage

Mean	0.0137

Standard Deviation	0.2061

2.4. Mapping Quality

Mean Mapping Quality	43.82

2.5. Mismatches and indels

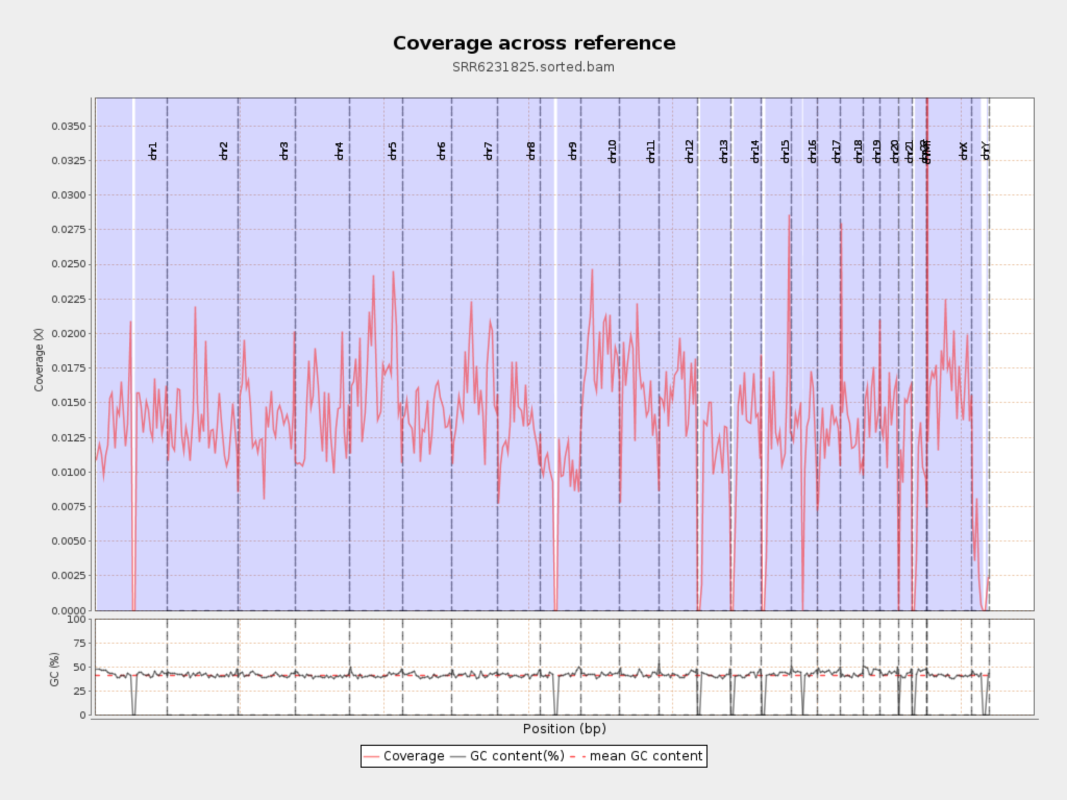
General error rate	0.86%
Mismatches	356,861
Insertions	4,135
Mapped reads with at least one insertion	0.61%
Deletions	11,867
Mapped reads with at least one deletion	1.75%
Homopolymer indels	43.93%

