Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 06:47:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231839.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_SRR6231839 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231839.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 06:47:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231839.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,131,391
Mapped reads	1,964,759 / 92.18%
Unmapped reads	166,632 / 7.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,132 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	130,951 / 6.14%
Duplication rate	4.47%
Clipped reads	831,830 / 39.03%

2.2. ACGT Content

Number/percentage of A's	36,512,236 / 27.73%
Number/percentage of C's	24,516,679 / 18.62%
Number/percentage of T's	41,214,876 / 31.3%
Number/percentage of G's	29,392,779 / 22.32%
Number/percentage of N's	48,868 / 0.04%
GC Percentage	40.94%

2.3. Coverage

Mean	0.0426

Standard Deviation	0.7876

2.4. Mapping Quality

Mean Mapping Quality	42.88

2.5. Mismatches and indels

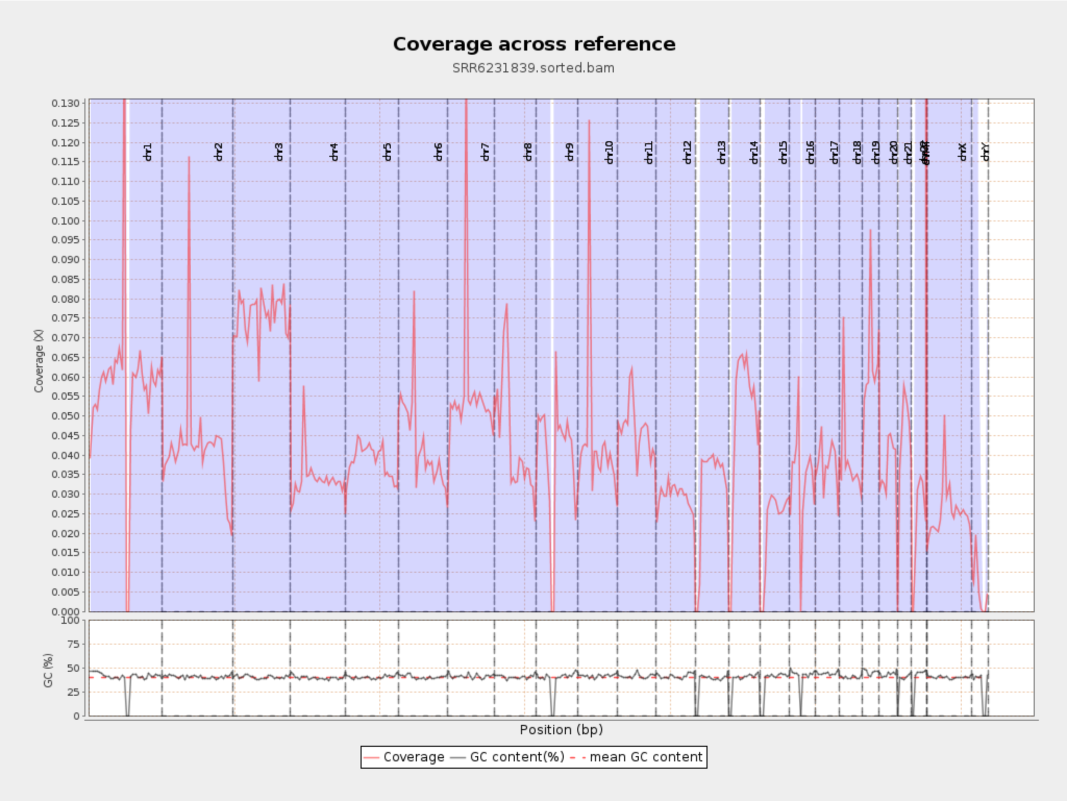
General error rate	0.83%
Mismatches	1,076,641
Insertions	10,508
Mapped reads with at least one insertion	0.53%
Deletions	33,600
Mapped reads with at least one deletion	1.69%
Homopolymer indels	44.24%

