

Population heterogeneity in the epithelial to mesenchymal transition is controlled by NFAT and phosphorylated Sp1

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Running Title: Modeling of TGF- β induced EMT

Character count: 56,659

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Abstract

Epithelial to mesenchymal transition (EMT) is an essential differentiation program during tissue morphogenesis and remodeling. EMT is induced by soluble transforming growth factor β (TGF- β) family members, and restricted by vascular endothelial growth factor family members. While many downstream molecular regulators of EMT have been identified, these have been largely evaluated individually without considering potential crosstalk. In this study, we created an ensemble of dynamic mathematical models describing TGF- β induced EMT to better understand the operational hierarchy of this complex molecular program. These models incorporate mass action kinetics within an ordinary differential equation (ODE) framework to describe the transcriptional and post-translational regulatory events driving EMT. Model parameters were estimated from multiple data sets using multiobjective optimization, in combination with cross-validation. TGF- β exposure drove the model population toward a mesenchymal phenotype, while an epithelial phenotype was maintained following vascular endothelial growth factor A (VEGF-A) exposure. Simulations predicted that the transcription factors phosphorylated SP1 and NFAT were master regulators promoting or inhibiting EMT, respectively. Surprisingly, simulations also predicted that a cellular population could exhibit phenotypic heterogeneity (characterized by a significant fraction of the population with both high epithelial and mesenchymal marker expression) if treated simultaneously with TGF- β and VEGF-A. We tested this prediction experimentally in both MCF10A and DLD1 cells and found that upwards of 45% of the cellular population acquired this hybrid state in the presence of both TGF- β and VEGF-A. We experimentally validated the predicted NFAT/Sp1 signaling axis for each phenotype response. Lastly, we found that cells in the hybrid state had significantly different functional behavior when compared to VEGF-A or TGF- β treatment alone. Together, these results establish a predictive mechanistic model of EMT susceptibility, and potentially reveal a novel signaling axis which regulates carcinoma progression through an EMT versus tubulogenesis response.

Author Summary

Tissue formation and remodeling requires a complex and dynamic balance of interactions between epithelial cells, which reside on the surface, and mesenchymal cells that reside in the tissue interior. During embryonic development, wound healing, and cancer, epithelial cells transform into a mesenchymal cell to form new types of tissues. It is important to understand this process so that it can be controlled to generate beneficial effects and limit pathological differentiation. Much research over the past 20 years has identified many different molecular species that are relevant, but these have mainly been studied one at a time. In this study, we developed and implemented a novel computational strategy to interrogate all of the known players in this transformation process to identify which are the major bottlenecks. We determined that NFATc1 and pSP1 are essential for promoting epithelial or mesenchymal differentiation, respectively. We then predicted the existence of a partially transformed cell that exhibits both epithelial and mesenchymal characteristics. We found this partial cell type develops a network of invasive but stunted vascular structures that may be a unique cell target for understanding cancer progression and angiogenesis.

1 Introduction

- 2 The epithelial to mesenchymal transition (EMT) is a broadly participating, evolutionarily
3 conserved differentiation program essential for tissue morphogenesis, remodeling and
4 pathological processes such as cancer (Thiery, 2003). During EMT polarized, tightly ad-
5 hered epithelial cell monolayers are transformed into non-interacting motile mesenchymal
6 cells that simultaneously degrade and synthesize extracellular matrix (ECM) components
7 and invade into the underlying tissue space (Stahl & Felsen, 2001). EMT is the funda-
8 mental initiator of developmental processes such as embryonic gastrulation and valvulo-
9 genesis (Eisenberg & Markwald, 1995) (also Kalluri J Clin Invest 2009, Thiery Cell 2009).
10 Transforming growth factor β (TGF- β) family members are important inducers of both de-

11 developmental and pathological EMT (Xu *et al.*, 2009, Zavadil & Böttinger, 2005). Decades
12 of research has focused on identifying molecular regulators of EMT, but almost all on a
13 single gene and in a nearly binary yes/no level of qualitative understanding. Medici and
14 coworkers recently identified a core signaling program by which TGF- β isoforms induce
15 EMT across a variety of cell lines (Medici *et al.*, 2006, 2008). This program involves
16 carefully orchestrated rounds of gene expression driven by the Smad and Snail families
17 of transcription factors as well as other key factors such as lymphoid enhancer-binding
18 factor 1 (LEF-1), nuclear factor of activated T-cells, cytoplasmic 1 (NFATc1), and speci-
19 fity protein 1 (Sp1). Coregulators such as β -catenin, NF- κ B, and the ErbB family of
20 receptor tyrosine kinases however also participate in EMT regulation, but the degree of
21 each's influence is difficult to ascertain in isolation (Hardy *et al.*, 2010, Huber *et al.*, 2004,
22 Jiang *et al.*, 2007, Kim *et al.*, 2002). EMT also exhibits complex temporal dynamics that
23 are often intractable in gain/loss of function studies. Elucidating the master regulatory ar-
24 chitecture controlling EMT therefore requires inclusion of these complex overlapping and
25 non-binary behaviors.

26 Systems biology and mathematical modeling are essential tools for understanding
27 complex developmental programs like EMT (Ahmed & Nawshad, 2007). Previous com-
28 putational models of TGF- β induced differentiation focused on single biological factors or
29 EMT in single cells. For example, Chung *et al.*, constructed a model of TGF- β receptor
30 activation and Smad signaling using ordinary differential equations and mass-action ki-
31 netics. Their model suggested that a reduction of functional TGF- β receptors in cancer
32 cells may lead to an attenuated Smad2 signal (Chung *et al.*, 2009). Similarly, Vilar *et al.*
33 suggested that specific changes in receptor trafficking patterns could lead to phenotypes
34 that favor tumorigenesis (Vilar *et al.*, 2006). Although these models provided insight into
35 the role of receptor dynamics, EMT induction involves many other components, includ-
36 ing competing second messengers and interconnected transcriptional regulatory loops.
37 Integrating these additional scales of molecular signaling while maintaining the capacity

38 for robust prediction requires a new and expanded computational and experimental strat-
39 egy. Data-driven systems approaches (Cirit & Haugh, 2012) or logical model formulations
40 (Morris *et al.*, 2011) are emerging paradigms that constrain model complexity through
41 the incorporation of training and validation data. These are interesting techniques be-
42 cause the data informs model structure (which can be expanded as more data becomes
43 available). Alternatively, Bailey proposed more than a decade ago that a qualitative un-
44 derstanding of a complex biological system should not require complete definition of its
45 structural and parametric content (Bailey, 2001). Shortly thereafter, Sethna and cowork-
46 ers showed that complex model behavior is often controlled by only a few parameter
47 combinations, a characteristic seemingly universal to multi-parameter models referred
48 to as “sloppiness” (Machta *et al.*, 2013). Thus, reasonable model predictions are often
49 possible with only limited parameter information. Taking advantage of this property, we
50 developed sloppy techniques for parameter identification using ensembles of determin-
51 istic models (Song *et al.*, 2010). Furthermore, we proposed that the sloppy behavior of
52 biological networks may also be seen as a source of cell-to-cell (Lequieu *et al.*, 2011) or
53 even patient-to-patient heterogeneity (Luan *et al.*, 2010). Recently, Bayesian parameter
54 identification techniques have also been used to explore cell-to-cell heterogeneity (Hase-
55 nauer *et al.*, 2011, Kalita *et al.*, 2011), where a population of cells could be viewed as a
56 dynamic ensemble of context-specific biochemical networks (Creixell *et al.*, 2012).

57 In this study, we developed a family of mechanistic models describing the induction
58 of EMT by TGF- β isoforms in the presence and absence of vascular endothelial growth
59 factor A (VEGF-A). We incorporated mass action kinetics within an ordinary differential
60 equation (ODE) framework to describe the EMT interaction network containing 97 gene,
61 protein or mRNA components interconnected through 169 interactions. A family of model
62 parameters was estimated using 41 molecular data sets generated in DLD1 colon carci-
63 noma, MDCKII and A375 melanoma cells using the Pareto optimal ensemble technique
64 (JuPOETs) multiobjective optimization algorithm. JuPOETs generated an ensemble of

65 approximately 1400 models for analysis. Analysis of the model population suggested that
66 both MCF10A and DLD1 cells could exhibit phenotypic heterogeneity if treated simultane-
67 ously with TGF- β 1/2 and VEGF-A. This heterogeneity was characterized by a significant
68 fraction of the population being in a “hybrid state” having both high E-cadherin and high
69 Vimentin expression. We tested these predictions using qRT-PCR and flow-cytometry
70 studies in a variety of experimental conditions. Validation studies confirmed that upwards
71 of 45% of the cellular population could be put into the hybrid state in the presence of both
72 TGF- β 1/2 and VEGF-A. Moreover, this response depended upon both activation of Sp1
73 by MAPK and NFATc1 transcriptional activity consistent with the predicted molecular sig-
74 naling. Lastly, the hybrid populations of both DLD1 and MCF10A cells exhibited different
75 functional behavior than those from either TGF- β or VEGF-A treatment. The extent of
76 ductal branch formation significantly increased with MCF10A cells in the hybrid pheno-
77 type, compared with cells treated with VEGF-A alone. Together, these results establish
78 a predictive mechanistic model of EMT susceptibility, and reveal a novel signaling axis,
79 which possibly regulates carcinoma progression through an EMT versus tubulogenesis
80 response.

81 **Results**

82 **The model population captured key features of TGF- β induced EMT** The EMT model
83 architecture, based upon curated molecular connectivity, described the expression of 23
84 genes following exposure to TGF- β isoforms and VEGF-A (Fig. 1). The EMT model con-
85 tained 74 molecular species interconnected by 169 interactions. Model equations were
86 formulated using either saturation or mass-action kinetics within an ordinary differential
87 equation (ODE) framework. ODEs and mass action kinetics are common tools to model
88 biochemical pathways (Chen *et al.*, 2009, Schoeberl *et al.*, 2002, Tasseff *et al.*, 2011).
89 However, while ODE models can simulate complex intracellular behavior, they require es-
90 timates for model parameters which are often difficult to obtain. The EMT model had 251
91 unknown model parameters, 169 kinetic constants and 45 non-zero initial conditions. As
92 expected, these parameters were not uniquely identifiable given the training data (Gad-
93 kar *et al.*, 2005). Thus, instead of identifying a single best fit (but uncertain) model, we
94 estimated a sloppy population of models (each consistent with the training data) by simul-
95 taneously minimizing the difference between model simulations and 41 molecular data
96 sets using the Pareto Optimal Ensemble Technique (JuPOETs). The training data were
97 generated in DLD1 colon carcinoma, MDCKII, and A375 melanoma cells following ex-
98 posure to TGF- β isoforms (Medici *et al.*, 2008). We organized these data sets into 11
99 objective functions which were simultaneously minimized by JuPOETs. Additionally, we
100 used 12 molecular data sets generated in HK-2 cells following VEGF-A exposure to train
101 VEGF-A responsive model processes (Lian *et al.*, 2011). To guard against overfitting,
102 we augmented the multiobjective optimization with leave-one-out cross validation to in-
103 dependently estimate both the training and prediction error for each objective. Thus, we
104 generated 11 different model ensembles. Lastly, we compared model predictions with in-
105 dependent data sets not used during training (both at the molecular and model population
106 levels) to evaluate the predictive power of the parameter ensemble.

107 JuPOETs generated a population of probable signaling models which captured the

multiple phases of EMT induction (Fig. 2). JuPOETs sampled well over 10^4 probable models during each stage of the cross-validation using global random sampling. From this analysis, $N \simeq 1400$ models were selected for further analysis. The selected models all had the same possible molecular connectivity, but different values for model parameters. Transcription and translation rates, as well as mRNA and protein degradation terms, were set using physical values from the literature (Milo *et al.*, 2010), and allowed to vary by a scaling factor, see methods. Model selection was based upon Pareto rank, the prediction and training error across all objectives. The model population recapitulated key signaling events following TGF- β exposure. We subdivided the response to TGF- β exposure into two phases. First, TGF- β 1/2 signaling initiated a program which downregulated E-cadherin expression in a MAPK dependent manner while simultaneously upregulating TGF- β 3 expression. Second, TGF- β 3 secretion initiated an autocrine feedback which upregulated the expression of mesenchymal markers such as Vimentin and key upstream transcription factors such as LEF-1 in a SMAD dependent manner. TGF- β 3 expression was also able to sustain β -catenin release by inhibiting its sequestration by the APC complex through PI3K mediated GSK3, which was captured by the model (Fig. 4B). Each phase involved the hierachal expression and/or post-translational modification of several key transcription factors. During the first phase, stimulation with TGF- β 1/2 (10 a.u.) activated both the SMAD and MAPK pathways. MAPK activation resulted in the phosphorylation of the transcription factor activator protein 1 (AP-1), which in-turn upregulated the expression of Snail, a well established transcriptional repressor (Fig. 2A). Snail expression was MAPK-dependent; the MEK inhibitor U0126 blocked AP-1 activation and Snail expression following TGF- β 1/2 exposure (Fig. 2A, Lane 3). Similar results were obtained for Slug expression, confirming initial activation through the MAPK pathway (data not shown). Overexpression of either Snail or Slug upregulated TGF- β 3 expression (Fig. 2C) while simultaneously downregulating E-cadherin expression (Fig. 2F). During the second phase, TGF- β 3 secretion and the subsequent autocrine signaling resulted in the

135 upregulation of mesenchymal marker expression. The TGF- β 3 induced gene expres-
136 sion program involves a complex hierarchy of transcriptional and post-translational reg-
137 ulatory events. Absence of E-cadherin indirectly promoted TGF- β 3 expression through
138 the β -catenin/TCF4 complex following Snail or Slug expression (Fig. 2C, Lane 2 or 3).
139 Conversely, over-expression of E-cadherin inhibited the TGF- β 3 autocrine production by
140 sequestering cytosolic β -catenin, thereby blocking EMT (Fig. 2C, Lane 4 or 5). TGF- β 3
141 signaled through the Smad pathway to regulate LEF-1 expression and downstream tar-
142 get EMT genes (Fig. 2G). TGF- β 3 (10 a.u.) in combination with downstream inhibitors
143 (DN-Smad4 and DN-LEF-1) completely inhibited Vimentin expression, while elevating E-
144 cadherin expression (Fig. 2H,I).

145 The predictive power of the ensemble was tested using both cross validation and by
146 comparing simulations with data sets not used for model training. In whole, 72% of our
147 training objectives were statistically significant (at a 95% confidence interval) compared to
148 a randomized parameter family ($N = 100$) generated from a random starting point. Con-
149 versely, we *predicted* approximately 72% of the training objectives, at a 95% confidence
150 interval compared to randomized parameters. The model also captured the temporal gene
151 expression responses of E-cadherin, pSmad2, and LEF-1 (not used for model training) to
152 within one-standard deviation (up to the 48 hr time-point) (Fig. 2J-L). Taken together, the
153 model captured the key signaling events revealed by Medici *et al.* (Medici *et al.*, 2008)
154 that drive the phenotypic conversion. A listing of objective function values resulting from
155 training, cross validation and the random parameter control is given in the supplement
156 (Fig. S1).

157 **Identification of a novel LEF-1 regulator** During model identification, we found that
158 consistent TGF- β induced EMT from a stable epithelial cell population required an addi-
159 tional regulatory protein. This protein, which we called hypothetical regulator 1 (YREG1),
160 was required to mediate between SNAIL/SLUG transcriptional activity and the upregu-
161 lation of LEF-1 expression following TGF- β 1/2 exposure. SNAIL/SLUG are well known

transcriptional repressors (Dhasarathy *et al.*, 2011, Hemavathy *et al.*, 2000a,b), although there are a few studies which suggest that at least SNAIL can also act as a transcriptional activator (Guaita *et al.*, 2002). In the model, we assumed the expression of SNAIL/SLUG was likely regulated by AP1/SP1 (Jackstadt *et al.*, 2013). Thus, upon receiving direct SNAIL/SLUG and TGF- β 3 signals, the model predicted enhanced SNAIL/SLUG expression, consistent with experimental observations. TGF- β 1/2 stimulation also induces LEF-1 expression. However, literature evidence suggested that LEF-1 expression was not strongly dependent upon AP1/SP1 activity (Eastman & Grosschedl, 1999). Thus, either SNAIL/SLUG are acting as inducers (contrary to substantial biochemical evidence) or, they are repressing the expression of an intermediate repressor. Given the biochemical evidence supporting SNAIL/SLUG as repressors, we created the hypothetical YREG1 repressor whose expression is downregulated by SNAIL/SLUG. The literature data therefore suggested that YREG1 had two transcriptional targets, LEF-1 and TGF- β 3. By adding this regulator, our simulations became consistent with training and literature data. Medici *et al.* suggested that feedback between β -catenin and LEF-1 was likely, although this feedback had yet to be identified (Medici *et al.*, 2008). Low levels of YREG1 expression were present in all simulations to regulate the formation of the β -catenin-LEF-1 complex. To test the effect of YREG1 on the epithelial population, we conducted over-expression and knockdown simulations on untreated cells (Fig. 4C and 4D). In the absence of YREG1, the population of models failed to consistently retain a stable epithelial state (Fig. 4D). Conversely, YREG1 amplification revealed an enhanced epithelial phenotype, while some inherently transformed cells moved towards a hybrid phenotype (Fig. 4C). Elevated YREG1 repressed LEF-1 and TGF- β 3 expression, thereby not allowing free β -catenin to form the β -catenin-LEF-1 complex, or TGF- β 3 induced SMAD activation. Taken together, low YREG1 expression was required for the maintenance of a stable epithelial phenotype that was simultaneously inducible across TGF- β 1/2, TGF- β 3 and SNAIL/SLUG transfection, as seen in the training objectives.

189 **TGF- β 1/2 and VEGF-A exposure promotes phenotype heterogeneity through NFATc
190 and phosphorylated Sp1** While we captured the central tendency of many of the molec-
191 ular features of EMT induction following TGF- β 1/2 exposure, an often neglected but im-
192 portant emergent feature of developmental and pathological programs is population het-
193 erogeneity (Park *et al.*, 2010). We (and others) have previously hypothesized that deter-
194 ministic model ensembles can simulate population behavior, at least at a course grained
195 level (Lequieu *et al.*, 2011). We tested this hypothesis by analyzing the response of the
196 population of EMT models to extracellular cues and then comparing this response to flow
197 cytometry studies. We quantified the phenotypic response of the individual members of
198 the ensemble to TGF- β 1/2 stimulation for two downstream phenotypic markers, Vimentin
199 (mesenchymal) and E-cadherin (epithelial) following the addition of TGF- β 1/2 alone (Fig.
200 3), and VEGF-A in combination with NFATc inhibitors (Fig. 3).

201 We identified model subpopulations that exhibited different behaviors following expo-
202 sure to TGF- β 1/2 (Fig. 3A). Analysis of the molecular signatures of these subpopulations
203 suggested the abundance, localization and state of the Sp1, AP-1 and NFATc transcription
204 factors controlled population heterogeneity. The majority of models (>80%) responded to
205 treatment, moving off of the untreated population (Fig 3A-C, gray). These models showed
206 the classically expected behavior, a switch from an epithelial to mesenchymal phenotype
207 following TGF- β 1/2 exposure. Models near resembling untreated cells had evaluated
208 nuclear localized phosphorylated Sp1, relative to non-induced cells. Elevated Sp1 ac-
209 tivity decreased E-cadherin expression through Slug-mediated inhibition, which in turn
210 increased Vimentin expression through TGF- β 3 autocrine signaling and the liberation
211 of β -catenin. However, the most biologically interesting behavior was exhibited by cells
212 achieving a hybrid phenotype, most notable in a dual treatment condition (black arrow),
213 but also present in a small percentage of untreated cells (Fig. 3A). Models with this hybrid
214 phenotype had elevated Sp1 and NFAT transcriptional activity, resulting in the simultane-
215 ous increase of *both* Vimentin and E-cadherin expression (Fig. 4A). Analysis of these

216 hypothetical cells suggested they had deregulated NFAT expression and nuclear local-
217 ization promoted E-cadherin expression while TGF- β 1/2 induced Sp1 action promoted
218 Vimentin expression.

219 To test this hypothesis, we simulated the response of the network to TGF- β 1/2 and
220 VEGF-A treatment with and without NFATc inhibitors (Fig. 4). As expected, stimulation
221 with VEGF-A (50 a.u.) maintained an epithelial population, while TGF- β 1/2 (10 a.u.) ex-
222 posure shifted the population from an epithelial to a mesenchymal phenotype (Fig. 3A and
223 Fig. 3B). On the other hand, combined stimulation with TGF- β 1/2 (10 a.u.) and VEGF-A
224 (50 a.u.) increased both E-cadherin and Vimentin expression, resulting in a hybrid phe-
225 notype with both epithelial and mesenchymal characteristics (Fig. 3C). Vimentin expres-
226 sion was correlated with high levels of nuclear phosphorylated Sp1, following TGF- β 1/2
227 exposure. Conversely, elevated E-cadherin expression depended upon the activity of
228 NFAT transcription factors downstream of VEGF-A stimulation. To further isolate the role
229 of NFAT on this hybrid state, we simulated the inhibition of NFAT transcriptional activity
230 across all conditions (all else being equal). NFAT inhibition in combination with VEGF-A
231 and TGF- β 1/2 treatments blocks increased activation of E-cadherin (Fig. 3D and Fig.
232 3E). Lastly, NFATc inhibition in combination with simultaneous TGF- β 1/2 and VEGF-A
233 exposure repressed nearly all E-cadherin expression, shifting nearly the entire population
234 towards a mesenchymal phenotype (Fig. 4F). Taken together, high levels of nuclear local-
235 ized phosphorylated Sp1 correlated with Vimentin expression, while NFATc transcriptional
236 activity was predicted to be critical for maintaining E-cadherin expression in the presence
237 of competing signals. In particular, when present, VEGF-A signaling through NFATc was
238 predicted to provide a protective up-regulation of E-cadherin.

239 **Combined TGF- β 2 and VEGF-A exposure drives heterogeneity in MCF10A and**
240 **DLD1 cells** The EMT model simulations suggested the transcriptional activity of NFATc
241 and Sp1 could be independently tuned to generate a hybrid cell population with both
242 epithelial and mesenchymal characteristics. To test this hypothesis, we exposed either

243 quiescent epithelial (MCFA10, (Fig. 5)) or transformed epithelial cells (DLD1, (Fig. S2))
244 to combinations of TGF- β 1/2 and/or VEGF-A. As expected, treatment with TGF- β 1/2
245 (10ng/ml) increased Slug and Vimentin expression, while repressing E-cadherin expres-
246 sion both at the transcript and protein levels in MCF10A (Fig. 5A-B) and DLD1 cells (Fig.
247 S3C, Fig S3 D,E). Both MCF10A (Fig. 5C) and DLD1 cells (Fig. S2E,G) transitioned
248 from quiescent cobblestone morphology to spread spindle shapes, consistent with EMT.
249 As predicted, we found increased nuclear localization of phosphorylated Sp1 following
250 TGF- β 1/2 stimulation in both MCF10A (Fig. 5B,C) and DLD1 cells (Fig. S2E,F). Con-
251 sistent with model predictions, VEGF-A (50ng/ml) treatment increased the abundance of
252 NFATc1 and E-cadherin at both the transcript and protein level in both MCF10A (Fig.
253 5A) and DLD1 (Fig. S2A) cells. We also found that NFATc1 nuclear localization signif-
254 icantly increased in both MCF10 and DLD1 treated with VEGF-A independently of the
255 abundance of nuclear localized phosphorylated Sp1 levels (Fig. 5B,C Fig.S3C,E). Inter-
256 estingly, combining VEGF-A (50ng/ml) with TGF- β 1/2 (10ng/ml) resulted in significantly
257 elevated expression of both E-cadherin and Vimentin at the transcript and protein levels
258 in both MCF10A and DLD1 cells (Fig 5A,B; Fig S3D,E; Fig S4C). NFATc1 expression
259 increased, while Sp1 expression was similar to the TGF- β 1/2 case alone (Fig. 5A-B,
260 Fig S3D,E; Fig S4C)), supporting their independent regulation. The expression of Slug,
261 and Vimentin significantly increased, while E-cadherin levels were increased in MCF10A
262 cells (Fig 5A) and maintained at control levels in DLD1 cells (Fig. S3D).y As further pre-
263 dicted, nuclear co-localization of both NFATc1 and phosphorylated Sp1 were apparent in
264 MCF10A and DLD1 cells treated with both ligands (Fig. 5B,C Fig S3E,F). Taken together,
265 combined VEGF-A and TGF- β 1/2 treatment elicited a hybrid phenotype expressing both
266 mesenchymal and epithelial characteristics in both MCF10A and DLD1 cells. This phe-
267 nototype was driven by the transcriptional activity of two key transcription factors, Sp1 and
268 NFATc, which could be modulated independently by TGF- β 1/2 and VEGF-A exposure.

269 Our phenotypic analysis predicted that NFATc transcriptional activity was critical to

270 maintaining E-cadherin expression in the presence of both VEGF-A and TGF- β 1/2. We
271 experimentally tested this hypothesis by exposing both MCF10A (Fig. 5E,F) and DLD1
272 cells (Fig. S3) to combinations of VEGF-A and TGF- β 1/2 in the presence or absence
273 of VIVIT, a soluble peptide inhibitor of NFATc transcriptional activity (Aramburu *et al.*,
274 1999). Treatment with VEGF-A (50ng/ml) and VIVIT (10 μ M) in MCF10A cells significantly
275 reduced E-cadherin expression compared to VEGF-A alone (Fig 5D,E). Co-treatment
276 with VIVIT and TGF- β 1/2 did not enhance EMT capacity of MCF10A cells above that
277 of TGF- β 1/2 alone (Fig 5A,B,E). Likewise, VIVIT in combination with both TGF- β 1/2
278 and VEGF-A resulted in a loss of E-cadherin gene and protein expression, while Slug
279 and Vimentin levels remained increased (Fig. 5D,E). Quantitative flow cytometry con-
280 firmed these results in both MCF10A (Fig. 5F) and DLD1 cells (Fig. S4C). Both epithelial
281 cell lines initially had high levels of E-cadherin expression, and low vimentin abundance
282 (Q1-99.5%), but both MCF10A and DLD1 cells shifted from an epithelial to mesenchymal
283 phenotype (Q1-33.4%, Q4-42.8%) following TGF- β 1/2 exposure. As expected, NFATc
284 nuclear localization was repressed with VIVIT treatment regardless of ligand stimulation,
285 while the abundance of nuclear phosphorylated Sp1 increased for both TGF- β 1/2 and
286 TGF- β 1/2 + VIVIT conditions (Fig. 5D,E). Combined TGF- β 1/2 and VEGF-A increased
287 both Vimentin and E-cadherin expression (Q1-42.1%, Q2-52.3%) compared to TGF- β 1/2
288 alone. Together, these results demonstrate that NFATc and phosphorylated Sp1 are criti-
289 cal for regulating E-cadherin and Vimentin expression during phenotype heterogeneity in
290 MCF10A and DLD1.

291 **Ductal branching during acini formation is dependent upon phenotype heterogene-
292 ity in MCF10A and DLD1 cells** We finally employed established three-dimensional
293 (3D) *in vitro* models of invasion, migration, compaction, and tubulogenesis (Dhimolea
294 *et al.*, 2010) to determine the functional consequences of the hybrid phenotype (Fig. 6).
295 MCF10A and DLD1 cells were aggregated via hanging drop, placed on the surface of a
296 collagen gel, and cultured for 72 hrs under various biochemical treatments. TGF- β 1/2

297 stimulation significantly enhanced cell matrix invasion and matrix compaction, while in
298 contrast VEGF-A stimulation promoted surface migration but no invasion or compaction
299 (Fig. 6B-D). Interestingly, combined TGF- β 1/2 and VEGF-A stimulation significantly in-
300 creased cell migration potential above that of VEGF-A alone while maintaining 3D matrix
301 compaction, though with decreased magnitude compared to TGF- β 1/2 alone. Inhibi-
302 tion of NFATc transcriptional activity by VIVIT decreased migration following treatment
303 with VEGF-A alone (Fig. 6B). Co-treatment of VIVIT significantly decreased migration,
304 while complementarily increasing invasion and compaction, when MCF10A cells were
305 stimulated with both VEGF-A and TGF- β 1/2 (Fig. 6B-D). The responses of DLD1 cells
306 followed a similar trend to MCF10A, although the magnitudes of migration, invasion, and
307 compaction were less. Cell circularity within 3D gels strongly and negatively correlated
308 with both invasion and compaction regardless of treatment (Fig. 6E). Circularity refers
309 to the morphology of the cells. In general, a quiescent epithelial cells assumes a circular
310 morphology in culture, while an active mesenchymal cell is highly elongated. The circular-
311 ity index, a common means of quantifying cell morphology, relates cell area to perimeter.
312 A perfect circle has a circularity index equal to 1.0, while a straight line has a circularity
313 index equal to 0.0, see Butcher et al. (Butcher et al., 2004). TGF- β 1/2 treatment alone
314 resulted in irregular and spindle shaped morphology, while VEGF-A exposure promoted
315 round quiescent cells (Fig. 6A). Combined VEGF-A and TGF- β 1/2 promoted morphology
316 between these extremes. VIVIT mediated NFATc inhibition significantly reduced the cir-
317 cularity index, similar to TGF- β 1/2 treatment (Fig. 6F). VEGF-A treatment also induced
318 the formation of tubular structures (acini), but the number of tubular branches relative to
319 total acini was significantly increased upon combined TGF- β 1/2 and VEGF-A. No tubular
320 structures were identified within the DLD1 constructs during the 7 day tubulogenesis end-
321 points, supporting that MCF10A and DLD1 cells have some cell-type specific EMT sensi-
322 tivity despite their underlying competency for acquiring a heterogeneous phenotype. This
323 suggests that initial EMT sensitivity of a cell influences downstream functional response

