

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 04:38:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174070.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_SRR10174070 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174070_1.fastq.gz SRR10174070_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 04:38:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174070.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,427,592
Mapped reads	8,261,780 / 98.03%
Unmapped reads	165,812 / 1.97%
Mapped paired reads	8,261,780 / 98.03%
Mapped reads, first in pair	4,129,649 / 49%
Mapped reads, second in pair	4,132,131 / 49.03%
Mapped reads, both in pair	8,151,302 / 96.72%
Mapped reads, singletons	110,478 / 1.31%
Secondary alignments	0
Supplementary alignments	1,062,885 / 12.61%
Read min/max/mean length	30 / 133 / 125.81
Duplicated reads (estimated)	6,712,087 / 79.64%
Duplication rate	66.57%
Clipped reads	4,333,285 / 51.42%

2.2. ACGT Content

Number/percentage of A's	279,447,916 / 29.63%
Number/percentage of C's	189,138,607 / 20.05%
Number/percentage of T's	277,340,934 / 29.4%
Number/percentage of G's	197,309,237 / 20.92%
Number/percentage of N's	6,772 / 0%

GC Percentage	40.97%
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2.3. Coverage

Mean	0.3049
Standard Deviation	5.3877

2.4. Mapping Quality

Mean Mapping Quality	52.79
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2.5. Insert size

Mean	1,104,464
Standard Deviation	9,764,125.99
P25/Median/P75	109 / 158 / 242

2.6. Mismatches and indels

General error rate	0.85%
Mismatches	7,757,295
Insertions	96,066
Mapped reads with at least one insertion	1.12%
Deletions	287,956
Mapped reads with at least one deletion	3.4%
Homopolymer indels	40.89%

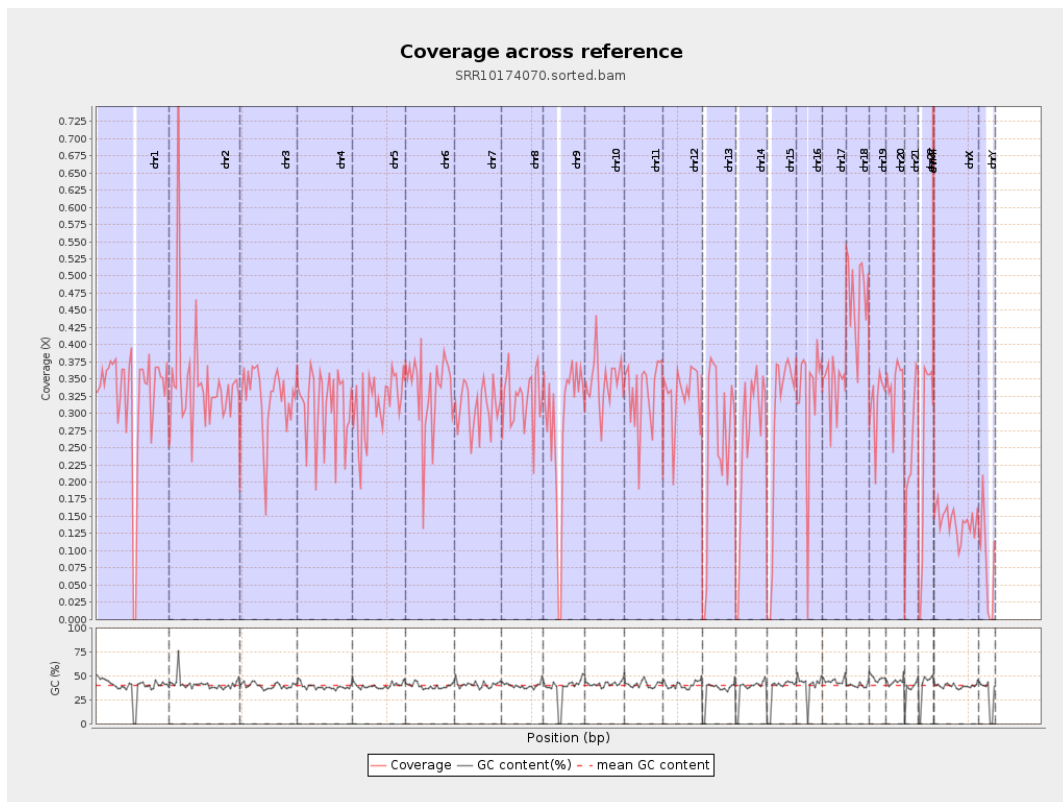
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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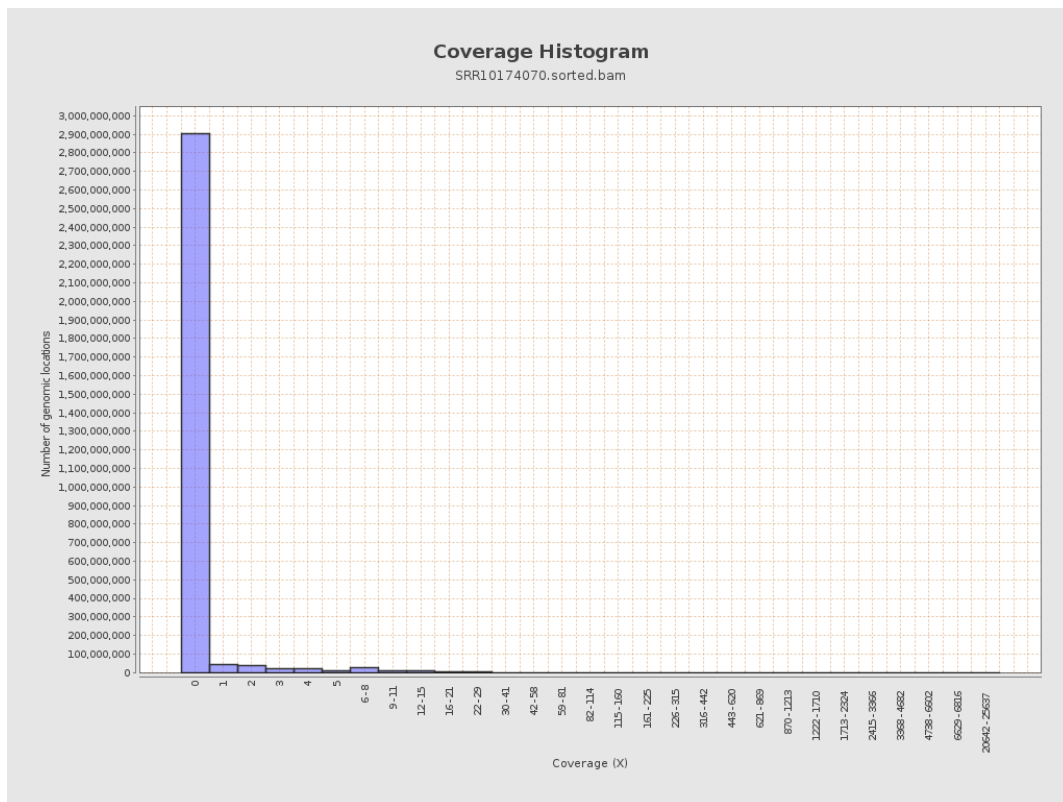
		bases	coverage	deviation
chr1	249250621	80551413	0.3232	2.6242
chr2	243199373	84438852	0.3472	17.937
chr3	198022430	63487115	0.3206	1.7363
chr4	191154276	58782311	0.3075	1.9681
chr5	180915260	56678161	0.3133	1.7033
chr6	171115067	56876048	0.3324	2.0868
chr7	159138663	49167785	0.309	2.0893
chr8	146364022	46908406	0.3205	2.2537
chr9	141213431	39936476	0.2828	2.2711
chr10	135534747	46888787	0.346	2.5136
chr11	135006516	44472671	0.3294	1.8656
chr12	133851895	44060260	0.3292	1.821
chr13	115169878	28854062	0.2505	1.5545
chr14	107349540	27989881	0.2607	1.5813
chr15	102531392	28692196	0.2798	1.6684
chr16	90354753	29454214	0.326	1.9656
chr17	81195210	27700967	0.3412	1.866
chr18	78077248	36982664	0.4737	3.0589
chr19	59128983	18691209	0.3161	2.1705
chr20	63025520	21307906	0.3381	1.8035
chr21	48129895	11822307	0.2456	1.7638
chr22	51304566	12437265	0.2424	1.6036
chrMT	16571	894594	53.9855	45.7625
chrX	155270560	22129865	0.1425	1.1575

chrY	59373566	4713185	0.0794	1.2411
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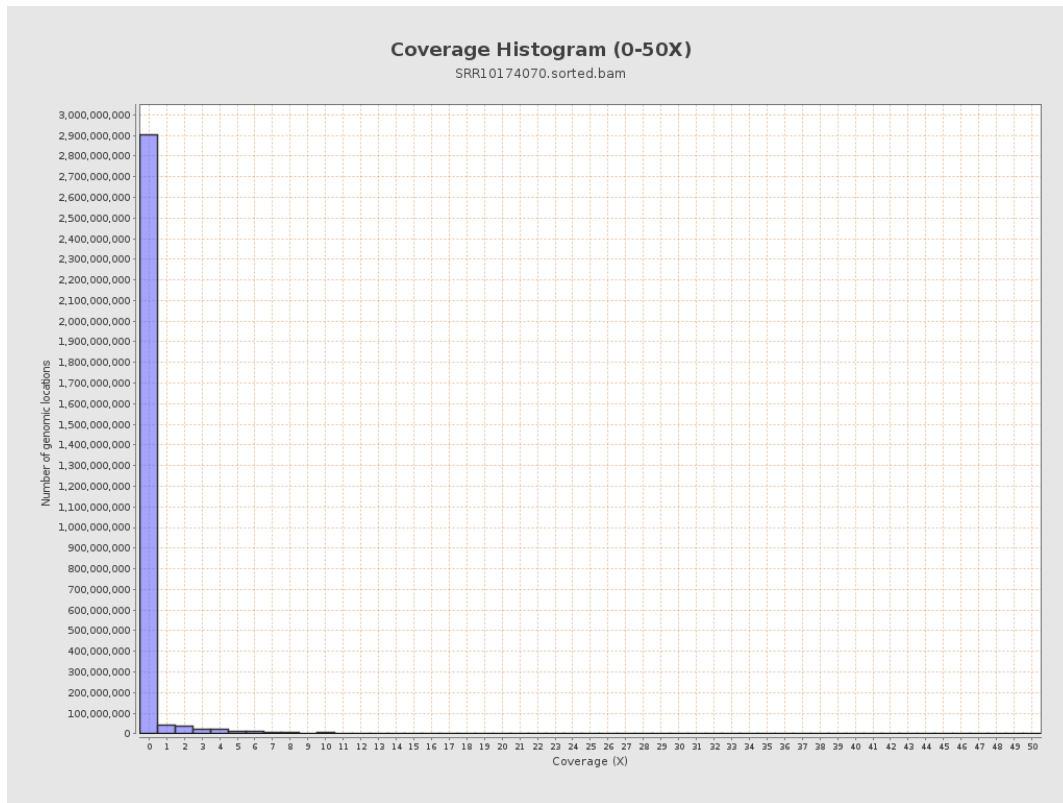
3. Results : Coverage across reference



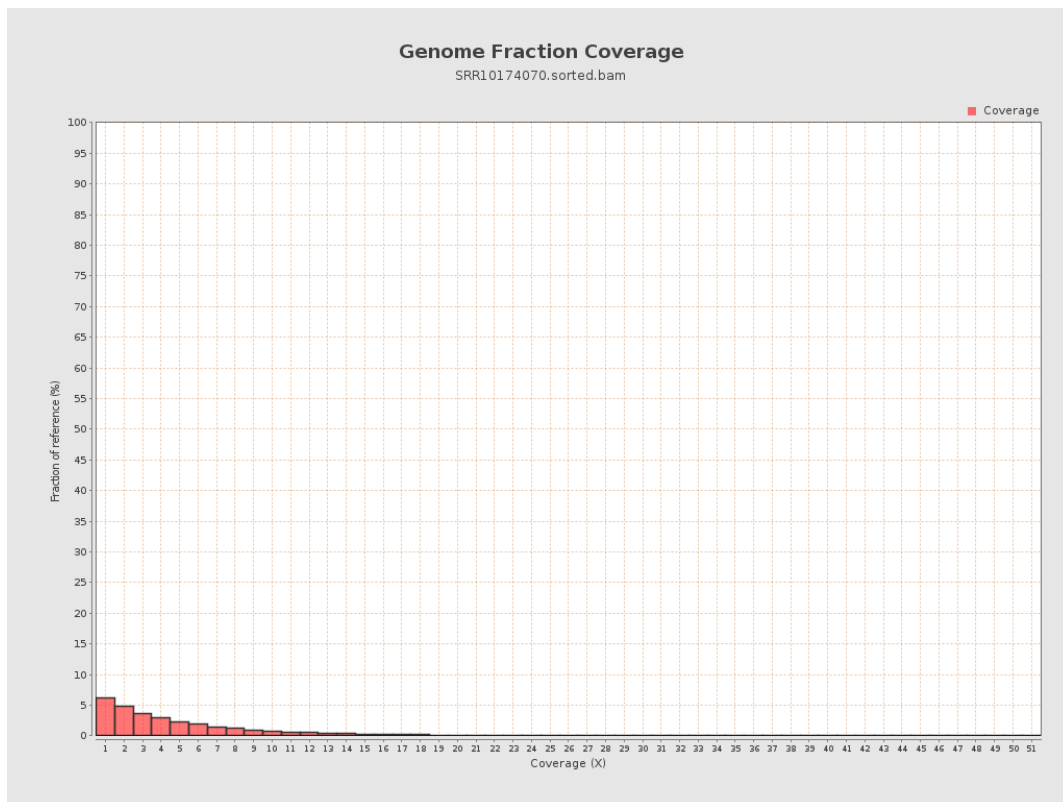
4. Results : Coverage Histogram



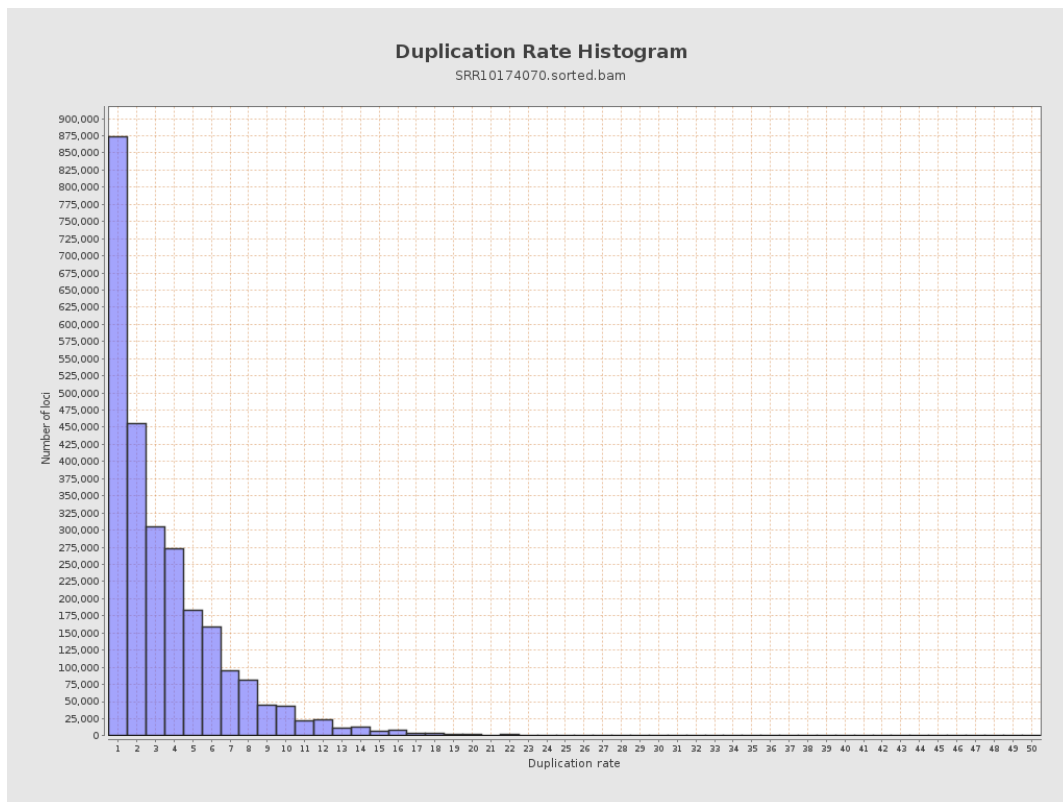
5. Results : Coverage Histogram (0-50X)



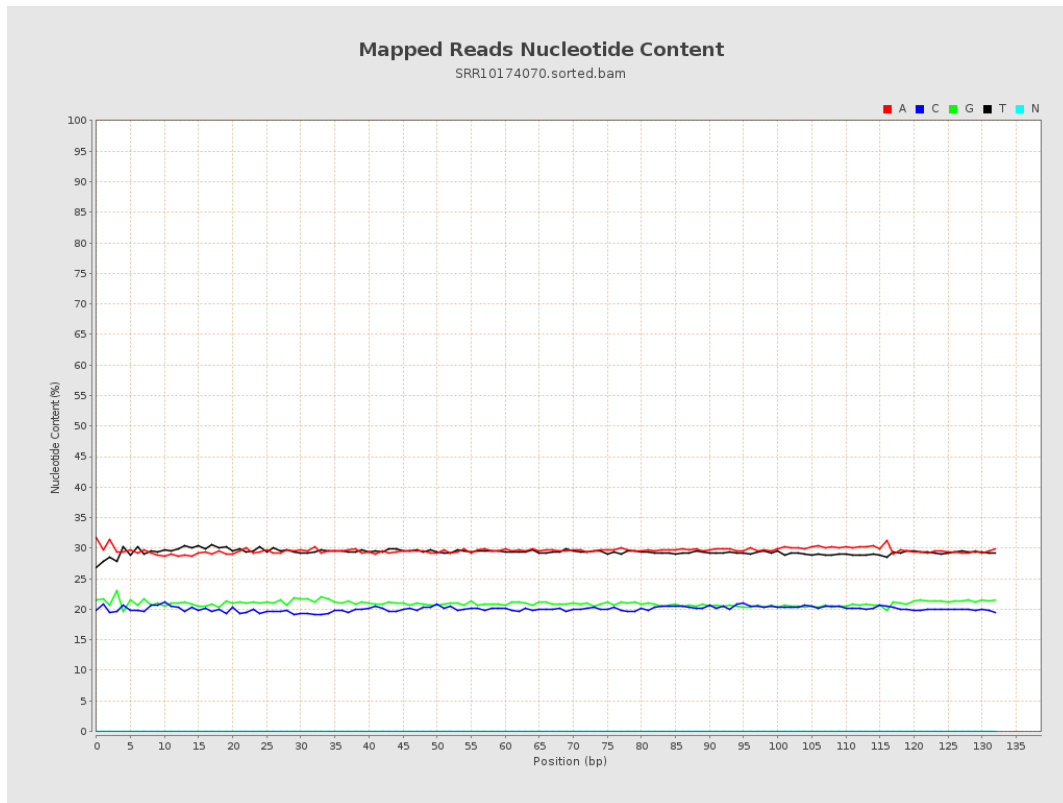
6. Results : Genome Fraction Coverage



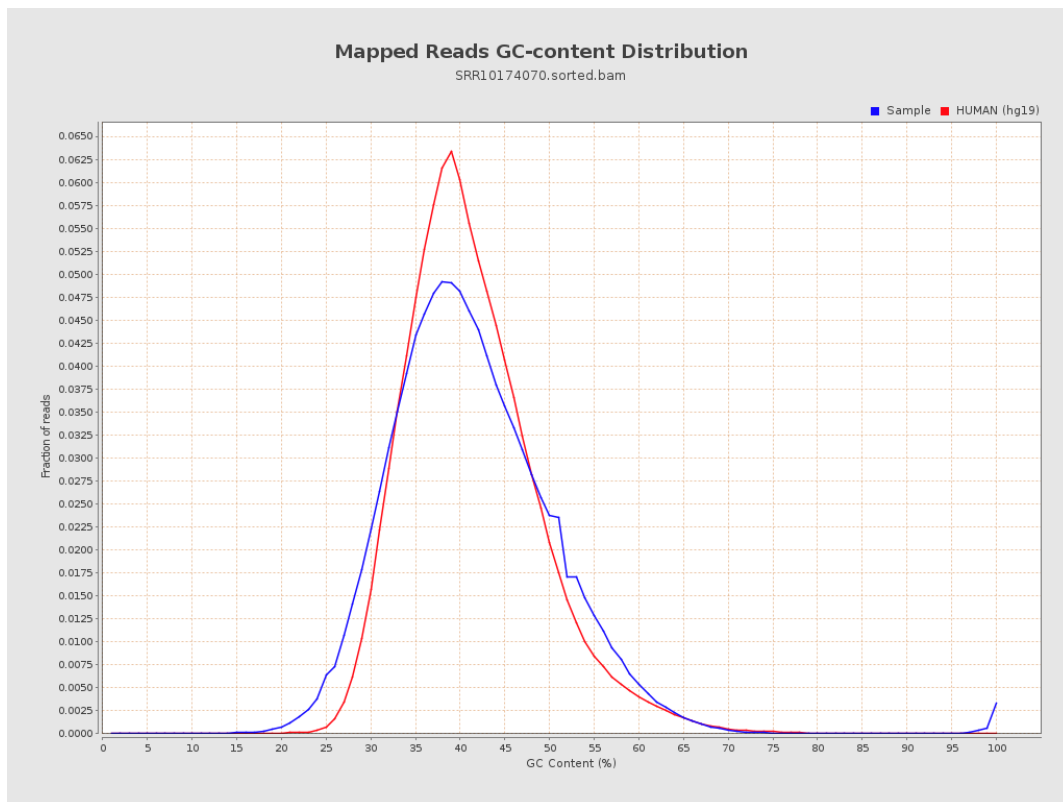
7. Results : Duplication Rate Histogram



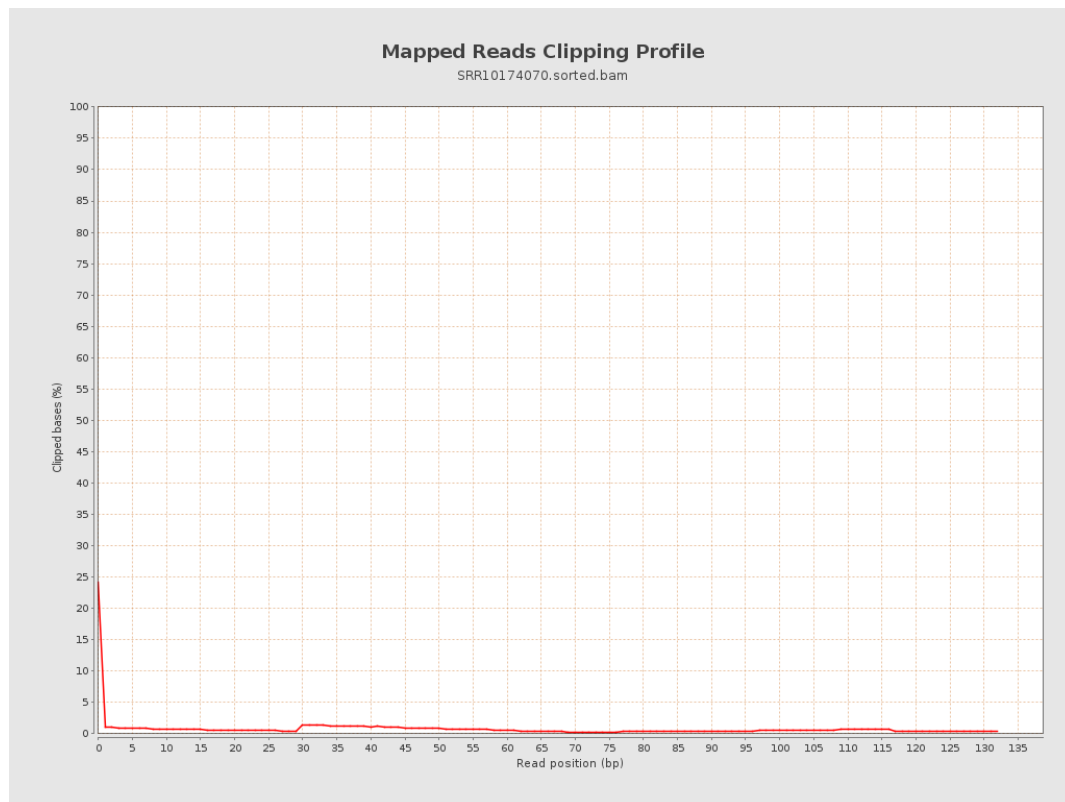
8. Results : Mapped Reads Nucleotide Content



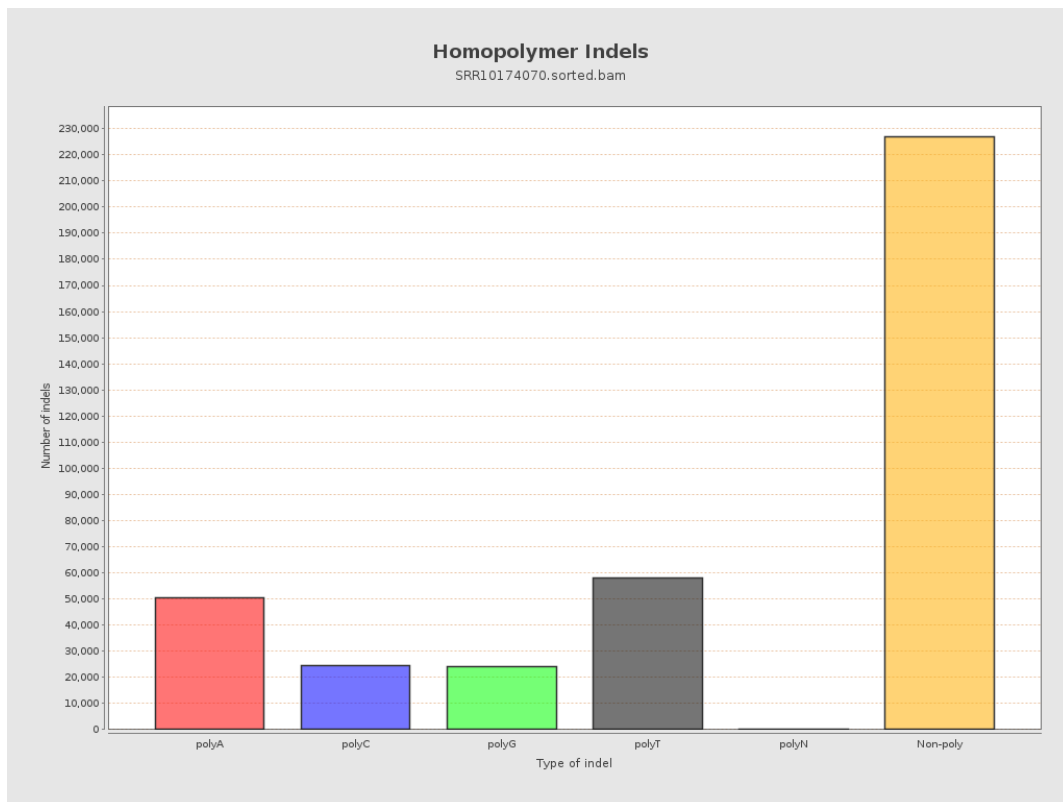
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



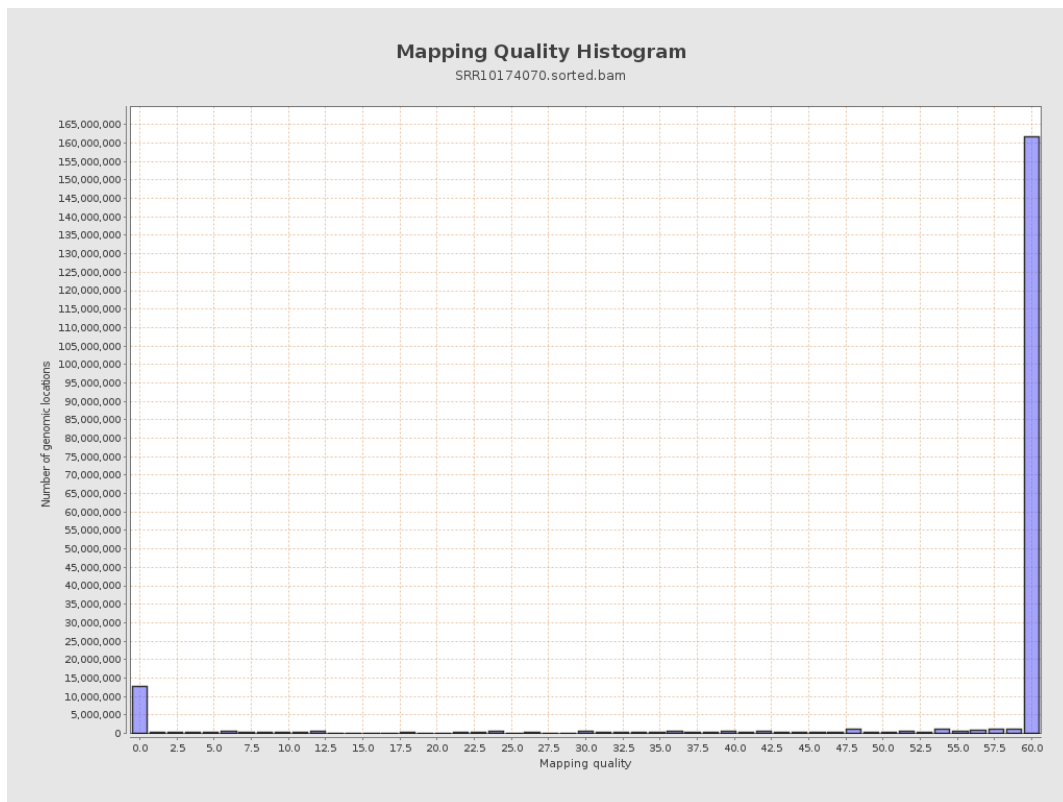
11. Results : Homopolymer Indels



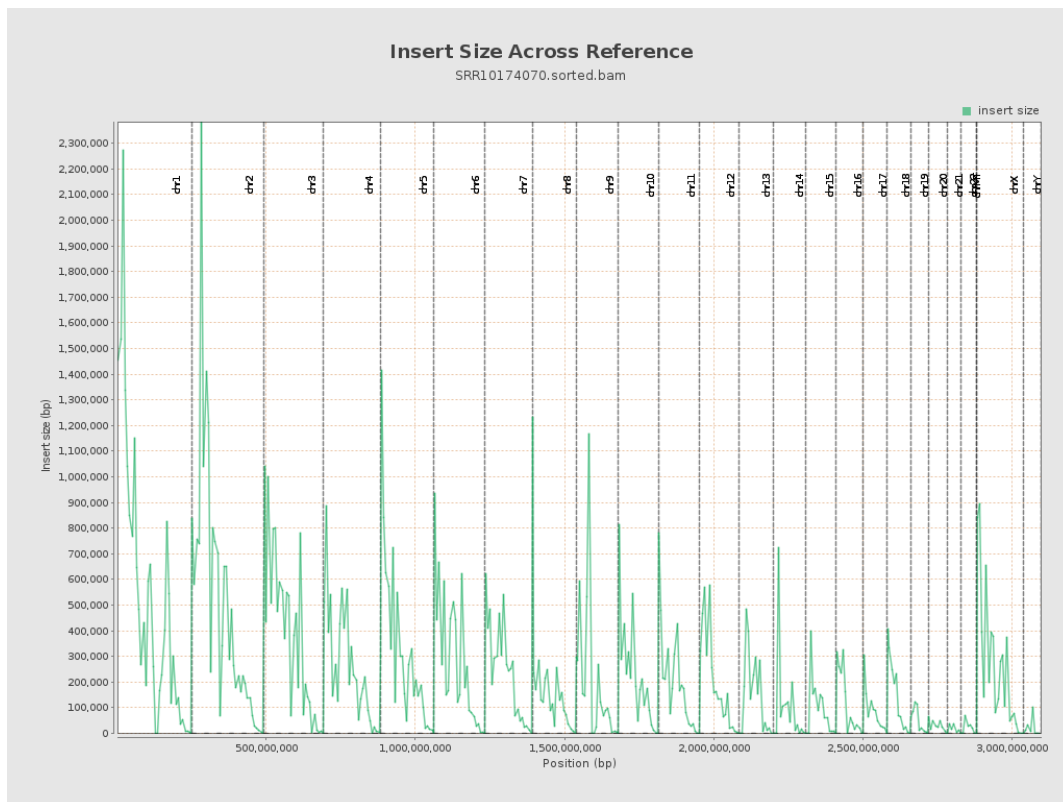
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

