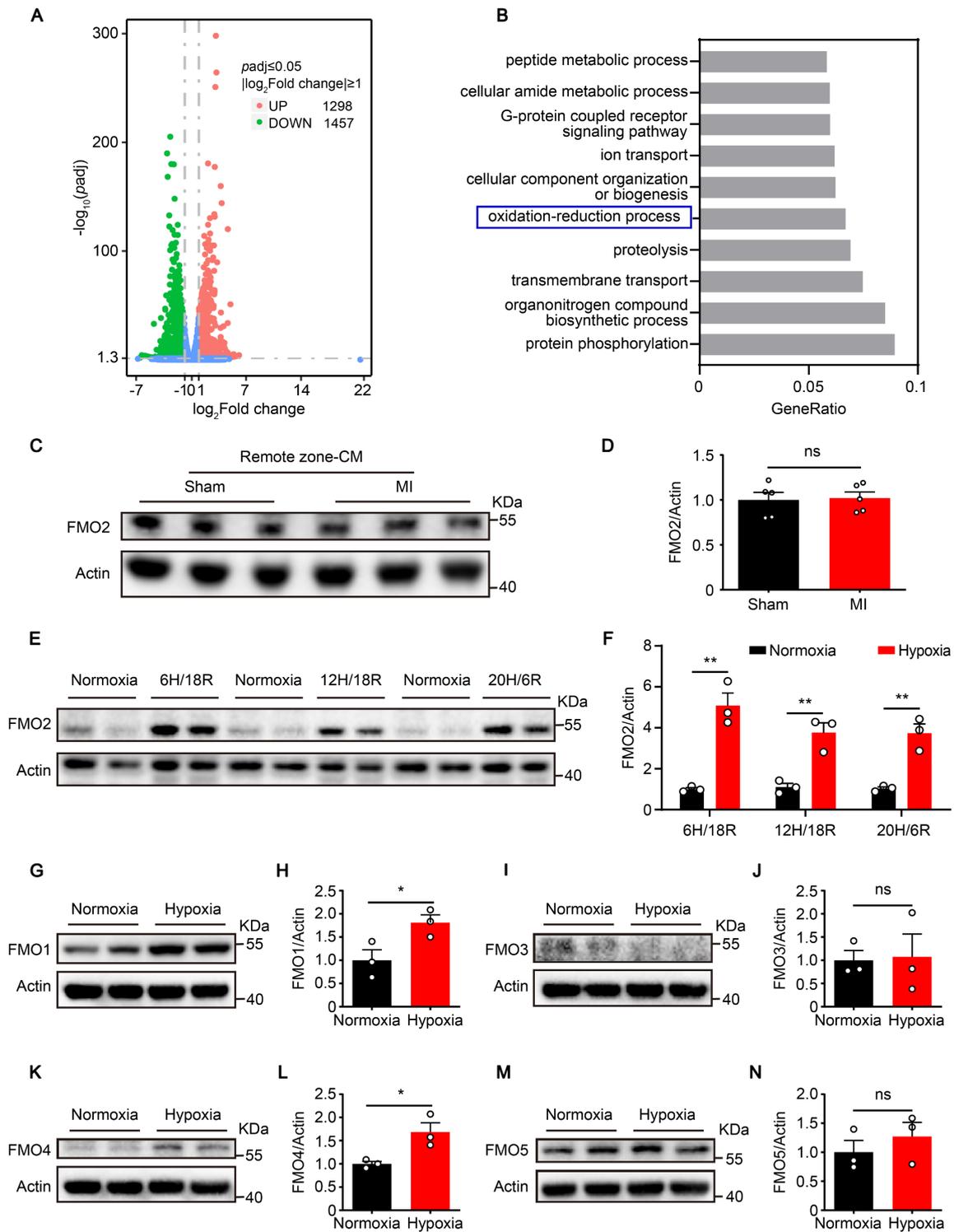


1 Supplemental materials

2 **–Flavin-containing monooxygenase 2 confers cardioprotection in ischemia**
3 **models through its disulfide-bond catalytic activity**

4
5 Qingnian Liu, Jiniu Huang, Hao Ding, Yue Tao, Jinliang Nan, Changchen Xiao, Yingchao
6 Wang, Rongrong Wu, Cheng Ni, Zhiwei Zhong, Wei Zhu, Jinghai Chen, Chenyun Zhang, Xiao
7 He, Danyang Xiong, Xinyang Hu, Jian'an Wang



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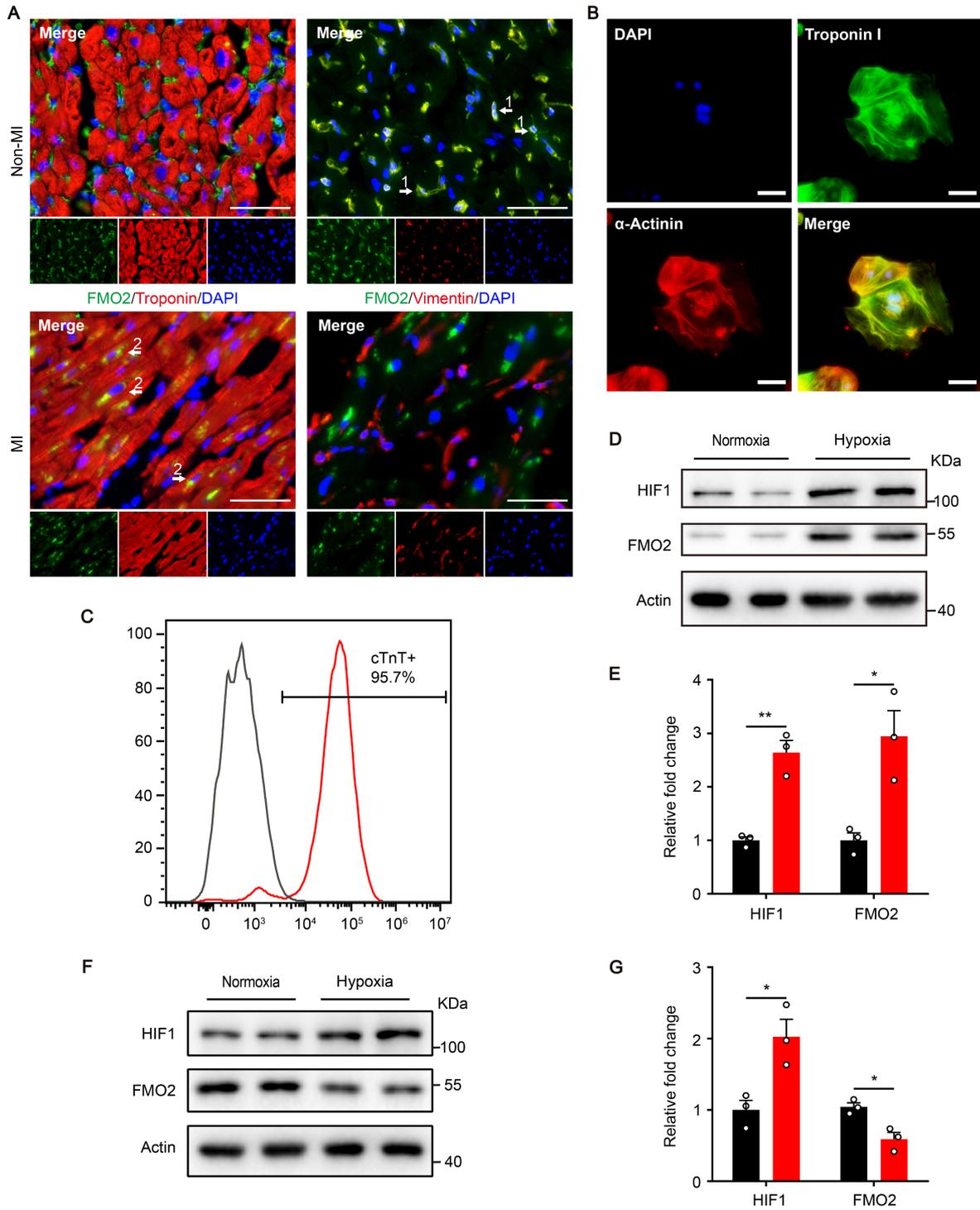
13 **Supplemental Figure 1. Expression of FMOs in cardiomyocytes upon hypoxia. (A)**

14 Volcano map showed differentially expressed genes in hypoxia NRCMs compared with

15 normoxia NRCMs. **(B)** Pathway enrichment analysis of significantly altered genes identified
16 between hypoxia and normoxia NRCMs. **(C and D)** Expression of FMO2 in CMs isolated from
17 the remote zone of adult normal and infarcted rat hearts (n = 5 per group). **(E and F)** Expression
18 of FMO2 in NRCMs under classical hypoxia/reoxygenation injuries. **(G-N)** Protein expression
19 of FMO1, FMO3, FMO4 and FMO5 in NRCMs subjected to hypoxia for 24 hours. The graphs
20 summarize data from 3 independent experiments. Quantified data are presented as means \pm
21 SEM, and significance was evaluated via t test. * $p < 0.05$, ** $p < 0.01$, ns: not significant. CM
22 indicates cardiomyocyte.

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26 **Supplemental Figure 2. Expression of FMO2 in different cardiac cells. (A)**

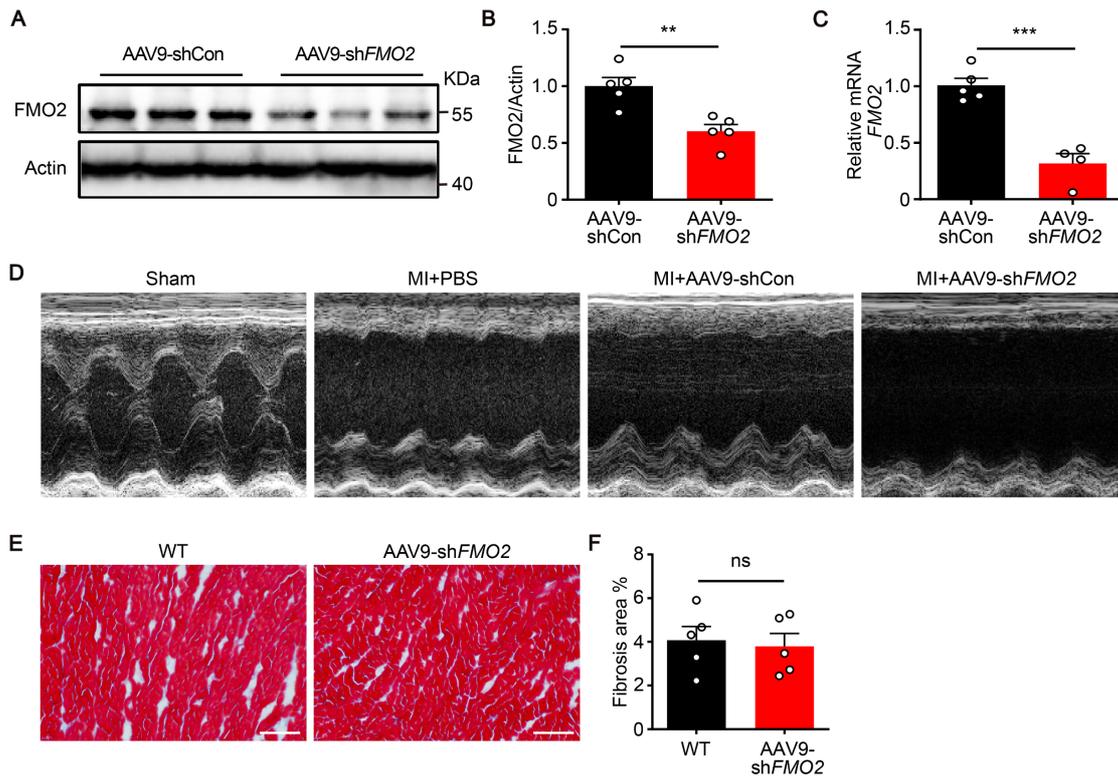
27 Immunofluorescence staining for FMO2 (green in respective image), Troponin I

28 (cardiomyocyte marker), and Vimentin (fibroblast marker) in heart section from MI patients

29 and non-MI controls. Arrow 1 indicates FMO2-positive fibroblast, and arrow 2 indicates
30 FMO2-positive cardiomyocyte. Bar = 50 μ m. **(B)** hiPSC-CMs were characterized via
31 immunofluorescent analyses of Troponin I and α -Actinin. Bar = 100 μ m. **(C)** The purity of
32 hiPSC-CMs that expressed Troponin T was determined via flow cytometry (n = 3 independent
33 experiments). **(D and E)** Protein expression of HIF1 and FMO2 in hiPSC-CMs subjected to
34 hypoxia. **(F and G)** Protein expression of HIF1 and FMO2 in neonatal rat cardiac fibroblasts
35 under hypoxia. The graphs summarize data from 3 independent experiments. Quantified data
36 are presented as means \pm SEM. Comparisons between two groups were assessed via the
37 Student's t-test. * p <0.05, ** p <0.01. α -Actinin indicates α -sarcomeric actinin. hiPSC-CMs
38 indicates human-induced pluripotent stem cell-derived cardiomyocytes.

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42 **Supplemental Figure 3. Effect of AAV9-shFMO2 in rat hearts.** (A-C) FMO2 protein and

43 mRNA levels in CMs isolated from control and AAV9-shFMO2 rat hearts (n = 4-5 per group).

