SUPPLEMENTARY INFORMATION

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Supplementary Fig. 17: Lentiviral vector-introduced xr-pegRNA increased prime editing efficiencies by PE2 in HEK293T cells.

Supplementary Fig. 18: Lentiviral vector-introduced xr-pegRNA increased prime editing efficiencies by PE3 in HEK293T cells.

Supplementary Fig. 19: The xrRNA motif increased pegRNA stability to preferentially impact its prime editing function.

Supplementary Fig. 20: Comparable editing efficiency by PE3 driven by xr-pegRNAs (with or without linkers) and epegRNAs in HEK293T cells.

Supplementary Fig. 21: Relative edit:indel ratios associated with prime editing experiments by xr-pegRNAs (with or without linkers) and epegRNAs shown in Fig. 5d and Supplementary Fig. 20.

Supplementary Table 1: Sequences for primers used for constructing WT pegRNA plasmids.

Supplementary Table 2: Primers used for human cells genomic DNA amplification and targeted deep sequencing.

Supplementary Table 3: Primers used for N2a cells genomic DNA amplification and targeted deep sequencing.

Supplementary Table 4: Information of predicted off-target sites related to Supplementary Fig. 16.
Supplementary Table 5: Primers used for off-target analysis related to Supplementary Fig. 16.
Supplementary Table 6: Primers used for pegRNA RT-qPCR analysis.

Supplementary Data 1: Sequences for pegRNAs and xr-pegRNAs. – This dataset is provided in a separate "xls" file.

MVE

WNV

Zika

TGTCAGGCCTGCTAGTCAGCCACAGTTTGGGGAAAGCTGTGCAGCCTGTAACCCCCCCA GGAGAAGCTGGGAAACCAAGCT

Dengue

AGTCAGGCCACTTGTGCCACGGTTTGAGCAAACCGTGCTGCCTGTAGCTCCGCCAATAA TGGGAGGCGT

YF

TGTCAGCCCAGAACCCCACACGAGTTTTGCCACTGCTAAGCTGTGAGGCAGTGCAGGCT GGGACAGCCGACCTCCAGGTTGCGAAAAACCTGGT

Supplementary Fig. 1: Sequences of five xrRNAs used.

Coding sequence of EGFP fluorescent report system

ATGAACAGCCTGATCAAAGAAAACATGCGGATGAAGGTGGTGCTGGAAGGCAGCGTGAA CGGCCACCAGTTCAAGTGCACCGGCGAGGGCGAGGGCAACCCCTACATGGGCACCCAGA CCATGCGGATCAAAGTGATCGAGGGCGGACCTCTGCCCTTCGCCTTCGACATCCTGGCCAC ATCCTTCATGTACGGCAGCCGGACCTTCATCAAGTACCCCCAAGGGCATCCCCGATTTCTTC AAGCAGAGCTTCCCCGAGGGCTTCACCTGGGAGAGAGTGACCAGATACGAGGACGGCGG CGTGATCACCGTGATGCAGGACACCAGCCTGGAAGATGGCTGCCTGGTGTACCATGCCCA GGTCAGGGGCGTGAATTTTCCCAGCAACGGCGCCGTGATGCAGAAGAAAACCAAGGGCT GGGAGCCCAACACCGAGATGATGTACCCCGCTGACGGCGGACTGAGAGGCTACACCCAC ATGGCCCTGAAGGTGGACGGCGGAGGGCACCTGAGCTGCAGCTTCGTGACCACCTACCGA TCCAAGAAAACCGTGGGCAACATCAAGATGCCCGGCATCCACGCCGTGGACCACCGGCTG GAAAGGCTGGAAGAGTCCGACAACGAGATGTTCGTGGTGCAGCGGGAGCACGCCGTGGC CAAGTTCGCCGGCCTGGGCGGAGGGAAGGATCCGCAGGGCGGAGGAGGCAGCGGCGGAG GAGGCAGCGGCGGAGGAGGCAGCGCCTGCTCGCGATGCTAGAGGGCTCTGCCAGGGGGG GTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTC GAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGA TGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCC CTGGCCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTCAGCCGCTACCCCGAC CACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGC ACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGC GACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATC CTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCATGGCCGACAAG CAGAAGAACGGCATCAAGGTGAACTTCAAGATCCGCCACAACATCGAGGACGGCAGCGT GCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCC CGACAACCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCG ATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGGATCACTCTCGGCATGGACGAGC TGTACAAGTAA

Supplementary Fig. 2: Coding sequences of pCMV-mRuby-linker-EGFP used in this study. The

coding sequences of mRuby, linker and EGFP are colored in red, grey and green, respectively. The

stop codon is background-highlighted in red.



Supplementary Fig. 3: The xr-pegRNAs enhanced prime editing of an EGFP reporter.

a. Schematic representation of WT pegRNA and xr-pegRNA. Five xrRNA motifs (derived from five different viruses: Murray Valley encephalitis (MVE), West Nile virus (WNV), Zika, Dengue (Dengue4), and Yellow Fever (YF)) were joined to the 3' end of pegRNA.

- b. Flow cytometry analyses of cell transfected with the PE2 (xr-pegRNAs) and the editing reporter are presented. The red boxes in the first two plots indicate gating for edited cells. The control pegRNA-transfectants and the mRuby-EGFP without the stop codon were used as negative and positive controls, respectively. The ratios of EGFP expression shown in Fig. 1d were calculated as: comp-GFP-A⁺/comp-DsRed-A⁺.
- c. The xr-pegRNAs increased targeted efficiency of A-to-G edit using PE2 strategy. PCR amplicons from the target regions were analyzed by targeted deep sequencing. The reads harboring only the correct edit were counted to evaluate the editing efficiency. Data are presented as mean values \pm SD, n = 3 biological replicates. Two-tailed student's t-tests were performed. *P* values are marked on the graph (*n.s.*: not significant)
- d. Relative edit:indel ratios associated with the above PE2-mediated reporter editing using different constructs of xr-pegRNAs are shown (mean ± SEM, n=3 biological replicates). The levels of the WT pegRNA group was set to 1 (the red dashed line).
- e. Sanger sequencing chromatograms of the A-to-G edit induced by PE2 with WT pegRNA and xr-pegRNAs. Asterisks indicate the desired editing. The PAM sequence and spacer sequence of pegRNA are underlined in red and black, respectively.

Source data are provided as a Source Data file.



Supplementary Fig. 4: The xr-pegRNAs increased prime editing efficiency of base transition and transversion in PE2.

- **a.** Gating strategy for flow cytometry sorting of cells transfected with PE plasmids is shown.
- b. Sanger sequencing chromatograms of the six sites in Fig. 2a. Asterisks indicate the desired editing. The PAM sequence and spacer sequence of pegRNA are underlined in red and black, respectively.



Supplementary Fig. 5: The xr-pegRNAs increased prime editing efficiency of base transition and transversion in PE3. Sanger sequencing chromatograms of the six sites in Fig. 2c. Asterisks indicate the desired editing. The PAM sequence and spacer sequence of pegRNA are underlined in red and black, respectively.



Supplementary Fig. 6: Relative edit:indel ratio by xrRNA motif-joined pegRNAs examined in Fig. 2.

a. Relative edit:indel ratios associated with PE2-mediated editing of 6 sites (in HEK293T cells) using different constructs of xr-pegRNAs are presented. The raw data are presented in the Source Data file. The levels of the WT pegRNA group was set as 1 (the red dashed line). The results correspond to those shown in Fig. 2a (mean ± SEM, n = 3 biological replicates).

- b. Relative edit:indel ratios associated with PE3-mediated editing of 6 sites (in HEK293T cells) using different constructs of xr-pegRNAs are presented. The raw data are presented in the Source Data file. The levels of the WT pegRNA group were set as 1 (the red dashed line). The results correspond to those shown in Fig. 2c (mean ± SEM, n = 3 biological replicates). The indel rates presented in the raw data also confirm that PE3 is associated with higher indel rates than PE2. For instance, the median indel rates by the WT pegRNAs at the *EMX1* and *HEXA* sites increase from 0.02% and 0.02% (by PE2) to 1.64% and 0.42% (by PE3), respectively.
- c. When all target sites (n=6) analyzed above were considered as a whole, the relative edit:indel ratios associated with PE3 using different constructs of xr-pegRNAs are presented. The levels of the WT pegRNA group was set as 1 (the red dashed line). In the violin plot, each point represents the averaged editing activity at the particular site. The thicker dotted line shows the medians of all data points, while the thinner dotted lines correspond to quartiles (1st and 3rd).

Source data are provided as a Source Data file.



Supplementary Fig. 7: The xrPE increased prime editing efficiency of base transition and transversion at a larger panel of sites in HEK293T cells. Sanger sequencing chromatograms of the 15 sites in Fig. 3b and Supplementary Fig. 8a are shown. Asterisks indicate the desired editing. The PAM sequence and spacer sequence of pegRNA are underlined in red and black, respectively.



Supplementary Fig. 8: The xrPE-dependent base conversions and the associated relative edit:indel ratios.

a. Comparison of efficiencies of base transition and transversion at 6 additional sites, as indicated, by xrPE and PE3 in HEK293T cells. The editing efficiencies were shown by red/blue-colored bars (mean ± SD, n=3 biological replicates). The grey bars immediately next to the red/blue-colored

bars indicate the indel frequencies associated with each editing group. Two-tailed student's t-tests were performed (with *P* values marked on the graph, *n.s.*: not significant).

- **b.** Relative edit:indel ratios associated with xrPE-mediated editing of 9 indicated sites (in HEK293T cells) are presented (mean ± SEM, n = 3 biological replicates). The levels of the PE3 group were set as 1 (the red dashed line). The results correspond to those shown in Fig. 3b.
- c. Relative edit:indel ratios associated with xrPE-mediated editing of 6 additional sites (in HEK293T cells) are presented (mean ± SEM, n = 3 biological replicates). The levels of the PE3 group were set as 1 (the red dashed line). The results correspond to those shown in panel (a) of this figure.
- d. Relative edit:indel ratios associated with xrPE-mediated editing of 9 indicated sites (in N2a cells) are presented (mean ± SEM, n = 3 biological replicates). The levels of the PE3 group were set as 1 (the red dashed line). The results correspond to those shown in Fig. 3d. Source data are provided as a Source Data file.



Supplementary Fig. 9: Effects of RT template length on the efficiency of xrPE and canonical PE3 in HEK293T cells. Targeted editing efficiency of base transition and transversion by canonical PE3 and xrPE using pegRNAs with different RT template lengths at 6 indicated sites in HEK293T. Analyses were carried out with editing rates from 3 biological replicates (mean ± SD). Source data are provided as a Source Data file.



Supplementary Fig. 10: The xrPE increased prime editing efficiency for base transition and transversion in HeLa cells in comparison to PE3, while featuring largely undiminished edit:indel ratios.

- a. Comparison of efficiencies of base transition and transversion at 8 sites by xrPE and PE3 in HeLa cells. The editing efficiencies were shown by red/blue-colored bars (mean ± SD, n=3 biological replicates). The grey bars immediately next to the red/blue-colored bars indicate the indel frequencies associated with each editing group. Multiple t tests (two-tailed) were performed. Statistical significance was determined using the Holm-Sidak method in GraphPad, with alpha = 0.05. When discoveries are made (5/8), the exact *P* values (unadjusted) are marked on graph. Otherwise, the comparisons are marked by "*n.s.*" (not significant), where the corresponding *P* values are 0.027 (*ALDOB*), 0.043 (*CTLA4*) and 0.451 (*FANCF*), respectively. The stringencies of such test design can be noted in some comparisons where the unadjusted *P* values are smaller than 0.05.
- b. The results in (a) are further analyzed by considering editing at all sites (n=8) as a whole. The editing frequencies induced by canonical PE3 were set as 100%. Each data point represents the averaged editing activity at the particular site. The center line shows medians of all data points and the box limits correspond to the upper the lower quartiles, while the whiskers extend to the largest and smallest values. Two-tailed one-sample student's t-test was performed (with *P* value marked).
- c. Sanger sequencing chromatograms of the 8 sites in HeLa cells. Asterisks indicate the desired editing. The PAM sequence and spacer sequence of pegRNA are underlined in red and black, respectively.
- d. Relative edit:indel ratios associated with xrPE-mediated editing of 8 indicated sites (in HeLa cells) are presented (mean ± SEM, n = 3 biological replicates). The levels of the PE3 group were set as 1 (the red dashed line). The results correspond to those shown in panel (a) of this figure. Source data are provided as a Source Data file.



Supplementary Fig. 11: The xrPE increased prime editing efficiency of base transition and

transversion in N2a cells. Sanger sequencing chromatograms of the 9 target sites in N2a cells (Fig. 3d). Asterisks indicate the desired editing. The PAM sequence and spacer sequence of pegRNA are underlined in red and black, respectively.



Supplementary Fig. 12: Relative edit:indel ratios associated with xrPE-mediated small insertions and deletions shown in Fig. 4.

- a. Relative edit:indel ratios associated with xrPE-mediated small deletions and insertions at 6 sites (in HEK293T cells) are presented (mean ± SEM, n = 3 biological replicates). The levels of the PE3 group were set as 1 (the red dashed line). The results correspond to those shown in Fig. 4a.
- b. Relative edit:indel ratios associated with xrPE-mediated small deletions and insertions at 6 sites (in N2a cells) are presented (mean ± SEM, n = 3 biological replicates). The levels of the PE3 group were set as 1 (the red dashed line). The results correspond to those shown in Fig. 4c. Source data are provided as a Source Data file.



Supplementary Fig. 13: The xrPE increased prime editing efficiency of precise deletion and insertion in HeLa cells in comparison to PE3, while featuring largely undiminished edit:indel ratios.

- **a.** Comparison of efficiencies of small deletions and insertions at 6 sites by xrPE and PE3 in HeLa cells. The editing efficiencies were shown by red/blue-colored bars (mean \pm SD, n=3 biological replicates). The grey bars immediately next to the red/blue-colored bars indicate the indel frequencies associated with each editing group. The same set of indel data from untreated cells (background) were presented for deletions and insertions. Multiple t tests (two-tailed) were performed. Discoveries were determined using the two-stage linear step-up procedure of Benjamini, Krieger and Yekutieli, with Q = 1%. When discoveries are made (10/12), only the exact *P* values (unadjusted) are shown on the graphs. Otherwise, the comparisons are marked by "*n.s.*" (not significant) along with the *P* values.
- **b.** The results in (a) are further analyzed by considering editing at all sites (n=6 for deletions and insertions, respectively) as a whole. The editing frequencies induced by canonical PE3 were set as

100%. In the box plot, each data point represents the averaged editing activity at the particular site. The center line shows medians of all (n=6) data points and the box limits correspond to the upper the lower quartiles, while the whiskers extend to the largest and smallest values. Two-tailed one-sample student's t-test was performed (with P values marked).

c. Relative edit:indel ratios associated with xrPE-mediated small deletions and insertions
 (corresponding to data in [a]) are presented (mean ± SEM, n = 3 biological replicates). The levels of the PE3 group were set as 1 (the red dashed line).

Source data are provided as a Source Data file.



Supplementary Fig. 14: Overall comparisons of undesired indel rates induced by canonical PE3 and xrPE in HEK293T cells.

- a. Overall levels of undesired indels associated with PE3- and xrPE-dependent base conversions (n=15 independent sites) in HEK293T cells (as shown in Fig. 3b and Supplementary Fig. 8a).
- b. Overall levels of undesired indels associated with PE3- and xrPE-dependent small deletions (n=6 independent sites) in HEK293T cells (as shown in Fig. 4a).
- c. Overall levels of undesired indels associated with PE3- and xrPE-dependent small insertions (n=6 independent sites) in HEK293T cells (as shown in Fig. 4a). In (a-c), data are presented as mean values ± SD. Two-tailed, paired student's t-tests were performed. *P* values are marked on the graphs (*n.s.*: not significant).

Source data are provided as a Source Data file.



Supplementary Fig. 15: Minimal levels of potential base conversion byproduct induced by canonical PE3 and xrPE at 15 edited sites in HEK293T cells. Analysis of potential base-change byproducts associated with PE3- and xrPE-dependent base conversions (shown in Fig. 3b and Supplementary Fig. 8a). The red triangles indicate the nCas9 nick site. The surrounding 10 bp sequences are shown. Light blue and light red indicate wild type base. The dark red indicates the desired base substitution. The data presented is representative of three independent measurements. Source data are provided as a Source Data file.



Supplementary Fig. 15 (continued)



Supplementary Fig. 16: Comparison of potential off-target rates for canonical PE3 and xrPE in 3 prime editing applications in HEK293T cells.

- a. Off-target analysis for PE3- and xrPE-mediated targeting of *EMX1*.
- **b.** Off-target analysis for PE3- and xrPE-mediated targeting of *FANCF*.
- c. Off-target analysis for PE3- and xrPE-mediated targeting of *HEXA*. In **a-c**, data are presented as mean values \pm SD (n = 3 biological replicates). Source data are provided as a Source Data file.



Supplementary Fig. 17: Lentiviral vector-introduced xr-pegRNA increased prime editing efficiencies by PE2 in HEK293T cells.

- a. HEK293T cells were transduced with WT pegRNAs or xr-pegRNAs in lentiviral vectors (LV). Six days after transduction, cells were further transfected with the PE2 plasmid for 4 days. Correct editing effeciencies were detemined by deep-sequencing. The editing efficiencies were shown by red/blue-colored bars (mean \pm SD, n=3 biological replicates). The grey bars immediately next to the red/blue-colored bars indicate the indel frequencies associated with each editing group. Twotailed student's t-tests were performed. *P* values are marked on the graph (*n.s.*: not significant).
- b. The results in (a) are further analyzed by considering editing at all sites (n=5) as a whole. The editing frequencies induced by WT pegRNAs were set as 100%. In the box plot, each data point represents the averaged editing activity at the particular site. The center line shows medians of all

data points and the box limits correspond to the upper the lower quartiles, while the whiskers extend to the largest and smallest values. Two-tailed one-sample student's t-test was performed (with *P* value marked).

c. Relative edit:indel ratios associated with prime editing by LV-introduced xr-pegRNAs (with PE2) are presented (mean ± SEM, n = 3 biological replicates). The levels of the WT pegRNA group were set as 1 (the red dashed line). The results correspond to those shown in (a). Source data are provided as a Source Data file.



Supplementary Fig. 18: Lentiviral vector-introduced xr-pegRNA increased prime editing efficiencies by PE3 in HEK293T cells.

- a. HEK293T cells were transduced with WT pegRNAs or xr-pegRNAs in LV. Six days after transduction, cells were further transfected with the PE3 plasmid for 4 days. Correct editing effeciencies were detemined by deep-sequencing. The editing efficiencies were shown by red/blue-colored bars (mean \pm SD, n=3 biological replicates). The grey bars immediately next to the red/blue-colored bars indicate the indel frequencies associated with each editing group. Two-tailed student's t-tests were performed. *P* values are marked on the graph (*n.s.*: not significant).
- b. The results in (a) are further analyzed by considering editing at all sites (n=5) as a whole (mean ± SD). The editing frequencies induced by WT pegRNAs were set as 100%. In the box plot, each data point represents the averaged editing activity at the particular site. The center line shows medians of all data points and the box limits correspond to the upper the lower quartiles, while the

whiskers extend to the largest and smallest values. One-tailed one-sample student's t-test was performed (with *P* value marked).

c. Relative edit:indel ratios associated with prime editing by LV-introduced xr-pegRNAs (with PE3) are presented (± SEM, n = 3). The levels of the WT pegRNA group were set as 1 (the red dashed line). The results correspond to those shown in (a).

Source data are provided as a Source Data file.



Supplementary Fig. 19: The xrRNA motif increased pegRNA stability to preferentially impact its prime editing function.

a. The *in vitro* transcribed WT pegRNAs or the corresponding xr-pegRNAs were first pre-incubated with (or without) a similar molar amount of Cas9 protein. The samples were then added with the HEK293T nuclear lysates. The levels of pegRNAs and xr-pegRNAs were determined by RT-

qPCR. Data presented are relative levels (mean \pm SD, n=3 biological replicates), with the remaining levels of WT pegRNAs (no Cas9) considered as 1.

- b. The levels of two targeting pegRNAs and their corresponding xr-pegRNAs in transfected HEK293T cells were determined by RT-qPCR. The cells were also co-transfected with a PE2 plasmid. The presented levels of pegRNAs or xr-pegRNAs have been normalzed to those of PE2. Data presented are relative levels (mean ± SD, n=3 biological replicates), with levels of each WT pegRNA considered as 1.
- c. Comparison of PE intermediates generated by PE2 with either WT pegRNAs or xr-pegRNAs at *RIT1* site in HEK293T cells. The black dotted line represents the end of the full-length RT template (14 nt). In the histogram, the x axis corresponds to the sizes of the 3' flaps, with the first base downstream of the PE2-induced nick denoted as position +1, while the y axis represents the relative abundance of the reads (percentage of all reads). The inset (box) contains pie charts showing percentages of reads with (red/blue) or without (grey) intended edits. The data presented are calculated from an average of three independent biological replicates.
- **d.** The abilities by two different groups of pegRNAs, xr-pegRNAs or sgRNAs (in combination with dCas9-VPR) to drive targeted activation of corresponding EGFP reporters were compared. On the left box, representative flow cytometry results shows an example of CRISPRa-dependent EGFP activation in transfected cells (mCherry). An sgRNA-mediated CRISPRa activity is shown in the example (corresponding to site in *EMX1* gene; N.T., a non-targeting pegRNA). On the right, the graph shows the MFI values for EGFP (normalized to those for mCherry), which indicate the levels of CRISPRa activities (mean \pm SD, n=3 biological replicates). Source data are provided as a Source Data file.



Supplementary Fig. 20: Comparable editing efficiency by PE3 driven by xr-pegRNAs (with or without linkers) and epegRNAs in HEK293T cells.

- a. Comparison of prime editing by xr-pegRNA and the epegRNA (containing evopreQ1 motif and Cr772 scaffold) in HEK293T cells at 3 sites analyzed in the newly published epegRNA study. The editing efficiencies are shown by red/blue-colored bars (mean ± SD, n=3 biological replicates).
- b. Comparison of prime editing by xr-pegRNA, xr-pegRNA with 8-bp linkers and epegRNA (containing tevopreQ1 motif) in a PE3 context. The 9 edits attempted were in reference to the newly published epegRNA study. The editing efficiencies are shown by red/blue-colored bars (mean ± SD, n=3 biological replicates).

