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The COP9 Signalosome Is Required for Autophagy, Proteasome-Mediated Proteolysis, and Cardiomyocyte Survival in Adult Mice

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Abstract

Background—The COP9 signalosome (CSN) is an evolutionarily conserved protein complex composed of 8 unique protein subunits (CSN1 through CSN8). We have recently discovered in perinatal mouse hearts that CSN regulates not only proteasome-mediated proteolysis but also macroautophagy. However, the physiological significance of CSN in a pots-mitotic organ of adult vertebrates has not been determined. We sought to study the physiological role of CSN8/CSN in adult mouse hearts.

Methods and Results—*Csn8* was conditionally ablated in the cardiomyocytes of adult mice ($CSN8^{CKO}$) using a temporally controlled Cre-LoxP system. Loss of CSN8 accumulated the neddylated forms of cullins and non-cullin proteins, increased ubiquitinated proteins, and stabilized a surrogate substrate of the proteasome in the heart. Autophagic flux was significantly decreased while autophagosomes were markedly increased in $CSN8^{CKO}$ hearts, indicative of impaired autophagosome removal. Furthermore, we observed increased oxidized proteins, massive necrotic cardiomyocytes, and morphological and functional changes characteristic of dilated cardiomyopathy in $CSN8^{CKO}$ mice.

Conclusions—CSN deneddylates substrates more than cullins and is indispensable to cardiomyocyte survival in not only perinatal hearts but also adult hearts. CSN8/CSN regulates both proteasome-mediated proteolysis and the autophagic-lysosomal pathway, critical to the removal of oxidized proteins in the heart.

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Disclosures
None.

Keywords

COP9 signalosome; autophagy; proteasome; NEDD8; heart

Protein quality control (PQC) is pivotal to proteostasis in the cell. Targeted removal of terminally misfolded/damaged proteins is the last line of defense in PQC and is performed by the ubiquitin proteasome system (UPS) and macroautophagy (hereafter referred to as autophagy), two main intracellular proteolytic pathways.[1] UPS-mediated proteolysis involves ubiquitination of a protein molecule and the subsequent proteasome-mediated degradation of the ubiquitinated protein. Autophagy uses specialized double-membrane structures to sequester a portion of the cytoplasm, proteins aggregates, or damaged organelles into autophagosomes for fusion with and degradation by lysosomes.[2, 3] UPS and autophagy dysfunctions are implicated in the pathogenesis of many cardiac disorders.[1–11] However, molecular mechanisms by which the UPS and autophagy are regulated in the heart remain poorly understood.

The COP9 signalosome (CSN), identified first in *Arabidopsis thaliana*,[12] is an evolutionarily conserved multi-protein complex consisting of eight unique subunits (CSN1 through CSN8).[13] The attachment of a ubiquitin-like protein NEDD8 to cullin via a process known as neddylation is critical for the activation of cullin-based RING ligases (CRLs).[14] The *bona fide* biochemical activity of CSN is to remove NEDD8 from cullin (i.e., deneddylation);[15] therefore, CSN is believed to play an important role in regulating CRLs. Studies from lower organisms and cultured mammalian cells have suggested that CSN participates in a variety of biological processes, including invertebrate development, DNA repair, cell cycle, kinase signaling, nuclear transport, and T cell proliferation.[16] These observed roles are more or less tied to the deneddylation activity of CSN; but this does not preclude other unidentified functions that CSN might possess. Despite these observations, the physiological role of the CSN in mammals has just begun to be investigated. Germ-line deletion of the genes encoding CSN subunits in mice all resulted in embryonic lethality, at least partially due to defect in cell proliferation, underscoring its essential role in embryonic development.[16, 17]

CSN8 is the smallest and least conserved subunit of CSN.[17] By conditional gene targeting at the perinatal stage of murine development, we have recently found that CSN8regulates both the UPS and the autophagic-lysosomal pathway in perinatal hearts and is essential to early postnatal cardiomyocyte survival and cardiac function.[9, 18] However, the biochemical function and physiological significance of CSN has never been tested in a post-mitotic organ of vertebral animals. Given that CSN is required for cell division and rodent cardiomyocytes do not stop proliferating until several days after birth,[13, 19] the phenotypes, including increased cell death which is often intimately linked to cell cycle perturbation, and resultant cardiac failure observed in mice with perinatal cardiomyocyte-restricted Csn8 knockout may be unique to the perinatal stage. In other words, the heart with cardiomyocytes undergoing active proliferation at the perinatal stage may respond to CSN8/CSN deficiency differently from an adult heart in which cardiomyocyte proliferation has ceased. Furthermore, neddylation and CSN are emerging therapeutic targets in adult malignancies.[20, 21] Understanding the impact of Csn8/CSN deficiency on adult hearts should help unveil the potential adverse impact of these new therapeutic strategies on adult hearts. Hence, the present study has determined the impact of cardiomyocyte-restricted ablation of the *csn8* gene initiated in adult mice ($CSN8^{CKO}$) on cardiac PQC and heart structure and function. The results demonstrate for the first time in a post-mitotic organ of intact adult vertebral animals that CSN8 is required for the deneddylation of cullins and unknown non-cullin proteins and regulates both the UPS and autophagy and thereby is essential to PQC and the functioning and survival of cardiomyocytes.

Methods

Animal models and experimental protocols

CSN8-floxed mice ($CSN8^{flox/+}$),[17] transgenic (tg) mice with cardiac expression of the mutant estrogen receptor fused *Cre* driven by the mouse *Mhc6* promoter ($MerCreMer^{tg}$),[22] GFPdgn tg mice,[23] and GFP-LC3 tg mice[24] were previously described. To generate mice suitable for $CSN8^{CKO}$, $CSN8^{flox/flox}$ mice were cross-bred with $MerCreMer^{tg}$. The resultant $MerCreMer^{tg}$::$Csn8^{flox/+}$ mice were then mated with $Csn8^{flox/flox}$ mice, which gave rise to littermate mice that have a genotype of (A) $MerCreMer^{ntg}$::$Csn8^{flox/+}$, (B) $MerCreMer^{ntg}$::$Csn8^{flox/flox}$, (C) $MerCreMer^{tg}$::$Csn8^{flox/+}$, or (D) $MerCreMer^{tg}$::$Csn8^{flox/flox}$ in the expected Mendelian frequency and appear healthy and indistinguishable from one another. To induce the MerCreMer mediated ablation of the floxed *csn8* alleles, 8- to 10-week-old littermate mice with the 4 different genotypes described above, as well as age- and gender- matched wild type mice were treated with daily intraperitoneal injection of tamoxifen (Sigma, 100μg/g/day) for 3 consecutive days. During the initial tests, no significant difference in CSN8 and neddylated cullin protein levels was detected among mice with genotypes (A), (B), and wild type mice after tamoxifen or mock treatments. Hence, mice of genotype (B) and (D) after tamoxifen treatments were respectively used as the control group (CTL) and the $CSN8^{CKO}$ group.

The protocol for the care and use of animals in this study was approved by the Institutional Animal Care and Use Committee of the University of South Dakota and conforms to the Guide for the Care and Use of Laboratory Animals published by the US National Institutes of Health (NIH Publication No. 85-23, revised 1996).

Immunofluorescence confocal microscopy

The fixation, embedding, immunostaining, and image acquisition were performed as previously described.[18]

Western blot analyses

Protein extraction from myocardium, protein concentration determination with BCA reagents (Pierce), SDS-PAGE, western blot analyses, and densitometry were performed as previously described.[9]

RNA analyses

Total RNA was extracted from ventricular tissue using the Tri-Reagent (Molecular Research Center). Northern blot analysis for Csn8 mRNA and RNA dot blot analyses for GFPdgn and genes of the fetal gene program were performed as previously described.[9, 25]

Proteasome peptidase activity assays

The synthetic fluorogenic substrate Suc-LLVY-minomethycoumarin (25μM) and Z-LLE-β naphthylamide (25μM, BIOMOL) were respectively used for measuring chymotrypsin-like and caspase-like activities in crude protein extracts from ventricular myocardium.[18]

Transmission electron microscopy

Transmission electron microscopy (TEM) of perfusion fixed myocardium was performed as previously described.[25]

Assessing autophagic flux in the heart

Mice were intraperitoneally injected with 2 doses of bafilomycin-A_1 (BFA, 3μmol/kg, Sigma) or vehicle control with 1 hour in between. At 2 hours after the first dose, the mice

were euthanized and the ventricular myocardium was sampled for western blot analyses of LC3-II levels. BFA induced increases of LC3-II reflect autophagic flux.[8]

Echocardiography

Mice were anesthetized by inhalation of isoflurane (2.5% for induction and 1.5% for maintenance) via a nose cone. The adequacy of anesthesia was monitored by toe pinch. Transthoracic echocardiograph was recorded using the Vevo770™ echocardiography system and a 30MHz transducer with a focal length of 12.7mm (Visual Sonics). The LV morphometric and functional parameters were analyzed off-line as previously described.[18]

Left ventricle (LV) hemodynamics

Mice anesthetized by inhalation of 2.5% isoflurane were intubated through the mouth and mechanically ventilated. The LV catheterization and hemodynamic assessments were performed as previously described.[26]

Statistical Analysis

All quantitative data are presented as dot plots with mean ± SD superimposed. Differences between two experimental groups were evaluated for statistical significance using the Wilcoxon rank sum test. Differences among multiple groups were evaluated using the Kruskal-Wallis test followed by the Dunn test. The P value <0.05 were considered statistically significant.

Results

Targeted ablation of the *Csn8* gene in cardiomyocytes of adult mice

We targeted the *Csn8* gene in adult mouse hearts using the MerCreMer mediated inducible Cre-Lox*P* system (Supplemental Figure S1A). Deletion of the Csn8 gene in adult hearts was induced by administration of tamoxifen to 8- to 10-week-old mice. Tamoxifen can bind to MerCreMer and moves the MerCreMer from cytoplasm to the nucleus where the MerCreMer performs the recombination of the floxed alleles.[22] The recombination were verified by PCR analyses, using genomic DNA extracted from myocardium of the CTL and $CSN8^{CKO}$ mice at 3 days after the first tamoxifen injection. The recombined $CSN8^{flox}$ allele was detected only in the $CSN8^{CKO}$ hearts but not in the CTL hearts (Supplemental Figure S1B). At 3 days after the first tamoxifen injection, the CSN8 mRNA level in the ventricle of $CSN8^{CKO}$ hearts fell nearly below the limit of northern blot analysis (Supplemental Figure S1C), indicative of efficient excision of $CSN8^{flox}$ alleles. Approximately 70% of CSN8 proteins were lost in the $CSN8^{CKO}$ hearts by 5 days after the first tamoxifen injection (Figure 1A). Consistent with the findings from western blot analyses, CSN8 immunostaining was significantly diminished in both the nucleus and cytoplasm of cardiomyocytes in $CSN8^{CKO}$ hearts (Supplemental Figure S1D). Together, these data indicate that highly efficient deletion of the *Csn8* gene was achieved in the cardiomyocytes of $CSN8^{CKO}$ adult mice within 5 days after the first tamoxifen injection.

Loss of CSN deneddylation activity in $CSN8^{CKO}$ hearts

The *bona fide* cullin deneddylation activity of CSN resides in CSN5.[13] Neither CSN5 nor CSN1 protein abundance were altered in $CSN8^{CKO}$ hearts (Figure 1A), but the neddylated form of cullin (Cul) proteins, including Cul1, Cul2, Cul3, and Cul4A was markedly increased in the $CSN8^{CKO}$ hearts (Figure 1B). A number of non-cullin proteins can also be neddylated.[27] Interestingly, increases in the neddylated form of unknown proteins were also detected in $CSN8^{CKO}$ hearts (Figure 1C). These data demonstrate that deletion of the *Csn8* gene suffices to compromise CSN deneddylation activity in adult cardiomyocytes.

Impairment of UPS proteolytic function in CSN8^{CKO} hearts

We recently showed that perinatal loss of CSN8 in cardiomyocytes caused cardiac PFI but this has not been tested in adult hearts.[18] To monitor UPS proteolytic function *in vivo*, a reporter mouse model was previously generated and validated.[23] In this tg mouse, a UPS surrogate substrate (GFPdgn) was ubiquitously and constitutively expressed and GFPdgn protein levels inversely reflect UPS proteolytic function. Tg GFPdgn was introduced into CSN8^{CKO} and littermate CTL mice through cross-breeding. GFPdgn protein levels in CSN8^{CKO}::GFPdgn mouse hearts were significantly increased at 3 days after the first tamoxifen injection, compared with the littermate CTL::GFPdgn mice (Figure 2A). Consistently, fluorescent confocal microscopy showed that GFPdgn fluorescence in cardiomyocytes was brighter in the CSN8^{CKO}::GFPdgn mice than in CTL::GFPdgn mice (Figure 2B). RNA dot blot analysis revealed that the GFPdgn transcripts were not significantly different between the CTL::GFPdgn mice and the CSN8^{CKO}::GFPdgn mice (Figure 2C), indicating that the increased GFPdgn protein levels likely result from decreased UPS-mediated degradation. These results reveal that cardiac UPS proteolytic function is severely impaired by CSN8^{CKO}. This impairment does not appear to be intrinsic to the proteasome because the proteasomal chymotrypsin-like and caspase-like activities both in presence or absence of ATP were significantly increased in the CSN8^{CKO} mice compared with the CTL (Figure 2D).

Accumulation of autophagosomes in CSN8^{CKO} hearts

Targeted protein degradation in the cell is carried out mainly by the UPS and the autophagic-lysosomal pathway. Proteasome functional insufficiency (PFI) can activate autophagy in cardiomyocytes;[5, 28] but chronic inhibition of autophagy has been shown to hinder the degradation of UPS substrates.[29] Since we have observed severe impairment in UPS-mediated protein degradation in CSN8^{CKO} hearts, we sought to investigate whether autophagy was altered. The conversion of LC3 from the cytosolic form (LC3-I) to the lipidated form (LC3-II) targets LC3-II to autophagosome membrane during autophagosome formation. Therefore, LC3-II protein levels are extensively used as a marker for autophagic vesicles. We found LC3-II were markedly increased in the CSN8^{CKO} hearts (Figure 3A, 3B), suggesting that Csn8 deficiency increases autophagosomes in adult mouse hearts. This was confirmed using the GFP-LC3 reporter and TEM. We cross-bred the GFP-LC3 tg mice with the CSN8^{CKO} mice. Direct fluorescent confocal microscopy revealed more GFP puncta in LV myocardium from the CSN8^{CKO} mice, compared with the CTL mice (Figure 3C). Quantification showed that GFP-LC3 puncta increased by a factor of >8 in CSN8^{CKO} compared with the littermate GFP-LC3 control mice (Figure 3D). Morphological detection of autophagic vacuoles via TEM remains the gold standard to visualize autophagosomes in the cell. Our TEM analyses further confirmed the markedly increase in autophagic vacuoles, especially the early stage ones (i.e., autophagosomes) in the cardiomyocytes of CSN8^{CKO} hearts (Figure 3E, 3F). These autophagosomes often contain organelles such as degenerative mitochondria.

Diminished autophagy flux in CSN8^{CKO} mouse hearts

The increase in autophagosomes could result from elevated formation or defective removal. Interestingly, the protein levels of p62, an autophagy substrate, were also significantly increased in CSN8^{CKO} hearts. This finding prompted us to test if autophagic flux is compromised. We used intraperitoneal injection of BFA to inhibit lysosomes. As expected, BFA treatment substantially accumulated LC3-II in the CTL mouse hearts. However, the BFA treatment failed to induce a significant increase in LC3-II in the CSN8^{CKO} hearts (Figure 4). These data indicate that the increase of autophagosomes in CSN8^{CKO} hearts is due to decreased lysosomal removal.

Accumulation of abnormal proteins in CSN8^{CKO} hearts

Terminally damaged/misfolded proteins are degraded by the UPS and autophagy. Consistent with PFI and the impaired autophagic-lysosomal pathway, the total ubiquitinated proteins (Figure 5A) in the form of aggregates (Figure 5B) and the level of protein carbonyls, a common feature of oxidized proteins (Figure 5C), were greatly increased in CSN8^{CKO} hearts. These ubiquitin-positive protein aggregates are frequently co-localized with GFP-LC3 puncta and enriched in p62 in CSN8^{CKO} hearts (Supplemental Figure S2).

Massive cardiomyocyte necrosis in CSN8^{CKO} hearts

A hallmark of necrotic cells is the loss of cell membrane integrity.[30] To assess the prevalence of cardiomyocyte necrosis, we first tested the uptake of intraperitoneally injected Evan's blue dye (EBD) by the cardiomyocytes in intact mice. Nearly none of the cardiomyocytes of CTL mice showed EBD uptake but over 10% of cardiomyocytes in the CSN8^{CKO} mice did (Figure 5D, 5E), suggesting that Csn8 deficiency causes cardiomyocytes to die in the necrotic form in adult mice. Consistently, TEM also revealed evidence of necrotic cardiomyocytes in the CSN8^{CKO} mice, including markedly cell swollen and mitochondrial swollen, decreased overall electron density, and myofibril fragmentation (Supplemental Figure S3).

CSN8^{CKO} mice developed dilated cardiomyopathy (DCM)

Five days after the first tamoxifen injection, the heart of CSN8^{CKO} mice appeared to be enlarged, compared to the CTL (Supplemental Figure S4A). Gravimetric analyses showed that CSN8^{CKO} mice had modest but statistically significant increases in the heart weight to body weight ratio, the ventricle weight to body weight ratio, and the lung weight to body weight ratio (Figure 6A) but not the kidney weight to body weight ratio (data not shown), compared with the CTL mice. The cross-sectional area of LV cardiomyocytes increased by 30%, compared with the CTL mice (Supplemental Figure S4B, S4C). A hallmark of cardiac hypertrophy/pathology is re-activation of the fetal gene program. The steady state transcript levels of atrial natriuretic factor (ANF) and skeletal α-actin in CSN8^{CKO} hearts were up-regulated by a factor of 8 and 9, respectively, whereas the SERCA2a mRNA levels were down-regulated by a factor of 4 (Figure 6B). These results show that *Csn8* ablation in adult cardiomyocytes triggers hypertrophic responses.

Morphometric and cardiac functional assessments further revealed that Csn8 deficiency initiated in adult hearts caused DCM. Echocardiography at 5 days after the first tamoxifen injection revealed significant increases in the LV end-diastolic dimension and end-systolic dimension and significant decreases in the posterior wall thickness at the end of diastole and LV fractional shortening in CSN8^{CKO} mice (Figure7A, Supplemental Figure S5). Hemodynamic analysis via monitoring LV pressure (Figure 7B) revealed a marked reduction of LV systolic pressure and the maximum dP/dt in CSN8^{CKO} mice, indicative of reduced cardiac contractility. The accompanying marked increase of LV end diastolic pressure and a significant reduction of the minimum dP/dt in CSN8^{CKO} hearts indicate that LV relaxation is also impaired. Taken together, these findings demonstrate that loss of CSN8 in the cardiomyocytes of adult mice causes rapidly severe congestive heart failure.

Discussion

The physiological significance of CSN has not been demonstrated in a post-mitotic organ of intact adult vertebral animals. Here we have shown that CSN8 deficiency initiated in adult mouse hearts caused severe duo-impairment of both the UPS and autophagy, resulted in cardiomyocyte necrosis, and led to rapid left heart failure. Along with the similar findings from perinatal mice,[18, 31] it is now comprehensively demonstrated that CSN8/CSN regulates

protein degradation by not only the UPS but also lysosomes in the heart during both the early development and adulthood. Moreover, we show here for the first time in intact animals that CSN8/CSN may modulate the redox state in the heart.

CSN8 is required for CSN-mediated deneddylation of a variety of substrates

Using the same *Csn8* floxed allele but temporally less controllable conditional gene targeting, we and others have previously showed that CSN-mediated cullin deneddylation in mouse hepatocytes, neonatal cardiomyocytes, and T cells was compromised by CSN8 deficiency.[17, 18, 32] In those previous studies, the accompanied down-regulation of other CSN subunits, such as CSN5 which harbors the deneddylase, could not be dissociated from the impaired deneddylation. Because the strategy used for the inducible *Csn8* targeting in the present study allows the timing of gene ablation to be controlled and pinpointed, we were able to observe severe impairment of CSN deneddylation in CSN8 ablated hearts before reduction of other key CSN subunits becomes evident, providing compelling evidence that CSN8 is required for CSN5-mediated deneddylation. Cullins are the first and best studied proteins that undergo neddylation but the list of the latter is growing.[27, 33] It is unknown whether CSN plays a role in the deneddylation of proteins other than cullins. Besides neddylated cullins, a large number of neddylated proteins of unknown idetities were also accumulated in $CSN8^{CKO}$ hearts. This is in agreement with our recent findings in postnatal CSN8-deficient heart.[18] Taken together, it is now strongly demonstrated that CSN-mediated deneddylation in the heart has an array of substrates besides neddylated cullins. It will be interesting to identify these non-cullin substrates using the CSN8 deficient hearts.

CSN8/CSN is central to protein degradation and quality control in cardiomyocytes

CSN has long been purported as a regulator of UPS-mediated proteolysis, by controlling the catalytic dynamics of CRLs,[34] serving as an alternate lid of the 19S proteasome,[35] or stabilizing the ubiquitin conjugation enzyme.[36] Our previous study showed impaired UPS function in postnatal CSN8-deficient hearts,[18] which may be caused by uncoupling of ubiquitination from proteasome-mediated degradation.[31] Consistent with this notion, we observed that loss of CSN8 in adult hearts rapidly accumulated the proteasome surrogate substrate GFPdgn but proteasomal peptidase activities were increased. Taken together, it is revealed that CSN8 is crucial to the functioning of the UPS in both neonatal and adult cardiomyocytes. Since DCM occurred immediately following the induction of $CSN8^{CKO}$ and cardiomyopathy can result in cardiac PFI,[1, 5] it cannot be ruled out that the concomitant DCM may contribute to the UPS malfunction.

Another exciting contribution of the current study is to have confirmed an important role of CSN8/CSN in the autophagic-lysosomal pathway that was initially revealed by our studies on the perinatal *Csn8* knockout.[18] Here we found the co-existence of increased autophagosomes with decreased autophagic flux in the adult mouse hearts with *Csn8* ablated in cardiomyocytes, confirming that CSN8/CSN is required for autophagosome removal. Impaired autophagosome removal can result from defective fusion between autophagosomes and lysosomes and/or from lysosome malfunction.

UPS-mediated protein degradation is a highly regulated process. Polyubiquitination of target proteins, the delivery of polyubiquitinated proteins to the proteasome, and proteasome activities can all impact on UPS functioning.[37] Given that the proteasome peptidase activities were increased in Csn8 deficient myocardium, the impairment of UPS proteolytic function as evidenced by GFPdgn accumulation is likely caused by defective ubiquitination and/or impaired delivery of ubiquitinated proteins to the proteasome. The latter is consistent with the increases of total ubiquitinated proteins in $Csn8^{CKO}$ hearts. As discussed below, macroautophagy is impaired and p62 increased in $Csn8^{CKO}$ hearts, which may impair

delivery of ubiquitinated proteins to the proteasome. Chronic inhibition of macroautophagy was shown to accumulate p62 which in turn binds ubiquitinated proteins and hinders their degradation by the proteasome.[29]

Selective autophagy contributes to quality control in the cell by targeted removal of defective organelles and protein aggregates. p62 is involved in the recruitment of autophagosome to misfolded proteins.[8] Consistent with PFI and inadequate PQC, both ubiquitinated proteins and oxidized proteins were markedly increased in CSN8^{CKO} hearts. The accumulation of ubiquitinated proteins in the form of aggregates and the co-localization of p62 and GFP-LC3 with the aggregates suggest that defective removal of autophagosomes at least contributes to, if is not the primary cause of, PQC inadequacy in CSN8^{CKO} hearts.

The increased level of protein carbonyls in CSN8^{CKO} hearts suggests that CSN8/CSN may regulate the redox state via supporting the removal of oxidized proteins and/or suppressing oxidative modifications. Indeed, a recent study on the transcriptome, proteome, and metabolome of the filamentous fungus Aspergillus nidulans with CSN5 gene deletion has revealed a critical role of CSN in mediating transcriptional and metabolic responses to oxidative stress.[38] Hence, the current study presents the first evidence that CSN8/CSN may regulate the redox state in vertebral animals.

CSN8 deficiency causes cardiomyocyte necrosis and DCM

We have previously reported that CSN8 deficiency causes primarily apoptosis in hepatocytes but predominantly necrosis in neonatal cardiomyocytes.[9, 18, 32] Here we observed massive cardiomyocyte necrosis in adult mice with CSN8^{CKO}. These results suggest that CSN8/CSN is essential for cardiomyocyte survival but the type of cell death caused by CSN8 deficiency is tissue/organ-specific. Similarly to *Csn8* knockout initiated at the perinatal stage,[18] cardiomyocyte-restricted *Csn8* ablation initiated in adult mice causes cardiac structural and functional changes that are characteristic of DCM. Interestingly, it takes a shorter time for cardiac *Csn8* ablation to cause DCM in adults than in neonates. This is strikingly reminiscent of the cardiac ablation of *Atg5*,[39] a protein required for autophagy, implicating that impairment of autophagy might be primarily responsible for the DCM in CSN8 deficient hearts. Massive cardiomyocyte necrosis is associated with, and likely an underlying cause of, the DCM in both perinatal and adult CSN8 deficient hearts. Indeed, inhibition of autophagosome removal is sufficient to cause cardiomyocyte necrosis in adult mice.[9] Moreover, accumulation of autophagic vacuoles was also observed in necrotic cardiomyocytes in diseased human and mouse hearts,[40, 41] raising an interesting possibility that impaired autophagosome removal may be a cause of cardiomyocyte necrosis in a diseased heart. It will be important to test this possibility and to investigate how impaired autophagosome removal causes necrotic cell death.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgments

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Clinical Summary

Targeted removal of terminally misfolded/damaged proteins by the ubiquitin proteasome system (UPS) and the autophagic-lysosomal pathways represents the last line of defense in protein quality control. UPS and autophagy dysfunctions are implicated in cardiac pathogenesis. However, the regulation of the UPS and autophagy is poorly understood. The attachment of a ubiquitin-like protein NEDD8 to cullin via a process known as neddylation activates cullin-based RING ligases (CRLs), a large family of ubiquitin ligases. The proper functioning of CRLs also requires cullin deneddylation catalyzed by the COP9 signalosome (CSN), a protein complex formed by eight unique proteins (CSN1 through CSN8). Hence, CSN may regulate cardiac UPS. By conditional gene targeting, we previously discovered that CSN8/CSN regulates both cardiac UPS and autophagy and is essential to cardiomyocyte survival at the perinatal stage when cardiomyocyte proliferation contributes actively to cardiac development. Here we report that CSN8/CSN also plays indispensable roles in adult hearts. Similarly to perinatal csn8 knockout, cardiac ablation of the *csn8* gene initiated in adult mice impairs both UPS proteolytic function and autophagosome removal, leading to massive cardiomyocyte necrosis and progressive dilated cardiomyopathy and heart failure. This has immediate clinical relevance because neddylation inhibition via NEDD8 activating enzyme (NAE) inhibitors (e.g., MLN4924) is in clinical trial to treat cancer and CSN inhibition is also being tested in the laboratory as a new therapeutic strategy. Similar to CSN8 deficiency, both NAE and CSN inhibitors effect to inhibit CRLs. Our findings caution that the use of these inhibitors may damage the heart.

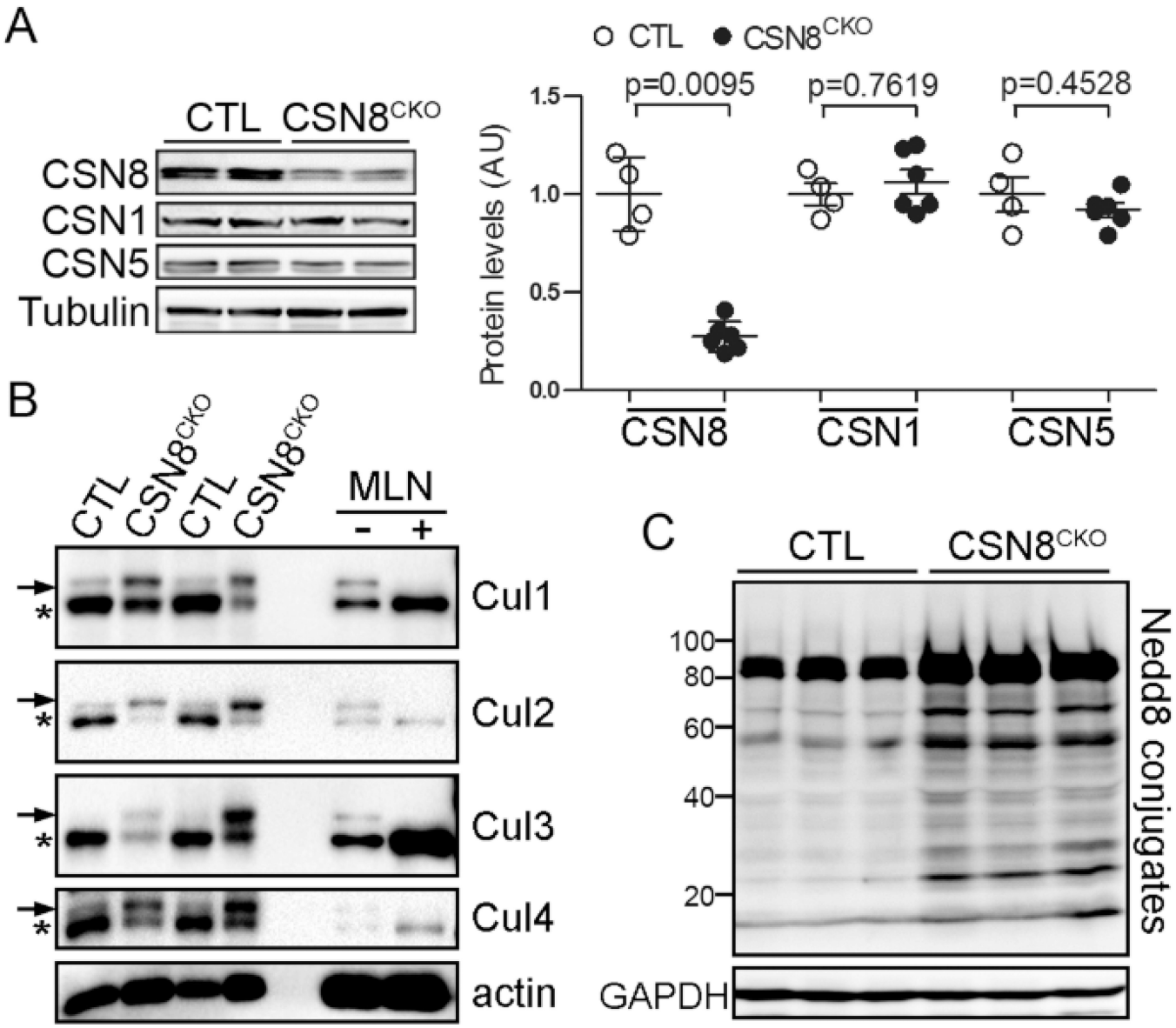

Figure 1. Cardiomyocyte-restricted *Csn8* knockout initiated in adult mice impairs deneddylation activities in the heart

At 5 days after the first tamoxifen injection, ventricular myocardium was sampled from $Csn8^{flox/flox}$ (CTL) or $Csn8^{flox/flox}$::$MerCreMer^{tg}$ ($CSN8^{CKO}$) littermate mice for western blot analyses. Representative images are shown with each lane representing a mouse. α-Tubulin or GAPDH was probed for loading control. (**A**) Changes in CSN8, CSN1 and CSN5. AU: arbitrary unit. (**B**) Increases in the neddylated form (arrow) and decreases in the native form (*) of cullin1 (Cul1), Cul 2, Cul3, and Cul4A in $CSN8^{CKO}$ hearts. To verify the identity of the neddylated cullins, cultured neonatal rat cardiomyocytes were treated with a specific NEDD8 E1 inhibitor MLN4924 (MLN, 1μM) (Active Biochem, Maplewood, NJ) or vehicle (−) for 24 hours. MLN4924, which inhibits neddylation, abolished the slow-migrating band of all cullins, confirming their identity as neddylated cullins. (**C**) Increased Nedd8 conjugates in $CSN8^{CKO}$ hearts.

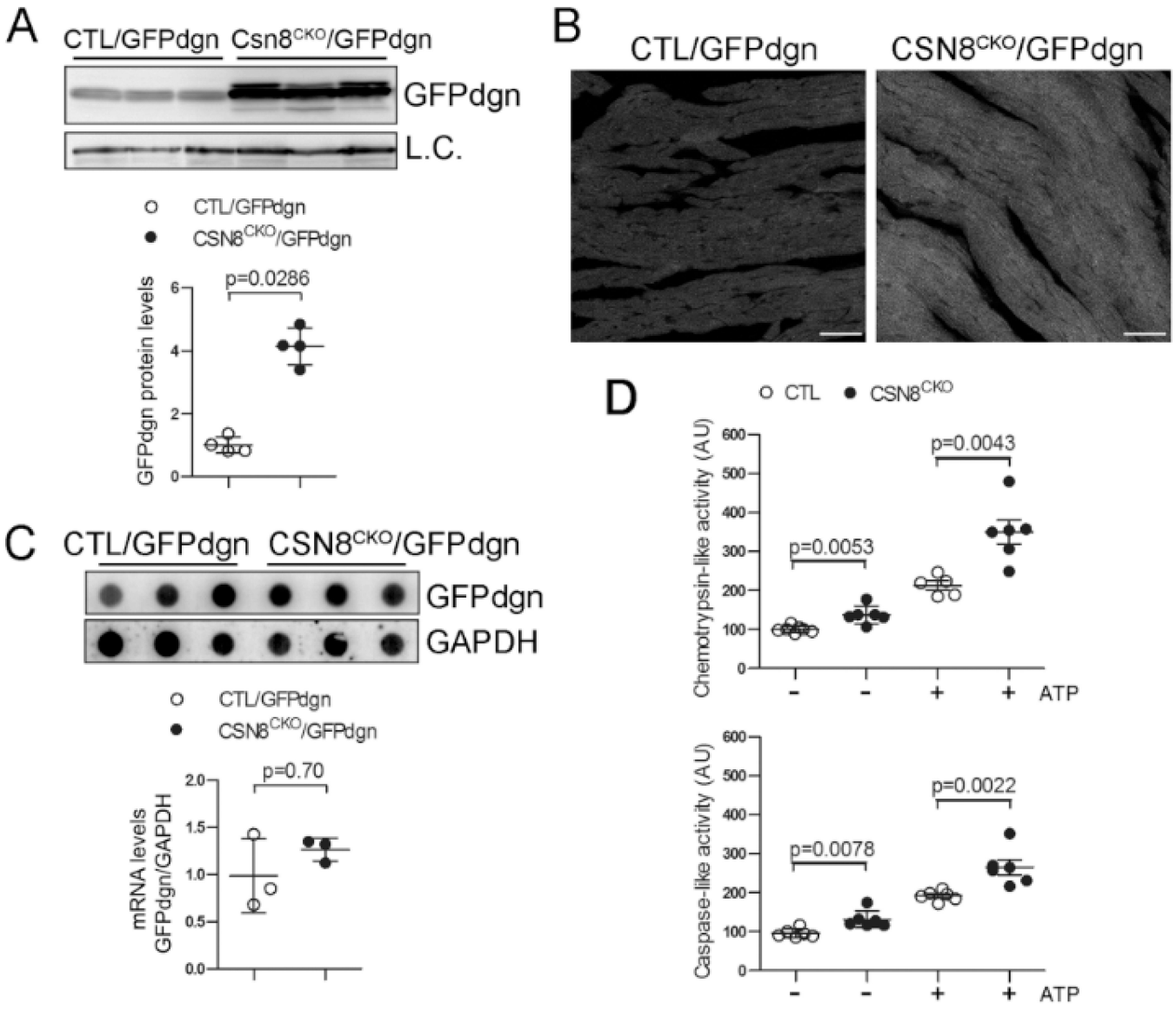

Figure 2. Proteasome functional insufficiency in CSN8^{CKO} hearts

(A~C) CSN8^{CKO} hearts accumulate GFPdgn, a surrogate substrate of the UPS. GFPdgn was introduced into the CTL and CSN8^{CKO} mice via cross-breeding. At 3 days after the first injection of tamoxifen, ventricular myocardium of littermate mice was collected for western blot analyses (**A**) and immunofluorescence/confocal microscopy (**B**) for GFPdgn or RNA dot blot analyses (**C**). L.C., loading control; Scale bar = 40μm. (**D**) Proteasomal peptidase activity assays of ventricular myocardium at 3 days after the first tamoxifen injection, in the presence (+) or absence (−) of ATP.

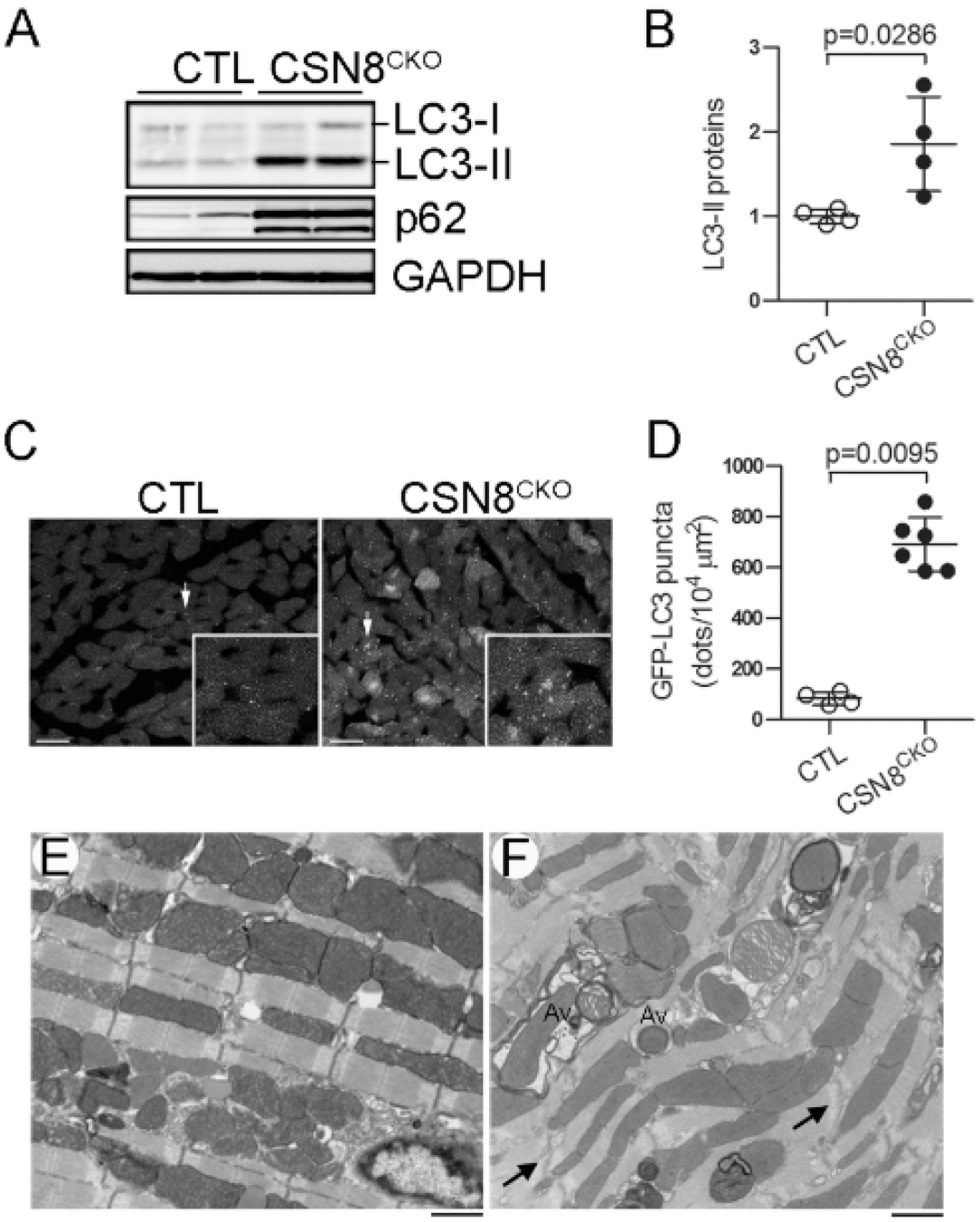

Figure 3. Marked increases of autophagic vacuoles in CSN8^{CKO} hearts

(**A, B**) Representative images of western blot analyses of LC3 and p62 (**A**) and a summary of LC3-II densitometry data (**B**) in CTL and CSN8^{CKO} hearts at 5 days after the first tamoxifen injection. (**C, D**) Probing autophagy in CSN8^{CKO} hearts using GFP-LC3. GFP-LC3 was introduced into the CTL and CSN8^{CKO} mice via cross-breeding. Perfusion-fixed ventricular myocardium from CTL::GFP-LC3 mice and CSN8KO::GFP-LC3 littermate mice at 5 days after the first injection of tamoxifen was subjected to GFP-LC3 direct fluorescence confocal microscopy. Images from a 2.1 μm-thick slide of tissue were projected (**C**, representative images) and analyzed for the GFP-LC3 puncta density (**D**). The

inset in panel C shows the area indicated by the arrow in a higher magnification. Bar=10 μm. (**E, F**) Electron micrographs of myocardium from CTL (**E**) and $CSN8^{CKO}$ (**F**) hearts. Abundant autophagosomes (Av) containing degenerating mitochondria and/or other cytoplasmic contents are evident in $CSN8^{CKO}$ hearts.

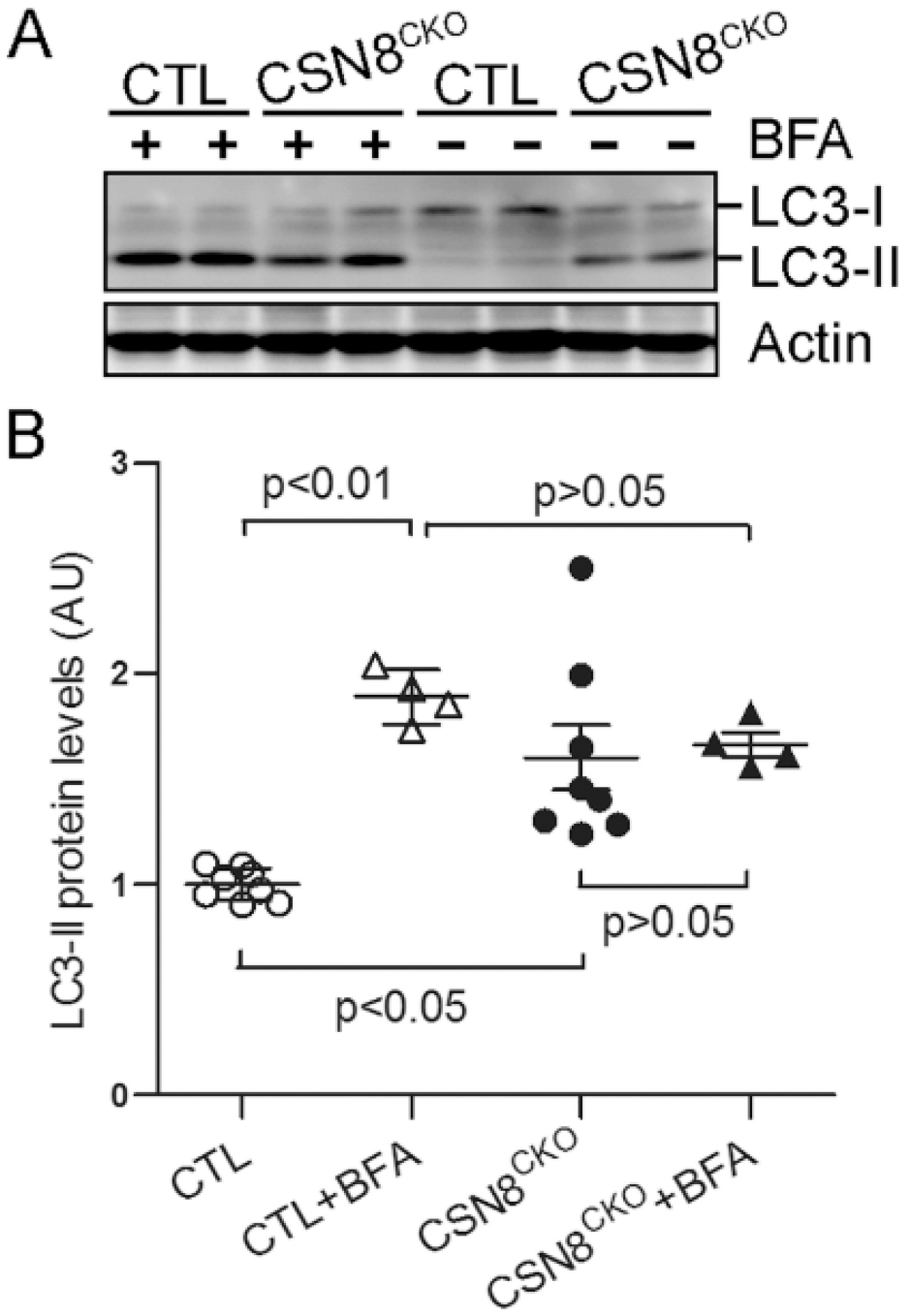

Figure 4. Impaired autophagic flux in CSN8^{CKO} hearts

Three days after the first tamoxifen injection, CTL and CSN8^{CKO} littermate mice were treated with two doses of BFA (3μmol/kg, i.p.) or vehicles with 1 hour in between, and sacrificed 2 hour after the first dose. LC3-II protein levels in ventricular myocardium were quantified using western blot analysis. Representative western blot images (**A**) and densitometric quantification (**B**) of LC3 proteins are presented.

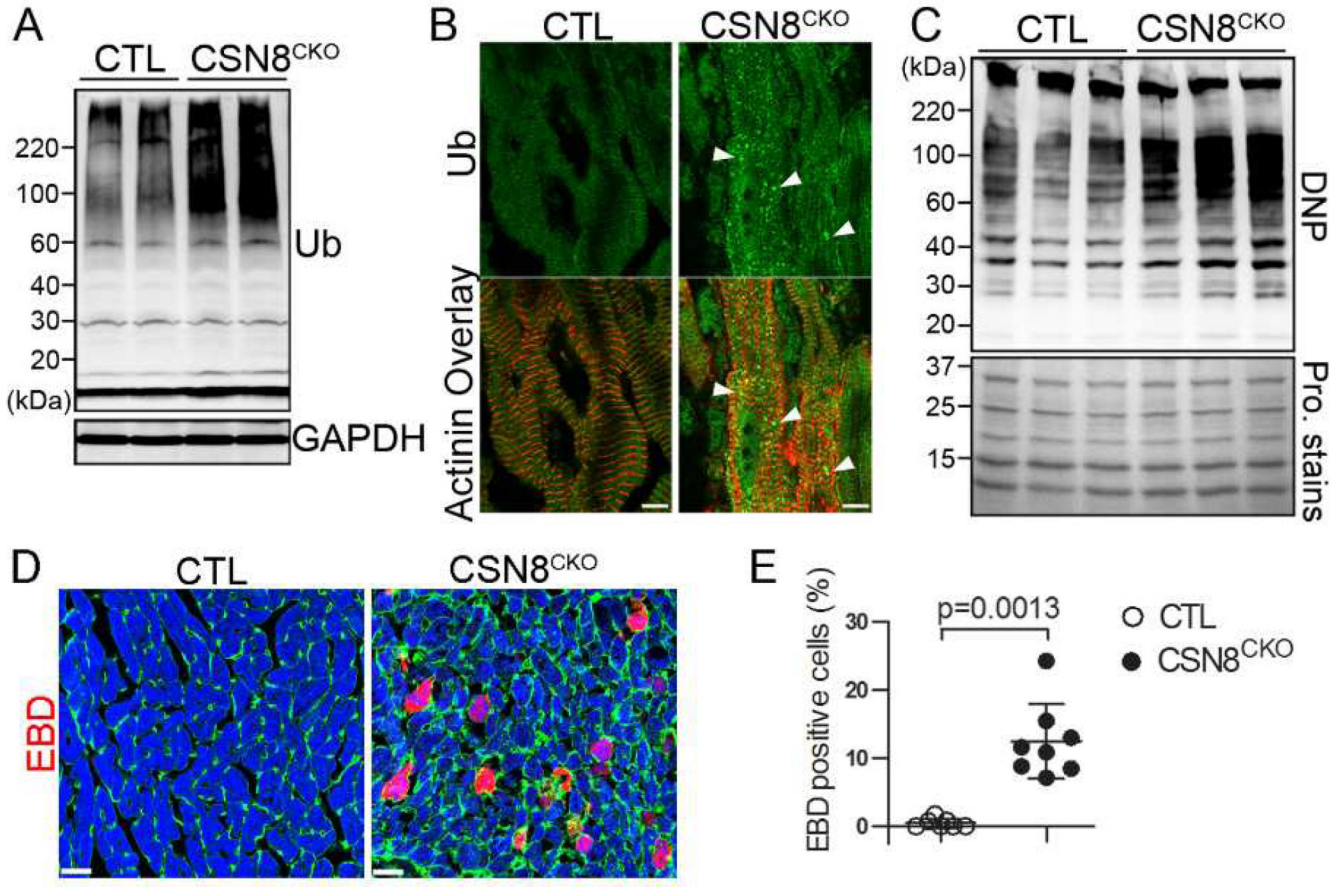

Figure 5. CSN8 deficiency in adult hearts accumulates abnormal proteins and increases cardiomyocyte necrosis

Ventricular myocardium from CTL and CSN8^{CKO} littermate mice at 5 days after the first tamoxifen injection were used for the following analyses. (**A**) Western blot analysis of myocardial total ubiquitinated proteins (Ub). (**B**) Immunofluorescence analysis of the subcellular localization of Ub (green) in cardiomyocytes. Sarcomeric α-actinin was counter-immunostained (red) to identify cardiomyocytes. Note increased ubiquitin-positive aggregates (arrowheads) in CSN8^{CKO} cardiomyocytes. (**C**) Western blot analysis of DNP-derivatized protein carbonyls. The carbonyls of oxidized proteins in the total myocardial protein extracts were first derivatized by DNP and then detected by immunoblot for DNP. The representative image is shown as the upper panel. Before the immunoblotting, the proteins on the same membrane were visualized by MemCode protein (Pro.) stains (Pierce) (bottom panel). (**D, E**) Increased Evans Blue Dye (EBD, red) incorporation into the cardiomyocytes of CSN8^{CKO} hearts. Perfusion-fixed ventricular myocardium was collected 18 hours after an intraperitoneal injection of EBD (100 mg/kg) and processed for cryosections. FITC-conjugated wheat germ agglutinin and rhodamine-conjugated phalloidin were used to stain cell membrane (green) and myofibrils (blue), respectively. The percentage of EBD positive cardiomyocytes in 2 or 3 random fields per heart and 3 hearts per group was measured and presented in panel **E**.

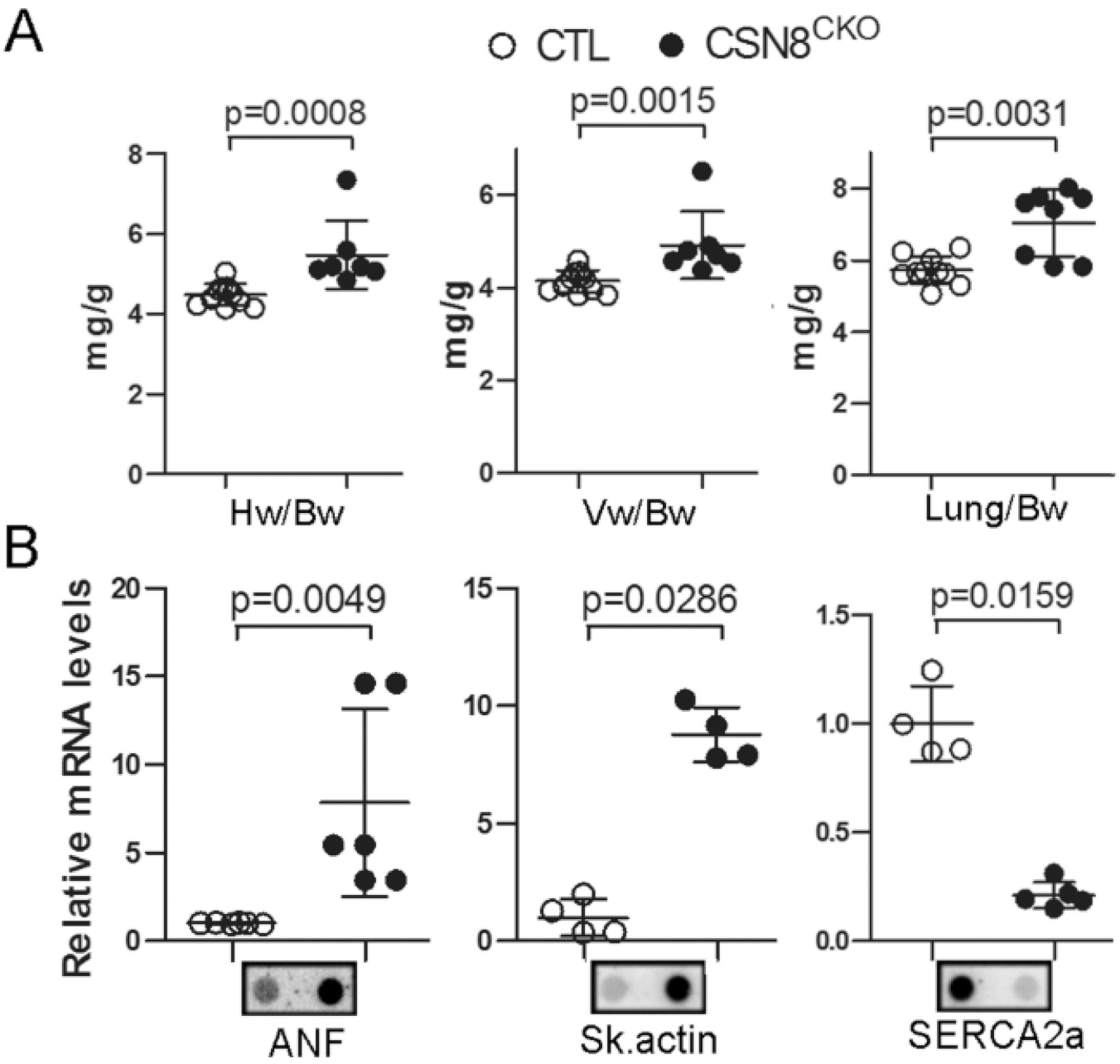

Figure 6. Gravimetric and cardiac fetal gene expression changes in CSN8^{CKO} mice

CTL and CSN8^{CKO} mice were used 5 days after the first injection of tamoxifen. (**A**) Gravimetric measurements. (**B**) Changes in the transcript levels of atrial natriuretic factor (ANF), skeletal (Sk.) α-actin, and sarcoplasmic reticulum calcium ATPase 2a (SERCA2a) in ventricular myocardium. RNA dot blot analyses were performed using radioactively labeled transcript-specific oligonucleotide probes.

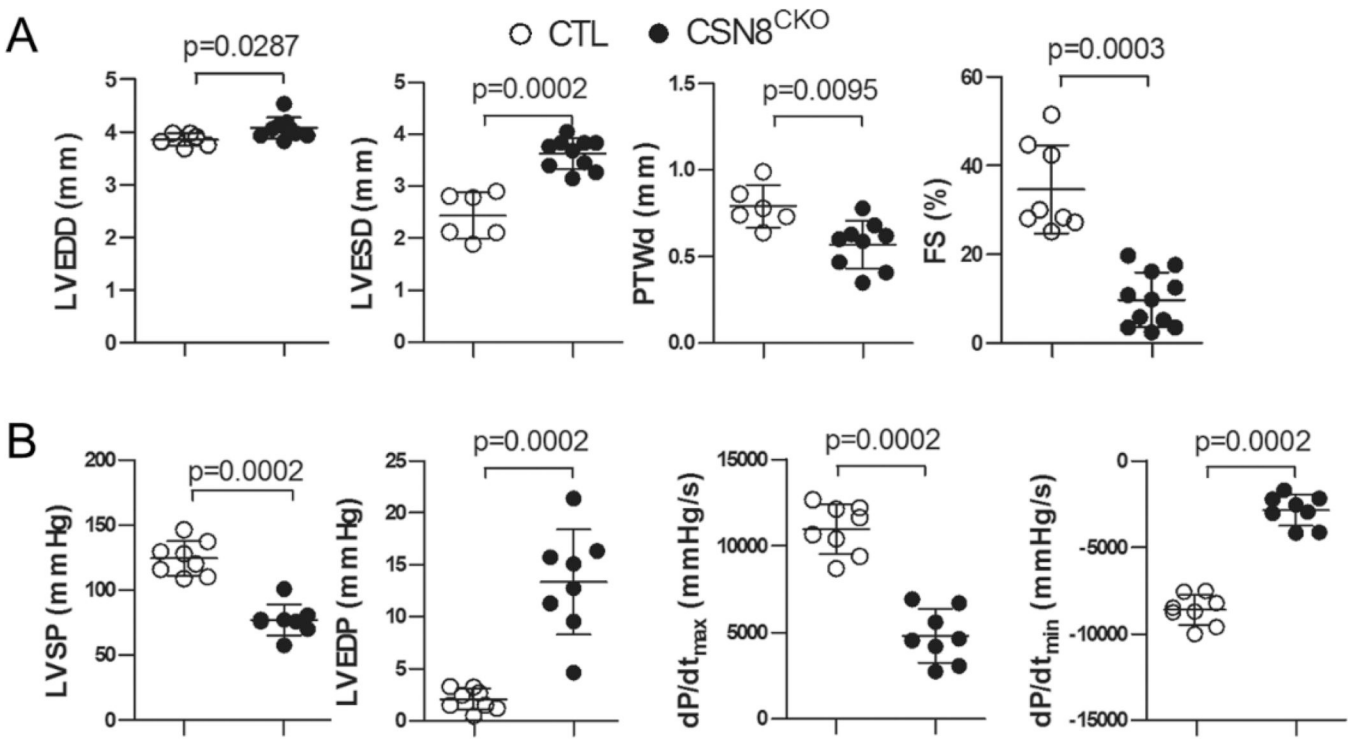

Figure 7. Changes in left ventricle (LV) geometry and function in CSN8^{CKO} mice

CTL and CSN8^{CKO} mice were used 5 days after the first injection of tamoxifen. (**A**) Echocardiographic assessments. LV end-diastolic dimension (LVEDD), end-systolic dimension (LVESD), posterior wall thickness in diastole (PWTd), and fraction shortening (FS) were determined using transthoracic M-mode echocardiography. (**B**) Hemodynamic assessments. LV systolic pressure (LVSP), LV end diastolic pressure (LVEDP), the maximum first derivative of LV pressure (dP/dt_{max}) and the minimum first derivative of LV pressure (dP/dt_{min}) were measured by LV catheterization via carotid artery.