

Supplementary Materials for

Attenuation of Dupuytren's fibrosis via targeting of the STAT1 modulated IL-13R α 1 response

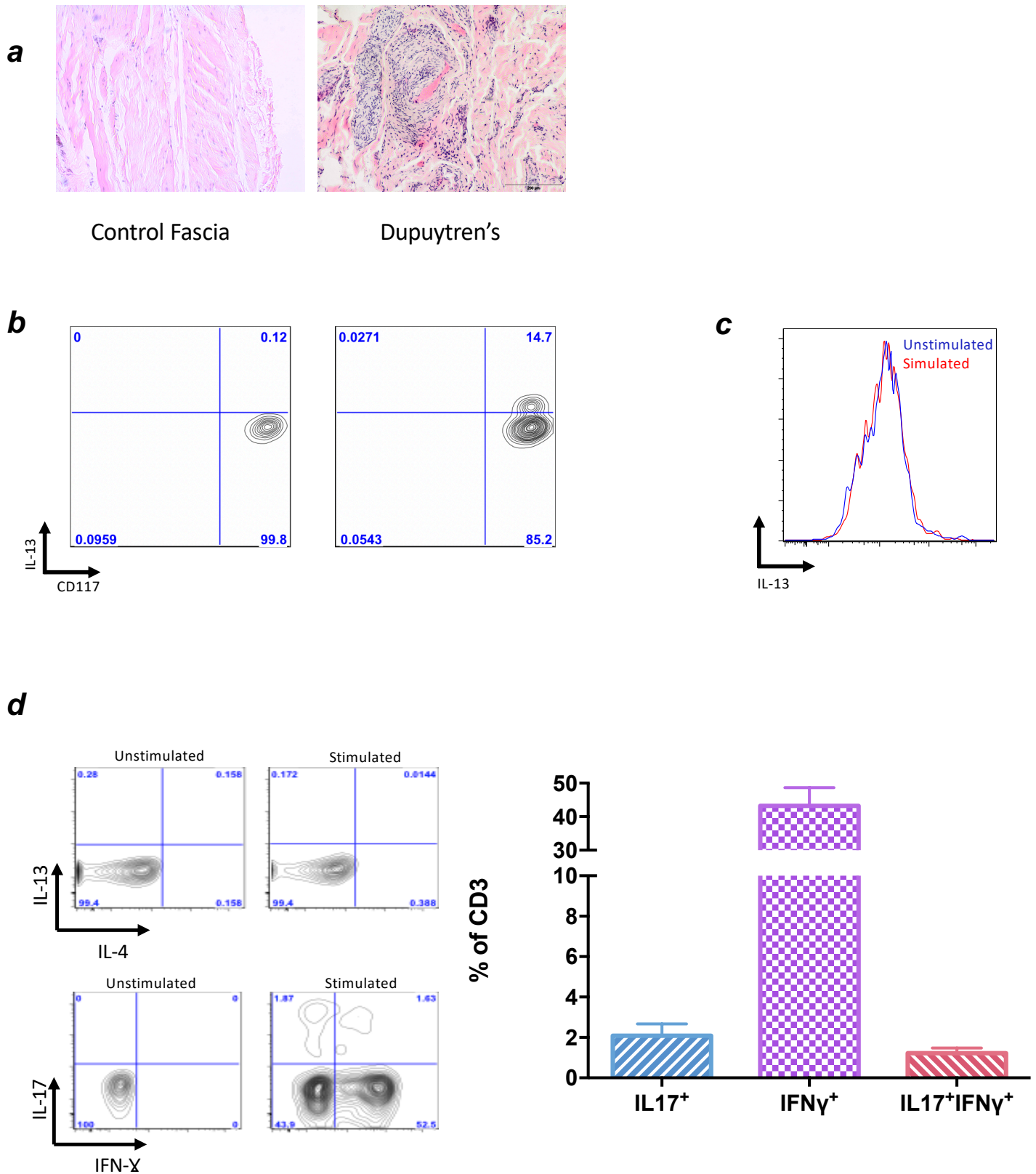
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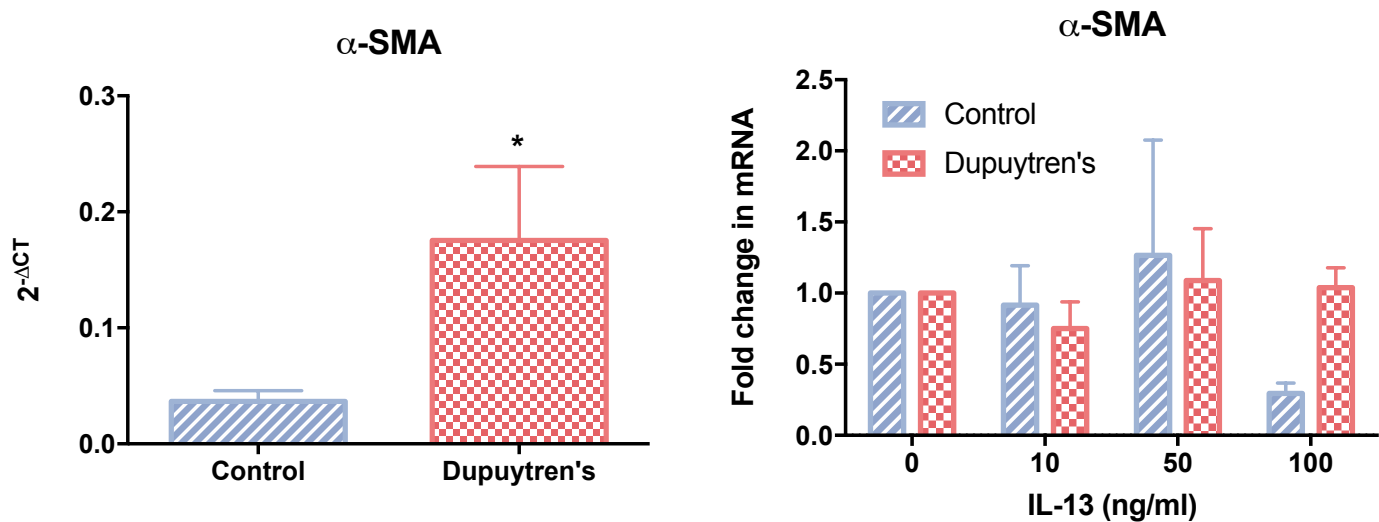
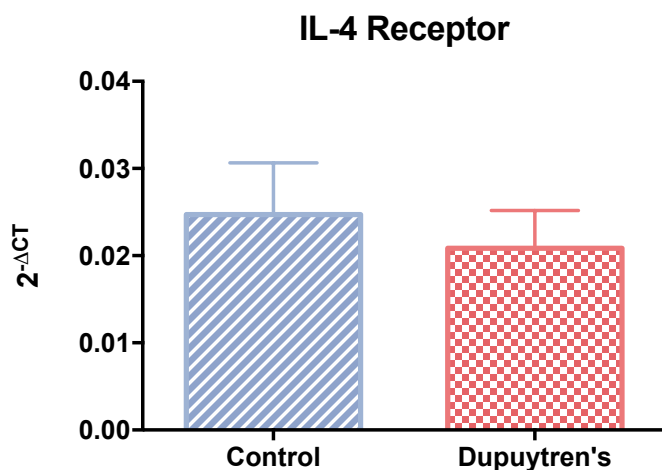
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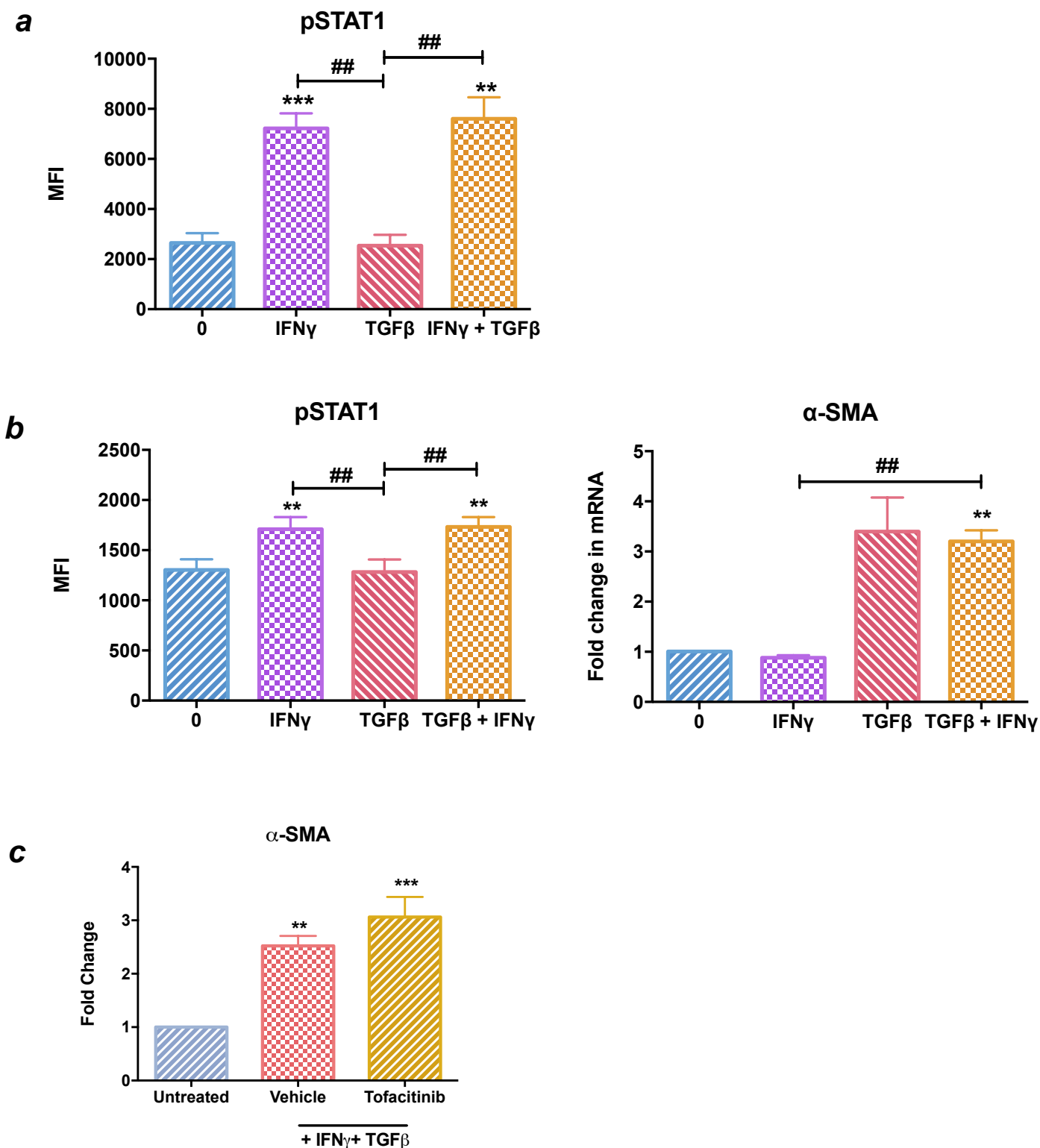
Figs. S1 to S3



Supplementary Figure 1. Inflammatory cells in Dupuytren's Disease. (A) Histological staining of control fascia and Dupuytren's tissue stained with H&E, at 10 × magnification. (B) Representative intracellular flow cytometry plot of unstimulated and stimulated CD117⁺ mast cells, from disaggregated Dupuytren's tissue, stained with anti-IL13. (C) Representative flow cytometry histogram of intracellular IL-13 in unstimulated and stimulated CD64⁺ macrophages, from disaggregated Dupuytren's tissue. (D) Characterisation of T-cells in disaggregated Dupuytren's tissue. Representative flow cytometric plots of unstimulated and stimulated CD3⁺ T-Cells following intracellular staining with antibodies against IL-4, IL-13, IL-17 and IFN alpha. Graph displays the proportion of T-cells positive for IFN-alpha.

a**b**

Supplementary Figure 2. (A) α -SMA expression in Dupuytren's disease. α -SMA expression in control fibroblasts and Dupuytren's myofibroblast, $2^{-\Delta CT}$ relative to GAPDH, mean \pm SEM, $n > 5$, $*p < 0.05$. α -SMA expression in control fibroblasts and Dupuytren's myofibroblast following IL-13 treatment, $n = 6$. mRNA gene expression expressed as fold change following normalisation to housekeeping gene (GAPDH) and then to relevant untreated cells. (B) IL-4 receptor expression in control fibroblasts and Dupuytren's myofibroblast, $2^{-\Delta CT}$ relative to GAPDH, mean \pm SEM, $n = 6$.



Supplementary Figure 3. IFN γ in Dupuytren's disease. (A) STAT1 phosphorylation and in human mast cells following IFN- γ and TGF- β exposure. (B) STAT1 phosphorylation and α -SMA gene expression in control fibroblasts following IFN- γ and TGF- β exposure. (C) α -SMA gene expression in control fibroblasts following IFN- γ and TGF- β exposure. Fibroblasts were pre-treated with tofacitinib or vehicle control (0.001% DMSO) for 30 mins prior to cytokine stimulation. All results are mean \pm SEM, mRNA gene expression expressed as fold change following normalisation to housekeeping gene (GAPDH) and then to relevant untreated cells, $n > 4$, * indicates significant difference from untreated cells, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.001$. # $p < 0.05$, ## $p < 0.01$, ### $p < 0.001$, #### $p < 0.0001$.