

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 04:14:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173900.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_SRR10173900 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173900_1.fastq.gz SRR10173900_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 04:14:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173900.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,225,972
Mapped reads	7,060,286 / 97.71%
Unmapped reads	165,686 / 2.29%
Mapped paired reads	7,060,286 / 97.71%
Mapped reads, first in pair	3,532,787 / 48.89%
Mapped reads, second in pair	3,527,499 / 48.82%
Mapped reads, both in pair	6,950,104 / 96.18%
Mapped reads, singletons	110,182 / 1.52%
Secondary alignments	0
Supplementary alignments	649,089 / 8.98%
Read min/max/mean length	30 / 133 / 127.77
Duplicated reads (estimated)	5,663,525 / 78.38%
Duplication rate	67.75%
Clipped reads	2,652,774 / 36.71%

2.2. ACGT Content

Number/percentage of A's	251,960,824 / 30.11%
Number/percentage of C's	164,224,911 / 19.62%
Number/percentage of T's	251,693,066 / 30.07%
Number/percentage of G's	169,004,509 / 20.19%
Number/percentage of N's	10,198 / 0%

GC Percentage	39.82%
---------------	--------

2.3. Coverage

Mean	0.2705
Standard Deviation	3.6884

2.4. Mapping Quality

Mean Mapping Quality	52.92
----------------------	-------

2.5. Insert size

Mean	804,612.83
Standard Deviation	8,359,703.7
P25/Median/P75	145 / 200 / 284

2.6. Mismatches and indels

General error rate	1.01%
Mismatches	8,262,830
Insertions	84,690
Mapped reads with at least one insertion	1.16%
Deletions	179,192
Mapped reads with at least one deletion	2.48%
Homopolymer indels	43.42%

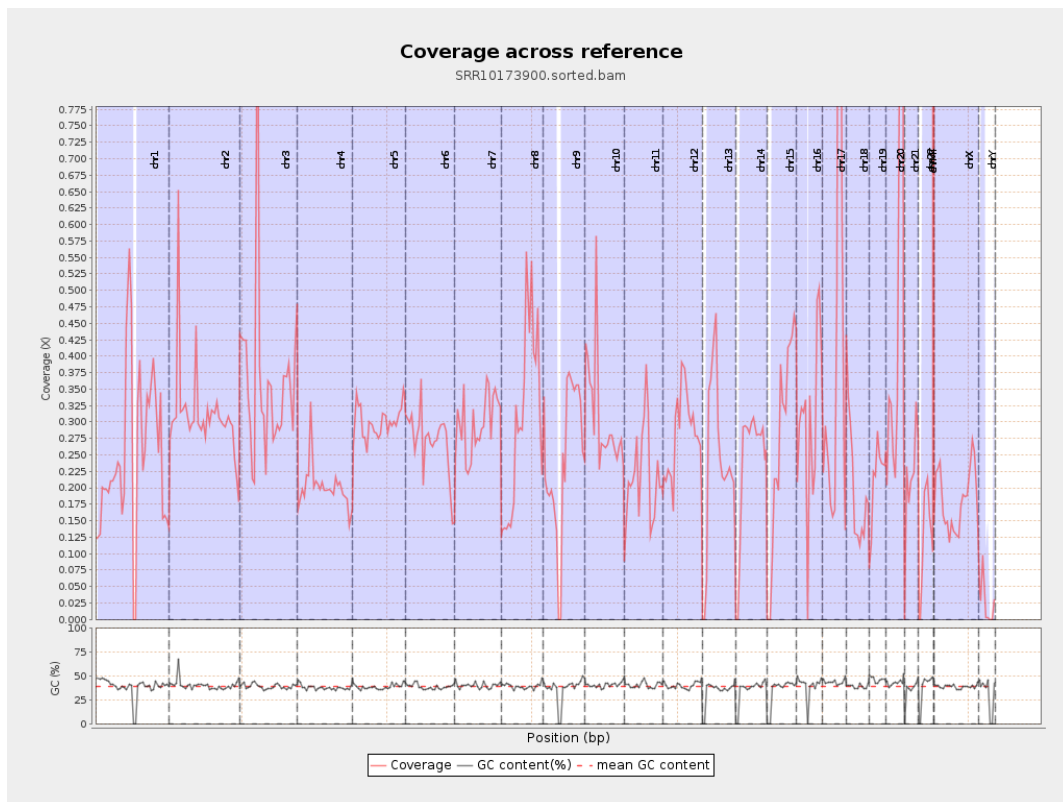
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

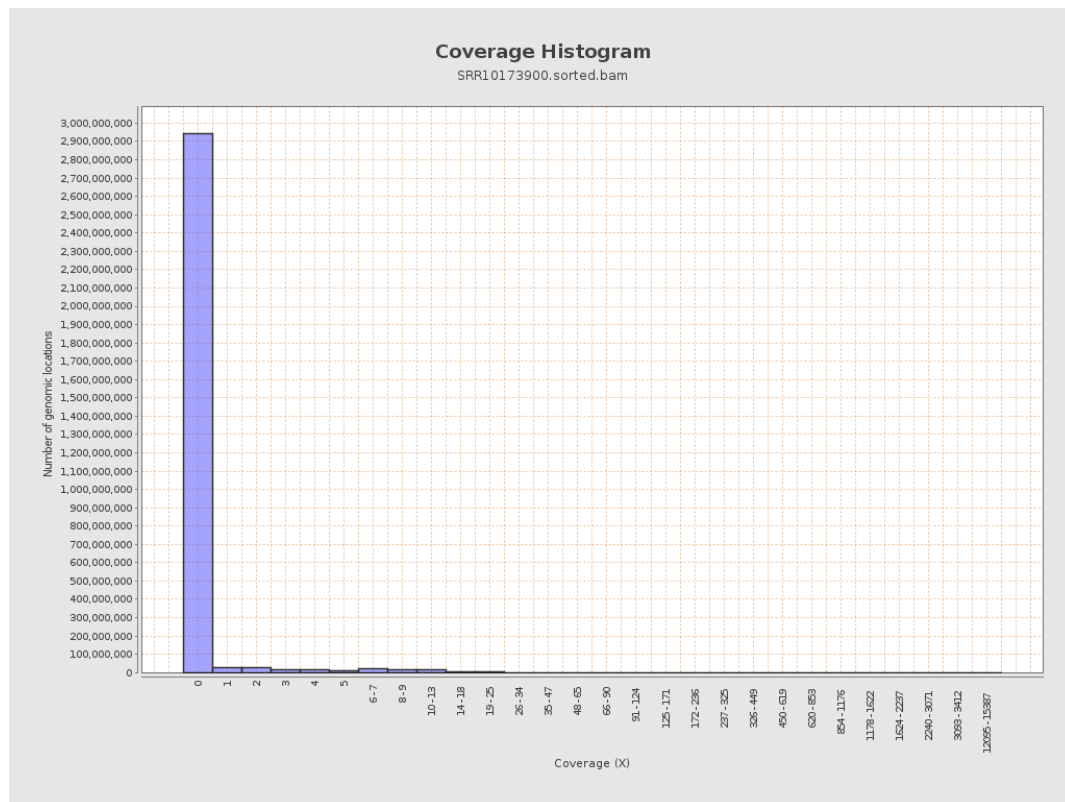
		bases	coverage	deviation
chr1	249250621	62347850	0.2501	2.815
chr2	243199373	75854917	0.3119	10.8552
chr3	198022430	70944268	0.3583	1.8489
chr4	191154276	38262095	0.2002	1.6996
chr5	180915260	54040500	0.2987	1.6478
chr6	171115067	46185056	0.2699	1.9274
chr7	159138663	47486494	0.2984	2.4223
chr8	146364022	44472586	0.3038	2.3163
chr9	141213431	33974664	0.2406	2.0969
chr10	135534747	41564344	0.3067	3.739
chr11	135006516	29545705	0.2188	1.4544
chr12	133851895	37841615	0.2827	1.6181
chr13	115169878	27397846	0.2379	1.4841
chr14	107349540	25378237	0.2364	1.4877
chr15	102531392	28186832	0.2749	1.5885
chr16	90354753	27672383	0.3063	2.2448
chr17	81195210	34124315	0.4203	2.2075
chr18	78077248	15564189	0.1993	3.409
chr19	59128983	12854128	0.2174	2.0656
chr20	63025520	34805115	0.5522	2.5447
chr21	48129895	10442409	0.217	1.5093
chr22	51304566	6196484	0.1208	1.0037
chrMT	16571	2461930	148.5686	117.5333
chrX	155270560	28249268	0.1819	1.2952

chrY	59373566	1480285	0.0249	0.9553
------	----------	---------	--------	--------

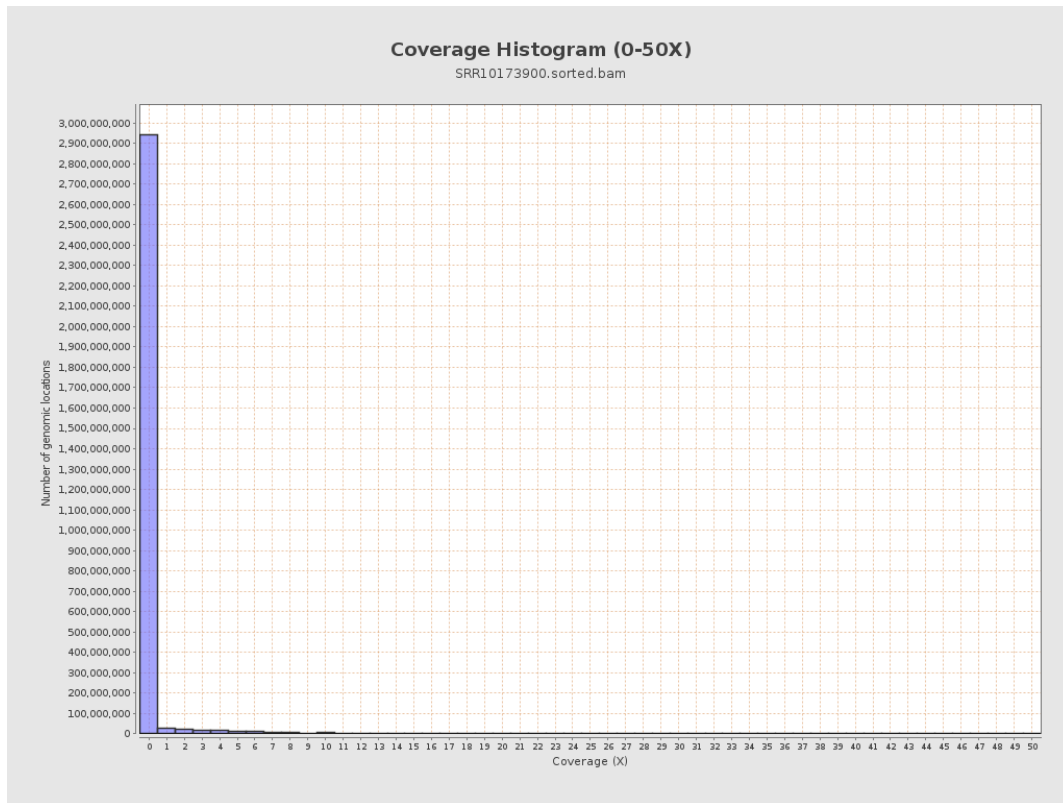
3. Results : Coverage across reference



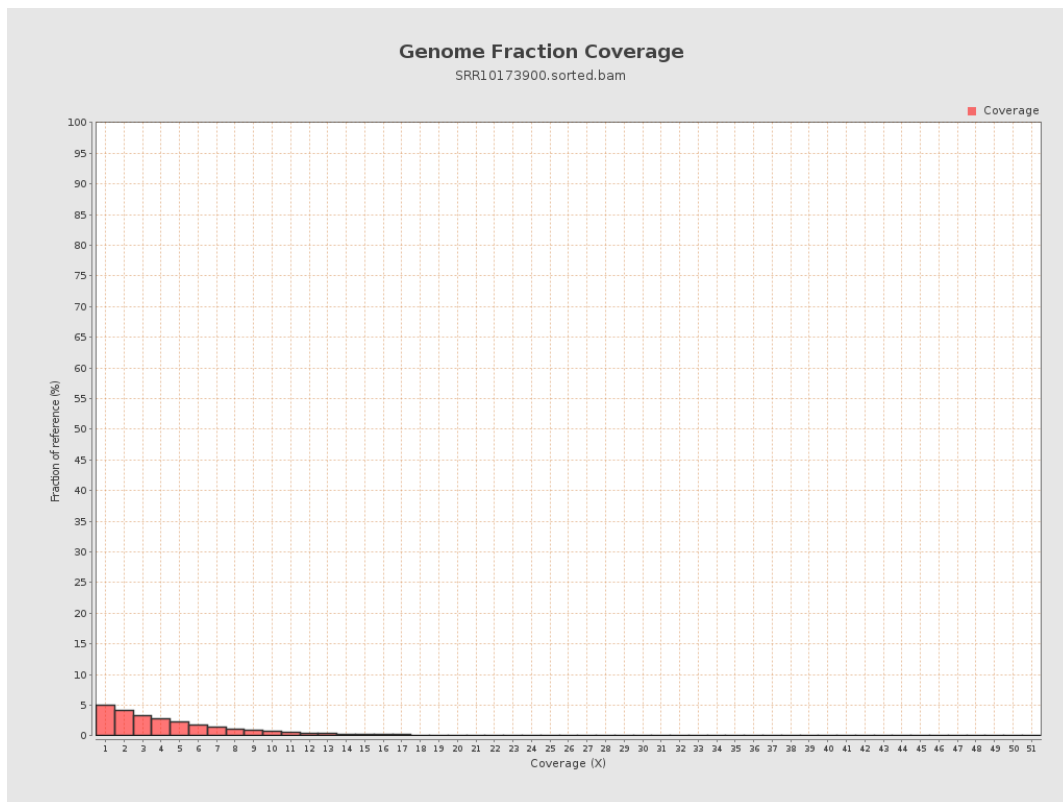
4. Results : Coverage Histogram



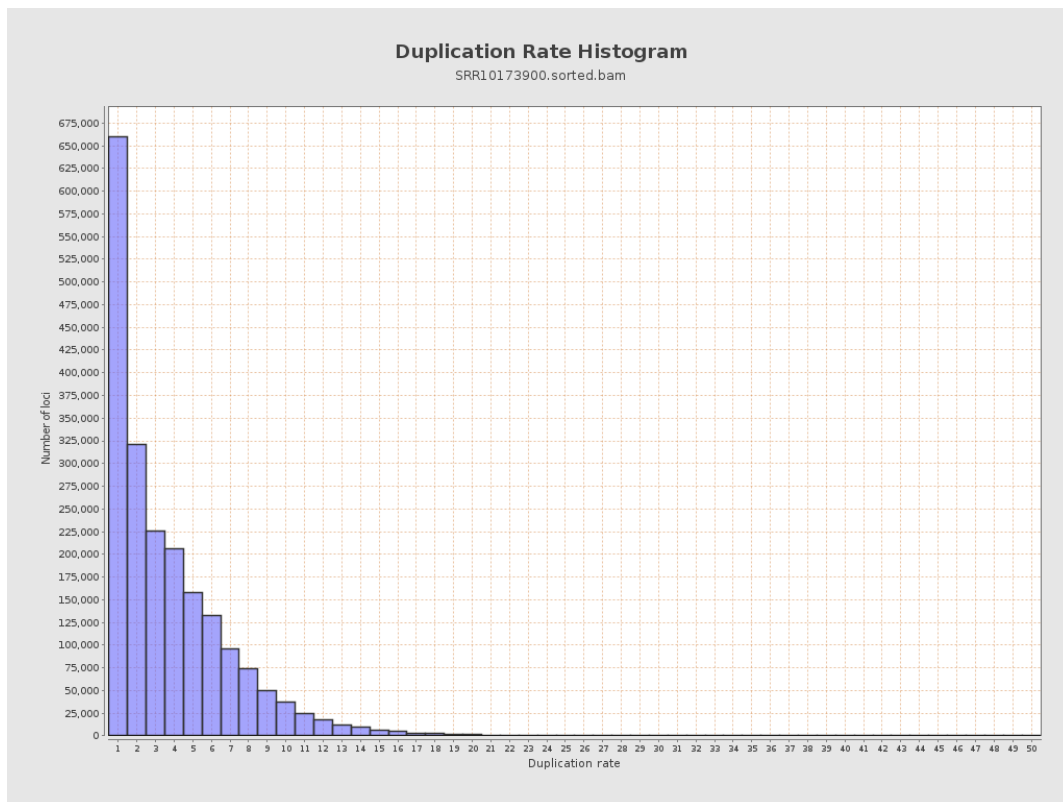
5. Results : Coverage Histogram (0-50X)



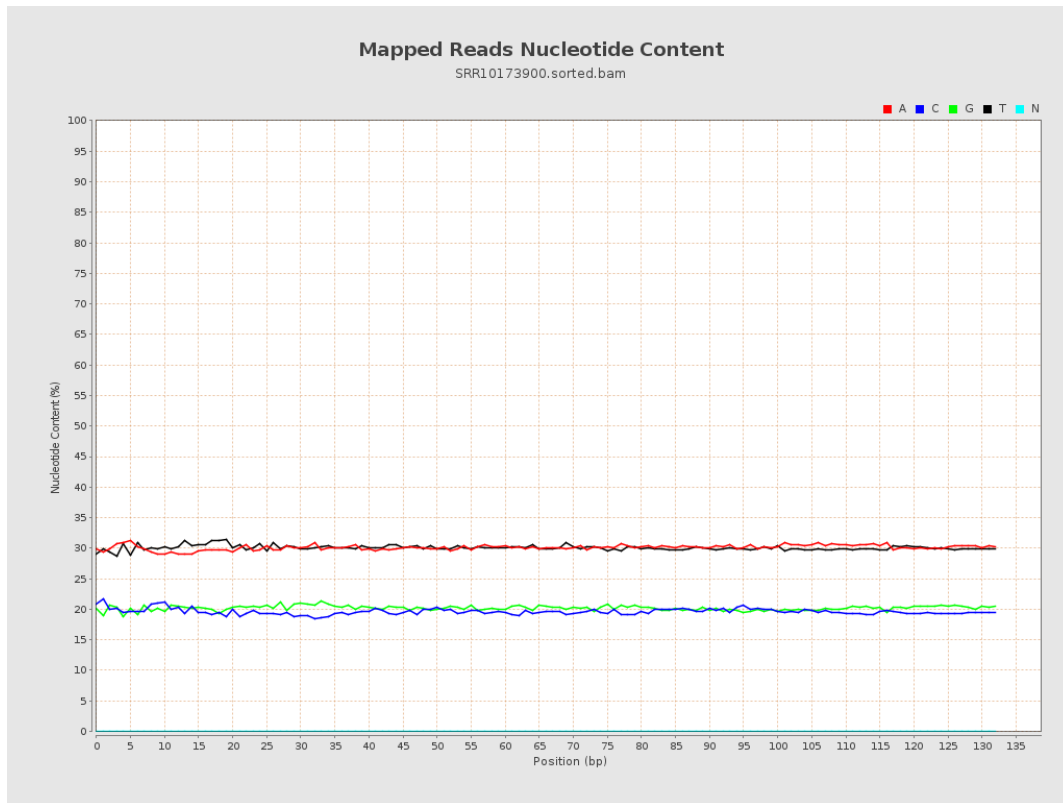
6. Results : Genome Fraction Coverage



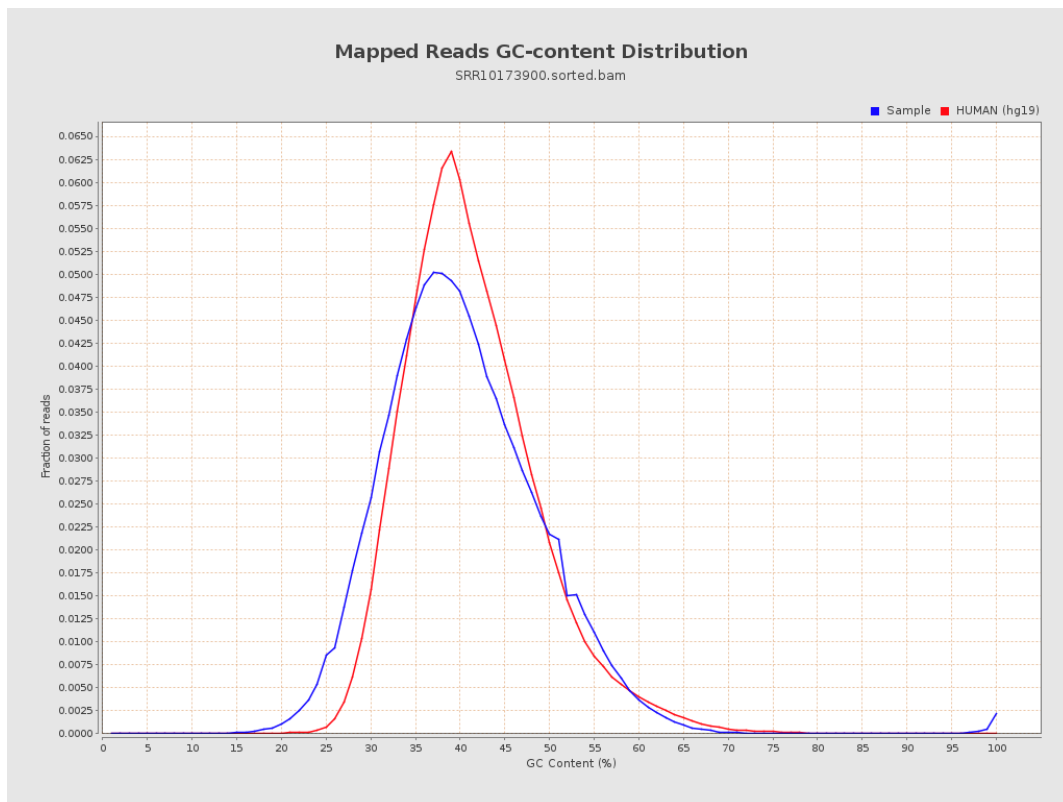
7. Results : Duplication Rate Histogram



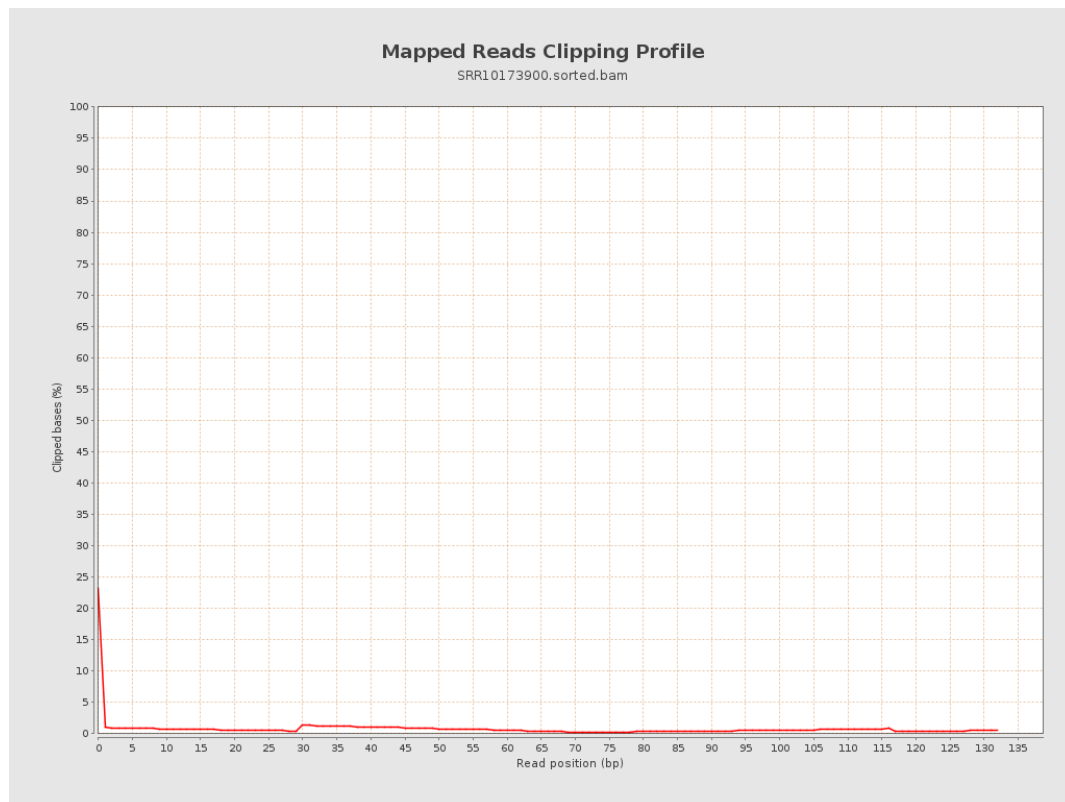
8. Results : Mapped Reads Nucleotide Content



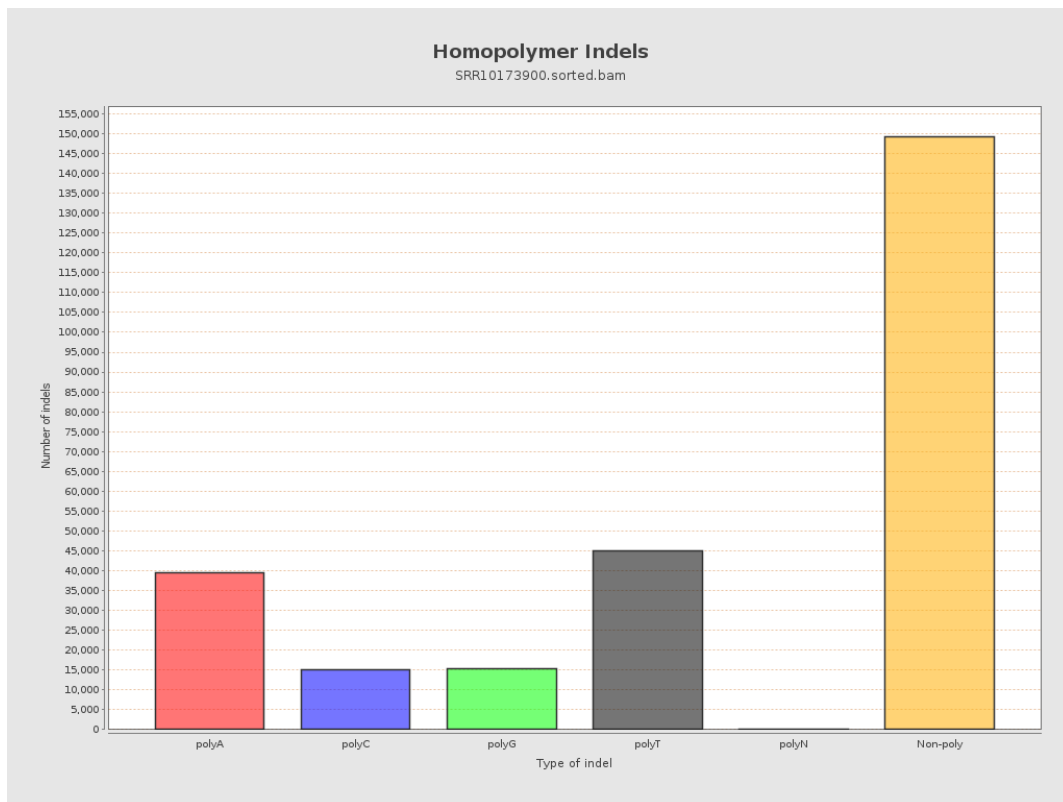
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



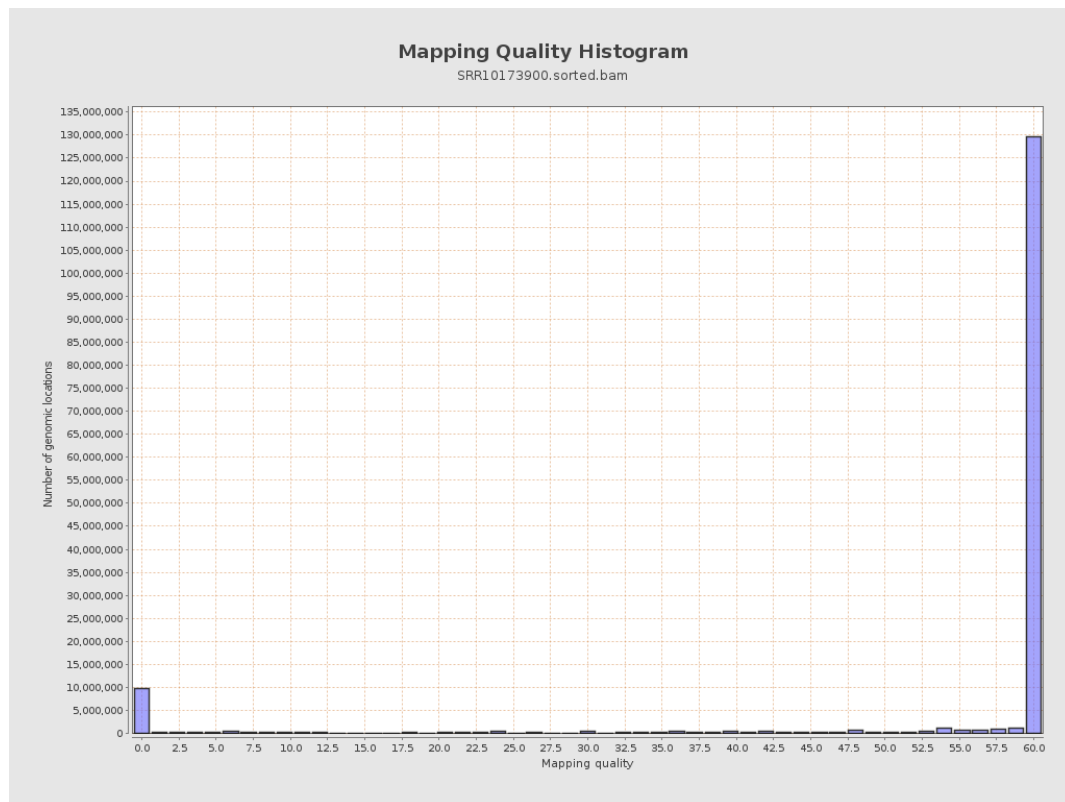
11. Results : Homopolymer Indels



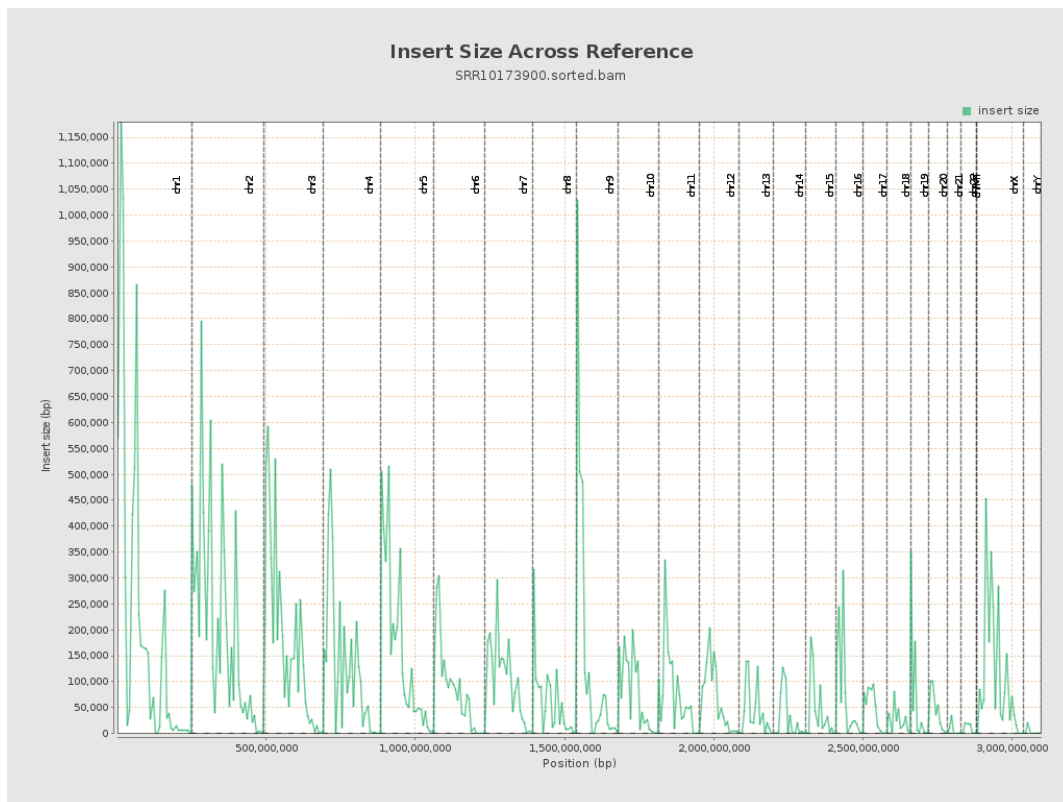
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

