Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 06:10:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231832.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_SRR6231832 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231832.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 06:10:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231832.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,338,269
Mapped reads	2,961,879 / 88.72%
Unmapped reads	376,390 / 11.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,028 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	764,973 / 22.92%
Duplication rate	17.42%
Clipped reads	1,785,400 / 53.48%

2.2. ACGT Content

Number/percentage of A's	46,288,240 / 25.11%
Number/percentage of C's	33,118,749 / 17.97%
Number/percentage of T's	60,868,647 / 33.02%
Number/percentage of G's	43,993,344 / 23.87%
Number/percentage of N's	70,283 / 0.04%
GC Percentage	41.83%

2.3. Coverage

Mean	0.0596

Standard Deviation	0.7769

2.4. Mapping Quality

Mean Mapping Quality	45.07

2.5. Mismatches and indels

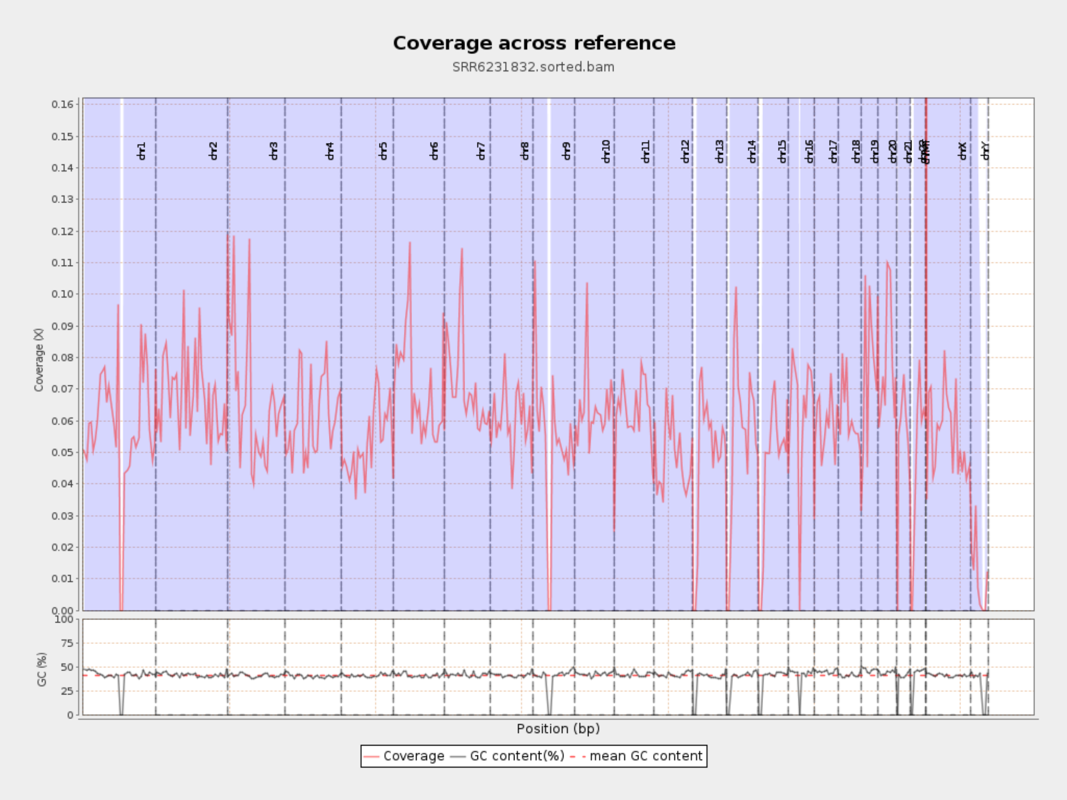
General error rate	0.68%
Mismatches	1,222,131
Insertions	12,174
Mapped reads with at least one insertion	0.41%
Deletions	39,744
Mapped reads with at least one deletion	1.33%
Homopolymer indels	42.81%

2.6. Chromosome stats

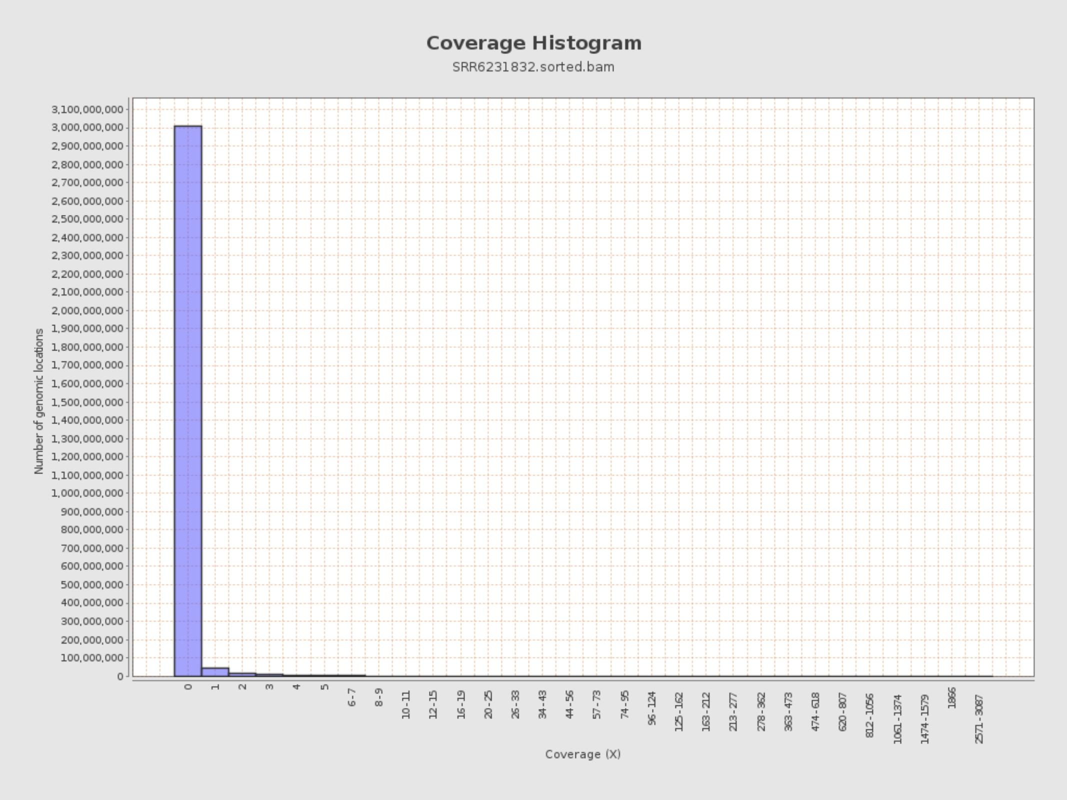
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14473198	0.0581	1.153
chr2	243199373	16514111	0.0679	1.5622
chr3	198022430	13199062	0.0667	0.491
chr4	191154276	11614683	0.0608	0.4861
chr5	180915260	9565434	0.0529	0.4382
chr6	171115067	12068026	0.0705	0.7545
chr7	159138663	11403968	0.0717	0.8253

chr8	146364022	8741534	0.0597	0.6779
chr9	141213431	7549650	0.0535	0.5555
chr10	135534747	8639843	0.0637	0.614
chr11	135006516	8576401	0.0635	0.5796
chr12	133851895	6457242	0.0482	0.4326
chr13	115169878	5663173	0.0492	0.4832
chr14	107349540	6119241	0.057	0.4776
chr15	102531392	4575661	0.0446	0.4646
chr16	90354753	5582617	0.0618	0.509
chr17	81195210	4819515	0.0594	0.4808
chr18	78077248	4850810	0.0621	1.2738
chr19	59128983	4511073	0.0763	0.8148
chr20	63025520	4891763	0.0776	0.5612
chr21	48129895	2557044	0.0531	0.4619
chr22	51304566	2382505	0.0464	0.4199
chrMT	16571	439535	26.5243	17.0463
chrX	155270560	8596536	0.0554	0.4803
chrY	59373566	616262	0.0104	0.2661

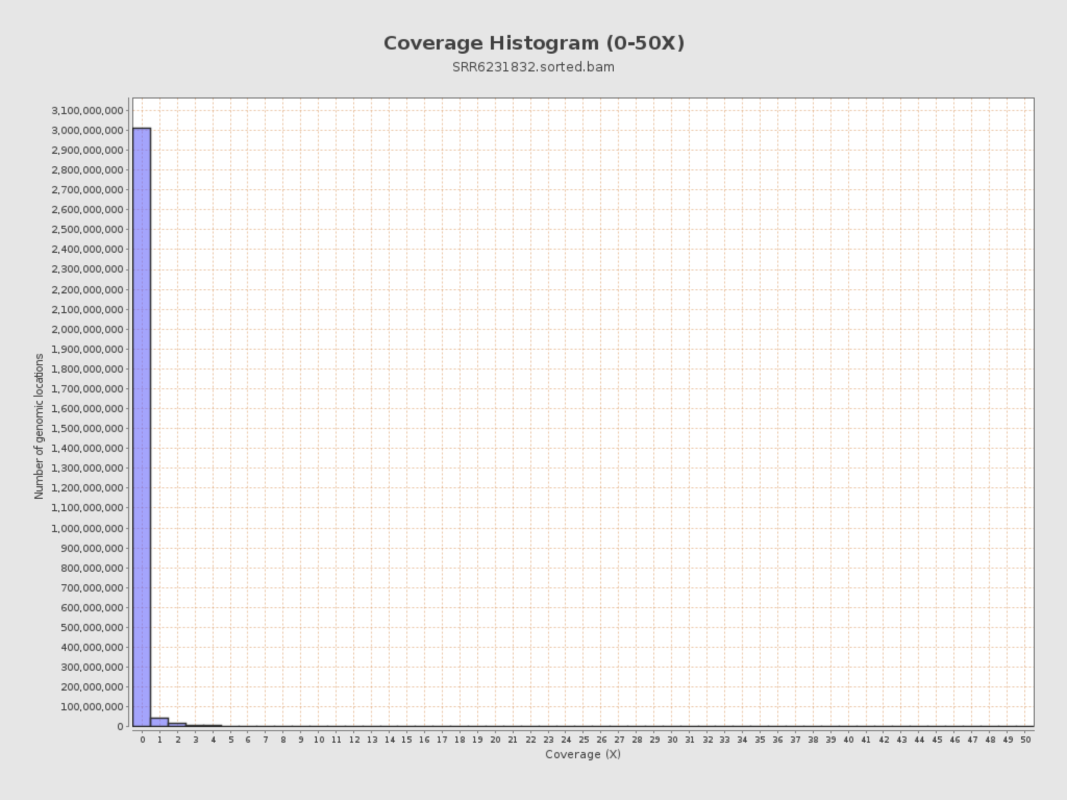
3. Results : Coverage across reference



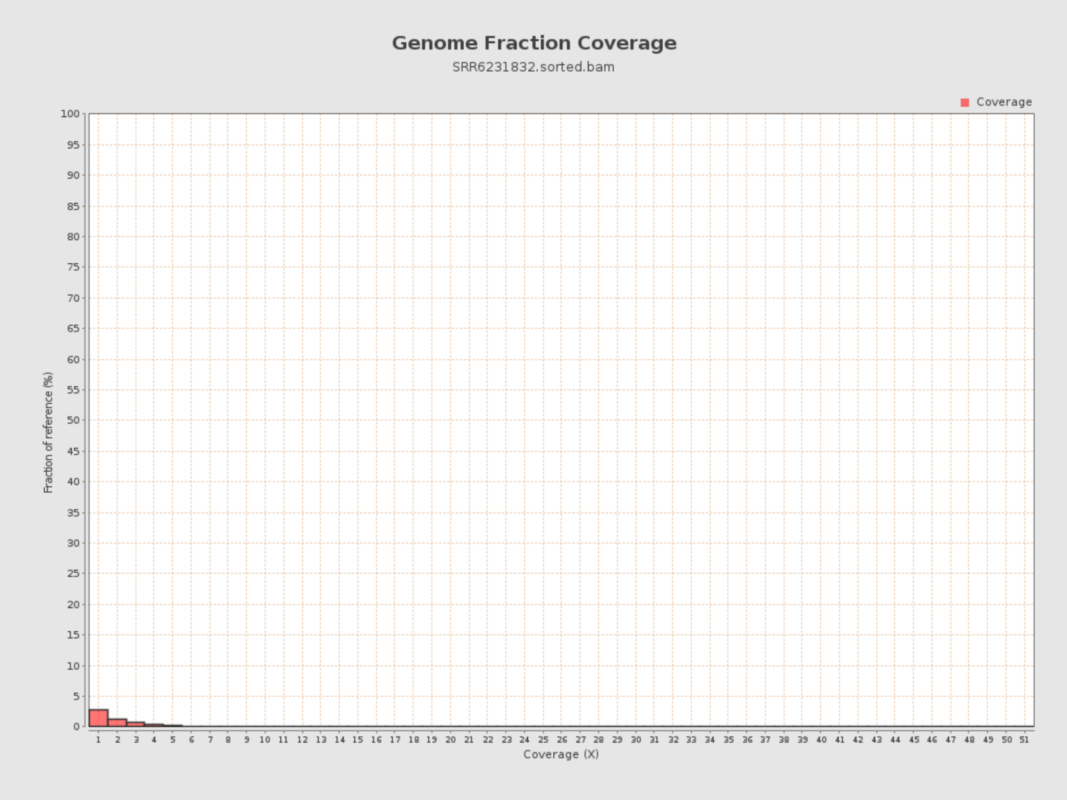
4. Results : Coverage Histogram



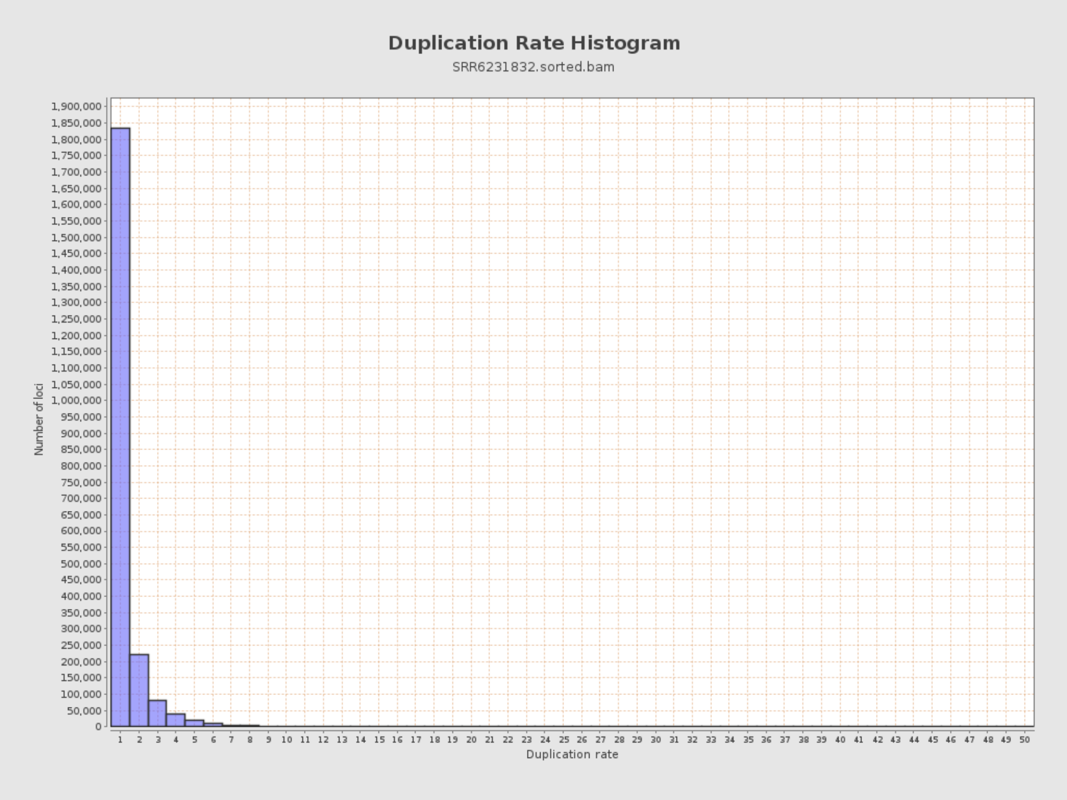
5. Results : Coverage Histogram (0-50X)



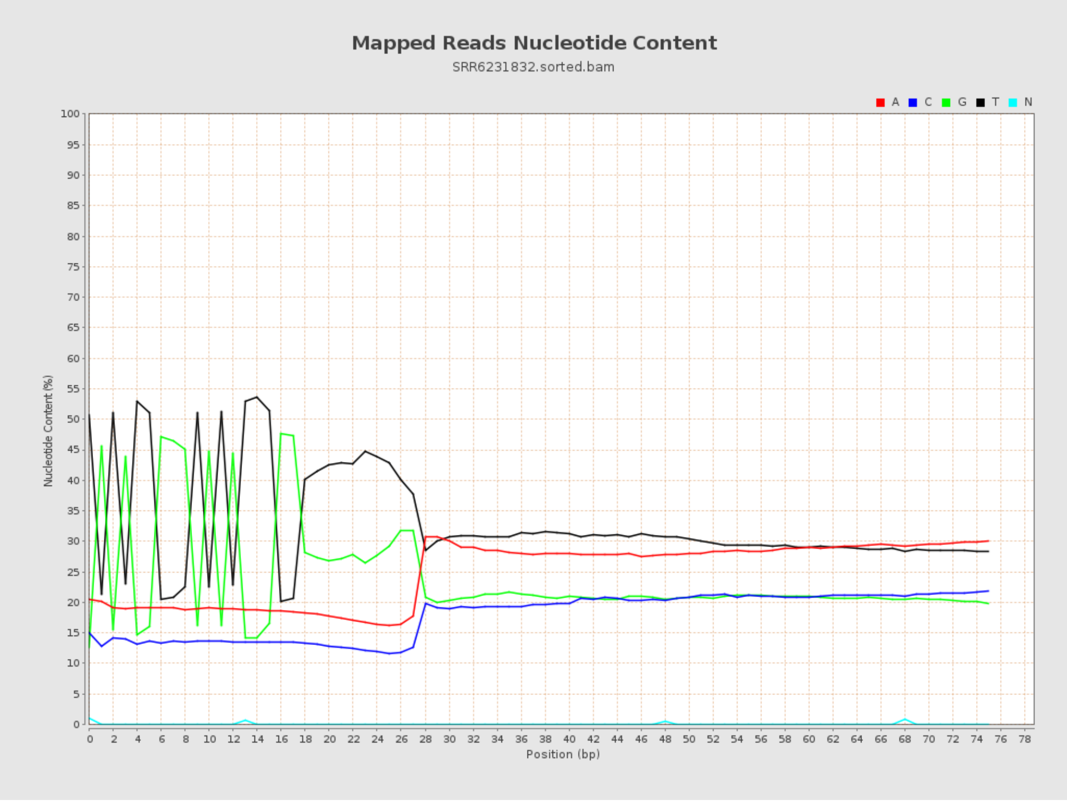
6. Results : Genome Fraction Coverage



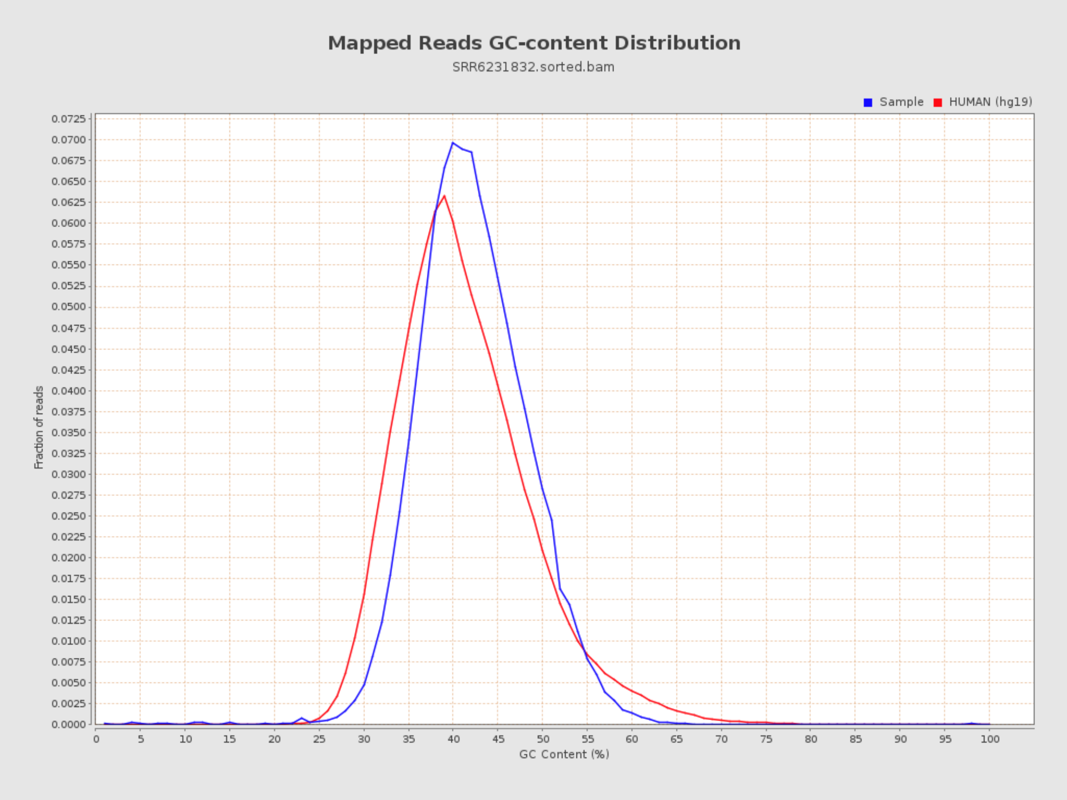
