RAW DATA FIGURE 1
Fig 1

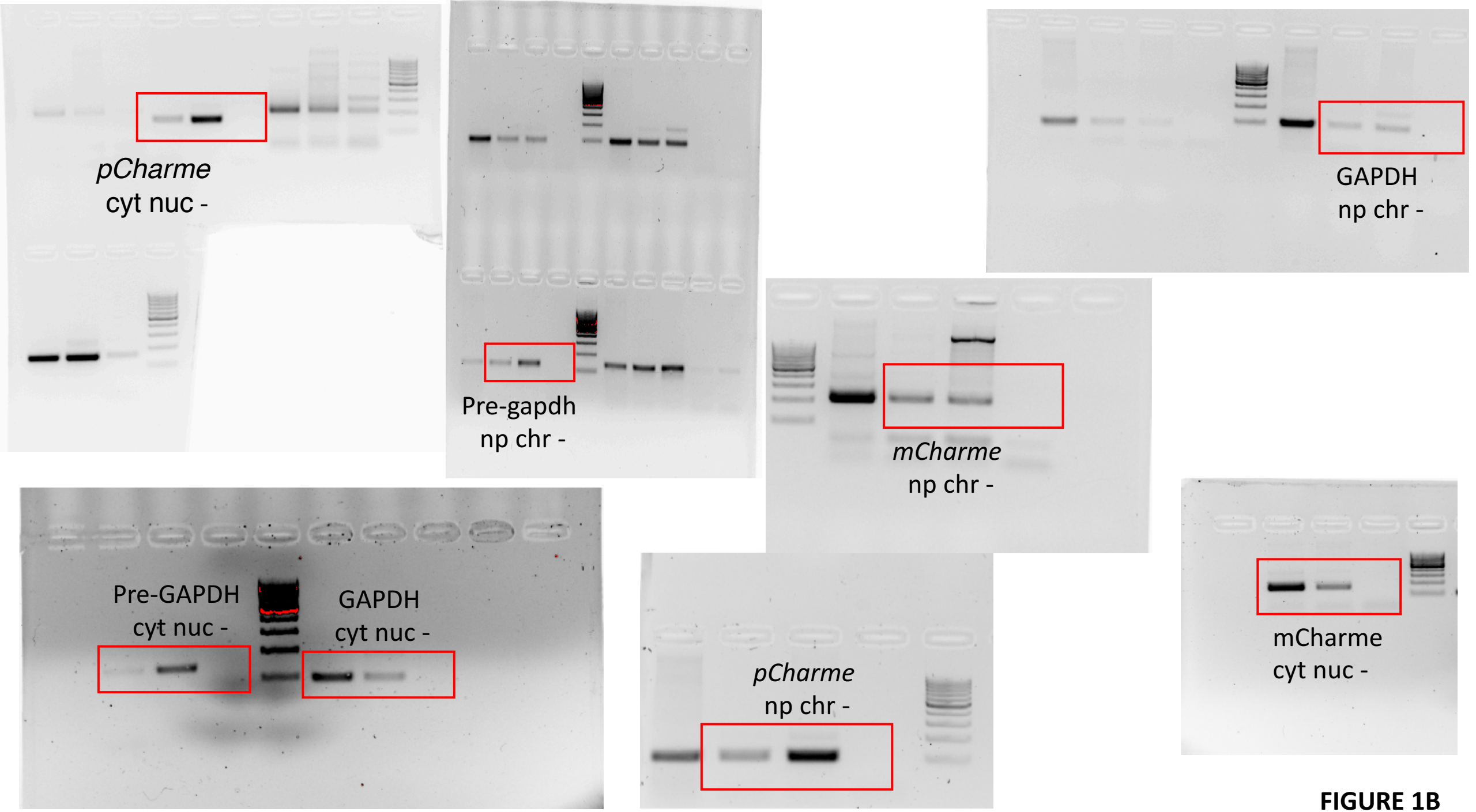
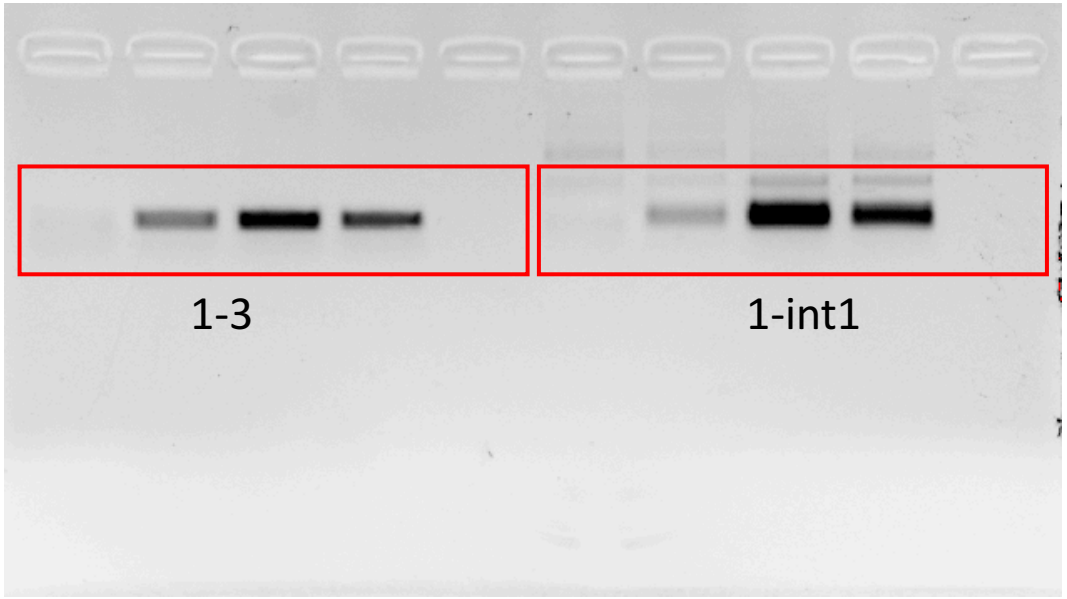
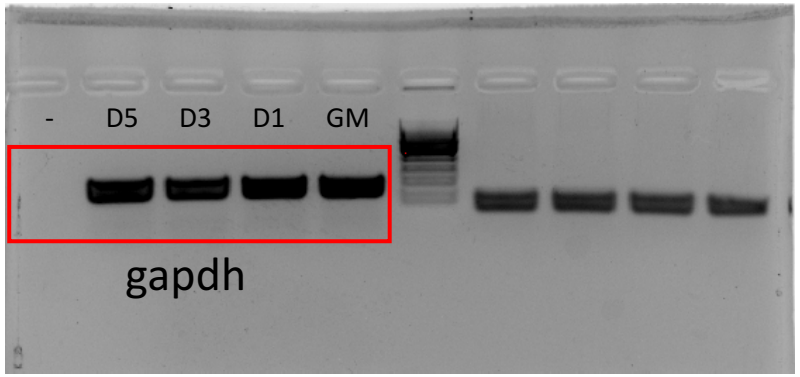

