

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 20:50:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472395.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR3472395 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472395_1.fastq.gz SRR3472395_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 20:50:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472395.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,376,156
Mapped reads	14,235,618 / 99.02%
Unmapped reads	140,538 / 0.98%
Mapped paired reads	14,235,618 / 99.02%
Mapped reads, first in pair	7,138,610 / 49.66%
Mapped reads, second in pair	7,097,008 / 49.37%
Mapped reads, both in pair	14,161,568 / 98.51%
Mapped reads, singletons	74,050 / 0.52%
Secondary alignments	0
Supplementary alignments	52,806 / 0.37%
Read min/max/mean length	30 / 100 / 99.25
Duplicated reads (estimated)	8,398,542 / 58.42%
Duplication rate	46.63%
Clipped reads	1,052,408 / 7.32%

2.2. ACGT Content

Number/percentage of A's	369,246,203 / 26.48%
Number/percentage of C's	328,519,848 / 23.56%
Number/percentage of T's	370,458,194 / 26.57%
Number/percentage of G's	325,854,317 / 23.37%
Number/percentage of N's	172,244 / 0.01%

GC Percentage	46.93%
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2.3. Coverage

Mean	0.4504
Standard Deviation	13.3862

2.4. Mapping Quality

Mean Mapping Quality	54.86
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2.5. Insert size

Mean	18,594.34
Standard Deviation	1,326,194.23
P25/Median/P75	153 / 212 / 285

2.6. Mismatches and indels

General error rate	0.56%
Mismatches	7,612,322
Insertions	77,024
Mapped reads with at least one insertion	0.54%
Deletions	70,562
Mapped reads with at least one deletion	0.48%
Homopolymer indels	45.26%

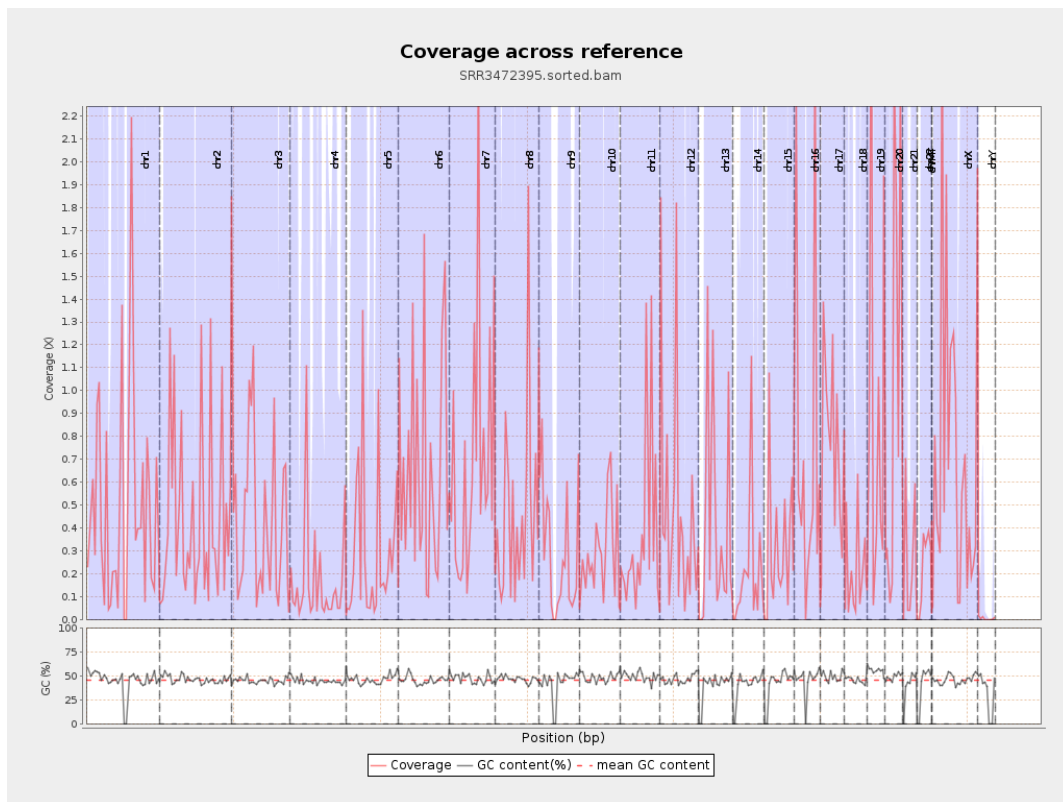
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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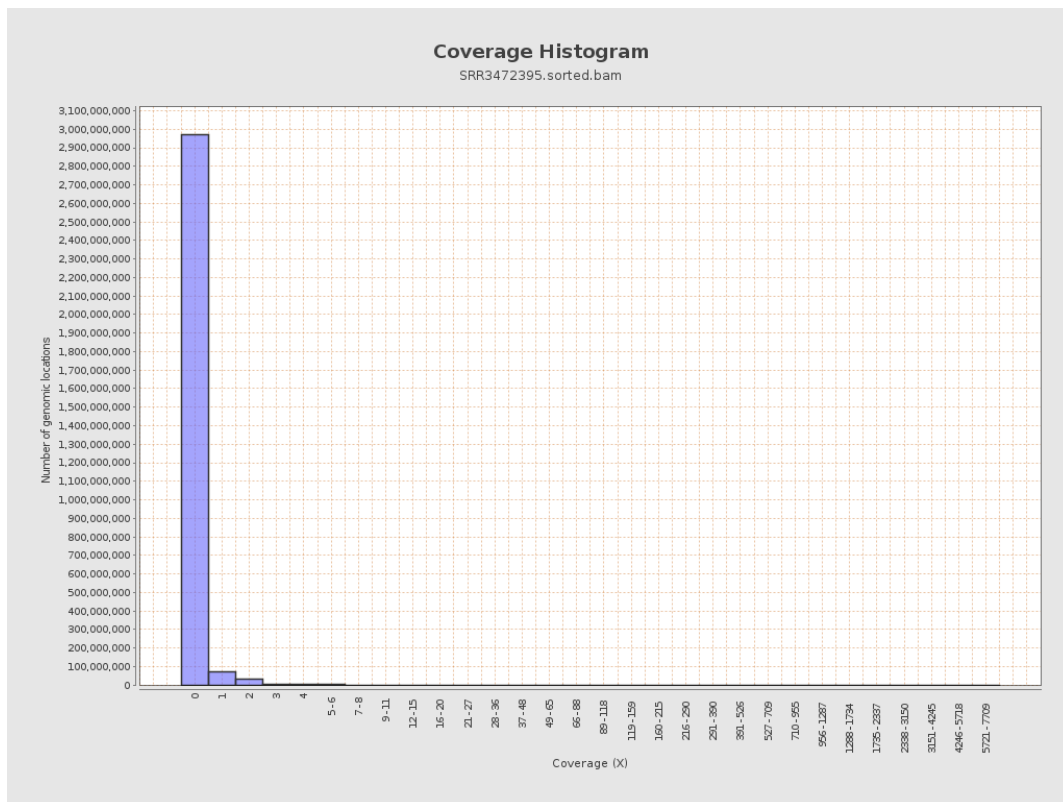
		bases	coverage	deviation
chr1	249250621	127630857	0.5121	14.769
chr2	243199373	108896982	0.4478	14.47
chr3	198022430	89197395	0.4504	11.3881
chr4	191154276	31016045	0.1623	5.8803
chr5	180915260	54992166	0.304	9.7365
chr6	171115067	110443500	0.6454	17.7803
chr7	159138663	111923593	0.7033	17.1928
chr8	146364022	66490918	0.4543	12.259
chr9	141213431	41236634	0.292	7.0848
chr10	135534747	40050825	0.2955	8.7701
chr11	135006516	49536270	0.3669	12.1391
chr12	133851895	65859488	0.492	11.2761
chr13	115169878	47225064	0.41	13.2208
chr14	107349540	21482429	0.2001	5.5055
chr15	102531392	31870231	0.3108	10.0994
chr16	90354753	69437390	0.7685	17.9359
chr17	81195210	61422996	0.7565	19.616
chr18	78077248	17081145	0.2188	7.8499
chr19	59128983	50831283	0.8597	21.0653
chr20	63025520	64554775	1.0243	25.1524
chr21	48129895	12596347	0.2617	11.6048
chr22	51304566	11545971	0.225	5.6303
chrMT	16571	7184	0.4335	0.8416
chrX	155270560	108830314	0.7009	17.7842

chrY	59373566	285545	0.0048	0.3377
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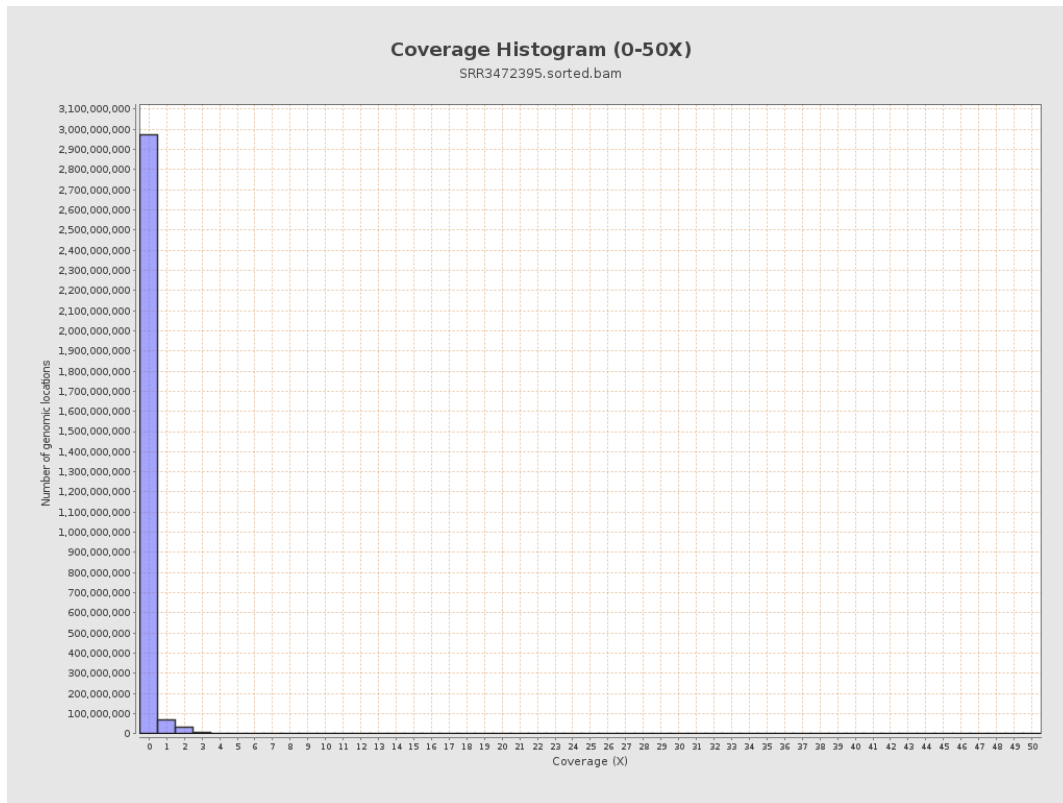
3. Results : Coverage across reference



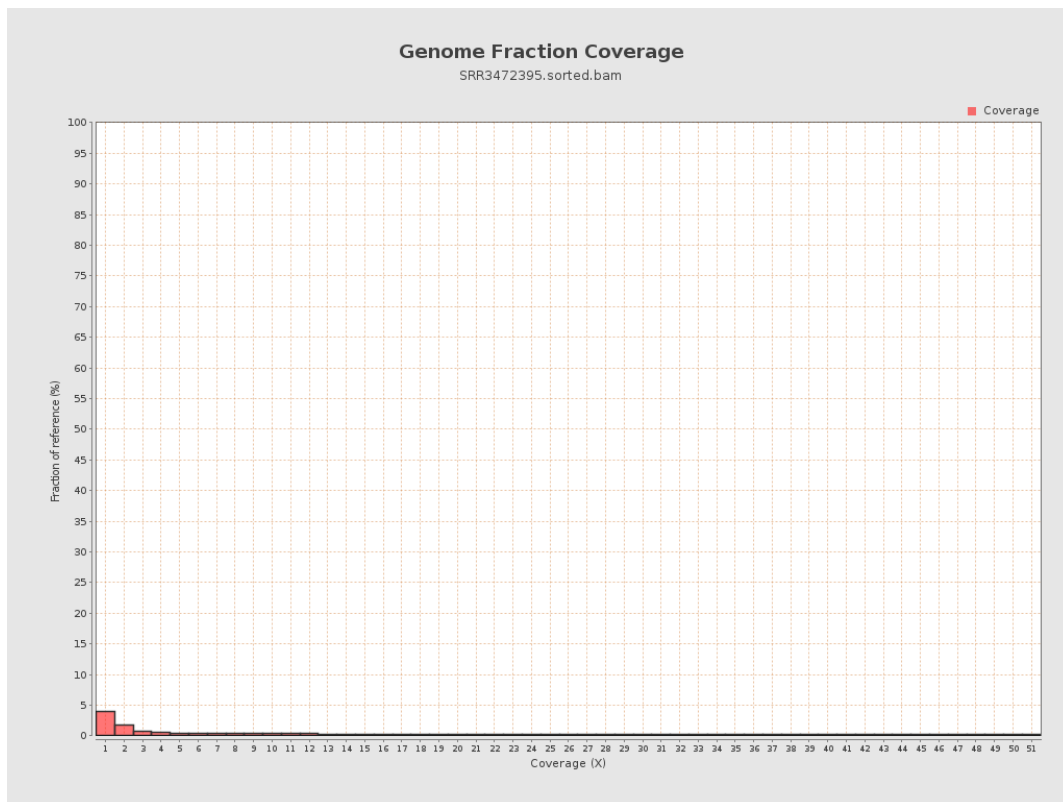
4. Results : Coverage Histogram



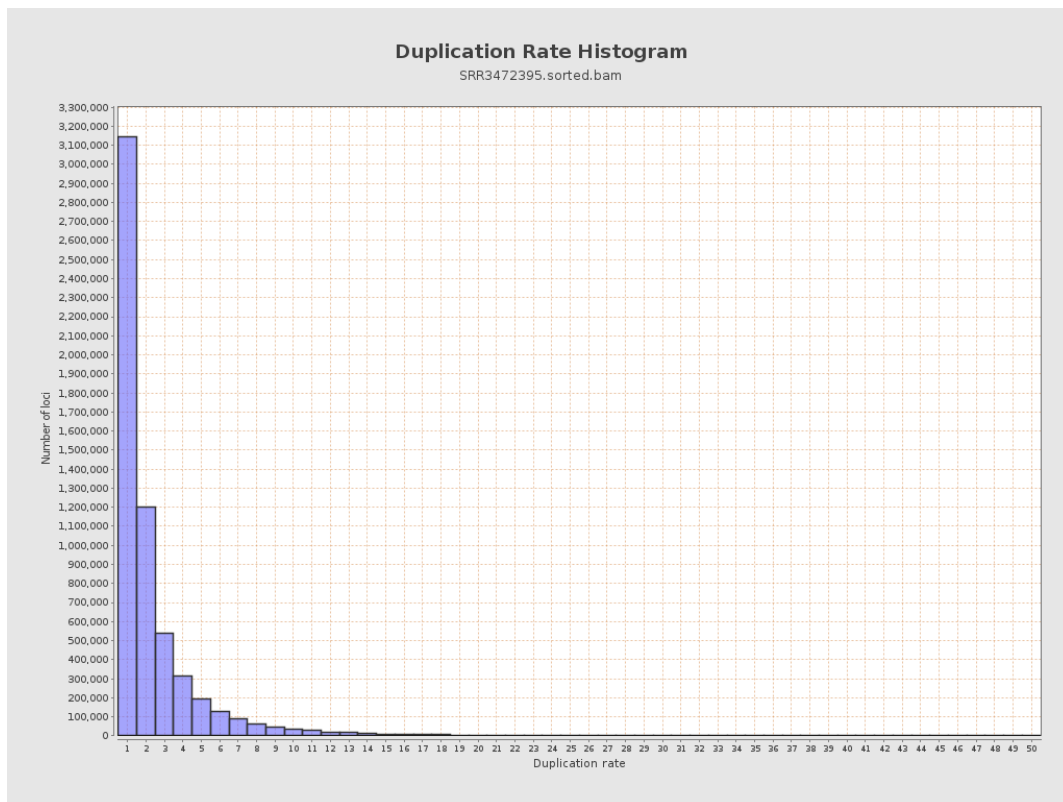
5. Results : Coverage Histogram (0-50X)



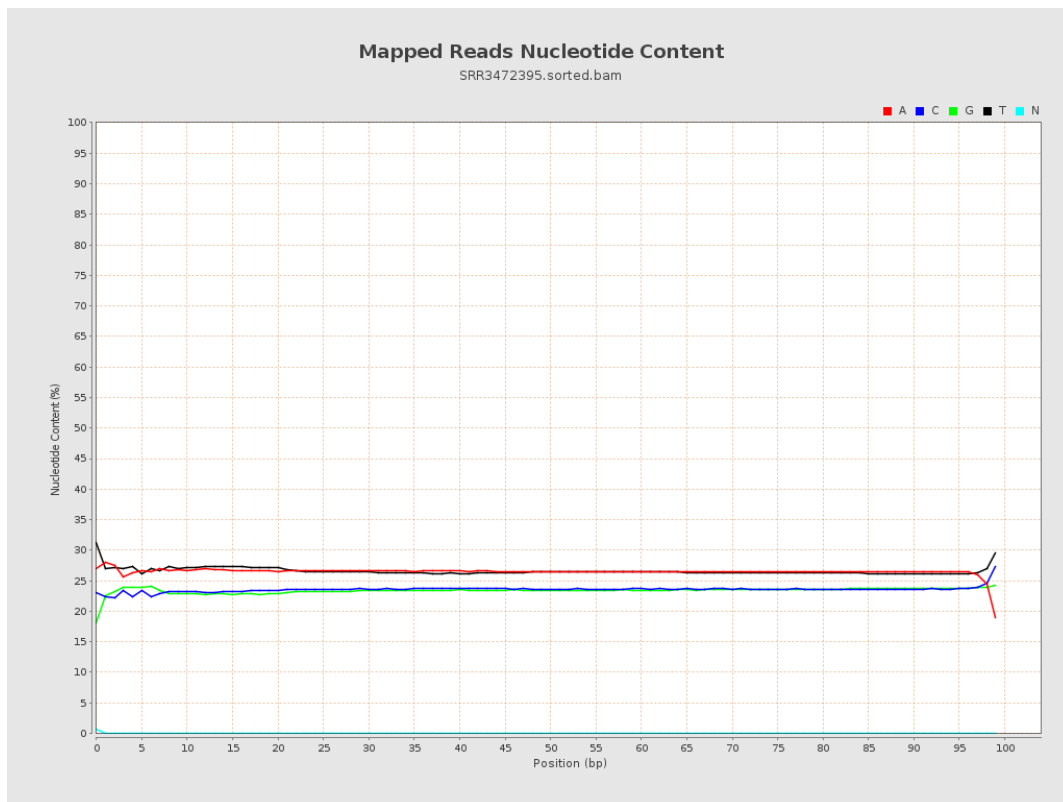
6. Results : Genome Fraction Coverage



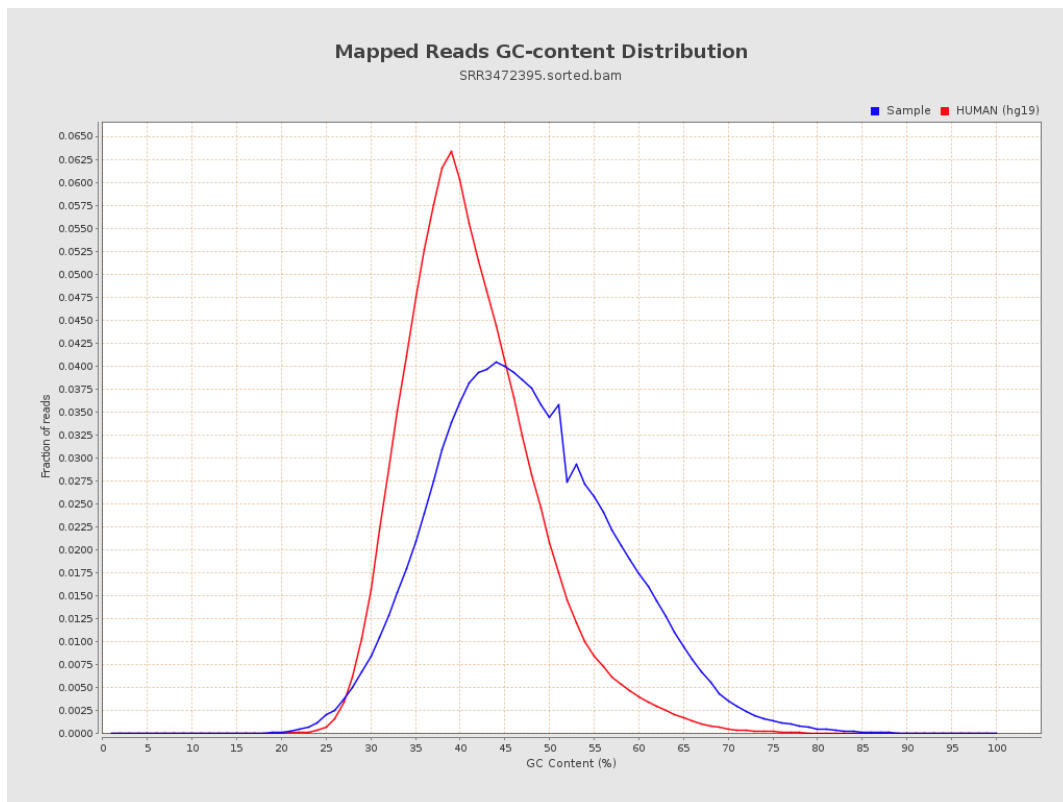
7. Results : Duplication Rate Histogram



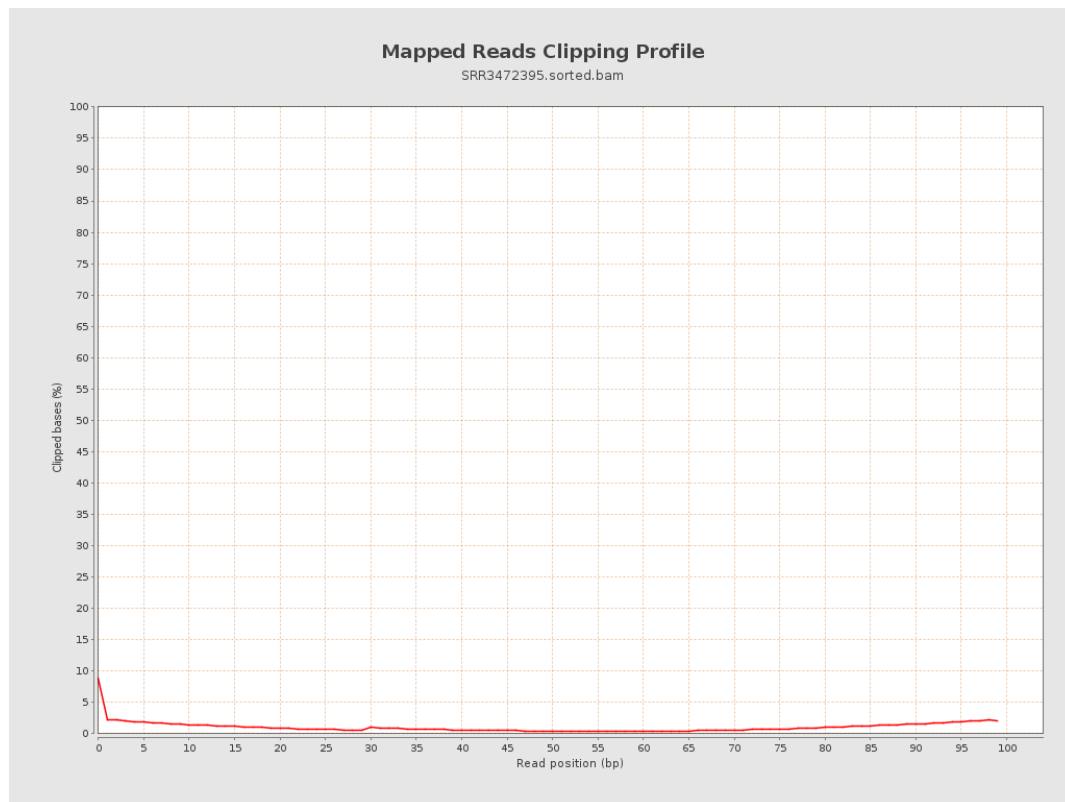
8. Results : Mapped Reads Nucleotide Content



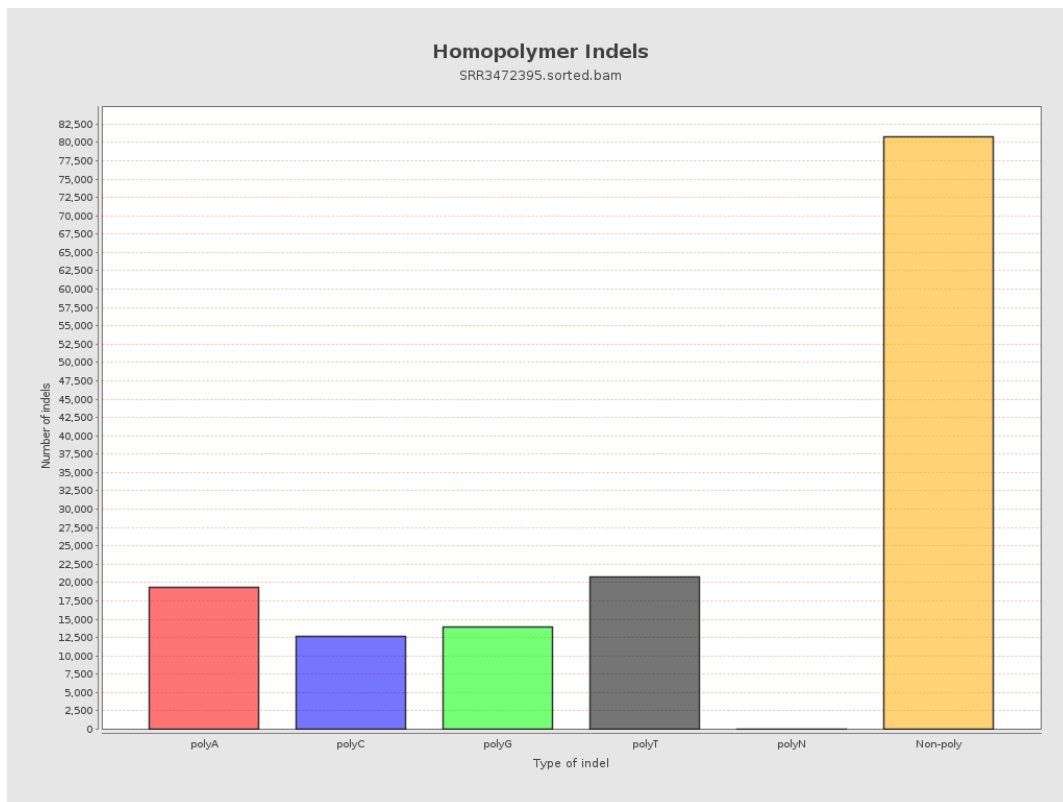
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



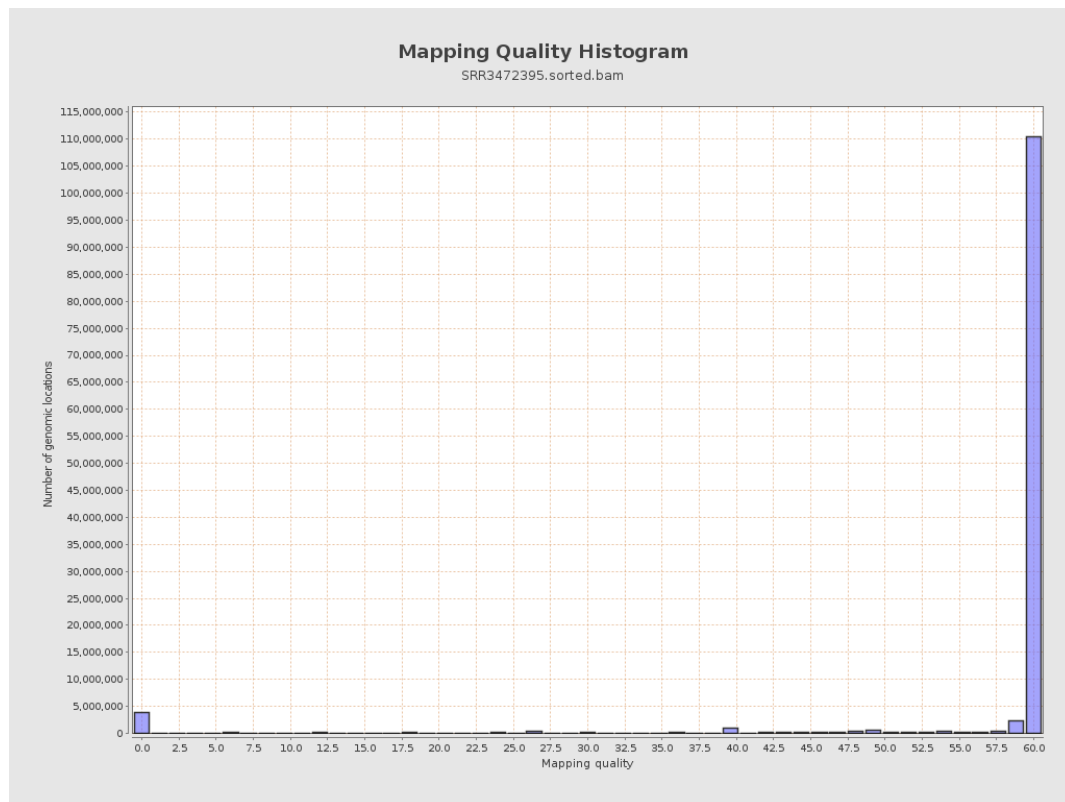
11. Results : Homopolymer Indels



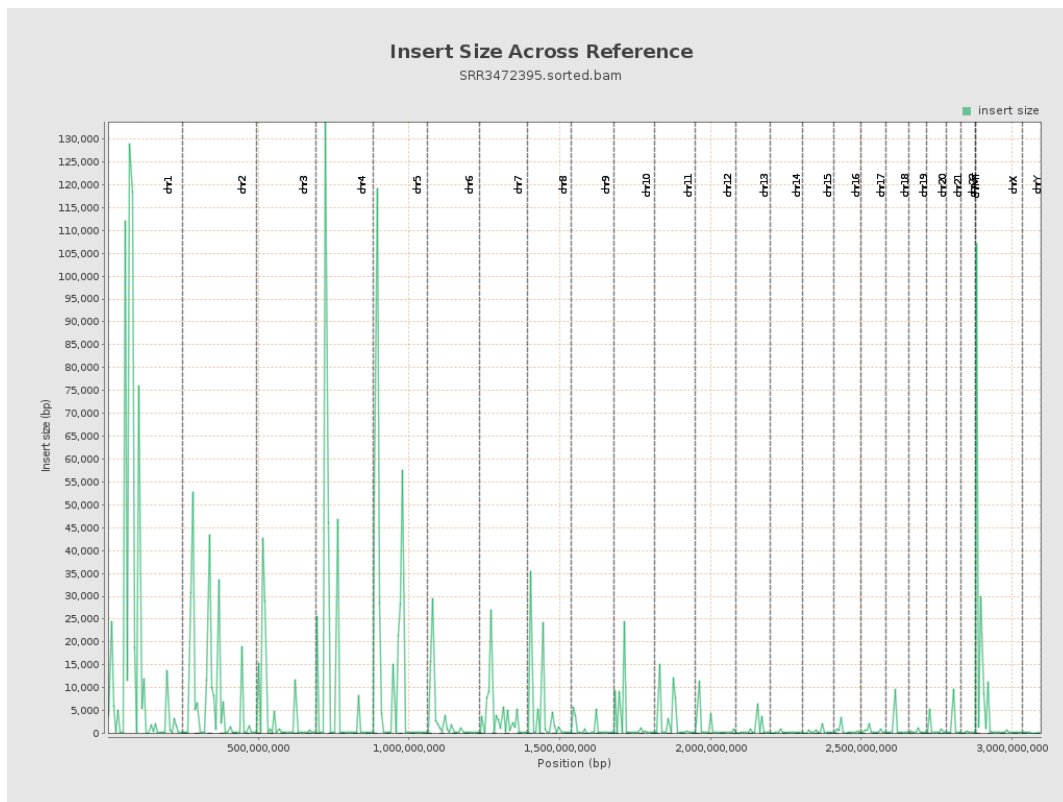
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

