

**Vagal Nerve Stimulation Modifies Neuronal Activity and the Proteome of Excitatory Synapses of Amygdala/Piriform Cortex**

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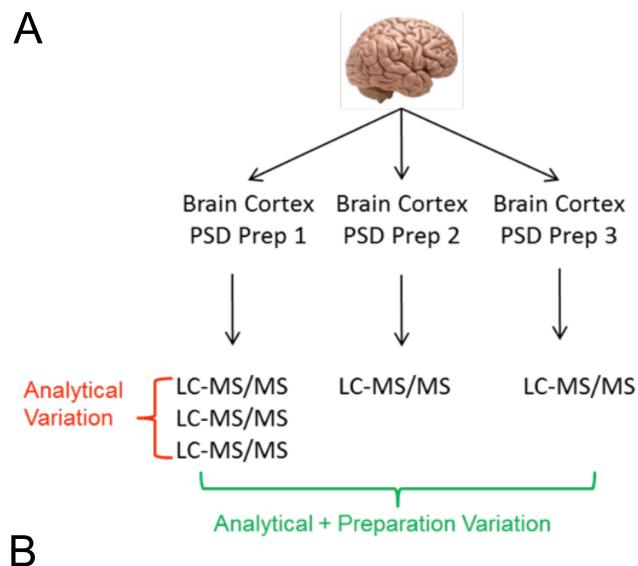
**Supplemental Materials**

Supplemental Figure Legends:

**Figure S1.** Assessment of reproducibility of the analytical approach employed in this study. A, Triplicate PSD fractions were generated and analyzed to determine the variation in any one protein's measured intensity across three replicate preparations. B, A histogram of the number of proteins within bins of measured variations (bins of 5% relative standard deviation) show that the sample preparation protocol is reproducible and the workflow is capable of quantitatively measuring differences in samples due to biology.

**Figure S2:** Three-dimensional principal component analysis (PCA) of the z-score corrected protein intensity values across control (n=4 animals, n=8 analytical injections) and VNS challenge (n=6 animals, n=12 analytical injections). For each unique biological (i.e., animal) sample, two datasets (i.e., technical duplicates) were acquired. A, The PCA analysis at the global protein level (n=436 proteins) indicated a VNS-stimulus dependent separation based on PC2. B, The PCA analysis using only those n=22 proteins classified as being differentially regulated in VNS versus Control indicated a VNS-stimulus dependent separation based on PC1.

**Figure S3.** A, Subcellular distribution of PSD proteins in the rat brain. Proteins (10 or 1  $\mu$ g) of each fraction isolated from rat hippocampus were analyzed by immunoblotting analysis with indicated antibodies. B, Quantification of enrichment of PSD-95 and synaptophysin in rat brain subcellular fractions. PSD-95, a marker of the postsynaptic density, was highly enriched in PSD-1T and PSD-2T fractions whereas synaptophysin, a marker of the presynaptic axon terminal, was highly enriched in presynaptic fraction and absent in PSD fractions. The enrichment of PSD-95 and absence of synaptophysin immunoreactivities in the PSD fractions validated the purification of the PSD fraction.



**B**

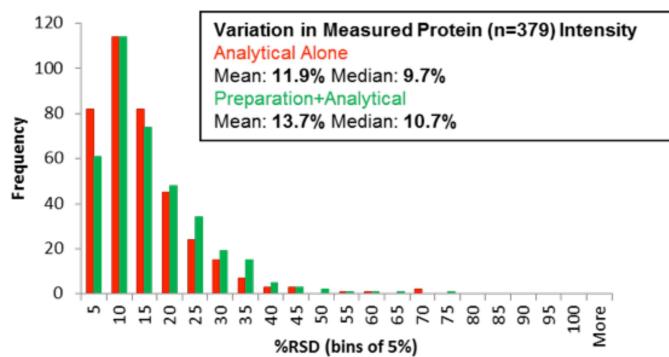


Figure S1.

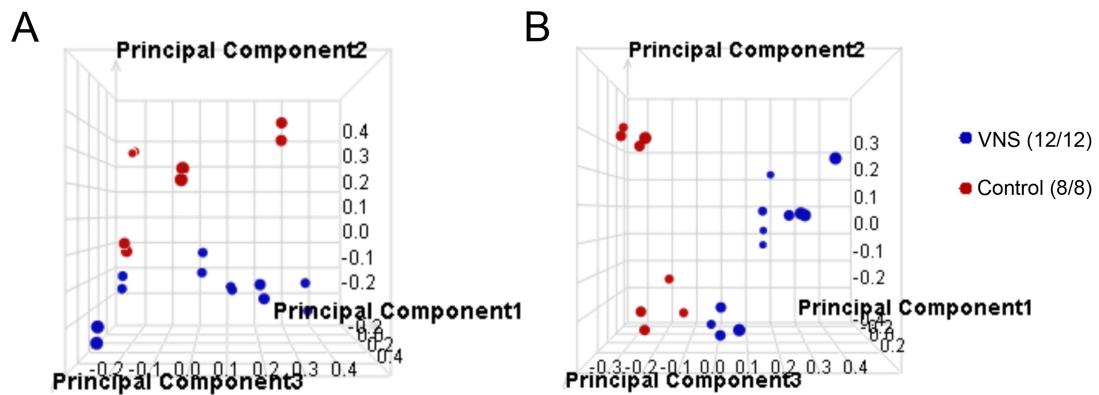


Figure S2.

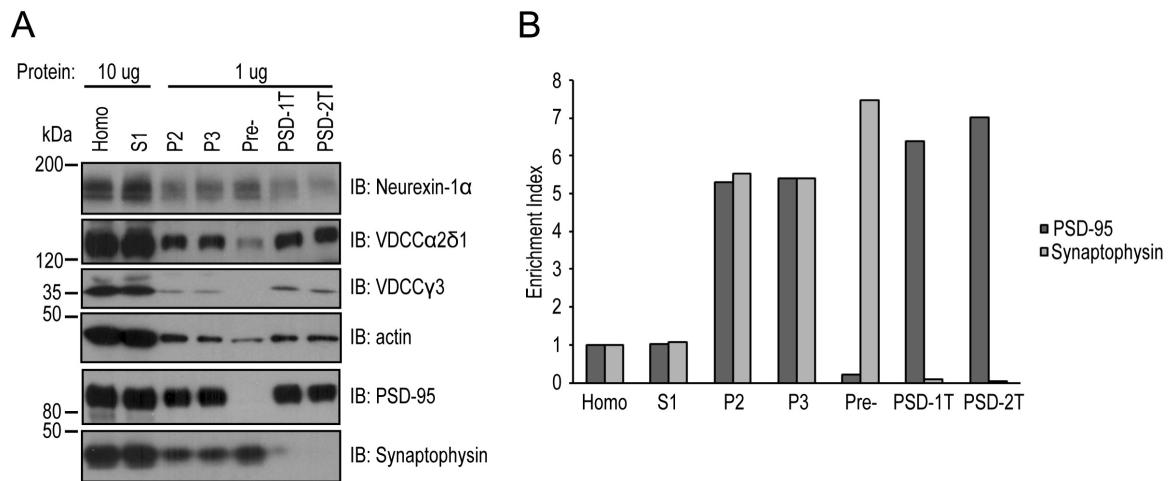


Figure S3.

**Supplemental Table 1.** Proteins identified in PSD fraction by LC-MS/MS grouped by function.

**Bold text indicates proteins not yet identified in the PSD fraction by proteomic analyses.**

Bracketed numbers indicate that the preceding residue was modified. C1160\_03071 indicates alkylation of cysteine, and M1147\_03541 indicates oxidation of methionine.







			Peptide 1	Peptide 2	Peptide 3	Peptide 4	Peptide 5	Peptide 6	Peptide 7	Peptide 8	Peptide 9	Peptide 10	Peptide 11	Peptide 12	Peptide 13	Peptide 14	Peptide 15	Peptide 16	Peptide 17	Peptide 18	Peptide 19	Peptide 20
PGAM5_RAT	Serine/threonine-protein phosphatase e PGAM5, mitochondrial	1	AVETTDIISK																			
SKP1_RAT	S-phase kinase-associated protein 1	1	NDFTEEEE AQVR																			
SRCN1_RAT	SRC kinase signaling inhibitor 1	8	SSGATPV SGPPPA TDPGPTPT PDHKPKK	SSGATPV VSSTPAG OPTAVSR	SLSTYSA ALQSDL EDSYLK	QVTLA QIR	LGGAPTS CGVSPS PSAILER	STGASTA GAPPSEL FPPGPE R	LOLONQE SVR	AGAGGPL YGDGYG FR												
<b>Membrane Trafficking</b>																						
AP2A2_MOUSE	AP-2 complex subunit alpha-2	5	KGPSTVTD LEETKRAAK	DDVQGY OR	NADVELO K	ALLLSTYI	ATIQDVL R															
AP2B1_MOUSE	AP-2 complex subunit beta-1	6	LQNNNNVY IAK	NINLIVQK	LAPPVLT LLSGEPE VQYVLR	LLSTDV TAK	FLELLPK	IQPGPNP YTSLK														
AP2M1_MOUSE	AP-2 complex subunit mu-1	5	LYNSDHDV IK	ECIYETR DIIPLPR	TFITQQ K	ISEENIK																
DYN1_MOUSE	Dynamin-1	4	VPVGDDQPP DIEFQIR	VGGCSA GK	SSVLENF VGR	GISPVPIN LR																
NPC1_MOUSE	Niemann-Pick C1 protein	1	GTERERLL NF																			
SYN1_RAT	Synapsin-1	15	VLLVIDEPH TDWAK	LPSPAA PQGSAS QGQGR	GSHSQT PSPGALP LGR	ASTAAPV ASPAAPS PGSSGG GGFVSSL SNAVK	TYATAEP FIDAK	EM 147.03 54 LSSTT YPVVK	MTQALPR	SQLSLNA FNLPPEA PPRPSLS	QTSSQP AGPPAQ QRPPQ GQGHLS	QPPPK QPPGAP GPGPQR	QASISGP APPK SPSPQR	QSRPVIA GGPGAP PAARPPA SPLPQR	CGPPLQ QRPPQ GQGHLS	EMLSSTT YPVVKK	TSVSGN WK					
SYN2_RAT	Synapsin-2	6	FPLIQCPTY PNHR	EMTLTPL FPVVK	QTAASAG LVDAPAP SAASR	OLITDVL SK	TPALSPQ RPLTTQQ PQSGLK EPDSKK															
SNP25_MOUSE	Synaptosomal-associated protein 25	5	RADQLADE SLESTRR	ADQLADE EQMAISG GFIIG	AWGNQNO DGVAS QPAR	MQLQVEE SK																
SYT1_MOUSE	Synaptotagmin-1	9	MDVGGSL DPYVK	NTLNPPY NESF-SFE VPFEQIK	LTVILEA K	DLOSAEK EEGEK	VFGYNS TGAEILR	VPYSELG GK	TLNPVFN EQFTFK	LGDIQ16 0.0307/FIS LR												
SYT7_MOUSE	Synaptotagmin-7	2	DLNPNIFES FAFDIPTEK	NDPGEV SIPLNK																		
SYT3_MOUSE	Synaptotagmin-like protein 3	1	ALGLLLNR																			
SNPH_RAT	Syntaphilin	8	HSELDLHP SGPR	VGQAQG C1160.03 7ISSVLK	EEGTGES AGGSPAR	EAEPIT NTPAEDR	OAGDPS ADSGFVA ADDTLSR	AIQDFTV YQYQDLS NITLEK		AIQDFTV YQYQDLS NITLEK	VEAQLAL K											
STX1A_RAT	Syntaxin-1A	3	SIEQSICE EGLNR	[AE]NVEE VK	QALSEIE TR																	
STX1B_MOUSE	Syntaxin-1B	4	OLEITGR	QALNEIE TR	LAIFTDI K	AIEQSIEQ EEGLNR																
STXB1_MOUSE	Syntaxin-binding protein 1	8	YETSGIGE AR	EPLPSLE EK	DNALLAQ LIQDK	SSASFST TAVASR	HIAEVSQ EVTR	ISEQTYQ LSR	SQILLDR	LNKTDEE ISS												
<b>Metabolism</b>																						
CN37_RAT	2',3'-cyclic-nucleotide 3'-phosphodiesterase	17	AGQVFLEE LGNHK	ADFSEYY KR	LSISALFV TPK	LDC 160.03 307 AQLK	LDEDLAG Y C 160.03 07 R	AIFTGYY GK	TAGAQVV LNEQELQ LWPSSDL KPSSSES LTPPGSR	HFSIGDE PKEK	GGSQGE EVGELPR	RPPGVHL C 160.030 7 JTTK	MVSADAY K	ADFSEYY K	HFISGDE PK	ATGAEEY AQQDVV R	VIVLDDT NHER	INQWQLS LDDLK	LDLVSYF GK			
THIL_RAT	Acetyl-CoA acetyltransferase, mitochondria	4	FANEITPITI SVK	AAFAFADA WDPIDFR LAPAYAV	AIK	LGTIAOG LEDIVK																
ADH1 YEAST	Alcohol dehydrogenase 1	8	ANGTTVL ANELLINVK	VGMPAG AK	YVVDTSK	EAIDFFA R	DIVGAVL K	C 160.030 7 C 160.0 307 SDVF NQVVK	VVGLSTL PEIYEK	SISIVGSY VGNR												
AOFA_RAT	Amine oxidase [flavin-containing] A	7	EVLNALGK	DIWVEE ESK	EIPVDAP WQAR	WWDVGG AVVGPTQ NR	INVLVLEA R	YVISAIPI LTAK	IFSVTNG GGER													
AATM_MOUSE	Aspartate aminotransferase, mitochondria	1	IAATILTSPD LR																			
KCRU_MOUSE	Creatine kinase ubiquitous	7	TVGMVAG DEETYEV AELFDPVQ ER	TVGM 147 DEETYEV AELFDPVQ VIQER	GTGGVD TAAATGSV FDISNLD R	VVDSL GLK	LGYILTC  160.0307 PSNLGTC LR	LYPPSAE YDPLR	SGYFDER													
QCR1_RAT	Cytochrome b-c1 complex subunit 1, mitochondrial	8	IEEVDQAM VR	EVEISGA HLNAYST R	LC 160.03 07 TSATE SEVTR	TDLTDYL SR	VWELLADI VONISLE DSQIEK	MVLAAAG GVK	IPLAEWE SR	FTGSEIR												
QCR2_RAT	Cytochrome b-c1 complex subunit 2, mitochondrial	12	AVAFQNPO TR	LASTLTT K	AVAQGNL SSADVQA F	TSAPGGV FETK	SMTASG NLGHTPF I DEI	NALANPL Y C 160.03 07 PDPYR NIR	EVAEQL AVK	RGNNTTS K	LLSQSVA I SOSVAK WVFAAI L SR						LPNGLVIA SLENYAP SR					



































	Peptide 65	Peptide 66	Peptide 67	Peptide 68	Peptide 69	Peptide 70
<b>Cytoskeleton-Actin</b>						
ACTG_RAT						
ARPC4_MOUSE						
ACTN1_RAT						
AINX_RAT						
ANK2_MOUSE						
E41L1_RAT						
E41L3_MOUSE						
COR1A_RAT						
COR1C_MOUSE						
DREB_RAT						
CAZA2_MOUSE						
SPTA2_RAT	DVDETIG WIK	DLAALD K	LQVASDE NYKOPTN LQK	LFQAAEV QR	EAALTSE EVGADLE QVEVLOKK	ILLEATEL
SPTB2_MOUSE						
SPTN2_RAT						
SYNPO_RAT						
<b>Cytoskeleton-Other</b>						
GFAP_RAT						
K1C10_MOUSE						
K2C1_MOUSE						
K2C6A_RAT						
MAP1A_RAT						
MAP1B_RAT						
MAP2_RAT						
MAP4_MOUSE						
MAP6_RAT						
TAU_RAT						
MLP3B_RAT						
NFH_RAT						
NFL_MOUSE						
NFM_RAT						
SEPT3_RAT						
PLEC1_RAT						
SEP11_RAT						
<b>SEP14_MOUSE</b>						
SEPT2_RAT						

**Supplemental Table 2. Ingenuity Pathway Analysis of 56 Proteins Significantly Changed by VNS (p<0.05), as detected by LC-MS/MS.**

### Top Canonical Pathways

Name	p-value	Overlap
Glutamate Receptor Signaling	5.46E-09	10.5 % 6/57
Amyotrophic Lateral Sclerosis Signaling	7.83E-06	4.5 % 5/111
RhoGDI Signaling	6.63E-05	2.9 % 5/173
Signaling by Rho Family GTPases	3.49E-04	2.0 % 5/247
phagosome maturation	4.36E-04	2.8 % 4/144

### Top Networks

ID Associated Network Functions	Score
1 Cell-To-Cell Signaling and Interaction, Nervous System Development and Function, Amino Acid Metabolism	50
2 Cell-To-Cell Signaling and Interaction, Hair and Skin Development and Function, Cellular Movement	32
3 Connective Tissue Disorders, Inflammatory Disease, Inflammatory Response	22
4 Cell Morphology, Nervous System Development and Function, Tissue Morphology	6
5 Cancer, Hematological Disease, Immunological Disease	3

### Top Diseases and Bio Functions

#### Diseases and Disorders

Name	p-value	#Molecules
Neurological Disease	7.37E-03 - 1.24E-08	38
Organismal Injury and Abnormalities	7.37E-03 - 3.31E-08	46
Psychological Disorders	7.37E-03 - 3.31E-08	22
Skeletal and Muscular Disorders	7.37E-03 - 2.14E-07	24
Hereditary Disorder	7.37E-03 - 2.38E-06	26

#### Molecular and Cellular Functions

Name	p-value	#Molecules
Cellular Assembly and Organization	7.37E-03 - 6.50E-11	30
Cellular Function and Maintenance	7.37E-03 - 6.50E-11	33
Cell Morphology	7.37E-03 - 5.25E-10	29
Cell-To-Cell Signaling and Interaction	7.37E-03 - 4.48E-09	28
Cellular Development	7.37E-03 - 6.89E-09	27

#### Physiological System Development and Function

Name	p-value	#Molecules
Behavior	7.37E-03 - 4.46E-10	20
Nervous System Development and Function	7.37E-03 - 5.25E-10	28
Tissue Morphology	7.37E-03 - 5.25E-10	22
Tissue Development	7.37E-03 - 6.89E-09	27
Embryonic Development	7.37E-03 - 3.85E-06	17