

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 19:26:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472393.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_SRR3472393 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472393_1.fastq.gz SRR3472393_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 19:26:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472393.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,700,192
Mapped reads	20,506,361 / 99.06%
Unmapped reads	193,831 / 0.94%
Mapped paired reads	20,506,361 / 99.06%
Mapped reads, first in pair	10,291,359 / 49.72%
Mapped reads, second in pair	10,215,002 / 49.35%
Mapped reads, both in pair	20,384,800 / 98.48%
Mapped reads, singletons	121,561 / 0.59%
Secondary alignments	0
Supplementary alignments	74,936 / 0.36%
Read min/max/mean length	30 / 100 / 99.48
Duplicated reads (estimated)	13,155,514 / 63.55%
Duplication rate	49.45%
Clipped reads	1,303,040 / 6.29%

2.2. ACGT Content

Number/percentage of A's	540,745,454 / 26.82%
Number/percentage of C's	468,664,684 / 23.25%
Number/percentage of T's	542,378,950 / 26.9%
Number/percentage of G's	463,874,432 / 23.01%
Number/percentage of N's	252,364 / 0.01%

GC Percentage	46.26%
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2.3. Coverage

Mean	0.6513
Standard Deviation	18.6303

2.4. Mapping Quality

Mean Mapping Quality	54.97
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2.5. Insert size

Mean	17,243.04
Standard Deviation	1,311,418.37
P25/Median/P75	164 / 226 / 302

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	11,464,343
Insertions	117,673
Mapped reads with at least one insertion	0.57%
Deletions	98,158
Mapped reads with at least one deletion	0.47%
Homopolymer indels	45.56%

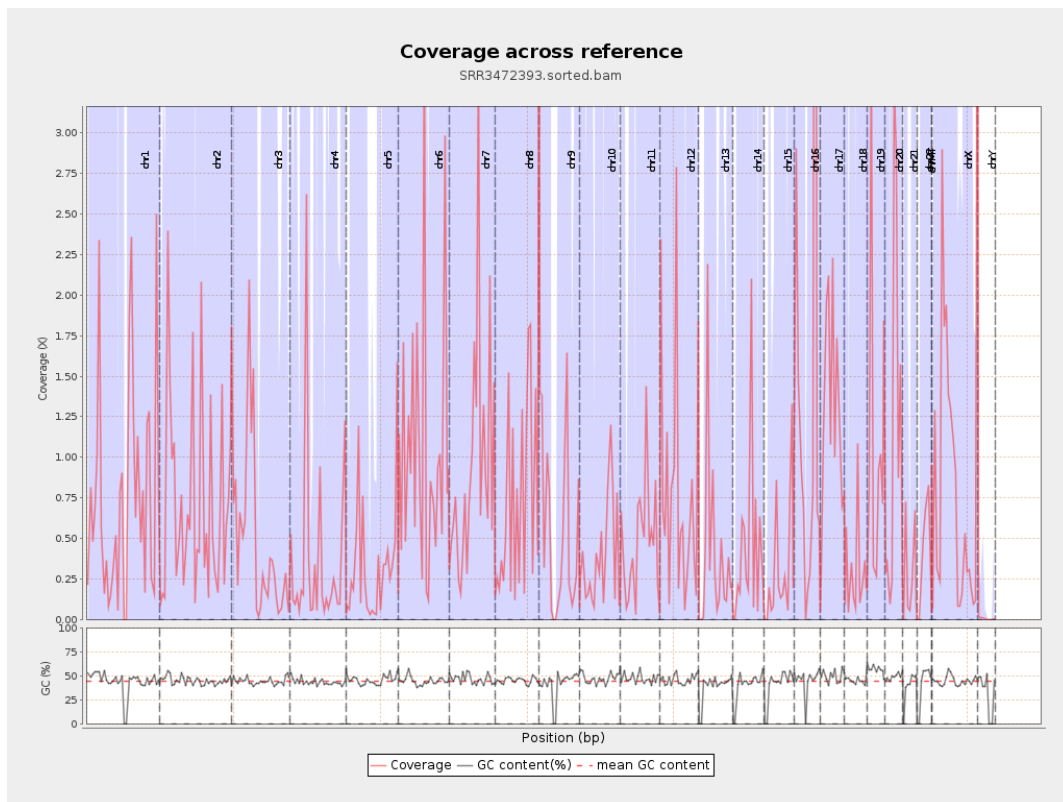
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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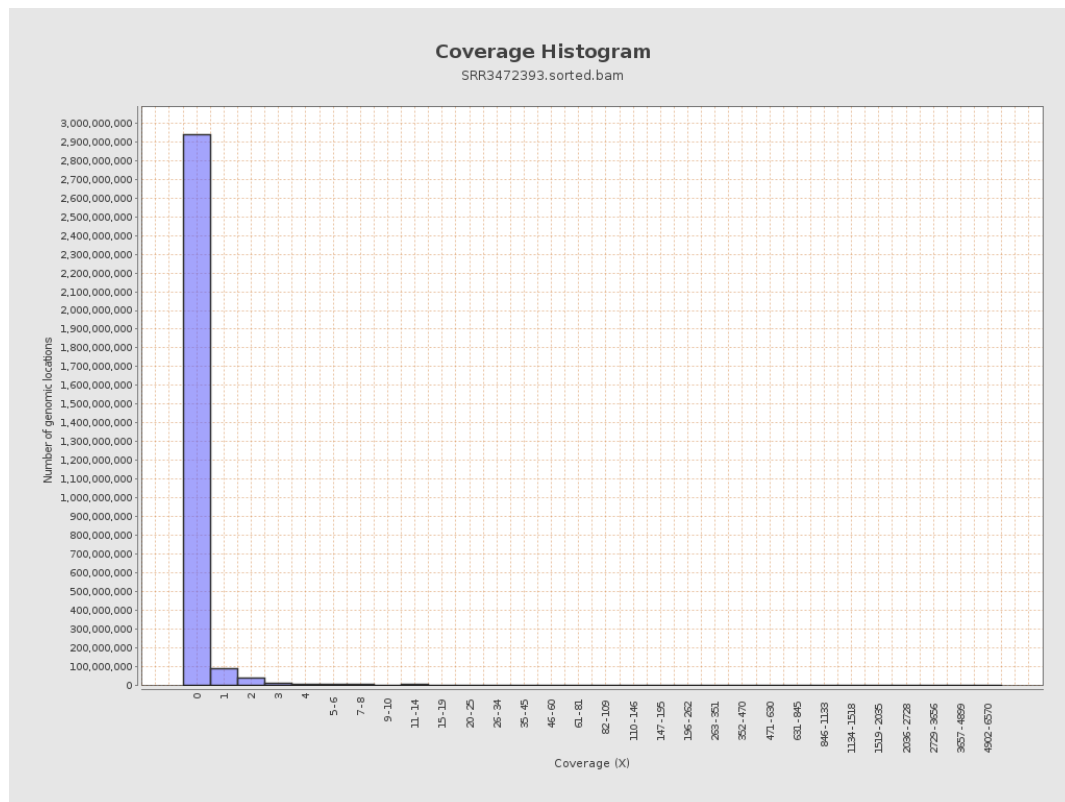
		bases	coverage	deviation
chr1	249250621	188507192	0.7563	20.4919
chr2	243199373	170773846	0.7022	19.3518
chr3	198022430	100537432	0.5077	11.22
chr4	191154276	65606526	0.3432	14.3689
chr5	180915260	60767957	0.3359	11.6239
chr6	171115067	180920788	1.0573	23.434
chr7	159138663	152275489	0.9569	22.8212
chr8	146364022	107326720	0.7333	20.5936
chr9	141213431	82959632	0.5875	14.447
chr10	135534747	53396474	0.394	13.4913
chr11	135006516	64910329	0.4808	13.4391
chr12	133851895	104617938	0.7816	17.1266
chr13	115169878	44617274	0.3874	11.6229
chr14	107349540	45411601	0.423	13.9615
chr15	102531392	32444525	0.3164	14.0742
chr16	90354753	129699403	1.4354	39.3945
chr17	81195210	106357558	1.3099	27.1277
chr18	78077248	23738281	0.304	11.8503
chr19	59128983	63296157	1.0705	20.7945
chr20	63025520	74398339	1.1804	29.818
chr21	48129895	13827092	0.2873	11.9018
chr22	51304566	19980360	0.3894	11.1373
chrMT	16571	15850	0.9565	1.3245
chrX	155270560	129484748	0.8339	21.2887

chrY	59373566	309871	0.0052	0.2871
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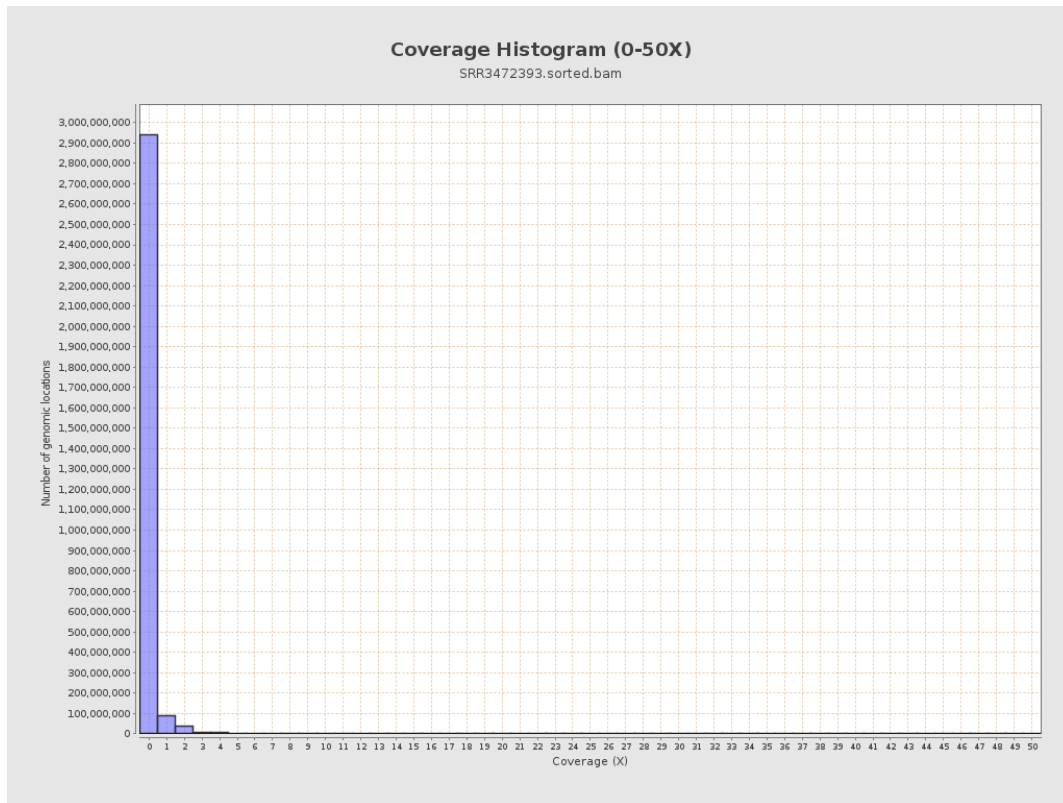
3. Results : Coverage across reference



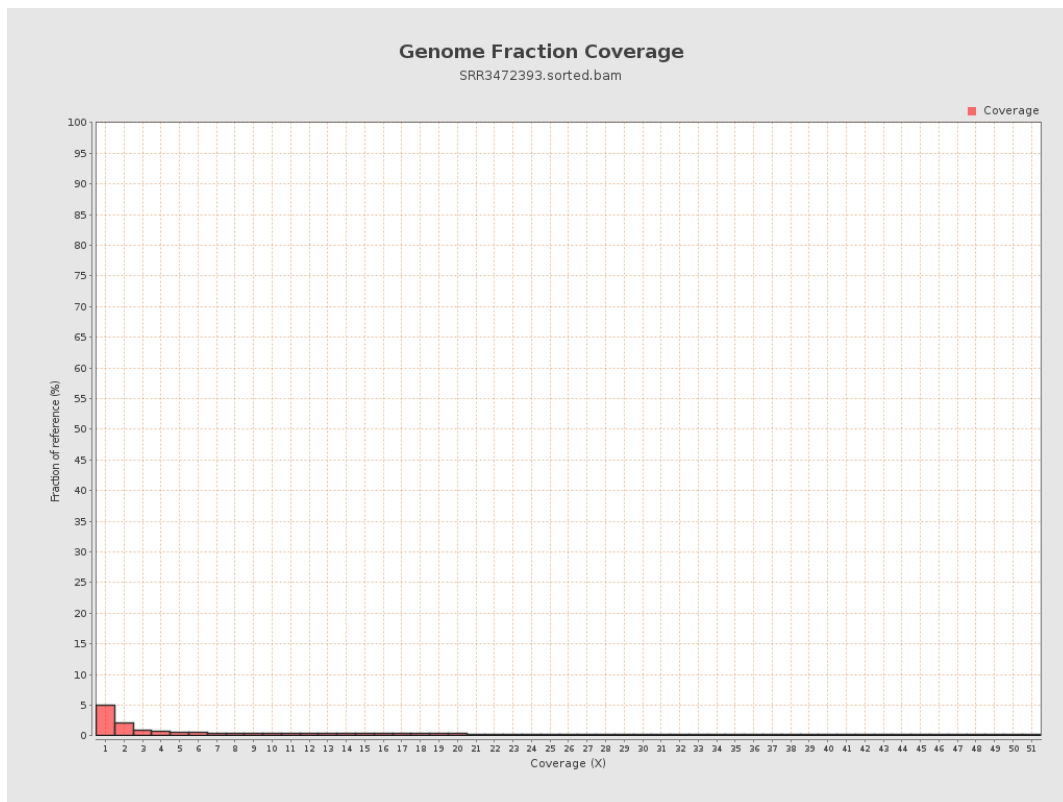
4. Results : Coverage Histogram



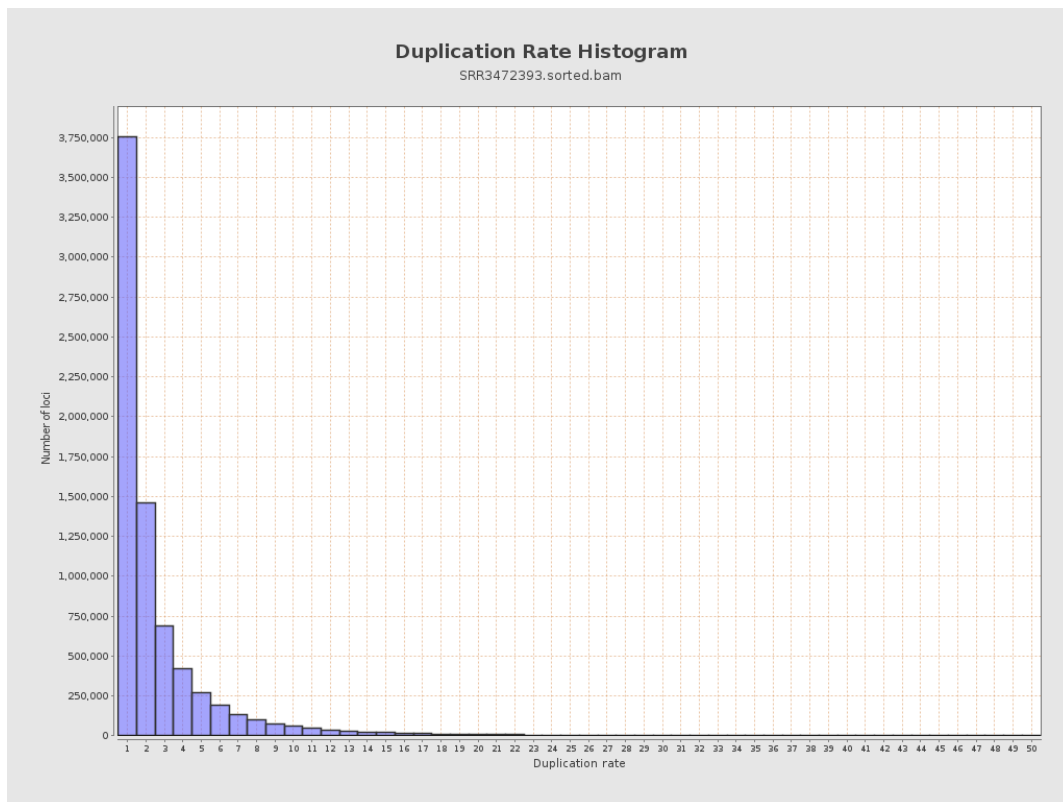
5. Results : Coverage Histogram (0-50X)



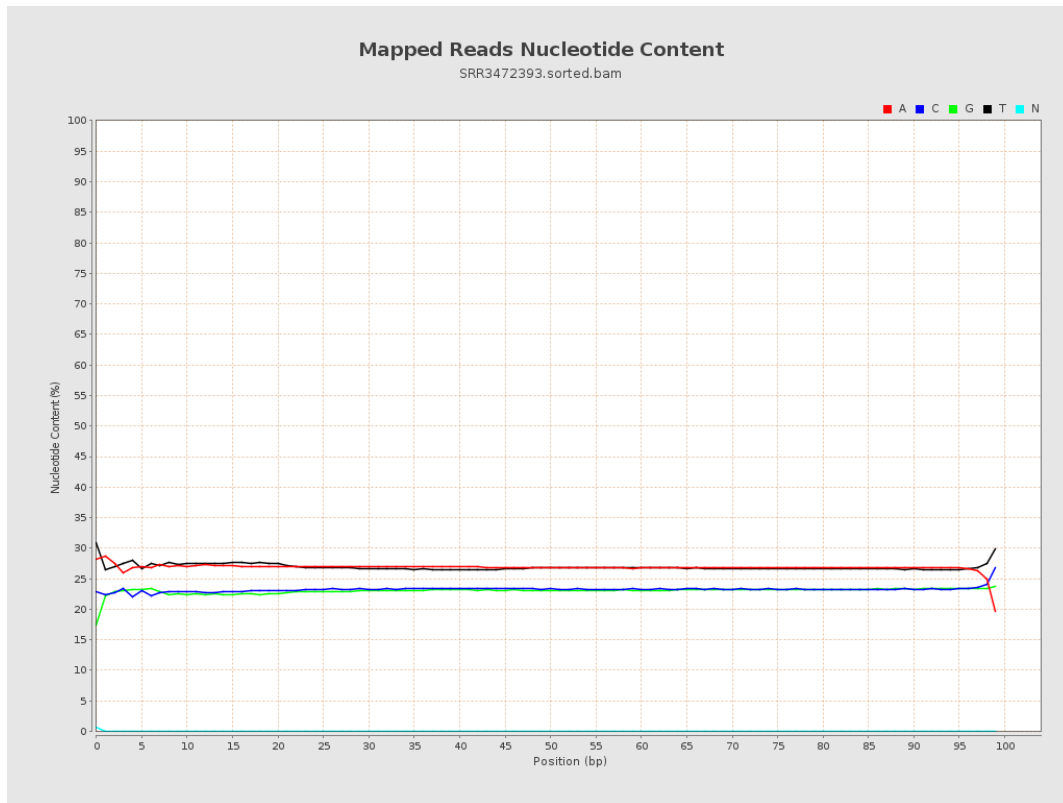
6. Results : Genome Fraction Coverage



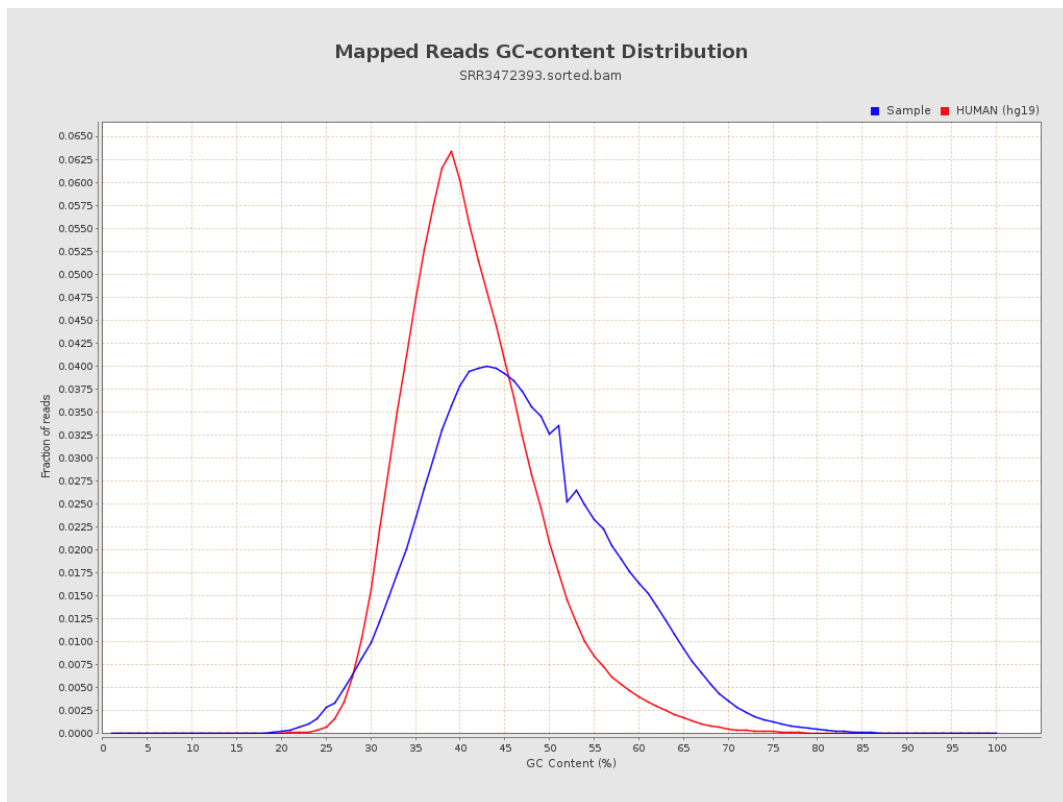
7. Results : Duplication Rate Histogram



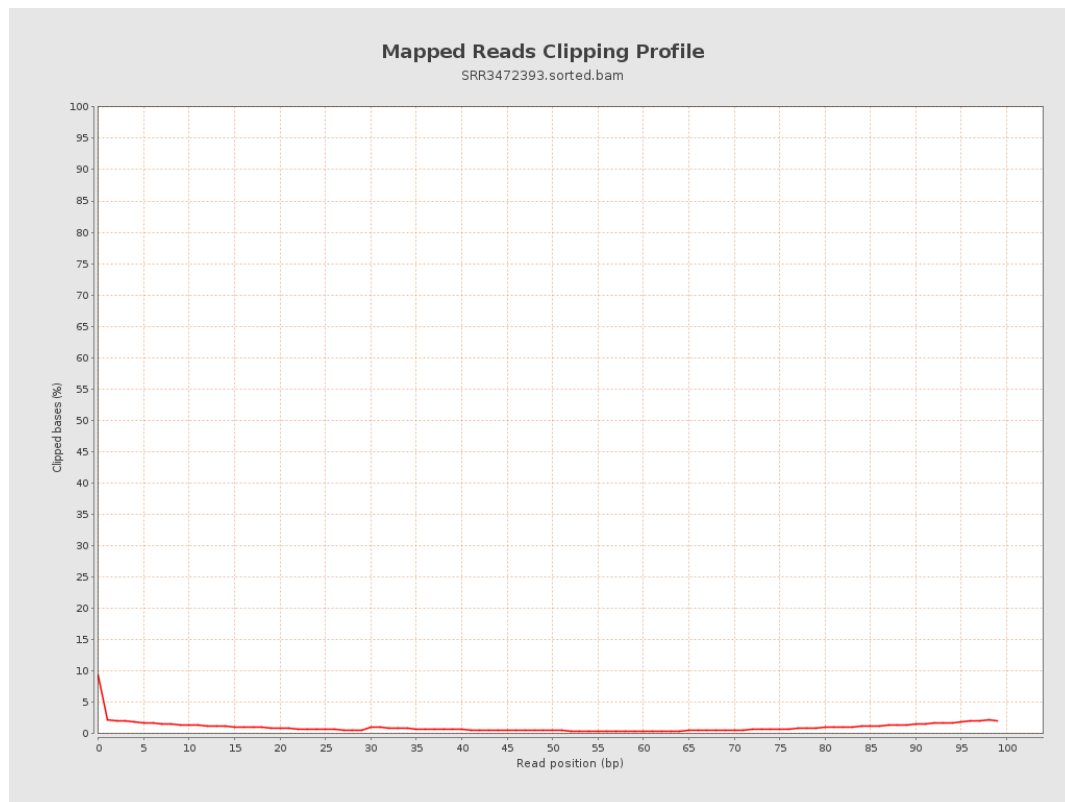
8. Results : Mapped Reads Nucleotide Content



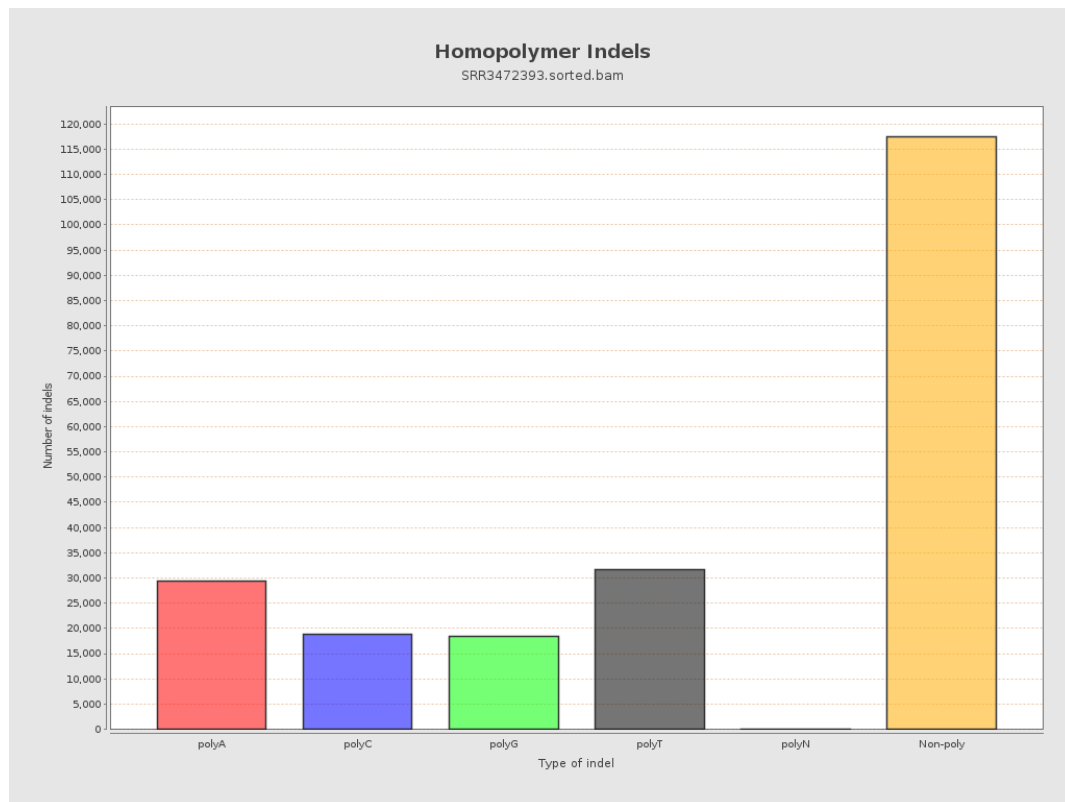
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



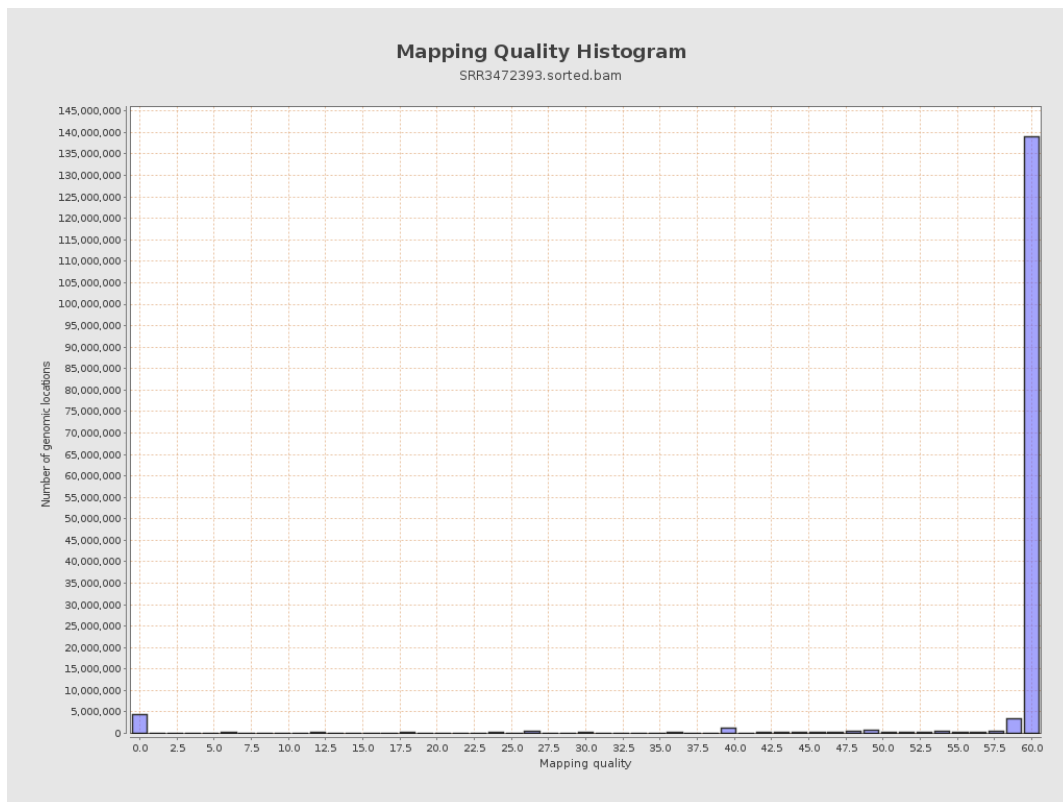
11. Results : Homopolymer Indels



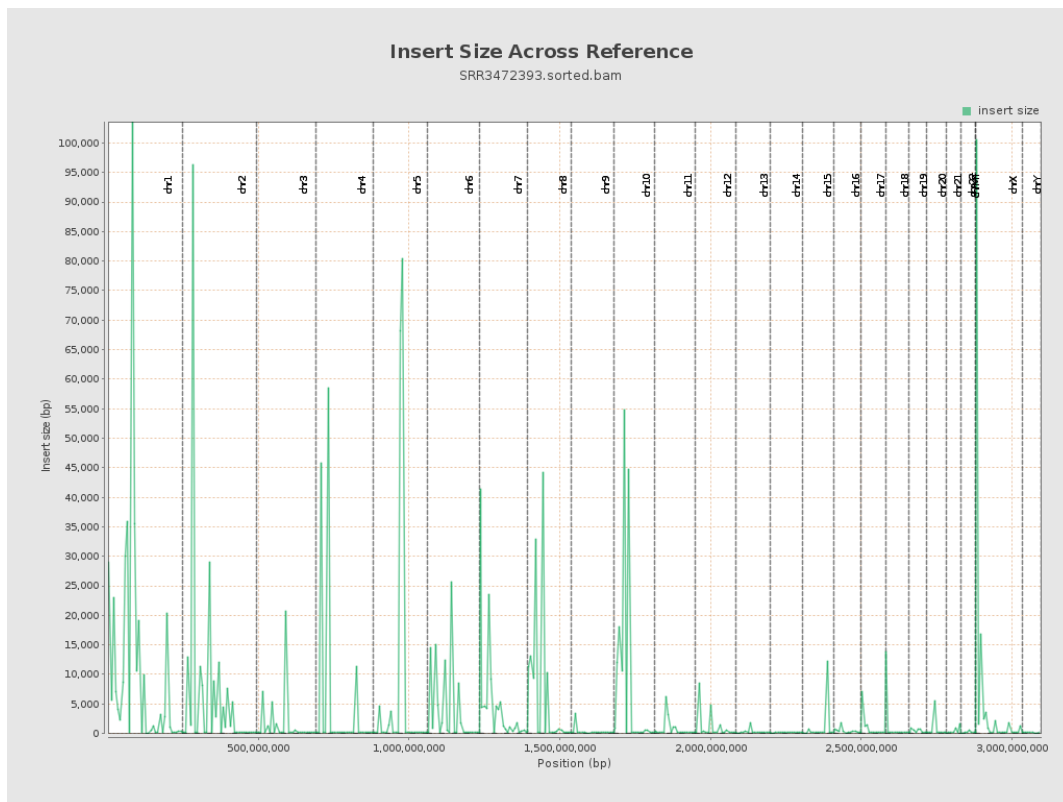
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