2.6. Chromosome stats

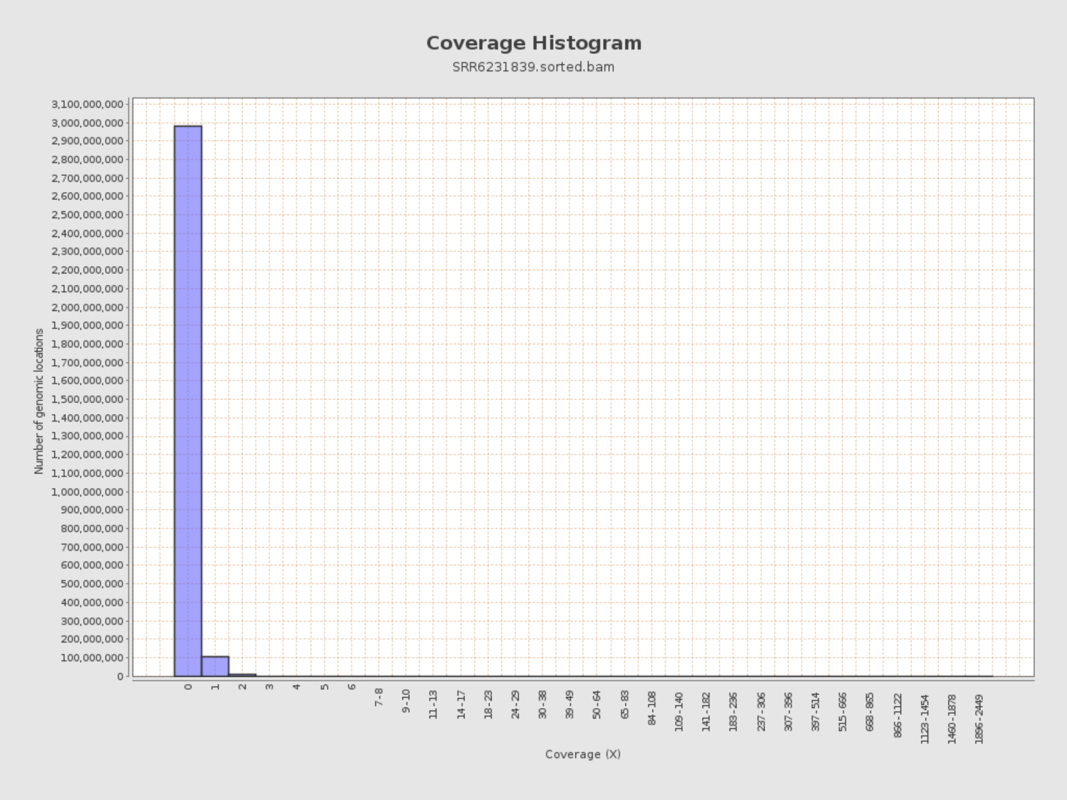
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14493080	0.0581	2.0624
chr2	243199373	10277892	0.0423	0.5941
chr3	198022430	15056649	0.076	0.3182
chr4	191154276	6482124	0.0339	0.2258
chr5	180915260	6994026	0.0387	0.2317
chr6	171115067	7405518	0.0433	0.392
chr7	159138663	9021736	0.0567	1.1903

chr8	146364022	6383206	0.0436	0.8102
chr9	141213431	5616486	0.0398	0.5295
chr10	135534747	5899373	0.0435	0.7326
chr11	135006516	6246052	0.0463	0.4937
chr12	133851895	3923453	0.0293	0.2145
chr13	115169878	3588244	0.0312	0.1942
chr14	107349540	5268378	0.0491	0.3043
chr15	102531392	2278545	0.0222	0.1788
chr16	90354753	3086336	0.0342	0.3125
chr17	81195210	3031225	0.0373	0.2904
chr18	78077248	3046620	0.039	1.1769
chr19	59128983	3748446	0.0634	1.1067
chr20	63025520	2340244	0.0371	0.2441
chr21	48129895	2065526	0.0429	0.2593
chr22	51304566	1133895	0.0221	0.1608
chrMT	16571	65276	3.9392	3.2734
chrX	155270560	3964900	0.0255	0.2722
chrY	59373566	329978	0.0056	0.1285

