

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 02:58:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237331.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_SRR6237331 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237331.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 02:58:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237331.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,715,881
Mapped reads	2,379,947 / 87.63%
Unmapped reads	335,934 / 12.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,683 / 1.02%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	755,832 / 27.83%
Duplication rate	20.81%
Clipped reads	1,502,871 / 55.34%

2.2. ACGT Content

Number/percentage of A's	38,757,030 / 26.32%
Number/percentage of C's	24,892,196 / 16.91%
Number/percentage of T's	49,936,718 / 33.92%
Number/percentage of G's	33,630,463 / 22.84%
Number/percentage of N's	15,993 / 0.01%
GC Percentage	39.75%

2.3. Coverage

Mean	0.0476

Standard Deviation	0.7177
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2.4. Mapping Quality

Mean Mapping Quality	42.45
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2.5. Mismatches and indels

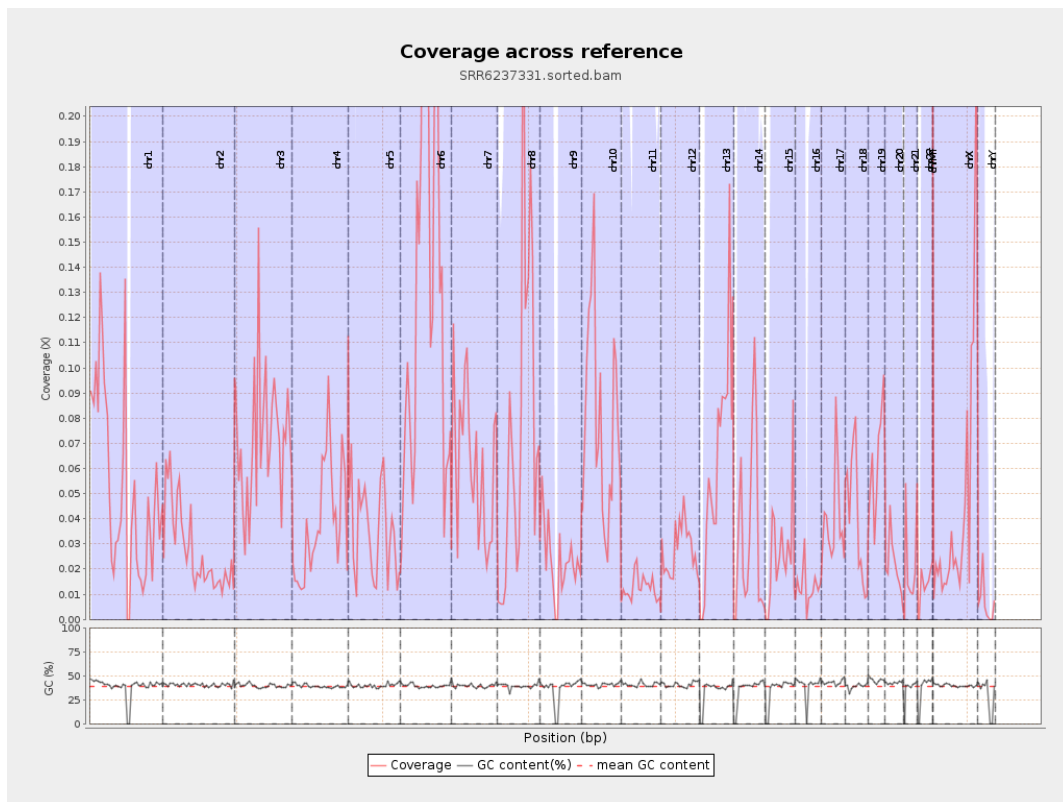
General error rate	0.65%
Mismatches	942,337
Insertions	9,810
Mapped reads with at least one insertion	0.41%
Deletions	54,646
Mapped reads with at least one deletion	2.26%
Homopolymer indels	42.16%

2.6. Chromosome stats

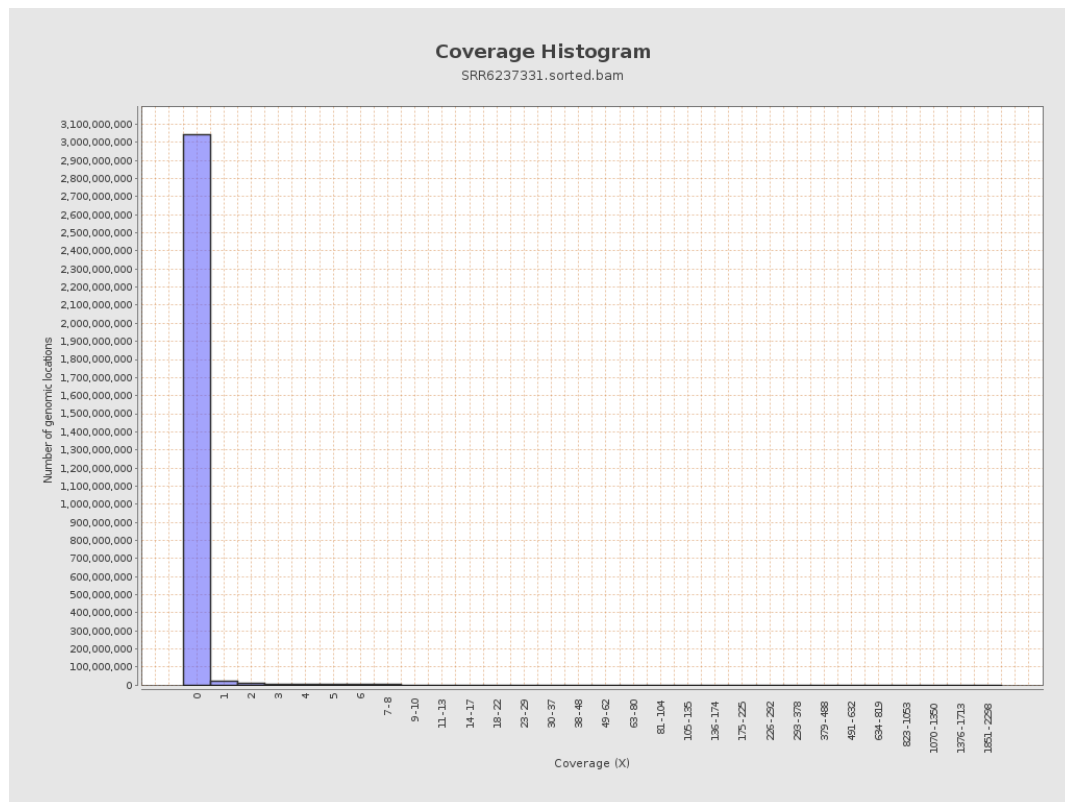
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12739834	0.0511	0.9365
chr2	243199373	6636779	0.0273	0.7337
chr3	198022430	14176448	0.0716	0.5882
chr4	191154276	7276351	0.0381	0.4389
chr5	180915260	6427493	0.0355	0.4206
chr6	171115067	24089031	0.1408	0.9485
chr7	159138663	9740757	0.0612	0.6243

chr8	146364022	11174425	0.0763	1.5935
chr9	141213431	3331193	0.0236	0.3589
chr10	135534747	10736794	0.0792	0.9697
chr11	135006516	1710771	0.0127	0.2819
chr12	133851895	3728155	0.0279	0.408
chr13	115169878	7257348	0.063	0.594
chr14	107349540	3656169	0.0341	0.4014
chr15	102531392	2777045	0.0271	0.3783
chr16	90354753	1136689	0.0126	0.254
chr17	81195210	3301022	0.0407	0.4734
chr18	78077248	3192015	0.0409	1.3936
chr19	59128983	3690079	0.0624	0.7524
chr20	63025520	1371404	0.0218	0.3335
chr21	48129895	1094827	0.0227	0.3474
chr22	51304566	668791	0.013	0.2371
chrMT	16571	3754	0.2265	0.704
chrX	155270560	6993417	0.045	0.4962
chrY	59373566	416314	0.007	0.2265

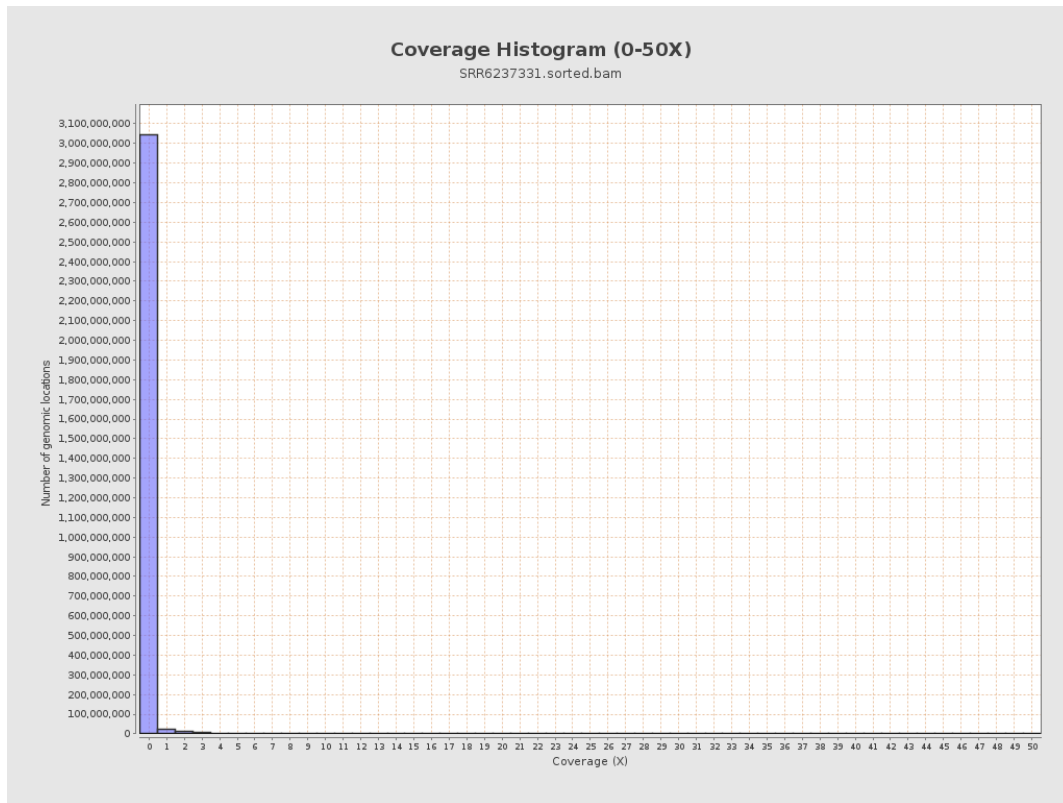
3. Results : Coverage across reference



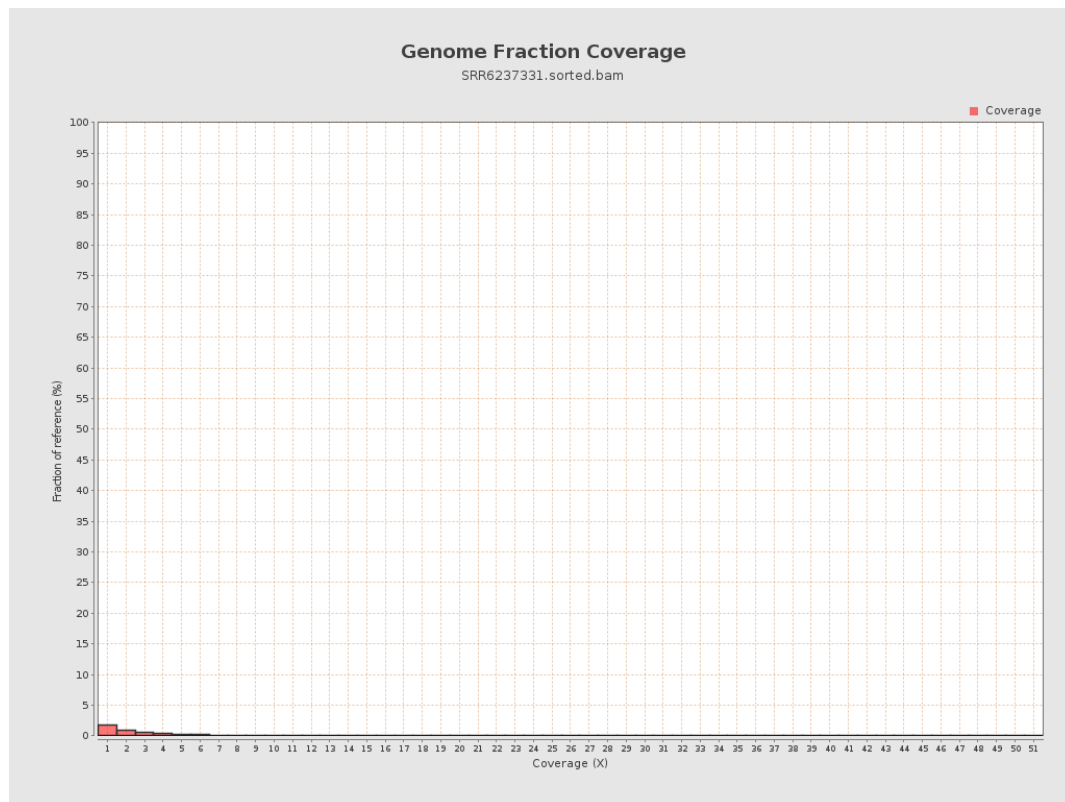
4. Results : Coverage Histogram



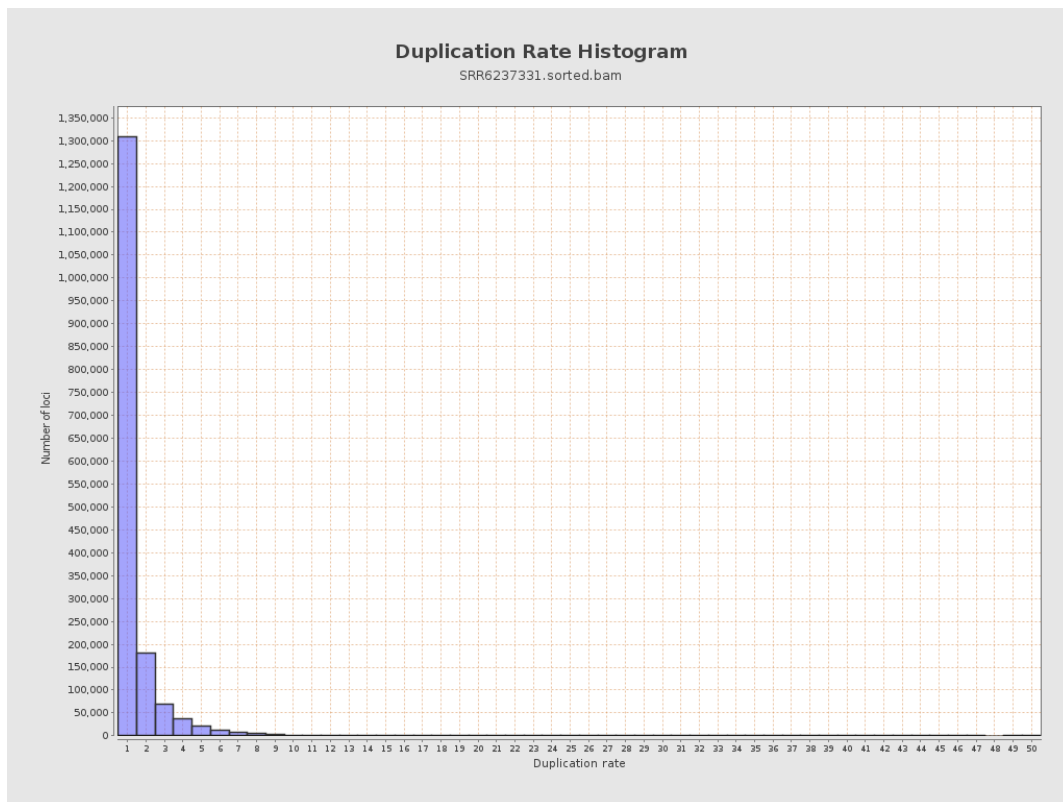
5. Results : Coverage Histogram (0-50X)



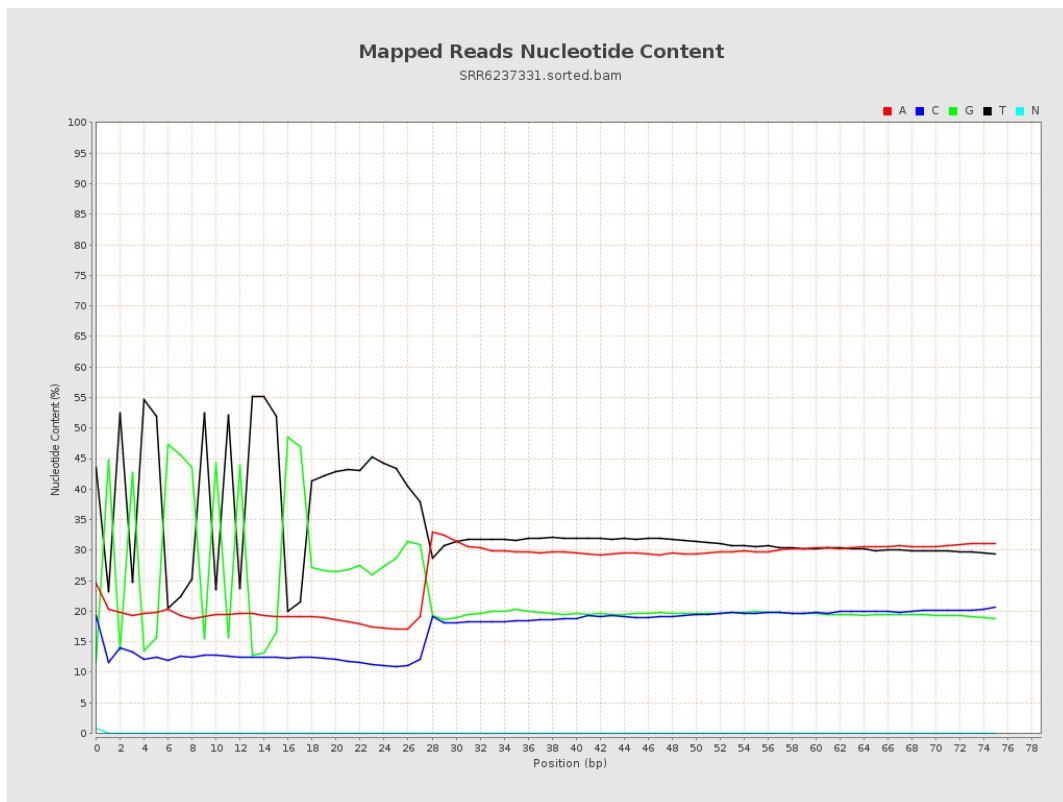
6. Results : Genome Fraction Coverage



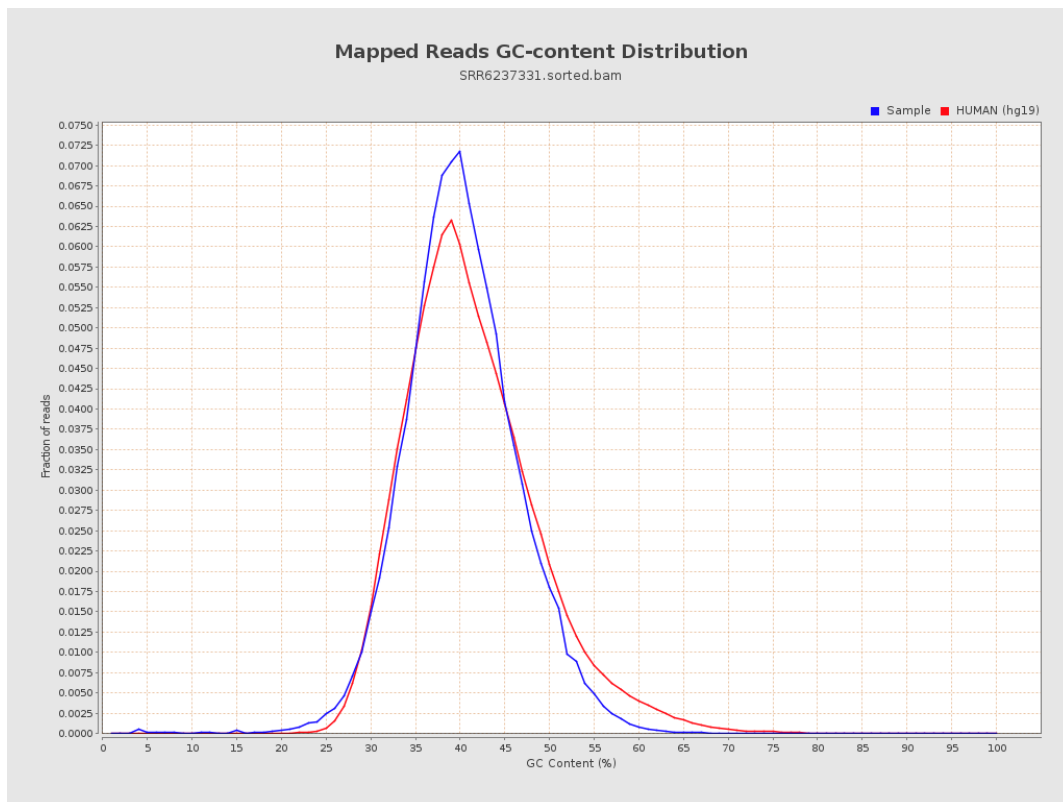
7. Results : Duplication Rate Histogram



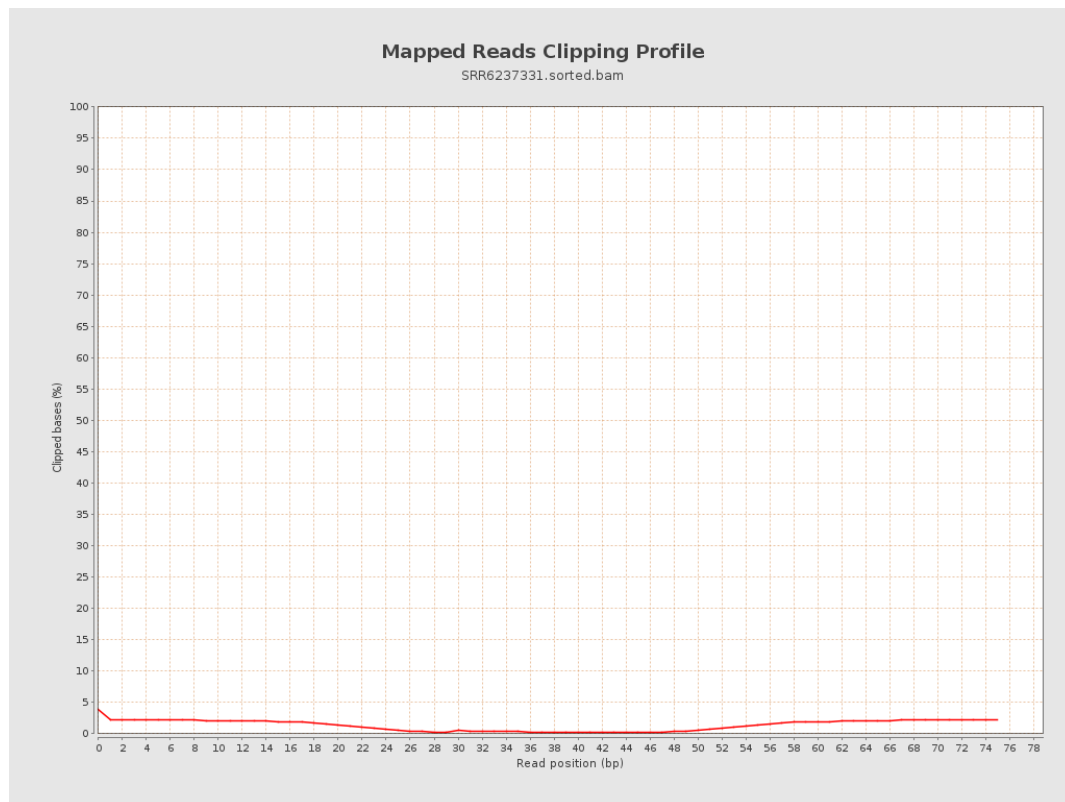
8. Results : Mapped Reads Nucleotide Content



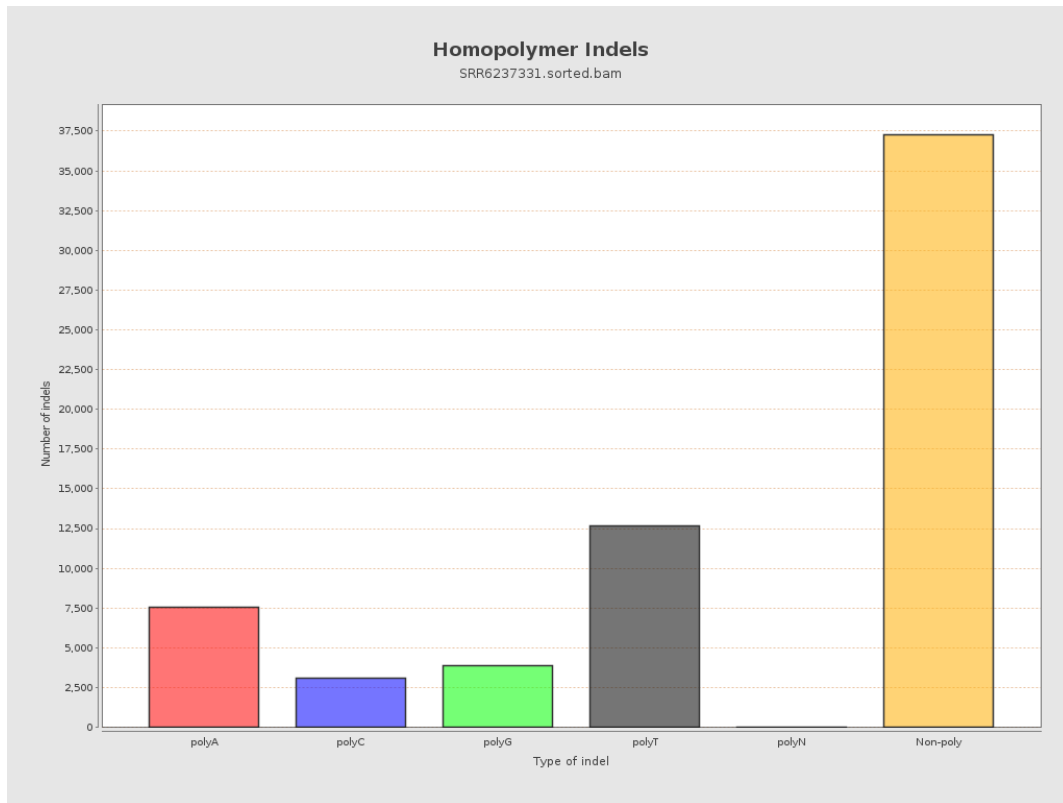
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