In both (a) and (b), the grey bars immediately next to the red/blue-colored bars indicate the indel frequencies associated with each editing group. Source data are provided as a Source Data file.



Supplementary Fig. 21: Relative edit:indel ratios associated with prime editing experiments by xr-pegRNAs (with or without linkers) and epegRNAs shown in Fig. 5d and Supplementary Fig. 20.

- a. Relative edit:indel ratios associated with xr-pegRNAs for 9 edits attempted earlier in our study are presented (mean ± SEM, n = 3 biological replicates). The levels of the epegRNA group were set as 1 (the red dashed line). The results correspond to those in Fig. 5d.
- b. Relative edit:indel ratios associated with xr-pegRNAs for 3 edits initially attempted in the epegRNA study are presented (mean ± SEM, n = 3 biological replicates). The levels of the epegRNA group were set as 1 (the red dashed line). The results correspond to those in Supplementary Fig. 20a.

c. Relative edit:indel ratios associated with xr-pegRNAs or their counterparts with 8-bp linkers are presented (mean ± SEM, n = 3 biological replicates). The levels of the epegRNA group were set as 1 (the red dashed line). The results correspond to those in Supplementary Fig. 20b. Source data are provided as a Source Data file.

Supplementary Table 1:	upplementary Table 1: Sequences for primers used for constructing WT pegRNA plasmids.		
NO. Forward primer			
backbone_pegRNA-F	AGCTAGGTCTCCTTTTTTTAAAGAATTCTCGACCTCGAGAC		
backbone_pegRNA-R	TCTCTCGGTCTCACGGTGTTTCGT		
scaffold-top	AGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCG		
scaffold-bottom	GCACCGACTCGGTGCCACTTTTTCAAGTTGATAACGGACTAGCCTTATTTTAACTTGCTATTTCTAG		

Supplementary	Table 2: Primers used for HEK293T and Hela cells genomic	DNA amplification and targeted deep se	quencing.
NO.	Forward primer	Reverse primer	Length of amplicon (nt
Reporter	NNNNNTGCCCGGCATCCACG	CCTCGCCCTTGCTCAC	237
ALDOB	NNNNNCTGAGTGAAGGTTTGACTGG	CTCCTACTAGAAGCACTGGAG	238
FAM171B	NNNNNGGTAATGAGGAGGCGTATGGGC	GGGCAAGGTCTGCGTAAAGT	213
FBN1	NNNNNTCGACCTCGAGGAGACAATG	GGGCTGAGAGGACTGATCTTT	252
RIT1	NNNNNGTATGGAAAGGTAAGGCACTG	CCTACCACTCTTCCCTACACC	237
EMX1	NNNNNAGGTGAAGGTGTGGTTCCAG	GCCAGCAGCAAGCAGCACTC	218
FANCF	NNNNNCCTGCGCCACATCCATCGGC	TGCACCAGGTGGTAACGAGC	219
RNF2	NNNNNCCTCGCTCGCTCGCTCCTTC	CAGCCCAGGGCTCCGCTGGC	208
DNMT1	NNNNNGCCTCACTGTGTGTGACAGC	TGGAGAGCCCTAAATAGAGC	221
PRNP	NNNNNTGAGCAGCTGATACCATTGC	GCGGTTGCCTCCAGGGCTGC	257
HEXA	NNNNNGAGAGCTCGCCCAACATCGC	CCTGTTCTTGCCAGCAGGGC	260
hAAVS1	NNNNNTAATGTGGCTCTGGTTCTGG	CTGGCAAGGAGAGAGATGGC	209
EGFR	NNNNNTGCCACCGTCATCACCTTCC	TGTGTTCCTTTGGAGGTGGC	238
PD1	NNNNNAACCAGACGGACAAGCTGGC	ACCTGTCACCCTGAGCTCTG	219
CCR5	NNNNNTACCTGGCTGTCGTCCATGC	CCAGCCCCAAGATGACTATC	232
CTLA4	NNNNNATGCATCTCCAGGCAAAGCC	CTTGCAGATGTAGAGTCCCG	212
Primers used t	o amplify Nelson et al-reported sites in HEK293T cells.		
NO.	Forward primer	Reverse primer	
DNMT1	CACAACAGCTTCATGTCAGC	GGTCCATGTCTGTTACTCGC	
HEK3	AGGGAAACGCCCATGCAAT	CCTCCCTAGGTGCTGGCTT	
RUNX1	AAGAAAGAGAGATGTAGGGC	CATTACAGGCAAAGCTGAGC	
VEGFA	ACTTGGTGCCAAATTCTTCTCC	AAGAGGGAATGGGCTTTGGA	
RNF2	AGCCAACATACAGAAGTCAG	TTTCCAGCAATGTCTCAGGC	
PRNP	CCACAGTCAGTGGAACAAGC	CACAAAGTTGTTCTGGTTGC	



Supplementary Table 3: Primers used for N2a cells genomic DNA amplification and targeted deep seque					
			Length of		
NO.	Forward primer	Reverse primer	amplicon		
			(nt)		
Trp53	TCTACCCTTTCCTATAAGCC	GCGGGATGTATCTTAAGGGC	220		
Tnf	AAACCACCAAGTGGAGGAGC	AGAGGAGGTTGACTTTCTCC	227		
ROSA26	AGGAGGCACTGTTAAGGAAC	ACCAAGGTACCTCAGGAGAG	237		
Tgfb1	ACGTCAGACATTCGGGAAGC	CTTAGGCTTCGACACTGTGC	234		
116	TGATGCTGGTGACAACCACG	AGCTTCAAATCCTAAGGGCC	265		
lfng	AATTCAAATAGTGCTGGCAG	CCAACAACTTGTATACTTGG	213		
lfnb1	CTCCATCAACTATAAGCAGC	AGTCTCATTCCACCCAGTGC	238		
Akt1	GATCTTATGTGCCTGGGTCC	TCTCAGTGGGCAGTTTCAGC	272		
Arg1	GGAGAAAGGACACAGGTTGC	CATAGGCACAGTACCTGAGC	225		

Supplementary Table 4: Information of predicted off-target sites related to Supplementary Fig. 16.				
NO.	Chr.	Off-target site	Mis-matches	
EMX1-peg-OT1	chr1	AtGGaTCaCATCACATCAACGGG	3	
EMX1-peg-OT2	chr16	AGGGgTCCCAgaACATCAACAGG	3	
EMX1-peg-OT3	chr11	AGaGCTCCCATCACAcCAtCTGG	3	
EMX1-peg-OT4	chr18	AGGGCTCCCAggAgATCAACAGG	3	
EMX1-peg-OT5	chr3	AGaGCTtCCATCACATCAcCTGG	3	
EMX1-peg-OT6	chr8	AtGtagCCCATCACATCAACAGG	4	
EMX1-peg-OT7	chr8	AtGtaaCCCATCACATCAACAGG	4	
EMX1-peg-OT8	chr8	AGGGCcCaCATCACtcCAACTGG	4	
EMX1-nick-OT1	chr8	GAaATCaAgGTCCTCCCCATAGG	3	
EMX1-nick -OT2	chr16	GACATCGATagCCTCCCCAcTGG	3	
EMX1-nick -OT3	chr16	cACATaGgTGTCCTCCCCATAGG	3	
EMX1-nick-OT4	chr8	GACATCGATGcaCcCCtCATGGG	4	
EMX1-nick-OT5	chr8	GACAggGAgGTCCTCCCaATGGG	4	
EMX1-nick-OT6	chr8	GACcTgGATGatCTCCCCATCGG	4	
EMX1-nick-OT7	chr15	aACtTCcATcTCCTCCCCATGGG	4	
EMX1-nick-OT8	chr15	GACcaCGATGTCtTCCCCAgGGG	4	
FANCF-peg-OT1	chr8	GggAGAGGGCtGCTTTGGGCAGG	3	
FANCF-peg-OT2	chr8	tCAAGAGGGCGGCTcgGGGCTGG	3	
FANCF-peg-OT3	chr1	GCAAGtGaGCGGCTgTGGGCAGG	3	
FANCF-peg-OT4	chr22	GCAAGAGGctGGgTTTGGGCAGG	3	
FANCF-peg-OT5	chr2	GCAAGAGGGGGGGGGTTGGGtCGG	3	
FANCF-peg-OT6	chr17		3	
FANCF-peg-OT7	chr16	GaAAGAGGGgGGCTgTGGGCGGG	3	
FANCF-peg-OT8	chrX	GCAAGAGGGtGGCcTTtGGCTGG	3	
FANCF-nick-OT1	chr8	gCAGCAGGCaCAGAGAGAGCTGG	2	
FANCF-nick -OT2	chr1	CCtGCAGGCcCAGAGAGAGCAGG	2	
FANCF-nick -OT3	chr15	CaAaCAGGaGCAGAGAGAGCTGG	3	
FANCF-nick-OT4	chr15	gCAGCAGGgGaAGAGAGAGCTGG	3	
FANCF-nick-OT5	chr5	CCtGCAGGCtCtGAGAGAGCAGG	3	
FANCF-nick-OT6	chr5	CCAGCAGGtGCtGAGAGAGCCGG	3	
FANCF-nick-OT7	chr5	CggGCAGGCGCcGAGAGAGCGGG	3	
FANCF-nick-OT8	chr20		3	
HEXA-peg-OT1	chr5	GAACGaGTTCCcCTaGCATCTGG	3	
HEXA-peg-012	chr20	GAAaGgGTTCtACTGGCATCTGG	3	
HEXA-peg-OT3	chr8		4	
HEXA-peg-O14	chr15		4	
HEXA-peg-O15	chr5	GAggGTGTgCtACTGGCATCTGG	4	
HEXA-peg-016	chr5	GAggGTGTgCtACTGGCATCTGG	4	
HEXA-peg-O17	chr5	GAAtGICIACCACaGGCAICAGG	4	
HEXA-peg-018	chr5		4	
HEXA-nick-OI1	chr1		2	
HEXA-NICK -012	cnr2		2	
HEXA-NICK -013	cnr8		3	
HEXA-nick-014	chr20	AAACTTGGTCaGAGTGAgAtGGG	3	
HEXA-NICK-U15			3	
HEXA-NICK-U16			3	
HEXA-NICK-UT/			3	
HEXA-nick-018	cnr1/	AAAAIIGGACIGtGIGAAACAGG	3	

NO. Forward primer Reverse primer Length of amplicon BW1:pep.012 GGTGAGTGACTTGACAGA GGTGATGCCAATCAGAGAC GTGTGACGCACTCAC 289 BW1:pep.013 GATCAGTGCAATCAGAGAC GTGTGTCAGGCACTCAC 281 BW1:pep.014 GACCCTCAGGTGTCAGATC TGTCTGTCAGCACCATCC 281 BW1:pep.014 GACCCTGGTGTCAGCTC TGTCTGTCGCACCACTCC 280 BW1:pep.017 TTATACCTGTGCCACACTGG IGCCTGTGTCGCACC 284 BW1:pep.017 TTATACCTGTGCCACACTGG GGGAGTGACCCCACTGGC 286 BW1:pep.017 TATACCTGGCGTCACACACGC CCCCACGCACTGAGTGACCC 286 BW1:pep.017 TGTGGGAGGGTGCACACAGC CCCCAGCTGTGCACCAC 281 BW1:pep.017 TGTGGGAGGGTGACCCCATCACCC CCCCAGCTGTGCGCACCACACGC 280 BW1:pep.017 TGTGGGAGGGGTGACCCCATCACCCCAC CCCCAGCTGTTGCGTCACC 280 BW1:pep.017 TGTGGGAGGCGTGACCCACACGC CCCCAGCTGTTGCGCCAC 280 BW1:pep.017 TGTGGGAGGCGTGACCCACACGC 280 280 BW1:pep.016 CCCAGCTGTGTGCGCCACAC CCCCAGCTGTGTGCGCCC 280	Supplementary	Table 5: Primers used for off-target analysis	related to Supplementary Fig. 16.	
EMX: psg.0T1 TGGTCAGGTAGTTGTTACAC AIXCATCCCTTGATAGCAC 288 EMX: psg.0T3 CGTCAGTCCAGATCACAGAC GTTGTCACAGGAGCACTGC 218 EMX: psg.0T3 CGTCAGTCCAGATCACAGAC GTTGTCACAGGAGCACTGC 218 EMX: psg.0T6 TATCATAGTCGTCGCCAC TGCTGTCGCAGCGC 219 EMX: psg.0T6 TATCATAGTCGTCGCCAC TGCTGTGCGCGCGC 241 EMX: psg.0T6 TAGCATTGCCCACACGG AGGAGTGGTCGTCGCAC 238 EMX: psg.0T6 AGGAGTGGTCGCCACCGG AGGAGTGTCGCGCGCC 238 EMX: psg.0T1 AGGCGGGGACCCACGG ATAGCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	NO.	Forward primer	Reverse primer	Length of amplicon
EMI: app.OT2 GGTGATGCCCAATCAAGAAC GTTGTCAAGGGTAACTGC 218 EMX: app.OTA GACCCCTCGTGTCAAGCATC TGTCGTGTCAAGC 241 EMX: app.OTA GACCCCTAGGTGTCAAGCATC TGTCGTGTCAAGCATCCC 208 EMX: app.OTA GACCCCTAGGTGTCAAGCATC TAGCTGGTCGACCCCTGCC 208 EMX: app.OTA TAATCACCTGGGTGTCAACCATCG TGGCTGGTCGACCCCCTGCC 204 EMX: app.OTA TAATCACCTGGTGTCAACCAGG TGGCGGTGTCACCCA 236 EMX: app.OTA TAATCCCAAGTGGTCAACCAGG CCCCAGGACTTAGTGCAAC 211 EMX: app.OTA CAGGTGTCAACCAGG CCCAGGACTTAGTGCAAC 211 EMX: app.OTA CCATGTCAAGAGGC CCCAGGACTTAGTGCAAC 281 EMX: app.OTA CCATGTCAAGAGGC CCCAGGACTTAGTGCAAC 283 EMX: app.OTA CCATGTCAGGAGGCAACAG CAGGAGATTGATGCGACAGG 281 EMX: app.OTA CCATGTCAGGAGGAGGCACACAGG CAGGCAGAGTTGATGCCAAC 283 EMX: app.OTA CCATGTCAGGAGGAGGAGCACAGG CAGGCAGAGTTGATGCGCGC 281 EMX: app.OTA CCATGTCAGGAGGAGGAGCACAGG CCCCATGTCAGTGCGCGCGCGCGGGGGGGGGGGGGGGGG	EMX1-peg-OT1	TGGTCAGGTAGTTTGTACAC	ATCATTCCTCTGATAAGCAC	209
EMX:psp-013 CATCCCTTCTCTCTCACACTC ACCTOTTACATCACTACC 241 EMX:psp-015 TAACATACCTTGGCACACC TGTGCTGCGGCCCCGCC 208 EMX:psp-015 AGACTACCTTGGCGACCAC TAACCTTGGCACACC 219 EMX:psp-015 AGACTACCTTGGCGACCAC 219 221 EMX:psp-015 AGACTACCTGGCGACAC 207 224 EMX:psp-017 ITAACCTTGGCGACCACC CGCCACACACTCTGTTC 221 EMX:psp-017 ITAACCCACGCACCC CCCCACGCACTGTGTCT 221 EMX:psp-013 GGCTGTACACACACTCTCT TTGCCACGCATTGTCC 221 EMX:psp-013 GGCACGTGTACACACACCC CCCCACGCACTTGCTCC 221 EMX:psp-013 TGTGCACGCATGTCC CTCTTCTCACACCTTGACC 220 EMX:psp-013 GGCACAGTGTAGGCACAGC CACCACGCACTGAGCTCC 220 EMX:psp-015 GGATAATGTGACGCAAGG ATAGCTAGTGCACCC 220 EMX:psp-016 CCACATGTGTGACACCACGC 220 220 EMX:psp-017 TGATGCACACTACGCAGCC 221 240 EMX:psp-017 CACTGCACACAGAGGCACCACC 226 224	EMX1-peg-OT2	GGTGATGCCAGATCAGAGAC	GTTGTACAGGAGGTAACTGC	218
EMI:psp:014 GACGCCTAGGTGTCAGCATC TGTGCTGCGCAGCTGCGC 208 EMI:psp:015 TATACATACCTGGCGCAAC TAAGCTTGGCGAGCAGCAGC 219 EMI:psp:016 AGGATTGGCCCAAC TGAGCTGGCGAGCAC 201 EMI:psp:017 TTATACCCTTGACGCCAAC GGCAATACCTTTATCGAT 201 EMI:psp:018 AAAGCTGGGCACACACAGTGG GGCAATACCTTATCTGAC 234 EMI:psp:018 AAAGCTGGGCATGGCAAAGA TGGCAGGAAGACACACAC 234 EMI:psp:017 ATAGCCTGGACACACACTGGC TTGGCAGGAATGAACTTGTGCACAC 234 EMI:psb:017 AGGCGGCTGGACAAGA CGGCAGTGGACTGGCACACAC 236 EMI:psb:013 CGTGGGGGGTGGACAAGA CGCCAGTGGGGCTGGCACACACCAC 230 EMI:psb:014 CCGTGGAGGGGGGGGGGAGTGC CTGTGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	EMX1-peg-OT3	CATCCCTTCTCTCTCAACTC	ACCTGTCTTAACTTCCTAGC	241
EMX1-psp-015 TAATCATACCTTGGGCCAAC TAAGCATACCTTGGGCCAAC 219 EMX1-psp-017 TTATACCTGGGCAACC GCACATCATCTTATCTGAT 207 EMX1-psp-017 TTATACCCTGGCCACCAC GCACATCATCTTATCTGAT 207 EMX1-psp-017 TTATACCCTGGCCACAC GCACATCATCTTATCTGAT 207 EMX1-psp-017 TTATACCTGGGCCGTGTGCAACAC GGCATTACCCAAGC 226 EMX1-msk-011 AGGCTGGGCGTGCACACAGC CCCCCACCACCTGGGTTCCCA 211 EMX1-msk-012 GGATTACCCAAGGCGTCGCACACGC CCCCCACCACCAGGCGTTCCCCA 211 EMX1-msk-013 GGAGTGAAGCGCGTGCCCCAGC CCCCCACCACCAGGCGCGTGCCCCA 220 EMX1-msk-016 GATGTGAAMGCTAGCCCAGC CCCCACCACCAGGCGCGTGCCCCAC 224 EMX1-msk-017 GCCCCACCACCAGGCGCGTGACCCCCA GCCCTCACCACCAGGCGCGTGGCCCCAC 224 EMX1-msk-017 GCCCCACCACCAGGCGCGTGGCCCCCAC CCCCACCACCAGGCGCGTGGCCCCCCCCC CCCCACCACCAGGCGCGCGCCCCCCCCC 224 EMX1-msk-018 GCGTGTGCACGGCGGCGGCGCCCCCCCCC CCCCACCACCAGGCGCGCCCCCCCCC 227 FANCF-psp-013 GCGTGTGCACGCCCCCCCC CCCCCACCACCAGGCGCGCCCCCCCC 227 FANCF-psp-013 GCGTGTG	EMX1-peg-OT4	GACGCCTAGGTGTCAGCATC	TGTGCTGCTGCAGCTCCTGC	208
EMX1-psp-016 AGGATTGAGTCCGGGTATGC GCACATCATTTATCTGAT 207 EMX1-psp-017 ITATCACCTTGACCACATCG AGGAAGTCCATTTGTTCTGTCC 204 EMX1-psp-018 MAGECTGGGCTGTGTCAAC TGGTCTTTGGTCGCGGCTCAC 221 EMX1-psp-017 ITATCCCTTGACCCATCTCT TGCCACGCACGTGGTTAGCCAC 221 EMX1-psp-017 GGATTATCCAAGGTCAACAGC CCCCACGCACGTGGTTAGCCAC 221 EMX1-psp-017 GGATTATCCAAGGTCAACAGC CCCCACGCATGGGTTAGCC 290 EMX1-psp-017 GGATGAAGTAGCCAACGCC CCCCAGCTTGAGGTCACCC 290 EMX1-psp-017 GGATGAAGTAGGCTAGTCC CCCAGCTTGAAGGTGGCC 291 EMX1-psp-017 GCCCACACGAGTGGCAGTAC CCAGCTCAAGGTGTGCCC 290 EMX1-psp-017 GCCCACACGAGTGGCAGTAC CCAGCTCAGCCCCGC 291 EMX1-psp-017 GCCCACACGAGTGGCAGTAC CCAGCTCAGGTGTCCCCCA 291 EMX1-psp-017 GCCCACCTTGCCCC CCCAGTCTCAGGGCCCTG 299 FANCF-psp-017 GCAGCGTAGTCAACGCC CCCAGTCTCAGAGGC 193 FANCF-psp-017 GCAGCGTAGTCAACGC AGGCGTGGTGTCAGCCGC 294 FANCF-p	EMX1-peg-OT5	TAATCATACCTTGGGCCAAC	TAAGCTTGGGCAGCAGTGAC	219
EMX1-psp-017 ITATACCCTTGACCACTGG AGGAATTCCTTTCTGTTCC 204 EMX1-psp-017 ITATACCCTTGACCAC TGGTCTTTGGTTCCC 236 EMX1-psp-017 GGATTATCCAAGCTGTGTCACAC TGGTCTTGGTCACCCA 211 EMX1-psp-017 GGATTATCCAAGCG CCCCAGCACTGGTTCACAGC 221 EMX1-psp-017 GGATTATCCAAGGTCACACGC CCCCAGCACTGGTTCACAGC 229 EMX1-psp-017 GGATTATCCAAGGTCACACGG ATAAGTAGCGCCC 220 EMX1-psp-017 GGATGAAAGGCACAGG ATAAGTAGCGCCC 220 EMX1-psp-017 GGATGAAAGGCACAGG CCCCACCACCAGCAGTGCACGC 220 EMX1-psp-017 GGATGAAAGGCACAGG CCCCACCACCAGCAGTGCAGCC 220 EMX1-psp-017 GGATGGTAAGCACCACGC CCCACCACCACGAGTGCAGCC 220 EMX1-psp-018 CCTTGGAGGTGTACCCCCA CCCACCACCACGCAGTGCAGCCCCCA 220 EMX1-psp-018 CCTTGGAGGTGTACACGTCCCCA CCCAGGTGCACACCAGTGCGCCCCCA 221 EANCP-psp-018 CCTTGGAGGTGTACAGCTCCCCA CCCCACCACCACGCAGTGCAGCCCCCACCACCAGCCCCCCACCACGCCCCCACCACC	EMX1-peg-OT6	AGGATTGAGTCCGGGTATGC	GCACATCATCTTATCTGAT	207
EMXT-pag-018 AAAGCCTGGGCTGTGAAC TGGTCTTGGTGTCCGCAC 296 EMXT-pack-071 AGGCTGGTAACCACACCAC TTGCCACGGAGTTGATCGA 211 EMXT-pack-073 TGTGGAGGCGTGCAGAAGA CACCAGCAGTTGACGAC 221 EMXT-pack-074 CGGATTATCCAAGGTCACACAGC CCACCAGCAGCTTGAGGAGTTGAGG 199 EMXT-pack-074 CGGATGATGTGAGGAGGAG CACCAGCAGCAGGC 229 EMXT-pack-074 CGATGTAGTAGGCAGCCA CCATGTGAGAGCCCACGC 220 EMXT-pack-075 GGATGAAGTGGCAGTAC CCAGGGAGTTGAGGCAGC 220 EMXT-pack-076 CCATGTGAAAGCTGACCCA CCAGGGAGTAGCACGCGC 220 EMXT-pack-078 CGTTGTGAAGTGGCAGTAC CCAGAGGAATGAAGCCGC 220 EMXT-pack-078 CGTTGTGAAGTGGCAGCA CCAGTGTGAAGCCGC 220 EMXT-pack-078 CGTTGTGAAGTGCCA CCAGTGTGGAGAGCCG 220 EMXT-pack-078 CGTTGTGAAGTGCCA CCAGTGTGGAGAGCGC 220 EMXT-pack-078 CGTTGTGAAGAGTGCAGCCA CCTTGTGGGCTGCAGACGC 220 FANCF-pag-071 CAGCTGTGGAGAGTGCGCA CTTGTGGGCGCAGCCAGGC 281 FANCF-pag-075	EMX1-peg-OT7	TTATACCCTTGACCAACTGG	AGGAAGTTCCTTTCTGTTCC	204
EMX-Ink-OT1 AGGCTGGTACACCCATCTCT TTGCCACGGAGTGTACCAC 211 EMX-Ink-OT2 GGATTATCCAAGGTCACACGC CCCCACGACGTAGTACACA 251 EMX-Ink-OT3 TGTGGAGGCGTTGCAAAGGTCACACGC CCCCAGGACGAGGGACTTGTGGGGGC 229 EMX-Ink-OT6 CCATGTATGCAAGGCACAGG ATAGTAAGCTTGTGCGGGC 229 EMX-Ink-OT6 CCATGTATGCAAGGCACACGG ATAGTAAGCTTGACGC 220 EMX-Ink-OT6 CCATGTATGCAGGCCAACCGG CCCCAGCTGCTGCACCCCT 220 EMX-Ink-OT7 GCCCACACGGTACCCCA CGCCAGCTGTCCCAACCCCT 229 EAX-Ink-OT8 GCGTGTGTATGCAGGTCAA CCACAGGCTTAGGCCCCCG 238 FANCF-peg-012 GGCTGGTATGCAAGCC GGCTGCGTATGCAACCCA 238 FANCF-peg-013 AGCTGTGTATGCAAGCC CCACAGTGCCTAAGCC 238 FANCF-peg-014 AGCCTGAGGTGCAACCCA CCACAGTGCTAAGCC 236 FANCF-peg-015 TGACTGGCTGAGCACCA AGTTTGCCAGCC 226 FANCF-peg-016 CCACAGTGCTATAGCC 226 227 FANCF-peg-017 GAACAGTGCAGCCCA 236 236 FANCF-peg-016 CTGAGGCTGAGCCACCCA <td>EMX1-peg-OT8</td> <td>AAAGCCTGGGCTGTGTCAAC</td> <td>TGGTCTTTGGTGTCCGTCAC</td> <td>236</td>	EMX1-peg-OT8	AAAGCCTGGGCTGTGTCAAC	TGGTCTTTGGTGTCCGTCAC	236
EMX-Inic-OT2 GGATTATCCAAGGTCACAGC CCCACGACCTAGGTACAG 251 EMX-Inick-OT3 GTGGGAGCGTTCACAAGAGA CACCAGGAGGAGTTGGG 199 EMX-Inick-OT4 CCATGTATGTGAAGCCACAGG ATAGTAAGCTTGCGCGC 229 EMX-Inick-OT5 GGATGAAGTGGCTAGTCCC CTCTTTCCAAGCTTGTGACC 250 EMX-Inick-OT6 CAGTGAAGACGTCAACCCAG CCCCAGTCTTGCACGCTGTCC 224 EMX-Inick-OT7 GCCCCACAGTGGCAGTGCC CCCTTCAGTGTGCACGCG 224 EMX-Inick-OT7 GCCCCACAGTGGCAGTGCC CCCAGTGTGTGACGCCGGG 238 FANEF-peg-OT1 TCATTCGCAGGCGTGTGCACGC CACTGCAAGCCGTGGCGGGGGGGGGGGGGGGGGGGGGGG	EMX1-nick-OT1	AGGCTGGTACACCCATCTCT	TTGCCACGGAGTTGATCCCA	211
EMX-Inick-073 TGTGGAGGCGTTGCAGAAGA CAGCAGGATGGAGTTGTGGC 199 EMX-Inick-074 CCATGTATGTGAAGGCACAGG ATAAGTAAGCTTGTGCGGC 229 EMX-Inick-075 GGATGAAAGTAGGCTAGTCC CTTTTCCAAGGTTGTGCGGC 250 EMX-Inick-076 CATGTGAAAGCTCAACCCAAG GCCCAGCTGTGACGTGTC 261 EMX-Inick-077 GCCCACACAGATGGCCAAGTGC CGAGGGATACACCTCCC16 224 EMX-Inick-078 CGCTTGGCAGGGTGTCCCAA GCCCAGGTGCCCAACCCT 229 FANCF-pse_071 TGATTGCACAGGGTGCCCAA GCCCTTCAGTGCCCAACCCT 229 FANCF-pse_0713 ACCCTCTGATGCGCA CAGCAGCCAGGGGCC 238 FANCF-pse_0714 AAGCCATGACAGGC CAGCAGCCAGGGGGCC 227 FANCF-pse_0715 IGACIGGCTGAGGCAGC AGCTGCCCCAC 206 FANCF-pse_0716 ACCCATGTGCAGCC AGCTGCCCCCCC 206 FANCF-pse_0717 GAAGGCTACACGC AGCCATGTGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	EMX1-nick -OT2	GGATTATCCAAGGTCACACAGC	CCCCAGCACCTAGGTTACAG	251
EMX1-nick-074 CCATGTATGTGAAGGCACAGG IATAGTAGCTTCTGCGGGC 229 EMX1-nick-075 GAGTGAAAGTGAGGCAGTCC CTCTTCCAAGCTGTGACCC 250 EMX1-nick-076 CATGTGAAAGCTCAACCCAG GCCCCACAGTGTGACCCC 251 EMX1-nick-077 GCCCCACAGAGTGGCAGTACC CAGAGGAATACACCTCCCTG 224 EMX1-nick-078 CGTTCTGCACGTGTGCTTACCCCA GCGTTCAGTGTCCCAAGCC 238 FANCF-peg-071 ITCATCCACATTTGCCCGC CACTTCAACAGTGCACAGCC 193 FANCF-peg-073 ACCTCTGTACACAGCTGCAC CAGTTGGCCCTTCCTGCCA 227 FANCF-peg-074 AACCTCTGTAGGTCTGAC ATTCGGCCATTCACGCAC 2261 FANCF-peg-075 ITCACTGCTTAGGTCTGAC ATTCGGCCATTCACGCAC 2261 FANCF-peg-076 CCCAGTTGACGTGCAC ATTCGGCCAGATTAATGGGC 248 FANCF-peg-077 GAAGATTACACTCTGTGTTCAC CCCAGTGTGCTGCACACG 248 FANCF-peg-078 GATGATAGACGCTGACG ACCCCAGGGTCTCACACCC 227 FANCF-nick-071 CCCAGTGACTGCTGCTGCACGC 248 244 FANCF-nick-071 CAGGTGACACG ACCCAGGTGTGTACACC 226 FANC	EMX1-nick -OT3	TGTGGAGGCGTTGCAGAAGA	CAGCAGGATGGAGTTTGTGG	199
EMX1-nick-075 GGATQAAAGTAGGCHAGTCC CTCTTTCCAAGCTTCTGACCC 280 EMX1-nick-076 CATGTGAAAGCTCACCCAG GCCCACCTTTCATGTGTGTCT 281 EMX1-nick-077 GCCCACACAGATGCCACCAG GCCCATGTGACGTGTCC 229 FANCF-peep.071 TCATTGCACGTTTAGTTCACACG GCCTGTGACACCTTCAGGGC 238 FANCF-peep.072 GGCTGGTGTTAGTTCACACGC CTCTGACACCCTTAGGGGC 238 FANCF-peep.073 ACCTCTGACACTGGACGC CGCTGGGGACGTGGAGGGC 290 FANCF-peep.073 ACCTCTGACACTGAGGTCGC CGTGTGGGCCTTAGGTGACAGC 206 FANCF-peep.074 AAGCCTACAGCGC CGCGGGTGTGAGGCC 281 FANCF-peep.075 TCACTGGCTTGAGGCGTGCGC TTGGGCCCTGCGCTAAGC 286 FANCF-peep.076 CCCCAGTGTCTGC CTTTGGGGCCCTGGCGCA 286 FANCF-peep.071 GAAGGTAACATGGTGCAC CTTTGGGGCCCTCAGGCACGACGA 286 FANCF-peep.071 GAAGGTAACATGGTGCAC CTTTGGGGCCCTGGCGCACGACGACGAGGACCATGACGACGACGAGGACGACGAGGACGACGAGGACGACGACG	EMX1-nick-OT4	CCATGTATGTGAAGGCACAGG	ATAAGTAAGCTTCTGCGGGC	229
EMX1-nick-076 CATGTGAAAGCTCAACCCAG GCCCAGTGTGAGTGCT 281 EMX1-nick-077 GCCCAACAGTGGCAGTGCC CAGGGAATCACCCT 229 FANCF-peg-071 TCATTCCACGATGGCAGTGC CAGCTCAAGTGTCCACAGC 238 FANCF-peg-071 GCCTGGTGTTAGTCACAGC CAGTTCAACACCT 229 FANCF-peg-072 GCGTGGTGTTAGTCACGC CAGTTCAACACCT 238 FANCF-peg-073 ACCTGTGTACACTCAGTTGC CAGTTGGACCCTCAGGGCC 227 FANCF-peg-074 AACCCATCACATCGATGCAC ACCTGTGTACACTCAGTTGCA ACCCCAGTTGTCACTCACAGTGCC 281 FANCF-peg-075 TCACTGGCTGACACG ATTGGCCCAGTTTAGTGCACC 281 FANCF-peg-076 CCCAGTTCCATGGCCCTGCAC ACCTGTGTACACCC 281 FANCF-peg-077 GAGAGTACACAGGGCACCACG ACCCGTGGTGCACCTGGTTTCCA 226 FANCF-peg-078 GATGTATGACACGG ACCCGTGCTCTCATACG 299 FANCF-nick-071 CCAGGGACCTCAGG CCCAGGTGCTCCATAGG 226 FANCF-nick-072 CCTTGCACACGGGGGGGGGC 226 225 FANCF-nick-073 TCTTGCGACAGGGACTAAC AGCCAGGGGCCTCAGGGGT 248	EMX1-nick-OT5	GGATGAAAGTAGGCTAGTCC	CTCTTTCCAAGCTTCTGACC	250
EMX1-nick-OT7 GCCCACACAGAGEGGAGTAC CAGAGGAATACACACTCCC 224 EMX1-nick-OT8 CGTTCGACAGGTGTACCCCA GCCTTCAGTCCCAAACCT 229 FANCF-peg-0T1 TCATTCCACTTTCTGCTCGC CACTTCAAGCACCTAAGGCACC 238 FANCF-peg-0T2 GGCTGGTGTTAGTTCACAGC CTTCGAGGCCCTAAGGCACC 237 FANCF-peg-0T3 ACCTCTGTACATCAGTTCCA CAGTTAGCCCCTTGCCCCCAC 206 FANCF-peg-0T4 AAGCCATCAGTTCCAAGTGCA ACTTCGAGCCTTAATGGCC 248 FANCF-peg-0T6 CCCAGTTCAGTCCAAGGC TTGGCCCTTCCCTGCCAC 206 FANCF-peg-0T7 GAAGACTACATGGTGGACAGG AACACTGGGCTTGAGGCC 248 FANCF-peg-0T6 CCCAGTTCTCTGTTCAGC CTTGGTGACCAGGC 267 FANCF-peg-0T7 GAAGACTACATGGTGGACAGG AACACTGGGCTCAAGCG 267 FANCF-peg-0T8 GATGATTAGACATGGTCGC CTTGTGTGCACCAGGGAACTCACC 209 FANCF-peg-0T8 GATGATTAGACATGACTGCG CTCTGTGCATACC 209 FANCF-peg-0T8 GATGATTAGACATGACCAG ACCCAGTGTCATAGC 225 FANCF-peg-0T8 CATGTGGCACCTGGTGGCAG CTCTGTGCATAGCAGGAAGCTCGCGCGCAGGAGGCAGGCA	EMX1-nick-OT6	CATGTGAAAGCTCAACCCAG	GCCCAGTCTTGAGTGTGTCT	261
EMX1-nick-OT8 CÓTTCTGCACGTGTACCCCA IGCTTCAGTGTGCCCACTTC 229 FANCF-peg-OT1 TCATTCCACTTCTGCCC CACTTCAGACCCTTTCACAGC 133 FANCF-peg-OT2 GGCTGGTGTTAGTCACAGC CCATTCAGAGCC 133 FANCF-peg-OT3 ACCTCTGACATCAGTTGC CAGTTGTGCACCC 227 FANCF-peg-OT3 ACCTCTGACATCAGTTGC CAGTTGGCACCC 227 FANCF-peg-OT3 ACCTCTGACTCACTGCTACCC CAGTTGGCACCC 227 FANCF-peg-OT3 ACCTCTGACGTCACAGTGCC CAGTTGGCACCC 227 FANCF-peg-OT4 AAGCCATGTGTGCACGC AGTTGGCACCCCC 227 FANCF-peg-OT5 TGACTGGCACAGTGCTGCACGC AGTTGGCACCCCCCACCCCCCCC 227 FANCF-peg-OT5 GAAGACTACATGGCACGC AGTTGGCACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	EMX1-nick-OT7	GCCCACAGATGGCAGTAC	CAGAGGAATACACCTCCCTG	224
FANCF-peg-071 TCATTCCACTTCTCCTCGC CACTTCAACATCTTCACACGC 238 FANCF-peg-013 ACCTCGTGTAGTTCACCACC CTCGGAGACCATGAGGAGC 199 FANCF-peg-013 ACCTCGTACATTCAGTTTGC CAGTTAGCCCTTACTCACC 227 FANCF-peg-013 ACCTCGTACATCAGTTGCAAGTGC AGTTCGCCCTCCCCCCACC 227 FANCF-peg-015 TGACTGCGCTGAGGTTGCAA ACCCAGTGTCCCTGCCA 206 FANCF-peg-016 CCCAGTTCTCACAGTCGTAGC AGCCAGTGTGCTTAGGC 281 FANCF-peg-017 GAAGATTGACAGTGGTCTGC TTGGGCCCTGTGAGACCG 248 FANCF-peg-017 GAAGATTAGACATGGTCTGC CTTTTGGTGACCTGTGTAGTCA 248 FANCF-nek-071 CCAGGCAGACTCCTGCTTTCAG CCACTGCCTCAGGTAGTA 248 FANCF-nek-071 CCAGGCAGCAGCACA AGCCAGGGTGCTCAGTAGTA 248 FANCF-nek-071 CCAGGCAGCAGCACA AGCCAGGGTGCTCAGTAGTA 248 FANCF-nek-071 CCAGGCAGCTGGTGTG TCCTGTCCTCATGTAG 224 FANCF-nek-074 CTGTGGCCCTGTGGTG TCCTGTCCTCATGTG 244 FANCF-nek-074 CTGGTGGAGTGCGGAG 266 249 FANCF-nek-075 <td>EMX1-nick-OT8</td> <td>CGTTCTGCACGTGTACCCCA</td> <td>GCCTTCAGTGTCCCAAACCT</td> <td>229</td>	EMX1-nick-OT8	CGTTCTGCACGTGTACCCCA	GCCTTCAGTGTCCCAAACCT	229
FANCE-beg-012 GCCTGGTGTTACTACAGC CTTCGGAGAGCCATGAGGAC 193 FANCE-beg-013 ACCTCTGTACATAGTTGCAAGTGC CACTTGGCCCTTAGTCACC 227 FANCE-beg-014 AAGCCATGAGTTGCAAGTGC ACTTGGCCCTTAGTCACC 227 FANCE-beg-015 TGCACTGGCTTGAGTCAGTGCA ACTTGGCCCTTAGTCCTAGC 261 FANCE-beg-015 TGCCAGTTCTAGTCCTAGC ITGGGCCCAGTTTAGGC 248 FANCE-beg-016 CCCAGTTCTAGTCCTAGC ACACTGGGTCTGAGCC 249 FANCE-beg-017 GAGAGTCCTCTGTTCAGC CTTTTGGTGACTGCAGCC 209 FANCE-beg-018 CATGATAGACAGGTCGC CCTGTCAGACGC 209 FANCE-beg-018 CATGATAGACAGGTCGC CCTGTGCAGCAGAGGAACTAAC AGCCAGGTCTCTCAGAGC 225 FANCE-hec-012 CCTGTGCAGCAGGAGGAACTAAC AGCCAGGTCTCTCATAGC 225 FANCE-hec-013 TCTTTGGACAGCAGGTCGCG CCTGTCCCATAGC 243 FANCE-hec-014 CTGTGTACTCAGGGAGTCCAG TCCTGTCCTCATAGC 244 FANCE-hec-015 CTGTGTCTCACAGG GCGTGGAGTCCGGGTGGC 249 FANCE-hec-016 CTTCTGCACAGG GCGTGGAACCCGGGGGGGGC 249 FANCE-hec-017 GACCCCGGCATGCCATAGC GCGGGGGGGGGGGGGGGGGGGG	FANCF-peg-OT1	TCATTCCACTTTCTGCTCGC	CACTTCAACATCTTCACAGC	238
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FANCF-nick-OT6CTTCCCTACTTCCTGACAGGGGCTGGAAACCTCGAACTCG217FANCF-nick-OT7GATCCTCGGACGCTTGAGGAGCCTTGGGATGGTGGGGGGAGGA268FANCF-nick-OT8AGCTGGGCATGGCTTCCTAAGCCAAATACCAAGGGAGGGT258HEXA-peg-OT1TGGAGGGGGGATGGCATATCCCGGTTGATTATTTCCATGC229HEXA-peg-OT2TATCTGTAGTCCCCTTCTGCAGATCAGGGTTCTTAATCTC240HEXA-peg-OT3GGAGAGGTGATGCAGTGACCACTTCTGCGCATTCC244HEXA-peg-OT4CCCAGATTACAGTCCAATCCGGCTGTGACTTTATCATCC247HEXA-peg-OT5TTCTTACCATCTGGTGGACAGTGCTTAAAATTCATCCG203HEXA-peg-OT6CACCCCACATTCTTCTTACCTCCTGCAGTGGAGGAGGC201HEXA-peg-OT7ACTTACTCCACTGGTGCCAGCAGTCCAAAGTGACC233HEXA-peg-OT8CCCGGGTGATTTTCCAGCTTGGTCTTACCCAGCAGGCC221HEXA-neg-OT8CCCGGGTGATTTTACCAGGAGACCTTGAGGAGGCAGGGAGAA269HEXA-nick-OT1GGAGACTAGGAAAGTCAGAGACCTTGAGGAGGCAGGGAGAA269HEXA-nick-OT3AATTAATGGGGAGAGGGAGCGGTGATAGGCAATGGCAGGCC241HEXA-nick-OT3AATTAATGGGGAGAGGGAGCGGTGATAGGCAATGGCAAGGC242HEXA-nick-OT6GTACCTGAGCTTAGGAGGGATTCCCCCAGAGGCC249HEXA-nick-OT6GTACCTGAGCTTAGGAGGGAATTCCCCCCCAGGGG234HEXA-nick-OT6GTACCTGAGCTTAGGAGGAATTCCCCCCAGAGGC247HEXA-nick-OT7CCAAGATATGGGCTACCGTG234TTCCCCCTCAGAGACACATGT252HEXA-nick-OT6GTACCTGAGCTTAGGAGGAATTCCCCTCCAGAGACACATGT252HEXA-nick-OT7CCAAGA	FANCE-nick-OT5	CTGTCTTCTCCACTTGTCTG	AAGAGAGGCTCTGCAAGGGT	249
FANCF-nick-OT7GATCCTCGGACGCTTGAGGAGCGTCTGGGATGGTGTGGGA268FANCF-nick-OT8AGCTGGCCATGGCTTCCTAAGCCAAATACCAAGGGAGGGT258HEXA-peg-OT1TGGAGGGGGATGGCATATCCCGGTTGATTATTTCCATGC229HEXA-peg-OT2TATCTGTAGTCCCCTTCTGCAGATCAGGGTTCTAAATCTC240HEXA-peg-OT3GAGAGGTGGATGCCAGTGACCACTTCTCTGCTCTCATTCC244HEXA-peg-OT4CCCAGATTACAGTCCAATCCGGCGTGTGACTTTATCATCCG247HEXA-peg-OT5TTCTTACCATCTGGTGGACAGTGCTTAAAATTCATCCTGC203HEXA-peg-OT6CACCCCACATTCTTTACCTCCTGCGATGAGCAGC201HEXA-peg-OT7ACTTACTCCACTGGCTTGCCAGCAGTCCAAAGTGACAGCC201HEXA-peg-OT8CCCCGGGTGATTTCCCAGGCTTGGTCTTACCAGGGCAGA269HEXA-nick-OT1GGGAGACTAGGAAAGTCAGAGACCTTGAGGAGGCAGGGAAA269HEXA-nick-OT2CCGGTTCTTAGCTCTGCTGTCCTGTGTTACCCCATGGGCT242HEXA-nick-OT3AATTAATGGGGAAGGGAGGCGGTATAGGCCAGCGGAGAAA269HEXA-nick-OT4GTTCCAGATGCCCATCTGCGTGGTCAGGATGGCAAGGC247HEXA-nick-OT5GGCACTGGGCTTCCTGTTCCCTGTGTTACCCCATGAGCC249HEXA-nick-OT5GGCACTGGGCTTCCTGTTCCCTGTGTACCCCATGGAGCC247HEXA-nick-OT6GTACCTGAGCTTAGGAGGAATTCCCCTCAGAGTAGCCAACGGC247HEXA-nick-OT6GTACCTGAGCTTAGGAGGGATTCCCCTCAGGAGAGCACATGT252HEXA-nick-OT7CCAAGATATGGGCTAGCGTGATGTCAGTCCTGACACGGC247HEXA-nick-OT7CCAAGATATGGGCTAGCGTGATGTCAGTCCTGACATGGC220HEXA-nick-OT6G	FANCE-nick-OT6	CTTCCCTACTTCCTGACAGG	GGCTGGAAACCTCGAACTCG	217
FANCF-nick-OT8AGCTGGGCATGGCTTCCTAAGGCAAATACCAAGGGAGGGT258HEXA-peg-OT1TGGAGGGGGGGGGCATGGCATATCCCGGTTGATTATTTCCATGC229HEXA-peg-OT2TATCTGTAGTCCCCTTCTGCAGATCGGGTCTTAATCTC240HEXA-peg-OT3GAGAGGTGTGATGCCAGTGACCACTTCTCGCTCTCATTCC244HEXA-peg-OT4CCCAGATTACAGTCCAATCCGGCTGTGACTTTATCATCCG244HEXA-peg-OT5TTCTTACCATCTGGTGGACAGTGCTTAAAATTCATCCTGC203HEXA-peg-OT6CACCCCCACATTCTTTTTCTCCCCGCAGTGAGGCC201HEXA-peg-OT7ACTTACTCCACTGGCTTGCCAGCAGTCCAAAGTGAGCC201HEXA-peg-OT8CCCGGGTGATTTCCCAGCTICGTCTTACCCAGGGCAGGCC221HEXA-nick-OT1GGAGACTAGGAAAGTCAGAGACCTTGAGGAGGGCAGGCC221HEXA-nick -OT2CCGGTTCTTAGCCACTGCTCCTGTGTTACCCAGGGCAGGCC249HEXA-nick -OT3AATTAATGGGGAGAGGGAGCGGTATAGGCCATCGGAGTGC247HEXA-nick-OT4GTTCCAGATGGCCACTCTGCGTGGTCAGAGTAGGCCAAGGC247HEXA-nick-OT5GGCACTGTGGCTTCCTGTTCCTTCCCACGCTGAGCAGGC247HEXA-nick-OT6GTACCTGAGCTTAGGAGGGATTCCCCACGAGCAGGGC247HEXA-nick-OT7CCAAGATATGGACTAGGGGATTCCCCTCGAGAGACACATGT252HEXA-nick-OT7CCAAGATATGGACTAGGGGATTCCCCTCGAGAGACACATGT252HEXA-nick-OT7CCAAGATATGGGCTAGCGGGGGCGGCGCACCGC220HEXA-nick-OT7CCAAGATATGGGCTAGCGGGGGCGGCGCCAACCG220HEXA-nick-OT7CCAAGATATGGCCAACGGGCGCGCCACCCCCACCGC220	FANCE-nick-OT7	GATCCTCGGACGCTTGAGGA	GCGTCTGGGGATGGTGTGGGGA	268
HEXA-peg-OT1TGGAGGGGGGATGGCATATCCCGGTTGATTATCTCCATGC229HEXA-peg-OT2TATCTGTAGTCCCCTTCTGCAGATCAGGGTTCTAATCTC240HEXA-peg-OT3GAGAGGTGTGATGCAGTGACCACTTCTCGCTCTCATTCC244HEXA-peg-OT4CCCAGATTACAGTCCAATCCGGCTGTGACTTTATCATCCG247HEXA-peg-OT5TTCTTACCATCTGGTGGACAGTGCTTAAAATTCATCCGC203HEXA-peg-OT6CACCCCCACATTCTTCTTACCTCCTGCAGTAGTGTCAAGGC201HEXA-peg-OT7ACTTACTCCACTGGCTGCCAGCAGTCCAAAGTGACTGAC233HEXA-peg-OT8CCCCGGGTGATTTCTCCAGCTTGGTCTTACCCAGCGCC221HEXA-nick-OT1GGAGACTAGGAAAGTCAGAGACCTTGAGGAGGCGCAGGAGAA269HEXA-nick-OT2CCCGGTTCTTAGCCTGCTGTCCTGTGTTACCCCAGGAGGAAA269HEXA-nick-OT3AATTAATGGGGAGAGGGAGCGGTATAGGCCATCGAGGTCT242HEXA-nick-OT5GGCACTGTGGCTCCTGCTGTCTTCCAAGCTCAAGGTC247HEXA-nick-OT6GTCCCAGATGCCACTCTGCGTGCCAGAGAGAGC247HEXA-nick-OT5GGCACTGTGGGCTCCGCGGGGGATTCCCCTCAGAGGACCACGGC247HEXA-nick-OT5GGCACTGTGGCTCCGCGGGGGATTCCCCTCAGAGACCACGGC247HEXA-nick-OT6GTACCTGAGCTTAGGAGGGATTCCCCTCAGAGACACATGT252HEXA-nick-OT7CCAAGATATGGCCTAGCGGATGTTCAGTCCTGACATGGC220HEXA-nick-OT7CCAAGATATGGCCTAGCGGGCCAGCCAACGC220HEXA-nick-OT7CCAAGATATGGCCTAGCGGGCCAGCCAACGC220	FANCE-nick-OT8	AGCTGGGCATGGCTTCCTAA	GGCAAATACCAAGGGAGGGT	258
IEXA-peg-OT2TATCTGTAGTCCCTTCTGCAGATCAGGGTTCTAATCC240HEXA-peg-OT3GAGAGGTGTGATGCAGTGACCACTTCTCGCCTCATTCC244HEXA-peg-OT4CCCAGATTACAGTCCAATCCGGCTGTGACTTTATCATCCG247HEXA-peg-OT5TTCTTACCATCTGGTGGACAGTGCTTAAAATTCATCCTGC203HEXA-peg-OT6CACCCCACATTCTCTTACCTCCTGCAGTAGTGCCAGGC201HEXA-peg-OT7ACTTACTCCACTGGCTTGCCAGCAGTCCAAAGTGACTGAC233HEXA-peg-OT8CCCGGGTGATTTTCTCCAGCTTGGTCTTACCCAGGAGGC221HEXA-peg-OT8CCCGGGTGATTTTCTCCAGCTTGGTCTTACCCAGGAGGCC221HEXA-nick-OT1GGAGACTAGGAAAGTCAGAGACCTTGAGGAGGGCAGGAGAAA269HEXA-nick-OT2CCGGTTCTTAGCTCTGCTGTCCTGTGTTACCCCATGATGC249HEXA-nick-OT3AATTAATGGGGAGGGGGGCGGTATAGGCCATCGGAGTCT242HEXA-nick-OT4GTTCCAGATGCCCACTCTGCGTGGTCAGAGTCACCCAGGC247HEXA-nick-OT5GGCACTGTGGCTTCCTGTTCCTTCCAAGCTCACCCAGGC247HEXA-nick-OT6GTACCTGAGCTTAGGAGGAGTTCCCCTCAAGGCCACGGC247HEXA-nick-OT7CCAAGATATGGCCAGCGTGATGTTCAGAGCACCACGTG234HEXA-nick-OT6GTACCTGAGCTTAGGAGGAGTTCCCCTCAAGACCACACGTG252HEXA-nick-OT7CCAAGATATGGCTAGCGGAGCCAGCTCATCCTGCCCCACCGC220HEXA-nick-OT8GGCCGGUTGGCAACAGGGCGAGCTACCCCACGTG228	HEXA-peg-OT1	TGGAGGGGGGGATGGCATATC	CCGGTTGATTATTTCCATGC	229
HEXA-peg-OT3GAGAGGTGTGATGCAGTGACCACTTCTCTGCTGTCTCATTCC244HEXA-peg-OT4CCCAGATTACAGTCCAATCCGGCTGTGACTTTATCATCCG247HEXA-peg-OT5TTCTTACCATCTGGTGGACAGTGCTTAAAATTCATCCTGC203HEXA-peg-OT6CACCCCACATTCTTCTACCTCCTGCAGTAGTGCCAGAGC201HEXA-peg-OT7ACTTACTCCACTGGCTTGCCAGCAGTCCAAAGTGACTGAC233HEXA-peg-OT8CCCGGGTGATTTTCTCCAGCTTGGTCTTACCCAGGAGGCC221HEXA-nick-OT1GGAGACTAGGAAAGTCAGAGACCTTGAGGAGGCAGGAGAA269HEXA-nick -OT2CCGGTCTTAGCTCTGCTGTCCTGTGTTACCCAGGAGGAGAA269HEXA-nick-OT3AATTAATGGGAGAGGGAGCGGTATAGGCCATCGGAGTCT242HEXA-nick-OT4GTTCCAGATGCCCACTCTGCGTGGTCAGAGTAGCCAAGGC247HEXA-nick-OT5GGCACTGTGGCTTCCTGTTCCTTCCAAGCTCACCACGTG234HEXA-nick-OT6GTACCTGAGCTTAGGAGGGGATTCCCCTCAGAGACACAGGC247HEXA-nick-OT7CCAAGATATGGGCTAGCGTGATGTTCAGTCCTCAGAGCACATGT252HEXA-nick-OT6GTACCTGAGCTTAGGAGGGAAGGCAGTGTCCGACATGGC220HEXA-nick-OT7CCAAGATATGGGCTAGCGTGATGTTCAGTCCTGCCACCCACTGC228	HEXA-peg-OT2	TATCTGTAGTCCCCTTCTGC	AGATCAGGGTTCTTAATCTC	240
HEXA-peg-OT4CCCAGATTACAGTCCAATCCGGCTGTGACTTATCATCCG247HEXA-peg-OT5TTCTTACCATCTGGTGGACAGTGCTTAAAATTCATCCTGC203HEXA-peg-OT6CACCCCACATTCTTCTTACCTCCTGCAGTAGTGTCAGAGC201HEXA-peg-OT7ACTTACTCCACTGGCTTGCCAGCAGTCCAAAGTGACTGAC233HEXA-peg-OT8CCCGGGTGATTTCTCCAGC211HEXA-nick-OT1GGAGACTAGGAAAGTCAGAGACCTTGAGGAGGCAGGAGAA269HEXA-nick -OT2CCGGTTCTTAGCTCTGCTGTCCTGTGTTACCCATGAGC242HEXA-nick -OT3AATTAATGGGGAGAGGGAGCGGTATAGGCCATCGGAGTCT242HEXA-nick-OT4GTTCCAGATGCCCACTCTGCGTGGTCAGAGTAGCCAAGGC247HEXA-nick-OT5GGCACTGTGGCTTCCTGTTCCTTCCAAGCTCACCCACGTG234HEXA-nick-OT6GTACCTGAGCTTAGGAGGGATTCCCCTCCAGAGACACATGT252HEXA-nick-OT7CCAAGATATGGCCAAACAGATGTTCAGTCCTGACATGGC220HEXA-nick-OT8GGCLGGTTGGCCAAACAGGCGCACTCCGCCCACCCC228	HEXA-peg-OT3	GAGAGGTGTGATGCAGTGAC		244
InEXA-peg-OT5TTCTTACCATCTGGTGGACAGTGCTTAAATTCATCCTGC203HEXA-peg-OT6CACCCCACATTCTTCTTACCTCCTGCAGTAGTGTCAGAGC201HEXA-peg-OT7ACTTACTCCACTGGCTTGCCAGCAGTCCAAAGTGACTGAC233HEXA-peg-OT8CCCGGGGTGATTTTCTCCAGCTTGGTCTTACCCAGCAGGCC221HEXA-nick-OT1GGAGACTAGGAAAGTCAGAGACCTTGAGGAGGCCAGGAGAA269HEXA-nick-OT2CCGGTTCTTAGCTGCTGCTCCTGTGTTACCCATGATGC249HEXA-nick-OT3AATTAATGGGGAGAGGGAGCGGTGATAGGCATCGGAGGC247HEXA-nick-OT4GTTCCAGATGCCCACTCTGCGTGGTCAGAGTAGCCAAGGC234HEXA-nick-OT6GGACCTGTGGCTTCCTGTTCCTTCCCAAGCTCACCCACGTG234HEXA-nick-OT7CCAGGATATGGGCTAGCGGGATGTTCAGTCCTGACCTGC220HEXA-nick-OT7CCAAGATATGGCCAACAGGCGCTGCTCCTGCC228	HEXA-peg-OT4	CCCAGATTACAGTCCAATCC	GGCTGTGACTITATCATCCG	247
HEXA-peg-OT6CACCCCACATTCTTCTTACCTCCTGCAGTAGTGTCAGAGC201HEXA-peg-OT7ACTTACTCCACTGGCTTGCCAGCAGTCCAAAGTGACTGAC233HEXA-peg-OT8CCCGGGTGATTTTCTCCAGCTTGGTCTTACCCAGCAGGCC221HEXA-nick-OT1GGAGACTAGGAAAGTCAGAGACCTTGAGGAGGCAGGAGAA269HEXA-nick -OT2CCGGTTCTTAGCTCTGCTGTCCTGTGTTACCCCATGATGC249HEXA-nick -OT3AATTAATGGGGAGAGGGAGCGGTATAGGCCATCGGAGTCT242HEXA-nick-OT4GTTCCAGATGCCCACTCTGCGTGGTCAGAGTAGCCAAGGC247HEXA-nick-OT5GGCACTGTGGCTTCCTGTTCCTTCCAAGCTCACCCACGTG234HEXA-nick-OT6GTACCTGAGCTTAGGAGGATTCCCCTCAGAGACACATGT252HEXA-nick-OT7CCAAGATATGGCCTAGCGTGATGTTCAGTCCTGACCCACTG220HEXA-nick-OT8GGCTGGTTTGGCGCAACCAGGGCAGCTCTGGCGCCC228	HEXA-peg-OT5	TTCTTACCATCTGGTGGACA	GTGCTTAAAATTCATCCTGC	203
HEXA-peg-017ACTACTCCACTGGCTTGCCAGCAGTCCAAAGTGACTGAC233HEXA-peg-018CCCGGGTGATTTTCTCCAGCTTGGTCTTACCCAGCAGGCC221HEXA-nick-011GGAGACTAGGAAAGTCAGAGACCTTGAGGAGGCAGGAGAA269HEXA-nick -012CCGGTTCTTAGCTCTGCTGTCCTGTGTTACCCCATGATGC249HEXA-nick -013AATTAATGGGAGAGGGAGCGGTATAGGCCATCGGAGTCT242HEXA-nick-014GTTCCAGATGCCCACTCTGCGTGGTCAGAGTAGCCAAGGC247HEXA-nick-015GGCACTGTGGCTTCCTGTTCCTTCCAAGCTCACCCACGTG234HEXA-nick-016GTACCTGAGCTTAGGAGGGAGTTCCCCTCAGAGACACATGT252HEXA-nick-017CCAAGATATGGGCTAGCGTGATGTTCAGCTCTGCACATGGC220HEXA-nick-018GGCTGGTTGGCTTAGCCAAGGCGCGCCATCTGGCCACCC228	HEXA-peg-OT6		TCCTGCAGTAGTGTCAGAGC	201
HEXA-peg-OT8CCCGGGTGATTTTCTCCAGCTTGGTCTACCCAGCAGGCC221HEXA-nick-OT1GGAGACTAGGAAAGTCAGAGACCTTGAGCAGGAGGAGGAGA269HEXA-nick -OT2CCGGTTCTTAGCTCTGCTGTCCTGTGTTACCCCATGATGC249HEXA-nick -OT3AATTAATGGGGAGGGGGGCGGTATAGGCCATCGGAGTCT242HEXA-nick-OT4GTTCCAGATGCCCACTCTGCGTGGTCAGAGTAGCCAAGGC247HEXA-nick-OT5GGCACTGTGGCTTCCTGTTCCTTCCAGGTCACCCACGTG234HEXA-nick-OT6GTACCTGAGCTTAGGAGGGATTCCCCTCAGAGACACATGT252HEXA-nick-OT7CCAAGATATGGGCTAGCGTGATGTCAGTCCTGACATGGC220HEXA-nick-OT8GGCCGGTTTGGCCCACGG228	HEXA-peg-OT7	ACTTACTCCACTGGCTTGCC		233
HEXA-nick-OT1GGAGACTAGGAAAGTCAGAGACCTTGAGGAGGCAGGAGAA269HEXA-nick-OT2CCGGTTCTTAGCTCTGCTGTCCTGTGTTACCCCATGATGC249HEXA-nick-OT3AATTAATGGGGAGAGGGAGCGGTATAGGCCATCGGAGTCT242HEXA-nick-OT4GTTCCAGATGCCCACTCTGCGTGCCAGAGTAGCCAAGGC247HEXA-nick-OT5GGCACTGTGGCTTCCTGTTCCTTCCAAGCTCACCCACGTG234HEXA-nick-OT6GTACCTGAGCTTAGGAGGGATTCCCCTCAGAGACCACTGT252HEXA-nick-OT7CCAAGATATGGGCTAGCGTGATTGCTCAGGTCCTGACATGGC220HEXA-nick-OT8GGCTGGTTTGACCCAAGC228	HEXA-peg-OT8			200
HEXA-nick OT2 CCGGTTCTAGCTCTGCTGT CCTGTGTTACCCCATGATGC 249 HEXA-nick -OT3 AATTAATGGGGAGAGGGAGC GGTATAGGCCATCGGAGTCT 242 HEXA-nick-OT4 GTTCCAGATGCCCACTCTGC GTGGCAGAGGCAGC 247 HEXA-nick-OT5 GGCACTGTGGCTTCCTGTTC CTTCCCAGGCTCACCCAGTG 234 HEXA-nick-OT6 GTACCTGAGCTTAGGAGGGA TTCCCCTCAGAGACCACTGT 252 HEXA-nick-OT7 CCAAGATATGGGCTAGCGTG ATGTTCAGTCCTGACATGGC 220 HEXA-nick-OT8 GGCTGGTTTGACCCAAGCG 228	HEXA-nick-OT1			269
HEXA-nick OT2 CONTRACTOR CONTRACTON CONTRACTOR CONTRA	HEXA-nick-OT2			203
HEXA-nick-OT4 GTTCCAGATGCCCACTCTGC GTGGTCAGAGTAGCCAAGGC 247 HEXA-nick-OT5 GGCACTGTGGCTTCCTGTTC CTTCCCAGGCTCACCCACGTG 234 HEXA-nick-OT6 GTACCTGAGCTTAGGAGGGA TTCCCCTCAGAGACCACTGT 252 HEXA-nick-OT7 CCAAGATATGGGCTAGCGTG ATGTTCAGTCCTGACATGGC 220 HEXA-nick-OT8 GGCTGGTTTGACCCAAGGC 228	HEXA-nick -OT3	AATTAATGGGGAGAGGGAGG	GGTATAGGCCATCGGAGTCT	242
HEXA-nick-OT5 GGCACTGTGGCTTCCTGTTC CTTCCAAGCTCACCCACGTG 234 HEXA-nick-OT6 GTACCTGAGCTTAGGAGGGA TTCCCCTCAGAGACACTGT 252 HEXA-nick-OT7 CCAAGATATGGGCTAGCGTG ATGTTCAGTCCTGACATGGC 220 HEXA-nick-OT8 GGCTGGTTTGACGCCAAACAG GGCAGTCATCTGGTGCCGATC 228	HEXA-nick-OT4	GTTCCAGATGCCCACTCTCC		247
HEXA-nick-OT6 GTACCTGAGCTTAGGAGGGA TTCCCCTCAGAGACACATGT 252 HEXA-nick-OT7 CCAAGATATGGGCTAGCGTG ATGTTCAGTCCTGACATGGC 220 HEXA-nick-OT8 GGCTGGTTTGACGCCAAACAG GGCAGTCATCTGGTGCCGATC 228	HEXA-nick-OT5	GGCACTGTGGCTTCCTGTTC		234
HEXA-nick-OT7 CCAAGATATGGGCTAGCGTG ATGTTCAGTCCTGACATGGC 220 HEXA-nick-OT8 GGCTGGTTTGACGCAAACAG GGCAGTCATCTGGTGCGATC 228	HEXA-nick-OT6	GTACCTGAGCTTAGGAGGGA	TTCCCCTCAGAGACACATGT	252
	HEXA-nick-OT7	CCAAGATATGGGCTAGCGTG	ATGTTCAGTCCTGACATGGC	220
	HEXA-nick-OT8	GGCTGGTTTGACGCAAACAG	GGGAGTCATCTGGTGCGATC	228

NO. Forward primer Reverse primer qPCR-RIT1 TGCTACAGCAGCTACCAACT CGACTCGGTGCCACTTTTC qPCR-EMX1 AGGGCTCCCATCACATCAAC CGACTCGGTGCCACTTTTC	Supplementary Table 6: Primers used for pegRNA RT-qPCR analysis.			
qPCR-RIT1 TGCTACAGCAGCTACCAACT CGACTCGGTGCCACTTTTC qPCR-EMX1 AGGGCTCCCATCACATCAAC CGACTCGGTGCCACTTTTC	NO.	Forward primer	Reverse primer	
qPCR-EMX1 AGGGCTCCCATCACATCAAC CGACTCGGTGCCACTTTTC	qPCR-RIT1	TGCTACAGCAGCTACCAACT	CGACTCGGTGCCACTTTTC	
	qPCR-EMX1	AGGGCTCCCATCACATCAAC	CGACTCGGTGCCACTTTTC	
	qPCR-Cas9	CTCTGTGGGCTGGGCC	TGCTGTGCCGGTCGG	