

Supplemental Table 2. 119 Dysregulated Genes in Postmortem Prefrontal Cortex (Brodmann's Area 46) from Patients with PTSD*

Gene	PTSD/C Log2	p-value	Gene	PTSD/C Log2	p-value	Gene	PTSD/C Log2	p-value	Gene	PTSD/C Log2	p-value
<u>DNAJC19</u>	-1.68	0.001	DUSP11	-0.59	0.038	MPO	-0.36	0.017	CLIC4	0.62	0.001
<u>SLC1A6</u>	-1.06	0.000	GLYAT	-0.58	0.027	SERPINA3	-0.35	0.011	CLIC1	0.62	0.011
<u>PPID</u>	-0.94	0.002	CD59	-0.57	0.041	SLC25A26	-0.35	0.008	MRPL55	0.64	0.039
<u>CS</u>	-0.91	0.005	ALDH18A1	-0.57	0.032	HSP90AB1	0.33	0.009	<u>TFAM</u>	0.70	0.025
<u>IMMP2L</u>	-0.89	0.003	ATP5E	-0.57	0.038	ECHDC1	0.36	0.019	<u>MYH3</u>	0.71	0.000
<u>VAMP1</u>	-0.88	0.010	C14orf121	-0.56	0.038	H3F3A	0.43	0.035	<u>CDH13</u>	0.71	0.011
<u>BRP44</u>	-0.87	0.032	FABP3	-0.55	0.049	ANXA3	0.45	0.011	<u>SLC25A30</u>	0.73	0.013
<u>MRPS18B</u>	-0.87	0.008	PECAM1	-0.55	0.006	ACADL	0.45	0.032	<u>RAB15</u>	0.75	0.034
<u>BCL2L10</u>	-0.83	0.016	HAGH	-0.54	0.048	EHD4	0.48	0.007	<u>HMGCL</u>	0.76	0.004
<u>PDHA1</u>	-0.79	0.003	MRPL4	-0.54	0.019	PSMD2	0.49	0.006	<u>PFKM</u>	0.79	0.009
<u>STARD3</u>	-0.75	0.027	RDH13	-0.54	0.046	FDX1	0.49	0.011	<u>RAB11FIP5</u>	0.80	0.026
<u>LOC153328</u>	-0.72	0.012	MGST1	-0.54	0.009	DDX39	0.50	0.024	<u>NDUFA10</u>	0.80	0.028
<u>TOM1L1</u>	-0.72	0.006	POLR3E	-0.51	0.006	MRPL9	0.51	0.005	<u>MRPL35</u>	0.83	0.012
<u>GFM1</u>	-0.72	0.005	SUCLG1	-0.50	0.011	MT1A	0.54	0.027	<u>B3GNT4</u>	0.85	0.019
<u>NDUFS2</u>	-0.71	0.004	SLC25A44	-0.49	0.022	CCDC56	0.54	0.019	<u>BCL2A1</u>	0.86	0.008
<u>MCAT</u>	-0.71	0.011	C9orf78	-0.49	0.001	CECR5	0.55	0.022	<u>ACAD8</u>	0.86	0.010
STCH	-0.67	0.033	BCL2	-0.49	0.005	IDH3B	0.56	0.022	<u>MRPS28</u>	0.89	0.017
BLK	-0.67	0.026	OXA1L	-0.49	0.042	OAS1	0.57	0.007	<u>HSPD1</u>	0.89	0.002
PPIF	-0.67	0.002	AKR1B1	-0.48	0.027	PPP2R1B	0.58	0.004	<u>HSPA1A</u>	0.90	0.003
NDUFB5	-0.66	0.002	MPHOSPH6	-0.47	0.042	UCP2	0.58	0.041	<u>DDX21</u>	0.95	0.044
DMGDH	-0.64	0.012	SLC25A6	-0.47	0.036	NP	0.59	0.005	<u>UVRAG</u>	0.95	0.006
CYBA	-0.63	0.030	PRKAR2B	-0.46	0.042	SLC25A46	0.60	0.012	<u>SURF1</u>	0.95	0.004
ATPAF1	-0.63	0.000	SPG7	-0.46	0.042	SLC25A20	0.60	0.037	<u>TLN2</u>	0.97	0.001
COX8A	-0.63	0.018	SLMAP	-0.45	0.026	ATP5C1	0.60	0.007	<u>ESR2</u>	0.98	0.025
PAPD1	-0.63	0.027	MTUS1	-0.44	0.008	TMCO6	0.60	0.013	<u>MPST</u>	1.02	0.000
LRP16	-0.62	0.018	MTERF	-0.42	0.012	RAB5B	0.60	0.038	<u>APP</u>	1.05	0.002
CRYAB	-0.61	0.046	RAB2A	-0.42	0.043	CCT6A	0.61	0.036	<u>DDX18</u>	1.09	0.000
LOC286208	-0.61	0.031	ATPIF1	-0.41	0.038	PRKCD	0.61	0.008	<u>SYK</u>	1.15	0.014
PDK1	-0.59	0.018	CASP4	-0.41	0.017	CAT	0.61	0.048	<u>SLC9A6</u>	1.58	0.002
PRMT2	-0.59	0.046	AGXT2	-0.36	0.021	OXR1	0.62	0.032			

All 119 genes were dysregulated ($p < 0.05$, $\pm \geq 1.25$) of which 42 had a fold change $\pm \geq 1.60$ (underlined).