2.6. Chromosome stats

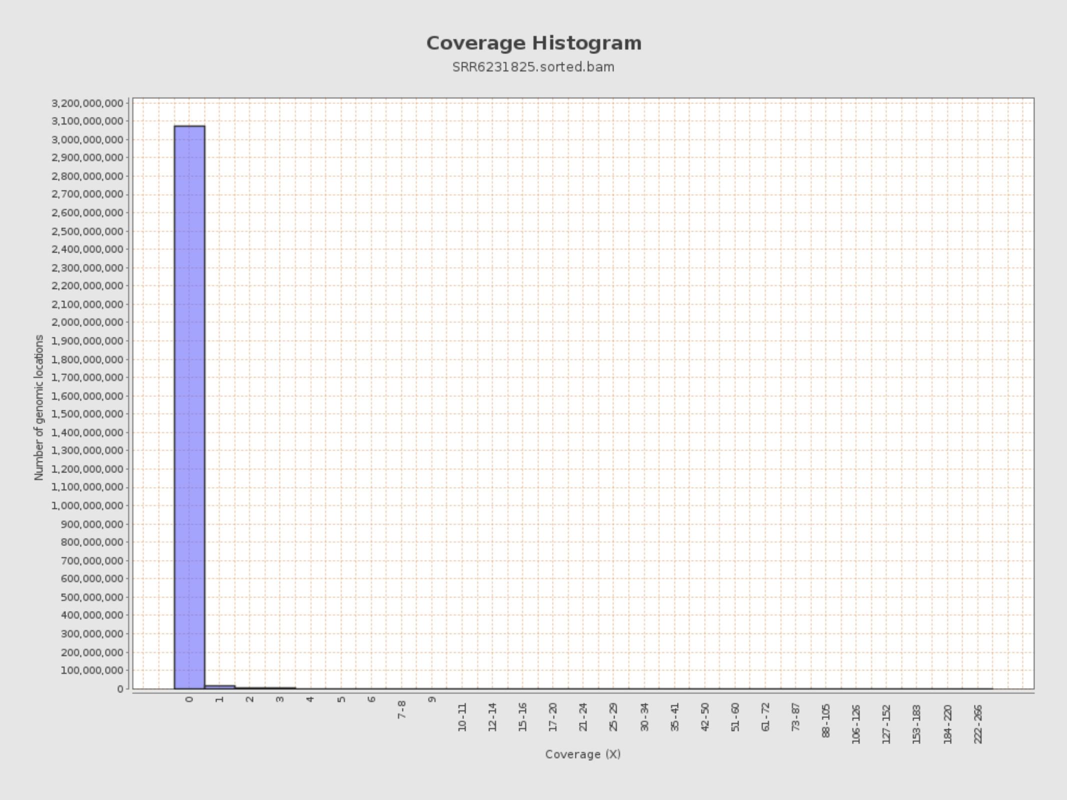
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3260100	0.0131	0.2771
chr2	243199373	3261570	0.0134	0.2178
chr3	198022430	2743967	0.0139	0.1858
chr4	191154276	2623502	0.0137	0.1891
chr5	180915260	3149052	0.0174	0.2122
chr6	171115067	2386635	0.0139	0.193
chr7	159138663	2528193	0.0159	0.2253

chr8	146364022	1945083	0.0133	0.1998
chr9	141213431	1296182	0.0092	0.1579
chr10	135534747	2528595	0.0187	0.2328
chr11	135006516	2142403	0.0159	0.2074
chr12	133851895	2140104	0.016	0.2014
chr13	115169878	1179999	0.0102	0.1928
chr14	107349540	1297578	0.0121	0.1857
chr15	102531392	1229971	0.012	0.1742
chr16	90354753	1117650	0.0124	0.1854
chr17	81195210	1015878	0.0125	0.1831
chr18	78077248	1065153	0.0136	0.2267
chr19	59128983	883840	0.0149	0.236
chr20	63025520	886059	0.0141	0.1925
chr21	48129895	600398	0.0125	0.177
chr22	51304566	394255	0.0077	0.1376
chrMT	16571	48327	2.9164	3.0639
chrX	155270560	2591243	0.0167	0.2093
chrY	59373566	164250	0.0028	0.0882

