

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 10:45:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251056.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_SRR10251056 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251056_1.fastq.gz SRR10251056_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 10:45:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251056.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,654,812
Mapped reads	1,509,074 / 91.19%
Unmapped reads	145,738 / 8.81%
Mapped paired reads	1,509,074 / 91.19%
Mapped reads, first in pair	757,247 / 45.76%
Mapped reads, second in pair	751,827 / 45.43%
Mapped reads, both in pair	1,498,836 / 90.57%
Mapped reads, singletons	10,238 / 0.62%
Secondary alignments	0
Supplementary alignments	48,702 / 2.94%
Read min/max/mean length	30 / 127 / 128.34
Duplicated reads (estimated)	245,612 / 14.84%
Duplication rate	14.44%
Clipped reads	381,702 / 23.07%

2.2. ACGT Content

Number/percentage of A's	54,898,505 / 29.63%
Number/percentage of C's	37,451,137 / 20.22%
Number/percentage of T's	54,798,653 / 29.58%
Number/percentage of G's	38,104,800 / 20.57%
Number/percentage of N's	6,555 / 0%

GC Percentage	40.78%
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2.3. Coverage

Mean	0.0599
Standard Deviation	0.695

2.4. Mapping Quality

Mean Mapping Quality	53.08
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2.5. Insert size

Mean	104,874.39
Standard Deviation	3,105,674.46
P25/Median/P75	152 / 193 / 261

2.6. Mismatches and indels

General error rate	0.81%
Mismatches	1,421,462
Insertions	32,601
Mapped reads with at least one insertion	2.02%
Deletions	84,381
Mapped reads with at least one deletion	5.35%
Homopolymer indels	43.88%

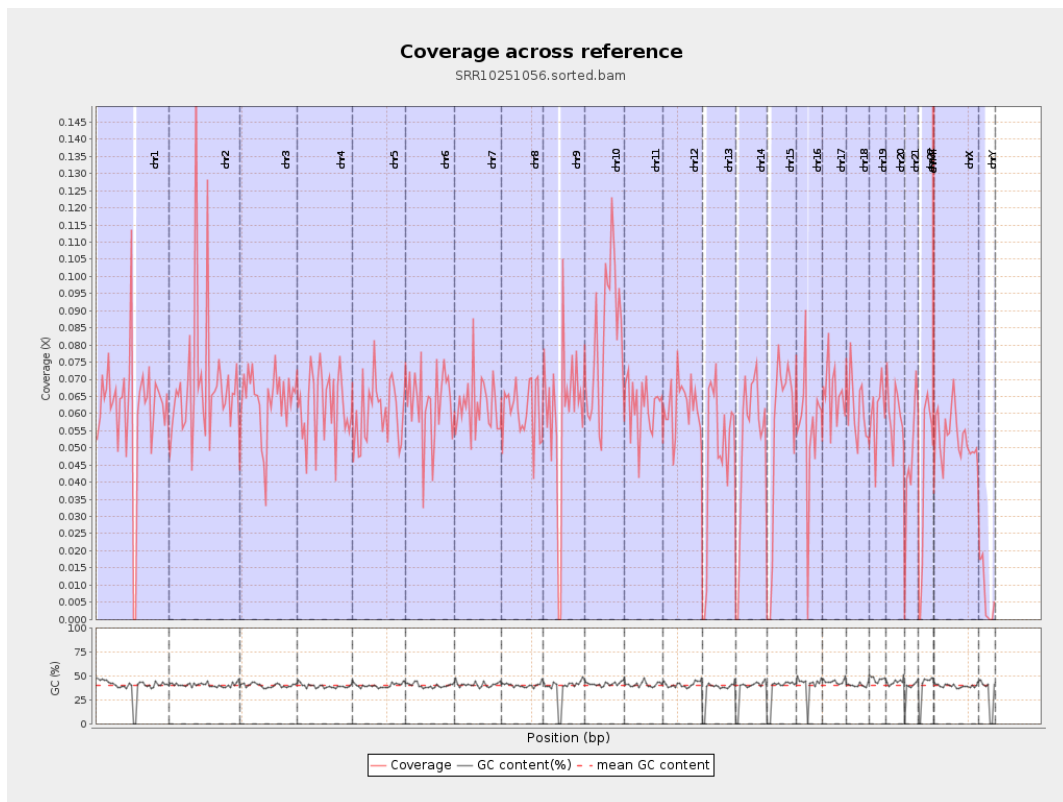
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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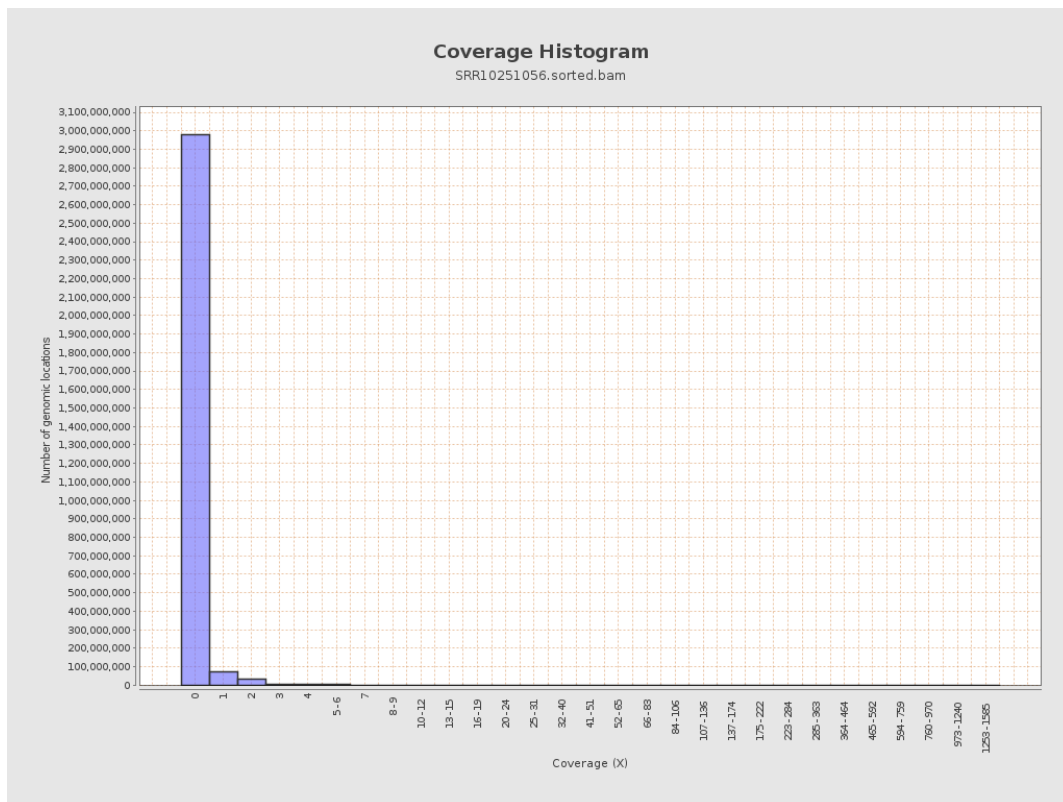
		bases	coverage	deviation
chr1	249250621	15214966	0.061	1.3395
chr2	243199373	16731090	0.0688	1.0635
chr3	198022430	12605824	0.0637	0.3621
chr4	191154276	11815569	0.0618	0.4144
chr5	180915260	10939115	0.0605	0.3571
chr6	171115067	10760248	0.0629	0.4212
chr7	159138663	9951789	0.0625	0.8467
chr8	146364022	8880141	0.0607	0.5004
chr9	141213431	8361912	0.0592	1.004
chr10	135534747	11016244	0.0813	0.8412
chr11	135006516	8388301	0.0621	0.4754
chr12	133851895	8326121	0.0622	0.3663
chr13	115169878	5506998	0.0478	0.3145
chr14	107349540	5581859	0.052	0.3431
chr15	102531392	5555245	0.0542	0.3321
chr16	90354753	5044690	0.0558	0.6282
chr17	81195210	5332936	0.0657	0.4933
chr18	78077248	4853061	0.0622	0.8176
chr19	59128983	3560657	0.0602	0.6929
chr20	63025520	3771414	0.0598	0.3615
chr21	48129895	2273538	0.0472	0.3255
chr22	51304566	2121755	0.0414	0.3068
chrMT	16571	193978	11.7059	7.2046
chrX	155270560	8223481	0.053	0.3455

chrY	59373566	424932	0.0072	0.4503
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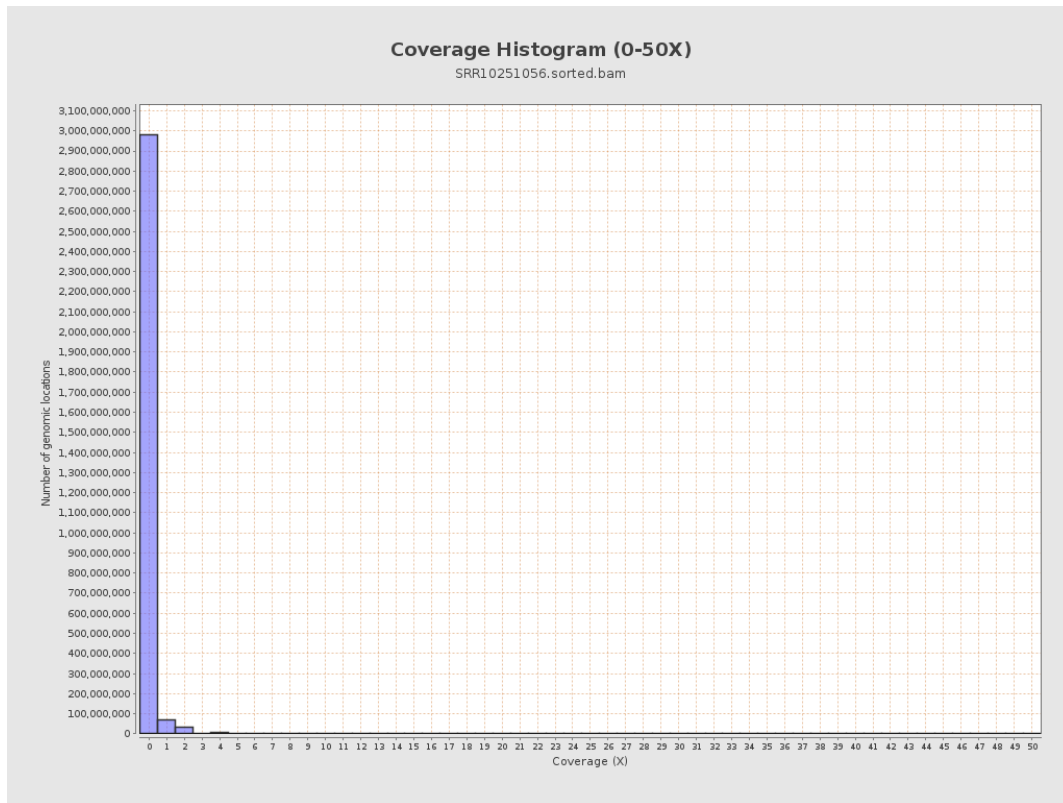
3. Results : Coverage across reference



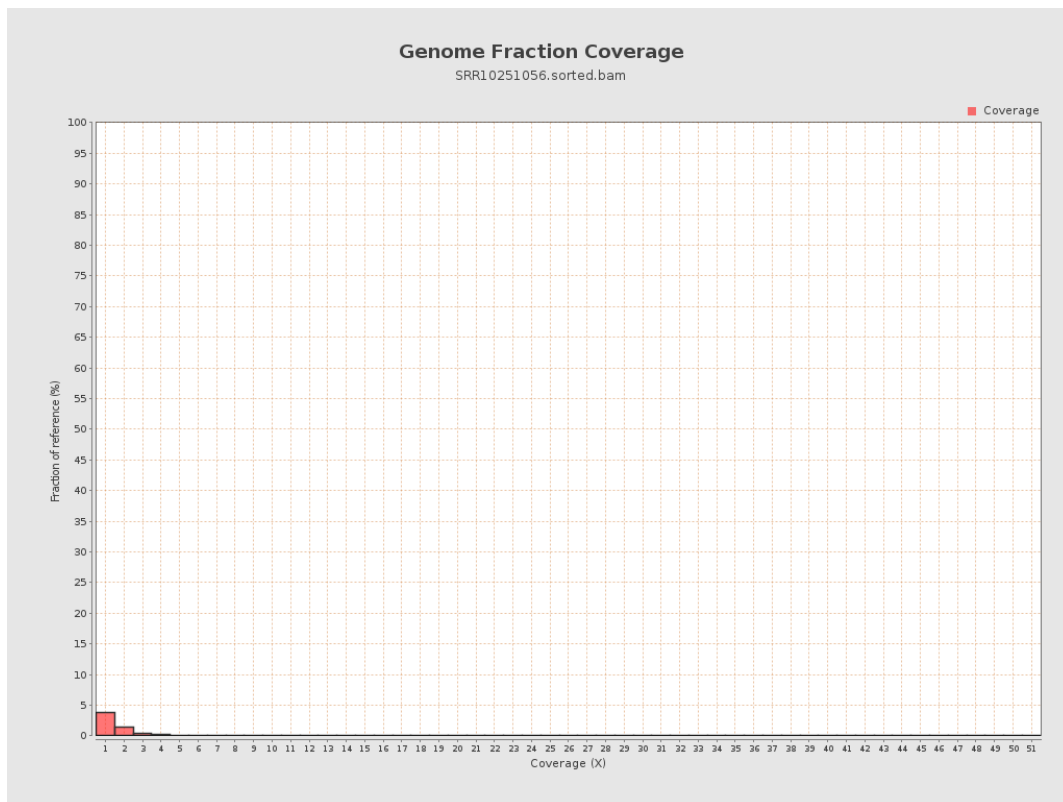
4. Results : Coverage Histogram



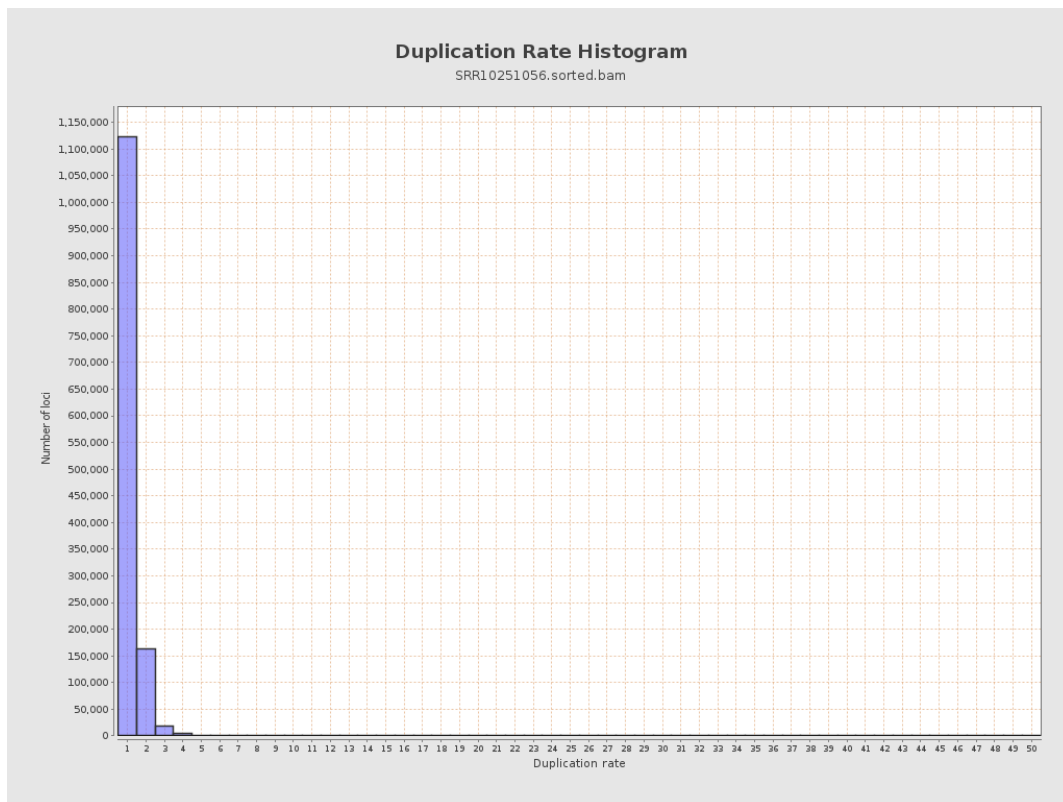
5. Results : Coverage Histogram (0-50X)



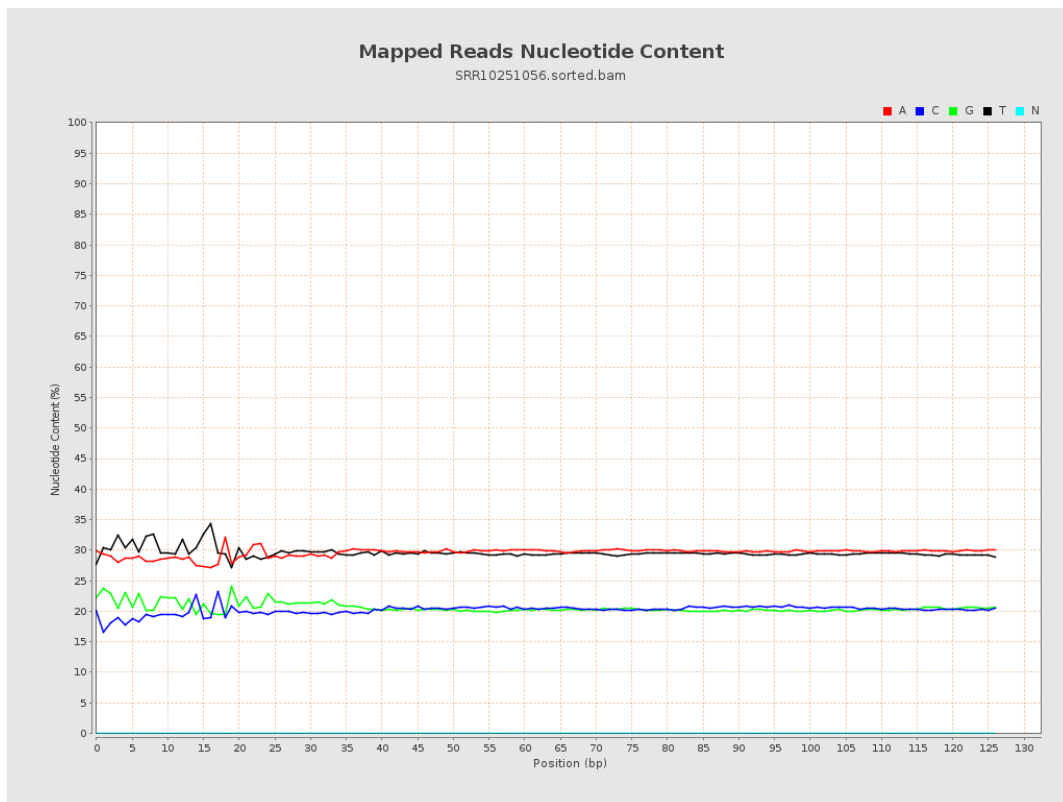
6. Results : Genome Fraction Coverage



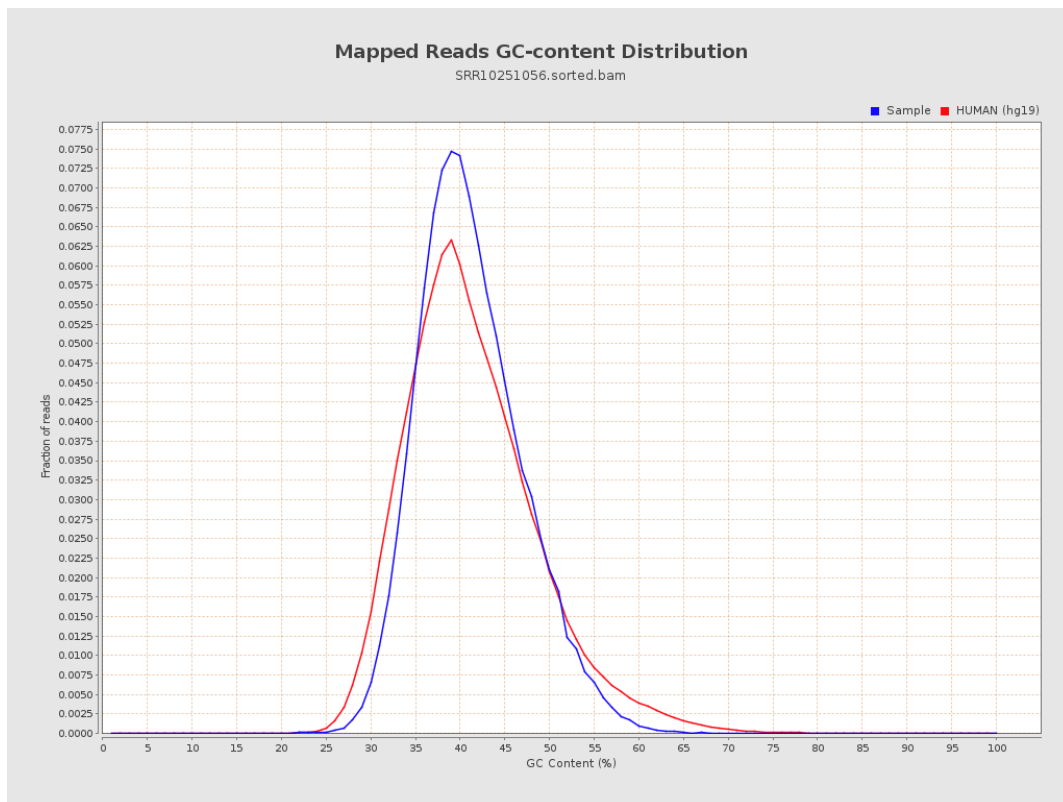
7. Results : Duplication Rate Histogram



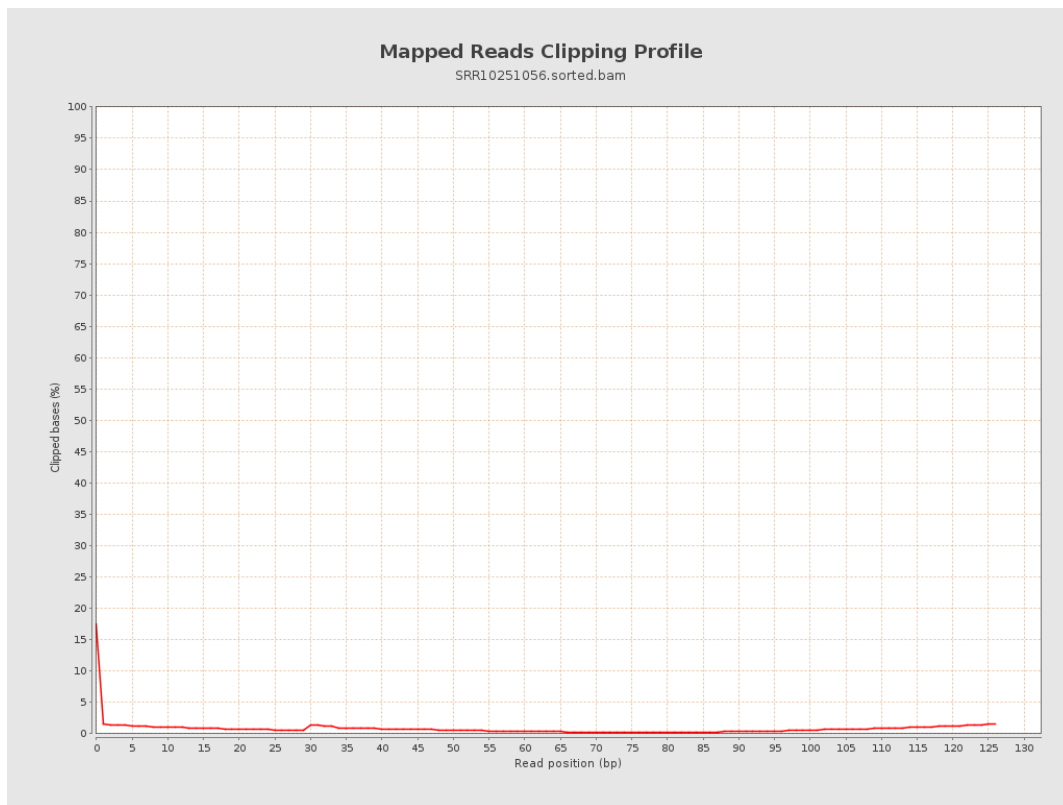
8. Results : Mapped Reads Nucleotide Content



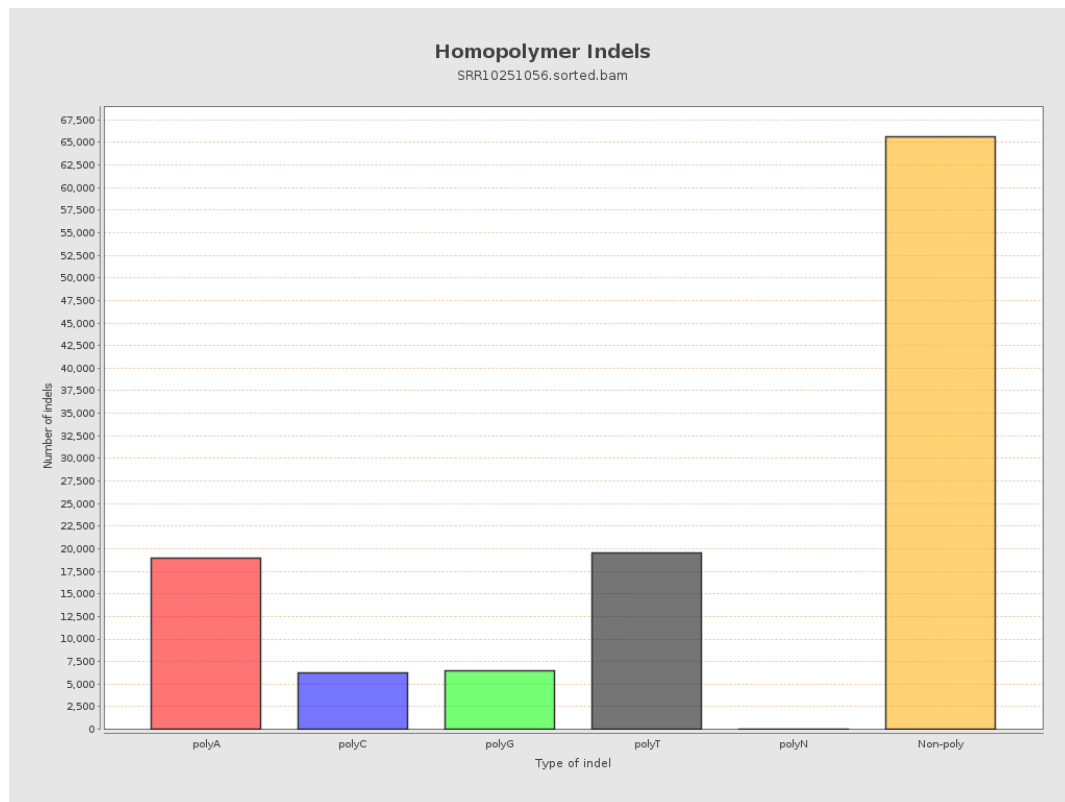
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



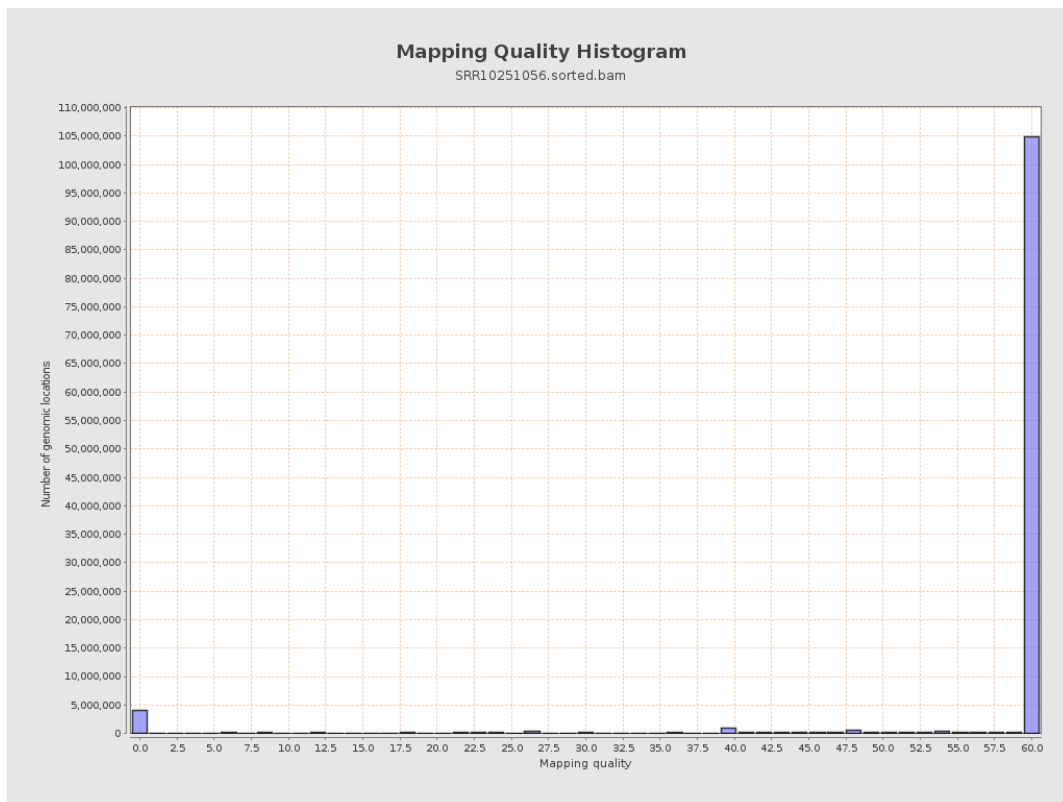
11. Results : Homopolymer Indels



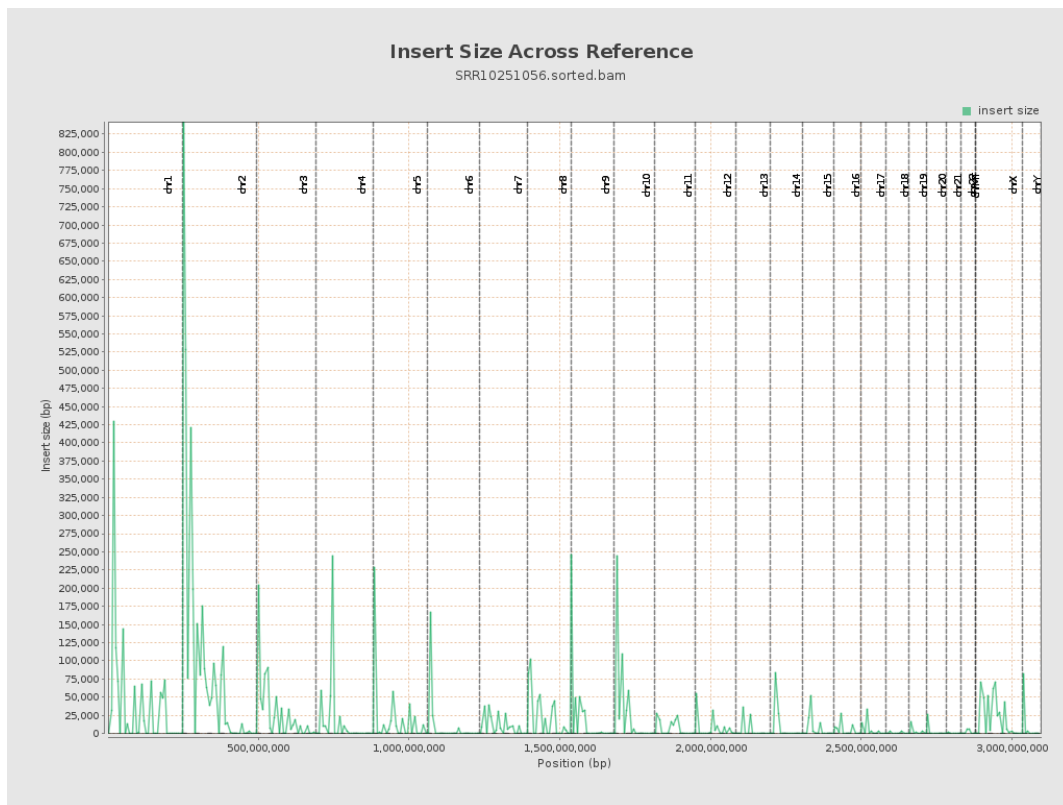
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

