Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 23:16:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231738.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_SRR6231738 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231738.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 23:16:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231738.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	841,386
Mapped reads	553,017 / 65.73%
Unmapped reads	288,369 / 34.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,065 / 0.36%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	18,943 / 2.25%
Duplication rate	2.93%
Clipped reads	280,787 / 33.37%

2.2. ACGT Content

Number/percentage of A's	10,104,160 / 28.33%
Number/percentage of C's	6,025,601 / 16.89%
Number/percentage of T's	11,761,110 / 32.97%
Number/percentage of G's	7,775,292 / 21.8%
Number/percentage of N's	1,483 / 0%
GC Percentage	38.69%

2.3. Coverage

Mean	0.0115

Standard Deviation	0.1477

2.4. Mapping Quality

Mean Mapping Quality	45.81

2.5. Mismatches and indels

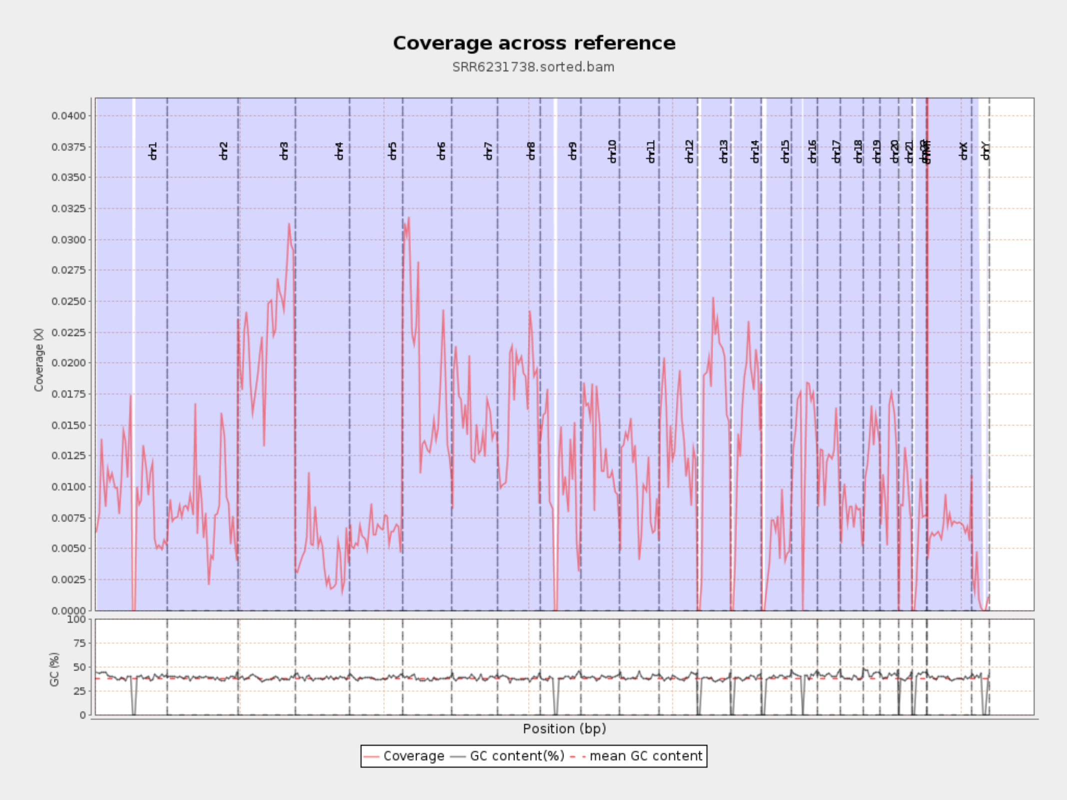
General error rate	0.89%
Mismatches	313,457
Insertions	2,952
Mapped reads with at least one insertion	0.53%
Deletions	11,518
Mapped reads with at least one deletion	2.05%
Homopolymer indels	45.01%

