

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 22:03:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231716.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_SRR6231716 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231716.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 22:03:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231716.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	569,350
Mapped reads	92,236 / 16.2%
Unmapped reads	477,114 / 83.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	810 / 0.14%
Read min/max/mean length	30 / 76 / 76.05
Duplicated reads (estimated)	8,299 / 1.46%
Duplication rate	6.54%
Clipped reads	57,816 / 10.15%

2.2. ACGT Content

Number/percentage of A's	1,489,408 / 26.85%
Number/percentage of C's	918,016 / 16.55%
Number/percentage of T's	1,885,095 / 33.98%
Number/percentage of G's	1,255,150 / 22.62%
Number/percentage of N's	249 / 0%
GC Percentage	39.17%

2.3. Coverage

Mean	0.0018

Standard Deviation	0.0747
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2.4. Mapping Quality

Mean Mapping Quality	40.95
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2.5. Mismatches and indels

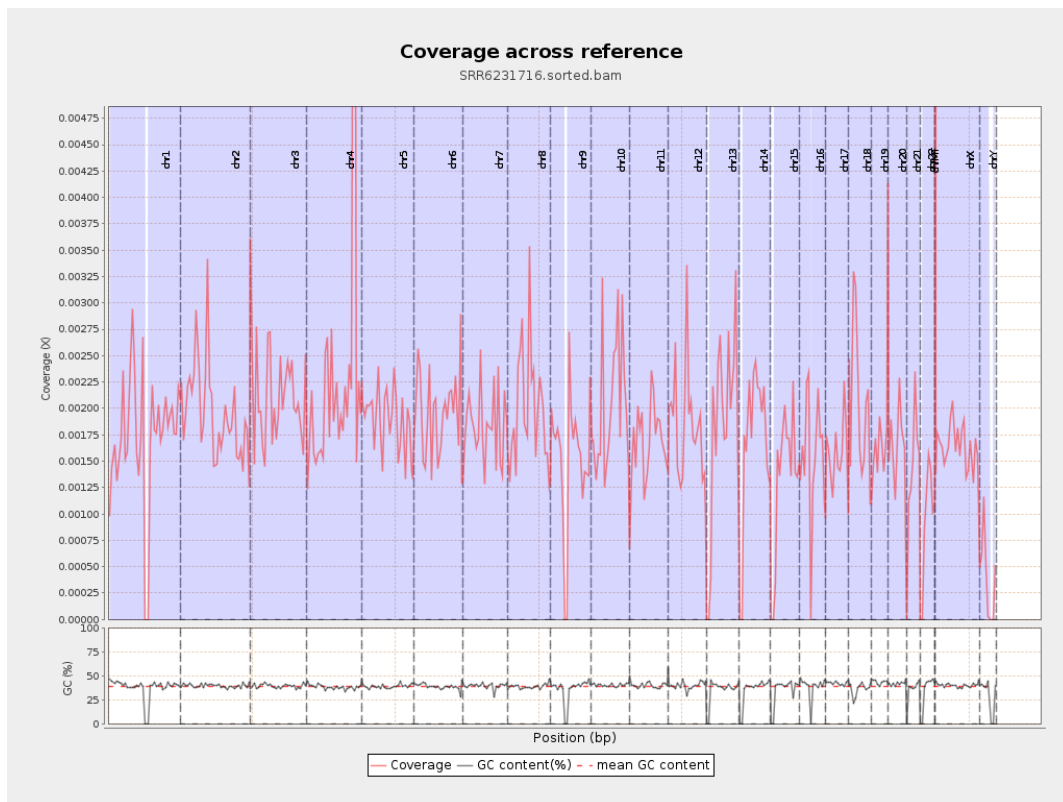
General error rate	0.98%
Mismatches	52,249
Insertions	836
Mapped reads with at least one insertion	0.88%
Deletions	1,530
Mapped reads with at least one deletion	1.63%
Homopolymer indels	39.69%

