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Supplementary Materials for

A conditional knockout rat resource of mitochondrial protein-coding genes via a DdCBE-induced premature stop codon

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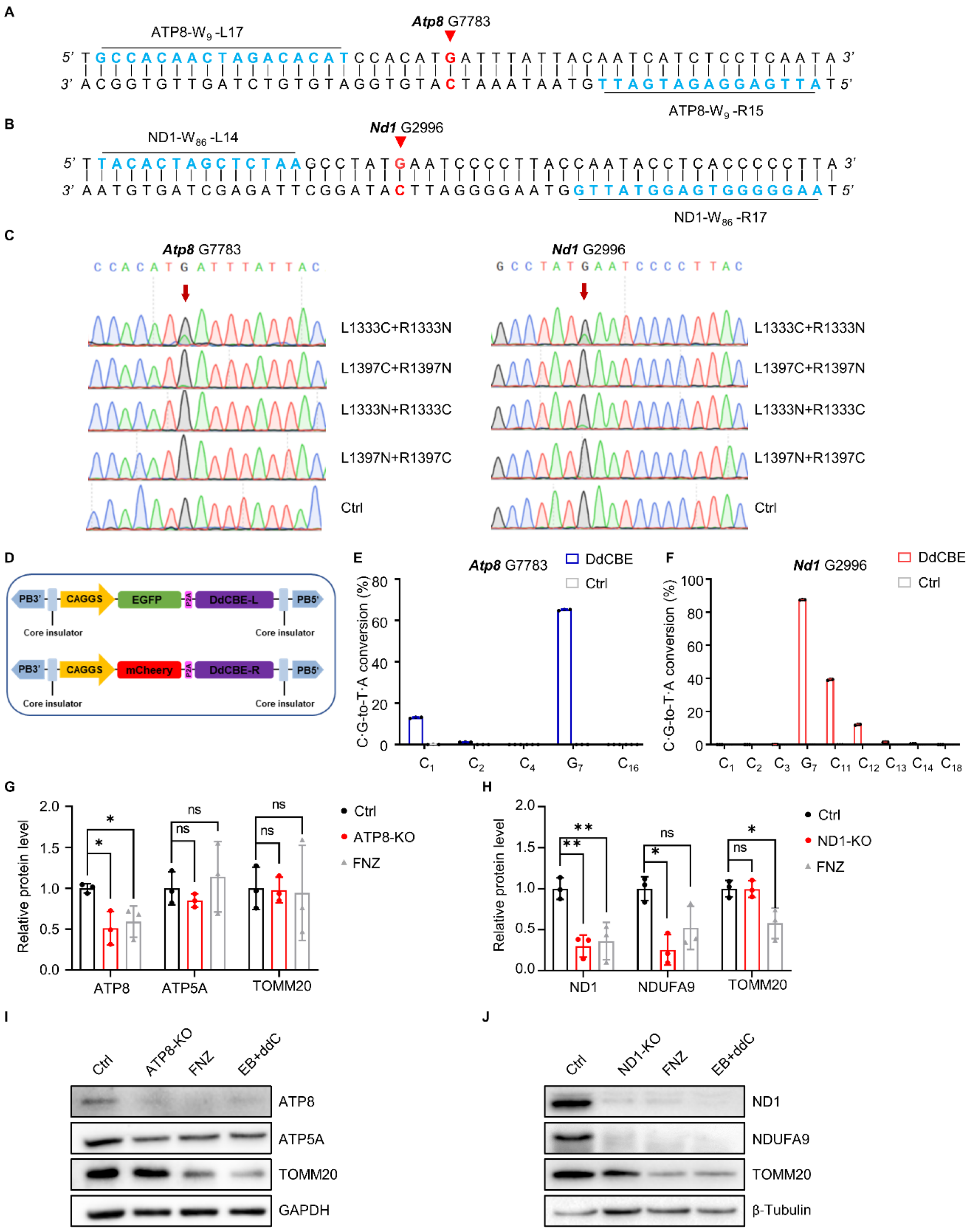


Fig. S1.

Screening efficient DdCBE pair for *Atp8* and *Nd1* targeting.

(A and B) Design overview of TALEs targeting rat *Atp8* G7783 site (A) and *Nd1* G2996 site (B). **(C)** The editing efficiency of four DdCBE pairs (L1333C + R1333N, L1397C + R1397N, L1333N + R1333C, and L1397N + R1397C) for *Atp8* G7783 site and *Nd1* G2996 site were analyzed by Sanger sequencing. **(D)** DdCBE pair with best performance was cloned into PB vector with EGFP or mCherry tags. **(E and F)** The frequencies of C•G to T•A conversion at *Atp8* G7783 site (E) and *Nd1* G2996 site (F) were analyzed by deep sequencing. n = 3 technical replicates. Data were presented as means ± SD. **(G and H)** The qualitative analysis of protein expression in treated C6 cells from Figure 1I and Figure 1J. n = 3 technical replicates. Data were presented as means ± SD. ns, not significant, $*P \leq 0.05$, $**P \leq 0.01$, $***P \leq 0.001$, $****P \leq 0.0001$ by one-way ANOVA test paired with a Tukey's Honest Significant Difference. **(I and J)** The protein level was detected by western blot in C6 cells treated with DdCBE, FNZ, or EB + ddC.

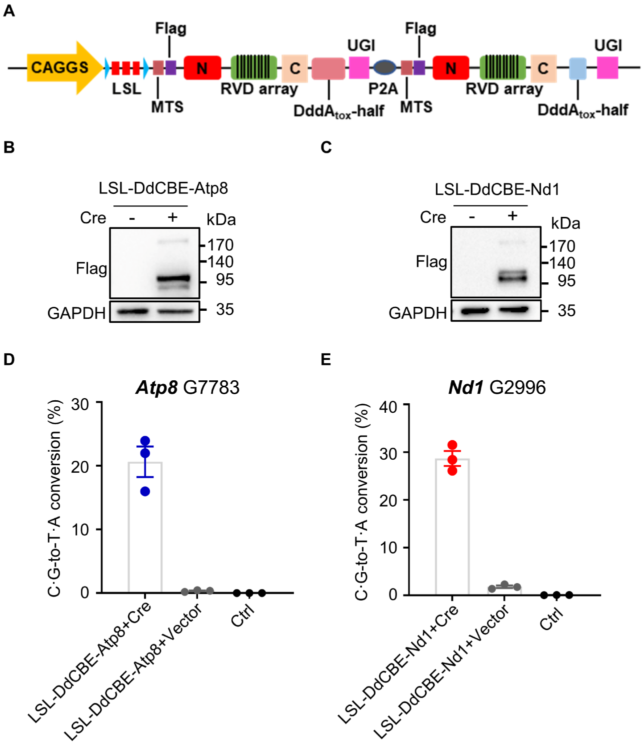


Fig. S2.

Construct a Cre-inducible DdCBE system in C6 cells.

(A) Schematic overview of Cre-inducible DdCBE system. The inducible DdCBE plasmid (LSL-DdCBE) contains a CAG promoter, two *loxP* sites flanking a triple repeat of poly(A) sequence, and a DdCBE pair linked by P2A peptides. **(B and C)** Expression of DdCBE for *Atp8* G7783 site (B) and *Nd1* G2996 site (C) were analyzed by western blot after 48h co-transfection of LSL-DdCBE plasmid with or without *Cre* plasmid. **(D and E)** The frequency of DdCBE-mediated C•G to T•A conversion at *Atp8* G7783 site (D) and *Nd1* G2996 site (E) were analyzed by deep sequencing. n = 3 biological replicates for each group, biological replicates. Data were presented as means ± SD.

