Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 10:42:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231890.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_SRR6231890 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231890.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 10:42:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231890.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,487,153
Mapped reads	3,248,353 / 93.15%
Unmapped reads	238,800 / 6.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,189 / 1.01%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	532,503 / 15.27%
Duplication rate	6.83%
Clipped reads	1,175,169 / 33.7%

2.2. ACGT Content

Number/percentage of A's	56,130,818 / 25.17%
Number/percentage of C's	40,002,430 / 17.94%
Number/percentage of T's	61,301,904 / 27.49%
Number/percentage of G's	65,536,128 / 29.39%
Number/percentage of N's	45,875 / 0.02%
GC Percentage	47.32%

2.3. Coverage

Mean	0.0721

Standard Deviation	40.3942

2.4. Mapping Quality

Mean Mapping Quality	40.38

2.5. Mismatches and indels

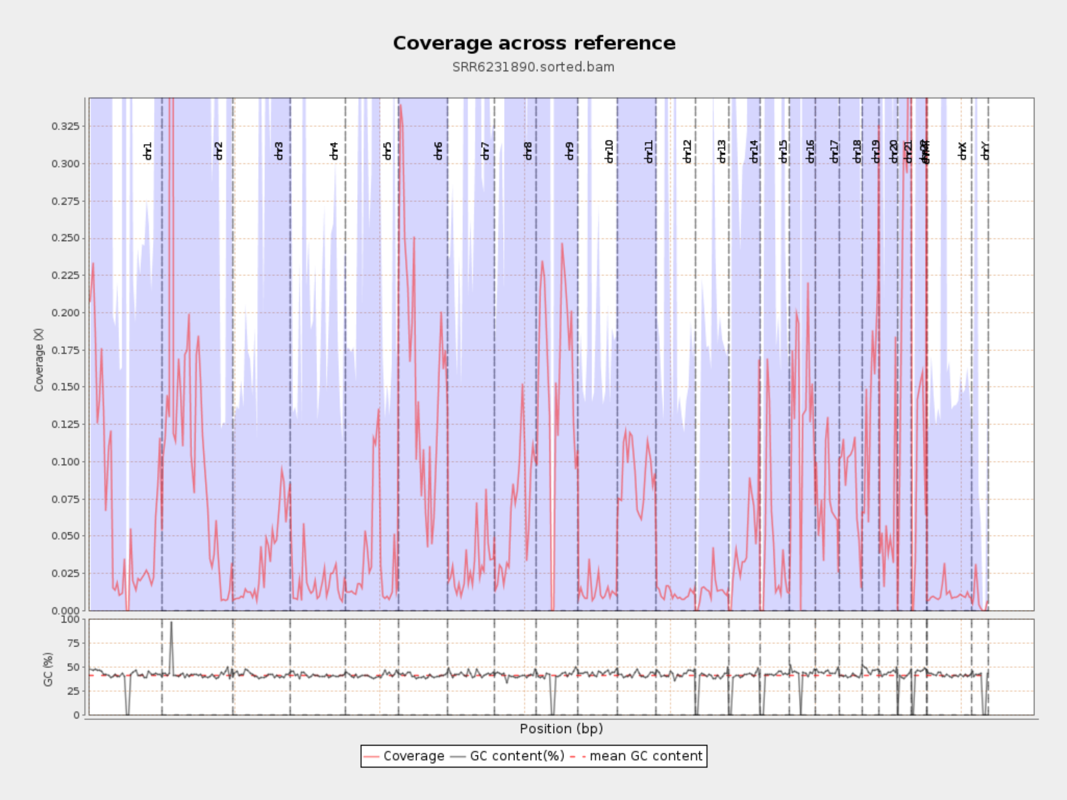
General error rate	0.68%
Mismatches	1,486,376
Insertions	15,279
Mapped reads with at least one insertion	0.47%
Deletions	49,540
Mapped reads with at least one deletion	1.51%
Homopolymer indels	46.16%

2.6. Chromosome stats

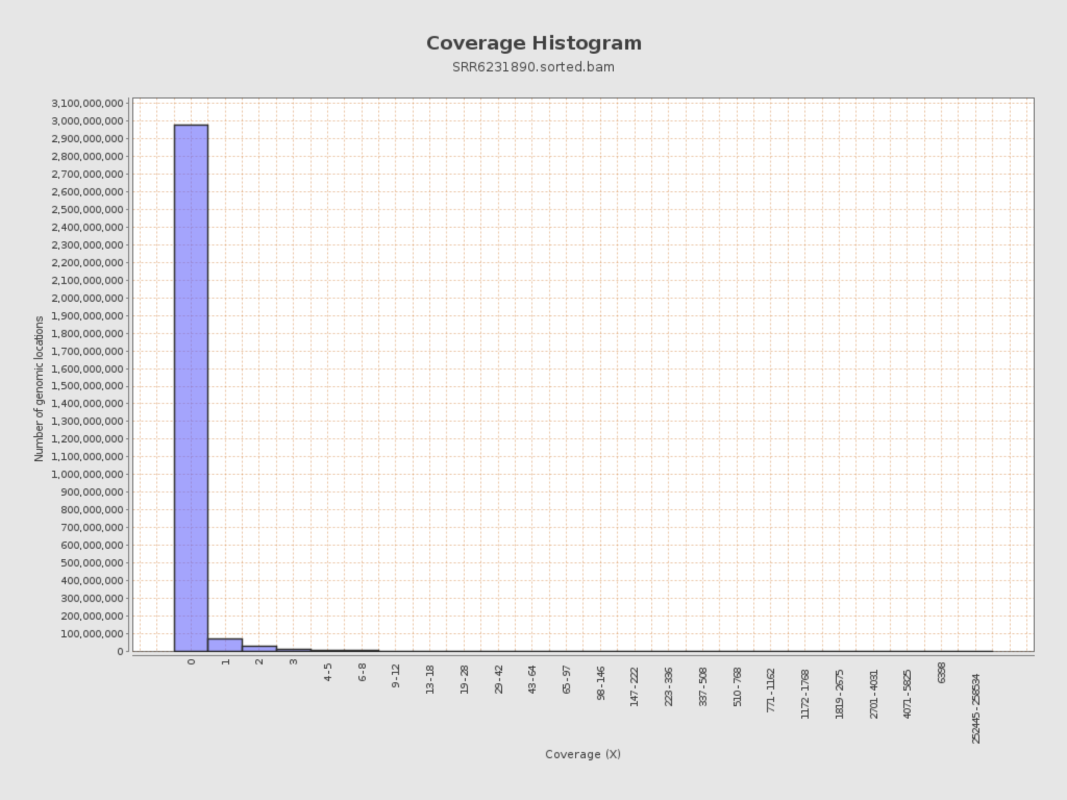
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16648906	0.0668	0.6616
chr2	243199373	43863777	0.1804	144.1024
chr3	198022430	6751690	0.0341	0.2856
chr4	191154276	3448794	0.018	0.2358
chr5	180915260	5983714	0.0331	0.293
chr6	171115067	27264507	0.1593	0.9429
chr7	159138663	4785451	0.0301	0.3885

chr8	146364022	9477555	0.0648	0.6382
chr9	141213431	22286262	0.1578	0.9099
chr10	135534747	1755251	0.013	0.2829
chr11	135006516	12310685	0.0912	1.0068
chr12	133851895	1501593	0.0112	0.2519
chr13	115169878	1556905	0.0135	0.1759
chr14	107349540	4570888	0.0426	0.5339
chr15	102531392	4588679	0.0448	0.3565
chr16	90354753	12332704	0.1365	0.6518
chr17	81195210	5998676	0.0739	0.5496
chr18	78077248	6955881	0.0891	1.3805
chr19	59128983	8456006	0.143	0.8837
chr20	63025520	3846961	0.061	0.4231
chr21	48129895	11982785	0.249	0.8876
chr22	51304566	4610686	0.0899	0.4756
chrMT	16571	9466	0.5712	1.1271
chrX	155270560	1684114	0.0108	0.3036
chrY	59373566	426731	0.0072	0.2019

