

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 19:42:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236081.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_SRR6236081 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236081.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 19:42:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236081.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,890,567
Mapped reads	2,558,442 / 88.51%
Unmapped reads	332,125 / 11.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,090 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	141,763 / 4.9%
Duplication rate	4.38%
Clipped reads	1,430,245 / 49.48%

2.2. ACGT Content

Number/percentage of A's	46,319,473 / 28.16%
Number/percentage of C's	30,682,584 / 18.66%
Number/percentage of T's	51,194,330 / 31.13%
Number/percentage of G's	36,273,886 / 22.05%
Number/percentage of N's	1,448 / 0%
GC Percentage	40.71%

2.3. Coverage

Mean	0.0532

Standard Deviation	0.4825
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2.4. Mapping Quality

Mean Mapping Quality	45.21
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2.5. Mismatches and indels

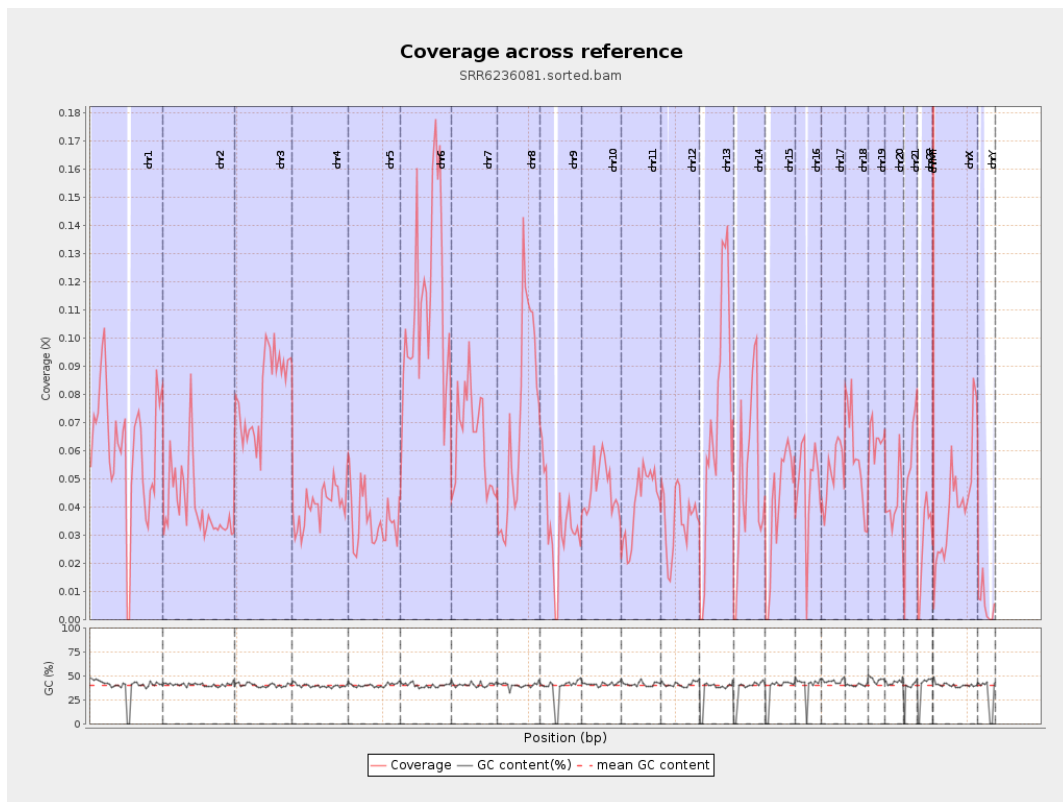
General error rate	0.76%
Mismatches	1,222,706
Insertions	12,014
Mapped reads with at least one insertion	0.47%
Deletions	46,351
Mapped reads with at least one deletion	1.79%
Homopolymer indels	46.69%

2.6. Chromosome stats

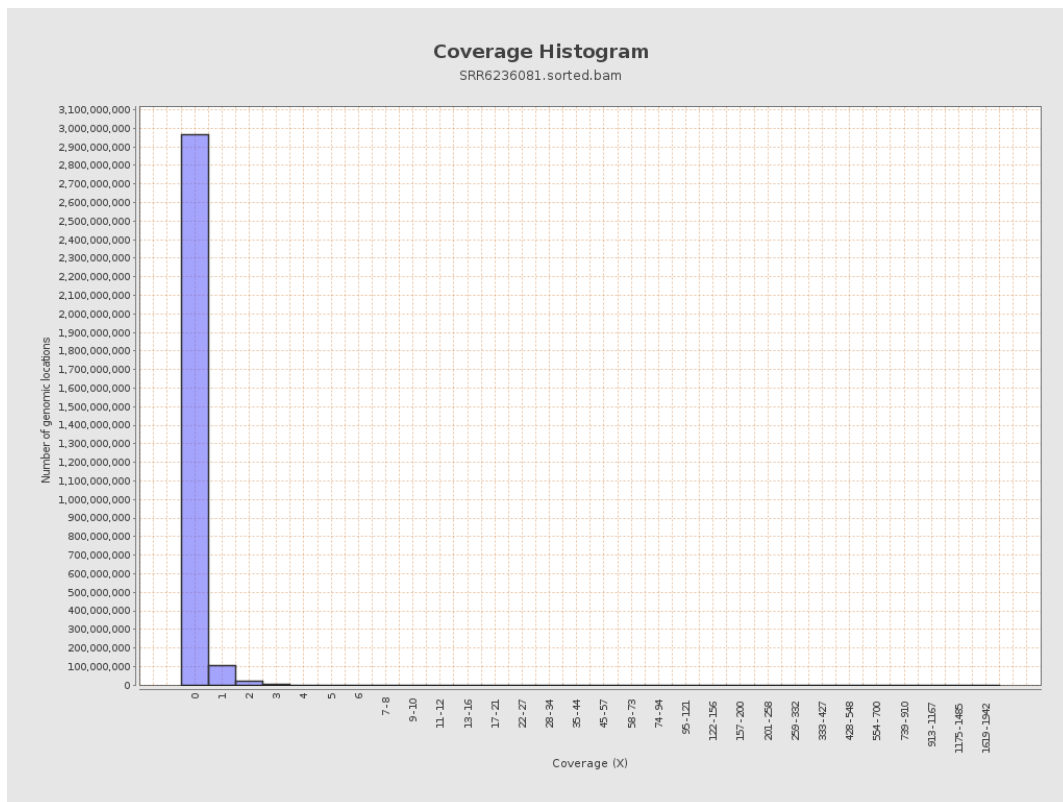
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15234948	0.0611	0.5908
chr2	243199373	9867969	0.0406	0.5299
chr3	198022430	15825701	0.0799	0.3456
chr4	191154276	7800146	0.0408	0.2961
chr5	180915260	6471063	0.0358	0.2317
chr6	171115067	19318324	0.1129	0.5989
chr7	159138663	10245878	0.0644	0.6042

chr8	146364022	10442177	0.0713	1.2654
chr9	141213431	4645794	0.0329	0.3304
chr10	135534747	6328781	0.0467	0.3336
chr11	135006516	5596238	0.0415	0.3518
chr12	133851895	4770194	0.0356	0.2342
chr13	115169878	8160494	0.0709	0.3322
chr14	107349540	5369007	0.05	0.2811
chr15	102531392	4198154	0.0409	0.2679
chr16	90354753	4249702	0.047	0.2764
chr17	81195210	4233322	0.0521	0.3034
chr18	78077248	4512055	0.0578	0.5449
chr19	59128983	3793086	0.0641	0.5108
chr20	63025520	2634678	0.0418	0.2524
chr21	48129895	2630566	0.0547	0.2945
chr22	51304566	1408098	0.0274	0.1954
chrMT	16571	113107	6.8256	5.928
chrX	155270560	6382458	0.0411	0.2732
chrY	59373566	318484	0.0054	0.1242

