

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/14 02:28:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695973.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_SRR1695973 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695973_1.fastq.gz SRR1695973_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 02:28:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695973.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,026,800
Mapped reads	13,625,552 / 97.14%
Unmapped reads	401,248 / 2.86%
Mapped paired reads	13,625,552 / 97.14%
Mapped reads, first in pair	6,904,625 / 49.22%
Mapped reads, second in pair	6,720,927 / 47.91%
Mapped reads, both in pair	13,381,280 / 95.4%
Mapped reads, singletons	244,272 / 1.74%
Secondary alignments	0
Supplementary alignments	43,376 / 0.31%
Read min/max/mean length	30 / 100 / 100.12
Duplicated reads (estimated)	696,920 / 4.97%
Duplication rate	1.63%
Clipped reads	1,016,515 / 7.25%

2.2. ACGT Content

Number/percentage of A's	394,630,349 / 29.49%
Number/percentage of C's	274,207,916 / 20.49%
Number/percentage of T's	393,049,002 / 29.37%
Number/percentage of G's	276,188,549 / 20.64%
Number/percentage of N's	110,908 / 0.01%

GC Percentage	41.13%
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2.3. Coverage

Mean	0.4324
Standard Deviation	4.9614

2.4. Mapping Quality

Mean Mapping Quality	53.63
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2.5. Insert size

Mean	50,573.76
Standard Deviation	2,149,831.71
P25/Median/P75	300 / 308 / 316

2.6. Mismatches and indels

General error rate	0.89%
Mismatches	11,553,731
Insertions	135,112
Mapped reads with at least one insertion	0.96%
Deletions	157,753
Mapped reads with at least one deletion	1.13%
Homopolymer indels	41.34%

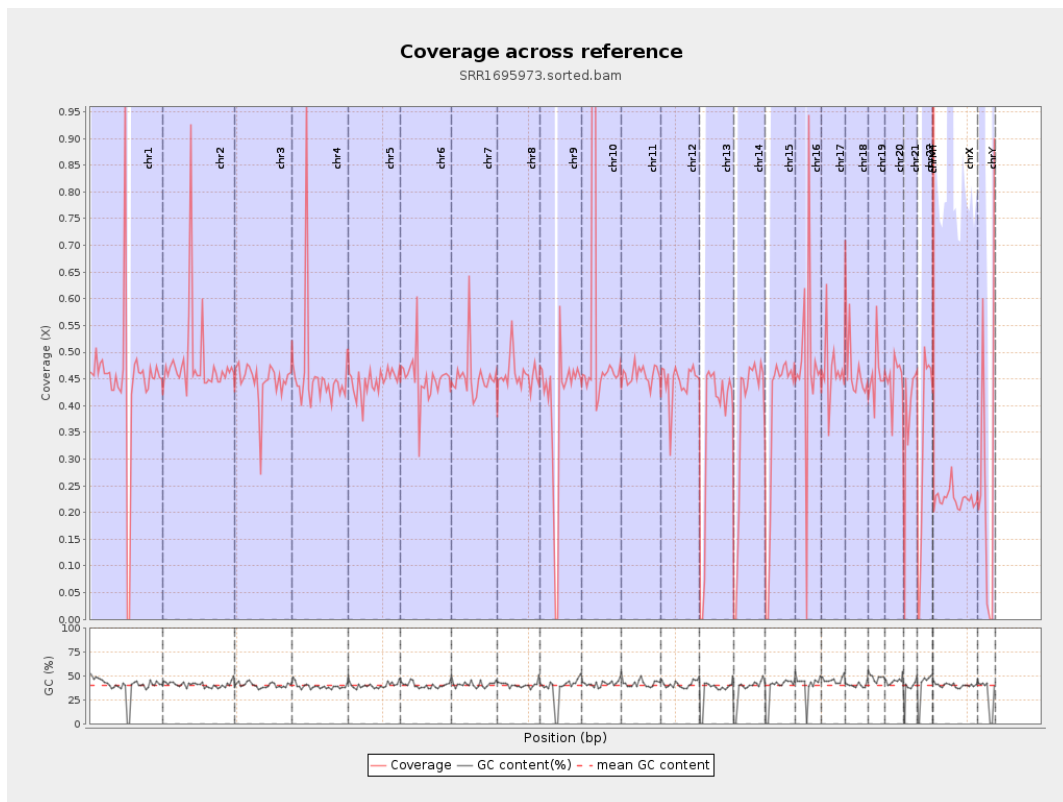
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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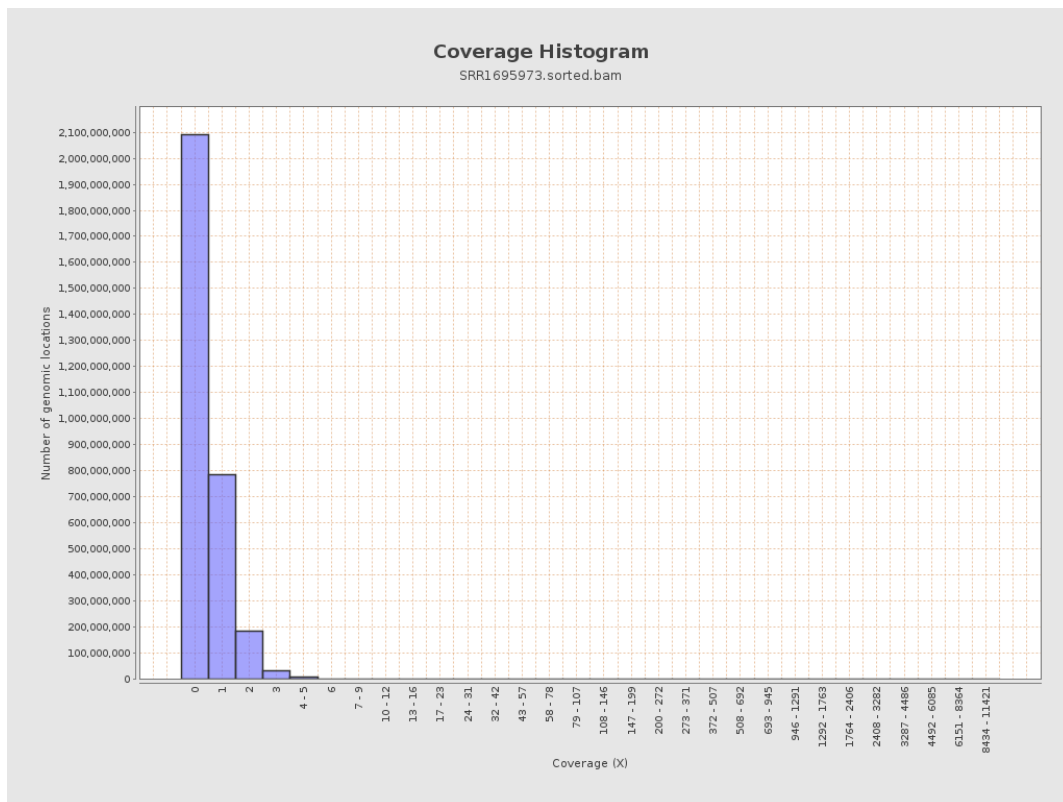
		bases	coverage	deviation
chr1	249250621	111052856	0.4455	11.1744
chr2	243199373	117144436	0.4817	3.209
chr3	198022430	88354317	0.4462	0.8373
chr4	191154276	88060547	0.4607	3.3584
chr5	180915260	80467330	0.4448	0.7845
chr6	171115067	77116521	0.4507	2.0061
chr7	159138663	72253157	0.454	4.1436
chr8	146364022	67102636	0.4585	3.0402
chr9	141213431	56354923	0.3991	4.1212
chr10	135534747	74458979	0.5494	13.0613
chr11	135006516	61658906	0.4567	2.269
chr12	133851895	59589003	0.4452	0.7757
chr13	115169878	41603862	0.3612	0.6733
chr14	107349540	40687698	0.379	0.7338
chr15	102531392	38495250	0.3754	0.7128
chr16	90354753	42880507	0.4746	3.6734
chr17	81195210	37955535	0.4675	2.1161
chr18	78077248	36600694	0.4688	5.3332
chr19	59128983	27155382	0.4593	5.9731
chr20	63025520	28350363	0.4498	1.6743
chr21	48129895	18541560	0.3852	1.9653
chr22	51304566	17018914	0.3317	1.8971
chrMT	16571	3706445	223.6706	42.5197
chrX	155270560	35162238	0.2265	0.9845

chrY	59373566	16795699	0.2829	4.9527
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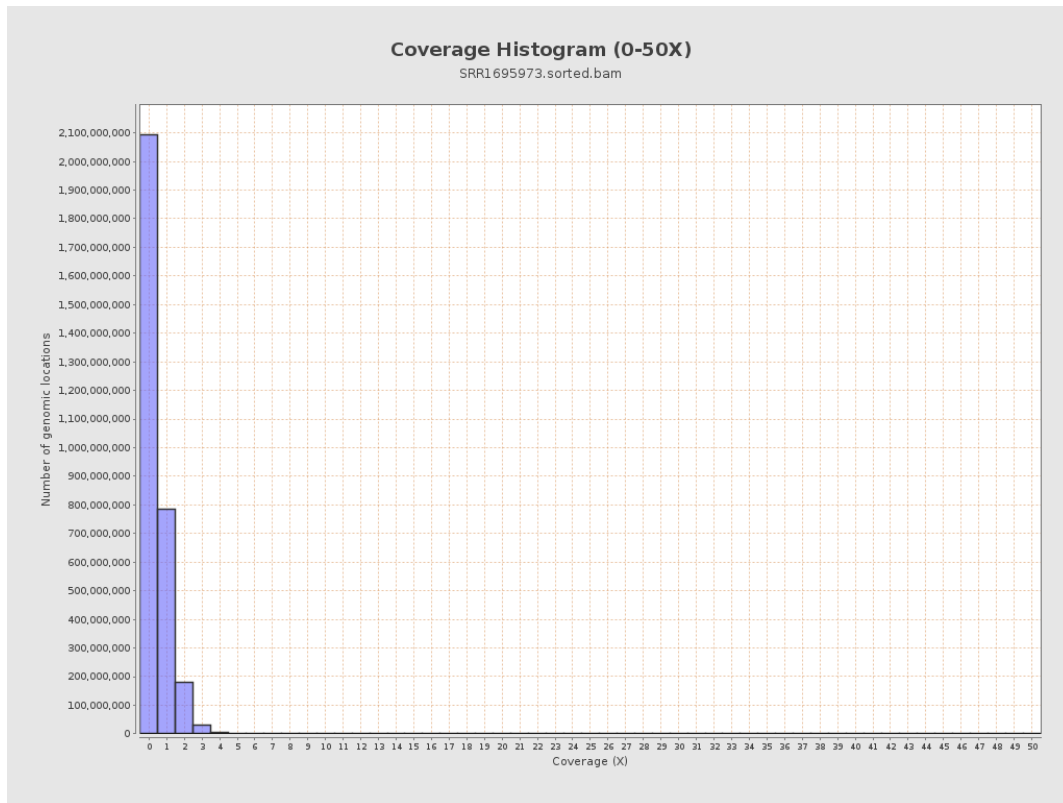
3. Results : Coverage across reference



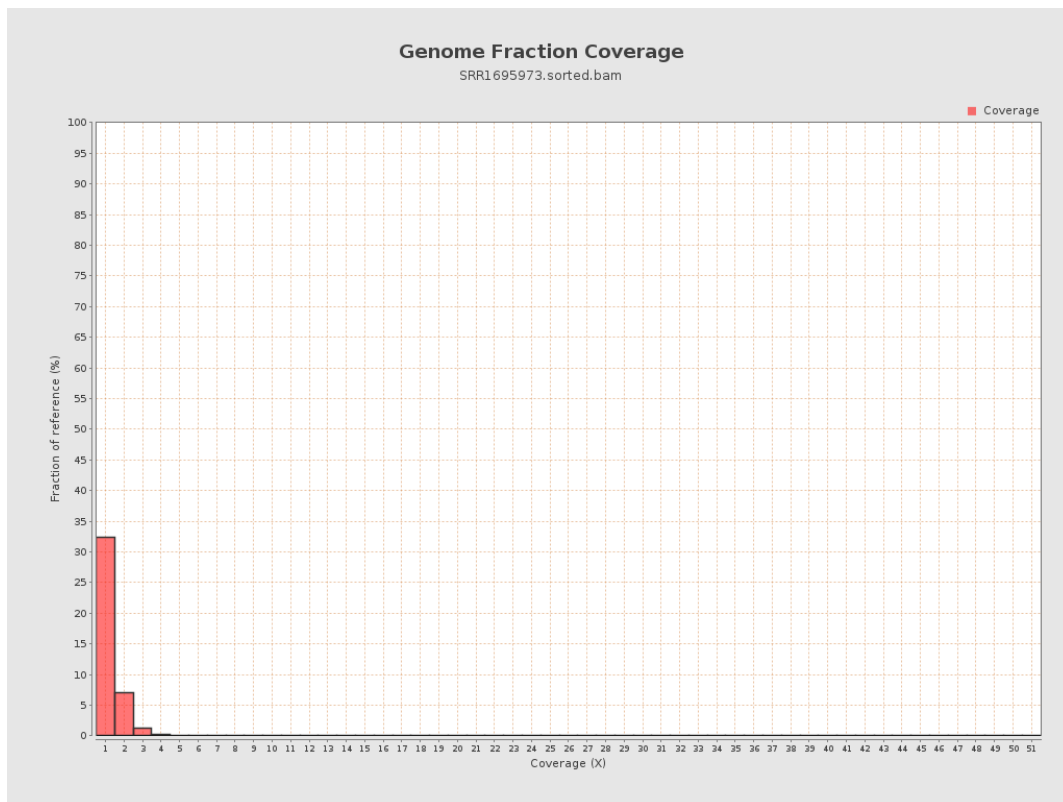
4. Results : Coverage Histogram



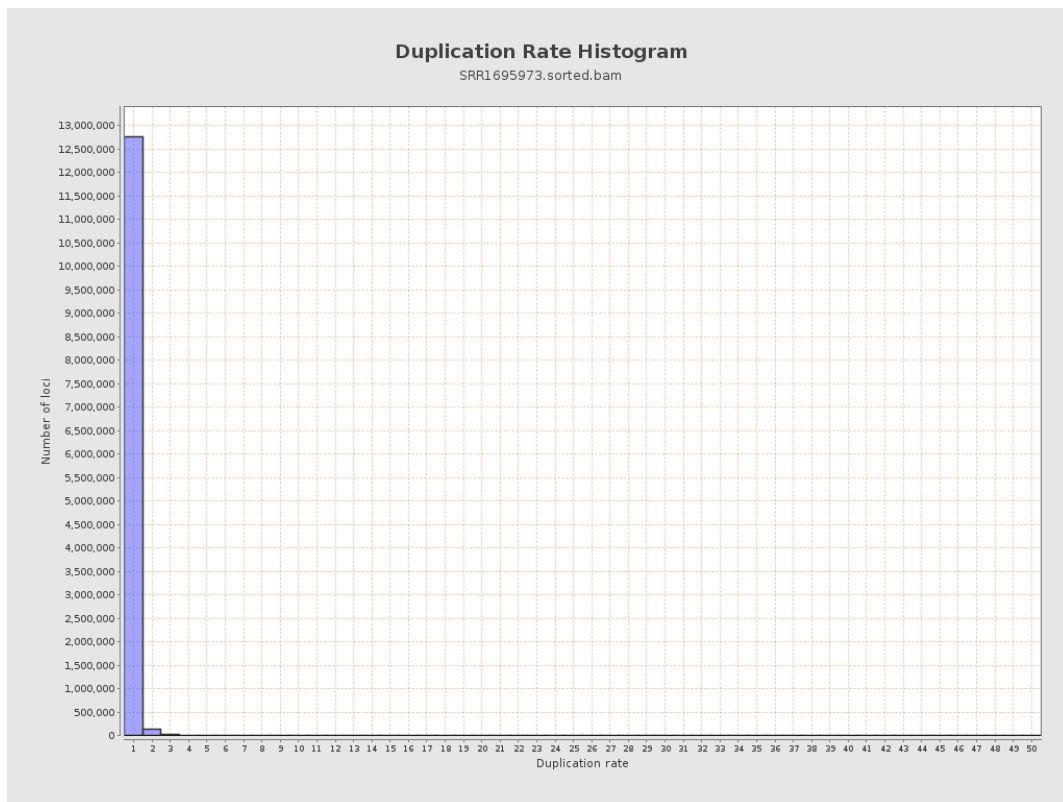
5. Results : Coverage Histogram (0-50X)



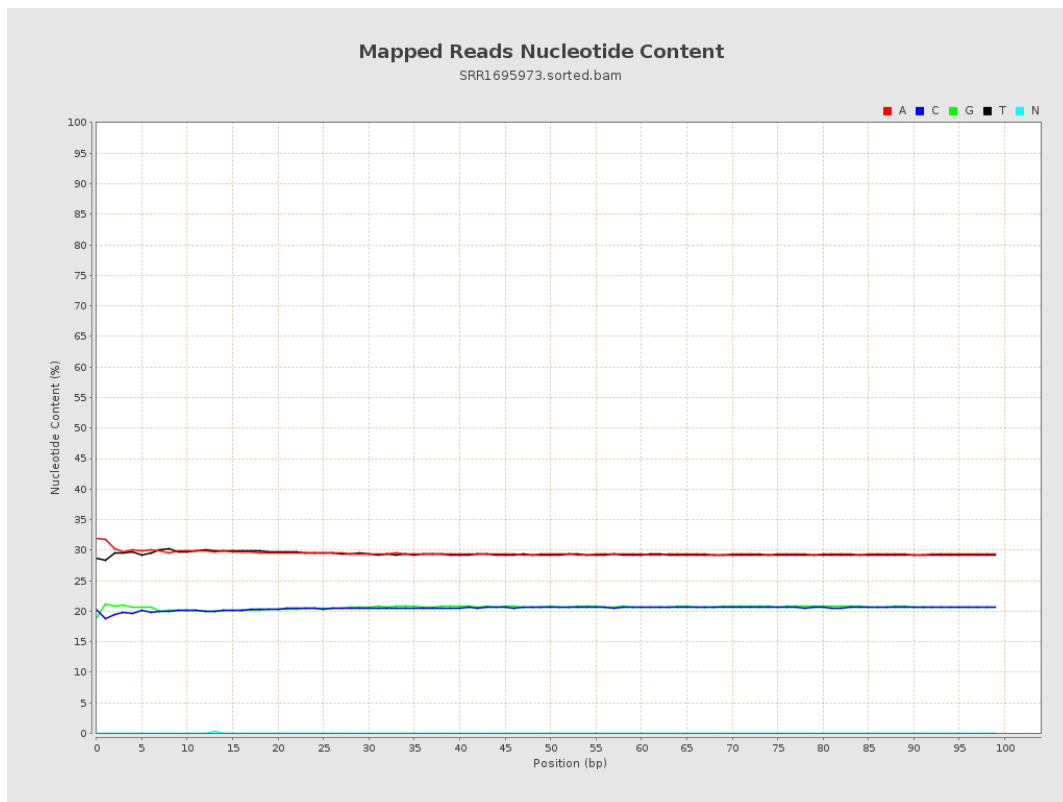
6. Results : Genome Fraction Coverage



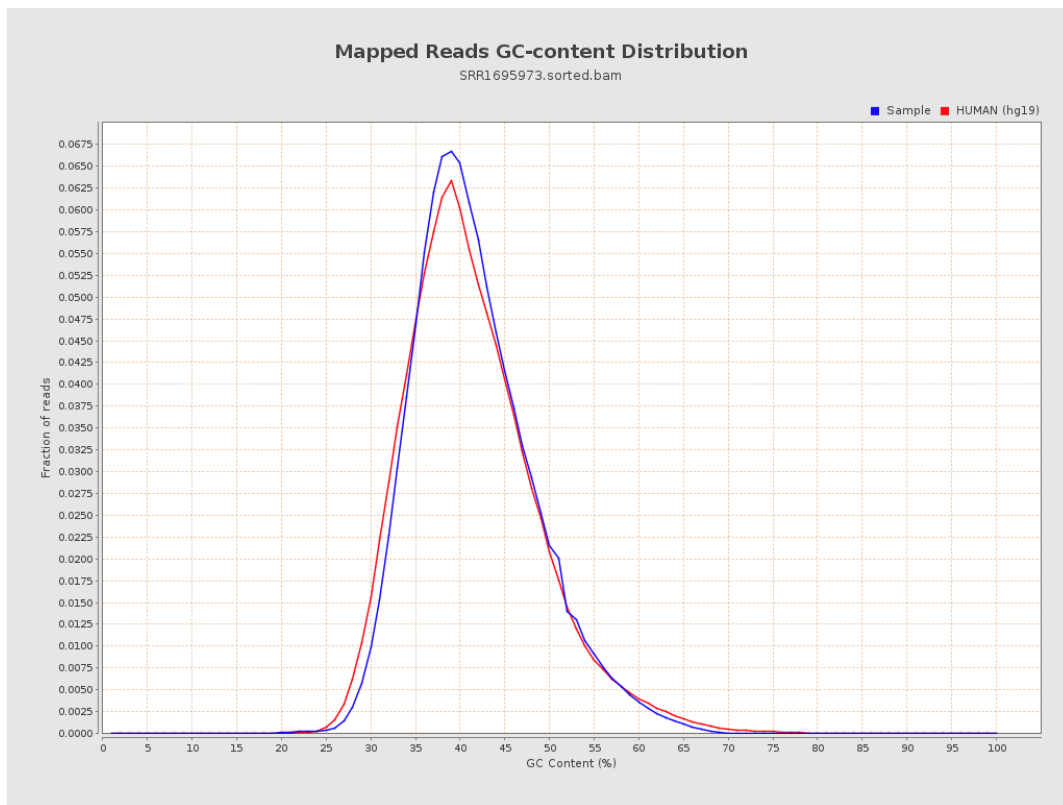
7. Results : Duplication Rate Histogram



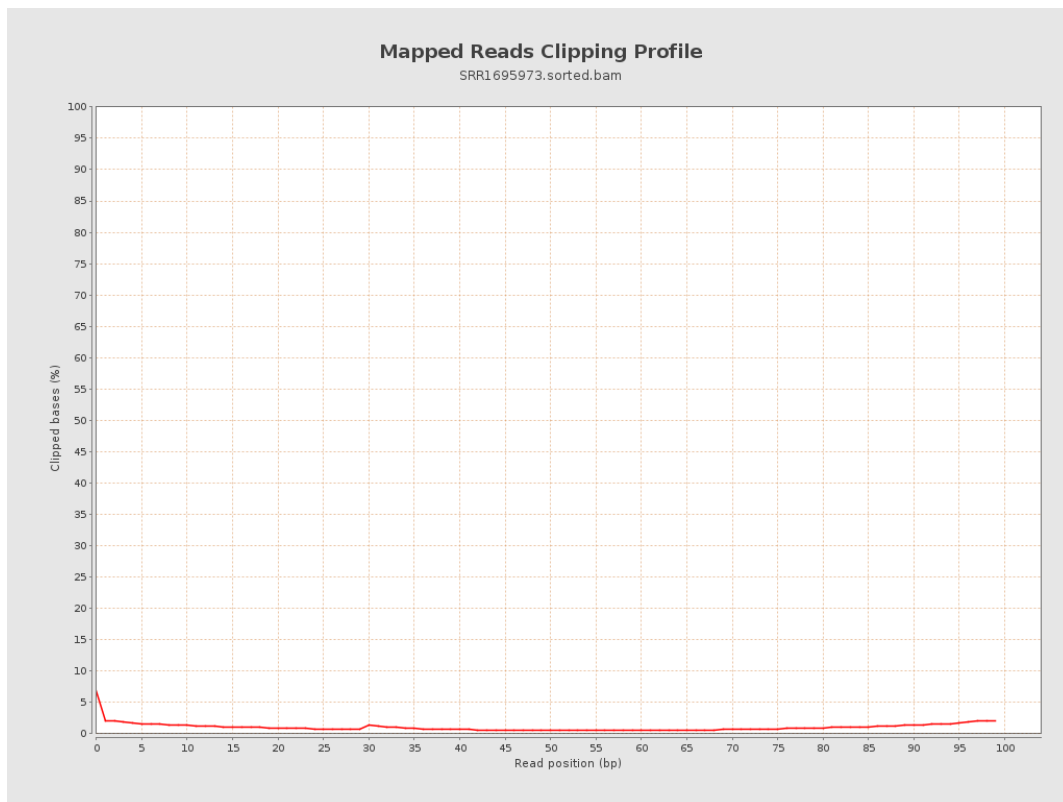
8. Results : Mapped Reads Nucleotide Content



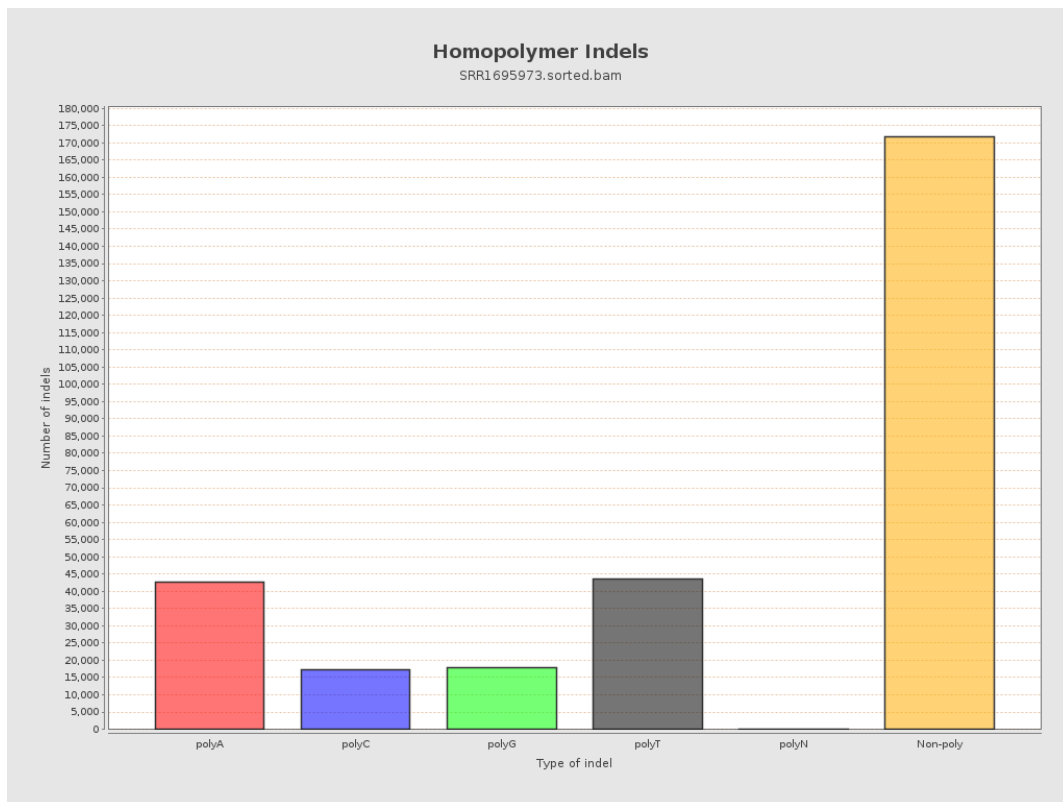
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



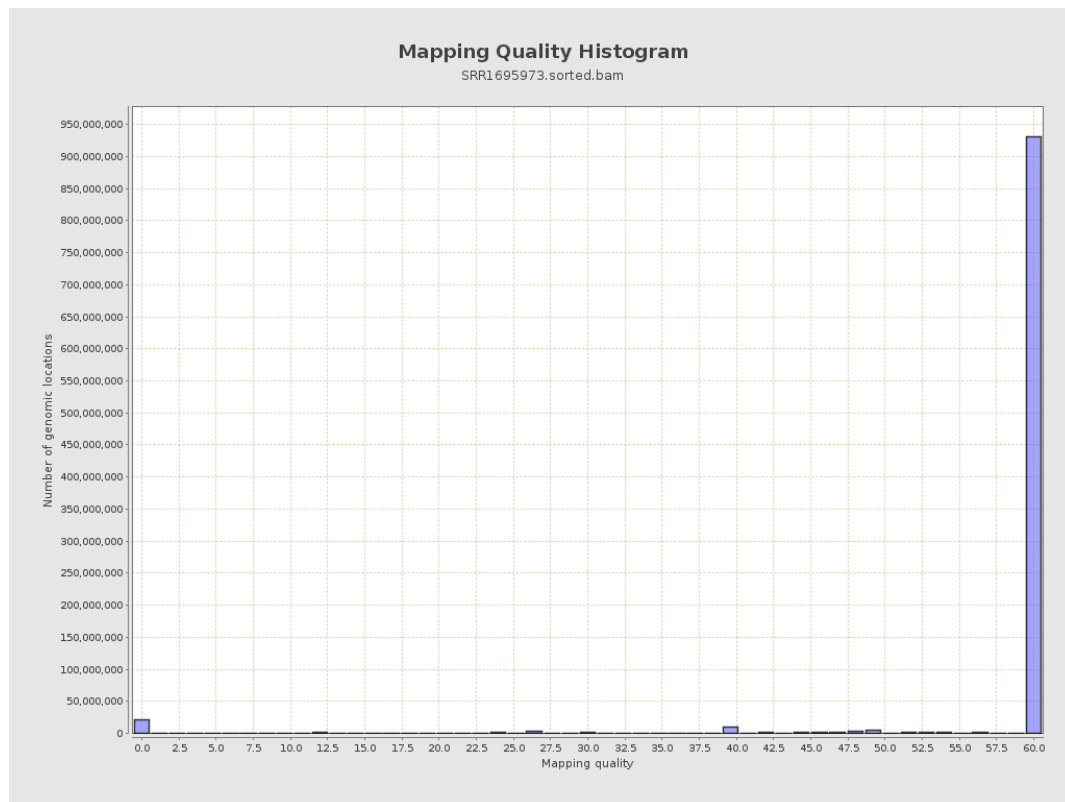
11. Results : Homopolymer Indels



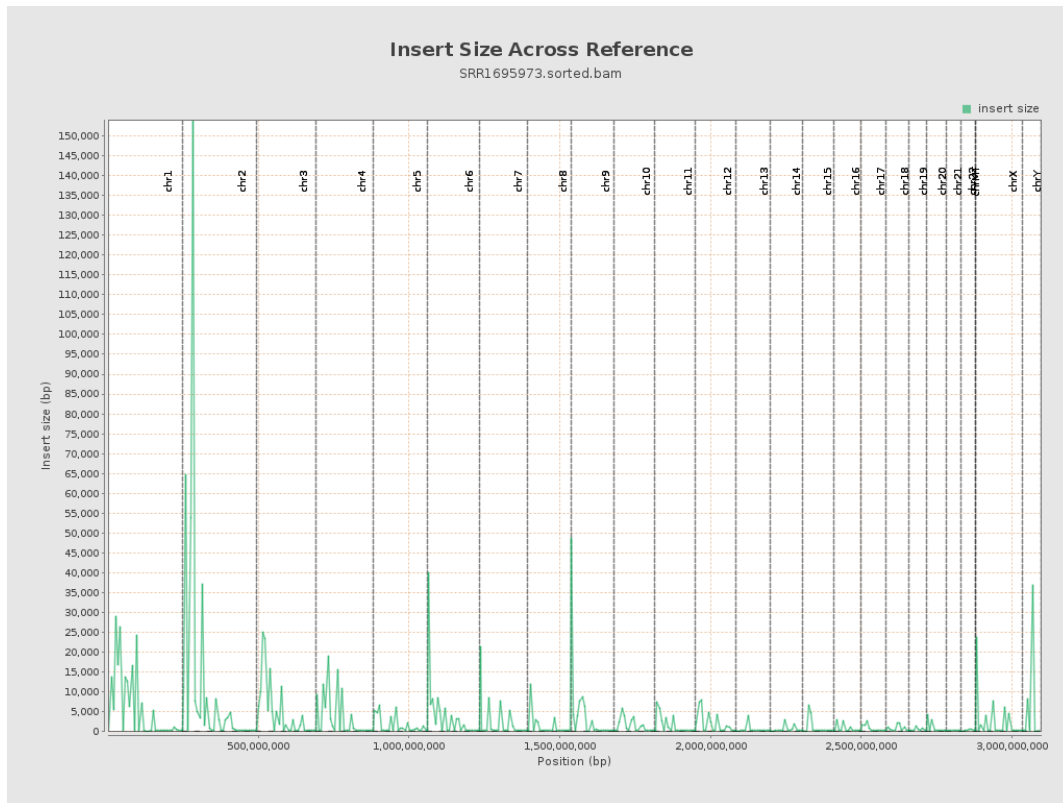
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

