

Supplementary Results

Time-course evaluation of TALE-TET1-induced effects on *HBB* promoter methylation and gene expression

To test whether the -266 CpG demethylation and increased *HBB* gene expression induced by HB-4, HB-5-, and HB-6 are stable over time, we assayed these parameters in a more extended time-course experiment. K562 cells transfected with expression plasmids encoding HB-4, HB-5, HB-6, or a control TALE-TET1 fusion targeted to the *KLF4* locus were assayed for -266 CpG demethylation and *HBB* gene expression at 4, 7, 14, and 30 days post-transfection. HB-4, HB-5, and HB-6 fusions all showed their highest levels of fold-activation at post-transfection day 4 with *HBB* expression steadily decreasing by day 30 to the same level observed with the control *KLF4*-targeted TALE-TET1 protein (**Supplementary Fig. 10a**). Strikingly, for all three *HBB*-targeted TALE-TET1 proteins, the extent of -266 CpG methylation over time in the population of transfected cells directly paralleled the fold-activation of *HBB* gene expression while the methylation status of another CpG at position -306 did not change significantly during the course of the experiment (**Supplementary Fig. 10b**).

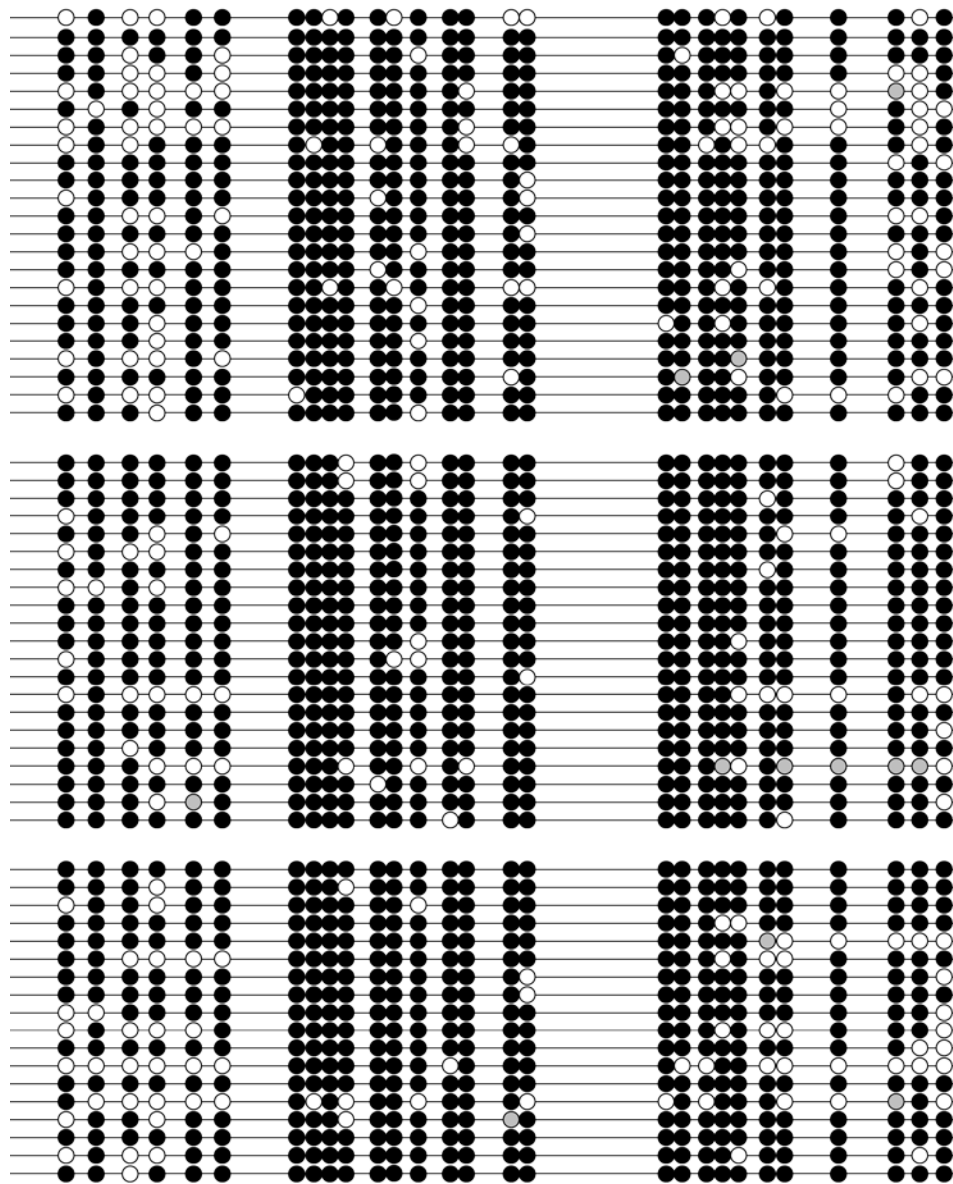
Construction and Testing of Engineered ZF-TET1 Fusion Proteins Targeted to the Human *KLF4* and *HBB* Genes

To test the feasibility of targeting TET1 activity using engineered zinc finger (ZF) proteins, we constructed ZF arrays targeted to two sites in the *KLF4* gene and to six sites in the *HBB* gene. These zinc finger arrays each consisted of six fingers and were assembled using two-finger units according to the method originally described by Moore et al.¹, and similar to the ZF engineering approach previously used by Sangamo Biosciences². Of the two ZF-TET1 fusions targeted to *KLF4*, one failed to demethylate nearby CpGs while the other was able to induce demethylation of CpGs located 6 and 24bp downstream of the ZF binding site by 61% and 18%,

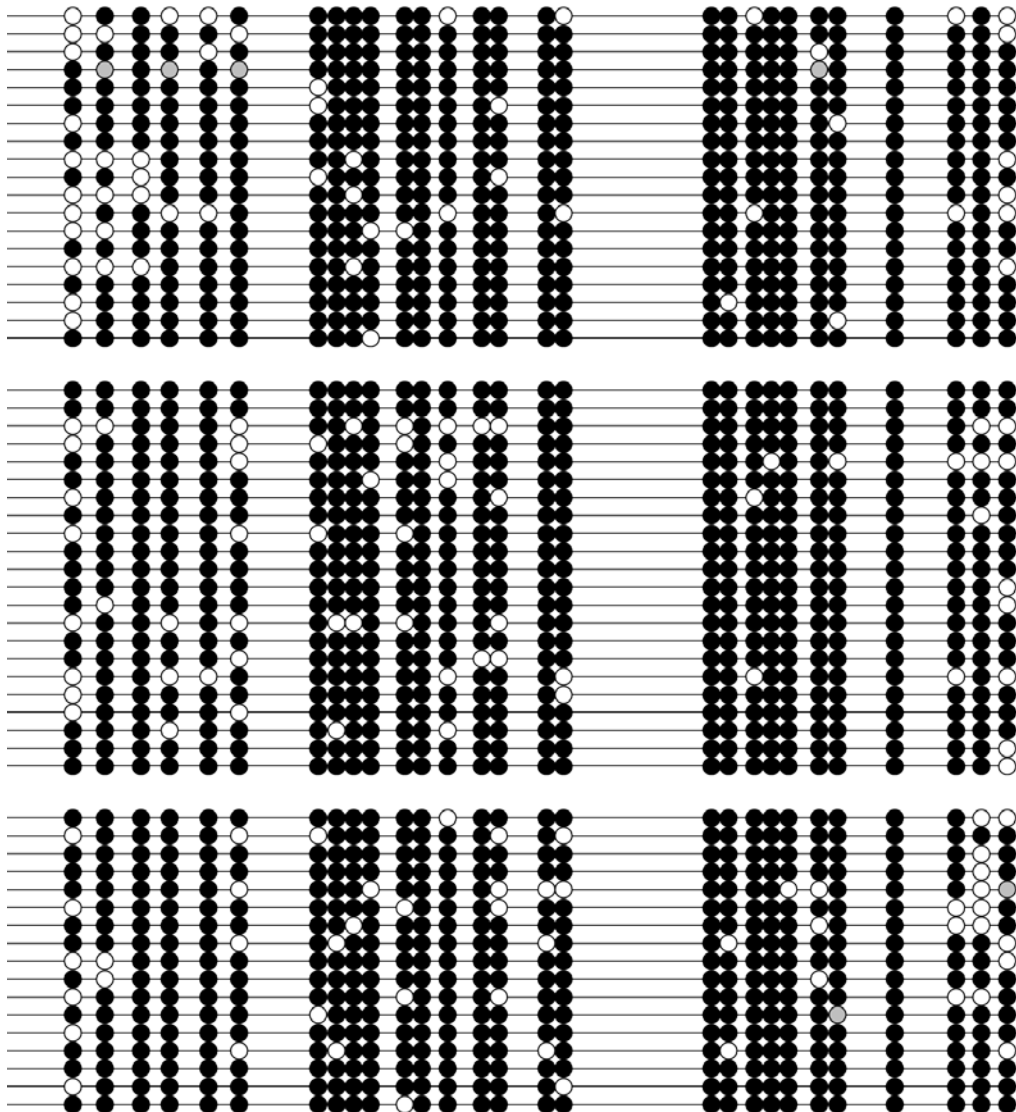
respectively (**Supplementary Fig. 11**). One ZF-TET1 fusion targeted to the -266 CpG in the *HBB* promoter failed to induce demethylation but all five fusions targeted to the region approximately 100 bp downstream of the transcription start site were able to demethylate target CpGs with efficiencies comparable to those observed with TALE-TET1 proteins (**Supplementary Fig. 12**).

A

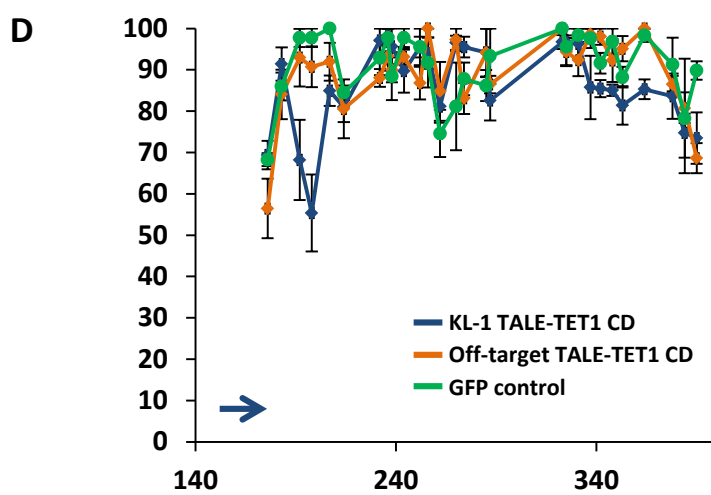
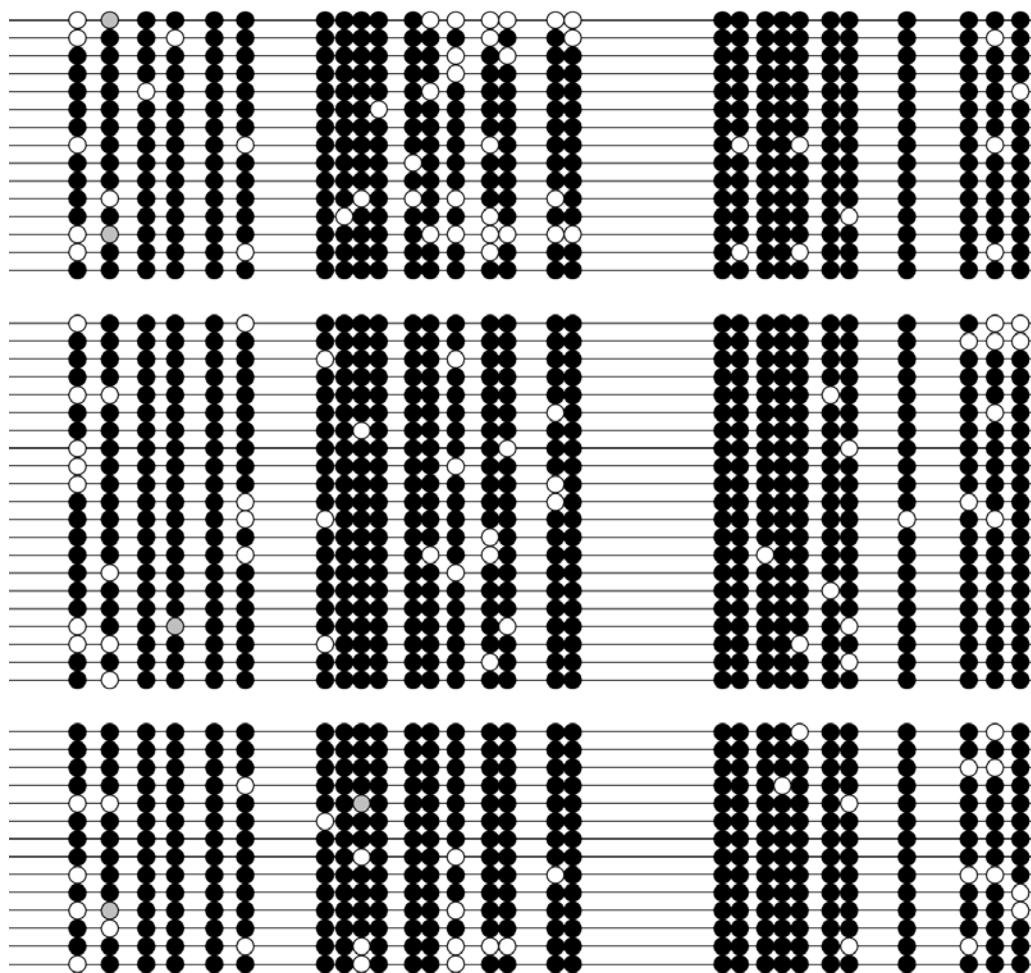
KL-1 TALE-TET1



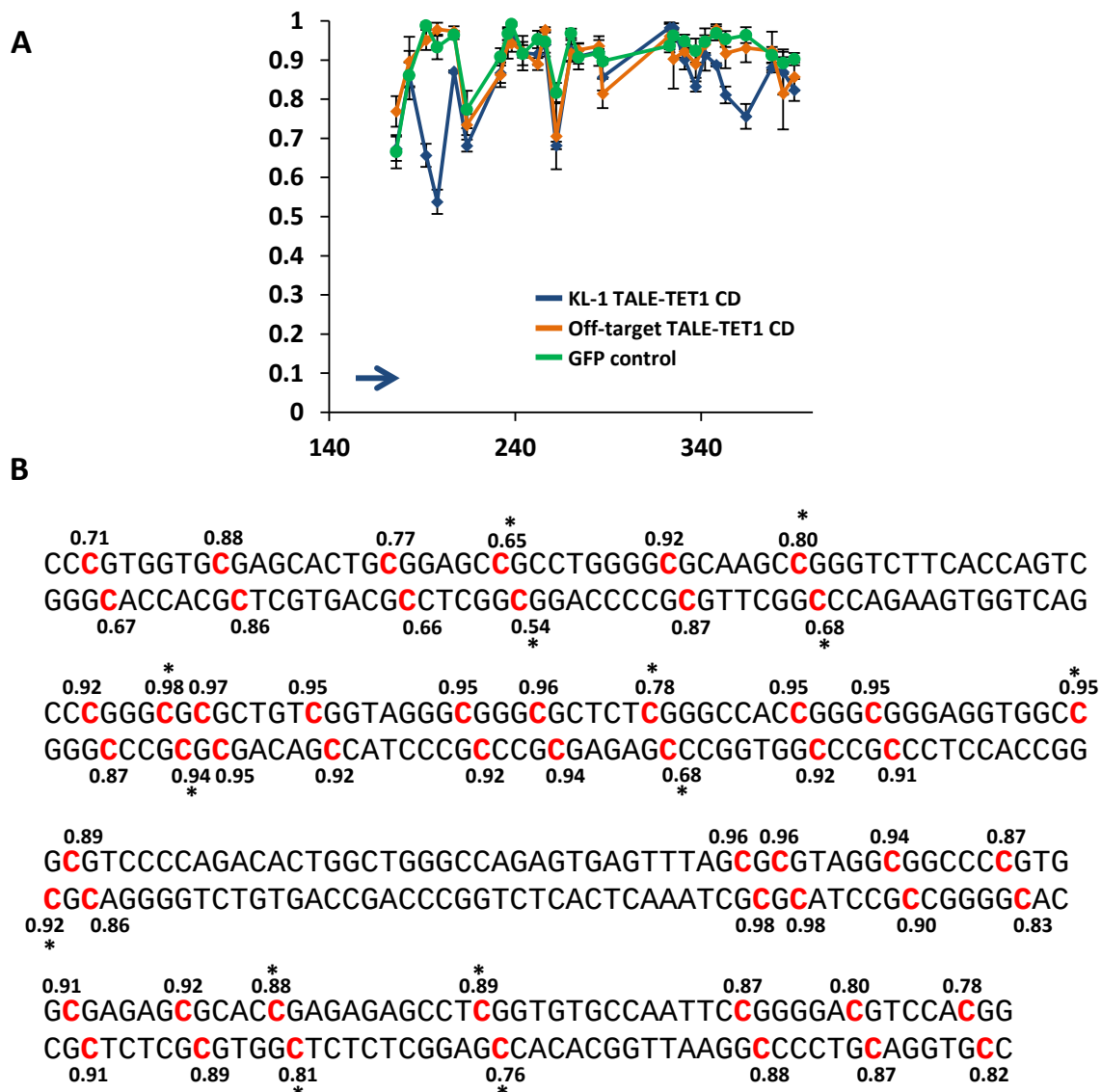
B Off-target TALE-TET1



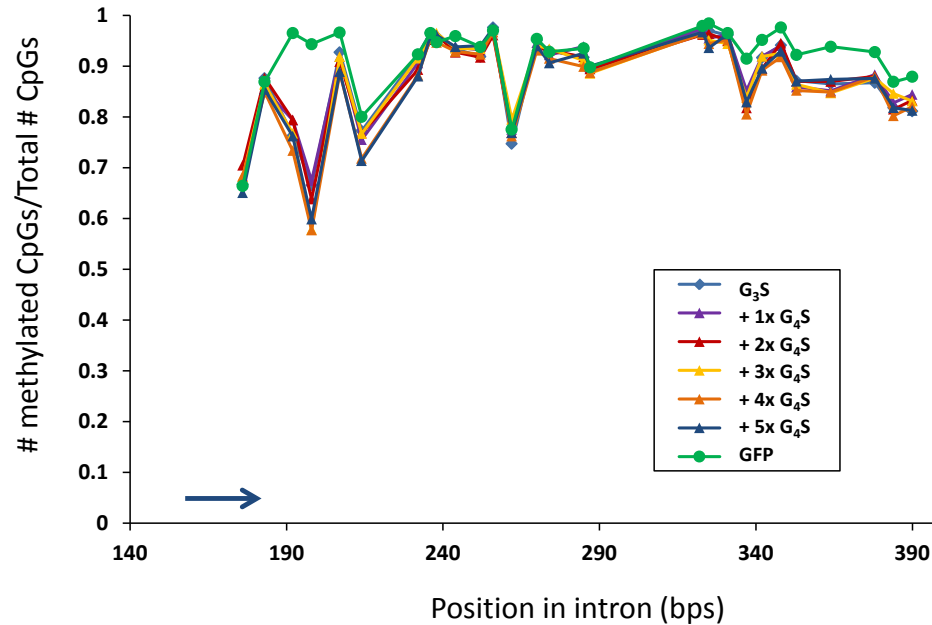
c GFP control



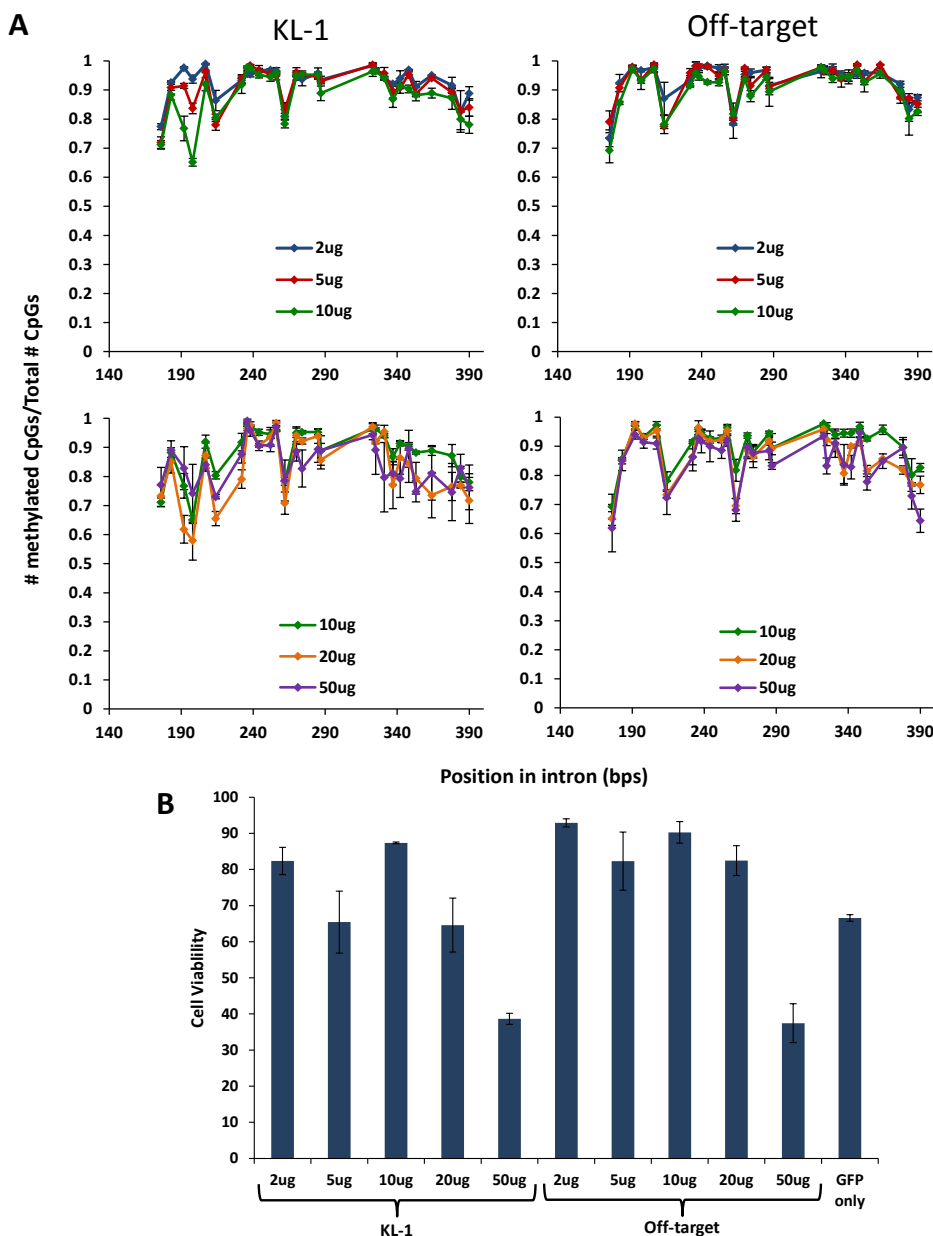
Supplementary Figure 1 Sanger sequencing of bisulfite PCR products. Figures depict methylation status of CpGs in the second *KLF4* intron in K562 cells transfected with plasmid expressing (a) the KL-1 TALE-TET1 fusion, (b) an off-target TALE-TET1 fusion (targeted to a sequence in the EGFP reporter gene), or (c) GFP. Genomic DNA is the same as that used in the 10 ug sample in Supplementary Fig. 1a and in Supplementary Fig. 2. Each panel shows three sets of sequences derived from three independent transfections. Black circles, methylated; white circles, non-methylated; grey circles, undetermined. (d) Summary of data from (a), (b), and (c) showing the fraction of methylated CpGs (y-axis) for different positions along the length of the second *KLF4* intron (x-axis, numbered relative to the start of the intron).



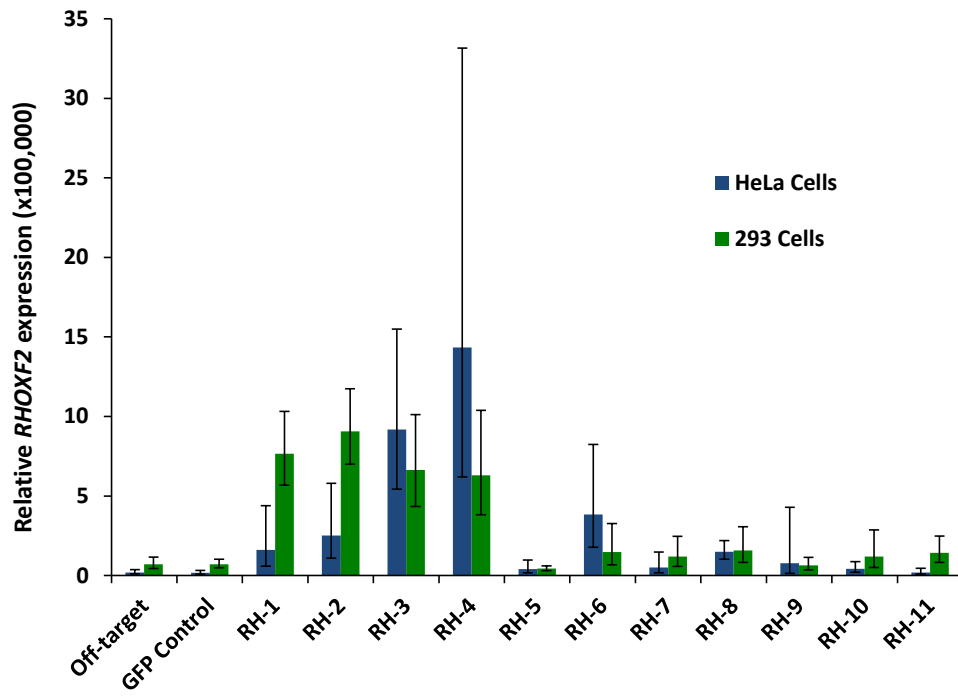
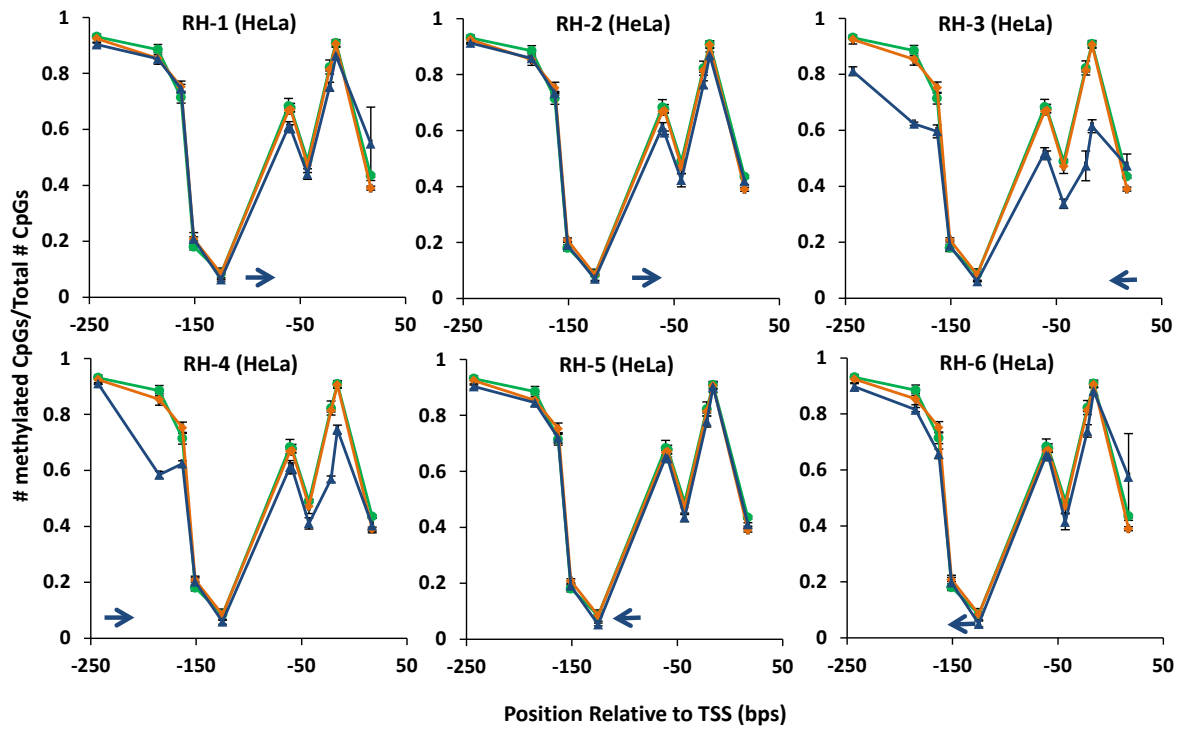
Supplementary Figure 2 TALE-TET1 fusion protein can induce demethylation of both DNA strands. (a) Graph shows the fraction of CpGs methylated (y-axis) for different positions along the length of the second *KLF4* intron (x-axis, numbered relative to the start of the intron) in K562 cells transfected with plasmid expressing KL-1 TALE-TET1 (blue), an off-target TALE-TET1 fusion protein (orange) or a GFP (control). Genomic DNA is the same as in Fig. 1d except that bisulfite PCR was performed to amplify the opposite DNA strand. (b) Schematic summary of mean CpG methylation at the KL-1 target locus from K562 cells transfected with plasmid encoding the KL-1 TALE-TET1 fusion protein. Data for this figure is derived from Fig. 1d (for the top strand) and Supplementary Fig. 2a (for the bottom strand). CpGs that have significantly different rates of methylation on the two strands in the KL-1 TALE-TET1 samples are indicated by asterisks, as determined by a two-sided t-test (n=3, p<0.05). No significant differences between methylation rates on the two strands were observed for cells transfected with plasmid encoding the off-target TALE-TET1 fusion protein or GFP (data not shown).

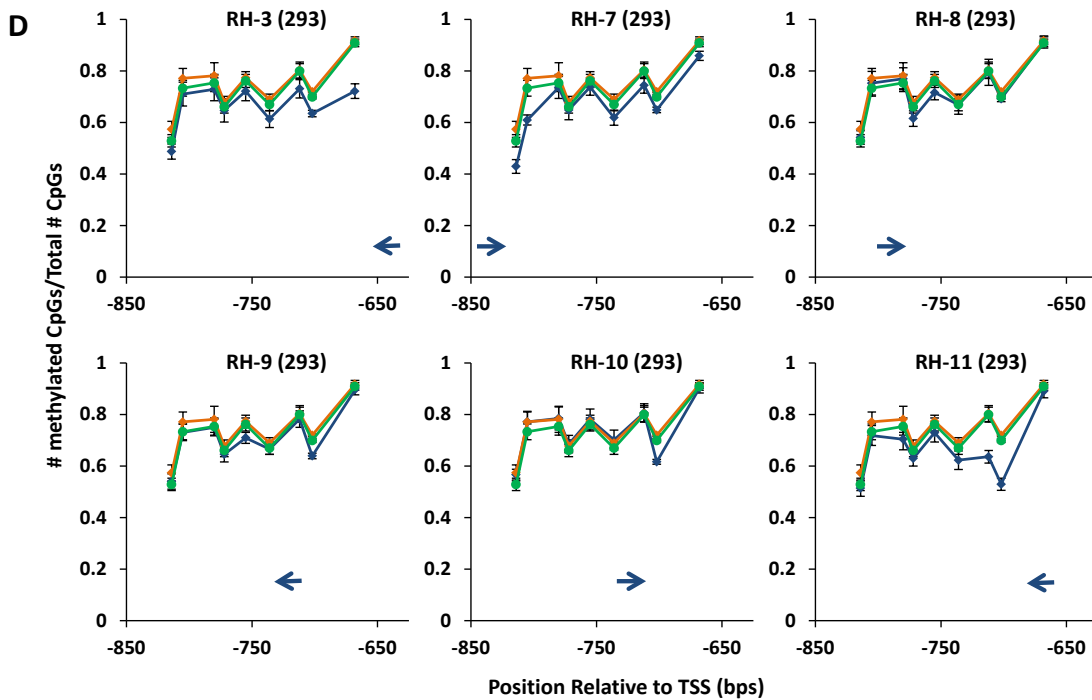
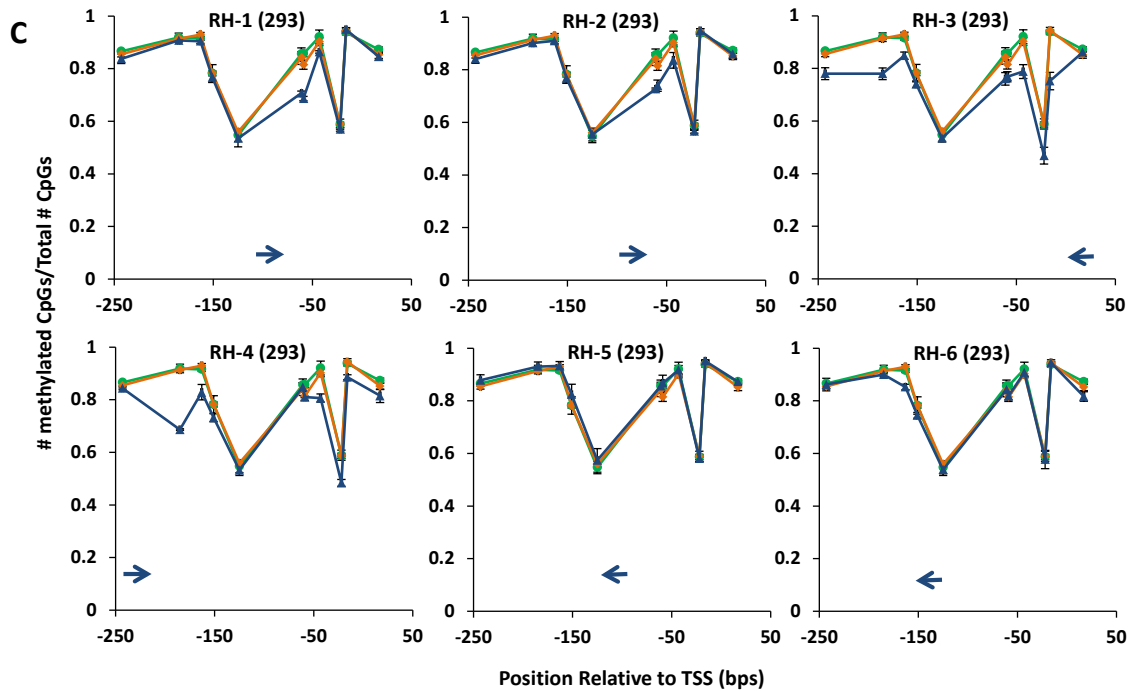


Supplementary Figure 3 CpG demethylation induced by TALE-TET1 fusion proteins bearing various length inter-domain linkers. Graphs show the fraction of CpGs methylated (y-axis) for different positions along the length of the second *KLF4* intron (x-axis, numbered relative to the start of the intron) in K562 cells transfected with plasmids expressing KL1 TALE-TET1 proteins bearing standard or variant linkers between the TALE and TET1 domains or a control plasmid expressing GFP. Blue arrow indicates the location and direction (5' to 3') of TALE target binding site. Each point represents data from a single transfection experiment. Methylation status was assessed using high-throughput bisulfite sequencing.



Supplementary Figure 4 Titration of TALE-TET1 plasmid. (a) Fraction of CpGs methylated (y-axis) for different positions along the length of the second *KLIF4* intron (x-axis, numbered relative to the start of the intron) in K562 cells transfected with indicated amounts of plasmid expressing KL-1 TALE-TET1 (left) or an off-target TALE-TET1 fusion protein targeted to an unrelated sequence in the *EGFP* reporter gene (right). Each point represents the mean of three independent transfection experiments with bars indicating standard errors of the mean. Methylation status for each experiment was assessed using high-throughput bisulfite sequencing. Note that 10ug samples are the same in top and bottom graphs and are depicted twice for ease of comparison. 10ug samples are also the same as those depicted in Fig. 1d and genomic DNA is the same as that used in **Supplementary Fig. 2**. (b) Cell viability of transfected K562 cells from (a) as determined by propidium iodide staining and FACS.

A**B**



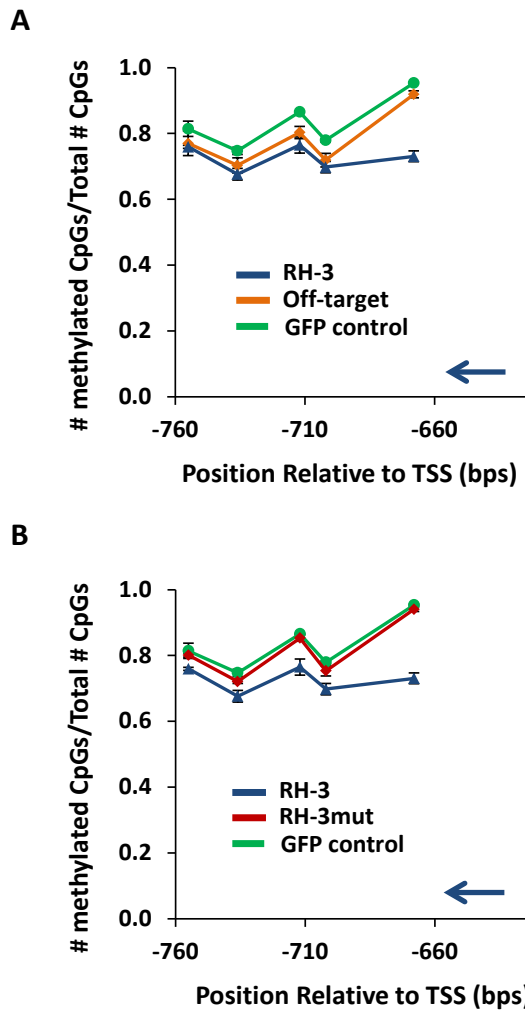
Supplementary Figure 5 Targeted demethylation and activation of the *RHOXF2* gene.

(a) Expression levels of *RHOXF2* mRNA (normalized to β -actin mRNA levels) as determined by quantitative RT-PCR in HeLa (blue) and 293 (green) cells transfected with plasmids encoding one of 11 different TALE-TET1 fusion proteins (RH-1 to RH-11), an off-target control (targeted to *KLF4*) or a GFP control. Means of three independent replicates are shown with error bars representing standard errors of the mean.

(b) Fraction of methylated CpGs (y-axis) for different positions within the -200 to +1 region of the *RHOXF2* promoter (x-axis, numbered relative to the transcription start site) in HeLa cells transfected with plasmids expressing *RHOXF2*-targeted TALE-TET1 proteins (blue), an off-target TALE-TET1 protein (targeted to a site in the *KLF4* gene) (orange), or GFP (green). Means of three independent transfection experiments are shown with bars representing standard errors of the mean. Methylation status for each experiment was assessed using high-throughput bisulfite sequencing. Note that the GFP and off-target TALE-TET1 control data points shown are the same in panels (c) and (d) and are depicted multiple times only for ease of comparison with experimental samples. Blue arrow indicates the location and direction (5' to 3') TALE-TET1 binding sites.

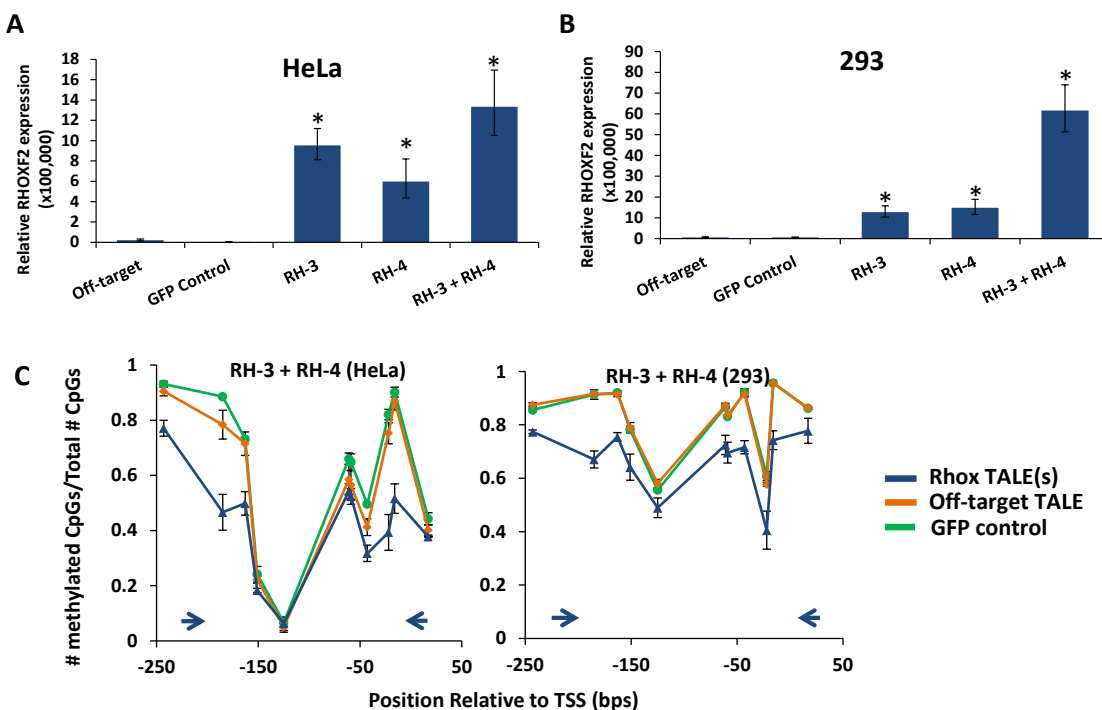
(c) Fraction of methylated CpGs for various positions within the -200 to +1 region of the *RHOXF2* promoter in 293 cells transfected with plasmids expressing *RHOXF2*-targeted TALE-TET1 proteins (blue), an off-target TALE-TET1 protein (targeted to a site in the *KLF4* gene) (orange), or GFP (green). Data depicted as in (b).

(d) Fraction of methylated CpGs for various positions within the -650 to -850 region of the *RHOXF2* promoter in 293 cells transfected with plasmids expressing *RHOXF2*-targeted TALE-TET1 proteins (blue), an off-target TALE-TET1 protein (targeted to a site in the *KLF4* gene) (orange), or GFP (green). Data depicted as in (b) and (c).



Supplementary Figure 6 RH-3 TALE-TET1 demethylates CpGs at its secondary upstream binding site in 293 cells.

(a) Graph shows the fraction of CpGs methylated (y-axis) for different positions along the length of the *RHOXF2* promoter (x-axis, numbered relative to the transcription start site) in cells transfected with plasmids expressing the RH-3 TALE-TET1 fusion (blue), a TALE-TET1 fusion targeted to an off-target site in the *KLF4* gene (orange), or GFP (green). Each data point represents the mean of three independent transfection experiments with bars indicating standard errors of the mean. Methylation status for each experiment was assessed using high-throughput bi-sulfite sequencing. Blue arrow indicates the location and direction (5' to 3') of the RH3 TALE-TET1 binding site. (b) Same as in (a) but showing data from cells transfected with plasmid encoding RH-3 TALE-TET1 fusion (blue), RH-3 TALE-TET1 fusion bearing mutations to inactivate the catalytic activity of TET1 (red), or GFP (green). Note that the data for the RH-3 TALE-TET1 and GFP samples are the same in both (a) and (b) and are depicted twice only for ease of comparison.

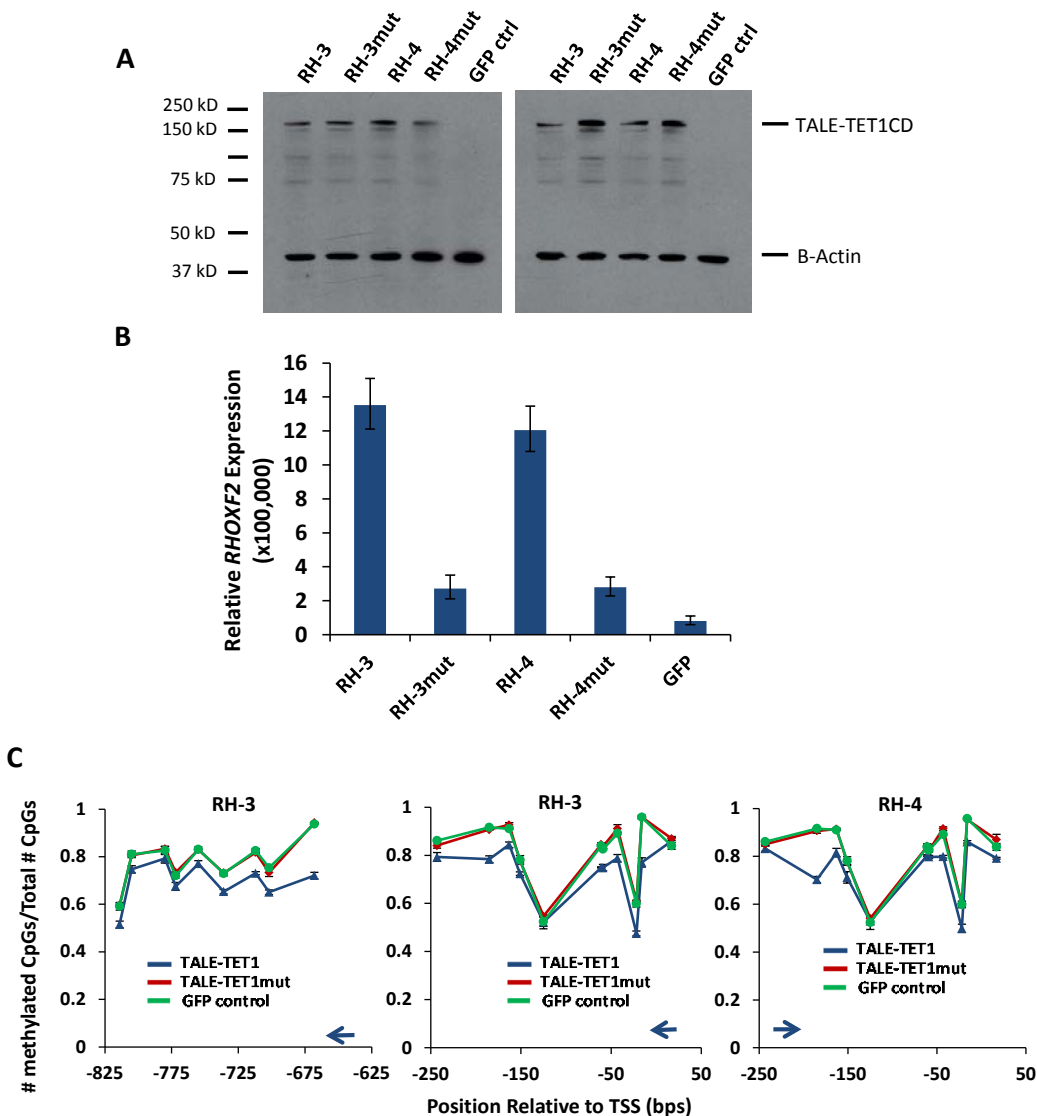


Supplementary Figure 7 Co-expression of RH-3 and RH-4 TALE-TET1 proteins.

(a) Expression levels of *RHOXF2* mRNA (normalized to β -actin mRNA levels) in HeLa cells transfected with plasmids expressing RH-3, RH-4, or both TALE-TET1 proteins, an off-target TALE-TET1 protein (targeted to *KLF4*), or GFP. Means of three independent transfection samples each assayed three times by quantitative RT-PCR are shown with bars representing standard errors of the mean. Asterisks indicate samples with values significantly greater than those obtained with the off-target control TALE-TET1 fusion protein as determined by a one-sided Welch's t-test ($n = 3$, $p < 0.05$).

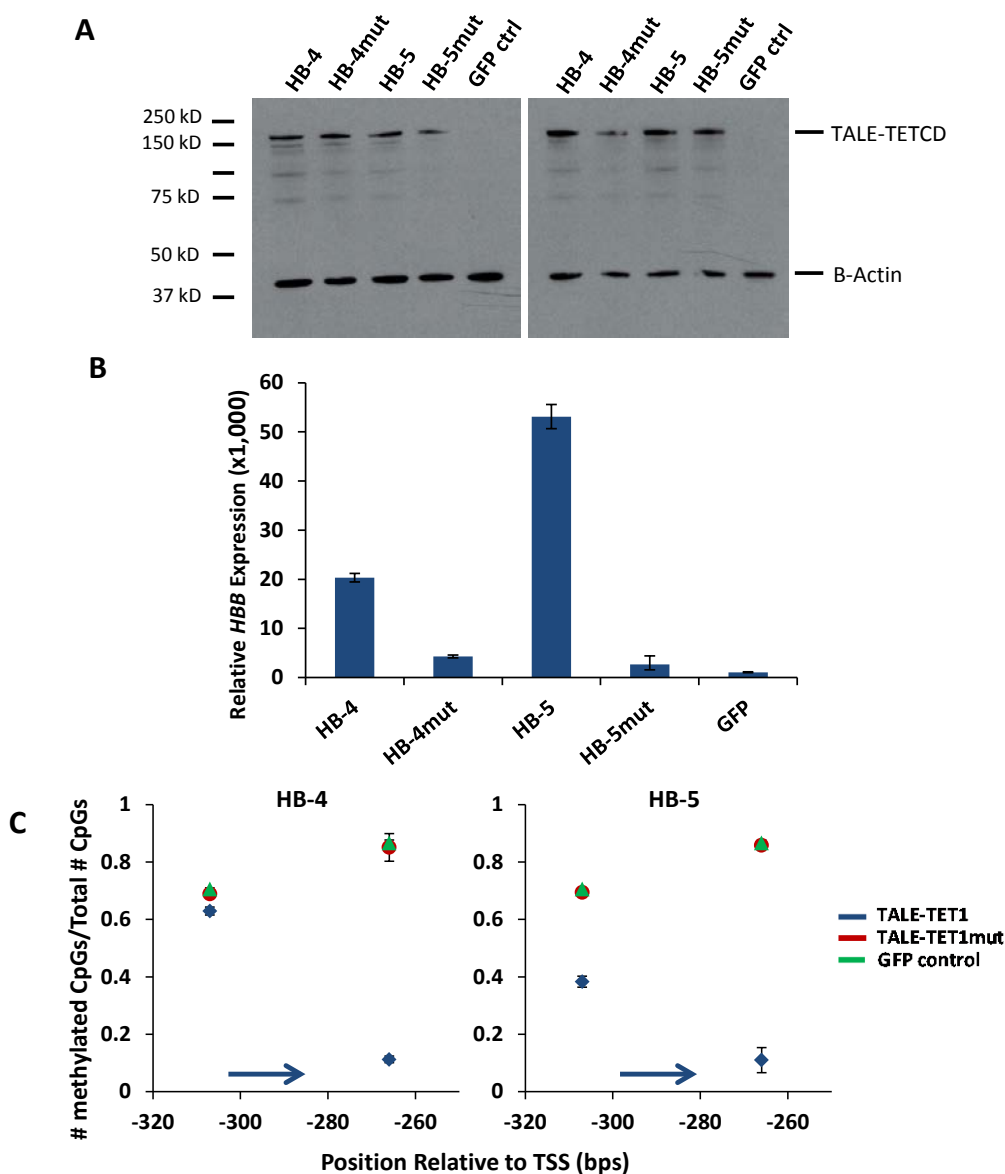
(b) Expression levels of *RHOXF2* mRNA (normalized to β -actin mRNA levels) in 293 cells transfected with plasmids expressing RH-3, RH-4, or both TALE-TET1 proteins, an off-target TALE-TET1 protein (targeted to *KLF4*) or GFP expression. Data presented as in (a).

(c) Fraction of methylated CpGs (y-axis) for different positions along the length of the *RHOXF2* promoter (x-axis, numbered relative to the transcription start site) in HeLa (left) and 293 (right) cells transfected with plasmids expressing RH-3, RH-4, or both (blue), an off-target TALE-TET1 fusion (to a site in the *KLF4* gene) (orange), or GFP (green). Each data point represents the mean of three independent transfection experiments with bars indicating standard errors of the mean. Methylation status for each experiment was assessed using high-throughput bisulfite sequencing. Blue arrow indicates the location and direction (5' to 3') of the RH3 (right) and/or RH4 (left) TALE-TET1 binding sites.



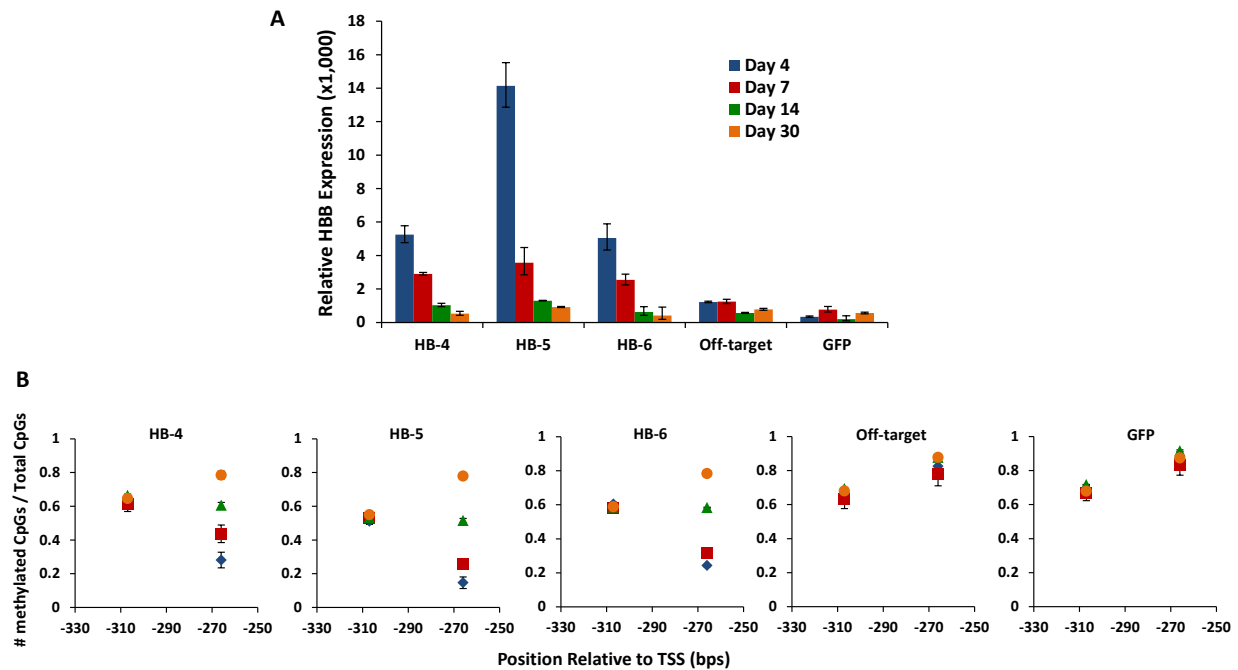
Supplementary Figure 8 *RhoxF2*-targeted TALE-TET1 proteins bearing mutations that inactivate TET1 catalytic function are stably expressed in 293 cells.

(a) Western blot analysis performed on 293 cells transfected with plasmids expressing triple-FLAG-tagged RH-3 or RH-4 TALE-TET1 fusions, FLAG-tagged RH-3 or RH-4 TALE-TET1 fusions bearing mutations that inactivate TET1 catalytic function, or GFP. Transfections were performed in triplicate and Western blots performed for two replicates using anti-FLAG antibody are shown. (b) Expression levels of *RHOXF2* mRNA (normalized to β -actin mRNA levels) from the same transfected cells described in (a). Means of three independent samples each assayed three times by quantitative RT-PCR are shown with bars representing standard errors of the mean. (c) Fraction of CpGs methylated (y-axis) for different positions along the length of the *RHOXF2* promoter (x-axis, numbered relative to the transcription start site) for the same transfected cells described in (a). Each data point represents the mean of the three independent transfection experiments with bars indicating standard errors of the mean. Methylation status for each experiment was assessed using high-throughput bisulfite sequencing. Note that the control GFP data in the second and third panels are the same and are presented twice for ease of comparison.



Supplementary Figure 9 *HBB*-targeted TALE-TET1 proteins bearing mutations that inactivate TET1 catalytic domain function are stably expressed in K562 cells.

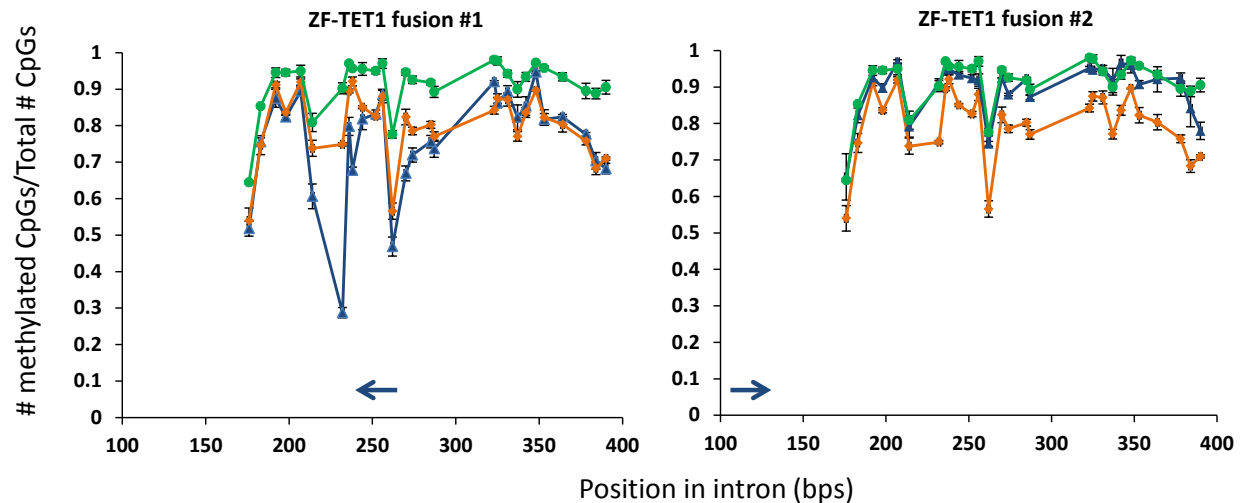
(a) Western blot analysis performed on K562 cells transfected with plasmids expressing triple-FLAG epitope-tagged HB-4 or HB-5 TALE-TET1 fusions, HB-4 or HB-5 TALE-TET1 fusions bearing mutations that inactivate TET1 catalytic function, or GFP. Transfections were performed in triplicate and Western blots performed for two replicates using anti-FLAG antibody are shown. (b) Expression levels of *HBB* mRNA (normalized to β -actin mRNA levels) from the same transfected cells described in (a). Means of three independent samples assayed by quantitative RT-PCR are shown with bars representing standard errors of the mean. (c) Fraction of CpGs methylated (y-axis) for different positions along the length of the *HBB* promoter (x-axis, numbered relative to the transcription start site) for the same transfected cells described in (a). Each data point represents the mean of the three independent transfection experiments with bars indicating standard errors of the mean. Methylation status for each experiment was assessed using high-throughput bisulfite sequencing. Note that the control GFP data in the left and right panels are the same and are presented twice for ease of comparison.



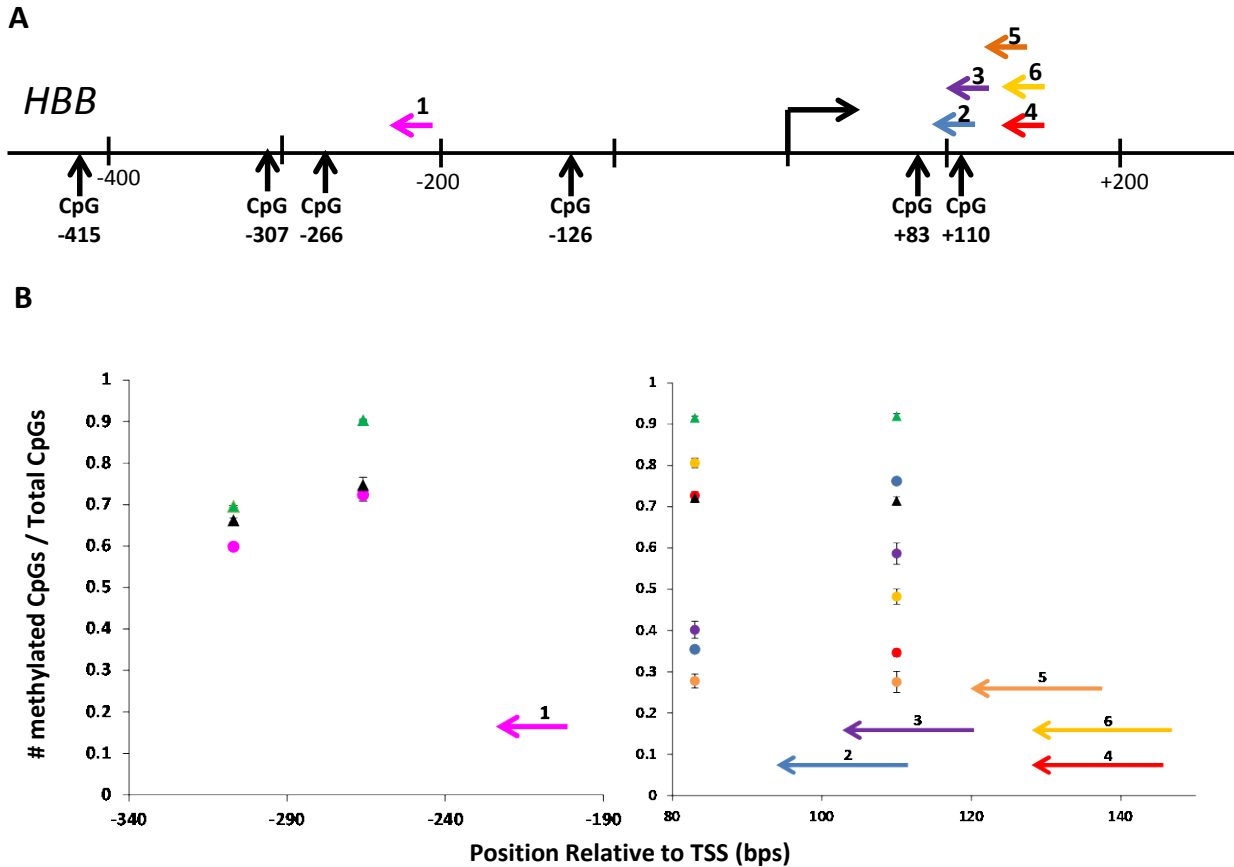
Supplementary Figure 10 Extended time-course experiment assessing promoter CpG methylation and expression of the human *HBB* gene in cells transfected with plasmids expressing TALE-TET1 fusion proteins

(a) Expression levels of *HBB* mRNA (normalized to β -actin mRNA levels) in K562 cells transfected with plasmids expressing HB-4, HB-5, HB-6, an off-target TALE-TET1 fusion protein (targeted to the human *KLF4* gene), or GFP were measured 4, 7, 14, and 30 days post-transfection. Means of three independent samples assayed by quantitative RT-PCR are shown with bars representing standard errors of the mean.

(b) Graphs showing the fraction of CpGs methylated (y-axis) for different positions along the length of the *HBB* promoter (x-axis, numbered relative to the transcription start site) for the same transfected cells described in (a). Each data point represents the mean of the three independent transfection experiments with bars indicating standard errors of the mean. Methylation status for each experiment was assessed using high-throughput bisulfite sequencing.



Supplementary Figure 11 ZF-TET1 fusion protein-induced demethylation of the human *KLF4* gene. Fraction of CpGs methylated (y-axis) for different positions along the length of the second *KLF4* intron (x-axis, numbered relative to the start of the intron) are shown for K562 cells transfected with plasmids expressing one of two *KLF4*-targeted ZF-TET1 fusions, an off-target ZF-TET1 fusion (targeted to an unrelated site in the human *VEGFA* gene), or GFP. Blue arrows indicate the location and direction (3' to 5') of the ZF target binding sites. Each point represents the mean of three independent transfection experiments with bars indicating standard errors of the mean. Methylation status for each experiment was assessed using high-throughput bisulfite sequencing. Note that the off-target ZF-TET1 fusion and GFP control data shown are the same for both graphs and are depicted twice for ease of comparison.



Supplementary Figure 12 ZF-TET1 fusion protein-induced demethylation of the human *HBB* gene.

(a) Schematic illustrating the human *HBB* locus with CpGs indicated with black arrows. Numbering indicates position on the DNA relative to the start site of transcription (right-angle arrow). Colored arrows indicate the location and direction (3' to 5') of six ZF-TET1 fusion protein binding sites.

(b) Fraction of CpGs methylated (y-axis) for different positions along the length of *HBB* gene (x-axis, numbered relative to *HBB* promoter transcription start site) for K562 cells transfected with plasmids expressing one of six *HBB*-targeted ZF-TET1 fusions (colored circles corresponding to colored arrows in (a)), an off-target ZF-TET1 fusion (targeted to an unrelated site in the human *VEGFA* gene) (black triangles), or GFP (green triangles). Colored arrows indicate the position, location and direction (3' to 5') of the ZF target binding sites. Data for ZF-TET1 proteins targeted to the -266 and +83/+110 CpGs are shown in the left and right panels, respectively. Each point represents the mean of three independent transfection experiments with bars indicating standard errors of the mean. Methylation status for each experiment was assessed using high-throughput bisulfite sequencing.

Supplementary Figure 13. Amino acid sequences of fusion proteins used in this work

Sequence of TALE-TET1CD Backbone (includes NLS, TALE N-terminal domain, TALE-C-terminal domain, TET1 catalytic domain):

MAPKKKRVGIHRGVPMVDLRTLGYSSQQQEQEKIKPKVRSTVAQHHEALVGHGFTHAHIVALSQHPAALGTVAVKYQD
MIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPQLDGTGQLLKIARGGVTAVEAVHAWRNALTGAPLN
...Insert TALE Repeat Arrays Here (see below) ...
SIVAQLSRDPALAAALTNDHLVALACLGGPALDAVKKGLPHAPALIKRTNRRIPERTSHRVADHAQVVRVLGFFQCHS
HPAQAFDDAMTQFGMSGGSLPTCCLDRVIQKDKGPYYTHLGAGPSVAAREIMENRYGQKGNIRIEIVVYTGE
GKSSHGCPKAKWVLRSSDEEKVLCVLRQRTGHHCTAVMVVLMVWDGIPLPMADRLYTELTENLSYNGHPTDRRC
TLNENRTCTCQGIDPETCGASFSFGCSWSMYFNGCKFGRSPSPRRFRIDPSSPLHEKNLEDNLQSLATRLAPIYKQYAPV
AYQNQVEYENVARECRLGSKEGRPFSGVTACLDCAHPHRDIHNMNNGSTVVCTLTREDNRLSGVIPQDEQLHVLPLY
KLSDTDEFGSKEGMEAKIKSGAIEVLAPRRKKRTCTQPVPRSGKKRAAMMTEVLAHKIRAVEKKPIPRIKRNSTTTN
NSKPSSLPTLGSNTETVQPEVKSETEPHFILKSSDNTKTYSLMPSAPHPVKEASPGFSWSPKTASATPAPLKNDATASCGF
SERSTPHCTMPSGRLSGANAAAADGPGISQLGEVAPLPTLSAPVMEPLINSEPSTGVTEPLTPHQPNHQPSFLTSPQDL
ASSPMEEDEQHSEADEPPSDEPLSDDPLSPAEEKLPHIDEYWSDEHIFLDANIGGVAIAPAHGSVLIECARRELHATTPV
EHPNRNHPTRLSLVFYQHKNLNKPQHGFELNKKIFEAKEAKNKKMKASEQKDQAANEGPEQSSEVNELNQIPSHKALT
LTHDNVVTVPYALTHVAGPYNHVV.

Sequence of TALE-TET1FL Backbone (includes NLS, TALE N-terminal domain, TALE-C-terminal domain, full length TET1):

MAPKKKRVGIHRGVPMVDLRTLGYSSQQQEQEKIKPKVRSTVAQHHEALVGHGFTHAHIVALSQHPAALGTVAVKYQD
MIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPQLDGTGQLLKIARGGVTAVEAVHAWRNALTGAPLN
...Insert TALE Repeat Arrays Here (see below) ...
SIVAQLSRDPALAAALTNDHLVALACLGGPALDAVKKGLPHAPALIKRTNRRIPERTSHRVADHAQVVRVLGFFQCHS
HPAQAFDDAMTQFGMSGGGSMSRSRHARPSRLVRKEDVNKKKKNSQLRKTGANKNVASVKTLSPGKLGKLIQER
DVKKKTEPKPPVVRSLTRAGAARMNLDRTEVLFQNPESLTCNGFTMALRSTSLRRLSQPPLVVAKSCKVPLSKGLEK
QHDCDYKILPALGVKHSENDSVPMQDTQVLPDIETLIGVQNPSSLKKGKSQETTQFWSQRVEDSKINIPTHSGPAEILPG
PLEGTRCGEGLFSEETLNDTSGSPKMFAQDTCAPFPQKATPKVTSQGNPSIQLEELGSRVESLKLSDSYLDPIKSEHDCY
PTSSLNKKVIPDLNLRNCLALGGSTSPSTVIKFLLAGSKQATLGAKPDHQEAFEATANQQEVSDTTSFLGQAFGAIPHQWE
LPGADPVHGEALGETPDLPEIPGAIPVQGEVFGTILDQQETLGMSSGVVDPDLPVFLPVPPNPIATFNAPSKWPEPQSTV
SYGLAVQGAIQILPLGSGHTPQSSSNSEKNSLPPVMAISNVENKQVHISFLPANTQGFPLAPERGLFHASLGIAQLSQA
GPSKSDRGSSQSVSTVHVNTTVTMPVPMVSTSSSYTTLLPTLEKKKRKRCGVCEPCQKTNCGECTYCKNRKNS
HQICKKRKCEELKKKPSVVVPLEVIKENKRPQREKKPKVLKADFDNKPVNGPKSESMDYSRCGHGEEQKLELNPHTVEN
VTKNEDSMTGIEVEKWTQNKKSQLTDHVKGDFSANVPEAEKSKNSEVDKKRTKSPKLFVQTVRNGIKHVHCLPAETNV
SFKKFNIEEFGKLENNYSYKFLKDTANHKNAMSSVATDMSCDHLKGRSNVLFQQPGFNCSSIPHSSHSIINHSHASIHNE
GDQPKTPENIPSKPKDGSPVQPSLLSLMKDRRLTLEQVVAIEALTQLSEAPSENSSPSKSEKDEESEQRTASLLNSCKAIL
YTVRKDLQDPNLQGEPPKLNHCPSLEKQSSCNTVVFNGQTTTSLNSHINSATNQASTKSHEYSKVTNSLSLFIKPSNSSKI
DTNKSIAQGIITLNCNLDLHQLPPRNNEVEYCNQLLDSSKKLSDDLSCQDATHQTIEEDVATQTLQLASIIKINYIKPED
KKVESTPTSLVTCNVQKYNQEKGTMMQKPPSSVHNNHGSSLTKQKNPTQKKTSTPSRDRRKKKPTVVSYQENDRQ
KWEKLSYMYGTICDIWASKFQNFQFCPHDFPTVFGKISSSTKIWKPLAQTRSIMQPKTVFPPLTQIKLQRPESAEKQV
KVEPLDSLFLHKTESNGKAFTDKAYNSQVQLTVNANQKAHPLTQPSSPPNQCANVMAGDDQIRFQQVQVKEQLMH
QRLPTLPGISHETPLPESALTNRNVNVVCSGGITVVSTKSEEEVCSSSFGTSEFSTVDSAQKNFNDYAMNFFTNPKNLVS
ITKDESLPTCCLDRVIQKDKGPYYTHLGAGPSVAAREIMENRYGQKGNIRIEIVVYTGEKKGSSHGCPKAKWVLRSS

DEEKVLCLVRQRTGHHCTAVMMVVLIMVWDGIPLPMADRLYTELTENLKSNGHPTDRRCTLNENRTCTCQGIDPETC
 GASFSFGCSWSMYFNGCKFGRSPSPRRFRIDPSSPLHEKNLEDNLQSLATRLAPIYKQYAPVAYQNQVEYENVARECRL
 GSKEGRPFSGVTACLDFAHPHRDIHNMNNGSTVVCTLTREDNRS LGVIPQDEQLHVLPLYKLSDTDEFGSKEGMEAKI
 KSGAIEVLAPRRKKRTCTFTQVPRSGKKRAAMMTEVLAHKIRAVEKKPIPRIKRKNNSTTTNNSKPSSLPTLGSNTETVQP
 EVKSETEPHFILKSSDNTKTYSLMPSAPHPVKEASPGFSWSPKTASATPAPLKNDATASCGFSERSSTPHCTMPSGRLSG
 ANAAAADGPGISQLGEVAPLPTLSAPVMEPLINSEPSTGVTEPLTPHQPNHQPSFLTSPQDLASSPMEEDEQHSEADEP
 PSDEPLSDDPLSPAEEKLP HIDEYWSDSEHIFLDANIGGVAIAPAHGSVLIECARRELHATTPVEHPNRNHPTRL SLVFYQ
 HKNLNKPQHGFE LN KIKFEAKEAKNKKMKASEQKDQAANEGPEQSSEVNELNQIPSHKALT LTHDNVTVSPYALTHV
 AGPYNHVW.

Sequence of Flag-tagged TALE-TET1CD Backbone (includes 3X FLAG, NLS, TALE N-terminal domain, TALE-
 C-terminal domain, TET1 catalytic domain):

MDYKDHDGDYKDHIDYKDDDDKMAPKKRKVG IHRGVPMVDLRTLGYSSQQQEKIKPKVRSTVAQHHEALVGHG
 FTHAHIVALSQHPAALGTAVVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAR
 GGVTAVEAVHAWRNALTGAPLN

...Insert TALE Repeat Arrays Here (see below)...

SIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKGLPHAPALIKRTNRRIPERTSHRVADHAQVVRVLGFFQCHS
 HPAQAFDDAMTQFGMSGGSLPTCSCLD RVIQKDKGPYYTHLGAGPSVAAVREIMENRYGQKGN AIRIEIVVYTGE
 GKSSHGCP IAKWVLRSSDEEKVLCLVRQRTGHHCTAVMMVVLIMVWDGIPLPMADRLYTELTENLKSNGHPTDRR
 TLNENRTCTCQGIDPETCGASFSFGCSWSMYFNGCKFGRSPSPRRFRIDPSSPLHEKNLEDNLQSLATRLAPIYKQYAPV
 AYQNQVEYENVARECRLGSKEGRPFSGVTACLDFAHPHRDIHNMNNGSTVVCTLTREDNRS LGVIPQDEQLHVLPLY
 KLSDTDEFGSKEGMEAKIKSGAIEVLAPRRKKRTCTFTQVPRSGKKRAAMMTEVLAHKIRAVEKKPIPRIKRKNNSTTTN
 NSKPSSLPTLGSNTETVQPEVKSETEPHFILKSSDNTKTYSLMPSAPHPVKEASPGFSWSPKTASATPAPLKNDATASCGF
 SERSSTPHCTMPSGRLSGANAAAADGPGISQLGEVAPLPTLSAPVMEPLINSEPSTGVTEPLTPHQPNHQPSFLTSPQDL
 ASSPMEEDEQHSEADEPPSDEPLSDDPLSPAEEKLP HIDEYWSDSEHIFLDANIGGVAIAPAHGSVLIECARRELHATTPV
 EHPNRNHPTRL SLVFYQHKNLNKPQHGFE LN KIKFEAKEAKNKKMKASEQKDQAANEGPEQSSEVNELNQIPSHKALT
 LTHDNVTVSPYALTHVAGPYNHVW

Specific TALE Repeat Array Sequences (insert into fusion protein framework sequences above):

KL-1:

LTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIA
 NNNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNNGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQAL
 ETVQRLLPVLCQDHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLC
 QAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPE
 QVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNG
 GGKQALETVQRLLPVLCQDHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETV
 QRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIANNNGGRPALE

KL-2

LTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAI
 ASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQA
 LETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLC
 QAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPE
 QVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGG
 GKQALETVQRLLPVLCQDHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNNGGKQALETVQ

RLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNNGGGKQALETVQRLLPVLCQDH
GLTPEQVVAIANNNNGGRPAAE

RH-1

LTPDQVVAIASNIGGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIAS
NIGGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALET
VQRLLPVLCQDHGLTPEQVVAIASNIGGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQ
AHGLTPAQVVAIASNNGGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNNGGGKQALETVQRLLPVLCQDHGLTPEQV
VAIASNIGGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGK
QALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLL
PVLCQAHGLTPDQVVAIASNNGGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGL
TPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIAS
HDGGGRPAAE

RH-2

LTPDQVVAIASNNGGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGGKQALETVQRLLPVLCQAHGLTPDQVVAIAS
HDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALE
TVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGGKQALETVQRLLPVLC
QAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQ
VVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDG
GKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQ
RLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGGKQALETVQRLLPVLCQDH
GLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGGKQALETVQRLLPVLCQAHGLTPEQVVAIA
SHDGGGRPAAE

RH-3

LTPDQVVAIASNIGGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNNGGGKQALETVQRLLPVLCQAHGLTPDQVVAIAS
NNGGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNNGGGKQALETVQRLLPVLCQDHGLTPDQVVAIANNNNGGKQAL
ETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGGKQALETVQRLLPVLC
QAHGLTPAQVVAIANNNNGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNNGGGKQALETVQRLLPVLCQDHGLTPE
QVVAIANNNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIANN
NNGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNNGGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNNGGGKQALET
VQRLLPVLCQAHGLTPDQVVAIANNNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNNGGKQALETVQRLLPVLC
QDHGLTPDQVVAIANNNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASHDGGGRPAAE

RH-4

LTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGGKQALETVQRLLPVLCQAHGLTPDQVVAIA
NNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGGKQAL
ETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGGKQALETVQRLLPVLC
QAHGLTPAQVVAIANNNNGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQ
VVAIASNIGGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGG
KQALETVQRLLPVLCQDHGLTPDQVVAIASNNGGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNNGGGKQALETVQRL
LPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGL
TPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIAS
HDGGGRPAAE

RH-5

LTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIA
SNGGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQVVAIANNNGGKQAL
ETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGLTP
EQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIANN
NGGKQALETVQRLLPVLCQDHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALE
TVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLC
QDHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPE
QVVAIANNNGGRPALE

RH-6

LTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAI
ANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQVVAIANNNGGKQA
LETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLP
VLCQAHGLTPAQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGL
TPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIAS
NIGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALE
TVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLC
QDHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIANNNGGRPALE

RH-7

LTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIAS
NIGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQVVAIANNNGGKQALE
TVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQ
AHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQV
AIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQ
ALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLP
VLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTP
DQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHD
GGRPALE

RH-8

LTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIAS
NIGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALE
TVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLC
QAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQ
VVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDG
GKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQR
LLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHG
LTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIA
SNIGGRPALE

RH-9

LTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIA
SNGGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPDQVVAIANNNGGKQA
LETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPV
CQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPE

QVVAIANNNGGKQALETVQRLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLPVLCQAHGLTPAQVVAIANN
NGGKQALETVQRLPVLCQDHGLTPDQVVAIANNNGGKQALETVQRLPVLCQDHGLTPEQVVAIASHDGGKQALET
VQRLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLPVLCQAHGLTPAQVVAIANNNGGKQALETVQRLPVLCQ
DHGLTPDQVVAIASNGGKQALETVQRLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLPVLCQAHGLTPEQV
AIANNNGGRPALE

RH-10

LTPDQVVAIASHDGGKQALETVQRLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLPVLCQAHGLTPDQVVAIA
SNGGKQALETVQRLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLPVLCQDHGLTPDQVVAIASHDGGKQALE
TVQRLPVLCQDHGLTPEQVVAIASNGGKQALETVQRLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLPVLC
QAHGLTPAQVVAIASHDGGKQALETVQRLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLPVLCQDHGLTPEQ
VVAIASHDGGKQALETVQRLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLPVLCQAHGLTPAQVVAIASHDG
GKQALETVQRLPVLCQDHGLTPDQVVAIASNIGGKQALETVQRLPVLCQDHGLTPEQVVAIASHDGGKQALETVQ
RLPVLCQAHGLTPDQVVAIASNGGKQALETVQRLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLPVLCQDHG
LTPDQVVAIASHDGGKQALETVQRLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLPVLCQAHGLTPEQVVAIAS
NIGGRPALE

RH-11

LTPDQVVAIANNNGGKQALETVQRLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLPVLCQAHGLTPDQVVAIA
SHDGGKQALETVQRLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLPVLCQDHGLTPDQVVAIASHDGGKQAL
ETVQRLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLPVLC
QAHGLTPAQVVAIANNNGGKQALETVQRLPVLCQDHGLTPDQVVAIANNNGGKQALETVQRLPVLCQDHGLTPE
QVVAIANNNGGKQALETVQRLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLPVLCQAHGLTPAQVVAIASNG
GGKQALETVQRLPVLCQDHGLTPDQVVAIASNGGKQALETVQRLPVLCQDHGLTPEQVVAIANNNGGKQALETV
QRLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLPVLCQ
DHGLTPDQVVAIASHDGGKQALETVQRLPVLCQDHGLTPEQVVAIASNGGKQALETVQRLPVLCQAHGLTPEQV
VAIASNGGGRPALE

HB-1

LTPDQVVAIASHDGGKQALETVQRLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLPVLCQAHGLTPDQVVAIAS
NIGGKQALETVQRLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLPVLCQDHGLTPDQVVAIASNGGKQALET
VQRLPVLCQDHGLTPEQVVAIASNGGKQALETVQRLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLPVLCQ
AHGLTPAQVVAIASNGGKQALETVQRLPVLCQDHGLTPDQVVAIASNGGKQALETVQRLPVLCQDHGLTPEQV
VAIASNIGGKQALETVQRLPVLCQAHGLTPDQVVAIASNGGKQALETVQRLPVLCQAHGLTPAQVVAIASNGGK
QALETVQRLPVLCQDHGLTPDQVVAIASNGGKQALETVQRLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRL
LPVLCQAHGLTPDQVVAIASNGGKQALETVQRLPVLCQAHGLTPAQVVAIANNNGGKQALETVQRLPVLCQDHG
LTPDQVVAIASNGGKQALETVQRLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLPVLCQAHGLTPEQVVAIAS
NIGGRPALE

HB-2

LTPDQVVAIASNGGKQALETVQRLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLPVLCQAHGLTPDQVVAIA
SNGGKQALETVQRLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLPVLCQDHGLTPDQVVAIASNIGGKQALE
TVQRLPVLCQDHGLTPEQVVAIASNGGKQALETVQRLPVLCQAHGLTPDQVVAIASNGGKQALETVQRLPVLC
QAHGLTPAQVVAIASNGGKQALETVQRLPVLCQDHGLTPDQVVAIANNNGGKQALETVQRLPVLCQDHGLTPEQ
VVAIASNGGKQALETVQRLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLPVLCQAHGLTPAQVVAIASNGG
GKQALETVQRLPVLCQDHGLTPDQVVAIASNIGGKQALETVQRLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRL
LPVLCQAHGLTPDQVVAIASNGGKQALETVQRLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLPVLCQDHGL

TPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIAS
NIGGRPALE

HB-3

LTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAI
ASNIGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQAL
ETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLC
QAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQV
VAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGK
KQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQR
LLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDH
GLTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIA
NNNGGRPALE

HB-4

LTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIA
SNGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQALE
TVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQ
AHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQV
AIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGK
QALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLL
VLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLT
PDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIANN
GGRPALE

HB-5

LTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIA
NNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQAL
ETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLC
QAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQ
VVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNGG
KQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRL
LPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHG
LTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIAS
NIGGGRPALE

HB-6

LTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIA
SNGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALE
TVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQ
AHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQV
AIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQ
ALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPV
CQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPD
QVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDG
GRPALE

HB-7

LTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIAS
NIGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALET
VQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNNGGKQALETVQRLLPVLCQ
AHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVV
AIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQ
ALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNGGGKQALETVQRLLPV
LCQAHGLTPDQVVAIANNNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNNGGKQALETVQRLLPVLCQDHGLTP
DQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASH
DGGRPAL

HB-8

LTPDQVVAIANNNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNNGGKQALETVQRLLPVLCQAHGLTPDQVVAI
ASNGGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNNGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQ
ALETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQDHGLTP
EQVVAIANNNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHD
GGKQALETVQRLLPVLCQDHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETV
QRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQD
HGLTPDQVVAIANNNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVA
IANNNNGGRP

HB-9

LTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIAS
HDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQALET
VQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQ
AHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPDQVVAIANNNNGGKQALETVQRLLPVLCQDHGLTPEQV
VAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGK
QALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNNGGKQALETVQRLL
PVLCQAHGLTPDQVVAIANNNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNNGGKQALETVQRLLPVLCQDHGL
TPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIAS
NGGGRP

HB-10

LTPDQVVAIANNNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIA
SNGGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALE
TVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQ
AHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVV
AIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNNGGK
QALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLL
PVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLT
PDQVVAIANNNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIAN
NNGGRP

Supplementary Table 1 Primers used in this study. All primers listed 5' to 3'.

See attached Excel file.

Supplementary Table 2 Binding sites of TALEs and Zinc Fingers used in this study. All binding sites listed 5' to 3' (bound N-terminus to C-terminus by TALEs and C-terminus to N-terminus by ZFs).

TALEs

KL-1	TGTGTATGCCCCGTGGTG
KL-2	TGGCCCAGCCAGTGTCTG
RH-1	TACACCACTTACCCCTCCCC
RH-2	TTACCCCTCCCCCCCACAC
RH-3	TATTTGCTGTGGGTTGGGCC
RH-4	TCAGCACAGCAGCTTCCCCC
RH-5	TAGTAGGGTGTGGGGGAGGG
RH-6	TGGGAGGGGGAGTAGGATGG
RH-7	TACATGCAAACACCCACCCC
RH-8	TACTCCCCCCTCCACCCTA
RH-9	TGTTGGAGTGGGGGCAGTAG
RH-10	TCCTACTGCCCCCACTCCAA
RH-11	TGCCTCAGGGGCTTGGCCTT
HB-1	TCAACTTCTTATTTGTGTAA
HB-2	TTCTTATTTGTGTAATAAGA
HB-3	TGGAATCACAGCTTGTAAG
HB-4	TCTTCAATATGCTTACCAAG
HB-5	TATGCTTACCAAGCTGTGAT
HB-6	TGCTACTAAAAACATCCTCC
HB-7	TCAAACAGACACCATGGTGC
HB-8	TGGTGCATCTGACTCCTGAG
HB-9	TACCAACCTGCCCAGGGCCT
HB-10	TGATACCAACCTGCCAGGG

Zinc Fingers

KL-ZF-1	GCTGTCGGTAGGGCGGGC
KL-ZF-2	GCGGAGTCCGCGCGGTGGC
HB-ZF-1	GATGGTATGGGGCCAAGAG
HB-ZF-2	TGTGGGGCAAGGTGAACG
HB-ZF-3	GGTGAACGTGGATGAAGTT
HB-ZF-4	GAGGCCCTGGGCAGGTTGG
HB-ZF-5	GGTGGTGAGGCCCTGGGCA
HB-ZF-6	GAGGCCCTGGGCAGGTTGGT

Supplementary References

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