³²⁴ from TGF- β and VEGFA stimulation. Together, these results establish that VEGF-A and
³²⁵ TGF- β 1/2 ligand concentrations potentiate between acini and ductal branch formation in
³²⁶ 3D culture, and are dependent upon NFATc activity.

327 **Discussion**

328 In this study, we developed a family of mechanistic models describing the induction of
329 EMT by TGF- β isoforms in the presence and absence of VEGF-A. The signaling architec-
330 ture encoded in the model, which contained 74 molecular species interconnected by 169
331 interactions, described the expression of 23 genes in response to growth factor stimula-
332 tion. This simulation incorporates an unprecedented level of detail compared to previous
333 models, but as a consequence created a large number of unknown model parameters.
334 Because these parameters could not be estimated uniquely apriori, we estimated an en-
335 semble of likely parameters using the JuPOETs multiobjective optimization framework.
336 The model population was trained and cross-validated to prescribe biological significance
337 using 41 data sets generated in DLD1 colon carcinoma, MDCKII, and A375 melanoma
338 cell lines (Medici *et al.*, 2008). The absence of TGF- β 1/2 or VEGF-A stimulation was
339 used as the baseline for the robustness calculations. Analysis of this population pre-
340 dicted possible phenotypic modes (and their associated signaling) that cells could exhibit
341 when stimulated with TGF- β and/or VEGF-A. The most novel hypothesis generated from
342 the analysis was that cells could operate in a hybrid state defined by both epithelial and
343 mesenchymal traits when stimulated simultaneously with TGF- β and VEGF-A. We tested
344 this hypothesis in MCF10A and DLD1 cells stimulated with combinations of TGF- β and
345 VEGF-A. As expected, in the presence of TGF- β or VEGF-A alone, MCF10A and DLD1
346 cells were either mesenchymal or epithelial, respectively. However, with both TGF- β and
347 VEGF-A, MCF10A and DLD1 cells exhibited a hybrid phenotype, having both epithe-
348 lial and mesenchymal characteristics. Furthermore, we found that functional traits such
349 as tubulogenesis and ductal branching were different for cells in this hybrid phenotype.
350 Together, this study established a predictive model of EMT induction, determined that
351 deterministic model ensembles could predict population heterogeneity, and proved the
352 existence of a unique hybrid phenotype resulting from the simultaneous integration of
353 extracellular growth factor signals.

354 Cells routinely process a multitude of signals simultaneously, especially when coordi-
355 nating developmental or pathological programs. For example, oncogenic cells integrate
356 both mechanical and chemical cues in their local microenvironment during tumorigenesis,
357 including cytokines VEGF and TGF- β (Hong *et al.*, 2013). VEGF-A mediates patholog-
358 ical angiogenic remodeling of tumors (Nagy *et al.*, 2007), while TGF- β can elicit both
359 protective and oncogenic responses (Ferrara, 2002, Willis & Borok, 2007). While much
360 research has tested signaling pathways individually, far less is understood about com-
361 binatorial stimulation, such as with both VEGF-A and TGF- β . Recent *in vitro* and *in*
362 *vivo* evidence has suggested that epithelial cells can exhibit heterogeneous phenotypes
363 in addition to classically defined epithelial or mesenchymal states (Polyak & Weinberg,
364 2009, Strauss *et al.*, 2011). For example, expression profiling in human epithelial cancer
365 cell lines demonstrated a spectrum of phenotypes, including some that expressed both
366 E-cadherin and Vimentin simultaneously (Neve *et al.*, 2006, Welch-Reardon *et al.*, 2014).
367 Zajchowski *et al.*, speculated that these expression profiles were somehow important for
368 maintaining epithelial properties, while simultaneously allowing other functional behavior
369 such as proliferation and migration (Zajchowski *et al.*, 2001). Whether and how heteroge-
370 neous phenotypes arise and participate in cancer progression, as well as their response
371 to pharmacological inhibition are fundamental questions that should receive increased at-
372 tention. In this study, we determined that a hybrid phenotype could be obtained through
373 combined treatment with VEGF-A and TGF- β , both common factors localized in the tu-
374 mor microenvironment. Furthermore, our systematic simulation-experimentation strategy
375 identified that the transcriptional activity of Sp1 and NFATc were the critical factors con-
376 trolling this phenotypic heterogeneity. Several studies have highlighted the importance
377 of NFATc as a key transcription factor involved in cell growth, survival, invasion, angio-
378 genesis and cancer (Mancini & Toker, 2009). For example, proliferation and anchorage-
379 independent growth of pancreatic tumor cells is dependent on calcineurin and NFATc1
380 activity, consistent with the high levels of nuclear NFATc1 found in pancreatic tumors

381 (Singh *et al.*, 2010). Likewise, our results found that VEGF-A was a potent inducer of
382 NFATc1 expression, which may be required for epithelial cell migration and tubulogenesis.
383 Although specific NFATc isoforms were not distinguished in the model, our simulations
384 suggested that NFATc transcriptional activity was capable of maintaining epithelial traits,
385 even during TGF- β induced EMT. Experimentally, we found that E-cadherin expression
386 was dependent upon NFATc dephosphorylation in response to simultaneous VEGF-A and
387 TGF- β 1/2 treatment. Thus, these results support the hypothesis that NFATc activity plays
388 a critical role in maintaining cell-cell contacts, even during partial EMT.

389 Epithelial cells reproduce tissue-like organization when grown in a three-dimensional
390 extracellular matrix (ECM) environment, and therefore are an attractive model to study
391 morphogenic mechanisms. It is well established that MCF10A cells form structures that
392 closely resemble acini (multi-lobed cluster of cells) in three-dimensional *in vitro* cultures
393 (Debnath *et al.*, 2003). It has been postulated that a cellular response reminiscent of
394 partial EMT underlies this process, stimulating further branching and formation of acini
395 (Pearson & Hunter, 2007). Normally well controlled process such as tubulogenesis can
396 be co-opted by cancer cells to break away from a primary lesion and invade through
397 the surrounding stroma (O'Brien *et al.*, 2004). However, by retaining a transient hybrid
398 EMT-like state, clusters of these tube-forming tumor cells can reform at a high rate af-
399 ter invasion, possibly explaining why invasive human carcinomas frequently appear to be
400 cellular collections with varying degrees of gland-like differentiation (Debnath & Brugge,
401 2005). In this study, we showed that our predicted hybrid phenotype generated by simu-
402 taneous treatment of epithelial cells with VEGF-A and TGF- β possessed altered migra-
403 tion and invasion, which enhanced tubular branching. A salient feature of this behavior,
404 however, was the retention of cell-cell contacts that allowed cells to migrate without com-
405 pletely dissociating from their neighbors. Thus, our results support a mechanism in which
406 hybrid cells can maintain some functional characteristics of epithelial cells such as cell-
407 cell adhesion, which are normally lost in a fully differentiated mesenchymal state. The

tumor microenvironment contains many soluble signals simultaneously, including VEGF and TGF- β . Thus, it is likely that some cancerous epithelial cells could exhibit hybrid EMT phenotypic states. This may explain why fibroblastoid morphology, a classical feature of EMT, is not commonly observed in human carcinomas (Debnath & Brugge, 2005). This study focused on the combinatorial effects of two very different ligand families present together in the tumor environment. Additional modeling studies are required to unravel the global response of epithelial cells to the full spectrum of chemical, substrate, and mechanical cues. The simulation strategy presented here is readily adaptable to larger species sets, with the major advantage that experimentally testable hypotheses can be generated regarding how signals get integrated to produce global cellular response. Furthermore, by simulating multiple ensembles of parameter sets, subpopulations across a constellation of phenotypes can be created and mined for common and/or divergent signaling characteristics. This is a significant advantage over forced convergence to a single unique solution and thereby generating a potentially non-physiological homogeneous population.

The deterministic population of EMT models predicted heterogeneous behavior that was qualitatively consistent with experimental studies. There is a diversity of algorithmic approaches to estimate model parameters (Moles *et al.*, 2003), as well as many strategies to integrate model identification with experimental design (Rodriguez-Fernandez *et al.*, 2013, Villaverde & Banga, 2014). However, despite these advances, the identification of models describing intracellular network behavior remains challenging. There are different schools of thought to deal with this challenge. One school has focused on model reduction. Data-driven approaches (Cirit & Haugh, 2012), boolean (Choi *et al.*, 2012) or other logical model formulations (Morris *et al.*, 2011, Terfve *et al.*, 2012) are emerging paradigms that constrain model complexity by the availability of the training and validation data. Other techniques such as constraints based modeling, which is commonly used to model metabolic networks, have also been applied to model transcriptional networks, although primarily in lower eukaryotes and prokaryotes (Hyduke & Palsson, 2010). These

435 techniques (and many others, see review (Wayman & Varner, 2013)) are certainly ex-
436 citing, with many interesting properties. However, we used the traditional approach of
437 mass action kinetics within an ordinary differential equation framework. The identifica-
438 tion problem for the EMT model was massively underdetermined. This is not uncommon
439 for differential equation models, especially those that are highly mechanistic. Of course,
440 we could have discarded mechanism or reduced the model scope to decrease the com-
441 plexity of the identification problem. However, a central criticism leveled by biologists is
442 that model simplification is often done at the cost of biological reality, or done for reasons
443 of computational expediency (Sainani, 2012). To avoid this criticism, we systematically
444 identified an ensemble of likely models each consistent with the training data, instead of a
445 single but uncertain best fit model. Previously, we (and others) have suggested that deter-
446 ministic ensembles could model heterogeneous populations in situations where stochastic
447 computation was not feasible (Lequieu *et al.*, 2011). Population heterogeneity using deter-
448 ministic model families has previously been explored for bacterial growth in batch cultures
449 (Lee *et al.*, 2009). In that case, distributions were generated because the model parame-
450 ters varied over the ensemble, i.e., extrinsic noise led to population heterogeneity. In this
451 study, parameters controlling physical interactions such as disassociation rates or the rate
452 of assembly or degradation of macromolecular machinery such as ribosomes were widely
453 distributed over the ensemble. Population heterogeneity can also arise from intrinsic ther-
454 mal fluctuations, which are not captured by a deterministic population of models (Swain
455 *et al.*, 2002). Thus, deterministic ensembles, provide a coarse-grained or extrinsic-only
456 ability to simulate population diversity. Despite this limitation, our prediction of phenotypic
457 heterogeneity (and the underlying signaling events responsible for the heterogeneity) was
458 consistent with experimental observations. This suggested that deterministic ensembles
459 could simulate disease or developmental processes in which heterogeneity plays an im-
460 portant role, without having to resort to stochastic simulation.

461 A common criticism of ODE modeling has been the poorly characterized effect of

462 structural and parametric uncertainty. In this study, parametric uncertainty was addressed
463 by developing an ensemble of probable models instead of a single best-fit but uncertain
464 model using multiobjective optimization. While computationally complex, multiobjective
465 optimization is an important tool to address qualitative conflicts in training data that arise
466 from experimental error or cell line artifacts (Handl *et al.*, 2007). On the other hand, struc-
467 tural uncertainty is defined as uncertainty in the biological connectivity. The EMT model
468 connectivity was assembled from an extensive literature review. However, several poten-
469 tially important signaling mechanisms were not included. First, we identified a potential
470 gap in biological knowledge surrounding the regulation of LEF-1 expression, that was filled
471 by the addition of the hypothetical YREG1 transcriptional repressor. The LEF-1 transcrip-
472 tion factor is expressed in tissues that undergo EMT during embryogenesis (Nawshad &
473 Hay, 2003, Vega *et al.*, 2004), and has been suggested to promote an invasive phenotype
474 in cancer cells (Cano *et al.*, 2000, Kim *et al.*, 2002). Low levels of YREG1 were important
475 for stabilizing the interaction between LEF-1 and β -catenin, while elevated levels inhibited
476 EMT by downregulating LEF-1 transcriptional activity. Recent evidence has established a
477 complex role of Amino terminal Enhancer of Split (AES) and Groucho/TLE on suppress-
478 ing LEF-1 activity. AES opposes LEF-1 transcriptional activation while Groucho/TLE binds
479 with LEF-1 for a histone deacetylase repression. In addition, β -catenin directly displaces
480 Groucho/TLE repressors from TCF/LEF-1 in Wnt-mediated transcription activation (Arce
481 *et al.*, 2009, Grumolato *et al.*, 2013). Our model agrees with this newly discovered feed-
482 back system, as YREG1 regulates LEF-1 activity leading to EMT stabilization.

483 Recent evidence has also suggested an essential role of NF- κ B in epithelial trans-
484 formation. NF- κ B may influence Snail expression through the AKT pathway and directly
485 stabilize Snail activity (Wu *et al.*, 2009). This is particularly important for integrating in-
486 flammation pathways, such as interleukin-6 (IL-6) and tumor necrosis factor- α (TNF- α),
487 which have been linked to EMT in pathological conditions (Sullivan *et al.*, 2009). Other
488 pathways such as Notch have also been shown to act synergistically with TGF- β to ex-

489 press Slug in the developing embryo (Niessen *et al.*, 2008). Lastly, while we have modeled
490 classical protein signaling, we have not considered the role of regulatory RNAs on EMT.
491 There is growing evidence that microRNAs (miRNAs) play a strong role in EMT, where
492 several miRNAs, for example miR-21 and miR-31 are strongly associated with TGF- β ex-
493 posure (Bullock *et al.*, 2012). Addressing missing structural components like these, could
494 generate more insight into TGF- β signaling and its role in phenotypic transformation.