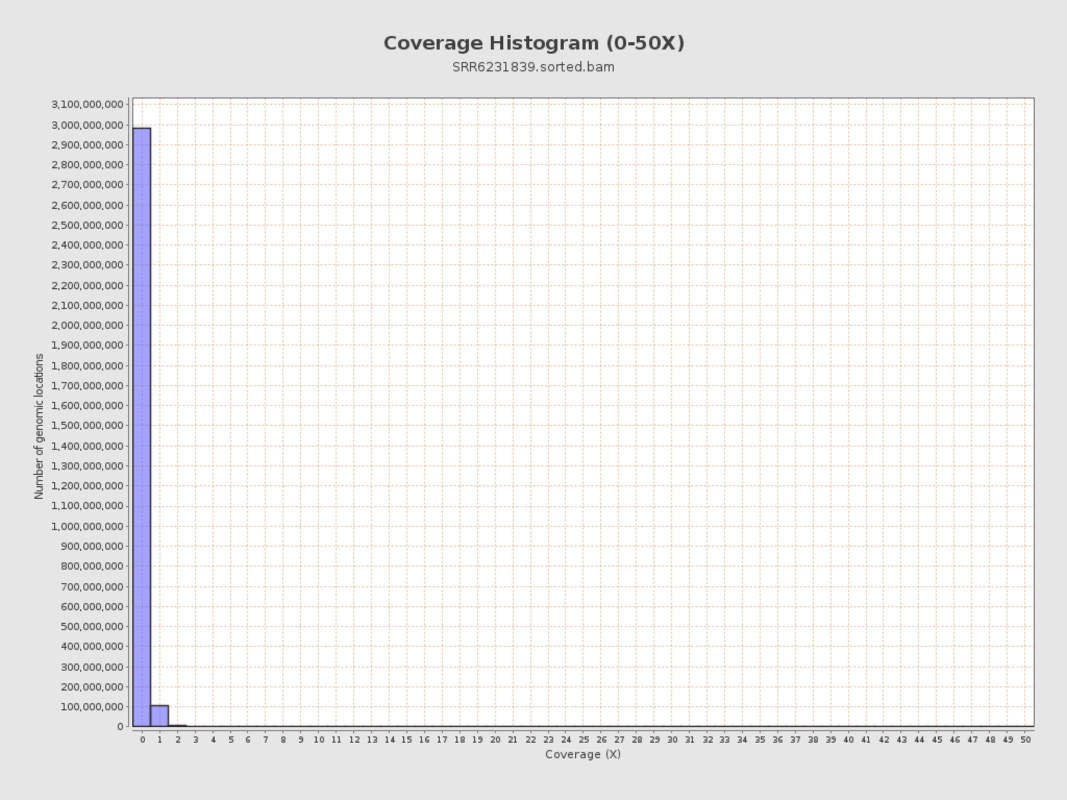
3. Results : Coverage across reference



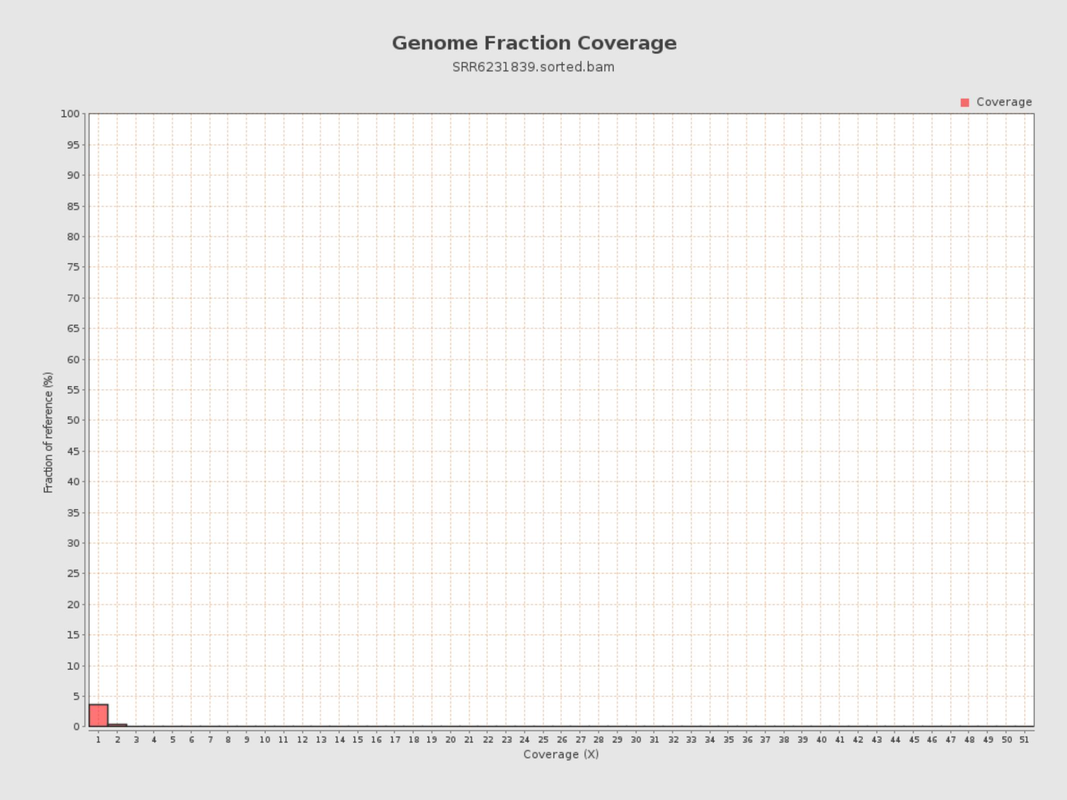