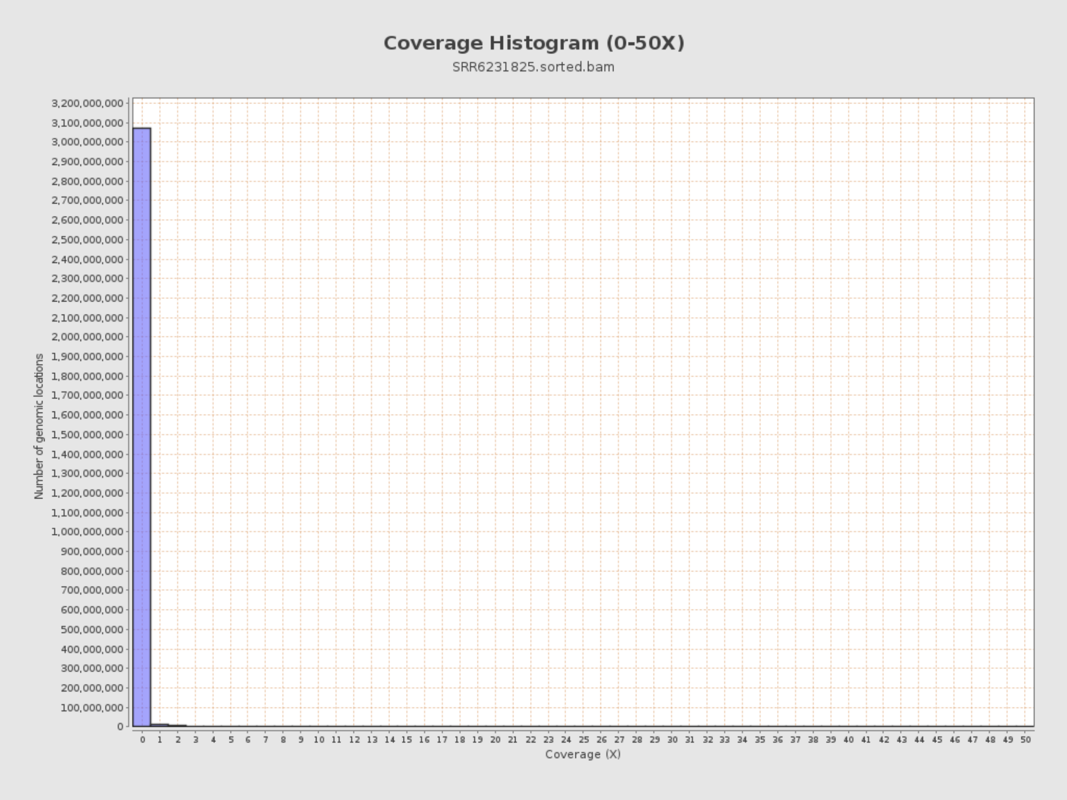
3. Results : Coverage across reference



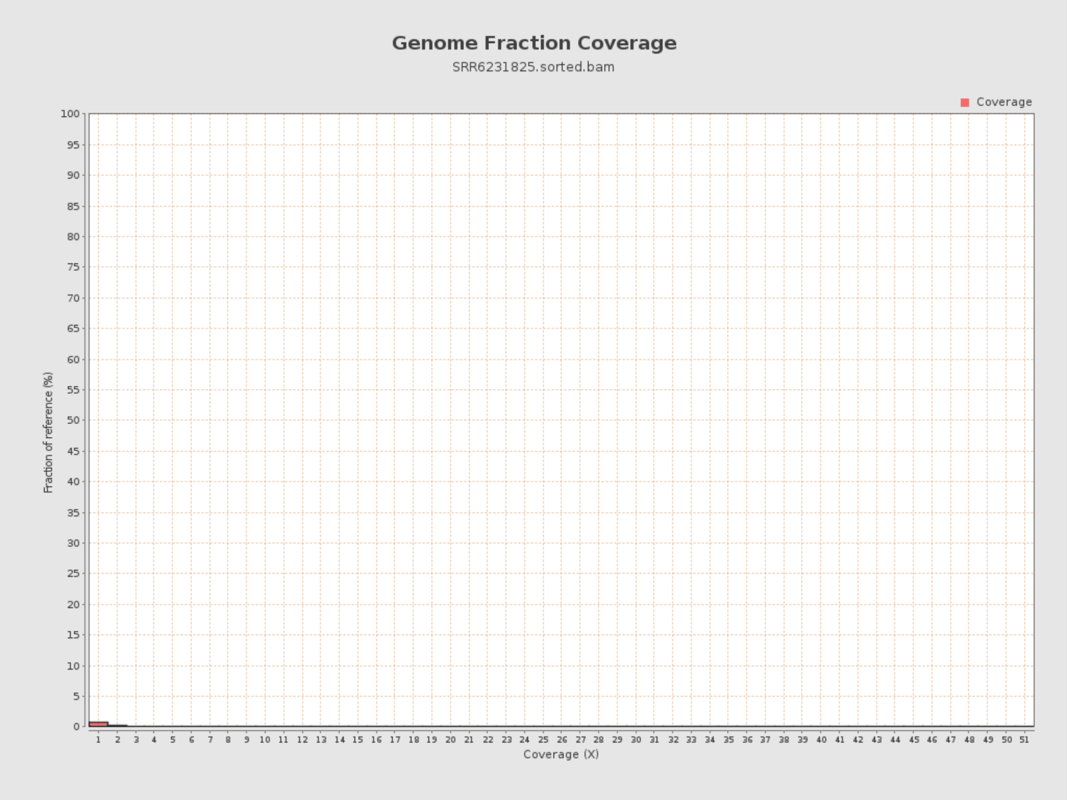
4. Results : Coverage Histogram



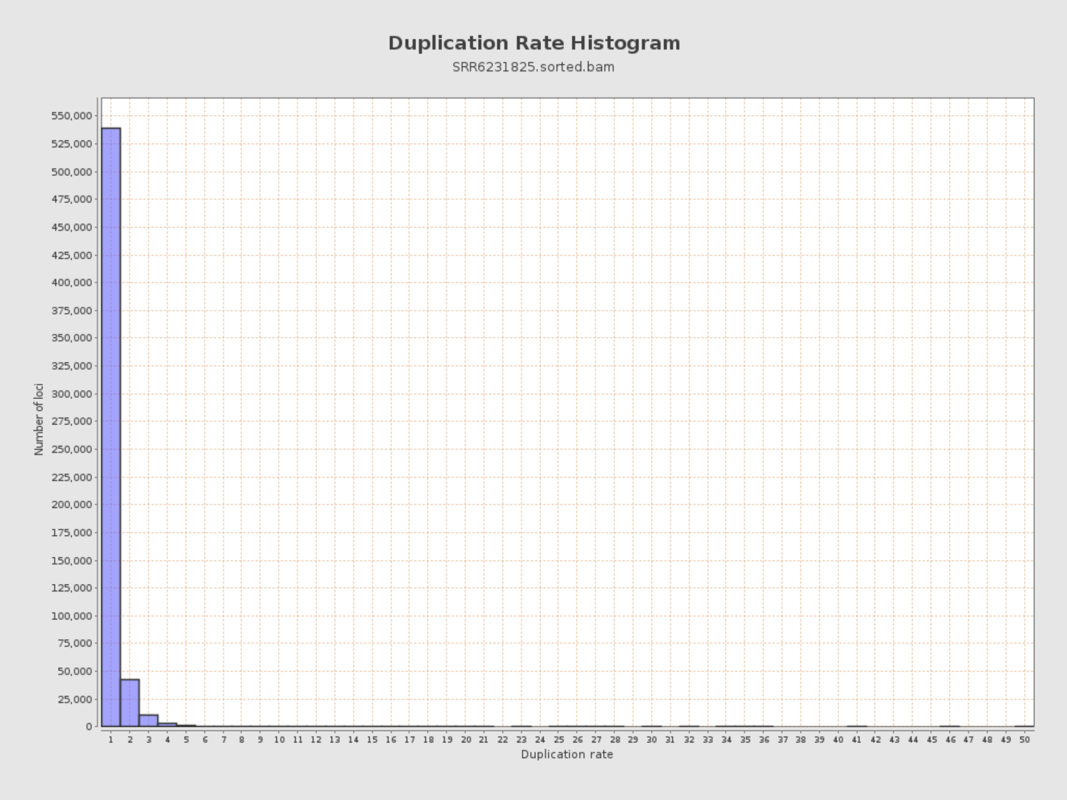
5. Results : Coverage Histogram (0-50X)



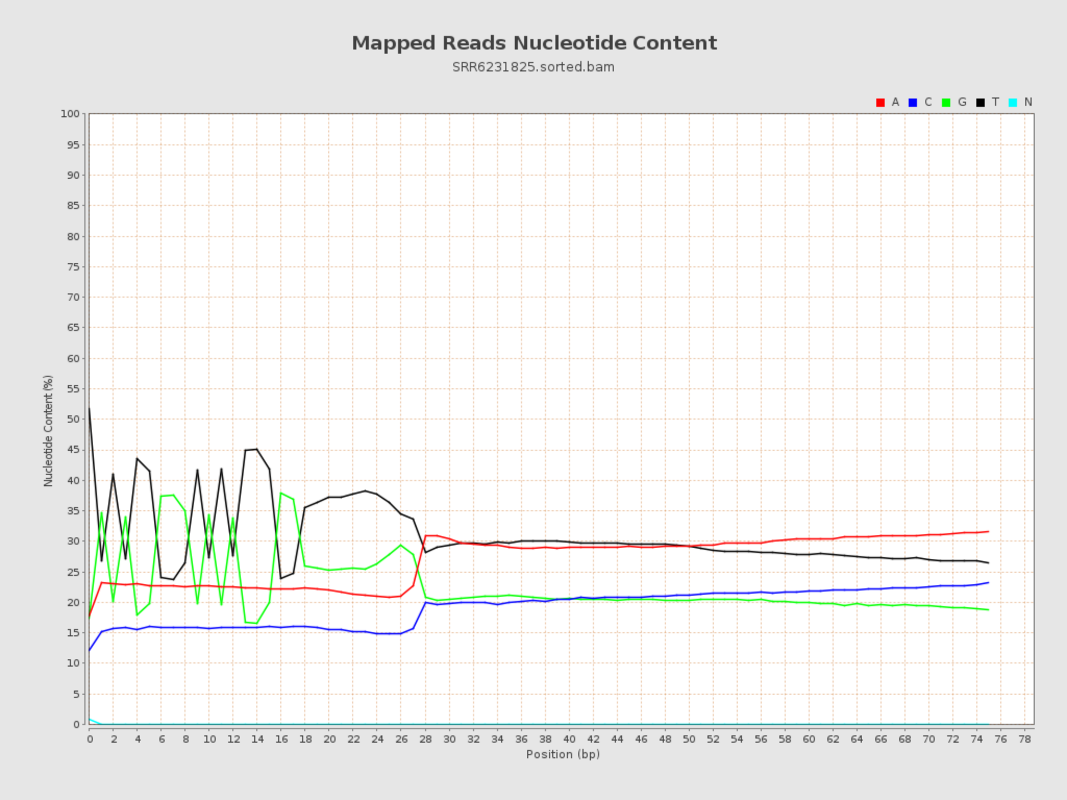
6. Results : Genome Fraction Coverage



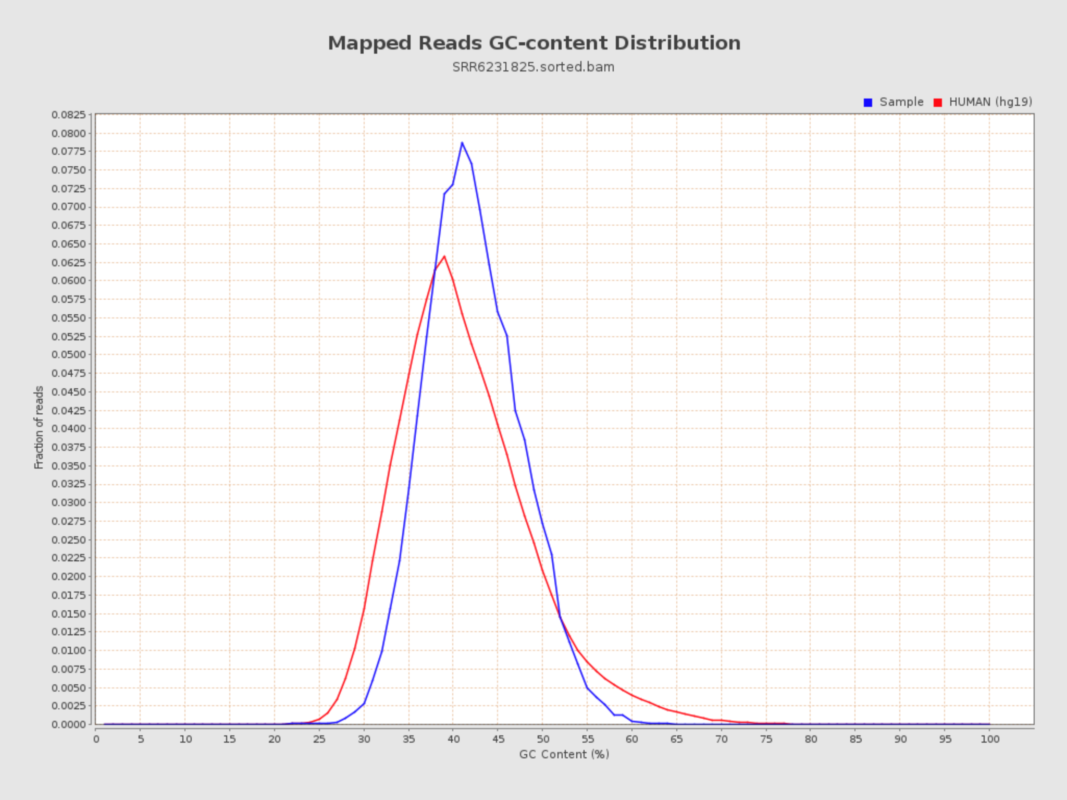
7. Results : Duplication Rate Histogram



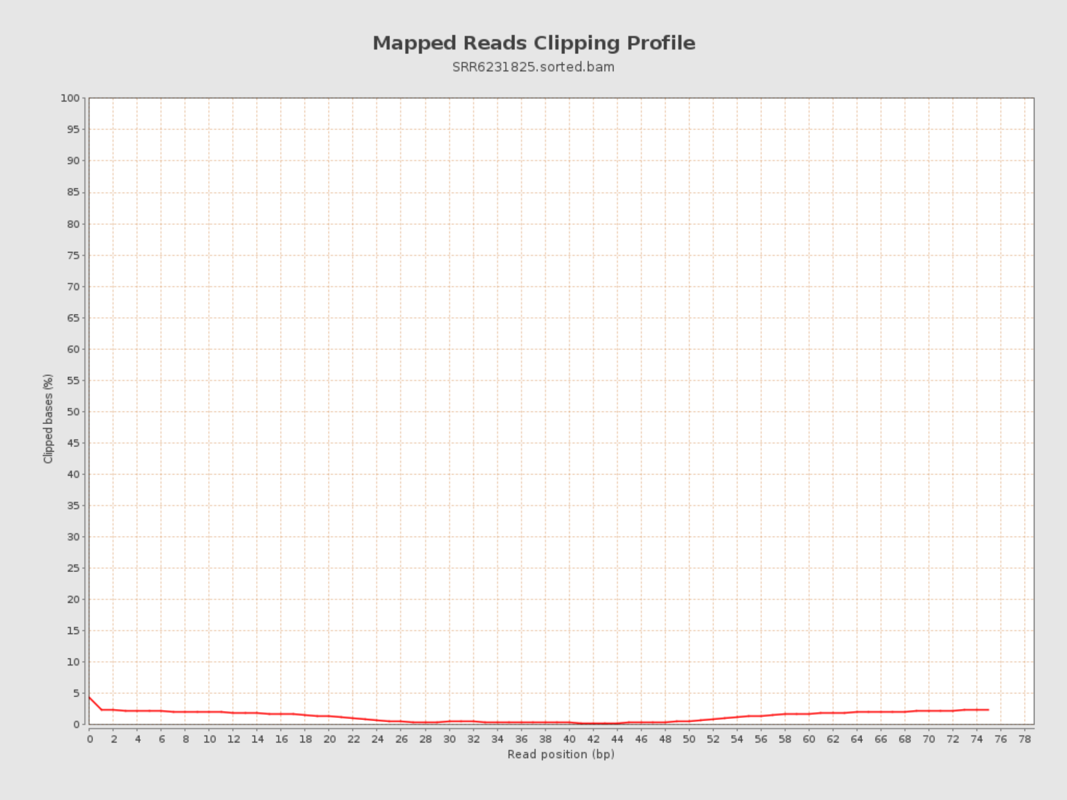
8. Results : Mapped Reads Nucleotide Content



