

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 05:43:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231827.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_SRR6231827 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231827.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 05:43:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231827.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	553,299
Mapped reads	371,708 / 67.18%
Unmapped reads	181,591 / 32.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	832 / 0.15%
Read min/max/mean length	30 / 76 / 76.05
Duplicated reads (estimated)	13,987 / 2.53%
Duplication rate	2.26%
Clipped reads	218,187 / 39.43%

2.2. ACGT Content

Number/percentage of A's	6,256,267 / 26.99%
Number/percentage of C's	3,833,551 / 16.54%
Number/percentage of T's	7,567,647 / 32.65%
Number/percentage of G's	5,520,278 / 23.82%
Number/percentage of N's	1,011 / 0%
GC Percentage	40.36%

2.3. Coverage

Mean	0.0075

Standard Deviation	0.5646
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2.4. Mapping Quality

Mean Mapping Quality	46.53
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2.5. Mismatches and indels

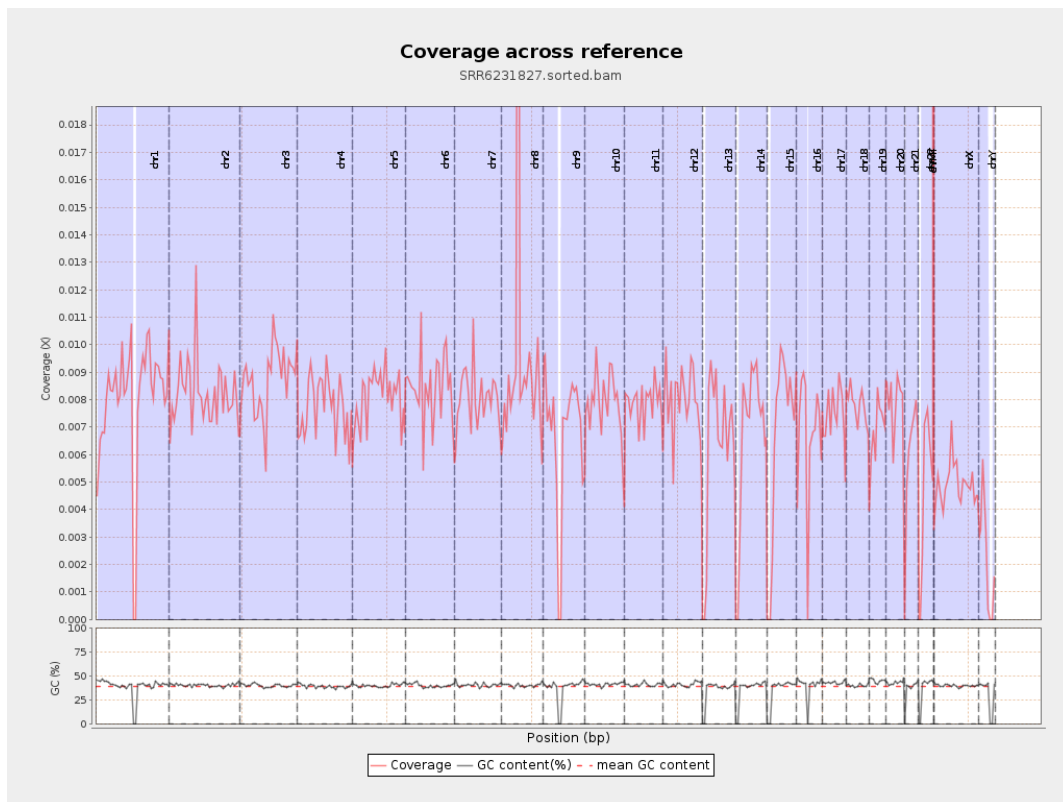
General error rate	0.97%
Mismatches	220,572
Insertions	1,854
Mapped reads with at least one insertion	0.49%
Deletions	6,836
Mapped reads with at least one deletion	1.82%
Homopolymer indels	48.72%

2.6. Chromosome stats

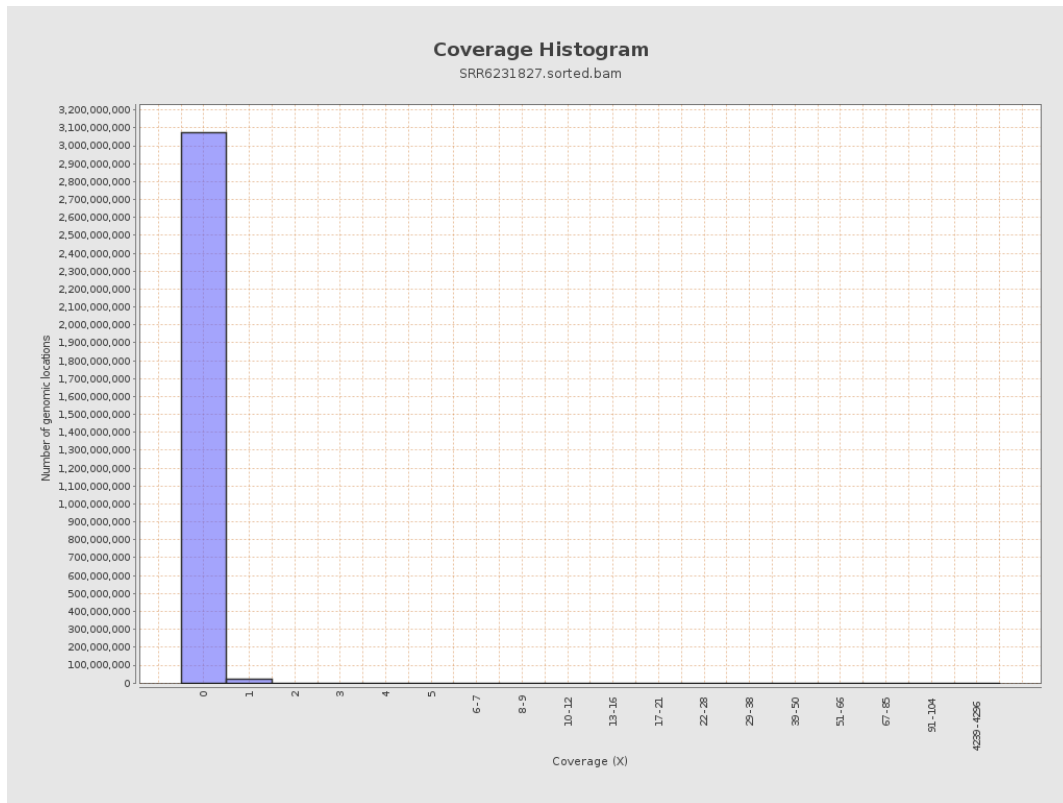
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1989071	0.008	0.1047
chr2	243199373	2001518	0.0082	0.1082
chr3	198022430	1721813	0.0087	0.0975
chr4	191154276	1472079	0.0077	0.0926
chr5	180915260	1461122	0.0081	0.0941
chr6	171115067	1436985	0.0084	0.1008
chr7	159138663	1292578	0.0081	0.1237

chr8	146364022	1426388	0.0097	2.5592
chr9	141213431	939282	0.0067	0.0943
chr10	135534747	1070951	0.0079	0.0989
chr11	135006516	1055754	0.0078	0.1107
chr12	133851895	1070026	0.008	0.0939
chr13	115169878	715776	0.0062	0.0823
chr14	107349540	717446	0.0067	0.0864
chr15	102531392	686506	0.0067	0.0861
chr16	90354753	606494	0.0067	0.0867
chr17	81195210	601364	0.0074	0.0925
chr18	78077248	611004	0.0078	0.1295
chr19	59128983	411444	0.007	0.0962
chr20	63025520	486188	0.0077	0.0921
chr21	48129895	288831	0.006	0.0827
chr22	51304566	235806	0.0046	0.0713
chrMT	16571	5343	0.3224	0.6335
chrX	155270560	761164	0.0049	0.0782
chrY	59373566	125565	0.0021	0.0495

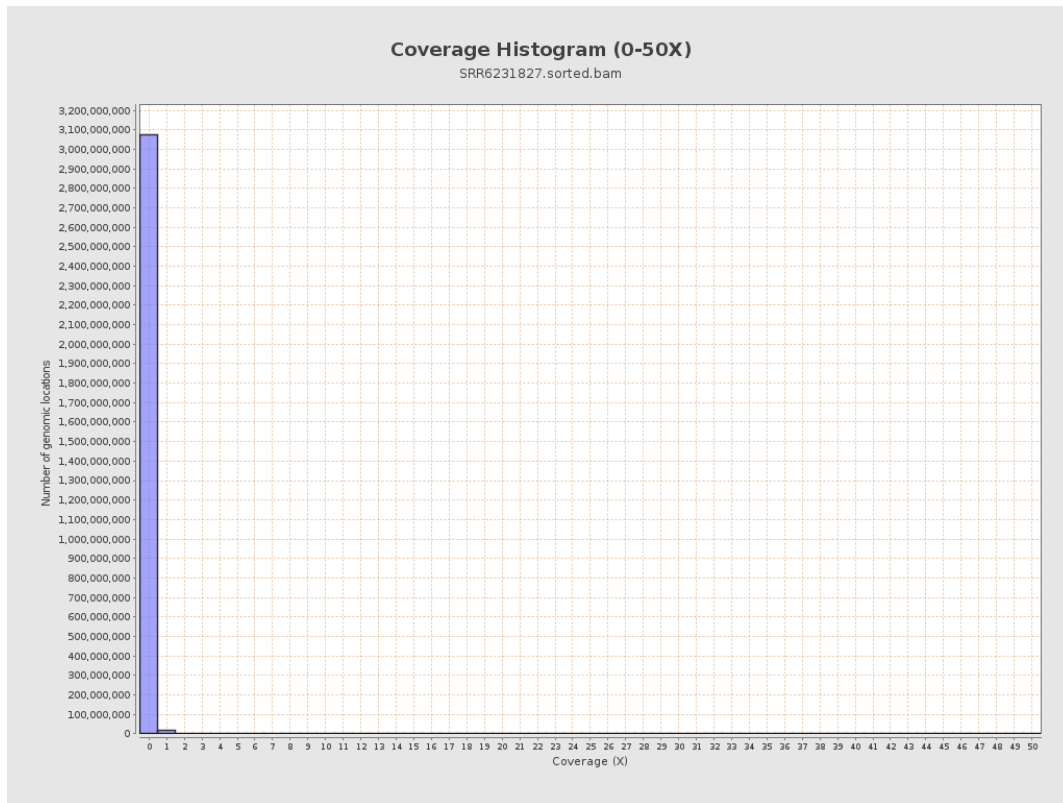
3. Results : Coverage across reference



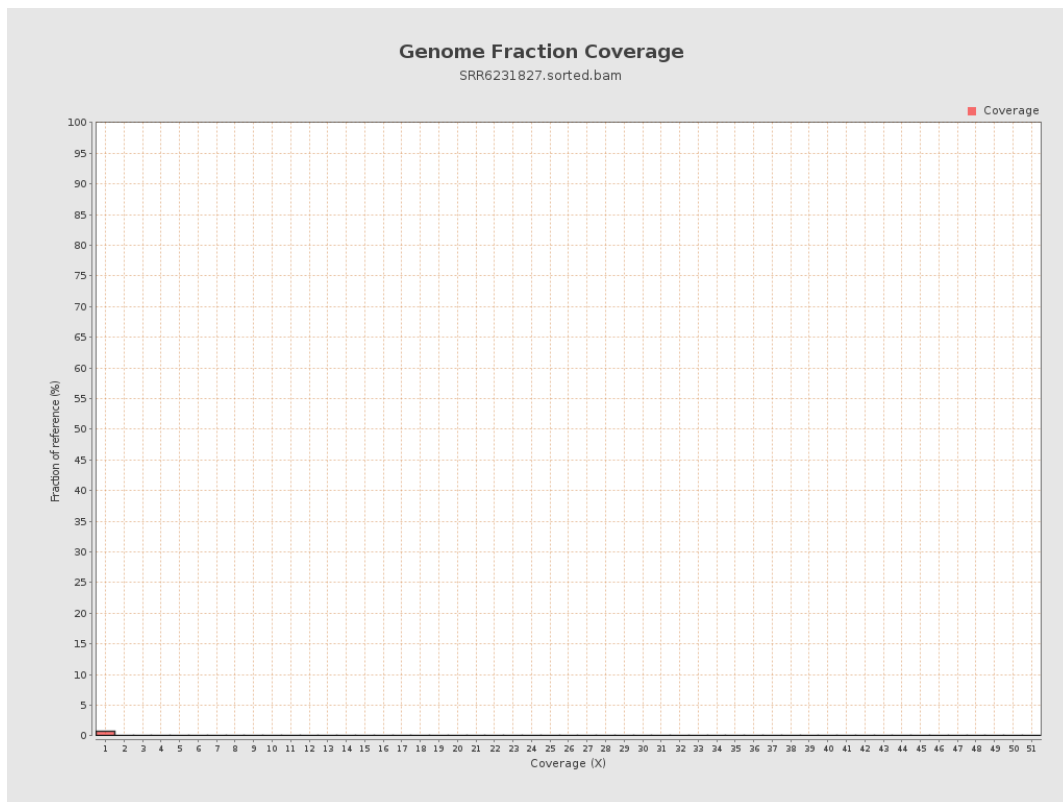
4. Results : Coverage Histogram



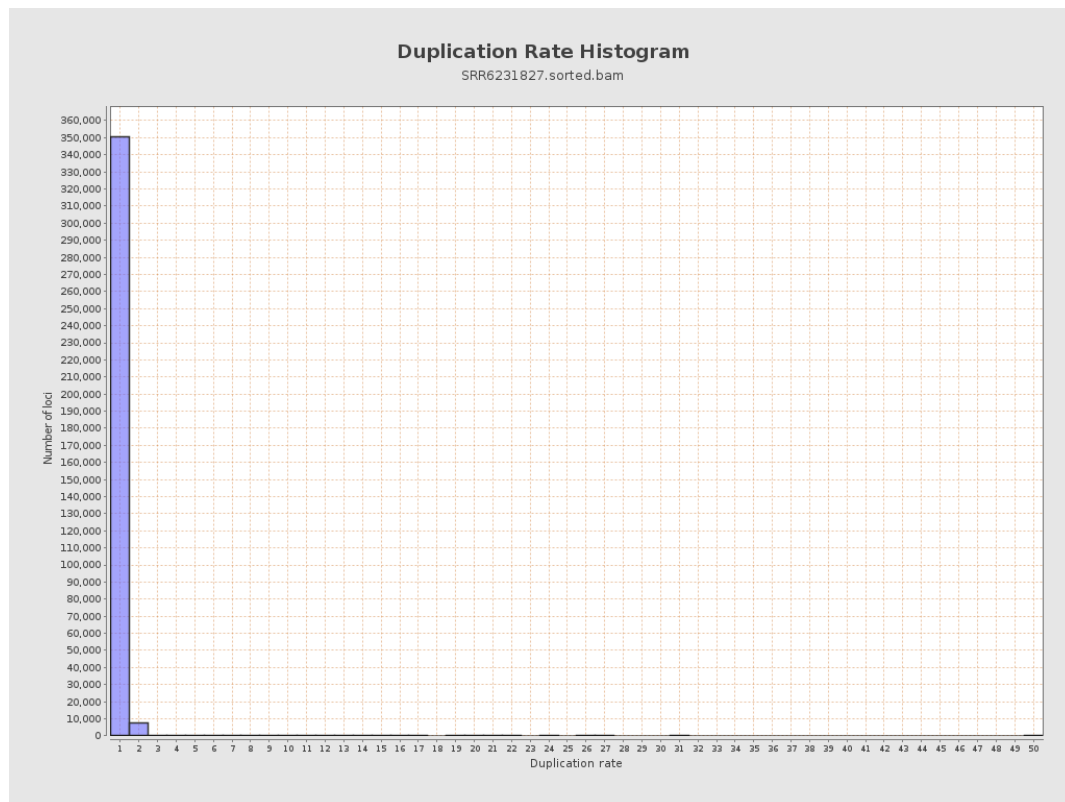
5. Results : Coverage Histogram (0-50X)



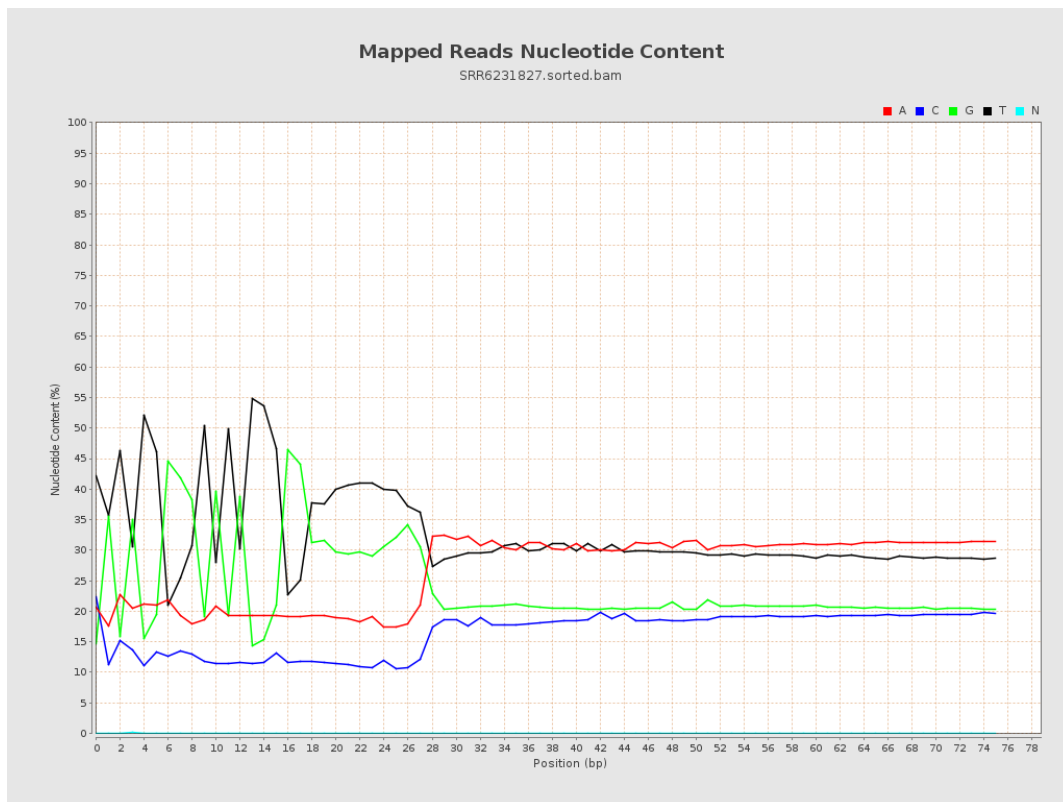
6. Results : Genome Fraction Coverage



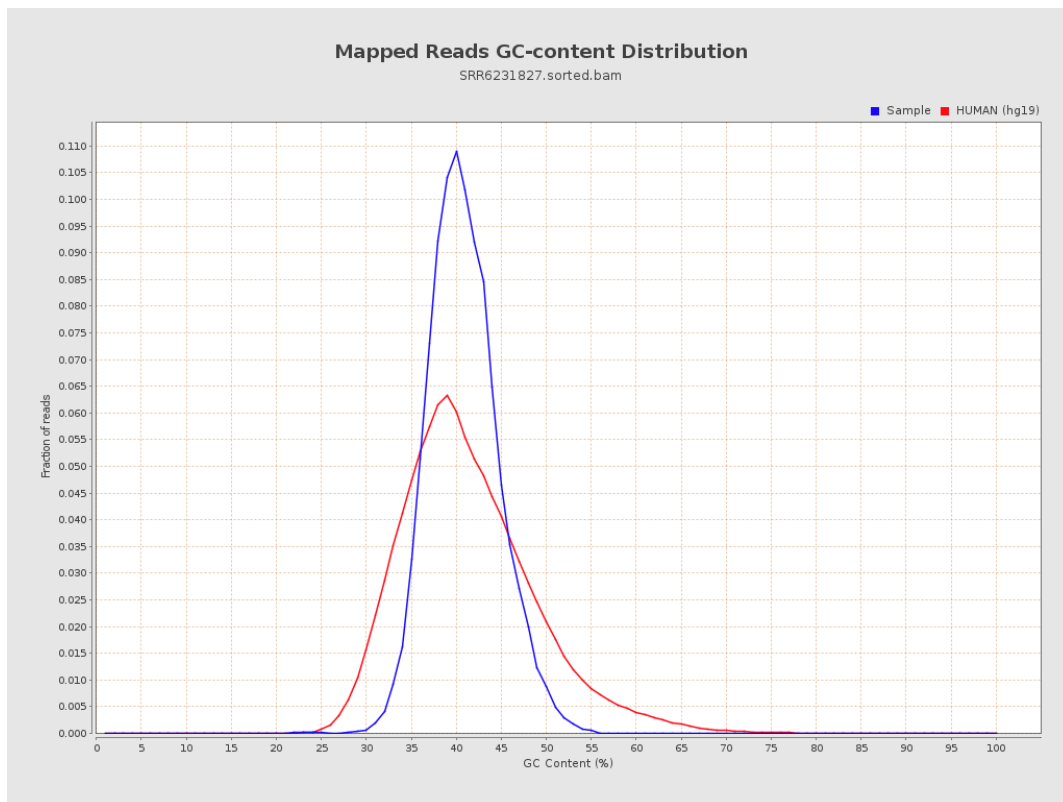
7. Results : Duplication Rate Histogram



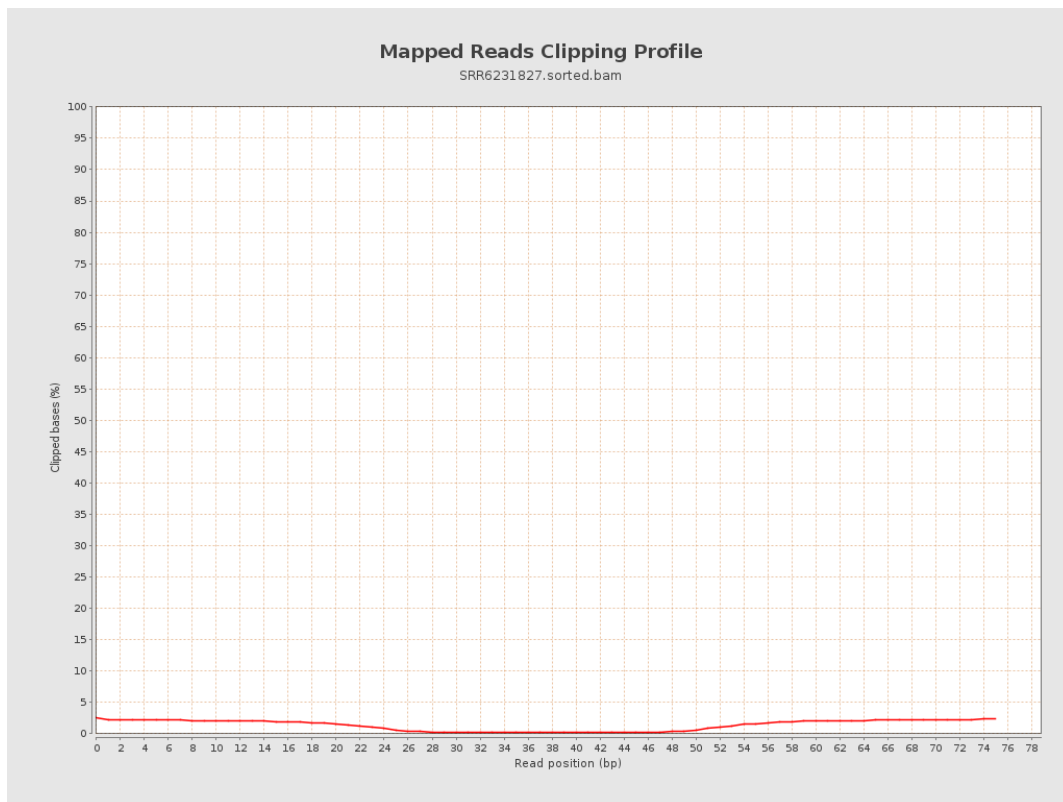
8. Results : Mapped Reads Nucleotide Content



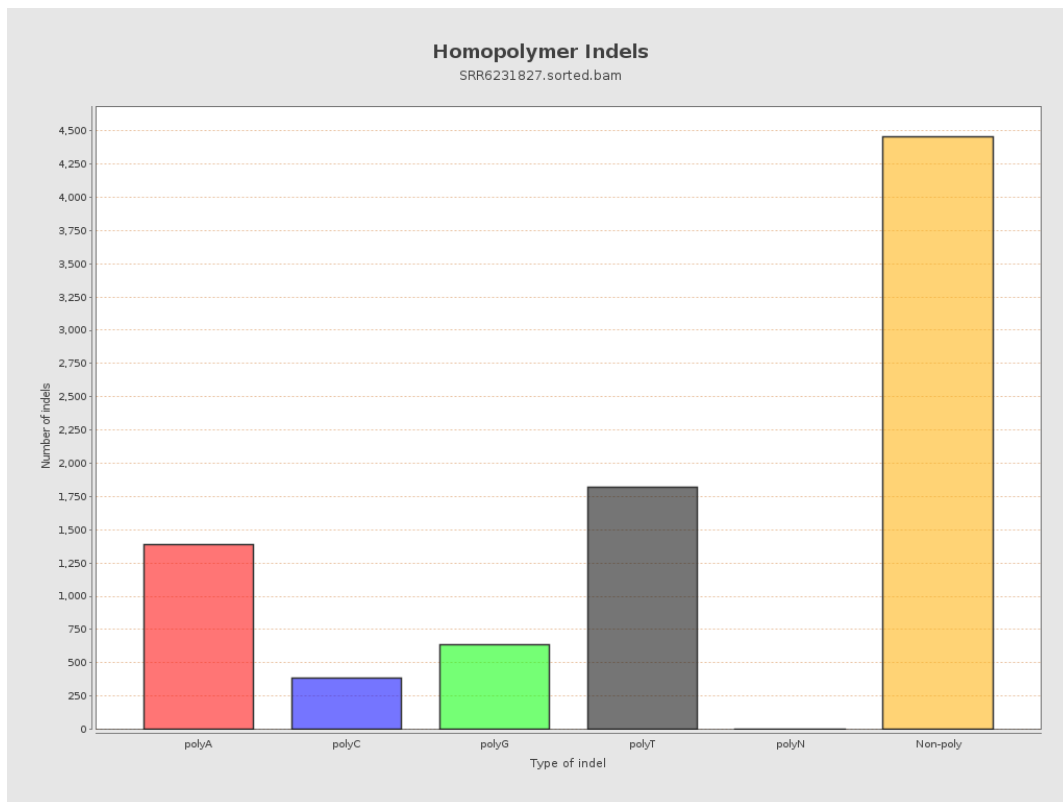
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