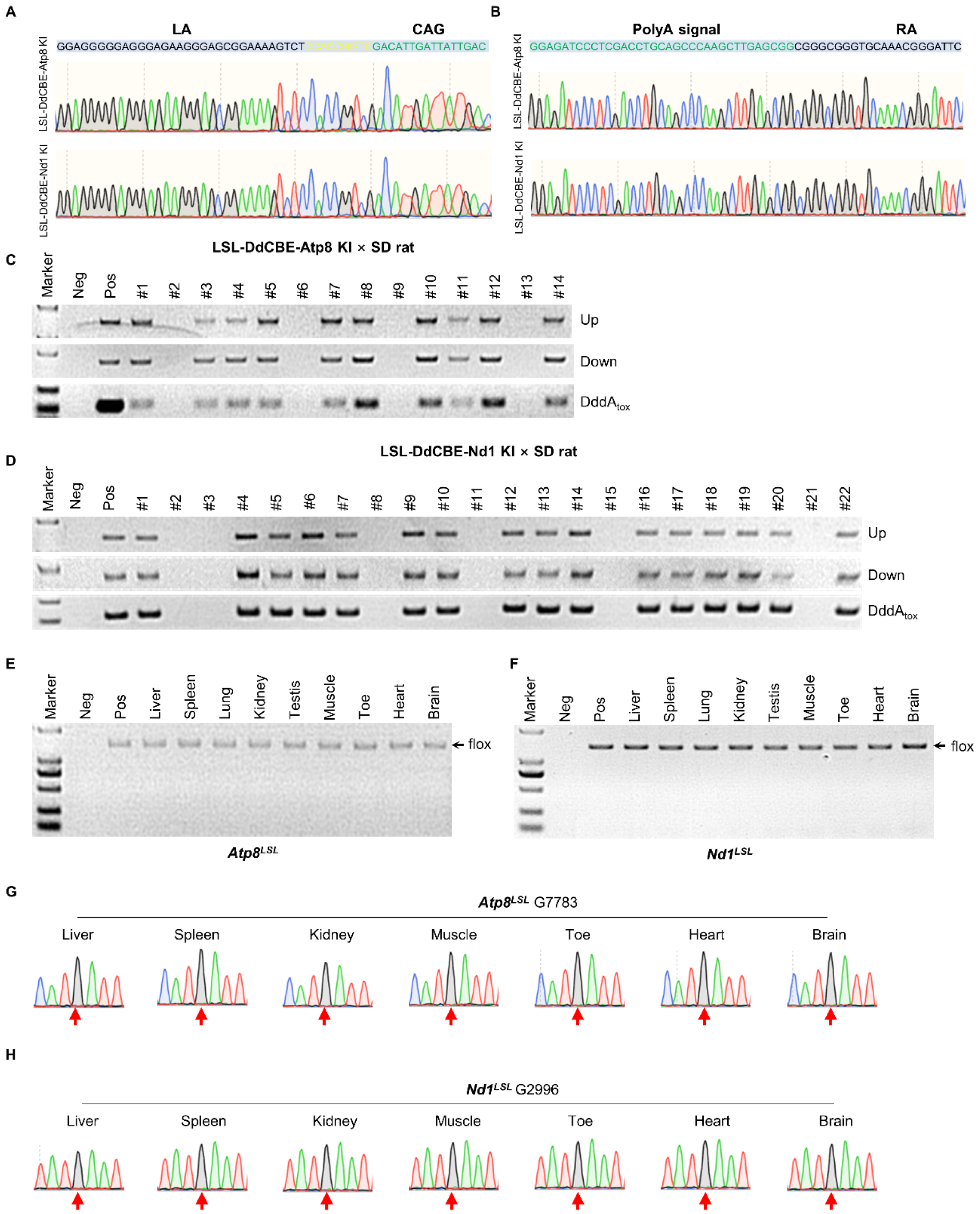


Fig. S3.

The germline transmission of LSL-DdCBE KI rats.

(A and B) The correct recombination of LSL-DdCBE cassettes were confirmed by Sanger sequencing for LA (A) and RA (B) in LSL-DdCBE-Atp8 KI F_0 rats and LSL-DdCBE-Nd1 KI F_0 rats. **(C and D)** Genotyping of LSL-DdCBE-Atp8 KI F_1 rats (C) and LSL-DdCBE-Nd1 KI F_1 rats (D) were analyzed using PCR with Up, Down, and DddA_{tox} primer pairs. **(E and F)** The LSL element in various tissues of LSL-DdCBE-Atp8 KI F_1 rat (E) and LSL-DdCBE-Nd1 KI F_1 rat (F) were analyzed using PCR with the loxP primer pair. **(G and H)** Sanger sequencing for *Atp8* G7783 site (G) and *Nd1* G2996 site (H) in various tissues of LSL-DdCBE-Atp8 KI F_1 rat and LSL-DdCBE-Nd1 KI F_1 rat.

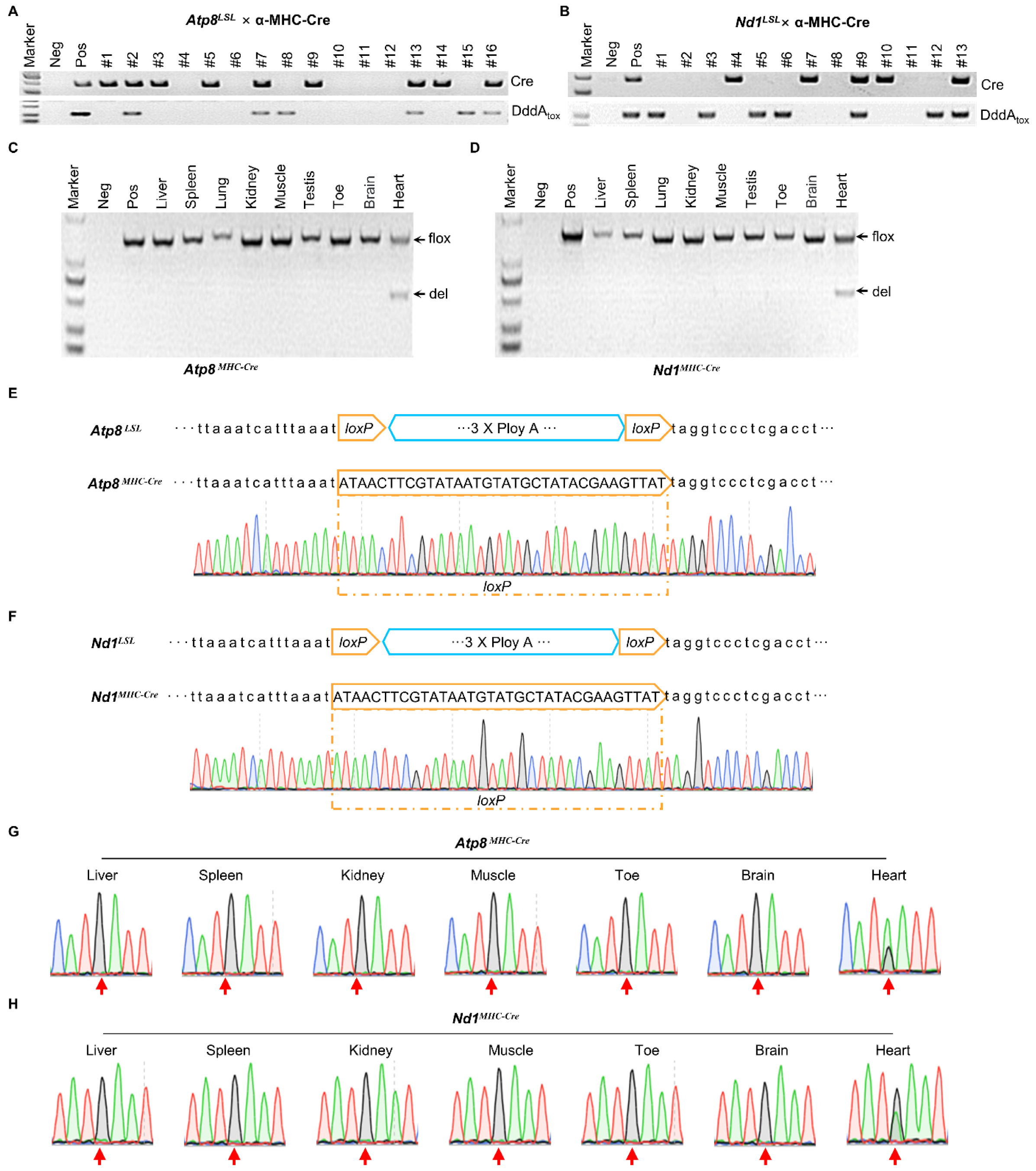


Fig. S4.

Heart-specific depletion of ATP8/ND1 using α-MHC-Cre rats.
(A and B) Genotyping of the offspring produced from *Atp8*^{LSL} × α-MHC-Cre rats (A) and *Nd1*^{LSL} × α-MHC-Cre rats (B) using Cre and DddA$_{tox}$ primer pairs. **(C and D)** The LSL element in various tissues of *Atp8*$^{MHC\text{-}Cre}$ rat (C) and *Nd1*$^{MHC\text{-}Cre}$ rat (D) was analyzed using the loxP primer pair. **(E and F)** Cre-mediated LSL deletion in heart tissues of *Atp8*$^{MHC\text{-}Cre}$ rat (E) and *Nd1*$^{MHC\text{-}Cre}$ rat (F) were confirmed by Sanger sequencing. **(G and H)** Sanger sequencing for *Atp8* G7783 site (G) and *Nd1* G2996 site (H) in various tissues of *Atp8*$^{MHC\text{-}Cre}$ and *Nd1*$^{MHC\text{-}Cre}$ rats.

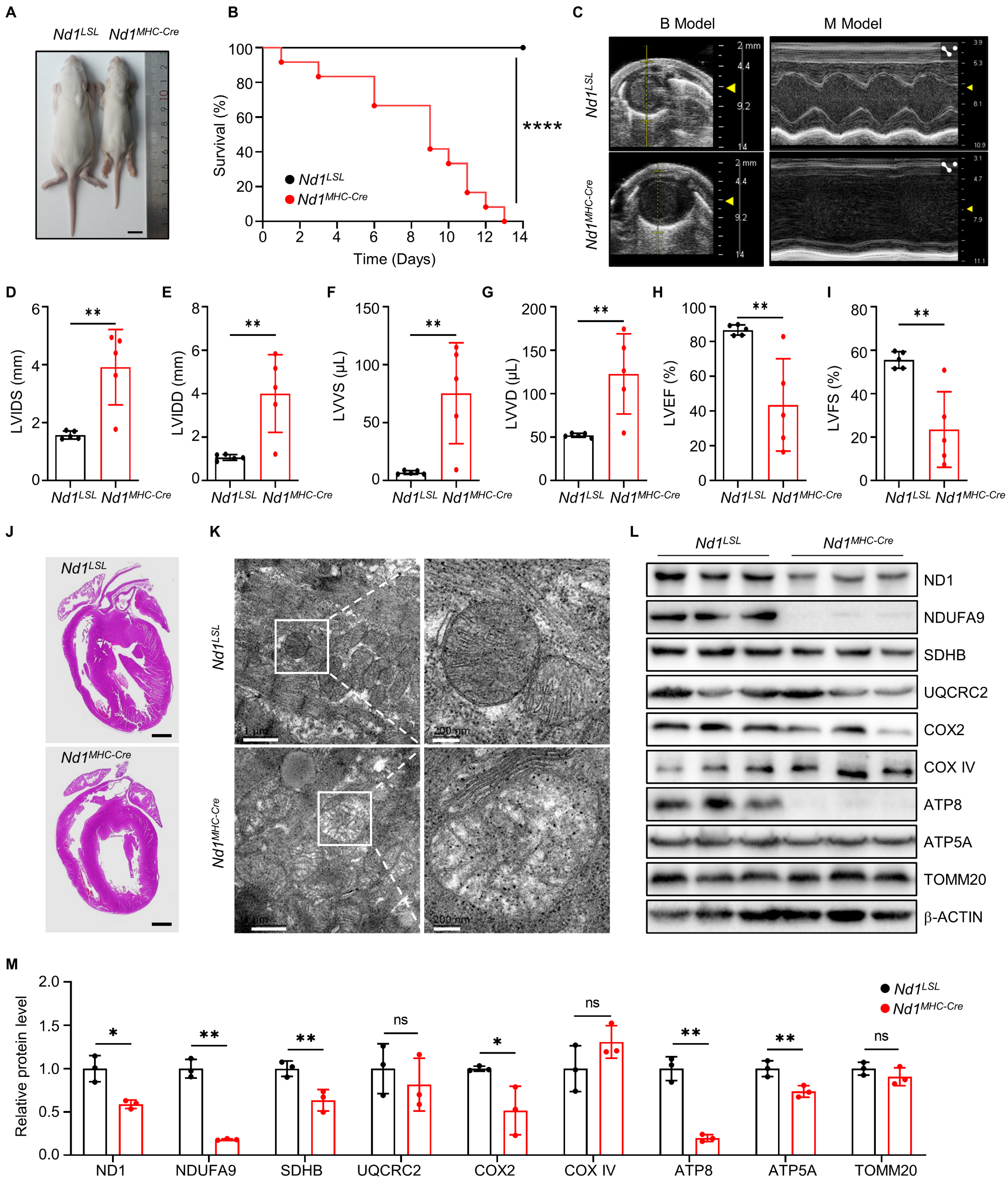


Fig. S5.

Heart-specific depletion of ND1 causes heart failure in rats.

(A) The whole-body image of ten-day-age $\mathit{Nd1}^{LSL}$ and $\mathit{Nd1}^{MHC\text{-}Cre}$ pups. Scale bar, 1 cm. **(B)** The survival curve of $\mathit{Nd1}^{LSL}$ and $\mathit{Nd1}^{MHC\text{-}Cre}$ rats. n = 10 biological replicates for each group. $^{****}P \leq 0.0001$ by Log-rank test. **(C)** The snap shot of echocardiography for $\mathit{Nd1}^{LSL}$ and $\mathit{Nd1}^{MHC\text{-}Cre}$ rats. **(D to I)** The cardiac structure and function parameters of $\mathit{Nd1}^{LSL}$ and $\mathit{Nd1}^{MHC\text{-}Cre}$ rats calculated from echocardiography in (C). Left ventricular (LV) diameter at end of systole (LVIDS) (D) and diastole (LVIDD) (E); LV volume at end of systole (LVVS) (F) and diastole (LVVD) (G); LV ejection fraction (LVEF) (H); LV percentage fractional shortening (LVFS) (I). n = 5 biological replicates for each group. Data were presented as means ± SD. $^{**}P \leq 0.01$ by Student's unpaired two-tailed *t*-test. (**J**) The H&E image of heart tissue from *Nd1*^{LSL} and *Nd1*$^{MHC\text{-}Cre}$ rats. Scale bar, 1 mm. (**K**) The TEM image of mitochondria in heart tissue of *Nd1*^{LSL} and *Nd1*$^{MHC\text{-}Cre}$ rats. **(L and M)** The mitochondrial protein level in heart tissues of *Nd1*^{LSL} and *Nd1*$^{MHC\text{-}Cre}$ rats were analyzed by western bot (L) and quantification (M). n = 3 biological replicates for each group. Data were presented as means ± SD. ns, not significant, $^{*}P \leq 0.05$, $^{**}P \leq 0.01$ by Student's unpaired two-tailed *t*-test.

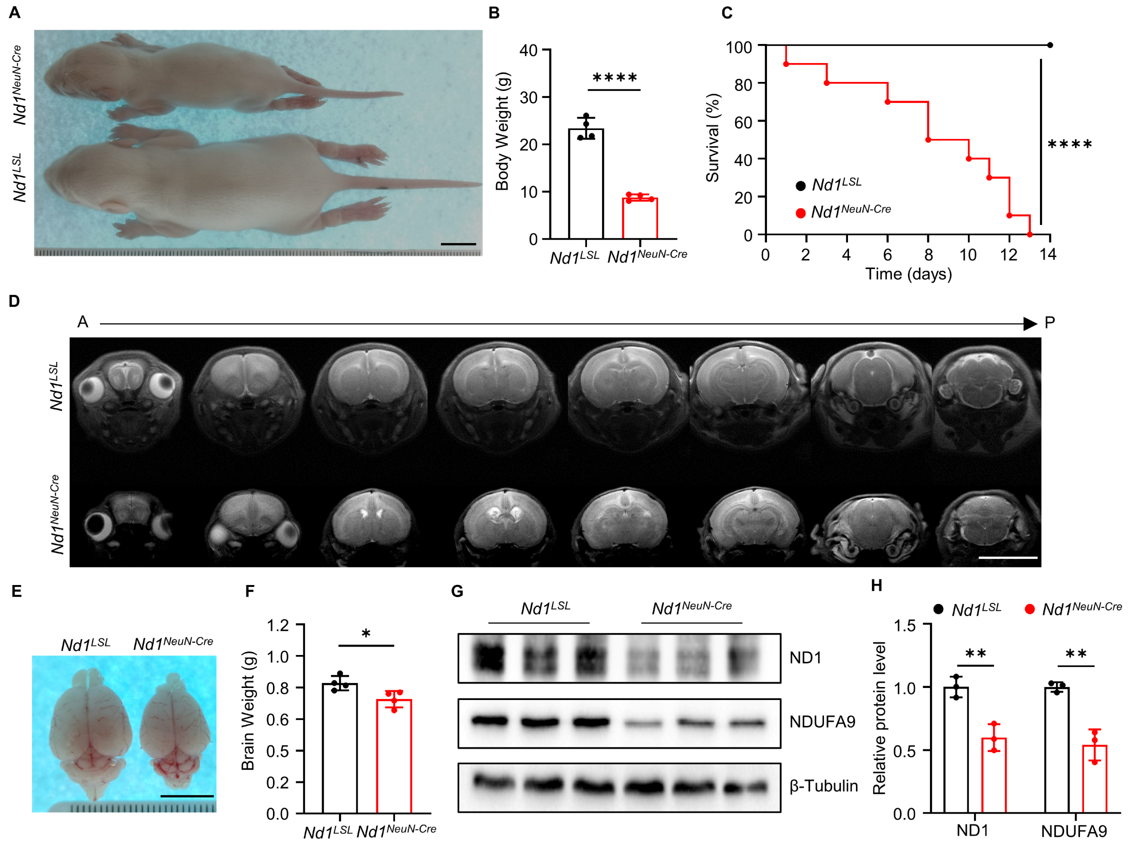


Fig. S6.

Neuron-specific knockout ND1 results in postnatal death in rats.

(A) The whole-body image of $Nd1^{LSL}$ and $Nd1^{NeuN\text{-}Cre}$ rats. Scale bar, 1 cm. **(B)** the body weight of $Nd1^{LSL}$ and $Nd1^{NeuN\text{-}Cre}$ rats. n = 4 biological replicates for each group. $****P \leq 0.0001$ by Student's unpaired two-tailed *t*-test. **(C)** The survival curve of $Nd1^{LSL}$ and $Nd1^{NeuN\text{-}Cre}$ rats. n = 10 biological replicates for each group. $****P \leq 0.0001$ by Log-rank test. **(D)** The brain MRI image of $Nd1^{LSL}$ and $Nd1^{NeuN\text{-}Cre}$ rats from anterior (A) to posterior (P). Scale bar, 1 cm. **(E)** The brain image of $Nd1^{LSL}$ and $Nd1^{NeuN\text{-}Cre}$ rats. Scale bar, 1 cm. **(F)** The brain weight of $Nd1^{LSL}$ and $Nd1^{NeuN\text{-}Cre}$ rats. n = 4 biological replicates for each group. $****P \leq 0.0001$ by Student's unpaired two-tailed *t*-test. **(G and H)** The protein level of ND1 and NDUFA9 in brain tissue of $Nd1^{LSL}$ and $Nd1^{NeuN\text{-}Cre}$ rats were analyzed by western blot (G) and quantification (H). n = 3 biological replicates for each group. Data were presented as means ± SD. $**P \leq 0.01$ by Student's unpaired two-tailed *t*-test.

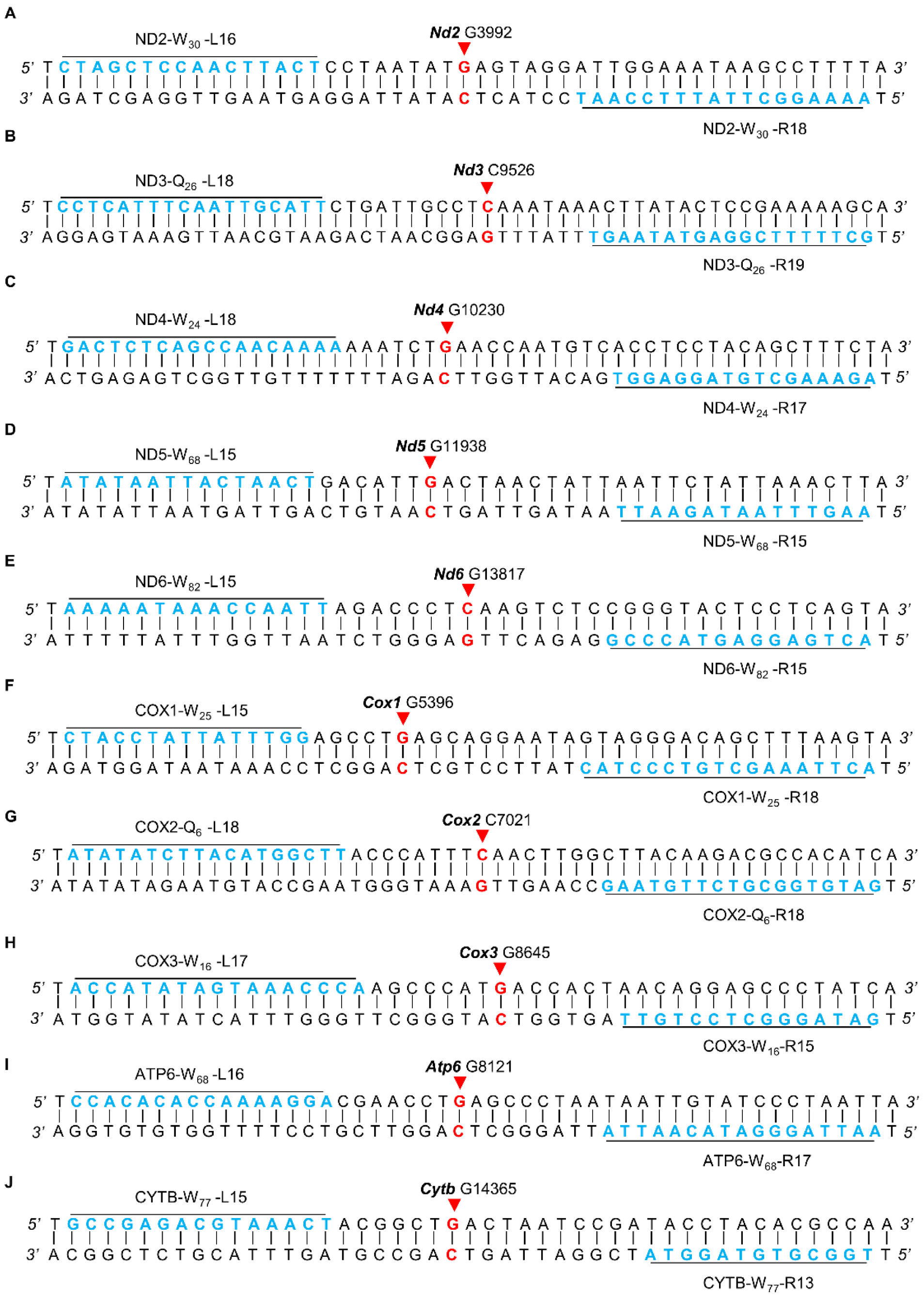


Fig. S7.

Design of knockout all rat mtDNA protein-coding genes.

(A to J) Design overview of DdCBEs for *Nd2* G3992 (A), *Nd3* C9526 (B), *Nd4* G10230 (C), *Nd5* G11938 (D), *Nd6* G13817 (E), *Cytb* G14365 (F), *Cox1* G5396 (G), *Cox2* C7021 (H), *Cox3* G8645 (I), and *Atp6* G8121 (J) sites.

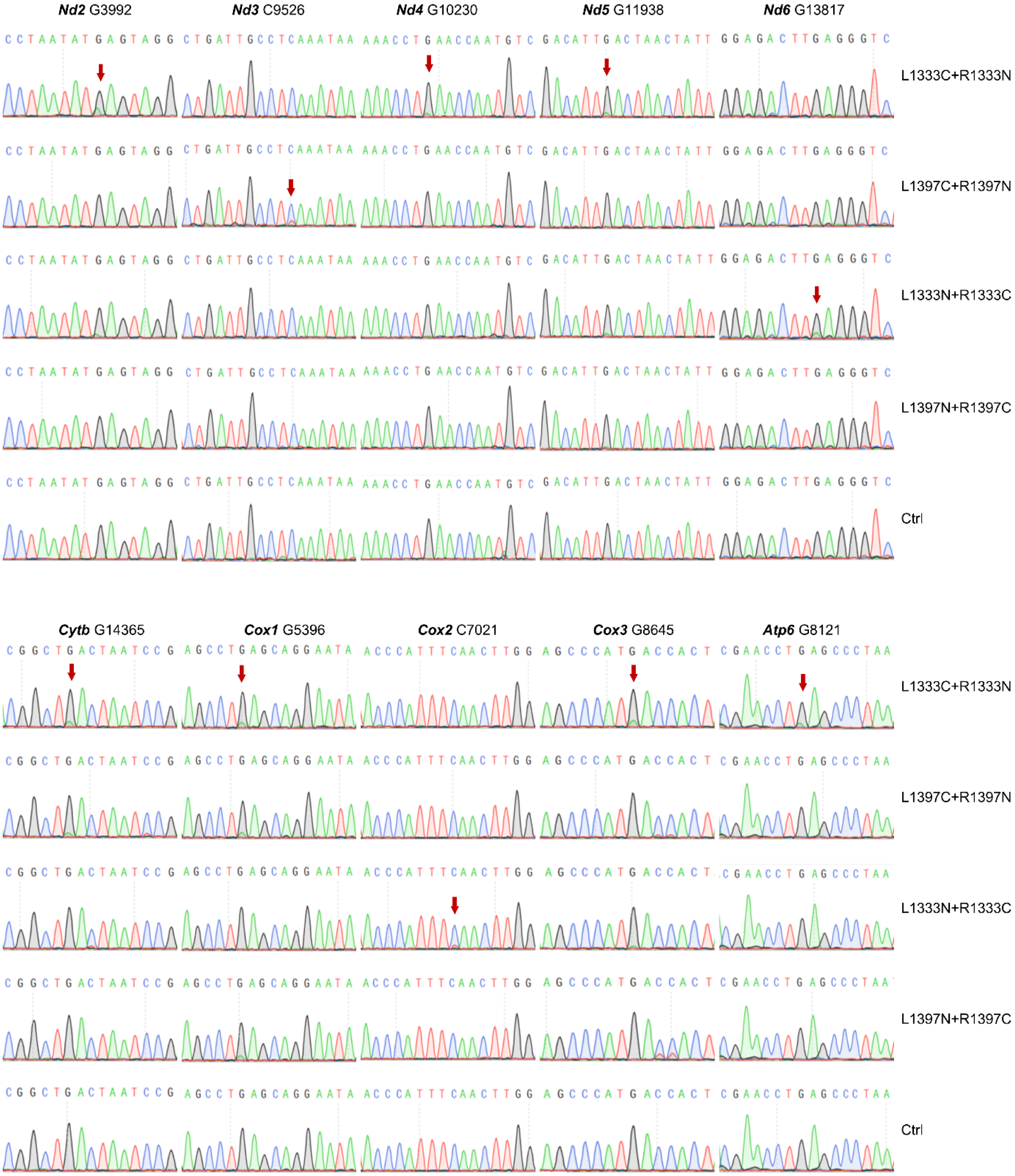


Fig. S8.

Screening of efficient DdCBE pairs for targeting mtDNA protein-coding genes in C6 cells. Sanger sequencing for *Nd2* G3992, *Nd3* C9526, *Nd4* G10230, *Nd5* G11938, *Nd6* G13817, *Cytb* G14365, *Cox1* G5396, *Cox2* C7021, *Cox3* G8645, and *Atp6* G8121 sites in C6 cells transfected with four DdCBE pairs for each target site.

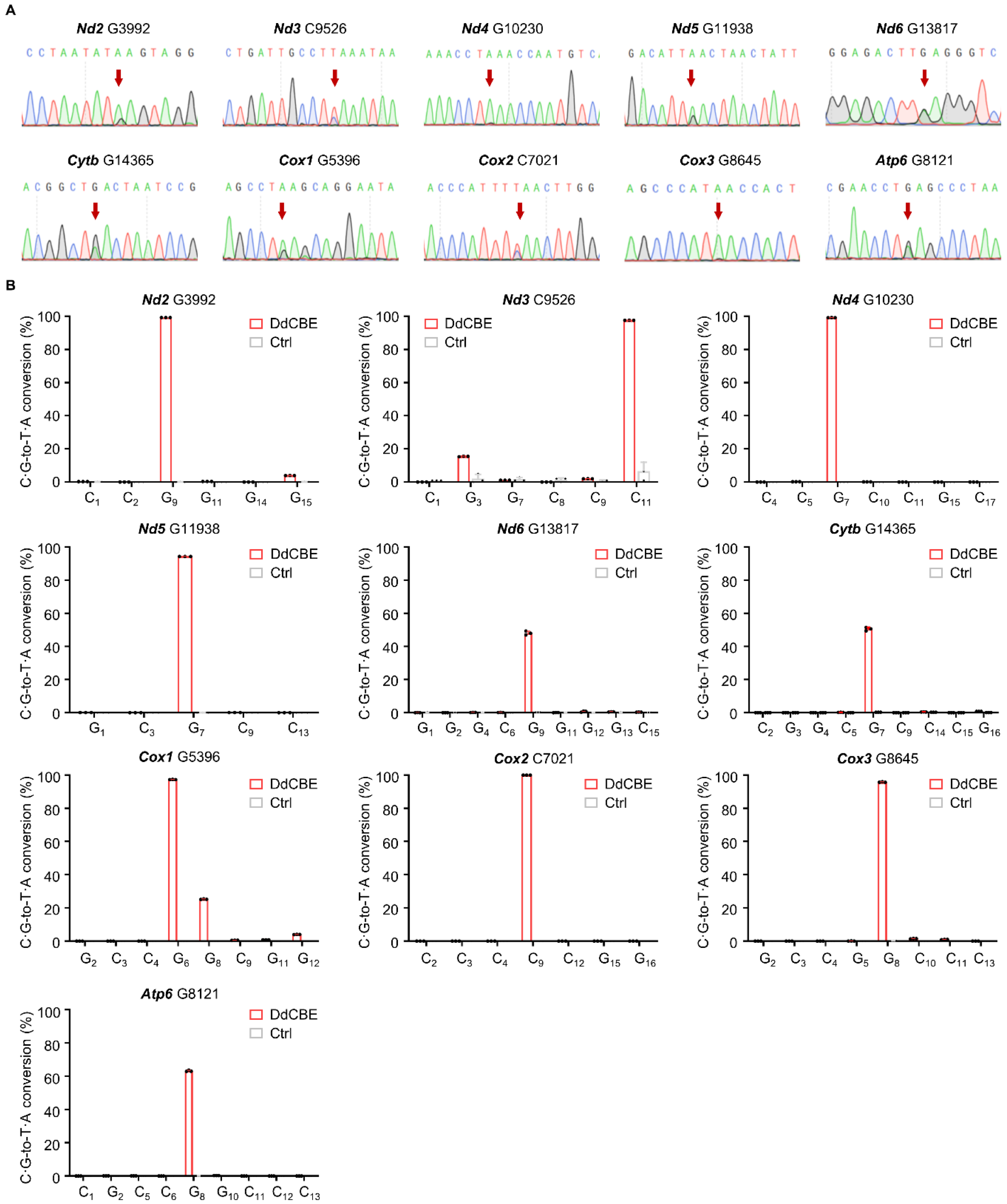


Fig. S9.

The editing efficiency of DdCBE for rat mtDNA protein-coding genes in C6 cells. **(A)** Sanger sequencing for *Nd2* G3992, *Nd3* C9526, *Nd4* G10230, *Nd5* G11938, *Nd6* G13817, *Cytb* G14365, *Cox1* G5396, *Cox2* C7021, *Cox3* G8645, and *Atp6* G8121 sites in PB-DdCBE plasmids transfected C6 cells. **(B)** The frequency of C•G to T•A conversion in the spacer region of *Nd2* G3992, *Nd3* C9526, *Nd4* G10230, *Nd5* G11938, *Nd6* G13817, *Cytb* G14365, *Cox1* G5396, *Cox2* C7021, *Cox3* G8645, and *Atp6* G8121 sites was analyzed by deep sequencing. n = 3 technical replicates. Data were presented as means ± SD.

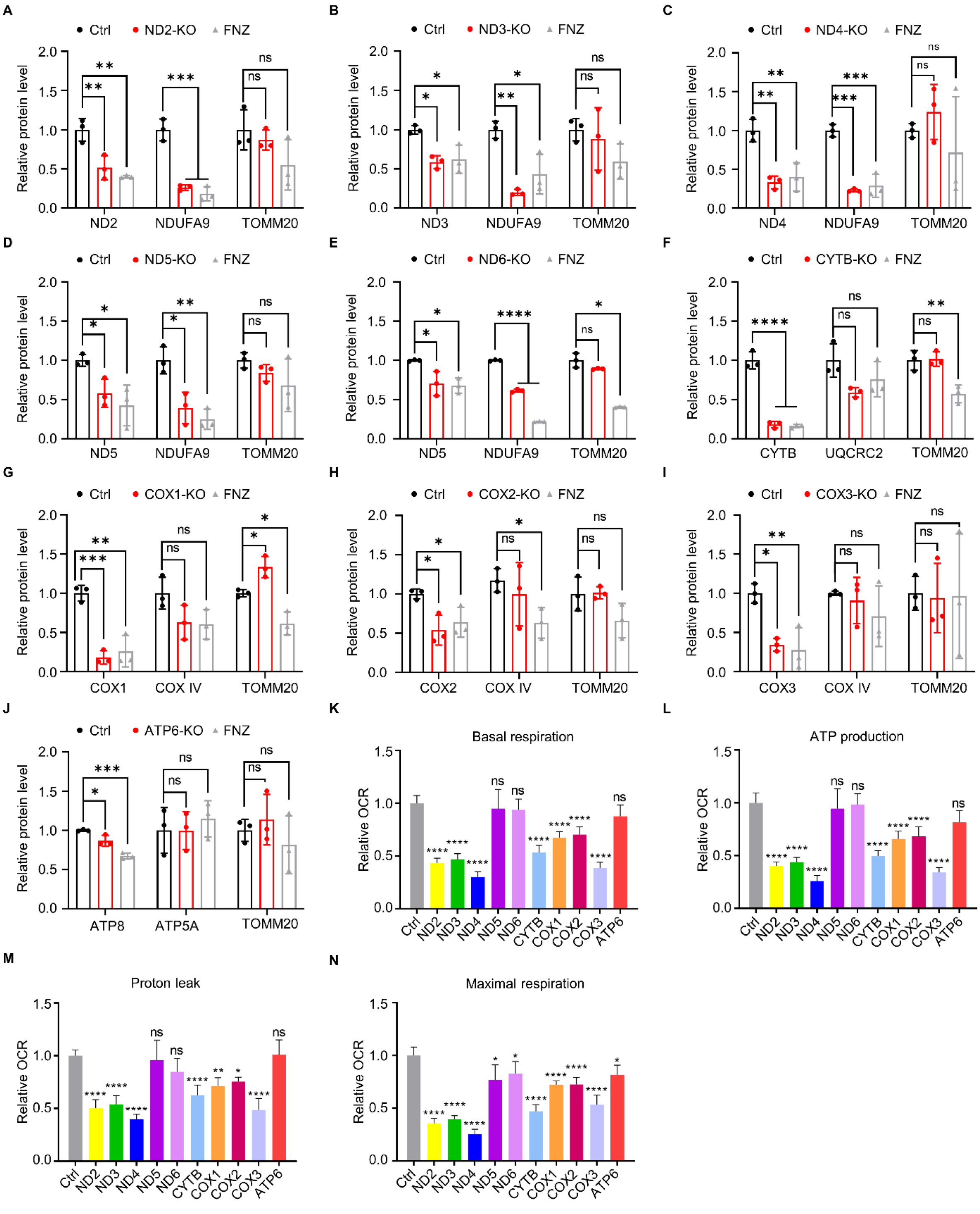


Fig. S10.

Depletion of mtDNA-encoded proteins in C6 cells.

(A to J) The quantitative analysis of protein expression in ND2-KO (A), ND3-KO (B), ND4-KO (C), ND5-KO (D), ND6-KO (E), CYTB-KO (F), COX1-KO (G), COX2-KO (H), COX3-KO (I), and ATP6-KO (J) C6 cells from Figure 5I to 5L. n = 3 technical replicates. Data were presented as means ± SD. ns, not significant, *$P \leq 0.05$, **$P \leq 0.01$, ***$P \leq 0.001$, ****$P \leq 0.0001$ by one-way ANOVA test paired with a Tukey's Honest Significant Difference. **(K to N)** Relative values of OXPHOX parameters from Figure 5C to 5L. n = 5 technical replicates for Ctrl and n = 6 technical replicates for each KO cell line. Data were presented as means ± SD. ns, not significant, *$P \leq 0.05$, **$P \leq 0.01$, ***$P \leq 0.001$, and ****$P \leq 0.0001$ by one-way ANOVA test paired with a Tukey's Honest Significant Difference.

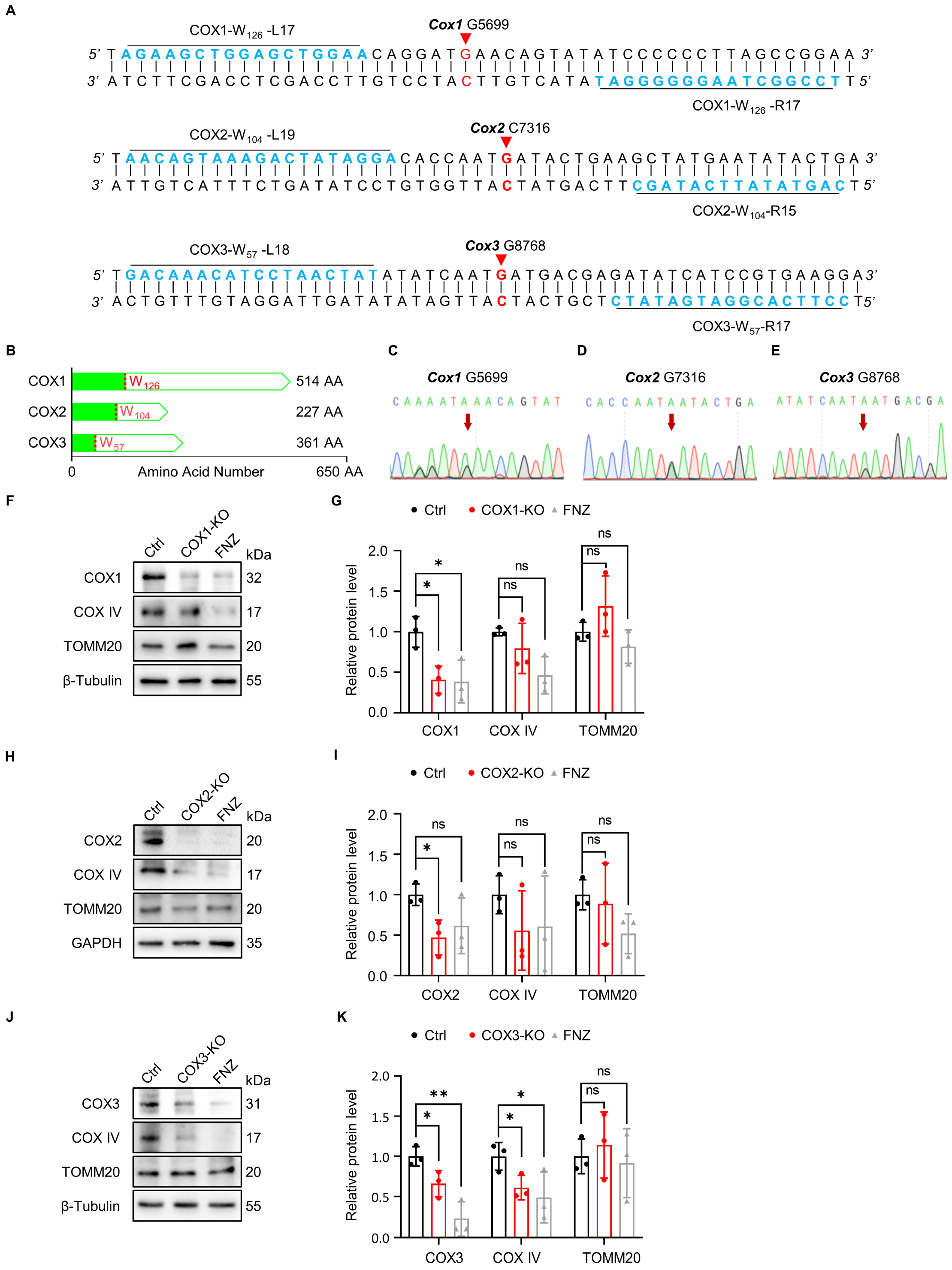
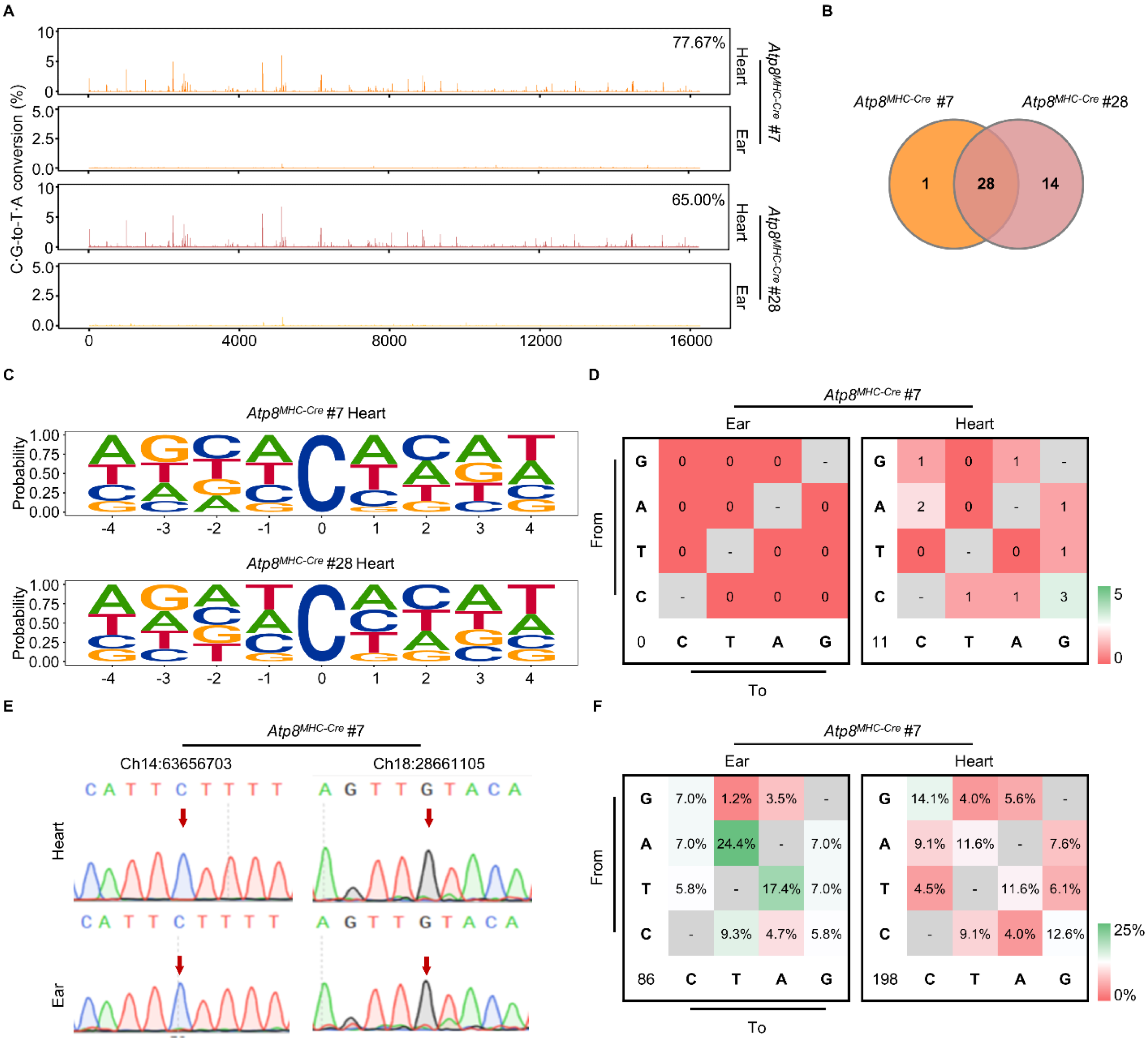


Fig. S11.

Depletion of mtDNA-encoded COXs in C6 cells.

(A) Design overview of DdCBEs for *Cox1* G5699, *Cox2* G7316, and *Cox3* G8768 sites. **(B)** The location of DdCBE-introduced stop codon at COX1, COX2, and COX3. **(C to E)** Sanger sequencing for *Cox1* G5699 (C), *Cox2* G7316 (D), and *Cox3* G9438 (E) sites in PB-DdCBE plasmids transfected C6 cells. **(F to K)** The protein level of COX1 (F and G), COX2 (H and I), and COX3 (J and K) in C6 cells treated with FNZ or targeted by corresponding DdCBEs were analyzed by western blot and quantification. n = 3 technical replicates. Data were presented as means ± SD. ns, not significant, $^{*}P \leq 0.05$, $^{**}P \leq 0.01$, $^{***}P \leq 0.001$, $^{****}P \leq 0.0001$ by one-way ANOVA test paired with a Tukey's Honest Significant Difference.



D Atp8MHC-Cre #7

Ear

G	0	0	0	-
A	0	0	-	0
T	0	-	0	0
C	-	0	0	0
0	C	T	A	G

Heart

G	1	0	1	-
A	2	0	-	1
T	0	-	0	1
C	-	1	1	3
11	C	T	A	G

F Atp8MHC-Cre #7

Ear

G	7.0%	1.2%	3.5%	-
A	7.0%	24.4%	-	7.0%
T	5.8%	-	17.4%	7.0%
C	-	9.3%	4.7%	5.8%
86	C	T	A	G

Heart

G	14.1%	4.0%	5.6%	-
A	9.1%	11.6%	-	7.6%
T	4.5%	-	11.6%	6.1%
C	-	9.1%	4.0%	12.6%
198	C	T	A	G

Fig. S12.

Off-target analysis on whole mitochondrial genome and nuclear genome.

(A) The frequencies of C·G-to-T·A conversion at off-target sites in the whole mitochondrial genome of *Atp8*$^{MHC\text{-}Cre}$ rats. The editing frequency of on-target was detected by Deep sequencing and marked in the upper right corner. **(B)** Venn diagram showing the overlap of off-target sites between *Atp8*$^{MHC\text{-}Cre}$ #7 rat and *ATP8*$^{MHC\text{-}Cre}$ #28 rat. **(C)** The motif analysis for non-target sites in heart tissue of *Atp8*$^{MHC\text{-}Cre}$ #7 and *ATP8*$^{MHC\text{-}Cre}$ #28 rats. **(D)** The distribution of base conversion type in the nuclear genome of *Atp8*$^{MHC\text{-}Cre}$ #7 rat. The numbers in each cell indicated the number of a certain mutation type. The number of detected SNVs was marked in the bottom left cell. **(E)** Sanger sequencing for putative off-target sites in *Atp8*$^{MHC\text{-}Cre}$#7. **(F)** The distribution of base conversion type in the nuclear genome of *Atp8*$^{MHC\text{-}Cre}$ #7 rat. The numbers in cell indicated the proportion of a certain mutation type.

Table S1.

Injection summary of CRISPR/Cas9-mediated LSL-DdCBE knockin (KI) rats.

Target gene	gRNA Con. (ng/µL)	Donor Con. (ng/µL)	Cas9 (ng/µL)	No. of injected zygotes	No. of transplanted zygotes	No. of pups	No. of KI pups
Atp8	12 + 12	7	30	75	44	10	5
Nd1	12 + 12	4	30	77	44	16	14
Cytb	12 + 12	8	30	79	43	8	8
Cox3	12 + 12	7	30	70	46	20	7
Nd2	12 + 12	4	30	60	41	10	6
Nd5	12 + 12	4	30	143	90	8	5

Table S2.
Primers used in this study.

	Primers	Sequence (5’-3’)
Primers for RVD	RVD seq Fwd	TGACCGCAGTGGAGGCAGTG
	RVD seq Rev	GCATCCAGCGCAGGAC
Primers for genotyping	Rat-Up-Fwd	GGGTGGCGAAGGTAATGTCT
	Rat-Up-Rev	GCTATGAACTAATGACCCCGTAATT
	Rat-Down-Fwd	GCATCTGACTTCTGGCTAATAAAG
	Rat-Down-Rev	CATTAACAGGAAATGGCTCAGTTTATAAATG
	Rat-G2966-Fwd	GAAAATCCTAGGCTACATACAACTACG
	Rat-G2966-Rev	GAGGATAATGGCTATTGTGACTT
	Rat-G7783- Fwd	TGCTCTGAAATTTGCGGCTC
	Rat-G7783-Rev	AGTCGGTTGCTGATTAGGCG
	Rat-loxP-Fwd	TCTGCTAACCATGTTCATGCC
	Rat-loxP-Rev	GCTACCTTTATCGTCGTCATCCT
Primers for DddA_{tox} halves	Halves Fwd	TTGCGGAGACTCACCCCTT
	Halves Rev	TGTAAACCCATGGCCGAC
Primers for on-target sanger-sequence	rND1KO-seq-Fwd	ATGGCCTTCCTCACCCTAGT
	rND1KO-seq-Rev	AATAGGGCGAATGGTCCTGC
	rND2KO-seq-Fwd	GGCCCATACCCCGAAAATGT
	rND2KO-seq-Rev	TCCTTGGGTGACTTCGGGTA
	rCOX1KO-seq-Fwd	AGGCGGGAGAAGCCTTAGTA
	rCOX1KO-seq-Rev	AGATAGAAGACACCCCGGCT
	rCOX2KO-seq-Fwd	AGCCTTCGCATCAAAACGAG
	rCOX2KO-seq-Rev	TAGGTGATGTGGCGTCTTGT
	rATP8KO-seq-Fwd	CCCGCCCCATCTAACATCTC
	rATP8KO-seq-Rev	AGAAGCGTGTTAGGGTTGCT
	rATP6KO-seq-Fwd	TCCCAAACCTTTCCTGCACC
	rATP6KO-seq-Rev	TCCTTGCGGTAAGAAGTGGG
	rCOX3KO-seq-Fwd	TTCTTACCGCAAGGAACCCC
	rCOX3KO-seq-Rev	TGGTGGCCTTGGTATGTTCC
	rND3KO-seq-Fwd	CGCAGCATGATACTGACACT
	rND3KO-seq-Rev	GTGCAGAACTTGTTGGGTCG
	rND4KO-seq-Fwd	TGCGAAGCAGCAGTAGGTTTA
	rND4KO-seq-Rev	AAGCGTTCTGTTTGGTTGCC
	rND5KO-seq-Fwd	ACCTTGGTGCAACTCCAAAT
	rND5KO-seq-Rev	CGGTTAATGTGGGGATCAGAGT
	rND6KO-seq-Fwd	GCATCCTAGCAGGCTTCCTT
	rND6KO-seq-Rev	GGTTGTCTAGGGTTGGCGTT
	rCYTBKO-seq-Fwd	CCCGCCCCATCTAACATCTC
	rCYTBKO-seq-Rev	AGAAGCGTGTTAGGGTTGCT
	rCOX1KO-2-seq-Fwd	AGGCGGGAGAAGCCTTAGTA
	rCOX1KO-2-seq-Rev	AGATAGAAGACACCCCGGCT
	rCOX2KO-2-seq-Fwd	CTTGGCTTACAAGACGCCAC
	rCOX2KO-2-seq-Rev	CCTAGTGAAGGGACGGCTCA
	rCOX3KO-2-seq-Fwd	TTCTTACCGCAAGGAACCCC
	rCOX3KO-2-seq-Rev	TGGTGGCCTTGGTATGTTCC
Barcoded Primers for on-target Deep-sequence	i5-rND1KO-Fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGCGAACCCATACGCCCCCTAAC
	i7-rND1KO-Rev	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACCGCTCGTAGGGCTCCGAATAG
	i5-rND2KO-Fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGCTGTTGGTCTAAACCCTTCCCG
	i7-rND2KO-Rev	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACCTTGAGGCTGTAGCTTGGGTT

	i5-rCOX1KO-Fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGCTGCTCGTAAACCGTTGACTCT
	i7-rCOX1KO-Rev	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACCTACGAATGCATGGGCTGTGA
	i5-rCOX2KO-Fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGCGGAAGGATTCGAACCCCCTACA
	i7-rCOX2KO-Rev	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACCTGGGCGTCTATTGTGCTTGT
	i5-rATP8KO-Fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGCAACTCATTGCGAAGCTTAGAGCG
	i7-rATP8KO-Rev	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACCTGTGGGGGTAATGAAAGAGGC
	i5-rATP6KO-Fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGCAACGCCTAATCAGCAACCGA
	i7-rATP6KO-Rev	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACCTGCTCATAGGGGGATGGCTA
	i5-rCOX3KO-Fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGCACTTGAATTTGCCGTAGCCT
	i7-rCOX3KO-Rev	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACCAGGATGTTTGTCAGGAGGCC
	i5-rND3KO-Fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGCGATGAGGATCCTACTCCCTTAGT
	i7-rND3KO-Rev	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACCGTGCAGAACTTGTTGGGTCG
	i5-rND4KO-Fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGCCTGCGAAGCAGCAGTAGGTT
	i7-rND4KO-Rev	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACCTGGGGTGGATAATGGATCGG
	i5-rND5KO-Fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGCTCCTCCTTAGCCTCTTACCTT
	i7-rND5KO-Rev	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACCCGGTTAATGTGGGGATCAGAG
	i5-rND6KO-Fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGCCAACTATAAATAGCCGCAACCCC
	i7-rND6KO-Rev	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACCTATTTGGGGGGGATGTTGGTTG
	i5-rCYTBKO-Fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGCTCCTCACAGGCTTATTCCTAGC
	i7-rCYTBKO-Rev	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACCTAGTCCTCGTCCCACATGGA
	i5-rCOX1KO-2-Fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGCAGGCTTCGGGAACTGACTTG
	i7-rCOX1KO-2-Rev	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACCAGATAGAAGACACCCCGGCT
	i5-rCOX2KO-2-Fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGCCACAAGCACAATAGACGCCC
	i7-rCOX2KO-2-Rev	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACCACGAAGTTCACCTGGTTTTAGGT
	i5-rCOX3KO-2-Fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGCACCCAAGCCCATGACCACTA
	i7-rCOX3KO-2-Rev	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACCATTCCGTATCGGAGGCCTTT
Primers for long-range PCR	rat-mt F1 Fwd	CCACCGCGGTCATACGATTA
	rat-mt F1 Rev	GGGGTAATTCCTGTTGGGGG
	rat-mt F2 Fwd	AAGGCCACCACACCCCTATT
	rat-mt F2 Rev	CCGCCAAGTCCTTTGAGTTT

Table S3.

The detailed information of the six cKO rat strains in Rat Resource Database.

Accession No.	**Strain Name**	**Gene**	**Type**	**Description**	**Links**
GC00215	SD. Rosa26(tm-CAG-LSL-MT-ND1(G2996A))-GC/ILAS	MT-*Nd1(G2996)*	Knock in and condition knockout	Knockout mitochondrial protein-coding gene *Nd1* by using a DdCBE-induced premature stop codon at G2996 locus in the presence of Cre recombinase.	https://www.ratresource.com/detail/12/1670.html
GC00216	SD. Rosa26(tm-CAG-LSL-MT-ND2(G3992A))-GC/ILAS	MT-*Nd2*(G3992)	Knock in and condition knockout	Knockout mitochondrial protein-coding gene *Nd2* by using a DdCBE-induced premature stop codon at G3992 locus in the presence of Cre recombinase.	https://www.ratresource.com/detail/12/1671.html
GC00217	SD. Rosa26(tm-CAG-LSL-MT-ND5(G11938A))-GC/ILAS	MT-*Nd5*(G11938)	Knock in and condition knockout	Knockout mitochondrial protein-coding gene *Nd5* by using a DdCBE-induced premature stop codon at G11938 locus in the presence of Cre recombinase.	https://www.ratresource.com/detail/12/1672.html
GC00218	SD. Rosa26(tm-CAG-LSL-MT-CYTB(G14365A))-GC/ILAS	MT-*Cytb*(G14365)	Knock in and condition knockout	Knockout mitochondrial protein-coding gene *Cytb* by using a DdCBE-induced premature stop codon at G14365 locus in the presence of Cre recombinase.	https://www.ratresource.com/detail/12/1673.html
GC00219	SD. Rosa26(tm-CAG-LSL-MT-COX3(G8645A))-GC/ILAS	MT-*Cox3*(G8645)	Knock in and condition knockout	Knockout mitochondrial protein-coding gene *Cox3* by using a DdCBE-induced premature stop codon at G8645 locus in the presence of Cre recombinase.	https://www.ratresource.com/detail/12/1674.html

GC00220	SD. Rosa26(tm-CAG-LSL-MT-ATP8(G7783A))-GC/ILAS	MT-*Atp8*(G7783)	Knock in and condition knockout	Knockout mitochondrial protein-coding gene *Atp8* by using a DdCBE-induced premature stop codon at G7783 locus in the presence of Cre recombinase.	https://www.ratresource.com/detail/12/1675.html

Sequence S1.

Amino acid sequences for DdCBEs.

Amino acid sequences of DdCBE-Nd1 for *Nd1* G2996 site targeting were annotated as: red for MTS, italics for linker, yellow for flag tag, green for N&C-terminal domain, underlined for RVDs, purple for split DddA$_{\text{tox}}$ halves, and cyan for UGI. Other targeting DdCBE only showed RVDs sequences.

ND1-W$_{86}$-L14 TALE-G1333C

MLGFVGRVAAAPASGALRRLTPSASLPPAQLLLRAAPTAVHPVRDYAAQTSESGGGGSPG*AAA*DYKDDDDK*GS*VDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLG*GS*PTPYPNYANAGHVEGQSALFMRDNGISEGLVFHNNPEGTCGFCVNMTETLLPENAKMTVVPPEGAIPVKRGATGETKVFTGNSNSPKSPTKGGC*SGGS*TNLSDIIEKETGKQLVIQESILMLPEEVEEVIGNKPESDILVHTAYDESTDENVMLLTSDAPEYKPWALVIQDSNGENKIKML

ND1-W$_{86}$-L14 TALE-G1397C

MLGFVGRVAAAPASGALRRLTPSASLPPAQLLLRAAPTAVHPVRDYAAQTSESGGGGSPG*AAA*DYKDDDDK*GS*VDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLG*GS*AIPVKRGATGETKVFTGNSNSPKSPTKGGC*SGGS*TNLSDIIEKETGKQLVIQESILMLPEEVEEVIGNKPESDILVHTAYDESTDENVMLLTSDAPEYKPWALVIQDSNGENKIKML

ND1-W$_{86}$-L14 TALE-G1333N

MLGFVGRVAAAPASGALRRLTPSASLPPAQLLLRAAPTAVHPVRDYAAQTSESGGGGSPG*AAA*DYKDDDDK*GS*VDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQV

VAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLG*GS*GSYALGPYQISAPQLPAYNGQTVGTFYYVNDAGGLESKVFSSGG*SGGS*TNLSDIIEKETGKQLVIQESILMLPEEVEEVIGNKPESDILVHTAYDESTDENVMLLTSDAPEYKPWALVIQDSNGENKIKML

ND1-W$_{86}$-L14 TALE-G1397N

MLGFVGRVAAAPASGALRRLTPSASLPPAQLLLRAAPTAVHPVRDYAAQTSESGGGGSPG*AAA*DYKDDDDK*GS*VDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLG*GS*GSYALGPYQISAPQLPAYNGQTVGTFYYVNDAGGLESKVFSSGGPTPYPNYANAGHVEGQSALFMRDNGISEGLVFHNNPEGTCGFCVNMTETLLPENAKMTVVPPEG*SGGS*TNLSDIIEKETGKQLVIQESILMLPEEVEEVIGNKPESDILVHTAYDESTDENVMLLTSDAPEYKPWALVIQDSNGENKIKML

ND1-W$_{86}$-R17 TALE-G1333C

MLGFVGRVAAAPASGALRRLTPSASLPPAQLLLRAAPTAVHPVRDYAAQTSESGGGGSPG*AAA*DYKDDDDK*GS*VDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLG*GS*PTPYPNYANAGHVEGQSALFMRDNGISEGLVFHNNPEGTCGFCVNMTETLLPENAKMTVVPPEGAIPVKRGATGETKVFTGNSNSPKSPTKGGCSGGSTNLSDIIEKETGKQLVIQESILMLPEEVEEVIGNKPESDILVHTAYDESTDENVMLLTSDAPEYKPWALVIQDSNGENKIKML

ND1-W$_{86}$-R17 TALE-G1397C

MLGFVGRVAAAPASGALRRLTPSASLPPAQLLLRAAPTAVHPVRDYAAQTSESGGGGSPG*AAA*DYKDDDDK*GS*VDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLG*GS*AIPVKRGATGETKVFTGNSNSPKSPTKGGC*SGGS*TNLSDIIEKETGKQLVIQESILMLPEEVEEVIGNKPESDILVHTAYDESTDENVMLLTSDAPEYKPWALVIQDSNGENKIKML

ND1-W$_{86}$-R17 TALE-G1333N

MLGFVGRVAAAPASGALRRLTPSASLPPAQLLLRAAPTAVHPVRDYAAQTSESGGGGSPG*AAA*DYKDDDDK*GS*VDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLG*GS*GSYALGPYQISAPQLPAYNGQTVGTFYYVNDAGGLESKVFSSGG*SGGS*TNLSDIIEKETGKQLVIQESILMLPEEVEEVIGNKPESDILVHTAYDESTDENVMLLTSDAPEYKPWALVIQDSNGENKIKML

ND1-W$_{86}$-R17 TALE-G1397N

MLGFVGRVAAAPASGALRRLTPSASLPPAQLLLRAAPTAVHPVRDYAAQTSESGGGGSPG*AAA*DYKDDDDK*GS*VDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQR

LLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLG*GS*GSYALGPYQISAPQLPAYNGQTVGTFYYVNDAGGLESKVFSSGGPTPYPNYANAGHVEGQSALFMRDNGISEGLVFHNNPEGTCGFCVNMTETLLPENAKMTVVPPEG*SGGS*TNLSDIIEKETGKQLVIQESILMLPEEVEEVIGNKPESDILVHTAYDESTDENVMLLTSDAPEYKPWALVIQDSNGENKIKML

ATP8-W$_9$-L17

LTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGRPALESIVAQLSRPDPAL

ATP8-W$_9$-R15

LTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGRPALESIVAQLSRPDPAL

ND2-W$_{30}$-L16

LTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGRPALESIVAQLSRPDPAL

ND2-W$_{30}$-R18

LTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASN

GGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGRPALESIVAQLSRPDPAL

ND3-Q$_{26}$-L18

LTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGRPALESIVAQLSRPDPAL

ND3-Q$_{26}$-R19

LTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGRPALESIVAQLSRPDPAL

ND4-W$_{24}$-L18

LTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGRPALESIVAQLSRPDPAL

ND4-W$_{24}$-R17

LTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVV

AIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQ
AHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALET
VQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
IGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTP
EQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPV
LCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQA
LETVQRLLPVLCQAHGLTPEQVVAIASNGGGRPALESIVAQLSRPDPAL

ND5-W_{68}-L15

LTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRL
LPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGK
QALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVV
AIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQ
AHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALET
VQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
IGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTP
EQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPV
LCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQA
LETVQRLLPVLCQAHGLTPEQVVAIASNGGGRPALESIVAQLSRPDPAL

ND5-W_{68}-R15

LTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLL
PVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGK
QALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQV
VAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQ
AHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALET
VQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASN
NGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTP
DQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQAHGLTPEQVVAIASNGGGRPALESIVAQLSRPDPAL

ND6-W_{82}-L15

LTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLL
PVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQ
ALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVA
IASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAH
GLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQR
LLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDG
GKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQ
VVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLC
QAHGLTPEQVVAIASNGGGRPALESIVAQLSRPDPAL

ND6-W_{82}-R15

LTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRL
LPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGG
KQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQV
VAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLC
QAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALET
VQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASN
IGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTP

AQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNNGGRPALESIVAQLSRPDPAL

COX1-W_{25}-L15

LTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGRPALESIVAQLSRPDPAL

COX1-W_{25}-R18

LTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGRPALESIVAQLSRPDPAL

COX2-Q_6-L18

LTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGRPALESIVAQLSRPDPAL

COX2-Q_6-R18

LTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGRPALESIVAQLSRPDPAL

COX3-W$_{16}$-L17

LTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAMASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGRPALESIVAQLSRPDPAL

COX3-W$_{16}$-R15

LTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGRPALESIVAQLSRPDPAL

ATP6-W$_{68}$-L16

LTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGRPALESIVAQLSRPDPAL

ATP6-W$_{68}$-R17

LTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNNGGRPALESIVAQLSRPDPAL

CYTB-W$_{77}$-L15

LTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQR
LLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNNG
GKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQ
VVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLC
QAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNNGGKQALE
TVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIAS
NIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLT
PDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLP
VLCQAHGLTPAQVVAIASNGGGRPALESIVAQLSRPDPAL

CYTB-W$_{77}$-R13

LTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQR
LLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGG
KQALETVQRLLPVLCQAHGLTPAQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVL
CQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALE
TVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIAS
NNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGL
TPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGRPALESIVAQLS
RPDPAL

COX1-W$_{126}$-L17

LTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRL
LPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGK
QALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQV
VAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLC
QAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALE
TVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIAS
NNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGL
TPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRL
LPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGK
QALETVQRLLPVLCQAHGLTPDQVVAIASNIGGRPALESIVAQLSRPDPAL

COX1-W$_{126}$-R17

LTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQR
LLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNNG
GKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPE
QVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPV
LCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQAL
ETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIA
SNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHG
LTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQR
LLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGG
KQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGRPALESIVAQLSRPDPAL

COX2-W$_{104}$-L19

LTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLL
PVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGK
QALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQV
VAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQ

AHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGRPALESIVAQLSRPDPAL

COX2-W$_{104}$-R15

LTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGRPALESIVAQLSRPDPAL

COX3-W$_{57}$-L18

LTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGRPALESIVAQLSRPDPAL

COX3-W$_{57}$-R17

LTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPALESIVAQLSRPDPAL

Sequence S2.

Amino acid sequences of ND1-W_{86}-L-EGFP/R-mCherry-DdCBE.

Amino acid sequences of ND1-W_{86}-L-EGFP/R-mCherry-DdCBE using for FASC are annotated as: green for EGFP, red for mCherry, italics for linker, pink for P2A, and purple for DdCBE.

ND1-W_{86}-EGFP-L-DdCBE

MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWP
TLVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEG
DTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSV
QLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMD
ELYK*GSG*ATNFSLLKQAGDVEENPGPMLGFVGRVAAAPASGALRRLTPSASLPPAQLLL
RAAPTAVHPVRDYAAQTSESGGGGSPGAAADYKDDDDKGSVDLRTLGYSQQQQEKIK
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TKVFTGNSNSPKSPTKGGCSGGSTNLSDIIEKETGKQLVIQESILMLPEEVEEVIGNKPESD
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ND1-W_{86}-mCherry-R-DdCBE

MVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGP
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KGGCSGGSTNLSDIIEKETGKQLVIQESILMLPEEVEEVIGNKPESDILVHTAYDESTDENVMLLTSDAPEYKPWALVIQDSNGENKIKML