Electronic Supplementary Information

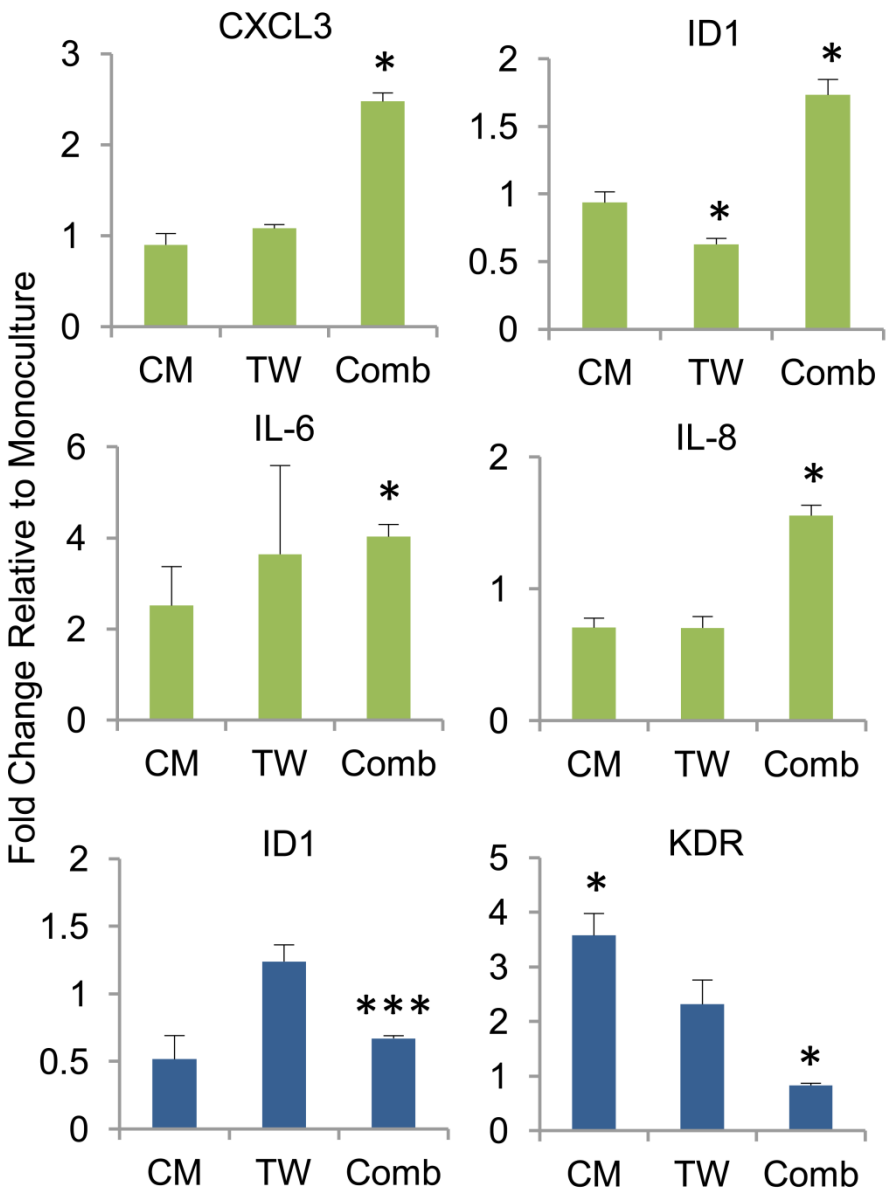

Figure S1. Gene induction as function of cell proximity. Quantification by conventional qRT-PCR of gene expression in conditioned media (CM), Transwell (TW), and comb gap (Comb) co-cultures. Here, CM and TW were performed conventionally, with cells in normal culture wells without comb substrates. In general, the trends are similar to Figure 2, in which all conditions were performed on comb substrates. Samples displaying statistically significant changes (Student's t-test) versus monoculture controls are indicated (* = $p < 0.05$, *** = $p < 0.005$). Bars are color-coded green for tumor-specific gene expression and blue for fibroblast-specific gene expression. Error bars are SEM.

Gene	Forward 5’ to 3’	Reverse 5’ to 3’
ANGPTL3	CCAAGCCAAGAGCACCAAGAACT	CTCCACACTCATCATGCCACCAC
ANGPTL4	GTCCTCCGCGTCTCCAGTCCT	CATCTCGGGCAGCCTCTTTCTT
CXCL3	TGCCCTTACCAGAGCTGAAAATGA	AAGAGAAACGCTGCAGAATGGACA
HPRT	GACCAGTCAACAGGGGACA	GTGTCAATTATATCCTTCCACAA
HPSE	CCCGCCTCAGCCTCTCAAAGT	GCCTCGGCCTCCCAAAGTG
ID1	CCTCAACGGCGAGATCAG	CGCTTCAGCGACACAAGAT
IL-1β	AGGCCGCGTCAGTTGTTGTG	TATATCCTGGCCGCCTTTGGTC
IL-6	CCCCAGTACCCCCAGGAGAAG	CTGCGCAGAATGAGATGAGTTGTC
IL-8	AGAAACCACCGGAAGGAACCATC	GCAACCCTACAACAGACCCACAC
KDR	GAGCCGGCCTGTGAGTGTAAAAA	AGGAGTTGGGGGTGTGGATGC
TERT	GGTCATCGCCAGCATCATCAAA	ACGGCTGGAGGTCTGTCAAGGTAG
THBS1	GCCACGGCCAACAAACAGGT	ACAGCGGTCTCCCACATCATCTC
VEGFA	AGATGTCCCGGCGAAGAGAAGA	GGGAGGGCAGAGCTGAGTGTTAG

Table S2. Primer sequences employed for qRT-PCR. These were employed for the validation experiments and may be different from the primers in the qRT-PCR arrays.