

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 12:52:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173959.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_SRR10173959 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173959_1.fastq.gz SRR10173959_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 12:52:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173959.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,216,420
Mapped reads	13,876,111 / 97.61%
Unmapped reads	340,309 / 2.39%
Mapped paired reads	13,876,111 / 97.61%
Mapped reads, first in pair	6,940,727 / 48.82%
Mapped reads, second in pair	6,935,384 / 48.78%
Mapped reads, both in pair	13,654,616 / 96.05%
Mapped reads, singletons	221,495 / 1.56%
Secondary alignments	0
Supplementary alignments	1,833,627 / 12.9%
Read min/max/mean length	30 / 133 / 125.99
Duplicated reads (estimated)	11,483,568 / 80.78%
Duplication rate	67.01%
Clipped reads	6,946,471 / 48.86%

2.2. ACGT Content

Number/percentage of A's	471,513,723 / 29.83%
Number/percentage of C's	314,522,547 / 19.9%
Number/percentage of T's	467,136,732 / 29.56%
Number/percentage of G's	327,291,076 / 20.71%
Number/percentage of N's	11,832 / 0%

GC Percentage	40.61%
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2.3. Coverage

Mean	0.5109
Standard Deviation	8.4869

2.4. Mapping Quality

Mean Mapping Quality	52.44
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2.5. Insert size

Mean	957,402.19
Standard Deviation	9,269,464.08
P25/Median/P75	109 / 161 / 249

2.6. Mismatches and indels

General error rate	0.9%
Mismatches	13,748,438
Insertions	178,628
Mapped reads with at least one insertion	1.23%
Deletions	436,028
Mapped reads with at least one deletion	3.06%
Homopolymer indels	41.35%

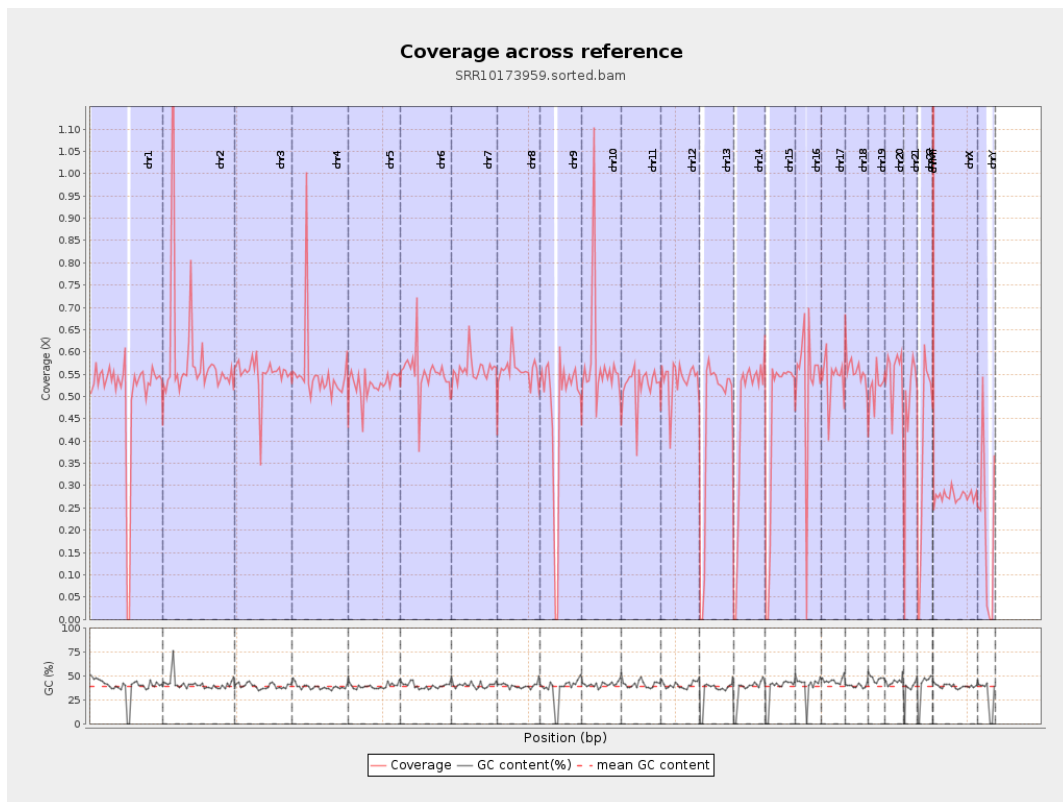
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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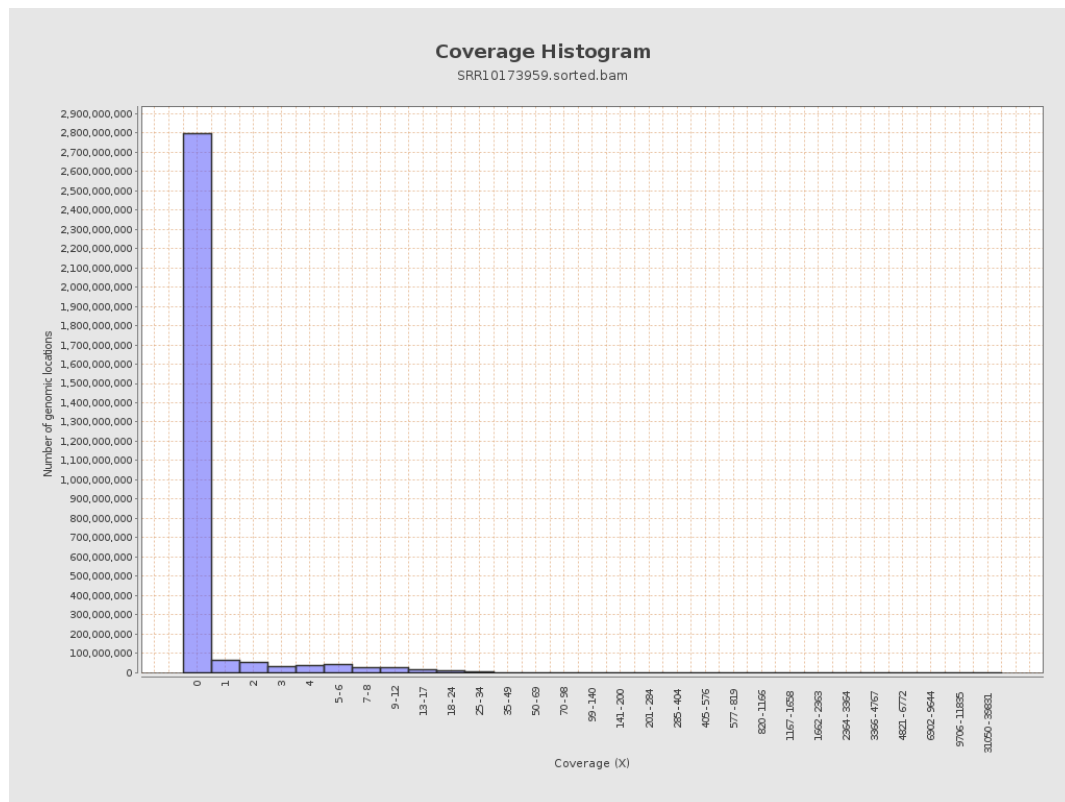
		bases	coverage	deviation
chr1	249250621	126255123	0.5065	4.1684
chr2	243199373	141965793	0.5837	27.7365
chr3	198022430	109116000	0.551	2.3407
chr4	191154276	105753002	0.5532	4.151
chr5	180915260	95513254	0.5279	2.2761
chr6	171115067	94729240	0.5536	3.2721
chr7	159138663	89269663	0.561	4.1653
chr8	146364022	81925434	0.5597	5.2524
chr9	141213431	67179683	0.4757	3.998
chr10	135534747	77765860	0.5738	5.4663
chr11	135006516	70975166	0.5257	2.461
chr12	133851895	72342377	0.5405	2.5013
chr13	115169878	51712897	0.449	2.0997
chr14	107349540	49062932	0.457	2.2118
chr15	102531392	45405912	0.4428	2.2243
chr16	90354753	47820249	0.5292	3.3893
chr17	81195210	44098499	0.5431	2.8191
chr18	78077248	43740027	0.5602	5.5126
chr19	59128983	30775327	0.5205	3.391
chr20	63025520	34893773	0.5536	2.6335
chr21	48129895	22932828	0.4765	3.6315
chr22	51304566	19865908	0.3872	2.7379
chrMT	16571	2924427	176.4786	135.6341
chrX	155270560	42888103	0.2762	1.6995

chrY	59373566	12606935	0.2123	3.2239
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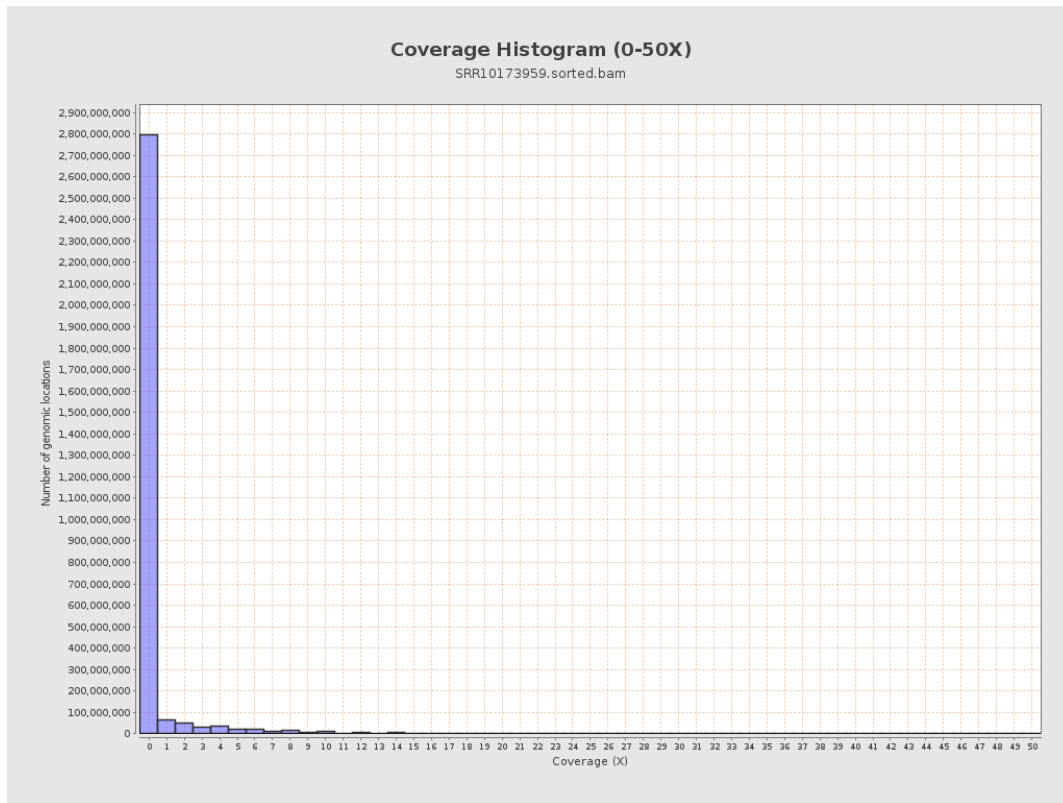
3. Results : Coverage across reference



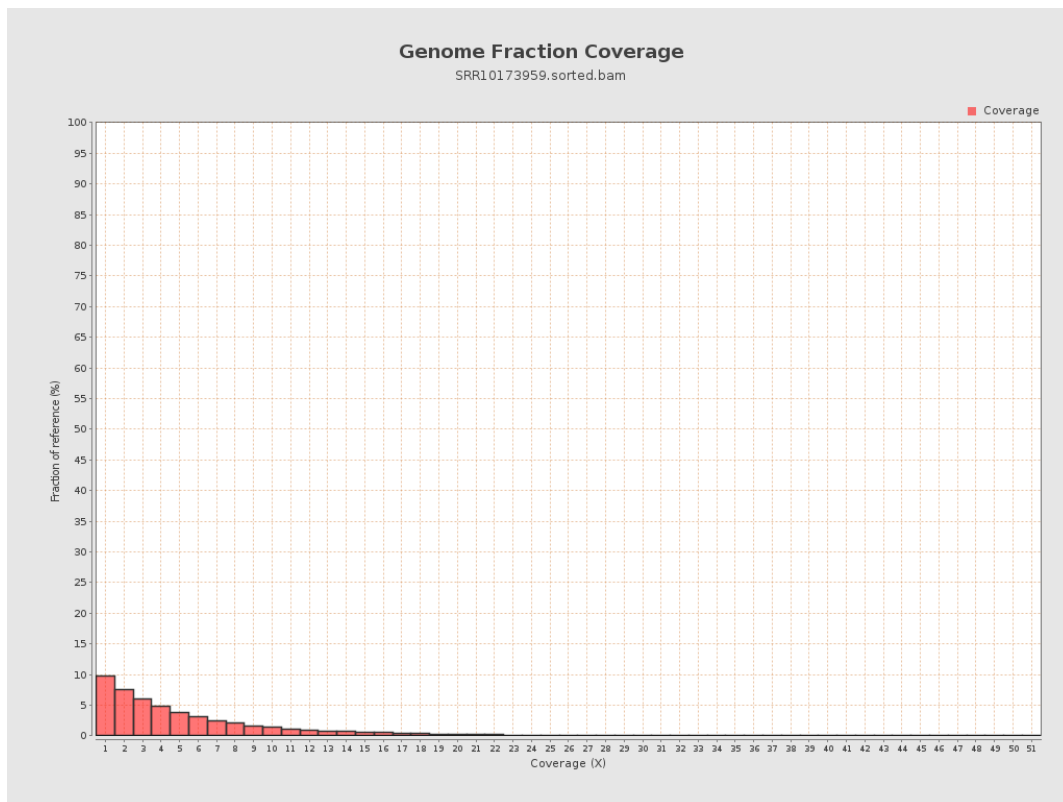
4. Results : Coverage Histogram



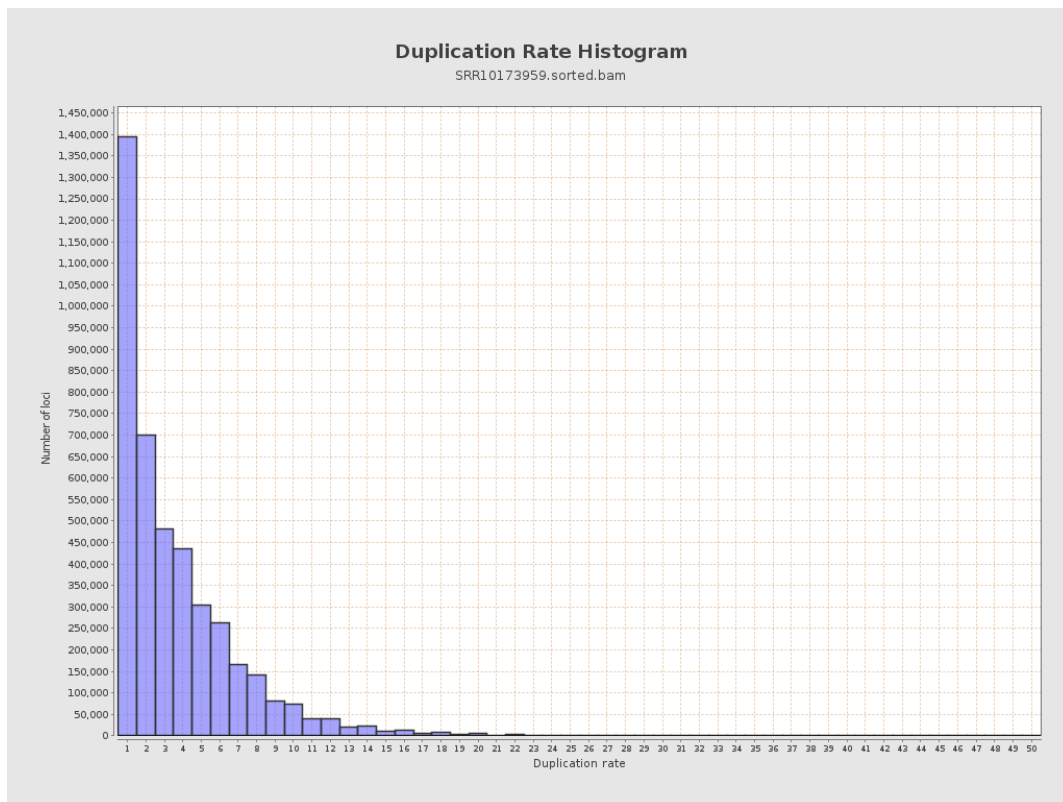
5. Results : Coverage Histogram (0-50X)



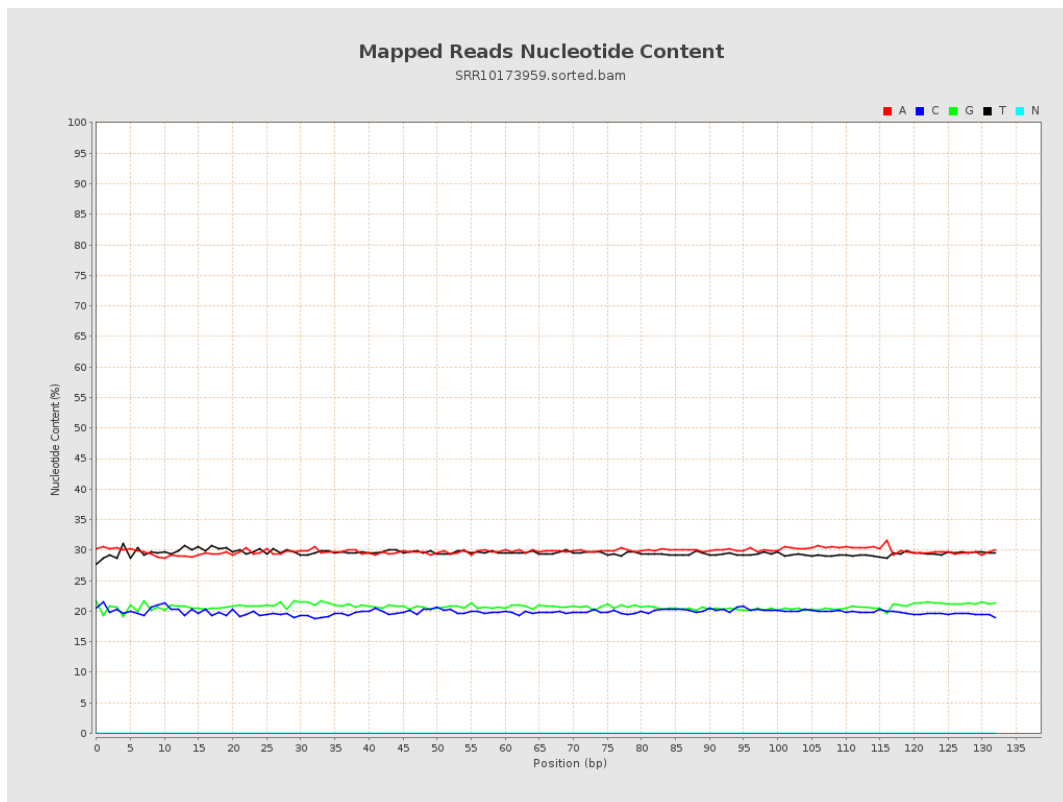
6. Results : Genome Fraction Coverage



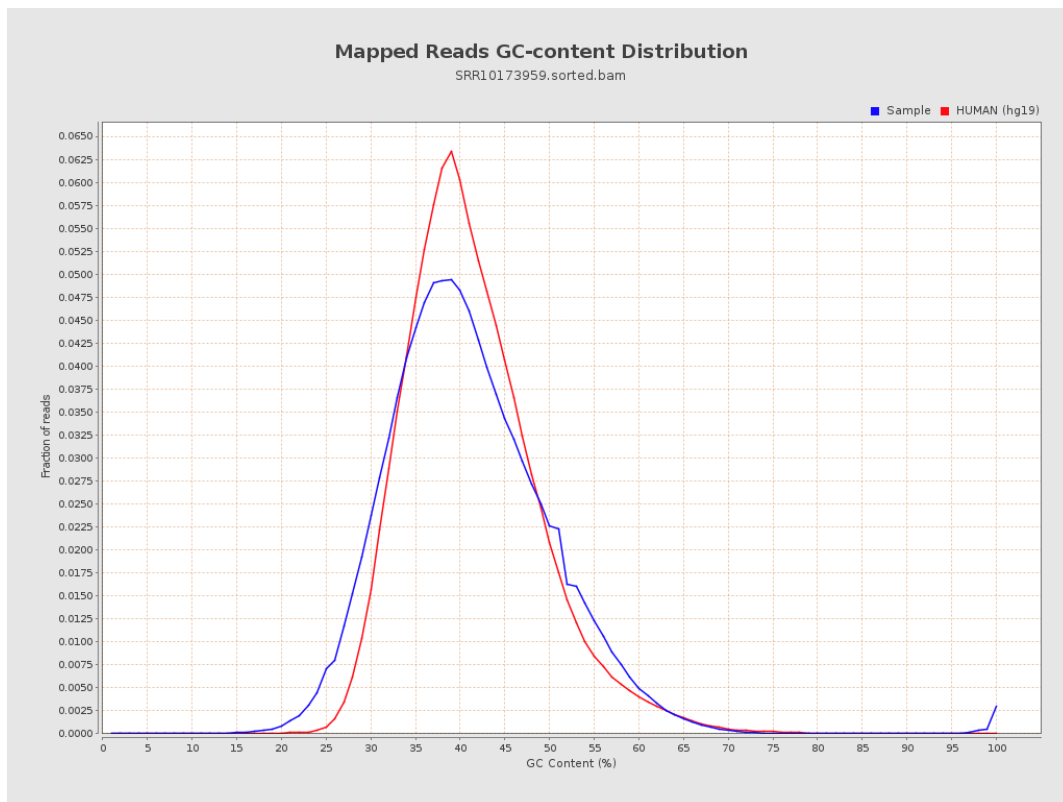
7. Results : Duplication Rate Histogram



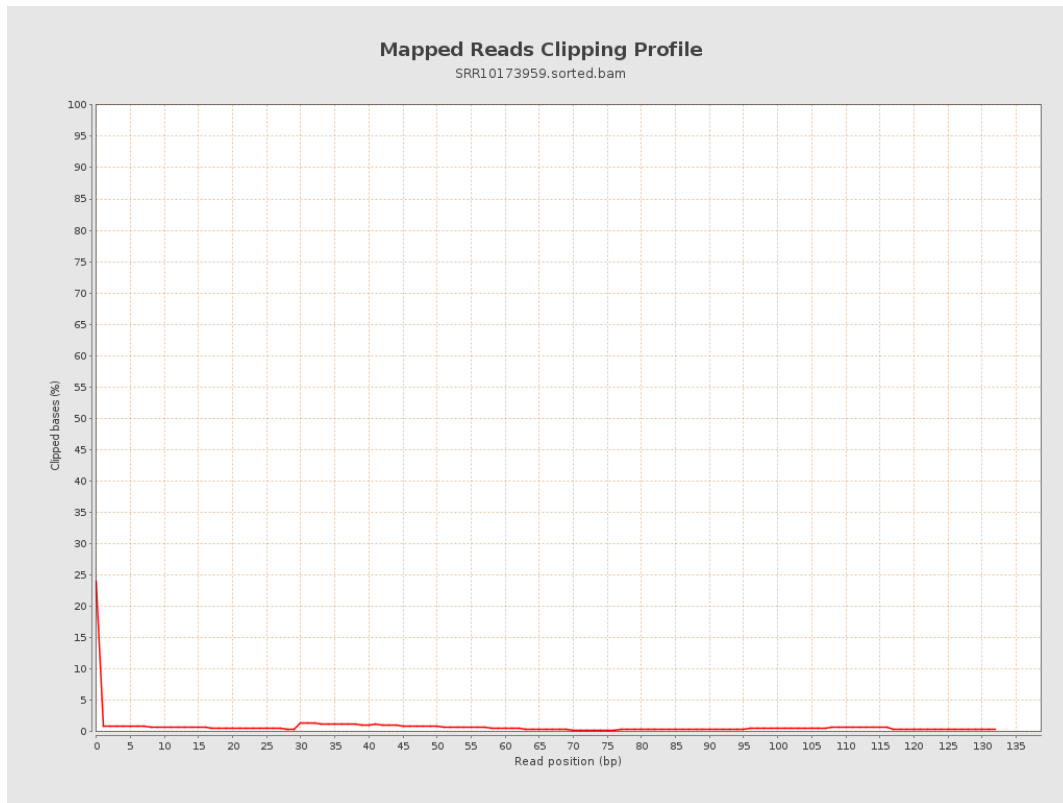
8. Results : Mapped Reads Nucleotide Content



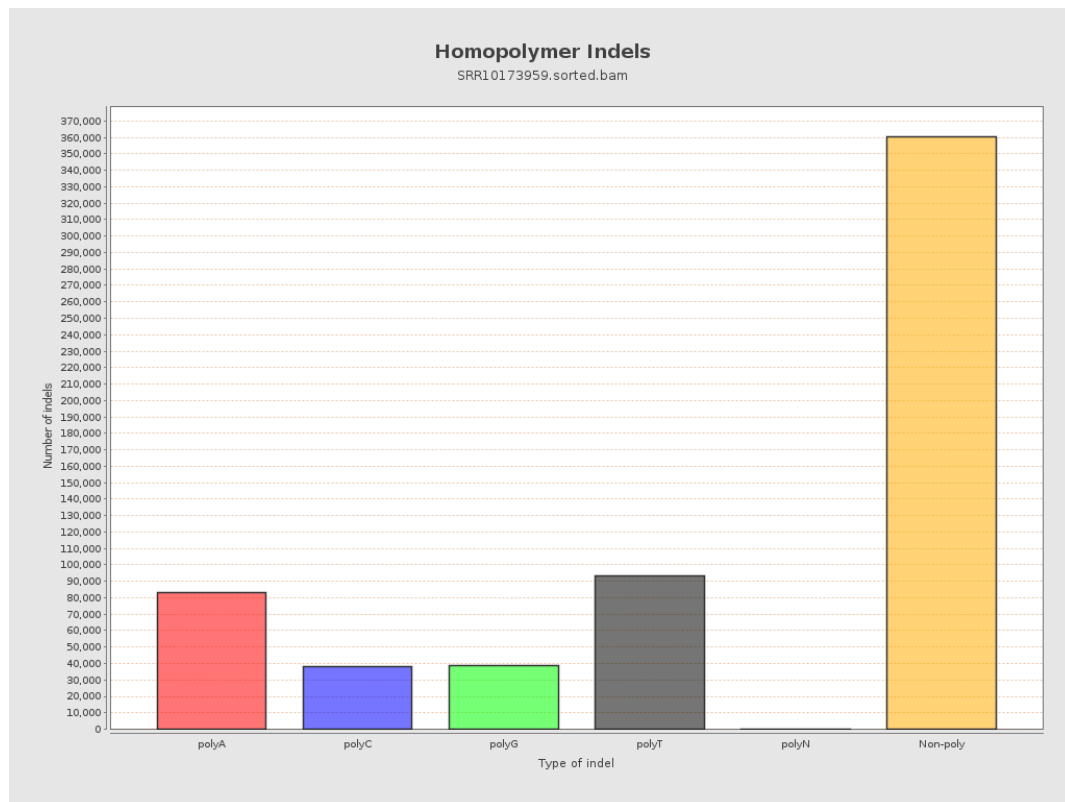
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



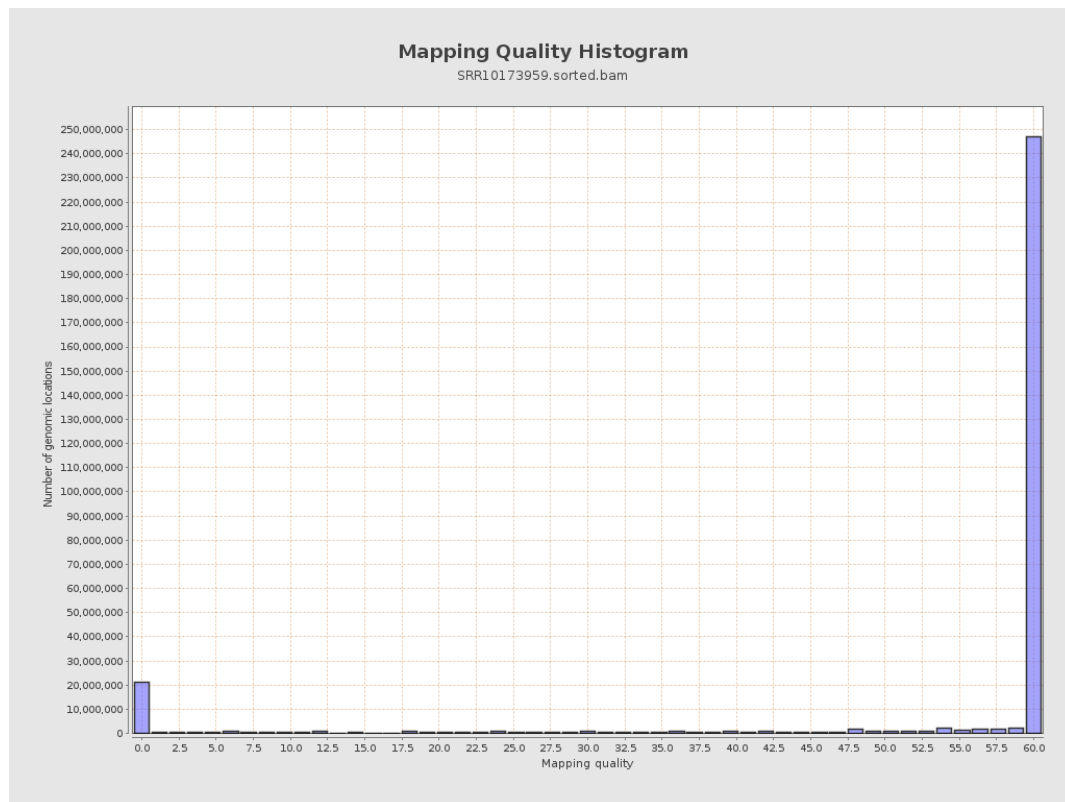
11. Results : Homopolymer Indels



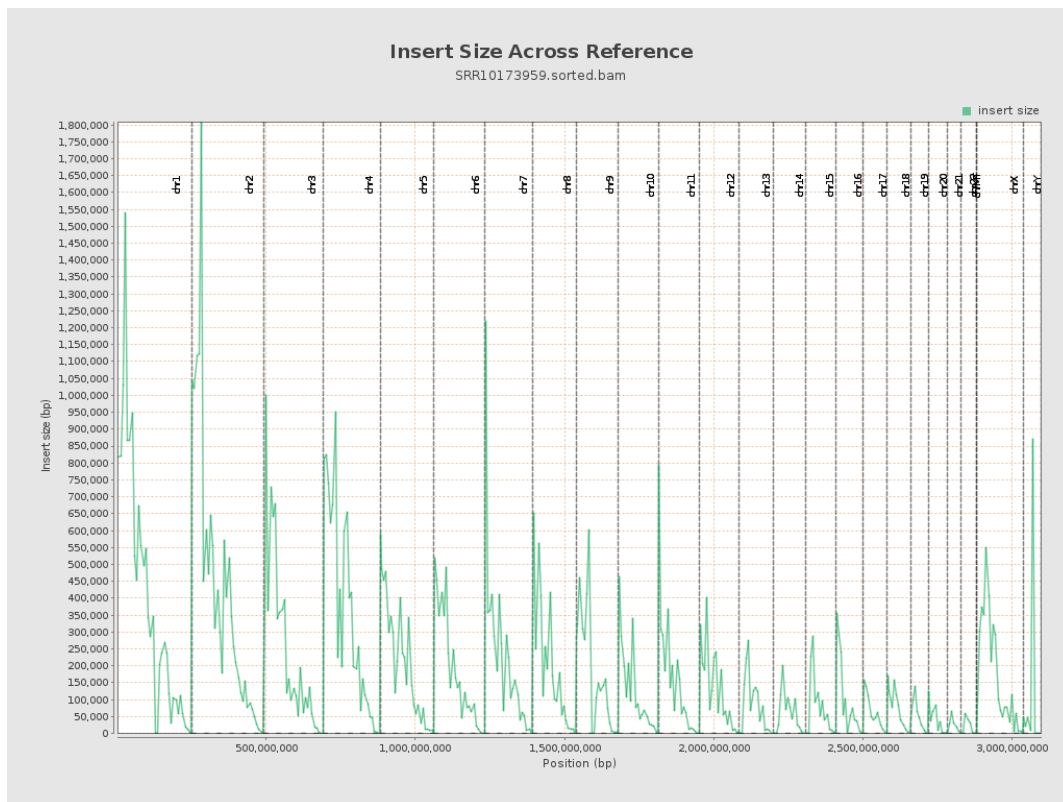
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

