

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 08:36:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR21672000.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_SRR21672000 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR21672000_1.fastq.gz SRR21672000_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 08:36:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR21672000.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	309,374,548
Mapped reads	307,917,902 / 99.53%
Unmapped reads	1,456,646 / 0.47%
Mapped paired reads	307,917,902 / 99.53%
Mapped reads, first in pair	154,007,893 / 49.78%
Mapped reads, second in pair	153,910,009 / 49.75%
Mapped reads, both in pair	307,377,032 / 99.35%
Mapped reads, singletons	540,870 / 0.17%
Secondary alignments	0
Supplementary alignments	1,404,584 / 0.45%
Read min/max/mean length	15 / 150 / 149.71
Duplicated reads (estimated)	90,364,861 / 29.21%
Duplication rate	26.47%
Clipped reads	15,968,149 / 5.16%

2.2. ACGT Content

Number/percentage of A's	13,360,190,265 / 29.28%
Number/percentage of C's	9,485,477,586 / 20.79%
Number/percentage of T's	13,285,787,116 / 29.12%
Number/percentage of G's	9,492,286,592 / 20.81%
Number/percentage of N's	225,974 / 0%

GC Percentage	41.6%
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2.3. Coverage

Mean	14.7438
Standard Deviation	143.2335

2.4. Mapping Quality

Mean Mapping Quality	54.56
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2.5. Insert size

Mean	60,183.35
Standard Deviation	2,354,244.1
P25/Median/P75	285 / 331 / 375

2.6. Mismatches and indels

General error rate	0.69%
Mismatches	298,497,082
Insertions	6,131,167
Mapped reads with at least one insertion	1.89%
Deletions	6,642,993
Mapped reads with at least one deletion	2.07%
Homopolymer indels	45.65%

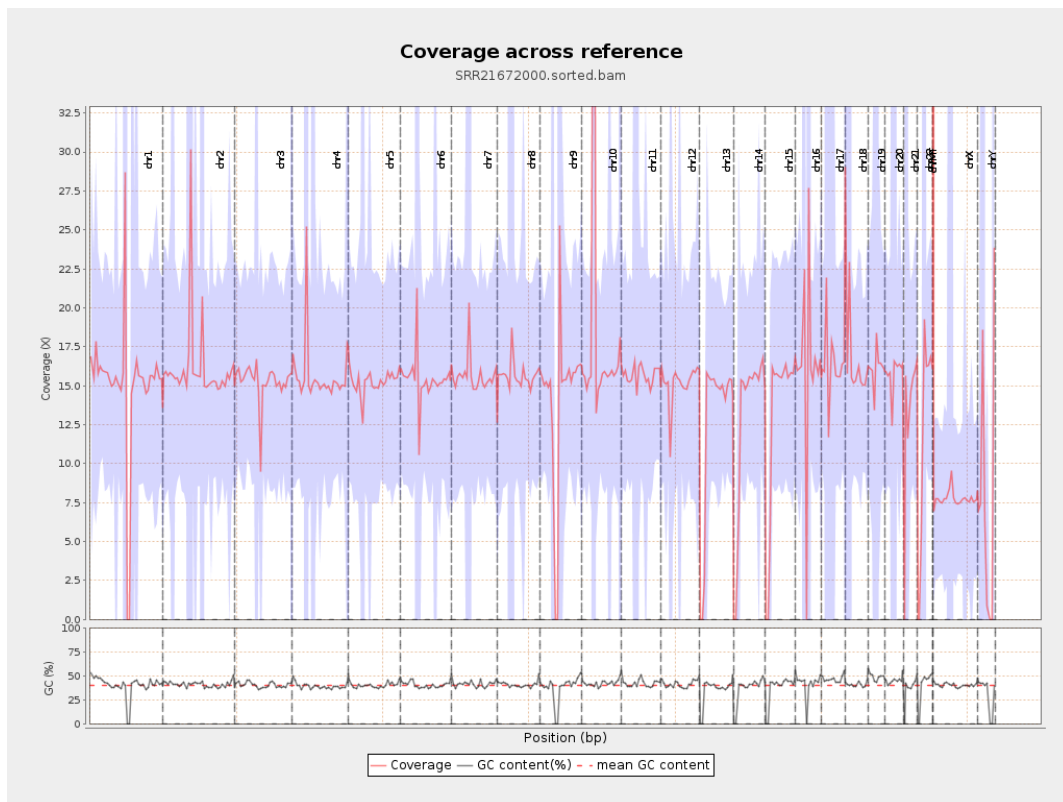
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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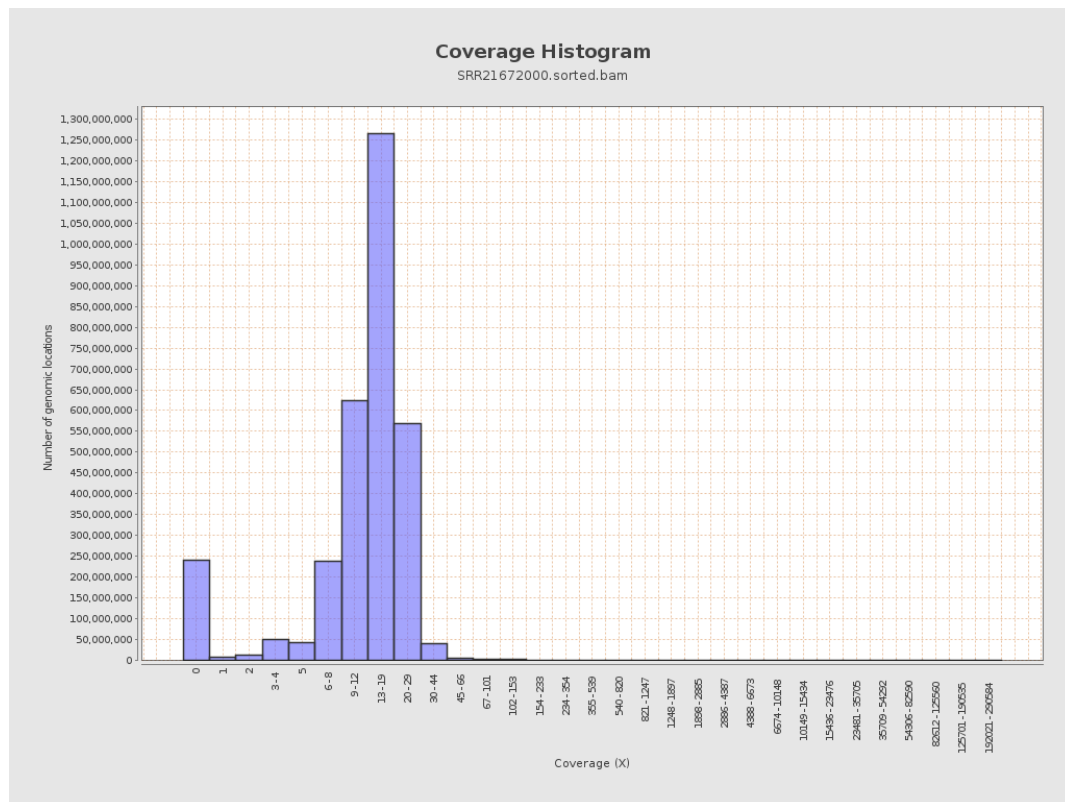
		bases	coverage	deviation
chr1	249250621	3752931120	15.0569	300.8707
chr2	243199373	3921464748	16.1245	89.4948
chr3	198022430	3021137947	15.2565	10.227
chr4	191154276	2990262807	15.6432	98.2297
chr5	180915260	2759289991	15.2518	12.4608
chr6	171115067	2637880641	15.4158	71.4616
chr7	159138663	2494172424	15.673	120.7607
chr8	146364022	2289209280	15.6405	95.1858
chr9	141213431	2003497016	14.1877	223.1333
chr10	135534747	2425569364	17.8963	347.5857
chr11	135006516	2114566592	15.6627	62.261
chr12	133851895	2033966121	15.1956	11.1429
chr13	115169878	1456363916	12.6454	8.6423
chr14	107349540	1396482800	13.0087	10.6382
chr15	102531392	1317469257	12.8494	8.9634
chr16	90354753	1473461057	16.3075	99.8628
chr17	81195210	1330463670	16.386	77.4218
chr18	78077248	1312259217	16.8072	227.8876
chr19	59128983	953755277	16.1301	133.7632
chr20	63025520	987599501	15.6698	36.4921
chr21	48129895	650455480	13.5146	67.0972
chr22	51304566	606461500	11.8208	69.127
chrMT	16571	31977728	1,929.7404	242.2272
chrX	155270560	1205086645	7.7612	25.0987

chrY	59373566	476401606	8.0238	153.0152
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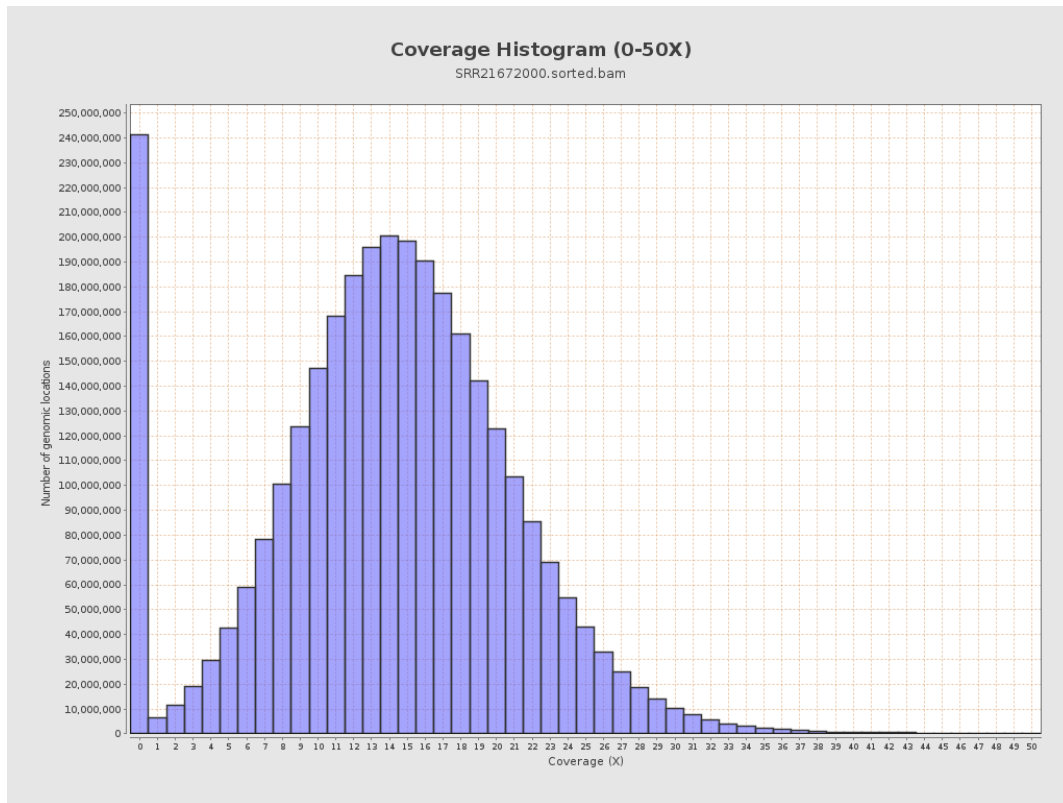
3. Results : Coverage across reference



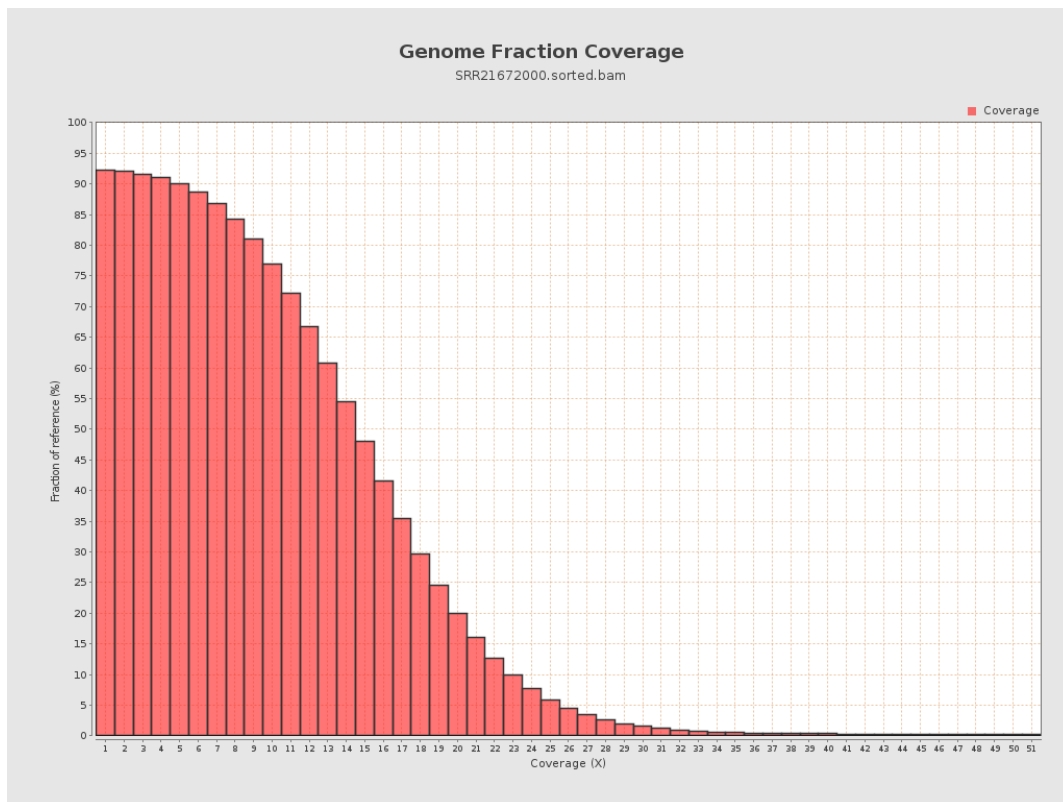
4. Results : Coverage Histogram



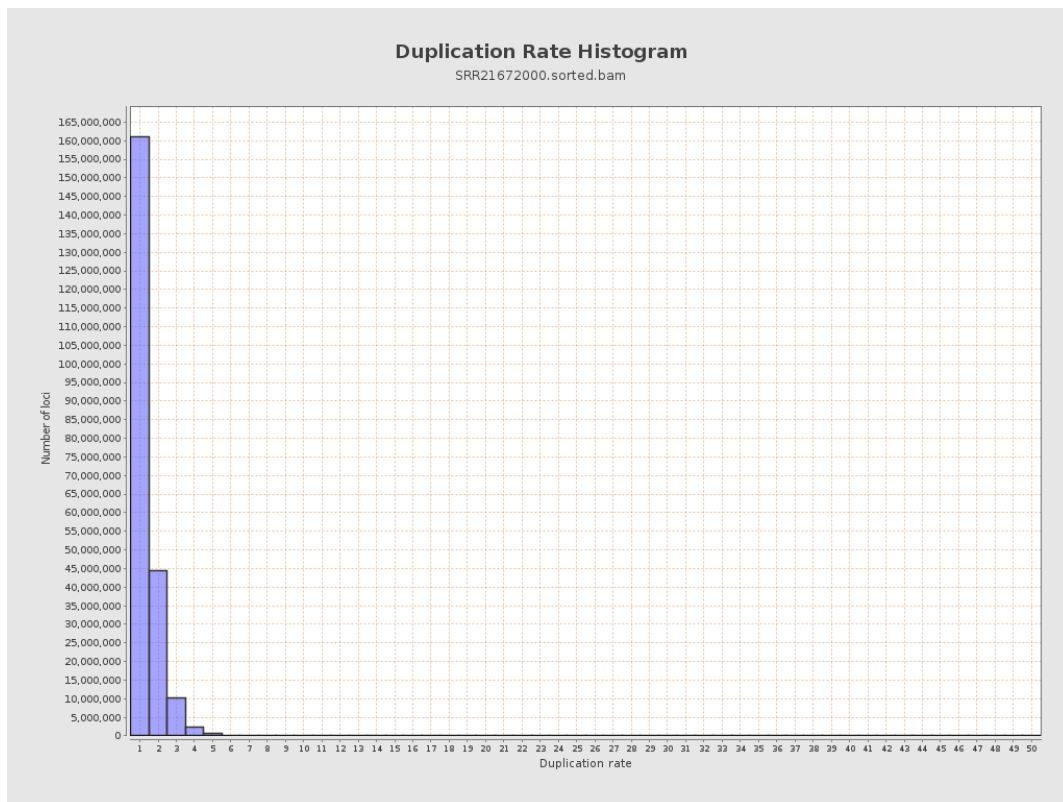
5. Results : Coverage Histogram (0-50X)



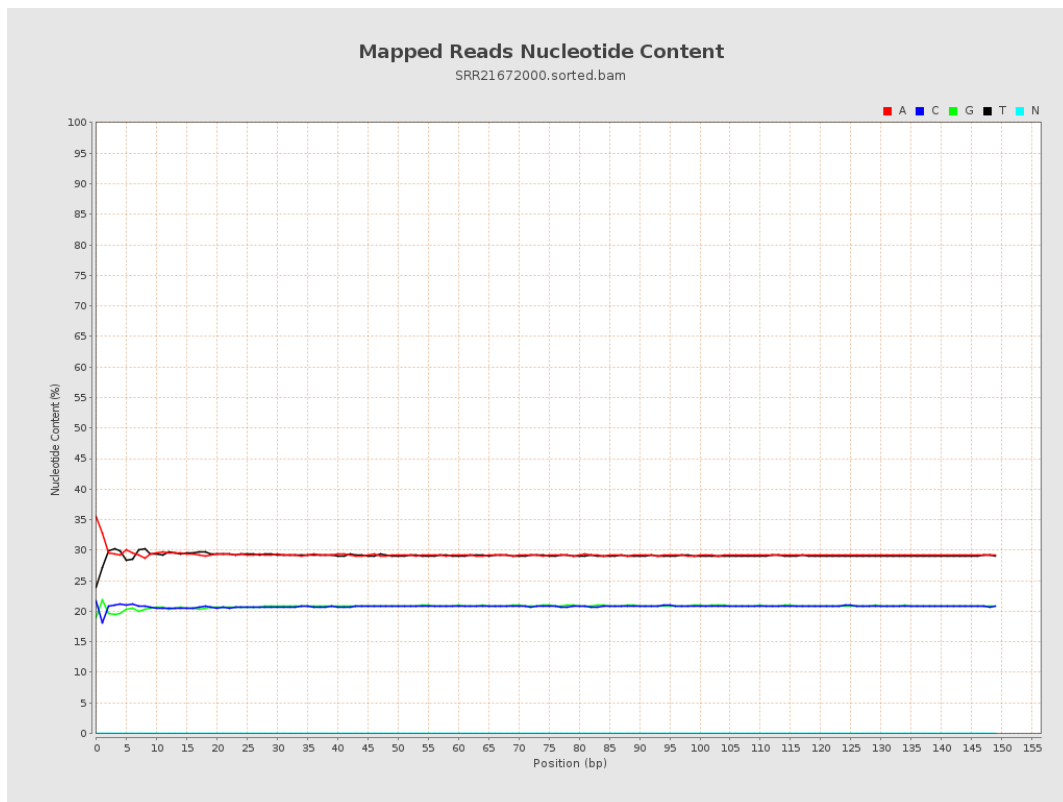
6. Results : Genome Fraction Coverage



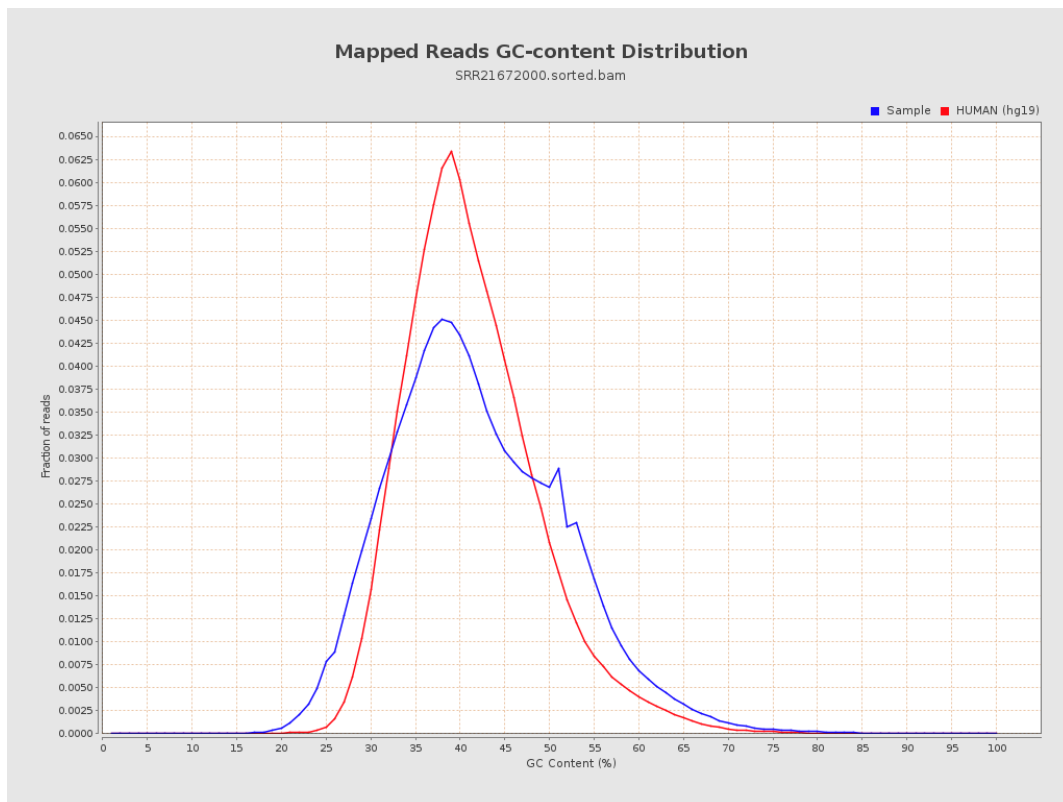
7. Results : Duplication Rate Histogram



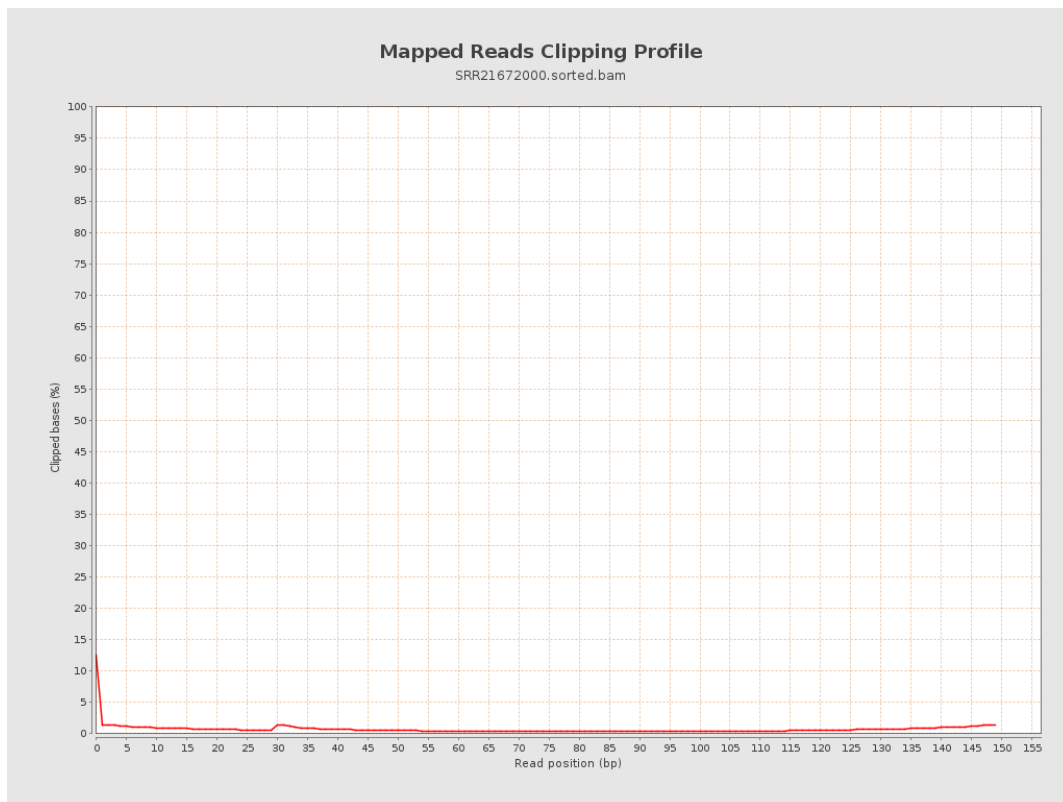
8. Results : Mapped Reads Nucleotide Content



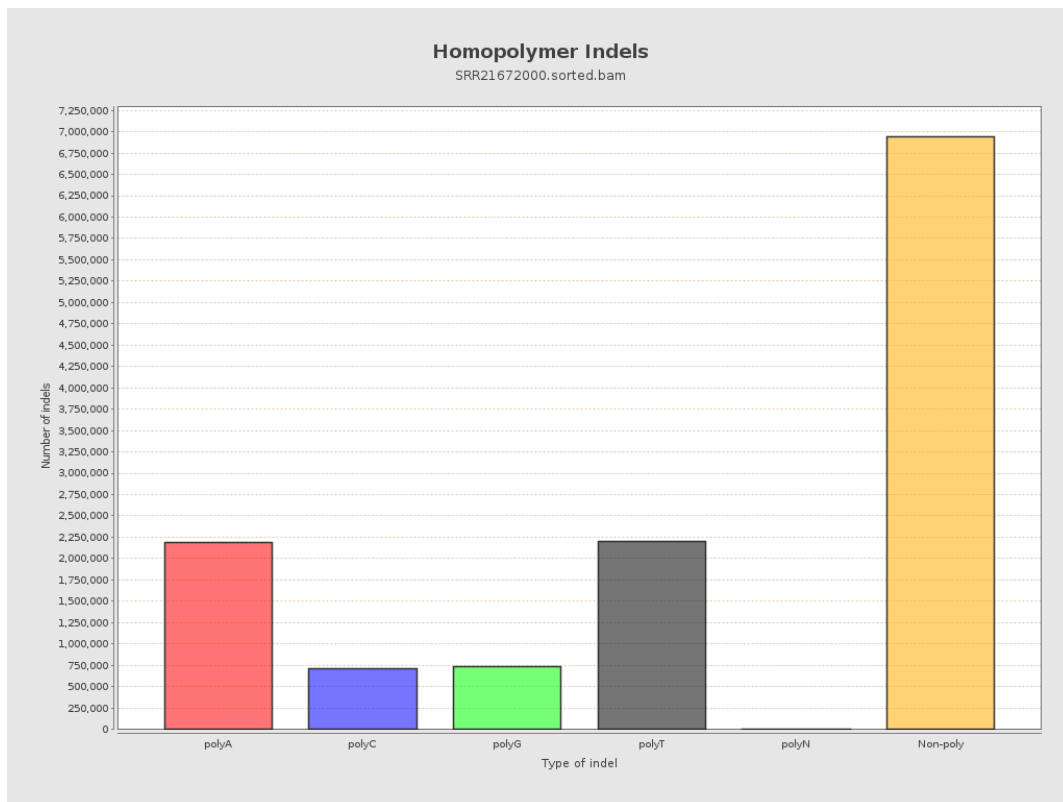
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



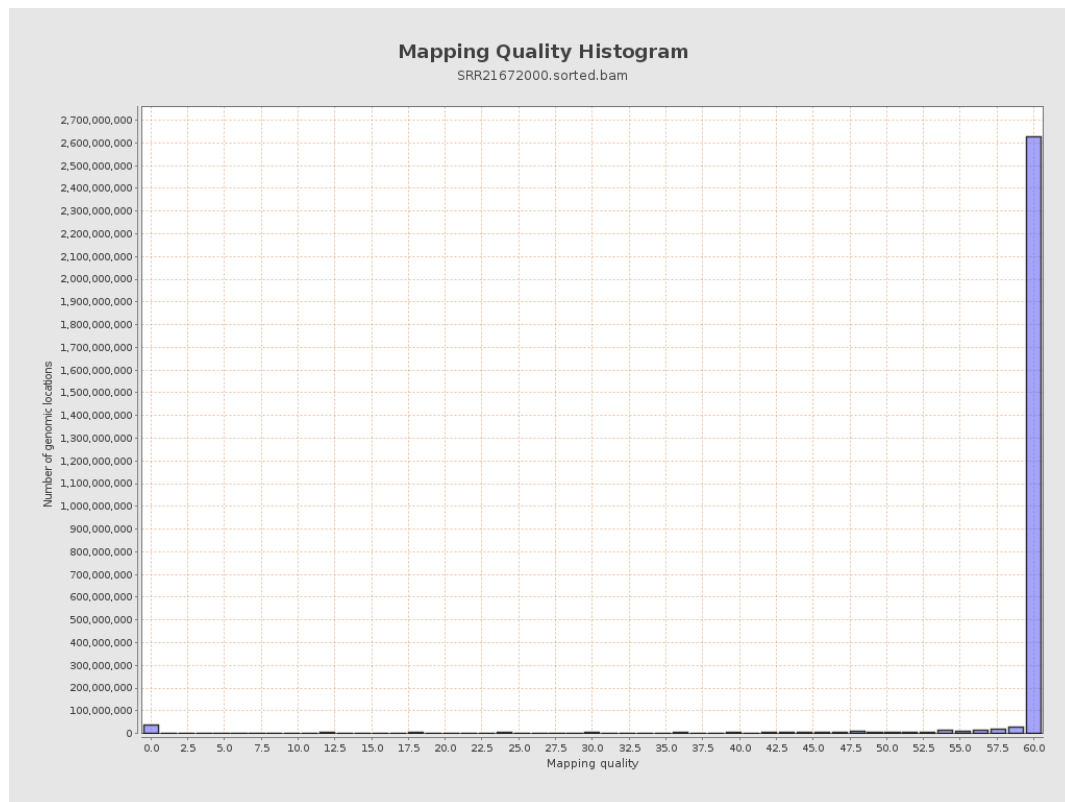
11. Results : Homopolymer Indels



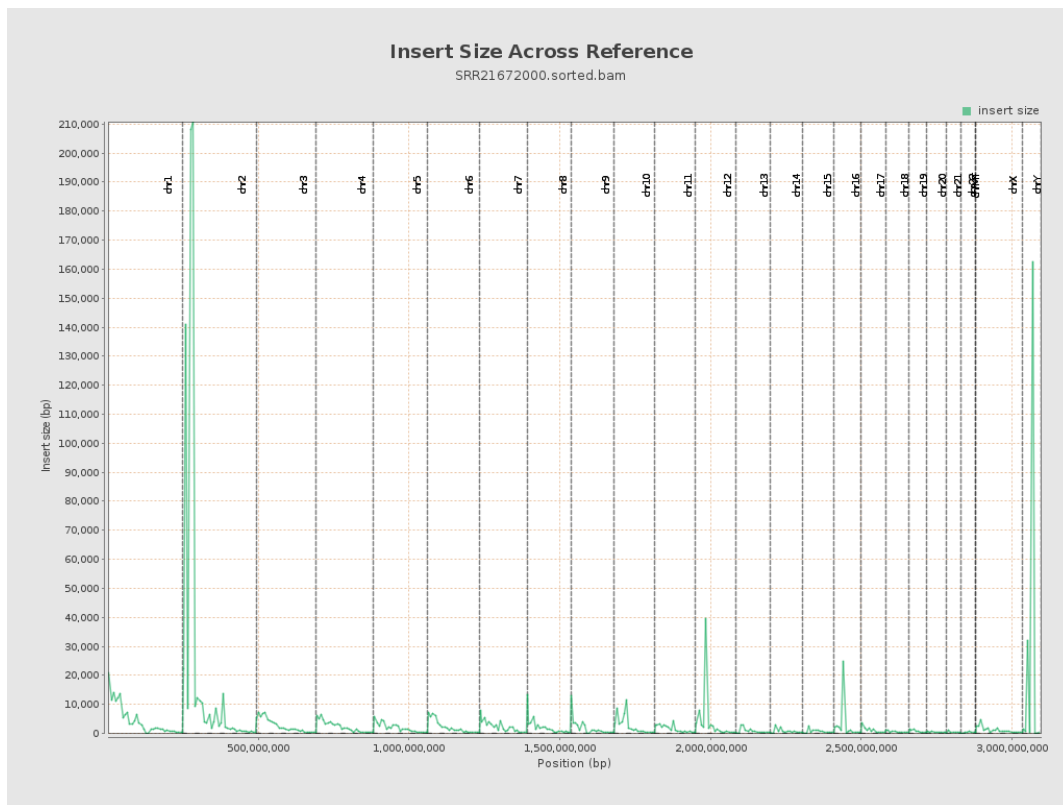
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

