

**Supplementary Materials:** The following are available online at <http://www.mdpi.com/2076-3425/9/12/340/s1>, Table S1: Gene expression data for Figure 3, Table S2: Gene expression data for Figure 4, Table S3: Gene expression data for Figure 5, Table S4: Gene expression data for Figure 6, Table S5: Gene expression data for GABA transporters in microglia from the STR at 2 hr and 3 days after METH, Table S6: Gene expression data for *Csf1*, *Csfr1*, *Il34* in microglia from the STR at 2 hr and 3 days after METH.

Table S1: Gene expression data for Figure 3. PG and LT biosynthetic enzymes and LT receptors in 2 hr post METH STR and PFC microglia. ND = Not Detected. NS = Not Significant.

Symbol	Gene Name	2 hr STR average log2cpm Saline (n=6), METH (n=8)	2 hr STR Fold Change, FDR	2 hr PFC average log2cpm S Saline (n=4), METH (n=5)	2 hr PFC Fold Change, FDR
Pla2	phospholipase A2, activating protein	5.34, 5.95	1.55, 3E-04	5.34, 5.64	1.25, 0.08 (NS)
Ptgs1	prostaglandin- endoperoxide synthase 1 (COX1)	10.36, 9.70	-1.55, 3E-05	10.15, 9.40	-1.65, 7.0E-07
Ptgs2	prostaglandin- endoperoxide synthase 2 (COX2)	-4.73, -0.62	47.3, 2E-03	ND	ND
Alox5	arachidonate 5- lipoxygenase	8.24, 8.11	-1.06, 0.79 (NS)	8.40, 8.98	1.51, 0.01
Alox5ap	arachidonate 5- lipoxygenase activating protein	7.67, 8.15	1.43, 5.5E-04	7.76, 8.49	1.68, 3.6E-06
Lta4h	leukotriene A4 hydrolase	7.16, 7.58	1.36, 4E-04	7.12, 7.65	1.46, 9E-06
Ptgr1	prostaglandin reductase 1	2.02, 0.91	-1.98, 8.8E-04	2.40, 0.89	-2.74, 7.0E-06
Ltb4r	Leukotriene B4 Receptor	ND	ND	ND	ND
Ltc4s	leukotriene C4 synthase	8.11, 6.91	-2.1, 1E-05	8.11, 7.35	-1.61, 9.0E-04
Ggt1	gamma- glutamyltransferase 1	ND	ND	ND	ND

Ggt7	gamma-glutamyltransferase 7	4.15, 3.65	-1.38, 0.045	4.20, 3.60	-1.55, 0.04
Dpep2	dipeptidase 2	3.59, 2.94	-1.6, 6E-03	3.81, 3.05	-1.72, 3.0E-04
Cysltr1	cysteinyl leukotriene receptor 1	4.48, 3.65	-1.7, 9E-04	4.45, 4.06	-1.3, 0.34 (NS)
Cysltr2	cysteinyl leukotriene receptor 2	ND	ND	ND	ND
P2ry12	purinergic receptor P2Y12	10.88, 9.77	-2.0, 5E-05	10.93, 10.23	-1.6, 5.0E-05

Table S2: Gene expression data for Figure 4. Biosynthetic enzymes and receptors for PG's, TxA2, and HETE's in 2 hr post METH STR and PFC microglia. ND = Not Detected. NS= Not Significant.

Symbol	Gene Name	2 hr STR average log2cpm Saline (n=6), METH (n=8)	2 hr STR Fold Change, FDR	2 hr PFC average log2cpm Saline (n=4), METH (n=5)	2 hr PFC Fold Change, FDR
Plaa	phospholipase A2, activating protein	5.34, 5.95	1.55, 3E-04	5.34, 5.64	1.25, 0.08 (NS)
Ptgs1	prostaglandin-endoperoxide synthase 1 (COX1)	10.36, 9.70	-1.55, 3E-05	10.15, 9.40	-1.65, 7E-07
Ptgs2	prostaglandin-endoperoxide synthase 2 (COX2)	-4.73, -0.62	47.3, 2E-03	ND	ND
Ptges2	prostaglandin E synthase 2	4.62, 5.41	1.76, 8E-06	1.24, 0.14 (NS)	4.63, 4.92
Ptges3	prostaglandin E synthase 3	6.70, 8.04	2.60, 3E-11	6.92, 8.18	2.43, 1E-07
Ptger1	prostaglandin E receptor 1	3.21, 3.86	1.61, 0.07 (NS)	3.32, 3.91	1.36, 0.22 (NS)
Ptger2	prostaglandin E receptor 2	0.32, 2.56	5.0, 2E-05	0.56, 1.82	2.50, 0.01
Ptger3	prostaglandin E receptor 3	ND	ND	ND	ND
Ptger4	prostaglandin E receptor 4	2.88, 5.19	6.5, 3E-05	3.16, 4.45	2.64, 6E-03

Alox15	arachidonate 15-Lipoxygenase	ND	ND	ND	ND
Alox12	arachidonate 12-lipoxygenase, 12S type	6.60, 6.13	-1.36, 0.11 (NS)	6.92, 5.29	-2.95, 3.3E-07
Alox5	arachidonate 5-lipoxygenase	8.24, 8.11	-1.06, 0.79 (NS)	8.40, 8.98	1.51, 0.01
Alox5ap	arachidonate 5-lipoxygenase activating protein	7.67, 8.15	1.43, 5.5E-04	7.76, 8.49	1.68, 3.6E-06
Ppard	peroxisome proliferator-activated receptor delta	3.63, 4.23	1.54, 0.04	3.60, 4.26	1.55, 0.01
Pparg	peroxisome proliferator activated receptor gamma	ND	ND	ND	ND
Angptl4	angiopoietin-like 4	0.94, 2.42	4.20, 1.2E-04	0.45, 2.39	3.78, 1.4E-07
Gpr31	G protein-coupled receptor 31	5.76, 3.30	-4.25, 1.6E-05	5.61, 4.46	-2.22, 4.3E-08
Oxer1	Oxoeicosanoid Receptor 1	ND	ND	ND	ND
Tbxas1	thromboxane A synthase 1	8.38, 8.17	-1.16, 0.11 (NS)	8.26, 7.92	-1.28, 0.09 (NS)
Tbxa2r	thromboxane A2 receptor	-1.11, -1.31	1.42, 0.53 (NS)	-1.07, -2.15	-2.19, 0.21 (NS)
Ptgds	prostaglandin D2 synthase	ND	ND	ND	ND
Ptgdr	prostaglandin D2 Receptor	ND	ND	ND	ND
Prx12b	peroxiredoxin like 2B (prostamide/prostaglandin F synthase)	ND	ND	ND	ND
Ptgfr	Prostaglandin F Receptor	ND	ND	ND	ND
Ptgis	Prostaglandin I2 Synthase	ND	ND	ND	ND
Ptgir	prostaglandin I2 receptor	-2.27, -0.59	2.82, 0.15 (NS)	-1.48, -1.04	1.83, 0.43 (NS)

Table S3: Gene expression data for Figure 5. Significantly changed RNAseq genes associated with NRF2-mediated oxidative stress response via IPA®.

Gene Symbol - rat (Entrez Gene)	Entrez Gene Name	Expr Fold Change	Expr False Discovery Rate (q-value)
<i>Bach1</i>	BTB domain and CNC homolog 1	2.01	5.62E-03
<i>Cct7</i>	chaperonin containing TCP1 subunit 7	2.95	1.54E-07
<i>Dnaja1</i>	DnaJ heat shock protein family (Hsp40) member A1	27.39	2.09E-07
<i>Dnaja4</i>	DnaJ heat shock protein family (Hsp40) member A4	37.00	3.84E-10
<i>Dnajb1</i>	DnaJ heat shock protein family (Hsp40) member B1	37.32	2.82E-05
<i>Dnajb4</i>	DnaJ heat shock protein family (Hsp40) member B4	6.25	2.76E-03
<i>Dnajb7</i>	DnaJ heat shock protein family (Hsp40) member B7	4.93	5.19E-04
<i>Dnajb11</i>	DnaJ heat shock protein family (Hsp40) member B11	2.59	1.47E-08
<i>Dnajc3</i>	DnaJ heat shock protein family (Hsp40) member C3	2.78	4.17E-08
<i>Enc1</i>	ectodermal-neural cortex 1	2.22	8.20E-04
<i>Ephx1</i>	epoxide hydrolase 1	-3.52	1.27E-03
<i>Fosl1</i>	FOS like 1, AP-1 transcription factor subunit (Fra1)	11.11	2.54E-03
<i>Fth1</i>	ferritin heavy chain 1	2.42	2.44E-06
<i>Ftl1</i>	ferritin light chain	2.09	3.18E-05

<i>Gclc</i>	glutamate-cysteine ligase catalytic subunit	9.13	2.01E-08
<i>LOC501110 (GSTA2)</i>	glutathione S-transferase alpha 2	-3.50	6.20E-05
<i>Hmox1</i>	heme oxygenase 1	74.84	1.53E-08
<i>Hspb8</i>	heat shock protein family B (small) member 8 (Hsp22)	4.86	1.72E-02
<i>Jun</i>	Jun proto-oncogene, AP- 1 transcription factor subunit	3.28	2.61E-02
<i>Maff</i>	MAF bZIP transcription factor F	4.95	1.46E-02
<i>Mafg</i>	MAF bZIP transcription factor G	2.08	5.09E-06
<i>Mafk</i>	MAF bZIP transcription factor K	4.00	2.35E-04
<i>Map2k6</i>	mitogen-activated protein kinase kinase 6	-2.67	1.66E-05
<i>Mgst3</i>	microsomal glutathione S-transferase 3	-2.13	5.60E-05
<i>Nfe2l2 (Nrf2)</i>	nuclear factor, erythroid 2 like 2 (Nrf2)	2.97	1.33E-06
<i>Nqo1</i>	NAD(P)H quinone dehydrogenase 1	11.63	6.32E-05
<i>Pik3c2b</i>	phosphatidylinositol-4- phosphate 3-kinase catalytic subunit type 2 beta	5.09	2.34E-04
<i>Pmf1</i>	polyamine modulated factor 1	-2.97	7.04E-08
<i>Sod1</i>	superoxide dismutase 1	3.98	2.16E-11
<i>Stip1</i>	stress induced phosphoprotein 1	16.07	3.34E-12
<i>Txnrd1</i>	thioredoxin reductase 1	3.39	5.67E-05
Additional gene expression data related to NRF2-mediated oxidative stress response via IPA®			

<i>Hsp90aa1</i>	heat shock protein 90, alpha (cytosolic), class A member 1	30.58	2.75E-09
<i>Hsp90ab1</i>	heat shock protein 90 alpha family class B member 1	12.78	2.76E-11

Table S4: Gene expression data for Figure 6. Hypothesized pathway and consequences of glutamine uptake in 2 hr post METH STR and PFC microglia. ND = Not Detected. NS = Not significant.

Symbol	Gene Name	2 hr STR average log2cpm Saline (n=6), METH (n=8)	2 hr STR Fold Change, FDR	2 hr PFC average log2cpm Saline (n=4), METH (n=5)	2 hr PFC Fold Change, FDR
<i>Slc7a6</i>	solute carrier family 7 member 6	6.67, 7.00	1.30, 0.02	6.69, 6.51	-1.09, 0.59 (NS)
<i>Slc38a7</i>	solute carrier family 38, member 7	5.34, 6.05	1.70, 2.8E-04	5.39, 5.83	1.38, 0.02
<i>Slc1a5</i>	solute carrier family 1 member 5	3.71, 5.50	3.52, 1.6E-03	3.69, 3.83	1.47, 0.42 (NS)
<i>Slc38a1</i>	solute carrier family 38, member 1	-2.78, -2.73	-1.20, 0.68 (NS)	-1.57, -2.03	-1.36, 0.71 (NS)
<i>Slc1a3</i>	solute carrier family 1 member 3 (EAAT1, GLAST1)	10.08, 9.33	-1.61, 6.3E-06	10.09, 8.90	-2.29, 8.3E-10
<i>Slc1a2</i>	solute carrier family 1 member 2 (EAAT2, GLT1)	0.33, 0.40	1.27, 0.61 (NS)	0.08, 0.33	1.03, 0.97 (NS)
<i>Slc7a11</i>	solute carrier family 7 member 11	-0.59, 1.11	4.22, 0.01	-0.75, -0.37	1.39, 0.63 (NS)

<i>Gls</i>	glutaminase	5.91, 5.92	1.02, 0.92 (NS)	5.99, 5.80	-1.17, 0.17 (NS)
<i>Gls2</i>	glutaminase 2	0.83, 1.50	1.58, 0.08 (NS)	0.88, 1.49	1.49, 0.16 (NS)
<i>Glul</i>	glutamate-ammonia ligase	10.26, 10.38	1.12, 0.41 (NS)	10.34, 10.83	1.41, 4.2E-03
<i>Glud1</i>	glutamate dehydrogenase 1	7.98, 7.42	-1.46, 3.4E-05	8.17, 7.64	-1.44, 3.1E-05
<i>Gclc</i>	glutamate-cysteine ligase, catalytic subunit	5.15, 8.14	9.13, 2.0E-08	5.09, 6.85	3.63, 2.8E-08
<i>Gss</i>	glutathione synthetase	4.09, 3.87	-1.11, 0.59 (NS)	4.13, 3.64	-1.39, 0.02
<i>Gpx8</i>	glutathione peroxidase 8	3.58, 2.69	-1.79, 1.8E-03	3.76, 3.27	-1.37, 0.02
Other Gpx's detected					
<i>Gpx1</i>	glutathione peroxidase 1	8.57, 8.28	-1.20, 0.12 (NS)	8.70, 8.82	1.10, 0.50 (NS)
<i>Gpx3</i>	glutathione peroxidase 3	-0.97, -0.80	1.11, 0.81 (NS)	-1.38, -2.08	-1.03, 0.97 (NS)
<i>Gpx4</i>	glutathione peroxidase 4	6.95, 6.79	-1.11, 0.30 (NS)	7.20, 7.10	-1.06, 0.66 (NS)
<i>Gpx7</i>	glutathione peroxidase 7	-3.87, -1.78	2.06, 0.22 (NS)	ND	ND
<i>Gsr</i>	glutathione-disulfide reductase	5.82, 6.04	1.20, 0.37 (NS)	5.79, 5.71	-1.06, 0.59 (NS)
Gst's: 17 glutathione-S-transferases were detected in the STR, 16 in the PFC. Those with FDR<0.05 are shown below.					
<i>LOC501110</i>	similar to glutathione S-transferase A1	1.58, -0.52	-3.50, 6.2E-05	ND	ND
<i>Gstm1</i>	glutathione S-transferase mu 1	ND	ND	3.68, 4.31	1.56, 0.01

<i>Gstm4</i>	glutathione S-transferase mu 4	ND	ND	4.41, 3.85	-1.47, 1.5E-03
<i>Gstt1</i>	glutathione S-transferase theta 1	0.58, -0.90	-2.76, 2.4E-04	ND	ND
<i>Gstz1</i>	glutathione S-transferase zeta 1	3.57, 2.89	-1.51, 0.03	3.76, 3.20	-1.45, 0.03
<i>Mgst3</i>	microsomal glutathione S-transferase 3	3.03, 1.91	-2.13, 5.6E-05	3.10, 2.28	-1.75, 1.9E-04
<i>Sod1</i>	superoxide dismutase 1, soluble	5.06, 7.00	3.98, 2.2E-11	5.12, 7.13	4.09, 1.1E-09
<i>Cat</i>	catalase	6.42, 5.96	-1.35, 5.8E-03	6.52, 6.34	-1.13, 0.37 (NS)

Table S5: Gene expression data for GABA transporters in microglia from the STR at 2 hr and 3 days after METH. NS = Not significant.

Symbol	Gene Name	2 hr STR average log2cpm Saline (n=6), METH (n=8)	2 hr STR Fold Change, FDR	3 day STR average log2cpm Saline (n=4), METH (n=5)	3 day STR Fold Change, FDR
<i>Slc6a12</i>	solute carrier family 6 member 12	-0.32, 3.84	16.60, 5.4E-07	-0.33, 1.07	2.76, 3.2E-04
<i>Slc6a1</i>	solute carrier family 6 member 1	1.27, 1.47	1.06, 0.91 (NS)	-0.73, -2.62	-2.00, 0.54 (NS)



Table S6: Gene expression data for *Csf1*, *Csfr1*, *Il34* in microglia from the STR at 2 hr and 3 days after METH. NS = Not significant.

Symbol	Gene Name	2 hr STR average log2cpm Saline (n=6), METH (n=8)	2 hr STR Fold Change, FDR	3 day STR average log2cpm Saline (n=4), METH (n=5)	3 day STR Fold Change, FDR
<i>Csf1</i>	colony stimulating factor 1	1.54, 4.91	12.52, 7.6E-09	-0.60, 0.52	2.42, 4.6E-03
<i>Csfr1</i>	colony stimulating factor 1 receptor	13.48, 13.62	1.10, 0.54 (NS)	11.73, 11.60	-1.06, 0.90 (NS)
<i>Il34</i>	interleukin 34	-1.52, -1.56	1.18, 0.76 (NS)	-2.01, -0.27	3.23, 0.02