

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/13 00:42:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695927.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 927 /seu_share/home/tujing/220232460/r eference/homo_bwa/hsa.fa SRR1695927_1.fastq.gz SRR1695927_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 00:42:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695927.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,780,044
Mapped reads	7,880,889 / 89.76%
Unmapped reads	899,155 / 10.24%
Mapped paired reads	7,880,889 / 89.76%
Mapped reads, first in pair	3,970,299 / 45.22%
Mapped reads, second in pair	3,910,590 / 44.54%
Mapped reads, both in pair	7,411,914 / 84.42%
Mapped reads, singletons	468,975 / 5.34%
Secondary alignments	0
Supplementary alignments	170,536 / 1.94%
Read min/max/mean length	30 / 100 / 100.72
Duplicated reads (estimated)	2,003,093 / 22.81%
Duplication rate	15.51%
Clipped reads	5,570,261 / 63.44%

2.2. ACGT Content

Number/percentage of A's	173,410,029 / 26.45%
Number/percentage of C's	116,160,844 / 17.71%
Number/percentage of T's	214,430,192 / 32.7%
Number/percentage of G's	151,521,560 / 23.11%
Number/percentage of N's	203,579 / 0.03%

GC Percentage	40.82%
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2.3. Coverage

Mean	0.2119
Standard Deviation	1.7805

2.4. Mapping Quality

Mean Mapping Quality	51.64
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2.5. Insert size

Mean	168,511.01
Standard Deviation	3,936,261.22
P25/Median/P75	277 / 294 / 307

2.6. Mismatches and indels

General error rate	1.39%
Mismatches	9,025,362
Insertions	53,088
Mapped reads with at least one insertion	0.66%
Deletions	135,369
Mapped reads with at least one deletion	1.69%
Homopolymer indels	45%

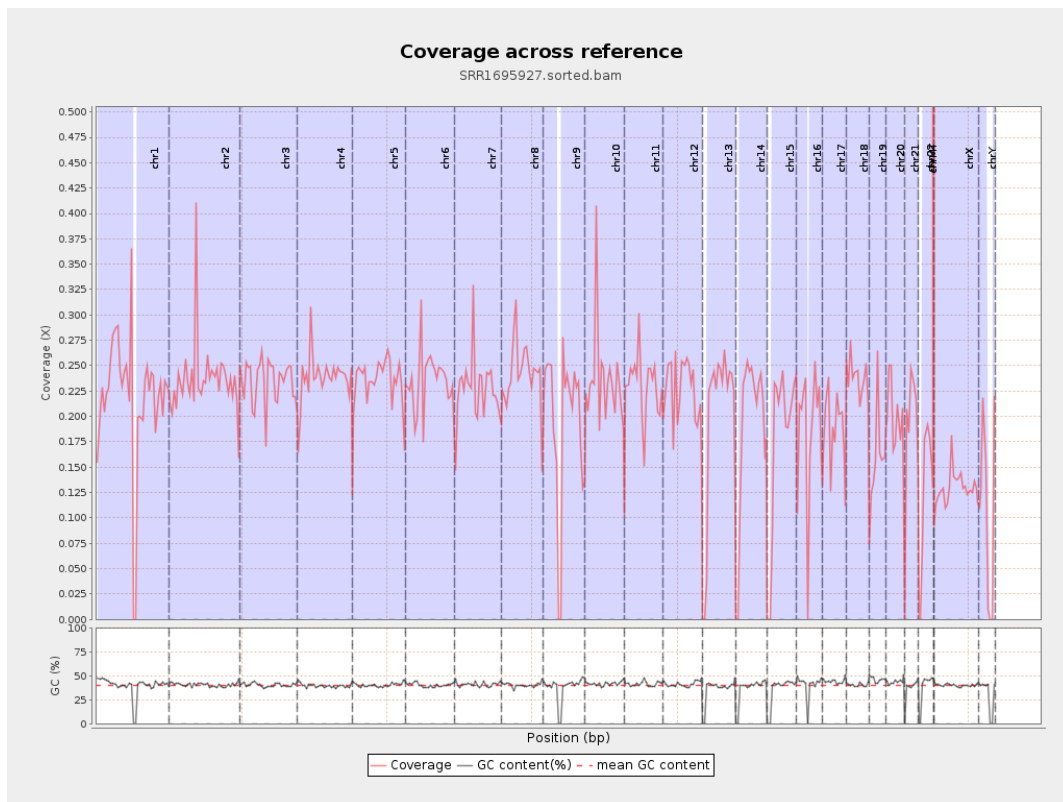
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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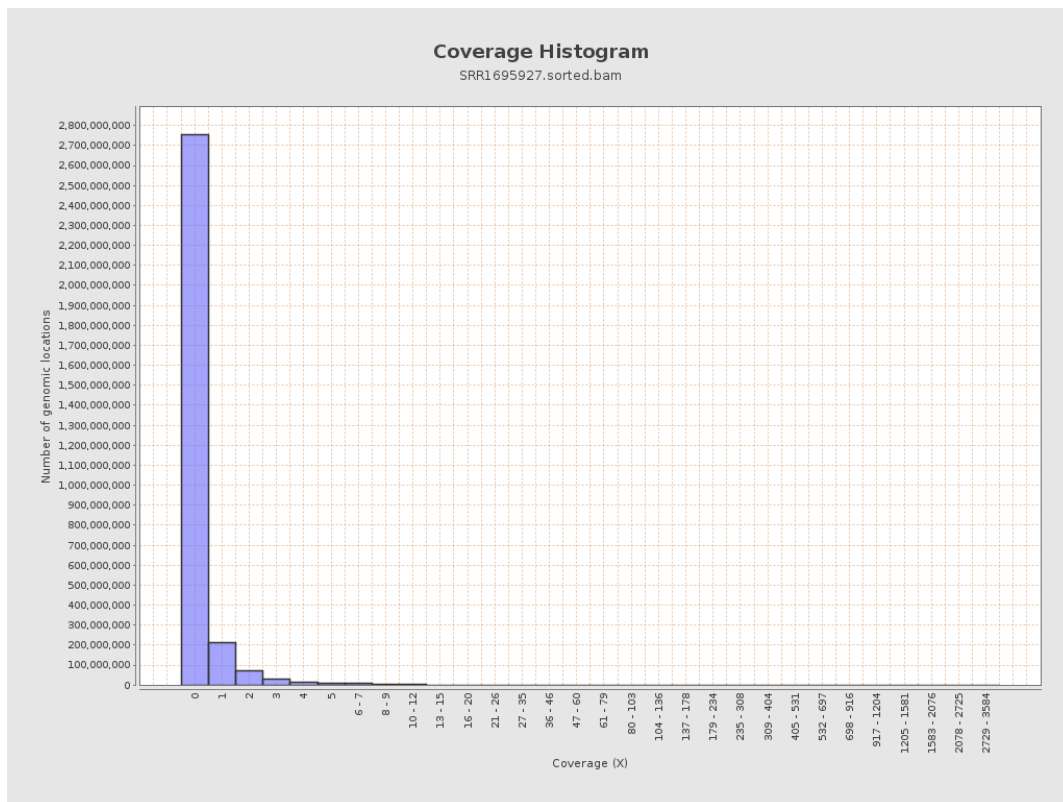
		bases	coverage	deviation
chr1	249250621	54551695	0.2189	2.9696
chr2	243199373	57602738	0.2369	2.2065
chr3	198022430	46514163	0.2349	0.9065
chr4	191154276	45534563	0.2382	1.0133
chr5	180915260	42717683	0.2361	0.9643
chr6	171115067	40122072	0.2345	1.2905
chr7	159138663	36334287	0.2283	2.3776
chr8	146364022	35365658	0.2416	2.7821
chr9	141213431	27656660	0.1959	1.7201
chr10	135534747	31900803	0.2354	2.0752
chr11	135006516	30779627	0.228	1.9953
chr12	133851895	30245976	0.226	0.9266
chr13	115169878	22760222	0.1976	0.8302
chr14	107349540	20506955	0.191	0.9449
chr15	102531392	18206009	0.1776	0.7961
chr16	90354753	16802633	0.186	0.9184
chr17	81195210	15092702	0.1859	1.0208
chr18	78077248	18595721	0.2382	2.9621
chr19	59128983	9598768	0.1623	2.3096
chr20	63025520	12600581	0.1999	0.8713
chr21	48129895	9131092	0.1897	1.6723
chr22	51304566	6230234	0.1214	1.2687
chrMT	16571	851369	51.377	40.0406
chrX	155270560	20071216	0.1293	0.8806

chrY	59373566	6192753	0.1043	1.1042
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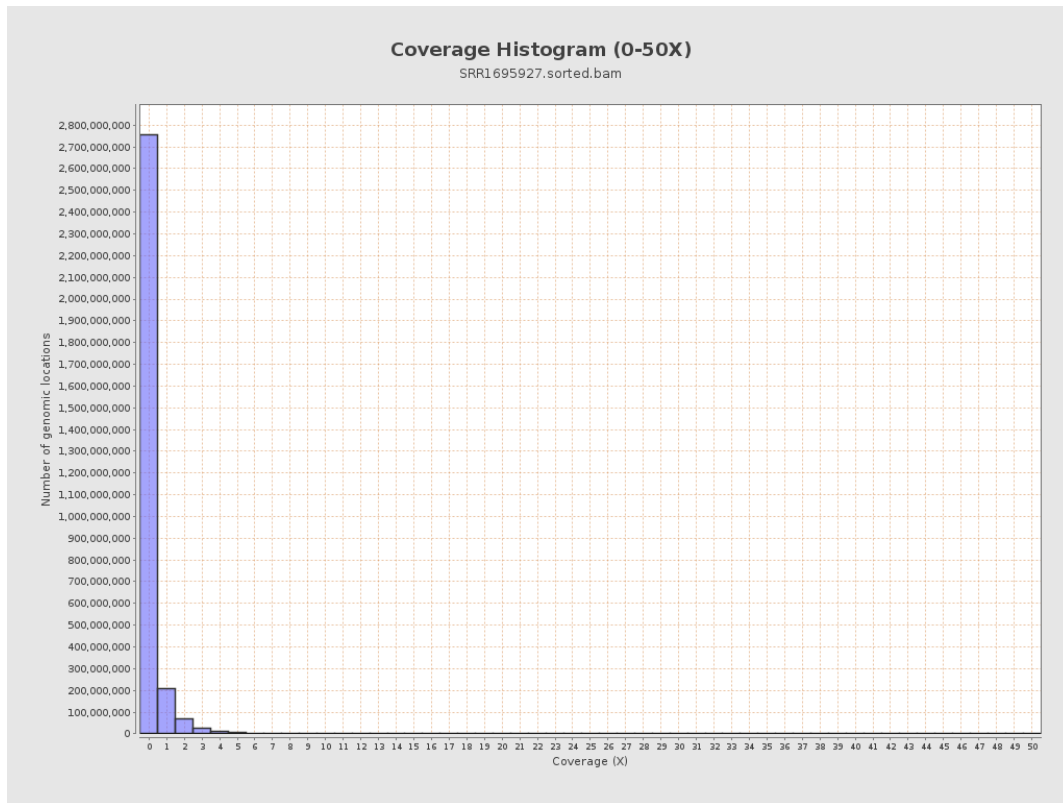
3. Results : Coverage across reference



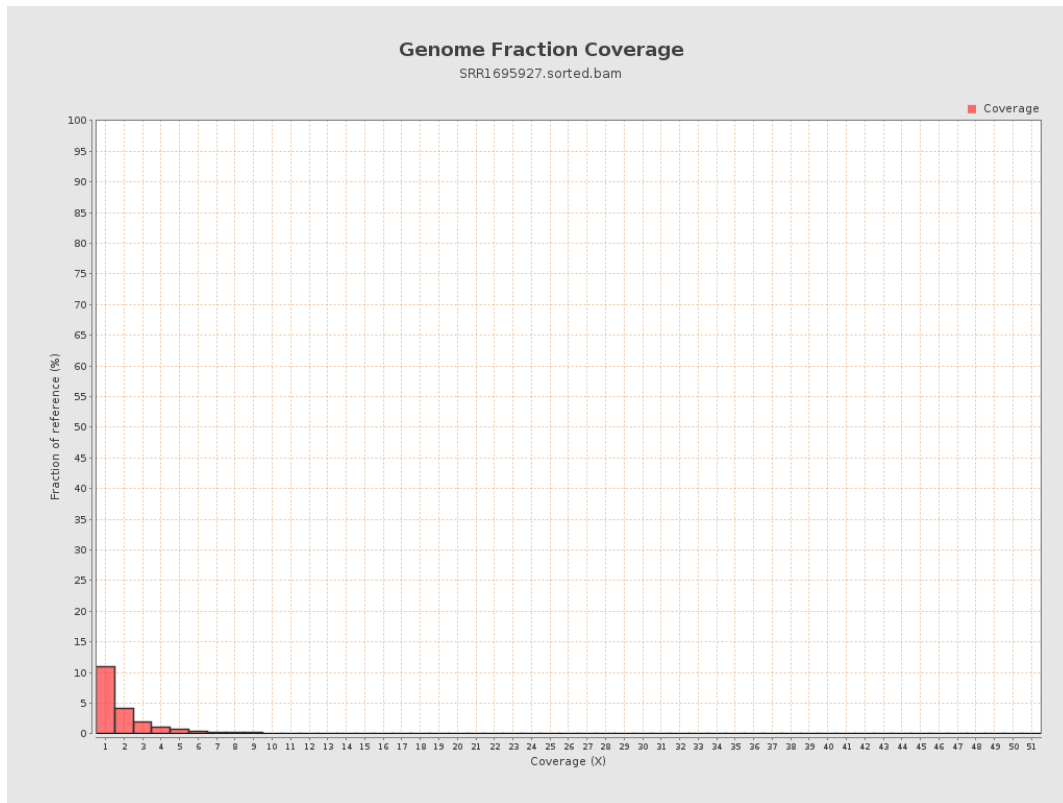
4. Results : Coverage Histogram



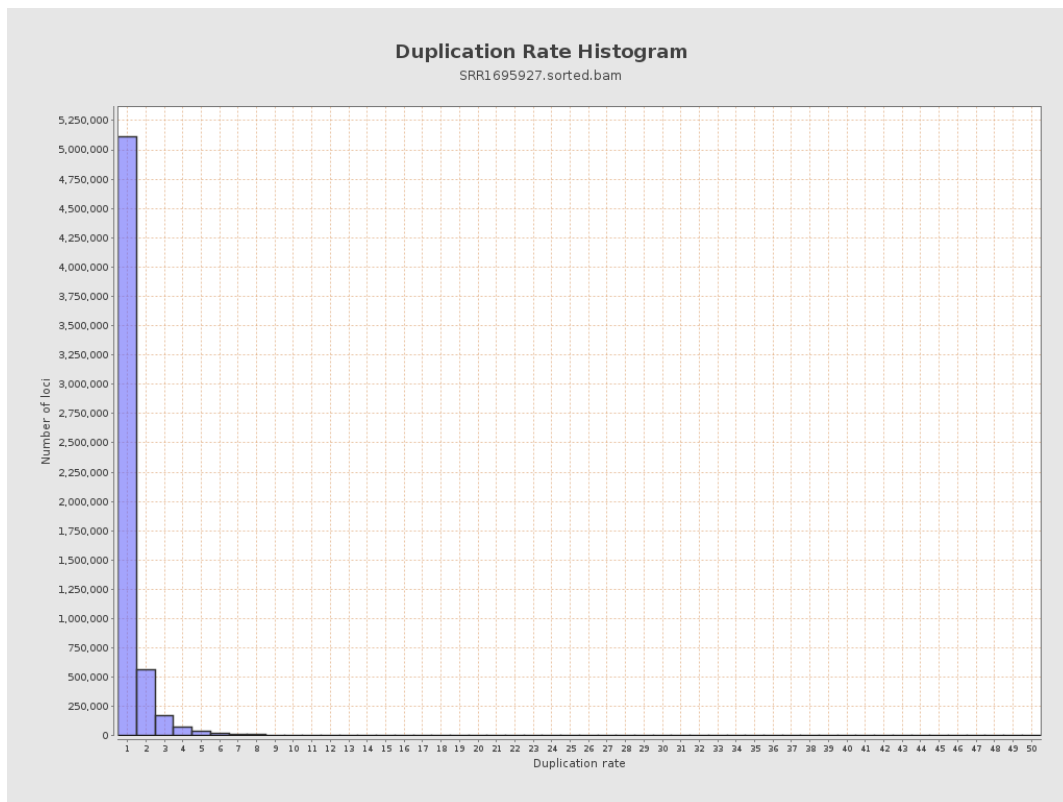
5. Results : Coverage Histogram (0-50X)



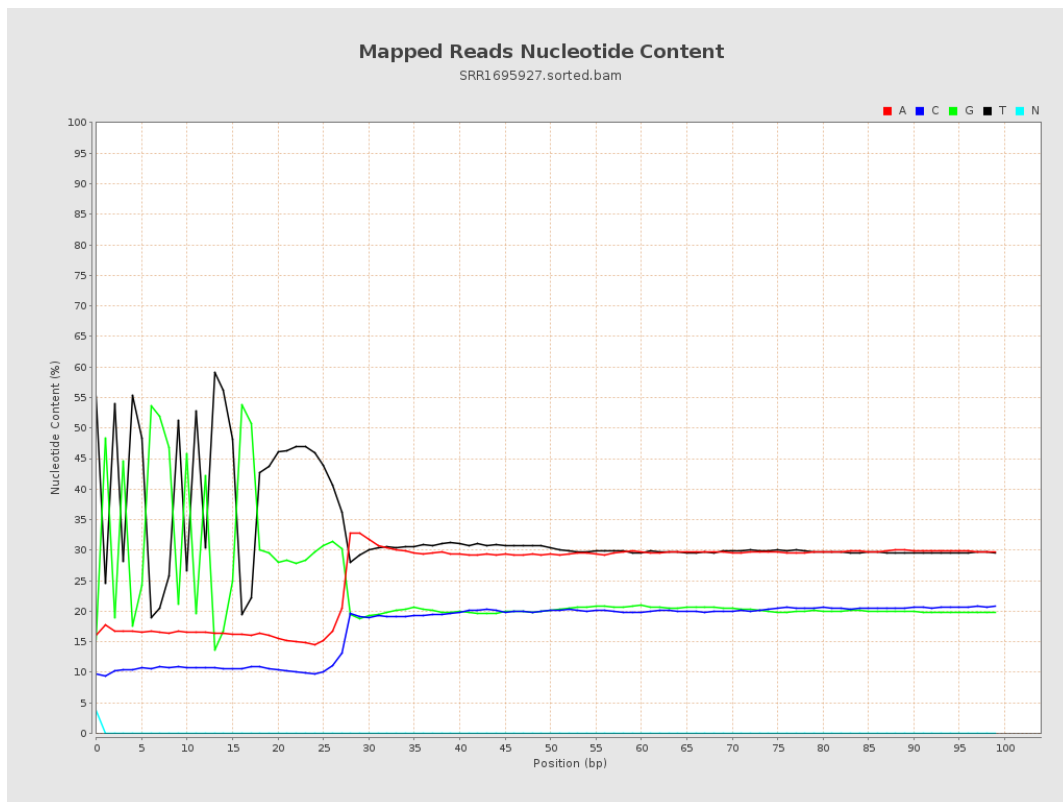
6. Results : Genome Fraction Coverage



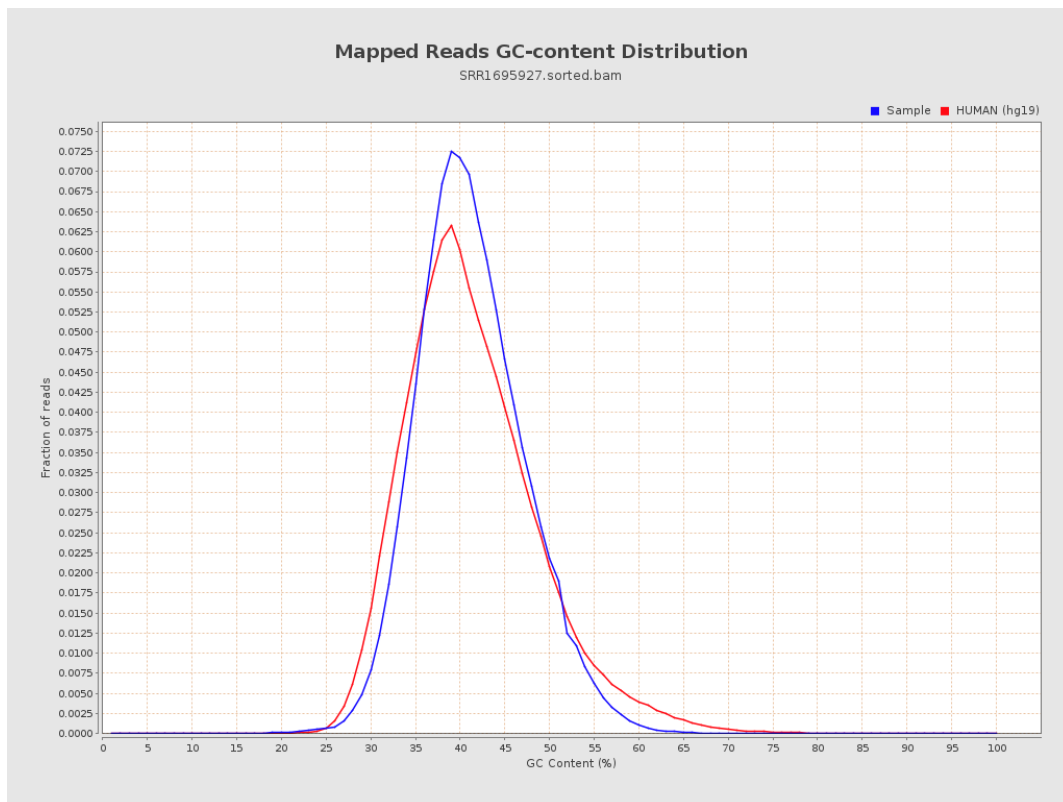
7. Results : Duplication Rate Histogram



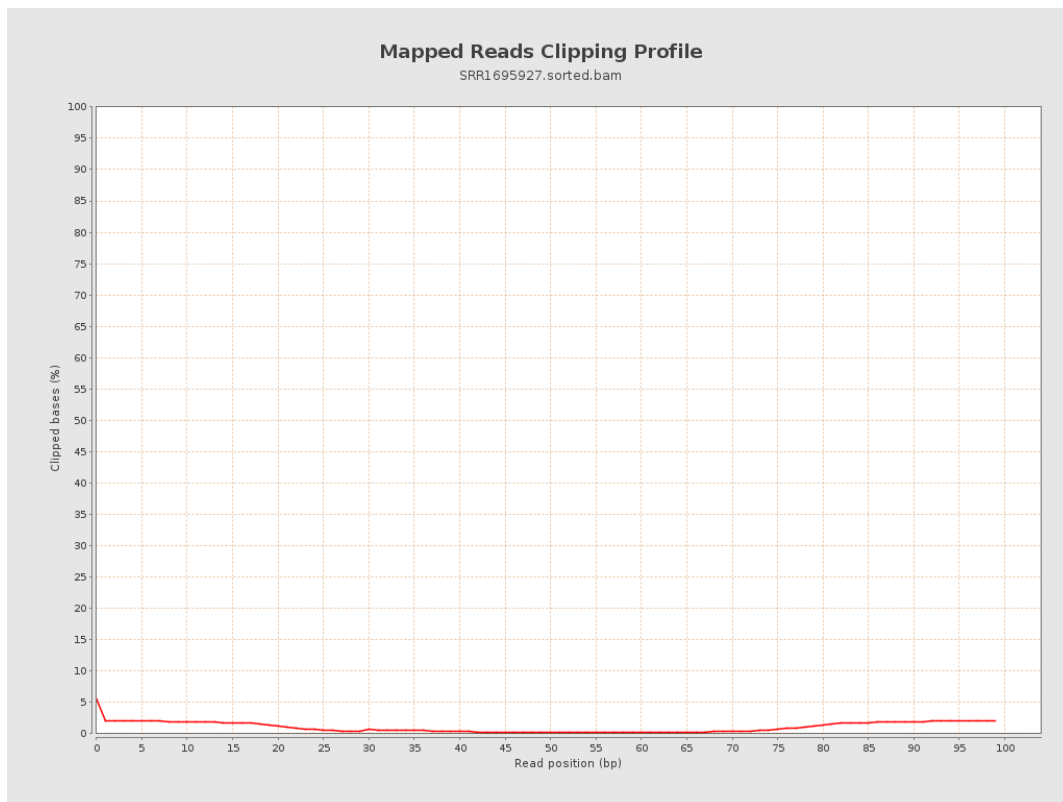
8. Results : Mapped Reads Nucleotide Content



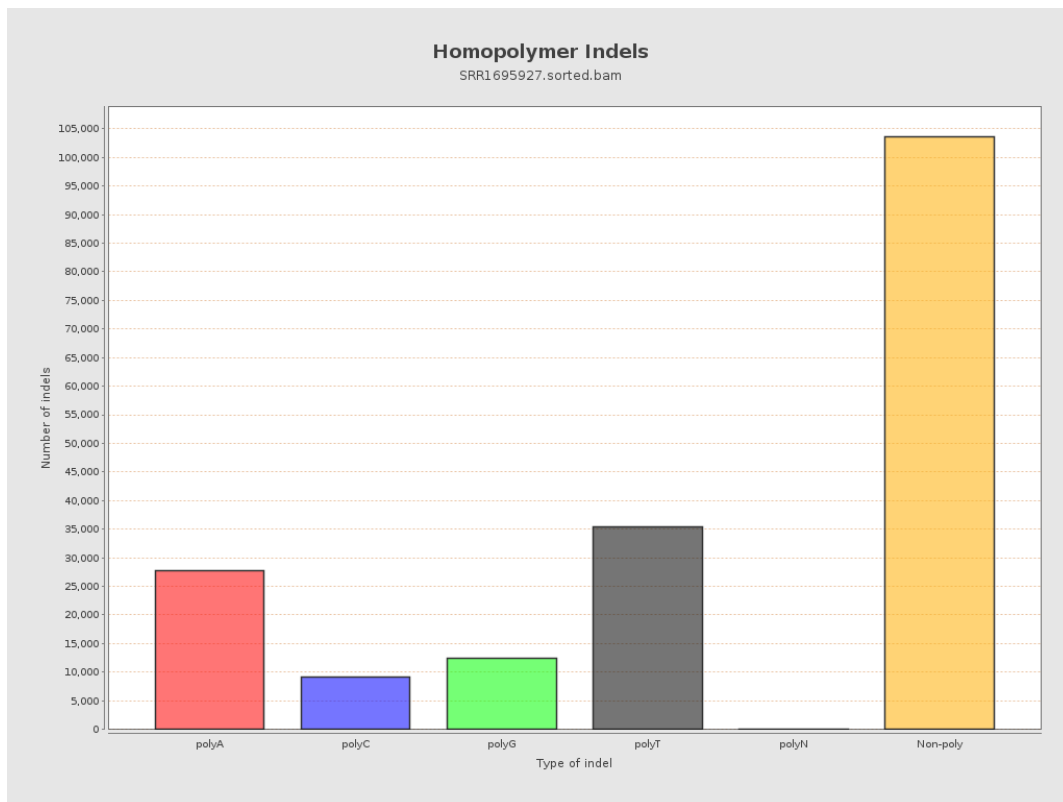
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



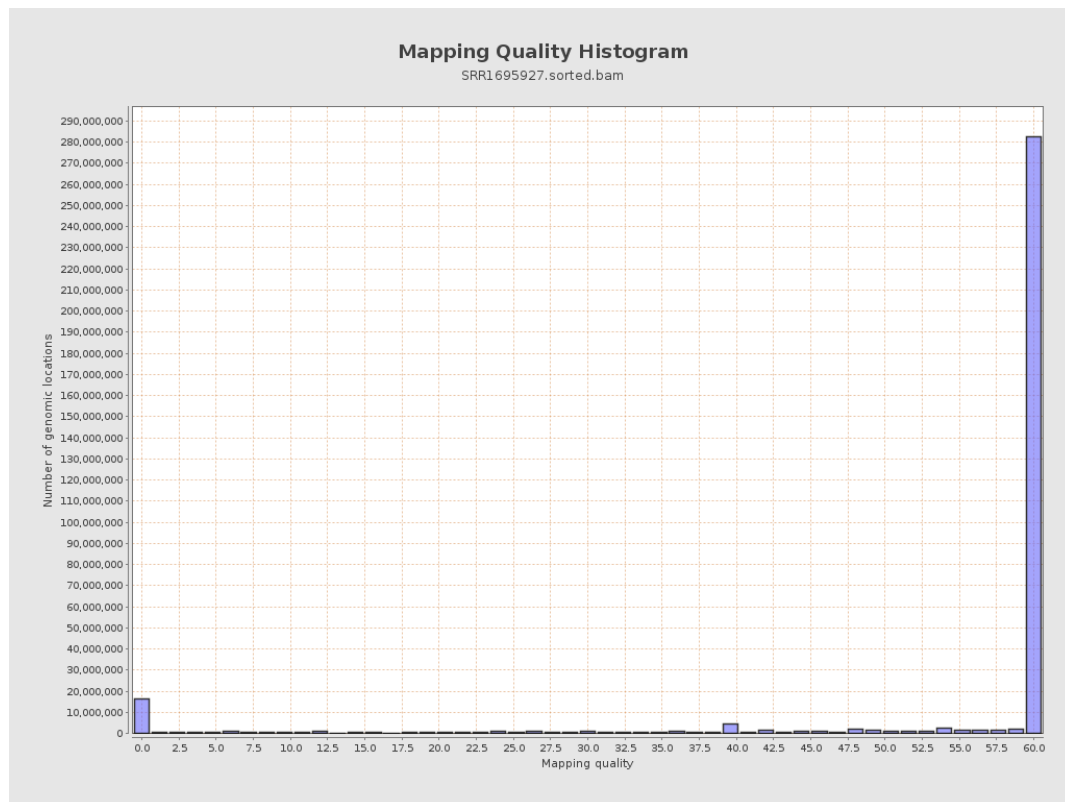
11. Results : Homopolymer Indels



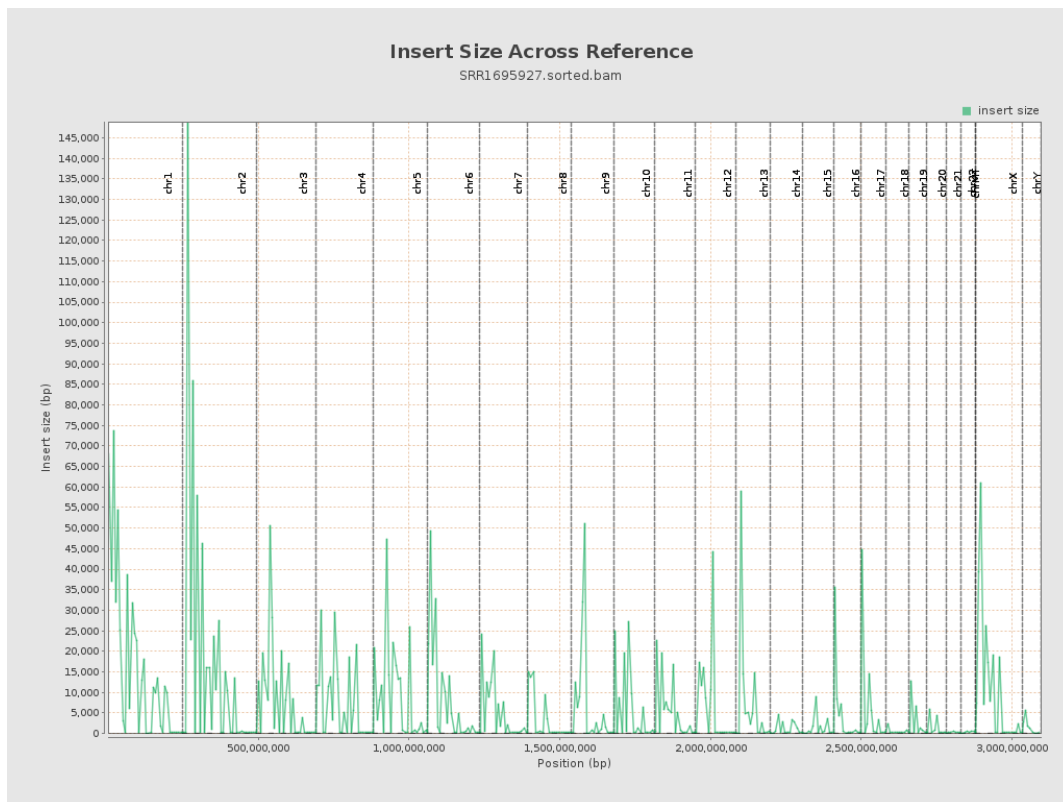
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

