

Neuropilin 1 mediates epicardial activation and revascularization in the regenerating zebrafish heart

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Abstract:

Unlike adult mammals, zebrafish can regenerate their heart. A key mechanism for regeneration is the activation of the epicardium, leading to the establishment of a supporting scaffold for new cardiomyocytes, angiogenesis and cytokine secretion. Neuropilins are co-receptors mediating signaling of kinase receptors for cytokines known to play critical roles in zebrafish heart regeneration. We investigated the role of neuropilins in response to cardiac injury and heart regeneration. All four neuropilin isoforms *nrp1a*, *nrp1b*, *nrp2a* and *nrp2b* were upregulated by the activated epicardium and a *nrp1a* knockout mutant showed a significant delay in heart regeneration and displayed persistent collagen deposition. The regenerating hearts of *nrp1a* mutants were less vascularized and epicardial-derived cell migration and re-expression of the developmental gene *wt1b* was impaired. Moreover, cryoinjury-induced activation and migration of epicardial cells in heart explants was reduced in *nrp1a* mutant. These results identify a key role for Nrp1 in zebrafish heart regeneration, mediated through epicardial activation, migration and revascularization.

Introduction:

Ischemic heart disease remains the leading cause of death worldwide, and, although improved therapeutic treatments have led to an increase in myocardial infarction (MI) survival rates (Cahill and Kharbanda, 2017, Roger, 2013, von Gise et al., 2011) cardiac function often remains severely compromised because adult mammalian hearts replace damaged tissue with an irreversible fibrotic scar (Dobaczewski et al., 2010, Porrello et al., 2011). This often leads to the development of chronic heart failure, further MIs, and fatal arrhythmias. In contrast to mammals, zebrafish have the remarkable ability to regenerate lost or damaged cardiac tissue *via* cardiomyocyte proliferation and resorption of fibrotic tissue, ultimately restoring cardiac function (Chablais et al., 2011, Gonzalez-Rosa et al., 2011, Jopling et al., 2010, Poss et al., 2002). Understanding the underlying mechanisms that govern zebrafish heart regeneration may identify therapeutic targets important for stimulating cardiac repair following MI in mammals.

Zebrafish heart regeneration involves a well described, but incompletely understood, sequence of cellular processes and signaling events. The epicardium, a mesothelial cell monolayer encasing the heart, has been strongly implicated as a key regulator of the regenerative response (Cao and Poss, 2018, Masters and Riley, 2014, Zhou and Pu, 2011). Upon cardiac damage, the epicardium is activated (Schnabel et al., 2011, van Wijk et al., 2012), undergoing proliferation and secreting cytokines that stimulate cardiomyocyte cell cycle re-entry (Kikuchi et al., 2010). Autocrine and paracrine signals induce a subpopulation of epicardial cells to undergo a process known as epithelial to mesenchymal transition (EMT) (Kim et al., 2010, Lepilina et al., 2006). These epicardial cells adopt an embryonic-like gene expression profile, migrate into the injured region, and differentiate into fibroblasts and mural cells that support revascularization (Gonzalez-Rosa et al., 2012, Lepilina et al., 2006). Some

of the signaling pathways required for the epicardial regenerative response in zebrafish have been identified and characterized. In particular, platelet-derived growth factor (PDGF)-BB and fibroblast growth factor (FGF) are both essential for epicardial EMT and coronary neovascularization in the regenerating zebrafish heart (Gonzalez-Rosa et al., 2012, Kim et al., 2010, Lepilina et al., 2006). Vascular endothelial growth factor (VEGF) was also found to play a key role in the early revascularization of the injured area (Marin-Juez et al., 2016). PDGF, FGF, and VEGF are all ligands for neuropilin (NRP) transmembrane receptors (Ball et al., 2010, Pellet-Many et al., 2011, West et al., 2005). NRP1 and NRP2 share similar homology domain organization, with a large extracellular region essential for ligand binding, a single transmembrane domain, and a short cytoplasmic domain (Pellet-Many et al., 2008). NRP1 was first identified as a regulator of angiogenesis and neurogenesis mediated *via* VEGF and semaphorin3A, respectively (Gu et al., 2003, Kawasaki et al., 1999, Kitsukawa et al., 1997). In zebrafish, it is also required for vascular development and is a mediator of VEGF-dependent angiogenesis (Lee et al., 2002). Furthermore, NRPs have been shown to mediate signaling pathways for other cytokines, including PDGF, FGF, and TGF- β in various tissues in both physiological and pathological settings (Glinka and Prud'homme, 2008, Kofler and Simons, 2016, Pellet-Many et al., 2011, West et al., 2005). NRPs have also been reported to play a role in EMT in carcinomas (Adham et al., 2014, Chu et al., 2014, Grandclement et al., 2011), but, despite their known interactions with cytokines implicated in EMT, their role in the epicardial response and the revascularization of the injured heart after cardiac damage is currently unknown. We used the zebrafish heart cryoinjury model (Gonzalez-Rosa and Mercader, 2012) to investigate the spatio-temporal expression of the four zebrafish neuropilin isoforms (*nrp1a*, *nrp1b*, *nrp2a*, and *nrp2b*, orthologues of human NRP1 and NRP2, respectively) in the regenerating heart. We show that all are upregulated in response to cryoinjury, with distinctive endocardial and epicardial expression during the

regenerative response. Neuropilins are expressed in activated epicardial cells and, zebrafish expressing a truncated loss-of-function Nrp1a (*nrp1a^{sa1485}*) show impaired epicardial response to injury indicated by a downregulation of *wt1b* expression. Epicardial explants from *nrp1a^{sa1485}* fish exhibit reduced epicardial cell migration compared to Wild-Type fish explants. Moreover, the revascularization of the injured area is also impaired in mutant fish. We also used a rat epicardial cell line (Wada et al., 2003) to investigate potential downstream targets of NRP1 and found that down-regulating the expression of NRP1 via shRNA adenovirus infection, led to a decrease in β -catenin expression which is an important regulator of epicardial to mesenchymal transition (Duan et al., 2012, von Gise et al., 2011, Zamora et al., 2007). These findings reveal an essential role for Nrps in zebrafish heart regeneration, mediated by a new function for Nrp1a in epicardial activation and cell movement.

Results:

Neuropilins are up-regulated during zebrafish heart regeneration

We quantified *nrp1a*, *nrp1b*, *nrp2a*, and *nrp2b* mRNA levels in whole ventricles following cardiac cryoinjury by absolute RT-qPCR and compared their expression with that in sham-operated hearts. *Nrp1a*, *nrp1b*, and *nrp2a* genes were up-regulated 3-5 fold in injured hearts compared to sham-operated hearts early in the regenerative process (1 and 3 days post-cryoinjury, dpci) and returned to endogenous basal levels thereafter ($p=0.0019$ and $p<0.0001$ for *nrp1a* at 1 dpci and 3 dpci respectively, $p=0.0007$ for *nrp1b* at 3 dpci and $p=0.0051$ and $p<0.0001$ for *nrp2a* at 1 dpci and 3 dpci respectively) (Fig.1A). In line with previous publications (Martyn and Schulte-Merker, 2004), we observed that *nrp2b* is the

most highly expressed isoform in the heart under control conditions (Fig.1A). However, qPCR did not show any significant *nrp2b* changes following cardiac damage, probably because any localized or cell type-specific cardiac up-regulation of this isoform was masked by its high basal expression.

We also analyzed the expression of molecules implicated in Nrp-mediated signaling pathways and others with a known role in zebrafish heart regeneration (Fig.S1). Consistent with previous work, *pdgfr β* , *pdgf-ab*, and *tgf β 1a* were all upregulated early after cryoinjury (Fig.S1) (Chablais and Jazwinska, 2012, Lepilina et al., 2006). Because Neuropilins are VEGF co-receptors, we examined the regulation of *vegfaa*, *vegfc*, and the VEGF receptors *kdrl* and *flt1*. In accordance with previous published data (Lien et al., 2006), *vegfc* was significantly upregulated following cardiac cryoinjury (Fig.S1), but we could not detect any significant change in the expression of *vegfaa*, *kdrl*, and *flt1*. In this context and at this time following the injury, *vegfc* is likely to be involved in inflammation and lymphangiogenesis as previously reported (Vieira et al., 2018).

Nrp1 protein expression in zebrafish ventricles, detected by Western blot, was observed as two bands of approximately 130 kDa and 150 kDa, corresponding to Nrp1a (916 amino acids) and Nrp1b (959 amino acids), respectively (Fig.1B). From 3 dpci and later, immunoblotting revealed an up-regulation of Nrp1 proteins in the injured hearts compared to sham-operated hearts, although this did not reach statistical significance (Fig.1B).

Neuropilins are upregulated in the epicardium and the endocardium following cryoinjury.

We used *in situ* hybridization to delineate the spatio-temporal expression of neuropilins following cryoinjury (Fig.1C). The specificity of the *nrp* RNA probes was initially analyzed in zebrafish embryos (Fig.S2), confirming expression patterns similar to previous observations in the literature (Martyn and Schulte-Merker, 2004, Yu et al., 2004). In control sham-operated adult zebrafish hearts, *nrp1a* was expressed by the epicardium and *nrp2b* was widely expressed by the myocardium (Fig.1C). One day post cryoinjury, *in situ* hybridization revealed mRNA up-regulation of all neuropilin isoforms in the epicardium and at the interface between the healthy myocardium and the injured tissue. At 3 dpci, both *nrp1a* and *nrp2a* were strongly and more widely upregulated by the activated epicardium, while *nrp1b* was expressed at the injury border. At 14 dpci, strong expression of *nrp1a* persisted in the epicardium adjacent to the injured area, and *nrp1b* was localized in the epicardium and the endocardium contiguous to the injured area. By 60 dpci, when heart regeneration was largely complete, expression of all *nrp* isoforms had returned to basal expression levels, which correlated with the gene expression data (data not shown).

To identify the Nrp1-expressing cells within the regenerating heart, we used co-immunofluorescent staining with specific endothelial, myocardial, and epicardial markers. In *tg(fli1a:EGFP)^{y1}* zebrafish, in which EGFP is specifically expressed in vascular endothelial cells, Nrp1 was co-expressed by *fli1a*-EGFP-expressing cells in sham hearts, consistent with expression of Nrp1 by coronary vessels and endocardium (Fig.2A, upper row). Nrp1 expression was also evident in *fli1a*-EGFP-expressing neovasculature and activated endocardium at the injured area in cryoinjured hearts (Fig.2A, lower row). These observations were supported by immunostaining of *tg(kdrl:mCherry)^{s896}* transgenic fish, in which mCherry expression is driven by the promoter for the endothelial VEGF receptor, *kdrl*.

Nrp1 immunostaining at 7 dpci in *tg(kdrl:mCherry)⁸⁹⁶* fish showed co-expression of mCherry-positive endocardium and Nrp1 (Fig.S3). Furthermore, neovascularization was observed as early as 1dpci in *tg(fli1a:EGFP)⁷* fish, consistent with previous findings (Marin-Juez et al., 2016), and these early neovessels also exhibited Nrp1 expression (Fig.S4). Nrp1 expression by tropomyosin-positive cardiomyocytes was low in control sham-operated hearts (Fig.2B, upper row). However, following cryoinjury, Nrp1 was expressed by a small population of cardiomyocytes located within the sub-epicardial layer at the lesion (Fig. 2B, lower row).

Epicardial expression of Nrp1 was examined in *tg(wt1b:EGFP)¹¹* zebrafish, in which EGFP expression is controlled by the promoter for the activated epicardial marker, Wilms' tumor 1b (*wt1b*). No detectable expression of EGFP was observed in sham-operated control hearts of *tg(wt1b:EGFP)¹¹* zebrafish (Fig.2C, upper row). In contrast, we observed high levels of colocalization between Nrp1 and EGFP in the epicardium covering the lesion in cryoinjured *tg(wt1b:EGFP)¹¹* zebrafish (Fig.2C, lower row). Furthermore, immunofluorescent staining of Wt1 and Nrp1 in cryoinjured Wild-Type zebrafish revealed a strong co-localization of Wt1 with Nrp1 in the epicardium adjacent to the injured area at 3dpci (Fig.S5).

***Nrp1a* mutant zebrafish (*nrp1a^{sa1485}*) display delayed heart regeneration following cryoinjury.**

The marked upregulation of Nrp1 mRNA and protein at the borders of healthy and cryoinjured myocardium, and the expression of Nrps by the endocardium and the activated epicardium suggested a role for Nrps in heart regeneration, particularly in the activated epicardium. Given the striking epicardial and endocardial expression of *nrp1a* after myocardial injury, we assessed the role of this isoform using the *nrp1a^{sa1485}* homozygous mutant zebrafish. This mutant carries a non-sense mutation (tyrosine to ochre, TAA) at

amino acid (aa) 206 (full length, 916 aa) in the second CUB domain of the *nrp1a* gene, resulting in the generation of a non-functional and truncated soluble N-terminal fragment (Fig.3A). Because the mutation occurs in the second CUB domain (also called a2), the binding of both Vegf and Semaphorin 3A (Sema3a) are predicted to be impaired in this mutant. The binding domain of other ligands such as Fgf, Pdgf, Tgf and Pdgf have not been fully characterized yet but it is known the deletion is likely to prevent receptor oligomerization or oligomerization and any resulting downstream signaling. Thus loss of *nrp1a* in these mutant fish, has been shown to induce axons to misproject to the dorsal and anterior dorsal zone protoglomerulus (Taku et al., 2016). *Nrp1a^{sa1485}* mutant fish were viable, born at expected Mendelian ratios (Fig.3B), displayed no obvious abnormal phenotype (Fig.S6A), and their body lengths and heart sizes were very similar to those of Wild-Type fish (Fig.S6B,C,D). In the *nrp1a^{sa1485}* fish, *nrp1a* endogenous basal expression was significantly reduced at both the mRNA ($p<0.0001$) (Fig.3C,D) and protein ($p<0.0001$) (Fig.3E,F) levels suggesting non-sense mediated decay, whereas the other neuropilin isoforms, *nrp1b*, *nrp2a* and *nrp2b*, were not significantly altered (*Nrp1b* $p=0.71$, *nrp2a* $p=0.09$, *nrp2b* $p=0.06$) (Fig.3C). AFOG staining was used to quantify the extent of the injury in both Wild-Type and *nrp1a^{sa1485}* fish over 60 days (Fig.4A). Following cryoinjury, the extent of lesions in *nrp1a^{sa1485}* and Wild-Type fish hearts was similar, affecting $22.6 \pm 5.2\%$ (S.E.M) and $25.2 \pm 5.5\%$ (S.E.M) of the ventricle, respectively (Fig.4B). By 60 dpci, the injured area was almost cleared and new healthy myocardium had replaced the damaged tissue in Wild-Type fish (Fig.4A,B). A reduction in the extent of heart repair was observed from as early as 7 dpci in the *nrp1a^{sa1485}* hearts compared with Wild-Type fish (Fig.4A, B). Whereas fibrin deposits (red staining in injury area) were mostly cleared from the injury scars in Wild-Type fish by 14 dpci, fibrin deposits were still evident at 30 and 60 dpci in the *nrp1a^{sa1485}* mutants (Fig.4A). Quantification of the size of the cryoinjuries revealed an overall significant delay in the

regeneration of mutant hearts in comparison to Wild-Type hearts (two-way ANOVA with Sidak's *post hoc* test for multiple comparisons, $p=0.0208$) (Fig.4B). Differences between *nrp1a*^{sa1485} and Wild-Type hearts were also observed in the regeneration of the cortical layer and wound closure. In Wild-Type zebrafish hearts regeneration typically led to formation of a continuous layer of cardiomyocytes enclosing the residual collagen scar, resulting in complete wound closure in the advanced stages of regeneration (30 and 60 dpci). In contrast, a larger proportion of mutant hearts at 30 and 60 dpci retained open wounds without complete closure of the lesion (Fig.4C). We also quantified the surface area of the epicardium normalized to the length of the injury border to determine relative epicardial thickness in Wild-Type and *nrp1a*^{sa1485} mutants (Fig.4D, E). We found that there was a modest but significant reduction in epicardial thickness in mutants heart at 3 dpci ($p=0.048$) suggesting a decrease in epicardial activation.

Revascularization of the cryoinjured heart tissue is impaired in *nrp1a*^{sa1485} mutant zebrafish

The impact of loss of functional Nrp1 on revascularization in cryoinjured hearts was examined by generating *nrp1a*^{sa1485} mutants in *tg(fli1a:EGFP)^{y1}* zebrafish, in which endothelial-specific GFP expression is driven by the *fli1a* promoter. Angiogenesis occurs rapidly following heart injury in zebrafish, with a marked neovascular response evident as early as 1 dpci (Marin-Juez et al., 2016). Therefore, we compared the extent of angiogenesis in control *tg(fli1a:EGFP)^{y1}* and *nrp1a*^{sa1485} *tg(fli1a:EGFP)^{y1}* mutant zebrafish at 1 and 3 dpci. GFP-positive vessels were clearly identified within the injured area at 1 and 3 dpci in both Wild-Type and mutant zebrafish (Fig.5A and B). However, the *nrp1a*^{sa1485} mutation was associated with a significant, 3 to 4-fold reduction in the extent of neovascularization. At 1 dpci, the average number of coronary vessels found within each microscopic field

(32,625 μm^2) of the injury was 13 in Wild-Type zebrafish compared to 3 in *nrp1a^{sa1485}* mutant zebrafish ($p=0.0087$) (Fig.5C). At 3 dpci, the average number of newly formed vessels within the injured area per microscopic field of the injury was 19 in Wild-Type zebrafish compared to 6 in *nrp1a^{sa1485}* mutant zebrafish ($p=0.0258$) (Fig.5D).

We further examined angiogenesis in cryoinjured hearts from Wild-Type and *nrp1a^{sa1485}* mutant zebrafish at 3 dpci by immunofluorescent staining for the endothelial-specific marker Tie2. Use of Tie2 immunostaining as a reliable method to identify neovessels was verified by comparing the number of vessels within the cryoinjury of *tg(fli1a:EGFP)^{y1}* zebrafish identified either using Tie2 or GFP immunostaining (data not shown). Similar to the results discussed above, obtained with GFP staining of the *tg(fli1a:EGFP)^{y1}* transgenic line, the *nrp1a^{sa1485}* mutation was associated with a significant reduction in the extent of neovascularization as quantified by Tie2 staining of the neovessels (Fig.S7). At 3dpci, the average number of coronary vessels found within each microscopic field of the injury was reduced by nearly 50% in *nrp1a^{sa1485}* mutant compared with Wild-Type zebrafish ($p=0.0058$).

Epicardial activation is inhibited in *nrp1a^{sa1485}* hearts

We next addressed whether the delayed heart regeneration caused by loss of functional Nrp1 in *nrp1a^{sa1485}* zebrafish could be due to an impact on activation of the epicardium and subsequent epicardial regeneration. Consistent with this possibility, our data showed epicardial upregulation of Nrp1 adjacent to the injured area, indicated by strong co-localization of Nrp1 with Wt1b, a specific marker for epicardial activation, at 3 dpci (see Fig.2, Fig.S8A), a time coincident with occurrence of robust epicardium activation during the reparative phase of the regeneration process (Gonzalez-Rosa et al., 2017). To investigate this hypothesis further, we examined epicardial activation in cryoinjured hearts of Wild-Type

and *nrp1a*^{sa1485} mutant *tg(wt1b:EGFP)^{li1}* zebrafish. Analysis of hearts at 3 dpci revealed a strong decrease in GFP expression under the control of the *wt1b* promoter in the *nrp1a*^{sa1485} mutants as compared to Wild-Type (Fig.6A). Quantification of the percentage of GFP-positive cells within the epicardium covering the cryoinjured area confirmed a marked and significant reduction in the number of GFP-expressing activated epicardial cells in *nrp1a*^{sa1485} mutants (14.08% versus 26.4% for *nrp1a*^{sa1485} and Wild-Type, respectively; $p=0.0071$) (Fig.6B). We also investigated whether loss of functional *nrp1a* impaired the proliferation of activated epicardial cells, using PCNA staining (Fig.6C). *Nrp1a*^{sa1485} hearts showed no statistically significant reduction in the proportion of proliferating epicardial cells expressing *wt1b* compared to Wild-Type hearts (37.25% versus 47.68% for *nrp1a*^{sa1485} and Wild-Type, respectively; $p=0.34$) (Fig.6D). Because WT1 is known to regulate epicardial EMT through the retinoic acid signaling pathway (von Gise et al., 2011), we investigated *raldh2* (*aldh1a2* – Zebrafish Information Network) gene and protein expression in 3 dpci hearts of Wild-Type and *nrp1a*^{sa1485} fish (Fig.7). *Aldh1a2* was upregulated following cryoinjury but there was no significant difference between *aldh1a2* gene expression in Wild-type and *nrp1a*^{sa1485} hearts ($p=0.99$ for uninjured, $p=0.97$ for 3 dpci) (Fig.7C). We also stained *aldh1a2*-positive cells in sections of 3 dpci heart (Fig.7A) and quantified these cells in the endocardium, as well as the number of proliferating (PCNA-positive) *aldh1a2*-positive cells (Fig.7B). Our results revealed no significant difference in *aldh1a2*-positive cells between Wild-Type and *nrp1a*^{sa1485} mutant hearts ($p=0.43$ *aldh1a2*+ cells, $p=0.59$ PCNA+ *aldh1a2*+ cells) (Fig.7B).

The gene expression of other known EMT effectors such as smooth muscle actin (*sma*), *tbx18*, *tgf β* receptors (*tgfbr1a*), *fgf*-receptor 2 and *fgf*-receptor 4 (*fgfr2* and *fgfr4*) were unchanged in *nrp1a^{sa1485}* as compared with Wild-type hearts (data not shown). It can be hypothesized that *nrp1b* may compensate for *nrp1a* inactivation in these pathways. Moreover, it is to be noted that, the *nrp1a^{sa1485}* mutation did not result in an upregulation of the other neuropilin isoforms following cryoinjury (Wild-Type vs *nrp1a^{sa1485}* for *nrp1b* $p=0.4674$, *nrp2a* $p=0.9026$, *nrp2b* $p=0.051$) (Fig.S9).

Another known epicardial signaling effector downstream of WT1 is β -catenin (von Gise et al., 2011). To investigate the possibility that NRP1 might be implicated in the regulation of β -catenin expression, we used the rat epicardial cell line described by Wada *et.al* (2003) (a generous gift from Dr Nicola Smart) and examined the effect in these cells of an adenovirus encoding for a shRNA targeting NRP1 or a control adenovirus. We found that, after 48 hours infection, there was a down-regulation of β -catenin in NRP1 depleted cells in comparison to control (Fig.7D).

Additionally, we examined whether cardiomyocyte proliferation was affected in *nrp1a^{sa1485}* mutant hearts by determining the number of Myocyte Enhancer Factor 2C (Mef2C)-positive cells that were also PCNA-positive. We counted double positive cells both at the border and within the injured area and found that there was no significant difference in the number of proliferating cardiomyocytes ($p=0.065$ and $p=0.54$ respectively) (Fig.S10A,B).

Epicardial expansion and activation of cryoinjury-induced *nrp1a*^{sa1485} heart explants is impaired

We next examined the role of Nrp1 in epicardial activation in an *ex vivo* heart explant model (Kim et al., 2012). Immunofluorescent staining of Nrp1 in explants of Wild-Type ventricular apexes collected at 5 dpci and cultured *in vitro* for 7 days showed perinuclear, cytoplasmic and membrane localization (Fig.S8B). Epicardial culture from *tg(wt1b:EGFP)^{li1}* ventricles showed that *Wt1b:EGFP* expression was variable in these explants and was strongly expressed by a subpopulation of explanted epicardial cells (top row, Fig.8C).

As shown in Fig.S11A and C, *wt1b:EGFP* expression was increased in explant outgrowths from cryoinjured as compared with those from control, sham-operated hearts and, similar to resected hearts (Kim et al., 2012), explants from Wild-Type cryoinjured hearts generated greater outgrowth in comparison with those from Wild-Type sham-operated hearts ($p=0.0001$) (Fig.8A,B). We next assessed the role of Nrp1a in injury-induced epicardial activation using epicardial explants from Wild-Type and *nrp1a*^{sa1485} *tg(wt1b:EGFP)^{li1}* zebrafish. Epicardial outgrowths of cryoinjury-induced *nrp1a*^{sa1485} heart explants were markedly impaired compared with Wild-Type explants ($p=0.0009$) (Fig.8A,B) and we observed no significant difference between the outgrowths of either Wild-Type or *nrp1a*^{sa1485} mutant sham-operated hearts ($p=0.93$ and $p=0.99$, respectively). Furthermore, *nrp1a*^{sa1485} explants showed a marked decrease of GFP expression in comparison with Wild-Type fish, both at the edge of the explant and within the region closest to the heart (Fig.8C), providing further support for a loss of epicardial activation in the *nrp1a*^{sa1485} mutants in comparison to Wild-Type hearts. This confirmed our observations of reduced GFP-positive epicardial cells in sections from cryoinjured *nrp1a*^{sa1485} *tg(wt1b:EGFP)^{li1}* zebrafish hearts (Fig. 6A,B). The less marked effect of the *nrp1a*^{sa1485} mutant on epicardial activation observed in heart sections as compared to cultured epicardial explants, may reflect compensatory effects of

other cell types (such as fibroblasts, immune cells) secreting paracrine factors to drive epicardial activation, and partially rescue the *nrp1a* mutant phenotype *in vivo*, which are lacking in epicardial cultures. Cao et al. (2017) recently showed that transient hypertrophy and polyploidization play an important role in epicardial regeneration following induced cell death in the zebrafish heart (Cao et al., 2017). To investigate whether changes in cell size or ploidy played a role in the effect of the *nrp1a*^{sa1485} mutant on injury-induced epicardial regeneration, we also analyzed the size and the ploidy of the cells at the center and at the edge of the ventricular explant (Fig.8D). There was no significant difference in cell size, neither at the center ($p=0.53$) nor at the edge of the explant ($p=0.57$), but we observed a reduction in the number of polyploid cells at the edge of the explant in the *nrp1a*^{sa1485} mutants in comparison to Wild-Type hearts ($p=0.016$), while there was no difference in the center of the explant ($p=0.46$).

Discussion:

Epicardial activation and angiogenesis are processes essential for zebrafish heart regeneration following injury. During these processes, revascularization and injury-induced epicardial-to-mesenchymal transition (EMT) are driven by Vegf, Fgf, and Pdgf (Chablais and Jazwinska, 2012, Kim et al., 2010, Lepilina et al., 2006), which are all ligands for the cell surface receptor Nrp1. Although it is known that NRPs are essential for angiogenesis and increasingly implicated in EMT in other contexts in mammalian species (Adham et al., 2014, Chu et al., 2014, Kawasaki et al., 1999), their role has not previously been characterized in zebrafish heart regeneration. Here, we show for the first time that *nrp1* and *nrp2* are upregulated in response to cardiac injury and that *nrp1a* plays a role in both revascularization and epicardial activation and migration, processes that are essential for the regeneration of the zebrafish heart.

Nrp1a, *nrp1b*, *nrp2a*, and *nrp2b* mRNAs were all strongly upregulated in the zebrafish heart 1-3 days after cryoinjury, coinciding with the time of epicardial activation, which occurs very early following cardiac injury (Cao and Cao, 2018). Increased protein expression of both Nrp1 isoforms also occurred 3-14 days following cryoinjury, further supporting the conclusion that Nrp1 is upregulated in the early regenerating heart. Our results also revealed a striking spatio-temporal upregulation of the *nrp* isoforms. Specifically, *nrp2a* was strongly upregulated in the endocardium (1dpci) and in the epicardium proximal to the injury (3 dpci), whereas *nrp1a* was strongly upregulated in the same regions at 1, 3 and 14 dpci. These findings support a sustained role for these isoforms in heart regeneration, particularly in the epicardial activation phase, which takes place during the first 3-7 days of regeneration. At present, the lack of suitable reagents made further detailed studies of Nrp2 problematic. However, a role for Nrp1 in epicardial activation in response to heart injury was further supported by immunofluorescent staining demonstrating co-localization of Nrp1 with both endogenous Wt1 and with EGFP under the control of the *wt1b* promoter, an embryonic gene that is upregulated following cardiac injury and is an activated epicardium marker (Peralta et al., 2014, von Gise et al., 2011).

Analysis of mutant *nrp1a*^{sa1485} fish lacking expression of full-length Nrp1a provided direct evidence that Nrp1a is required for zebrafish heart regeneration. *Nrp1a*^{sa1485} fish displayed no morphological or pathological phenotype. It was previously reported that knockdown of *nrp1* using morpholino oligomers produces a lethal phenotype in zebrafish embryos (Martyn and Schulte-Merker, 2004). The absence of embryonic lethality in *nrp1a*^{sa1485} fish as compared with *nrp1a* morpholino knock-down probably reflects redundancy due to adaptive mechanisms relying on compensation by *nrp1b* and may also suggest morpholino off-target effects in *nrp1a* morphants (Kok et al., 2015). The genetic robustness of the *nrp1a*^{sa1485} mutant fish could also be due to the allele displaying mutant

mRNA decay (El-Brolosy et al., 2019), although we could not detect any compensative up-regulation of the other neuropilin related genes. Following cardiac damage, *nrp1a*^{sa1485} mutants exhibited a significantly reduced regenerative response in comparison with Wild-Type controls. The importance of *nrp1a* for heart regeneration was demonstrated by the delayed and incomplete removal of fibrin deposits essential for the scar resolution process in *nrp1a*^{sa1485} mutant fish. Given that myocardial proliferation was not significantly affected in *nrp1a*^{sa1485} mutant fish, delayed wound closure in *nrp1a*^{sa1485} fish likely indicates a failure of the myocardium to migrate efficiently towards the subepicardial layer after cryoinjury. Together, these findings provide strong evidence that *nrp1a* is required for zebrafish heart regeneration following cryoinjury. Since we examined the loss of only the *nrp1a* isoform, due to anticipated embryonic lethality of a double *nrp1a* and *nrp1b* knock out, it is possible that Nrp1 loss may have an even more prominent role in heart regeneration in species that did not undergo genome duplication. Furthermore, our data also showed epicardial expression of *nrp2a* and *nrp2b*, indicating a possible role of Nrp2 isoforms in epicardial activation and heart regeneration, something that warrants further investigation.

Activation of the epicardium and subsequent regeneration involves multiple cellular processes, including cell migration, proliferation, and EMT. It is well established that NRP1 modulates cell migration in diverse mammalian cell types (Evans et al., 2011, Pellet-Many et al., 2008, Wang et al., 2003). The conclusion that *nrp1a* is important for zebrafish epicardial migration is supported by our finding that *ex vivo* outgrowth from epicardial explants of *nrp1a*^{sa1485} hearts was also impaired. Furthermore, we observed a reduction in polyploidization of explanted epicardial cells in *nrp1a*^{sa1485} hearts, a process which has recently been implicated as an important mechanism underlying epicardial regeneration following induced cell death in zebrafish (Cao et al., 2017). In contrast, we observed no effect on epicardial cell proliferation in cryoinjured *nrp1a*^{sa1485} hearts, indicating that *nrp1a*

is not critical for proliferation, in line with studies of NRP1 function in primary mammalian cells. However, we cannot preclude the possibility that one of the other *nrp* isoforms has a role in epicardial proliferation.

Reduced *in vitro* expansion of *nrp1a*-deficient epicardial cells is likely due to impaired detection of cellular cues promoting migration. Consistent with this possibility, we observed upregulation of *nrp* isoform expression concomitant with increased expression of *tgfb*, *pdgfab*, *vegfc*, and the receptor *pdgfrb*, chemotactic factors and receptors implicated in zebrafish heart regeneration, and also shown to act as ligands and co-receptors for NRP1 in mediating mammalian cellular functions. Interestingly, using the (*wt1b:EGFP*)^{li1} transgenic fish line, we also noted that the *nrp1a*^{sa1485} epicardial cells failed to re-express the *wt1b* embryonic marker *in vitro* as well as *in vivo*. Previously, Gonzalez-Rosa *et al.* (2012) demonstrated the importance of the *wt1b:EGFP*⁺ epicardial derived cells (EPDCs) in the regeneration process which gave rise to perivascular fibroblasts and myofibroblasts and also participated in the regeneration process by secreting essential pro-angiogenic paracrine factors (Gonzalez-Rosa *et al.*, 2012). The decreased number of GFP-expressing (and therefore *wt1b*⁺) EPDCs in the *nrp1a*^{sa1485} hearts therefore likely explains their delayed regeneration in comparison to WT hearts. It is known that WT1 regulates epicardial EMT through β -catenin and retinoic acid signaling pathways in mice (von Gise *et al.*, 2011) and, that interruption of Wnt/ β -catenin signaling in epicardial cells disrupts EMT and compromises cardiac function after acute cardiac injury (Duan *et al.*, 2012). Although we observed an upregulation of *aldh1a2* gene and protein expression in cryoinjured hearts in both *nrp1a*^{sa1485} Wild-Type fish, there was no significant difference in either gene or protein expression at 3 dpci, indicating that Nrp1 functions in epicardial regeneration via *aldh1a2*-independent pathways downstream of Wt1b.

Our study also revealed Nrp1 upregulation following cardiac damage by the activated endocardium, which undergoes endothelial to mesenchymal transition (endoMT) in response to injury (Kikuchi et al., 2011), by the neovasculature, and by some subepicardial cardiomyocytes known to be a primary source of new myocardium (Kikuchi et al., 2010). Following injury, these cells acquire a migratory phenotype to contribute to the regenerative processes in the heart. It is likely that the *nrp1a^{sa1485}* endocardium is less able to perform this function, further contributing to the overall observed delay in regeneration.

Nrp1 has an essential role in angiogenesis in mammalian and zebrafish development, and is required in post-natal and adult angiogenic processes (Lee et al., 2002, Soker et al., 1998). Marin-Juez *et al.* recently reported transient upregulation of *vegfaa* at 1 dpci, with a return to baseline expression by 3 dpci, and showed an important role for *vegfaa* in inducing rapid early revascularization of the injured heart (Marin-Juez et al., 2016). Our data showed a trend towards increased *vegfaa* expression at 1 dpci, using RT-qPCR, although this was not statistically significant, unlike the concomitant changes in *nrp1*. Similarly to its major endothelial ligand *vegfaa*, the main Nrp1 co-receptor *kdrl* was also not significantly upregulated. However, we observed revascularization of the injured area as early as 1 dpci, in line with previous findings (Marin-Juez et al., 2016). These neovessels also expressed Nrp1 and studies in *nrp1a^{sa1485}* mutants co-expressing *fli1a:EGFP^{y1}* demonstrated a role for *nrp1a* in the revascularization of the cryoinjured area. As expected, the loss of Nrp1a reduced the number of neovessels in the regenerating heart of *nrp1a^{sa1485}* fish in comparison to their Wild-Type counterparts. While our findings are consistent with a role for Nrp1 in mediating Vegfaa-driven angiogenesis in the regenerating heart, recent findings indicate that the role of NRP1 in developmental angiogenesis may be largely independent of VEGF, since NRP1 mutations which prevent VEGF-A binding impair post-natal angiogenesis but are compatible with normal embryonic development (Fantin et al., 2015, Fantin et al., 2014).

It is therefore plausible that the angiogenic role of Nrp1 in revascularization of the regenerating zebrafish heart is also mediated via binding of other ligands to Nrp1 (Ball et al., 2010, Pellet-Many et al., 2011, West et al., 2005).

This study establishes a novel role for Nrp1 in epicardial activation and angiogenesis during zebrafish heart regeneration following injury. Further work to elucidate the extracellular ligands for Nrp1 in epicardial and endothelial cells and the signaling pathways that mediate its role further downstream will shed new light on the mechanisms involved in epicardial activation in heart regeneration.

Materials and Methods:

An extended version of the Material and Methods section is available as supplementary information online.

Zebrafish husbandry and cryoinjury

Procedures were performed in accordance with the Animals (Scientific Procedures) Act 1986, and husbandry was regulated by the central University College London fish facility. Cryoinjury procedure was carried out as described in (Gonzalez-Rosa and Mercader, 2012), and more details are provided in the supplementary 'Materials and Methods'.

RT-qPCR

Ventricles from corresponding time-points and treatments were pooled for RNA extraction using the RNeasy Mini Kit (Qiagen). RNA was reverse transcribed using the QuantiTect® Reverse Transcription Kit (Qiagen). All primers (details are described in table S1) and standards were purchased from qStandard© and absolute qPCR were performed by qStandard©.

Histological procedures

In situ hybridization, immunofluorescence and Acid Fuchsin Orange G (AFOG) procedures are described in the supplementary information file.

Fibrin gel heart explants

In vitro epicardial cell outgrowth experiments were performed as previously described (Kim et al., 2012b). The apex of cryoinjured and sham-operated zebrafish hearts were isolated 5 days post-surgery and placed firmly on set fibrin gel matrices, ensuring epicardial surface contact with the gel. Medium was changed every 2 days and cells were cultured for 7 days before harvesting epicardial outgrowths for protein extraction or immunofluorescence imaging.

Statistical analysis

All results are presented as mean \pm standard error of the mean (S.E.M). Experimental repeat *n* values are indicated as individual data points in graphs or specified in figure legends. When samples were pooled to produce 1 *n* (e.g. for qPCR) or several sections per tissue were analyzed, this is indicated in figure legends or the main text. All data were visualized and analyzed using Graphpad prism 6.0 software. All data were first tested for normal distribution using histograms and the D'Agostino-Pearson Omnibus test. Comparisons of more than 2 groups, e.g. AFOG cryoinjury area and qPCR data, were analyzed for statistical significance using one-way ANOVA with pre-selected pairs and the Sidak's *post hoc* test for multiple comparisons and, for overall effect, a two-way ANOVA with Tukey post-test was conducted. Student's unpaired *t*-test analysis was applied to all other data sets, (*i.e.* for data sets comparing only 2 groups). The Mann-Whitney test was applied for comparisons of two groups if data was not normally distributed. Statistical significance values are indicated in

figure legends and in the main text. Data were considered significant for $p < 0.05$, indicated by single asterisk * in graphs, two ** indicate $p < 0.01$, three *** indicate $p < 0.001$ and four **** indicate $p < 0.0001$. All immunostaining data was analyzed by a blinded investigator.

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Figures

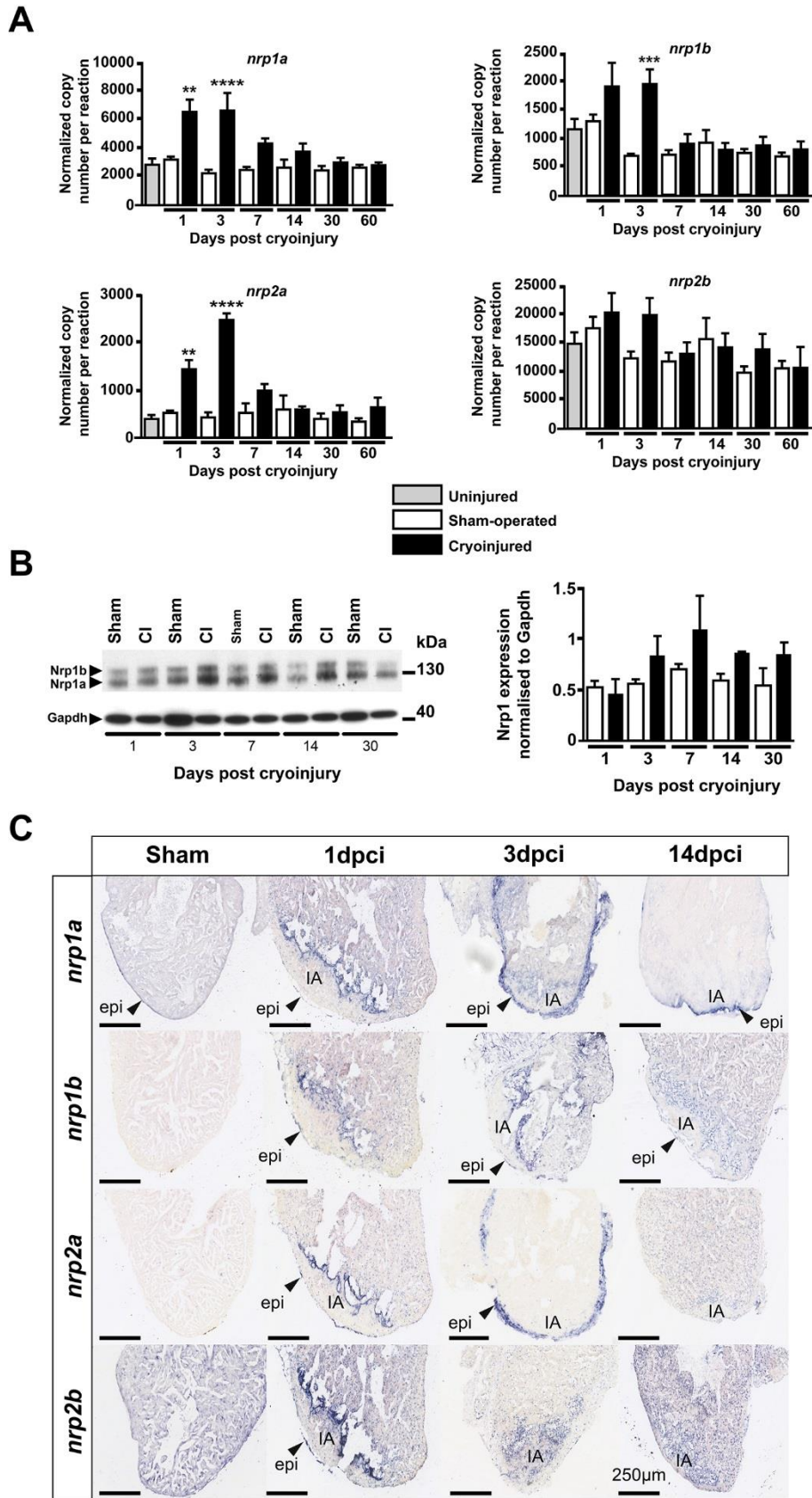


Figure 1 Neuropilins are upregulated during zebrafish heart regeneration.

(A) Absolute quantitative PCR analysis of neuropilins at 1, 3, 7, 14, 30, and 60 days following cryoinjury or sham surgery. Basal expression was evaluated in uninjured hearts of age-matched Wild-Type fish. Bars represent normalized copy number per reaction means \pm S.E.M, ** $p < 0.01$, *** $p < 0.005$, **** $p < 0.001$ (one-way ANOVA with Sidak's *post hoc* test for multiple comparisons of $n = 4$ or 5 with each n being a pool of 5 ventricles). **(B, left)** Adult zebrafish ventricle lysates 1, 3, 7, 14 and 30 days following surgery immunoblotted for Nrp1 and Gapdh. **(B, right)** Western blot quantification of Nrp1 protein in sham and cryoinjured ventricles 1, 3, 7, 14 and 30 days following surgery ($n = 4$ or 5 , with each n being a pool of 3 ventricles). **(C)** *In situ* hybridization with digoxigenin-labelled anti-sense riboprobes were used to detect *nrp* isoforms in sham-operated and cryoinjured adult zebrafish hearts 1, 3 and 14 days post-cryoinjury (dpci). IA– injured area, epi– epicardium. Arrows indicate gene expression within the epicardium. Scale bar 250 μ m ($n \geq 3$).

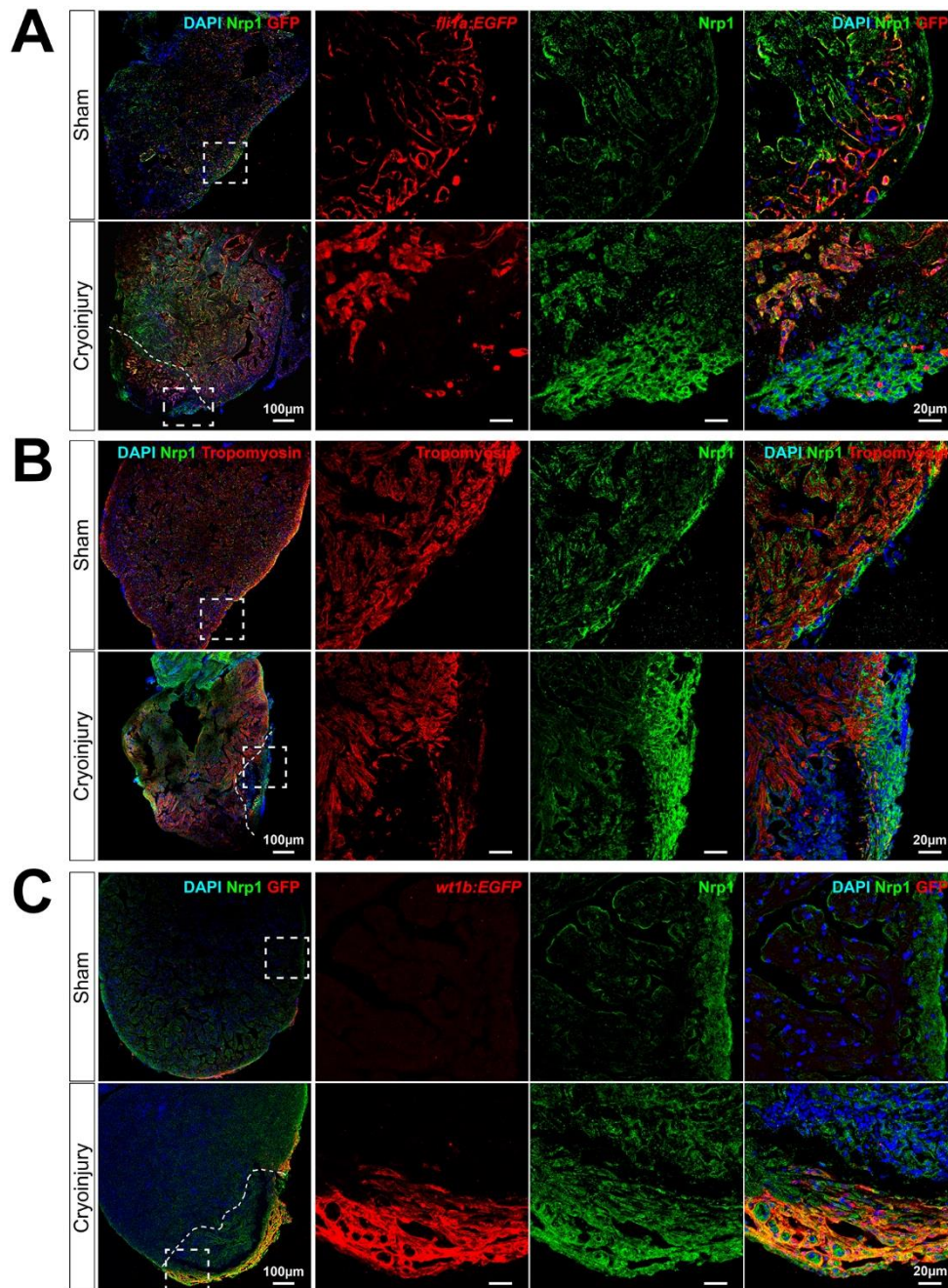


Figure 2 Nrp1 is expressed by the endocardium and the epicardium in sham and cryoinjured hearts.

Immunostaining of 7 days post sham-operated (upper rows) and cryoinjured (lower rows) hearts. *Tg(fli1a:EGFP)^{y1}* (A), Wild-Type fish immunostained for tropomyosin (B), and *tg(wt1b:EGFP)^{li1}* (C) zebrafish hearts were used to identify endothelium, myocardium and activated epicardium, respectively. Overlay of the two colors are displayed with DAPI nuclei staining. White dotted boxes denote location of enlarged images and dashed line indicate injury interface. ($n \geq 3$)

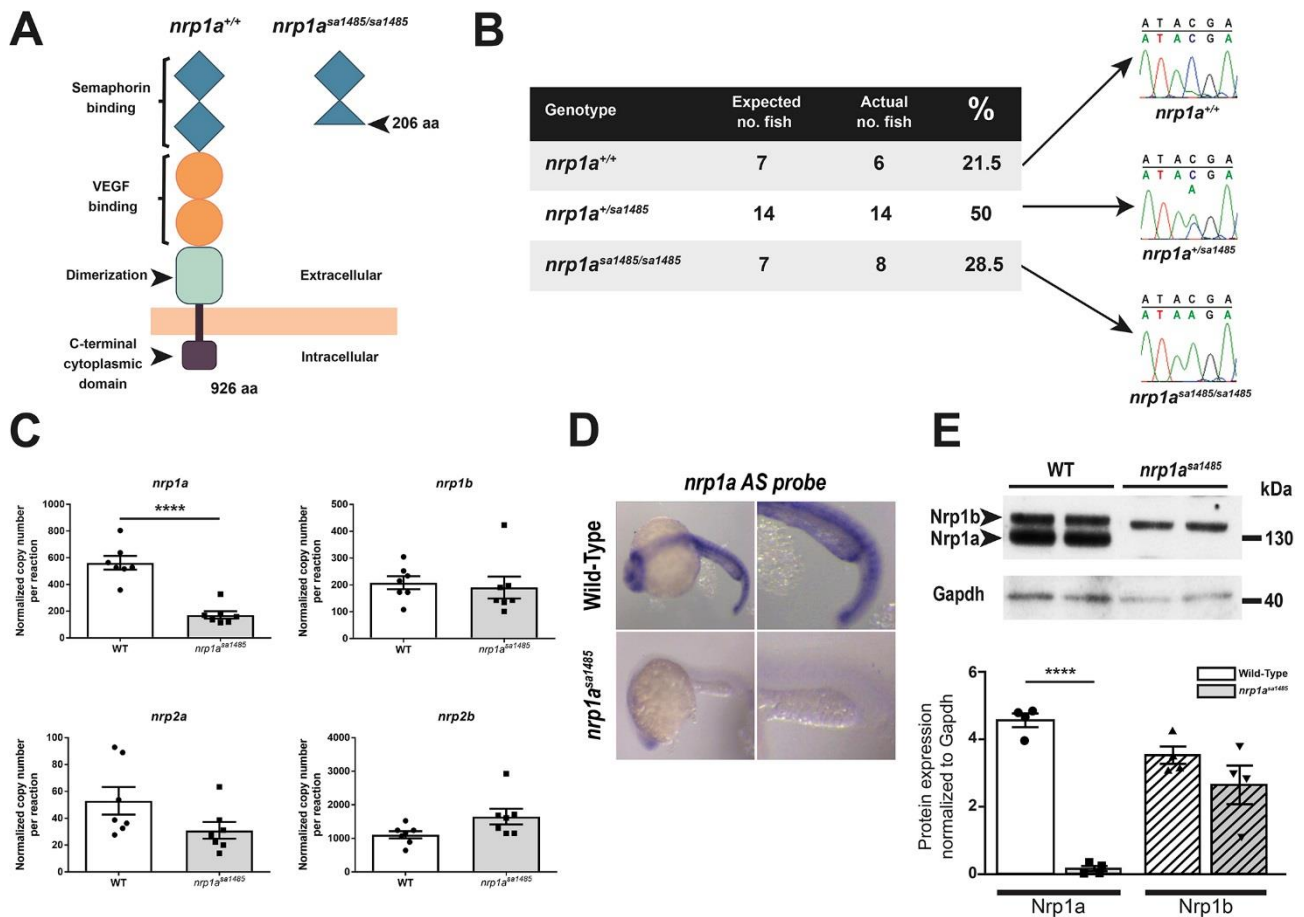


Figure 3 *nrp1a*^{sa1485} mutant fish characterization

(A) Diagram of Wild-Type (WT) (left) and *nrp1a*^{sa1485} mutant fish (right) Nrp1a structure. The point mutation results in the generation of a premature stop codon at amino acid 206 resulting in a truncated Nrp1a fragment. Blue diamonds - CUB (a1 and a2) domains, orange circles – FA58C (b1 and b2) domains, green square – MAM domain, brown square – C-terminal domain. **(B)** Sequencing chromatograms of Wild-Type fish, heterozygous *nrp1a*^{sa1485/+} and homozygous *nrp1a*^{sa1485/sa1485} mutant fish. An early stop codon (nonsense mutation) TAA, replaces the Wild-Type TAC codon at amino acid 206. The genotypes of 14 zebrafish embryos 48 hours post fertilization (hpf) were compared against the expected Mendelian ratio after heterozygous fish incross. **(C)** Absolute RT-qPCR of Wild-Type (white bar) or *nrp1a*^{sa1485} homozygous mutant (grey bar) uninjured adult zebrafish hearts under basal conditions. Results are represented as means of normalized copy numbers per reaction ± S.E.M (error bars) **** $p < 0.0001$ with two-tailed t -test of $n = 7$ with each n being a pool of 3 ventricles. *nrp1a* expression is significantly decreased in *nrp1a*^{sa1485} samples suggesting non-sense mediating decay. **(D)** *Nrp1a* anti-sense (AS) *in situ* hybridization of Wild-Type (upper row) or *nrp1a*^{sa1485} homozygous mutant (lower row) embryos 24 hpf. *Nrp1a* expression is clearly decreased in *nrp1a*^{sa1485} samples. **(E) (upper blot)** Western blot of Wild-Type (WT) or *nrp1a*^{sa1485} homozygous mutant uninjured adult zebrafish ventricle lysates. Lysates were immunoblotted with an antibody targeting the Nrp1 cytoplasmic domain and Gapdh. Note the absence of C-terminus detection of Nrp1a in the *nrp1a*^{sa1485}

samples. **(Lower graph)** Western blot quantification of Nrp1a and Nrp1b normalized to Gapdh (one-way ANOVA with Sidak's *post hoc* test for multiple comparisons of $n=4$), confirming significant reduction of Nrp1a expression ($p<0.0001$), whereas Nrp1b is not significantly different between Wild-Type and *nrp1a*^{sa1485} ($p=0.219$).

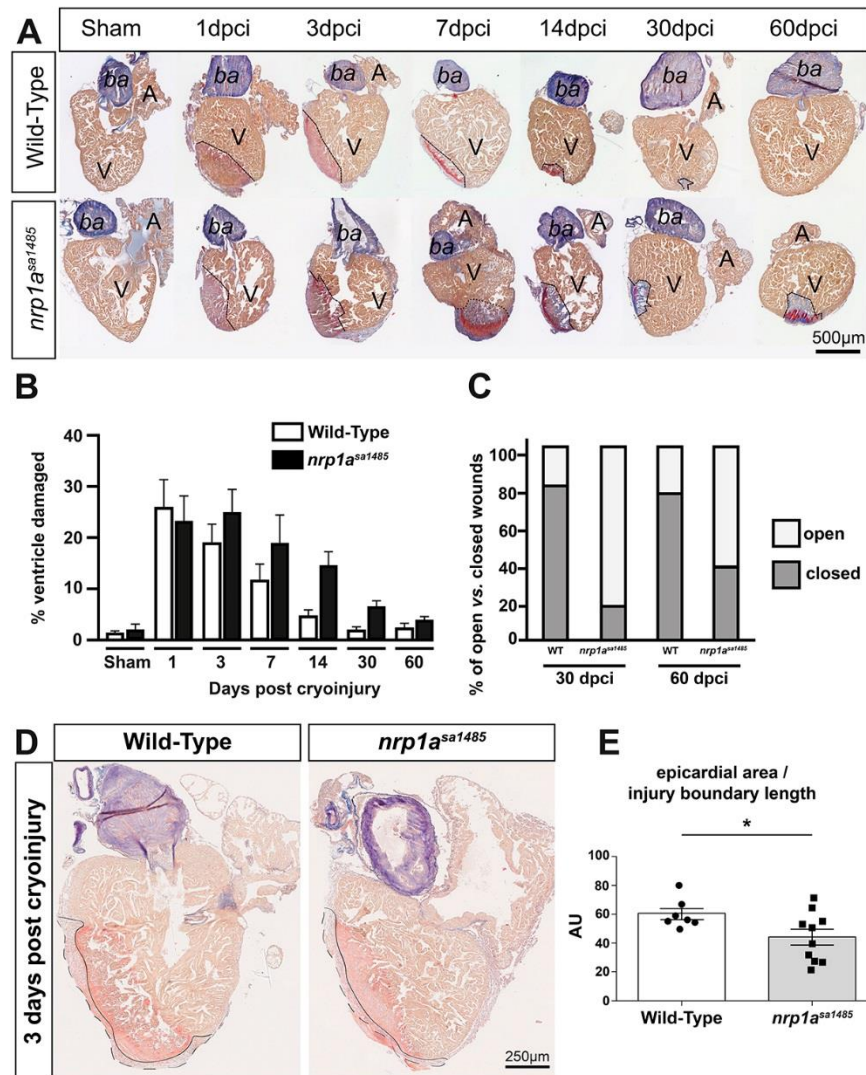


Figure 4 Cardiac regeneration is delayed in *nrp1a^{sa1485}* mutants following cryoinjury. (A) Heart sections from Wild-Type and *nrp1a^{sa1485}* mutant fish obtained at 1, 3, 7, 14, 30 and 60 dpci and stained with AFOG to identify the injured region. (B) Cryoinjured areas were measured and represented as mean percentage of total ventricle area \pm S.E.M (two-way ANOVA with Sidak's *post hoc* test for multiple comparisons of $n = 4-8$) $*p < 0.05$. (C) The compact myocardium recovers following cryoinjury and encases the scar tissue, this is defined as a closed wound; whereas a scar exposed to the surface is defined as an open wound. Wound closure was examined in Wild-Type and *nrp1a^{sa1485}* mutant hearts at 30 and 60 dpci and open vs closed wounds were expressed as percentage of total number of hearts ($n = 4-8$), (D) AFOG staining of Wild-Type and *nrp1a^{sa1485}* mutant hearts at 3 dpci used to evaluate epicardial thickness and injury boundaries to calculate the epicardial area normalized to the length of the injury boundary (continuous line) (E) (two-tailed *t*-test of $n=7$ for Wild-Type and $n=10$ for *nrp1a^{sa1485}* hearts, $*p < 0.05$) A– atrium, ba– *bulbus arteriosus*, V– ventricle.

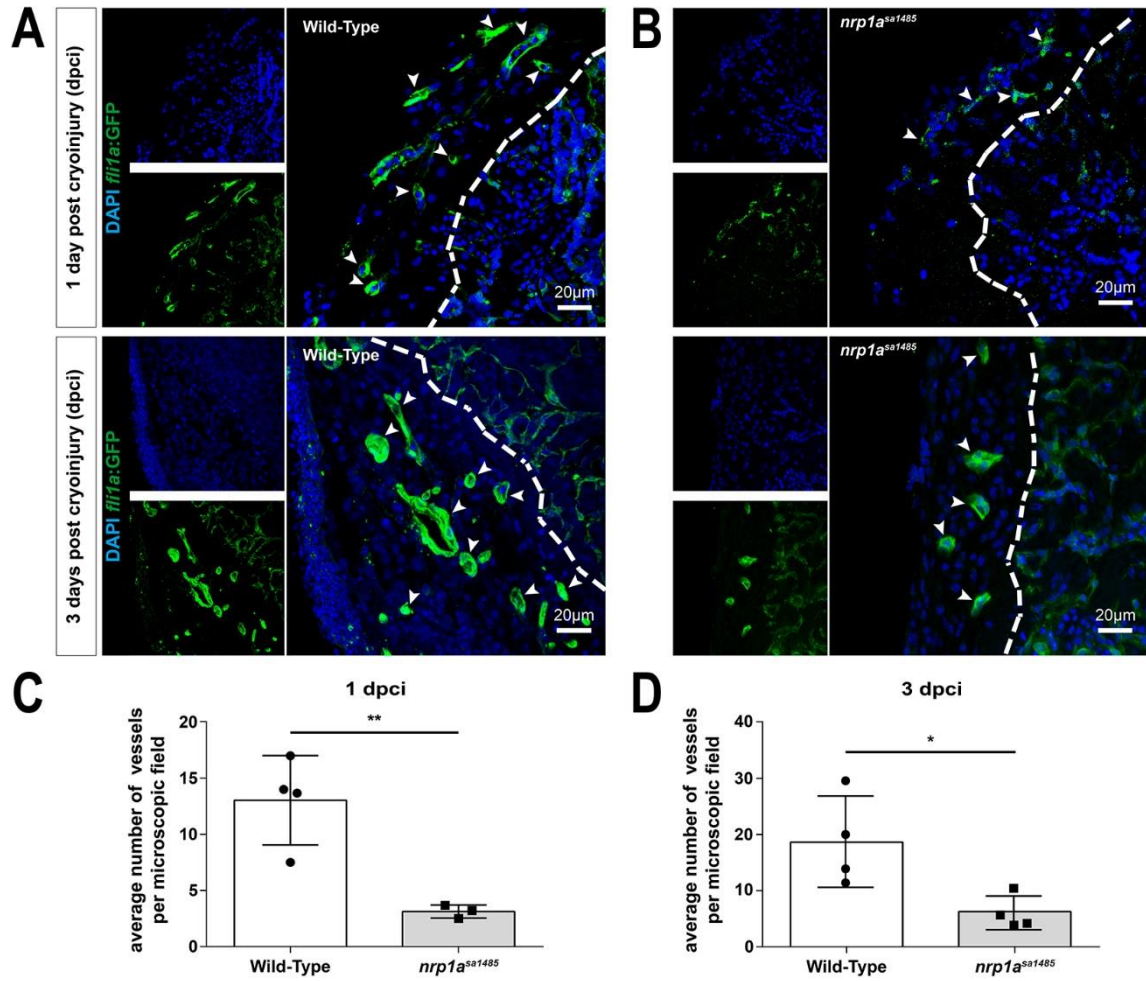


Figure 5 Neovascularization of the cryoinjured area is impaired in *nrp1a^{sa1485}* mutants.

Blood vessels in either Wild-type **(A)** or *nrp1a^{sa1485}* **(B)** *tg(fli1a:EGFP)^{y1}* zebrafish at 1 day (upper row) and 3 days (lower row) post cryoinjury were identified in heart sections by GFP immunofluorescence in vascular structures. Heart sections were also counterstained with DAPI. The dashed white line delineates the border of the area of injury. White arrows indicate blood vessels. Quantification of GFP-positive vessels were then quantified at **(C)** 1dpci (two-tailed *t*-test of $n = 3$ and 4) $** p < 0.01$ and **(D)** 3dpci (two-tailed *t*-test of $n = 4$) $* p < 0.05$, for Wild-Type *versus* *nrp1a^{sa1485}* hearts; individual data points represent individual hearts, each averaged from vessel counts in 3-4 different sections covering the injury site.

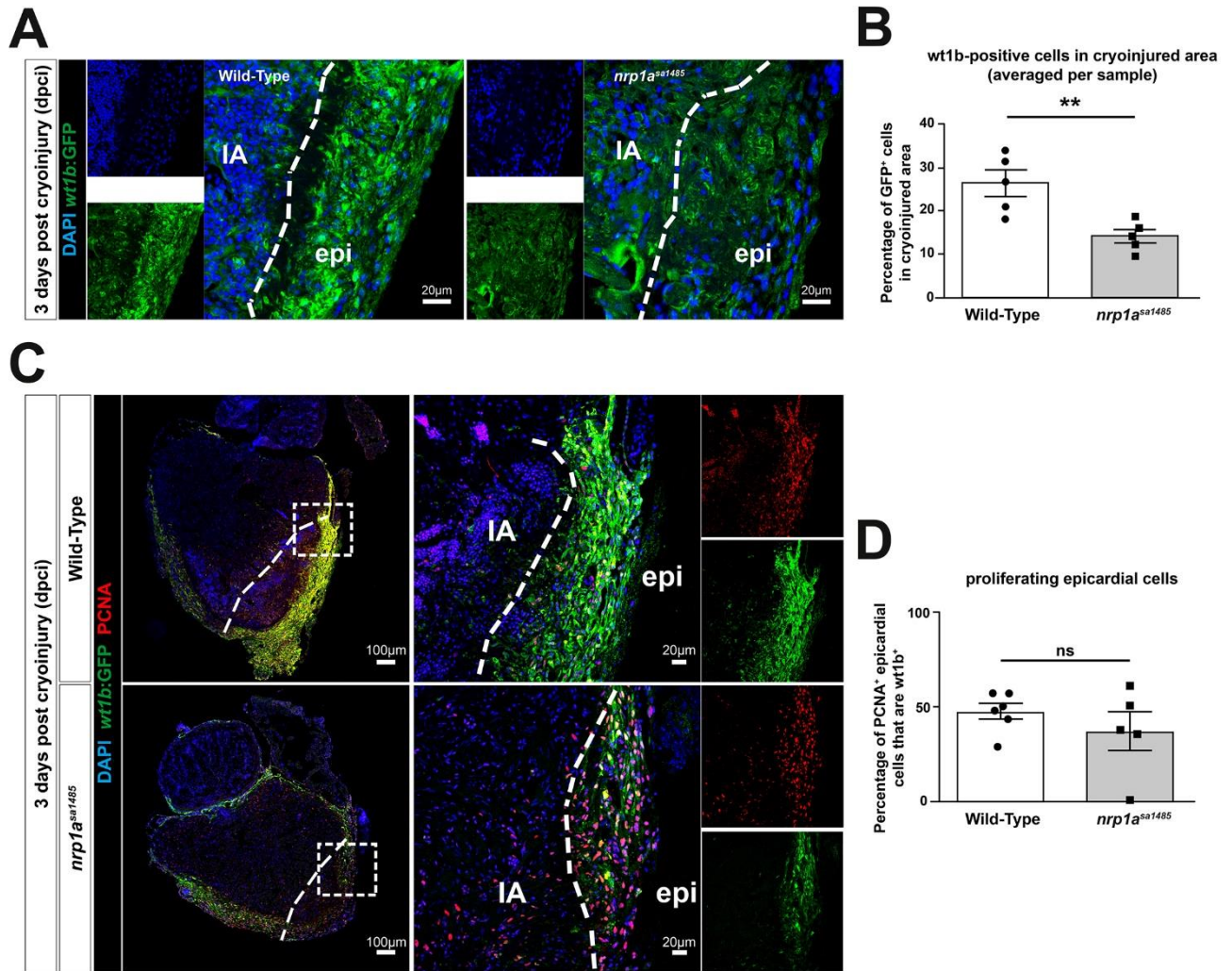


Figure 6 Epicardial activation is decreased in *nrp1a^{sa1485}* hearts following cryoinjury. Wild-Type and *nrp1a^{sa1485}* mutant cryoinjured fish on the *tg(wt1b:EGFP)^{li1}* background were analyzed for epicardial activation at 3 dpici by identification of *wt1b:EGFP*-positive cells (**A,C**), and were also stained with DAPI (**A,C**), and anti-PCNA antibody (**C**), as indicated. (**B**) The percentages of *wt1b:EGFP*-positive cells adjacent to the area of cryoinjury (indicated by the dashed line) were quantified in Wild-Type and *nrp1a^{sa1485}* mutant fish (two-tailed *t*-test of $n = 5$) $**p < 0.01$, for WT vs *nrp1a^{sa1485}* hearts. (**D**) The percentages of cells positive for *wt1b:EGFP* and PCNA were also quantified in the area of cryoinjury (two-tailed *t*-test of $n = 6$ and 5 for Wild-Type and *nrp1a^{sa1485}* respectively, $p > 0.05$). Individual data points represent percentages in individual hearts, each averaged from counts in 2-4 different sections covering the injury borders. (IA– injury area, epi– epicardium, white dotted line delineates injury/epicardial border).

