Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 05:22:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231818.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_SRR6231818 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231818.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 05:22:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231818.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	976,793
Mapped reads	537,784 / 55.06%
Unmapped reads	439,009 / 44.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,546 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	34,542 / 3.54%
Duplication rate	5.42%
Clipped reads	296,447 / 30.35%

2.2. ACGT Content

Number/percentage of A's	9,628,240 / 28.19%
Number/percentage of C's	5,758,922 / 16.86%
Number/percentage of T's	11,443,287 / 33.51%
Number/percentage of G's	7,318,322 / 21.43%
Number/percentage of N's	1,477 / 0%
GC Percentage	38.29%

2.3. Coverage

Mean	0.011

Standard Deviation	0.175

2.4. Mapping Quality

Mean Mapping Quality	45.72

2.5. Mismatches and indels

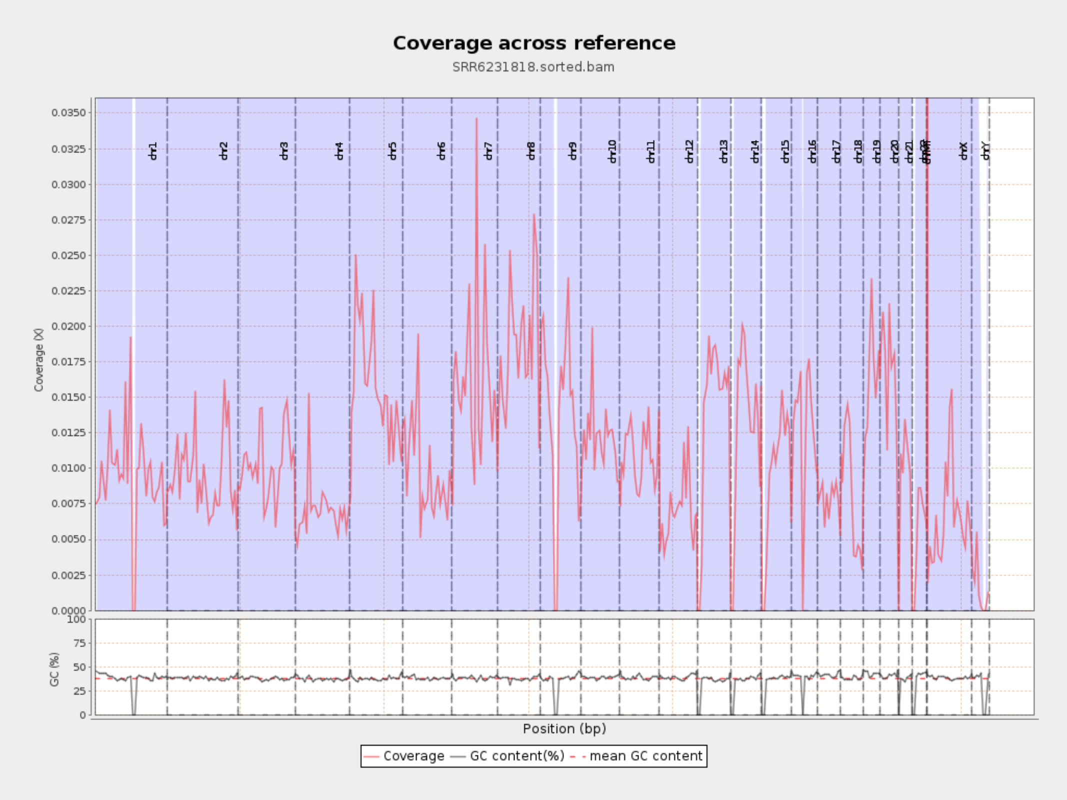
General error rate	0.95%
Mismatches	318,370
Insertions	3,068
Mapped reads with at least one insertion	0.56%
Deletions	17,363
Mapped reads with at least one deletion	3.15%
Homopolymer indels	41.72%

