

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/13 16:17:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695952.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_SRR1695952 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695952_1.fastq.gz SRR1695952_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 16:17:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695952.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	89,012,154
Mapped reads	88,164,933 / 99.05%
Unmapped reads	847,221 / 0.95%
Mapped paired reads	88,164,933 / 99.05%
Mapped reads, first in pair	44,192,664 / 49.65%
Mapped reads, second in pair	43,972,269 / 49.4%
Mapped reads, both in pair	87,666,846 / 98.49%
Mapped reads, singletons	498,087 / 0.56%
Secondary alignments	0
Supplementary alignments	1,415,294 / 1.59%
Read min/max/mean length	30 / 100 / 100.65
Duplicated reads (estimated)	6,237,242 / 7.01%
Duplication rate	5.03%
Clipped reads	6,965,759 / 7.83%

2.2. ACGT Content

Number/percentage of A's	2,445,556,083 / 28.02%
Number/percentage of C's	1,893,641,595 / 21.7%
Number/percentage of T's	2,434,162,402 / 27.89%
Number/percentage of G's	1,953,986,931 / 22.39%
Number/percentage of N's	137,891 / 0%

GC Percentage	44.09%
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2.3. Coverage

Mean	2.8202
Standard Deviation	10.6203

2.4. Mapping Quality

Mean Mapping Quality	53.91
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2.5. Insert size

Mean	87,813.27
Standard Deviation	2,841,237.6
P25/Median/P75	341 / 350 / 358

2.6. Mismatches and indels

General error rate	0.44%
Mismatches	35,456,015
Insertions	1,331,867
Mapped reads with at least one insertion	1.46%
Deletions	1,128,478
Mapped reads with at least one deletion	1.23%
Homopolymer indels	41.42%

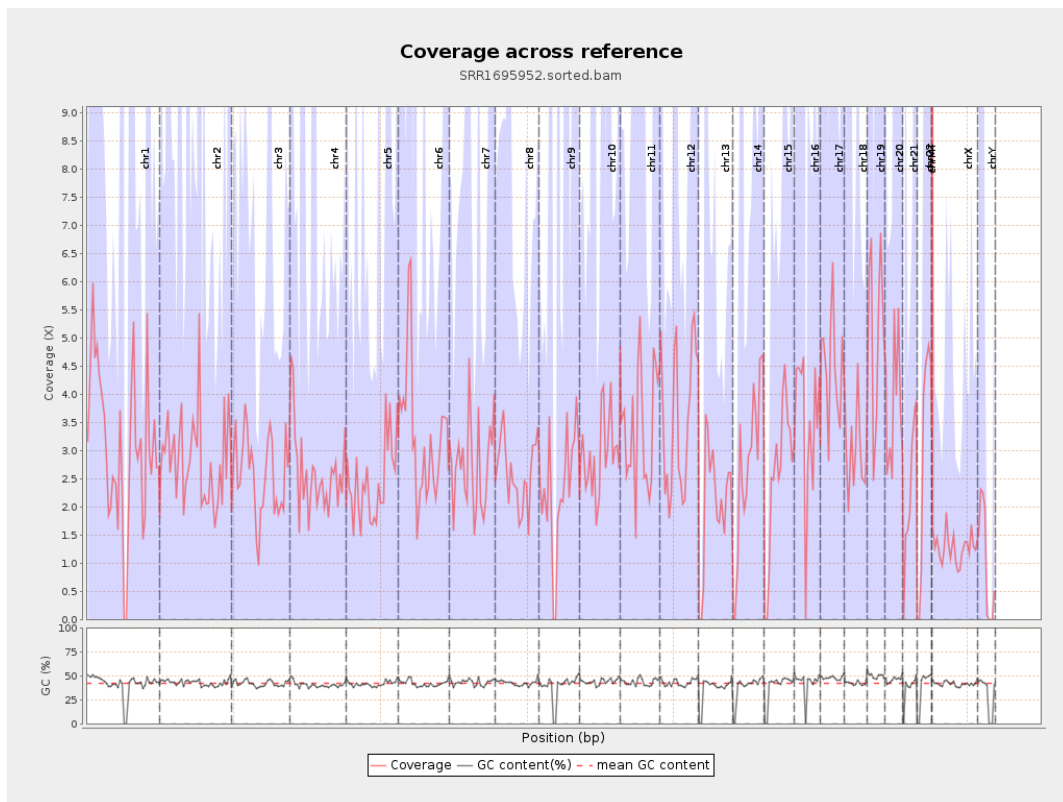
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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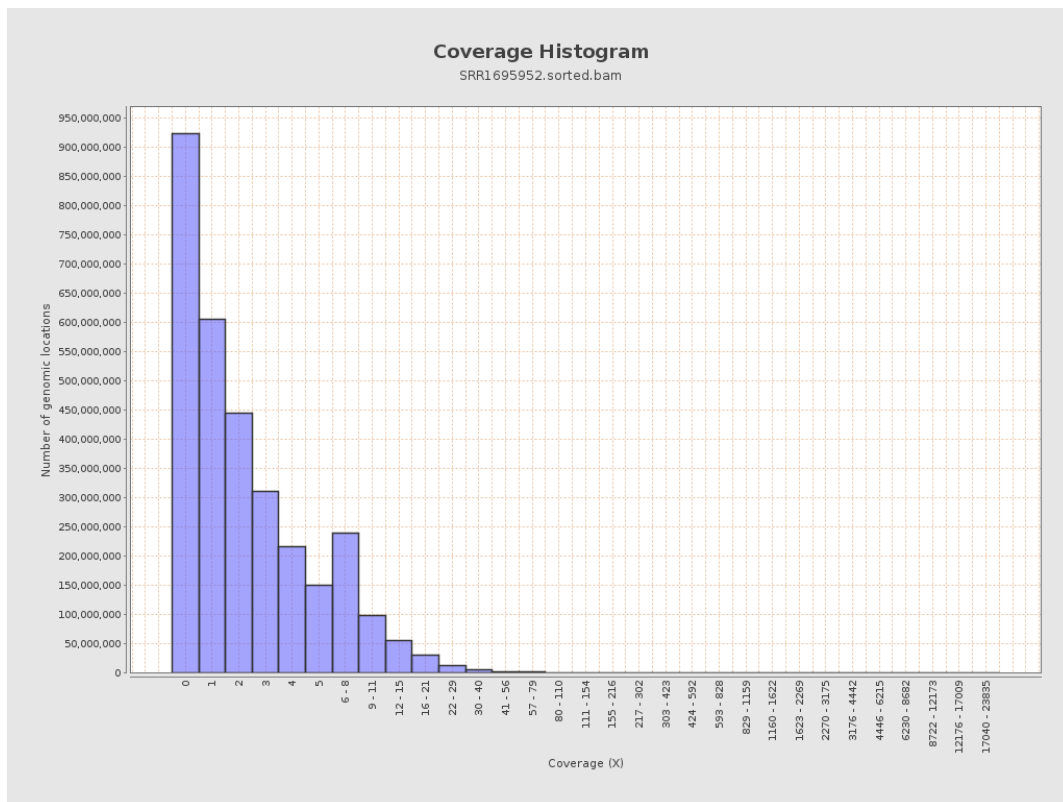
		bases	coverage	deviation
chr1	249250621	770298787	3.0905	8.8967
chr2	243199373	691072202	2.8416	22.4705
chr3	198022430	510781938	2.5794	4.5926
chr4	191154276	494428365	2.5865	6.3282
chr5	180915260	444447872	2.4567	5.1486
chr6	171115067	557126821	3.2559	7.8276
chr7	159138663	433661789	2.7251	5.9135
chr8	146364022	383300541	2.6188	7.1654
chr9	141213431	327250435	2.3174	14.0787
chr10	135534747	396701820	2.9269	15.1276
chr11	135006516	463698218	3.4346	7.22
chr12	133851895	474849085	3.5476	5.4002
chr13	115169878	239250132	2.0774	4.8159
chr14	107349540	289750071	2.6991	10.2812
chr15	102531392	259363906	2.5296	5.4239
chr16	90354753	315161436	3.488	16.3001
chr17	81195210	367547732	4.5267	9.0662
chr18	78077248	230939707	2.9578	11.1788
chr19	59128983	308845859	5.2233	9.7806
chr20	63025520	241804730	3.8366	6.0452
chr21	48129895	110878943	2.3037	6.4575
chr22	51304566	152372163	2.97	6.3614
chrMT	16571	5727240	345.6182	121.017
chrX	155270560	197899848	1.2745	3.4905

chrY	59373566	63301892	1.0662	18.9495
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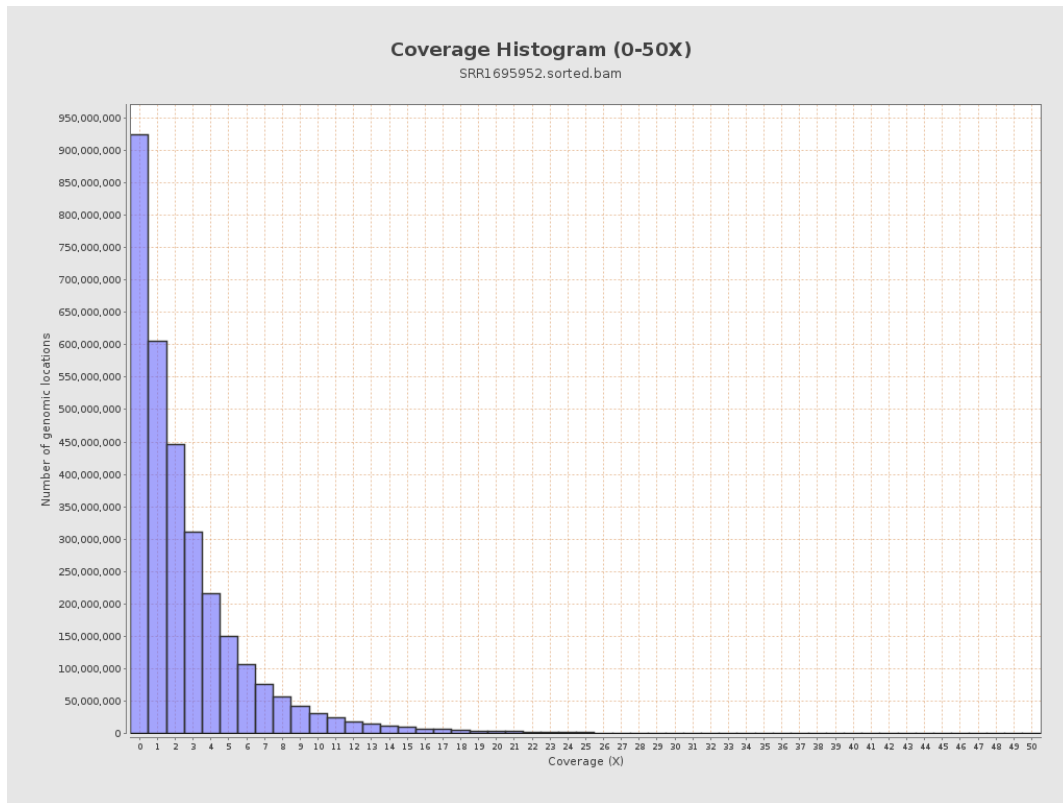
3. Results : Coverage across reference



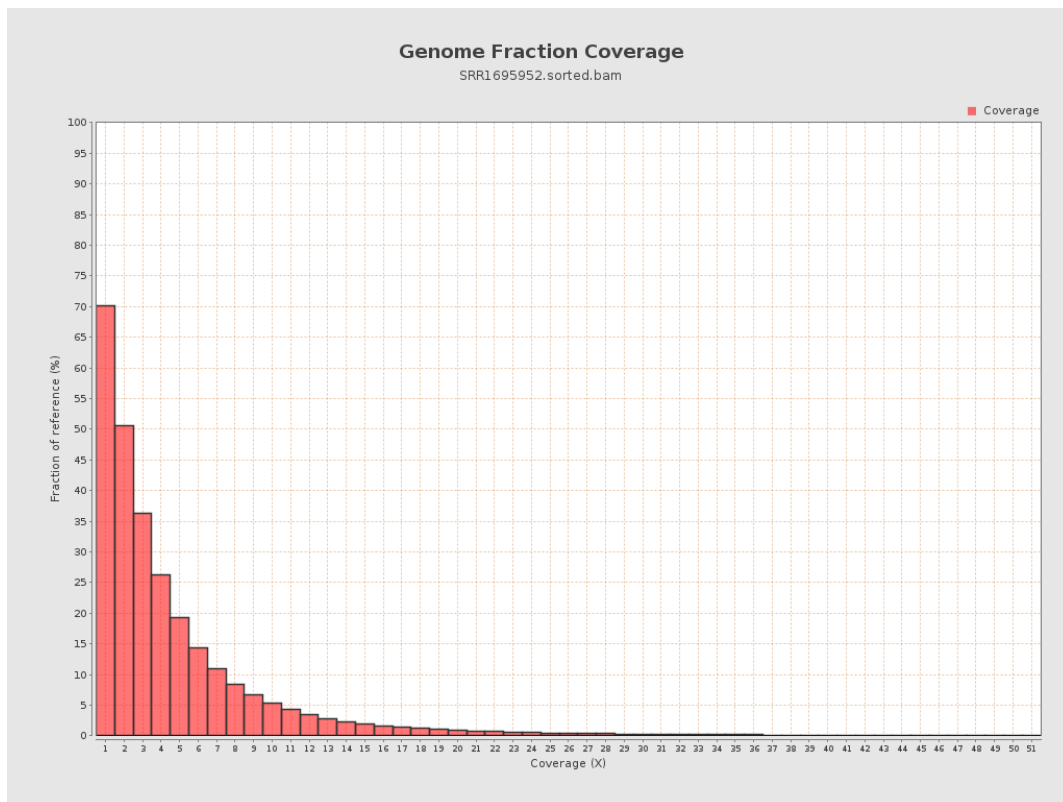
4. Results : Coverage Histogram



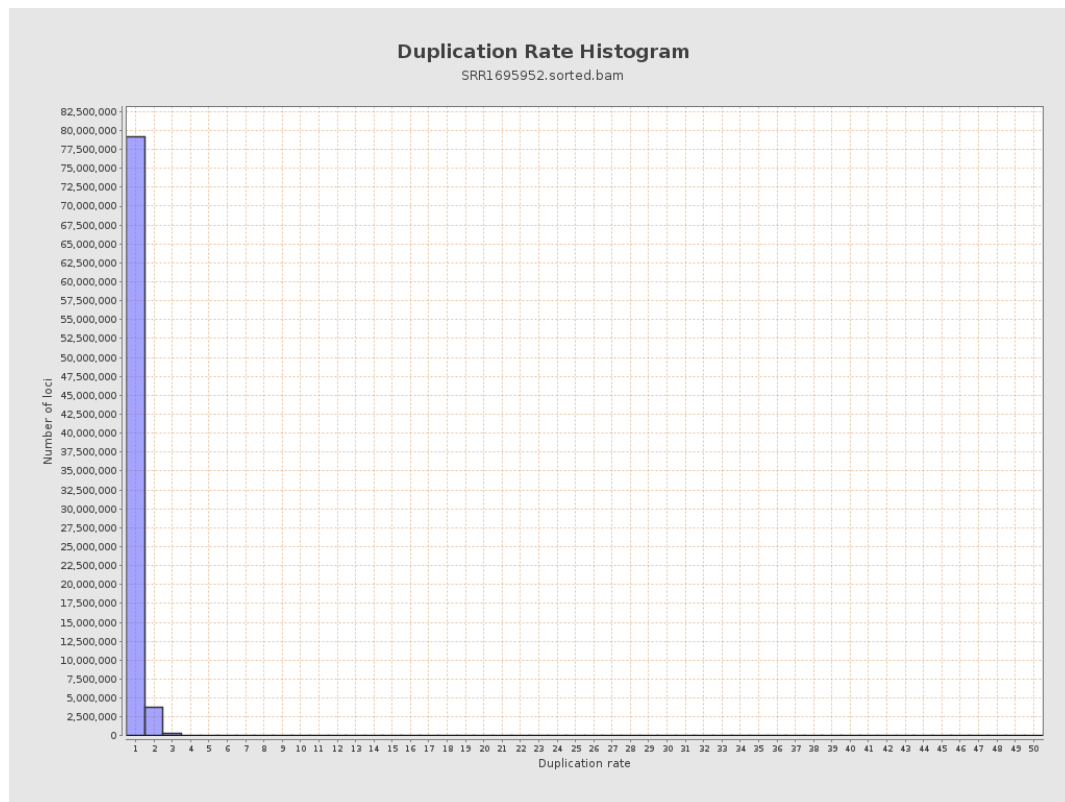
5. Results : Coverage Histogram (0-50X)



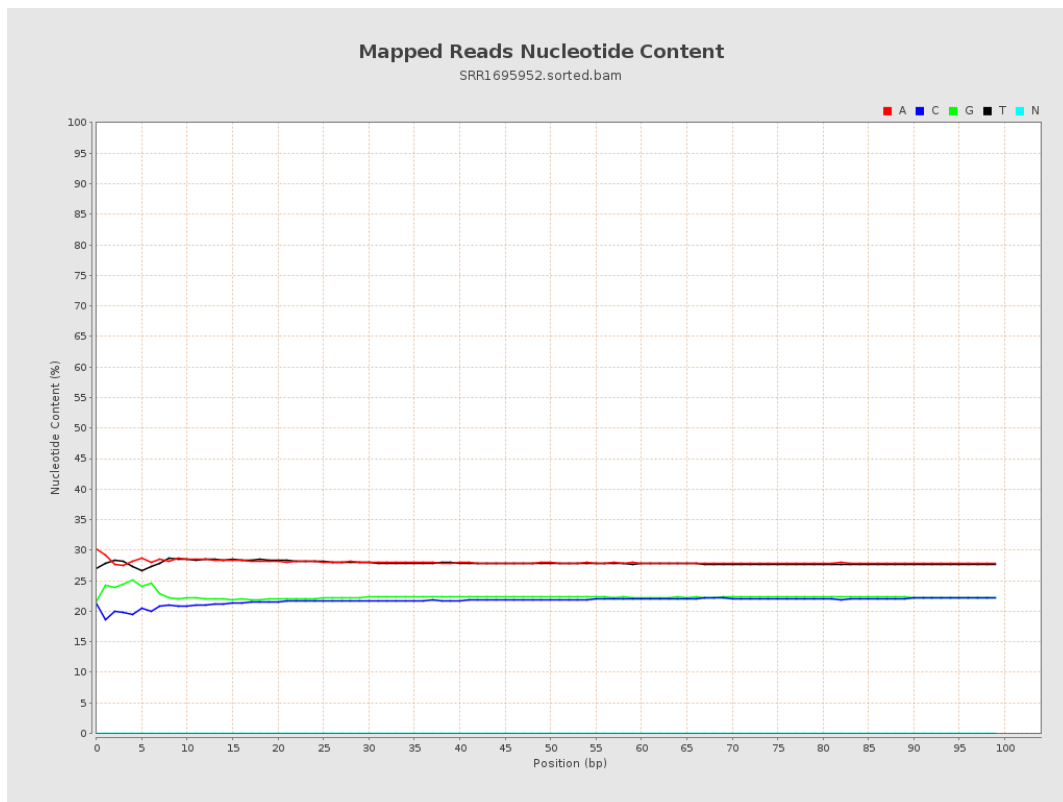
6. Results : Genome Fraction Coverage



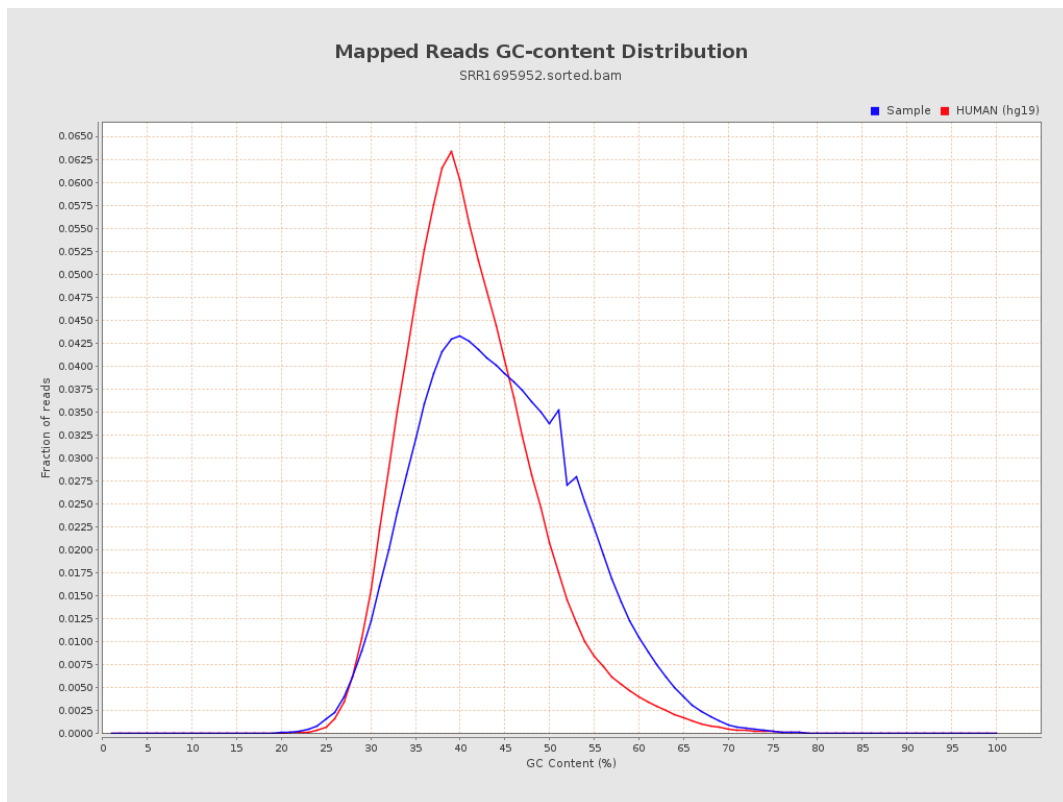
7. Results : Duplication Rate Histogram



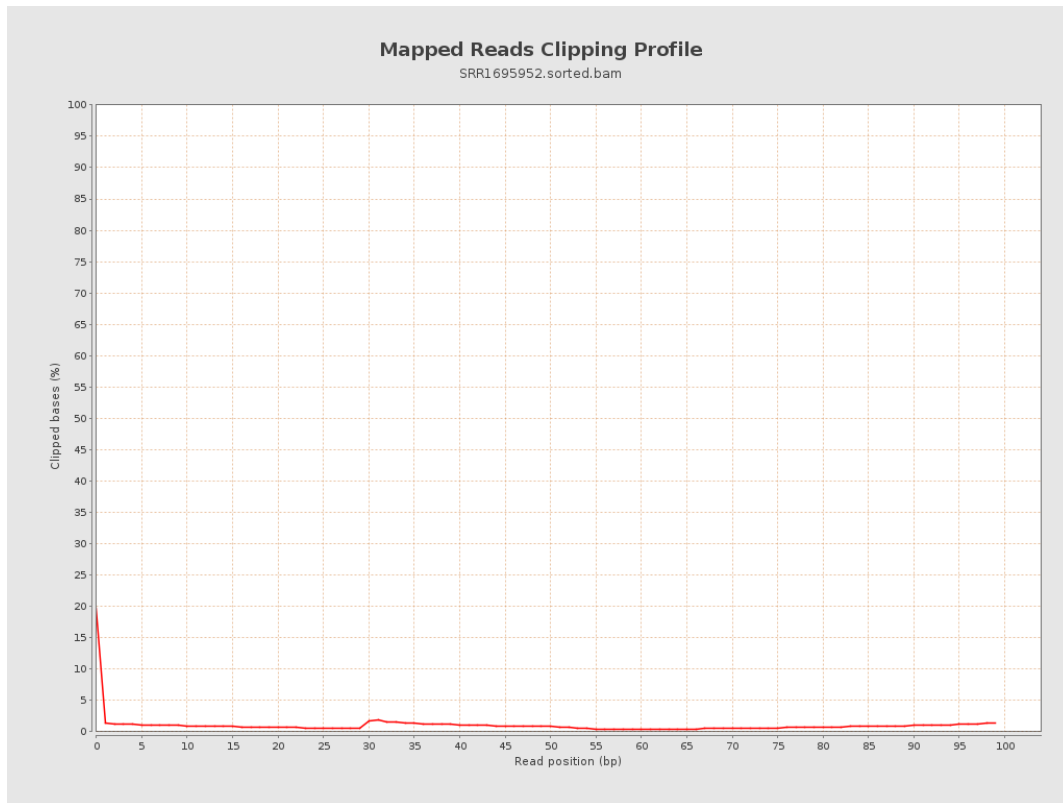
8. Results : Mapped Reads Nucleotide Content



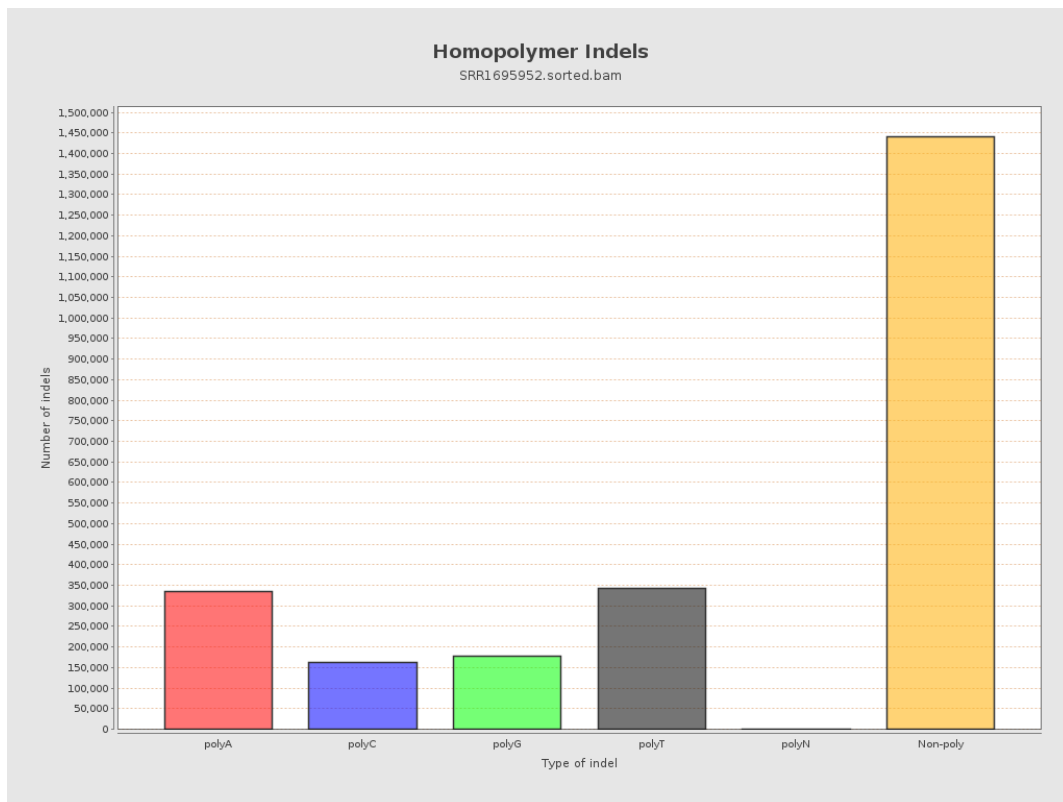
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



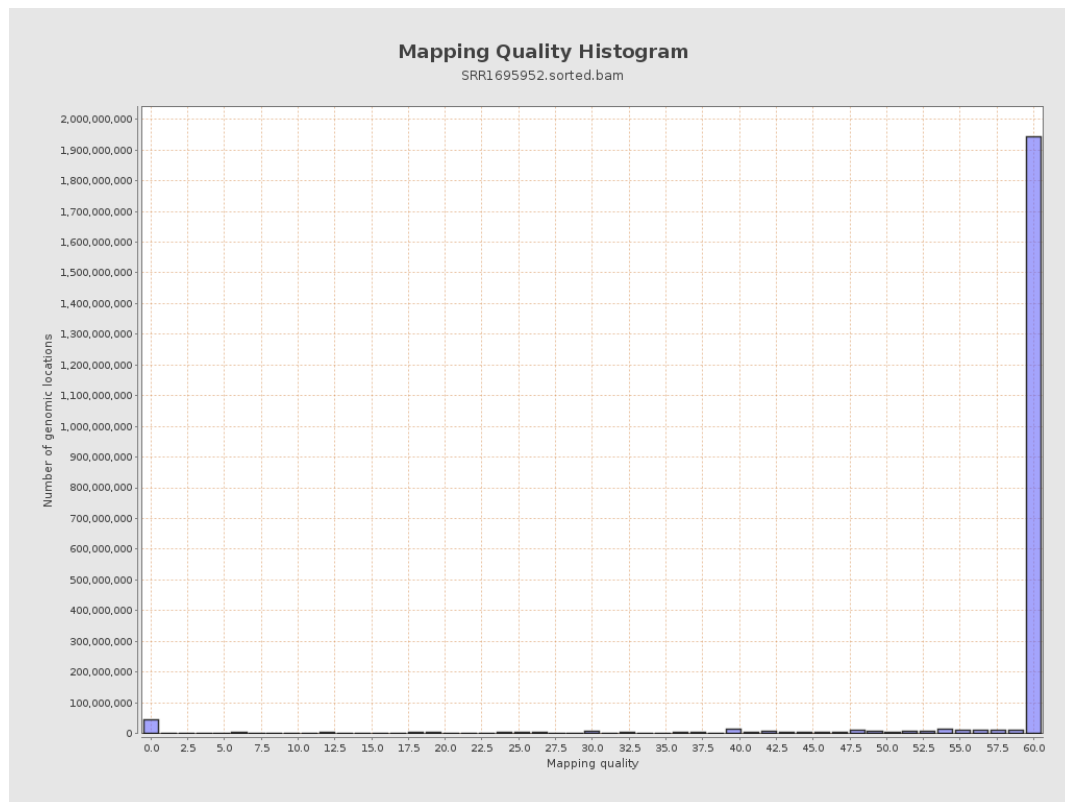
11. Results : Homopolymer Indels



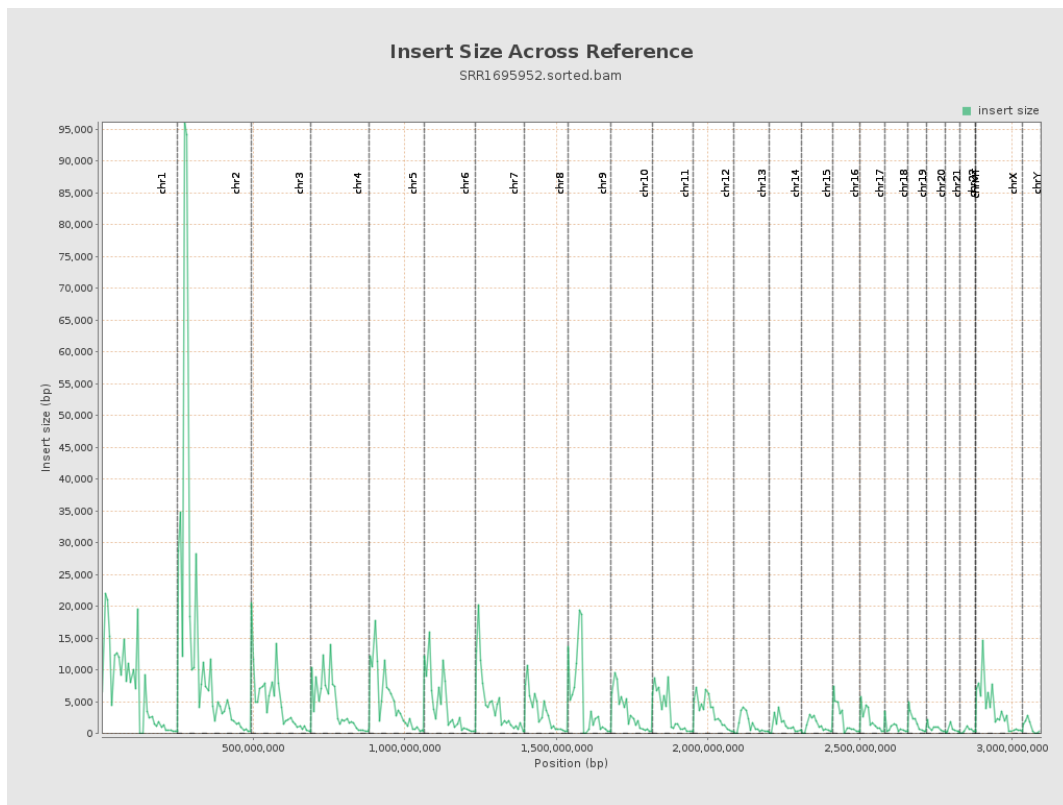
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