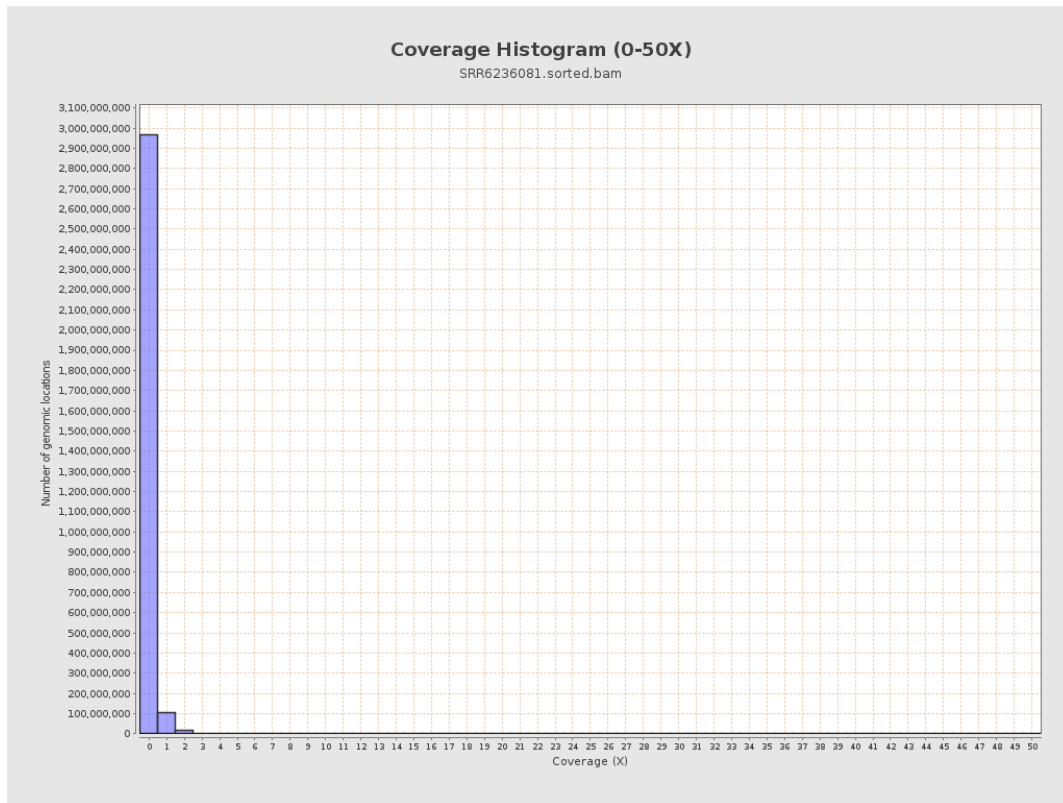
3. Results : Coverage across reference



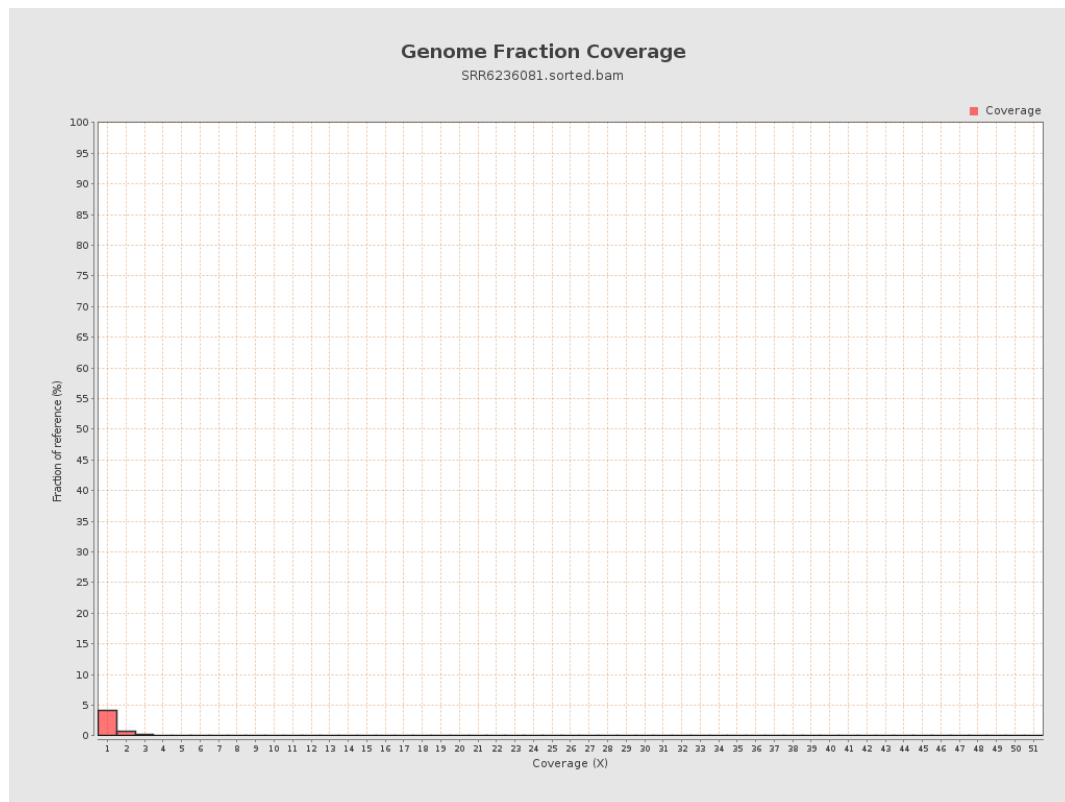
4. Results : Coverage Histogram



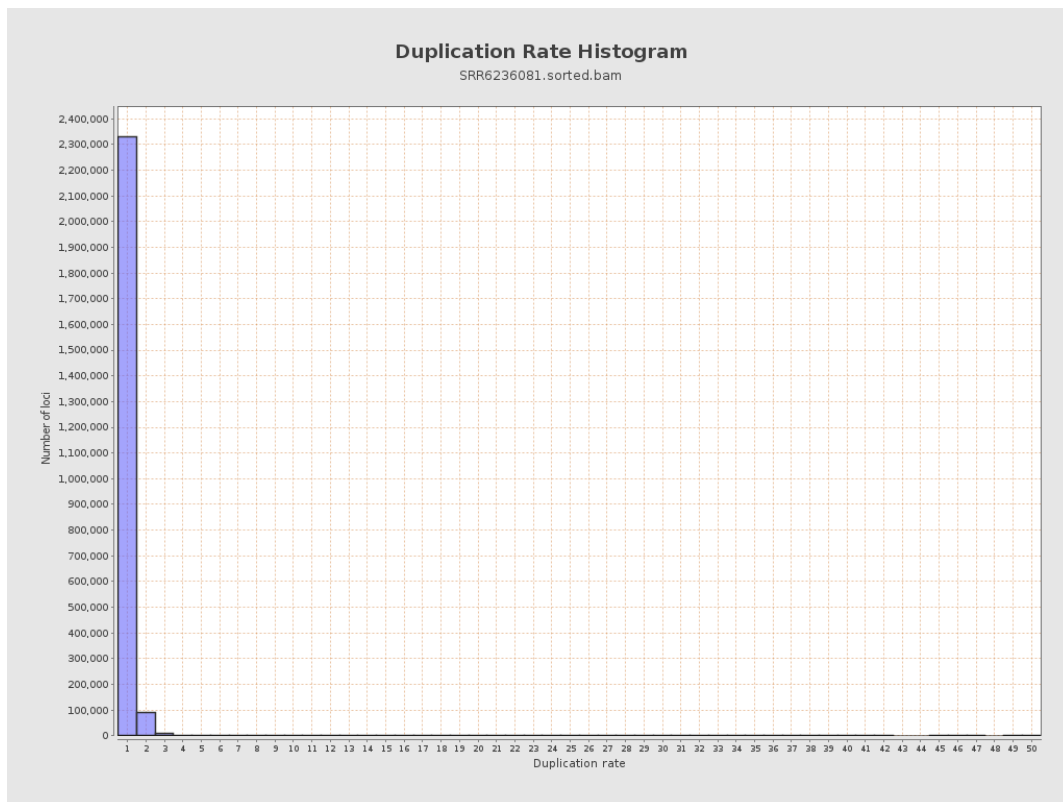
5. Results : Coverage Histogram (0-50X)



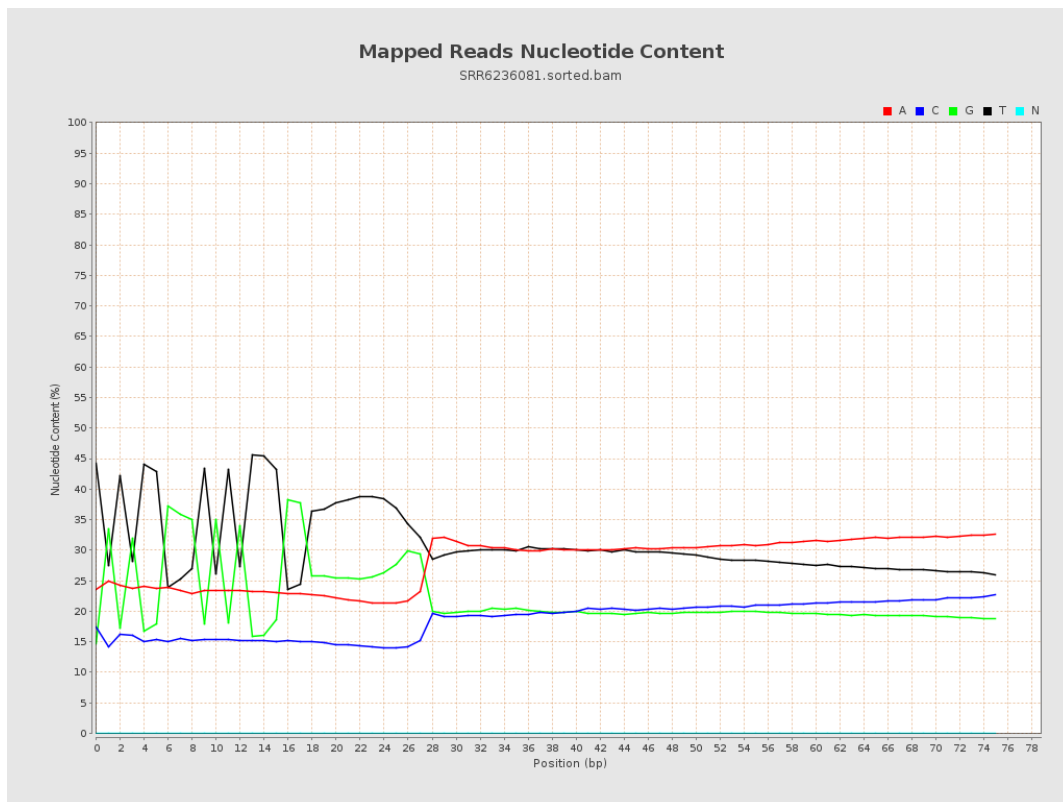
6. Results : Genome Fraction Coverage



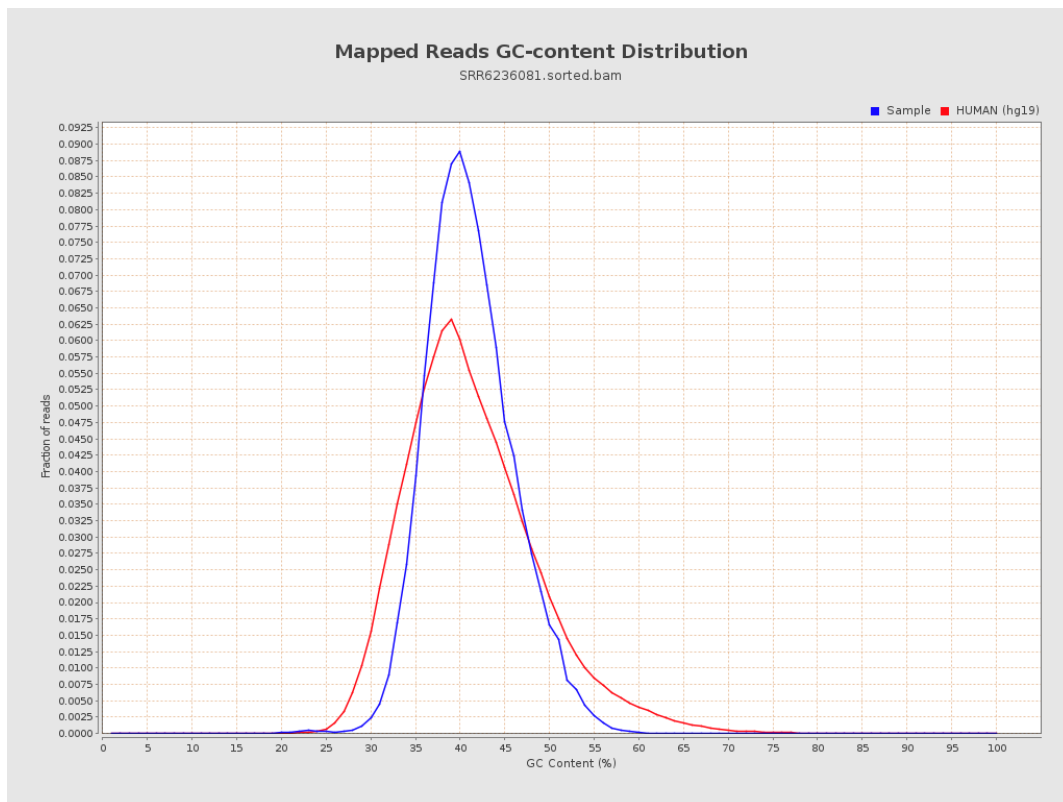
7. Results : Duplication Rate Histogram



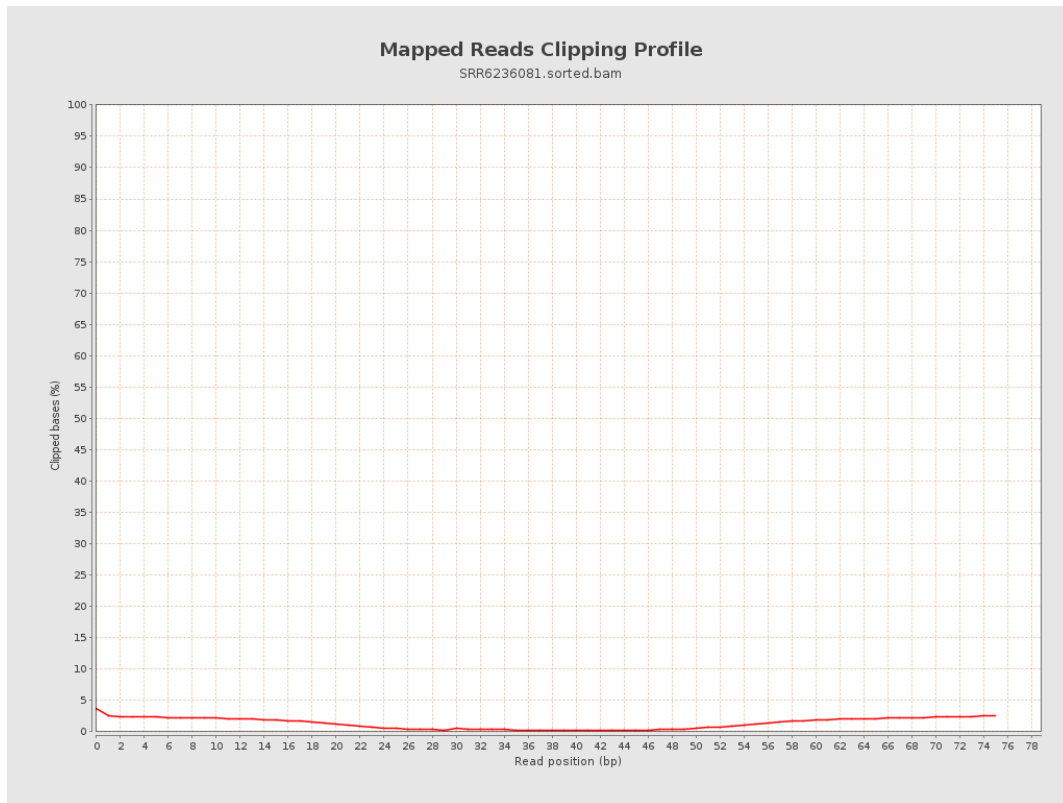
8. Results : Mapped Reads Nucleotide Content



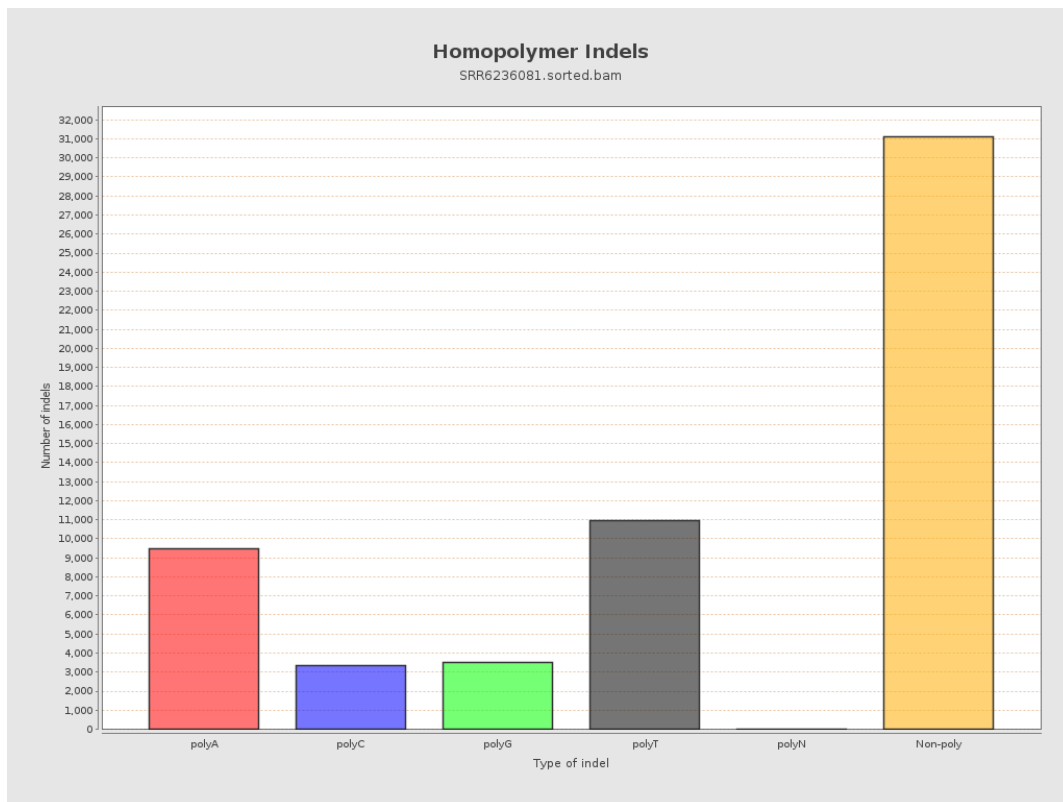
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

