Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 03:53:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231803.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_SRR6231803 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231803.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 03:53:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231803.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,885,687
Mapped reads	2,402,188 / 83.24%
Unmapped reads	483,499 / 16.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,966 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	109,789 / 3.8%
Duplication rate	2.89%
Clipped reads	1,321,550 / 45.8%

2.2. ACGT Content

Number/percentage of A's	45,448,253 / 29.31%
Number/percentage of C's	30,905,852 / 19.93%
Number/percentage of T's	44,612,808 / 28.77%
Number/percentage of G's	34,070,022 / 21.97%
Number/percentage of N's	11,188 / 0.01%
GC Percentage	41.91%

2.3. Coverage

Mean	0.0501

Standard Deviation	3.3262

2.4. Mapping Quality

Mean Mapping Quality	45.02

2.5. Mismatches and indels

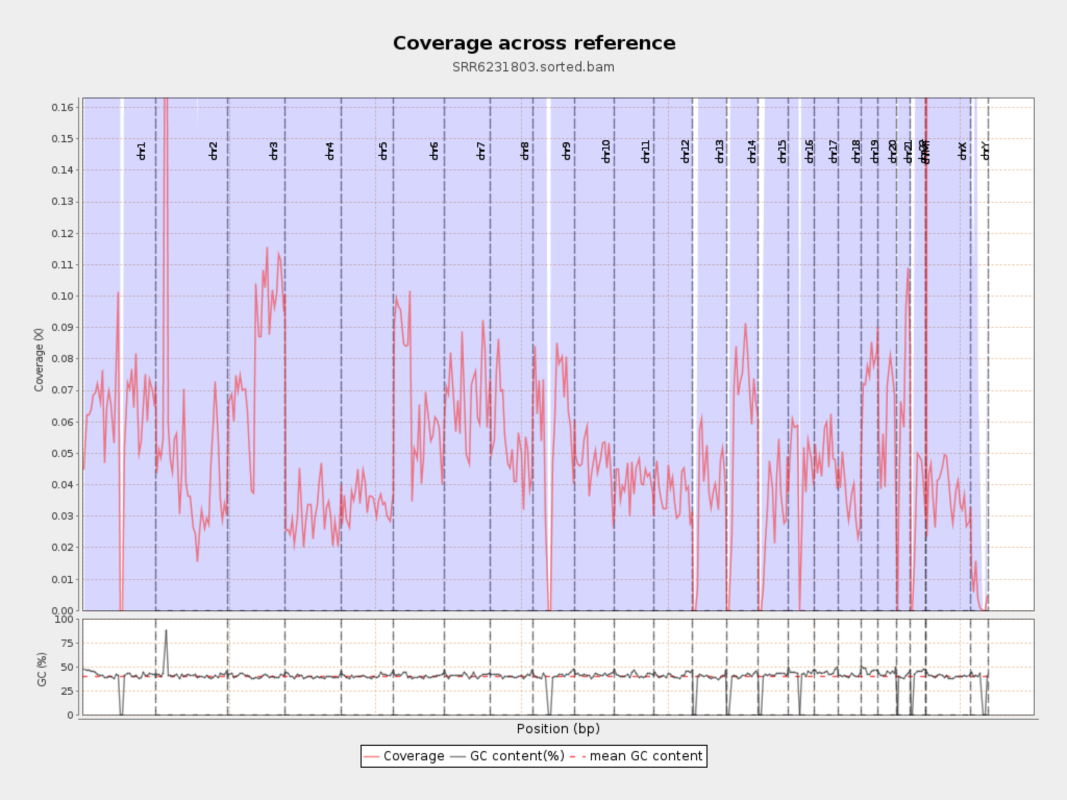
General error rate	0.59%
Mismatches	889,113
Insertions	10,938
Mapped reads with at least one insertion	0.45%
Deletions	36,569
Mapped reads with at least one deletion	1.51%
Homopolymer indels	45.27%

2.6. Chromosome stats

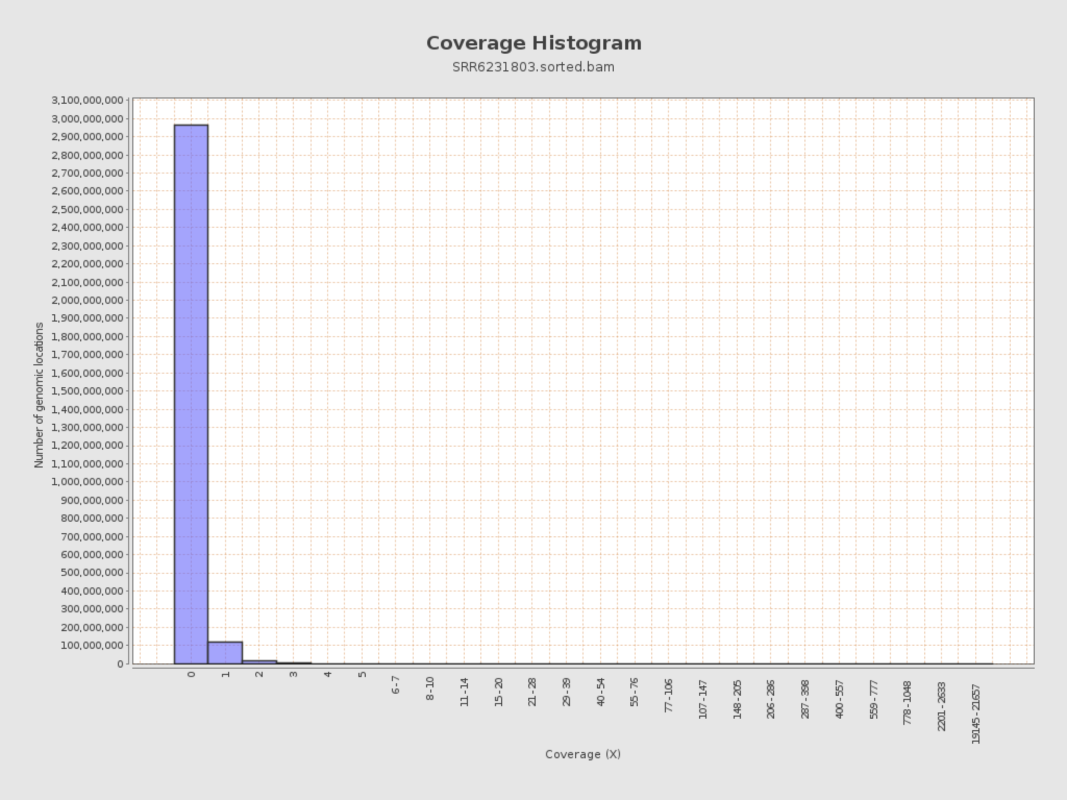
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15548366	0.0624	0.8535
chr2	243199373	11943715	0.0491	11.7839
chr3	198022430	16215284	0.0819	0.3211
chr4	191154276	5717230	0.0299	0.2098
chr5	180915260	6287259	0.0348	0.2112
chr6	171115067	11458839	0.067	0.3335
chr7	159138663	10894665	0.0685	0.5723

chr8	146364022	7830518	0.0535	0.5651
chr9	141213431	8165613	0.0578	0.3349
chr10	135534747	6432119	0.0475	0.3345
chr11	135006516	5569883	0.0413	0.2925
chr12	133851895	5054599	0.0378	0.2206
chr13	115169878	4263721	0.037	0.2142
chr14	107349540	6559905	0.0611	0.2959
chr15	102531392	2918825	0.0285	0.1889
chr16	90354753	3970144	0.0439	0.2574
chr17	81195210	4095256	0.0504	0.2657
chr18	78077248	2810145	0.036	0.5477
chr19	59128983	4522126	0.0765	0.5279
chr20	63025520	3776573	0.0599	0.2785
chr21	48129895	3208734	0.0667	0.2985
chr22	51304566	1608376	0.0313	0.1953
chrMT	16571	161971	9.7744	6.386
chrX	155270560	5787830	0.0373	0.2329
chrY	59373566	307671	0.0052	0.1117

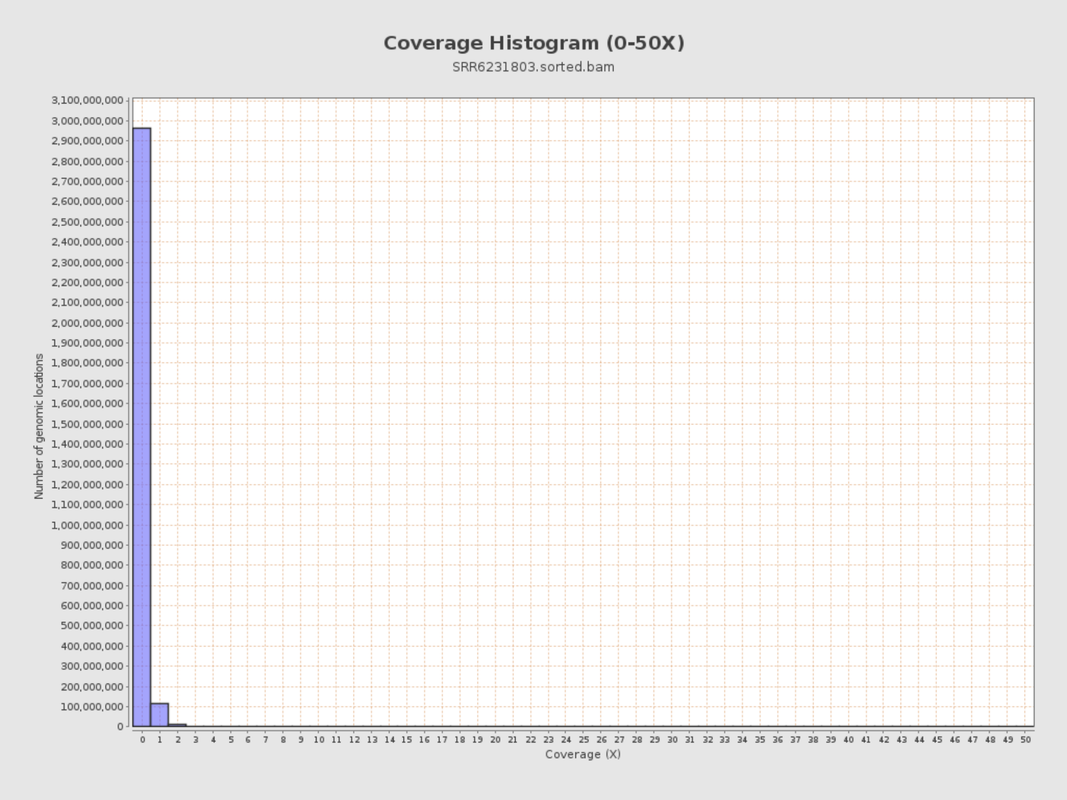
3. Results : Coverage across reference



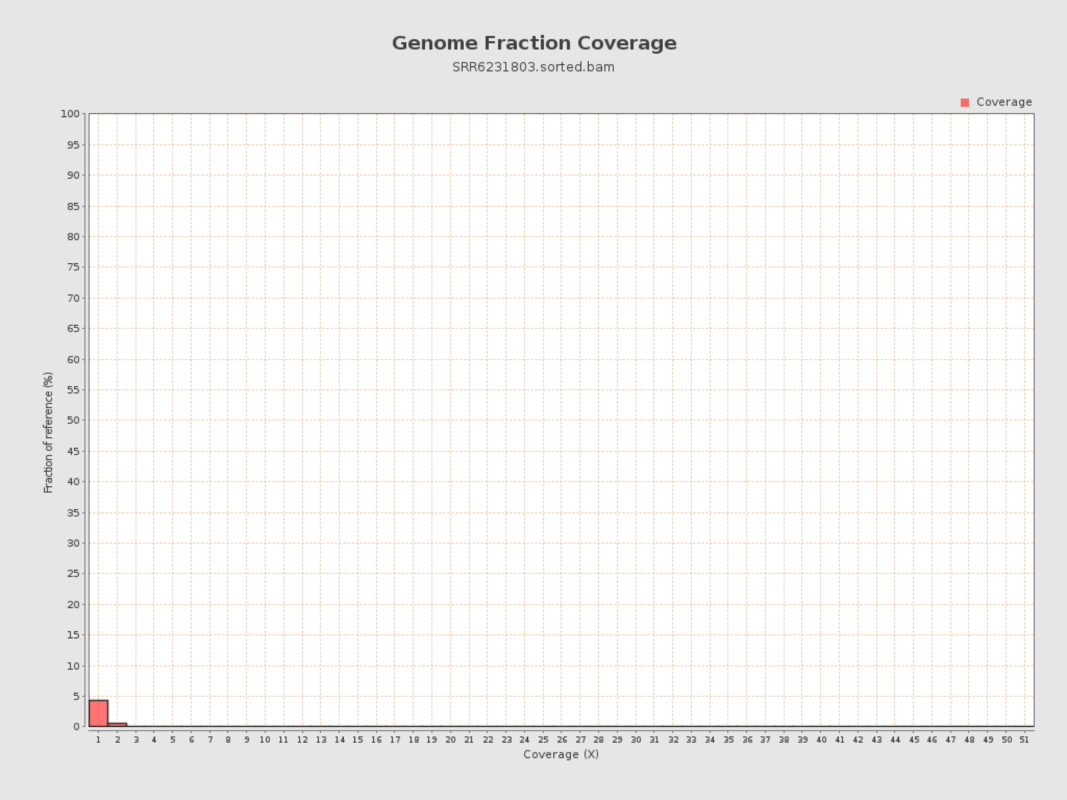
4. Results : Coverage Histogram



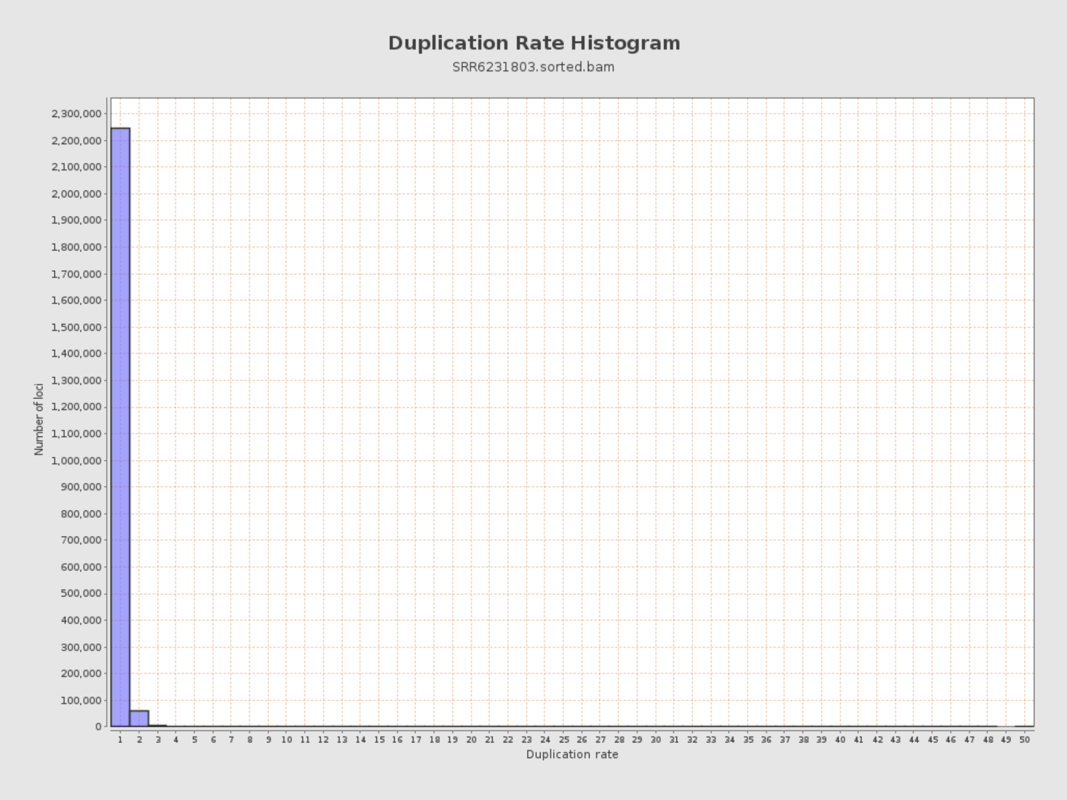
5. Results : Coverage Histogram (0-50X)



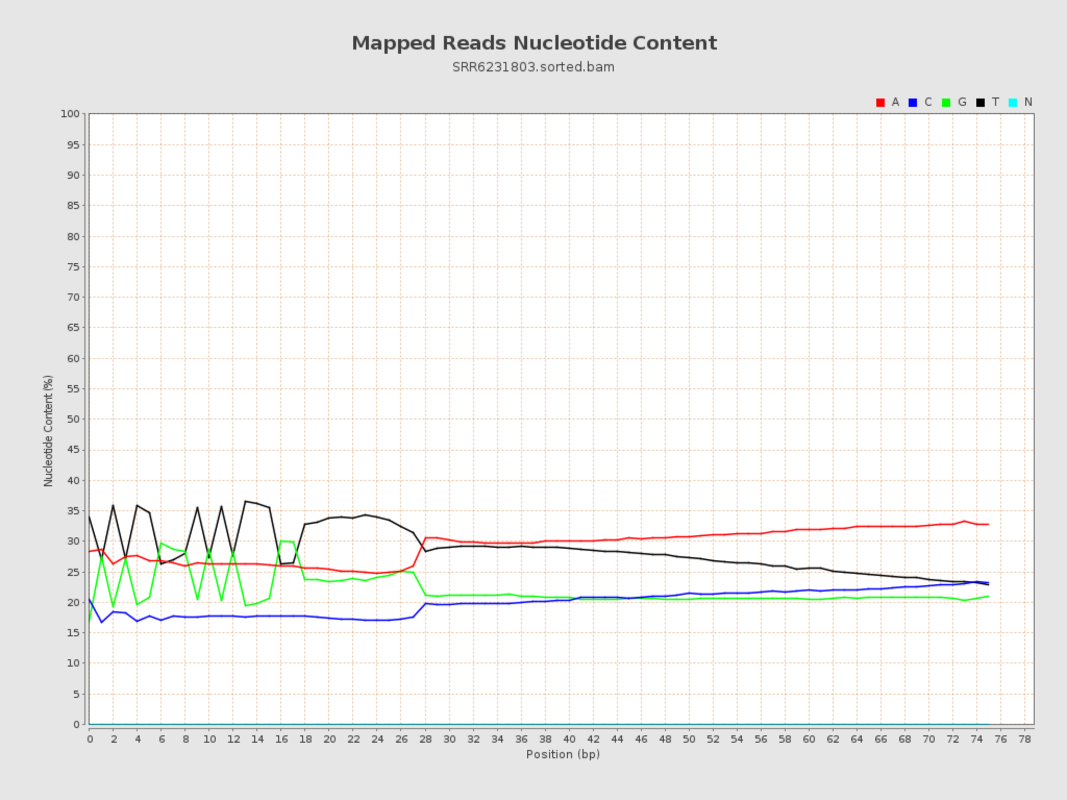
6. Results : Genome Fraction Coverage



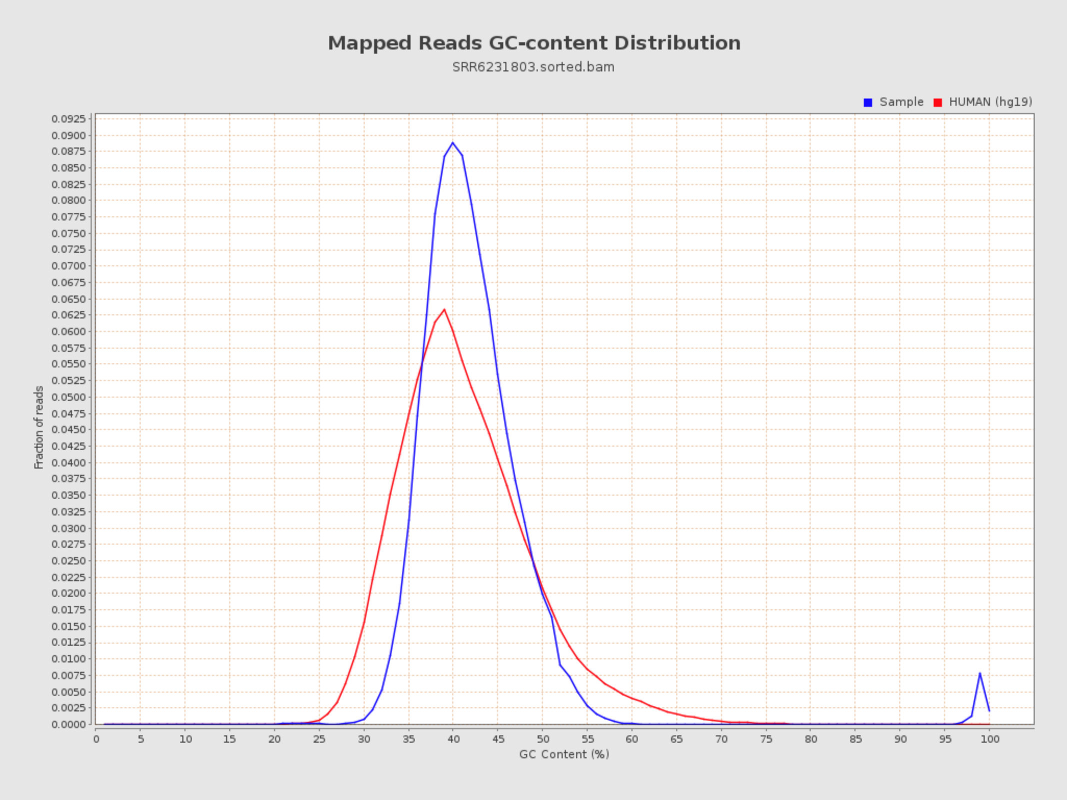
7. Results : Duplication Rate Histogram



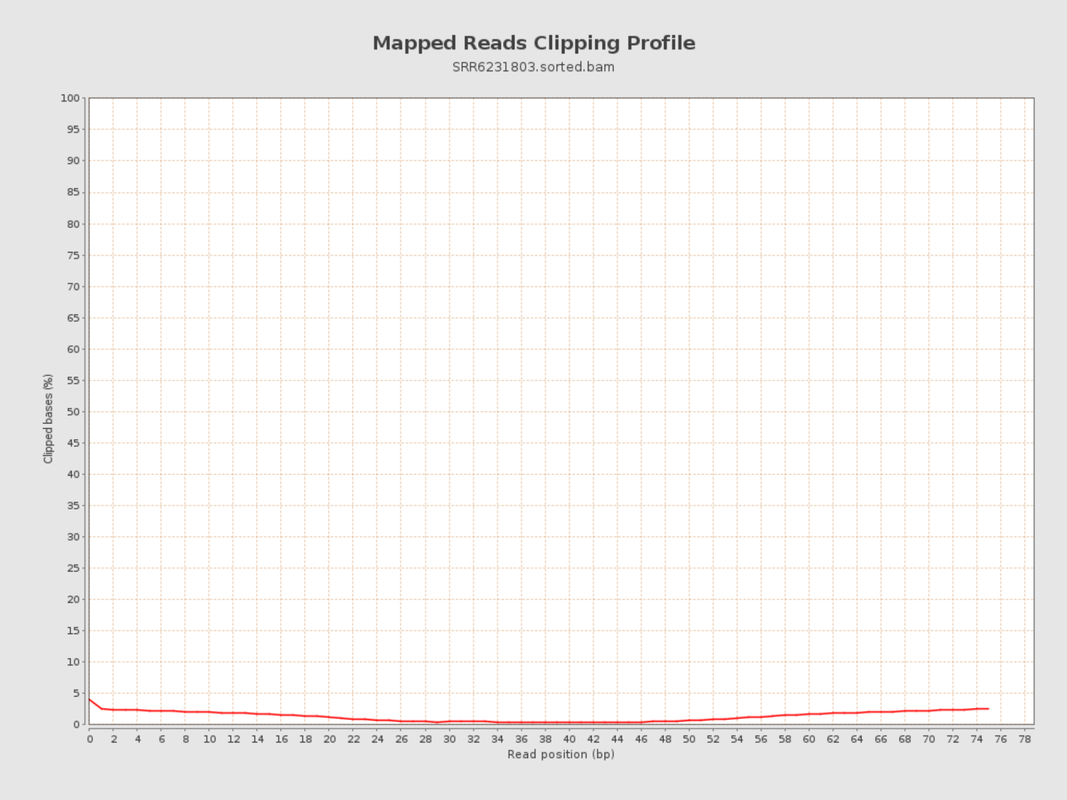
8. Results : Mapped Reads Nucleotide Content



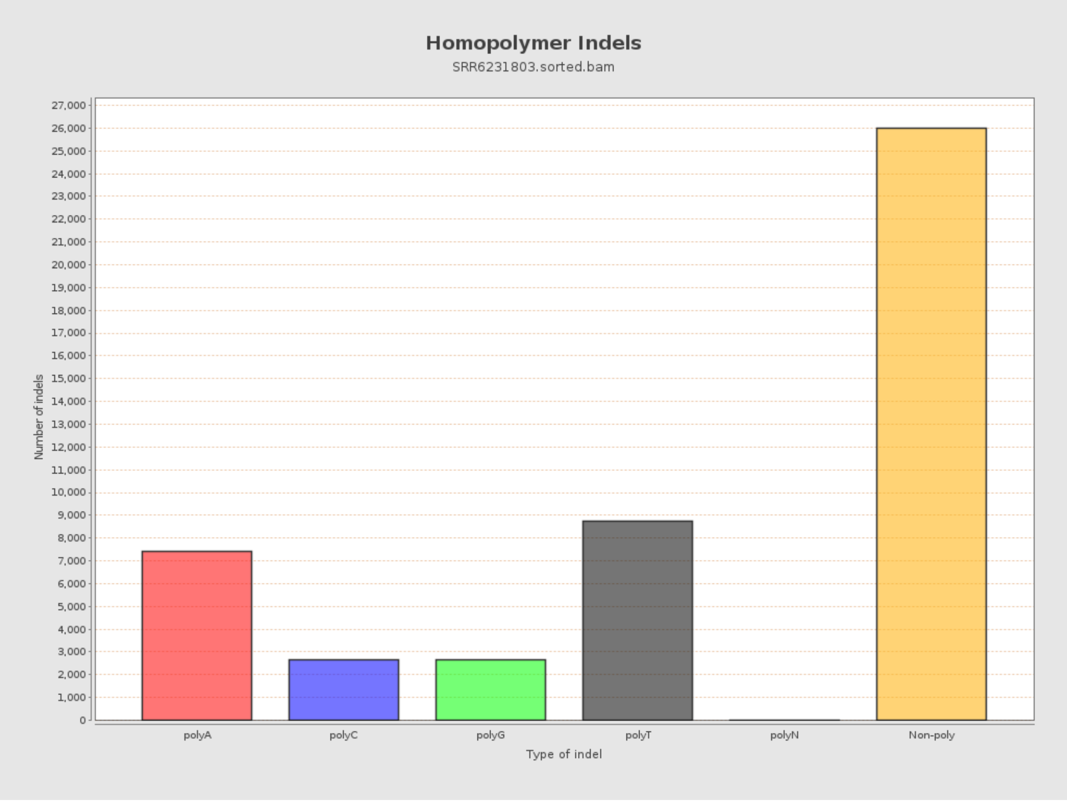
9. Results : Mapped Reads GC-content Distribution



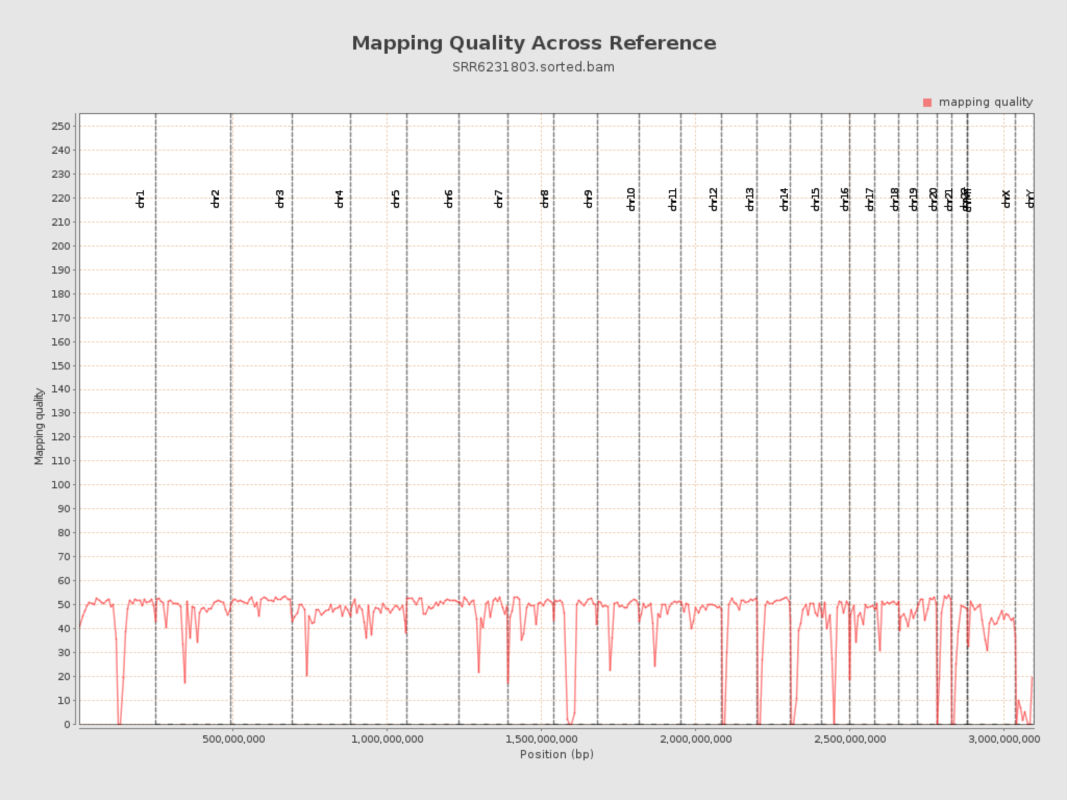
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram