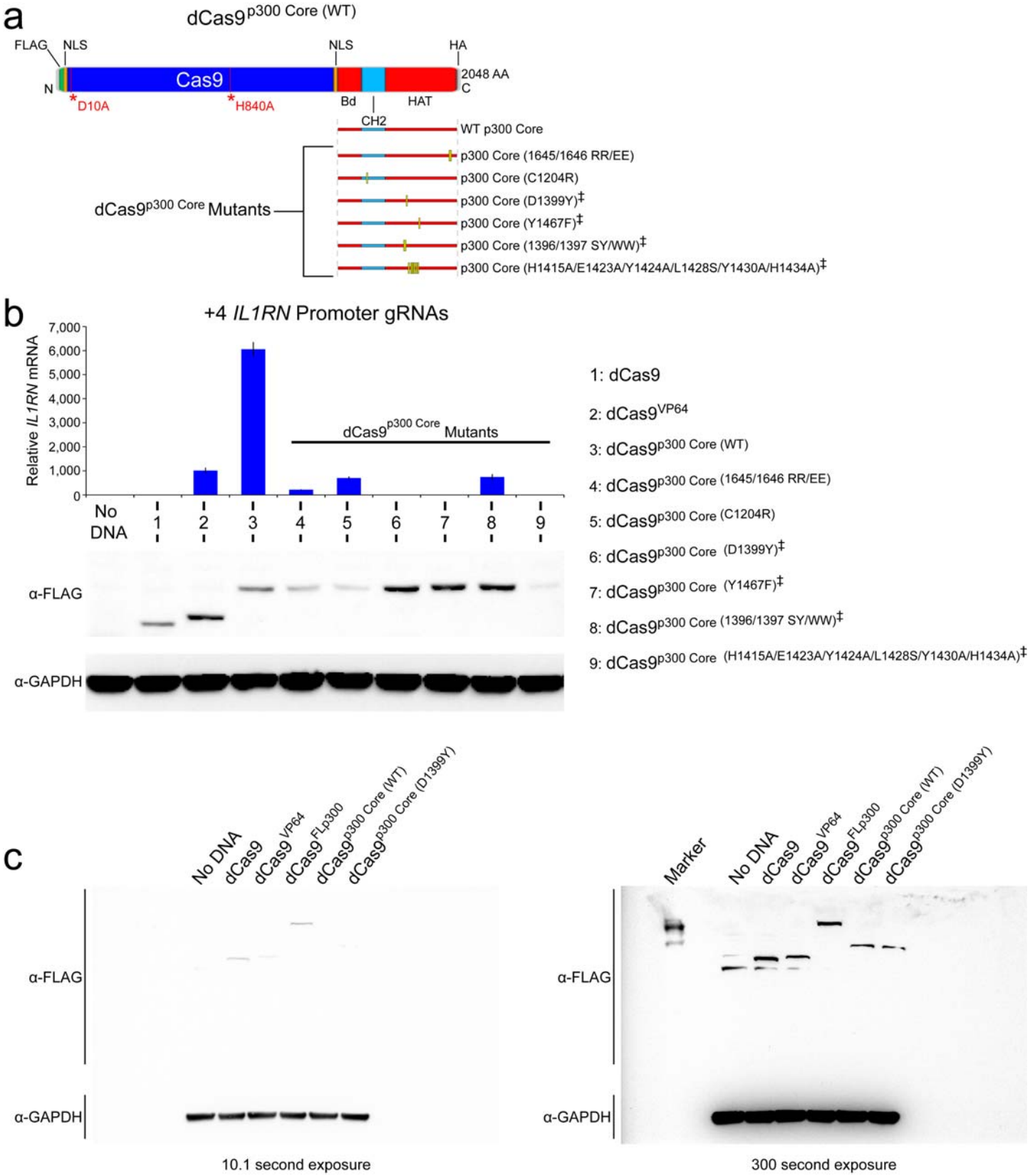
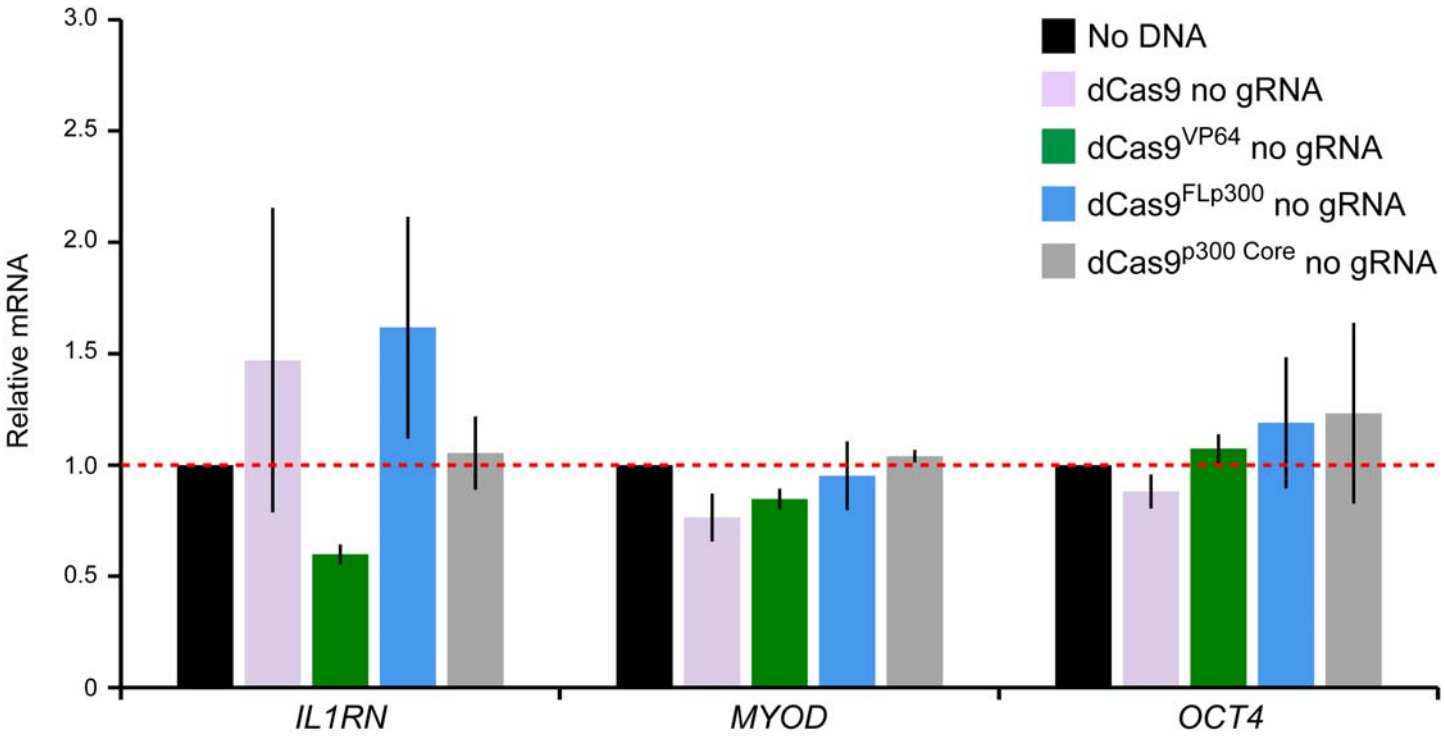



**Supplementary Figure 1**

dCas9$^{p300\ Core}$ mutant fusion protein activities.

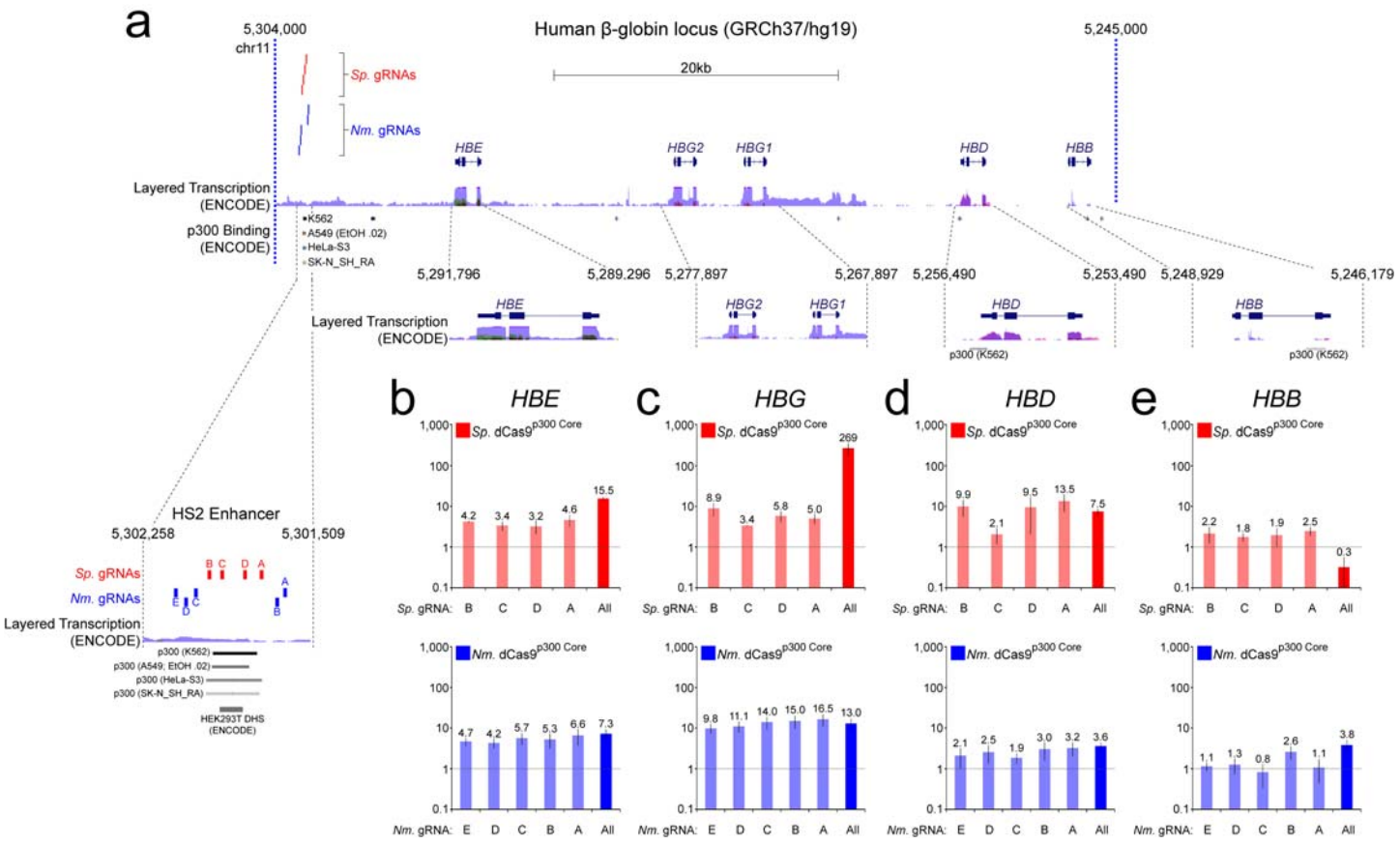
(**a**) Schematic depiction of the WT dCas9$^{p300\ Core}$ fusion protein and p300 Core mutant derivatives. Relative locations of mutated amino acids are displayed as yellow bars within the p300 Core effector domain. (**b**) dCas9$^{p300\ Core}$ variants were transiently co-transfected with four *IL1RN* promoter gRNAs and were screened for hyperactivity[1] (amino acid 1645/1646 RR/EE and C1204R mutations) or hypoactivity[1, 2] (denoted by ‡) via mRNA production from the *IL1RN* locus (top panel, n=2 independent experiments, error bars: s.e.m.). Experiments were performed in duplicate with one well used for RNA isolation and the other for western blotting to validate expression (bottom panels). The nitrocellulose membrane was cut and incubated with α-FLAG primary antibody (top, Sigma-Aldrich cat.# F7425) or α-GAPDH (bottom, Cell Signaling Technology cat.# 14C10) then α-Rabbit HRP secondary antibody (Sigma-Aldrich cat.# A6154). (**c**) Full membranes from western blot shown in main text (**Figure 1b**). The nitrocellulose membrane was cut and incubated with α-FLAG primary antibody (top, Sigma-Aldrich cat.# F7425) or α-GAPDH (bottom, Cell Signaling Technology cat.# 14C10) then α-Rabbit HRP secondary antibody (Sigma-Aldrich cat.# A6154). Membrane was imaged for the indicated durations after careful re-alignment of trimmed pieces.




**Supplementary Figure 2**

Target gene activation is unaffected by overexpression of synthetic dCas9 fusion proteins.

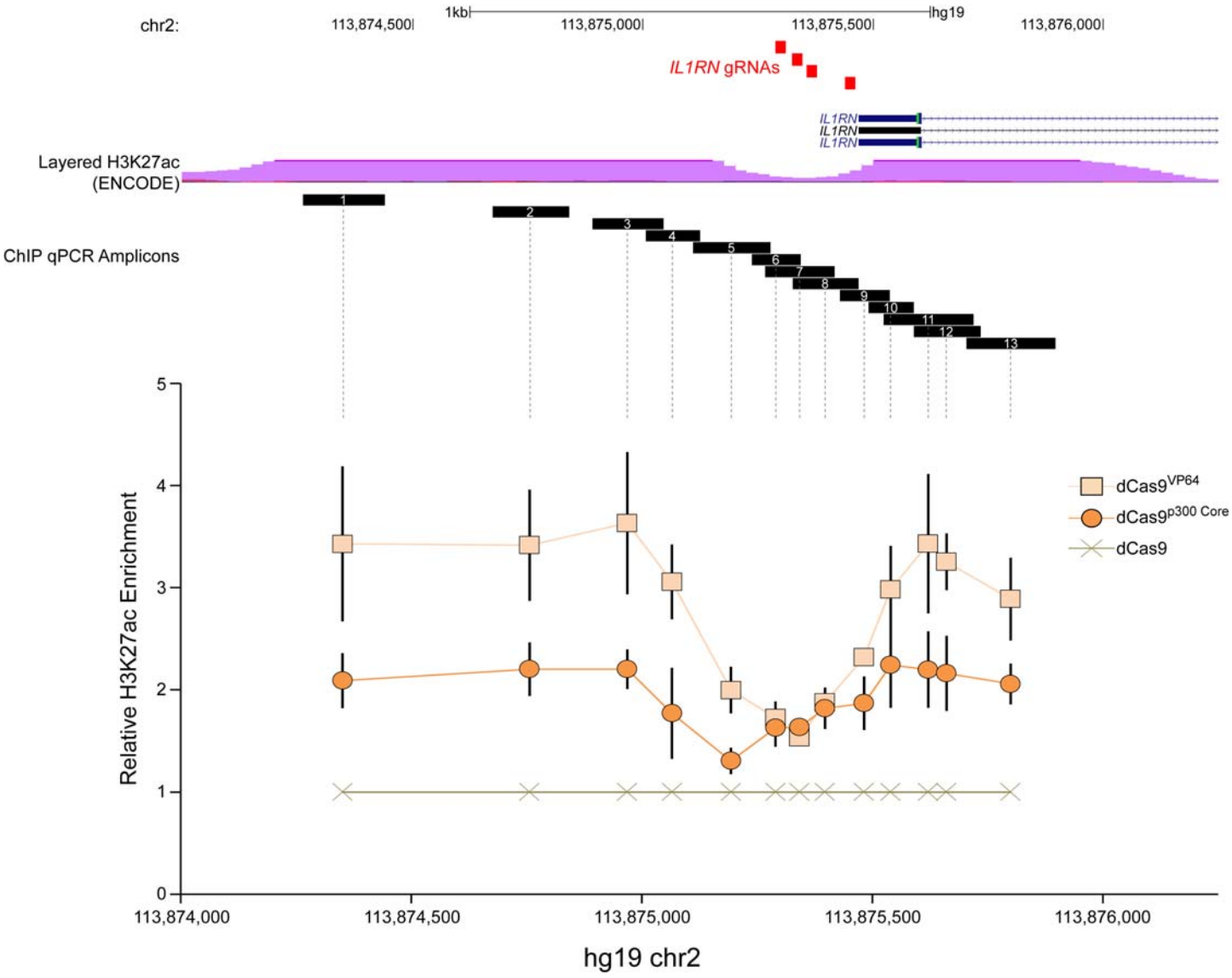
dCas9 fusion proteins were transiently co-transfected with an empty gRNA vector backbone and mRNA expression of *IL1RN*, *MYOD*, and *OCT4* was assayed as in the main text. Red dashed line indicates background expression level from No DNA-transfected cells. n=2 independent experiments, error bars: s.e.m., no significant activation was observed for any target gene assayed.




**Supplementary Figure 3**

Comparison of *Sp*. dCas9 and *Nm*. dCas9 gene induction from the HS2 enhancer with individual and pooled gRNAs.

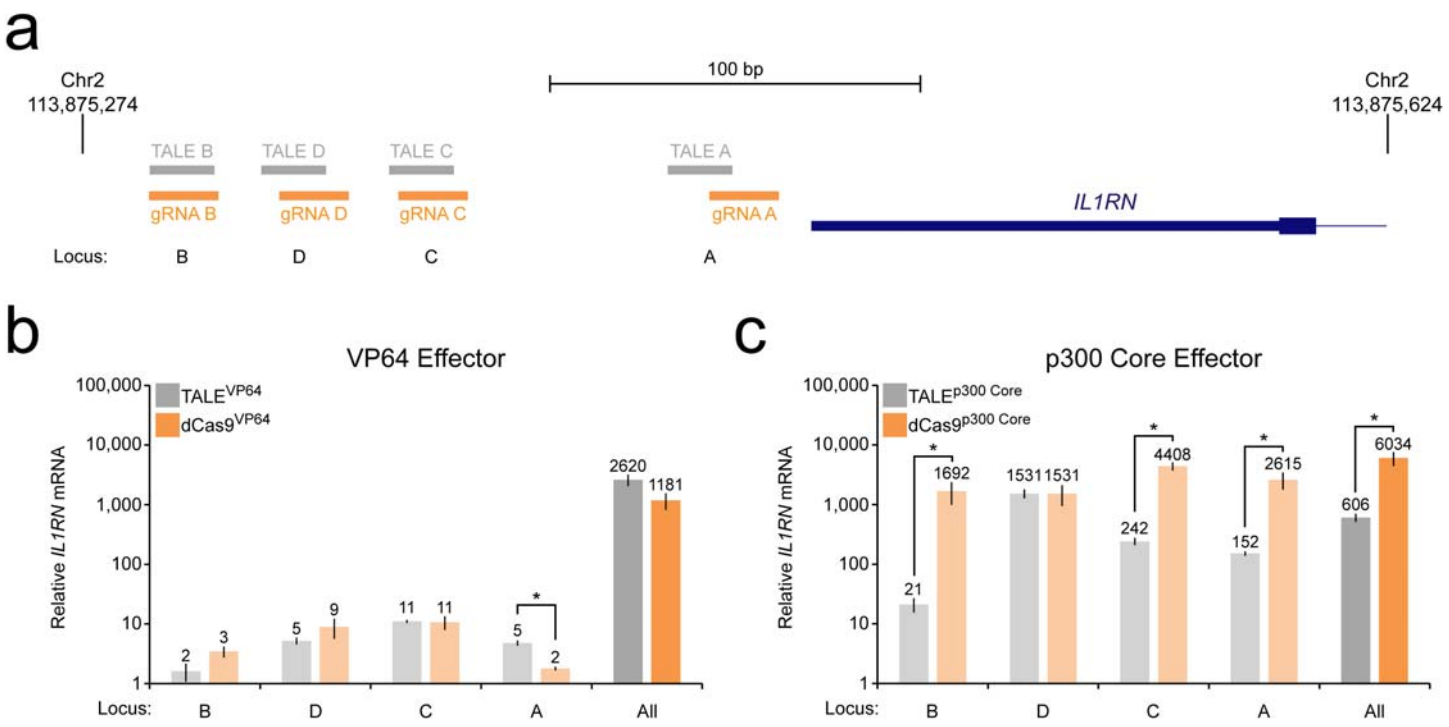
(**a**) Schematic display of the human β-globin locus including *Streptococcus pyogenes* dCas9 (*Sp*. dCas9) and *Neisseria meningitidis* dCas9 (*Nm*. dCas9) gRNA locations at the HS2 enhancer. Layered transcription profiles scaled to a vertical viewing range of 8 from nine ENCODE cell lines (GM12878, H1-hESC, HeLa-S3, HepG2, HSMM, HUVEC, K562, NHEK, and NHLF) is shown in addition to ENCODE p300 binding peaks in K562, A549 (EtOH.02), HeLA-S3, and SKN_SH_RA cell lines. An ENCODE HEK293T DNase hypersensitive site (HEK293T DHS) is shown in the HS2 Enhancer inset. (**b–e**) Relative transcriptional induction of *HBE*, *HBG*, *HBD*, and *HBD* transcripts from single and pooled *Sp*. dCas9 gRNAs (A–D) or single and pooled *Nm*. dCas9 gRNAs (A–E) in response to co-transfection with *Sp*. dCas9$^{p300\ Core}$ or *Nm*. dCas9$^{p300\ Core}$ respectively. gRNAs are tiled for each dCas9 ortholog corresponding to their location in GRCh37/hg19. Gray dashed line indicates background expression level in transiently co-transfected HEK293T cells. Note shared logarithmic scale among panels **b–e**. Numbers above bars in **b–e** indicate mean expression (n = at least 3 independent experiments, error bars: s.e.m.).




**Supplementary Figure 4**

dCas9$^{VP64}$ and dCas9$^{p300\ Core}$ induce H3K27ac enrichment at *IL1RN* gRNA-targeted chromatin.

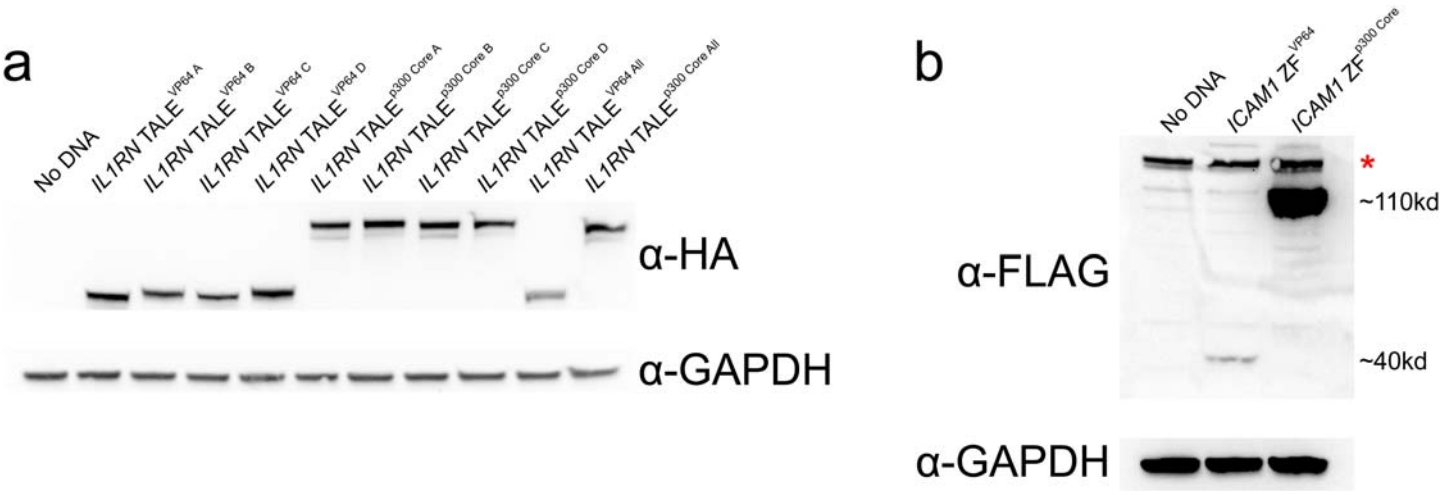
The *IL1RN* locus on GRCh37/hg19 is shown along with *IL1RN* gRNA target sites. In addition layered ENCODE H3K27ac enrichment from seven cell lines (GM12878, H1-hESC, HSMM, HUVEC, K562, NHEK, and NHLF) is indicated with the vertical range setting set to 50. Tiled *IL1RN* ChIP qPCR amplicons (1–13) are also shown in corresponding locations on GRCh37/hg19. H3K27ac enrichment for dCas9$^{VP64}$ and dCas9$^{p300\ Core}$ co-transfected with four *IL1RN*-targeted gRNAs and normalized to dCas9 co-transfected with four *IL1RN* gRNAs is indicated for each ChIP qPCR locus assayed. 5ng of ChIP-prepared DNA was used for each reacton (n = 3 independent experiments, error bars: s.e.m.)




**Supplementary Figure 5**

Direct comparison of VP64 and p300 Core effector domains between TALE and dCas9 programmable DNA binding proteins.

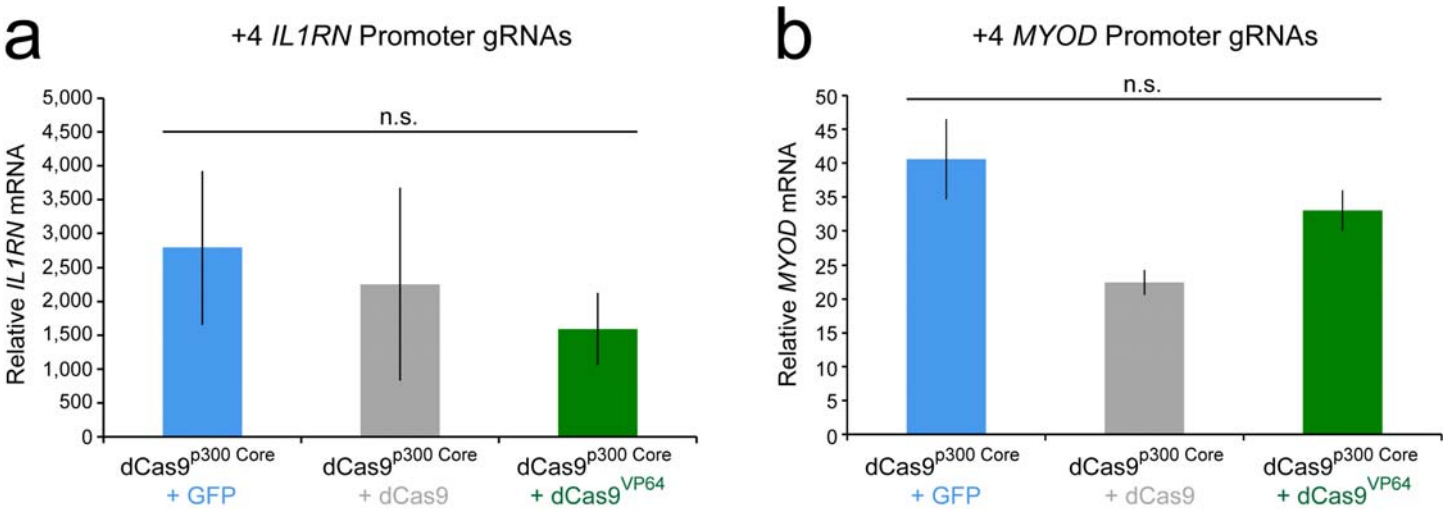
(**a**) The GRCh37/hg19 region encompassing the *IL1RN* transcription start site is shown schematically along with *IL1RN* TALE binding sites and dCas9 *IL1RN* gRNA target sites. (**b**) Direct comparison of *IL1RN* activation in HEK293T cells when transfected with individual or pooled (A–D) *IL1RN* TALE$^{VP64}$ fusion proteins or when co-transfected with dCas9$^{VP64}$ and individual or pooled (A–D) *IL1RN*-targeting gRNAs. (**c**) Direct comparison of *IL1RN* activation in HEK293T cells when transfected with individual or pooled (A–D) *IL1RN* TALE$^{p300\ Core}$ fusion proteins or when co-transfected with dCas9$^{p300\ Core}$ and individual or pooled (A–D) *IL1RN*-targeting gRNAs. Note shared logarithmic scale between panels **b** and **c**. Numbers above bars in panels **b** and **c** indicate mean values. Tukey test, **P*-value <0.05, n = at least 3 independent experiments, error bars: s.e.m.




**Supplementary Figure 6**

TALE and ZF fusion protein expression.

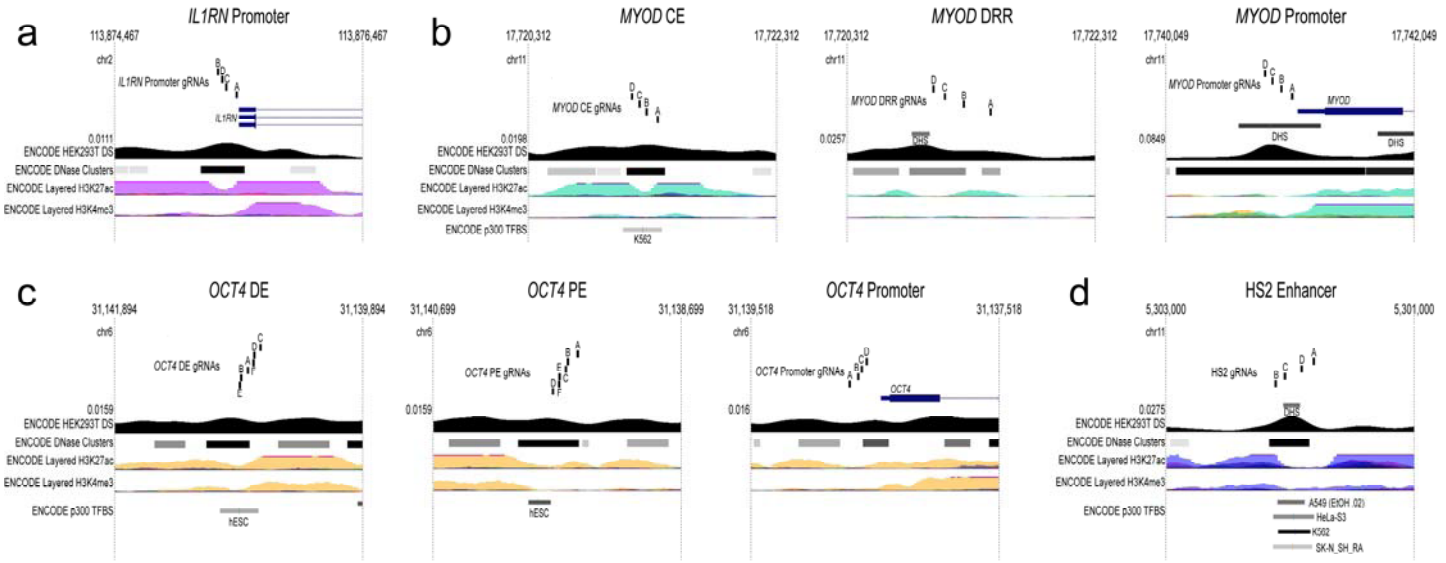
(**a**) Western blotting was carried out on cells transiently transfected with individual or pooled *IL1RN* TALE proteins. Nitrocellulose membranes were cut and probed with α-HA primary antibody (1:1000 dilution in TBST + 5% Milk, top, Covance cat.# MMS-101P) or α-GAPDH (bottom, Cell Signaling Technology cat.# 14C10) then α-Mouse HRP (Santa Cruz, sc-2005) or α-Rabbit HRP (Sigma-Aldrich cat.# A6154) secondary antibody, respectively. (**b**) Western blotting was carried out on cells transiently transfected with *ICAM1* ZF-effector proteins and nitrocellulose membranes were cut and probed with α-FLAG primary antibody (top, Sigma-Aldrich cat.# F7425) or α-GAPDH (bottom, Cell Signaling Technology cat.# 14C10) then α-Rabbit HRP secondary antibody (Sigma-Aldrich cat.# A6154). Red asterisk indicates non-specific band.




**Supplementary Figure 7**

dCas9$^{p300\ Core}$ and dCas9$^{VP64}$ do not display synergy in transactivation.

(**a**) dCas9$^{p300\ Core}$ was co-transfected at a 1:1 mass ratio to PL-SIN-EF1α-EGFP[3] (GFP), dCas9, or dCas9$^{VP64}$ with four *IL1RN* promoter gRNAs as indicated (n = 2 independent experiments, error bars: s.e.m.). (**b**) dCas9$^{p300\ Core}$ was co-transfected at a 1:1 mass ratio to GFP, dCas9, or dCas9$^{VP64}$ with four *MYOD* promoter gRNAs as indicated (n = 2 independent experiments, error bars: s.e.m.). No significant differences were observed using Tukey's test (n.s).




e

| gRNA-Targeted Locus | Overlap DHS in HEK293T | Overlap DHS in Other ENCODE Lines | Multiple gRNAs Required for Maximal dCas9$^{p300\ Core}$ Target Activation | Overlap Endogenous p300 in ENCODE Lines |
|---|---|---|---|---|
| *IL1RN* Promoter | N | Y | N | N |
| *MYOD* CE | N | Y | N | Y |
| *MYOD* DRR | Marginal | Y | N | N |
| *MYOD* Promoter | N | Y | N | N |
| *OCT4* DE | N | Y | Y | Y |
| *OCT4* PE | N | Y | N | Marginal |
| *OCT4* Promoter | N | Y | N | N |
| HS2 Enhancer | Y | Y | Y | Y |

**Supplementary Figure 8**

Underlying chromatin context of dCas9$^{p300\ Core}$ target loci.

(**a–d**) Indicated loci are shown along with associated *Streptococcus pyogenes* gRNAs used in this study at corresponding genomic locations in GRCh37/hg19. ENCODE HEK293T DNase hypersensitivity enrichment is shown (note changes in scale) along with regions of significant DNase hypersensitivity in HEK293T cells ("DHS"). In addition ENCODE master DNase clusters across 125 cell types are shown. Layered ENCODE H3K27ac and H3K4me3 enrichment across seven cell lines (GM12878, H1-hESC, HSMM, HUVEC, K562, NHEK, and NHLF) is also displayed and scaled to a vertical viewing range of 50 and 150 respectively. Endogenous p300 binding profiles are also indicated for each locus and respective cell line. (**e**) An overview of the information provided in **a–d**.

**Supplementary Table 1.** Ten most enriched mRNAs for dCas9 *IL1RN*-targeted RNA-seq experiments

| **dCas9$^{VP64}$ + 4 *IL1RN* gRNAs compared to dCas9 + 4 *IL1RN* gRNAs** | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | Refseq ID | Gene | baseMean | log2FoldChange | lfcSE | stat | pvalue | padj |
| 1 | **NM_173842** | ***IL1RN* (transcript variant 1)** | **14.764** | **0.529** | **0.152** | **3.48** | **0.000494857** | **0.99992134** |
| 2 | **NM_173843** | ***IL1RN* (transcript variant 4)** | **13.606** | **0.517** | **0.149** | **3.47** | **0.000530109** | **0.99992134** |
| 3 | NR_073102 | ZNF551 | 21.505 | 0.505 | 0.159 | 3.17 | 0.00152863 | 0.99992134 |
| 4 | **NM_000577** | ***IL1RN* (transcript variant 3)** | **14.890** | **0.497** | **0.152** | **3.28** | **0.001039353** | **0.99992134** |
| 5 | NM_001077441 | BCLAF1(transcript variant 3) | 437.814 | 0.482 | 0.153 | 3.14 | 0.001665925 | 0.99992134 |
| 6 | **NM_173841** | ***IL1RN* (transcript variant 2)** | **13.711** | **0.448** | **0.15** | **3.00** | **0.002716294** | **0.99992134** |
| 7 | NM_001268 | *RCBTB2* | 46.265 | 0.440 | 0.167 | 2.64 | 0.008335513 | 0.99992134 |
| 8 | NM_000922 | *PDE3B* | 143.947 | 0.439 | 0.167 | 2.63 | 0.008471891 | 0.99992134 |
| 9 | NM_001077440 | *BCLAF1* (transcript variant 2) | 463.743 | 0.439 | 0.156 | 2.82 | 0.004790762 | 0.99992134 |
| 10 | NM_014739 | *BCLAF1* (transcript variant 1) | 474.598 | 0.432 | 0.158 | 2.74 | 0.006232218 | 0.99992134 |
| **dCas9$^{p300\ Core}$ + 4 *IL1RN* gRNAs compared to dCas9 + 4 *IL1RN* gRNAs** | | | | | | | | |
| | Refseq ID | Gene | baseMean | log2FoldChange | lfcSE | stat | pvalue | padj |
| 1 | **NM_173843** | ***IL1RN* (transcript variant 4)** | **45.517** | **1.548** | **0.171** | **9.04** | **1.52E-19** | **5.24E-15** |
| 2 | **NM_173841** | ***IL1RN* (transcript variant 2)** | **40.690** | **1.457** | **0.171** | **8.50** | **1.83E-17** | **3.16E-13** |
| 3 | **NM_173842** | ***IL1RN* (transcript variant 1)** | **39.568** | **1.448** | **0.171** | **8.45** | **2.88E-17** | **3.30E-13** |
| 4 | **NM_000577** | ***IL1RN* (transcript variant 3)** | **41.821** | **1.437** | **0.171** | **8.39** | **4.88E-17** | **4.20E-13** |
| 5 | NM_001429 | *p300* | 928.435 | 0.955 | 0.171 | 5.57 | 2.50E-08 | 0.000171838 |
| 6 | NM_002253 | *KDR* | 17.477 | 0.842 | 0.163 | 5.17 | 2.36E-07 | 0.00135472 |
| 7 | NM_030797 | *FAM49A* | 21.286 | 0.736 | 0.166 | 4.44 | 8.91E-06 | 0.043823927 |
| 8 | NM_012074 | *DPF3* | 17.111 | 0.609 | 0.164 | 3.72 | 0.000202676 | 0.871938986 |
| 9 | NM_031476 | *CRISPLD2* | 25.148 | 0.569 | 0.167 | 3.41 | 0.000653132 | 0.999954424 |
| 10 | NM_007365 | *PADI2* | 99.012 | 0.554 | 0.162 | 3.41 | 0.000641145 | 0.999954424 |
| **dCas9$^{p300\ Core\ (D1399Y)}$ + 4 *IL1RN* gRNAs compared to dCas9 + 4 *IL1RN* gRNAs** | | | | | | | | |
| | Refseq ID | Gene | baseMean | log2FoldChange | lfcSE | stat | pvalue | padj |
| 1 | NM_001429 | *p300* | 935.659 | 1.234 | 0.198 | 6.24 | 4.36E-10 | 1.49E-05 |
| 2 | NM_001270493 | *SREK1* (transcript variant 4) | 30.118 | 0.651 | 0.203 | 3.20 | 0.001388089 | 0.999938051 |
| 3 | NM_001079802 | *FKTN* (transcript variant 1) | 148.558 | 0.546 | 0.203 | 2.69 | 0.007212168 | 0.999938051 |
| 4 | NM_000922 | *PDE3B* | 140.122 | 0.535 | 0.201 | 2.66 | 0.007805491 | 0.999938051 |
| 5 | NM_206937 | *LIG4* (transcript variant 2) | 30.589 | 0.521 | 0.203 | 2.56 | 0.010513626 | 0.999938051 |
| 6 | NM_001136116 | *ZNF879* | 18.421 | 0.520 | 0.201 | 2.59 | 0.009600802 | 0.999938051 |
| 7 | NM_018374 | *TMEM106B* (transcript variant 1) | 280.758 | 0.516 | 0.196 | 2.64 | 0.008329592 | 0.999938051 |
| 8 | NM_019863 | *F8* (transcript variant 2) | 8.048 | 0.515 | 0.178 | 2.89 | 0.003827553 | 0.999938051 |
| 9 | NM_001193349 | *MEF2C* (transcript variant 5) | 18.934 | 0.510 | 0.202 | 2.53 | 0.011492452 | 0.999938051 |
| 10 | NM_183245 | *INVS* (transcript variant 2) | 38.545 | 0.497 | 0.203 | 2.45 | 0.014125973 | 0.999938051 |

**Supplementary Table 2.** *IL1RN* TAL effector information.

| Name | Target Site | Location* | Reference |
|---|---|---|---|
| *IL1RN* TALE$^{VP64\ A}$ | GGGCTCCTCCTTGTACT | chr2:113875431-113875447 | Perez-Pinera et al., Nat. Methods, 2013[3] |
| *IL1RN* TALE$^{VP64\ B}$ | ACGCAGATAAGAACCAGT | chr2:113875291-113875308 | Perez-Pinera et al., Nat. Methods, 2013[3] |
| *IL1RN* TALE$^{VP64\ C}$ | GGCATCAAGTCAGCCAT | chr2:113875356-113875372 | Perez-Pinera et al., Nat. Methods, 2013[3] |
| *IL1RN* TALE$^{VP64\ D}$ | AGCCTGAGTCACCCTCCT | chr2:113875321-113875338 | Perez-Pinera et al., Nat. Methods, 2013[3] |
| *IL1RN* TALE$^{p300\ Core\ A}$ | GGGCTCCTCCTTGTACT | chr2:113875431-113875447 | This study |
| *IL1RN* TALE$^{p300\ Core\ B}$ | ACGCAGATAAGAACCAGT | chr2:113875291-113875308 | This study |
| *IL1RN* TALE$^{p300\ Core\ C}$ | GGCATCAAGTCAGCCAT | chr2:113875356-113875372 | This study |
| *IL1RN* TALE$^{p300\ Core\ D}$ | AGCCTGAGTCACCCTCCT | chr2:113875321-113875338 | This study |

*GRCh37/hg19 assembly

**Supplementary Table 3.** Referenced plasmids in this study available at Addgene.

| Plasmid Name | Addgene Plasmid # | Reference |
|---|---|---|
| pcDNA-dCas9$^{VP64}$ | 47107 | Perez-Pinera et al., Nat. Methods, 2013[4] |
| pcDNA-dCas9-HA | 61355 | This study |
| pcDNA3.1-p300 | 23252 | Chen et al., EMBO J., 2002[5] |
| pcDNA-dCas9$^{FLp300}$ | 61356 | This study |
| pcDNA-dCas9$^{p300\ Core}$ | 61357 | This study |
| pcDNA-dCas9$^{p300\ Core\ (D1399Y)}$ | 61358 | This study |
| pcDNA-dCas9$^{p300\ Core\ (1645/1646\ RR/EE)}$ | 61359 | This study |
| pcDNA-dCas9$^{p300\ Core\ (C1204R)}$ | 61361 | This study |
| pcDNA-dCas9$^{p300\ Core\ (Y1467F)}$ | 61362 | This study |
| pcDNA-dCas9$^{p300\ Core\ (1396/1397\ SY/WW)}$ | 61363 | This study |
| pcDNA-dCas9$^{p300\ Core\ (H1415A/E1423A/Y1424A/L1428S/Y1430A/H1434A)}$ | 61364 | This study |
| pZdonor-pSPgRNA | 47108 | Perez-Pinera et al., Nat. Methods, 2013[4] |
| pcDNA3.1-300(HAT-) | 23254 | Chen et al., EMBO J., 2002[5]; Kraus et al., Mol. Cell Biol.,1999[6] |
| pcDNA3.3-Nm-dCas9$^{VP64}$ | 48676 | Esvelt and Mali et al., Nat. Methods, 2013[7] |
| pcDNA3.3-Nm-dCas9$^{p300\ Core}$ | 61365 | This study |
| pZDonor-NmCas9-gRNA-hU6 | 61366 | This study |
| PL-SIN-EF1 -EGFP | 21320 | Hotta et al., Nat. Methods, 2009[8] |

**Supplementary Table 4.** gRNA information.

| *Sp*-dCas9 | | | |
|---|---|---|---|
| **Target Location** | **Protospacer Sequence (5'- 3')** | **Genomic Location (GRCh37/hg19 Assembly)** | **Reference** |
| *IL1RN* Promoter A | TGTACTCTCTGAGGTGCTC | chr2:113875442-113875460 | Perez-Pinera et al., Nat. Methods, 2013[4] |
| *IL1RN* Promoter B | ACGCAGATAAGAACCAGTT | chr2:113875291-113875309 | Perez-Pinera et al., Nat. Methods, 2013[4] |
| *IL1RN* Promoter C | CATCAAGTCAGCCATCAGC | chr2:113875358-113875376 | Perez-Pinera et al., Nat. Methods, 2013[4] |
| *IL1RN* Promoter D | GAGTCACCCTCCTGGAAAC | chr2:113875326-113875344 | Perez-Pinera et al., Nat. Methods, 2013[4] |
| *MYOD* Promoter A | CCTGGGCTCCGGGGCGTTT | chr11:17741056-17741074 | Perez-Pinera et al., Nat. Methods, 2013[4] |
| *MYOD* Promoter B | GGCCCCTGCGGCCACCCCG | chr11:17740969-17740987 | Perez-Pinera et al., Nat. Methods, 2013[4] |
| *MYOD* Promoter C | CTCCCTCCCTGCCCGGTAG | chr11:17740897-17740915 | Perez-Pinera et al., Nat. Methods, 2013[4] |
| *MYOD* Promoter D | AGGTTTGGAAAGGGCGTGC | chr11:17740837-17740855 | Perez-Pinera et al., Nat. Methods, 2013[4] |
| *OCT4* Promoter A | ACTCCACTGCACTCCAGTCT | chr6:31138711-31138730 | Hu et al., Nucleic Acids Res., 2014[9] |
| *OCT4* Promoter B | TCTGTGGGGGACCTGCACTG | chr6:31138643-31138662 | Hu et al., Nucleic Acids Res., 2014[9] |
| *OCT4* Promoter C | GGGGCGCCAGTTGTGTCTCC | chr6:31138613-31138632 | Hu et al., Nucleic Acids Res., 2014[9] |
| *OCT4* Promoter D | ACACCATTGCCACCACCATT | chr6:31138574-31138593 | Hu et al., Nucleic Acids Res., 2014[9] |
| *MYOD* DRR A | TGTTTTCAGCTTCCAAACT | chr11:17736528-17736546 | This Study |
| *MYOD* DRR B | CATGAAGACAGCAGAAGCC | chr11:17736311-17736329 | This Study |
| *MYOD* DRR C | GGCCCACATTCCTTTCCAG | chr11:17736158-17736176 | This Study |
| *MYOD* DRR D | GGCTGGATTGGGTTTCCAG | chr11:17736065-17736083 | This Study |
| *MYOD* CE A | CAACTGAGTCCTGAGGTTT | chr11:17721347-17721365 | This Study |
| *MYOD* CE B | CTCACAGCACAGCCAGTGT | chr11:17721257-17721275 | This Study |
| *MYOD* CE C | CAGCAGCTGGTCACAAAGC | chr11:17721200-17721218 | This Study |
| *MYOD* CE D | CTTCCTATAAACTTCTGAG | chr11:17721139-17721157 | This Study |
| *OCT4* PE A | AGTGATAAGACACCCGCTTT | chr6:31139524-31139543 | This Study |
| *OCT4* PE B | CAGACATCTAATACCACGGT | chr6:31139604-31139623 | This Study |
| *OCT4* PE C | AGGGAGAACGGGGCCTACCG | chr6:31139620-31139639 | This Study |
| *OCT4* PE D | ACTTCAGGTTCAAAGAAGCC | chr6:31139725-31139744 | This Study |
| *OCT4* PE E | TTTTCCCCACCCAGGGCCTA | chr6:31139671-31139690 | This Study |
| *OCT4* PE F | CCCTGGGTGGGGAAAACCAG | chr6:31139675-31139694 | This Study |
| *OCT4* DE A | GGAGGAACATGCTTCGGAAC | chr6:31140809-31140828 | This Study |
| *OCT4* DE B | GTGCCGTGATGGTTCTGTCC | chr6:31140864-31140883 | This Study |

| | | | |
|---|---|---|---|
| *OCT4* DE C | GGTCTGCCGGAAGGTCTACA | chr6:31140707-31140726 | This Study |
| *OCT4* DE D | TCGGCCTTTAACTGCCCAAA | chr6:31140757-31140776 | This Study |
| *OCT4* DE E | GCATGACAAAGGTGCCGTGA | chr6:31140875-31140894 | This Study |
| *OCT4* DE F | CCTGCCTTTTGGGCAGTTAA | chr6:31140764-31140783 | This Study |
| HS2 A | AATATGTCACATTCTGTCTC | chr11:5301800-5301819 | This Study |
| HS2 B | GGACTATGGGAGGTCACTAA | chr11:5302108-5302127 | This Study |
| HS2 C | GAAGGTTACACAGAACCAGA | chr11:5302033-5302052 | This Study |
| HS2 D | GCCCTGTAAGCATCCTGCTG | chr11:5301898-5301917 | This Study |

| ***Nm*-dCas9** | | | |
|---|---|---|---|
| **Target Location** | **Protospacer Sequence (5'- 3')** | **Genomic Location (GRCh37/hg19 Assembly)** | **Reference** |
| *HBG* Promoter A | CCACTGCTAACTGAAAGAGA | chr11:5271570-5271589 | This Study |
| *HBG* Promoter B | AGCCACAGTTTCAGCGCAGT | chr11:5271692-5271711 | This Study |
| *HBG* Promoter C | CTGTTTCATCTTAGAAAAAT | chr11:5271793-5271812 | This Study |
| *HBG* Promoter D | GAATGTTCTTTGGCAGGTAC | chr11:5271942-5271961 | This Study |
| *HBG* Promoter E | CGCACATCTTATGTCTTAGA | chr11:5272021-5272040 | This Study |
| *HBE* Promoter A | CTTAAGAGAGCTAGAACTGG | chr11:5291618-5291637 | This Study |
| *HBE* Promoter B | TCCCAAAGTACAGTACCTTG | chr11:5291758-5291777 | This Study |
| *HBE* Promoter C | TCCCTAGAGAGGACAGACAG | chr11:5291785-5291804 | This Study |
| *HBE* Promoter D | TCATAGAGAAATGAAAAGAG | chr11:5291840-5291859 | This Study |
| *HBE* Promoter E | ATAATATACCCTGACTCCTA | chr11:5292038-5292057 | This Study |
| HS2 A | AGGCCACCTGCAAGATAAAT | chr11:5301662-5301681 | This Study |
| HS2 B | TGTTGTTATCAATTGCCATA | chr11:5301708-5301727 | This Study |
| HS2 C | ATCCCTTCCAGCATCCTCAT | chr11:5302187-5302206 | This Study |
| HS2 D | GTGCTTCAAAACCATTTGCT | chr11:5302245-5302264 | This Study |
| HS2 E | GATACATGTTTTATTCTTAT | chr11:5302306-5302325 | This Study |

**Supplementary Table 5.** Quantitative reverse transcription PCR and ChIP-qPCR primers and conditions.

| Target | Forward Primer (5'-3') | Reverse Primer (5'-3') | Cycling Parameters |
|---|---|---|---|
| *GAPDH* | CAATGACCCCTTCATTGACC | TTGATTTTGGAGGGATCTCG | 95˚C 30 sec<br>95˚C 5 sec<br>53˚C 20 sec \| 45X |
| *IL1RN* | GGAATCCATGGAGGGAAGAT | TGTTCTCGCTCAGGTCAGTG | 95˚C 30 sec<br>95˚C 5 sec<br>58˚C 20 sec \| 45X |
| *MYOD* | TCCCTCTTTCACGGTCTCAC | AACACCCGACTGCTGTATCC | 95˚C 30 sec<br>95˚C 5 sec<br>53˚C 20 sec \| 45X |
| *OCT4* | CGAAAGAGAAAGCGAACCAGTATCGAGAAC | CGTTGTGCATAGTCGCTGCTTGATCGC | 95˚C 30 sec<br>95˚C 5 sec<br>53˚C 20 sec \| 45X |
| *HBB* | GCACGTGGATCCTGAGAACT | ATTGGACAGCAAGAAAGCGAG | 95˚C 30 sec<br>95˚C 5 sec<br>58˚C 20 sec \| 45X |
| *HBD* | GCACGTGGATCCTGAGAACT | CAGGAAACAGTCCAGGATCTCA | 95˚C 30 sec<br>95˚C 5 sec<br>58˚C 20 sec \| 45X |
| *HBG* | GCTGAGTGAACTGCACTGTGA | GAATTCTTTGCCGAAATGGA | 95˚C 30 sec<br>95˚C 5 sec<br>58˚C 20 sec \| 45X |
| *HBE* | TCACTAGCAAGCTCTCAGGC | AACAACGAGGAGTCTGCCC | 95˚C 30 sec<br>95˚C 5 sec<br>62˚C 20 sec \| 45X |
| *ICAM1* | GCAGACAGTGACCATCTACAGCTT | CAATCCCTCTCGTCCAGTCG | 95˚C 30 sec<br>95˚C 5 sec<br>58˚C 20 sec \| 45X |
| HS2 ChIP Region 1 | TGCTTGGACTATGGGAGGTC | GCAGGTGCTTCAAAACCATT | 95˚C 30 sec<br>95˚C 5 sec<br>60˚C 20 sec \| 45X |
| HS2 ChIP Region 2 | TCAGGTGGTCAGCTTCTCCT | AAGCAAACCTTCTGGCTCAA | 95˚C 30 sec<br>95˚C 5 sec<br>60˚C 20 sec \| 45X |
| HS2 ChIP Region 3 | CCACACAGGTGAACCCTTTT | GGACACATGCTCACATACGG | 95˚C 30 sec<br>95˚C 5 sec<br>60˚C 20 sec \| 45X |
| *HBE* ChIP Region 1 | ATTCGATCCATGTGCCTGA | CAATGCTGGAATTTGTGGAA | 95˚C 30 sec<br>95˚C 5 sec<br>60˚C 20 sec \| 45X |
| *HBE* ChIP Region 2 | GGGGTGATTCCCTAGAGAGG | AAGCAGGACAGACAGGCAAG | 95˚C 30 sec<br>95˚C 5 sec<br>60˚C 20 sec \| 45X |
| *HBE* ChIP Region 3 | GAGGGTCAGCAGTGATGGAT | TGGAAAAGGAGAATGGGAGA | 95˚C 30 sec<br>95˚C 5 sec<br>60˚C 20 sec \| 45X |
| *HBG1/2* ChIP Region 1 | TGGTCAAGTTTGCCTTGTCA | GGAATGACTGAATCGGAACAA | 95˚C 30 sec<br>95˚C 5 sec<br>60˚C 20 sec \| 45X |
| *HBG1/2* ChIP Region 2 | CCTCCAGCATCTTCCACATT | GAAGCACCCTTCAGCAGTTC | 95˚C 30 sec<br>95˚C 5 sec<br>60˚C 20 sec \| 45X |
| *HBG*1/2 ChIP Region 3 | CCACAGTTTCAGCGCAGTAATA | ATCAGCCAGCACACACACTT | 95˚C 30 sec<br>95˚C 5 sec<br>60˚C 20 sec \| 45X |
| *IL1RN* ChIP Region 1 | CCCTGTCAGGAGGGACAGAT | GGCTCACCGGAAGCATGAAT | 95˚C 30 sec<br>95˚C 5 sec<br>60˚C 20 sec \| 45X |
| *IL1RN* ChIP Region 2 | AAGCTACAAGCAGGTTCGCT | AATAACAGGGTCCATCCCGC | 95˚C 30 sec<br>95˚C 5 sec<br>60˚C 20 sec \| 45X |
| *IL1RN* ChIP Region 3 | TGTTCCCTCCACCTGGAATA | GGGAAAATCCAAAGCAGGAT | 95˚C 30 sec<br>95˚C 5 sec<br>60˚C 20 sec \| 45X |

| | | | |
|---|---|---|---|
| *IL1RN* ChIP Region 4 | TCCTAGGTCCCTCAAAAGCA | GTCCCCAACGCTCTAACAAA | 95˚C 30 sec<br>95˚C 5 sec<br>60˚C 20 sec 45X |
| *IL1RN* ChIP Region 5 | GTTAGAGCGTTGGGGACCTT | CACATGCAGAGAACTGAGCTG | 95˚C 30 sec<br>95˚C 5 sec<br>60˚C 20 sec 45X |
| *IL1RN* ChIP Region 6 | GTTGGGGTAAGCACGAAGG | TTTCCAGGAGGGTGACTCAG | 95˚C 30 sec<br>95˚C 5 sec<br>60˚C 20 sec 45X |
| *IL1RN* ChIP Region 7 | TTCTCTGCATGTGACCTCCC | ACACACTCACAGAGGGTTGG | 95˚C 30 sec<br>95˚C 5 sec<br>60˚C 20 sec 45X |
| *IL1RN* ChIP Region 8 | TGAGTCACCCTCCTGGAAAC | CTCCTTCCAGAGCACCTCAG | 95˚C 30 sec<br>95˚C 5 sec<br>60˚C 20 sec 45X |
| *IL1RN* ChIP Region 9 | GCTGGGCTCCTCCTTGTACT | GCTGCTGCCCATAAAGTAGC | 95˚C 30 sec<br>95˚C 5 sec<br>60˚C 20 sec 45X |
| *IL1RN* ChIP Region 10 | GGACTGTGGCCCAGGTACT | GGCCTCATAGGACAGGAGGT | 95˚C 30 sec<br>95˚C 5 sec<br>60˚C 20 sec 45X |
| *IL1RN* ChIP Region 11 | TTATGGGCAGCAGCTCAGTT | GACATTTTCCTGGACGCTTG | 95˚C 30 sec<br>95˚C 5 sec<br>60˚C 20 sec 45X |
| *IL1RN* ChIP Region 12 | CCCTCCCCATGGCTTTAGGT | AGCTCCATGCGCTTGACATT | 95˚C 30 sec<br>95˚C 5 sec<br>60˚C 20 sec 45X |
| *IL1RN* ChIP Region 13 | AGCGTCCAGGAAAATGTCAA | ATGACCCTCACACTCCAAGG | 95˚C 30 sec<br>95˚C 5 sec<br>60˚C 20 sec 45X |
| Upstream - *actin* ChIP NEG CTRL | GTTGGGTGCTCCAGCTTTTA | CCTCAAAACTCCTGGACTCG | 95˚C 30 sec<br>95˚C 5 sec<br>60˚C 20 sec 45X |

**Supplementary Note 1.** Amino acid sequences of dCas9 constructs.

**dCas9 HA:**(Addgene plasmid 61355) amino acid sequence; 3X "Flag" Epitope, **Nuclear Localization Sequence,** ***Streptococcus pyogenes*** **Cas9 (D10A, H840A), "HA" Epitope**

MDYKDHDGDYKDHDIDYKDDDDKMA**PKKKRKVG**RGMDKKYSIGLAIGTNSVGWAVITDEY
KVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEI
FSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDS
TDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASG
VDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQ
LSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY
DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDG
TEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILT
FRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNE
KVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLK
EDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTL
FEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKS
DGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVD
ELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQ
LQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRG
KSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETR
QITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAH
DAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNF
FKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGF
SKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLG
ITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNE
LALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADA
NLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDA
TLIHQSITGLYETRIDLSQLGGDPIAGSKAS**PKKKRKVG**RALIN**YPYDVPDYAS**

**dCas9$^{VP64}$:** (Addgene Plasmid 47107)[4] amino acid sequence; 3X "Flag" Epitope, **Nuclear Localization Sequence,** ***Streptococcus pyogenes*** **Cas9 (D10A, H840A), VP64 Effector, "HA"Epitope**

MDYKDHDGDYKDHDIDYKDDDDKMA**PKKKRKVG**RGMDKKYSIGLAIGTNSVGWAVITDEY
KVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEI
FSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDS
TDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASG
VDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQ
LSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY
DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDG
TEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILT
FRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNE
KVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLK
EDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTL
FEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKS
DGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVD
ELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQ
LQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRG
KSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETR
QITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAH

DAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNF
FKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGF
SKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLG
ITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNE
LALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADA
NLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDA
TLIHQSITGLYETRIDLSQLGGDPIAGSKASPKKKRKVGRADALDDFDLDMLGSDALDDF
DLDMLGSDALDDFDLDMLGSDALDDFDLDMLINYPYDVPDYAS

**dCas9$^{FL\ p300}$:** (Addgene Plasmid 61356) amino acid sequence; 3X "Flag" Epitope, **Nuclear Localization Sequence,** ***Streptococcus pyogenes*** **Cas9 (D10A, H840A), Human p300 aa 2-2414, L553M, "HA" Epitope**

MDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGRGMDKKYSIGLAIGTNSVGWAVITDEY
KVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEI
FSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDS
TDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASG
VDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQ
LSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY
DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDG
TEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILT
FRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNE
KVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLK
EDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTL
FEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKS
DGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVD
ELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQ
LQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRG
KSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETR
QITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAH
DAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNF
FKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGF
SKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLG
ITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNE
LALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADA
NLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDA
TLIHQSITGLYETRIDLSQLGGDPIAGSKASPKKKRKVGRAAENVVEPGPPSAKRPKLSS
PALSASASDGTDFGSLFDLEHDLPDELINSTELGLTNGGDINQLQTSLGMVQDAASKHKQ
LSELLRSGSSPNLNMGVGGPGQVMASQAQQSSPGLGLINSMVKSPMTQAGLTSPNMGMGT
SGPNQGPTQSTGMMNSPVNQPAMGMNTGMNAGMNPGMLAAGNGQGIMPNQVMNGSIGAGR
GRQNMQYPNPGMGSAGNLLTEPLQQGSPQMGGQTGLRGPQPLKMGMMNNPNPYGSPYTQN
PGQQIGASGLGLQIQTKTVLSNNLSPFAMDKKAVPGGGMPNMGQQPAPQVQQPGLVTPVA
QGMGSGAHTADPEKRKLIQQQLVLLLHAHKCQRREQANGEVRQCNLPHCRTMKNVLNHMT
HCQSGKSCQVAHCASSRQIISHWKNCTRHDCPVCLPLKNAGDKRNQQPILTGAPVGLGNP
SSLGVGQQSAPNLSTVSQIDPSSIERAYAALGLPYQVNQMPTQPQVQAKNQQNQQPGQSP
QGMRPMSNMSASPMGVNGGVGVQTPSLLSDSMLHSAINSQNPMMSENASVPSMGPMPTAA
QPSTTGIRKQWHEDITQDLRNHLVHKLVQAIFPTPDPAALKDRRMENLVAYARKVEGDMY
ESANNRAEYYHLLAEKIYKIQKELEEKRRTRLQKQNMLPNAAGMVPVSMNPGPNMGQPQP
GMTSNGPLPDPSMIRGSVPNQMMPRITPQSGLNQFGQMSMAQPPIVPRQTPPLQHHGQLA
QPGALNPPMGYGPRMQQPSNQGQFLPQTQFPSQGMNVTNIPLAPSSGQAPVSQAQMSSSS
CPVNSPIMPPGSQGSHIHCPQLPQPALHQNSPSPVPSRTPTPHHTPPSIGAQQPPATTIP
APVPTPPAMPPGPQSQALHPPPRQTPTPPTTQLPQQVQPSLPAAPSADQPQQQPRSQQST

**AASVPTPTAPLLPPQPATPLSQPAVSIEGQVSNPPSTSSTEVNSQAIAEKQPSQEVKMEA**
**KMEVDQPEPADTQPEDISESKVEDCKMESTETEERSTELKTEIKEEEDQPSTSATQSSPA**
**PGQSKKKIFKPEELRQALMPTLEALYRQDPESLPFRQPVDPQLLGIPDYFDIVKSPMDLS**
**TIKRKLDTGQYQEPWQYVDDIWLMFNNAWLYNRKTSRVYKYCSKLSEVFEQEIDPVMQSL**
**GYCCGRKLEFSPQTLCCYGKQLCTIPRDATYYSYQNRYHFCEKCFNEIQGESVSLGDDPS**
**QPQTTINKEQFSKRKNDTLDPELFVECTECGRKMHQICVLHHEIIWPAGFVCDGCLKKSA**
**RTRKENKFSAKRLPSTRLGTFLENRVNDFLRRQNHPESGEVTVRVVHASDKTVEVKPGMK**
**ARFVDSGEMAESFPYRTKALFAFEEIDGVDLCFFGMHVQEYGSDCPPPNQRRVYISYLDS**
**VHFFRPKCLRTAVYHEILIGYLEYVKKLGYTTGHIWACPPSEGDDYIFHCHPPDQKIPKP**
**KRLQEWYKKMLDKAVSERIVHDYKDIFKQATEDRLTSAKELPYFEGDFWPNVLEESIKEL**
**EQEEEERKREENTSNESTDVTKGDSKNAKKKNNKKTSKNKSSLSRGNKKKPGMPNVSNDL**
**SQKLYATMEKHKEVFFVIRLIAGPAANSLPPIVDPDPLIPCDLMDGRDAFLTLARDKHLE**
**FSSLRRAQWSTMCMLVELHTQSQDRFVYTCNECKHHVETRWHCTVCEDYDLCITCYNTKN**
**HDHKMEKLGLGLDDESNNQQAAATQSPGDSRRLSIQRCIQSLVHACQCRNANCSLPSCQK**
**MKRVVQHTKGCKRKTNGGCPICKQLIALCCYHAKHCQENKCPVPFCLNIKQKLRQQQLQH**
**RLQQAQMLRRRMASMQRTGVVGQQQGLPSPTPATPTTPTGQQPTTPQTPQPTSQPQPTPP**
**NSMPPYLPRTQAAGPVSQGKAAGQVTPPTPPQTAQPPLPGPPPAAVEMAMQIQRAAETQR**
**QMAHVQIFQRPIQHQMPPMTPMAPMGMNPPPMTRGPSGHLEPGMGPTGMQQQPPWSQGGL**
**PQPQQLQSGMPRPAMMSVAQHGQPLNMAPQPGLGQVGISPLKPGTVSQQALQNLLRTLRS**
**PSSPLQQQQVLSILHANPQLLAAFIKQRAAKYANSNPQPIPGQPGMPQGQPGLQPPTMPG**
**QQGVHSNPAMQNMNPMQAGVQRAGLPQQQPQQQLQPPMGGMSPQAQQMNMNHNTMPSQFR**
**DILRRQQMMQQQQQQGAGPGIGPGMANHNQFQQPQGVGYPPQQQQRMQHHMQQMQQGNMG**
**QIGQLPQALGAEAGASLQAYQQRLLQQQMGSPVQPNPMSPQQHMLPNQAQSPHLQGQQIP**
**NSLSNQVRSPQPVPSPRPQSQPPHSSPSPRMQPQPSPHHVSPQTSSPHPGLVAAQANPME**
**QGHFASPDQNSMLSQLASNPGMANLHGASATDLGLSTDNSDLNSNLSQSTLDIHYPYDVP**
**DYAS**

**dCas9$^{p300\ Core}$:** (Addgene Plasmid 61357) amino acid sequence; 3X "Flag" Epitope, **Nuclear Localization Sequence,** ***Streptococcus pyogenes*** **Cas9 (D10A, H840A), p300 Core Effector, "HA" Epitope**

MDYKDHDGDYKDHDIDYKDDDDKMA**PKKKRKVG**RGMDKKYSIGLAIGTNSVGWAVITDEY
KVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEI
FSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDS
TDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASG
VDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQ
LSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY
DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDG
TEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILT
FRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNE
KVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLK
EDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTL
FEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKS
DGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVD
ELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQ
LQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRG
KSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETR
QITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAH
DAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNF
FKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGF
SKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLG
ITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNE
LALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADA

NLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDA
TLIHQSITGLYETRIDLSQLGGDPIAGSKASPKKKRKVGRAIFKPEELRQALMPTLEALY
RQDPESLPFRQPVDPQLLGIPDYFDIVKSPMDLSTIKRKLDTGQYQEPWQYVDDIWLMFN
NAWLYNRKTSRVYKYCSKLSEVFEQEIDPVMQSLGYCCGRKLEFSPQTLCCYGKQLCTIP
RDATYYSYQNRYHFCEKCFNEIQGESVSLGDDPSQPQTTINKEQFSKRKNDTLDPELFVE
CTECGRKMHQICVLHHEIIWPAGFVCDGCLKKSARTRKENKFSAKRLPSTRLGTFLENRV
NDFLRRQNHPESGEVTVRVVHASDKTVEVKPGMKARFVDSGEMAESFPYRTKALFAFEEI
DGVDLCFFGMHVQEYGSDCPPPNQRRVYISYLDSVHFFRPKCLRTAVYHEILIGYLEYVK
KLGYTTGHIWACPPSEGDDYIFHCHPPDQKIPKPKRLQEWYKKMLDKAVSERIVHDYKDI
FKQATEDRLTSAKELPYFEGDFWPNVLEESIKELEQEEEERKREENTSNESTDVTKGDSK
NAKKKNNKKTSKNKSSLSRGNKKKPGMPNVSNDLSQKLYATMEKHKEVFFVIRLIAGPAA
NSLPPIVDPDPLIPCDLMDGRDAFLTLARDKHLEFSSLRRAQWSTMCMLVELHTQSQDYP
YDVPDYAS

**dCas9$^{p300\ Core\ (D1399Y)}$:** (Addgene Plasmid 61358) amino acid sequence; 3X “Flag” Epitope, **Nuclear Localization Sequence,** ***Streptococcus pyogenes*** **Cas9 (D10A, H840A), p300 Core Effector, D1399Y, “HA” Epitope**

MDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGRGMDKKYSIGLAIGTNSVGWAVITDEY
KVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEI
FSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDS
TDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASG
VDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQ
LSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY
DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDG
TEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILT
FRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNE
KVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLK
EDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTL
FEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKS
DGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVD
ELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQ
LQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRG
KSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETR
QITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAH
DAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNF
FKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGF
SKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLG
ITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNE
LALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADA
NLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDA
TLIHQSITGLYETRIDLSQLGGDPIAGSKASPKKKRKVGRAIFKPEELRQALMPTLEALY
RQDPESLPFRQPVDPQLLGIPDYFDIVKSPMDLSTIKRKLDTGQYQEPWQYVDDIWLMFN
NAWLYNRKTSRVYKYCSKLSEVFEQEIDPVMQSLGYCCGRKLEFSPQTLCCYGKQLCTIP
RDATYYSYQNRYHFCEKCFNEIQGESVSLGDDPSQPQTTINKEQFSKRKNDTLDPELFVE
CTECGRKMHQICVLHHEIIWPAGFVCDGCLKKSARTRKENKFSAKRLPSTRLGTFLENRV
NDFLRRQNHPESGEVTVRVVHASDKTVEVKPGMKARFVDSGEMAESFPYRTKALFAFEEI
DGVDLCFFGMHVQEYGSDCPPPNQRRVYISYLYSVHFFRPKCLRTAVYHEILIGYLEYVK
KLGYTTGHIWACPPSEGDDYIFHCHPPDQKIPKPKRLQEWYKKMLDKAVSERIVHDYKDI
FKQATEDRLTSAKELPYFEGDFWPNVLEESIKELEQEEEERKREENTSNESTDVTKGDSK
NAKKKNNKKTSKNKSSLSRGNKKKPGMPNVSNDLSQKLYATMEKHKEVFFVIRLIAGPAA
NSLPPIVDPDPLIPCDLMDGRDAFLTLARDKHLEFSSLRRAQWSTMCMLVELHTQSQDYP

**YDVPDYAS**

**dCas9 $^{p300\ Core\ (1645/1646\ RR/EE)}$:** (Addgene Plasmid 61359) amino acid sequence; 3X "Flag" Epitope, **Nuclear Localization Sequence,** ***Streptococcus pyogenes*** **Cas9 (D10A, H840A), p300 Core Effector, 1645/1646 RR/EE, "HA" Epitope**

MDYKDHDGDYKDHDIDYKDDDDKMA**PKKKRKVG**RGMDKKYSIGLAIGTNSVGWAVITDEY
KVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEI
FSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDS
TDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASG
VDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQ
LSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY
DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDG
TEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILT
FRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNE
KVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLK
EDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTL
FEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKS
DGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVD
ELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQ
LQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRG
KSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETR
QITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAH
DAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNF
FKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGF
SKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLG
ITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNE
LALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADA
NLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDA
TLIHQSITGLYETRIDLSQLGGDPIAGSKAS**PKKKRKVG**RA**IFKPEELRQALMPTLEALY
RQDPESLPFRQPVDPQLLGIPDYFDIVKSPMDLSTIKRKLDTGQYQEPWQYVDDIWLMFN
NAWLYNRKTSRVYKYCSKLSEVFEQEIDPVMQSLGYCCGRKLEFSPQTLCCYGKQLCTIP
RDATYYSYQNRYHFCEKCFNEIQGESVSLGDDPSQPQTTINKEQFSKRKNDTLDPELFVE
CTECGRKMHQICVLHHEIIWPAGFVCDGCLKKSARTRKENKFSAKRLPSTRLGTFLENRV
NDFLRRQNHPESGEVTVRVVHASDKTVEVKPGMKARFVDSGEMAESFPYRTKALFAFEEI
DGVDLCFFGMHVQEYGSDCPPPNQRRVYISYLDSVHFFRPKCLRTAVYHEILIGYLEYVK
KLGYTTGHIWACPPSEGDDYIFHCHPPDQKIPKPKRLQEWYKKMLDKAVSERIVHDYKDI
FKQATEDRLTSAKELPYFEGDFWPNVLEESIKELEQEEEERKREENTSNESTDVTKGDSK
NAKKKNNKKTSKNKSSLSRGNKKKPGMPNVSNDLSQKLYATMEKHKEVFFVIRLIAGPAA
NSLPPIVDPDPLIPCDLMDGRDAFLTLARDKHLEFSSL**EEAQWSTMCMLVELHTQSQD**YP
**YDVPDYAS**

**dCas9$^{p300\ Core\ (C1204R)}$:** (Addgene Plasmid 61361) amino acid sequence; 3X "Flag" Epitope, **Nuclear Localization Sequence,** ***Streptococcus pyogenes*** **Cas9 (D10A, H840A), p300 Core Effector, C1204R, "HA" Epitope**

MDYKDHDGDYKDHDIDYKDDDDKMA**PKKKRKVG**RGMDKKYSIGLAIGTNSVGWAVITDEY
KVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEI
FSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDS
TDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASG

VDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQ
LSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY
DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDG
TEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILT
FRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNE
KVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLK
EDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTL
FEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKS
DGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVD
ELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQ
LQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRG
KSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETR
QITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAH
DAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNF
FKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGF
SKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLG
ITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNE
LALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADA
NLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDA
TLIHQSITGLYETRIDLSQLGGDPIAGSKASPKKKRKVGRAIFKPEELRQALMPTLEALY
RQDPESLPFRQPVDPQLLGIPDYFDIVKSPMDLSTIKRKLDTGQYQEPWQYVDDIWLMFN
NAWLYNRKTSRVYKYCSKLSEVFEQEIDPVMQSLGYCCGRKLEFSPQTLCCYGKQLCTIP
RDATYYSYQNRYHFCEKRFNEIQGESVSLGDDPSQPQTTINKEQFSKRKNDTLDPELFVE
CTECGRKMHQICVLHHEIIWPAGFVCDGCLKKSARTRKENKFSAKRLPSTRLGTFLENRV
NDFLRRQNHPESGEVTVRVVHASDKTVEVKPGMKARFVDSGEMAESFPYRTKALFAFEEI
DGVDLCFFGMHVQEYGSDCPPPNQRRVYISYLDSVHFFRPKCLRTAVYHEILIGYLEYVK
KLGYTTGHIWACPPSEGDDYIFHCHPPDQKIPKPKRLQEWYKKMLDKAVSERIVHDYKDI
FKQATEDRLTSAKELPYFEGDFWPNVLEESIKELEQEEEERKREENTSNESTDVTKGDSK
NAKKKNNKKTSKNKSSLSRGNKKKPGMPNVSNDLSQKLYATMEKHKEVFFVIRLIAGPAA
NSLPPIVDPDPLIPCDLMDGRDAFLTLARDKHLEFSSLRRAQWSTMCMLVELHTQSQDYP
YDVPDYAS

**dCas9$^{p300\ Core\ (Y1467F)}$:** (Addgene Plasmid 61362) amino acid sequence; 3X “Flag” Epitope, **Nuclear Localization Sequence,** ***Streptococcus pyogenes*** **Cas9 (D10A, H840A), p300 Core Effector, Y1467F, “HA” Epitope**

MDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGRGMDKKYSIGLAIGTNSVGWAVITDEY
KVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEI
FSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDS
TDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASG
VDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQ
LSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY
DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDG
TEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILT
FRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNE
KVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLK
EDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTL
FEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKS
DGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVD
ELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQ
LQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRG
KSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETR

QITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAH
DAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNF
FKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGF
SKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLG
ITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNE
LALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADA
NLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDA
TLIHQSITGLYETRIDLSQLGGDPIAGSKASPKKKRKVGRAIFKPEELRQALMPTLEALY
RQDPESLPFRQPVDPQLLGIPDYFDIVKSPMDLSTIKRKLDTGQYQEPWQYVDDIWLMFN
NAWLYNRKTSRVYKYCSKLSEVFEQEIDPVMQSLGYCCGRKLEFSPQTLCCYGKQLCTIP
RDATYYSYQNRYHFCEKCFNEIQGESVSLGDDPSQPQTTINKEQFSKRKNDTLDPELFVE
CTECGRKMHQICVLHHEIIWPAGFVCDGCLKKSARTRKENKFSAKRLPSTRLGTFLENRV
NDFLRRQNHPESGEVTVRVVHASDKTVEVKPGMKARFVDSGEMAESFPYRTKALFAFEEI
DGVDLCFFGMHVQEYGSDCPPPNQRRVYISYLDSVHFFRPKCLRTAVYHEILIGYLEYVK
KLGYTTGHIWACPPSEGDDYIFHCHPPDQKIPKPKRLQEWFKKMLDKAVSERIVHDYKDI
FKQATEDRLTSAKELPYFEGDFWPNVLEESIKELEQEEEERKREENTSNESTDVTKGDSK
NAKKKNNKKTSKNKSSLSRGNKKKPGMPNVSNDLSQKLYATMEKHKEVFFVIRLIAGPAA
NSLPPIVDPDPLIPCDLMDGRDAFLTLARDKHLEFSSLRRAQWSTMCMLVELHTQSQDYP
YDVPDYAS

**dCas9$^{p300\ Core(1396/1397\ SY/WW)}$**: (Addgene Plasmid 61363) amino acid sequence; 3X “Flag” Epitope, **Nuclear Localization Sequence,** ***Streptococcus pyogenes*** **Cas9 (D10A, H840A), p300 Core Effector, 1396/1397 SY/WW, “HA” Epitope**

MDYKDHDGDYKDHDIDYKDDDDKMA**PKKKRKVG**RGMDKKYSIGLAIGTNSVGWAVITDEY
KVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEI
FSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDS
TDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASG
VDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQ
LSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY
DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDG
TEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILT
FRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNE
KVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLK
EDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTL
FEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKS
DGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVD
ELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQ
LQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRG
KSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETR
QITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAH
DAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNF
FKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGF
SKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLG
ITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNE
LALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADA
NLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDA
TLIHQSITGLYETRIDLSQLGGDPIAGSKASPKKKRKVGRAIFKPEELRQALMPTLEALY
RQDPESLPFRQPVDPQLLGIPDYFDIVKSPMDLSTIKRKLDTGQYQEPWQYVDDIWLMFN
NAWLYNRKTSRVYKYCSKLSEVFEQEIDPVMQSLGYCCGRKLEFSPQTLCCYGKQLCTIP
RDATYYSYQNRYHFCEKCFNEIQGESVSLGDDPSQPQTTINKEQFSKRKNDTLDPELFVE
CTECGRKMHQICVLHHEIIWPAGFVCDGCLKKSARTRKENKFSAKRLPSTRLGTFLENRV

NDFLRRQNHPESGEVTVRVVHASDKTVEVKPGMKARFVDSGEMAESFPYRTKALFAFEEI
DGVDLCFFGMHVQEYGSDCPPPNQRRVYIWWLDSVHFFRPKCLRTAVYHEILIGYLEYVK
KLGYTTGHIWACPPSEGDDYIFHCHPPDQKIPKPKRLQEWYKKMLDKAVSERIVHDYKDI
FKQATEDRLTSAKELPYFEGDFWPNVLEESIKELEQEEEERKREENTSNESTDVTKGDSK
NAKKKNNKKTSKNKSSLSRGNKKKPGMPNVSNDLSQKLYATMEKHKEVFFVIRLIAGPAA
NSLPPIVDPDPLIPCDLMDGRDAFLTLARDKHLEFSSLRRAQWSTMCMLVELHTQSQDYP
YDVPDYAS

**dCas9$^{p300\ Core}$** (H1415A E1423A Y1424A L1428S Y1430A H1434A): (Addgene Plasmid 61364) amino acid sequence; 3X "Flag" Epitope, **Nuclear Localization Sequence,** ***Streptococcus pyogenes*** **Cas9 (D10A, H840A), p300 Core Effector, H1415A E1423A Y1424A L1428S Y1430A H1434A, "HA" Epitope**

MDYKDHDGDYKDHDIDYKDDDDKMA**PKKKRKVG**RGMDKKYSIGLAIGTNSVGWAVITDEY
KVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEI
FSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDS
TDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASG
VDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQ
LSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY
DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDG
TEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILT
FRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNE
KVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLK
EDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTL
FEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKS
DGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVD
ELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQ
LQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRG
KSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETR
QITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAH
DAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNF
FKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGF
SKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLG
ITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNE
LALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADA
NLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDA
TLIHQSITGLYETRIDLSQLGGDPIAGSKAS**PKKKRKVG**RA**IFKPEELRQALMPTLEALY**
**RQDPESLPFRQPVDPQLLGIPDYFDIVKSPMDLSTIKRKLDTGQYQEPWQYVDDIWLMFN**
**NAWLYNRKTSRVYKYCSKLSEVFEQEIDPVMQSLGYCCGRKLEFSPQTLCCYGKQLCTIP**
**RDATYYSYQNRYHFCEKCFNEIQGESVSLGDDPSQPQTTINKEQFSKRKNDTLDPELFVE**
**CTECGRKMHQICVLHHEIIWPAGFVCDGCLKKSARTRKENKFSAKRLPSTRLGTFLENRV**
**NDFLRRQNHPESGEVTVRVVHASDKTVEVKPGMKARFVDSGEMAESFPYRTKALFAFEEI**
**DGVDLCFFGMHVQEYGSDCPPPNQRRVYISYLDSVHFFRPKCLRTAVYAEILIGYLAAVK**
**KSGATTGAIWACPPSEGDDYIFHCHPPDQKIPKPKRLQEWYKKMLDKAVSERIVHDYKDI**
**FKQATEDRLTSAKELPYFEGDFWPNVLEESIKELEQEEEERKREENTSNESTDVTKGDSK**
**NAKKKNNKKTSKNKSSLSRGNKKKPGMPNVSNDLSQKLYATMEKHKEVFFVIRLIAGPAA**
**NSLPPIVDPDPLIPCDLMDGRDAFLTLARDKHLEFSSLRRAQWSTMCMLVELHTQSQDYP**
**YDVPDYAS**

**Nm-dCas9$^{VP64}$:** amino acid sequence (Addgene Plasmid #48676)[7]; ***Neisseria meningitidis*** **Cas9 (D16A, D587A, H588A, N611A), Nuclear Localization Sequence, VP64 Effector**

MAAFKPNPINYILGLAIGIASVGWAMVEIDEDENPICLIDLGVRVFERAEVPKTGDSLAMARRLARS
VRRLTRRRAHRLLRARRLLKREGVLQAADFDENGLIKSLPNTPWQLRAAALDRKLTPLEW
SAVLLHLIKHRGYLSQRKNEGETADKELGALLKGVADNAHALQTGDFRTPAELALNKFEK
ESGHIRNQRGDYSHTFSRKDLQAELILLFEKQKEFGNPHVSGGLKEGIETLLMTQRPALS
GDAVQKMLGHCTFEPAEPKAAKNTYTAERFIWLTKLNNLRILEQGSERPLTDTERATLMD
EPYRKSKLTYAQARKLLGLEDTAFFKGLRYGKDNAEASTLMEMKAYHAISRALEKEGLKD
KKSPLNLSPELQDEIGTAFSLFKTDEDITGRLKDRIQPEILEALLKHISFDKFVQISLKA
LRRIVPLMEQGKRYDEACAEIYGDHYGKKNTEEKIYLPPIPADEIRNPVVLRALSQARKV
INGVVRRYGSPARIHIETAREVGKSFKDRKEIEKRQEENRKDREKAAAKFREYFPNFVGE
PKSKDILKLRLYEQQHGKCLYSGKEINLGRLNEKGYVEIAAALPFSRTWDDSFNNKVLVL
GSEAQNKGNQTPYEYFNGKDNSREWQEFKARVETSRFPRSKKQRILLQKFDEDGFKERNL
NDTRYVNRFLCQFVADRMRLTGKGKKRVFASNGQITNLLRGFWGLRKVRAENDRHHALDA
VVVACSTVAMQQKITRFVRYKEMNAFDGKTIDKETGEVLHQKTHFPQPWEFFAQEVMIRV
FGKPDGKPEFEEADTPEKLRTLLAEKLSSRPEAVHEYVTPLFVSRAPNRKMSGQGHMETV
KSAKRLDEGVSVLRVPLTQLKLKDLEKMVNREREPKLYEALKARLEAHKDDPAKAFAEPF
YKYDKAGNRTQQVKAVRVEQVQKTGVWVRNHNGIADNATMVRVDVFEKGDKYYLVPIYSW
QVAKGILPDRAVVQGKDEEDWQLIDDSFNFKFSLHPNDLVEVITKKARMFGYFASCHRGT
GNINIRIHDLDHKIGKNGILEGIGVKTALSFQKYQIDELGKEIRPCRLKKRPPVRSRADP
KKKRKVEASGSGRADALDDFDLDMLGSDALDDFDLDMLGSDALDDFDLDMLGSDALDDFD
LDMLINSR

**Nm-dCas9$^{p300\ Core}$:** (Addgene Plasmid 61365) amino acid sequence; ***Neisseria meningitidis*** **Cas9 (D16A, D587A, H588A, N611A), Nuclear Localization Sequence, p300 Core Effector, "HA" Epitope**

MAAFKPNPINYILGLAIGIASVGWAMVEIDEDENPICLIDLGVRVFERAEVPKTGDSLAMARRLARS
VRRLTRRRAHRLLRARRLLKREGVLQAADFDENGLIKSLPNTPWQLRAAALDRKLTPLEW
SAVLLHLIKHRGYLSQRKNEGETADKELGALLKGVADNAHALQTGDFRTPAELALNKFEK
ESGHIRNQRGDYSHTFSRKDLQAELILLFEKQKEFGNPHVSGGLKEGIETLLMTQRPALS
GDAVQKMLGHCTFEPAEPKAAKNTYTAERFIWLTKLNNLRILEQGSERPLTDTERATLMD
EPYRKSKLTYAQARKLLGLEDTAFFKGLRYGKDNAEASTLMEMKAYHAISRALEKEGLKD
KKSPLNLSPELQDEIGTAFSLFKTDEDITGRLKDRIQPEILEALLKHISFDKFVQISLKA
LRRIVPLMEQGKRYDEACAEIYGDHYGKKNTEEKIYLPPIPADEIRNPVVLRALSQARKV
INGVVRRYGSPARIHIETAREVGKSFKDRKEIEKRQEENRKDREKAAAKFREYFPNFVGE
PKSKDILKLRLYEQQHGKCLYSGKEINLGRLNEKGYVEIAAALPFSRTWDDSFNNKVLVL
GSEAQNKGNQTPYEYFNGKDNSREWQEFKARVETSRFPRSKKQRILLQKFDEDGFKERNL
NDTRYVNRFLCQFVADRMRLTGKGKKRVFASNGQITNLLRGFWGLRKVRAENDRHHALDA
VVVACSTVAMQQKITRFVRYKEMNAFDGKTIDKETGEVLHQKTHFPQPWEFFAQEVMIRV
FGKPDGKPEFEEADTPEKLRTLLAEKLSSRPEAVHEYVTPLFVSRAPNRKMSGQGHMETV
KSAKRLDEGVSVLRVPLTQLKLKDLEKMVNREREPKLYEALKARLEAHKDDPAKAFAEPF
YKYDKAGNRTQQVKAVRVEQVQKTGVWVRNHNGIADNATMVRVDVFEKGDKYYLVPIYSW
QVAKGILPDRAVVQGKDEEDWQLIDDSFNFKFSLHPNDLVEVITKKARMFGYFASCHRGT
GNINIRIHDLDHKIGKNGILEGIGVKTALSFQKYQIDELGKEIRPCRLKKRPPVRSRADP
KKKRKVEASGRAIFKPEELRQALMPTLEALYRQDPESLPFRQPVDPQLLGIPDYFDIVKS
PMDLSTIKRKLDTGQYQEPWQYVDDIWLMFNNAWLYNRKTSRVYKYCSKLSEVFEQEIDP
VMQSLGYCCGRKLEFSPQTLCCYGKQLCTIPRDATYYSYQNRYHFCEKCFNEIQGESVSL
GDDPSQPQTTINKEQFSKRKNDTLDPELFVECTECGRKMHQICVLHHEIIWPAGFVCDGC
LKKSARTRKENKFSAKRLPSTRLGTFLENRVNDFLRRQNHPESGEVTVRVVHASDKTVEV
KPGMKARFVDSGEMAESFPYRTKALFAFEEIDGVDLCFFGMHVQEYGSDCPPPNQRRVYI
SYLDSVHFFRPKCLRTAVYHEILIGYLEYVKKLGYTTGHIWACPPSEGDDYIFHCHPPDQ
KIPKPKRLQEWYKKMLDKAVSERIVHDYKDIFKQATEDRLTSAKELPYFEGDFWPNVLEE
SIKELEQEEEERKREENTSNESTDVTKGDSKNAKKKNNKKTSKNKSSLSRGNKKKPGMPN
VSNDLSQKLYATMEKHKEVFFVIRLIAGPAANSLPPIVDPDPLIPCDLMDGRDAFLTLAR
DKHLEFSSLRRAQWSTMCMLVELHTQSQDYPYDVPDYAS

**Supplementary Note 2.** Amino acid sequences of *ICAM1* Zinc Finger[10] effectors.

***ICAM1* ZF$^{VP64}$** amino acid sequence; 3X "Flag" Epitope, **Nuclear Localization Sequence,** **Zinc Finger Helix**, **VP64 Effector**, **"HA" Epitope**

MDYKDHDGDYKDHDIDYKDDDDKMA**PKKKRKVG**RGMAQAALEPGEKPYACPECGKSFS**DC**
**RDLAR**HQRTHTGEKPYKCPECGKSFS**RSDDLVR**HQRTHTGEKPYKCPECGKSFS**QSSNLV**
**R**HQRTHTGEKPYACPECGKSFS**TSGELVR**HQRTHTGEKPYKCPECGKSFS**QRAHLER**HQR
THTGEKPYKCPECGKSFS**QAGHLAS**HQRTHTGKKTSGQAGQAS**PKKKRKVG**RA**DALDDFD**
**LDMLGSDALDDFDLDMLGSDALDDFDLDMLGSDALDDFDLDML**IN**YPYDVPDYAS**

***ICAM1* ZF$^{p300\ Core}$** amino acid sequence; 3X "Flag" Epitope, **Nuclear Localization Sequence,** **Zinc Finger Helix**, **p300 Core Effector**, **"HA" Epitope**

MDYKDHDGDYKDHDIDYKDDDDKMA**PKKKRKVG**RGMAQAALEPGEKPYACPECGKSFS**DC**
**RDLAR**HQRTHTGEKPYKCPECGKSFS**RSDDLVR**HQRTHTGEKPYKCPECGKSFS**QSSNLV**
**R**HQRTHTGEKPYACPECGKSFS**TSGELVR**HQRTHTGEKPYKCPECGKSFS**QRAHLER**HQR
THTGEKPYKCPECGKSFS**QAGHLAS**HQRTHTGKKTSGQAGQAS**PKKKRKVG**RA**IFKPEEL**
**RQALMPTLEALYRQDPESLPFRQPVDPQLLGIPDYFDIVKSPMDLSTIKRKLDTGQYQEP**
**WQYVDDIWLMFNNAWLYNRKTSRVYKYCSKLSEVFEQEIDPVMQSLGYCCGRKLEFSPQT**
**LCCYGKQLCTIPRDATYYSYQNRYHFCEKCFNEIQGESVSLGDDPSQPQTTINKEQFSKR**
**KNDTLDPELFVECTECGRKMHQICVLHHEIIWPAGFVCDGCLKKSARTRKENKFSAKRLP**
**STRLGTFLENRVNDFLRRQNHPESGEVTVRVVHASDKTVEVKPGMKARFVDSGEMAESFP**
**YRTKALFAFEEIDGVDLCFFGMHVQEYGSDCPPPNQRRVYISYLDSVHFFRPKCLRTAVY**
**HEILIGYLEYVKKLGYTTGHIWACPPSEGDDYIFHCHPPDQKIPKPKRLQEWYKKMLDKA**
**VSERIVHDYKDIFKQATEDRLTSAKELPYFEGDFWPNVLEESIKELEQEEEERKREENTS**
**NESTDVTKGDSKNAKKKNNKKTSKNKSSLSRGNKKKPGMPNVSNDLSQKLYATMEKHKEV**
**FFVIRLIAGPAANSLPPIVDPDPLIPCDLMDGRDAFLTLARDKHLEFSSLRRAQWSTMCM**
**LVELHTQSQDYPYDVPDYAS**