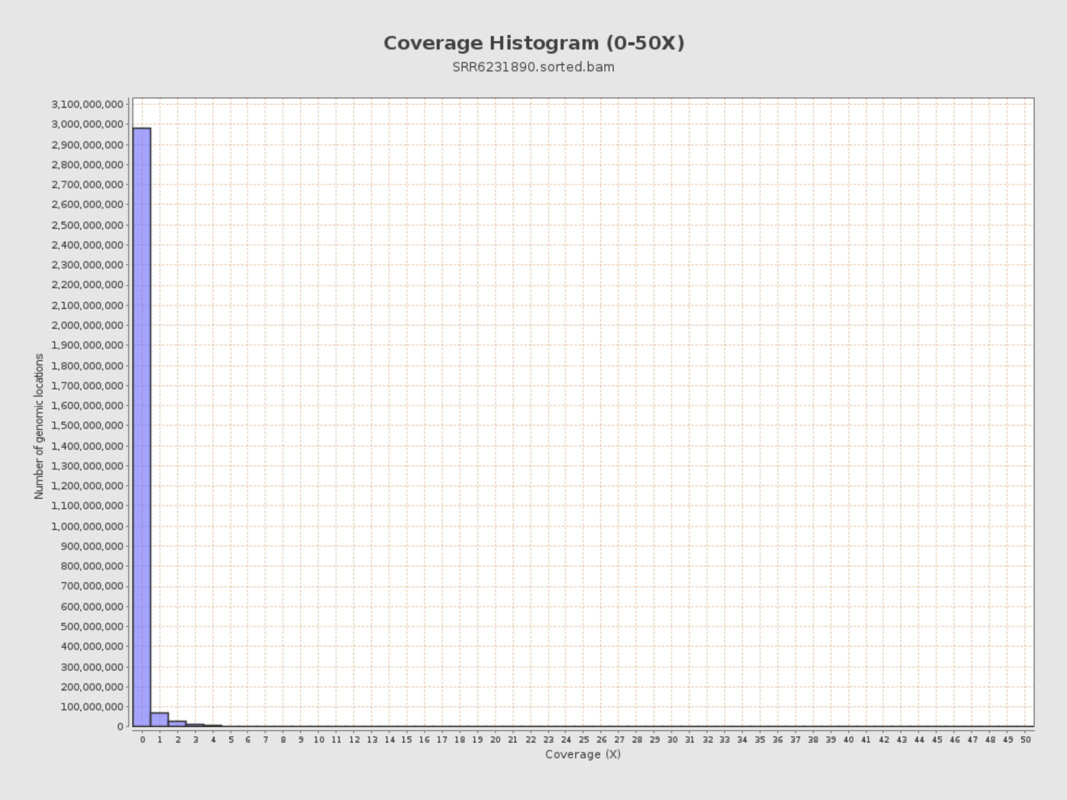
3. Results : Coverage across reference



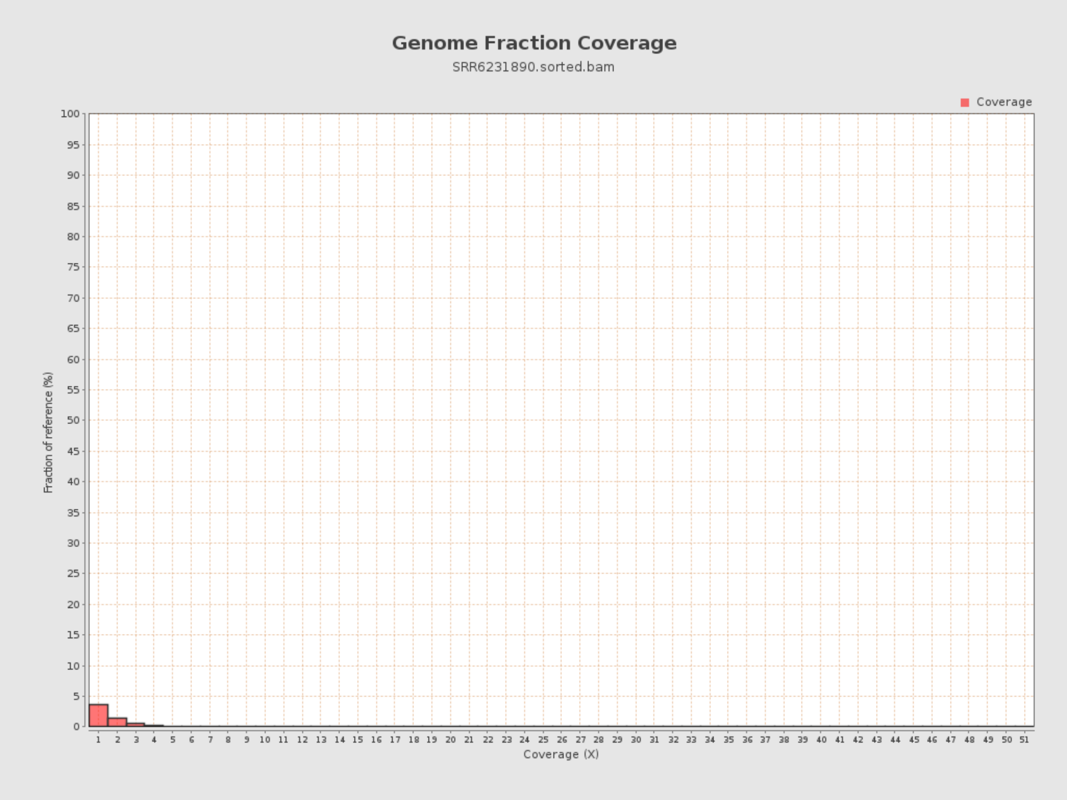
4. Results : Coverage Histogram



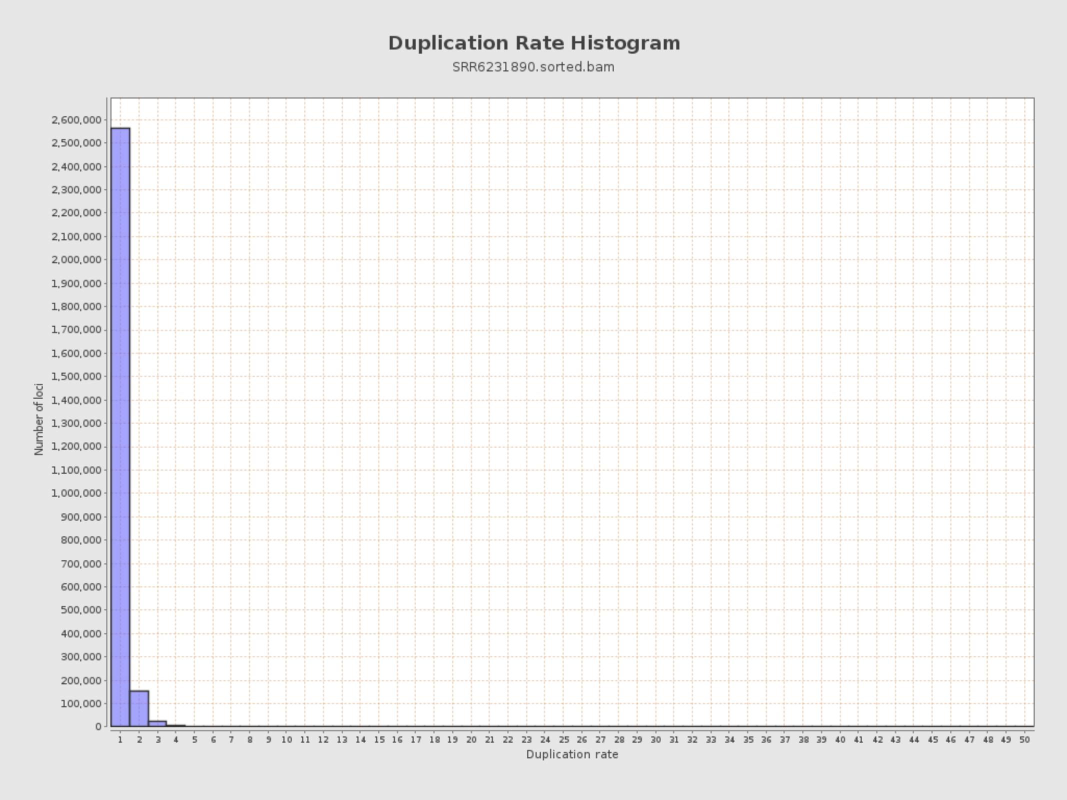
5. Results : Coverage Histogram (0-50X)



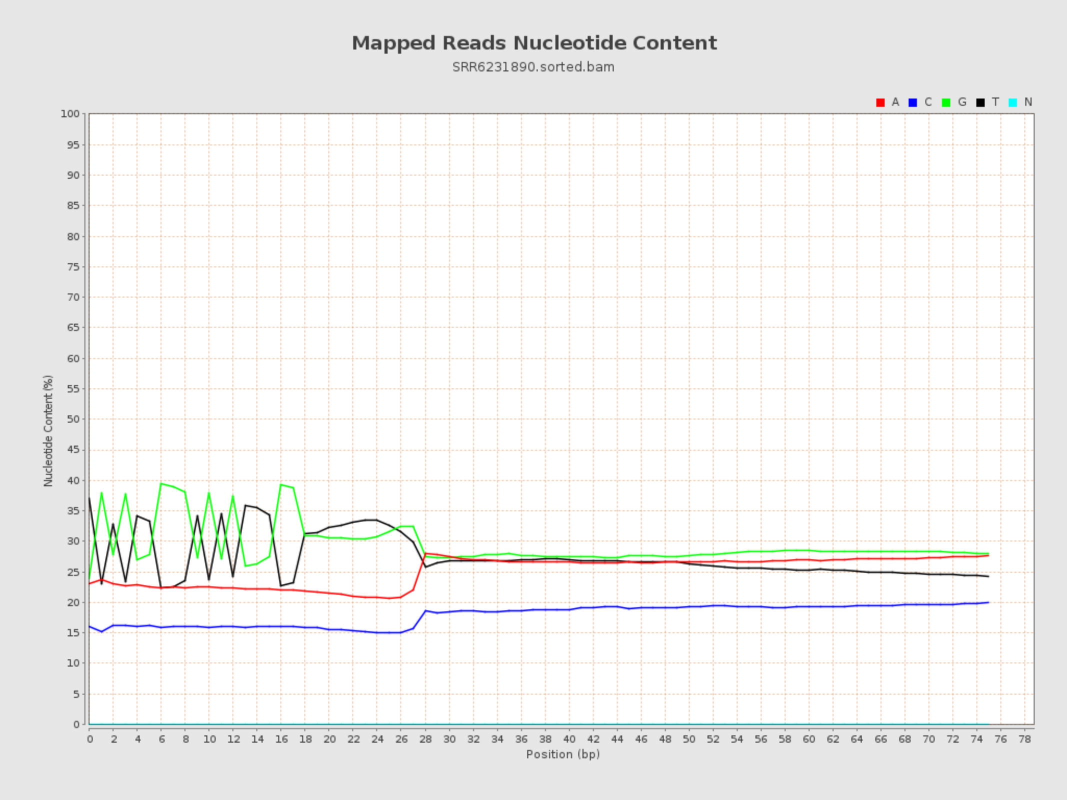
6. Results : Genome Fraction Coverage



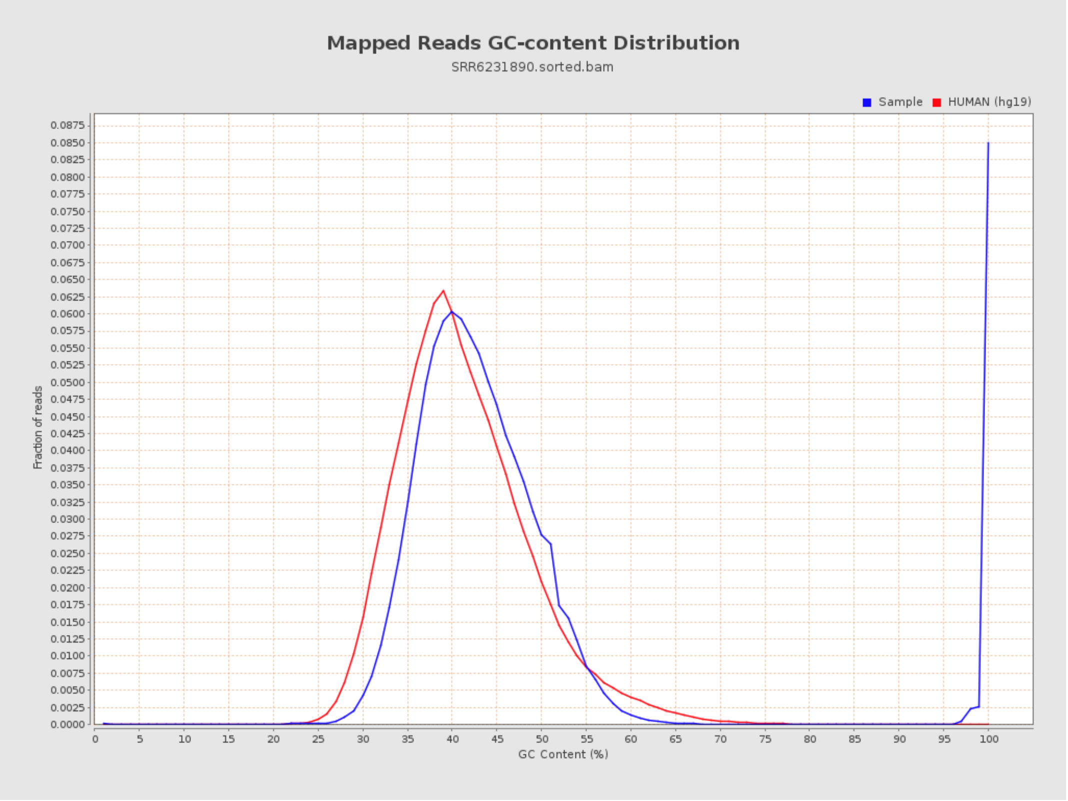
7. Results : Duplication Rate Histogram



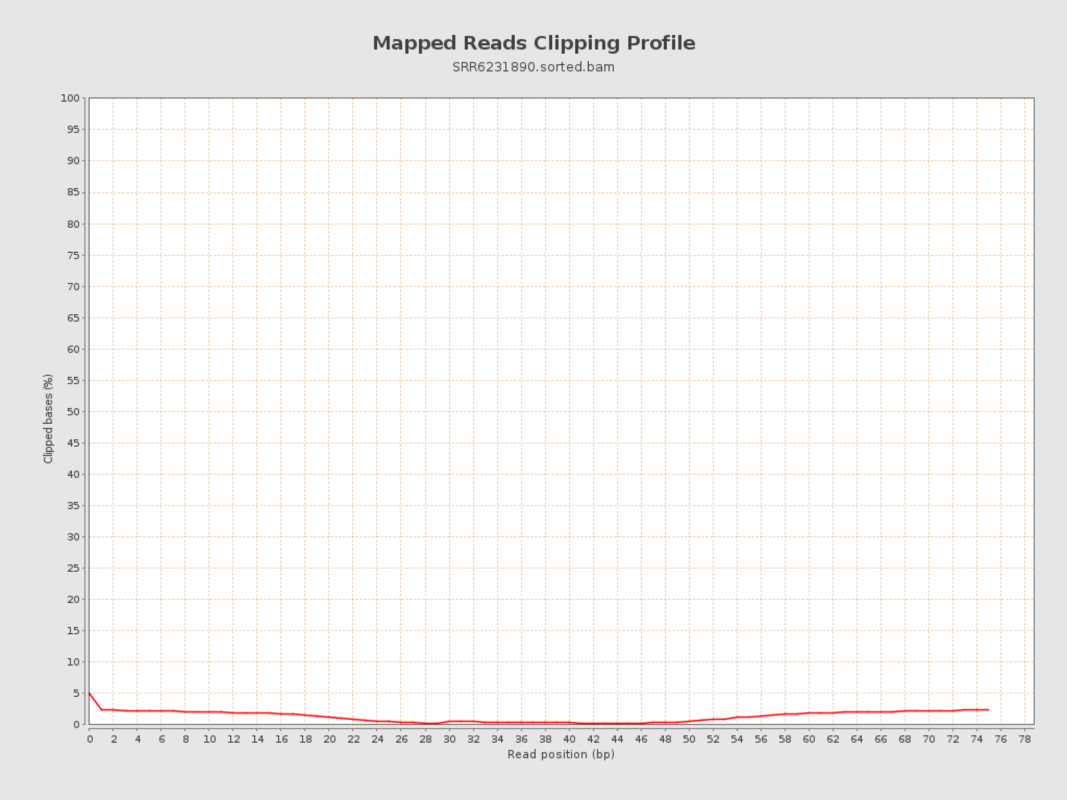
8. Results : Mapped Reads Nucleotide Content



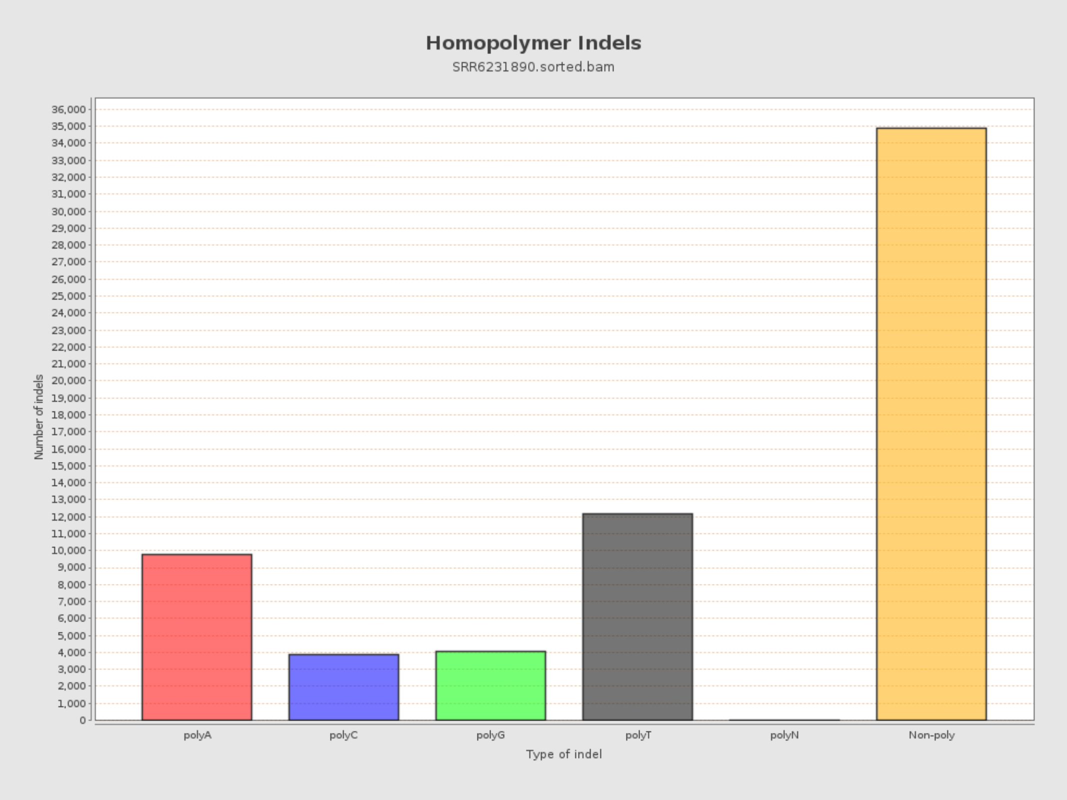
9. Results : Mapped Reads GC-content Distribution



