

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 23:04:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173856.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_SRR10173856 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173856_1.fastq.gz SRR10173856_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 23:04:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173856.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,165,128
Mapped reads	3,076,978 / 97.21%
Unmapped reads	88,150 / 2.79%
Mapped paired reads	3,076,978 / 97.21%
Mapped reads, first in pair	1,543,174 / 48.76%
Mapped reads, second in pair	1,533,804 / 48.46%
Mapped reads, both in pair	3,019,630 / 95.4%
Mapped reads, singletons	57,348 / 1.81%
Secondary alignments	0
Supplementary alignments	320,099 / 10.11%
Read min/max/mean length	30 / 133 / 127.8
Duplicated reads (estimated)	2,275,923 / 71.91%
Duplication rate	62.51%
Clipped reads	1,320,206 / 41.71%

2.2. ACGT Content

Number/percentage of A's	108,598,067 / 30.14%
Number/percentage of C's	70,308,054 / 19.51%
Number/percentage of T's	108,491,075 / 30.11%
Number/percentage of G's	72,930,441 / 20.24%
Number/percentage of N's	4,163 / 0%

GC Percentage	39.75%
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2.3. Coverage

Mean	0.1165
Standard Deviation	1.826

2.4. Mapping Quality

Mean Mapping Quality	52.95
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2.5. Insert size

Mean	945,651.54
Standard Deviation	8,980,134.06
P25/Median/P75	136 / 190 / 271

2.6. Mismatches and indels

General error rate	1.09%
Mismatches	3,792,570
Insertions	42,309
Mapped reads with at least one insertion	1.32%
Deletions	108,484
Mapped reads with at least one deletion	3.43%
Homopolymer indels	41.48%

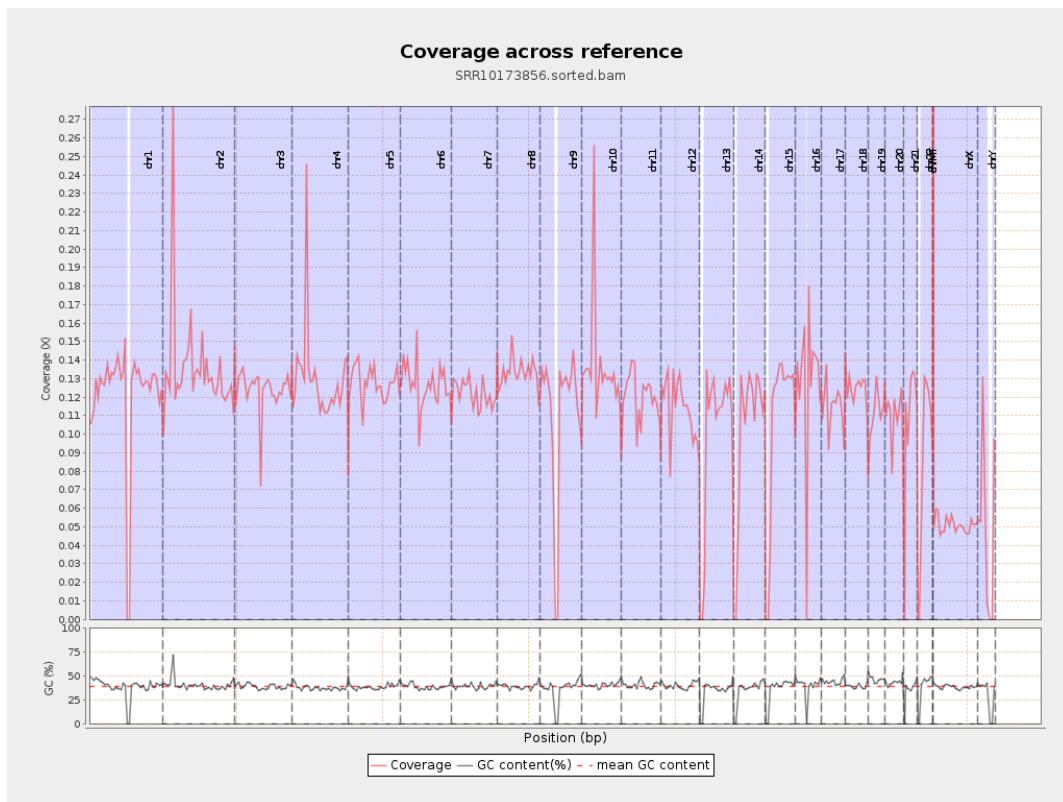
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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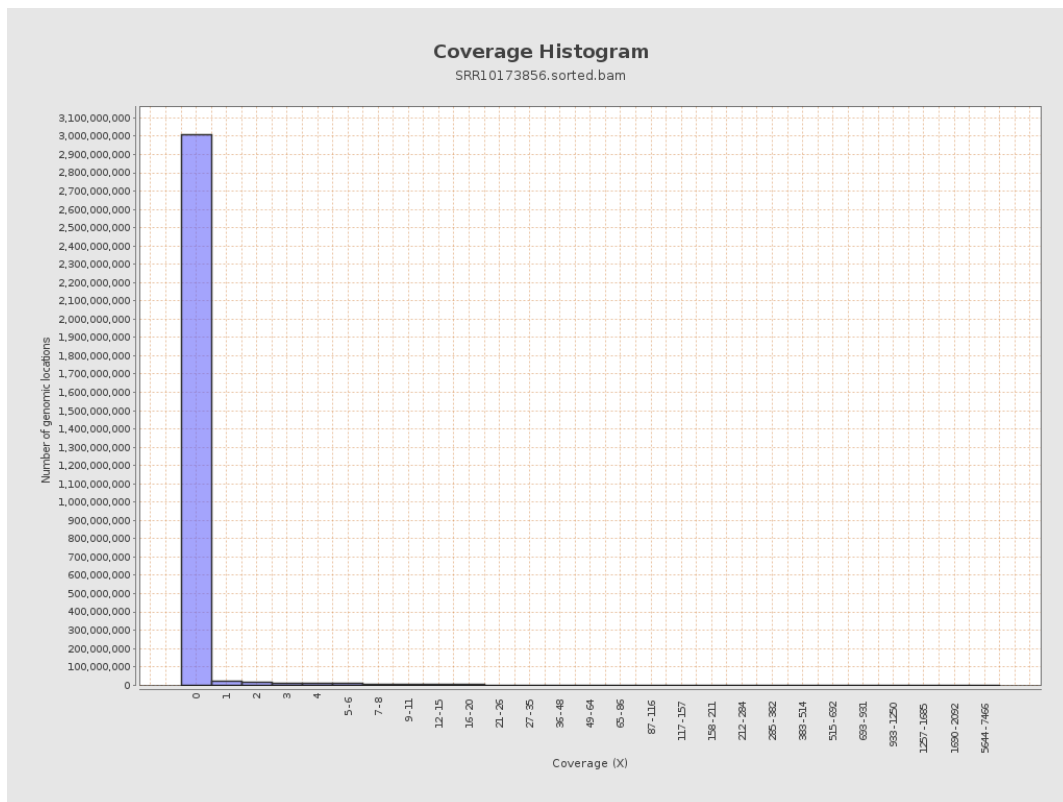
		bases	coverage	deviation
chr1	249250621	30248340	0.1214	1.2223
chr2	243199373	32858165	0.1351	5.257
chr3	198022430	24614933	0.1243	0.9678
chr4	191154276	24869449	0.1301	1.3015
chr5	180915260	23041231	0.1274	0.973
chr6	171115067	21751004	0.1271	1.0378
chr7	159138663	19386495	0.1218	1.1838
chr8	146364022	19519160	0.1334	1.6291
chr9	141213431	15751377	0.1115	1.1443
chr10	135534747	18452495	0.1361	1.5415
chr11	135006516	16182186	0.1199	0.9592
chr12	133851895	15353126	0.1147	0.9236
chr13	115169878	11526429	0.1001	0.8731
chr14	107349540	10954024	0.102	0.879
chr15	102531392	10724544	0.1046	0.8622
chr16	90354753	11380771	0.126	1.1506
chr17	81195210	9368311	0.1154	0.9858
chr18	78077248	9791790	0.1254	1.572
chr19	59128983	6631518	0.1122	1.0274
chr20	63025520	6937855	0.1101	0.9447
chr21	48129895	5267281	0.1094	1.0956
chr22	51304566	4414248	0.086	0.8419
chrMT	16571	577958	34.8777	31.5981
chrX	155270560	7920546	0.051	0.6143

chrY	59373566	3066335	0.0516	0.9964
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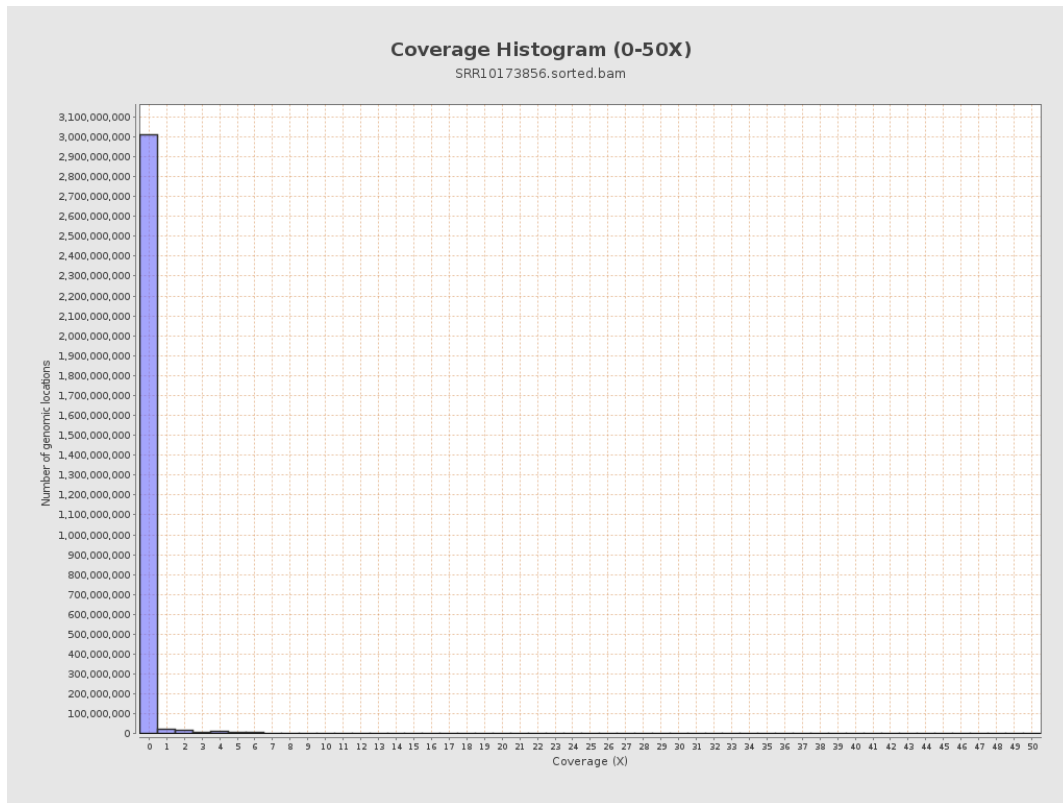
3. Results : Coverage across reference



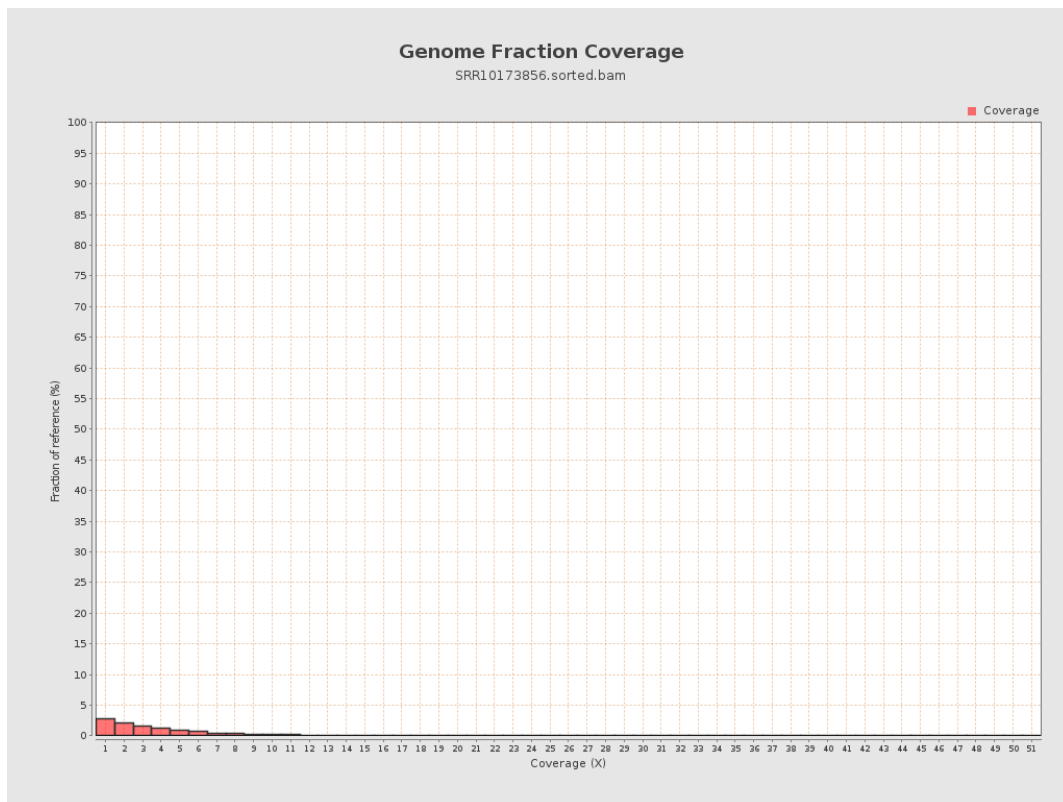
4. Results : Coverage Histogram



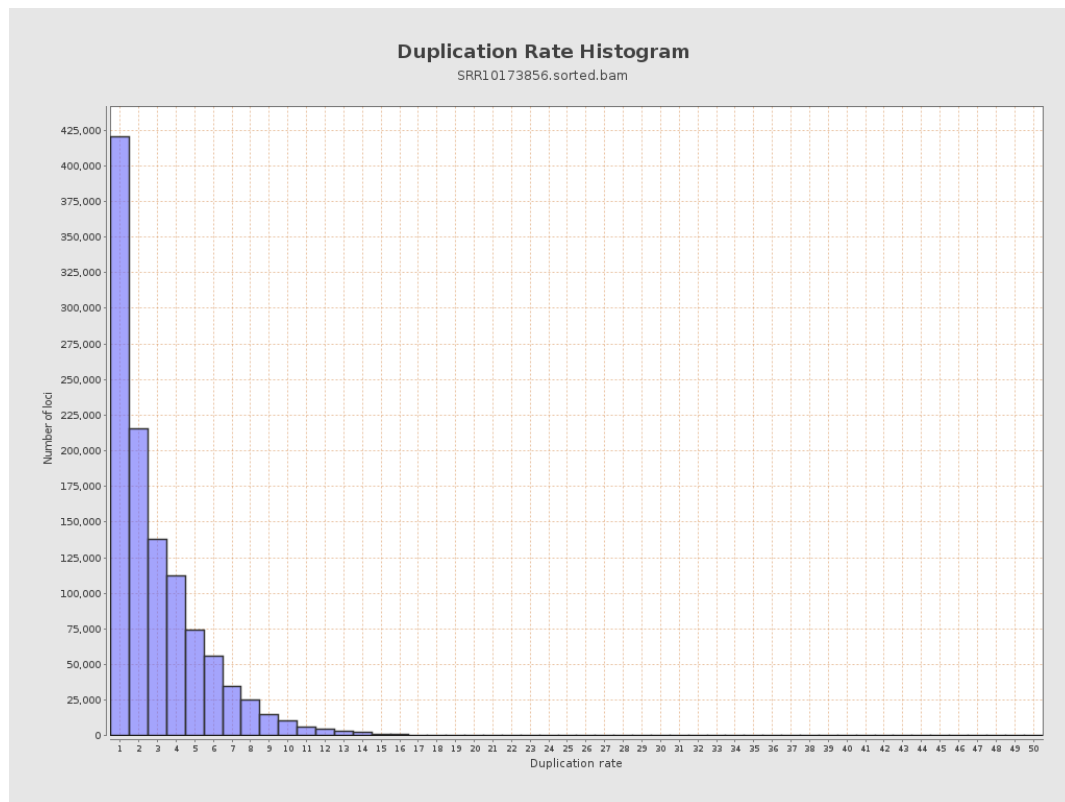
5. Results : Coverage Histogram (0-50X)



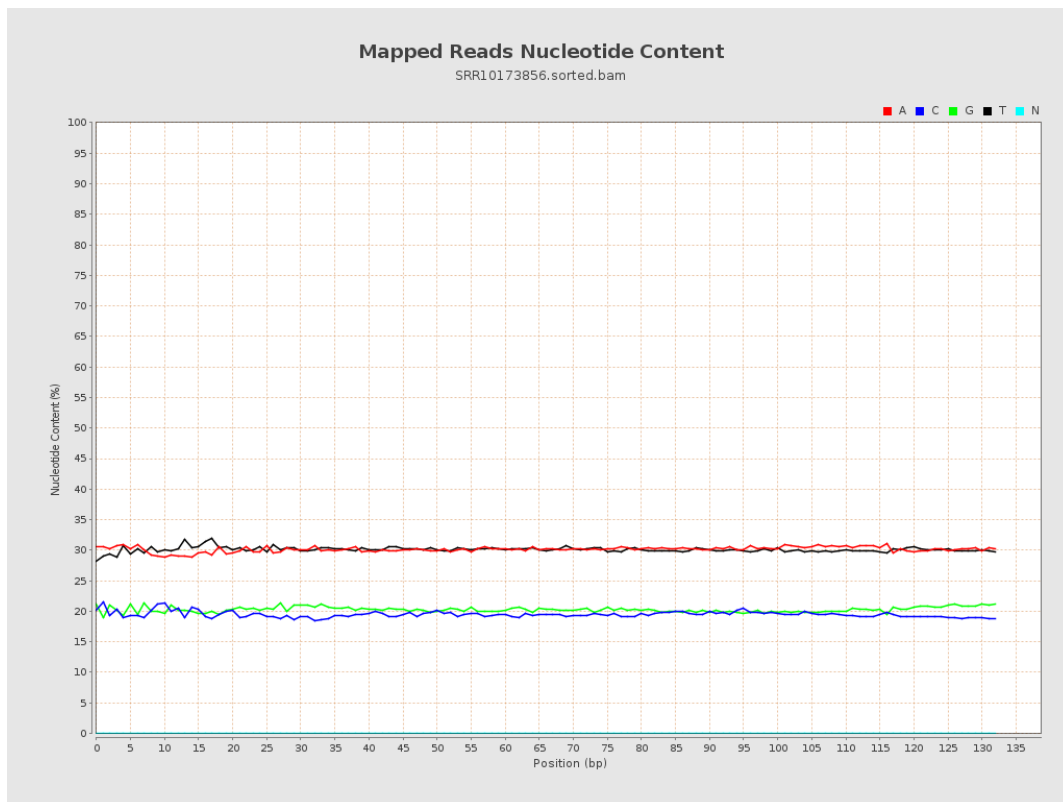
6. Results : Genome Fraction Coverage



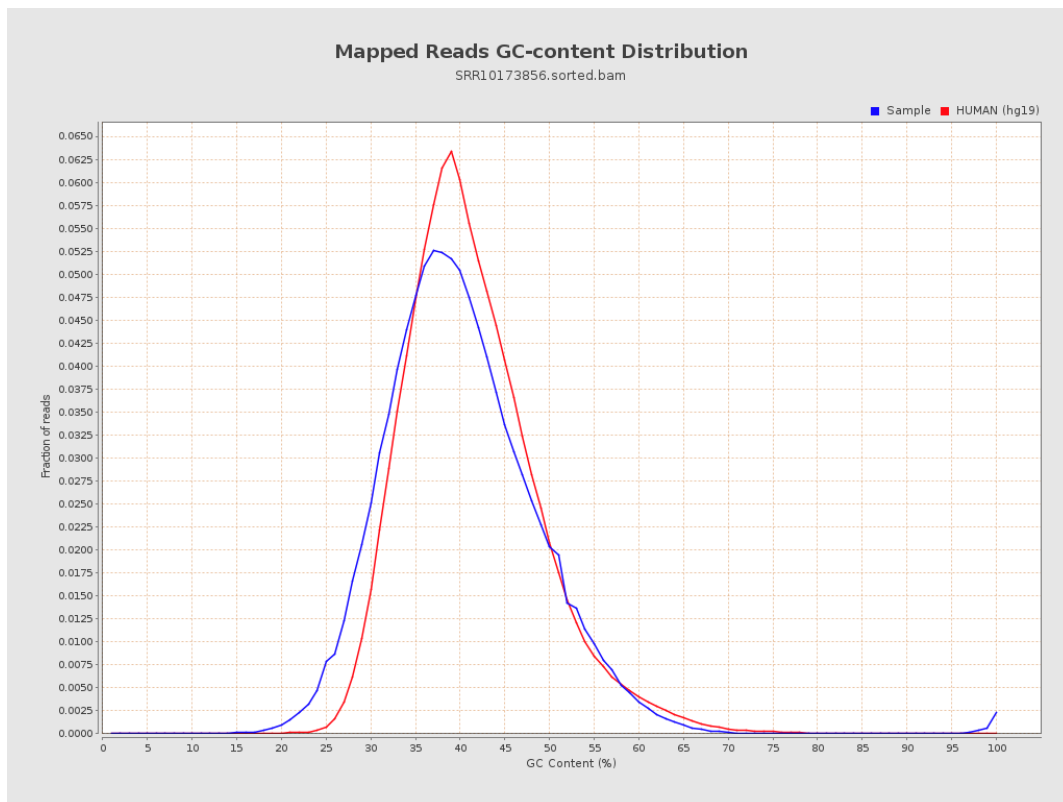
7. Results : Duplication Rate Histogram



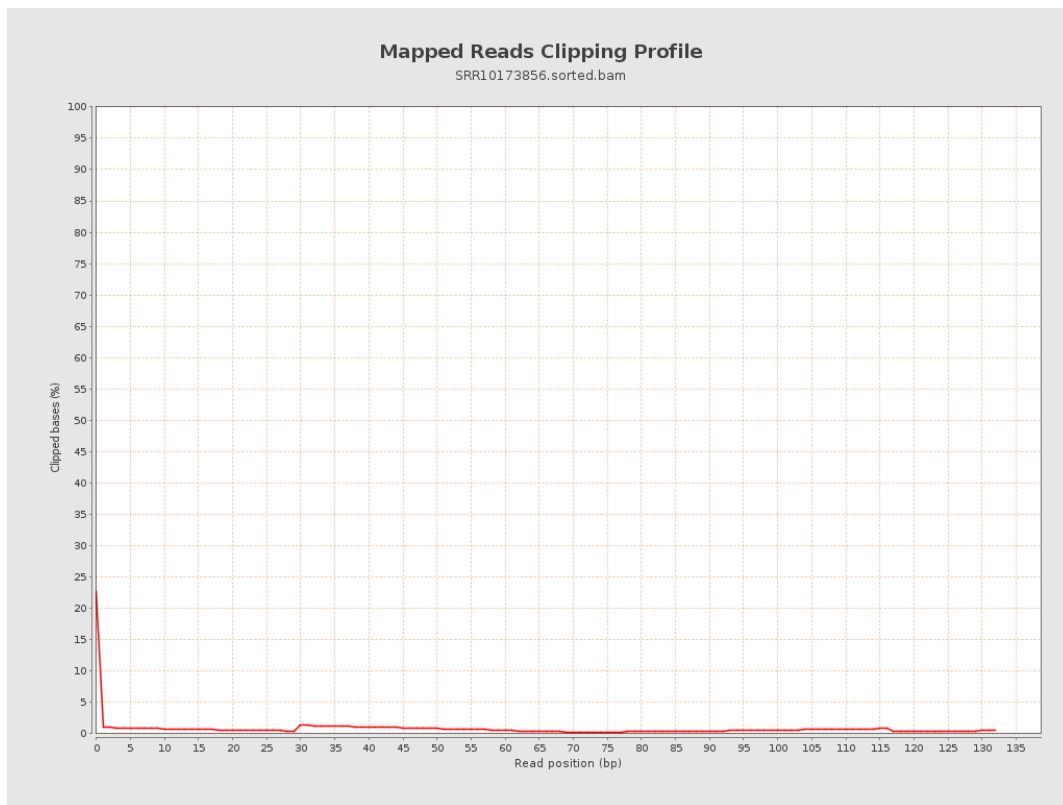
8. Results : Mapped Reads Nucleotide Content



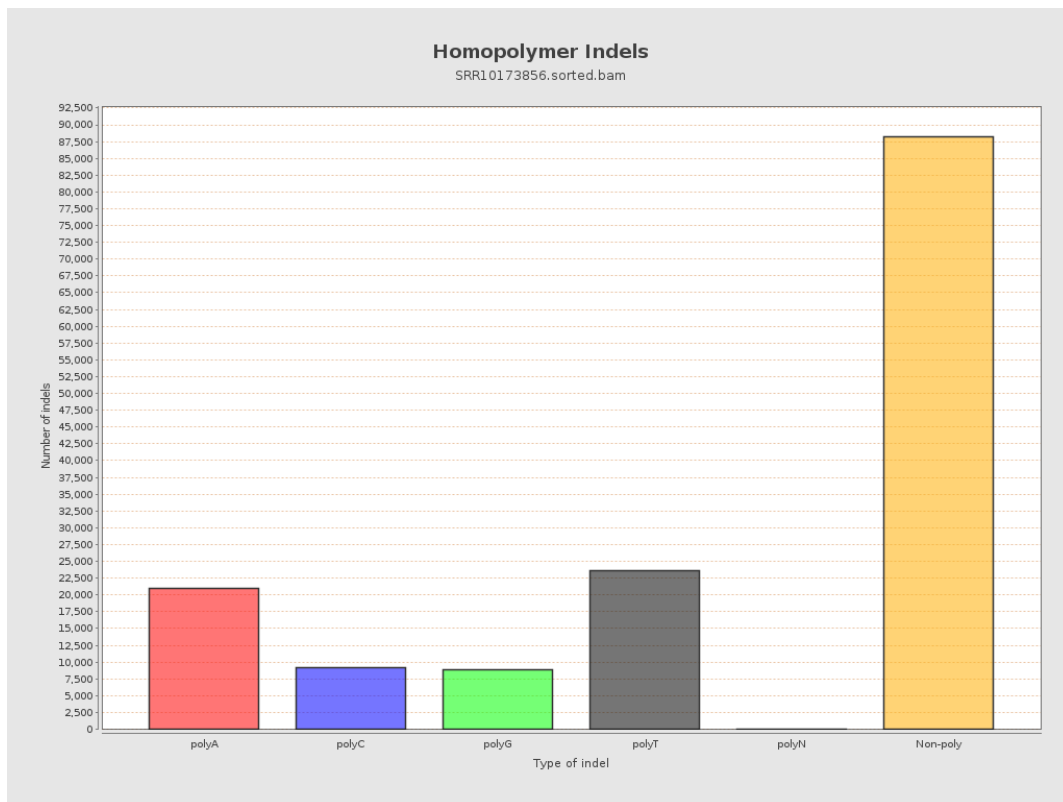
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



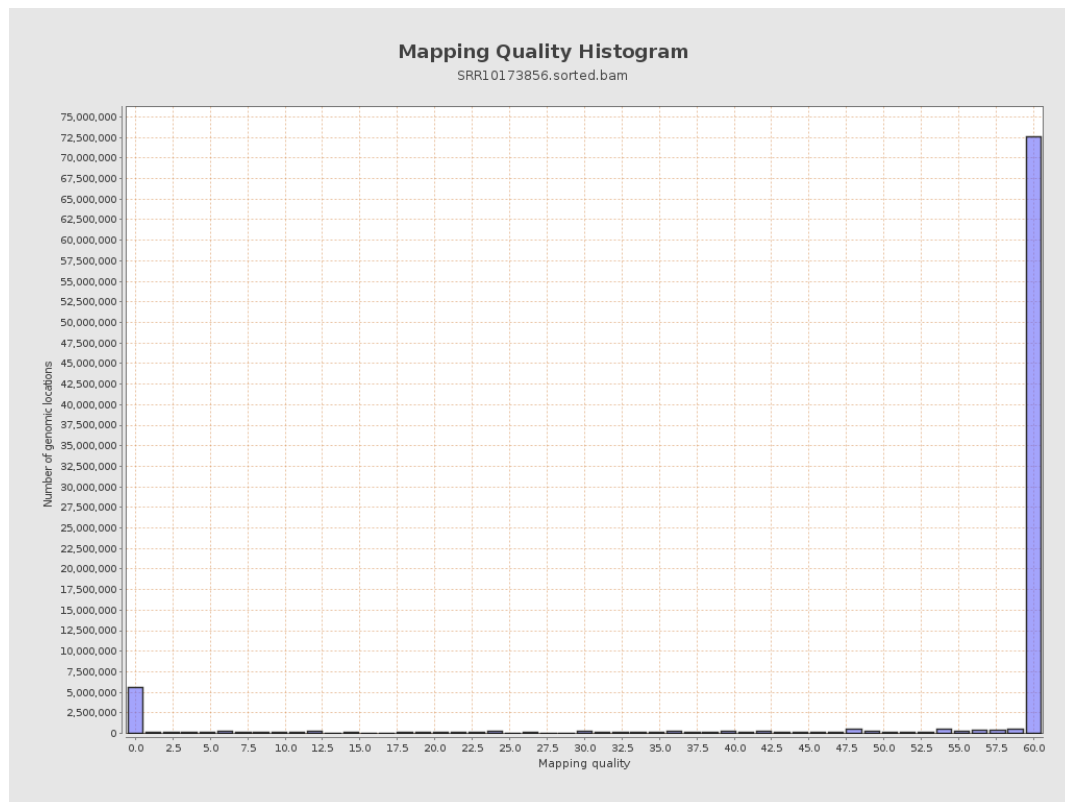
11. Results : Homopolymer Indels



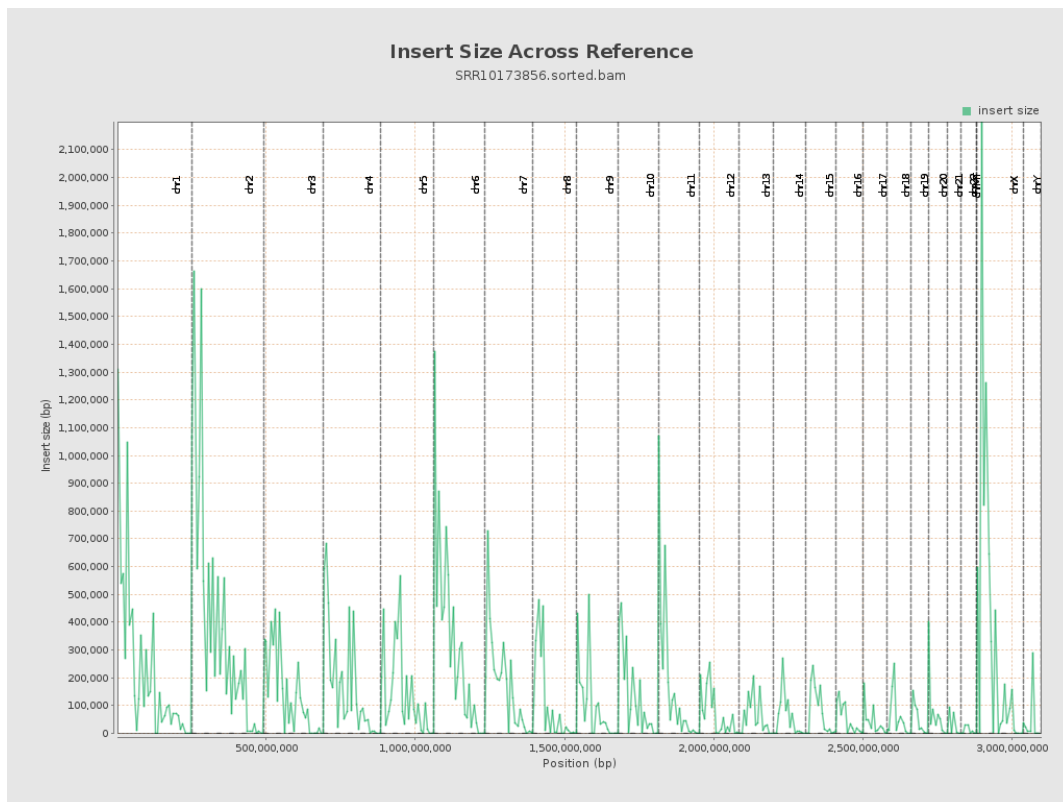
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

