

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/13 16:35:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695954.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/seu_share/home/tujing/220232460/s oftware/bwa-0.7.18/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\t PL:ILLUMINA\tSM:sample_SRR1695 954 /seu_share/home/tujing/220232460/r eference/homo_bwa/hsa.fa SRR1695954_1.fastq.gz SRR1695954_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Fri Sep 13 16:35:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695954.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,159,388
Mapped reads	18,998,492 / 99.16%
Unmapped reads	160,896 / 0.84%
Mapped paired reads	18,998,492 / 99.16%
Mapped reads, first in pair	9,544,764 / 49.82%
Mapped reads, second in pair	9,453,728 / 49.34%
Mapped reads, both in pair	18,879,106 / 98.54%
Mapped reads, singletons	119,386 / 0.62%
Secondary alignments	0
Supplementary alignments	245,349 / 1.28%
Read min/max/mean length	30 / 100 / 100.53
Duplicated reads (estimated)	304,938 / 1.59%
Duplication rate	1.43%
Clipped reads	1,564,600 / 8.17%

2.2. ACGT Content

Number/percentage of A's	555,616,138 / 29.54%
Number/percentage of C's	380,608,629 / 20.24%
Number/percentage of T's	553,262,559 / 29.42%
Number/percentage of G's	390,485,496 / 20.76%
Number/percentage of N's	806,596 / 0.04%

GC Percentage	41%
---------------	-----

2.3. Coverage

Mean	0.6077
Standard Deviation	1.074

2.4. Mapping Quality

Mean Mapping Quality	53.83
----------------------	-------

2.5. Insert size

Mean	80,794.47
Standard Deviation	2,740,997.5
P25/Median/P75	310 / 317 / 325

2.6. Mismatches and indels

General error rate	0.71%
Mismatches	12,996,908
Insertions	187,138
Mapped reads with at least one insertion	0.97%
Deletions	176,263
Mapped reads with at least one deletion	0.91%
Homopolymer indels	45.01%