2.6. Chromosome stats

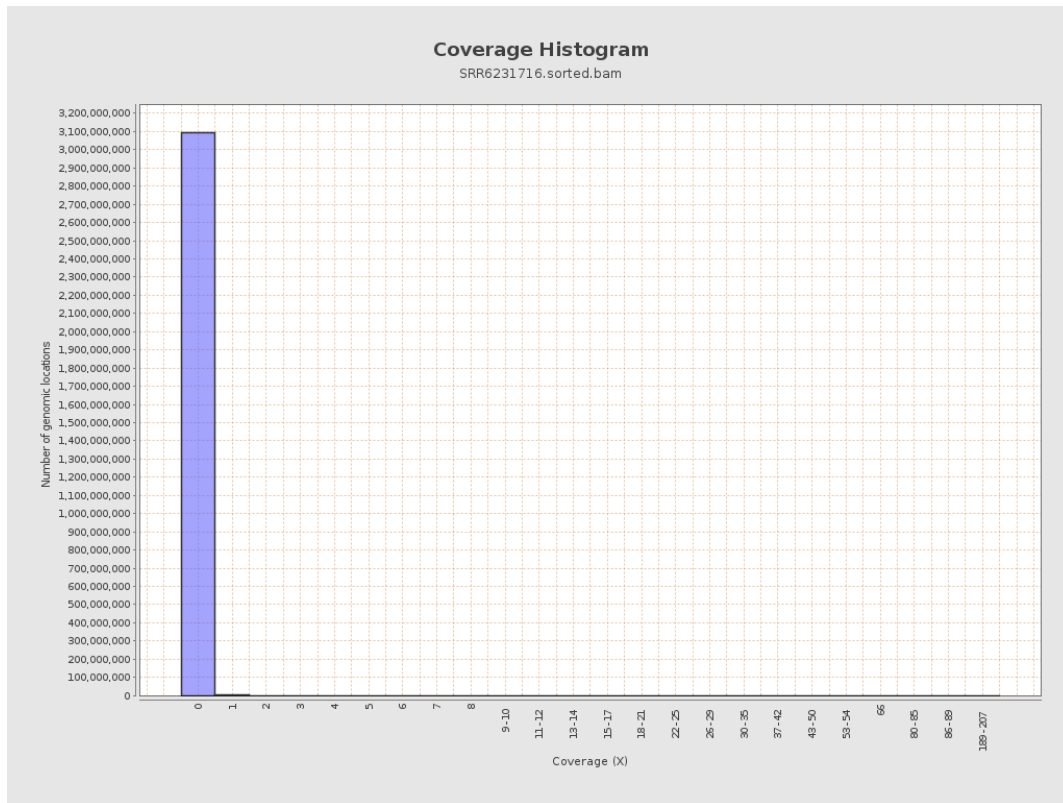
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	434497	0.0017	0.0586
chr2	243199373	476640	0.002	0.0659
chr3	198022430	418526	0.0021	0.0607
chr4	191154276	435101	0.0023	0.0675
chr5	180915260	342186	0.0019	0.0593
chr6	171115067	336496	0.002	0.083
chr7	159138663	291520	0.0018	0.0751

chr8	146364022	293140	0.002	0.066
chr9	141213431	210234	0.0015	0.0494
chr10	135534747	275394	0.002	0.0586
chr11	135006516	230204	0.0017	0.054
chr12	133851895	248641	0.0019	0.0871
chr13	115169878	208709	0.0018	0.0622
chr14	107349540	182855	0.0017	0.0536
chr15	102531392	134352	0.0013	0.0864
chr16	90354753	139391	0.0015	0.0506
chr17	81195210	128522	0.0016	0.052
chr18	78077248	161238	0.0021	0.259
chr19	59128983	100098	0.0017	0.0504
chr20	63025520	103470	0.0016	0.0523
chr21	48129895	69131	0.0014	0.0484
chr22	51304566	49137	0.001	0.0387
chrMT	16571	3096	0.1868	0.5414
chrX	155270560	253566	0.0016	0.0535
chrY	59373566	24489	0.0004	0.0254

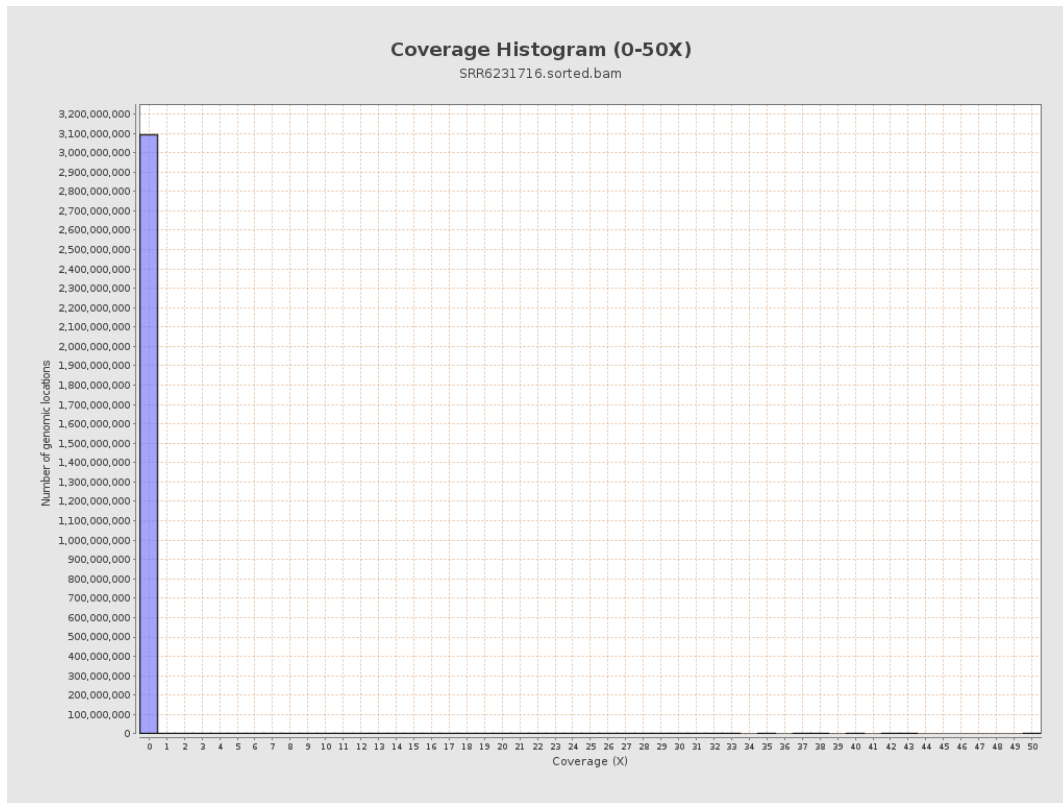
3. Results : Coverage across reference



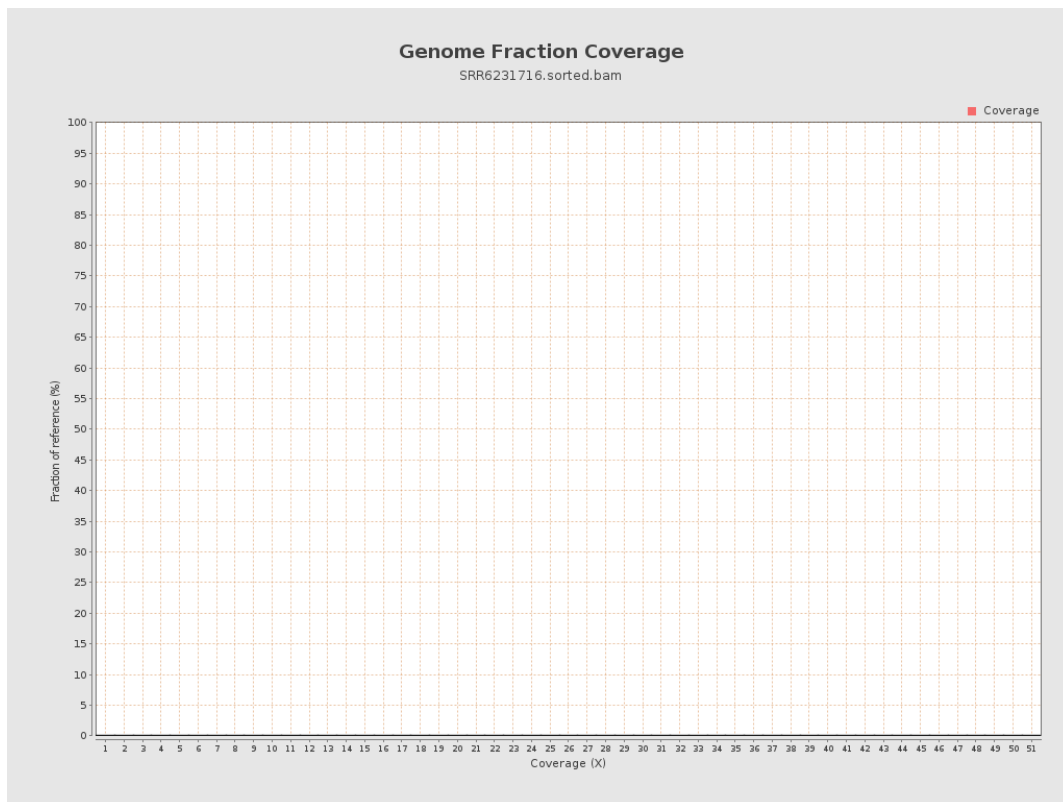
4. Results : Coverage Histogram



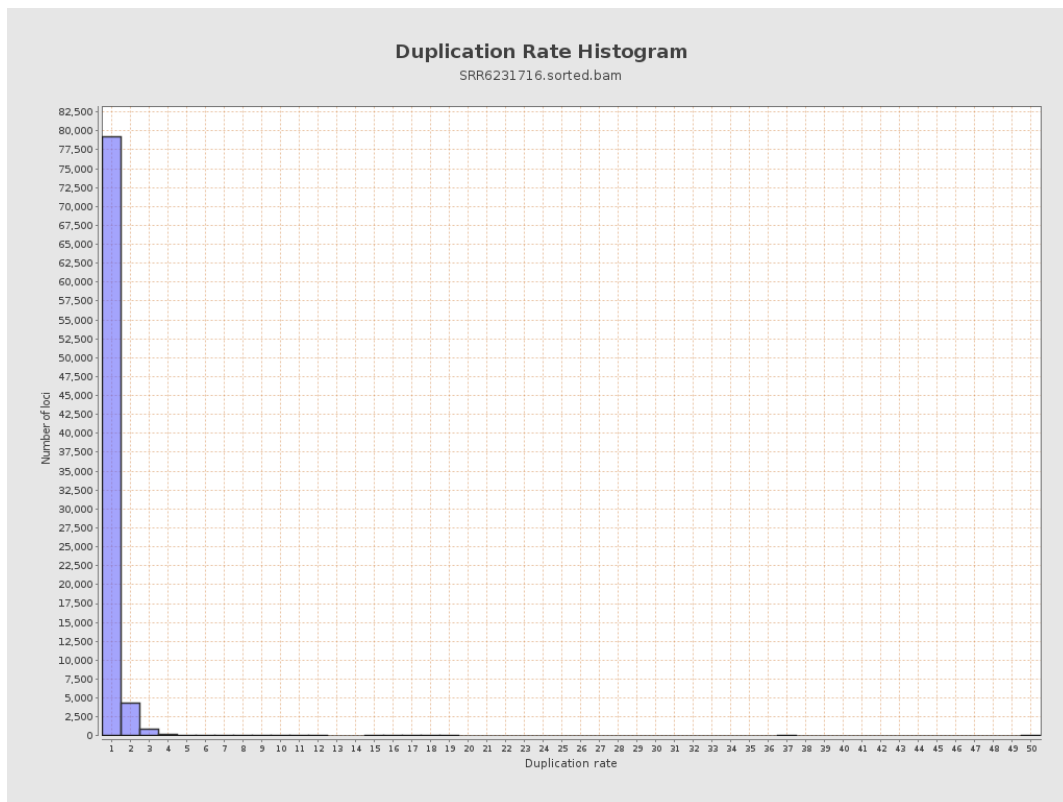
5. Results : Coverage Histogram (0-50X)



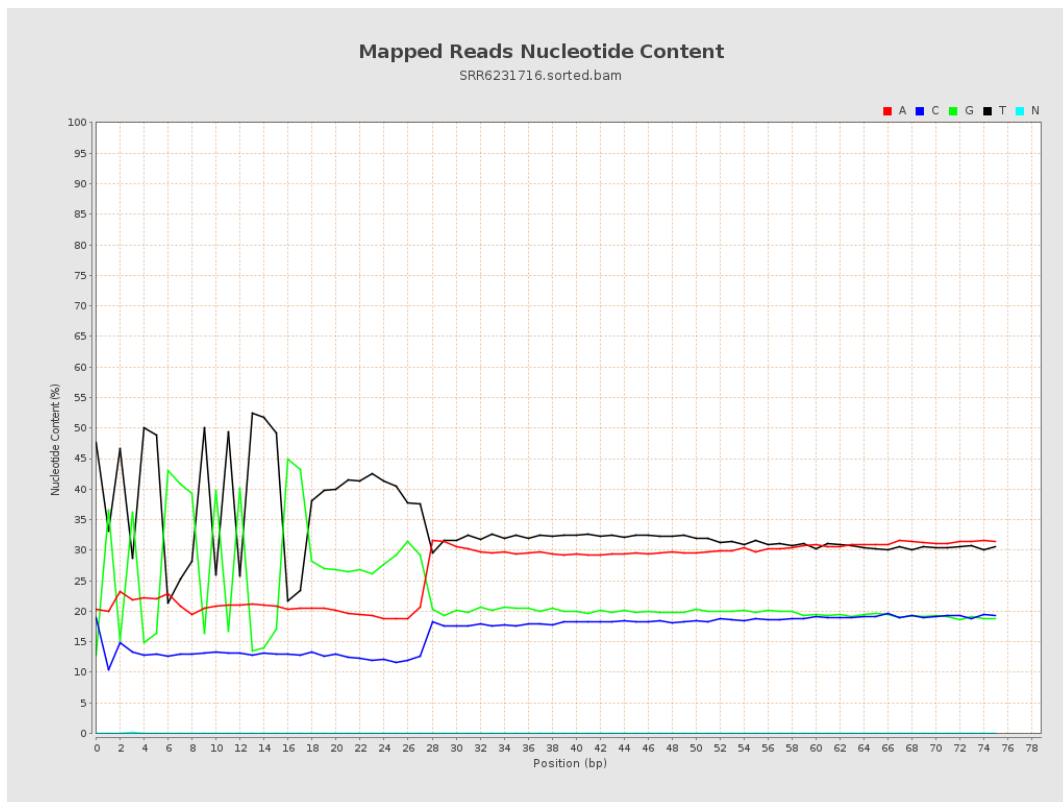
6. Results : Genome Fraction Coverage



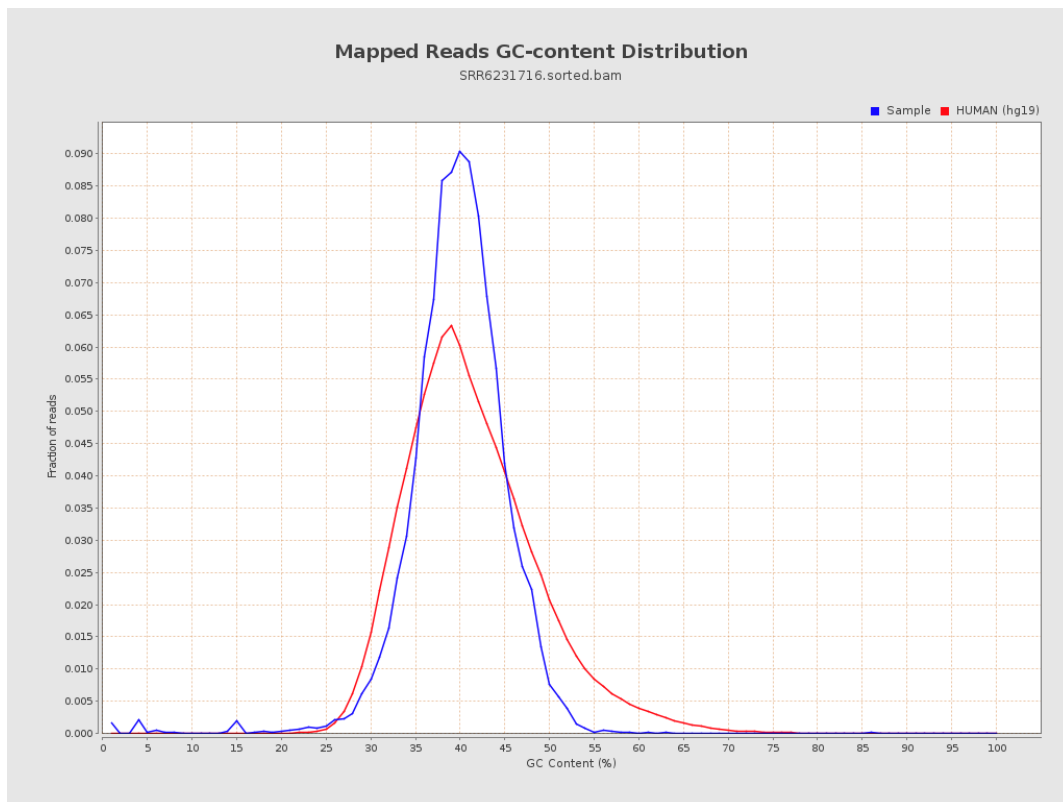
7. Results : Duplication Rate Histogram



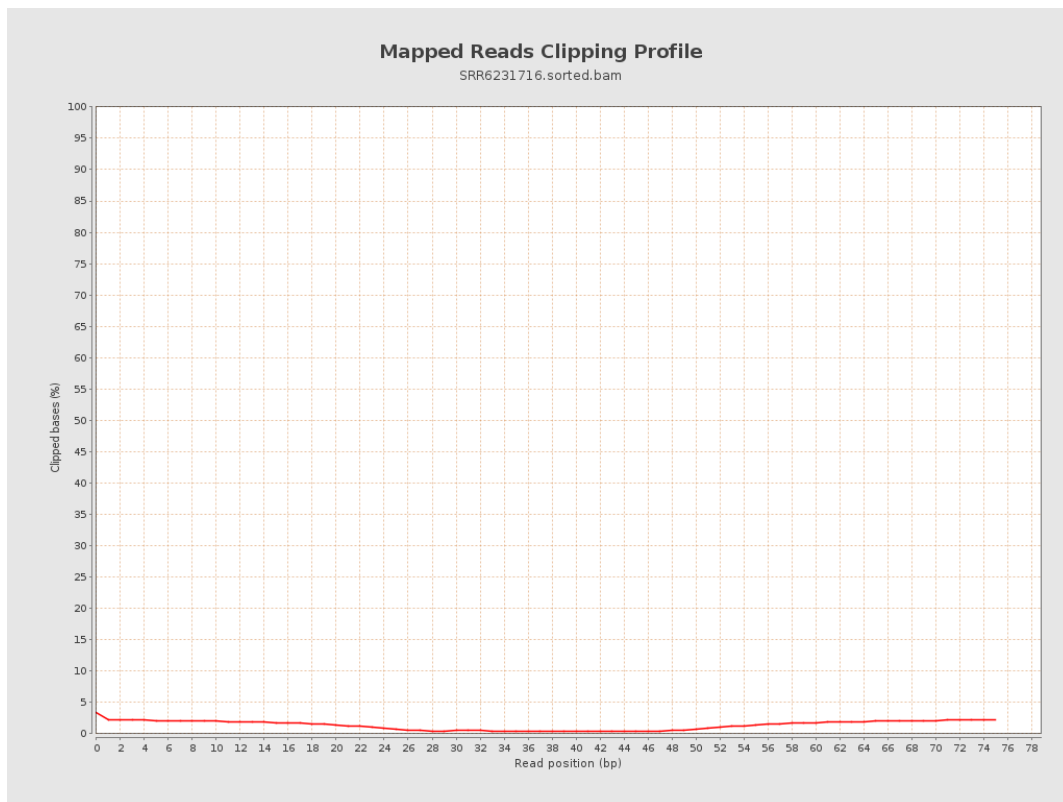
8. Results : Mapped Reads Nucleotide Content



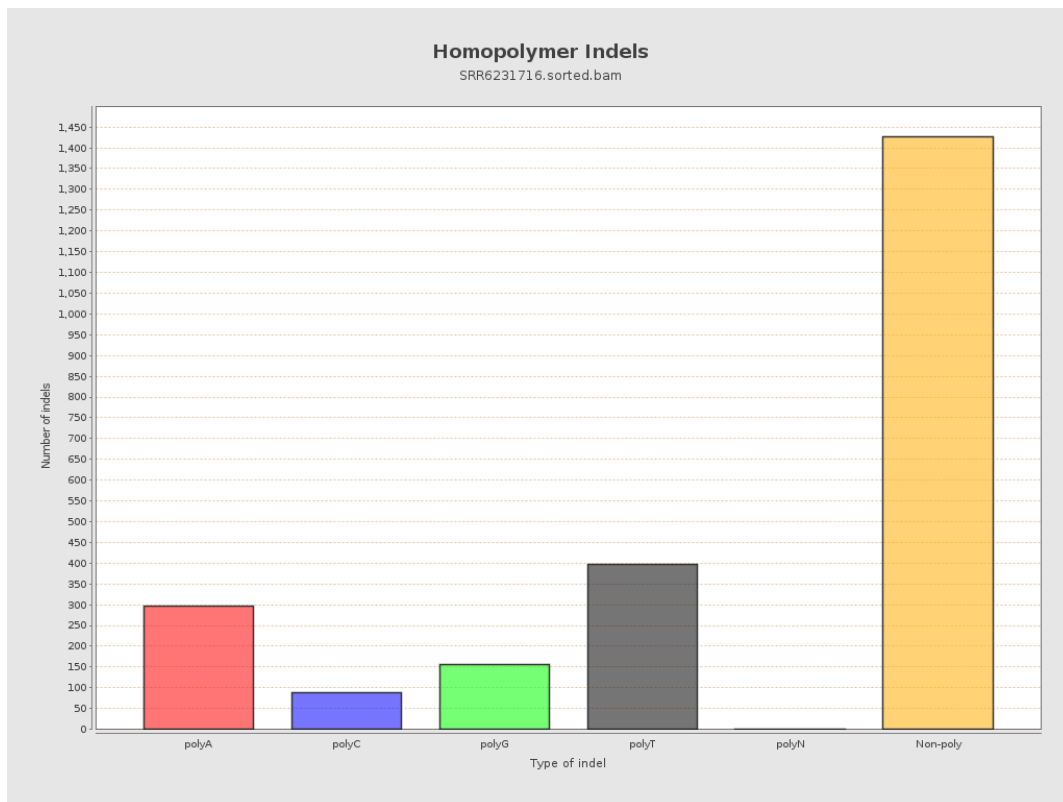
9. Results : Mapped Reads GC-content Distribution



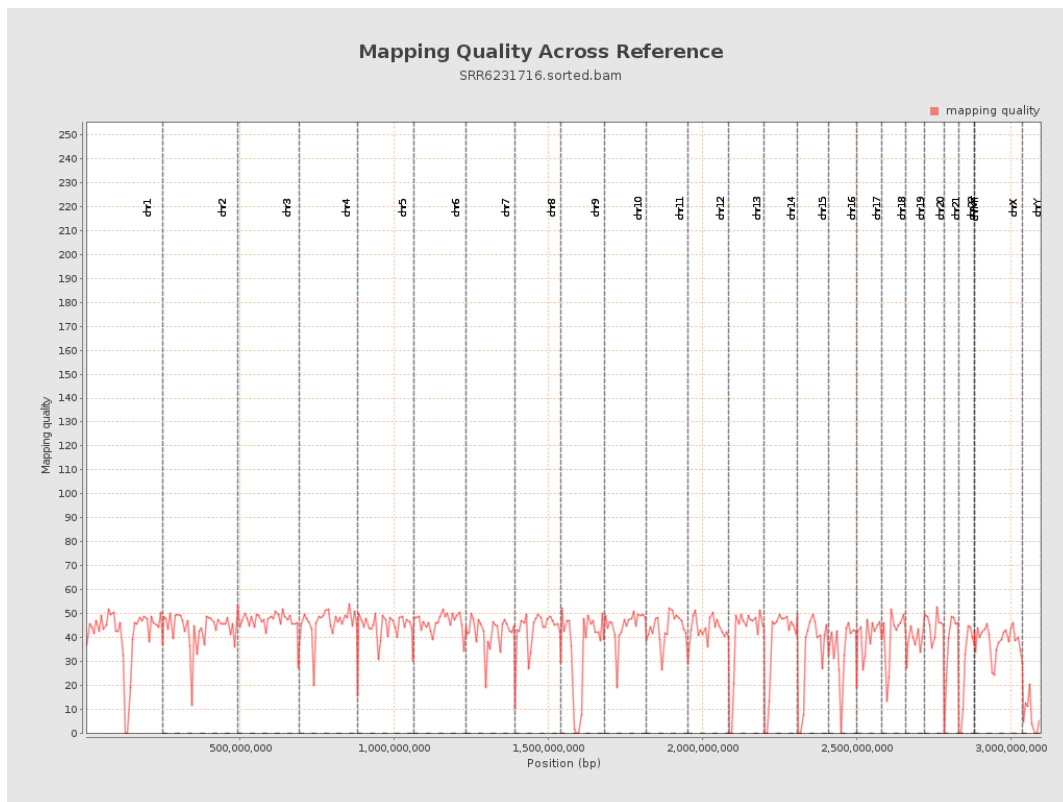
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

