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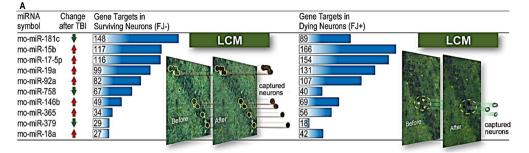
OPEN Publisher Correction: Evidence linking microRNA suppression of essential prosurvival genes with hippocampal cell death after traumatic brain injury

Deborah Kennedy Boone¹, Harris A. Weisz¹, Min Bi¹, Michael T. Falduto², Karen E. O. Torres², Hannah E. Willey¹, Christina M. Volsko¹, Anjali M. Kumar¹, Maria-Adelaide Micci¹, Douglas S. Dewitt¹, Donald S. Prough¹ & Helen L. Hellmich¹

Correction to: Scientific Reports https://doi.org/10.1038/s41598-017-06341-6, published online 27 July 2017

In this Article, Figure 1B is omitted. The correct Figure 1 appears below.

¹Department of Anesthesiology, University of Texas Medical Branch, Galveston, Texas, USA. ²Genus Biosystems, Inc., Northbrook, Illinois, USA. Correspondence and requests for materials should be addressed to H.L.H. (email: hhellmic@utmb.edu)



В		

_		Fold Change				
Gene Name	miRNA Symbol	miRNA changes	Dying (FJ+)	Surviving (FJ-)	OMIM Acc#	RM ID
Prosurviva	I Response	-		3 1		
ABCG4	miR-379/miR-3529/miR-1193-5p	-1.272	7.270	NA	607784	3
ADCYAP1	miR-365	1.330	-13.986	NA	102980	8
CAT	miR-146a/miR-146b/miR-146b-5p	1.268	-3.922	NA	115500	28
DDX3X	miR-758/miR-153*	-1.458	13.100	10.730	300160	57
IGF1	miR-758/miR-153*	-1.458	NA	12.860	147440	109
MAPK1	miR-19b/miR-19a	1.950	-9.434	NA	176948	124
MAPK9	miR-20a/miR-106b/miR-17-5p (includes others)	1.774	-9.524	NA	602896	125
NFAT5	miR-181a/miR-181b/miR-181d (includes others)	-1.285	NA	8.788	604708	148
NOTCH2	miR-181a/miR-181b/miR-181d (includes others)	-1.285	NA	7.185	600275	154
Synaptic F						
BDNF	miR-365	1.330	-7.752	-2.865	113505	22
EPHA4	miR-20a/miR-106b/miR-17-5p (includes others)	1.774	-10.246	NA	602188	67
GABRA4	miR-18a/miR-18b/miR-4735-3p	2.761	-6.061	NA	137141	76
NETO2	miR-20a/miR-106b/miR-17-5p (includes others)	1.774	-13.316	NA	607974	146
NLGN1	miR-16/miR-497/miR-195 (includes others)	1.317	-13.532	NA	600568	15
NPTX1	miR-92a/miR-92b/miR-32 (includes others)	1.605	-16.779	-3.300	602367	157
SNAP25	miR-16/miR-497/miR-195 (includes others)	1.317	-6.757	NA	600322	209
Cell Cycle		1.517	-0.131	INA	000322	20;
ABCE1	miR-19b/miR-19a	1.950	-4.016	NA	601213	2
CCNG1	miR-190/miR-190 miR-365	1.330	-4.016	-1.883	601213	2 30
CCNGT	miR-305 miR-16/miR-497/miR-195 (includes others)	1.330	-0.757 -7.576	-1.003 NA	612786	30
		1.317	-1.010	INA	012700	31
	tic Cell Function	4.047	7 750	0.700	000457	
ACSL4	miR-16/miR-497/miR-195 (includes others)	1.317	-7.752	-2.732	<u>300157</u>	5
ARCN1	miR-16/miR-497/miR-195 (includes others)	1.317	-9.091	NA	<u>600820</u>	15
JKAMP	miR-19b/miR-19a	1.950	-8.772	-3.012	<u>611176</u>	11(
MGEA5	miR-18a/miR-18b/miR-4735-3p	2.761	-21.008	NA	<u>604039</u>	13
PPM1K	miR-146a/miR-146b/miR-146b-5p	1.268	-9.346	-2.801	<u>611065</u>	177
RRAGA	miR-16/miR-497/miR-195 (includes others)	1.317	-6.098	NA	<u>612194</u>	193
SLC9A6	miR-16/miR-497/miR-195 (includes others)	1.317	-5.618	-2.882	<u>300231</u>	205
	d Development					
CDH10	miR-92a/miR-92b/miR-32 (includes others)	1.605	-8.929	-1.751	<u>604555</u>	34
GHRHR	miR-379/miR-3529/miR-1193-5p	-1.272	NA	7.238	<u>139191</u>	79
NAP1L2	miR-19b/miR-19a	1.950	-10.799	-2.725	<u>300026</u>	14(
NFASC	miR-146a/miR-146b/miR-146b-5p	1.268	-12.870	NA	<u>609145</u>	147
VRK1	miR-20a/miR-106b/miR-17-5p (includes others)	1.774	-9.174	NA	<u>602168</u>	248
DNA Repa	r					
NHEJ1	miR-379/miR-3529/miR-1193-5p	-1.272	3.999	NA	<u>611290</u>	150
SMC5	miR-146a/miR-146b/miR-146b-5p	1.268	-4.902	NA	609386	208
USP47	miR-146a/miR-146b/miR-146b-5p	1.268	-15.267	NA	<u>614460</u>	244
RNA Proce	essing					
CELF2	miR-146a/miR-146b/miR-146b-5p	1.268	-6.173	NA	602538	35
HNRNPD	miR-19b/miR-19a	1.950	-8.264	NA	601324	100
PAPD4	miR-19b/miR-19a	1.950	-10.823	NA	614121	164
	ssion Linked to Disease					
ARFGEF2	miR-181a/miR-181b/miR-181d (includes others)	-1.285	10.330	NA	605371	16
SOAT1	miR-758/miR-153*	-1.458	7.548	NA	102642	21

Figure 1. Ten Traumatic brain injury (TBI)-altered microRNAs target approximately 600 pro-survival and/ or pro-death genes in dying and surviving hippocampal pyramidal neurons that were obtained by laser capture microdissection 24 h after TBI. (**A**) Ingenuity pathway analysis miRNA target filter was used to identify predicted gene targets in dying, Fluoro-Jade-positive (FJ+) and surviving, Fluoro-Jade-negative (FJ-) neurons. These genes were identified in our previous microarray study as significantly differentially expressed in dying and surviving neurons. (**B**) Differentially expressed miRNA target genes in dying and surviving neurons play essential roles in neuronal function and their misregulation is associated with human disease (see Online Mendelian Inheritance in Man database). The complete, annotated list of differentially expressed miRNA target genes in dying and surviving neurons is shown in Supplementary Table 3.

As a result, the Figure legend,

"Ten Traumatic brain injury (TBI)-altered microRNAs target approximately 600 pro-survival and/or pro-death genes in dying and surviving hippocampal neurons. In our previous microarray study, we showed that these genes were significantly differentially expressed in dying and surviving neurons 24 h after TBI. Ingenuity pathway analysis miRNA target filter was used to identify predicted gene targets in laser captured dying, Fluoro-Jade-positive (FJ+) and surviving, Fluoro-Jade-negative (FJ-) hippocampal pyramidal neurons".

should read:

"Ten Traumatic brain injury (TBI)-altered microRNAs target approximately 600 pro-survival and/or pro-death genes in dying and surviving hippocampal pyramidal neurons that were obtained by laser capture microdissection 24 h after TBI. (A) Ingenuity pathway analysis miRNA target filter was used to identify predicted gene targets in dying, Fluoro-Jade-positive (FJ+) and surviving, Fluoro-Jade-negative (FJ-) neurons. These genes were identified in our previous microarray study as significantly differentially expressed in dying and surviving neurons. (B) Differentially expressed miRNA target genes in dying and surviving neurons play essential roles in neuronal function and their misregulation is associated with human disease (see Online Mendelian Inheritance in Man database). The complete, annotated list of differentially expressed miRNA target genes in dying and surviving neurons is shown in Supplementary Table 3".

Additionally, there are typographical errors in the text. In the Results section:

"We found that ten TBI-dysregulated miRNAs targeted, either singly or frequently in combination, about 600 TBI-dysregulated genes (Fig. 1, manually curated functional data including GeneCard and PubMed links for all miRNA gene targets with gene information shown left of the blue line and miRNA data shown right of the blue line, are provided in Supplementary Tables 1 and 2)".

should read:

"We found that ten TBI-dysregulated miRNAs targeted, either singly or frequently in combination, about 600 TBI-dysregulated genes (Fig. 1A, manually curated functional data including GeneCard and PubMed links for all miRNA gene targets with gene information shown left of the blue line and miRNA data shown right of the blue line, are provided in Supplementary Tables 1 and 2)".

In the same section:

"Analysis of the annotated genes that displayed strikingly disparate expression levels in dying and surviving neurons (Table 1, the complete list of differentially expressed miRNA target genes in dying and surviving neurons described in the manuscript are shown in Supplementary Table 3 along with links to OMIM and supporting literature for each gene in Supplementary References) showed that the majority of transcripts are thought to play essential roles in cell function".

should read:

"Analysis of the annotated genes that displayed strikingly disparate expression levels in dying and surviving neurons (Fig. 1B, the complete list of differentially expressed miRNA target genes in dying and surviving neurons described in the manuscript are shown in Supplementary Table 3 along with links to OMIM and supporting literature for each gene in Supplementary References) showed that the majority of transcripts are thought to play essential roles in cell function".

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