

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/14 01:48:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695970.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_SRR1695970 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695970_1.fastq.gz SRR1695970_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 01:48:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695970.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	60,266,000
Mapped reads	59,912,022 / 99.41%
Unmapped reads	353,978 / 0.59%
Mapped paired reads	59,912,022 / 99.41%
Mapped reads, first in pair	30,049,017 / 49.86%
Mapped reads, second in pair	29,863,005 / 49.55%
Mapped reads, both in pair	59,658,522 / 98.99%
Mapped reads, singletons	253,500 / 0.42%
Secondary alignments	0
Supplementary alignments	596,045 / 0.99%
Read min/max/mean length	30 / 100 / 100.41
Duplicated reads (estimated)	1,800,505 / 2.99%
Duplication rate	2.6%
Clipped reads	4,119,137 / 6.83%

2.2. ACGT Content

Number/percentage of A's	1,759,553,868 / 29.6%
Number/percentage of C's	1,195,714,781 / 20.12%
Number/percentage of T's	1,749,868,006 / 29.44%
Number/percentage of G's	1,230,882,957 / 20.71%
Number/percentage of N's	8,182,121 / 0.14%

GC Percentage	40.82%
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2.3. Coverage

Mean	1.9206
Standard Deviation	2.7718

2.4. Mapping Quality

Mean Mapping Quality	53.91
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2.5. Insert size

Mean	73,949.86
Standard Deviation	2,610,717.94
P25/Median/P75	315 / 325 / 334

2.6. Mismatches and indels

General error rate	0.68%
Mismatches	39,508,837
Insertions	557,984
Mapped reads with at least one insertion	0.92%
Deletions	562,607
Mapped reads with at least one deletion	0.92%
Homopolymer indels	45.78%

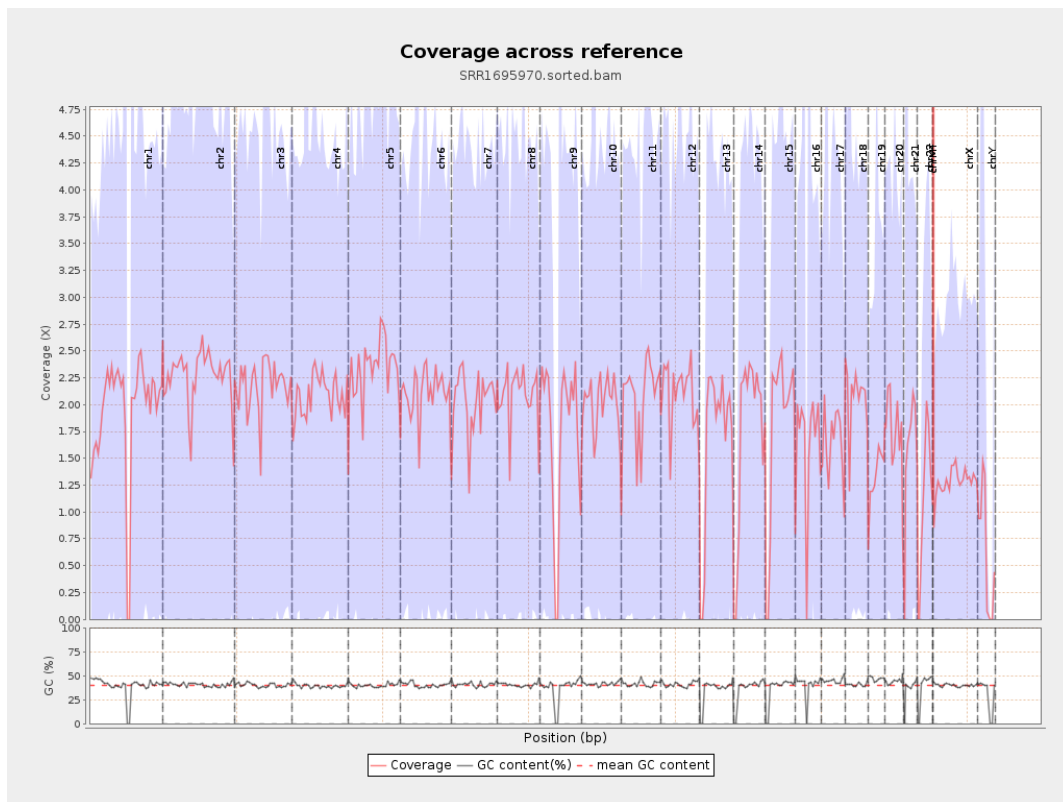
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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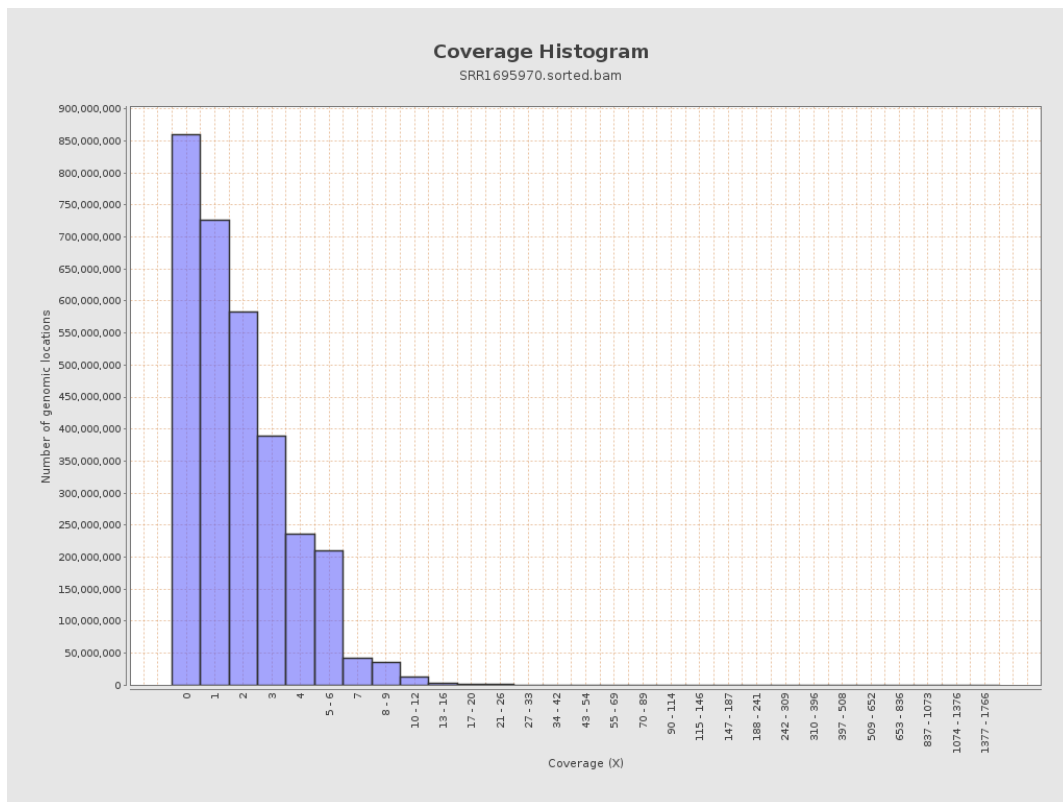
		bases	coverage	deviation
chr1	249250621	484244741	1.9428	2.8843
chr2	243199373	551173676	2.2663	2.6809
chr3	198022430	431207596	2.1776	2.0214
chr4	191154276	400141514	2.0933	2.5088
chr5	180915260	422022866	2.3327	2.1209
chr6	171115067	361599475	2.1132	2.3119
chr7	159138663	322019920	2.0235	2.0907
chr8	146364022	305259704	2.0856	2.0525
chr9	141213431	247300575	1.7513	2.3306
chr10	135534747	274535079	2.0256	3.0761
chr11	135006516	281367025	2.0841	2.1136
chr12	133851895	282666307	2.1118	2.0963
chr13	115169878	193164280	1.6772	1.9201
chr14	107349540	191011549	1.7793	2.0276
chr15	102531392	182695054	1.7818	2.1166
chr16	90354753	144310245	1.5972	2.6428
chr17	81195210	135060090	1.6634	2.3196
chr18	78077248	160967405	2.0616	2.9151
chr19	59128983	80644269	1.3639	2.0777
chr20	63025520	111606445	1.7708	2.0884
chr21	48129895	76543799	1.5904	3.236
chr22	51304566	58654378	1.1433	1.7716
chrMT	16571	9934130	599.4889	158.2778
chrX	155270560	199341460	1.2838	1.4822

chrY	59373566	38023318	0.6404	2.5831
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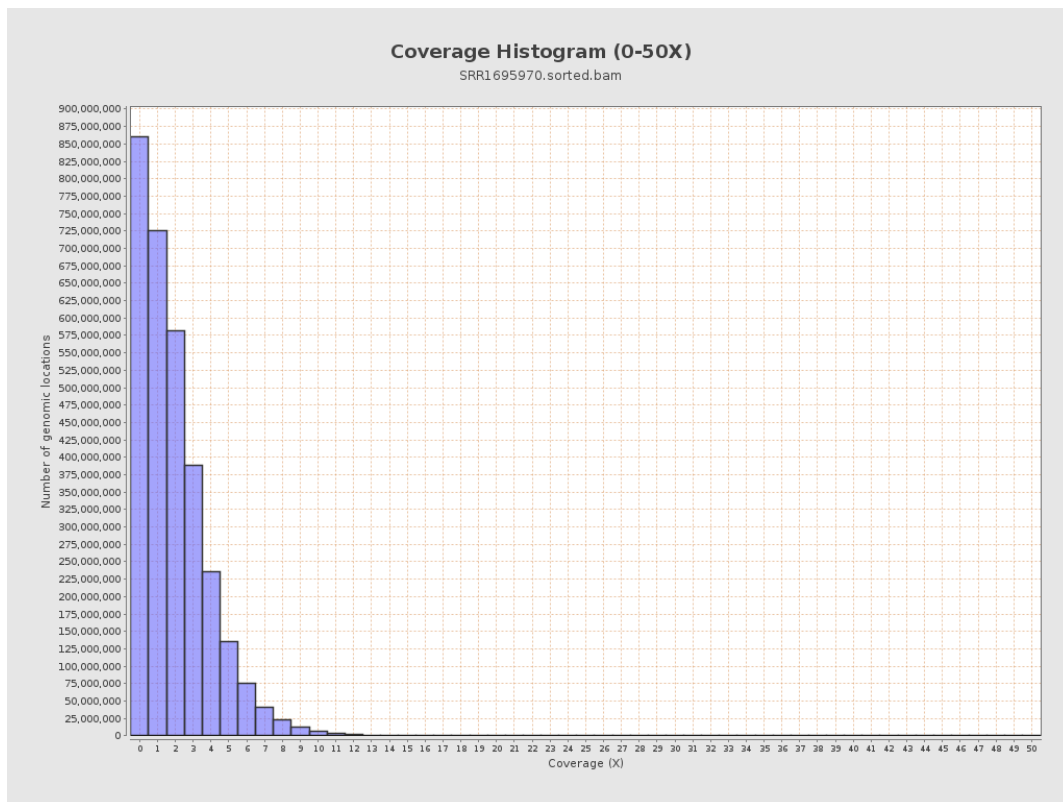
3. Results : Coverage across reference



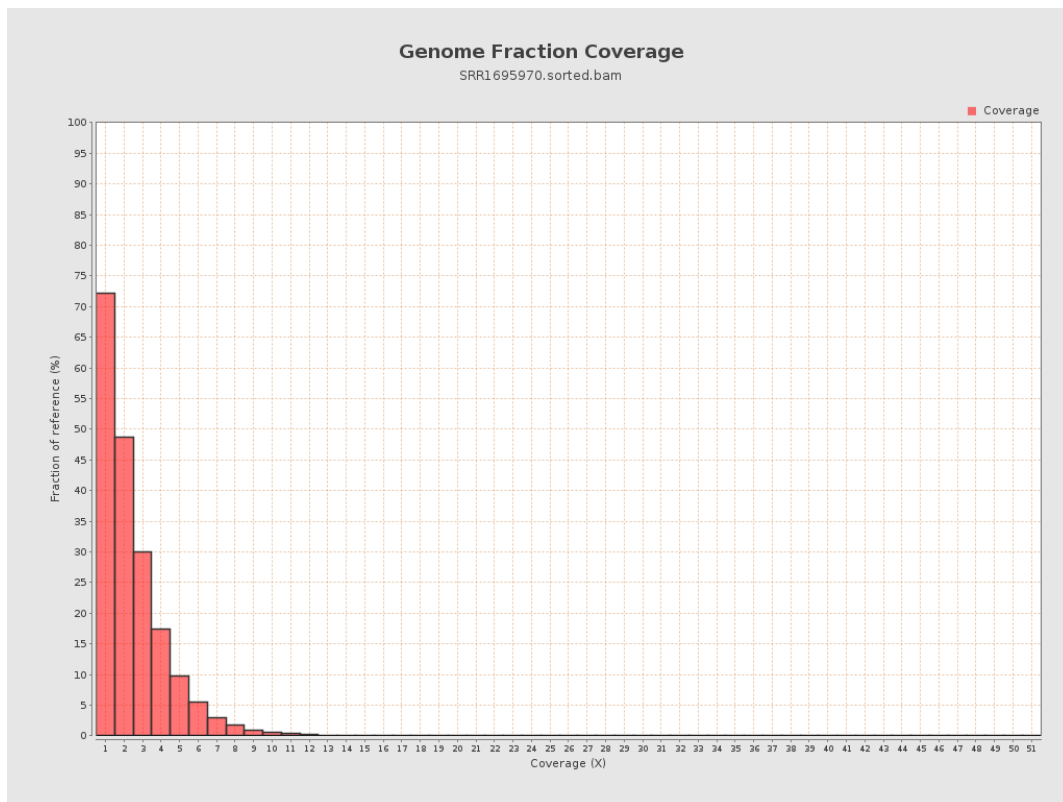
4. Results : Coverage Histogram



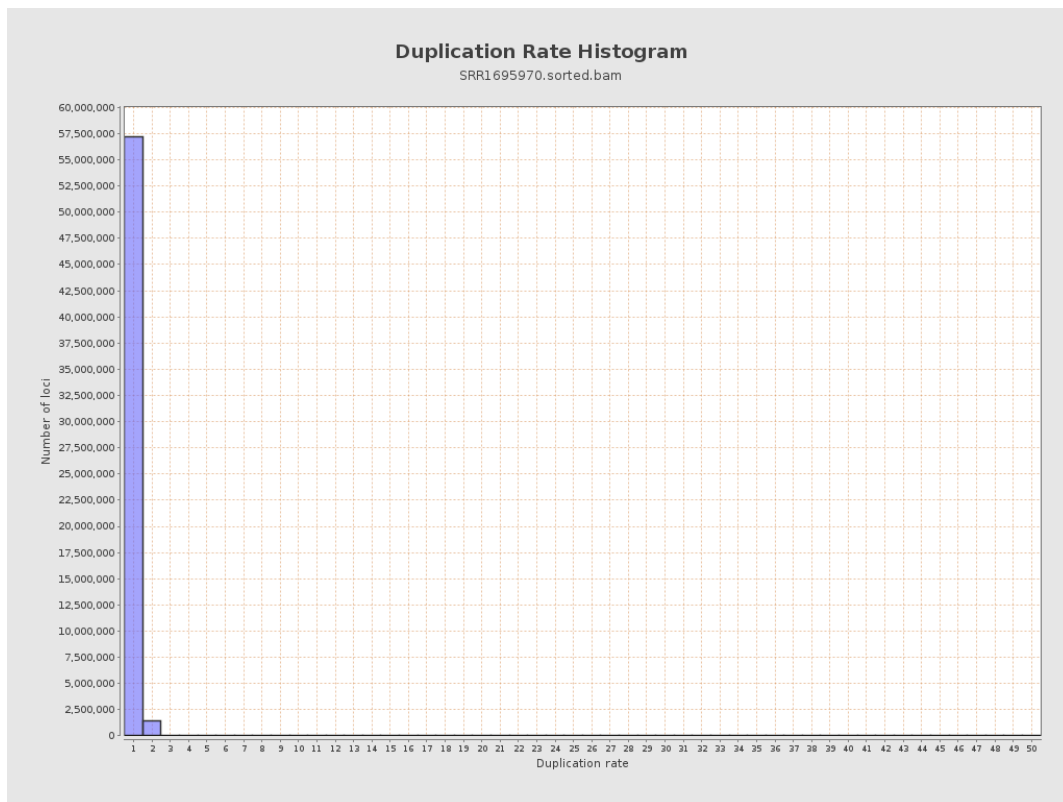
5. Results : Coverage Histogram (0-50X)



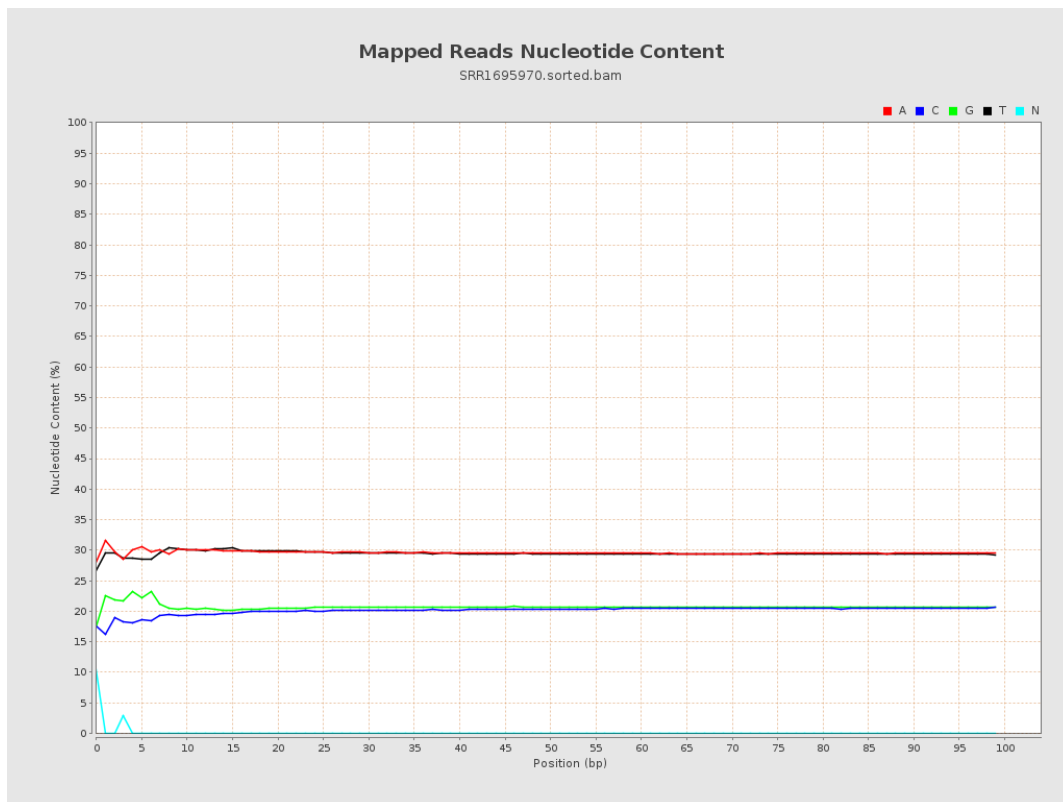
6. Results : Genome Fraction Coverage



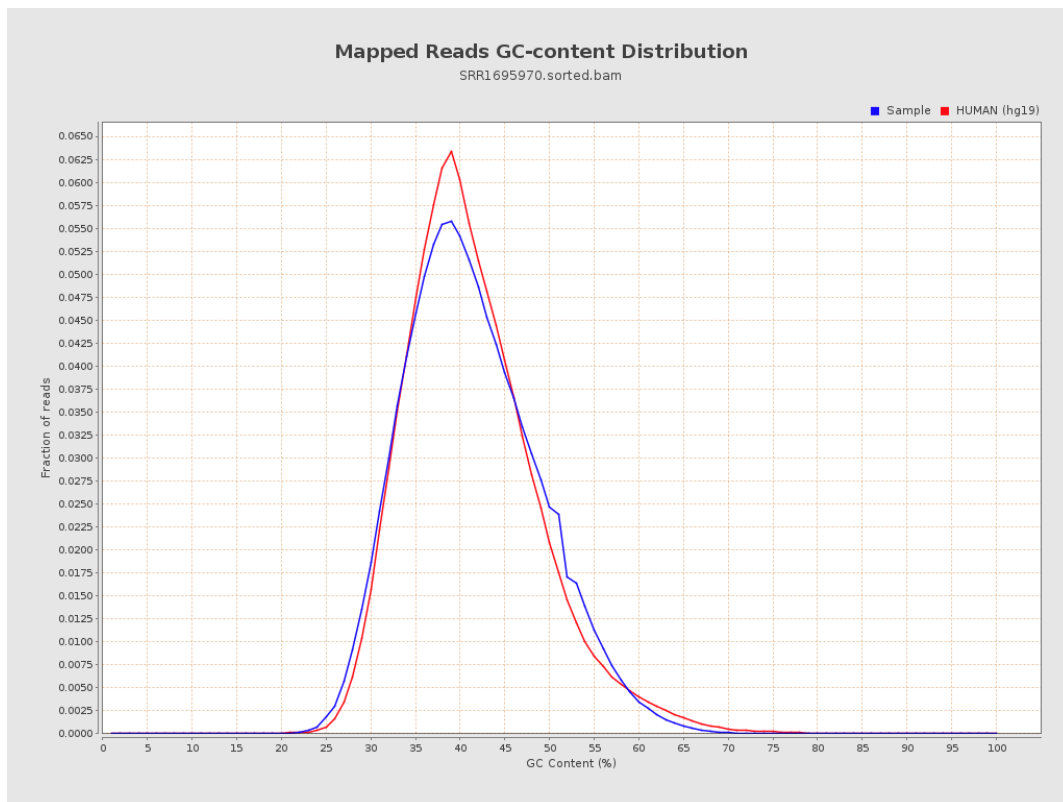
7. Results : Duplication Rate Histogram



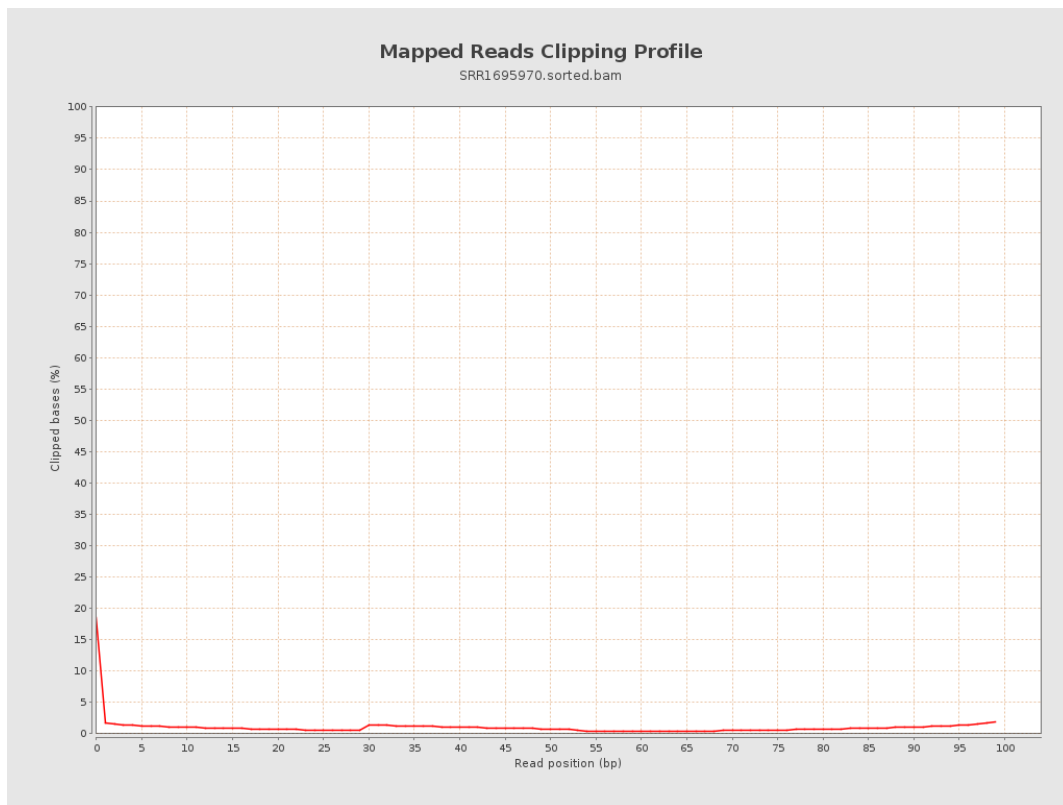
8. Results : Mapped Reads Nucleotide Content



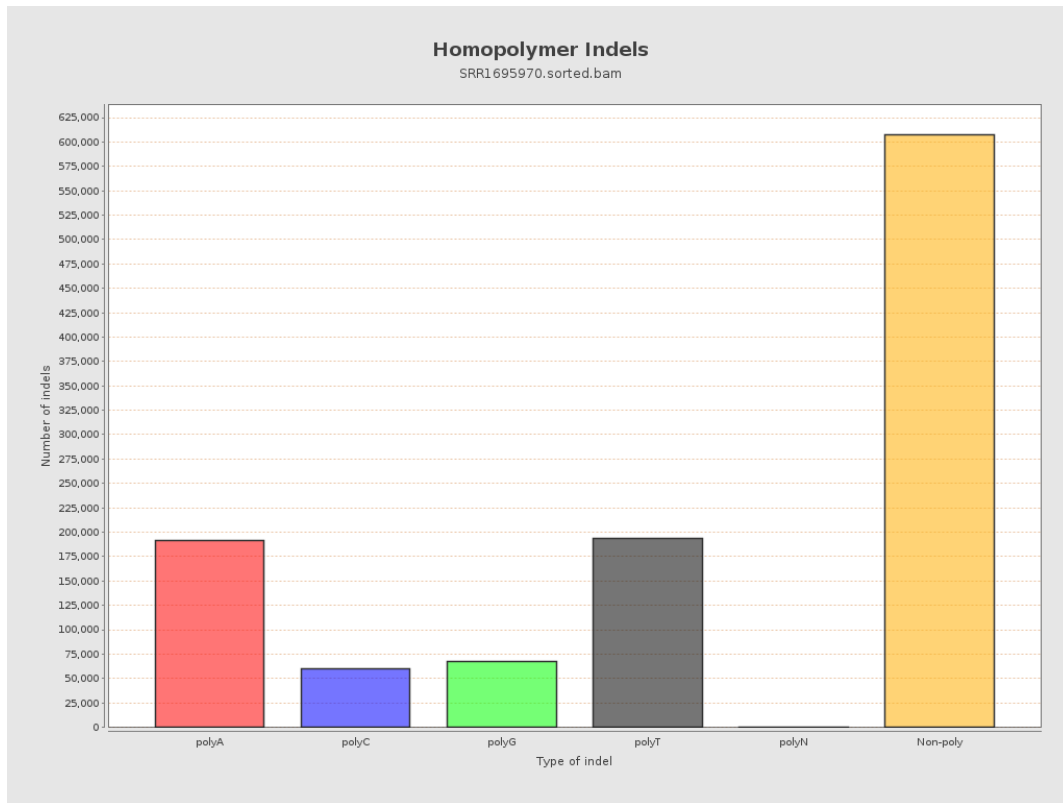
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



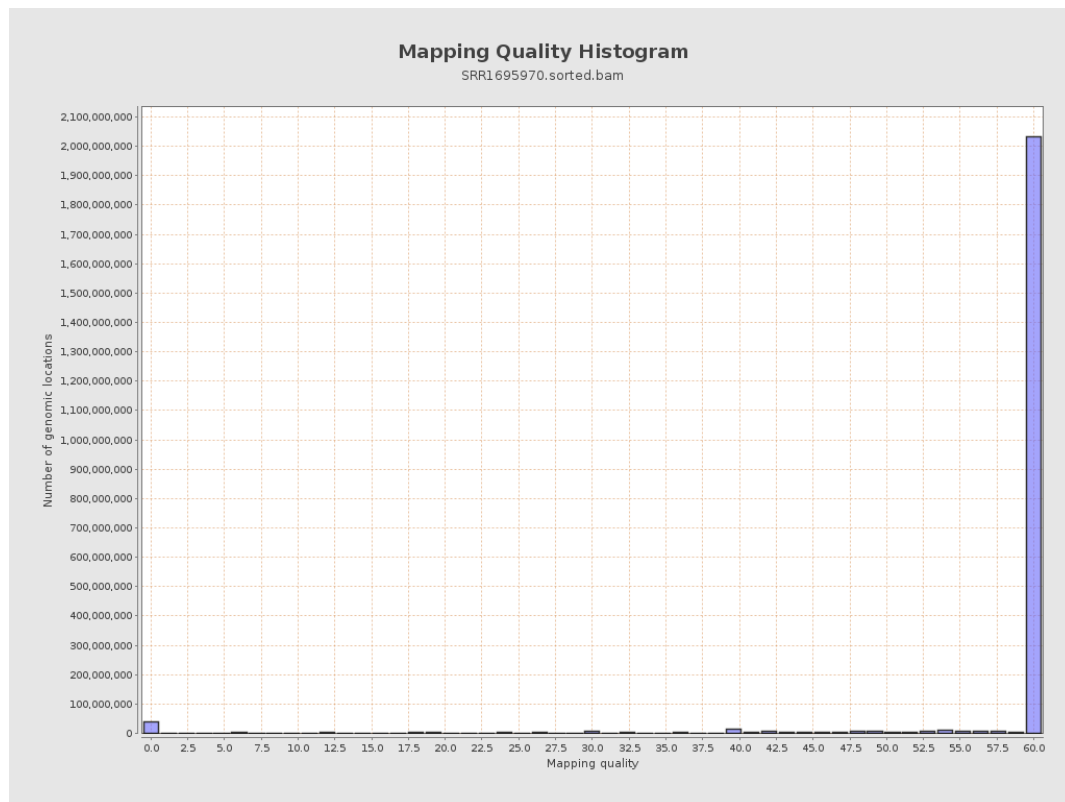
11. Results : Homopolymer Indels



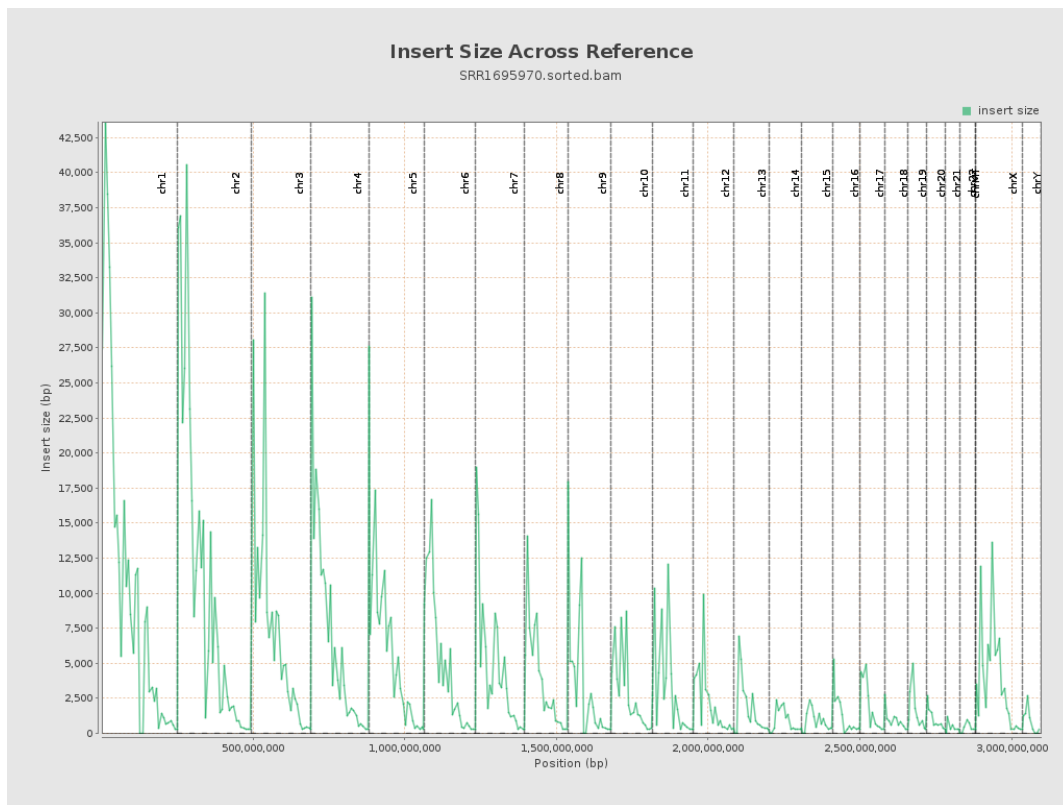
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

