

Fig S1

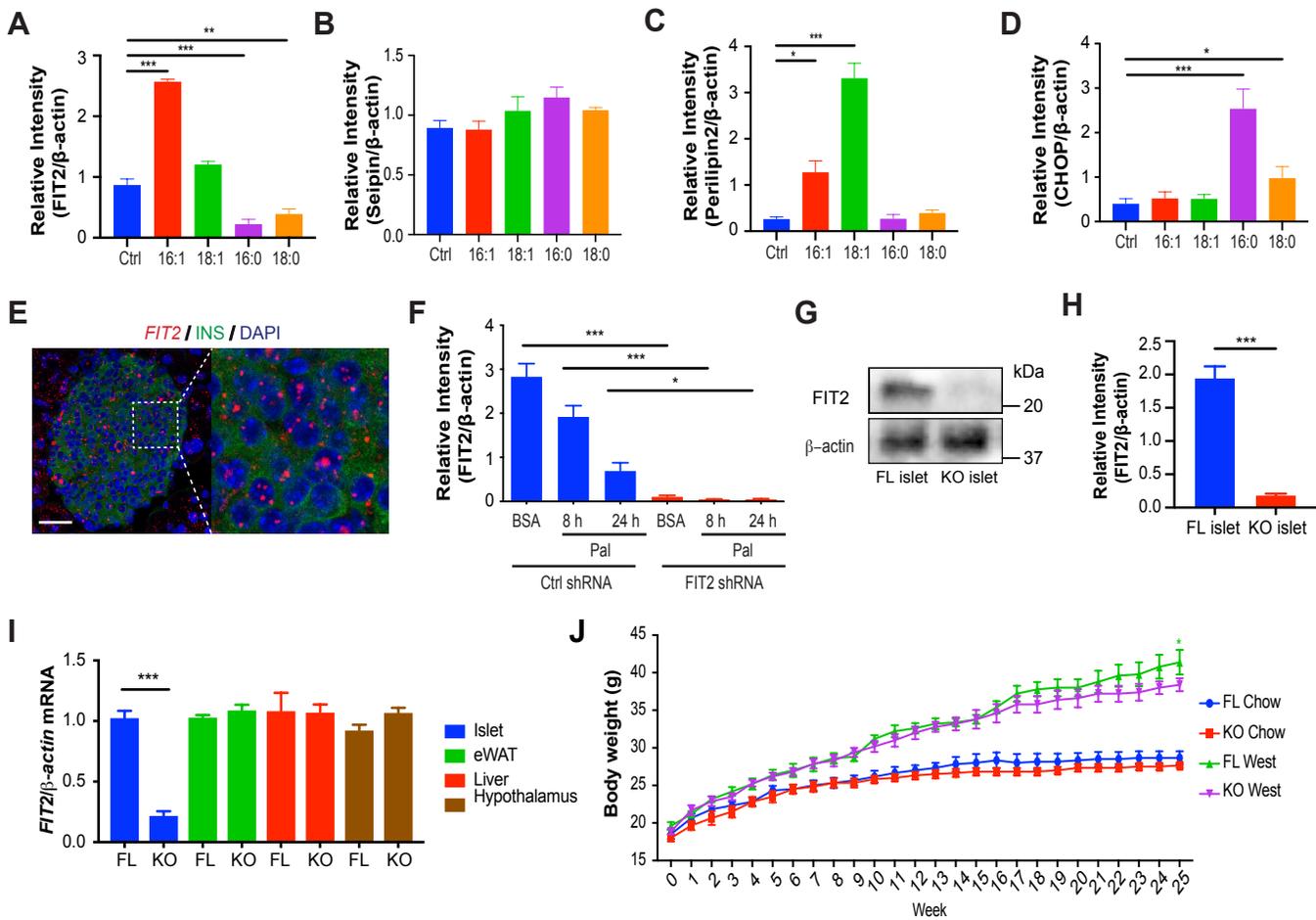


Fig S2

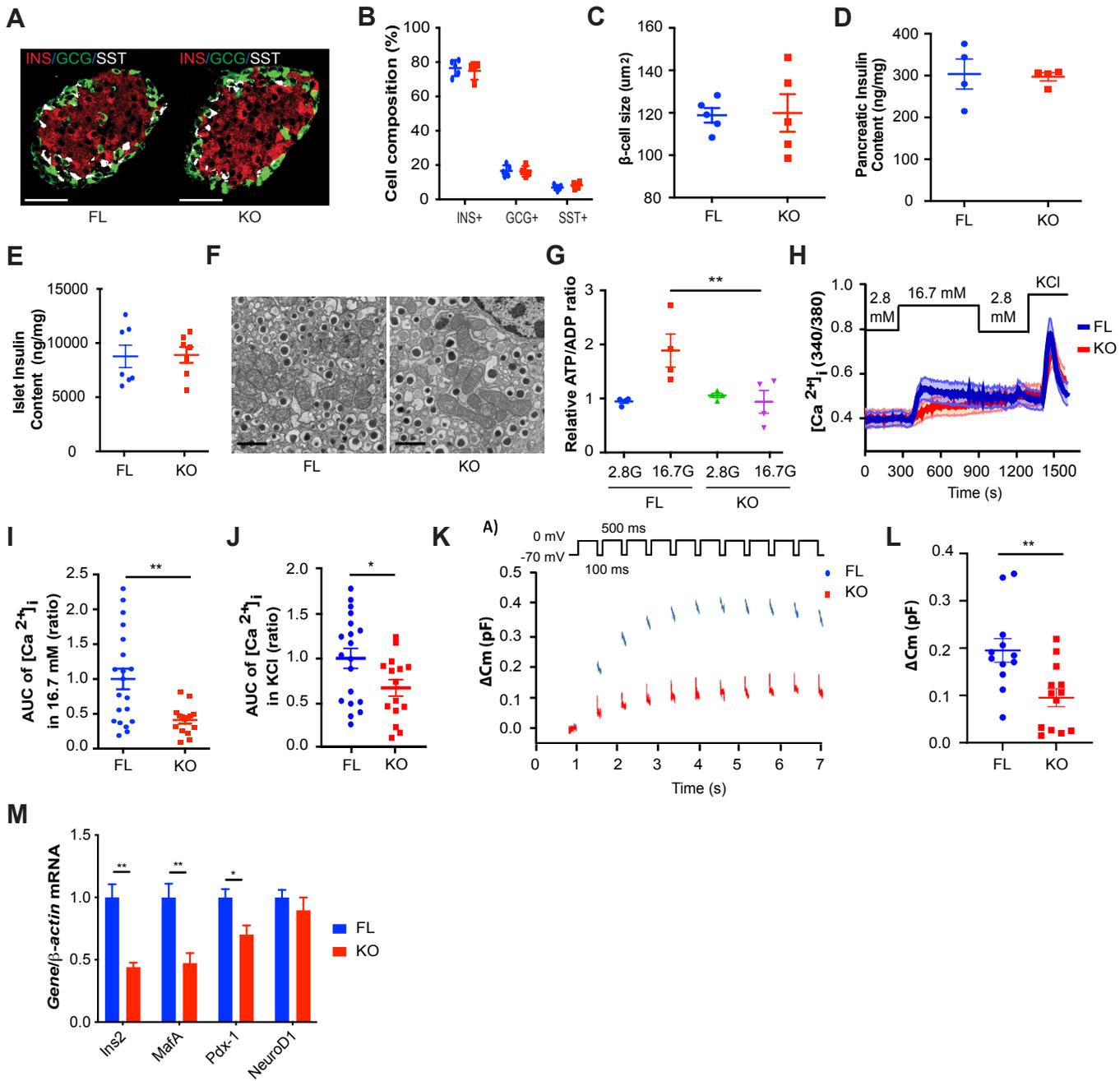


Fig S3

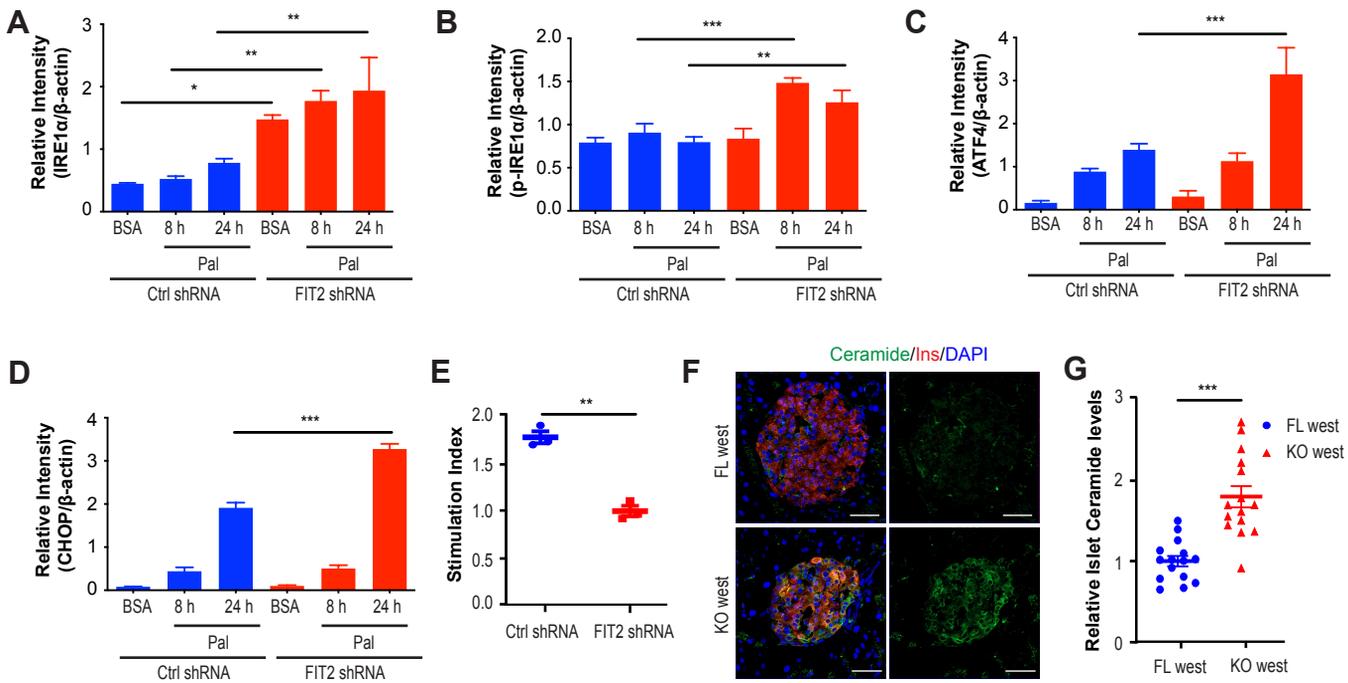
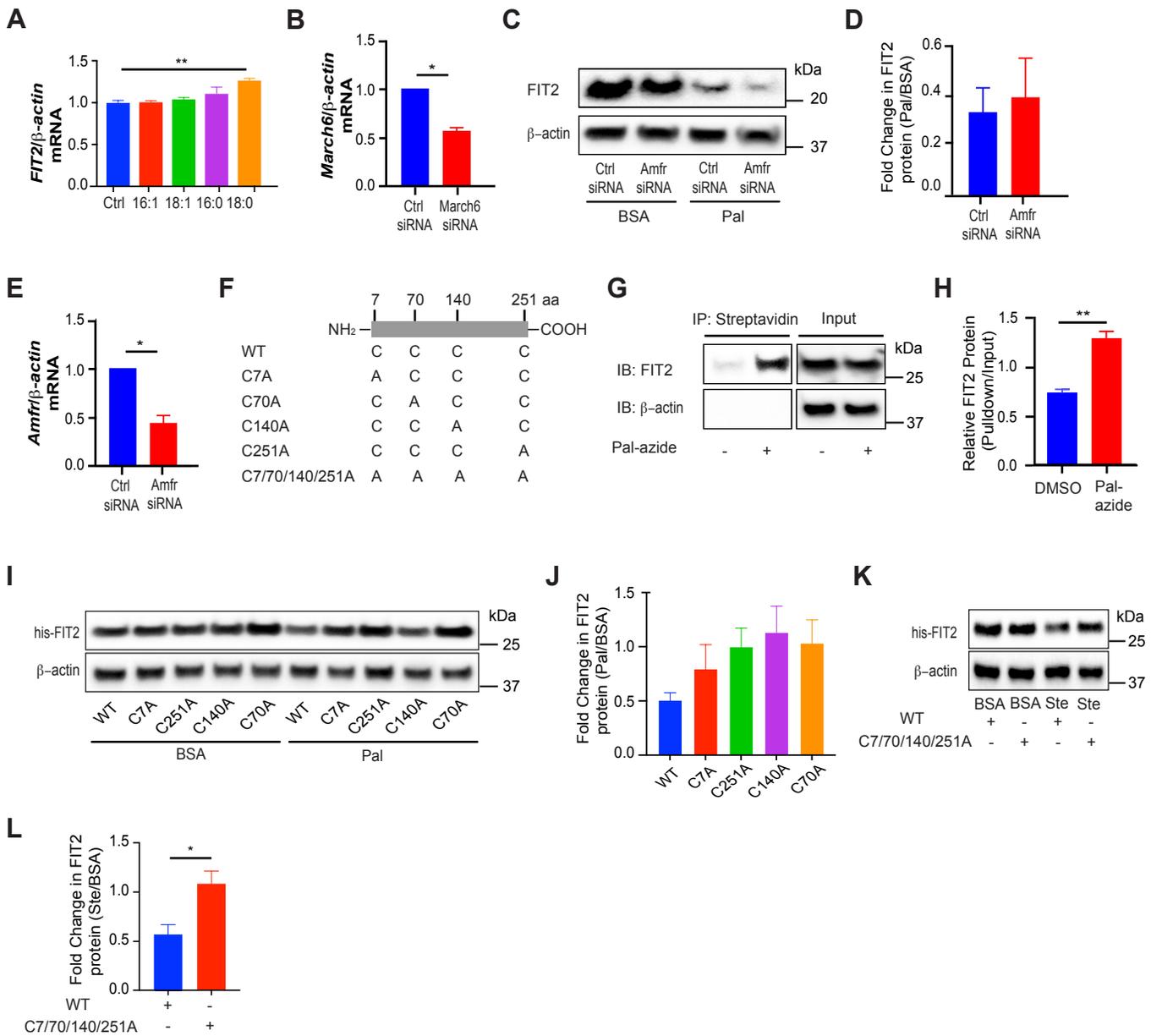


Fig S4



1 **Supplementary Information (SI) Appendix**

2
3 **SUPPLEMENTARY FIGURE LEGENDS**

4
5 **Supplementary Fig 1: Relative levels of LD formation proteins following FA**
6 **treatment as well as analysis of FIT2 in islets of β FIT2KO mice.**

7 **A-D**, Semi-quantitation of immunoblots for FIT2, Seipin, Perilipin2 and CHOP protein
8 levels in MIN6 cells treated with palmitoleate (16:1), oleate (18:1), palmitate (16:0),
9 stearate (18:0) (300 μ M, 24 h) or BSA control (N=3). **E**, Representative *in situ*
10 hybridization image for *FIT2* mRNA (red) combined with immunohistochemistry for
11 insulin (green) in pancreatic cryosections from C57BL/6 mice. DAPI was used to
12 counterstain the cell nucleus (blue). Expanded image (right) of the demarcated
13 section. Images shown are maximum-intensity projections. Scale bar = 50 μ m. **F**,
14 Semi-quantitation of immunoblot analysis of FIT2 expression in vector only (Ctrl
15 shRNA) or stable FIT2 knockdown (FIT2 shRNA) MIN6 cells treated with or without
16 palmitate (300 μ M, 24 h). **G**, Representative immunoblot and **H**, corresponding semi-
17 quantitation of FIT2 protein in isolated islets from floxed control (FL) and β FIT2KO
18 (KO) mice (12 wk-old male, N=7). **I**, Gene expression (qPCR) analysis of *FIT2*
19 mRNA levels in pancreatic islets, adipose tissue, liver and hypothalamus of floxed
20 control (FL) and β FIT2KO (KO) mice (12 wk-old male, N=3-4). **J**, Body weight of
21 floxed control (FL) and β FIT2KO (KO) fed with chow diet (FL Chow, KO Chow) or
22 West diet (FL West, KO West) for 25 weeks (30 wk-old at time of analysis, male,
23 N=6). Values shown are mean \pm SEM; *, P < 0.05; **, P < 0.01; ***, P < 0.001
24 relative to control (A, B, C, D: one-way ANOVA with Tukey's post-hoc test, F, J: two-
25 way ANOVA with Šidák post-hoc test), H, I: two-tailed Student's T-test.

26
27 **Supplementary Fig 2: Islet characteristics of β FIT2KO mice.**

28 **A**, Representative immunostaining for insulin (red), glucagon (green) and
29 somatostatin (white) in pancreas sections from FL and KO mice (12 wk-old male).
30 Scale bar = 50 μ m. **B, C**, Cell-type distribution and β -cell size analysis of *in situ* islets
31 in pancreas sections from floxed control (FL) and β FIT2KO (KO) mice (12 wk-old
32 male, N=4-5). **D, E**, Measurements of total pancreas (N=4) and islet (N=7) insulin
33 content. **F**, Representative Transmission Electron Microscope (TEM) images of
34 insulin granules of FL and KO pancreata (N=3). Scale bar = 1 μ m. **G**, ATP/ADP ratio
35 of FL and KO islets in 2.8 mM glucose (2.8 G) followed by stimulation with 16.7 mM
36 glucose (16.7 G). (N=4). **H**, Measurements of changes in $[Ca^{2+}]_i$ in FL and KO islets
37 exposed to varying concentrations of glucose "G" as indicated (15-20 islets from four
38 independent experiments were analyzed per group). **I**, AUC of $[Ca^{2+}]_i$ at 16.7 mM
39 glucose (N=15-20). **J**, AUC of $[Ca^{2+}]_i$ at 25 mM KCl (N=15-20). **L, K**, Measurements
40 of capacitance change in FL and KO islets. **L**, Representative traces of capacitance
41 recording obtained with a train of 10 consecutive depolarising pulses (500 ms steps,
42 100 ms interval) from -70 mV to 0 mV on FL (blue) and KO (red) islets. **K**,
43 Quantification of changes in capacitance upon the 10th depolarising pulse induction
44 between FL and KO islets (N=12 islets from 3 different 12-wk old mice each). **M**,
45 qPCR validation of RNA-Seq results with respect to changes seen in key β -cell
46 genes (N=5). Values shown are mean \pm SEM; *, P < 0.05; **, P < 0.01; ***, P < 0.001
47 (B, C, D, E, I, J, L, M: two-tailed Student's T-test, G: two-way ANOVA with Šidák
48 post-hoc test).

50 **Supplementary Fig 3: Relative levels of ER stress proteins and ceramide**
51 **immunodetection in pancreas of β FIT2KO mice.**

52 **A-D**, Semi-quantitation of immunoblot analysis of IRE1 α , p-IRE1 α , ATF4 and CHOP
53 protein levels in scrambled (Ctrl shRNA) or FIT2 knockdown (FIT2 shRNA) MIN6
54 cells in the absence (BSA) or presence of palmitate (300 μ M, 24 h). **E**, *Ex vivo*
55 insulin secretion, represented as Stimulation Index (16.7 mM / 2.8 mM), from
56 scrambled (Ctrl shRNA) or FIT2 knockdown (FIT2 shRNA) MIN6 cells. **F**,
57 Representative immunostaining image for insulin (red), ceramide (green) and DAPI
58 (blue) in pancreas sections from western diet fed FL and KO mice (30 wk-old, male,
59 N=3). Scale bar = 50 μ m. **G**, Quantitation of ceramide fluorescence intensities from
60 floxed control (FL) and β FIT2KO (KO) islets of western diet fed mice (30 wk-old,
61 male, N=3) (normalised to FL) using Image-J. Values shown are mean \pm SEM; *, P <
62 0.05; **, P < 0.01; ***, P < 0.001 (A, B, C, D: two-way ANOVA with Šidák post-hoc
63 test, E, G: two-tailed Student's T-test.

64

65 **Supplementary Fig 4: Relative changes in gene and protein levels of FIT2**
66 **following exposure to different FAs and separately on MARCH6 and AMFR**
67 **knockdown in MIN6 cells.**

68 **A**, Relative *FIT2* mRNA levels (qPCR) in MIN6 cells treated with BSA or different
69 FAs (300 μ M) for 24 h (N=3). **B-E**, MIN6 cells were transiently transfected with a
70 scrambled (ctrl siRNA) or different siRNA oligonucleotides targeting either *March6* or
71 *Amfr*. 48 h after transfection, cells were serum-starved for 2 h followed by treatment
72 with either BSA or palmitate (300 μ M) for 4 h. **B**, Relative *March6* gene expression
73 levels following siRNA mediated knockdown. **C**, **D**, Changes in FIT2 protein following
74 AMFR knockdown and palmitate (300 μ M, 4h) exposure. **E**, Relative *Amfr* gene
75 expression levels following siRNA mediated knockdown. **F**, Schematic
76 representation of point mutants (C \rightarrow A) of FIT2. **G**, **H**, Click-iT palmitoylation assay
77 of FIT2 protein in MIN6 cells transiently transfected with pcDNA3.1-FIT2/V5-His and
78 pre-treated with 10 μ M MG132 for 2 h followed by DMSO (Vehicle control) or 200 μ M
79 Click-IT™ Palmitic Acid, Azide treatment for 6 h. **I**, **J**, Representative immunoblot
80 analysis and semi-quantification of FIT2 protein levels in MIN6 cells transfected with
81 pcDNA3.1-FIT2/V5-His (WT) or mutants followed by treatment with BSA or palmitate
82 (300 μ M, 24 h). **K**, treatment of wild-type or quadruple mutant FIT2 with stearate
83 (300 μ M) for 24 h (N=3-4). Values shown are mean \pm SEM; *, P < 0.05; **, P < 0.01;
84 ***, P < 0.001 (A, J: one-way ANOVA with Tukey's post-hoc test, B, D, E, H, L: two-
85 tailed Student's T-test.

86

87 SUPPLEMENTARY MATERIALS AND METHODS

88

89 Islet isolation, dispersion and cell culture

90 Mouse pancreatic islets were isolated by perfusing the pancreas through the
91 common bile duct with collagenase. The isolated islets were dispersed into single
92 cells by incubation with Accutase at 37°C for 3-5 min. The primary islet cells were
93 cultured in CMRL medium supplemented with 10% heat-inactivated fetal bovine
94 serum (FBS), 100 U/ml penicillin and 100 µg/ml streptomycin. The mouse pancreatic
95 β-cell line MIN6 was kindly provided by Dr. Jun-ichi Miyazaki, Osaka University,
96 Japan (1). MIN6 cells (passages 30–35) were cultured in DMEM containing 25 mM
97 glucose, 10% heat-inactivated fetal bovine serum, 4 mM L-glutamine, 100 U/ml
98 penicillin, 100 µg/ml streptomycin and 50 µM 2-mercaptoethanol. HEK 293T/17 cells
99 were cultured in Dulbecco's modified Eagles medium (DMEM, 25 mM glucose)
100 containing 10% fetal bovine serum, 4 mM L-glutamine, 100 U/ml penicillin and
101 100 µg/ml streptomycin. Cells were maintained at 37 °C under 5% CO₂ and 95% air
102 condition. Transient transfections of Min6 and HEK 293T/17 cells were performed
103 using Liofectamine 2000 (Thermo Fisher Scientific) according to the manufacturer's
104 instructions. FFAs (palmitate, stearate, oleate and linoleate) were conjugated with
105 FFA-free BSA at a 2:1 molar ratio and used at a final concentration of 300 µM.

106

107 Lentiviral transduction for generation of shRNA-mediated stable knockdown cell
108 lines.

109 MISSION lentiviral transduction particles expressing shRNA targeting FIT2
110 (SHCLNV-NM_173397) and lentiviral-negative control particles (SHC002V) were
111 purchased from Sigma-Aldrich. Stable transduced cell lines were generated
112 according to the manufacturer's instructions. Briefly, cells were seeded on a 12-well
113 plate and infected with the lentiviral particles the following day. After 24 h medium
114 was changed. Selection of lentiviral expressing cells started 24 h later with the
115 addition of 2 µg/ml puromycin. Knockdown efficiency of different cell lines was
116 determined by immunoblotting and real-time PCR.

117

118 Protein extraction and immunoblotting assays

119 Cells and isolated islets were lysed in RIPA buffer supplemented with protease
120 inhibitor cocktail. Proteins were separated by SDS-PAGE and transferred onto
121 nitrocellulose membranes. Blocking was performed at room temperature for 1 h in
122 Tris-buffered saline (TBS) with 5% non-fat milk, followed by incubation with the
123 different primary antibodies (described below) in TBS with 5% non-fat milk for either
124 1 h at room temperature or overnight at 4 °C. After several washes with TBS
125 containing 0.5% Tween 20 (TBST), the membranes were incubated with secondary
126 antibodies of anti-mouse/rabbit IgG/HRP (as appropriate) in TBS with 1% non-fat
127 milk. Following several washes, the protein bands were visualized using enhanced
128 chemiluminescence (Cell Signaling Technology) and quantified using ImageJ.

129

130 RNA extraction and quantitative RT-PCR

131 Total RNA was prepared from tissues or cells using NucleoSpin RNA II kit
132 (Macherey-Nagel), or prepared from the isolated islets using the RNeasy® Plus Mini
133 Kit (Qiagen). 1 µg of RNA was reversely transcribed using High Capacity cDNA
134 Reverse Transcription Kit (Applied Biosystems) according to the manufacturer's
135 instructions. Real-time PCR was performed on QuantStudio 6 Flex Real-Time PCR
136 System (Applied Biosystems) using Power SYBR Green PCR Master Mix (Applied

137 Biosystems). The PCR primers used are summarized in Supplementary Table 3.

138

139 RNA-seq library preparation

140 Pancreatic islets were isolated from 12 week old wild type (WT) and β -cell specific
141 FIT2 knockout (β -FIT2KO, KO) mice in quintuplicate. Isolated pancreatic islets then
142 cultured in complete CMRL medium overnight for recovery. Total RNA was
143 harvested using RNeasy Plus Mini Kit (Qiagen). RNA-seq library construction was
144 conducted by Seqmatic. Briefly, polyA-tail specific mRNA libraries were prepared
145 from 1 μ g of total RNA with Illumina TruSeq stranded mRNA library preparation
146 protocol followed by single-end 75bp sequencing with the Illumina NextSeq to
147 generate an average of 50,578,630 reads per sample.

148

149 RNA-Seq data processing

150 Sequenced reads were aligned to the mm10 (GRCm38) mouse genome with STAR
151 version 2.5.2a (2) and transcripts were assembled with RSEM version 1.3.0 (3).
152 Cuffnorm version 2.2.1 (4, 5) was used to obtain quartile-normalized fragments per
153 kilobase per million reads (FPKM) expression matrix of genes across all samples.
154 Cuffdiff2 version 2.2.1 (4, 5) was used to identify differential genes between
155 samples. Genes were considered to be significantly differentially expressed when
156 false discovery rate (FDR) ≤ 0.05 , with FPKM ≥ 1 in one sample group retained for
157 subsequent analysis. GO clustering enrichment analysis was carried out on
158 differential genes using the Functional Annotation tool in DAVID version 6.8 under
159 medium stringency for all default annotation categories except protein domains. We
160 identified significant clustered groups having group enrichment scores of ≥ 1.3 , with
161 higher scores indicative of more significant annotated GO clusters. Heatmaps were
162 generated with R package pheatmap version 1.0.10 ([https://cran.r-](https://cran.r-project.org/web/packages/pheatmap/index.html)
163 [project.org/web/packages/pheatmap/index.html](https://cran.r-project.org/web/packages/pheatmap/index.html)).

164

165 Immunofluorescence

166 Pancreata were fixed with 4% paraformaldehyde for 6 h, followed by incubation with
167 30% sucrose overnight at 4 °C. Cryosections of 10 μ m thickness were used for
168 immunofluorescence analysis. Sections were rinsed with TBS, permeabilized, and
169 blocked with 10% normal goat serum plus 0.2% Triton X-100 in TBS for 1 h at room
170 temperature and then incubated overnight with primary antibodies at 4°C in a
171 humidified atmosphere. After gentle washing with TBS and incubating with
172 fluorescence secondary antibodies for 1 h at room temperature, sections were
173 mounted with Vecta Mount solution (Vector Labs) and analysed by confocal imaging
174 (Leica). For LD staining, cryosections were stained with BODIPY 493/503
175 (0.01mg/ml) and DAPI (5 μ g/ml) for 15 min at RT. For propidium iodide (PI) staining,
176 cells were incubated with 10 μ g/ml PI and 5 μ g/ml DAPI in medium for 1h at 37 °C
177 followed by RT fixation. Images were captured using a SP8 confocal microscope
178 (Leica). BODIPY-positive puncta per cell and percentage of PI-positive cells were
179 quantified using Image-J and Prism 7 (GraphPad).

180

181 LD staining

182 Cells were fixed with 4% paraformaldehyde solution for 15 min at RT. Fixed cells or
183 pancreas cryosections of 10 μ m thickness were stained with BODIPY 493/503
184 (0.01mg/ml) and DAPI (5 μ g/ml) for 15 min at RT. Images were captured using a
185 SP8 confocal microscope (Leica). BODIPY-positive puncta per cell was quantified
186 using Image-J and Prism 7 (GraphPad).

187

188 Propidium Iodide staining

189 Cells were incubated with 10 µg/ml propidium iodide (PI) and 5 µg/ml DAPI in
190 medium for 1h at 37 °C. After 3 times washing with phosphate-buffered saline (PBS),
191 cells were fixed with 4% paraformaldehyde solution for 15 min at RT and subjected
192 to confocal imaging. Percentage of PI-positive cells was quantified using Image-J
193 Prism 7 (GraphPad).

194

195 Islet cell composition and beta β-cell size

196 Islet cell composition was determined by dividing the number of individual cell types
197 (α, β or δ cells) by the total islet cell number per islet. β-cell size was determined by
198 dividing the insulin-positive area of each islet by the number of insulin-positive cells
199 within the same islet. For each group, >40 islets from non-serial sections of
200 pancreatic tissues from 5 animals were analyzed for both β-cell size and islet cell
201 composition.

202

203 Transmission electron microscopy

204 Mouse pancreas were either directly fixed at room temperature using 4%
205 formaldehyde/2% glutaraldehyde (Electron Microscopy Sciences, Hatfield, PA) in 0.1
206 M sodium cacodylate, pH 7.4, or cryo-fixed overnight as described previously (47).
207 Tissue samples were then washed twice with 0.1 M cacodylate buffer, post-fixed for
208 2 h in a mixture consisting of 1% osmium tetroxide (EMS) and 1.5% potassium
209 ferrocyanide (EMS) in 0.1M cacodylate, pH 7.4. Post-fixed tissues were washed with
210 distilled H₂O and dehydrated through an ethanol series (25%, 50%, 75%, 85%, 90%,
211 95%, 100%) and then in propylene oxide (EMS). Samples were subsequently
212 embedded in Epoxy resin for 1 h at 42 °C followed by 48 h at 65 °C. For all samples,
213 ultrathin sections of 50 nm were cut with diamond knife (Diatome, Switzerland) on
214 Leica Ultracut EM UC7 ultramicrotome (Leica Microsystems, Germany) and
215 collected onto formvar/carbon copper slot grids (EMS). Sections on grids were
216 contrasted with 4% aqueous uranyl acetate followed by Reynold's lead citrate and
217 analysed with a JEM-1010 Jeol transmission electron microscope (JEOL Ltd.,
218 Japan) operating at 80 kV. Images were acquired with SIA model 12C high
219 resolution full-frame CCD camera.

220

221 Total islet and pancreatic insulin content

222 To determine islet insulin content, around 10 isolated islets were washed twice with
223 ice-cold D-PBS and then lysed with RIPA buffer. Insulin and protein content of the
224 lysate were measured using Mercodia Mouse Insulin ELISA (Mercodia) and BCA
225 assay (Thermo Fisher Scientific), respectively. Total islet insulin content was
226 normalized to total protein content. To determine pancreatic insulin content, half of
227 the whole pancreas was collected and placed into 5 ml Acid-Ethanol solution (1.5%
228 HCl in 70% EtOH) overnight at -20°C. Tissue was then homogenized and incubated
229 in the same solution overnight at -20°C. Supernatant was collected by centrifugation
230 at 3000 x g for 10 min at 4°C, followed by neutralization with 1 M Tris pH 7.5 at 1:1
231 (vol/vol). Insulin and protein content of the neutralized solution were measured. Total
232 pancreatic insulin content was normalized by total protein content.

233

234 Glucose Stimulated Insulin Secretion (GSIS) Assay

235 To measure GSIS in Min6 cells, cells were pre-incubated at 37°C for 2 hr in KRBH
236 buffer (119 mM NaCl, 4.74 mM KCl, 2.54 mM CaCl₂, 1.19 mM MgCl₂, 1.19 mM

237 KH₂PO₄, 25 mM NaHCO₃, and 10 mM HEPES, pH 7.4) containing 0.1% BSA and
238 0.1 mM glucose. After washing with the same buffer, cells were then incubated in the
239 KRBH buffer containing 0.1% BSA and 0.1 mM glucose at 37°C for 30 min, followed
240 by incubation with KRBH buffer containing 0.1% BSA and 25 mM glucose for
241 another 30 min. The supernatant was collected for insulin measurements.

242 To measure GSIS in the isolated islets, islets were pre-incubated at 37°C for 2 hr in
243 buffer containing 125 mM NaCl, 5.9 mM KCl, 2.56 mM CaCl₂, 1.2 mM MgCl₂, 25
244 mM HEPES, 0.1% BSA and 2.8 mM glucose, pH 7.4 (2.8 G buffer). Batches of
245 around 50 islets were placed between two layers of bio-gel (Bio-Rad) in a perfusion
246 chamber and perfused at a flow rate of 200 µL/min, at 37°C, with 2.8 G buffer for 20
247 min prior to the start of collecting samples. To determine the dynamic response of
248 insulin secretion, islets were first perfused for 10 min with 2.8 G buffer, followed by
249 10 min with buffer containing 125 mM NaCl, 5.9 mM KCl, 2.56 mM CaCl₂, 1.2 mM
250 MgCl₂, 25 mM HEPES, 0.1% BSA and 16.7 mM glucose, pH 7.4 (16.7 G buffer),
251 prior to incubation with 2.8 G buffer for 30 min. Samples were collected every 2 min
252 for insulin measurements. At the end of the perfusion assay, islets were lysed in
253 RIPA buffer and total insulin content was measured. GSIS was normalized by total
254 islet insulin content.

255 To measure GSIS *in vivo*, mice were starved for 6 hr and blood were collected from
256 tail vein to determine basal insulin levels. Mice were then injected with 2 g
257 glucose/kg of body weight, intraperitoneally. Blood samples were collected from the
258 tail vein 15 min after glucose injection. Total blood was centrifuged at 10,000 x g for
259 10 min and the supernatant (serum) was collected for insulin measurements using
260 Mercodia Mouse Insulin ELISA (Mercodia).

261

262 Insulin and glucose tolerance tests

263 Prior to GTT or ITT, mice were fasted for 6 h with ad libitum access to water and
264 then administered glucose (2 g/kg) or insulin (0.75 unit/kg) intraperitoneally. Blood
265 glucose was measured in blood samples collected from tail vein using a glucometer
266 (Accu-Chek Performa Nano System).

267

268 *In vitro* [Ca²⁺]_i imaging and data analysis

269 *In vitro* imaging of whole intact islets was carried out 1-2 days after isolation from FL
270 and KO animals. Changes in cytosolic free Ca²⁺ concentration were measured
271 using fura2-AM on a fluorescence wide-field microscope (Leica DMI6000B). Single
272 islets were attached to glass coverslips using a peptide hydrogel (Corning Inc.,
273 354250) inside an open recording chamber (Warner Instruments), with the whole
274 system maintained at 37°C. Prior to imaging, islets were starved for 1 h in 2.8 G
275 buffer containing 4 µM Fura2-AM. Islets were stimulated with a glucose
276 concentration of 16.7 mM, Fura-2 fluorescence was measured using the excitation
277 from a xenon lamp (Sutter DG-4) and fura-2 filter set (Excitation 340/380 nm;
278 Dichroic 415 nm; Emission 510 nm). Responses were measured as area under the
279 curve (AUC), computed using the trapezoidal method. Due to the lack of a clear
280 peak and drifting baseline for the FIT2 KO group, the AUC was measured for only
281 the first 120 s of the response to high glucose. Analysis was carried out using
282 ImageJ and Prism 7 (GraphPad).

283

284 ATP/ADP Ratio

285 FL or KO islets were pre-incubated in 2.8 G buffer for 2 hr, then incubated with a 2.8
286 G or a 16.7 G buffer for 15 min. ATP/ADP ratio was determined with ADP/ATP Ratio

287 Bioluminescence Assay Kit (Biovision), according to manufacturer's instruction.

288

289 Membrane Capacitance

290 Membrane capacitance were recorded from intact pancreatic islets using the
291 standard whole cell patch clamp technique and software lock-in module of the
292 Patchmaster software together with an EPC10/2 amplifier (HEKA Elektronik). An 800
293 Hz, 25 mV peak-to-peak sinusoidal wave was applied around a holding potential of –
294 70 mV. β -cell exocytosis was triggered with 10 consecutive 500 ms depolarization
295 pulses (-70 to 0 mV) with 100 ms intervals. β -Cells were identified based on their
296 size ($C_m > 5$ pF) and discernible voltage-gated Na^+ currents (6). Islets are bathed in
297 extracellular solution containing the following: 118 mmol/L NaCl, 5.6 mmol/L KCl, 1.2
298 mmol/L $MgCl_2$, 10 mmol/L $CaCl_2$, 20 mmol/L tetraethylammonium chloride, 5
299 mmol/L HEPES, and 5 mmol/L glucose (310 mOsm, pH 7.4). The bath was perfused
300 continuously, and all recordings were carried out at room temperature. Recording
301 pipettes were pulled with P-1000 (4-7 M Ω ; Sutter Instrument Co.) and filled with an
302 internal solution containing the following: 125 mmol/L Cs-glutamate, 10 mmol/L
303 CsCl, 10 mmol/L NaCl, 1 mmol/L $MgCl_2$, 5 mmol/L HEPES, 0.05 mmol/L EGTA, and
304 3 mmol/L MgATP (300 mOsm, pH 7.3).

305

306 In situ RNA hybridization

307 In situ hybridization for FIT2 mRNA on pancreas tissue was performed using
308 RNAscope 2.5 HD Detection Kit - RED (Advanced Cell Diagnostics) according to the
309 manufacturer's instructions. Briefly, mouse pancreas was fixed with 4% PFA for 6 hr
310 at 4 °C. The fixed tissues were then immersed gradually through a series of 10%,
311 20% and 30% sucrose, frozen in the Optimal Cutting Temperature (OCT) embedding
312 media and cut at 10 μ m thickness. Tissue sections were sequentially pretreated with
313 RNAscope Hydrogen Peroxide, RNAscope Target Retrieval and RNAscope
314 Protease Plus reagents prior to hybridization with the target oligo probes. The
315 signals were then amplified and developed, followed by counterstaining insulin and
316 nuclei with IHC using anti-insulin antibody, Alexa 488-labeled anti-guinea pig
317 antibody and DAPI. Images were captured using the SP8 confocal microscope
318 (Leica).

319

320 Ceramide analysis

321 Pancreatic islets were resuspended in 100 μ L of butanol/methanol (1:1, v:v) spiked
322 with 66.07 nM of C8 Ceramide (d18:1/8:0) purchased from Avanti Polar Lipids
323 (860508). Cells were sonicated for 30 min followed by centrifugation at 14,000 g for
324 10 min at 22 °C. The supernatant was transferred to MS vials for analysis. The
325 samples were analysed using an Agilent 1290 series UHPLC system connected to
326 an Agilent 6495 QQQ mass spectrometer after separation on a ZORBAX Eclipse
327 plus C18 column (2.1 x 50 mm, 1.8 μ m, 95 Å, Agilent) at 40 °C. The injection volume
328 was 2 μ L. Solvent A consisted of 60% water/40% acetonitrile (v/v) with 10mM
329 ammonium formate; solvent B consisted of 90% isopropanol/10% acetonitrile (v/v)
330 with 10mM ammonium formate. The gradient started with a flow rate of 0.4 mL/min
331 at 20%B and increased to 60% B at 2 min, 100% B at 7 min, held at 100% B until 9
332 min, followed by equilibration with 20% B from 9.01 min until 10.8 min. The column
333 effluent was introduced to the Agilent 6495 QQQ mass spectrometer via AJS-ESI ion
334 source operating under the following conditions: Gas temperature, 200°C; gas flow,
335 14 L/min; nebulizer, 20 psi; sheath gas temperature, 250°C; sheath gas flow, 11
336 L/min; capillary, 3500 V. Mass spectrometry analysis was performed in positive ion

337 mode with dynamic scheduled multiple reaction monitoring (dMRM). Mass
338 spectrometry settings, LC-MS gradient and MRM transitions for each lipid class were
339 adapted from a previously published method (53). Data analysis was performed on
340 Agilent MassHunter Quantitative analysis software. Relative quantitation was based
341 on one-point calibration with Ceramide d18:1/8:0. The data were further normalized
342 to the total number of islets in each sample.

343

344 Co-immunoprecipitation assay

345 MIN6 cells, transiently co-transfected with pcDNA3.1-FIT2/V5-His and GFP-tagged
346 MARCH6 (BC059190) Mouse Tagged ORF Clone (Origene), were pre-treated with
347 10 μ M MG132 (Cell Signaling Technology) for 2 h and subsequently treated with 300
348 μ M palmitate (BSA-conjugated) for 6 h. Cells were then lysed in IP lysis buffer
349 (ThermoFisher Scientific), supplemented with protease inhibitor cocktail. Co-
350 immunoprecipitation assay was then performed on the protein lysates using Pierce™
351 Classic IP Kit (ThermoFisher Scientific) with either Anti-6X His tag antibody (Abcam)
352 or Rabbit IgG (Cell Signaling Technology) in accordance with the manufacturer's
353 instructions. The eluted fraction was then subjected to immunoblotting assay and
354 MARCH6 was detected using Mouse monoclonal turboGFP antibody (Origene).

355

356 S-Palmitoylation Assays

357 Thiol side-chain protection assay: MIN6 cells, transiently transfected with pcDNA3.1-
358 FIT2/V5-His, were pre-treated with 10 μ M MG132 (Cell Signaling Technology) for 2 h
359 and thereafter treated with 300 μ M palmitate (BSA-conjugated) for 6 h. S-
360 palmitoylation assay was then performed using CAPTUREome™ S-Palmitoylated
361 Protein Kit (Badrilla) in accordance with manufacturer's instruction. Briefly, cell lysis
362 and free thiol blocking (blocking of free thiols on non-palmitoylated cysteine residue)
363 was performed by incubating cells with the provided lysis buffer for 4 h with constant
364 shaking. Proteins were then precipitated using acetone, and subsequently
365 resuspended in the provided binding buffer. 30 μ l of resuspended proteins were
366 collected as the Input Fraction (IF), while the remainder was split into two tubes:
367 "experimental" and "negative control". In the experimental tube, proteins were treated
368 with thioester cleavage reagent, which cleaves off acyl groups from the protein,
369 resulting in the exposure of a free thiol group. Treated samples were then subjected
370 to CAPTUREome™ resin for 2.5 h at room temperature, where proteins with free
371 thiols were captured by the resin. 50 μ l of flowthroughs were collected as the cleaved
372 unbound fraction (cUF). S-acylated proteins, which were captured by the
373 CAPTUREome™ resin, were eluted by incubating the resin in 50 μ l of 2x laemmli
374 buffer at 60°C for 10 min (cleaved Bound Fraction (cBF)). In the negative control
375 tube, proteins were treated with acyl-preservation reagent, which preserves acyl
376 groups on the protein. Treated samples were then subjected to CAPTUREome™
377 resin for 2.5 h at room temperature. 50 μ l of flowthroughs were collected as
378 preserved unbound fraction (pUF). Proteins were eluted from the CAPTUREome™
379 resin by incubation of resin with 50 μ l of 2x laemmli buffer at 60°C for 10 min
380 (preserved Bound Fraction (pBF)).

381 Click-chemistry S-palmitoylation Assay: MIN6 cells, transiently transfected with
382 pcDNA3.1-FIT2/V5-His, were pre-treated with 10 μ M MG132 (Cell Signaling
383 Technology) for 2 h and thereafter treated with 200 μ M Click-IT™ Palmitic Acid,
384 Azide (ThermoFisher Scientific) for 6 h. Cells were then lysed in 50 mM Tris-HCL,
385 pH 8.0, supplemented with 1% SDS and protease inhibitor cocktail. Palmitoylated
386 proteins were conjugated using the Click-iT® Protein Reaction Buffer Kit

387 (ThermoFisher Scientific), in accordance with manufacturer's instructions, without
388 modifications.
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390

391 SUPPLEMENTARY TABLE OF REAGENTS
392

REAGENT or RESOURCE	SOURCE	IDENTIFIER	Lot
Antibodies			
Rabbit polyclonal anti-FIT2	Dr. David L. Silver	(7)	
Rabbit polyclonal anti-Seipin	Abcam	Cat# ab106793	
Rabbit polyclonal anti-Perilipin-2	Novus Biologicals	Cat#NB110-40877	Lot# F-1
Rabbit polyclonal anti-CHOP (F-168)	Santa Cruz Biotechnology	Cat# sc-575	Lot# F2613
Rabbit polyclonal anti-ATF4 (C-20)	Santa Cruz Biotechnology	Cat# sc-200	Lot# G0115
Rabbit polyclonal anti-p-eIF2 α (Ser 52)	Santa Cruz Biotechnology	Cat# sc-101670	Lot# C0714
Rabbit monoclonal anti-IRE1 α (14C10)	Cell Signaling Technology	Cat#3294	Lot# 9
Rabbit polyclonal anti-p-IRE1 α (p Ser724)	Novus Biologicals	Cat#NB100-2323	Lot# AF-3
Mouse monoclonal anti- β -actin (AC-15)	Abcam	Cat#6276	Lot# GRC3207325-9
Rabbit polyclonal anti-6XHis	Abcam	Cat#ab9108	Lot# GR3246563-1
Mouse monoclonal turboGFP antibody, clone OTI2H8	Origene	Cat#TA150041	Lot#W004
Normal Rabbit IgG	Cell Signaling Technology	Cat#2729	Lot#8
Horse anti-mouse IgG (HRP-linked)	Cell Signaling Technology	Cat#7076	Lot# 31
Goat anti-rabbit IgG (HRP-linked)	Cell Signaling Technology	Cat#7074	Lot# 28
Guinea pig polyclonal anti-Insulin	Dako	Cat#A0564	Lot# 10088287
Mouse monoclonal anti-glucagon (K79bB10)	Sigma-Aldrich	Cat#G2654	
Monoclonal Anti-Ceramide antibody produced in mouse	Sigma-Aldrich	Cat#C8104	Lot# SLCC3937
Rat monoclonal anti-somatostatin (YC7)	Merk Millipore	Cat#MAB354	
Goat anti-guinea pig IgG, Alexa Fluor 488	Thermo Scientific Fisher	Cat#A11073	Lot# 1737010
Goat anti-guinea pig IgG, Alexa Fluor 568	Thermo Scientific Fisher	Cat#A11075	Lot# 1692965
Goat anti-mouse IgG, Alexa Fluor 488	Thermo Scientific Fisher	Cat#A28175	Lot# 1611153
Goat anti-Mouse IgM (Heavy chain) Cross-Adsorbed Secondary Antibody, Alexa Fluor 488	Thermo Scientific Fisher	Cat#A21042	Lot# 2079371
Goat anti-rat IgG, Alexa Fluor 647	Thermo Scientific Fisher	Cat#A21247	
Goat anti-rabbit IgG, Alexa Fluor 488	Thermo Scientific Fisher	Cat#A32731	Lot# 1622775
Bacterial and Virus Strains			
FIT2 MISSION shRNA lentiviral transduction particles	Sigma-Aldrich	Cat#SHCLNV-NM_173397 (TRCN0000125380)	
MISSION pLKO.1-puro non-target shRNA control transduction particles	Sigma-Aldrich	Cat#SHC016V	
Chemicals, Peptides, and Recombinant Proteins			
BODIPY 493/503	Thermo Scientific Fisher	Cat#D3922	

Fura-2, AM	Thermo Scientific	Fisher	Cat#F1225	
DAPI	Thermo Scientific	Fisher	Cat#D1306	
Propidium iodide	Thermo Scientific	Fisher	Cat#P1304MP	
Palmitic acid	Sigma-Aldrich		Cat#57-10-3	
Click-IT™ Palmitic Acid, Azide (15-Azidopentadecanoic Acid)	Thermo Scientific	Fisher	Cat#C10265	
Biotin Alkyne (PEG4 carboxamide-Propargyl Biotin)	Thermo Scientific	Fisher	Cat#B10185	
Oleic acid	Sigma-Aldrich		Cat#112-80-1	
Stearic acid	Sigma-Aldrich		Cat#57-11-4	
Palmitoleic acid	Sigma-Aldrich		Cat#P9417	
Sodium hydroxide	Sigma-Aldrich		Cat#1310-73-2	
D-(+)-Glucose	Sigma-Aldrich		Cat#50-99-7	
Humalog U-100 insulin	Eli Lilly		Cat#HP8799	
MG-132	Cell Signaling Technology		Cat#2194	
2-Bromopalmitic acid	Sigma-Aldrich		Cat#21604	
Eeyarestatin	Sigma-Aldrich		Cat#E1286	
Cerulenin	Sigma-Aldrich		Cat#C2389	
Critical Commercial Assays				
RNAscope 2.5 HD detection kit (red)	Advanced Diagnostics	Cell	Cat#322360	
Pierce BCA protein assay kit	Thermo Scientific	Fisher	Cat#23225	
Lipofectamine 2000 transfection reagent	Thermo Scientific	Fisher	Cat#11668019	
Fast SYBR green master mix	Thermo Scientific	Fisher	Cat#4385617	
Pierce™ Classic IP Kit	Thermo Scientific	Fisher	Cat#26146	
Pierce® IP Lysis Buffer	Thermo Scientific	Fisher	Cat# 87788	
RIPA buffer	Sigma-Aldrich		Cat#R0278	
Protease inhibitor cocktail	Sigma-Aldrich		Cat#P8340	
SignalFire ECL reagent	Cell Signaling Technology		Cat#6883	
ADP/ATP ratio bioluminescence assay kit	BioVision		Cat#255-200	
NucleoSpin RNA XS	Macherey-Nagel		Cat#740902	
NucleoSpin RNA	Macherey-Nagel		Cat#740955	
Mouse Insulin ELISA	Mercodia		Cat#10-1247-01	
Ultrasensitive mouse Insulin ELISA	Mercodia		Cat#10-1249-01	
Apo-ONE homogeneous caspase-3/7 assay	Promega		Cat#G7790	
CAPTUREome™ S-Palmitoylated Protein Kit	Badrilla		Cat#K010-311	
Deposited Data				
RNAseq Data	GEO		GEO: GSE133939	
Experimental Models: Cell Lines				
Min6 cells	Dr. Jun-ichi Miyazaki		(1)	

Min6 cells stably expressing control shRNA	This study	N/A	
Min6 cells stably expressing FIT2 shRNA	This study	N/A	
Human: HEK 293T/17	ATCC	Cat#CRL-11268	
Experimental Models: Organisms/Strains			
Mouse: C57BL/6J	The Jackson Laboratory	Cat#000664	
Mouse: FIT2fl/fl	Dr. David L. Silver	(8)	
Mouse: B6.Cg-Tg (Ins2-cre) 25Mgn/J	The Jackson Laboratory	Cat#003573	
Mouse: 129S1/SvImJ	The Jackson Laboratory	Cat#002448	
Mouse: B6.Cg-Tg (Ins2-cre) 25Mgn/J:129S1/SvImJ	This study	N/A	
Mouse: C57BL/6J:129S1/SvImJ	This study	N/A	
Mouse: B6.Cg-Tg(Ins2-cre)25Mgn/J:FIT2fl/fl	This study	N/A	
Mouse: B6.BKS (D)-Lepr ^{db} /J	The Jackson Laboratory	Cat#000697	
Oligonucleotides			
ON-TARGETplus March6 siRNA SmartPool	Horizon Discovery	Cat# L-055065-01-0020	
ON-TARGETplus Amfr siRNA SmartPool	Horizon Discovery	Cat#L-048676-01-0020	
See Supplemental Table 2 for primer sequences	This study	N/A	
Recombinant DNA			
pcDNA3.1 mammalian expression vector	Thermo Fisher Scientific	Cat#V79020	
pcDNA3.1-FIT2	Dr. David L. Silver	(9)	
pcDNA3.1-FIT2/V5-His	Dr. David L. Silver	(9)	
pcDNA3.1-FIT2(C7A)/V5-His	Bio Basic Inc.	N/A	
pcDNA3.1-FIT2(C70A)/V5-His	Bio Basic Inc.	N/A	
pcDNA3.1-FIT2(C140A)/V5-His	Bio Basic Inc.	N/A	
pcDNA3.1-FIT2(C251A)/V5-His	Bio Basic Inc.	N/A	
pcDNA3.1-FIT2(C7/70/140/251A)/V5-His	Bio Basic Inc.	N/A	
March6 (BC059190) Mouse Tagged ORF Clone	Origene	CAT#MG207831	
Software and Algorithms			
GraphPad Prism 7	GraphPad	https://www.graphpad.com	
Image Lab 5.0	Bio-Rad	https://www.bio-rad.com/en-sg/product/image-lab-software	
Leica LAS X software	Leica	https://www.leica-microsystems.com/products/microscope-software	
NIS-Elements software	Nikon	https://www.microscope.healthcare.nikon.com/products/software	
ImageJ	N/A	https://imagej.net/Welcome	

Other			
Chow diet	Altromin	Cat#1324	
Western diet	Research Diets	Cat#D12079B	

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Data Table S1. Oligonucleotides

Name	Forward primer (5' - 3')	Reverse primer (5' - 3')
qPCR		
<i>Fit2</i>	CACGACTTGACCCAGAAAGTG	GGAGGAAGTCCTGGAGAGAAA
<i>Ins2</i>	CCATCAGCAAGCAGGAAGCCTATC	CCCCACACACCAGGTAGAGAGCC
<i>MafA</i>	GAGGTCATCCGACTGAAAC	CACTTCTCGCTCTCCAGA
<i>Pdx-1</i>	GAAATCCACCAAAGCTCAC	AAGAATTCCTTCTCCAGCTC
<i>NeuroD1</i>	AACAACAGGAAGTGGAAC	TTTCTTGTCTGCCTCGTG
<i>β-actin</i>	GACAGGATGCAGAAGGAGAT	TTGCTGATCCACATCTGCTG
Genotyping		
Cre5	GCAAGTTGAATAACCGGAAATGGTT	AGGGTGTTATAAGCAATCCCCAGAA
FL146	CCCATGTTAGTAGAAGCAAGCGTGA	ACAAGGAAAGCCTCGTTAAAACCAA