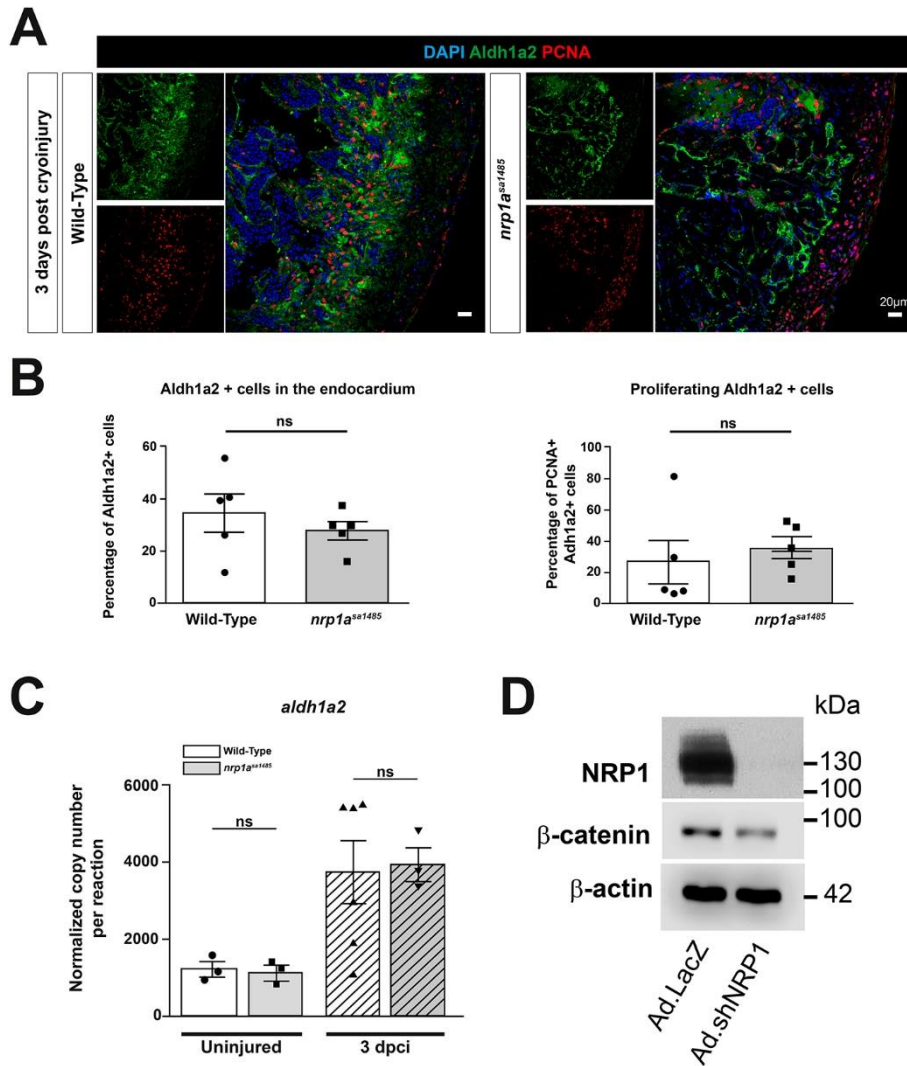


Figure 7 Aldh1a2 expression is unchanged in *nrp1a^{sa1485}* fish following cryoinjury. β -catenin expression is downregulated in rat epicardial cells.

(A) Cryoinjured Wild-Type and *nrp1a^{sa1485}* fish were analyzed for *aldh1a2* expression and were also stained with DAPI and anti-PCNA antibody at 3 dpci. **(B)** Percentage of *aldh1a2*-positive cells in the endocardium of the cryoinjury area (left) and percentage of proliferating endocardial cells (PCNA+ and *aldh1a2*+ cells) (two-tailed *t*-test of $n = 5$) $p=0.43$ *aldh1a2*+ cells and $p=0.59$ PCNA+ *aldh1a2*+ cells. **(C)** Absolute quantitative PCR analysis of *aldh1a2* (*aldh1a2*) gene expression was performed on uninjured and 3 dpci ventricles from Wild-Type and *nrp1a^{sa1485}* mutant fish. Bars represent normalized copy number per reaction means \pm S.E.M (one-way ANOVA with Sidak's *post hoc* test for multiple comparisons of $n \geq 3$). **(D)** Rat epicardial cells were cultured *in vitro* and infected with control (Ad.LacZ) and shRNA NRP1 (Ad.shNRP1) adenoviral constructs. Cell lysates immunoblotted for NRP1, β -catenin and β -actin ($n = 2$).

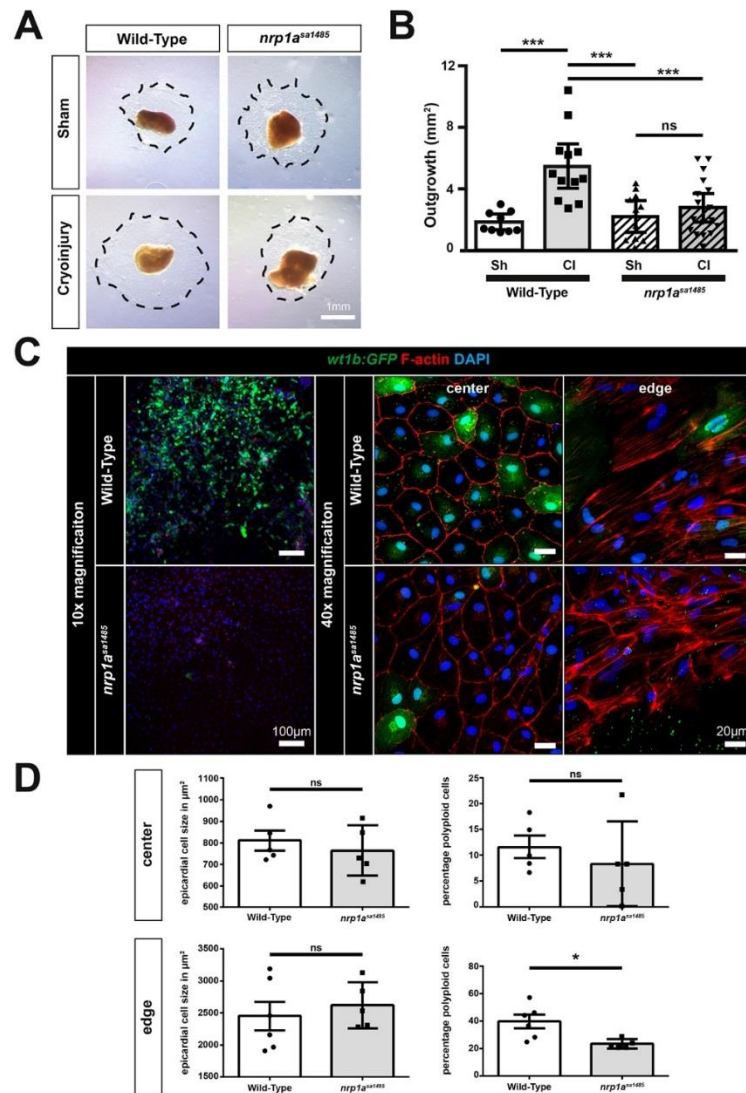


Figure 8 Epicardial cryoinjury induced expansion and activation are impaired in *nrp1a^{sa1485}* mutants.

The apices of Wild-Type and *nrp1a^{sa1485}* zebrafish ventricles were collected 5 days post sham surgery or cryoinjury and cultured on fibrin gels for 7 days. **(A)** Epicardial cells migrate into the fibrin gels (dotted black lines). **(B)** Epicardial outgrowths were measured for each condition (sh – sham-operated and CI – cryoinjured hearts) after 7 days culture, data are represented as mean outgrowth area (mm^2) \pm S.E.M (one-way ANOVA with Sidak's *post hoc* test for multiple comparisons of $n > 9$) *** $p < 0.001$. **(C)** Epicardial explant recovered from Wild-Type and *nrp1a^{sa1485}* *tg(wt1b:EGFP)^{li1}* cryoinjured fish at 5 dpci were left to grow on fibrin gels for 7 days and stained for GFP. GFP fluorescence was observed at 10x (**left column**) and 40x magnification at the center and the periphery of the explants (**middle and right columns** respectively). **(D)** Cell size (left) and ploidy (right) were quantified both at the center (top row) and at the edge (bottom row) of the explant. Data are expressed as percentage of cells per field of view \pm S.E.M. Each n represents an average of 3 fields of view per explant (two-tailed *t*-test of $n \geq 5$) $p < 0.05$.

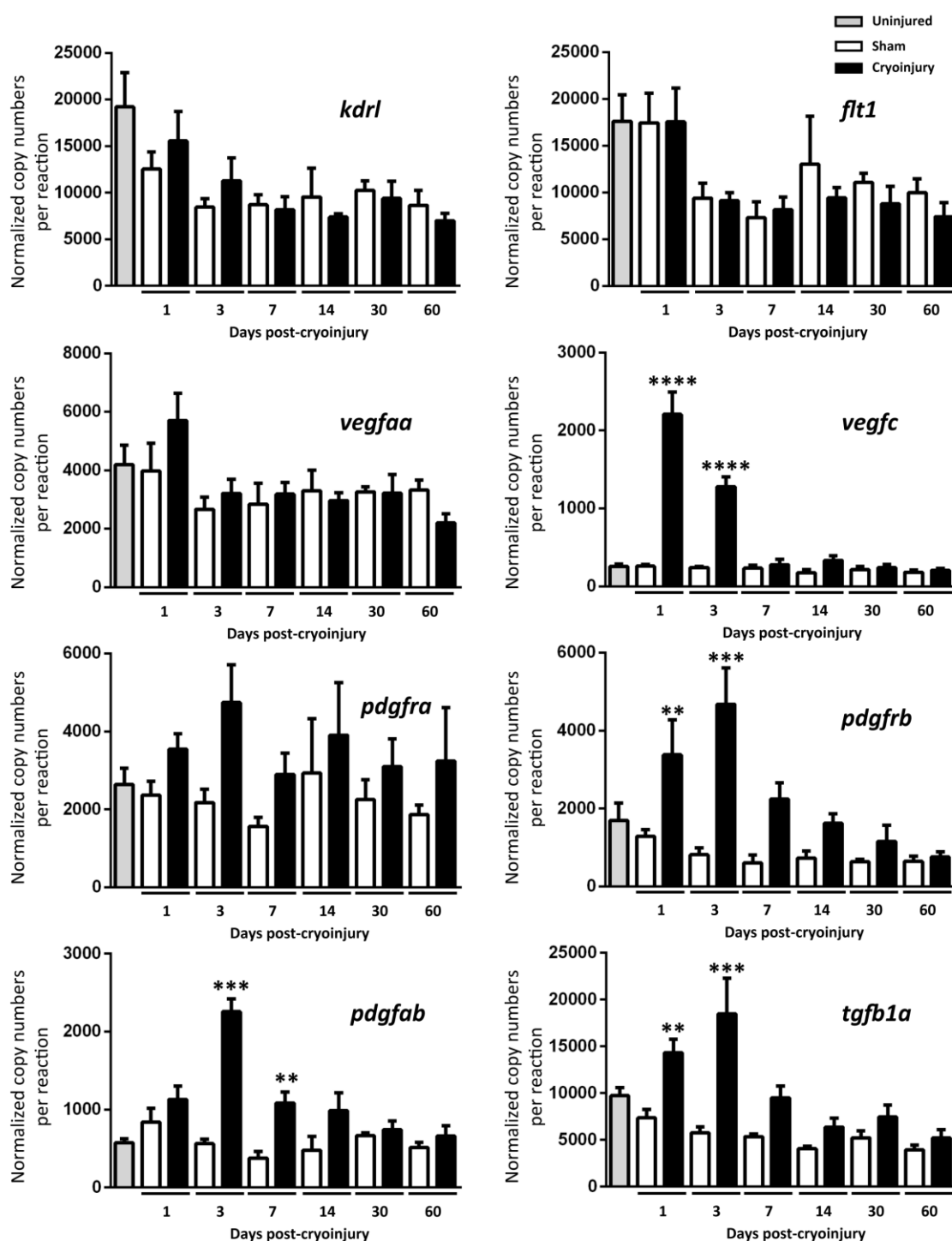


Figure S1 Gene expression of vascular endothelial growth factors (*vegf*), platelet-derived growth factor (*pdgf*) and transforming growth factor (*tgf*) and their receptors in adult zebrafish cryoinjured ventricles.

Absolute quantitative PCR analysis 1, 3, 7, 14, 30, and 60 days following cryoinjury or sham surgery of zebrafish ventricles. Basal expression was evaluated in uninjured hearts. *Vegf* receptors *kdr1* and *flt1* and *vegf* isoforms (*vegfaa* and *vegfc*) mRNA levels

were assessed to evaluate expression of genes associated with angiogenesis. *Pdgf* receptors *pdgfra* (*pdgfr* α) and *pdgfrb* (*pdgfr* β), additional to *pdgf* (*pdgfab*) and *tgf* (*tgfb1a*) gene expression were measured to evaluate expression of genes associated epithelial-to-mesenchymal transition. Bars represent means of normalized copy numbers per reaction \pm S.E.M, ** $p < 0.01$, *** $p < 0.005$, **** $p < 0.001$ (one-way ANOVA with Sidak's *post hoc* test for multiple comparisons of $n = 4-5$ with each n being a pool of 5 ventricles).

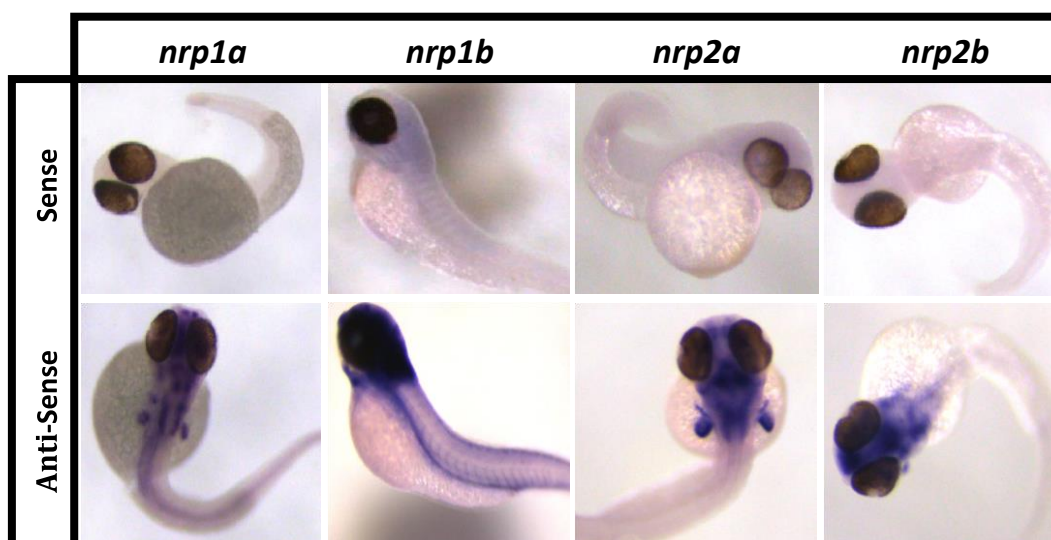


Figure S2 *nrp* riboprobes validation.

In situ hybridization of TraNac transgenic zebrafish embryos 48 hours post fertilization (hpf) with *nrp* sense riboprobes (**upper row**) and *nrp* anti-sense riboprobes (**lower row**). Anti-sense riboprobes differential staining patterns were compared to previous reports (43) to confirm specific *nrp* isoform detection. All neuropilin isoforms are observed in the brain with additional differential expression patterns observed between different isoforms. *Nrp1a* is observed in the fin buds and otic vesicles, *nrp1b* is expressed in the dorsal aorta and intersegmental vessels, *nrp2a* is observed in the hind brain and fin buds, whereas *nrp2b* is largely restricted to the brain and hind brain, $n \geq 8$.

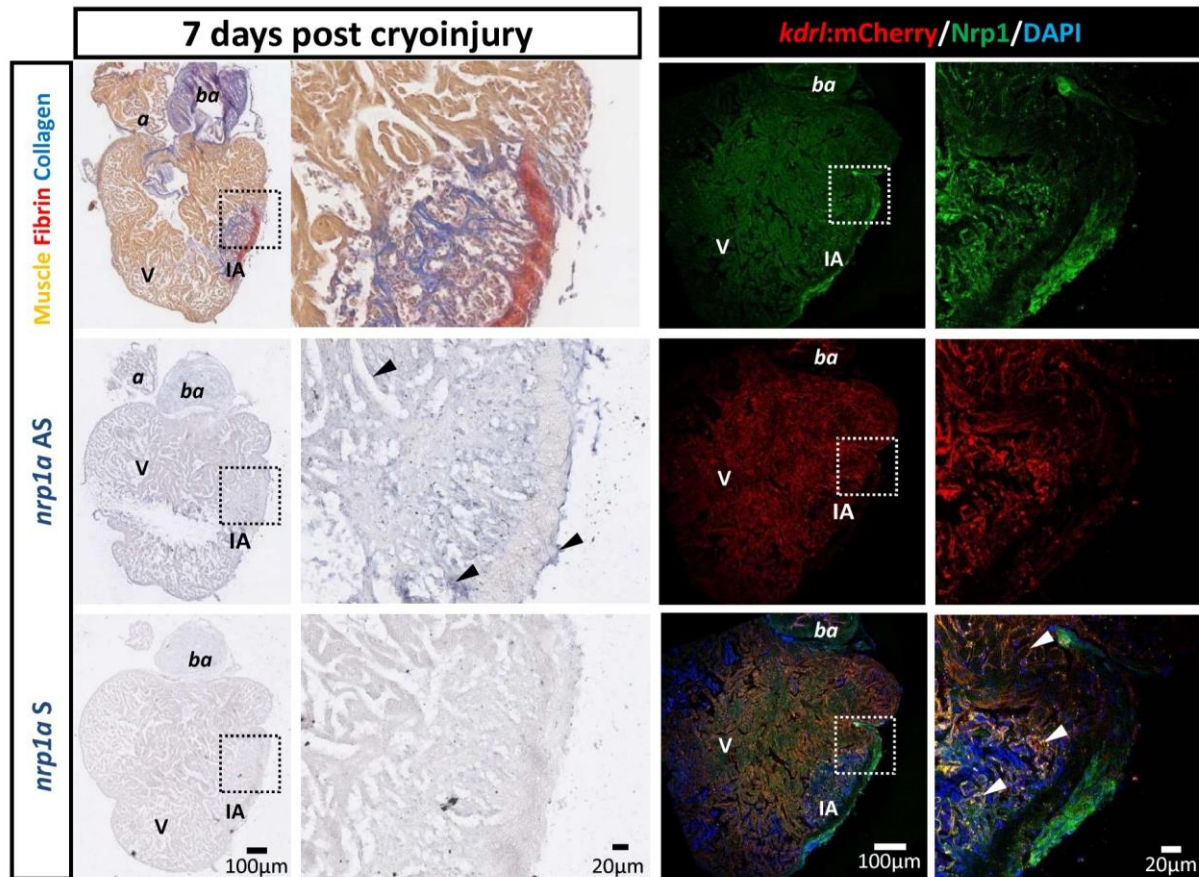


Figure S3 Nrp1 is expressed by the endocardium.

AFOG staining (**upper left panels**), *in situ* hybridization (ISH) (**middle and lower left panels**) and immunofluorescence (**two right columns**) of *tg(kdr:mCherry)^{s896}* zebrafish heart 7 days post cryoinjury (dpci). AFOG staining gives reference to cryoinjury location and tissue composition. ISH of *nrp1a* anti-sense riboprobe (*nrp1a* AS) (**middle left panels**) and negative control sense (*nrp1a* S) riboprobe (**lower left panels**), signal is observed as a dark blue stain within the section, black arrows indicate mRNA expression. *kdr* expression by viable endocardium is immunolabeled with anti-mCherry antibody (red) (**middle right panels**) and Nrp1-expressing cells are labelled in green (**upper right panels**). Overlay of the two colors is displayed with DAPI nuclei staining (**lower right panels**). White arrows indicate regions of colocalization. Dotted boxes highlight magnified regions. V– ventricle, *ba*– *bulbus arteriosus*, *a*– atrium, IA– injured area ($n = 2$).

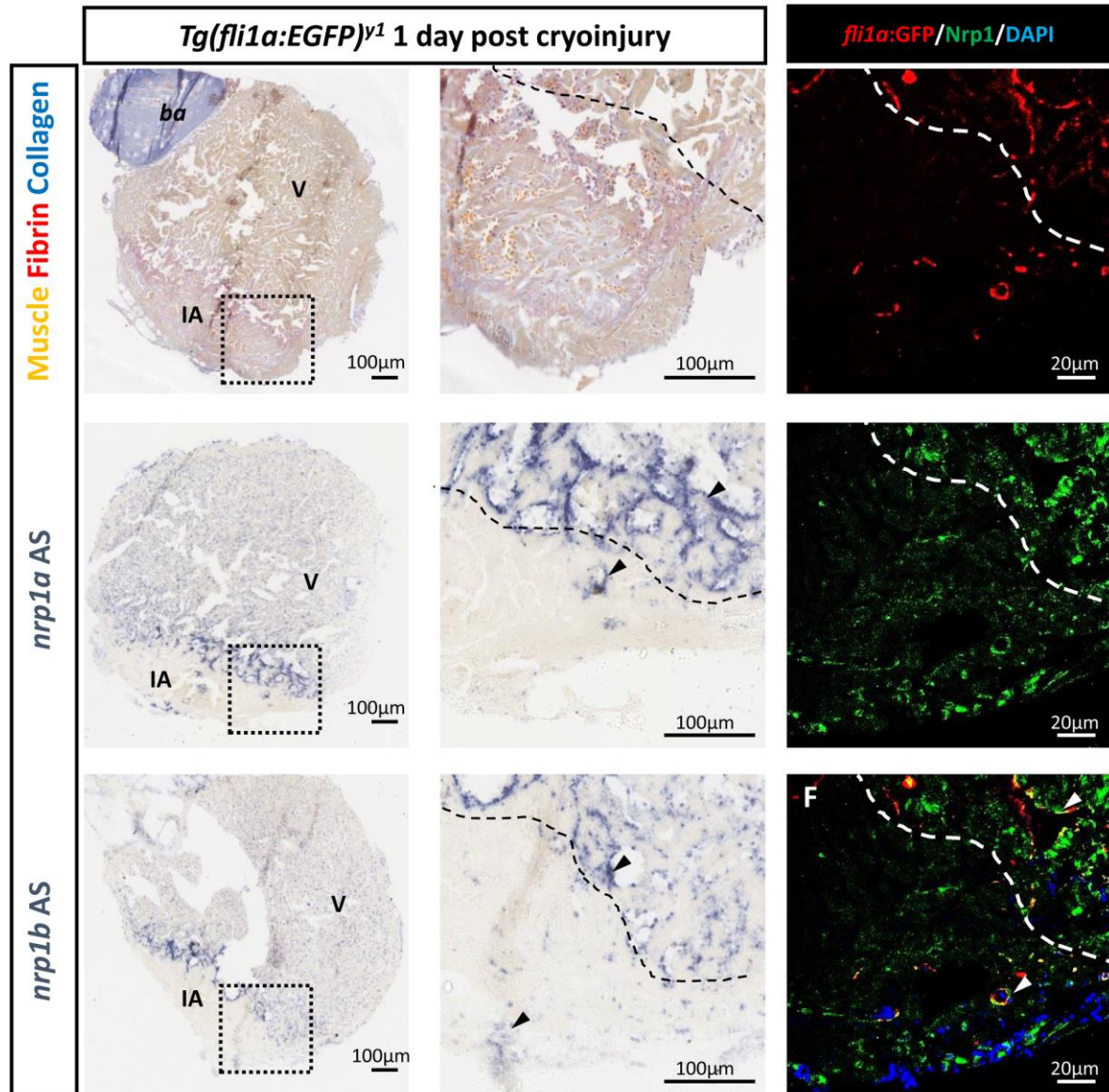


Figure S4 Nrp1 is expressed by early neovasculature in the cryoinjured lesion of *tg(fli1a:EGFP)^{y1}* zebrafish heart 1 day post cryoinjury.

AFOG staining (**upper left**) identifies cryoinjured lesion. *Nrp1a* (**middle left**) and *nrp1b* (**lower left**) mRNA localization is detected with *in situ* hybridization, black arrows indicate mRNA expression within the injury and at the injury/healthy myocardium border. Immunofluorescence imaging was used to locate *fli1a:EGFP* positive cells expressed by viable endothelium and endocardium (red) (**upper right**) and Nrp1-expressing cells (green) (**middle right**). Overlay of the two colors are displayed with DAPI nuclei staining (**lower right pane**), white arrows indicate areas of colocalization. Dotted boxes highlight magnified regions. Dashed lines define injury interface. V– ventricle, *ba*– *bulbus arteriosus*, IA– injured area, HM– healthy myocardium, *n* = 3.

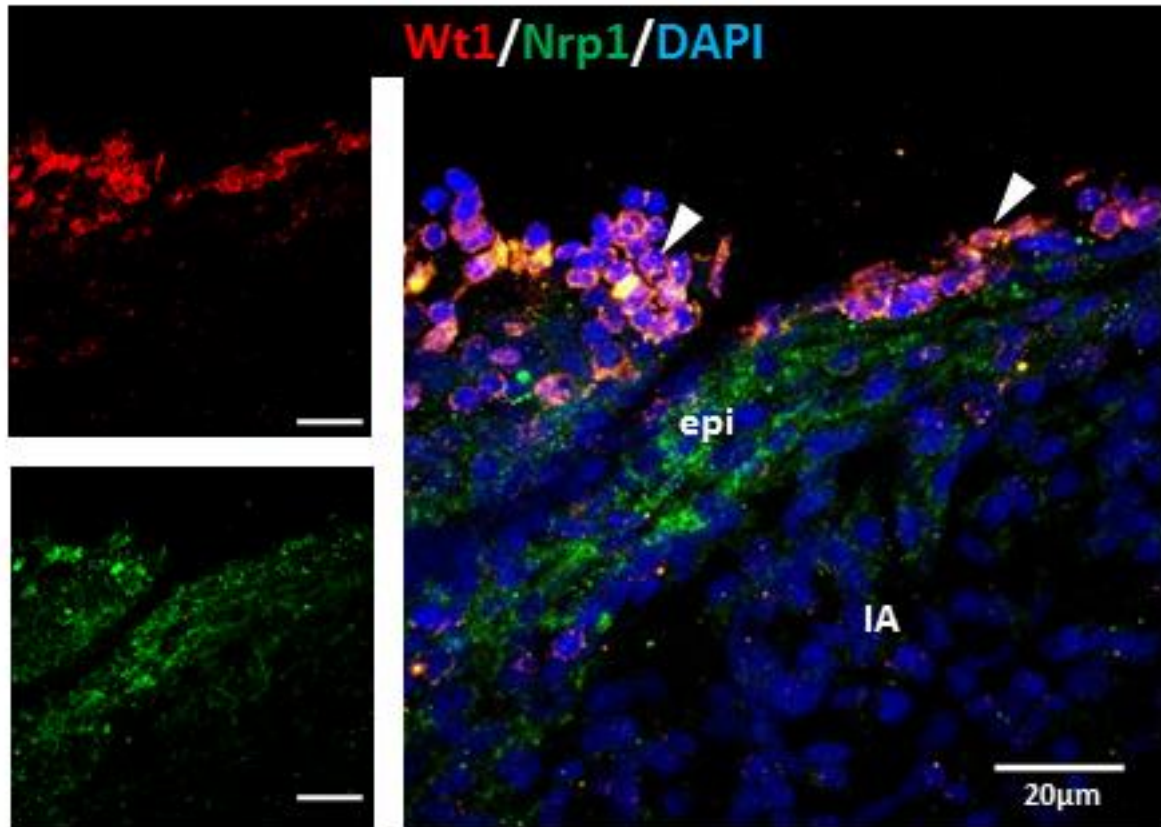


Figure S5 Wt1-positive epicardial cells express Nrp1.

Immunofluorescence of Wild-Type adult zebrafish heart 3 days post cryoinjury (dpci). Activated epicardial cells were identified with Wt1 antibody (red) and assessed for Nrp1 expression (green). White arrows indicate regions of colocalization. Scale bars = 20µm. IA– injured area, epi– epicardium ($n = 2$).

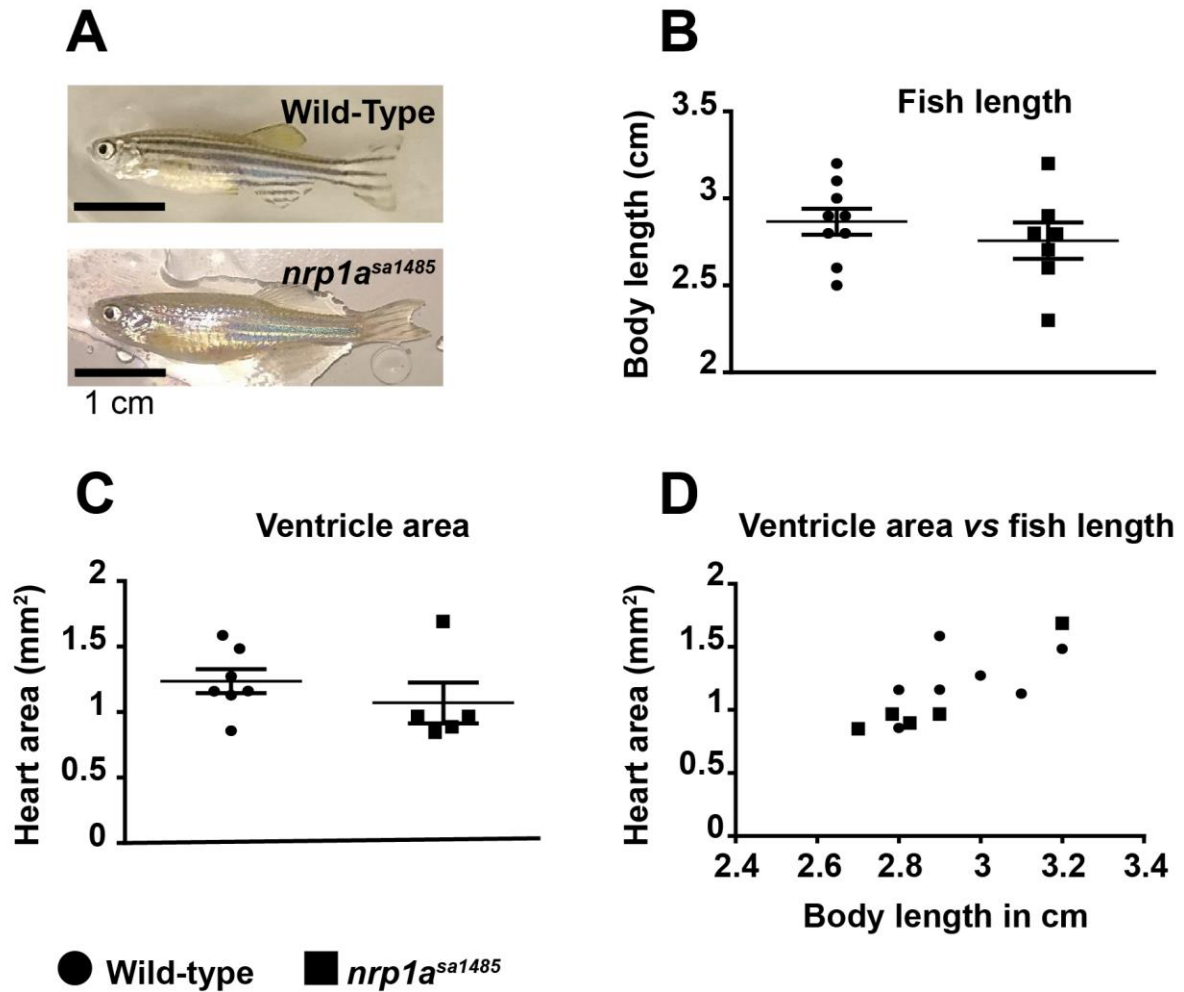


Figure S6 *nrp1a*^{sa1485} mutant fish characterization

(A) Representative picture of Wild-Type (upper panel) and *nrp1a*^{sa1485} mutant zebrafish (lower panel), scale bar 1 cm. The body length (B), and heart size (C) of age matched Wild-Type (black dots) and *nrp1a*^{sa1485} mutant (black squares) zebrafish were measured and compared (two-tailed *t*-test of $n \geq 5$, $p > 0.05$). (D) Scatter graph values are displayed as means \pm S.E.M and individual measurements of fish indicated as black dots (Wild-Type) or squares (*nrp1a*^{sa1485}).

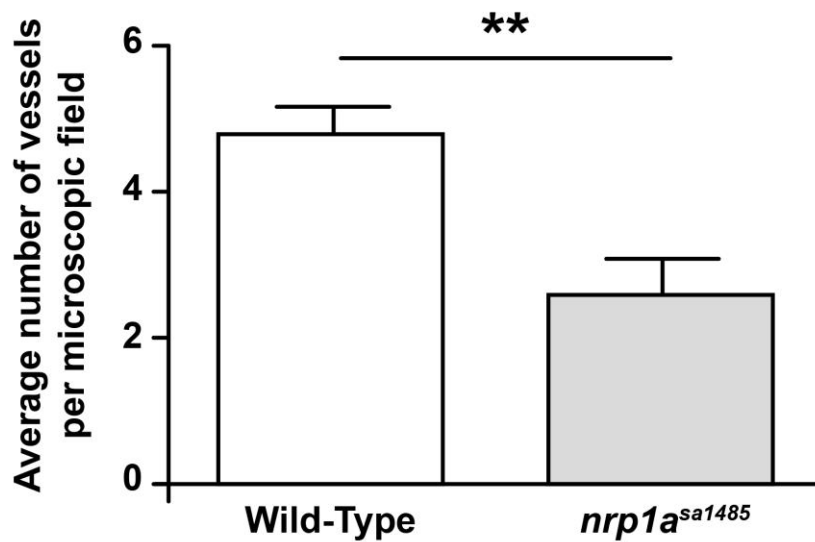
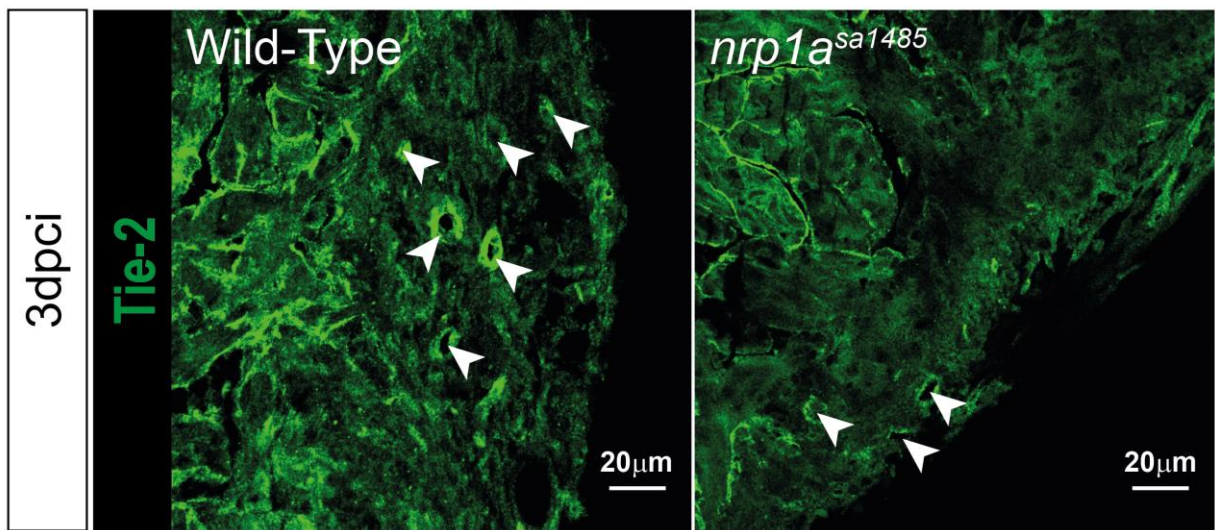


Figure S7 Neovascularization of the cryoinjured area is impaired in *nrp1a*^{sa1485} fish.

Tie2 immunostaining of Wild-Type (top left) and *nrp1a*^{sa1485} (top right) hearts 3 days post cryoinjury. Bars represent average numbers of newly formed vessels per microscopic field (32625 μm²) within the injured area ± S.E.M, samples were quantified at least at 3 levels across the whole hearts (two-tailed *t*-test of *n* = 6, ** *p* < 0.01).

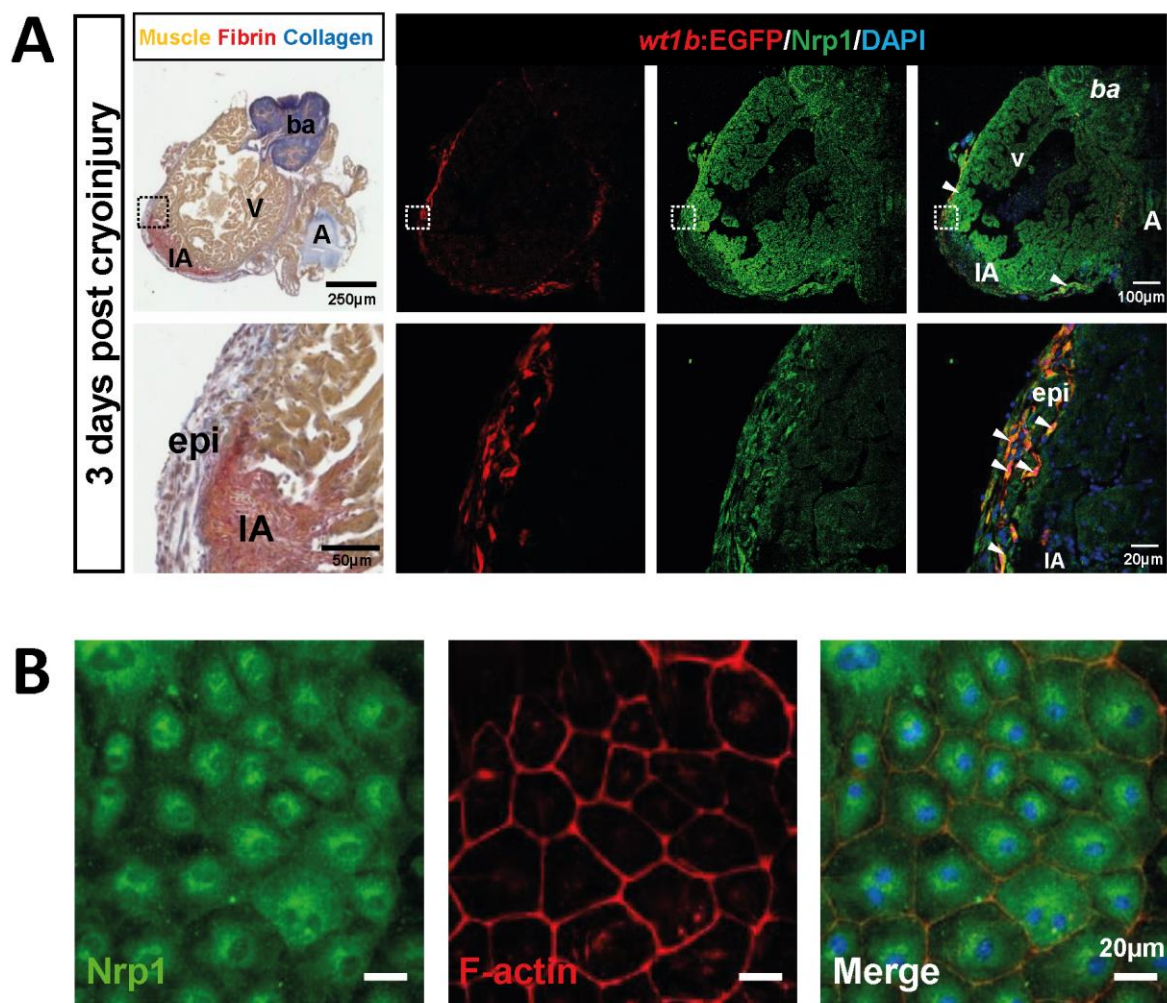


Figure S8 Epicardial cells express Nrp1 *in vivo* and *in vitro*.

(A) Serial sections of *tg(wt1b:EGFP)^{li1}* adult zebrafish heart 3 dpci stained with AFOG for lesion location and immunostained for GFP (red), Nrp1 (green) and DAPI (right panels). Dotted boxes indicate magnified region in panels below. White arrows identify cells co-expressing GFP and Nrp1. V– ventricle, *ba*– *bulbus arteriosus*, A– atrium, IA– injured area, epi– epicardium, HM– healthy myocardium ($n = 3$). **(B)** Wild-Type ventricle apices were collected 5 dpci and cultured *in vitro* for 7 days and epicardial outgrowths immunostained for Nrp1. All epicardial cells of the explant were Nrp1 positive. Phalloidin conjugated to Alexa-555 was used to identify F-actin and highlight cellular tight junctions and DAPI staining applied to located individual cells. Scale bar 20 μm ($n = 4$).

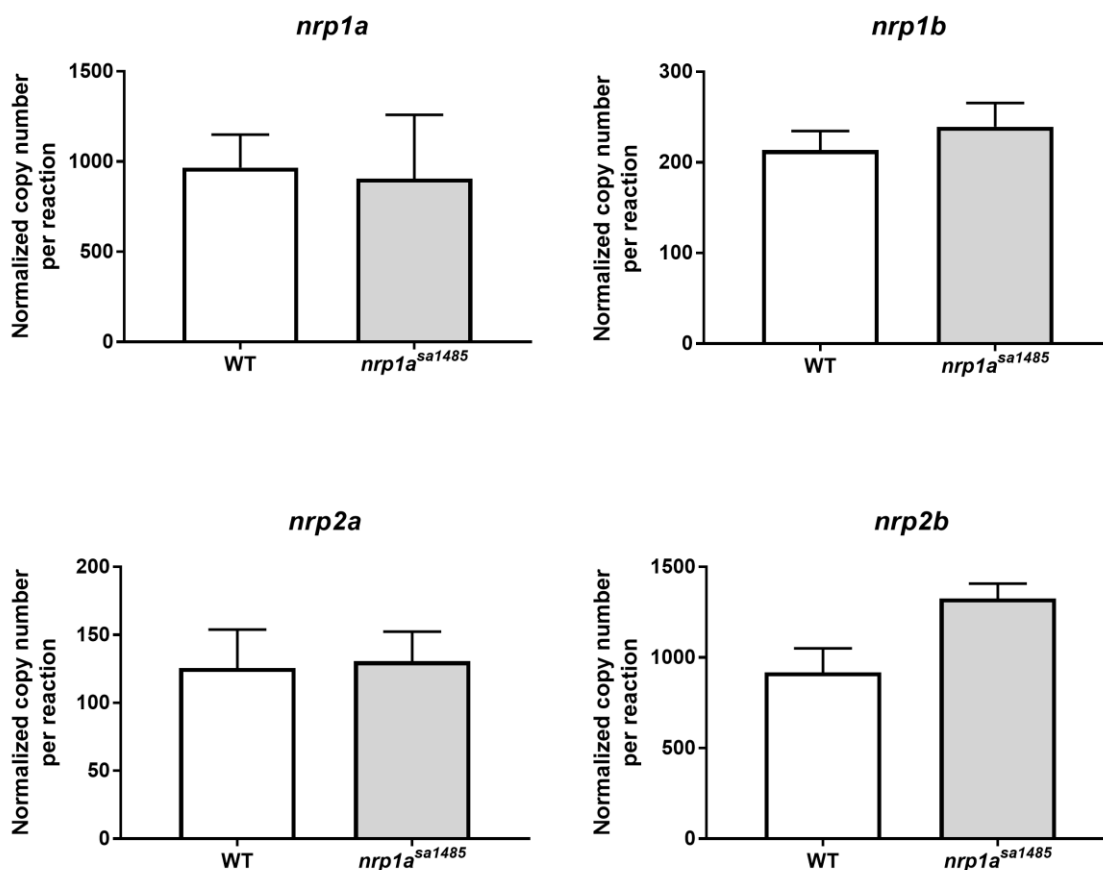


Figure S9 Gene expression of all neuropilin isoform remain unchanged in *nrp1a^{sa1485}* fish after cryoinjury.

Absolute quantitative PCR analysis at 3 days following cryoinjury of Wild-Type or *nrp1a^{sa1485}* zebrafish ventricles. Bars represent means of normalized copy numbers per reaction \pm S.E.M, (two-tailed *t*-tests of $n=6$ for Wild-Type and $n=4$ for *nrp1a^{sa1485}* fish, each n is one heart, $p<0.05$).

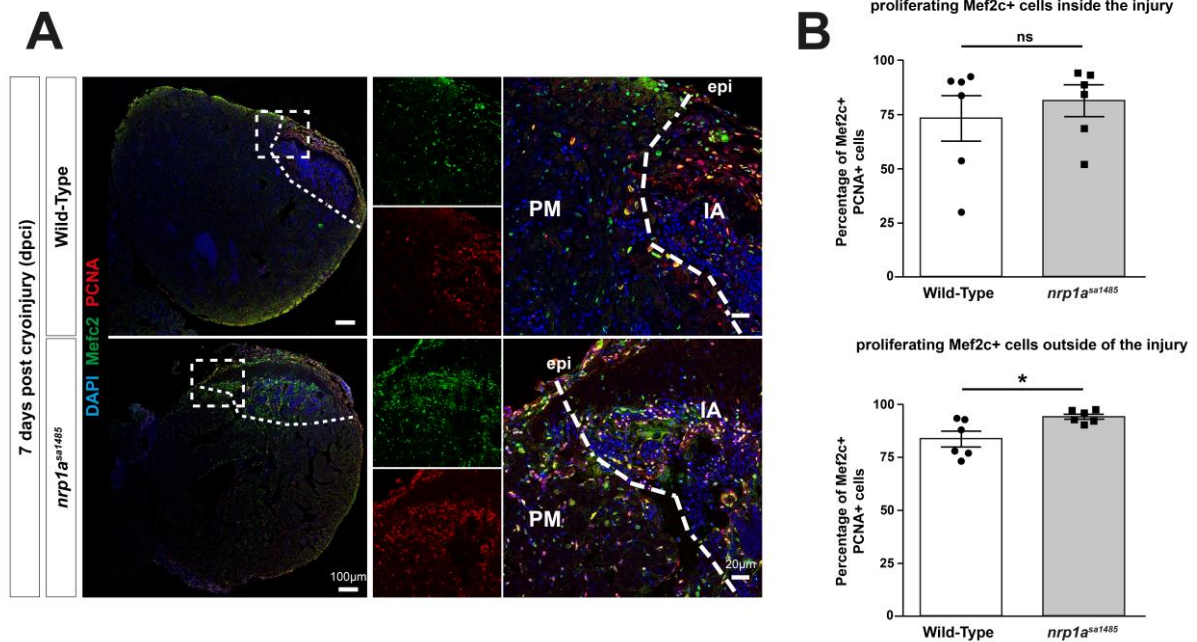


Figure S10 Cardiomyocyte proliferation of *nrp1a^{sa1485}* mutant is not affected following cryoinjury.

Sections of Wild-Type and *nrp1a^{sa1485}* mutant cryoinjured hearts (7 dpci) were examined by immunofluorescent staining for Mef2c and PCNA and counterstained with DAPI. The percentage of PCNA+ cardiomyocytes (i.e., also Mef2c-positive) inside the injury as well as at the injury periphery were quantified. Data points represent average values of individual hearts, obtained from 2-3 sections per heart, (two-tailed *t*-test of $n=6$, $p=0.542$ inside the injury, Mann-Whitney non parametric test of $n=6$, $p=0.065$ in the periphery).

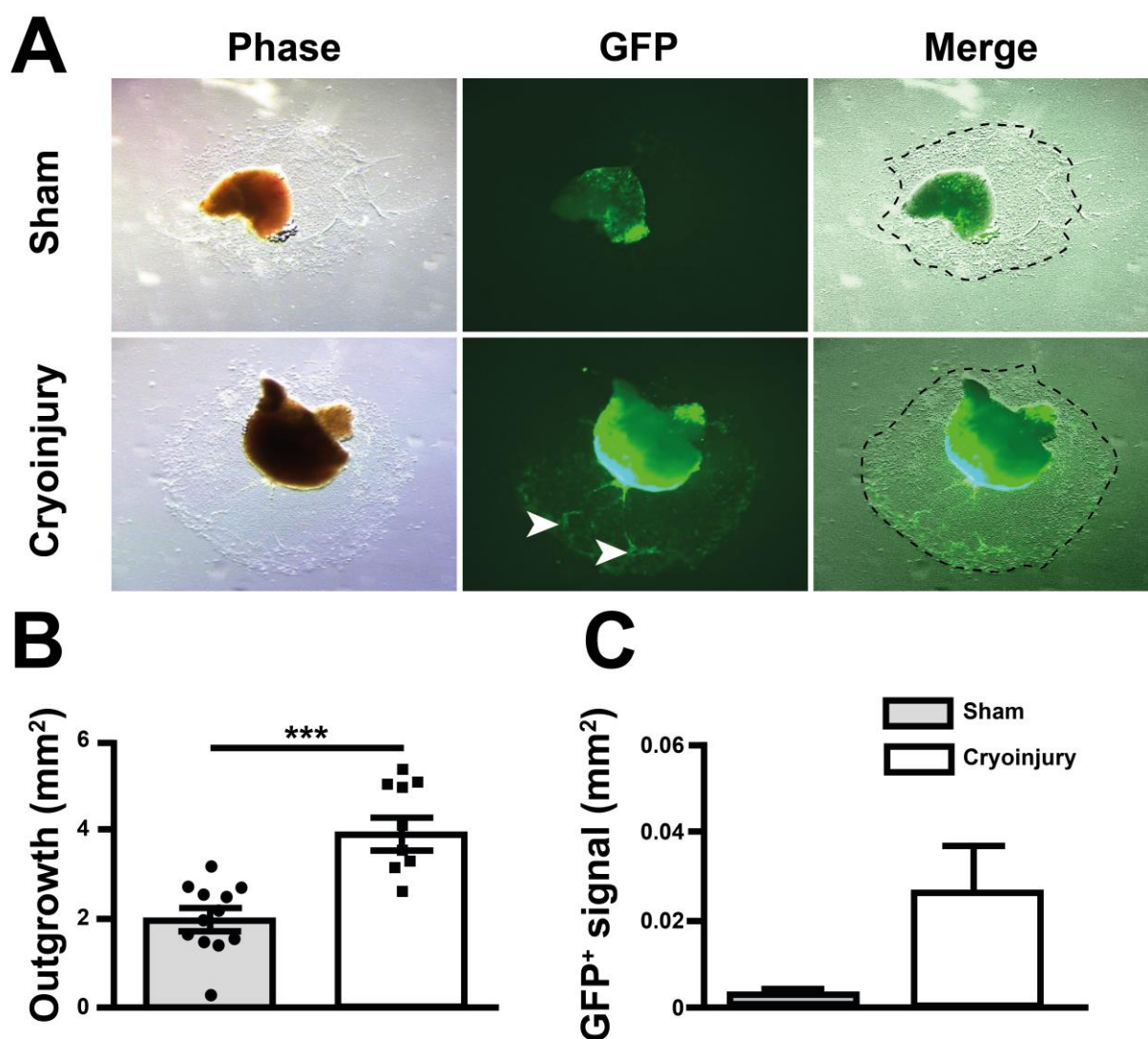


Figure S11 Cryoinjury induces epicardial activation and expansion in heart explants.

The apices of *tg(wt1b:EGFP)^{li1}* zebrafish ventricles were collected 5 days post sham surgery or cryoinjury and cultured on fibrin gels for 7 days. **(A)** Explants were imaged using a stereomicroscope under phase contrast and green-fluorescence, then overlaid to visualize GFP-positive epicardial outgrowth (white arrows), scale bar 500 μ m. **(B)** Epicardial outgrowths from sham (white bar) and cryoinjury (grey bar) surgeries were quantified. Results are presented as mean outgrowth in mm² \pm S.E.M (two-tailed *t*-test of *n* = 12 sham and *n* = 10 cryoinjury, ****p*=0.0003). **(C)** GFP+ signal in the epicardial outgrowth was measured for sham (white bar) and cryoinjury (grey bar) surgeries. Results are presented as mean GFP+ signal area in mm² \pm S.E.M (two-tailed *t*-test of *n* = 4, *p*=0.0713).

Supplementary Materials and Methods:

Zebrafish husbandry, cryoinjury and sample collection

Procedures were performed in line with the Animals (Scientific Procedures) Act 1986, and husbandry was regulated by the Central University College London fish facility. Adult zebrafish between 6-18 months of age were used for the study. Wild-Type ABxTupLF (ABxTübingen-long fin) (Max-Planck, Tübingen, Germany) and *nrp1a*^{sa1485/sa1485} (Zebrafish Mutation Project, Sanger Center, Cambridge, UK) fish were used for *in vitro* culture, histological samples, RNA, and protein expression analysis. Additionally, the following transgenic fish were used for histological and *in vitro* preparations: *Tg(fli1a:EGFP)^{y1}* and *tg(kdrl:mCherry)^{s896}* to identify endocardial cells, *tg(wt1b:EGFP)^{li1}* to detect activated epicardial cells. TraNac zebrafish embryos (gift from Paul Frankel, University College London) were used for whole-mount *in situ* hybridization probe validation.

The cryoinjury procedure was carried out as described in (Gonzalez-Rosa and Mercader, 2012). Briefly, fish were anaesthetized and a small incision was made to expose the ventricle. A stainless steel probe (0.75 mm diameter), cooled in liquid nitrogen, was pressed onto the ventricle apex for 5 seconds. Sham surgeries were performed as above, with the absence of probe application.

For RNA extraction, ventricles were rinsed briefly in PBS and stored at -20°C in RNAlater® stabilization reagent (Qiagen). For protein extraction, ventricles were snap frozen in liquid nitrogen and stored at -80°C until processing. For histological preparations, the entire heart (atrium, ventricle and *bulbus arteriosus*) was kept intact and placed in PBS/0.1 M KCL to arrest heart in diastole before fixing with 4% (wt/vol) paraformaldehyde overnight at 4°C. After fixation, hearts were rinsed several times in PBS, dehydrated in graded concentrations of ethanol solutions and embedded in

paraffin wax. Sections were cut in serial sections at 10 μm to slides. Sections used for Acid Fuchsin Orange G (AFOG) staining and immunohistochemistry were mounted to Superfrost® Plus slides and stored at room temperature, while sections prepared for *in situ* hybridization were mounted to Superfrost® ultra plus (both Thermo Fisher Scientific) and stored at -80°C for *in situ* hybridization procedures. For whole-mount *in situ* preparations, embryos were collected 48 hours post fertilization and fixed with 4% (wt/vol) paraformaldehyde overnight at 4°C . The following day, embryos were rinsed several times with PBS, dechorionated, and stored in 100% methanol at -20°C until processing.

RT-qPCR

Five ventricles from corresponding time points and treatments were pooled for RNA extraction and homogenized in lysis buffer (Qiagen) in 1.4mm ceramic bead-containing tubes and mechanically disrupted in a Minilys homogenizer (Peqlab). Homogenates were passed through a QIAshredder spin column (Qiagen) then total RNA was extracted using the RNeasy Mini Kit (Qiagen). The quantity and purity of RNA were evaluated using a NanoDrop 2000 spectrophotometer (Thermo Fisher Scientific) and RNA integrity was assessed with a Bioanalyzer (Agilent). 250-500 ng of total RNA was reverse transcribed using the QuantiTect® Reverse Transcription Kit (Qiagen).

All primers (see table S1) and standards were purchased from qStandard: Absolute RT-qPCR values were measured using Brilliant III Ultra-Fast QPCR Master Mix (Agilent Technologies Inc.) and the Rotor-Gene PCR thermocycler (Qiagen). Values were normalized using a normalization factor generated using GeNorm software from the following three reference genes: *gapdh*, *Rpl13a* and *eef1a1a* to calculate the expression of the genes of interest.

Gene	Name	Accession Number	Primer Sequence 5'-3'
<i>rpl13a</i>	Ribosomal protein L 13A	NM_212784	Fwd gtctgaaacccacacgcaaat Rev cgttctttcagcctgcttagt
<i>eef1a1a</i>	Eukaryotic translation elongation factor 1a	NM_200009	Fwd ctctctgggtcgtttctgct Rev tatgtgtctctggagtggca
<i>gapdh</i>	Glyceraldehyde 3-phosphate dehydrogenase	NM_001115114	Fwd ttctgagctcaatggcaagc Rev agacggactgtcagatccaca
<i>nrp1a</i>	Neuropilin 1a	NM_001040326 & NM_181497	Fwd ctccaacaaaccctaccaggt Rev tcggtgatgtccaccatgattc
<i>nrp1b</i>	Neuropilin 1b	AY493415	Fwd gaccaaagcagatggagggaa Rev catctctgtattctctggatcttgc
<i>nrp2a</i>	Neuropilin 2a	NM_212965	Fwd gattctgacttcagctgggtatg Rev cgatgtacaggtagttcccaaa
<i>nrp2b</i>	Neuropilin 2b	NM_212966	Fwd cagcattgagcttgagcagt Rev tcaggctctcgctcagtcac
<i>kdrl</i>	Kinase insert domain receptor like	NM_131472	Fwd ccttgagacgcagatgaatcc Rev ctgctgtatccaccctggct
<i>flt1</i>	Fms-related tyrosine kinase 1	NM_001014829 & NM_001257153	Fwd aactcacagaccagtgaacaaga Rev ttagccttctgtgggtatgtcca
<i>vegfaa</i>	Vascular endothelial growth factor Aa	NM_001190933	Fwd ccatctgtctgctgtaaaggct Rev gatgatgtctaccagcagctctc

vegfc	Vascular endothelial growth factor c	NM_205734	Fwd tgccatgcaggagcattcaga Rev gcctcctccgacctgtttc
tgfb1a	Transforming growth factor beta 1a	NM_212965	Fwd gctggctctcatttgacgtg Rev ctctgctgtctagccctga
pdgfra	Platelet-derived growth factor receptor alpha	NM_131459	Fwd tgataatctctacacaacgctgagt Rev cctatagacatcactggacgcat
pdgfrb	Platelet-derived growth Factor receptor beta	NM_001190933	Fwd gctatcacaacaggactggttc Rev ctctgtgcgaaagtctggga
pdgfab	Platelet derived growth factor alpha b	NM_001076757	Fwd tgataatctctacacaacgctgagt Rev caggggtctgaggtaaagtc
aldh1a2	retinaldehyde dehydrogenase 2	NM031850	Fwd gcgatgacctccagtgaagttg Rev acctgccgctcacagaatcat

Table S1 RT-qPCR primers used for zebrafish gene expression analyses

Immunofluorescence

Whole heart sections were rehydrated in graded concentrations of ethanol solutions. Citrate buffer heat-induced antigen retrieval was performed (10 minutes) and samples were permeabilized in 0.5% Triton X-100 for 15 minutes followed by blocking for 1 hour at room temperature in blocking solution (PBS 0.1% Tween-20 (PBST) supplemented with 5% BSA and 10% donkey serum). Primary antibodies were diluted in blocking solution and incubated overnight at 4°C. The following antibodies were used for immunofluorescence: anti-Neuropilin 1, Genetex GTX62190; anti-WT1 6F-H2, Novus NB110-6001; anti-GFP, Roche 11 814 460 001; anti-Tropomyosin, sigma T2780; anti-mCherry, Novus NBP1-96752; anti-PCNA PC-10, Santa Cruz sc-56; anti-ALDH2 (RALDH2), Genetex GTX101429; anti-Mef2, biorbyt orb256682; anti-L-plastin, antibody kindly donated by Marie-Christine Ramel, Imperial College London; normal rabbit IgG, alpha diagnostics 200009-1-200; normal mouse IgG, Invitrogen 026502. The following day, slides were washed in PBST and incubated with fluorescent secondary antibodies: anti-rabbit Alexa 488 and anti-mouse Alexa 555 (both Thermo Fisher Scientific, A31570 and A11034) for 1 hour at room temperature. Slides were washed with PBST and incubated in 1% (wt/vol) Sudan Black B in 70% ethanol for 15 minutes at room temperature to quench background fluorescence and rinsed 8 times rapidly with PBS before mounting with ProLong DAPI mounting medium (Thermo Fisher Scientific). Images were captured on the Leica TCS SPE1 confocal microscope system and processed using the publicly available ImageJ software.

AFOG staining

Deparaffinized and rehydrated sections were fixed in Bouins fixative (Thermo Fisher Scientific) for 2 hours at 60°C followed by overnight incubation at room temperature. The following day, slides were washed for 10 minutes in constant tap water stream. Nuclei were

stained with Weigert's iron hematoxylin (Amresco, Sigma-Aldrich), and treated for 5 minutes with 1% phosphomolybdic acid in ddH₂O (Sigma-Aldrich). Slides were then incubated in AFOG staining solution (5g Methyl Blue (Sigma), 10g Orange G (Sigma-Aldrich), 15g acid fuchsin (Acros organics) per litre of double distilled water (ddH₂O), pH=1.09) for 10 minutes and washed in ddH₂O 5 times. Slides were then rapidly dehydrated in a series of ethanol solutions of increasing concentrations to a final incubation in xylene and mounted for imaging in NanoZoomer automated slide scanner (Hamamatsu).

***In situ* hybridization**

Digoxigenin-labelled RNA (Roche) probe templates were generated from adult zebrafish heart cDNA, the primers used were as follows (5'-3'):

nrp1a fwd TACAGTGCCGCCTACTACAC, rev CACGCTTCCGAGTACGAGTT;

nrp1b fwd CAAAACCATGACACGCCAGA rev TGCCCTCACAGTTCACGATTT;

nrp2a fwd AGACCAGCACGACACAGAAA, rev GTGAGGGGTTTGGTGTGGTC;

nrp2b fwd ACCACCATTCTGACTGTC, rev GTGAGGGGTTTGGTGTGGTC.

Previously established probes, such as: *cmlc2*, *raldh2*, *wt1b* and *tbx18* (gift from Nadia Mercader, Universität Bern, Switzerland) were synthesized in a similar manner. Primers were used in a PCR reaction to amplify probe sequence region and amplicons cloned to pGEM®-T plasmid vectors. Each plasmid was used in two RNA polymerase reactions (either SP6 or T7) to generate the sense and the anti-sense probes.

After deparaffinization in xylene, sections were rehydrated, fixed with 4% (wt/vol) paraformaldehyde at room temperature for 10 minutes and digested with proteinase K (10µg/ml in PBS) at 37°C for 10 minutes. Sections were then post-fixed with 4% (wt/vol) paraformaldehyde for 5 minutes at room temperature, washed twice in PBS, and acetylated for 10 minutes with 0.25% acetic anhydride in 0.1 M triethanolamine (DEPC-treated), then

washed in PBS. Hybridization solution (50% deionised formamide, 10% dextran sulphate, 1X Denhardt's, 5X Saline-Sodium Citrate (SSC), 1 mg/ml yeast tRNA, 0.1% Tween 20) was placed on samples and incubated at 67°C for 2 hours in a humidifying chamber. Either anti-sense (AS) or sense (S) digoxigenin-labelled probes (0.5µg probe/ml) in hybridization solution were added to the samples overnight at 67°C in a humidifying chamber. Slides were washed at 67°C in graded salt solutions (5X SSC/50% formamide, 2X SSC/50% formamide, 2X SSC and 0.2X SSC) for 30 minutes per wash, then washed with malate buffer (100 mM maleic acid, 150 mM NaCl, pH7.5, 0.1% Tween 20) (MAB) 3 times, and blocked (MAB/ 2% Boehringer blocking reagent/10% sheep serum) at room temperature for 2 hours. Alkaline phosphatase-conjugated anti-digoxigenin antibody (Roche) was incubated on samples overnight at 4°C and, the following day, slides were washed with MAB and equilibrated in staining buffer (100 mM Tris pH9.5, 50 mM MgCl₂, 100 mM NaCl, 0.1% Tween 20). Gene detection by alkaline phosphatase/NBT/BCIP reaction (containing 5% polyvinyl alcohol) was carried out at 37°C in the dark until a signal was detected. Slides were fixed with 4% (wt/vol) paraformaldehyde before rapid dehydration in graded concentrations of ethanol solutions to xylene for imaging in NanoZoomer automated slide scanner (Hamamatsu).

Neuropilin probes were validated with whole-mount *in situ* hybridization of dechorionated embryos. Embryos were rehydrated in graded concentrations of methanol, permeabilized with proteinase K (10 µg/ml) at RT for 20 minutes and further fixed in 4% (wt/vol) paraformaldehyde. Hybridization buffer (50% formamide, 5X Saline-Sodium Citrate buffer (SSC), heparin (50 µg/ml), torula yeast tRNA (5 mg/ml), 0.1% Tween 20) was used to block embryos at 67°C for one hour. Probes were diluted to 0.5 µg probe/ml in the same hybridization buffer and denatured at 80°C for 3 minutes. Equilibrated embryos were then incubated in probe-containing hybridization solution at 67°C overnight. Similarly, detection was performed using alkaline phosphatase-conjugated anti-DIG antibodies (Roche).

Visualization was done using alkaline phosphatase substrate BM purple (Roche) in the dark at room temperature until a dark purple precipitant developed. Embryos were then post fixed with 4% (wt/vol) paraformaldehyde overnight at 4°C and stored in 80% glycerol/PBS for microscopic analysis.

***In vitro* epicardial cell culture (heart explants)**

Thrombin/fibrin reaction in Dulbecco's Modified Eagle Medium (DMEM, Thermo Fisher Scientific) was performed as described previously (Kim et al., 2012) to produce a fibrin gel matrix in either 24-well plates or Lab-Tek™II 4-chamber slides (Thermo Fisher Scientific). The apex of cryoinjured and sham-operated zebrafish hearts 5 days post-surgery were isolated and rinsed several times with HDMEM (23mM HEPES, 15mM NaCl in DMEM) to remove residual blood. One apex per well/chamber was placed firmly on set fibrin gel matrices, ensuring epicardial surface contact with the gel. Excess HDMEM was removed from heart tissue and left to adhere for 1 hour in a tissue culture incubator (28°C, 5% CO₂) before careful addition of DMEM supplemented with 0.5% fetal bovine serum (FBS), Normocin™ (invivoGen) and penicillin/streptomycin antibiotics (Sigma-Aldrich) into the wells or slide chambers. Medium was changed every 2 days and cells were cultured for 7 days before harvesting epicardial outgrowths for immunofluorescence imaging. For immunofluorescence analysis, heart tissue was discarded and cells were fixed in 4% (wt/vol) paraformaldehyde for 15 mins and permeabilized with 0.1% Triton X-100 for 10 mins before blocking in PBST (1% BSA, 10% donkey serum) at room temperature for 1 hour and incubated overnight at 4°C with primary antibody diluted in blocking solution. The antibodies used to stain epicardial cells from heart explants are the following: anti-Neuropilin 1, Genetex GTX62190; anti-GFP, Roche 11 814 460 001; anti-ALDH2, Genetex GTX124302, normal rabbit IgG, alpha diagnostics 200009-1-200; normal mouse IgG, Invitrogen 026502.

The following day, samples were incubated for one hour at room temperature with fluorescent-tagged secondary antibodies (anti-rabbit Alexa 488 and Alexa Fluor 555 Phalloidin, both Thermo Fisher Scientific). Slides were mounted with ProLong DAPI mounting medium (Thermo Fisher Scientific).

Immunoblotting

Lysates were obtained from zebrafish hearts by homogenizing 3 ventricles in RIPA buffer (Sigma-Aldrich) supplemented with TCEP, protease inhibitor cocktail (Roche) and phosphatase inhibitor cocktails (Sigma-Aldrich) in 1.4mm ceramic bead-containing tubes using the Minilys homogenizer (Peqlab). Lysates were supplemented with Lithium dodecyl sulfate anionic detergent (Thermo Fisher Scientific) and RIPA buffer to load equal amount of proteins. All samples were then denatured by heating for 3 minutes at 95°C before loading to gels. Proteins were separated by electrophoresis on 4–12% Bis-Tris polyacrylamide gels, and electrotransferred to PVDF membranes (all Thermo Fisher Scientific). Membranes were blocked with 5% (w/v) non-fat dried milk in PBS containing 0.1% Tween 20 (PBST), incubated with primary antibodies in PBS/blocking solution overnight at 4°C, washed five times in PBST, incubated for 1 hour with horseradish peroxidase-labelled IgG (Santa Cruz biotechnology, Inc.) at room temperature. The antibodies used for immunoblotting are the following: anti-Neuropilin 1 (Abcam ab81321); anti-GAPDH V-18 (Santa Cruz sc-20357), β actin clone AC-15 (Sigma-Aldrich, Cat No. A5441), β catenin (Sigma-Aldrich, Cat No. C2206). Proteins were detected using the ECL Plus™ Western blotting detection system and Hyperfilm (both Amersham).

Recombinant adenovirus generation

All reagents used for the generation of the adenoviruses constructs were from Life Technologies™.

Rat specific NRP1 shRNA construct was generated as previously described (Pellet-Many et al., 2015) using the BLOCK-iT™ U6 RNAi Entry Vector Kit, the primers used to form the hairpins are listed below. The shRNA cassette was recombined into the pAd/BLOCK-iT™-DEST vector and virus produced as described above. The primers used to generate the construct were:

Ad.shNRP1:

5'- CACCGCAGCATCTCTGAAGATTTACGAATGAAATCTTCAGAGATGCTG -3' and,
5'- AAAAGCAGCATCTCTGAAGATTTCAATTCGTGAAATCTTCAGAGATGCTGC -3'

Viral particles were released from the HEK-293A cells by three freeze-thaw cycles and purified using the Adenopure® adenovirus purification kit (Puresyn, Inc.). Purified adenoviruses were dialyzed (Slide-A-Lyzer Dialysis kit: 10,000 MWCO, 2-12 ml capacity, extra strength (Catalogue number 66807) from Thermo Scientific and stored at -20°C until needed.

Epicardial cell NRP1 knock down

Rat Epicardial cells were a generous gift from Dr Nicola Smart and described in (Wada et al., 2003). Cells were tested prior to their use in experiment and were found to be free of mycoplasma. Cells were seeded and left to adhere for 6 to 8 hours. They were then infected with shNRP1 adenovirus constructs for 24 hours as described in Pellet-Many et al. (2015). Protein lysates were harvested and immunoblotting performed as described above.

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