

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/08 10:39:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354885.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_SRR22354885 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354885_1.fastq.gz SRR22354885_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 08 10:39:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354885.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	25,046,022
Mapped reads	19,938,228 / 79.61%
Unmapped reads	5,107,794 / 20.39%
Mapped paired reads	19,938,228 / 79.61%
Mapped reads, first in pair	9,971,698 / 39.81%
Mapped reads, second in pair	9,966,530 / 39.79%
Mapped reads, both in pair	19,805,098 / 79.07%
Mapped reads, singletons	133,130 / 0.53%
Secondary alignments	0
Supplementary alignments	461,392 / 1.84%
Read min/max/mean length	30 / 150 / 150.8
Duplicated reads (estimated)	13,595,435 / 54.28%
Duplication rate	60.81%
Clipped reads	7,602,114 / 30.35%

2.2. ACGT Content

Number/percentage of A's	658,034,311 / 24.3%
Number/percentage of C's	671,048,423 / 24.79%
Number/percentage of T's	657,354,491 / 24.28%
Number/percentage of G's	721,001,947 / 26.63%
Number/percentage of N's	7,391 / 0%

GC Percentage	51.42%
---------------	--------

2.3. Coverage

Mean	0.8753
Standard Deviation	32.2472

2.4. Mapping Quality

Mean Mapping Quality	53.5
----------------------	------

2.5. Insert size

Mean	150,532.03
Standard Deviation	4,014,564.19
P25/Median/P75	154 / 238 / 346

2.6. Mismatches and indels

General error rate	1.54%
Mismatches	40,390,115
Insertions	543,791
Mapped reads with at least one insertion	2.62%
Deletions	1,361,185
Mapped reads with at least one deletion	6.51%
Homopolymer indels	47.25%

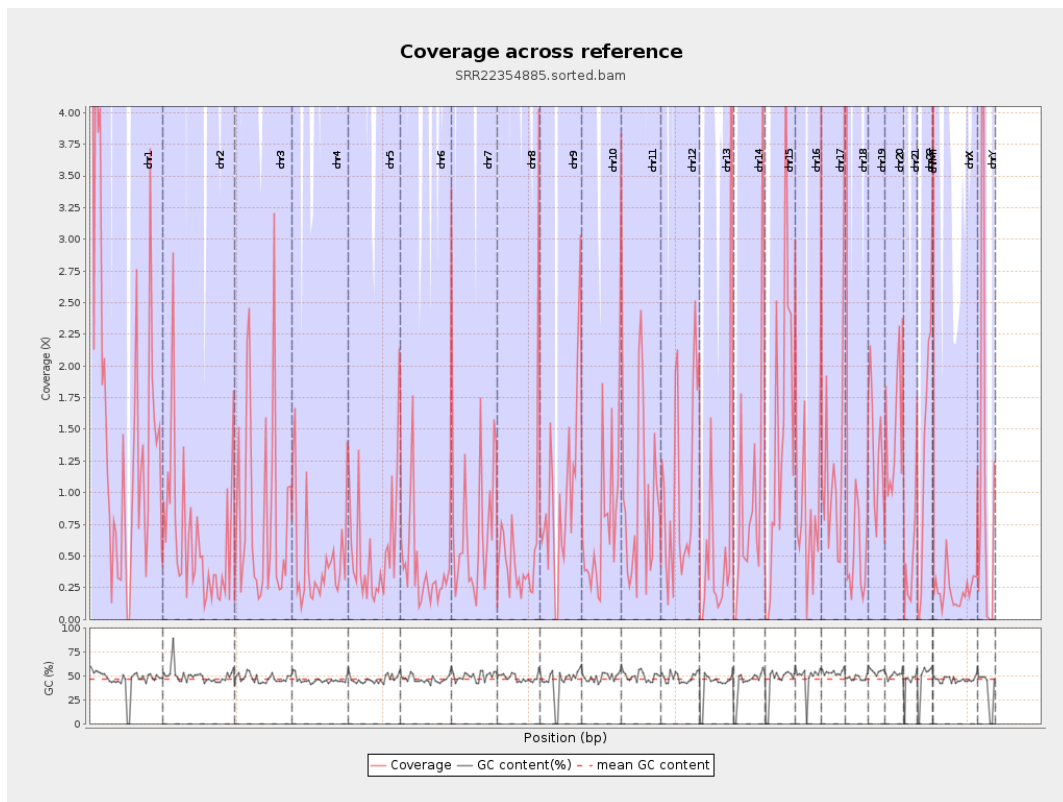
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

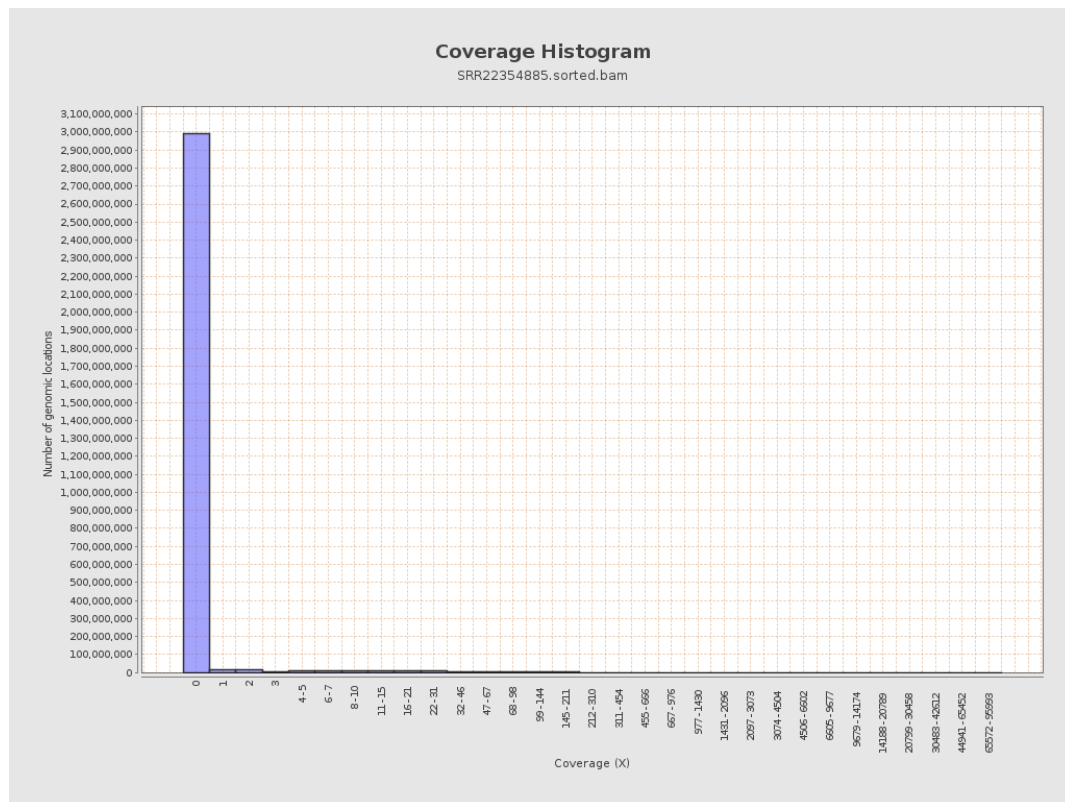
		bases	coverage	deviation
chr1	249250621	420828913	1.6884	15.8395
chr2	243199373	151364762	0.6224	70.7961
chr3	198022430	158376657	0.7998	9.3607
chr4	191154276	91517416	0.4788	8.1588
chr5	180915260	106821631	0.5905	7.7258
chr6	171115067	70231458	0.4104	6.3485
chr7	159138663	120169861	0.7551	20.8915
chr8	146364022	85365178	0.5832	7.932
chr9	141213431	139727907	0.9895	13.5263
chr10	135534747	99764906	0.7361	13.4405
chr11	135006516	131232913	0.972	10.9351
chr12	133851895	140066817	1.0464	10.7612
chr13	115169878	87833181	0.7626	9.8095
chr14	107349540	106891624	0.9957	14.5072
chr15	102531392	147089776	1.4346	13.1082
chr16	90354753	81810340	0.9054	9.8296
chr17	81195210	91993244	1.133	11.4066
chr18	78077248	98497929	1.2615	131.793
chr19	59128983	77607482	1.3125	11.8414
chr20	63025520	93337123	1.4809	13.2669
chr21	48129895	24826483	0.5158	7.7453
chr22	51304566	68367175	1.3326	12.928
chrMT	16571	555889	33.5459	23.9754
chrX	155270560	37447850	0.2412	4.2338

chrY	59373566	77937350	1.3127	67.2371
------	----------	----------	--------	---------

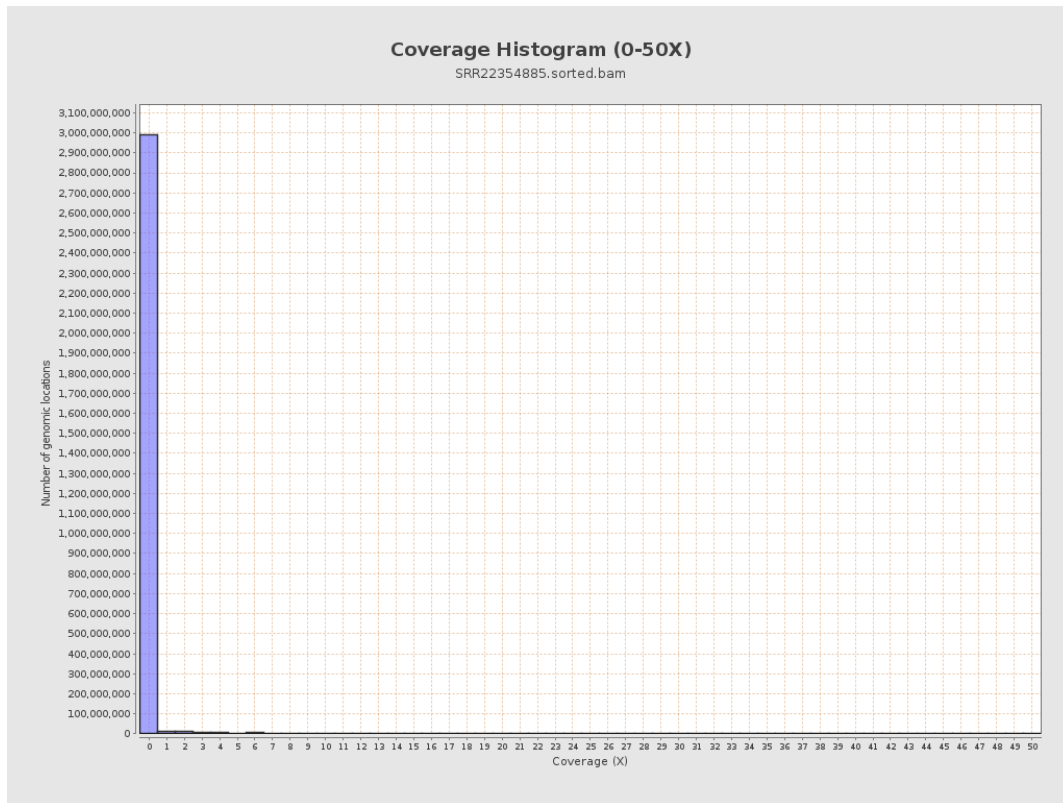
3. Results : Coverage across reference



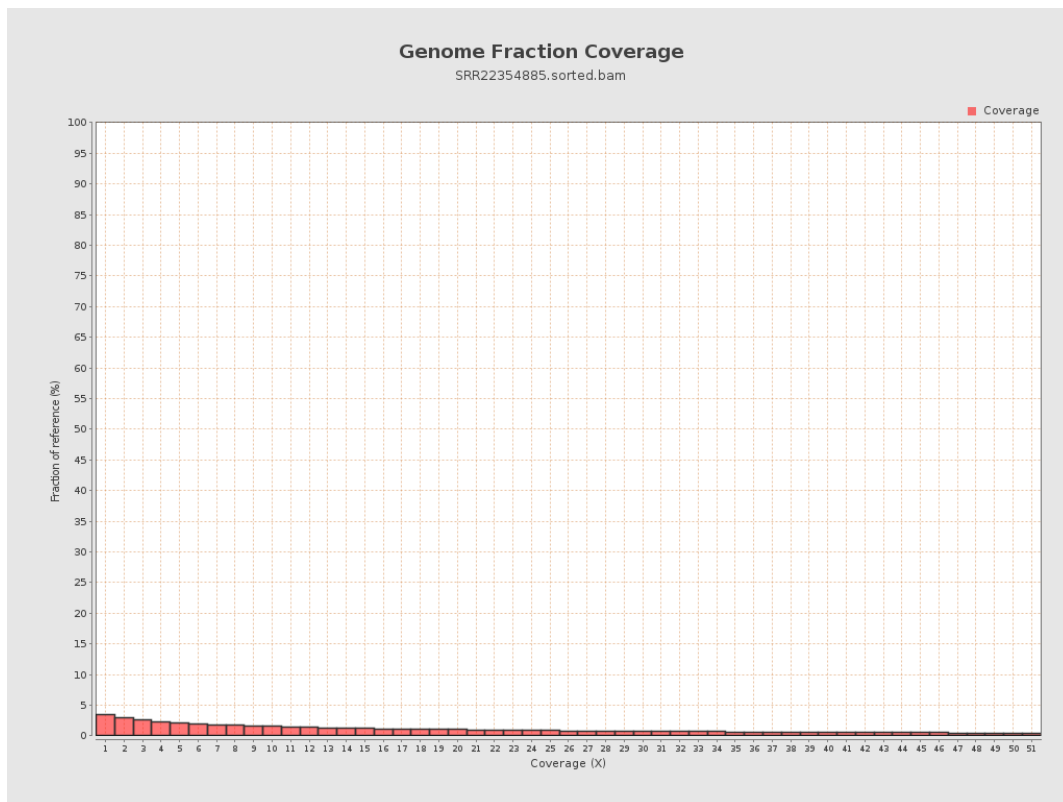
4. Results : Coverage Histogram



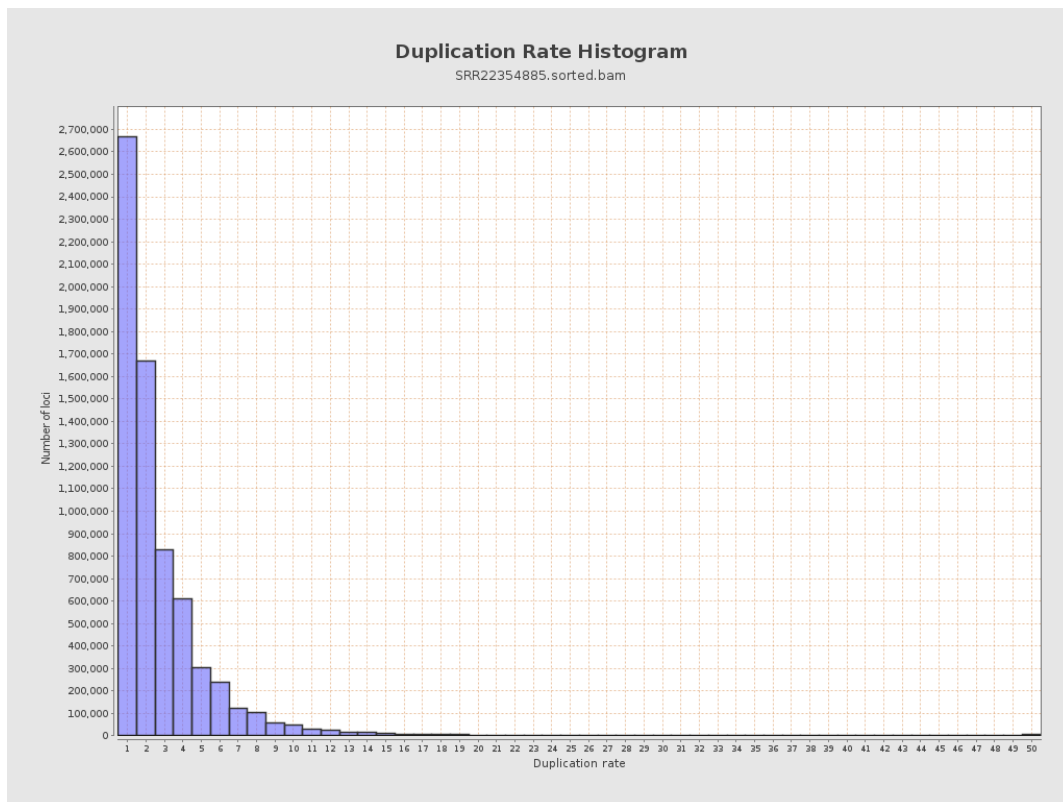
5. Results : Coverage Histogram (0-50X)



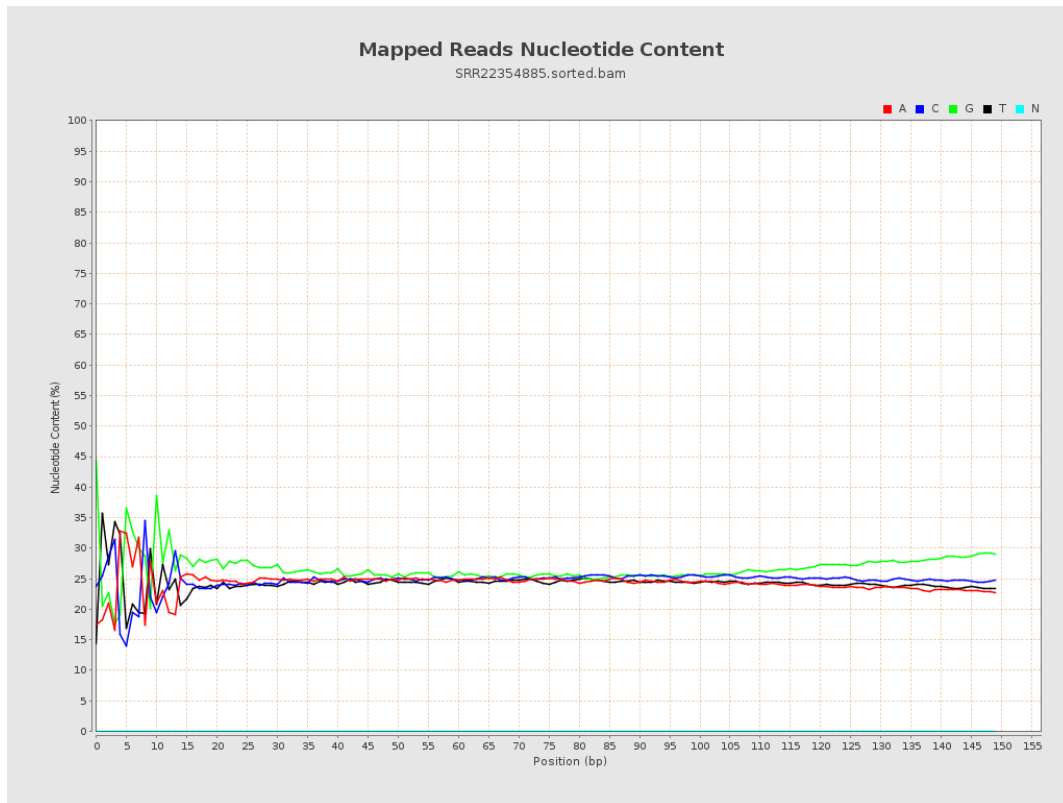
6. Results : Genome Fraction Coverage



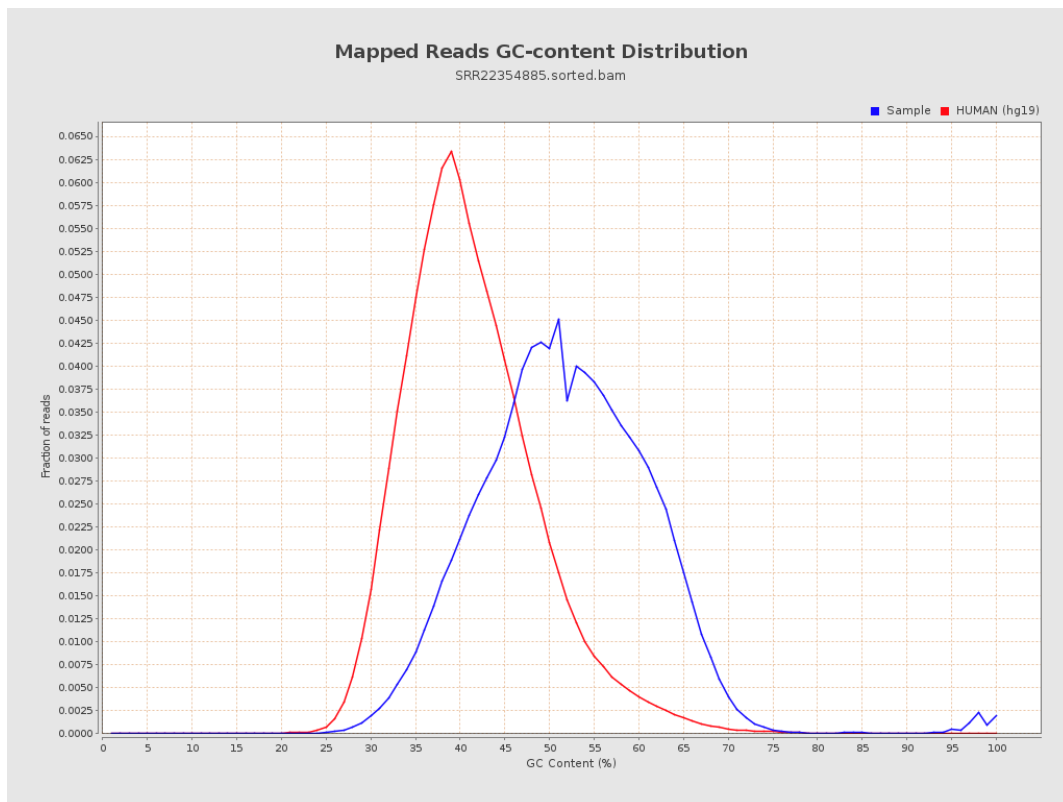
7. Results : Duplication Rate Histogram



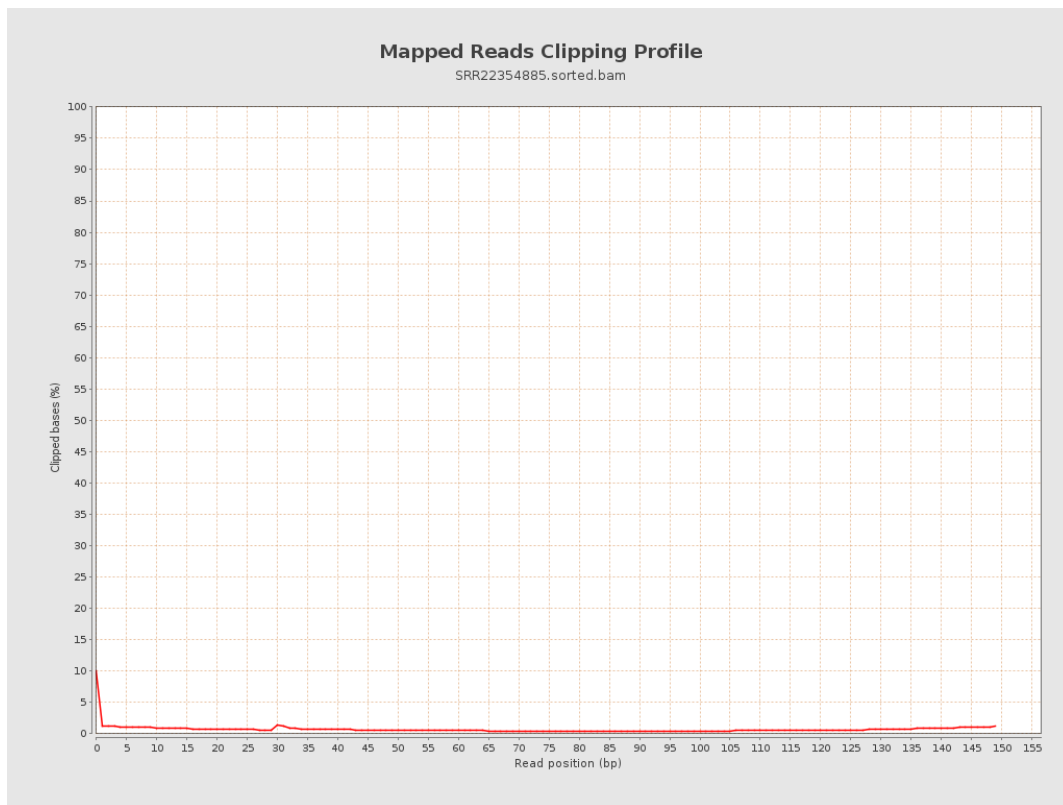
8. Results : Mapped Reads Nucleotide Content



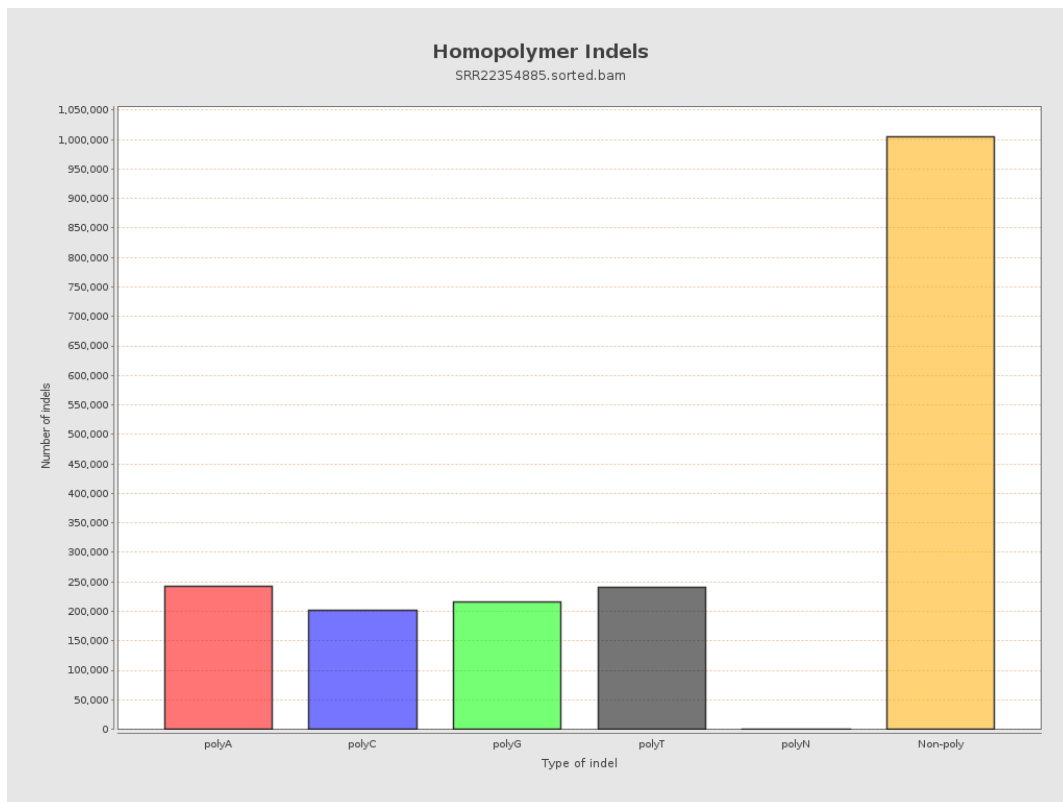
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



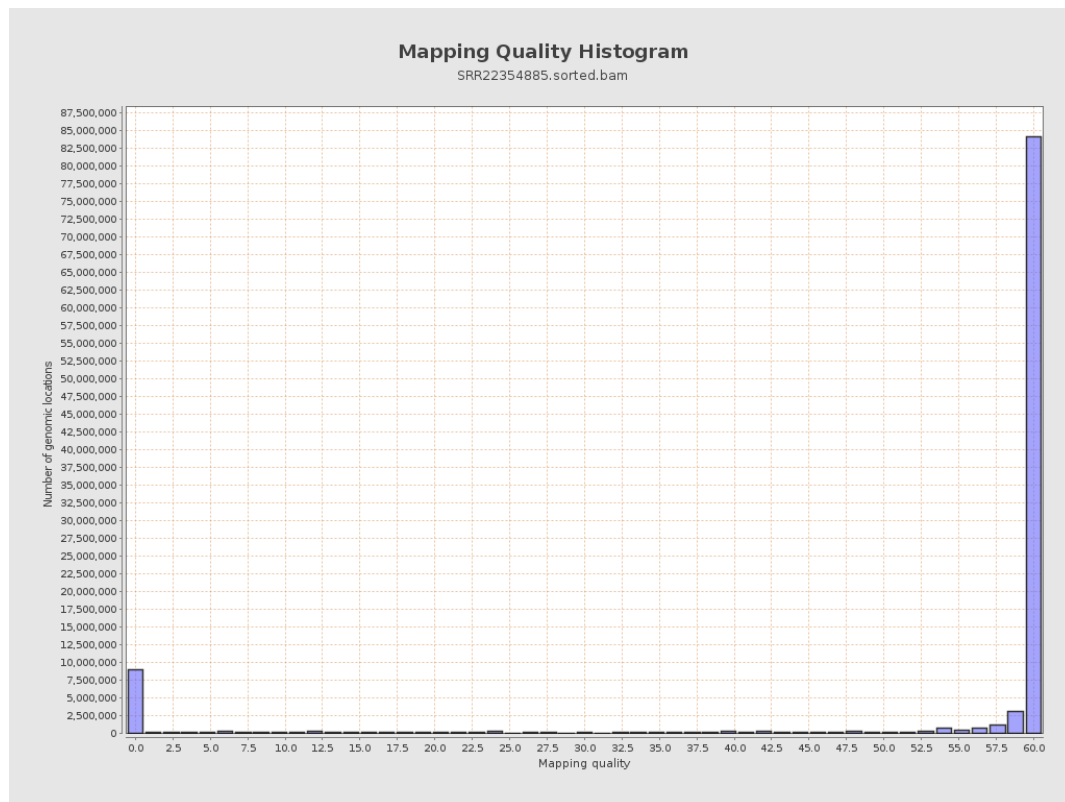
11. Results : Homopolymer Indels



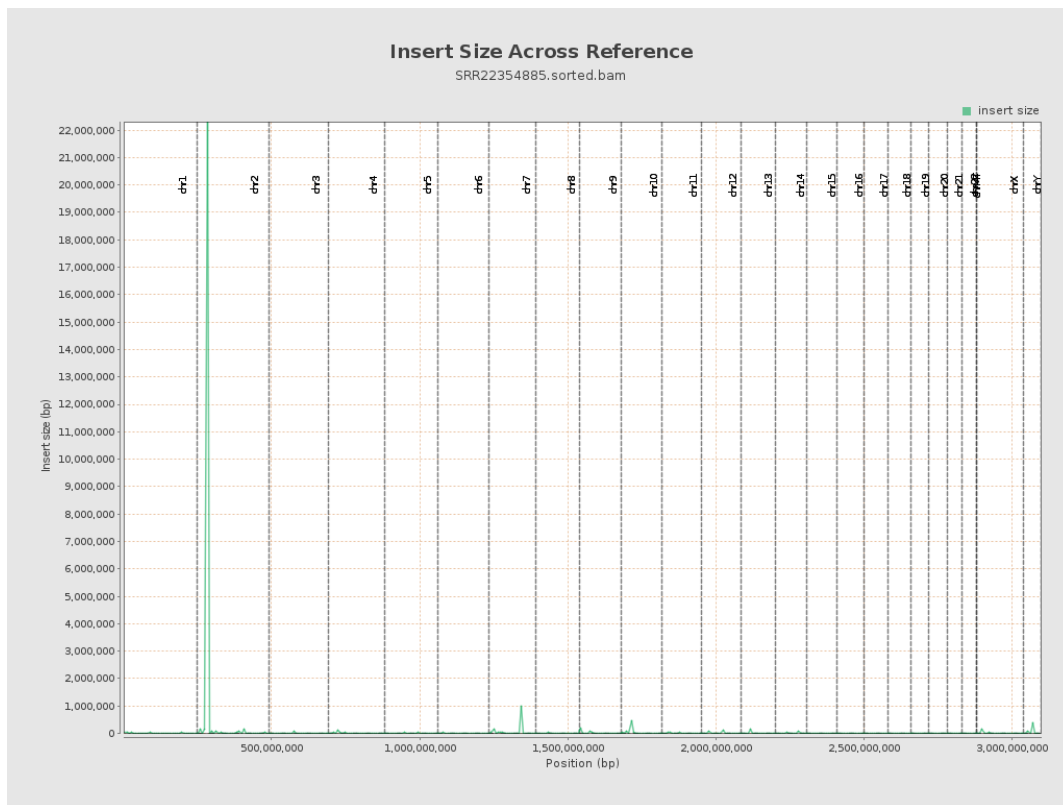
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

