

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/14 04:16:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695974.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/seu_share/home/tujing/220232460/software/bwa-0.7.18/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1695974 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695974_1.fastq.gz SRR1695974_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Sat Sep 14 04:16:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695974.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	400,168,992
Mapped reads	392,184,680 / 98%
Unmapped reads	7,984,312 / 2%
Mapped paired reads	392,184,680 / 98%
Mapped reads, first in pair	197,766,943 / 49.42%
Mapped reads, second in pair	194,417,737 / 48.58%
Mapped reads, both in pair	387,385,938 / 96.81%
Mapped reads, singletons	4,798,742 / 1.2%
Secondary alignments	0
Supplementary alignments	1,181,070 / 0.3%
Read min/max/mean length	30 / 100 / 100.11
Duplicated reads (estimated)	60,367,009 / 15.09%
Duplication rate	10.03%
Clipped reads	24,344,094 / 6.08%

2.2. ACGT Content

Number/percentage of A's	11,296,833,002 / 29.24%
Number/percentage of C's	7,998,459,664 / 20.71%
Number/percentage of T's	11,287,538,629 / 29.22%
Number/percentage of G's	8,038,055,715 / 20.81%
Number/percentage of N's	8,723,779 / 0.02%

GC Percentage	41.51%
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2.3. Coverage

Mean	12.4821
Standard Deviation	137.4573

2.4. Mapping Quality

Mean Mapping Quality	53.71
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2.5. Insert size

Mean	47,073.08
Standard Deviation	2,050,415.72
P25/Median/P75	301 / 308 / 316

2.6. Mismatches and indels

General error rate	0.71%
Mismatches	265,119,419
Insertions	3,938,749
Mapped reads with at least one insertion	0.97%
Deletions	4,633,860
Mapped reads with at least one deletion	1.15%
Homopolymer indels	41.84%

2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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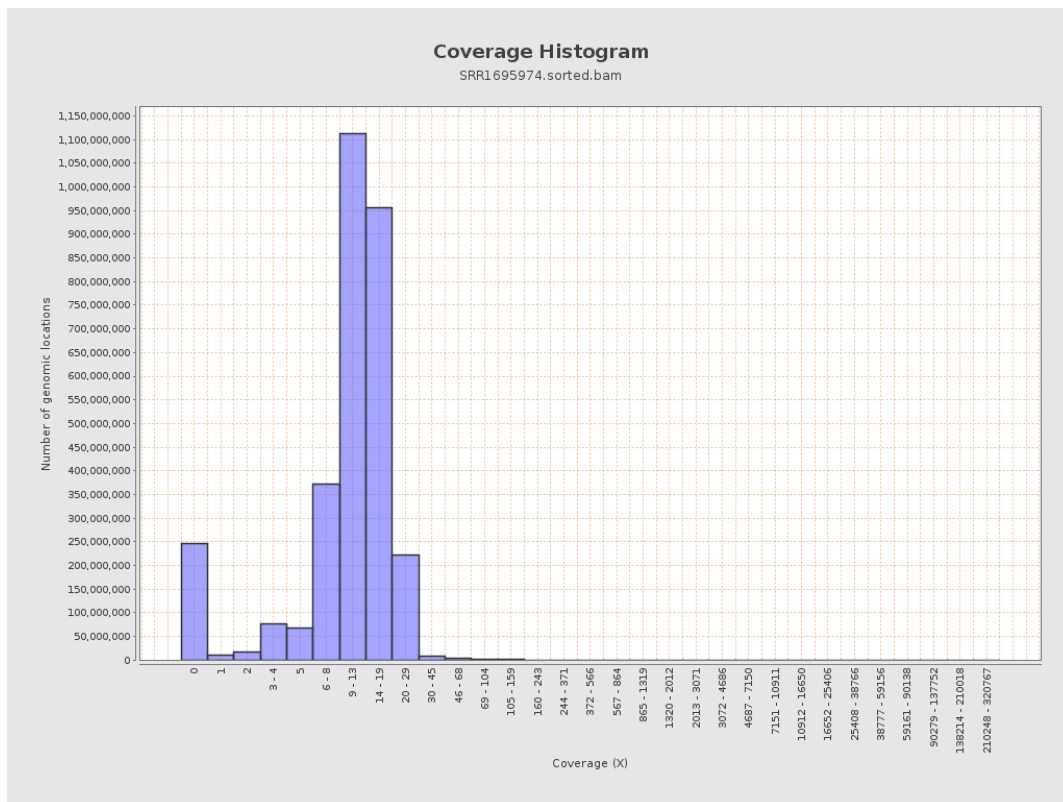
		bases	coverage	deviation
chr1	249250621	3217283285	12.9078	313.6674
chr2	243199373	3366806761	13.8438	87.1571
chr3	198022430	2532703100	12.79	13.888
chr4	191154276	2509492494	13.1281	94.3314
chr5	180915260	2302010306	12.7242	11.9703
chr6	171115067	2209432872	12.912	52.7189
chr7	159138663	2087849734	13.1197	114.0642
chr8	146364022	1921234656	13.1264	78.7462
chr9	141213431	1632528236	11.5607	116.479
chr10	135534747	2137801834	15.7731	358.9789
chr11	135006516	1784953087	13.2212	61.5478
chr12	133851895	1722312159	12.8673	11.5813
chr13	115169878	1189879829	10.3315	8.8507
chr14	107349540	1175259345	10.948	11.0953
chr15	102531392	1116754945	10.8918	9.8033
chr16	90354753	1259575036	13.9403	98.5143
chr17	81195210	1130268689	13.9204	58.0766
chr18	78077248	1050853879	13.4592	150.1214
chr19	59128983	819366204	13.8573	167.6426
chr20	63025520	834745724	13.2446	45.0812
chr21	48129895	535426308	11.1246	55.8959
chr22	51304566	512924535	9.9976	52.9881
chrMT	16571	109688953	6,619.3321	1,033.0894
chrX	155270560	1006917553	6.4849	23.9473

chrY	59373566	474829780	7.9973	137.5545
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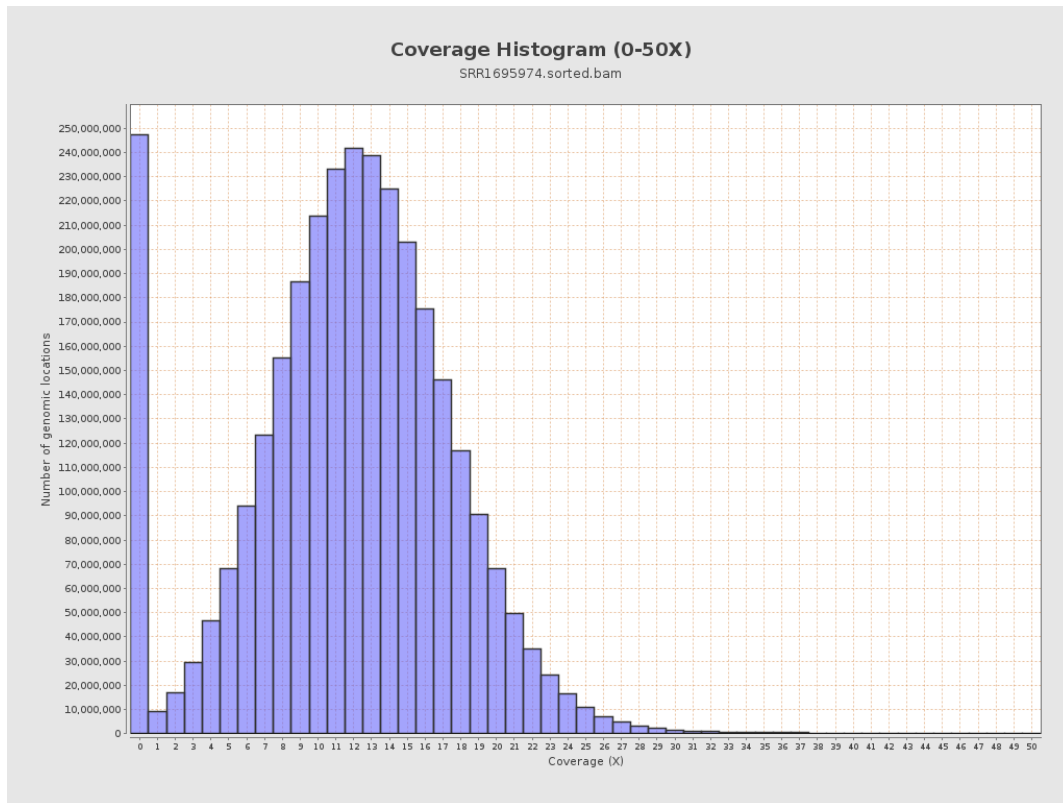
3. Results : Coverage across reference



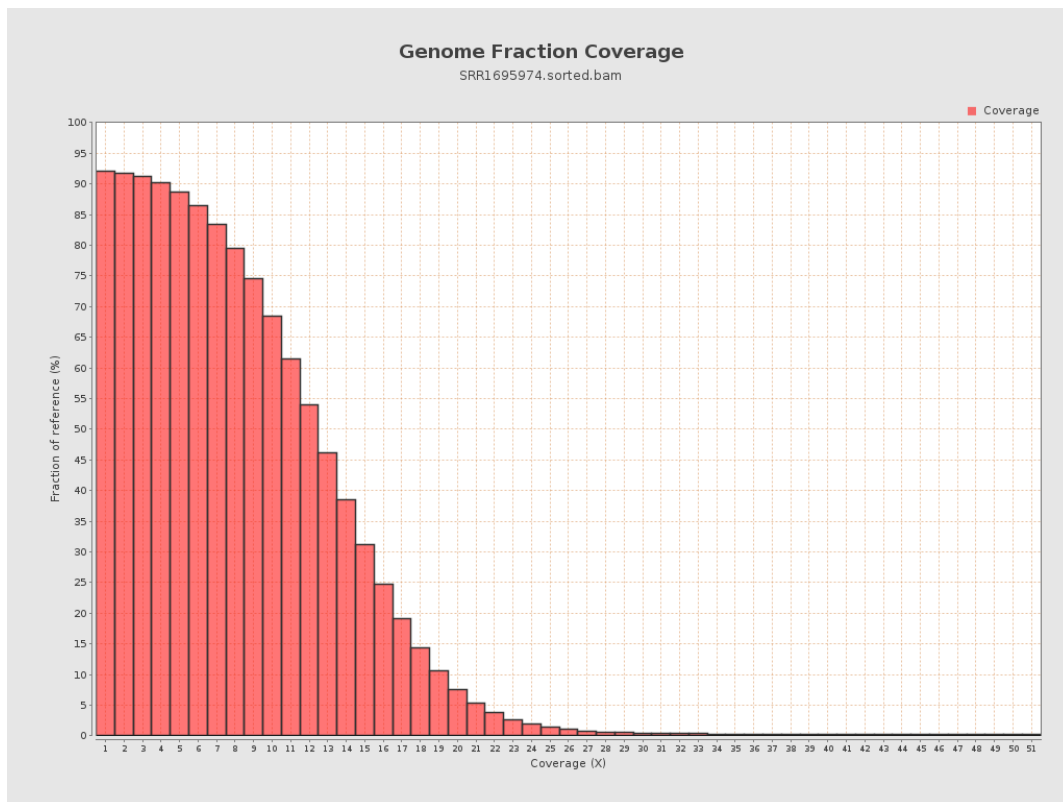
4. Results : Coverage Histogram



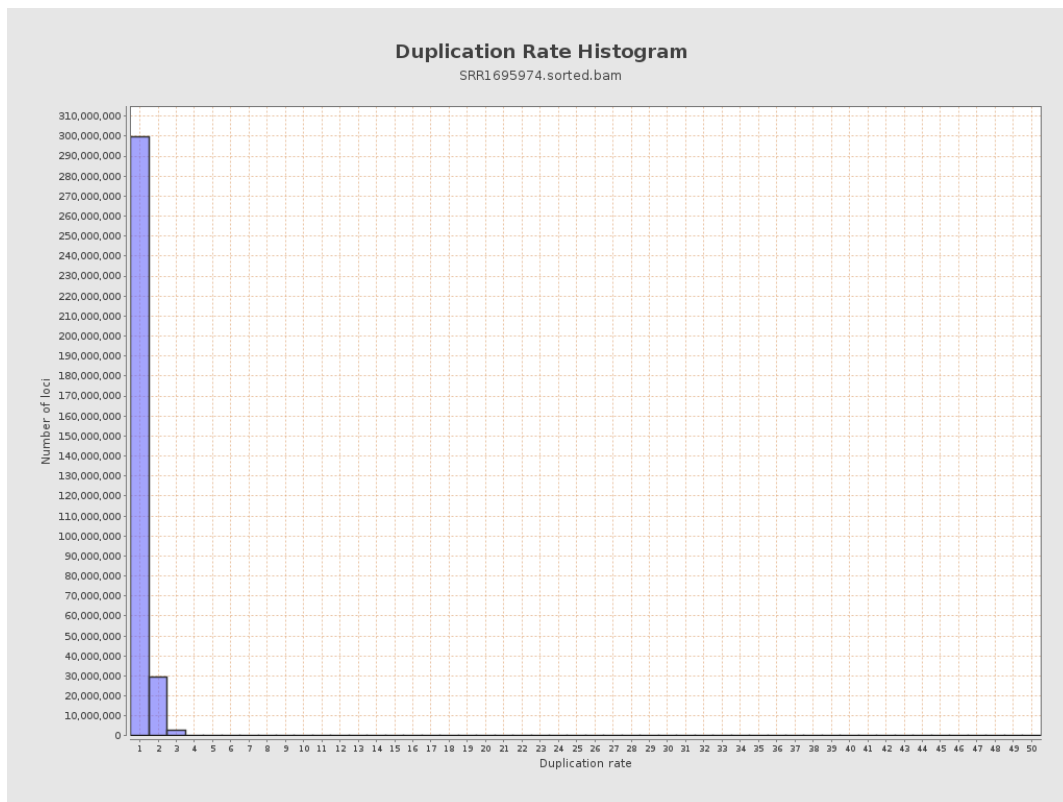
5. Results : Coverage Histogram (0-50X)



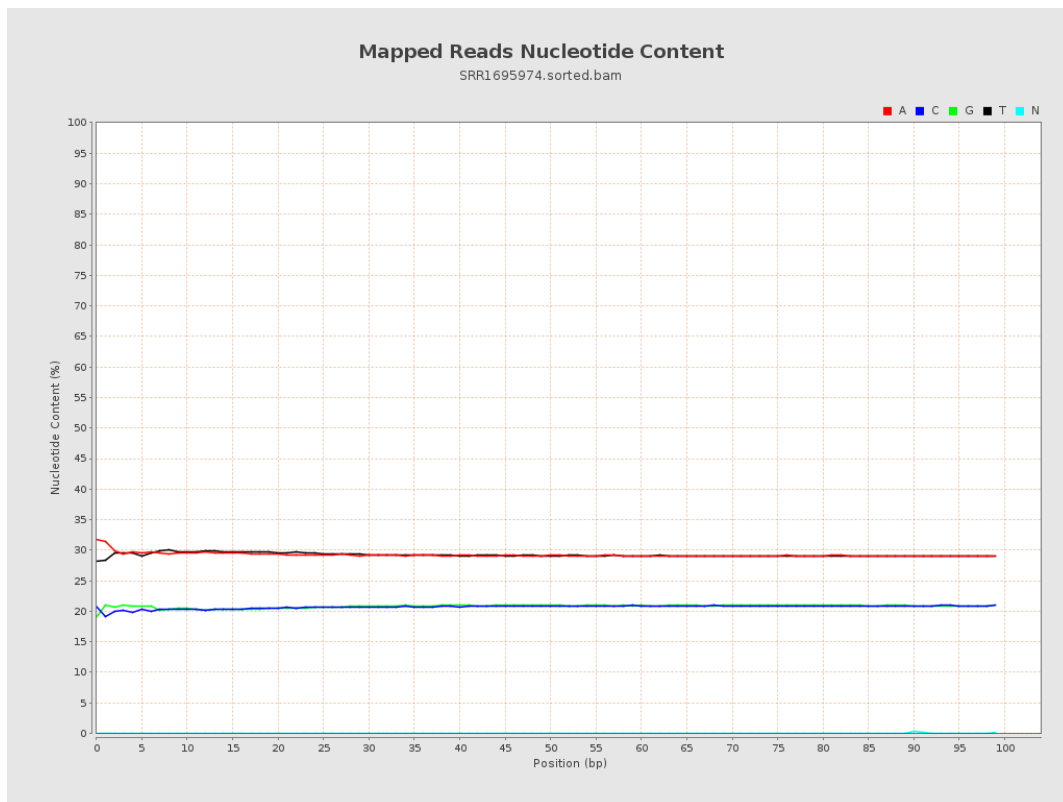
6. Results : Genome Fraction Coverage



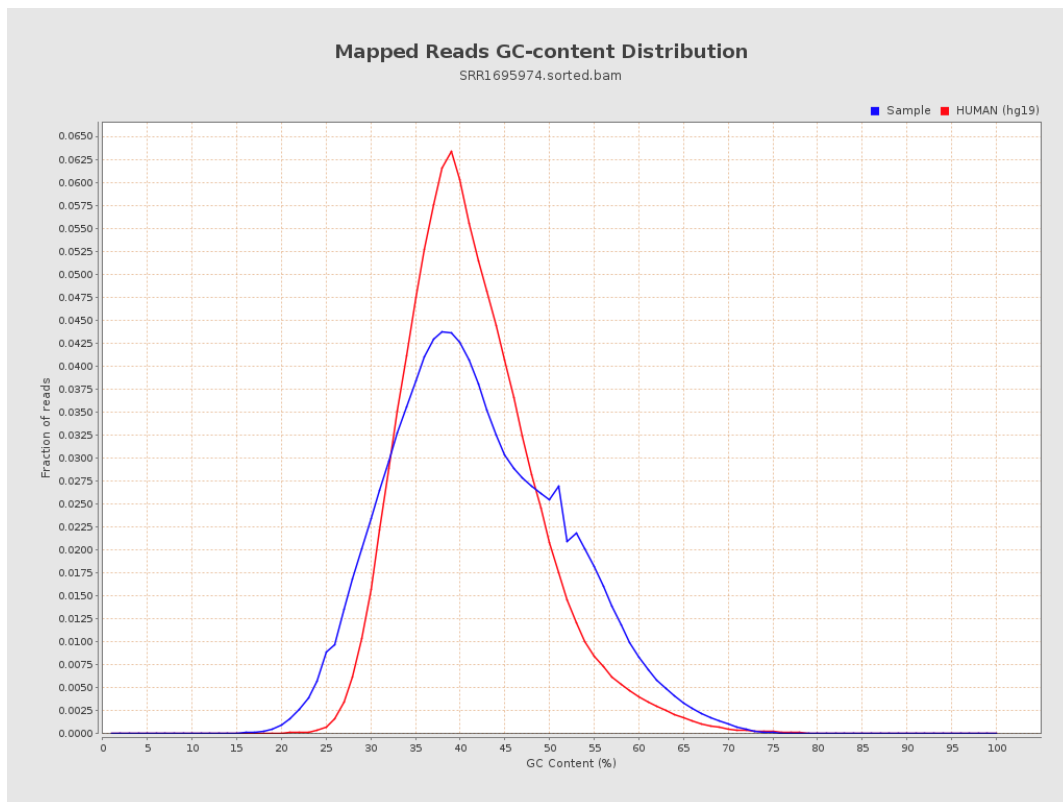
7. Results : Duplication Rate Histogram



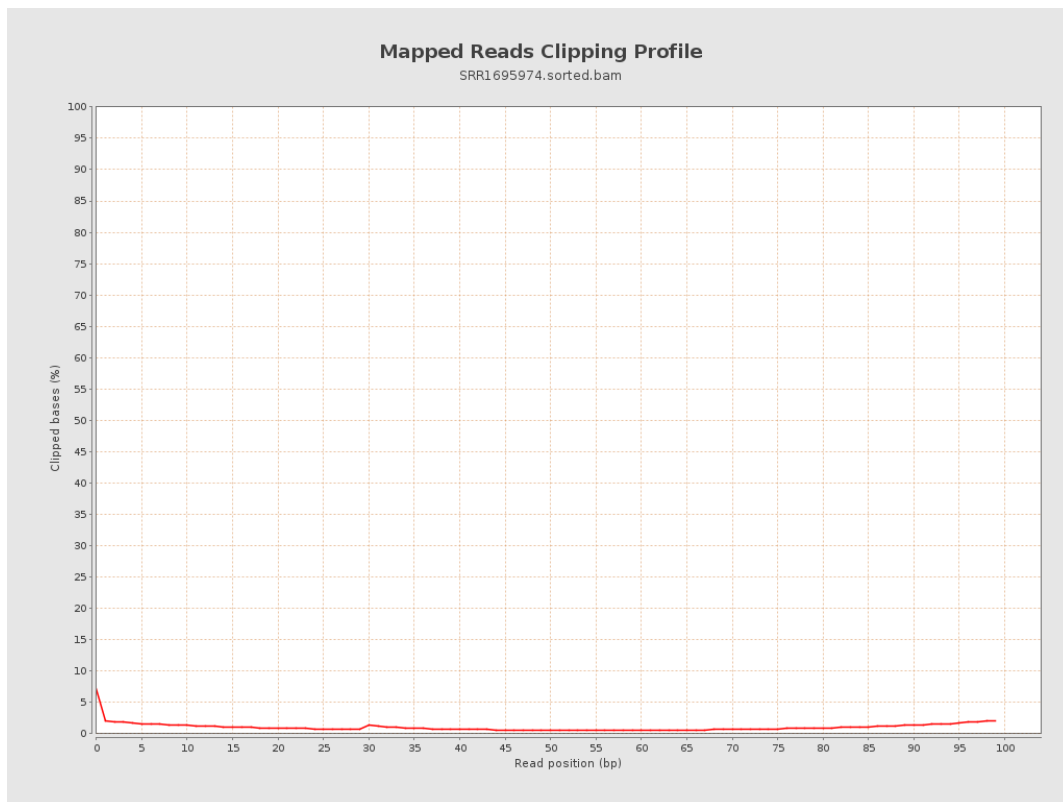
8. Results : Mapped Reads Nucleotide Content



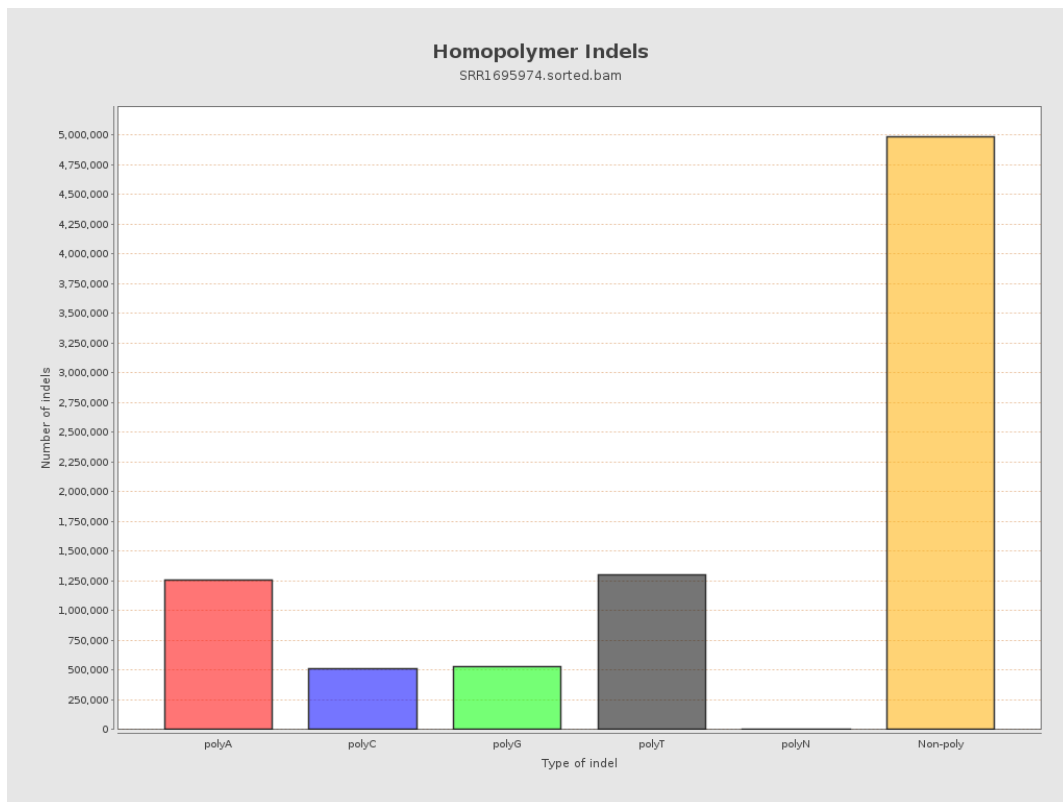
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



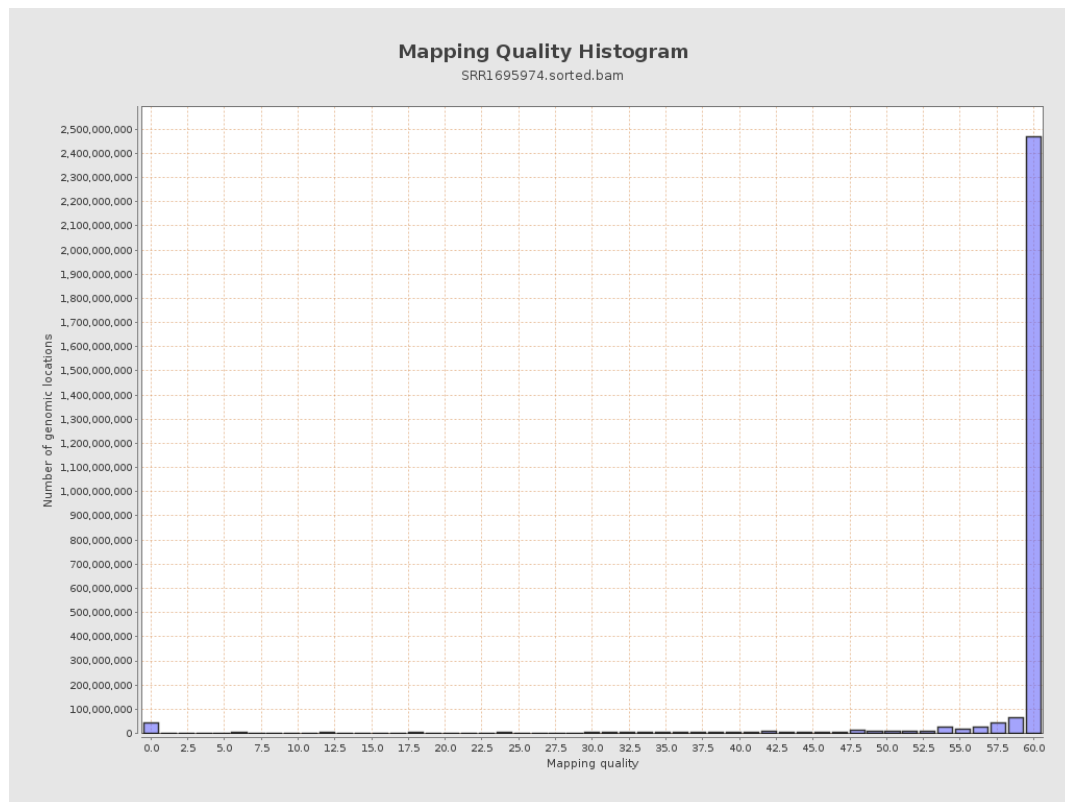
11. Results : Homopolymer Indels



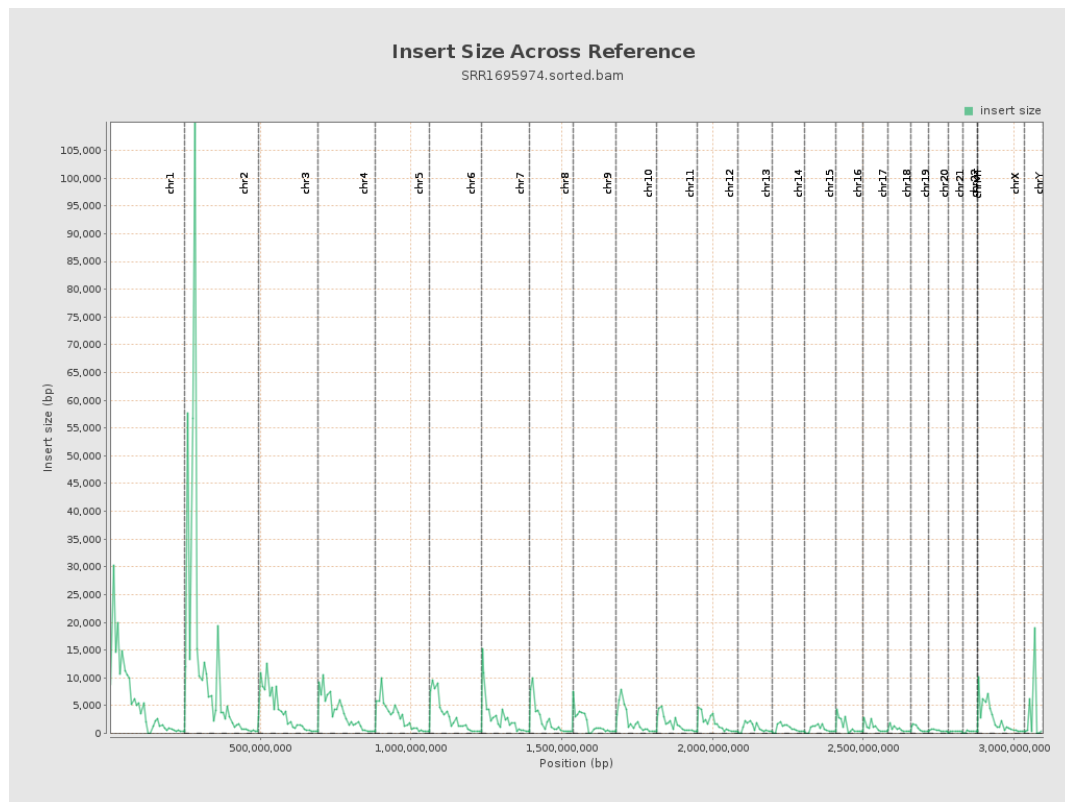
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