pCharme
cyt nuc -
Pre-gapdh
np chr -
GAPDH
np chr -
mCharme
np chr -
Pre-GAPDH
cyt nuc -
GAPDH
cyt nuc -
pCharme
np chr -
mCharme
cyt nuc -

FIGURE 1B





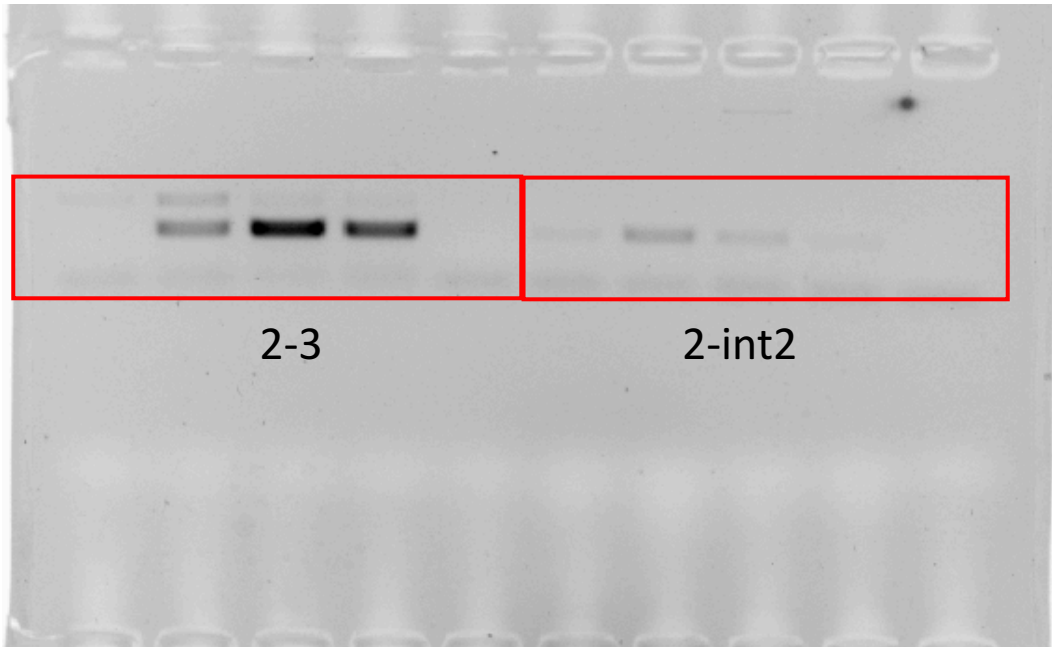


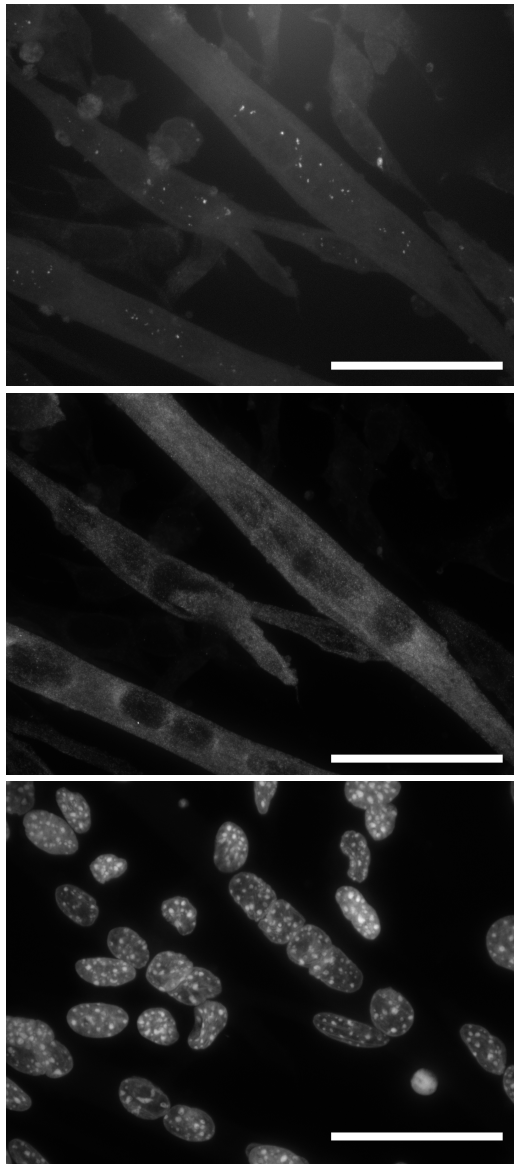
FIGURE 1D

Figure 1C

Charme RNA

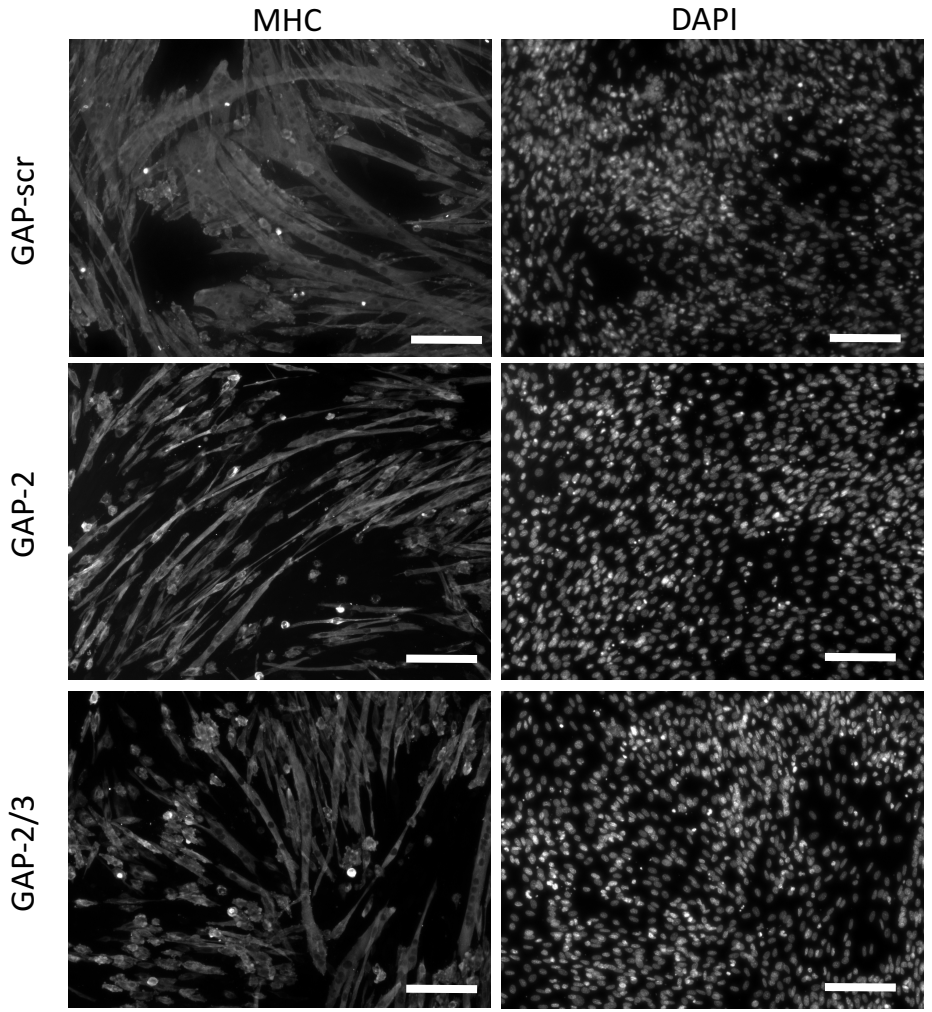
myosin heavy chain (MHC)

DAPI



Full size confocal images of co-staining for *MHC* protein and *Charme* RNA and DAPI (4',6-diamidino-2-phenylindole) in fully differentiated C_2C_{12} myotubes.
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 images were processed in post-acquisition analysis with FIJI software, in contrast and brightness for MHC immunolabeling; the RNA-FISH Z-stacks were processed with a Laplacian of Gaussian filter (sigma XYZ 3px) to enhance the spots signal over background. For both channels, Intensity threshold was manually adjusted using MetaMorph software. All adjustement were applied to the entire image. Z-stacks were merged with maximum intensity projection and combine in multicolour image. Scale bar = 50 µm.

Figure 1F



Full size images of immunofluorescence for *MHC* protein and DAPI (4',6-diamidino-2-phenylindole) in fully differentiated C2C12 myotubes.
The images were acquired as 8 bit depth by using a Plan-Neofluar EC 10×/0.3 M27 and collected with AxioVision Rel.4.8 software. The images were processed in post-acquisition analysis with FIJI software, in contrast and brightness for MHC and DAPI and all adjustement were applied to the entire image. For both channels, pseudocolor were added and color combine applied. Scale bar = 100 µm.