Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 07:25:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231845.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_SRR6231845 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231845.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 07:25:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231845.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,080,941
Mapped reads	5,422,371 / 76.58%
Unmapped reads	1,658,570 / 23.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	51,757 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	415,517 / 5.87%
Duplication rate	5.03%
Clipped reads	2,745,223 / 38.77%

2.2. ACGT Content

Number/percentage of A's	103,808,023 / 29.33%
Number/percentage of C's	67,705,550 / 19.13%
Number/percentage of T's	106,231,134 / 30.01%
Number/percentage of G's	76,183,884 / 21.52%
Number/percentage of N's	25,995 / 0.01%
GC Percentage	40.65%

2.3. Coverage

Mean	0.1144

Standard Deviation	4.9371

2.4. Mapping Quality

Mean Mapping Quality	40.49

2.5. Mismatches and indels

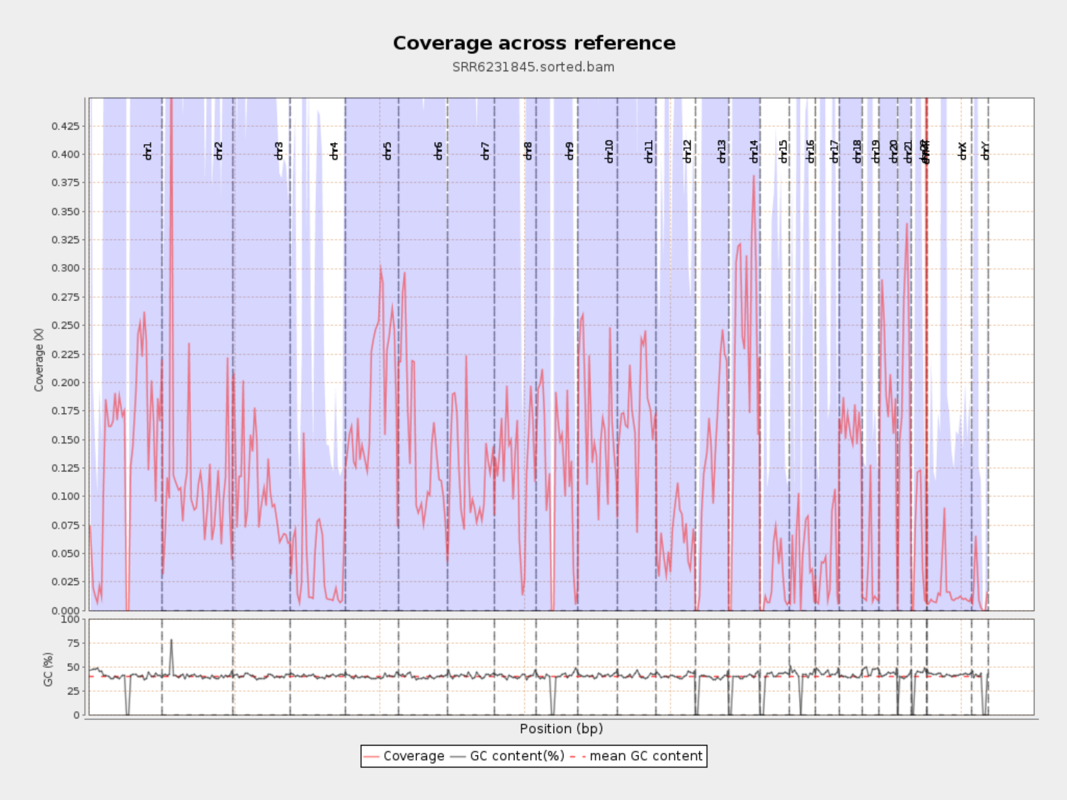
General error rate	0.65%
Mismatches	2,256,365
Insertions	26,792
Mapped reads with at least one insertion	0.49%
Deletions	88,658
Mapped reads with at least one deletion	1.62%
Homopolymer indels	45.39%

2.6. Chromosome stats

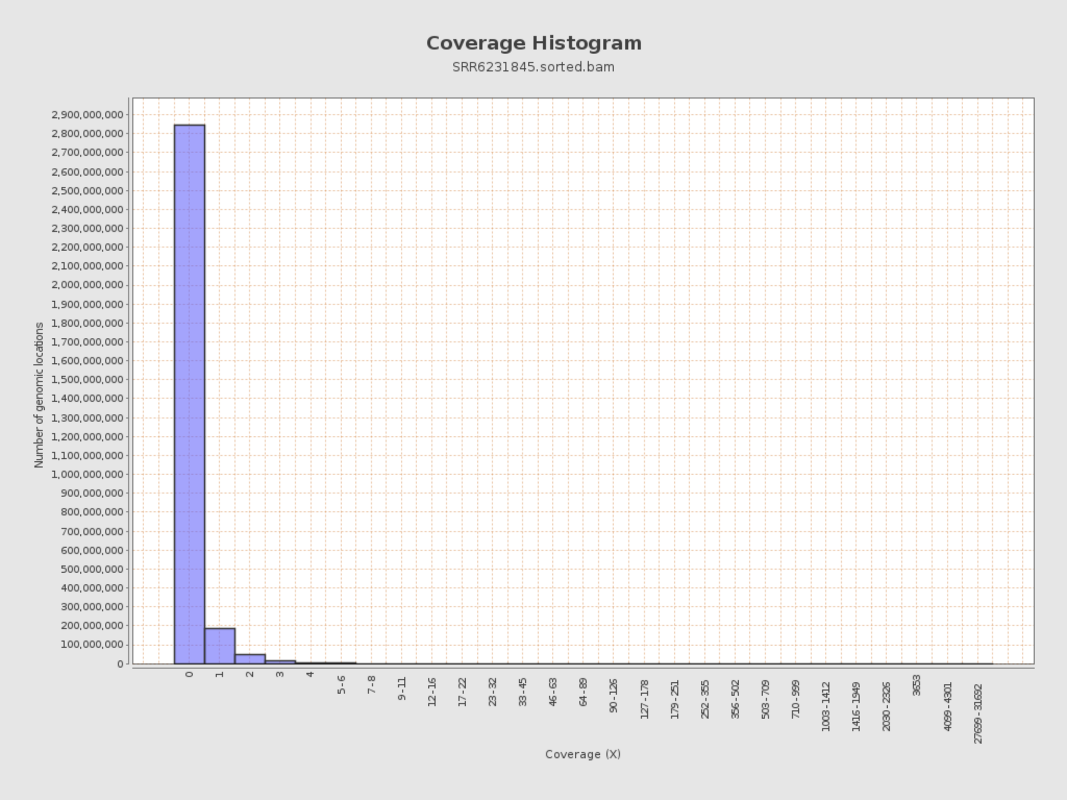
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	34722236	0.1393	1.9309
chr2	243199373	28487933	0.1171	17.2527
chr3	198022430	21442339	0.1083	0.424
chr4	191154276	6885279	0.036	0.4779
chr5	180915260	34391259	0.1901	0.5685
chr6	171115067	24731702	0.1445	0.8752
chr7	159138663	19550466	0.1229	1.3925

chr8	146364022	18678978	0.1276	1.6267
chr9	141213431	17367488	0.123	0.964
chr10	135534747	22585039	0.1666	0.9163
chr11	135006516	23484171	0.1739	1.2476
chr12	133851895	8154495	0.0609	0.3493
chr13	115169878	15730118	0.1366	0.477
chr14	107349540	24866538	0.2316	0.676
chr15	102531392	2552812	0.0249	0.2242
chr16	90354753	4185499	0.0463	0.4956
chr17	81195210	2972567	0.0366	0.4793
chr18	78077248	12652781	0.1621	2.0398
chr19	59128983	1765108	0.0299	1.2633
chr20	63025520	12434533	0.1973	0.601
chr21	48129895	9318502	0.1936	0.6776
chr22	51304566	2851897	0.0556	0.3018
chrMT	16571	822723	49.6484	27.1825
chrX	155270560	2563587	0.0165	0.4918
chrY	59373566	906896	0.0153	0.4401

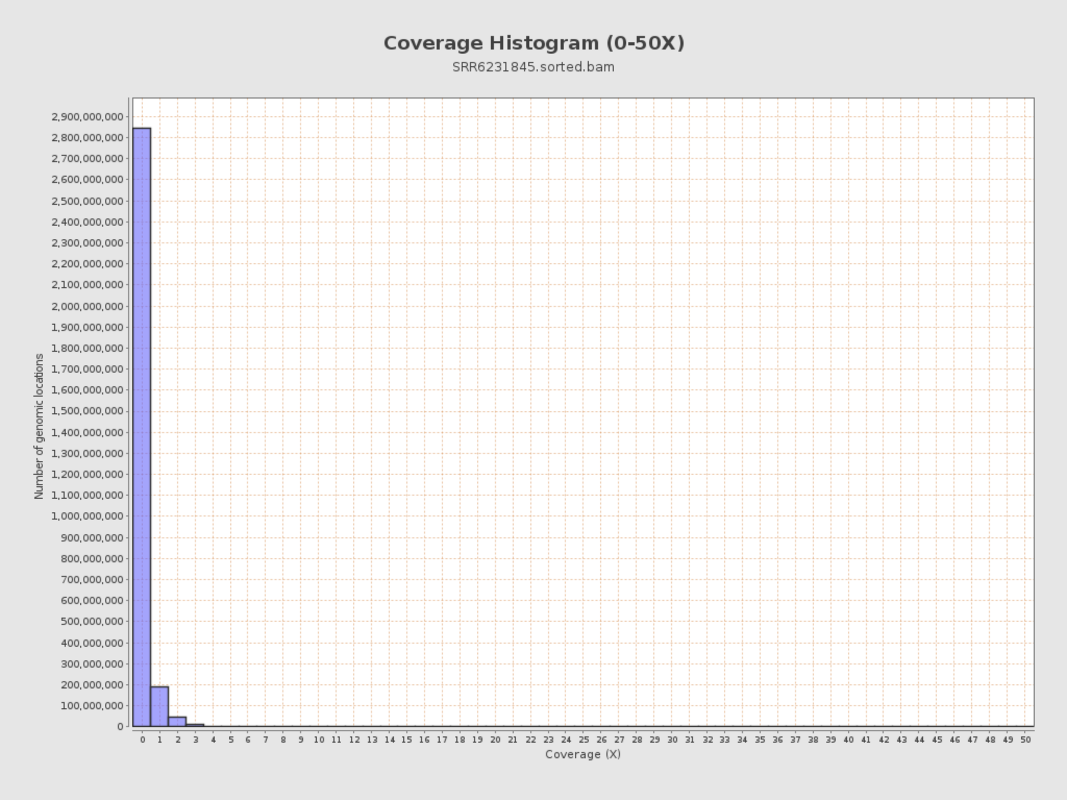
3. Results : Coverage across reference



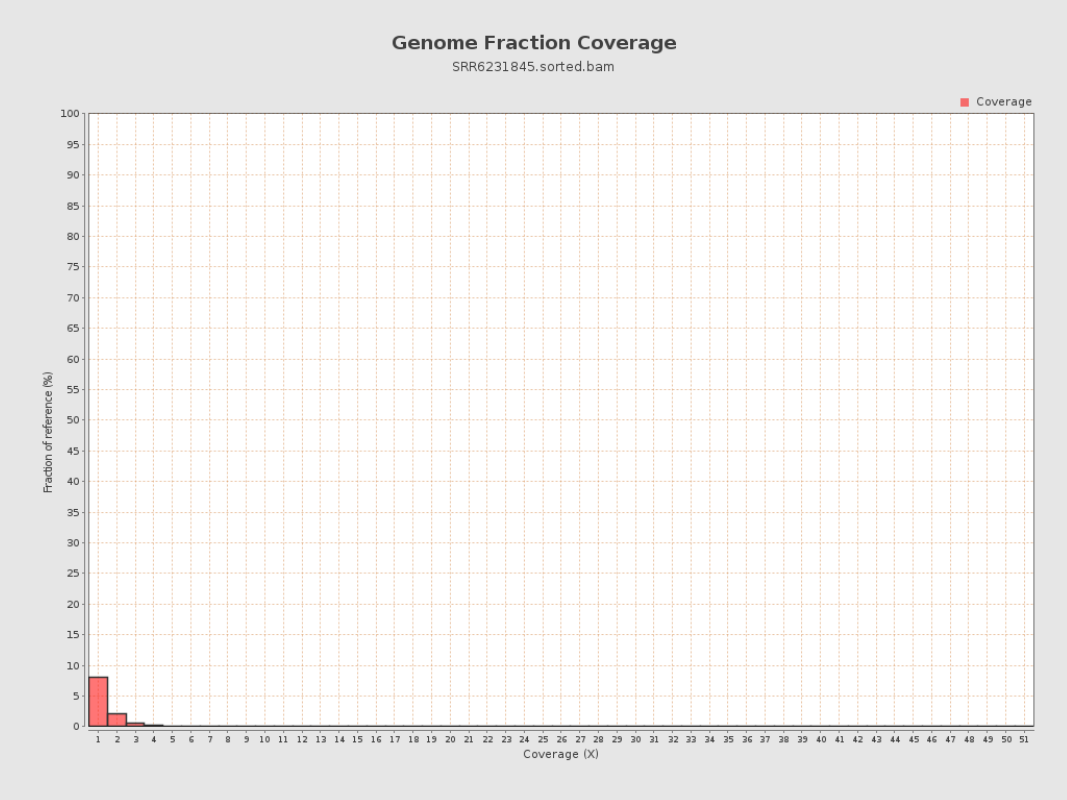
4. Results : Coverage Histogram



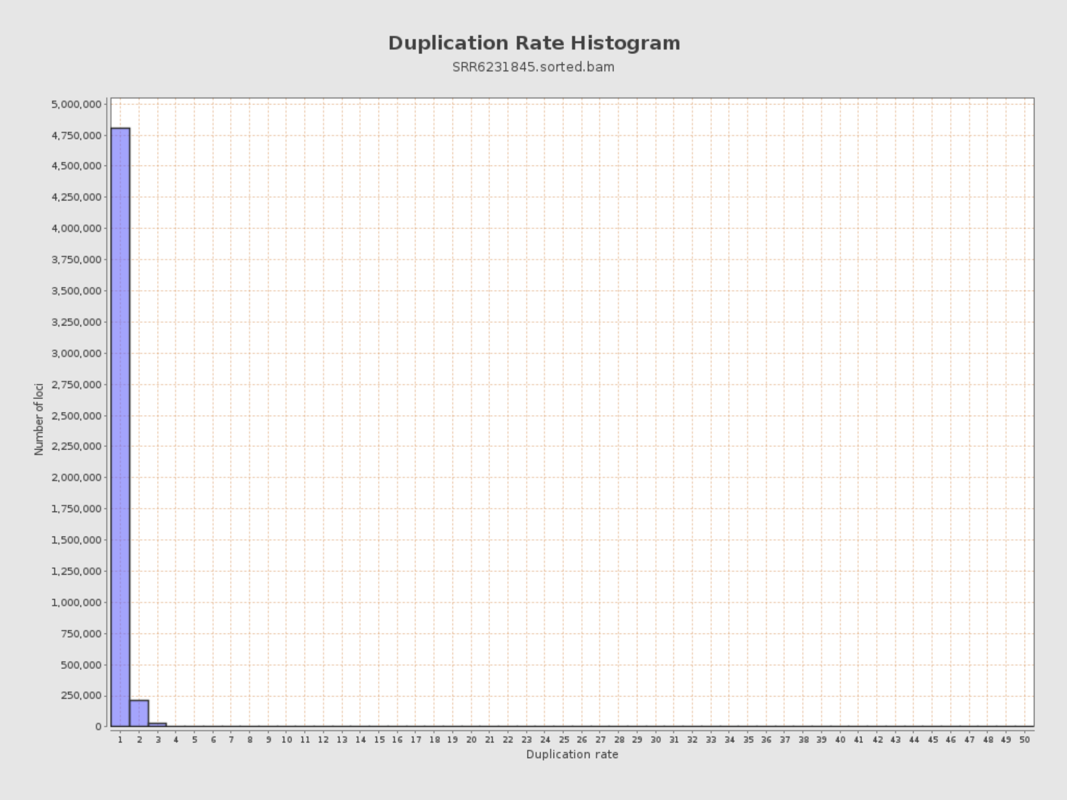
5. Results : Coverage Histogram (0-50X)



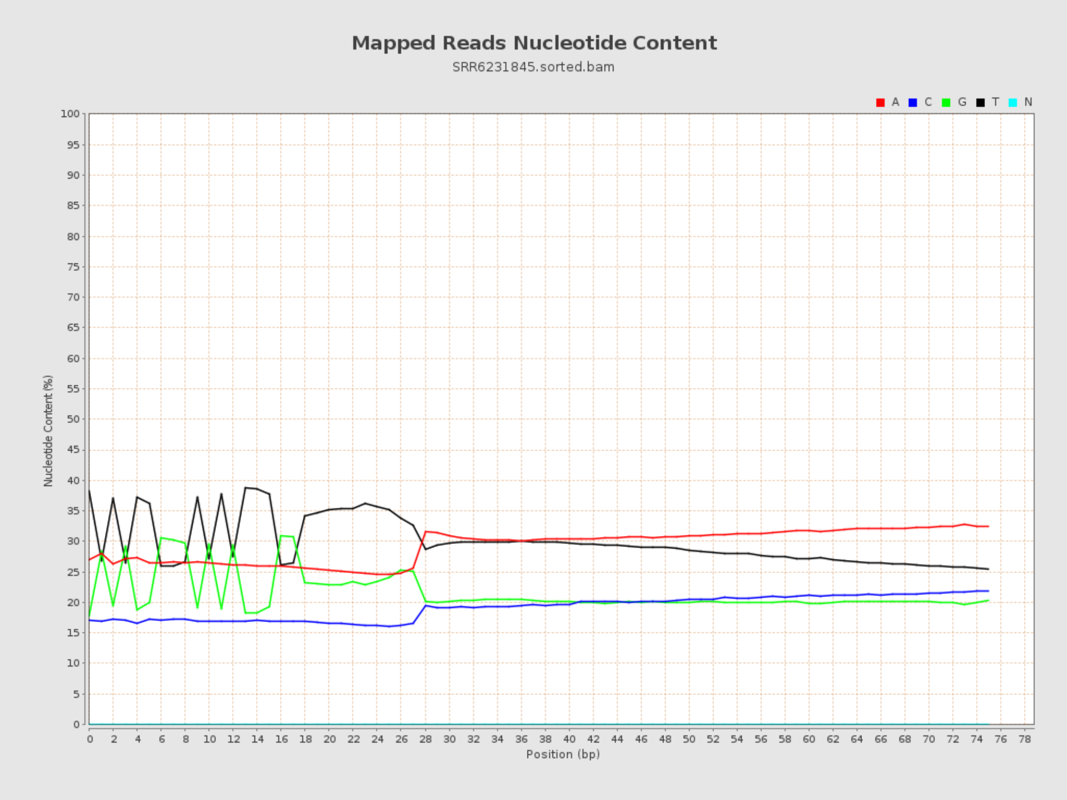
6. Results : Genome Fraction Coverage



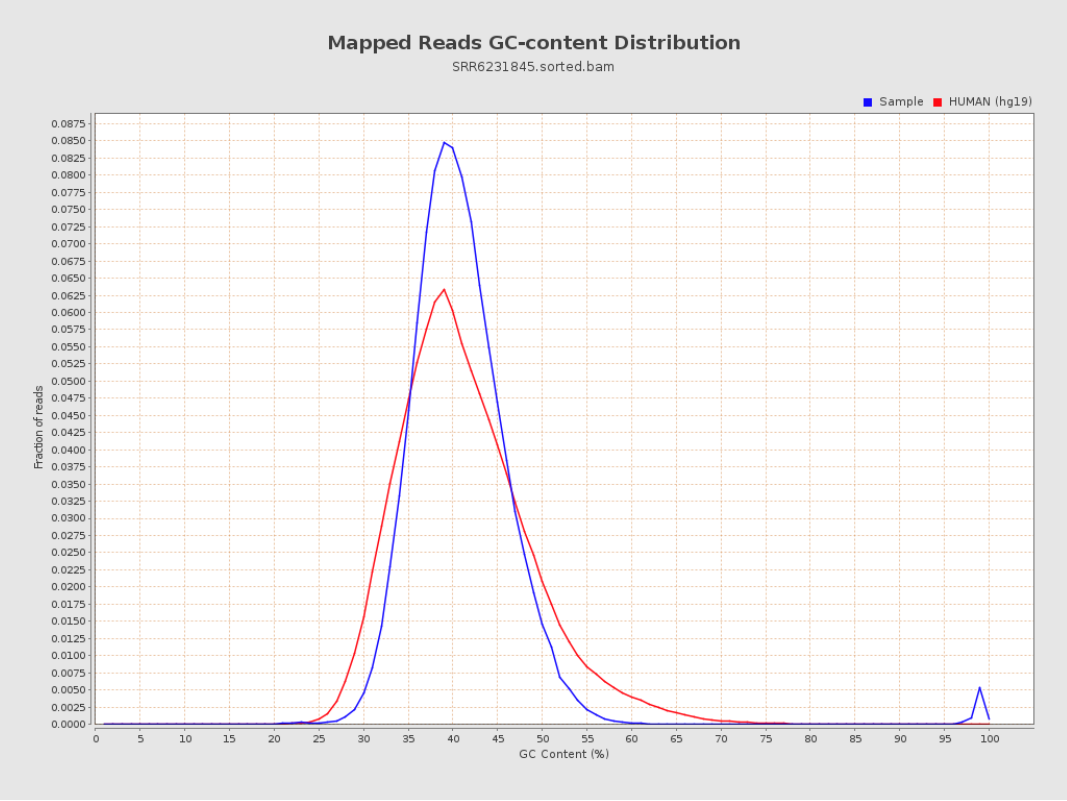
7. Results : Duplication Rate Histogram



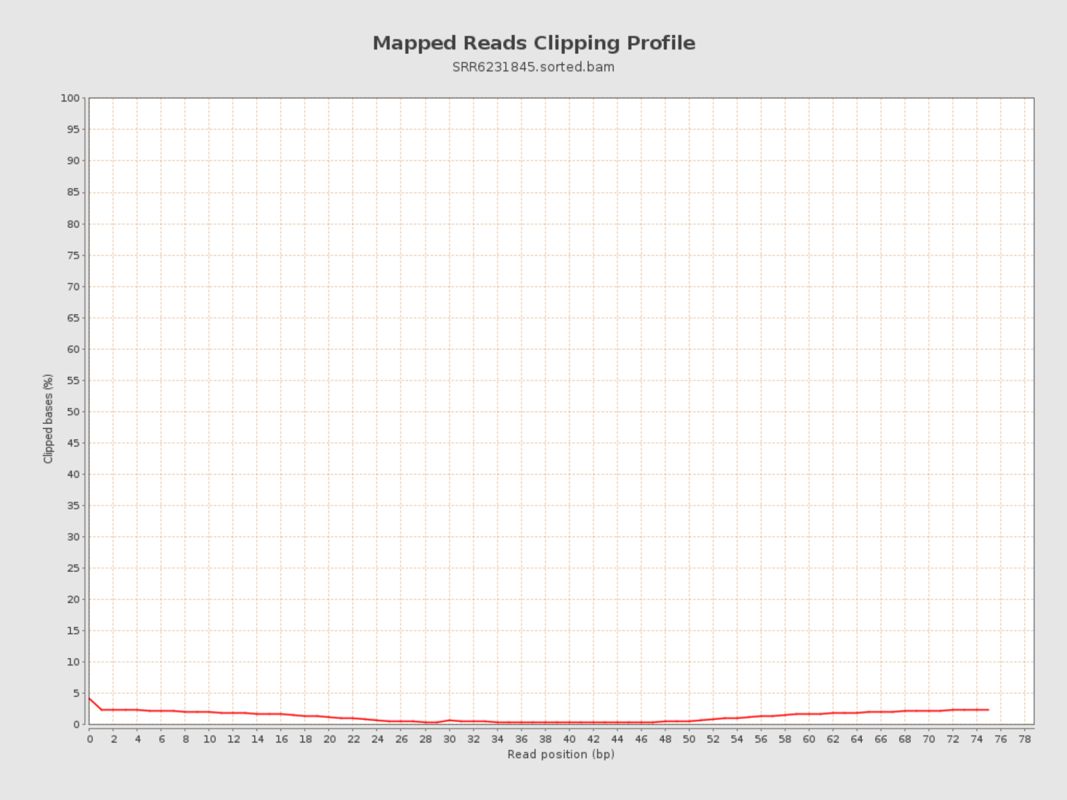
8. Results : Mapped Reads Nucleotide Content



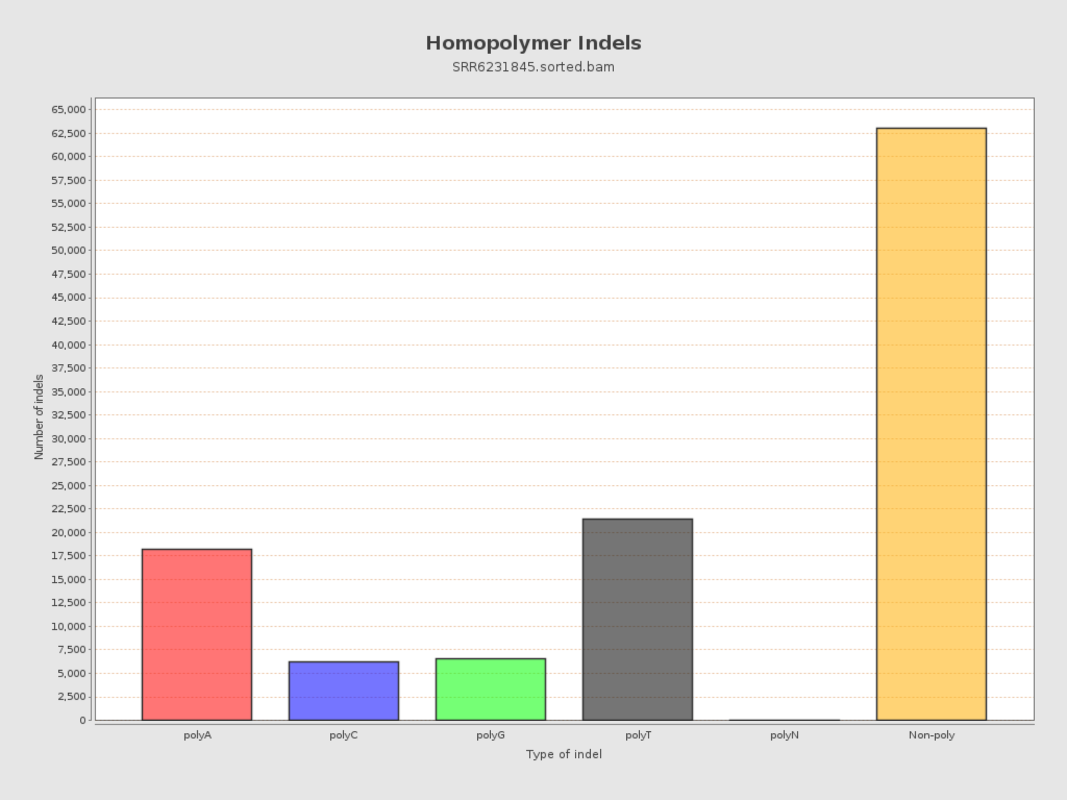
9. Results : Mapped Reads GC-content Distribution



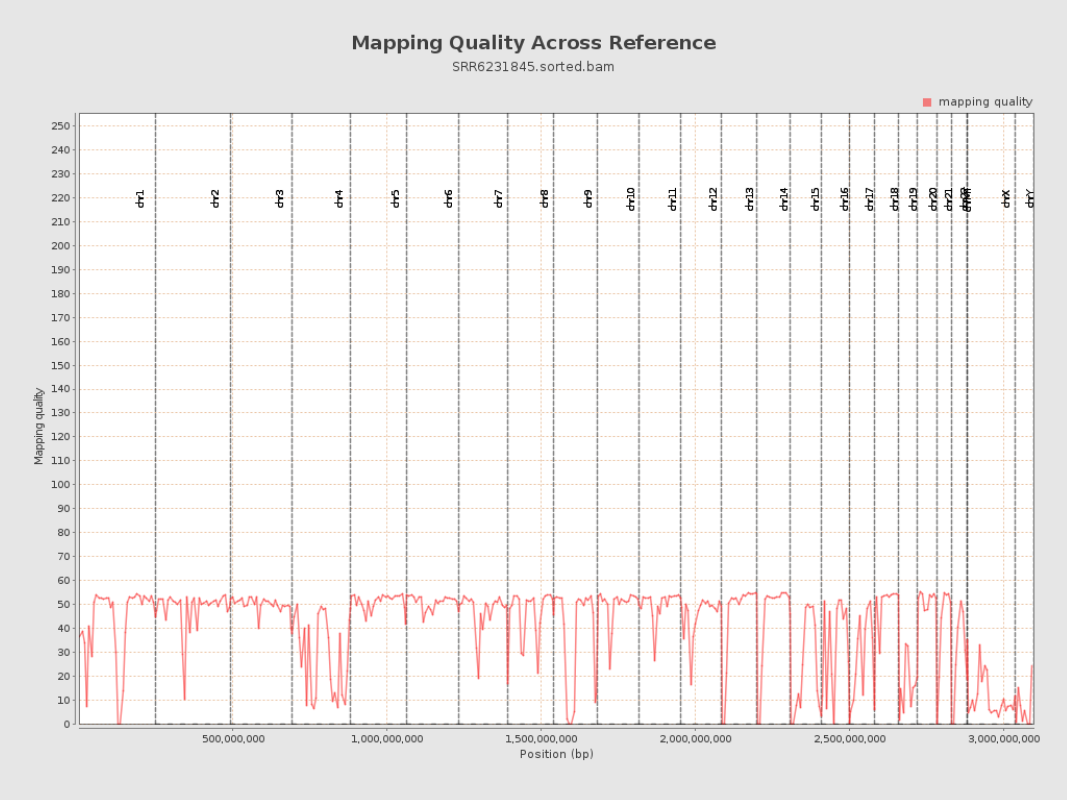
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram