

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/13 00:45:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695928.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_SRR1695928 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695928_1.fastq.gz SRR1695928_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 00:45:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695928.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,641,988
Mapped reads	6,567,461 / 85.94%
Unmapped reads	1,074,527 / 14.06%
Mapped paired reads	6,567,461 / 85.94%
Mapped reads, first in pair	3,320,847 / 43.46%
Mapped reads, second in pair	3,246,614 / 42.48%
Mapped reads, both in pair	6,053,040 / 79.21%
Mapped reads, singletons	514,421 / 6.73%
Secondary alignments	0
Supplementary alignments	162,313 / 2.12%
Read min/max/mean length	30 / 100 / 100.79
Duplicated reads (estimated)	1,992,818 / 26.08%
Duplication rate	17.25%
Clipped reads	4,267,319 / 55.84%

2.2. ACGT Content

Number/percentage of A's	146,581,837 / 26.49%
Number/percentage of C's	101,234,107 / 18.3%
Number/percentage of T's	177,943,288 / 32.16%
Number/percentage of G's	127,385,266 / 23.02%
Number/percentage of N's	177,141 / 0.03%

GC Percentage	41.32%
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2.3. Coverage

Mean	0.1788
Standard Deviation	1.6336

2.4. Mapping Quality

Mean Mapping Quality	51.78
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2.5. Insert size

Mean	146,226.08
Standard Deviation	3,701,985.89
P25/Median/P75	303 / 322 / 335

2.6. Mismatches and indels

General error rate	1.51%
Mismatches	8,266,603
Insertions	45,826
Mapped reads with at least one insertion	0.69%
Deletions	123,507
Mapped reads with at least one deletion	1.85%
Homopolymer indels	45.22%

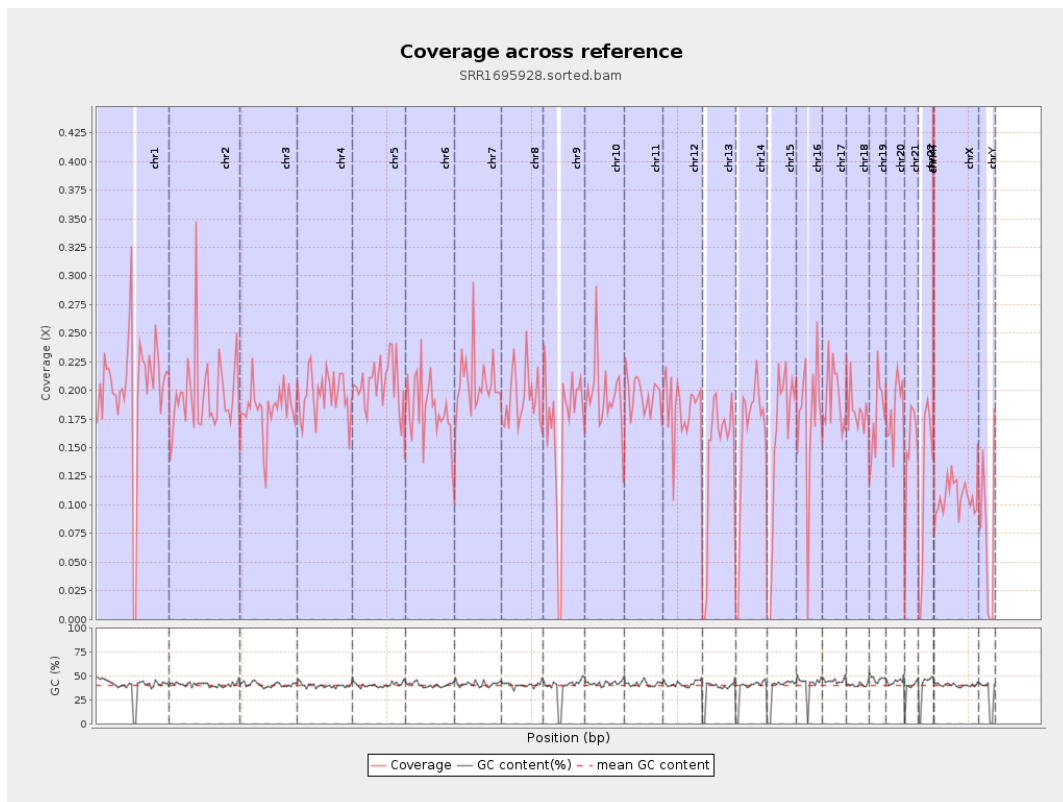
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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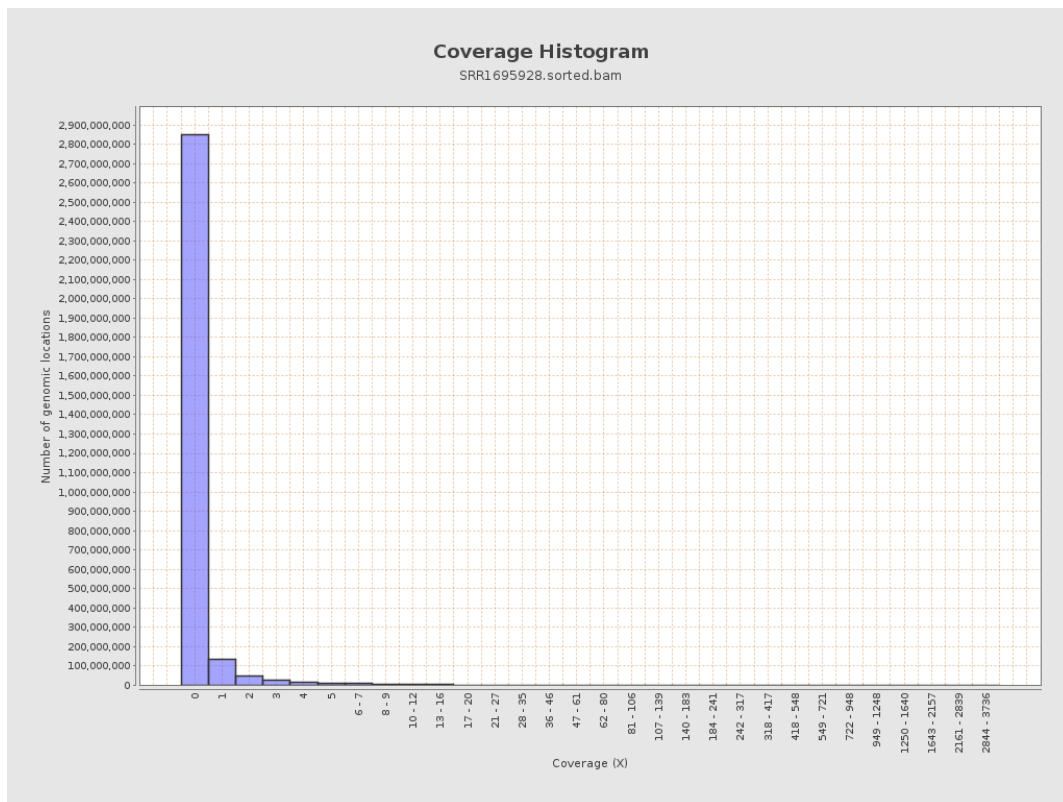
		bases	coverage	deviation
chr1	249250621	50100273	0.201	2.7403
chr2	243199373	47933902	0.1971	2.0915
chr3	198022430	36252114	0.1831	0.9131
chr4	191154276	37368457	0.1955	1.0064
chr5	180915260	37132144	0.2052	0.9868
chr6	171115067	31171688	0.1822	1.2372
chr7	159138663	33061438	0.2078	2.0681
chr8	146364022	28068102	0.1918	2.6876
chr9	141213431	23466775	0.1662	1.4191
chr10	135534747	26499859	0.1955	1.5251
chr11	135006516	26145425	0.1937	1.4086
chr12	133851895	24602847	0.1838	0.9395
chr13	115169878	16210516	0.1408	0.8061
chr14	107349540	16810826	0.1566	0.9005
chr15	102531392	15926359	0.1553	0.8553
chr16	90354753	15907265	0.1761	0.932
chr17	81195210	15751072	0.194	1.0927
chr18	78077248	14333150	0.1836	3.2908
chr19	59128983	10523214	0.178	1.7827
chr20	63025520	11505487	0.1826	0.9737
chr21	48129895	7026984	0.146	0.9405
chr22	51304566	6003340	0.117	0.8349
chrMT	16571	862998	52.0788	33.9343
chrX	155270560	16558992	0.1066	0.8135

chrY	59373566	4315466	0.0727	0.94
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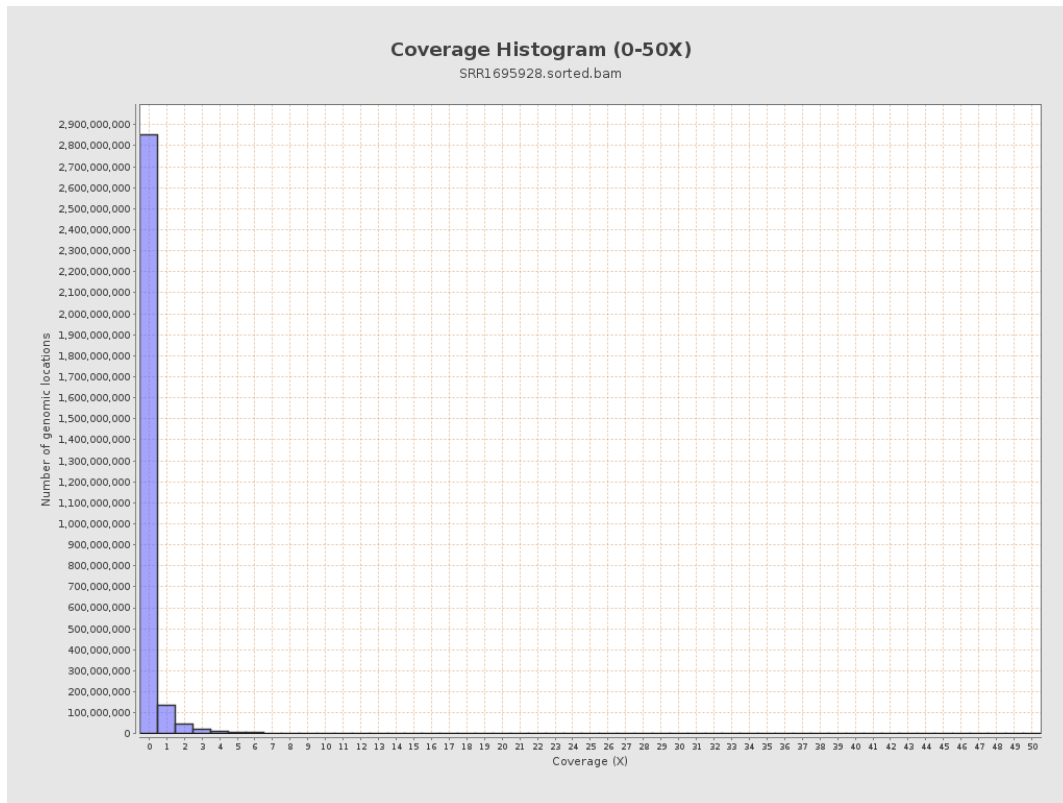
3. Results : Coverage across reference



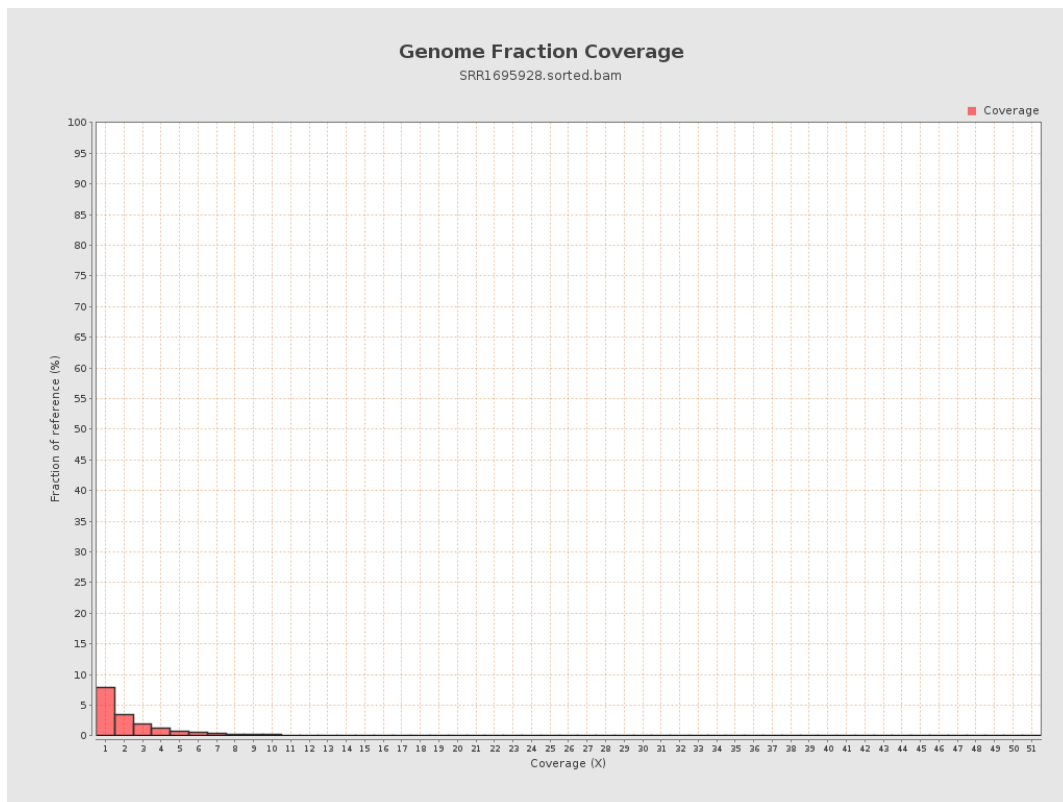
4. Results : Coverage Histogram



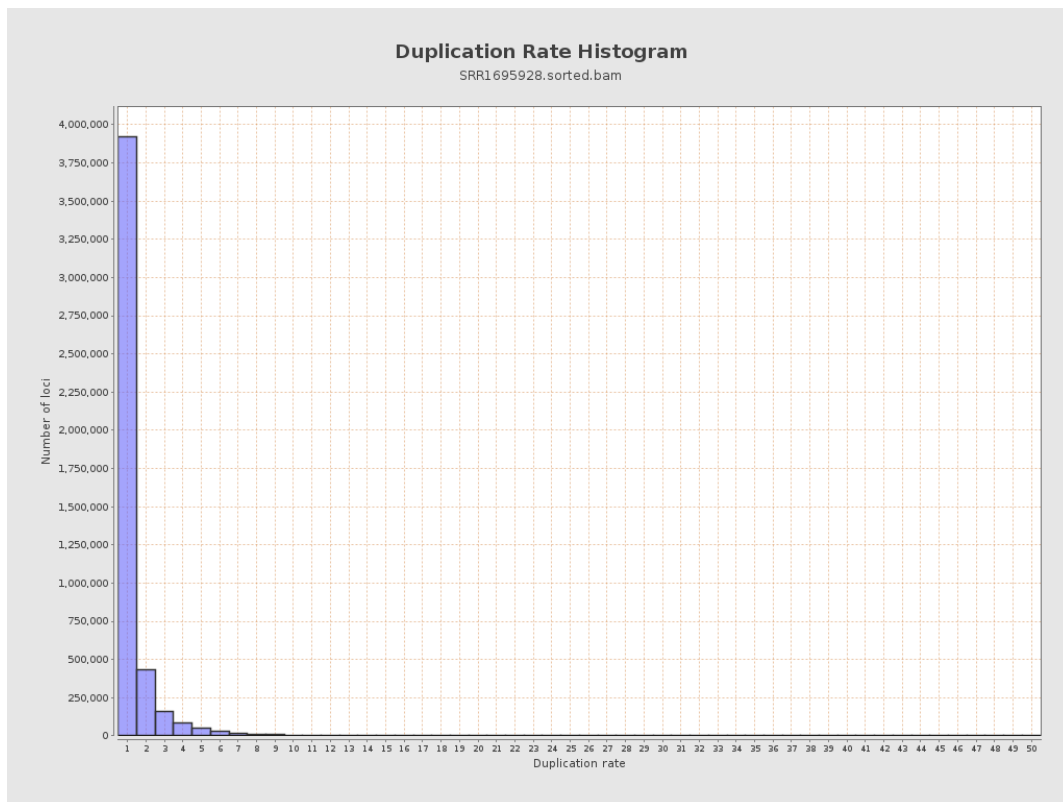
5. Results : Coverage Histogram (0-50X)



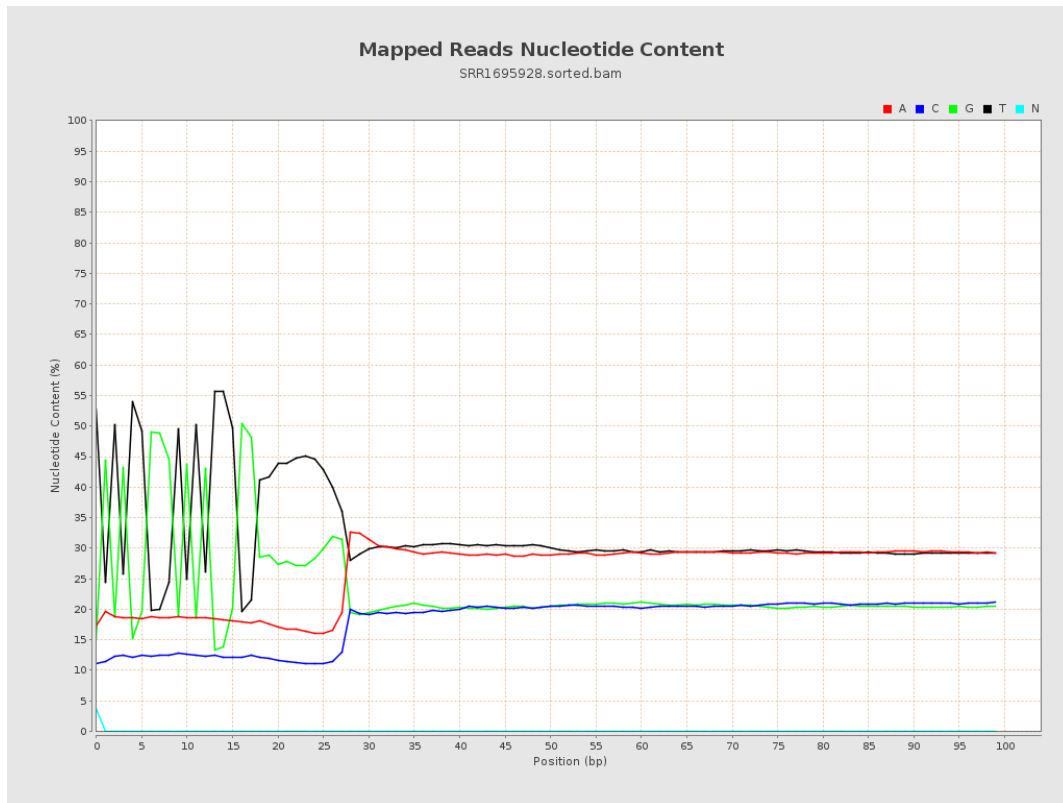
6. Results : Genome Fraction Coverage



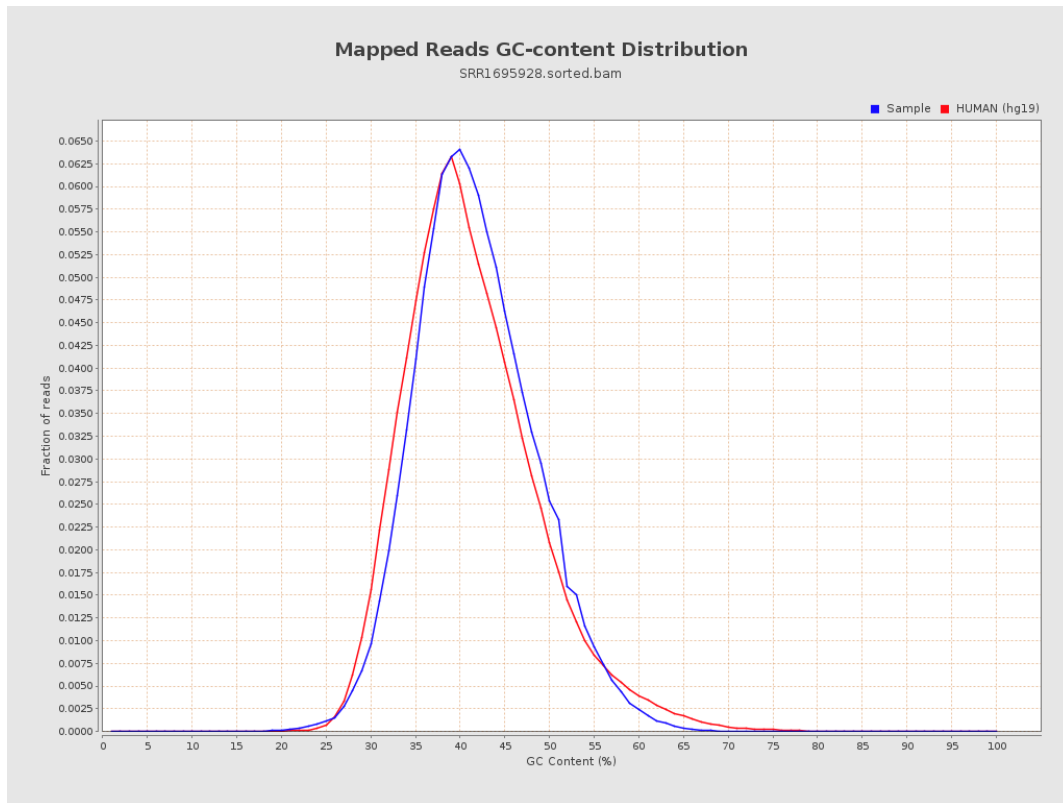
7. Results : Duplication Rate Histogram



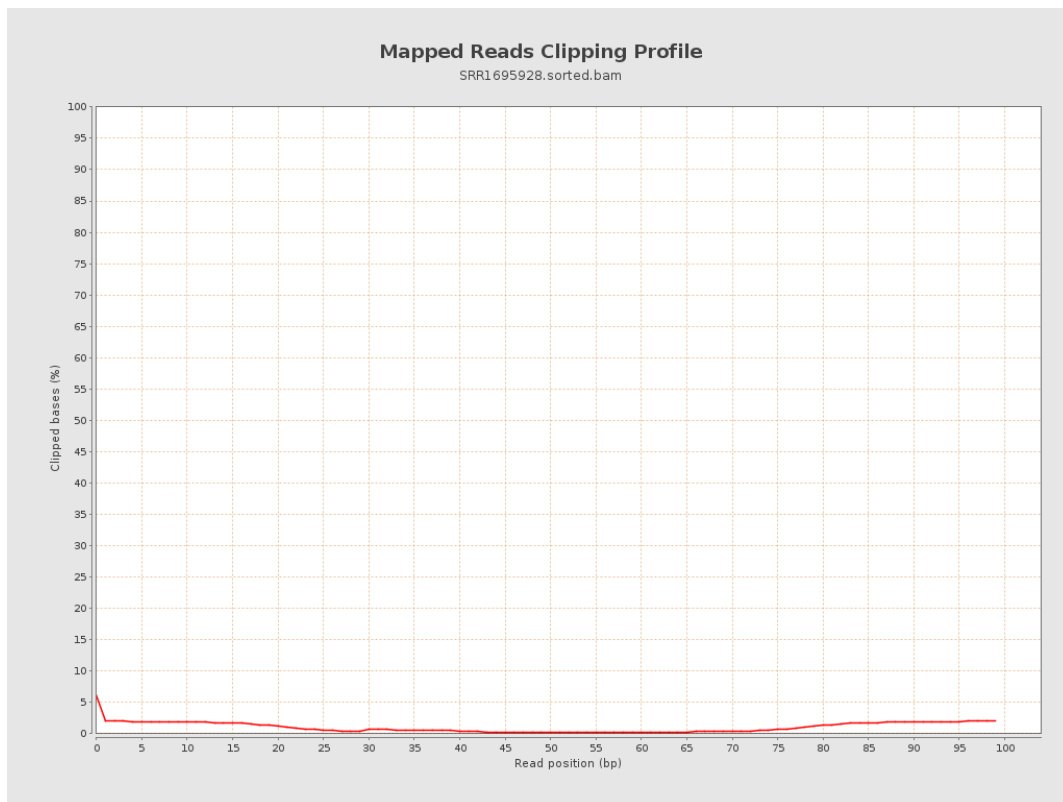
8. Results : Mapped Reads Nucleotide Content



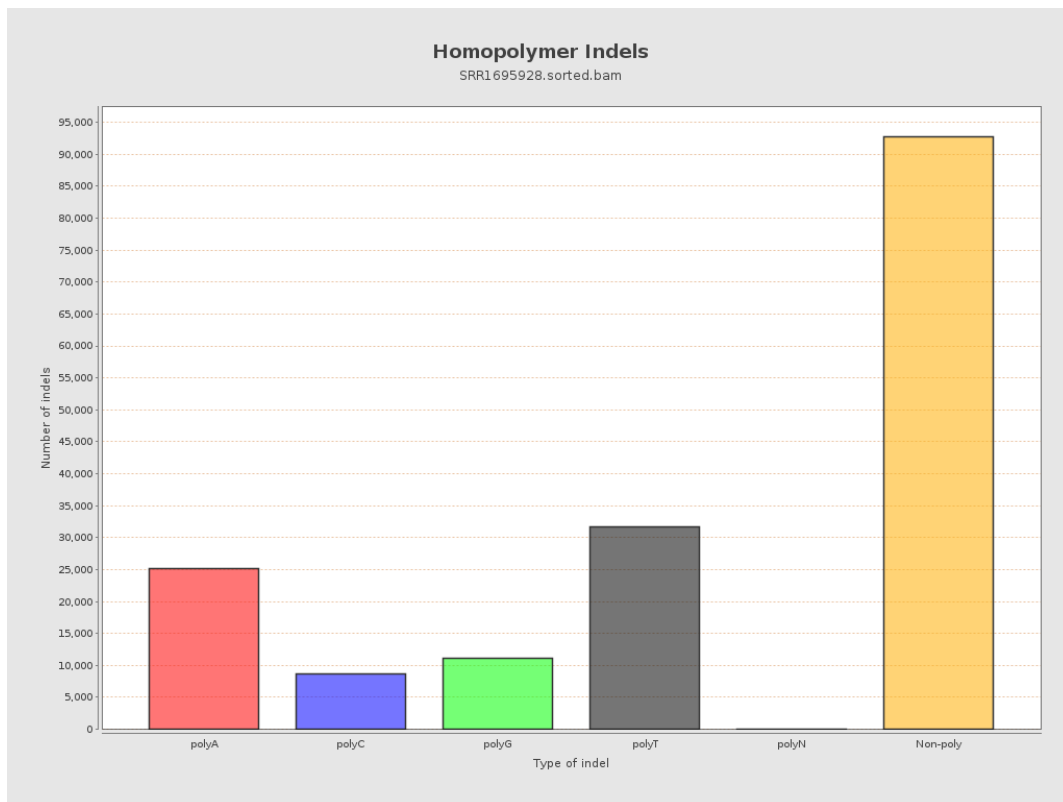
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



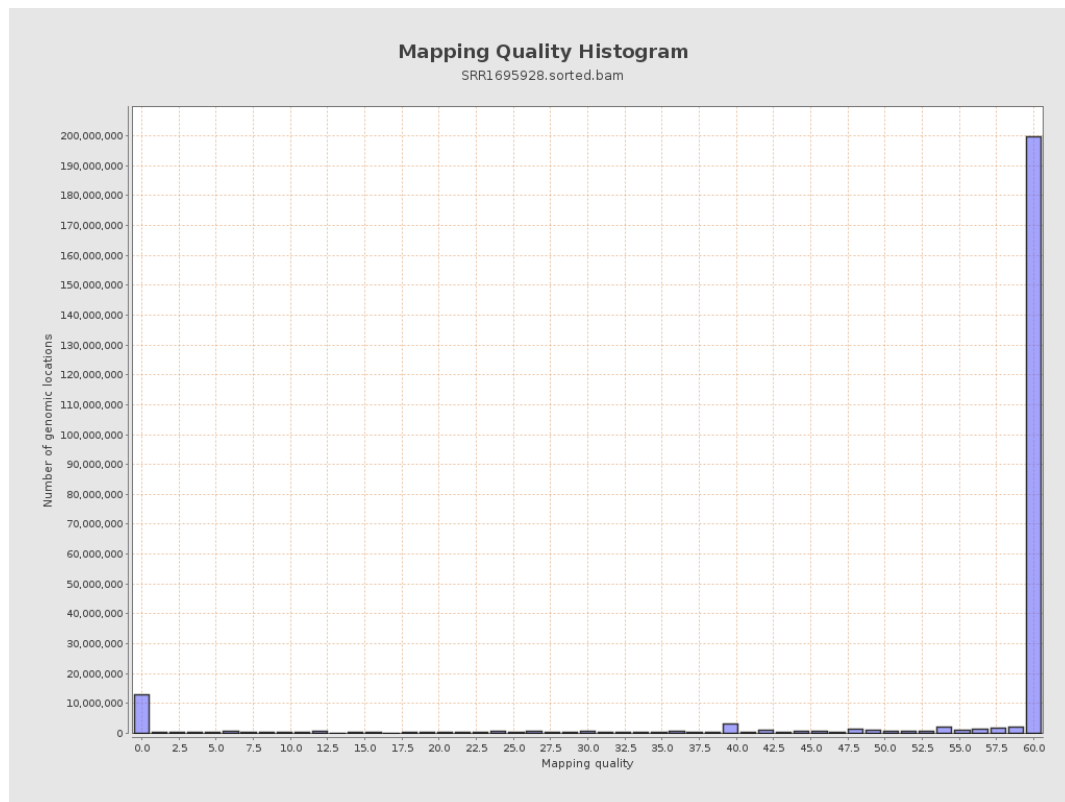
11. Results : Homopolymer Indels



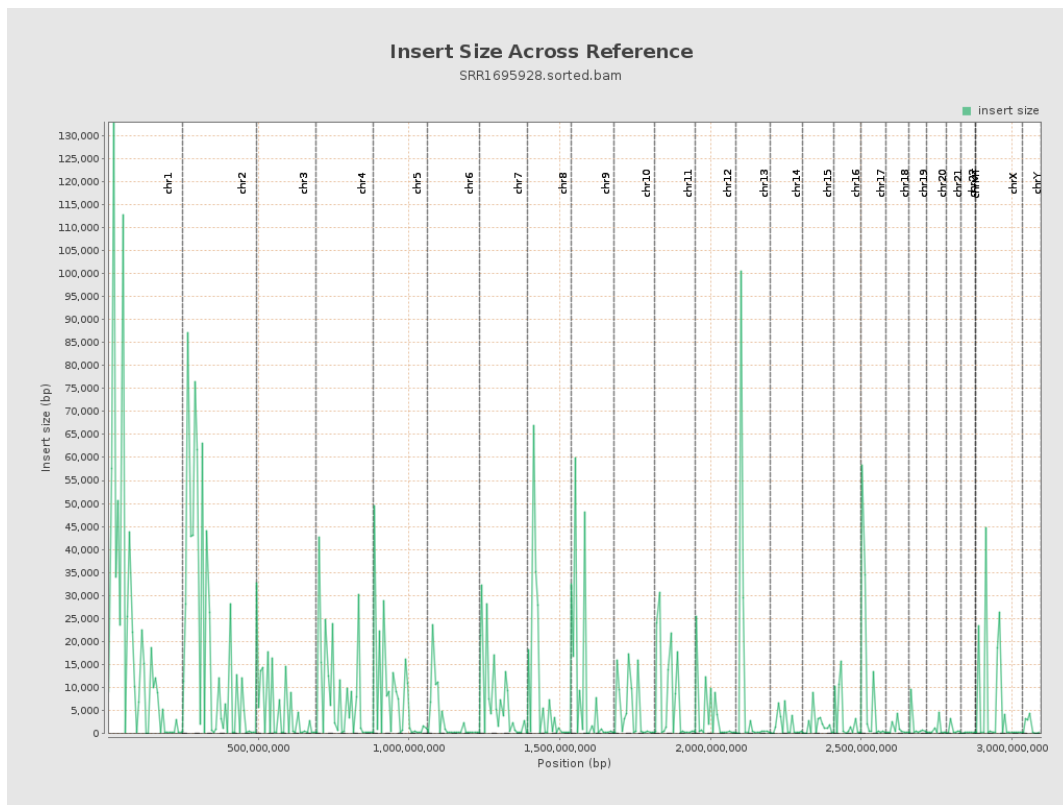
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