2.6. Chromosome stats

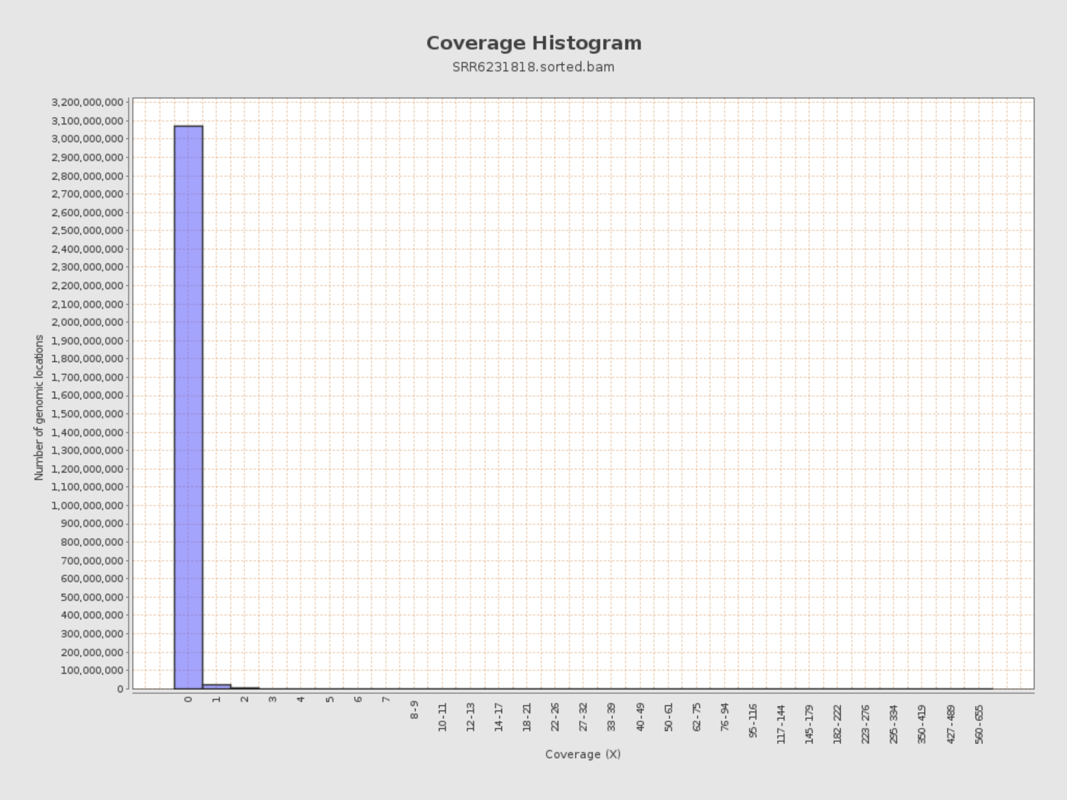
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2334969	0.0094	0.2488
chr2	243199373	2316047	0.0095	0.1446
chr3	198022430	2022428	0.0102	0.1239
chr4	191154276	1343926	0.007	0.1084
chr5	180915260	2905869	0.0161	0.1571
chr6	171115067	1679587	0.0098	0.1388
chr7	159138663	2608868	0.0164	0.1979

chr8	146364022	2734597	0.0187	0.4255
chr9	141213431	1949104	0.0138	0.1521
chr10	135534747	1645200	0.0121	0.147
chr11	135006516	1449873	0.0107	0.1298
chr12	133851895	931782	0.007	0.1047
chr13	115169878	1604057	0.0139	0.147
chr14	107349540	1379534	0.0129	0.1396
chr15	102531392	984955	0.0096	0.1198
chr16	90354753	1121024	0.0124	0.1371
chr17	81195210	634840	0.0078	0.1081
chr18	78077248	629823	0.0081	0.2046
chr19	59128983	969442	0.0164	0.1769
chr20	63025520	1051018	0.0167	0.1616
chr21	48129895	459499	0.0095	0.1226
chr22	51304566	281073	0.0055	0.0873
chrMT	16571	23057	1.3914	1.5364
chrX	155270560	1026440	0.0066	0.1037
chrY	59373566	93760	0.0016	0.0583