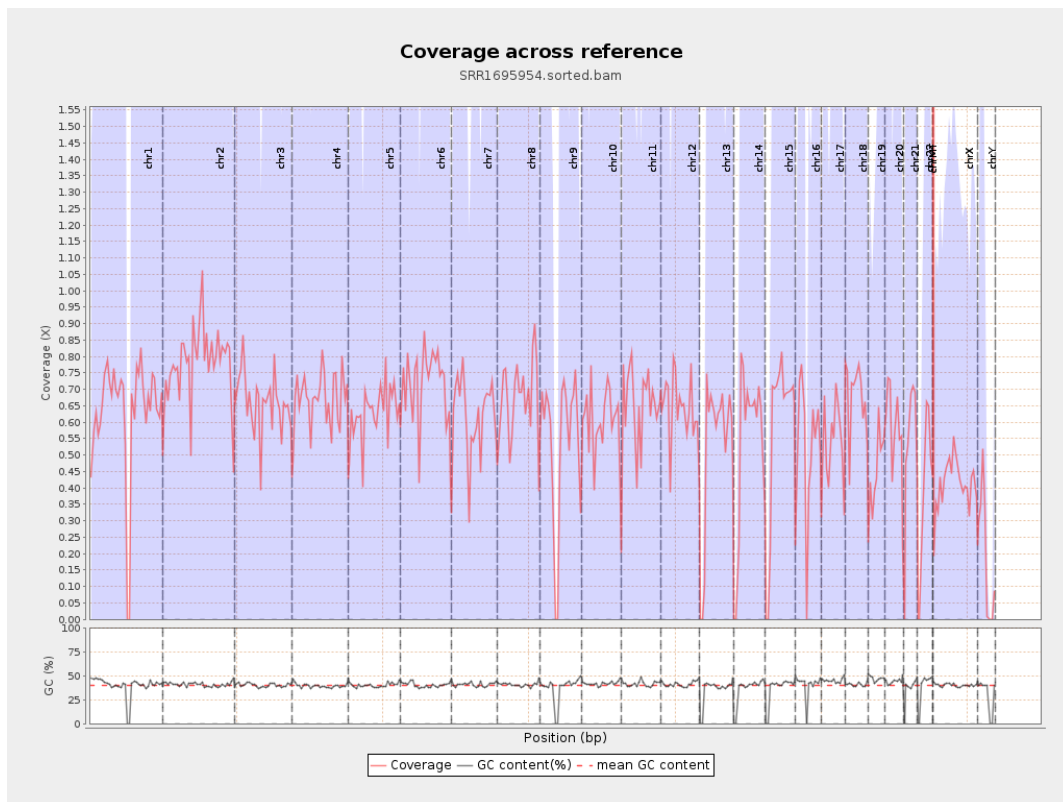
2.7. Chromosome stats

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

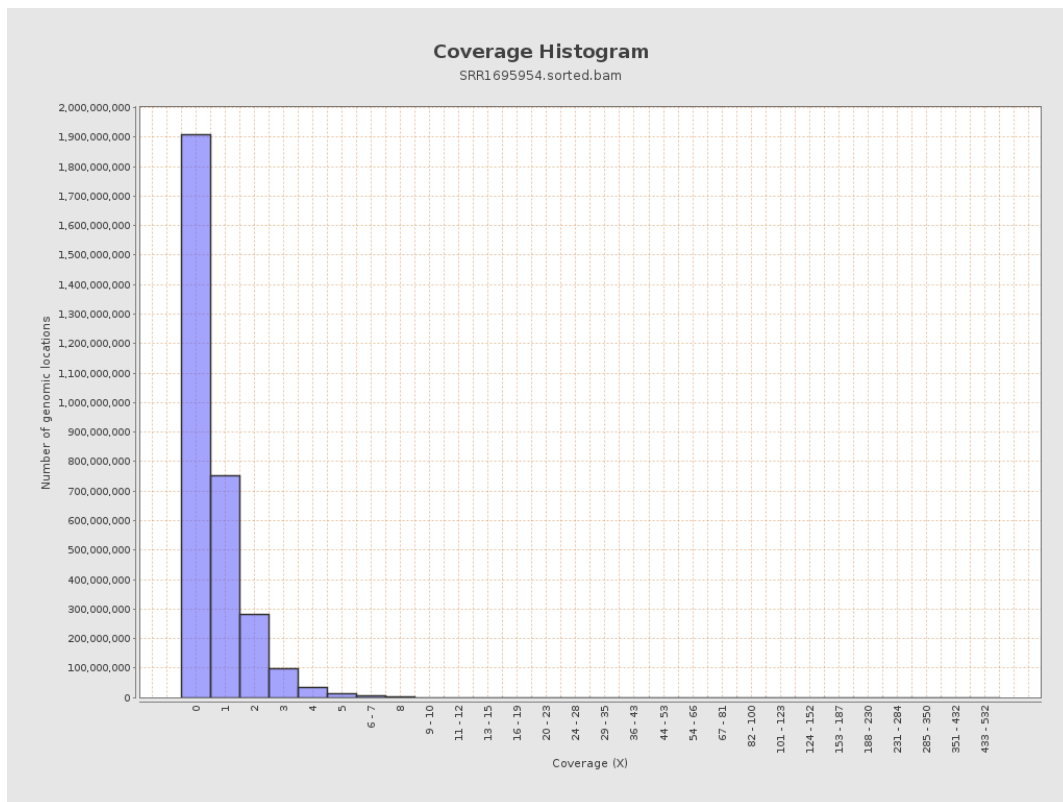
		bases	coverage	deviation
chr1	249250621	157052185	0.6301	1.1076
chr2	243199373	190510208	0.7833	1.3279
chr3	198022430	130544764	0.6592	0.9964
chr4	191154276	128774187	0.6737	1.1304
chr5	180915260	113703936	0.6285	0.9614
chr6	171115067	122547760	0.7162	1.0748
chr7	159138663	97680527	0.6138	0.9745
chr8	146364022	98882075	0.6756	1.019
chr9	141213431	76447445	0.5414	0.994
chr10	135534747	82225343	0.6067	1.0536
chr11	135006516	87814480	0.6504	1.0134
chr12	133851895	86038901	0.6428	0.9951
chr13	115169878	60844027	0.5283	0.9171
chr14	107349540	58550685	0.5454	0.9513
chr15	102531392	58936239	0.5748	0.9949
chr16	90354753	46331369	0.5128	1.0938
chr17	81195210	44690205	0.5504	0.9864
chr18	78077248	52605356	0.6738	1.1091
chr19	59128983	27037846	0.4573	0.8845
chr20	63025520	36872989	0.585	0.9876
chr21	48129895	26115979	0.5426	1.3429
chr22	51304566	20024047	0.3903	0.8359
chrMT	16571	1673340	100.98	29.464
chrX	155270560	63669954	0.4101	0.7749

chrY	59373566	11615828	0.1956	0.889
------	----------	----------	--------	-------

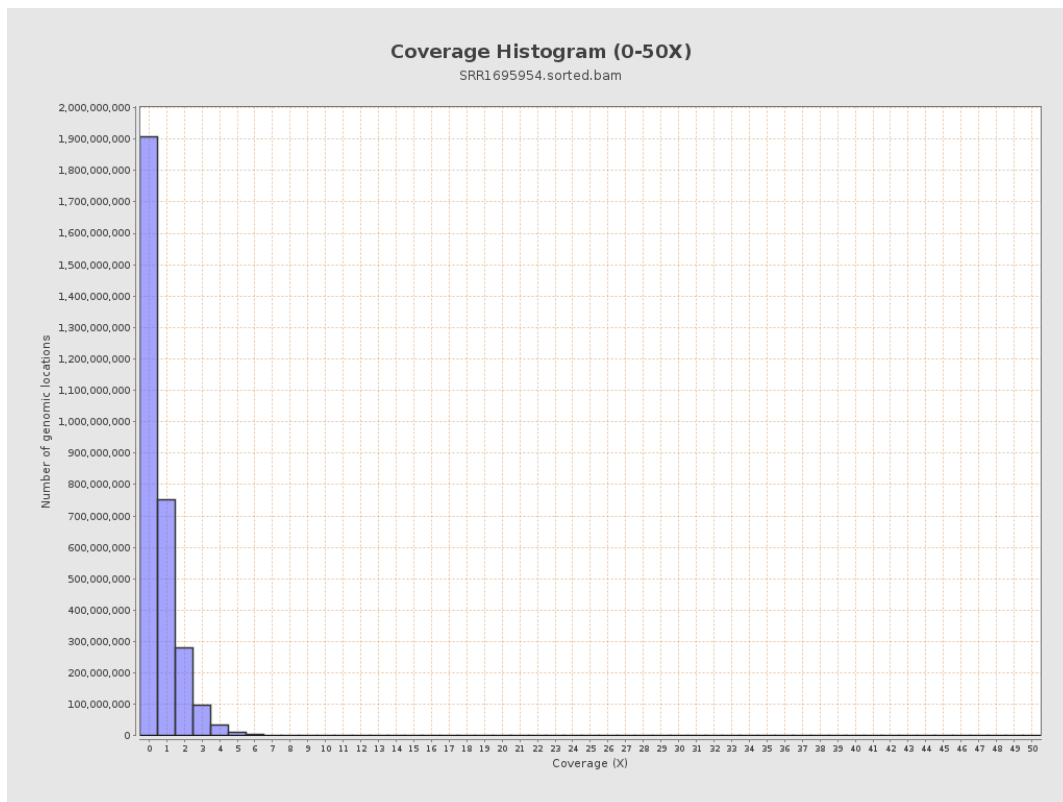
3. Results : Coverage across reference



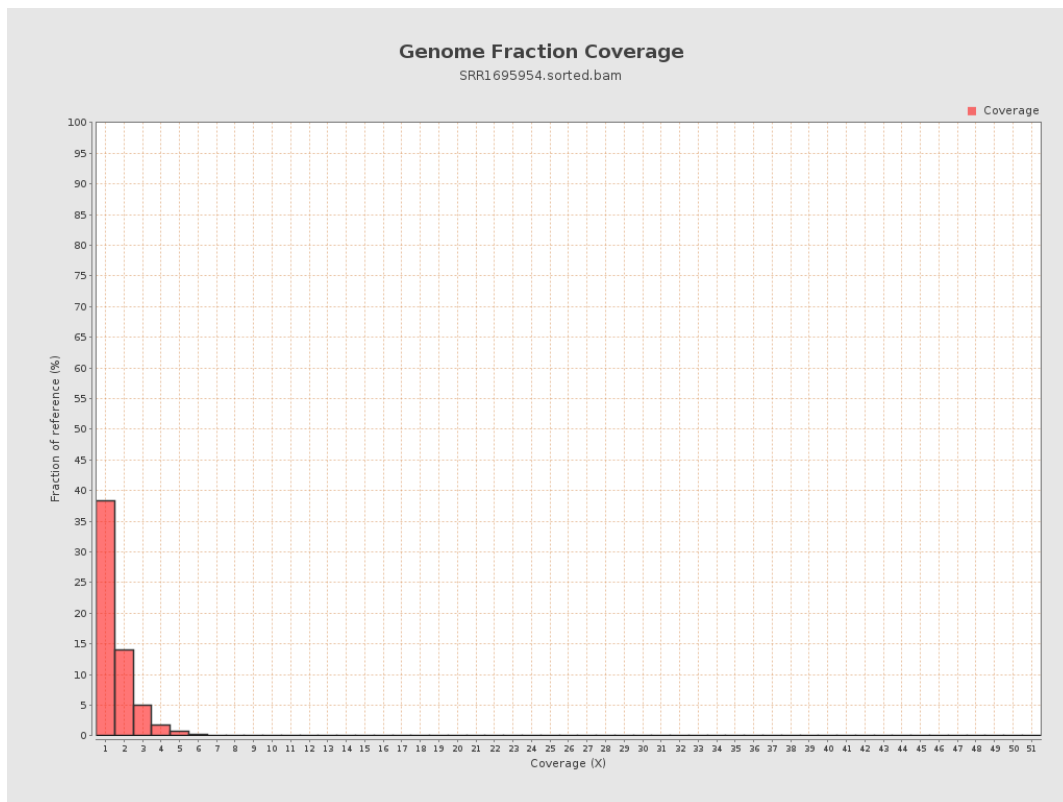
