Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 12:21:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354851.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_SRR22354851 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354851_1.fastq.gz SRR22354851_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 12:21:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354851.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,277,036
Mapped reads	20,065,478 / 98.96%
Unmapped reads	211,558 / 1.04%
Mapped paired reads	20,065,478 / 98.96%
Mapped reads, first in pair	10,052,033 / 49.57%
Mapped reads, second in pair	10,013,445 / 49.38%
Mapped reads, both in pair	19,986,950 / 98.57%
Mapped reads, singletons	78,528 / 0.39%
Secondary alignments	0
Supplementary alignments	368,452 / 1.82%
Read min/max/mean length	30 / 150 / 150.8
Duplicated reads (estimated)	6,536,272 / 32.23%
Duplication rate	27.65%
Clipped reads	5,379,754 / 26.53%

2.2. ACGT Content

Number/percentage of A's	799,154,133 / 28.74%
Number/percentage of C's	583,696,931 / 20.99%
Number/percentage of T's	803,471,448 / 28.89%
Number/percentage of G's	594,421,740 / 21.38%
Number/percentage of N's	47,251 / 0%

GC Percentage	42.37%

2.3. Coverage

Mean	0.8988
Standard Deviation	18.1453

2.4. Mapping Quality

Mean Mapping Quality	53.93

2.5. Insert size

Mean	141,854.89
Standard Deviation	4,196,739.86
P25/Median/P75	170 / 270 / 398

2.6. Mismatches and indels

General error rate	0.91%
Mismatches	23,140,151
Insertions	545,974
Mapped reads with at least one insertion	2.47%
Deletions	518,768
Mapped reads with at least one deletion	2.4%
Homopolymer indels	39%

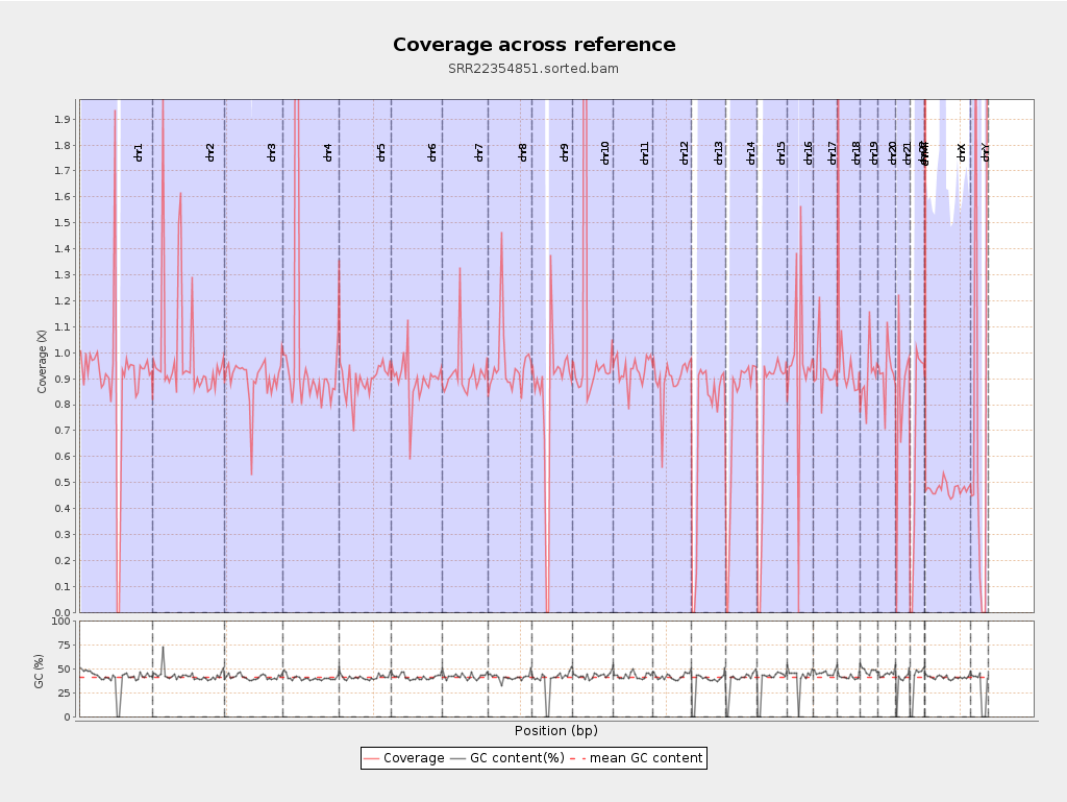
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard

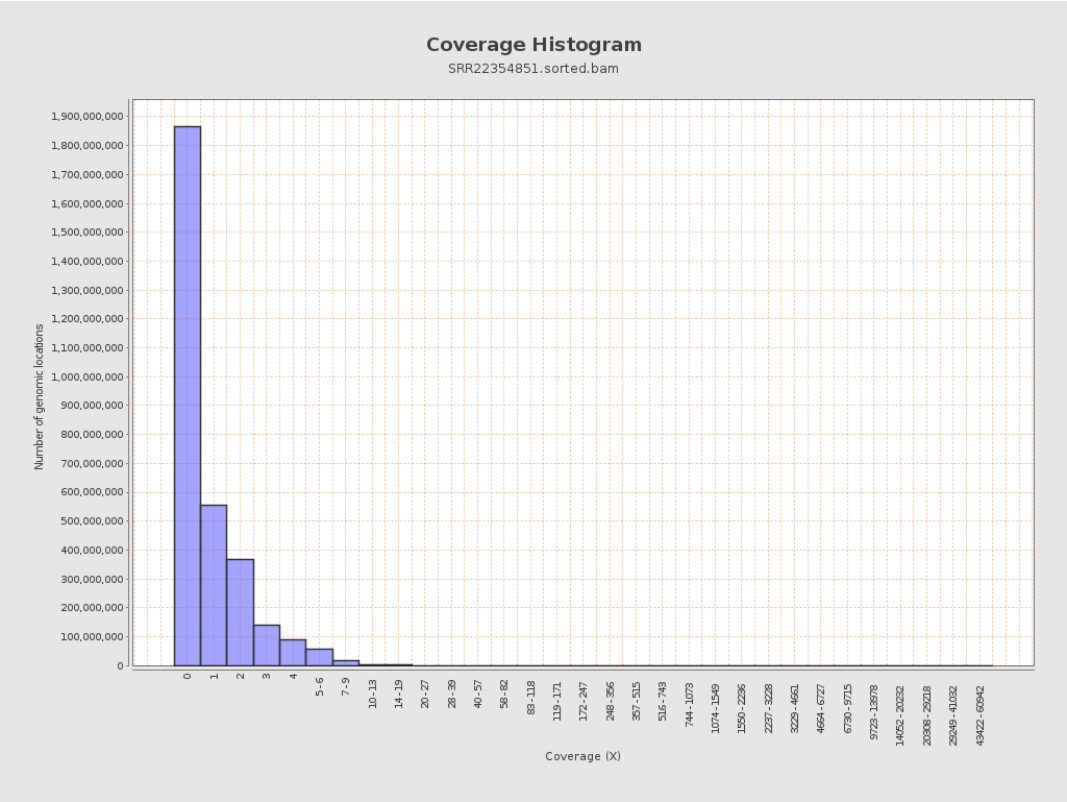
		bases	coverage	deviation
chr1	249250621	225184141	0.9034	24.2057
chr2	243199373	242785753	0.9983	36.3716
chr3	198022430	178226270	0.9	1.7473
chr4	191154276	196386585	1.0274	25.8663
chr5	180915260	162231221	0.8967	1.578
chr6	171115067	153604326	0.8977	3.2365
chr7	159138663	146438547	0.9202	11.0102
chr8	146364022	139616785	0.9539	25.6201
chr9	141213431	117221226	0.8301	12.0854
chr10	135534747	157445885	1.1617	31.6669
chr11	135006516	126194458	0.9347	3.6909
chr12	133851895	119949174	0.8961	1.5696
chr13	115169878	84432113	0.7331	1.3335
chr14	107349540	82100876	0.7648	2.3298
chr15	102531392	77515614	0.756	1.3542
chr16	90354753	85907856	0.9508	6.5013
chr17	81195210	75077714	0.9247	5.0502
chr18	78077248	77193623	0.9887	15.3053
chr19	59128983	53714483	0.9084	13.8006
chr20	63025520	58545647	0.9289	8.5335
chr21	48129895	40095534	0.8331	13.2465
chr22	51304566	34702915	0.6764	2.5263
chrMT	16571	27532420	1,661.4821	514.6299
chrX	155270560	73745845	0.475	1.5123

chrY	59373566	46623635	0.7853	27.963

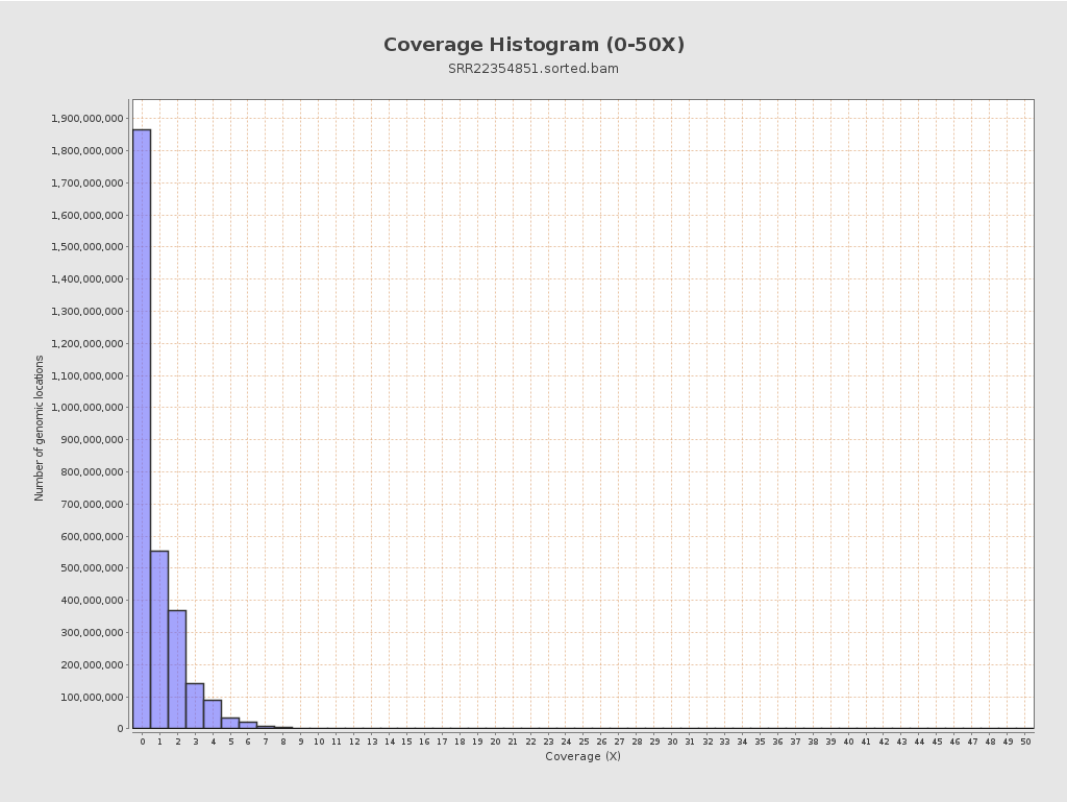
3. Results : Coverage across reference



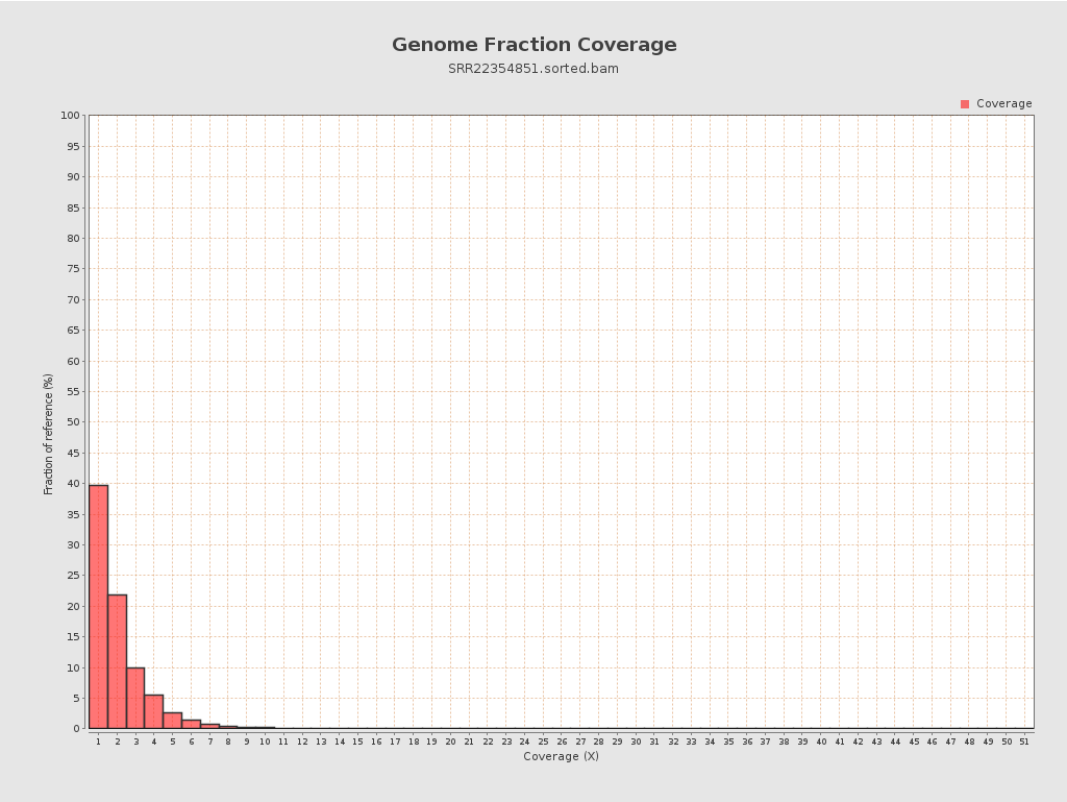
4. Results : Coverage Histogram



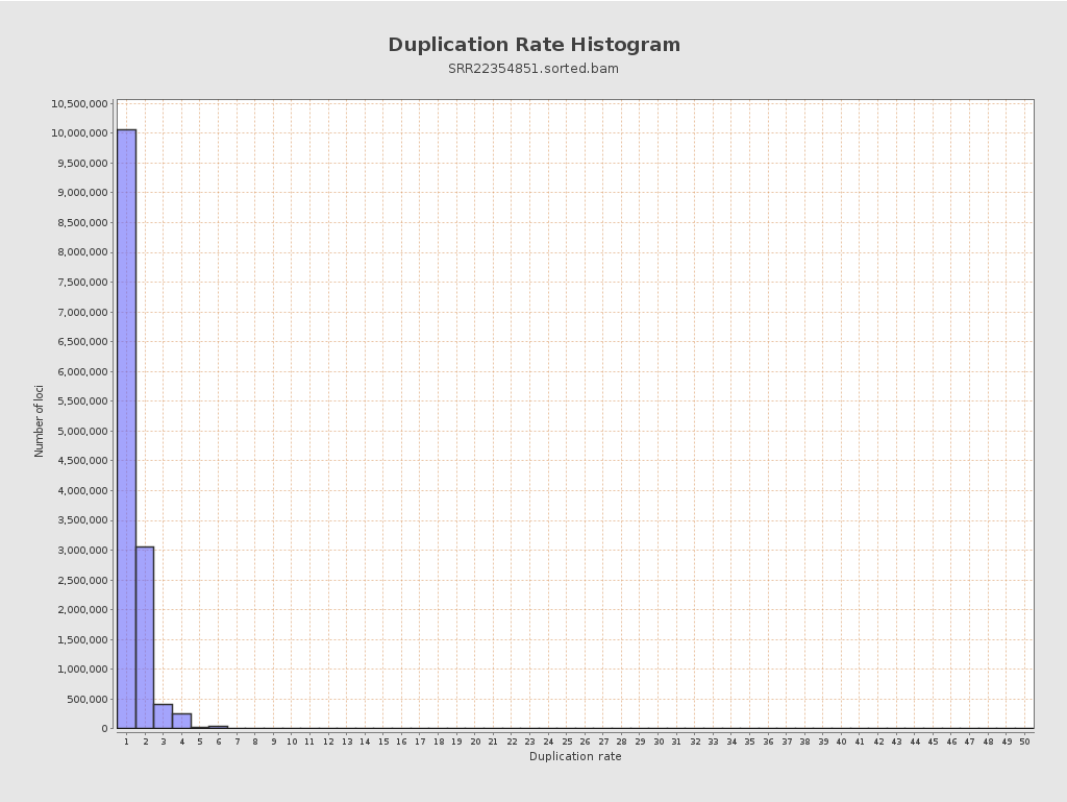
5. Results : Coverage Histogram (0-50X)



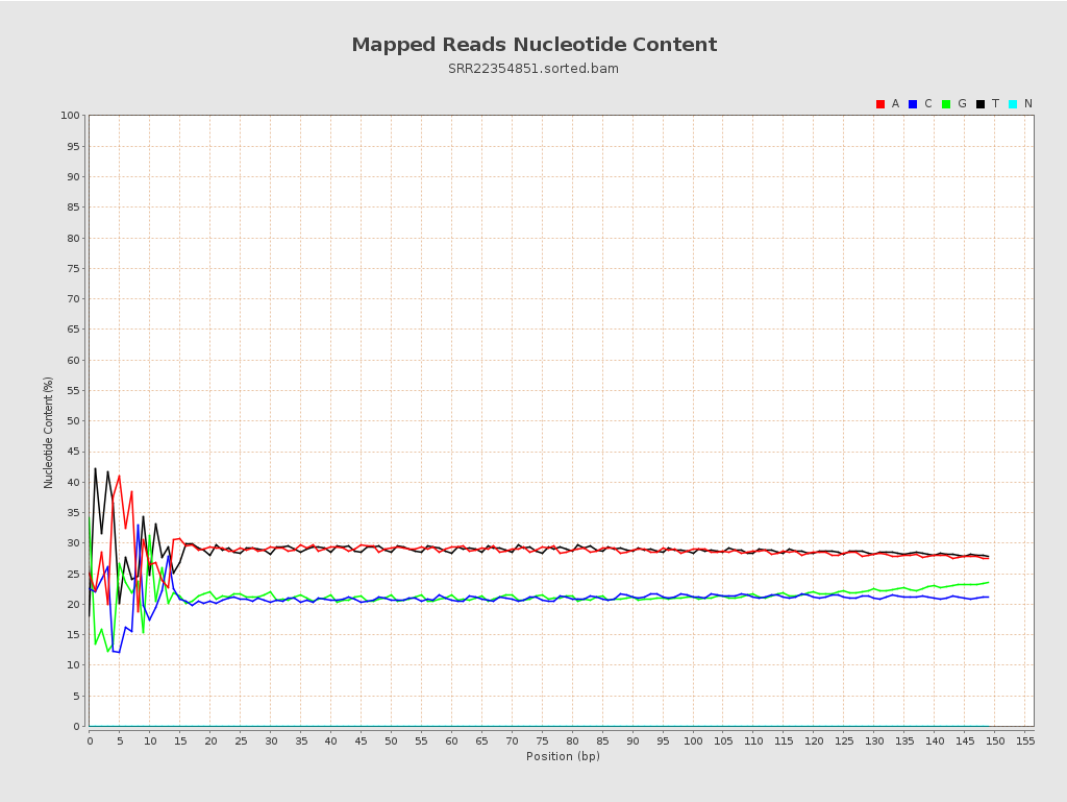
6. Results : Genome Fraction Coverage



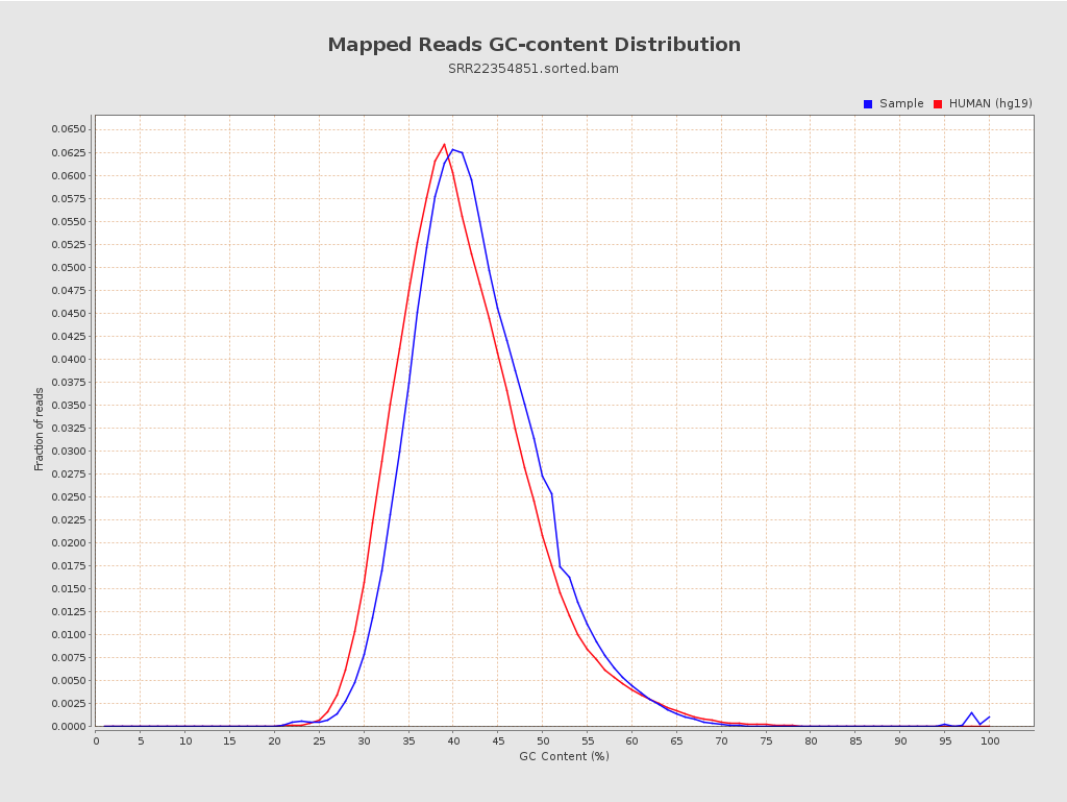
7. Results : Duplication Rate Histogram



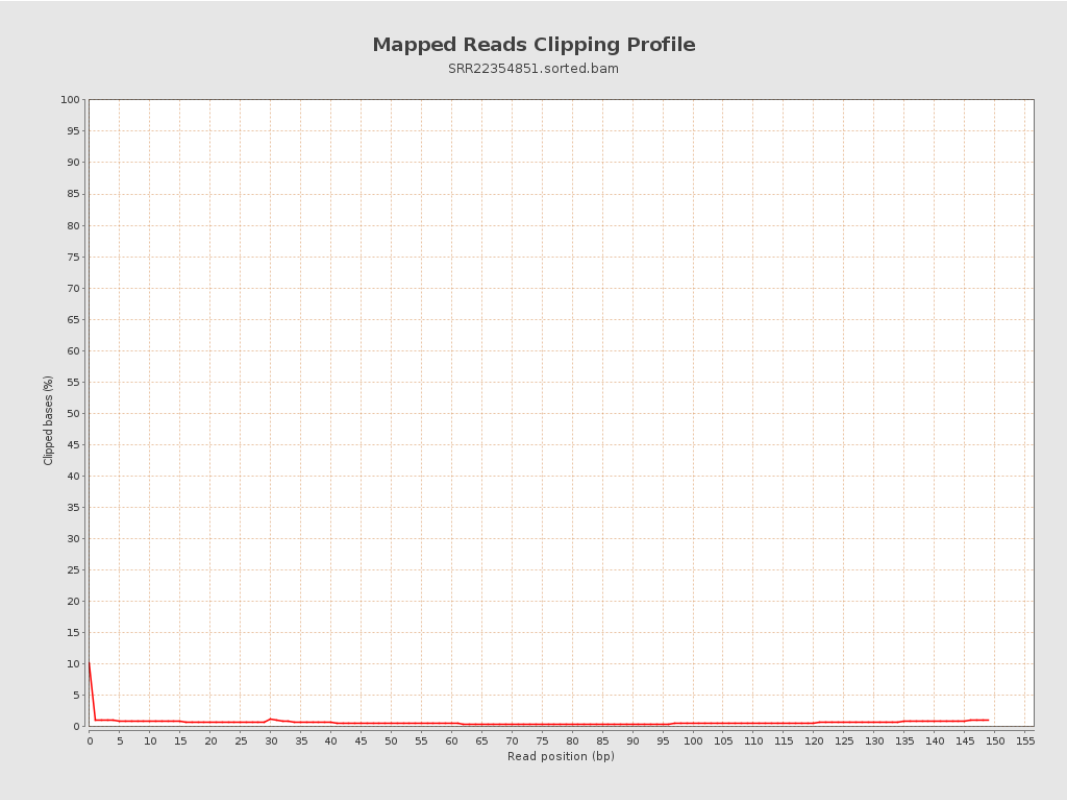
8. Results : Mapped Reads Nucleotide Content



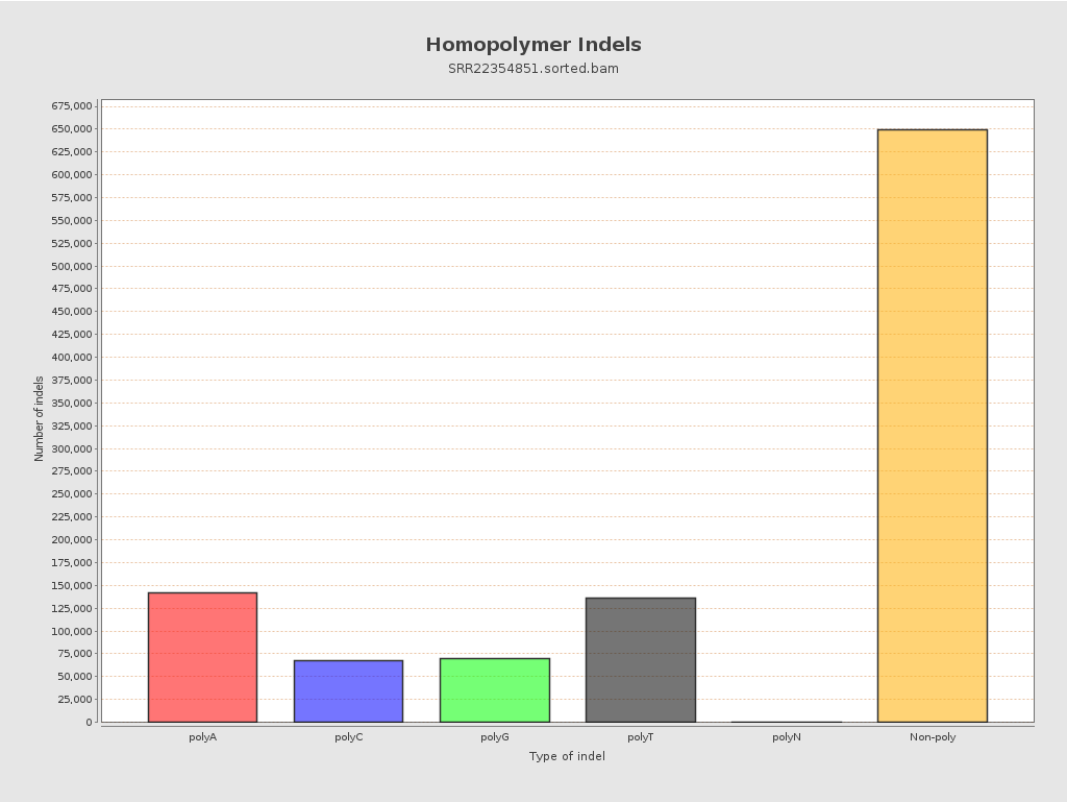
9. Results : Mapped Reads GC-content Distribution



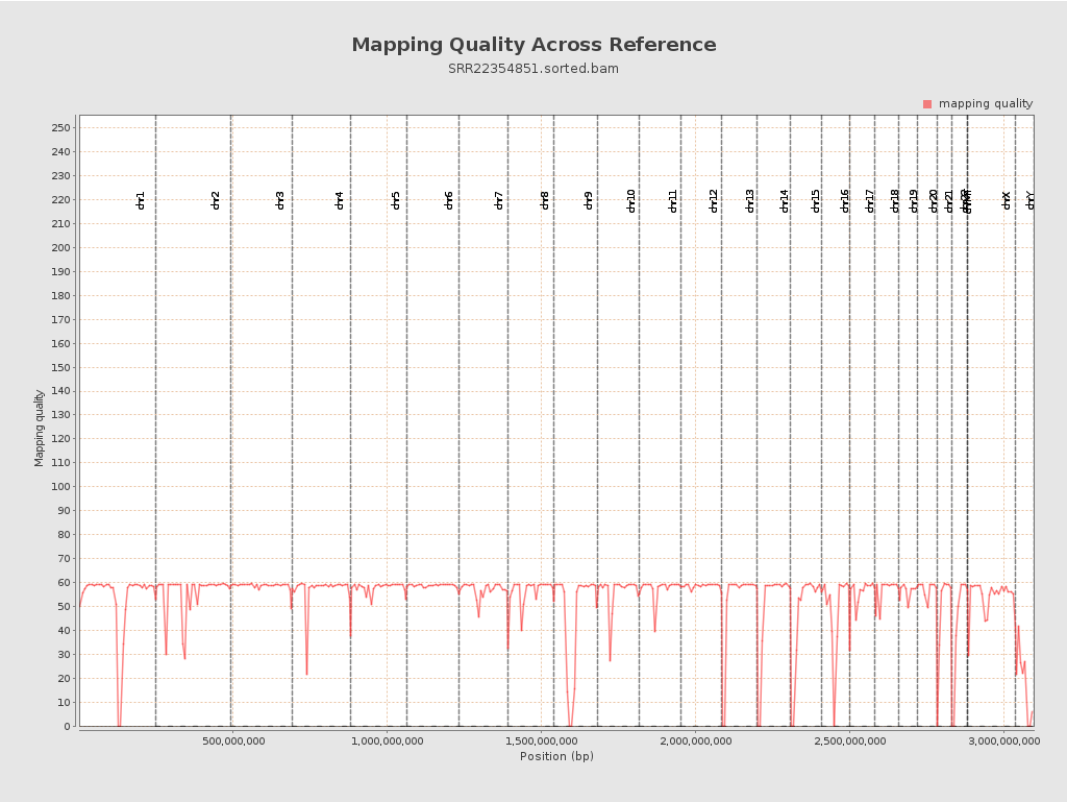
10. Results : Mapped Reads Clipping Profile



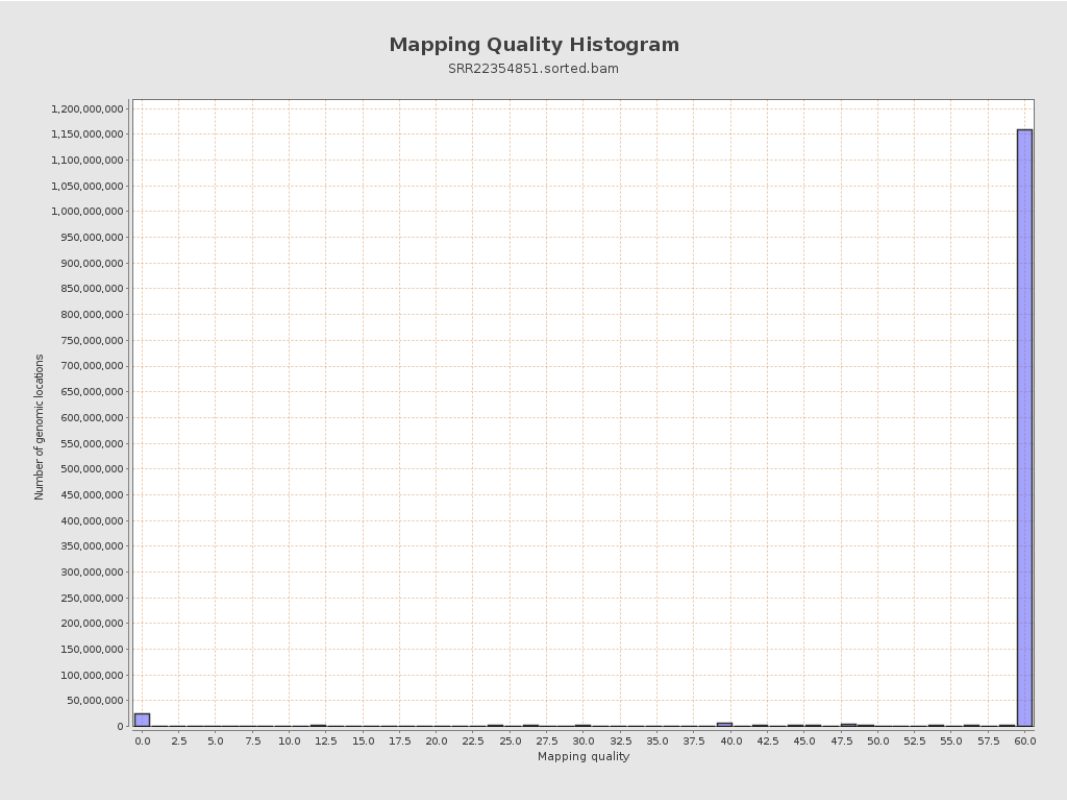
11. Results : Homopolymer Indels



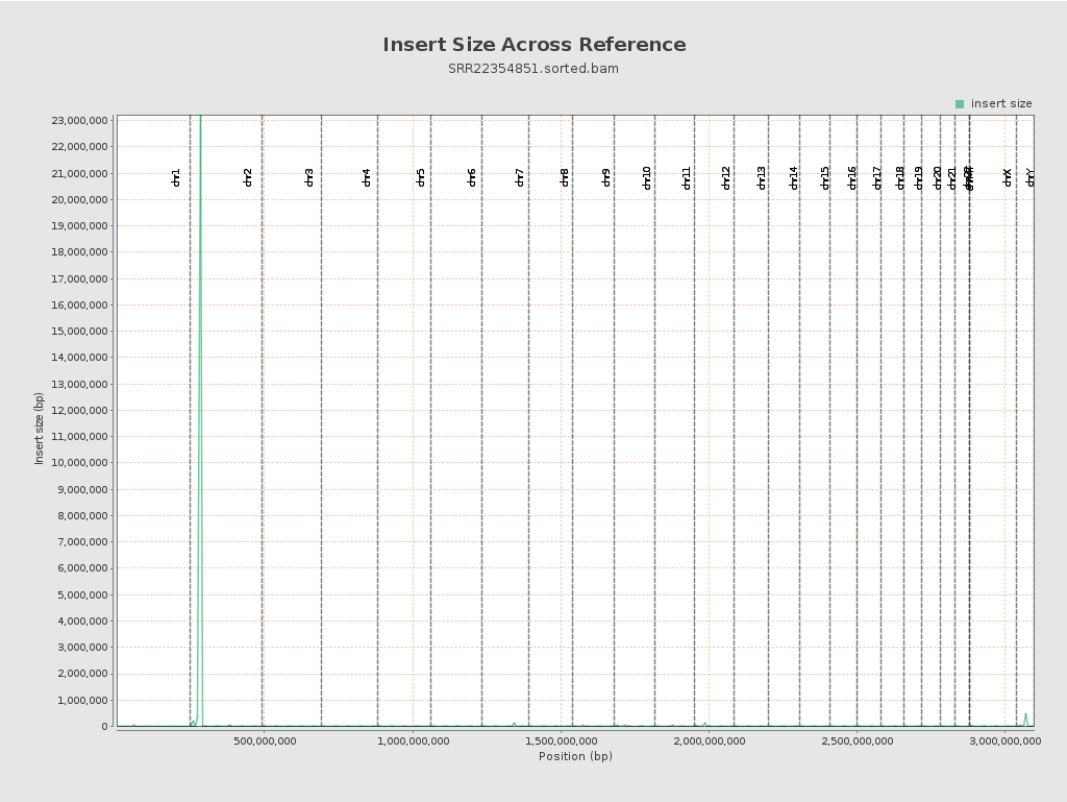
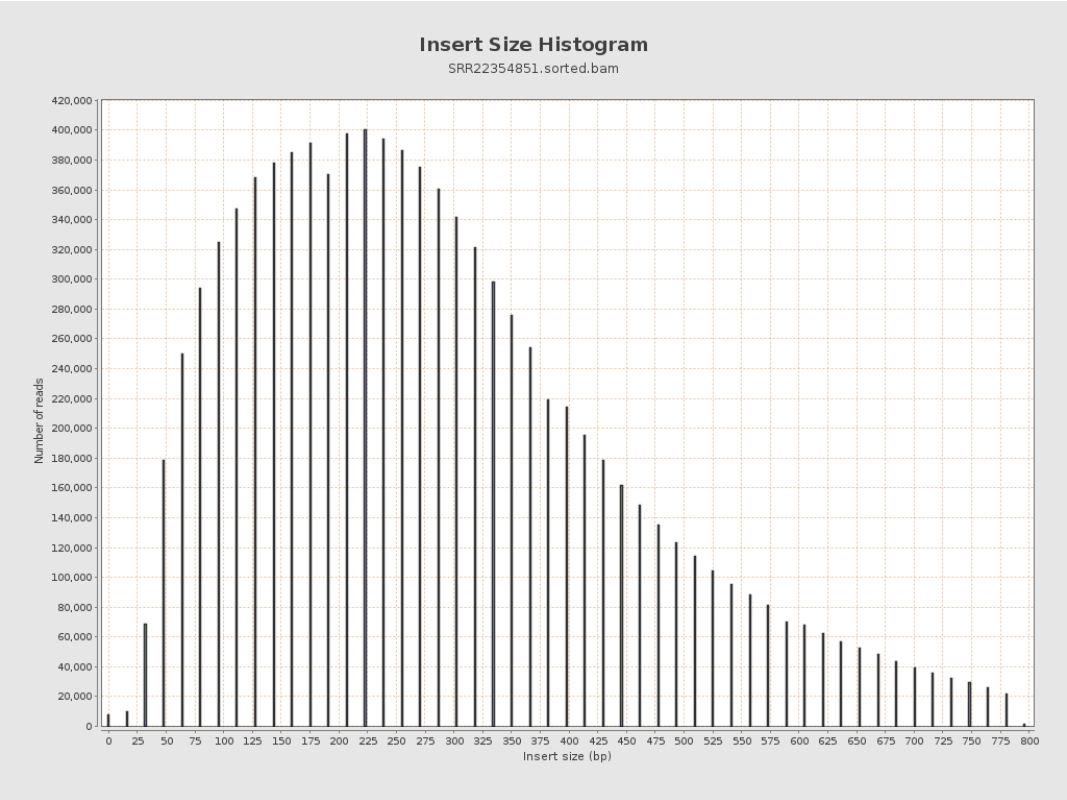
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram