

Adipose-derived mesenchymal stromal cells modulate tendon fibroblast responses to macrophage-induced inflammation

- Supplemental Document -

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Table S1: Primers used for TF qRT-PCR.

Gene	QuantiTect Primer
IL-1 β	QT01048355
TNF α	QT00104006
Cox2	QT00165347
MMP1a	QT00138894
MMP3	QT00107751
MMP13	QT00111104
Col1	QT0016220
Col3	QT02331301
Bgn	QT00108682
Dcn	QT00131068
Scx	QT00166271
Tnmd	QT00126427
GAPDH	QT01658692

Table S2: Primers used for macrophage qRT-PCR.

Gene	TaqMan Primer
IL-1 β	Mm00434228 ml
TNF α	Mm00443258 ml
IL-1Ra	Mm00446186 ml
IL-10	Mm00439614 ml
IL-12	Mm00434174 ml
IL-23	Mm01160011 gl
Cxcl9	Mm00434946 ml
CCL22	Mm00436439 ml
Arg1	Mm00475988 ml
MMP9	Mm00442991 ml
TGF β -1	Mm01178820 ml
GAPDH	Mm99999915 gl

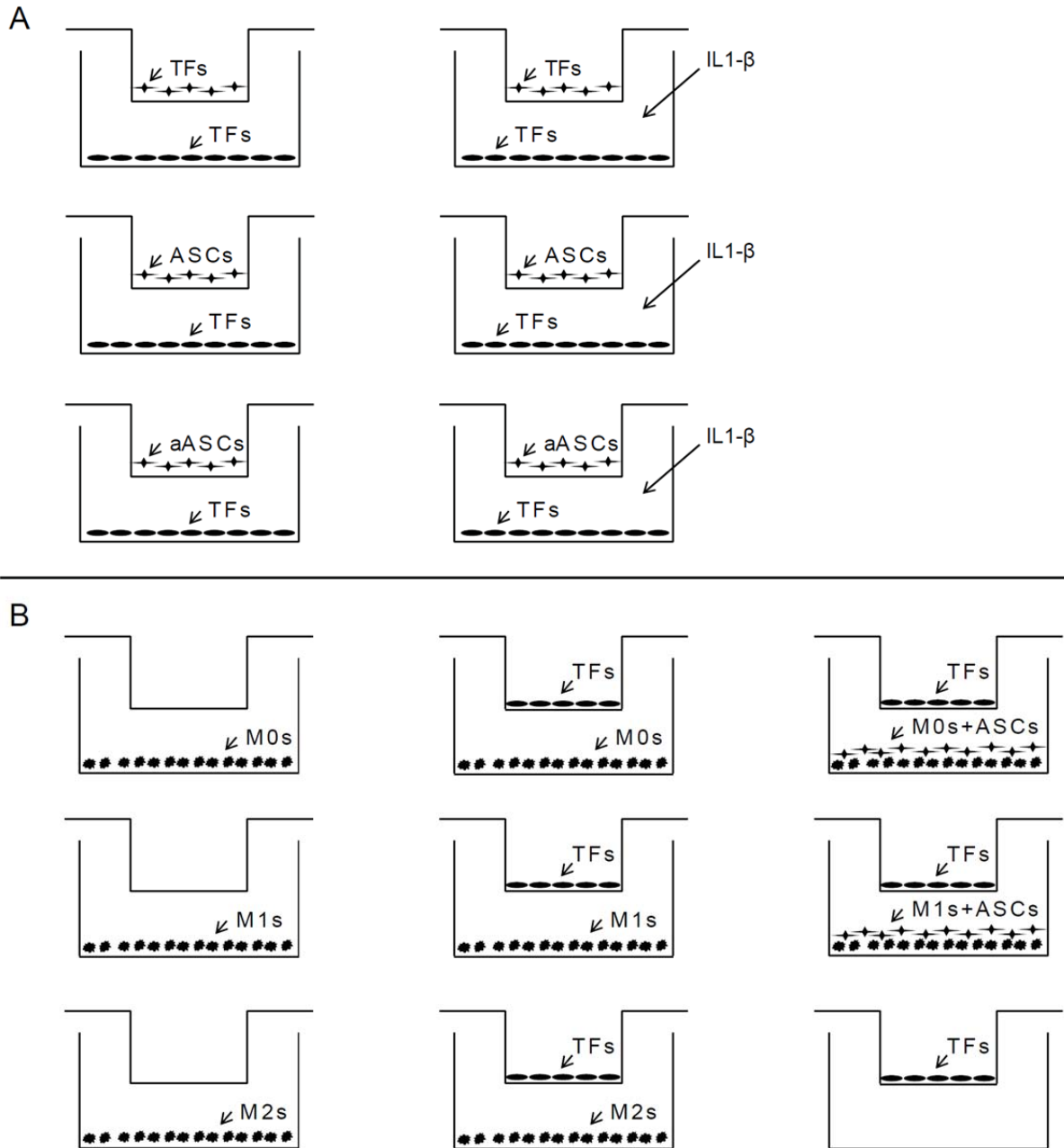


Figure S1: Schematics of *in vitro* experimental design. (A) Schematic of experimental design for the IL-1 β -induced inflammation model. TFs were cultured alone or co-cultured with either naïve ASCs (ASCs) or activated ASCs (aASCs) in the presence of IL-1 β . Controls consisted of the same experimental