

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/02/04 20:06:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR16352032.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_SRR16352032 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR16352032_1.fastq.gz SRR16352032_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Feb 04 20:06:09 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR16352032.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,289,884,690
Mapped reads	1,250,606,879 / 96.95%
Unmapped reads	39,277,811 / 3.05%
Mapped paired reads	1,250,606,879 / 96.95%
Mapped reads, first in pair	626,093,063 / 48.54%
Mapped reads, second in pair	624,513,816 / 48.42%
Mapped reads, both in pair	1,239,585,596 / 96.1%
Mapped reads, singletons	11,021,283 / 0.85%
Secondary alignments	0
Supplementary alignments	29,094,813 / 2.26%
Read min/max/mean length	30 / 100 / 92.9
Duplicated reads (estimated)	421,953,553 / 32.71%
Duplication rate	29.33%
Clipped reads	185,187,524 / 14.36%

2.2. ACGT Content

Number/percentage of A's	33,137,002,635 / 29.35%
Number/percentage of C's	23,164,592,030 / 20.51%
Number/percentage of T's	32,811,177,004 / 29.06%
Number/percentage of G's	23,800,597,167 / 21.08%
Number/percentage of N's	2,355,053 / 0%

GC Percentage	41.59%
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2.3. Coverage

Mean	36.4984
Standard Deviation	392.0862

2.4. Mapping Quality

Mean Mapping Quality	52.81
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2.5. Insert size

Mean	165,961.75
Standard Deviation	3,950,413.72
P25/Median/P75	212 / 280 / 395

2.6. Mismatches and indels

General error rate	0.78%
Mismatches	853,329,094
Insertions	14,644,840
Mapped reads with at least one insertion	1.15%
Deletions	47,668,752
Mapped reads with at least one deletion	3.73%
Homopolymer indels	45.13%

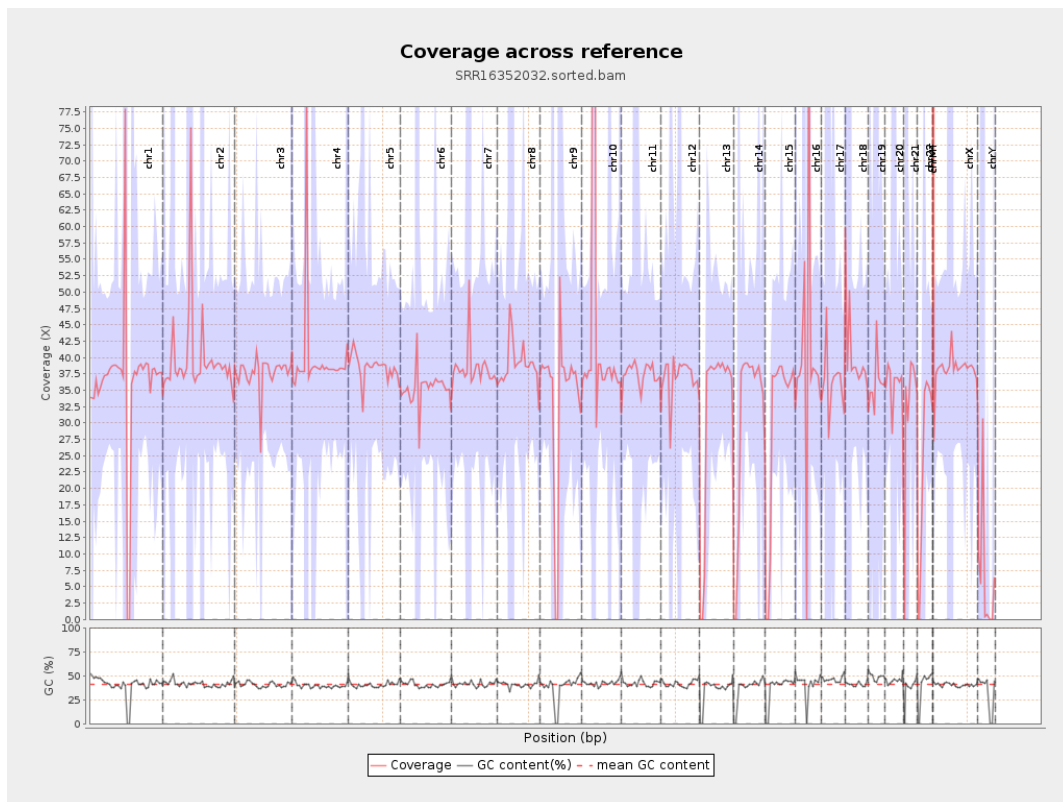
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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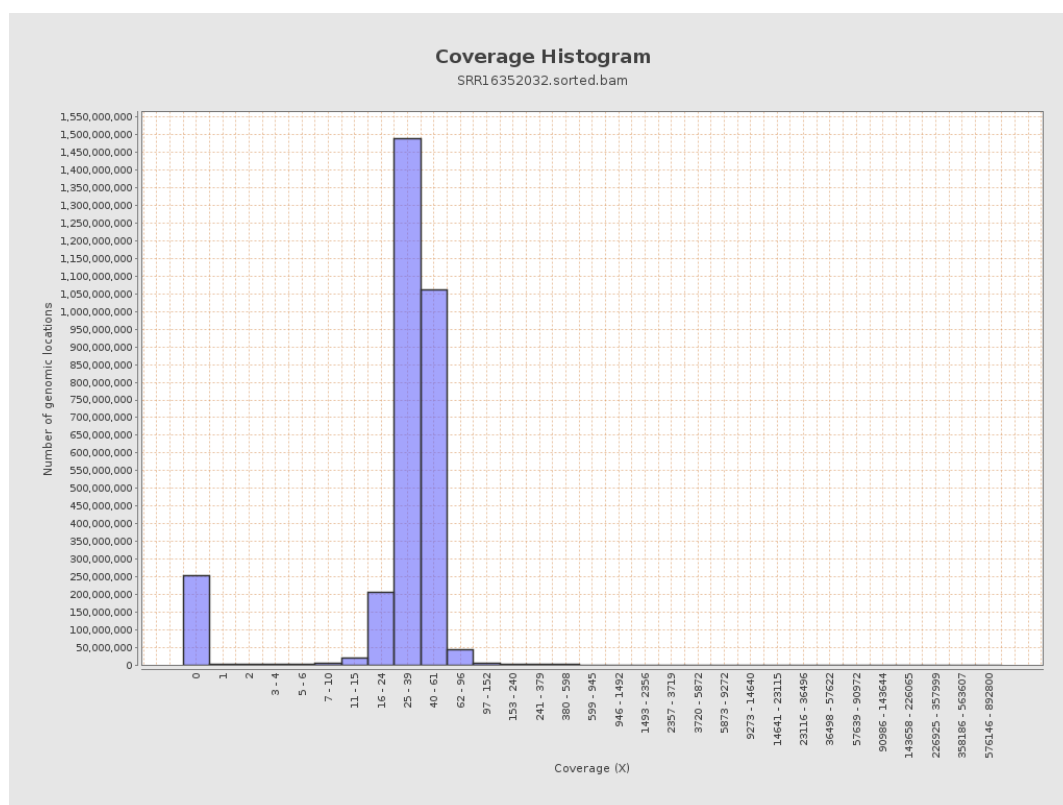
		bases	coverage	deviation
chr1	249250621	9031775292	36.2357	889.1728
chr2	243199373	9688312313	39.8369	367.0317
chr3	198022430	7457842418	37.6616	36.3353
chr4	191154276	7609888502	39.8102	269.4993
chr5	180915260	6934578593	38.3305	26.7427
chr6	171115067	6048280415	35.3463	98.8674
chr7	159138663	6100097480	38.332	268.4983
chr8	146364022	5710895858	39.0184	577.6678
chr9	141213431	4802929521	34.0118	279.106
chr10	135534747	5979733197	44.1196	878.5945
chr11	135006516	5060130888	37.4806	147.0926
chr12	133851895	4958973229	37.0482	38.8307
chr13	115169878	3666900742	31.8391	20.8079
chr14	107349540	3368468063	31.3785	35.6206
chr15	102531392	3059325144	29.8379	22.7208
chr16	90354753	3601039775	39.8545	358.158
chr17	81195210	2956038480	36.4066	156.4472
chr18	78077248	3124336596	40.016	482.2762
chr19	59128983	2141309493	36.2142	369.9602
chr20	63025520	2252031177	35.7321	48.5556
chr21	48129895	1569624335	32.6123	88.6233
chr22	51304566	1259546130	24.5504	31.2717
chrMT	16571	294933823	17,798.191	3,060.1609
chrX	155270560	5921343349	38.1356	74.059

chrY	59373566	389506938	6.5603	262.9279
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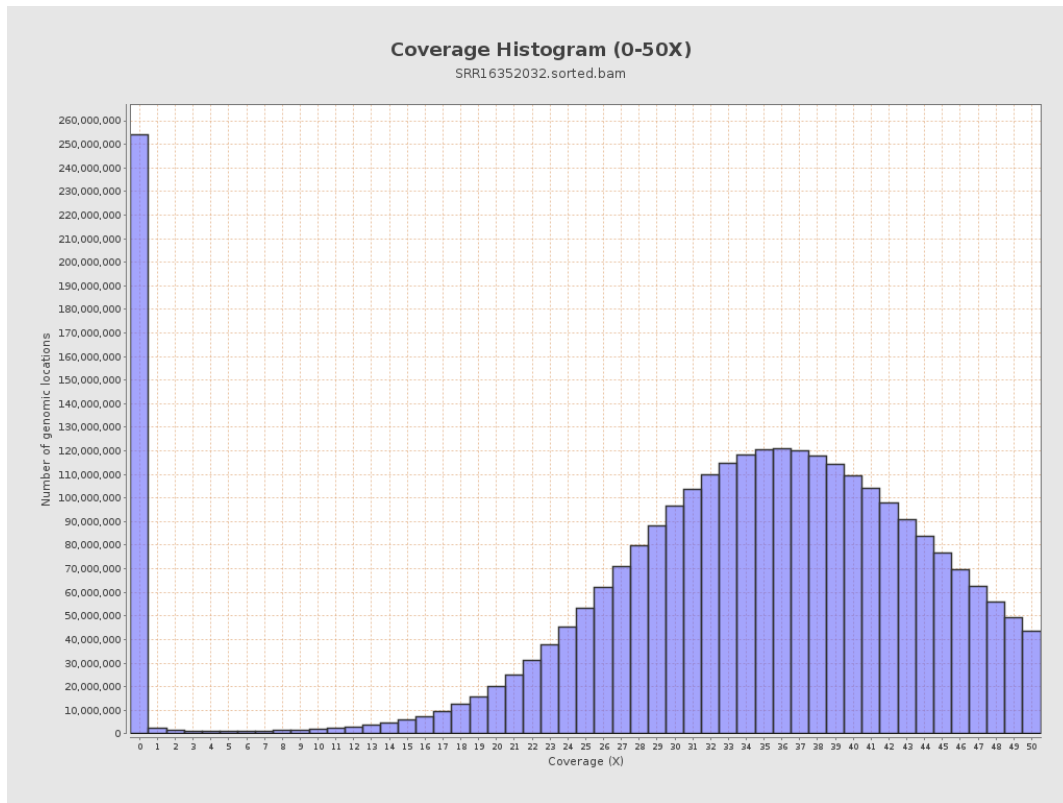
3. Results : Coverage across reference



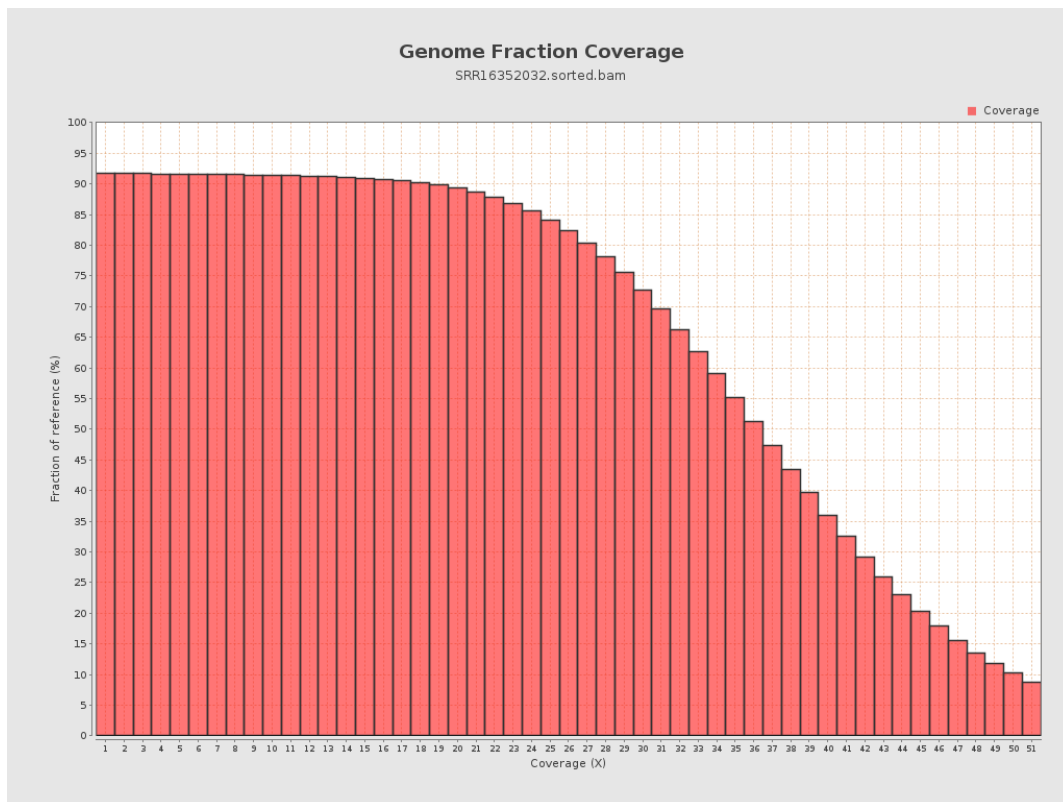
4. Results : Coverage Histogram



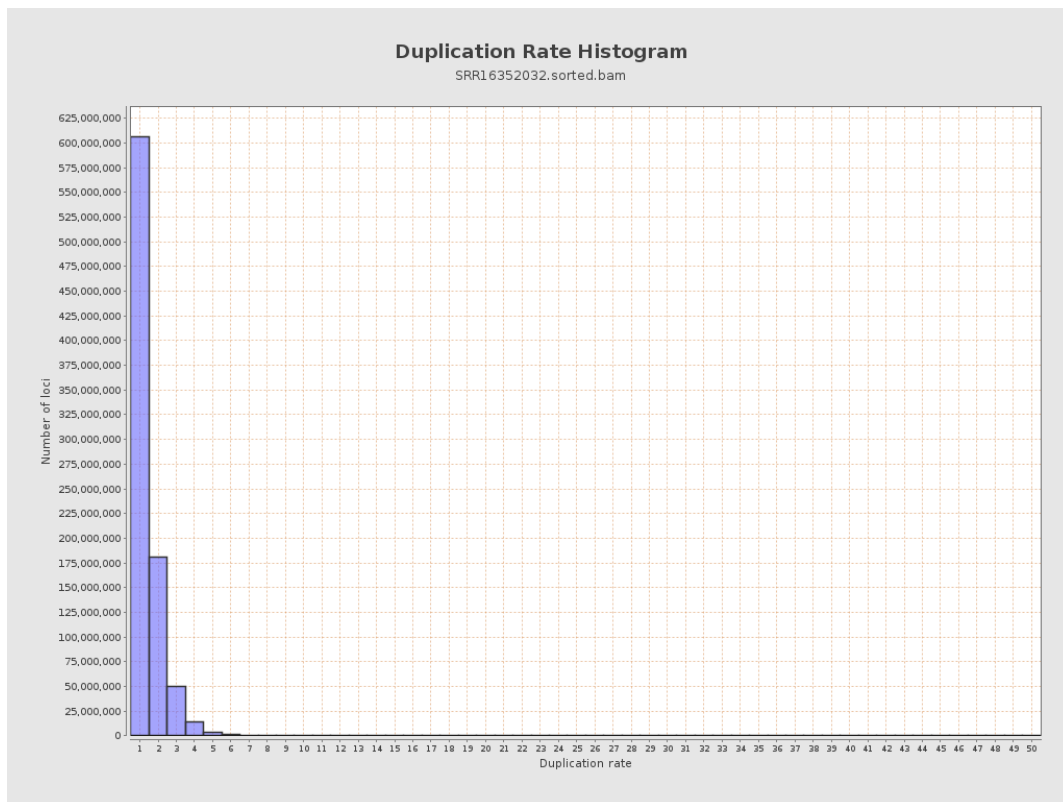
5. Results : Coverage Histogram (0-50X)



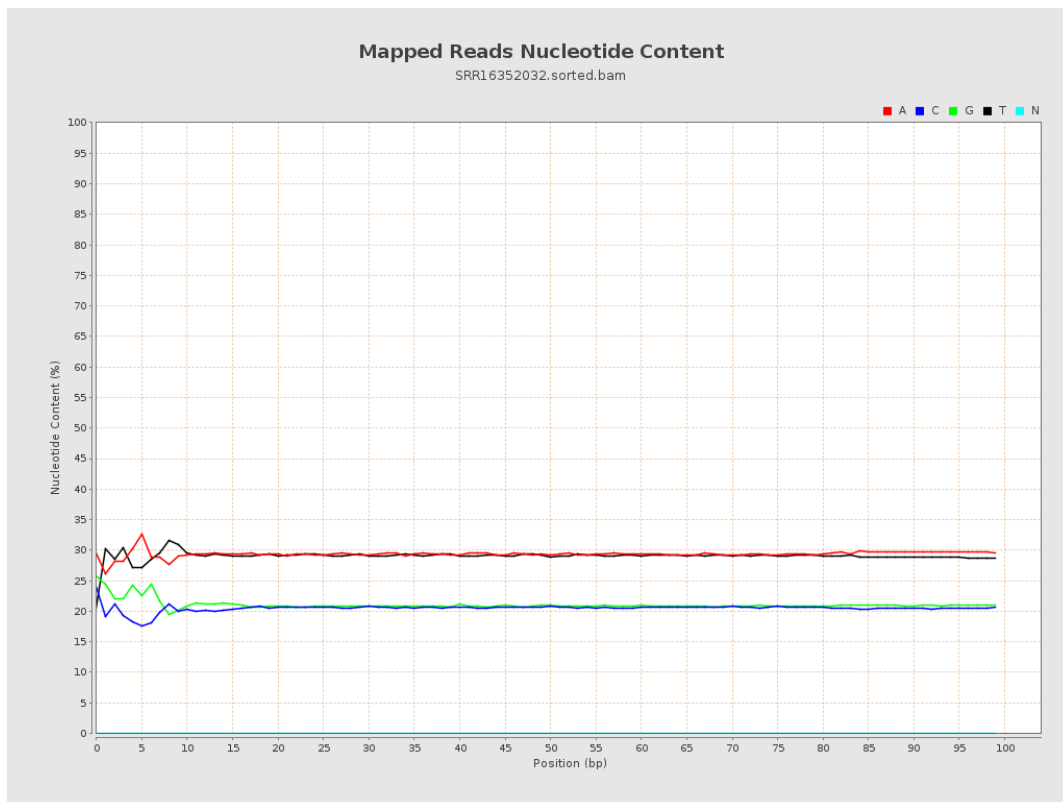
6. Results : Genome Fraction Coverage



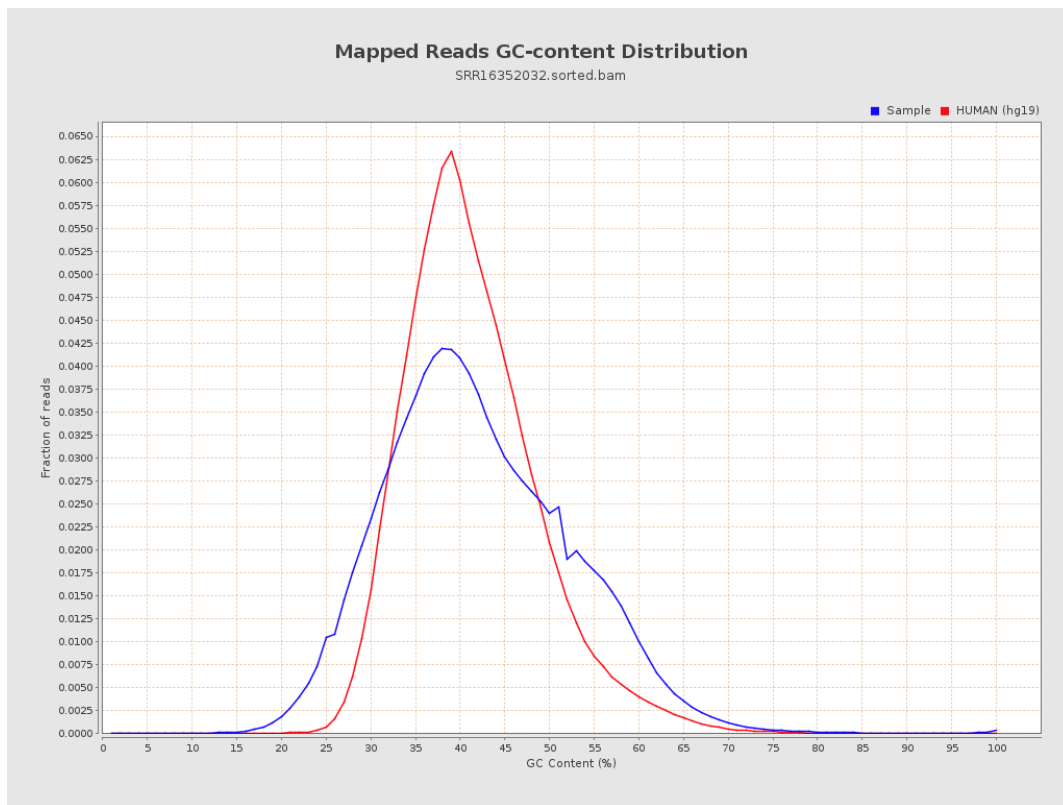
7. Results : Duplication Rate Histogram



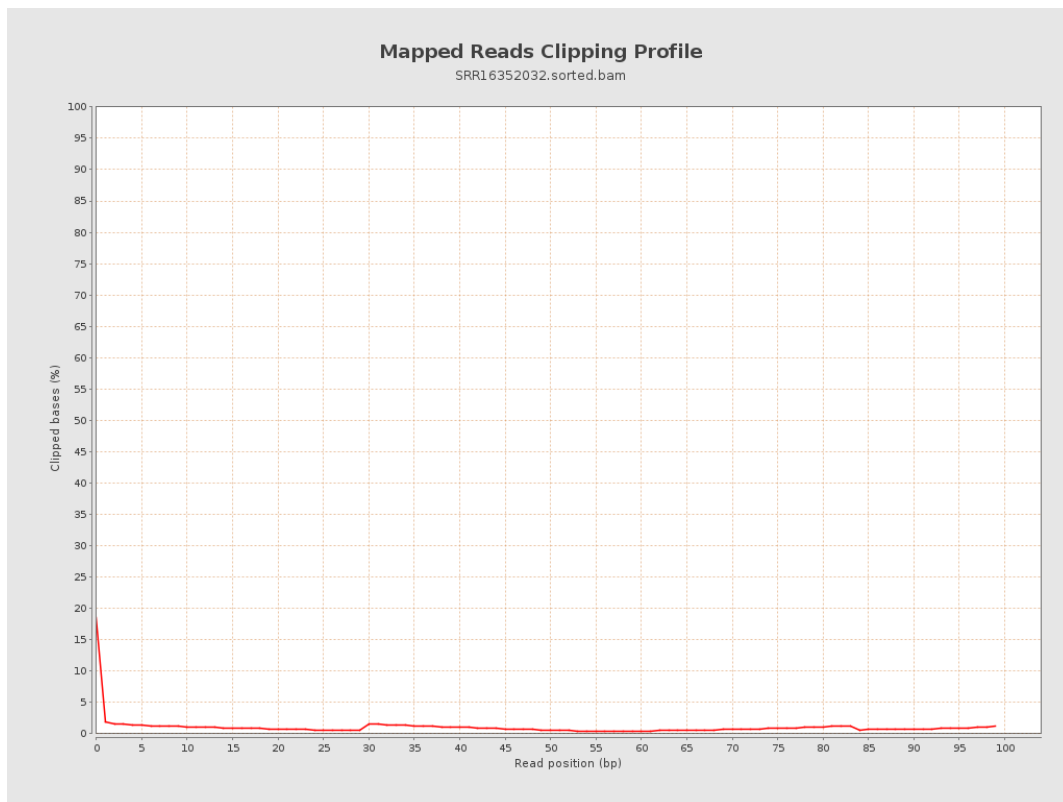
8. Results : Mapped Reads Nucleotide Content



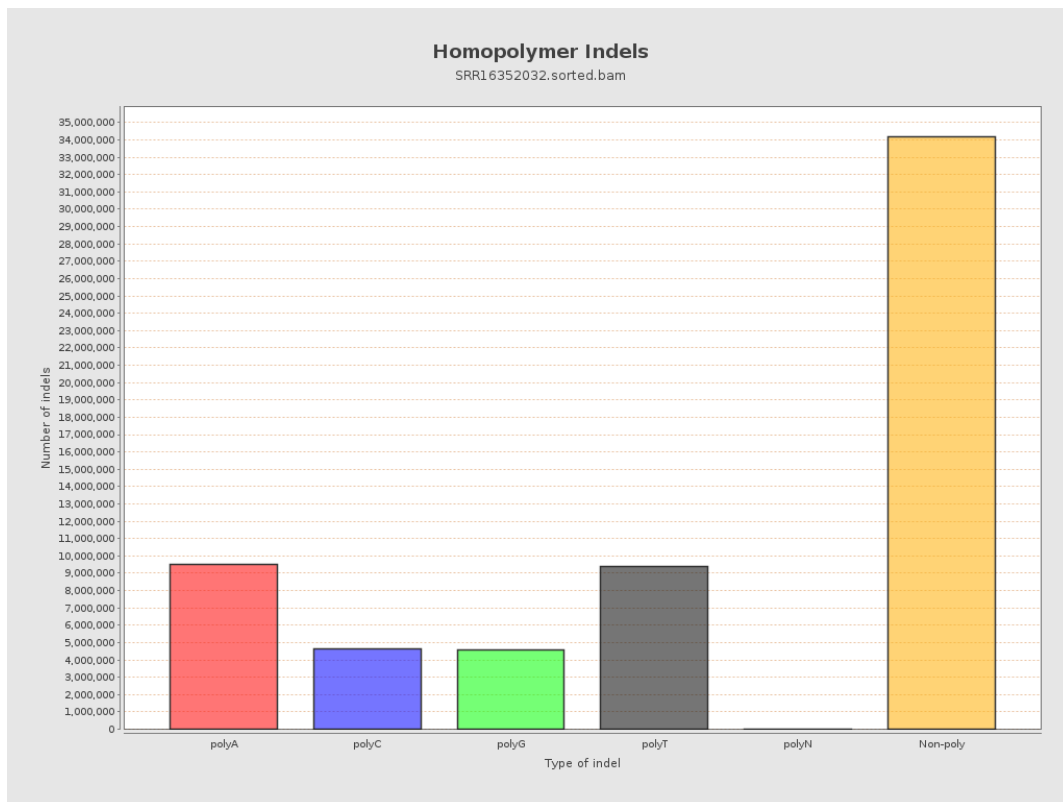
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



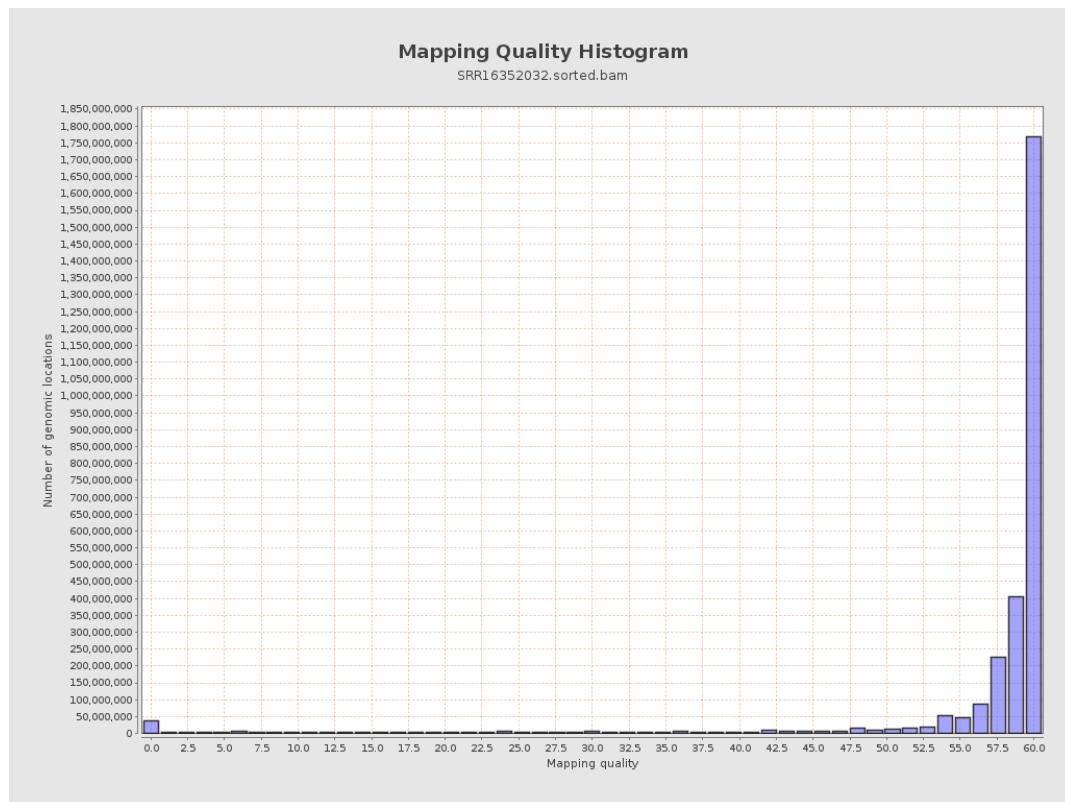
11. Results : Homopolymer Indels



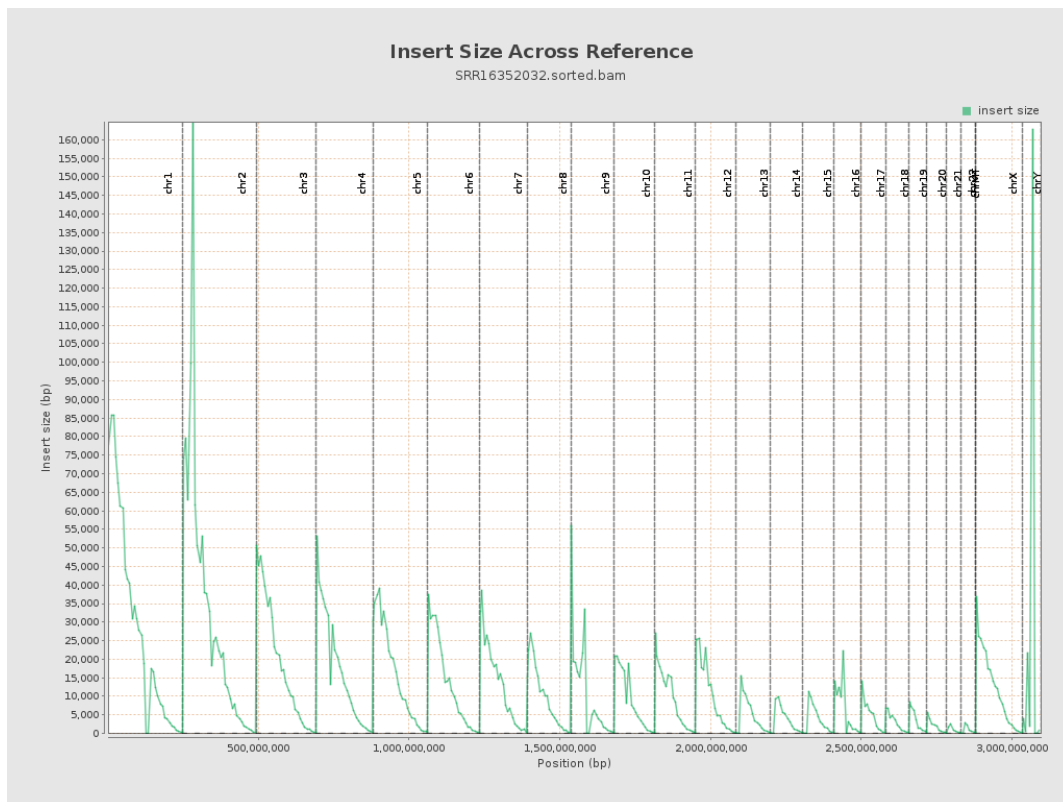
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

