1	TiTle: mitoNEET Regulates Mitochondrial Iron Homeostasis Interacting with
2	Transferrin Receptor
3	
4	Running Title: mitoNEET Regulates Mitoiron Homeostasis
5	
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7	mitochondrial respiration; cardiac dysfunction
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33 Abstract

34 Iron is an essential trace element for regulation of redox and mitochondrial function, 35 and then mitochondrial iron content is tightly regulated in mammals. We focused on a 36 novel protein localized at the outer mitochondrial membrane. Immunoelectron 37 microscopy revealed transferrin receptor (TfR) displayed an intimate relationship with 38 the mitochondria, and mass spectrometry analysis also revealed mitoNEET interacted 39 with TfR in vitro. Moreover, mitoNEET was endogenously coprecipitated with TfR in 40 the heart, which indicates that mitoNEET also interacts with TfR in vivo. We generated 41 mice with cardiac-specific deletion of mitoNEET (mitoNEET-knockout). Iron contents 42 in isolated mitochondria were significantly increased in mitoNEET-knockout mice 43 compared to control mice. Mitochondrial reactive oxygen species (ROS) were higher, 44 and mitochondrial maximal capacity and reserve capacity were significantly decreased 45 in mitoNEET-knockout mice, which was consistent with cardiac dysfunction evaluated by echocardiography. The complex formation of mitoNEET with TfR may regulate 46 47 mitochondrial iron contents via an influx of iron. A disruption of mitoNEET could thus 48 be involved in mitochondrial ROS production by iron overload in the heart. 49

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50 Introduction

51	Mitochondrial function is impaired with aging in various organs, including the
52	heart, brain, and skeletal muscle (Bagh, Thakurta et al., 2011, Kwong & Sohal, 2000, Li,
53	Kumar Sharma et al., 2013, Sugiyama, Takasawa et al., 1993). Age-dependent
54	mitochondrial dysfunction is one of the main causes of organ failure and cellular
55	dysfunction (Dai & Rabinovitch, 2009). Mitochondria are one of the main sources of
56	reactive oxygen species (ROS) generation, which is associated with mitochondrial
57	dysfunction. Conversely, mitochondria are highly susceptible to attack by ROS, because
58	they contain iron/sulfur clusters (ISCs). Thus, once the mitochondria are impaired for
59	any reason, an increase in ROS generation can, in itself, induce a vicious cycle of
60	further impairment in mitochondria function, further ROS generation, and cellular
61	injury (Ikeuchi, Matsusaka et al., 2005, Suematsu, Tsutsui et al., 2003).
62	Iron is one of the most abundant metals on earth and an essential trace element
63	for both cellular energy and metabolism and the maintenance of body homoeostasis.
64	Excessive iron damages cells via iron toxicity and ROS production, while iron
65	deficiency impairs cellular proliferation (Oliveira, Rocha et al., 2014). Thus iron
66	concentrations in mammals need to be tightly and constantly regulated at the dietary,
67	plasma, extracellular, cellular and mitochondrial levels (Ganz, 2013). Despite the
68	numerous studies on iron homeostasis in the last few decade (Anderson, Shen et al.,
69	2012, Anderson & Vulpe, 2009), mitochondrial iron homeostasis remains largely
70	unexplored. ISCs and heme are produced only within mitochondria (Richardson, Lane
71	et al., 2010), and are used as components of many enzymes in the cytosol and
72	mitochondria. Therefore, iron-homeostasis regulation is closely associated with
73	mitochondrial function and cellular function. Some proteins involved in influx of iron to

74	mitochondria, transfer of iron within mitochondria, and efflux of iron from
75	mitochondria have been identified, and all these proteins exist in the mitochondrial
76	inner membrane or within mitochondria (Branda, Cavadini et al., 1999, Ichikawa,
77	Bayeva et al., 2012, Paradkar, Zumbrennen et al., 2009, Srinivasan, Pierik et al., 2014,
78	Vigani, Tarantino et al., 2013). Iron bound on transferrin (Tf) and transferrin receptor
79	(TfR), namely Tf-TfR complex, is carried to the cytosol as endosomes, and then iron
80	dissociated from the complex transports across the endosomal membrane to the labile
81	iron pool in the cytosol. Iron from the labile iron pool is carried into the mitochondria to
82	utilize this iron for mitochondrial iron homeostasis (Gkouvatsos, Papanikolaou et al.,
83	2012). Whereas some proteins involved in iron inflow into the mitochondria are known
84	to be in the inner mitochondrial membrane (Richardson et al., 2010), novel proteins
85	involved in mitochondrial iron homeostasis may also exist in the outer mitochondrial
86	membrane (OMM).
87	It has recently been reported that mitoNEET is a novel protein localized at the
88	OMM and a target protein of the insulin-sensitizing drug pioglitazone (Wiley, Murphy
89	et al., 2007a). Analysis of the expression of mRNAs from murine tissues revealed that
90	mitoNEET was widely expressed in mice, with especially high levels in the heart.
91	Experiments using optical and electron paramagnetic resonance spectroscopy clarified
92	that mitoNEET contained iron/sulfur clusters that were redox-active and functioned as
93	electron-transfer proteins (Wiley, Paddock et al., 2007b). Moreover, complex I-linked
94	state 3 respiration was significantly decreased in isolated mitochondria from the hearts
95	of mitoNEET-null mice. These results allowed us to hypothesize that mitoNEET was a
96	candidate for the regulatory protein of iron homeostasis.

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97	The regulation of mitochondrial function is especially important for the
98	maintenance of cardiac function, because the heart is a mitochondria-rich organ (Rosca
99	& Hoppel, 2010). In the present study, we focused on the mechanisms underlying the
100	regulation of mitochondrial iron homeostasis in the heart, and verified our hypothesis
101	that mitoNEET is the regulator of iron homeostasis. To accomplish this, we used lox-P
102	and homologous recombination to establish mice with cardiac-specific deletion of
103	mitoNEET.

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105 Results

106 mitoNEET combines with TfR and is regulated by iron

107 TfR have been known to be located in plasma membrane or endosome (Das, 108 Nag et al., 2016). Surprisingly, in mitochondrial fraction, TfR were detected evaluated 109 by immunoblot, though there existed no other proteins localized in cellular matrix 110 (glyceraldehyde phosphate dehydrogenase; GAPDH), endosome (Ras-related protein 111 Rab-5; Rab5) or plasma membrane (Cadherin) (Fig 1A). The silver-intensified 112 immunogold method for electron microscopy revealed the subcellular localization of 113 TfR in the C2C12 cells incubated with iron. Immunogold particles showing the 114 localization of TfR were frequently associated with (cytoplasmic) vesicles and vacuoles 115 of various sizes and shapes, which might correspond to endosomes. In addition, gold 116 particles displayed an intimate relationship with mitochondria, where they attached the 117 outer membrane of mitochondria. (Fig 1B). Protein-protein interactions are often 118 important to realize biological functions in vivo. To elucidate what kind of 119 mitochondrial protein is involved in mitochondrial iron homeostasis, we focused on TfR. 120 That is because TfR is thought to have a critical role in iron uptake into the cell. So 121 silver-stained gels with the immunoprecipitated protein by TfR antibody in the 122 mitochondria from the mouse heart acquired some bands (Fig 1C), suggesting that 123 endogenous TfR coprecipitated with some endogenous mitochondrial proteins. We 124 think that mitoNEET could play a critical role in mitochondrial iron homeostasis, for 125 mitoNEET simultaneously fulfill below conditions; localized at the OMM (Das et al., 126 2016, Wiley et al., 2007a), containing ISCs (Paddock, Wiley et al., 2007), and involved 127 in iron metabolism (Kusminski, Holland et al., 2012) (Fig 1D). Actually, candidate proteins were picked up by using mass spectrometry, and what we focused on as the 128

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129 strongest candidate was just TfR (**Fig 1E, Appendix Table S1, S2**). Moreover,

130 mitoNEET was endogenously coprecipitated with TfR in the heart, which indicates that

- 131 mitoNEET also interacts with TfR in vivo (Fig 1F, 1G). The levels of mitoNEET
- 132 protein expression were higher in the addition of ferric ammonium citrate, and lower in
- 133 the addition of desferioxamine compared to control (Fig 1H), and the changes in iron
- 134 content were consistent with the changes in mitoNEET protein expression (Appendix
- 135 Fig S1), suggesting that there may be some connections between mitoNEET and iron

136 homeostasis. There was a significant positive correlation between mitoNEET expression

137 levels and mitochondrial respiration (**Fig 1I**), suggesting that mitoNEET may have an

138 important role in regulating cellular function via iron homeostasis.

139

140 mitoNEET and Tranferrin Receptor Colocalizes on the Mitochondria

141 If mitoNEET interact with transferrin receptor, these proteins should colocalize 142 in the mitochondria. We subsequently performed immunoprecipitation by using 143 mitochondrial fraction. As we expected, mitoNEET coprecipitated with TfR in 144 mitochondria from the heart in mice, suggesting that TfR, which has been thought to be 145 only plasma membrane or endosomes, did exist with mitochondria (Fig 2A). Moreover, 146 to determine whether TfR localizes to the OMM, we used digitonin, which is efficiently 147 able to extract cholesterol in the OMM protein (Arasaki, Shimizu et al., 2015). To 148 confirm the purity of isolated mitochondria, Cadherin and GAPDH were analyzed by 149 immunoblot. These were not detected in supernatant and pellet. Heat-shock protein 60 150 was not detected in supernatant even with the treatment of digitonin, suggesting that 151 digitonin used in the present study did not affect the inner mitochondrial membrane. 152 Voltage-dependent anion channel (VDAC), a known OMM protein, was dose-

153	dependently increased in supernatant and decreased in pellet by digitonin treatment. The
154	changes in mitoNEET and TfR protein levels by the treatment with digitonin were
155	similar to VDAC (Fig 2B). These data strongly suggest that TfR localizes to the OMM
156	interacting with mitoNEET, besides plasma membrane or endosome. Immunostaining
157	for mitoNEET (green) merged with TfR (red) in mouse C2C12 cells. In control,
158	mitoNEET was localized at the OMM along surface of the mitochondria, and TfR
159	mainly existed on the inside of cytosolic membrane. In iron overload circumstances,
160	TfR partially transferred from membrane to cytosol, some of which colocalized with
161	mitoNEET, suggesting that this increase of colocalization helps TfR to stay on the
162	mitochondria in order to cope with iron overload (Fig 2C).
163	
164	Creation of Cardiac-Specific mitoNEET-knockout Mice
101	•
165	To establish mice with cardiac-specific deletion of mitoNEET, lox-P and
	-
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 165 166 167 168 169 170 171 172 173 174 	To establish mice with cardiac-specific deletion of mitoNEET, lox-P and homologous recombination strategies were used (Appendix Fig S2A). As controls, we generated mitoNEET flox/flox mice in similar manner. Cardiac-specific deletion of mitoNEET was achieved using αMHC-Cre (Appendix Fig S2B). The cardiac-specific mitoNEET-knockout mice were viable and fertile, and there were no differences in appearance, body weight or cardiac phenotype between control and mitoNEET- knockout mice at a young age (about 3 months). Levels of the mRNA of <i>CISD1</i> , encoding the mitoNEET protein, were significantly lower in the whole heart of mitoNEET-knockout than control mice (Appendix Fig S2C). To characterize the mitoNEET protein expression, we generated a mitoNEET polyclonal antibody using a

177	electrophoresis (SDS-PAGE), confirmed the mitoNEET expression in the hearts of
178	control mice. The C-terminal fragment of mitoNEET (below 2 kDa) is also shown as a
179	positive control. As expected, immunoblot analysis revealed that mitoNEET protein
180	expression was widely detected in the brain, heart, liver, kidney and skeletal muscle of
181	control mice, but was absent in the hearts of mitoNEET-knockout mice (Fig 3A).
182	Immunohistochemical analysis of mitoNEET expression indicated that mitoNEET was
183	broadly present in cardiac cells (Appendix Fig S2E).
184	
185	Interaction between mitoNEET and TfR in mitoNEET-knockout Mice
186	To confirm the complex formation of other proteins with mitoNEET, we
187	performed a Blue Native Polyacrylamide Gel Electrophoresis (BN-PAGE) retardation
188	assay in mitochondrial fractions derived from control mice and mitoNEET-knockout
189	mice. This assay identified the smear in control mice (Appendix Fig S3, left lane). In
190	contrast, these bands were almost completely absent in mitoNEET-knockout mice,
191	especially in the range of 50-150 kDa (Appendix Fig S3, right lane). This clearly
192	shows the specific formation of complexes with mitoNEET. TfR expression levels in
193	the mitochondria from mitoNEET-knockout mice was lower than from control mice,
194	suggesting that mitoNEET interact with TfR on the OMM in vivo (Fig 3B).
195	
196	mitoNEET Regulates Mitochondrial Iron Contents
197	The iron contents in isolated mitochondria were significantly higher in
198	mitoNEET-knockout than control mice (Fig 3C). In parallel with the iron contents, the
199	levels of mitochondrial ferritin, a mitochondrial iron storage protein, was significantly
200	higher in mitoNEET-knockout than control mice (Appendix Fig S4A). However, there

201	was no difference between the two groups in levels of other proteins involved in
202	mitochondrial iron homeostasis, i.e., mitoferin2 (MFRN2, Appendix Fig S4B), frataxin
203	(FXN, Appendix Fig S4C), adenosine triphosphate (ATP)-binding cassette protein B7
204	(ABCB7, Appendix Fig S4D), and ATP-binding cassette protein B8 (ABCB8,
205	Appendix Fig S4E); proteins involved in cytosolic iron homeostasis, i.e., TfR
206	(Appendix Fig S4F), divalent metal transporter 1 (DMT1, Appendix Fig S4G), and
207	ferroportin (Fpn, Appendix Fig S4H); proteins involved in cellular iron homeostasis,
208	i.e., iron regulatory protein 1 (IRP1, Appendix Fig S4I) and iron regulatory protein 2
209	(IRP2, Appendix Fig S4J). Heme was not increased in the whole hearts and
210	mitochondria of mitoNEET-knockout mice (Appendix Fig S4K, S4L), and proteins
211	involved in heme synthesis also did not differ between the groups (Appendix Fig S4M,
212	S4N).
213	
214	Deletion of mitoNEET Affects Mitochondrial ROS and Respiration
215	To assess mitochondrial ROS, we measured the mitochondrial Hydrogen
216	peroxide (H ₂ O ₂) release rate from isolated mitochondria during mitochondrial
217	respiration. The mitochondrial H_2O_2 release rate during state 3 with glutamate and
218	malate (complex I-linked substrates; GM3) was significantly higher in mitoNEET-
219	knockout than control mice (0.062 ± 0.003 vs. 0.045 ± 0.003 nmol/min/mg
220	mitochondrial protein, P<0.05, Fig 3D). After the addition of carbonyl cyanide-p-
221	trifluoromethoxyphenylhydrazone (FCCP), an uncoupler, mitochondrial ROS release
222	during maximal capacity of the electron-transfer system was higher in mitoNEET-
222 223	during maximal capacity of the electron-transfer system was higher in mitoNEET-knockout than control mice (0.068 ± 0.004 vs. 0.049 ± 0.004 nmol/min/mg

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229	3E).
228	between the groups (2331 \pm 146 vs. 2689 \pm 168 pmol/s/mg mitochondrial protein, Fig
227	Fig $3E$). There was also no significant difference in mitochondrial maximal capacity
226	knockout and control mice (620 \pm 120 vs. 712 \pm 118 pmol/s/mg mitochondrial protein,
225	state 3 respiration with glutamate and malate was comparable between the mitoNEET-

230

231	Deletion of mitoNEET Promotes Mitochondrial and Cardiac Dysfunction by Aging
232	At the age of 12 months, the iron contents in isolated mitochondria were higher
233	in mitoNEET-knockout than control mice (Fig 3F). Mitochondrial H_2O_2 release was
234	significantly higher in mitoNEET-knockout mice than control mice both during state 3
235	respiration (0.080 \pm 0.007 vs. 0.049 \pm 0.004 nmol/min/mg mitochondrial protein,
236	P<0.05) and maximal capacity (0.084 \pm 0.007 vs. 0.056 \pm 0.005 nmol/min/mg
237	mitochondrial protein, P<0.05), respectively (Fig 3G). Mitochondrial state 3 respiration
238	with glutamate and malate was comparable between mitoNEET-knockout and control
239	mice at 12 months of age (545 \pm 52 vs. 571 \pm 59 pmol/s/mg mitochondrial protein, Fig
240	3H). In contrast, mitochondrial maximal capacity was significantly lower in mitoNEET-
241	knockout than control mice at 12 months of age (1960 \pm 73 vs. 2458 \pm 57 pmol/s/mg
242	mitochondrial protein, P<0.05, Fig 3H). In short, the mitochondrial reserve capacity,
243	calculated by subtracting state 3 respiration from potential maximum respiratory
244	capacity, was significantly lower in mitoNEET-knockout than control mice (512 ± 83 vs.
245	$1057 \pm 48 \text{ pmol/s/mg}$ mitochondrial protein, P<0.05, Fig 3I).
246	Cardiac function was evaluated by echocardiography in control and mitoNEET-
247	knockout mice at 12 months of age. Left ventricle (LV) end-diastolic diameter and LV
248	end-systolic diameter, each of which typically dilates in the state of cardiac failure, were

249	significantly higher. As a simple and widely used measure of LV contractility, fractional
250	shortening was significantly lower compared to control mice, suggesting that the heart
251	of 12 months-old mitoNEET-knockout mice had LV dysfunction. LV wall thickness
252	was not different between 12-month-old control and mitoNEET-knockout mice,
253	representing no evidence of cardiac hypertrophy by deletion of mitoNEET (Fig 4A, 4B).
254	Histological analysis showed that myocyte cross-sectional area did not differ between
255	groups (Appendix Fig S5A, S5B).
256	
257	Aging Decreases mitoNEET Expression and Increases Mitochondrial Iron
258	Contents
259	Time course of mitoNEET protein expression was examined in the whole heart
260	of C57BL/6J mice at the ages of 3, 6, 9, and 12 months. The expressions of mitoNEET,
261	which were normalized by GAPDH and cytochrome c oxidase IV (COX IV), were
262	significantly lower in the 12-month-old than the 3-month-old mice (Fig 5A, 5B). This
263	suggests that mitoNEET protein is decreased in the aged heart independently of
264	mitochondrial quantity. The iron content in isolated mitochondria was higher in 12-
265	month-old than 3-month-old mice (Fig 5C). Moreover, the levels of mitoNEET protein
266	tended to be lower in the kidneys of 12-month-old than in those of 3-month-old mice
267	(Appendix Fig S6).
268	

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269 **Discussion**

270	The main findings of our study were that the endogenous mitoNEET interacted
271	with TfR, a carrier protein for transferrin with iron. Interestingly, mitochondrial iron
272	contents from the hearts of cardiac-specific mitoNEET-knockout mice were higher than
273	control mice. The increase in mitochondrial iron contents corresponded with increased
274	mitochondrial ROS release without affecting mitochondrial respiratory function at the
275	age of 3 months. Therefore, these results suggested that mitoNEET regulated
276	mitochondrial iron homeostasis by protein-protein interaction with TfR.
277	
278	We focused on a newly discovered novel protein, mitoNEET, located at the
279	OMM (Wiley et al., 2007a). To realize the importance of mitoNEET in vivo, we search
280	for clues from the aspect of protein-protein interactions. Namely mitoNEET were
281	selected as target protein for its location of TfR (Fig 1). We for the first time clarified
282	that mitoNEET protein interacted with TfR, by using mass spectrometry analysis and
283	immunoprecipitation (Fig 1B, 1C, 1D, 1E, 2A, 2B, Appendix Table S1, S2). TfR
284	enters the cellular cytosol in the form of the iron-Tf-TfR complex via endocytosis from
285	the cytoplasmic membrane. To date, TfR has been considered to be in the plasma
286	membrane and endosomes. On the other hand, we also clearly showed that TfR existed
287	with the mitochondria facing the OMM (Fig 2), even if we did not probe direct
288	interaction between mitoNEET and TfR. As a previous study said, there are possibility
289	that mitoNEET indirectly interact with TfR via endosomes containging iron-Tf-TfR
290	complex (Das et al., 2016). Because of its location, mitoNEET could play a central role
291	in its complexation with TfR to form TfR-mitoNEET. We propose that mitoNEET may
292	help TfR to primary function as negative regulator of iron inflow into the mitochondria

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293 by its interaction with TfR. In other words, that TfR exists on the mitochondria with 294 mitoNEET, not in the membrane or cytosol, may limit iron inflow into the mitochondria, 295 even if the way of its regulation is not elucidated yet. 296 The relation between mitoNEET protein levels and mitochondrial iron contents 297 does not always reveal the inverse correlation. Because mitochondrial iron 298 concentrations in mammals need to be tightly regulated, iron increase by mitoNEET 299 decrease may be compensated by other known regulatory mechanism in mitochondrial 300 iron homeostasis. Even if that is case, mitoNEET plays a primary role in mitochondrial 301 iron homeostasis. Next, we created mice with cardiac specific deletion of mitoNEET 302 (Fig 3A, Appendix Fig S2) and clearly demonstrated that absence of mitoNEET 303 directly increased mitochondrial iron contents (Fig 3C). This increase in mitochondrial 304 iron sustained in 12-moths-old mitoNEET-knockout mice as well (Fig 3F). Furthermore, 305 there were no differences in the expressions of proteins known to be involved in 306 mitochondrial iron homeostasis, suggesting the existence of an undisclosed pathway of 307 mitochondrial iron homeostasis via mitoNEET. The mitoNEET protein is known to be 308 an acceptor of ISCs (Wiley et al., 2007b). It has also been proposed that the mitoNEET 309 protein transfers iron/sulfur clusters by redox regulation, and donates the clusters and 310 iron ions to mitochondria (Paddock et al., 2007). However, the details of the 311 mechanisms for the acceptance and donation of iron in the mitoNEET protein have not 312 been elucidated. 313 In the preset study, under the condition of mitochondrial iron overload with the

315 using Amplex UltraRed, which was monitored as the fluorescent compound resorufin

deletion of mitoNEET, the increase in ROS release was detected (Fig 3D), measured by

314

after converting superoxide anion $(O_2 \cdot \overline{})$ into H_2O_2 . Although we could not clarify the

317	cause-and-effect relationship between iron overload and H_2O_2 release, iron plays a
318	crucial role in the redox reaction in vivo, and its overload can cause free radical
319	production through many pathways via reduction of O2. Moreover, highly reactive ROS
320	are generated by means of the Fenton reaction in the presence of endogenous iron.
321	Therefore, mitochondrial iron overload can easily enhance O_2 . production via
322	mitochondrial oxidative phosphorylation (OXPHOS), even if overall mitochondrial
323	function is preserved (Fig $3E$). It was consistent with the overall mitochondrial function
324	and cardiac function in 3-month-old mice (Fig 3E). These results suggest that disruption
325	of mitoNEET primarily causes mitochondrial iron overload and enhances ROS
326	production, which secondarily leads to mitochondrial dysfunction. Many previous
327	reports have shown that enhanced ROS production leads to cardiac dysfunction and
328	development of heart failure (HF). We previously reported that an exposure of H_2O_2 to
329	cardiac myocytes lead to their injury (Ide, Tsutsui et al., 1999). Furthermore we
330	reported that mitochondria-derived ROS production was increased in the heart from HF
331	model mice (Kinugawa, Tsutsui et al., 2000), and that the treatment with anti-oxidant
332	and overexpression of mitochondrial antioxidant, such as peroxiredoxin-3, improved
333	cardiac function and HF (Matsushima, Ide et al., 2006). Therefore, long-term exposure
334	of ROS over physiological level could lead to cardiac dysfunction. A previous study
335	reported that strong ROS exposure decreased mitochondrial OXPHOS capacity and
336	reserve capacity, resulting in cell death (Dranka, Hill et al., 2010). In contrast, mild
337	ROS exposure decreased mitochondrial reserve capacity, but mitochondrial OXPHOS
338	capacity was almost constant (Dranka et al., 2010). Although the increase in ROS
339	release was the same between 3-month-old mice and 12-month-old mice, the
340	mitochondrial reserve capacity was decreased in 12-month-old mitoNEET-knockout

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341 mice, but the mitochondrial OXPHOS capacity was not decreased (Fig 3G, 3H, 3I). A 342 previous study showed that deletion of mitoNEET in the liver after high-fat diet feeding 343 increased mitochondrial iron contents and mitochondrial respiration (Kusminski et al., 344 2012). In contrast, another study reported that the maximal uncoupler-stimulated (state 345 3u) respiration and complex I-dependent (state 3) respiration were decreased in the 346 isolated mitochondria from the heart of systemic mitoNEET-knockout mice compared 347 to WT mice (Wiley et al., 2007a). This data supports our results. The reason for these 348 discrepancies remains unknown. However, the deletion of mitoNEET can increase 349 mitochondrial iron contents, and decrease mitochondrial respiration at least in the heart. 350 In accordance with mitochondrial reserve capacity, chronic ROS exposure caused 351 cardiac dysfunction (Fig 4). 352 Finally, we showed that mitochondrial iron was increased by aging in 353 association with a decrease in mitoNEET protein (Fig 5). This suggests that the 354 mitoNEET-iron relationship is an important physiological and universal phenomenon, 355 but not one specific to cardiac diseases. Moreover, in the kidney, the decrease of 356 mitoNEET expression in aging mice were observed as well, this result also support the 357 importance of mitoNEET (Appendix Fig S6). 358 Mitochondrial iron has been reported to play an important role in some cardiac

diseases. Doxorubicin, an anthracycline antibiotic, is one of the most widely used agents as chemotherapy for hematological malignancies and solid tumor, which often induces cardiac dysfunction and HF, i.e. doxorubicin-induced cardiomyopathy (Minotti, Menna et al., 2004). Previous clinical study showed that levels of mitochondrial iron were significantly higher in the explanted heart from patients with doxorubicin-induced cardiomyopathy than in the heart from normal subjects and patients with other

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365	cardiomyopathies (Ichikawa, Ghanefar et al., 2014). Increased ROS caused by iron
366	overload are thought to be its major cause. Thus, mitochondrial iron homeostasis plays
367	an important role on cardiac function. Its regulation has been controlled by several
368	proteins in mitochondria. FXN, located in mitochondria matrix, plays a role in synthesis
369	of iron/sulfur cluster (Vaubel & Isaya, 2013). Friedreich's ataxia (FRDA), a human
370	genetic disease caused by GAA triplet expansion of FXN gene, leads to hypertrophic
371	cardiomyopathy, as well as neurodegeneration (Isaya, 2014). Mouse model of FXN
372	deletion in the heart, which mimic FRDA cardiomyopathy, by gene therapy with adeno-
373	associated virus rh10 vector expressing human FXN, prevents cardiomyopathy
374	progressing and also reverse cardiomyopathy with HF (Perdomini, Belbellaa et al.,
375	2014). In addition, Mice with knockout of ABCB8, which is localized in the inner
376	mitochondrial membrane and functions as iron exporter from the mitochondrial matrix,
377	showed the progression of LV dysfunction in association with iron accumulation and an
378	increase in ROS (Ichikawa et al., 2012). In contrast, iron within mitochondria is used for
379	the synthase of iron/sulfur clusters and heme. Therefore, mitochondrial iron needs to be
380	finely controlled under every kind of conditions around mitochondria. In the present
381	study, we clearly demonstrated that mitoNEET was the regulator of iron homeostasis.
382	In summary, we show that the increase in mitochondrial iron contents
383	corresponded with increased mitochondrial ROS release in the hearts of cardiac-specific
384	mitoNEET-knockout mice. The endogenous mitoNEET interacted with TfR, suggesting
385	that mitoNEET regulated mitochondrial iron homeostasis by protein complex formation.
386	These results suggest that the regulation of mitochondrial iron would be a potential
387	target for the treatment of cardiac diseases and other conditions.

388

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389 Methods

All experimental procedures and methods of animal care were approved by the
Institutional Animal Care and Use Committee of National University Corporation
Hokkaido University (Permit Number: 16-0101) and also conformed to the Guide for
the Care and Use of Laboratory Animals published by the US National Institutes of
Health.

395

396 Immunoblot

397 Samples, 10-20 µg of total protein from heart tissues, were separated by SDS-398 PAGE and transferred to a polyvinylidene fluoride (PVDF) membrane (Bio-Rad, USA). 399 The membrane was blocked for 1 h at room temperature in TBS-T buffer (Tris buffered 400 saline containing 0.1% Tween 20) containing 3% BSA or milk, and was incubated with 401 the primary antibodies at a dilution of 1:1000 overnight at 4°C. After 3 washings with 402 TBS-T, the membrane was incubated with a horseradish peroxide-conjugated secondary 403 antibody at a dilution 1:5000 for 1 h at room temperature. After washing, the membrane 404 was developed with ECL or ECL Prime Reagent (GE, USA) and then processed for 405 detection with ChemiDoc XRS+ (Bio-Rad, USA). The density of the signals of bands 406 was quantified with Image J (NIH) software.

407

408 Silver-intensified immunogold method for electron microscopy

409 Cultured C2C12 cells were fixed for 2 hr with 4% paraformaldehyde in 0.1 M

410 phosphate buffer, pH 7.3. After pretreatment in normal donkey serum for 30 min, they

411 were incubated with the mouse anti-TfR monoclonal antibody (1: 2000 in dilution,

412 Thermo Fisher) at 4oC overnight, and subsequently reacted at 4oC overnight with goat

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413	anti-mouse IgG covalently linked with 1-nm gold particles (1: 400 in dilution;
414	Nanoprobes, Yaphank, NY). Following silver enhancement using a kit (HQ silver;
415	Nanoprobes), the samples were osmificated, dehydrated, and directly embedded in Epon
416	(Nisshin EM, Tokyo, Japan). Ultrathin sections were prepared and stained with both
417	uranyl acetate and lead citrate for observation under an electron microscope (H-7100;
418	Hitachi, Tokyo, Japan).
419	
420	Immunoprecipitation of Endogenous Proteins
421	To analyze the interaction between endogenous mitoNEET and other proteins,
422	including TfR, the whole cell lysates from mouse heart were solubilized with lysis
423	buffer (Cell Signaling Technology, USA). The lysates were centrifuged at 15,000 rpm
424	for 20 min at 4°C, and then the supernatant fluid was collected. The lysates were mixed
425	with an anti-TfR Ab (Abcam, UK) and normal rabbit IgG as a control, and incubated
426	overnight at 4°C. After the addition of protein-A (rProtein A Sepharose Fast Flow, GE,
427	USA), the lysates were incubated for 4 h at 4°C. Protein-A was washed with buffer (150
428	mM NaCl, 50 mM Tris-HCl, 0.5% Triton-X) and then mixed with $2 \times SDS$ sample
429	buffer with boiling for 5 min at 95°C.
430	
431	Cell Culture
432	The mouse C2C12 myoblast cell line was purchased from the American Type
433	Culture Collection (Manassas, USA). Mouse C2C12 myoblasts were seeded at a
434	concentration of 4×10^5 cells/ml in 6-well culture plates. Differentiation of C2C12
435	myoblasts into myotubes was induced by medium containing 2% horse serum for 24 h,

436 as previously described(Fukushima, Kinugawa et al., 2014).

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437

438 Iron Addition or Reduction for Cells

When mouse C2C12 cells reached confluence, 20 μM ferric ammonium citrate
(FAC) (Sigma) in addition to iron, and desferioxamine (DFO) (Sigma) in reduction of
iron, were added 24h.

442

443 **Preparation of Isolated Mitochondria**

444 Heart tissues were quickly harvested, and mitochondria were isolated

445 (Tonkonogi & Sahlin, 1997). Briefly, heart tissues were minced on ice, and incubated

446 with mitochondrial isolation buffer containing 0.1 mg/ml proteinase (Sigma-Aldrich,

447 USA) for 2 min. The heart tissue was gently homogenized with six strokes using a

448 motor-driven Teflon pestle in glass chamber. The homogenate was centrifuged at 750 g

for 10 min. The supernatant was centrifuged at 10,000 g for 10 min, and the pellet was

450 washed and centrifuged at 7,000 g for 3 min. The final pellet was suspended in

451 suspension buffer (containing 225 mmol/l mannitol, 75 mmol/l sucrose, 10 mmol/l Tris,

452 and 0.1 mmol/l EDTA; pH 7.4). Finally, the mitochondrial protein concentration was

453 measured using a BCA assay.

454

455 **Digitonin treatment**

456 Digitonin was dissolved in DMSO. To extract cholesterol from the OMM, 457 isolated mitochondria were incubated for 5 min at room temperature with 0.03 mg/ml 458 digitonin. To solubilize isolated mitochondria, digitonin at the indicated final 459 concentrations was added to 100 μ l of 1.2 mg/ml mitochondria in mitochondrial 460 suspension buffer (Tris-HCl (pH 7.4), 75 mM sucrose, and 225 mM mannitol). After 5

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461	min incubation at room temperature and centrifugation at $10,000 g$, the pellet was
462	suspended in 100 μ l of 2 X sample buffer. Equivalent portions of the supernatant and
463	pellet were subjected to SDS-PAGE and evaluated by immunoblot (Arasaki et al., 2015).
464	
465	Immunohistochemical Staining
466	For immunohistochemical staining, the mouse C2C12 cells were plated onto
467	cover-glasses coated with 50 μ g/ml fibronectin. After 24-hr incubation at 37°C, the cells
468	were fixed with 2% formaldehyde in phosphate-buffered saline (PBS) at 37°C for 10
469	min, followed by ice-cold methanol for a 5-min fixation at -20° C. After blocking with
470	1% bovine serum albumin (BSA) in PBS for 30 min, the samples were incubated with
471	antibodies against mitoNEET and TfR in 1% BSA/PBS overnight at 4°C. After being
472	rinsed with blocking buffer, the samples were incubated with secondary antibodies
473	conjugated with Alexa Fluor Plus 488 (against rabbit IgG) and Alexa Fluor Plus 555
474	(against mouse IgG) at a dilution of 1:1000 for 30 min at room temperature.
475	Fluorescence images were obtained with a structured illumination microscopy (N-SIM,
476	Nikon, Japan).
477	
478	Experimental Animals
479	All mice were bred in a pathogen-free environment and housed in an animal
480	room under controlled condition on a 12 h: 12 h light/dark cycle at a temperature of

481 23°C to 25°C.

482 C57BL/6J mice (CLEA Japan Inc.) were bred under controlled conditions and
483 euthanized under deep anesthesia with tribromoethanol-amylene hydrate (Avertin; 250

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484 mg/kg body weight, i.p.) (Kinugawa et al., 2000) at the age of 3, 6, 9 or 12 months (n=6,
485 each). The heart and kidney were excised.

486 Mice with disruption of cardiac-specific mitoNEET were newly generated (Fig 487 S1). Briefly, the conditional mitoNEET allele was created using clones isolated by 488 restriction mapping with a genome library, and a C57BL/6 genetic background clone 489 was used to construct the targeting vector. A neo cassette was inserted downstream from 490 exon 2 and was flanked by FRT sites for later excision by FLP recombinase. The lox-P 491 sites were inserted upstream from exon 2 and downstream from the neo cassette. The 492 targeting vector was transfected by electroporation of embryonic stem cells. After 493 selection, the surviving clones were expanded for polymerase chain reaction analysis to 494 identify recombinant embryonic stem clones. Targeted embryonic stem cells were 495 microinjected into C57BL/6 blastocysts, and chimera mice were mated with wild type 496 C57BL/6 homozygous FLP mice to remove the neo cassette. Heterozygous mice with 497 neo deletion and confirmed lox-P sites were crossed with C57/BL6 mice to obtain 498 heterozygous mice. Finally, mitoNEET flox/flox mice were also crossed with aMHC-499 Cre mice to obtain cardiac-specific deletion of mitoNEET (mitoNEET-knockout mice). 500 mitoNEET flox/flox mice were used as control mice. Most of experiments were 501 performed at the age of 3 months, with others performed at the age of 12 months. 502

503 Measurement of Mitochondrial Iron Contents

- 504 Isolated mitochondria, collected by using a Mitochondrial Isolation Kit for
- 505 Tissue (Pierce, USA), were diluted with EDTA-free buffer after sonication.
- 506 Mitochondrial "non-heme" iron contents were measured by using a commercial Iron
- 507 Assay Kit (BioAssay Systems, USA), which directly detect total iron in the sample,

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508 according to the manufacturer's protocol(Kusminski et al., 2012). Isolated mitochondria

509 with sonication were diluted with EDTA-free buffer, and normalized to the

- 510 mitochondria concentration of each sample.
- 511

512 Mitochondrial OXPHOS Capacity and ROS Release

513 The mitochondrial respiratory capacity was measured in isolated mitochondria at

514 37°C with a high-resolution respirometer (Oxygraph-2k, Oroboros Instruments, Austria)

515 (Christiansen, Dela et al., 2015, Takada, Masaki et al., 2016). H₂O₂ release from

516 isolated mitochondria was measured at 37°C by spectrofluorometry (O2k-Fluorescence

517 LED2-Module, Oroboros Instruments, Austria). The release of H₂O₂ that we measured

518 reflected intrinsic O_2 . and H_2O_2 release in the mitochondria under the presence of

519 superoxide dismutase (SOD) (Hey-Mogensen, Hojlund et al., 2010). O_2 , unstable

substance, needs to be converted into H_2O_2 , relatively stable one, to evaluate ROS

521 production. H₂O₂ reacts with Amplex UltraRed (Life Technologies, USA) in an equal

522 amount of stoichiometry catalyzed by horseradish peroxidase, which yields the

523 fluorescent compound resorufin (excitation: 560 nm; emission: 590 nm). Resorufin was

524 monitored throughout the experiment. Beforehand five different concentrations of H₂O₂

525 were added to establish a standard curve in advance. The H_2O_2 release rate from

526 isolated mitochondria is expressed as nanomoles per minute per milligram of

527 mitochondrial protein.

After the addition of isolated mitochondria (approximately 100-200 μg) to the
chamber in the respirometer filled with 2 ml of MiR05 medium with 5 U/ml SOD, 25
μmol/l Amplex ultrared, and 1 U/ml horseradish peroxidase, substrates, adenosine
diphosphate (ADP), and inhibitors were added in the following order: 1) glutamate 10

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532 mr	nol/l + malate	2 mmol/l (c	complex	I-linked	substrates).	2) ADP	10 mmol/l	3)
--------	----------------	--------------	---------	----------	--------------	--------	------------	----

- 533 succinate 10 mmol/l (a complex II-linked substrate), 4) oligomycin 2.5 μmol/l, 5) FCCP
- 534 1 μmol/l, 6) rotenone 0.5 μmol/l, 7) antimycin a 2.5 μmol/l. O₂ consumption rates, i.e.,
- 535 respiratory rates, were expressed as O₂ flux normalized to mitochondrial protein
- 536 concentration ($\mu g/\mu l$). Datlab software (Oroboros Instruments) was used for data
- 537 acquisition and data analysis.
- 538
- 539 Echocardiographic Measurements
- 540 Echocardiographic measurements were performed under light anesthesia with
- 541 tribromoethanol/amylene hydrate (avertin; 2.5% wt/vol, 8 μL/g i.p.). Two-dimensional
- 542 parasternal short-axis views were obtained at the levels of the papillary muscles. Two-
- 543 dimensional targeted M-mode tracings were recorded at a paper speed of 50 mm/sec.
- 544

545 Statistical Analysis

- 546 Data are expressed as the mean \pm the standard error of the mean (SE). Student's
- 547 unpaired *t*-tests were performed to compare means between two independent groups.
- 548 One-way ANOVA followed by the Tukey's test was performed for multiple-group
- 549 comparisons of means. Values of P<0.05 were considered statistically significant.
- 550
- 551

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568 Author contributions

569 T.F., S.T. and S.K. designed the study. M.W., H.T., S.H., M.M. and K.I.N.

- 570 performed Mass Spectrometry Analysis. N.K., Y.O., H.S. performed IHC analysis. J.N-
- 571 K and T.I performed immune electron microscopy. T.F., S.T., S.M., A.F., M.T., and
- 572 J.M. performed the other experiments. T.F. and S.K. wrote the manuscript with help
- 573 from T.Y., S.M., and H.T.
- 574

575 **Conflict of interset**

- 576 The authors have no conflicts of interest to disclose.
- 577
- 578
- 579

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705

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706 Figure Legends

707

708 Figure 1. The Role of mitoNEET in Mitochondrial Iron Homeostasis.

(A) Immunoblot of supernatant and pellet from mitochondrial fractions of the mouse

710 heart. (B) Electron microscopy of TfR in C2C12 cells. In upper panel, Gold particles,

711 black dots in figures, showing the existence of TfR are broadly distributed throughout

the cytoplasm but tend to be condensed around vacuoles (arrows) and mitochondria.

713 Lower panel shows an intimate relationship of gold particles with a long mitochondrion.

714 Bar, 0.5 μm. (C) Silver-stained gels with the immunoprecipitated protein by TfR

antibody in the mitochondrial protein from the mouse heart (black arrows). (D) Venn

716 diagram showing the central role of mitoNEET in new mitochondrial iron regulation

717 involved in iron metabolism, outer mitochondrial proteins, and iron sulfur-cluster(ISC).

(E) Silver-stained gels with the immunoprecipitated protein from HEK 293 cells

719 transfected with and without 3×FLAG-mitoNEET containing the pcDNA3 promoter.

720 (F) Interaction of endogenous TfR and mitoNEET. The whole cell lysate of the mouse

heart was subjected to immunoprecipitation with anti-TfR antibody or normal rabbit

IgG followed by immunoblot with mitoNEET antibody. An input representing 5 µg of

the whole cell lysate was used for each immunoprepicitation. (G) Interaction of

real endogenous mitoNEET and TfR. (H) Representative immunoblot and summary data of

725 mitoNEET protein expression normalized to beta-actin in mouse C2C12 cells in the

addition of iron or the reduction of iron with DFO compared to control. Data are shown

as the mean \pm SE. n=7. *P<0.05 vs. Ctrl. (I) Correlation between mitochondrial

respiration and mitoNEET protein expression normalized to beta-action.

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729	WCL, whole cell lysate; IB, immunoblot; IP, immunoprecipitation; TfR, transferrin
730	receptor; mNT, mitoNEET; M, mitochondria; Ctrl, control; Fe, the addition of ferric

- ammonium citrate; DFO, desferioxamine.
- 732

733 Figure 2. The Colocalization of mitoNEET and Transferrin Receptor on the Outer

734 Mitochondrial Membrane.

- 735 (A) Interaction of mitoNEET and TfR with mitochondria of the mouse heart. An input
- representing 100 µg of the mitochondria lysate was used. (B) Immunoblot of
- supernatant and pellet from mitochondrial fractions after digitonin treatment with the
- 738 indicated concentrations. (C)_Representative images obtained from structured
- 739 illumination microscopy of C2C12 cell stained for mitoNEET and TfR. mitoNEET
- 740 (green) and TfR (red) visualized using Alexa Fluoro Plus 488 and Alexa Fluoro Plus
- 741 555. Left, C2C12 cell imaged with 488 nm filter. Center, C2C12 cell imaged with 555
- 742 nm filter. Right, merged image. Bar, 10 μm.
- 743 IB, immunoblot; IP, immunoprecipitation; KO, knockout; mNT, mitoNEET; TfR,
- 744 transferrin receptor; ANT, adenine nucleotide translocator; WCL, whole cell lysate; Sup,
- supernatant; PPT, pellet; VDAC, voltage-dependent anion channel; HSP60, heat-shock
- 746 protein 60; Ctrl, control; Fe, the addition of ferric ammonium citrate.
- 747

748 Figure 3. Mitochondrial Iron, ROS, and Respiration in the Heart of mitoNEET-

- 749 knockout mice.
- 750 (A) Representative immunoblot of the mitoNEET protein in various organs from
- 751 mitoNEET-knockout mice and control mice. (B) Representative immunoblot of the
- transferrin receptor protein from control mice (n=6) and mitoNEET-konckout (n=6)

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753	mice in the mitochondrial fraction of the heart normalized to COX IV. (C) Levels of
754	mitochondrial iron contents in 3-month-old mitoNEET-knockout mice relative to
755	control mice (n=8-9). (D) H_2O_2 release originating from isolated mitochondria in the
756	heart of 3-month-old control mice (n=5) and 3-month-old mitoNEET-knockout mice
757	(n=5) during state 3 respiration with complex I-linked substrates (left bars) and in
758	maximal capacity of an electron-transfer system with FCCP (right bars). (E)
759	Mitochondrial respiration in isolated mitochondria from the heart of 3-month-old mice
760	during state 3 with complex I-linked substrates (left bars) and maximal capacity of the
761	electron-transfer system with FCCP (right bars). (F) Levels of mitochondrial iron
762	contents in 12-month-old mitoNEET-knockout mice relative to 12-month-old control
763	mice (n=11-14). (G) H_2O_2 release in 12-month-old control mice (n=5) and 12-month-
764	old mitoNEET-knockout mice (n=5). (H) Mitochondrial respiration in isolated
765	mitochondria from the heart of 12-month-old mice. (I) Reserve capacity in 12-month-
766	old control mice (left bar) and mitoNEET-knockout mice (right bar).
767	mNT, mitoNEET; GAPDH, glyceraldehyde phosphate dehydrogenase; B, brain; H,
768	heart; Li, liver; K, kidney; SM, skeletal muscle; COX, cytochrome c oxidase; M, month.
769	GM3, state 3 respiration with glutamate and malate; FCCP, carbonyl cyanide-p-
770	trifluoromethoxyphenylhydrazone.
771	
772	Figure 4. Cardiac Function of 12-month-old mitoNEET-knockout mice assessed by
773	Echocardiography.
774	(A) Representative echocardiography; Control mice(left panel) and mitoNEET-

knockout mice (right panel) at the age of 12 months. (B) Summary data of LVEDD

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776 (mm), LV	'ESD (mm)	, %FS,	and LV	wall	thickness i	n 12	2-month-old	control a	and
--------------	-----------	--------	--------	------	-------------	------	-------------	-----------	-----

777 mitoNEET-knockout mice.

- 778 Data are shown as the mean \pm SE. *P<0.05 vs. the Control. LV, left ventricle; EDD,
- end-diastolic diameter; ESD, end-systolic diameter; %FS, percent fractional shortening.

780

```
781 Figure 5. Expression of mitoNEET and Accumulation of Mitochondrial Iron in 12-
```

782 Month Old C57B6/J Mice.

- 783 Representative immunoblot and summary data of mitoNEET protein expression
- normalized to GAPDH (A) and COX IV (B) in the hearts of 3, 6, 9, and 12-month old
- 785 mice. (C) Levels of mitochondrial iron contents in 12-month old mice relative to 3-

786 month old mice.

787 Data are shown as the mean \pm SE. n=5-6. *P<0.05 vs. 3M. M, month; mNT,

mitoNEET; GAPDH, glyceraldehyde phosphate dehydrogenase; COX, cytochrome c
oxidase.

790

791 Figure 6. A schematic mechanism of iron overload in mitoNEET-knockout mice.

792 The interaction between mitoNEET and transferrin receptor causes mitoNEET to be

793 colocalize with transferrin receptor, which in control limits inflow of iron. In contrast,

- the absence of mitoNEET in mitoNEET-knockout mice increases inflow of iron, for
- ransferrin receptor was separated from mitochondrial outer membrane, leading to
- 796 mitochondrial iron overload and consequently enhancing mitochondrial ROS production.
- 797 ROS, reactive oxygen species.

798

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799	Appendix
800	
801	Methods
802	
803	Mass Spectrometry Analysis
804	HEK 293 cells were transfected with or without expressed $3 \times FLAG$ -
805	mitoNEET under the control of a cytomegalovirus constitutive promoter in the pcDNA3
806	expression vector. The cells were lysed, and the lysate was centrifuged. The resultant
807	supernatant was incubated at 4°C with the antibody to FLAG (M2, Sigma-Aldrich,
808	USA) immobilized on protein-A (rProtein A Sepharose Fast Flow, GE, USA), and the
809	beads were washed with the lysis buffer. The immunoprecipitated proteins were eluted
810	with the $3 \times$ FLAG peptide (Sigma-Aldrich, USA).
811	The proteins collected proteins by immunoprecipitation were separated by SDS-
812	PAGE gel and stained with silver staining. These silver-stained bands were excised
813	from the gels. The proteins therein were subjected to in-gel reduction, S-
814	carboxyamidomethylation and digestion with sequence-grade trypsin (Promega,
815	Fitchburg). The resultant peptides were analyzed by LCESI-MS/MS (LCQ DECA and
816	LTQ XL; Thermo Fisher Scientific, USA). The data were analyzed using Mascot
817	software (Matrix Science, USA) (Yamamoto, Takeya et al., 2013).
818	
819	Genotyping for mitoNEET KO Mice
820	Genotyping of mitoNEET KO mice was performed by PCR with DNA extracted
821	from the tail. To detect the Cre recombinase, the following primers were used: 5'-

822 CTGAAAAGTTAACCAGGTGAGAATG -3' (forward) and 5'-

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- 823 AGGTAGTTATTCGGATCATCAGCTA -3' (reverse). To distinguish mitoNEET
- 824 flox/flox or wild type, the following primers were used: 5'-
- 825 TCTAAAATGTACAGCAGCCATGAAG -3' (forward) and 5'-
- 826 ACCAAGATACTTAGCGGTAGAAGTG -3' (reverse). The protocol of PCR
- amplification was as follows: 35 cycles of 10 sec at 98 °C, 5 sec at 65 °C, and 120 sec at
- 828 72 °C; followed by 35 cycles of 10 sec at 98 °C, 5 sec at 66 °C, and 60 sec at 72 °C,
- 829 respectively.
- 830

831 Quantitative Reverse Transcriptase PCR

Total RNA was extracted from heart tissues with QuickGene-810 (FujiFilm,

833 Japan) according to the manufacturer's instructions. The total RNA concentration and

purity were assessed by measuring the optical density (230, 260, and 280 nm) with a

835 Nanodrop 1000 Spectrophotometer (Thermo Fisher Scientific, USA). cDNA was

836 synthesized with a high capacity cDNA reverse transcription kit (Applied Biosystems,

USA). Reverse transcription was performed for 10 min at 25°C, for 120 min at 37°C,

838 for 5 sec at 85°C, and then solution was cooled at 4°C. TaqMan quantitative realtime

- 839 PCR was performed with the 7300 real-time PCR system (Applied Biosystems) to
- amplify samples for Cisd1 (Mm01172641_g1) cDNA in the heart. After 2 min at 50°C
- and 10 min at 95°C, the PCR amplification was performed for 40 cycles of 15 sec at
- 842 95°C and 1 min at 60°C. GAPDH was used as an internal control. Data were analyzed

843 using a comparative $2^{-\Delta\Delta CT}$ method.

844

845 Generation of mitoNEET Antibody

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846	The peptide antigen, a C-terminal fragment of mitoNEET, was chemically
847	synthesized. Samples using the peptide were injected into 4-month-old female New
848	Zealand white rabbits. After multiple immunizations, the blood samples were collected
849	from the ear vein of the rabbits. The generation of antibodies was examined by
850	immunoblot, and levels of anti-peptide antibody were determined with the conventional
851	ELISA method.
852	
853	Blue Native Page Electrophoresis (BN-PAGE)
854	BN-PAGE was performed as previously described (Wittig, Braun et al., 2006).
855	The proteins from the whole heart were extracted with 5% digitonin (Invitrogen)
856	(protein : detergent ratio of 1 : 10) and $4 \times$ buffer on ice for 30 min. After centrifugation
857	at 10,000 g for 10 min at 4 °C, the supernatants were collected. The remaining lysate
858	was combined with Coomasie blue G-250 dye (Invitrogen) (protein : detergent ratio of
859	1:10) and added to 3-12% NativePAGETM Novex Bis-Tris Gel (Invitrogen), then
860	separated electrophoretically by SDS-PAGE using an Anode and Cathode buffer
861	(Invitrogen) at 10 mA for 1 h and at 150V for 2 h on ice. The protein complex in the
862	samples after SDS-PAGE was denatured by denaturing buffer (in mmol; Tris 20,
863	glycine 200, 1% SDS). Then the gels were transferred by electroblotting to PVDF
864	membranes (Bio-Rad) using transfer buffer at 30 V for 3 h.
865	
866	Measurement of Heme
867	About 2-3 mg of heart tissue was homogenized in 1% Triton-X100 in Tris-
868	buffered saline and centrifuged at 5,000 g for 10 min. The supernatants were collected,

the lysate for total heme measurement was prepared and then the protein concentration

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870 was quantified by BCA assay. The lysa	ate for mitochondrial heme measurement was
---	--

- 871 prepared using a Mitochondrial Isolation Kit for Tissue (Pierce, USA).
- 872 Levels of total and mitochondrial heme were quantified as previously
- described(Khechaduri, Bayeva et al., 2013). Briefly, equal amounts of total or
- 874 mitochondrial proteins were mixed with 2 M oxalic acid and boiled to 95°C for 30 min.
- After centrifugation at 1,000 g for 10 min at 4° C, the supernatants containing release
- 876 iron from heme and generated fluorescent PPIX were collected. The fluorescence of the
- 877 supernatant was assessed at 405 nm/600 nm on a Spectra Max Gemini fluorescence
- 878 microplate reader, which was normalized to the protein concentration of each sample.

879

880 Organ Histology

- 881 For histological analysis, tissue was fixed in 10% formaldehyde, cut into three
- transverse sections; apex, middle ring, and base, then stained with hematoxylin-eosin.
- 883 Myocyte cross-sectional area was determined as described previously(Kinugawa et al.,

884 2000).

885

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886 Figure Legends

887

888 Appendix Figure S1. Mitochondrial Iron Contents Influenced by Iron or DFO.

- 889 Representative images obtained from super-resolution microscopy by using Mito-
- 890 ferroGreen (Dojindo, Japan). Bar, 50 μm.
- 891 DFO, desferioxamine; Fe, the addition of ferric ammonium citrate.
- 892

893 Appendix Figure S2. Generation of mitoNEET KO Mice.

- (A) Design of the mitoNEET targeting construct and the genomic structure of the
- mitoNEET. LoxP sites were inserted to delete the entire exon 2, resulting in early
- termination and truncation of the C-terminal region of mitoNEET. This resulted in the
- 897 complete destruction of mitoNEET function. The indicated primers were used for
- 898 detecting mitoNEET flox allele. (B) WT and mitoNEET floxed alleles were
- distinguished by polymerase chain reaction (PCR) analysis. Genomic PCR confirmed
- 900 the mitoNEET floxed alleles and Cre allele in mitoNEET-knockout mice. (C)
- 901 Quantitative analysis of the gene expression of *CISD1* in the heart (n=10-11). Data are
- 902 shown as the mean \pm SE. *P<0.05 vs. Control. (D) Representative immunoblot by Tris-
- 903 Tricine SDS-PAGE of the lysate from control (Ctrl) and mitoNEET-knockout mice
- 904 (KO), and the peptide of the mitoNEET fragment as positive control (PC). The black
- 905 arrow (about 14 kDa) indicates mitoNEET, and the white arrow (below 2 kDa) indicates
- 906 mitoNEET fragment as PC. (E) Representative positive immunostaining for mitoNEET
- 907 in myocardial sections. Upper Panel: Control; Lower Panel: mNT KO. Scale Bar, 50 μm.
- 908 WT, wild-type; mNT KO, mitoNEET-knockout; *CISD1*, CDGSH iron sulfur domain 1;

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- 909 CZ, cruz marker; PC, positive control; Ctrl, control; CM, color marker; GAPDH,
- 910 glyceraldehyde phosphate dehydrogenase.
- 911

912 Appendix Figure S3. Complex of mitoNEET in mitoNEET-knockout mice.

- 913 (A) Representative BN-PAGE retardation assays performed on the whole cell lysate
- 914 from the heart of control mice or mitoNEET-knockout mice. Black arrows (about 120
- 915 kDa) indicate the complex consisting of mitoNEET and TfR. IB, immunoblot; IP,
- 916 immunoprecipitation; KO, knockout.
- 917
- 918 Appendix Figure S4. Proteins Related to Iron Homeostasis and Levels of Heme
- 919 and Expression of Proteins Related to Heme Synthesis in the Heart of 3 Months-

920 Old mitoNEET-knockout mice.

- 921 Representative immunoblot and summary data of FtMt (A), MFRN2 (B), FXN (C),
- 922 ABCB7 (D), ABCB8 (E), TfR (F), DMT1 (G), Fpn (H), IRP1 (I), and IRP2 (J) protein
- 923 expressions normalized to GAPDH in the heart from control and mitoNEET KO mice
- 924 (n=10-11). Levels of total heme (K) and mitochondrial heme (L) in mitoNEET KO
- 925 mice relative to control mice (n=7-9). Representative immunoblot and summary data of
- 926 ALAS1 (M) and FECH (N) protein expressions normalized to GAPDH in the heart
- 927 from control and mitoNEET KO mice (n=10-11). Data are shown as the mean \pm SE.
- 928 *P<0.05 vs. Control. Ctrl, control; NS, not significant; FtMt, mitochondrial ferritin;
- 929 MFRN2, mitoferin2; FXN, frataxin; ABCB7, ATP-binding cassette protein B7; ABCB8,
- ATP-binding cassette protein B8; TfR, transferrin receptor; DMT1, divalent metal
- transporter 1; Fpn, ferroportin; IRP1, iron regulatory protein 1; IRP2, iron regulatory

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- 932 protein 2; ALAS1, 5'-aminolevulinate synthase 1; FECH, ferrochelatase; GAPDH,
- 933 glyceraldehyde phosphate dehydrogenase.
- 934

935 Appendix Figure S5. Representative Histological Images of the Heart.

- 936 (A) Representative Hematoxylin and eosin (HE) stains from 12-month old control mice
- and 12-month old mitoNEET-knockout mice. Scale Bar, 100µm. (B) Summary data for
- 938 cross sectional area. n=3 for each.
- 939

940 Appendix Figure S6. Expression of mitoNEET in the kidney of 12-Month Old

- 941 **C57B6/J Mice.**
- 942 (A) Representative immunoblot and summary data of mitoNEET protein expression
- normalized to GAPDH in the kidneys of 3 and 12-month old mice. Data are shown as
- 944 the mean \pm SE. n=5-6. *P<0.05 vs. 3M. M, month; mNT, mitoNEET; GAPDH,
- 945 glyceraldehyde phosphate dehydrogenase.
- 946

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947 Appendix Table S1.

Identifie	d Protein	Score	Molecular	Expected	NCBI
			weight	value	accession
			(kDa)		number
<band a<="" td=""><td>round 100 kDa></td><td></td><td></td><td></td><td></td></band>	round 100 kDa>				
Transferr	rin receptor				
protein 1		131	85274	9.2e-009	cd09848
MASCO	T Scores and Nat	tional Center for	Biotechnology I	nformation (NC	CBI)
Accessio	n Numbers of Pro	oteins. Generated	d by the MASCC	T database (M	atrix Scienc
Boston, I	MA).				
Appendi	ix Table S2.				
	ix Table S2.	e: 5%			
Protein s					
Protein s	equence coverage peptides shown i		RFSLARQVDGDN	ISHVEMKLAVI	DEEENADN
Protein so Matched	equence coverage peptides shown i MMDQARSAFS	in <mark>red</mark> .	-		
Protein so Matched 1 51 101	equence coverage peptides shown i MMDQARSAFS NTKANVTKPK LAGTESPVREH	in <mark>red</mark> . SNLFGGEPLSYTI CRCSGSICYGTIA EPGEDFPAARRL	VIVFFLIGFMIGY YWDDLKRKLSE	LGYCKGVEPK KLDSTDFTGTI	TECER K <mark>LLNEN</mark>
Protein so Matched 1 51 101 151	equence coverage peptides shown i MMDQARSAFS NTKANVTKPK LAGTESPVREF SYVPREAGSQ	in <mark>red</mark> . SNLFGGEPLSYTI CRCSGSICYGTIA EPGEDFPAARRL [*] KDENLALYVEN(VIVFFLIGFMIGY YWDDLKRKLSE QFREFKLSKVWF	LGYCKGVEPK KLDSTDFTGTII RDQHFVKIQVK	TECER K <mark>LLNEN</mark> IDSAQNSV
Protein se Matched 1 51 101 151 201	equence coverage peptides shown i MMDQARSAFS NTKANVTKPK LAGTESPVREE SYVPREAGSQI IIVDKNGRLVY	in <mark>red</mark> . SNLFGGEPLSYTH RCSGSICYGTIA EPGEDFPAARRL KDENLALYVEN (LVENPGGYVA)	VIVFFLIGFMIGY YWDDLKRKLSE QFREFKLSKVWF /SKAATVTGKLV	LGYCKGVEPK KLDSTDFTGTII RDQHFVKIQVK 'HANFGTKKDF	TECER K <mark>LLNEN</mark> DSAQNSV EDLYTPV
Protein se Matched 1 51 101 151 201 251	equence coverage peptides shown i MMDQARSAFS NTKANVTKPK LAGTESPVREH SYVPREAGSQ IIVDKNGRLVY NGSIVIVRAGK	in <mark>red</mark> . SNLFGGEPLSYTH RCSGSICYGTIA EPGEDFPAARRL KDENLALYVEN KLVENPGGYVAY	VIVFFLIGFMIGY YWDDLKRKLSE QFREFKLSKVWF (SKAATVTGKLV SLNAIGVLIYMD)	LGYCKGVEPK KLDSTDFTGTI RDQHFVKIQVK HANFGTKKDF QTKFPIVNAEL	TECER K <mark>LLNEN</mark> DSAQNSV FEDLYTPV SFFGH
Protein se Matched 1 51 101 151 201 251 301	equence coverage peptides shown i MMDQARSAFS NTKANVTKPK LAGTESPVREF SYVPREAGSQ IIVDKNGRLVY NGSIVIVRAGK AHLGTGDPYT	in red . SNLFGGEPLSYTH CRCSGSICYGTIA EPGEDFPAARRL KDENLALYVEN KUENPGGYVAY KITFAEKVANAES	VIVFFLIGFMIGY YWDDLKRKLSE QFREFKLSKVWF (SKAATVTGKLV SLNAIGVLIYMDO PSRSSGLPNIPVQ	LGYCKGVEPK KLDSTDFTGTI RDQHFVKIQVK HANFGTKKDF QTKFPIVNAEL TISRAAAEKLF	TECER KLLNEN DSAQNSV FEDLYTPV SFFGH FGNME
Protein se Matched 1 51 101 151 201 251 301 351	equence coverage peptides shown i MMDQARSAFS NTKANVTKPK LAGTESPVREH SYVPREAGSQJ IIVDKNGRLVY NGSIVIVRAGK AHLGTGDPYT GDCPSDWKTE	in red. SNLFGGEPLSYTH CRCSGSICYGTIA EPGEDFPAARRL KDENLALYVEN (LVENPGGYVAY KITFAEKVANAES PGFPSFNHTQFP DSTCRMVTSESK)	VIVFFLIGFMIGY YWDDLKRKLSE QFREFKLSKVWF (SKAATVTGKLV SLNAIGVLIYMDO PSRSSGLPNIPVQ NVKLTVSNVLKI	LGYCKGVEPK KLDSTDFTGTII RDQHFVKIQVK HANFGTKKDF QTKFPIVNAEL TISRAAAEKLF EIKILNIFGVIKG	TECER KLLNEN DSAQNSV FEDLYTPV SFFGH FGNME GFVEPD
Protein se Matched 1 51 101 151 201 251 301 351 401	equence coverage peptides shown i MMDQARSAFS NTKANVTKPK LAGTESPVREH SYVPREAGSQI IIVDKNGRLVY NGSIVIVRAGK AHLGTGDPYT GDCPSDWKTE HYVVVGAQRI	in red. SNLFGGEPLSYTH RCSGSICYGTIA EPGEDFPAARRL KDENLALYVENG (LVENPGGYVAY KITFAEKVANAES PGFPSFNHTQFP OSTCRMVTSESKI DAWGPGAAK <mark>SG</mark>	VIVFFLIGFMIGY YWDDLKRKLSE QFREFKLSKVWF (SKAATVTGKLV SLNAIGVLIYMD PSRSSGLPNIPVQ NVKLTVSNVLKI VGTALLLKLAQ)	LGYCKGVEPK KLDSTDFTGTII RDQHFVKIQVK HANFGTKKDF QTKFPIVNAEL TISRAAAEKLF EIKILNIFGVIKO MFSDMVLKDG	TECER KLLNEN DSAQNSV ÆDLYTPV SFFGH GNME GFVEPD FQPSRSIIF
Protein se Matched 1 51 101 151 201 251 301 351 401 451	equence coverage peptides shown i MMDQARSAFS NTKANVTKPK LAGTESPVREH SYVPREAGSQI IIVDKNGRLVY NGSIVIVRAGK AHLGTGDPYT GDCPSDWKTE HYVVVGAQRI ASWSAGDFGS	in red. SNLFGGEPLSYTH RCSGSICYGTIA EPGEDFPAARRL KDENLALYVEN (LVENPGGYVAY KITFAEKVANAES PGFPSFNHTQFP DSTCRMVTSESK) DAWGPGAAKSG	VIVFFLIGFMIGY YWDDLKRKLSE QFREFKLSKVWF ZSKAATVTGKLV SLNAIGVLIYMD PSRSSGLPNIPVQ NVKLTVSNVLKI VGTALLLKLAQI LSSLHLKAFTYIN	LGYCKGVEPK KLDSTDFTGTI RDQHFVKIQVK HANFGTKKDF QTKFPIVNAEL TISRAAAEKLF EIKILNIFGVIKC MFSDMVLKDG LDKAVLGTSN	TECER KLLNEN DSAQNSV FEDLYTPV SFFGH FGNME GFVEPD FQPSRSIIF FKVSASP
Protein se Matched 1 51 101 151 201 251 301 351 401	equence coverage peptides shown i MMDQARSAFS NTKANVTKPK LAGTESPVREF SYVPREAGSQU IIVDKNGRLVY NGSIVIVRAGK AHLGTGDPYT GDCPSDWKTE HYVVVGAQRI ASWSAGDFGS LLYTLIEKTM(in red. SNLFGGEPLSYTH RCSGSICYGTIA EPGEDFPAARRL KDENLALYVENG (LVENPGGYVAY KITFAEKVANAES PGFPSFNHTQFP OSTCRMVTSESKI DAWGPGAAK <mark>SG</mark>	VIVFFLIGFMIGY YWDDLKRKLSE QFREFKLSKVWF (SKAATVTGKLV SLNAIGVLIYMD PSRSSGLPNIPVQ NVKLTVSNVLKI VGTALLLKLAQ SSLHLKAFTYIN .YQDSNWASKVI	LGYCKGVEPK KLDSTDFTGTI RDQHFVKIQVK HANFGTKKDF QTKFPIVNAEL TISRAAAEKLF EIKILNIFGVIKC MFSDMVLKDG LDKAVLGTSN EKLTLDNAAFP	TECER KLLNEN DSAQNSV FEDLYTPV SFFGH FGNME GFVEPD FQPSRSIIF FKVSASP FLAYSGI

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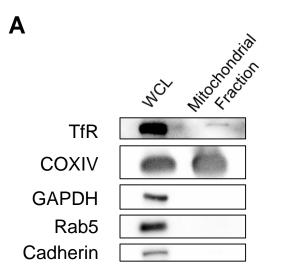
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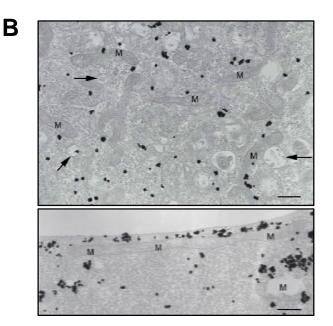
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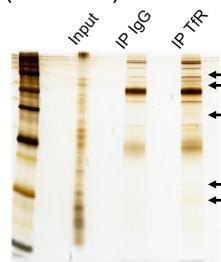
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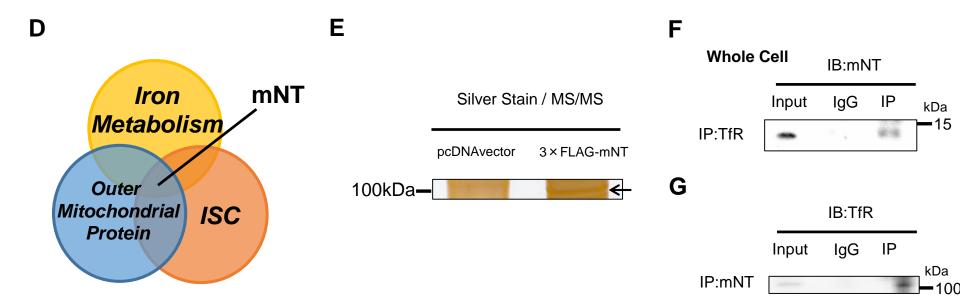
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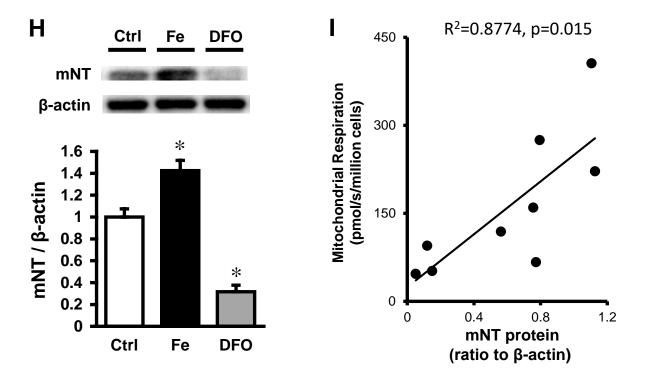


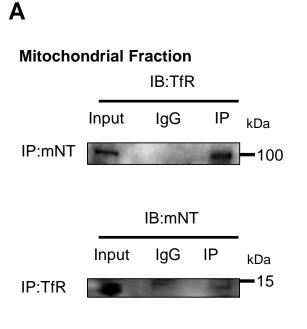


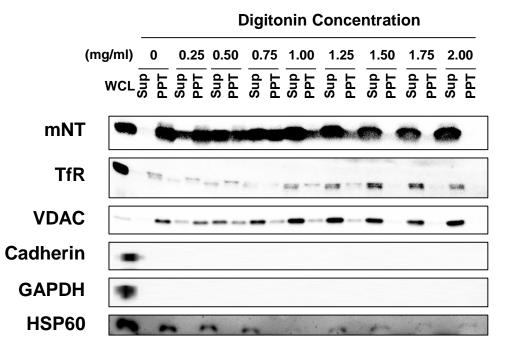
C Mouse Heart (mitochondria)

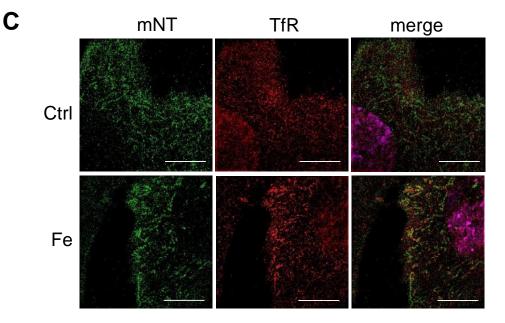




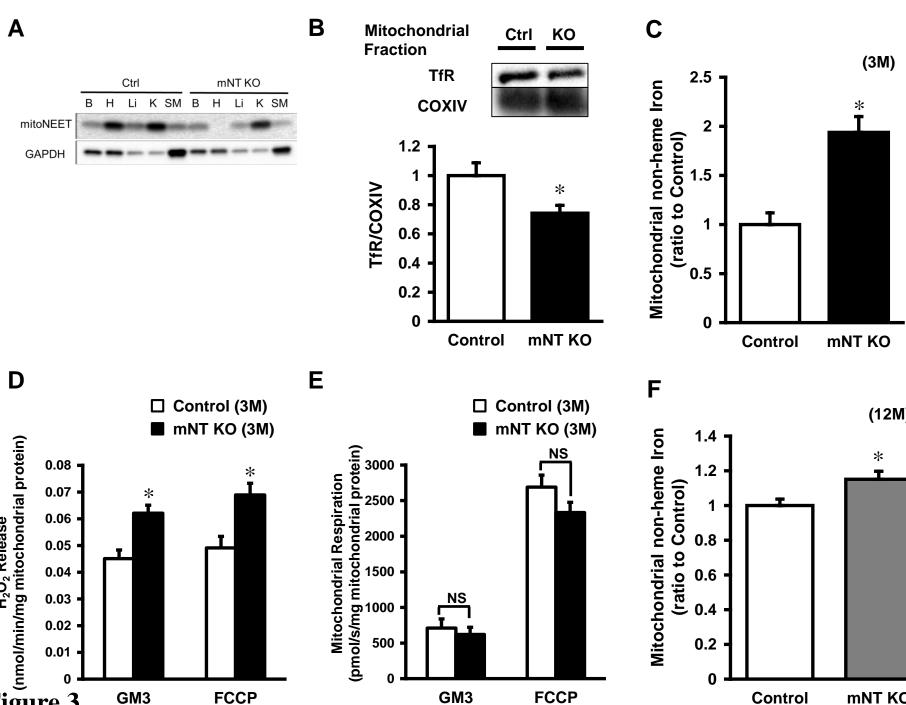


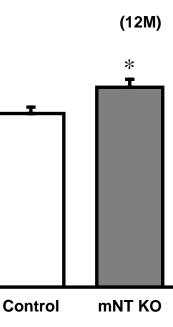


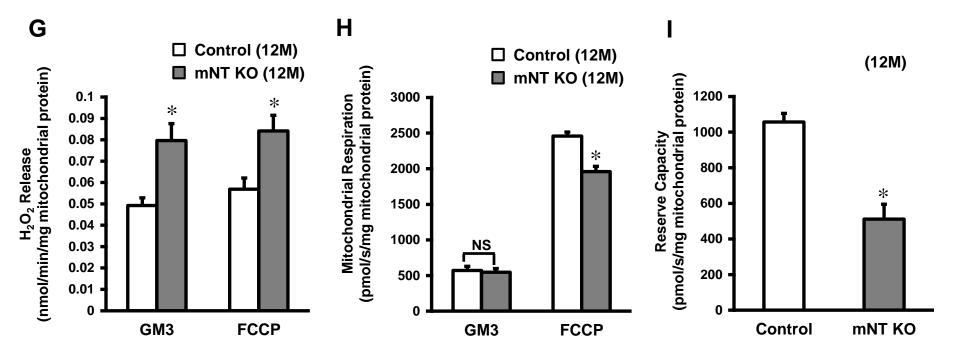


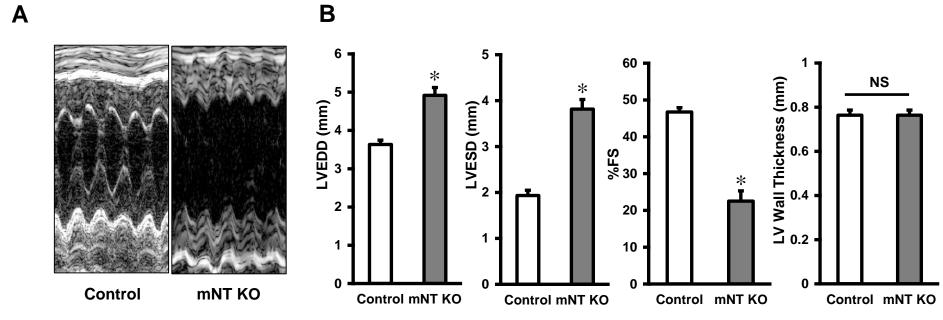


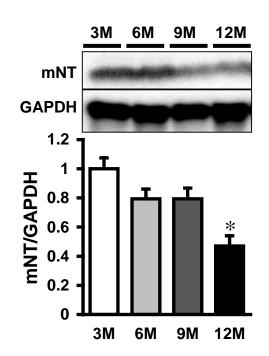
Β



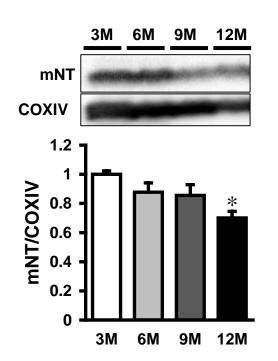


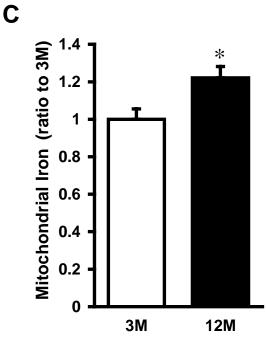




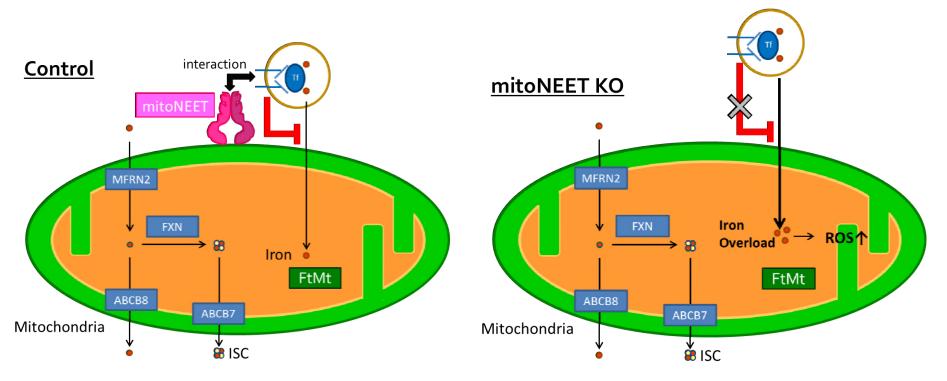


В



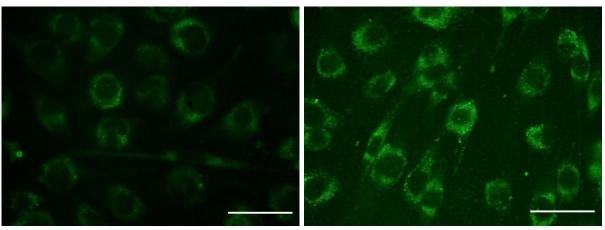


Α

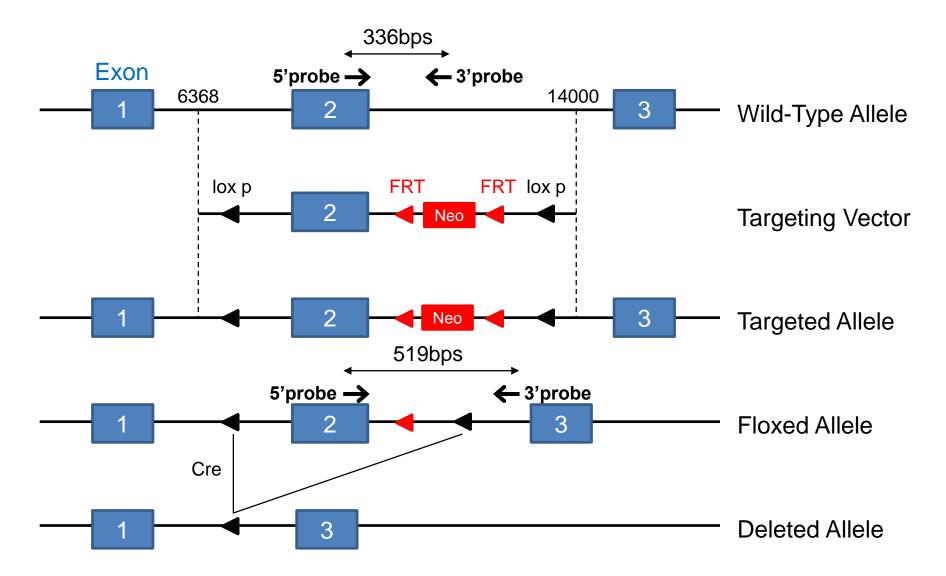




Α

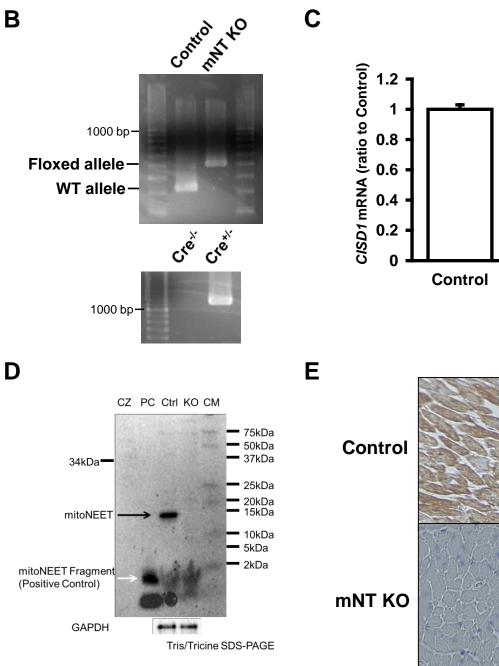


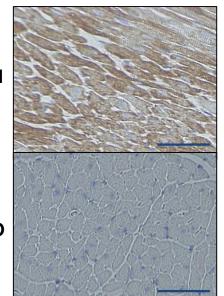
Chromosome 10 (C57/BL Background)



Appendix Figure S2

Α

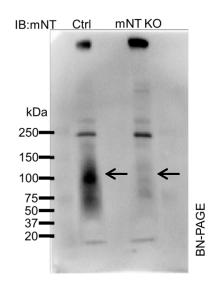




*

mNT KO

Figure S2



Α