groups, but in the absence of IL-1 β . Note: TFs were cultured in the inserts of the transwell plates for some groups to keep the total number of cells uniform between all groups. **(B)** Schematic of experimental setup for the macrophage-induced inflammation model. M0, M1, and M2 macrophages were cultured alone to characterize macrophage phenotype. TFs were co-cultured with M0, M1, or M2 macrophages to determine the effects of macrophages on TFs. TFs were cultured with ASCs and either M0 or M1 macrophages to determine if ASCs can protect TFs from the effects of macrophages. TFs also cultured alone to serve as controls.

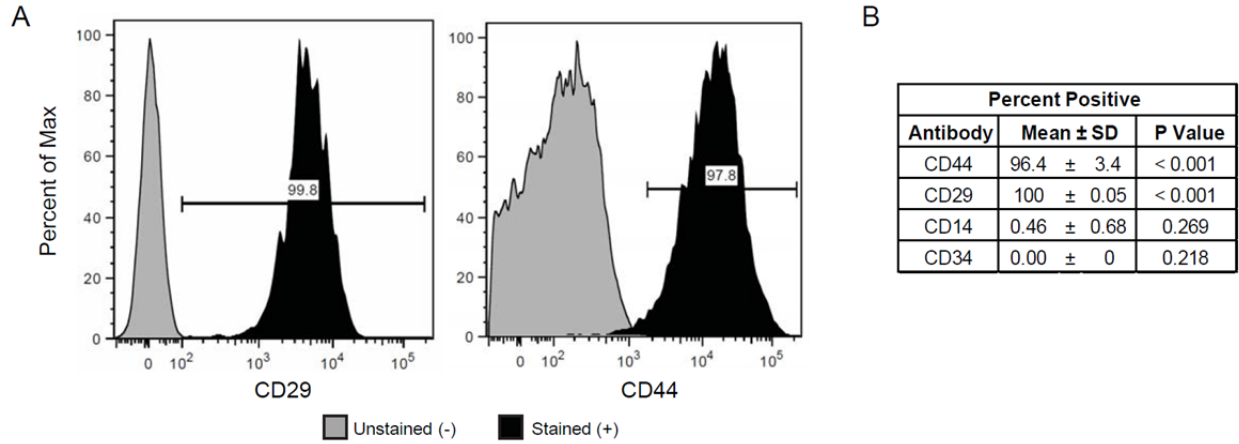


Figure S2: ASCs characterization using flow cytometry. ASCs were labeled with antibodies against mesenchymal stem cell markers (CD29, CD44) and hematopoietic stem cell markers (CD14, CD34). The percentage of cells staining positive for the various markers was determined by comparing the expression of the stained ASCs to unstained cells. **(A)** Results are shown for representative samples. **(B)** The data are presented as mean percent positive \pm SD (N=4).

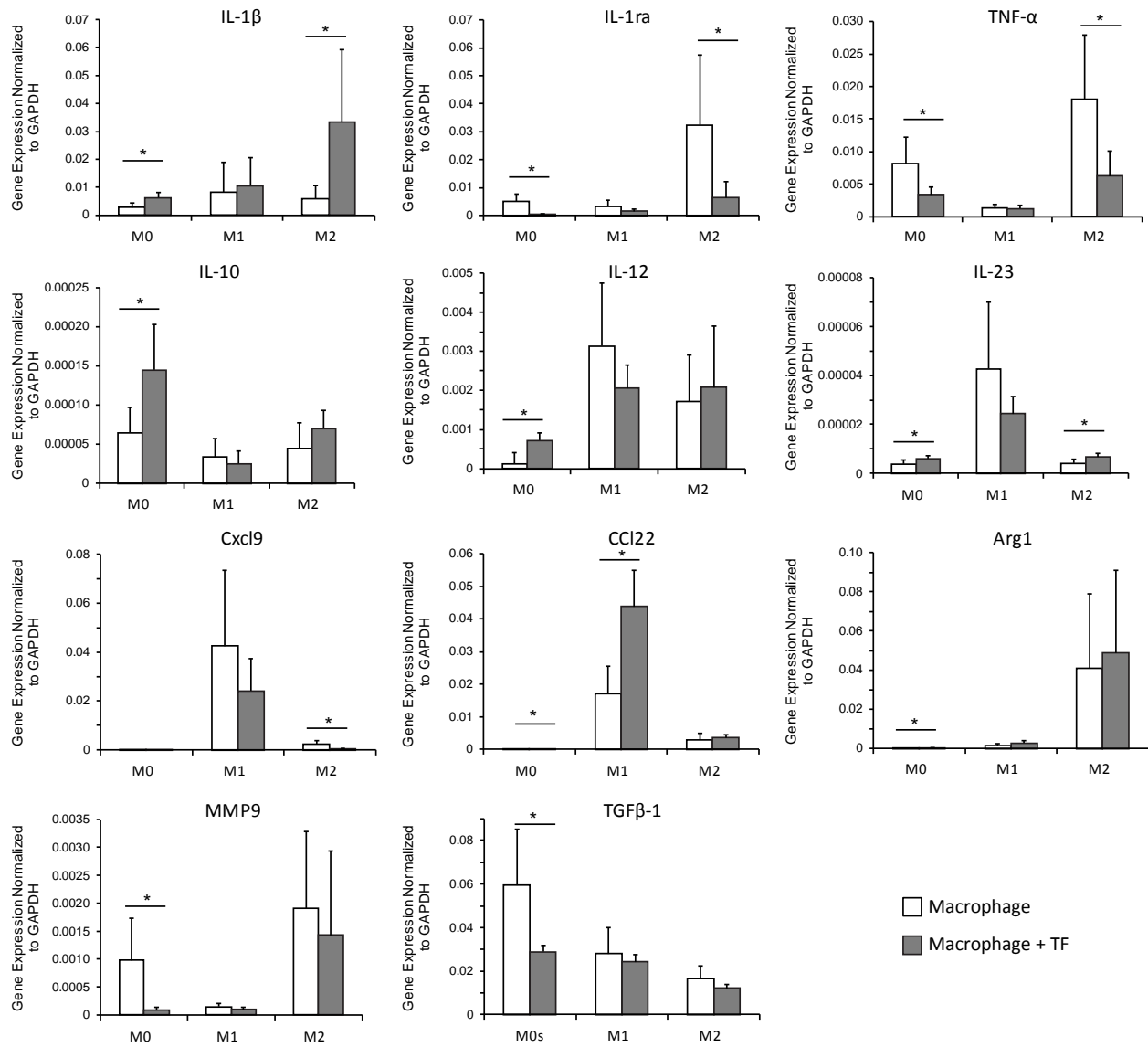


Figure S3: Macrophage gene expression. Changes in gene expression for macrophages was examined after culture alone (white bars) or co-culture with TFs (gray bars) for 1 day. There were significant effects of macrophage phenotype and presence of TFs on macrophage gene expression. Gene expression was normalized to GAPDH (* $p < 0.05$, $N=10$ for macrophage alone and $N=6$ for macrophage/TF co-culture).

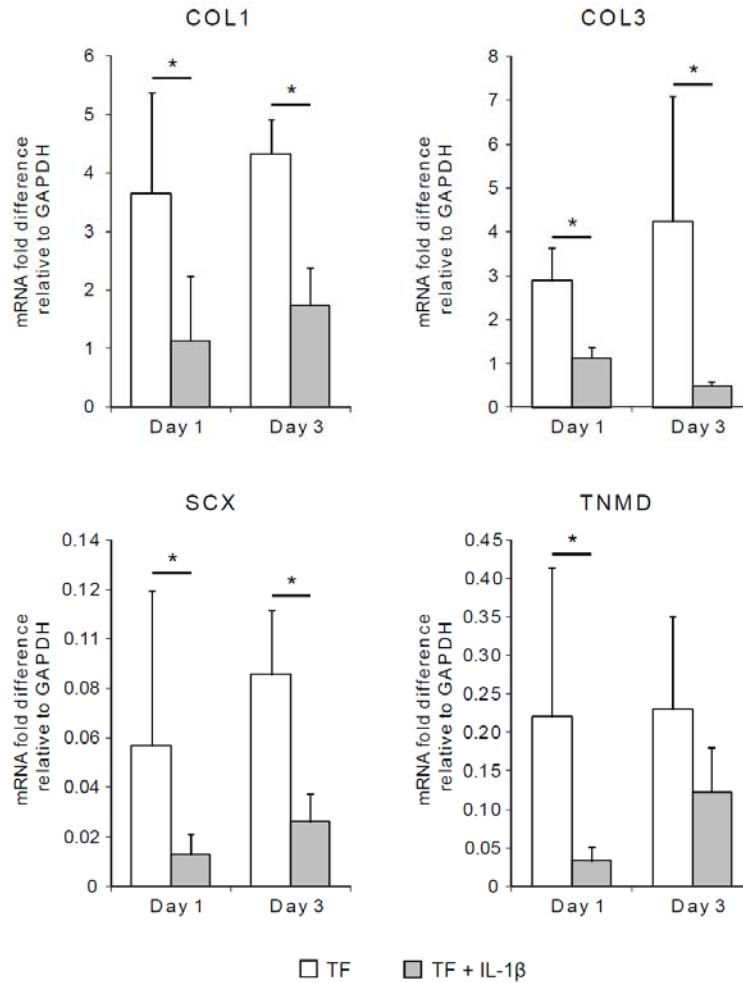


Figure S4: Changes in TF gene expression due to IL-1β. IL-1β induced down-regulation of tendon ECM- and differentiation-related genes by TFs. Results are shown for tendon ECM (COL1, COL3) and differentiation (SCX, TNMD) genes for TFs and in TFs treated with 10 ng/ml of IL-1β for 1 or 3 days (* p < 0.05, two-way ANOVA, N=4).

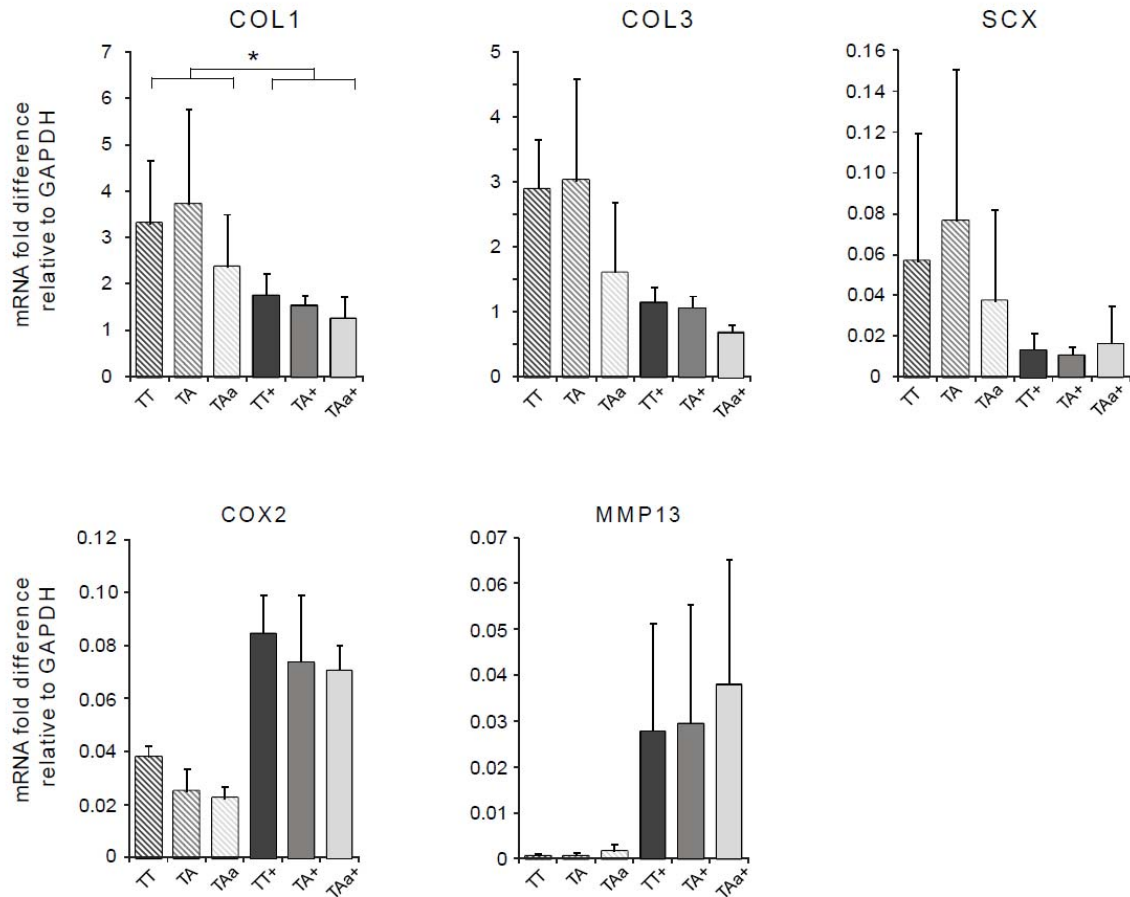


Figure S5: ASCs failed to suppress the IL-1 β -induced effects on TF gene expression. TFs were cultured alone (TT), co-cultured with naïve ASCs (TA), or co-cultured with activated ASCs (TAa), with or without IL-1 β for 1 day (inclusion of IL-1 β indicated with “+”). Data was normalized to the housekeeping gene GAPDH (* $p < 0.05$, based on a multi-factor ANOVA with Fisher’s post-hoc tests there was a significant effects of IL-1 β but no effect of ASCs, N=4). [TT: TFs cultured alone, TT+: TFs treated with IL-1 β , TA: TFs co-cultured with naïve ASCs, TA+: TFs co-cultured with naïve ASCs and treated with IL-1 β , TAa: TFs co-cultured with activated ASCs, TAa+: TFs co-cultured with activated ASCs and treated with IL-1 β].

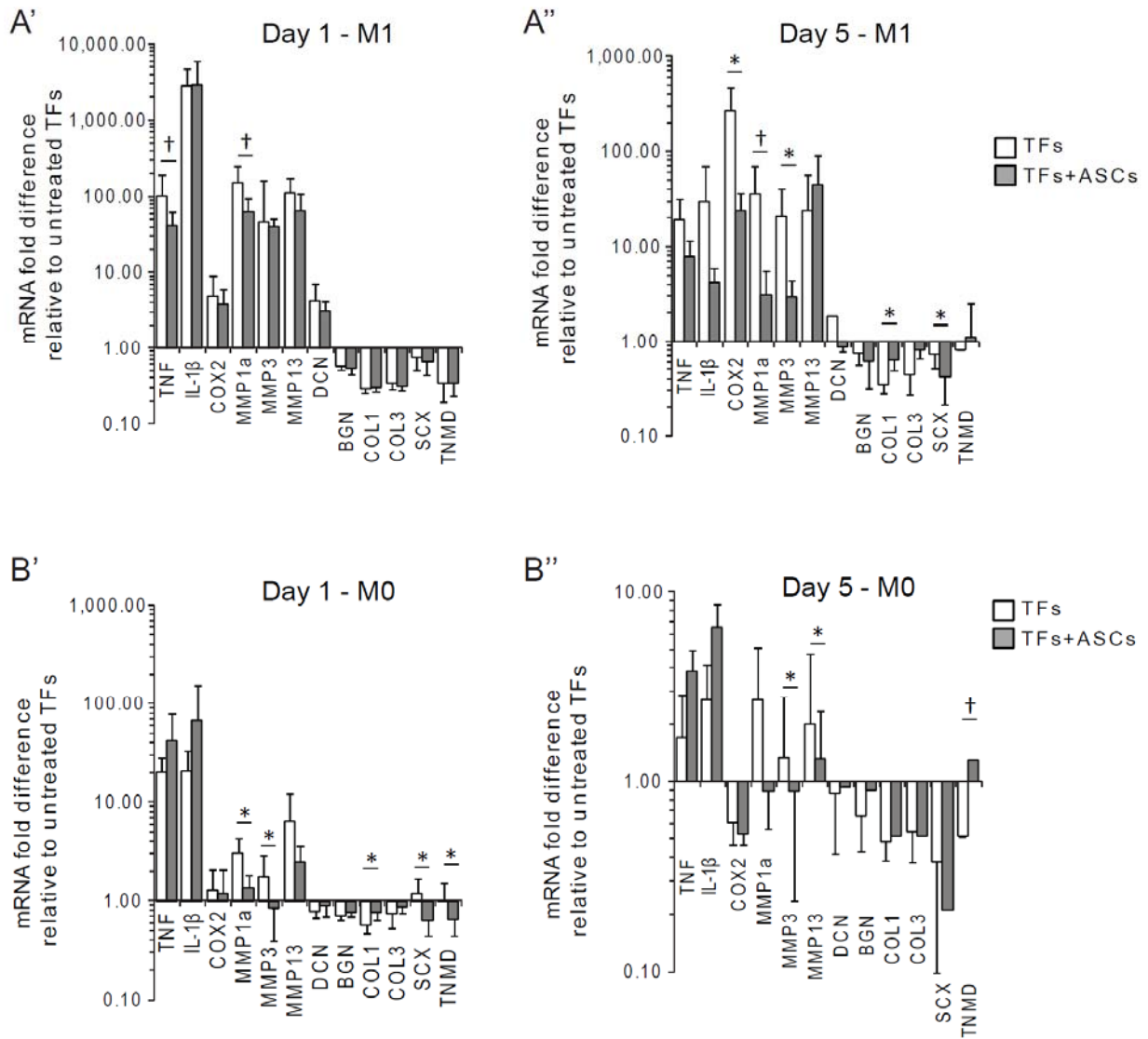


Figure S6: Changes in gene expression for TFs after culture with macrophages with and without ASCs. TFs were cultured with macrophages alone (white bars) or with macrophages and ASCs (grey bars) for 1 or 5 days. ASCs suppressed the effects of (A) M1 and (B) M0 macrophages on TF gene expression. The greatest effect of ASCs was seen for M1 macrophages on day 5 (A''). Gene expression was normalized to untreated TFs (* $p < 0.05$, $N=5$ for day 1, $N=3$ for day 5 except for bars without standard deviations, for which $N=2$ due to insufficient amounts of RNA for analysis).