

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/12 20:58:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695922.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 922 /seu_share/home/tujing/220232460/r eference/homo_bwa/hsa.fa SRR1695922_1.fastq.gz SRR1695922_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Thu Sep 12 20:58:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695922.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,113,204
Mapped reads	2,070,193 / 97.96%
Unmapped reads	43,011 / 2.04%
Mapped paired reads	2,070,193 / 97.96%
Mapped reads, first in pair	1,037,079 / 49.08%
Mapped reads, second in pair	1,033,114 / 48.89%
Mapped reads, both in pair	2,065,188 / 97.73%
Mapped reads, singletons	5,005 / 0.24%
Secondary alignments	0
Supplementary alignments	61,058 / 2.89%
Read min/max/mean length	30 / 150 / 151.54
Duplicated reads (estimated)	15,051 / 0.71%
Duplication rate	0.62%
Clipped reads	194,755 / 9.22%

2.2. ACGT Content

Number/percentage of A's	91,007,462 / 29.48%
Number/percentage of C's	63,248,978 / 20.49%
Number/percentage of T's	90,746,564 / 29.4%
Number/percentage of G's	63,639,181 / 20.62%
Number/percentage of N's	40,677 / 0.01%

GC Percentage	41.11%
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2.3. Coverage

Mean	0.0997
Standard Deviation	0.5137

2.4. Mapping Quality

Mean Mapping Quality	55.16
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2.5. Insert size

Mean	35,134.32
Standard Deviation	1,737,584.75
P25/Median/P75	286 / 295 / 303

2.6. Mismatches and indels

General error rate	0.37%
Mismatches	1,068,883
Insertions	27,460
Mapped reads with at least one insertion	1.29%
Deletions	34,565
Mapped reads with at least one deletion	1.63%
Homopolymer indels	48.72%

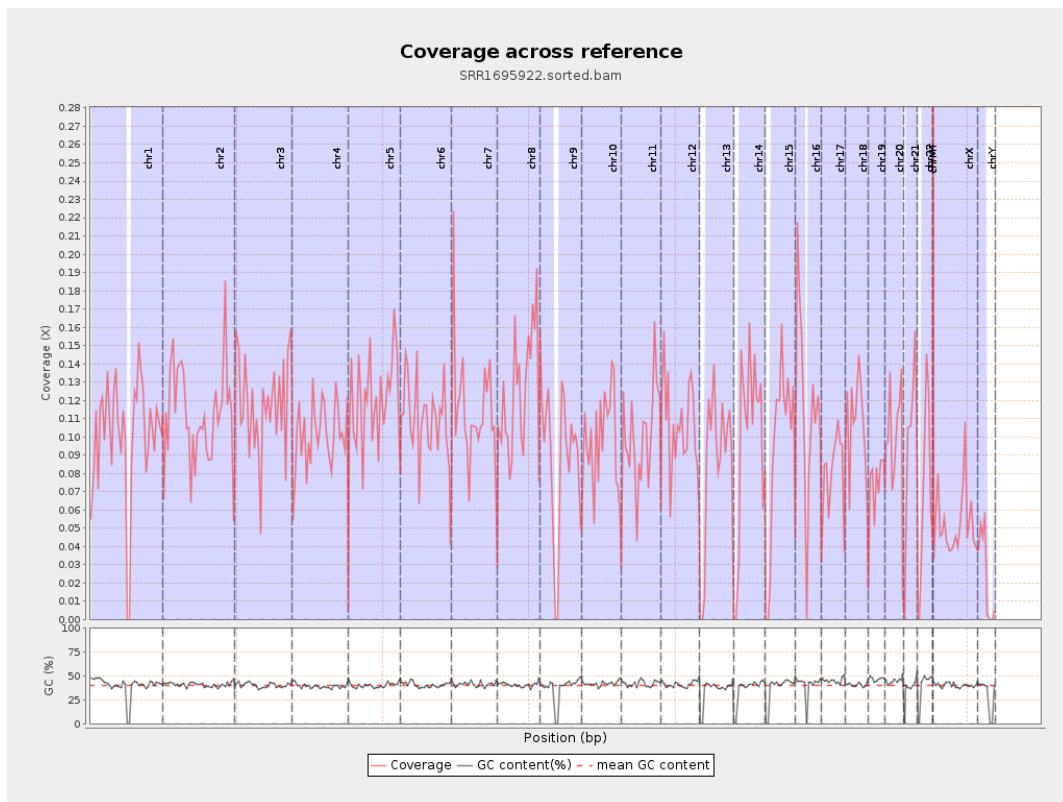
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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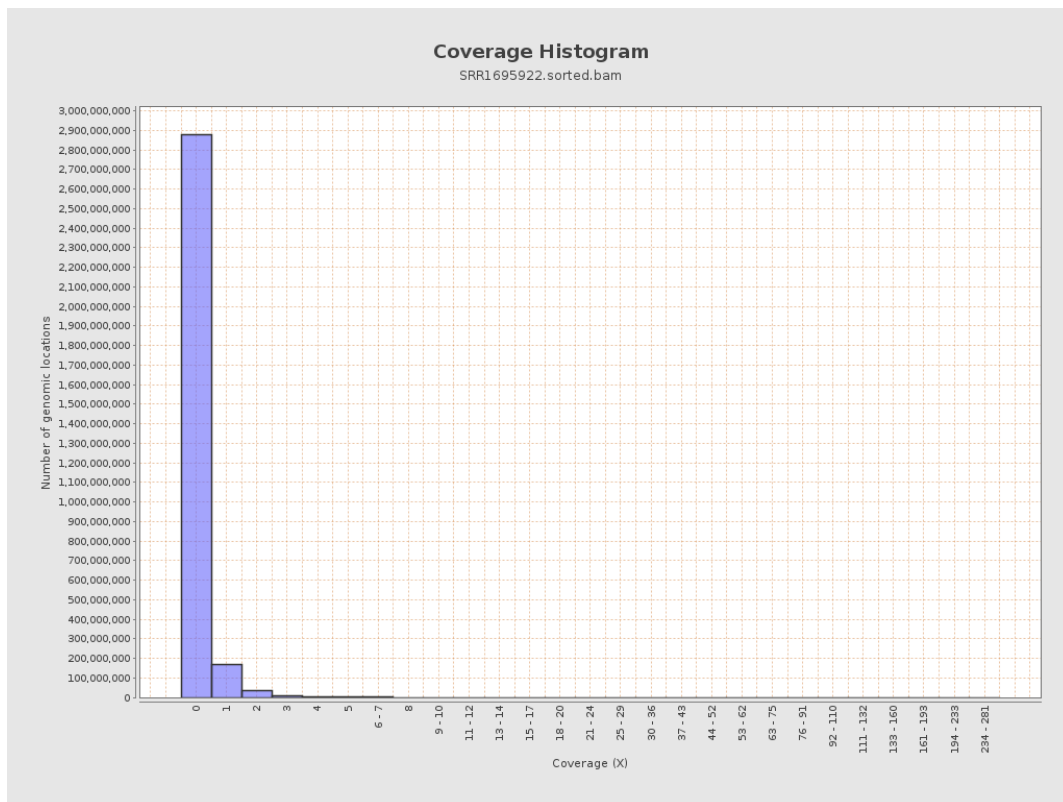
		bases	coverage	deviation
chr1	249250621	25125860	0.1008	0.4501
chr2	243199373	27209251	0.1119	0.5114
chr3	198022430	23212064	0.1172	0.478
chr4	191154276	19458323	0.1018	0.438
chr5	180915260	21558691	0.1192	0.5011
chr6	171115067	18761862	0.1096	0.4933
chr7	159138663	17890563	0.1124	1.071
chr8	146364022	18119676	0.1238	0.5517
chr9	141213431	12308150	0.0872	0.3978
chr10	135534747	13385565	0.0988	0.4527
chr11	135006516	13398042	0.0992	0.4481
chr12	133851895	14398379	0.1076	0.4714
chr13	115169878	9835149	0.0854	0.391
chr14	107349540	10682236	0.0995	0.4464
chr15	102531392	9596280	0.0936	0.4196
chr16	90354753	10154011	0.1124	0.5441
chr17	81195210	6713260	0.0827	0.3874
chr18	78077248	8399094	0.1076	0.4316
chr19	59128983	4366931	0.0739	0.7146
chr20	63025520	6404999	0.1016	0.5015
chr21	48129895	4559675	0.0947	0.5416
chr22	51304566	3635109	0.0709	0.4142
chrMT	16571	7943	0.4793	0.8604
chrX	155270560	8118471	0.0523	0.3254

chrY	59373566	1466247	0.0247	0.2095
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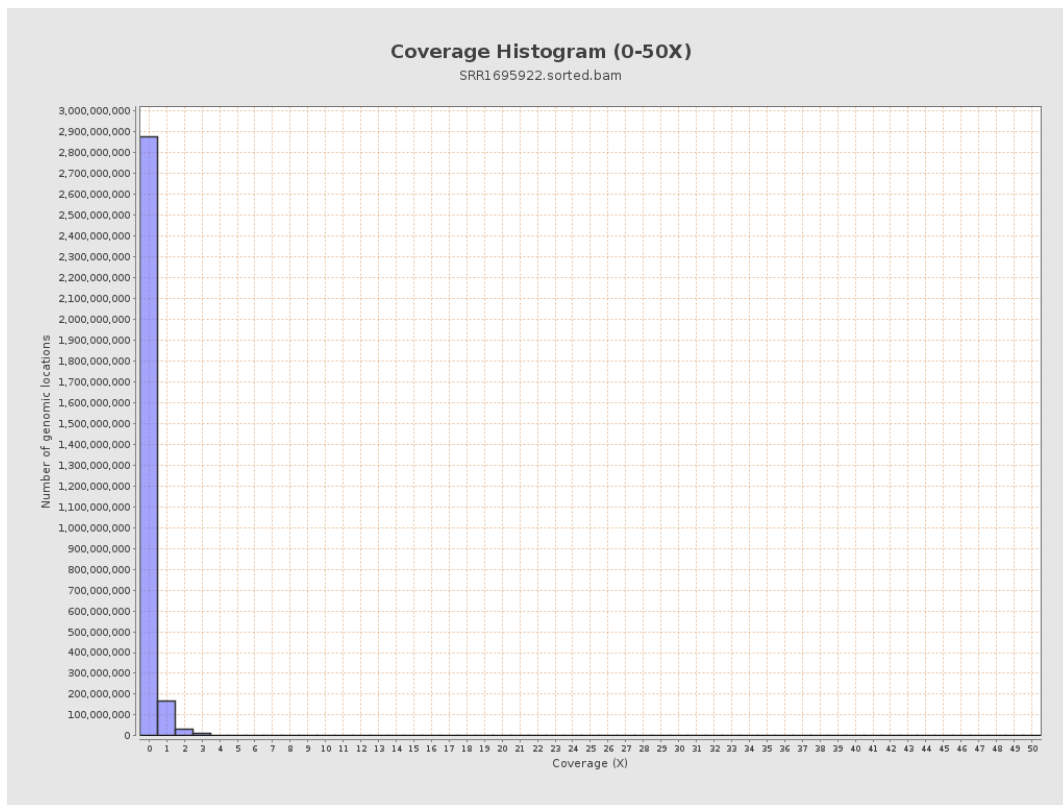
3. Results : Coverage across reference



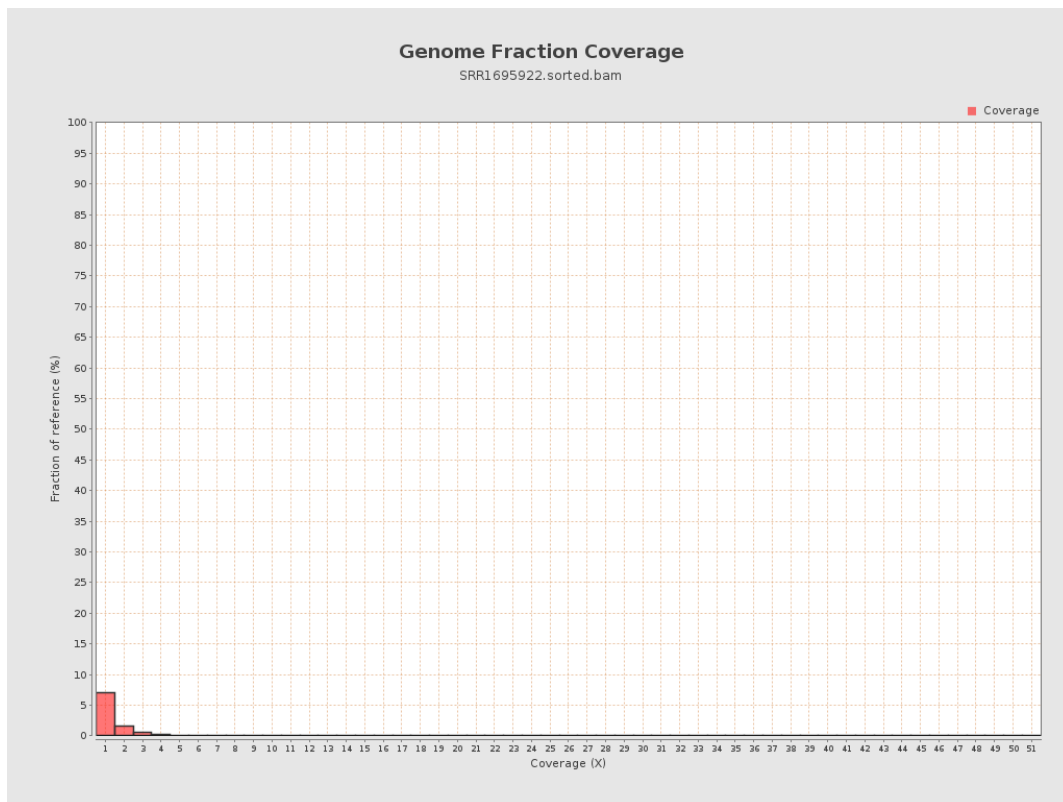
4. Results : Coverage Histogram



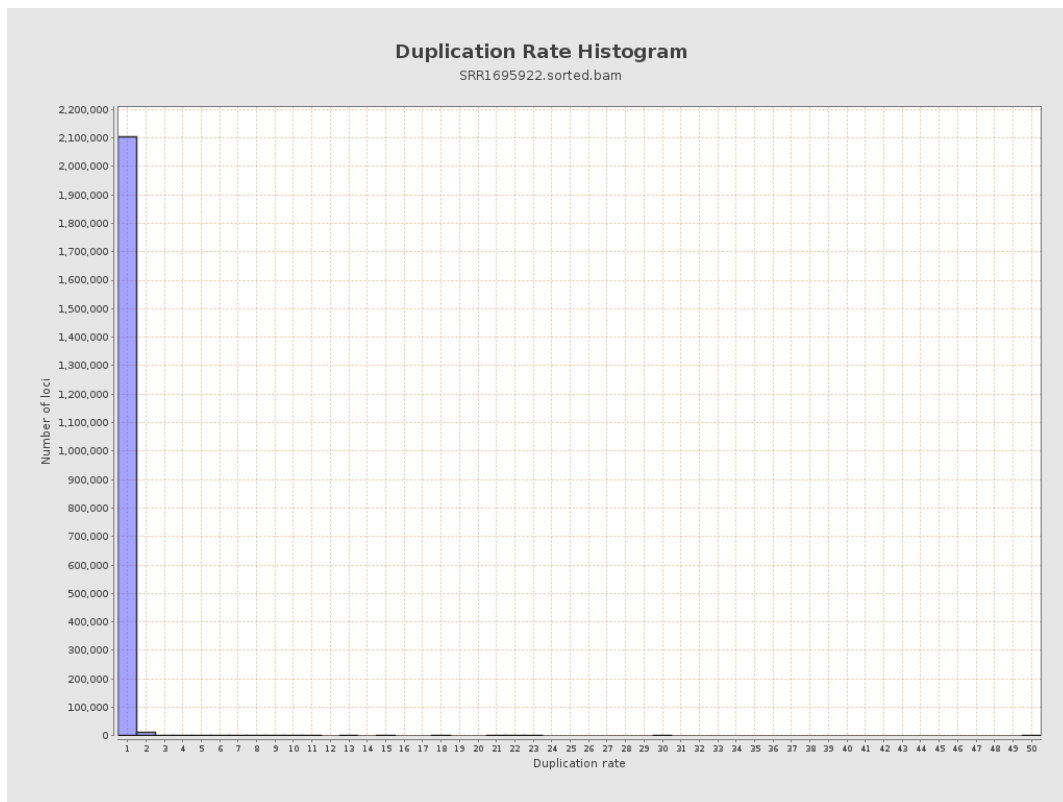
5. Results : Coverage Histogram (0-50X)



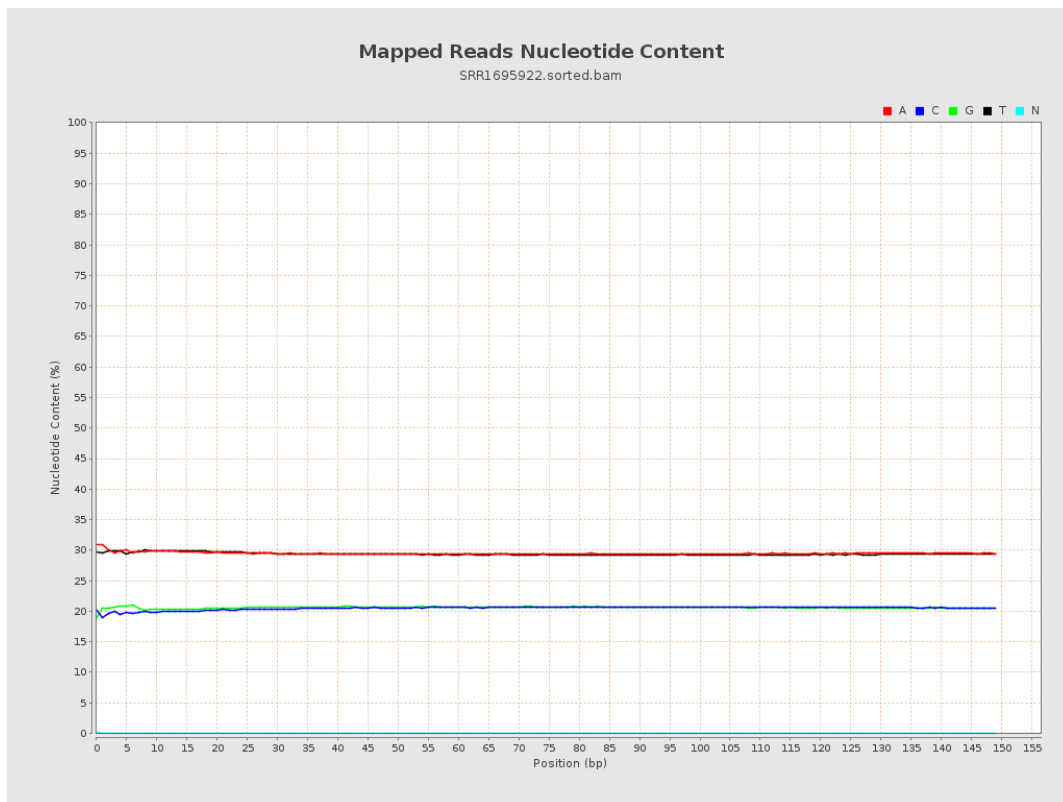
6. Results : Genome Fraction Coverage



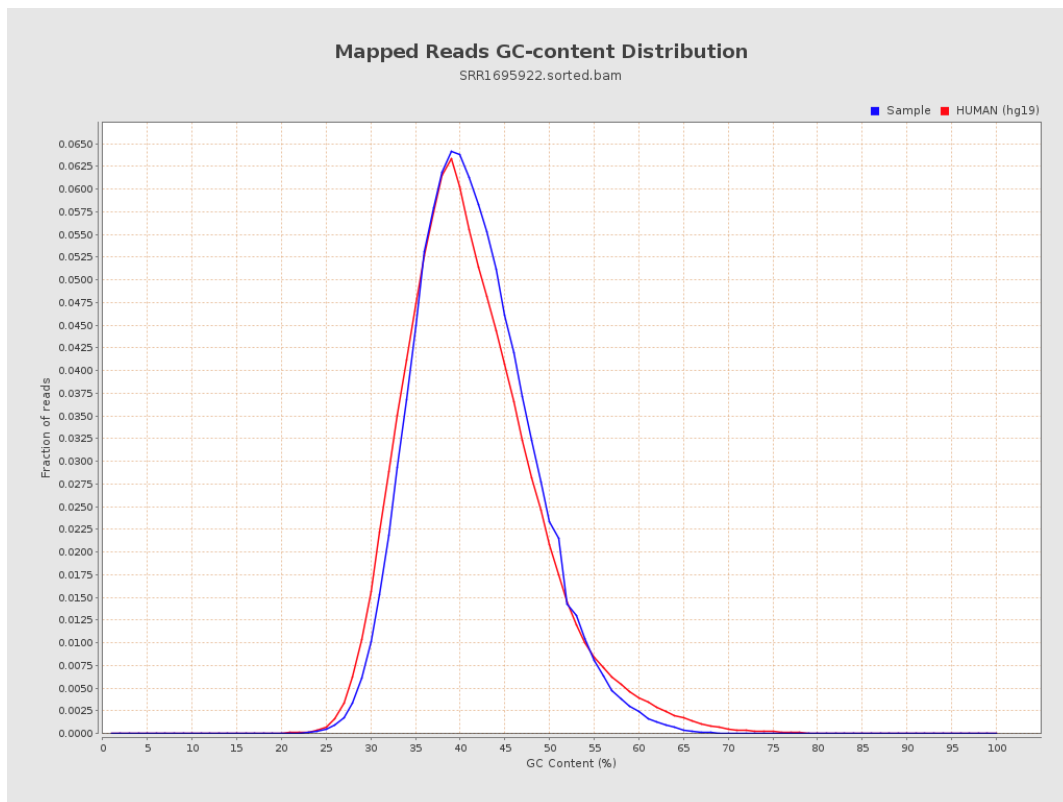
7. Results : Duplication Rate Histogram



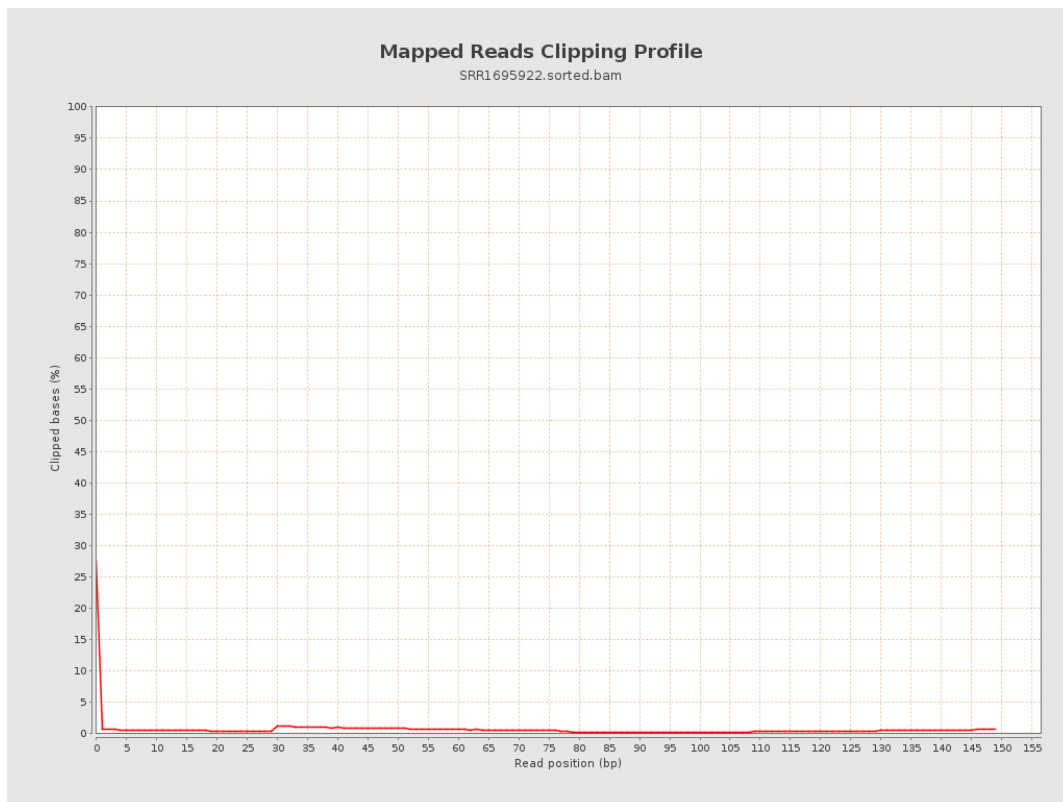
8. Results : Mapped Reads Nucleotide Content



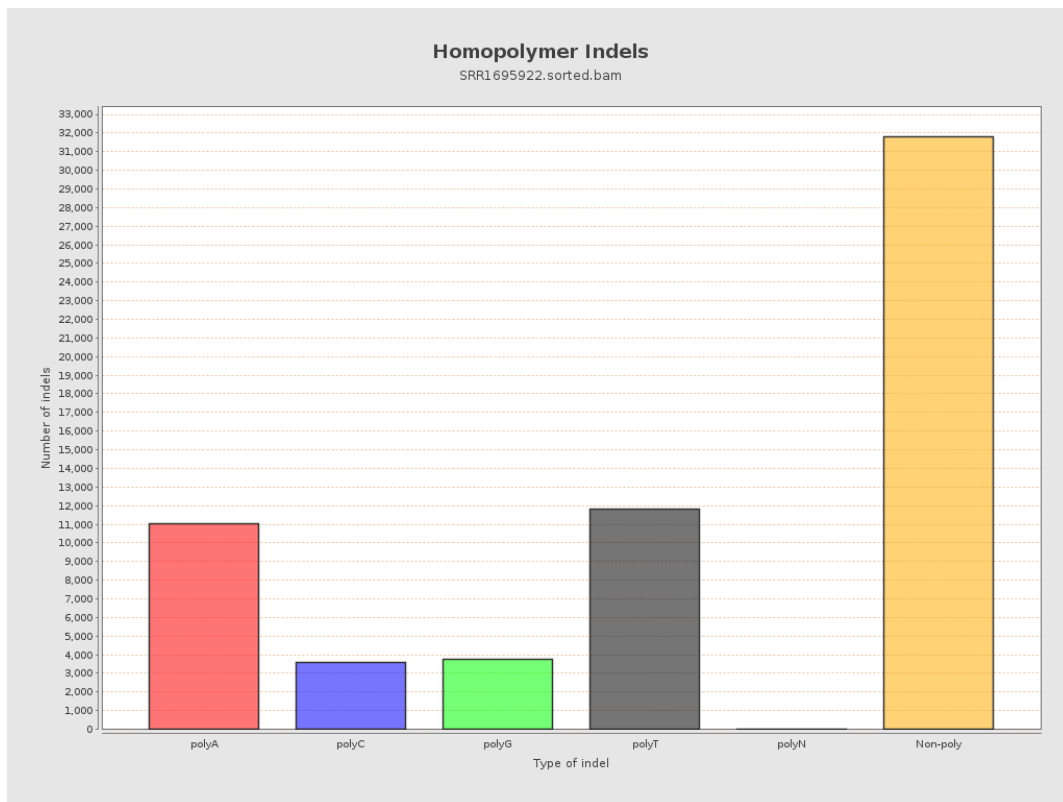
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



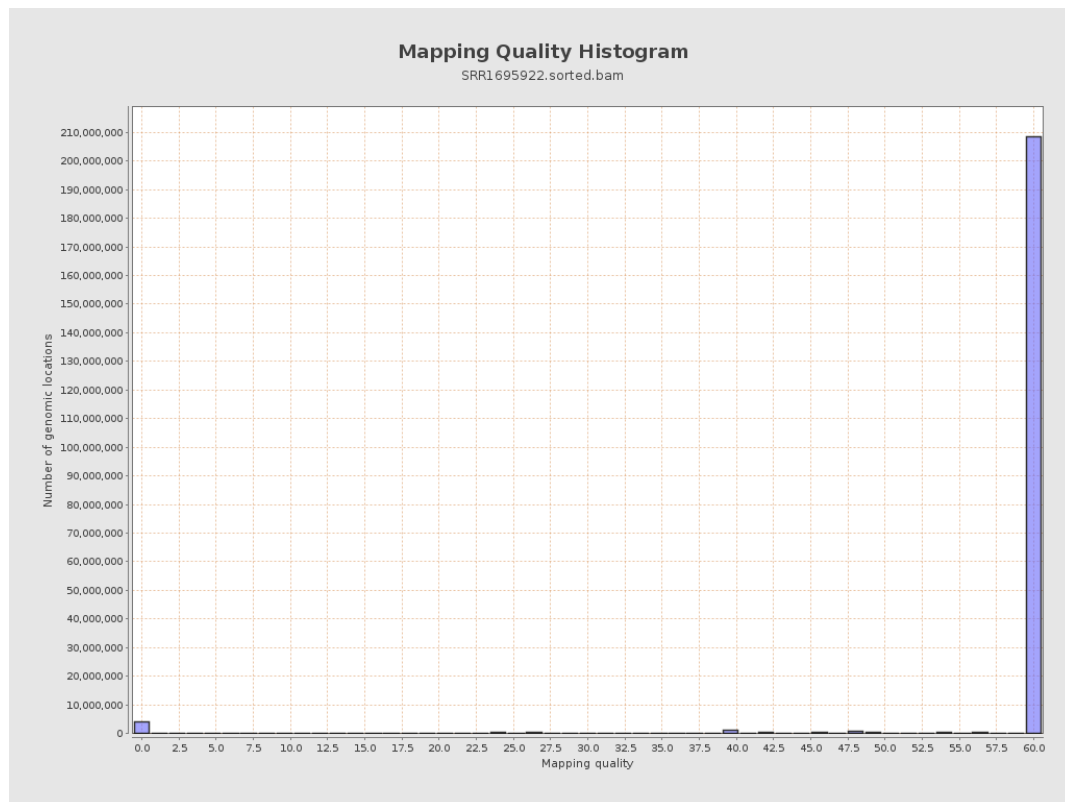
11. Results : Homopolymer Indels



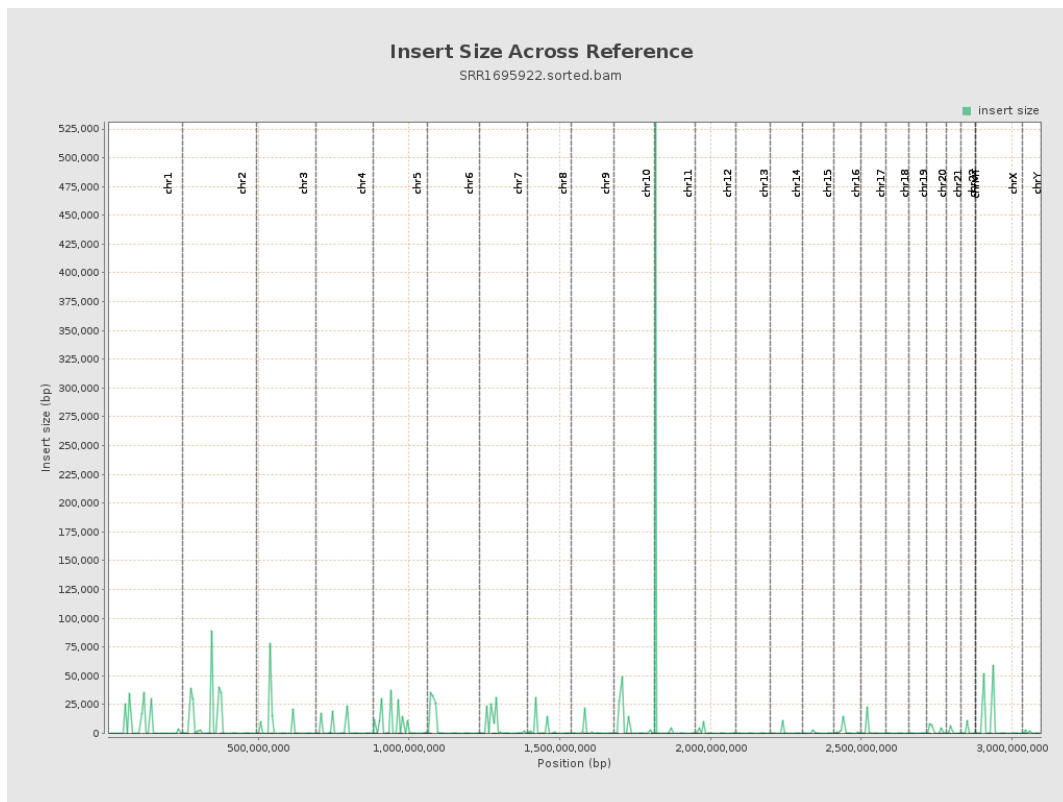
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

