

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 06:12:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10156426.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_SRR10156426 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10156426_1.fastq.gz SRR10156426_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 06:12:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10156426.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,445,518
Mapped reads	13,144,679 / 97.76%
Unmapped reads	300,839 / 2.24%
Mapped paired reads	13,144,679 / 97.76%
Mapped reads, first in pair	6,572,415 / 48.88%
Mapped reads, second in pair	6,572,264 / 48.88%
Mapped reads, both in pair	12,953,870 / 96.34%
Mapped reads, singletons	190,809 / 1.42%
Secondary alignments	0
Supplementary alignments	1,867,973 / 13.89%
Read min/max/mean length	30 / 133 / 126.15
Duplicated reads (estimated)	10,866,305 / 80.82%
Duplication rate	65.87%
Clipped reads	6,879,381 / 51.16%

2.2. ACGT Content

Number/percentage of A's	447,104,500 / 29.92%
Number/percentage of C's	295,709,206 / 19.79%
Number/percentage of T's	443,426,941 / 29.68%
Number/percentage of G's	307,855,160 / 20.6%
Number/percentage of N's	11,896 / 0%

GC Percentage	40.4%
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2.3. Coverage

Mean	0.483
Standard Deviation	8.9226

2.4. Mapping Quality

Mean Mapping Quality	52.37
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2.5. Insert size

Mean	1,059,419.48
Standard Deviation	9,579,912.96
P25/Median/P75	106 / 157 / 245

2.6. Mismatches and indels

General error rate	0.9%
Mismatches	12,951,499
Insertions	166,674
Mapped reads with at least one insertion	1.22%
Deletions	419,355
Mapped reads with at least one deletion	3.11%
Homopolymer indels	41.24%

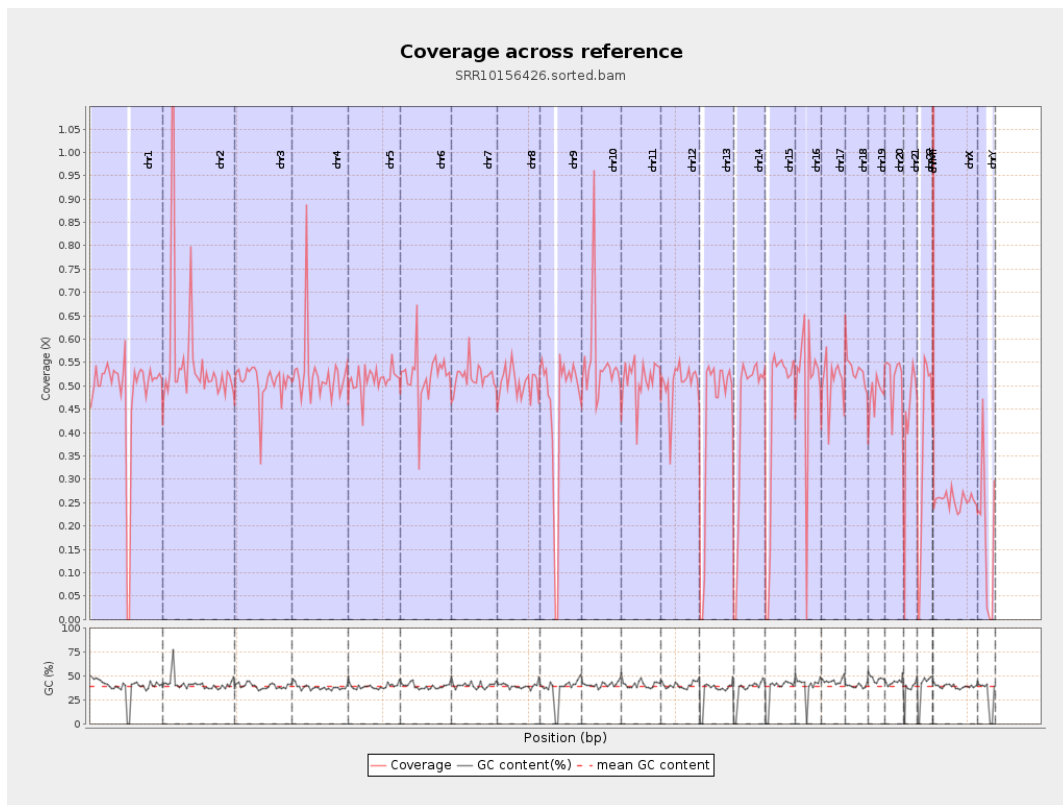
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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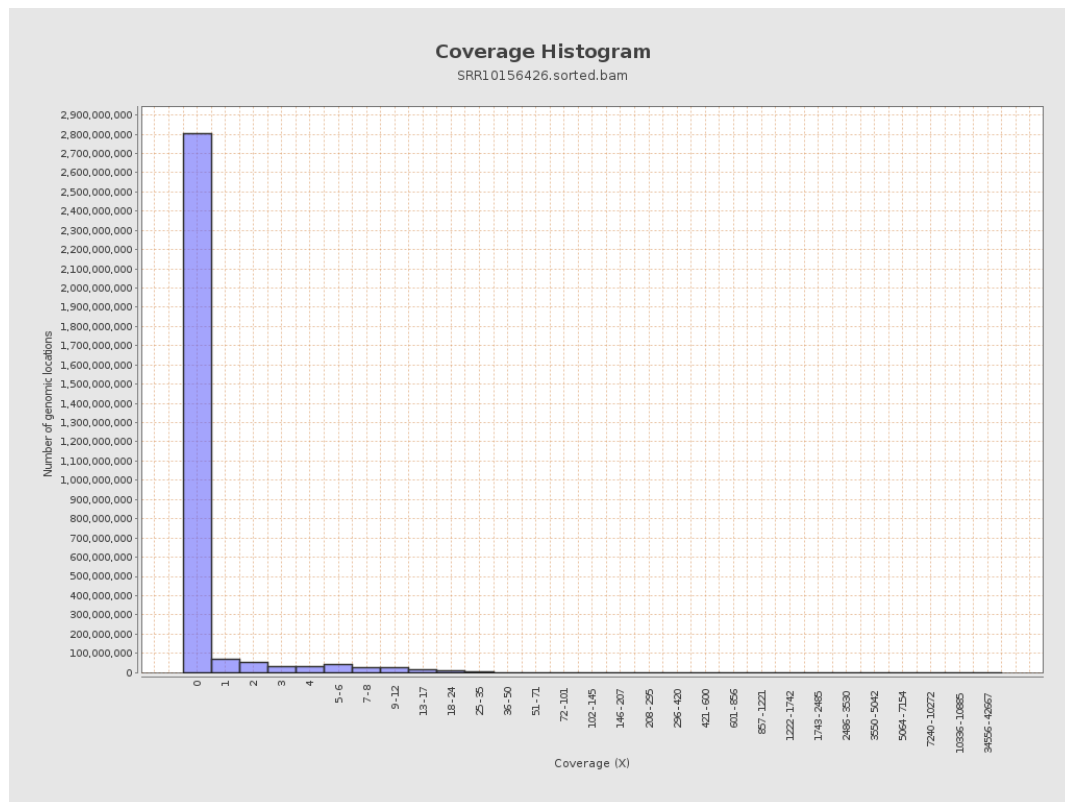
		bases	coverage	deviation
chr1	249250621	120639063	0.484	3.8443
chr2	243199373	134889926	0.5546	29.833
chr3	198022430	100415843	0.5071	2.2206
chr4	191154276	100835120	0.5275	3.6494
chr5	180915260	92914183	0.5136	2.2453
chr6	171115067	89334462	0.5221	2.9819
chr7	159138663	82551864	0.5187	3.8413
chr8	146364022	74039547	0.5059	4.7511
chr9	141213431	64369733	0.4558	3.9602
chr10	135534747	74362195	0.5487	4.6691
chr11	135006516	69424996	0.5142	2.4206
chr12	133851895	67950318	0.5077	2.4036
chr13	115169878	49390882	0.4289	2.0465
chr14	107349540	47247185	0.4401	2.1641
chr15	102531392	44764565	0.4366	2.1901
chr16	90354753	45389023	0.5023	3.206
chr17	81195210	41587556	0.5122	2.7017
chr18	78077248	41772753	0.535	5.2521
chr19	59128983	28669714	0.4849	3.0357
chr20	63025520	32511679	0.5158	2.4622
chr21	48129895	20957279	0.4354	3.1097
chr22	51304566	19000289	0.3703	2.5652
chrMT	16571	1532889	92.5043	72.3845
chrX	155270560	39550095	0.2547	1.6161

chrY	59373566	11018026	0.1856	2.7557
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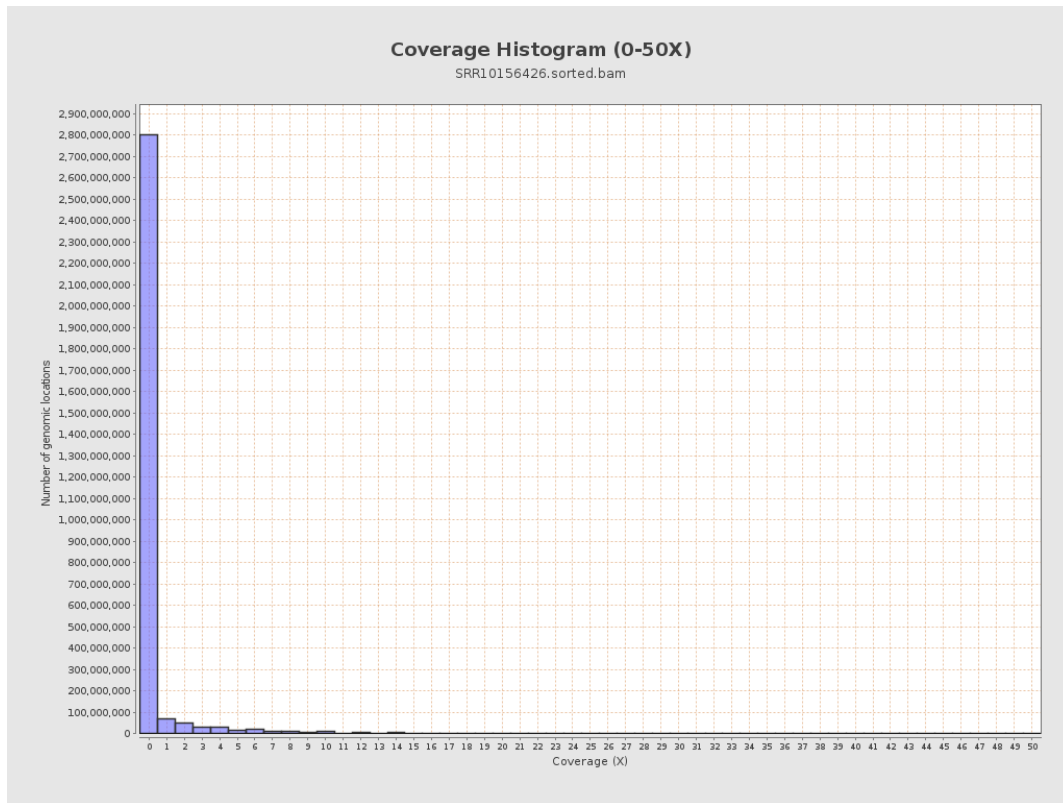
3. Results : Coverage across reference



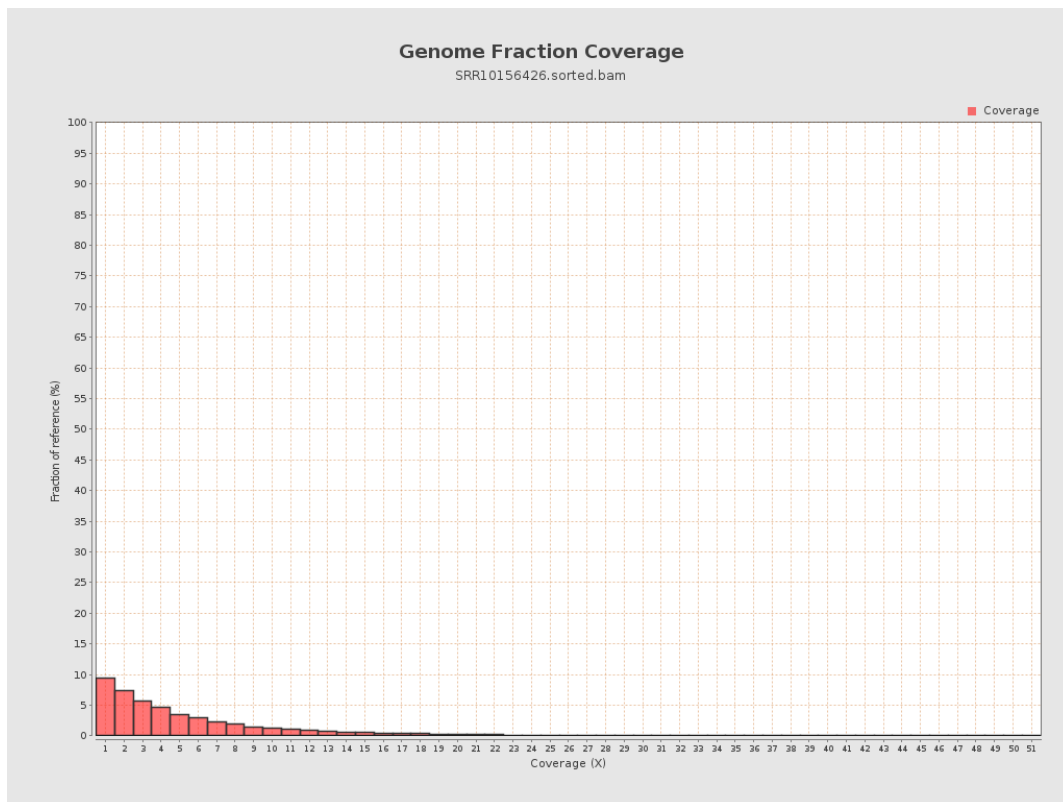
4. Results : Coverage Histogram



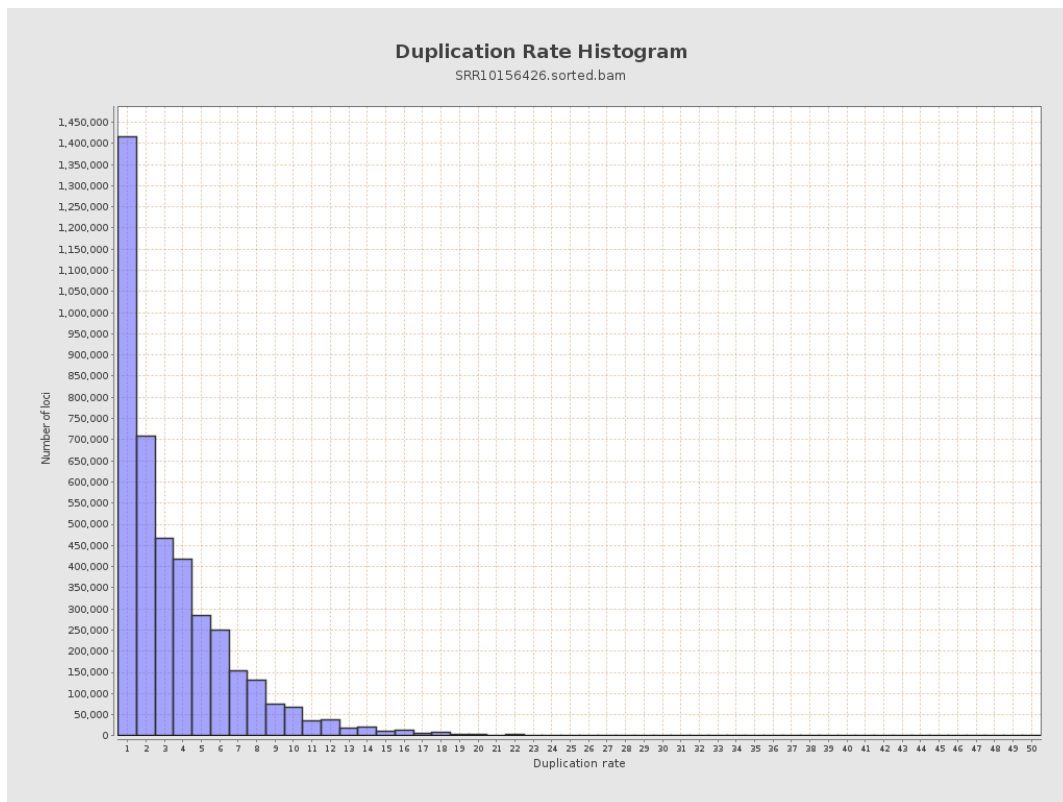
5. Results : Coverage Histogram (0-50X)



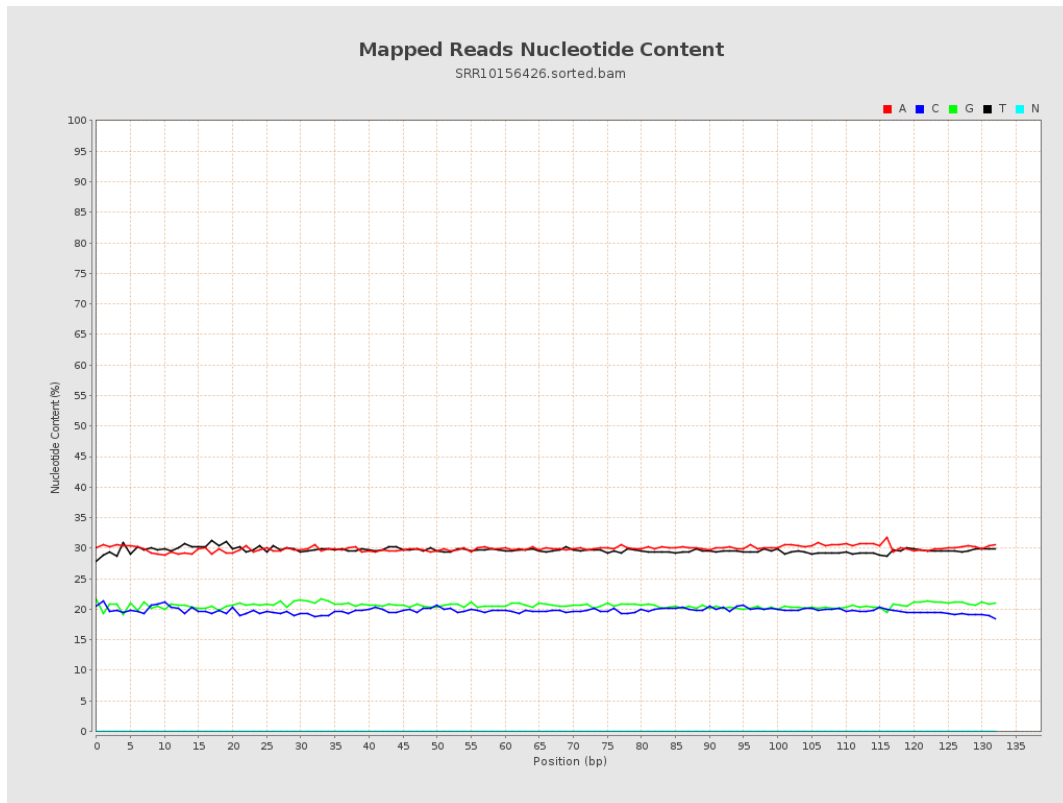
6. Results : Genome Fraction Coverage



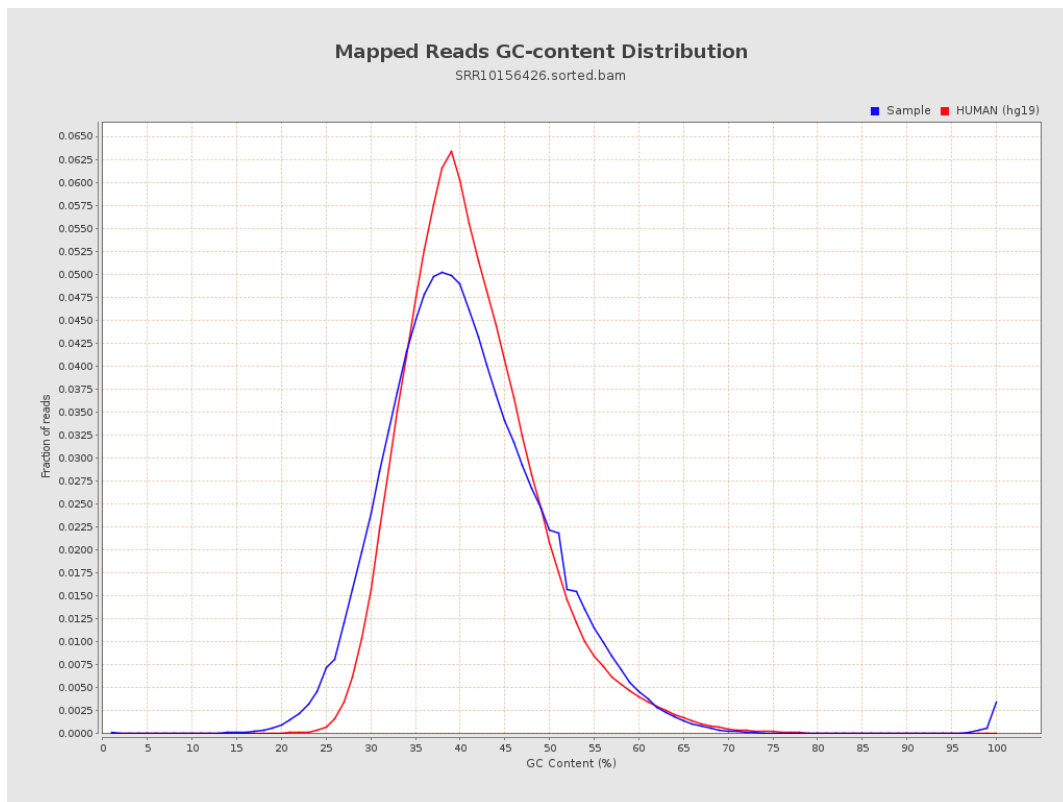
7. Results : Duplication Rate Histogram



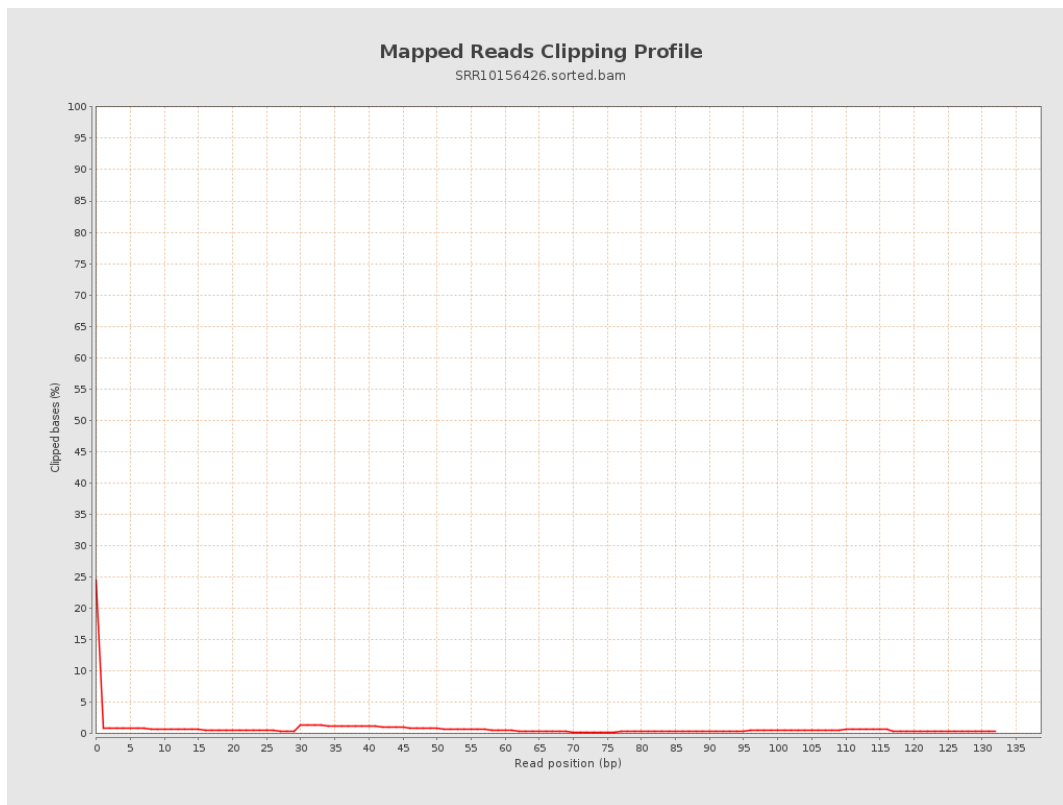
8. Results : Mapped Reads Nucleotide Content



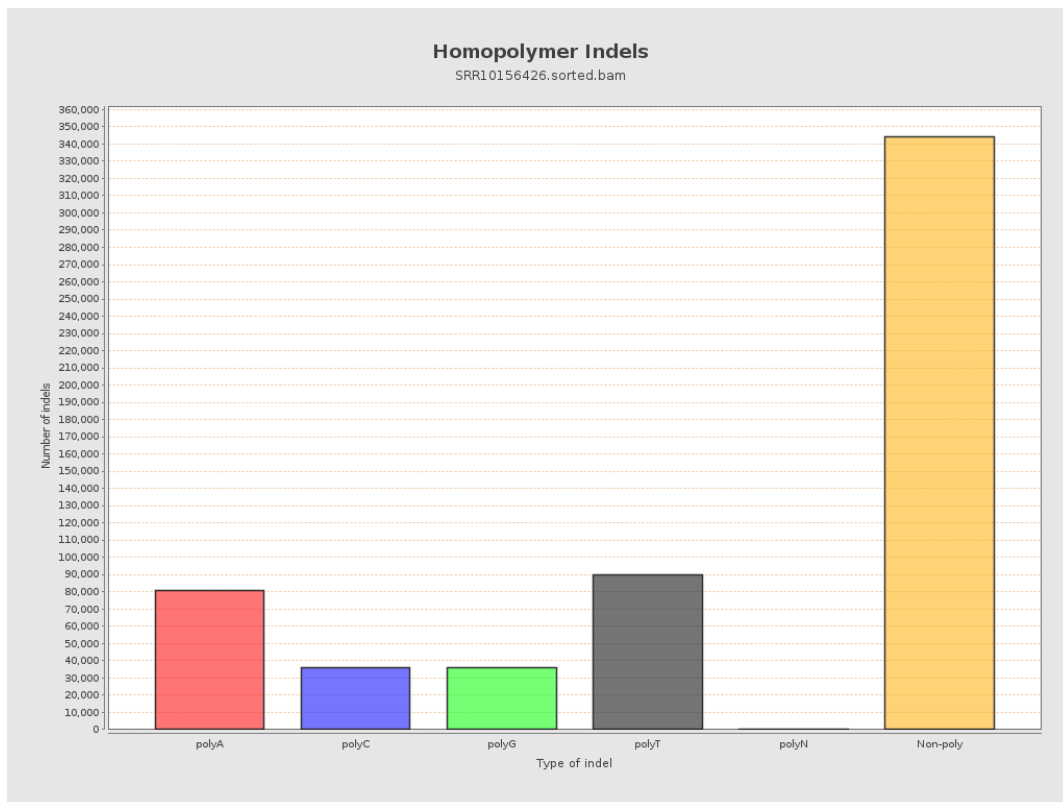
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



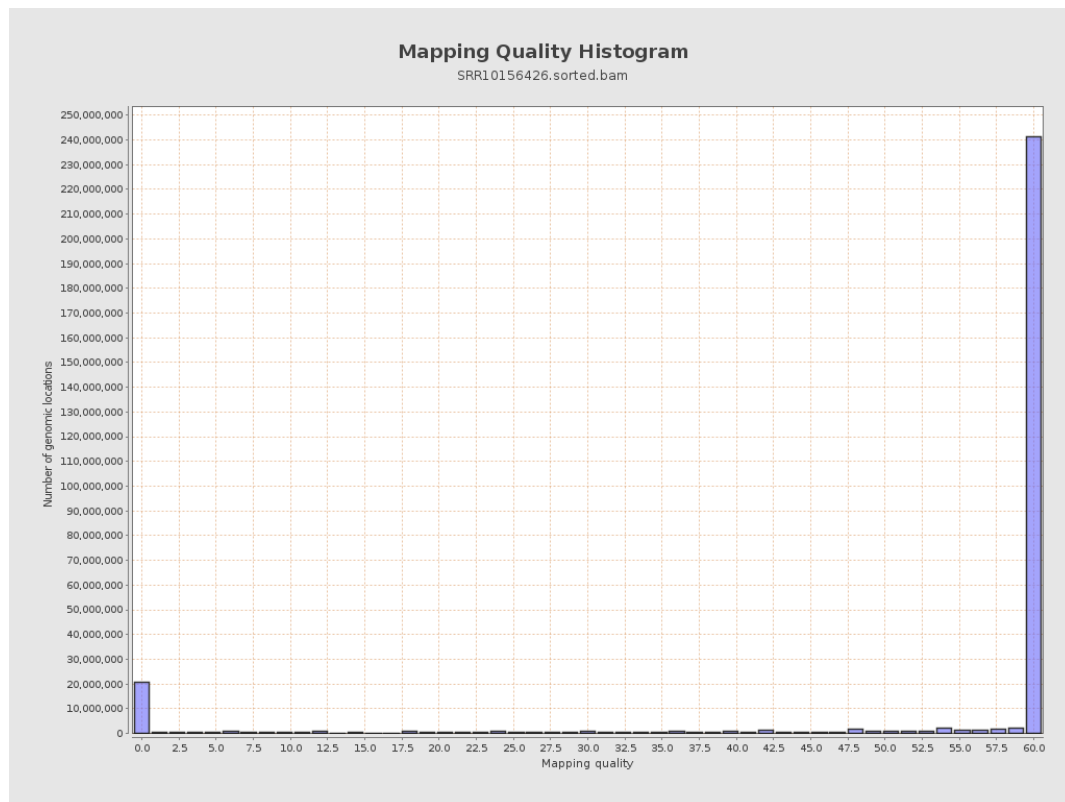
11. Results : Homopolymer Indels



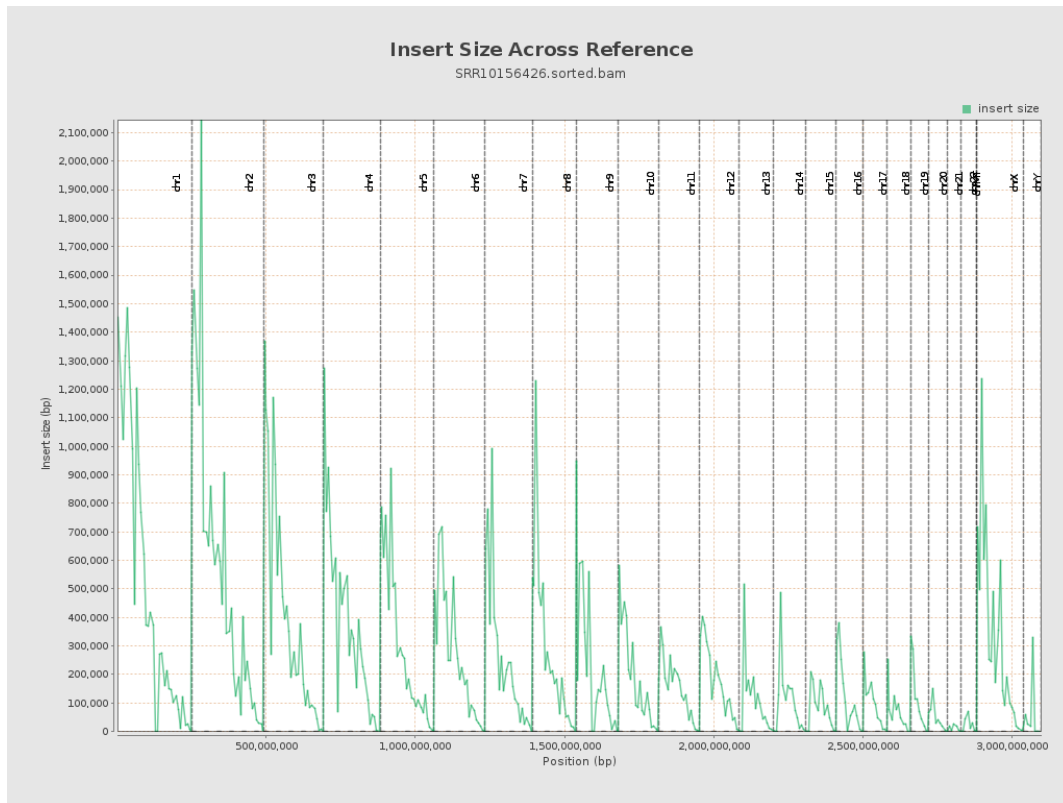
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

