

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 08:31:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173931.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_SRR10173931 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173931_1.fastq.gz SRR10173931_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 08:31:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173931.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,079,468
Mapped reads	13,756,488 / 97.71%
Unmapped reads	322,980 / 2.29%
Mapped paired reads	13,756,488 / 97.71%
Mapped reads, first in pair	6,882,417 / 48.88%
Mapped reads, second in pair	6,874,071 / 48.82%
Mapped reads, both in pair	13,552,964 / 96.26%
Mapped reads, singletons	203,524 / 1.45%
Secondary alignments	0
Supplementary alignments	1,870,108 / 13.28%
Read min/max/mean length	30 / 133 / 126.02
Duplicated reads (estimated)	11,036,102 / 78.38%
Duplication rate	65.07%
Clipped reads	7,430,126 / 52.77%

2.2. ACGT Content

Number/percentage of A's	463,227,545 / 29.77%
Number/percentage of C's	310,005,978 / 19.92%
Number/percentage of T's	460,128,184 / 29.57%
Number/percentage of G's	322,576,316 / 20.73%
Number/percentage of N's	12,256 / 0%

GC Percentage	40.66%
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2.3. Coverage

Mean	0.503
Standard Deviation	8.9023

2.4. Mapping Quality

Mean Mapping Quality	52.43
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2.5. Insert size

Mean	1,122,111.58
Standard Deviation	9,741,989.41
P25/Median/P75	107 / 159 / 248

2.6. Mismatches and indels

General error rate	0.91%
Mismatches	13,585,325
Insertions	179,392
Mapped reads with at least one insertion	1.25%
Deletions	469,548
Mapped reads with at least one deletion	3.32%
Homopolymer indels	40.94%

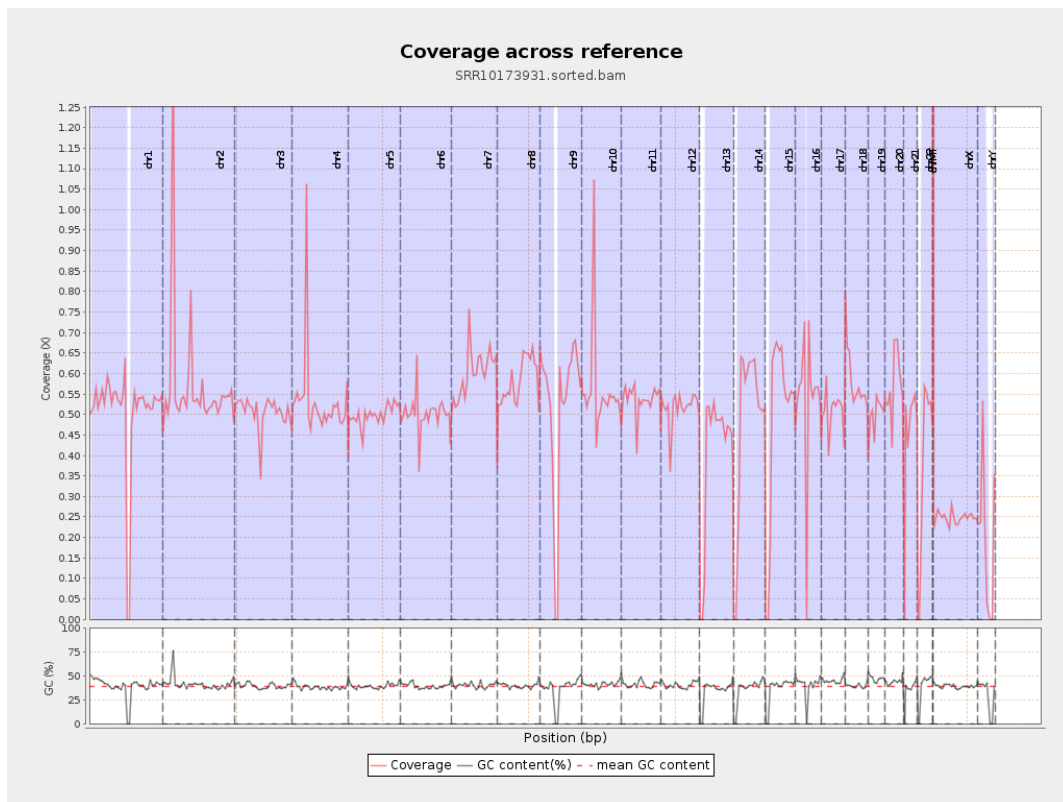
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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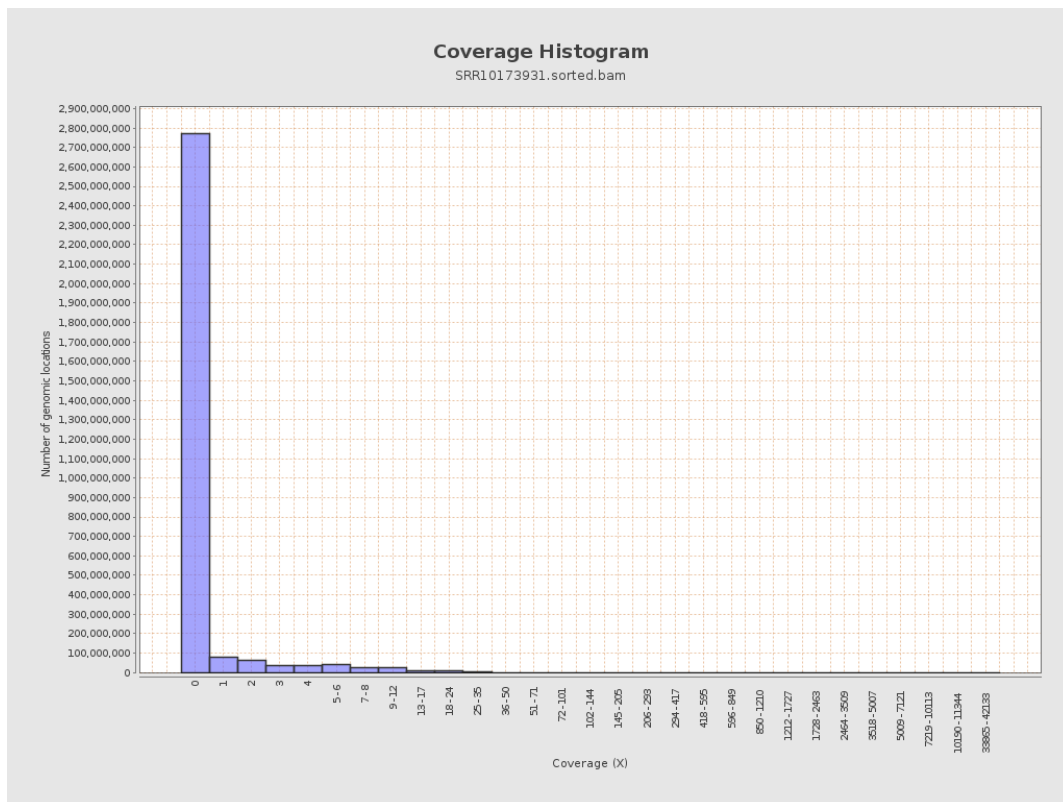
		bases	coverage	deviation
chr1	249250621	125893691	0.5051	4.2123
chr2	243199373	138159259	0.5681	29.4061
chr3	198022430	100021943	0.5051	2.1381
chr4	191154276	102126266	0.5343	4.3109
chr5	180915260	90264849	0.4989	2.115
chr6	171115067	85966127	0.5024	2.8239
chr7	159138663	95758952	0.6017	4.5129
chr8	146364022	85326670	0.583	5.3142
chr9	141213431	73244340	0.5187	3.9607
chr10	135534747	75376893	0.5561	5.4244
chr11	135006516	72358226	0.536	2.4065
chr12	133851895	69304614	0.5178	2.3454
chr13	115169878	46647058	0.405	1.9241
chr14	107349540	52749586	0.4914	2.1843
chr15	102531392	49780872	0.4855	2.2119
chr16	90354753	48087357	0.5322	3.4518
chr17	81195210	41462225	0.5106	2.595
chr18	78077248	45319125	0.5804	5.7319
chr19	59128983	29699250	0.5023	3.297
chr20	63025520	35984967	0.571	2.6913
chr21	48129895	22030697	0.4577	3.3272
chr22	51304566	19413436	0.3784	2.4888
chrMT	16571	1558905	94.0743	68.2158
chrX	155270560	38554634	0.2483	1.5426

chrY	59373566	11974479	0.2017	3.419
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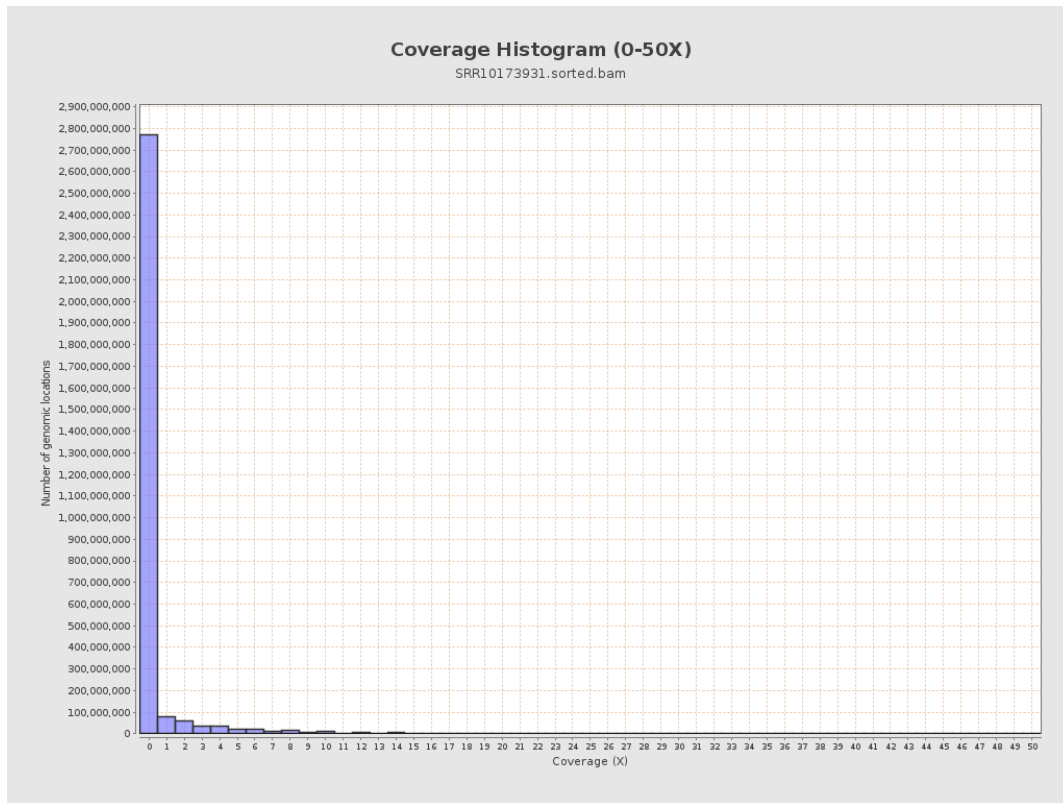
3. Results : Coverage across reference



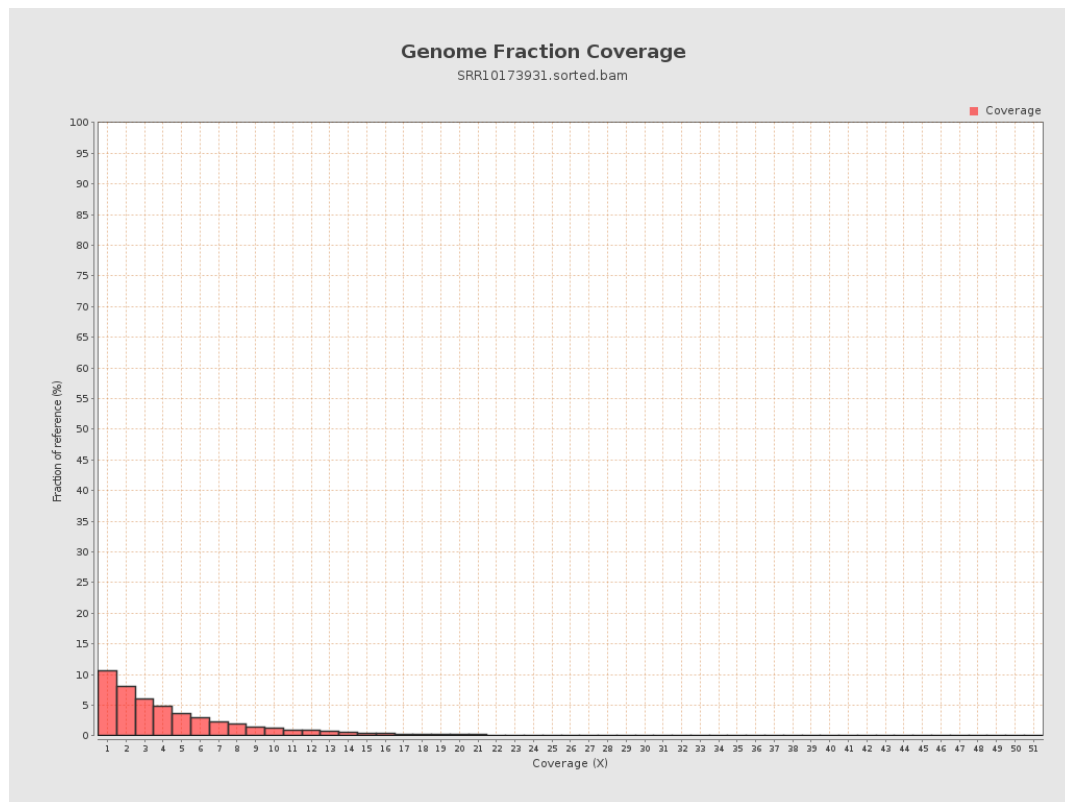
4. Results : Coverage Histogram



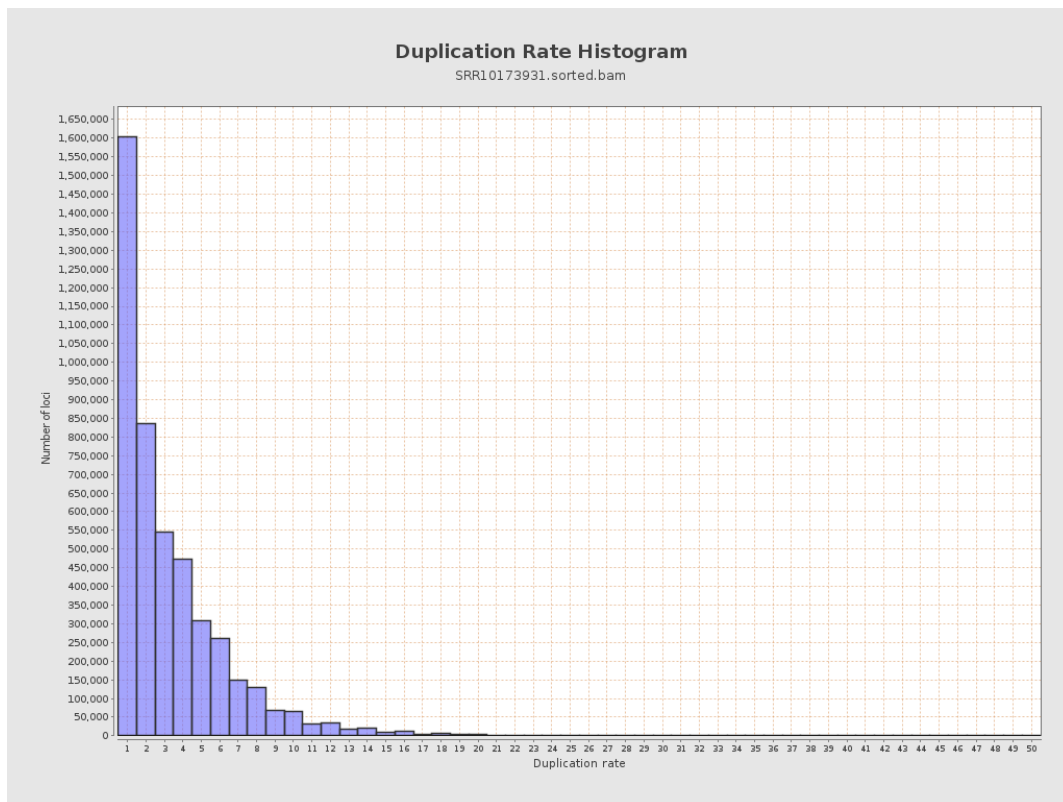
5. Results : Coverage Histogram (0-50X)



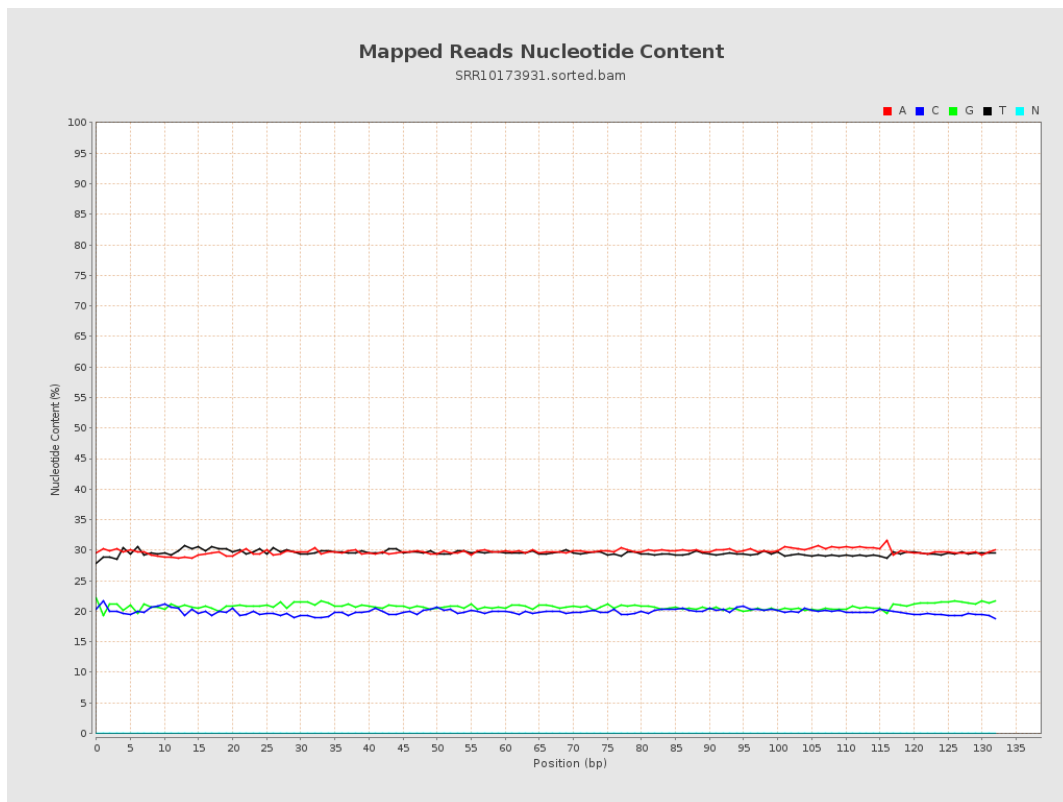
6. Results : Genome Fraction Coverage



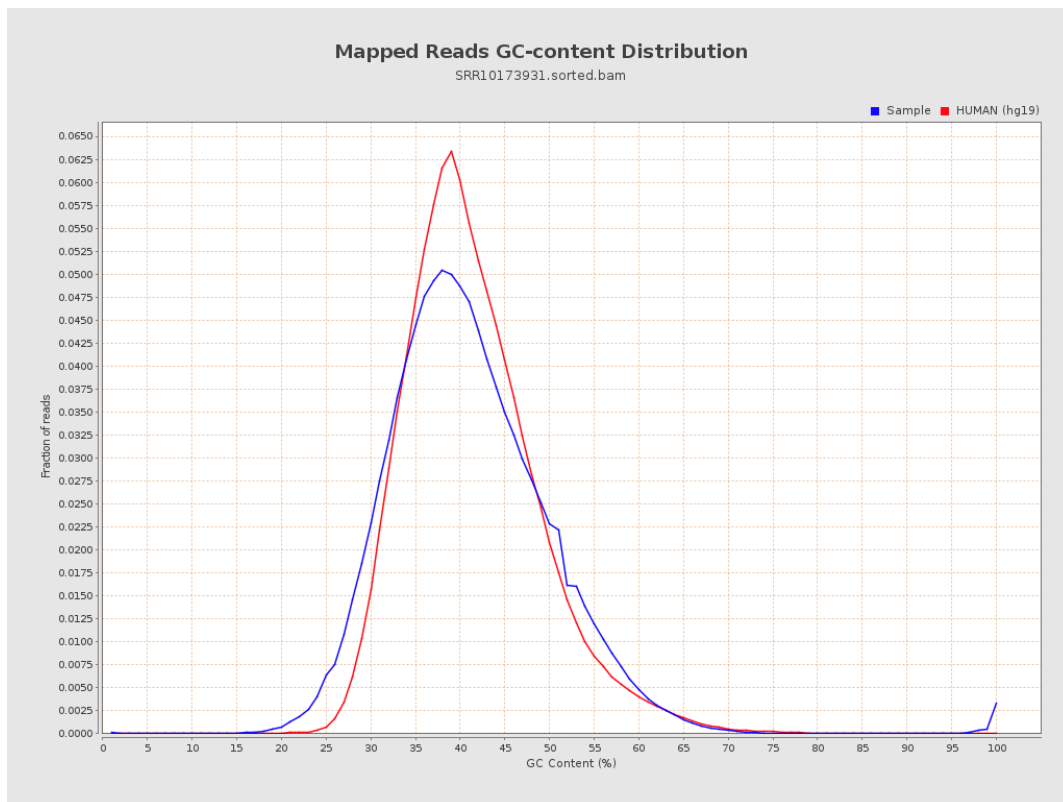
7. Results : Duplication Rate Histogram



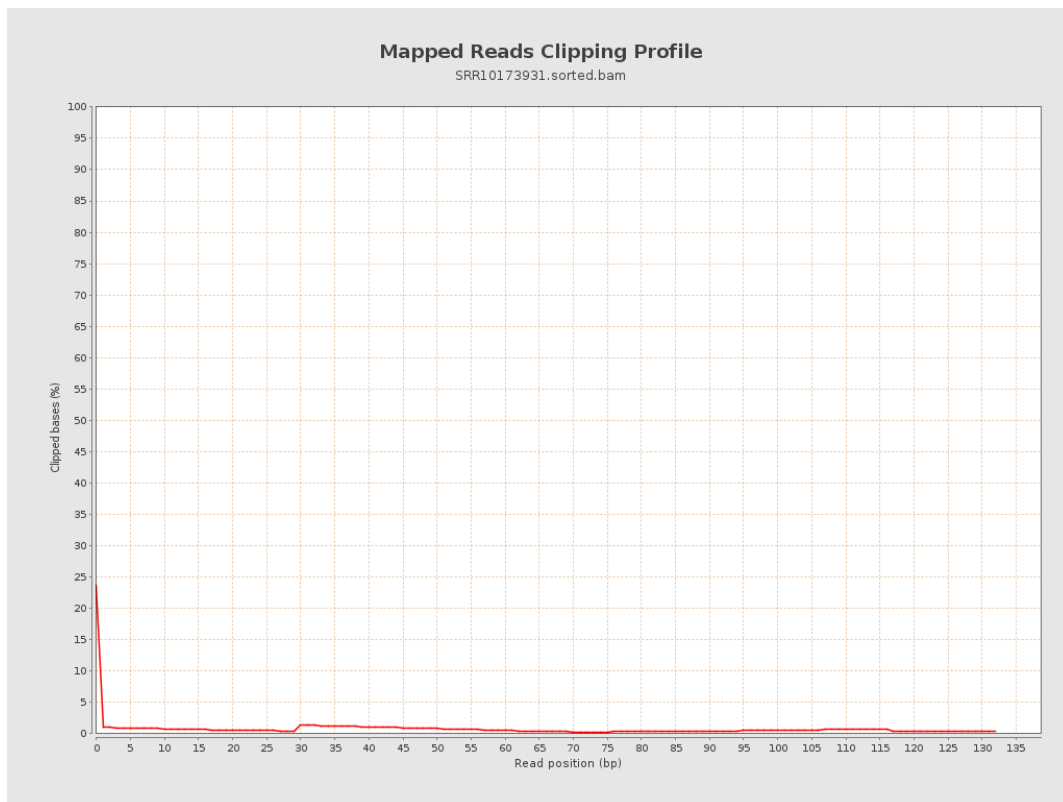
8. Results : Mapped Reads Nucleotide Content



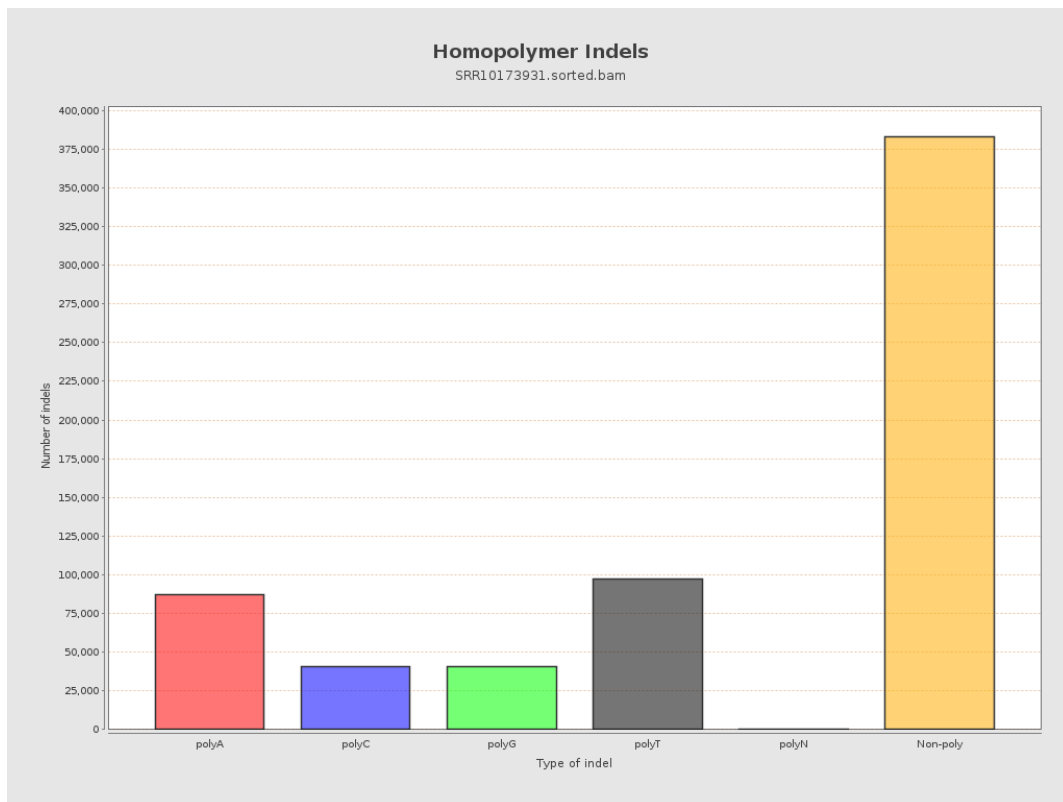
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



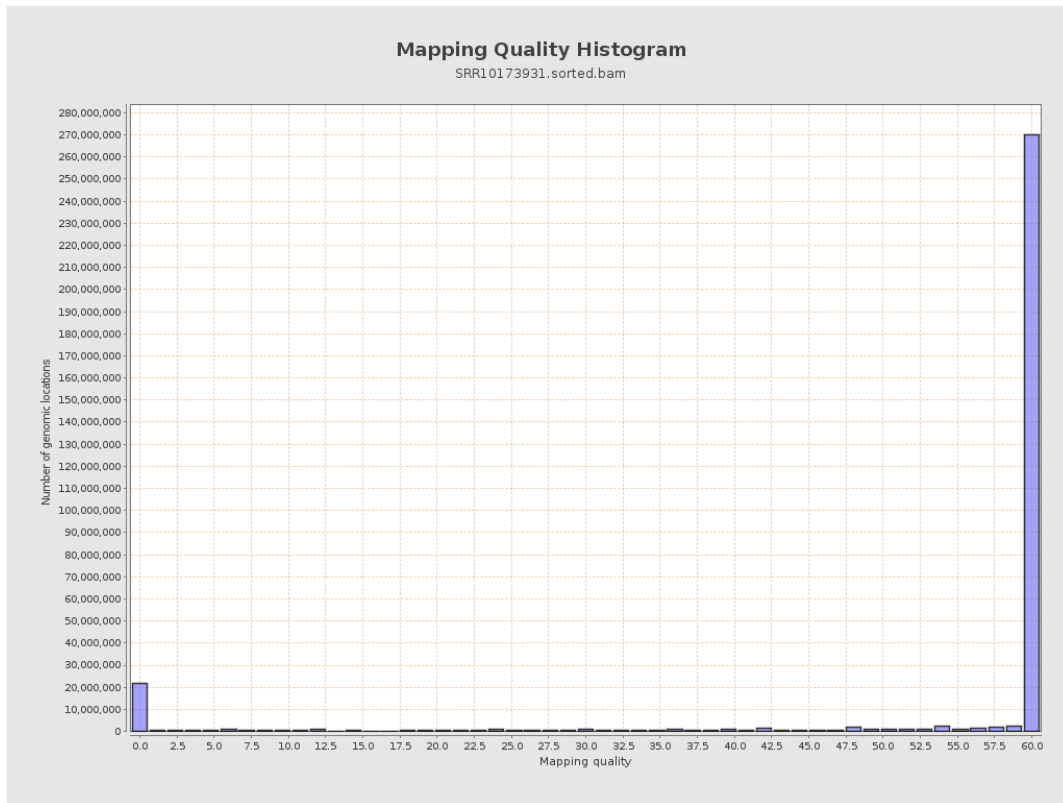
11. Results : Homopolymer Indels



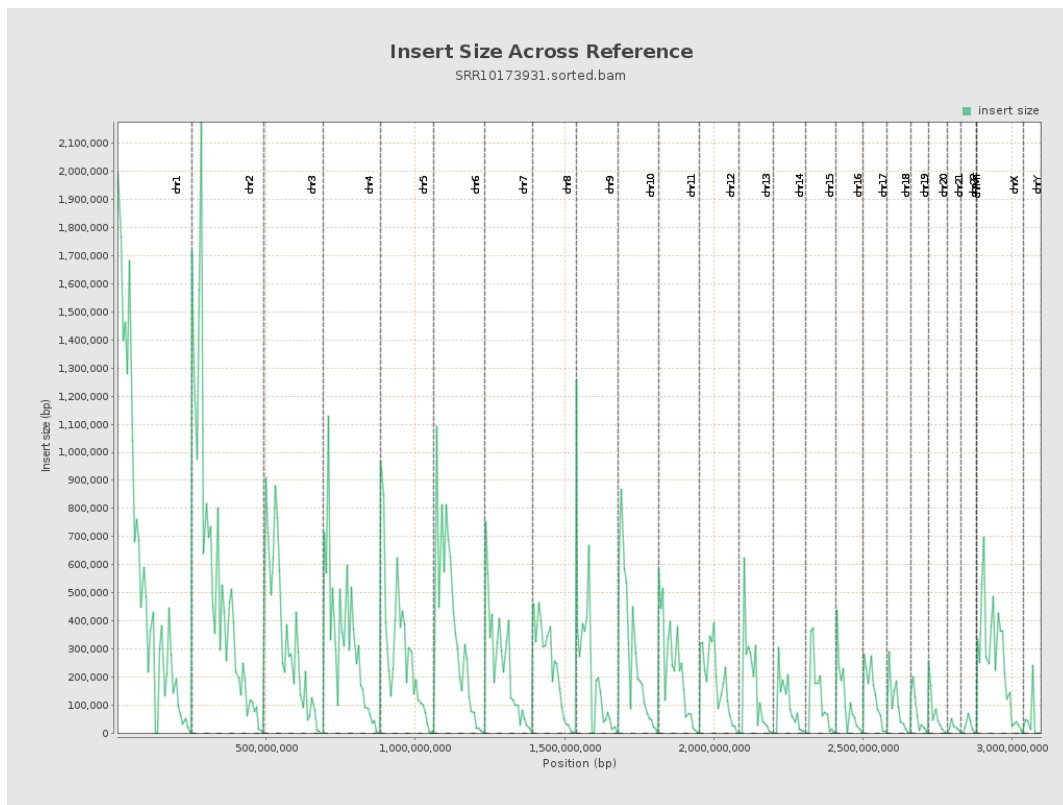
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

