

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 06:18:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR21671997.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_SRR21671997 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR21671997_1.fastq.gz SRR21671997_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 06:18:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR21671997.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	303,531,990
Mapped reads	294,873,216 / 97.15%
Unmapped reads	8,658,774 / 2.85%
Mapped paired reads	294,873,216 / 97.15%
Mapped reads, first in pair	147,468,611 / 48.58%
Mapped reads, second in pair	147,404,605 / 48.56%
Mapped reads, both in pair	294,358,612 / 96.98%
Mapped reads, singletons	514,604 / 0.17%
Secondary alignments	0
Supplementary alignments	1,226,045 / 0.4%
Read min/max/mean length	15 / 150 / 149.8
Duplicated reads (estimated)	109,450,257 / 36.06%
Duplication rate	34.82%
Clipped reads	13,623,789 / 4.49%

2.2. ACGT Content

Number/percentage of A's	12,775,152,958 / 29.2%
Number/percentage of C's	9,130,386,868 / 20.87%
Number/percentage of T's	12,672,062,638 / 28.97%
Number/percentage of G's	9,171,358,709 / 20.96%
Number/percentage of N's	373,764 / 0%

GC Percentage	41.83%
---------------	--------

2.3. Coverage

Mean	14.1381
Standard Deviation	140.7622

2.4. Mapping Quality

Mean Mapping Quality	54.58
----------------------	-------

2.5. Insert size

Mean	25,913.33
Standard Deviation	1,483,254.29
P25/Median/P75	269 / 307 / 348

2.6. Mismatches and indels

General error rate	0.69%
Mismatches	286,344,297
Insertions	5,977,147
Mapped reads with at least one insertion	1.92%
Deletions	6,535,511
Mapped reads with at least one deletion	2.13%
Homopolymer indels	45.76%

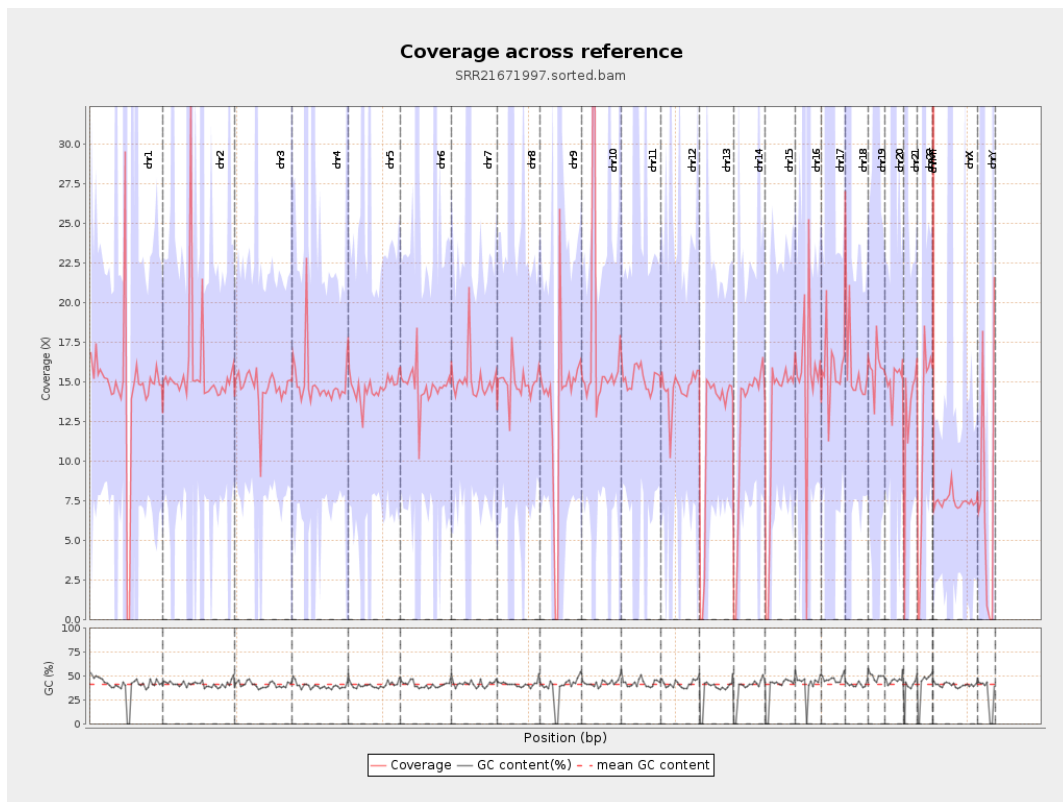
2.7. Chromosome stats

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

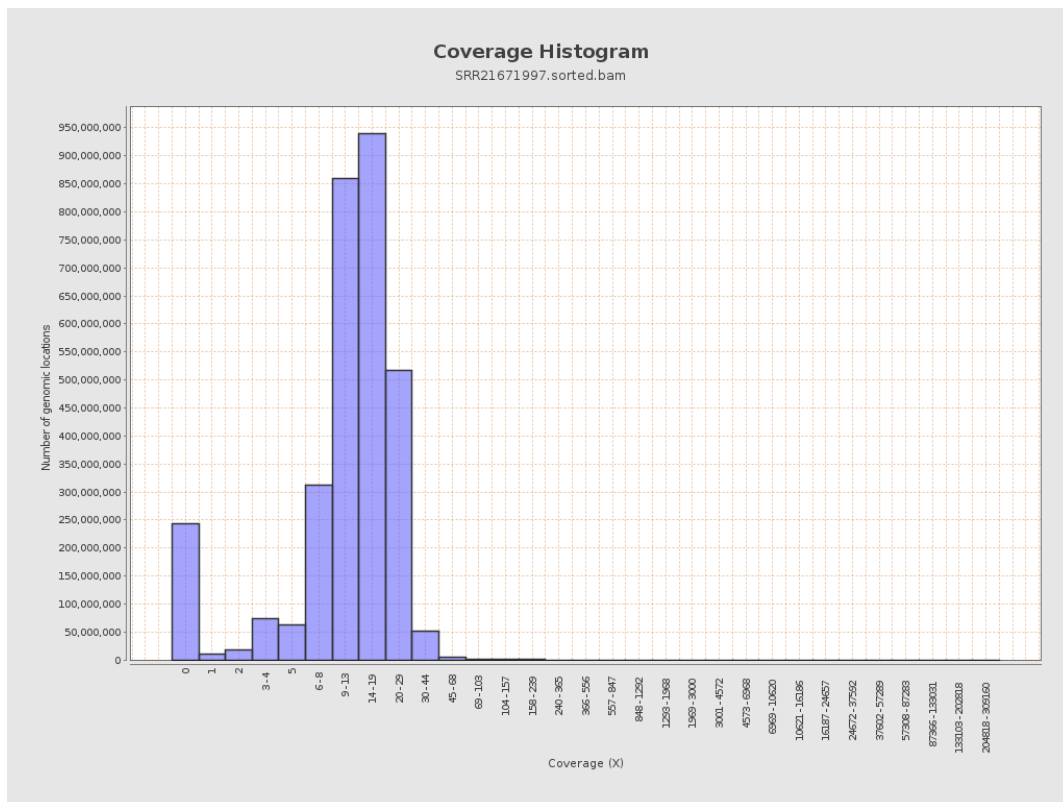
		bases	coverage	deviation
chr1	249250621	3627108957	14.5521	321.6198
chr2	243199373	3803363677	15.6389	103.9654
chr3	198022430	2890574127	14.5972	9.877
chr4	191154276	2855051866	14.9359	85.2908
chr5	180915260	2643480163	14.6117	13.8618
chr6	171115067	2512581663	14.6836	49.2536
chr7	159138663	2402550067	15.0972	142.5309
chr8	146364022	2178938205	14.8871	36.7017
chr9	141213431	1933158255	13.6896	252.5278
chr10	135534747	2271868015	16.7623	266.8984
chr11	135006516	2048505287	15.1734	89.2088
chr12	133851895	1951642545	14.5806	11.9206
chr13	115169878	1387803714	12.0501	9.3941
chr14	107349540	1346025907	12.5387	11.9419
chr15	102531392	1271094305	12.3971	9.3766
chr16	90354753	1393894081	15.4269	90.9567
chr17	81195210	1279811788	15.7622	70.6147
chr18	78077248	1239630801	15.877	212.0014
chr19	59128983	940072179	15.8987	148.083
chr20	63025520	948406997	15.048	36.8119
chr21	48129895	623953537	12.9639	66.6912
chr22	51304566	590395305	11.5077	64.7869
chrMT	16571	16508077	996.2028	111.3818
chrX	155270560	1158248076	7.4595	25.5013

chrY	59373566	452430347	7.6201	144.8201
------	----------	-----------	--------	----------

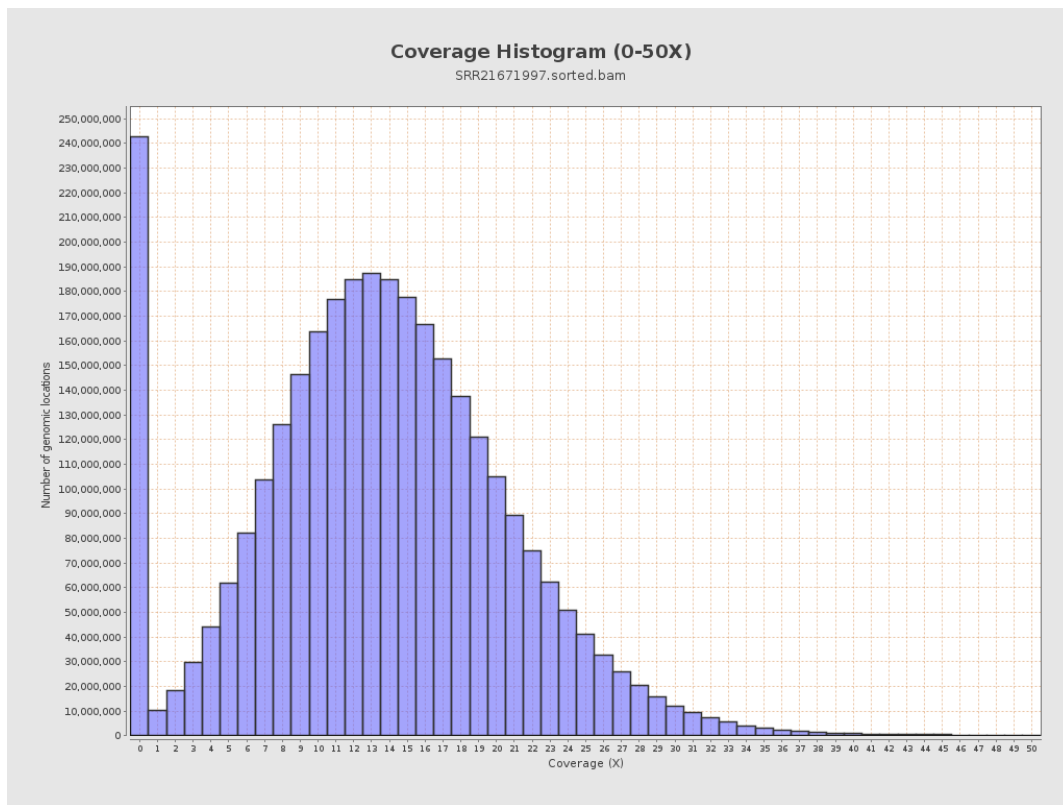
3. Results : Coverage across reference



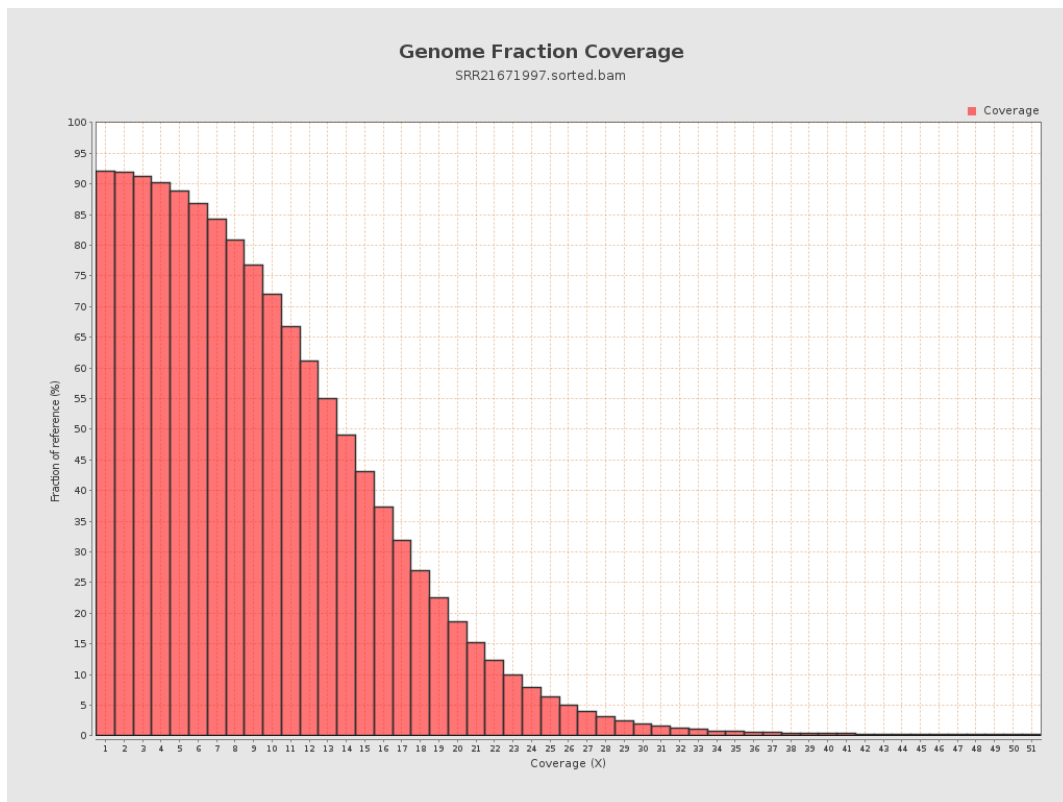
4. Results : Coverage Histogram



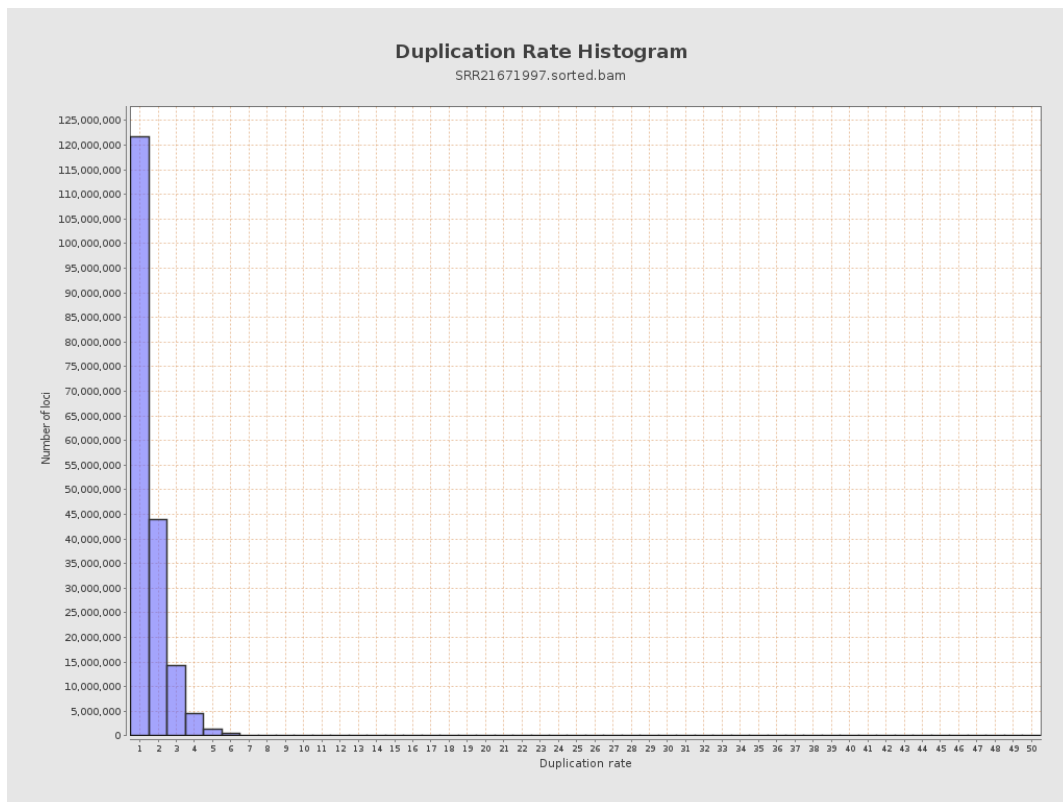
5. Results : Coverage Histogram (0-50X)



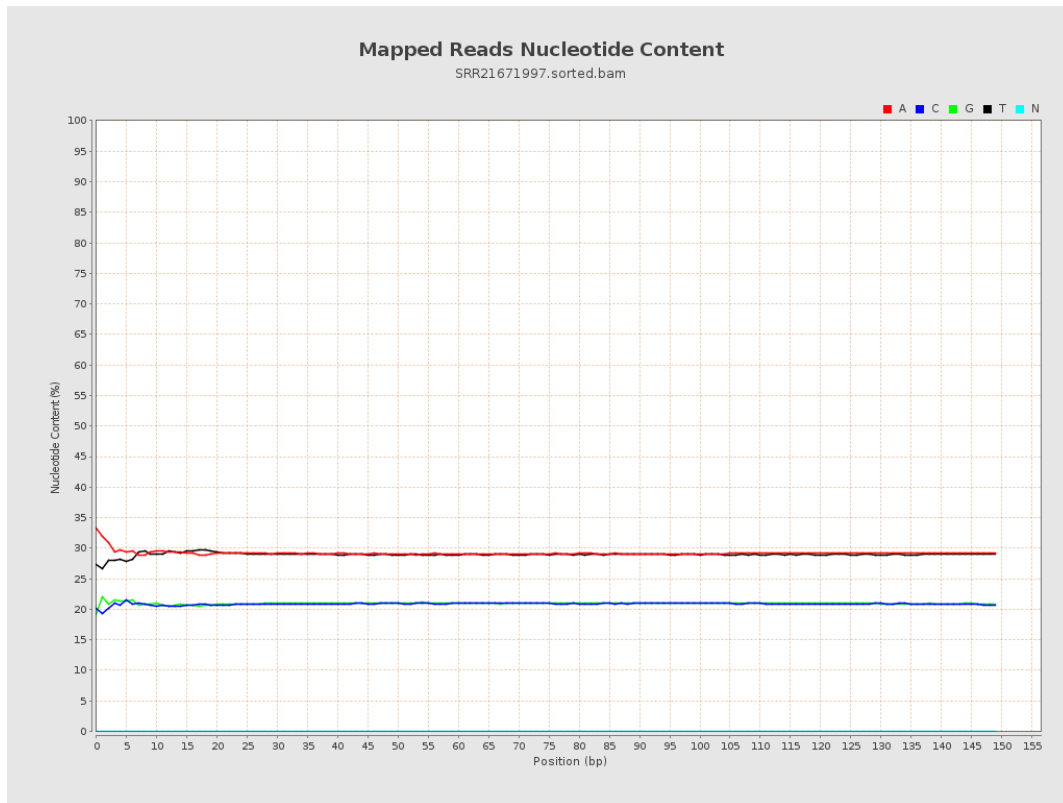
6. Results : Genome Fraction Coverage



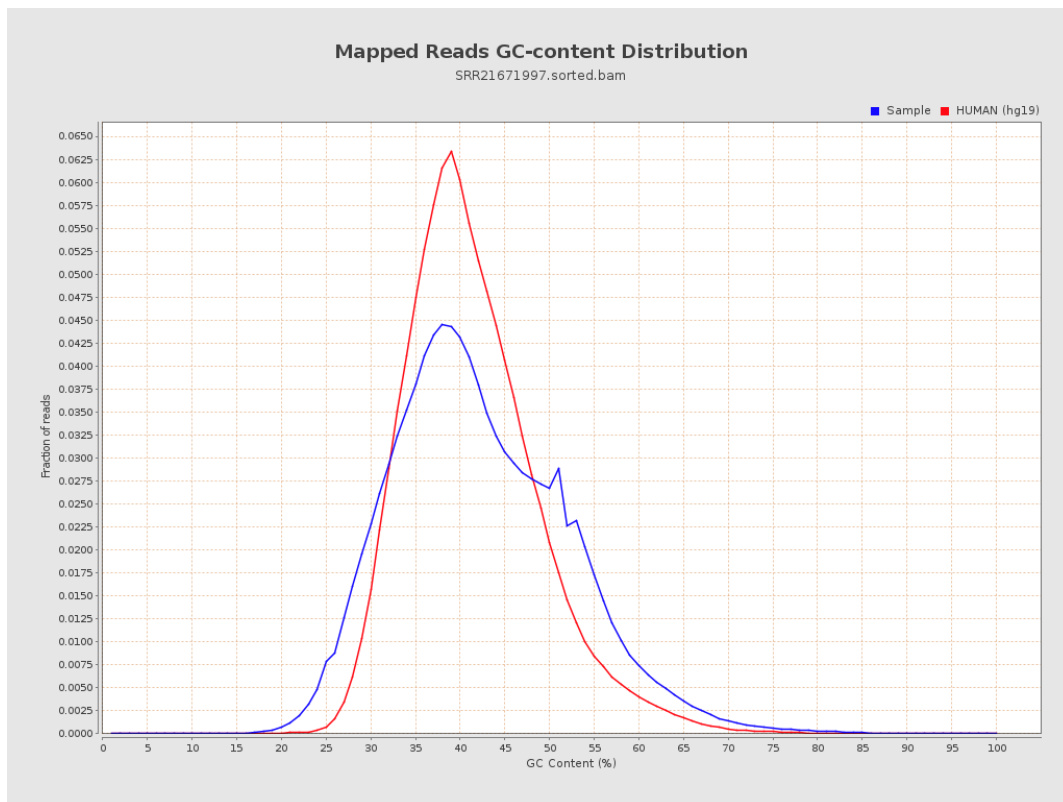
7. Results : Duplication Rate Histogram



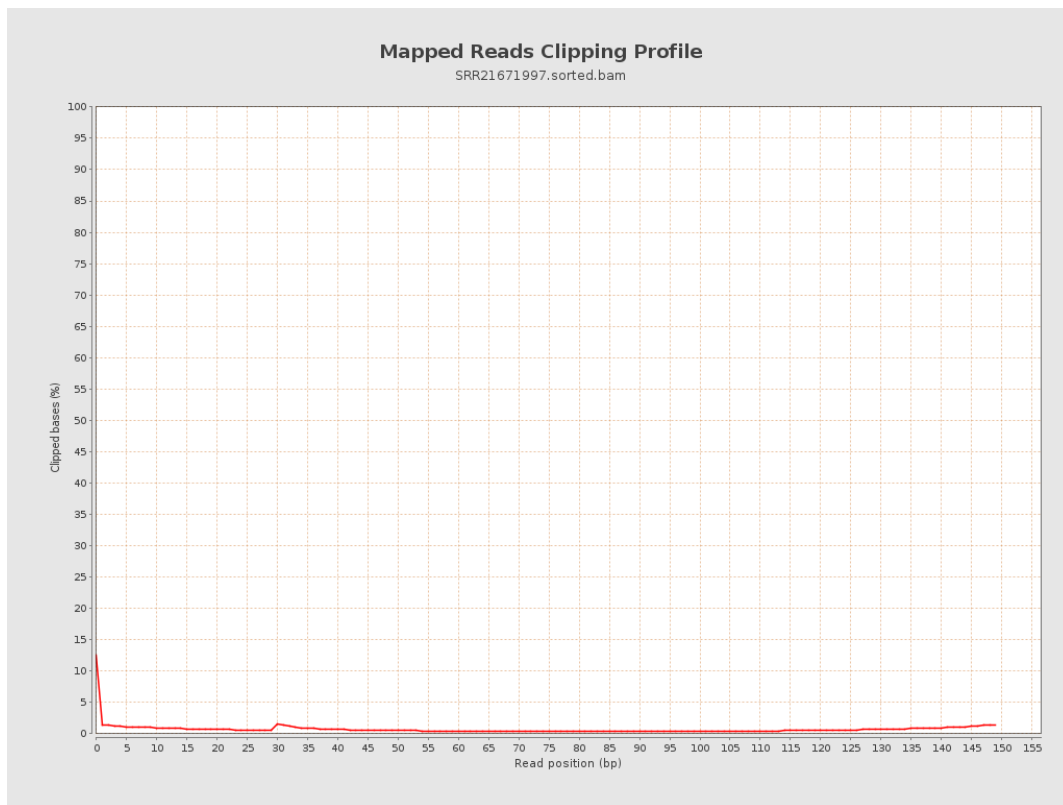
8. Results : Mapped Reads Nucleotide Content



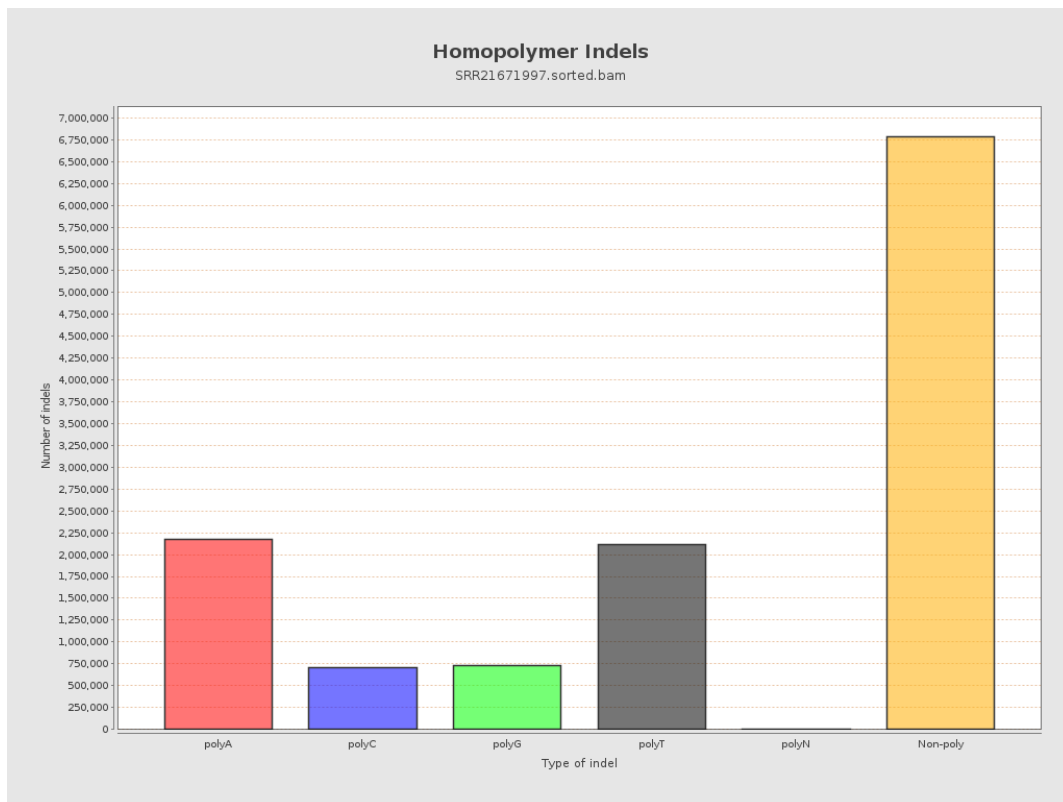
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



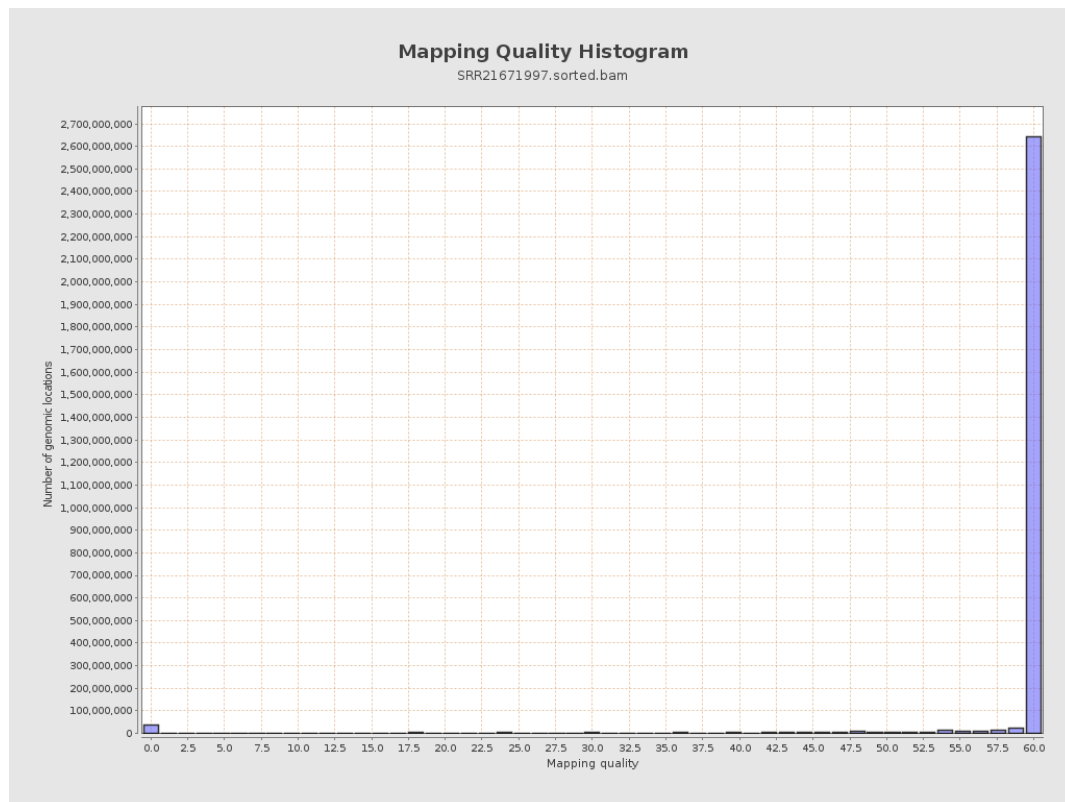
11. Results : Homopolymer Indels



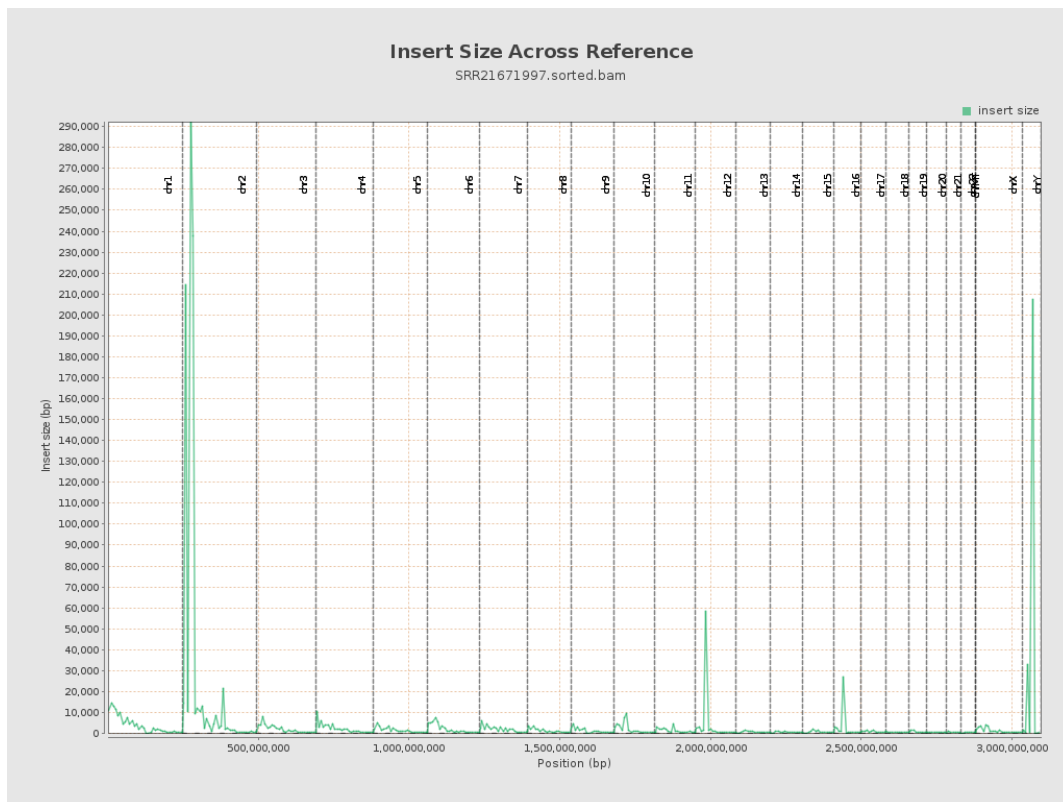
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

