Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 01:23:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231767.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_SRR6231767 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231767.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 01:23:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231767.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,046,265
Mapped reads	721,066 / 68.92%
Unmapped reads	325,199 / 31.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,787 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	20,543 / 1.96%
Duplication rate	2.33%
Clipped reads	382,827 / 36.59%

2.2. ACGT Content

Number/percentage of A's	13,082,473 / 28.22%
Number/percentage of C's	7,840,858 / 16.91%
Number/percentage of T's	15,063,778 / 32.49%
Number/percentage of G's	10,377,145 / 22.38%
Number/percentage of N's	2,093 / 0%
GC Percentage	39.29%

2.3. Coverage

Mean	0.015

Standard Deviation	0.1666

2.4. Mapping Quality

Mean Mapping Quality	45.87

2.5. Mismatches and indels

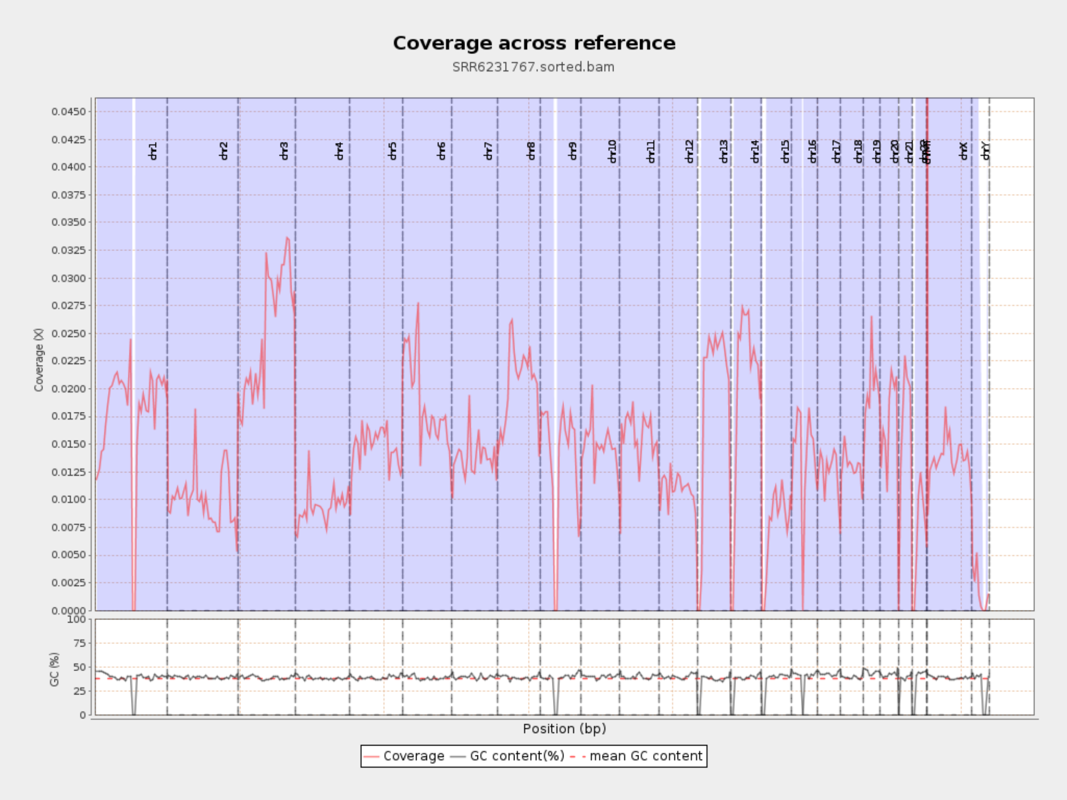
General error rate	0.95%
Mismatches	435,375
Insertions	3,816
Mapped reads with at least one insertion	0.53%
Deletions	15,963
Mapped reads with at least one deletion	2.19%
Homopolymer indels	44.3%

2.6. Chromosome stats

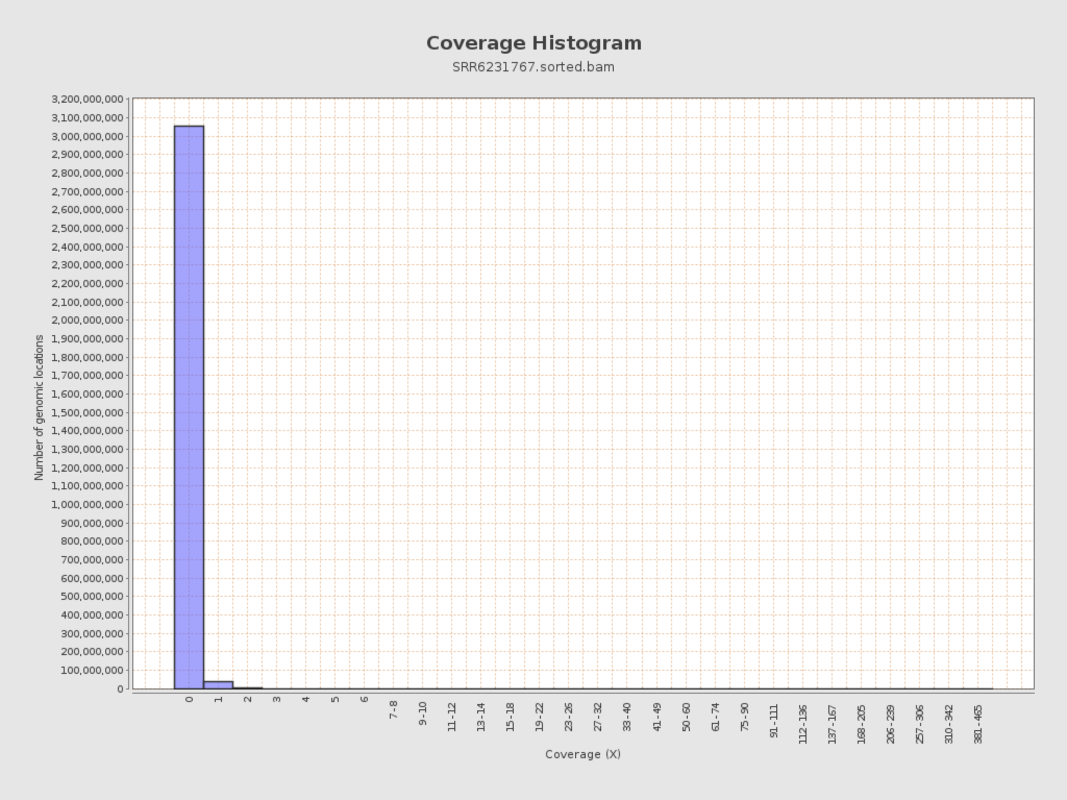
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4408075	0.0177	0.2484
chr2	243199373	2445378	0.0101	0.1622
chr3	198022430	4990171	0.0252	0.1689
chr4	191154276	1784323	0.0093	0.1044
chr5	180915260	2678612	0.0148	0.1295
chr6	171115067	3219015	0.0188	0.1594
chr7	159138663	2200665	0.0138	0.1601

chr8	146364022	3008593	0.0206	0.3219
chr9	141213431	1939424	0.0137	0.1391
chr10	135534747	2019814	0.0149	0.1492
chr11	135006516	2127734	0.0158	0.1455
chr12	133851895	1459683	0.0109	0.1106
chr13	115169878	2231093	0.0194	0.1485
chr14	107349540	2157684	0.0201	0.1546
chr15	102531392	769809	0.0075	0.0925
chr16	90354753	1240633	0.0137	0.1282
chr17	81195210	1019593	0.0126	0.1224
chr18	78077248	1018397	0.013	0.2064
chr19	59128983	1180516	0.02	0.1891
chr20	63025520	1069050	0.017	0.141
chr21	48129895	806898	0.0168	0.14
chr22	51304566	360971	0.007	0.0877
chrMT	16571	6545	0.395	0.7828
chrX	155270560	2144707	0.0138	0.1284
chrY	59373566	106799	0.0018	0.0494

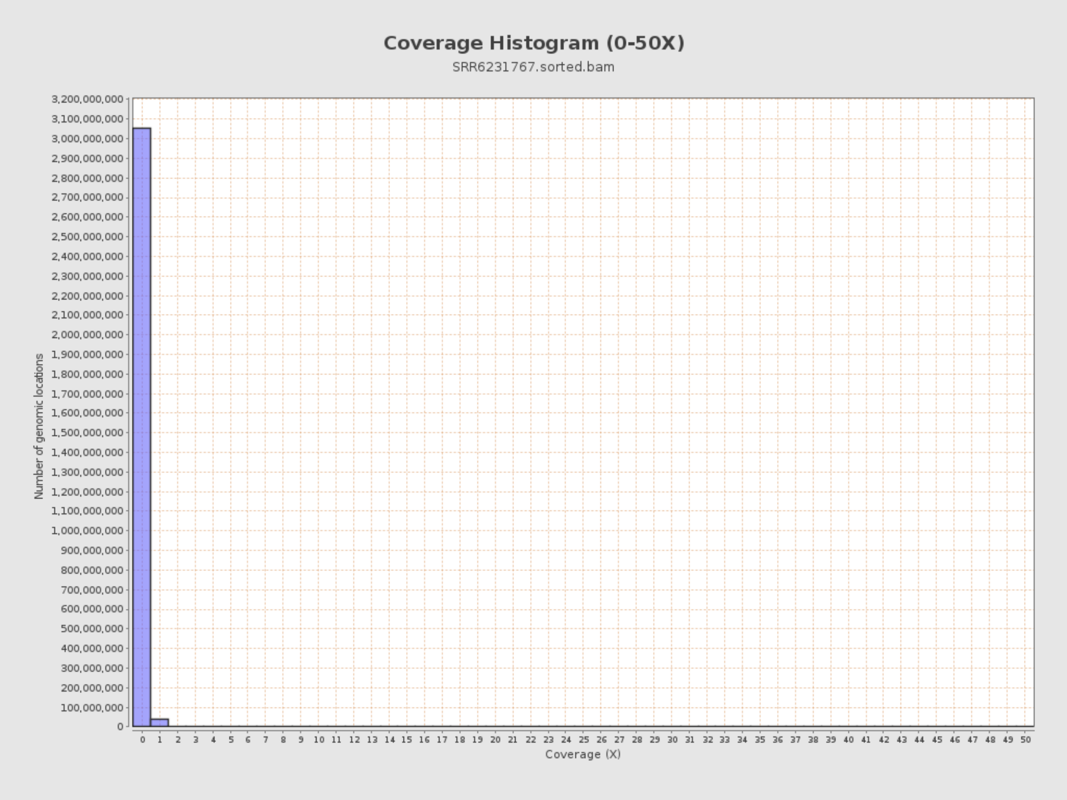
3. Results : Coverage across reference



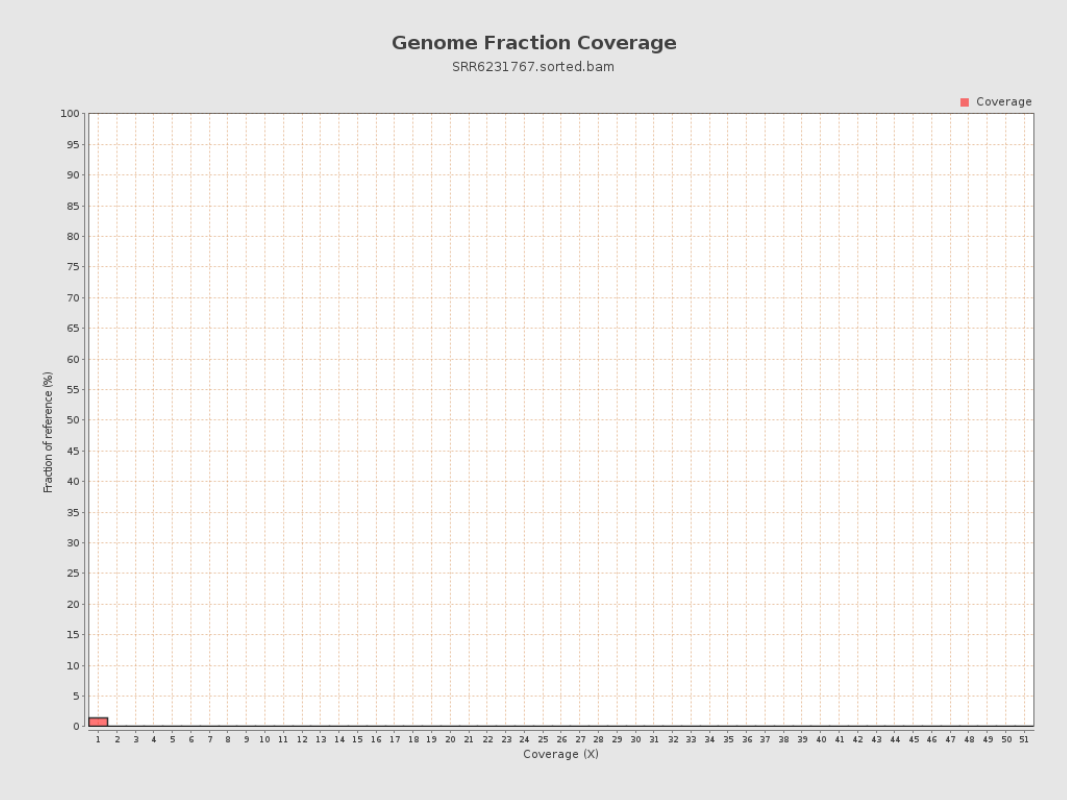
4. Results : Coverage Histogram



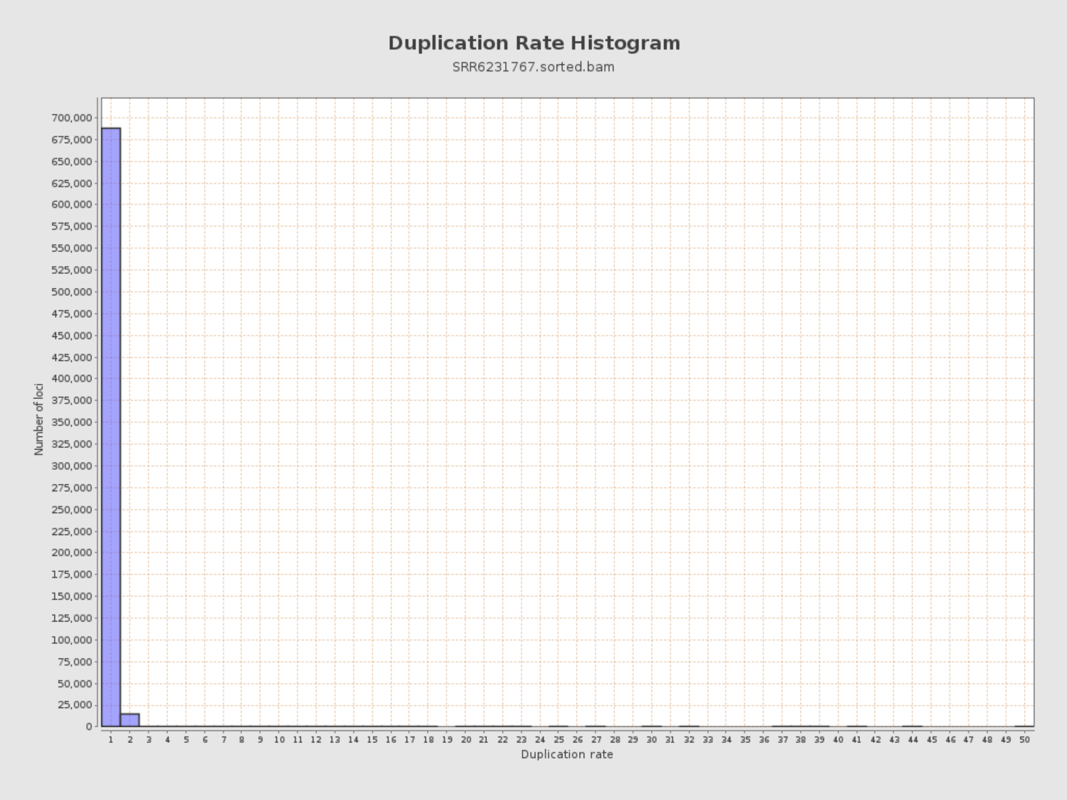
5. Results : Coverage Histogram (0-50X)



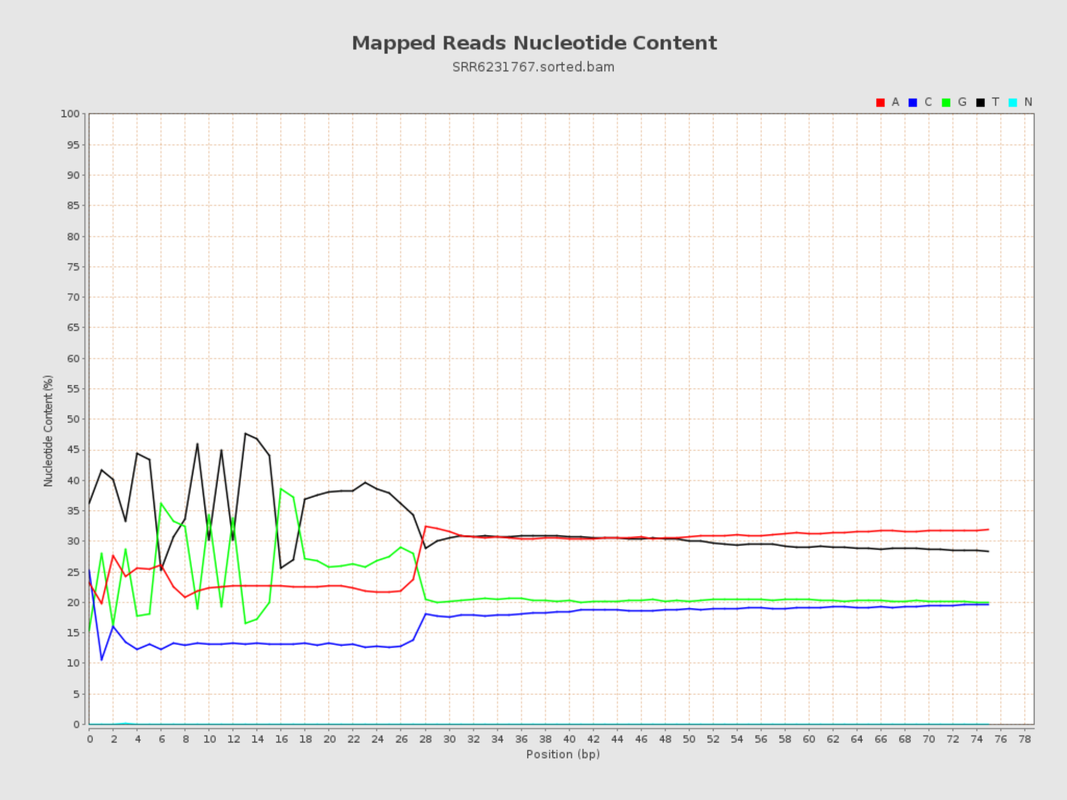
6. Results : Genome Fraction Coverage



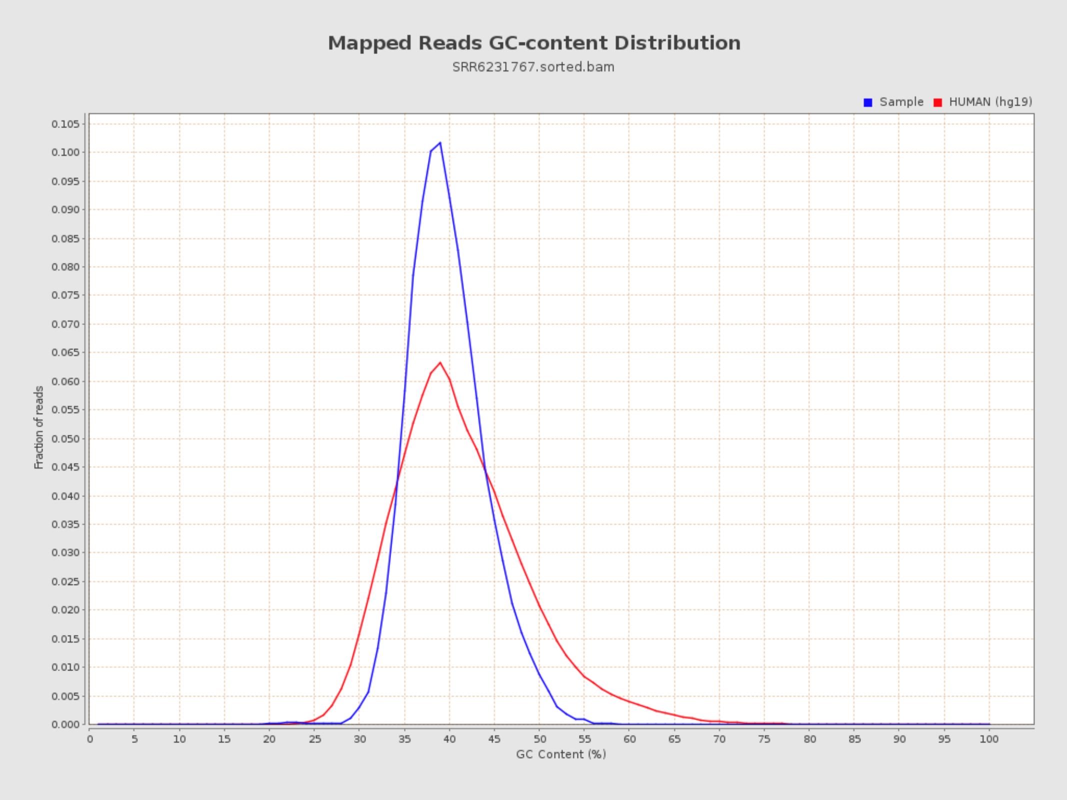
7. Results : Duplication Rate Histogram



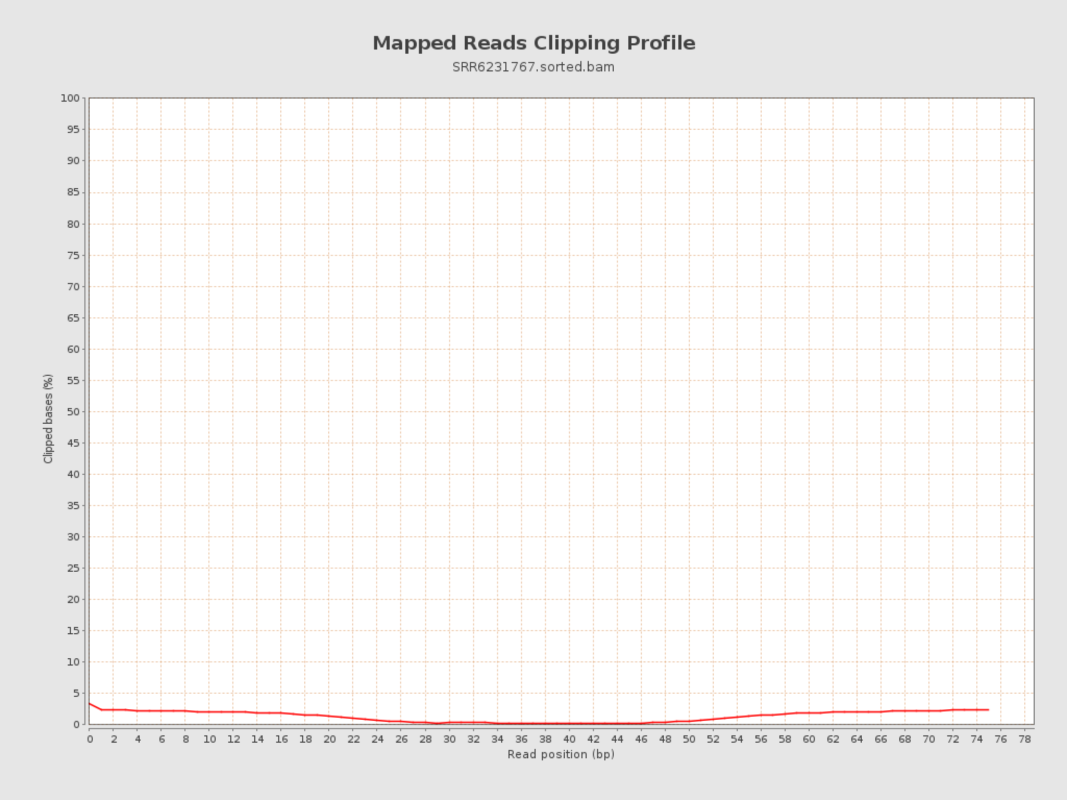
8. Results : Mapped Reads Nucleotide Content



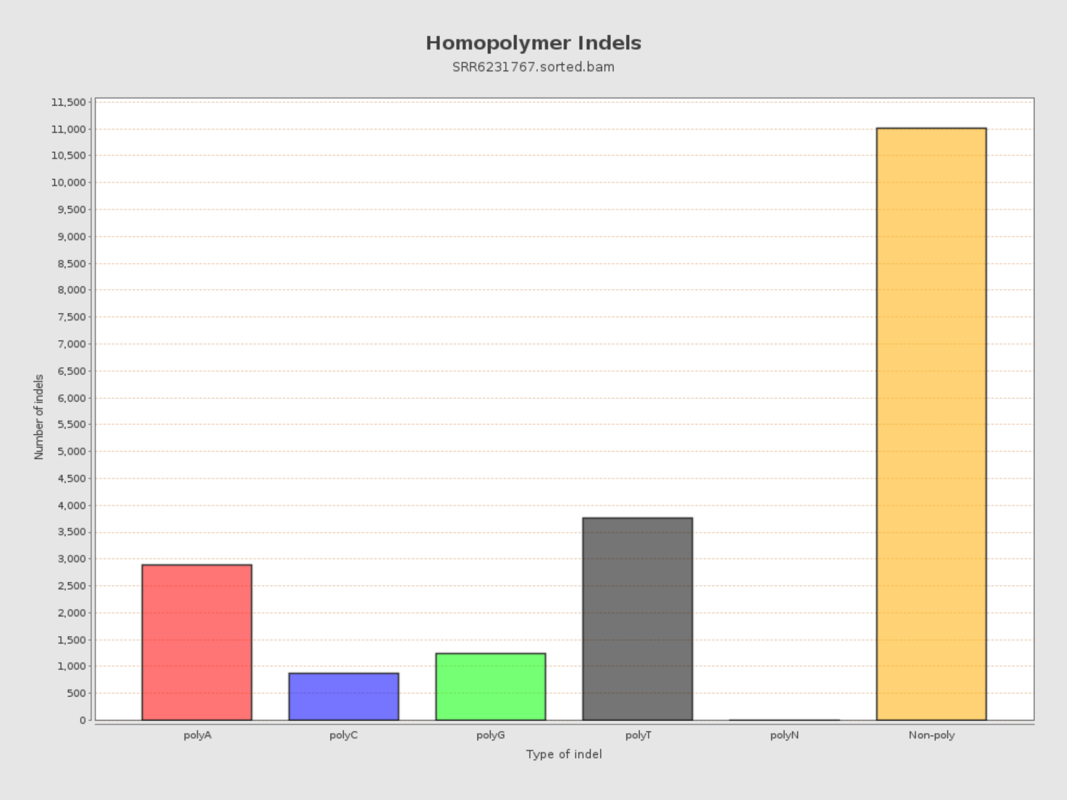
9. Results : Mapped Reads GC-content Distribution



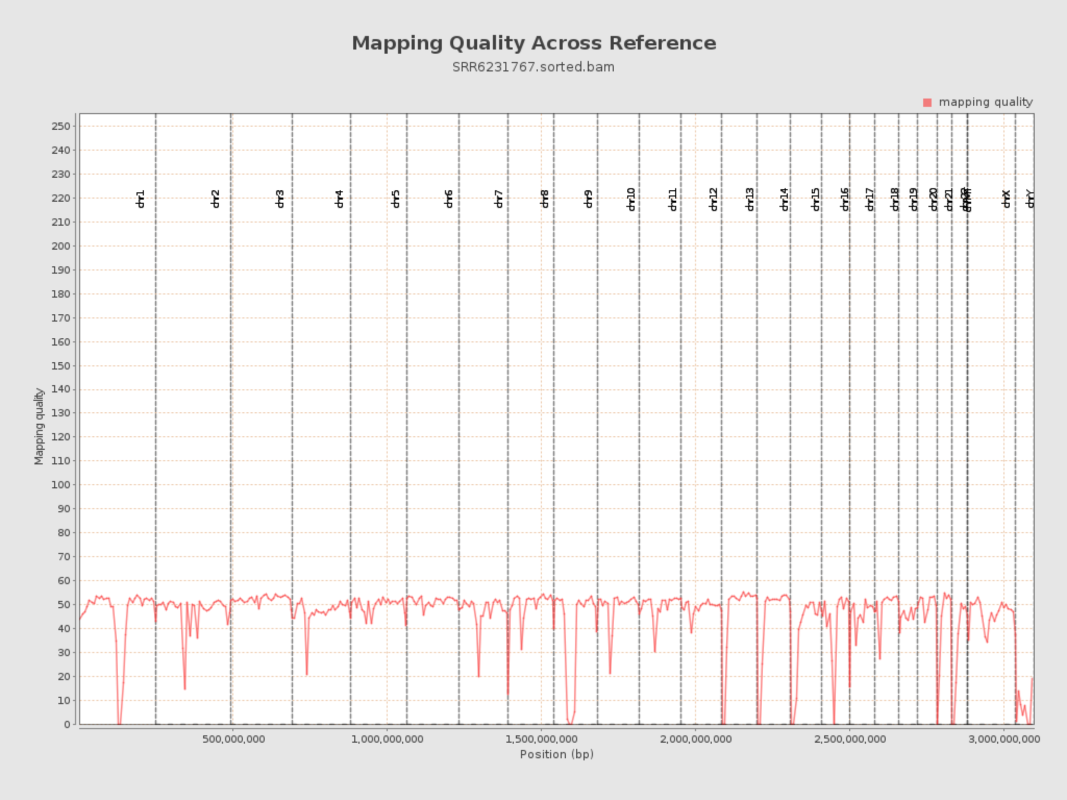
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram