Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 08:57:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231868.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_SRR6231868 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231868.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 08:57:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231868.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,466,314
Mapped reads	3,997,358 / 89.5%
Unmapped reads	468,956 / 10.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,375 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	352,124 / 7.88%
Duplication rate	6.95%
Clipped reads	2,296,792 / 51.42%

2.2. ACGT Content

Number/percentage of A's	66,846,356 / 26.27%
Number/percentage of C's	45,907,949 / 18.04%
Number/percentage of T's	81,774,734 / 32.14%
Number/percentage of G's	59,819,625 / 23.51%
Number/percentage of N's	95,487 / 0.04%
GC Percentage	41.55%

2.3. Coverage

Mean	0.0822

Standard Deviation	0.919

2.4. Mapping Quality

Mean Mapping Quality	42.72

2.5. Mismatches and indels

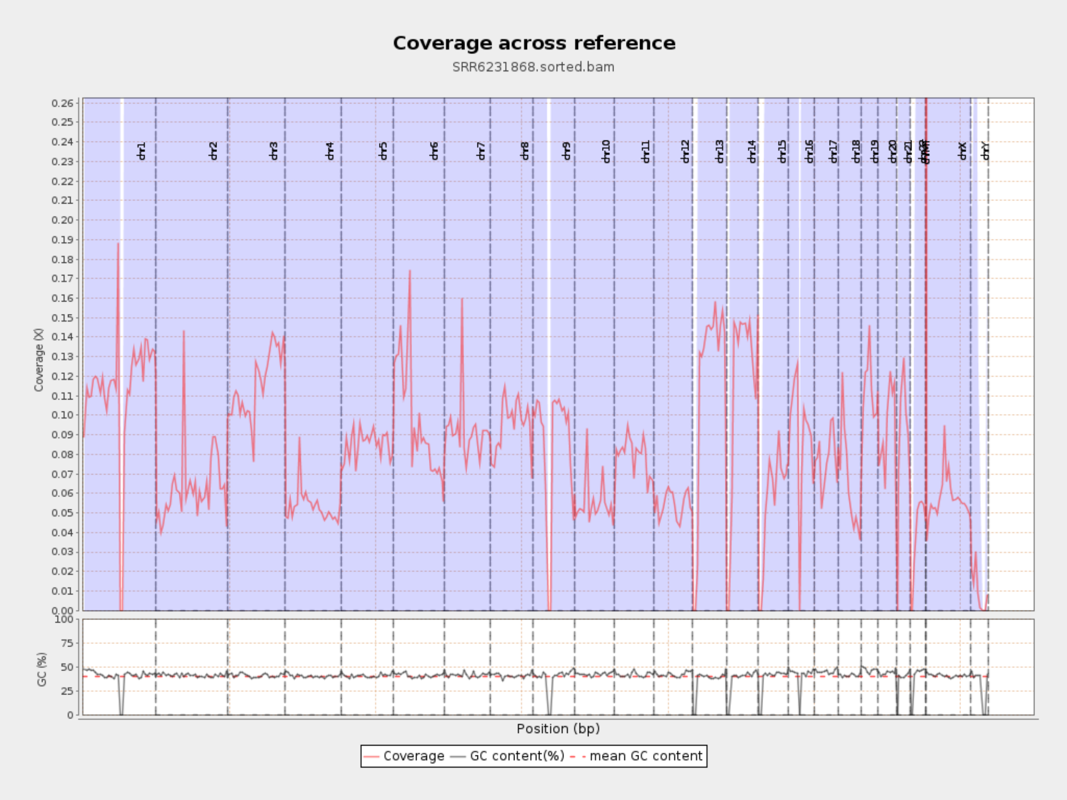
General error rate	0.67%
Mismatches	1,684,305
Insertions	18,050
Mapped reads with at least one insertion	0.45%
Deletions	55,576
Mapped reads with at least one deletion	1.38%
Homopolymer indels	44%

2.6. Chromosome stats

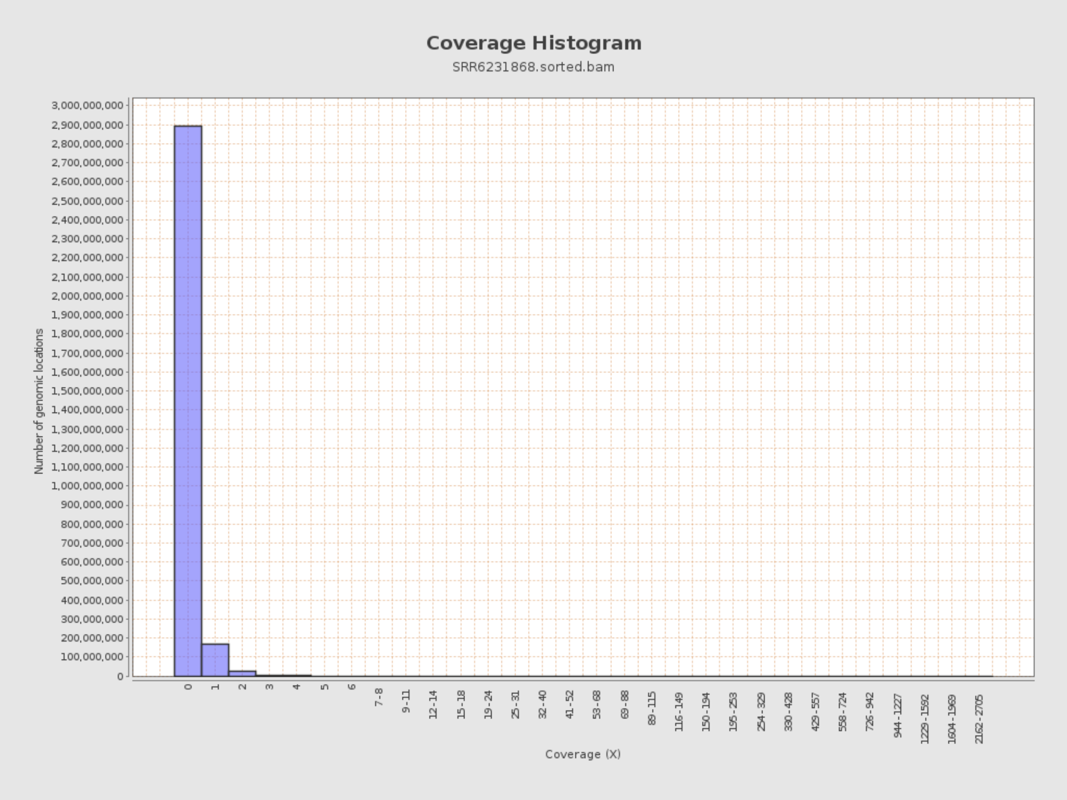
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28265598	0.1134	1.917
chr2	243199373	15366603	0.0632	1.3695
chr3	198022430	22870119	0.1155	0.4212
chr4	191154276	10241525	0.0536	0.3822
chr5	180915260	15402764	0.0851	0.3704
chr6	171115067	16888980	0.0987	0.6365
chr7	159138663	14714878	0.0925	1.1661

chr8	146364022	13863346	0.0947	1.2023
chr9	141213431	11945977	0.0846	0.7135
chr10	135534747	7468619	0.0551	0.4953
chr11	135006516	10692097	0.0792	0.7019
chr12	133851895	7289911	0.0545	0.3197
chr13	115169878	13597180	0.1181	0.4504
chr14	107349540	12363767	0.1152	0.5041
chr15	102531392	5635427	0.055	0.4076
chr16	90354753	7931291	0.0878	0.4713
chr17	81195210	6383097	0.0786	0.4283
chr18	78077248	5196726	0.0666	1.7248
chr19	59128983	6691073	0.1132	1.1519
chr20	63025520	5901218	0.0936	0.4452
chr21	48129895	4210437	0.0875	0.3977
chr22	51304566	1974262	0.0385	0.233
chrMT	16571	97921	5.9092	4.3484
chrX	155270560	8954059	0.0577	0.4441
chrY	59373566	592165	0.01	0.1956

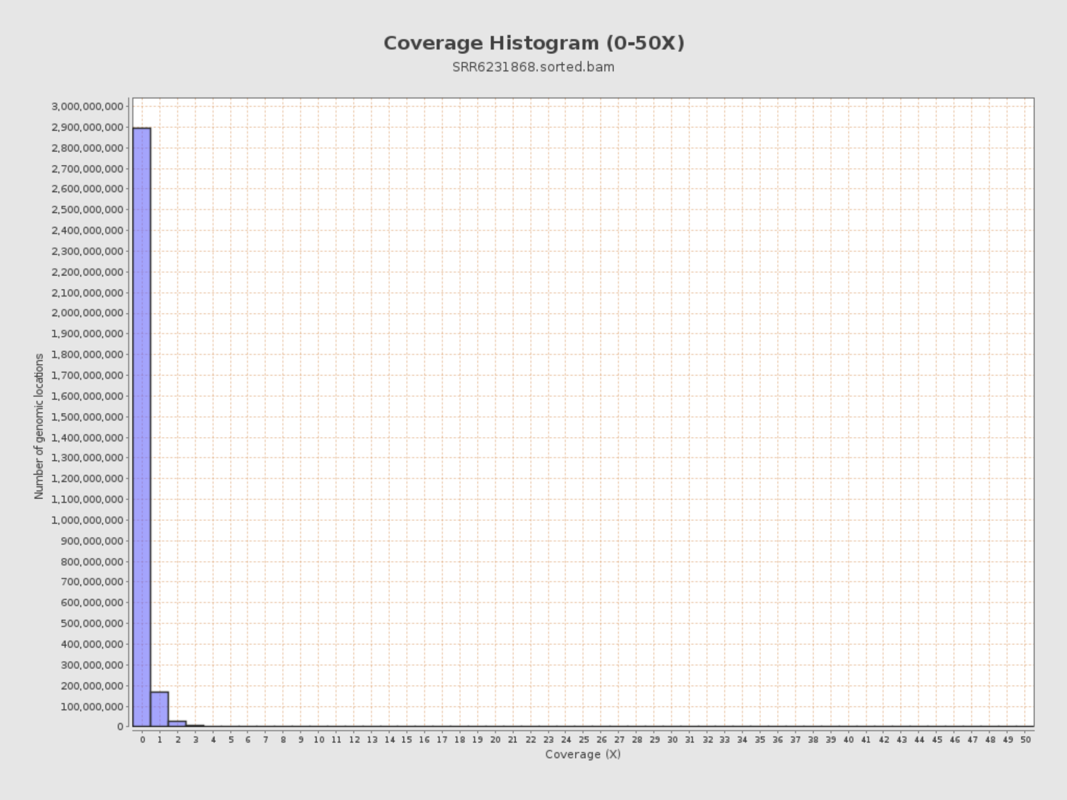
3. Results : Coverage across reference



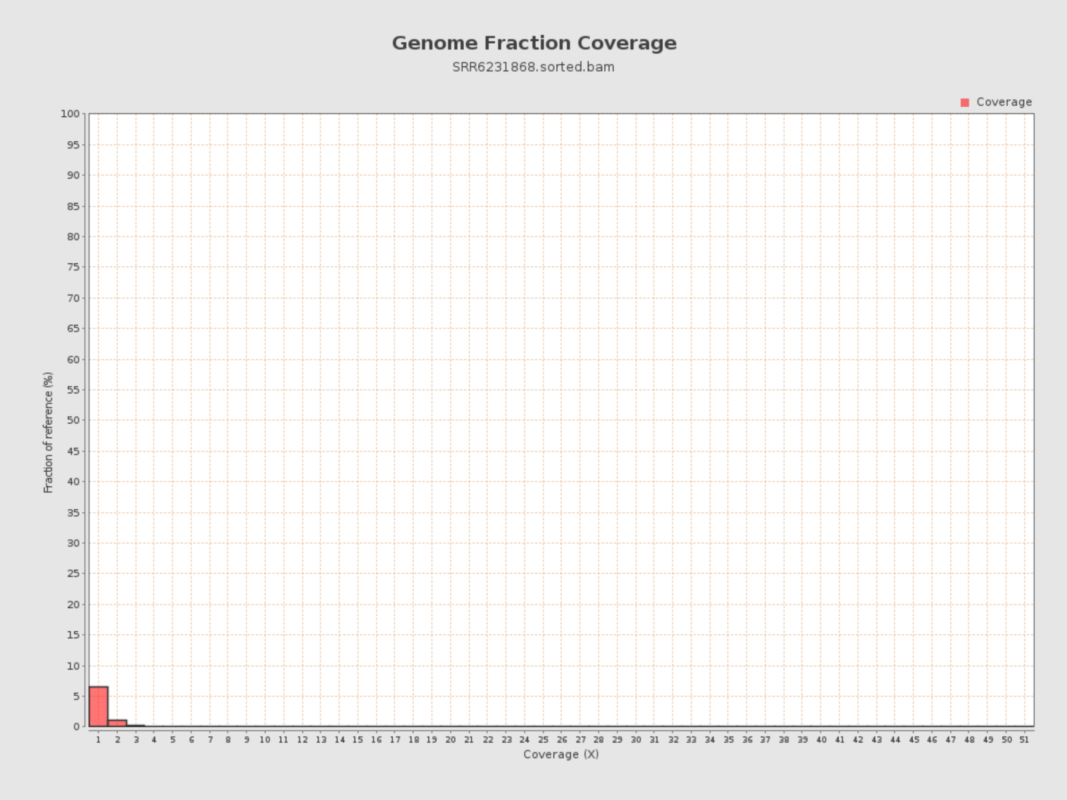
4. Results : Coverage Histogram



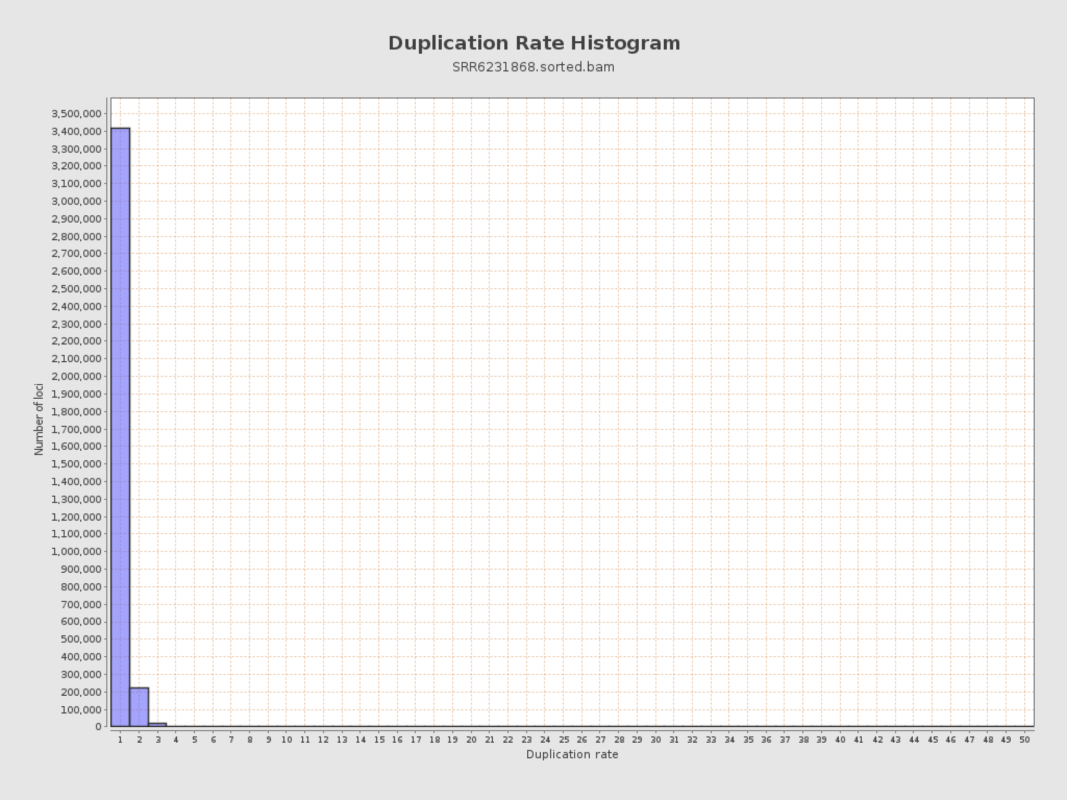
5. Results : Coverage Histogram (0-50X)



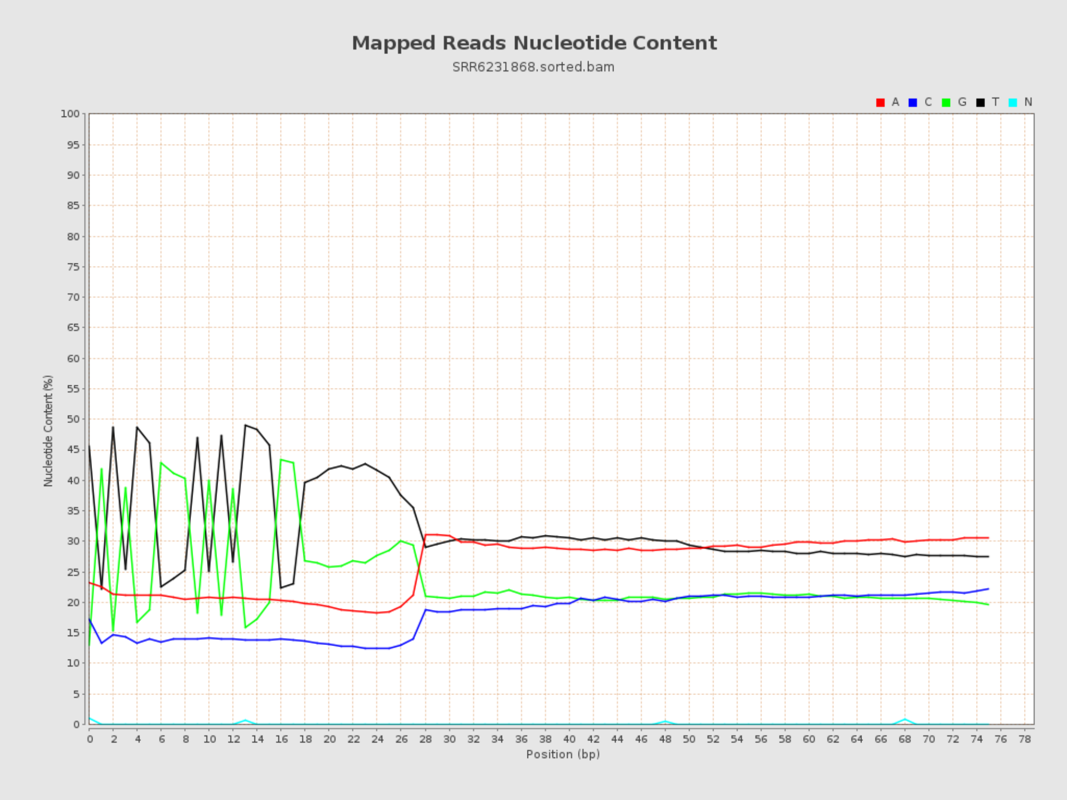
6. Results : Genome Fraction Coverage



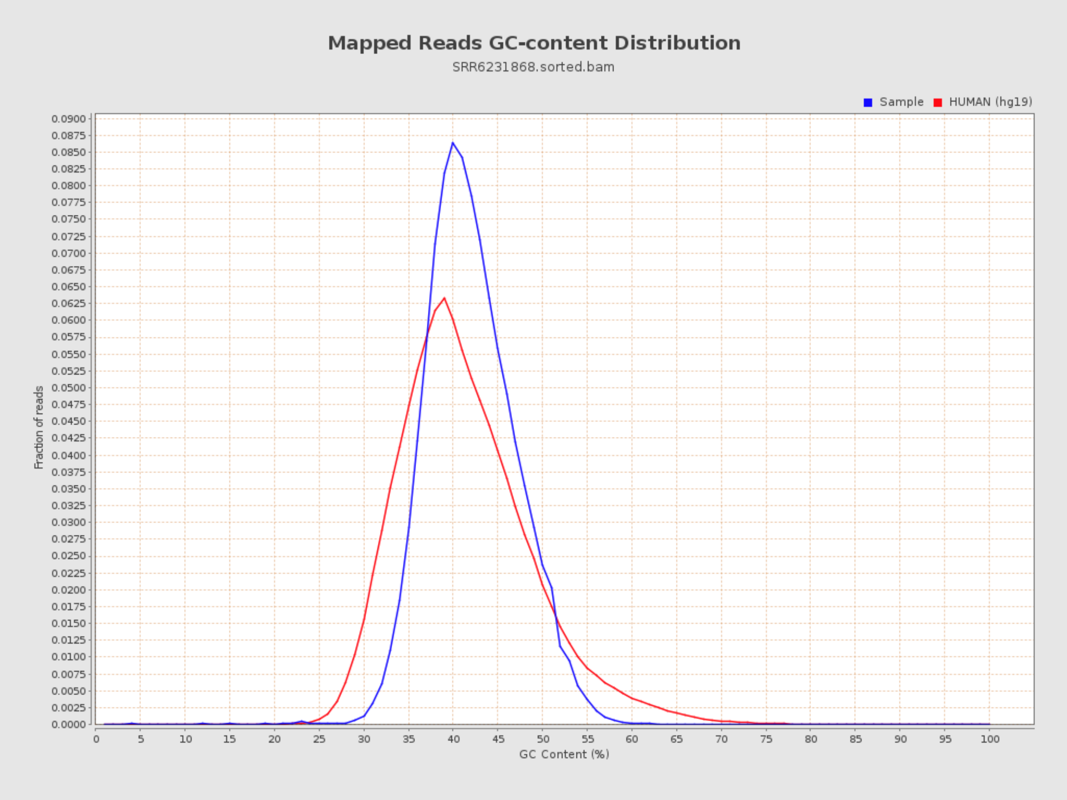
7. Results : Duplication Rate Histogram



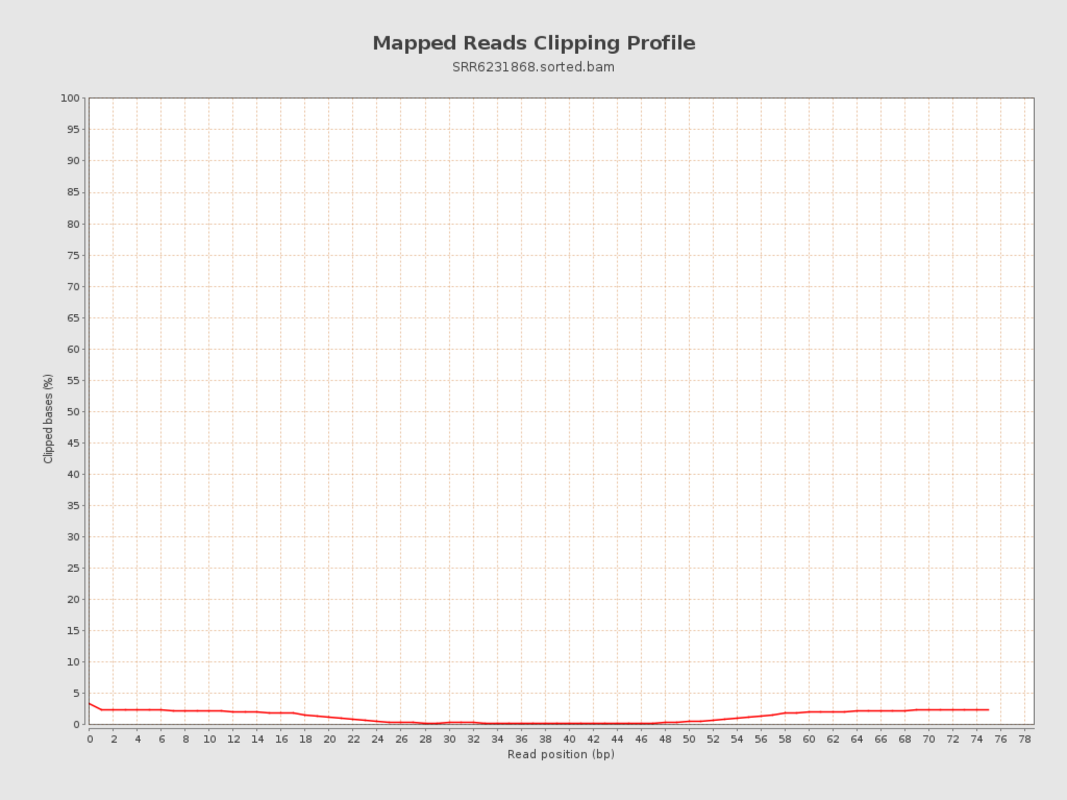
8. Results : Mapped Reads Nucleotide Content



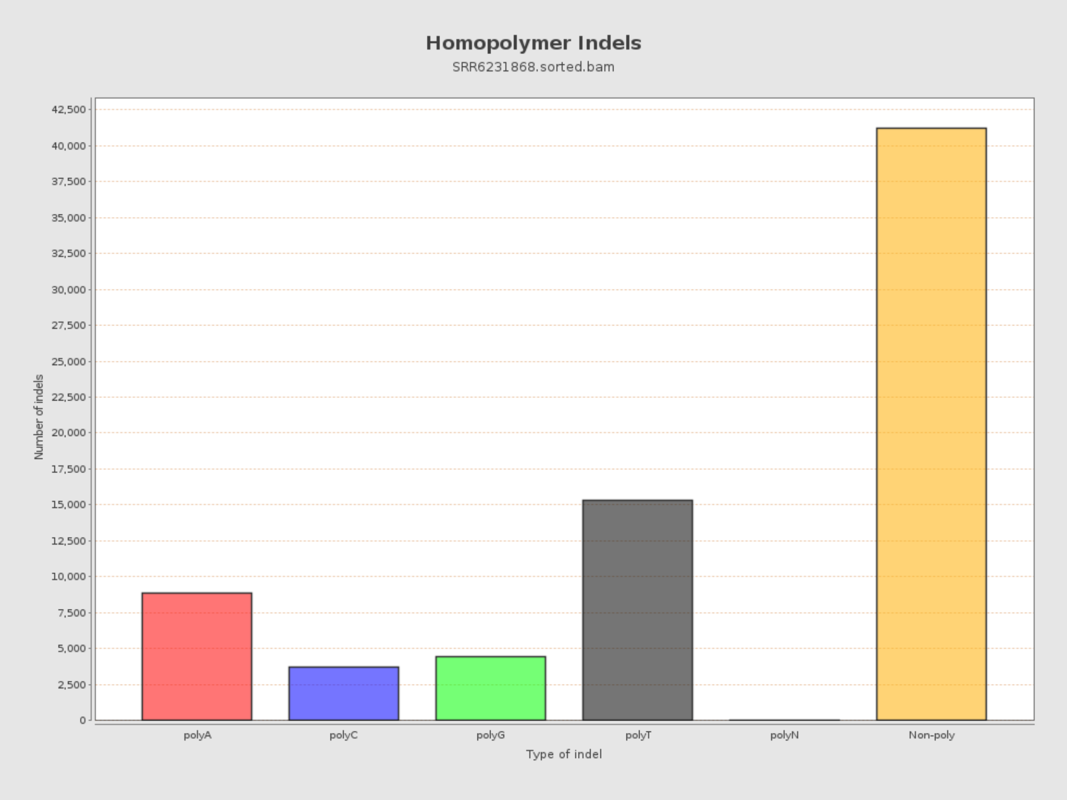
9. Results : Mapped Reads GC-content Distribution



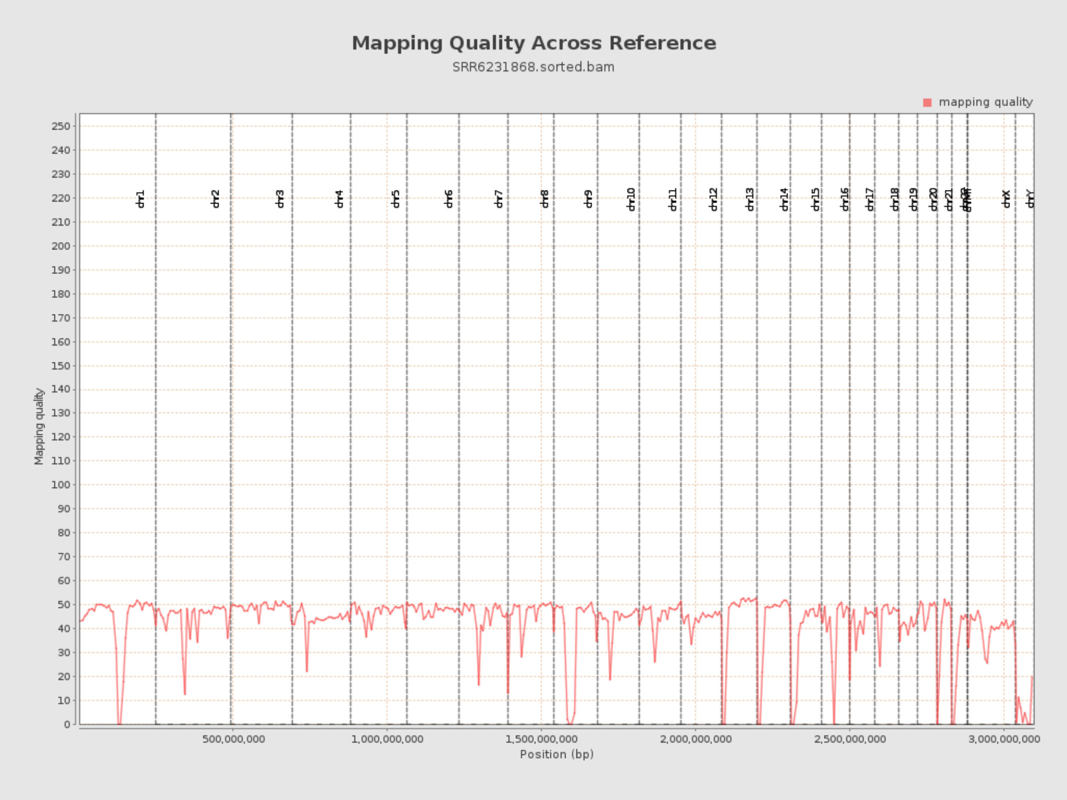
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram