3. 治療法開発に向けて

他の遺伝性疾患同様に，AVMも現在のところ完全な治療法は確立されていない。しかしながら，酸マルターゼ欠損症およびDMRVに対して，今後の展開が期待される治療法が開発されつつある。

酸マルターゼ欠損症に対しては，アメリカのGenzyme社が開発した組み換え型ヒトα-グルコシダーゼによる酵素補充療法剤による治療がおこなわれており，乳児型では明らかな効果が得られている。しかしながら，問題点として，効果が長続きせず，2週間に1回の点滴静注が必要となることがあげられている。

また，我々の研究室では，DMRVのモデルマウスを世界で初めて作成し，そのマウスを用いた研究から，原因遺伝子*GNE*によりコードされる酵素の最終代謝産物であるシアル酸，シアリル乳糖または生合成中間体であるN-アセチルマンノサミンを投与することにより，病態の進行をほぼ完全に抑制することが可能であることを明らかにし，DMRVの治療に向け大きな1歩を進めることに成功した。

おわりに

筋細胞におけるオートファジーの研究は，AVM患者数の問題などからもいまだ十分になされているとは言い難い。しかしながら我々や他の研究者たちの成果により確実にその役割・重要性が明らかになりつつある。オートファジーの異常をしめす筋疾患は，オートファジー/リソソーム系の異常によるものと，オートファジーそのものの異常ではなく，2次的にオートファジーの機能が惹起されているものがあり，前者ではAVSF，後者では縁取り空胞が特徴的な病理症状としてあげられる。現在のところ，酸マルターゼ欠損症・DMRVに対しては，我々や他の研究者により治療の可能性が示されているものの，他のAVMに対する効果的な治療法は開発されておらず，今後のより詳細な病態解明および，それに基づいた治療法の開発が期待される。また，AVMにおける自己貪食空胞の蓄積メカニズムは十分に解明されたとは言いがたく，その詳細を解明することは，正常組織でのオートファジーの役割を理解する上で重要であると考えられる。

Cell

Resource

A Global In Vivo *Drosophila* RNAi Screen Identifies *NOT3* as a Conserved Regulator of Heart Function

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SUMMARY

Heart diseases are the most common causes of morbidity and death in humans. Using cardiac-specific RNAi-silencing in *Drosophila*, we knocked down 7061 evolutionarily conserved genes under conditions of stress. We present a first global roadmap of pathways potentially playing conserved roles in the cardiovascular system. One critical pathway identified was the CCR4-Not complex implicated in transcriptional and posttranscriptional regulatory mechanisms. Silencing of CCR4-Not components in adult *Drosophila* resulted in myofibrillar disarray and dilated cardiomyopathy. Heterozygous *not3* knockout mice showed spontaneous impairment of cardiac contractility and increased susceptibility to heart failure. These heart defects were reversed via inhibition of HDACs, suggesting a mechanistic link to epigenetic chromatin remodeling. In humans, we show that a common *NOT3* SNP correlates with altered cardiac QT intervals, a known cause of potentially lethal ventricular tachyarrhythmias. Thus, our functional genome-wide screen in *Drosophila* can identify candidates that directly translate into conserved mammalian genes involved in heart function.

INTRODUCTION

Cardiovascular diseases are the most common cause of death in North America and Europe (Yusuf et al., 2001) killing more than 860,000 people annually in the United States (A.H.A., 2005; Lloyd-Jones et al., 2009). Moreover, 80 million people in the United States are estimated to suffer from cardiovascular diseases (A.H.A., 2005; Lloyd-Jones et al., 2009). Known or associated causes of cardiovascular disease include diabetes mellitus, inflammation, high cholesterol, hypertension, overweight and obesity, physical inactivity, or smoking (A.H.A., 2005; Lloyd-Jones et al., 2009). Although there have been great advances in the understanding of heart failure in recent decades (Mudd and Kass, 2008), there is still a gap in understanding the genetic causes and an unmet need for better therapies. In particular, the complex interplay of lifestyle, genetic susceptibilities,

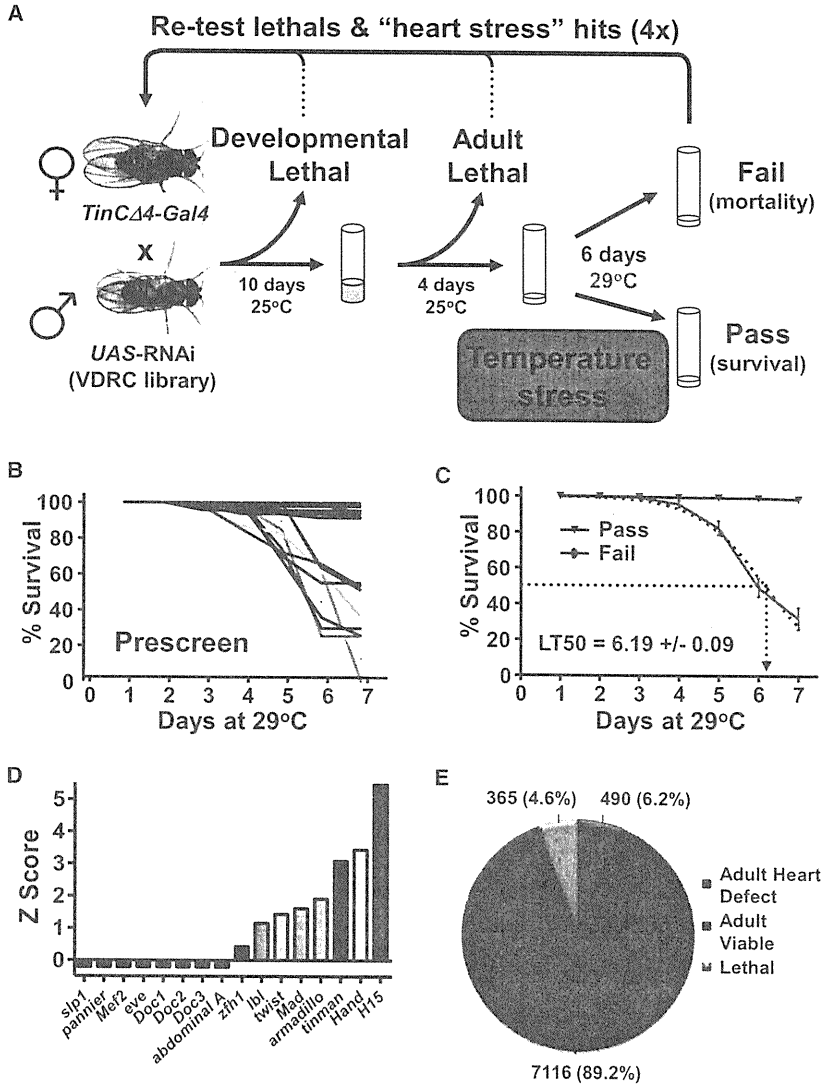

Figure 1. Genome-wide Screen for Conserved Heart Genes

(A) Schematic for screen setup. *TinΔ4-Gal4*, a cardiac tissue specific driver, was used to drive conserved *UAS*-RNAi hairpins in the developing heart. Developmental lethality and baseline adult viability was scored. Viable adult flies were then given a heart stress (continued exposure to 29°C) and survival was scored on day 6. Fly lines showing a potential developmental or heart function phenotype were then retested to confirm the candidate gene.

(B) Eighty randomly selected *UAS*-RNAi lines were crossed to *TinCΔ4-Gal4* and evaluated for adult lethality after an increase in ambient temperature as a cardiac stressor. Lines were either viable (black) or died starting around day 3. Data from individual lines are shown as percent survival on the indicated days.

(C) Mean responses from viable and failing (death after exposure to 29°C) flies revealed an average lethal time at which 50% of failing flies died (LT50) of 6.19 days.

(D) Efficacy of *TinCΔ4-Gal4* x *UAS*-RNAi lines to knock down transcription factors known to play a role in heart formation.

(E) With this system, a genome-wide screen was performed to search for conserved candidate genes for adult heart function under conditions of cardiac stress; 4.6% *TinCΔ4-Gal4* x *UAS*-RNAi lines were developmental lethal. Among the 7971 viable lines, 490 transformant lines exhibited significantly increased death (Z score >3, determined on day 6 after shifting the ambient temperature to 29°C).

See also Figure S1 and Tables S1 and S2.

diseases, and aging have made it difficult to understand the underlying pathogenic principles (Yusuf et al., 2001). In addition to large-scale genetic mapping and phenotyping in humans (Gordon et al., 1977; Morita et al., 2005; Nabel, 2003), a genetic dissection of the cardiovascular system in less complex model organisms would greatly facilitate the understanding of basic controls of cardiac physiology and mechanisms of disease.

Multiple proteins that control contraction in cardiomyocytes are highly conserved between species. For instance, the fly heart is capable of spontaneous rhythmic activity required for the circulation of hemolymph, and the same genes control heart rhythm in humans and flies (Ocorr et al., 2007a). In aging flies, the heartbeat becomes irregular with increased episodes of arrhythmias (Ocorr et al., 2007b), reminiscent of increased atrial fibrillation and heart failure in older humans (Lakatta and Levy, 2003). Moreover, genes involved in specification and differentiation of the heart are also conserved between *Drosophila* and mammals (reviewed in Bodmer, 1995; Cripps and Olson, 2002; Ocorr et al., 2007a). Mutations in subunits of repolarizing voltage gated potassium channels I_{Kr} (*eag, KCNH2*) and I_{Ks} (*kvLQT1, KCNQ1*) perturb heart function in *Drosophila* and in vertebrates can cause long QT syndrome (Ocorr et al., 2007b; Sanguinetti and Tristani-Firouzi, 2006). Moreover, the sarco-endoplasmic reticulum Ca^{2+}-ATPase (*serca2a*, *ATP2A2*) and the Ca^{2+}-channel *Cacophony* control heart function also in *Drosophila* (Ray and Dowse, 2005; Sanyal et al., 2006). Thus, *Drosophila* has become a powerful genetic model system to identify conserved genes involved in heart function.

RESULTS

A *Drosophila* High-Throughput Assay to Identify Candidate Heart Genes

To identify candidate genes for heart development and heart function (Figure 1A), we used cardiac tissue-specific RNA interference (RNAi) silencing of all genes that we identified as showing possible conservation between mammalian species and *Drosophila melanogaster* (Table S1, part A, available online).

TinCΔ4-Gal4 specifically drives expression in cardioblasts (Lo and Frasch, 2001) and has been previously used to study genes involved in heart function of the adult fly (Qian et al., 2008). Because RNAi-mediated downregulation of gene expression in many cases permits the circumvention of lethality commonly associated with classical mutations (Dietzl et al., 2007), cardiac tissue-specific *TinCΔ4-Gal4* RNAi-mediated gene silencing therefore allowed us to assay the functional roles of the respective target genes in adult flies. Since elevated ambient temperature results in an increase in *Drosophila* heart rate (Paternostro et al., 2001; Ray and Dowse, 2005), we combined cardiac tissue-specific RNAi knockdown with an increased ambient temperature to reveal cardiac phenotypes under conditions of stress. Elevated temperature also enhances the activity of the UAS/GAL4 system, without affecting survival within the timeframe of the experiment (Figure S1A).

To evaluate the efficacy of this experimental setup (Figure 1A), we performed a prescreen with 80 randomly selected genes that were targeted by *TinCΔ4-Gal4* RNAi (Table S1, part B). Whereas ~10% of these *TinCΔ4-Gal4* RNAi lines started to die at the increased ambient temperature, the vast majority survived for more than 7 days (Figure 1B). From these pilot experiments, we calculated an average time of 6.19 days at which 50% of flies among the susceptible lines had died (lethal time 50 [LT50]) (Figure 1C). Thus, our large-scale genome-wide screen was carried out at 29°C and lethality was recorded for each line at day 6. As a control, *TinCΔ4-Gal4* RNAi knockdown of known cardiogenic transcription factors resulted in viable lines at 25°C (data not shown), but a shift to 29°C resulted in increased death of nearly half of the transcription factor RNAi lines tested, including *Tinman*, *Hand*, and *H15* (*neuromancer-1/Tbx20*) (Figure 1D). Cardiac knockdown of *pannier/Gata4* and the *Doc* genes (*Tbx5/6*) did not cause premature lethality at 29°C, even though they are known to contribute to adult heart function (Qian and Bodmer, 2009; Qian et al., 2008). As negative controls, we used RNAi lines targeting *eve* and *zfh-1*, which are not expressed in the myocardium targeted by *TinCΔ4-Gal4* (Figure 1D). Thus, we have set up a model system that allows for efficient high-throughput screening and has the capacity to pick up known heart genes.

A Genome-wide In Vivo Fly RNAi Screen for Conserved Genes

In total we screened 8417 transgenic RNAi lines corresponding to 7061 conserved genes for potential developmental and adult heart functional defects (Table S1, part C). We only included 7971 lines representing 6751 genes that fit the previously defined criteria of specificity (Dietzl et al., 2007) for further analyses, i.e., only lines with an S19 score ≥ 0.8 and having six or fewer CAN repeats were considered specific (Table S1, part D). Progeny of each RNAi line crossed to *TinCΔ4-Gal4* were first monitored for viability (reared at 25°C). Among these 7971 RNAi lines, 365 lines resulted in lethality (Figure 1E and Table S1, part E), indicating that many of these genes function in heart development. Developmental lethality was further staged as lethal (embryonic lethal or we never observed any offspring), larval lethal, pupal lethal, or early adult (within 4 days after eclosion) lethal (Table S1, part F).

To identify candidate genes for adult heart function, we assayed 7804 adult *TinCΔ4-Gal4* RNAi progeny (Dietzl et al., 2007) for survival after shifting the flies to 29°C (Figures S1B–S1D). To categorize our hits from the screen, we used the Z score, which is a measure of the distance in standard deviations of a sample from the mean. All RNAi lines with a Z score of 2 in the primary screen were tested on average 4.18 independent times (an average of 90 flies per genotype) using in some cases second RNAi transformants to control for transgenic insertion effects and second independent RNAi hairpins to target a different region of the gene (Table S2). After repeated screening, we identified 498 genes that passed the more stringent Z score of 3 (Figure 1E and Table S2), indicating that these hits exhibit a death score of three standard deviations from the mean. Using gene ontology (GO) annotations, our candidate hits were classified according to their predicted biological processes (BP), molecular functions (MF), and cellular components (CC). Of the classified genes, those involved in signaling, ion transporter activity, metabolism and mitochondrial structure, development and morphogenesis, transcriptional regulation, or nucleic acid binding were highly represented among the entire data set (Figure S2 and Table S4, part A). To remove any artificial bias in the gene list created by the ad hoc Z score cutoff >3, we performed a gene set analysis (GSA) to confirm enrichment of selected GO terms (Table S4, part B). In addition, 121 candidate heart genes had no annotated function by GO. With panther (http://www.pantherdb.org/), we were able to functionally annotate 116 of these genes (Table S4, part C).

Given that the RNAi library screened is known to generate a level of false negative phenotypes because of inefficient targeting of genes to levels required to reveal phenotypes (Dietzl et al., 2007), and based on the assumption that our candidate heart hits perform some of their functions in protein complexes, we next identified first-degree binding partners (Table S4, part D). Using this list of primary heart hits and their binding partners, we performed fly KEGG pathway analyses. Moreover, we included developmental lethal hits to generate a global interaction network. KEGG analyses showed enrichment of multiple pathways, such as mTOR signaling and PI3K/AKT, amino acid metabolism, JAK-STAT signaling, ErbB signaling, the Wnt, Notch, hedgehog, or TGFβ pathways, protein degradation, VEGF signaling, DNA repair, and calcium homeostasis (Table S3 and Table S4, part E). Besides the identification of multiple known genes, our screen has also revealed hundreds of candidate genes and pathways that have not been previously associated with heart function.

A Global View of Heart Function

To extend our *Drosophila* results to mammalian systems, we used the power of data mining and bioinformatics at a global systems level. Potential mouse and human orthologs of our candidate heart screen hits were evaluated for GO enrichment. The GO analyses of the human and mouse orthologs showed marked enrichment of genes involved in PIP3 and calcium signaling, ion transporter activity, metabolism, development, fatty acid metabolism, and muscle contraction (Table S4, part F). We next performed KEGG pathway as well as Broad Institute C2 gene set analysis on the mouse and human orthologs and

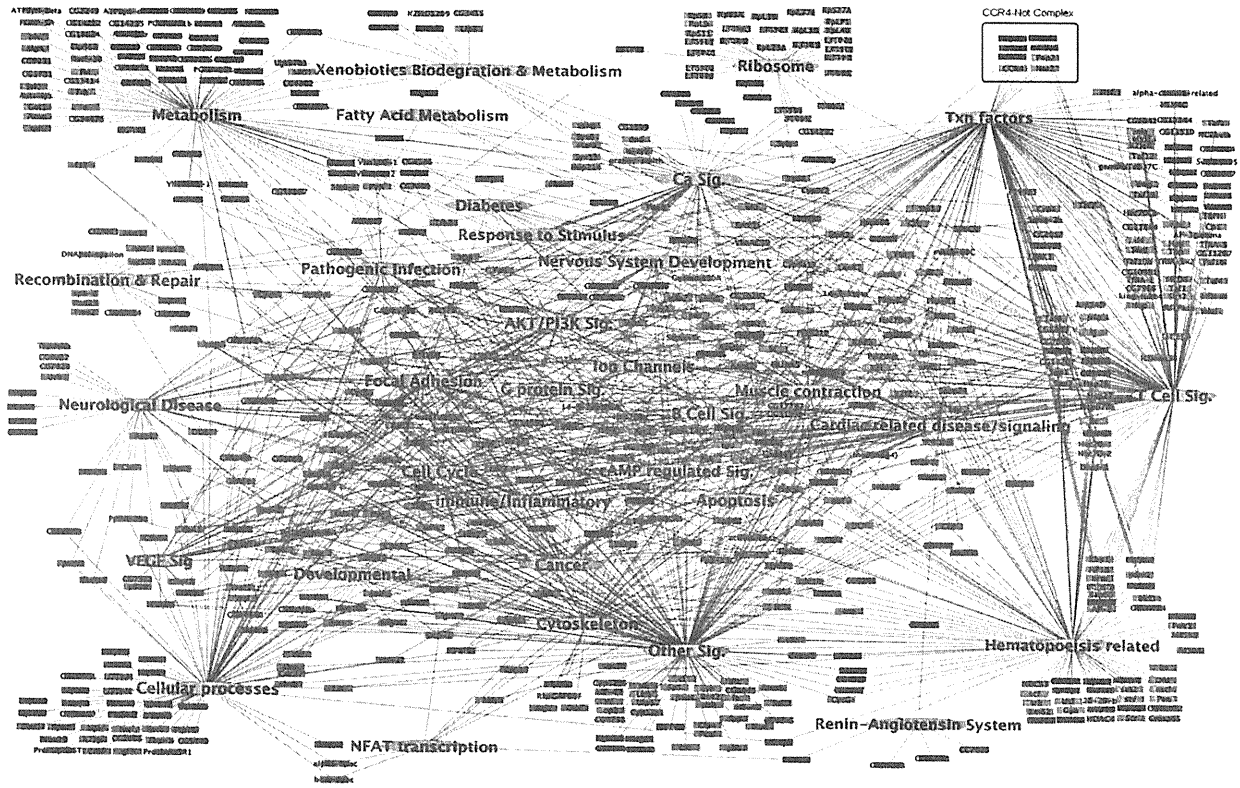

Figure 2. A Global Network of Heart Function

The systems network includes data from the significantly enriched *Drosophila* KEGG and mouse and human KEGG and C2 data sets. Pathways and gene sets from the same biological processes were grouped into common functional categories. Orange nodes represent statistically enriched functional categories of pathways, red nodes represent direct primary fly RNAi hits, green nodes represent their first degree binding partners, and blue nodes indicate genes that were scored as developmentally lethal in our *Drosophila* heart screen. Lines indicate associations of the genes to the appropriate functional category. All KEGG pathways and selected C2 gene sets have been represented in the systems map. See also Tables S3, S4, and S5.

their first-degree binding partners. Based on the mammalian KEGG (Table S4, part E) and C2 (Table S4, part G) analyses, we found significant enrichment for gene sets involved in signaling, metabolism, ion channels, inflammation, aging, and transcription.

To generate a network map that includes our functional data in *Drosophila*, their human and mouse orthologs, and first-degree binding partners, we combined KEGG pathways from *Drosophila*, mouse, and human with relevant gene sets from the Broad Institute C2 annotations (Table S4). A combined systems map and the interactions between the individual genes in the indicated nodes are shown in Figure 2 and Table S4, part H. A systems map using only direct screening hits was also generated, yielding a comparable network map (Table S3). Importantly, by using this network approach, we identified multiple pathways known to play key roles in heart function and cardiovascular disease. For instance, we found significant enrichment in NFAT transcription, AKT activation, and PI3K signaling, calcium signaling and muscle contraction, GPCR- and cAMP signaling, ion channels and proton-transporting ATPase complexes, and transcription. We also found associations with the renin-angiotensin system, a key pathway involved in cardiovascular function in humans (Figure 2 and Table S4, part H). In support of our network approach, advanced data mining revealed that 171 of our primary fly hits and their first-degree binding partners corresponded to mouse knockouts with known cardiovascular phenotypes (Table S5). Thus, our genome-wide screen for candidate heart genes and in silico analyses provides a first attempt at a global roadmap of essential molecular components and key pathways potentially involved in heart function and cardiac failure.

RNAi Silencing of *not3* and *UBC4* Results in Dilated Cardiomyopathy in *Drosophila*

One of the pathways we found in our global network analysis was the CCR4-Not complex (Figure 2 and Table S3). Intriguingly, among the eight members of this complex assayed, we hit the subunits *not1*, *not3* (*not3/5* in fly), *not4*, *UBC4*, and *Hsp83* (Figure 3A). In addition, the subunits *not2* and *CG8759* were "weak" hits (Figure 3A). The CCR4-Not complex was first identified in yeast (Denis, 1984) and is highly conserved in evolution (Albert et al., 2000). Components of the CCR4-Not complex

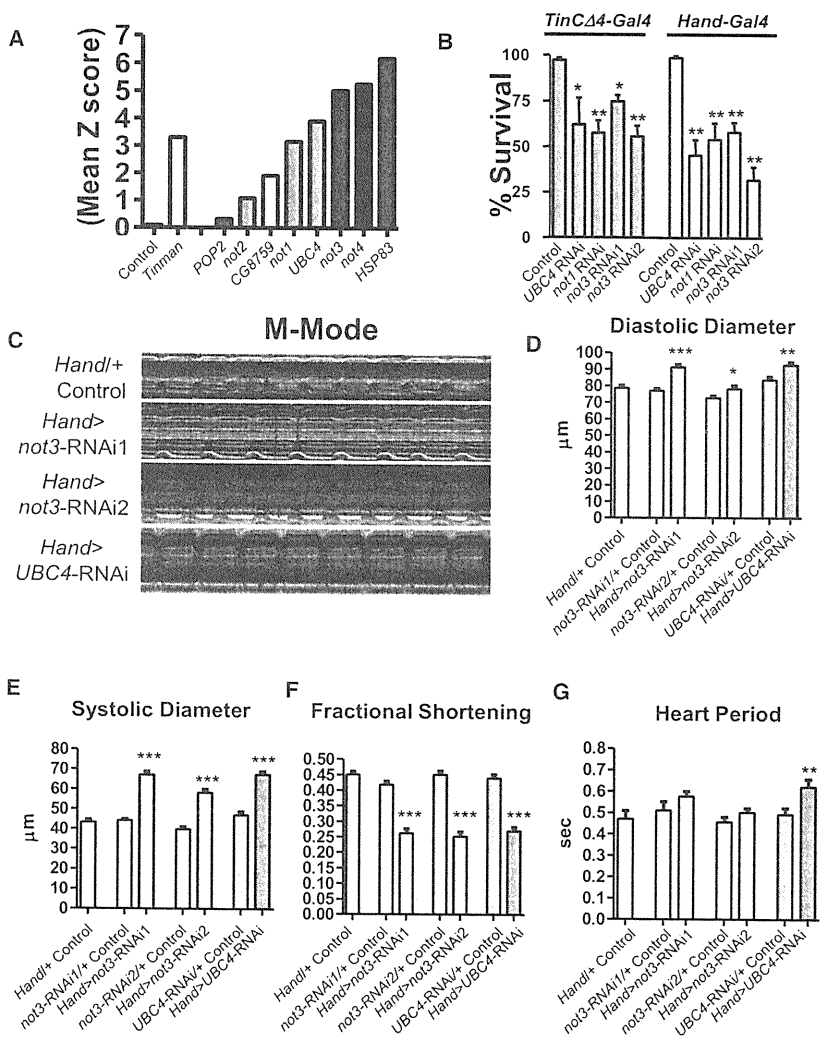

Figure 3. The CCR4-Not Complex Is a Central Regulator of Adult Heart Function, and Loss of not3 Results in Dilated Cardiomyopathy in *Drosophila*

(A) Mean Z scores for *TinCΔ4-Gal4* x *UAS*-RNAi lines targeting the indicated members of the fly CCR4-Not complex. A negative control (w^{1118} [isogenic to the RNAi library] X *TinΔ4-Gal4*) and the positive control *Tinman* RNAi line are shown.

(B) *not1*, *not3*, and *UBC4* are essential for proper adult heart function in both *Tinman*- and *Hand*-expressing cells. Data are shown as mean ± SEM for at least three replicates. RNAi1 and RNAi2 indicate different transgenic hairpins targeting *not3* . *p < 0.05, **p < 0.01 by ANOVA.

(C) One-week-old adult flies with *Hand-Gal4* driving *not3* or *UBC4* cardiac-specific knockdown exhibit impaired heart function. M modes provide traces of the heart contractions to document the movements in a 1 pixel wide region of the heart tube over time. *HandG4/+* control are the progeny of *Hand-Gal4* crossed to w^{1118}. *Hand>Not3* complex flies are the progeny of *Hand-Gal4* crossed to either *UAS-not3*-RNAi (−1 or −2) or to UAS-*UBC4*-RNAi lines. Fly heart analysis was performed with a MatLab-based image analysis program (Fink et al., 2009; Ocorr et al., 2007b). M modes of the RNAi knockdown hearts reveal dilated diastolic and systolic diameters (double-headed red arrows) and reduced shortening properties (difference between diameters) when compared to M modes of control hearts. Each trace represents a 5 s recording.

(D–G) *Not3* or *UBC4* heart-specific knockdown perturbs several indices of cardiac performance. Progeny of *Hand-Gal4* crossed to two different *UAS-not3*-RNAi lines or an *UAS-UBC4*-RNAi line (experimental) and w^{1118} crossed to *UAS*-RNAi or *Hand-Gal4* driver (controls) were used for these experiments as in (C). *not3* and *UBC4* knockdown led to significantly wider diastolic (D) and systolic (E) diameters, and as a result significantly depressed (F) fractional shortening in all experimental lines relative to controls. *not3* knockdown trended toward a slight lengthening in the heart period (time between consecutive diastolic intervals), while *UBC4* knockdown led to a significant increase in heart period (G). Mean values ± SEM are shown for each group (n = 29–40). Unpaired t tests were performed between each *Hand-Gal4>UAS*-RNAi and each corresponding *UAS*-RNAi/+ control (progeny of w^{1118} crossed to *UAS*-RNAi line). Additionally, one-way ANOVAs with Bonferroni multiple comparison tests revealed no significant differences between the *HandG4/+* control and all *UAS*-RNAi/+ control lines, for any cardiac parameter measured.

*p < 0.05, **p < 0.01, ***p < 0.001. See also Figure S3 and Movie S1.

have not yet been associated with cardiovascular function. We therefore retested components of this pathway using *TinCΔ4-Gal4*-driven knockdown in the heart, which confirmed the phenotype (Figure 3B). Moreover, use of a second heart driver, *Hand-Gal4*, which is expressed with high specificity in myocardial and pericardial cells throughout development and in the adult fly heart (Han and Olson, 2005), showed that silencing of *not1*, *not3*, and *UBC4* resulted in early death when adult flies were shifted to 29°C (Figure 3B).

Since *not3* RNAi gave a strong phenotype with two different *UAS*-RNAi lines (Figure 3B), we focused on the CCR4-Not component *not3*. Cardiac-specific knockdown of *not3* with two different RNAi lines (*Hand>not3*-RNAi: progeny from *Hand*-Gal4 crossed to *UAS-not3*-RNAi) significantly increased both diastolic and systolic diameters and resulted in reduced systolic fractional shortening relative to control flies (Figures 3C–3F and Movie S1). Hearts with cardiac *not3* knockdown also showed slight increases in heart periods (Figure 3G); however, this was not statistically significant. Fluorescent microscopy revealed that *not3* RNAi lines exhibit marked myofibrillar disarray, especially in the conical chamber (Figures 4A–4D). Heart-restricted *not3*-RNAi-mediated knockdown was confirmed by qRT-PCR (Figure S3). In addition, we observed transcriptional downregulation of the Sarcoplasmic/endoplasmic reticulum calcium ATPase

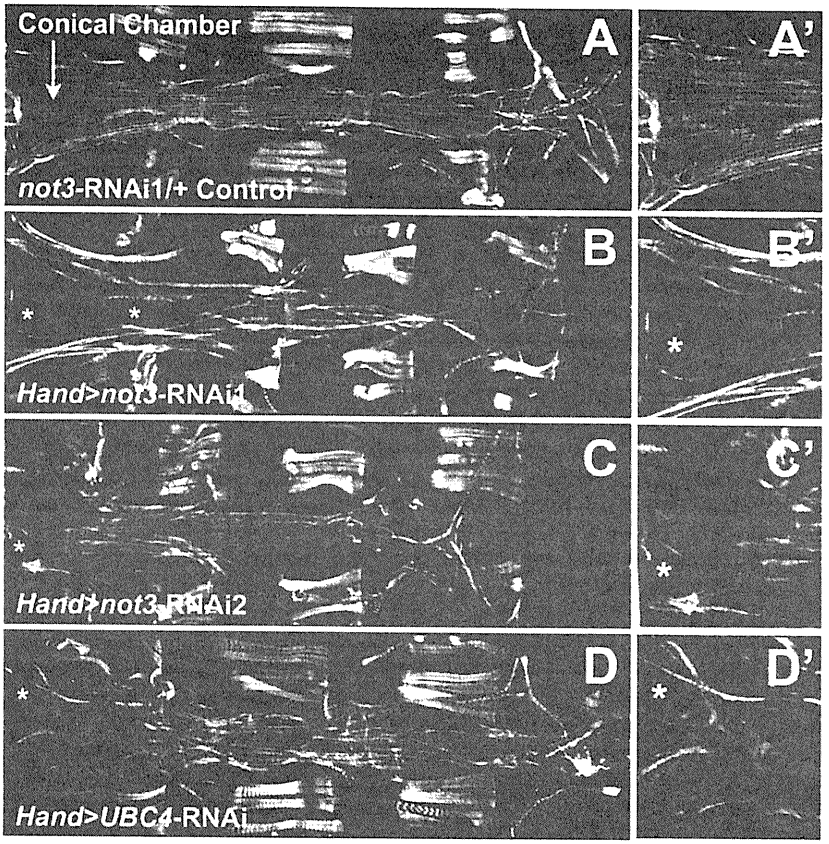

Figure 4. *not3* and *UBC4* Cardiac-Specific RNAi Knockdown Substantially Perturb Myofibrillar Organization and Content

(A) Alexa584-phalloidin staining of control *Drosophila* cardiac tubes reveals typical spiraling myofibrillar arrangements within the cardiomyocytes. The fibers, especially those in the conical chamber, located anteriorly, are densely packed with F-actin.

(B–D) Relative to control hearts, *not3* or *UBC4* RNAi knockdown severely disrupts myofibrillar organization and leads to an apparent loss of myofilaments as noted by large gaps in F-actin staining (*) as well as by a lack of myosin heavy chain transcripts (Figure S3F).

(A'–D') Enlarged images of the conical chambers from (A)–(D), respectively, which illustrate the high degree of myofibrillar disarray and large gaps in F-actin staining within the cardiomyocytes of *not3* and *UBC4* RNAi knockdown hearts. Original images were taken at 10× magnification with a Zeiss Imager Z1 fluorescent microscope.

(*Serca2a*, *ATP2A2*), myosin heavy chain (*mhc*, *MYH7*), and the potassium channel *KCNQ* (*kcnq1*, *KCNQ1*) (Figure S3) involved in heart rhythm control. Cardiac-specific knockdown of *not3* increased the number of flies exhibiting contractile irregularities (Figures S3H and S3I), a finding similar to what is seen in response to cardiac-specific knockdown of the *KCNQ* K^+ channel (Figure S3I) and what has been reported for *KCNQ* mutant flies (Ocorr et al., 2007b). Of note, a *not3 P* element mutant was developmentally lethal, exhibiting a late stage defect in embryonic heart tube organization, which could be rescued by *P* element excision (Figure S3C).

The CCR4-Not complex component *UBC4* was also a major hit identified by our heart screen. Moreover, *UBC4* expression was reduced after *not3* knockdown (Figure S3B). *Hand-Gal4>UAS-UBC4*-RNAi flies also exhibited significantly longer heart periods and showed dramatically altered diastolic and systolic diameters and reduced fractional shortening relative to control hearts (Figures 3C–3G). Fluorescent imaging again revealed severe myofibrillar disarray (Figure 4D) that was strikingly similar to that observed in *not3* knockdown hearts. Further, we observed similar structural and functional phenotypes in *not1* cardiac-specific knockdown flies (A.C., G.N., J.P., and R.B., unpublished data). Thus, knockdown of different components of the CCR4-Not complex result in abnormal heart structure and severely impaired cardiac function indicative of dilated cardiomyopathy.

Functional Assessment of Additional *Drosophila* Heart Hits

To extend our confirmations beyond the CCR4-Not complex, we assayed heart function in adult flies with heart-specific knockdown of four additional candidates identified in our heart screen (Figure S3). One candidate heart gene tested was *CG1216* (*Mrityu*), which encodes a mesoderm-expressed BTB-POZ domain-containing protein (Rusconi and Challa, 2007). Cardiac knockdown of *CG1216* resulted in a significant increase in systolic diameter. Another candidate heart gene, *CG8933* (*extradenticle*), encodes a PBX-family transcription factor. Cardiac knockdown of *CG8933* resulted in increased systolic diameter and reduced fractional shortening. Cardiac knockdown of *CG33261* (*Trithorax-like*) resulted in significantly altered diastolic and systolic diameters as well as impaired fractional shortening. Finally, knockdown of *CG7371*, which encodes a Vps52 domain-containing protein predicted to participate in Golgi trafficking, resulted in a marked increase in heart period and affected the diastolic diameter. These data further demonstrate that our screen indeed has the capacity to identify novel factors involved in and required for normal adult heart function.

Generation of *not3* Knockout Mice

We next tested whether our data on *Drosophila* can be directly translated into a mammalian species. The mouse and human NOT3 proteins (official gene name *Cnot3*) share 60% identity with the *Drosophila not3* ortholog. Expression of human and mouse *not3* messenger RNA (mRNA) transcripts can be found in the majority of tissues analyzed. Although *not3* is evolutionarily conserved from yeast to mammals, essentially nothing is known about the in vivo role of mammalian *not3*. We therefore generated *not3* knockout mice.

We disrupted the *not3* gene in murine embryonic stem cells (ESCs) using a targeting vector in which nucleotides encompassing exons 2 through 9 are deleted (Figure 5A and Figure S4A). Both $not3^{+/-}$ male and $not3^{+/-}$ female mice are viable and exhibit normal fertility. We never obtained viable $not3^{-/-}$ newborn mice, indicating that loss of *not3* results in embryonic lethality. We staged embryonic development but failed to recover *not3* null embryos from placental implantations (Figures S4B and S4C). We therefore assayed early embryogenesis and observed that $not3^{-/-}$ blastocysts can develop. These mutant blastocysts have a normal appearance (Figure S4D), occur at Mendelian frequencies (Figures S4E and S4F), and express key markers of early embryonic differentiation at normal levels (Figure S4G). *not3* mRNA transcripts and NOT3 protein were undetectable in $not3^{-/-}$ blastocysts by RT-PCR and immunostaining (Figures S4F and S4G). In $not3^{+/+}$ and $not3^{-/-}$ epiblast cultures (Figure S4H), trophoblast cells started to spread and supported the outgrowths of the inner cell mass (ICM). While the ICM of $not3^{+/+}$ blastocysts continued to grow, $not3^{-/-}$ ICM cells exhibited a severe outgrowth defect. Thus, complete loss of mouse *not3* results in early embryonic death at the implantation stage.

not3 Haploinsufficiency Results in Impaired Heart Function

We speculated that similar to RNAi-mediated downregulation of *not3* in *Drosophila*, *not3* haploinsufficiency might also reveal a role in mammalian heart function. In *not3* heterozygote mice, *not3* expression is indeed downregulated in the heart (Figure 5B). We failed to observe overt structural changes in the hearts of $not3^{+/-}$ mice. However, both male and female *not3* haploinsufficient mice exhibited a reduction in cardiac contractility as determined by decreased left ventricle fractional shortening and increased left ventricular diameter in systole (Figures 5C and 5D).

To address whether the defects in cardiac function are intrinsic to the heart per se or whether the observed impairment of contractility was secondary because of haploinsufficiency of *not3* in other tissues, we subjected explanted hearts from wild-type and $not3^{+/-}$ littermate mice to Langendorff perfusion, assessing ex vivo heart function (Joza et al., 2005). When isoproterenol was used to activate β-adrenergic receptors, $not3^{+/-}$ hearts exhibited severe contractile abnormalities as defined by impaired generation of left ventricular pressure (LVP) (Figure 5E and Figure S5A). Hemodynamic measurements confirmed that all functional heart parameters such as dP/dT_{max} or dP/dT_{min}, indicative of generated contractile pressure, were markedly reduced in $not3^{+/-}$ hearts (data not shown). Moreover, when explanted hearts were electrically stimulated, $not3^{+/-}$ hearts exhibited a striking defect in contractility (Figure 5F). Thus, downregulation of *not3* expression in *not3* haploinsufficient mice results in an intrinsic impairment in heart function.

Yeast strains mutant for components of the CCR4-Not complex, including *not3*, display reduced acetylation levels of lysine residues on histone tails (e.g., H3K9) (Peng et al., 2008) and/or reduced trimethylation of H3K4 (Laribee et al., 2007). H3K9 acetylation and H3K4 trimethylation are indicative of transcriptionally active states of chromatin. Moreover, promoter regions of NOT3 target genes were shown to recruit trimethylated H3K4 in mouse ESCs (Hu et al., 2009), suggesting that NOT3 may regulate chromatin modifications. Our gene expression and bioinformatic analyses of mouse *not3* knockout cells revealed that histone deacetylases (HDACs) and mRNA metabolisms are localized central in gene networks (K.K., unpublished data). We therefore assessed the state of histone modifications in hearts from $not3^{+/-}$ mice. Histone extracts of whole hearts from *not3* haploinsufficient mice showed a slight but significant reduction in active histone marks such as acetylation of H3K9 and trimethylation of H3K4 (Figures 5G and 5H and Figure S5). H3K27 trimethylation was not changed (Figure 5I and Figure S5). Treatment of $not3^{+/-}$ hearts with the HDAC inhibitor VPA restored the reduced acetylation of H3K9 and H3K4 trimethylation to that of wild-type levels (Figures 5G–5I and Figure S5). Most importantly, administration of HDAC inhibitors rescued the impairment in heart function in $not3^{+/-}$ mice; i.e., ex vivo heart functions of VPA treated mice were similar to control mice in response to both isoproterenol (Figure 5J) and electrical stimulation (Figure 5K). These data were confirmed with TSA, a second HDAC inhibitor (Figures S5H and S5I). Together, these data show that $not3^{+/-}$ mice exhibit a spontaneous and intrinsic defect in cardiac function that can be rescued with HDAC inhibitors.

$not3^{+/-}$ Mice Develop Severe Cardiomyopathy in Response to Cardiac Stress

We next exposed control and $not3^{+/-}$ littermates to chronic pressure overload by surgical constriction of the aorta (transverse aortic constriction, TAC). Three weeks after TAC, heart weight/body weight ratios (HW/BW) increased in both $not3^{+/+}$ and $not3^{+/-}$ mice, although this increase was significantly larger in the $not3^{+/-}$ mice (Figure 6A). Cardiac hypertrophy was also seen by histology (Figure 6D and Figure S6A). Aortic banding of $not3^{+/-}$ mice resulted in severe heart failure characterized by decreased fractional shortening (Figure 6B) and a dilation of the left ventrical as determined by echocardiography (Figure 6C). In addition, $not3^{+/-}$ mice develop severe cardiac fibrosis after TAC, as shown by Masson-trichrome staining of hearts 3 weeks after TAC (Figure 6D and Figure S6B). Thus, $not3^{+/-}$ mice develop severe symptoms of heart failure in response to cardiac stress.

We next assessed whether HDAC inhibitors can also rescue stress-induced heart failure. HDAC inhibitor treatment could indeed block the augmented loss of cardiac function observed in $not3^{+/-}$ mice after TAC (Figures 7A and 7B). In vivo treatment of $not3^{+/-}$ mice with HDAC inhibitors also blocked the exaggerated induction of heart failure markers such as *ANF* (Figure S6C) and *βMyhc* (Figure S6D). Moreover, treatment with an HDAC inhibitor restored the observed histone alterations in $not3^{+/-}$ mice to that of wild-type littermates (Figure 7C and Figures S6E and S6F). Thus, *not3* haploinsufficiency results in exaggerated heart failure that can be rescued by HDAC inhibition in vivo.

A Common Genomic Variant in the *NOT3* Promoter Correlates with Cardiac Repolarization Duration in Humans

Using an in silico search to identify NOT3 target genes, we found that NOT3 has been shown to bind to the *Kcnq1* promoter in

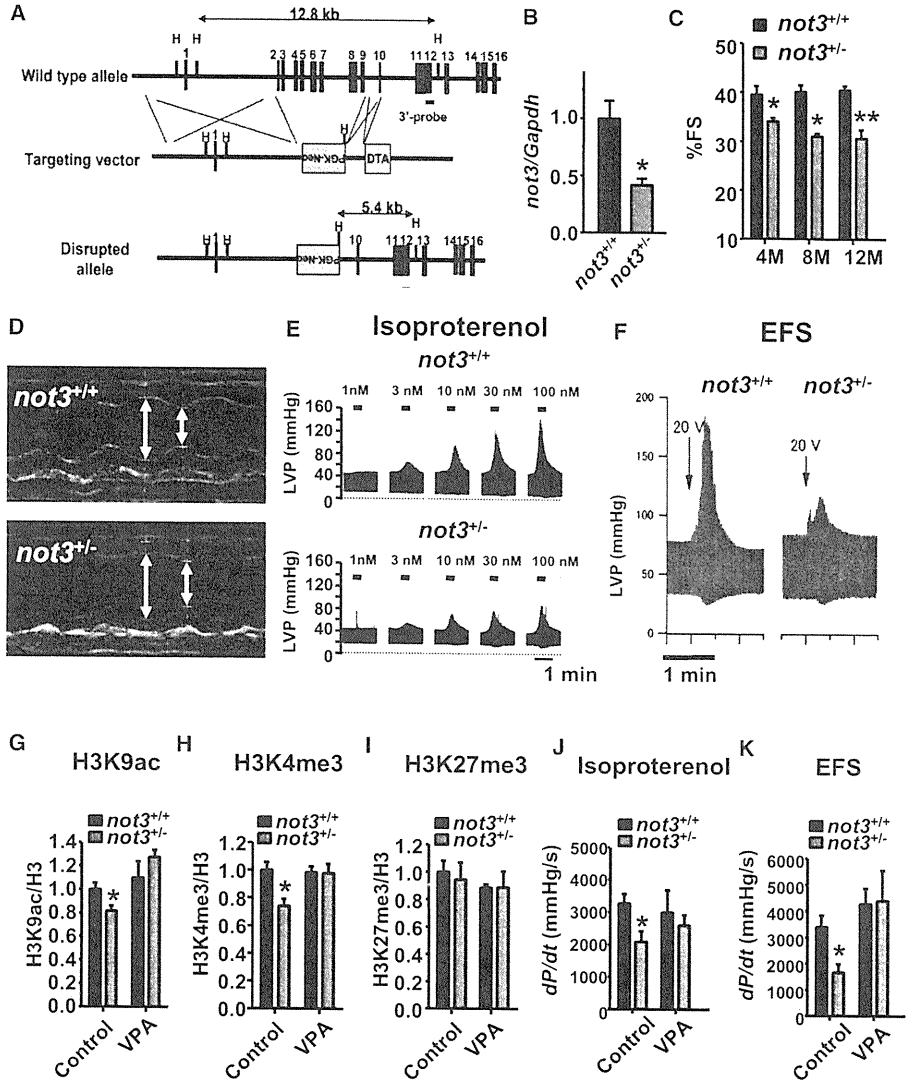

Figure 5. *not3*$^{+/-}$ **Mice Exhibit Reduced Heart Contractility, Ex Vivo Function, and Histone Modifications that Can Be Rescued by Treatment with HDAC Inhibitors**

(A) Gene targeting strategy. Exons 2 to 9 of the *not3* gene (official symbol *cnot3*) were replaced with a PGK-Neo cassette by homologous recombination in A9 ESCs. The wild-type allele, targeting vector, mutant allele, and PGK-Neo and DTH selection cassettes are shown. Blue boxes indicate exons.

(B) Real-time PCR analyses for *not3* mRNA expression in 3-month-old wild-type and *not3*$^{+/-}$ hearts. Values were normalized to *gapdh* mRNA expression. n = 6 mice per group.

(C) *not3*$^{+/-}$ mice display a significant reduction in percent fractional shortening at 4 months of age, which became more pronounced with age. n = 6–8 mice per group. Fractional shortening was determined by echocardiography.

(D) Representative M mode echocardiography for wild-type and *not3*$^{+/-}$ mice at 8 months of age.

(E) Left ventricular pressure (LVP) measurements in isolated ex vivo *not3*$^{+/-}$ and *not3*$^{+/+}$ hearts under isoproterenol perfusion. *not3*$^{+/-}$ hearts from 4-month-old mice showed impaired contractile responses to different doses of isoproterenol perfusion in the retrograde Langendorff mode as compared to age-matched controls.

(F) Impaired contractile response of ex vivo *not3*$^{+/-}$ hearts to electrical field stimulation (EFS) compared with littermate *not3*$^{+/+}$ hearts. Representative data for left ventricular pressure (LVP) at 20 V stimulation are shown.

(G–I) H3K9 acetylation (H3K9ac) (G), H3K4 trimethylation (H3K4me3) (H), and H3K27 trimethylation (H3K27me3) (I) levels were analyzed by western blot for acid-extracted histones from whole heart ventricles of wild-type and *not3*$^{+/-}$ mice treated with vehicle or VPA (0.71% w/v in drinking water for 1 week) Band intensities were normalized to total H3 levels.

(J and K) Treatment (1 week) with the HDAC inhibitor VPA rescue impaired ex vivo heart contractility of *not3*$^{+/-}$ hearts to isoproterenol (100 nM) perfusion or 25 V EFS.

All values are mean ± SEM. *p < 0.05; **p < 0.01. n = 5–12 per group. See also Figures S4 and S5.

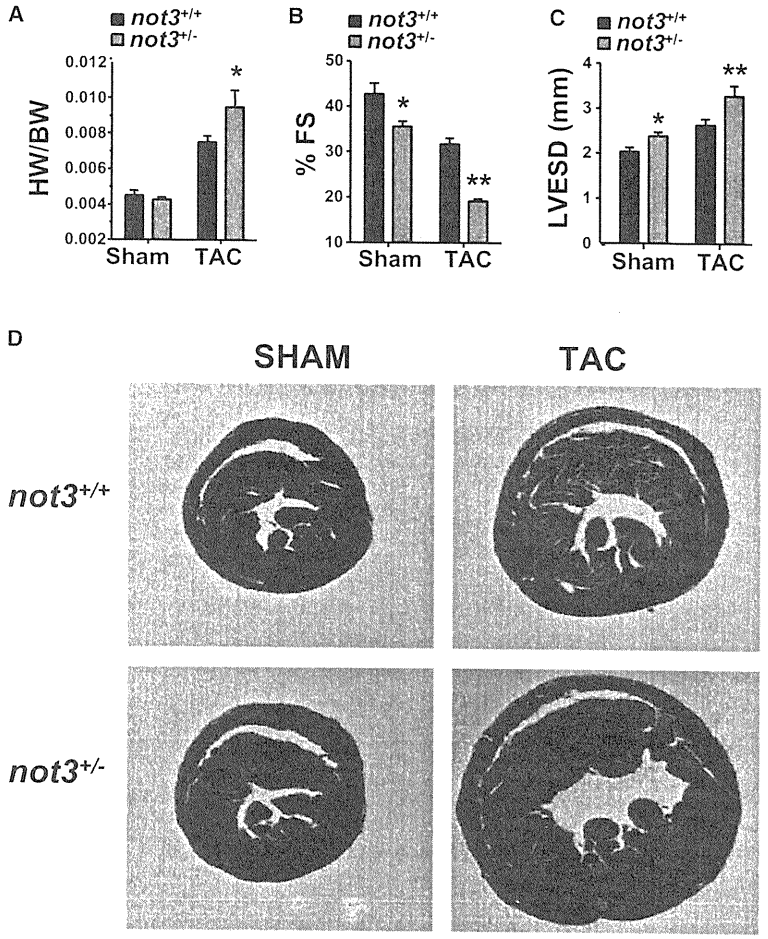

Figure 6. *Not3*$^{+/}$ Mice Exhibit Severe Heart Failure in Response to Pressure Overload

(A) Heart weight to body weight ratios (HW/BW) in *not3*$^{+/-}$ and *not3*$^{+/+}$ littermate mice 3 weeks after transverse aortic constriction (TAC). Animals receiving sham surgery are shown as controls.

(B and C) Echocardiography of male *not3*$^{+/-}$ and wild-type littermates 3 weeks after TAC. *not3*$^{+/-}$ mice with TAC show decreased percent fractional shortening (%FS) (B) and increased left ventricular diameter in systolic phase (LVESD) (C) compared with *not3*$^{+/+}$ mice that received TAC. All values are mean ± SEM. *$p < 0.05$; **$p < 0.01$.

(D) Representative sections of *not3*$^{+/+}$ and *not3*$^{+/-}$ hearts analyzed 3 weeks after sham or TAC surgery. Masson-trichrome stainings are shown to visualize collagen deposits indicative of fibrotic changes. Note the severe cardiac hypertrophy and ventricular dilation in *not3*$^{+/-}$ mice after TAC.

ESCs (Hu et al., 2009). *Kcnq1* encodes the α subunit of the repolarizing voltage gated potassium channel I_{Ks}, mutations in which are the most common cause of long-QT syndrome (LQT1) in humans (Wang et al., 1996). Abnormalities of cardiac repolarization, measured as alterations in QT interval, predispose to sudden cardiac death in humans (Moss and Kass, 2005). Indeed, while sham-operated *not3*$^{+/-}$ mice exhibit a subtle reduction in cardiac *Kcnq1* expression, this decrease was pronounced after TAC (Figure 7D). Reduced *Kcnq1* expression was rescued after HDAC inhibitor treatment. Also, for *Kcne1*, the β subunit of I_{Ks}, we observed a TAC-inducible and HDAC-sensitive defect in expression in *not3*$^{+/-}$ hearts (Figure 7E). In fly *not3*-RNAi hearts, *KCNQ* expression is also reduced (Figure S3D), and these flies exhibit cardiac contractile irregularities (Figures S3H and S3I).

Recently, two consortia have published genome-wide association studies (GWAS) for QT interval, QT-Interval and Sudden Cardiac Death (QTSCD) (Pfeufer et al., 2009) and Genetics of QT-Interval (QTGEN) (Newton-Cheh et al., 2009). One of the 12 identified genomic regions contains the *NOT1* gene, which we also found as a hit in our *Drosophila* screen (Figures 3A and 3B). Because of the stringent requirements to achieve a genome-wide significance threshold of $p < 5 \times 10^{-8}$ (Dudbridge and Gusnanto, 2008), many genuinely associated alleles will be missed because of both a failure to exceed this statistical threshold and the absence of functional confirmatory data for genes within loci of interest. We therefore evaluated whether common variants in and near the human *NOT3* locus are also associated with alterations in QT interval. Intriguingly, SNP rs36643 (chromosome 19: 59.3 Mb), located in the promoter region ~969 base pairs upstream from the *NOT3* transcriptional start site (924 bases upstream of the TATA box), is significantly associated with QT interval in the QTSCD data set (Figure 7F). Patients carrying the common T allele (minor allele frequency = 0.65) showed a dose-dependent increase in QT interval (ES = +1.03 ± 0.29 ms QT interval per copy of T allele, $p = 3.66E^{-04}$) (Figure 7G). Of note, similar to adult *kcnq1* mutant mice (Nerbonne, 2004), we did not observe an increased QT interval in *not3* heterozygous mice (except for one mouse with arrhythmia, K.K., M.M., H.Y., and K.F., unpublished data). Thus, our genome-wide screening data for death in flies can be used to identify candidate variants in humans that predispose individuals to heart disease, i.e., in the case of *NOT3* to arrhythmia and sudden death.

DISCUSSION

Here, we present the first in vivo RNAi adult heart screen in *Drosophila* assaying conserved genes. Using functional imaging, we were able to observe cardiac defects in all flies with heart-specific knockdown of candidate genes evaluated to date. Our experimental approach to screen for conserved heart genes in *Drosophila* in concert with advanced bioinformatics has the potency to reveal human and mouse genes involved in heart function and heart disease. Moreover, we uncovered a plethora of additional genes, a large proportion of which had

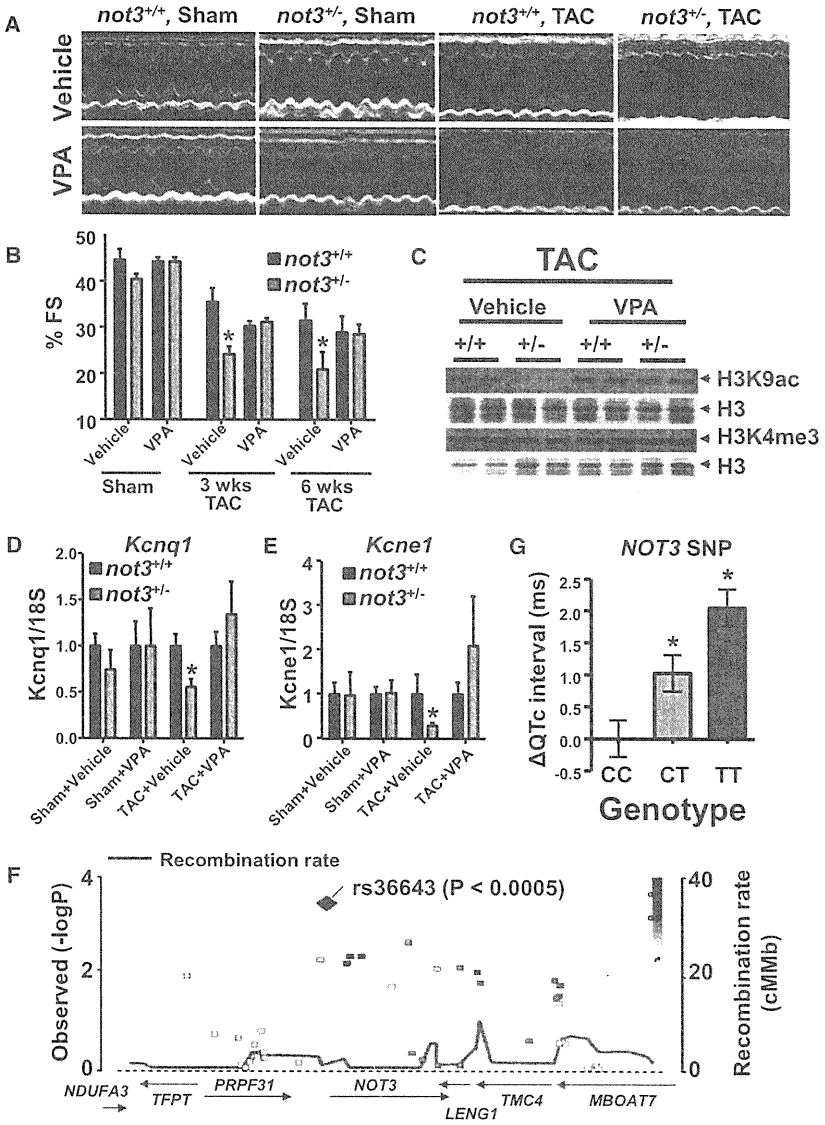

Figure 7. *not3* Is a Conserved Regulator of Heart Function

(A and B) Rescue of severe heart failure in TAC $not3^{+/-}$ hearts by the HDAC inhibitor VPA. One day after TAC or sham surgery, the mice received treatment with vehicle or VPA (0.71% w/v in drinking water) for 6 weeks. Representative M mode echocardiography (A) and percent FS (B) in $not3^{+/-}$ and $not3^{+/+}$ littermate mice 6 weeks after TAC or sham surgery with or without VPA treatment are shown. Values are mean ± SEM. *$p < 0.05$.

(C) Reduced H3K9 acetylation (H3K9ac) and H3K4 trimethylation (H3K4me3) levels were rescued by VPA treatment. Acid-extracted histones from the hearts 6 weeks after TAC surgery were immunoblotted with antibodies for H3K9ac and H3K4me3. H3 is shown as a loading control.

(D and E) Real-time PCR analyses for the QT interval-associated potassium channel genes *Kcnq1* and *Kcne1*. Total RNA was isolated from hearts 6 weeks after TAC or sham surgery with or without VPA treatment, and *Kcnq1* and *Kcne1* mRNA levels were measured and normalized to *18S* mRNA. Data are shown as fold changes compared to $not3^{+/+}$ mice for each treatment group. Values are mean ± SEM. *$p < 0.05$; **$p < 0.01$. $n = 5–10$ per group.

(F) Regional visualization of the association signal between common variants in the *NOT3* region and the adjusted QT interval (QTc). SNP rs36643 in the 5′ region of *NOT3* (−969 bp from the transcription start and −924 bp from the TATA box) showed a significant regional association ($p = 0.000366$).

(G) Association between the T allele of SNP rs36643 and a prolongation of QTc. * $p < 0.0005$ from linear regression with inverse variance weighting using an additive genetic model. Data are derived from a meta-analysis of genome-wide association scans in several populations (Pfeufer et al., 2009).

See also Figure S6.

completely unknown functions until now. Future experiments are required to test whether our candidate genes indeed control cardiac development, regulate adult heart function, and/or influence the outcome of heart failure in response to cardiac stress.

One pathway we identified was the CCR4-Not complex. Functional heart analyses in *Drosophila* confirmed that RNAi-mediated silencing of the CCR4-Not components *not3* and *UBC4* resulted in a severe impairment of cardiac function that resembles dilated cardiomyopathy in experimental mouse models and human patients. To provide a first proof of principle that our fly hits can indeed have similar functions in the more complex mammalian heart, we generated knockout mice for a component of the CCR4-Not complex. *not3* haploinsufficient mice develop spontaneous impairment of heart function and severe heart failure after aortic banding. Mechanistically, *not3* downregulation results in a defect in active histone marks and cardiac defects observed in $not3^{+/-}$ mice could be rescued by treatment with HDAC inhibitors. Besides regulating transcriptionally active states of chromatin (Hu et al., 2009; Jayne et al., 2006; Laribee et al., 2007; Peng et al., 2008), the CCR4-Not complex has also been implicated in RNA deadenylation (Tucker et al., 2001) and microRNA-mediated mRNA degradation (Behm-Ansmant et al., 2006). Thus, we cannot exclude that CCR4-Not components affect additional mechanisms regulating heart function. Importantly, our work on *not3* in flies and mice has also allowed us to identify a single-nucleotide polymorphism in the human *NOT3* promoter that is associated with prolonged QT intervals and sudden cardiac death in humans. Thus, large-scale screens in *Drosophila* can be directly translated to

mammalian species and, in combination with other genome-wide approaches, can reveal regulators of heart function and heart failure.

EXPERIMENTAL PROCEDURES

Detailed experimental procedures are provided in the Extended Experimental Procedures.

Fly Stocks

All RNAi transgenic fly lines were obtained from the Vienna *Drosophila* RNAi Center (VDRC) RNAi stocks (Dietzl et al., 2007). The cardiac tissue-specific *TinCΔ4 12a-Gal4* was a kind gift from Manfred Frasch, (Lo and Frasch, 2001) and *Hand-Gal4* was a gift from Eric Olsen (Han and Olson, 2005).

Screening System

Transgenic RNAi males were crossed to *TinCΔ4* virgin females. Viable lines were then incubated at 29°C for 6 days to expose flies to temperature stress (Paternostro et al., 2001). Initially, a Z score cutoff of 2 (mean control-test)/SD was used to select RNAi lines for retesting.

Drosophila Cardiac Function, Morphology, and Gene Expression

UAS-RNAi fly lines obtained from the Vienna *Drosophila* RNAi Center were crossed to *Hand-Gal4* (II) driver flies and to w^{1118} wild-type control flies. Flies were assessed for heart morphology and physiology with high-speed digital video imaging (Ocorr et al., 2007b). M modes were generated and cardiac parameters including heart periods, diastolic and systolic diameters, and fractional shortening were recorded for each group with a MatLab-based image analysis program (Fink et al., 2009). Fluorescent imaging of *Drosophila* heart tubes was performed as described (Alayari et al., 2009).

Bioinformatics Analysis

For a detailed description of full bioinformatics analysis, please see the Extended Experimental Procedures.

Phenotyping of *not3* Knockout Mice

A targeting vector was constructed to replace exons 2 and 9 of the murine *not3* gene. Fractional shortening (FS) was calculated as follows: FS = [(LVEDD − LVESD)/LVEDD] × 100. For ex vivo heart studies, hearts were assayed with a Langendorff apparatus. The heart was paced electrically at 400 beats/min (bpm), and the electrical field stimulation (EFS) was applied in conjunction with the pacing stimulation. Isoproterenol was perfused for 30 s with the indicated doses. For HDAC inhibition, wild-type and $not3^{+/-}$ mice were treated with vehicle, Trichostatin A (TSA), or Valproic acid (VPA) for 1 week. Acid-extracted histones were prepared, resolved, and transferred to nitrocellulose membranes for western blotting. Transverse aorta constriction (TAC) was performed as described (Kuba et al., 2007). For heart histology, hearts were arrested, fixed, embedded in paraffin, and stained with hematoxylin and eosin (H&E) or Masson-Trichrome.

Human QT Interval Association

Human QT interval association signals over the NOT3 region were obtained from data generated by the QTSCD Consortium (Pfeufer et al., 2009).

SUPPLEMENTAL INFORMATION

Supplemental Information includes Extended Experimental Procedures, six figures, five tables, and one movie and can be found with this article online at doi:10.1016/j.cell.2010.02.023.

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EXTENDED EXPERIMENTAL PROCEDURES

Fly Stocks

All RNAi transgenic fly lines were obtained from the VDRC RNAi stocks. The whole genome VDCR library has been previously reported (Dietzl et al., 2007). The cardiac-tissue specific *TinCΔ4 12a-Gal4* was kind gift from Manfred Frasch, (Lo and Frasch, 2001) and *Hand-Gal4* was kind gift from Eric Olsen, (Han and Olson, 2005) driver lines have been previously described and used to study genes involved in *Drosophila* heart development and cardiac function in adult flies (Wolf et al., 2006). w^{1118} wild-type control flies obtained from the VDRC were used when indicated since the *Drosophila melanogaster* w^{1118} background is isogenic to the VDRC RNAi library. The fly stock for the *not3* associated P-element ($CG8426^{KG10496}$) was obtained from Bloomington (#15271).

Screening System

Transgenic *UAS*-RNAi males were crossed to *TinCΔ4 12a-Gal4* virgin females and 4 day old viable F1 adult progeny were transferred to test chambers containing 2 filter pads with 2 ml of a 50 mMol sucrose solution. The viable RNAi lines were then incubated at 29°C for 6 days to expose flies to temperature stress as described previously (Paternostro et al., 2001) and the number of dead and surviving flies were counted. Initially a Z-score cut-off of 2 (Mean control-test)/SD was used to select RNAi lines for re-testing. Developmental lethality was assessed in a semiquantitative fashion, with lethal crosses scored as 0, semi-lethal crosses scored as 0.5, and viable crosses scored as 1. During re-testing, lethality was staged when apparent. In all cases, crosses were scored based on the furthest developmental stage reached: 0 = lethal (embryonic lethal or no off-spring), 1 = larval lethal, 2 = pupal lethal, 3 = adult lethal (die within 4 days after eclosion), 4 = adult viable.

Drosophila Cardiac Analysis

UAS-RNAi fly lines obtained from the VDRC were crossed to *Hand-Gal4* (II) driver-flies and to w^{1118} wild-type control flies. As an additional control, *Hand-Gal4* (II) driver-flies were crossed to w^{1118} wild-type flies. The progeny were raised at 25°C on standard cornmeal-agar medium. At 1 week of age, 29-40 female offspring from each cross were anaesthetized and dissected. All procedures were done at room temperature (18-22°C) as previously described (Cammarato et al., 2008; Ocorr et al., 2007). Briefly, each head, ventral thorax and ventral abdominal cuticle was removed exposing the abdomen. All internal organs and abdominal fat were removed leaving only the heart and associated muscles for each fly. Dissections were performed in oxygenated artificial adult hemolymph. The semi-intact preparations were allowed to equilibrate with oxygenation for 20–30 min prior to filming. Analysis of gross heart morphology and physiology was performed using high speed movies. 30 s movies were taken at rates of 100–200 frames/sec using a Hamamatsu EM-CCD digital camera on a Leica DM LFSA microscope with a 10x immersion lens. All images were acquired and contrast enhanced using Simple PCI imaging software (Compix, Inc.). M-modes were generated and determination of cardiac parameters, including heart periods, diastolic and systolic diameters and fractional shortening for each group was performed using a MatLab-based image analysis program (Fink, 2009). ANOVA of genotype as a function of each measured cardiac parameter was employed to test for significant differences between w^{1118}>*UAS-Not3*-RNAi or w^{1118}>*UAS-UBC4*-RNAi control flies and both *Hand-Gal4*>*UAS-Not3*-RNAi or the *Hand-Gal4*>*UAS-UBC4*-RNAi mutants, respectively. Additionally, one-way ANOVAs with Bonferroni multiple comparison post tests were employed to determine if significant differences between w^{1118}>*Hand-Gal4* and all w^{1118}>*UAS*-RNAi control lines were present.

Fluorescent Staining

Fluorescent staining and imaging of *Drosophila* heart tubes were performed as described (Alayari et al., 2009). Briefly, beating hearts of semi-intact *Drosophila* were placed in artificial adult *Drosophila* hemolymph containing 10mM EGTA. Cardiac tubes were examined to ensure contractions were inhibited. Hearts were fixed in 1xPBS containing 4% formaldehyde at room temperature for 20 min with gentle shaking. Washing of hearts was performed three times for 10 min with PBSTx (PBS containing 0.1% Triton X-100) at room temperature with continual shaking. After washing, the hearts were incubated with Alexa584-phalloidin in PBSTx (1:1000) for 20 min with continual agitation. Washing of the hearts was carried out three times for 10 min with PBSTx at room temperature. The hearts were rinsed in 100 μl of PBS for 10 min. The specimens were mounted on microscope slides and viewed at 10X magnification using a Zeiss Imager Z1 fluorescent microscope equipped with an Apotome sliding module.

Q-RT-PCR of *Drosophila* Cardiac Associated Transcripts

Quantitative RT-PCR was performed using standard procedures according to (Akasaka et al., 2006) with minor modifications. Total RNA was extracted from 30 hearts per genotype (all female flies). Quantitative Real Time-PCR was performed with the LightCycler FastStart DNA Master PLUS SYBR Green I kit (Roche) using single strand cDNA."

The primer sets were as follows:

*not3*_05 CGCAAAGCAGTATCGGAAGT
*not3*_06 CCGCAGGATTGTTACCAG
*UBC4*_01 CGCAGCTTTGTGTTTCGTTT
*UBC4*_02 GTTGGTGTCTCGCGTATT

*SERCA*_01 CAAGTCCTACTCGGGTCGTG
*SERCA*_02 CATAGCGGAGATTTCGTTCAT
*KCNQ*_11 ACCATCAAGGAGTACGAAGA
*KCNQ*_12 CGATGACCAGAGTCGAG
*Mhc*_01 AGTCCGAGCGTCGCGTCAAG
*Mhc*_02 TGAGGGCGGCGATTTC
*rp49*_01 GAC GCT TCA AGG GAC AGT ATC TG
*rp49*_02 AAA CGC GGT TCT GCA TGA G
*actin*_01 ATCCGCAAGGATCTGTATGC
*actin*_02 ACATCTGCTGGAAGGTGGAC
*actinin*_03 CCTGACCGCCAACGACATGA
*actinin*_04 CATTTGCCGCTCGATCCA

Whole Mount Fluorescent Staining of *Drosophila* Embryos

Following dechorionization in 7.5% bleach, embryos from overnight collections were devitellinized and fixed in heptane with 4% formaldehyde in 0.3% PBT buffer (1x PBS with 0.3% Triton) for 25 min. Dechorionisation and dehydration was accomplished by vortexing and washing in methanol. Primary antibodies used: anti-ßGal (mouse 1:1000; Cappel), anti-Tin (rabbit 1:800; R. Bodmer). The secondary antibodies used were donkey anti-mouse-Alexa488 and anti-rabbit-Alexa568 (1:500, Molecular Probes). Flat preparations of embryos were mounted in Vectashield mounting medium and 70% glycerol (1:1). Stained embryos were examined under a confocal microscope (Zeiss LSM510) and images were processed using Adobe Photoshop.

Identification of Mouse and Human Orthologs

To identify orthologs between *Drosophila* and mouse and between *Drosophila* and human, we used pre-computed orthology predictions obtained from compara49, inparanoid, inparanoid6.1, inparanoid6.1 to ensembl, homologen08, and orthomclv2 (Kuzniar et al., 2008) databases. One-to-one and one-to-many mappings were observed between the *Drosophila* and the mammalian genes. In case of one–to–many mappings, all the ortholog targets for a given gene were considered for downstream analysis.

Functional Annotation of "Heart Function" Hits

Of the 490 RNAi hits (498 genes) with potential defects in heart function, we could annotate 377 genes by GO terms. To annotate the remaining 121 genes, we searched Panther db (http://www.pantherdb.org/). We were able to annotate an additional 116 genes with previously unknown functions.

Gene Ontology (GO) Classification and Gene Set Enrichment

GO analysis was performed using GOstat (http://gostat.wehi.edu.au/). GO analysis was run with *Drosophila* genes (and mouse or human orthologs) whose RNAi hits had a Z-score > 3. Over and under-represented ($p < 0.1$) GO terms with corrections for multiple testing (Yekutieli correction), were identified in the above list, compared to the FlyBase (fb) for *Drosophila*, Mouse Genome Informatics (mgi) for mouse and goa_human for human genes, respectively. Since terms that occur at a deeper level in the GO tree hierarchy and contain lesser number of genes are considered more biologically informative, we discarded terms containing more than 500 genes from further analysis. Significant GO terms were manually curated, pooled and organized into "functional groups," for visual representation of the GO data. A complete list of significantly enriched GO terms pooled into functional groups is provided in Table S4.

To remove any artificial bias in the gene list created by the ad hoc Z-score cut-off (>3) that we used previously in the GO analysis, we performed the Gene Set Analysis (GSA) to confirm enrichment of selected GO terms. GSA uses the entire list of genes corresponding to the selected biological terms and assesses if the process as a whole has been significantly altered in the entire dataset. A null hypothesis is that "Genes of a functionally irrelevant pathway are not clustered at the top of a rank ordered (based on Z-score) list of all genes in the experiment." Based upon the Z-score of the RNAi hit phenotype, a rank order list of 6892 unique genes corresponding to 8291 (with reported Z-score) RNAi transformants was created. Individual gene lists were constructed corresponding to 45 GO terms rendered significant by GO analysis (corrected $p < 0.1$). An enrichment score (Es) for a gene list (s) was calculated based upon the "heart function" Z-score using the formula:

Es = (Sum of average z-scores of all genes in s) / $\sqrt{}$ (Number of genes in s).

For every **s**, 100 bootstrap permutations were carried out to generate random functionally unrelated gene lists of the same size and their enrichment scores calculated as Er. A gene set s is considered enriched when Es > Er (90th quantile) and we reject the null hypothesis (p-value < 0.1). Enrichment of the GO term is also reported at p-value < 0.05 and 0.01.

Pathway Analyses

Pathway analysis was performed using the *Drosophila* Pathway database in GeneSpring GX. Briefly, the Pathway database in GeneSpring GX contains molecular relations from two sources: (1) those reported in open-source public databases like BIND and IntAct

(IMEX consortium) or (2) extracted from PubMed abstracts using a proprietary natural language processing technique. The tool UI allows a query of the database to build networks of molecular relations (edges) among molecules (nodes) of interest. Relations are classified as binding, expression, transport, protein modification, general regulation, metabolism and promoter binding. We constructed a network of "heart function" genes along with their first degree protein-protein interaction neighbors. Using filters in GeneSpring GX, we selected molecular relations reported by the IMEX consortium which represent "binding" interactions between the molecules. These interactions found the majority of binding partners for the heart hits. We also included the highest quality (Quality score $\geq$ 9) expression and promoter binding interactions using appropriate filter settings in GeneSpring GX. These interactions were manually curated and included in the final network.

Pathway Enrichment Analysis

A hypergeometric test, similar to the test used for GO enrichment analysis, was used to identify over-represented gene lists (C2 from Msigdb, BROAD Institute) and pathways (KEGG) among the "heart" hits. The hypergeometric test considers only the percentage representation of genes corresponding to a biological pathway in the pre-computed heart function gene list. This analysis was performed on the gene list identified as adult "heart" hits (Z-score $\geq$ 3) in *Drosophila* and their corresponding mouse or human orthologs, respectively.

Pathway Systems Map

For the combined systems map, all significant KEGG pathways and C2 gene sets were manually grouped into uniform functional categories as shown in Table S4, parts E–H. For uniformity, both lists have been manually annotated by the same functional classification terms. Functional classifications were assigned relevant to the biology of heart functions. For the systems map, we included all the functional categories assigned to the significant KEGG pathways. The information obtained from KEGG pathway analysis was supplemented with significant C2 gene sets from the appropriate functional categories: AKT/PI3K signaling activation, Calcium Signaling, cAMP regulated signaling, Cardiac related disease/signaling, Cytoskeleton, Hematopoeisis related, Ion Channels, muscle contraction, NFAT transcription, PI3K signaling, Txn factors. For each functional category, the corresponding genes that mapped to the KEGG pathways or C2 gene set were extracted. *Drosophila* orthologs for these genes were found and assigned to the respective pathway in the visual representation of the systems map. For the *Drosophila* systems map, *Drosophila* pathways that were over 90% enriched were manually annotated into functional groups. Corresponding heart hit genes and their first degree binding partners that overlapped with the gene set of the pathway were extracted and assigned to each pathway node in the systems map. We found both primary heart hits as well as binding partners filtered into the systems map are significantly enriched ($p < 0.01$) in cardiac genes of known function from independent studies, compared to any random list of the same size. We observe an almost equal enrichment of cardiac genes with known functions among the RNAi hits as well as binding partners included in the systems map.

Generation of *not3* Knockout Mice

For gene targeting of *not3* in mice, a targeting vector was constructed to replace exons 2 and 9 of the murine *not3* gene. The linearized construct was electroporated into A9 embryonic stem (ES) cells derived from 129/Ola and C57BL/6J hybrids. Approximately 2-3 in 100 ES cell clones were identified as correctly targeted by genomic Southern blotting. Chimeric mice from two independent clones transmitted the mutant allele through the germ line, and the targeted allele was confirmed by Southern blot. F1 mice were backcrossed for 5 times onto a C57BL/6 background. F5-F7 intercrossed mice were used for all experiments reported in this study. Mice were genotyped by PCR and Southern blotting and maintained at the animal facilities of the Institute of Molecular Biotechnology (IMBA), Akita University Graduate School of Medicine and Tokyo Medical and Dental University. All animal experiments were performed in accordance with institutional guidelines.

Mouse Embryo Analyses

To analyze blastocyst-stage mouse emryos, embryos at 3.5 dpc were flushed out from the uteri of pregnant mice of heterozygous x heterozygous breeding. RNA and Genomic DNA were extracted from individual blastocysts with Trizol (Invitrogen). Genotypes were determined by nested PCR, and reverse transcription was performed with Primescript RT reagent kit (TAKARA) followed by RT-PCR with ExTaq PCR kit (TAKARA). For immunohistochemistry of whole embryos, blastocysts were fixed in 4% PFA for 20 min, permealized with 0.4% Triton X-100 in PBS for 20 min, and blocked with 0.1% Triton X-100, 1% BSA or 10% donkey serum in PBS for 30 min. After each step embryos were washed five times for 5 min in PBS, and anti-Not3 antibody (Protein Tech Group, 11135-1-AP) staining was performed at 4°C overnight followed by Alexa543 secondary antibody for 1 hr. Embryos were mounted with VECTASHIELD with DAPI (Vector Labs) and observed under LSM500 confocal microscopy (Carl Zeiss). Embryos were collected and genotyped by nested PCR. For in vitro culture of inner cell mass outgrowth, blastocysts were individually cultured onto gelatinized tissue culture plates (Nunc) in standard ES medium with leukemia inhibitory factor (Chemicon) and photographed every few days. After cultivation, embryos were harvested by trypsinization and genotyped by PCR.

mRNA and Protein Expression Analyses in Mice

For real-time PCR analysis of mouse *not3*, 3 μg of DNase-treated total RNA was extracted from hearts and reverse transcribed using First-Strand Beads (GE Healthcare) with random primers. SYBR green real-time PCR reactions were carried out in 96-well plates

using an iQ-Cycler (Bio-Rad). Immunohistochemistry to detect *not3* was carried out with antibodies to NOT3 (Abcam 55681). Blastocysts were then counterstained DAPI.

The primer sets were as follows:

Not3-F: GTATAGCAAGGAGGGTCTGGGTCTGGCTCAG
Not3-R: TCGGGGTCCTGGGATGAGTCAACGTAGTAC
ANF-F: GAGAGACGGCAGTGCTTCTAGGC
ANF-R: CGTGACACACCACAAGGGCTTAGG
βMyhc-F: GACGAGGCAGAGCAGATCGC
βMyhc-R: GGGCTTCACAGGCATCCTTAGGG
Kcnq1-F: ATCAGGCGCATGCAGTACTTTG
Kcnq1-R: TGACATCTCGCACGTCGTAGG
Kcne1-F: TAGTGAATGTCGCCTTGTTTGGAA
Kcne1-R: TGGCATCTCACGGTGCTCTC
Oct4-F: CCAATCAGCTTGGGCTAGAG
Oct4-R: TGTCTACCTCCCTTGCCTTG
GATA6-F: GAGCTGGTGCTACCAAGAGG
GATA6-R: TGCAAAAGCCCATCTCTTCT
Eomesodermin-F: GGCAAAGCGGACAATAACAT
Eomesodermin-R: GACCTCCAGGGACAATCTGA
18S-F: CTGCCGTCTGAGTGTATCGC
18S-R: GCTGGGGCTGAGGAAAGTG
GAPDH-F: GGCCAAGGTCATCCATGACAAC
GAPDH-R: GTTGTCATGGATGACCTTGGCC

Echocardiography

Echocardiographic measurements were performed as described previously (Kuba et al., 2007). Briefly, mice were anesthetized with isoflurane(1%)/oxygen, and echocardiography was performed using an Acuson Sequoia C256 equipped with a 15-MHz linear transducer. Fractional shortening (FS) was calculated as follows: FS = [(LVEDD – LVESD)/LVEDD] x 100.

Langendorff Perfusion Experiments

not3 heterozygous and littermate control mice were anaesthetized with ketamine/xylazine and isolated hearts immediately placed in cold PBS. The isolated heart was mounted on a Langendorff apparatus and perfused at a constant hydrostatic pressure of 75 mm Hg with an oxygenated Tyrode solution (37°C) composed of 136.9 mM NaCl, 5.4 mM KCl, 1.8 mM $CaCl_2$, 0.5 mM $MgCl_2$, 0.33 mM NaH_2PO_4, 10.0 mM glucose, and 5.0 mM HEPES as described (Murakami et al., 2007). Atropine (5.5 μM) was added to the perfusate, and a fluid-filled balloon catheter connected to a pressure transducer (CD200; NihonKoden) was inserted into the left ventricle via the left atrium. The sinoatrial node region was removed, and the heart was paced electrically at 400 beats/min (bpm). The electrical field stimulation (EFS) was applied in conjunction with the pacing stimulation (delay, 4 ms; duration, 1 ms for 5 s). Isoproterenol was perfused for 30 s using the indicated doses.

Transverse Aorta Constriction (TAC)

Eight to ten weeks old control wild-type littermates and *not3* heterozygous mice were subjected to pressure overload by TAC through constriction of the thoracic aorta as described (Kuba et al., 2007). Heart function was determined by echocardiography. For histology, hearts were arrested with 1 M KCl, fixed with 10% formalin, and embedded in paraffin. 5 μm thick sections were then cut and stained with hematoxylin and eosin (H&E). For detection of fibrotic areas, sections were stained with Masson-Trichrome.

Treatment with HDAC Inhibitors

For baseline measurements, wild-type and $not3^{+/-}$ mice were treated with vehicle, Trichostatin A (TSA) (Sigma, 0.6 mg/kg/day, i.p.), or Valproic acid (VPA) (Na Valproate (WAKO) 0.71% w/v in drinking water) for 1 week. For TAC heart failure experiments, the mice were given vehicle or VPA (0.71% w/v in drinking water) for 6 weeks starting one day after TAC or sham surgery.

Western Blot Analysis for Histone Tail Modifications

Acid-extracted histones were prepared from whole ventricles of mouse hearts as described (Cheung et al., 2000). Histones were resolved by SDS-PAGE (15%; 30:0.8) gels and transferred to nitrocellulose membranes for Western blotting. The amount of histone H3 was precalibrated with ponceau-S (Sigma) staining. Covalent modification status of H3 tails was analyzed using antibodies detecting acetylated H3K9 (Upstate), trimethylated H3K4 (Abcam), and anti-trimethylated H3K27 (kind gift from T. Jenuwein). Band intensities were quantified and normalized to total H3 levels.

Human QT Interval Association

Human QT interval association signals over the *NOT3* region (official gene name *CNOT3*) were obtained from data generated by the QTSCD Consortium as described in (Pfeufer et al., 2009).

Statistical Analyses

Data are presented as mean values ± SEM and were analyzed for differences between wild-type and *not3* heterozygous mice at discrete time points. *Drosophila* survival and heart function was analyzed by t test for single comparisons and ANOVA for multiple comparisons. Gene set enrichment is described above. GO enrichment was calculated using the online tool GOstat (http://gostat.wehi.edu.au/). For mouse heart function, normally distributed data were analyzed by t test. Data not normally distributed were analyzed using the Mann-Whitney test. $p < 0.05$ was considered significant. GWAS association results are presented as mean values ± SD.

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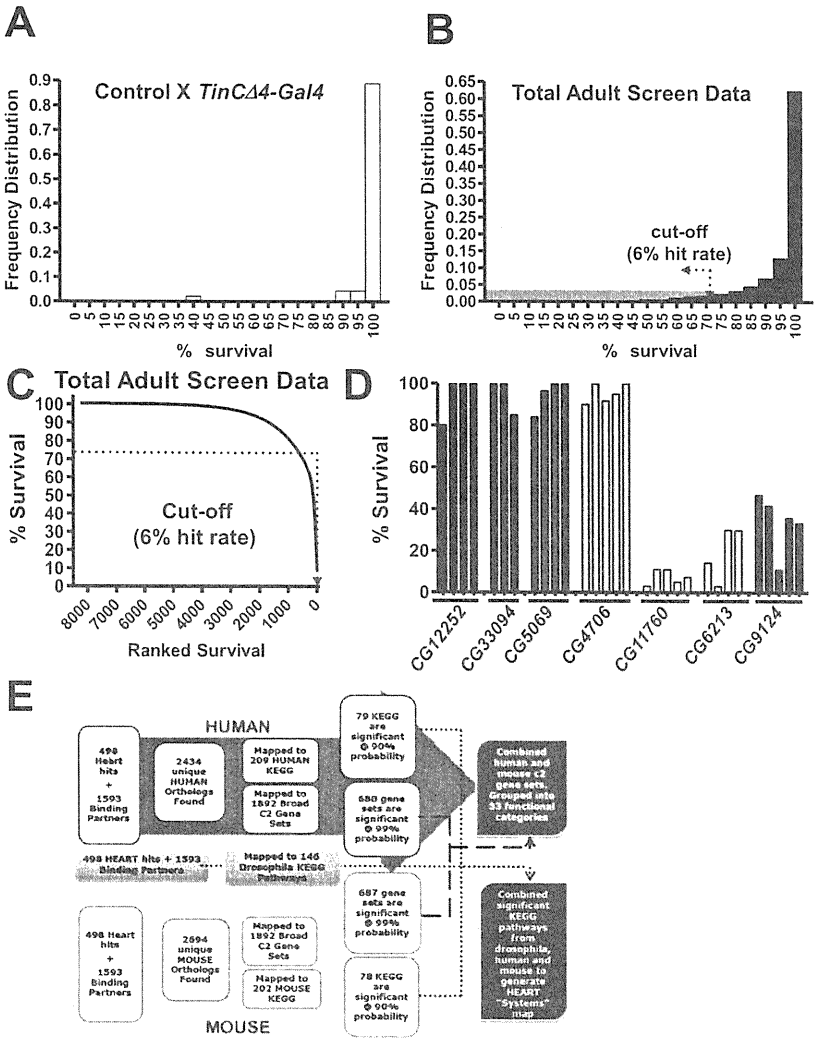

Figure S1. Screen Set-up, Related to Figure 1

(A) Repeated testing of our background control (w^{1118}) X heart driver (*TinCΔ4-Gal4*) line on multiple days shows a consistent ability of these flies to pass the increased ambient temperature. The *x* axis shows percent survival and the *y* axis the frequency of flies that passed (survival) or failed (death) the experimental challenge. n = 966 flies.

(B) Histogram for the entire heart screen shows the distribution of survival for all tested *TinCΔ4-Gal4*_RNAi lines. The cut-off used for *TinCΔ4-Gal4*_RNAi lines to pass the threshold for further analyses is indicated (Z-score > 3 corresponding to 72% survival). The *x* axis shows percent survival and the *y* axis the frequency of flies that passed (survival) or failed (death) the experimental challenge.

(C) Ranked Best Fit curve for the entire screen data set. The cut-off used for *TinCΔ4-Gal4*_RNAi lines to be included into our data-set for further analyses is indicated (Z-score > 3 corresponding to 72% survival.

(D) Representative repeat experiments for select *TinCΔ4-Gal4*_RNAi lines that passed or failed (recorded as % survival on day 6 after a shift to 29°C) to show reproducibility of the experimental model. Bar represent individual experiments for each RNAi line.

(E) Flow chart indicating KEGG and C2 gene set analysis in *Drosophila*, mice, and humans. Data from all three organisms were pooled to generate a global network map. See the Experimental Procedures for details.

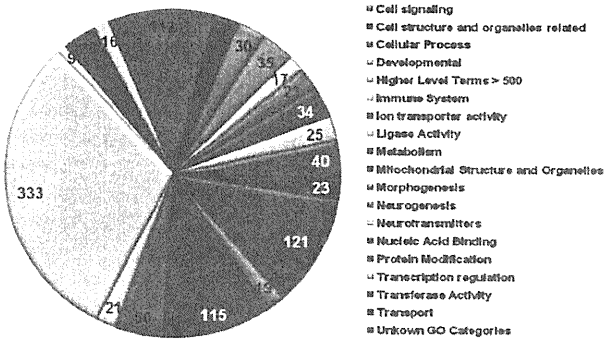

Figure S2. *Drosophila* GO and KEGG Analysis, Related to Figure 2

Functional classification of statistically enriched GO (gene ontology) terms for adult heart hits in *Drosophila*. Numbers indicate gene counts from all the GO terms included in each functional category. See Suppl. Table S4A contains the entire list of enriched GO terms and their classification into functional categories.