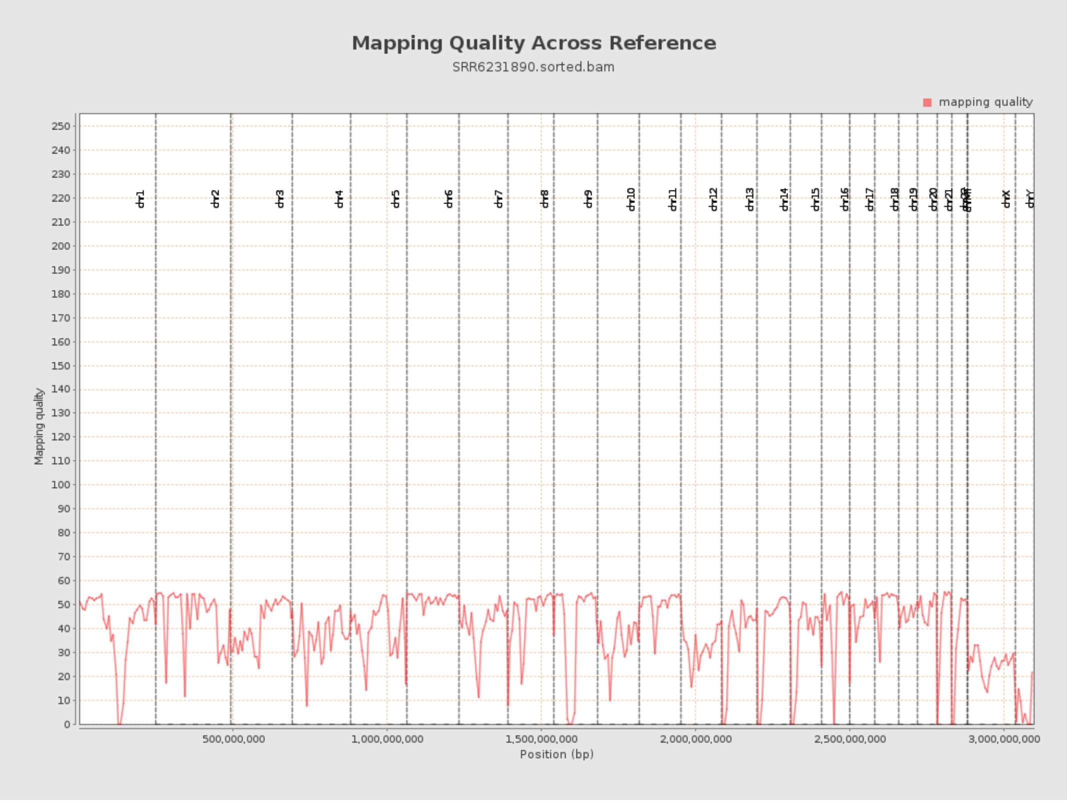
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram