Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 04:42:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231810.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_SRR6231810 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231810.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 04:42:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231810.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,667,232
Mapped reads	4,904,572 / 86.54%
Unmapped reads	762,660 / 13.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	36,451 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	666,779 / 11.77%
Duplication rate	11.55%
Clipped reads	2,631,827 / 46.44%

2.2. ACGT Content

Number/percentage of A's	82,105,741 / 26.09%
Number/percentage of C's	55,844,073 / 17.74%
Number/percentage of T's	103,551,779 / 32.9%
Number/percentage of G's	73,097,983 / 23.23%
Number/percentage of N's	121,550 / 0.04%
GC Percentage	40.97%

2.3. Coverage

Mean	0.1017

Standard Deviation	0.9087

2.4. Mapping Quality

Mean Mapping Quality	45.46

2.5. Mismatches and indels

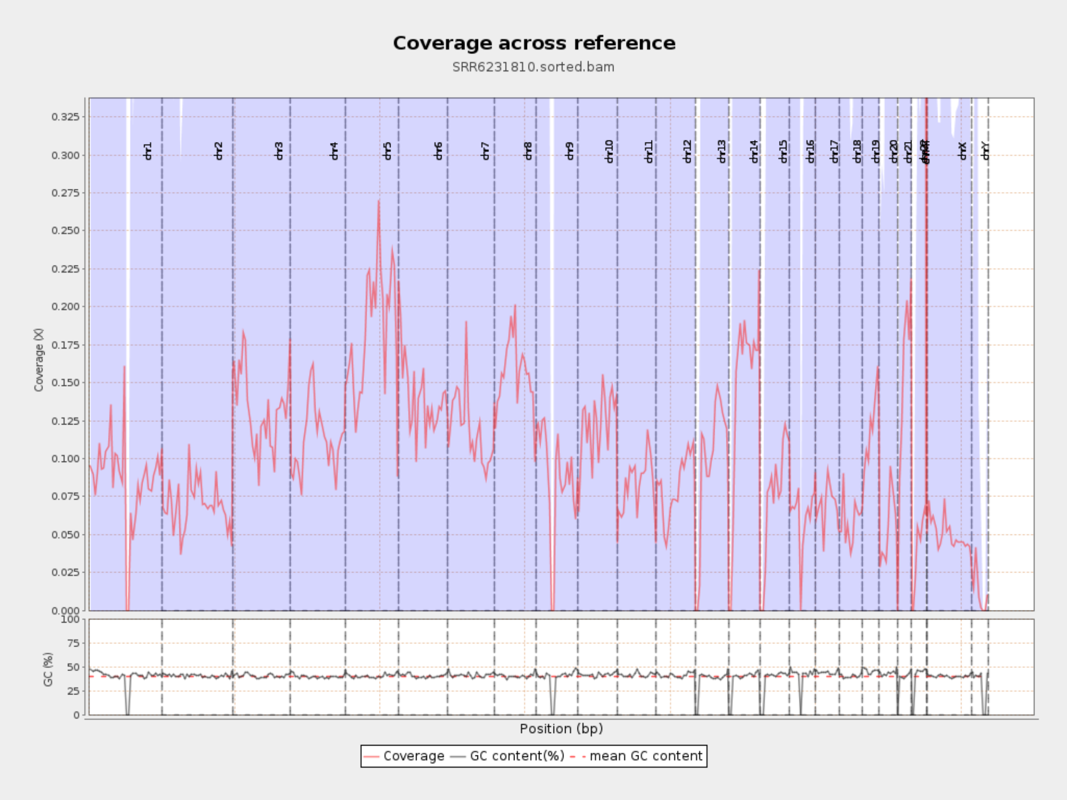
General error rate	0.61%
Mismatches	1,896,429
Insertions	20,301
Mapped reads with at least one insertion	0.41%
Deletions	67,431
Mapped reads with at least one deletion	1.36%
Homopolymer indels	44.52%

2.6. Chromosome stats

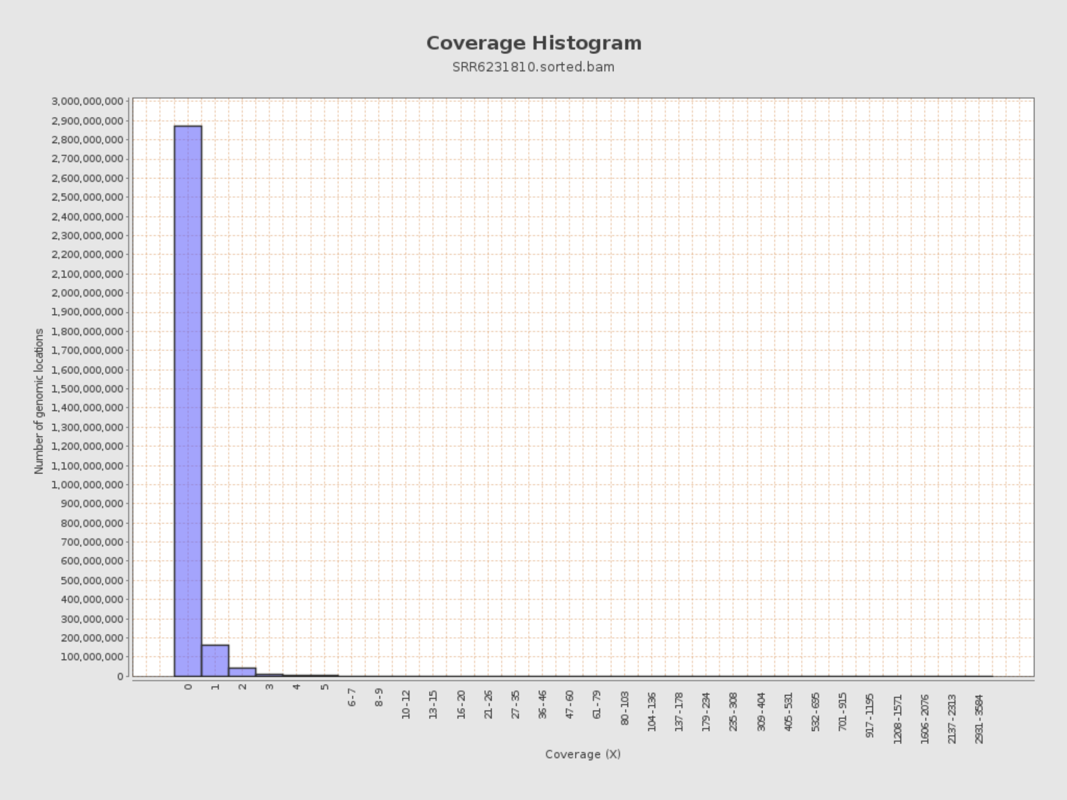
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21479315	0.0862	1.5455
chr2	243199373	16850021	0.0693	1.6179
chr3	198022430	26093126	0.1318	0.4842
chr4	191154276	21561429	0.1128	0.4831
chr5	180915260	33472754	0.185	0.5832
chr6	171115067	24150001	0.1411	0.7664
chr7	159138663	19011811	0.1195	1.1787

chr8	146364022	22859705	0.1562	1.4654
chr9	141213431	12175138	0.0862	0.5757
chr10	135534747	16609076	0.1225	0.6574
chr11	135006516	11178964	0.0828	0.5772
chr12	133851895	10994646	0.0821	0.4068
chr13	115169878	11244454	0.0976	0.4628
chr14	107349540	15398394	0.1434	0.5393
chr15	102531392	7642368	0.0745	0.4124
chr16	90354753	5561803	0.0616	0.3929
chr17	81195210	5664392	0.0698	0.3956
chr18	78077248	4574543	0.0586	1.3304
chr19	59128983	6965004	0.1178	0.9909
chr20	63025520	3399368	0.0539	0.3557
chr21	48129895	7049645	0.1465	0.5375
chr22	51304566	2057306	0.0401	0.2539
chrMT	16571	347070	20.9444	12.3526
chrX	155270560	7804543	0.0503	0.3825
chrY	59373566	693244	0.0117	0.2835

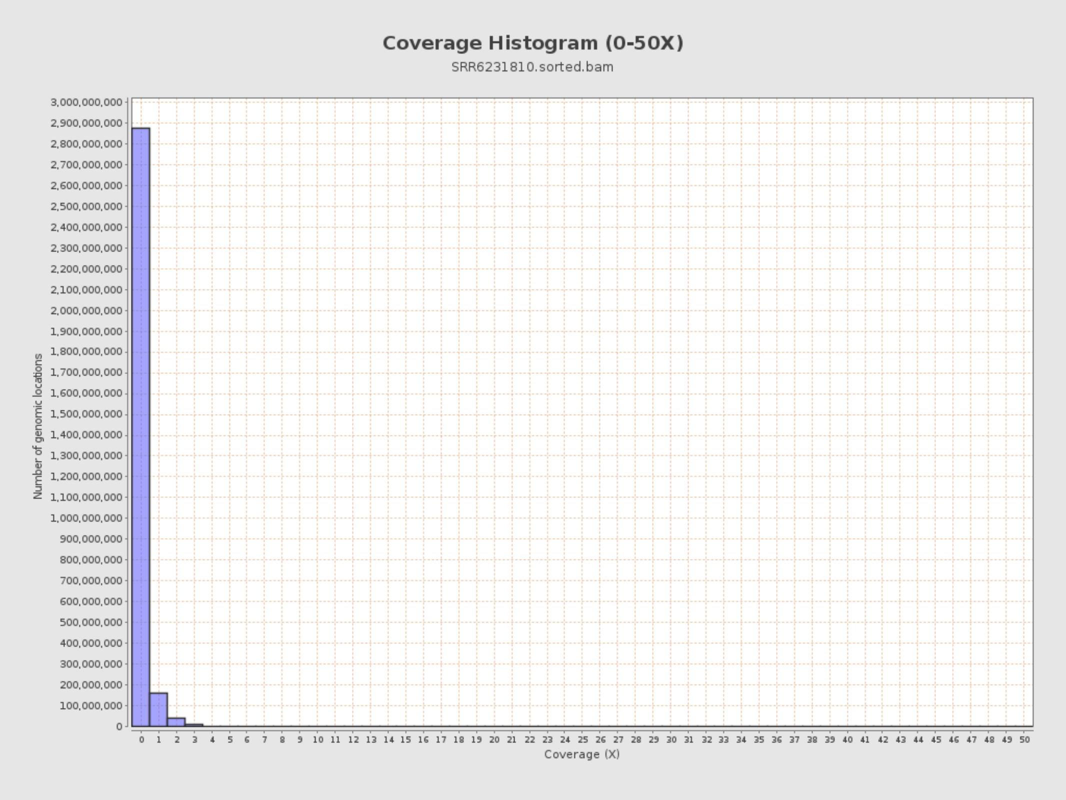
3. Results : Coverage across reference



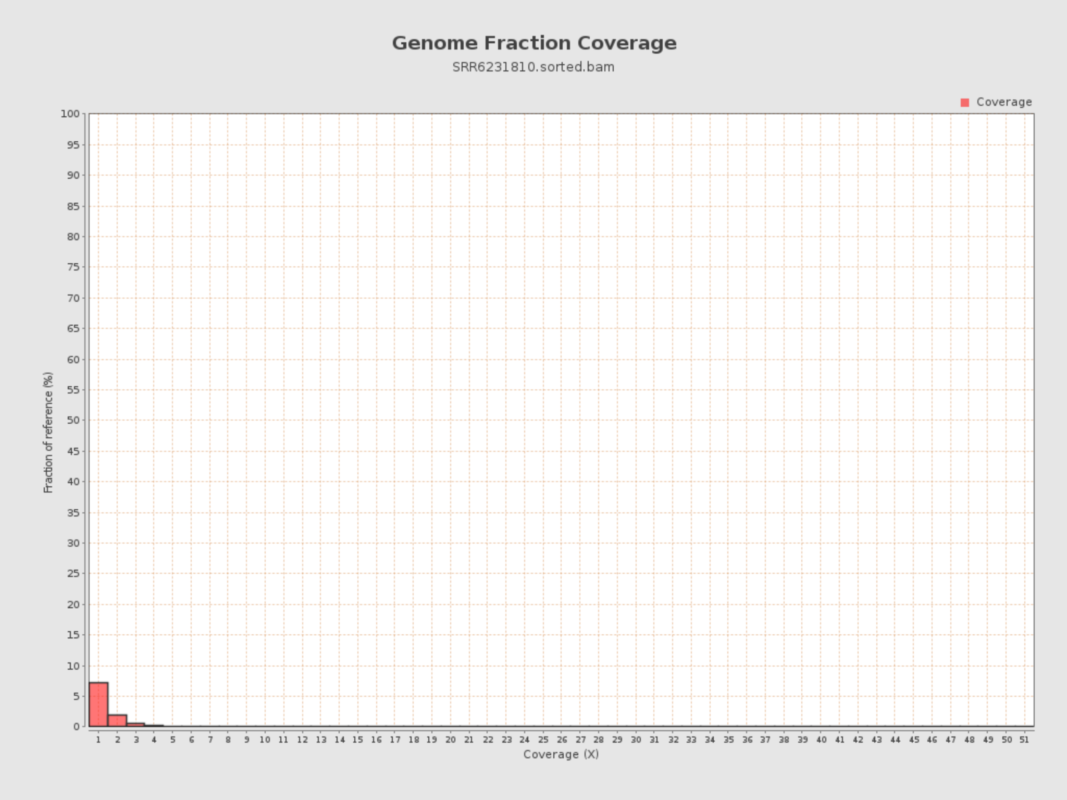
4. Results : Coverage Histogram



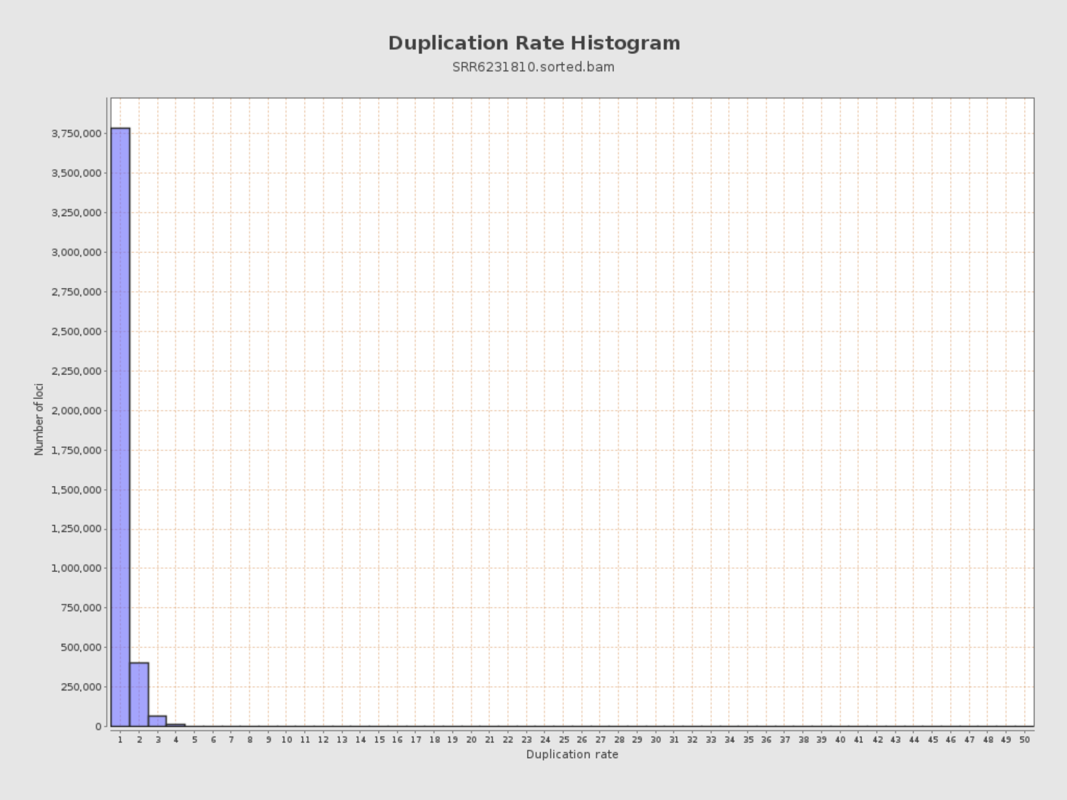
5. Results : Coverage Histogram (0-50X)



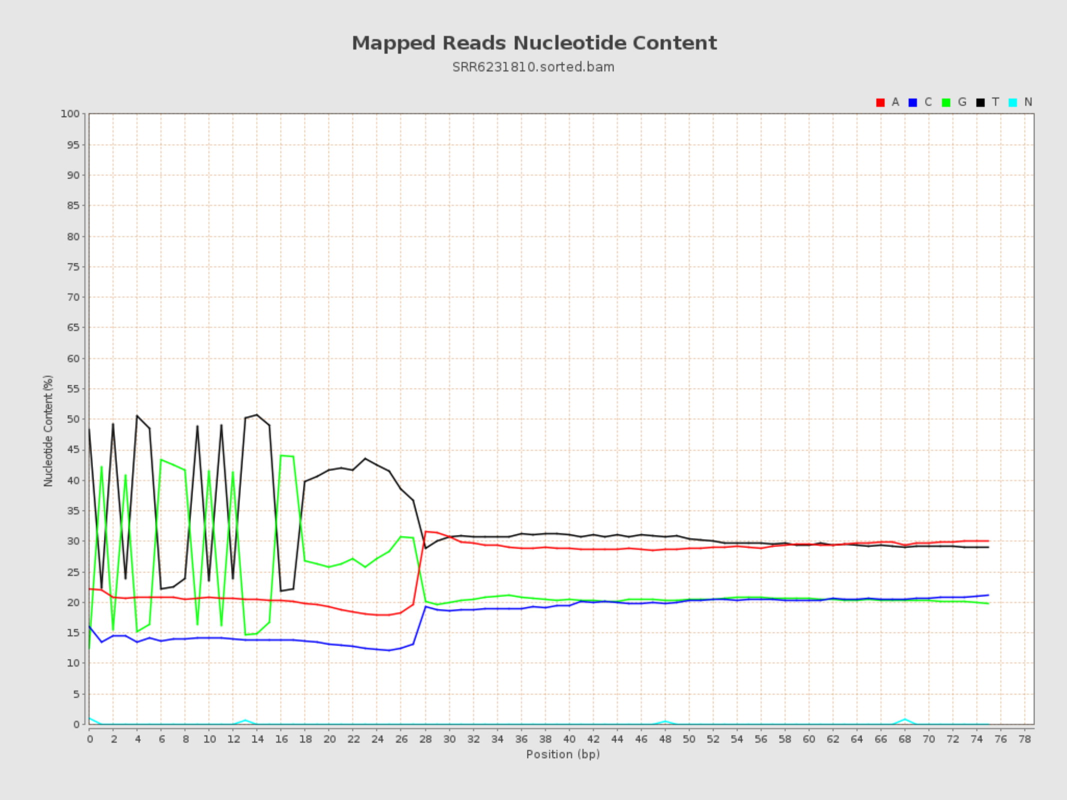
6. Results : Genome Fraction Coverage



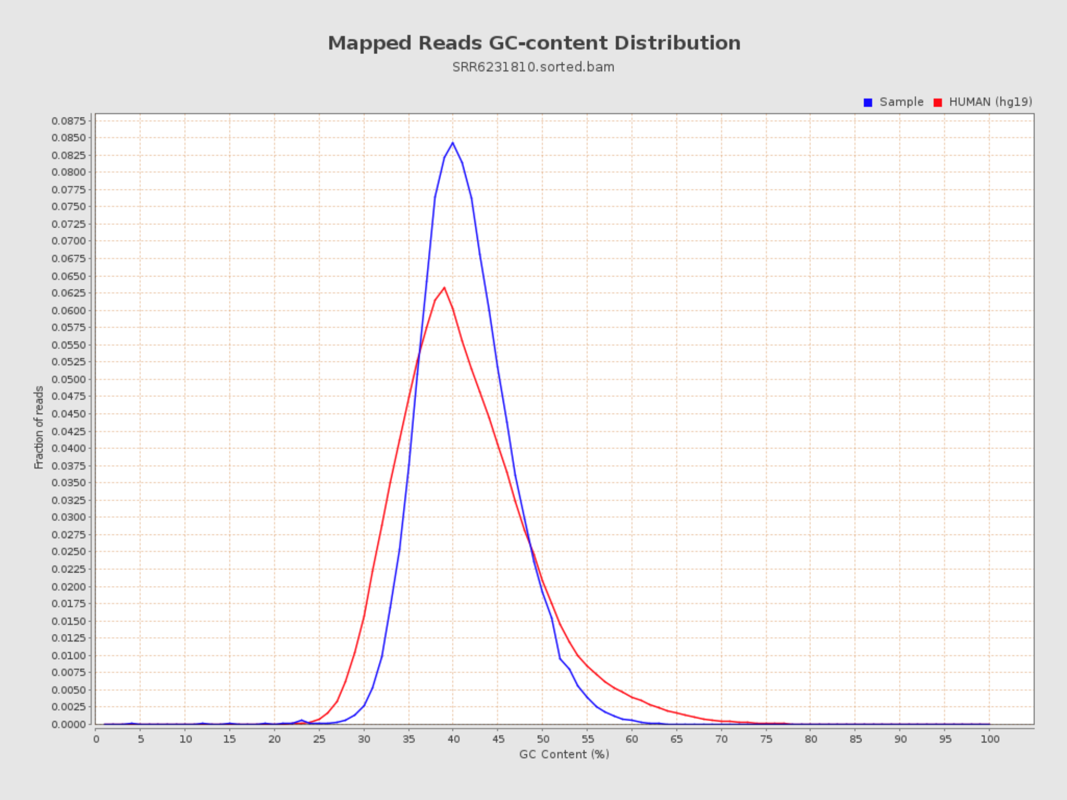
7. Results : Duplication Rate Histogram



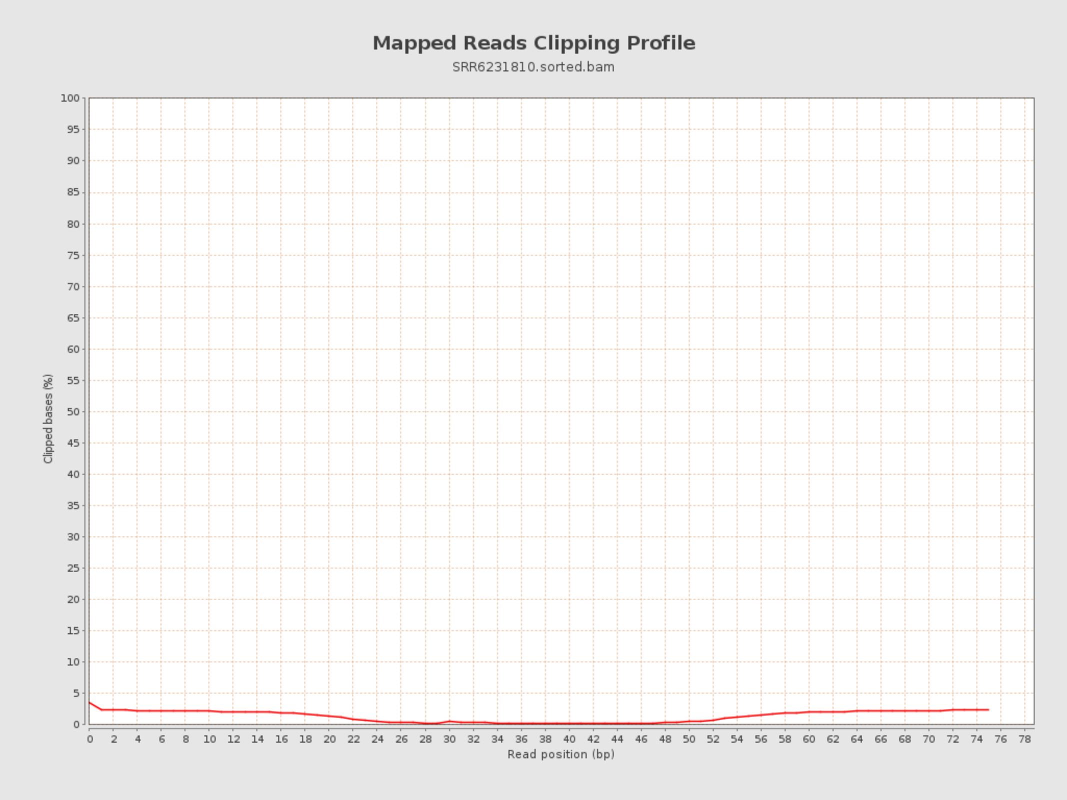
8. Results : Mapped Reads Nucleotide Content



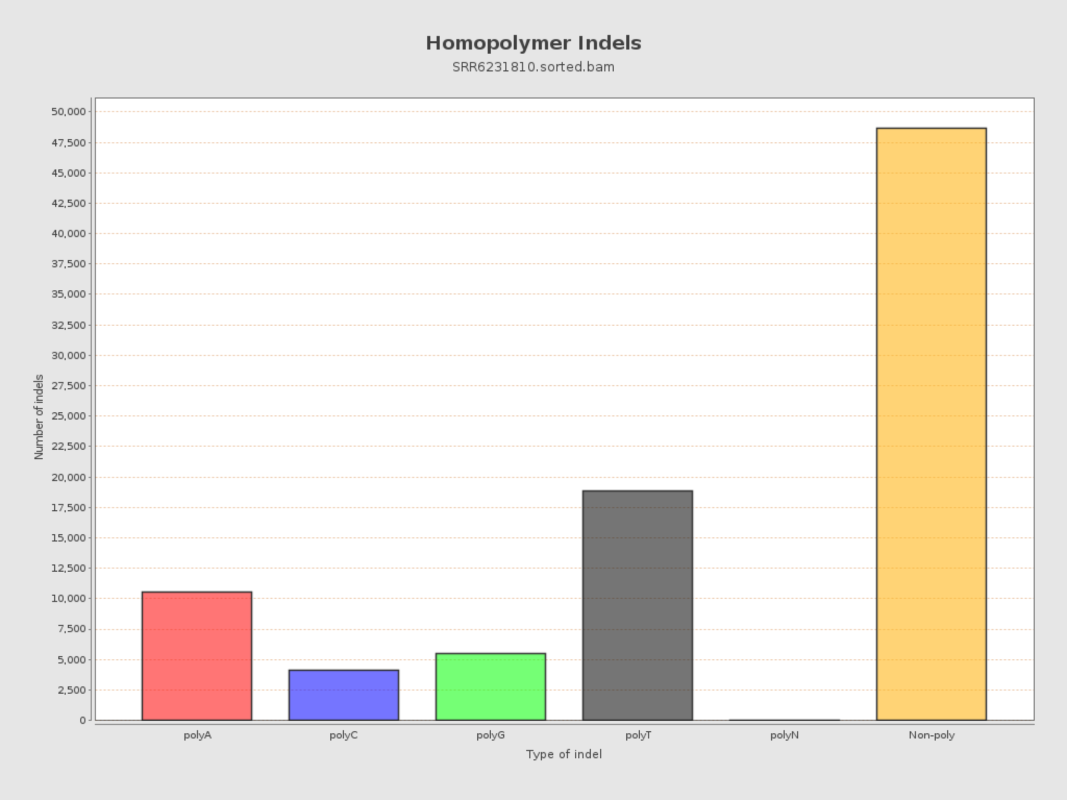
9. Results : Mapped Reads GC-content Distribution



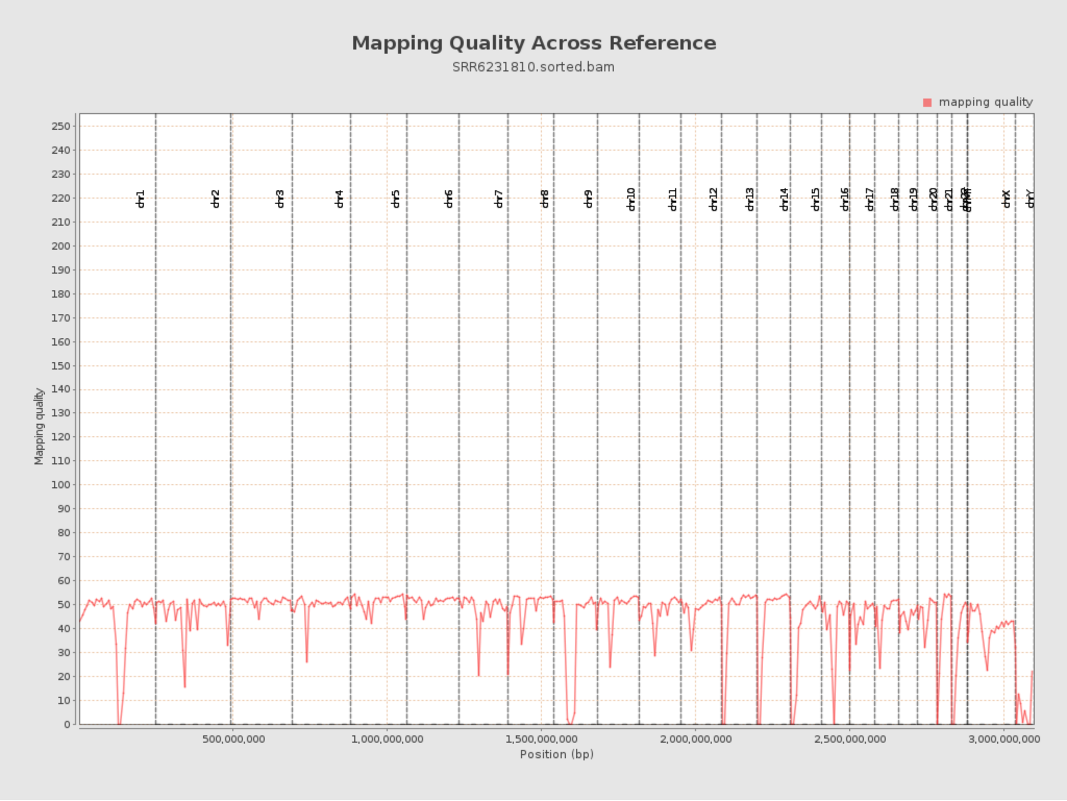
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram