

# High Resolution Metabolite Imaging in the Hippocampus Following Neonatal Exposure to the Environmental Toxin BMAA using ToF-SIMS

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## **Content:**

**SI Table 1+2:** OPLS DA results

**SI Figures 1-4:** alternative color scheme for Figures 2,3,4,8

**SI Table 1:** Molecular species that were found changed in the CA1 between BMAA and control animals as revealed by OPLS DA.

<b>positive ions</b>				
Increased in				
BMAA				
m/z	I.D. <sup>1</sup>	Ratio BMAA/Ctrl <sup>2</sup>	Loading <sup>3</sup>	
22.99	Na+	1.20	0.023	
86.1	TME, C5H12N+	1.04	0.010	
104.1	choline, C5H14NO+	1.09	0.025	
119.87	K2CNO+	1.21	0.013	
166.88	C5H13PNO3	1.07	0.001	
184.09	C5H15PNO4+	1.02	0.016	
369.29	cholesterol C27H45+	2.22	0.014	
496.25	LPC (16:0)	1.76	0.030	
520.25	LPC (18:2)	1.49	0.031	
523.42	DAG(30:0-OH)	1.57	0.021	
524.48	LPC (18:0)	1.78	0.027	
551.28	DAG(32:0-OH)	1.66	0.031	
568.09	PC (22:6)	2.47	0.033	
577.38	DAG(34:1-OH)	1.81	0.032	
725.23	SM(d18:1/16:0)+Na	1.64	0.031	
731.41	SM(d18:1/18:0)	1.73	0.022	
734.39	PC(32:0)	1.44	0.020	
753.54	SM(d18:1/18:0)+Na	2.02	0.030	
756.39	PC(32:0)+Na	1.94	0.032	
758.35	PC(34:2)	1.76	0.014	
760.4	PC(34:1)	1.22	0.003	
769.41	SM(d18:1/18:0)+K	2.00	0.032	
770.15	PC (32:0)+K	2.15	0.027	
770.41	PC(32:1)+K	1.55	0.034	
772.36	PC(32:0)+K	1.57	0.029	
780.19	PC (34:2)+Na	2.12	0.021	
782.38	PC(36:4)	1.55	0.010	
784.39	PC(36:3)	1.52	0.021	
786.39	PC(36:2)	1.63	0.015	
788.42	PC(36:1)	1.51	0.008	
804.31	PC(36:4)+Na	1.44	0.007	
806.31	PC(38:6)	1.74	0.014	
810.4	PC(38:4)	1.86	0.015	
820.31	PC(36:4)+K	1.63	0.008	
822.27	PC (36:3)+K	2.65	0.010	
824.29	PC(36:2)+K	1.34	0.006	
826.36	PC(36:1)+K	1.45	0.007	
832.42	PC(38:4)+Na	1.71	0.006	
834.46	PC (40:6)	2.21	0.010	

**negative ions**

Increased in

BMAA

m/z	I.D. <sup>1</sup>	Ratio BMAA/Ctrl <sup>2</sup>	Loading <sup>3</sup>
385.33	cholesterol, C27H45O-	1.38	0.002
675.49	PA(34:0)	1.07	0.011
701.47	PA(36:1)	1.23	0.008
716.53	PE(16:0/18:1)	1.08	0.005
722.46	PE(16:0p/20:4)	1.56	0.027
726.52	PE(18:1p/18:0)	1.46	0.019
728.51	PE(18:0p/18:0)	1.19	0.006
742.52	PE(18:1/18:1)	1.24	0.008
746.48	PE(16:0p/22:6)	1.13	0.012
750.47	PE(18:0p/20:4)	1.55	0.025
762.52	PE(16:0/22:6)	1.55	0.024
764.52	PE(18:1/20:4)	1.30	0.019
766.49	PE(18:0/20:4)	1.19	0.006
774.59	PE(18:0p/22:6)	1.08	0.003
778.49	ST(d18:1/16:0)	2.45	0.034
786.54	PS(36:2)	1.32	0.006
788.51	PS(36:1)	1.45	0.011
790.49	PE(18:0/22:6)	1.28	0.013
794.5	PE(18:0/22:4)	1.82	0.032
806.55	ST(d18:1/18:0)	1.81	0.033
810.47	PS(18:0/20:4)	1.62	0.024
816.5	PS(18:0/20:1)	1.48	0.023
805.29	TAG(48:0)	1.95	0.015
829.32	TAG(50:0)	2.04	0.013

Decreased in

BMAA

78.97	PO3-	0.73	-0.034
96.99	H2PO4-	0.91	-0.020
747.45	PG(16:0/18:1)	0.89	-0.007
833.43	PI(16:0/18:2)	0.93	-0.002
837.59	PI(16:0/18:0)	0.68	-0.014

<sup>1</sup> Tentative assignment based on accurate mass, isotope pattern and literature values. Lipid annotation is based on lipid maps (*1, 2*). Abbreviations: **TME**: trimethylethylimine; **PC**: phosphatidylcholine; **LPC**: lysophosphatidylcholine; **DAG**: diacylglyceride; **TAG**: triacylglyceride; **SM**: sphingomyelin; **PA**: diacylphosphate, **FA**: fatty acids; **AA**: arachnoid acid; **PE**: phosphoethanolamine; **ST**: sulfatide; **PS**: phosphatidylserine; **PG**: phosphatidylglycerol; **PI**: phosphatidylinositol

<sup>2</sup> average fold change in intensity in BMAA compared to Controls.

<sup>3</sup> Loadings on component 1. Positive loadings indicate contribution to BMAA, while negative loading values indicate association with control.

**SI Table 2:** Molecular species that were found changed in the DG between BMAA and control animals as revealed by OPLS DA.

<b>positive ions</b>				
Increased in BMAA				
m/z	I.D. <sup>1</sup>	Ratio BMAA/Ctrl <sup>2</sup>	Loading <sup>3</sup>	
22.99	Na+	1.24	0.033	
38.97	K+	1.08	0.018	
86.1	TME, C5H12N+	1.19	0.030	
104.1	Choline, C5H14NO+	1.13	0.030	
184.09	C5H15PNO4+	1.06	0.014	
496.49	LPC (16:0)	1.28	0.012	
520.25	LPC (18:2)	1.30	0.029	
524.48	LPC (18:0)	1.46	0.023	
523.42	DAG(30:0-OH)	1.46	0.020	
551.28	DAG(32:0-OH)	1.52	0.029	
577.38	DAG(34:1-OH)	1.82	0.037	
603.29	DAG(36:2-OH)	1.52	0.032	
731.41	SM(d18:1/18:0)	1.40	0.031	
734.39	PC(32:0)	1.26	0.020	
753.19	SM(d18:1/18:0)+Na	1.49	0.026	
756.39	PC(32:0)+Na	1.64	0.035	
758.35	PC(34:2)	1.60	0.022	
770.41	PC(32:1)+K	1.32	0.030	
772.12	PC(32:0)+K	1.54	0.032	
780.19	PC (34:2+Na)	1.62	0.020	
784.39	PC(36:3)	1.27	0.023	
796.29	PC (34:2+K)	1.09	0.010	
Decreased in BMAA				
369.29	cholesterol C27H45+	0.77	-0.011	
385.27	cholesterol C27H45O+	0.54	-0.024	
430.27	Vitamin E, C29H50O2+	0.33	-0.029	
<b>negative ions</b>				
Decreased in BMAA				
26.01	CN-	0.72	-0.026	
42.01	CNO-	0.66	-0.028	
62.97	PO2-	0.78	-0.024	
78.97	PO3-	0.83	-0.027	
96.99	H2PO4-	0.84	-0.032	
281.25	FA (18:1)	0.67	-0.018	
283.26	FA (18:0)	0.80	-0.019	
303.24	AA	0.76	-0.013	

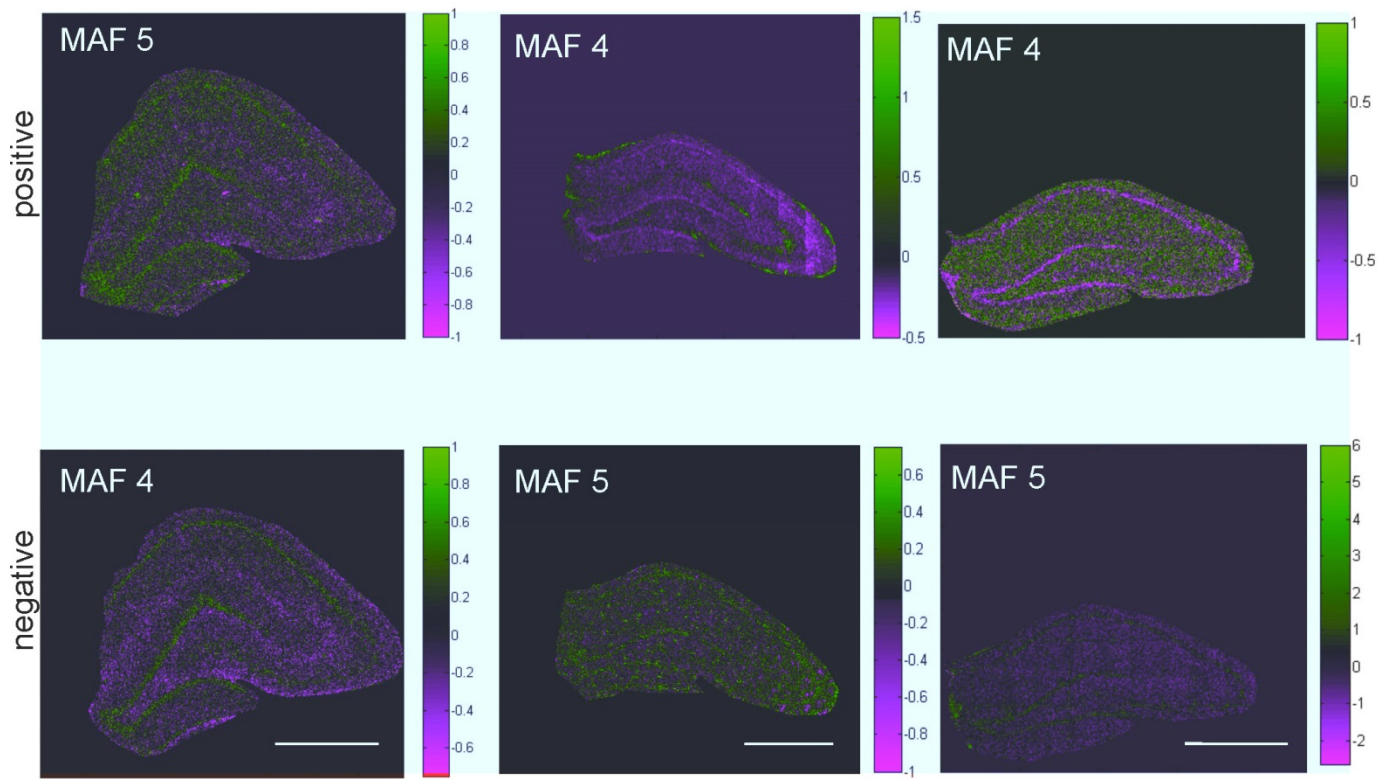
m/z	I.D. <sup>1</sup>	Ratio BMAA/Ctrl <sup>2</sup>	Loading <sup>3</sup>
385.33	cholesterol, C27H45O-	0.55	-0.020
429.3	Vitamin E, C29H49O2-	0.49	-0.027
722.46	PE(16:0/18:1)	0.94	-0.009
726.52	PE(16:0p/20:4)	0.94	-0.008
728.51	PE(18:1p/18:0)	0.84	-0.015
742.52	PE(18:0p/18:0)	0.84	-0.013
744.51	PE(18:1/18:0)	0.80	-0.015
746.48	PE(16:0p/22:6)	0.88	-0.013
747.45	PG(16:0/18:1)	0.88	-0.007
750.47	PE(18:0p/20:4)	0.81	-0.020
762.52	PE(16:0/22:6)	0.93	-0.007
764.52	PE(18:1/20:4)	0.90	-0.014
766.49	PE(18:0/20:4)	0.88	-0.007
770.49	PE(20:0/18:2)	0.75	-0.021
774.59	PE(18:0p/22:6)	0.74	-0.019
778.49	ST(d18:1/16:0)	1.15	0.018
786.54	PS(36:2)	0.66	-0.019
788.51	PS(36:1)	0.73	-0.018
790.49	PE(18:0/22:6)	0.79	-0.013
806.55	ST(d18:1/18:0)	0.93	-0.017
810.47	PS(18:0/20:4)	0.86	-0.013
833.43	PI(16:0/18:2)	0.76	-0.018
223.19	PI fragment	0.71	-0.032
241.25	PI fragment	0.64	-0.031
837.59	PI(16:0/18:0)	0.36	-0.029
805.51	TAG(48:0)	0.95	-0.006

1 Tentative assignment based on accurate mass, isotope pattern and literature values. Lipid annotation is based on lipid maps (1, 2). Abbreviations: **TME**: trimethylethylamine; **PC**: phosphatidylcholine; **LPC**: lysophosphatidylcholine; **DAG**: diacylglyceride; **TAG**: triacylglyceride; **SM**: sphingomyelin; **PA**: diacylphosphate, **FA**: fatty acids; **AA**: arachnoid acid; **PE**: phosphoethanolamine; **ST**: sulfatide; **PS**: phosphatidylserine; **PG**: phosphatidylglycerol; **PI**: phosphatidylinositol

2 average fold change in intensity in BMAA compared to Controls.

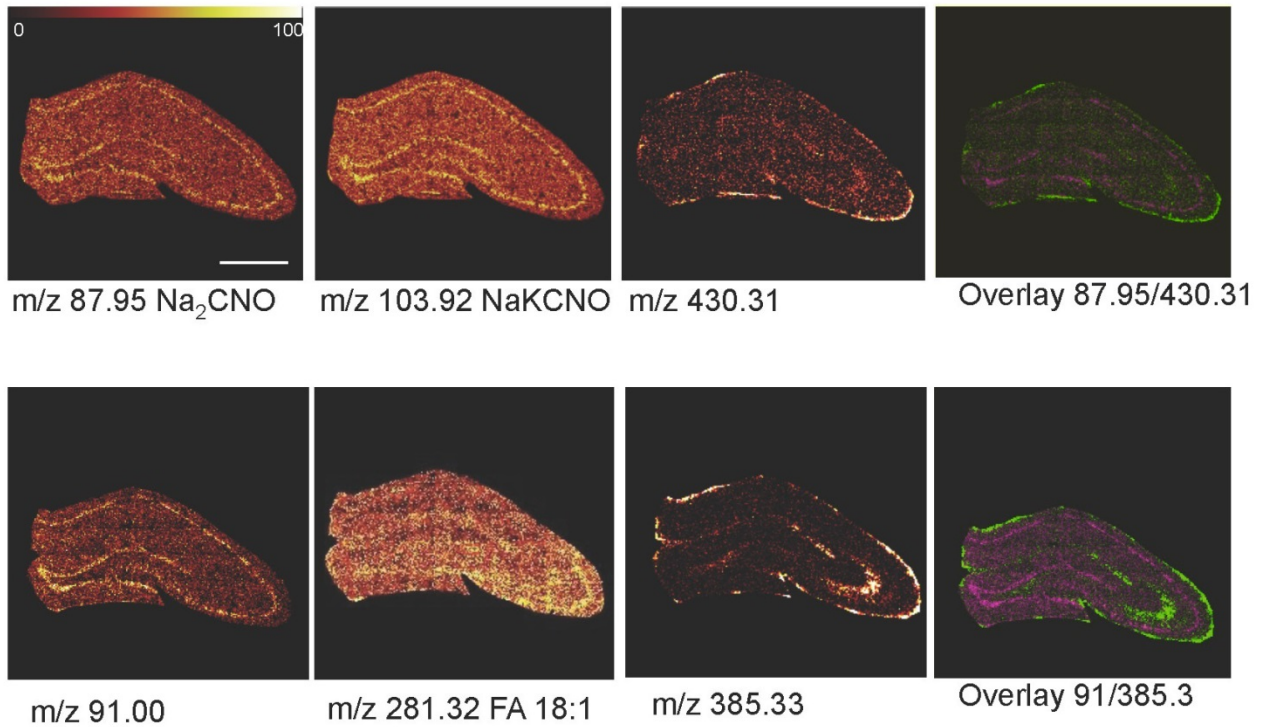
3 Loadings on component 1. Positive loadings indicate contribution to BMAA, while negative loading values indicate association with control.

1. Fahy, E., Subramaniam, S., Murphy, R. C., Nishijima, M., Raetz, C. R., Shimizu, T., Spener, F., van Meer, G., Wakelam, M. J., and Dennis, E. A. (2009) Update of the LIPID MAPS comprehensive classification system for lipids, *Journal of lipid research* 50 Suppl, S9-14.
2. Fahy, E., Subramaniam, S., Brown, H. A., Glass, C. K., Merrill, A. H., Jr., Murphy, R. C., Raetz, C. R., Russell, D. W., Seyama, Y., Shaw, W., Shimizu, T., Spener, F., van Meer, G., VanNieuwenhze, M. S., White, S. H., Witztum, J. L., and Dennis, E. A. (2005) A comprehensive classification system for lipids, *Journal of lipid research* 46, 839-861.



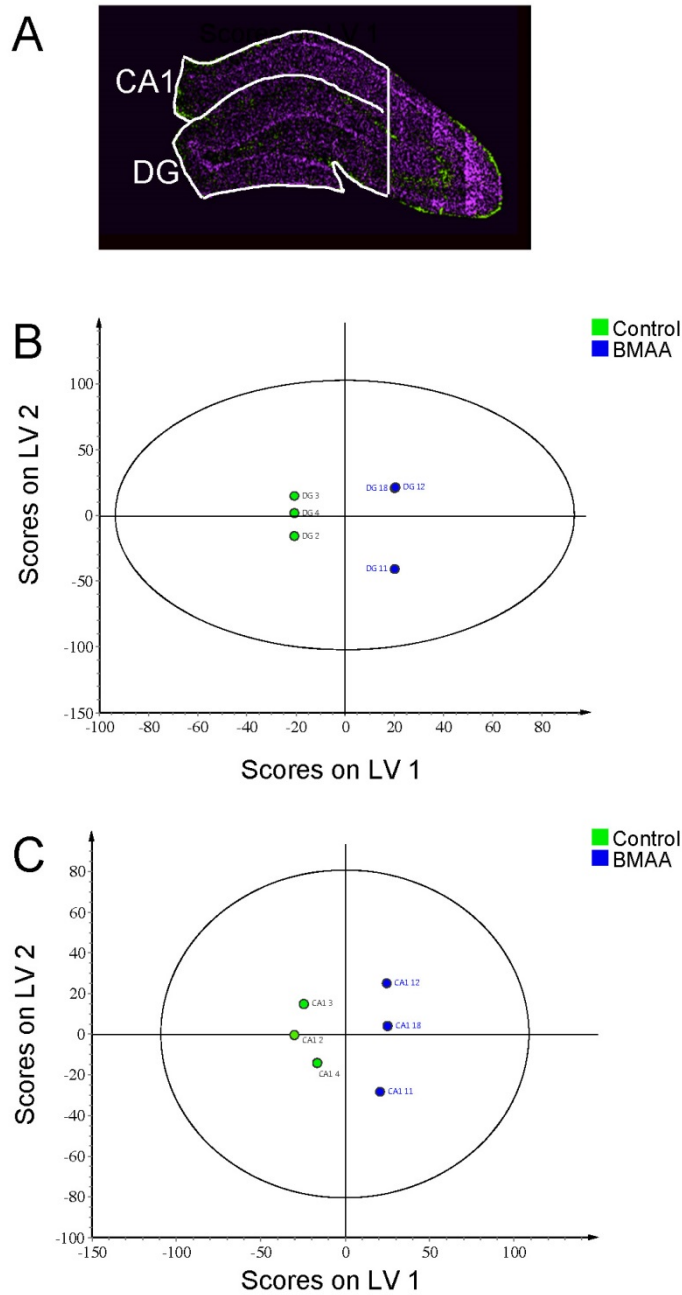
**SI Figure 1. Multivariate image analysis for identification of anatomical regions of interest.**

ToF-SIMS imaging data of the hippocampus of 6-month old control animals (n=3) were acquired in positive and negative ion mode and analyzed by means of maximum autocorrelation factor (MAF) analysis. The composition images depict individual scores (eigenvalues) for each pixel (spectrum) in the corresponding factors (MAF 3-5). The factors capture the variances over the tissue section and allow for an unbiased annotation of regions in the hippocampus based on chemical differences (scale bar = 1 mm).



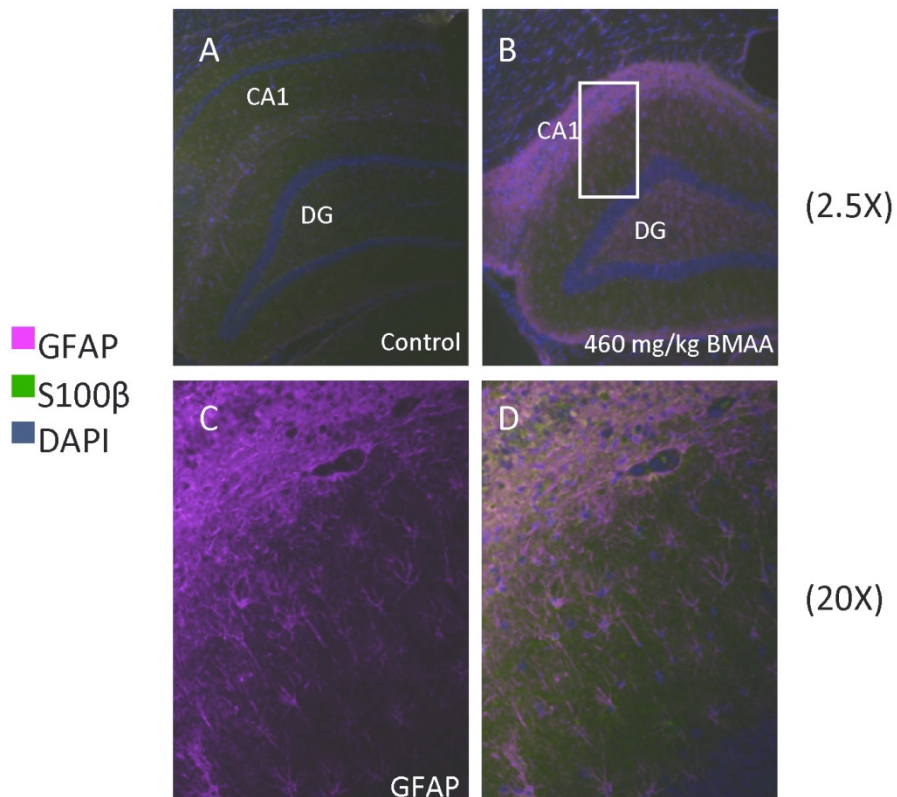
**SI Figure 2. Single ion images of biochemical species that show region specific distributions.**

Positive and negative ion species show characteristic localization patterns that are well in line with anatomical regions of the hippocampus of 6-month old control animals. Protein specific fragments (pos: NaKCNO, Na<sub>2</sub>CNO) were found in highest levels in the CA1-4 and the granular cell layer of the DG. Similar observations were made for a yet unidentified species at m/z 91.00 in negative mode. Vitamin E (Vit.E, [M+H]<sup>+</sup> 430.31), fatty acids (FA 18:1, [M-H]<sup>-</sup> 281.32) and cholesterol (Chol., [M-H]<sup>-</sup> 385.33) were localized to the molecular layer of the DG as well as mossy fibers projecting from the DG to the CA3. Overlay: 87.95: cyan, 430.31 green; 91.00: cyan, 385.3 green. (scale bar = 1mm)



**SI Figure 3. Multivariate analysis of spectral data reveal BMAA-induced hippocampal changes.** MAF analysis was used to segment the hippocampal images into regions representing CA1 and DG (A). OPLS-DA models were calculated for both regions, clearly separating the control group from the BMAA group. (B) The analysis resulted in a 1+3 (1 predictive- + 3 orthogonal components) model for DG. The model explained 86% of the variation in the dataset (R2X cumulative) with a predictive power of 0.96 (Q2 cumulative). (C) For the CA1 a 1+1 (1 predictive- + 3 orthogonal components) model where 53% variation was explained at 0.61 predictive power (Q2 cumulative).





**SI Figure 4. Immunohistochemistry of hippocampus.** Double antigen staining was performed against GFAP and S100 beta on hippocampal sections of control (A) and BMAA exposed animals (B). The data show massive gliosis and reactive astrocyte species localizing to the histopathologically altered region in the hippocampus of BMAA-treated rats. This was indicated by increased GFAP immunoreactivity (cyan) in the CA1 of BMAA exposed animals (B) compared to controls (A). (C) Magnification of outlined area indicated in (B). GFAP positive cells (C) were also found to stain positively for S100 beta (white) serving as additional astrocyte marker (D). Magnifications. A-B lens x 10; C-D lens x 20.