

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 23:09:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472656.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_SRR3472656 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472656_1.fastq.gz SRR3472656_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 23:09:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472656.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,700,190
Mapped reads	14,526,009 / 98.82%
Unmapped reads	174,181 / 1.18%
Mapped paired reads	14,526,009 / 98.82%
Mapped reads, first in pair	7,299,255 / 49.65%
Mapped reads, second in pair	7,226,754 / 49.16%
Mapped reads, both in pair	14,405,644 / 98%
Mapped reads, singletons	120,365 / 0.82%
Secondary alignments	0
Supplementary alignments	92,012 / 0.63%
Read min/max/mean length	30 / 101 / 99.85
Duplicated reads (estimated)	9,726,599 / 66.17%
Duplication rate	47.34%
Clipped reads	998,426 / 6.79%

2.2. ACGT Content

Number/percentage of A's	394,814,770 / 27.57%
Number/percentage of C's	322,539,478 / 22.52%
Number/percentage of T's	395,780,476 / 27.64%
Number/percentage of G's	318,543,787 / 22.25%
Number/percentage of N's	271,319 / 0.02%

GC Percentage	44.77%
---------------	--------

2.3. Coverage

Mean	0.4626
Standard Deviation	21.4034

2.4. Mapping Quality

Mean Mapping Quality	54.76
----------------------	-------

2.5. Insert size

Mean	25,836.14
Standard Deviation	1,559,720.83
P25/Median/P75	173 / 238 / 315

2.6. Mismatches and indels

General error rate	0.67%
Mismatches	9,461,667
Insertions	96,944
Mapped reads with at least one insertion	0.66%
Deletions	83,575
Mapped reads with at least one deletion	0.57%
Homopolymer indels	45.54%

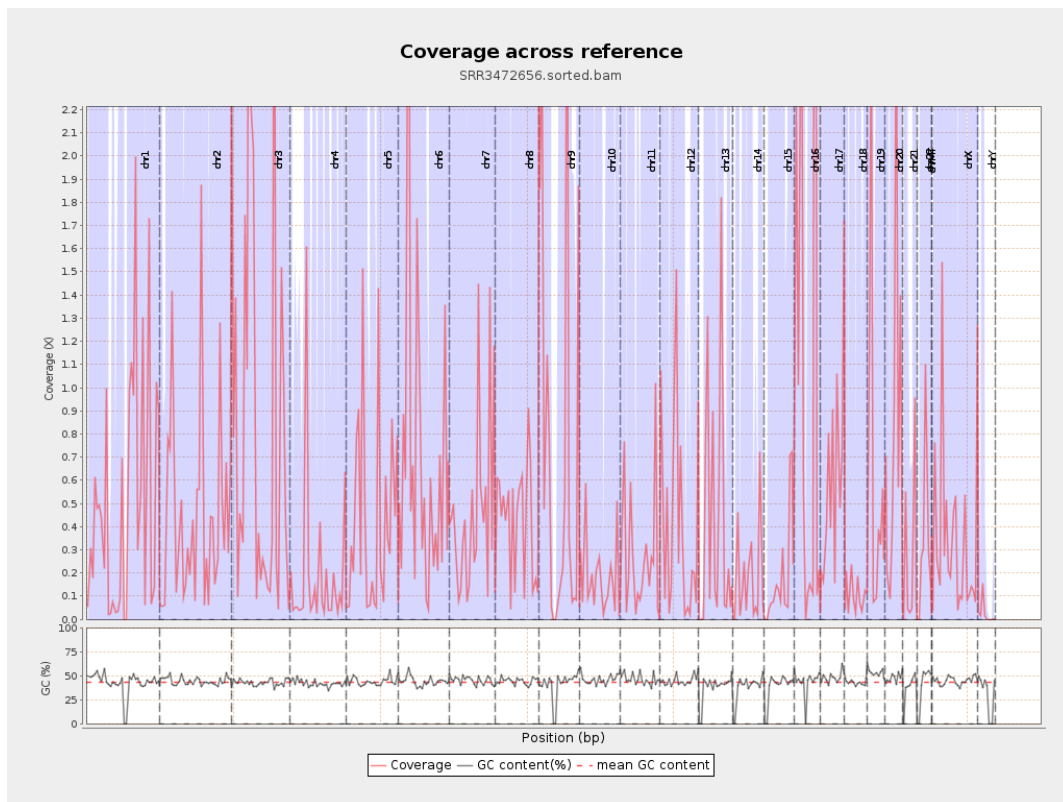
2.7. Chromosome stats

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

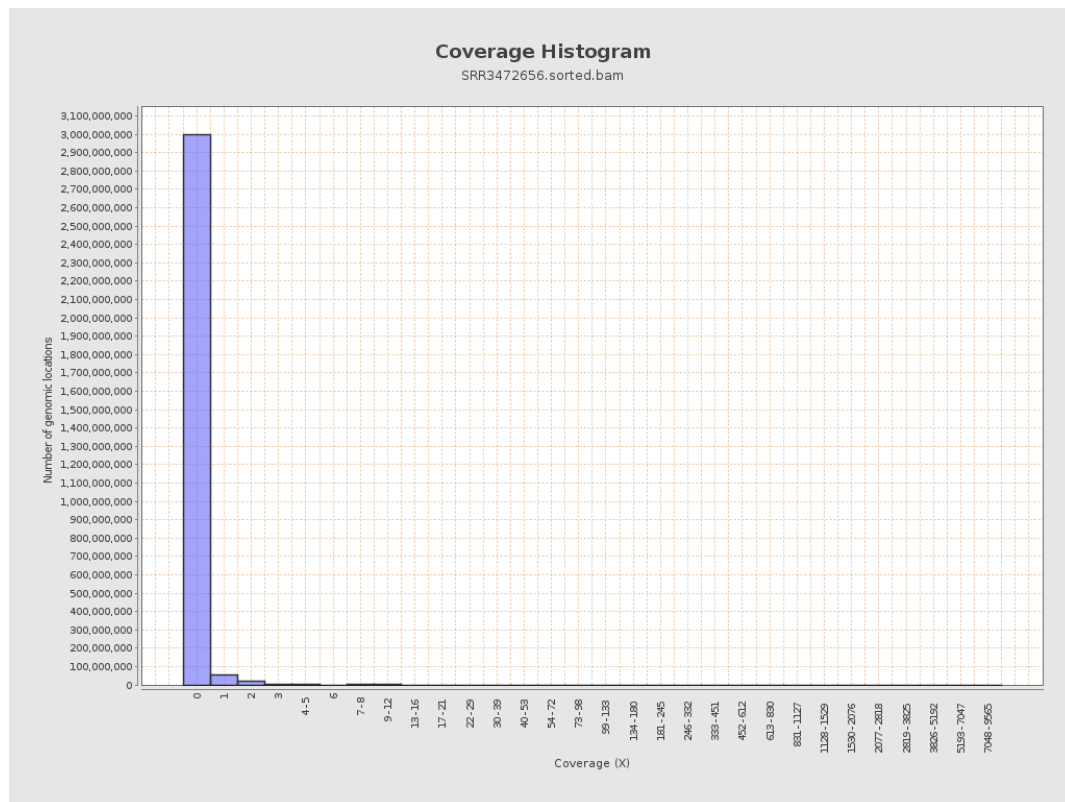
		bases	coverage	deviation
chr1	249250621	129051322	0.5178	23.9733
chr2	243199373	109943343	0.4521	22.4202
chr3	198022430	181578991	0.917	31.3875
chr4	191154276	34144170	0.1786	11.0271
chr5	180915260	77663146	0.4293	17.3993
chr6	171115067	115263351	0.6736	27.4155
chr7	159138663	75620764	0.4752	15.4773
chr8	146364022	63242189	0.4321	14.3997
chr9	141213431	107319270	0.76	29.1579
chr10	135534747	24457443	0.1805	9.0785
chr11	135006516	37223250	0.2757	12.9755
chr12	133851895	55198636	0.4124	16.7396
chr13	115169878	47461908	0.4121	22.1076
chr14	107349540	17834714	0.1661	9.1487
chr15	102531392	19324273	0.1885	8.5769
chr16	90354753	104052972	1.1516	51.6652
chr17	81195210	48068920	0.592	18.1521
chr18	78077248	8461126	0.1084	4.6405
chr19	59128983	40305624	0.6817	19.8102
chr20	63025520	53216820	0.8444	35.329
chr21	48129895	13065970	0.2715	22.1385
chr22	51304566	16470758	0.321	13.1872
chrMT	16571	6013	0.3629	0.945
chrX	155270560	51523650	0.3318	9.42

chrY	59373566	1672558	0.0282	1.9204
------	----------	---------	--------	--------

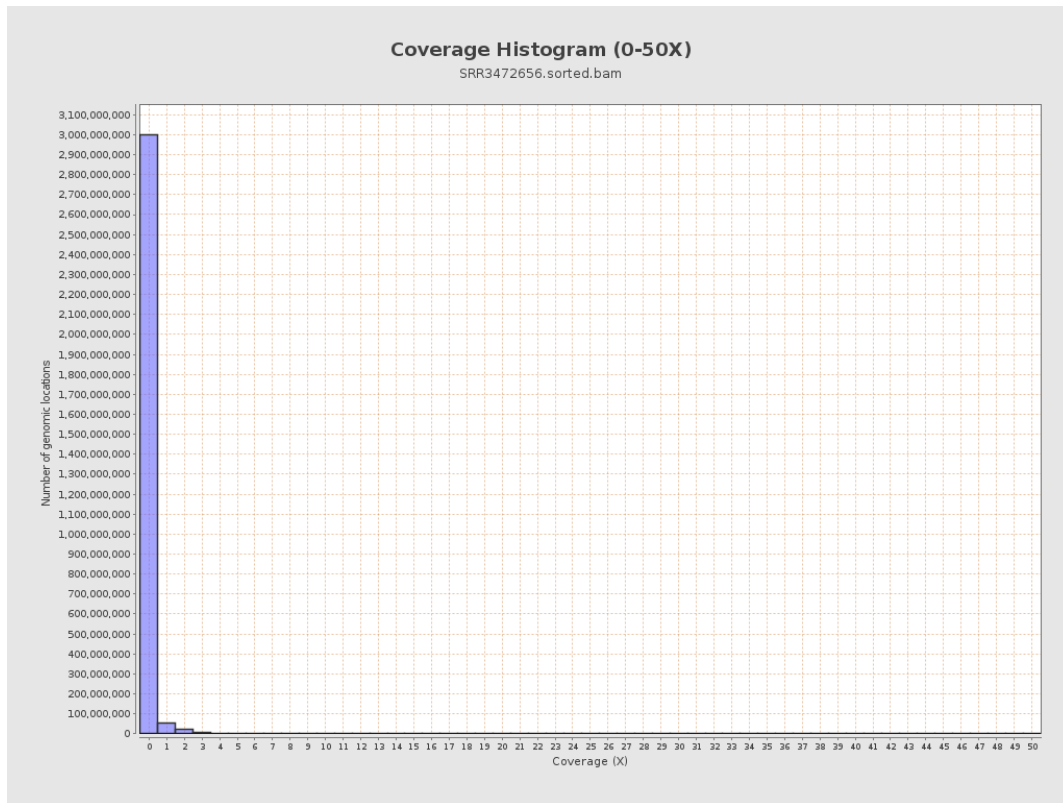
3. Results : Coverage across reference



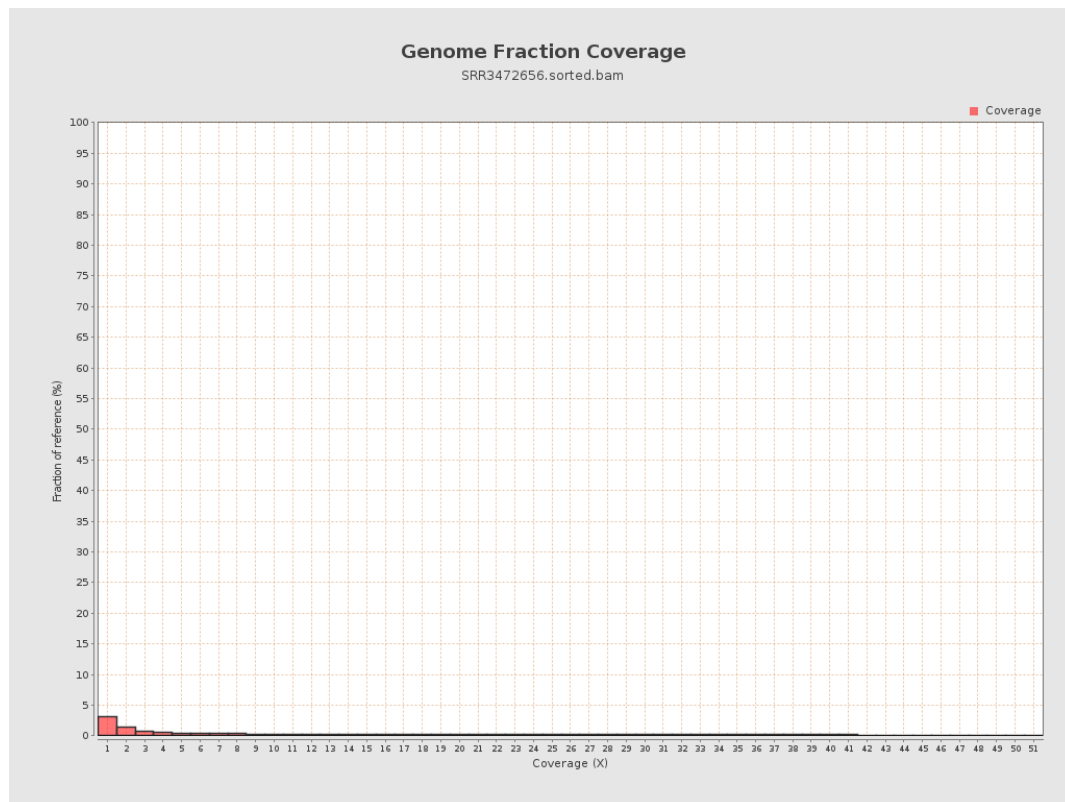
4. Results : Coverage Histogram



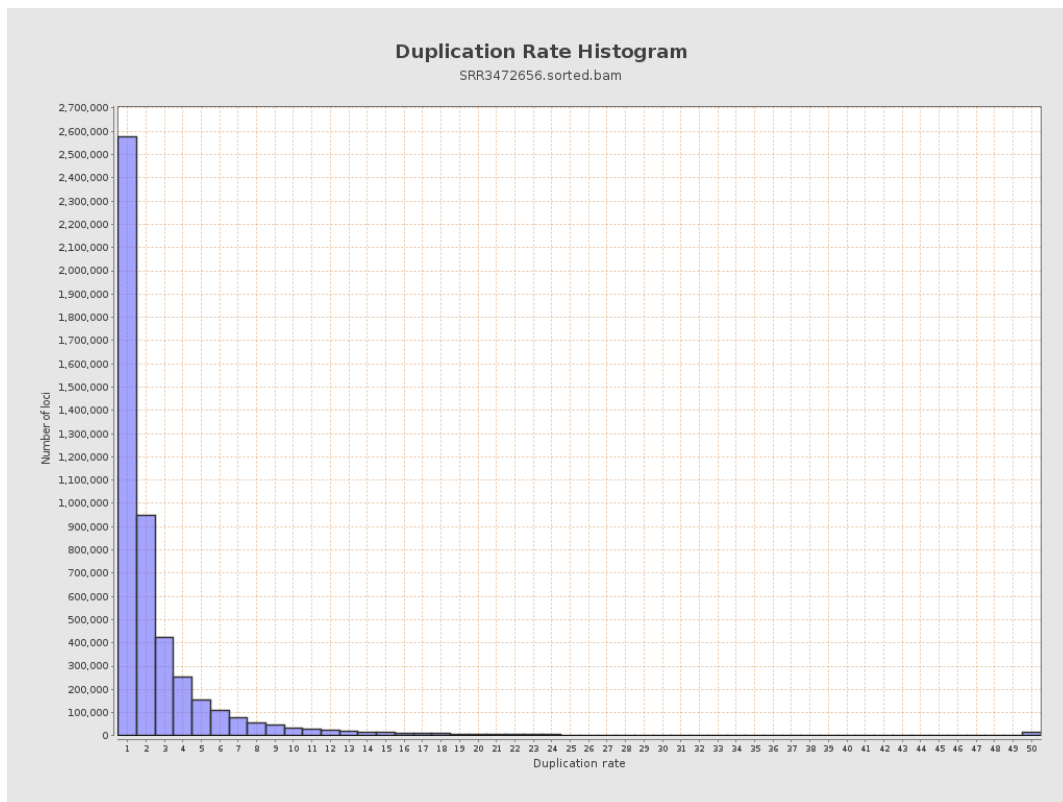
5. Results : Coverage Histogram (0-50X)



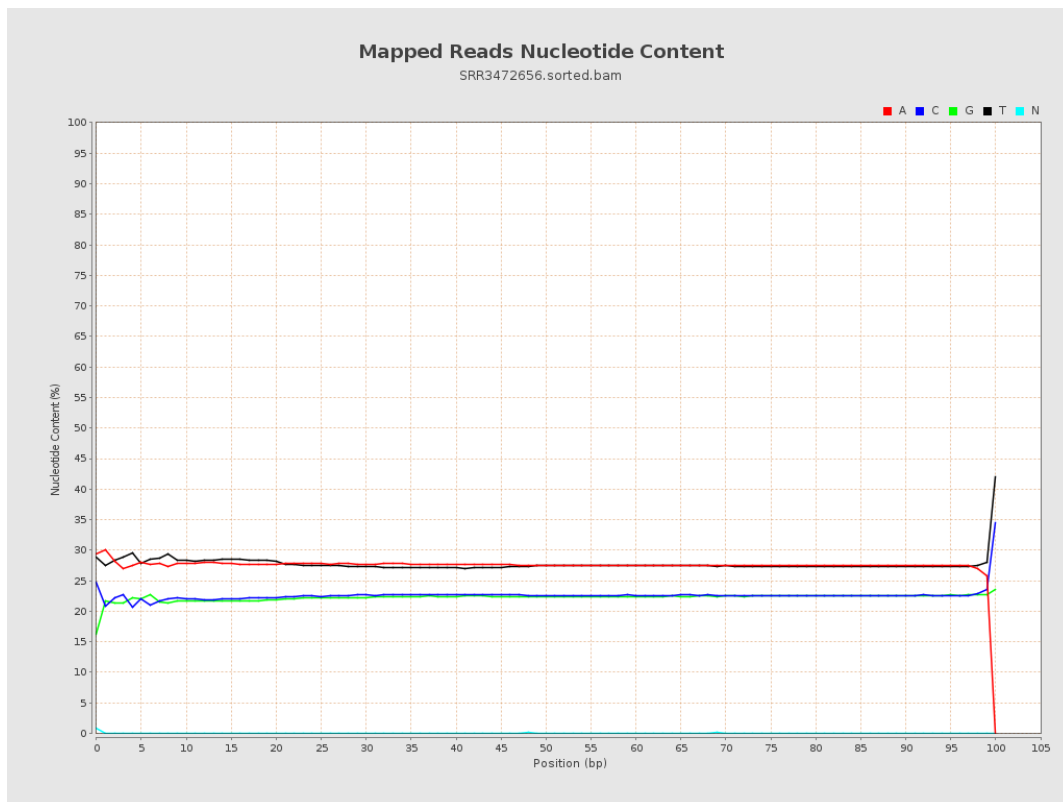
6. Results : Genome Fraction Coverage



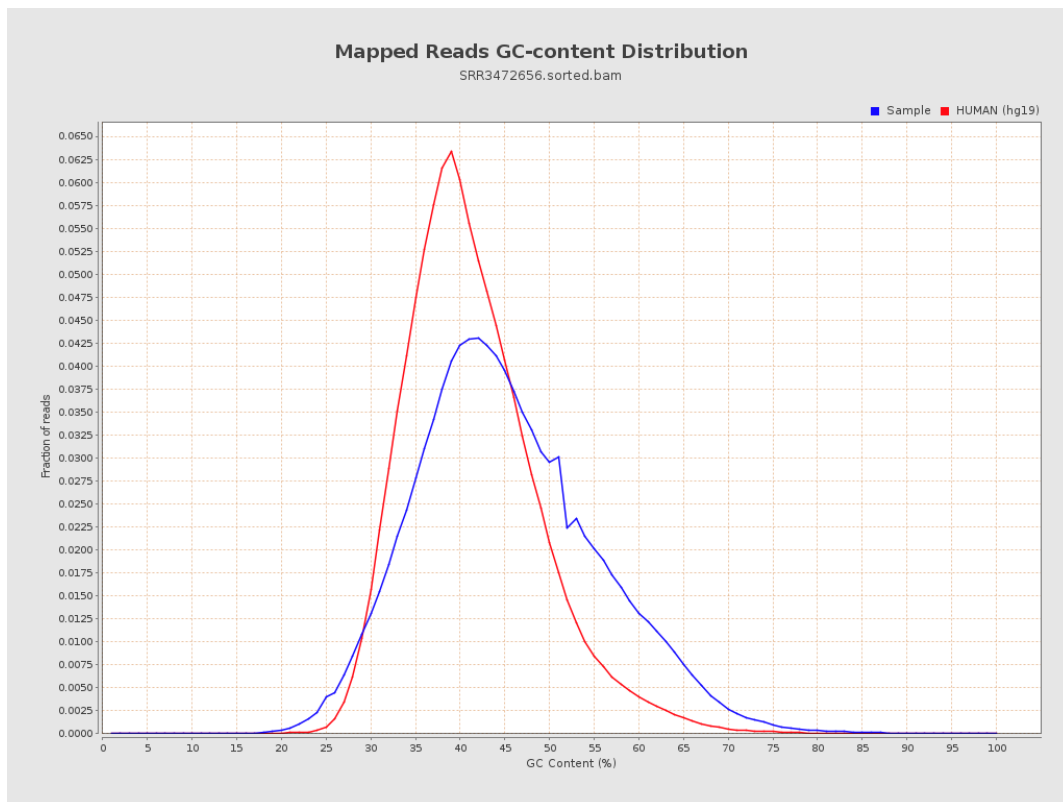
7. Results : Duplication Rate Histogram



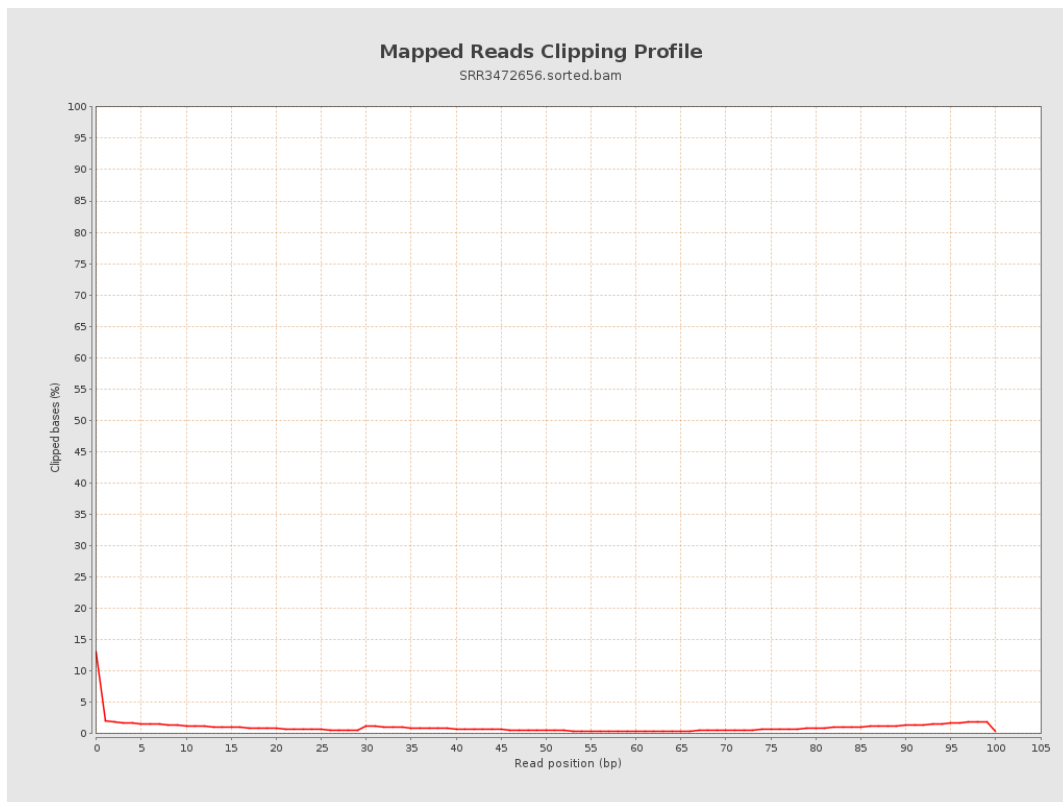
8. Results : Mapped Reads Nucleotide Content



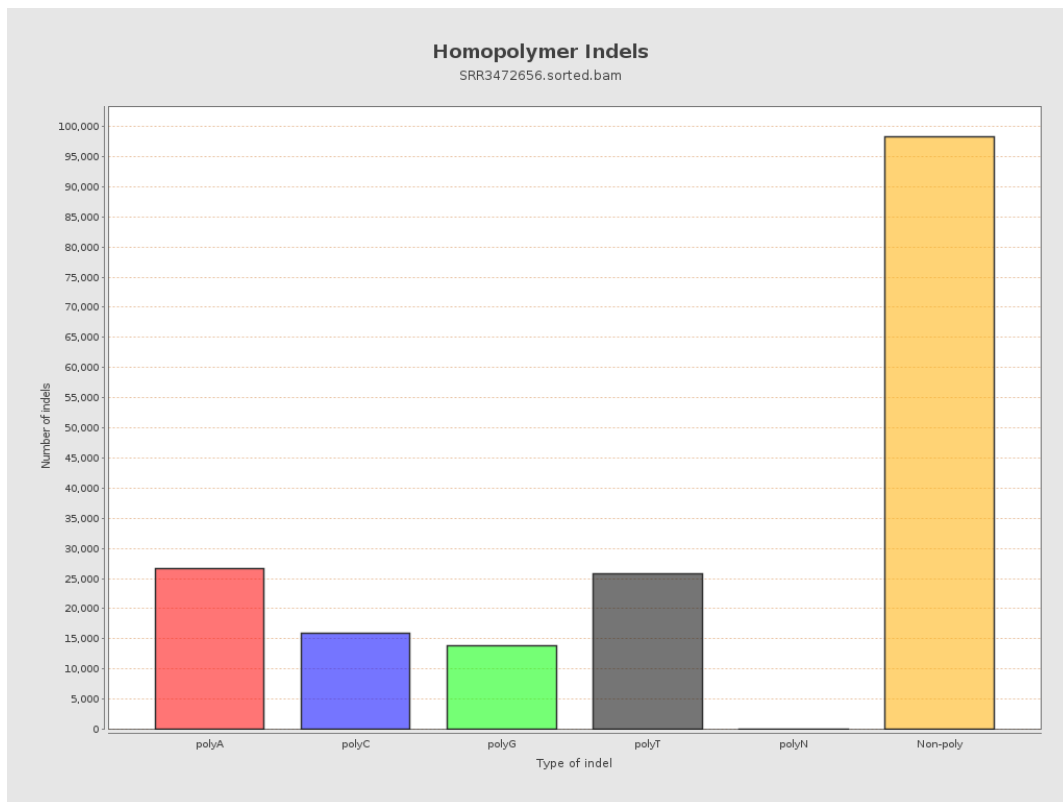
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



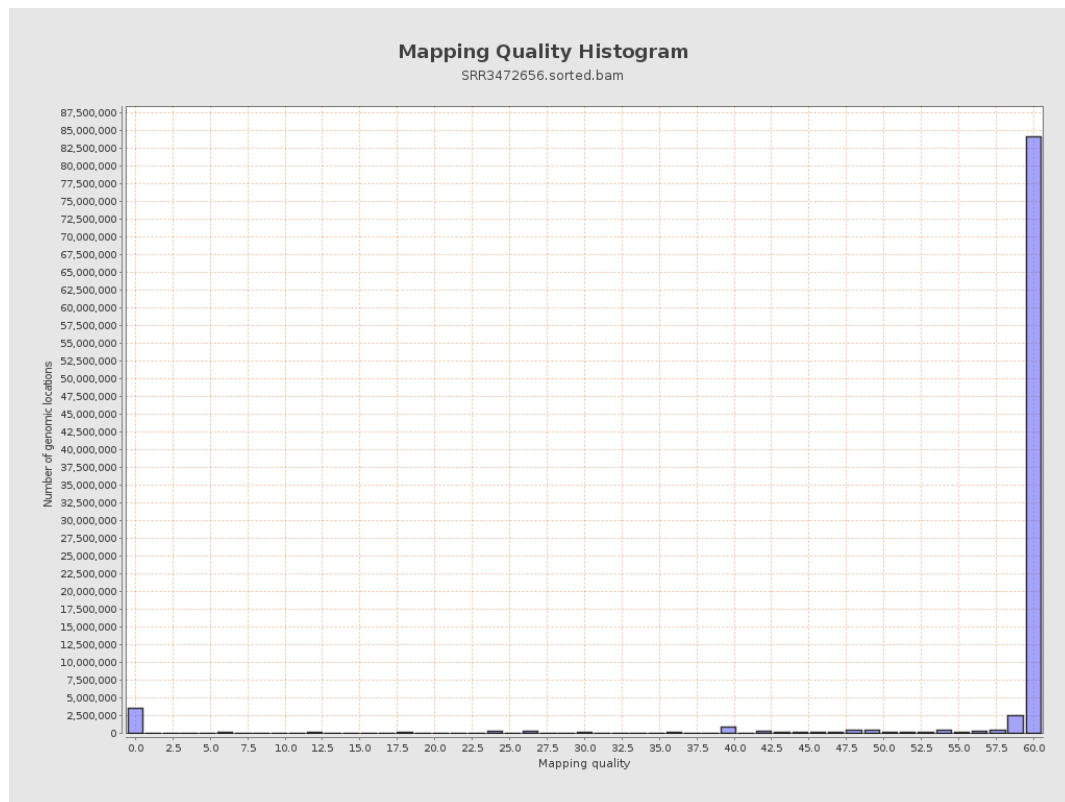
11. Results : Homopolymer Indels



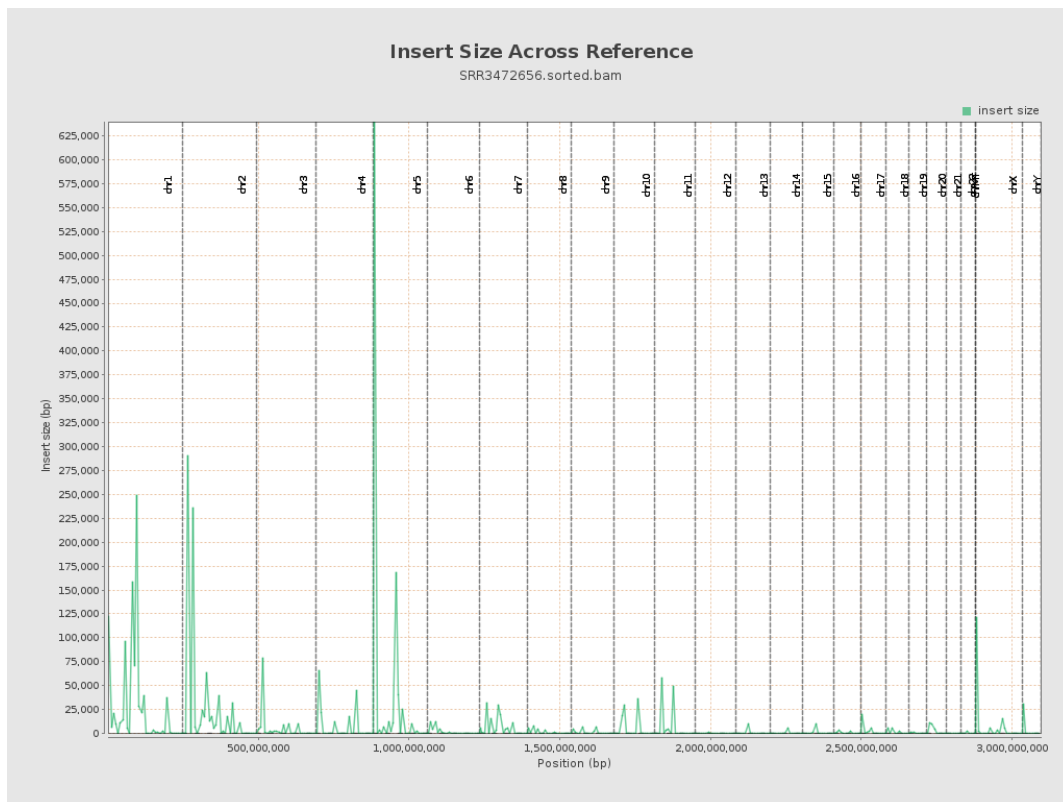
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

