

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/13 01:36:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695930.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 930 /seu_share/home/tujing/220232460/r eference/homo_bwa/hsa.fa SRR1695930_1.fastq.gz SRR1695930_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 01:36:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695930.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	29,872,826
Mapped reads	25,736,935 / 86.16%
Unmapped reads	4,135,891 / 13.84%
Mapped paired reads	25,736,935 / 86.16%
Mapped reads, first in pair	13,210,146 / 44.22%
Mapped reads, second in pair	12,526,789 / 41.93%
Mapped reads, both in pair	24,056,142 / 80.53%
Mapped reads, singletons	1,680,793 / 5.63%
Secondary alignments	0
Supplementary alignments	800,419 / 2.68%
Read min/max/mean length	30 / 100 / 100.99
Duplicated reads (estimated)	14,213,363 / 47.58%
Duplication rate	21.9%
Clipped reads	18,962,124 / 63.48%

2.2. ACGT Content

Number/percentage of A's	549,018,601 / 25.82%
Number/percentage of C's	376,308,117 / 17.69%
Number/percentage of T's	698,541,508 / 32.85%
Number/percentage of G's	500,626,121 / 23.54%
Number/percentage of N's	2,226,254 / 0.1%

GC Percentage	41.23%
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2.3. Coverage

Mean	0.6873
Standard Deviation	7.0163

2.4. Mapping Quality

Mean Mapping Quality	51.71
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2.5. Insert size

Mean	140,062.04
Standard Deviation	3,596,720.96
P25/Median/P75	297 / 317 / 331

2.6. Mismatches and indels

General error rate	1.27%
Mismatches	26,712,158
Insertions	170,538
Mapped reads with at least one insertion	0.65%
Deletions	478,419
Mapped reads with at least one deletion	1.83%
Homopolymer indels	46.89%

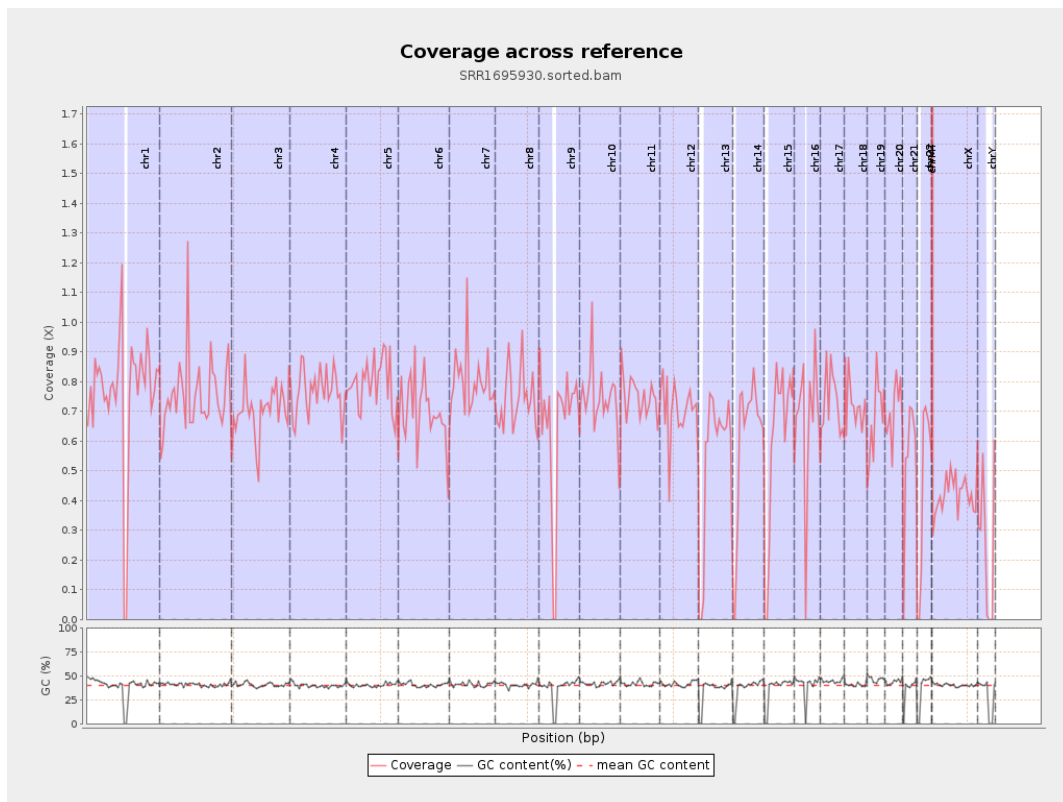
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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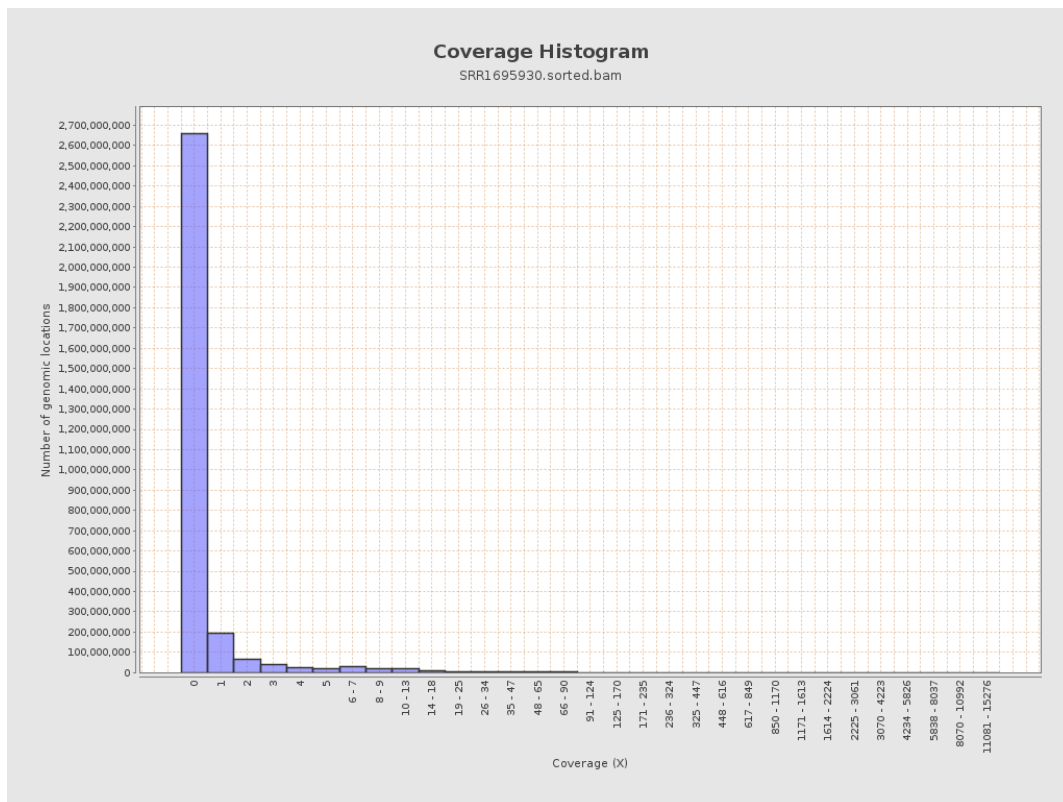
		bases	coverage	deviation
chr1	249250621	192285297	0.7715	10.2411
chr2	243199373	184137178	0.7571	7.8806
chr3	198022430	139063236	0.7023	4.3951
chr4	191154276	146199836	0.7648	4.7772
chr5	180915260	143155332	0.7913	4.7682
chr6	171115067	120096769	0.7018	5.3118
chr7	159138663	127215482	0.7994	9.9044
chr8	146364022	107233897	0.7327	11.8772
chr9	141213431	90551709	0.6412	5.8579
chr10	135534747	101173420	0.7465	6.4751
chr11	135006516	100405347	0.7437	5.9661
chr12	133851895	94071764	0.7028	4.4748
chr13	115169878	62620893	0.5437	3.8359
chr14	107349540	64663200	0.6024	4.255
chr15	102531392	61391559	0.5988	4.0855
chr16	90354753	59868352	0.6626	4.2081
chr17	81195210	59464880	0.7324	4.736
chr18	78077248	56028875	0.7176	16.191
chr19	59128983	39992331	0.6764	7.5391
chr20	63025520	44192826	0.7012	4.5996
chr21	48129895	26735825	0.5555	4.2819
chr22	51304566	23001552	0.4483	4.0115
chrMT	16571	3440478	207.6204	163.4822
chrX	155270560	64978668	0.4185	3.7874

chrY	59373566	15594060	0.2626	3.4088
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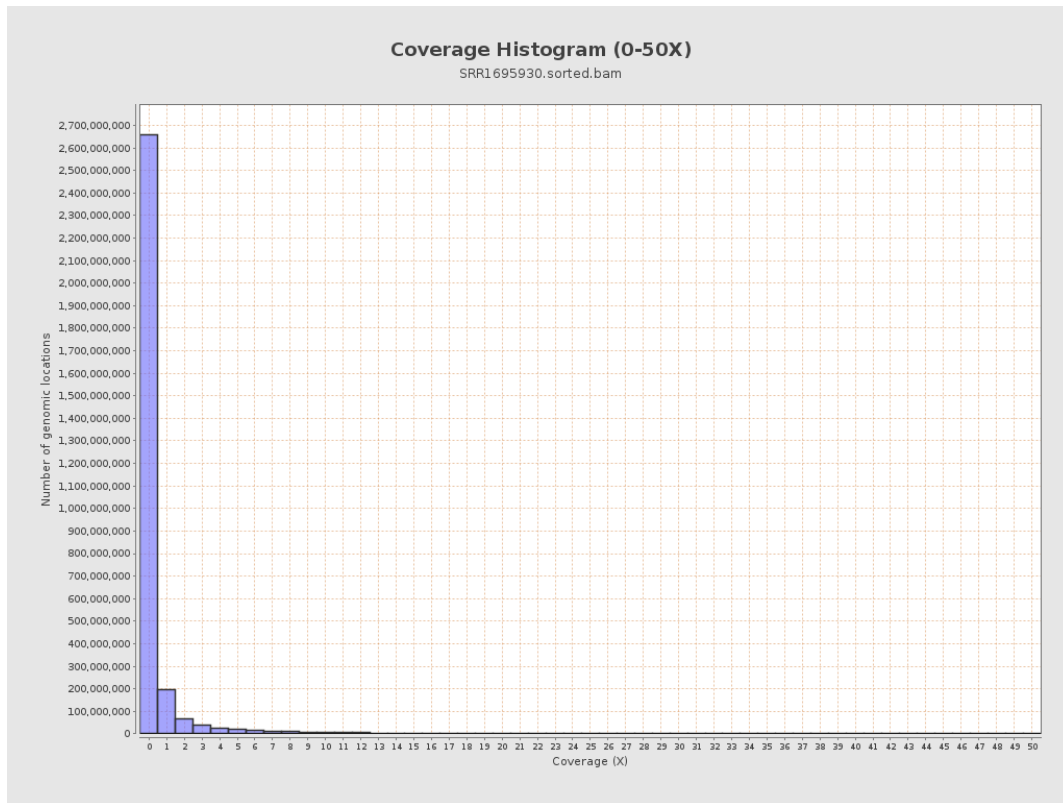
3. Results : Coverage across reference



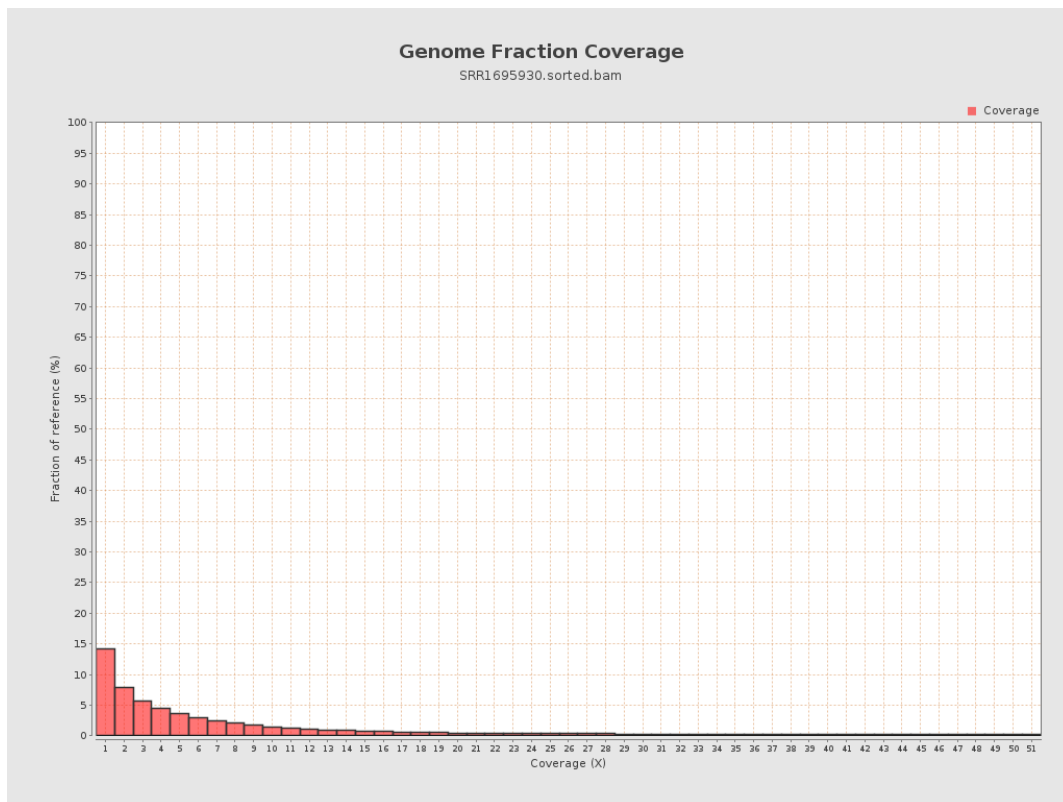
4. Results : Coverage Histogram



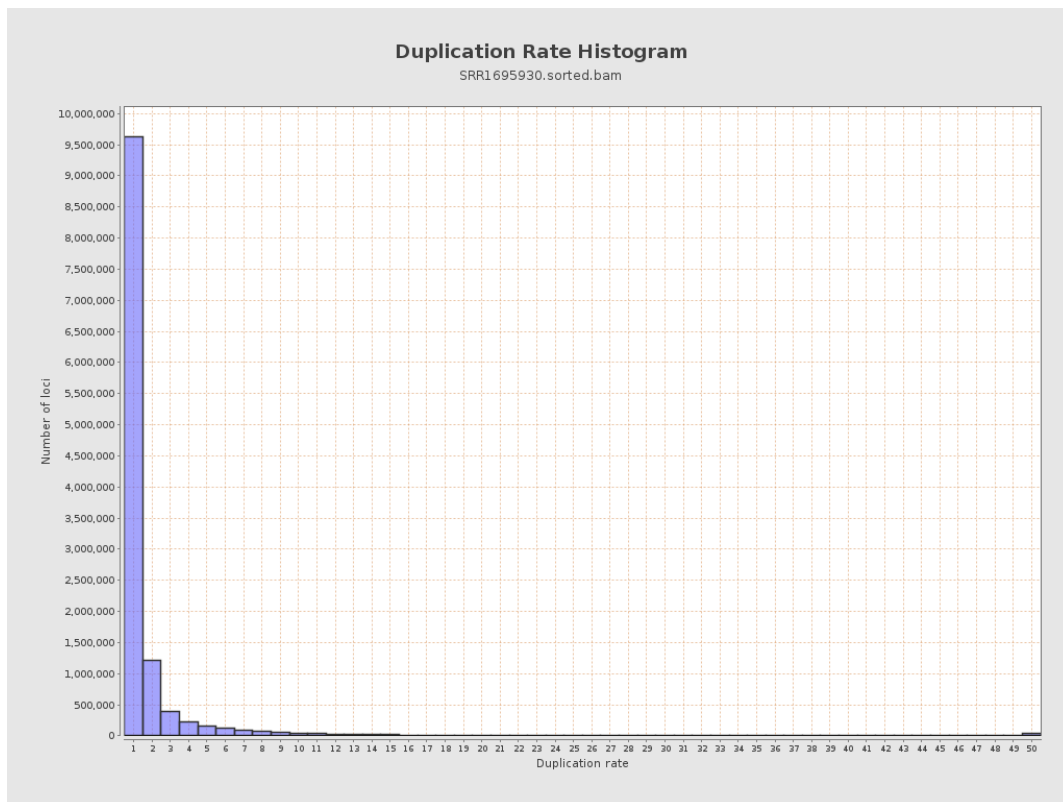
5. Results : Coverage Histogram (0-50X)



