Supplementary Information

Optical Control of Mammalian Endogenous Transcription and Epigenetic States

Silvana Konermann[1,2*], Mark D. Brigham[1,2,3*], Alexandro Trevino[1,2], Patrick D. Hsu[1,2,4], Matthias Heidenreich[1,2], Le Cong[1,2,4], Randall J. Platt[1,2], David A. Scott[1,2], George M. Church[1],[6], and Feng Zhang[1,2†]

[1] Broad Institute of MIT and Harvard
7 Cambridge Center
Cambridge, MA 02142, USA

[2]McGovern Institute for Brain Research
Department of Brain and Cognitive Sciences
Department of Biological Engineering
Massachusetts Institute of Technology
Cambridge, MA 02139, USA

[3] School of Engineering and Applied Sciences
Harvard University
Cambridge, MA 02138, USA

[4] Department of Molecular and Cellular Biology
Harvard University
Cambridge, MA 02138, USA

[5] Program in Biological and Biomedical Sciences
Harvard Medical School
Boston, MA 02115, USA

[6] Department of Genetics
Harvard Medical School
Boston, MA 02115, USA

*These authors contributed equally to this work.
[†]To whom correspondence should be addressed: zhang@broadinstitute.org

SUPPLEMENTARY METHODS

Photostimulation Hardware – *in vitro*

In vitro light stimulation experiments were performed using a custom built LED photostimulation device. All electronic elements were mounted on a custom printed circuit board (ExpressPCB). Blue LEDs with peaks 466 nm (model #: YSL-R542B5C-A11, China Young Sun LED Technology; distributed by SparkFun Electronics as 'LED – Super Bright Blue' COM-00529), were arrayed in groups of three aligned with the wells of a Corning 24-well plate. LED current flow was regulated by a 25 mA DynaOhm driver (LEDdymanics #4006-025). Columns of the LED array were addressed by TTL control (Fairchild Semiconductor PN2222BU-ND) via an Arduino UNO microcontroller board. Light output was modulated via pulse width modulation. Light output was measured from a distance of 80 mm above the array utilizing a Thorlabs PM100D power meter and S120VC photodiode detector. In order to provide space for ventilation and to maximize light field uniformity, an 80 mm tall ventilation spacer was placed between the LED array and the 24-well sample plate. Fans (Evercool EC5015M12CA) were mounted along one wall of the spacer unit, while the opposite wall was fabricated with gaps to allow for increased airflow.

Quantification of LIVE/DEAD® assay using ImageJ software.

Images of LIVE/DEAD (Life Technologies) stained cells were captured by fluorescence microscopy and processed as follows: Background was subtracted (*Process* → *Subtract Background*). A threshold based on fluorescence area was set to ensure accurate identification of cell state (*Image* → *Adjust* → *Threshold*). A segmentation analysis was performed to enable automated counting of individual cells (*Process* → *Binary* → *Watershed*). Finally, debris signals were filtered and cells were counted (*Analyze* → *Analyze Particles*). Toxicity was determined as the percentage of dead cells.

Chemically-inducible TALEs

Neuro2A cells were grown in a medium containing a 1:1 ratio of OptiMEM (Life Technologies) to high-glucose DMEM with GlutaMax and Sodium Pyruvate (Life Technologies) supplemented with 5% HyClone heat-inactivated FBS (Thermo Scientific), 1% penicillin/streptomycin (Life

Technologies) and 25mM HEPES (Sigma Aldrich). 150,000 cells were plated in each well of a 24-well plate 18-24 hours prior to transfection. Cells were transfected with 1 μg total of construct DNA (at equimolar ratios) per well and 2 μL of Lipofectamine 2000 (Life Technologies) according to the manufacturer's recommended protocols. Media was exchanged 12 hours post-transfection. For the kinetics test, chemical induction was started 24 hours post-transfection, when abscisic acid (ABA, Sigma Aldrich) was added to fresh media to a final concentration of 250 μM. RNA was extracted using the RNeasy kit (Qiagen) according to manufacturer's instructions and 1 μg of RNA per sample was reverse-transcribed using qScript (Quanta Biosystems). Relative mRNA levels were measured by quantitative real-time PCR (qRT-PCR) using Taqman probes specific for the targeted gene as well as mouse GAPDH as an endogenous control (Life Technologies, see Supplementary Table 2 for Taqman probe IDs). ΔΔCt analysis was used to obtain fold-changes relative to negative controls where cells were subjected to mock transfection with GFP.

Cas9 transcriptional effectors

HEK 293FT cells were co-transfected with mutant Cas9 fusion protein and a synthetic guide RNA (sgRNA) using Lipofectamine 2000 (Life Technologies) 24 hours after seeding into a 24 well dish. 72 hours post-transfection, total RNA was purified (RNeasy Plus, Qiagen). 1ug of RNA was reverse transcribed into cDNA (qScript, Quanta BioSciences). Quantitative real-time PCR was done according to the manufacturer's protocol (Life Technologies) and performed in triplicate using TaqMan Assays for hKlf4 (Hs00358836_m1), hSox2 (Hs01053049_s1), and the endogenous control GAPDH (Hs02758991_g1).

The hSpCas9 activator plasmid was cloned into a lentiviral vector under the expression of the hEF1a promoter (pLenti-EF1a-Cas9-NLS-VP64). The hSpCas9 repressor plasmid was cloned into the same vector (pLenti-EF1a-SID4x-NLS-Cas9-NLS). Guide sequences (20bp) targeted to the *KLF4* locus are: 5'-GCGCGCTCCACACAACTCAC, 5'-GCAAAAATAGACAATCAGCA, GAAGGATCTCGGCCAATTTG. Spacer sequences for guide RNAs targeted to the *SOX2* locus are: 5'-GCTGCCGGGTTTTGCATGAA, 5'-CCGGGCCCGCAGCAAACTTC, 5'-GGGGCTGTCAGGGAATAAAT.

SUPPLEMENTARY DISCUSSION

Optogenetic actuators

Microbial and plant-derived light-sensitive proteins have been engineered as optogenetic actuators, allowing optical control of cellular functions including membrane potential[2-4], intracellular signaling[5], protein interactions[6-9], and heterologous gene expression[7,9-13].

Ambient light exposure

All cells were cultured at low light levels (<0.01 mW/cm^2) at all times except during stimulation. These precautions were taken as ambient light in the room (0.1-0.2 mW/cm^2) was found to significantly activate the LITE system (**Extended Data Fig. 2c**). No special precautions were taken to shield animals from light during *in vivo* experiments – even assuming ideal propagation within the implanted optical fiber, an estimation of light transmission at the fiber terminal due to ambient light was <0.01 mW (based on 200 μm fiber core diameter and 0.22 numerical aperture).

Optimization of light stimulation parameters in Neuro2A cells

To minimize near-UV induced cytotoxicity, we selected 466 nm blue LEDs to activate TALE-CRY2, a wavelength slightly red-shifted from the CRY2 absorption maxima of 450 nm but still maintaining over 80% activity[14] (**Extended Data Fig. 2a**). To minimize light exposure, we selected a mild stimulation protocol (1 s light pulses at 0.067 Hz, ~7% duty cycle). This was based on our finding that light duty cycle had no significant effect on LITE-mediated transcriptional activation over a wide range of duty cycle parameters (1.7% to 100% duty cycles, **Extended Data Fig. 2b**). Illumination with a range of light intensities from 0 to 10 mW/cm^2 revealed that *Ngn2* mRNA levels increased as a function of intensity up to 5 mW/cm^2.

However, increases in *Ngn2* mRNA levels declined at 10 mW/cm^2 (**Extended Data Fig. 2c**), suggesting that higher intensity light may have detrimental effects on either LITE function or on cell physiology. To better characterize this observation, we performed an ethidium homodimer-1 cytotoxicity assay with a calcein counterstain for living cells and found a significantly higher percentage of ethidium-positive cells at the higher stimulation intensity of 10 mW/cm^2.

Conversely, the ethidium-positive cell count from 5 mW/cm^2 stimulation was indistinguishable from unstimulated controls (**Extended Data Fig. 2d**). Thus 5 mW/cm^2 appeared to be optimal for achieving robust LITE activation while maintaining low cytotoxicity.

Reduction of light-induced toxicity in primary neurons: Initial application of LITEs in neurons revealed that cultured neurons were much more sensitive to blue light than Neuro 2a cells. Stimulation parameters previously optimized for Neuro 2a cells (466 nm, 5 mW/cm^2 intensity, 7% duty cycle with 1 s light pulse at 0.067 Hz for a total of 24 h) caused >50% toxicity in primary neurons. We therefore tested survival with a lower duty cycle, as we had previously observed that a wide range of duty cycles had little effect on LITE-mediated transcriptional activation (**Extended Data Fig. 2b**). A reduced duty cycle of 0.8% (0.5 s light pulses at 0.0167 Hz) at the same light intensity (5 mW/cm^2) was sufficient to maintain a high survival rate that was indistinguishable from that of unstimulated cultures (**Extended Data Fig. 5a**).

Light propagation and toxicity in *in vivo* experiments

Previous studies have investigated the propagation efficiency of different wavelengths of light in brain tissue. For 473 nm light (wavelength used in this study), there was a >90% attenuation after passing through 0.35 mm of tissue[15]. An estimated 5 mW/cm^2 light power density was estimated based on a tissue depth of 0.35 mm of tissue (the diameter of brain punch used in this study) and a total power output of 5 mW. The light stimulation duty cycle used *in vivo* was the same (0.8%, 0.5 s at 0.0167 Hz) as that used for primary neurons (**Extended Data Fig. 5a**).

CRY2 absorption spectrum

An illustration of the absorption spectrum of CRY2 was shown in **Extended Data Fig. 2a**. The spectrum showed a sharp drop in absorption above 480 nm[1]. Wavelengths > 500 nm were virtually not absorbed, which could be useful for future multimodal optical control with yellow or red-light sensitive proteins.

Development of AAV1 supernatant process

Traditional AAV particle generation require laborious production and purification processes, making the testing of many constructs in parallel impractical[16]. In this study, a simple yet highly effective process of AAV production using filtered supernatant from transfected 293FT cells (**Extended Data Fig. 4**). A previous study indicated that AAV particles produced in 293FT cells could be found not only within the cytoplasm but also in considerable amounts within the culture media[17]. The ratio of viral particles between the supernatant and cytosol of host cells varied depending on the AAV serotype, and secretion was enhanced if polyethylenimine (PEI) was used to transfect the viral packaging plasmids[17].

In the current study, we demonstrated that 2×10^5 293FT cells transfected with AAV vectors carrying TALEs (**Extended Data Fig. 2b**) and packaged using AAV1 serotype were capable of producing 250 μl of AAV1 at a concentration of $5.6 \pm 0.24 \times 10^{10}$ DNaseI resistant genome copies (GC) per mL. 250 μl of filtered supernatant was able to transduce 150,000 primary cortical neurons at efficiencies of 80-90% (**Fig. 2b** and **Extended Data Fig. 4b**). This process was also successfully adapted to a 96-well format, enabling the production of 125 μl AAV1 supernatant from up to 96 different constructs in parallel. 35ul of supernatant can then be used to transduce one well of primary neurons cultured in 96-well format, enabling transductions in biological triplicates from a single well.

Modification strategies for background elimination

CRY2PHR-VP64 Constructs: Three new constructs were designed with the goal of improving CRY2PHR-VP64 nuclear import. First, the mutations L70A and L74A within a predicted endogenous nuclear export sequence of CRY2PHR were induced to limit nuclear export of the protein (referred to as '*' in the Effector column of **Extended Data Fig. 6**). Second, the α-importin nuclear localization sequence was fused to the N-terminus of CRY2PHR-VP64 (referred to as 'A' in the Effector column of **Extended Data Fig. 6**). Third, the SV40 nuclear localization sequence was fused to the C-terminus of CRY2PHR-VP64 (referred to as 'P' in the Effector column of **Extended Data Fig. 6**).

TALE-CIB1 Linkers: The SV40 NLS linker between TALE and CIB1 used in LITE 1.0 was replaced with one of several linkers designed to increase nuclear export of the TALE-CIB1 protein (The symbols used in the CIB1 Linker column of **Extended Data Fig. 6** are shown in parentheses): a flexible glycine-serine linker (G), an adenovirus type 5 E1B nuclear export sequence (W), an HIV nuclear export sequence (M), a MAPKK nuclear export sequence (K), and a PTK2 nuclear export sequence (P).

NLS* Endogenous CIB1 Nuclear Localization Sequence Mutation: A nuclear localization signal exists within the wild type CIB1 sequence. This signal was mutated in NLS* constructs at K92A, R93A, K105A, and K106A in order to diminish TALE-CIB1 nuclear localization (referred to as 'N' in the NLS* column of **Extended Data Fig. 6**).

ΔCIB1 Transcription Factor Homology Deletions: In an effort to eliminate possible basal CIB1 transcriptional activation, deletion constructs were designed in which regions of high homology to basic helix-loop-helix transcription factors in higher plants were removed. These deleted regions consisted of Δaa230-256, Δaa276-307, Δaa308-334 (referred to as '1' '2' and '3' in the ΔCIB1 column of **Extended Data Fig. 6**). In each case, the deleted region was replaced with a 3 residue GGS link.

NES Insertions into CIB1: One strategy to facilitate light-dependent nuclear import of TALE-CIB1 was to insert an NES in CIB1 at its dimerization interface with CRY2PHR such that the signal would be concealed upon binding with CRY2PHR. To this end, an NES was inserted at different positions within the known CRY2 interaction domain CIBN (aa 1-170). The positions are as follows (The symbols used in the NES column of **Extended Data Fig. 6** are shown in parentheses): aa28 (1), aa52 (2), aa73 (3), aa120 (4), aa140 (5), aa160 (6).

***bHLH basic Helix-Loop-Helix Mutation:** To reduce direct CIB1-DNA interactions, several basic residues of the basic helix-loop-helix region in CIB1 were mutated. The following mutations are present in all *bHLH constructs (referred to as 'B' in the *bHLH column of **Extended Data Fig. 6**): R175A, G176A, R187A, and R189A.

Supplementary Table 1 | HDAC Recruiter Effector Domains

Subtype/ Complex	Name	Substrate (if known)	Modification (if known)	Organism	Full size (aa)	Selected truncation (aa)	Final size (aa)	Catalytic domain
Sin3a	**MeCP2**	-	-	*R. norvegicus*	492	207-492[18]	286	-
Sin3a	**MBD2b**	-	-	*H. sapiens*	262	45-262[19]	218	-
Sin3a	**Sin3a**	-	-	*H. sapiens*	1273	524-851[20]	328	627-829: HDAC1 interaction
NcoR	**NcoR**	-	-	*H. sapiens*	2440	420-488[21]	69	-
NuRD	**SALL1**	-	-	*M. musculus*	1322	1-93[22]	93	-
CoREST	**RCOR1**	-	-	*H. sapiens*	482	81-300[23,24]	220	-

Supplementary Table 2 | HDAC Effector Domains

Subtype/ Complex	Name	Substrate (if known)	Modification (if known)	Organism	Full size (aa)	Selected truncation (aa)	Final size (aa)	Catalytic domain
HDAC I	**HDAC 8**	-	-	*X. laevis*	325	1-325	325	1-272: HDAC
HDAC I	**RPD3**	-	-	*S. cerevisiae*	433	19-340	322[25]	19-331: HDAC
HDAC IV	**MesoLo4**	-	-	*M. loti*	300	1-300[26]	300	-
HDAC IV	**HDAC 11**	-	-	*H. sapiens*	347	1-347[27]	347	14-326: HDAC
HD2	**HDT1**	-	-	*A. thaliana*	245	1-211[28]	211	-
SIRT I	**SIRT3**	H3K9Ac H4K16Ac H3K56Ac	-	*H. sapiens*	399	143-399[29]	257	126-382: SIRT
SIRT I	**HST2**	-	-	*C. albicans*	331	1-331[30]	331	-
SIRT I	**CobB**	-	-	*E. coli (K12)*	242	1-242[31]	242	-
SIRT I	**HST2**	-	-	*S. cerevisiae*	357	8-298[32]	291	-
SIRT III	**SIRT5**	H4K8Ac H4K16Ac	-	*H. sapiens*	310	37-310[33]	274	41-309: SIRT
SIRT III	**Sir2A**	-	-	*P. falciparum*	273	1-273[34]	273	19-273: SIRT
SIRT IV	**SIRT6**	H3K9Ac H3K56Ac	-	*H. sapiens*	355	1-289[35]	289	35-274: SIRT

Supplementary Table 3 | Histone Methyltransferase (HMT) Effector Domains

Subtype/ Complex	Name	Substrate (if known)	Modification (if known)	Organism	Full size (aa)	Selected truncation (aa)	Final size (aa)	Catalytic domain
SET	**NUE**	H2B, H3, H4	-	*C. trachomatis*	219	1-219[36]	219	-
SET	**vSET**	-	H3K27me3	*P. bursaria chlorella virus*	119	1-119[37]	119	4-112: SET2
SUV39 family	**EHMT 2/G9A**	H1.4K2, H3K9, H3K27	H3K9me1/ 2, H1K25me1	*M. musculus*	1263	969-1263[38]	295	1025-1233: preSET, SET, postSET
SUV39	**SUV39 H1**	-	H3K9me2/ 3	*H. sapiens*	412	79-412[39]	334	172-412: preSET, SET, postSET
Suvar3-9	**dim-5**	-	H3K9me3	*N. crassa*	331	1-331[40]	331	77-331: preSET, SET, postSET
Suvar3-9 (SUVH subfamily)	**KYP**	-	H3K9me1/ 2	*A. thaliana*	624	335-601	267[41]	-
Suvar3-9 (SUVR subfamily)	**SUVR4**	H3K9me 1	H3K9me2/ 3	*A. thaliana*	492	180-492	313[42]	192-462: preSET, SET, postSET
Suvar4-20	**SET4**	-	H4K20me3	*C. elegans*	288	1-288[43]	288	-
SET8	**SET1**	-	H4K20me1	*C. elegans*	242	1-242[43]	242	-
SET8	**SETD8**	-	H4K20me1	*H. sapiens*	393	185-393	209[44]	256-382: SET
SET8	**TgSET 8**	-	H4K20me1 /2/3	*T. gondii*	1893	1590-1893[45]	304	1749-1884: SET

Supplementary Table 4 | Histone Methyltransferase (HMT) Recruiter Effector Domains

Subtype/ Complex	Name	Substrate (if known)	Modification (if known)	Organism	Full size (aa)	Selected truncation (aa)	Final size (aa)	Catalytic domain
-	**Hp1a**	-	H3K9me3	*M. musculus*	191	73-191	119[46]	121-179: chromoshadow
-	**PHF19**	-	H3K27me3	*H. sapiens*	580	(1-250) + GGSG linker + (500-580)	335[47]	163-250: PHD2
-	**NIPP1**	-	H3K27me3	*H. sapiens*	351	1-329[48]	329	310-329: EED

Supplementary Table 5 | Histone Acetyltransferase Inhibitor Effector Domains

Subtype/ Complex	Name	Substrate (if known)	Modification (if known)	Organism	Full size (aa)	Selected truncation (aa)	Final size (aa)	Catalytic domain
-	**SET/TAF-1β**	-	-	*M. musculus*	289	1-289[49]	289	-

Supplementary Table 6 | genomic sequences targeted by TALEs (5' to 3')

5-HT1B	TATCTGAACTCTCC
5-HTT	TGTCTGTCTTGCAT
Arc	TGGCTGTTGCCAGG
BDNF	TACCTGGAGCTAGC
c-Fos	TACACAGGATGTCC
DNMT3a	TTGGCCCTGTGCAG
DNMT3b	TAGCGCAGCGATCG
gad65	TATTGCCAAGAGAG
gad67	TGACTGGAACATAC
GR (GCR, NR3C1)	TGATGGACTTGTAT
HAT1	TGGACCTTCTCCCT
HCRTR1	TAGGTCTCCTGGAG
HCRTR2	TGGCTCAGGAACTT
HDAC1	TTCTCTAAGCTGCC
HDAC2	TGAGCCCTGGAGGA
HDAC4	TGCCTAAGATGGAG
JMJD2A	TGTAGTGAGTGTTC
MCH-R1	TGTCTAGGTGATGT
NET	TCTCTGCTAGAAGG
Scn1a	TCTAGGTCAAGTGT
SIRT1	TCCTCTGCTCCGCT
tet1	TCTAGGAGTGTAGC
tet3	TGCCTGGCTGCTGG
5-HT1B	TATCTGAACTCTCC
Grm2	TCAGAGCTGTCCTC
Grm5	TGCAAGAGTAGGAG
5-HT2A	TAGTGACTGATTCC
Grin2a	TTGGAGGAGCACCA
Neurog2	TGAATGATGATAATAC

Supplementary Table 7 | Product information for all Taqman probes (Life Technologies)

Target	Species	Probe #
Ngn2	mouse	Mm00437603_g1
Grm5 (mGluR5)	mouse	Mm00690332_m1
Grm2 (mGluR2)	mouse	Mm01235831_m1
Grin2a (NMDAR2A)	mouse	Mm00433802_m1
GAPD (GAPDH)	mouse	4352932E
KLF4	human	Hs00358836_m1
GAPD (GAPDH)	human	4352934E
WPRE	custom	
5-HT1A	mouse	Mm00434106_s1
5-HT1B	mouse	Mm00439377_s1
5-HTT	mouse	Mm00439391_m1
Arc	mouse	Mm00479619_g1
BDNF	mouse	Mm04230607_s1
c-Fos	mouse	Mm00487425_m1
CBP/P300	mouse	Mm01342452_m1
CREB	mouse	Mm00501607_m1
CRHR1	mouse	Mm00432670_m1
DNMT1	mouse	Mm01151063_m1
DNMT3a	mouse	Mm00432881_m1
DNMT3b	mouse	Mm01240113_m1
egr-1 (zif-268)	mouse	Mm00656724_m1
Gad65	mouse	Mm00484623_m1
Gad67	mouse	Mm00725661_s1
GR (GCR, NR3C1)	mouse	Mm00433832_m1
HAT1	mouse	Mm00509140_m1
HCRTR1	mouse	Mm01185776_m1
HCRTR2	mouse	Mm01179312_m1
HDAC1	mouse	Mm02391771_g1
HDAC2	mouse	Mm00515108_m1
HDAC4	mouse	Mm01299557_m1
JMJD2A	mouse	Mm00805000_m1
M1 (CHRM1)	mouse	Mm00432509_s1
MCH-R1	mouse	Mm00653044_m1
NET (SLC6A2)	mouse	Mm00436661_m1
NR2B subunit	mouse	Mm00433820_m1
OXTR	mouse	Mm01182684_m1
Scn1a	mouse	Mm00450580_m1
SIRT1	mouse	Mm00490758_m1
Tet1	mouse	Mm01169087_m1
Tet2	mouse	Mm00524395_m1
Tet3	mouse	Mm00805756_m1

Supplementary Table 8 | Clone, product numbers and concentrations for antibodies used in this study

Primary Antibodies

Target	Host	Clone #	Manufacturer	Product #	IsoType	Concentration
mGluR2	mouse	mG2Na-s	Abcam	Ab15672	IgG	1:1000
α-tubulin	mouse	B-5-1-2	Sigma-Aldrich	T5168	IgG1	1:20000
NeuN	mouse	A60	Millipore	MAB377	IgG1	1:200
HA (Alexa Fluor 594	mouse	6E2	Cell Signaling	3444	IgG1	1:100
GFP	chicken	polyclonal	Aves Labs	GFP-1020	IgY	1:500

Target	Host	Conjugate	Manufacturer	Product #		Concentration
mouse IgG	goat	HRP	Sigma-Aldrich	A9917		1:5000-10000
mouse IgG	goat	Alexa Fluor 594	Life Technologies	A11005		1:1000
chicken IgG	Goat	Alexa Fluor 488	Life Technologies	A11039		1:1000

Target	Host	Epitope	Manufacturer	Product #	IsoType	Concentration
H3K9me1	mouse	1-18	Millipore	17-680	IgG	2 µl/IP
H3K9me2	mouse	1-18	Millipore	17-681	IgG	4 µl/IP
H3K9Ac	rabbit	polyclonal	Millipore	17-658	IgG	3 µg/IP
H4K20me1	rabbit	15-24	Millipore	17-651	IgG	4 µg/IP
H4K8Ac	rabbit	polyclonal	Millipore	17-10099	IgG	1.5 µl/IP
H4K20me3	rabbit	18-22	Millipore	17-671	IgG	7 µl/IP
H3K27me3	rabbit	polyclonal	Millipore	17-622	IgG	4 µg/IP

Supplementary Table 9 | Viral transduction and light stimulation parameters for *in vivo* LITE-mediated activation of *Grm2* in the mouse infralimbic cortex (ILC). *Grm2* mRNA levels in the ipsilateral LITE-expressing hemisphere are compared with the contralateral mCherry-expressing control hemisphere for all three experimental conditions shown in **Fig. 3h.**

Experimental condition	*ILC Hemisphere (ipsilateral)*		*ILC Hemisphere (contralateral)*
	AAV vector	**Light stimulation**	**AAV vector**
GFP	GFP	yes	mCherry
LITEs / no Light	TALE-CIB1::CRY2PHR-VP64	no	mCherry
LITEs / + Light	TALE-CIB1::CRY2PHR-VP64	yes	mCherry

Supplementary Table 10 | qPCR primers used for CHIP-qPCR

target	**Primers**
Grm2 promoter	Forward: CTGTGCTGAAGGATCTGGGG Reverse: ATGCTGCAGGCATAGGACAA
Neurog2 promoter	Forward: GAGGGGGAGAGGGACTAAAGA Reverse: GCTCTCCCTCCCCAGCTTA
Myt-1 promoter control	Cell Signaling Technologies SimpleChIP® Mouse MYT-1 Promoter Primers #8985
RPL30 Intron 2 control	Cell Signaling Technologies SimpleChIP® Mouse RPL30 Intron 2 Primers #7015

Supplementary Sequences

> TALE(*Ngn2*)-NLS-CRY2

MSRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLRAADAPPPT
MRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFT
HAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQ
LLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQV
VAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVA
IASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
GGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIG
GKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGK
QALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQAL
ETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETV
QRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRL
LPVLCQAHGLTPEQVVAIASHDGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPH
APALIKRTNRRIPERTSHRVADHAQVVRVLGFFQCHSHPAQAFDDAMTQFGMSRHGLLQLFRRVGVTELE
ARSGTLPPASQRWDRILQASGMKRAKPSPTSTQTPDQASLHAFADSLERDLDAPSPMHEGDQTRASASPKK
KRKVEASKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHL
SQSLKALGSDLTLIKTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLY
EPWEIYCEKGKPFTSFNSYWKKCLDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLT
RAWSPGWSNADKLLNEFIEKQLIDYAKNSKKVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNS
EGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFFPWDADVDKFKAWRQGRTGYPLVDAGMRELW
ATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLECDILGWQYISGSIPDGHELDRLDNPALQ
GAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPIVDIDTARELLAKAISRTRE
AQIMIGAAPDEIVADSFEALGANTIKEPGLCPSVSSNDQQVPSAVRYNGSKRVKPEEEEERDMKKSRGFDER
ELFSTAESSSSSSVFFVSQSCSLASEGKNLEGIQDSSDQITTSLGKNG

> TALE(*Ngn2*)-NLS-CRY2PHR

MSRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLRAADAPPPT
MRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFT
HAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQ
LLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQV
VAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVA
IASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
GGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIG
GKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGK
QALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQAL
ETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETV
QRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRL
LPVLCQAHGLTPEQVVAIASHDGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPH
APALIKRTNRRIPERTSHRVADHAQVVRVLGFFQCHSHPAQAFDDAMTQFGMSRHGLLQLFRRVGVTELE
ARSGTLPPASQRWDRILQASGMKRAKPSPTSTQTPDQASLHAFADSLERDLDAPSPMHEGDQTRASASPKK
KRKVEASKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHL
SQSLKALGSDLTLIKTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLY
EPWEIYCEKGKPFTSFNSYWKKCLDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLT
RAWSPGWSNADKLLNEFIEKQLIDYAKNSKKVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNS

EGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFFPWDADVDKFKAWRQGRTGYPLVDAGMRELW
ATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLECDILGWQYISGSIPDGHELDRLDNPALQ
GAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPIVDIDTARELLAKAISRTRE
AQIMIGAAP

> CIB1-NLS-VP64_2A_GFP

MNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPMMYGET
TVEGDSRLSISPETTLGTGNFKKRKFDTETKDCNEKKKKMTMNRDDLVEEGEEEKSKITEQNNGSTKSIKK
MKHKAKKEENNFSNDSSKVTKELEKTDYIHVRARRGQATDSHSIAERVRREKISERMKFLQDLVPGCDKIT
GKAGMLDEIINYVQSLQRQIEFLSMKLAIVNPRPDFDMDDIFAKEVASTPMTVVPSPEMVLSGYSHEMVHS
GYSSEMVNSGYLHVNPMQQVNTSSDPLSCFNNGEAPSMWDSHVQNLYGNLGVASPKKKRKVEASGSGR
ADALDDFDLDMLGSDALDDFDLDMLGSDALDDFDLDMLGSDALDDFDLDMLINSRGSGEGRGSLLTCGD
VEENPGPVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLT
YGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNI
LGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSA
LSKDPNEKRDHMVLLEFVTAAGITLGMDELYK

> CIBN-NLS-VP64_2A_GFP

MNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPMMYGET
TVEGDSRLSISPETTLGTGNFKKRKFDTETKDCNEKKKKMTMNRDDLVEEGEEEKSKITEQNNGSTKSIKK
MKHKAKKEENNFSNDSSKVTKELEKTDYIASPKKKRKVEASGSGRADALDDFDLDMLGSDALDDFDLDM
LGSDALDDFDLDMLGSDALDDFDLDMLINSRGSGEGRGSLLTCGDVEENPGPVSKGEELFTGVVPILVELD
GDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLTYGVQCFSRYPDHMKQHDFFKSAMP
EGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKN
GIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITL
GMDELYK

> CIB1-NLS-VP16_2A_GFP

MNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPMMYGET
TVEGDSRLSISPETTLGTGNFKKRKFDTETKDCNEKKKKMTMNRDDLVEEGEEEKSKITEQNNGSTKSIKK
MKHKAKKEENNFSNDSSKVTKELEKTDYIHVRARRGQATDSHSIAERVRREKISERMKFLQDLVPGCDKIT
GKAGMLDEIINYVQSLQRQIEFLSMKLAIVNPRPDFDMDDIFAKEVASTPMTVVPSPEMVLSGYSHEMVHS
GYSSEMVNSGYLHVNPMQQVNTSSDPLSCFNNGEAPSMWDSHVQNLYGNLGVASPKKKRKVEASAPPTD
VSLGDELHLDGEDVAMAHADALDDFDLDMLGDGDSPGPGFTPHDSAPYGALDMADFEFEQMFTDALGID
EYGGEFPGIRRSRGSGEGRGSLLTCGDVEENPGPVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDAT
YGKLTLKFICTTGKLPVPWPTLVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKT
RAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA
DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK

> CIB1-NLS-p65_2A_GFP

MNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPMMYGET
TVEGDSRLSISPETTLGTGNFKKRKFDTETKDCNEKKKKMTMNRDDLVEEGEEEKSKITEQNNGSTKSIKK
MKHKAKKEENNFSNDSSKVTKELEKTDYIHVRARRGQATDSHSIAERVRREKISERMKFLQDLVPGCDKIT
GKAGMLDEIINYVQSLQRQIEFLSMKLAIVNPRPDFDMDDIFAKEVASTPMTVVPSPEMVLSGYSHEMVHS
GYSSEMVNSGYLHVNPMQQVNTSSDPLSCFNNGEAPSMWDSHVQNLYGNLGVASPKKKRKVEASPSGQI
SNQALALAPSSAPVLAQTMVPSSAMVPLAQPPAPAPVLTPGPPQSLSAPVPKSTQAGEGTLSEALLHLQFDA
DEDLGALLGNSTDPGVFTDLASVDNSEFQQLLNQGVSMSHSTAEPMLMEYPEAITRLVTGSQRPPDPAPTP
LGTSGLPNGLSGDEDFSSIADMDFSALLSQISSSGQSRGSGEGRGSLLTCGDVEENPGPVSKGEELFTGVVPI
LVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLTYGVQCFSRYPDHMKQHDFF
KSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMAD
KQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTA
AGITLGMDELYK

.> **HA-TALE(12mer)-NLS-VP64_2A_GFP**

MYPYDVPDYAVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFTHAHIVALSQHPAALGTVAVKYQ
DMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKRGGVTAVEAVHAWRN
ALTGAPLNLTPEQVVAIASXXGGKQALETVQRLLPVLCQAHGLTPEQVVAIASXXGGKQALETVQRLLPV
LCQAHGLTPEQVVAIASXXGGKQALETVQRLLPVLCQAHGLTPEQVVAIASXXGGKQALETVQRLLPVLC
QAHGLTPEQVVAIASXXGGKQALETVQRLLPVLCQAHGLTPEQVVAIASXXGGKQALETVQRLLPVLCQA
HGLTPEQVVAIASXXGGKQALETVQRLLPVLCQAHGLTPEQVVAIASXXGGKQALETVQRLLPVLCQAHG
LTPEQVVAIASXXGGKQALETVQRLLPVLCQAHGLTPEQVVAIASXXGGKQALETVQRLLPVLCQAHGLT
PEQVVAIASXXGGKQALETVQRLLPVLCQAHGLTPEQVVAIASXXGGKQALETVQRLLPVLCQAHGLTPE
QVVAIASXXGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIP
ERTSHRVAASPKKKRKVEASGSGRADALDDFDLDMLGSDALDDFDLDMLGSDALDDFDLDMLGSDALD
DFDLDMLINSRGSGEGRGSLLTCGDVEENPGPVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATY
GKLTLKFICTTGKLPVPWPTLVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTR
AEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD
HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK

> **HA-TALE(12mer)-NLS-SID4X_2A_phiLOV2.1**

MYPYDVPDYAVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFTHAHIVALSQHPAALGTVAVKYQ
DMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKRGGVTAVEAVHAWRN
ALTGAPLNLTPEQVVAIASXXGGKQALETVQRLLPVLCQAHGLTPEQVVAIASXXGGKQALETVQRLLPV
LCQAHGLTPEQVVAIASXXGGKQALETVQRLLPVLCQAHGLTPEQVVAIASXXGGKQALETVQRLLPVLC
QAHGLTPEQVVAIASXXGGKQALETVQRLLPVLCQAHGLTPEQVVAIASXXGGKQALETVQRLLPVLCQA
HGLTPEQVVAIASXXGGKQALETVQRLLPVLCQAHGLTPEQVVAIASXXGGKQALETVQRLLPVLCQAHG
LTPEQVVAIASXXGGKQALETVQRLLPVLCQAHGLTPEQVVAIASXXGGKQALETVQRLLPVLCQAHGLT
PEQVVAIASXXGGKQALETVQRLLPVLCQAHGLTPEQVVAIASXXGGKQALETVQRLLPVLCQAHGLTPE
QVVAIASXXGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIP
ERTSHRVAASPKKKRKVEASPKKKRKVEASGSGMNIQMLLEAADYLERREREAEHGYASMLPGSGMNIQ
MLLEAADYLERREREAEHGYASMLPGSGMNIQMLLEAADYLERREREAEHGYASMLPGSGMNIQMLLEA
ADYLERREREAEHGYASMLPSRSRGSGEGRGSLLTCGDVEENPGPIEKSFVITDPRLPDYPIIFASDGFLELTE
YSREEIMGRNARFLQGPETDQATVQKIRDAIRDQRETTVQLINYTKSGKKFWNLLHLQPVRDRKGGLQYFI
GVQLVGSDHV

> **HA-TALE(12mer)-NLS-CIB1**

MYPYDVPDYAVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFTHAHIVALSQHPAALGTVAVKYQ
DMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKRGGVTAVEAVHAWRN
ALTGAPLNLTPEQVVAIASXXGGKQALETVQRLLPVLCQAHGLTPEQVVAIASXXGGKQALETVQRLLPV
LCQAHGLTPEQVVAIASXXGGKQALETVQRLLPVLCQAHGLTPEQVVAIASXXGGKQALETVQRLLPVLC
QAHGLTPEQVVAIASXXGGKQALETVQRLLPVLCQAHGLTPEQVVAIASXXGGKQALETVQRLLPVLCQA
HGLTPEQVVAIASXXGGKQALETVQRLLPVLCQAHGLTPEQVVAIASXXGGKQALETVQRLLPVLCQAHG
LTPEQVVAIASXXGGKQALETVQRLLPVLCQAHGLTPEQVVAIASXXGGKQALETVQRLLPVLCQAHGLT
PEQVVAIASXXGGKQALETVQRLLPVLCQAHGLTPEQVVAIASXXGGKQALETVQRLLPVLCQAHGLTPE
QVVAIASXXGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIP
ERTSHRVAASPKKKRKVEASNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEM
DSYLSTAGLNLPMMYGETTVEGDSRLSISPETTLGTGNFKKRKFDTETKDCNEKKKKMTMNRDDLVEEGE
EEKSKITEQNNGSTKSIKKMKHKAKKEENNFSNDSSKVTKELEKTDYIHVRARRGQATDSHSIAERVRREKI
SERMKFLQDLVPGCDKITGKAGMLDEIINYVQSLQRQIEFLSMKLAIVNPRPDFDMDDIFAKEVASTPMTV
VPSPEMVLSGYSHEMVHSGYSSEMVNSGYLHVNPMQQVNTSSDPLSCFNNGEAPSMWDSHVQNLYGNLG
V

> **CRY2PHR-NLS-VP64_2A_GFP**

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKA
LGSDLTLIKTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIY
CEKGKPFTSFNSYWKKCLDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSP
GWSNADKLLNEFIEKQLIDYAKNSKKVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEES
ADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFFPWDADVDKFKAWRQGRTGYPLVDAGMRELWATGW
MHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLECDILGWQYISGSIPDGHELDRLDNPALQGAKY
DPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPIVDIDTARELLAKAISRTREAQIMI
GAAPASPKKKRKVEASGSGRADALDDFDLDMLGSDALDDFDLDMLGSDALDDFDLDMLGSDALDDFDL
DMLINSRGSGEGRGSLLTCGDVEENPGPVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLT
LKFICTTGKLPVPWPTLVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKF
EGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQN
TPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYKV

> **CRY2PHR-NLS-SID4X_2A_phiLOV2.1**

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKA
LGSDLTLIKTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIY
CEKGKPFTSFNSYWKKCLDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSP
GWSNADKLLNEFIEKQLIDYAKNSKKVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEES
ADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFFPWDADVDKFKAWRQGRTGYPLVDAGMRELWATGW
MHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLECDILGWQYISGSIPDGHELDRLDNPALQGAKY
DPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPIVDIDTARELLAKAISRTREAQIMI
GAAPASPKKKRKVEASGSGMNIQMLLEAADYLERREREAEHGYASMLPGSGMNIQMLLEAADYLERRER
EAEHGYASMLPGSGMNIQMLLEAADYLERREREAEHGYASMLPGSGMNIQMLLEAADYLERREREAEHG
YASMLPSRSRGSGEGRGSLLTCGDVEENPGPIEKSFVITDPRLPDYPIIFASDGFLELTEYSREEIMGRNARFL
QGPETDQATVQKIRDAIRDQRETTVQLINYTKSGKKFWNLLHLQPVRDRKGGLQYFIGVQLVGSDHV

> TALE(*KLF4*)-NLS-CRY2PHR

MSRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLRAADAPPPT
MRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFT
HAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQ
LLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQV
VAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVA
IASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIAS
HDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNG
GGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGG
KQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQA
LETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDA
VKKGLPHAPALIKRTNRRIPERTSHRVADHAQVVRVLGFFQCHSHPAQAFDDAMTQFGMSRHGLLQLFRR
VGVTELEARSGTLPPASQRWDRILQASGMKRAKPSPTSTQTPDQASLHAFADSLERDLDAPSPMHEGDQTR
ASASPKKKRKVEASKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWM
KQSLAHLSQSLKALGSDLTLIKTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQS
YNGDLLYEPWEIYCEKGKPFTSFNSYWKKCLDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAE
KPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSKKVVGNSTSLLSPYLHFGEISVRHVFQCARMKQII
WARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFFPWDADVDKFKAWRQGRTGYPLVD
AGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLECDILGWQYISGSIPDGHELD
RLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPIVDIDTARELLA
KAISRTREAQIMIGAAP

> HA-NLS-TALE(*p11*, N136)-SID

MYPYDVPDYASPKKKRKVEASVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFTHAHIVALSQHP
AALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKRGGV
TAVEAVHAWRNALTGAPLNLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGK
QALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQA
LETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALE
TVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETV
QRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQR
LLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLP
VLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVL
CQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQ
AHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASHDGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRT
NRRIPERTSHRVADHAQVVRVLGFFQCHSHPAQAFDDAMTQFGMSRHGLLQLFRRVGVTELEARSGTLPP
ASQRWDRILQASGMKRAKPSPTSTQTPDQASLHAFADSLERDLDAPSPMHEGDQTRASASGSGMNIQMLL
EAADYLERREREAEHGYASMLP.

> HA-NLS-TALE(*p11*, N136)-SID4X

MYPYDVPDYASPKKKRKVEASVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFTHAHIVALSQHP
AALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKRGGV
TAVEAVHAWRNALTGAPLNLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGK
QALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQA
LETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALE
TVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETV
QRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQR

LLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLP
VLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVL
CQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQ
AHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASHDGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRT
NRRIPERTSHRVADHAQVVRVLGFFQCHSHPAQAFDDAMTQFGMSRHGLLQLFRRVGVTELEARSGTLPP
ASQRWDRILQASGMKRAKPSPTSTQTPDQASLHAFADSLERDLDAPSPMHEGDQTRASASGSGMNIQMLL
EAADYLERREREAEHGYASMLPGSGMNIQMLLEAADYLERREREAEHGYASMLPGSGMNIQMLLEAADY
LERREREAEHGYASMLPGSGMNIQMLLEAADYLERREREAEHGYASMLPSR

>HA-TALE(*ng2,* C63)-GS-cib1-mutNLS

YPYDVPDYASRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLR
AADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEA
LVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPP
LQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLT
PEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVV
AIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAI
ASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
IGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGG
KQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPA
LESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAASGGGG
SGGGGSNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPM
MYGETTVEGDSRLSISPETTLGTGNFKAAKFDTETKDCNEAAKKMTMNRDDLVEEGEEEKSKITEQNNGS
TKSIKKMKHKAKKEENNFSNDSSKVTKELEKTDYIHVRARRGQATDSHSIAERVRREKISERMKFLQDLVP
GCDKITGKAGMLDEIINYVQSLQRQIEFLSMKLAIVNPRPDFDMDDIFAKEVASTPMTVVPSPEMVLSGYSH
EMVHSGYSSEMVNSGYLHVNPMQQVNTSSDPLSCFNNGEAPSMWDSHVQNLYGNLGV

> HA-TALE(*ng2,* C63)-wNES-cib1-mutNLS

YPYDVPDYASRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLR
AADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEA
LVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPP
LQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLT
PEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVV
AIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAI
ASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
IGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGG
KQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPA
LESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAASLYPER
LRRILTNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPMM
YGETTVEGDSRLSISPETTLGTGNFKAAKFDTETKDCNEAAKKMTMNRDDLVEEGEEEKSKITEQNNGSTK
SIKKMKHKAKKEENNFSNDSSKVTKELEKTDYIHVRARRGQATDSHSIAERVRREKISERMKFLQDLVPGC
DKITGKAGMLDEIINYVQSLQRQIEFLSMKLAIVNPRPDFDMDDIFAKEVASTPMTVVPSPEMVLSGYSHEM
VHSGYSSEMVNSGYLHVNPMQQVNTSSDPLSCFNNGEAPSMWDSHVQNLYGNLGV

> HA-TALE(*ng2,* C63)-mNES-cib1-mutNLS

YPYDVPDYASRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLR
AADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEA
LVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPP
LQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLT
PEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVV
AIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAI
ASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
IGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGG
KQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPA
LESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAASLQLPP
LERLTLNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPMM
YGETTVEGDSRLSISPETTLGTGNFKAAKFDTETKDCNEAAKKMTMNRDDLVEEGEEEKSKITEQNNGSTK
SIKKMKHKAKKEENNFSNDSSKVTKELEKTDYIHVRARRGQATDSHSIAERVRREKISERMKFLQDLVPGC
DKITGKAGMLDEIINYVQSLQRQIEFLSMKLAIVNPRPDFDMDDIFAKEVASTPMTVVPSPEMVLSGYSHEM
VHSGYSSEMVNSGYLHVNPMQQVNTSSDPLSCFNNGEAPSMWDSHVQNLYGNLGV

> HA-TALE(*ng2,* C63)-ptk2NES-cib1-mutNLS

YPYDVPDYASRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLR
AADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEA
LVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPP
LQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLT
PEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVV
AIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAI
ASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
IGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGG
KQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPA
LESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAASLDLAS
LILNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPMMYGE
TTVEGDSRLSISPETTLGTGNFKAAKFDTETKDCNEAAKKMTMNRDDLVEEGEEEKSKITEQNNGSTKSIK
KMKHKAKKEENNFSNDSSKVTKELEKTDYIHVRARRGQATDSHSIAERVRREKISERMKFLQDLVPGCDKI
TGKAGMLDEIINYVQSLQRQIEFLSMKLAIVNPRPDFDMDDIFAKEVASTPMTVVPSPEMVLSGYSHEMVH
SGYSSEMVNSGYLHVNPMQQVNTSSDPLSCFNNGEAPSMWDSHVQNLYGNLGV

> HA-TALE(*ng2,* C63)-mapkkNES-cib1-mutNLS

YPYDVPDYASRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLR
AADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEA
LVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPP
LQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLT
PEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVV
AIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAI

ASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
IGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGG
KQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPA
LESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAASLQKK
LEELELNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPMM
YGETTVEGDSRLSISPETTLGTGNFKAAKFDTETKDCNEAAKKMTMNRDDLVEEGEEEKSKITEQNNGSTK
SIKKMKHKAKKEENNFSNDSSKVTKELEKTDYIHVRARRGQATDSHSIAERVRREKISERMKFLQDLVPGC
DKITGKAGMLDEIINYVQSLQRQIEFLSMKLAIVNPRPDFDMDDIFAKEVASTPMTVVPSPEMVLSGYSHEM
VHSGYSSEMVNSGYLHVNPMQQVNTSSDPLSCFNNGEAPSMWDSHVQNLYGNLGV

> HA-TALE(*ng2,* C63)-GS-cib1Δ3-mutNLS

YPYDVPDYASRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLR
AADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEA
LVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPP
LQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLT
PEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVV
AIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAI
ASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
IGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGG
KQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPA
LESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAASGGGG
SGGGGSNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPM
MYGETTVEGDSRLSISPETTLGTGNFKAAKFDTETKDCNEAAKKMTMNRDDLVEEGEEEKSKITEQNNGS
TKSIKKMKHKAKKEENNFSNDSSKVTKELEKTDYIHVRARRGQATDSHSIAERVRREKISERMKFLQDLVP
GCDKITGKAGMLDEIINYVQSLQRQIEFLSMKLAIVNPRPDFDMDDIFAKEVASTPMTVVPSPEMVLSGYSH
EMVHSGYSSEMVNSGYLHVNPMQQVNTSS

> HA-TALE(*ng2,* C63)-wNLS-cib1Δ3-mutNLS

YPYDVPDYASRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLR
AADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEA
LVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPP
LQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLT
PEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVV
AIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAI
ASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
IGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGG
KQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPA
LESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAASLYPER
LRRILTNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPMM
YGETTVEGDSRLSISPETTLGTGNFKAAKFDTETKDCNEAAKKMTMNRDDLVEEGEEEKSKITEQNNGSTK
SIKKMKHKAKKEENNFSNDSSKVTKELEKTDYIHVRARRGQATDSHSIAERVRREKISERMKFLQDLVPGC
DKITGKAGMLDEIINYVQSLQRQIEFLSMKLAIVNPRPDFDMDDIFAKEVASTPMTVVPSPEMVLSGYSHEM
VHSGYSSEMVNSGYLHVNPMQQVNTSS

> HA-TALE(*ng2*, C63)-mNLS-cib1Δ3-mutNLS

YPYDVPDYASRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLR
AADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEA
LVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPP
LQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLT
PEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVV
AIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAI
ASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
IGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGG
KQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPA
LESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAASSPKKK
RKVEASNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPM
MYGETTVEGDSRLSISPETTLGTGNFKAAKFDTETKDCNEAAKKMTMNRDDLVEEGEEEKSKITEQNNGS
TKSIKKMKHKAKKEENNFSNDSSKVTKELEKTDYIHVRARRGQATDSHSIAERVRREKISERMKFLQDLVP
GCDKITGKAGMLDEIINYVQSLQRQIEFLSMKLAIVNPRPDFDMDDIFAKEVASTPMTVVPSPEMVLSGYSH
EMVHSGYSSEMVNSGYLHVNPMQQVNTSS

> HA-TALE(*ng2*, C63)-GS-cib1-mutNLS-mutbHLH

YPYDVPDYASRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLR
AADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEA
LVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPP
LQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLT
PEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVV
AIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAI
ASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
IGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGG
KQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPA
LESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAASGGGG
SGGGGSNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPM
MYGETTVEGDSRLSISPETTLGTGNFKAAKFDTETKDCNEAAKKMTMNRDDLVEEGEEEKSKITEQNNGS
TKSIKKMKHKAKKEENNFSNDSSKVTKELEKTDYIHVRARAAQATDSHSIAEAVAREKISERMKFLQDLVP
GCDKITGKAGMLDEIINYVQSLQRQIEFLSMKLAIVNPRPDFDMDDIFAKEVASTPMTVVPSPEMVLSGYSH
EMVHSGYSSEMVNSGYLHVNPMQQVNTSSDPLSCFNNGEAPSMWDSHVQNLYGNLGV

> HA-TALE(*ng2*, C63)-wNES-cib1-mutNLS-mutbHLH

SRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLRAADAPPPTMR
VAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFTHAH
IVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLK
IAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIA
SNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNI
GGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGG
KQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQ
ALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALE

TVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQ
RLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLL
PVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPALESIVAQLSRPD
PALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAASLYPERLRRILTNGAIGG
DLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPMMYGETTVEGDSR
LSISPETTLGTGNFKAAKFDTETKDCNEAAKKMTMNRDDLVEEGEEEKSKITEQNNGSTKSIKKMKHKAK
KEENNFSNDSSKVTKELEKTDYIHVRARAAQATDSHSIAEAVAREKISERMKFLQDLVPGCDKITGKAGML
DEIINYVQSLQRQIEFLSMKLAIVNPRPDFDMDDIFAKEVASTPMTVVPSPEMVLSGYSHEMVHSGYSSEMV
NSGYLHVNPMQQVNTSSDPLSCFNNGEAPSMWDSHVQNLYGNLGV

> HA-TALE(*ng2,* C63)-GS-cib1Δ1-mutNLS

YPYDVPDYASRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLR
AADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEA
LVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPP
LQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLT
PEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVV
AIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAI
ASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
IGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGG
KQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPA
LESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAASGGGG
SGGGGSNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPM
MYGETTVEGDSRLSISPETTLGTGNFKAAKFDTETKDCNEAAKKMTMNRDDLVEEGEEEKSKITEQNNGS
TKSIKKMKHKAKKEENNFSNDSSKVTKELEKTDYIHVRARRGQATDSHSIAERVRREKISERMKFLQDLVP
GCDKITGKAGMLDEIINYVQSLQRGGSVASTPMTVVPSPEMVLSGYSHEMVHSGYSSEMVNSGYLHVNPM
QQVNTSSDPLSCFNNGEAPSMWDSHVQNLYGNLGV

> HA-TALE(*ng2,* C63)-wNLS-cib1Δ1-mutNLS

YPYDVPDYASRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLR
AADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEA
LVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPP
LQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLT
PEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVV
AIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAI
ASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
IGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGG
KQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPA
LESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAASLYPER
LRRILTNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPMM
YGETTVEGDSRLSISPETTLGTGNFKAAKFDTETKDCNEAAKKMTMNRDDLVEEGEEEKSKITEQNNGSTK
SIKKMKHKAKKEENNFSNDSSKVTKELEKTDYIHVRARRGQATDSHSIAERVRREKISERMKFLQDLVPGC
DKITGKAGMLDEIINYVQSLQRGGSGEEEKSKITEQNNGSTKSIKKMKHKAKKEENNFSNDSSKVTKELEK
TDYIHVRARRGQATDSHSIAERVRREKISERMKFLQDLVPGCDKITGKAGMLDEIINYVQSLQRGGSVASTP

MTVVPSPEMVLSGYSHEMVHSGYSSEMVNSGYLHVNPMQQVNTSSDPLSCFNNGEAPSMWDSHVQNLY
GNLGV

> HA-TALE(*ng2,* C63)-GS-cib1Δ2-mutNLS

YPYDVPDYASRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLR
AADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEA
LVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPP
LQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLT
PEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVV
AIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAI
ASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
IGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGG
KQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPA
LESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAASGGGG
SGGGGSNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPM
MYGETTVEGDSRLSISPETTLGTGNFKAAKFDTETKDCNEAAKKMTMNRDDLVEEGEEEKSKITEQNNGS
TKSIKKMKHKAKKEENNFSNDSSKVTKELEKTDYIHVRARRGQATDSHSIAERVRREKISERMKFLQDLVP
GCDKITGKAGMLDEIINYVQSLQRQIEFLSMKLAIVNPRPDFDMDDIFAKEVASTPMTVVPSPEMVLSGYG
GSPLSCFNNGEAPSMWDSHVQNLYGNLGV

> HA-TALE(*ng2,* C63)-wNES-cib1Δ2-mutNLS

YPYDVPDYASRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLR
AADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEA
LVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPP
LQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLT
PEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVV
AIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAI
ASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
IGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGG
KQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPA
LESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAASLYPER
LRRILTNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPMM
YGETTVEGDSRLSISPETTLGTGNFKAAKFDTETKDCNEAAKKMTMNRDDLVEEGEEEKSKITEQNNGSTK
SIKKMKHKAKKEENNFSNDSSKVTKELEKTDYIHVRARRGQATDSHSIAERVRREKISERMKFLQDLVPGC
DKITGKAGMLDEIINYVQSLQRQIEFLSMKLAIVNPRPDFDMDDIFAKEVASTPMTVVPSPEMVLSGYGGSP
LSCFNNGEAPSMWDSHVQNLYGNLGV

> HA-TALE(*ng2,* C63)-NLS-cib1-mutNLS-mutbHLH

YPYDVPDYASRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLR
AADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEA
LVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPP
LQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLT

PEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVV
AIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAI
ASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
IGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGG
KQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPA
LESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAASSPKKK
RKVEASNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPM
MYGETTVEGDSRLSISPETTLGTGNFKAAKFDTETKDCNEAAKKMTMNRDDLVEEGEEEKSKITEQNNGS
TKSIKKMKHKAKKEENNFSNDSSKVTKELEKTDYIHVRARAAQATDSHSIAEAVAREKISERMKFLQDLVP
GCDKITGKAGMLDEIINYVQSLQRQIEFLSMKLAIVNPRPDFDMDDIFAKEVASTPMTVVPSPEMVLSGYSH
EMVHSGYSSEMVNSGYLHVNPMQQVNTSSDPLSCFNNGEAPSMWDSHVQNLYGNLGV

> HA-TALE(*ng2,* C63)-NLS-cib1Δ1-mutNLS

YPYDVPDYASRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLR
AADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEA
LVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPP
LQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLT
PEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVV
AIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAI
ASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
IGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGG
KQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPA
LESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAASSPKKK
RKVEASNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPM
MYGETTVEGDSRLSISPETTLGTGNFKAAKFDTETKDCNEAAKKMTMNRDDLVEEGEEEKSKITEQNNGS
TKSIKKMKHKAKKEENNFSNDSSKVTKELEKTDYIHVRARRGQATDSHSIAERVRREKISERMKFLQDLVP
GCDKITGKAGMLDEIINYVQSLQRGGSVASTPMTVVPSPEMVLSGYSHEMVHSGYSSEMVNSGYLHVNPM
QQVNTSSDPLSCFNNGEAPSMWDSHVQNLYGNLGV

> HA-TALE(*ng2,* C63)-NLS-cib1Δ2-mutNLS

YPYDVPDYASRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLR
AADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEA
LVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPP
LQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLT
PEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVV
AIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAI
ASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
IGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGG
KQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPA
LESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAASLYPER
LRRILTNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPMM
YGETTVEGDSRLSISPETTLGTGNFKAAKFDTETKDCNEAAKKMTMNRDDLVEEGEEEKSKITEQNNGSTK
SIKKMKHKAKKEENNFSNDSSKVTKELEKTDYIHVRARRGQATDSHSIAERVRREKISERMKFLQDLVPGC

DKITGKAGMLDEIINYVQSLQRQIEFLSMKLAIVNPRPDFDMDDIFAKEVASTPMTVVPSPEMVLSGYGGSP
LSCFNNGEAPSMWDSHVQNLYGNLGV

> HA-TALE(*ng2,* C63)-GS-iNES1-cib1-mutNLS

YPYDVPDYASRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLR
AADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEA
LVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPP
LQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLT
PEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVV
AIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAI
ASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
IGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGG
KQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPA
LESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAASGGGG
SGGGGSNGAIGGDLLLNFPDMSVLERQRAHLKYLLYPERLRRILTNPTFDSPLAGFFADSSMITGGEMDSYL
STAGLNLPMMYGETTVEGDSRLSISPETTLGTGNFKAAKFDTETKDCNEAAKKMTMNRDDLVEEGEEEKS
KITEQNNGSTKSIKKMKHKAKKEENNFSNDSSKVTKELEKTDYIHVRARRGQATDSHSIAERVRREKISER
MKFLQDLVPGCDKITGKAGMLDEIINYVQSLQRQIEFLSMKLAIVNPRPDFDMDDIFAKEVASTPMTVVPSP
EMVLSGYSHEMVHSGYSSEMVNSGYLHVNPMQQVNTSSDPLSCFNNGEAPSMWDSHVQNLYGNLGV

> HA-TALE(*ng2,* C63)-GS-iNES2-cib1-mutNLS

YPYDVPDYASRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLR
AADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEA
LVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPP
LQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLT
PEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVV
AIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAI
ASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
IGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGG
KQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPA
LESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAASGGGG
SGGGGSNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDLYPERLRRILTSYL
STAGLNLPMMYGETTVEGDSRLSISPETTLGTGNFKAAKFDTETKDCNEAAKKMTMNRDDLVEEGEEEKS
KITEQNNGSTKSIKKMKHKAKKEENNFSNDSSKVTKELEKTDYIHVRARRGQATDSHSIAERVRREKISER
MKFLQDLVPGCDKITGKAGMLDEIINYVQSLQRQIEFLSMKLAIVNPRPDFDMDDIFAKEVASTPMTVVPSP
EMVLSGYSHEMVHSGYSSEMVNSGYLHVNPMQQVNTSSDPLSCFNNGEAPSMWDSHVQNLYGNLGV

> HA-TALE(*ng2,* C63)-GS-iNES3-cib1-mutNLS

YPYDVPDYASRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLR
AADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEA
LVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPP
LQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLT

PEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVV
AIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAI
ASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
IGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGG
KQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPA
LESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAASGGGG
SGGGGSNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPM
MYGETTVEGLYPERLRRILTDSRLSISPETTLGTGNFKAAKFDTETKDCNEAAKKMTMNRDDLVEEGEEEK
SKITEQNNGSTKSIKKMKHKAKKEENNFSNDSSKVTKELEKTDYIHVRARRGQATDSHSIAERVRREKISER
MKFLQDLVPGCDKITGKAGMLDEIINYVQSLQRQIEFLSMKLAIVNPRPDFDMDDIFAKEVASTPMTVVPSP
EMVLSGYSHEMVHSGYSSEMVNSGYLHVNPMQQVNTSSDPLSCFNNGEAPSMWDSHVQNLYGNLGV

> HA-TALE(*ng2,* C63)-GS-iNES4-cib1-mutNLS

YPYDVPDYASRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLR
AADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEA
LVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPP
LQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLT
PEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVV
AIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAI
ASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
IGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGG
KQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPA
LESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAASGGGG
SGGGGSNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPM
MYGETTVEGDSRLSISPETTLGTGNFKAAKFDTETKDCNEAAAAKKMTMNRDDLVEEGLYPERLRRILTEE
EKSKITEQNNGSTKSIKKMKHKAKKEENNFSNDSSKVTKELEKTDYIHVRARRGQATDSHSIAERVRREKIS
ERMKFLQDLVPGCDKITGKAGMLDEIINYVQSLQRQIEFLSMKLAIVNPRPDFDMDDIFAKEVASTPMTVV
PSPEMVLSGYSHEMVHSGYSSEMVNSGYLHVNPMQQVNTSSDPLSCFNNGEAPSMWDSHVQNLYGNLGV

> HA-TALE(*ng2,* C63)-GS-iNES5-cib1-mutNLS

YPYDVPDYASRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLR
AADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEA
LVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPP
LQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLT
PEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVV
AIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAI
ASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
IGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGG
KQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPA
LESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAASGGGG
SGGGGSNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPM
MYGETTVEGDSRLSISPETTLGTGNFKAAKFDTETKDCNEAAKKMTMNRDDLVEEGEEEKSKITEQNNGS
TKSIKKLYPERLRRILTMKHKAKKEENNFSNDSSKVTKELEKTDYIHVRARRGQATDSHSIAERVRREKISE

RMKFLQDLVPGCDKITGKAGMLDEIINYVQSLQRQIEFLSMKLAIVNPRPDFDMDDIFAKEVASTPMTVVPS
PEMVLSGYSHEMVHSGYSSEMVNSGYLHVNPMQQVNTSSDPLSCFNNGEAPSMWDSHVQNLYGNLGV

> HA-TALE(*ng2,* C63)-GS-iNES6-cib1-mutNLS

YPYDVPDYASRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLR
AADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEA
LVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPP
LQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLT
PEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVV
AIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAI
ASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
IGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGG
KQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPA
LESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAASGGGG
SGGGGSNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPM
MYGETTVEGDSRLSISPETTLGTGNFKAAKFDTETKDCNEAAKKMTMNRDDLVEEGEEEKSKITEQNNGS
TKSIKKMKHKAKKEENNFSNDSSKVTLYPERLRRILTKELEKTDYIHVRARRGQATDSHSIAERVRREKISE
RMKFLQDLVPGCDKITGKAGMLDEIINYVQSLQRQIEFLSMKLAIVNPRPDFDMDDIFAKEVASTPMTVVPS
PEMVLSGYSHEMVHSGYSSEMVNSGYLHVNPMQQVNTSSDPLSCFNNGEAPSMWDSHVQNLYGNLGV

> HA-TALE(*ng2,* C63)-NLS-cib1Δ1

MYPYDVPDYASRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGL
RAADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHE
ALVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRG
PPLQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQA
HGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGL
TPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPE
QVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQV
VAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVA
IASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIAS
NIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGG
GKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRP
ALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAASSPKK
KRKVEASNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPM
MYGETTVEGDSRLSISPETTLGTGNFKKRKFDTETKDCNEKKKKMTMNRDDLVEEGEEEKSKITEQNNGST
KSIKKMKHKAKKEENNFSNDSSKVTKELEKTDYIHVRARRGQATDSHSIAERVRREKISERMKFLQDLVPG
CDKITGKAGMLDEIINYVQSLQRGGSVASTPMTVVPSPEMVLSGYSHEMVHSGYSSEMVNSGYLHVNPMQ
QVNTSSDPLSCFNNGEAPSMWDSHVQNLYGNLGV

> HA-TALE(*ng2,* C63)-NLS-cib1Δ2

YPYDVPDYASRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLR
AADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEA
LVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPP
LQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLT

PEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVV
AIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAI
ASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
IGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGG
KQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPA
LESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAASSPKKK
RKVEASNGAIGGDLLLNFPDMSVLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPM
MYGETTVEGDSRLSISPETTLGTGNFKKRKFDTETKDCNEKKKKMTMNRDDLVEEGEEEKSKITEQNNGST
KSIKKMKHKAKKEENNFSNDSSKVTKELEKTDYIHVRARRGQATDSHSIAERVRREKISERMKFLQDLVPG
CDKITGKAGMLDEIINYVQSLQRQIEFLSMKLAIVNPRPDFDMDDIFAKEVASTPMTVVPSPEMVLSGYGGS
PLSCFNNGEAPSMWDSHVQNLYGNLGV

> **alpha-importin-NLS-CRY2PHR-NLS-VP64_2A_GFP**

MKRPAATKKAGQAKKKKKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASR
WWMKQSLAHLSQSLKALGSDLTLIKTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGI
SVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKCLDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLE
NEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSKKVVGNSTSLLSPYLHFGEISVRHVFQCAR
MKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFFPWDADVDKFKAWRQGRTG
YPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLECDILGWQYISGSIPD
GHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPIVDIDTA
RELLAKAISRTREAQIMIGAAPASPKKKRKVEASGSGRADALDDFDLDMLGSDALDDFDLDMLGSDALDD
FDLDMLGSDALDDFDLDMLINSRGSGEGRGSLLTCGDVEENPGPVSKGEELFTGVVPILVELDGDVNGHKF
SVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTI
FFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRH
NIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYKV

> **mutNES-CRY2PHR-NLS-VP64_2A_GFP**

MEQKLISEEDLKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSL
AHLSQSLKAAGSDATLIKTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGD
LLYEPWEIYCEKGKPFTSFNSYWKKCLDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNA
LLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSKKVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARD
KNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFFPWDADVDKFKAWRQGRTGYPLVDAGMR
ELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLECDILGWQYISGSIPDGHELDRLDNP
ALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPIVDIDTARELLAKAISR
TREAQIMIGAAPASPKKKRKVEASGSGRADALDDFDLDMLGSDALDDFDLDMLGSDALDDFDLDMLGSD
ALDDFDLDMLINSRGSGEGRGSLLTCGDVEENPGPVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGD
ATYGKLTLKFICTTGKLPVPWPTLVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNY
KTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQ
LADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYKV

> CRY2PHR-NLS-VP64-NLS_2A_GFP

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKA
LGSDLTLIKTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIY
CEKGKPFTSFNSYWKKCLDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSP
GWSNADKLLNEFIEKQLIDYAKNSKKVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEES
ADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFFPWDADVDKFKAWRQGRTGYPLVDAGMRELWATGW
MHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLECDILGWQYISGSIPDGHELDRLDNPALQGAKY
DPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPIVDIDTARELLAKAISRTREAQIMI
GAAPASPKKKRKVEASGSGRADALDDFDLDMLGSDALDDFDLDMLGSDALDDFDLDMLGSDALDDFDL
DMLINSPKKKRKVEASSRGSGEGRGSLLTCGDVEENPGPVSKGEELFTGVVPILVELDGDVNGHKFSVSGE
GEGDATYGKLTLKFICTTGKLPVPWPTLVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDD
GNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDG
SVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYKV

> Neurog2-TALE(N240,C63)-PYL

MSRTRLPSPPAPSPAFSADSFSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLRAADAPPPT
MRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFT
HAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQ
LLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASHNGGKQALETVQRLLPVLCQAHGLTPEQV
VAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAI
ASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHNGGKQALETVQRLLPVLCQAHGLTPEQVVAIAS
NIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHN
GGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGG
KQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQA
LETVQRLLPVLCQAHGLTPEQVVAIASNGGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDA
VKKGLPHAPALIKRTNRRIPERTSHRVAASMANSESSSSPVNEEENSQRISTLHHQTMPSDLTQDEFTQLSQS
IAEFHTYQLGNGRCSSLLAQRIHAPPETVWSVVRRFDRPQIYKHFIKSCNVSEDFEMRVGCTRDVNVISGLP
ANTSRERLDLLDDDRRVTGFSITGGEHRLRNYKSVTTVHRFEKEEEEERIWTVVLESYVVDVPEGNSEEDT
RLFADTVIRLNLQKLASITEAMNRNNNNNNNSSQVR

>ABI-NLS-VP64

MVPLYGFTSICGRRPEMEAAVSTIPRFLQSSSGSMLDGRFDPQSAAHFFGVYDGHGGSQVANYCRERMHL
ALAEEIAKEKPMLCDGDTWLEKWKKALFNSFLRVDSEIESVAPETVGSTSVVAVVFPSHIFVANCGDSRAV
LCRGKTALPLSVDHKPDREDEAARIEAAGGKVIQWNGARVFGVLAMSRSIGDRYLKPSIIPDPEVTAVKRV
KEDDCLILASDGVWDVMTDEEACEMARKRILLWHKKNAVAGDASLLADERRKEGKDPAAMSAAEYLSK
LAIQRGSKDNISVVVVDLKPRRKLKSKPLNASPKKKRKVEASGSGRADALDDFDLDMLGSDALDDFDLDM
LGSDALDDFDLDMLGSDALDDFDLDMLIN

>hSpCas9(D10A,H840A)-Linker-NLS-VP64

MDKKYSIGLAIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRR
YTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLV
DSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSAR
LSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQY
ADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNG
YAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYP
FLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLP
NEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIE

CFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDK
VMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQG
DSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGI
KELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTR
SDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITK
HVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEI
VWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYS
VLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRML
ASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADAN
LDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRI
DLSQLGGDSAGGGGSGGGGSGGGGSGPKKKRKVAAAGSGRADALDDFDLDMLGSDALDDFDLDMLGSD
ALDDFDLDMLGSDALDDFDLDMLIN

>SID4X-NLS-FLAG-Linker-hSpCas9(D10A,H840A)-NLS

MGSGMNIQMLLEAADYLERREREAEHGYASMLPGSGMNIQMLLEAADYLERREREAEHGYASMLPGSG
MNIQMLLEAADYLERREREAEHGYASMLPGSGMNIQMLLEAADYLERREREAEHGYASMLPSRSAGPKK
KRKVAAADYKDDDDKSRLEPGEKPYKCPECGKSFSQSGALTRHQRTHTRDKKYSIGLAIGTNSVGWAVIT
DEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKV
DDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFR
GHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLF
GNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNT
EITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEK
MDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPL
ARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTK
VKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDL
LKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLING
IRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTV
KVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLY
LYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKN
YWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIRE
VKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMI
AKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNI
VKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELL
GITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFL
YLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAEN
IIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDKRPAATKKAGQAK
KKK

Epigenetic effector domain sequences

>hs_NCoR
ASSPKKKRKVEASMNGLMEDPMKVYKDRQFMNVWTDHEKEIFKDKFIQHPKNFGLIASYLERKSVPDCVL
YYYLTKKNENYKEF

>pf_Sir2A
ASSPKKKRKVEASMGNLMISFLKKDTQSITLEELAKIIKKCKHVVALTGSGTSAESNIPSFRGSSNSIWSKYD
PRIYGTIWGFWKYPEKIWEVIRDISSDYEIEINNGHVALSTLESLGYLKSVVTQNVDGLHEASGNTKVISLHG

NVFEAVCCTCNKIVKLNKIMLQKTSHFMHQLPPECPCGGIFKPNIILFGEVVSSDLLKEAEEEIAKCDLLLVI
GTSSTVSTATNLCHFACKKKKKIVEINISKTYITNKMSDYHVCAKFSELTKVANILKGSSEKNKKIMEF

>nc_DIM5
ASSPKKKRKVEASMEKAFRPHFFNHGKPDANPKEKKNCHWCQIRSFATHAQLPISIVNREDDAFLNPNFRFI
DHSIIGKNVPVADQSFRVGCSCASDEECMYSTCQCLDEMAPDSDEEADPYTRKKRFAYYSQGAKKGLLRD
RVLQSQEPIYECHQGCACSKDCPNRVVERGRTVPLQIFRTKDRGWGVKCPVNIKRGQFVDRYLGEIITSEEA
DRRRAESTIARRKDVYLFALDKFSDPDSLDPLLAGQPLEVDGEYMSGPTRFINHSCDPNMAIFARVGDHAD
KHIHDLALFAIKDIPKGTELTFDYVNGLTGLESDAHDPSKISEMTKCLCGTAKCRGYLWEF

>sc_HST2
ASSPKKKRKVEASTEMSVRKIAAHMKSNPNAKVIFMVGAGISTSCGIPDFRSPGTGLYHNLARLKLPYPEA
VFDVDFFQSDPLPFYTLAKELYPGNFRPSKFHYLLKLFQDKDVLKRVYTQNIDTLERQAGVKDDLIIEAHGS
FAHCHCIGCGKVYPPQVFKSKLAEHPIKDFVKCDVCGELVKPAIVFFGEDLPDSFSETWLNDSEWLREKITT
SGKHPQQPLVIVVGTSLAVYPFASLPEEIPRKVKRVLCNLETVGDFKANKRPTDLIVHQYSDEFAEQLVEEL
GWQEDFEKILTAQGGMGEF

>hs_SIRT3
ASSPKKKRKVEASMVGAGISTPSGIPDFRSPGSGLYSNLQQYDLPYPEAIFELPFFFHNPKPFFTLAKELYPG
NYKPNVTHYFLRLLHDKGLLLRLYTQNIDGLERVSGIPASKLVEAHGTFASATCTVCQRPFPGEDIRADVM
ADRVPRCPVCTGVVKPDIVFFGEPLPQRFLLHVVDFPMADLLLILGTSLEVEPFASLTEAVRSSVPRLLINRD
LVGPLAWHPRSRDVAQLGDVVHGVESLVELLGWTEEMRDLVQRETGKLDGPDKEF

>hs_NIPP1
ASSPKKKRKVEASMAAAANSGSSLPLFDCPTWAGKPPPGLHLDVVKGDKLIEKLIIDEKKYYLFGRNPDLC
DFTIDHQSCSRVHAALVYHKHLKRVFLIDLNSTHGTFLGHIRLEPHKPQQIPIDSTVSFGASTRAYTLREKPQ
TLPSAVKGDEKMGGEDDELKGLLGLPEEETELDNLTEFNTAHNKRISTLTIEEGNLDIQRPKRKRKNSRVTF
SEDDEIINPEDVDPSVGRFRNMVQTAVVPVKKKRVEGPGSLGLEESGSRRMQNFAFSGGLYGGLPPTHSEA
GSQPHGIHGTALIGGLPMPYPNLAPDVDLTPVVPSAVNMNPAPNPAVYNPEAVNEEF

>ct_NUE
ASSPKKKRKVEASMTTNSTQDTLYLSLHGGIDSAIPYPVRRVEQLLQFSFLPELQFQNAAVKQRIQRLCYRE
EKRLAVSSLAKWLGQLHKQRLRAPKNPPVAICWINSYVGYGVFARESIPAWSYIGEYTGILRRRQALWLDE
NDYCFRYPVPRYSFRYFTIDSGMQGNVTRFINHSDNPNLEAIGAFENGIFHIIIRAIKDILPGEELCYHYGPLY
WKHRKKREEFVPQEEEF

>hs_MBD2b
ASSPKKKRKVEASARYLGNTVDLSSFDFRTGKMMPSKLQKNKQRLRNDPLNQNKGKPDLNTTLPIRQTASI
FKQPVTKVTNHPSNKVKSDPQRMNEQPRQLFWEKRLQGLSASDVTEQIIKTMELPKGLQGVGPGSNDETL
LSAVASALHTSSAPITGQVSAAVEKNPAVWLNTSQPLCKAFIVTDEDIRKQEERVQQVRKILEDALMADILS
RAADTEEMDIEMDSGDEAEF

>ca_HST2
ASSPKKKRKVEASMPSLDDILKPVAEAVKNGKKVTFFNGAGISTGAGIPDFRSPDTGLYANLAKLNLPFAE
AVFDIDFFKEDPKPFYTLAEELYPGNFAPTKFHHFIKLLQDQGSLKRVYTQNIDTLERLAGVEDKYIVEAHG
SFASNHCVDCHKEMTTETLKTYMKDKKIPSCQHCEGYVKPDIVFFGEGLPVKFFDLWEDDCEDVEVAIVA
GTSLTVFPFASLPGEVNKKCLRVLVNKEKVGTFKHEPRKSDIIALHDCDIVAERLCTLLGLDDKLNEVYEKE
KIKYSKAETKEIKMHEIEDKLKEEAHLKEDKHTTKVDKKEKQNDANDKELEQLIDKAKAEF

>hs_PHF19
ASSPKKKRKVEASMENRALDPGTRDSYGATSHLPNKGALAKVKNNFKDLMSKLTEGQYVLCRWTDGLY
YLGKIKRVSSSKQSCLVTFEDNSKYWVLWKDIQHAGVPGEEPKCNICLGKTSGPLNEILICGKCGLGYHQQ
CHIPIAGSADQPLLTPWFCRRCIFALAVRKGGALKKGAIARTLQAVKMVLSYQPEELEWDSPHRTNQQQCY
CYCGGPGEWYLRMLQCYRCRQWFHEACTQCLNEPMMFGDRFYLFFCSVCNQGPGGSGSDSSAEGASVPE
RPDEGIDSHTFESISEDDSSLSHLKSSITNYFGAAGRLACGEKYQVLARRVTPEGKVQYLVEWEGTTPYEF

>hs_HDAC11
ASSPKKKRKVEASMLHTTQLYQHVPETRWPIVYSPRYNITFMGLEKLHPFDAGKWGKVINFLKEEKLLSDS
MLVEAREASEEDLLVVHTRRYLNELKWSFAVATITEIPPVIFLPNFLVQRKVLRPLRTQTGGTIMAGKLAVE
RGWAINVGGGFHHCSSDRGGGFCAYADITLAIKFLFERVEGISRATIIDLDAHQGNGHERDFMDDKRVYIM
DVYNRHIYPGDRFAKQAIRRKVELEWGTEDDEYLDKVERNIKKSLQEHLPDVVVYNAGTDILEGDRLGGL
SISPAGIVKRDELVFRMVRGRRVPILMVTSGGYQKRTARIIADSILNLFGLGLIGPESPSVSAQNSDTPLLPPA
VPEF

>ml_MesoLo4
ASSPKKKRKVEASMPLQIVHHPDYDAGFATNHRFPMSKYPLLMEALRARGLASPDALNTTEPAPASWLKL
AHAADYVDQVISCSVPEKIEREIGFPVGPRVSLRAQLATGGTILAARLALRHGIACNTAGGSHHARRAQGA
GFCTFNDVAVASLVLLDEGAAQNILVVDLDVHQGDGTADILSDEPGVFTFSMHGERNYPVRKIASDLDIAL
PDGTGDAAYLRRLATILPELSARARWDIVFYNAGVDVHAEDRLGRLALSNGGLRARDEMVIGHFRALGIP
VCGVIGGGYSTDVPALASRHAILFEVASTYAEF

>pbcv1_vSET
ASSPKKKRKVEASMFNDRVIVKKSPLGGYGVFARKSFEKGELVEECLCIVRHNDDWGTALEDYLFSRKNM
SAMALGFGAIFNHSKDPNARHELTAGLKRMRIFTIKPIAIGEEITISYGDDYWLSRPRLTQNEF

>at_KYP
ASSPKKKRKVEASDISGGLEFKGIPATNRVDDSPVSPTSGFTYIKSLIIEPNVIIPKSSTGCNCRGSCTDSKKCA
CAKLNGGNFPYVDLNDGRLIESRDVVFECGPHCGCGPKCVNRTSQKRLRFNLEVFRSAKKGWAVRSWEYI
PAGSPVCEYIGVVRRTADVDTISDNEYIFEIDCQQTMQGLGGRQRRLRDVAVPMNNGVSQSSEDENAPEFC
IDAGSTGNFARFINHSCEPNLFVQCVLSSHQDIRLARVVLFAADNISPMQELTYDYGYALDSVHEF

>tg_TgSET8
ASSPKKKRKVEASASRRTGEFLRDAQAPSRWLKRSKTGQDDGAFCLETWLAGAGDDAAGGERGRDREGA
ADKAKQREERRQKELEERFEEMKVEFEEKAQRMIARRAALTGEIYSDGKGSKKPRVPSLPENDDDALIEIII
DPEQGILKWPLSVMSIRQRTVIYQECLRRDLTACIHLTKVPGKGRAVFAADTILKDDFVVEYKGELCSEREA
REREQRYNRSKVPMGSFMFYFKNGSRMMAIDATDEKQDFGPARLINHSRRNPNMTPRAITLGDFNSEPRLI
FVARRNIEKGEELLVDYGERDPDVIKEHPWLNSEF

>hs_SIRT6
ASSPKKKRKVEASMSVNYAAGLSPYADKGKCGLPEIFDPPEELERKVWELARLVWQSSSVVFHTGAGISTA
SGIPDFRGPHGVWTMEERGLAPKFDTTFESARPTQTHMALVQLERVGLLRFLVSQNVDGLHVRSGFPRDK
LAELHGNMFVEECAKCKTQYVRDTVVGTMGLKATGRLCTVAKARGLRACRGELRDTILDWEDSLPDRDL
ALADEASRNADLSITLGTSLQIRPSGNLPLATKRRGGRLVIVNLQPTKHDRHADLRIHGYVDEVMTRLMKH
LGLEIPAWDGPRVLERALPPLEF

>ce_Set1
ASSPKKKRKVEASMKVAAKKLATSRMRKDRAAAASPSSDIENSENPSSLASHSSSSGRMTPSKNTRSRKGV
SVKDVSNHKITEFFQVRRSNRKTSKQISDEAKHALRDTVLKGTNERLLEVYKDVVKGRGIRTKVNFEKGDF
VVEYRGVMMEYSEAKVIEEQYSNDEEIGSYMYFFEHNNKKWCIDATKESPWKGRLINHSVLRPNLKTKVV
EIDGSHHLILVARRQIAQGEELLYDYGDRSAETIAKNPWLVNTEF

>mm_G9a
ASSPKKKRKVEASVRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHC
TCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRSCKNRVVQSGIKVRLQLYRT
AKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCD
PNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRL
ARLDPHPELLPDLSSLPPINTEF

>hs_SIRT5
ASSPKKKRKVEASSSSMADFRKFFAKAKHIVIISGAGVSAESGVPTFRGAGGYWRKWQAQDLATPLAFAH
NPSRVWEFYHYRREVMGSKEPNAGHRAIAECETRLGKQGRRVVVITQNIDELHRKAGTKNLLEIHGSLFKT
RCTSCGVVAENYKSPICPALSGKGAPEPGTQDASIPVEKLPRCEEAGCGGLLRPHVVWFGENLDPAILEEVD

RELAHCDLCLVVGTSSVVYPAAMFAPQVAARGVPVAEFNTETTPATNRFRFHFQGPCGTTLPEALACHEN
ETVSEF

>xl_HDAC8
ASSPKKKRKVEASMSRVVKPKVASMEEMAAFHTDAYLQHLHKVSEEGDNDDPETLEYGLGYDCPITEGIY
DYAAAVGGATLTAAEQLIEGKTRIAVNWPGGWHHAKKDEASGFCYLNDAVLGILKLREKFDRVLYVDM
DLHHGDGVEDAFSFTSKVMTVSLHKFSPGFFPGTGDVSDIGLGKGRYYSINVPLQDGIQDDKYYQICEGVL
KEVFTTFNPEAVVLQLGADTIAGDPMCSFNMTPEGIGKCLKYVLQWQLPTLILGGGGYHLPNTARCWTYL
TALIVGRTLSSEIPDHEFFTEYGPDYVLEITPSCRPDRNDTQKVQEILQSIKGNLKRVVEF

>mm_HP1a
ASSPKKKRKVEASMKEGENNKPREKSEGNKRKSSFSNSADDIKSKKKREQSNDIARGFERGLEPEKIIGATD
SCGDLMFLMKWKDTDEADLVLAKEANVKCPQIVIAFYEERLTWHAYPEDAENKEKESAKSEF

>at_HDT1
ASSPKKKRKVEASMEFWGIEVKSGKPVTVTPEEGILIHVSQASLGECKNKKGEFVPLHVKVGNQNLVLGTL
STENIPQLFCDLVFDKEFELSHTWGKGSVYFVGYKTPNIEPQGYSEEEEEEEEEVPAGNAAKAVAKPKAKP
AEVKPAVDDEEDESDSDGMDEDDSDGEDSEEEEPTPKKPASSKKRANETTPKAPVSAKKAKVAVTPQKTD
EKKKGGKAANQSEF

>mm_SAll
ASSPKKKRKVEASMSRRKQAKPQHFQSDPEVASLPRRDGDTEKGQPSRPTKSKDAHVCGRCCAEFFELSDL
LLHKKSCTKNQLVLIVNESPASPAKTFPPGPSLNDEF

>hs_SETD8
ASSPKKKRKVEASSCDSTNAAIAKQALKKPIKGKQAPRKKAQGKTQQNRKLTDFYPVRRSSRKSKAELQSE
ERKRIDELIESGKEEGMKIDLIDGKGRGVIATKQFSRGDFVVEYHGDLIEITDAKKREALYAQDPSTGCYMY
YFQYLSKTYCVDATRETNRLGRLINHSKCGNCQTKLHDIDGVPHLILIASRDIAAGEELLYDYGDRSKASIE
AFPWLKHEF

>sc_RPD3
ASSPKKKRKVEASRRVAYFYDADVGNYAYGAGHPMKPHRIRMAHSLIMNYGLYKKMEIYRAKPATKQE
MCQFHTDEYIDFLSRVTPDNLEMFKRESVKFNVGDDCPVFDGLYEYCSISGGGSMEGAARLNRGKCDVAV
NYAGGLHHAKKSEASGFCYLNDIVLGIIELLRYHPRVLYIDIDVHHGDGVEEAFYTTDRVMTCSFHKYGEF
FPGTGELRDIGVGAGKNYAVNVPLRDGIDDATYRSVFEPVIKKIMEWYQPSAVVLQCGGDSLSGDRLGCF
NLSMEGHANCVNYVKSFGIPMMVVGGGGYTMRNVARTWCFETGLLNNVVLDKDLPYEF

>ec_CobB
ASSPKKKRKVEASMEKPRVLVLTGAGISAESGIRTFRAADGLWEEHRVEDVATPEGFDRDPELVQAFYNA
RRRQLQQPEIQPNAAHLALAKLQDALGDRFLLVTQNIDNLHERAGNTNVIHMHGELLKVRCSQSGQVLDW
TGDVTPEDKCHCCQFPAPLRPHVVWFGEMPLGMDEIYMALSMADIFIAIGTSGHVYPAAGFVHEAKLHGA
HTVELNLEPSQVGNEFAEKYYGPASQVVPEFVEKLLKGLKAGSIAEF
>hs_SUV39H1
ASSPKKKRKVEASNLKCVRILKQFHKDLERELLRRHHRSKTPRHLDPSLANYLVQKAKQRRALRRWEQEL
NAKRSHLGRITVENEVDLDGPPRAFVYINEYRVGEGITLNQVAVGCECQDCLWAPTGGCCPGASLHKFAY
NDQGQVRLRAGLPIYECNSRCRCGYDCPNRVVQKGIRYDLCIFRTDDGRGWGVRTLEKIRKNSFVMEYVG
EIITSEEAERRGQIYDRQGATYLFDLDYVEDVYTVDAAYYGNISHFVNHSCDPNLQVYNVFIDNLDERLPRI
AFFATRTIRAGEELTFDYNMQVDPVDMESTRMDSNFGLAGLPGSPKKRVRIECKCGTESCRKYLFEF

>hs_RCOR1
ASSPKKKRKVEASSNSWEEGSSGSSSDEEHGGGGMRVGPQYQAVVPDFDPAKLARRSQERDNLGMLVWS
PNQNLSEAKLDEYIAIAKEKHGYNMEQALGMLFWHKHNIEKSLADLPNFTPFPDEWTVEDKVLFEQAFSF
HGKTFHRIQQMLPDKSIASLVKFYYSWKKTRTKTSVMDRHARKQKREREESEDELEEANGNNPIDIEVDQN
KESKKEVPPTETVPQVKKEKHSTEF

>hs_sin3a

ASSPKKKRKVEASYKESVHLETYPKERATEGIAMEIDYASCKRLGSSYRALPKSYQQPKCTGRTPLCKEVL
NDTWVSFPSWSEDSTFVSSKKTQYEEHIYRCEDERFELDVVLETNLATIRVLEAIQKKLSRLSAEEQAKFRL
DNTLGGTSEVIHRKALQRIYADKAADIIDGLRKNPSIAVPIVLKRLKMKEEEWREAQRGFNKVWREQNEKY
YLKSLDHQGINFKQNDTKVLRSKSLLNEIESIYDERQEQATEENAGVPVGPHLSLAYEDKQILEDAAALIIH
HVKRQTGIQKEDKYKIKQIMHHFIPDLLFAQRGDLSDVEEEEEEEMDVDEATGAVEF

>at_SUVR4
ASSPKKKRKVEASQSAYLHVSLARISDEDCCANCKGNCLSADFPCTCARETSGEYAYTKEGLLKEKFLDTC
LKMKKEPDSFPKVYCKDCPLERDHDKGTYGKCDGHLIRKFIKECWRKCGCDMQCGNRVVQRGIRCQLQV
YFTQEGKGWGLRTLQDLPKGTFICEYIGEILTNTELYDRNVRSSSERHTYPVTLDADWGSEKDLKDEEALC
LDATICGNVARFINHRCEDANMIDIPIEIETPDRHYYHIAFFTLRDVKAMDELTWDYMIDFNDKSHPVKAFR
CCCGSESCRDRKIKGSQGKSIERRKIVSAKKQQGSKEVSKKRKEF

>rn_MeCP2_NLS
ASSPKKKRKVEASVQVKRVLEKSPGKLLVKMPFQASPGGKGEGGGATTSAQVMVIKRPGRKRKAEADPQ
AIPKKRGRKPGSVVAAAAAEAKKKAVKESSIRSVQETVLPIKKRKTRETVSIEVKEVVKPLLVSTLGEKSGK
GLKTCKSPGRKSKESSPKGRSSSASSPPKKEHHHHHHHAESPKAPMPLLPPPPPPEPQSSEDPISPPEPQDLSS
SICKEEKMPRAGSLESDGCPKEPAKTQPMVAAAATTTTTTTTTVAEKYKHRGEGERKDIVSSSMPRPNREE
PVDSRTPVTERVSEF

>mm_SET-TAF1B
ASSPKKKRKVEASMAPKRQSAILPQPKKPRPAAAPKLEDKSASPGLPKGEKEQQEAIEHIDEVQNEIDRLNE
QASEEILKVEQKYNKLRQPFFQKRSELIAKIPNFWVTTFVNHPQVSALLGEEDEEALHYLTRVEVTEFEDIKS
GYRIDFYFDENPYFENKVLSKEFHLNESGDPSSKSTEIKWKSGKDLTKRSSQTQNKASRKRQHEEPESFFTW
FTDHSDAGADELGEVIKDDIWPNPLQYYLVPDMDDEEGEAEDDDDDDEEEEGLEDIDEEGDEDEGEEDDD
EDEGEEGEEDEGEDDEF

>ce_Set4
ASSPKKKRKVEASMQLHEQIANISVTFNDIPRSDHSMTPTELCYFDDFATTLVVDSVLNFTTHKMSKKRRY
LYQDEYRTARTVMKTFREQRDWTNAIYGLLTLRSVSHFLSKLPPNKLFEFRDHIVRFLNMFILDSGYTIQEC
KRYSQEGHQGAKLVSTGVWSRGDKIERLSGVVCLLSSEDEDSILAQEGSDFSVMYSTRKRCSTLWLGPGA
YINHDCRPTCEFVSHGSTAHIRVLRDMVPGDEITCFYGSEFFGPNNIDCECCTCEKNMNGAFSYLRGNENAE
PIISEKKTKYELRSRSEF

Photostimulation Hardware Control Scripts

The following Arduino script was used to enable the individual control of each 4-well column of a light-stimulated 24-well plate

```
//Basic control code for LITE LED array using Arduino UNO

//LED column address initialization to PWM-ready Arduino outputs
int led1_pin = 3;
int led2_pin = 5;
int led3_pin = 6;
int led4_pin = 9;
int led5_pin = 10;
int led6_pin = 11;

//Maximum setting for Arduino PWM
int uniform_brightness = 255;

//PWM settings for individual LED columns
int led1_brightness = uniform_brightness/2;
int led2_brightness = uniform_brightness/2;
int led3_brightness = uniform_brightness/2;
int led4_brightness = uniform_brightness/2;
int led5_brightness = uniform_brightness/2;
int led6_brightness = uniform_brightness/2;

//'on' time in msec
unsigned long uniform_stim_time = 1000; /

//individual 'on' time settings for LED columns
unsigned long led1_stim_time = uniform_stim_time;
unsigned long led2_stim_time = uniform_stim_time;
unsigned long led3_stim_time = uniform_stim_time;
unsigned long led4_stim_time = uniform_stim_time;
unsigned long led5_stim_time = uniform_stim_time;
unsigned long led6_stim_time = uniform_stim_time;

//'off' time in msec
unsigned long uniform_off_time = 14000;

//individual 'off' time settings for LED columns
unsigned long led1_off_time = uniform_off_time;
unsigned long led2_off_time = uniform_off_time;
unsigned long led3_off_time = uniform_off_time;
unsigned long led4_off_time = uniform_off_time;
unsigned long led5_off_time = uniform_off_time;
unsigned long led6_off_time = uniform_off_time;

unsigned long currentMillis = 0;

//initialize timing and state variables
unsigned long led1_last_change = 0;
unsigned long led2_last_change = 0;
unsigned long led3_last_change = 0;
unsigned long led4_last_change = 0;
unsigned long led5_last_change = 0;
unsigned long led6_last_change = 0;

int led1_state = HIGH;
int led2_state = HIGH;
int led3_state = HIGH;
int led4_state = HIGH;
int led5_state = HIGH;
int led6_state = HIGH;

unsigned long led1_timer = 0;
```

```
unsigned long led2_timer = 0;
unsigned long led3_timer = 0;
unsigned long led4_timer = 0;
unsigned long led5_timer = 0;
unsigned long led6_timer = 0;

void setup() {
  // setup PWM pins for output
  pinMode(led1_pin, OUTPUT);
  pinMode(led2_pin, OUTPUT);
  pinMode(led3_pin, OUTPUT);
  pinMode(led4_pin, OUTPUT);
  pinMode(led5_pin, OUTPUT);
  pinMode(led6_pin, OUTPUT);

  //LED starting state
  analogWrite(led1_pin, led1_brightness);
  analogWrite(led2_pin, led2_brightness);
  analogWrite(led3_pin, led3_brightness);
  analogWrite(led4_pin, led4_brightness);
  analogWrite(led5_pin, led5_brightness);
  analogWrite(led6_pin, led6_brightness);
}

void loop() {
  currentMillis = millis();

  //identical timing loops for the 6 PWM output pins
  led1_timer = currentMillis - led1_last_change;
  if (led1_state == HIGH){ //led state is on
    if (led1_timer >= led1_stim_time){ //TRUE if stim time is complete
      analogWrite(led1_pin, 0); //turn LED off
      led1_state = LOW;        //change LED state variable
      led1_last_change = currentMillis;  //mark time of most recent change
    }
  }
  else{ //led1 state is off
    if (led1_timer >= led1_off_time){ //TRUE if off time is complete
      analogWrite(led1_pin, led1_brightness); //turn LED on
      led1_state = HIGH;                      //change LED state variable
      led1_last_change = currentMillis;      //mark time of most recent change
    }
  }

  led2_timer = currentMillis - led2_last_change;
  if (led2_state == HIGH){
    if (led2_timer >= led2_stim_time){
      analogWrite(led2_pin, 0);
      led2_state = LOW;
      led2_last_change = currentMillis;
    }
  }
  else{ //led2 state is off
    if (led2_timer >= led2_off_time){
      analogWrite(led2_pin, led2_brightness);
      led2_state = HIGH;
      led2_last_change = currentMillis;
    }
  }

  led3_timer = currentMillis - led3_last_change;
  if (led3_state == HIGH){
    if (led3_timer >= led3_stim_time){
      analogWrite(led3_pin, 0);
      led3_state = LOW;
      led3_last_change = currentMillis;
    }
  }
  else{ //led3 state is off
    if (led3_timer >= led3_off_time){
      analogWrite(led3_pin, led3_brightness);
      led3_state = HIGH;
```

```
      led3_last_change = currentMillis;
    }
  }

  led4_timer = currentMillis - led4_last_change;
  if (led4_state == HIGH){
    if (led4_timer >= led4_stim_time){
      analogWrite(led4_pin, 0);
      led4_state = LOW;
      led4_last_change = currentMillis;
    }
  }
  else{ //led4 state is off
    if (led4_timer >= led4_off_time){
      analogWrite(led4_pin, led4_brightness);
      led4_state = HIGH;
      led4_last_change = currentMillis;
    }
  }

  led5_timer = currentMillis - led5_last_change;
  if (led5_state == HIGH){
    if (led5_timer >= led5_stim_time){
      analogWrite(led5_pin, 0);
      led5_state = LOW;
      led5_last_change = currentMillis;
    }
  }
  else{ //led5 state is off
    if (led5_timer >= led5_off_time){
      analogWrite(led5_pin, led5_brightness);
      led5_state = HIGH;
      led5_last_change = currentMillis;
    }
  }

  led6_timer = currentMillis - led6_last_change;
  if (led6_state == HIGH){
    if (led6_timer >= led6_stim_time){
      analogWrite(led6_pin, 0);
      led6_state = LOW;
      led6_last_change = currentMillis;
    }
  }
  else{ //led6 state is off
    if (led6_timer >= led6_off_time){
      analogWrite(led6_pin, led6_brightness);
      led6_state = HIGH;
      led6_last_change = currentMillis;
    }
  }
}
```

Supplementary References

1 Banerjee, R. *et al.* The Signaling State of Arabidopsis Cryptochrome 2 Contains Flavin Semiquinone. *Journal of Biological Chemistry* 282, 14916-14922, doi:10.1074/jbc.M700616200 (2007).

2 Deisseroth, K. Optogenetics. *Nature methods* 8, 26-29, doi:10.1038/nmeth.f.324 (2011).

3 Zhang, F. *et al.* The microbial opsin family of optogenetic tools. *Cell* 147, 1446-1457, doi:10.1016/j.cell.2011.12.004 (2011).

4 Yizhar, O., Fenno, L. E., Davidson, T. J., Mogri, M. & Deisseroth, K. Optogenetics in neural systems. *Neuron* 71, 9-34, doi:10.1016/j.neuron.2011.06.004 (2011).

5 Airan, R. D., Thompson, K. R., Fenno, L. E., Bernstein, H. & Deisseroth, K. Temporally precise in vivo control of intracellular signalling. *Nature* 458, 1025-1029, doi:10.1038/nature07926 (2009).

6 Levskaya, A., Weiner, O. D., Lim, W. A. & Voigt, C. A. Spatiotemporal control of cell signalling using a light-switchable protein interaction. *Nature* 461, 997-1001, doi:10.1038/nature08446 (2009).

7 Yazawa, M., Sadaghiani, A. M., Hsueh, B. & Dolmetsch, R. E. Induction of protein-protein interactions in live cells using light. *Nat Biotechnol* 27, 941-945, doi:10.1038/nbt.1569 (2009).

8 Strickland, D. *et al.* TULIPs: tunable, light-controlled interacting protein tags for cell biology. *Nature methods* 9, 379-384, doi:10.1038/nmeth.1904 (2012).

9 Kennedy, M. J. *et al.* Rapid blue-light-mediated induction of protein interactions in living cells. *Nature methods* 7, 973-975, doi:10.1038/nmeth.1524 (2010).

10 Shimizu-Sato, S., Huq, E., Tepperman, J. M. & Quail, P. H. A light-switchable gene promoter system. *Nat Biotechnol* 20, 1041-1044, doi:10.1038/nbt734 (2002).

11 Ye, H., Daoud-El Baba, M., Peng, R. W. & Fussenegger, M. A synthetic optogenetic transcription device enhances blood-glucose homeostasis in mice. *Science* 332, 1565-1568, doi:10.1126/science.1203535 (2011).

12 Wang, X., Chen, X. & Yang, Y. Spatiotemporal control of gene expression by a light-switchable transgene system. *Nature methods* 9, 266-269, doi:10.1038/nmeth.1892 (2012).

13 Polstein, L. R. & Gersbach, C. A. Light-inducible spatiotemporal control of gene activation by customizable zinc finger transcription factors. *J Am Chem Soc* 134, 16480-16483, doi:10.1021/ja3065667 (2012).

14 Banerjee, R. *et al.* The signaling state of Arabidopsis cryptochrome 2 contains flavin semiquinone. *J Biol Chem* 282, 14916-14922, doi:10.1074/jbc.M700616200 (2007).

15 Witten, Ilana B. *et al.* Recombinase-Driver Rat Lines: Tools, Techniques, and Optogenetic Application to Dopamine-Mediated Reinforcement. *Neuron* 72, 721-733, doi:http://dx.doi.org/10.1016/j.neuron.2011.10.028 (2011).

16 Grieger, J. C., Choi, V. W. & Samulski, R. J. Production and characterization of adeno-associated viral vectors. *Nat Protoc* 1, 1412-1428, doi:10.1038/nprot.2006.207 (2006).

17 Lock M, A. M., Vandenberghe LH, Samanta A, Toelen J, Debyser Z, Wilson JM. Rapid, Simple, and Versatile Manufacturing of Recombinant Adeno-Associated Viral Vectors at Scale. *Human Gene Therapy* 21, 1259-1271, doi:10.1089/hum.2010.055 (2010).

18 Nan, X. *et al.* Transcriptional repression by the methyl-CpG-binding protein MeCP2 involves a histone deacetylase complex. *Nature* 393, 386-389 (1998).

19 Boeke, J., Ammerpohl, O., Kegel, S., Moehren, U. & Renkawitz, R. The minimal repression domain of MBD2b overlaps with the methyl-CpG-binding domain and binds directly to Sin3A. *Journal of Biological Chemistry* 275, 34963-34967 (2000).
20 Laherty, C. D. *et al.* Histone deacetylases associated with the mSin3 corepressor mediate mad transcriptional repression. *Cell* 89, 349-356 (1997).
21 Zhang, J., Kalkum, M., Chait, B. T. & Roeder, R. G. The N-CoR-HDAC3 nuclear receptor corepressor complex inhibits the JNK pathway through the integral subunit GPS2. *Molecular cell* 9, 611-623 (2002).
22 Lauberth, S. M. & Rauchman, M. A conserved 12-amino acid motif in Sall1 recruits the nucleosome remodeling and deacetylase corepressor complex. *Journal of Biological Chemistry* 281, 23922-23931 (2006).
23 Gu, H. & Roizman, B. Herpes simplex virus-infected cell protein 0 blocks the silencing of viral DNA by dissociating histone deacetylases from the CoREST‚ÄìREST complex. *Proceedings of the National Academy of Sciences* 104, 17134-17139 (2007).
24 Ouyang, J., Shi, Y., Valin, A., Xuan, Y. & Gill, G. Direct binding of CoREST1 to SUMO-2/3 contributes to gene-specific repression by the LSD1/CoREST1/HDAC complex. *Molecular cell* 34, 145-154 (2009).
25 Vannier, D., Balderes, D. & Shore, D. Evidence that the transcriptional regulators SIN3 and RPD3, and a novel gene (SDS3) with similar functions, are involved in transcriptional silencing in S. cerevisiae. *Genetics* 144, 1343-1353 (1996).
26 Gregoretti, I., Lee, Y.-M. & Goodson, H. V. Molecular evolution of the histone deacetylase family: functional implications of phylogenetic analysis. *Journal of molecular biology* 338, 17-31 (2004).
27 Gao, L., Cueto, M. A., Asselbergs, F. & Atadja, P. Cloning and functional characterization of HDAC11, a novel member of the human histone deacetylase family. *Journal of Biological Chemistry* 277, 25748-25755 (2002).
28 Wu, K., Tian, L., Malik, K., Brown, D. & Miki, B. Functional analysis of HD2 histone deacetylase homologues in Arabidopsis thaliana. *The Plant Journal* 22, 19-27 (2000).
29 Scher, M. B., Vaquero, A. & Reinberg, D. SirT3 is a nuclear NAD+-dependent histone deacetylase that translocates to the mitochondria upon cellular stress. *Genes & development* 21, 920-928 (2007).
30 Hnisz, D., Schwarzm√ºller, T. & Kuchler, K. Transcriptional loops meet chromatin: a dual‚Äêlayer network controls white‚Äìopaque switching in Candida albicans. *Molecular microbiology* 74, 1-15 (2009).
31 Landry, J. *et al.* The silencing protein SIR2 and its homologs are NAD-dependent protein deacetylases. *Proceedings of the National Academy of Sciences* 97, 5807-5811 (2000).
32 Wilson, J. M., Le, V. Q., Zimmerman, C., Marmorstein, R. & Pillus, L. Nuclear export modulates the cytoplasmic Sir2 homologue Hst2. *EMBO reports* 7, 1247-1251 (2006).
33 Gertz, M. & Steegborn, C. Function and regulation of the mitochondrial Sirtuin isoform Sirt5 in Mammalia. *Biochimica et Biophysica Acta (BBA)-Proteins and Proteomics* 1804, 1658-1665 (2010).
34 Zhu, A. Y. *et al.* Plasmodium falciparum Sir2A preferentially hydrolyzes medium and long chain fatty acyl lysine. *ACS chemical biology* 7, 155-159 (2011).
35 Tennen, R. I., Berber, E. & Chua, K. F. Functional dissection of SIRT6: identification of domains that regulate histone deacetylase activity and chromatin localization. *Mechanisms of ageing and development* 131, 185-192 (2010).

36 Pennini, M. E., Perrinet, S. p., Dautry-Varsat, A. & Subtil, A. Histone methylation by NUE, a novel nuclear effector of the intracellular pathogen Chlamydia trachomatis. *PLoS pathogens* 6, e1000995 (2010).
37 Mujtaba, S. *et al.* Epigenetic transcriptional repression of cellular genes by a viral SET protein. *Nature cell biology* 10, 1114-1122 (2008).
38 Tachibana, M., Matsumura, Y., Fukuda, M., Kimura, H. & Shinkai, Y. G9a/GLP complexes independently mediate H3K9 and DNA methylation to silence transcription. *The EMBO journal* 27, 2681-2690 (2008).
39 Snowden, A. W., Gregory, P. D., Case, C. C. & Pabo, C. O. Gene-specific targeting of H3K9 methylation is sufficient for initiating repression in vivo. *Current biology* 12, 2159-2166 (2002).
40 Rathert, P., Zhang, X., Freund, C., Cheng, X. & Jeltsch, A. Analysis of the substrate specificity of the Dim-5 histone lysine methyltransferase using peptide arrays. *Chemistry & biology* 15, 5-11 (2008).
41 Jackson, J. P. *et al.* Dimethylation of histone H3 lysine 9 is a critical mark for DNA methylation and gene silencing in Arabidopsis thaliana. *Chromosoma* 112, 308-315 (2004).
42 Thorstensen, T. *et al.* The Arabidopsis SUVR4 protein is a nucleolar histone methyltransferase with preference for monomethylated H3K9. *Nucleic acids research* 34, 5461-5470 (2006).
43 Vielle, A. *et al.* H4K20me1 Contributes to Downregulation of X-Linked Genes for C. elegans Dosage Compensation. *PLoS Genetics* 8, e1002933 (2012).
44 Couture, J.-F., Collazo, E., Brunzelle, J. S. & Trievel, R. C. Structural and functional analysis of SET8, a histone H4 Lys-20 methyltransferase. *Genes & development* 19, 1455-1465 (2005).
45 Sautel, C. l. F. *et al.* SET8-mediated methylations of histone H4 lysine 20 mark silent heterochromatic domains in apicomplexan genomes. *Molecular and cellular biology* 27, 5711-5724 (2007).
46 Hathaway, N. A. *et al.* Dynamics and memory of heterochromatin in living cells. *Cell* (2012).
47 Ballaré, C. *et al.* Phf19 links methylated Lys36 of histone H3 to regulation of Polycomb activity. *Nature structural & molecular biology* 19, 1257-1265 (2012).
48 Jin, Q. *et al.* The protein phosphatase-1 (PP1) regulator, nuclear inhibitor of PP1 (NIPP1), interacts with the polycomb group protein, embryonic ectoderm development (EED), and functions as a transcriptional repressor. *Journal of Biological Chemistry* 278, 30677-30685 (2003).
49 Cervoni, N., Detich, N., Seo, S.-B., Chakravarti, D. & Szyf, M. The oncoprotein Set/TAF-1Œ≤, an inhibitor of histone acetyltransferase, inhibits active demethylation of DNA, integrating DNA methylation and transcriptional silencing. *Journal of Biological Chemistry* 277, 25026-25031 (2002).