7. Results : Duplication Rate Histogram



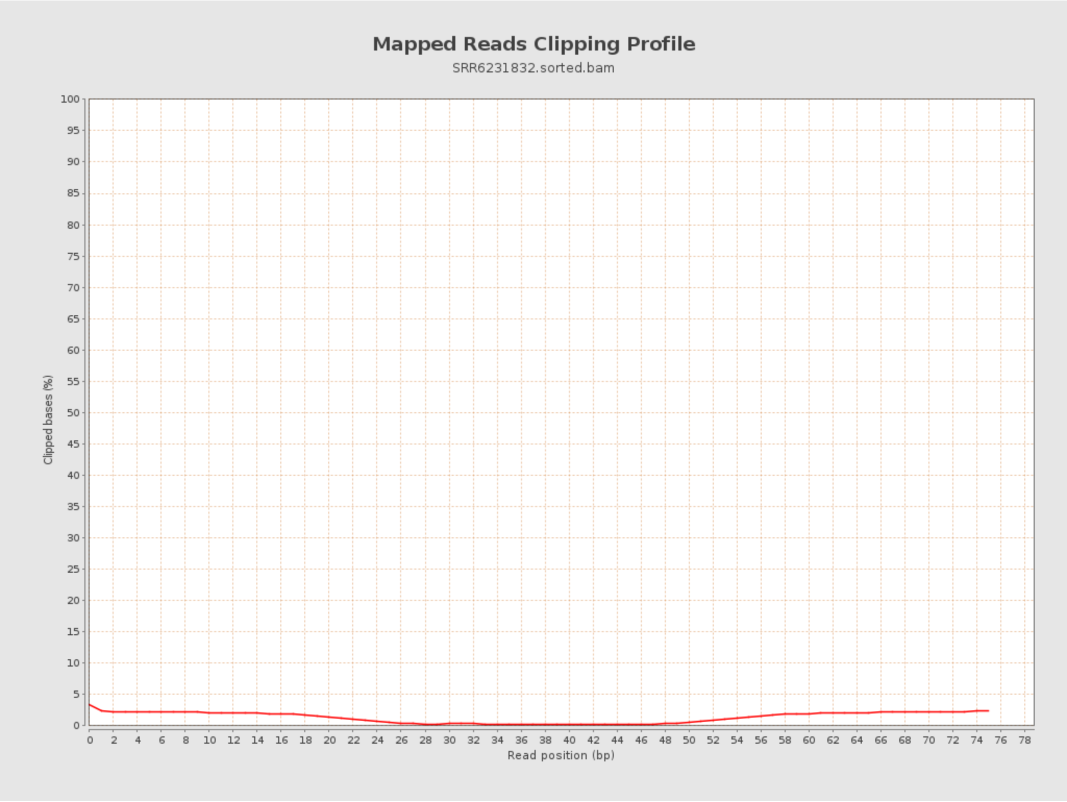
8. Results : Mapped Reads Nucleotide Content



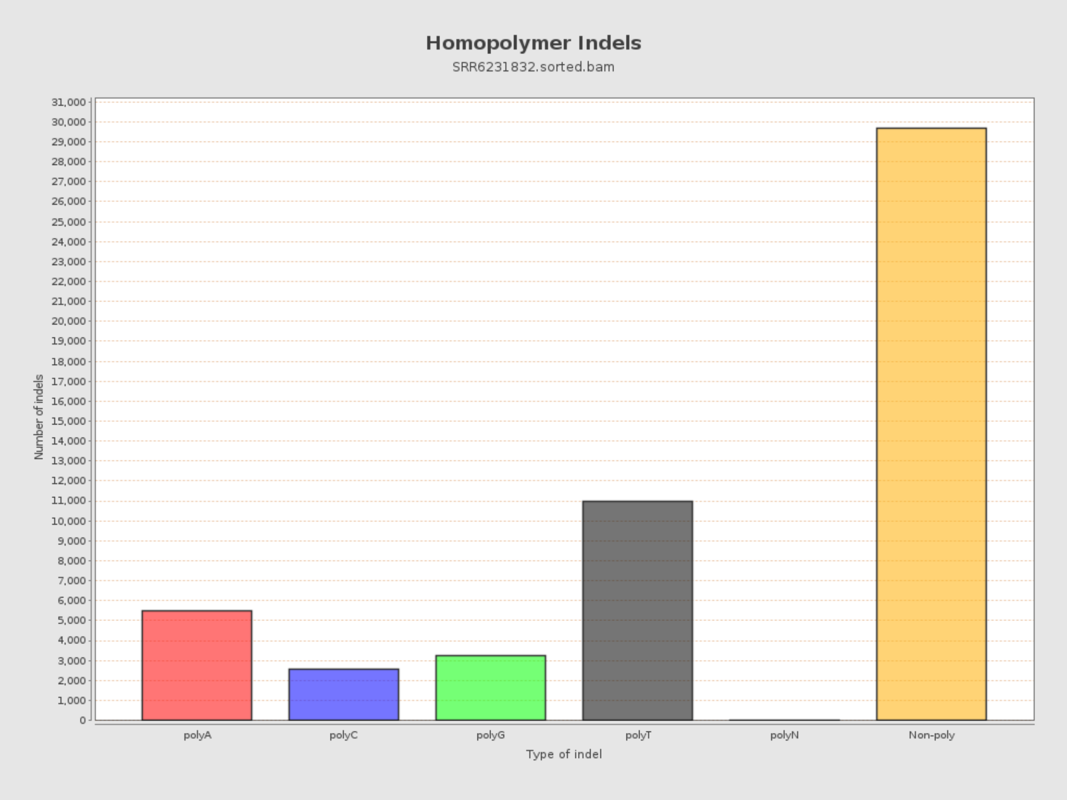
9. Results : Mapped Reads GC-content Distribution



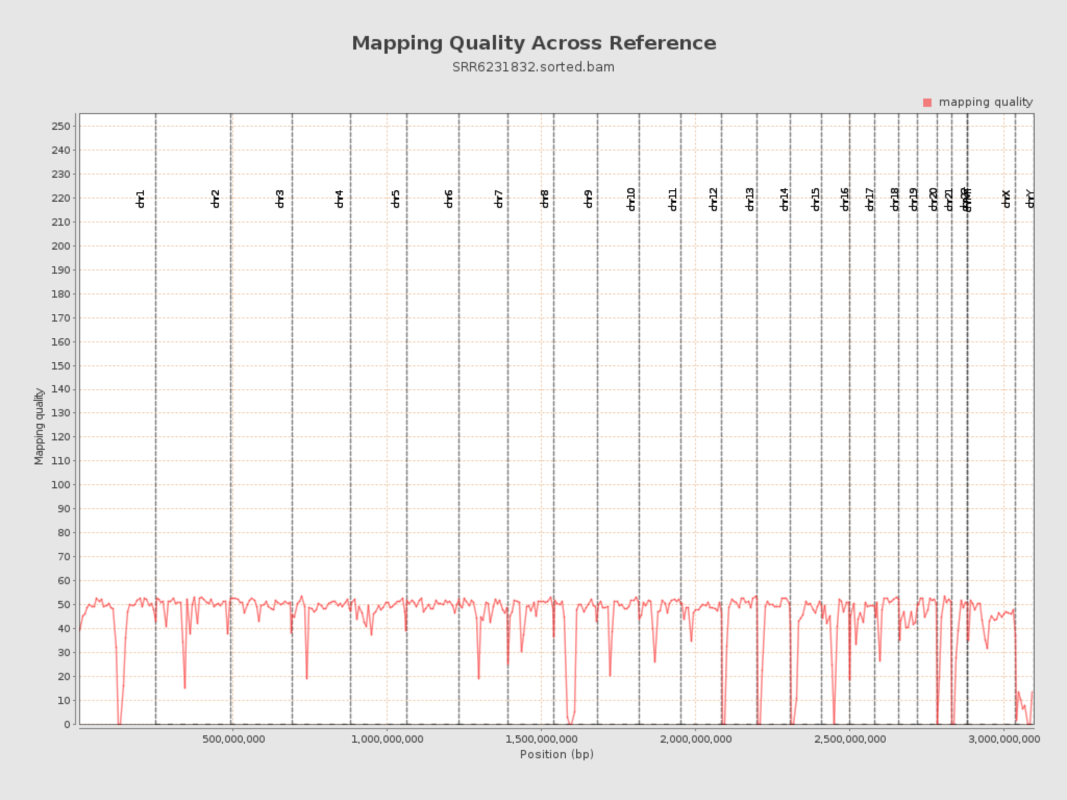
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram