

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 21:53:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013331.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_SRR6013331 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013331.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 21:53:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013331.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,242,590
Mapped reads	838,745 / 67.5%
Unmapped reads	403,845 / 32.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,334 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	17,416 / 1.4%
Duplication rate	1.75%
Clipped reads	469,839 / 37.81%

2.2. ACGT Content

Number/percentage of A's	15,928,850 / 29.94%
Number/percentage of C's	9,377,245 / 17.62%
Number/percentage of T's	16,082,496 / 30.23%
Number/percentage of G's	11,819,071 / 22.21%
Number/percentage of N's	432 / 0%
GC Percentage	39.84%

2.3. Coverage

Mean	0.0172

Standard Deviation	0.1606
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2.4. Mapping Quality

Mean Mapping Quality	46.45
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2.5. Mismatches and indels

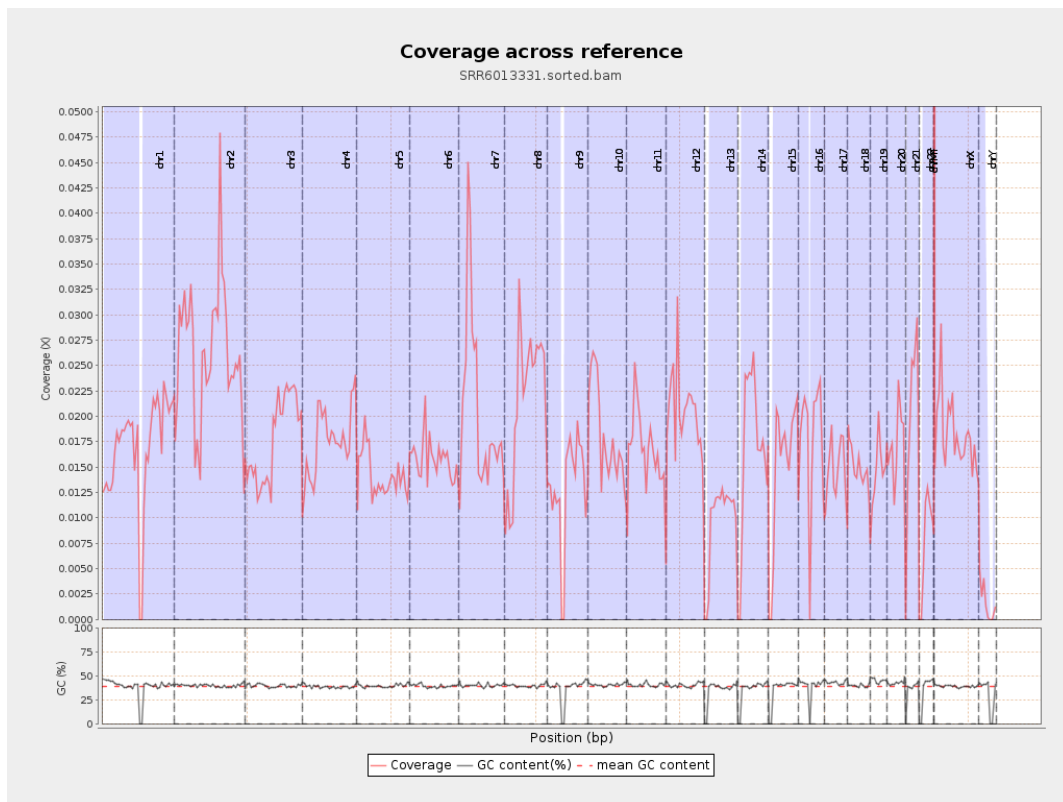
General error rate	0.96%
Mismatches	505,809
Insertions	3,571
Mapped reads with at least one insertion	0.42%
Deletions	15,213
Mapped reads with at least one deletion	1.8%
Homopolymer indels	49.19%

2.6. Chromosome stats

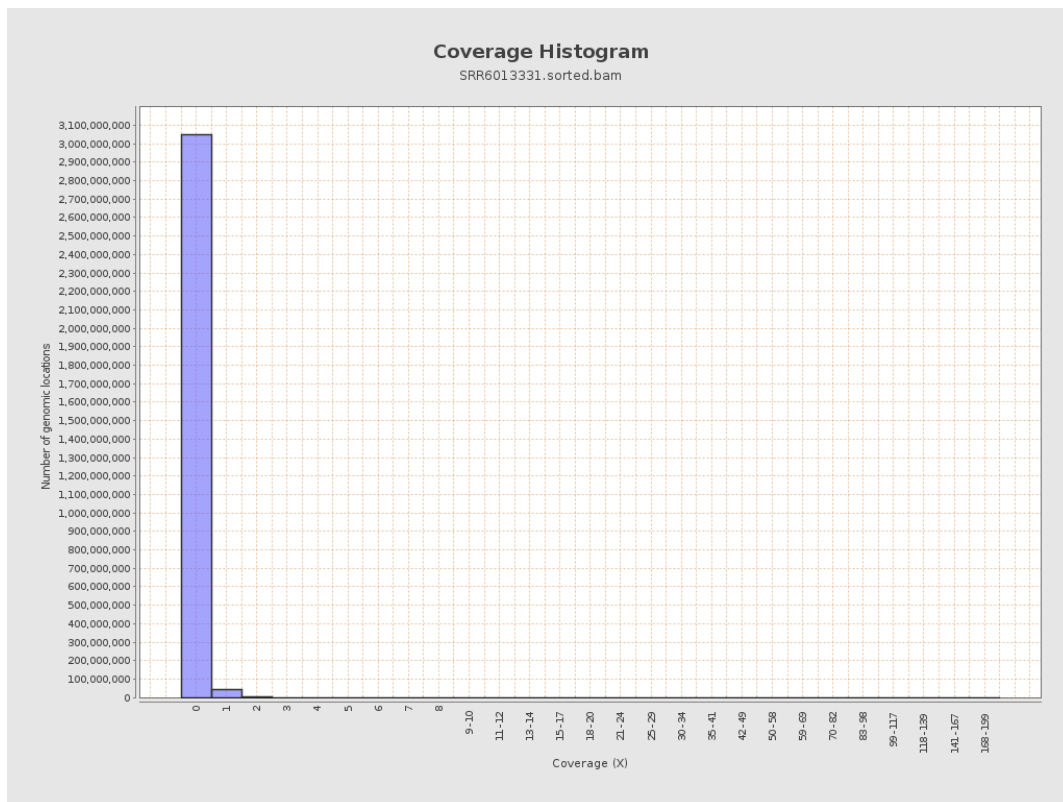
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4196313	0.0168	0.2013
chr2	243199373	6418527	0.0264	0.1942
chr3	198022430	3494426	0.0176	0.142
chr4	191154276	3349675	0.0175	0.1431
chr5	180915260	2574654	0.0142	0.128
chr6	171115067	2712259	0.0159	0.1448
chr7	159138663	3280939	0.0206	0.227

chr8	146364022	3192204	0.0218	0.1994
chr9	141213431	1829583	0.013	0.1376
chr10	135534747	2466973	0.0182	0.157
chr11	135006516	2275846	0.0169	0.1556
chr12	133851895	2754833	0.0206	0.1551
chr13	115169878	1108757	0.0096	0.1043
chr14	107349540	1819591	0.017	0.1416
chr15	102531392	1531149	0.0149	0.1334
chr16	90354753	1582253	0.0175	0.1427
chr17	81195210	1195981	0.0147	0.1346
chr18	78077248	1177222	0.0151	0.193
chr19	59128983	873734	0.0148	0.1681
chr20	63025520	1066325	0.0169	0.1397
chr21	48129895	976819	0.0203	0.1551
chr22	51304566	408699	0.008	0.094
chrMT	16571	10296	0.6213	0.9032
chrX	155270560	2840124	0.0183	0.1487
chrY	59373566	96447	0.0016	0.0448

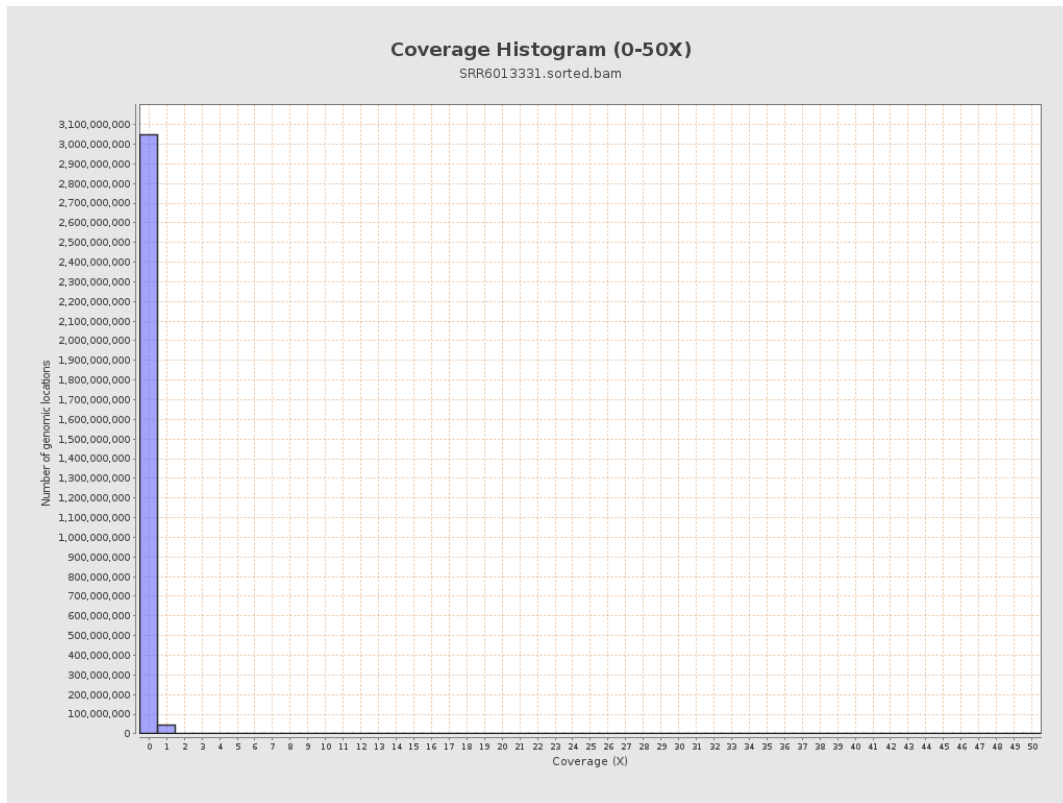
3. Results : Coverage across reference



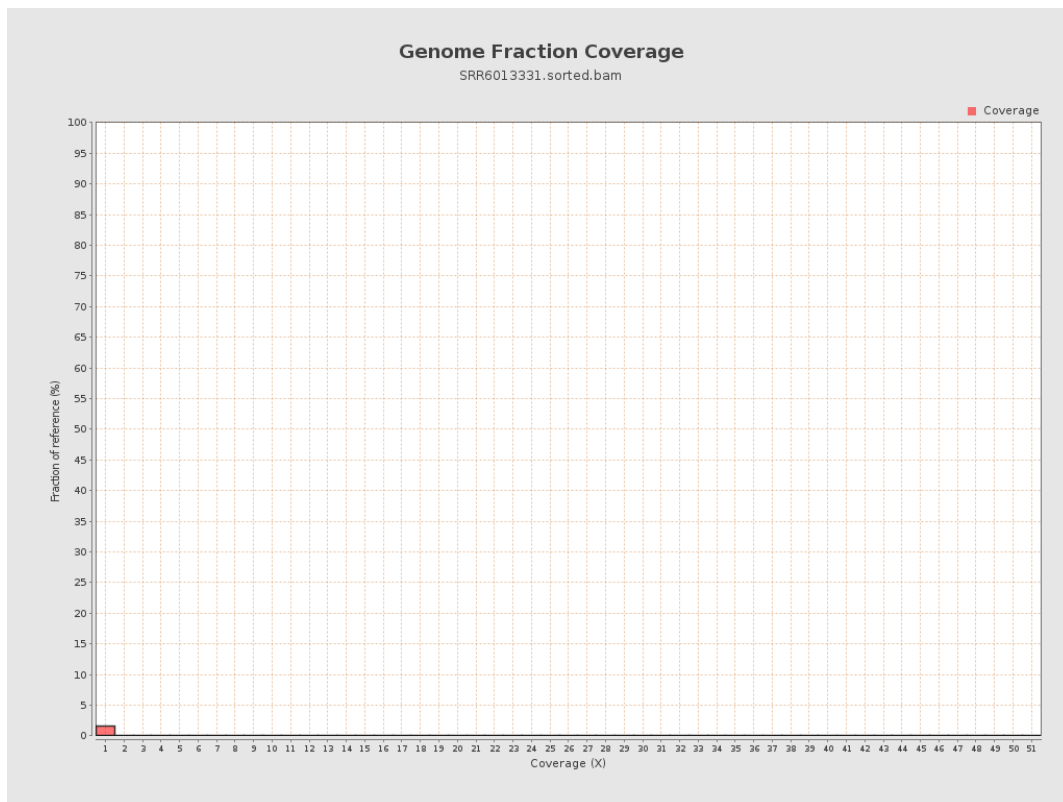
4. Results : Coverage Histogram



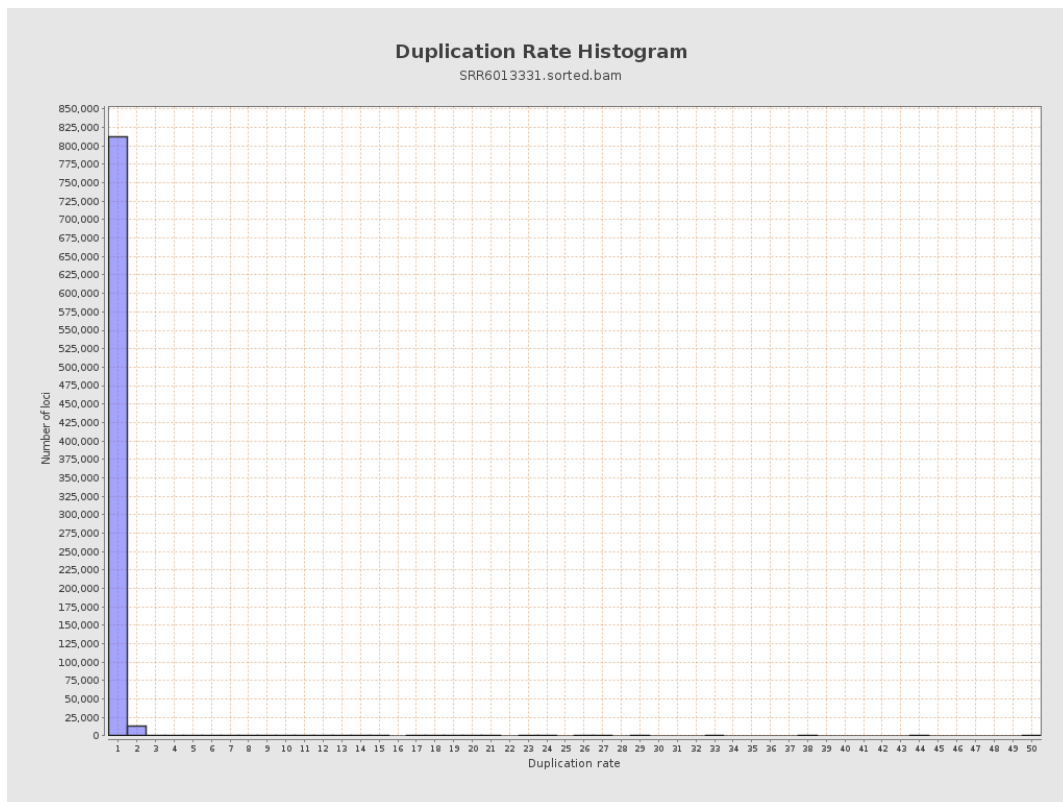
5. Results : Coverage Histogram (0-50X)



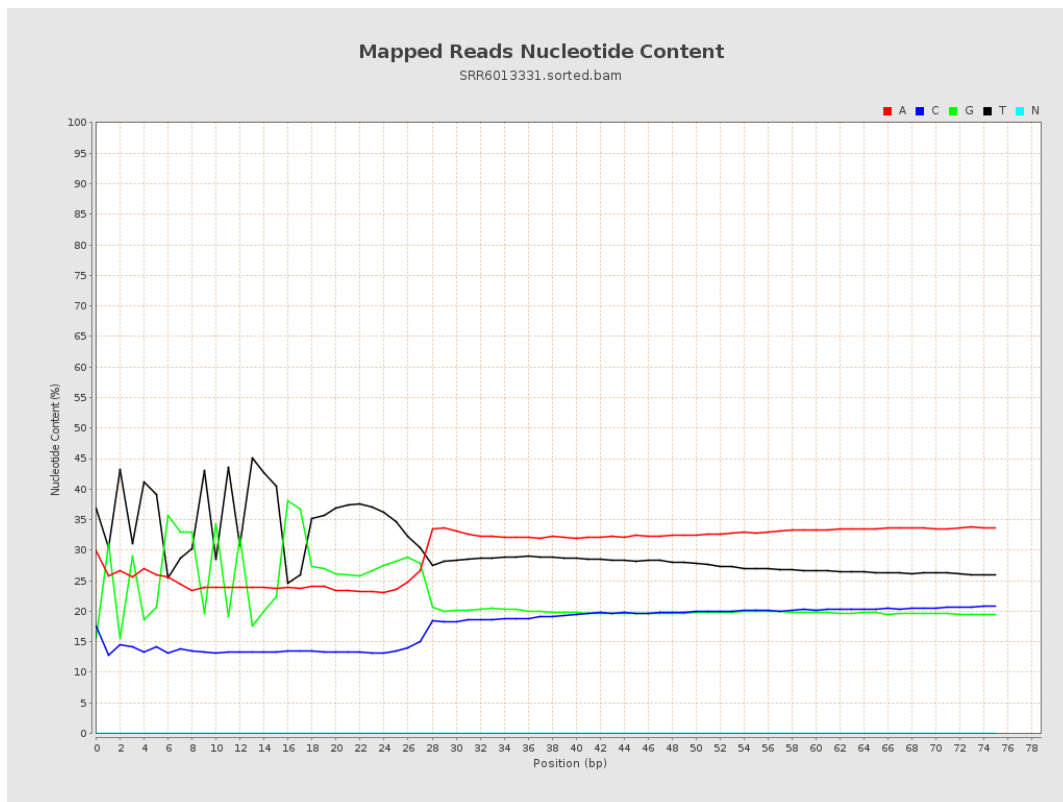
6. Results : Genome Fraction Coverage



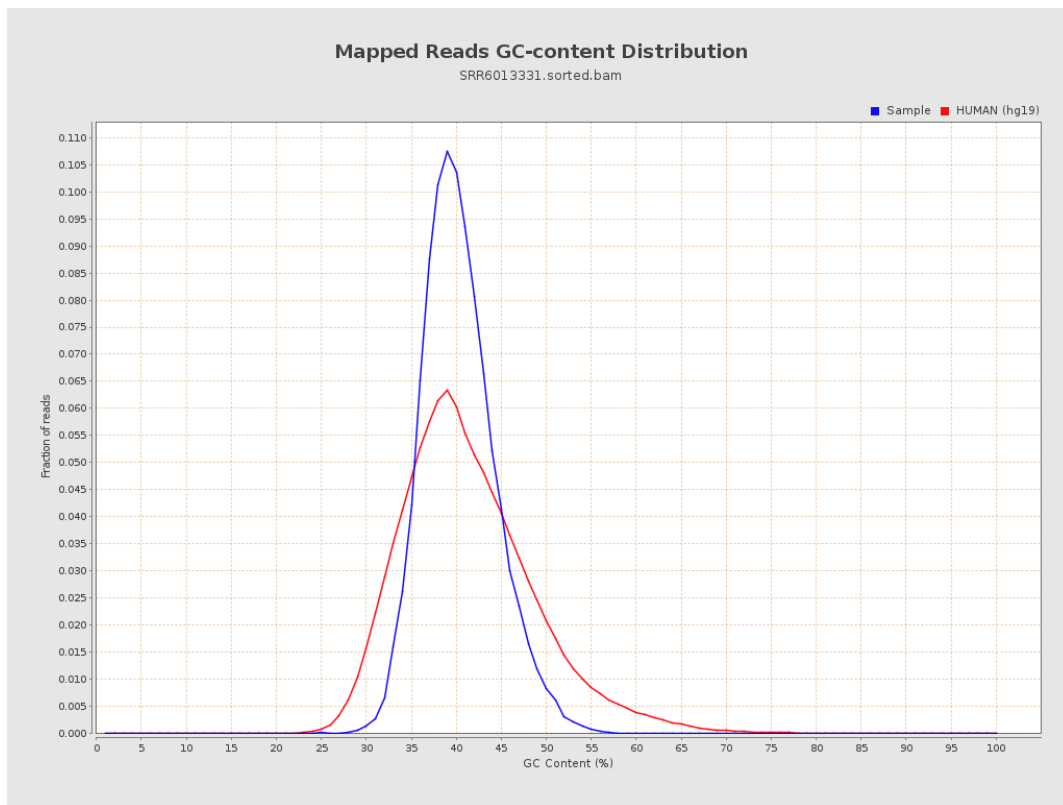
7. Results : Duplication Rate Histogram



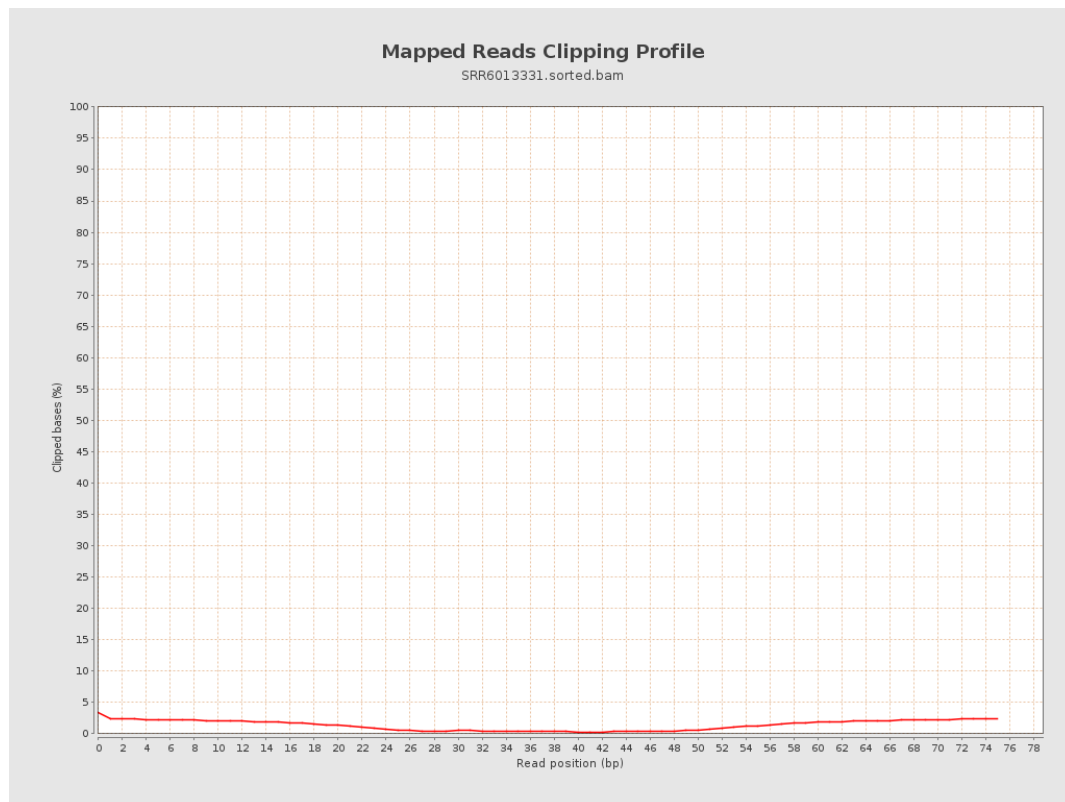
8. Results : Mapped Reads Nucleotide Content



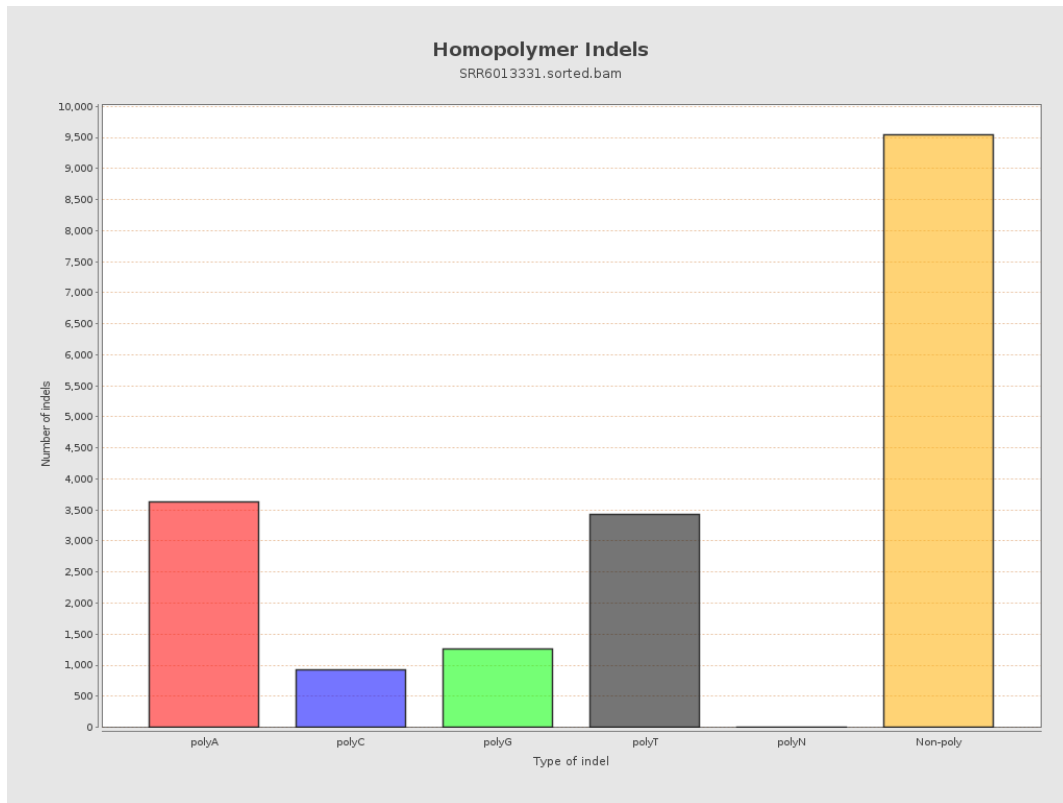
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