4. Results : Coverage Histogram



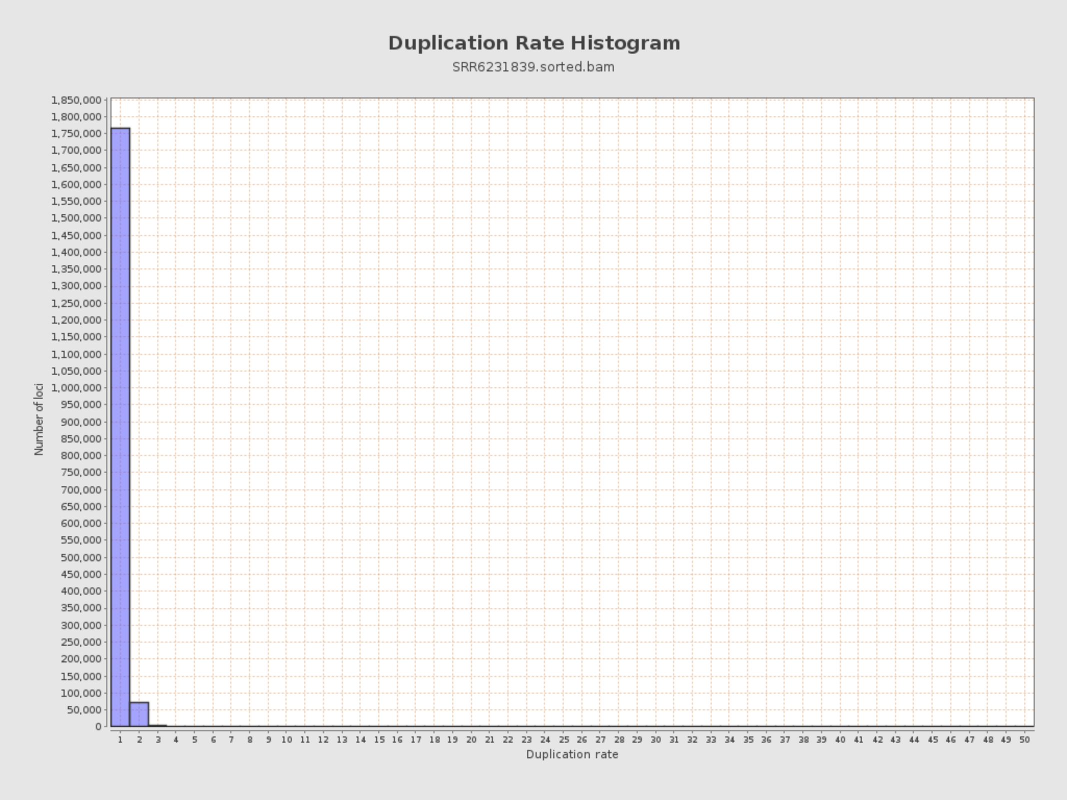
5. Results : Coverage Histogram (0-50X)



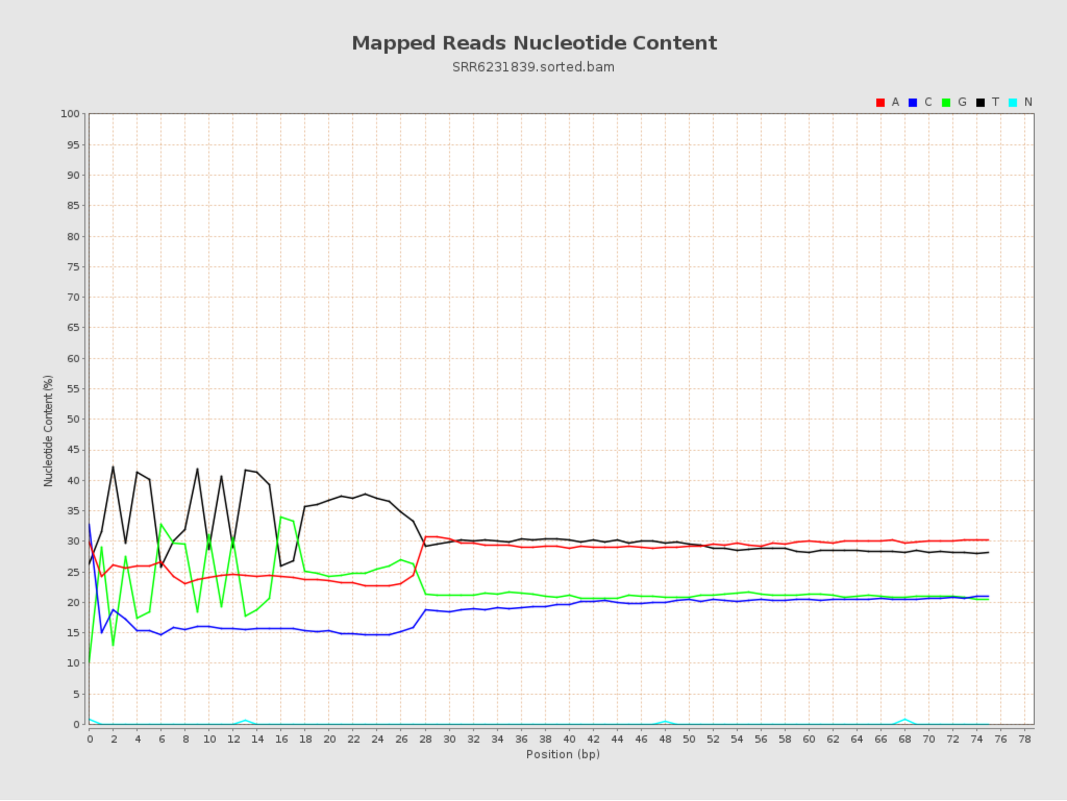
6. Results : Genome Fraction Coverage



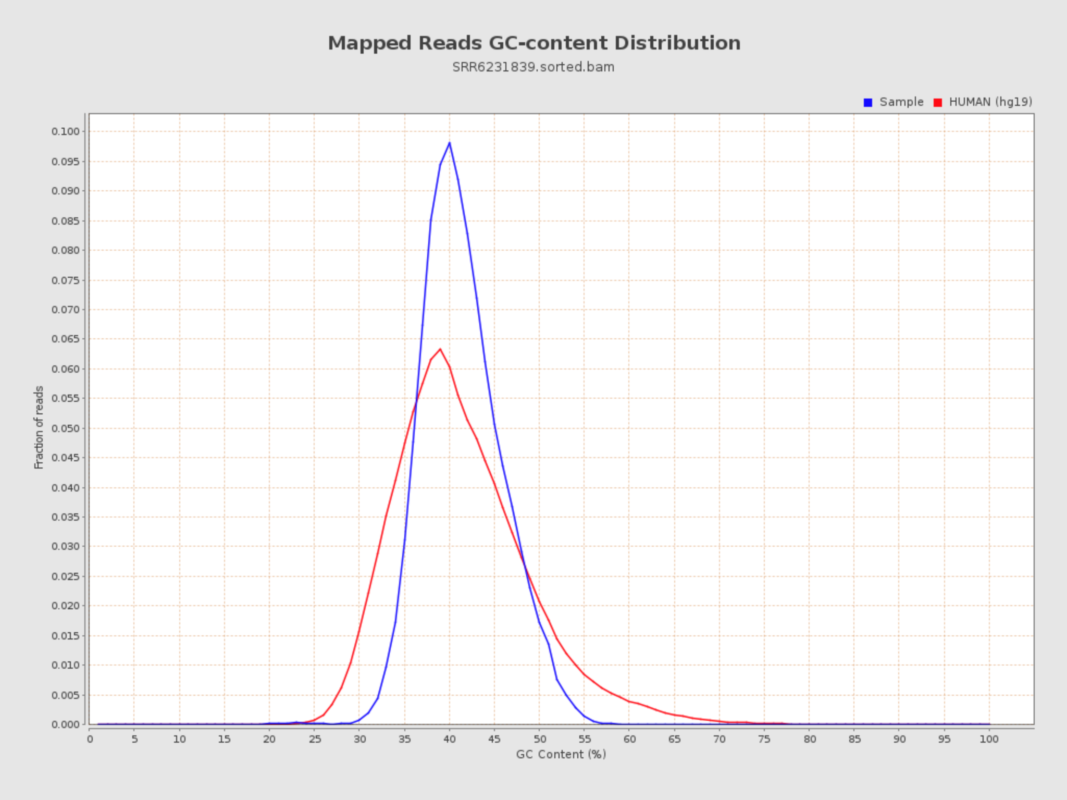