4. Results : Coverage Histogram



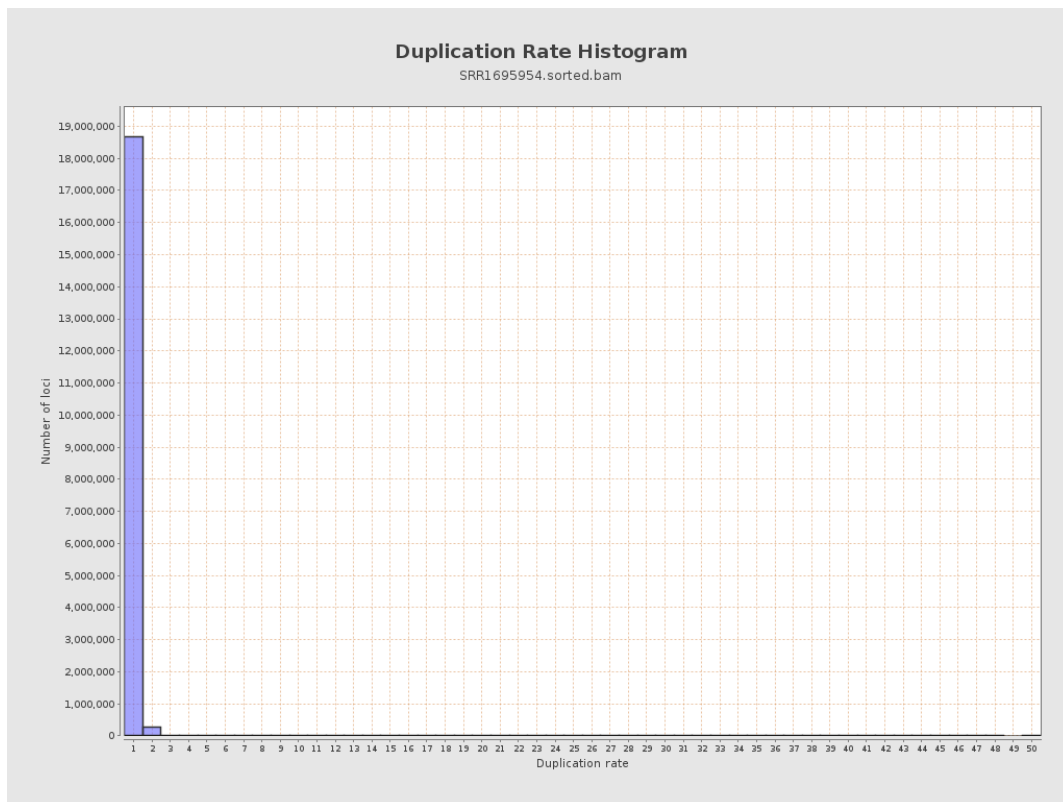
5. Results : Coverage Histogram (0-50X)



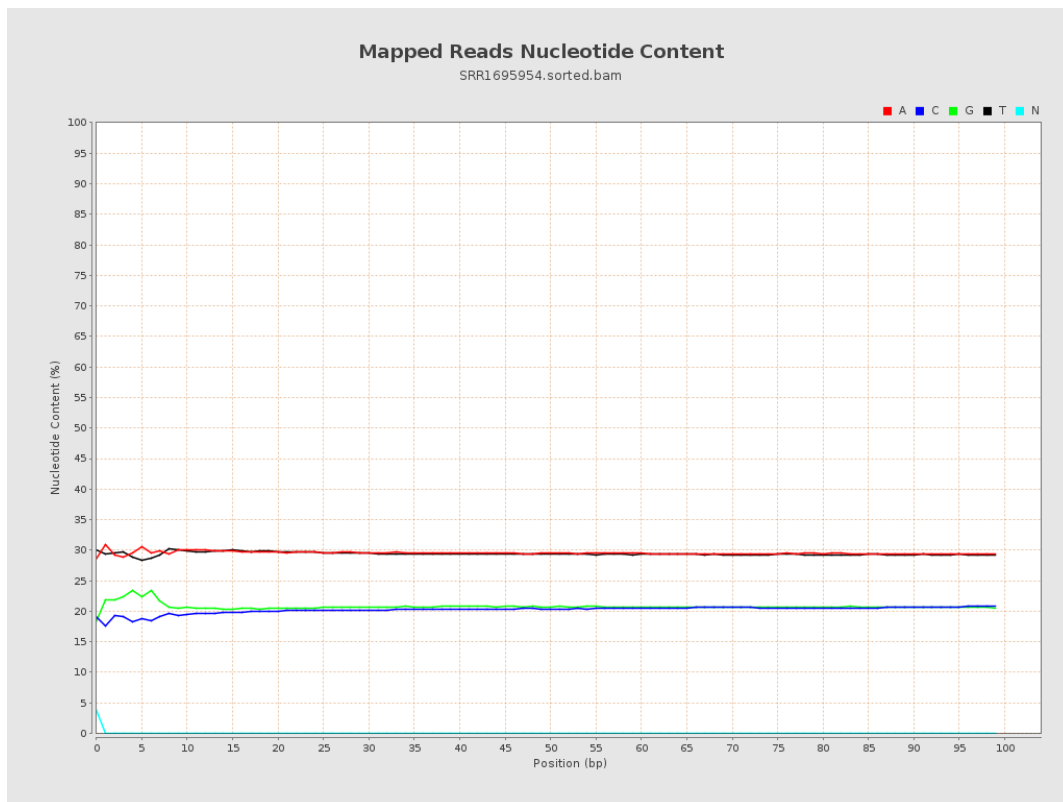
6. Results : Genome Fraction Coverage



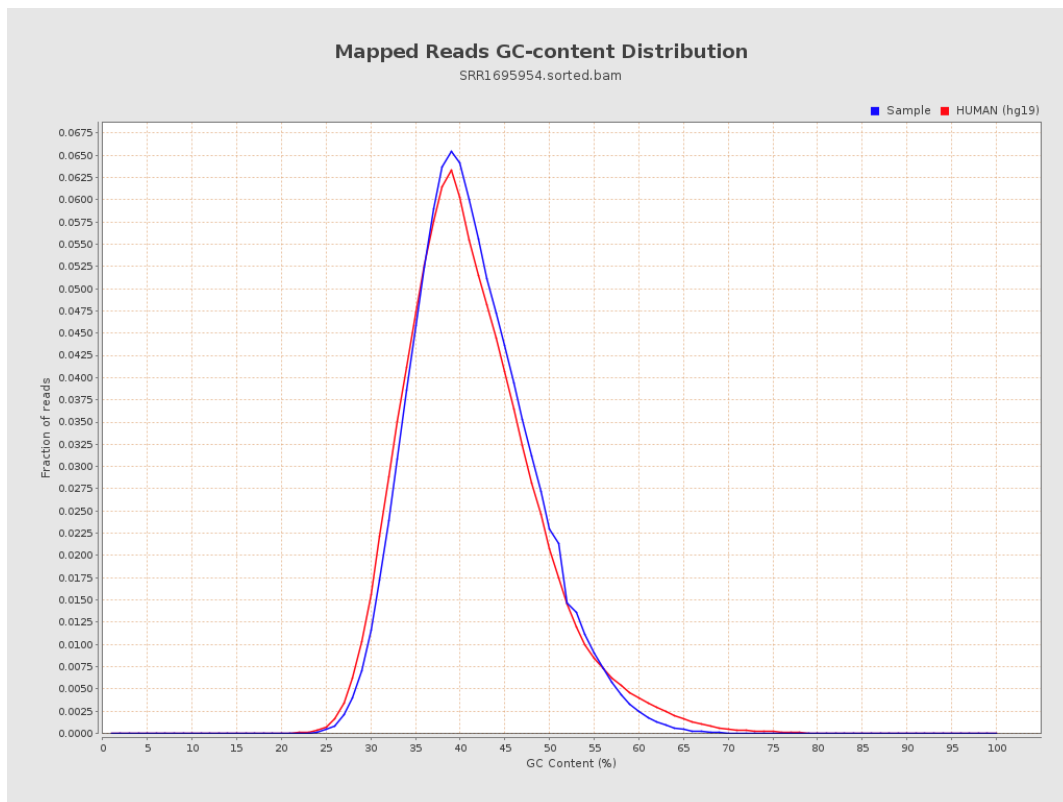
7. Results : Duplication Rate Histogram



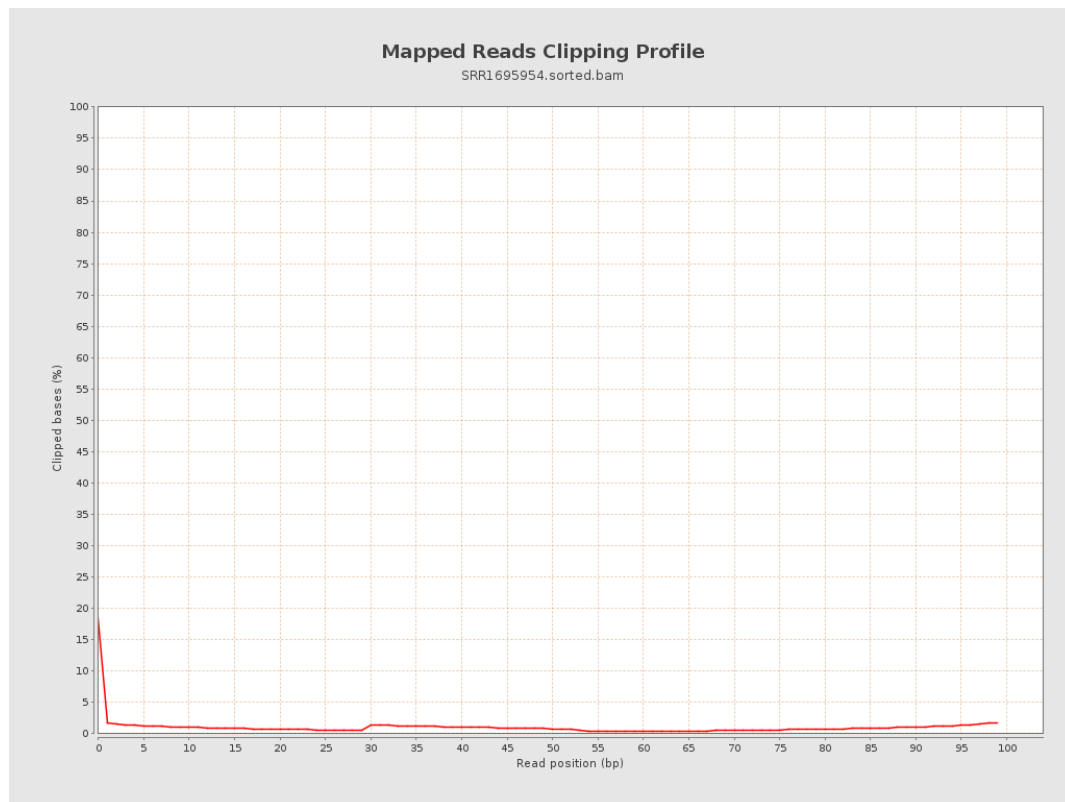
8. Results : Mapped Reads Nucleotide Content



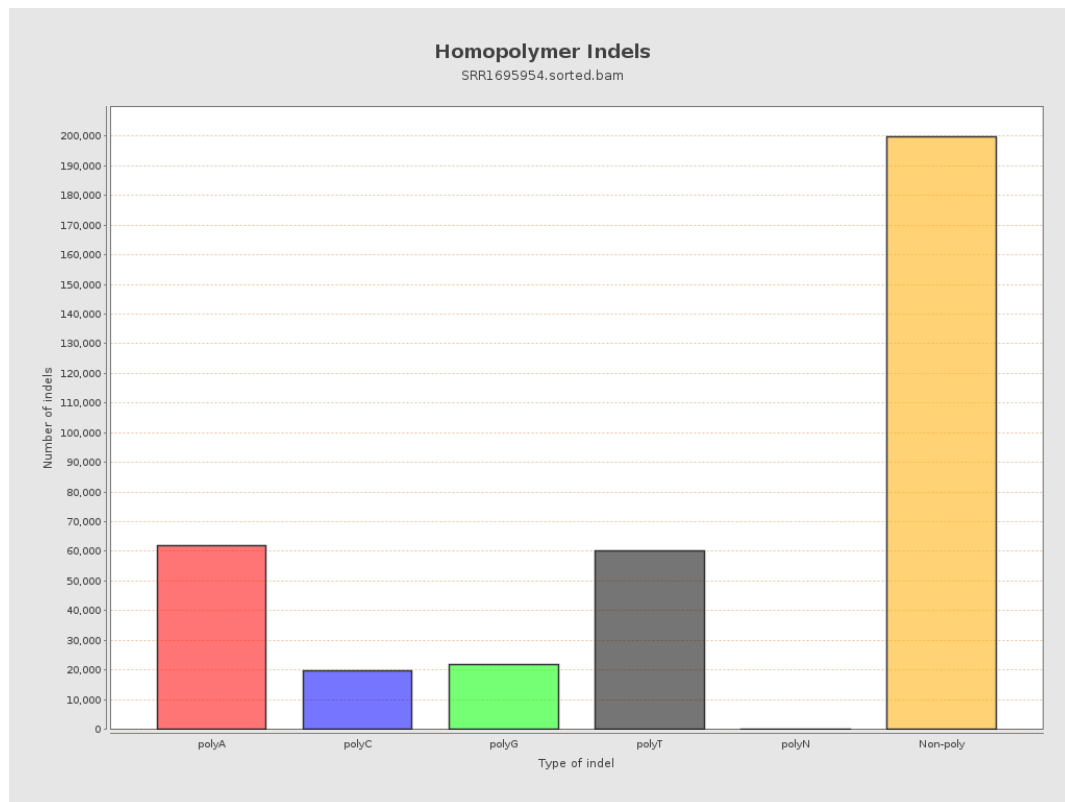
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



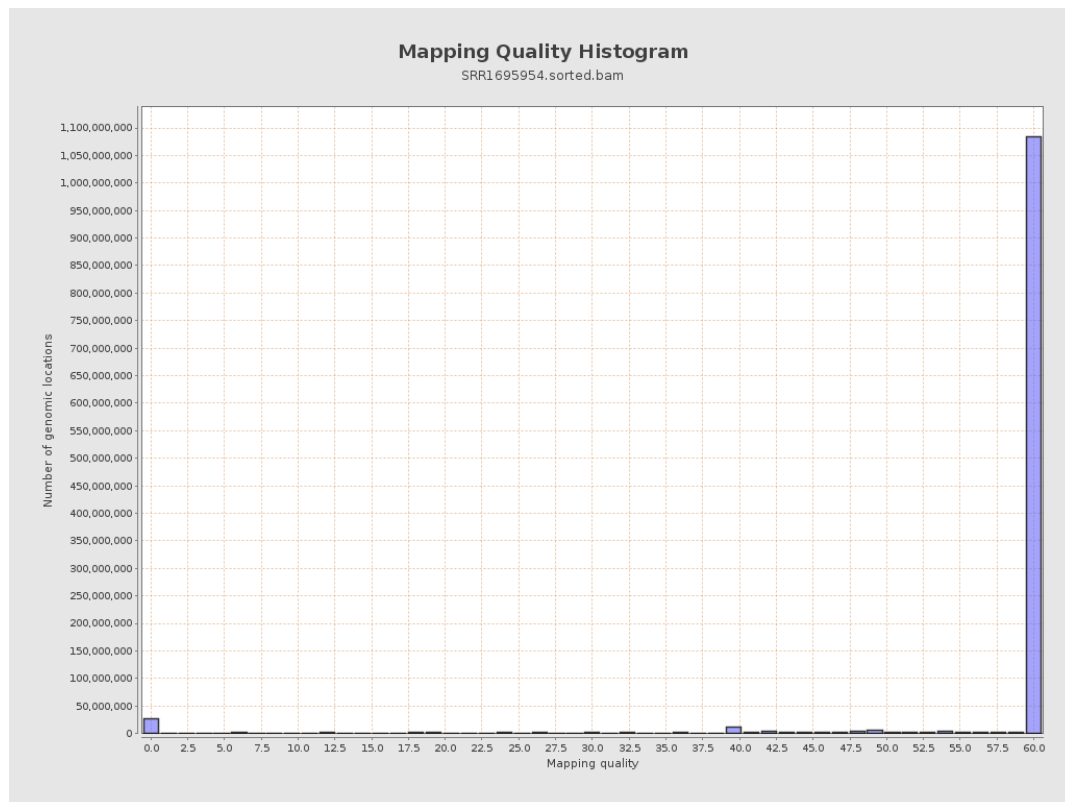
11. Results : Homopolymer Indels



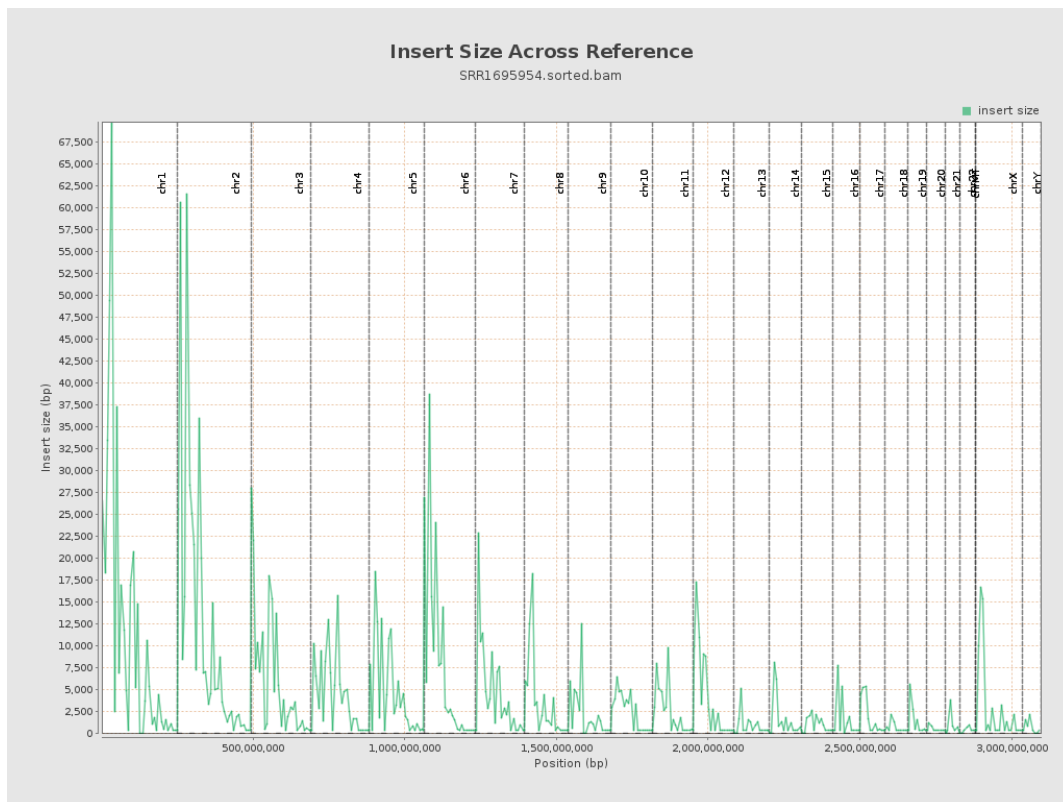
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

