Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 04:33:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231808.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_SRR6231808 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231808.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 04:33:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231808.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,120,015
Mapped reads	3,775,583 / 91.64%
Unmapped reads	344,432 / 8.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,042 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	615,304 / 14.93%
Duplication rate	13.41%
Clipped reads	2,137,995 / 51.89%

2.2. ACGT Content

Number/percentage of A's	61,276,029 / 25.58%
Number/percentage of C's	42,302,861 / 17.66%
Number/percentage of T's	79,272,943 / 33.1%
Number/percentage of G's	56,568,015 / 23.62%
Number/percentage of N's	89,833 / 0.04%
GC Percentage	41.28%

2.3. Coverage

Mean	0.0774

Standard Deviation	0.9278

2.4. Mapping Quality

Mean Mapping Quality	45

2.5. Mismatches and indels

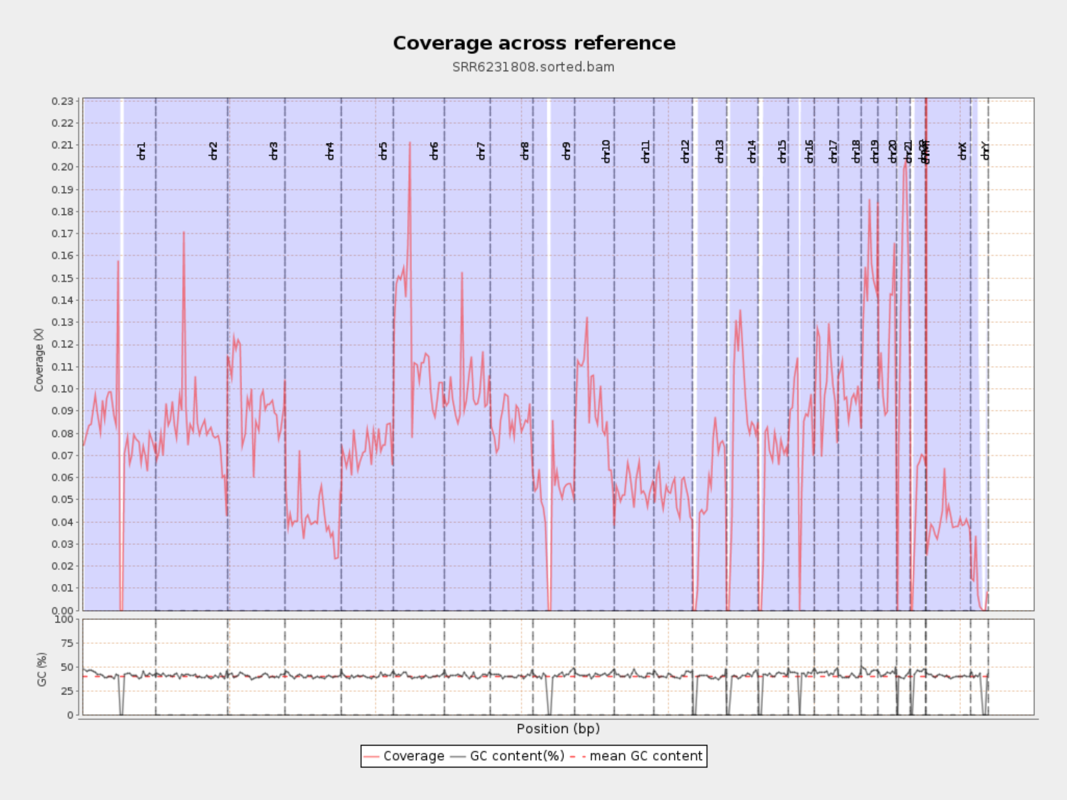
General error rate	0.65%
Mismatches	1,535,884
Insertions	15,885
Mapped reads with at least one insertion	0.42%
Deletions	51,137
Mapped reads with at least one deletion	1.34%
Homopolymer indels	44.09%

2.6. Chromosome stats

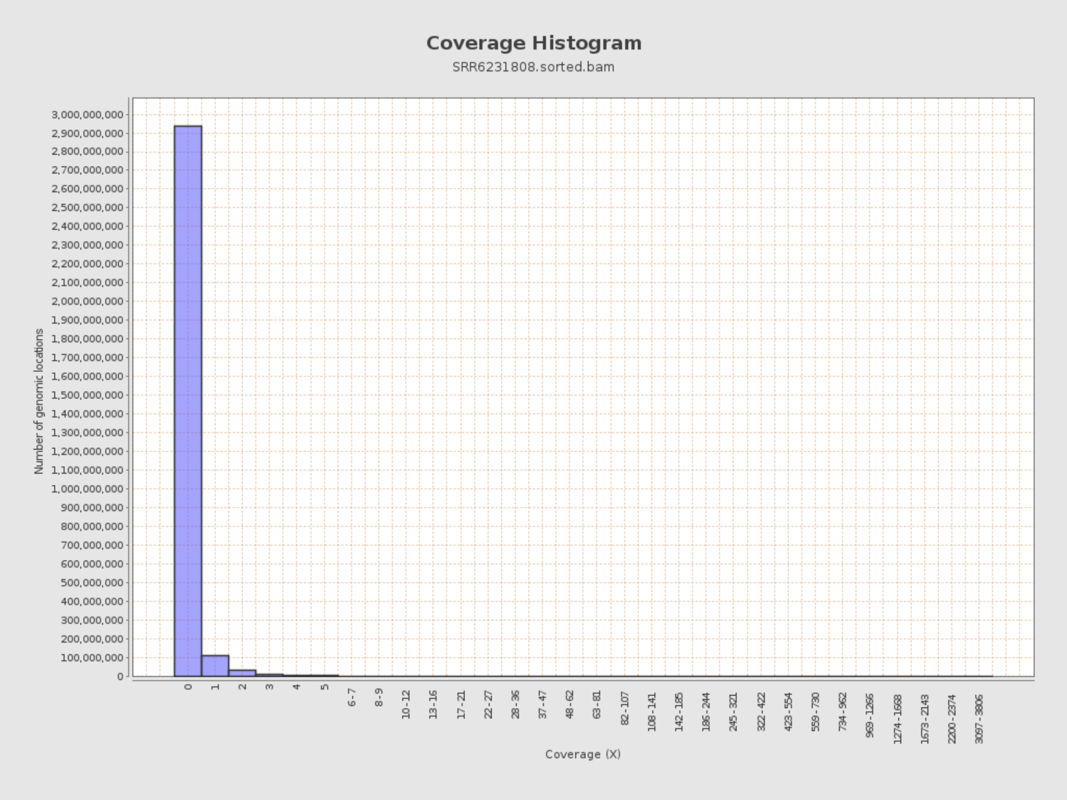
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19495211	0.0782	1.8809
chr2	243199373	20286667	0.0834	1.8078
chr3	198022430	18807596	0.095	0.4382
chr4	191154276	7899652	0.0413	0.3161
chr5	180915260	13237651	0.0732	0.3957
chr6	171115067	20764823	0.1214	0.8863
chr7	159138663	15858728	0.0997	0.997

chr8	146364022	12345611	0.0843	0.7896
chr9	141213431	7065939	0.05	0.5897
chr10	135534747	12626911	0.0932	0.6155
chr11	135006516	7380402	0.0547	0.4778
chr12	133851895	7135095	0.0533	0.3427
chr13	115169878	6038402	0.0524	0.3919
chr14	107349540	9090602	0.0847	0.4268
chr15	102531392	6138794	0.0599	0.4088
chr16	90354753	7244295	0.0802	0.4349
chr17	81195210	8467056	0.1043	0.5263
chr18	78077248	7670228	0.0982	1.3356
chr19	59128983	8820676	0.1492	1.1364
chr20	63025520	7424829	0.1178	0.5007
chr21	48129895	6498764	0.135	0.548
chr22	51304566	2444373	0.0476	0.3006
chrMT	16571	157729	9.5184	6.3613
chrX	155270560	6130918	0.0395	0.3545
chrY	59373566	568497	0.0096	0.2477

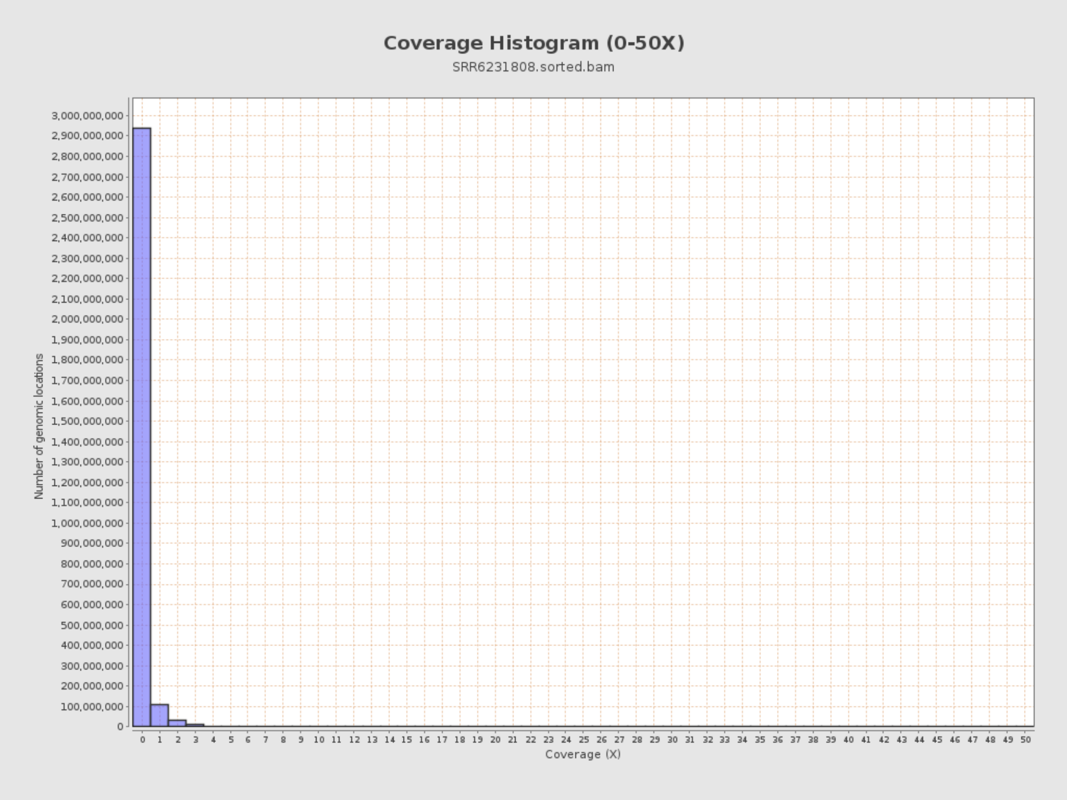
3. Results : Coverage across reference



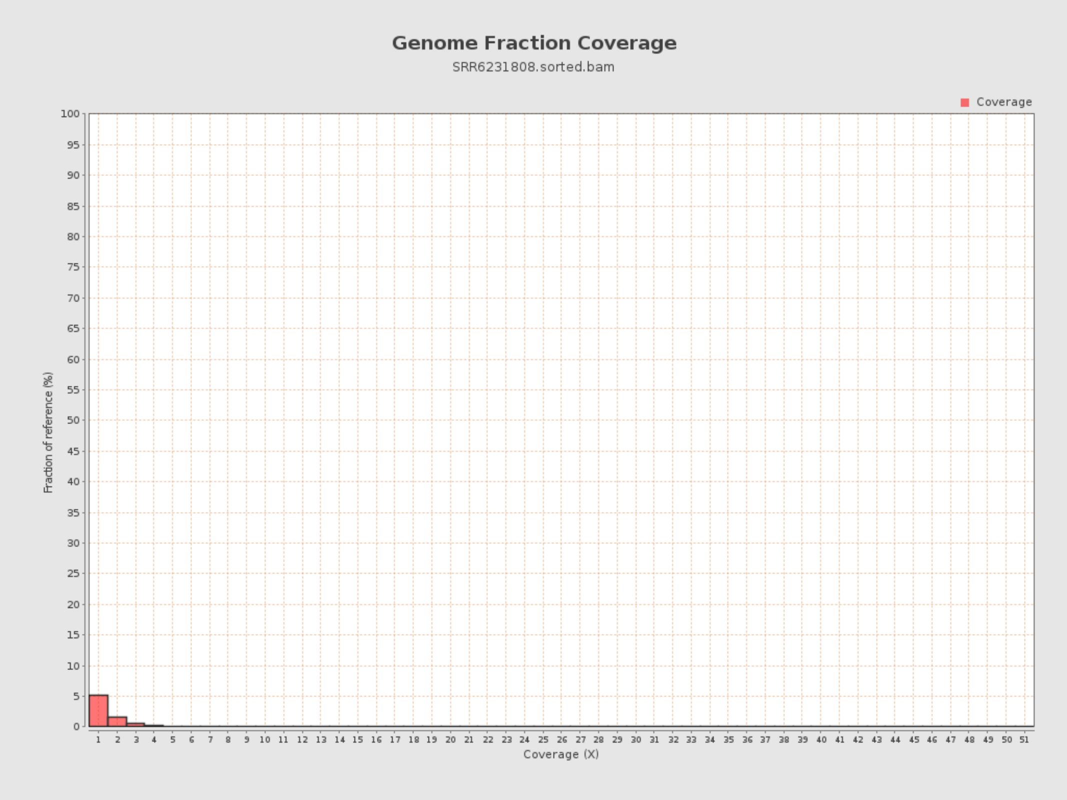
4. Results : Coverage Histogram



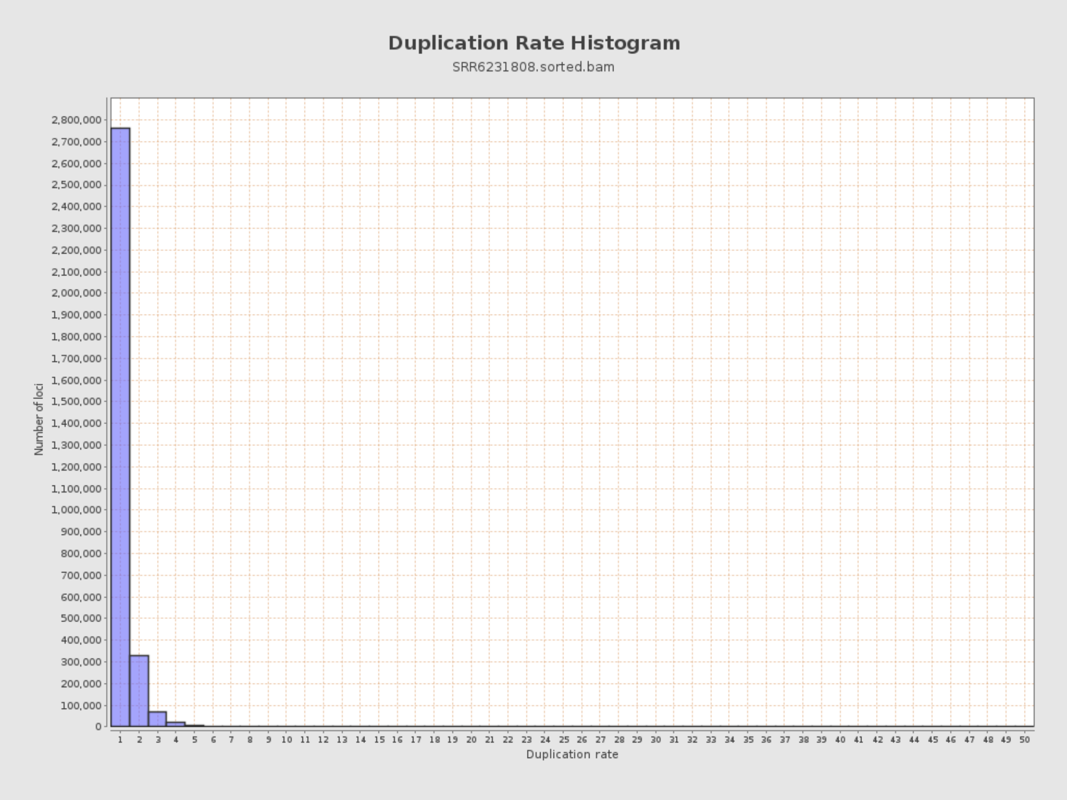
5. Results : Coverage Histogram (0-50X)



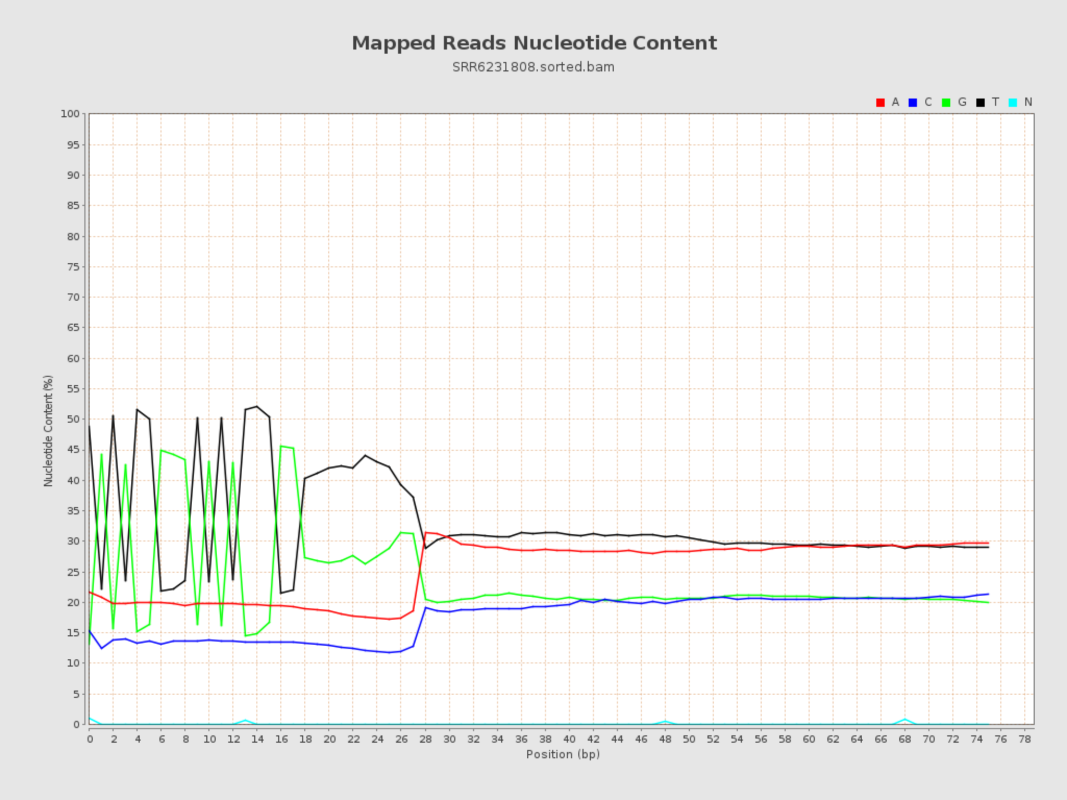
6. Results : Genome Fraction Coverage



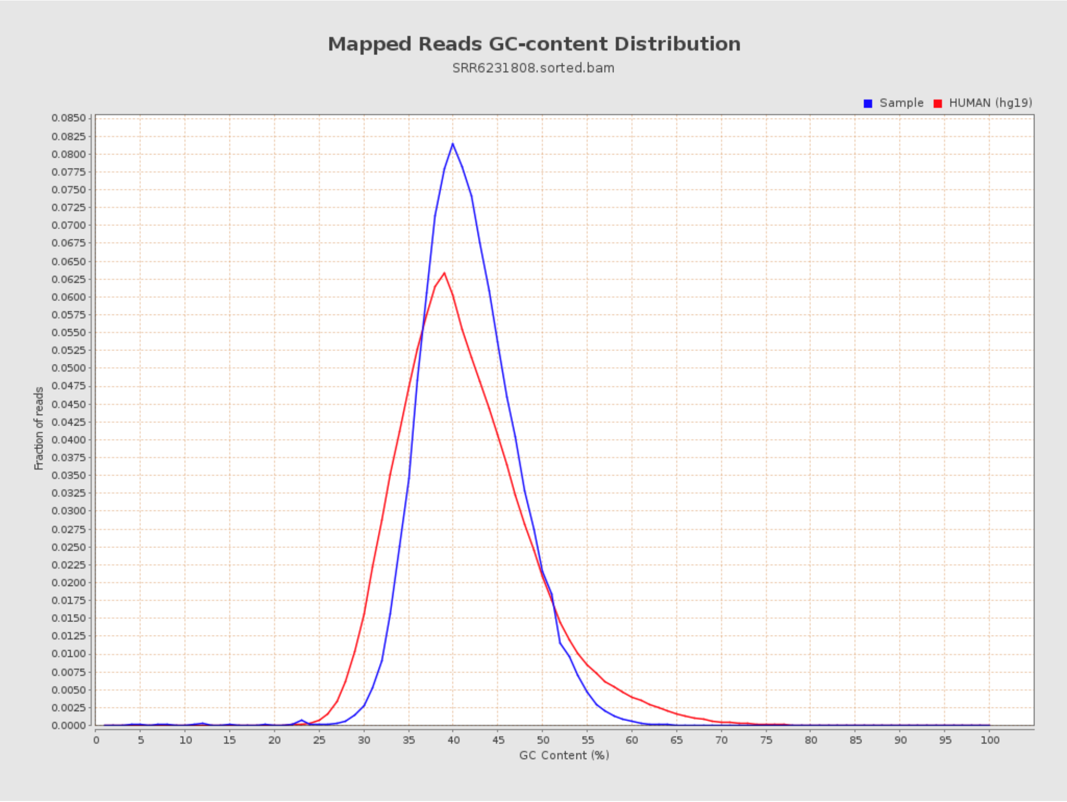
7. Results : Duplication Rate Histogram



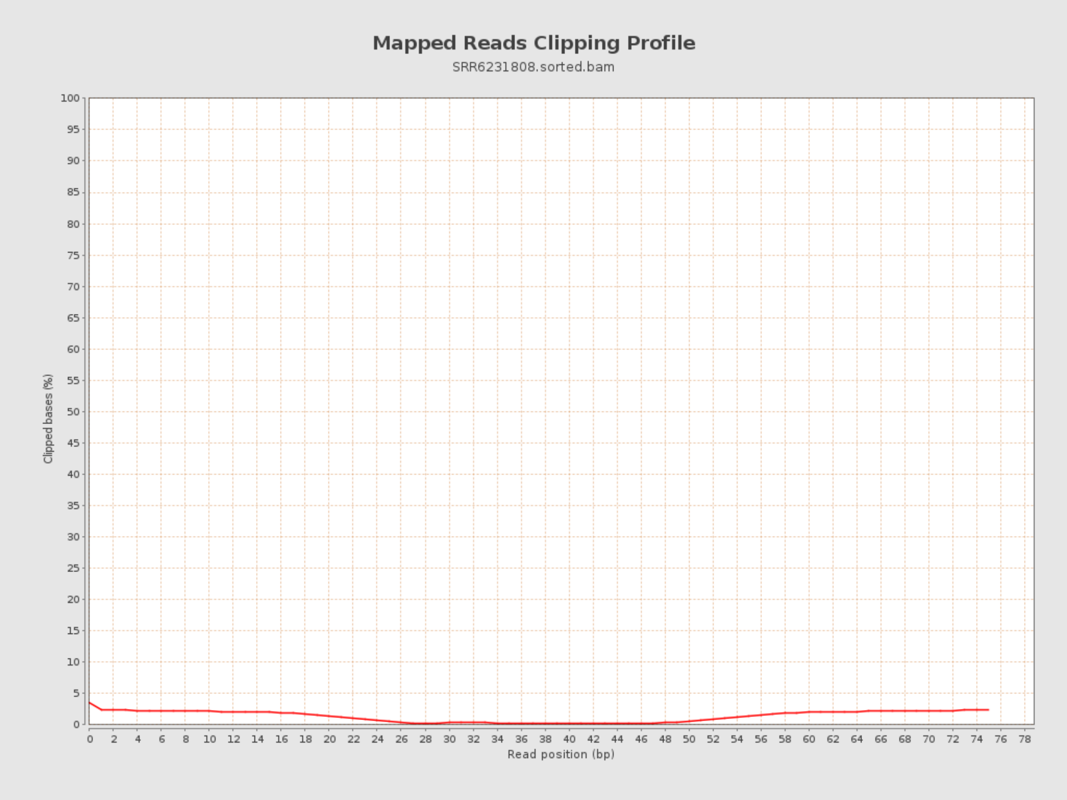
8. Results : Mapped Reads Nucleotide Content



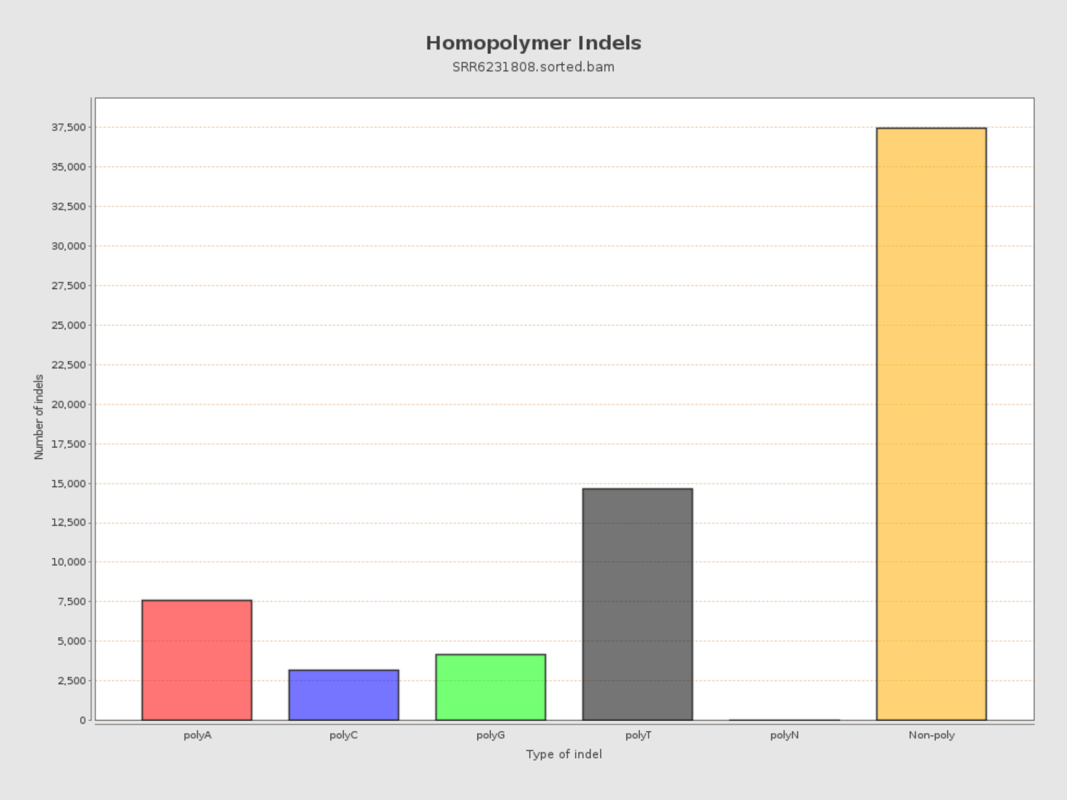
9. Results : Mapped Reads GC-content Distribution



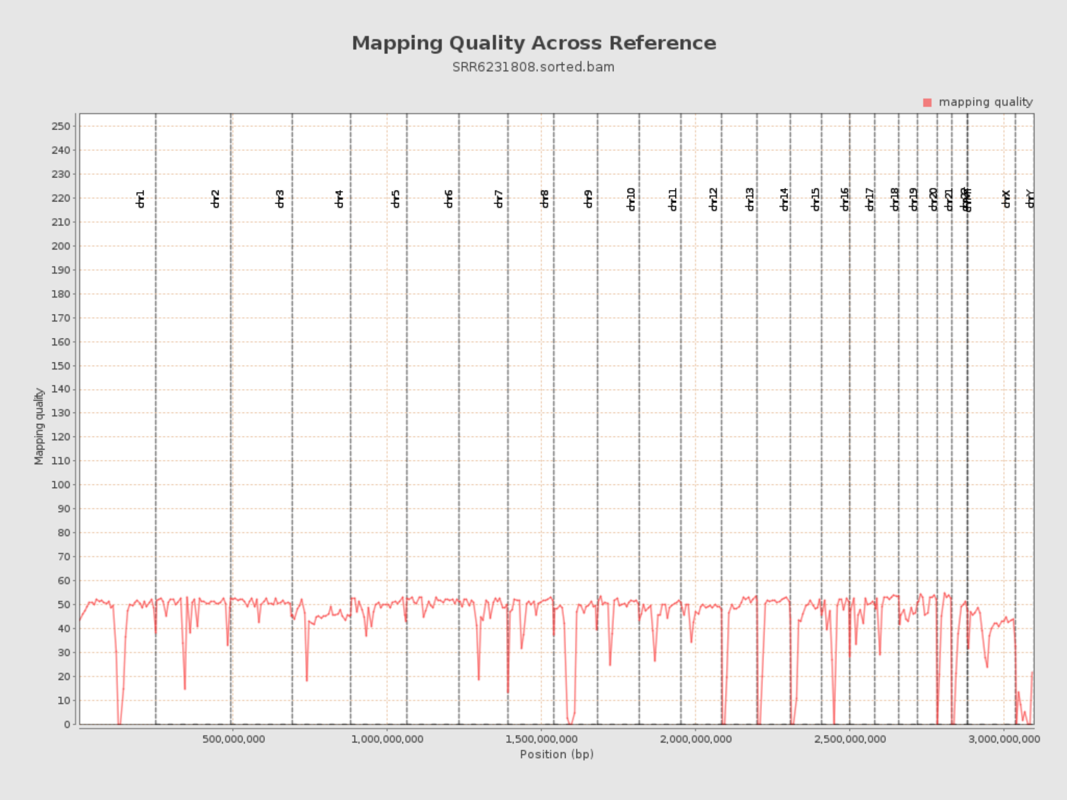
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram