

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 18:49:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472638.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_SRR3472638 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472638_1.fastq.gz SRR3472638_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 18:49:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472638.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,876,578
Mapped reads	15,737,603 / 99.12%
Unmapped reads	138,975 / 0.88%
Mapped paired reads	15,737,603 / 99.12%
Mapped reads, first in pair	7,886,953 / 49.68%
Mapped reads, second in pair	7,850,650 / 49.45%
Mapped reads, both in pair	15,645,104 / 98.54%
Mapped reads, singletons	92,499 / 0.58%
Secondary alignments	0
Supplementary alignments	77,029 / 0.49%
Read min/max/mean length	30 / 101 / 99.43
Duplicated reads (estimated)	10,490,478 / 66.08%
Duplication rate	49.86%
Clipped reads	1,229,739 / 7.75%

2.2. ACGT Content

Number/percentage of A's	427,605,458 / 27.76%
Number/percentage of C's	344,020,610 / 22.34%
Number/percentage of T's	428,297,322 / 27.81%
Number/percentage of G's	339,972,067 / 22.07%
Number/percentage of N's	282,052 / 0.02%

GC Percentage	44.41%
---------------	--------

2.3. Coverage

Mean	0.4976
Standard Deviation	19.8685

2.4. Mapping Quality

Mean Mapping Quality	54.79
----------------------	-------

2.5. Insert size

Mean	21,095.14
Standard Deviation	1,456,216.01
P25/Median/P75	146 / 208 / 286

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	9,539,302
Insertions	92,535
Mapped reads with at least one insertion	0.58%
Deletions	80,326
Mapped reads with at least one deletion	0.5%
Homopolymer indels	45.92%

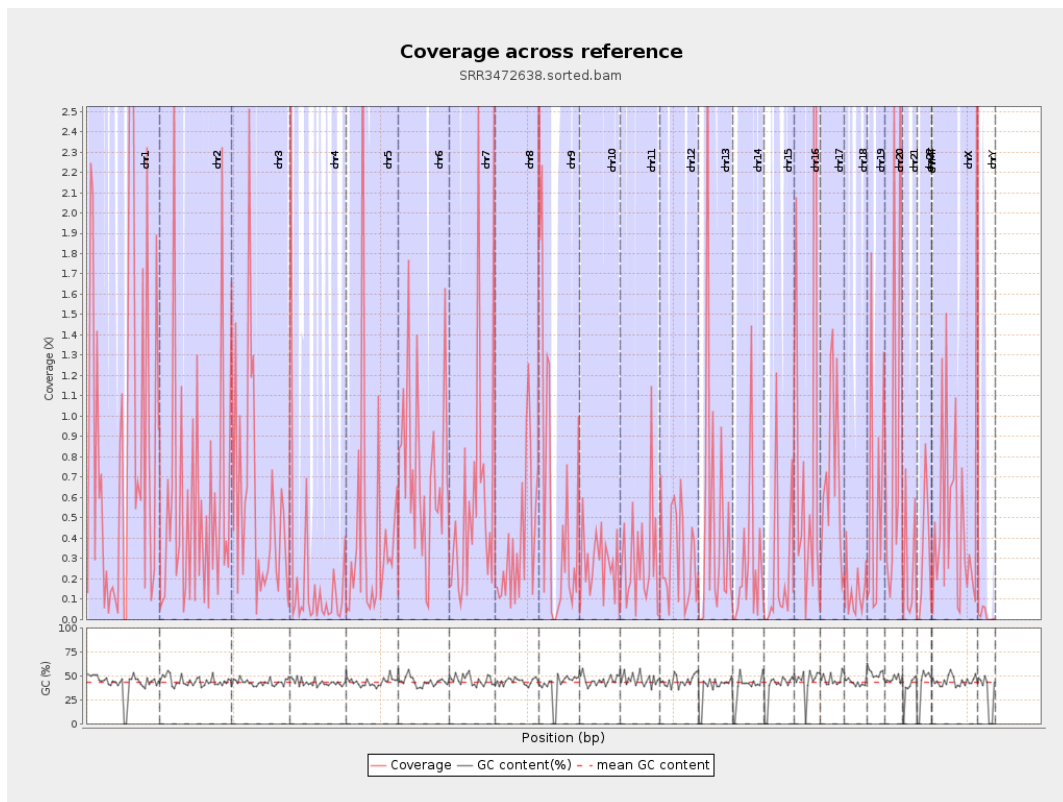
2.7. Chromosome stats

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

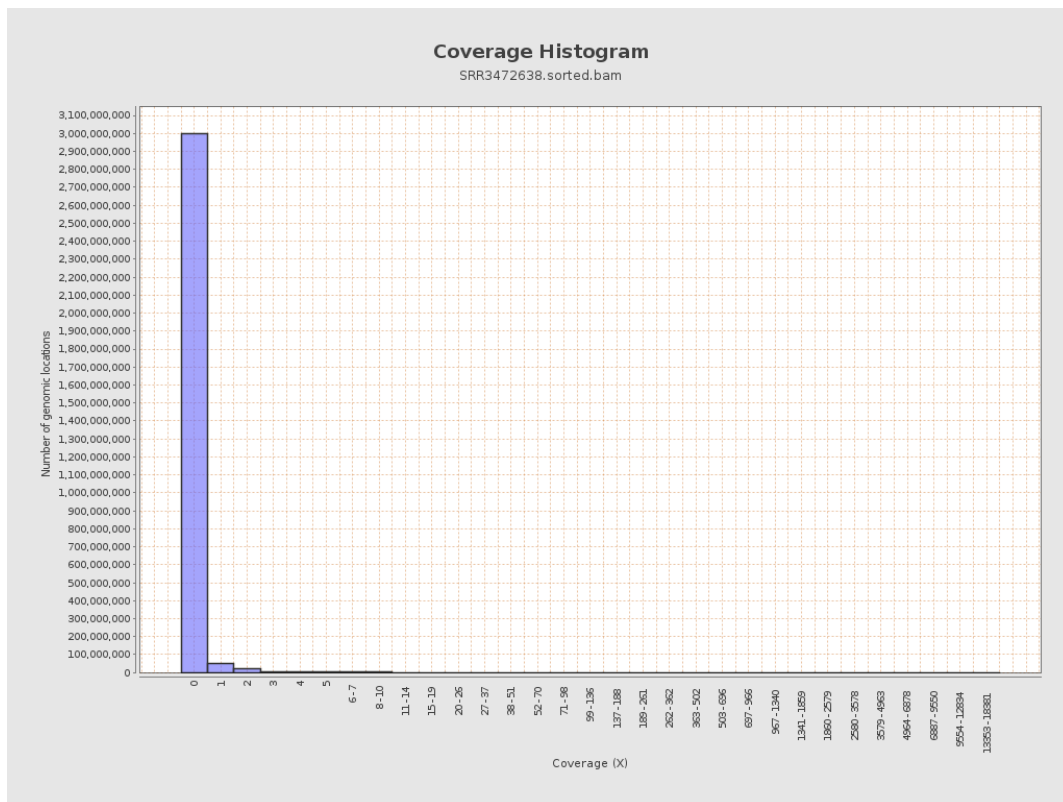
		bases	coverage	deviation
chr1	249250621	226680321	0.9094	27.5293
chr2	243199373	136272250	0.5603	25.765
chr3	198022430	114066311	0.576	15.5161
chr4	191154276	37584583	0.1966	11.7853
chr5	180915260	78423073	0.4335	16.8151
chr6	171115067	123125796	0.7195	20.2976
chr7	159138663	96614448	0.6071	20.2074
chr8	146364022	57684133	0.3941	12.9701
chr9	141213431	81769020	0.579	18.828
chr10	135534747	37432234	0.2762	12.5826
chr11	135006516	39917462	0.2957	11.8279
chr12	133851895	42419544	0.3169	11.4331
chr13	115169878	56488894	0.4905	21.4888
chr14	107349540	27242297	0.2538	10.8569
chr15	102531392	23814225	0.2323	12.064
chr16	90354753	87411069	0.9674	37.1115
chr17	81195210	57245440	0.705	20.622
chr18	78077248	11291311	0.1446	5.8088
chr19	59128983	35158024	0.5946	16.139
chr20	63025520	60506088	0.96	49.2647
chr21	48129895	12056500	0.2505	13.8279
chr22	51304566	15739863	0.3068	11.7456
chrMT	16571	6814	0.4112	0.8347
chrX	155270560	80175250	0.5164	18.1364

chrY	59373566	1263411	0.0213	1.1247
------	----------	---------	--------	--------

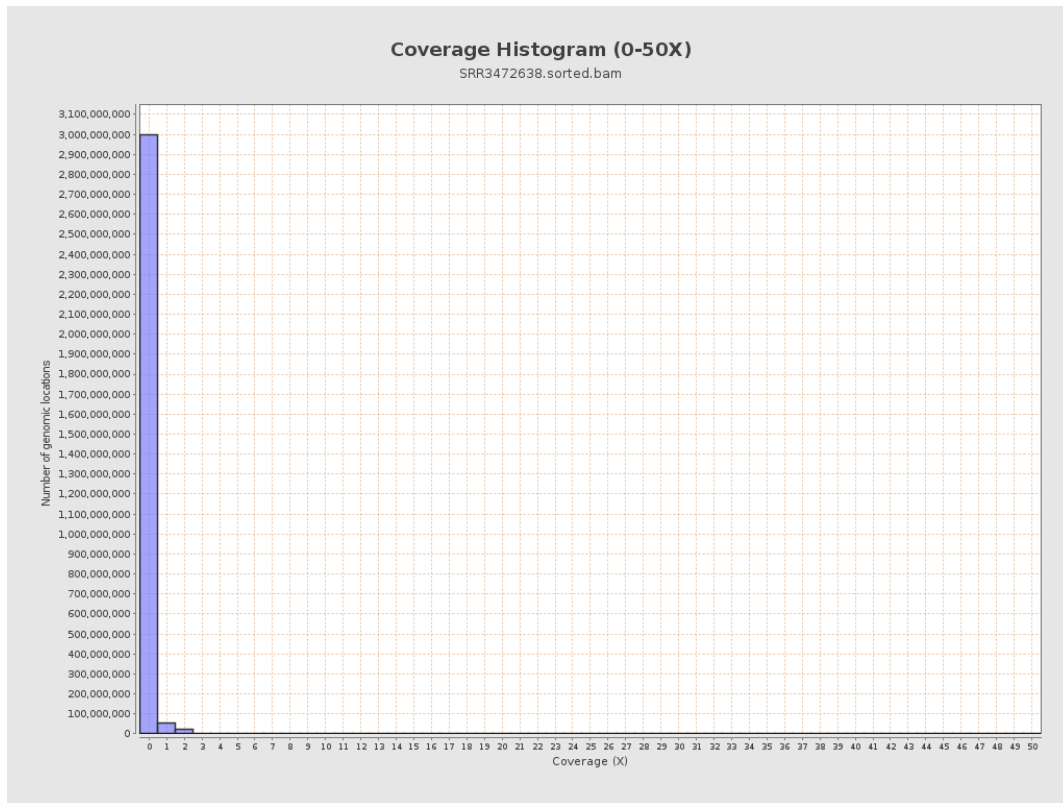
3. Results : Coverage across reference



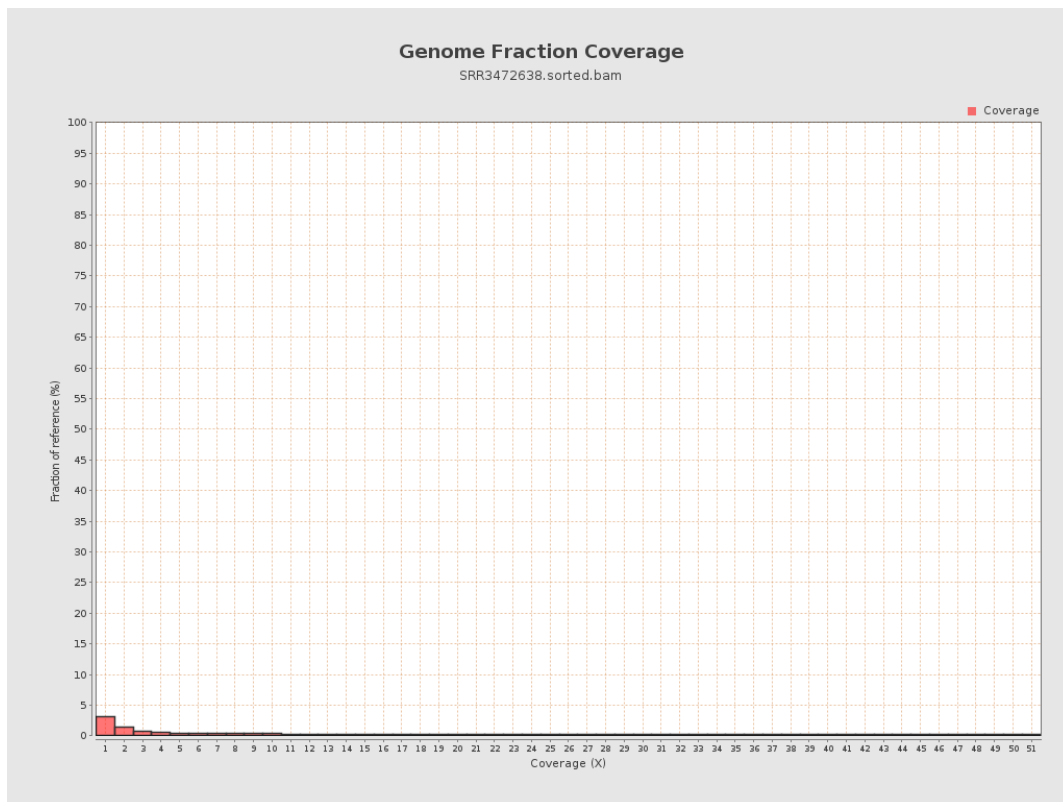
4. Results : Coverage Histogram



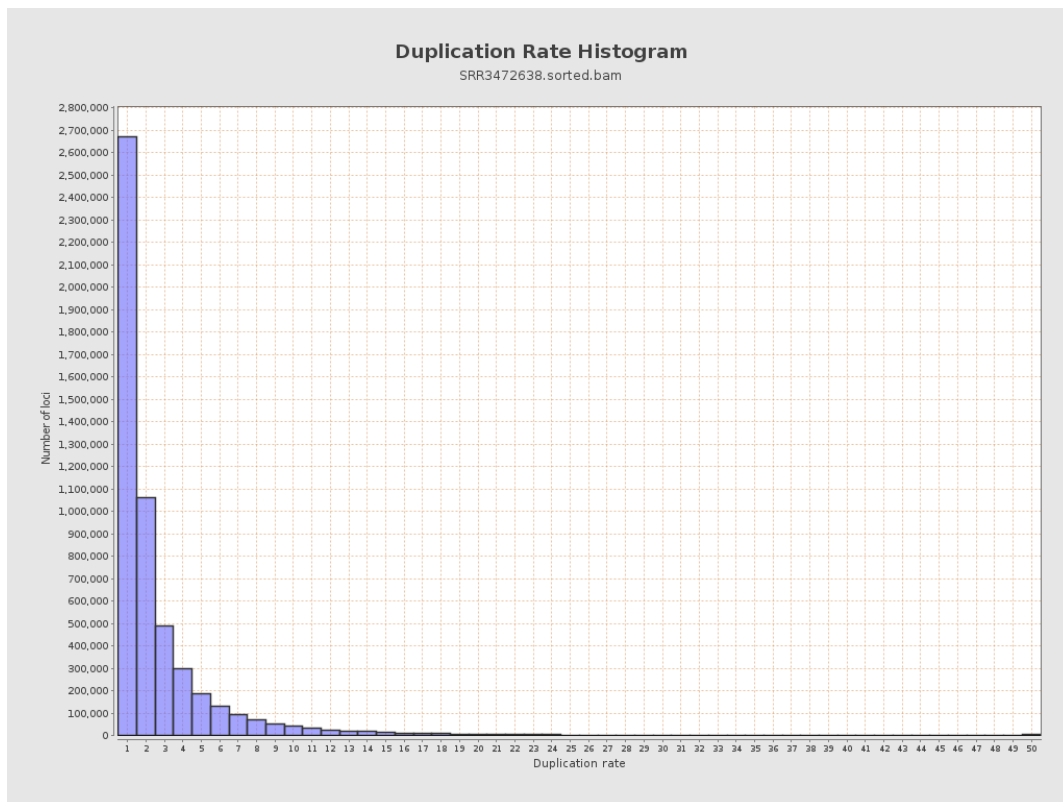
5. Results : Coverage Histogram (0-50X)



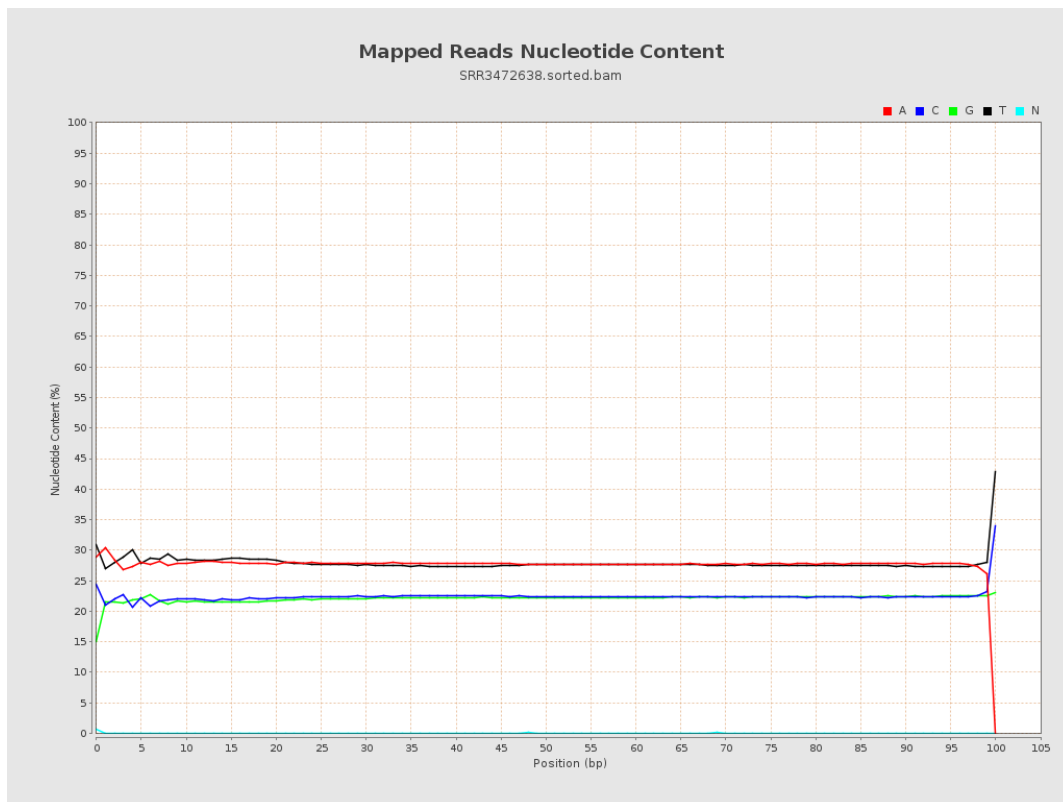
6. Results : Genome Fraction Coverage



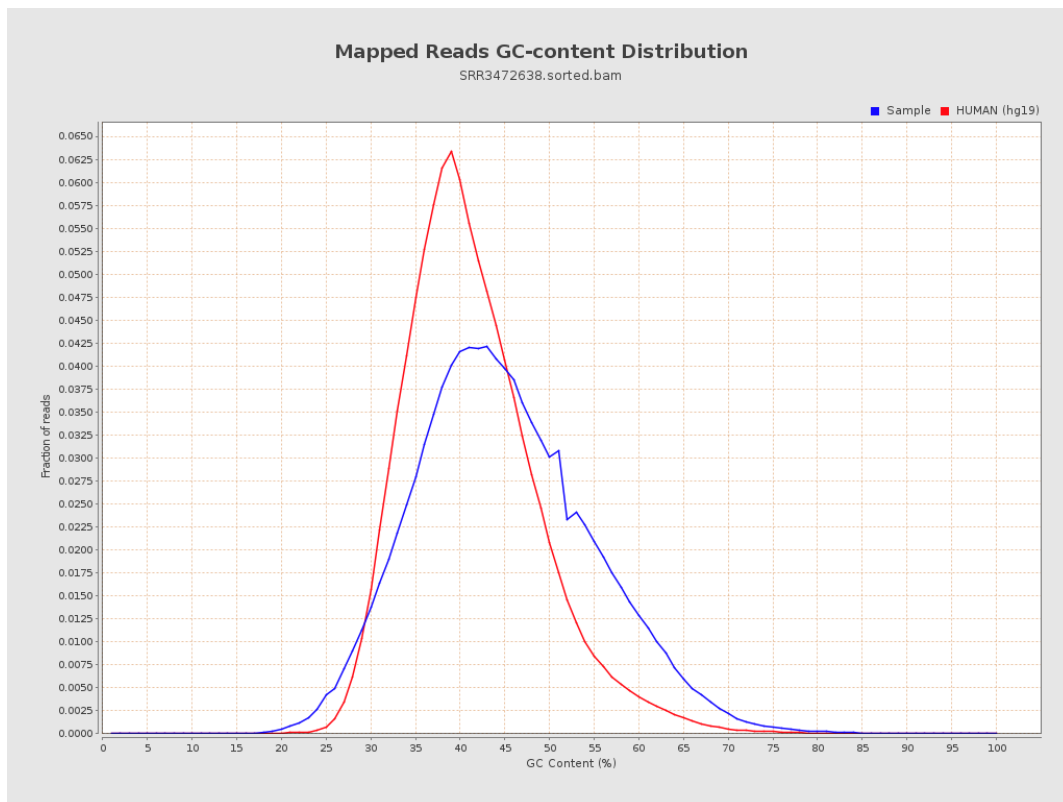
7. Results : Duplication Rate Histogram



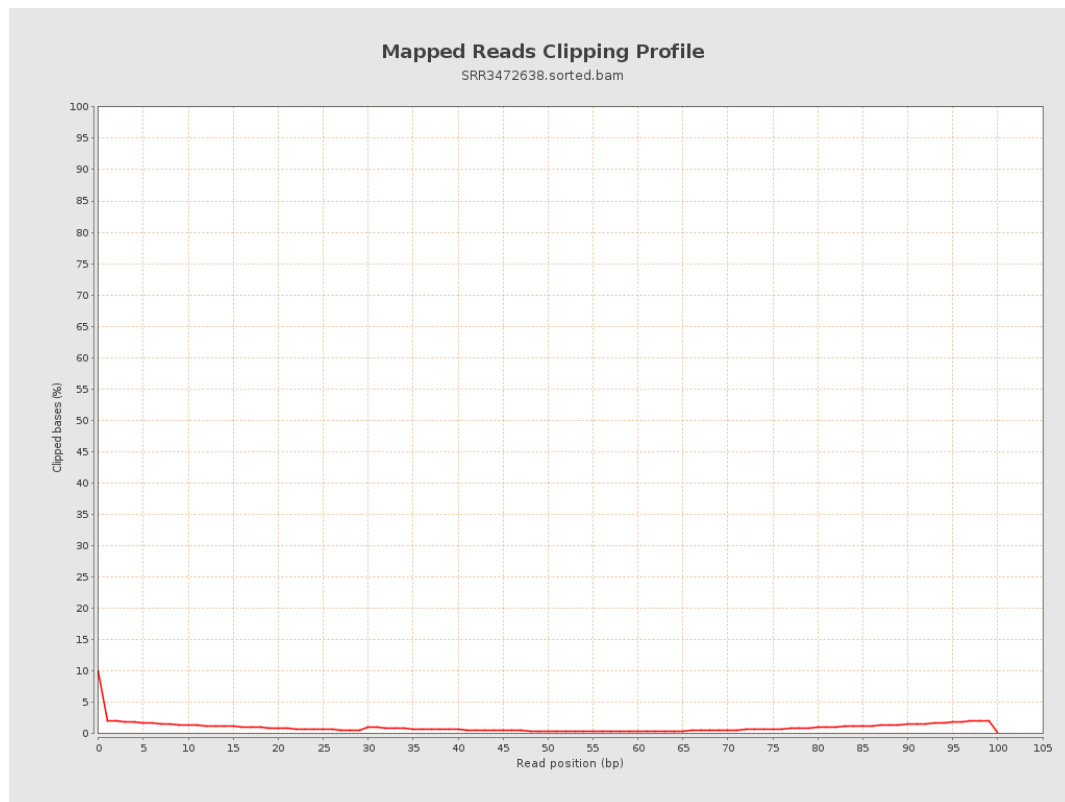
8. Results : Mapped Reads Nucleotide Content



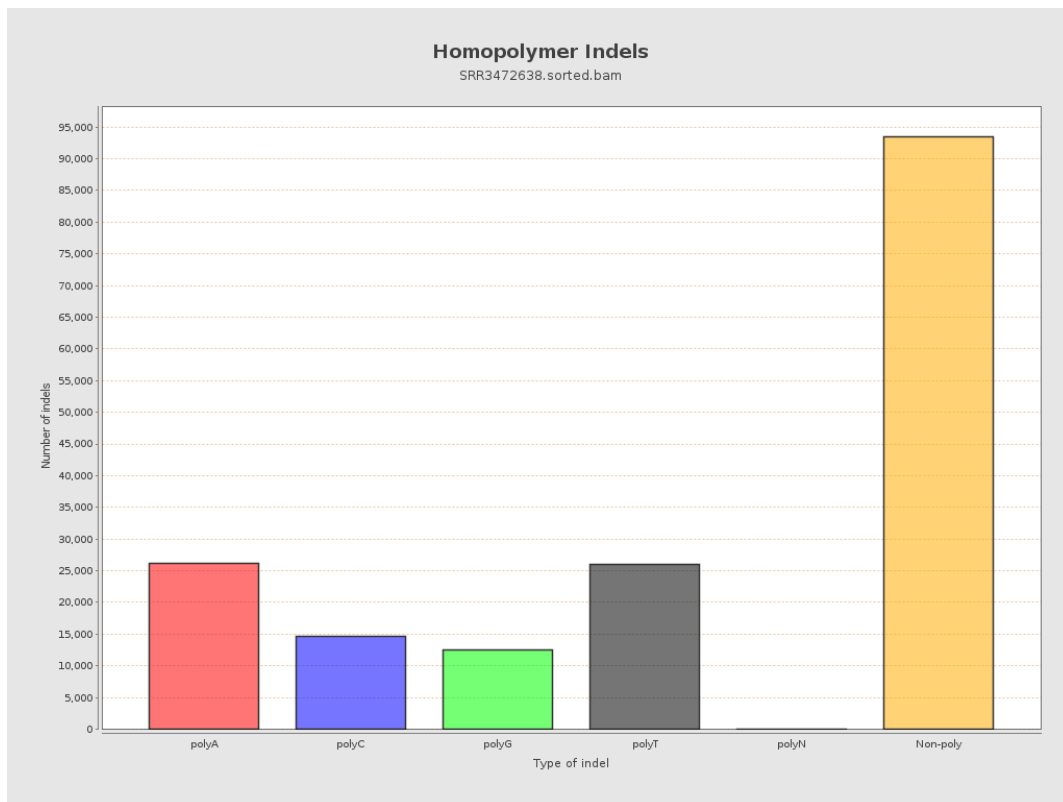
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



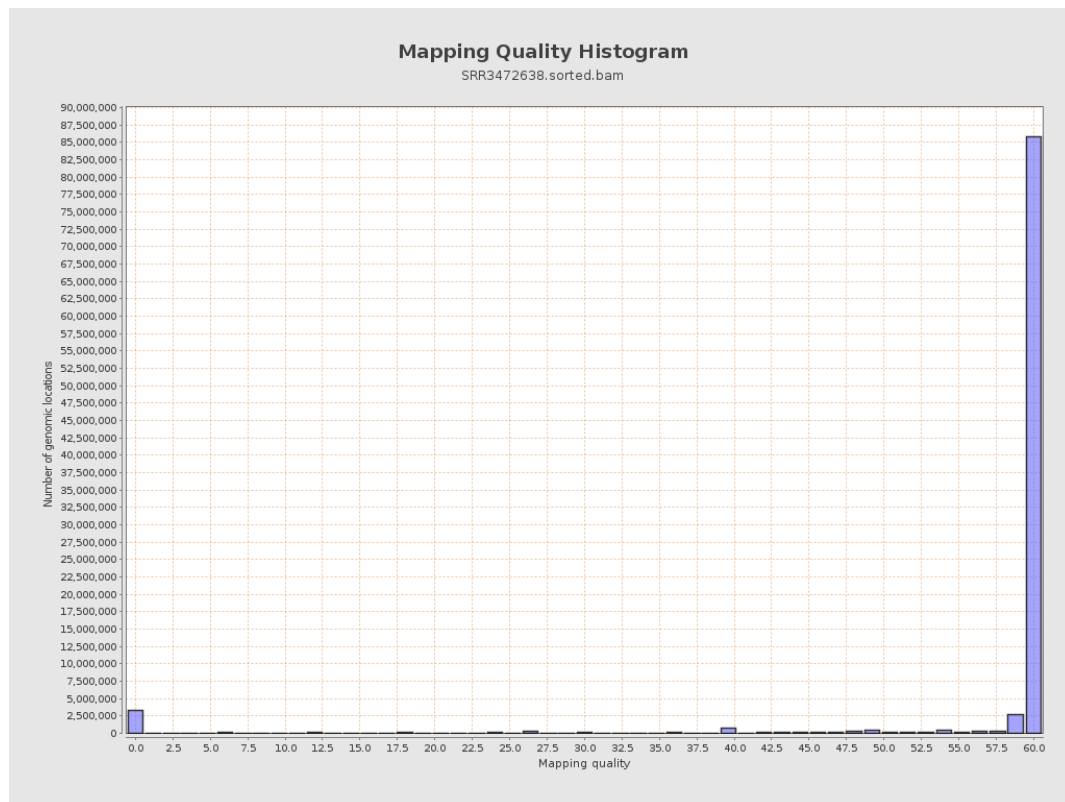
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



15. Results : Insert Size Histogram

