

SUPPLEMENTARY DATA

Supplementary Figures.

Supplementary Figure 1. Knockdown of LANP promotes neurite outgrowth in N2A cells.

A-D. N2A cells were transfected with control siRNA (A and C) or siRNA targeting LANP (B and D) in the presence of cAMP. 48h post transfection, the cells were fixed and stained with anti-tubulin (A and B) and anti-LANP (C and D) antibodies.

E. Quantitation of number of cells displaying neurites longer than two cell body length. Mock represents untransfected cells. Scale bar= 20 μ m. Cells were counted in 3 sets of high power fields representing triplicate transfections (typically 6 fields or more were counted with total number of cells >75 per set). Error bars represent SEM; $p < 0.005$.

F. N2A cells were transfected with siRNA targeting LANP and control siRNA. 48h post transfection, western blot analysis was performed with anti-LANP antibody. Actin was used as a loading control. Mock represents untransfected cells.

Supplementary Figure 2. Knockdown of LANP by RNA interference results in upregulation of NF-L transcripts 24h post-transfection.

A. PC12 cells transfected with siRNA targeting LANP show reduced expression at the RNA level 24h post transfection as demonstrated by RT-PCR. In these experiments, GAPDH message was measured as an internal control.

B. PC12 cells transfected with a pool of siRNA targeting LANP and control siRNA show reduced level of LANP protein 24h post transfection by western blot analysis. Actin was used as a loading control.

C. Semi-quantitative analysis from triplicate samples depicts 66% knockdown of LANP protein levels. LANP protein levels are relative to actin and normalized to protein levels of LANP upon transfection with control siRNA.

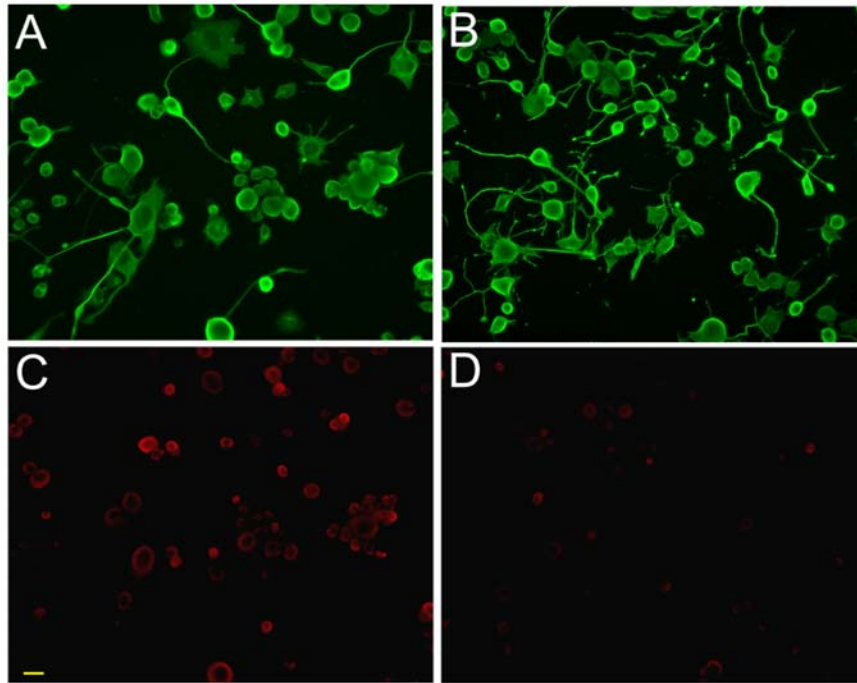
D. RNA was isolated from PC12 cells 24 hours after transfection with siRNA targeting LANP and control siRNA. DNase treated RNA was subjected to quantitative-RT-PCR analysis employing primers to amplify NF-L transcripts. Ct value of each sample is normalized to GAPDH and fold change is relative to control transfected PC12 cells.

Supplementary Figure 3. Knockdown of LANP does not alter histone acetylation status at the control β -globin promoter. PC12 cells were transfected with siRNA targeting LANP or control siRNA. 48h post transfection, cells were processed for chromatin immunoprecipitation with anti-acetyl H3 (H3 ac), anti-H3 total antibody or IgG (serving as a negative control). PCR was performed to amplify the promoter region of β -globin gene (serving as a control). Pre-immunoprecipitated lysate served as input.

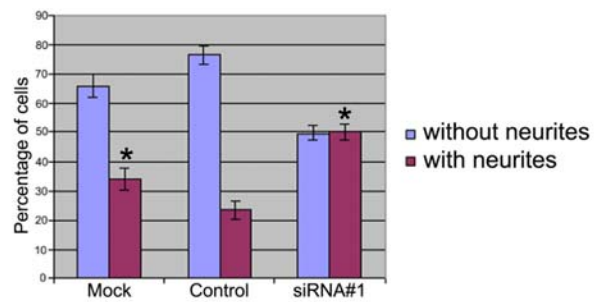
Supplementary Figure 4. Depletion of LANP does not alter histone acetylation status at the β -globin promoter. Postnatal day 2 mice were sacrificed and brains were processed for chromatin immunoprecipitation with anti-acetyl H3, anti-H3 total or IgG (serving as control) antibody. PCR was performed to amplify the promoter region of β -globin (serving as a control). Pre-immunoprecipitated lysate served as input.

Supplementary Table 1. The list of differentially expressed genes in control and siRNA transfected PC12 cells as depicted in Figure 3. Signal intensity, fold-change, p value and gene symbol annotation with accession numbers are displayed. Genes are grouped according to their major biological function.

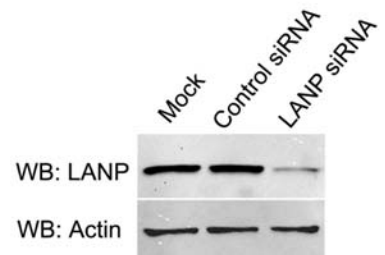
Supplementary Figure 1



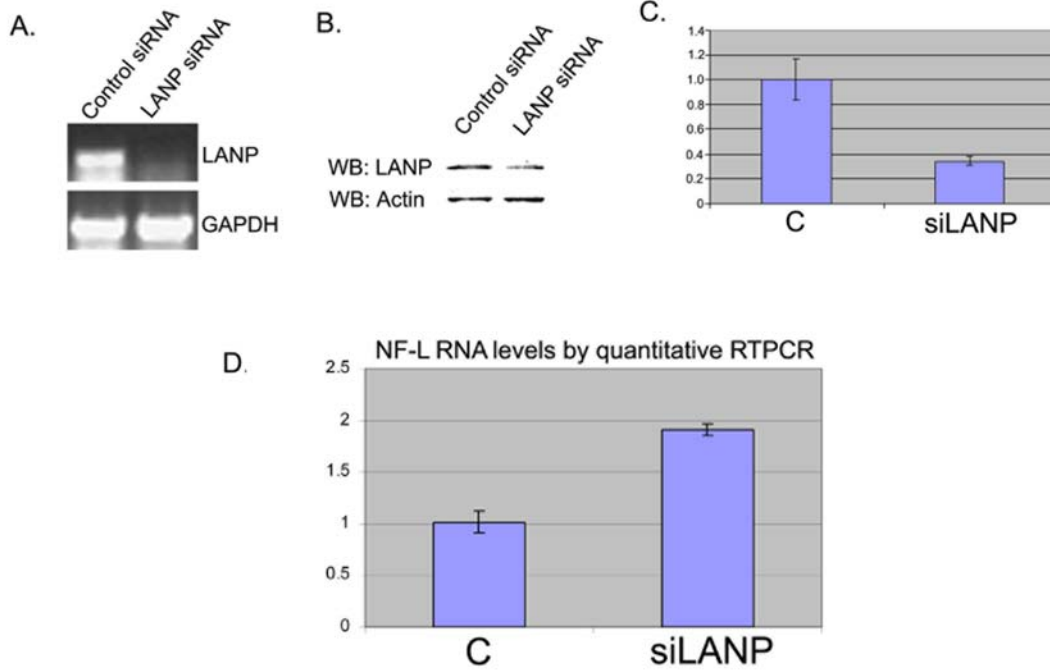
E.



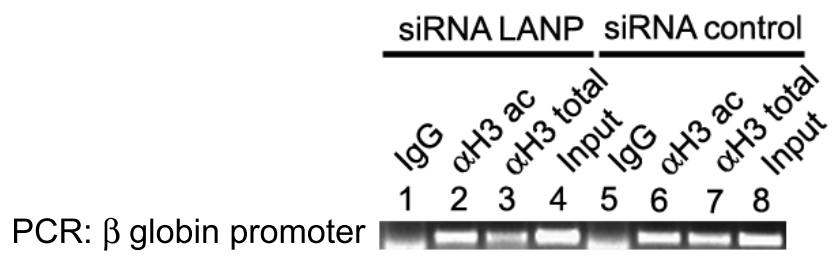
F.



Supplementary Figure 2



Supplementary Figure 3



Supplementary Figure 4



PCR: β -globin promoter

Supplementary Table 1

Gene_Descriptor	Control Group Signal	Exp Group Signal	Raw Est Fold Change	p-value	Gene_Symbol	SeqDerivedFrom
acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	1151.4	203.0	-5.67	0.0152	Anp32a	NM_012903
acidic (leucine-rich) nuclear phosphoprotein 32 family, member E (predicted)	2473.0	2057.1	-1.20	0.0012	Anp32e	AI008642
acidic nuclear phosphoprotein 32 family, member B	4342.8	4068.0	-1.07	0.4954	Anp32b	NM_131911
Differentiation						
epidermal growth factor	60.9	304.1	5.00	0.0021	Egf	NM_012842
vascular endothelial growth factor C	15.0	65.5	4.37	0.0097	Vegfc	NM_053653
brain derived neurotrophic factor	77.0	246.2	3.23	0.0000	Bdnf	X67108
Synapsin I	266.8	490.6	1.84	0.0016	Syn1	BG378858
neurofilament 3, medium	3750.4	6524.0	1.74	0.0001	Nef3	NM_017029
growth associated protein 43	413.7	617.6	1.49	0.0088	Gap43	NM_017195
neurofilament, light polypeptide	2595.6	3601.0	1.39	0.0006	RGD:621458	BF394545
neurofilament, heavy polypeptide	1912.9	2457.2	1.29	0.0232	Nefh	AF031879
Vascular endothelial growth factor A	777.0	456.0	-1.70	0.0302	Vegf	AF080594
neural precursor cell expressed, developmentally down-regulated gene 9 (predicted)	708.8	368.5	-1.92	0.0012	Nedd9	BF555968
colony stimulating factor 1 (macrophage)	189.9	95.0	-2.00	0.0059	Csf1	AW535553
keratinocyte differentiation associated protein	143.9	71.1	-2.02	0.0036	Krt1dap	BI282568
fibroblast growth factor 7	1290.5	611.3	-2.11	0.0276	Fgf7	NM_022182
insulin-like growth factor binding protein 5	3265.7	1101.8	-2.98	0.0309	Igf1bp5	BF399783
Cell cycle/Cancer						
similar to downregulated in renal cell carcinoma (predicted)	36.7	129.3	3.52	0.0032		BG380826
similar to squamous cell carcinoma antigen 2	169.9	435.7	2.56	0.0009	LOC498209	BM390325
Tumor necrosis factor receptor superfamily, member 26 (predicted)	305.6	671.5	2.20	0.0018		BE098317
RAB15, member RAS oncogene family	895.2	1927.4	2.15	0.0006	Rab15	BM384841
high mobility group AT-hook 1	755.6	1576.9	2.09	0.0002	Hmga1	BG378885
cyclin D1	851.0	1814.8	2.13	0.0361	Ccnd1	BI295861
Death-associated protein	111.5	218.3	1.96	0.0016	Dap	BE110708
cyclin D1	1004.2	1689.6	1.68	0.0186	Ccnd1	AW143798
Cyclin G2 (predicted)	300.9	181.8	-1.66	0.0186	Ccng2	AI408309
cyclin E	713.1	423.4	-1.68	0.0078	Ccne1	AW913890
cyclin L2 (predicted)	329.2	169.0	-1.95	0.0110	Ccrl2	BE098333
CDC23 (cell division cycle 23, yeast, homolog) (predicted)	359.9	138.6	-2.60	0.0625	Cdc23	AI013729
Neurodegeneration						
homer homolog 1 (Drosophila)	32.8	73.1	2.23	0.0077	Homer1	AF030088
bone morphogenetic protein 2	1276.1	2773.8	2.17	0.0045	Bmp2	AA944627
VGF nerve growth factor inducible	4813.3	9470.8	1.97	0.0025	Vgf	NM_030997
Huntingtin interactor protein E	396.3	726.3	1.84	0.0021	LOC288741	BM384029
ataxin 2	280.6	497.0	1.77	0.0040		AI060139
Purkinje cell protein 4	296.8	159.6	-1.86	0.0182	Pcp4	NM_013002
gamma-aminobutyric acid receptor, subunit beta 3	119.0	59.2	-2.01	0.0001	Gabbr3	NM_017065
gamma-aminobutyric acid (GABA) A receptor, pi	224.3	79.7	-2.82	0.0484	Gabpr	NM_031029
ataxin 3	136.6	37.6	-3.64	0.0434	Atxn3	NM_021702
Transcription/Translation						
Cbp/p300-interacting transactivator	944.7	1923.8	2.04	0.0012	Cited2	AI013390
histone 3, H2ba (predicted)	414.9	232.3	-1.79	0.0364	Hist3h2ba	AW533007
H3 histone, family 3B	11898.5	6653.1	-1.79	0.0265	RGD:621095	AI177503
Histone 1, H4a (predicted)	4690.4	2584.9	-1.82	0.0004		AA848821
CCAAT/enhancer binding protein (C/EBP), gamma	268.2	141.4	-1.90	0.0087	Cebpg	X64403
meringoma expressed antigen 5 (hyaluronidase)	602.7	304.6	-1.98	0.0021	Mgea5	NM_131904
histone 2	97.2	49.1	-1.98	0.0170	Hist2h2aa	AI235236
general transcription factor II H, polypeptide 1 (predicted)	284.8	132.9	-2.14	0.0032	Gtf2h1	BF524412
histone 2a	533.8	243.7	-2.19	0.0178	RGD:621437	AA850895
histone 1, H2bh (predicted)	1382.4	614.0	-2.25	0.0181	Hist1h2bh	BM391206
eukaryotic translation initiation factor 4, gamma 2 (predicted)	7868.9	3194.2	-2.46	0.0308	Eif4g2	BG672378
histone 1, H2bl	37.5	10.3	-3.66	0.0001	Hist1h2bl	NM_022647
Signal transduction						
microfibrillar associated protein 5 (predicted)	44.2	141.7	3.20	0.0010	Mfap5	BI283094
serine (or cysteine) proteinase inhibitor, clade B, member 2	40.4	126.3	3.17	0.0035	Serp1nb2	NM_021696
similar to MAP kinase phosphatase 4	221.5	667.8	3.02	0.0008	LOC293847	AI179321
bradykinin receptor b2	118.5	303.6	2.56	0.0001	Bdkrb2	BF408558
Mitogen activated protein kinase kinase kinase 12	46.4	102.9	2.22	0.0036	Map3k12	BI303658
interleukin 1 receptor accessory protein	98.0	202.8	2.07	0.0019	Il1rap	BF391914
Rho GTPase activating protein 27	221.0	445.0	2.01	0.0037	Arhgap15	BE100015
G protein-coupled receptor 48	429.0	221.2	-1.94	0.0026	Gpr48	BI300274
alpha-2-macroglobulin	828.9	412.7	-2.01	0.0000	A2m	NM_012488
adrenergic receptor, beta 3	208.8	99.1	-2.11	0.0026	Adrb3	NM_013108
guanine nucleotide binding protein (G protein), gamma 5 subunit	264.9	123.6	-2.14	0.0048	Gng5	NM_024377
prostaglandin E receptor 3 (subtype EP3)	1472.1	686.1	-2.15	0.0009	Ptger3	NM_012704
guanylate nucleotide binding protein 2	464.7	211.2	-2.20	0.0017	Gbp2	NM_133624
lamin B receptor	747.6	318.7	-2.35	0.0056	Lbr	NM_134453
matrix metalloproteinase 2	153.7	62.2	-2.47	0.0011	Mmp2	U65656
serine (or cysteine) proteinase inhibitor, clade A	2303.7	876.3	-2.63	0.0001	Serpina6	AA893495
interleukin 1 receptor, type 1	280.9	68.9	-4.08	0.0121	Il1r1	NM_013123
Miscellaneous						
prostaglandin-endoperoxide synthase 2	517.9	2866.1	5.53	0.0000	Ptgs2	U03389
aquaporin 8	648.1	2743.5	4.23	0.0000	Aqp8	NM_019158
kallikrein 10	110.6	324.1	2.93	0.0000	RGD:1303242	BI283346
Kruppel-like factor 5	47.5	135.2	2.84	0.0036	Klf5	BM382886
Potassium voltage-gated channel, subfamily G, member 1	61.8	166.6	2.70	0.0010	Kcng1	BF387447
NOD3-like protein (has Leucine-rich repeats)	119.2	256.1	2.15	0.0005	nod3	BE106776
DnaJ (Hsp40) homolog, subfamily C, member 4 (predicted)	230.0	118.4	-1.94	0.0004	Dnajc4	BG380252
SET binding factor 1 (predicted)	332.7	162.6	-2.05	0.0360	Sbf1	AW434982
adrenergic receptor, beta 3	208.8	99.1	-2.11	0.0026	Adrb3	NM_013108
Nuclear pore associated protein	551.3	243.7	-2.26	0.0066		BI283822
lamin B receptor	747.6	318.7	-2.35	0.0056	Lbr	NM_134453
crystallin, gamma E	369.3	146.6	-2.52	0.0068	Cryge	J00716
calcium channel, voltage-dependent, alpha2/delta subunit 1	909.4	351.4	-2.59	0.0003	Cacna2d1	AF400662
sodium channel, voltage-gated, type III, beta	3578.8	1274.8	-2.81	0.0000	Scn3b	AA685184
5-hydroxytryptamine (serotonin) receptor 2C	58.6	18.4	-3.19	0.0006	Htr2c	U35315
angiotensin II receptor, type 2	327.2	95.7	-3.42	0.0011	Agtr2	BF552873
tubby homolog (mouse)	52.4	1.9	-27.75	0.0008	Tub	NM_013077