

Supplementary Information

An innovative approach using CRISPR-ribonucleoprotein packaged in virus-like particles to generate genetically engineered mouse models

Supplementary Fig. 1 Gene editing efficiencies at human or mouse targets using varying volumes of SpCas9/sgRNA or ABE8e/sgRNA packaged in VLPs in cell lines.

Supplementary Fig. 2 Comparison of embryo editing efficiency using SpCas9/sgRNA RNP alone versus SpCas9/sgRNA RNP packaged in VLPs targeting the *Gata3* gene in mouse embryos.

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Supplementary Fig. 6 Mutation rate distributions in embryos edited via the CRISPR-VIM method.

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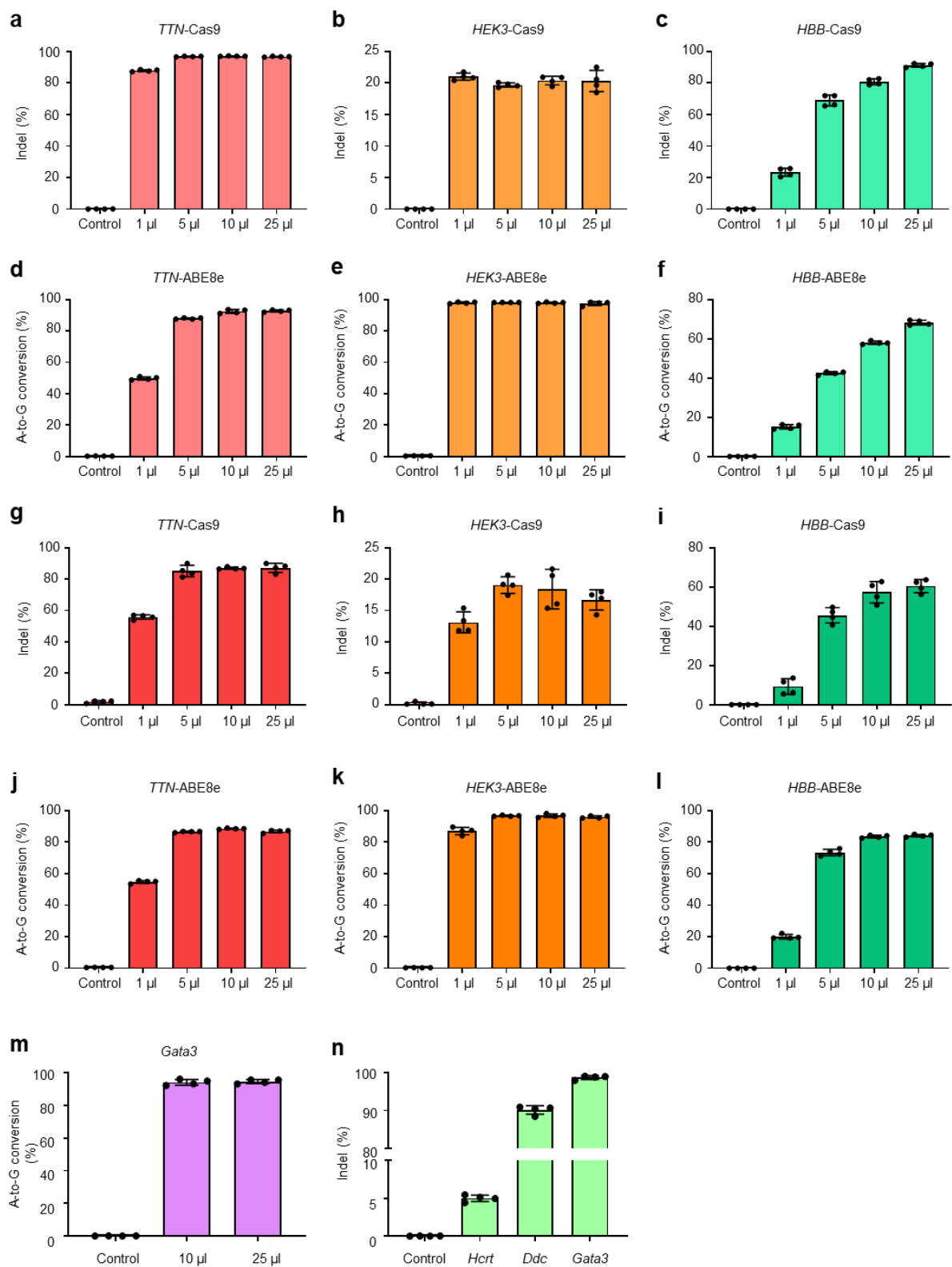
Supplementary Fig. 8 Knock-in or indel mutation efficiencies using the CRISPR-VIM-based HDR strategy in mouse Neuro-2a cells and mESCs.

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Supplementary Fig. 10 Quantification of VLPs for all experimental targets using P30 ELISA.

Supplementary Table 1. Sequences of single guide RNAs targeting human and mouse genomes.

- 22 Supplementary Table 2. Primer sequences for on-target gene editing analysis.
- 23 Supplementary Table 3. Sequences of off-target candidate sites for *Tyr* and *Plin1*.
- 24 Supplementary Table 4. Primer sequences for analyzing off-target effects of *Tyr* and *Plin1*.



Supplementary Fig. 1 Gene editing efficiencies at human or mouse targets using varying volumes of SpCas9/sgRNA or ABE8e/sgRNA packaged in VLPs in cell lines. a-c, g-i, Indel frequencies at *TTN*, *HEK3*, and *HBB* targets in (a-c) HEK293T or (g-i) ARPE19 cells, based on the treatment volume of SpCas9/sgRNA packaged in VLPs. d-f, j-l, A-to-G conversion efficiencies using ABE8e/sgRNA packaged in VLPs in two human cell lines: (d-f) HEK293T or (j-l) ARPE19 cells (n = 4 for all conditions). m, A-to-G conversion frequencies at the *Gata3* locus in mESCs treated with 10 or 25 μ l volumes of ABE8e/sgRNA packaged in VLPs (n = 4 for all conditions). n, Analysis of indel mutations at *Hcrt*, *Ddc*, and *Gata3* genes in mESCs treated with SpCas9/sgRNA packaged in VLPs (n = 4 for all conditions). Source data are provided as a Source Data file.

a

<i>Plin1</i> 10%		Frequency (%)
WT	TCTGTGTGCAATGCCTATGAGAAGGGGTGACAGGGTGCCAGCAAC	
#1M	TCTGTGTGCAATGCCTATGAGAAGGGGTGTACAGGGTGCCAGCAAC	14.3
	TCTGTGTGCAATGCCTATGAGAAGG--GTACAGGGTGCCAGCAAC	13.9
#5F	TCTGTGTGCAATGCCTATGAGA-----AGGGTGCCAGCAAC	2.7
#6M	TCTGTGTGCAATGCCTATGAGAAGG--GTACAGGGTGCCAGCAAC	2.0
#10M	TCTGTGTGCAATGCCTATGAGA-----AGGGTGCCAGCAAC	1.4
#11M	TCTGTGTGCAATGCCTATGAGA-----AGGGTGCCAGCAAC	7.1
	TCTGTGTGCAATGCCTATGAGAAGGGT-TACAGGGTGCCAGCAAC	6.0
#16M	TCTGTGTGCAATGCCTATGAGA-----AGGGTGCCAGCAAC	10.5
#21F	TCTGTGTGCAATGCCTATGAGAAGGGTG--CAGGGTGCCAGCAAC	6.7
#32M	TCTGTGTGCAATGCCTATGAGAAGGT--ACAGGGTGCCAGCAAC	11.8
#42M	TCTGTGTGCAATGCCTATGAGA-----AGGGTGCCAGCAAC	26.0
	TCTGTGTGCAATGCCTATGAGAAGGGGTGTACAGGGTGCCAGCAAC	8.4
#48F	TCTGTGTGCAATGCCTATGAGA-----AGGGTGCCAGCAAC	1.6
#54M	TCTGTGTGCAATGCCTATGA-----TTACAGGGTGCCAGCAAC	19.4
#66M	TCTGTGTGCAATGCCTATGAGAAGGGT-----GGGTGCCAGCAAC	1.8

b

<i>Plin1</i> 20%		Frequency (%)
WT	TCTGTGTGCAATGCCTATGAGAAGGGGTGACAGGGTGCCAGCAAC	
#23F	TCTGTGTGCAATGCCTATGAGA-----AGGGTGCCAGCAAC	6.0
#31M	TCTGTGTGCAATGCCTATGAGA-----AGGGTGCCAGCAAC	21.8
	TCTGTGTGCAATGCCT-----AGGGTGCCAGCAAC	16.5
#41F	TCTGTGTGCAATGCCTATGAGA-----AGGGTGCCAGCAAC	15.1
	TCTGTGTGCAATGCCTATGAGAAGGGGTGTACAGGGTGCCAGCAAC	6.5
	TCTGTGTGCAATGCCTATGAGA-----TACAGGGTGCCAGCAAC	2.9
#47M	TCTGTGTGCAATGCCTATGAGA-----AGGGTGCCAGCAAC	22.0
#52M	TCTGTGTGCAATGCC-----TACAGGGTGCCAGCAAC	4.7
#53M	TC-----AGGGTGCCAGCAAC	44.7
#63F	TCTGTGTGCAATGCCTATGAGAAGG--GTACAGGGTGCCAGCAAC	23.1

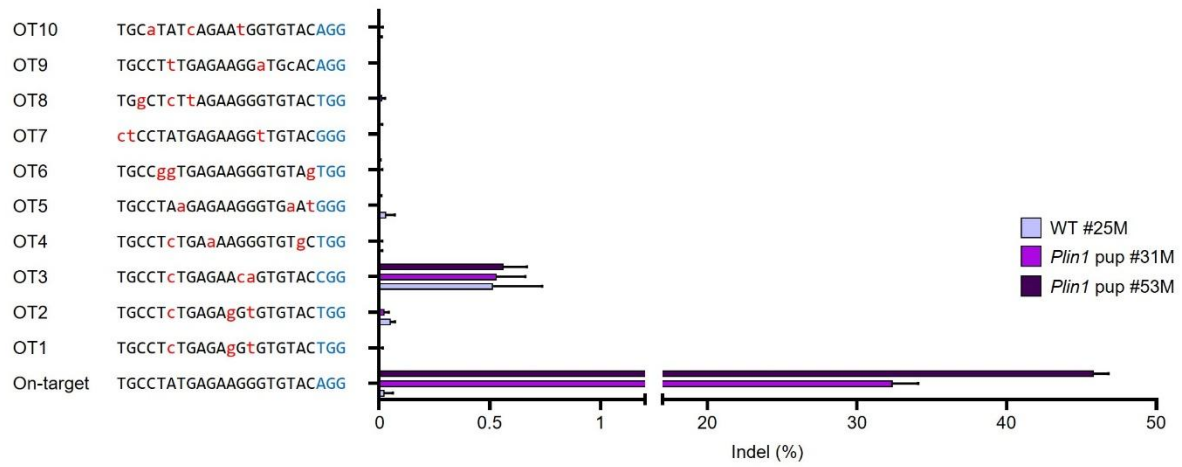
c

<i>Tyr</i> 20%		Frequency (%)
WT	AATGCACCTATCGGCATAACAGAGACTCTTACATGGTTCCTTTTCATACCG	
#2M	AATGCACCTATCGGCCGTGGCGGAGACTCTTACATGGTTCCTTTTCATACCG	42.4
#3F	AATGCACCTGTGGCCGTGGCGGAGACTCTTACATGGTTCCTTTTCATACCG	15.0
	AATGCACCTATCGGCCGTGGCGGAGACTCTTACATGGTTCCTTTTCATACCG	14.9

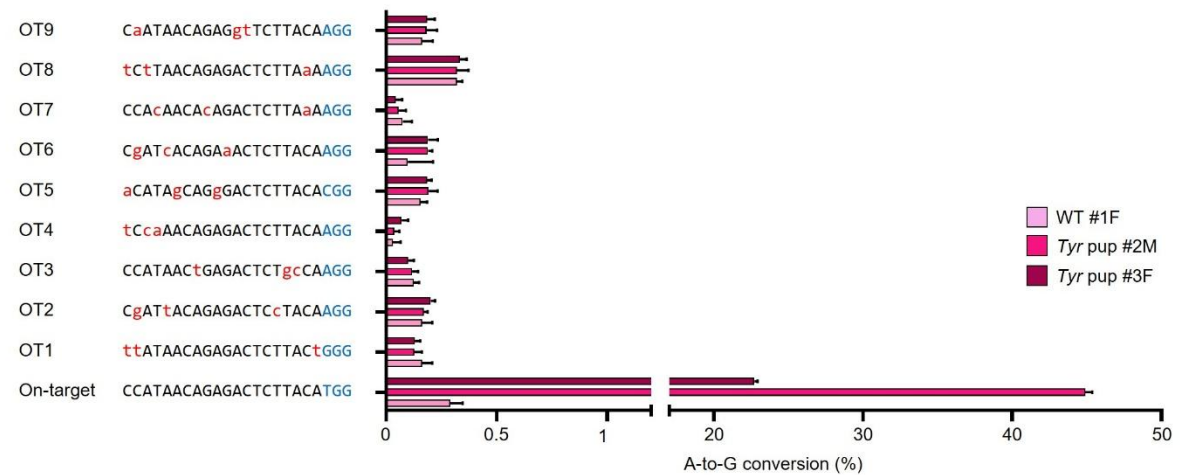
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55 **Supplementary Fig. 3 Mutation patterns in newborn mice generated via the CRISPR-VIM**
56 **method. a, b,** Mutation patterns in pups from mouse zygotes treated with (a) 10% or (b) 20%
57 SpCas9/sgRNA packaged in VLPs targeting *Plin1*. **c,** Mutation patterns of newborn mice with the *Tyr*
58 H420R induced by ABE8e/sgRNA packaged in VLPs. Red letters indicate mutation sites, green letters
59 represent PAM sequences, and the underline indicates the target spacer sequence. The blue letter
60 indicates substitution target A of the H420R mutation at the *Tyr* locus.

a



b

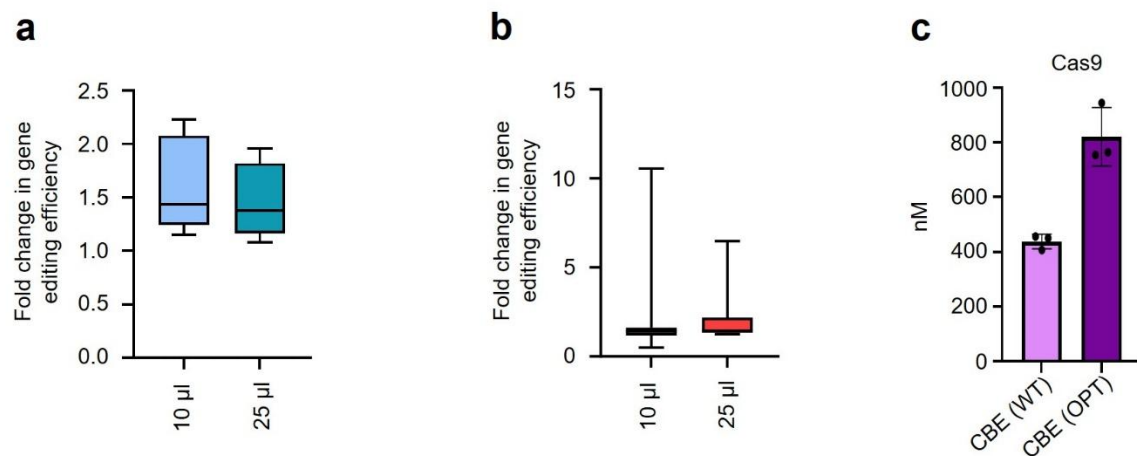


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62 **Supplementary Fig. 4 Off-target effects in *Plin1* and *Tyr* mutant mice generated via CRISPR-**

63 **VIM method. a, b, Off-target effects analyzed by next-generation sequencing in *Plin1*- or *Tyr*-mutant**

64 **mice. Source data are provided as a Source Data file.**



Supplementary Fig. 5 Gene editing efficiency and Cas9 protein quantification of codon-optimized VLPs in Neuro-2a cells. **a**, Fold changes in C-to-T conversion efficiency in human targets. **b**, Fold changes in C-to-T conversion efficiency at mouse target genes. **c**, Cas9 protein levels in VLPs packaged with CBE (WT) and codon-optimized VLPs packaged with CBE (OPT) measured by anti-FLAG or anti MLV(p30) ELISA (n = 3 for condition). Source data are provided as a Source Data file.

a

		Number of edited embryos (%)							Total embryos
Treatment time		< 1%	1~5 %	5~10 %	10~20 %	20~30%	30~40 %	> 40%	
0 h	<i>Tyr</i> -ABE	8 (100.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	8
1 h		54 (96.4)	1 (1.8)	1 (1.8)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	56
5 h		42 (85.7)	1 (2.0)	2 (4.1)	3 (6.1)	1 (2.0)	0 (0.0)	0 (0.0)	49
10 h		29 (78.4)	4 (10.8)	3 (8.1)	1 (2.7)	0 (0.0)	0 (0.0)	0 (0.0)	37
20 h		18 (43.9)	6 (14.6)	8 (19.5)	6 (14.6)	1 (2.4)	1 (2.4)	1 (2.4)	41

b

		Number of edited embryos (%)							Total embryos
Treatment time		< 1%	1~5 %	5~10 %	10~20 %	20~30%	30~40 %	> 40%	
0 h	<i>Plin1</i> -ABE	4 (100.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	4
1 h		35 (94.6)	0 (0.0)	0 (0.0)	0 (0.0)	2 (5.4)	0 (0.0)	0 (0.0)	37
5 h		25 (62.5)	6 (15.0)	4 (10.0)	3 (7.5)	1 (2.5)	0 (0.0)	1 (2.5)	40
10 h		19 (55.9)	7 (20.6)	4 (11.8)	3 (8.8)	0 (0.0)	1 (2.9)	0 (0.0)	34
20 h		12 (25.5)	3 (6.4)	8 (17.0)	8 (17.0)	5 (10.6)	3 (6.4)	8 (17.0)	47

c

		Number of edited embryos (%)							Total embryos
VLP treatment %		< 1%	1~5 %	5~10 %	10~20 %	20~30%	30~40 %	> 40%	
10%	<i>Plin1</i> -ABE	7 (41.2)	1 (5.9)	4 (23.5)	2 (11.8)	0 (0.0)	1 (5.9)	2 (11.8)	17
20%		1 (5.0)	0 (0.0)	2 (10.0)	3 (15.0)	5 (25.0)	3 (15.0)	6 (30.0)	20

d

		Number of edited embryos (%)							Total embryos
VLP treatment %		< 1%	1~5 %	5~10 %	10~20 %	20~30%	30~40 %	> 40%	
10%	<i>Dnmt1</i> -ABE	18 (60.0)	6 (20.0)	2 (6.7)	2 (6.7)	0 (0.0)	2 (6.7)	0 (0.0)	30
20%		7 (29.2)	4 (16.7)	2 (8.3)	3 (12.5)	4 (16.7)	2 (8.3)	2 (8.3)	24

e

		Number of edited embryos (%)							Total embryos
VLP treatment %		< 1%	1~5 %	5~10 %	10~20 %	20~30%	30~40 %	> 40%	
10%	<i>Gata3</i> -ABE	18 (29.5)	5 (8.2)	5 (8.2)	7 (11.5)	4 (6.6)	4 (6.6)	18 (29.5)	61
20%		7 (10.4)	6 (9)	7 (10.4)	12 (17.9)	8 (11.9)	5 (7.5)	22 (32.8)	67

f

		Number of edited pups (%)							Total pups
VLP treatment %		< 1%	1~5 %	5~10 %	10~20 %	20~30%	30~40 %	> 40%	
10%	<i>Plin1</i> -Cas	31 (88.6)	1 (2.9)	1 (2.9)	2 (5.7)	0 (0.0)	0 (0.0)	0 (0.0)	35
20%		24 (88.9)	1 (3.7)	2 (7.4)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	27

g

VLP treatment (+: 10%, ++: 20%)			Number of edited embryos (%)							Total embryos
Sperm	Fertilization	Culture	< 1%	1~5 %	5~10 %	10~20 %	20~30%	30~40 %	> 40%	
-	-	-	<i>Gata3</i> -ABE	20 (100.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	20
-	-	+		3 (20.0)	1 (6.7)	3 (20.0)	3 (20.0)	2 (13.3)	3 (20.0)	15
-	-	++		2 (16.7)	1 (8.3)	1 (8.3)	2 (16.7)	1 (8.3)	2 (16.7)	12
+	+	-		5 (83.3)	0 (0.0)	0 (0.0)	1 (16.7)	0 (0.0)	0 (0.0)	6
+	+	+		1 (11.1)	2 (22.2)	1 (11.1)	3 (33.3)	0 (0.0)	1 (11.1)	9
++	++	-		2 (40.0)	0 (0.0)	1 (20.0)	2 (40.0)	0 (0.0)	0 (0.0)	5
++	++	+		2 (40.0)	0 (0.0)	2 (40.0)	1 (20.0)	0 (0.0)	0 (0.0)	5
++	++	++		2 (40.0)	0 (0.0)	2 (40.0)	1 (20.0)	0 (0.0)	0 (0.0)	5

h

VLP treatment (+: 10%, ++: 20%)			Number of edited embryos (%)							Total embryos
Sperm	Fertilization	Culture	< 1%	1~5 %	5~10 %	10~20 %	20~30%	30~40 %	> 40%	
-	-	-	<i>Plin1</i> -ABE	24 (100.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	24
-	-	+		1 (3.8)	2 (7.7)	5 (19.2)	3 (11.5)	5 (19.2)	4 (15.4)	26
-	-	++		7 (31.8)	3 (13.6)	0 (0.0)	2 (9.1)	1 (4.5)	2 (9.1)	22
+	+	-		20 (83.3)	2 (8.3)	2 (8.3)	0 (0.0)	0 (0.0)	0 (0.0)	24
+	+	+		3 (23.1)	2 (15.4)	2 (15.4)	1 (7.7)	2 (15.4)	1 (7.7)	13
++	++	-		6 (66.7)	1 (11.1)	1 (11.1)	0 (0.0)	1 (11.1)	0 (0.0)	9
++	++	+		0 (0.0)	0 (0.0)	0 (0.0)	2 (40.0)	1 (20.0)	1 (20.0)	5
++	++	++		0 (0.0)	0 (0.0)	0 (0.0)	2 (40.0)	1 (20.0)	1 (20.0)	5

i

		Number of edited pups (%)							Total pups
VLP treatment %		< 1%	1~5 %	5~10 %	10~20 %	20~30%	30~40 %	> 40%	
10%	<i>Tyr-Ex4</i> -ABE	1 (14.3)	0 (0.0)	2 (28.6)	3 (42.9)	1 (14.3)	0 (0.0)	0 (0.0)	7
20%		57 (89.1)	1 (1.6)	1 (1.6)	0 (0)	3 (4.7)	0 (0.0)	2 (3.1)	8

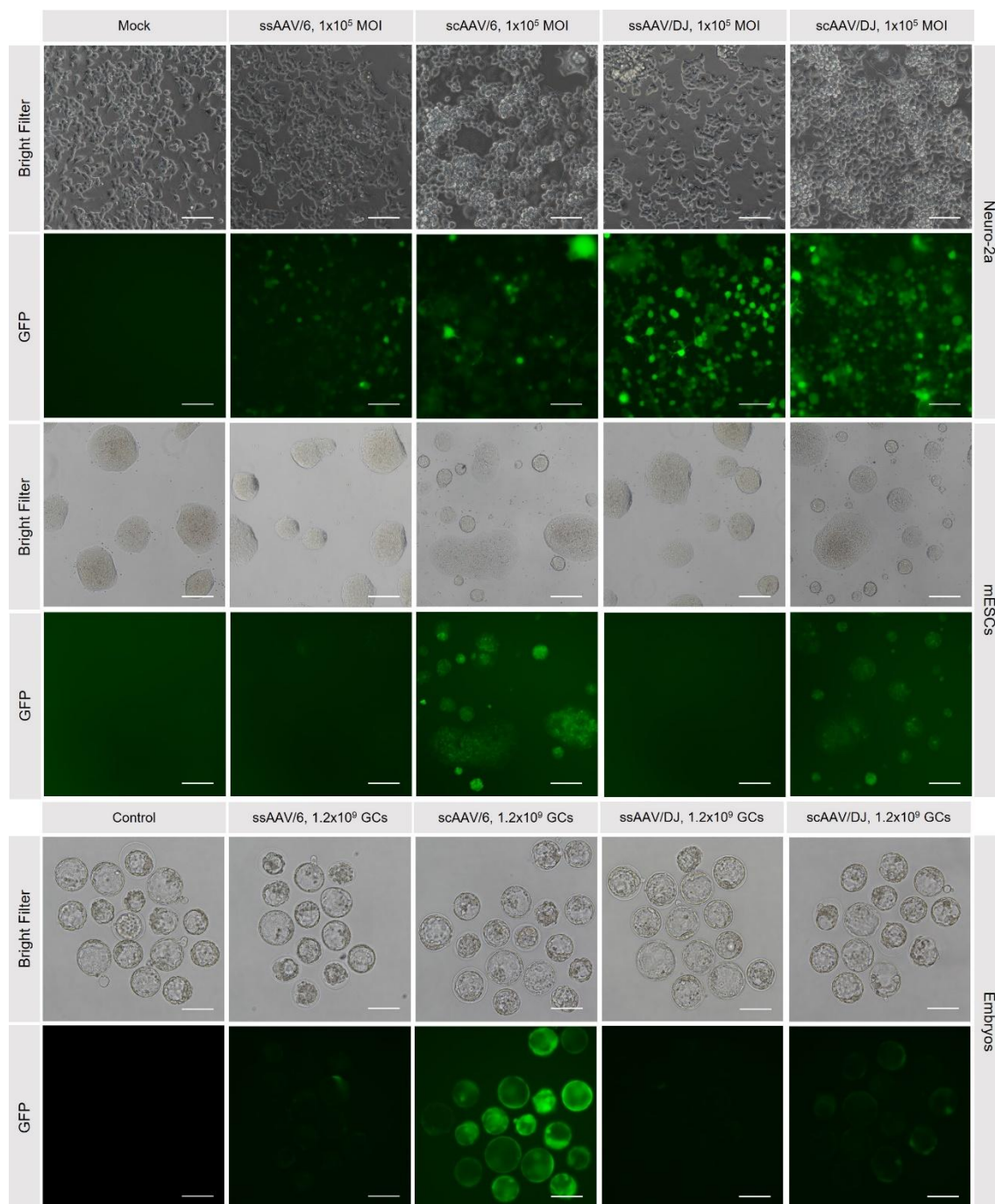
j

		Edited embryo number (%)							Total embryos
VLP treatment %		< 1%	1~5 %	5~10 %	10~20 %	20~30%	30~40 %	> 40%	
10%	<i>Dnmt1</i> -CBE	46 (92.0)	2 (4.0)	2 (4.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	50
20%		31 (96.9)	0 (0.0)	1 (3.1)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	32

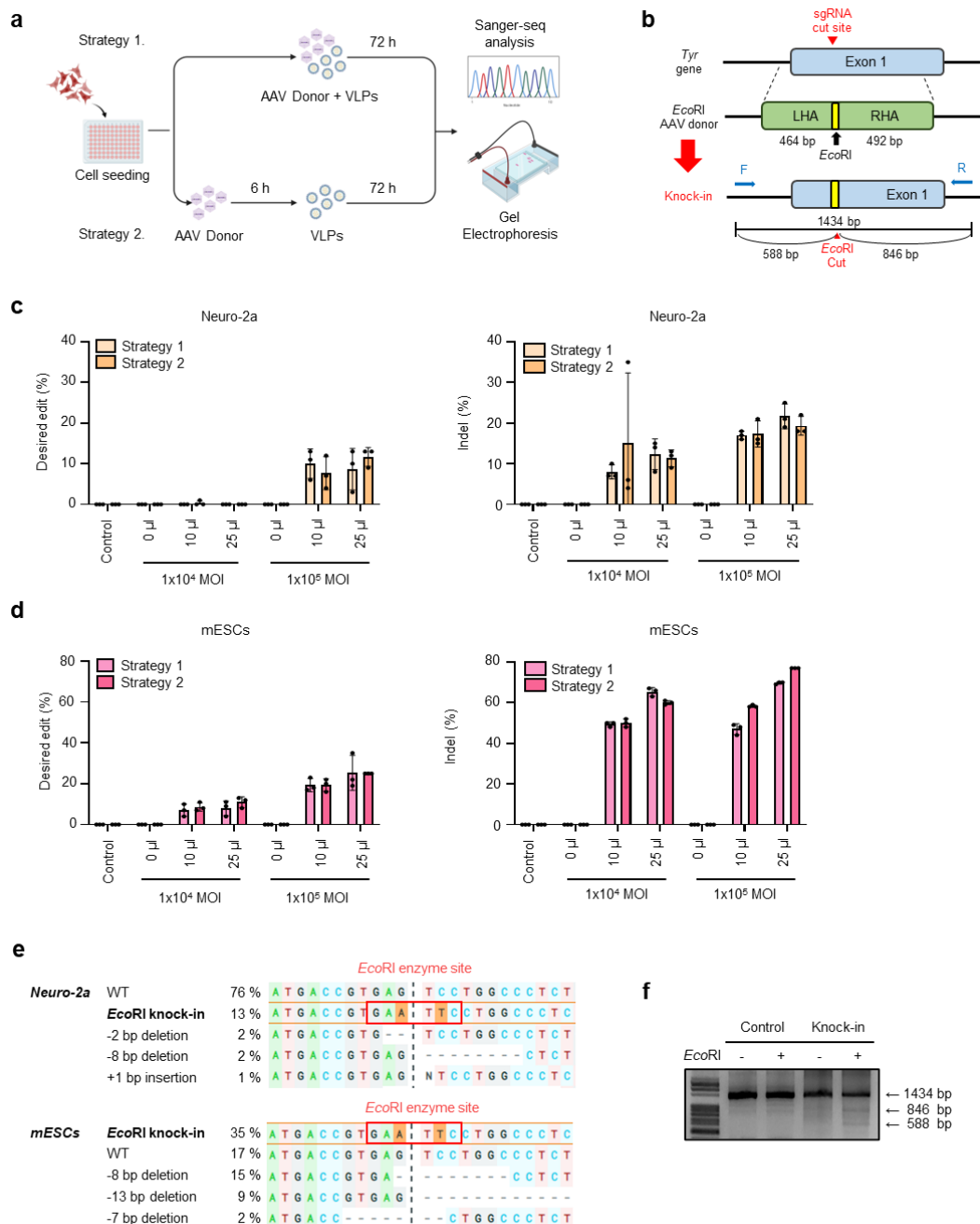
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		Edited embryo number (%)							Total embryos
VLP treatment %		< 1%	1~5 %	5~10 %	10~20 %	20~30%	30~40 %	> 40%	
10%	<i>Hpd</i> -CBE	31 (88.6)	1 (2.9)	1 (2.9)	2 (5.7)	0 (0.0)	0 (0.0)	0 (0.0)	35
20%		24 (88.9)	1 (3.7)	2 (7.4)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	27

Supplementary Fig. 6 Mutation rate distributions in embryos edited via the CRISPR-VIM method. **a, b,** Mutation rate distributions in edited embryos at **(a)** *Tyr* and **(b)** *Plin1* targets, depending on treatment duration (0, 1, 5, 10, and 20 h) with ABE8e/sgRNA in VLPs. **c, d, e,** Mutation rate distributions in edited embryos at **(c)** *Plin1*, **(d)** *Dnmt1*, and **(e)** *Gata3* targets, depending on treatment rates (10% or 20%) with ABE8e/sgRNA in VLPs. **f,** Mutation rate distributions in edited pups at the *Plin1* target, depending on treatment rates (10% or 20%) with SpCas9/sgRNA in VLPs. **g, h,** Mutation rate distributions in edited embryos at **(g)** *Gata3* and **(h)** *Plin1* targets, depending on treatment rates (10% or 20%) with ABE8e/sgRNA in VLPs during IVF process. **i,** Mutation rate distributions in mice born by treatment rates (10% or 20%) with ABE8e/sgRNA in VLPs targeting *Tyr-Ex4* after IVF. **j, k,** Mutation rate distributions in edited embryos using human codon-optimized VLPs with AncBE4max/sgRNA targeting **(j)** *Dnmt1* or **(k)** *Hpd*, depending on the treatment rates (10% or 20%).



Supplementary Fig. 7 Validation of transduction efficiency of AAV6 and DJ serotypes in mouse Neuro-2a cells, mESCs, and embryos through GFP expression. Transduction efficiency of single-stranded AAV (ssAAV) and self-complementary AAV (scAAV) based on GFP expression levels in mouse Neuro-2a cells (Scale bars: 200 μ m), mESCs (Scale bars: 100 μ m), and embryos (Scale bars: 100 μ m) across AAV/6 and AAV/DJ serotypes. Source data are provided as a Source Data file.



Supplementary Fig. 8 Knock-in or indel mutation efficiencies using the CRISPR-VIM-based HDR strategy in mouse Neuro-2a cells and mESCs. **a**, Schematic of the CRISPR-VIM-based HDR strategy using AAV-based donors. In Strategy 1, AAV donors and VLPs are added simultaneously the day after cell seeding. In Strategy 2, the AAV donors are added first and incubated for 6 hours, followed by VLP addition. Created in BioRender. Kim, K. (2025) <https://BioRender.com/m78p943>. **b**, Strategy

103 to insert the *EcoRI* enzyme sequence into exon 1 of the *Tyr* gene. LHA: left homology arm; RHA: right
104 homology arm. **c, d**, Comparison of knock-in and indel mutation efficiencies between two CRISPR-
105 VIM-mediated HDR strategies targeting *Tyr* in mouse Neuro-2a cells and mESCs (n = 3 for all
106 condition). **e**, *EcoRI* knock-in efficiency analyzed by Sanger sequencing. **f**, Verification of *EcoRI* knock-
107 in efficiency in mESCs by in vitro cleavage assay. Source data are provided as a Source Data file.

VLP treatment		No. of examined embryos	No. of two-cell stage embryos (%)	No. of blastocysts (%)	No. of transferred embryos	No. of offspring (%)	Mutant ratio (%)	
Target							No. of desired mutants/total blastocyst (%)	No. of desired mutants/total offspring (%)
0%	-	362	224 (62)	167 (75)	-	-	0/46 (0)	-
	<i>Plin1</i> -ABE8e	50	21 (42)	17 (81)	-	-	10/17 (59)	-
	<i>Dnmt1</i> -ABE8e	50	42 (84)	33 (79)	-	-	12/30 (40)	-
	<i>Gata3</i> -ABE8e	98	70 (71)	65 (93)	-	-	43/71 (61)	-
10%	<i>Plin1</i> -Cas9	594	445 (75)	-	445	68 (15)	-	12/68 (18)
	<i>Dnmt1</i> -CBE	35	28 (80)	24 (86)	-	-	-	-
	<i>Hpd</i> -CBE	98	70 (71)	35 (50)	-	-	-	-
	<i>Plin1</i> -ABE8e	50	28 (56)	20 (71)	-	-	19/20 (95)	-
	<i>Dnmt1</i> -ABE8e	51	33 (65)	24 (73)	-	-	17/24 (71)	-
	<i>Gata3</i> -ABE8e	103	86 (83)	67 (78)	-	-	60/67 (90)	-
20%	<i>Plin1</i> -Cas9	548	322 (59)	-	322	64 (20)	-	7/64 (11)
	<i>Dnmt1</i> -CBE	35	28 (80)	20 (71)	-	-	-	-
	<i>Hpd</i> -CBE	98	66 (67)	27 (40)	-	-	-	-

VLP treatment				No. of examined embryos	No. of two-cell stage embryos (%)	No. of blastocysts (%)	No. of transferred embryos	No. of offspring (%)	Mutant ratio (%)	
Target	Sperm	IVF	Culture						No. of desired mutants/total blastocyst (%)	No. of desired mutants/total offspring (%)
Control	-	-	-	101	74 (73)	39 (53)	-	-	0/33 (0)	-
	-	-	+	40	32 (80)	18 (56)	-	-	12/18 (67)	-
	-	-	++	39	28 (72)	12 (43)	-	-	10/12 (83)	-
	+	+	-	52	23 (44)	6 (26)	-	-	1/6 (17)	-
	+	+	+	51	25 (49)	9 (36)	-	-	8/9 (89)	-
	++	++	-	46	16 (35)	6 (38)	-	-	3/5 (60)	-
	++	++	++	45	13 (29)	5 (38)	-	-	3/5 (60)	-
	-	-	+	55	45 (82)	26 (58)	-	-	25/26 (96)	-
	-	-	++	59	38 (64)	22 (58)	-	-	15/22 (68)	-
	+	+	-	87	54 (62)	24 (44)	-	-	4/24 (17)	-
	+	+	+	88	53 (60)	13 (25)	-	-	10/13 (77)	-
	++	++	-	85	38 (45)	9 (24)	-	-	3/9 (33)	-
	++	++	++	87	37 (43)	5 (14)	-	-	5/5 (100)	-
	-	-	+	30	19 (63)	11 (58)	-	-	6/7 (86)	-
	-	-	++	32	13 (41)	8 (62)	-	-	5/8 (63)	-
	-	-	++	95	46 (48)	-	46	9 (20)	-	2/9 (22)

VLP treatment		No. of examined embryos	No. of two-cell stage embryos (%)	No. of blastocysts (%)	No. of transferred embryos	No. of offspring (%)	Mutant ratio (%)	
Target							No. of desired mutants/total blastocyst (%)	No. of desired mutants/total offspring (%)
0%	-	33	22 (67)	17 (77)	-	-	0	-
5%	<i>Kcnq4</i>	737	501 (68)	8/70 (11)	390	12 (3)	1/8 (13)	1/12 (8)

VLP treatment		No. of examined embryos	No. of two-cell stage embryos (%)	No. of blastocysts (%)	No. of transferred embryos	No. of offspring (%)	Mutant ratio (%)	
Target							No. of desired mutants/total blastocyst (%)	No. of desired mutants/total offspring (%)
Control		81	36 (44)	31 (86)	-	-	0 (0)	-
Combi	<i>Plin1</i> + <i>Kcnq4</i> -Cas	99	63 (64)	31 (54)	-	-	5 (16)	-
Double	<i>Plin1</i> -Cas <i>Kcnq4</i> -Cas	100	61 (61)	44 (72)	-	-	2 (5)	-
Triple	<i>Plin1</i> -Cas <i>Kcnq4</i> -Cas <i>Fgfr3</i> -Cas	99	54 (55)	34 (63)	-	-	3 (9)	-

Supplementary Fig. 9 Embryonic development rates following the application of CRISPR-VIM method. **a, b,** Analysis of embryonic development rates and offspring ratios following the CRISPR-VIM method in **(a)** zygotes and **(b)** IVF. + indicates 10% and ++ indicates 20% VLP treatment of the total medium volume. **c, d,** Evaluation of developmental rates and offspring proportions in mouse embryos resulting from **(c)** the knock-in approach at the *Kcnq4* gene and **(d)** multi-gene targeting.

Cargo protein	Target sgRNA	VLPs/ μ l	Cargo protein	Target sgRNA	VLPs/ μ l
Cas9	<i>Clcn7</i>	2.60×10^8	CBE(WT)	<i>Cftr</i>	4.41×10^8
	<i>Ddc</i>	3.61×10^8		<i>Dip2a</i>	2.69×10^8
	<i>Dnmt1</i>	2.24×10^8		<i>Dnmt1</i>	2.71×10^8
	<i>Fgfr3</i>	3.59×10^8		<i>F9</i>	5.09×10^8
	<i>Fgfr3+Kcnq4</i>	3.96×10^8		<i>Gjb2</i>	4.63×10^8
	<i>Gata3</i>	3.50×10^8		<i>Hpd</i>	5.52×10^8
	<i>Gjb2</i>	2.96×10^8		<i>Kcnq4</i>	4.13×10^8
	<i>Hcrt</i>	1.90×10^8		<i>Rpe65</i>	1.84×10^8
	<i>Igf2</i>	2.01×10^8		<i>Tyr-Ex4</i>	4.03×10^8
	<i>Kcnq4</i>	3.94×10^8		<i>ADAMTS4</i>	3.90×10^8
	<i>Kcnq4-sgRNA1</i>	5.10×10^{10}		<i>CCR5</i>	4.65×10^8
	<i>Kcnq4-sgRNA2</i>	1.45×10^{10}		<i>EIF3D</i>	4.14×10^8
	<i>Kcnq4+Plin1</i>	2.57×10^8		<i>EMX1</i>	4.93×10^8
	<i>Lep</i>	2.43×10^8		<i>HEK3</i>	6.34×10^8
	<i>Nanog</i>	1.54×10^8		<i>MYOCD</i>	4.08×10^8
	<i>Pdgfra</i>	2.26×10^8		<i>RNF2</i>	3.51×10^8
	<i>Plin1</i>	3.00×10^8	CBE(OPT)	<i>Cftr</i>	2.43×10^8
	<i>Tyr-Ex1</i>	2.76×10^8		<i>Dip2a</i>	1.54×10^8
	<i>Tyr-Ex4</i>	1.76×10^8		<i>Dnmt1</i>	4.62×10^8
	<i>HBB</i>	1.84×10^8		<i>F9</i>	3.00×10^8
	<i>HEK3</i>	2.47×10^8		<i>Gjb2</i>	3.61×10^8
	<i>TTN</i>	2.91×10^8		<i>Hpd</i>	4.30×10^8
ABE8e	<i>Dnmt1</i>	2.82×10^8		<i>Kcnq4</i>	1.76×10^8
	<i>Gata3</i>	3.07×10^8		<i>Rpe65</i>	1.84×10^8
	<i>Gata3+Kcnq4</i>	1.25×10^8		<i>Tyr-Ex4</i>	2.47×10^8
	<i>Igf2</i>	2.27×10^8		<i>ADAMTS4</i>	2.13×10^8
	<i>Kcnq4</i>	1.64×10^8		<i>CCR5</i>	2.15×10^8
	<i>Lep</i>	3.02×10^8		<i>EIF3D</i>	1.31×10^8
	<i>Nanog</i>	2.64×10^8		<i>EMX1</i>	1.65×10^8
	<i>Pdgfra</i>	1.97×10^8		<i>HEK3</i>	4.47×10^8
	<i>Plin1</i>	1.78×10^8		<i>MYOCD</i>	3.25×10^8
	<i>Tyr-Ex4</i>	2.27×10^8		<i>RNF2</i>	2.73×10^8
	<i>HBB</i>	1.42×10^8			
	<i>HEK3</i>	2.27×10^8			
	<i>TTN</i>	1.42×10^8			

Supplementary Fig. 10 Quantification of VLPs for all experimental targets using P30 ELISA. P30 ELISA for quantifying VLP concentrations across all experimental targets.

118 **Supplementary Table 1. Sequences of single guide RNAs targeting human and mouse genomes.**

Target	Sequence with PAM (5' to 3')
<i>ADAMTS4</i>	TGGCACCATCAATGGAGATCCGG
<i>CCR5</i>	TGACATCAATTATTATACATCGG
<i>EIF3D</i>	AGACGACCCTGTCATCCGCAAGG
<i>EMX1</i>	GAGTCCGAGCAGAAGAAGAAGGG
<i>HBB</i>	TCAGAAAGTGGTGGCTGGTGTGG
<i>HEK3</i>	GGCCCAGACTGAGCACGTGATGG
<i>MYOCD</i>	ACTTCAACAAAGAAGGACCCAGG
<i>RNF2</i>	GTCATCTTAGTCATTACCTGAGG
<i>TTN</i>	GGTACTTCAGCAGCCTTCACTGG
<i>Cfir</i>	CTTATATCTGTACTCATCATAGG
<i>Cln7</i>	GGGGGATCTTCACCCCATTGAGG
<i>Ddc</i>	AATGAAAGCAGAGCTGCTTCAGG
<i>Dip2a</i>	CATTCAAGGTATGGGCAGCGTGG
<i>Dnmt1</i>	AACAGCTCTGAACGAGACCCCGG
<i>F9</i>	CTACTCAGTACCGAATGTGCAGG
<i>Fgfr3</i>	GAGGCTGGCAGCGTGACGCAGG
<i>Gata3</i>	GTCACCGCCATGGGTTAGAGAGG
<i>Gjb2</i>	ACTTCCCCATCTCTCACATCCGG
<i>Hcrt</i>	TCAGGACAAGGATAGAAGATGGG
<i>Hpd</i>	CAACCCAGAAGGTCACCGAGTGG
<i>Igf2</i>	TATTGGAAGAACTTGCCCACGGG
<i>Kcnq4</i>	CCTATGCCGACTCGCTCTGGTGG
<i>Kcnq4-1</i>	CTGGGTTGAAGCCTGAAAGATGG
<i>Kcnq4-2</i>	GATACAAACAGGTTGCCCATAGG
<i>Lep</i>	CCAGCAGATGGAGGAGGTCTCGG
<i>Nanog</i>	TATGAGACTTACGCAACATCTGG
<i>Pdgfra</i>	ACCCGGAGCGTGTCAGTTACAGG
<i>Plin1</i>	TGCCTATGAGAAGGGTGACAGG
<i>Rpe65</i>	GTCTCCTCCGATGTGGGCCAGGG
<i>Tyr-Ex1</i>	GGGTGGATGACCGTGAGTCCTGG
<i>Tyr-Ex4</i>	CCATAACAGAGACTCTTACATGG

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Supplementary Table 2. Primer sequences for on-target gene editing analysis.

Target	1 st PCR		2 nd PCR	
	Forward (5' to 3')	Reverse (5' to 3')	Forward (5' to 3')	Reverse (5' to 3')
<i>ADAMTS4</i>	GGAGATCGTGTTCCTCA GAGAAG	GAACGGCCAGAAGTG TAAGT	ACACTCTTTCCCTACACGACGCT CTTCCGATCTGGCTGACAGTGC AGTACC	GTGACTGGAGTTCAGACGTGTG CTCTTCCGATCTACTCTTCCGGC GTAGGAT
<i>CCR5</i>	AGAGCCAAGCTCTCC ATCTA	GAAGATTCCAGAGAA GAAGCCTATAA	ACACTCTTTCCCTACACGACGCT CTTCCGATCTCATTCATGGAGGG CAACTAAATAC	GTGACTGGAGTTCAGACGTGTG CTCTTCCGATCTAAGATGAACAC CAGTGAGTAGAG
<i>EIF3D</i>	GTTGTGCTTGCTGTGT TCTATG	GCTTCAGATGCTTTCA CCTTTG	ACACTCTTTCCCTACACGACGCT CTTCCGATCTATGTCTTTGCCTG CTCTTCC	GTGACTGGAGTTCAGACGTGTG CTCTTCCGATCTAAGCCGACAGC ATTCCTAAC
<i>EMX1</i>	CAGCTCTGTGACCCTT TGTT	TGCTTGTCCTCTGTG AATG	ACACTCTTTCCCTACACGACGCT CTTCCGATCTCTGGCCAGGTGA AGGT	GTGACTGGAGTTCAGACGTGTG CTCTTCCGATCTCGTGGGTTTG TGGTTGC
<i>HBB</i>	CTCTTTCTTTAGGGC AATAATGATAC	GGCAGAATCCAGATGC TCAA	ACACTCTTTCCCTACACGACGCT CTTCCGATCTACCTCTTATCTTCC TCCCACA	GTGACTGGAGTTCAGACGTGTG CTCTTCCGATCTAGTTGGACTTA GGGAACAAAGG
<i>HEK3</i>	GTTGAGCTCGACCCTG AAG	GGCATGAGAAACCTT GGAGA	ACACTCTTTCCCTACACGACGCT CTTCCGATCTCCAACTTGTCAG CCAGTATCC	GTGACTGGAGTTCAGACGTGTG CTCTTCCGATCTGCATGCATTG TAGGCTTGA
<i>MYOCD</i>	CAGAGTGTAGAGAGA GAGAGCA	CCCTGAGAACAAATCC ACTACA	ACACTCTTTCCCTACACGACGCT CTTCCGATCTTGAATGATATTTA GCCCAACTCAC	GTGACTGGAGTTCAGACGTGTG CTCTTCCGATCTTGGCTTAAAC TAAATGACCTCTG
<i>RNF2</i>	CATAACCTGATCACCT CCCAAA	AGGACTTGCCCAACTT TCTAC	ACACTCTTTCCCTACACGACGCT CTTCCGATCTTGCAGACAAACG GAACTCAA	GTGACTGGAGTTCAGACGTGTG CTCTTCCGATCTGCCAACATACA GAAGTCAGGAA
<i>TTN</i>	CTGCCTGCCAGAACT ACA	TCTGAACTCCAGGACT GACT	ACACTCTTTCCCTACACGACGCT CTTCCGATCTTTTGTGCGGAGAAG ACTCCATTC	GTGACTGGAGTTCAGACGTGTG CTCTTCCGATCTCTGTTACCTT TACCTTTCCTTTC
<i>Cln7</i>	GCAGAACCTGCTCTGT GTATAG	CCAGATGTGGAGAAG GATCAAG	ACACTCTTTCCCTACACGACGCT CTTCCGATCTCCCTTACTTTACC TGCTCAATTGG	GTGACTGGAGTTCAGACGTGTG CTCTTCCGATCTGGAGAAAGGAT CAAGCAAAGAC
<i>Ddc</i>	GTCTACCCTCTCTAGG TGTTACT	GCTTTGGTCAGTGCTG TTTG	ACACTCTTTCCCTACACGACGCT CTTCCGATCTCTCGCACTGTGGA GTCTG	GTGACTGGAGTTCAGACGTGTG CTCTTCCGATCTCACAGCCACTC AGCACTAA
<i>Dip2a</i>	CTGGGAAGGCAGAGA AGAAA	CCCAAGACCTATCCCA TGTTAG	ACACTCTTTCCCTACACGACGCT CTTCCGATCTTCCCATGTTGTA GGTGACATC	GTGACTGGAGTTCAGACGTGTG CTCTTCCGATCTCCCATGTTAGC AAGGGTTCTAC
<i>Dnmt1</i>	TGGCAAGCAAACCAG AGT	TGGCGCCAACAGCTA AG	ACACTCTTTCCCTACACGACGCT CTTCCGATCTTCCCTTCGGGCA TAGCAT	GTGACTGGAGTTCAGACGTGTG CTCTTCCGATCTCTCGGGCTGGA GCTGTT
<i>F9</i>	CAAAGATACACCGAG GGAGATG	CCACAAGCCCTGTAAA TGTAAT	ACACTCTTTCCCTACACGACGCT CTTCCGATCTAACACCGTCATGG CAGAAT	GTGACTGGAGTTCAGACGTGTG CTCTTCCGATCTGACGTGCTTCC TGCTACAATA
<i>Fgf3</i>	CTTGGTGTGGAAACAT GAATCT	CTAGCTGCTCGGACTT CTATAC	ACACTCTTTCCCTACACGACGCT CTTCCGATCTTCTTCTCCAAGTA TCCCAGGT	GTGACTGGAGTTCAGACGTGTG CTCTTCCGATCTGCCACCACAG GATGAAG
<i>Gata3</i>	ATCCCTGAGCCACATC TCT	CCGGATTCACTGGTTG GAAT	ACACTCTTTCCCTACACGACGCT CTTCCGATCTCACTCCAGCCACA TGCT	GTGACTGGAGTTCAGACGTGTG CTCTTCCGATCTGTGCTTTCCGG GCTTCA
<i>Gjb2</i>	CTCCACCAGCATTGGA AAGA	AAAGATGACCCGGAA GAAGATG	ACACTCTTTCCCTACACGACGCT CTTCCGATCTTATGCTACGACCA CCACTTC	GTGACTGGAGTTCAGACGTGTG CTCTTCCGATCTGATACGGACCT TCTGGGTTT
<i>Hcrt</i>	GTATCCTGACTCTGGG AAAGC	AGTCACACCAACAGA GAATCG	ACACTCTTTCCCTACACGACGCT CTTCCGATCTTAGAGCCACATCC CTGCTC	GTGACTGGAGTTCAGACGTGTG CTCTTCCGATCTACACCAACAGA GAATCGTCTTTAT
<i>Hpd</i>	GTGGTCACCCATACTG TTCTC	CAGAGGTTCAAAGCC CATCT	ACACTCTTTCCCTACACGACGCT CTTCCGATCTTTGGGCTTGAGG CTGA	GTGACTGGAGTTCAGACGTGTG CTCTTCCGATCTGAGGCCCTTTG GCTTGT
<i>Igf2</i>	GTGAGACAAAGAGAC CACTCAC	CTCAAGAGGAGGTCA CAGATTG	ACACTCTTTCCCTACACGACGCT CTTCCGATCTTAGATGGGAGCTC AGGCTAA	GTGACTGGAGTTCAGACGTGTG CTCTTCCGATCTGACGTTGGCC TCTCTGAA
<i>Kcnq4</i>	GCCTGAAAGATGGAG CAAGA	CCACAGCCTTAGTGTG AAGAG	ACACTCTTTCCCTACACGACGCT CTTCCGATCTTGATCACCAGCTG	GTGACTGGAGTTCAGACGTGTG CTCTTCCGATCTTAGGAAGACA

			GTACAT	GAACCTGGGAAG
<i>Lep</i>	TGGCTCGGAATGAAC AGAAA	CTTTGGATGGGTGGTC TACAG	ACACTCTTTCCCTACACGACGCT CTTCCGATCTCCCAATTCTGAGTT TGTCCAAGAT	GTGACTGGAGTTCAGACGTGTG CTCTTCCGATCTTTCCAGGACGC CATCCA
<i>Nanog</i>	AGGACTTTCTGCAGCC TTAC	TGGTGGCTCACAACC ATAC	ACACTCTTTCCCTACACGACGCT CTTCCGATCTACTAGGGAAAGC CATGCG	GTGACTGGAGTTCAGACGTGTG CTCTTCCGATCTGTGTCTGAAGA CAGCTACAGTG
<i>Pdgfra</i>	GTTCCAGTAGTTCCAC CTTCAT	ACTCTCTTGTCCATCC ATTTCC	ACACTCTTTCCCTACACGACGCT CTTCCGATCTCATCGACATGATG GATGACATTG	GTGACTGGAGTTCAGACGTGTG CTCTTCCGATCTGCCTCGGGAAC TTTCTCTC
<i>Plin1</i>	GGAAAGGACCACAGT TCTATCA	CACATACCCACAAGCC TCTATC	ACACTCTTTCCCTACACGACGCT CTTCCGATCTTTCTTTGCTGACA GGAGCAG	GTGACTGGAGTTCAGACGTGTG CTCTTCCGATCTAGTCTATGAGG ACTCACACTGG
<i>Rpe65</i>	TCCTGACACTTATCCC TGTATCT	GTCATGGACTTACCTT CTGTGG	ACACTCTTTCCCTACACGACGCT CTTCCGATCTGTTCTGTCTATAG GTAAGCTGACAA	GTGACTGGAGTTCAGACGTGTG CTCTTCCGATCTGCCCTCCTTGA AGTCAAAC
<i>Tyr-Ex1</i>	AGTGCTATTCAAACCA TCCAGTAA	ACCTTTGCTATTTACC AACAATGC	TCAGAATCTAGATGTTTCATGAC CT	GTGAACCAATCAGTCCTTGTTTA TAG
<i>Tyr-Ex4</i>	CCTCACACTACTTCTG ATGAATGA	CCCACATTGCATTCCA TAGTTC	ACACTCTTTCCCTACACGACGCT CTTCCGATCTTCTGACTCTGAG TAACCCTTC	GTGACTGGAGTTCAGACGTGTG CTCTTCCGATCTGACTCTTGGAG GTAGCTGTAGT
<i>Tyr-Ex1</i> (1434 bp)	TCAGAATCTAGATGTT TCATGACCT	GTGAACCAATCAGTCC TTGTTTATAG		
<i>Kcnq4</i> (680 bp)	AACCTGGGCTTCTGTT CTTC	CTTGGTTCCTCTCACC TTTCTC		
<i>Kcnq4</i> (985 bp)	CCCTTCTGTGTCATCG GTATAAA	CCACACGGGAAAGGG ATAAA		
<i>Kcnq4</i> (3929 bp)	AACACTTCCTTGGGAC CTTAAA	ACCAGAGCAGGGAGA TATAGAA		
<i>Kcnq4</i> (2046bp)	TTTATCCCTTTCCCGTG TGG	CCTTTGGGTGCCTCTT GT		

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124 **Supplementary Table 3. Sequences of off-target candidate sites for *Tyr* and *Plin1*.**

Target	Sequence with PAM (5' to 3')
<i>Tyr</i> -OT1	ttATAACAGAGACTCTTACtGGG
<i>Tyr</i> -OT2	CgATtACAGAGACTCcTACAAGG
<i>Tyr</i> -OT3	CCATAACtGAGACTCTgcCAAGG
<i>Tyr</i> -OT4	tCcaAACAGAGACTCTTACAAGG
<i>Tyr</i> -OT5	aCATAgCAGgGACTCTTACACGG
<i>Tyr</i> -OT6	CgATcACAGAAcACTCTTACAAGG
<i>Tyr</i> -OT7	CCAcAACAcAGACTCTTAaAAGG
<i>Tyr</i> -OT8	tCtTAACAGAGACTCTTAaAAGG
<i>Tyr</i> -OT9	CaATAACAGAGgtTCTTACAAGG
<i>Plin1</i> -OT1	TGCCTcTGAGAgGtGTGTACTGG
<i>Plin1</i> -OT2	TGCCTcTGAGAgGtGTGTACTGG
<i>Plin1</i> -OT3	TGCCTcTGAGAAcaGTGTACCGG
<i>Plin1</i> -OT4	TGCCTcTGAAaAAGGGTGTgCTGG
<i>Plin1</i> -OT5	TGCCTAaGAGAAGGGTGaAtaGGG
<i>Plin1</i> -OT6	TGCCggTGAGAAGGGTGTAgtGG
<i>Plin1</i> -OT7	ctCCTATGAGAAGGtTGTACGGG
<i>Plin1</i> -OT8	TGgCTcTtAGAAGGGTGTACTGG
<i>Plin1</i> -OT9	TGCCTtTGAGAAGGaTGcACAGG
<i>Plin1</i> -OT10	TGCaTATcAGAAtGGTGTACAGG

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Supplementary Table 4. Primer sequences for analyzing off-target effects of *Tyr* and *Plin1*.

Target	1st PCR		2nd PCR	
	Forward (5' to 3')	Reverse (5' to 3')	Forward (5' to 3')	Reverse (5' to 3')
<i>Tyr</i> -OT1	GGGTGTCATTCCTC AGTTCTTT	CCCACAAGTAATTC TCTCCTGATAC	ACACTCTTTCCTACACGACGCT CTTCCGATCTTCTGGGTGTGGA ATTACAGG	GTGACTGGAGTTCAGACGTGTG CTCTCCGATCTACCAGAGAAAG CTGATGGTAAG
<i>Tyr</i> -OT2	CCAAAGTATGTACA CAGTTGCTT	TCAGCAGGAATTCT GGTTCTC	ACACTCTTTCCTACACGACGCT CTTCCGATCTGACTTGTGTGGA AAGAGCAAAG	GTGACTGGAGTTCAGACGTGTG CTCTCCGATCTGTTTGAAGGTT ACCCGTACA
<i>Tyr</i> -OT3	ACAACAGGCACAG GATTAGG	GCTGCAGAGACTCT TGATTGA	ACACTCTTTCCTACACGACGCT CTTCCGATCTCAACAGGCACAG GATTAGGA	GTGACTGGAGTTCAGACGTGTG CTCTCCGATCTCCTGCTACGTA GATGGCATA
<i>Tyr</i> -OT4	GGGAAGTAATCAGT CGCAGAG	GTCTGGCAAGCAA ACCTAGA	ACACTCTTTCCTACACGACGCT CTTCCGATCTCCCAACAACTGT GGGAAATAAA	GTGACTGGAGTTCAGACGTGTG CTCTCCGATCTTGTAAAGAGCAT CGAGCCATTT
<i>Tyr</i> -OT5	TAACAGAAGCCTCT TGTTCCT	CAGCCATACCTCTG GTCAAA	ACACTCTTTCCTACACGACGCT CTTCCGATCTTAAAGGTCAGCTGG GTCCATTAG	GTGACTGGAGTTCAGACGTGTG CTCTCCGATCTAGAAAAGAGCA GAGGAGAGAA
<i>Tyr</i> -OT6	GCATTGGCAGCAG GAATAAAT	GCGGTACTACTTGA GAAGATTAG	ACACTCTTTCCTACACGACGCT CTTCCGATCTCTATTGCTGTGAA GAGATGCC	GTGACTGGAGTTCAGACGTGTG CTCTCCGATCTGGAAGTATGAC CTTGCTGGAG
<i>Tyr</i> -OT7	CTTGTTGGTGCTGGA GATCAA	CGAAGCTCTTTAGA GGAGCATAA	ACACTCTTTCCTACACGACGCT CTTCCGATCTGTGGTGTGGAGA TCAAACCT	GTGACTGGAGTTCAGACGTGTG CTCTCCGATCTGCTTCTCTACTT CCCAAGTTCTC
<i>Tyr</i> -OT8	TGAGGAGTCCCAG TTCTGA	GGCTGGATTGTGG GTAGAT	ACACTCTTTCCTACACGACGCT CTTCCGATCTTGCTCCTGCCACA TAATAGTC	GTGACTGGAGTTCAGACGTGTG CTCTCCGATCTGGCTGGATTG TGGGTAGAT
<i>Tyr</i> -OT9	GCATGAATGAGGCT TTGTTCTC	TCGGAGGACCCTG GATTT	ACACTCTTTCCTACACGACGCT CTTCCGATCTGTGTAGGTGCATG GAGGTATTAG	GTGACTGGAGTTCAGACGTGTG CTCTCCGATCTGGCTTACAGAT GGGTGCTTTT
<i>Plin1</i> -OT1	CCCATTGAGGCTGC AGTTAT	CATGGACAGGTGGT GTAGAAAG	ACACTCTTTCCTACACGACGCT CTTCCGATCTACTGTGTTCCAGC CCTTTG	GTGACTGGAGTTCAGACGTGTG CTCTCCGATCTCTGCACACTAC TGACCATGAC
<i>Plin1</i> -OT2	CTTATCCTTCCAGG TCACTG	CATGGACAGGTGGT GTAGAAA	ACACTCTTTCCTACACGACGCT CTTCCGATCTCTTTGTAGACCT GTCAAGAGG	GTGACTGGAGTTCAGACGTGTG CTCTCCGATCTCCAGAAAAGTA TGGGTGTCAAT
<i>Plin1</i> -OT3	GCCAAAGCCAAA TGGTTAT	GGACTCGTTTGTCC AGTATGT	ACACTCTTTCCTACACGACGCT CTTCCGATCTGTGCCATGTCAAT AGCAGATAAG	GTGACTGGAGTTCAGACGTGTG CTCTCCGATCTGGGATGGGTAA GCTAGAAATGT
<i>Plin1</i> -OT4	GAATGTGGGTAGGA GGACTTAAC	CTAATTGGGAAGTC TCGAAGGG	ACACTCTTTCCTACACGACGCT CTTCCGATCTTGGAGGTGAGAA CCATCTCT	GTGACTGGAGTTCAGACGTGTG CTCTCCGATCTACAAAGCAATG AGGTGCCTA
<i>Plin1</i> -OT5	CTTCGTACCCCTGC TCATTTA	CCTAGAACTTGCTT CTCTTAIGG	ACACTCTTTCCTACACGACGCT CTTCCGATCTCGCCTCAAGGCAG TTTCA	GTGACTGGAGTTCAGACGTGTG CTCTCCGATCTCAGAGTTTCTG AGTCTGGTAAATAA
<i>Plin1</i> -OT6	ACTGAGACCCAGA GGGAATAA	GTCAGGATGACACC CATCTTC	ACACTCTTTCCTACACGACGCT CTTCCGATCTGGCTGTAGAAAGG CAGGTATTT	GTGACTGGAGTTCAGACGTGTG CTCTCCGATCTACCTGTACCA CAGGTCTC
<i>Plin1</i> -OT7	GTGTGATGTGAGGG TCAGAAA	GGAGTAAGAAGGG CCGTAAAG	ACACTCTTTCCTACACGACGCT CTTCCGATCTGAGACAGACATGT GACCAAGAG	GTGACTGGAGTTCAGACGTGTG CTCTCCGATCTTGAAGTATAG GGAGGACAGA
<i>Plin1</i> -OT8	GTCAACCTCTGGTA CTGTGAAA	AACTCAAGCAGGT CCGAAAG	ACACTCTTTCCTACACGACGCT CTTCCGATCTAACAATAGGGACT TGCCTTGA	GTGACTGGAGTTCAGACGTGTG CTCTCCGATCTCTGAAGCTCCT TTCTCTGTGAT
<i>Plin1</i> -OT9	AACCATCACGTGGG AGAATG	CCTGTGGCTCAGAA GTCATTTA	ACACTCTTTCCTACACGACGCT CTTCCGATCTCCGGGAGGAAGA ATCAAATGTA	GTGACTGGAGTTCAGACGTGTG CTCTCCGATCTCTGTGGCTCA GAAGTCATTTA
<i>Plin1</i> -OT10	CTGAACAAGGGCA ACACTAGA	CCAATACCAGTTGA CCCAGAA	ACACTCTTTCCTACACGACGCT CTTCCGATCTCCATCTACACAA AGACCTACA	GTGACTGGAGTTCAGACGTGTG CTCTCCGATCTGGACCAACAGA ACAAACGATAC