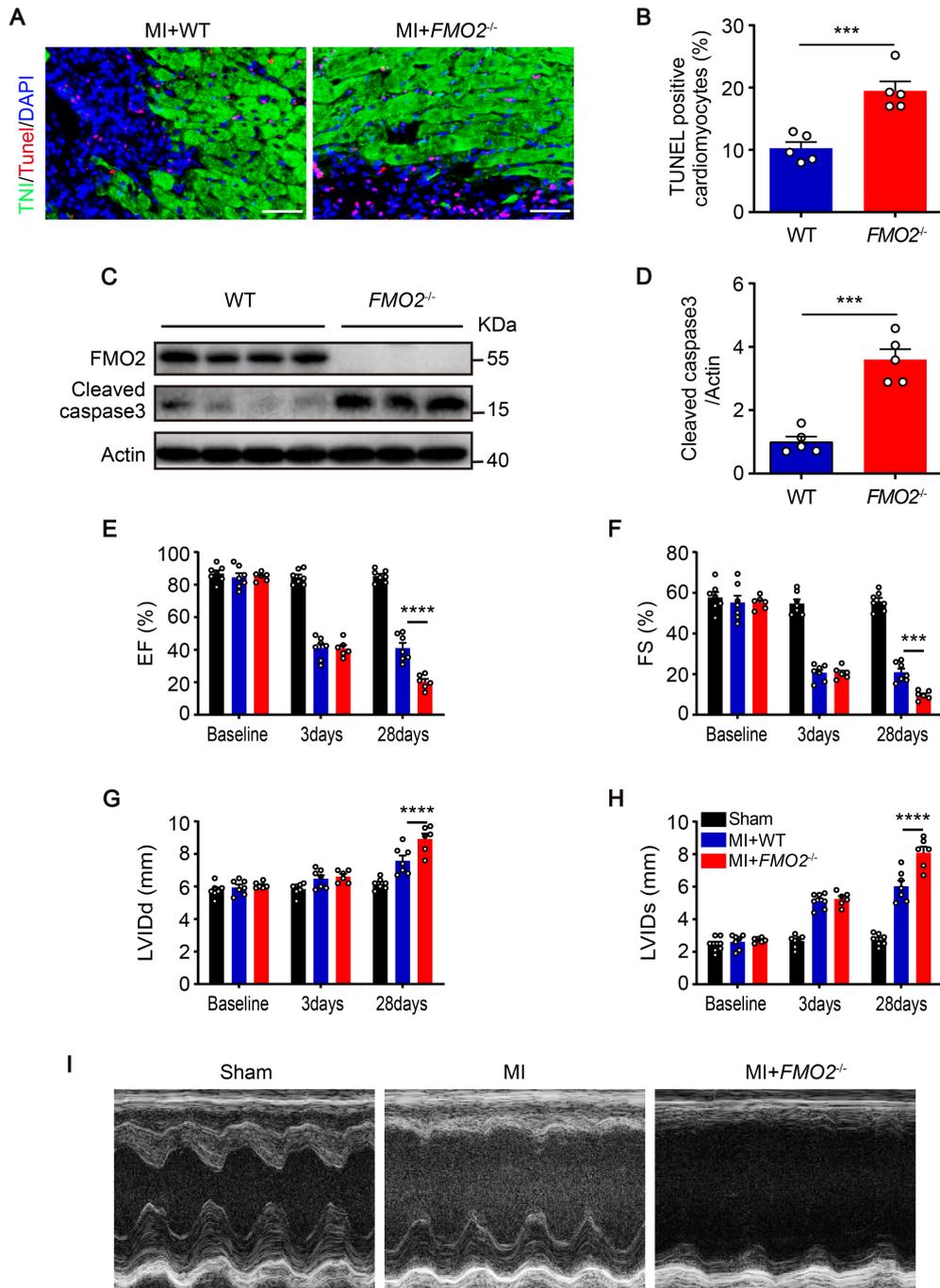
44 (D) Representative photographs of M-mode echocardiography. (E and F) Masson staining

45 showing different degrees of fibrosis in heart from WT and AAV9-shFMO2 rats. Bar = 100

46 μm . The summary data of fibrosis are shown in (right, n = 5 per group). Quantified data are

47 presented as means \pm SEM. Comparisons between two groups were assessed via the Student's

48 t-test. ** $p < 0.01$, *** $p < 0.001$, ns: not significant.



49

50 **Supplemental Figure 4. Knockout of FMO2 impairs cardiac function accompanied by**

51 **increased cardiomyocyte apoptotic level after MI. (A and B) Analysis of TUNEL-Troponin**

52 **I positive cardiomyocytes in the border zone of WT and FMO2^{-/-} infarcted rat hearts (n = 5 per**

53 group). Bar = 50 μ m. (C and D) Protein expression of cleaved caspase 3 in each group of rats
54 as described above (n = 5 per group). (E-H) Quantitative analysis of echocardiography in each
55 group of rats (n = 6-7 per group). (I) Representative photographs of M-mode echocardiography.
56 Quantified data are presented as means \pm SEM. Comparisons between two groups were
57 assessed via the Student's t-test, comparisons among groups after multiple treatments were
58 evaluated via two-way ANOVA with Tukey test. *** p <0.001, **** p <0.0001.

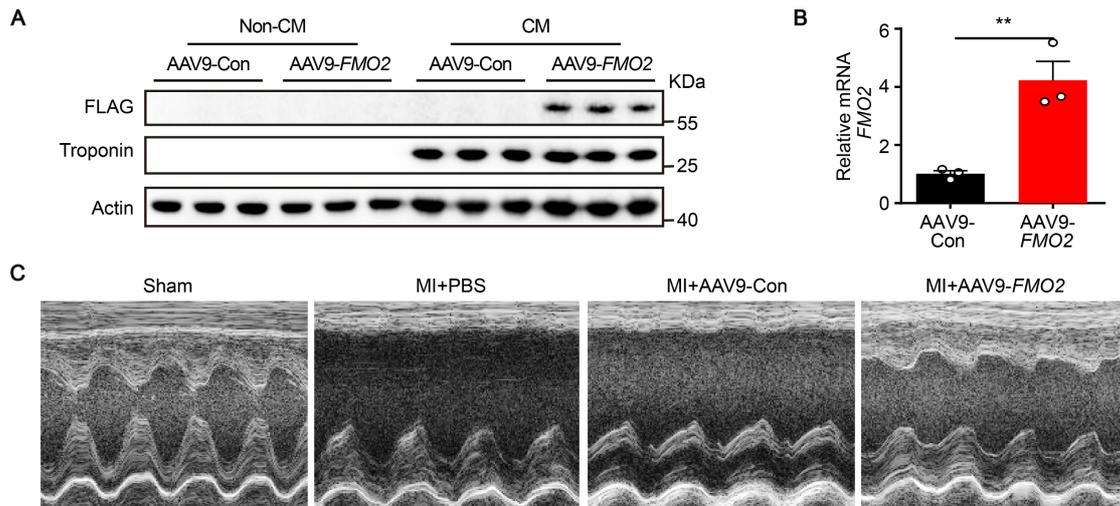
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65 **Supplemental Figure 5. Effect of AAV9-FMO2 in rat hearts.** (A) Expression of FMO2-

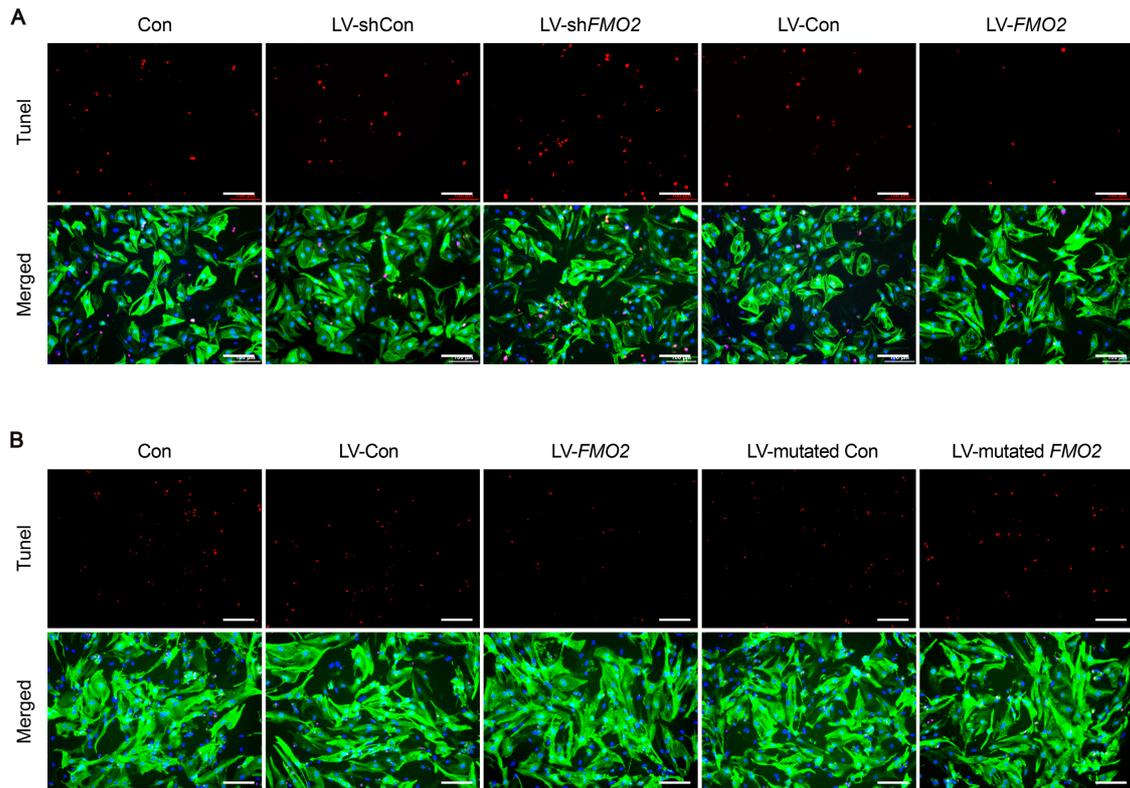
66 FLAG and Troponin in CMs and Non-CMs following AAV9-FMO2 injection. (B) FMO2

67 mRNA level in CMs isolated from control and AAV9-FMO2 rat hearts (n = 3 per group). (C)

68 Representative photographs of M-mode echocardiography. Quantified data are presented as

69 means ± SEM. Comparisons between two groups were assessed via the Student's t-test.

70 ** $p < 0.01$.



71

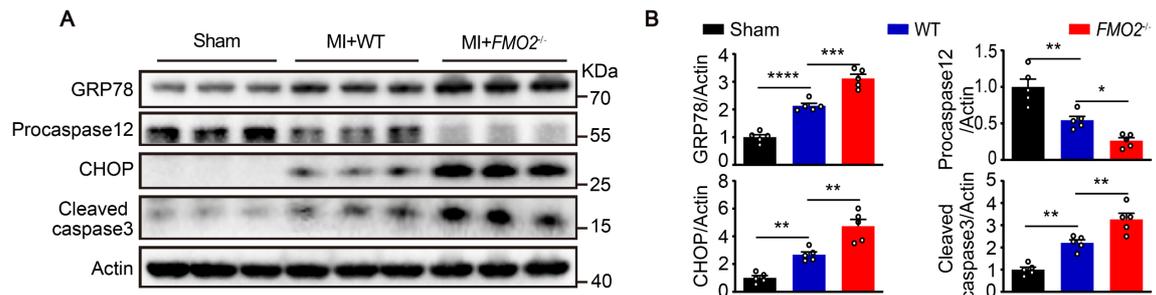
72 **Supplemental Figure 6. *FMO2* confers protection against hypoxia-induced apoptosis in**

73 **cultured cardiomyocytes. (A)** NRCMs were transfected with either LV-sh*FMO2* or LV-

74 *FMO2* lentivirus, then subjected to hypoxia for 24 hours. Representative views of TUNEL-

75 positive cardiomyocytes are shown. Bar = 100 um. **(B)** TUNEL staining of hypoxia-exposed

76 NRCMs with LV-*FMO2* or enzyme-inactivated *FMO2* (LV-mutated *FMO2*). Bar = 100 um.



77

78 **Supplemental Figure 7. Knockout of FMO2 exacerbates ER stress in infarcted hearts.**

79 (A and B) Protein expression of GRP78 and ER stress-induced apoptotic proteins in infarcted

80 hearts of *FMO2*^{-/-} rats, compared with WT. The graphs summarize data from 5 rats per group.

81 Quantified data are presented as means ± SEM, and significance was evaluated via one-way

82 ANOVA with Tukey test among three or more groups. **p*<0.05, ***p*<0.01, ****p*<0.001,

83 *****p*<0.0001.

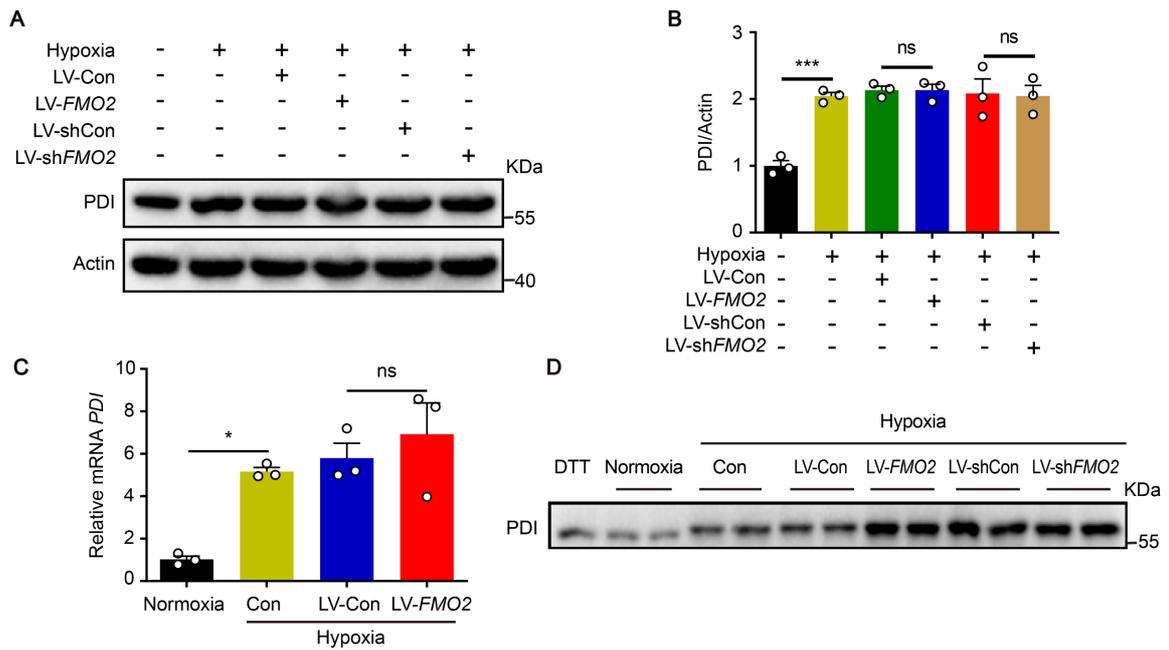
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90 **Supplemental Figure 8. Effect of FMO2 on disulfide-bond modification is independent**

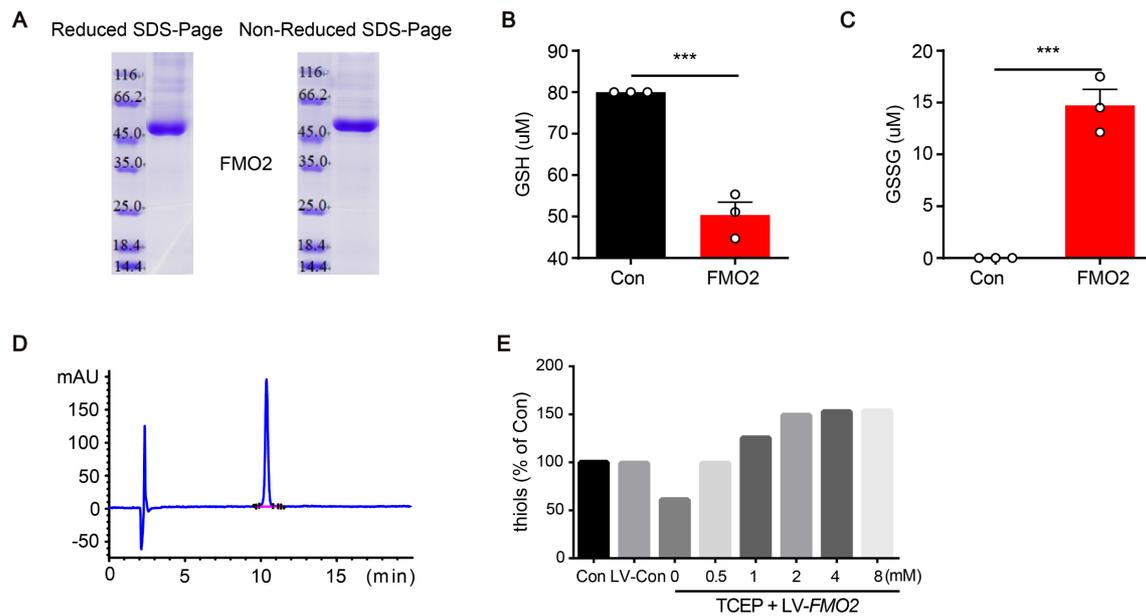
91 **on PDI.** (A-C) Effect of FMO2 on PDI protein and mRNA levels in NRCMs. (D) The redox

92 status of PDI in NRCMs transfected with LV-shFMO2 or LV-FMO2. DTT was used as

93 reduced control. The graphs summarize data from 3 independent experiments. Quantified data

94 are presented as means \pm SEM, and significance was evaluated via one-way ANOVA with

95 Tukey test among three or more groups. * $p < 0.05$, *** $p < 0.001$, ns: not significant.



96

97 **Supplemental Figure 9. FMO2 catalyzes disulfide-bond formation. (A)** FMO2 protein was

98 purified from insect cells and estimated on the Coomassie Blue-stained SDS-PAGE gel under

99 reduced and non-reduced conditions. **(B and C)** Contents of GSH and GSSG were measured

100 after reaction with or without FMO2. **(D)** Purity of peptide NRCSQGSCWN was analyzed by

101 High Performance Liquid Chromatography (HPLC). **(E)** TCEP inhibited disulfide-bond

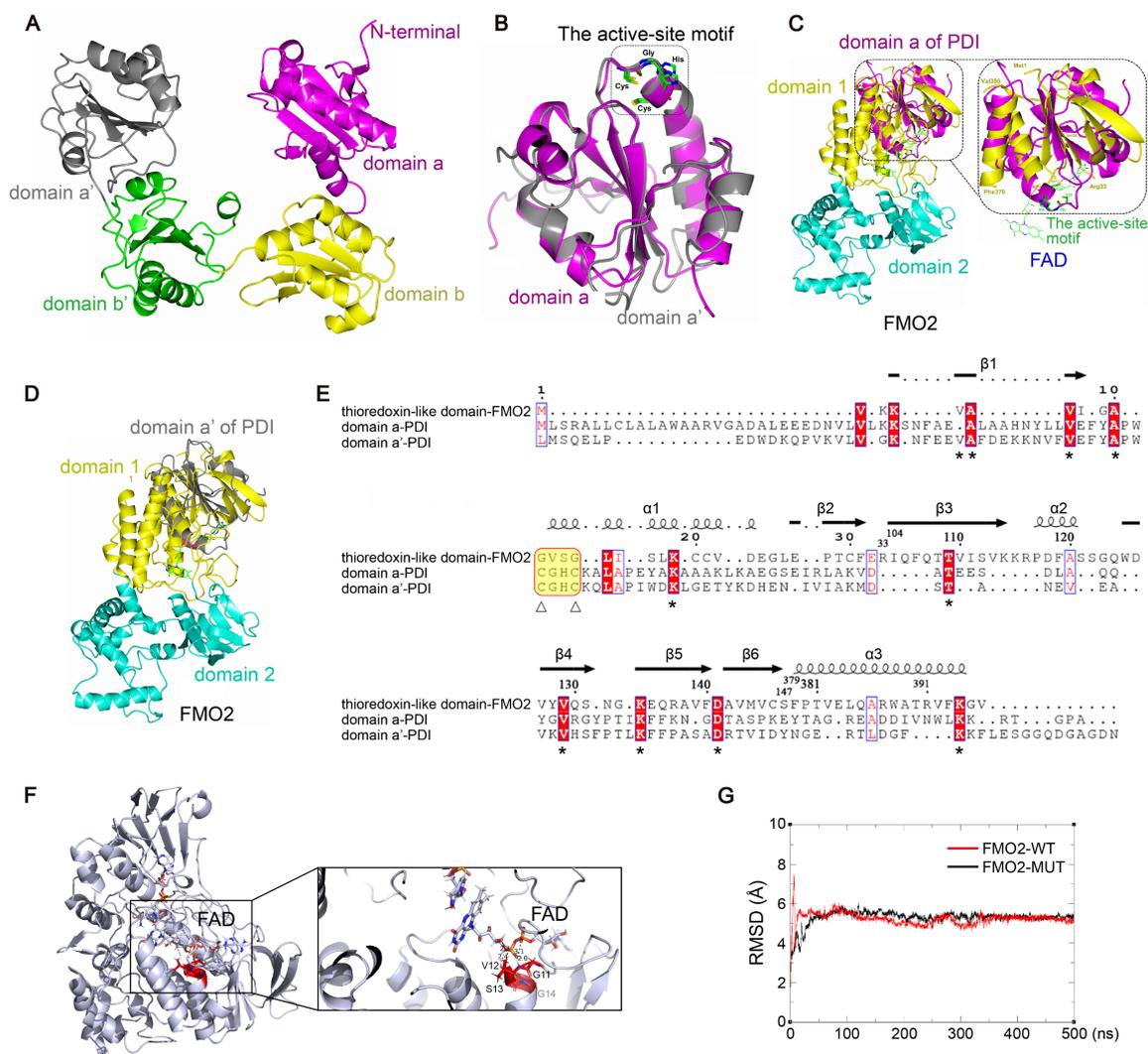
102 formation in a dose-dependent manner. Bar diagram of differently treated groups was

103 normalized to the hypoxia control. Quantified data are presented as means \pm SEM, and

104 significance was evaluated via one-way ANOVA with Tukey test among three or more groups.

105 *** p <0.001.

106



107

108 **Supplemental Figure 10. Structures of PDI and FMO2. (A and B)** Overall structure of PDI.

109 (A) N-terminal, domain a, b, b' and a' are colored in magenta, yellow, green and grey,

110 respectively. (B) The active-site motif in domain a and a' (colored in magenta and grey). (C)

111 Ribbon diagram of FMO2 (domain 1 and domain 2 colored in yellow and cyan, respectively)

112 was superposed with that of PDI domain a (colored in magenta). Close-up view of the active

113 site is shown in right. (D) Ribbon diagram of FMO2 (domain 1 and 2 colored in yellow and

114 cyan, respectively) was superposed with that of PDI domain a' (colored in magenta). (E)

115 Structure-based sequence alignment of the thioredoxin-like domain from FMO2 and domains

116 a and a' from PDI. Arrows represent β -strands and helices represent α -helices. The active-site

117 motif CGHC is colored in yellow and the conserved residues are colored in red and marked by

118 *. (F) The GVSG motif of FMO2 anchors FAD through hydrogen bonding. The amino acids

119 in the GVSG motif are highlighted in red. The hydrogen bonding interaction between GVSG

120 and FAD is depicted by black dotted lines. (G) Molecular dynamics simulations for FMO2-

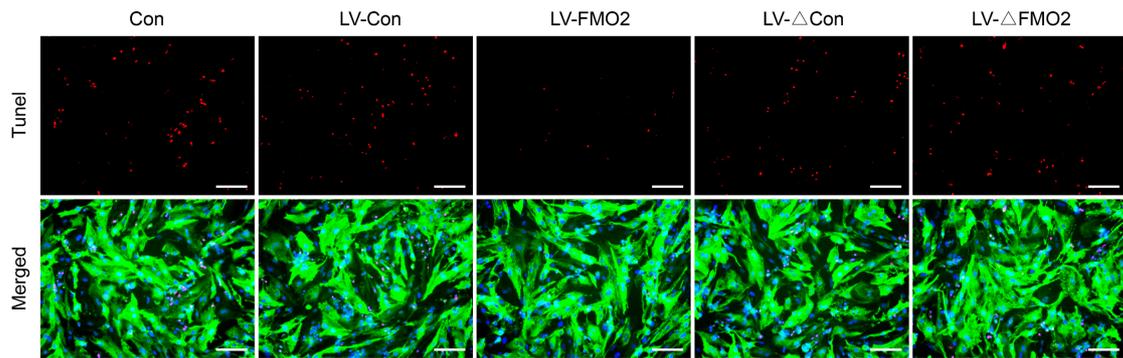
121 WT and FMO2-MUT were conducted. Both FMO2-WT and FMO2-MUT were subjected to a

122 500 ns molecular dynamics simulation, and the RMSD (\AA) was calculated during the

123 simulation.

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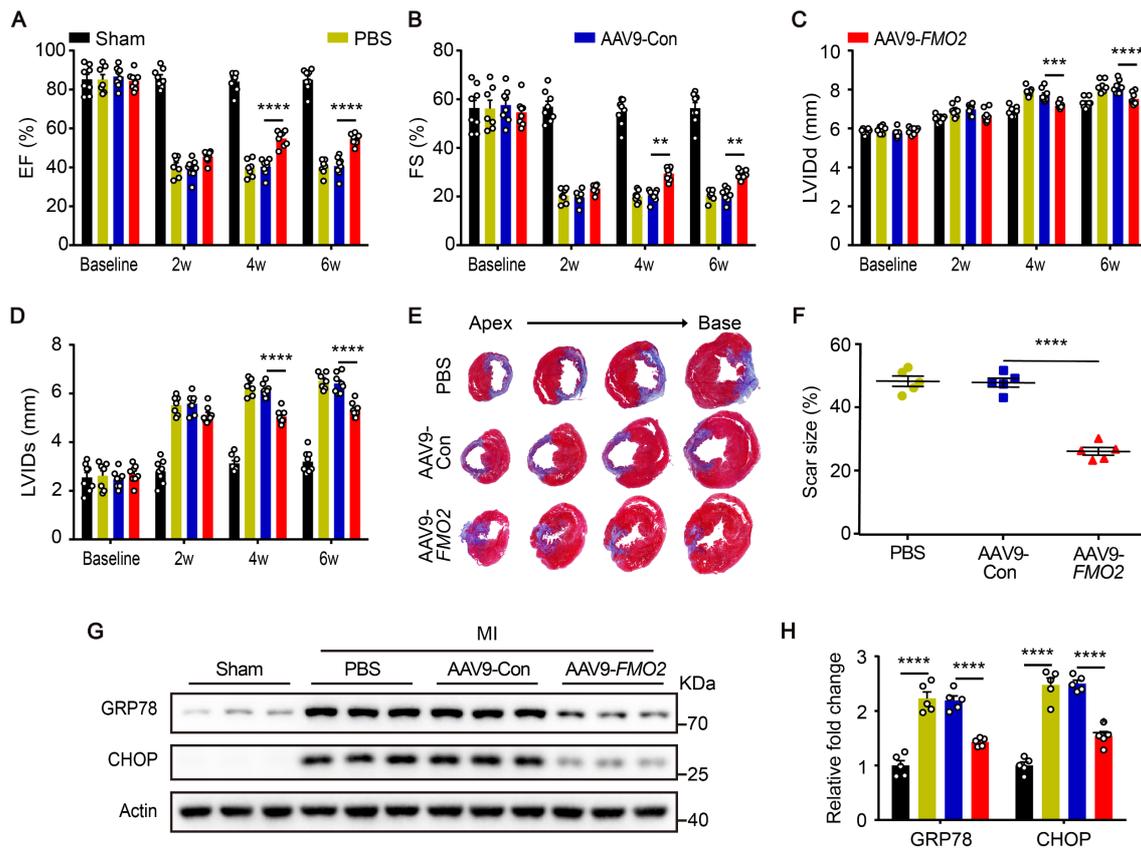
127 **Supplemental Figure 11. GVSG-mutated FMO2 fails to reduce cardiomyocyte apoptosis.**

128 TUNEL staining of hypoxia-exposed NRCMs with LV-*FMO2* or LV- Δ *FMO2*. Bar = 100 μ m.

129 Δ FMO2 indicates GVSG-mutant FMO2.

130

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133 **Supplemental Figure 12. AAV9-mediated overexpression of FMO2 protects the heart**

134 **from myocardial infarction. (A-D) Quantitative analysis of echocardiography (n = 7-8 per**

135 **group). (E and F) Representative tissue sections stained with Masson at 28 days after MI injury.**

136 **Percentage of scar size in is shown in (right, n = 5 per group). (G and H) Protein expression of**

137 **ER stress markers in rats that either received AAV9-FMO2 or AAV9-Con virus. Protein lysates**

138 **were harvested from infarct border zone of hearts (n = 5 per group). Quantified data are**

139 **presented as means ± SEM. Comparisons among three or more groups were evaluated via one-**

140 **way analysis of variance (ANOVA) with Tukey test, and comparisons among groups after**

141 multiple treatments were evaluated via two-way ANOVA with Tukey test. ** $p < 0.01$,

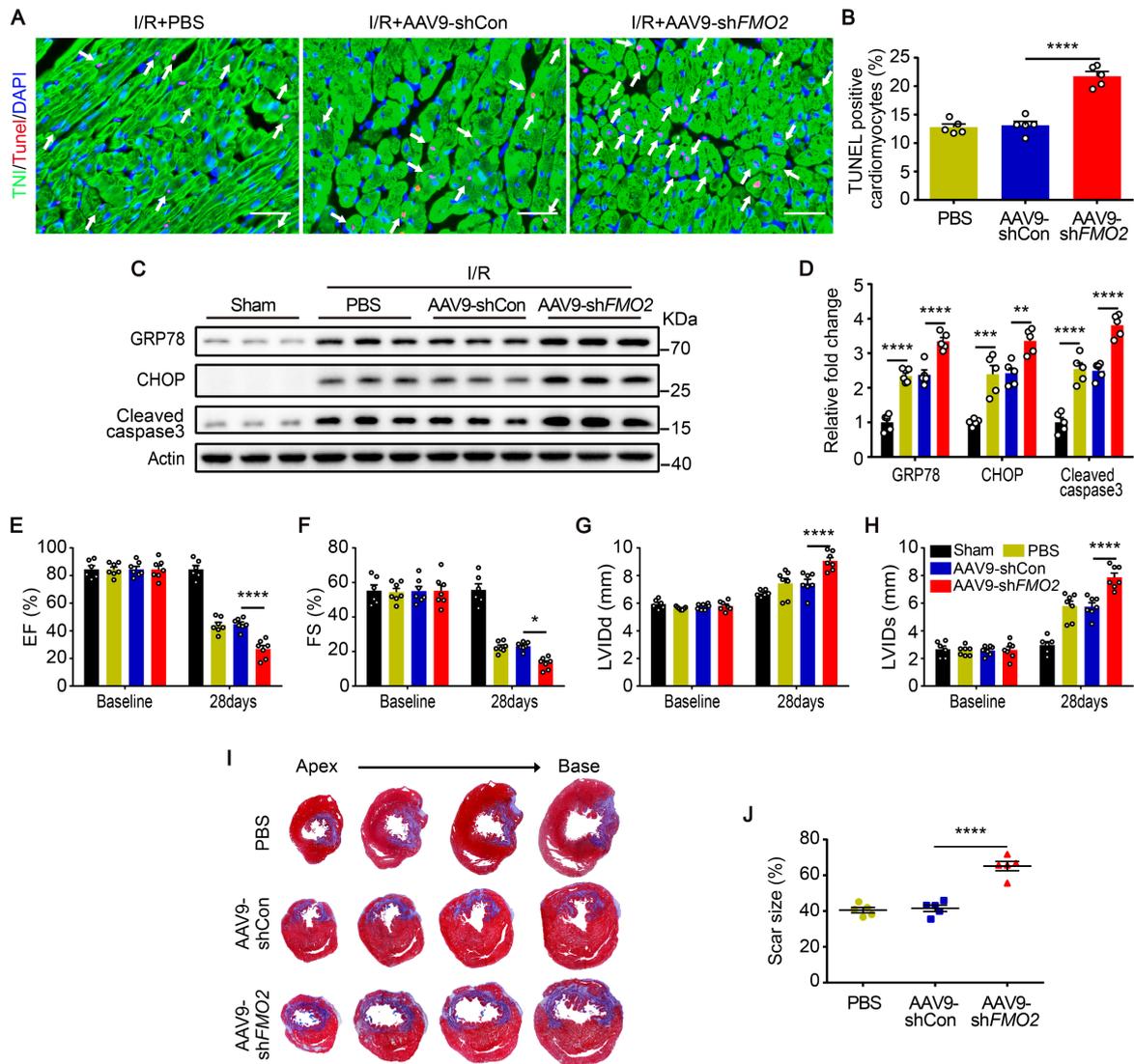
142 *** $p < 0.001$, **** $p < 0.0001$.

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148 **Supplemental Figure 13. Cardiomyocyte-specific FMO2 knockdown impairs cardiac**

149 **function accompanied by increased cardiomyocyte apoptotic level after I/R. (A and B)**

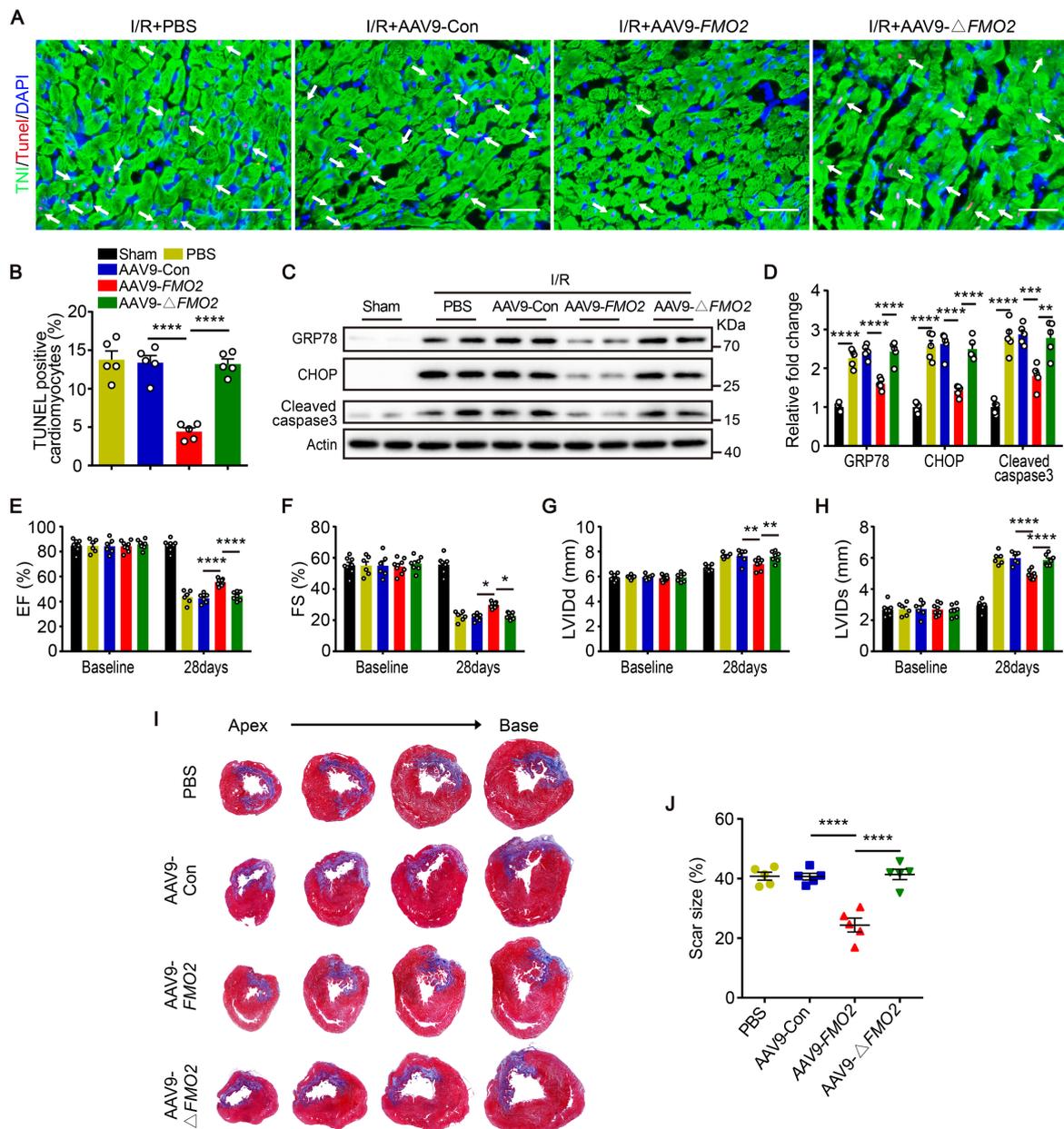
150 Representative TUNEL staining images of rat heart sections and quantitative results after I/R

151 surgery (n = 5 per group). Bar = 50 μ m. (C and D) Protein expression of GRP78 and ER stress-

152 induced apoptotic proteins in rats that either received AAV9-shFMO2 or AAV9-shCon virus.

153 Protein lysates were harvested from infarct border zone of hearts (n = 5 per group). (E-H)

154 Quantitative analysis of echocardiography (n = 6 in Sham group, n = 7 in other groups). (I and
155 J) Representative tissue sections stained with Masson at 28 days post-I/R. Percentage of scar
156 size in is shown in (right, n = 5 per group). Quantified data are presented as means \pm SEM.
157 Comparisons among three or more groups were evaluated via one-way analysis of variance
158 (ANOVA) with Tukey test, and comparisons among groups after multiple treatments were
159 evaluated via two-way ANOVA with Tukey test. * p <0.05, ** p <0.01, *** p <0.001,
160 **** p <0.0001.



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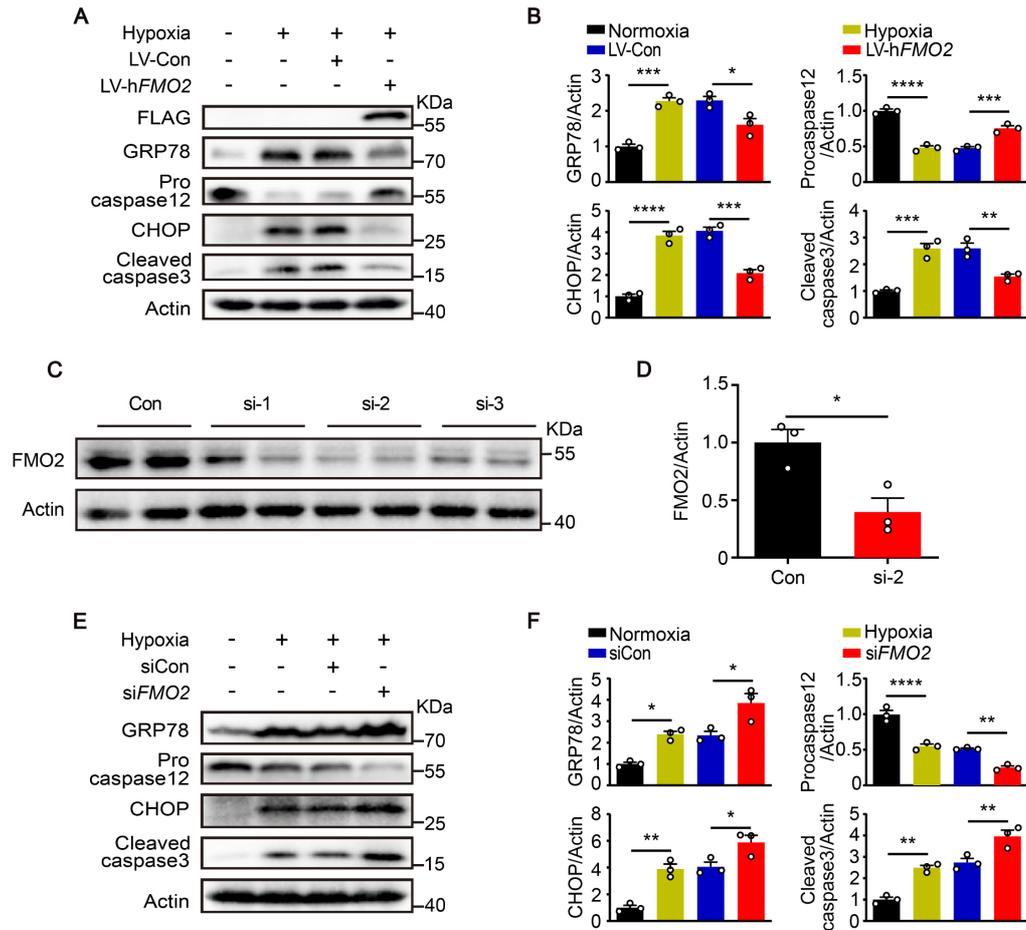
162 **Supplemental Figure 14. Cardiomyocyte-specific FMO2 overexpression decreases**

163 **cardiomyocyte apoptosis and improves cardiac function after I/R. (A and B)**

164 Representative sections of rat hearts subjected to I/R were analyzed for apoptosis by TUNEL

165 staining. Bar = 50 μ m. Quantitative analysis of TUNEL-Troponin I positive cardiomyocytes is

166 shown in (right, n = 5 per group). (C and D) Protein expression of GRP78 and ER stress-
167 induced apoptotic proteins in rats that either received AAV9-FMO2 or AAV9- Δ FMO2 virus.
168 Protein lysates were harvested from infarct border zone of hearts (n = 5 per group). (E-H)
169 Quantitative analysis of echocardiography (n = 6-8 per group). (I and J) Representative tissue
170 sections stained with Masson at 28 days after I/R injury. Percentage of scar size in is shown in
171 (right, n = 5 per group). Quantified data are presented as means \pm SEM. Comparisons among
172 three or more groups were evaluated via one-way analysis of variance (ANOVA) with Tukey
173 test, and comparisons among groups after multiple treatments were evaluated via two-way
174 ANOVA with Tukey test. * p <0.05, ** p <0.01, *** p <0.001, **** p <0.0001. Δ FMO2
175 indicates GVSG-mutant FMO2.



176

177 **Supplemental Figure 15. FMO2 inhibits ER stress and ER stress-induced apoptotic**

178 **response in hiPSC-CMs. (A and B) Protein expression of GRP78 and ER stress-induced**

179 **apoptotic proteins in hypoxia-exposed hiPSC-CMs transfected with LV-hFMO2 lentivirus. (C**

180 **and D) FMO2 protein expression in hiPSC-CMs after siRNA (siFMO2) transfection. si-2**

181 **siRNA targeting human FMO2 was used in the following experiments. (E and F) Protein**

182 **expression of GRP78 and ER stress-induced apoptotic proteins in hypoxia-exposed hiPSC-**

183 **CMs transfected with FMO2 siRNA. The graphs summarize data from 3 independent**

184 experiments. Quantified data are presented as means \pm SEM, and significance was evaluated
185 via one-way ANOVA with Tukey test among three or more groups. * $p < 0.05$, ** $p < 0.01$,
186 *** $p < 0.001$, **** $p < 0.0001$, ns: not significant.

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| SNP | Chr:Position (GRCh38) | Effect allele | Other allele | Exposure: <i>FMO2</i> expression in left ventricle | | | Outcome: HF | | | MR results | | | | |
|------------|--------------------------|------------------|-----------------|---|-------|-----------------------|-------------|-------|--------------|---------------|--------|-------|------------------------|--------------|
| | | | | Beta | SE | <i>p</i> val | Beta | SE | <i>p</i> val | Method | Beta | SE | OR (95% CI) | <i>p</i> val |
| rs78893152 | 1:171167180 | A | G | -0.440 | 0.071 | 5.4x10 ⁻¹⁰ | 0.040 | 0.019 | 0.034 | Wald ratio | -0.090 | 0.043 | 0.914 (0.841-0.993) | 0.034 |

197

198 **Supplemental Table 1. Causality analysis between *FMO2* and heart failure.** SE, standard

199 error; CI, confidence interval; OR, odds ratio.