

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 11:55:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354850.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_SRR22354850 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354850_1.fastq.gz SRR22354850_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 11:55:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354850.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,533,674
Mapped reads	14,408,979 / 99.14%
Unmapped reads	124,695 / 0.86%
Mapped paired reads	14,408,979 / 99.14%
Mapped reads, first in pair	7,211,131 / 49.62%
Mapped reads, second in pair	7,197,848 / 49.53%
Mapped reads, both in pair	14,384,378 / 98.97%
Mapped reads, singletons	24,601 / 0.17%
Secondary alignments	0
Supplementary alignments	346,953 / 2.39%
Read min/max/mean length	30 / 150 / 150.89
Duplicated reads (estimated)	10,630,147 / 73.14%
Duplication rate	73.63%
Clipped reads	7,100,733 / 48.86%

2.2. ACGT Content

Number/percentage of A's	535,856,562 / 29.12%
Number/percentage of C's	374,538,101 / 20.35%
Number/percentage of T's	544,699,195 / 29.6%
Number/percentage of G's	385,190,900 / 20.93%
Number/percentage of N's	4,629 / 0%

GC Percentage	41.28%
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2.3. Coverage

Mean	0.5947
Standard Deviation	16.6199

2.4. Mapping Quality

Mean Mapping Quality	54.06
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2.5. Insert size

Mean	223,677.04
Standard Deviation	5,440,019.85
P25/Median/P75	109 / 160 / 231

2.6. Mismatches and indels

General error rate	0.69%
Mismatches	11,843,080
Insertions	273,850
Mapped reads with at least one insertion	1.8%
Deletions	296,769
Mapped reads with at least one deletion	1.98%
Homopolymer indels	44.23%

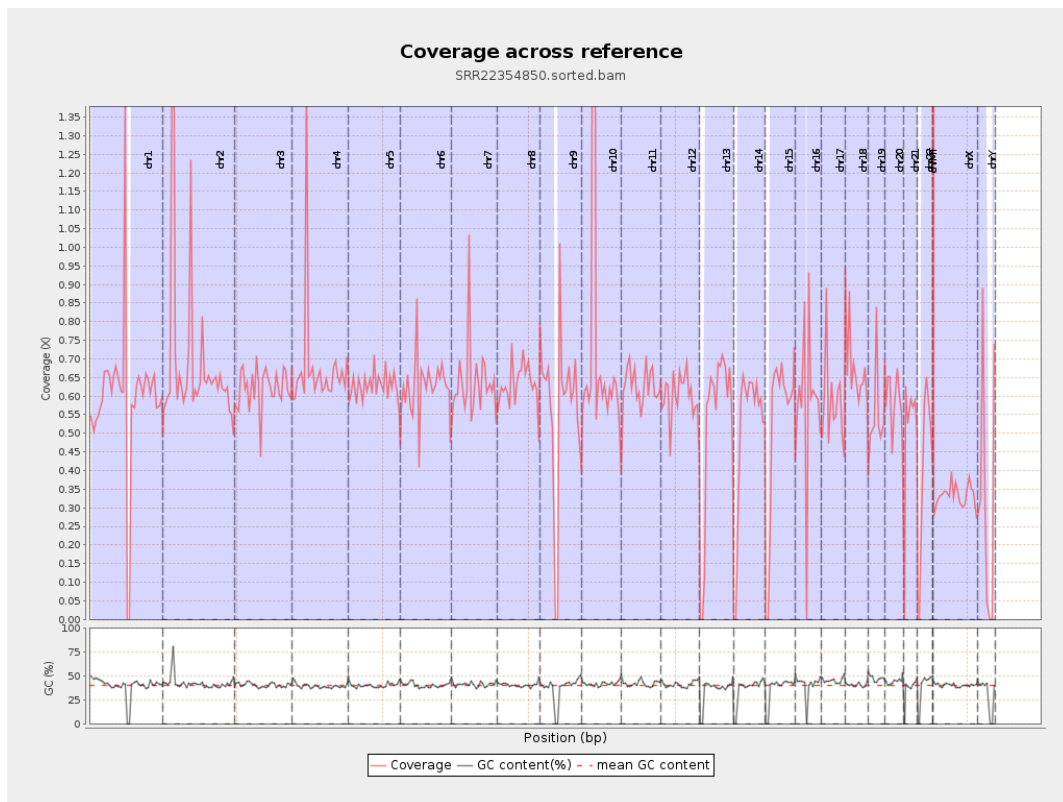
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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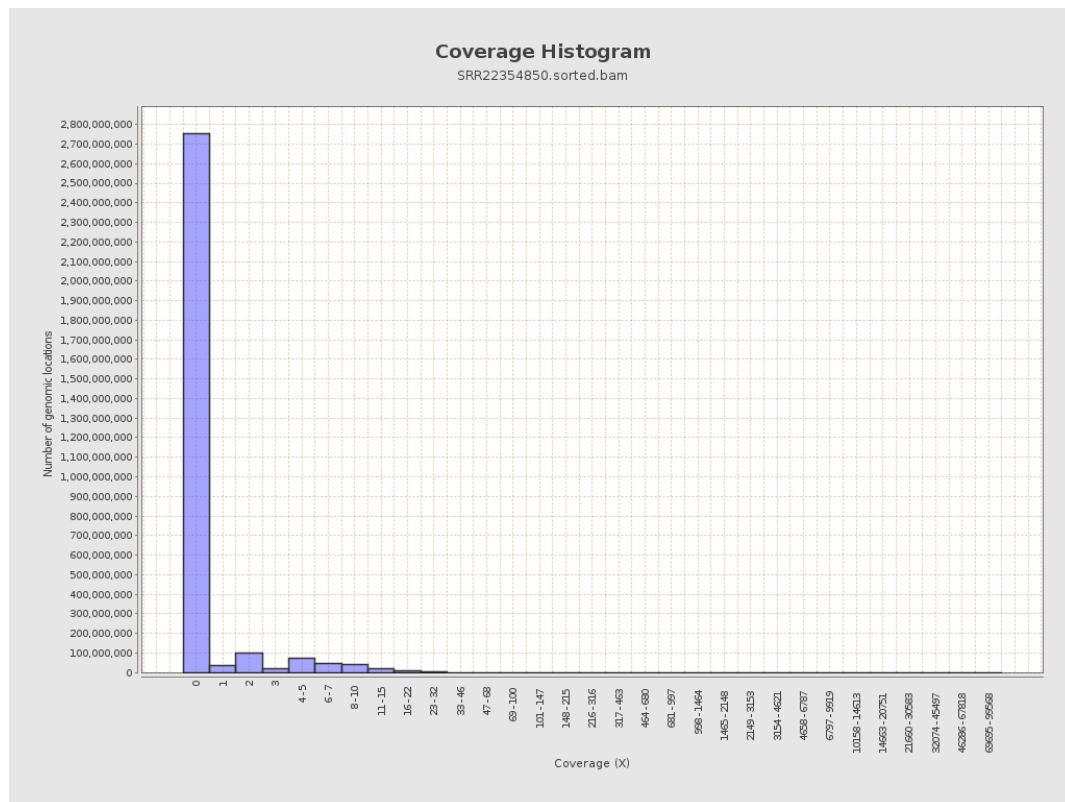
		bases	coverage	deviation
chr1	249250621	148666773	0.5965	18.1053
chr2	243199373	167866764	0.6902	52.2207
chr3	198022430	123119929	0.6217	2.4295
chr4	191154276	129388170	0.6769	6.41
chr5	180915260	113054054	0.6249	2.2833
chr6	171115067	107587947	0.6287	3.0761
chr7	159138663	100765333	0.6332	10.0142
chr8	146364022	92317058	0.6307	3.817
chr9	141213431	79773953	0.5649	9.3601
chr10	135534747	98333830	0.7255	17.376
chr11	135006516	84665320	0.6271	3.6017
chr12	133851895	80206893	0.5992	2.2572
chr13	115169878	60768415	0.5276	2.0878
chr14	107349540	55020633	0.5125	3.4108
chr15	102531392	52876389	0.5157	2.0392
chr16	90354753	52284343	0.5787	3.9008
chr17	81195210	47510914	0.5851	3.8284
chr18	78077248	52819095	0.6765	8.1812
chr19	59128983	32756430	0.554	9.4374
chr20	63025520	36717628	0.5826	2.9003
chr21	48129895	24965339	0.5187	3.8243
chr22	51304566	20816097	0.4057	2.1549
chrMT	16571	7649085	461.5947	93.9013
chrX	155270560	51606091	0.3324	1.9182

chrY	59373566	19538611	0.3291	8.0126
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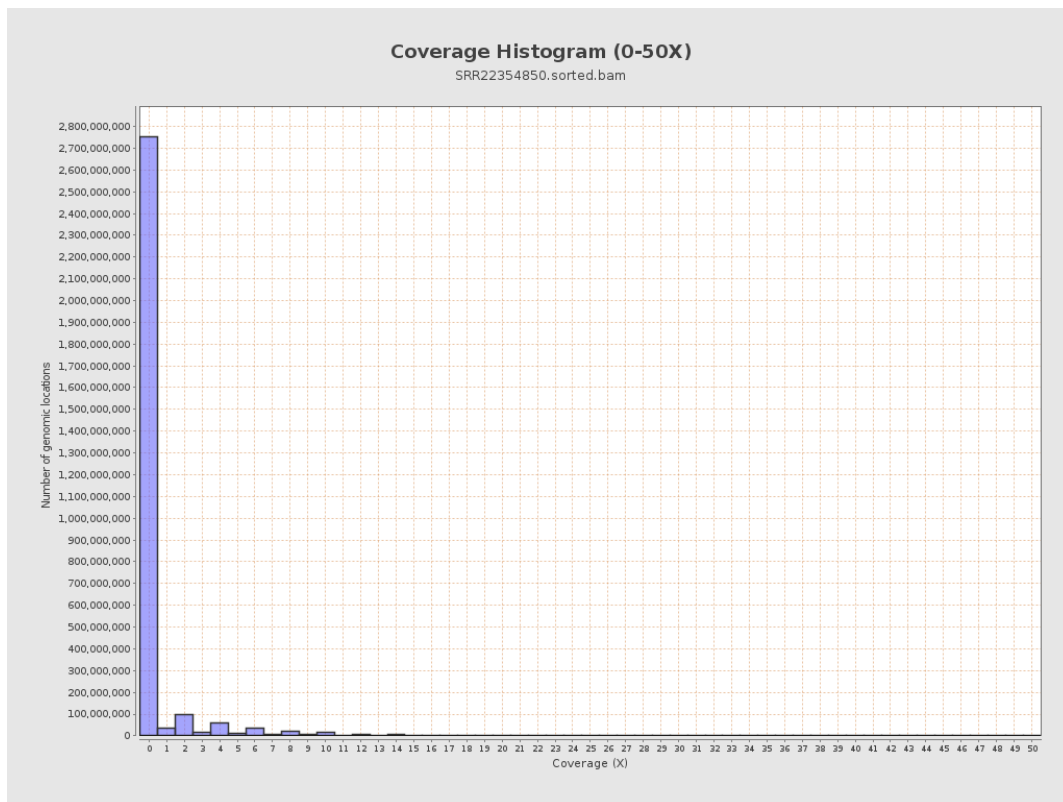
3. Results : Coverage across reference



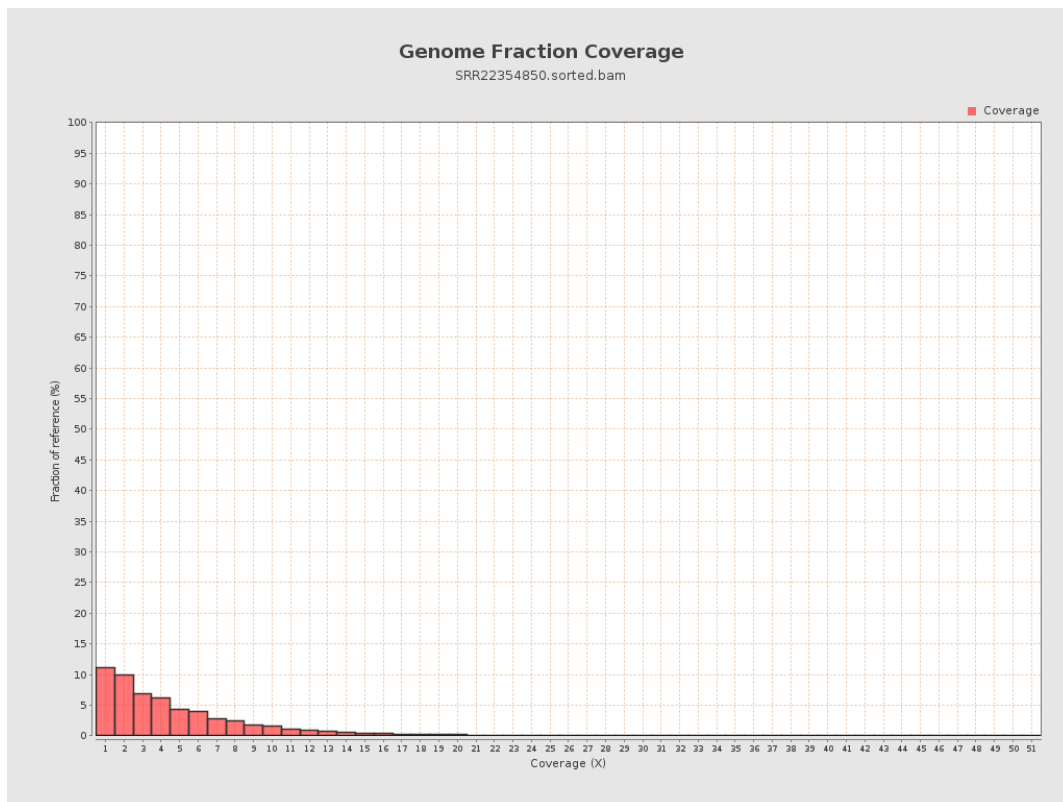
4. Results : Coverage Histogram



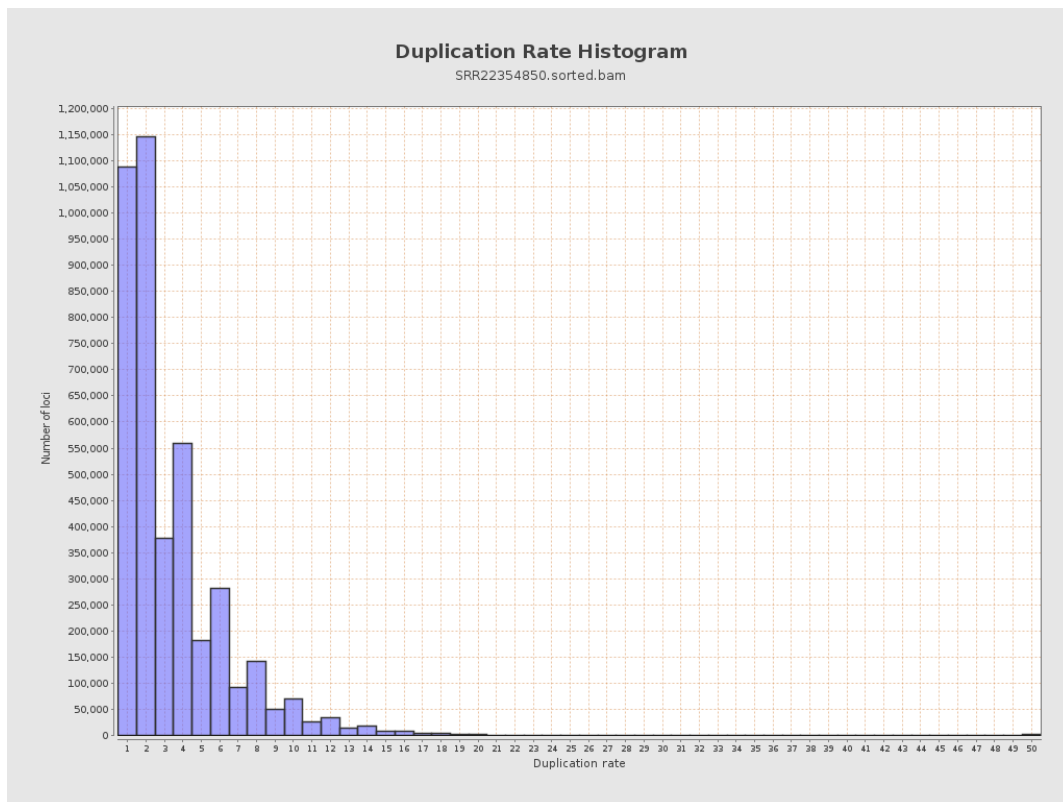
5. Results : Coverage Histogram (0-50X)



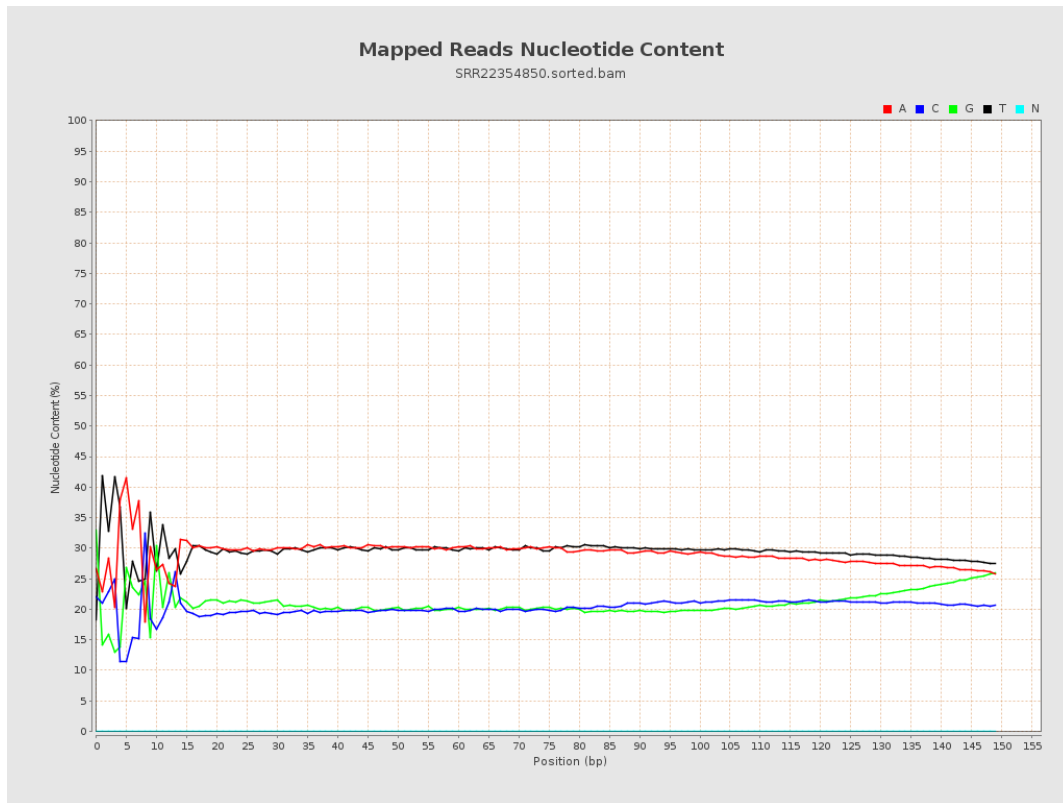
6. Results : Genome Fraction Coverage



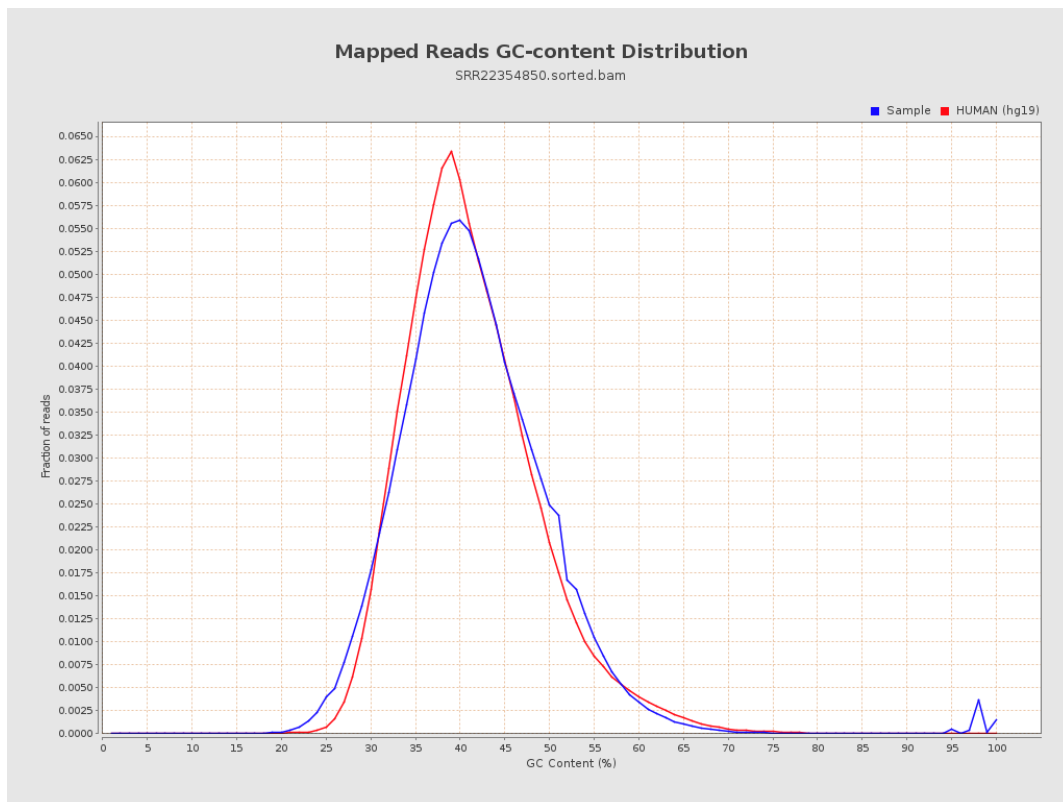
7. Results : Duplication Rate Histogram



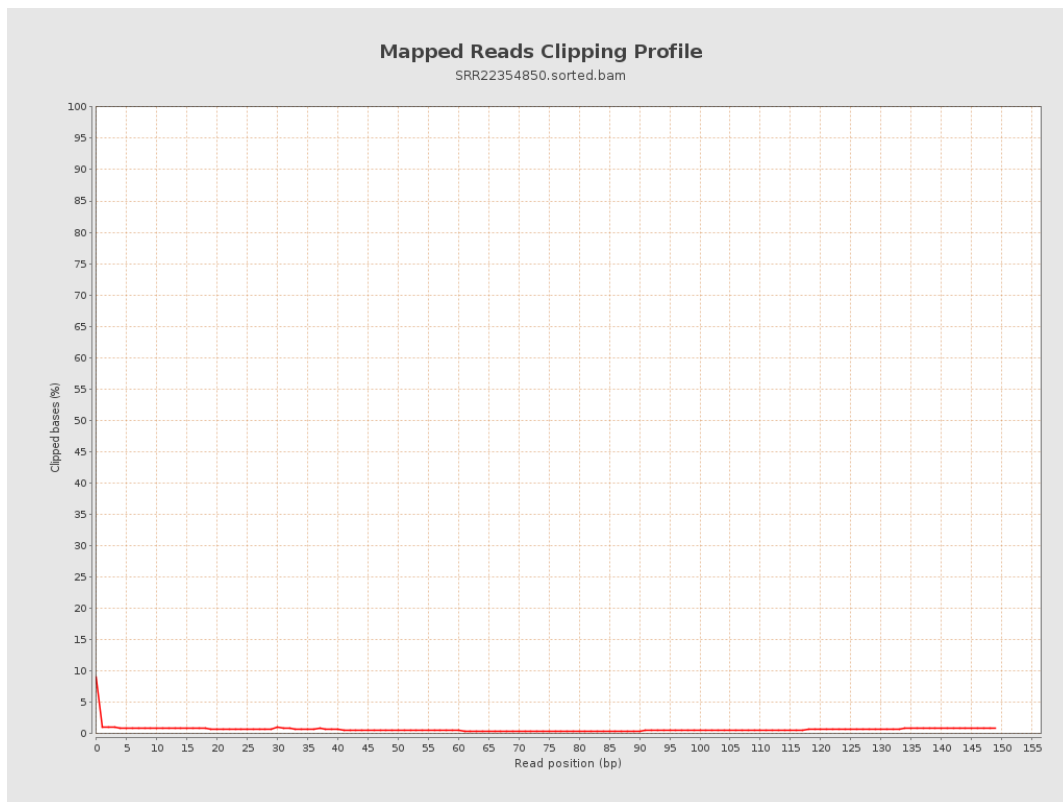
8. Results : Mapped Reads Nucleotide Content



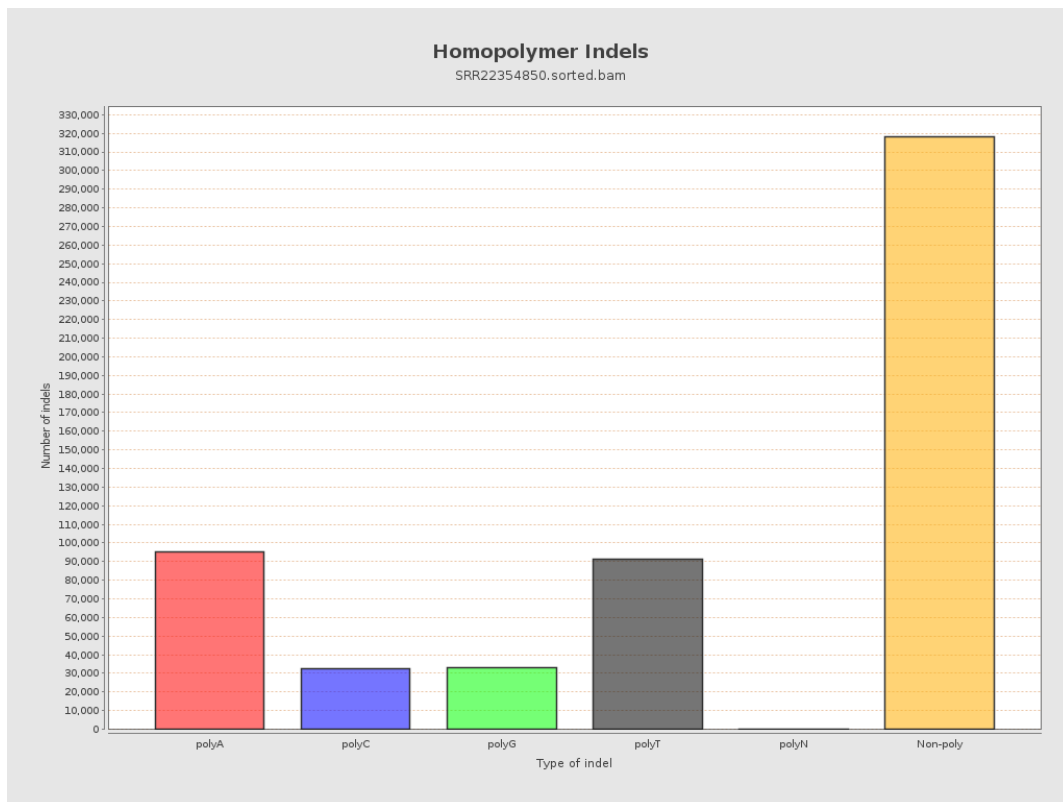
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



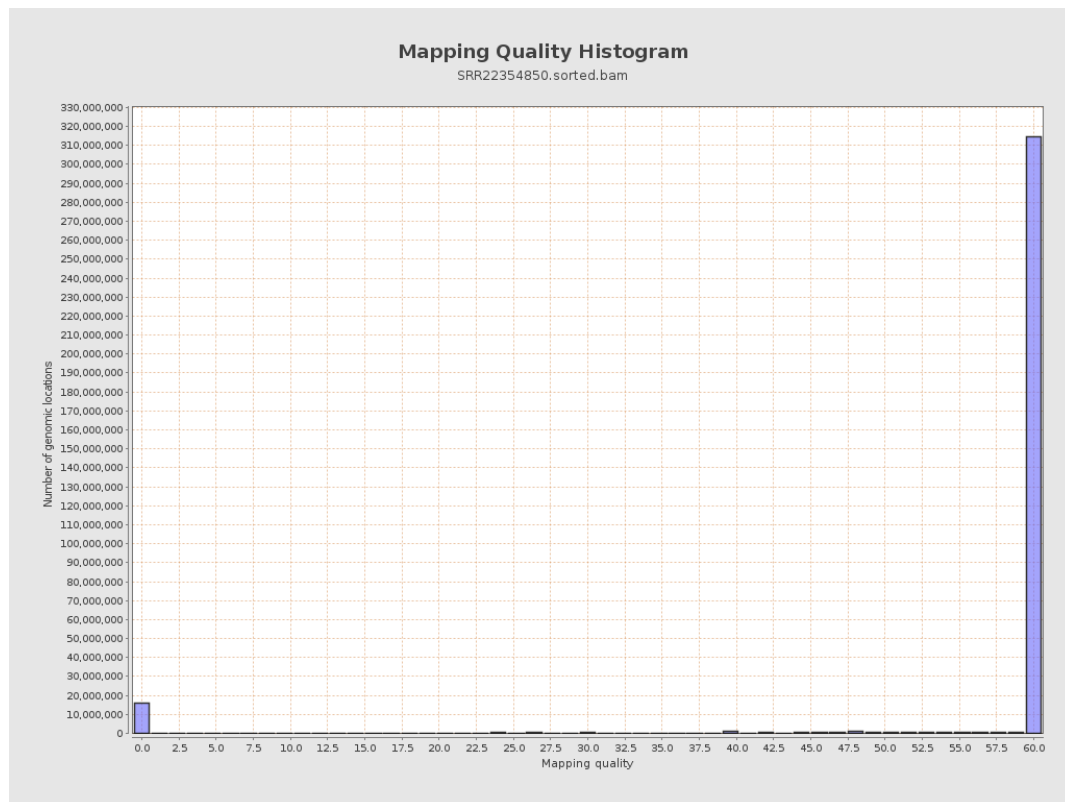
11. Results : Homopolymer Indels



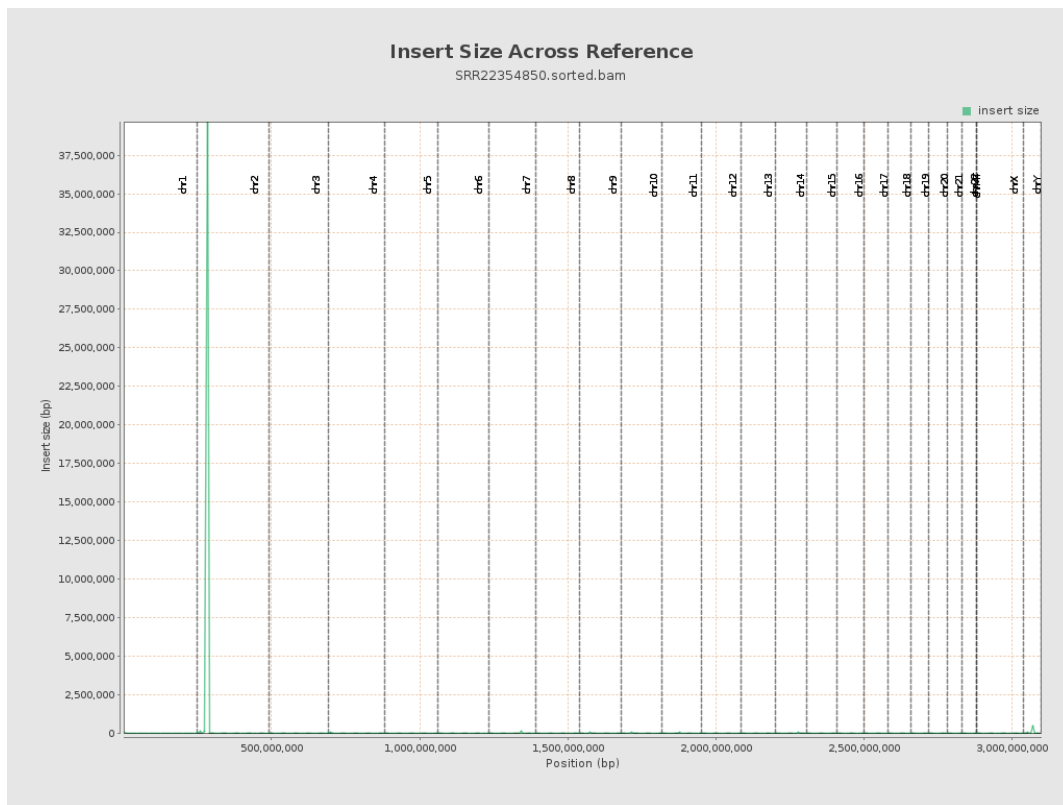
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