2.6. Chromosome stats

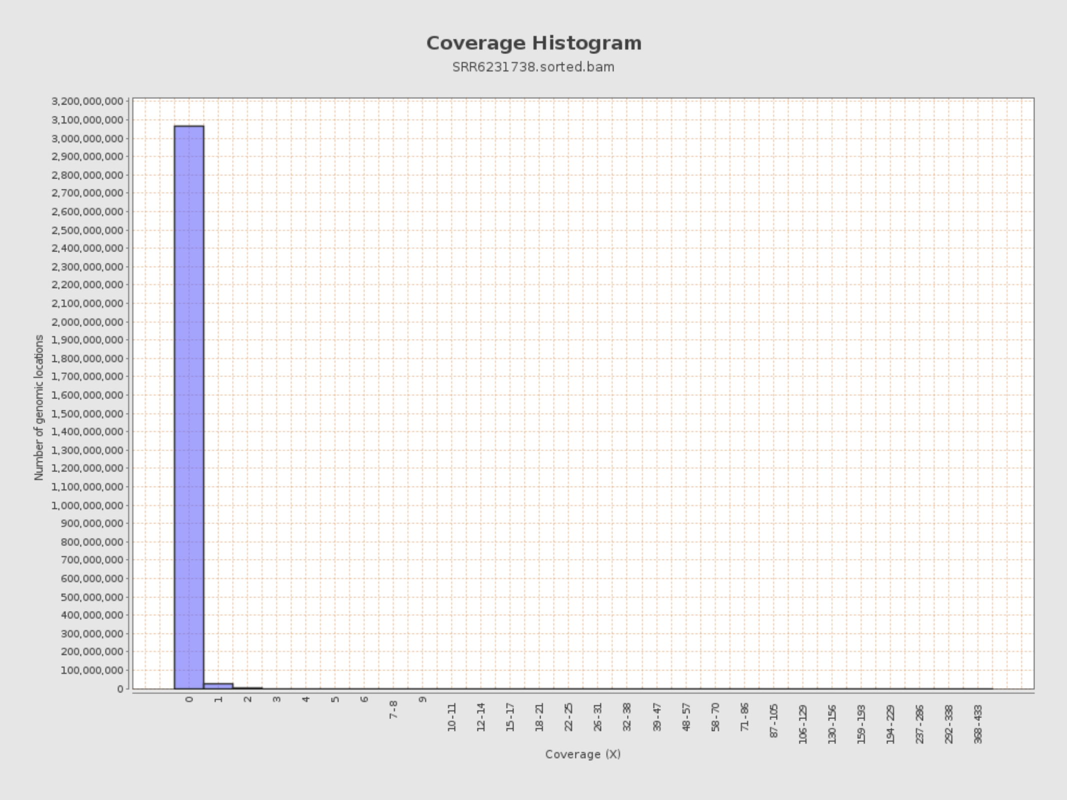
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2266909	0.0091	0.1971
chr2	243199373	1975700	0.0081	0.1198
chr3	198022430	4508544	0.0228	0.1653
chr4	191154276	846862	0.0044	0.0761
chr5	180915260	1141112	0.0063	0.0861
chr6	171115067	3250533	0.019	0.167
chr7	159138663	2426694	0.0152	0.1808

chr8	146364022	2498966	0.0171	0.2962
chr9	141213431	1452134	0.0103	0.1184
chr10	135534747	1778912	0.0131	0.1417
chr11	135006516	1384218	0.0103	0.1253
chr12	133851895	1898779	0.0142	0.1304
chr13	115169878	1920173	0.0167	0.1416
chr14	107349540	1584639	0.0148	0.1349
chr15	102531392	495118	0.0048	0.0765
chr16	90354753	1272532	0.0141	0.1317
chr17	81195210	967444	0.0119	0.1236
chr18	78077248	619418	0.0079	0.1688
chr19	59128983	787657	0.0133	0.15
chr20	63025520	748158	0.0119	0.1189
chr21	48129895	420601	0.0087	0.1033
chr22	51304566	281673	0.0055	0.0799
chrMT	16571	32221	1.9444	1.8829
chrX	155270560	1048590	0.0068	0.092
chrY	59373566	80158	0.0014	0.0462

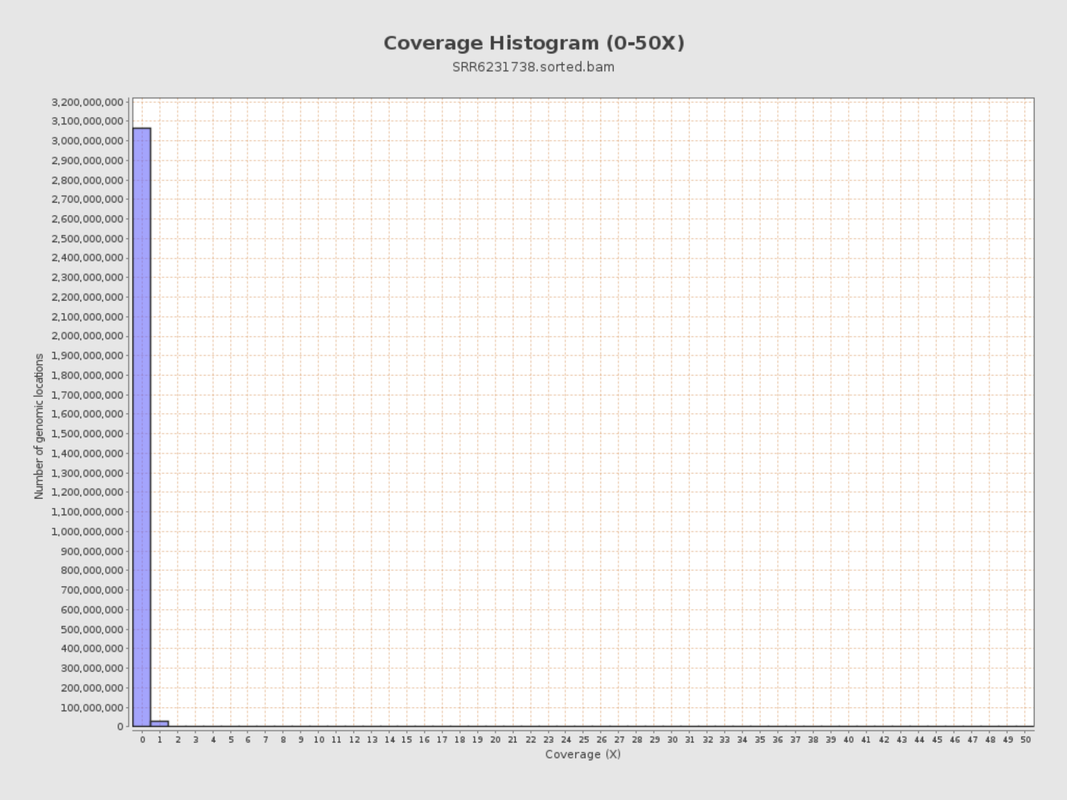
3. Results : Coverage across reference



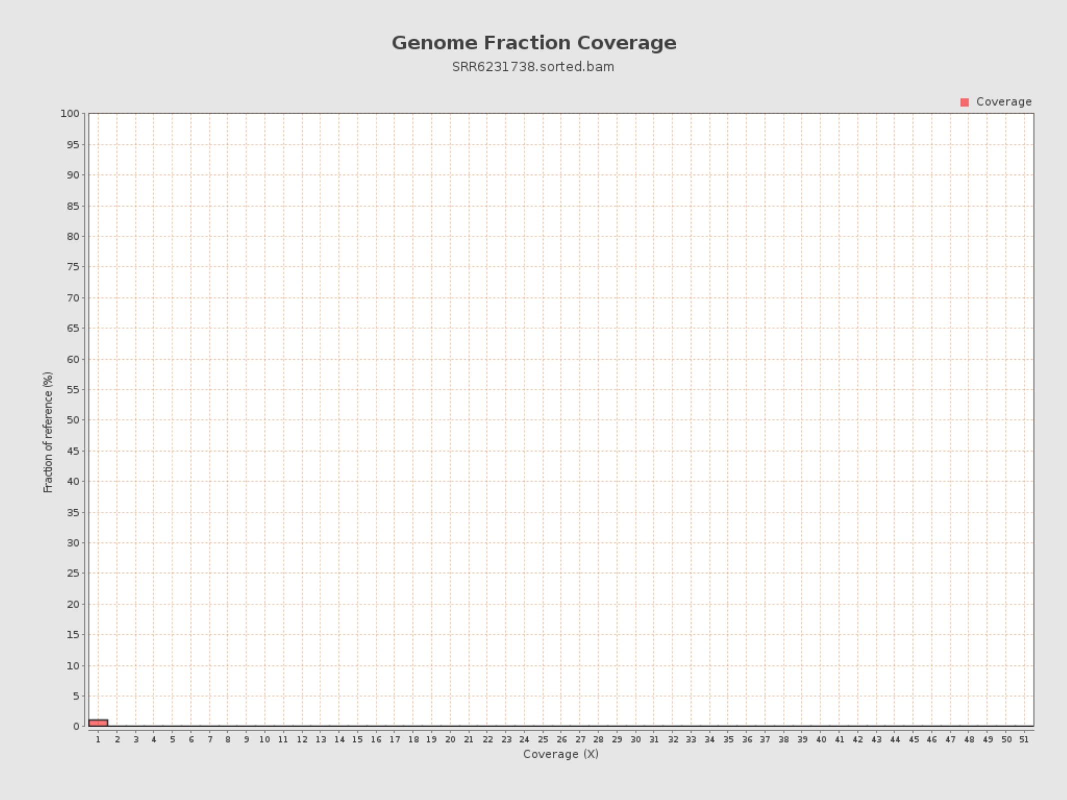
4. Results : Coverage Histogram



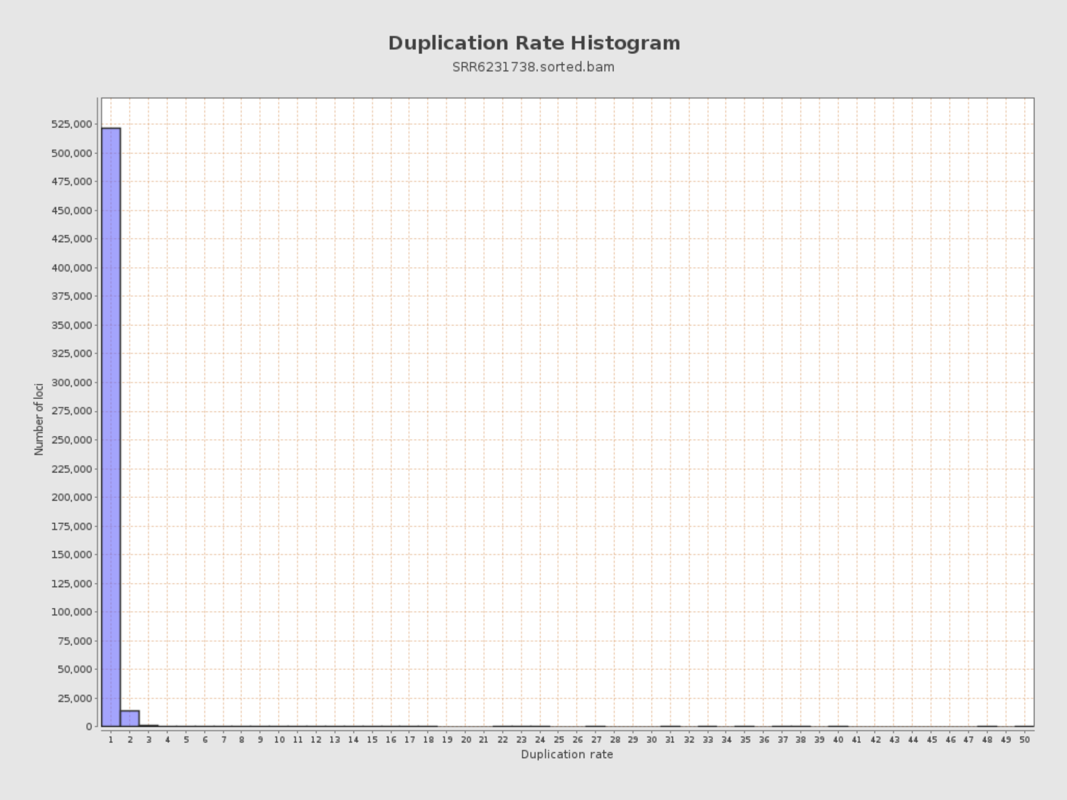
5. Results : Coverage Histogram (0-50X)



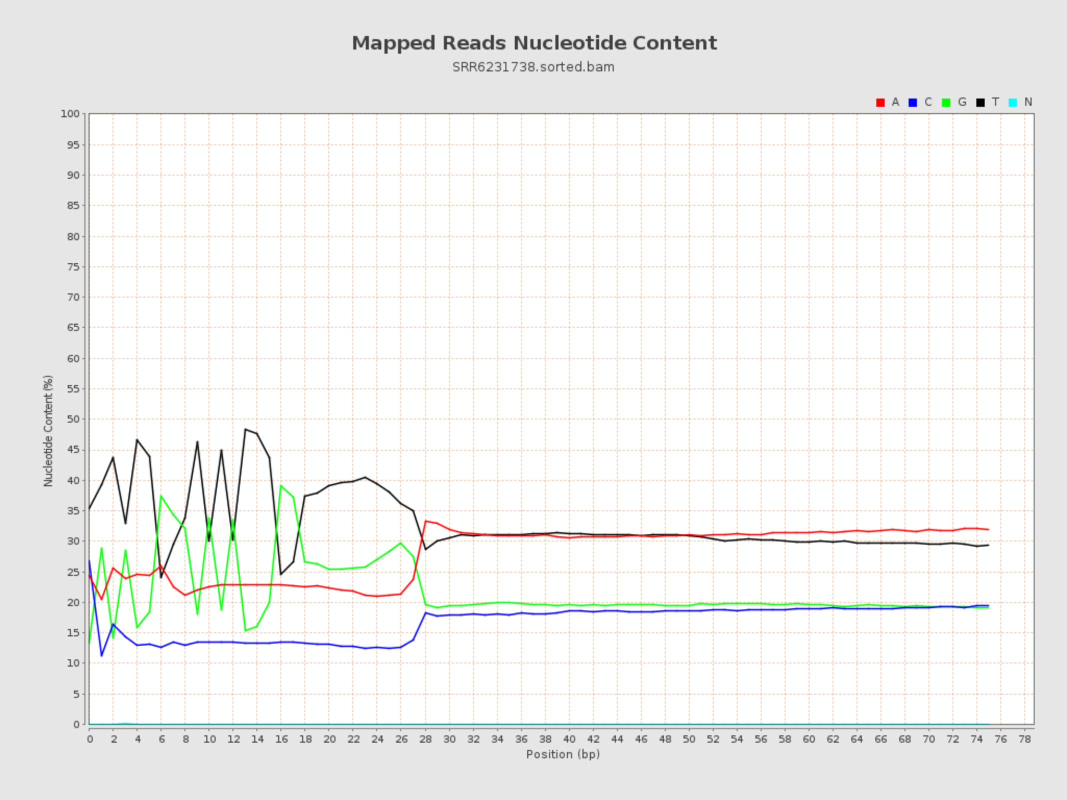
6. Results : Genome Fraction Coverage



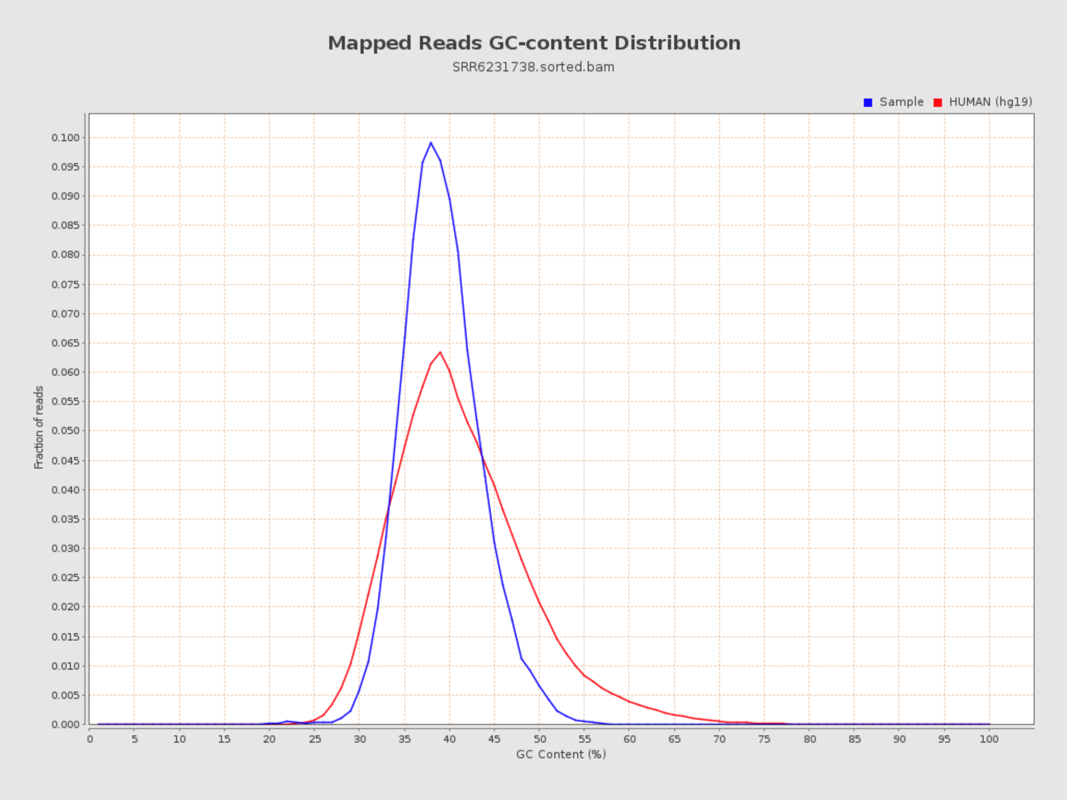
7. Results : Duplication Rate Histogram



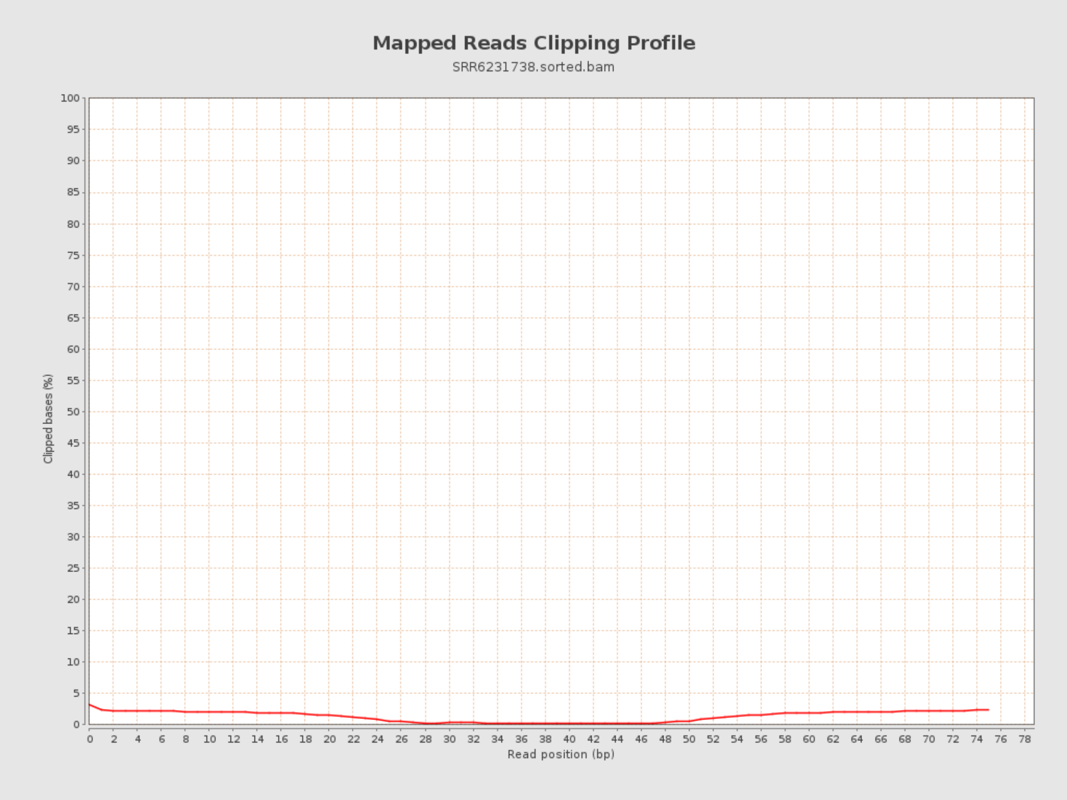
8. Results : Mapped Reads Nucleotide Content



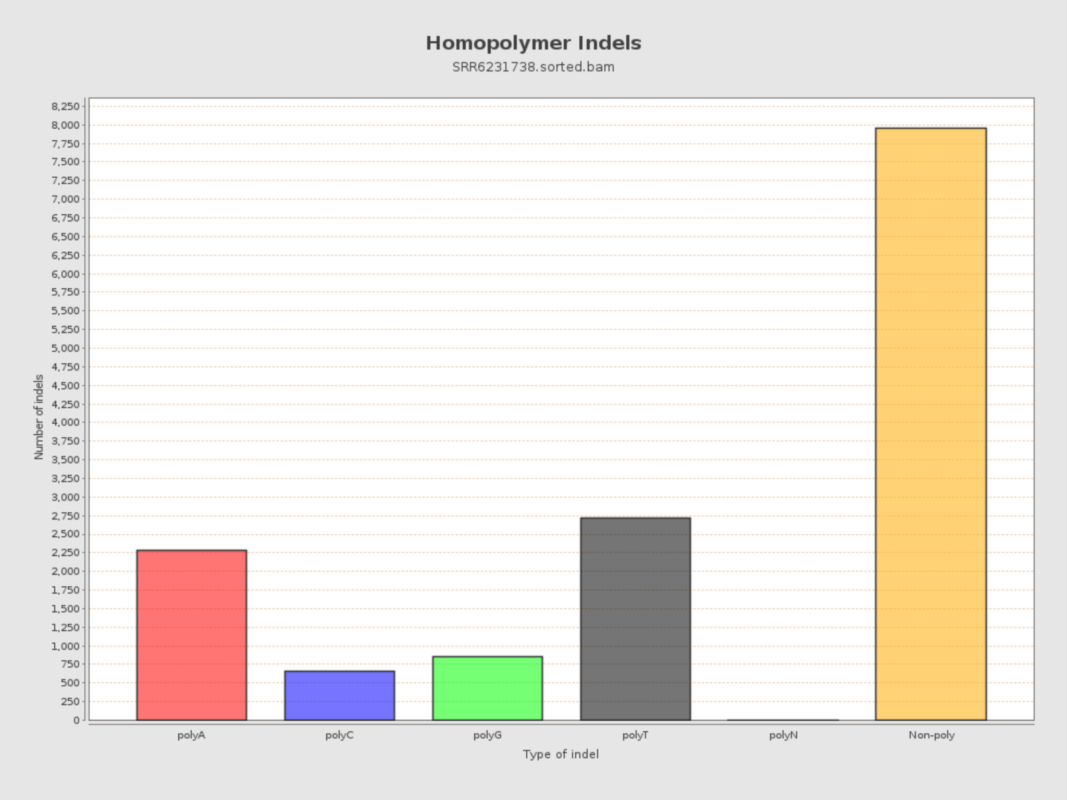
9. Results : Mapped Reads GC-content Distribution



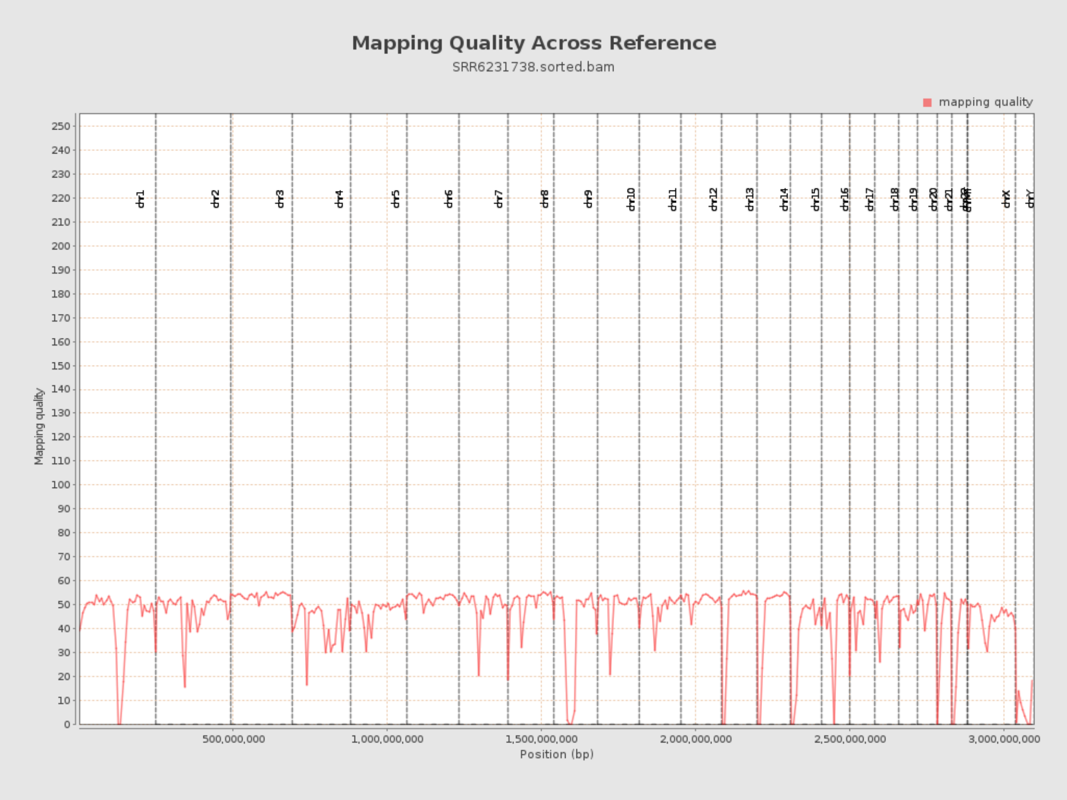
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram