

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:49:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081039.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_SRR3081039 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081039.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:49:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081039.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,416,911
Mapped reads	1,162,400 / 82.04%
Unmapped reads	254,511 / 17.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,370 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	21,441 / 1.51%
Duplication rate	1.43%
Clipped reads	512,594 / 36.18%

2.2. ACGT Content

Number/percentage of A's	23,010,681 / 29.88%
Number/percentage of C's	14,557,261 / 18.9%
Number/percentage of T's	22,668,741 / 29.44%
Number/percentage of G's	16,765,213 / 21.77%
Number/percentage of N's	1,043 / 0%
GC Percentage	40.68%

2.3. Coverage

Mean	0.0249

Standard Deviation	0.2114
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2.4. Mapping Quality

Mean Mapping Quality	47.13
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2.5. Mismatches and indels

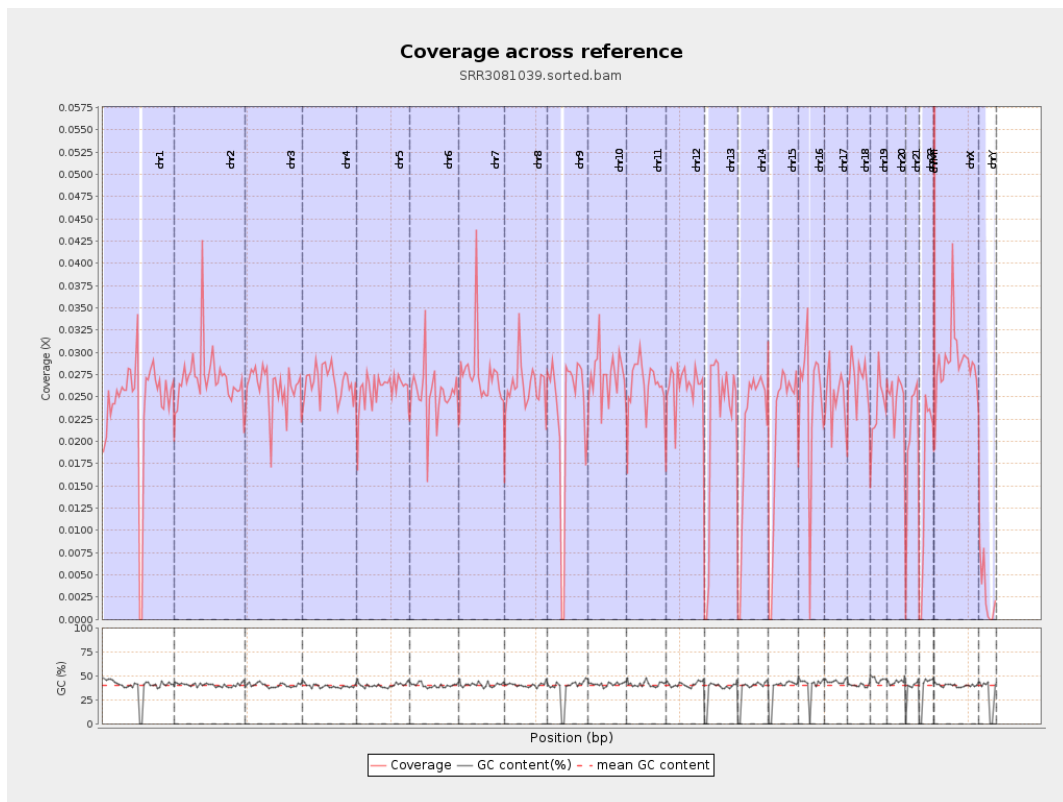
General error rate	0.84%
Mismatches	637,343
Insertions	4,957
Mapped reads with at least one insertion	0.42%
Deletions	16,330
Mapped reads with at least one deletion	1.39%
Homopolymer indels	47.39%

2.6. Chromosome stats

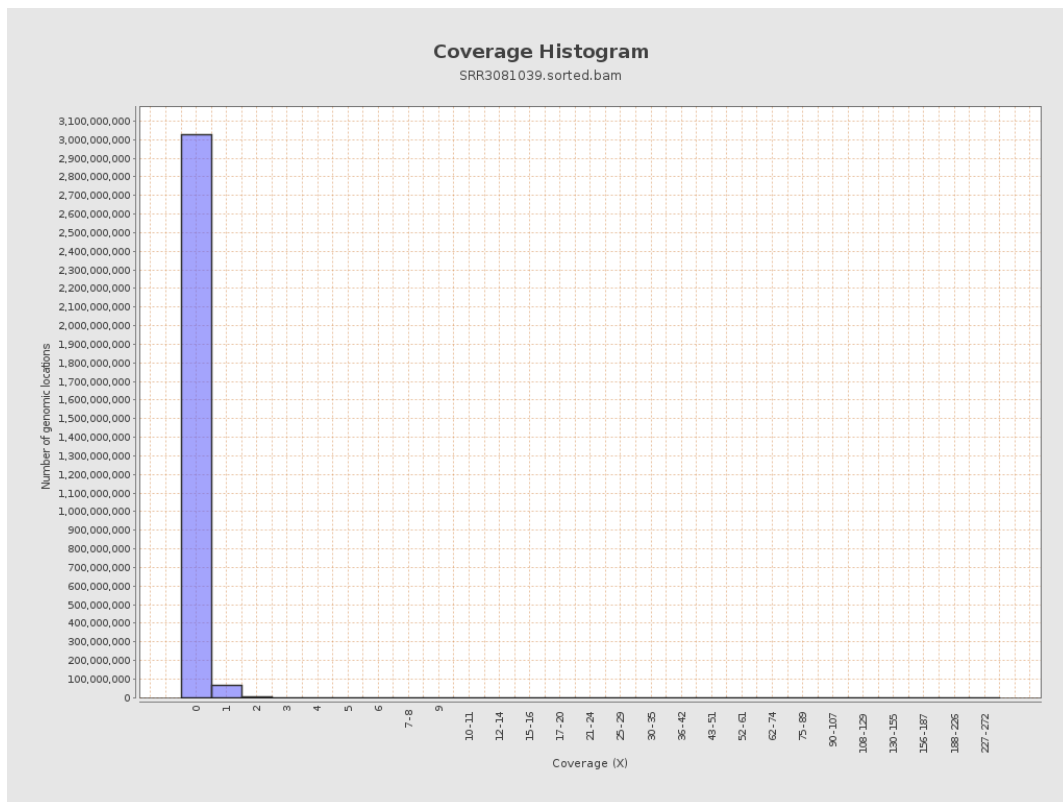
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5999677	0.0241	0.2902
chr2	243199373	6612144	0.0272	0.2258
chr3	198022430	5151730	0.026	0.1712
chr4	191154276	5092422	0.0266	0.1768
chr5	180915260	4707122	0.026	0.1717
chr6	171115067	4323112	0.0253	0.2021
chr7	159138663	4379337	0.0275	0.3055

chr8	146364022	3842749	0.0263	0.2198
chr9	141213431	3298483	0.0234	0.2
chr10	135534747	3705381	0.0273	0.2073
chr11	135006516	3574165	0.0265	0.2139
chr12	133851895	3516536	0.0263	0.1734
chr13	115169878	2522077	0.0219	0.1565
chr14	107349540	2281396	0.0213	0.1604
chr15	102531392	2180678	0.0213	0.1571
chr16	90354753	2214763	0.0245	0.1757
chr17	81195210	2019185	0.0249	0.1865
chr18	78077248	2110773	0.027	0.3612
chr19	59128983	1416465	0.024	0.2286
chr20	63025520	1560902	0.0248	0.1686
chr21	48129895	997211	0.0207	0.1607
chr22	51304566	832469	0.0162	0.1347
chrMT	16571	11203	0.6761	0.8915
chrX	155270560	4509925	0.029	0.196
chrY	59373566	170878	0.0029	0.07

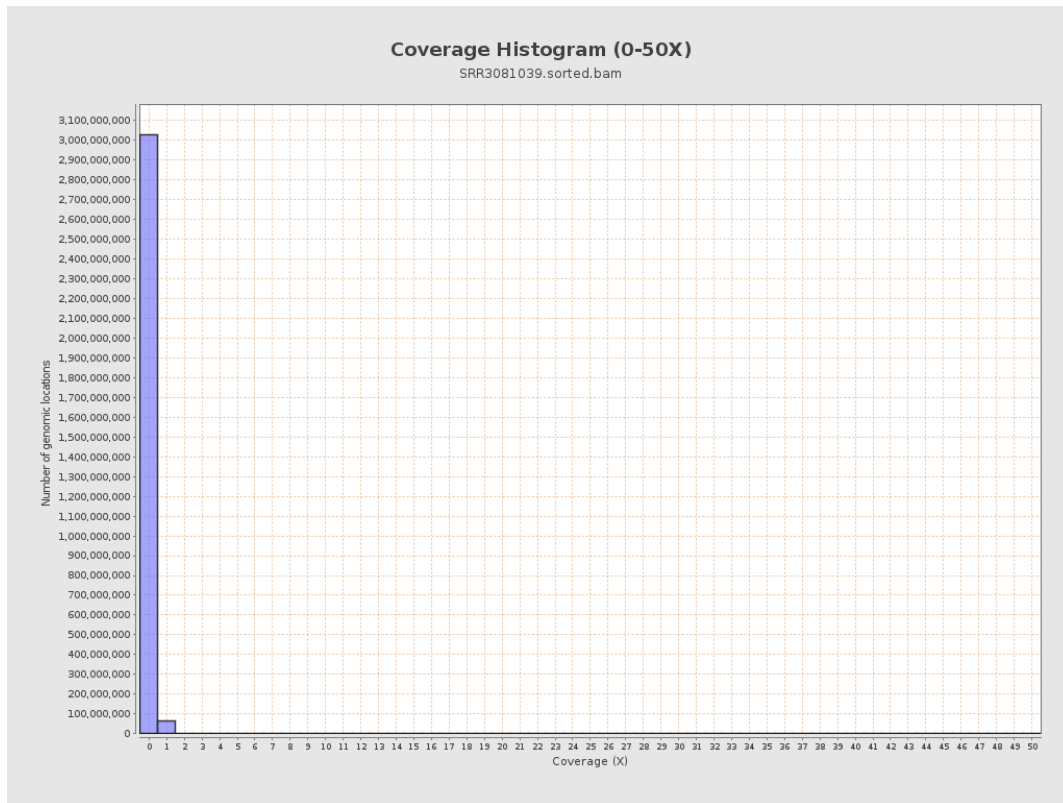
3. Results : Coverage across reference



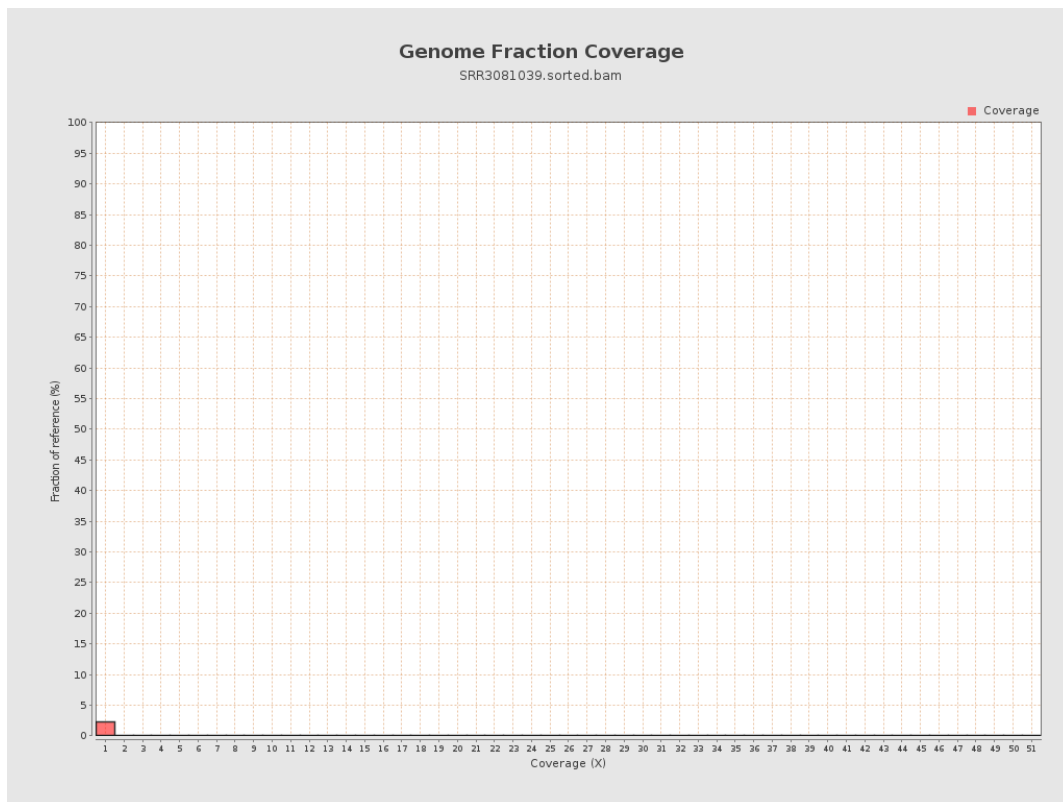
4. Results : Coverage Histogram



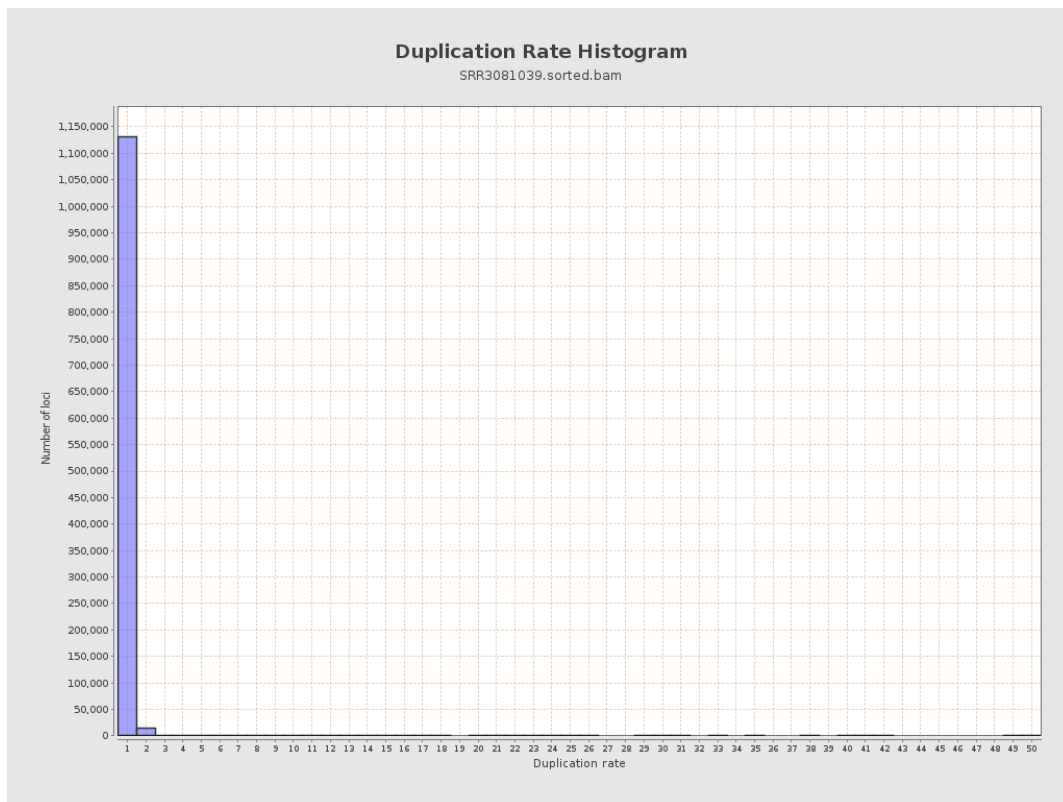
5. Results : Coverage Histogram (0-50X)



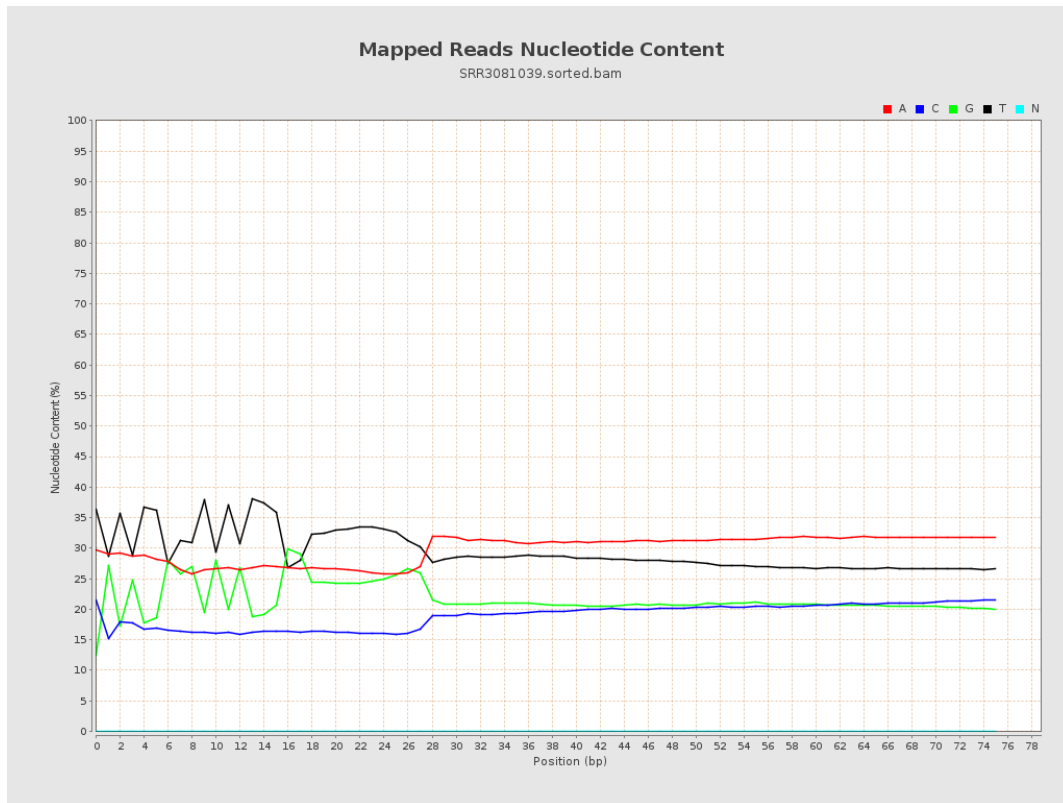
6. Results : Genome Fraction Coverage



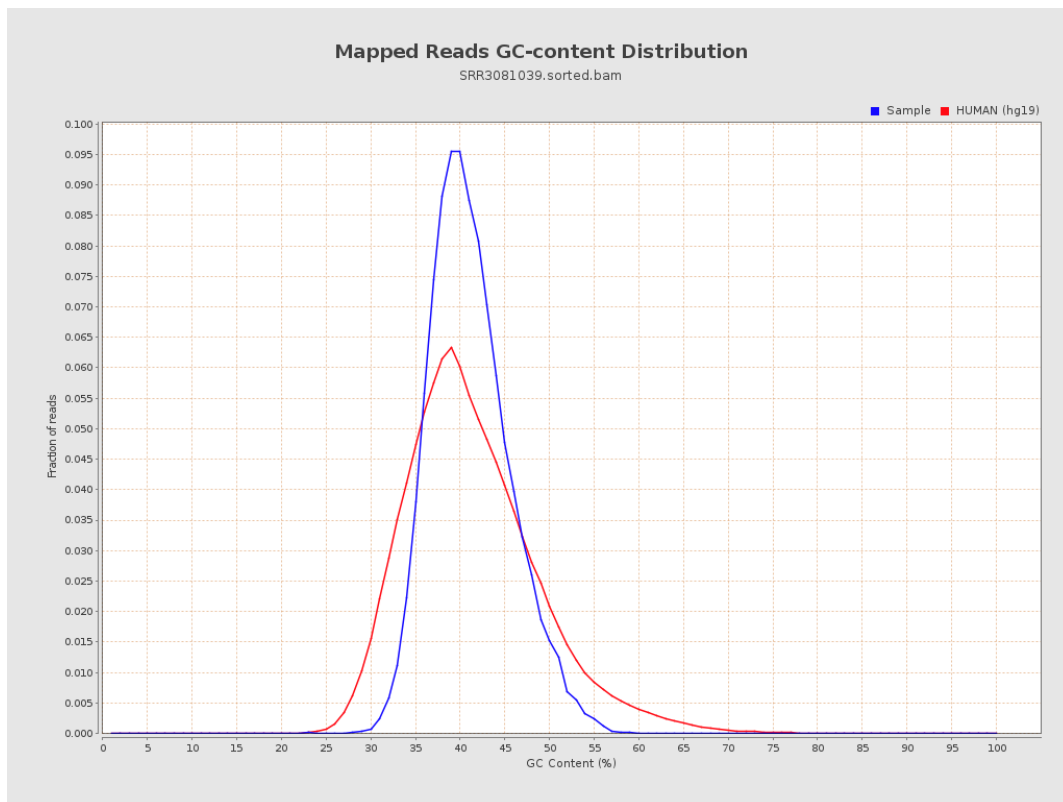
7. Results : Duplication Rate Histogram



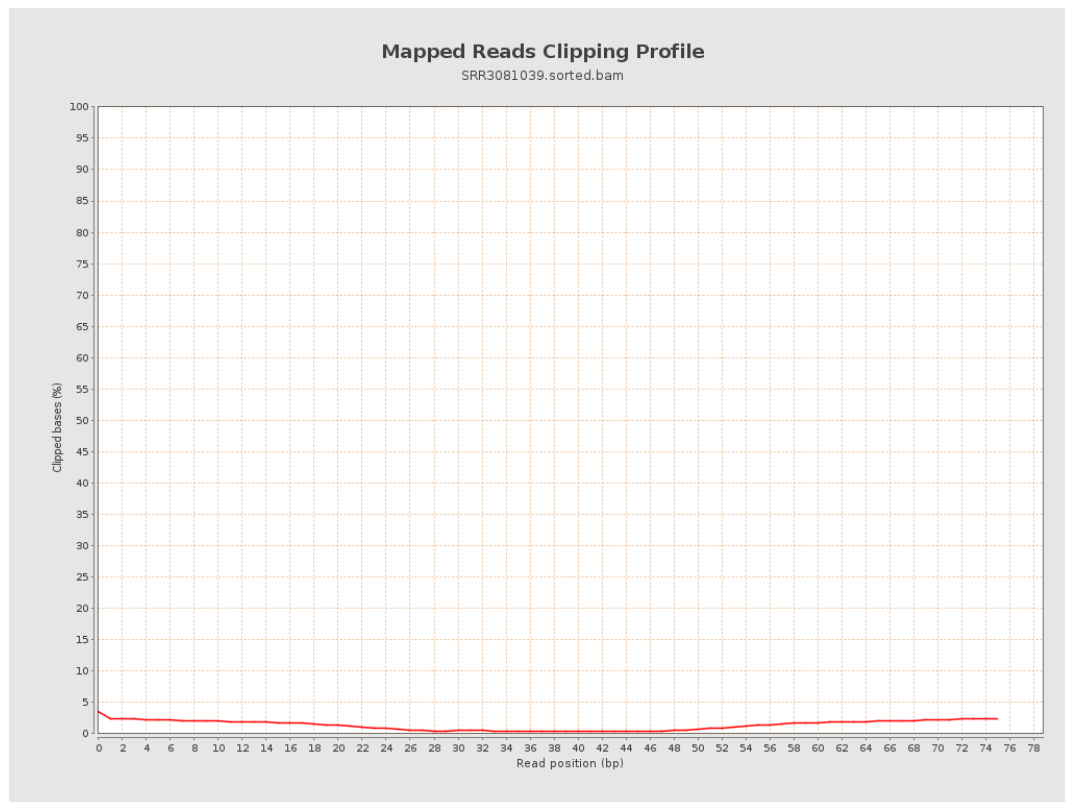
8. Results : Mapped Reads Nucleotide Content



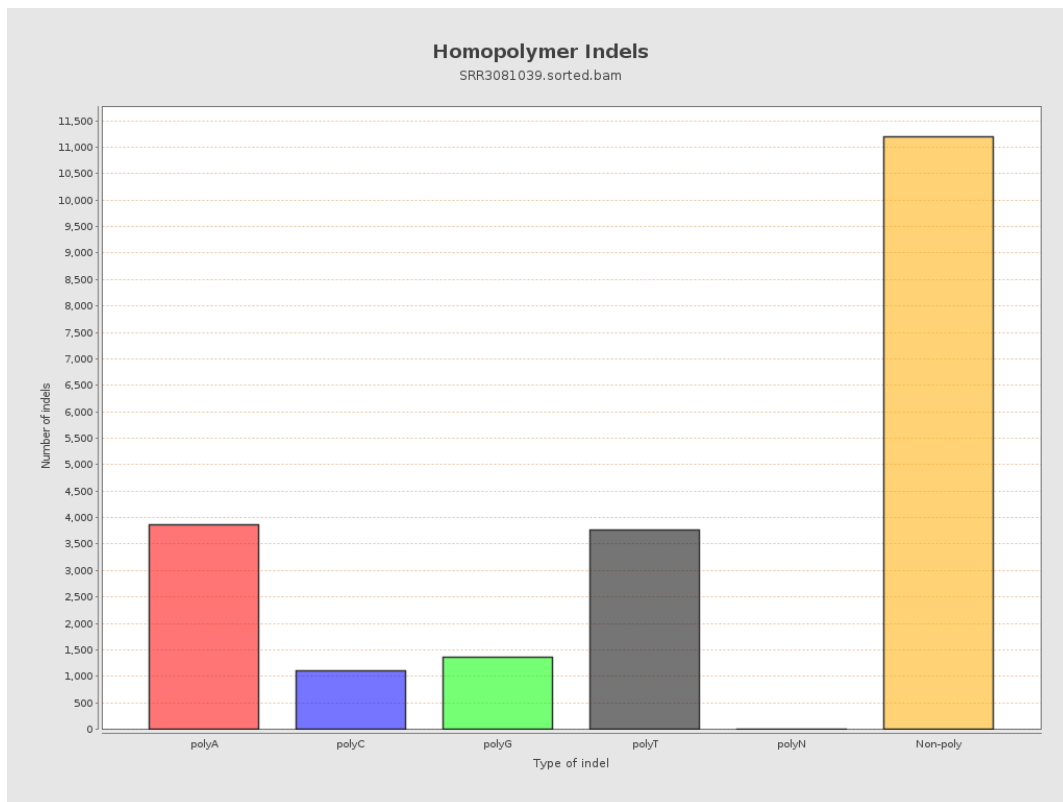
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

