

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 23:19:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472657.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_SRR3472657 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472657_1.fastq.gz SRR3472657_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 23:19:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472657.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	162,530
Mapped reads	160,876 / 98.98%
Unmapped reads	1,654 / 1.02%
Mapped paired reads	160,876 / 98.98%
Mapped reads, first in pair	80,738 / 49.68%
Mapped reads, second in pair	80,138 / 49.31%
Mapped reads, both in pair	159,772 / 98.3%
Mapped reads, singletons	1,104 / 0.68%
Secondary alignments	0
Supplementary alignments	944 / 0.58%
Read min/max/mean length	30 / 101 / 99.78
Duplicated reads (estimated)	34,245 / 21.07%
Duplication rate	21.07%
Clipped reads	11,635 / 7.16%

2.2. ACGT Content

Number/percentage of A's	4,307,433 / 27.22%
Number/percentage of C's	3,631,115 / 22.94%
Number/percentage of T's	4,308,662 / 27.22%
Number/percentage of G's	3,576,581 / 22.6%
Number/percentage of N's	3,580 / 0.02%

GC Percentage	45.54%
---------------	--------

2.3. Coverage

Mean	0.0051
Standard Deviation	0.2187

2.4. Mapping Quality

Mean Mapping Quality	54.54
----------------------	-------

2.5. Insert size

Mean	18,374.11
Standard Deviation	1,193,090.37
P25/Median/P75	157 / 215 / 287

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	98,286
Insertions	917
Mapped reads with at least one insertion	0.56%
Deletions	838
Mapped reads with at least one deletion	0.51%
Homopolymer indels	45.58%

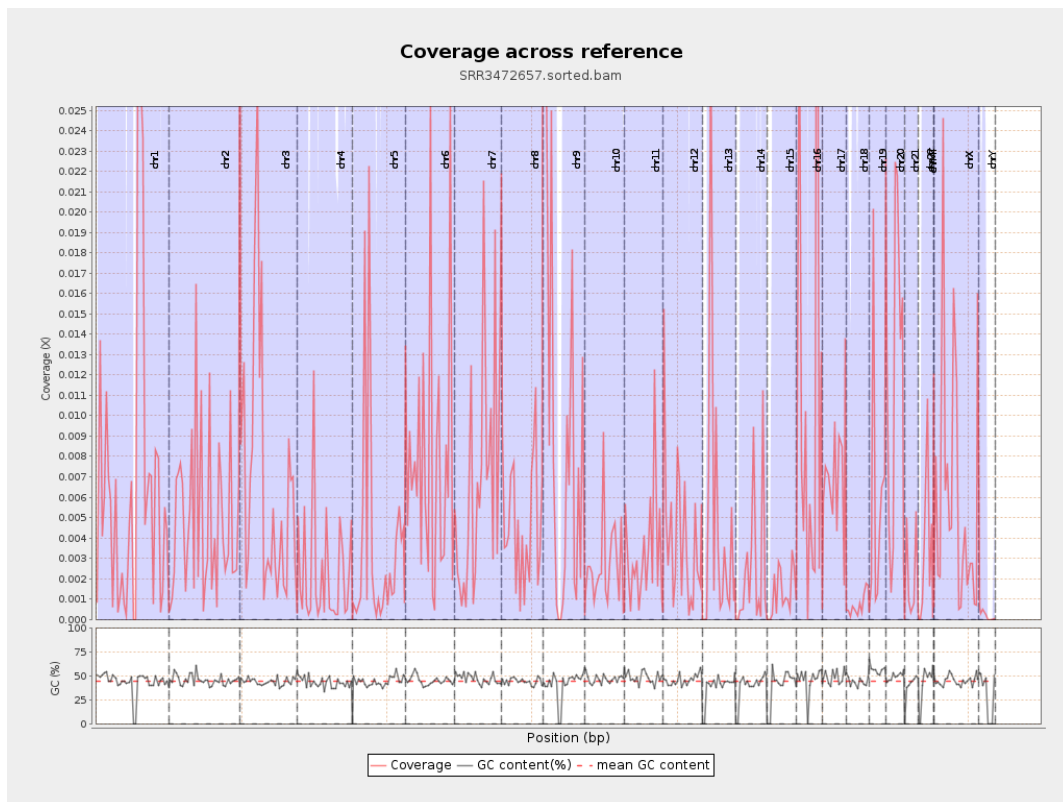
2.7. Chromosome stats

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

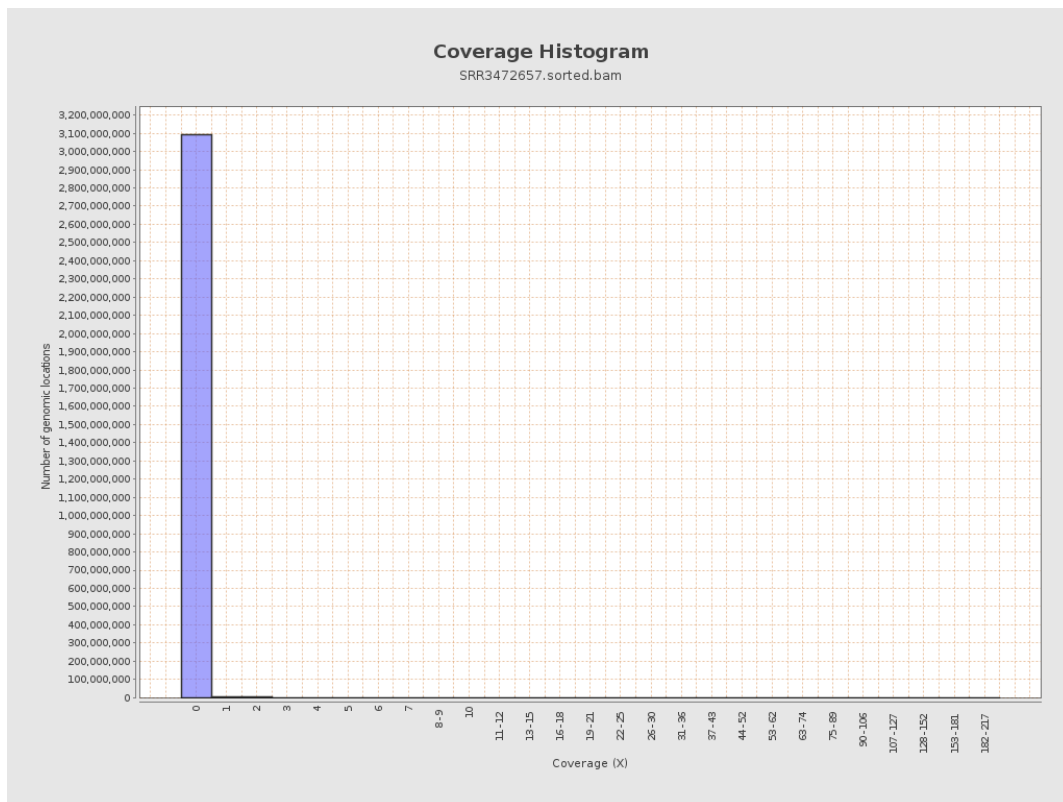
		bases	coverage	deviation
chr1	249250621	1568745	0.0063	0.2998
chr2	243199373	1193660	0.0049	0.2312
chr3	198022430	1401318	0.0071	0.2024
chr4	191154276	417225	0.0022	0.1152
chr5	180915260	631594	0.0035	0.1733
chr6	171115067	1379031	0.0081	0.272
chr7	159138663	1047186	0.0066	0.2559
chr8	146364022	704134	0.0048	0.186
chr9	141213431	1339513	0.0095	0.346
chr10	135534747	369162	0.0027	0.1391
chr11	135006516	432993	0.0032	0.1358
chr12	133851895	541698	0.004	0.1406
chr13	115169878	511575	0.0044	0.2223
chr14	107349540	262420	0.0024	0.1684
chr15	102531392	137314	0.0013	0.0756
chr16	90354753	1041338	0.0115	0.4119
chr17	81195210	558465	0.0069	0.2065
chr18	78077248	56112	0.0007	0.0409
chr19	59128983	374110	0.0063	0.1966
chr20	63025520	725245	0.0115	0.2999
chr21	48129895	97072	0.002	0.125
chr22	51304566	170652	0.0033	0.1868
chrMT	16571	200	0.0121	0.1092
chrX	155270560	857249	0.0055	0.1785

chrY	59373566	11532	0.0002	0.0188
------	----------	-------	--------	--------

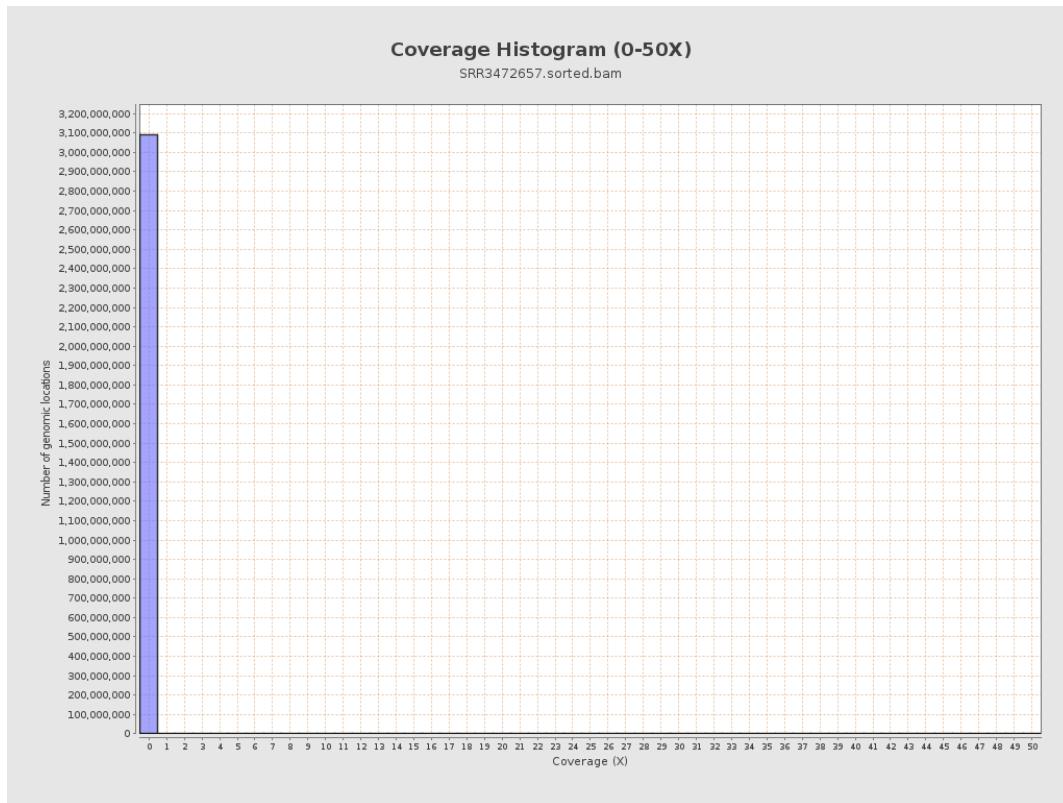
3. Results : Coverage across reference



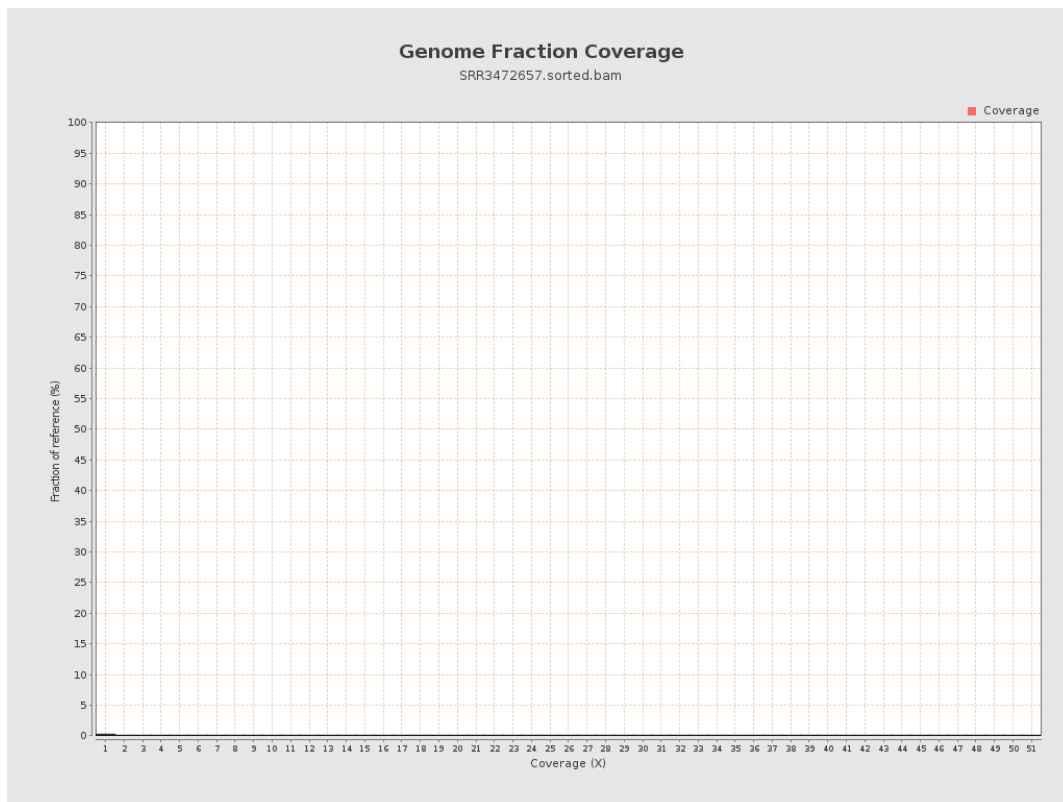
4. Results : Coverage Histogram



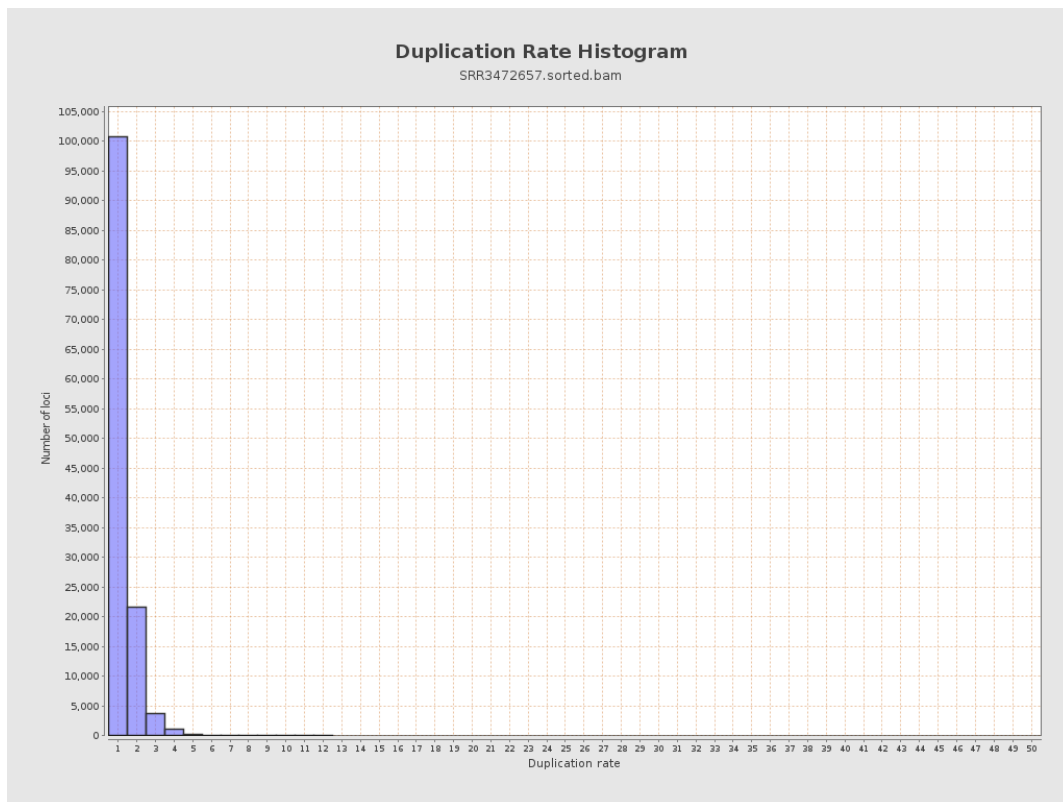
5. Results : Coverage Histogram (0-50X)



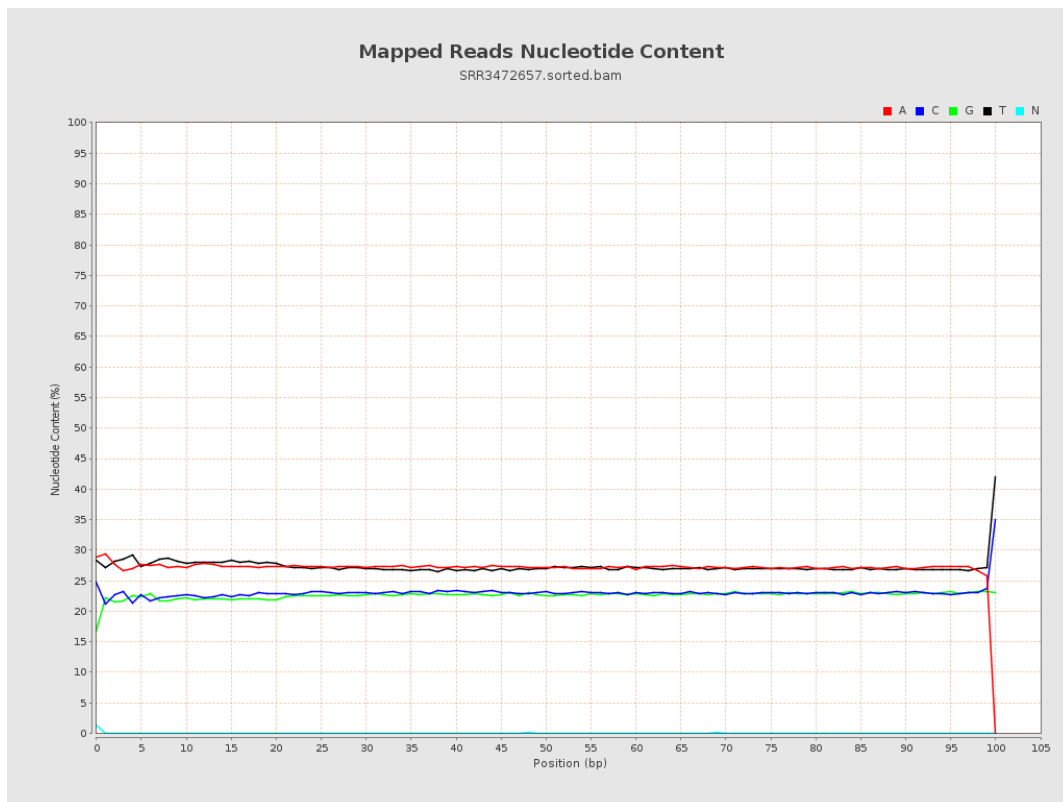
6. Results : Genome Fraction Coverage



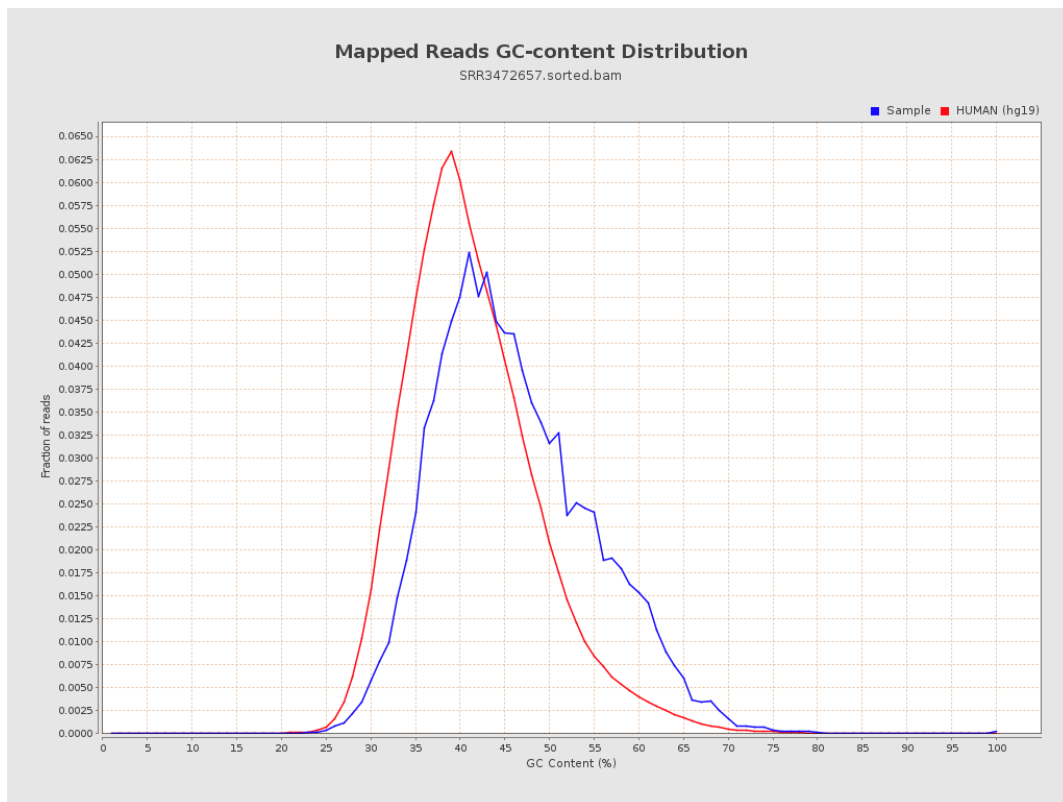
7. Results : Duplication Rate Histogram



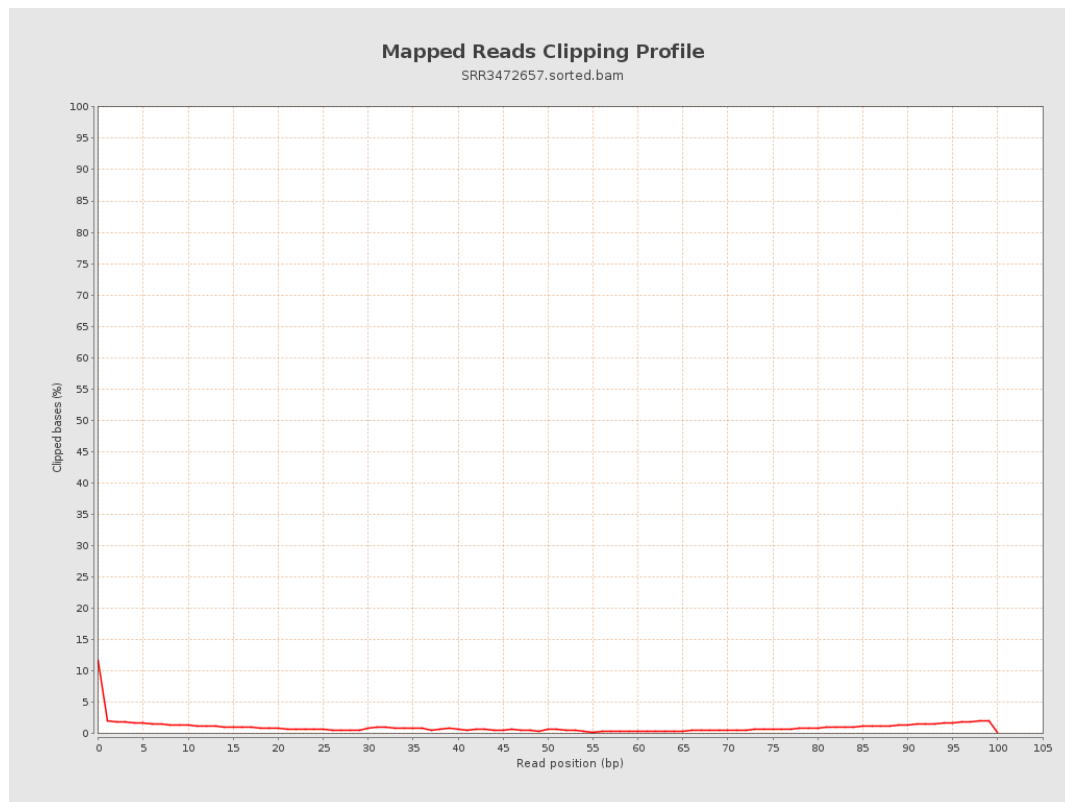
8. Results : Mapped Reads Nucleotide Content



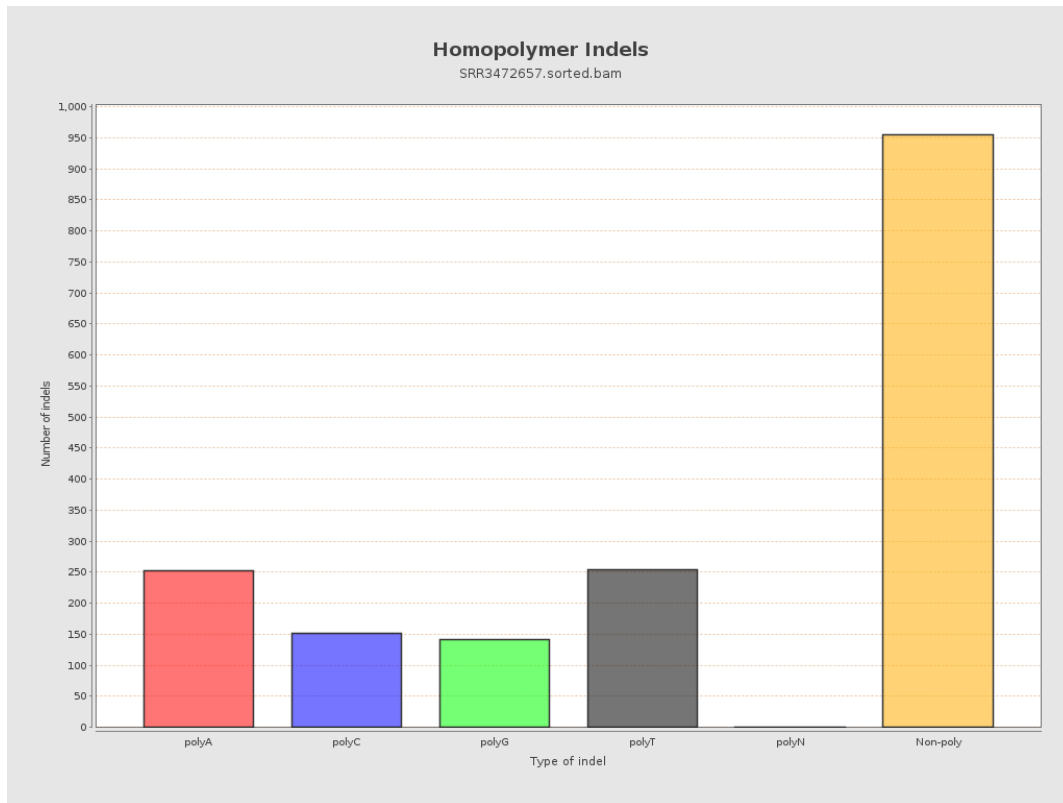
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



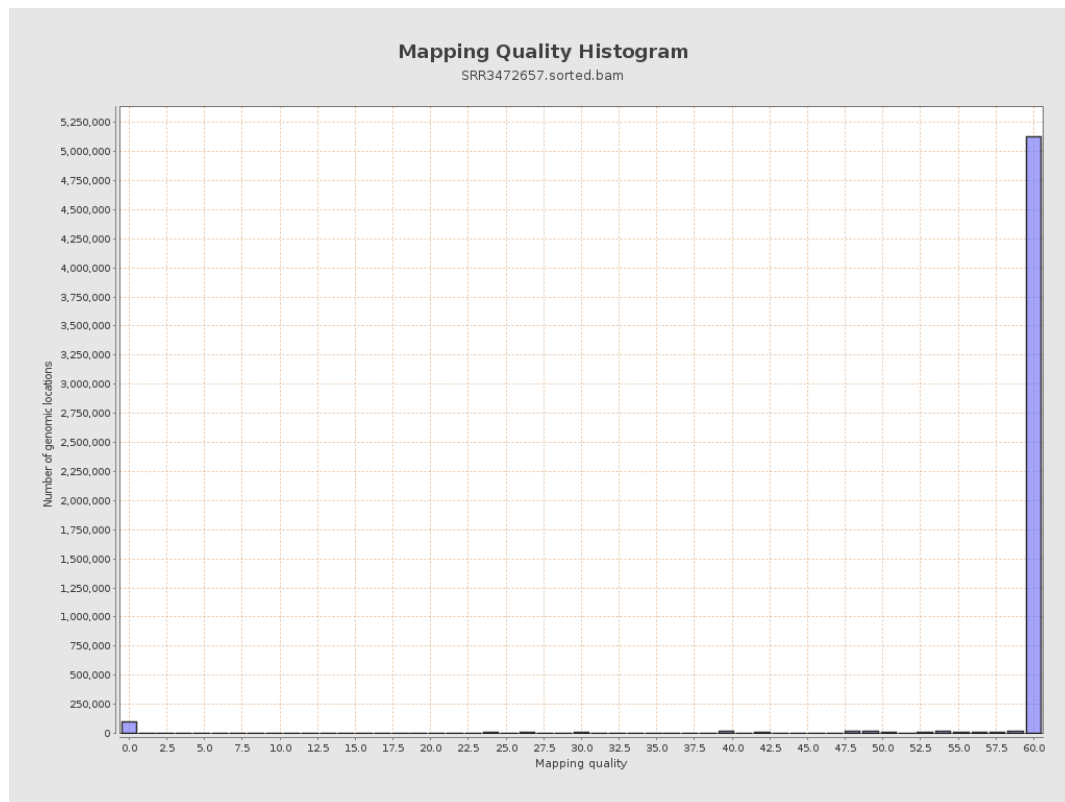
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

