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Supplemental information

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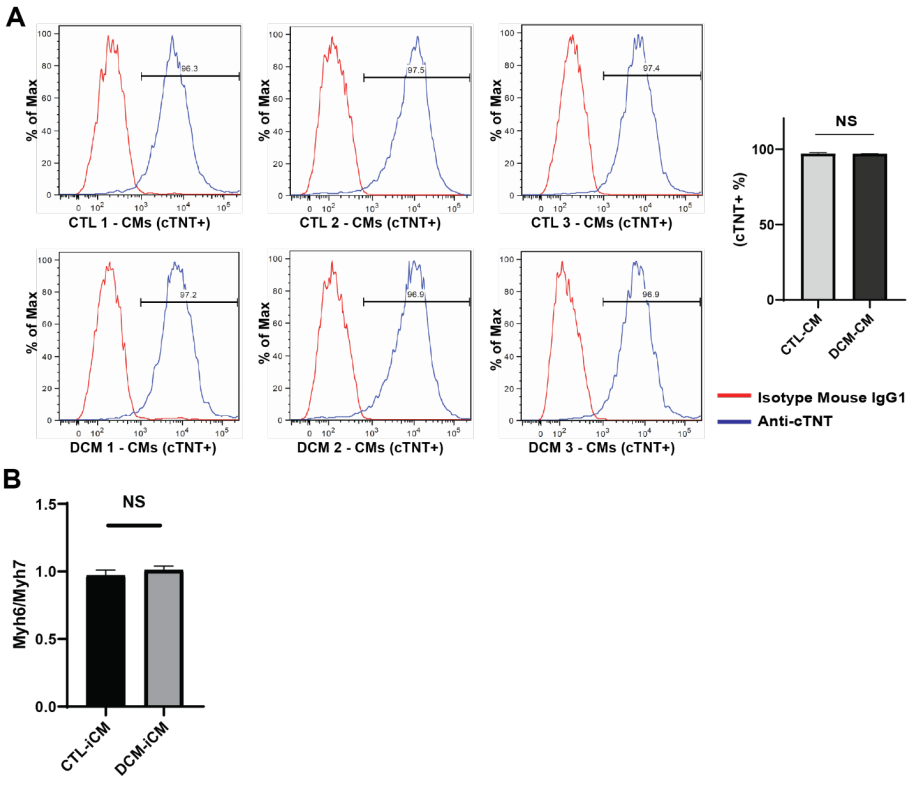

Figure S1. The purity and maturation of CTL- and DCM-iPSC differentiated cardiomyocytes were determined by flow cytometry and RT-PCR. (A) Histograms for flow cytometric analysis of $cTNT^{+}$ in CTL-iCMs and DCM-iCMs. (B) Quantification of myh6 to myh7 ratio in CTL- and DCM-iCMs. Three CTL lines and 3 DCM lines were used in the experiments. Related to Figure 1.

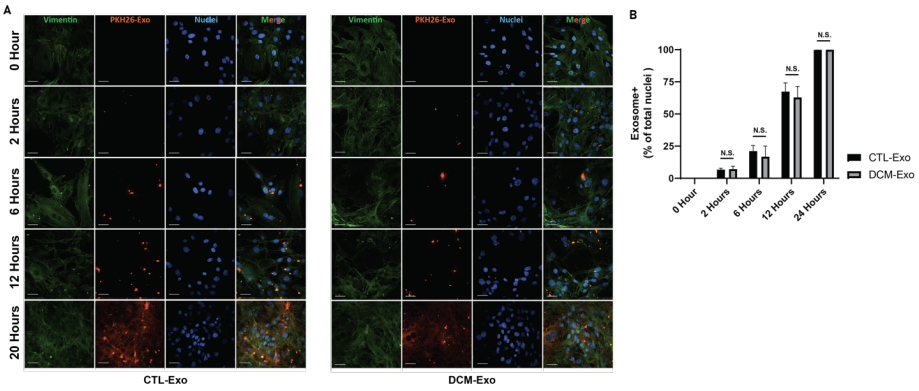

Figure S2. Time course assay of PKH26-labeled Exos treatment in vitro. The pictures were taken from different time-points after Exos treatment (A). Bar = 50um. The Exos update at different time points was analyzed (B). Related to Figure 2.

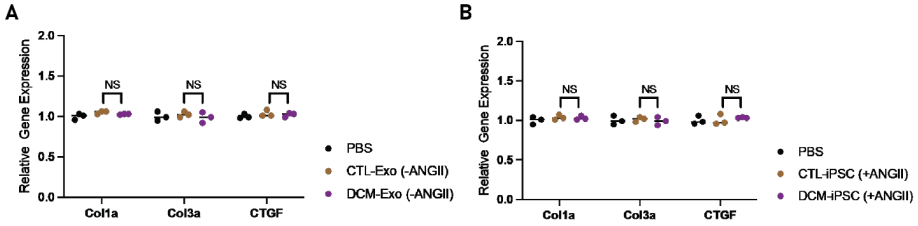

Figure S3. Neither Exos derived from basal media nor the Exos derived from iPSCs promoted fibrogenesis. The expression of fibrotic markers was determined by qRT-PCR. (A), CFs were treated with vehicle (PBS), CTL-Exo, or DCM-Exo derived from cardiomyocytes cultured in basal media. N= 3; One-way ANOVA. (B), CFs were treated with vehicle (PBS) or Exos derived from ANG II stimulated CTL-iPSC or DCM-iPSC. N= 3; One-way ANOVA; NS = no significance. Related to Figure 2.

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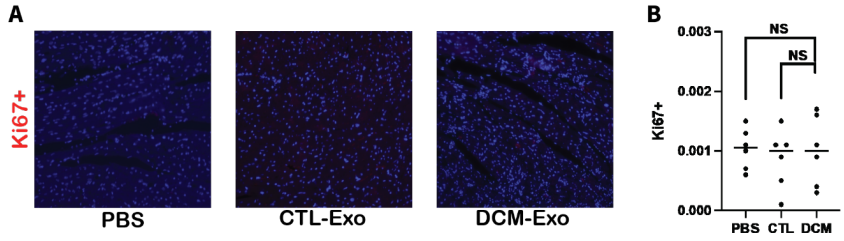

Figure S4. The injection of Exos did not induce proliferation in the hearts. (A) Immunofluorescent staining of detecting Ki67 (Red) in the vehicle, CTL-Exo, or DCM-Exo injection heart sections. The positive Ki67 indicated the proliferative cells in the hearts. (B) Statistical analysis showed positive Ki67 showed no significant differences. N= 6; One-way ANOVA; NS = nonsignificant. Related to Figure 3.

A

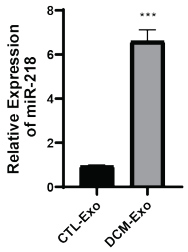

Figure S5. RT-PCR determined the expression of miR-218 in Exos. (A) Compared with CTL-Exos, miR-218-5p expression in DCM-Exos was significantly increased. N=3; Student's *t*-test; ***=P < 0.005. Related to Figure 4.

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Table S1. IPSCs used in this study. Related to Figure 1.

Patient No.	Cell Type	Disease	Age	Gender	Race	Passage
SCVI479	Sendai virus reprogrammed hiPSC	Healthy Donor	24	Male	African American	10
SCVI480	Sendai virus reprogrammed hiPSC	Healthy Donor	18	Female	African American	8
SCVI15	Sendai virus reprogrammed hiPSC	Healthy Donor	16	Male	Caucasian	8
SCVI17	Sendai virus reprogrammed hiPSC	DCM,TNNT2^{R173W}	75	Female	Caucasian	8
SCVI18	Sendai virus reprogrammed hiPSC	DCM,TNNT2^{R173W}	39	Male	Caucasian	11
SCVI19	Sendai virus reprogrammed hiPSC	DCM,TNNT2^{R173W}	46	Male	Asian	9

Table S2. Sequence of wild-type 5'UTR and mutated 5'UTR. Related to Figure 7.

Name	Sequence
Wild-type	gcagtctgca gtcttcgtgg cgggccaagc gagcttggag cccgcggggg cggagcggtg agagcggccg ccaagagaga tcacaccccc agccgaccct gccagcgagc gagcccgacc ccaggcgtcc atggagcgtc gcctccgccc ggtccctgcc ccgacccccg cctgcggcgc gctcctgcct tgaccaggac ttgggacttt gcgaaaggat cgcggggccc ggagaggtaa ccgccgcgcc tcccggagag gtgttggaga gcacaatggc tgaacaagtc cttcctcagg
Mutation	gcagtctgca gtcttcgtgg cgggccaagc gagcttggag cccgcggggg cggagcggtg agagcggccg ccaagagaga tcacaccccc agccgaccct gccagcgagc gagcccgacc ccaggcgtcc atggagcgtc gcctccgccc ggtccctgcc ccgacccccg cctgcggcgc gctcctgcct tgaccaggac ttgggacttt gcgaaaggat cgcggggccc ggagaggtaa ccgccgcgcc tcccggagag ctatacccgc tcttggc tgaacaagtc cttcctcagg