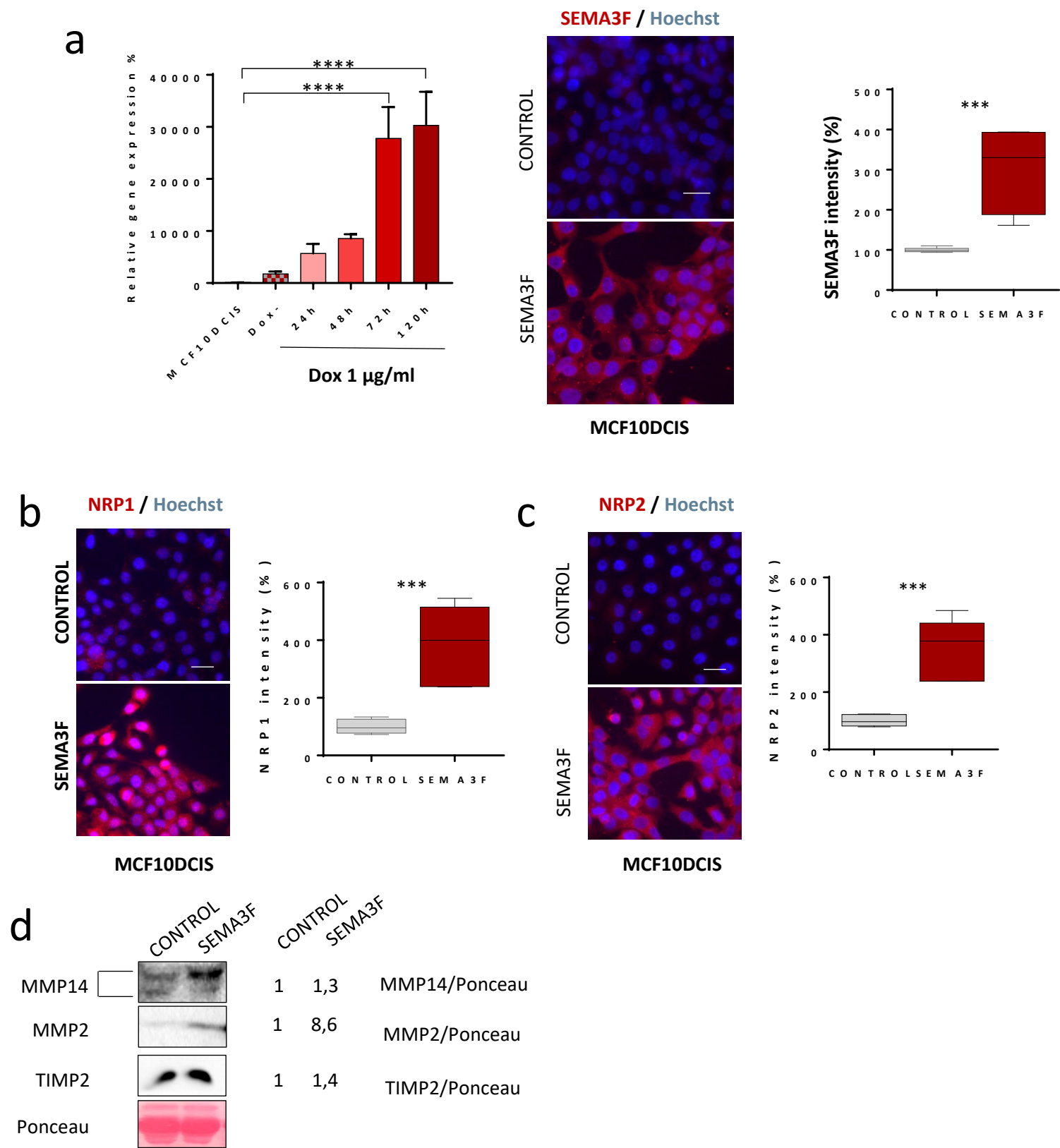


Supplementary Figure 3



Suppl. Figure 3. Effects of SEMA3F over-expression in MCF10DCIS cell line. A) Left panel, analysis of *SEMA3F* mRNA relative expression in MCF10DCIS cells. *SEMA3F* expression was induced by 24, 48, 72 or 120h of doxycycline (Dox; 1µg/mL) treatment. The graph represents the % of mRNA levels ± S.E.M. referred to non-treated MCF10DCIS cells (control); ****P < 0.0001 comparing non-treated vs *SEMA3F* overexpressing MCF10DCIS cells by one-way ANOVA, Mann-Whitney's test. Middle and right panels, representative IF images (middle panel; scale bar: 20µm) and mfi quantification (right panel) for *SEMA3F* in control or *SEMA3F* overexpressing MCF10DCIS cells. The graph represents the % of mfi levels ± S.E.M. referred to control cells; ***P < 0.001 comparing control vs *SEMA3F* overexpressing MCF10DCIS cells by one-way ANOVA, Mann-Whitney's test. **B, C)** Representative IF images (left panel; scale bar: 20µm) and mfi quantification (right panel) for NRP1 (**B**) and NRP2 (**C**) in control or *SEMA3F* overexpressing MCF10DCIS cells. The graphs represent the % of mfi levels ± S.E.M. referred to control cells; ***P < 0.001 comparing control vs *SEMA3F* overexpressing MCF10DCIS cells by one-way ANOVA, Mann-Whitney's test. **D)** Representative Western blot analysis (left panel) of protein levels of MMP14, MMP2 and TIMP2 and a representative image of Ponceau staining. Quantification normalised to total Ponceau-stained lane (right panel) in *SEMA3F* overexpressing MCF10DCIS cells.