Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 04:00:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231804.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_SRR6231804 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231804.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 04:00:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231804.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,349,481
Mapped reads	10,256,843 / 83.05%
Unmapped reads	2,092,638 / 16.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	103,956 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	1,079,031 / 8.74%
Duplication rate	7.26%
Clipped reads	5,586,635 / 45.24%

2.2. ACGT Content

Number/percentage of A's	192,745,716 / 29.01%
Number/percentage of C's	134,627,977 / 20.26%
Number/percentage of T's	191,576,233 / 28.84%
Number/percentage of G's	145,384,909 / 21.88%
Number/percentage of N's	50,363 / 0.01%
GC Percentage	42.15%

2.3. Coverage

Mean	0.2147

Standard Deviation	8.8311

2.4. Mapping Quality

Mean Mapping Quality	45.27

2.5. Mismatches and indels

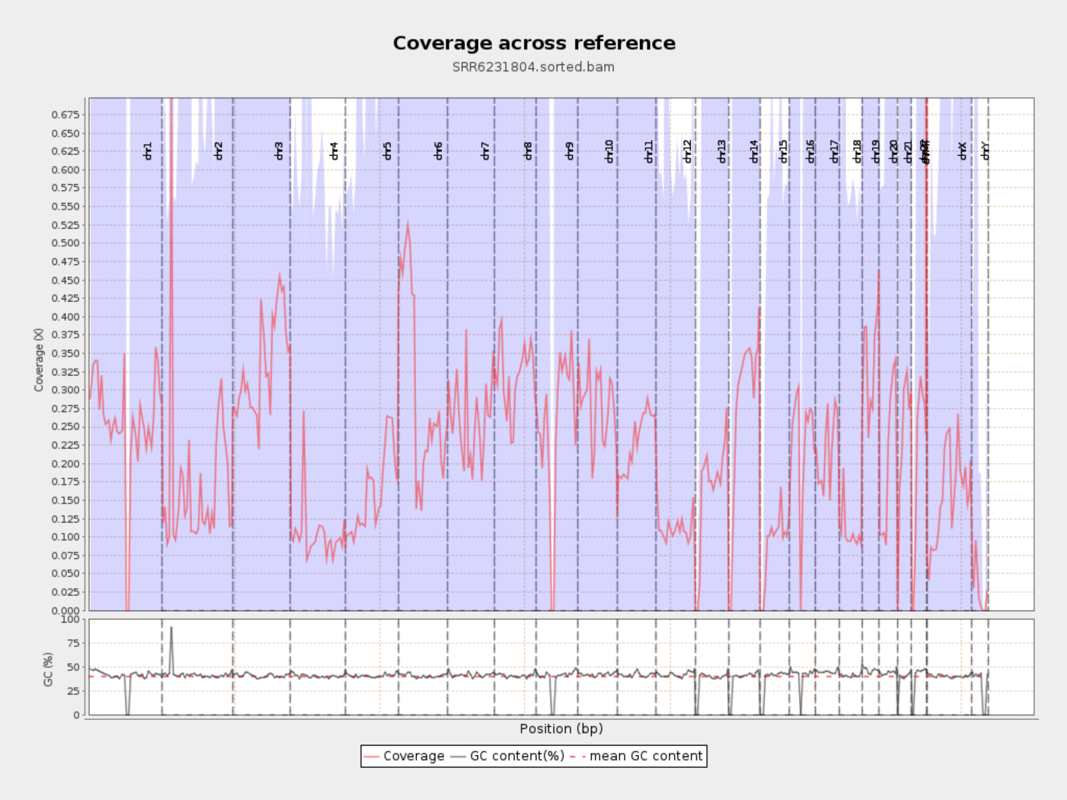
General error rate	0.59%
Mismatches	3,843,707
Insertions	47,769
Mapped reads with at least one insertion	0.46%
Deletions	144,397
Mapped reads with at least one deletion	1.39%
Homopolymer indels	45.81%

2.6. Chromosome stats

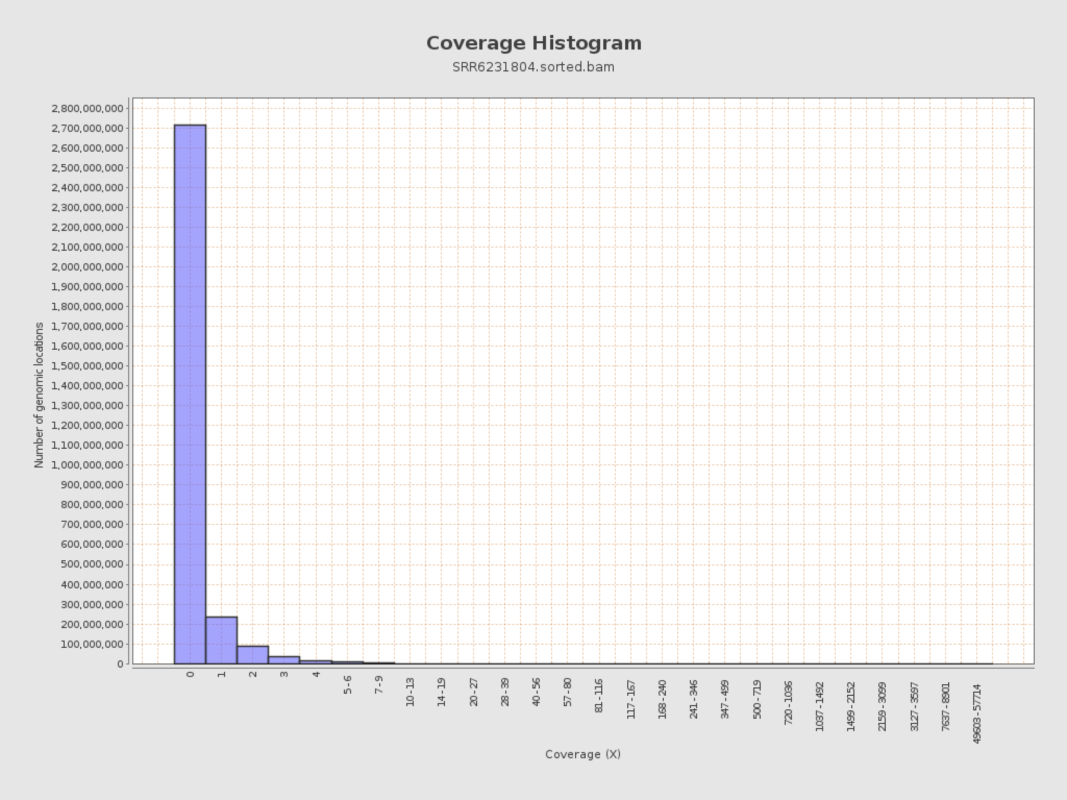
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	63573098	0.2551	3.0299
chr2	243199373	41507571	0.1707	31.0565
chr3	198022430	66001359	0.3333	0.8979
chr4	191154276	19684809	0.103	0.8169
chr5	180915260	29275899	0.1618	0.6302
chr6	171115067	51837435	0.3029	1.3616
chr7	159138663	41189756	0.2588	2.3859

chr8	146364022	46865931	0.3202	2.0197
chr9	141213431	35420313	0.2508	1.2611
chr10	135534747	38300413	0.2826	1.5959
chr11	135006516	30930430	0.2291	1.4479
chr12	133851895	15079788	0.1127	0.574
chr13	115169878	18887667	0.164	0.614
chr14	107349540	29353797	0.2734	0.9392
chr15	102531392	9277124	0.0905	0.4549
chr16	90354753	20926724	0.2316	0.9385
chr17	81195210	17747832	0.2186	0.8692
chr18	78077248	8450891	0.1082	2.9561
chr19	59128983	19974036	0.3378	1.9746
chr20	63025520	12788762	0.2029	0.7668
chr21	48129895	11380844	0.2365	0.9052
chr22	51304566	10067311	0.1962	0.6725
chrMT	16571	603639	36.4274	21.4946
chrX	155270560	23922552	0.1541	0.8267
chrY	59373566	1580264	0.0266	0.6808

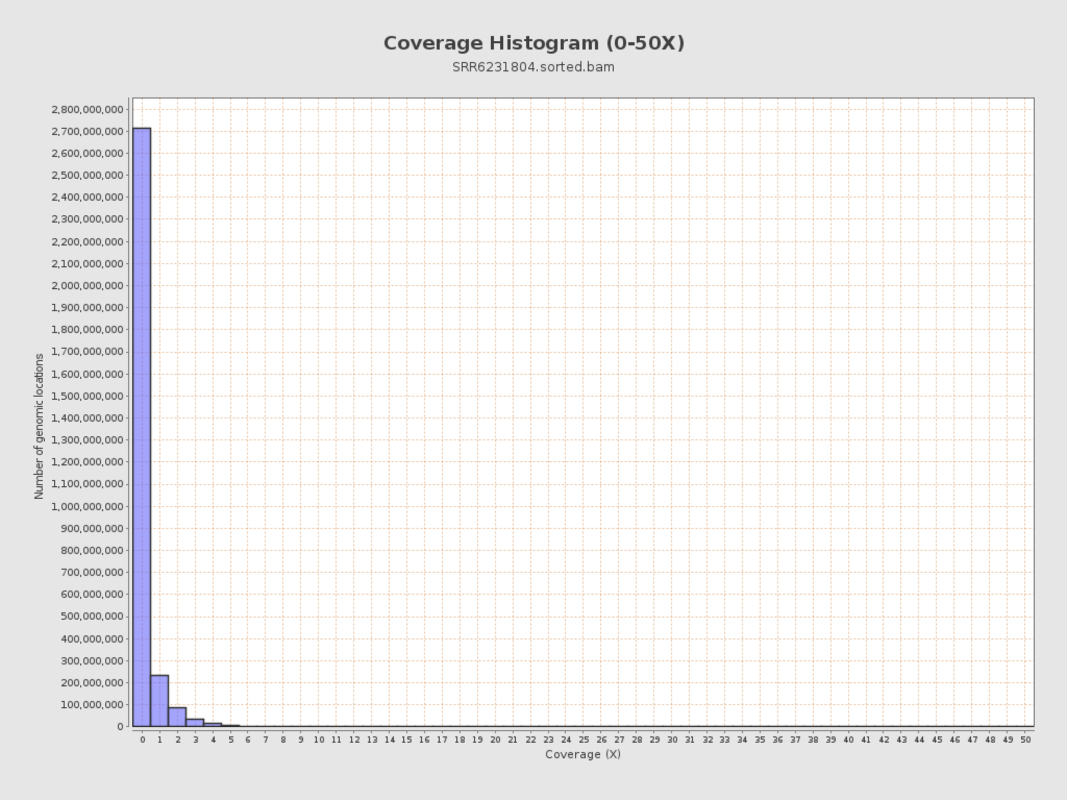
3. Results : Coverage across reference



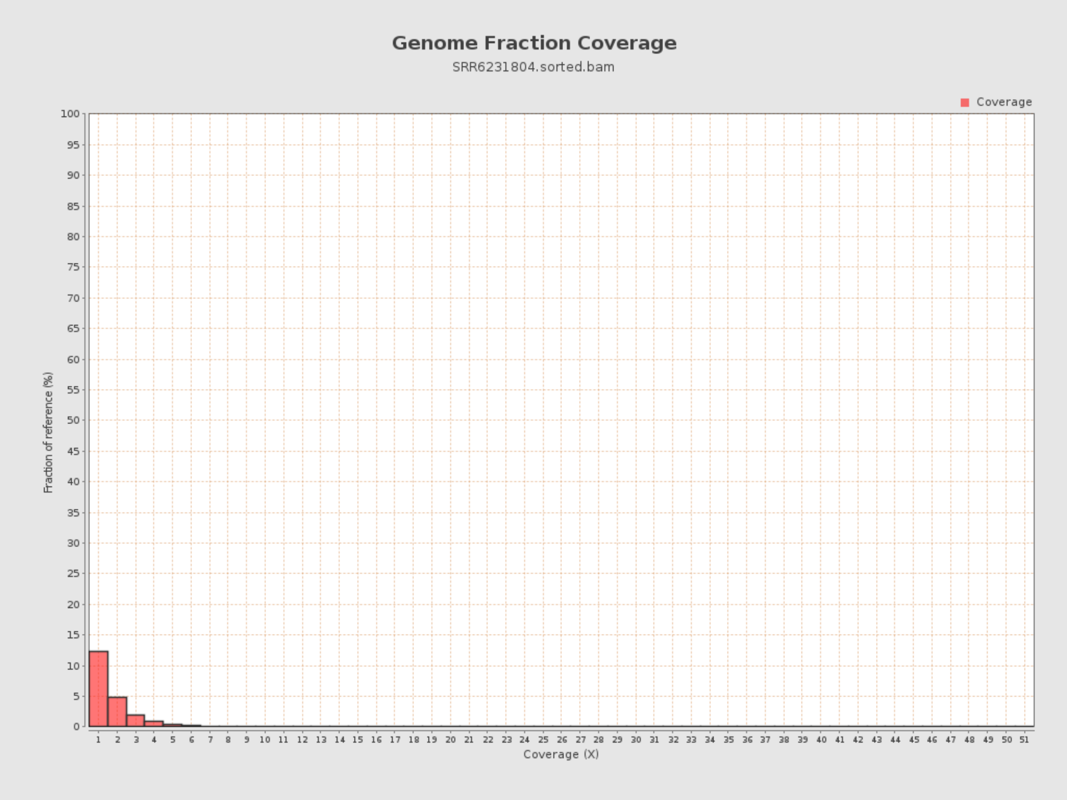
4. Results : Coverage Histogram



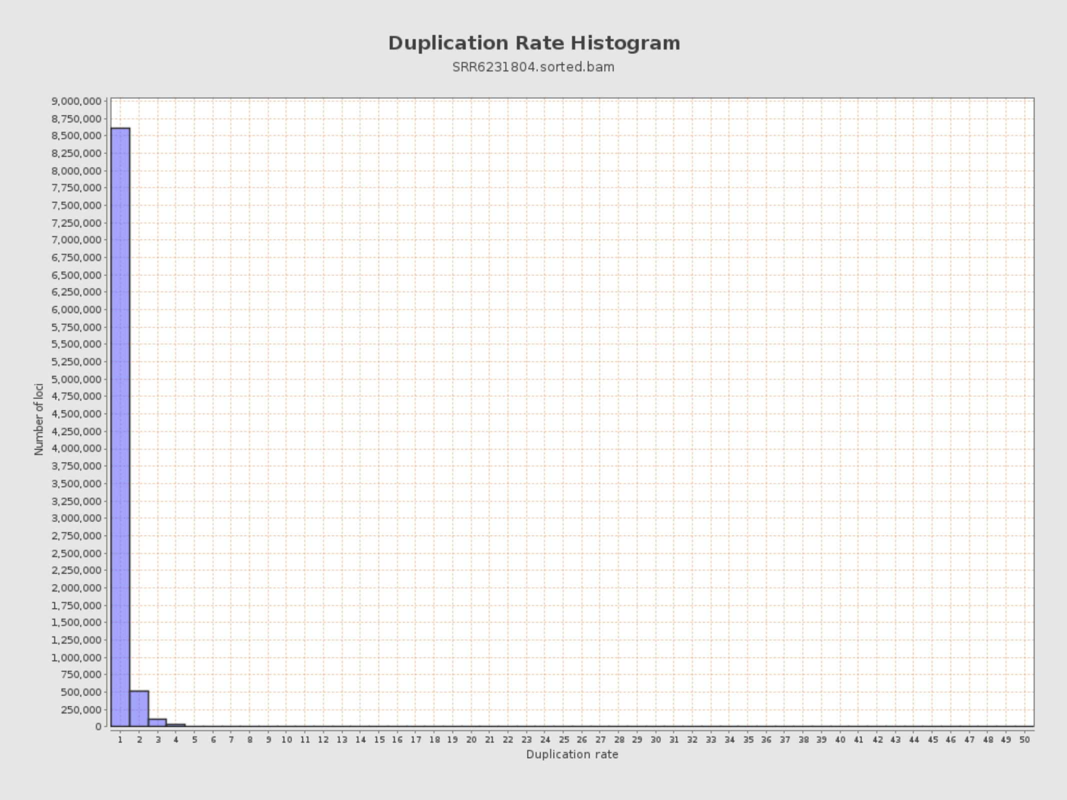
5. Results : Coverage Histogram (0-50X)



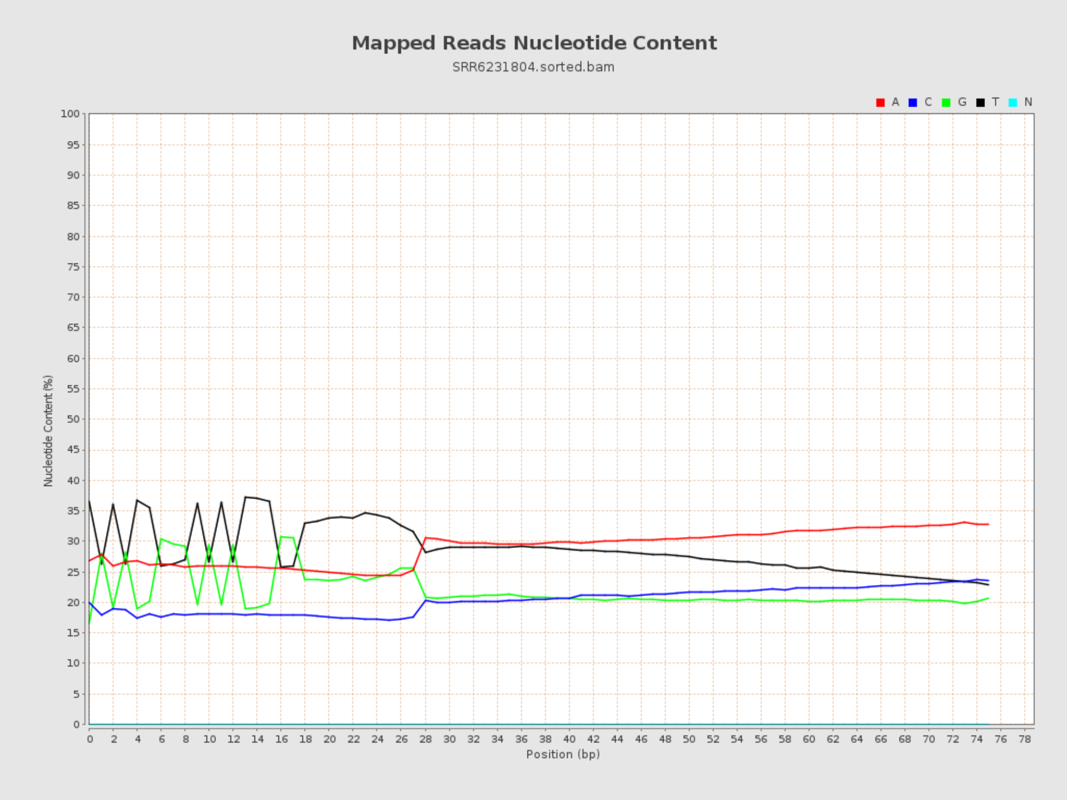
6. Results : Genome Fraction Coverage



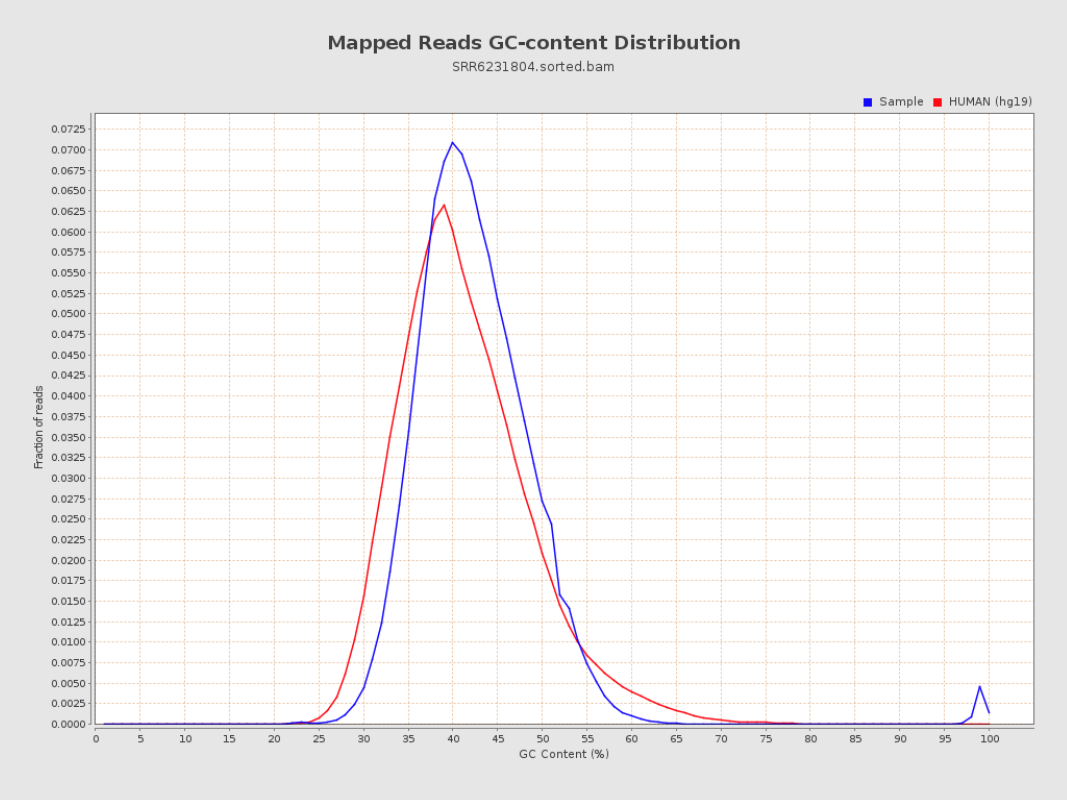
7. Results : Duplication Rate Histogram



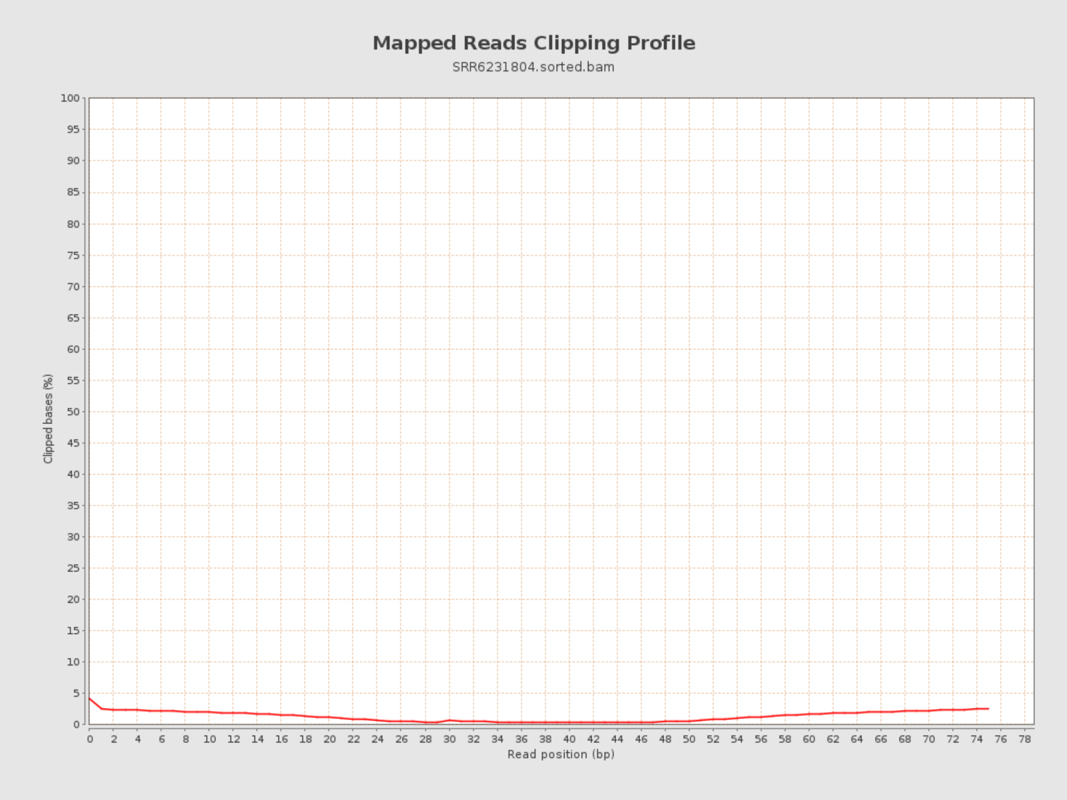
8. Results : Mapped Reads Nucleotide Content



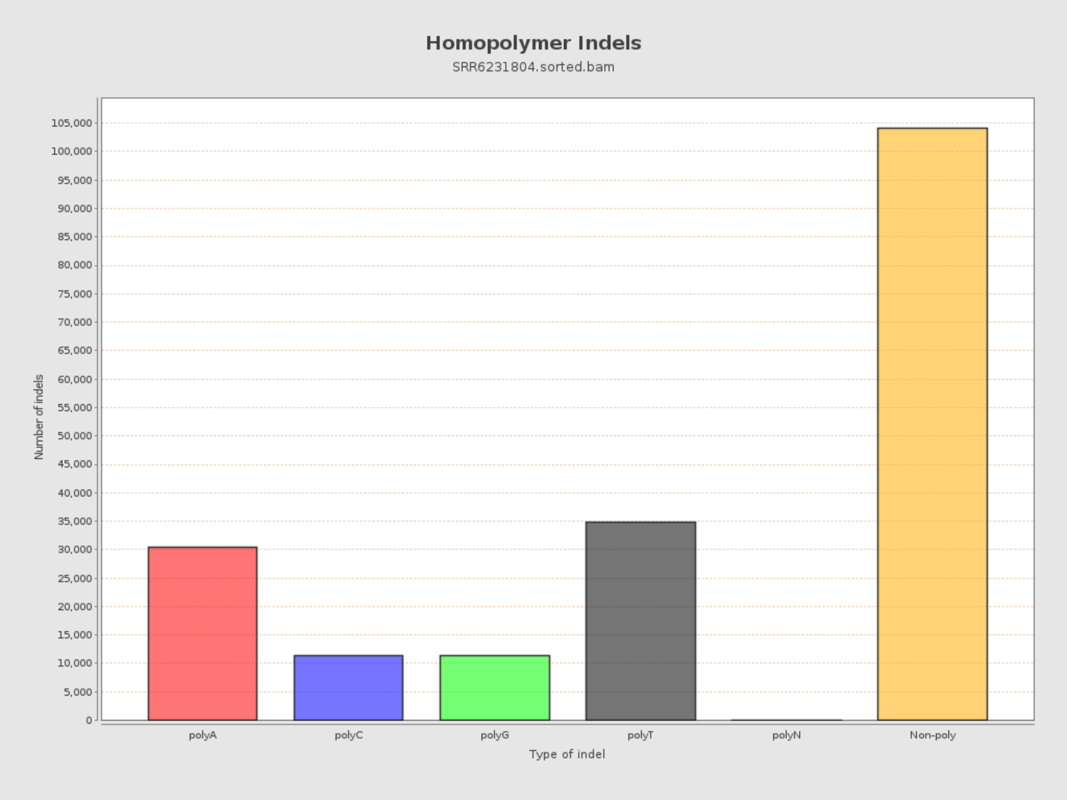
9. Results : Mapped Reads GC-content Distribution



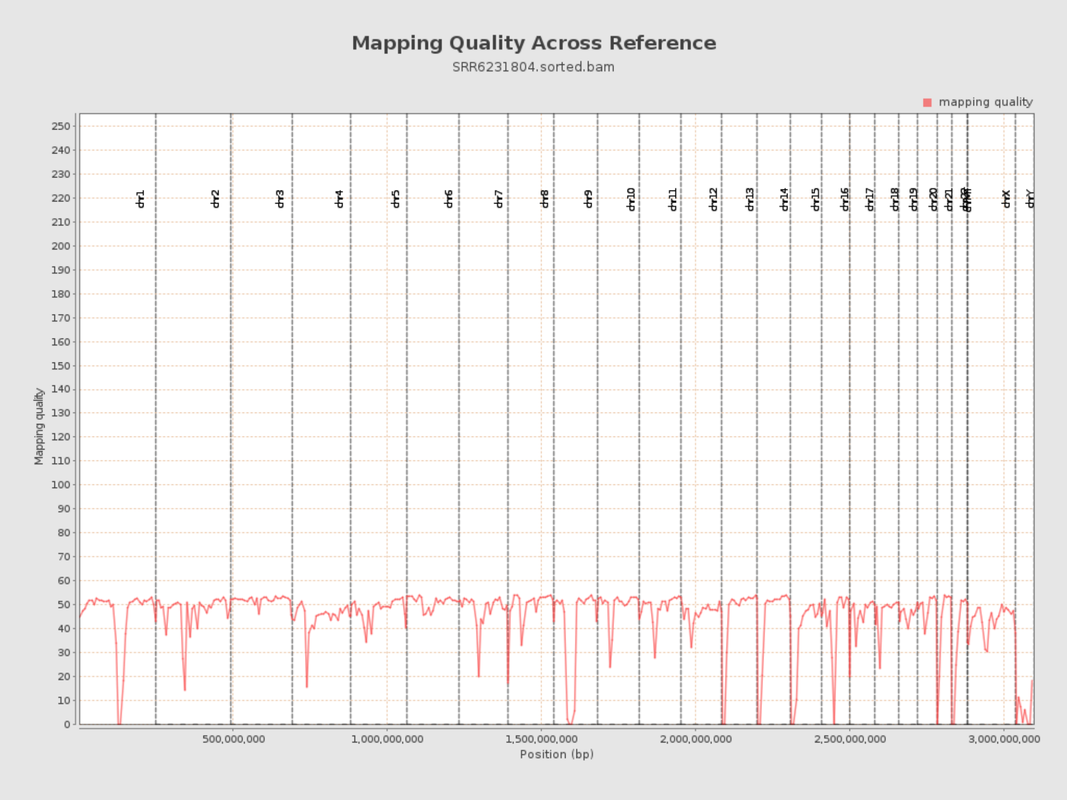
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram