

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/02/03 23:11:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR16352031.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_SRR16352031 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR16352031_1.fastq.gz SRR16352031_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Feb 03 23:11:29 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR16352031.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,669,981,148
Mapped reads	1,621,574,852 / 97.1%
Unmapped reads	48,406,296 / 2.9%
Mapped paired reads	1,621,574,852 / 97.1%
Mapped reads, first in pair	811,735,421 / 48.61%
Mapped reads, second in pair	809,839,431 / 48.49%
Mapped reads, both in pair	1,607,370,294 / 96.25%
Mapped reads, singletons	14,204,558 / 0.85%
Secondary alignments	0
Supplementary alignments	39,396,406 / 2.36%
Read min/max/mean length	30 / 100 / 92.93
Duplicated reads (estimated)	639,800,565 / 38.31%
Duplication rate	35.95%
Clipped reads	240,683,590 / 14.41%

2.2. ACGT Content

Number/percentage of A's	42,243,552,486 / 28.84%
Number/percentage of C's	30,727,988,466 / 20.98%
Number/percentage of T's	41,844,404,666 / 28.57%
Number/percentage of G's	31,661,019,516 / 21.61%
Number/percentage of N's	3,062,450 / 0%

GC Percentage	42.59%
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2.3. Coverage

Mean	47.3475
Standard Deviation	389.8482

2.4. Mapping Quality

Mean Mapping Quality	52.96
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2.5. Insert size

Mean	155,716.43
Standard Deviation	3,869,616.97
P25/Median/P75	209 / 276 / 385

2.6. Mismatches and indels

General error rate	0.75%
Mismatches	1,052,758,656
Insertions	18,956,685
Mapped reads with at least one insertion	1.15%
Deletions	61,707,593
Mapped reads with at least one deletion	3.73%
Homopolymer indels	45.35%

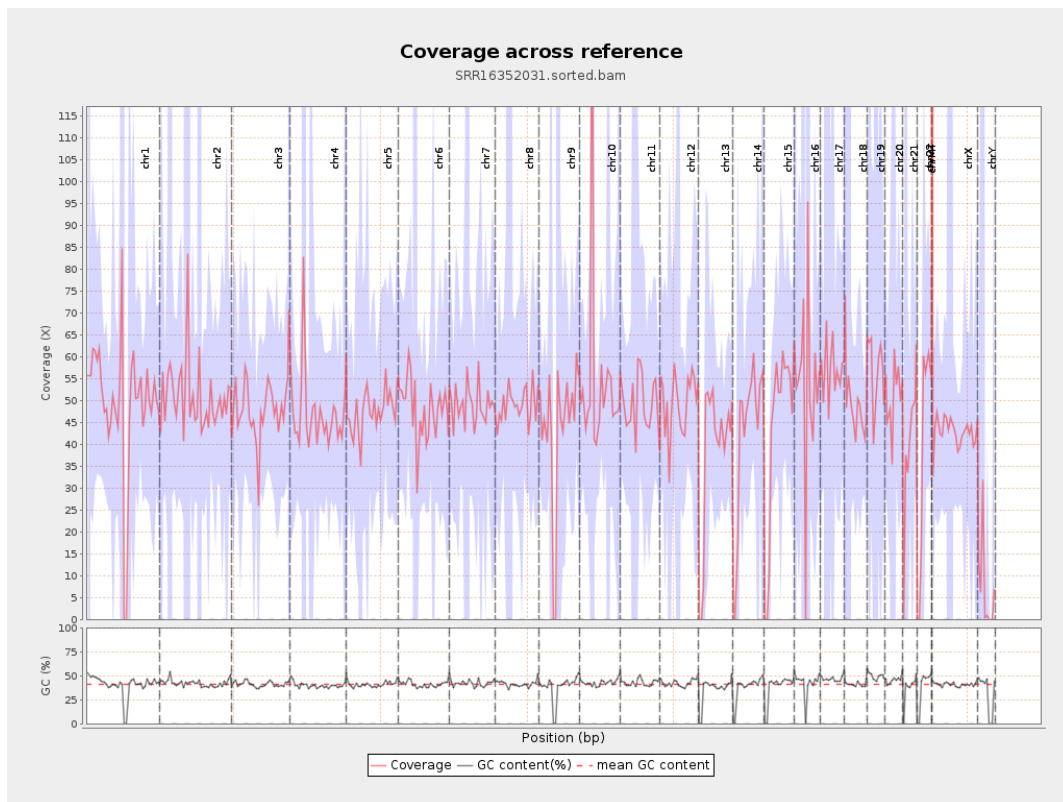
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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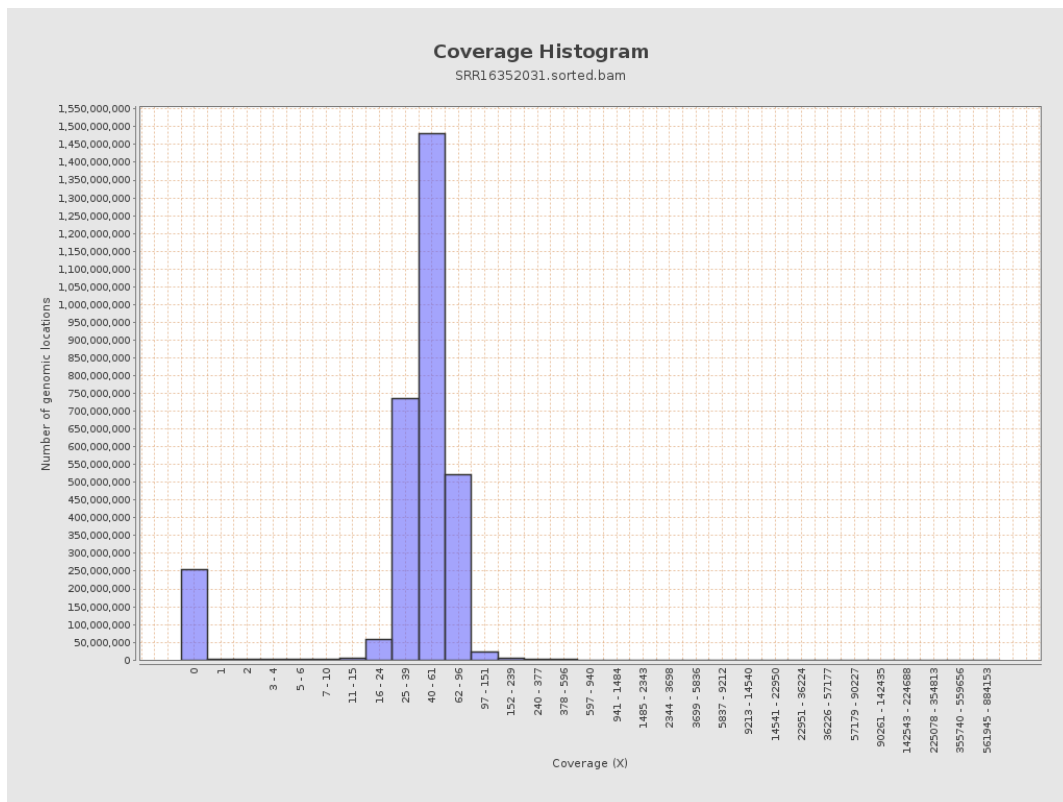
		bases	coverage	deviation
chr1	249250621	12393472880	49.7229	880.3972
chr2	243199373	12395471861	50.9684	456.2094
chr3	198022430	9494912094	47.9487	37.2523
chr4	191154276	8926413107	46.6974	259.0911
chr5	180915260	8615555386	47.622	34.4657
chr6	171115067	8195205933	47.893	103.8649
chr7	159138663	7798635162	49.0053	264.2816
chr8	146364022	7168466774	48.977	552.3544
chr9	141213431	6165695369	43.6622	270.8442
chr10	135534747	7418457483	54.7347	797.6166
chr11	135006516	6702822067	49.6481	146.166
chr12	133851895	6605987039	49.353	48.3192
chr13	115169878	4387501245	38.0959	28.3966
chr14	107349540	4495767205	41.8797	45.2628
chr15	102531392	4387885321	42.7955	32.5244
chr16	90354753	4909290510	54.3335	325.039
chr17	81195210	4626275001	56.9772	153.9084
chr18	78077248	3755644502	48.1017	453.7209
chr19	59128983	3387600506	57.2917	365.4663
chr20	63025520	3207308514	50.889	53.4649
chr21	48129895	1939732382	40.302	94.4731
chr22	51304566	2052483113	40.0059	42.1714
chrMT	16571	482242987	29,101.6225	5,546.1732
chrX	155270560	6629954841	42.6994	77.2214

chrY	59373566	430474546	7.2503	253.9522
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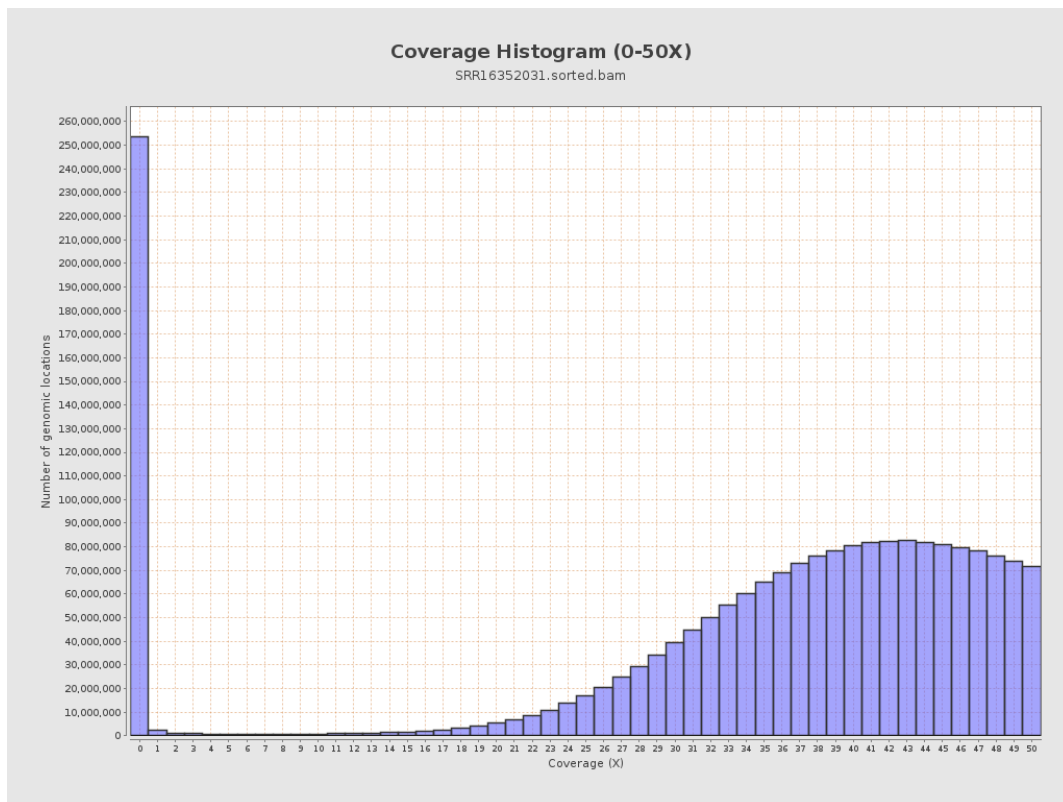
3. Results : Coverage across reference



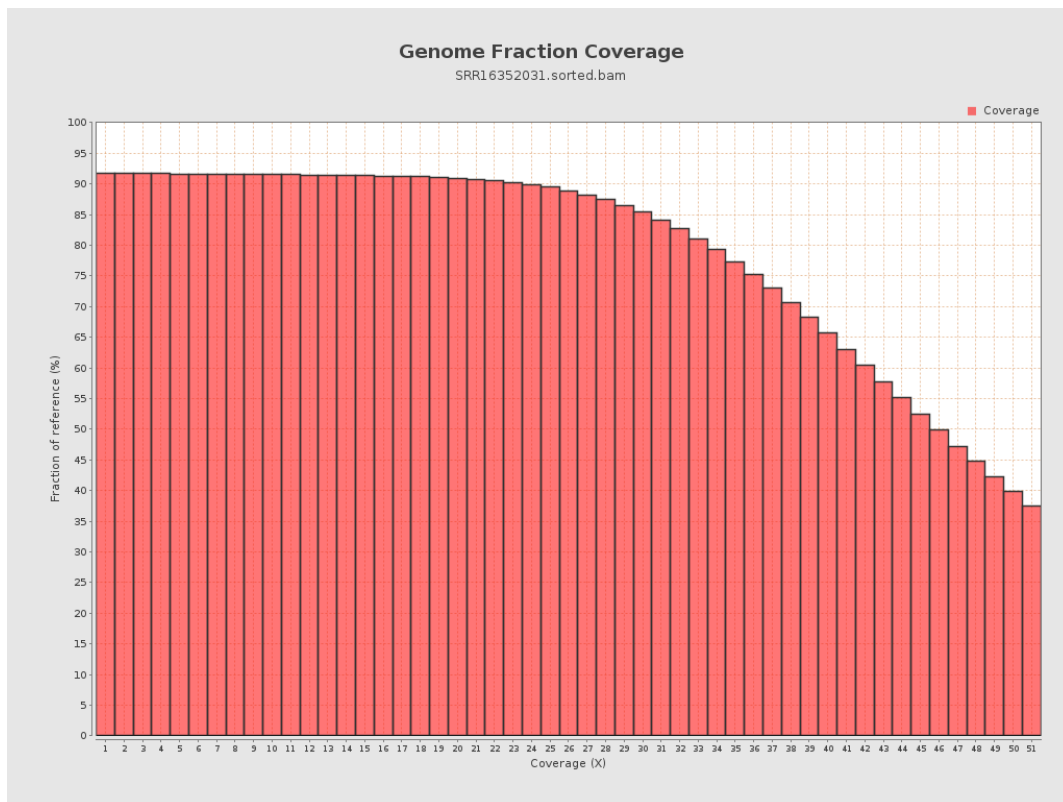
4. Results : Coverage Histogram



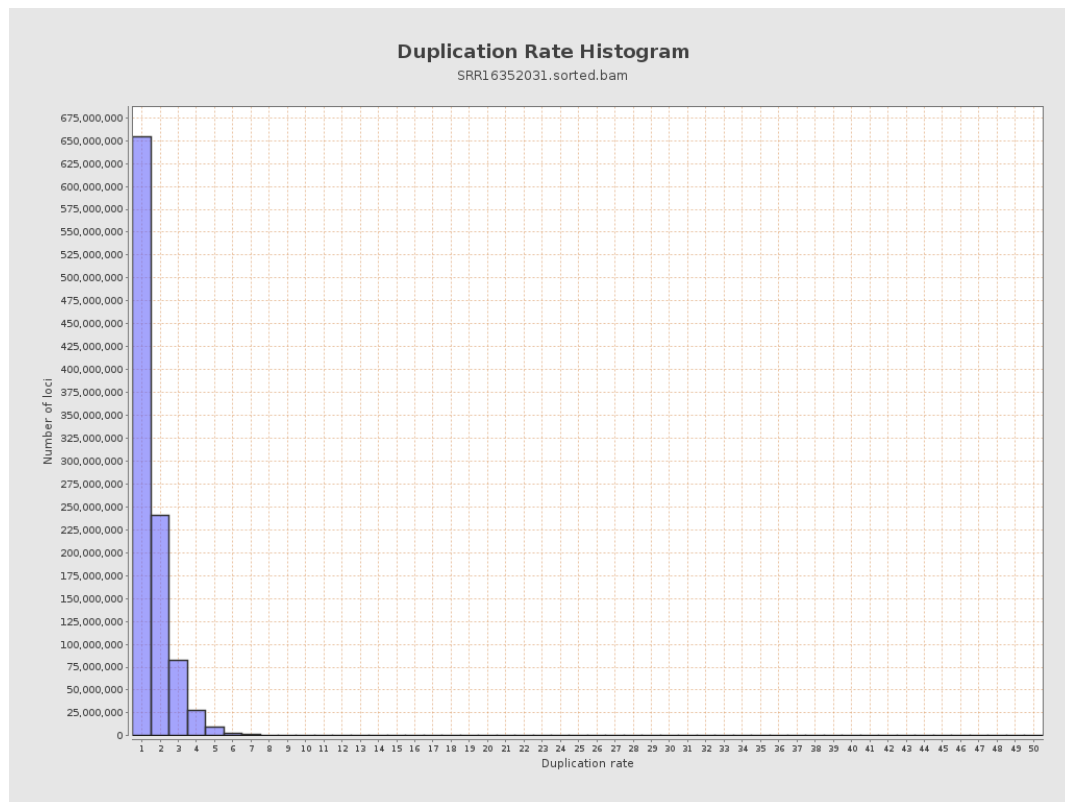
5. Results : Coverage Histogram (0-50X)



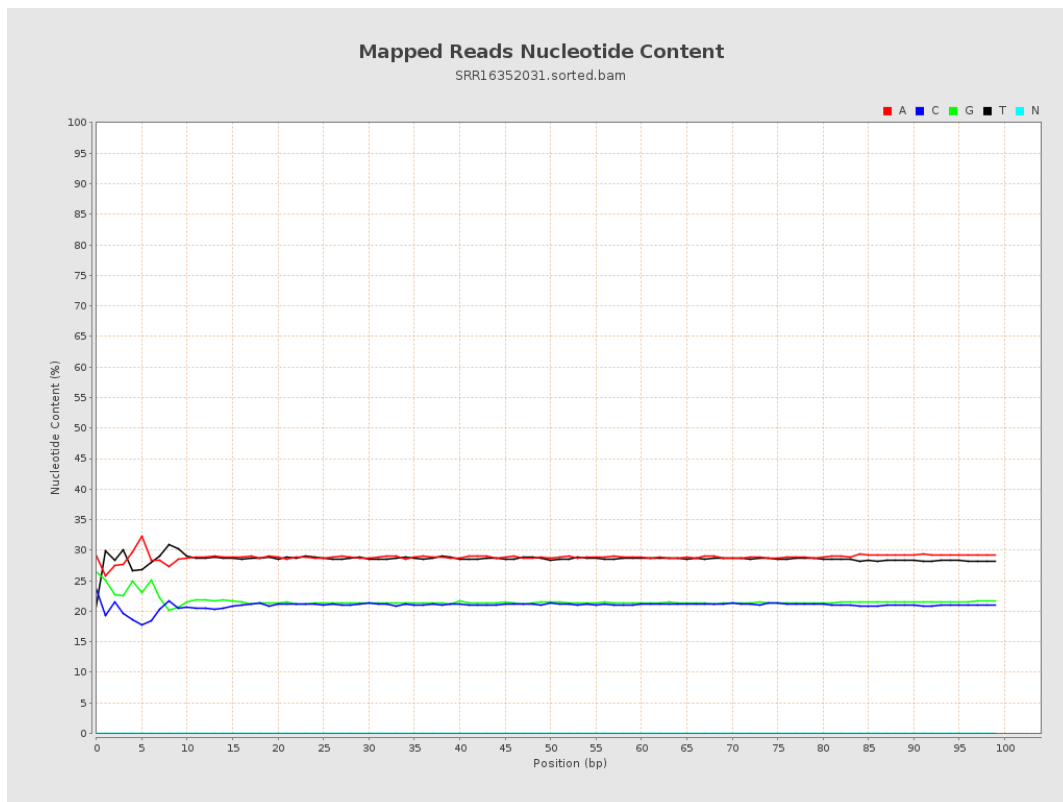
6. Results : Genome Fraction Coverage



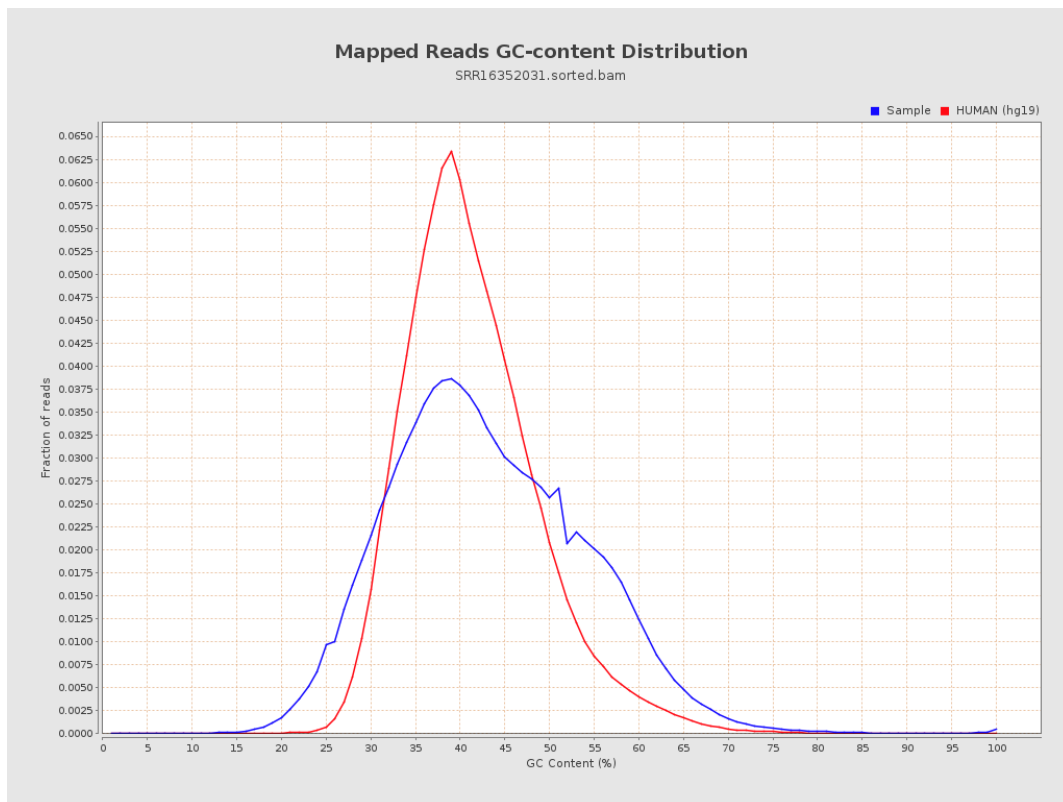
7. Results : Duplication Rate Histogram



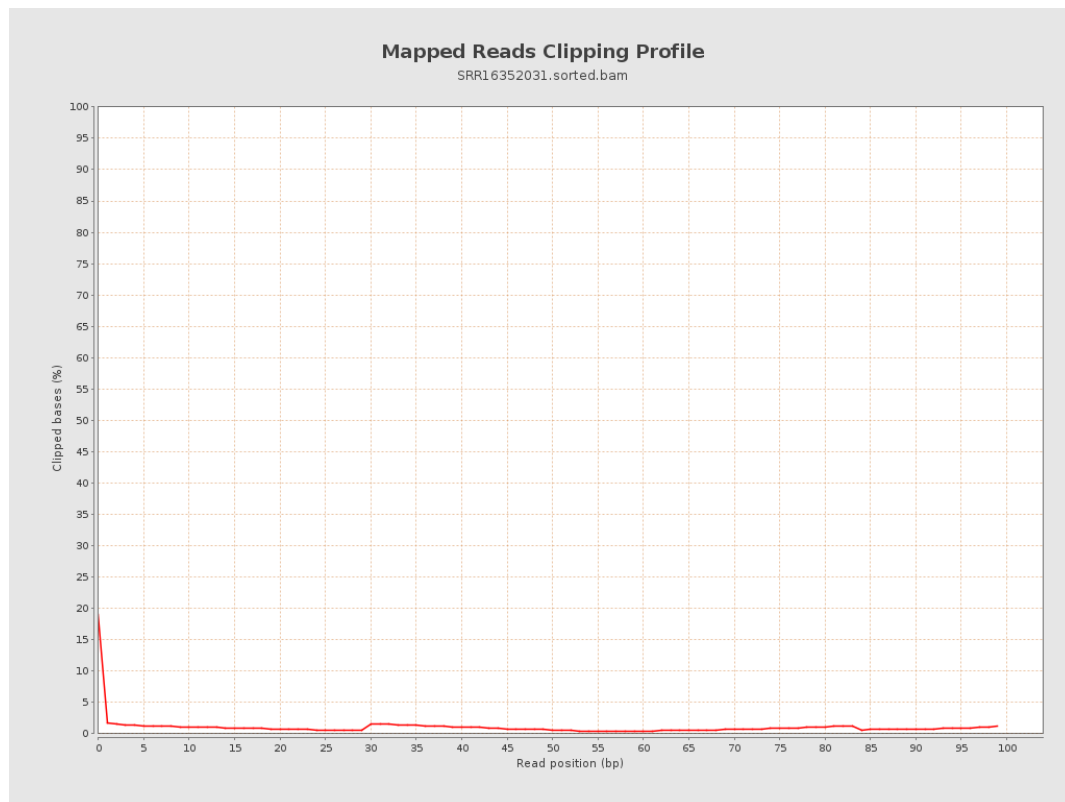
8. Results : Mapped Reads Nucleotide Content



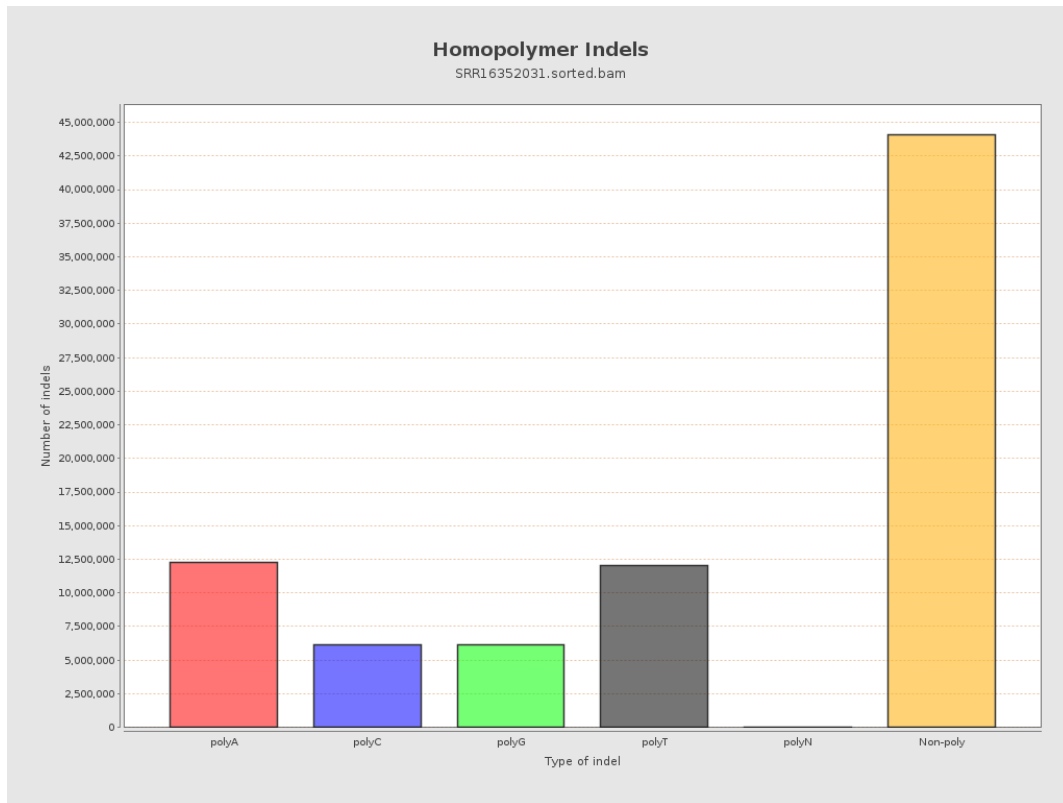
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



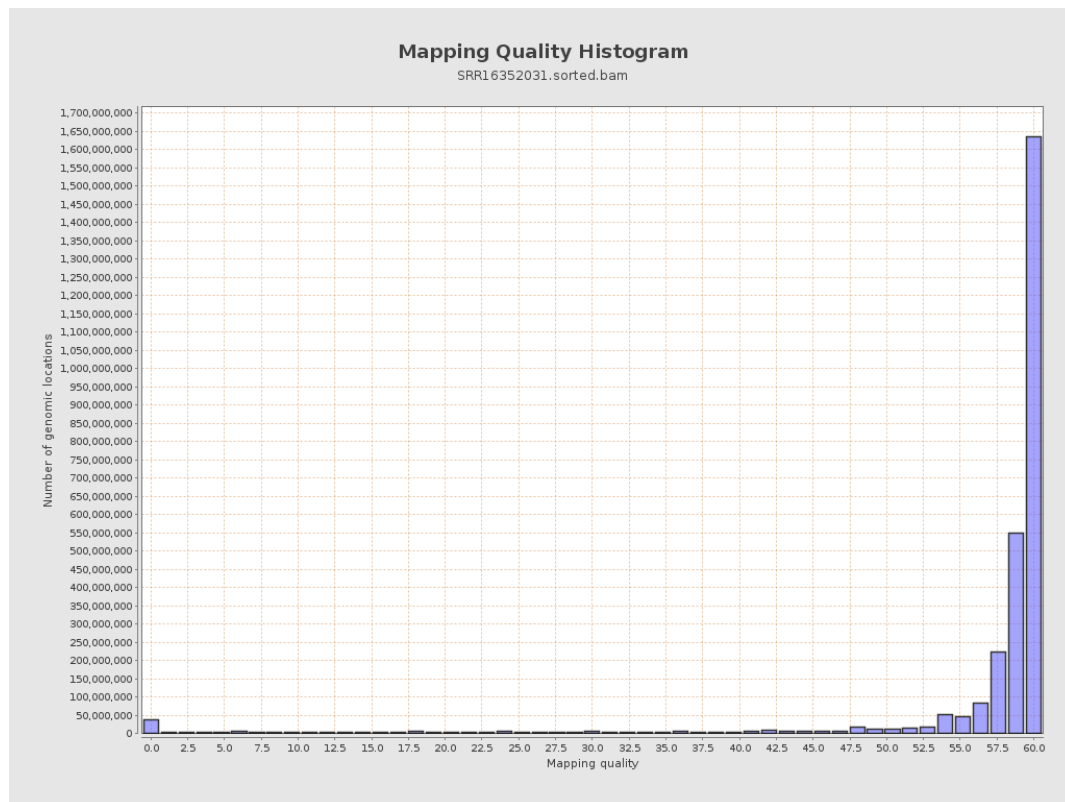
11. Results : Homopolymer Indels



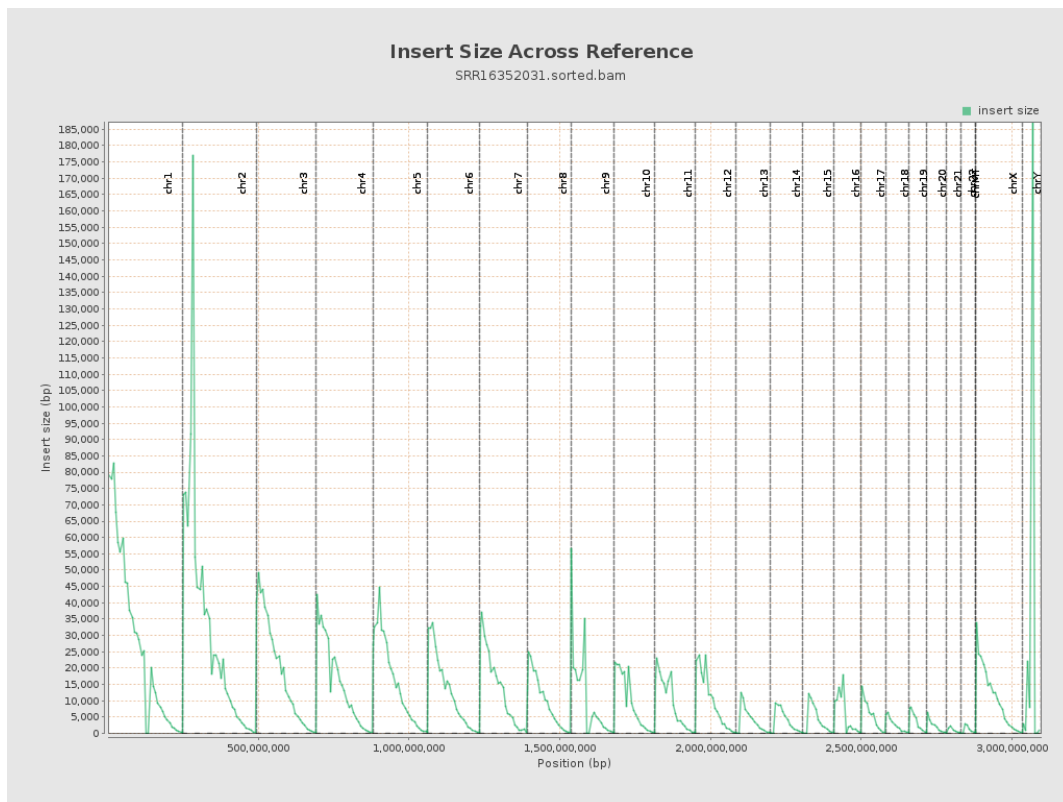
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