7. Results : Duplication Rate Histogram



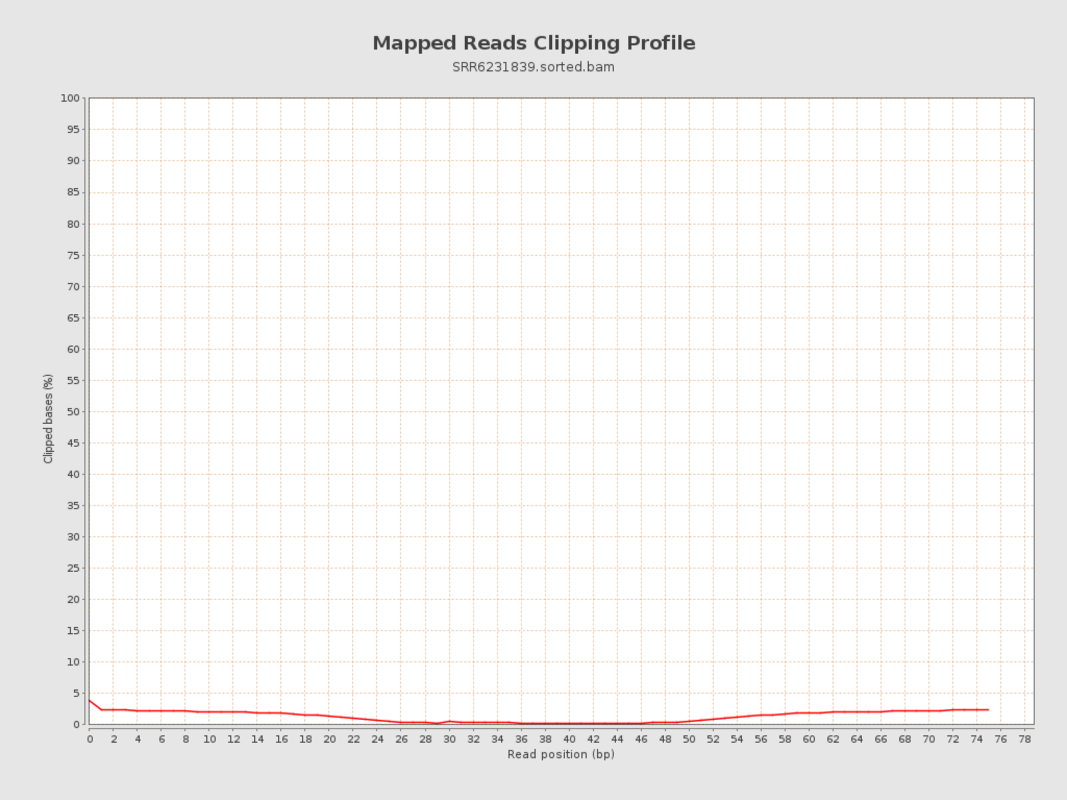
8. Results : Mapped Reads