

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 17:41:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354871.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_SRR22354871 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354871_1.fastq.gz SRR22354871_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 17:41:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354871.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	27,272,112
Mapped reads	26,983,295 / 98.94%
Unmapped reads	288,817 / 1.06%
Mapped paired reads	26,983,295 / 98.94%
Mapped reads, first in pair	13,504,762 / 49.52%
Mapped reads, second in pair	13,478,533 / 49.42%
Mapped reads, both in pair	26,937,064 / 98.77%
Mapped reads, singletons	46,231 / 0.17%
Secondary alignments	0
Supplementary alignments	1,369,907 / 5.02%
Read min/max/mean length	30 / 150 / 151.82
Duplicated reads (estimated)	17,763,347 / 65.13%
Duplication rate	65.59%
Clipped reads	15,267,202 / 55.98%

2.2. ACGT Content

Number/percentage of A's	913,861,687 / 27.59%
Number/percentage of C's	706,336,089 / 21.32%
Number/percentage of T's	934,959,717 / 28.22%
Number/percentage of G's	757,339,598 / 22.86%
Number/percentage of N's	29,925 / 0%

GC Percentage	44.19%
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2.3. Coverage

Mean	1.0705
Standard Deviation	73.3211

2.4. Mapping Quality

Mean Mapping Quality	53.59
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2.5. Insert size

Mean	493,597.56
Standard Deviation	8,108,405.6
P25/Median/P75	97 / 150 / 224

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	17,594,984
Insertions	517,298
Mapped reads with at least one insertion	1.79%
Deletions	539,268
Mapped reads with at least one deletion	1.91%
Homopolymer indels	43.77%

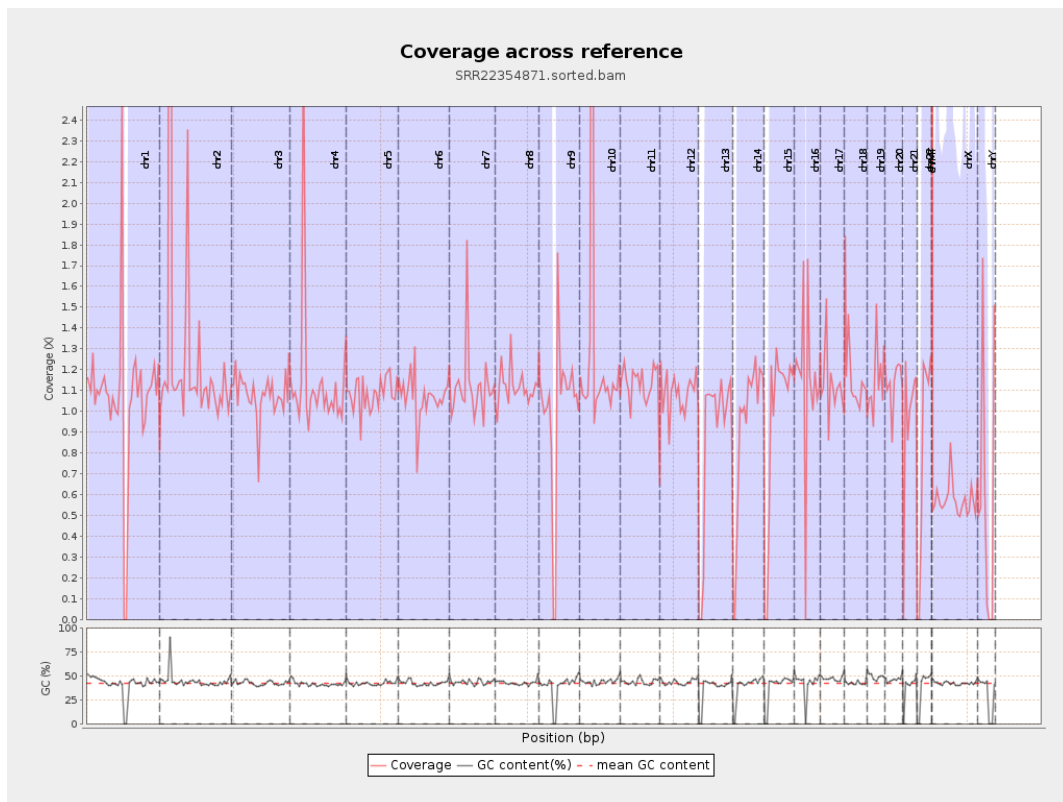
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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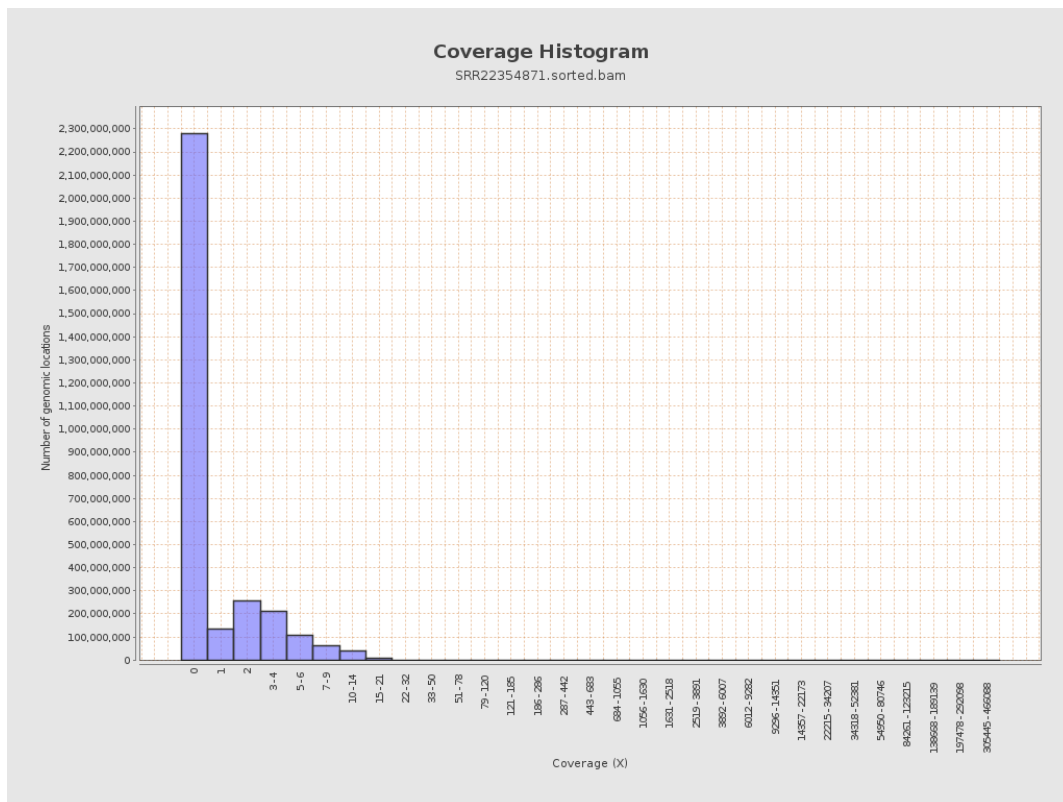
		bases	coverage	deviation
chr1	249250621	267387525	1.0728	29.9939
chr2	243199373	330458928	1.3588	256.7601
chr3	198022430	212721066	1.0742	2.9449
chr4	191154276	215746661	1.1287	12.8052
chr5	180915260	196958721	1.0887	2.432
chr6	171115067	183391023	1.0717	4.2491
chr7	159138663	178210773	1.1198	19.592
chr8	146364022	163585225	1.1177	6.0102
chr9	141213431	140676919	0.9962	16.235
chr10	135534747	182415860	1.3459	35.0743
chr11	135006516	153813123	1.1393	6.433
chr12	133851895	145617621	1.0879	2.43
chr13	115169878	101776160	0.8837	2.14
chr14	107349540	99192473	0.924	9.0219
chr15	102531392	98191552	0.9577	2.2459
chr16	90354753	103748220	1.1482	6.6024
chr17	81195210	90693661	1.117	6.0023
chr18	78077248	90702046	1.1617	14.3288
chr19	59128983	67091881	1.1347	15.9855
chr20	63025520	71282575	1.131	4.7276
chr21	48129895	46940318	0.9753	7.3182
chr22	51304566	43313348	0.8442	3.2632
chrMT	16571	4054873	244.6969	55.8139
chrX	155270560	88895172	0.5725	2.8722

chrY	59373566	37172142	0.6261	16.6167
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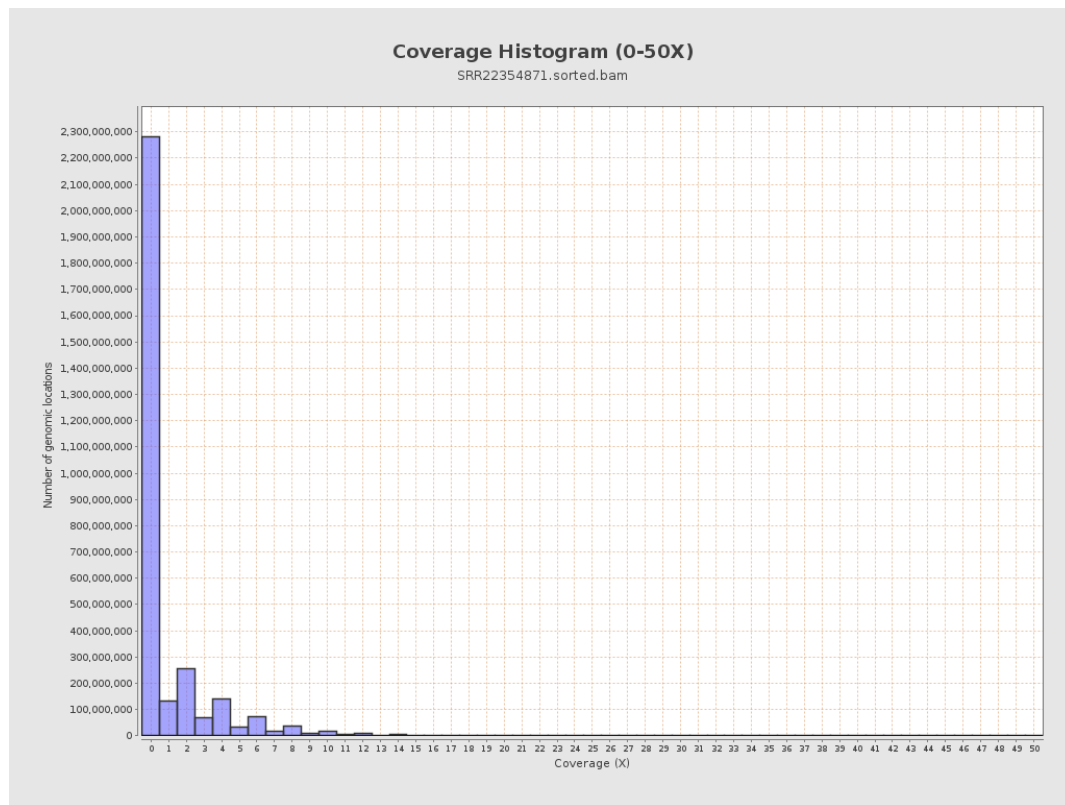
3. Results : Coverage across reference



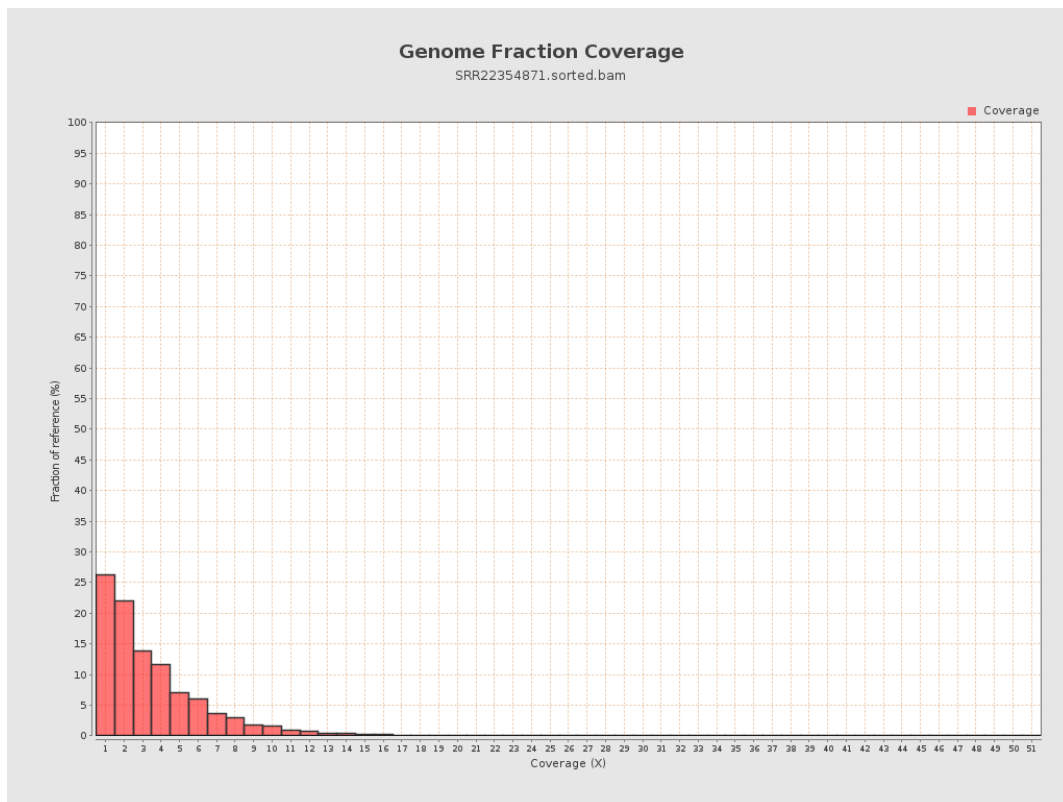
4. Results : Coverage Histogram



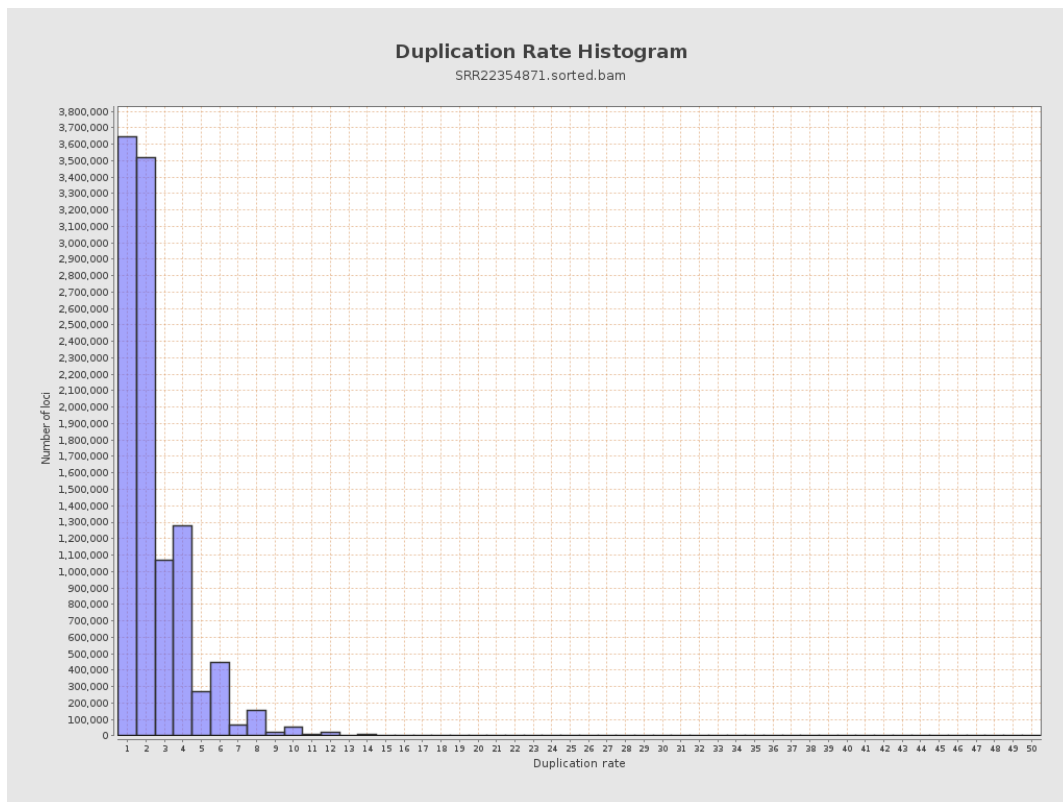
5. Results : Coverage Histogram (0-50X)



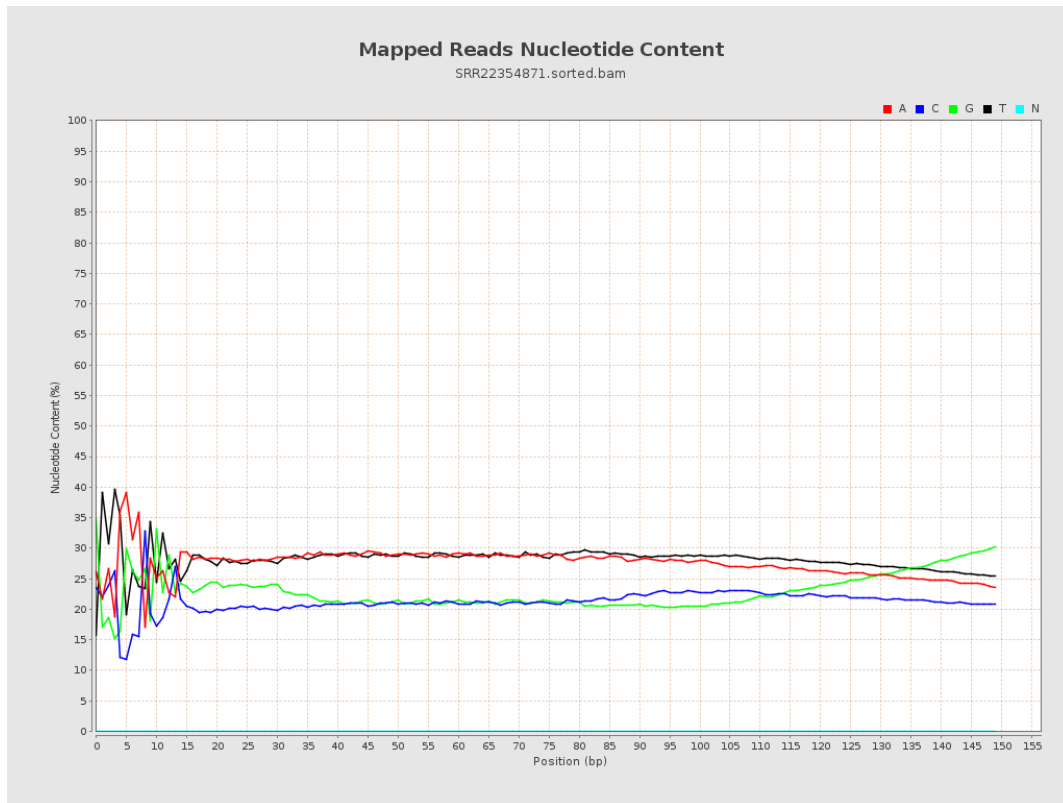
6. Results : Genome Fraction Coverage



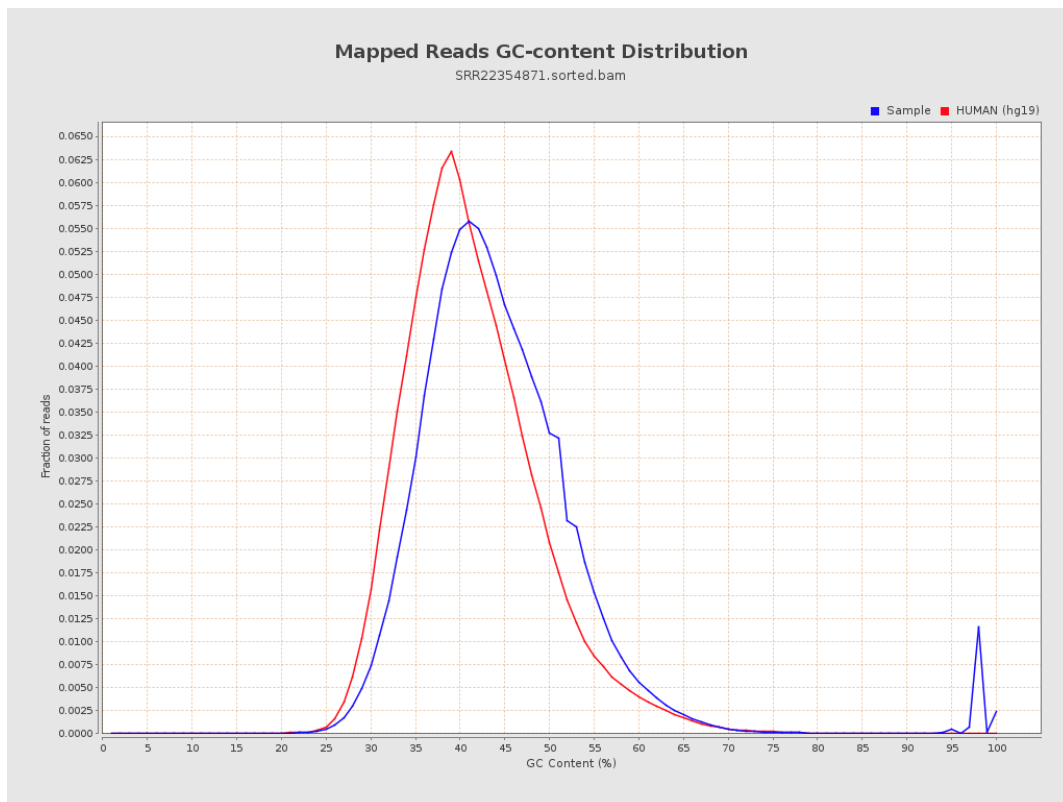
7. Results : Duplication Rate Histogram



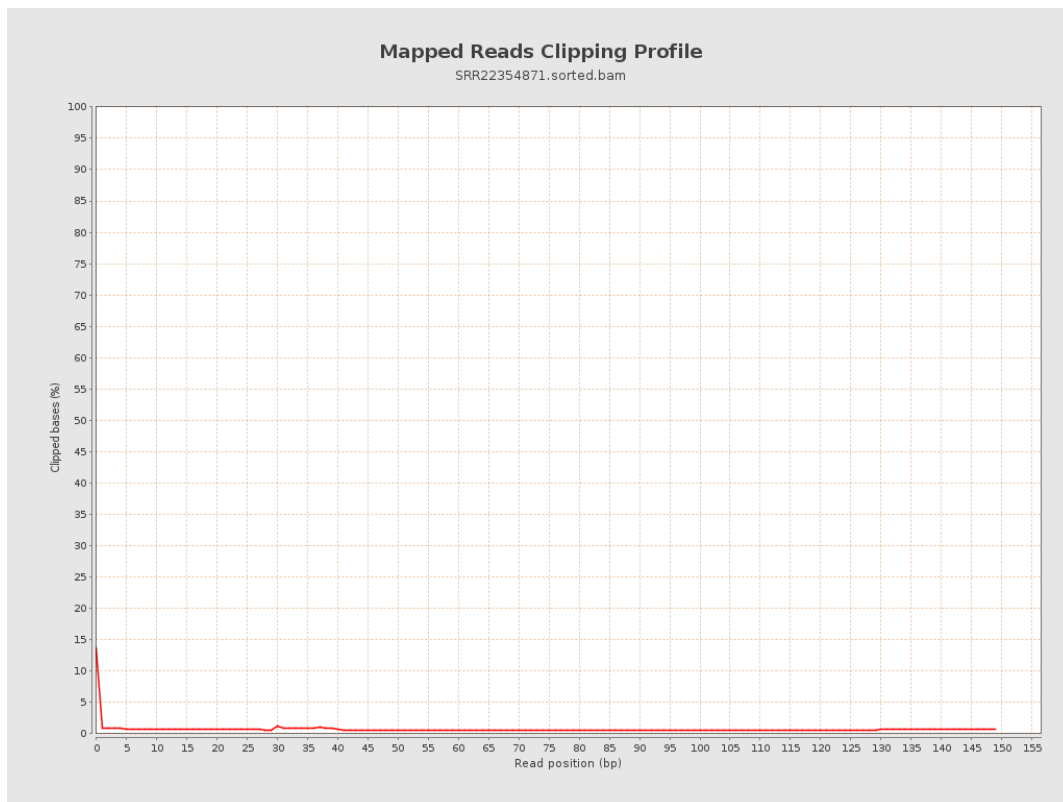
8. Results : Mapped Reads Nucleotide Content



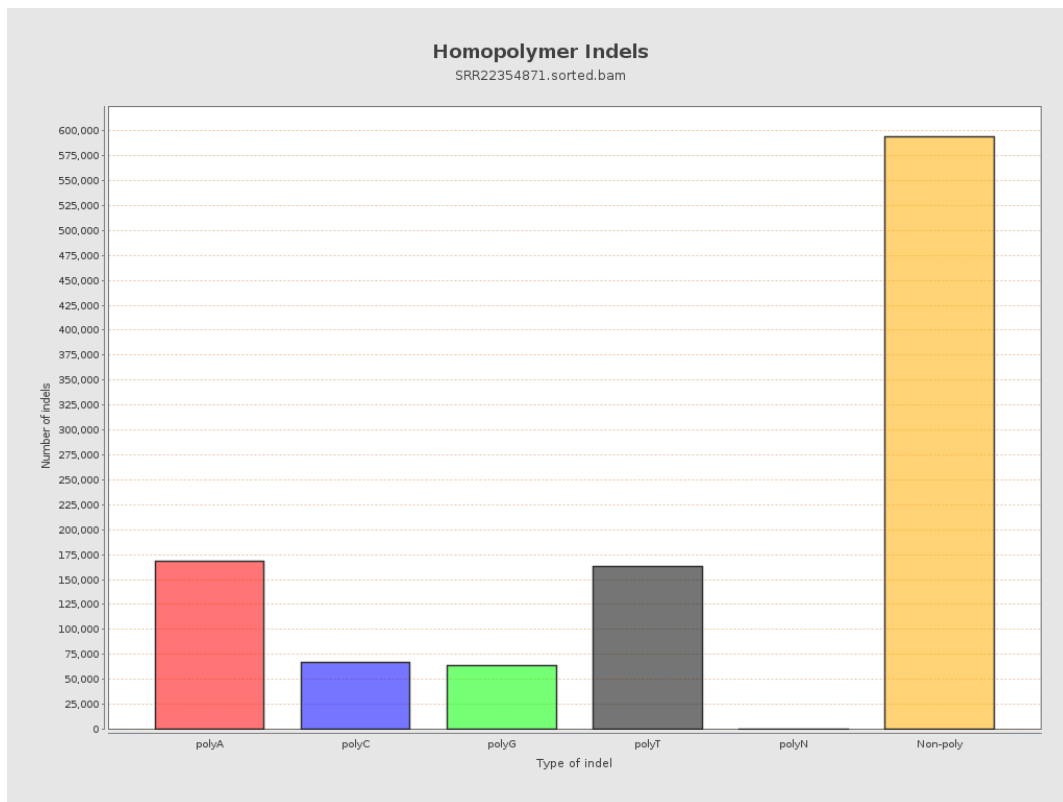
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



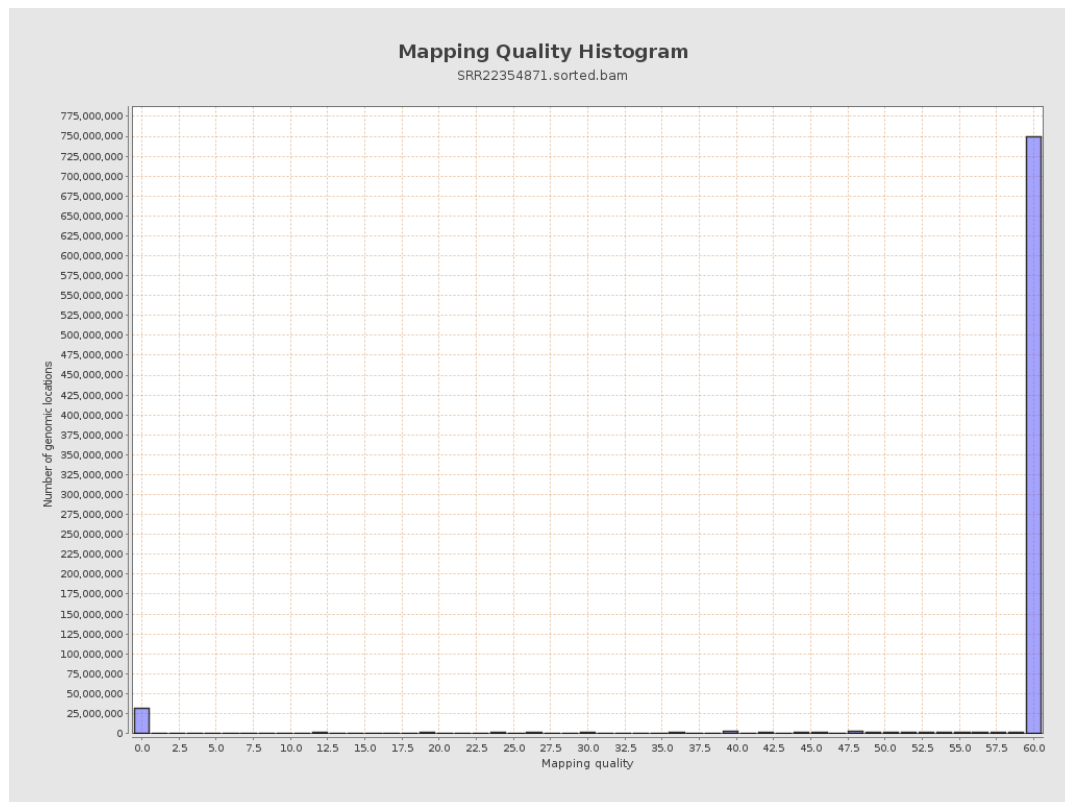
11. Results : Homopolymer Indels



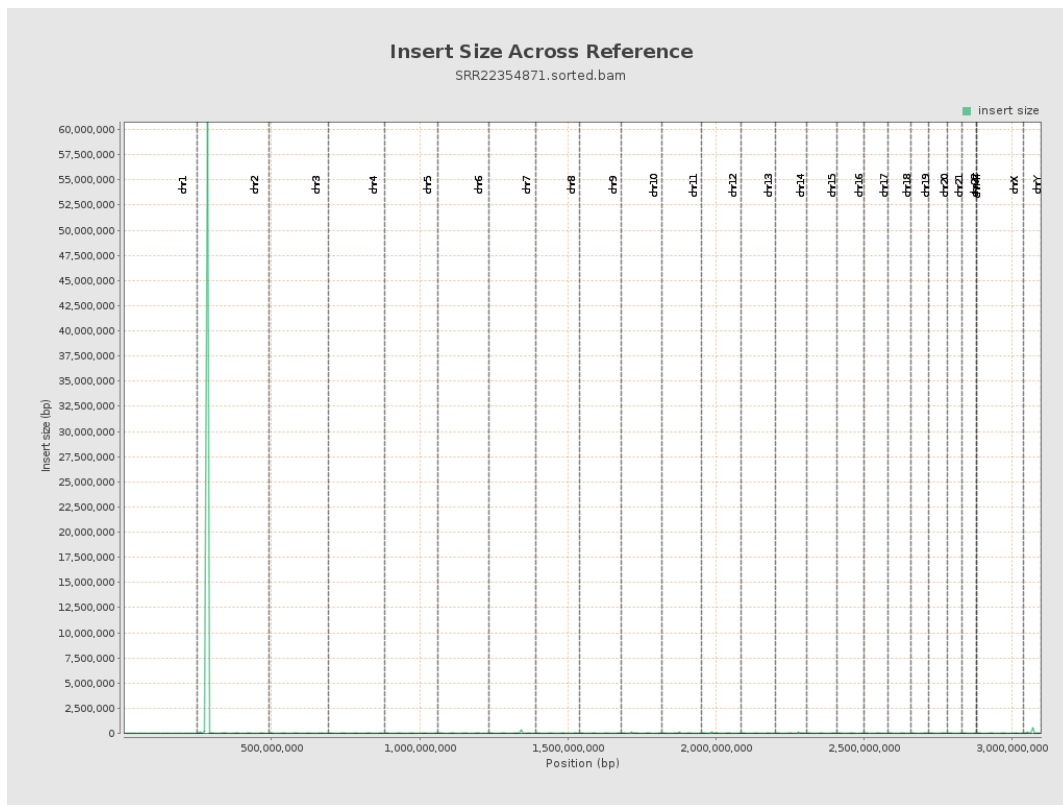
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