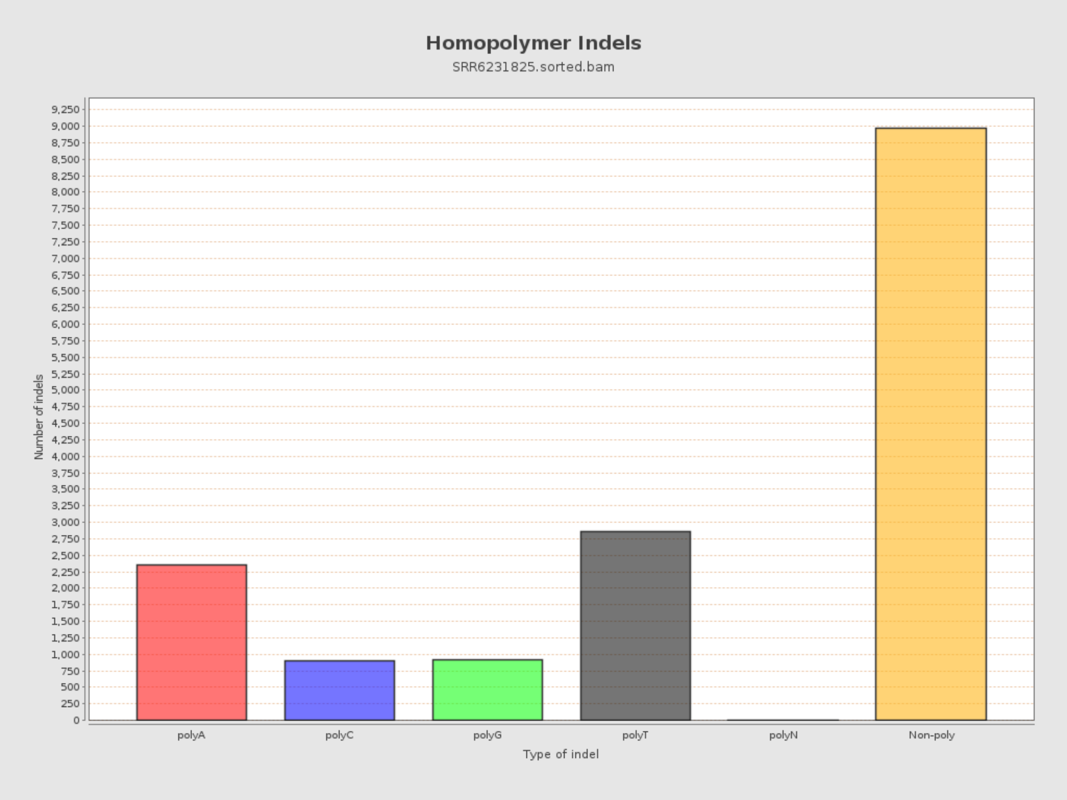
9. Results : Mapped Reads GC-content Distribution



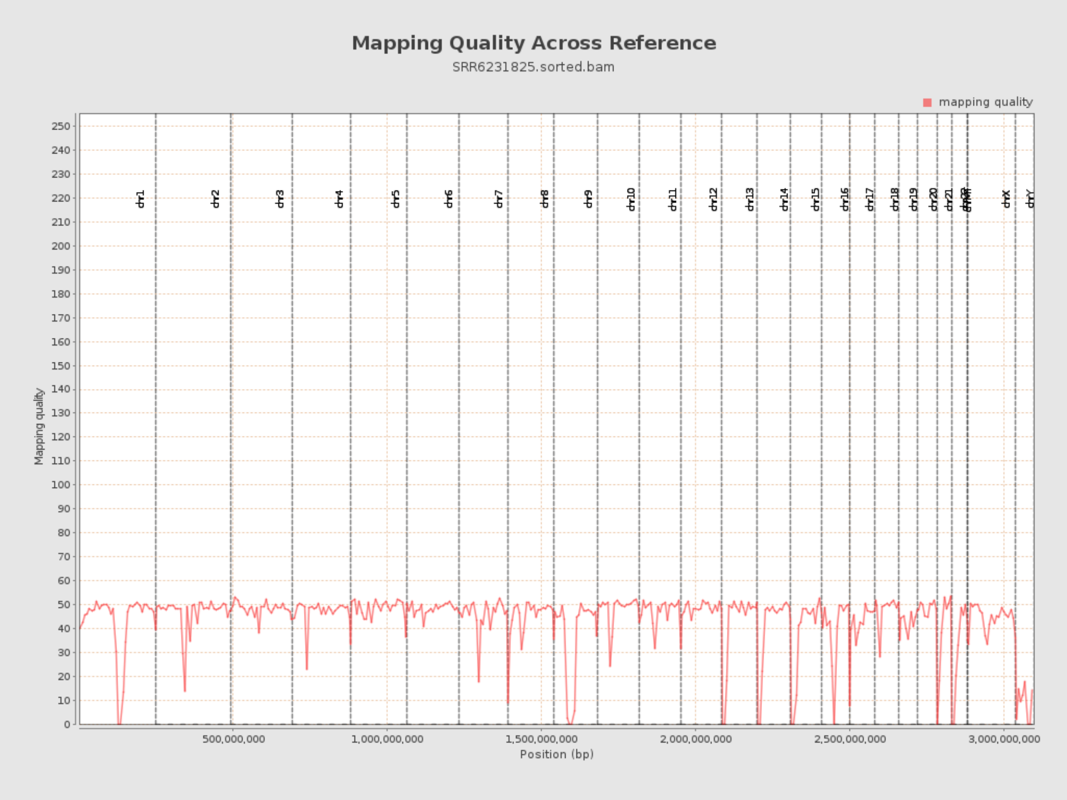
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram