

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/13 21:42:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695961.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_SRR1695961 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695961_1.fastq.gz SRR1695961_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 21:42:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695961.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	97,032,106
Mapped reads	96,497,722 / 99.45%
Unmapped reads	534,384 / 0.55%
Mapped paired reads	96,497,722 / 99.45%
Mapped reads, first in pair	48,349,389 / 49.83%
Mapped reads, second in pair	48,148,333 / 49.62%
Mapped reads, both in pair	96,153,054 / 99.09%
Mapped reads, singletons	344,668 / 0.36%
Secondary alignments	0
Supplementary alignments	945,372 / 0.97%
Read min/max/mean length	30 / 100 / 100.4
Duplicated reads (estimated)	4,201,309 / 4.33%
Duplication rate	3.75%
Clipped reads	5,339,291 / 5.5%

2.2. ACGT Content

Number/percentage of A's	2,772,864,112 / 28.95%
Number/percentage of C's	1,994,357,448 / 20.82%
Number/percentage of T's	2,759,635,924 / 28.82%
Number/percentage of G's	2,049,995,868 / 21.41%
Number/percentage of N's	166,136 / 0%

GC Percentage	42.23%
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2.3. Coverage

Mean	3.0944
Standard Deviation	4.5179

2.4. Mapping Quality

Mean Mapping Quality	54.08
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2.5. Insert size

Mean	74,063.54
Standard Deviation	2,632,642.53
P25/Median/P75	329 / 337 / 345

2.6. Mismatches and indels

General error rate	0.36%
Mismatches	32,343,473
Insertions	973,598
Mapped reads with at least one insertion	0.99%
Deletions	984,700
Mapped reads with at least one deletion	1%
Homopolymer indels	45.57%

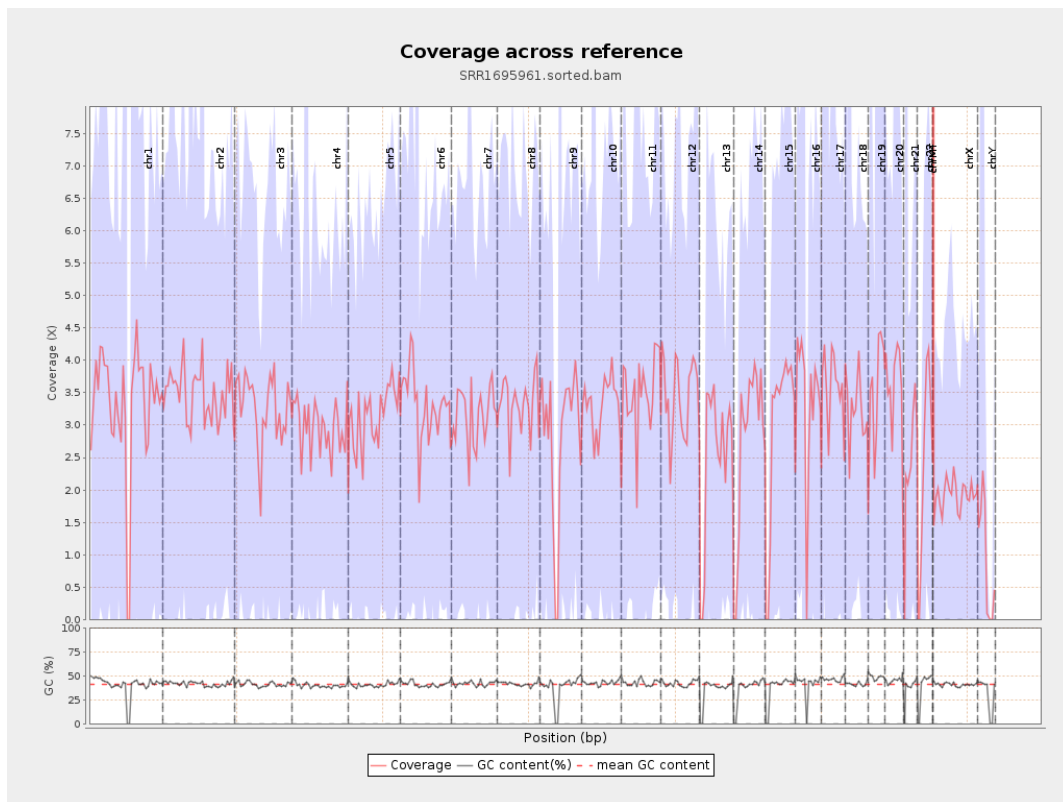
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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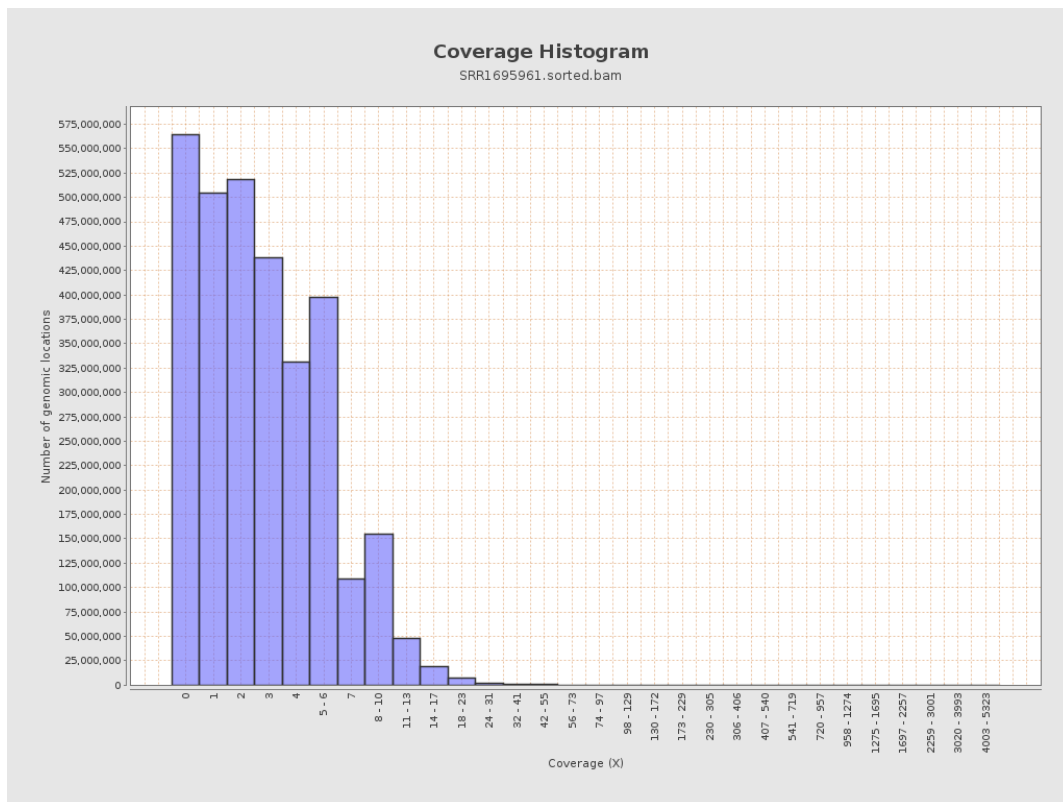
		bases	coverage	deviation
chr1	249250621	826008317	3.314	6.5779
chr2	243199373	847365057	3.4842	4.9202
chr3	198022430	643646551	3.2504	2.8702
chr4	191154276	569533447	2.9794	4.2703
chr5	180915260	571459040	3.1587	2.843
chr6	171115067	566380523	3.3099	3.6863
chr7	159138663	500073034	3.1424	3.3373
chr8	146364022	485679936	3.3183	3.2555
chr9	141213431	399552489	2.8294	4.1759
chr10	135534747	451127043	3.3285	5.2969
chr11	135006516	470186042	3.4827	3.5201
chr12	133851895	465629646	3.4787	3.3446
chr13	115169878	288481032	2.5048	2.8673
chr14	107349540	303267025	2.825	3.1006
chr15	102531392	303172272	2.9569	3.2589
chr16	90354753	296195027	3.2781	4.442
chr17	81195210	294147315	3.6227	5.2703
chr18	78077248	251837282	3.2255	7.1061
chr19	59128983	209606878	3.5449	5.3596
chr20	63025520	227045166	3.6024	3.6167
chr21	48129895	118935353	2.4711	6.0777
chr22	51304566	126036690	2.4566	3.2967
chrMT	16571	9484212	572.3379	170.4266
chrX	155270560	298238829	1.9208	2.252

chrY	59373566	56214503	0.9468	5.1017
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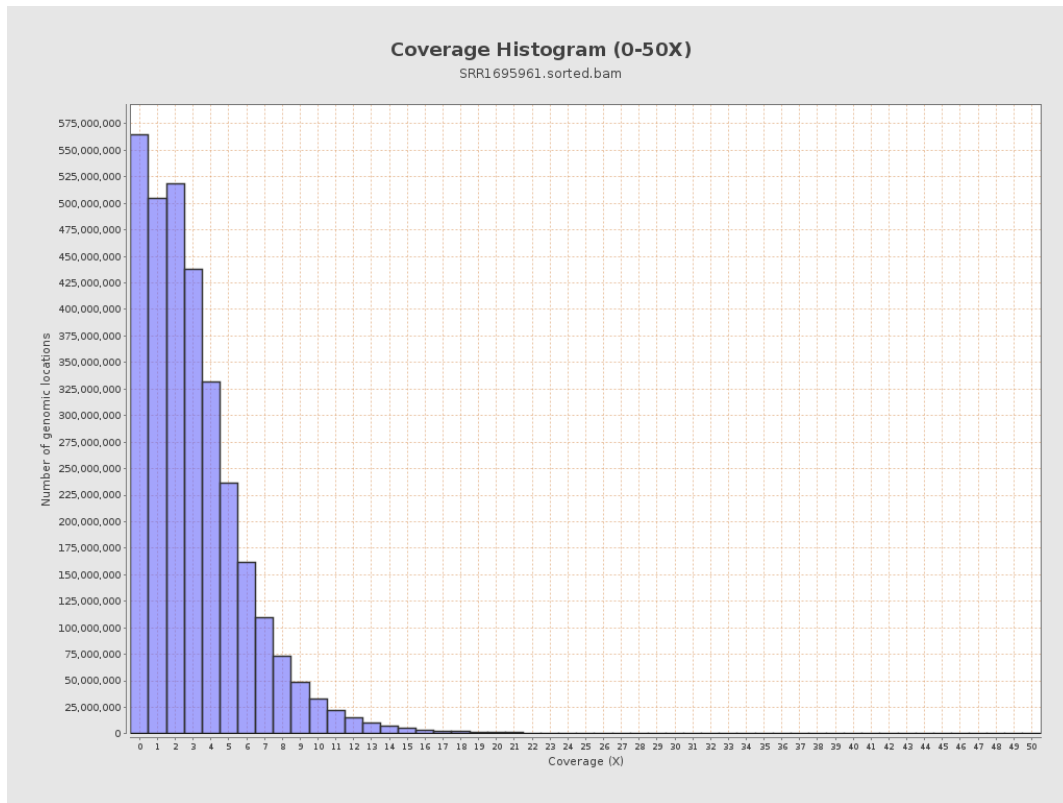
3. Results : Coverage across reference



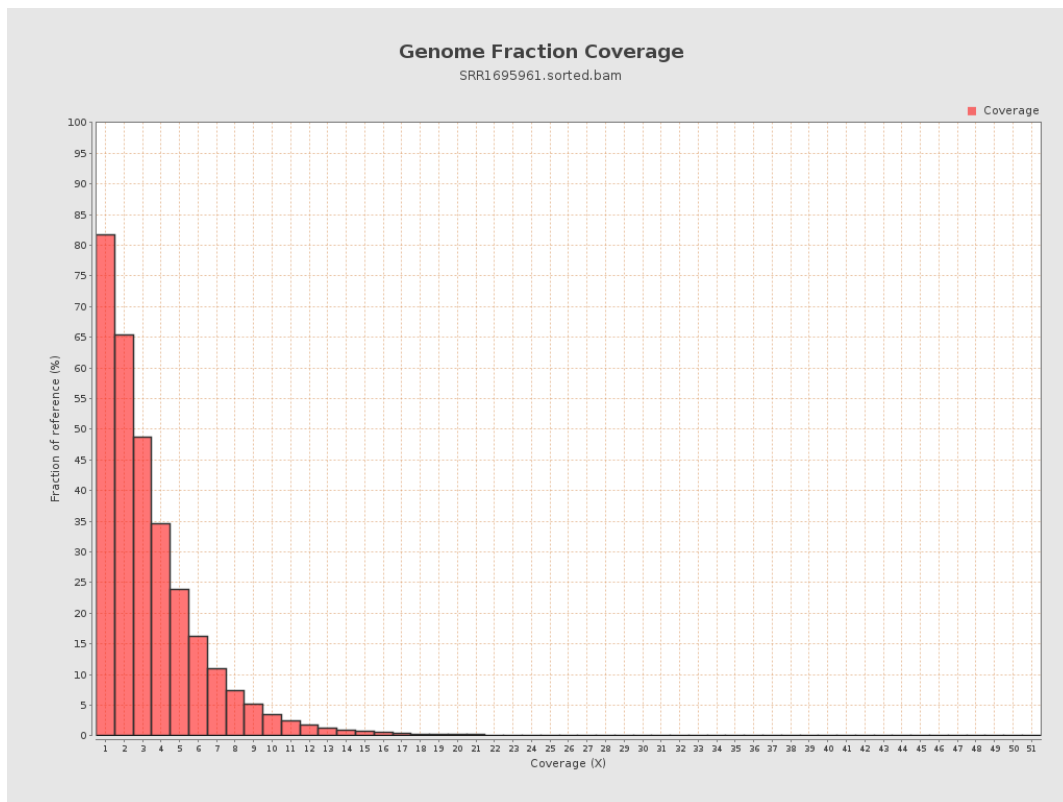
4. Results : Coverage Histogram



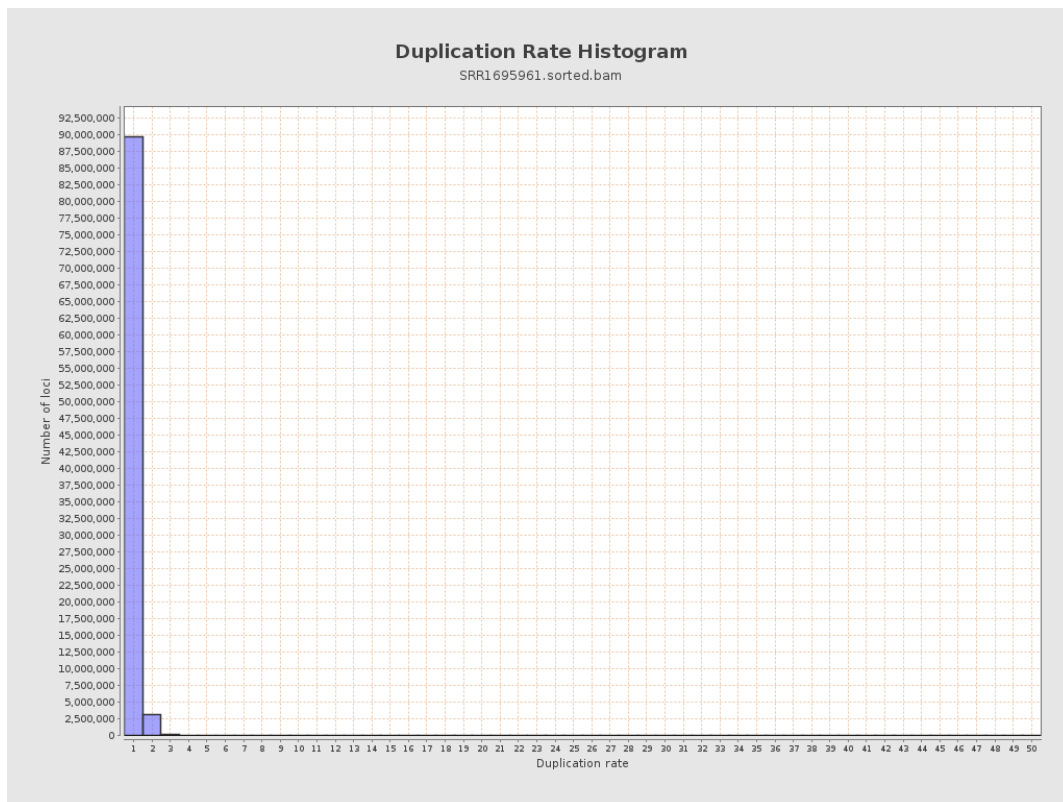
5. Results : Coverage Histogram (0-50X)



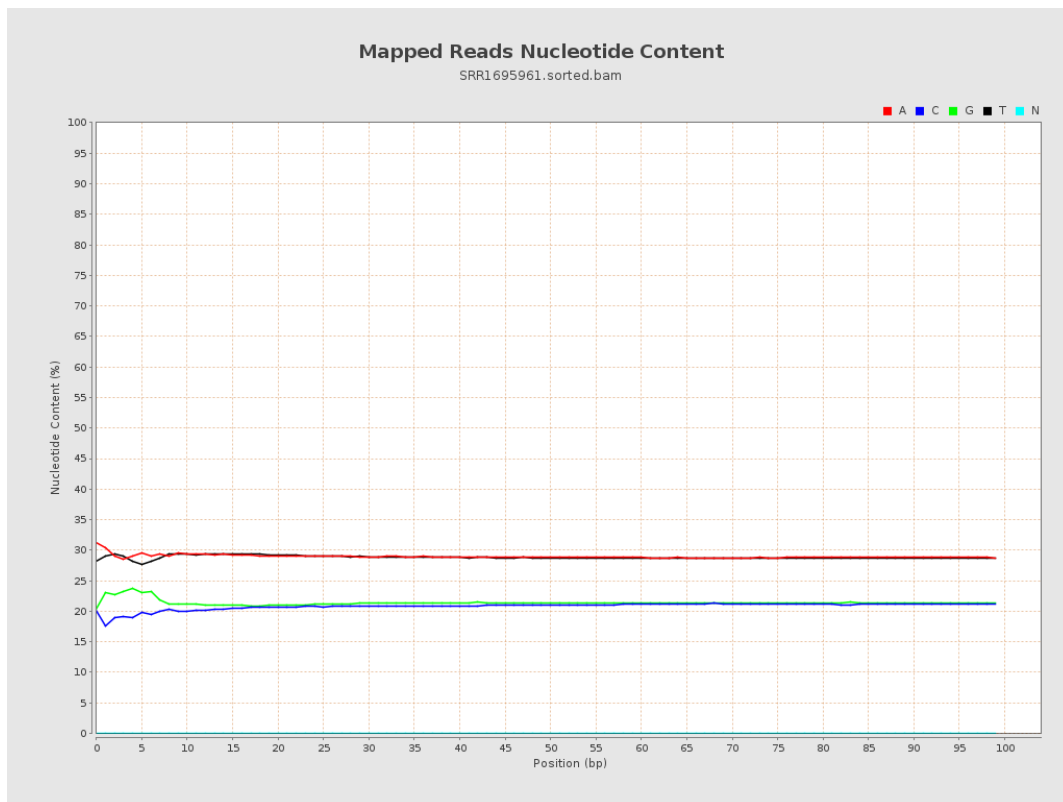
6. Results : Genome Fraction Coverage



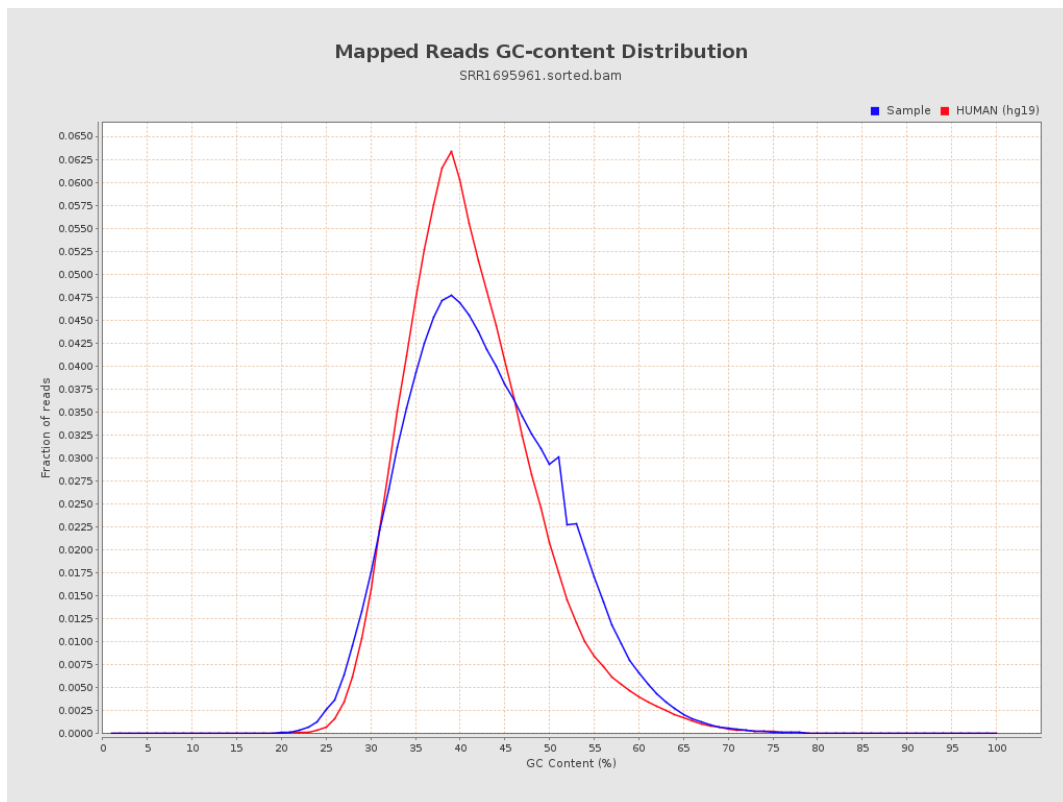
7. Results : Duplication Rate Histogram



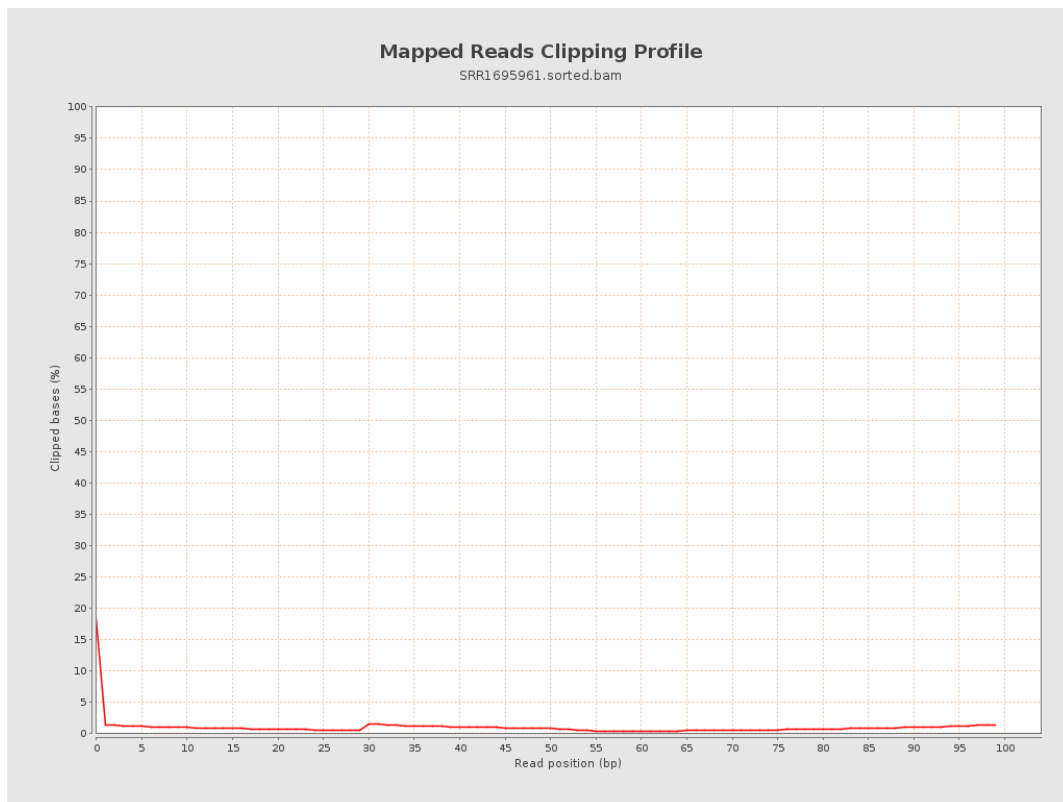
8. Results : Mapped Reads Nucleotide Content



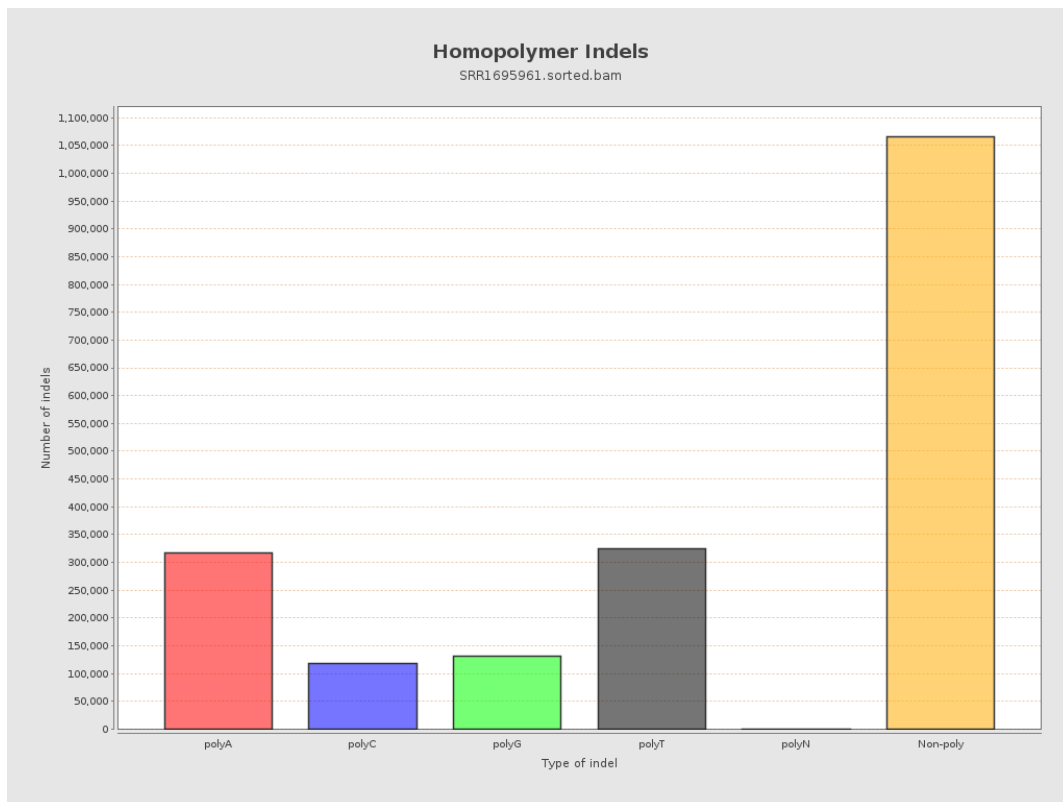
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



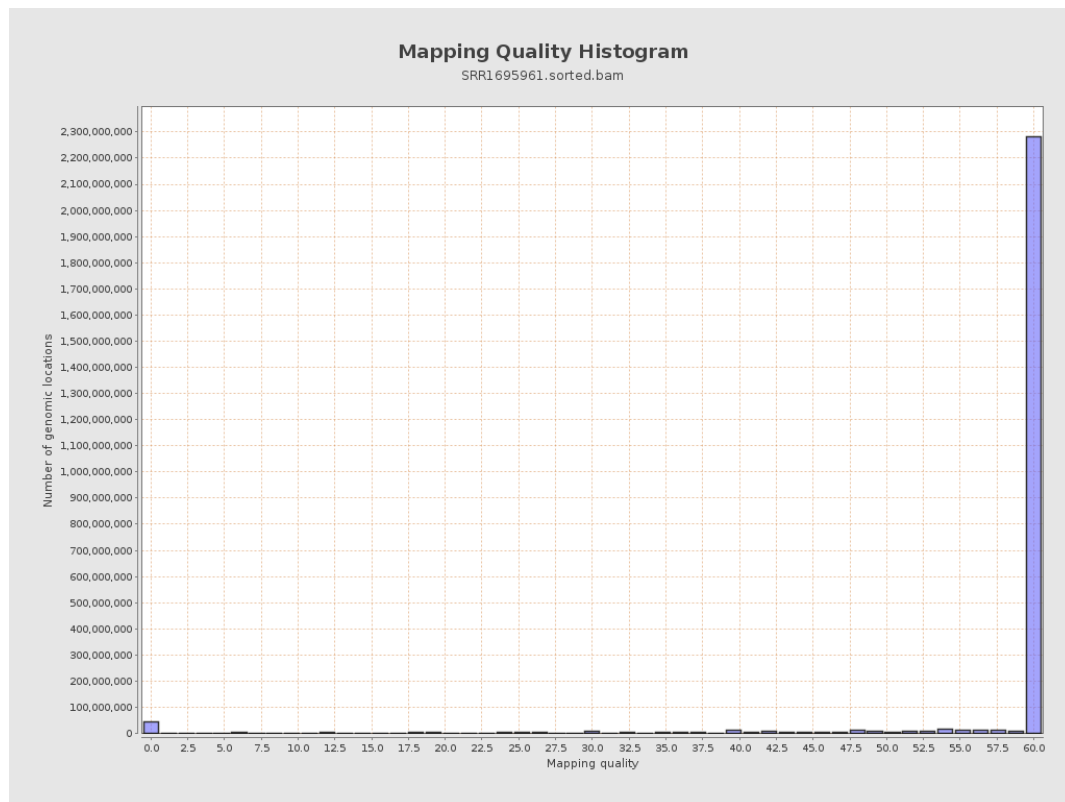
11. Results : Homopolymer Indels



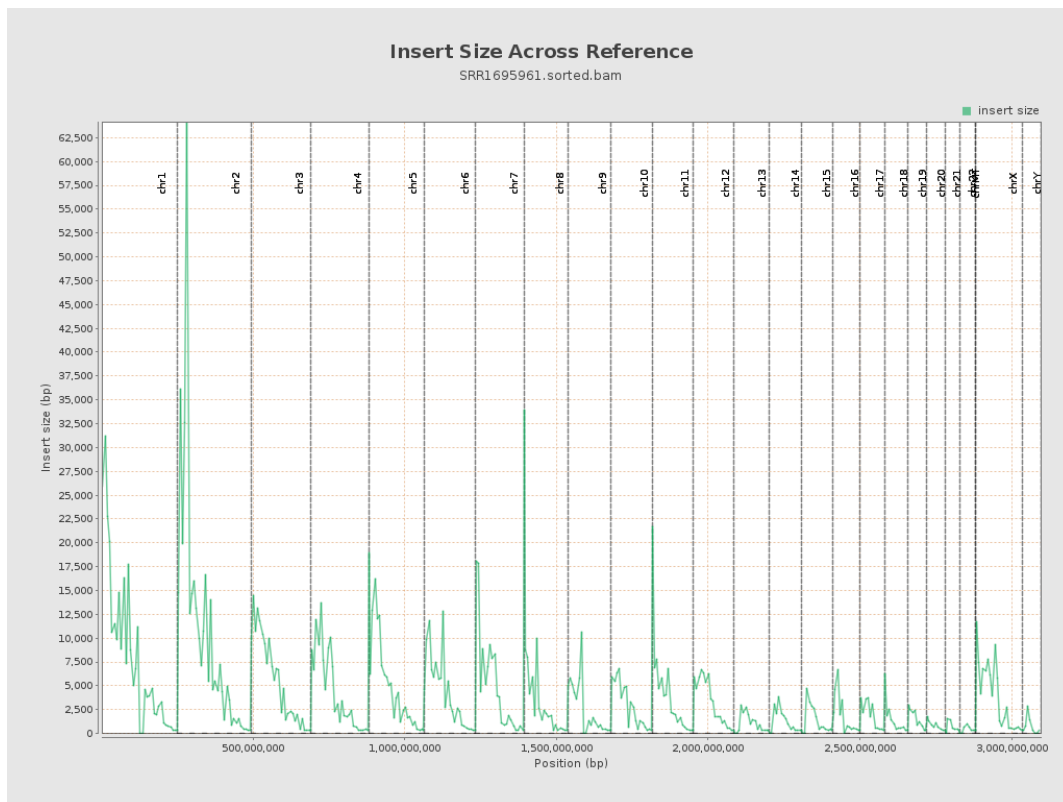
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

