### SUPPLEMENTAL METHODS Cell cultures

Mouse neonatal hearts were dissected and incubated with F-10 nutrient medium, containing 140  $\mu$ g/ml of collagenase type-2 (Sigma) and 440  $\mu$ g/ml pancreatin (Sigma) until cells were dissociated. The cells were then washed, resuspended in 1:1 mix of Dulbecco's minimal Eagle's medium (DMEM) and F10 nutrient mix with 5% each of equine and bovine calf serum. These cells were pre-plated in tissue culture dishes for 1 h to allow for attachment of nonmyocytes. The resulting non-adherent myocytes were plated on fibronectin-coated (Sigma) tissue culture dishes. Cells from one heart were plated in each 35 mm² petridish and cultured for 24 h, after which the medium was replaced with 1:1 mix of DMEM and F10 nutrient medium containing 1  $\mu$ g/ml thyroxin, 5  $\mu$ g/ml of transferrin, 1  $\mu$ g/ml of insulin, 10 pM each of LiCl and selenite. A 0.1 mM bromodeoxyuridine concentration was used to check fibroblast growth.

#### CaMKIIN mice

The HA eptiope and membrane association domain (MEM), encoding a palmitoylation sequence, were added to the 5' of  $\beta$ CaMKIIN sequence by PCR using the 5' primer: gccattaagcttatgctctgctgtatgagaagaaccaaacaggttgaaaagaatgatgaggaccaaaagatcatgtccgagatcctaccctacggc and the 3' primer ccgtatggatccctacactccggacggaggcttctc (Integrated DNA Technologies) with *Hin*dIII and *Bam*HI sites at the extreme ends. The DNA template for PCR was pSB3-His-CaMKIIN. CaMKIIN cDNA construct was a kind gift from Dr. Tom Soderling (Vollum Institute). The product (~360 base pairs) was purified from agarose gel (Quiagen gel extraction kit) and was digested with restriction enzymes, *Hin*dIII and *Bam*HI. The resulting DNA product was ligated into pCMV5-HA1 previously digested with *Hin*dIII and *Bam*HI. The HA-tagged MEM-CaMKIIN sequence was subcloned into p $\alpha$ -MHC promoter vector by PCR using the following primers: 5'-ccatgagtcgacgccgccaccatgtacccatacgacgtcccagactatgctgg taccacgcgtatcgataaactt and 3'-gccattaagcttctacactccggacggagggtcttct that incorporated *Sal*I and

kozak sites in the 5' region and a HindIII site in the 3' region. PCR products digested with SalI and HIndIII were ligated into the p $\alpha$ MHC-script-Hgh vector (9.2 kb). Mouse embryonic stem cells were injected with the linearized DNA (digested with NotI) in the Vanderbilt Transgenic Mouse Core Facility and implanted into B6D2 pseudo-pregnant females. Insertion of the transgene into the mouse genome was confirmed by PCR analysis (not shown) using the above primers.

#### **Quantitative RT-PCR**

For quantitative RT-PCR, 1  $\mu$ l of reverse transcription reaction was mixed with 10 pmoles each specific primer and 12.5  $\mu$ l SYBR PCR Master Mix (BioRad). The reaction was incubated in an iQ5 model thermocycler (BioRad) for 40 cycles consisting of denaturation at 95°C for 10 s and annealing/extension at 59.9°C for 1 min. The quality of the PCR product was routinely checked by thermal denaturation curve following the qPCR reactions. The threshold cycle ( $C_T$ ) was determined by the iCycler software, and quantification of relative mRNA levels was performed by  $\Delta\Delta C_T$  method. We thank Dr. Mollie Meffert (Johns Hopkins) for IkB-DN lentivirus expression construct. mCfbFor 5'-GAAACCCTGTCACTGTCATTC-3' and mCfbRev 5'-CCCCAAACACATACACA TCC-3'.

### SUPPLEMENTAL FIGURE LEGENDS Suppl. Figure 1:

Complement factor B expression in normal hearts. (**A**) Quantitative RT-PCR analyses of RNA from hearts (n=3) shows increased *Cfb* mRNA levels in AC3-I compared to WT. (**B**) Immunoblotting of heart extracts (n=3) shows similar amounts of CFB in both WT and AC3-I. (**C**) Immunoblot of WT and AC3-I heart extracts was probed with anti-CFB antibody (upper panel) as described in the Methods. Following the signal detection, the blot was stained with coomassie blue (lower panel).

#### Suppl. Figure 2:

Cfb expression in cardiomyocytes. (A) RT-PCR analysis of Cfb and Hprt performed on cultured neonatal (Neo) and isolated adult cardiomyocytes. The RT-PCR lanes representing reverse transcriptase reaction with and without reverse transcriptase enzyme are designated as '+' and '-', respectively. The far left and far right columns show molecular size markers marked in base pairs (bp). (B) Immunoblotting for CFB protein expression in neonatal and adult cardiomyocytes, and heart tissue. Equal amount of total protein from each sample was fractionated using NuPAGE gels. Antibody to CFB was used to detect the CFB protein band. Immunoblots of actin were used as a loading control.

#### Suppl. Figure 3:

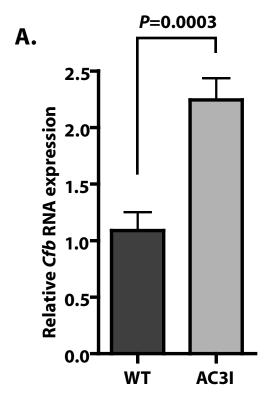
Death and apoptosis markers in neonatal cardiomyocytes treated with LPS. (A) Fraction of dead cardiomyocytes determined by flow cytometry using propidium iodide (PI) fluorescent vital dye (Molecular Probes). A total of 18,344 and 14,647 cells were sorted for control (serum alone) and treatment (serum and LPS), respectively. The significance of the results of PI-positive cells in each treatment was determined by Fisher's Exact test. (B) TUNEL staining data from mouse serum and LPS treated cultured cardiomyocytes. All data are from n>3 separate experiments.

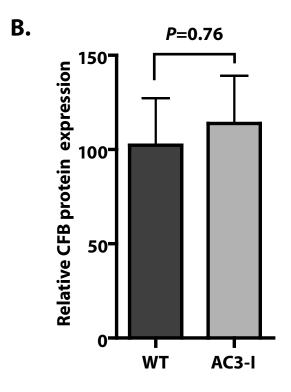
#### Suppl. Figure 4:

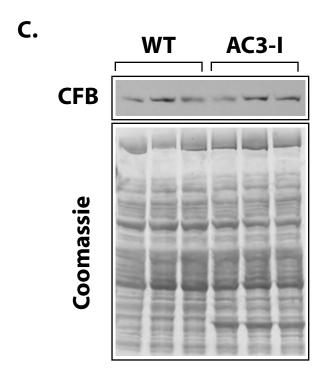
(A) Expression of βCaMKIIN in transgenic mouse heart and inhibition of CaMKII mediated phosphorylation of T17 residue of phospholamban (PLN). Heart extracts from wild type (WT) and βCaMKIIN transgenic mice (CaMKIIN) were fractionated on a NuPage gel (Invitrogen) and transferred onto a PVDF membrane (BioRad). Blots were probed with either a monoclonal

antibody to detect HA-epitope tagged cardiomyocyte-delimited expression of transgenic  $\beta$ CaMKIIN or antibodies to phospholamban (PLN). Specific antibodies to either total or phospho-specific epitope were used. For PLN, the same blot was stripped and reprobed in the following order: PLN-T17, PLN-S16, and PLN-total. (**B**) Membrane localization of  $\beta$ CaMKIIN. DNA binding fluorescent stain DAPI was used to visualize the nuclei. Images were obtained by BioRad multiphoton confocal microscopy and rendered pseudocolors (Red= anti-HA, Blue= DAPI). Scale bars = 20  $\mu$ m.

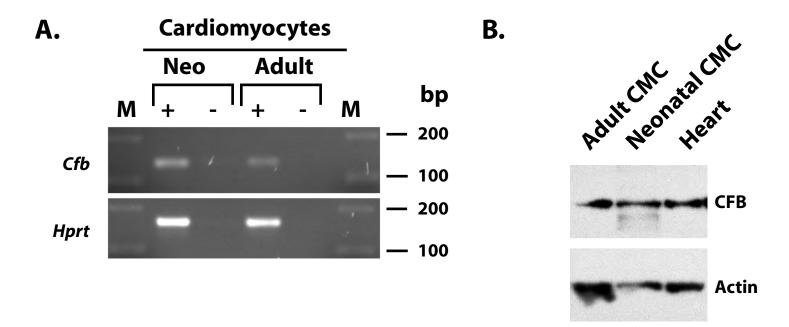
## **Suppl Figure-1**





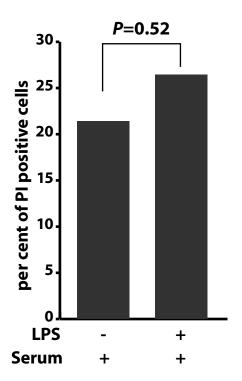


### **Suppl Figure-2**

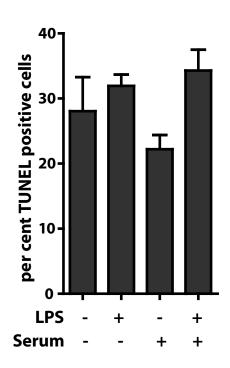


# **Suppl Figure-3.**

A.

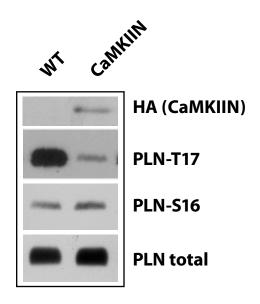


В.

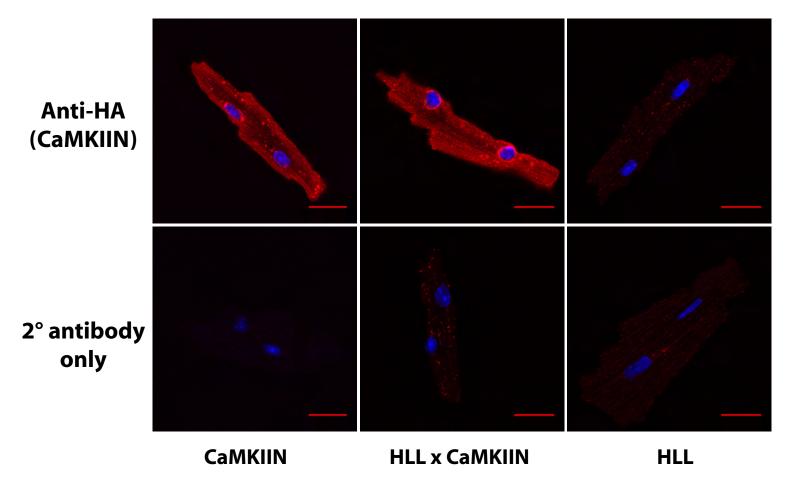


## **Suppl Figure-4.**





### В.



# Supplemental Table 1. cutoff)

List of genes upregulated in post-MI AC3-C hearts (1.8-fold increase  $\,$ 

1110002B05Rik

AC124413.2

AC138640.7

Adamts15

Adn

AK024941.1

AL732556.7

Ankrd1

Arntl

Atp13a1

ATXN1

AY172581.1

Bf

Btnl2

BX883045.1

C1s

C2

C4a

Ca3

Cacna2d1

Cald1

Cap1

Capzb

Cd2

Cd37

Cd74

Cdo1

Centg1

Cetn3

Cfp

Cish

Clk4

Cma1

Col3a1

Col5a2

Cpne3

Cpxm1

Ctgf

Ctss

Cyp2e1

Cyp2f2

Cyp4f5

Dym

Efemp1

Eif3s10

Eln

Enpp2

Eprs

Fasn

Fn1

Fos

Gpc3

Gpnmb

Hbg1

Hmgn3

Hspa1a

Ifi30

IgG-2a

Igh-6

II18

Itgam

Itih4

KIf9

Kras

L22655

LOC64305

Loxl1

M21780.1

Man2a1

Map2k6

Matr3

Mbnl2

MgI1

Mgp

Mmp9

MsIn

Myo1g

Ncl

Neb

Nfia

Nif3I1

Nppa

Nppb

Nr3c1

Plcb1

Plcb4

Plk2

Pnkd

Postn

Ppp4r2

Prei3

Prkcb1

Ptk2b

Rasa1

Rcan1

RGD1564450

Rock2

Rpl5

RT1-Aw2

Rtn4

S100a9

Saa

Sacm1I

Scd1

Sfrs12

Sorl1

Stat1

Stch

Stk25

Sv2b

Tbc1d5

Tbca

Tf

Tgfb2

Timp1

Tpp2

Ttc3

Ugt1a1

Uqcrfs1

Usp15

Vcp

Vps54

X53054

X68312

XM\_234581.2

XM\_341386.1

Zfp265

Zfp692

### Supplementary Table 2. Genes downregulated in post-MI AC3-C hearts (1.8 fold decrease cutoff).

Angptl4 AY172581.1

BX883045.1

Camk2b

Cd164

Cd36

Cd63

Cish

Dbp

Dhrs7c

Dtx2

Eno3

ldh1

Irx3

Kbtbd10

Pam

Pdk4

Pfkfb1

Pim3

Ptgds

Ptp4a3

Pttg1

Rbp7

Slc9a3r1

Tcap

Uqcrbl

XM\_342364.1

XM\_347242.1