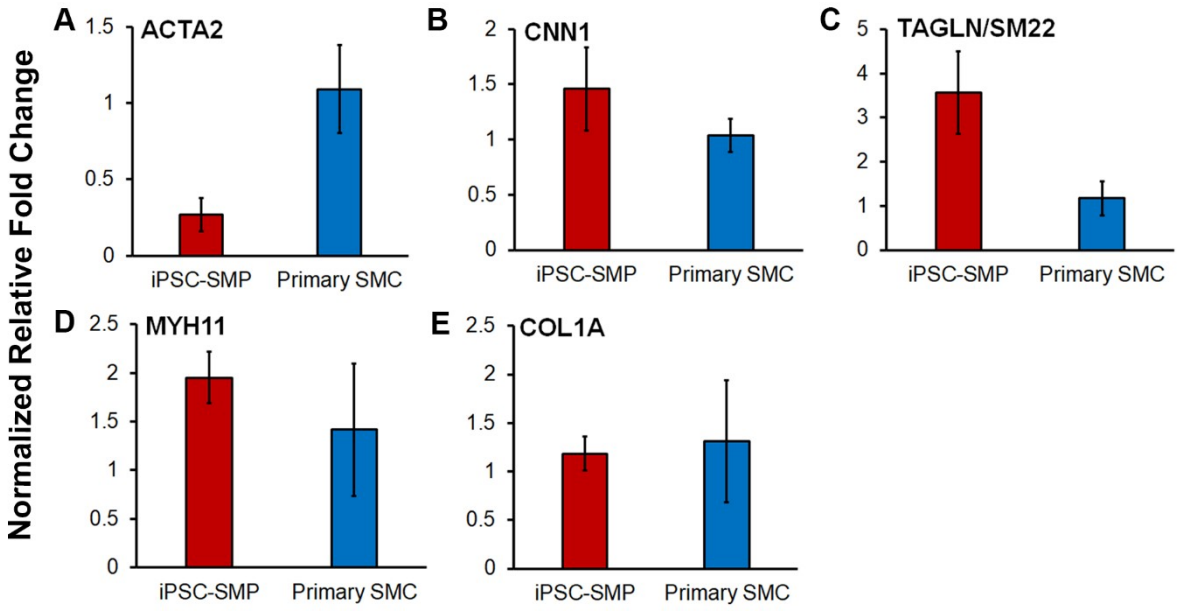
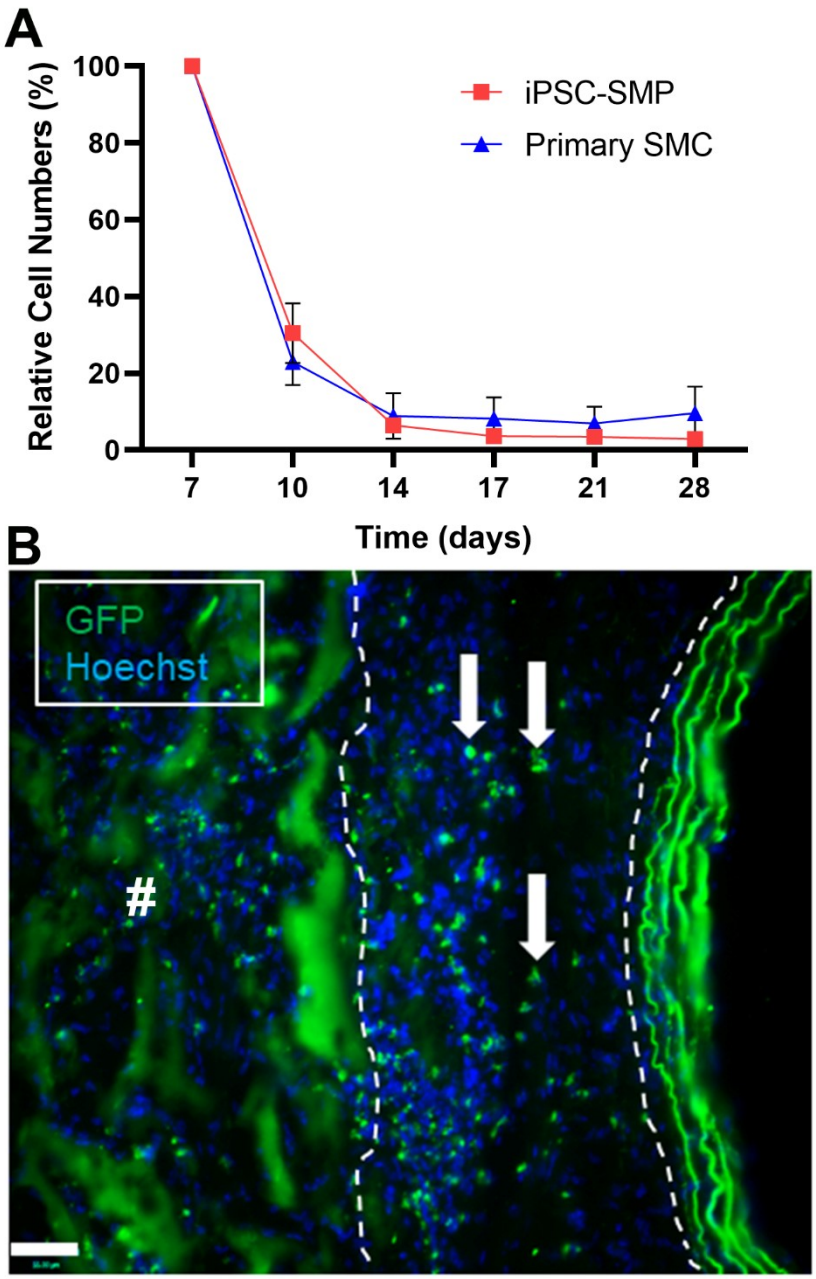
Electronic Supplementary Material (ESI) for Biomaterials Science.

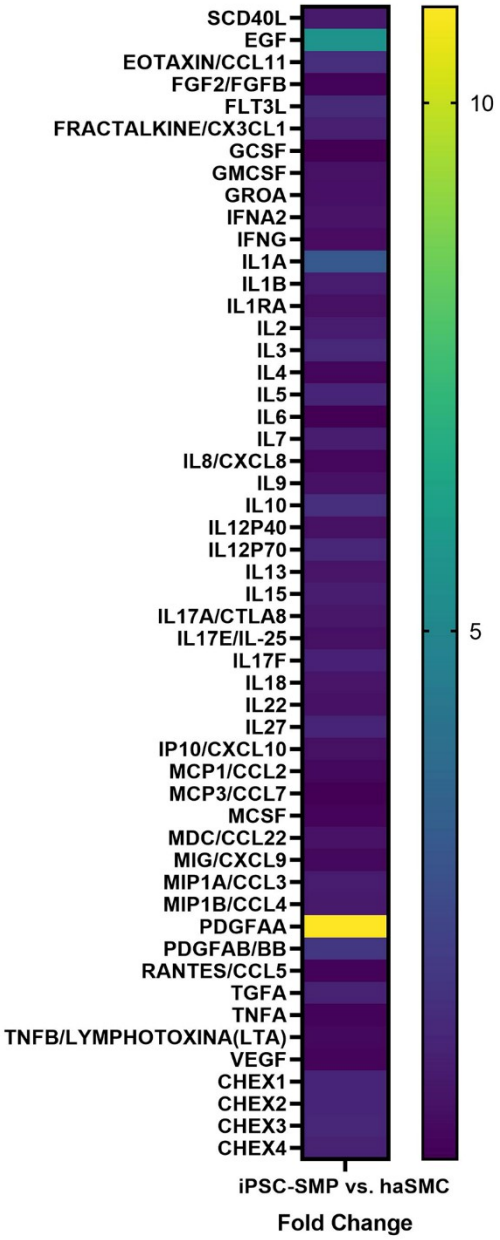
Supplemental Figures:



Supplemental Figure 1. Quantitaive PCR analysis of phenotypic smooth muscle markers in primary human SMCs and iPSC-SMPs cultured *in vitro* (n=4-5)**.**



Supplemental Figure 2. Quantification and localization of transplanted cells *in vivo*. A. Relative transplant cell numbers, quantified as bioluminescence signal intensity relative to baseline (day of implantation on day 7) (n=5 for SMC; n=15 for iPSC-SMP). **B.** Visualization of primary SMCs on day 28 in tissue sections by fluorescence imaging of green fluorescence protein (GFP). Based on autofluorescence of the internal elastic laminae, some of the GFP^+ primary SMCs (green), denoted by the white arrows, appeared to be migrating from the scaffold towards the weakened media (area marked between the dotted lines). Data shown as mean ± SEM. # denotes scaffold region. Scale bar is 55 μm.



Supplemental Figure 3. Proteomic analysis of conditioned media derived from cell-seeded scaffolds *in vitro*. Heat-map denoting fold changes in proteomic expression of pro- and anti-inflammatory-related signalling cytokines from conditioned media obtained from scaffolds seeded with iPSC-SMPs vs. human primary SMCs (haSMC) *in vitro* (n=4). The conditioned media were analyzed with a Luminex proteomic array. Overall, iPSC-SMPs show less expression for most cytokines.