

RAW DATA FIGURE 3

Fig 3

Figure 3A

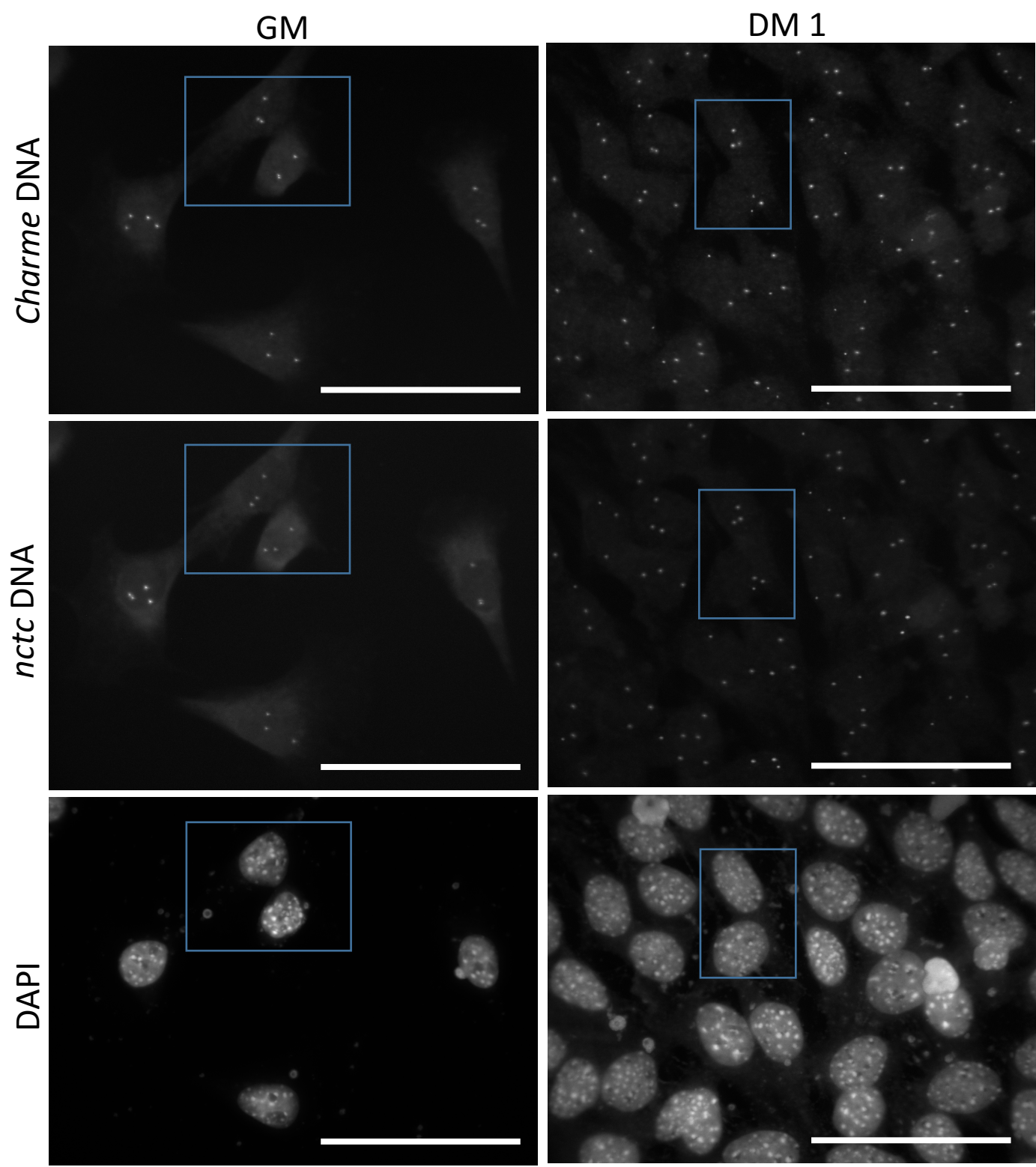


Figure 3A

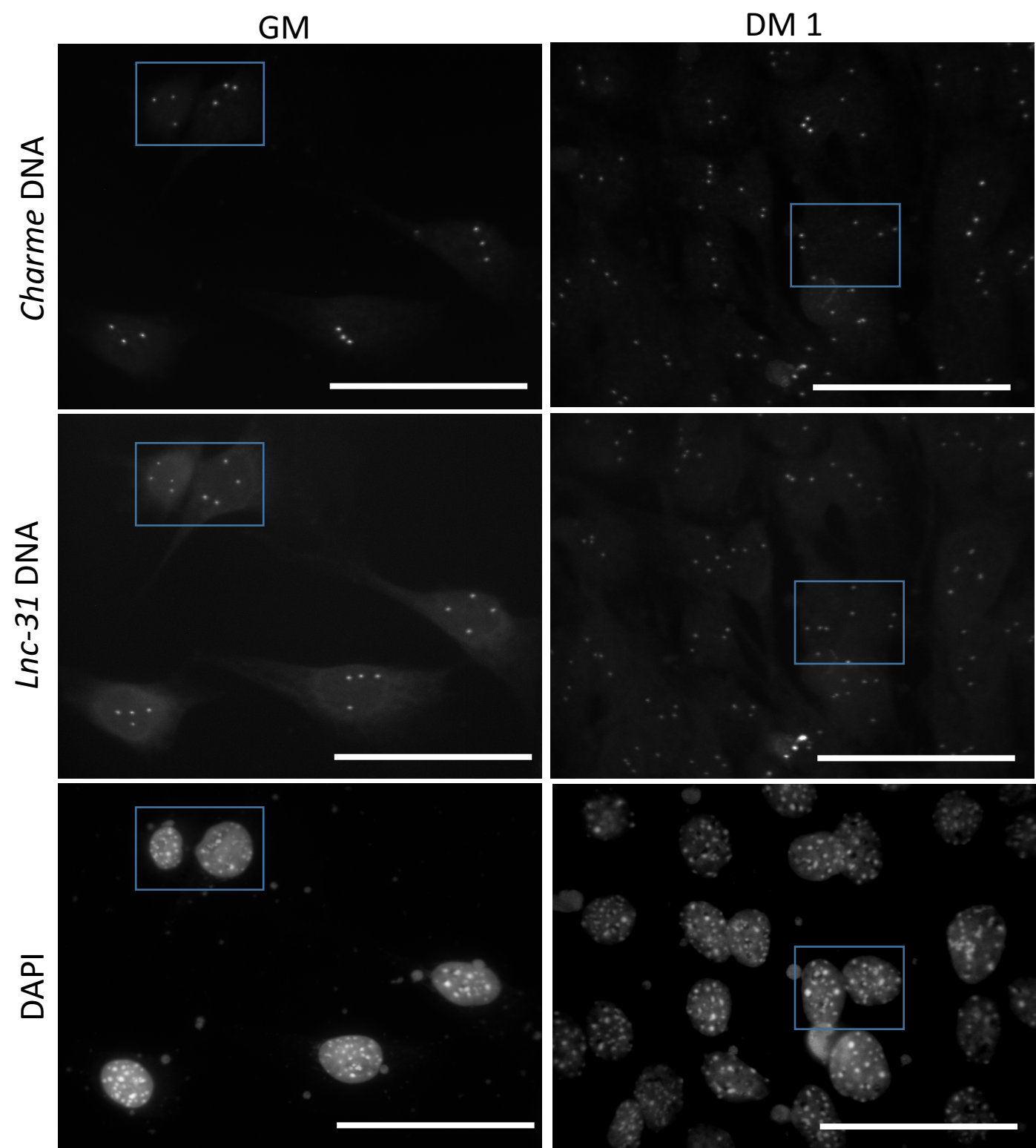
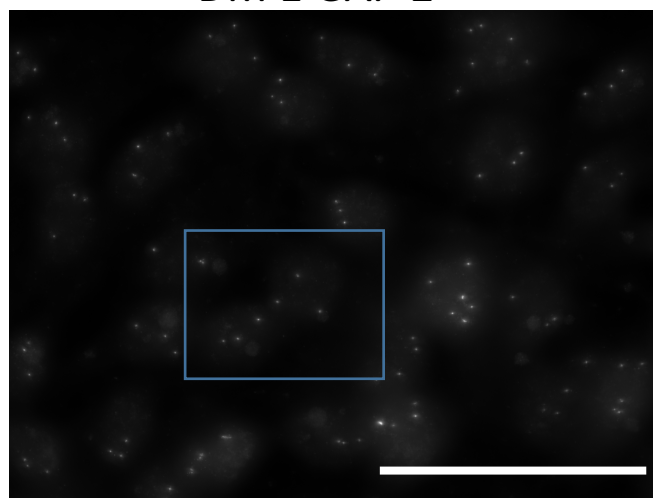
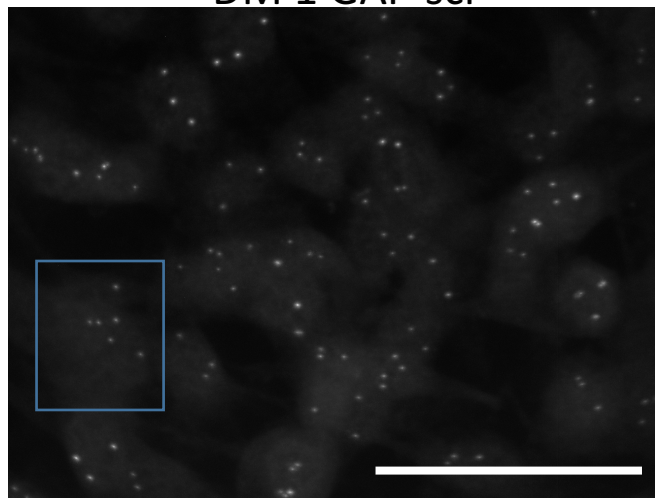


Figure 3B

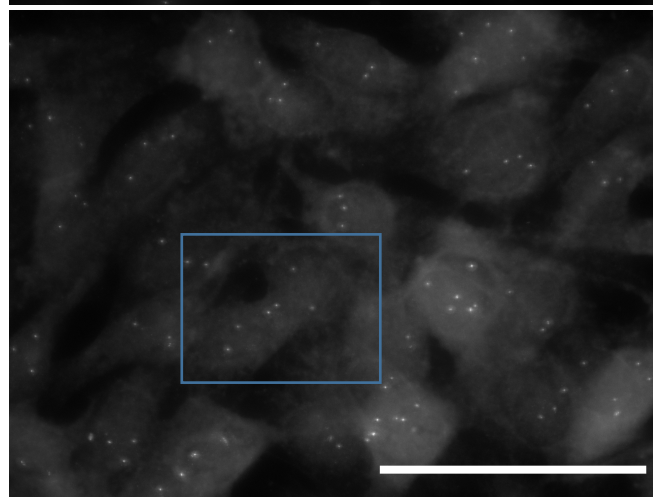
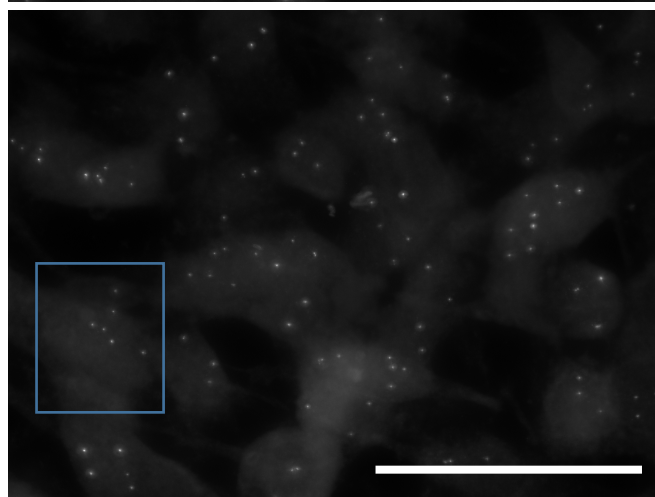
DM 1 GAP-scr

DM 1 GAP-2

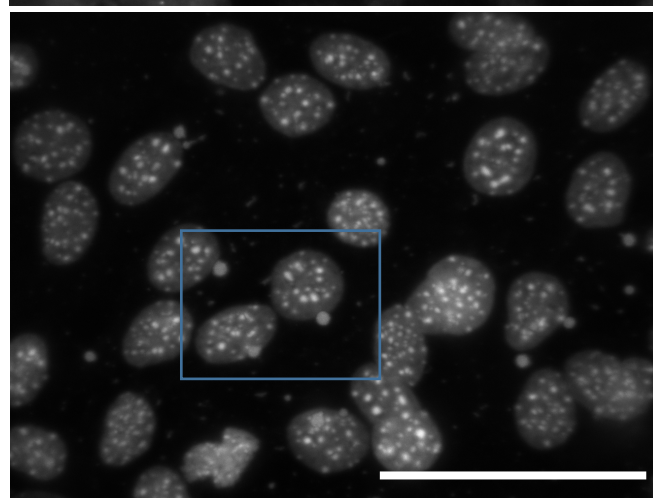
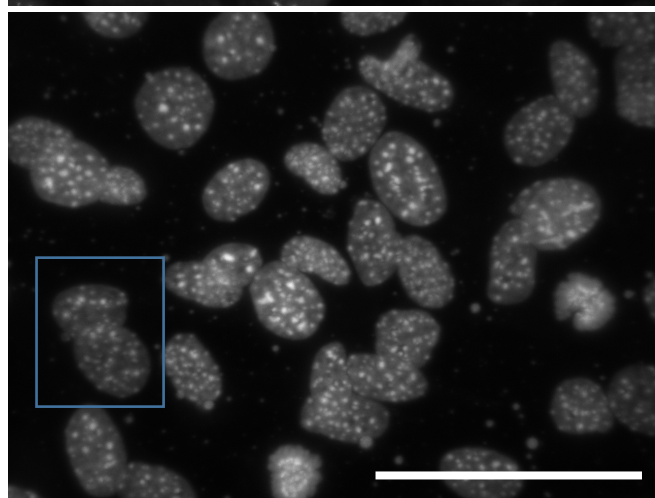
Charme DNA



nctc DNA



DAPI



Full size confocal images of DNA/DNA FISH for *Charme* and *nctc* genomic regions and DAPI (4',6-diamidino-2-phenylindole) in proliferating (GM) and differentiated (DM1 and DM1,5) C_2C_{12} cell cultures.

The images were acquired as 16 bit depth with a resolution XY of 0,075 micron, by using a UPLANS Apo 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 and all adjustment were applied to the entire image.

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 μ m.