Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 00:42:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231758.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_SRR6231758 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231758.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 00:42:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231758.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,494,591
Mapped reads	4,107,141 / 91.38%
Unmapped reads	387,450 / 8.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	36,111 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	604,813 / 13.46%
Duplication rate	7.08%
Clipped reads	1,421,741 / 31.63%

2.2. ACGT Content

Number/percentage of A's	73,060,666 / 25.83%
Number/percentage of C's	52,495,529 / 18.56%
Number/percentage of T's	79,429,340 / 28.08%
Number/percentage of G's	77,855,516 / 27.52%
Number/percentage of N's	60,593 / 0.02%
GC Percentage	46.08%

2.3. Coverage

Mean	0.0914

Standard Deviation	37.4391

2.4. Mapping Quality

Mean Mapping Quality	46.34

2.5. Mismatches and indels

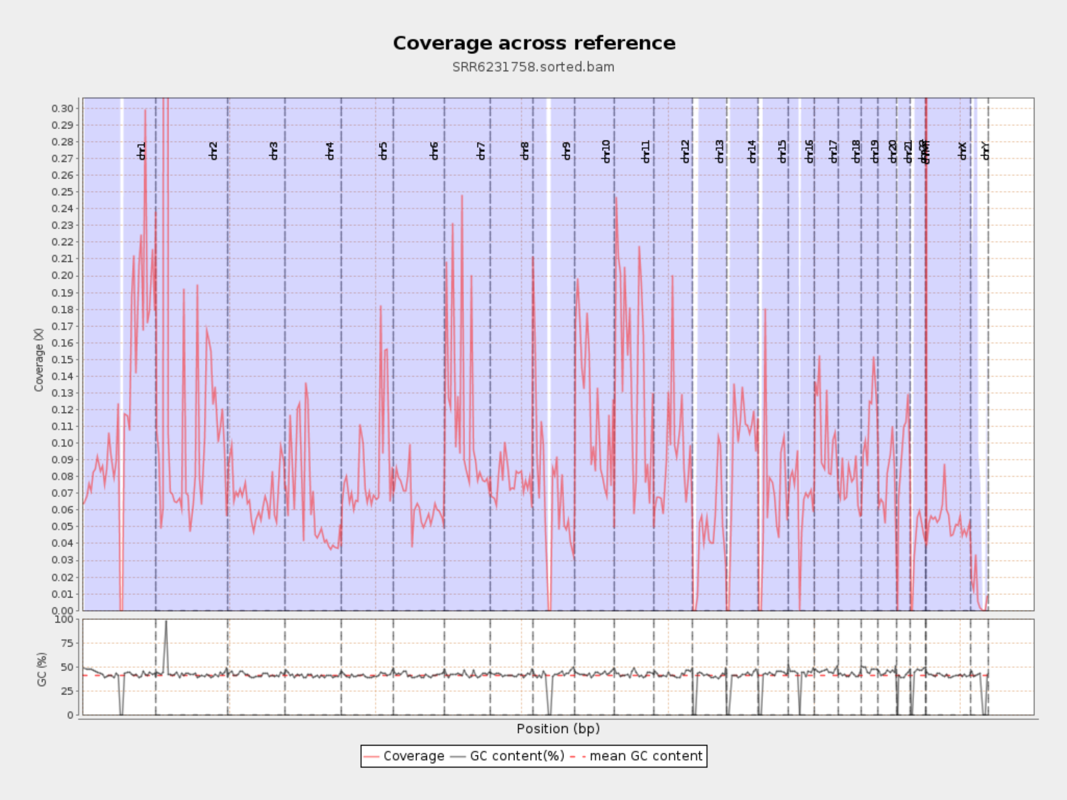
General error rate	0.65%
Mismatches	1,791,613
Insertions	18,235
Mapped reads with at least one insertion	0.44%
Deletions	58,028
Mapped reads with at least one deletion	1.4%
Homopolymer indels	47.11%

2.6. Chromosome stats

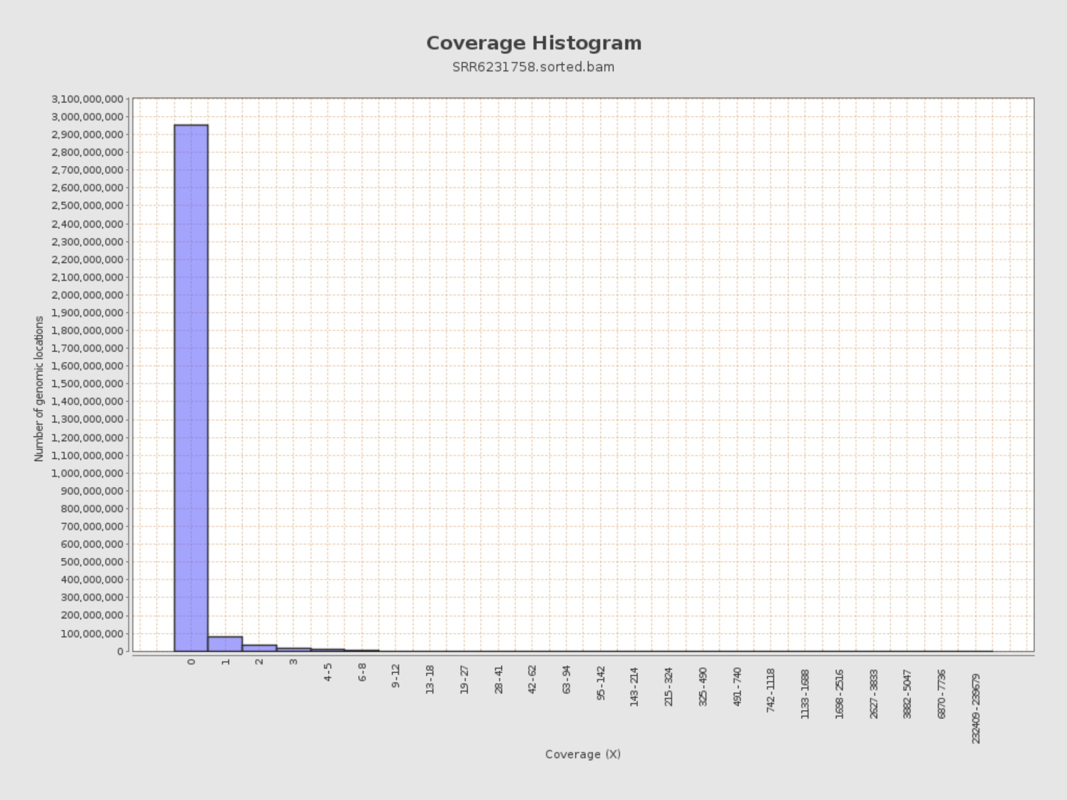
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	30459581	0.1222	1.0581
chr2	243199373	42200051	0.1735	133.5442
chr3	198022430	13555541	0.0685	0.435
chr4	191154276	12727622	0.0666	0.4571
chr5	180915260	15433467	0.0853	0.4896
chr6	171115067	11002866	0.0643	0.5085
chr7	159138663	18584652	0.1168	2.0229

chr8	146364022	11311031	0.0773	0.5779
chr9	141213431	9519108	0.0674	0.6057
chr10	135534747	16334672	0.1205	0.814
chr11	135006516	19648040	0.1455	1.4052
chr12	133851895	12468563	0.0932	0.5247
chr13	115169878	5337285	0.0463	0.3685
chr14	107349540	10349968	0.0964	0.6263
chr15	102531392	6861525	0.0669	0.4476
chr16	90354753	5873288	0.065	0.469
chr17	81195210	8769741	0.108	0.9488
chr18	78077248	5879913	0.0753	1.1145
chr19	59128983	6618239	0.1119	0.7733
chr20	63025520	4803063	0.0762	0.4733
chr21	48129895	4310596	0.0896	0.5301
chr22	51304566	1988494	0.0388	0.3262
chrMT	16571	60618	3.6581	3.5572
chrX	155270560	8329033	0.0536	0.4989
chrY	59373566	569962	0.0096	0.2365

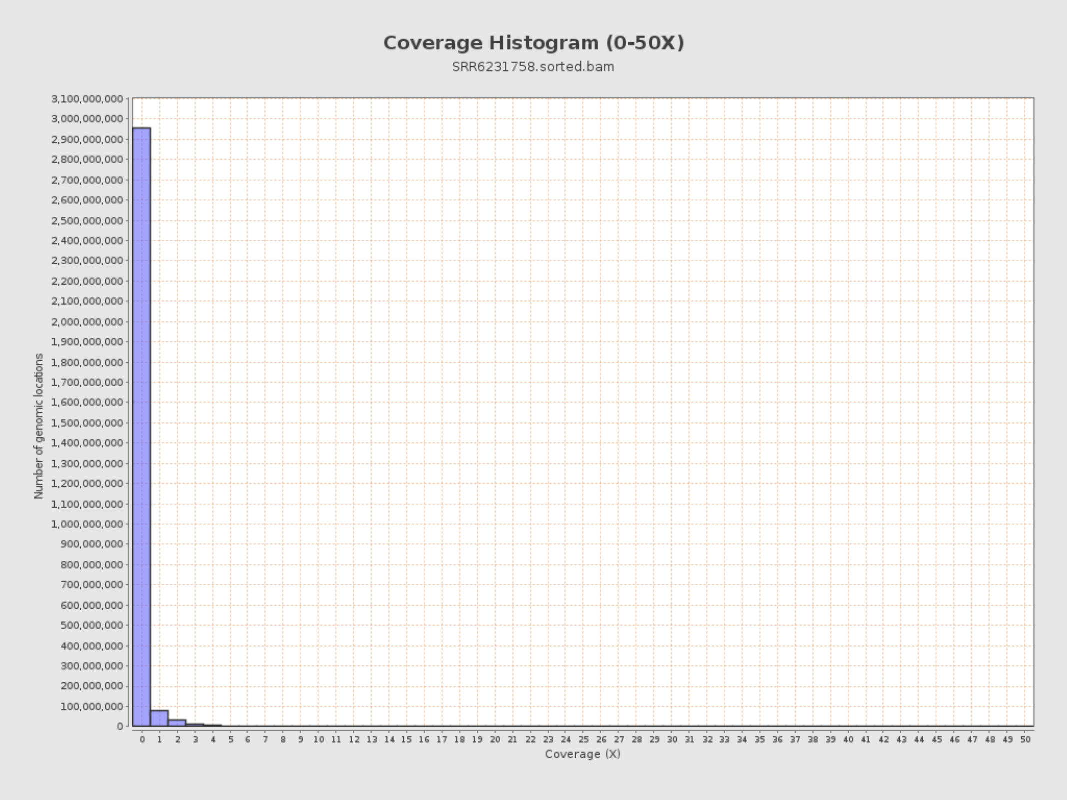
3. Results : Coverage across reference



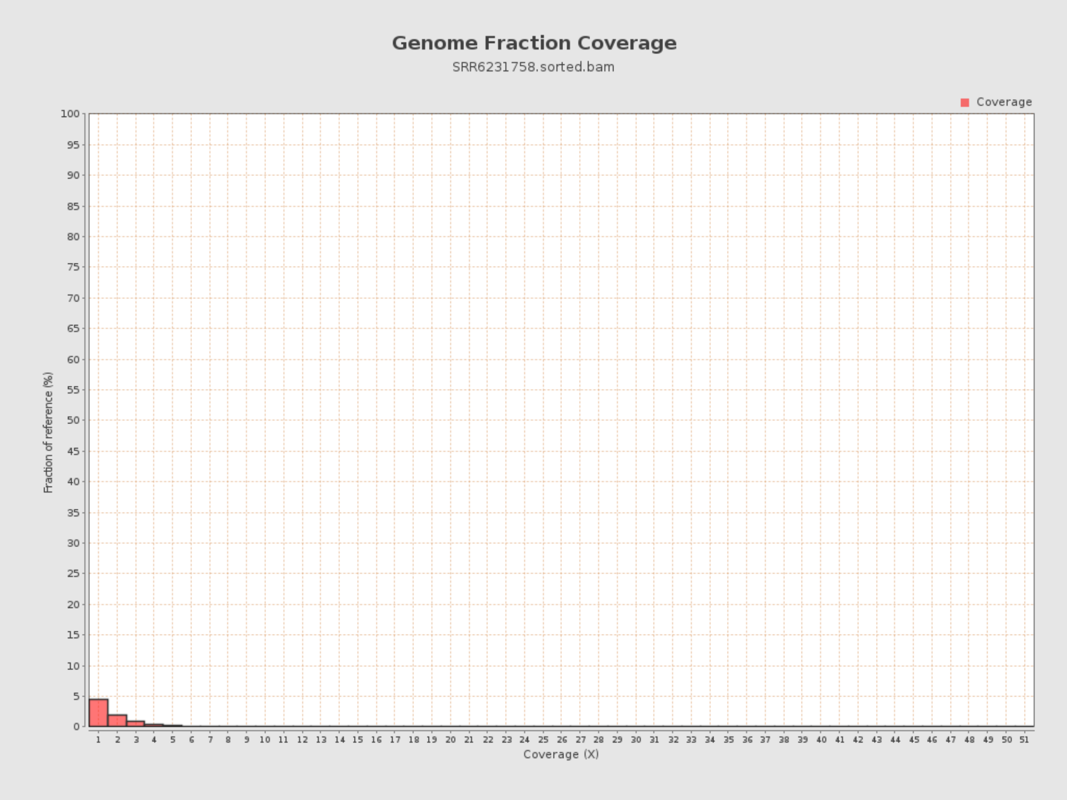
4. Results : Coverage Histogram



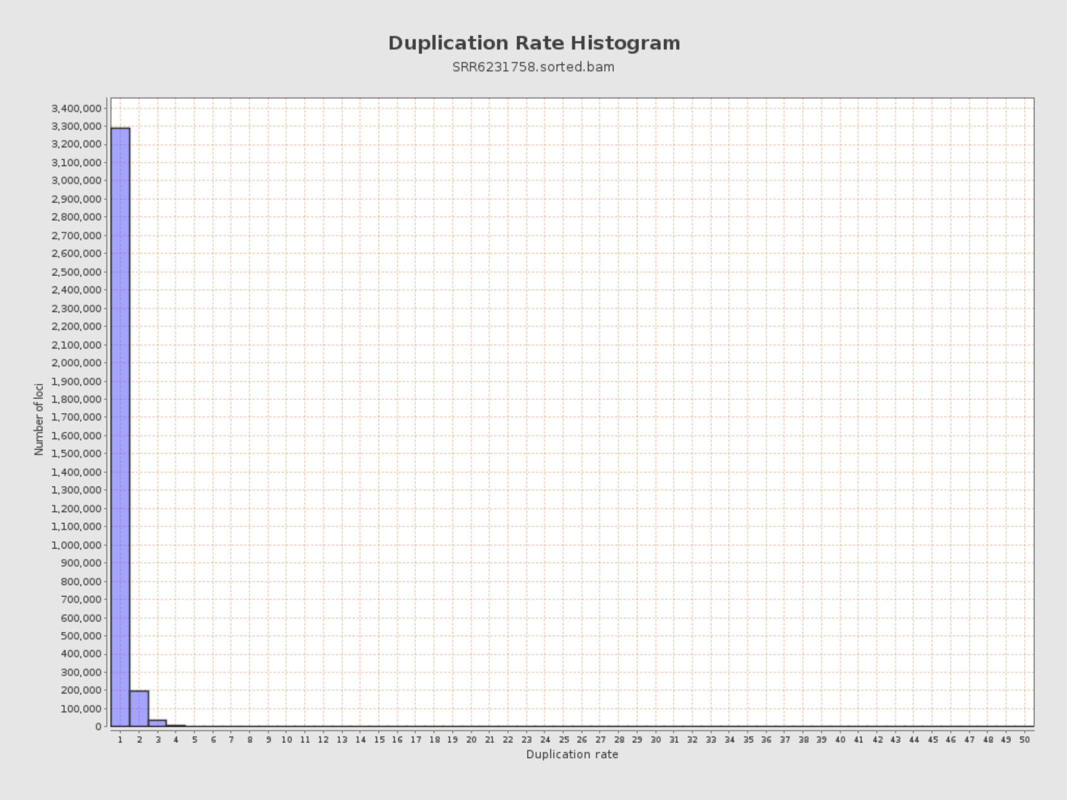
5. Results : Coverage Histogram (0-50X)



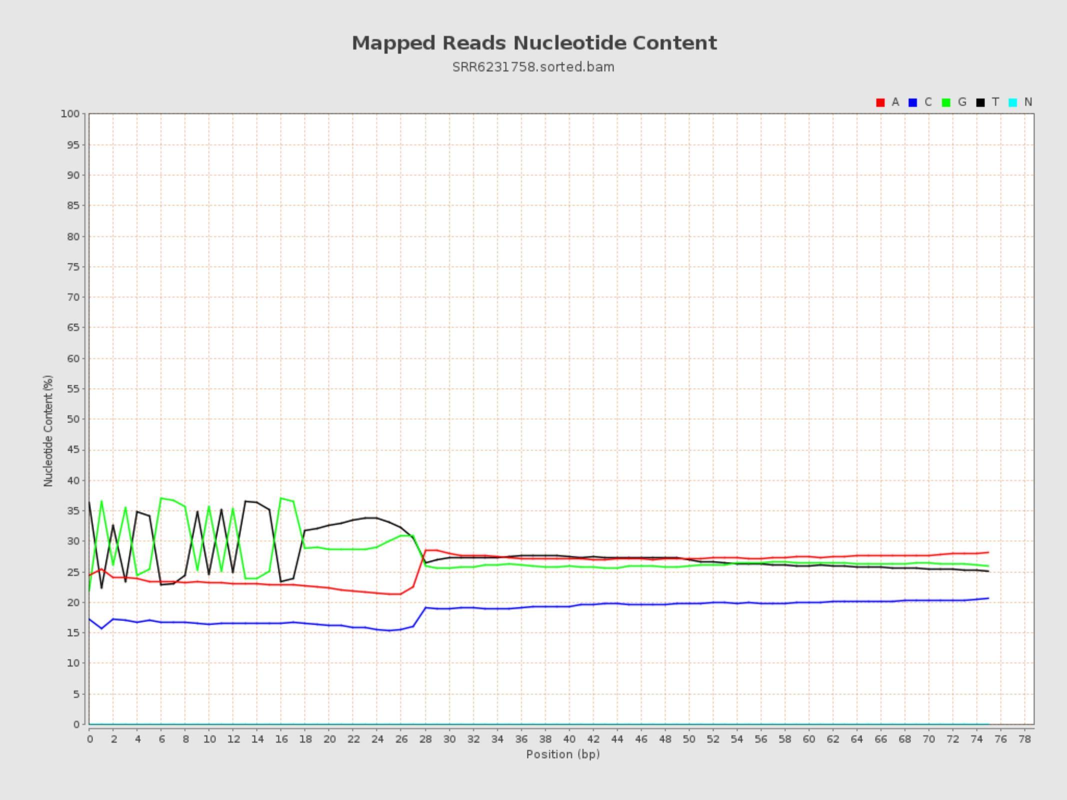
6. Results : Genome Fraction Coverage



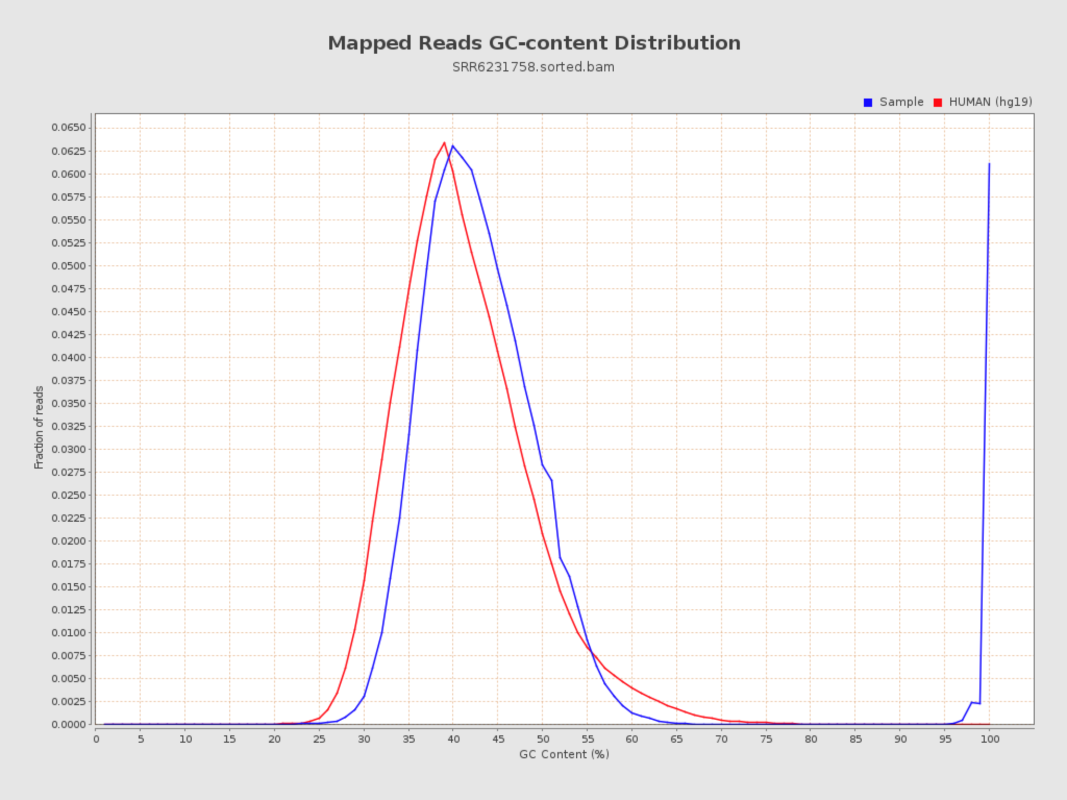
7. Results : Duplication Rate Histogram



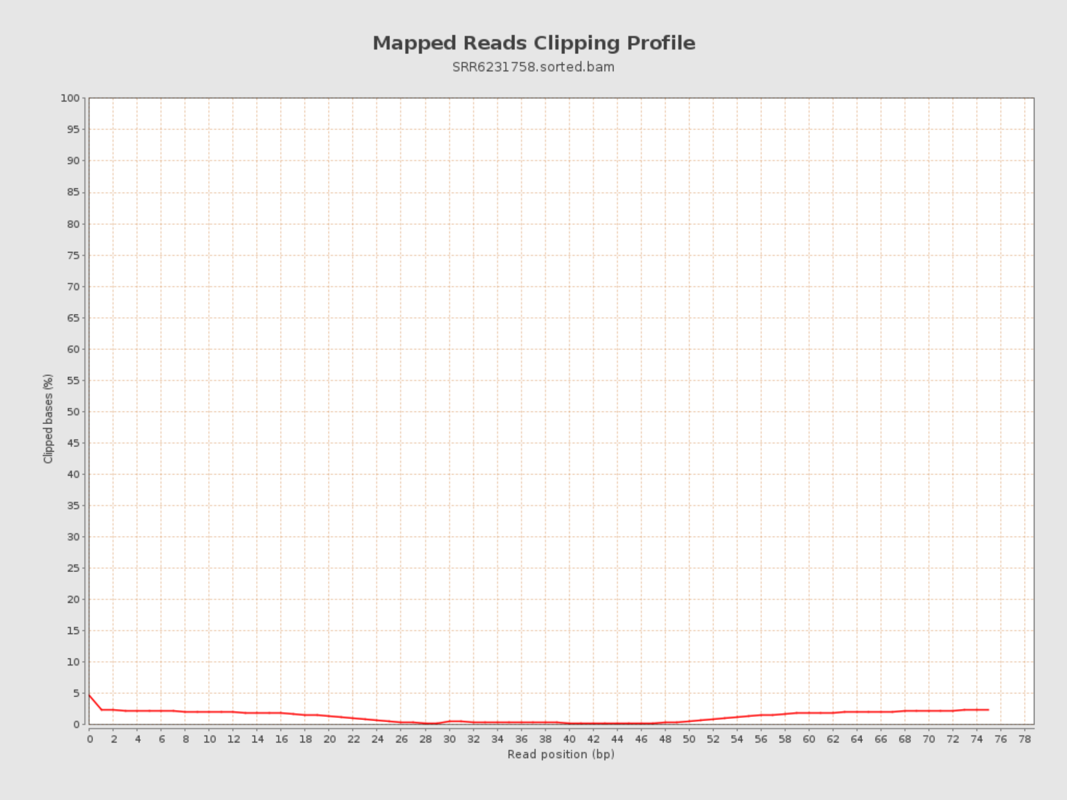
8. Results : Mapped Reads Nucleotide Content



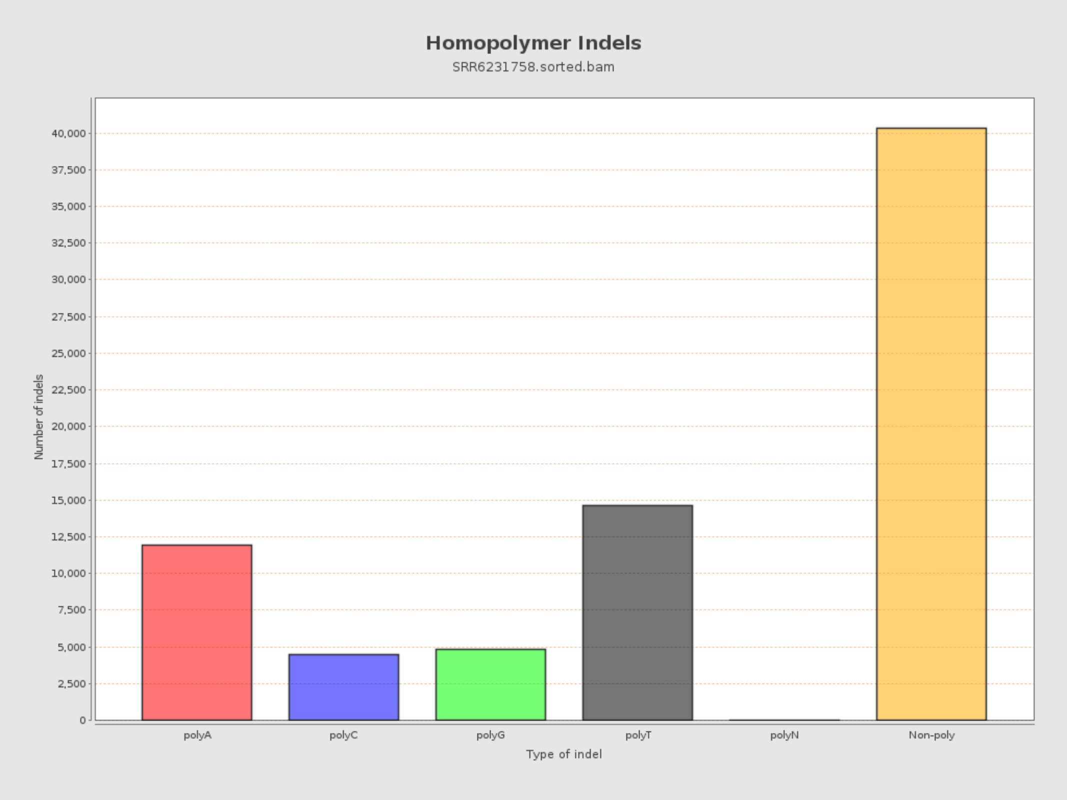
9. Results : Mapped Reads GC-content Distribution



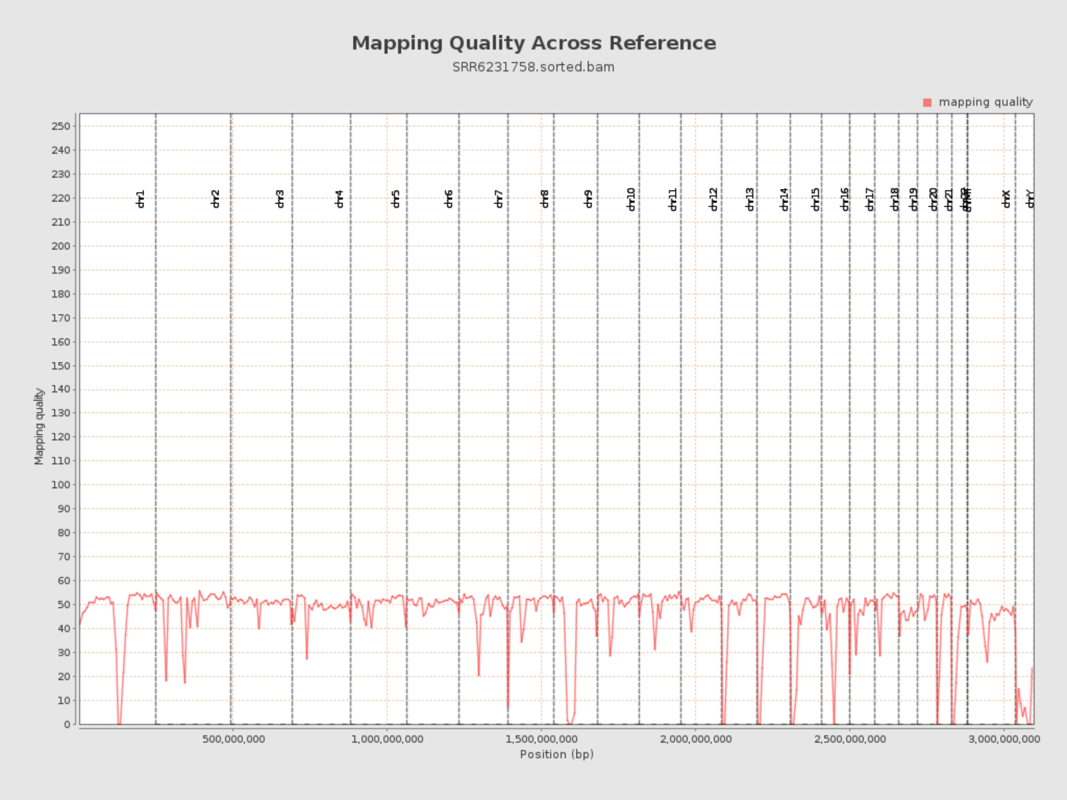
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram