

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 05:59:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231830.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_SRR6231830 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231830.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 05:59:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231830.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,757,763
Mapped reads	4,354,463 / 91.52%
Unmapped reads	403,300 / 8.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,345 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	373,300 / 7.85%
Duplication rate	6.09%
Clipped reads	2,509,675 / 52.75%

2.2. ACGT Content

Number/percentage of A's	67,669,998 / 24.61%
Number/percentage of C's	51,109,540 / 18.59%
Number/percentage of T's	87,284,187 / 31.74%
Number/percentage of G's	68,831,980 / 25.03%
Number/percentage of N's	101,830 / 0.04%
GC Percentage	43.62%

2.3. Coverage

Mean	0.0889

Standard Deviation	1.2465
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2.4. Mapping Quality

Mean Mapping Quality	40.62
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2.5. Mismatches and indels

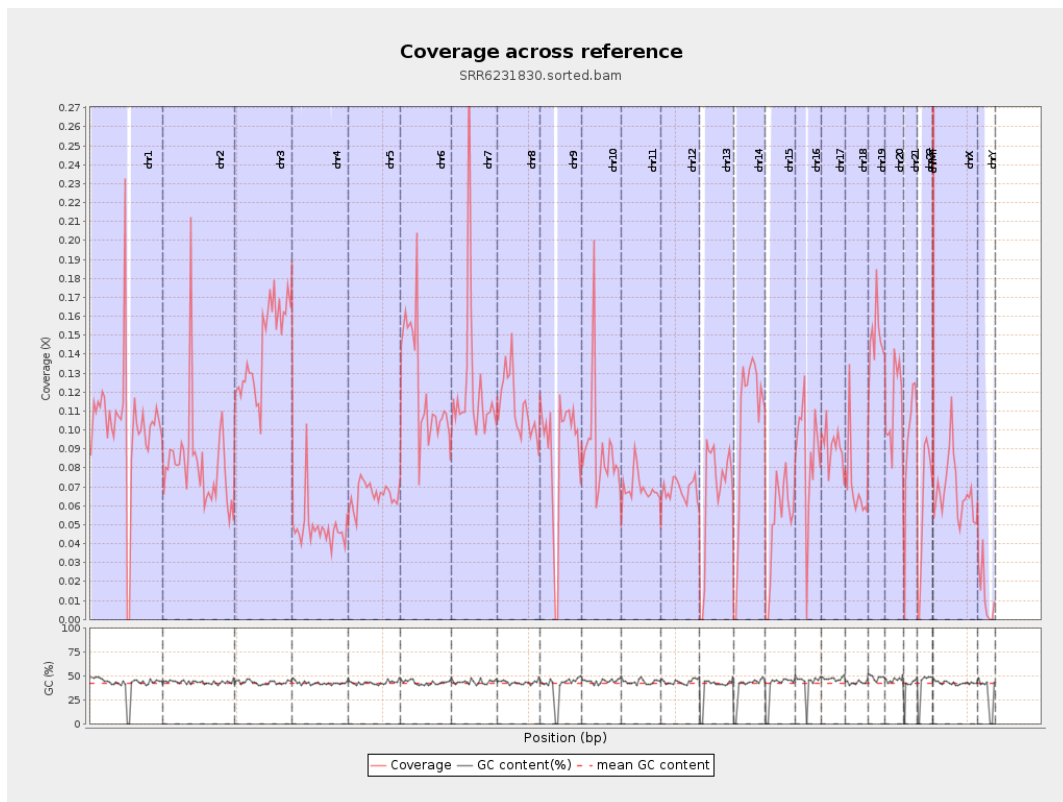
General error rate	0.69%
Mismatches	1,866,985
Insertions	19,967
Mapped reads with at least one insertion	0.45%
Deletions	64,867
Mapped reads with at least one deletion	1.47%
Homopolymer indels	43.71%

2.6. Chromosome stats

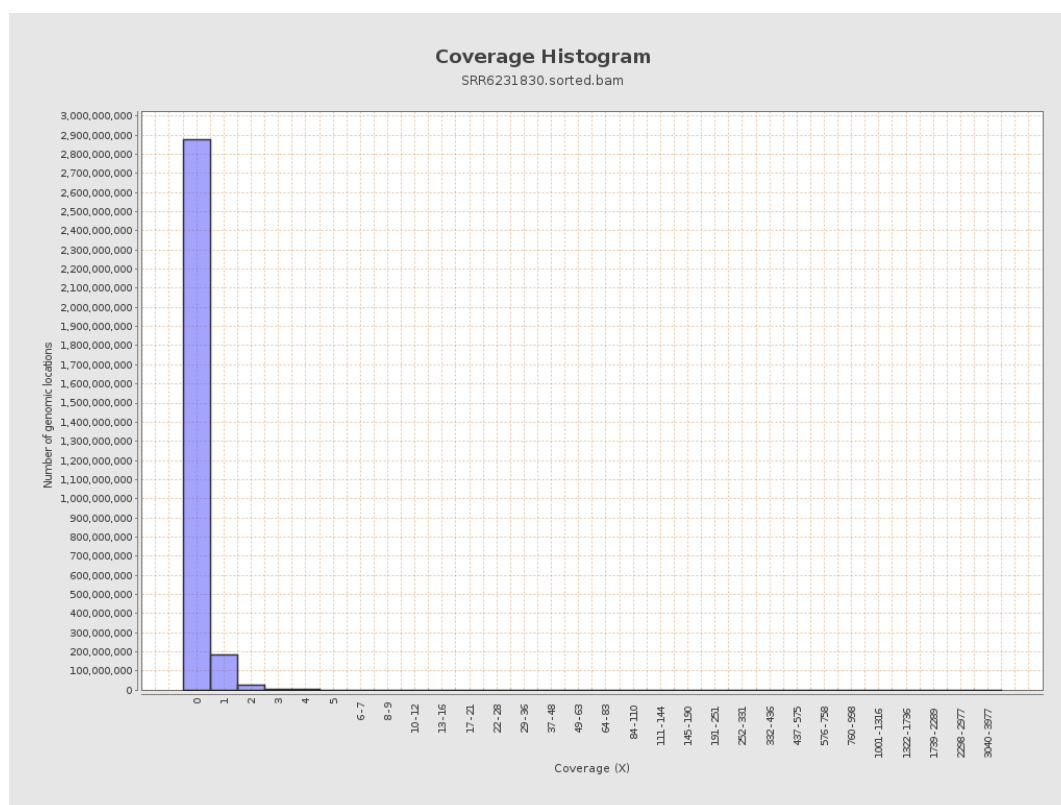
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	25401615	0.1019	2.9055
chr2	243199373	19951543	0.082	1.4113
chr3	198022430	28360785	0.1432	0.4733
chr4	191154276	9305537	0.0487	0.3506
chr5	180915260	11972940	0.0662	0.348
chr6	171115067	20857163	0.1219	0.9234
chr7	159138663	19593839	0.1231	2.4048

chr8	146364022	16363385	0.1118	0.8517
chr9	141213431	12607383	0.0893	0.832
chr10	135534747	12103464	0.0893	1.037
chr11	135006516	9365370	0.0694	0.7455
chr12	133851895	9188548	0.0686	0.3693
chr13	115169878	7783287	0.0676	0.3415
chr14	107349540	11183480	0.1042	0.4907
chr15	102531392	5152107	0.0502	0.3726
chr16	90354753	7757840	0.0859	0.5162
chr17	81195210	7458629	0.0919	0.4912
chr18	78077248	5526487	0.0708	1.9239
chr19	59128983	8831573	0.1494	1.6337
chr20	63025520	7094243	0.1126	0.4676
chr21	48129895	4605902	0.0957	0.436
chr22	51304566	3176955	0.0619	0.2991
chrMT	16571	160215	9.6684	5.881
chrX	155270560	10554303	0.068	0.5189
chrY	59373566	757896	0.0128	0.2754

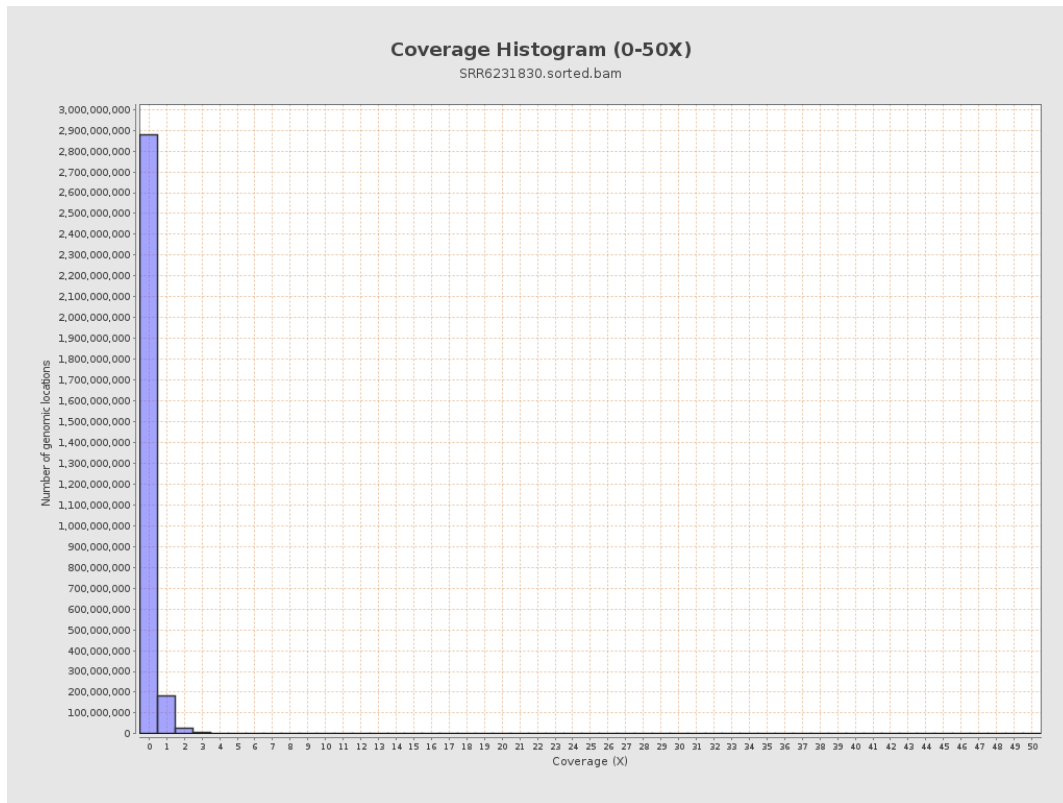
3. Results : Coverage across reference



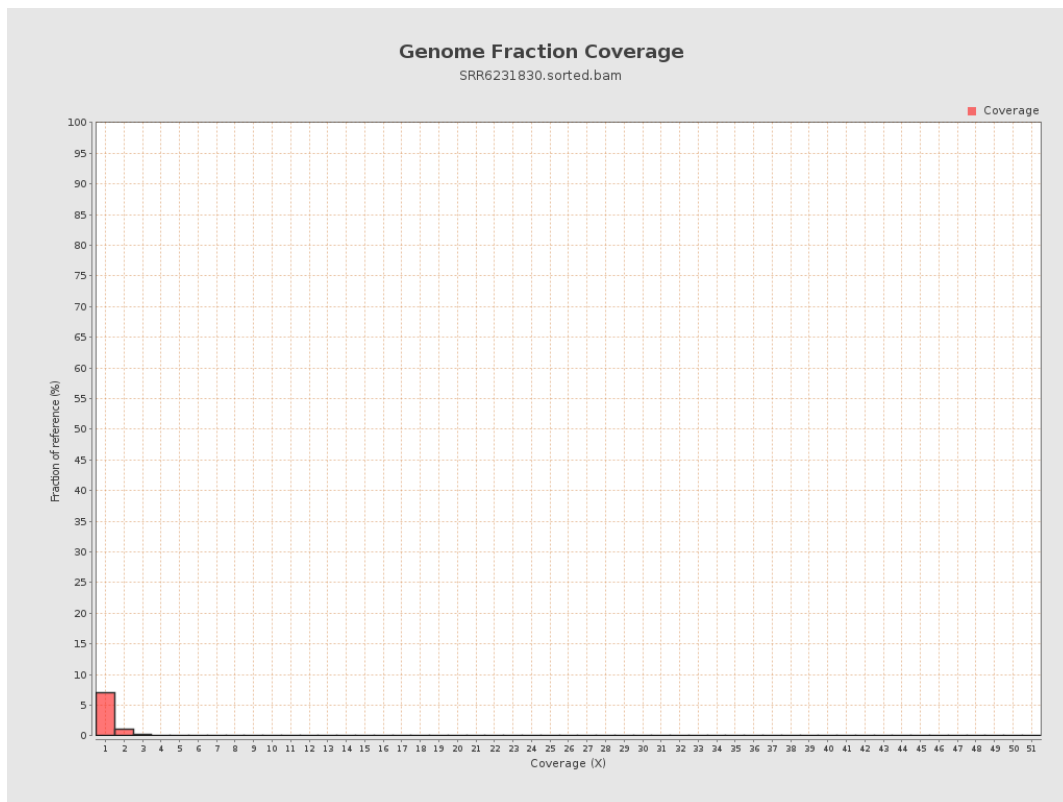
4. Results : Coverage Histogram



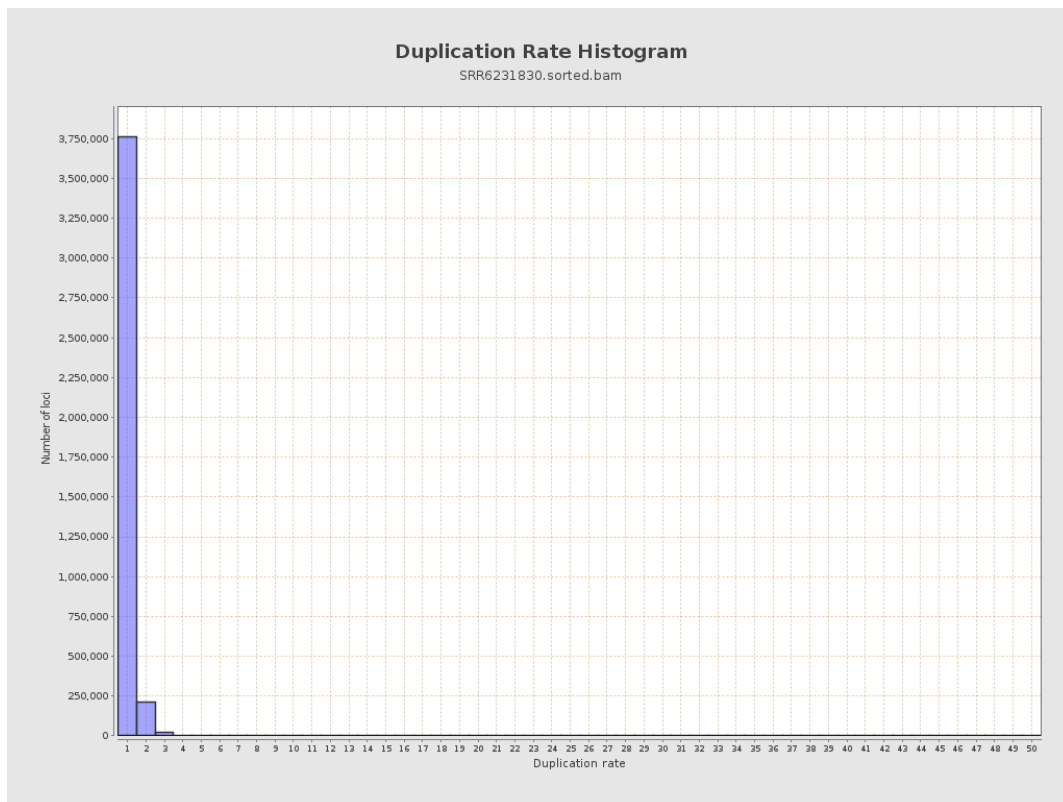
5. Results : Coverage Histogram (0-50X)



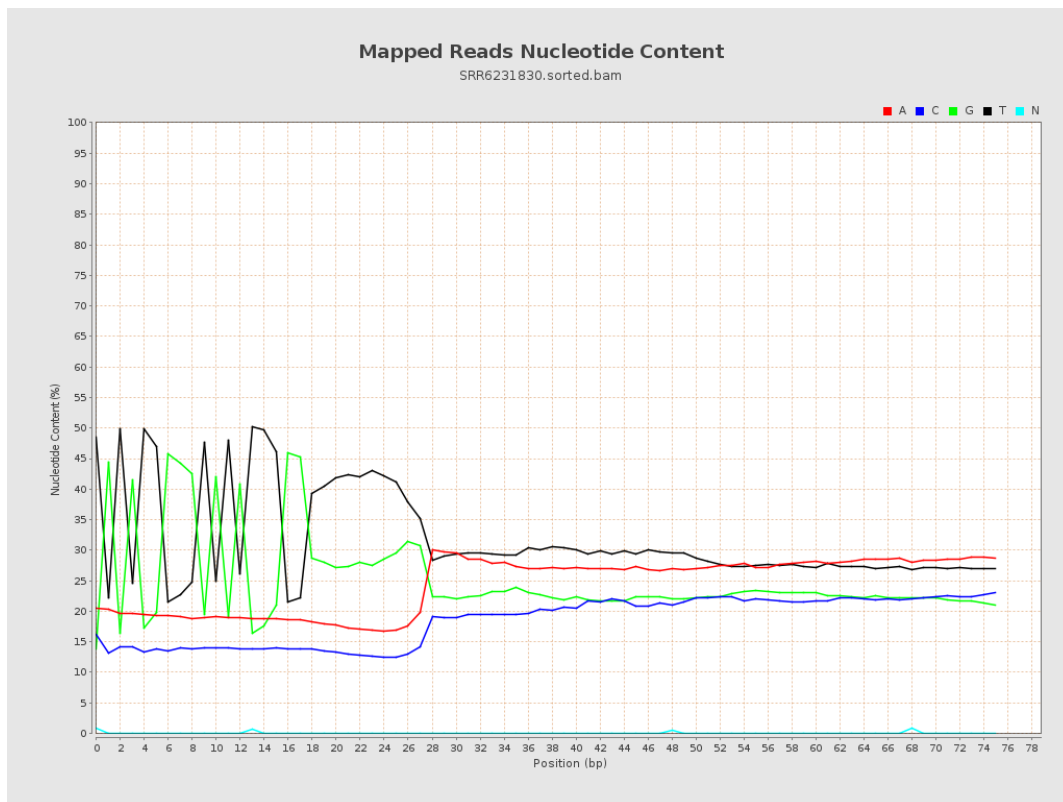
6. Results : Genome Fraction Coverage



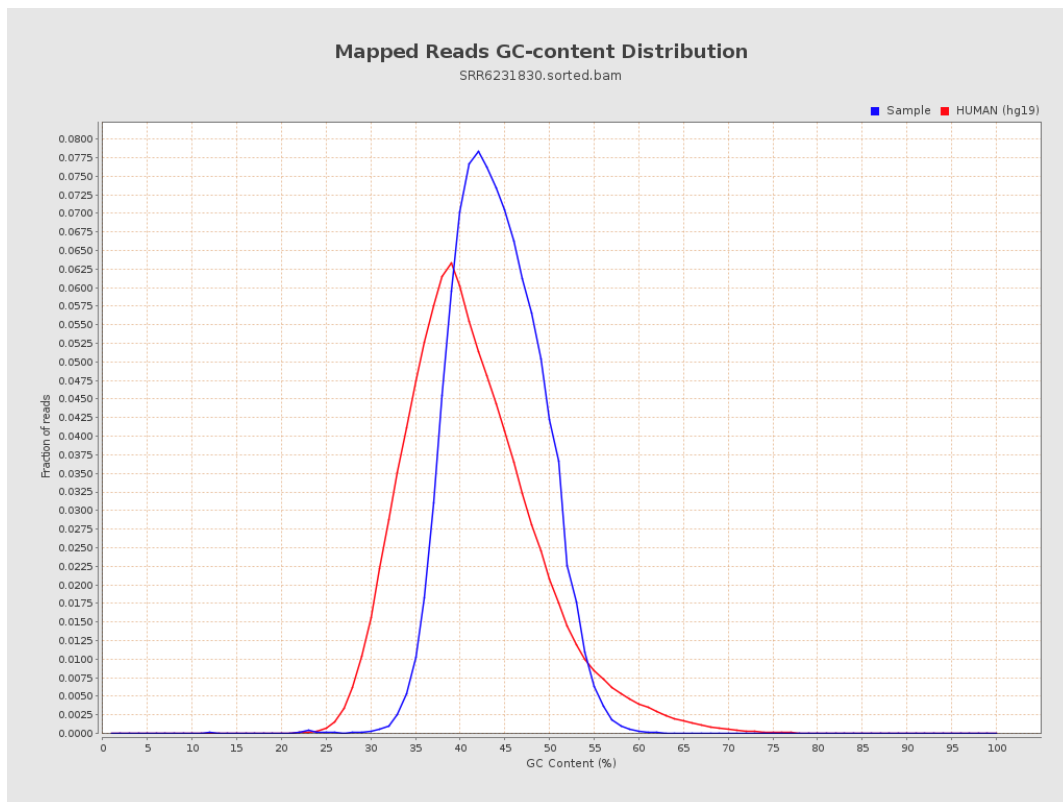
7. Results : Duplication Rate Histogram



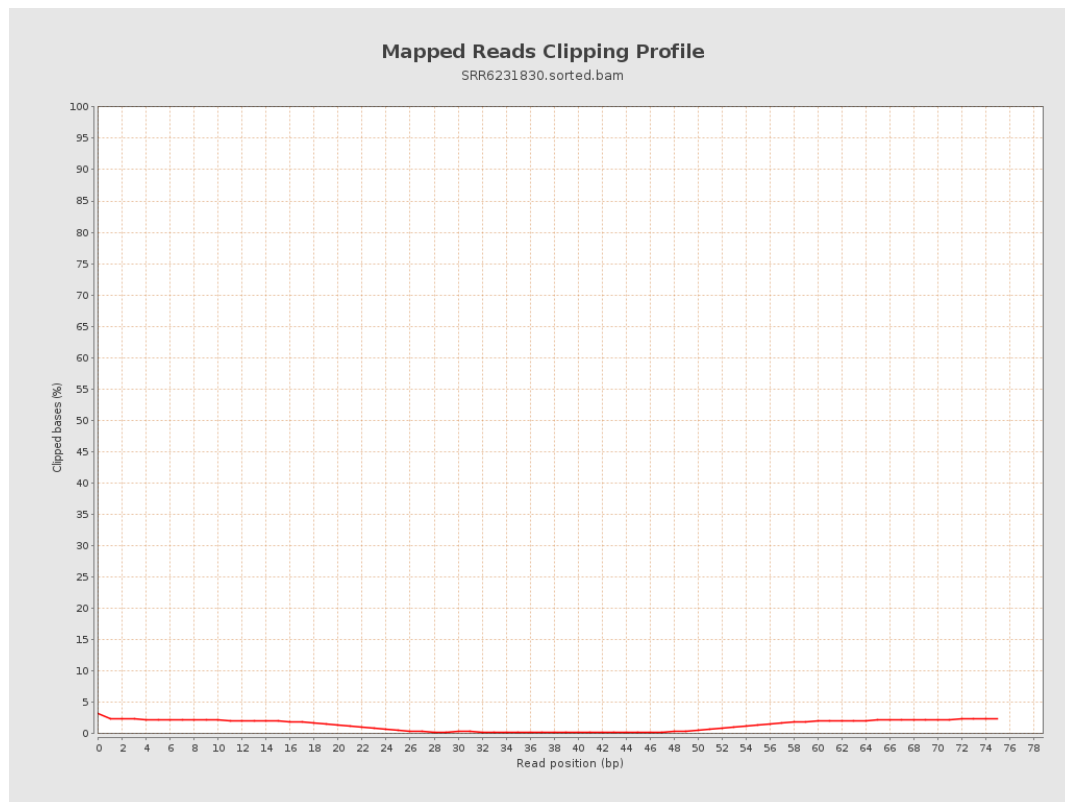
8. Results : Mapped Reads Nucleotide Content



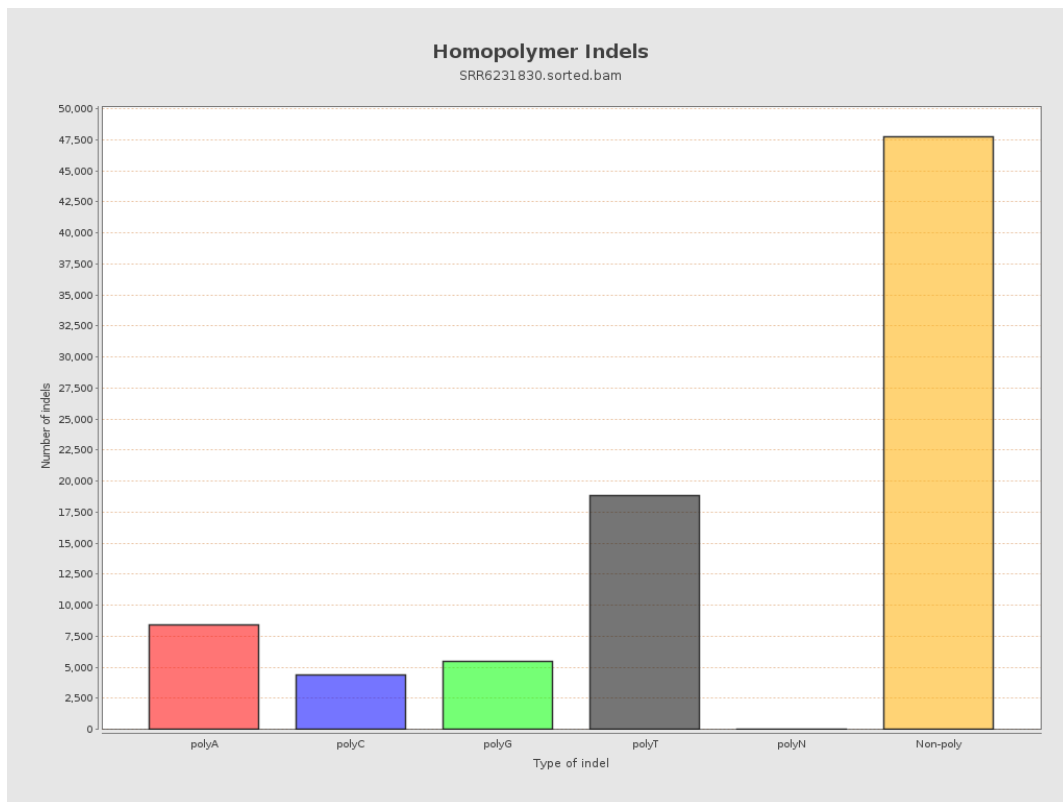
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

