

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/02/03 01:25:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR16352030.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_SRR16352030 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR16352030_1.fastq.gz SRR16352030_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Feb 03 01:25:19 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR16352030.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,336,675,720
Mapped reads	1,298,801,732 / 97.17%
Unmapped reads	37,873,988 / 2.83%
Mapped paired reads	1,298,801,732 / 97.17%
Mapped reads, first in pair	650,371,204 / 48.66%
Mapped reads, second in pair	648,430,528 / 48.51%
Mapped reads, both in pair	1,287,814,374 / 96.34%
Mapped reads, singletons	10,987,358 / 0.82%
Secondary alignments	0
Supplementary alignments	29,274,740 / 2.19%
Read min/max/mean length	30 / 100 / 92.87
Duplicated reads (estimated)	442,779,823 / 33.13%
Duplication rate	30.53%
Clipped reads	185,146,690 / 13.85%

2.2. ACGT Content

Number/percentage of A's	33,959,488,488 / 28.92%
Number/percentage of C's	24,527,098,627 / 20.89%
Number/percentage of T's	33,666,772,840 / 28.67%
Number/percentage of G's	25,257,061,333 / 21.51%
Number/percentage of N's	2,356,499 / 0%

GC Percentage	42.4%
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2.3. Coverage

Mean	37.952
Standard Deviation	319.1197

2.4. Mapping Quality

Mean Mapping Quality	52.96
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2.5. Insert size

Mean	153,627.38
Standard Deviation	3,834,024.35
P25/Median/P75	214 / 284 / 399

2.6. Mismatches and indels

General error rate	0.75%
Mismatches	848,059,447
Insertions	15,126,461
Mapped reads with at least one insertion	1.14%
Deletions	50,182,853
Mapped reads with at least one deletion	3.78%
Homopolymer indels	45.42%

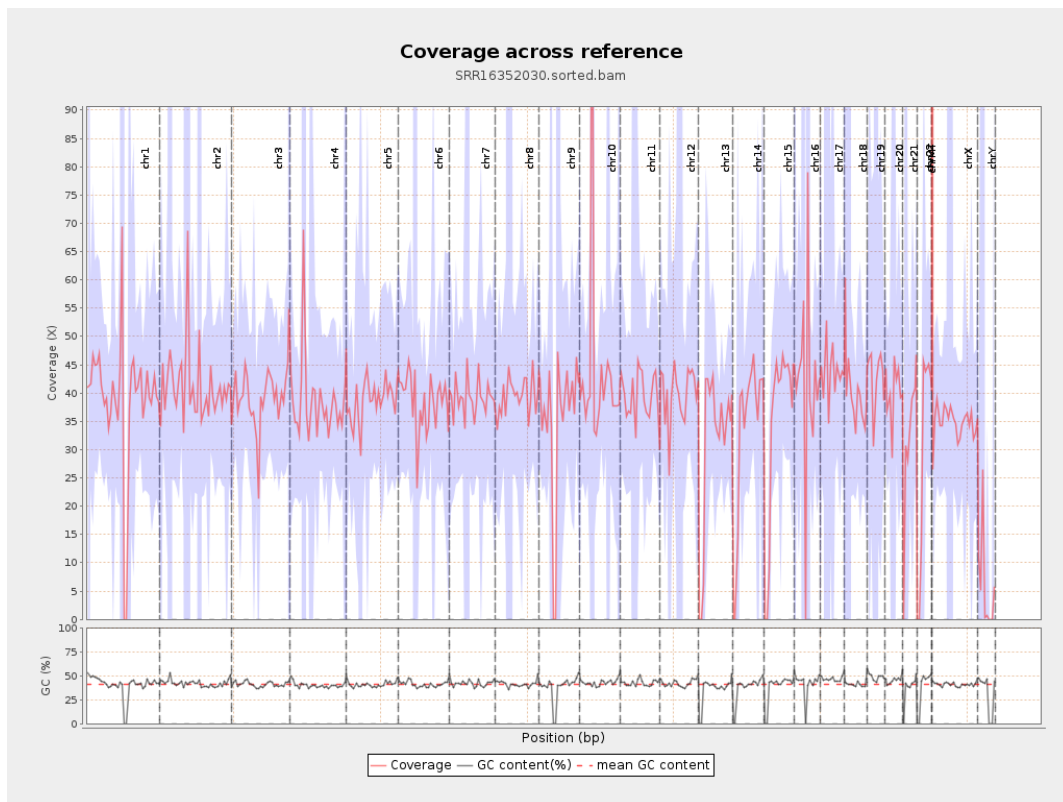
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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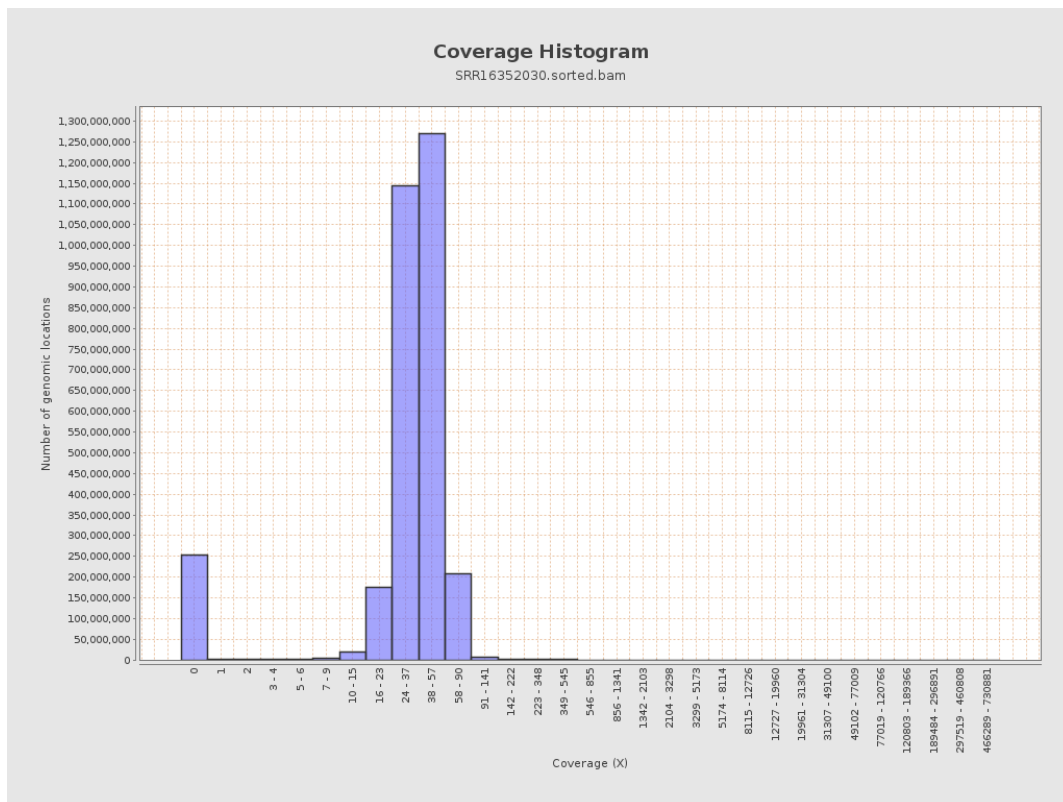
		bases	coverage	deviation
chr1	249250621	9761110089	39.1618	722.0093
chr2	243199373	10044008009	41.2995	359.2544
chr3	198022430	7754041916	39.1574	30.4196
chr4	191154276	7317047252	38.2782	216.3971
chr5	180915260	7013591187	38.7673	25.2842
chr6	171115067	6577200700	38.4373	83.7639
chr7	159138663	6236601517	39.1897	215.1145
chr8	146364022	5774058410	39.45	453.5828
chr9	141213431	4970759958	35.2003	227.8365
chr10	135534747	5989844594	44.1942	663.6936
chr11	135006516	5378200685	39.8366	127.9464
chr12	133851895	5321468995	39.7564	55.5312
chr13	115169878	3578277535	31.0696	21.8211
chr14	107349540	3572862283	33.2825	34.9536
chr15	102531392	3464418532	33.7889	24.6827
chr16	90354753	3816693937	42.2412	273.6618
chr17	81195210	3542854182	43.6338	127.6571
chr18	78077248	3067634673	39.2897	380.6353
chr19	59128983	2551131533	43.1452	298.6944
chr20	63025520	2525465847	40.0705	41.6453
chr21	48129895	1564759522	32.5112	75.7572
chr22	51304566	1559624215	30.3993	32.5615
chrMT	16571	349166542	21,070.9397	4,035.7343
chrX	155270560	5403726106	34.802	62.2241

chrY	59373566	353361939	5.9515	213.1386
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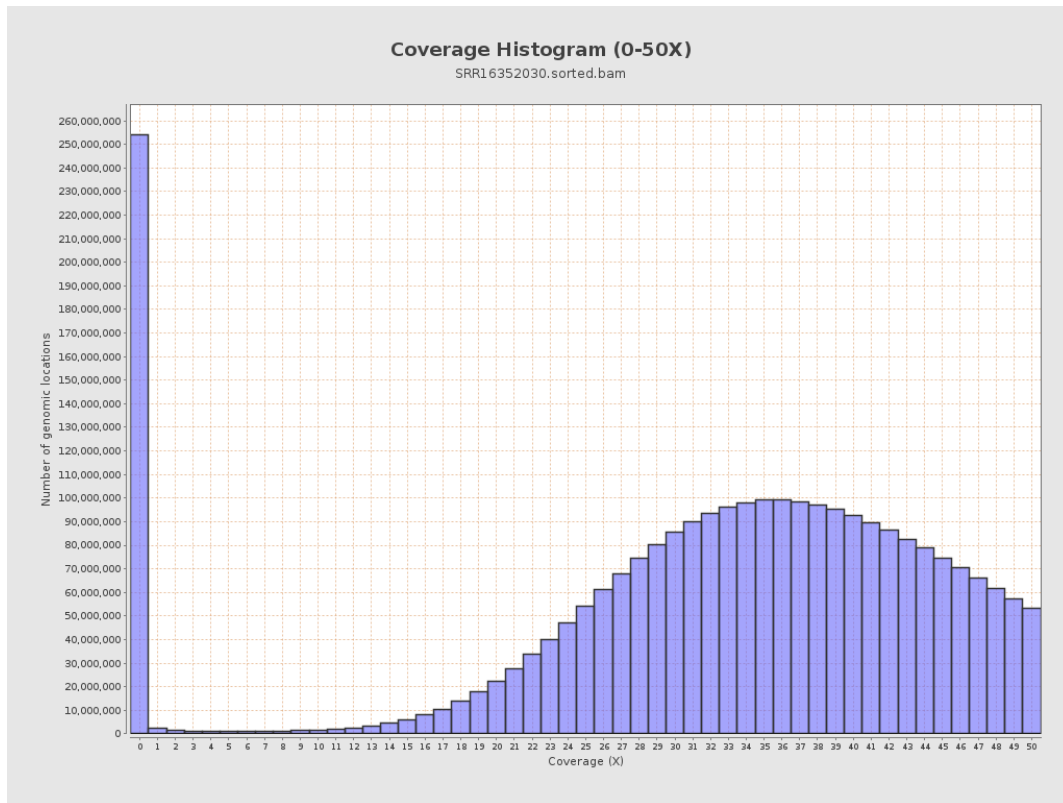
3. Results : Coverage across reference



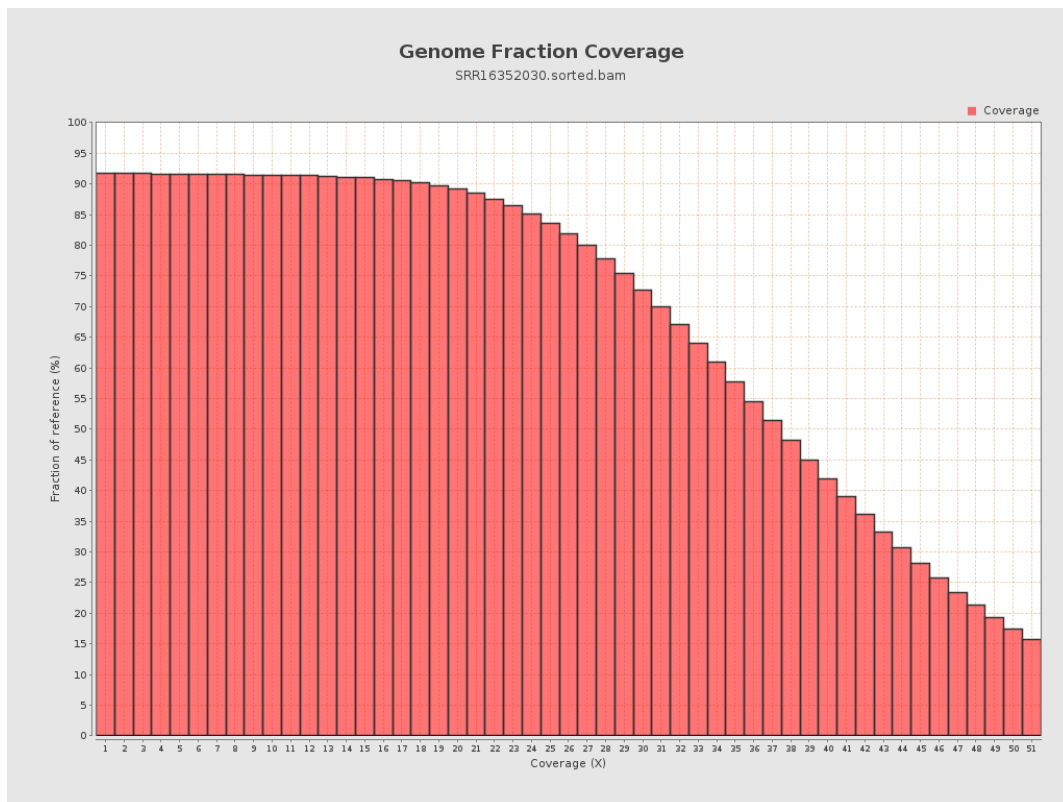
4. Results : Coverage Histogram



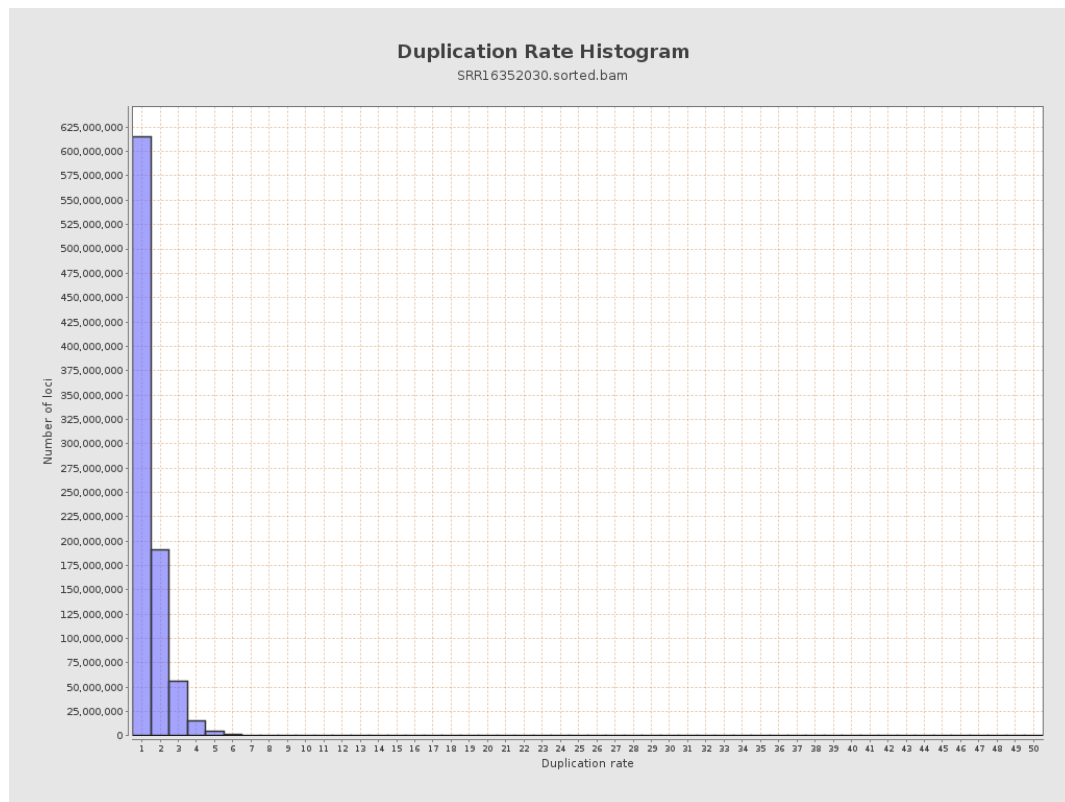
5. Results : Coverage Histogram (0-50X)



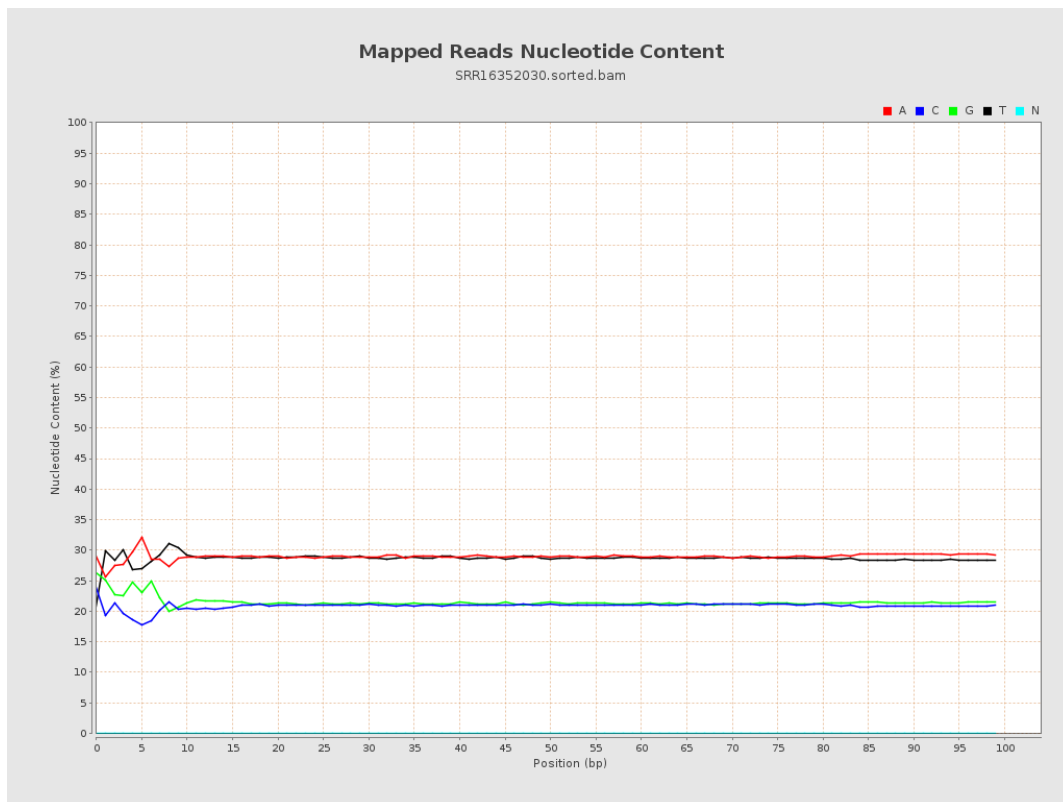
6. Results : Genome Fraction Coverage



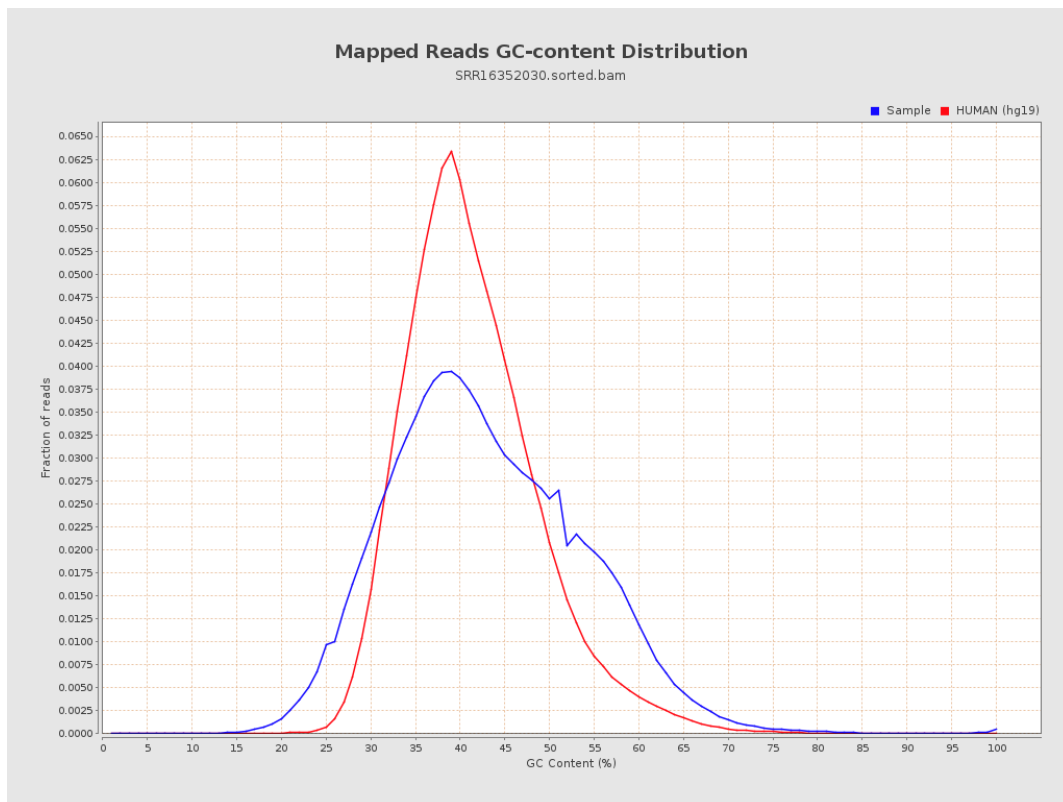
7. Results : Duplication Rate Histogram



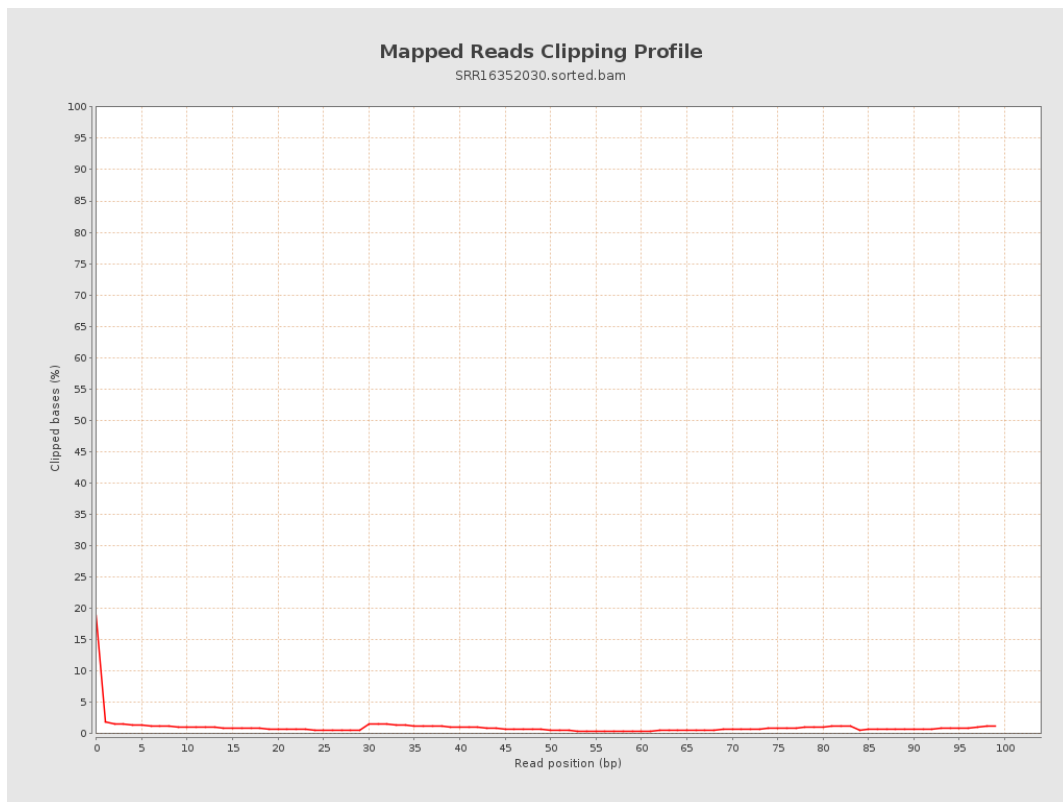
8. Results : Mapped Reads Nucleotide Content



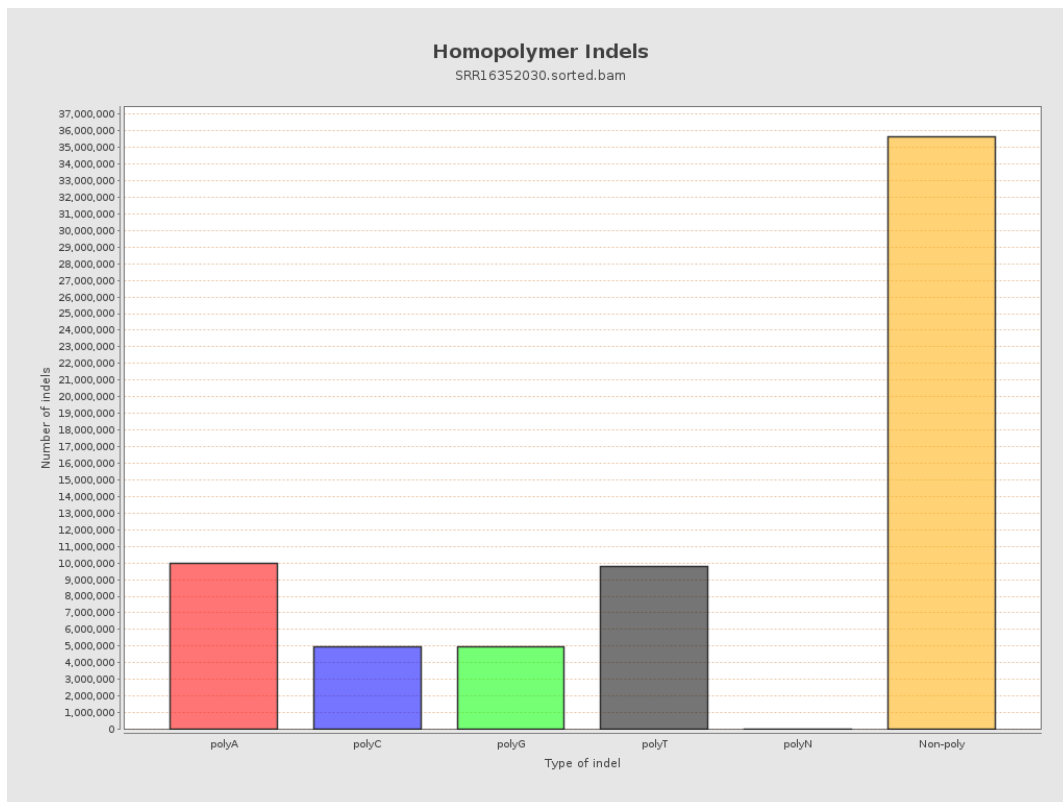
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



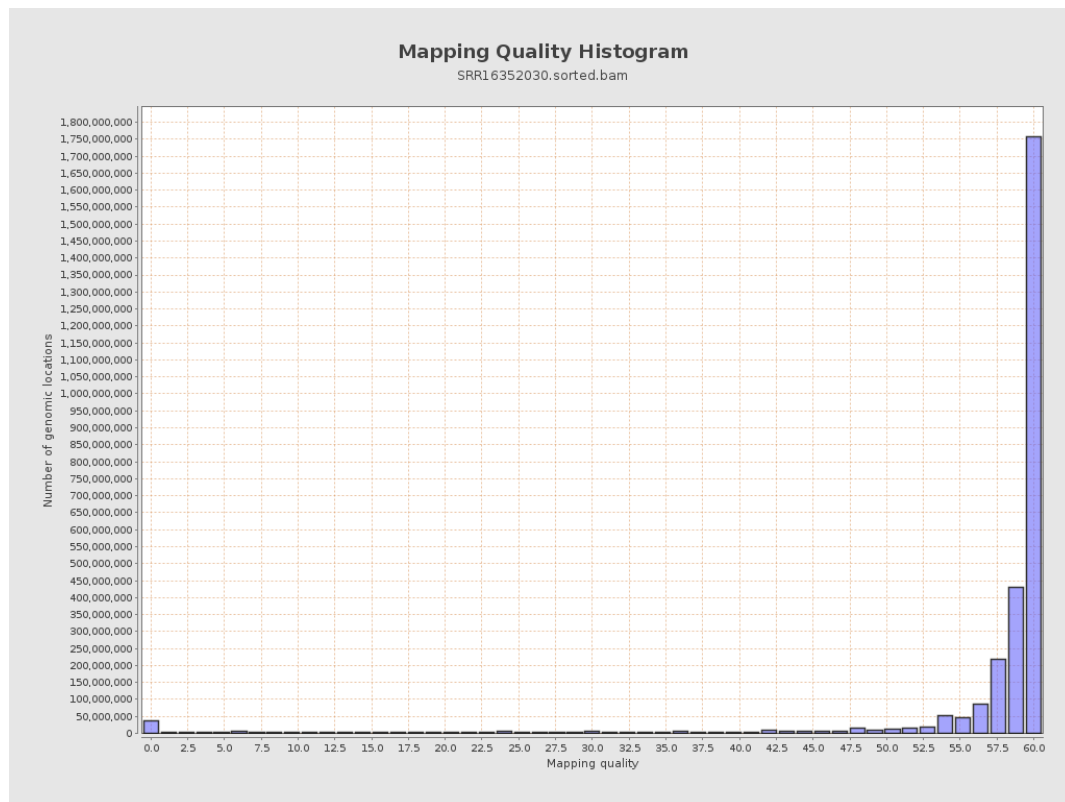
11. Results : Homopolymer Indels



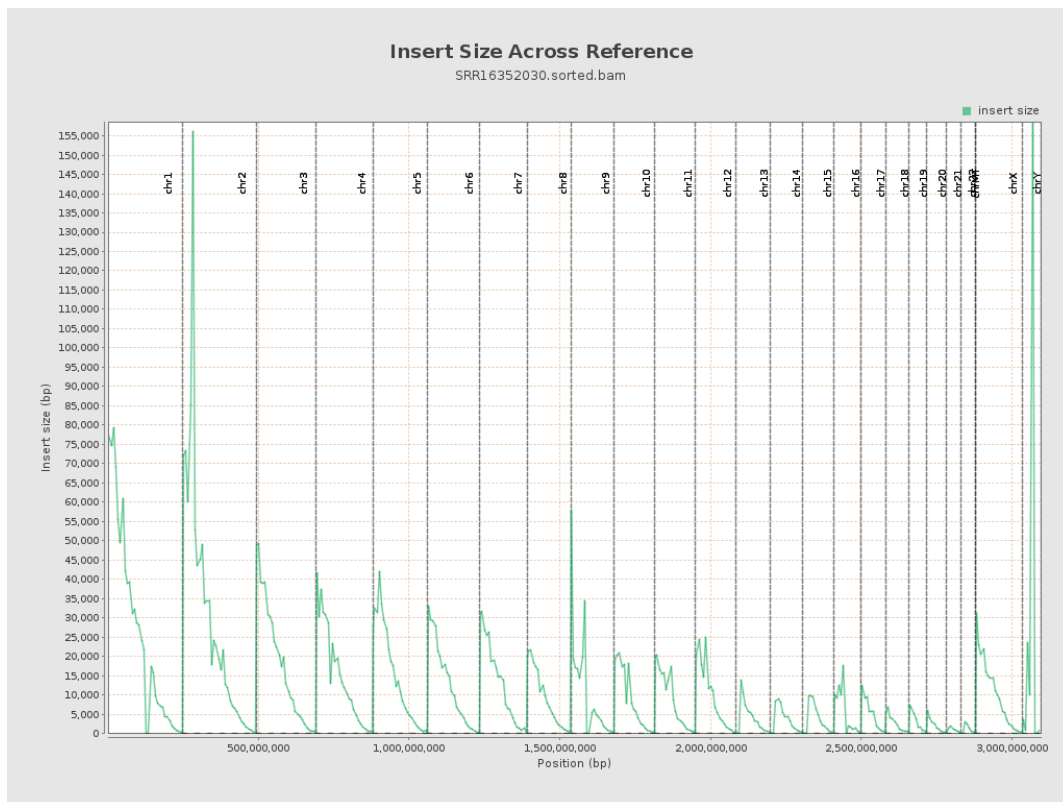
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

