

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 04:40:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472470.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_SRR3472470 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472470_1.fastq.gz SRR3472470_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 04:40:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472470.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,378,418
Mapped reads	16,102,511 / 98.32%
Unmapped reads	275,907 / 1.68%
Mapped paired reads	16,102,511 / 98.32%
Mapped reads, first in pair	8,071,571 / 49.28%
Mapped reads, second in pair	8,030,940 / 49.03%
Mapped reads, both in pair	15,993,068 / 97.65%
Mapped reads, singletons	109,443 / 0.67%
Secondary alignments	0
Supplementary alignments	54,243 / 0.33%
Read min/max/mean length	30 / 100 / 100.13
Duplicated reads (estimated)	10,057,703 / 61.41%
Duplication rate	46.73%
Clipped reads	1,639,041 / 10.01%

2.2. ACGT Content

Number/percentage of A's	430,260,037 / 27.32%
Number/percentage of C's	359,959,034 / 22.85%
Number/percentage of T's	426,962,815 / 27.11%
Number/percentage of G's	357,578,509 / 22.7%
Number/percentage of N's	247,579 / 0.02%

GC Percentage	45.56%
---------------	--------

2.3. Coverage

Mean	0.5088
Standard Deviation	17.8708

2.4. Mapping Quality

Mean Mapping Quality	54.94
----------------------	-------

2.5. Insert size

Mean	28,510.52
Standard Deviation	1,664,501.14
P25/Median/P75	156 / 220 / 299

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	8,964,014
Insertions	77,660
Mapped reads with at least one insertion	0.48%
Deletions	76,697
Mapped reads with at least one deletion	0.47%
Homopolymer indels	44.62%

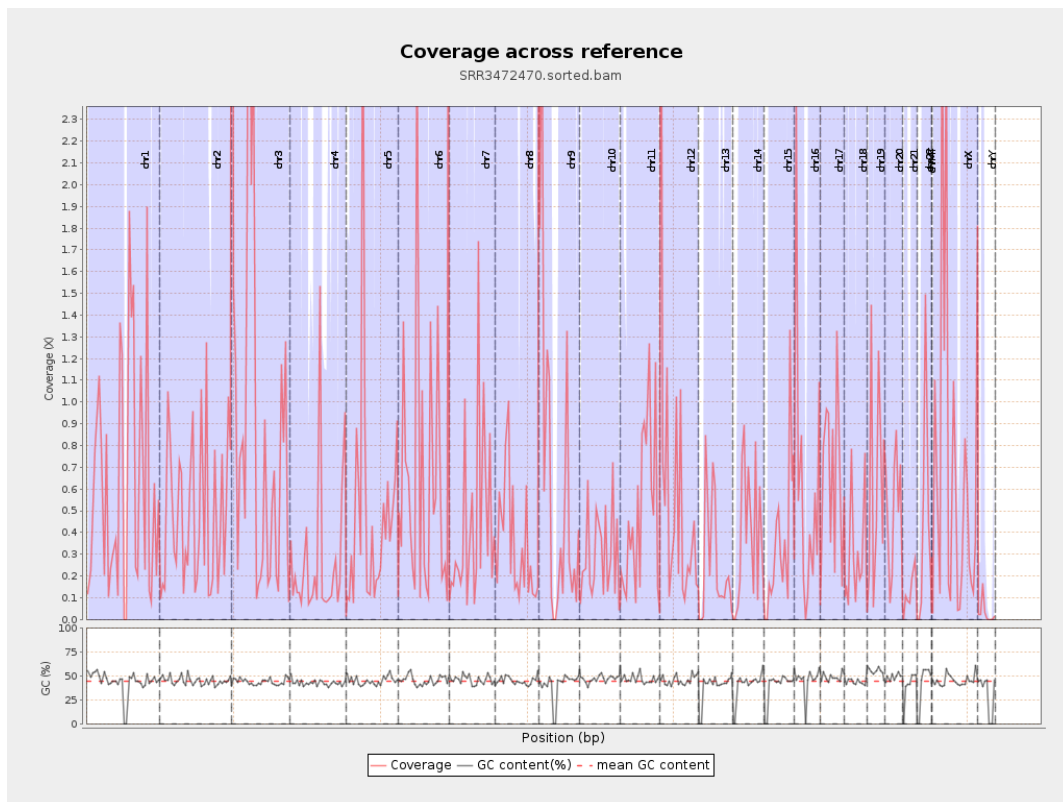
2.7. Chromosome stats

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

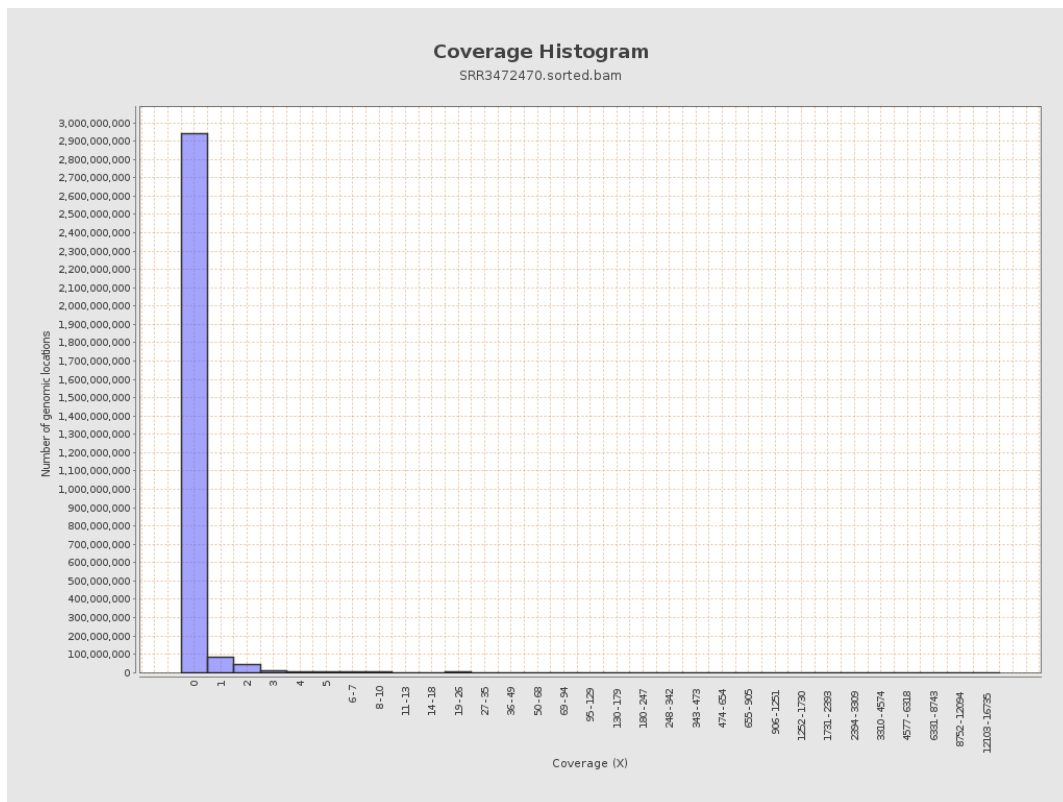
		bases	coverage	deviation
chr1	249250621	156877687	0.6294	20.0809
chr2	243199373	115929451	0.4767	15.757
chr3	198022430	198354848	1.0017	22.863
chr4	191154276	48916717	0.2559	10.8499
chr5	180915260	90816612	0.502	17.4307
chr6	171115067	117408957	0.6861	22.7377
chr7	159138663	69250987	0.4352	13.4372
chr8	146364022	50478174	0.3449	10.4299
chr9	141213431	92240070	0.6532	17.1903
chr10	135534747	41197941	0.304	12.534
chr11	135006516	67923515	0.5031	16.1557
chr12	133851895	81895370	0.6118	22.9229
chr13	115169878	30260083	0.2627	10.0689
chr14	107349540	40237365	0.3748	12.8025
chr15	102531392	35392740	0.3452	9.5546
chr16	90354753	53151495	0.5883	17.9778
chr17	81195210	52731532	0.6494	15.4993
chr18	78077248	23560614	0.3018	10.354
chr19	59128983	37318704	0.6311	17.4017
chr20	63025520	32009811	0.5079	14.6047
chr21	48129895	6523948	0.1355	4.631
chr22	51304566	21685544	0.4227	16.4198
chrMT	16571	4761	0.2873	0.8013
chrX	155270560	109107180	0.7027	36.1413

chrY	59373566	1937528	0.0326	1.8678
------	----------	---------	--------	--------

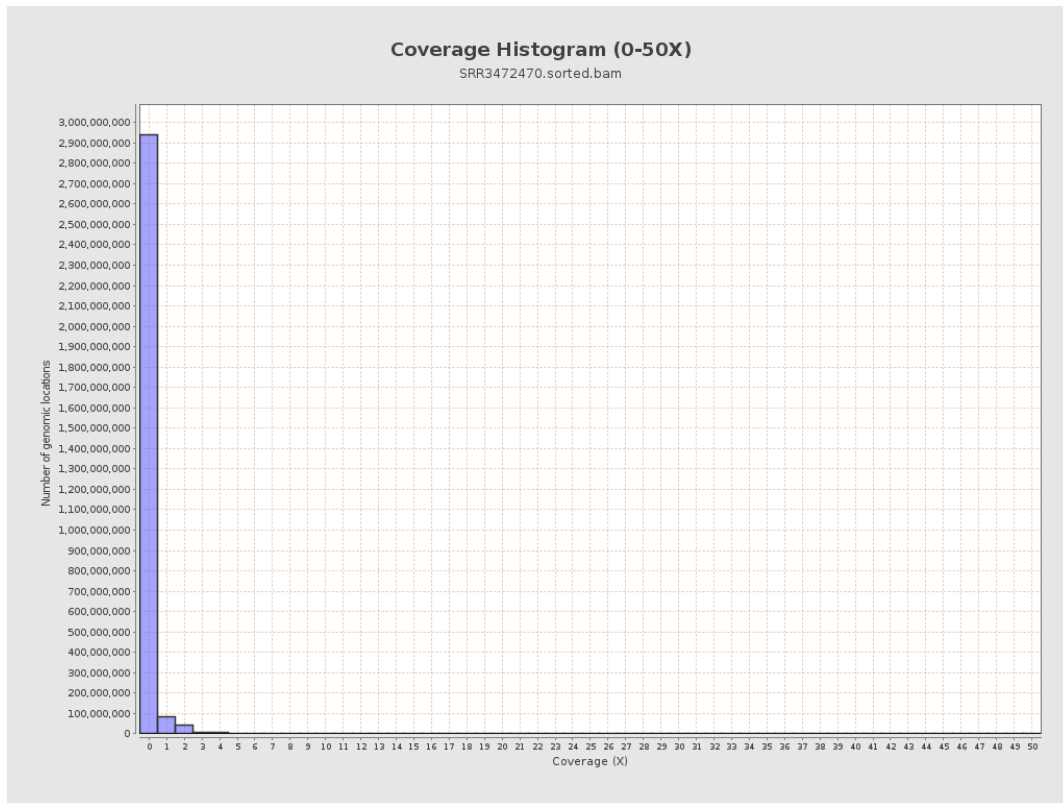
3. Results : Coverage across reference



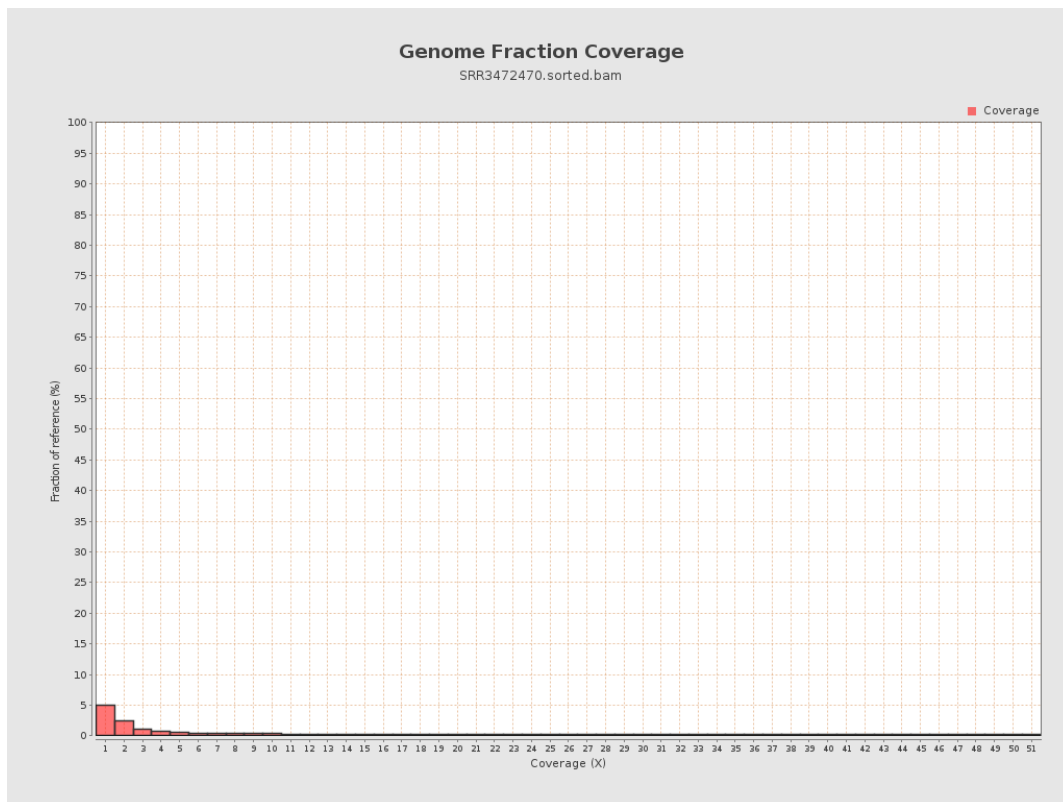
4. Results : Coverage Histogram



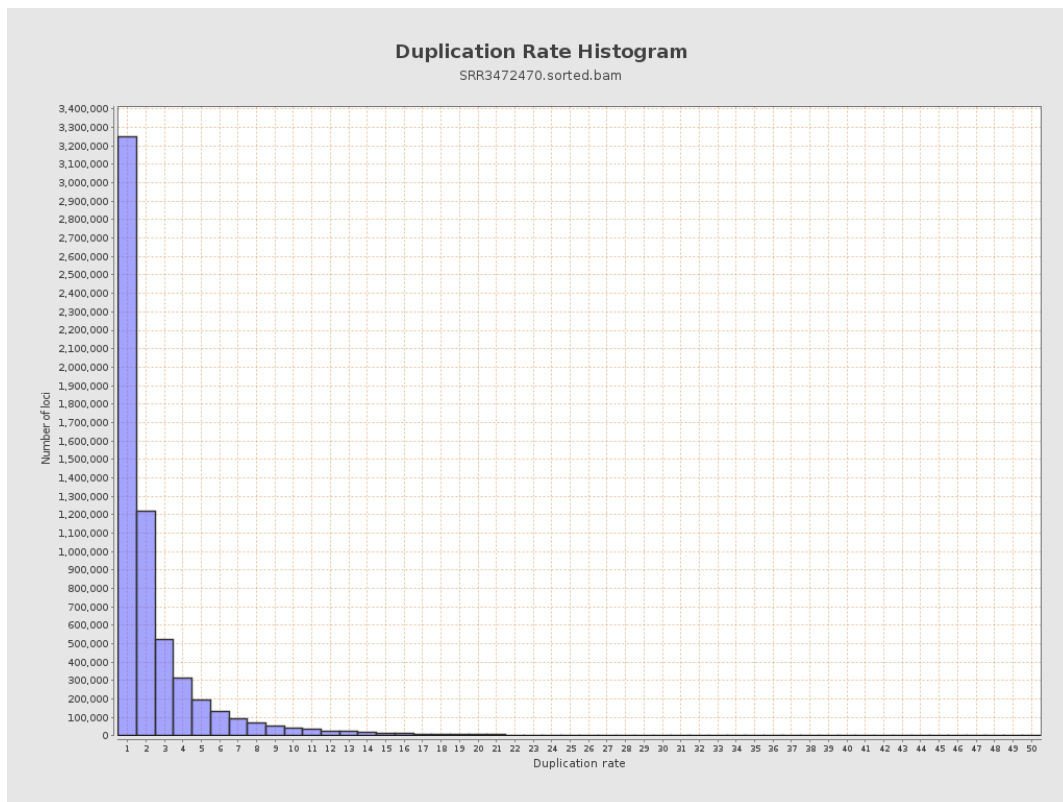
5. Results : Coverage Histogram (0-50X)



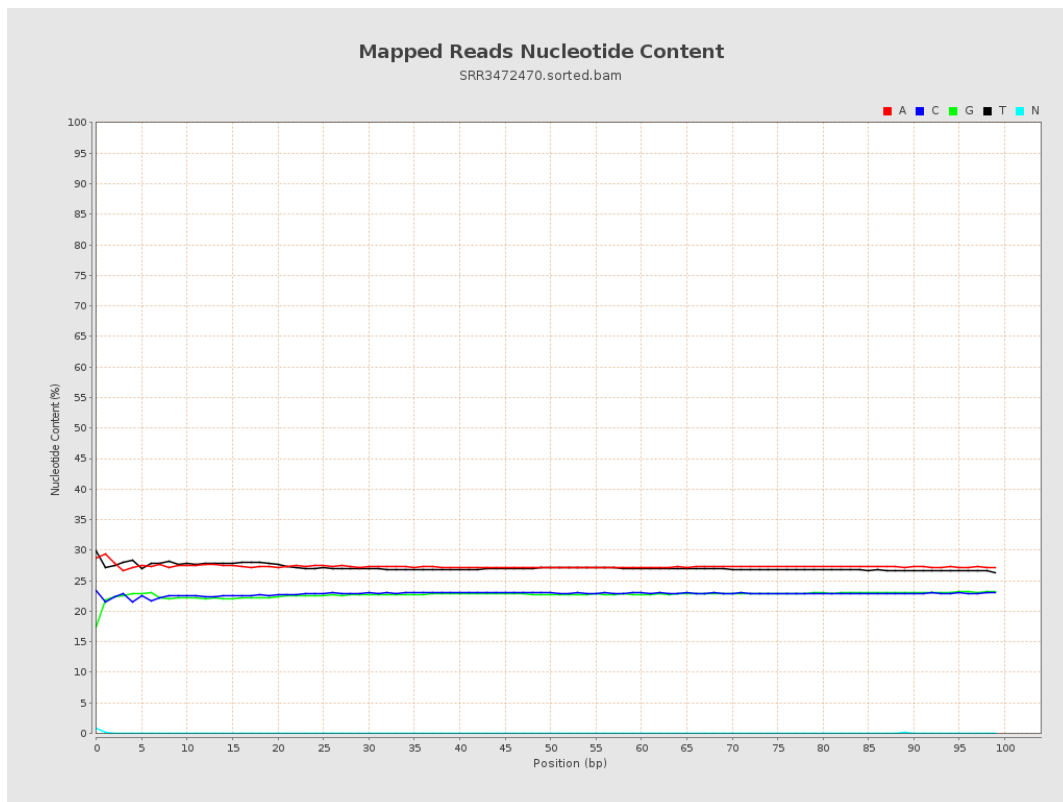
6. Results : Genome Fraction Coverage



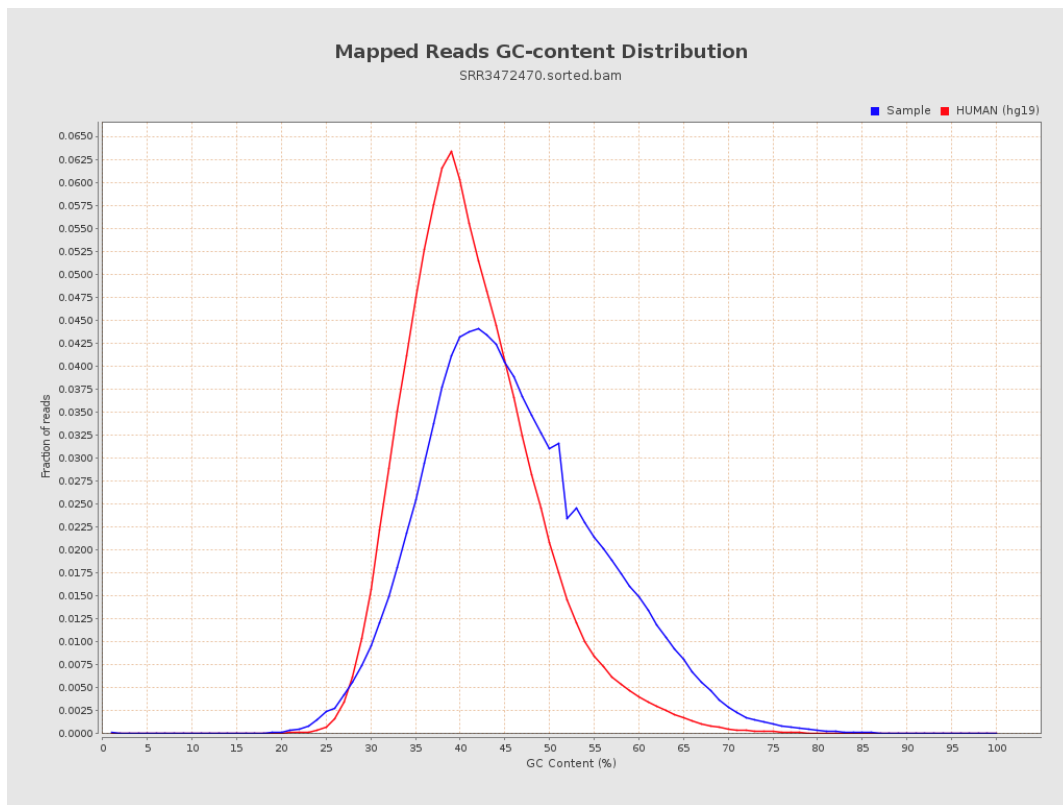
7. Results : Duplication Rate Histogram



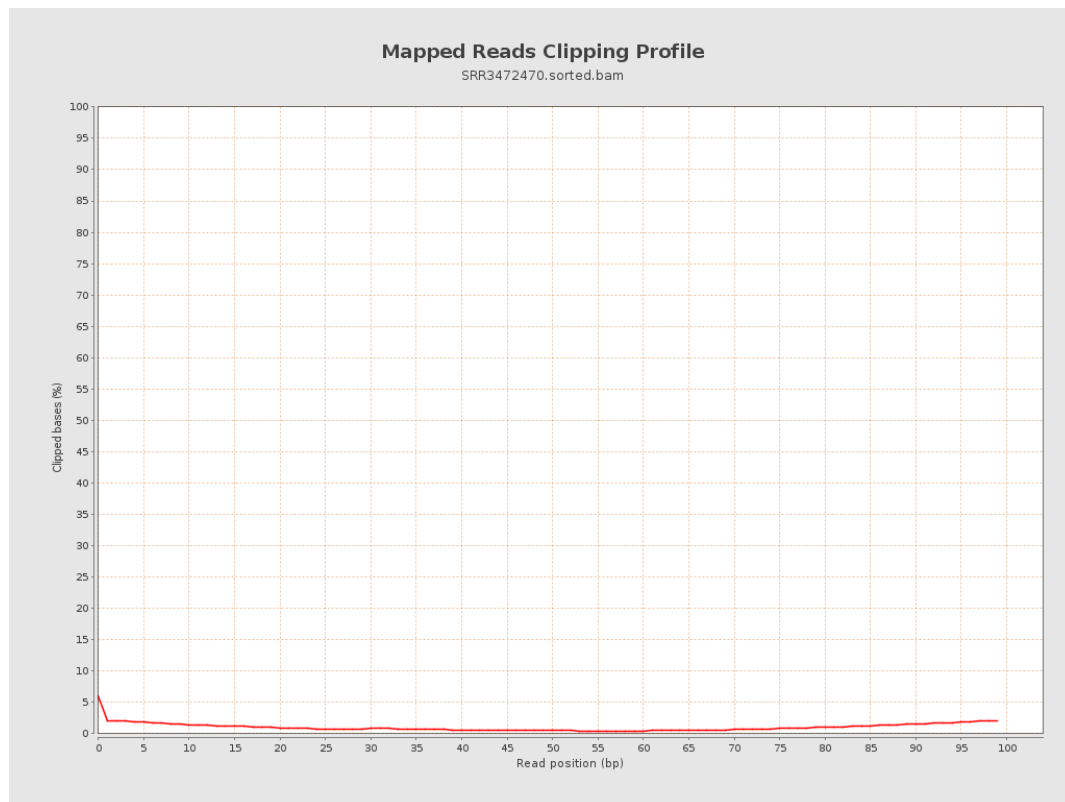
8. Results : Mapped Reads Nucleotide Content



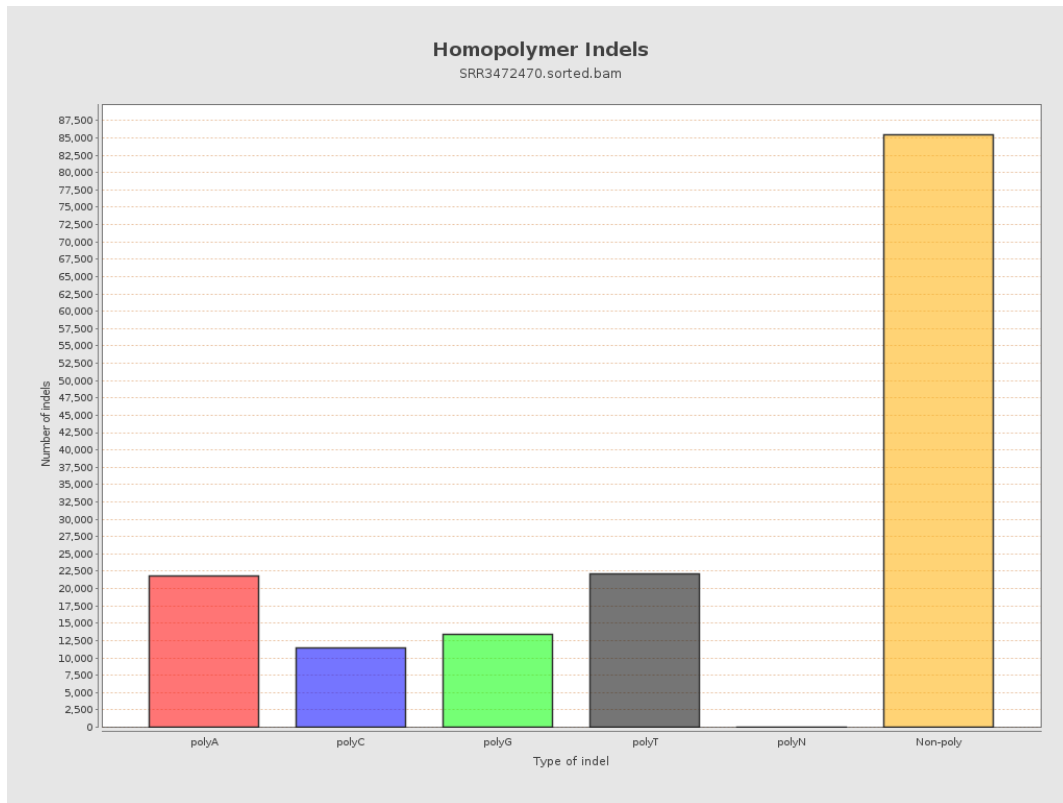
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



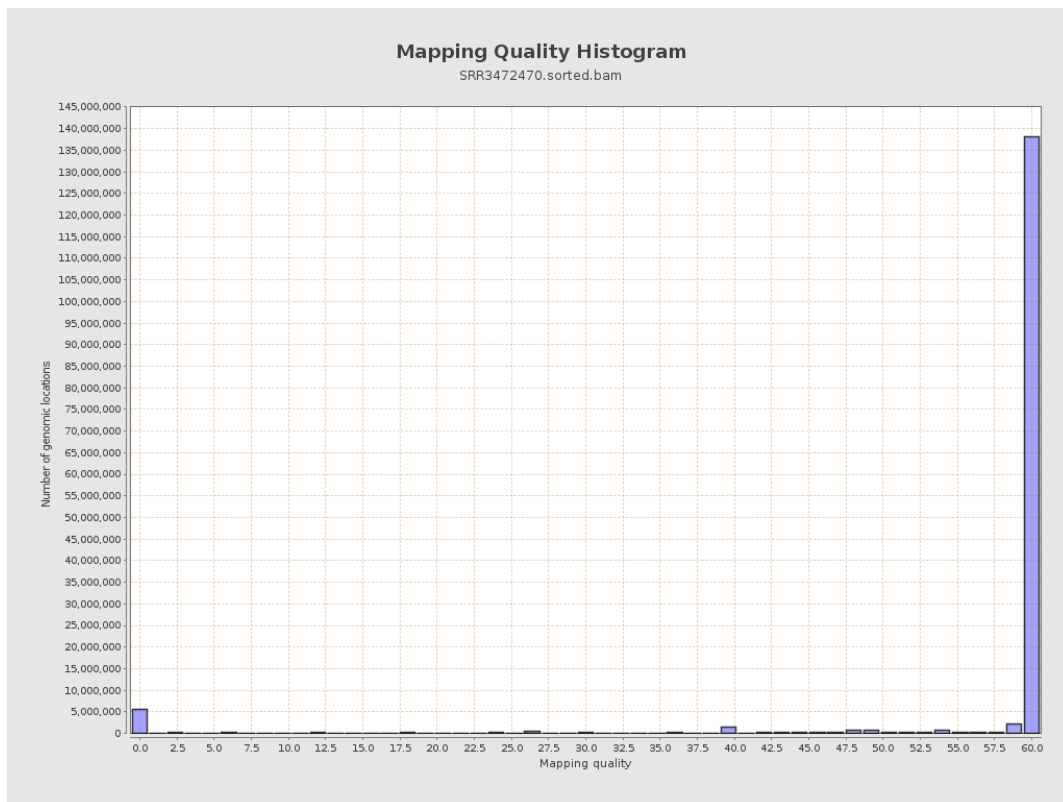
11. Results : Homopolymer Indels



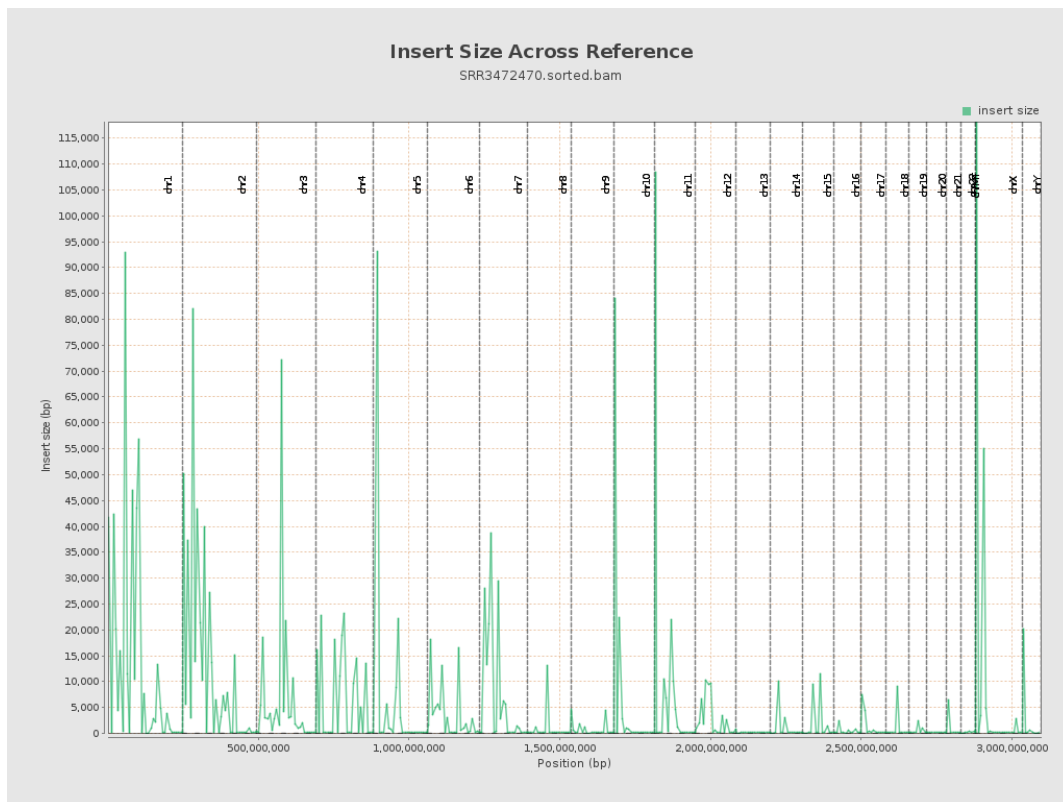
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

