

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 20:16:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR21672003.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_SRR21672003 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR21672003_1.fastq.gz SRR21672003_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 20:16:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR21672003.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	136,722,800
Mapped reads	103,652,859 / 75.81%
Unmapped reads	33,069,941 / 24.19%
Mapped paired reads	103,652,859 / 75.81%
Mapped reads, first in pair	51,834,238 / 37.91%
Mapped reads, second in pair	51,818,621 / 37.9%
Mapped reads, both in pair	102,811,590 / 75.2%
Mapped reads, singletons	841,269 / 0.62%
Secondary alignments	0
Supplementary alignments	2,666,357 / 1.95%
Read min/max/mean length	15 / 150 / 150.34
Duplicated reads (estimated)	39,076,003 / 28.58%
Duplication rate	28.53%
Clipped reads	61,963,343 / 45.32%

2.2. ACGT Content

Number/percentage of A's	3,750,753,298 / 27.08%
Number/percentage of C's	2,780,731,446 / 20.08%
Number/percentage of T's	4,104,901,690 / 29.64%
Number/percentage of G's	3,213,498,062 / 23.2%
Number/percentage of N's	48,975 / 0%

GC Percentage	43.28%
---------------	--------

2.3. Coverage

Mean	4.4773
Standard Deviation	99.4916

2.4. Mapping Quality

Mean Mapping Quality	52.93
----------------------	-------

2.5. Insert size

Mean	202,135.31
Standard Deviation	4,379,678.24
P25/Median/P75	235 / 289 / 342

2.6. Mismatches and indels

General error rate	1.36%
Mismatches	177,400,554
Insertions	3,180,506
Mapped reads with at least one insertion	2.83%
Deletions	4,366,444
Mapped reads with at least one deletion	4.02%
Homopolymer indels	43.38%

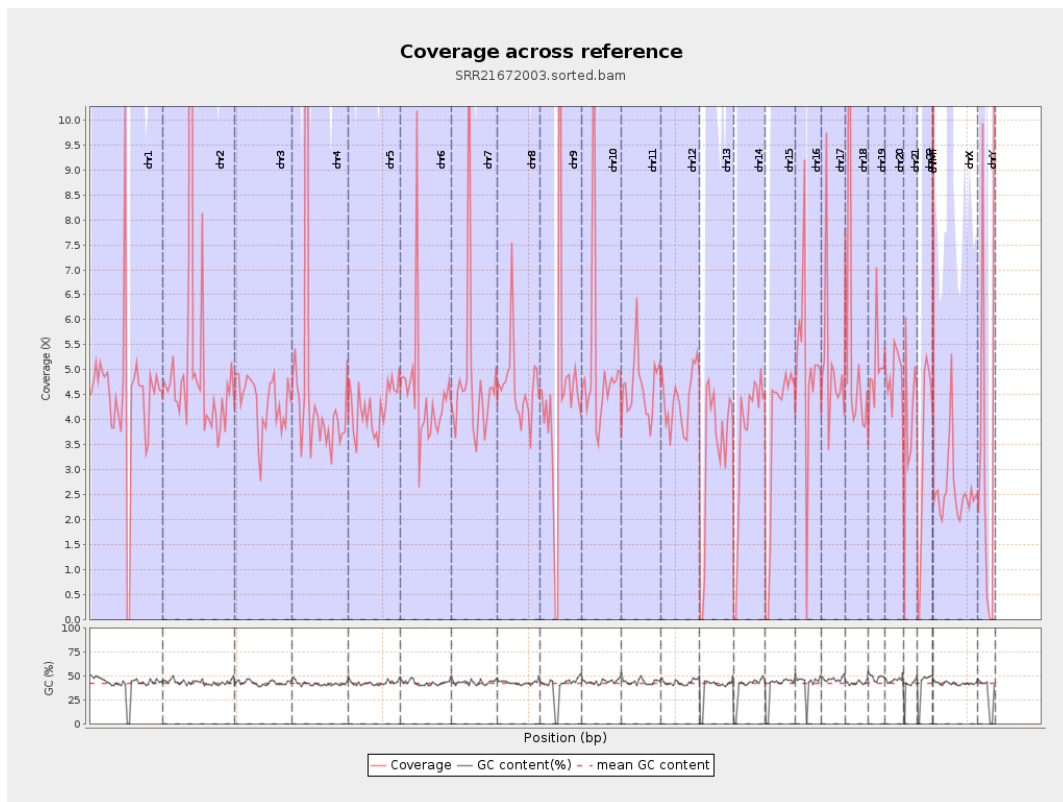
2.7. Chromosome stats

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

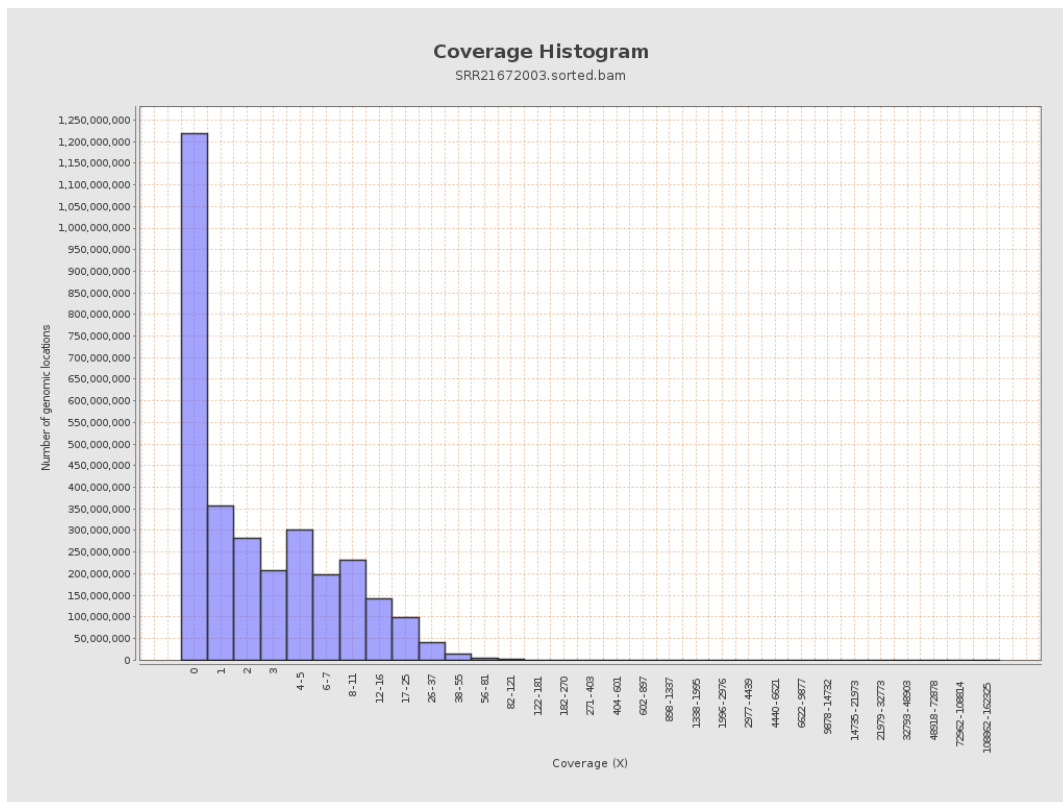
		bases	coverage	deviation
chr1	249250621	1111396008	4.4589	109.1115
chr2	243199373	1334148018	5.4858	157.0697
chr3	198022430	861630542	4.3512	7.663
chr4	191154276	940174862	4.9184	142.79
chr5	180915260	769493781	4.2533	9.3186
chr6	171115067	771975859	4.5114	71.7971
chr7	159138663	759293467	4.7713	126.0078
chr8	146364022	680930411	4.6523	33.7443
chr9	141213431	650335816	4.6053	224.3168
chr10	135534747	678524514	5.0063	64.9574
chr11	135006516	628179536	4.653	42.373
chr12	133851895	590970178	4.4151	9.5141
chr13	115169878	387959894	3.3686	6.9014
chr14	107349540	395980540	3.6887	11.1709
chr15	102531392	384011838	3.7453	7.2676
chr16	90354753	451371722	4.9956	50.631
chr17	81195210	415791441	5.1209	71.6559
chr18	78077248	447561156	5.7323	221.0178
chr19	59128983	299181429	5.0598	69.531
chr20	63025520	309355852	4.9084	40.7034
chr21	48129895	192441303	3.9984	57.7069
chr22	51304566	175712443	3.4249	11.313
chrMT	16571	4180002	252.248	260.601
chrX	155270560	403502708	2.5987	22.5148

chrY	59373566	216140974	3.6404	137.164
------	----------	-----------	--------	---------

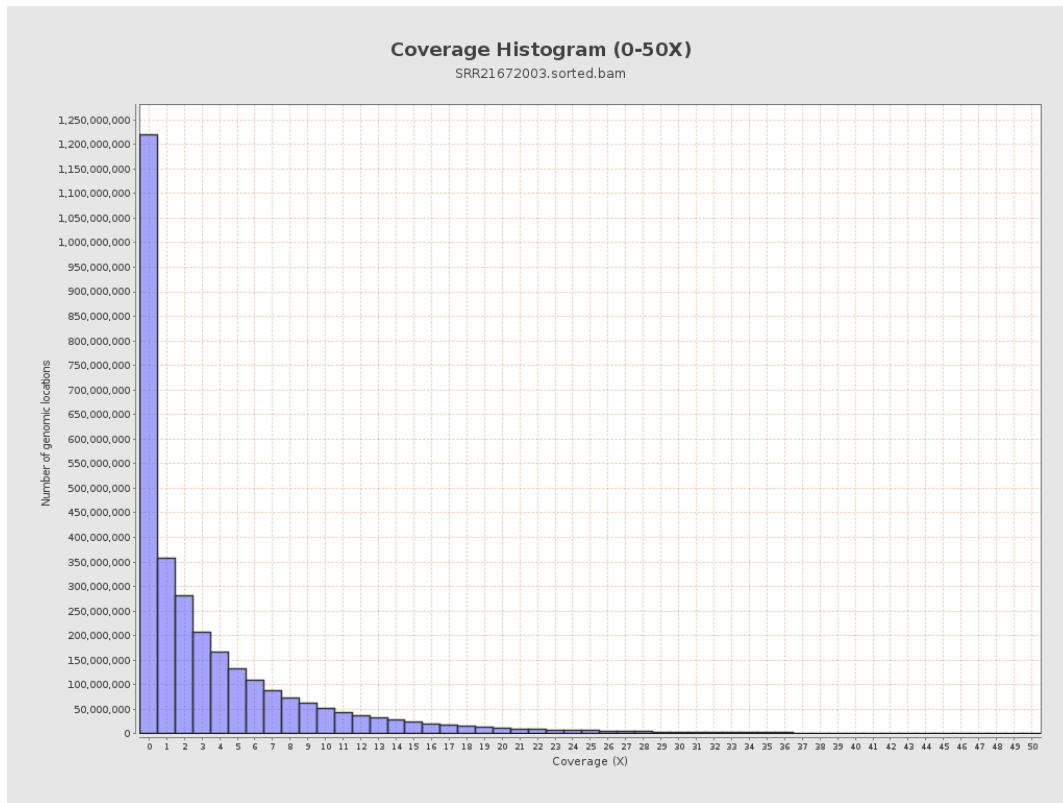
3. Results : Coverage across reference



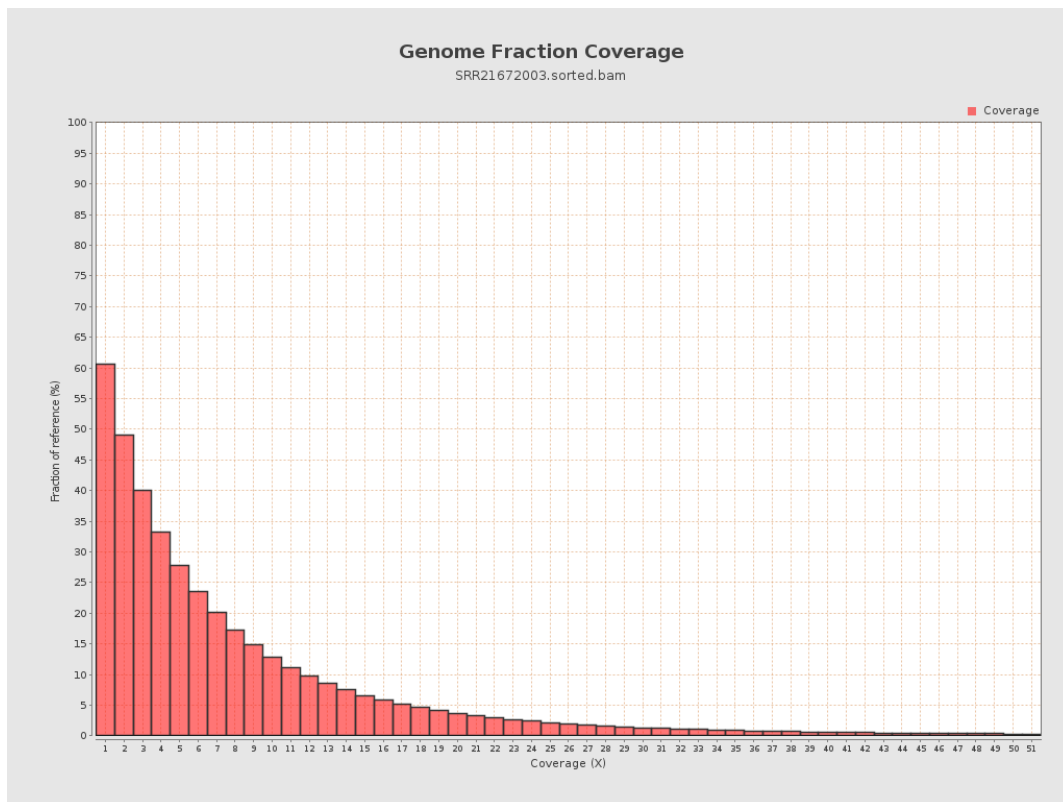
4. Results : Coverage Histogram



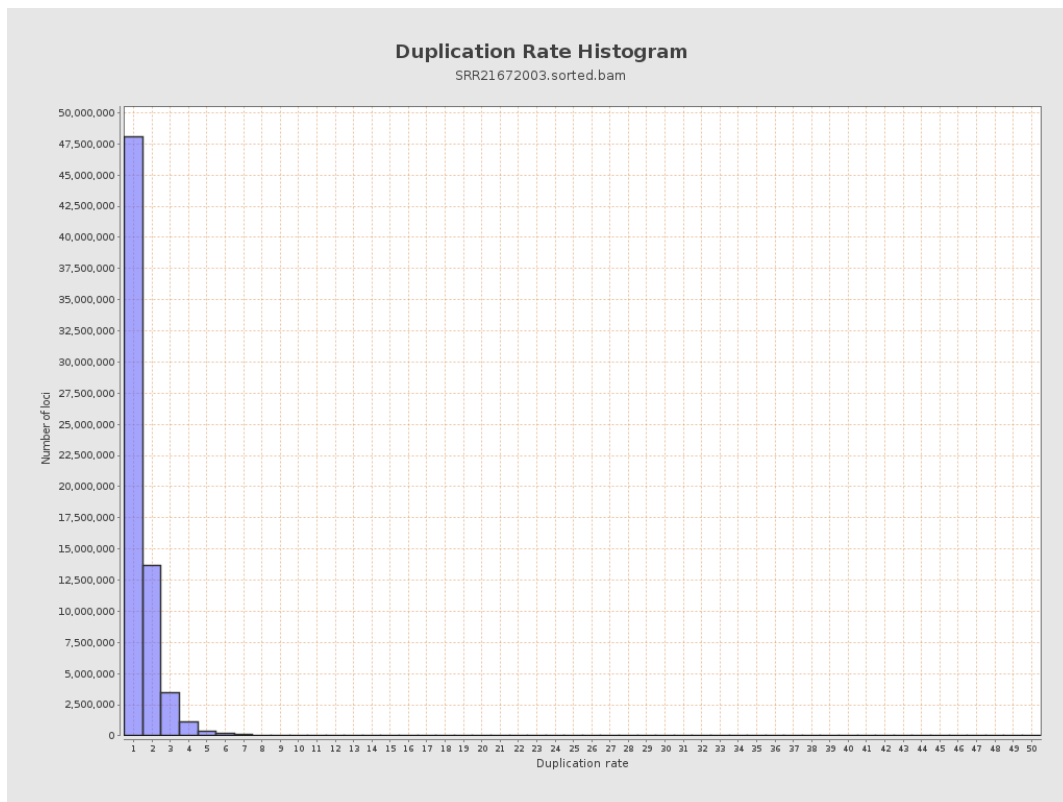
5. Results : Coverage Histogram (0-50X)



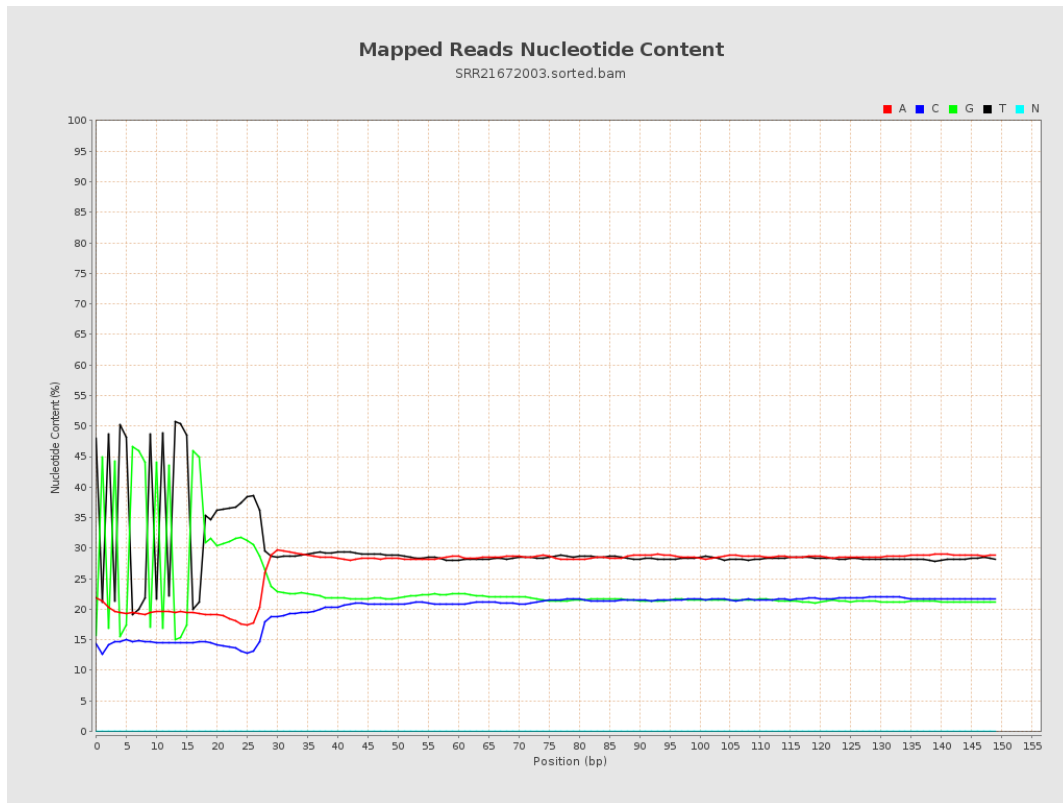
6. Results : Genome Fraction Coverage



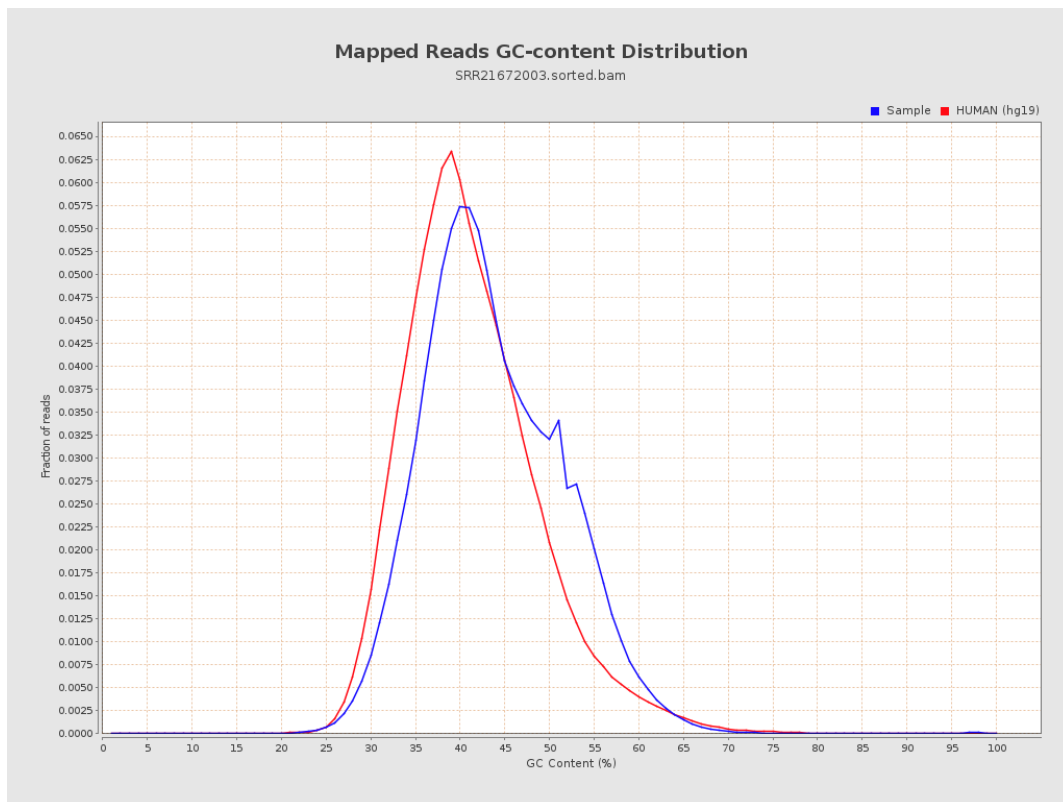
7. Results : Duplication Rate Histogram



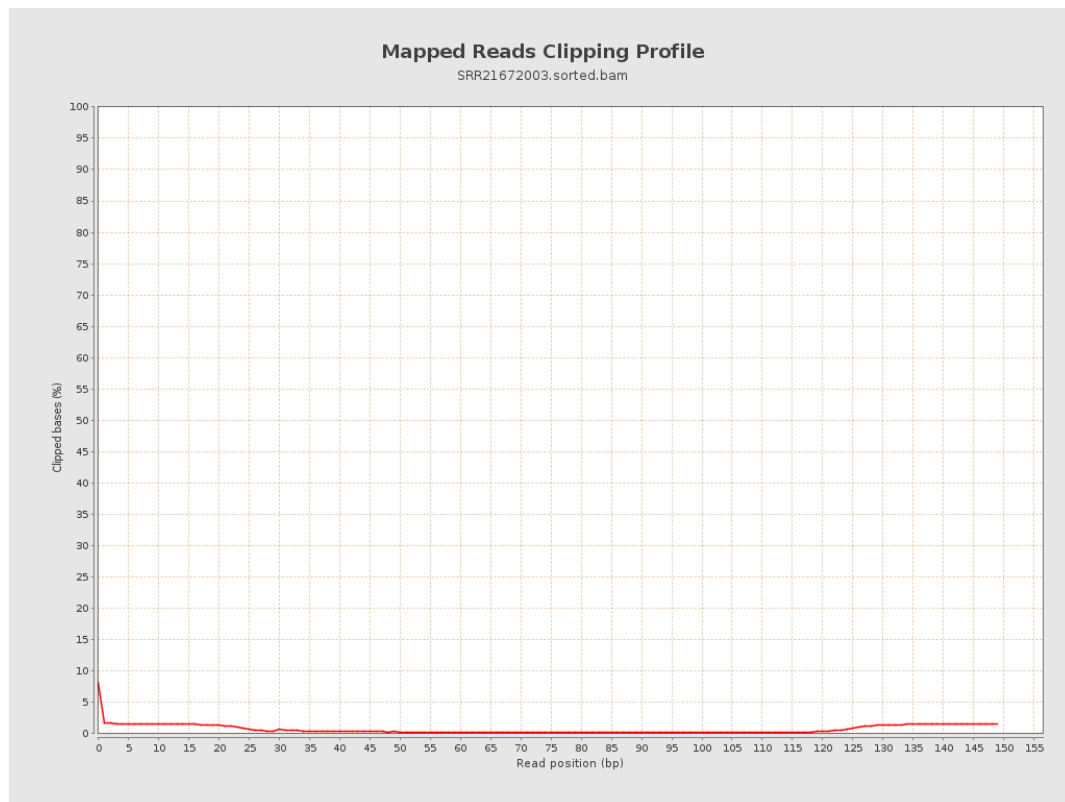
8. Results : Mapped Reads Nucleotide Content



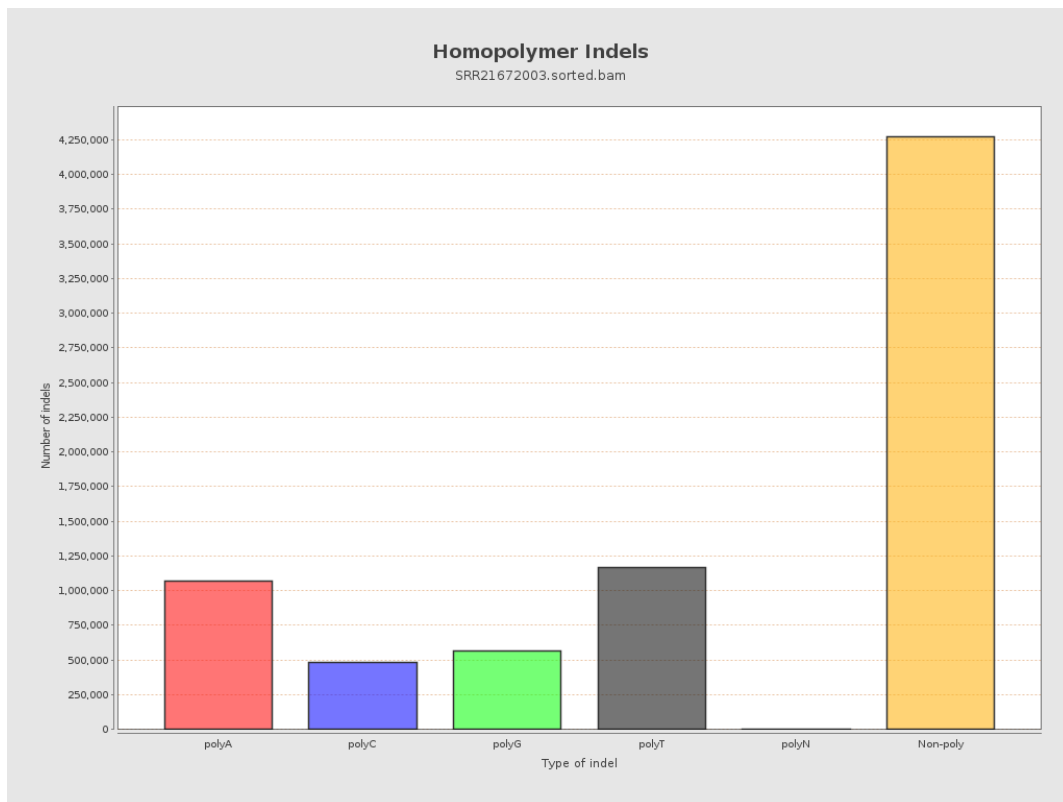
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



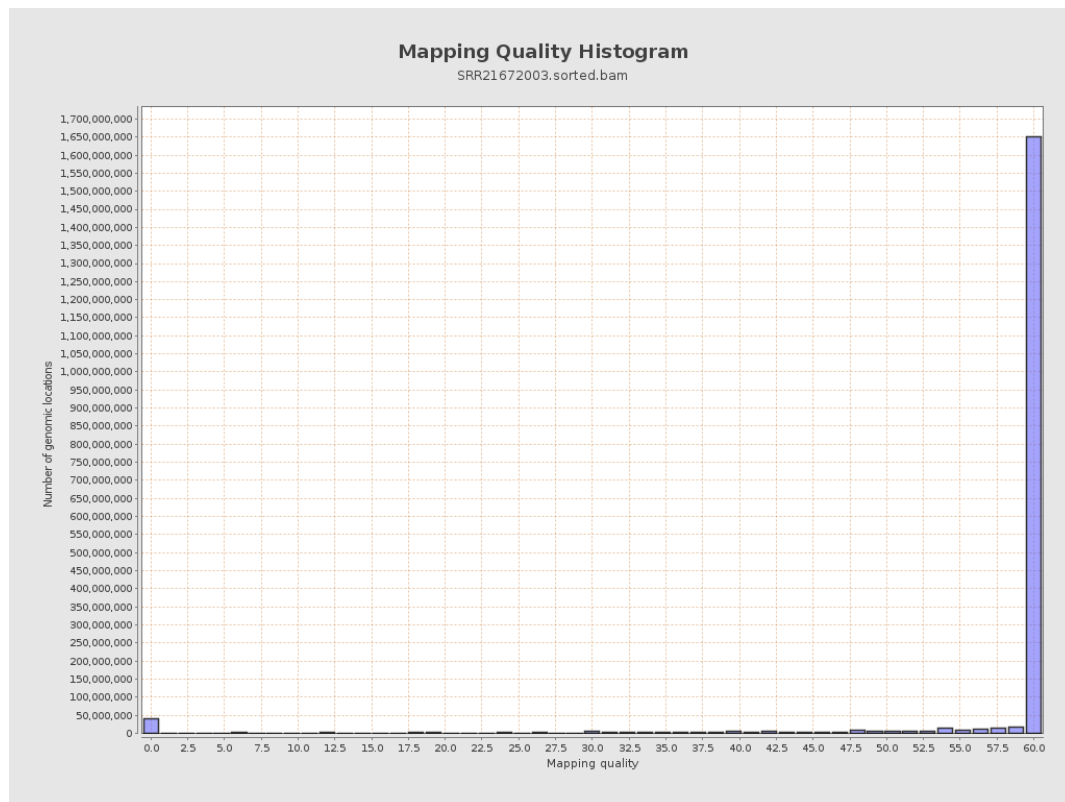
11. Results : Homopolymer Indels



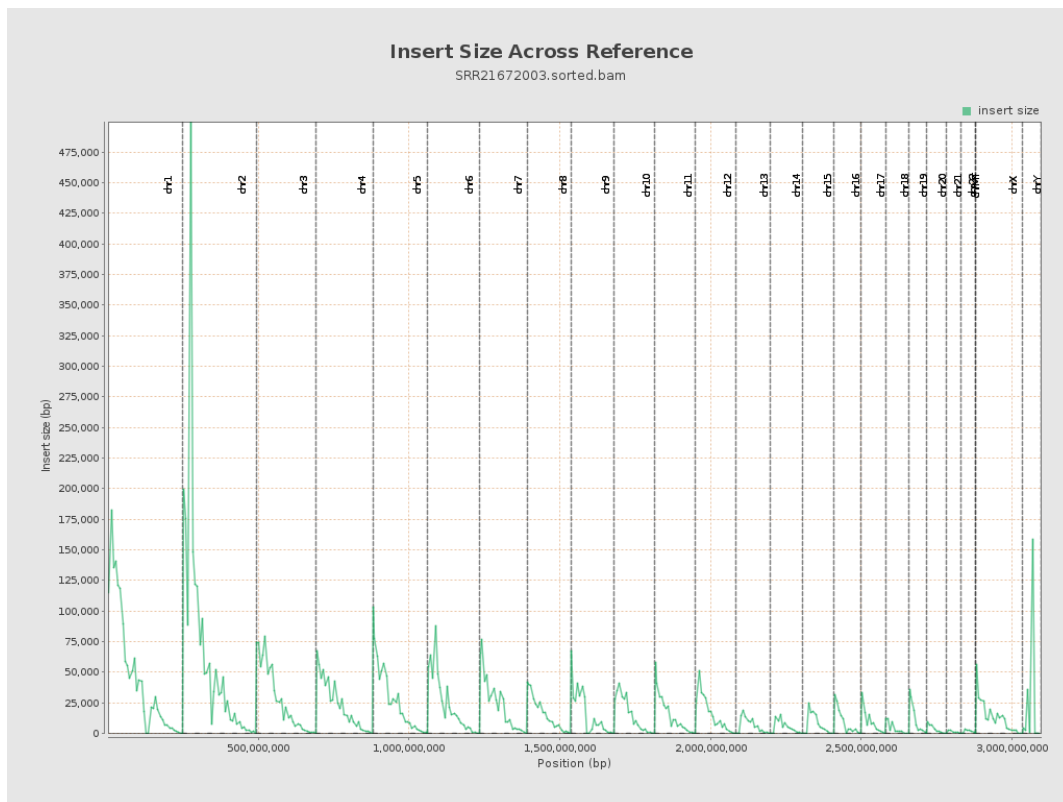
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

