

**Table S1.** Differential expression of genes in CSC-exposed (10 µg/mL) versus vehicle control cells.

Symbol	Entrez Gene Name	Expr <i>p</i> -Value	Expr Fold Change	Location
<i>FOXC2</i>	forkhead box C2	3.26E-02	12.10	Nucleus
<i>CDH2</i>	cadherin 2	1.69E-05	6.34	Plasma Membrane
<i>SNAI1</i>	snail family transcriptional repressor 1	8.45E-03	2.80	Nucleus
<i>CTNNB1</i>	catenin beta 1	8.23E-05	2.66	Nucleus
<i>SNAI2</i>	snail family transcriptional repressor 2	1.65E-03	2.60	Nucleus
<i>FN1</i>	fibronectin 1	1.38E-04	2.39	Extracellular Space
<i>TGFB2</i>	transforming growth factor beta 2	1.54E-02	2.30	Extracellular Space
<i>SMAD2</i>	SMAD family member 2	1.54E-03	2.13	Nucleus
<i>PDGFRB</i>	platelet derived growth factor receptor beta	1.81E-04	2.08	Plasma Membrane

Note: This table was derived from IPA Canonical Pathway analysis on RT<sup>2</sup> EMT Profiler Array.  
Red = Upregulated gene expression fold changes.