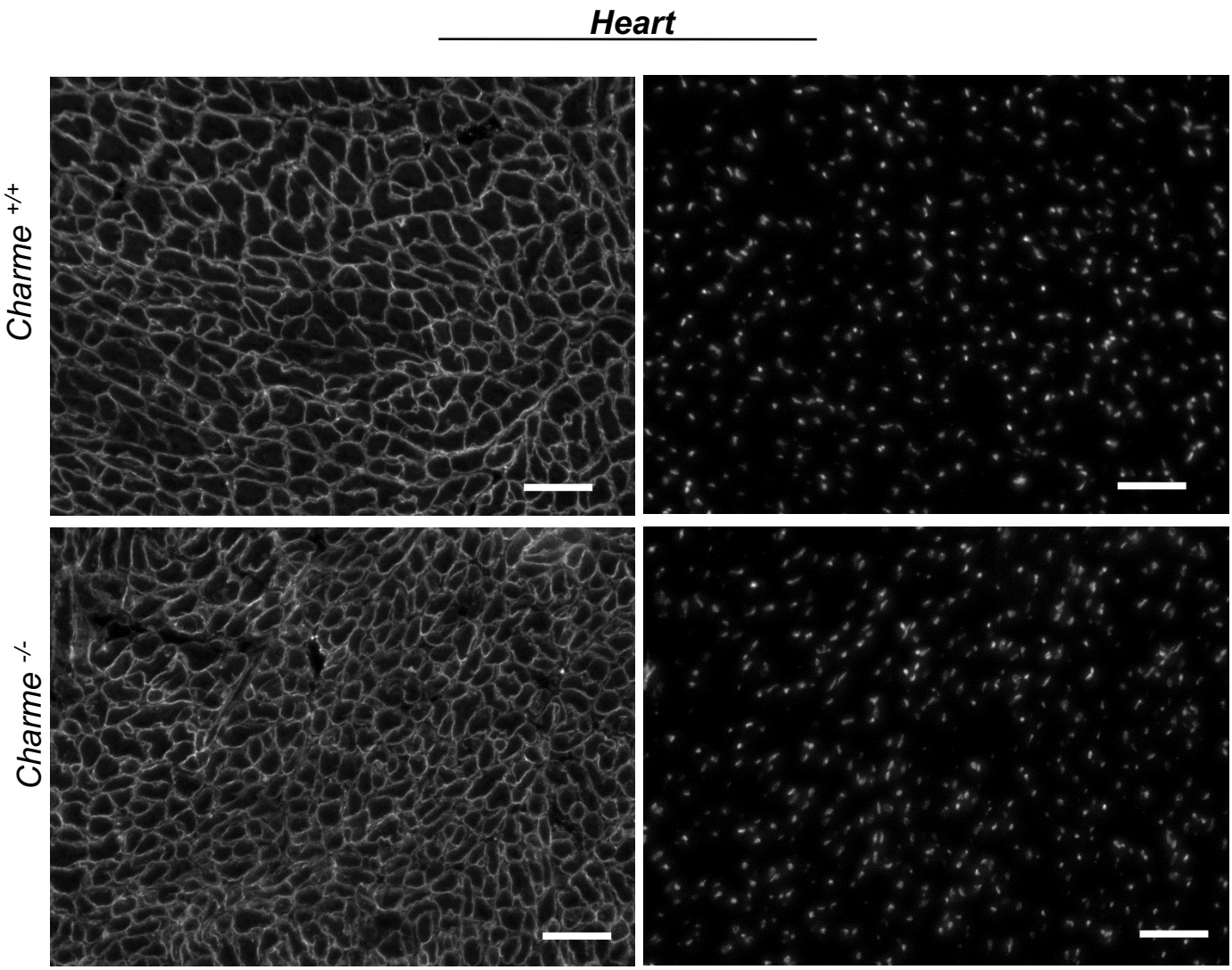
RAW DATA FIGURE 5
Fig 5

Figure 5C



Full size images of immunofluorescence for dystrophin protein and DAPI (4',6-diamidino-2-phenylindole) on *Charme*$^{+/+}$ and *Charme*$^{-/-}$ skeletal gastrocnemius and heart biopsies.
The images were acquired as 8 bit depth by using a Plan-Neofluar EC 10×/0.3 M27 (gastrocnemius) or LD 20×/0.4 Korr (heart) and collected with AxioVision Rel.4.8 software. The entire images were processed in post-acquisition analysis with FIJI software, in contrast and brightness for Dystrophin and DAPI. For both channels, pseudocolor were added and color combine applied. Scale bar = 100 μm.

Figure 5E

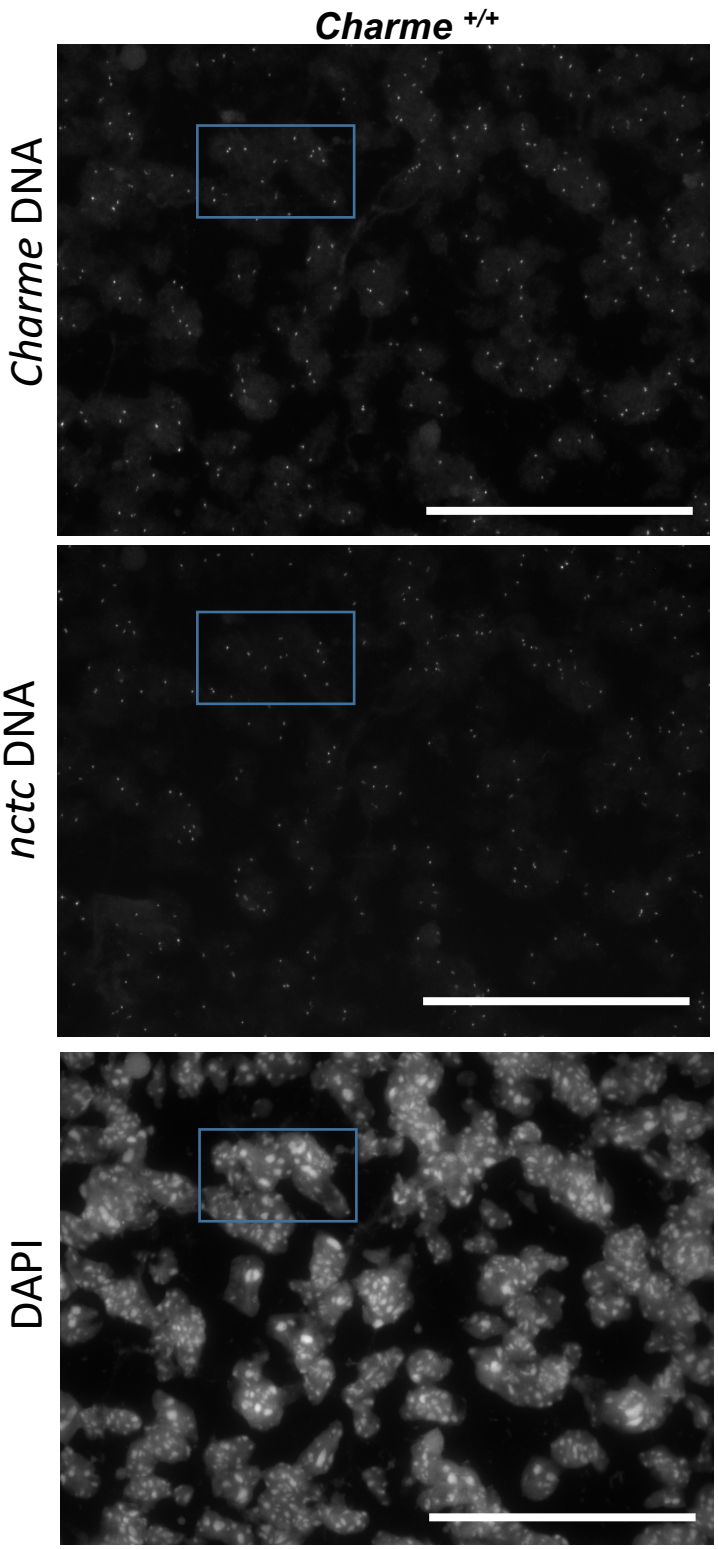
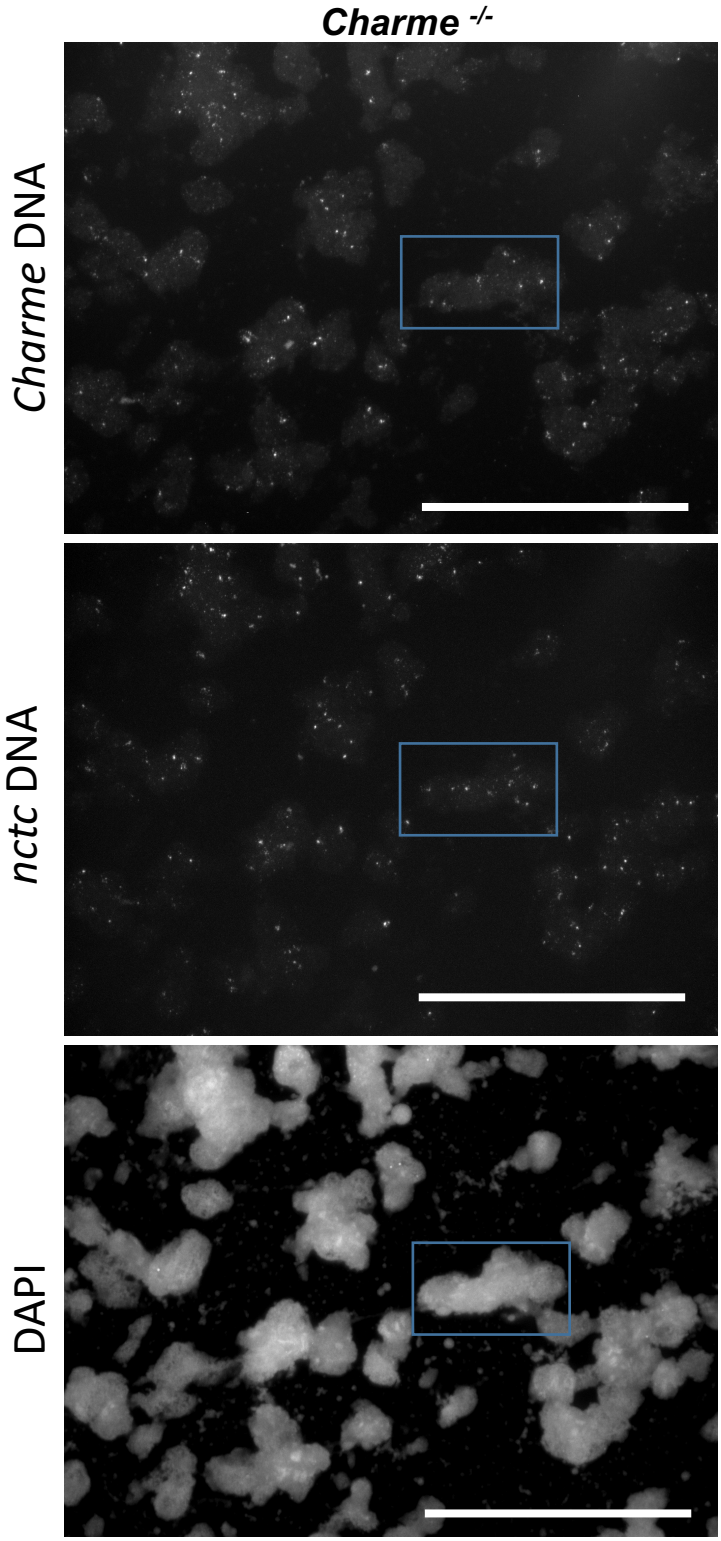


Figure 5E



Full size confocal images of DNA/DNA FISH for *Charme* and *nctc* genomic regions **and DAPI (4',6-diamidino-2-phenylindole) in** *Charme*$^{+/+}$ and *Charme*$^{-/-}$ neonatal (1 day old) cardiac tissues**.**

The images were acquired as 16 bit depth with a resolution XY of 0,075 micron, by using a UPLANSApo 60 X oil objective (NA 1.35) and collected with MetaMorph software (Molecular Devices). Stacks of images were taken automatically with 0,2 micron between the Z-slices.

The entire images were processed in post-acquisition analysis with FIJI software:

DNA FISH 16 bit Z-stacks were processed with a Laplacian of Gaussian filter (sigma XYZ 3px) to enhance the spots signal over background and color balance was manually adjusted using MetaMorph or ImageJ softwares setting a reference value considering the without specific staining as a background.

All Z stacks were merged with maximum intensity projection and combine in multicolour image. Blue square: area enlarged in the figure. Scale bar = 50 µm.