

# Supporting Information

## Engineered PROTAC-CID systems for mammalian inducible gene regulation

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## Table of contents

<b>Section 1. Supplementary Text.....</b>	<b>3</b>
<b>Fluorescence Protein Activation Assay Protocol.....</b>	<b>3</b>
<b>Section 2. Supplementary Figures.....</b>	<b>5</b>
<b>Promotor configurations and degrader Types.....</b>	<b>5</b>
<b>Basal level analysis.....</b>	<b>7</b>
<b>Truncated CRBN.....</b>	<b>8</b>
<b>Dosage curves and modularity of PROTAC-CIDs.....</b>	<b>9</b>
<b>Orthogonality analysis.....</b>	<b>10</b>
<b>TetR binding domain.....</b>	<b>11</b>
<b>Multiplexing Gene Regulation.....</b>	<b>12</b>
<b>Inducible Cre Recombinase.....</b>	<b>13</b>
<b>Inducible Prime Editor.....</b>	<b>14</b>
<b>AAV-loaded PROTAC-CID system.....</b>	<b>15</b>
<b>In-vivo injection timeline.....</b>	<b>16</b>
<b>Immunoblot of BRD4 in mice liver.....</b>	<b>17</b>
<b>Immunoblot of BRD4 in HEK293T.....</b>	<b>18</b>
<b>Weight loss analysis.....</b>	<b>19</b>
<b>FACS gating strategy.....</b>	<b>20</b>
<b>Uncropped immunoblots S12.....</b>	<b>21</b>
<b>Uncropped immunoblots S13.....</b>	<b>22</b>
<b>Section 3. Supplementary Table.....</b>	<b>23</b>
<b>Small molecule dosages.....</b>	<b>23</b>
<b>gRNA and primers designed for base editing.....</b>	<b>24</b>
<b>Prime Editing components.....</b>	<b>25</b>
<b>EC<sub>50</sub> profiles.....</b>	<b>26</b>
<b>Section 4. Supplementary Sequences.....</b>	<b>29</b>
<b>Amino Acid Sequences.....</b>	<b>29</b>
<b>Primers.....</b>	<b>46</b>
<b>DNA sequence of <i>Cre</i>.....</b>	<b>58</b>
<b>DNA sequence of LoxP and Rox sites.....</b>	<b>59</b>

## Section 1. Supplementary Text

### Step-by-step fluorescence protein activation assay protocol

#### Reagents:

1. PEI Max (Polysciences no. 24765-1)
2. DMEM, high glucose, GlutaMAX™ Supplement, pyruvate (Thermo Fisher Scientific no. 10569044)
3. Penicillin-Streptomycin (10,000 U/mL) (Thermo Fisher Scientific no. 15140122)
4. Fetal Bovine Serum 500ML(FBS) (Thermo Fisher Scientific no. 10437028)
5. TrypLE™ Express Enzyme (1X), phenol red (Thermo Fisher Scientific no. 12605068)
6. PBS pH=7.4 (Thermo Fisher Scientific no. 10010023)
7. Sony sorting chip 100  $\mu$ M for MA900 (SONY no. LE-C3210)
8. Automatic Setup Beads kit (SONY no. LE-B3001)
9. DMSO (Sigma, no. D8418)

#### Procedure:

##### 1. Preparation of PEI Max solution

50 mg PEI Max is dissolved in 45 mL Mill-Q Water. pH is adjusted to 7.1 by adding 10 M NaOH dropwise. Use Mill-Q water to adjust the volume to 50 mL. Filter the solution with 0.45  $\mu$ M pore size Membrane filter (Millipore no. HAWP03700). Allocate the PEI Max solution to 1 mL and store at -20°C for use (avoiding multiple freeze-thaw cycles). Before using, PEI Max solution is heated at 65°C for 2 min.

##### 2. Cell culture

HEK293T cells are seeded into 96 well plates (Corning no. 3598), 12-24 h early before transfection when cell confluence achieves 50% (Caution: HEK293T cells should be divided every 2 days to avoid overcrowding).

##### 3. Transfection

4.5  $\mu$ L PEI Max solution and 300  $\mu$ L DMEM are mixed (Caution: Do not use DMEM medium with FBS, FBS would interfere with transfection). Shake gently to mix. 180 ng of pUAS-1-EYFP, 180 ng of pHef1a-BFP, 180 ng of plasmids encoding GAL4 fused protein, and 180 ng of plasmids encoding VPR fused protein were mixed into a 1.7 mL tube (Caution: plasmids should be prepared freshly with good quality and preservation. Bad plasmid preservation would affect the gene activation ability dramatically). Mix the PEI-DMEM solution with plasmids and incubate at room temperature for 30 min. Add 1/3 volume of the mixture to one well of 96 well plate gently. Return the 96 well plates for culture.

##### 4. Gene induction

12 h after transfection, the cell culture medium is replaced with DMEM with 10% FBS and 100 U Penicillin-Streptomycin. DMSO dissolved inducer or DMSO as control is added according to the experiments.

##### 5. Flow cytometry sample collection

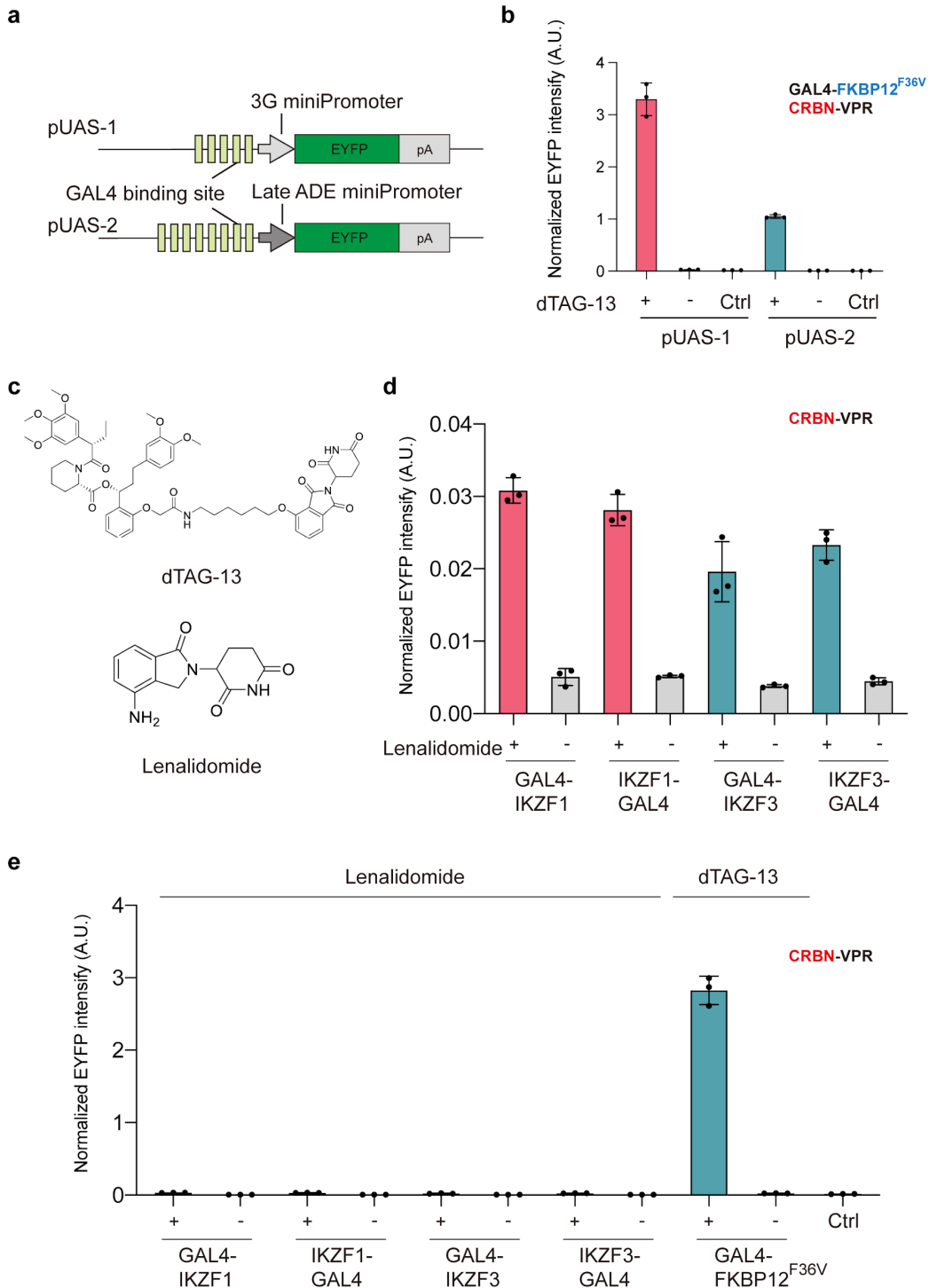
2 d after transfection, remove the cultured medium, and  $\sim$  50  $\mu$ L trypLE is added into each well. After 3 min of digestion (Caution: cells should be thoroughly digested to avoid cell clusters to block the flow cytometry, but too long time of digestion will be harmful to the cells). 100  $\mu$ L of DMEM with 10% FBS are added into wells to inactivate the tryple. Cell-containing medium is moved to a 1.7 mL tube. Centrifuge the medium with 3000 g at 5 min. Remove the

supernatant and 200  $\mu$ L PBS is added to make the single cell solution. Transfer the cells to 12 $\times$ 75 mm flow tubes.

#### 6. Flow cytometry data collection

Before running, change the sorting chip on MA900 every 24 h and check the MA900 flow cytometry with setup beads. Collect the cells as the parameter described in Methods. Clean the MA900 flow cytometry with 10% bleach and water after using.

## Section 2. Supplementary Figures



**Figure S1.** Activity comparisons between promoter configurations and between degrader types for inducible EYFP expression. a, Schematic of the pUAS promoters used for evaluating PROTAC-CID-based gene activation systems. pUAS-1 promoter was designed by connecting 5 copies GAL4 binding sites with miniPromoter derived from TRE3G promoter (3G miniPromoter). pUAS-2 was engineered with 8 copies

GAL4 binding sites with mini-promoter derived from Late ADE gene. b, Quantitative EYFP gene activation efficiency for the comparison of pUAS-1 and pUAS-2 promoter-based reporter systems. HEK293T cells transfected dTAG-13 PROTAC-CID systems and reporter plasmid induced by 100 nM dTAG-13 (+) or DMSO (-) for 2 days. c, Chemical structure of dTAG-13 (PROTAC) (Top) and Lenalidomide (Molecular glue) (Below). d and e, Fluorescence quantification of EYFP intensity for dTAG-13 and Lenalidomide inducible gene activation in HEK293T cells. IKZF1 or IKZF3 fused to GAL4 at N-terminal or C-terminal. HEK293T cells were induced by Lenalidomide (1  $\mu$ M) and 100 nM dTAG-13 for 2 days. The same data are shown in Figure S1e and Figure 1b for the dTAG-13 group of gene activation. b-e, Error bars reflect the mean with SD from n =3 biological replicates. “+” represents treatment with inducers. “-” represents treatment with DMSO. Ctrl, control. HEK293T cells were transfected with the reporter plasmid only as in the control group.

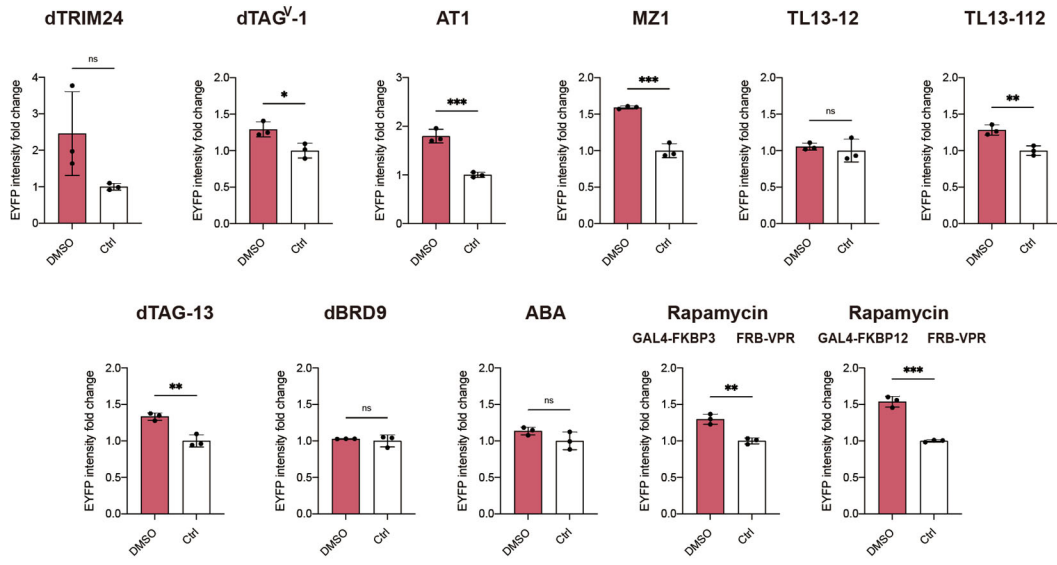
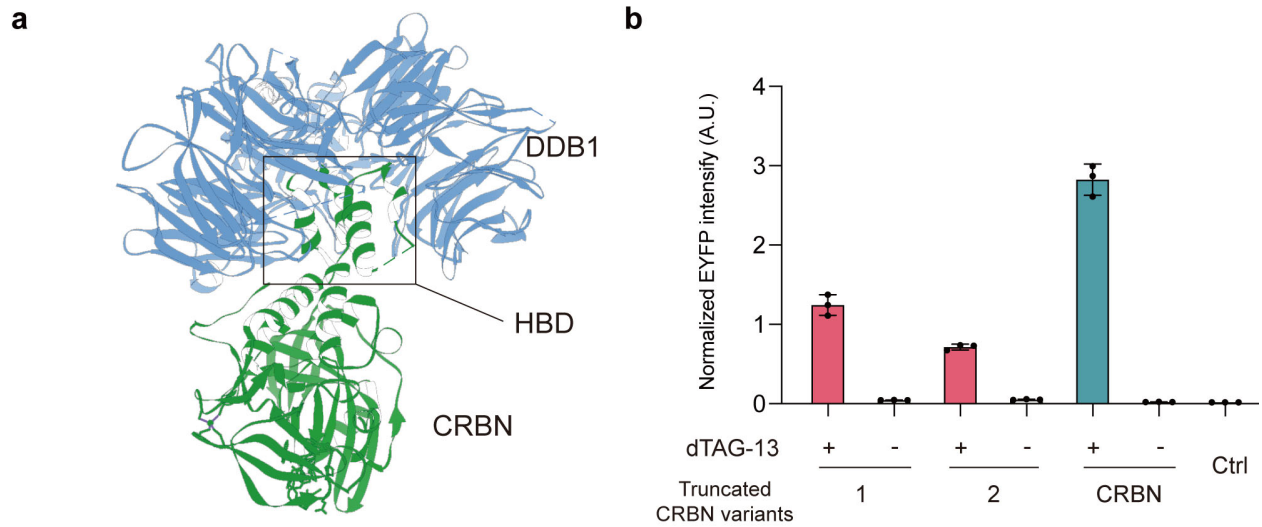
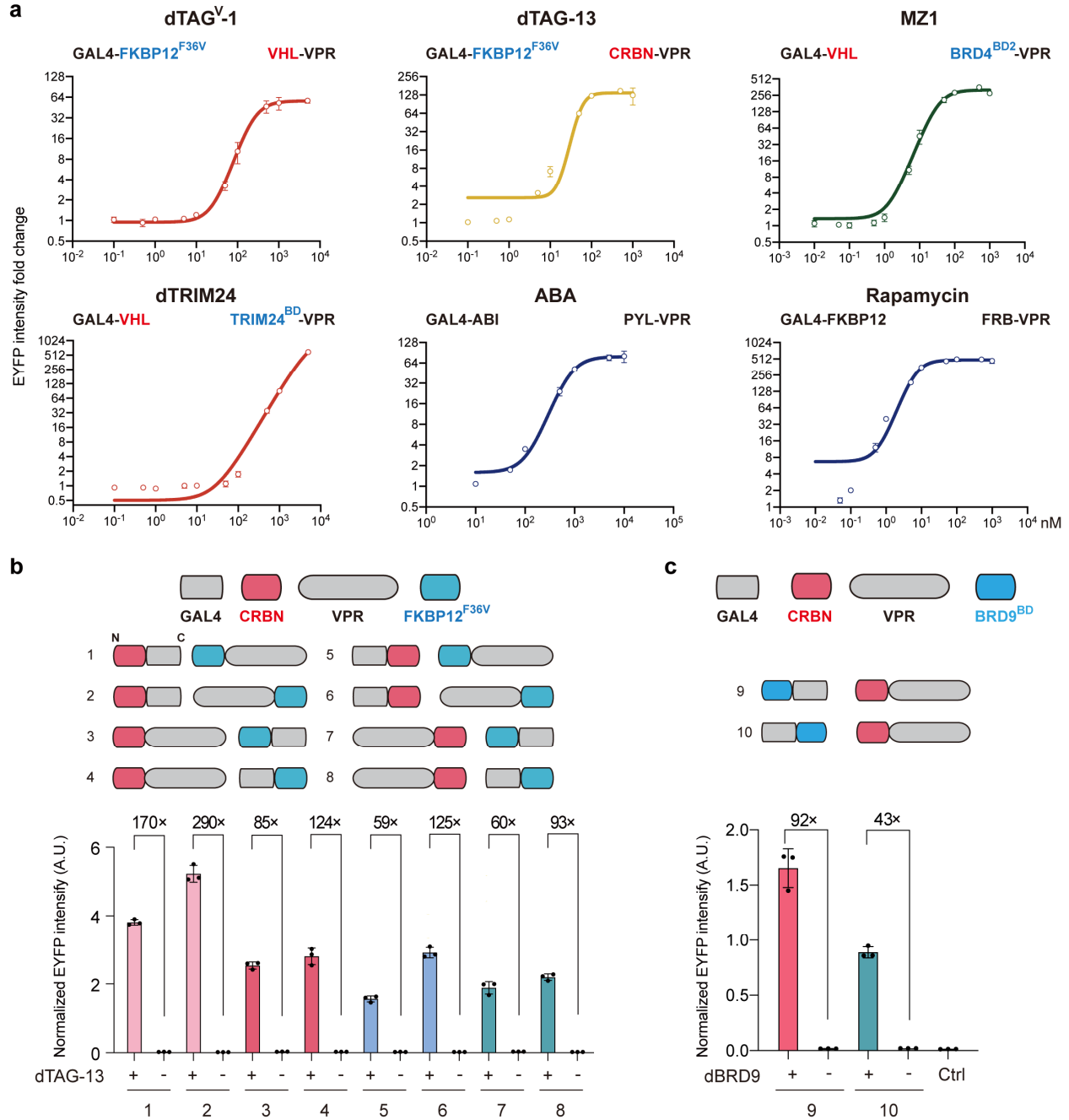


Figure S2. Basal level of the PROTAC-CID based gene activation systems. The differences between red column (w/ PROTAC-CID proteins, w/o inducer,  $\geq 1$ ) and white column (w/o PROTAC-CID proteins, w/o inducer, normalized as 1) represent the basal leaky effect. P value was calculated by two tailed unpaired t-test. \*  $p < 0.05$ ; \*\*  $p < 0.01$ ; \*\*\*  $p < 0.001$ ; n.s., non-significant. Data are from Fig. 1b,  $n = 3$  biologically independent repeats with an error bar of SD.

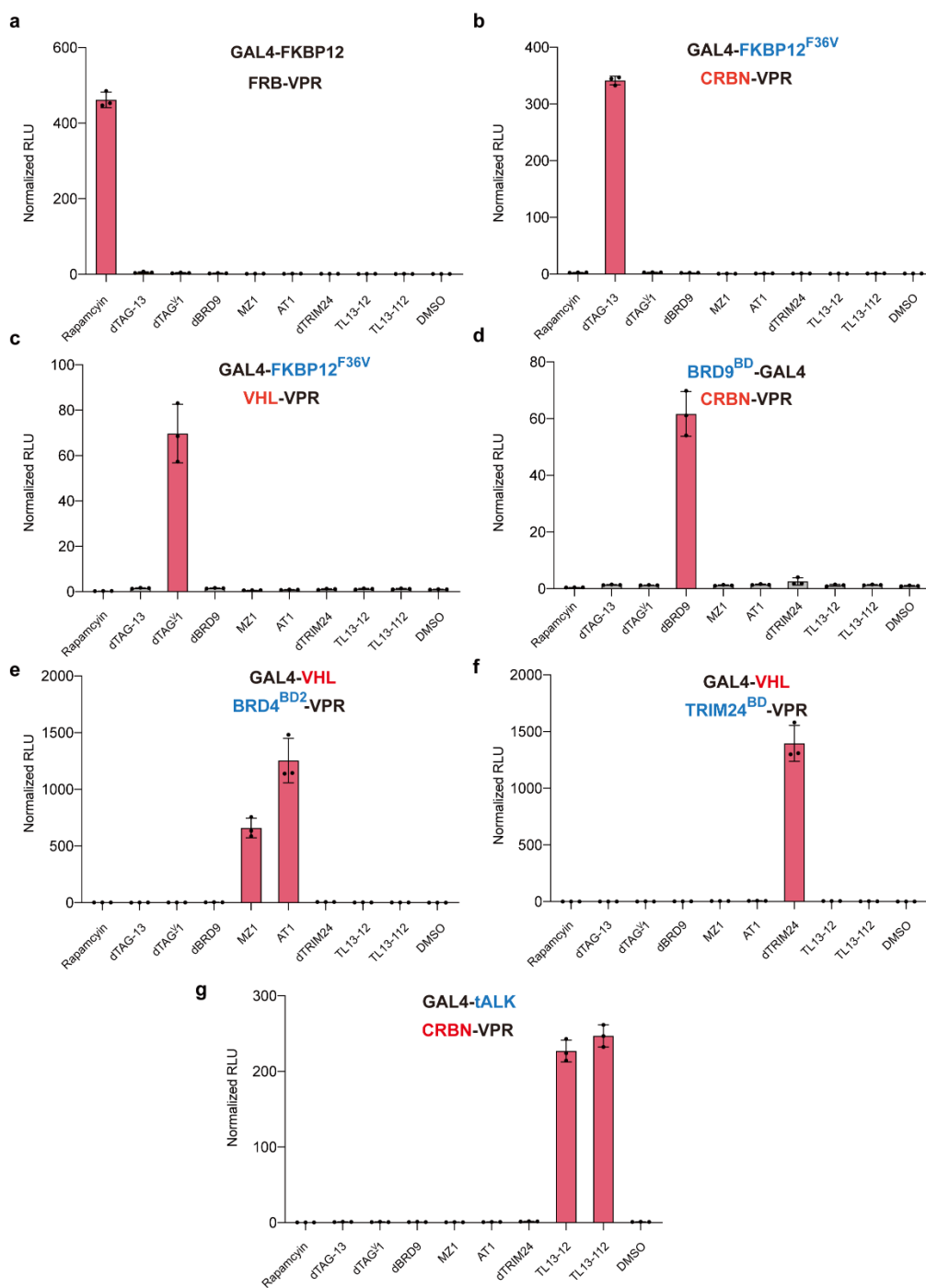


**Figure S3.** Truncated CRBN with disabled E3 ubiquitin ligase function for PROTAC-CID platform. a, Crystal structure of CRBN with DDB1<sup>1</sup>. 7- $\alpha$ -helical bundle domain (HBD) in CRBN interacts with DDB1 and was labeled in the rectangle. b, Two truncated CRBN variants by removing the HBD domain to disable the E3 ubiquitin ligase function were fused with VPR (tCRBN-VPR). Full-length CRBN fused with VPR (CRBN-VPR) for comparison. HEK293T cells transfected with reporter plasmid (pUAS-1-EYFP), GAL4-FKBP12<sup>F36V</sup>, and CRBN-VPR or tCRBN-VPR were treated with 100 nM dTAG-13 (+) or DMSO (-). HEK293T cells transfected with reporter plasmid as the control group (Ctrl). The same data of the full-length CRBN fused with VPR from Fig. 1b were used for comparison. n = 3 biologically independent repeats with an error bar of SD.

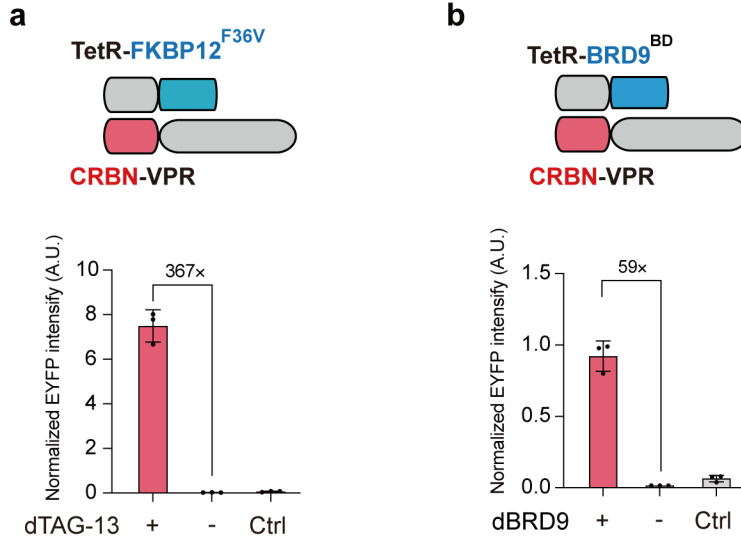




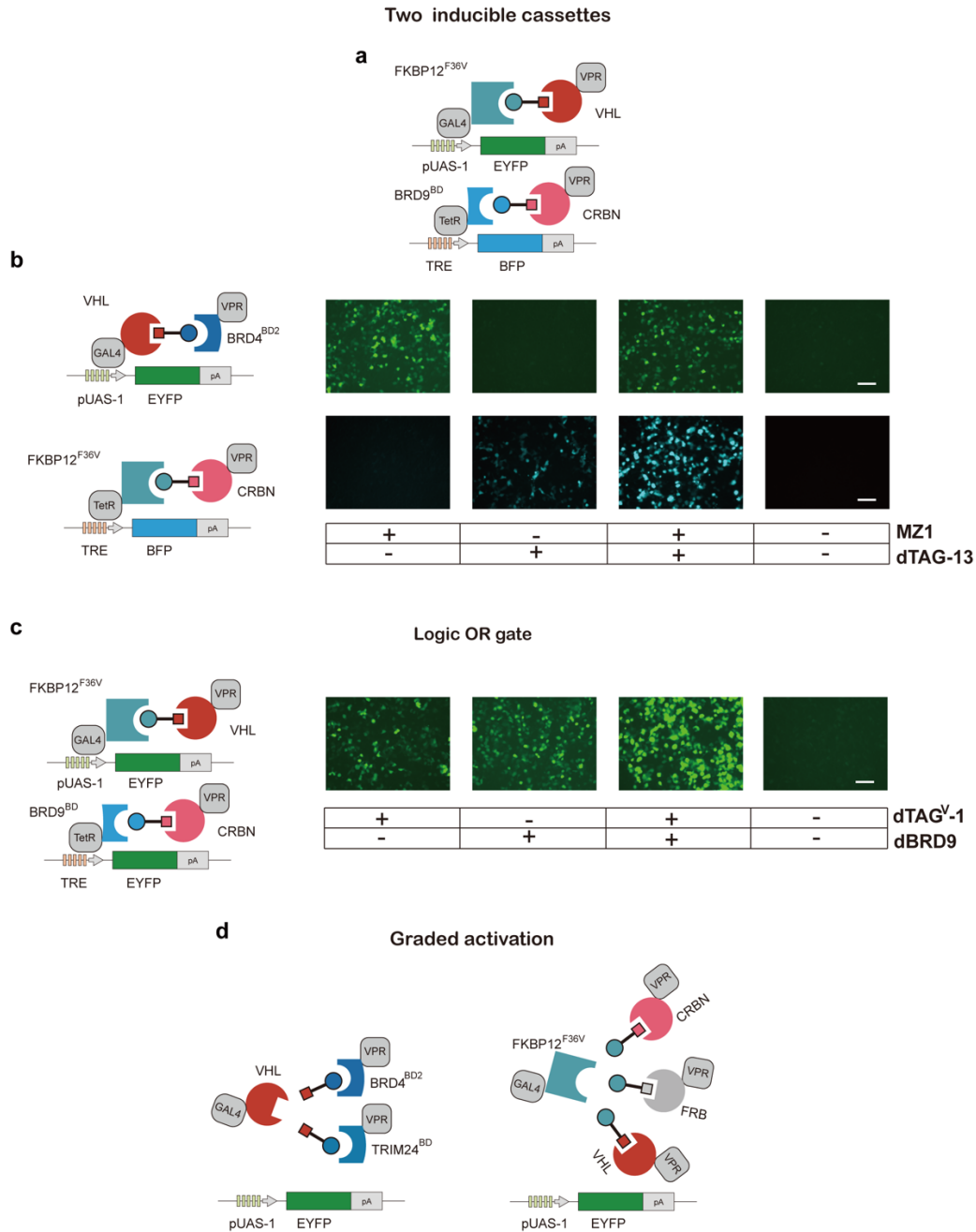
**Figure S4.** Sensitivity and modularity of the PROTAC-CID systems. **a**, The dose-response curve of PROTAC small molecules, Rapamycin and ABA. The  $EC_{50}$  of PROTAC-CID tools was calculated by Prism 9 (Graphpad) using the “[Agonist] vs. response -- Variable slope (four parameters)” model. The nonlinear regression results were listed in Table 4. **b**, dTAG-13 interacting protein partners (CRBN or  $FKBP12^{F36V}$ ) fused with GAL4 or VPR in N-terminal or C-terminal. EYFP induction efficiency was measured by all combinations of fusion proteins with either 100 nM dTAG-13 (+) or DMSO (-). For the protein fusion configuration, unless stated otherwise, fuse protein starts with N-terminal and ends with C-terminal. When CRBN was fused with VPR in N-terminally and GAL4 was placed in the N-terminal of  $FKBP12^{F36V}$ , the same data are shown in Fig. 1b and Fig. S3 for comparison. **c**,  $BRD9^{BD}$  fused with GAL4 in N-terminal or C-terminal treated with 1  $\mu$ M dBRD9 or DMSO. Data are shown in  $n = 3$  independent biological replications with an error bar of SD.



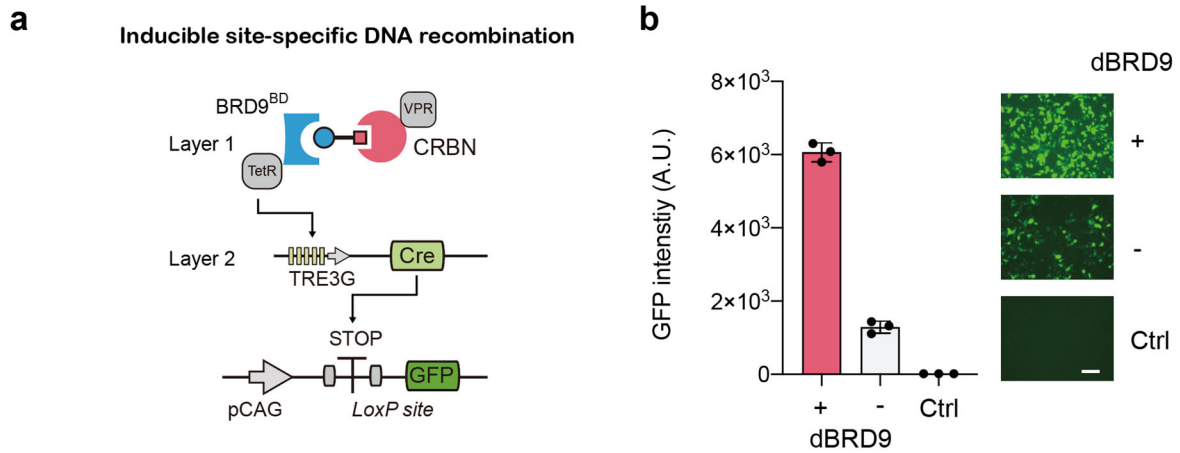
**Figure S5.** Orthogonal analysis of the PROTAC-CID systems. a-g, Firefly luciferase expression induced by PROTAC-CID systems (100 nM dTAG-13, 1  $\mu$ M dTAG<sup>V</sup>-1, 1  $\mu$ M dBRD9, 100 nM MZ1, 1  $\mu$ M AT1, 5  $\mu$ M dTRIM24, 1  $\mu$ M TL13-12, 1  $\mu$ M TL13-112), 100 nM Rapamycin or DMSO. HEK293T cells pre-transfected with plasmids encoding GAL4 or VPR fused with protein partners. Cells were lysed 2 days post-induction to measure the intensity of bioluminescence. RLU, relative light units. See Materials and Methods for the RLU normalization calculation. Data are shown in n = 3 independent biological replications with an error bar of SD.



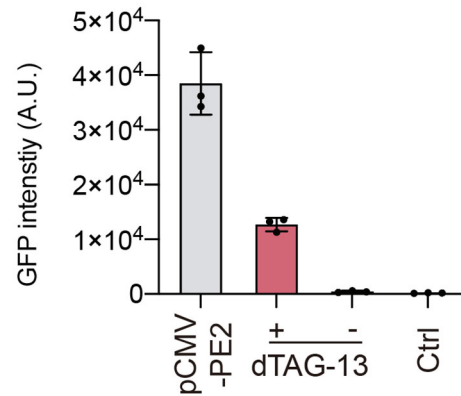
**Figure S6.** TetR DNA binding domain for PROTAC-CID platform. a and b, Schematic of the inducible PROTAC-CID systems with the replacement of the DNA binding domain from GAL4 to TetR. FKBP12<sup>F36V</sup> or BRD9<sup>BD</sup> fused with TetR C-terminally (Above). Efficacy of dTAG-13 or dBRD9 to induce TRE promoter-driven EYFP expression. HEK293T cells transfected with plasmids treated with 100 nM dTAG-13 (+), 1  $\mu$ M dBRD9 (+) or DMSO (-) for 2 days. Data are shown in n = 3 independent biological replications with an error bar of SD.



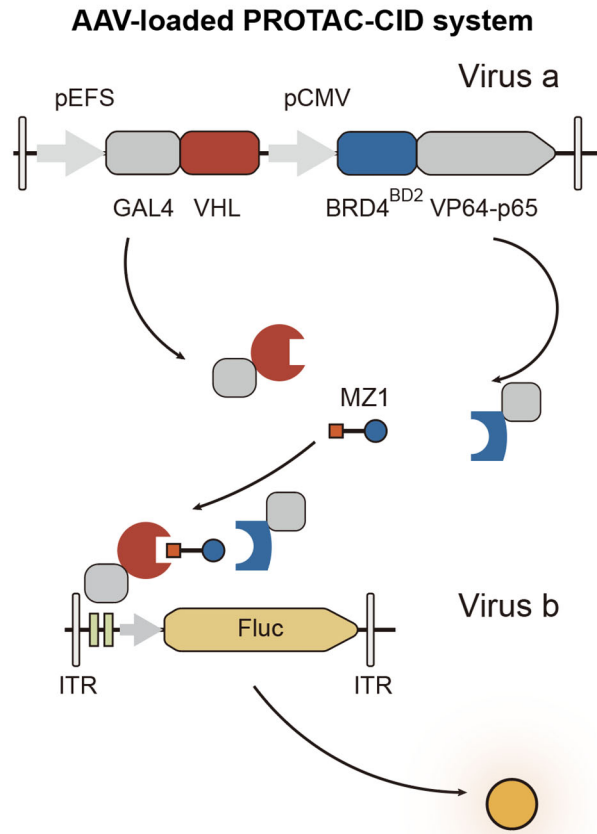
**Figure S7.** Multiplexing gene regulation by PROTAC-CID small molecules. a and b, Dual inducible expression cassettes to drive EYFP and BFP regulated by two PROTACs. c, Dual inducible expression cassettes to drive the same EYFP gene forming a logic OR gate. b and c, Representative images of EYFP or BFP intensity 2 days post-induction in HEK293T cells transfected with constructs in the presence of dTAG-13 (100 nM), MZ1 (100 nM), dTAG<sup>V</sup>-1 (1  $\mu$ M) or dBRD9 (1  $\mu$ M). Data are shown in  $n = 3$  biologically independent repeats. d, Schematic design of the graded activation systems. b and c, Scale bar, 125  $\mu$ m. Images of each condition were taken independently for  $n = 3$  times with similar results shown above.



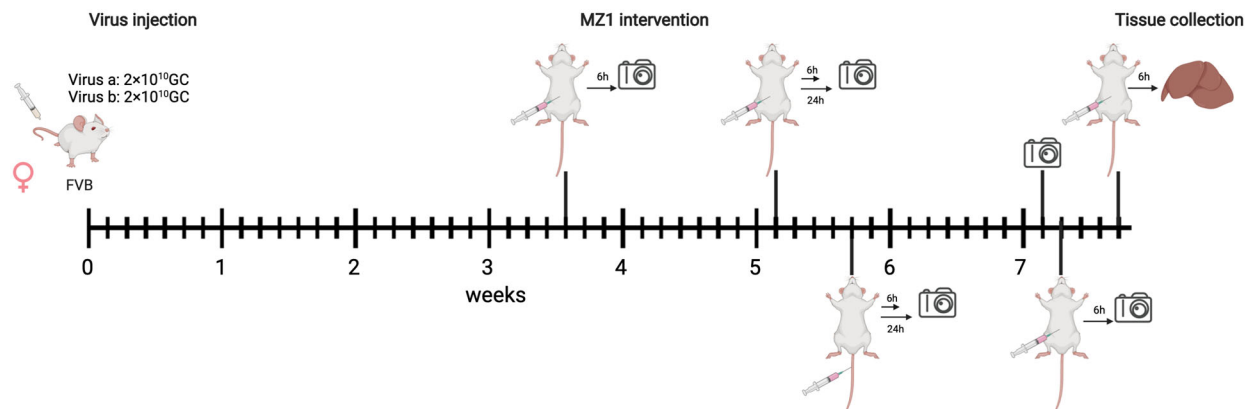
**Figure S8.** Inducible Cre DNA recombinase by PROTAC-CID. a, Schematic of the PROTAC-CID based inducible site-specific DNA recombination platform. Cre gene was placed downstream of TRE3G promoter. Pre-mature STOP transcriptional signal was put between constitutive pCAG promoter and *Gfp* gene. The induced Cre protein will remove the STOP signal to activate the GFP expression. b, Representative images and fluorescence quantification of the GFP intensity induced by dBRD9 (+) after 2 days of induction. The red bar represents the GFP intensity of induced cells, and the grey bar represents the uninduced cells (-) transfected with the PROTAC-CID system, TRE3G driven Cre, and the LoxP-STOP-LoxP-GFP reporter plasmids. The control (Ctrl) group refers to the HEK293T cells transfected with the LoxP-STOP-LoxP-GFP reporter plasmid. Data are shown in n = 3 biologically independent repeats with an error bar of SD. b. Scale bar, 125  $\mu$ m.



**Figure S9.** Inducible PE to repair micro-deleted *Cre* gene. Quantitative GFP intensity for the evaluation of inducible PE activity compared with pCMV-driven PE2 in HEK293T cells. The micro-deleted *Cre* gene was repaired by the PE system to express functional Cre protein. GFP will be expressed once the pre-mature STOP signal is removed by Cre protein. HEK293T cells transfected with LoxP-STOP-LoxP-GFP reporter plasmid as control (Ctrl). HEK293T cells were treated with 100 nM dTAG-13 (+) or DMSO (-). (n=3 biological repeats with an error bar of SD).

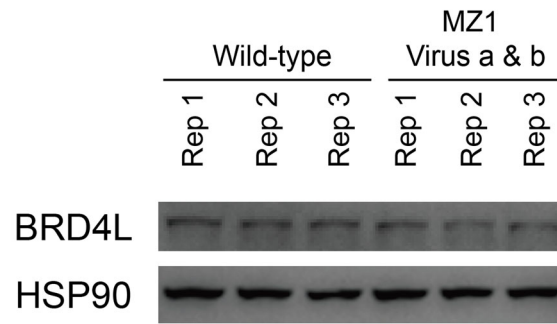


**Figure S10.** Schematic depicting the compact PROTAC-CID system loaded by AAV vectors to induce the *Fluc* expression. pEFS, elongation factor 1 $\alpha$  short promoter. pCMV, truncated human cytomegalovirus promoter. ITR, inverted terminal repeat. In Virus a, GAL4 fused with VHL and BRD4<sup>BD2</sup> fused with VP64-p65 gene activation domain was expressed constitutively. GAL4-VHL fusion protein binds with the pUAS-2 promoter upstream of the *Firefly luciferase* (*Fluc*) gene in Virus b. In the presence of MZ1, BRD4<sup>BD2</sup>-VP64-p65 will be brought in proximity to the pUAS-2 promoter to drive the *Fluc* gene expression.

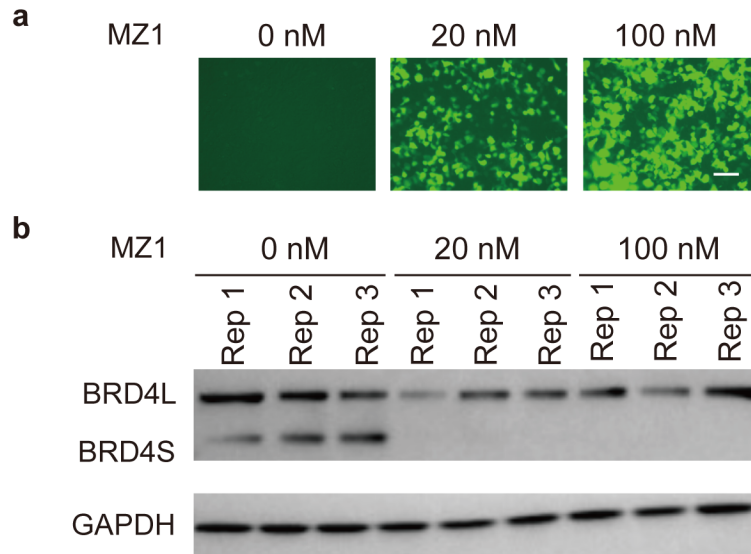


**Figure S11.** Schematic of in vivo studies of PROTAC-CID gene activation in FVB mice model treated with AAV virus and MZ1. 8-week-old FVB female mice were injected with either Virus a or Virus a and Virus b at a dose of  $2 \times 10^{10}$  genome copies (GC) per mouse by i.v. injection. 25 days post-injection, mice were administrated with MZ1 (10 mg/kg) by i.p. injection. 6 h post-MZ1 treatment, the bioluminescence was monitored. Mice were treated with 50 mg/kg MZ1 by i.p. injection or 10 mg/kg by i.v. injection to compare the route of administration. On day 52, mice were treated with 50 mg/kg MZ1 by i.p. injection and observed the luciferase bioluminescence. On day 54, after being treated with 50 mg/kg MZ1 by i.p. injection, liver tissue was collected for protein detection.

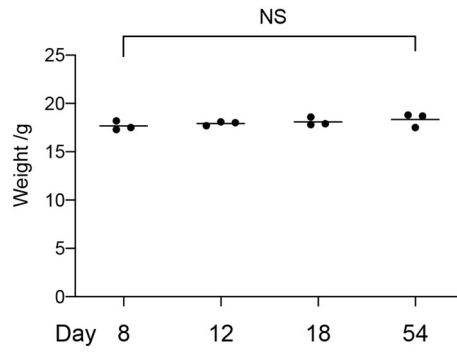




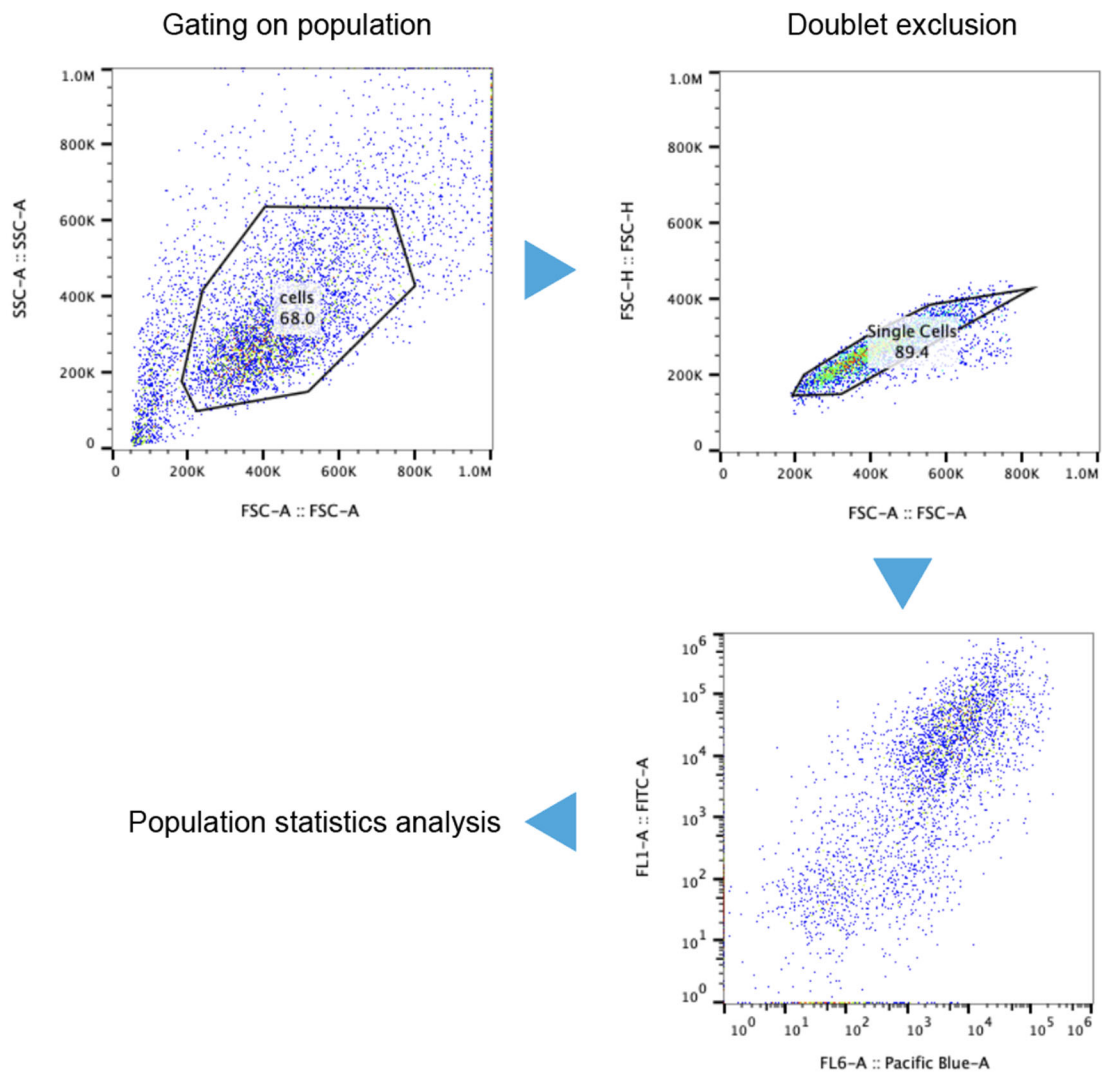
**Figure S12.** Immunoblot analysis of endogenous BRD4 expression in FVB mice liver tissue. Immunoblot analysis of endogenous long isoform BRD4 (BRD4L) after 50 mg/kg MZ1 treatment by i.p. injection. The short isoform BRD4 (BRD4S) was undetectable in the liver tissue. Uncropped immunoblots are displayed in Fig. S16.



**Figure S13.** Immunoblot analysis of endogenous BRD4 expression in HEK293T cells. HEK293T cells were pre-transfected with MZ1 (GAL4-VHL and BRD4<sup>BD2</sup>-VPR) PROTAC-CID systems to activate the pUAS-1 driven EYFP. 48 h post-induction, the EYFP intensity was observed (a) and cells were lysed for immunoblot to detect the BRD4 expression. Scale bar 125  $\mu$ m. b, Long isoform BRD4 (BRD4L). Short isoform BRD4 (BRD4S). Uncropped immunoblots are displayed in Figure S17. Rep, Replication.

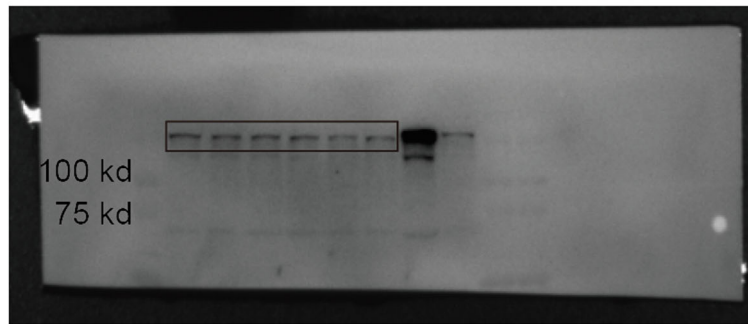


**Figure S14.** Weight loss analysis of AAV and MZ1-treated mice. FVB mice receiving Virus a and Virus b were treated by MZ1 as in Figure S10 and S11. The dotted line represents the mean weight of tested mice. Statistical analysis was performed using an unpaired two-tailed Student's t-test. NS, not significant.



**Figure S15.** FACS gating examples for flow cytometry data analysis in this study. FL1-FITC-A channel is used for measuring the intensity of EYFP and GFP. FL6-Pacific blue-A channel is used for measuring the intensity of BFP.

## BRD4



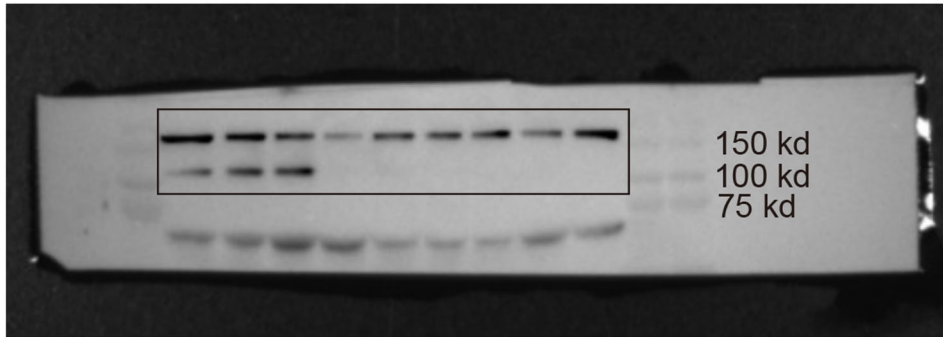
## HSP90



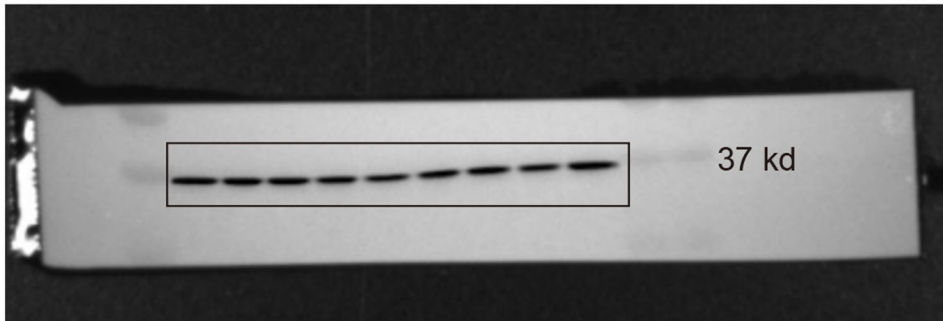
Testis positive control  
Pancreas positive control

**Figure S16.** Uncropped original immunoblots data in Figure S12. Mice testis and pancreas tissue as the positive control for BRD4 detection.

BRD4



GAPDH



**Figure S17.** Uncropped original immunoblots data in Figure S13.

### Section 3. Supplementary Tables

**Table S1. Protein partners and fusion strategies in Figure 1b.**

	<b>Fusion protein 1</b> (E3 ubiquitin ligases are shown in <b>red</b> )	<b>Fusion protein 2</b> (Target proteins are shown in <b>blue</b> )	<b>Concentration of the small molecules</b>
<b>PROTACs</b>			
dTRIM24	GAL4- <b>VHL</b>	<b>TRIM24</b> -VPR	5 $\mu$ M
dTAG <sup>V</sup> -1	<b>VHL</b> -VPR	GAL4- <b>FKBP12</b> <sup>F36V</sup>	5 $\mu$ M
AT1	GAL4- <b>VHL</b>	<b>BRD4</b> -VPR	1 $\mu$ M
MZ1	GAL4- <b>VHL</b>	<b>BRD4</b> -VPR	100 nM
TL13-12	<b>CRBN</b> -VPR	GAL4- <b>tALK</b>	1 $\mu$ M
TL13-112	<b>CRBN</b> -VPR	GAL4- <b>tALK</b>	1 $\mu$ M
dTAG-13	<b>CRBN</b> -VPR	GAL4- <b>FKBP12</b> <sup>F36V</sup>	100 nM
dBRD9	<b>CRBN</b> -VPR	GAL4- <b>BRD9</b>	1 $\mu$ M
ZXH3-26	<b>CRBN</b> -VPR	GAL4- <b>BRD4</b>	1 $\mu$ M
<b>CID inducers</b>			
ABA	GAL4-ABI	PYL-VPR	250 $\mu$ M
Rapamycin	GAL4-FKBP3	FRB-VPR	1 $\mu$ M
Rapamycin	GAL4-FKBP12	FRB-VPR	10 nM

**Table S2. gRNA sequences and primers for amplifying the genome sites in Figure 3c and 3e.**

Description	gRNA sequence (5' to 3')	Forward primer (5' to 3')	Reverse primer (5' to 3')
A3G site 1	GTTACGAAAA CCTAGGGGTG	TGAAAGTGGCATCTTGAA AGGG	ACCCTTGCATTCCAATACCAC
A3G site 2	AGATCCAGG GACACGGTGC T	GTGGGAAACAGCCGTCAG	CACTGAGCACTGAAGGCC
A3G site 3	AAAACCGA GGGGTAAGA ATC	ACACTCTTTCCTACACG ACGCTCTTCCGATCTATA GGATAGGAGTGATGGACA GG	GACTGGAGTTCAGACGTGTGCTC TTCCGATCTCTGCTGCTCCTCAAT ACACC
ABE site 1	GACAAACCA GAAGCCGCTC C	TCTCTTGTGGTTTCCTAGC TTCTGA	ACTTCCCCTGAGTTTAAGTGATG
ABE site 2	GAACACAAA GCATAGACTG C	ACATTTGGGCTTCTTTCTA GTTGA	CCTGATGTAATGACTAGACTGAG GC



**Table S3. pegRNA sequences, nicking sgRNA and primers for measuring prime editing efficiency in Figure 3h.**

<b>pegRNA</b>	<b>space sequence (5' to 3')</b>	<b>3' extension (5' to 3')</b>	<b>PBS length (nt)</b>	<b>RT template length (nt)</b>
HEK3_His <sub>6</sub> ins	GGCCCAGACTGAGCA CGTGA	TGGAGGAAGCAGGGCTTCCTT TCCTCTGCCATCAATGATGGT GATGATGGTGCGTGCTCAGTC TG	13	52
Cre_2ATins	AAATGCCAGATTACG TATCC	TCGCTGCCAGGATATACGTAA TCTGGC	11	14

<b>Nicking sgRNA</b>	<b>spacer sequence (5' to 3')</b>
HEK3_His <sub>6</sub> ins	GTCAACCAGTATCCCGGTGC
Cre_2ATins	CGAACGCACTGATTTCGACC

<b>Description</b>	<b>sequence</b>
HEK3 fwd	CTTTTCCTCTGTTGAGCTCG
HEK3 rev	GAATCAGTGCTGGAGAATGG

**Table S4. Nonlinear regression analysis for calculating EC<sub>50</sub> of PROTAC-CID tools.**

**ABA**

<b>Description</b>	<b>Number</b>
<b>Best-fit values</b>	
Bottom	1.587
Hillslope	2.083
Top	79.43
EC <sub>50</sub>	762.6
logEC <sub>50</sub>	2.882
Span	77.84
<b>Goodness of Fit</b>	
Degrees of Freedom	17
R squared	0.9724
Sum of Squares	631.1
Sy.x	6.093
<b>Constraints</b>	
EC <sub>50</sub>	EC <sub>50</sub> > 0

**dTAG<sup>V</sup>-1**

<b>Description</b>	<b>Number</b>
<b>Best-fit values</b>	
Bottom	0.9420
Hillslope	1.937
Top	56.67
EC <sub>50</sub>	227.8
logEC <sub>50</sub>	2.358
Span	55.73
<b>Goodness of Fit</b>	
Degrees of Freedom	26
R squared	0.9697
Sum of Squares	496.3
Sy.x	4.369
<b>Constraints</b>	
EC <sub>50</sub>	EC <sub>50</sub> > 0

### dTAG-13

<b>Description</b>	<b>Number</b>
<b>Best-fit values</b>	
Bottom	2.581
Hillslope	3.384
Top	138.3
EC <sub>50</sub>	52.98
logEC <sub>50</sub>	1.724
Span	135.7
<b>Goodness of Fit</b>	
Degrees of Freedom	23
R squared	0.9579
Sum of Squares	4269
Sy.x	13.62
<b>Constraints</b>	
EC <sub>50</sub>	EC <sub>50</sub> > 0

### dTRIM24

<b>Description</b>	<b>Number</b>
<b>Best-fit values</b>	
Bottom	0.5037
Hillslope	1.463
Top	1431
EC <sub>50</sub>	6347
logEC <sub>50</sub>	3.803
Span	1430
<b>Goodness of Fit</b>	
Degrees of Freedom	26
R squared	0.9968
Sum of Squares	2974
Sy.x	10.69
<b>Constraints</b>	
EC <sub>50</sub>	EC <sub>50</sub> > 0

## Rapamycin

<b>Description</b>	<b>Number</b>
<b>Best-fit values</b>	
Bottom	6.692
Hillslope	1.871
Top	490.6
EC <sub>50</sub>	6.322
logEC <sub>50</sub>	0.8008
Span	483.9
<b>Goodness of Fit</b>	
Degrees of Freedom	29
R squared	0.9914
Sum of Squares	13564
Sy.x	21.63
<b>Constraints</b>	
EC <sub>50</sub>	EC <sub>50</sub> > 0

## MZ1

<b>Description</b>	<b>Number</b>
<b>Best-fit values</b>	
Bottom	1.416
Hillslope	1.728
Top	321
EC <sub>50</sub>	32.39
logEC <sub>50</sub>	1.51
Span	319.6
<b>Goodness of Fit</b>	
Degrees of Freedom	29
R squared	0.9781
Sum of Squares	13560
Sy.x	21.62
<b>Constraints</b>	
EC <sub>50</sub>	EC <sub>50</sub> > 0

## Section 4. Supplementary Sequences

### Sequences S1. Amino acid sequences of PROTAC-CID protein partners used in this study.

GAL4-FKBP12<sup>F36V</sup>:

SV40 NLS

GAL4 DBD

FKBP12<sup>F36V</sup>

Nucleoplasmin NLS

MPKKKRKVGGGSPGGGSMKLLSSIEQACDICRLKKLKCSKEKPKCAKCLKNNWECRY  
SPKTKRSPLTRAHLTEVESRLERLEQLFLLIFPREDLDMILKMDSLQDIKALLTGLFVQDN  
VNKDAVTDRLASVETDMPLTLRQHRISATSSSEESSNKGQRQLTVSGGGSMGVQVETIS  
PGDGRTFPKRGQTCVVHYTGMLEDGKKVDSSRDRNKPFKFMLGKQEVIRGWEEGVAQ  
MSVGQRAKL TISPDYAYGATGHPGIIPPHATLVFDVELLKLETSGGGSKRPAATKKAGQ  
AKKKKSR

CRBN-VPR:

SV40 NLS

CRBN

VPR

Nucleoplasmin NLS

MPKKKRKVGGGSPGGGSMAGEGDQDAAAHNMGNHLPLLPESEEEDEMEVEDQDSK  
EAKKPNINFDTSLPTSHTYLGADMEEFHGRTLHDDSDSCQVIPVLPQVMMILIPGQTLPL  
QLFHPQEVSMVRNLIQKDRTFVLAYSNVQEREAQFGTTAEIYAYREEQDFGIEIVKVK  
AIGRQRFKVLRLTQSDGIQQAKVQILPECVLPSTMSAVQLESLNKCQIFPSKPVSRDQC  
SYKWWQKYQKRKFHCANLTSWPRWLYSLYDAETLMDRIKKQLREWENLKDSDLPS  
NPIDFSYRVAACLPIDDVLRIQLLKIGSAIQRLRCELDMNKCTSLCCKQCQETEITTKNEI  
FSLSLCGPMAAYVNPFGYVHETLTVYKACNLNLIGRPSTEHSWFPGYAWTVAQCKICA  
SHIGWKFTATKKDMSPQKFWGLTRSALLPTIPDTEDEISPDK VILCLGGGSRADPKKKRK  
VEASGSGRADALDDFDLMLGSDALDDFDLMLGSDALDDFDLMLGSDALDDFDL  
MLINSRSQYLPDTPDRHRIEEKRKRTYETFKSIMKKS PFGPTDPRPPPRRIAVPSRSSASV  
PKPAPQPYPFTSSLSTINYDEFPTMVFPSPGQISQASALAPAPPQVLPQAPAPAPAMVSA  
LAQAPAPVPVLPAGPPQAVAPPAPKPTQAGEGTLSEALLQLQFDDDELGALLGNSTDPA  
VFTDLASVDNSEFQQLLNQGIPVAPHTTEPMLMEYPEAITRLVTGAQRPPDPAPAPLGP  
GLPNGLLSGDEDFSSIADMDFSALLGSGSGSRDSREGMFLPKPEAGSAISDVFE GREVCQ  
PKRIRPFHPPGSPWANRPLPASLAPTPTGPVHEPVGSLTPAPVPQPLDPAPAVTPEASHLL  
EDPDEETSQAVKALREMA DTVIPQKEEA AICGQMDLSHPPPRGHLDELTTTLESMTEDL  
NLDSP LTPELNEILD TFLNDECLLHAMHISTGLSIFDTS LFTSGGGSKRPAATKKAGQAKK  
KKS R

GAL4-VHL:

SV40 NLS  
GAL4 DBD  
VHL

MPKKKRKVGGGSPGGGSMKLLSSIEQACDICRLKKLKCSKEKPKCAKCLKNNWECRY  
SPKTKRSPLTRAHLTEVESRLERLEQLFLLIFPREDLDMILKMDSLQDIKALLTGLFVQDN  
VNKDAVTDRLASVETDMPLTLRQHRISATSSSEESSNKGQRQLTVSGGGSMPRRAENW  
DEAEVGAEAGVEEYGPPEEDGGEESGAEESGPEESGPEELGAEEMEAGRPRPVLRSVN  
SREPSQVIFCNRSPRVVLPVWLNFDGEPQPYPTLPPGTGRRIHSYRGHLWFRDAGTHDG  
LLVNQTELFVPSLNVDDGQPIFANITLPVYTLKERCLQVVRSLVKPENYRRLDIVRSLYED  
LEDHPNVQKDLERLTQERIAHQRMGD

TRIM24<sup>BD</sup>-VPR:

SV40 NLS  
TRIM24<sup>BD</sup>  
VPR  
Nucleoplasmin NLS

MPKKKRKVGGGSPGGGGSPNEDWCAVCQNGGELLCCCEKCPKVFHLSCHVPTLTNFPSG  
EWICTFCRDLKPEVEYDCDAPSHNSEKKKTEGLVKLTPIDKRKCERLLLFLYCHEMSL  
AFQDPVPLTVPDYYKIIKNPMDLSTIKKRLQEDYSMYSKPEDFVADFRLIFQNCAEFNEP  
DSEVANAGIKLENYFEELLKNLYPGGGSRADPKKKRKVEASGSGRADALDDFDLDMLG  
SDALDDFDLDMLGSDALDDFDLDMLGSDALDDFDLDMLINRSQYLPDTPDRHRIEEK  
RKRTYETFKSIMKKSFPSTGPTDPRPPPRRIAVPSRSSASVPKPAPQYPFTSSLSTINYDEF  
TMVFPSTGQISQASALAPAPPQVLPQAPAPAPAMVSALAQAPAPVPLAPGPPQAVAP  
PAPKPTQAGEGTLSEALLQLQFDDDELGALLGNSTDPVFTDLASVDNSEFQQLLNQGIP  
VAPHTTEPMLMEYPEAITRLVTGAQRPPDPAPAPLGAPGLPNGLLSGDEDFSSIADMDFS  
ALLGSGSGSRDSREGMFLPKPEAGSAISDVFEGREVCQPKRIRPFHPPGSPWANRPLPASL  
APTPTGPVHEPVGSLTPAPVPQPLDPAPAVTPEASHLLEDPEETSQAVKALREMAADTVI  
PQKEEAICGQMDLSHPPRGLDELTTTLESMTEDLNLDSPLELNEILDFTLNDECLL  
HAMHISTGLSIFDTSLFTSGGGSKRPAATKKAGQAKKKKSR

TRIM24-VPR:

SV40 NLS  
TRIM24  
VPR  
Nucleoplasmin NLS

MPKKKRKVGGGSPGGGGSGTSRRSRTMEVAVEKAVAAAAAASAAASGGPSAAPS  
GENEAESRQGPDSERGGEAARLNLLDTCVCHQNIQSRAKLLPCLHSFCQRCLPAPQRYLM  
LPAPMLGSAETPPPVPAPGSPVSGSSPFATQVGVIRCPVCSQECAERHIIDNFFVKDTTEV  
PSSTVEKSNQVCTSCEDNAEANGFCVECWEWLCKTCIRAHQRVKFTKDHTVVRQKEEVS

PEAVGVTSQRPVFCPFHKKEQLKLYCETCDKLTCDKLCQLEHKEHRYQFIEEAFQNQKV  
IIDTLITKLMKTKYIKFTGNQIQNRIIEVNNQKQVEQDIKVAIFTLMVEINKKKGKALLH  
QLESLAKDHRMKLMQQQQEVAGLSKQLEHVMHFSKWAVSSGSSTALLYSKRLITYRLR  
HLLRARCDASPVNTNTIQFHCDPSFWAQNIINLGS�VIEDKESQPQMPKQNPVVEQNSQP  
PSGLSSNQLSKFPTQISLAQLRLQHMQQQVMAQRQQVQRRPAPVGLPNPRMQGPIQQPS  
ISHQQPPRLINFQNHSPKPNGPVLPPHPQQLRYPPNQIPRQAIKPNPLQMAFLAQQAIK  
QWQISSGQGTPTTNTSSTPSSPTITSAAGYDGKAFGSPMIDLSSPVGGSYNLPSLPDIDC  
SSTIMLDNIVRKDTNIDHGQPRPPSNRTVQSPNSSVSPGLAGPVTMTSVHPPIRSPSASSV  
GSRGSSGSSSKPAGADSTHKVPVVMLEPIRIKQENSGPPENYDFPVVIVKQESDEESRPQ  
NANYPRSILTSLLNSSQSSTSEETVLRSDAPDSTGDQPGLHQDNSSNGKSEWLDPSQKS  
PLHVGETRKEDDPNEDWCAVCQNGGELLCEKCPKVFHLSCHVPTLTNFPSGEWICTFC  
RDLSKPEVEYDCDAPSHNSEKKKTEGLVKLTPIDKRKCERLLLFLYCHEMSLAFQDPVP  
LTVPDYKIIKNPMDLSTIKKRLQEDYSMYSKPEDFVADFRLIFQNCAEFNEPDSEVANA  
GIKLENYFEELLKNLYPEKRFKPEFRNESEDNKFSDSDDDDFVQPRKKRLKSIEERQLL  
KLERPPDITLQGSWPASGGGSRADPKKKRKVEASGSGRADALDDFDLDMLGSDALDDF  
DLMLGSDALDDFDLDMLGSDALDDFDLDMLINSRSQYLPDTDDRHRIEEKRKRTYET  
FKSIMKKSPPSGPTDPRPPPRRIAVPSRSSASVPKPAPQYPFTSSLSTINYDEFPTMVFP  
QISQASALAPAPPQVLPQAPAPAPAPAMVSALAQAPAPVPVLAPGPPQAVAPPAPKPTQ  
AGEGTLSEALLQLQFDEDLGALLGNSTDPVFTDLASVDNSEFQQLLNQGPVAPHTT  
EPMLMEYPEAITRLVTGAQRPPDPAPAPLGLPGLNGLLSGDEDFSSIADMDFSALLGSG  
SGSRDSREGMFLPKPEAGSAISDVFEGREVCQPKRIRPFHPPGSPWANRPLPASLAPTPTG  
PVHEPVGSLTPAPVPQPLDPAPAVTPEASHLLEDPEETSQAVKALREMADTVIPQKEEA  
AICGQMDLSHPPPRGHLDELTTTLESMTEDLNLDSPLTPELNEILDFTLNDECLLHAMHIS  
TGLSIFDTSLFTSGGGSKRPAATKKAGQAKKKSR

BRD4-VPR:

SV40 NLS

BRD4

VPR

Nucleoplasmin NLS

MPKKKKRKGGGSPGGGGSMSAESGPGTRLRNLPMVMDGLETSQMSTTQAQAQPQAN  
AASNPPPPETSNNPKPKRQTNQLQYLLRVVLKTLWKHQFAWPFQQPVDAVKLNLPDY  
YKIIKTPMDMGTIKKRLENNYYWNAQECIQDFNTMFTNCYIYNKPGDDIVLMAEALEKL  
FLQKINELPTEETEIMIVQAKGRGRGRKETGTAKPGVSTVPNTTQASTPPQTQTPQNP  
VQATPHPPFAVTPDLIVQTPVMTVPPQPLQTPPPVPPQPPAPAPQPVQSHPPHIAATP  
QPVKTKKGVKRKADTTTPTTIDPIHEPPSLPPEPKTTKLGQRRESSRPVKPPKDVPSQ  
HPAPEKSSKVSEQLKCCSGILKEMFAKKHAAAYAWPFYKPVDEALGLHDYCDIHKHPM  
DMSTIKSKLEAREYRDAQEFGADVRLMFSNCYKYNPPDHEVVAMARKLQDVFEMRFA  
KMPDEPEEPVAVSSPAVPPPTKVVAPPSSSDSSSDSSSDSDSSTDDSEERAQRLAELQE  
QLKAVHEQLAALSQPQONKPKKKEKDKKEKKEKHKRKEEVEENKSKAKEPPPKKT  
KNNSSNSNVSKKEPAPMKSPPPTYESEEDKCKPMSYEEKRQLSLDINKLPGEKLR  
VVHIIQSREPSLKN SNPDEIEIDFETLKPSTLRELERVYVTSCLRKKRKPQAEKVDVIAGSSK  
MKGFSSESSESSSSSDSEDSETGPAAGGGSRADPKKKRKVEASGSGRADALDDFDLD  
MLGSDALDDFDLDMLGSDALDDFDLDMLGSDALDDFDLDMLINSRSQYLPDTDDRHRH

EEKRKRITYETFKSIMKKSPFSGPTDPRPPRRRIAVPSRSSASVPKPAPQYPFTSSLSTINY  
DEFPTMVFPSGQISQASALAPAPPQVLPQAPAPAPAPAMVSALAQAPAPVPLAPGPPQA  
VAPPAPKPTQAGEGTLSEALLQLQFDDDLGALLGNSTDPVFTDLASVDNSEFQQLN  
QGIPVAPHTTEPMLMEYPEAITRLVTGAQRPPDPAPAPLAPGLPNGLLSGDEDFSSIAD  
MDFSALLGSGSGSRDSREGMFLPKPEAGSAISDVFEGREVCQPKRIRPFHPPGSPWANRP  
LPASLAPTPTGPVHEPVGSLTPAPVPQPLDPAPAVTPEASHLLEDPDEETSQAVKALREM  
ADTVIPQKEEAICGQMDLSHPPRGRHLDELTTTLESMTEDLNLDSPLELNEILDFTLN  
DECLLHAMHISTGLSIFDTSLFTSGGGSKRPAATKKAGQAKKKSR

BRD4<sup>BD2</sup>-VPR:

SV40 NLS

BRD4<sup>BD2</sup>

VPR

Nucleoplasmin NLS

MPKKKRRKVGGGSPGGGSSKVVSEQLKCCSGILKEMFAKKHAAAYAWPFYKPVDVEALG  
LHDYCDIHKHPMDMSTIKSKLEAREYRDAQEFGADVRLMFSNCYKYNPPDHEVVAMAR  
KLQDVFEMRFAKMPDGGGSRADPKKKRKRKVEASGSGRADALDDFDLDM LGSDALDDF  
DLDM LGSDALDDFDLDM LGSDALDDFDLDM LINSRSQYLPDTDDRHRIEEKRKRITYET  
FKSIMKKSPFSGPTDPRPPRRRIAVPSRSSASVPKPAPQYPFTSSLSTINYDEFPTMVFPSG  
QISQASALAPAPPQVLPQAPAPAPAPAMVSALAQAPAPVPLAPGPPQAVAPPAPKPTQ  
AGEGTLSEALLQLQFDDDLGALLGNSTDPVFTDLASVDNSEFQQLNQGIPVAPHTT  
EPMLMEYPEAITRLVTGAQRPPDPAPAPLAPGLPNGLLSGDEDFSSIADMDFSALLGSG  
SGSRDSREGMFLPKPEAGSAISDVFEGREVCQPKRIRPFHPPGSPWANRPLPASLAPTPTG  
PVHEPVGSLTPAPVPQPLDPAPAVTPEASHLLEDPDEETSQAVKALREMAADTVIPQKEEA  
AICGQMDLSHPPRGRHLDELTTTLESMTEDLNLDSPLELNEILDFTLNDECLLHAMHIS  
TGLSIFDTSLFTSGGGSKRPAATKKAGQAKKKSR

BRD4<sup>BD1</sup>-VPR:

SV40 NLS

BRD4<sup>BD1</sup>

VPR

Nucleoplasmin NLS

MPKKKRRKVGGGSPGGGGSNPPPPETSNPKNPKRQTNQLQYLLRVVLKTLWKHQFAWP  
FQQPVDAVKLNLPDYYKIIKTPMDMGTIKKRLENNYYWNAQECIQDFNTMFTNCYIYN  
KPGDDIVLMAEAELEKLFQKINELPTGGGSRADPKKKRKRKVEASGSGRADALDDFDLDM  
LGSDALDDFDLDM LGSDALDDFDLDM LGSDALDDFDLDM LINSRSQYLPDTDDRHRIE  
EKRKRITYETFKSIMKKSPFSGPTDPRPPRRRIAVPSRSSASVPKPAPQYPFTSSLSTINYD  
EFPTMVFPSGQISQASALAPAPPQVLPQAPAPAPAPAMVSALAQAPAPVPLAPGPPQAV  
APPAPKPTQAGEGTLSEALLQLQFDDDLGALLGNSTDPVFTDLASVDNSEFQQLNQ  
GIPVAPHTTEPMLMEYPEAITRLVTGAQRPPDPAPAPLAPGLPNGLLSGDEDFSSIADM  
DFSALLGSGSGSRDSREGMFLPKPEAGSAISDVFEGREVCQPKRIRPFHPPGSPWANRPL  
ASLAPTPTGPVHEPVGSLTPAPVPQPLDPAPAVTPEASHLLEDPDEETSQAVKALREMA



TVIPQKEEAAICGQMDLSHPPPRGHLDELTTTLESMTEDLNLDSPLTPELNEILDFTLNDE  
CLLHAMHISTGLSIFDTSLFTSGGGSKRPAATKKAGQAKKKSR

GAL4-FKBP12:

SV40 NLS

GAL4 DBD

FKBP12

Nucleoplasmin NLS

MPKKKRKVGGGSPGGGSMKLLSSIEQACDICRLKKLKCSKEKPKCAKCLKNNWECRY  
SPKTKRSPLTRAHLTEVESRLERLEQLFLLIFPREDLDMILKMDSLQDIKALLTGLFVQDN  
VNKDAVTDRLASVETDMPLTLRQHRISATSSSEESSNKGQRQLTVSGGGSMGVQVETIS  
PGDGRTPFKRGQTCVVHYTGMLEDGKKFDSSRDNRNPKFKFMLGKQEVIRGWEEGVAQ  
MSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLETSGGGSKRPAATKKAGQ  
AKKKSR

GAL4-tALK:

SV40 NLS

GAL4 DBD

tALK

Nucleoplasmin NLS

MPKKKRKVGGGSPGGGSMKLLSSIEQACDICRLKKLKCSKEKPKCAKCLKNNWECRY  
SPKTKRSPLTRAHLTEVESRLERLEQLFLLIFPREDLDMILKMDSLQDIKALLTGLFVQDN  
VNKDAVTDRLASVETDMPLTLRQHRISATSSSEESSNKGQRQLTVSGGGSRTSTIMTDY  
NPNYCFAGKTSSISDLKEVPRKNITLIRGLGHGAFGEVYEGQVSGMPNDPSPLQVAVKTL  
PEVCSEQDELDFLMEALIISKFNHQIVRCIGVSLQSLPRFILLELMAGGDLKSFLRETRPR  
PSQPSSLAMLDLLHVARDIACGCQYLEENHFIHRDIAARNCLLTCGPGRVAKIGDFGM  
ARDIYRASYYRKGGCAMLPVKWMPPEAFMEGIFTSKTDTSFVLLWEIFSLGYMPYP  
SKSNQEVLEFVTSGGRMDPPKNCPGPVYRIMTQCWQHQPEDRPNFAILERIEYCTQDPD  
VINTALPIEYGPLVEEEEKTSGGGSKRPAATKKAGQAKKKSR

VHL-VPR:

SV40 NLS

VHL

VPR

Nucleoplasmin NLS

MPKKKRKVGGGSPGGGSMPRRAENWDEAEVGAEEAGVEEYGPEEDGGEEESGAEESG  
PEESGPEELGAEEMEAGRPRPVLRSVNSREPSQVIFCNRSPRVLPVWLNFDGEPQYP  
TLPPGTGRRHSYRGHLWFRDAGTHDGLLVNQTSELFVPSLNVGQPIFANITLPVYTLK  
ERCLQVVRSLVKPENYRRLDIVRSLYEDLEDHPNVQKDLERLTQERIAHQRMGDGGGS



GAL4-FKBP3:

SV40 NLS

GAL4 DBD

FKBP3

Nucleoplasmin NLS

MPKKKRKVGGGSPGGGSMKLLSSIEQACDICRLKKLKCSKEKPKCAKCLKNNWECRY  
SPKTKRSPLTRAHLTEVESRLERLEQLFLLIFPREDLDMILKMDSLQDIKALLTGLFVQDN  
VNKDAVTDRLASVETDMPLTLRQHRISATSSSEESSNKGQRQLTVSGGGSSPKYTKSVL  
KKGDKTNFPKGDVVHCWYTGTLQDGTVFDTNIQTSAKKKKNAKPLSFKVGVGKVR  
GWDEALLTMSKGEKARLEIEPEWAYGKKKGQPDAKIPPNAKLTFEVELVDIDTSGGGSKR  
PAATKKAGQAKKKSR

GAL4-ABI:

SV40 NLS

GAL4 DBD

ABI

Nucleoplasmin NLS

MPKKKRKVGGGSPGGGSMKLLSSIEQACDICRLKKLKCSKEKPKCAKCLKNNWECRY  
SPKTKRSPLTRAHLTEVESRLERLEQLFLLIFPREDLDMILKMDSLQDIKALLTGLFVQDN  
VNKDAVTDRLASVETDMPLTLRQHRISATSSSEESSNKGQRQLTVSGGGSMVPLYGFTSI  
CGRPEMEEAAVSTIPRFLQSSSGSMLDGRFDPQSAAHFFGVYDGHGGSQVANYCRERM  
HLALAEIIEAKEKPMLCDGDTWLEKWKALFNSFLRVDSEIESVAPETVGTSTVAVVFP  
SHIFVANCGDSRAVLCRGKTALPLSVDHKPDREDEAARIEAAGGKVIQWNGARVFGVL  
AMRSIGDRYLKPSIIPDPEVTAVKRVKEDDCLILASDGVWDVMTDEEACEMARKRILL  
WHKKNVAVAGDASLLADERRKEGKDPAAAMSAEYLSKLAIQRGSKDNISVVVVDLKKL  
TSGGGSKRPAATKKAGQAKKKSR

PYL-VPR:

SV40 NLS

FRB

VPR

Nucleoplasmin NLS

MPKKKRKVGGGSPGGGSAPTQDEFTQLSQSIAEFHTYQLGNGRCSSLLAQRIHAPPET  
VWSVRRFRDPQIYKHFIKSCNVSEDFEMRVGCTRDVNVISGLPANTSRRERLDLDDDR  
RVTGFSITGGEHRLRNYKSVTTVHRFEKEEEEEERIWTVVLESYVVDVPEGNSEEDTRLFA  
DTVIRLNLQKLASITEAMNGGGSRADPKKKRKVEASGSGRADALDDFDLMLGSDALD  
DFDLMLGSDALDDFDLMLGSDALDDFDLMLINSRSQYLPDTDDRHRIEEKRKRTY  
ETFKSIMKKSPFSGPTDPRPPPRRIA VPSRSSASVPKPAPQYPFTSSLSTINYDEFPTMVFP  
SGQISQASALAPAPPQVLPQAPAPAPAPAMVSALAQAPAPVPVLPAGPPQAVAPPAPKPT

QAGEGTLSEALLQLQFDDDELGALLGNSTDPVFTDLASVDNSEFQQLLNQGIPVAPHT  
TEPMLMEYPEAITRLVTGAQRPPDPAPAPLGAPGLPNGLLSGDEDFSSIADMDFSALLGS  
GSGSRDSREGMFLPKPEAGSAISDVFEGREVCQPKRIRPFHPPGSPWANRPLPASLAPTPT  
GPVHEPVGSLTPAPVPQPLDPAPA VTPEASHLLEDPDEETSQAVKALREMADTVIPQKEE  
AAICGQMDLSHPPPRGHLEDELTTTLESMTEDLNLDSP LTPELNEILD TFLNDECLLHAMH  
ISTGLSIFD TSLFTSGGGSKRPAATKKAGQAKKKKSR

FRB-VPR:

SV40 NLS

FRB

VPR

Nucleoplasmin NLS

MPKKKRKVGGGSPGGGGSSILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAM  
MERGPQTLKETSFNQAYGRDLMEAQEWCRKYMKSGNVKDLTQAWDLYHVFRRISG  
GGSRADPKKKRKEASGSGRADALDDFDLDM LGSDALDDFDLDM LGSDALDDFDLD  
MLGSDALDDFDLDM LINSRSQYLPDTDDRHRIEEKRKRTYETFKSIMKKS PFSGPTDPRP  
PPRIA VPSRSSASVPKPAPQYPFTSSLSTINYDEFPTMVFP SGQISQASALAPAPPQVLP  
QAPAPAPAPAMVSALAQAPAPVPVLAPGPPQAVAPPAPKPTQAGEGTLSEALLQLQFDD  
EDLGALLGNSTDPVFTDLASVDNSEFQQLLNQGIPVAPHTTEPMLMEYPEAITRLVTG  
AQRPPDPAPAPLGAPGLPNGLLSGDEDFSSIADMDFSALLGSGSGSRDSREGMFLPKPEA  
GSAISDVFEGREVCQPKRIRPFHPPGSPWANRPLPASLAPTPTGPVHEPVGSLTPAPVPQP  
LDPAPA VTPEASHLLEDPDEETSQAVKALREMADTVIPQKEEAAICGQMDLSHPPPRGH  
LDELTTTLESMTEDLNLDSP LTPELNEILD TFLNDECLLHAMHISTGLSIFD TSLFTSGGGG  
KRPAATKKAGQAKKKKSR

GAL4-IKZF1:

SV40 NLS

GAL4 DBD

IKZF1

Nucleoplasmin NLS

MPKKKRKVGGGSPGGGGSMKLLSSIEQACDICRLKKLKCSEKPKCAKCLKNNWECRY  
SPKTKRSPLTRAHLTEVESRLERLEQLFLLIFPREDLDMILKMDSLQDIKALLTGLFVQDN  
VNKDAVTDRLASVETDMPLTLRQHRISATSSSEESSNKGQRQLTVS GSGSMDADEGQD  
MSQVSGKESPPVSDTPDEGDEPMPIPEDLSTTSGGQQSSKSDRVVASNVKVETQSDEEN  
GRACEMNGEECAEDLRMLDASGEKMNGSHRDQGSSALSGVGGIRLPNGKCLKDCIGIIC  
IGPNVLMVHKRSHTGERPFQCNCQCGASFTQKGNLLRHIKLHSGEKPFKCHLCNYACRRR  
DALTGHLRTHSVIKEETNHSEMAEDLCKIGSERSLVLDRLASNVAKRKSSMPQKFLGDK  
GLSDTPYDSSASYEKENEMMKSHVMDQAINNAINYLGAESLRPLVQTPPGGSEVVPVIS  
PMYQLHKPLAEGTPRSNHSQAQDSAVENLLLLSKAKLVPSEREASPSNSCQDSTD TESNN  
EEQRSGLIYLTNHIAPHARNGLSLKEEHRAYDLLRAASENSQDALRVVSTSGEQMKVYK  
CEHCRVFLDHV MYTIHMGCHGFRDPFECNMC GYHSQDRYEFSSHITRGEHRFHMSTS  
GGGSKRPAATKKAGQAKKKKSR

GAL4-IKZF3:

SV40 NLS

GAL4 DBD

IKZF3

Nucleoplasmin NLS

MPKKKRKVGGGSPGGGSMKLLSSIEQACDICRLKCLKCSKEKPKCAKCLKNNWECRY  
SPKTKRSPLTRAHLTEVESRLERLEQLFLLIFPREDLDMILKMDSLQDIKALLTGLFVQDN  
VNKDAVTDRLASVETDMPLTLRQHRISATSSSEESSNKGQRQLTVSGSGSMEDIQTNAE  
LKSTQEQSVAESA AVLNDYSLTKSHEMENVDSGEGPANEDEDIGDDSMKVKDEYSER  
DENVLKSEPMGNAEPEIPYSYSREYNEYENIKLERHVVSFDSSRPTSGKMNCDCVGLSC  
ISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYACQRR  
DALTGHLRTHSVKPYKCEFCGRSYKQRSSLEEHEKERCRTFLQSTDPGDTASAEARHIK  
AEMGSERALVLDRLASNVAKRKSSMPQKFIGEKRHCFDVNYNSSYMYEKESELIQTRM  
MDQAINNAISYLGAEALRPLVQTPPAPTSEMVPVISSMYPIALTRAEMSNGAPQELEKKS  
IHLPEKSVPSERGLSPNNSGHDSTDTDSNHEERQNHYYQQNHMVLSRARNGMPLLKEVP  
RSYELLKPPPICPRDSVKVINKEGEVMDVYRCDHCRVFLFDYVMFTIHMGCCHGFRDPFE  
CNMCGYRSHDRYEFSSHIARGEHRALLKTSGGGSKRPAATKKAGQAKKKKSR

IKZF1-GAL4:

SV40 NLS

IKZF1

GAL4 DBD

Nucleoplasmin NLS

MPKKKRKVGGGSPGGGGSMDADEGQDMSQVSGKESPPVSDTPDEGDPEMPPIPEDLSTT  
SGGQSSKSDRVVASNVKVETQSDEENGRACEMNGEECAEDLRMLDASGEKMNGSHR  
DQGSSALSGVGGIRLPNGKCLKCDICGIICIGPNVLMVHKRSHTGERPFQCNQCGASFTQK  
GNLLRHIKLHSGEKPFKCHLCNYACRRRDAL TGHLRTHSVIKEETNHSEMAEDLCKIGS  
ERSLVLDRLASNVAKRKSSMPQKFLGDKGLSDTPYDSSASYEKENEMMKSHVMDQAIN  
NAINYLGAESLRPLVQTPPGGSEVVPVISPMYQLHKPLAEGTPRSNHSQAQDSAVENLLLL  
SKAKLVPSEREASPSNSCQDSTDTESNNEEQRSGLIYLTNHIAPHARNGLSLKEEHAYD  
LLRAASENSQDALRVVSTSGEQMKVYKCEHCRVFLFDHVMYTIHMGCCHGFRDPFECN  
MCGYHSQDRYEFSSHITRGEHRFHMSGSGSMKLLSSIEQACDICRLKCLKCSKEKPKCA  
KCLKNNWECRYSPKTKRSPLTRAHLTEVESRLERLEQLFLLIFPREDLDMILKMDSLQDI  
KALLTGLFVQDNVNKDAVTDRLASVETDMPLTLRQHRISATSSSEESSNKGQRQLTVST  
SGGGSKRPAATKKAGQAKKKKSR

IKZF3-GAL4:

SV40 NLS

IKZF3

GAL4 DBD

## Nucleoplasmin NLS

MPKKKRKVGGGSPGGGSMEDIQTNAELKSTQEQSVPAESA AVLNDYSLTKSHEMENV  
DSGEGPANEDIDIGDDSMKVKDEYSERDENVLKSEPMGNAEPEPEIPYSYSREYNEYENI  
KLERHVVSFDSSRPTSGKMNCDCVGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQK  
GNLLRHILKHTGEKPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSL  
EEHKERCRTFLQSTDPGDTASAEARHIKAEMGSERALVLDRLASNVAKRKSSMPQKFIG  
EKRHCDFVNYNSSYMYEKESELIQTRMMDQAINNAISYLGAEALRPLVQTPPAPTSEMV  
PVISSMYPIALTRAEMSNGAPQELEKKSIIHLPEKSVPSERGLSPNNSGHDSTDTDSNHEER  
QNHYYQQNHMVLSRARNGMPLLKEVPRSYELLKPPPICPRDSVKVINKEGEVMDVYRC  
DHCRVFLDYVMFTIHMGCHEFRDPFECNMCGRYSHDRYEFSSHIARGEHRALLKGGG  
SMKLLSSIEQACDICRLKCLKCSKEKPKCAKCLKNNWECRYSPKTKRSPLTRAHLTEVE  
SRLERLEQLFLLIFPREDLDMILKMDSLQDIKALLTGLFVQDNVNKDAVTDRLASVETD  
MPLTLRQHRISATSSSEESSNKGQRQLTVSTSGGSKRPAATKKAGQAKKKSR

CRBN-GAL4:

SV40 NLS

CRBN

GAL4 DBD

Nucleoplasmin NLS

MPKKKRKVGGGSPGGGSMAGEGDQQDAAHNMGNHLPLLPESEEEDEMEVEDQDSK  
EAKKPNIINFDTSLPTSHTYLGADMEEFHGRTLHDDDDSCQVIPVLPQVMMILIPGQTLPL  
QLFHPQEVSMVRNLIQKDRTFVLAYSNVQEREAQFGTTAEIYAYREEQDFGIEIVKVK  
AIGRQRFKVLRLTQSDGIQQAQVQILPECVLPSTMSAVQLESLNKCQIFPSKPVSRDQC  
SYKWWQKYQKRKFHCANLTSWPRWLYSLYDAETLMDRIKKQLREWDENLKDDSLPS  
NPIDFSYRVAACLPIDDVLRIQLLKIGSAIQRLRCELDIMNKCTSLCCKQCQETEITTKNEI  
FSLSLCGPMAAYVNPHGYVHETLTVYKACNLNLIGRPSTEHSWFPGYAWTVAQCKICA  
SHIGWKFTATKKDMSPQKFWGLTRSALLPTIPDTEDEISPDK VILCLGGGSMKLLSSIEQA  
CDICRLKCLKCSKEKPKCAKCLKNNWECRYSPKTKRSPLTRAHLTEVESRLERLEQLFL  
LIFPREDLDMILKMDSLQDIKALLTGLFVQDNVNKDAVTDRLASVETDMPLTLRQHRIS  
ATSSSEESSNKGQRQLTVSTSGGSKRPAATKKAGQAKKKSR

GAL4-CRBN:

SV40 NLS

GAL4 DBD

CRBN

Nucleoplasmin NLS

MPKKKRKVGGGSPGGGSMKLLSSIEQACDICRLKCLKCSKEKPKCAKCLKNNWECRY  
SPKTKRSPLTRAHLTEVESRLERLEQLFLLIFPREDLDMILKMDSLQDIKALLTGLFVQDN  
VNKDAVTDRLASVETDMPLTLRQHRISATSSSEESSNKGQRQLTVSGGSMAGEGDQQ  
DAAHNMGNHLPLLPESEEEDEMEVEDQDSKEAKKPNIINFDTSLPTSHTYLGADMEEFH  
GRTLHDDDDSCQVIPVLPQVMMILIPGQTLPLQLFHPQEVSMVRNLIQKDRTFVLAYSN

VQEREAQFGTTAEIYAYREEQDFGIEIVKVKAIQRQRFKVLRLRTQSDGIQQAKVQILPEC  
VLPSTMSAVQLESLNKCQIFPSKPVSRREDQCSYKWWQKYQKRKFHCANLTSWPRWLYS  
LYDAETLMDRIKKQLREWDENLKDDSLPSNPIDFSYRVAACLPIDDVLRIQLLKIGSAIQR  
LRCELDIMNKCTSLCCKQCQETEITTKNEIFSLSLCGPMAAYVNPHGYVHETLTVYKAC  
NLNLIGRPSTEHSWFPGYAWTVAQCKICASHIGWKFTATKKDMSPQKFWGLTRSALLPT  
IPDTEDEISPKVILCLTSGGGSKRPAATKKAGQAKKKSR

VPR-CRBN:

SV40 NLS

VPR

CRBN

Nucleoplasmin NLS

MPKKKRKVGGGSPGGGSRADPKKKRKEASGSGRADALDDFDLMLGSDALDDFDL  
DMLGSDALDDFDLMLGSDALDDFDLMLINSRSQYLPDTDDRHRIEEKRRRTYETFK  
SIMKKS PFSGPTDPRPPPRRIA VPSRSSASVPKPAPQYPFTSSLSTINYDEFPTMVFP  
SQASALAPAPPQVLPQAPAPAPAMVSALAQAPAPVPLAPGPPQAVAPPAPKPTQAG  
EGTLSEALLQLQFDDEDL GALLGNSTDP AVFTDLASVDNSEFQQLLNQGIPVAPHTTEP  
MLMEYPEAITRLVTGAQRPPDPAPAPL GAPGLPNGLLSGDEDFSSIADMDFSALLGSGSG  
SRDSREGMFLPKPEAGSAISDVFE GREVCQPKRIRPFHPPGSPWANRPLPASLAPTPTGPV  
HEPVGSLTPAPVPQPLDPAPAVTPEASHLLEDPEETSQAVKALREMA DTVIPQKEEAAI  
CGQMDLSHPPPRGHLDELTTTLESMTEDLNLDSP LTPELNEILD TFLNDECLLHAMHIST  
GLSIFDTSLFGGGSMAGEGDQQA AHNMGNHLPLLPES EEEDEMEVEDQDSKEAKKPN  
IINFDTSLPTSHTYLGADMEEFHGRTLHDDSDCQVIPVLPQVMMILIPGQTLPLQLFHPQE  
VSMVRNLIQKDRTF AVLAYS NVQEREAQFGTTAEIYAYREEQDFGIEIVKVKAIQRQRFK  
VLELRTQSDGIQQAKVQILPECVLPSTMSAVQLESLNKCQIFPSKPVSRREDQCSYKWWQ  
KYQKRKFHCANLTSWPRWLYSLYDAETLMDRIKKQLREWDENLKDDSLPSNPIDFSYR  
VAACLPIDDVLRIQLLKIGSAIQR LRCELDIMNKCTSLCCKQCQETEITTKNEIFSLSLCGP  
MAAYVNPHGYVHETLTVYKACNLNLIGRPSTEHSWFPGYAWTVAQCKICASHIGWKFT  
ATKKDMSPQKFWGLTRSALLPTIPDTEDEISPKVILCLTSGGGSKRPAATKKAGQAKK  
KKSR

FKBP12<sup>F36V</sup>-GAL4:

SV40 NLS

FKBP12<sup>F36V</sup>

GAL4 DBD

Nucleoplasmin NLS

MPKKKRKVGGGSPGGGSMGVQVETISPGDGRTFPKRGQTCVVHYTG MLEDGKKVDS  
SRDRNPKPFKMLGKQEVIRGWEEGVAQMSV GQRAKLTISPDYAYGATGHPGIIPPHATL  
VFDVELLKLEGGGSMKLLSSIEQACDICRLK LKCSKEKPKCAKCLKNNWECRYSPKTK  
RSPLTRAHLTEVESRLERLEQLFLLIFPREDLDMILKMDSLQDIKALLTGLFVQDNVND  
AVTDLASVETDMPLTLRQHRISATSSSEESSNKGQRQLTVSTSGGGSKRPAATKKAGQ  
AKKKKSR

FKBP12<sup>F36V</sup>-VPR:

SV40 NLS

FKBP12<sup>F36V</sup>

VPR

Nucleoplasmin NLS

MPKKKRKVGGGSPGGGSMGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKVDS  
SRDRNKPFKMLGKQEVIRGWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATL  
VFDVELLKLEGGGSRADPKKKRKVEASGSGRADALDDFDLMLGSDALDDFDLMLG  
SDALDDFDLMLGSDALDDFDLMLINSRSQYLPDTDDRHRIEEKRKRTYETFKSIMKK  
SPFSGPTDPRPPRRIAVPSRSSASVPKPAPQYPFTSSLSTINYDEFPTMVFPSPGQISQASA  
LAPAPPQVLPQAPAPAPAPAMVSALAQAPAPVPLAPGPPQAVAPPAPKPTQAGEGTLS  
EALLQLQFDDDELGALLGNSTDPAVFTDLASVDNSEFQQLLNQGIPVAPHTTEPMLMEY  
PEAITRLVTGAQRPPDPAPAPLGAAPGLPNGLLSGDEDFSSIADMDFSALLGSGSGSRDSRE  
GMFLPKPEAGSAISDVFEGREVCQPKRIRPFHPPGSPWANRPLPASLAPTPTGPVHEPVGS  
LTPAPVPQPLDPAPA VTPPEASHLLEDPEETSQAVKALREMA DTVIPQKEEAAICGQMD  
LSHPPRGHLDELTTTLESMTEDLNLDSP LTPELNEILD TFLNDECLLHAMHISTGLSIFDT  
SLFTSGGGSKRPAATKKAGQAKKKKSR

VPR-FKBP12<sup>F36V</sup>:

SV40 NLS

VPR

FKBP12<sup>F36V</sup>

Nucleoplasmin NLS

MPKKKRKVGGGSPGGGSRADPKKKRKVEASGSGRADALDDFDLMLGSDALDDFDL  
DMLGSDALDDFDLMLGSDALDDFDLMLINSRSQYLPDTDDRHRIEEKRKRTYETFK  
SIMKKS PFSGPTDPRPPRRIAVPSRSSASVPKPAPQYPFTSSLSTINYDEFPTMVFPSPGQI  
SQASALAPAPPQVLPQAPAPAPAPAMVSALAQAPAPVPLAPGPPQAVAPPAPKPTQAG  
EGTLSEALLQLQFDDDELGALLGNSTDPAVFTDLASVDNSEFQQLLNQGIPVAPHTTEP  
MLMEYPEAITRLVTGAQRPPDPAPAPLGAAPGLPNGLLSGDEDFSSIADMDFSALLGSGSG  
SRDSREGMFLPKPEAGSAISDVFEGREVCQPKRIRPFHPPGSPWANRPLPASLAPTPTGPV  
HEPVGSLTPAPVPQPLDPAPA VTPPEASHLLEDPEETSQAVKALREMA DTVIPQKEEAAI  
CGQMDLSHPPRGHLDELTTTLESMTEDLNLDSP LTPELNEILD TFLNDECLLHAMHIST  
GLSIFDTSLFGGGSMGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKVDS SRDRNK  
PFKMLGKQEVIRGWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVEL  
LKLETSGGGSKRPAATKKAGQAKKKKSR

BRD9<sup>BD</sup>-GAL4:

SV40 NLS

BRD9<sup>BD</sup>



GAL4 DBD

Nucleoplasmin NLS

MPKKKRKVGGGSPGGGGSESTPIQQLLEHFLRQLQRKDPHGFFAFPVTDIAIPGYSMIIK  
HPMDFGTMKDKIVANEYKSVTEFKADFKLMCDNAMTYNRPDTVYYKLAKKILHAGFK  
MMSGGSMKLLSSIEQACDICRLKCLKSKEKPKCAKCLKNNWECRYSPKTKRSPLTR  
AHLTEVESRLERLEQLFLLIFPREDLDMILKMDSLQDIKALLTGLFVQDNVNKDAVTDRL  
ASVETDMPLTLRQHRISATSSSEESSNKGQRQLTVSTSGGGSKRPAATKKAGQAKKKKS  
R

TetR-FKBP12<sup>F36V</sup>:

SV40 NLS

TetR

FKBP12<sup>F36V</sup>

Nucleoplasmin NLS

MPKKKRKVGGGSPGGGMSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTL  
YWHVKNKRALLDALAIEMLDLRHHTHFCPLEGESWQDFLRNNAKSFRCALLSHRDGAK  
VHLGTRPTEKQYETLENQLAFLCQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKE  
ERETPTTDSMPLLRQAIELFDHQGAEP AFLFGLELIICGLEKQLKCESGGPAGGGSMGV  
QVETISPGDGRTPFKRGQTCVVHYTGMLEDGKKVDSSRDRNKPFKFMLGKQEVIRGWE  
EGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLETSGGGSKRPAAT  
KKAGQAKKKKSR

TetR-BRD9<sup>BD</sup>:

SV40 NLS

TetR

FKBP12<sup>F36V</sup>

Nucleoplasmin NLS

MPKKKRKVGGGSPGGGMSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTL  
YWHVKNKRALLDALAIEMLDLRHHTHFCPLEGESWQDFLRNNAKSFRCALLSHRDGAK  
VHLGTRPTEKQYETLENQLAFLCQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKE  
ERETPTTDSMPLLRQAIELFDHQGAEP AFLFGLELIICGLEKQLKCESGGPAGGGSESTPI  
QQLLEHFLRQLQRKDPHGFFAFPVTDIAIPGYSMIIKHPMDFGTMKDKIVANEYKSVTE  
FKADFKLMCDNAMTYNRPDTVYYKLAKKILHAGFKMMSTSGGGSKRPAATKKAGQA  
KKKKS

ABE8e-SpG:

SV40 NLS

ABE8e

SpG Cas9 nickase

MKRTADGSEFESPKKKRKVSEVEFSHEYWMRHALTLAKRARDEREVPVGAVLVLNNR  
VIGEGWNRAIGLHDPTAHAEIMALRQGGLVMQNYRLIDATLYVTFEPCVMCAGAMIHS  
RIGRVVFGVRNSKRGAAGSLMNVLNYPGMNHRVEITEGILADECAALLCDFYRMPRQV  
FNAQKKAQSSINSGGSSGGSSGSETPGTSESATPESSGGSSGSDKKYSIGLAIGTNSVGW  
AVITDEYKVPSSKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKN  
RICYLQEIFSNEMAKVDDSFHRLSEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHL  
RKKLVDSTDKADRLIYLALAHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEE  
NPINASGVDAKAILSARLSKSRLENLIAQLPGEKKNLFGNLIASLGLTPNFKSNFDLA  
EDAKLQLSKDQYDDDLNLLAQIGDQYADFLAAKNLSDAILLSDILRVNTEITKAPLSA  
SMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPI  
LEKMDGTEELLVKNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFLKDNREK  
IEKILTRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASASQSFIERMTNFD  
KNLPNEKVLPHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNR  
KVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIKDKDFLDNEENEDILE  
DIVLTLTLFEDREMIEERLKYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSG  
KTILDFLKSDFANRNFMLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKG  
ILQTVKVVDELVKVMGRHKPENIVEMARENQTTQKGQKNSRERMKRIEELGKELGSQI  
LKEHPVENTQLQNEKLYLYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSID  
NKVLTRSDKNRSGSDNVPSEEVVKMKMKNYWRQLLNAKLITQRKFDNLTKAERGGGLSE  
LDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSCLVSDFRKDF  
QFYKREINNYHHAHDAYLNAVVGTAIIKKYPKLESEFVYGDYKVVYDVRKMIKSEQE  
IGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLS  
MPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFLWPTVAYSVLVV  
AKVEKGGKSKKLKSVKELLGITIMERSSEFEKNPIDFLEAKGYKEVKKDLIILPKYSLFELE  
NGRKRMLASAKQLQKGNELALPSKYVNFYLYASHYEKLGKSPEDNEQKQLFVEQHKH  
YLDEIIEQISEFSKRVLADANLDKVL SAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKY  
FDTTIDRKQYRSTKEVLDA TLHQ SITGLYETRIDLSQLGGDSGPKKKRKV

tCRBN-VPR-1:

SV40 NLS

tCRBN

VPR

Nucleoplasmin NLS

MPKKKKRKVGGGSPGGGSLKDDSLPSNPIDFSYRVAACLPIDDVLRIQLLKIGSAIQRLR  
CELDIMNKCTSLCCKQCQETEITTKNEIFSLSLCGPMAAYVNPBGYVHETLTVYKACNL  
NLIGRPSTEHSWFPGYAWTVAQCKICASHIGWKFTATKKDMSPQKFWGLTRSALLPTIP  
DTEDEISPDKVLCLGGGSRADPKKKRKVEASGSGRADALDDFDLMLGSDALDDFDL  
DMLGSDALDDFDLMLGSDALDDFDLMLINSRSQYLPDTDDRHRRIEEKRKRRTYETFK  
SIMKKSPPSGPTDPRPPRRRIAVPSRSSASVPKPAPQPYPFTSSLSTINYDEFPTMVFPDQI  
SQASALAPAPPQVLPQAPAPAPAPAMVSALAQAPAPVPVLAPGPPQAVAPPAPKPTQAG  
EGTLSEALLQLQFDDEDLGALLGNSTDPVFTDLASVDNSEFQQLLNQGIPVAPHTTEP  
MLMEYPEAITRLVTGAQRPPDPAPAPLGAPGLPNGLLSGDEDFSSIADMDFSALLGSGSG  
SRDSREGMFLPKPEAGSAISDVFEGREVCQPKRIRPFHPPGSPWANRPLPASLAPTPTGPV  
HEPVGSLTPAPVPQPLDPAPAVTPEASHLLEDPEETSQAVKALREMADTVIPQKEEAAI

CGQMDLSHPPPRGHLDELTTTLESMTEDLNLDSPLELNEILDFTLNDECLLHAMHIST  
GLSIFDTSLFTSGGGSKRPAATKKAGQAKKKSR

tCRBN-VPR-2:

SV40 NLS

tCRBN

VPR

Nucleoplasmin NLS

MPKKKRKVGGGSPGGGGSMAEGEQDQDAAHNMGNHLPLLPESSEEDEMEVEDQDSK  
EAKKPNINFDTSLPTSHTYLADMEEFHGRTLHDDSDSCQVIPVLPQVMMILIPGQTLPL  
QLFHPQEVSMVRNLIQKDRTFVLAYSINVQEREAQFGTTAEIYAYREEQDFGIEIVKVK  
AIGRQRFKVLRLTQSDGIQQAQVQILPECVLPATLMDRIKKQLREWDENLKDDSLPSN  
PIDFSYRVAACLPIDDVLRIQLLKIGSAIQLRCELDIMNKCTSLCCKQCQETEITTKNEIF  
SLSLCGPMAAYVNPBGYVHETLTVYKACNLNLIGRPSTESHSWFPGYAWTVAQCKICAS  
HIGWKFTATKKDMSPQKFWGLTRSALLPTIPDTEDEISPDK VILCLGGGSRADPKKKRK  
VEASGSGRADALDDFDLDMLGSDALDDFDLDMLGSDALDDFDLDMLGSDALDDFDLD  
MLNSRSQYLPDTDDRHRIEEKRKRTYETFKSIMKKSPPSGPTDPRPPRRRIAVPSRSSASV  
PKPAPQYPFTSSLSTINYDEFPTMVFPSPGQISQASALAPAPPQVLPQAPAPAPAPAMVSA  
LAQAPAPVPVLAPGPPQAVAPPAPKPTQAGEGTLSEALLQLQFDDDELGALLGNSTDPA  
VFTDLASVDNSEFQQLLNQGIPVAPHTTEPMLMEYPEAITRLVTGAQRPPDPAPAPLGA  
PLNGLLSGDEDFSSIADMDFSALLGSGSGSRDSREGMFLPKPEAGSAISDVFEGREVCQ  
PKRIRPFHPPGSPWANRPLPASLAPTPTGPVHEPVGSLTPAPVPQPLDPAPAVTPEASHLL  
EDPDEETSQAVKALREMA DTVIPQKEEAAICGQMDLSHPPPRGHLDELTTTLESMTEDL  
NLDSPLTPELNEILDFTLNDECLLHAMHISTGLSIFDTSLFTSGGGSKRPAATKKAGQAKK  
KSR

BRD4<sup>BD2</sup>-VP64-p65

SV40 NLS

BRD4<sup>BD2</sup>

VP64-p65

MPKKKRKVGGGSPGGGGS SKVSEQLKCCSGILKEMFAKKHAAAYAWPFYKPV DVEALG  
LHDYCDIHKHPMDMSTIKSKLEAREYRDAQEFGADVRLMFSNCYKYNPPDHEVVAMAR  
KLQDVFEMRFAKMPDGGGSRADPKKKRKVEASGSGRADALDDFDLDMLGSDALDDF  
DLMLGSDALDDFDLDMLGSDALDDFDLDMLNSRSQYLPDTDDRHRIEEKRKRTYET  
FKSIMKKSPPSGPTDPRPPRRRIAVPSRSSASV PKPAPQYPFTSSLSTINYDEFPTMVFPSPG  
QISQASALAPAPPQVLPQAPAPAPAPAMVSALAQAPAPVPVLAPGPPQAVAPPAPKPTQ  
AGEGTLSEALLQLQFDDDELGALLGNSTDPAVFTDLASVDNSEFQQLLNQGIPVAPHTT  
EPMLMEYPEAITRLVTGAQRPPDPAPAPLGA PLNGLLSGDEDFSSIADMDFSALLTTN  
PG

Fluc:

Fluc  
PEST Tag

MEDAKNIKKGPAPFYPLEDGTAGEQLHKAMKRYALVPGTIAFTDAHIEVDITYAEYFEM  
SVRLAEAMKRYGLNTNHRIVVCSENSLQFFMPVLGALFIGVAVAPANDIYNERELLSM  
GISQPTVVVFSKGLQKILNVQKLPPIQKIIIMDSKTDYQGFQSMYTFVTSHLPPGFNEY  
DFVPESFDRDKTIALIMNSSGSTGLPKGVALPHRTACVRFSHARDPIFGNQIIPDTAILS  
PFHHGFGMFTTLGYLICGFRVVLMYRFEELFLRSLQDYKIQSALLVPTLFSFFAKSTLID  
KYDLSNLHEIASGGAPLSKEVGEAVAKRFHLPGIRQGYGLTETTSAILITPEGDDKPGAV  
GKVVPFFEAKVVDLDTGKTLGVNQRGELCVRGPMIMSGYVNNPEATNALIDKDGWLH  
SGDIAYWDEDEHFFIVDRLKSLIKYKGYQVAPAELESILLQHPNIFDAGVAGLPDDDAGE  
LPAVVVLEHGKTMTEKEIVDYVASQVTTAKKLRGGVVVFVDEVPKGLTGKLDARKIRE  
ILIKAKKGGKIAVGSTGSSHGFPPEVEEQDDGTLPMSCAQESGMDRHPAACASARINV

Hel1a-BFP:

EBFP2

MVSKGEELFTGVVPILVELDGDVNGHKFSVRGEGEGDATNGKLTCLKFICTTGKLPVWP  
TLVTTLSHGVCQFARYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGTYKTRAEVKFEG  
DTLVNRIELKGVDFKEDGNILGHKLEYNFNHSHNIYIMAVKQKNGIKVNFKIRHNVEDGS  
VQLADHYQQNTPIGDGPVLLPDSHYLSTQSVLSKDPNEKRDHMLLEFRTAAGITLGM  
DELYK

EYFP:

MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGLKLTCLKFICTTGKLPVWP  
TLVTTFGYGLQCFARYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEG  
DTLVNRIELKGVDFKEDGNILGHKLEYNFNHSHNVYIMADKQKNGIKVNFKIRHNIEDGSV  
QLADHYQQNTPIGDGPVLLPDNHYSYQSKLSKDPNEKRDHMLLEFVTAAGITLGM  
ELYK

TRE-BFP:

TagBFP

MSELIKENMHMKLYMEGTVDNHHFKCTSEGEGKPYEGTQTMRIKVVEGGPLPFAFDIL  
ATSFLYGSKTFINHTQGIPDFFKQSFPEGFTWERVTTYEDGGVLTATQDQDTSQDGLIYN  
VKIRGVNFTSNGPVMQKKTGLWEAFTETLYPADGGLEGRNDMALKLVGGSHLIANIKT  
TYRSKKPAKNLKMGPVYYVDYRLRIKEANNETYVEQHEVAVARYCDLPSKLGH

TRE3G-Dre:

SV40 NLS

HA Tag

Dre

MPKKKRKVYPYDVPDYAGSSELIISGSSGGFLRNIGKEYQEAAENFMRFMNDQGAYAP  
NLRDLRLVFHSWARWCHARQLAWFISPEMAREYFLQLHDADLASTTIDKHYAMLN  
MLLSHCGLPPLSDDKSVSLAMRRIRREAATEKGERTGQAIPLRWDDLKLLDVLLSRSER  
LVDLNRNFLVAVYNTLMRMSEISRIRVGDLDQTGDTVTLHISHTKTITTAAGLDKVLRSR  
RTTAVLNDWLDVSGLREHPDAVLFPPIHRSNKARITTTPLTAPAMEKIFSDAWVLLNKR  
DATPNKGRYRTWTGHSARVGAIDMAEKQVSMVEIMQEGTWKKPETLMRYLRRGGV  
SVGANSRLMDS

TRE3G-Cre:

SV40 NLS

Cre

MPKKKRKVNLLTVHQNLPALPVDATSDEVKRNLMDFRDRQAFSEHTWKMLLSVCRS  
WAAWCKLNNRKWFPAEPEDVRDYLLYLQARGLAVKTIQQHLGQLNMLHRRSGLPRPS  
DSNAVSLVMRRIRKENVDAGERAKQALAFERTDFDQVRSLMENS DRCQDIRNLAFLGI  
AYNTLLRIAEIARIRVKDISRTDGGRM LIHIGRTKTLVSTAGVEKALS LGVTKLVERWISV  
SGVADDPNNYLCFRVRKNGVAAPSATSQ LSTRALEGIFEATHRLIYGAKDDSGQRYLA  
WSGHSARVGAARDMARAGVSIPEIMQAGGWTNVNIVMNYIRNLDSETGAMVRLLEDG  
DPKKKRKV

**Sequences S2. Sequences of primers used for plasmid cloning in this study.**

<b>Aim</b>	<b>Name</b>	<b>Sequence (5' to 3')</b>
GAL4-VHL	GAL4-F-d270	TAGCATGGTCTCACTCAATGAAGCTACTGTCTTCTATCGAACA AGCA
GAL4-VHL	GAL4-R-d270	ATAGGTCTCTCGATACAGTCAACTGTCTTTGACCTTTGTTACT
GAL4-VHL	VHL-F-d270	TAGTAGGTCTCAATCGGGTGGCGGCTCAATGCCCCGGAGGGC GGAGAACTGGG
GAL4-VHL	VHL-R-d270	TAGTAGGTCTCATAGTGGCAATCAATCTCCCATCCGT
TRIM24- VPR	TRIM24-1-F	TAGTGGTCTCACTCAGGTACCTCTAGAAGATCTAGGACAATGG AGGTGGCGGTGGAG
TRIM24- VPR	TRIM24-1-R	TAGTAGGTCTCACGGAGTCTCGGCCGAGCCCAGCATGGGCGC GGCAG
TRIM24- VPR	TRIM24-2-F	TAGTAGGTCTCATCCGCCACCCGTCCCTG
TRIM24- VPR	TRIM24-m-R	AGTAGGTCTCACATTCTAGGGTTTGGTAAACCCACAGGTGCTG GCC
TRIM24- VPR	TRIM24-m-F	TAGTAGGTCTCAAATGCAGGGGCCCATCCAGCA
TRIM24- VPR	TRIM24-2-R-c	TAGGTCTCACACCGCTAGCTGGCCAGGATCCCTGCAGGGTGAT ATCGGGCGGCCGCT
TRIM24- VPR	VPR-F	TAGTAGGTCTCAGGTGGCGGGTCGAGAGCTGACCCCAAGAAG AAGAG
TRIM24- VPR	VPR(L)-R	TAGGGTCTCATAGTAAACAACTTGTGTCAAATATACTCAGCC CGGTGCTGATGTGCAT
BRD4-VPR	BRD4-Front-F	AGGTCTCACTCAATGTCTGCGGAGAGCGGCCCTGGGACGAGA TTGAGAAATCTGCCAGT
BRD4-VPR	BRD4-front-R	TAGTGGTCTCACACCAGCGGGACCTGTTTCGGAGTCTTCGCTG TCAGAGGAGCTGGACT
BRD4-VPR	VPR-behind-F	TAGTAGGTCTCAGGTGGCGGGTCGAGAGCTGACCCCAAGAAG AAGAG

BRD4-VPR	VPR-behind-R	TAGGGTCTCATAGTAAACAAACTTGTGTCAAATATACTCAGCC CGGTGCTGATGTGCAT
GAL4-tALK	GAL4-F-d270	TAGCATGGTCTCACTCAATGAAGCTACTGTCTTCTATCGAACA AGCA
GAL4-tALK	GAL4-R-d270	ATAGGTCTCTCGATACAGTCAACTGTCTTTGACCTTTGTTACT
GAL4-tALK	ALK-1-F-d351-c	TATAGTGGTCTCAATCGGGTGGCGGCTCACGCACCTCGACCAT CATGACCG
GAL4-tALK	ALK-1-R-d351	TATAGGTCTCAGAGGAAGGACTTGAGATCTCCCCCGCCATGA GCTCCA
GAL4-tALK	ALK-2-F-d351	TAGTACGGTCTCACCTCCGAGAAACCCGCCCTCGCCCGAGCCA GCCCTCCTCC
GAL4-tALK	ALK-2-R-d351	TAGTAGGTCTCATAGTTTTTCTTCTTCTTCCACAAGTGGACCA TATTCTATCGGC
VHL-VPR	VHL-front-F	TAGTAGGTCTCACTCAATGCCCCGGAGGGCGGAGAACTGGG
VHL-VPR	VHL-front-F	TAGTAGGTCTCACACCATCTCCCATCCGTTGATGTGCAATGCG CTCCT
VHL-VPR	VPR-behind-F	TAGTAGGTCTCAGGTGGCGGGTCGAGAGCTGACCCCAAGAAG AAGAG
VHL-VPR	VPR-behind-R	TAGGGTCTCATAGTAAACAAACTTGTGTCAAATATACTCAGCC CGGTGCTGATGTGCAT
GAL4-BRD9	GAL4-F	TAGCATGGTCTCACTCAATGAAGCTACTGTCTTCTATCGAACA AGCA
GAL4-BRD9	GAL4-R	ATAGGTCTCTCGATACAGTCAACTGTCTTTGACCTTTGTTACT
GAL4-BRD9	BRD9-1-F	TAGTAGGTCTCAATCGGGTGGCGGCTCAATGGGCAAGAAGCA CAAGAAGCACA
GAL4-BRD9	BRD9-R	TAGTAGGTCTCATAGTGGTCTTGGCAGAGGCCGCAGGCTCTGG AGACTGAAGAAAC
GAL4-BRD4	BRD4-behind-F-c	TAGTAGGTCTCAGGTGGCGGCTCAATGTCTGCGGAGAGCGGC CCTGGGACGAGATTGAG

GAL4-BRD4	BRD4-behind-R-c	AGATGGTCTCATAGTAGCGGGACCTGTTTCGGAGTCTTCGCTG TCAGAGGAGCTGGACT
GAL4-BRD4	GAL4-front-F	AGTAGGTCTCACTCAATGAAGCTACTGTCTTCTATCGAACAAG CA
GAL4-BRD4	GAL4-front-R	TAGTAGGTCTCACACCCGATACAGTCAACTGTCTTTGACCTTT GTTACT
GAL4-ABI	ABI-F	TAGTAGGTCTCAGGTGGCGGCTCAATGGTGCCTTTGTATGGTT TTACT
GAL4-ABI	ABI-R	TAGTAGGTCTCATAGTTAGCTTCTTCAAATCAACCACCACC
GAL4-ABI	GAL4-front-F	AGTAGGTCTCACTCAATGAAGCTACTGTCTTCTATCGAACAAG CA
GAL4-ABI	GAL4-front-R	TAGTAGGTCTCACACCCGATACAGTCAACTGTCTTTGACCTTT GTTACT
PYL-VPR	PYL-F	TAGTAGGTCTCACTCAGCGCCAACCTCAAGACGA
PYL-VPR	VPR(L)-R	TAGGGTCTCATAGTAAACAAACTTGTGTCAAATATACTCAGCC CGGTGCTGATGTGCAT
GAL4- FKBP3	FKBP3-F	TATAGTAGGTCTCAATCGGGTGGCGGCTCAAGCCCCAAGTACA CCAAGAGC
GAL4- FKBP3	FKBP3-R	TAGTAGGTCTCATAGTGTGCGATGTCCACCAGCTCCACCTCA
GAL4- FKBP3	GAL4-F	TAGCATGGTCTCACTCAATGAAGCTACTGTCTTCTATCGAACA AGCA
GAL4- FKBP3	GAL4-R	ATAGGTCTCTCGATACAGTCAACTGTCTTTGACCTTTGTTACT
GAL4- FKBP12	GAL4-front-F	AGTAGGTCTCACTCAATGAAGCTACTGTCTTCTATCGAACAAG CA
GAL4- FKBP12	GAL4-front-R	TAGTAGGTCTCACACCCGATACAGTCAACTGTCTTTGACCTTT GTTACT
GAL4- FKBP12	FKBP12F36V- behind-F	TAGTAGGTCTCAGGTGGCGGCTCAATGGGAGTGCAGGTGGAA ACC



GAL4- FKBP12	FKBP12F36V- behind-R	TAGTAGGTCTCATAGTTTCCAGTTTTAGAAAGCTCCACATCGAA GACG
FRB-VPR	FRB-F	TAATGTGGTCTCACTCATCGAGCATCCTGTGGCA
FRB-VPR	FRB-R	TAGTAGGTCTCACACCCTGATCCTCCTGAACACGTGGT
FRB-VPR	VPR-behind-F	TAGTAGGTCTCAGGTGGCGGGTCGAGAGCTGACCCCAAGAAG AAGAG
FRB-VPR	VPR-behind-R	TAGGGTCTCATAGTAAACAAACTTGTGTCAAATATACTCAGCC CGGTGCTGATGTGCAT
TRIM24 <sup>BD</sup> - VPR	TRIM-F	TAGTAGGTCTCACTCACCCAATGAGGACTGGTGTGC
TRIM24 <sup>BD</sup> - VPR	TRIM-R	TAGTAGGTCTCACACCTGGATAGAGGTTCTTTAGAAGTTCTTC A
TRIM24 <sup>BD</sup> - VPR	VPR(L)-R	TAGGGTCTCATAGTAAACAAACTTGTGTCAAATATACTCAGCC CGGTGCTGATGTGCAT
TRIM24 <sup>BD</sup> - VPR	VPR-F	TAGTAGGTCTCAGGTGGCGGGTCGAGAGCTGACCCCAAGAAG AAGAG
BRD4 <sup>BD1</sup> - VPR	BRD4-BD1-F	TAGTAGGTCTCACTCAAACCCCCCGCCCCCAGAGACTT
BRD4 <sup>BD1</sup> - VPR	VPR-R	TAGGGTCTCATAGTAAACAAACTTGTGTCAAATATACTCAGCC CGGTGCTGATGTGCAT
BRD4 <sup>BD2</sup> - VPR	BRD4-BD2-F	TATAGGTCTCACTCAAGCAAGGTGTCGGAGCAGC
BRD4 <sup>BD2</sup> - VPR	VPR-R	TAGGGTCTCATAGTAAACAAACTTGTGTCAAATATACTCAGCC CGGTGCTGATGTGCAT
GAL4- BRD9 <sup>BD</sup>	GAL4-F	TAGCATGGTCTCACTCAATGAAGCTACTGTCTTCTATCGAACA AGCA
GAL4- BRD9 <sup>BD</sup>	GAL4-R	ATAGGTCTCTCGATACAGTCAACTGTCTTTGACCTTTGTTACT
GAL4- BRD9 <sup>BD</sup>	tBRD9-F	TAGTAGGTCTCAATCGGGTGGCGGCTCAGAGAGCACACCTATT CAGCAACTCCT

GAL4- BRD9 <sup>BD</sup>	tBRD9-R	TAGTGGTCTCATAGTGCTCATCATCTTAAAGCCTGCGTGAAGG ATCTTCT
pUAS-2-Fluc	UAS-F	AGCGAGGTCTCACTATTGCAGGCGATAGGTACCGAG
pUAS-2-Fluc	UAS-R	AGCGAGGTCTCAAAGCGCGCCCAGTACCGGAATG
pUAS-2-Fluc	Fluc-F	TAGTAGGTCTCAGCTTGGCAATCCGGTACTGT
pUAS-2-Fluc	Luci-R	TATAGGTCTCAATCCCACGGCGATCTTGCCGCCCTTCTTGG
pUAS-2-Fluc	PEST-R	ATAGGGTCTCATAGTTACACATTGATCCTAGCAGAAGCACAGG CTGCAGGGTGACG
pUAS-2-Fluc	PEST-F	TAGGGTCTCAGGATCCACCGGATCTAGCCATGGCTTCCCGCCG GAGGTGGAGGAGCAGG
TRE-EYFP	EYFP-F	TAGTAGGTCTCAGCTTATGGTGAGCAAGGGCGAGGAGCTGTTC ACCGGGGT
TRE-EYFP	EYFP-R	ATACGTAGGTCTCATAGTTTACTTGTACAGCTCGTCCATGCC
TRE-EYFP	TRE-F	AGCGAGGTCTCACTCATTGTATAGAAAAGTTGGCTCCGAA
TRE-EYFP	TRE-R	AGCGAGGTCTCAAAGCCGACCGGTAATCAGCCTGC
pUAS-1-Dre	UAS-F	TAGTAGGTCTCACTCAGCAGTTTATGGCGGGCGT
pUAS-1-Dre	569-6-1-R	TAGTAGGTCTCAGGTCCCGACATGGTGGCTCAGC
pUAS-1-Dre	dre-R	TAGTAGGTCTCATAGTGCCACAATCAGCTATCCATCAGTCGAG AATTGGCTCCCACGG
pUAS-1-Dre	dre-F	TAGTGGTCTCAGACCATGCCTAAGAAGAAGAGGAAGGTTTAC CCATACGATGTTCCAGA
TRE3G-Cre	TRE-3G-R	TAGTAGGTCTCAGGTCACTTTACGAGGGTAGGAAGTGGTACG
TRE3G-Cre	TRE3G-F	TAGTAGGTCTCACTCATTCGTCTTCAAGAATTCCTCGAG

TRE3G-Cre	TRE-cre-F	AGGTCTCAGACCATGCCAAAGAAGAAGCGGAAGGTCAATTTA CTGACCGTACACCAAAA
TRE3G-Cre	CreNLS-R-ACTA	TAGGTCTCATAGTTTAGACCTTCCGCTTCTTCTTATCGCCATCT TCCAGCAGGCGCACC
TRE3G-Dre	TRE-F	TAGTAGGTCTCACTCATTTCGTCTTCAAGAATTCCTCGAG
TRE3G-Dre	Dre-R	TAGTAGGTCTCATAGTGCCACAATCAGCTATCCATCAGTCGAG AATTGGCTCCCACGG
TRE3G- LoxP-STOP- LoxP-Cre	CreNLS-R-ACTA	TAGGTCTCATAGTTTAGACCTTCCGCTTCTTCTTATCGCCATCT TCCAGCAGGCGCACC
TRE3G- LoxP-STOP- LoxP-Cre	TRE-F	TAGTAGGTCTCACTCATTTCGTCTTCAAGAATTCCTCGAG
TRE3G- LoxP-STOP- LoxP-Cre	TRE3G-F	TAGTAGGTCTCACTCATTTCGTCTTCAAGAATTCCTCGAG
TRE3G- LoxP-STOP- LoxP-Cre	TRE-3G-R	TAGTAGGTCTCAGGTCACCTTACGAGGGTAGGAAGTGGTACG
TRE3G- LoxP-STOP- LoxP-Cre	A3G-1-F	TAGTAGGTCTCAGACCTAGAGATCCGCGGCCGC
TRE3G- LoxP-STOP- LoxP-Cre	A3G-m-R	TAGTAGGTCTCAGTTTCGTGTCTGCCCCGCA
TRE3G- LoxP-STOP- LoxP-Cre	A3G-m-F	TAGTAGGTCTCAAAACCTACCTGTGCTATGAGGTGGAGCGGAT GCACAACG
TRE3G- LoxP-STOP- LoxP-Cre	A3G-2-R	TAGTAGGTCTCACCTTTTTCTGCTCGCCGCTCAGGAAGGCGGG CT
TRE3G- LoxP-STOP- LoxP-Cre	A3G-3-F	TAGTAGGTCTCAAAGGCCATCGTGGACCTGCTGT
TRE3G- LoxP-STOP- LoxP-Cre	A3G-3-R	TAGTAGGTCTCATAGTAGGCACAGTCGAGGCTGA
TRE3G- ABE8e-SpG	TRE3G-F	TAGTAGGTCTCACTCATTTCGTCTTCAAGAATTCCTCGAG
TRE3G- ABE8e-SpG	TRE-3G-R-GACC	TAGTAGGTCTCAGGTCACCTTACGAGGGTAGGAAGTGGTACG

TRE3G- ABE8e-SpG	ABE(TRE-F)-gacc	TATGTGGTCTCAGACCGGAGAGCCGCCACCATGA
TRE3G- ABE8e-SpG	SpG-1-R	TATGAGGTCTCACCACGTACATATCCCGCCCATTCTGCAGG
TRE3G- ABE8e-SpG	SpG-2-F	TAGTGGTCTCAGTGGACCAGGAACTGGACATCAACCGGC
TRE3G- ABE8e-SpG	SpG-2-R	TAGTGGTCTCATAGTTTAGACTTTCCTCTTCTTCTTGGGGCCGC TGTCACCTCCCA
TRE3G- LoxP-STOP- LoxP- ABE8e-SpG	TRE3G-F	TAGTAGGTCTCACTCATTCGTCTTCAAGAATTCCTCGAG
TRE3G- LoxP-STOP- LoxP- ABE8e-SpG	TRE-3G-R-GACC	TAGTAGGTCTCAGGTCACTTTACGAGGGTAGGAAGTGGTACG
TRE3G- LoxP-STOP- LoxP- ABE8e-SpG	loxP-F	TAAGTAGGTCTCAGACCGGTGACCCGCCACCAA
TRE3G- LoxP-STOP- LoxP- ABE8e-SpG	loxP-R	TAGTAGGTCTCATGGGCTGCAGGTGAGG
TRE3G- LoxP-STOP- LoxP- ABE8e-SpG	ABE-F	TAGTAGGTCTCACCCAAGCCGCCACCATGAAACG
TRE3G- LoxP-STOP- LoxP- ABE8e-SpG	SpG-1-R	TATGAGGTCTCACCACGTACATATCCCGCCCATTCTGCAGG
TRE3G- LoxP-STOP- LoxP- ABE8e-SpG	SpG-2-F	TAGTGGTCTCAGTGGACCAGGAACTGGACATCAACCGGC
TRE3G- LoxP-STOP- LoxP- ABE8e-SpG	SpG-2-R	TAGTGGTCTCATAGTTTAGACTTTCCTCTTCTTCTTGGGGCCGC TGTCACCTCCCA
TRE3G-PE2	TRE3G-R	TAGTAGGTCTCAGGTCACTTTACGAGGGTAGGAAGTGGTACG
TRE3G-PE2	TRE3G-F	TAGTAGGTCTCACTCATTCGTCTTCAAGAATTCCTCGAG

TRE3G-PE2	Protac-PE-F	TAGTAGGTCTCAGACCATGAAACGGACAGCCGACGGAAGCGA GTT
TRE3G-PE2	Cas9-SpG-R	ATGATGGTCTCATCATGATGTTGCTGTAGAAGAAGTACTTGGC GGTAGC
TRE3G-PE2	Cas9-SpG-F	AGTAGGTCTCAATGAACTTTTTCAAGACCGAGATTACCCTGGC C
TRE3G-PE2	PE-1-R	TAGTAGGTCTCAGTCTCATGTAGCCGATACTCA
TRE3G-PE2	PE-2-F	TAGTAGGTCTCAAGACTTCAAAGAGCCAGATGTTTCTCTAGG GTCCACATGGCT
TRE3G-PE2	PE-4-R	TAGTAGGTCTCATAGTAAGGCACAGTCGAGGCTGA
microdeleted Cre	Cre-F	ATAGTGGTCTCACTCAATGAATTTACTGACCGTACACCAAAT TTGCCTGC
microdeleted Cre	Cre-deletion-1-R	ACCAGGTTTCGTTCACTCATGGAAAATAGCGATCGCTGCCAGGA TA
microdeleted Cre	Cre-deletion-2-F	TAGTAGGTCTCAGATACGTAATCTGGCATTCTGGGGATTGCT T
microdeleted Cre	Cre-R	ACTAGGTCTCTTAGTTTAGACTTTCCGCTTCTTCTTTGGATCGC CATCTTCCAGCAGGC
cre pegRNA	his6-U6-F	AGTGGTCTCACTCATGATAGTAGGAGGCTTGGTAGGT
cre pegRNA	His6-U6-R	TAGTAGGTCTCCCGGTGTTTCGTCCTTTCCA
His pegRNA	his6-U6-F	AGTGGTCTCACTCATGATAGTAGGAGGCTTGGTAGGT
His pegRNA	His6-U6-R	TAGTAGGTCTCCCGGTGTTTCGTCCTTTCCA
Virus a	EFS-F	CTCAGGTCTCACTATATTTGGCTCCGGTGCCCGTCAGTGGGCA GAGCG
Virus a	EFS-R	TAGTAGGTCTCATACTGTGTTCTGGCGGCA
Virus a	VHL-R-d550	AGTGGGTCTCAACGGGAAAGCTGGGTAGATCAGT
Virus a	GAL4-F	TAGTAGGTCTCAGGTACACCGGTGCCACCATGC
Virus a	CMV-R57	TAGTAGGTCTCAGCAGAAGTGGGTCTCTAGTTAGCC

Virus a	CMV-For-d459-v2	CTCAGGTCTCACCGTACGTATGTTCCCATAGTAACGCC
Virus a	P65-R	TAGTGGTCTCATAGTCAACAGGGCGCTAAAATCCATGTCTGGCG ATTGA
Virus a	BD2-F	TATAGGTCTCACTGCCACCGGTGCCACCATGC
Virus a	P65-R	TAGTGGTCTCATAGTCAACAGGGCGCTAAAATCCATGTCTGGCG ATTGA
Virus a	BD2-F	TATAGGTCTCACTGCCACCGGTGCCACCATGC
pUAS-1- EYFP	mini3G-F	TAGTAGGTCTCAGACTGGCGTGTACGGTGGGCGCCT
pUAS-1- EYFP	EYFP-R	ATACGTAGGTCTCATAGTTTACTTGTACAGCTCGTCCATGCC
Plasmids in SI	GAL4-F	TAGCATGGTCTCACTCAATGAAGCTACTGTCTTCTATCGAACA AGCA
Plasmids in SI	GAL4-R	TAGTAGGTCTCAAGCCCGATACAGTCAACTGTCTTTGACCTTT GTTACT
Plasmids in SI	ikzf1-F	TAGTAGGTCTCAGGCTCAGGCTCAATGGATGCTGATGAGGGTC AAGA
Plasmids in SI	ikzf1-R	TAGTAGGTCTCATAGTGCTCATGTGGAAGCGGTGCTCCCCT
Plasmids in SI	IZKF3-F	ATAGGTCTCAGGCTCAGGCTCAATGGAAGATATACAAACAAA TGCGGAACTGAAAAGCA
Plasmids in SI	izkf3-R	TAGTAGGTCTCATAGTCTTCAGCAGGGCTCTGTGTTCTCCT
Plasmids in SI	GAL4-F	TAGCATGGTCTCAATGAAGCTACTGTCTTCTATCGAACAAGCA
Plasmids in SI	GAL4-R	TAGTAGGTCTCATAGTCGATACAGTCAACTGTCTTTGACCTTT GTTACT
Plasmids in SI	ikzf1-F	TAGTAGGTCTCACTCAATGGATGCTGATGAGGGTCAAGA
Plasmids in SI	ikzf1-R	TAGTAGGTCTCATCATTGAGCCTGAGCCGCTCATGTGGAAGCG GTGCTCCCCT

Plasmids in SI	IZKF3-F	TAGTAGGTCTCACTCAATGGAAGATATACAAACAAATGCGGA ACTGAAAAGCACTCA
Plasmids in SI	izkf3-R	TAGTAGGTCTCATCATTGAGCCTGAGCCCTTCAGCAGGGCTCT GTGTTCTCCT
Plasmids in SI	CRBN-behind-F	AGGTCTCAGGTGGCGGCTCAATGGCCGGCGAAGGAGATCAGC AGGACGCTGCGCACAAC
Plasmids in SI	CRBN-behind-R	TAGTGGTCTCATAGTCAAGCAAAGTATTACTTTGTCTGGACTT ATTTCA
Plasmids in SI	CRBN-Front-F	TAGTAGGTCTCACTCAATGGCCGGCGAAGGAGATCAGCAGGA CGCTGCGCACAAC
Plasmids in SI	CRBN-Front-R	TAGTGGTCTCACACCCAAGCAAAGTATTACTTTGTCTGGACTT ATTTCA
Plasmids in SI	FKBP12F36V-behind-F	TAGTAGGTCTCAGGTGGCGGCTCAATGGGAGTGCAGGTGGAA ACC
Plasmids in SI	FKBP12F36V-behind-R	TAGTAGGTCTCATAGTTTCCAGTTTTAGAAGCTCCACATCGAA GACG
Plasmids in SI	FKBP12F36V-front-F	TATAGTGGTCTCACTCAATGGGAGTGCAGGTGGAAACC
Plasmids in SI	FKBP12F36V-front-R	TAGTAGGTCTCACACCTTCCAGTTTTAGAAGCTCCACATCGAA GACG
Plasmids in SI	GAL4-behind-F	TAGTAGGTCTCAGGTGGCGGCTCAATGAAGCTACTGTCTTCTA TCGAACAAGCA
Plasmids in SI	GAL4-behind-R	TAGTAGGTCTCATAGTCGATACAGTCAACTGTCTTTGACCTTT GTTACT
Plasmids in SI	GAL4-front-F	AGTAGGTCTCACTCAATGAAGCTACTGTCTTCTATCGAACAAG CA
Plasmids in SI	GAL4-front-R	TAGTAGGTCTCACACCCGATACAGTCAACTGTCTTTGACCTTT GTTACT
Plasmids in SI	VPR-front-F	TAGTAGGTCTCACTCAAGAGCTGACCCCAAGAAGAAGAG
Plasmids in SI	VPR-front-R	TAGGGTCTCACACCAAACAAACTTGTGTCAAATATACTCAGCC CGGTGCTGATGTGCAT

Plasmids in SI	VPR-behind-F	TAGTAGGTCTCAGGTGGCGGGTCGAGAGCTGACCCCAAGAAG AAGAG
Plasmids in SI	VPR-behind-R	TAGGGTCTCATAGTAAACAAACTTGTGTCAAATATACTCAGCC CGGTGCTGATGTGCAT
BRD9 <sup>BD</sup> -GAL4	d565-GAL4-F	TAGTAGGTCTCAGGTGGCGGCTCAATGAAGCTACTGTCTTCTA TCGAACAAGCA
BRD9 <sup>BD</sup> -GAL4	GAL4-R	TAGTAGGTCTCATAGTCGATACAGTCAACTGTCTTTGACCTTT GTTACT
BRD9 <sup>BD</sup> -GAL4	BRD9BD-F	TAGTAGGTCTCACTCAGAGAGCACACCTATTCAGCAACTCCT
BRD9 <sup>BD</sup> -GAL4	BRD9D-R	TAGTAGGTCTCACACCGCTCATCATCTTAAAGCCTGCGTGAAG GATCT
TetR-FKBP12 <sup>F36V</sup>	tetR-1-F	TAGTGGTCTCACTCAATGAGTCGGCTGGATAAAATCTAAAGTCA TAAACTCTGCTCTGGA
TetR-FKBP12 <sup>F36V</sup>	tetR-1-R	TAGTAGGTCTCACGGTGGTAGGTGTCTCTCTTTTCCT
TetR-FKBP12 <sup>F36V</sup>	tetR-2-F	TAGTAGGTCTCAACCGATTCTATGCCACCACTTCTGAGACAAG CA
TetR-FKBP12 <sup>F36V</sup>	tetR-2-R	TAGTGGTCTCACGATACTGAGCCGCCACCGGCCGGCCCGCCGC TTTCGCACTT
TetR-FKBP12 <sup>F36V</sup>	FKBP12F36V-behind-F	TAGTAGGTCTCAGGTGGCGGCTCAATGGGAGTGCAGGTGGAA ACC
TetR-FKBP12 <sup>F36V</sup>	FKBP12F36V-behind-R	TAGTAGGTCTCATAGTTTCCAGTTTTAGAAAGCTCCACATCGAA GACG
TetR-BRD9 <sup>BD</sup>	tetR-1-F	TAGTGGTCTCACTCAATGAGTCGGCTGGATAAAATCTAAAGTCA TAAACTCTGCTCTGGA
TetR-BRD9 <sup>BD</sup>	tetR-1-R	TAGTAGGTCTCACGGTGGTAGGTGTCTCTCTTTTCCT
TetR-BRD9 <sup>BD</sup>	tetR-2-F	TAGTAGGTCTCAACCGATTCTATGCCACCACTTCTGAGACAAG CA
TetR-BRD9 <sup>BD</sup>	tetR-2-R	TAGTGGTCTCACGATACTGAGCCGCCACCGGCCGGCCCGCCGC TTTCGCACTT



TetR- BRD9 <sup>BD</sup>	tBRD9-behind-F	TAGTAGGTCTCAGGTGGCGGCTCAGAGAGCACACCTATTCAGC AACTCCT
TetR- BRD9 <sup>BD</sup>	tBRD9-behind-R	TAGTGGTCTCATAGTGCTCATCATCTTAAAGCCTGCGTGAAGG ATCTTCT
tCRBN-1- VPR	CRBN-v7-F-c55	GATATGGTCTCACTCACTAAAAGATGATTCTCTTCCTTCAAAT CCA
tCRBN-1- VPR	VPR-behind-R	TAGGGTCTCATAGTAAACAAACTTGTGTCAAATATACTCAGCC CGGTGCTGATGTGCAT
tCRBN-2- VPR	CRBN-2-F-d420	TAGTAGGTCTCAAATGGACAGAATCAAGAAACAGCTACGTGA ATGGGATGA
tCRBN-2- VPR	VPR-behind-R	TAGGGTCTCATAGTAAACAAACTTGTGTCAAATATACTCAGCC CGGTGCTGATGTGCAT
tCRBN-2- VPR	CRBN-1-R-d420	TAGTAGGTCTCACATTAAGGTTTCAGCAGGCAACACACATTCG GGAA
tCRBN-2- VPR	CRBN-Front-F	TAGTAGGTCTCACTCAATGGCCGGCGAAGGAGATCAGCAGGA CGCTGCGCACAAC

**Sequences S3. DNA sequences of micro-deleted *Cre* used in this study (5' to 3' direction).**

^ Deleted region

SV40 NLS (underlined)

*Micro-deleted Cre*

*Nucleoplasmin NLS*

ATGCCAAAGAAGAAGCGGAAGGTCGGTGGCGGCTCACCCGGGGGTGGCGGCTCA  
ATGAATTTACTGACCGTACACCAAAATTTGCCTGCATTACCGGTCGATGCAACGAGT  
GATGAGGTTTCGAAGAACCTGATGGACATGTTTCAGGGATCGCCAGGCGTTTTCTGAG  
CATACTGGAAAATGCTTCTGTCCGTTTGCCGGTCGTGGGCGGCATGGTGCAAGTTG  
AATAACCGGAAATGGTTTCCCGCAGAACCTGAAGATGTTTCGCGATTATCTTCTATAT  
CTTCAGGCGCGCGGTCTGGCAGTAAAACTATCCAGCAACATTTGGGCCAGCTAAA  
CATGCTTCATCGTCGGTCCGGGCTGCCACGACCAAGTGACAGCAATGCTGTTTCACT  
GGTTATGCGGCGGATCCGAAAAGAAAACGTTGATGCCGGTGAACGTGCAAAACAGG  
CTCTAGCGTTTCGAACGCACTGATTTTCGACCAGGTTTCGTTCACTCATGGAAAATAGCG  
ATCGCTGCCAGGATA^CGTAATCTGGCATTCTGGGGATTGCTTATAACACCCTGTTA  
CGTATAGCCGAAATTGCCAGGATCAGGGTTAAAGATATCTCACGTAAGTACGGTGG  
GAGAATGTTAATCCATATTGGCAGAACGAAAACGCTGGTTAGCACCGCAGGTGTAG  
AGAAGGCACTTAGCCTGGGGGTAATAACTGGTTCGAGCGATGGATTTCCGTCTCTG  
GTGTAGCTGATGATCCGAATAACTACCTGTTTTGCCGGGTCAGAAAAAATGGTGTG  
CCGCGCCATCTGCCACCAGCCAGCTATCAACTCGCGCCCTGGAAGGGATTTTTGAAG  
CAACTCATCGATTGATTTACGGCGCTAAGGATGACTCTGGTCAGAGATACCTGGCCT  
GGTCTGGACACAGTGCCCGTGTTCGGAGCCGCGCGAGATATGGCCCGCGCTGGAGTT  
TCAATACCGGAGATCATGCAAGCTGGTGGCTGGACCAATGTAAATATTGTCATGAAC  
TATATCCGTAACCTGGATAGTGAAACAGGGGCAATGGTGCGCCTGCTGGAAGATGG  
CGATCCAAAGAAGAAGCGGAAAGTCACTAGTGGTGGCGGCTCAAAGCGTCCTGCTG  
CTACTAAGAAAGCTGGTCAAGCTAAGAAAAAGAAATCTAGA

#### Sequences S4. DNA sequences of LoxP and Rox sites used in this study.

LoxP site (5' to 3' direction):

ATAACTTCGTATAGCATACATTATACGAAGTTAT

Rox site (5' to 3' direction):

TAACTTTAAATAATTGGCATTATTTAAAGTTA

#### Sequences S5. DNA sequences of pUAS promoters used in this study (5' to 3' direction).

pUAS-1:

5×GAL4 DBD binding sites

3G miniPromoter

CGGAGTACTGTCCTCCGAGCGGAGTACTGTCCTCCGAGCGGAGTACTGTCCTCCGAG  
CGGAGTACTGTCCTCCGAGCGGAGTTCTGTCCTCCGAGCGGAGACTCTAGACTGGCG  
TGTACGGTGGGCGCCTATAAAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGG  
AGCAATTCACAACACTTTTGTCTTATACCAACTTCCGTACCACTTCCTACCCTCGT  
AAAGTGACC

pUAS-2:

8×GAL4 DBD binding sites

LateADE miniPromoter

CGATAGGTACCGAGTTTCTAGACGGAGTACTGTCCTCCGAGCGGAGTACTGTCCTCC  
GACTCGAGCGGAGTACTGTCCTCCGATCGGAGTACTGTCCTCCGCGAATTCGGAGT  
ACTGTCCTCCGAAGACGCTAGACGGAGTACTGTCCTCCGAGCGGAGTACTGTCCTCC  
GACTCGAGCGGAGTACTGTCCTCCGGCTAGCGGGGGGCTATAAAAGGGGGGTGGGGG  
CGTTCGTCCTCACTCTAGATCTGCGATCTAAGTAAGCTTGGCATTCCGGTACTG

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