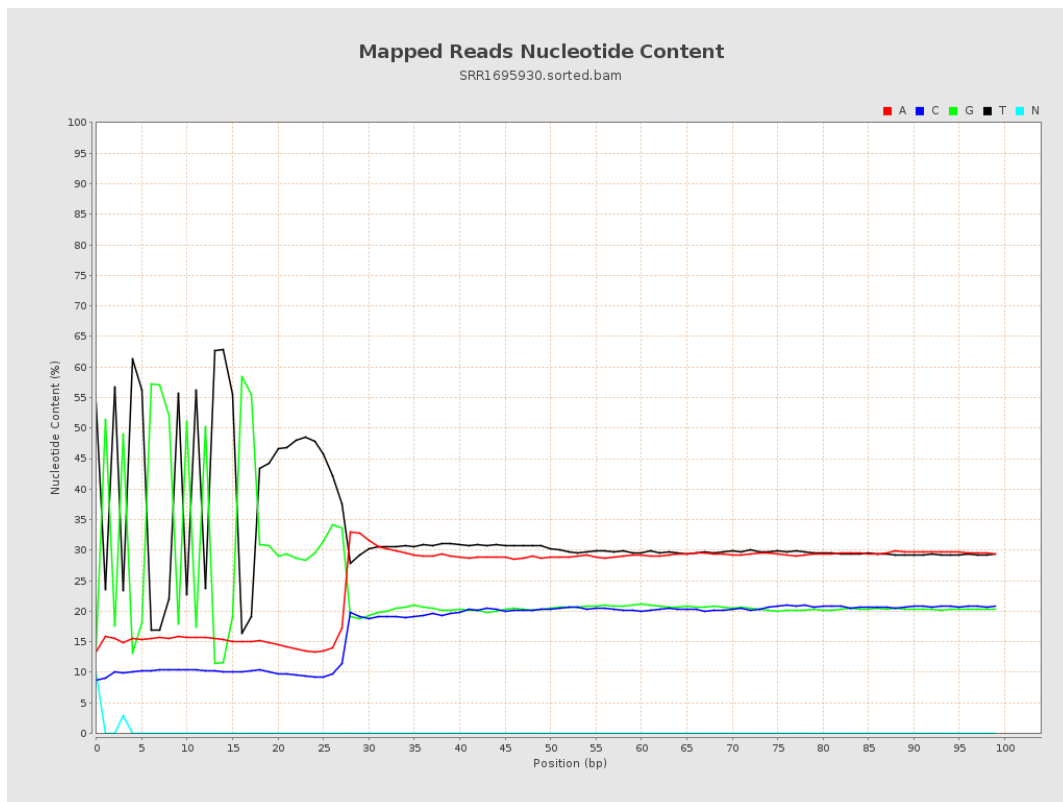
6. Results : Genome Fraction Coverage



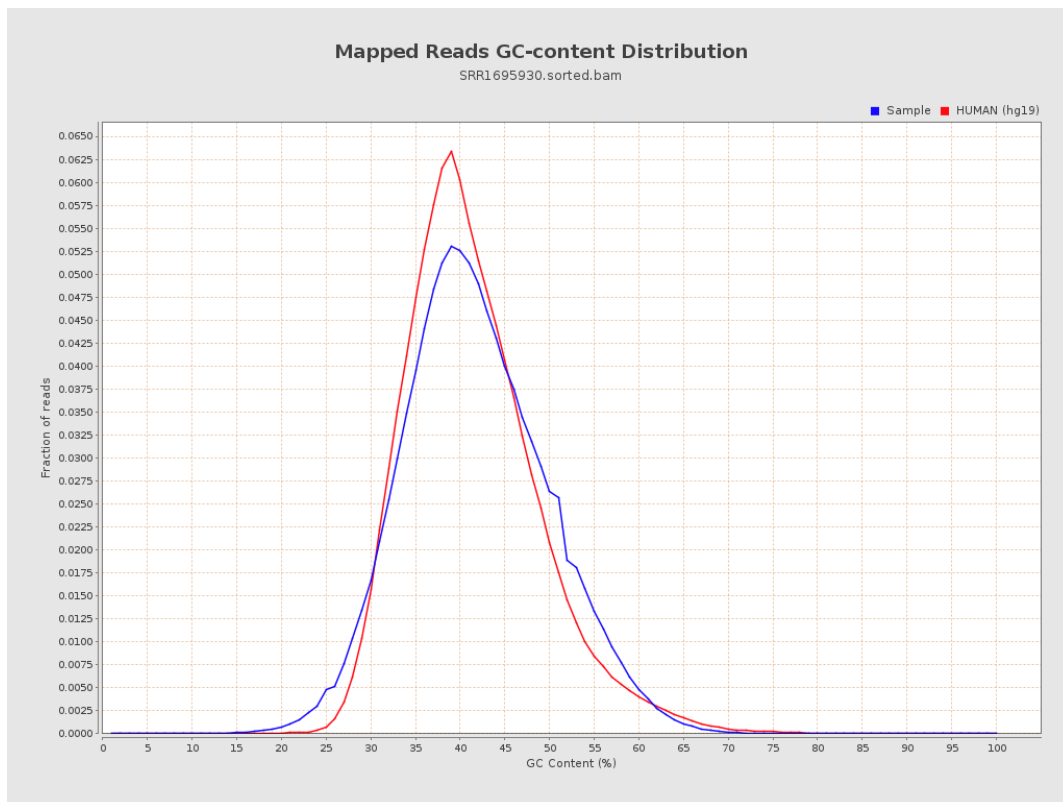
7. Results : Duplication Rate Histogram



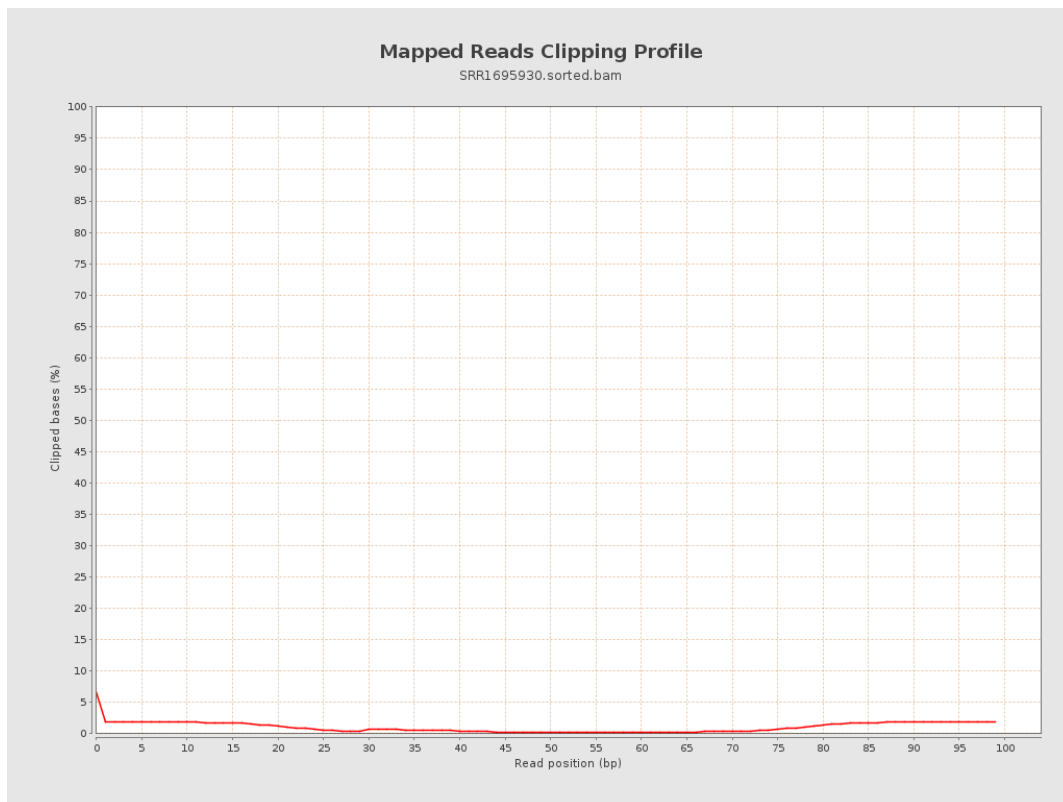
8. Results : Mapped Reads Nucleotide Content



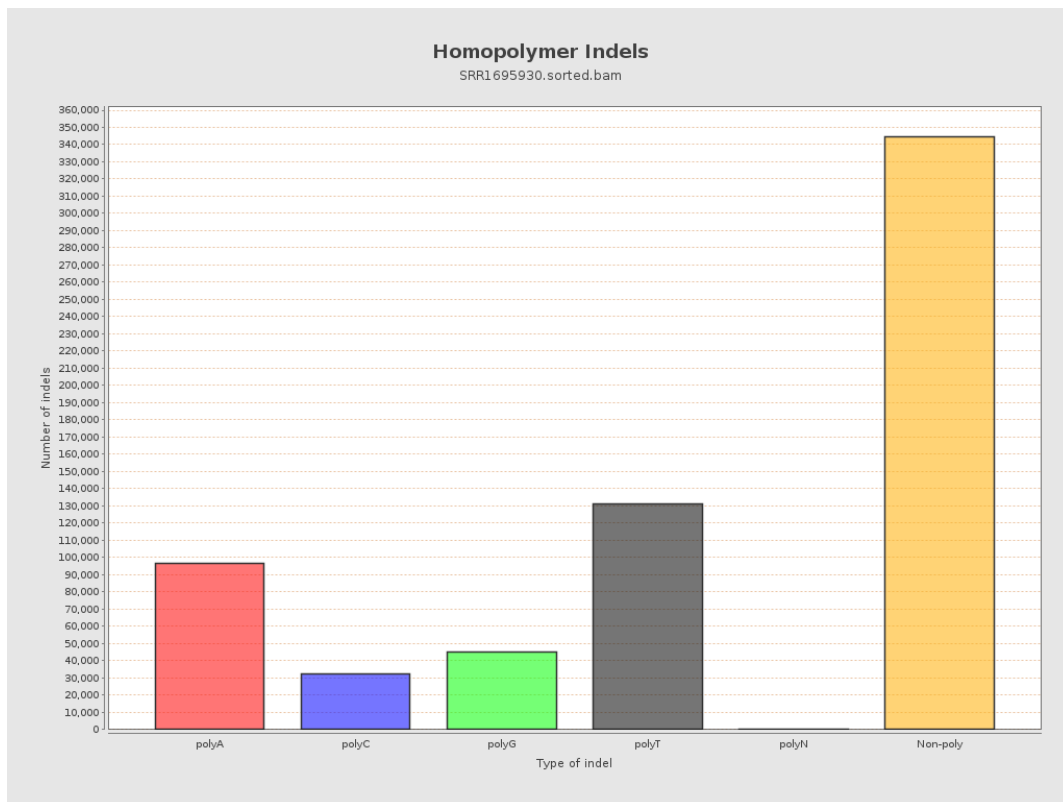
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



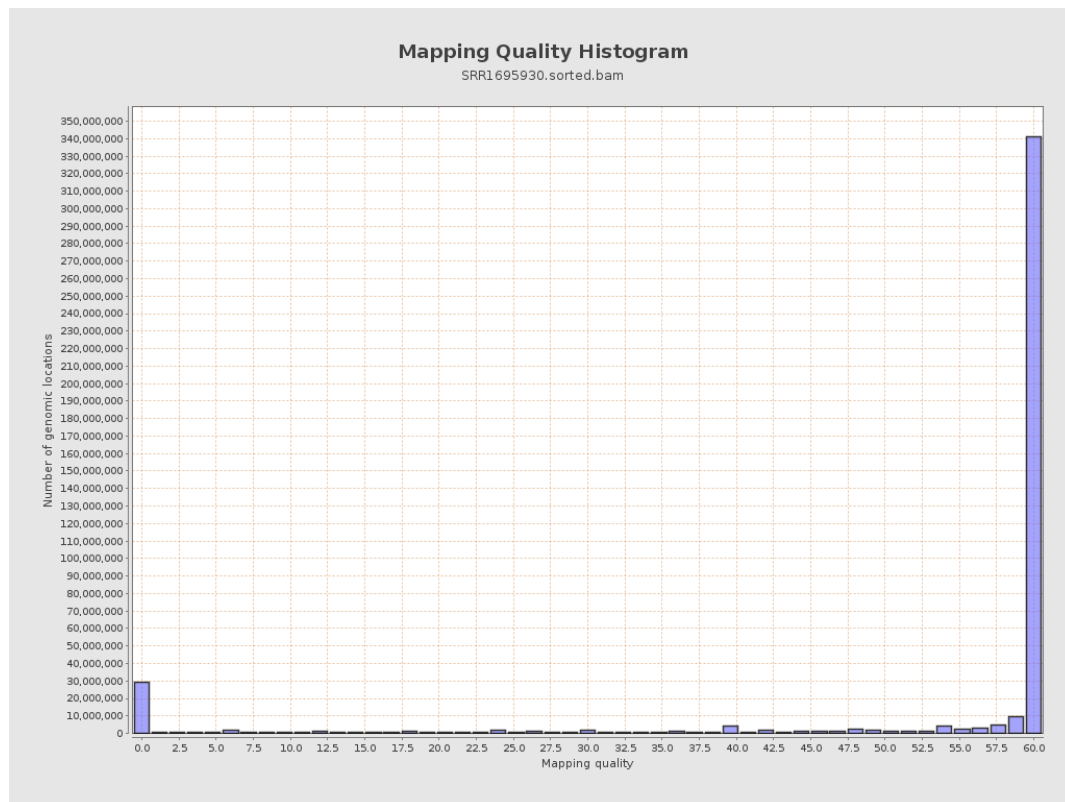
11. Results : Homopolymer Indels



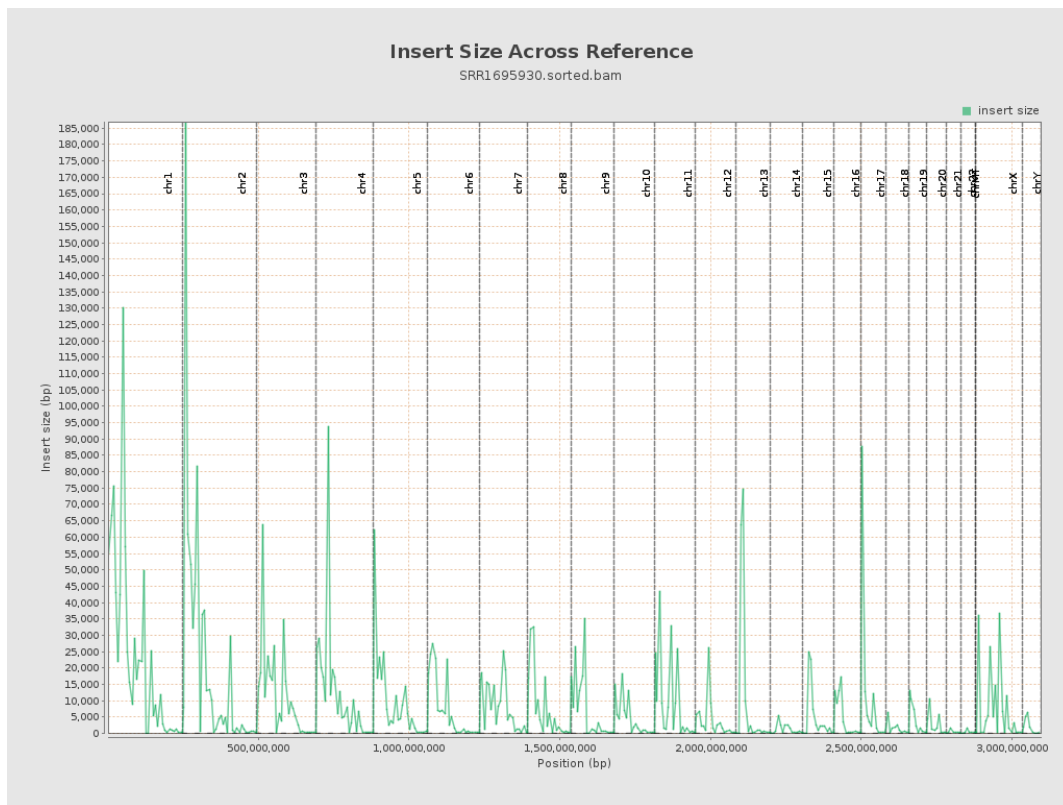
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

