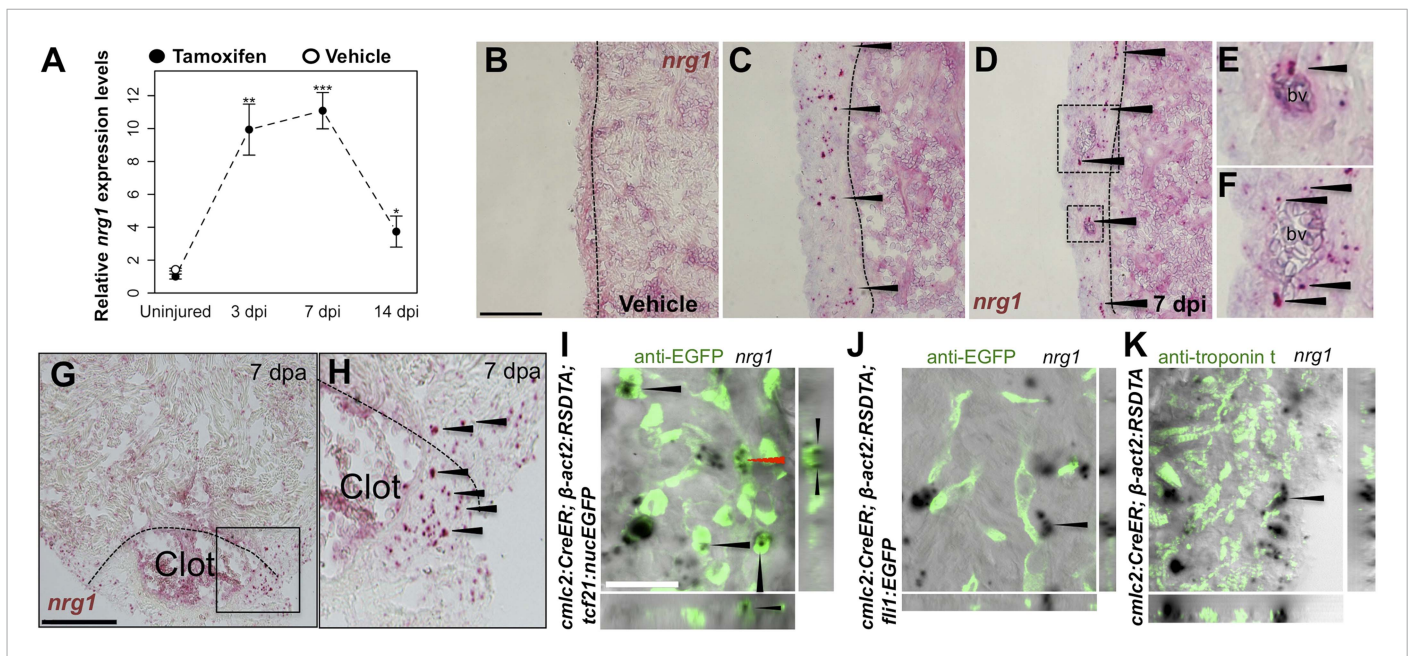


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## Figures and figure supplements

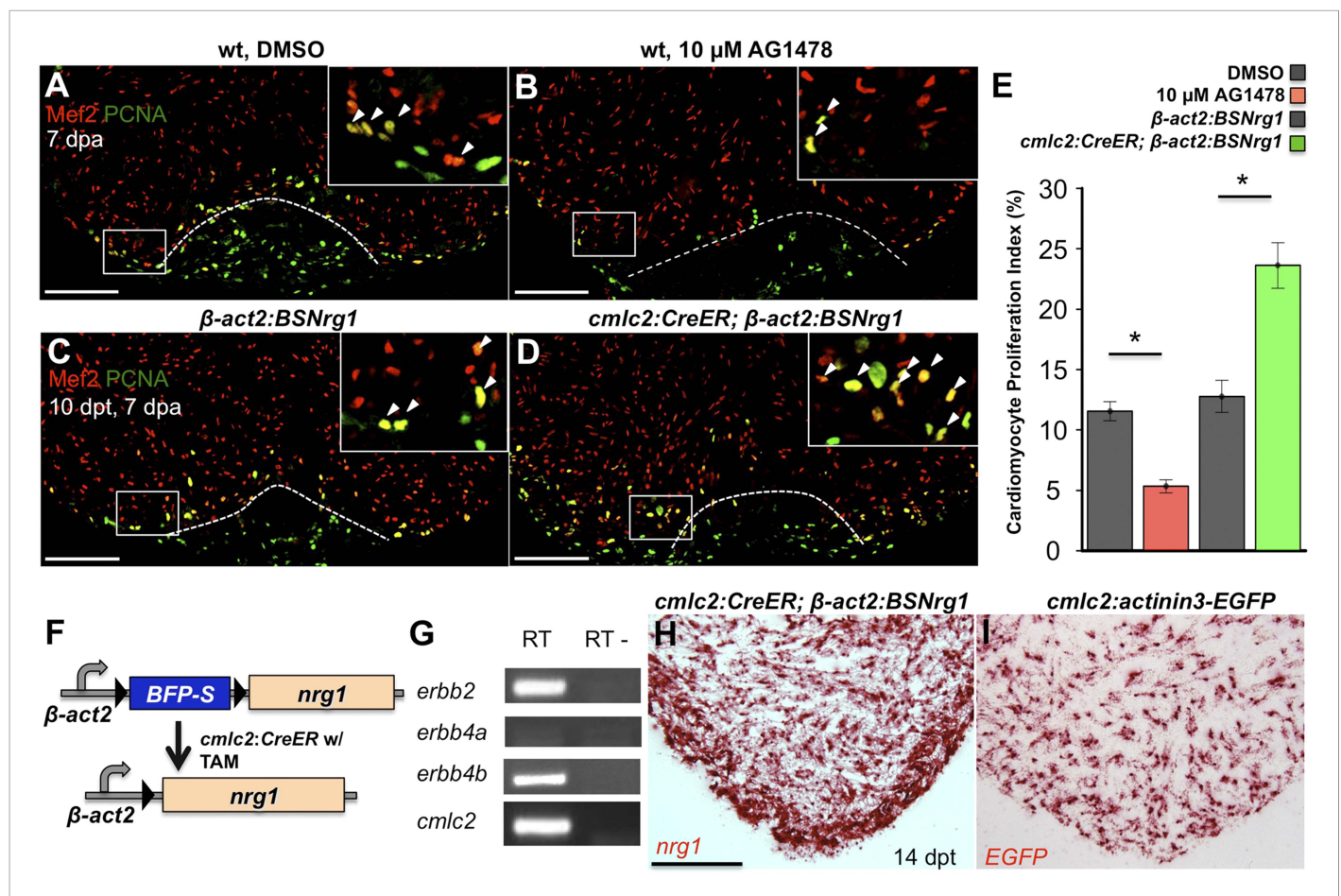
Nrg1 is an injury-induced cardiomyocyte mitogen for the endogenous heart regeneration program in zebrafish

**Matthew Gemberling, et al.**



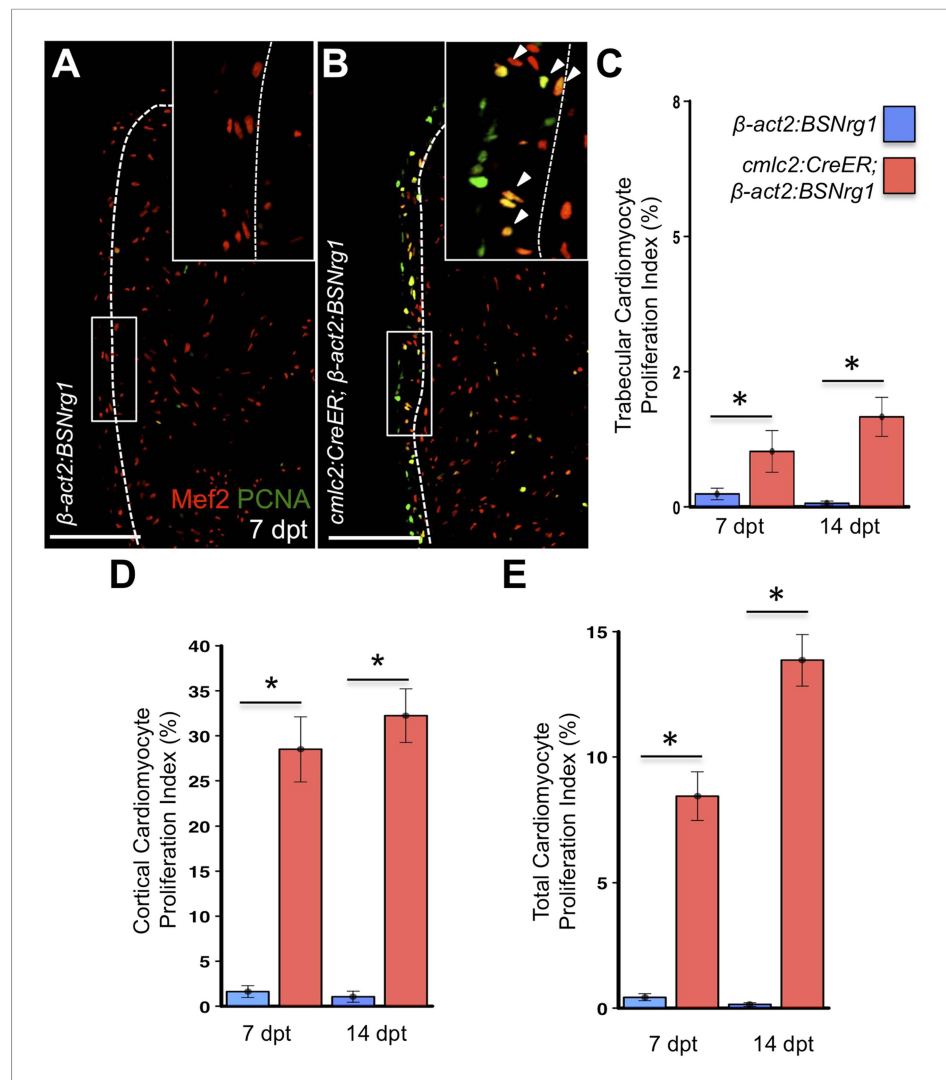
**Figure 1.** Induction of *Nrg1* after cardiac injury. **(A)** Time course of *nrg1* induction in cardiac ventricles following severe genetic ablation of cardiomyocytes. *nrg1* mRNA levels were assessed by qPCR at 3, 7, and 14 days after ablation injury in tamoxifen-treated *cmlc2:CreER*; *β-act2:RSDTA* animals relative to control *cmlc2:CreER* animals (closed circles). *cmlc2:CreER*; *β-act2:RSDTA* (open circle) vehicle-treated animals serve as an additional control. Data are presented as mean  $\pm$  SE. \* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ , Student's *t*-test, two-tailed. **(B–F)** Section images of in situ hybridization experiments assessed for *nrg1* expression in uninjured ventricles **(B)** or at 7 days after induced cardiomyocyte ablation **(C and D)**. Dashed lines delineate the ventricular wall from the trabecular compartment. Higher magnification of boxes in **(E)** and **(F)** reveal *nrg1* signals surrounding vessels (bv). Arrowheads indicate examples of RNAscope signals. Scale bar represents 100  $\mu$ m. **(G and H)** Section images of RNAscope in situ hybridization analysis for *nrg1* expression at 7 days after ventricular resection surgery. Image in **(H)** is a higher magnification of box in **(G)**. Arrowheads indicate examples of RNAscope signals. Scale bar represents 100  $\mu$ m. **(I–K)** Confocal slice images, with accompanying orthogonal views, of *nrg1* expression colocalized with *tcf21:nucEGFP* **(I)**, *flil1:EGFP* **(J)**, or cardiac muscle (Troponin, **K**). Arrows point to RNAscope signal, and red arrows indicate area for orthogonal views. Scale bar represents 20  $\mu$ m.

DOI: [10.7554/eLife.05871.003](https://doi.org/10.7554/eLife.05871.003)



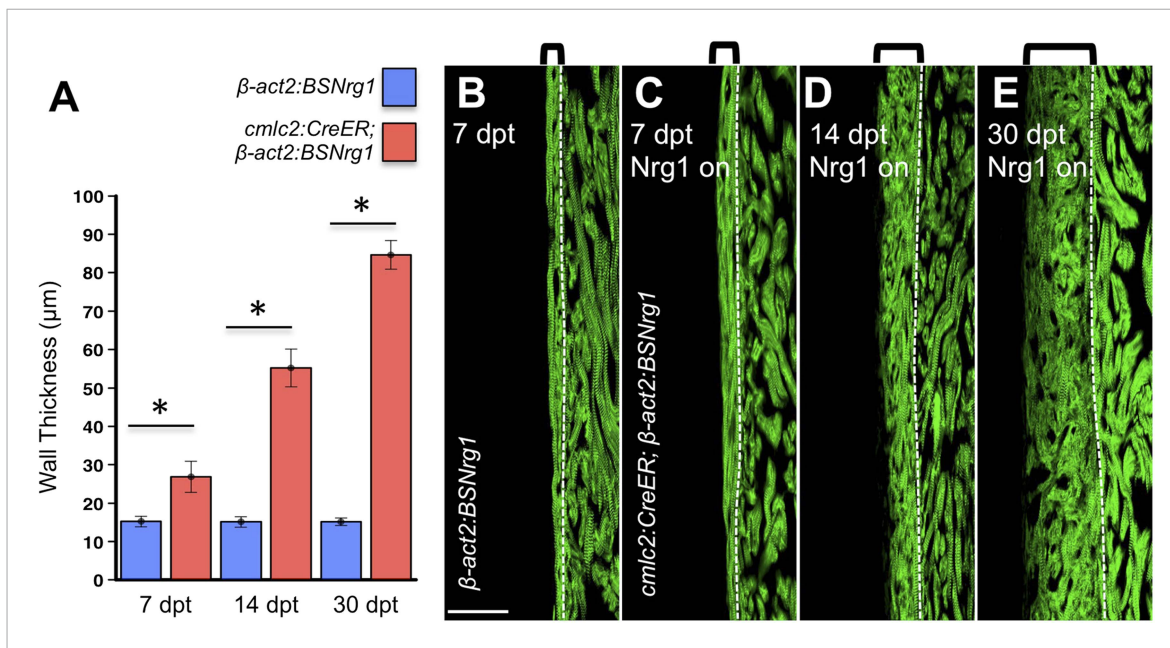
**Figure 2.** Nrg1 signaling modulates cardiomyocyte proliferation during regeneration. (**A** and **B**) Section images of injured ventricular apices of animals treated from 6 to 7 dpa with DMSO (**A**) or 10  $\mu$ M AG1478 (**B**) and stained for Mef2<sup>+</sup>PCNA<sup>+</sup> cells (arrowheads). Wounds are indicated by dotted lines. Scale bar represents 100  $\mu$ m. (**C** and **D**) Section images of 7 dpa ventricular apices of control  *$\beta$ -act2:BSNrg1* (**C**) or *cmlc2:CreER;  $\beta$ -act2:BSNrg1* (**D**) animals treated with tamoxifen at 3 days before injury, stained for Mef2<sup>+</sup>PCNA<sup>+</sup> cells (arrowheads). Scale bar represents 100  $\mu$ m. (**E**) Quantification of cardiomyocyte proliferation at 7 dpa. DMSO-treated wild-type clutchmates (n = 22) were used as controls for 10  $\mu$ M AG1478 treatment (n = 20), and tamoxifen-treated  *$\beta$ -act2:BSNrg1* clutchmates (n = 15) were controls for *cmlc2:CreER;  $\beta$ -act2:BSNrg1* (n = 18) animals. Data are represented as mean  $\pm$  SEM. \*p < 0.05, Mann–Whitney Ranked Sum Test. (**F**) Cartoon schematic of  *$\beta$ -act2:BSNrg1* transgene. (**G**) RT-PCR results for *erbb2*, *erbb4a*, and *erbb4b*, indicating the presence of *erbb2* and *erbb4b* messages in the uninjured adult ventricle. *cmlc2* is shown as a control. (**H**) Section image of RNA scope in situ hybridization analysis for *nrg1* expression at 14 days after tamoxifen-released expression in uninjured *cmlc2:CreER;  $\beta$ -act2:BSNrg1* ventricles. (**I**) Section image of RNA scope in situ hybridization analysis for *EGFP* expression in uninjured *cmlc2:actinin3-EGFP* ventricles, used as a control to detect transgenic signals. Scale bar represents 100  $\mu$ m.

DOI: 10.7554/eLife.05871.004



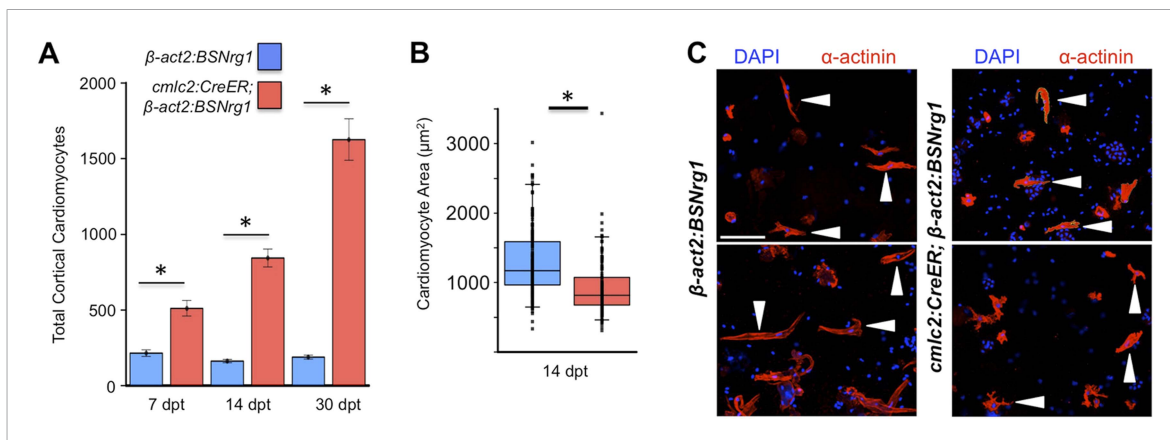
**Figure 3.** Nrg1 reactivation without injury induces proliferation of ventricular wall cardiomyocytes. (A and B) Section images from uninjured *cmlc2:CreER; β-act2:BSNrg1* and control ventricles at 7 days post-tamoxifen treatment (dpt), stained for Mef2<sup>+</sup>PCNA<sup>+</sup> cells. Insets show high-zoom views of the boxed regions, and arrowheads indicate Mef2<sup>+</sup>PCNA<sup>+</sup> nuclei. Dashed lines delineate cortical (wall) from trabecular muscle. Scale bars represent 100 μm. (C) Quantification of cardiomyocyte proliferation in *cmlc2:CreER; β-act2:BSNrg1* and controls in the trabecular muscle compartment at 7 (n = 8, 9) and 14 dpt (n = 10, 10). Data are represented as mean ± SEM. \*p < 0.05, Mann-Whitney Ranked Sum Test. (D) Quantification of cardiomyocyte proliferation in cortical muscle at 7 (n = 8, 9) and 14 dpt (n = 10, 10), from groups in (A and B). Data are represented as mean ± SEM. \*p < 0.05, Mann-Whitney Ranked Sum Test. (E) Quantification of total cardiomyocyte proliferation at 7 (n = 8, 9) and 14 dpt (n = 10, 10), from groups in (C and D). Data are represented as mean ± SEM. \*p < 0.05, Mann-Whitney Ranked Sum Test.

DOI: [10.7554/eLife.05871.005](https://doi.org/10.7554/eLife.05871.005)



**Figure 4.** Nrg1-induced cardiomyocyte proliferation expands the ventricular wall. **(A)** Quantification of cortical muscle thickness at 7 (n = 8, 9), 14 (n = 10, 11), and 30 dpt (n = 11, 11). Data are represented as mean  $\pm$  SEM. \*p < 0.05, \*\*p < 0.01, Student's t-test, two-tailed. **(B–E)** Section images of *cmlc2:CreER*;  $\beta$ -act2:BSNrg1 (Nrg1 on) and control ventricles from 7 to 30 dpt, using animals also transgenic for *cmlc2:actinin3-EGFP* to indicate sarcomere organization. Brackets indicate cortical muscle, and dashed lines delineate cortical from trabecular muscle. Scale bar represents 100  $\mu$ m.

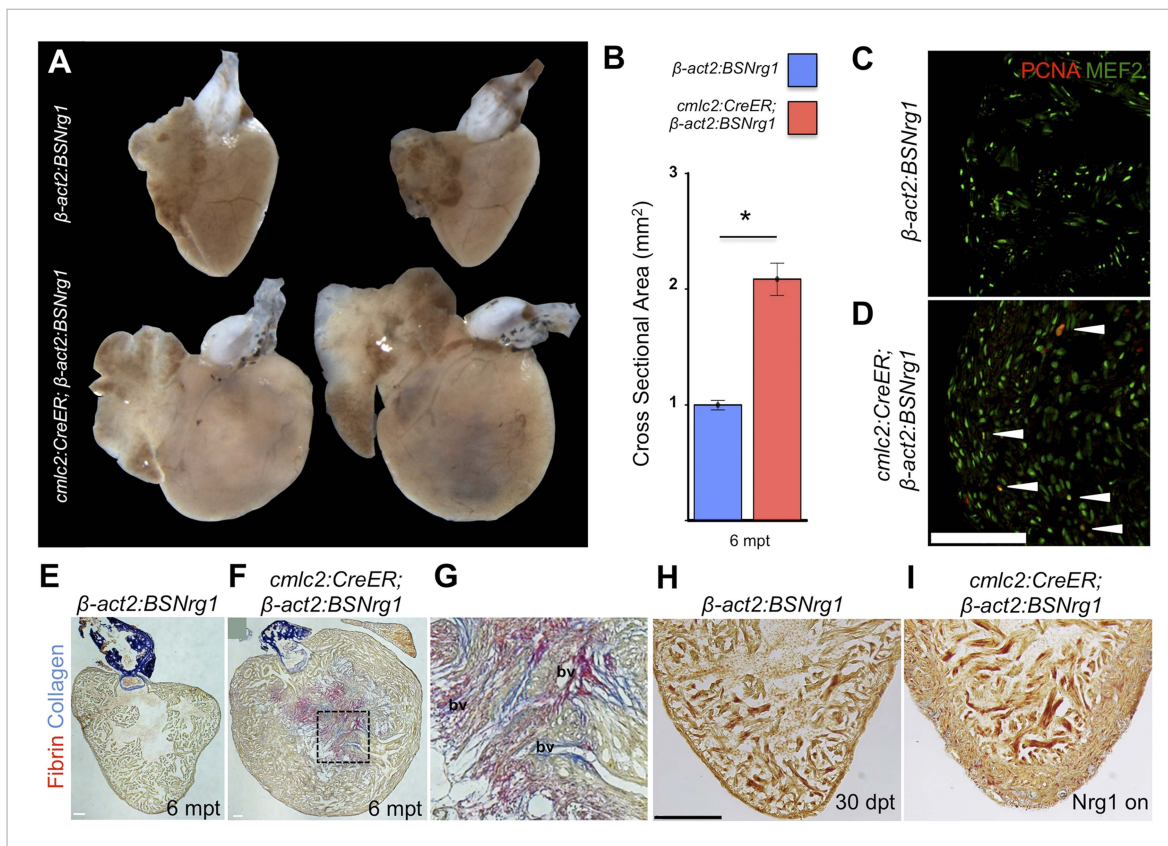
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**Figure 5.** Nrg1 induces a hyperplastic, not hypertrophic, response. **(A)** Quantification of total ventricular wall cardiomyocytes in *cmlc2:CreER*;  $\beta$ -act2:BSNrg1 animals and controls at 7 (n = 8, 9) and 14 dpt (n = 10, 10). Data are represented as mean  $\pm$  SEM. \*p < 0.05, Student's t-test, two-tailed. **(B)** Quantification of cardiomyocyte area in *cmlc2:CreER*;  $\beta$ -act2:BSNrg1 animals and controls at 14 dpt. Data are represented as mean  $\pm$  SD, with all data points represented. \*p < 0.05, Student's t-test, two-tailed. **(C and D)** Confocal images of dissociated cardiomyocytes from *cmlc2:CreER*;  $\beta$ -act2:BSNrg1 and controls at 14 dpt (n = 124, 172). Only cardiomyocytes with visible sarcomeres and nuclei were measured. Examples of quantified cells are marked with arrows. Scale bar represents 100  $\mu$ m.

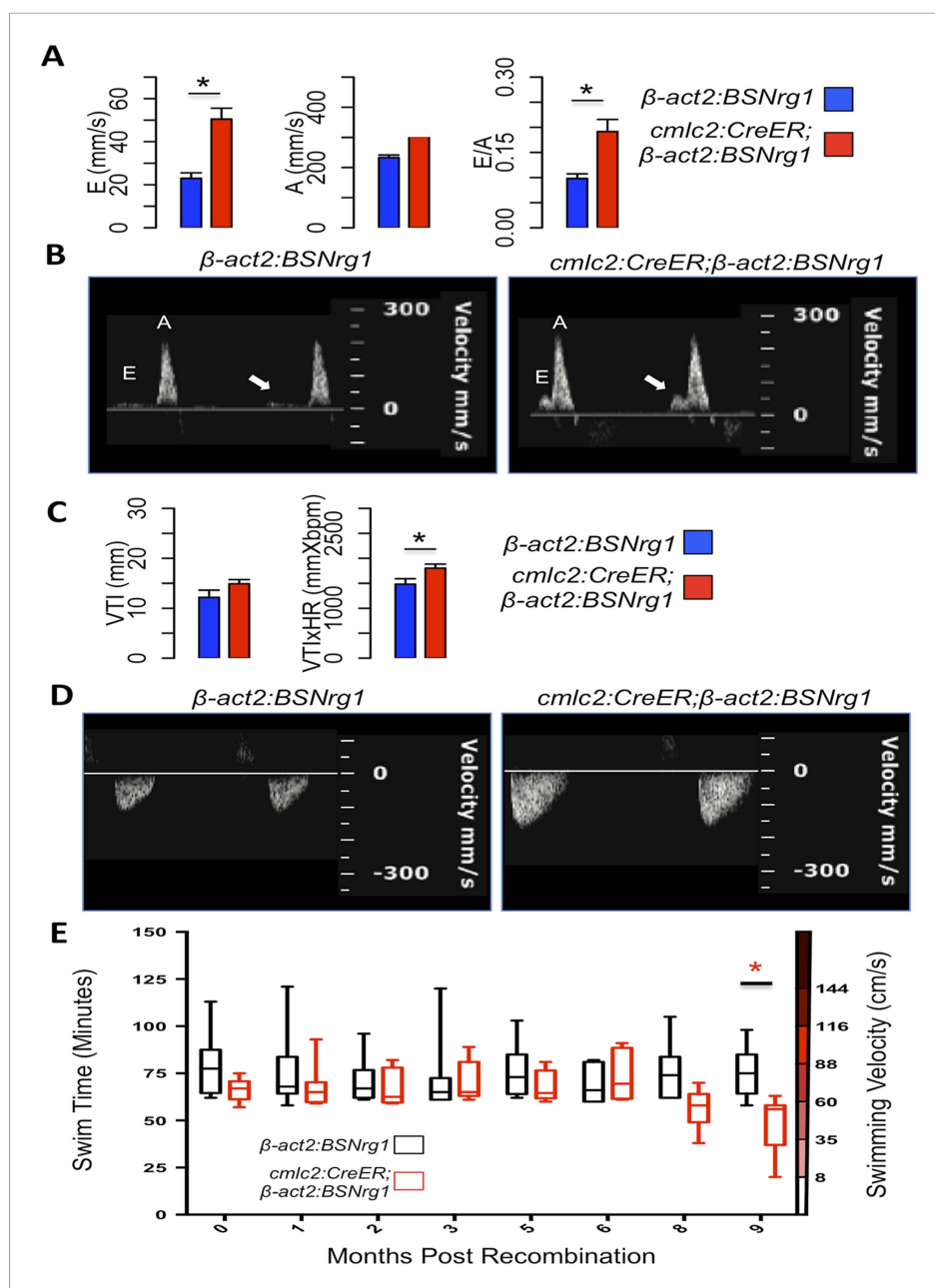
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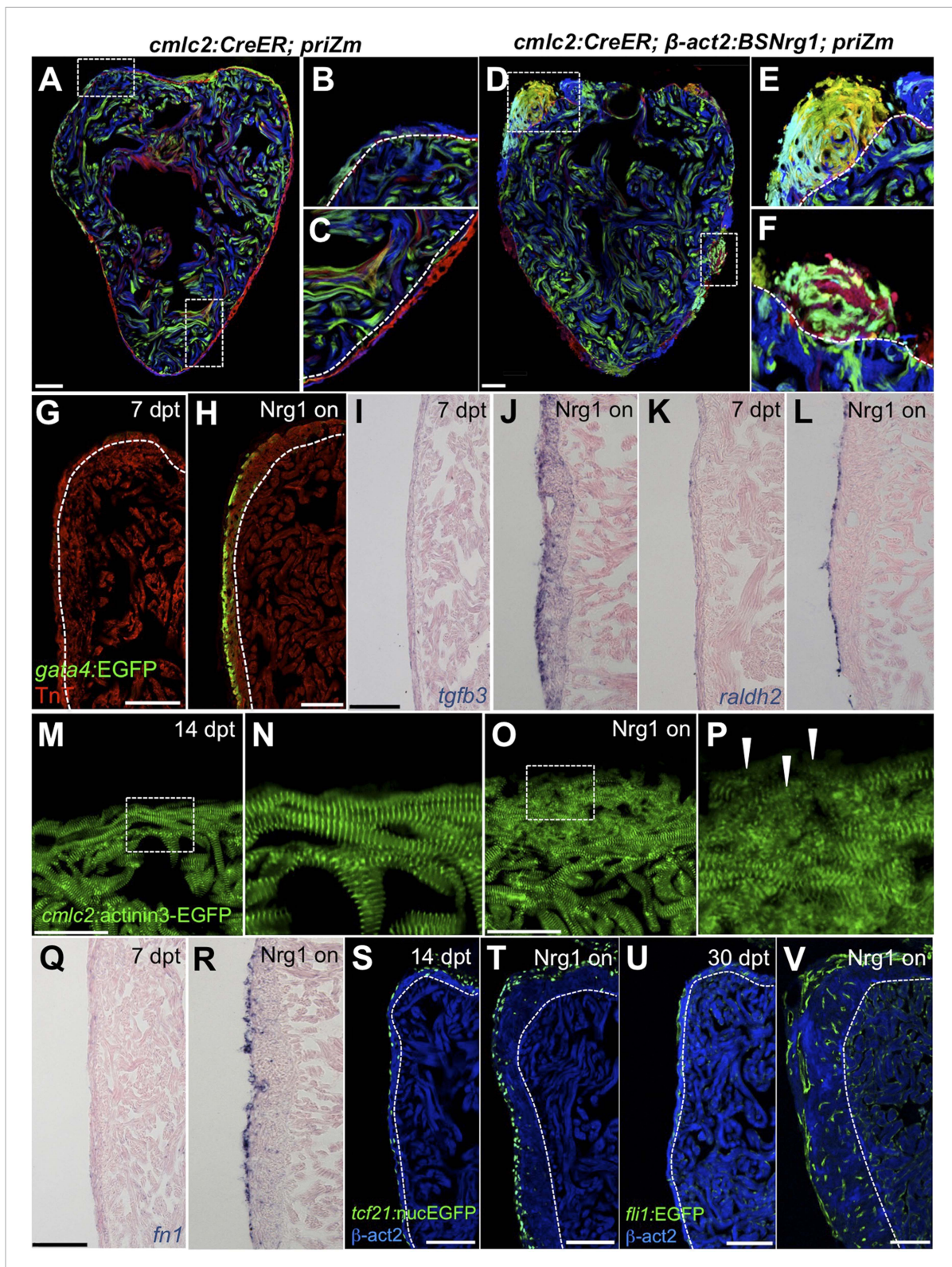
**Figure 6.** Nrg1-induced hyperplasia causes cardiomegaly. **(A)** Whole-mount images of *cmlc2:CreER*;  $\beta$ -act2:BSNrg1 and control ventricles at 6 months post-tamoxifen treatment. **(B)** Quantification of the cross-sectional surface area of *cmlc2:CreER*;  $\beta$ -act2:BSNrg1 ( $n = 9$ ) and control ventricles ( $n = 10$ ) 6 months post-treatment, revealing cardiomegaly effects of *nrg1* overexpression. Data are represented as mean  $\pm$  SEM. \* $p < 0.05$ , Student's *t*-test, two-tailed. **(C and D)** Section images of ventricular walls of 6 mpt control  $\beta$ -act2:BSNrg1 **(C)** or *cmlc2:CreER*;  $\beta$ -act2:BSNrg1 animals **(D)** stained for Mef2\*PCNA<sup>+</sup> cells (arrowheads). Scale bar represents 100  $\mu$ m. **(E)** Section images of control  $\beta$ -act2:BSNrg1 ventricles stained with Acid-Fuchsin Orange G (AFOG), revealing minimal collagen (blue), or fibrin deposition (red). Scale bar represents 100  $\mu$ m. **(F and G)** Section images of *cmlc2:CreER*;  $\beta$ -act2:BSNrg1 ventricles stained with AFOG, revealing collagen (blue) and fibrin deposition (red) in the inner portions of the thickened ventricular wall. Image in **(G)** is a high-zoom view of box in **(F)** and also indicates two examples of large coronary vessels (bv). **(H and I)** Acid-Fuchsin Orange (AFOG) staining reveals minimal fibrosis in *cmlc2:CreER*;  $\beta$ -act2:BSNrg1 ventricle at 30 dpt despite the thickened ventricular wall ( $n = 7, 7$ ). Scale bar represents 100  $\mu$ m.

DOI: 10.7554/eLife.05871.008



**Figure 7.** Effects of Nrg1 reactivation on cardiac function. **(A)** Doppler measures of ventricular filling obtained at the AV valve in *cmlc2:CreER*;  $\beta$ -act2:BSNrg1 and  $\beta$ -act2:BSNrg1 animals ( $n = 9$  and  $7$ ). Data are represented as mean  $\pm$  SEM.  $*p < 0.05$ , Student's  $t$ -test, two-tailed. **(B)** Representative PW Doppler at the AV valve in *cmlc2:CreER*;  $\beta$ -act2:BSNrg1 and  $\beta$ -act2:BSNrg1 animals. **(C)** Doppler measures of cardiac output and stroke volume using the velocity time integral (VTI) obtained at the outflow tract (OFT) in *cmlc2:CreER*;  $\beta$ -act2:BSNrg1 and  $\beta$ -act2:BSNrg1 animals ( $n = 9$ ,  $7$ ). Data are represented as mean  $\pm$  SEM.  $*p < 0.05$ , Student's  $t$ -test, two-tailed. **(D)** Representative PW Doppler at the OFT in *cmlc2:CreER*;  $\beta$ -act2:BSNrg1 and  $\beta$ -act2:BSNrg1 animals. **(E)** Quantification of graded swimming performance of animals at varying times of *nrg1* overexpression plotted as box and whisker plots. Two-way ANOVA was performed looking at the effect of Nrg1 overexpression ( $p < 0.05$ ), age ( $p = 0.38$ ), and the interaction of Nrg1 overexpression and age ( $p < 0.05$ ).

DOI: [10.7554/eLife.05871.009](https://doi.org/10.7554/eLife.05871.009)



**Figure 8.** *Nrg1* reactivation is sufficient to induce the heart regeneration program. (A–F) Section images of ventricles from control *cmlc2:CreER; priZM* (A–C) and *cmlc2:CreER; β-act2:BSNrg1; priZM* (D–F) animals treated with tamoxifen at 5 weeks post-fertilization (wpf) and assessed at 10 wpf. Cortical myocyte clones show clear boundaries between clones in control ventricles (B and C; n = 11). During *nrg1* overexpression, cortical muscle thickens appreciably via mixing and radial growth of distinct clones (E and F; n = 14). Dashed lines delineate cortical from trabecular muscle. Scale bar represents Figure 8. continued on next page



Figure 8. Continued

100  $\mu\text{m}$ . (**G** and **H**) Section images of ventricles from *cmlc2:CreER*;  $\beta$ -act2:BSNrg1 (Nrg1 on) and control animals at 7 days post-treatment, using animals also transgenic for *gata4:EGFP*. EGFP induction is clear in the cortical layer during *nrg1* overexpression. Scale bar represents 100  $\mu\text{m}$ . (**I** and **J**) Section images of ventricles from *cmlc2:CreER*;  $\beta$ -act2:BSNrg1 and control animals at 7 days post-treatment, visualized for *tgfb3* expression by in situ hybridization. Scale bar represents 100  $\mu\text{m}$ . (**K**, **L**, **Q**, **R**) Section images of ventricles from *cmlc2:CreER*;  $\beta$ -act2:BSNrg1 and control animals at 7 days post-treatment, visualized for *raldh2* (**K** and **L**) or *fn1* expression (**Q** and **R**) in epicardial cells by in situ hybridization. Scale bar represents 100  $\mu\text{m}$ . (**M** and **N**) Section images of the ventricular wall from *cmlc2:CreER*;  $\beta$ -act2:BSNrg1 and control animals at 14 days post-treatment, using animals transgenic for *cmlc2:actinin3-EGFP*. EGFP marks sarcomeric z-bands. Control animals (**M**) show organized sarcomeres in ventricular wall. *nrg1* overexpression (**O**) leads to reduced EGFP fluorescence and disorganization of sarcomeres. Arrowheads point to areas of reduced EGFP intensity and sarcomere organization. Boxes in (**M** and **O**) are represented as high-zoom in (**N** and **P**). Scale bars represents 50  $\mu\text{m}$ . (**S** and **T**) Section images of ventricles from *cmlc2:CreER*;  $\beta$ -act2:BSNrg1 and control animals at 14 days post-treatment, visualized for epicardial cells using a *tcf21:nucEGFP* transgene. *nrg1* overexpression grossly increases epicardial cell presence. Scale bar represents 100  $\mu\text{m}$ . (**U** and **V**) Section images of ventricles from *cmlc2:CreER*;  $\beta$ -act2:BSNrg1 and control animals at 30 days post-treatment, visualized for endothelial cells using a *fli1:EGFP* transgene. Increased endothelial cells and vasculature are evident in the thickened ventricular wall. Scale bar represents 100  $\mu\text{m}$ .

DOI: [10.7554/eLife.05871.012](https://doi.org/10.7554/eLife.05871.012)