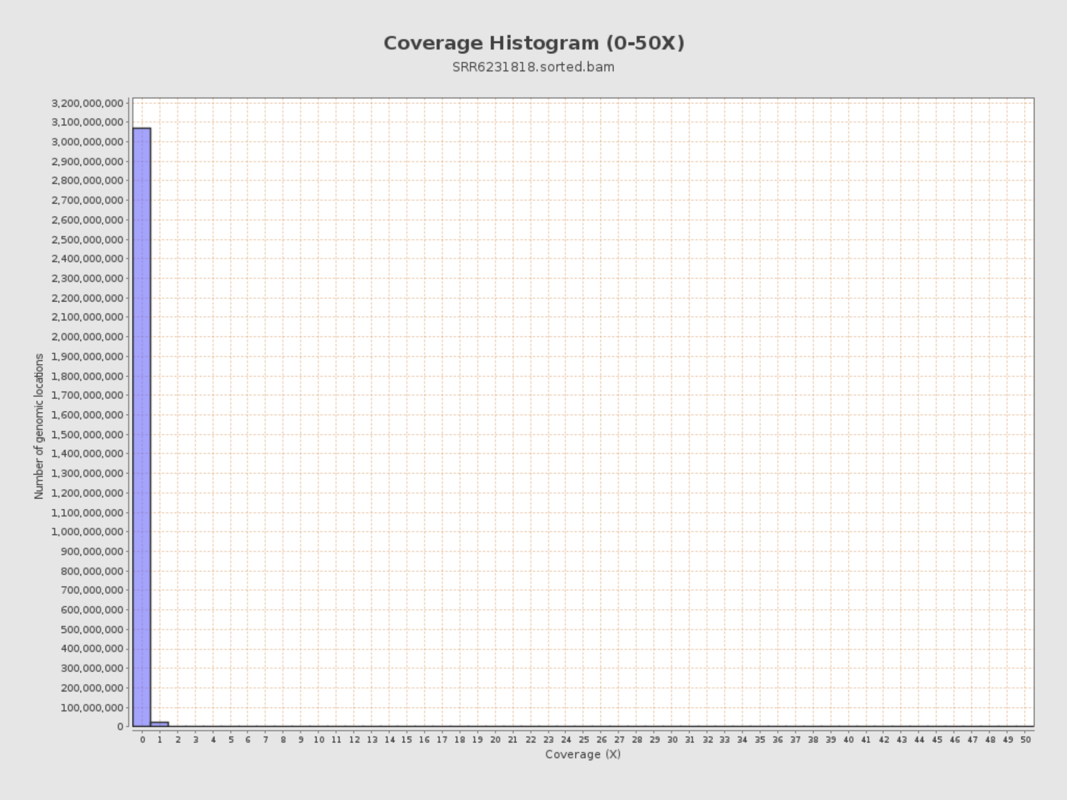
3. Results : Coverage across reference



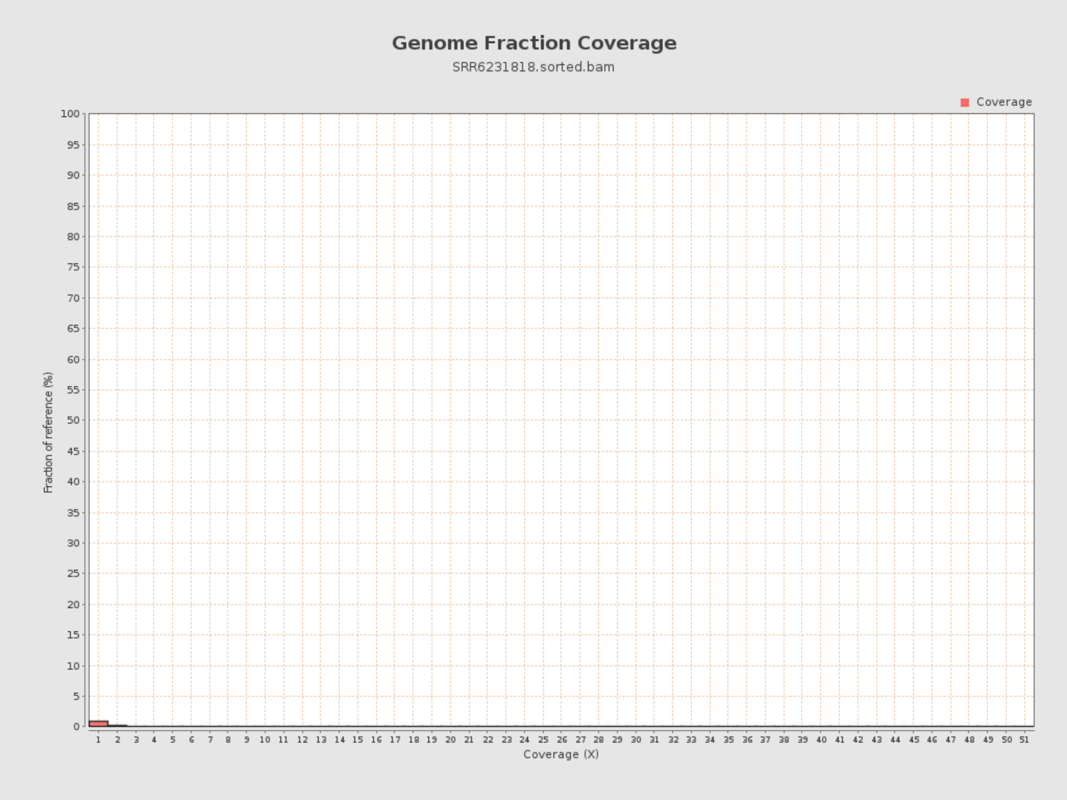
4. Results : Coverage Histogram



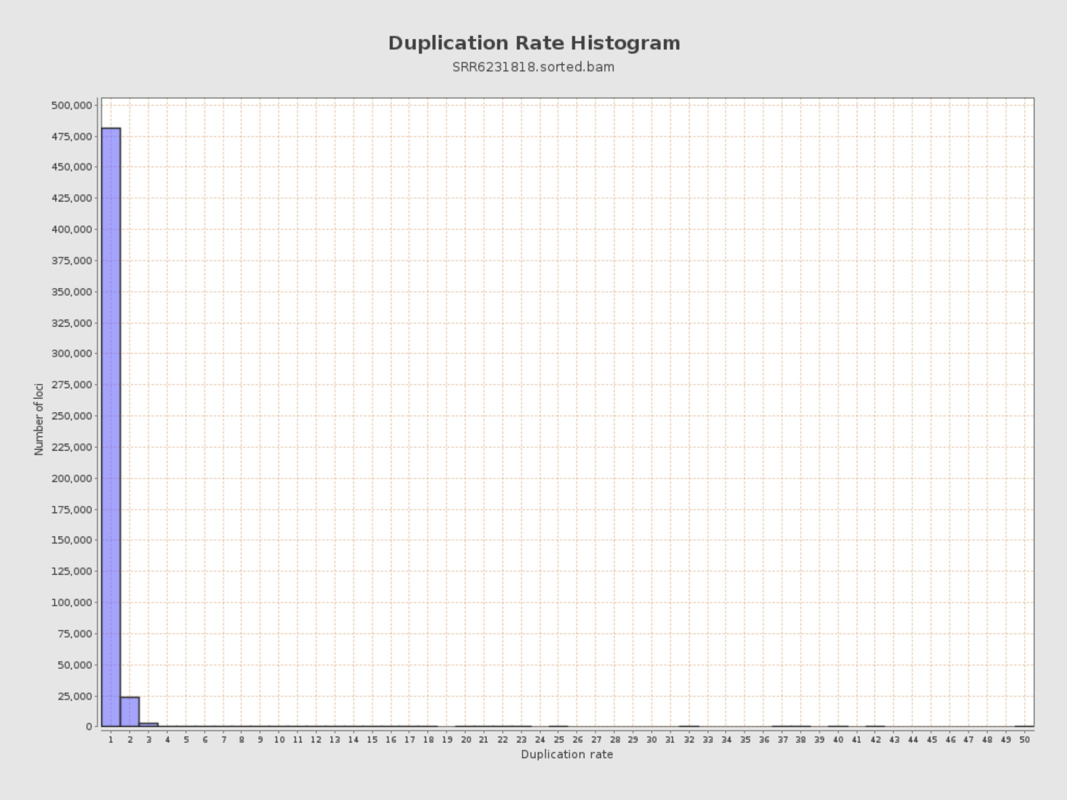
5. Results : Coverage Histogram (0-50X)



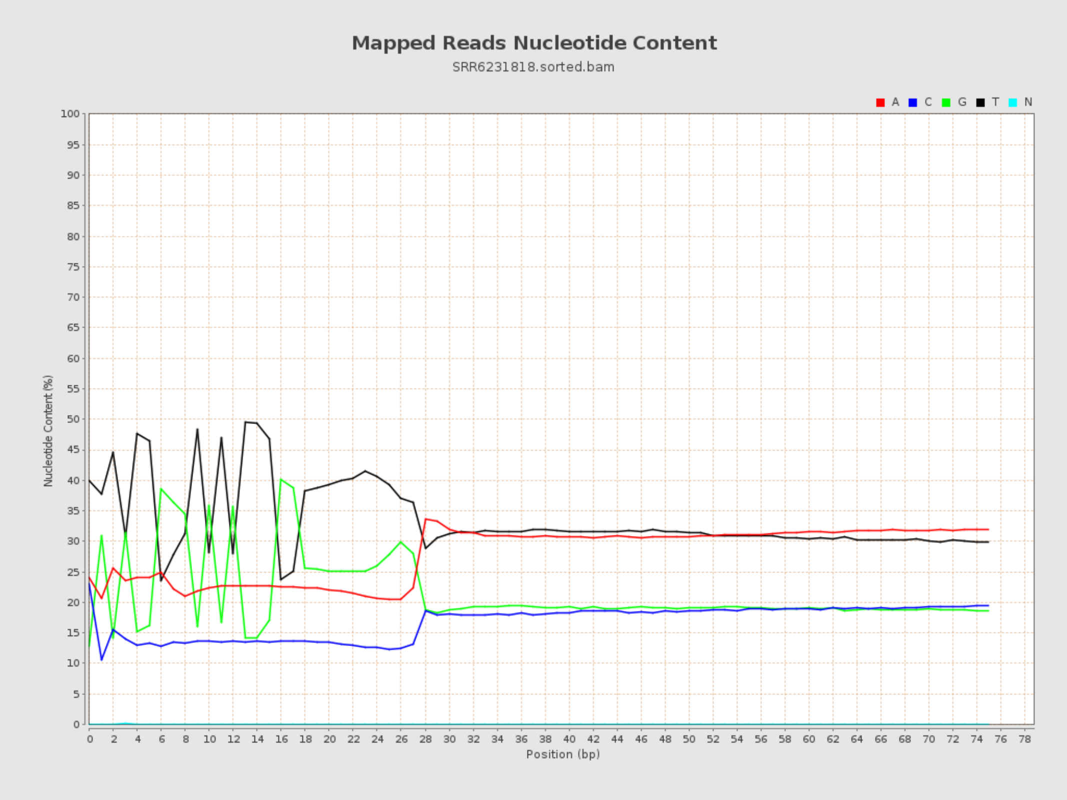
6. Results : Genome Fraction Coverage



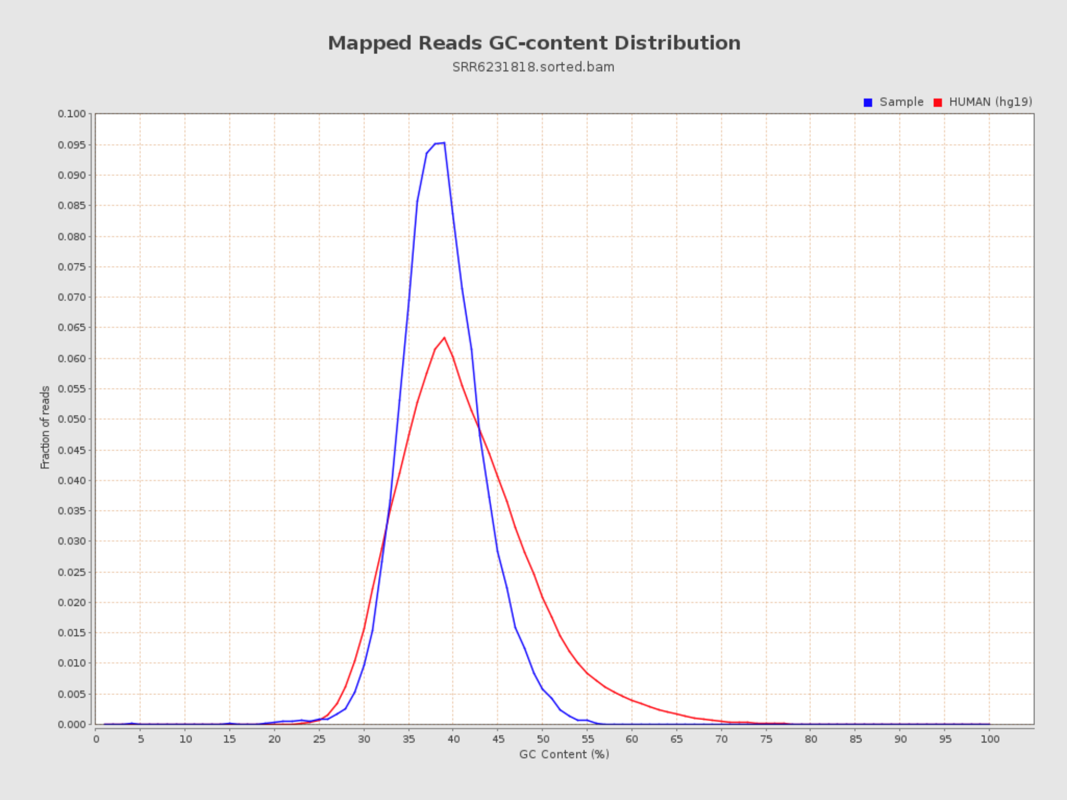
7. Results : Duplication Rate Histogram



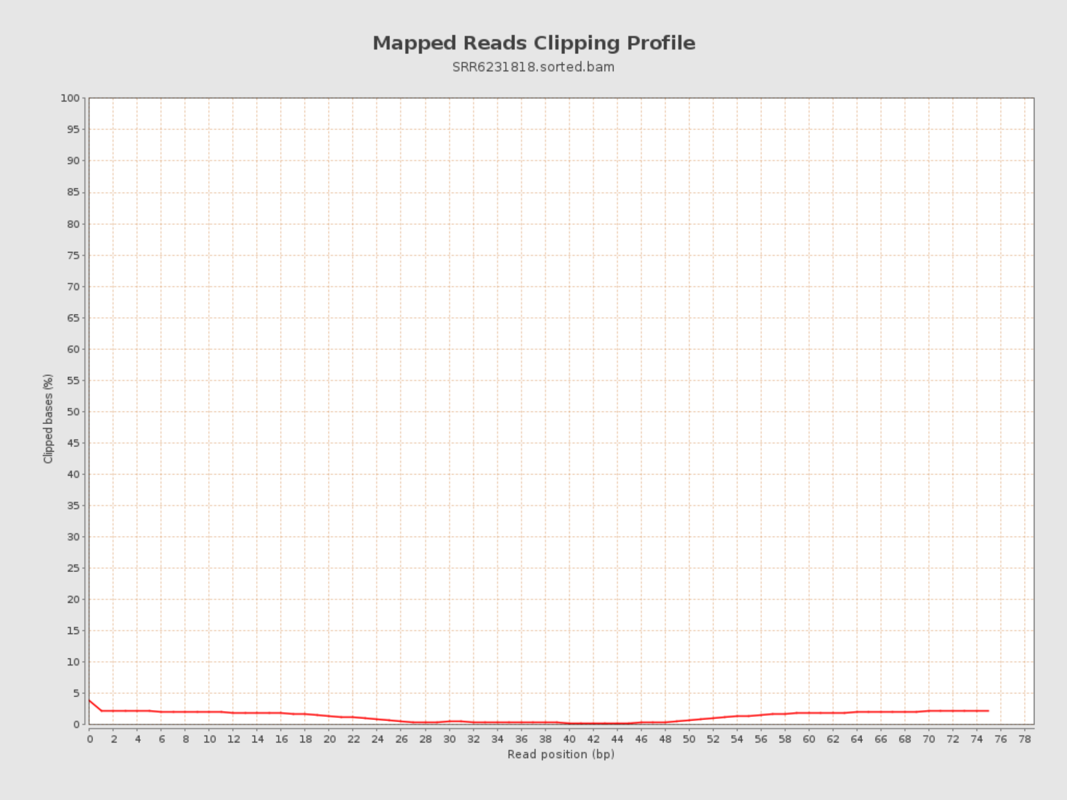
8. Results : Mapped Reads Nucleotide Content



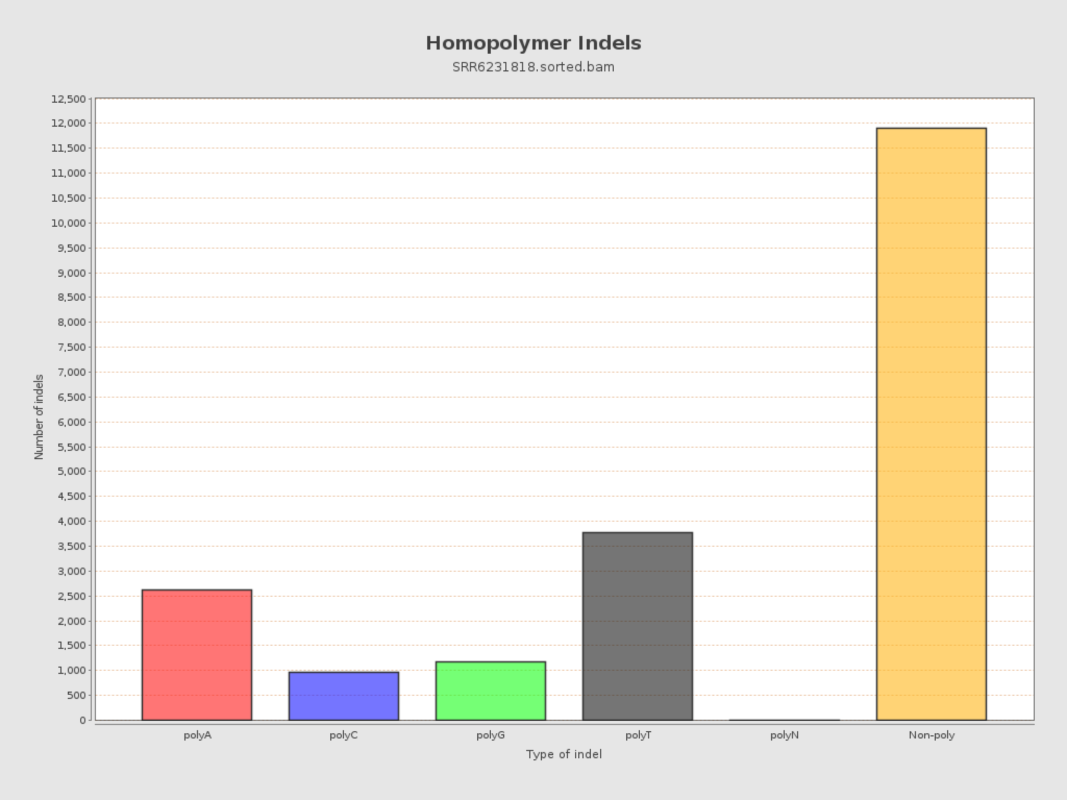
9. Results : Mapped Reads GC-content Distribution



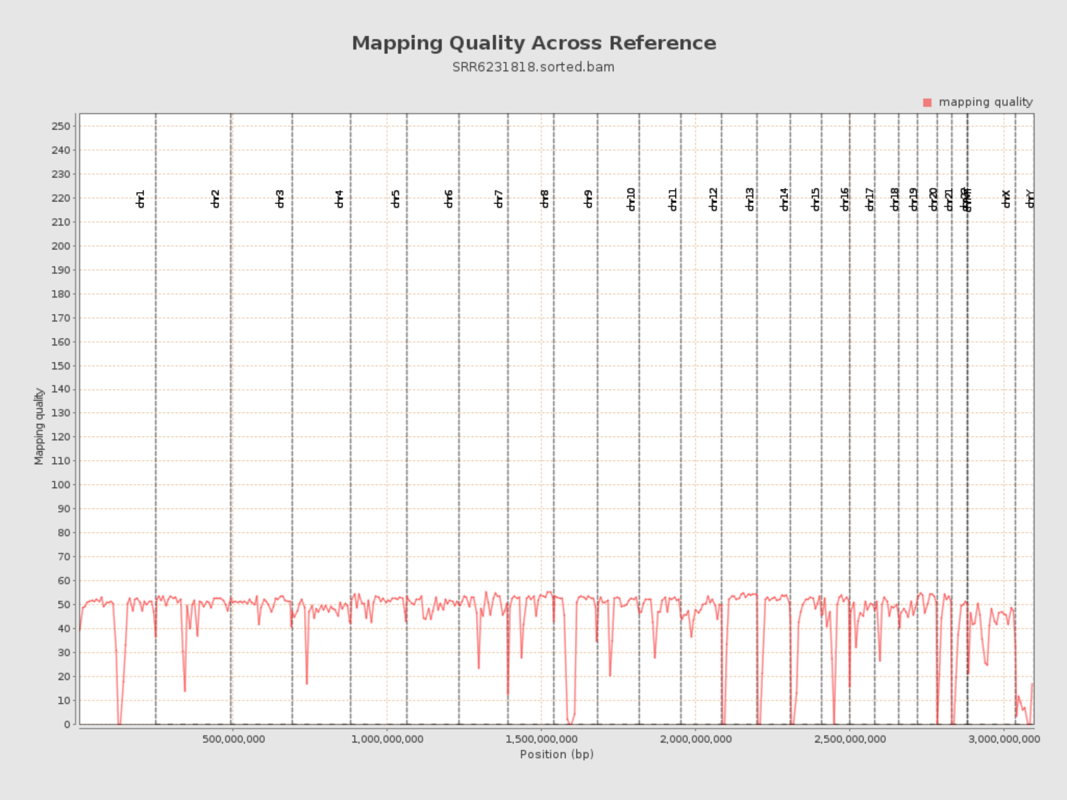
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram