

## SUPPLEMENTARY MATERIALS

for

### “Calmodulin suppresses synaptotagmin-2 transcription in cortical neurons” by

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#### Supplementary Figure 1

*Activity blockade and activation of CaM Kinase II $\alpha$  do not increase the expression of Syt2.*

**A.** Activity blockade does not activate Syt2 expression in cultured cortical neurons from wild-type mice. Neurons were treated at DIV12 with TTX (1  $\mu$ M, to block action potentials), DL-APV (50  $\mu$ M, to block NMDA receptors) or nifedipine (20  $\mu$ M, to block L-type Ca<sup>2+</sup>-channels), and harvested after 48, 72, or 96 hrs. To ensure the continued activity of different blockers, the same amounts of blockers were added again at 48 hrs for the 72 and 96 hrs treatments. Samples were analyzed by immunoblotting for the indicated proteins (abbreviations same as above).

**B.** CaMKII $\alpha$  does not mediate the CaM-dependent suppression of Syt2 expression. Cultured cortical neurons from newborn wild-type mice were infected at DIV5 with control lentivirus or with CaM KD lentivirus expressing CaM shRNAs without a rescue construct, or with wild-type CaMKII $\alpha$  or constitutively active mutant CamKII $\alpha$ <sup>T286D</sup> as rescue constructs. Neurons were analyzed by immunoblotting for Syt2 and syntaxin-1 (Synt.) at DIV 14.

#### Supplemental Table 1

##### List of genes whose expression levels are affected by CaM-RNAi

Accession No.	Gene Symbol	Description	Relative mRNA Level			
			CaM KD1		CaM KD2	
			-	+ Res.	-	+ Res.
<b>Category 1: Transcription Regulation</b>						
NM_001081338	L3mbtl	l(3)mbt-like (Drosophila)	1.59	0.71	1.77	1.12
NM_130893	Scrt1	scratch homolog 1, zinc finger protein (Drosophila)	1.51	0.93	1.42	0.97
NM_008671	Nap1l2	nucleosome assembly protein 1-like 2	1.49	1.06	1.46	0.97
NM_009035	Rbpj	recombination signal binding protein for immunoglobulin kap	1.48	1.20	1.79	1.11
NM_001077398	Ldb2	LIM domain binding 2	0.71	0.87	0.66	1.31
NM_019743	Rybp	RING1 and YY1 binding protein	0.69	1.05	0.49	1.03
NM_173780	Klf8	Kruppel-like factor 8	0.69	1.08	0.60	1.06
NM_053123	Smarca1	SWI	0.67	1.03	0.50	0.93
NM_025282	Mef2c	myocyte enhancer factor 2C	0.65	0.89	0.54	1.23
NM_009769	Klf5	Kruppel-like factor 5	0.65	1.03	0.66	0.99
NM_008719	Npas2	neuronal PAS domain protein 2	0.65	1.20	0.64	1.07
NM_009234	Sox11	SRY-box containing gene 11	0.62	1.00	0.61	1.06
NM_175045	Bcor	Bcl6 interacting corepressor	0.60	1.10	0.67	1.34
NM_024124	Hdac9	histone deacetylase 9	0.58	1.07	0.65	1.20

Accession No.	Gene Symbol	Description	Relative mRNA Level			
			CaM KD1		CaM KD2	
			-	+ Res.	-	+ Res.
NM_009717	Neurod6	neurogenic differentiation 6	0.57	1.87	0.18	0.88
NM_001081557	Camta1	calmodulin binding transcription activator 1	0.53	0.90	0.63	1.19
NM_018781	Egr3	early growth response 3	0.30	1.18	0.59	1.53
<b>Category 2: Membrane Receptors</b>						
NM_172659	Slc2a6	solute carrier family 2 (facilitated glucose transporter)	2.12	0.88	2.09	0.99
NM_054055	Slc13a3	solute carrier family 13 (sodium-dependent dicarboxylate	1.69	0.82	1.65	0.77
NM_153145	Abca8a	ATP-binding cassette, sub-family A (ABC1), member 8a	1.67	0.68	1.40	0.87
NM_178405	Atp1a2	ATPase, Na+	1.43	1.00	1.41	0.91
NM_030682	Tlr1	toll-like receptor 1	1.42	0.96	1.50	1.21
NM_009199	Slc1a1	solute carrier family 1 (neuronal)	0.70	1.11	0.63	1.01
NM_011216	Ptpro	protein tyrosine phosphatase, receptor type, O	0.70	1.01	0.57	1.15
NM_008983	Ptprk	protein tyrosine phosphatase, receptor type, K	0.69	0.88	0.45	1.46
NM_011391	Slc16a7	solute carrier family 16 (monocarboxylic acid transporter	0.69	0.96	0.70	1.28
NM_177328	Grm7	glutamate receptor, metabotropic 7	0.67	1.20	0.50	1.25
NM_001004761	Gpr158	G protein-coupled receptor 158	0.67	1.06	0.60	1.36
NM_008746	Ntrk3	neurotrophic tyrosine kinase, receptor, type 3	0.65	1.17	0.55	1.11
NM_010077	Drd2	dopamine receptor 2	0.64	0.87	0.62	1.10
NM_148946	Slc8a2	solute carrier family 8	0.63	1.01	0.54	1.67
NM_145066	Gpr85	G protein-coupled receptor 85	0.61	0.91	0.46	1.11
NM_199058	Gpr6	G protein-coupled receptor 6	0.61	0.87	0.64	1.80
NM_173410	Gpr26	G protein-coupled receptor 26	0.36	1.17	0.46	1.31
<b>Category 3: Membrane Ion Channels</b>						
NM_001013390	Scn4b	sodium channel, type IV, beta	2.31	1.09	6.81	1.06
NM_009783	Cacna1g	calcium channel, voltage-dependent, T type, alpha 1G	1.59	0.70	1.57	1.18
NM_011322	Scn1b	sodium channel, voltage-gated, type I, beta	1.47	1.00	1.69	0.88
NM_133207	Kcnh7	potassium voltage-gated channel, subfamily H (eag-related)	0.71	1.14	0.54	1.36
NM_001099298	Scn2a1	sodium channel, voltage-gated, type II, alpha 1	0.71	1.03	0.60	1.30
NM_009782	Cacna1e	calcium channel, voltage-dependent, R type, alpha 1E sub	0.68	0.93	0.61	1.25
NM_019697	Kcnd2	potassium voltage-gated channel, Shal-related family, member 2	0.66	0.94	0.54	0.95
NM_008170	Grin2a	glutamate receptor, ionotropic, NMDA2A (epsilon 1)	0.65	1.01	0.45	1.00
NM_001034013	Accn1	amiloride-sensitive cation channel 1, neuronal	0.65	0.84	0.65	1.13
NM_153512	Kcng3	potassium voltage-gated channel, subfamily G, member 3	0.65	1.07	0.45	1.22
NM_007583	Cacng2	calcium channel, voltage-dependent, gamma subunit 2	0.61	0.95	0.69	0.98
NM_023872	Kcnq5	potassium voltage-gated channel, subfamily Q, member 5	0.60	1.02	0.42	0.99

Accession No.	Gene Symbol	Description	Relative mRNA Level			
			CaM KD1		CaM KD2	
			-	+ Res.	-	+ Res.
NM_010601	Kcnh3	potassium voltage-gated channel, subfamily H (eag-related)	0.58	1.10	0.50	1.52
NM_001044308	Cacna1i	calcium channel, voltage-dependent, alpha 1I subunit	0.46	0.99	0.47	1.04
NM_019430	Cacng3	calcium channel, voltage-dependent, gamma subunit 3	0.44	1.28	0.64	1.74
NM_026200	Kcnv1	potassium channel, subfamily V, member 1	0.37	1.19	0.47	2.27
<b>Category 4: Cytoskeleton</b>						
NM_139128	Coro6	coronin, actin binding protein 6	3.46	0.99	4.45	1.11
NM_010904	Nefh	neurofilament, heavy polypeptide	2.78	0.74	2.73	0.62
NM_032393	Mtap1a	microtubule-associated protein 1 A	2.42	0.92	2.40	0.87
NM_001039546	Myo6	myosin VI	1.43	0.96	1.43	1.05
NM_026369	Arpc5	actin related protein 2	0.71	1.07	0.55	0.96
NM_001081230	Mtap9	microtubule-associated protein 9	0.71	0.92	0.63	1.00
NM_016747	Dlg3	discs, large homolog 3 (Drosophila)	0.68	1.00	0.60	0.90
NM_011983	Homer2	homer homolog 2 (Drosophila)	0.67	1.00	0.52	1.14
NM_019824	Arpc3	actin related protein 2	0.67	1.11	0.61	0.93
NM_198618	Dlgap3	discs, large (Drosophila) homolog-associated protein 3	0.67	1.20	0.69	1.17
NM_172910	Dlgap2	discs, large (Drosophila) homolog-associated protein 2	0.66	0.92	0.58	0.93
NM_007864	Dlg4	PSD-95	0.62	0.94	0.69	1.11
NM_021883	Tmod1	tropomodulin 1	0.60	1.21	0.70	1.57
NM_016695	Mpp2	membrane protein, palmitoylated 2 (MAGUK p55 subfamily memb	0.58	0.91	0.54	1.10
NM_021287	Spnb3	spectrin beta 3	0.52	0.90	0.58	1.23
NM_147176	Homer1	homer homolog 1 (Drosophila)	0.45	1.24	0.48	1.20
NM_019518	Grasp	GRP1 (general receptor for phosphoinositides 1)-associated	0.36	1.34	0.69	1.49
NM_018790	Arc	activity regulated cytoskeletal-associated protein	0.35	1.99	0.71	1.90
<b>Category 5: Calcium signaling (Channels not included)</b>						
NM_011242	Rasgrp2	RAS, guanyl releasing protein 2	2.87	1.17	2.03	1.03
NM_011311	S100a4	S100 calcium binding protein A4	1.54	1.09	1.60	0.87
NM_178617	Necab1	N-terminal EF-hand calcium binding protein 1	0.71	1.06	0.51	1.58
NM_134094	Ncald	neurocalcin delta	0.69	0.89	0.63	1.02
NM_007873	Doc2b	double C2, beta	0.68	0.84	0.48	1.07
NM_009790	Calm1	calmodulin 1	0.60	0.35	0.38	0.26
NM_153166	Cpne5	copine V	0.58	1.38	0.54	1.52
NM_007589	Calm2	calmodulin 2	0.47	0.53	0.34	0.39
NM_010471	Hpca	hippocalcin	0.40	0.96	0.40	1.31
NM_007590	Calm3	calmodulin 3	0.40	0.19	0.19	0.09
<b>Category 6: Intracellular signal transduction</b>						

Accession No.	Gene Symbol	Description	Relative mRNA Level			
			CaM KD1		CaM KD2	
			-	+ Res.	-	+ Res.
NM_010229	Flt3	FMS-like tyrosine kinase 3	2.32	1.00	2.80	1.06
NM_175178	Aifm3	apoptosis-inducing factor, mitochondrion-associated 3	1.72	0.72	2.51	0.96
NM_010404	Hap1	huntingtin-associated protein 1	1.69	0.79	1.55	0.53
NM_011756	Zfp36	zinc finger protein 36	1.65	1.10	1.61	0.98
NM_008832	Phka1	phosphorylase kinase alpha 1	1.58	0.97	1.54	1.11
NM_008817	Peg3	paternally expressed 3	1.57	0.73	2.15	1.10
NM_013834	Sfrp1	secreted frizzled-related protein 1	1.56	0.96	1.83	1.09
NM_010717	Limk1	LIM-domain containing, protein kinase	1.54	0.90	1.57	0.67
ENSMUST00000055576	Pcsk6	proprotein convertase subtilisin	1.49	0.86	1.53	0.82
NM_172778	Maob	monoamine oxidase B	1.48	0.93	1.76	1.02
NM_009035	Rbpj	recombination signal binding protein for immunoglobulin kap	1.48	1.20	1.79	1.11
NM_029094	Pik3cb	phosphatidylinositol 3-kinase, catalytic, beta polypeptid	1.46	0.72	2.07	1.04
NM_172263	Pde8b	phosphodiesterase 8B	1.46	0.95	1.44	1.17
NM_007928	Mark2	MAP	0.71	1.01	0.71	0.97
ENSMUST00000076810	Kalrn	kalirin, RhoGEF kinase	0.71	0.95	0.59	1.28
NM_029933	Bcl9	B-cell CLL	0.71	0.85	0.62	0.88
NM_033264	Arpp21	cyclic AMP-regulated phosphoprotein, 21	0.71	0.95	0.62	1.48
NM_207223	Centb5	centaurin, beta 5	0.71	0.98	0.67	0.93
NM_178681	Dgkb	diacylglycerol kinase, beta	0.69	1.16	0.70	1.12
NM_153171	Rgs13	regulator of G-protein signaling 13	0.69	1.62	0.67	1.72
NM_011104	Prkce	protein kinase C, epsilon	0.69	0.86	0.64	1.16
NM_008083	Gap43	growth associated protein 43	0.69	1.25	0.69	0.98
NM_139147	Rab40b	Rab40b, member RAS oncogene family	0.67	1.05	0.57	1.01
NM_177751	Cnksr2	connector enhancer of kinase suppressor of Ras 2	0.66	0.99	0.48	1.24
NM_183315	Ctxn1	cortexin 1	0.65	0.96	0.55	1.01
NM_007634	Ccnf	cyclin F	0.65	1.21	0.61	0.86
NM_172858	Pak7	p21 (CDKN1A)-activated kinase 7	0.65	0.90	0.51	1.07
BC024265	Mast3	microtubule associated serine	0.65	1.03	0.68	1.08
NM_021389	Sh3kbp1	SH3-domain kinase binding protein 1	0.64	1.24	0.62	0.94
NM_198114	Dagla	diacylglycerol lipase, alpha	0.64	0.93	0.61	1.04
NM_080428	Fbxw7	F-box and WD-40 domain protein 7, archipelago homolog (Dro	0.64	0.98	0.59	1.01
NM_029761	Dok5	docking protein 5	0.63	1.24	0.67	1.25
NM_011201	Ptpn1	protein tyrosine phosphatase, non-receptor type 1	0.63	0.92	0.65	1.27
NM_001122998	Tiam2	T-cell lymphoma invasion and metastasis 2	0.63	1.02	0.61	1.18
NM_026878	Ras11b	RAS-like, family 11, member B	0.62	1.11	0.70	0.87

Accession No.	Gene Symbol	Description	Relative mRNA Level			
			CaM KD1		CaM KD2	
			-	+ Res.	-	+ Res.
NM_175930	Rapgef5	Rap guanine nucleotide exchange factor (GEF) 5	0.60	1.23	0.41	1.19
NM_198419	Phactr1	phosphatase and actin regulator 1	0.60	0.92	0.69	1.17
NM_015743	Nr4a3	nuclear receptor subfamily 4, group A, member 3	0.58	1.17	0.68	1.10
NM_130862	Baiap2	brain-specific angiogenesis inhibitor 1-associated protei	0.56	0.85	0.60	1.20
NM_008926	Prkg2	protein kinase, cGMP-dependent, type II	0.48	1.35	0.63	1.35
NM_009528	Wnt7b	wingless-related MMTV integration site 7B	0.47	0.86	0.50	1.04
<b>Category 7 :Vesicle and trafficking</b>						
NM_009307	Syt2	synaptotagmin II	5.31	0.84	5.95	0.89
NM_001080557	Vamp1	vesicle-associated membrane protein 1	2.61	1.05	3.06	1.03
NM_016900	Cav2	caveolin 2	1.85	1.15	1.70	1.09
NM_016908	Syt9	synaptotagmin IX	0.69	1.05	0.58	0.99
NM_016801	Stx1a	syntaxin 1A (brain)	0.68	1.01	0.54	0.91
NM_182993	Slc17a7	vGluT1	0.67	0.96	0.49	0.89
NM_009308	Syt4	synaptotagmin IV	0.65	1.09	0.64	0.86
<b>Category 8: Cell Adhesion molecules</b>						
NM_177129	Cntn2	contactin 2	2.54	1.06	1.89	0.80
NM_016782	Cntnap1	contactin associated protein-like 1	2.31	0.77	2.19	0.91
NM_145219	Lgi3	leucine-rich repeat LGI family, member 3	1.87	0.63	2.36	0.77
NM_028880	Lrrtm1	leucine rich repeat transmembrane neuronal 1	0.71	0.96	0.66	0.98
NM_001080814	Fat3	FAT tumor suppressor homolog 3 (Drosophila)	0.70	1.19	0.58	1.35
NM_080285	Cttnbp2	contactin binding protein 2	0.66	0.89	0.66	1.44
NM_020278	Lgi1	leucine-rich repeat LGI family, member 1	0.62	1.11	0.36	1.03
NM_008319	Icam5	intercellular adhesion molecule 5, telencephalin	0.62	0.92	0.45	1.05
NM_177906	Opcml	opioid binding protein	0.62	0.91	0.58	0.98
NM_021424	Pvr1	poliovirus receptor-related 1	0.62	1.12	0.57	1.13
NM_011858	Odz4	odd Oz	0.61	0.93	0.66	1.08
NM_011855	Odz1	odd Oz	0.61	1.01	0.67	1.09
NM_178678	Lrrtm3	leucine rich repeat transmembrane neuronal 3	0.57	1.04	0.67	1.31
NM_001081298	Lphn2	latrophilin 2	0.57	0.84	0.59	1.36
<b>Category 9: Intercellular Signaling</b>						
NM_172815	Rspo2	R-spondin 2 homolog (Xenopus laevis)	0.71	1.30	0.68	1.06
NM_009472	Unc5c	unc-5 homolog C (C. elegans)	0.71	0.98	0.43	0.86
NM_008882	Plxna2	plexin A2	0.71	1.02	0.58	1.06
NM_021436	Tmeff1	transmembrane protein with EGF-like and two follistatin-l	0.71	0.99	0.69	1.11

Accession No.	Gene Symbol	Description	Relative mRNA Level			
			CaM KD1		CaM KD2	
			-	+ Res.	-	+ Res.
NM_010141	Epha7	Eph receptor A7	0.69	0.94	0.54	0.93
NM_198962	Hcrtr2	hypocretin (orexin) receptor 2	0.69	0.87	0.61	1.07
NM_007938	Epha6	Eph receptor A6	0.68	0.92	0.43	0.84
NM_001126047	Sema4c	sema domain, immunoglobulin domain (Ig), transmembrane	0.68	1.13	0.67	1.17
NM_007680	Ephb6	Eph receptor B6	0.66	1.00	0.71	1.10
NM_181074	Lingo1	leucine rich repeat and Ig domain containing 1	0.63	1.28	0.48	1.15
NM_013658	Sema4a	sema domain, immunoglobulin domain (Ig), transmembrane do	0.59	1.54	0.50	1.62
NM_009217	Sstr2	somatostatin receptor 2	0.54	1.12	0.52	1.36
NM_031161	Cck	cholecystokinin	0.50	1.22	0.35	1.18
NM_009152	Sema3a	sema domain, immunoglobulin domain (Ig), short basic doma	0.50	1.85	0.60	1.14
NM_010140	Epha3	Eph receptor A3	0.50	1.40	0.33	1.13
<b>Category 10: Other</b>						
NM_030700	Maged2	melanoma antigen, family D, 2	2.68	1.08	2.70	0.80
NM_001040611	Peg10	paternally expressed 10	2.44	0.67	6.11	0.91
NM_027100	Rwdd2a	RWD domain containing 2A	2.22	0.86	1.94	0.93
NM_153104	Phospho1	phosphatase, orphan 1	2.08	1.20	2.22	1.19
NM_153169	Pnma3	paraneoplastic antigen MA3	1.98	0.79	1.80	0.82
NM_009801	Car2	carbonic anhydrase 2	1.74	1.12	1.44	0.96
NM_011921	Aldh1a7	aldehyde dehydrogenase family 1, subfamily A7	1.73	0.99	1.84	1.19
NM_027533	Tspan2	tetraspanin 2	1.65	1.04	1.85	1.09
NM_028841	Tspan17	tetraspanin 17	1.64	1.14	1.78	0.78
NM_009780	C4b	complement component 4B (Childo blood group)	1.63	1.11	2.12	0.81
NM_011123	Plp1	proteolipid protein (myelin) 1	1.63	1.07	1.61	1.02
NM_025943	Dzip1	DAZ interacting protein 1	1.57	1.05	1.49	0.94
NM_182991	Tmem59l	transmembrane protein 59-like	1.53	0.86	1.67	0.94
NM_001001985	Nat8l	N-acetyltransferase 8-like	1.50	1.00	1.42	0.89
NM_010171	F3	coagulation factor III	1.48	1.03	1.43	1.03
NM_013813	Epb4.1l3	erythrocyte protein band 4.1-like 3	1.48	0.78	1.59	0.82
NM_172604	Scara3	scavenger receptor class A, member 3	1.46	1.11	1.82	1.17
ENSMUST00000029046	Fabp5	fatty acid binding protein 5, epidermal	1.46	1.00	1.40	0.96
NM_001038699	Fn3k	fructosamine 3 kinase	1.45	0.97	1.55	1.22
ENSMUST00000067439	Prune2	prune homolog 2 (Drosophila)	1.45	0.71	1.82	1.20
NM_009155	Sepp1	selenoprotein P, plasma, 1	1.45	0.87	1.66	1.10
NM_011020	Hspa4l	heat shock protein 4 like	1.45	1.07	1.57	1.11
NM_011843	Mbc2	membrane bound C2 domain containing protein	1.44	0.96	2.69	1.06

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			CaM KD1		CaM KD2	
			-	+ Res.	-	+ Res.
NM_145570	Tmem166	transmembrane protein 166	1.44	0.77	1.57	1.03
NM_011994	Abcd2	ATP-binding cassette, sub-family D (ALD), member 2	1.43	0.86	1.43	0.83
NM_184109	Rtl1	retrotransposon-like 1	1.42	1.00	1.52	1.01
NM_026203	Ahi1	Abelson helper integration site 1	1.41	1.06	1.72	1.07
NM_011157	Srgn	serglycin	1.40	0.80	1.63	1.08
NM_173739	Galnt4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgl	0.70	1.02	0.65	1.07
NM_026898	Wdr53	WD repeat domain 53	0.70	0.87	0.60	0.96
NM_001081146	Prickle2	prickle-like 2 (Drosophila)	0.70	0.96	0.52	1.08
NM_013500	Hapln1	hyaluronan and proteoglycan link protein 1	0.70	1.13	0.60	0.92
NM_173777	Olfm2	olfactomedin 2	0.69	0.90	0.71	0.99
NM_021286	Sez6	seizure related gene 6	0.69	0.98	0.57	1.14
NM_010266	Gda	guanine deaminase	0.69	0.88	0.67	1.39
BC021311	Zswim6	zinc finger, SWIM domain containing 6	0.69	1.06	0.69	0.98
NM_133706	Tmem97	transmembrane protein 97	0.69	1.59	0.67	1.47
NM_172637	Hectd2	HECT domain containing 2	0.68	1.60	0.60	1.30
NM_001024928	Zfp667	zinc finger protein 667	0.68	1.07	0.63	1.52
NM_009262	Spock1	sparc	0.68	0.93	0.48	1.07
NM_146073	Zdhhc14	zinc finger, DHHC domain containing 14	0.68	0.91	0.48	1.07
NM_009270	Sqle	squalene epoxidase	0.68	1.18	0.46	1.20
NM_133706	Tmem97	transmembrane protein 97	0.67	1.27	0.71	1.18
NM_011119	Pa2g4	proliferation-associated 2G4	0.67	1.01	0.67	0.88
NM_153407	Csnrp2	cysteine-serine-rich nuclear protein 2	0.67	0.99	0.64	1.11
NM_198627	Vstm2l	V-set and transmembrane domain containing 2-like	0.67	1.14	0.57	1.02
NM_011846	Mmp17	matrix metalloproteinase 17	0.67	1.15	0.57	1.04
NM_178920	Mal2	mal, T-cell differentiation protein 2	0.66	1.15	0.65	0.91
NM_028185	Lsm11	U7 snRNP-specific Sm-like protein LSM11	0.66	1.09	0.65	1.08
NM_153155	C1qf3	C1q-like 3	0.66	1.28	0.57	1.05
U88401	Mtag2	metastasis associated gene 2	0.66	0.95	0.71	1.00
NM_199024	Nol4	nucleolar protein 4	0.65	0.84	0.61	1.26
NM_033567	Cecr6	cat eye syndrome chromosome region, candidate 6 homolog (h)	0.64	1.05	0.64	1.05
NM_178252	Snx26	sorting nexin 26	0.64	1.03	0.48	0.88
NM_201529	Lmo7	LIM domain only 7	0.64	0.92	0.45	1.12
NM_001033212	Rprml	reprimin-like	0.64	1.32	0.65	1.19
NM_175645	Xylt1	xylosyltransferase 1	0.63	0.84	0.59	1.21
NM_001081388	Rimbp2	RIMS binding protein 2	0.62	0.84	0.42	0.95

Accession No.	Gene Symbol	Description	Relative mRNA Level			
			CaM KD1		CaM KD2	
			-	+ Res.	-	+ Res.
ENSMUST00000074081	Csmd2	CUB and Sushi multiple domains 2	0.62	0.91	0.56	1.18
NM_172434	Tnrc4	trinucleotide repeat containing 4	0.62	0.84	0.42	1.15
NM_001005341	Ypel2	yippee-like 2 (Drosophila)	0.60	1.04	0.60	1.33
NM_175502	Tmem74	transmembrane protein 74	0.60	0.92	0.50	0.96
NM_145981	Phyhip	phytanoyl-CoA hydroxylase interacting protein	0.59	0.87	0.41	0.98
NM_001039376	Pde4dip	phosphodiesterase 4D interacting protein (myomegalin)	0.58	0.93	0.70	1.24
NM_001081064	Pdzd2	PDZ domain containing 2	0.56	1.10	0.62	1.21
AK032191	Nol4	nucleolar protein 4	0.55	0.98	0.64	1.06
NM_008255	Hmgcr	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	0.54	1.41	0.52	1.27
AK162044	March11	membrane-associated ring finger (C3HC4) 11	0.54	1.66	0.70	1.61
NM_019967	Dbc1	deleted in bladder cancer 1 (human)	0.54	1.31	0.68	1.41
NM_019675	Stmn4	stathmin-like 4	0.52	1.00	0.50	0.86
NM_201371	Prmt8	protein arginine N-methyltransferase 8	0.52	0.90	0.49	0.92
NM_198306	Galnt9	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylga	0.46	1.37	0.70	1.03
Category 11: Uncharacterized						
BC052055	BC052055	cDNA sequence BC052055	3.33	0.83	2.66	0.99
BC125016	EG328644	predicted gene, EG328644	2.44	0.67	3.01	1.10
AF529169	AF529169	cDNA sequence AF529169	1.85	1.04	1.99	0.88
NM_001114174	Gm967	gene model 967, (NCBI)	1.60	0.76	1.57	1.05
NM_001081029	4930420K17Rik	RIKEN cDNA 4930420K17 gene	1.57	1.04	1.56	1.20
ENSMUST00000049544	2610301F02Rik	RIKEN cDNA 2610301F02 gene	1.43	1.14	1.47	1.12
BC055818	D330028D13Rik	RIKEN cDNA D330028D13 gene	1.41	1.01	1.56	0.85
NM_001039167	D11Bwg0517e	DNA segment, Chr 11, Brigham & Women's Genetics 0	0.71	0.92	0.58	1.27
NM_026279	2310026E23Rik	RIKEN cDNA 2310026E23 gene	0.69	1.04	0.69	0.90
BC119515	1700001L19Rik	RIKEN cDNA 1700001L19 gene	0.69	0.94	0.57	1.14
NM_144935	BC018242	cDNA sequence BC018242	0.68	0.90	0.52	0.93
NM_001033166	2700094K13Rik	RIKEN cDNA 2700094K13 gene	0.67	0.93	0.70	1.02
ENSMUST00000059500	BC028663	cDNA sequence BC028663	0.65	1.04	0.68	0.87
ENSMUST00000057768	4930429B21Rik	RIKEN cDNA 4930429B21 gene	0.61	1.23	0.69	1.40
ENSMUST00000061282	OTTMUSG00000013918	predicted gene, OTTMUSG00000013918	0.60	1.00	0.41	1.83
BC072639	2010300C02Rik	RIKEN cDNA 2010300C02 gene	0.59	0.90	0.58	1.22
NM_001033391	A130090K04Rik	RIKEN cDNA A130090K04 gene	0.57	1.09	0.48	1.41
BC092532	2900046G09Rik	RIKEN cDNA 2900046G09 gene	0.51	0.97	0.48	1.06
ENSMUST00000068927	A330084C13Rik	RIKEN cDNA A330084C13 gene	0.50	1.13	0.58	0.87



Accession No.	Gene Symbol	Description	Relative mRNA Level			
			CaM KD1		CaM KD2	
			-	+ Res.	-	+ Res.
XM_001473525	LOC100039795	similar to C1orf32 putative protein	0.46	0.97	0.62	1.32
NM_029530	6330527O06Rik	RIKEN cDNA 6330527O06 gene	0.44	1.56	0.69	1.53
ENSMUST00000101196	3110047P20Rik	RIKEN cDNA 3110047P20 gene	0.40	0.99	0.29	1.12
NM_182808	C630007B19Rik	RIKEN cDNA C630007B19 gene	0.39	1.60	0.28	1.49

Data shown are from two independent experiments performed with neurons that contained the CaM KD shRNAs, without or with full-length CaM rescue. Data are shown as fold of change (normalized to the control).

**Supplementary Table 2**  
 Numeric data presented in the paper

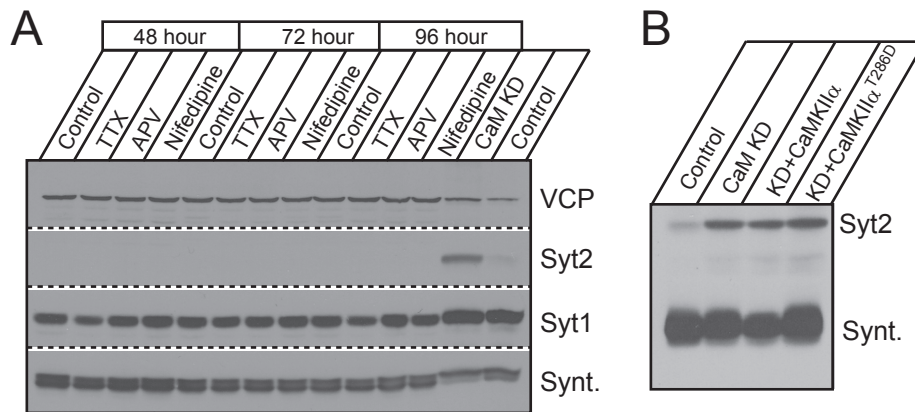
Figure number	Descriptions	Mean	±	SEM	n	p Value*
Figure 1	1E Syt1 KO mIPSC Frequency (Hz)					
	Control	7.46	±	0.42	18	
	CaM KD	3.55	±	0.45	21	P<0.001
	CaM KD+WT CaM	6.59	±	0.65	17	n.s.
	1F Syt1 KO mIPSC Amplitude (pA)					
	Control	26.5	±	1.6	18	
	CaM KD	30.5	±	1.8	21	n.s.
	CaM KD+WT CaM	28.4	±	2.7	17	n.s.
	1G Syt1 KO mIPSC Rise Time (ms)					
	Control	1.92	±	0.11	18	
	CaM KD	1.83	±	0.11	21	n.s.
	CaM KD+WT CaM	1.79	±	0.12	17	n.s.
		21.0222		2.8229		
		23.7286		0.6222		
		22.5706		0.7204		
	1G Syt1 KO mIPSC Decay Time (ms)					
	Control	21.02	±	2.82	18	
	CaM KD	23.73	±	0.62	21	n.s.
	CaM KD+WT CaM	22.57	±	0.72	17	n.s.
Figure 2	2B Syt1 KO evoked IPSC Amplitude (nA)					
	Control	0.24	±	0.02	44	
	CaM KD	1.32	±	0.13	49	P<0.001
	CaM KD+WT CaM	0.21	±	0.03	15	n.s.
Figure 4	4A Relative mRNA level					
	Syt2 (Control)	1.00	±	0.00	5	
	Syt2 (CaM KD)	10.42	±	3.12	5	P<0.05
	Syt2 (CaM KD+WT Res.)	0.92	±	0.15	4	n.s.
	Lrrtm3 (Control)	1.00	±	0.00	3	
	Lrrtm 3 (CaM KD)	0.47	±	0.02	3	P<0.001

Figure number	Descriptions	Mean	±	SEM	n	p Value*
	CaM 3 (Control)	1.00	±	0.00	4	
	CaM 3 (CaM KD)	0.26	±	0.08	4	P<0.01
	CaM 3 ((CaM KD+WT Res.)	0.10	±	0.03	4	P<0.001
Figure 5	5B Protein expression level (%)					
	CaM (Control)	100	±	13	3	
	CaM (CaM KD)	23	±	3	3	P<0.01
	CaM (CaM KD+WT Res)	200	±	19	3	P<0.05
	CaM (CaM KD+CaM1,2,3,4)	467	±	54	3	P<0.01
	Syt2 (Control)	100	±	39	3	
	Syt2 (CaM KD)	1045	±	37	3	P<0.001
	Syt2 (CaM KD+WT Res)	107	±	41	3	n.s.
	Syt2 (CaM KD+CaM1,2,3,4)	401	±	59	3	P<0.05
	Rab3A (Control)	100	±	29	3	n.s.
	Rab3A (CaM KD)	59	±	21	3	n.s.
	Rab3A (CaM KD+WT Res)	92	±	27	3	n.s.
	Rab3A (CaM KD+CaM1,2,3,4)	58	±	9	3	n.s.
	Syt1 (Control)	100	±	5	3	
	Syt1 (CaM KD)	55	±	15	3	P<0.05
	Syt1 (CaM KD+WT Res)	102	±	6	3	n.s.
	Syt1 (CaM KD+CaM1,2,3,4)	44	±	15	3	P<0.05
	Synt1 (Control)	100	±	16	3	
	Synt1 (CaM KD)	97	±	28	3	n.s.
	Synt1(CaM KD+WT Res)	85	±	10	3	n.s.
	Synt1 (CaM KD+CaM1,2,3,4)	75	±	9	3	n.s.
	SNAP25 (Control)	100	±	19	3	
	SNAP25 (CaM KD)	87	±	35	3	n.s.
	SNAP25 (CaM KD+WT Res)	101	±	14	3	n.s.
	SNAP25 (CaM KD+CaM1,2,3,4)	64	±	22	3	n.s.
	Rabphilin (Control)	100	±	16	3	

Figure number	Descriptions	Mean	±	SEM	n	p Value*
	Rabphilin (CaM KD)	36	±	5	3	P<0.05
	Rabphilin (CaM KD+WT Res)	126	±	14	3	n.s.
	Rabphilin (CaM KD+CaM1,2,3,4)	31	±	2	3	P<0.05
	CSP (Control)	100	±	2	3	
	CSP (CaM KD)	75	±	11	3	n.s.
	CSP (CaM KD+WT Res)	90	±	17	3	n.s.
	CSP (CaM KD+CaM1,2,3,4)	56	±	13	3	P<0.05
	Munc 18 (Control)	100	±	29	3	
	Munc 18 (CaM KD)	69	±	21	3	n.s.
	Munc 18 (CaM KD+WT Res)	93	±	22	3	n.s.
	Munc 18 (CaM KD+CaM1,2,3,4)	92	±	32	3	n.s.
	SCAMP (Control)	100	±	32	3	
	SCAMP (CaM KD)	60	±	16	3	n.s.
	SCAMP (CaM KD+WT Res)	113	±	29	3	n.s.
	SCAMP (CaM KD+CaM1,2,3,4)	73	±	23	3	n.s.
	PSD95 (Control)	100	±	6	3	
	PSD95 (CaM KD)	81	±	1	3	P<0.05
	PSD95 (CaM KD+WT Res)	90	±	7	3	n.s.
	PSD95 (CaM KD+CaM1,2,3,4)	76	±	7	3	P<0.05
	NSF (Control)	100	±	5	3	
	NSF (CaM KD)	69	±	1	3	P<0.01
	NSF (CaM KD+WT Res)	95	±	8	3	n.s.
	NSF (CaM KD+CaM1,2,3,4)	78	±	6	3	n.s.
	Neuroigin 1 (Control)	100	±	25	3	
	Neuroigin 1 (CaM KD)	70	±	15	3	n.s.
	Neuroigin 1 (CaM KD+WT Res)	85	±	14	3	n.s.
	Neuroigin 1 (CaM KD+CaM1,2,3,4)	74	±	19	3	n.s.
	Neuroigin 2 (Control)	100	±	20	3	
	Neuroigin 2 (CaM KD)	88	±	6	3	n.s.
	Neuroigin 2 (CaM KD+WT Res)	95	±	7	3	n.s.

Figure number	Descriptions	Mean	±	SEM	n	p Value*
	Neurologin 2 (CaM KD+CaM1,2,3,4)	84	±	5	3	n.s.
Figure 6	6B CaM/VCP					
	Cortex	1.66	±	0.04	4	
	Cerebellum	1.16	±	0.06	4	P<0.001
	Spinal cord	0.85	±	0.06	4	P<0.001
	Syt1/VCP					
	Cortex	6.97	±	0.12	4	
	Cerebellum	2.55	±	0.26	4	P<0.001
	Spinal cord	1.05	±	0.15	4	P<0.001
	Syt2/VCP					
	Cortex	0.46	±	0.02	4	
	Cerebellum	1.46	±	0.03	4	P<0.001
	Spinal cord	1.04	±	0.04	4	P<0.001
	Syb1/VCP					
	Cortex	0.73	±	0.04	4	
	Cerebellum	2.77	±	0.09	4	P<0.001
	Spinal cord	2.33	±	0.20	4	P<0.001
Figure 7	7D Rescue evoked IPSCs Amplitude in Syt1 KO					
	Control (same data set as in 1b)	0.24	±	0.02	44	
	CaM KD+CaM1,2	0.22	±	0.04	17	n.s.
	CaM KD+CaM3,4	0.82	±	0.12	13	P<0.001
	CaM KD+CaM1,2,3,4	0.95	±	0.18	16	P<0.001

\* P value obtained by Student t-test, compared to control group.



Suppl. Figure 1  
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