

Table SI. Significantly altered protein abundances in the mPFC of rats upon RWIS.

Group 1, Structural proteins					
Gene symbol	Protein name	Accession no.	Lesioned mPFC (↑ or ↓)	MW (Da)	FC
Plp1	Myelin proteolipid protein	MYPR_RAT	↑	30,077	0.8299
Cdh11	Cadherin 11	F1MAH6_RAT	↑	88,036	0.6468
Rps25	40S ribosomal protein S25	A0A0H2UHU0_RAT	↑	13,611	0.6174
LOC100909481	Eukaryotic translation initiation factor 3 subunit E	A0A0G2K273_RAT	↑	52,229	0.5706
Sf3b2	Splicing factor 3b, subunit 2	D3ZMS1_RAT	↑	98,147	0.5561
Camsap2	Calmodulin-regulated spectrin-associated protein 2	A0A0G2K7K9_RAT	↑	165,612	0.5300
Eif4a3	Eukaryotic initiation factor 4A-III	IF4A3_RAT	↑	46,841	0.5039
Psmd5	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 5 (Predicted), isoform CRA_a	G3V8G2_RAT	↑	55,853	0.5008
Sf3b4	Splicing factor 3B subunit 4	SF3B4_RAT	↑	44,356	0.4863
Mpv17	Protein Mpv17	F1LNG8_RAT	↑	18,750	0.4807
Cd151	CD151 antigen	CD151_RAT	↑	28,355	0.4708
Mrpl9	39S ribosomal protein L9, mitochondrial	RM09_RAT	↑	30,076	0.3625
Vcan	Versican core protein	CSPG2_RAT	↑	300,008	0.4502
Nefl	Neurofilament light polypeptide	NFL_RAT	↑	61,335	0.4381
Nefm	Neurofilament medium polypeptide	NFM_RAT	↑	95,791	0.3863
Rpl23a	RCG33340	B5DES1_RAT	↑	17,695	0.3703
Rpl15	60S ribosomal protein L15	RL15_RAT	↑	24,146	0.4602
Sptbn4	Spectrin beta chain	A0A0G2K677_RAT	↑	288,817	0.3412
Surf4	Ab1-205	Q7TP91_RAT	↑	83,263	0.3102
Strn3	Striatin-3	E9PT82_RAT	↑	77,629	0.3063
Mog	Myelin-oligodendrocyte glycoprotein	MOG_RAT	↑	27,882	0.2948
Dmtn	Dematin actin-binding protein	B2GUY4_RAT	↑	39,524	0.2899
Eif4b	Eukaryotic translation initiation factor 4B	Q5RKG9_RAT	↑	69,064	0.2868
Hist1h4b	Histone H4	H4_RAT	↑	11,367	0.2699
cpg2	CPG2 protein	Q63128_RAT	↓	109,037	-0.6926
Cav1	Caveolin	A2VCW2_RAT	↓	19,714	-0.5047
Coa3	Cytochrome C oxidase assembly factor 3	D3Z9I1_RAT	↓	11,929	-0.5005
Mapre2	Microtubule-associated protein RP/EB family member 2	M0R8A4_RAT	↓	28,137	-0.3187
Ndufb11	NADH dehydrogenase (Ubiquinone)1 beta subcomplex, 11 (Predicted)	D4A7L4_RAT	↓	17,634	-0.2895
Dlg4	Disks large homolog 4	DLG4_RAT	↓	80,465	-0.2774

Group 2, Regulating proteins					
Gene symbol	Protein name	Accession no.	Lesioned mPFC (↑ or ↓)	MW (Da)	FC
Cstb	Cystatin-B	CYTB_RAT	↑	11,196	0.8891
Mindy2	Family with sequence similarity 63, member B	D3ZWA1_RAT	↑	65,697	0.8734
Arl3	ADP-ribosylation factor-like protein 3	ARL3_RAT	↑	20,457	0.8304
Slc6a9	Sodium- and chloride-dependent glycine transporter 1	SC6A9_RAT	↑	71,061	0.7901
Lama1	Laminin subunit alpha 1	D4A409_RAT	↑	338,195	0.7887
Cd9	Tetraspanin	B1WBM0_RAT	↑	25,215	0.7843
Ptma	Prothymosin alpha	PTMA_RAT	↑	12,382	0.7816
Shh	Hedgehog protein	G3V6T0_RAT	↑	47,577	0.6817
Tars	Threonine-tRNA ligase, cytoplasmic	A0A0G2K9V6_RAT	↑	83,389	0.4759

Table SI. Continued.

Group 2, Regulating proteins

Gene symbol	Protein name	Accession no.	Lesioned mPFC (↑ or ↓)	MW (Da)	FC
Pebp1	Phosphatidylethanolamine-binding protein 1	PEBP1_RAT	↑	20,801	0.4709
Ppt1	Palmitoyl-protein thioesterase 1	PPT1_RAT	↑	34,455	0.4382
Sri	LOC683667 protein	B0BNJ1_RAT	↑	21,624	0.4150
N/A	Uncharacterized protein	A0A0G2K3Z9_RAT	↑	22,164	0.3898
Prdx6	Protein phosphatase 1H	PRDX6_RAT	↑	24,819	0.3895
N/A	Glutathione S-transferase omega 1	B6DYQ5_RAT	↑	27,669	0.3879
Hpx	Hemopexin	HEMO_RAT	↑	51,351	0.3619
Ppm1h	Echinoderm microtubule-associated	PPM1H_RAT	↑	56,380	0.3583
Park7	Protein/nucleic acid deglycase DJ-1	PARK7_RAT	↑	19,974	0.3574
Ppid	Peptidyl-prolyl cis-trans isomerase D	PPID_RAT	↑	40,766	0.3549
Cmpk1	UMP-CMP kinase	KCY_RAT	↑	22,169	0.3488
Ppp5c	Serine/threonine-protein phosphatase 5	PPP5_RAT	↑	56,917	0.3466
Adh5	Alcohol dehydrogenase class-3	ADHX_RAT	↑	39,576	0.3455
Eml2	Echinoderm microtubule-associated protein-like 2	EMAL2_RAT	↑	70,711	0.3402
Epb4112	Erythrocyte membrane protein band 4.1-like 2	D3ZAY7_RAT	↑	89,129	0.3322
Gstm3	Glutathione S-transferase Yb-3	GSTM4_RAT	↑	25,681	0.2798
Chga	Chromogranin-A	CMGA_RAT	↓	52,024	-0.9774
Apex1	DNA-(apurinic or apyrimidinic site) lyase	APEX1_RAT	↓	35,538	-0.7542
Lama4	Laminin subunit alpha 4	F1LTF8_RAT	↓	196,949	-0.7228
Plgrkt	Plasminogen receptor (KT)	PLRKT_RAT	↓	17,312	-0.5036
Atp2b2	Plasma membrane calcium-transporting ATPase 2	AT2B2_RAT	↓	136,811	-0.4124
LOC100360940	Diablo-like	D4A7Z5_RAT	↓	28,772	-0.3866
Ttbk1	Tau tubulin kinase 1	A0A0G2JTK1_RAT	↓	147,665	-0.3666

Group 3, Transport proteins

Gene symbol	Protein name	Accession no.	Lesioned mPFC (↑ or ↓)	MW (Da)	FC
Reep1	Receptor expression-enhancing protein	D4A193_RAT	↑	22,241	0.4704
Vps11	Vps11 protein	B5DF01_RAT	↑	103,693	0.3776
Synrg	Synergism gamma	SYNRG_RAT	↓	141,359	-0.6484
Vamp2	Vesicle associated membrane protein 2B	Q9WUW2_RAT	↓	14,509	-0.4841
Xpr1	Xenotropic and polytropic retrovirus receptor 1	A0A0G2JXZ7_RAT	↓	78,978	-0.4584
Abcd3	ATP-binding cassette sub-family D member 3	ABCD3_RAT	↓	75,316	-0.3770
Stx1a	Syntaxin-1A	STX1A_RAT	↓	33,067	-0.2740

Group 4, Chaperones

Gene symbol	Protein name	Accession no.	Lesioned mPFC (↑ or ↓)	MW (Da)	FC
Cotl1	Coactosin-like protein	COTL1_RAT	↑	15,932	0.2981
Fkbp8	Peptidyl-prolyl cis-trans isomerase FKBP8	FKBP8_RAT	↓	43,556	-0.2842

Group 5, Cell cycle

Gene symbol	Protein name	Accession no.	Lesioned mPFC (↑ or ↓)	MW (Da)	FC
Pum1	Pumilio RNA-binding family member 1	D3Z8L5_RAT	↑	126,290	0.8621

Table SI. Continued.

Group 5, Cell cycle

Gene symbol	Protein name	Accession no.	Lesioned mPFC (↑ or ↓)	MW (Da)	FC
Ccdc155	Coiled-coil domain-containing 155	D3ZPX3_RAT	↑	67,805	0.4538
Ube2l3	Ube2l3 protein	B2RZA9_RAT	↑	17,862	0.2631
Cetn2	Centrin 2	G3V9W0_RAT	↓	19,842	-0.8289
Ttc19	Tetratricopeptide repeat protein 19, mitochondrial	TTC19_RAT	↓	41,333	-0.4946
Dhx15	DEAH (Asp-Glu-Ala-His) box polypeptide 15 (Predicted), isoform CRA_b	D3ZD97_RAT	↓	90,977	-0.2928

Group 6, Signal transduction

Gene symbol	Protein name	Accession no.	Lesioned mPFC (↑ or ↓)	MW (Da)	FC
Ndrp1	Protein NDRG1	NDRG1_RAT	↑	42,955	1.2931
Rhof	RCG21806	D3ZRB3_RAT	↑	23,601	0.7477
Ncam1	Neural cell adhesion molecule 1	F1LUV9_RAT	↑	91,636	0.6624
Pacs1	Phosphofurin acidic cluster sorting protein 1	F1LPG3_RAT	↑	104,751	0.5371
Rhog	Ras homolog family member G	A0A096MJM1_RAT	↑	20,623	0.2650
NEWGENE_1305560	Neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adaptor 2	F1M3A4_RAT	↓	78,341	-4.7968
Cacna1b	Voltage-dependent N-type calcium channel subunit alpha-1B	CAC1B_RAT	↓	262,256	-0.7177
Srpk2	SRSF protein kinase 2	A0A0G2JX62_RAT	↓	80,596	-0.4203
Gpr162	G protein-coupled receptor 162	D4AAS1_RAT	↓	64,048	-0.3999
Rap1gap2	RAP1 GTPase-activating protein 2	A0A0G2K0S7_RAT	↓	80,514	-0.2788

Group 7, Transcription

Gene symbol	Protein name	Accession no.	Lesioned mPFC (↑ or ↓)	MW (Da)	FC
Eef1a1	Elongation factor 1-alpha 1	EF1A1_RAT	↑	50,114	0.5322
Hmgn2	Non-histone chromosomal protein HMG-17	HMGN2_RAT	↑	9,366	0.5302
Mtpn	Myotrophin	MTPN_RAT	↑	12,861	0.4264
Hint1	Histidine triad nucleotide-binding protein 1	HINT1_RAT	↑	13,777	0.3804
Ruvbl1	RuvB-like 1	RUVB1_RAT	↑	50,214	0.3343
Celf2	CUGBP Elav-like family member 2	CELF2_RAT	↑	54,271	0.3243
Rbmxtl	RNA-binding motif protein, X chromosome retrogene-like	RMXRL_RAT	↑	42,204	0.2877
Wbp2	WW domain binding protein 2, isoform CRA_b	G3V721_RAT	↓	28,159	-0.7003
Cc2d1a	Coiled-coil and C2 domain-containing protein 1A	C2D1A_RAT	↓	103,587	-0.6298
N/A	Uncharacterized protein	M0R7E6_RAT	↓	54,985	-0.4906
Zbed5	RCG21454	D3ZTR5_RAT	↓	84,035	-0.4189
Pura	Transcriptional activator protein Pur-alpha	F1LPS8_RAT	↓	31,904	-0.2713

Group 8, Enzymes

Group 8a, Energy metabolism

Gene symbol	Protein name	Accession no.	Lesioned mPFC (↑ or ↓)	MW (Da)	FC
Arhgap5	Rho-GTPase-activating protein 5	A0A0G2K7N9_RAT	↑	172,291	1.1866

Table SI. Continued.

Group 8a, Energy metabolism					
Gene symbol	Protein name	Accession no.	Lesioned mPFC (↑ or ↓)	MW (Da)	FC
Rab8b	RAB8B, member RAS oncogene family	B0BMV5_RAT	↑	23,603	0.3387
Ddx1	ATP-dependent RNA helicase DDX1	DDX1_RAT	↑	82,497	0.3196
Abcc8	ATP-binding cassette sub-family C member 8	ABCC8_RAT	↓	177,185	-0.9285
Atp6v0c	V-type proton ATPase 16 kDa proteolipid subunit	VATL_RAT	↓	15,808	-0.7745
LOC100911485	Mitofusin-2-like	F7FHF7_RAT	↓	86,813	-0.3755
Ndufs3	NADH dehydrogenase (Ubiquinone) Fe-S protein 3 (Predicted), isoform CRA_c	D3ZG43_RAT	↓	30,226	-0.3363
Ndufa12	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	F1LXA0_RAT	↓	17,178	-0.2861
Group 8b, Carbohydrate metabolism					
Gene symbol	Protein name	Accession no.	Lesioned mPFC (↑ or ↓)	MW (Da)	FC
Mpi	Mannose-6-phosphate isomerase	MPI_RAT	↑	46,424	0.5859
Clybl	Citramalyl-CoA lyase, mitochondrial	CLYBL_RAT	↑	37,321	0.5523
Gpd1	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic	GPDA_RAT	↑	37,453	0.4995
Akr1b1	Aldose reductase	ALDR_RAT	↑	35,797	0.3566
Lcmt1	Leucine carboxyl methyltransferase 1	G3V7V9_RAT	↑	38,356	0.2935
Mdh1	Malate dehydrogenase, cytoplasmic	MDHC_RAT	↑	36,483	0.2803
Group 8c, Amino acid metabolism					
Gene symbol	Protein name	Accession no.	Lesioned mPFC (↑ or ↓)	MW (Da)	FC
Rida	2-iminobutanoate/2-iminopropanoate deaminase	UK114_RAT	↑	14,303	0.6229
Gstm1	Glutathione S-transferase Mu 1	GSTM1_RAT	↑	25,914	0.3413
Oat	Ornithine aminotransferase, mitochondrial	OAT_RAT	↑	48,333	0.3193
Srr	Serine racemase	SRR_RAT	↑	35,693	0.2822
Gstz1	Maleylacetoacetate isomerase	A0A0G2K6H2_RAT	↓	23,863	-0.5499
Group 8d, Cofactors and vitamins					
Gene symbol	Protein name	Accession no.	Lesioned mPFC (↑ or ↓)	MW (Da)	FC
B3gat3	Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase	B2GV35_RAT	↓	37,073	-0.8201
Group 8e, Lipid metabolism					
Gene symbol	Protein name	Accession no.	Lesioned mPFC (↑ or ↓)	MW (Da)	FC
Sirt2	NAD-dependent protein deacetylase	A0A0G2JWM2_RAT	↑	43,163	0.4775
Pafah1b2	Platelet-activating factor acetylhydrolase IB subunit beta	PA1B2_RAT	↓	25,581	-0.6040

Table SI. Continued.

Group 8f, Nucleic acid metabolism

Gene symbol	Protein name	Accession no.	Lesioned mPFC (↑ or ↓)	MW (Da)	FC
Cnp	2',3'-cyclic-nucleotide 3'-phosphodiesterase	CN37_RAT	↑	47,268	0.5092
Adsl	Adenylosuccinate lyase	D3ZW08_RAT	↓	54,852	-0.2632

Group 8g, Proteasome

Gene symbol	Protein name	Accession no.	Lesioned mPFC (↑ or ↓)	MW (Da)	FC
C4a	Complement component 4A (Rodgers blood group)	A0A0G2JW12_RAT	↑	192,248	1.2328
Psm13	26S proteasome non-ATPase regulatory subunit 13	PSD13_RAT	↑	42,817	0.2923

Group 9, unknown function

Gene symbol	Protein name	Accession no.	Lesioned mPFC (↑ or ↓)	MW (Da)	FC
Bcas1	Breast carcinoma-amplified sequence 1 homolog	A0A0G2K079_RAT	↑	37,500	0.5937
Rnf214	Ring finger protein 214	D4A3V4_RAT	↑	77,723	0.5647
-		F1LNY0_RAT	↑		
-		M0RA17_RAT	↑		

The FC represents the ratio of the absolute intensities of proteins in the RWIS 4 h and control groups. ↑, upregulated; ↓, downregulated; MW, theoretical molecular weight; FC, fold change; mPFC, medial prefrontal cortex; RWIS, restraint water-immersion stress.

Table SII. Original membrane data for SYN, NDRG1 and PSD95 in western blotting.

Protein	Group	β -tubulin (IOD)	SYN (IOD)	Relative IOD	Mean	MSE	P-value
SYN	Control	3179.174	1532.268	0.481971	0.414	0.04	0.365
	RWIS 4h	1694.835	574.8303	0.339166	0.368	0.022	
	Control	3754.38	1294.393	0.344769			
	RWIS 4h	4950.379	1747.145	0.352932			
	Control	5116.998	2132.146	0.416679			
	RWIS 4h	2666.318	1098.263	0.411902			
NDRG1	Group	GAPDH	NDRG1	Relative IOD	Mean	MSE	P-value
	Control	55.9391	3314.2666	0.01687827	0.012	0.003	0.117
	RWIS 4h	52.6666	2907.7028	0.01811279	0.024	0.005	
	Control	24.5403	4145.2253	0.00592014			
	RWIS 4h	52.6689	2677.6432	0.01966987			
	Control	53.9262	3930.1444	0.01372118			
	RWIS 4h	102.9894	3132.7437	0.03287514			
PSD95	Group	GAPDH (IOD)	PSD95 (IOD)	Relative IOD	Mean	MSE	P-value
	Control	2658.4163	1259.9595	0.47395116	0.616	0.082	0.022
	RWIS 4h	3428.6698	840.1849	0.2450469	0.273	0.075	
	Control	2335.9288	1121.6678	0.48018065			
	RWIS 4h	2146.2009	152.14872	0.07089211			
	Control	2677.6432	1916.3271	0.71567679			
	RWIS 4h	4145.2253	1648.9489	0.39779476			
	Control	3053.8061	2428.937	0.79538023			
	RWIS 4h	3314.2666	1253.4831	0.37820829			

IOD, integrated optical density; MSE, mean squared error; sNDRG1, N-myc downstream regulated 1; PSD95, postsynaptic density protein 95; RWIS, restraint water-immersion stress.