
Transcriptomic Profiling of circRNAs in rat Hippocampus after Deep Hypothermic Circulatory Arrest

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Supplementary Figure

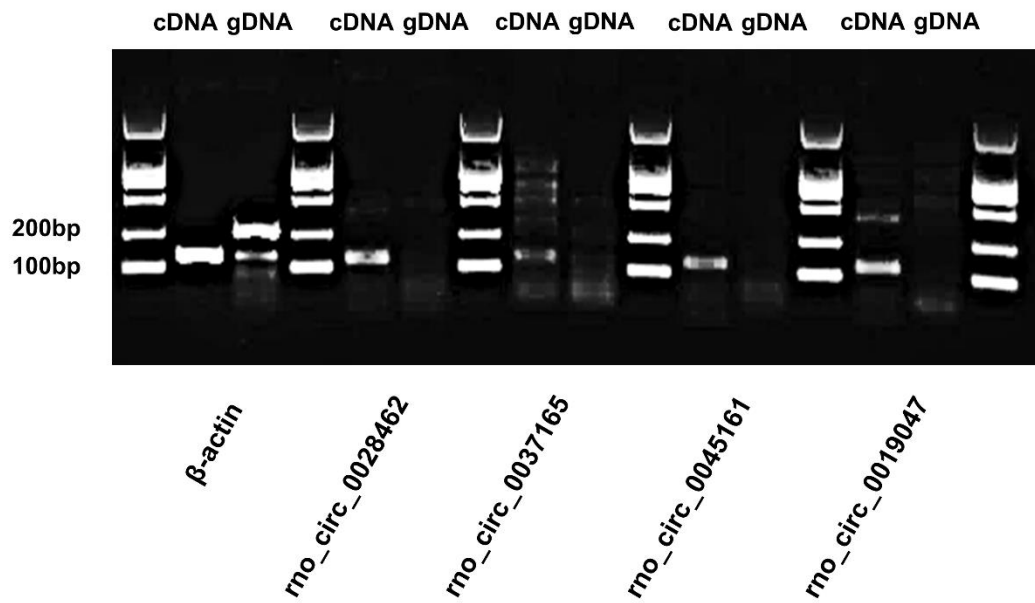


Figure S1. The existence of 4 candidate circRNAs were validated by agarose gel electrophoresis.

cDNA: complementary DNA; gDNA: genomic DNA.

Supplementary Tables

Table S1. The sequences of primers for reverse transcription-quantitative polymerase chain reaction.

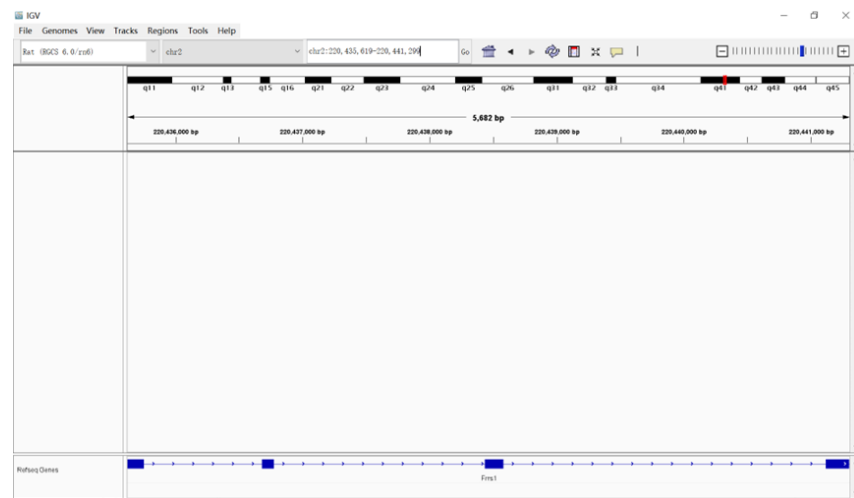
Primer	Forward	Reverse
rno_circ_0028462	GAAATGAGCGGACCCAGTGA	CGCTCAAATCCTCAGCGTTC
rno_circ_0021340	AGGTCTAGGAAGCTCACTCCA	GCACCCAGAAGTCACTGGTA
rno_circ_0035220	AAGATAGATCACTTCCTGGTGCC	GCATAGCACACAATGCAGGT
rno_circ_0017358	TTGGAGAATTACGATTAGGAGCCC	TCTCGGTGATATAAGCTGGTGC
rno_circ_0049747	AAGAGCTGGTCTACCTCGTG	CATGCTTGACCTTCATGCTCG
rno_circ_0028047	CCCAACACTCCAGTGAAAATGG	ACAAAATCATCAGCTCTCTGGGT
rno_circ_0023535	GCTACTGTGCTCCTGAGTATGT	TTCACCTGCACTGATTATACGCAA
rno_circ_0024062	CCACTCGAGTCCGTCAGAAC	AAAGGGCAGTGTACTGGTCG
rno_circ_0037165	TCCATGGGAACGAGCTTTAC	TTCTCCCTTCCTTCCTTTC
rno_circ_0038739	AAGAAGCTTTTGGTCTTCGGGA	TGATGACTCAAGCCTTCCATC
rno_circ_0004551	GTACACAGCACCACACGGAA	CAAGCTGCAAAGTCCCTCTG
rno_circ_0037247	GGACAGGACAAGGAAAAGCC	TCCCGCTCAGGACTAGATTCA
rno_circ_0027463	GCGGATCCAGCTGACATTTG	CTCTCATGCCGGGGATCTTG
rno_circ_0002585	GGCCATGCTTATGAGGAAGACT	AACGGCCACATTGCTGGATT
rno_circ_0030003	GACTGGTCAAACCTTGCTGCC	CCCAGTTTCTCCTTGCTCCA
rno_circ_0005842	AAAACCAACCAGGGAGTGGG	TTCTCGACCTCCTCTTCGGT
rno_circ_0054079	CCATGACTGACAAGCTGACCT	GAAGCATGGGGACCACCGT
rno_circ_0033398	GAGTCAAGGAAGCCAGGATGAT	CCACCAGTGAGGCCTGTTCA
rno_circ_0043052	AAATCAGACCCCTATGGAATCATCC	TGTCCAGTTAATCTCTAAAAGCTCA
rno_circ_0031837	CTCGAGCTGGGACTTTGGTAT	GAGCTTGCCCAGGGAGTATTT
rno_circ_0045161	TCTCCTACCTCATCCTGGCTT	TCGTTCAGATCCACCTCTCCA
rno_circ_0019047	CTGTTGCTGCTGCTATGTGTG	CTGTGACACTCAGTCACGTCT
rno_circ_0035410	CACCATGAAGCCATCTTCCCC	ATGAGGATCTGCTGGATTGGG
rno_circ_0039004	ACCTGCAAGAATTCCACTCTCA	TGCTGACGTCACTGGCTTAG
rno_circ_0033973	TTAAAGACTCTACAGCCGCCG	GAACCCAGACTCTGTTCCCTGC
rno_circ_0007116	TCAATGTTCCCTCGTGACCC	AAATGCCGGACTGGAGATGG
rno_circ_0031737	ACAGTAGGTGGAAGCAACGG	CTGGTGTGTGCCCTCCATTA
rno_circ_0030500	ATATCCCCTTGGTCCCTTCA	GCTGAAGATTTGCCATACC
rno_circ_0004035	AAGACGTCAGGCAGTAAGCC	TCAGAATTGCAGTTCCGCCT
rno_circ_0016962	TTTGCAGGTTTACAAATCAAAG	GTCTTTGGAAAACAACCTTAGCAA
β-Actin	GGAGATTACTGCCCTGGCTCCTA	GACTCATCGTACTCCTGCTTGCTG

Table S2. Integrated genome viewer (IGV) screen shots of 4 validated circRNAs.

rno_circ_0028462

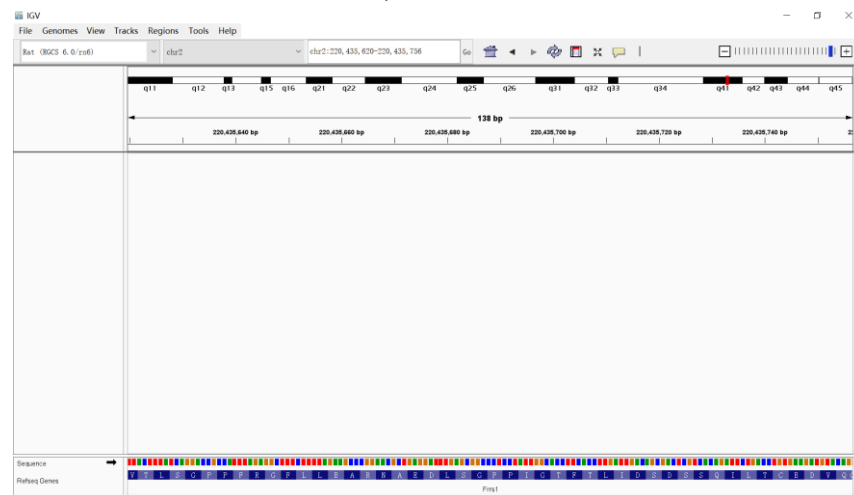
Chr location

chr 2: 220435619-220441299

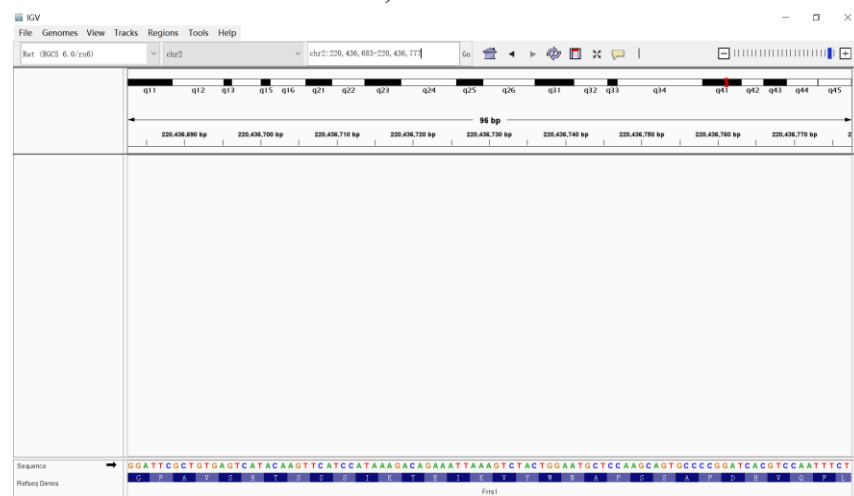


circRNA feature

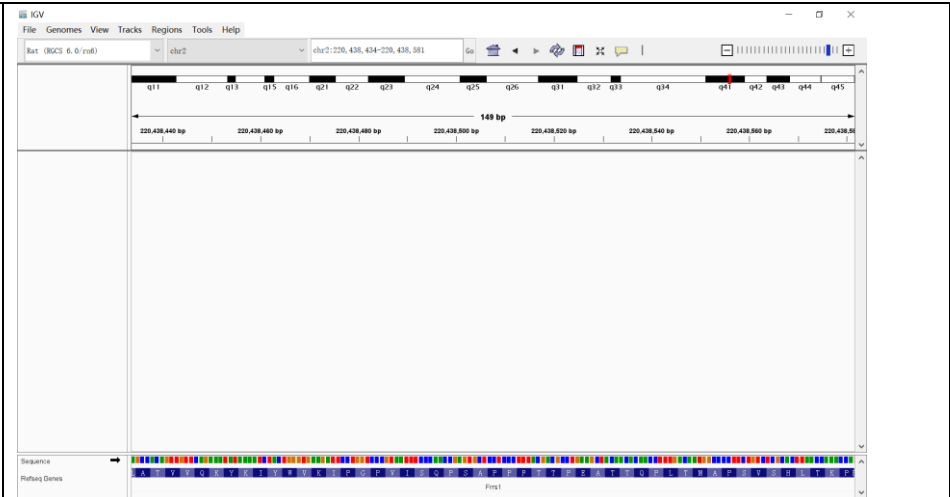
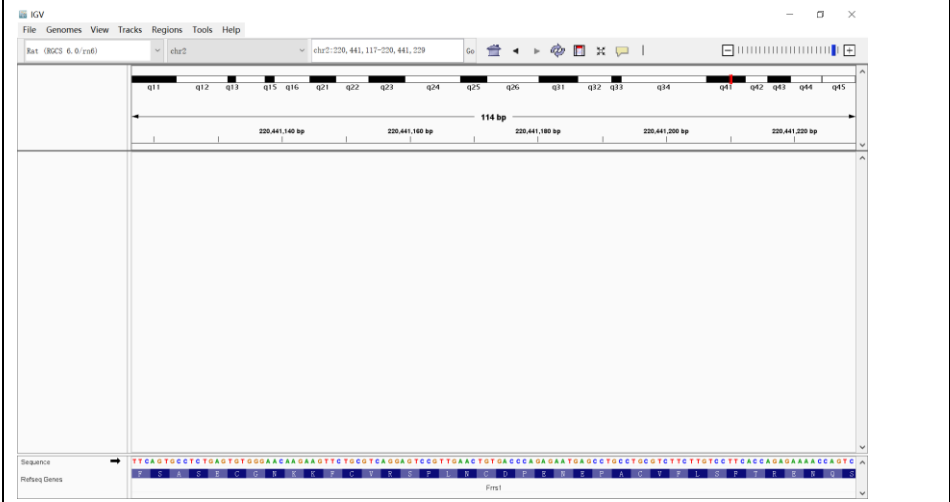
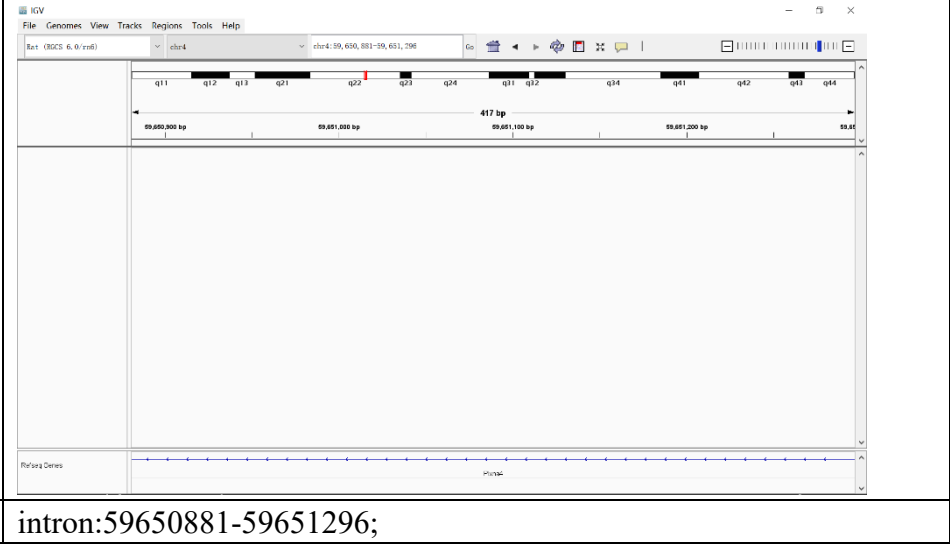
exon:220435620-220435756;

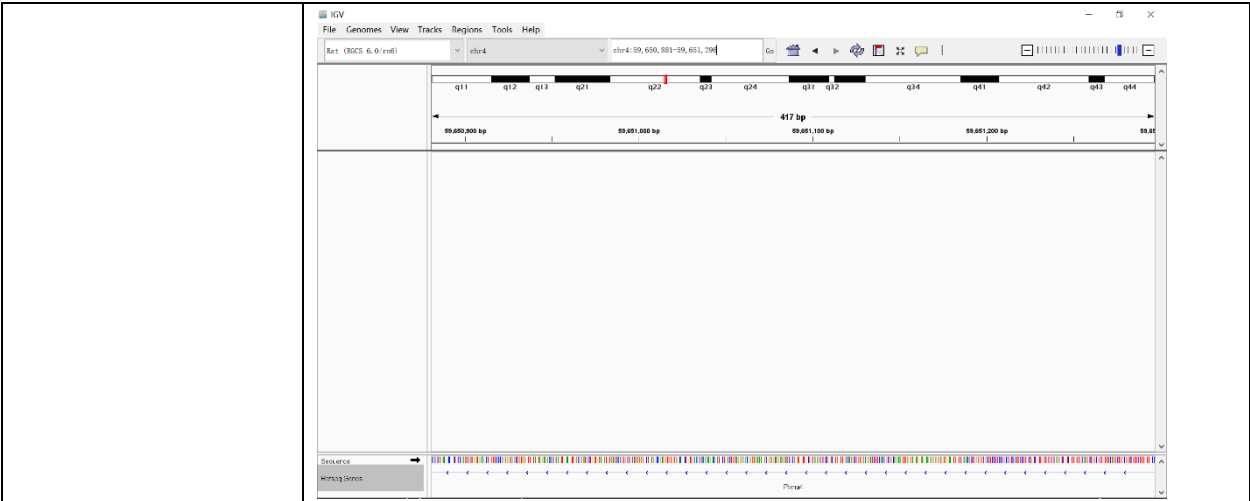


exon:220436683-220436777;



exon:220438434-220438581;

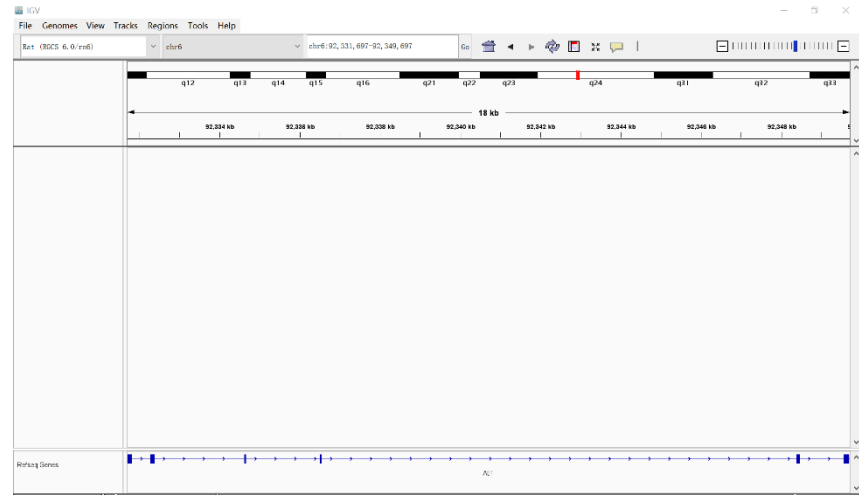
	 exon:220441117-220441299; 
rno_circ_0037165	
Chr location	chr 4: 59650881-59651296 
circRNA feature	intron:59650881-59651296;



rno_circ_0045161

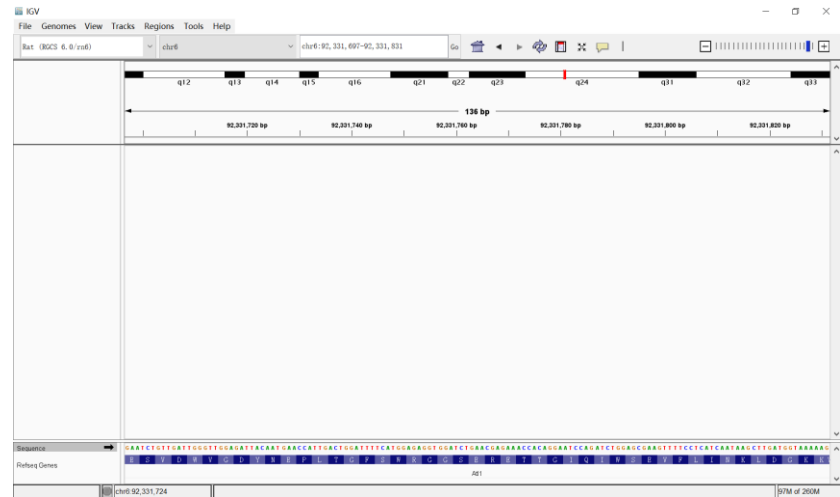
Chr location

chr 6: 92331696-92349697



circRNA feature

exon:92331697-92331831;



[illegible]

Chr location

The screenshot displays the IGV (Integrative Genomics Viewer) interface. At the top, a menu bar includes 'File', 'Genomes', 'View', 'Tracks', 'Regions', 'Tools', and 'Help'. Below the menu is a toolbar with icons for file operations, navigation, and analysis. The main window shows a genomic track for chromosome 19, specifically the region chr19:43,394,726-43,401,075. The track is labeled with p14, p13, p12, p11, q11, and q12. A scale bar indicates a 6,851 bp region, with coordinates 43,395,000 bp, 43,396,000 bp, 43,397,000 bp, 43,398,000 bp, 43,399,000 bp, 43,400,000 bp, and 43,401,000 bp. Below the track, a 'RefSeq Genes' track shows several gene models represented by blue boxes and arrows. The interface is clean and professional, with a white background and clear labeling.

IGV

File Genomes View Tracks Regions Tools Help

RefSeq chr19:43,394,727-43,394,363

Go

138 bp

43,394,240 bp 43,394,280 bp 43,394,300 bp 43,394,320 bp 43,394,340 bp 43,394,360 bp

Sequences

RefSeq Genes

SRR3

exon:43400972-43401075;

