

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/17 05:00:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618567.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_SRR618567 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618567_1.fastq.gz SRR618567_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 17 05:00:54 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618567.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	239,882,962
Mapped reads	229,605,172 / 95.72%
Unmapped reads	10,277,790 / 4.28%
Mapped paired reads	229,605,172 / 95.72%
Mapped reads, first in pair	115,418,811 / 48.11%
Mapped reads, second in pair	114,186,361 / 47.6%
Mapped reads, both in pair	226,499,804 / 94.42%
Mapped reads, singletons	3,105,368 / 1.29%
Secondary alignments	0
Supplementary alignments	1,945,332 / 0.81%
Read min/max/mean length	30 / 100 / 100.33
Duplicated reads (estimated)	89,557,839 / 37.33%
Duplication rate	31.3%
Clipped reads	54,598,684 / 22.76%

2.2. ACGT Content

Number/percentage of A's	5,704,473,611 / 26.38%
Number/percentage of C's	4,887,387,857 / 22.6%
Number/percentage of T's	5,760,955,695 / 26.64%
Number/percentage of G's	5,267,475,334 / 24.36%
Number/percentage of N's	1,287,973 / 0.01%

GC Percentage	46.97%
---------------	--------

2.3. Coverage

Mean	6.9891
Standard Deviation	27.5373

2.4. Mapping Quality

Mean Mapping Quality	52.32
----------------------	-------

2.5. Insert size

Mean	114,799.64
Standard Deviation	3,386,466.85
P25/Median/P75	175 / 193 / 214

2.6. Mismatches and indels

General error rate	1.32%
Mismatches	280,591,816
Insertions	3,587,547
Mapped reads with at least one insertion	1.54%
Deletions	10,491,280
Mapped reads with at least one deletion	4.46%
Homopolymer indels	52.24%

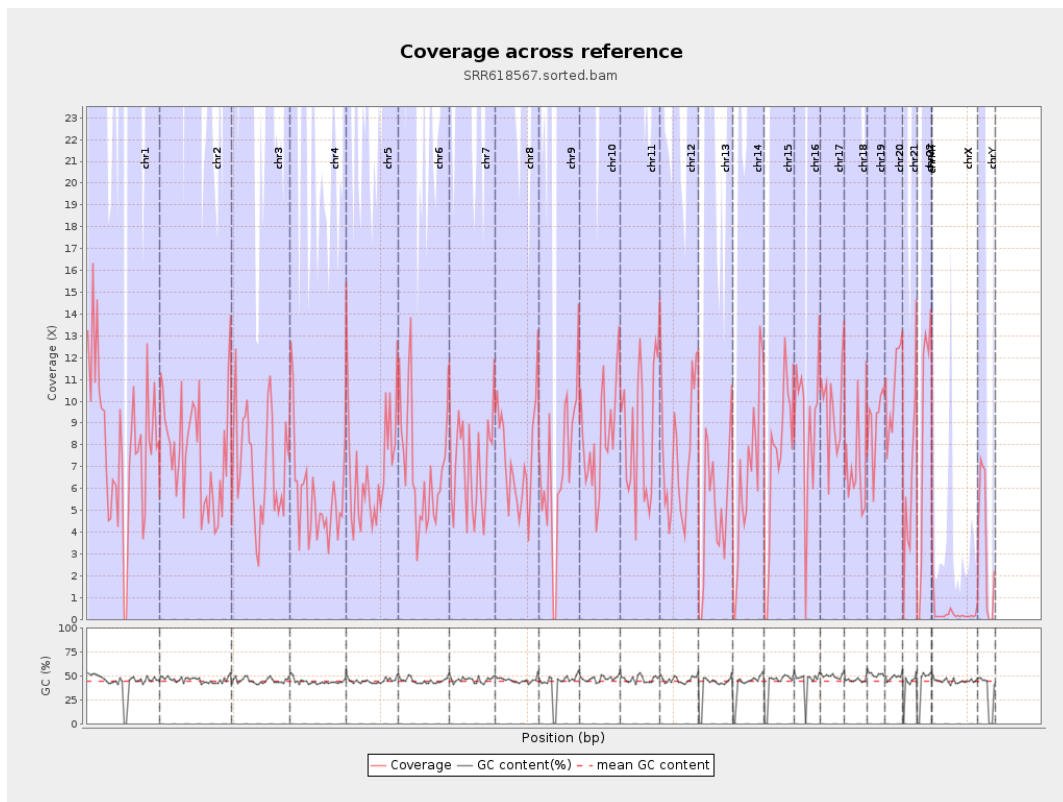
2.7. Chromosome stats

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

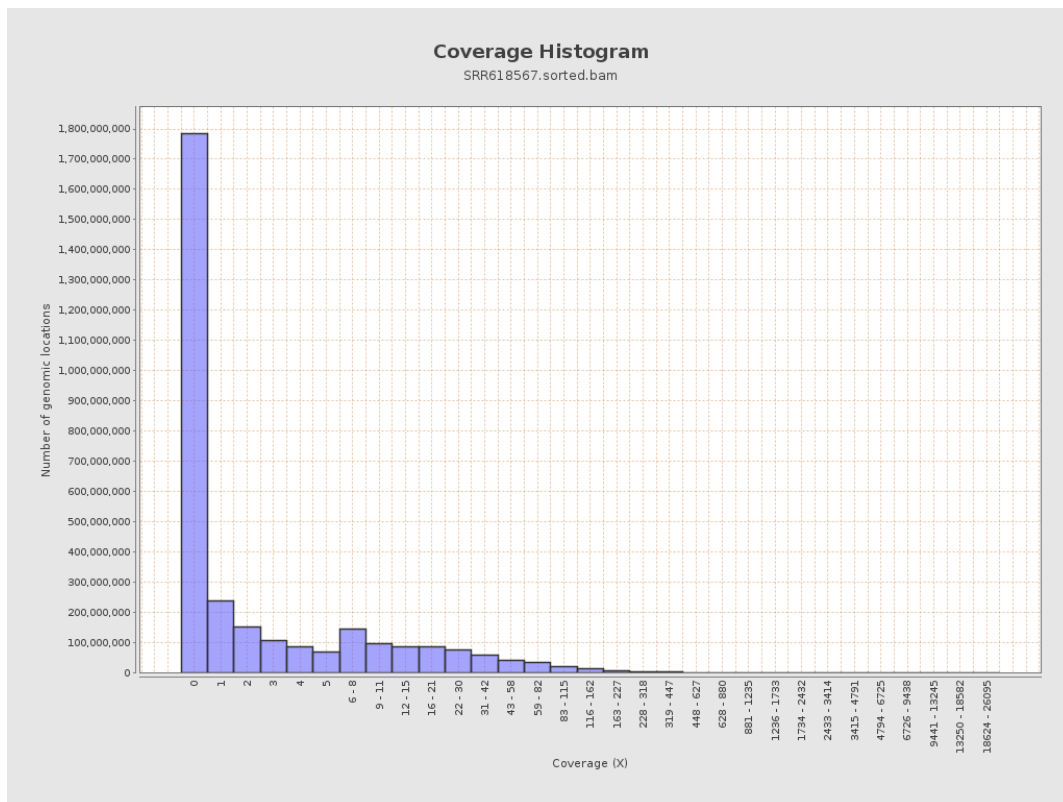
		bases	coverage	deviation
chr1	249250621	2006948759	8.0519	34.186
chr2	243199373	1854716349	7.6263	31.2035
chr3	198022430	1401129497	7.0756	22.1675
chr4	191154276	1072842138	5.6124	22.9183
chr5	180915260	1240659635	6.8577	21.4402
chr6	171115067	1177145758	6.8793	22.3434
chr7	159138663	1129216432	7.0958	23.5561
chr8	146364022	1073656492	7.3355	23.0932
chr9	141213431	982188670	6.9553	28.6014
chr10	135534747	1141211073	8.4201	26.1619
chr11	135006516	1160422187	8.5953	31.357
chr12	133851895	1007700309	7.5285	24.1435
chr13	115169878	588628094	5.111	18.2097
chr14	107349540	697357126	6.4961	23.0939
chr15	102531392	743272317	7.2492	24.0787
chr16	90354753	813278756	9.001	49.2903
chr17	81195210	788180775	9.7072	30.6281
chr18	78077248	550506119	7.0508	29.0177
chr19	59128983	540050223	9.1334	31.7673
chr20	63025520	671116439	10.6483	31.9238
chr21	48129895	302890172	6.2932	51.6183
chr22	51304566	442992288	8.6346	30.8922
chrMT	16571	76743	4.6312	12.8581
chrX	155270560	41190970	0.2653	5.3659

chrY	59373566	208733422	3.5156	23.9078
------	----------	-----------	--------	---------

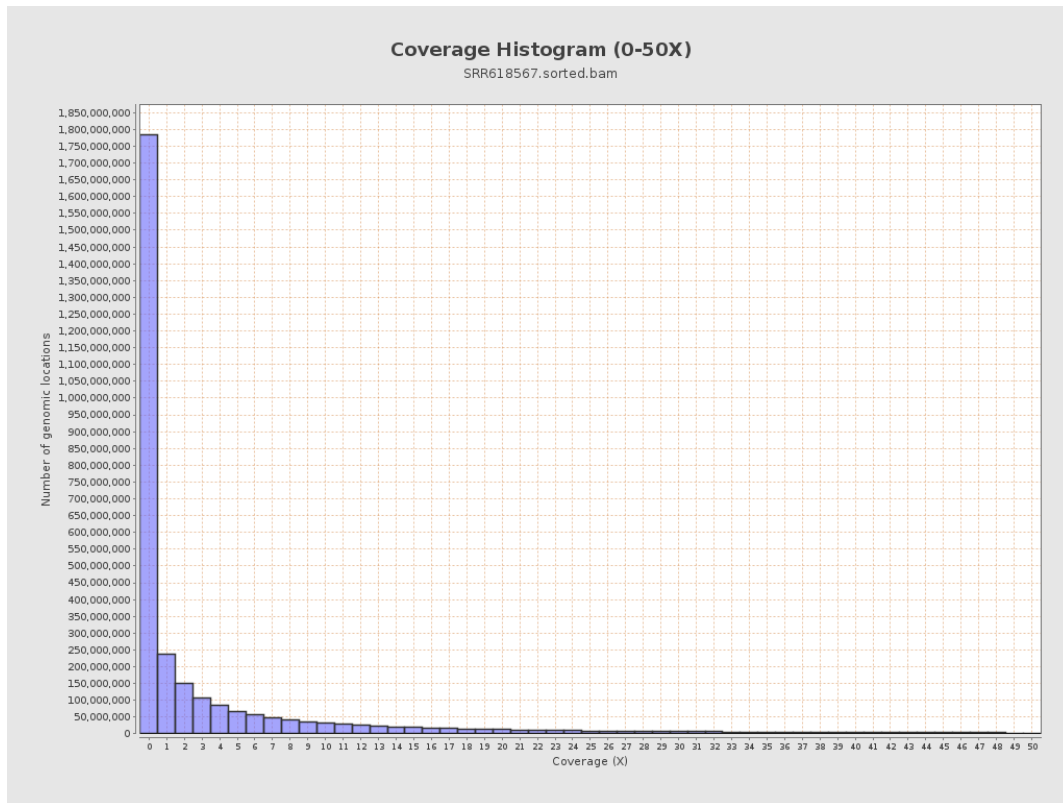
3. Results : Coverage across reference



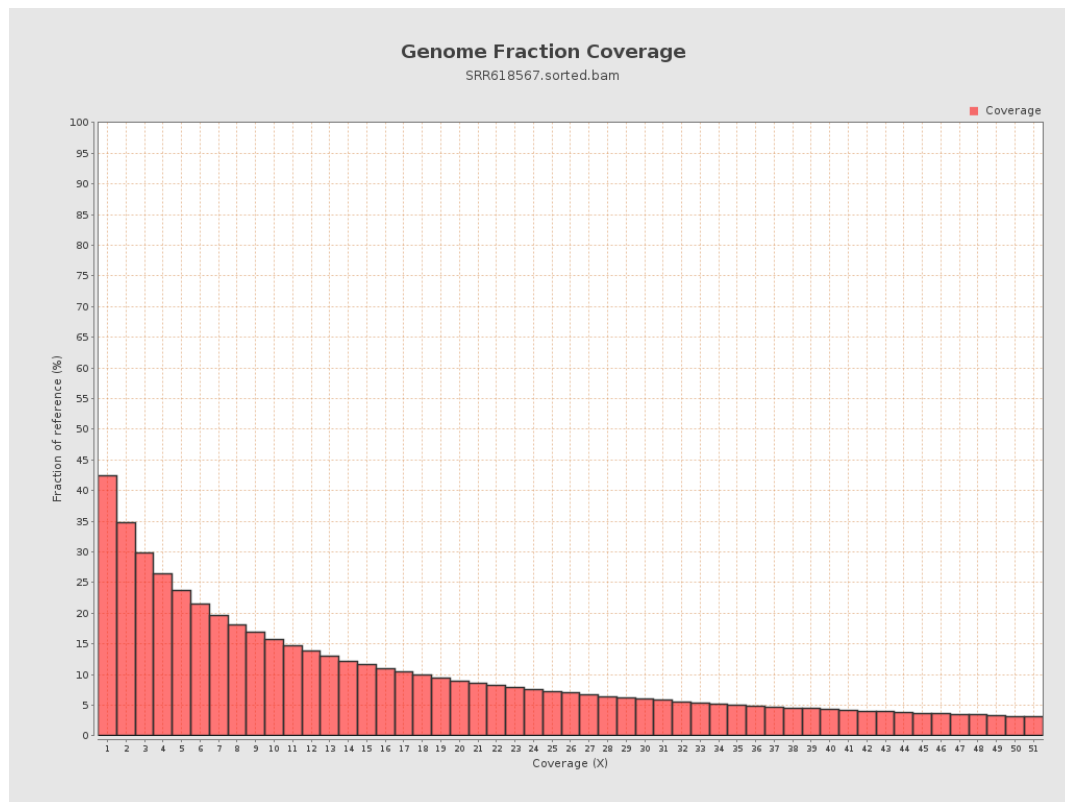
4. Results : Coverage Histogram



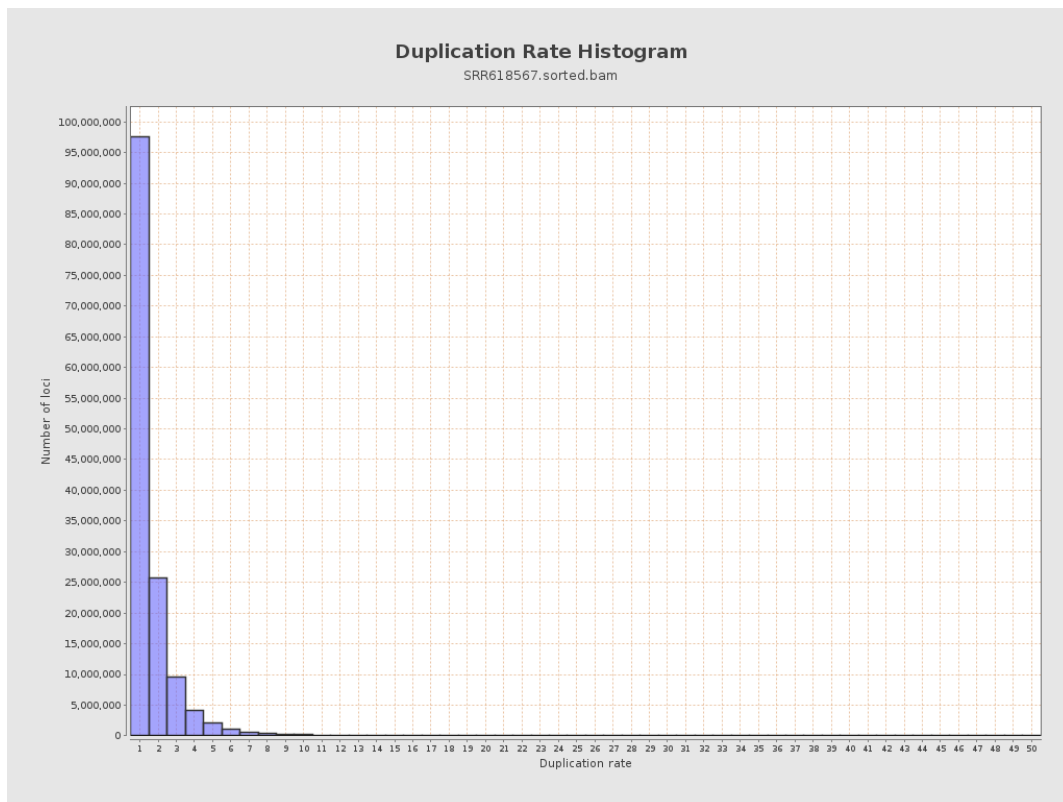
5. Results : Coverage Histogram (0-50X)



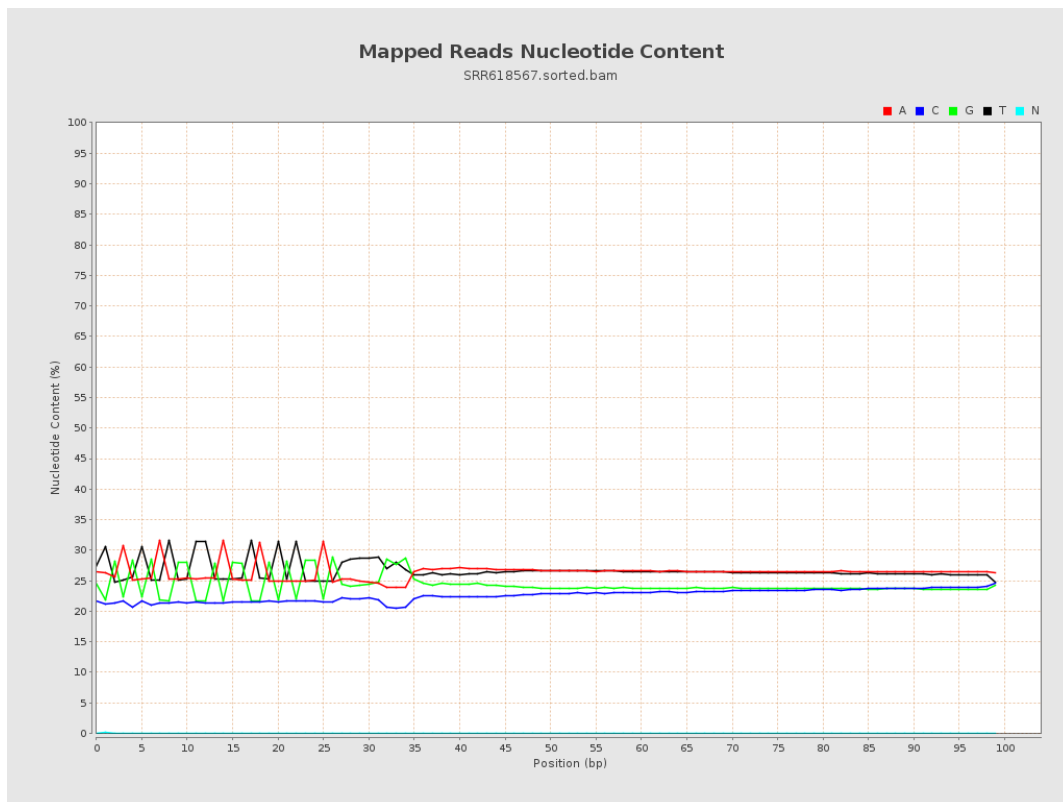
6. Results : Genome Fraction Coverage



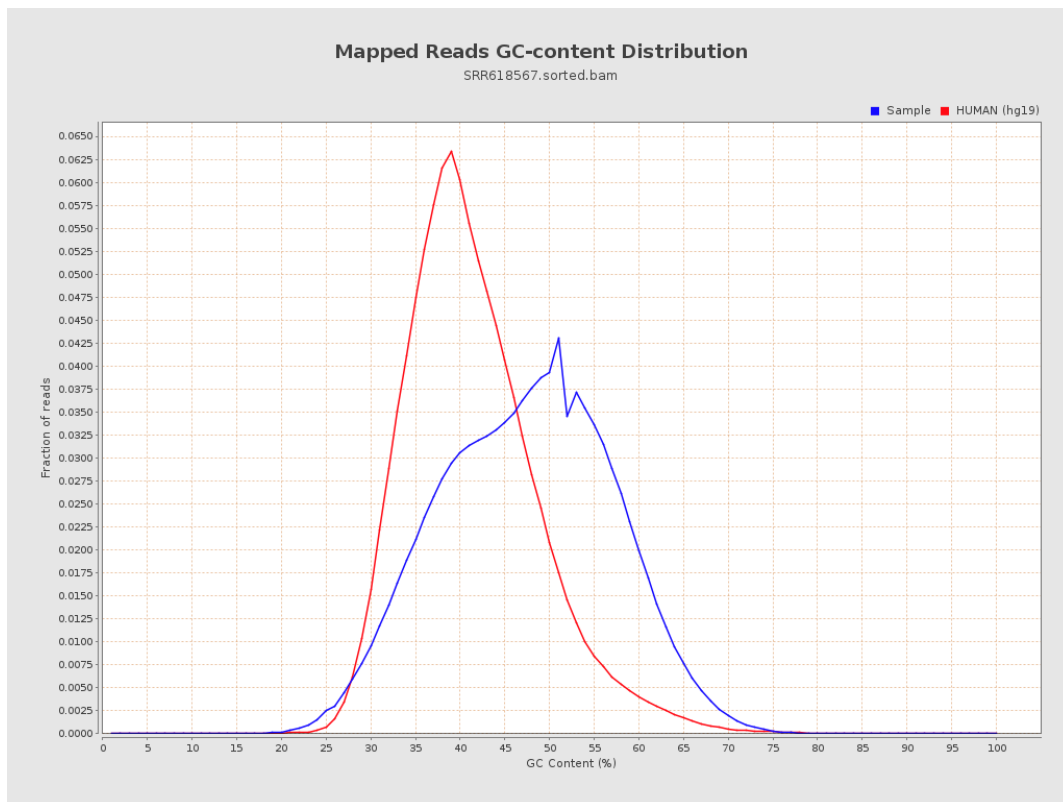
7. Results : Duplication Rate Histogram



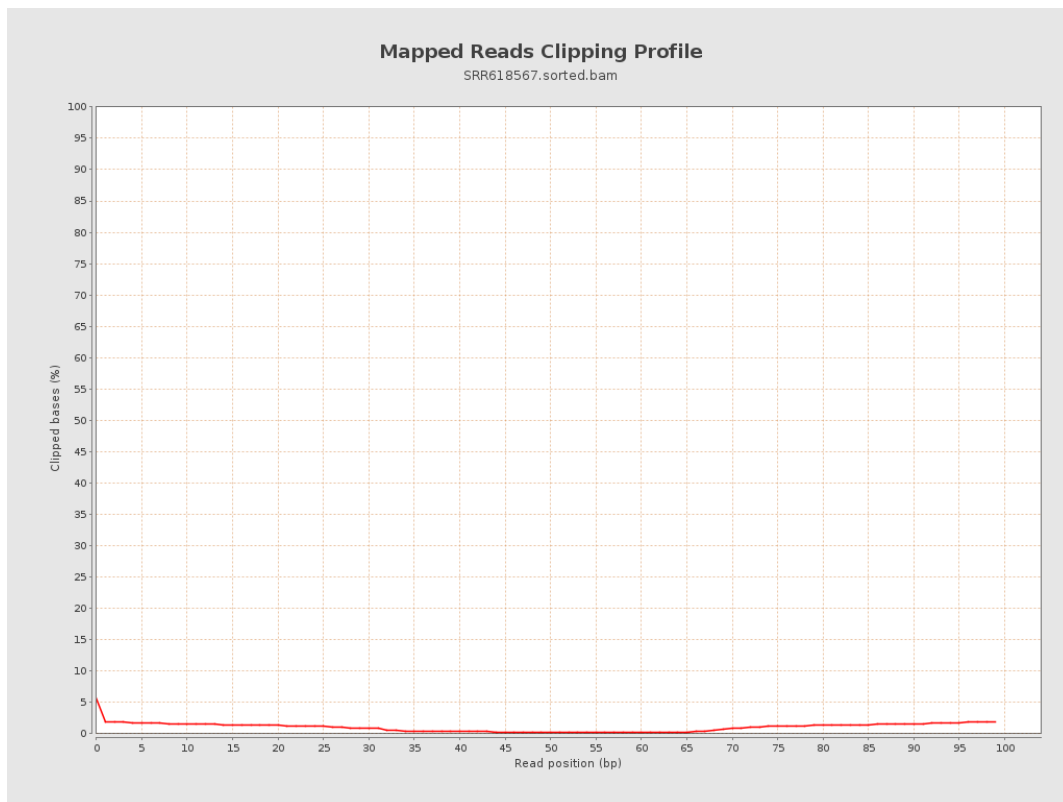
8. Results : Mapped Reads Nucleotide Content



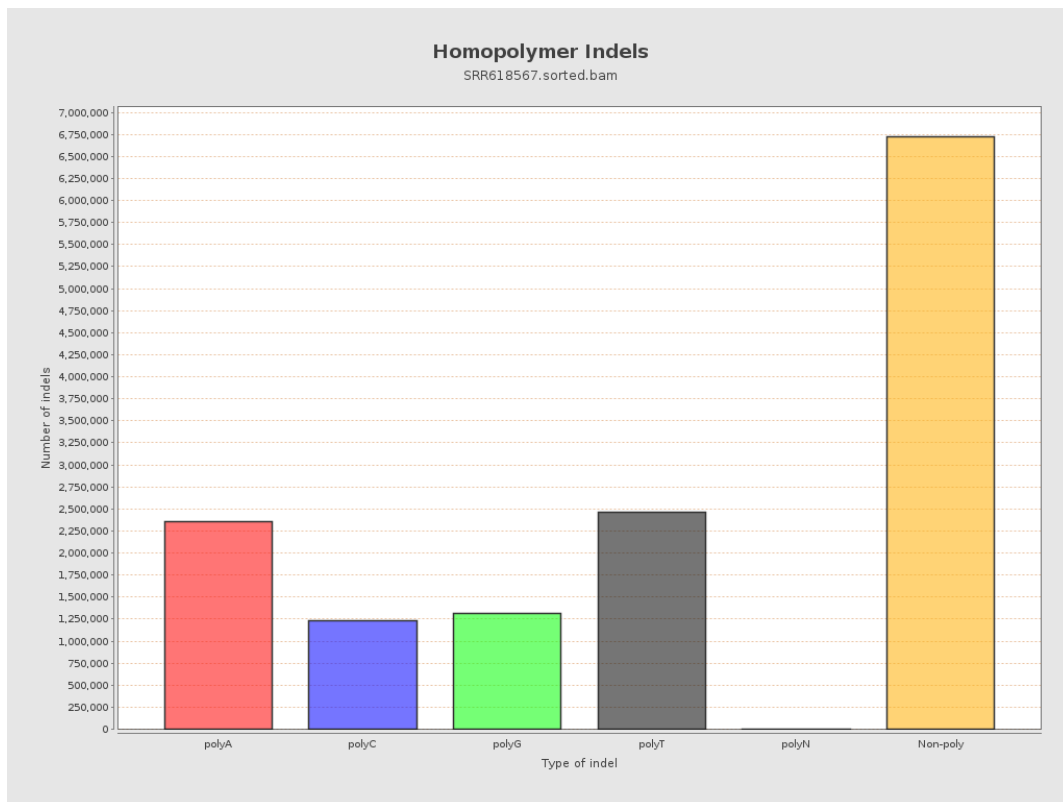
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



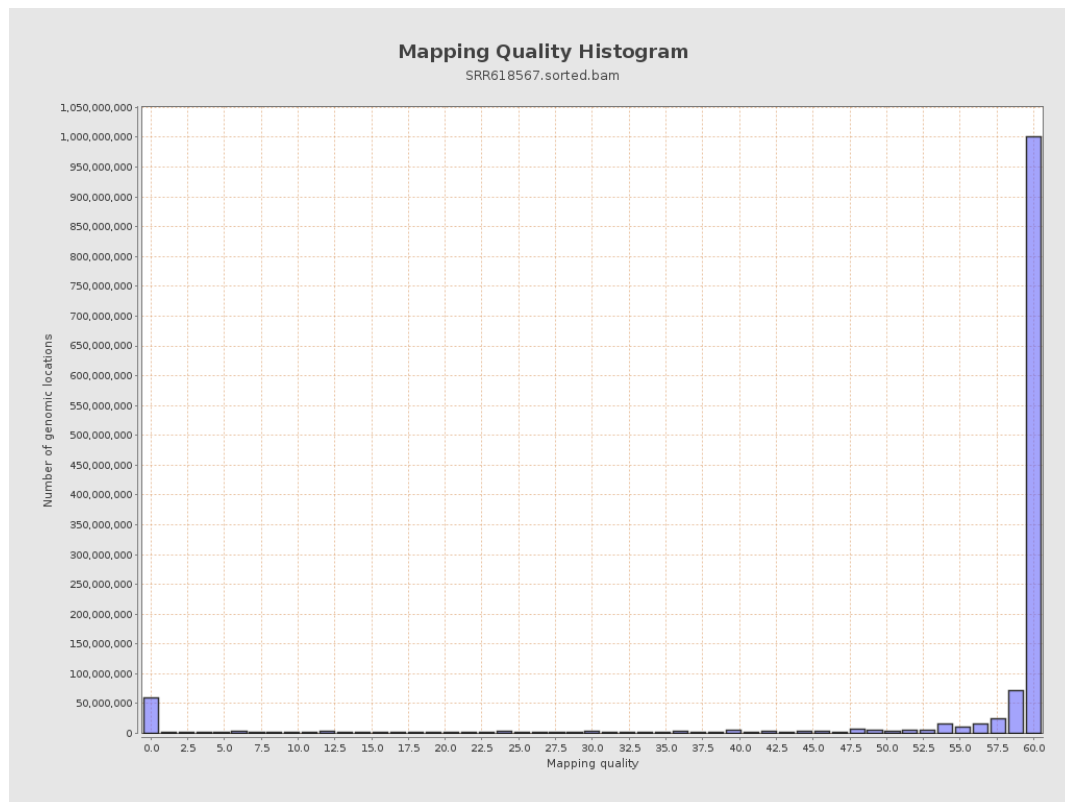
11. Results : Homopolymer Indels



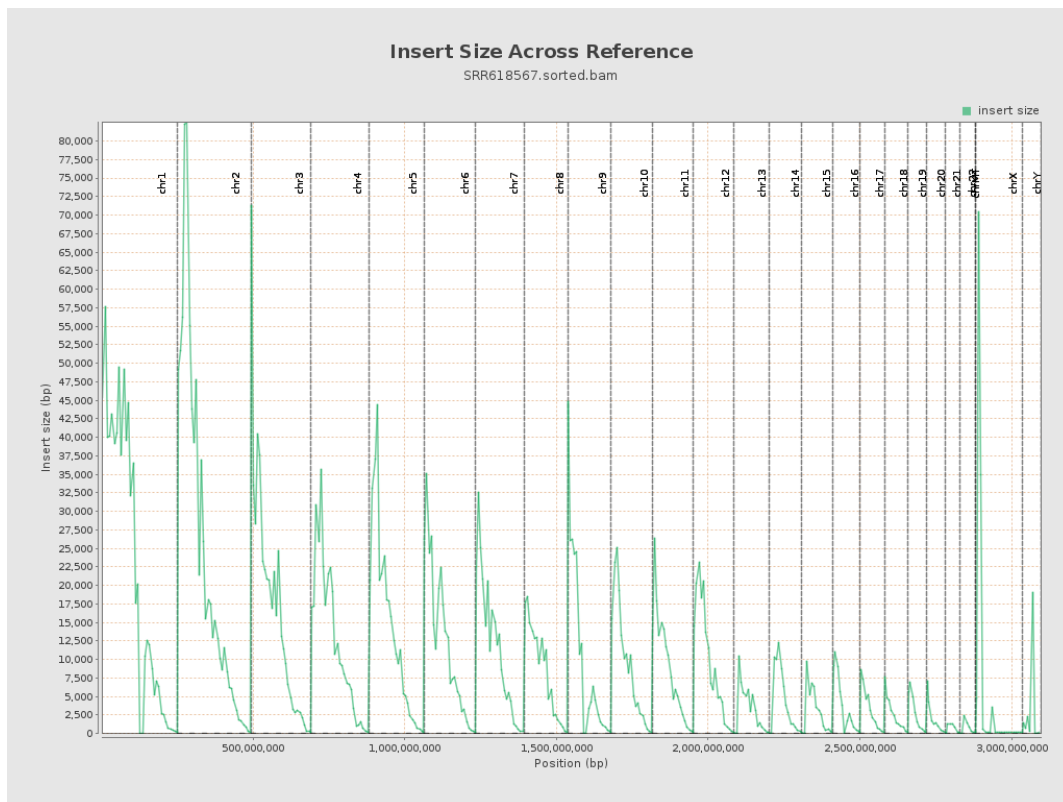
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