Nucleotide Content



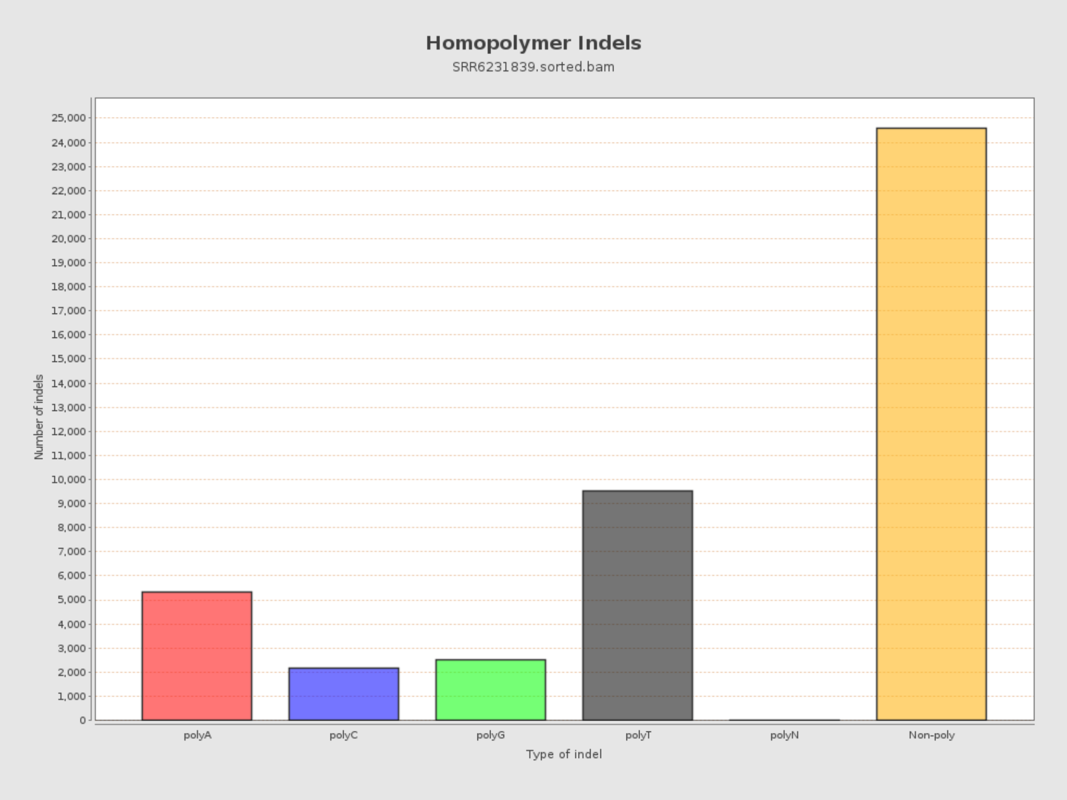
9. Results : Mapped Reads GC-content Distribution



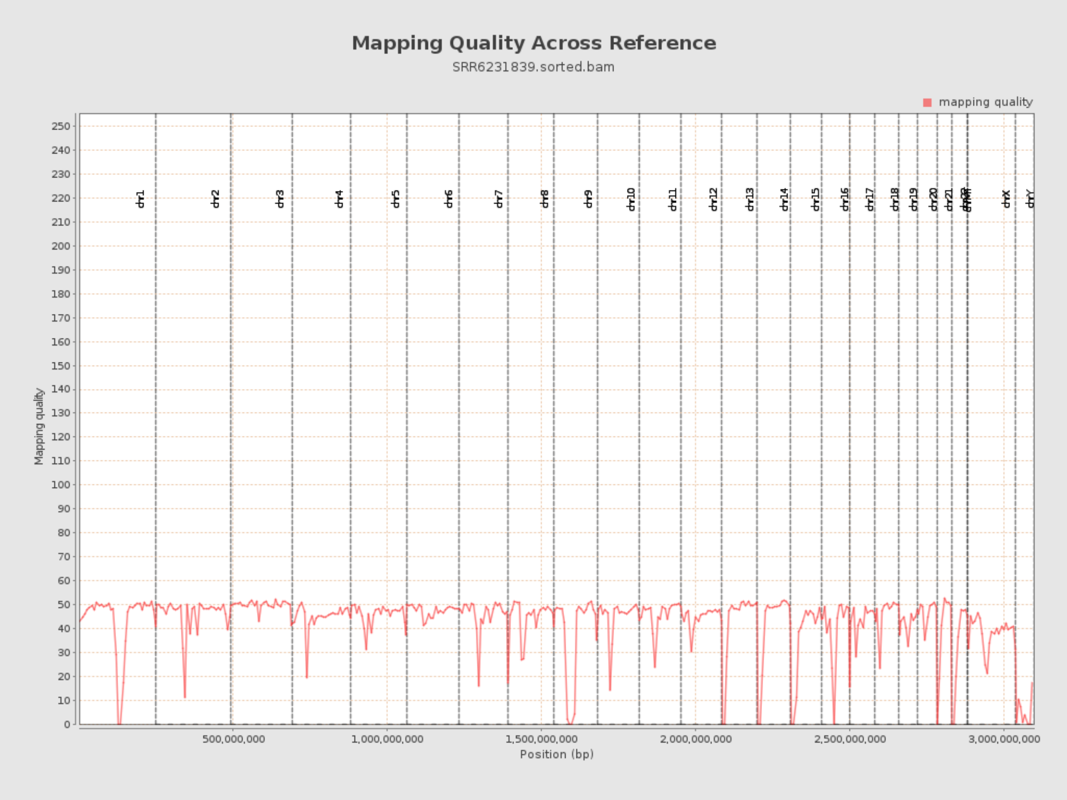
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram