Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 10:00:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231882.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_SRR6231882 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231882.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 10:00:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231882.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,852,583
Mapped reads	1,413,497 / 76.3%
Unmapped reads	439,086 / 23.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,795 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	158,075 / 8.53%
Duplication rate	9.34%
Clipped reads	857,970 / 46.31%

2.2. ACGT Content

Number/percentage of A's	23,597,391 / 26.43%
Number/percentage of C's	14,964,965 / 16.76%
Number/percentage of T's	30,179,331 / 33.8%
Number/percentage of G's	20,530,164 / 23%
Number/percentage of N's	4,055 / 0%
GC Percentage	39.76%

2.3. Coverage

Mean	0.0289

Standard Deviation	0.2754

2.4. Mapping Quality

Mean Mapping Quality	46.07

2.5. Mismatches and indels

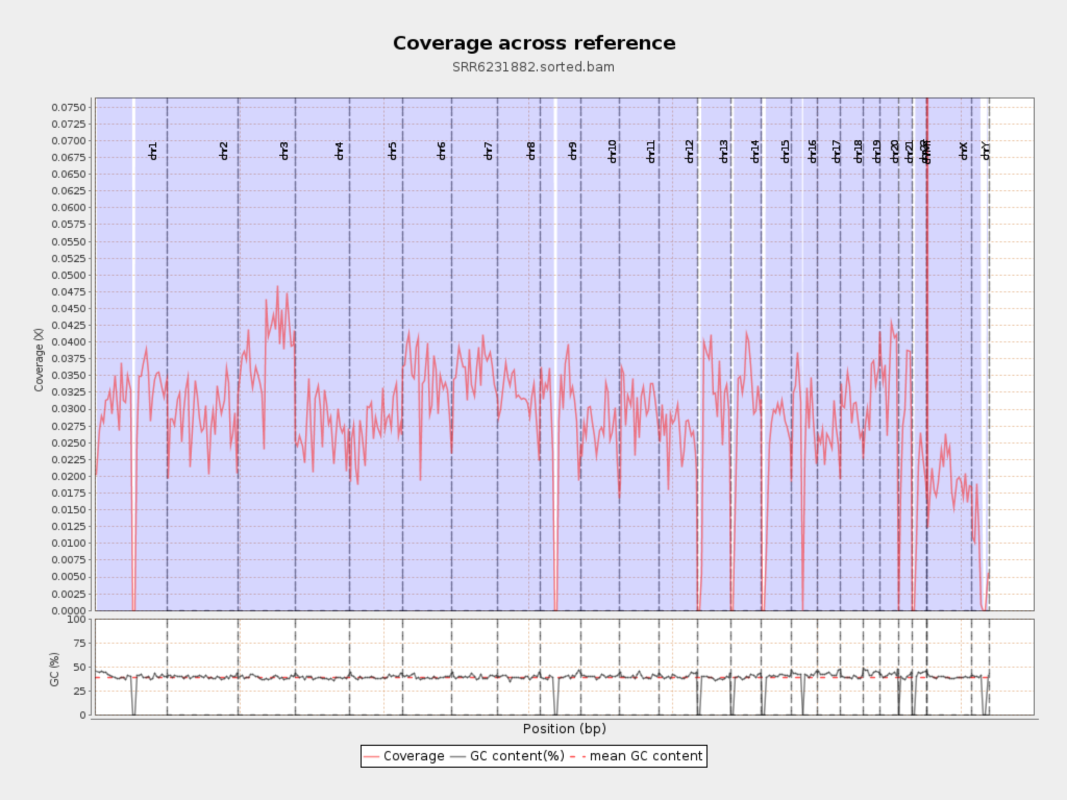
General error rate	0.81%
Mismatches	712,234
Insertions	7,755
Mapped reads with at least one insertion	0.54%
Deletions	27,669
Mapped reads with at least one deletion	1.93%
Homopolymer indels	48.85%

2.6. Chromosome stats

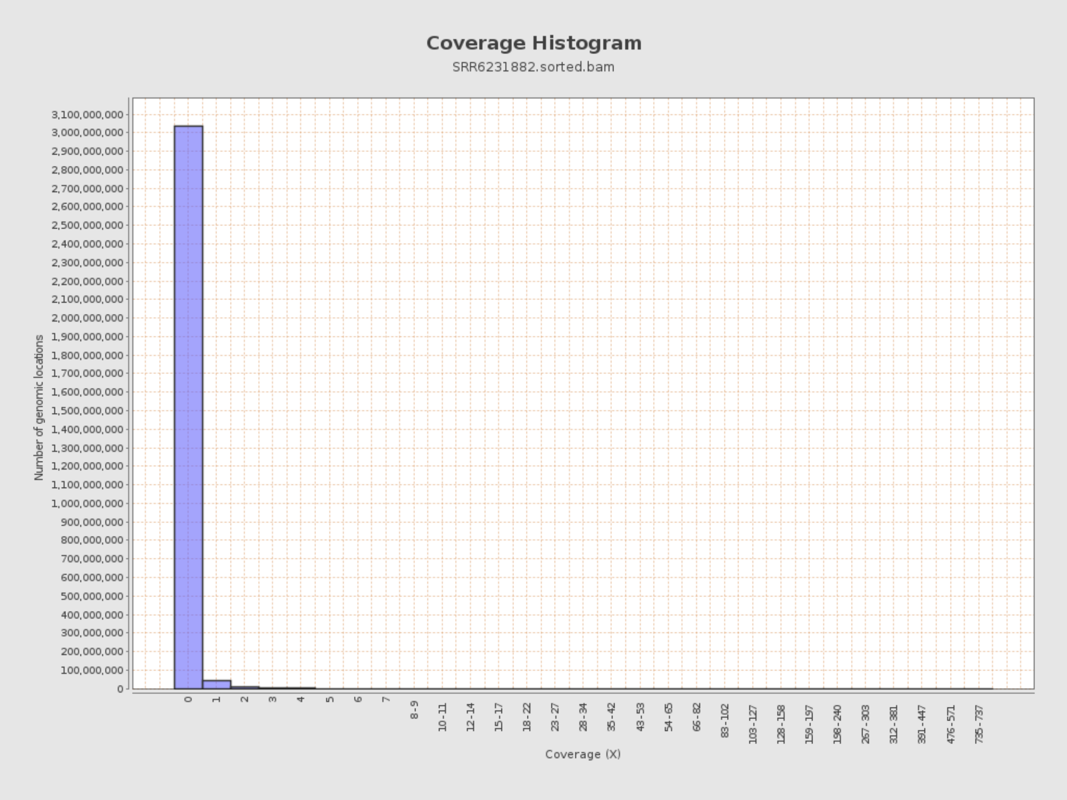
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7485095	0.03	0.2705
chr2	243199373	7035602	0.0289	0.3843
chr3	198022430	7735537	0.0391	0.2728
chr4	191154276	5208651	0.0272	0.2395
chr5	180915260	4973848	0.0275	0.2278
chr6	171115067	5851398	0.0342	0.278
chr7	159138663	5696730	0.0358	0.3332

chr8	146364022	4634031	0.0317	0.4261
chr9	141213431	3993729	0.0283	0.2474
chr10	135534747	3665795	0.027	0.2348
chr11	135006516	4171948	0.0309	0.29
chr12	133851895	3525100	0.0263	0.2243
chr13	115169878	3247057	0.0282	0.234
chr14	107349540	3062054	0.0285	0.2348
chr15	102531392	2349248	0.0229	0.2132
chr16	90354753	2452948	0.0271	0.2254
chr17	81195210	2079389	0.0256	0.2279
chr18	78077248	2366679	0.0303	0.3374
chr19	59128983	1917809	0.0324	0.2561
chr20	63025520	2261005	0.0359	0.2659
chr21	48129895	1325026	0.0275	0.2298
chr22	51304566	808043	0.0157	0.1698
chrMT	16571	35247	2.127	2.4782
chrX	155270560	3017855	0.0194	0.1943
chrY	59373566	425400	0.0072	0.1191

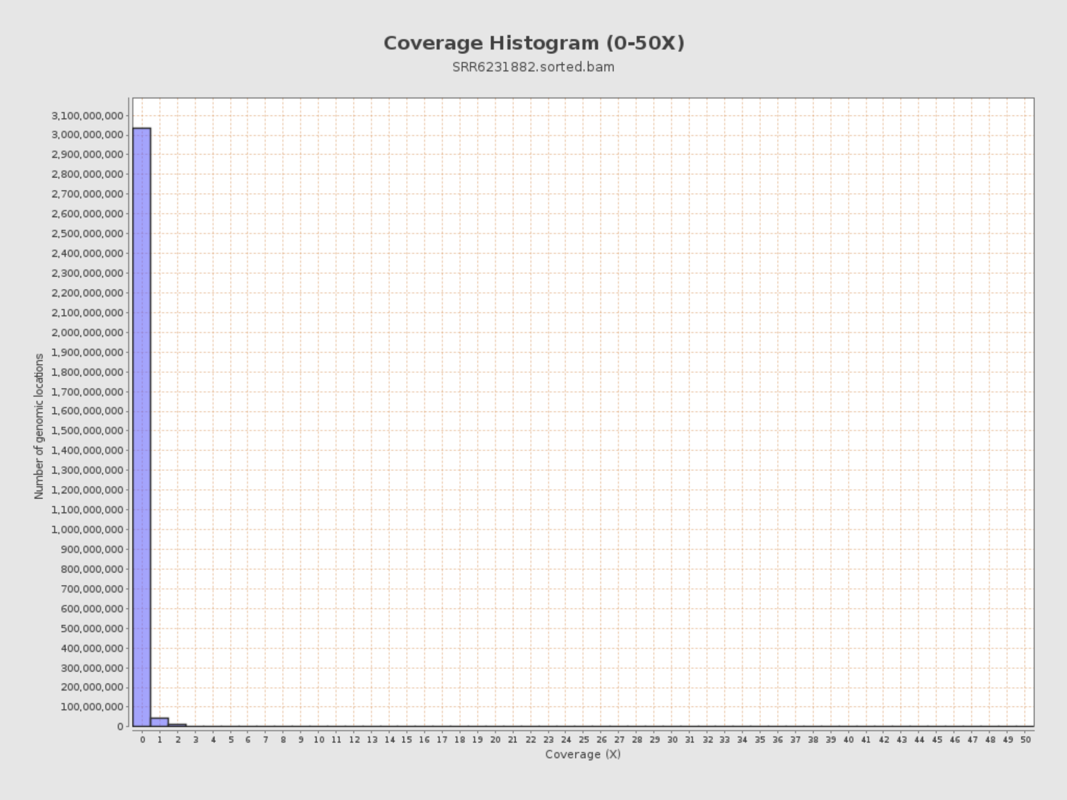
3. Results : Coverage across reference



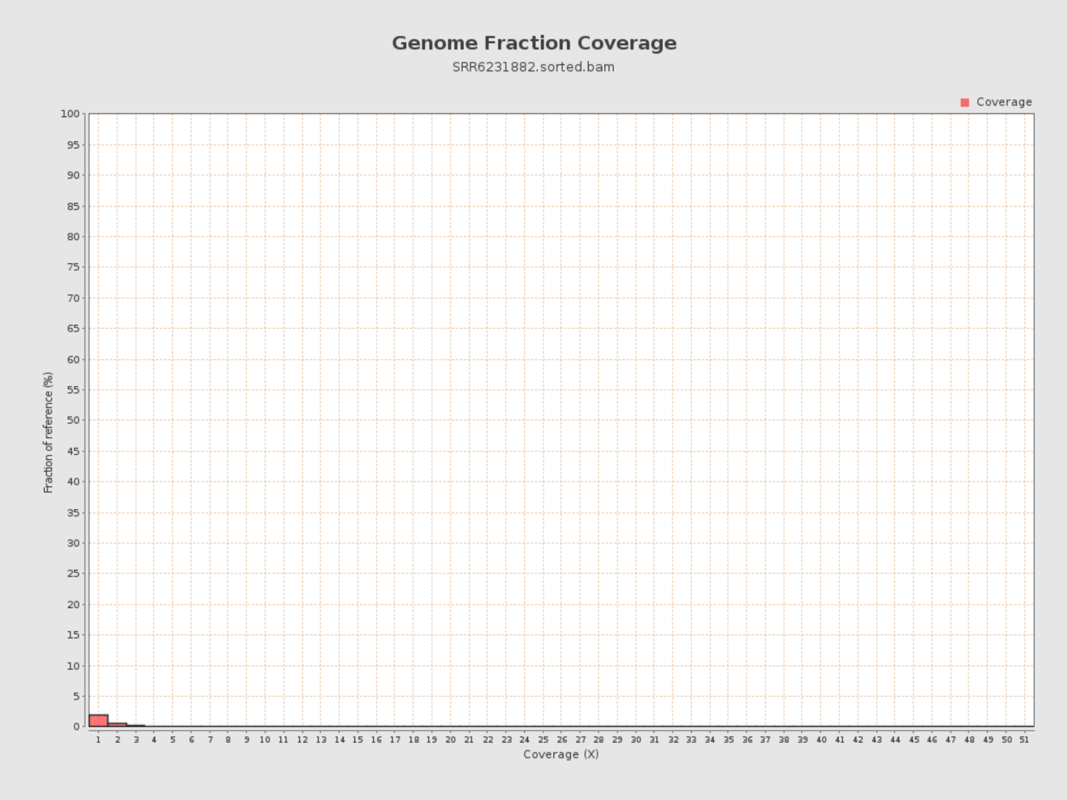
4. Results : Coverage Histogram



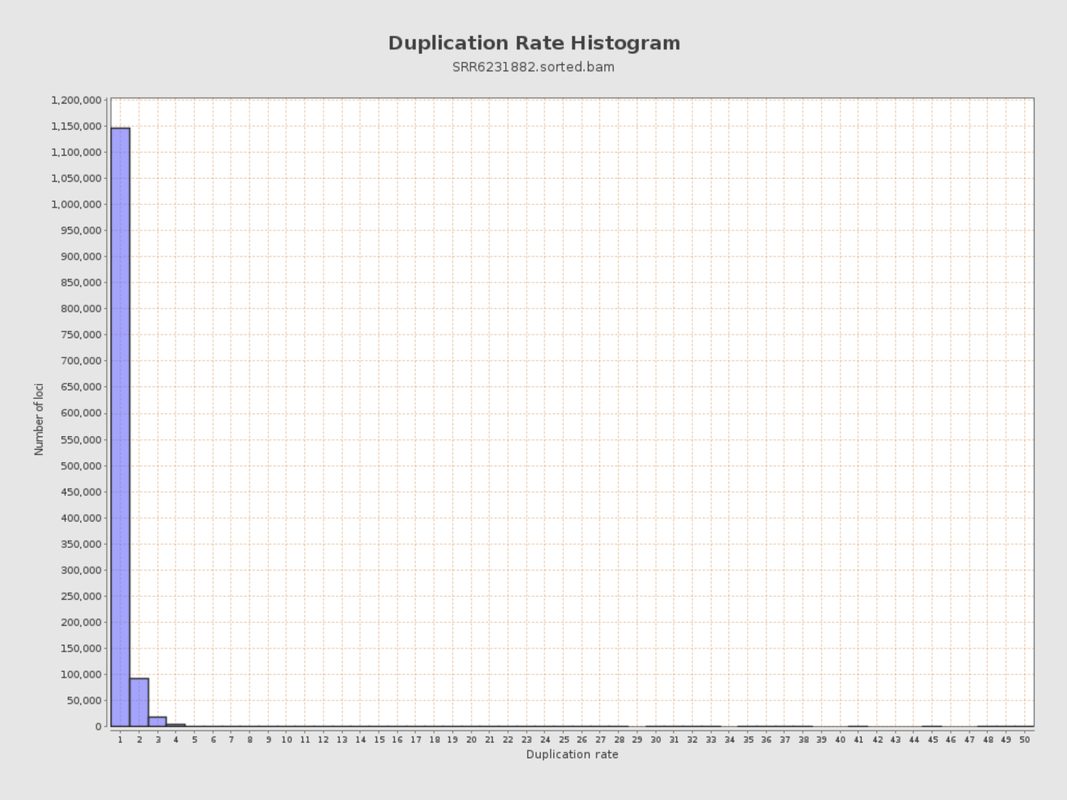
5. Results : Coverage Histogram (0-50X)



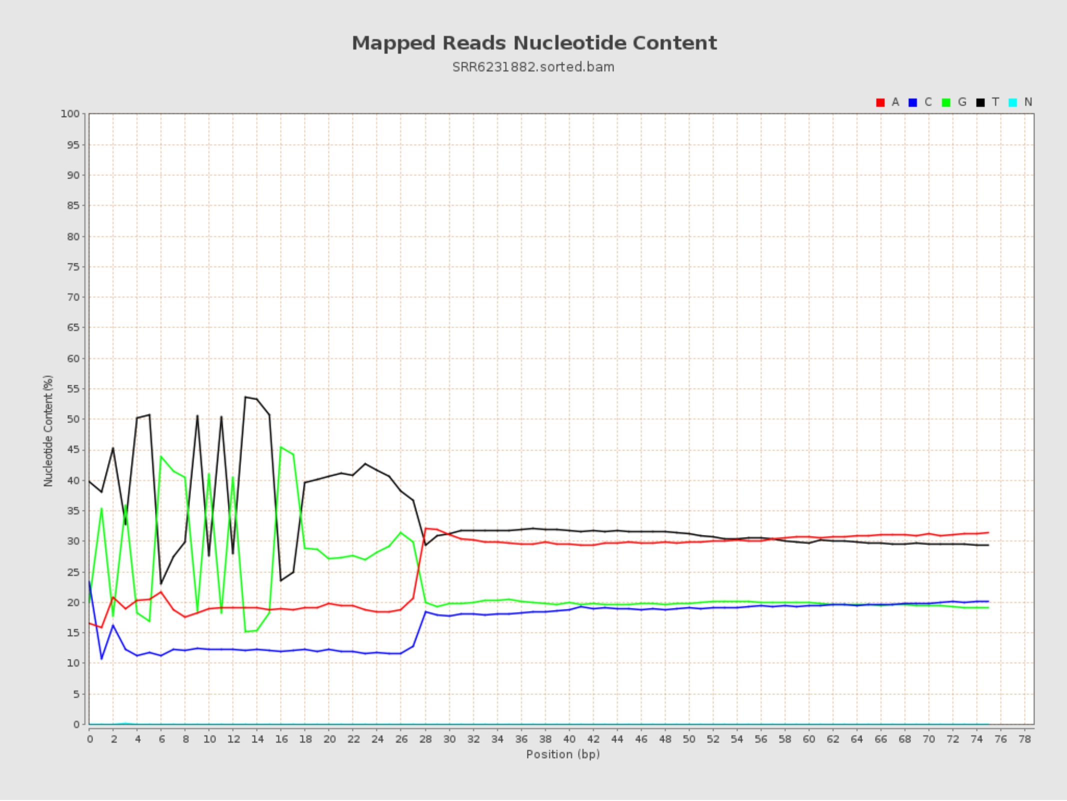
6. Results : Genome Fraction Coverage



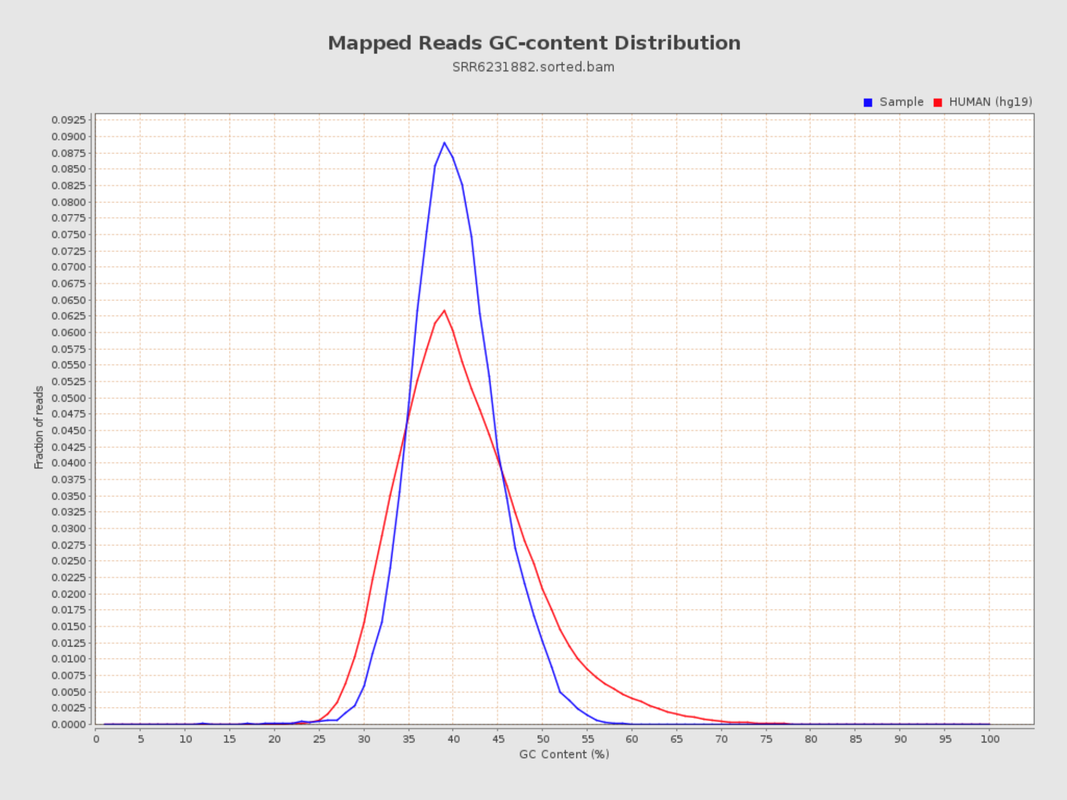
7. Results : Duplication Rate Histogram



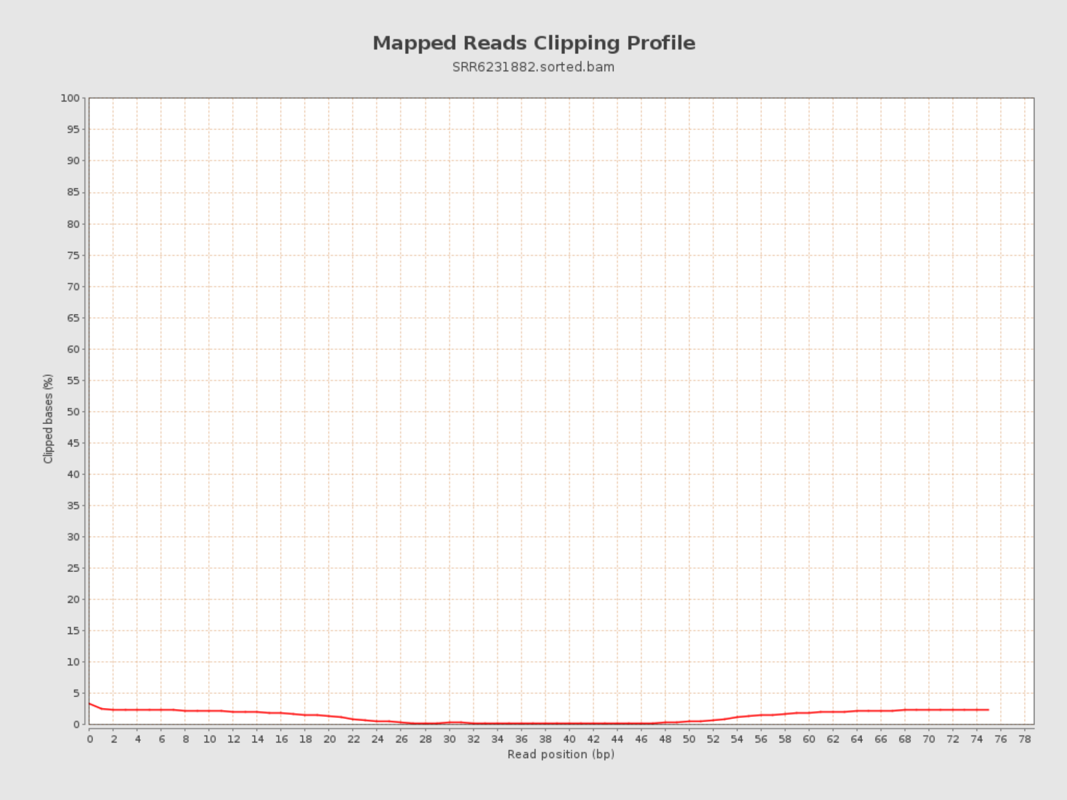
8. Results : Mapped Reads Nucleotide Content



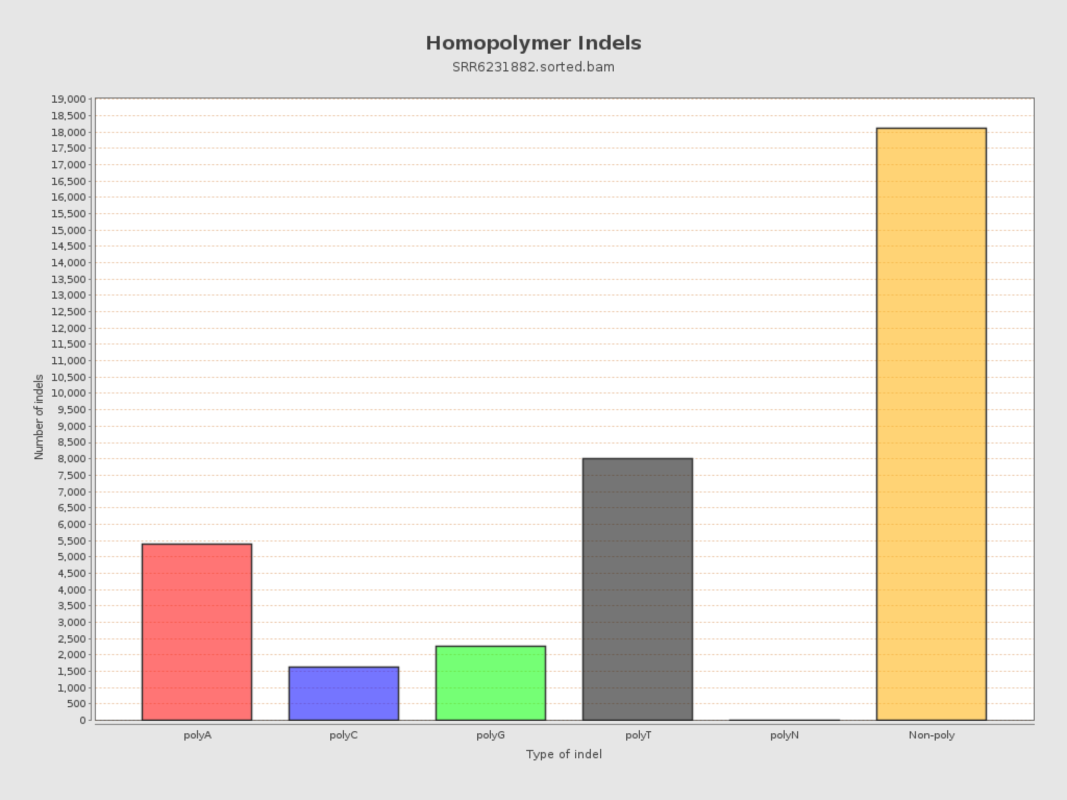
9. Results : Mapped Reads GC-content Distribution



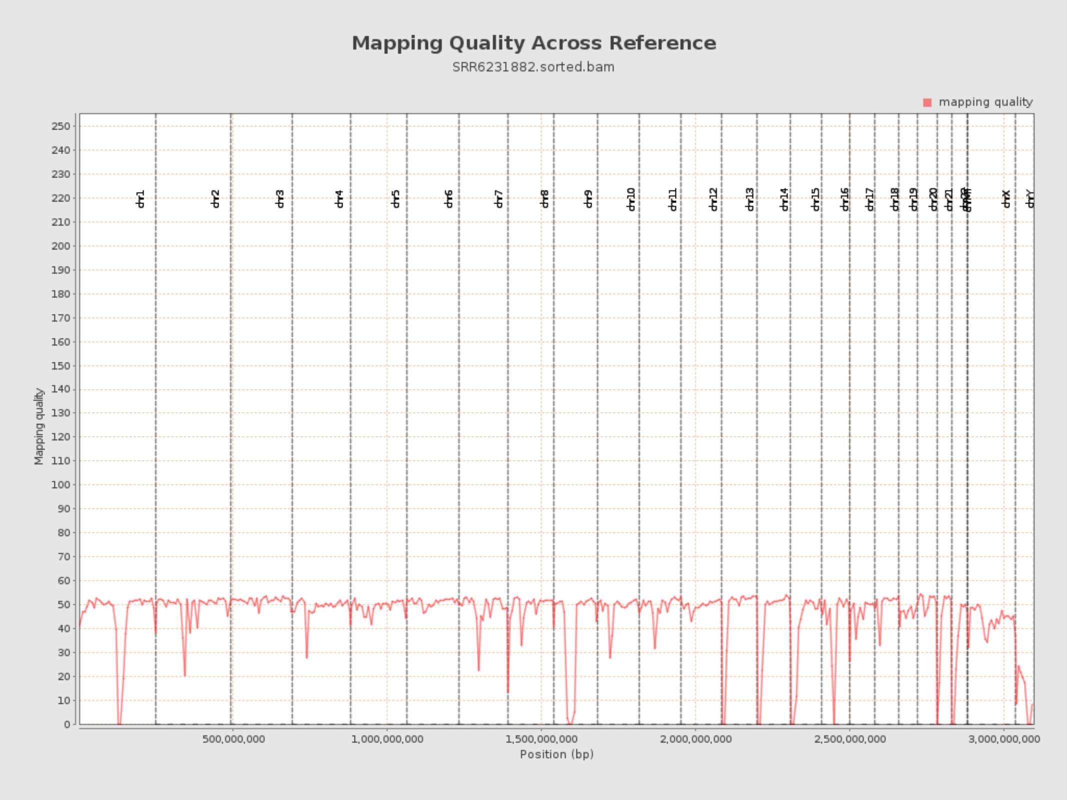
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram