

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 17:08:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR21672002.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_SRR21672002 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR21672002_1.fastq.gz SRR21672002_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 17:08:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR21672002.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,748,204
Mapped reads	16,403,901 / 97.94%
Unmapped reads	344,303 / 2.06%
Mapped paired reads	16,403,901 / 97.94%
Mapped reads, first in pair	8,203,380 / 48.98%
Mapped reads, second in pair	8,200,521 / 48.96%
Mapped reads, both in pair	16,383,072 / 97.82%
Mapped reads, singletons	20,829 / 0.12%
Secondary alignments	0
Supplementary alignments	140,115 / 0.84%
Read min/max/mean length	15 / 150 / 147.2
Duplicated reads (estimated)	13,698,987 / 81.79%
Duplication rate	58.75%
Clipped reads	8,053,157 / 48.08%

2.2. ACGT Content

Number/percentage of A's	569,260,061 / 25.52%
Number/percentage of C's	505,500,199 / 22.66%
Number/percentage of T's	598,931,468 / 26.85%
Number/percentage of G's	557,204,691 / 24.98%
Number/percentage of N's	5,871 / 0%

GC Percentage	47.64%
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2.3. Coverage

Mean	0.7209
Standard Deviation	40.9867

2.4. Mapping Quality

Mean Mapping Quality	52.54
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2.5. Insert size

Mean	41,469.18
Standard Deviation	1,990,304.85
P25/Median/P75	172 / 235 / 309

2.6. Mismatches and indels

General error rate	0.77%
Mismatches	16,762,416
Insertions	165,856
Mapped reads with at least one insertion	0.97%
Deletions	417,100
Mapped reads with at least one deletion	2.5%
Homopolymer indels	45.66%

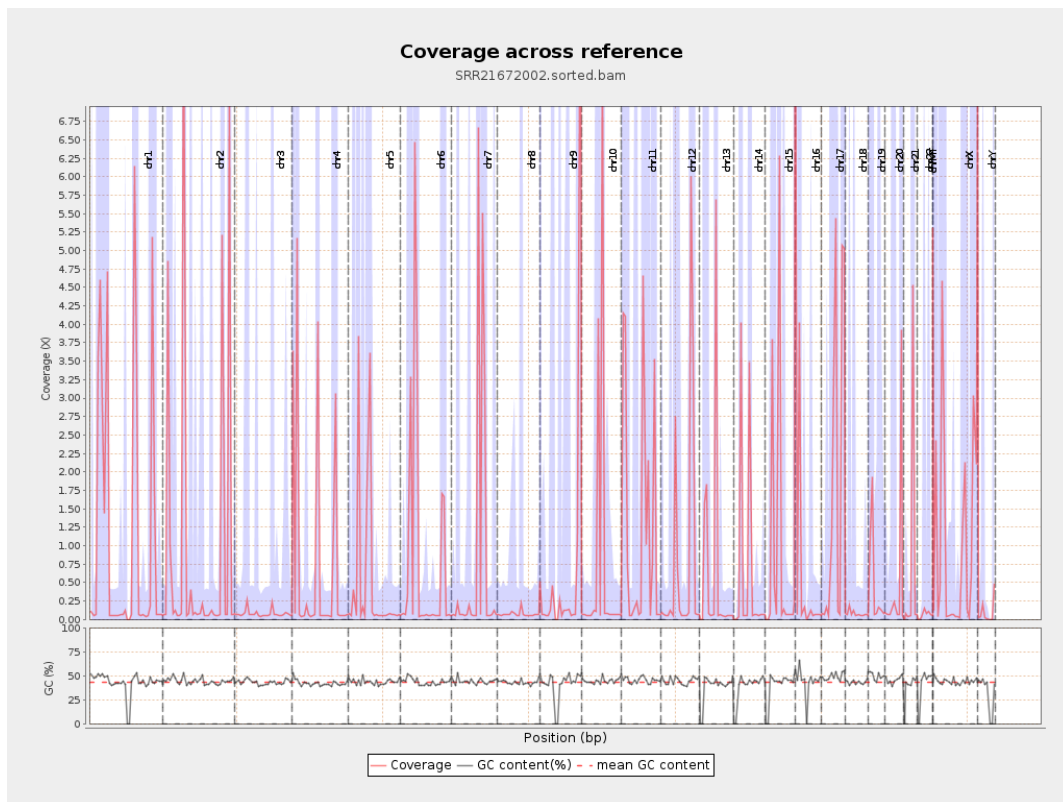
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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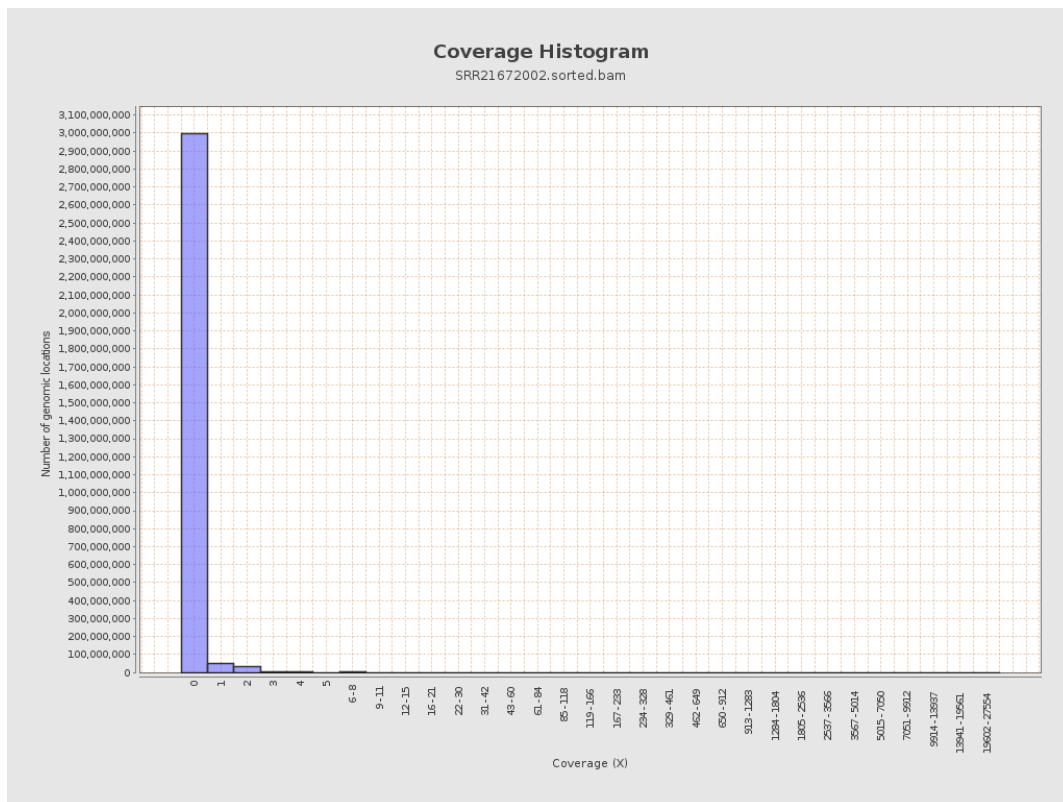
		bases	coverage	deviation
chr1	249250621	273339262	1.0966	52.7133
chr2	243199373	223327357	0.9183	48.9513
chr3	198022430	15723618	0.0794	5.8298
chr4	191154276	136530018	0.7142	40.2456
chr5	180915260	84282658	0.4659	32.4937
chr6	171115067	141138495	0.8248	42.2049
chr7	159138663	130891372	0.8225	47.6611
chr8	146364022	10573737	0.0722	4.758
chr9	141213431	98678348	0.6988	41.7368
chr10	135534747	100286015	0.7399	42.0303
chr11	135006516	170360249	1.2619	55.8018
chr12	133851895	109565879	0.8186	44.2852
chr13	115169878	75122441	0.6523	38.6258
chr14	107349540	62603629	0.5832	32.9376
chr15	102531392	86858899	0.8471	40.718
chr16	90354753	83784931	0.9273	39.2958
chr17	81195210	140535480	1.7308	62.0019
chr18	78077248	6292393	0.0806	4.002
chr19	59128983	28256961	0.4779	30.1401
chr20	63025520	35989821	0.571	33.4817
chr21	48129895	37107453	0.771	70.5457
chr22	51304566	3409710	0.0665	4.1817
chrMT	16571	88028	5.3122	9.6872
chrX	155270560	170800620	1.1	43.9841

chrY	59373566	6074370	0.1023	7.145
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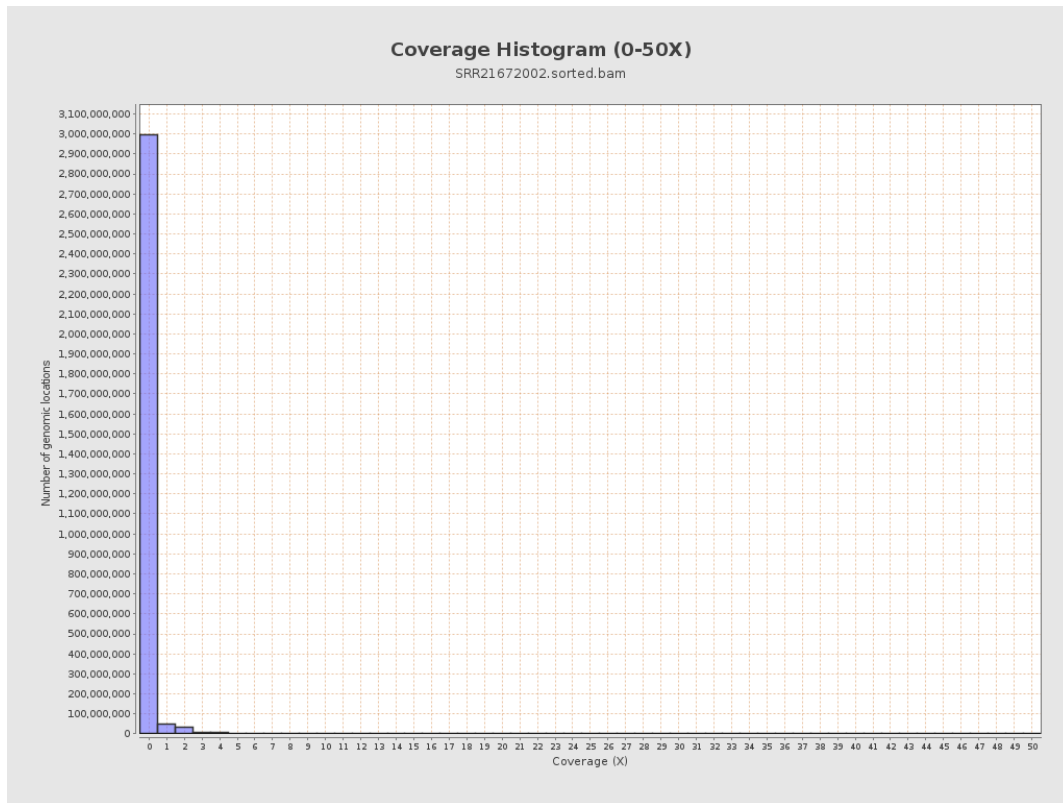
3. Results : Coverage across reference



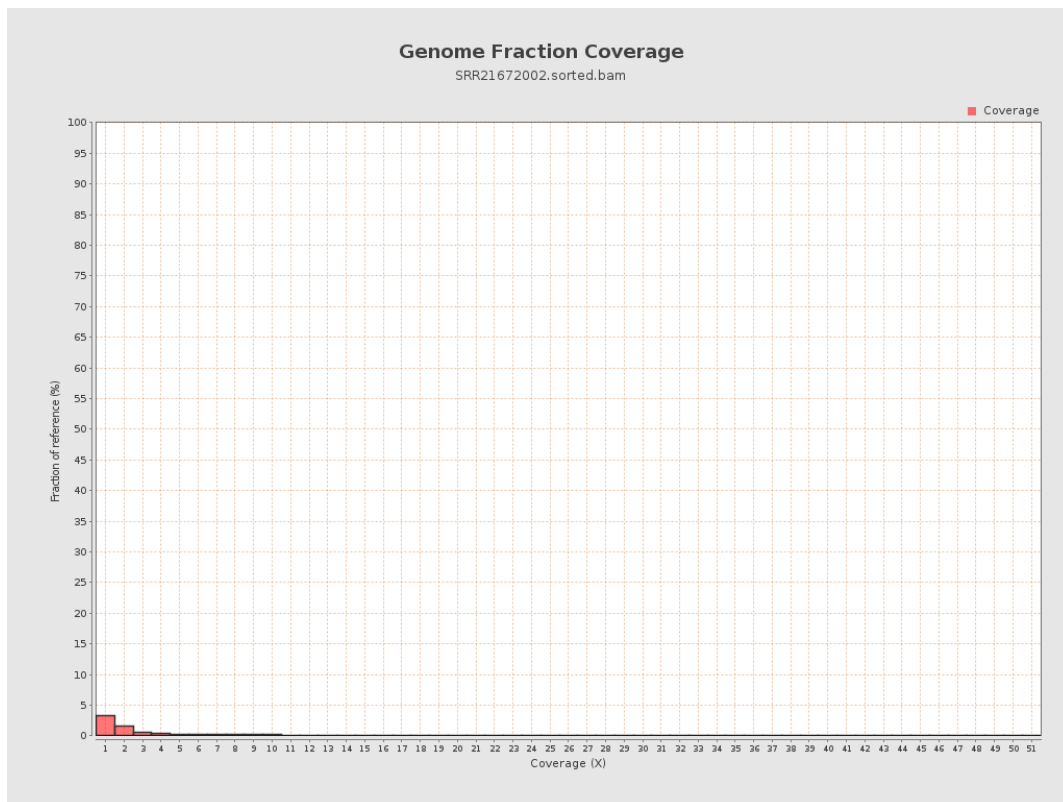
4. Results : Coverage Histogram



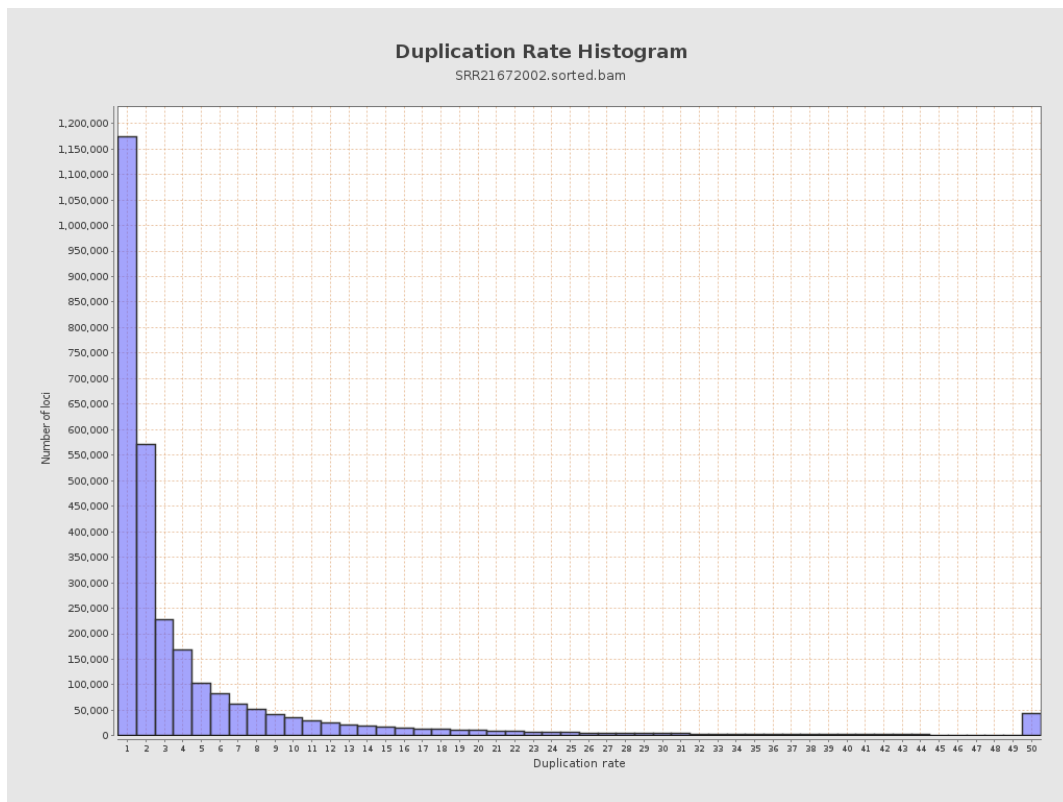
5. Results : Coverage Histogram (0-50X)



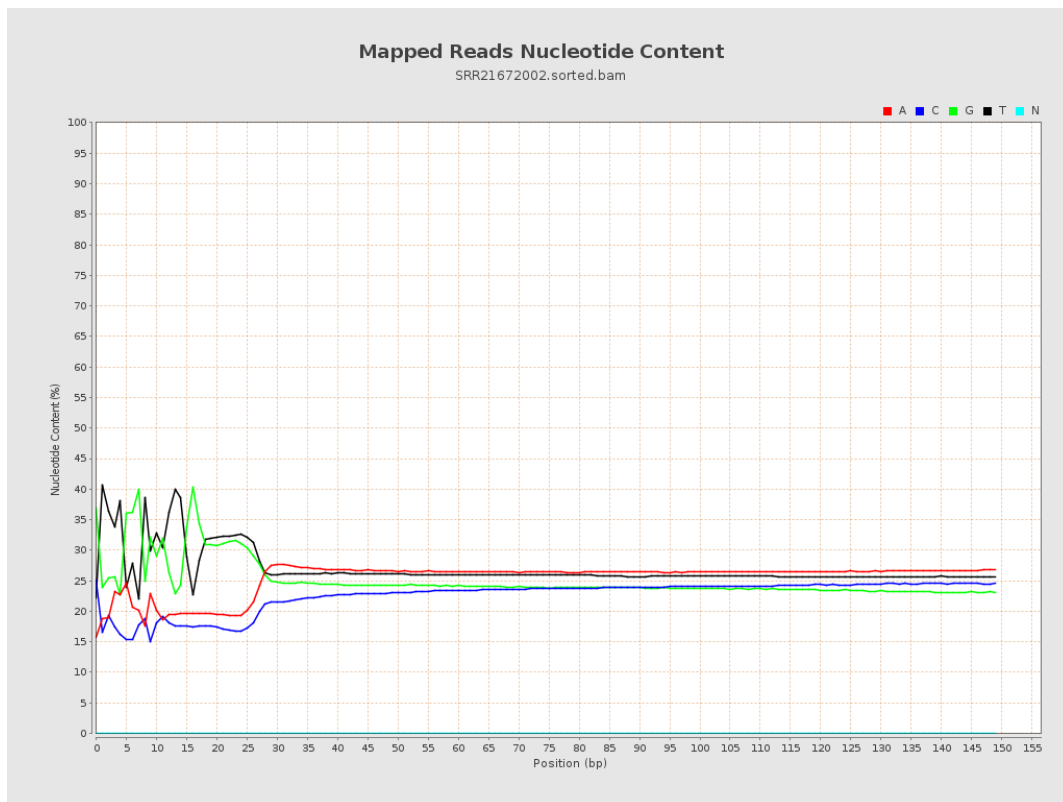
6. Results : Genome Fraction Coverage



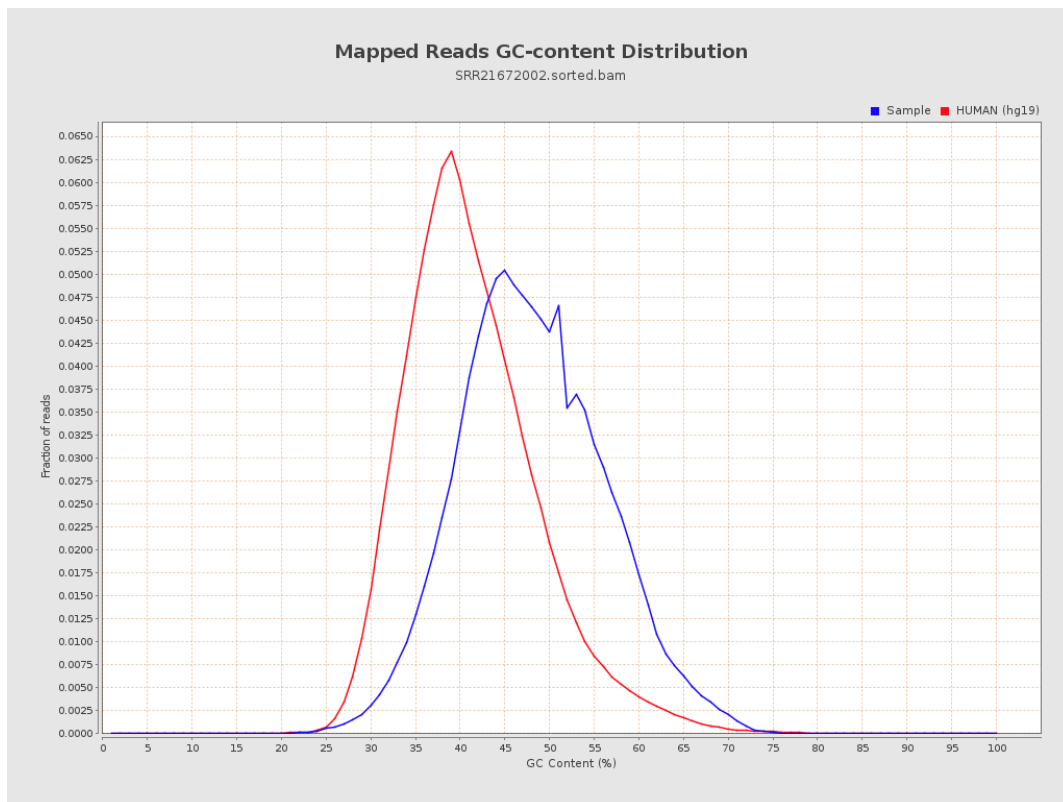
7. Results : Duplication Rate Histogram



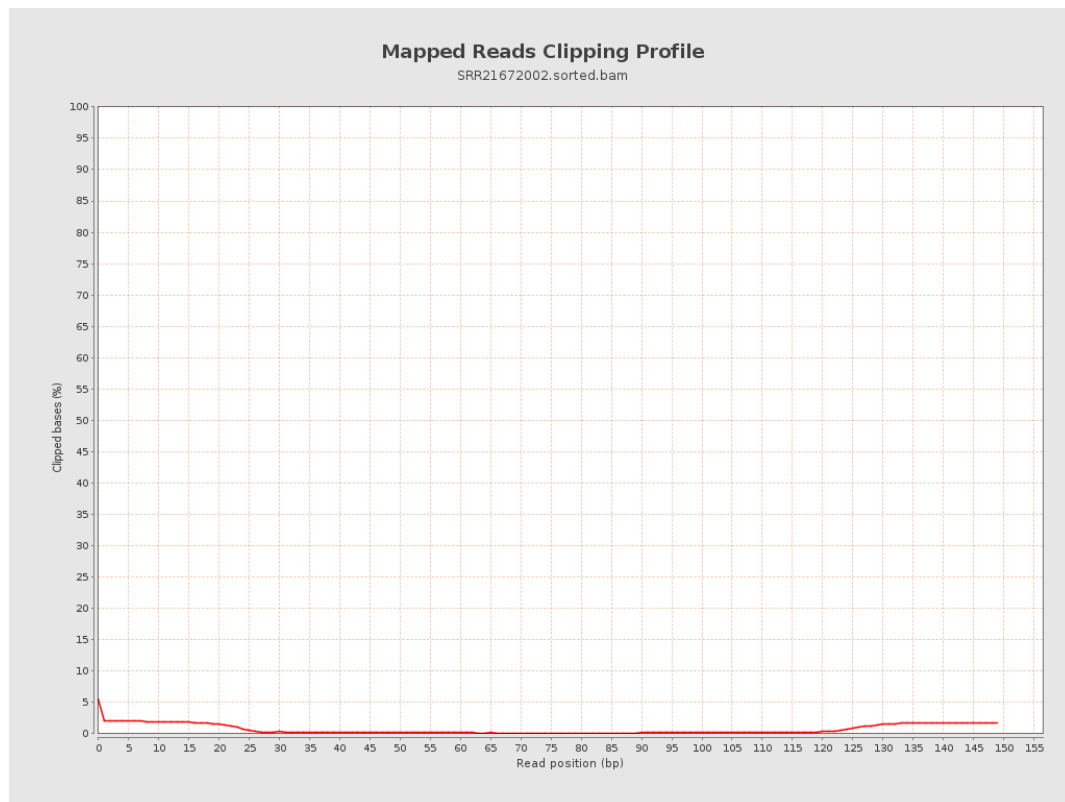
8. Results : Mapped Reads Nucleotide Content



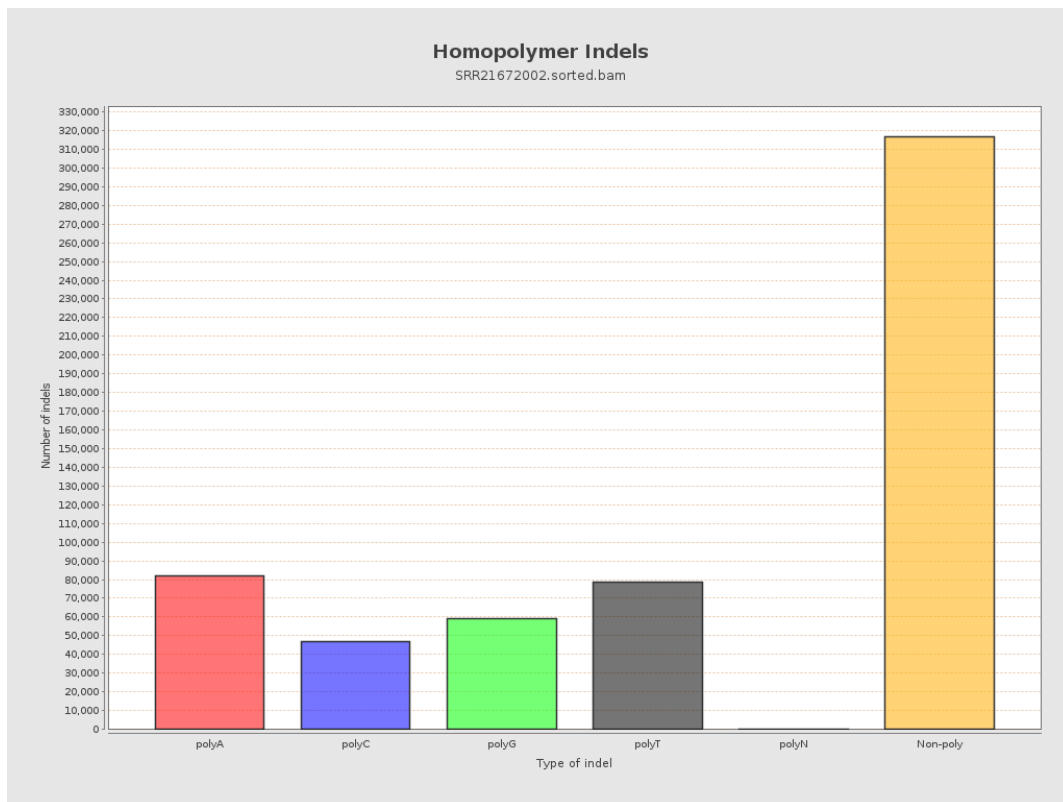
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



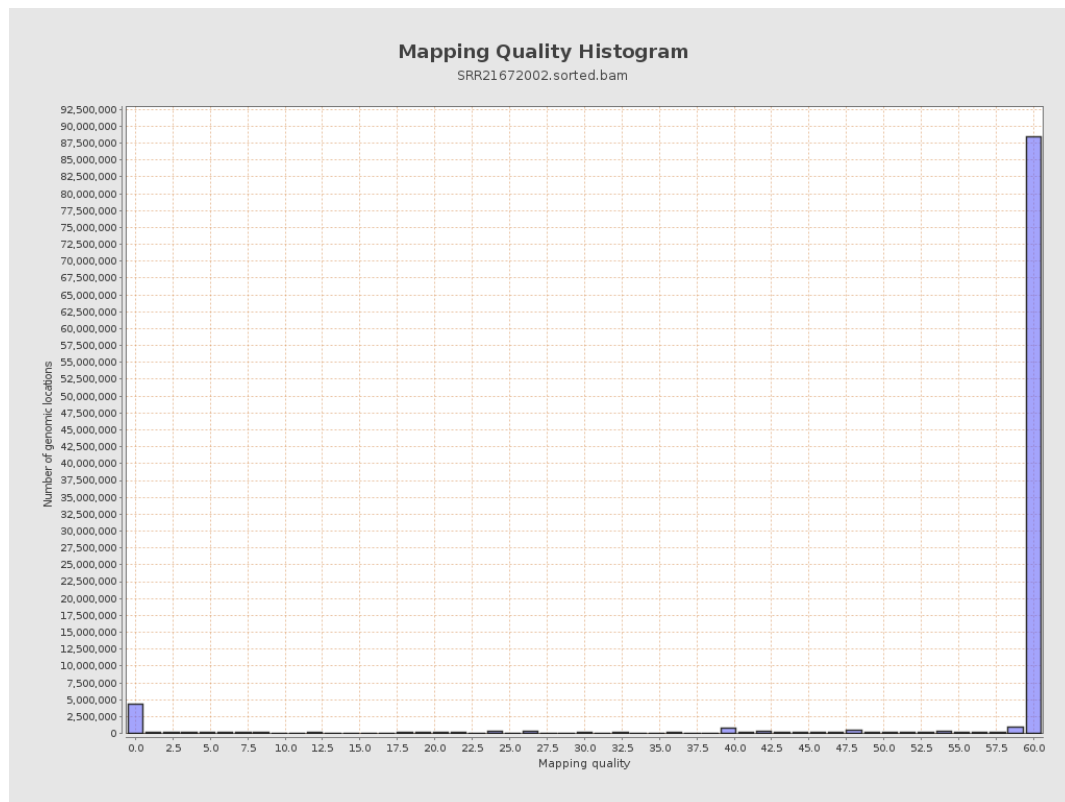
11. Results : Homopolymer Indels



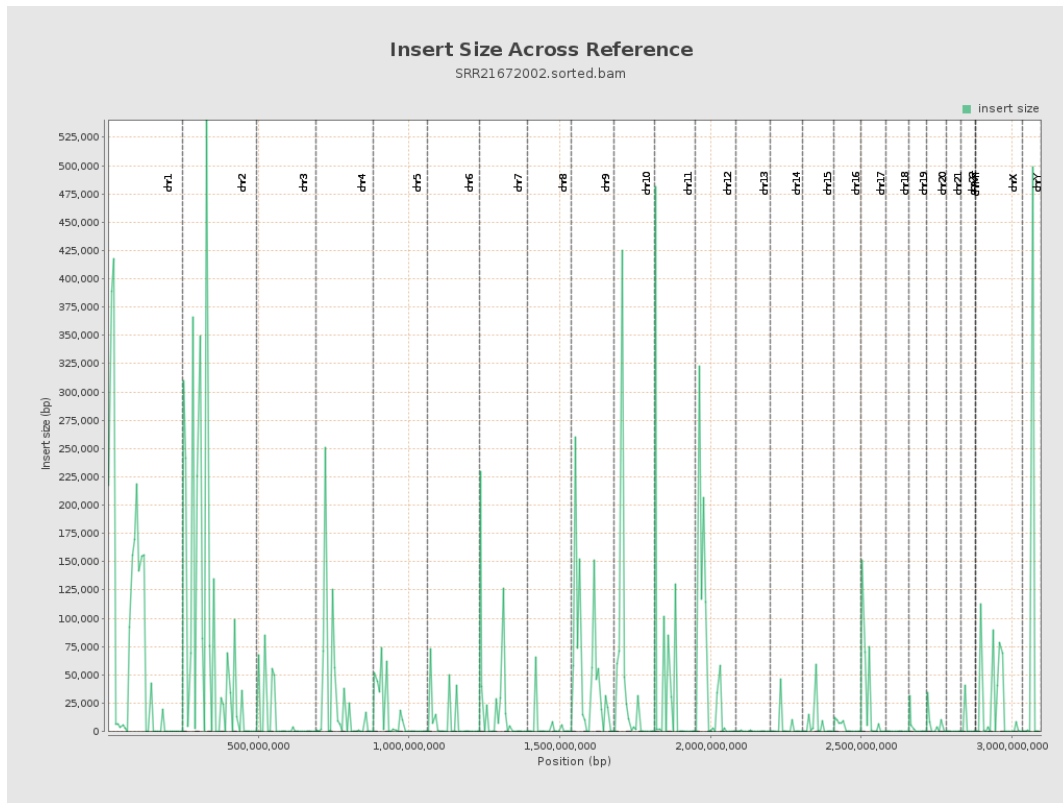
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