495 **Materials and Methods**

496 All model code and parameter ensemble is freely available under an MIT software license
497 and can be downloaded from <http://www.varnerlab.org>.

498 **Signaling network connectivity** The EMT model described the gene expression pro-
499 gram resulting from TGF- β and VEGF-A signaling in a prototypical epithelial cell. The
500 TGF- β -EMT network contained 97 nodes (proteins, mRNA or genes) interconnected by
501 251 interactions. The network connectivity was curated from more than 40 primary liter-
502 ature sources in combination with on-line databases (Jensen *et al.*, 2009, Linding *et al.*,
503 2007). The model interactome was not specific to a single epithelial cell line. Rather, we
504 assembled canonical pathways involved in TGF- β and VEGF-A signaling, defaulting to
505 human connectivity when possible. Using a canonical architecture allowed us to explore
506 general features of TGF- β induced EMT without cell line specific artifacts. On the other
507 hand, because of the canonical architecture, we can test the model against several cell
508 lines to test the generality of our conclusions.

509 Our signaling network reconstruction was based on Medici *et al.* who identified the
510 pathways through which MDCKII, DLD1 colon carcinoma, and A375 melanoma cells tran-
511 sition towards a mesenchymal phenotype (Medici *et al.*, 2008). Sequential activation of
512 MAPK and Smad pathways were initiated upon addition of TGF- β 1/2. Briefly, TGF- β 2
513 signals through the RAS-RAF-MEK-ERK pathway to up-regulate Snail and Slug expres-
514 sion (Medici *et al.*, 2006). Snail, a known repressor of junctional proteins, inhibits the ex-
515 pression of E-cadherin (Cano *et al.*, 2000). This initial repression of E-cadherin leads to a
516 release of β -catenin from the cell membrane. This release of β -catenin can then translo-
517 cate to the nucleus and form transcriptional complexes with TCF-4 to drive TGF- β 3 ex-
518 pression (Medici *et al.*, 2008). The PI3K to GSK3 pathway was included and acted as an
519 activating mechanism of β -catenin signaling through TGF- β 3 signaling ,itepMedici:2008fk.
520 GSK3 is known to act on β -catenin signaling through the ubiquitin-proteasome pathway
521 (Larue & Bellacosa, 2005, Zhou *et al.*, 2004). Thereby, further β -catenin release also re-

522 sulted from by TGF- β 3 signals to the cells interior by binding to type II receptors, which
523 form heterodimers with type I receptors (ALK5) (Derynck & Zhang, 2003). This activates
524 the receptors serine/threonine kinase activity to phosphorylate and activate the recep-
525 tor Smads 2/3 (Massagué *et al.*, 2005). In the model, receptors are represented as either
526 bound or unbound complexes. Phosphorylated Smads 2/3 (pSmad2/3) form heterodimers
527 and translocate to the nucleus. pSmads complexes up-regulate other transcription factors,
528 such as LEF-1. The pSmad2/4-LEF-1 complex has been shown to directly repress the E-
529 cadherin gene (Nawshad *et al.*, 2007). LEF-1 also binds with β -catenin to upregulate mes-
530 enchymal proteins such as fibronectin (Medici *et al.*, 2011). In the model, Smad signaling
531 is lumped into a single smad species that can act in a co-dependent fashion with LEF1 to
532 downregulate E-cadherin. The EMT gene expression program was initiated by the binding
533 of TGF- β isoforms to TGF- β surface receptors. Binding of extracellular TGF- β 1/2 with
534 TGF- β surface receptors I/II (TGF- β R-I/II) initiates the assembly of adapter complexes
535 which starts the downstream signaling program. In the model, TGF- β 1/2 binds TGF- β R-
536 I/II followed by the recruitment of activin receptor-like kinase 1 (ALK1) and TGF- β sur-
537 face receptor III (TGF- β R-III) to form the activated receptor complex (Derynck & Zhang,
538 2003). Alternatively, we also included activin receptor-like kinase 5 (ALK5) recruitment in
539 combination with Endoglin and TGF- β R-III as a second (redundant) activated receptor
540 complex (Gatza *et al.*, 2010). Complex assembly activates the serine/threonine kinase
541 activity on the receptor, leading to the recruitment and phosphorylation of Smad partners
542 (Massagué *et al.*, 2005). Phosphorylated Smads2/3 (pSmad2/3) form heterodimers with
543 partner Smad4 and then translocate to the nucleus where they act as both transcriptional
544 activators and repressors. Nuclear pSmad2/3-Smad4 form transcriptional complexes with
545 several genes in the model including lymphoid enhancer-binding factor 1 (*LEF-1*), Nuclear
546 factor of activated T-cells, cytoplasmic 1 (*NFACT1*), and Specificity Protein 1 (*SP1*). On
547 the other hand, nuclear pSmad2/3-Smad4 represses (in combination with the LEF-1 pro-
548 tein) the expression of E-cadherin (*Cdh1*) (Nawshad *et al.*, 2007) and Cadherin 5, type

549 2 (VE-Cadherin encoded by *Cdh5*). Repression of E-cadherin expression is the central
 550 event in the transition from an epithelial to a mesenchymal phenotype (Cano *et al.*, 2000).
 551 However, this transition is not solely driven by transcriptional events. At the protein level,
 552 the repression of E-cadherin leads to a release of β -catenin from cell membrane. Cytosolic
 553 β -catenin then translocates to the nucleus and forms transcriptionally-active complexes
 554 with immunoglobulin transcription factor 2 (TCF-4) to drive TGF- β 3 expression (Medici
 555 *et al.*, 2008). The PI3K to GSK3 pathway was included and acted as an activating mech-
 556 anism of β -catenin signaling through TGF- β 3 signaling (Medici *et al.*, 2008). GSK3 is
 557 known to act on β -catenin signaling through the ubiquitin-proteasome pathway (Larue &
 558 Bellacosa, 2005, Zhou *et al.*, 2004). Lastly, VEGF-A activation of NFATc1 takes place
 559 through calcineurin signaling leading to an enhancement of E-cadherin expression (Sue-
 560 hiro *et al.*, 2014), as supported by our VEGF-A experimental data (Fig. S4).

561 **Formulation, solution and analysis of the EMT model equations**

562 *EMT signaling events.* EMT signaling events were modeled using either saturation or
 563 mass-action kinetics within an ordinary differential equation (ODE) framework:

$$\frac{1}{\tau_i} \frac{dx_i}{dt} = \sum_{j=1}^{\mathcal{R}} \sigma_{ij} r_j(\mathbf{x}, \epsilon, \mathbf{k}) - \mu x_i \quad i = 1, 2, \dots, \mathcal{M} \quad (1)$$

564 where \mathcal{R} denotes the number of signaling reactions and \mathcal{M} denotes the number of pro-
 565 teins in the model. The quantity τ_i denotes a time scale parameter for species i which
 566 captures unmodeled effects. In the current study $\tau_i = 1$ for all species. The quantity
 567 $r_j(\mathbf{x}, \epsilon, \mathbf{k})$ denotes the rate of reaction j . Typically, reaction j is a non-linear function of
 568 biochemical and enzyme species abundance, as well as unknown model parameters \mathbf{k}
 569 ($\mathcal{K} \times 1$). The quantity σ_{ij} denotes the stoichiometric coefficient for species i in reaction j . If
 570 $\sigma_{ij} > 0$, species i is produced by reaction j . Conversely, if $\sigma_{ij} < 0$, species i is consumed
 571 by reaction j , while $\sigma_{ij} = 0$ indicates species i is not connected with reaction j . Species
 572 balances were subject to the initial conditions $\mathbf{x}(t_0) = \mathbf{x}_0$.

573 Rate processes were written as the product of a kinetic term (\bar{r}_j) and a control term (v_j)
 574 in the EMT model. The rate of enzyme catalyzed reactions was modeled using saturation
 575 kinetics:

$$\bar{r}_j = k_j^{cat} \epsilon_i \left(\frac{x_s}{K_{js} + x_s} \right) \quad (2)$$

576 where k_j^{cat} denotes the catalytic rate constant for reaction j , ϵ_i denotes the abundance of
 577 the enzyme catalyzing reaction j , and K_{js} denotes the saturation constant for species s
 578 in reaction j . On the other hand, mass action kinetics were used to model protein-protein
 579 binding interactions within the network:

$$\bar{r}_j = k_j^{max} \prod_{s \in m_j^-} x_s^{-\sigma_{sj}} \quad (3)$$

580 where k_j^{max} denotes the maximum rate for reaction j , σ_{sj} denotes the stoichiometric coef-
 581 ficient for species s in reaction j , and $s \in m_j$ denotes the set of *reactants* for reaction j .
 582 We assumed all binding interactions were irreversible.

583 The control terms $0 \leq v_j \leq 1$ depended upon the combination of factors which in-
 584 fluenced rate process j . For each rate, we used a rule-based approach to select from
 585 competing control factors. If rate j was influenced by $1, \dots, m$ factors, we modeled this re-
 586 lationship as $v_j = \mathcal{I}_j(f_{1j}(\cdot), \dots, f_{mj}(\cdot))$ where $0 \leq f_{ij}(\cdot) \leq 1$ denotes a regulatory transfer
 587 function quantifying the influence of factor i on rate j . The function $\mathcal{I}_j(\cdot)$ is an integration
 588 rule which maps the output of regulatory transfer functions into a control variable. In this
 589 study, we used $\mathcal{I}_j \in \{\min, \max\}$ (Sagar & Varner, 2015). If a process has no modifying
 590 factors, $v_j = 1$.

591 *EMT gene expression processes.* The EMT model described both signal transduction
 592 and gene expression events following the addition of TGF- β and VEGF-A. For each

593 gene, we modeled both the resulting mRNA (m_j) and protein (p_j):

$$\frac{dm_j}{dt} = r_{T,j} - (\mu + \delta_{m,j}) m_j + \lambda_j \quad (4)$$

$$\frac{dp_j}{dt} = r_{X,j} - (\mu + \delta_{p,j}) p_j \quad (5)$$

594 where $j = 1, 2, \dots, \mathcal{G}$. The terms $r_{T,j}$ and $r_{X,j}$ denote the specific rate of transcription,
 595 and translation while the terms $\delta_{m,j}$ and $\delta_{p,j}$ denote degradation constants for mRNA and
 596 protein, respectively. Lastly, μ denotes the specific growth rate, and λ_j denotes the con-
 597 stitutive rate of gene expression for gene j . The specific transcription rate was modeled
 598 as the product of a kinetic term $\bar{r}_{T,j}$ and a control term u_j which described how the abun-
 599 dance of transcription factors, or other regulators influenced the expression of gene j .

600 The kinetic rate of transcription was modeled as:

$$\bar{r}_{T,j} = \alpha_j \left[V_T^{max} \left(\frac{G_j}{K_T + G_j} \right) \right] \quad (6)$$

601 where the maximum gene expression rate was defined as the product of a character-
 602 istic transcription rate constant (k_T) and the abundance of RNA polymerase, $V_T^{max} =$
 603 $k_T (RNAP)$. The parameter α_j was used to adjust the transcription to that of gene j (es-
 604 timated in this study), while k_T , G_j and $RNAP$ were estimated from literature (Milo *et al.*,
 605 2010). Similar to the signaling processes, the gene expression control term $0 \leq u_j \leq 1$
 606 depended upon the combination of factors which influenced rate process j . For each
 607 rate, we used a rule-based approach to select from competing control factors. If the ex-
 608 pression of gene j was influenced by $1, \dots, m$ factors, we modeled this relationship as
 609 $u_j = \mathcal{I}_j(f_{1j}(\cdot), \dots, f_{mj}(\cdot))$ where $0 \leq f_{ij}(\cdot) \leq 1$ denotes a regulatory transfer function
 610 quantifying the influence of factor i on the expression of gene j . The function $\mathcal{I}_j(\cdot)$ is an
 611 integration rule which maps the output of regulatory transfer functions into a control vari-
 612 able. In this study, we used $\mathcal{I}_j \in \{\min, \max\}$ (Sagar & Varner, 2015). If a gene expression
 613 process has no modifying factors, $u_j = 1$. Lastly, the specific translation rate was modeled

614 as:

$$r_{X,j} = \beta_j \left[V_X^{max} \left(\frac{m_j}{K_X + m_j} \right) \right] \quad (7)$$

615 where V_X^{max} denotes a characteristic maximum translation rate estimated from literature,
616 β_j denotes the transcript specific correction the characteristic translation rate, and K_X
617 denotes a translation saturation constant. The characteristic maximum translation rate
618 was defined as the product of a characteristic translation rate constant (k_X) and the abun-
619 dance of Ribosomes ($RIBO$), $V_X^{max} = k_X (RIBO)$, where both k_X and $RIBO$ abundance
620 were estimated from literature (Milo *et al.*, 2010).

621 The signaling and gene expression model equations were implemented in Julia and
622 solved using the CVODE routine of the Sundials package (Bezanson *et al.*, 2014, Hindmarsh
623 *et al.*, 2005). The model code and parameter ensemble is freely available under an MIT
624 software license and can be downloaded from <http://www.varnerlab.org>.

625 *Estimation of model parameters using multiobjective optimization.* The EMT model had
626 296 unknown parameters (169 kinetic constants, 44 saturation constants, 38 control logic
627 paramters, and 45 non-zero initial conditions) which were not uniquely identifiable given
628 the training data. Instead, we estimated a population of likely models (each consistent
629 with the training data) using 41 data sets generated in DLD1 colon carcinoma, MDCKII,
630 and A375 melanoma cells taken from Medici *et al.* (Medici *et al.*, 2008). We used the
631 Pareto Optimal Ensemble Technique (JuPOETs) multiobjective optimization framework in
632 combination with leave-one-out cross-validation to estimate an ensemble of model param-
633 eters (Song *et al.*, 2010). Cross-validation was used to calculate both training and predic-
634 tion error during the parameter estimation procedure (Kohavi, 1995). The 41 intracellular
635 protein and mRNA data-sets used for identification were organized into 11 objective func-
636 tions. These 11 objective functions were then partitioned, where each partition contained
637 ten training objectives and one validation objective. The training and validation data were
638 Western blots. We achived a physical simulation scale by establishing characteristic rates
639 of transcription, translation, mRNA and protein degradation, as well as characteristic con-

640 concentrations of ribosomes and RNAPs (Milo *et al.*, 2010). The concentration scale is in nM,
641 with proteins ranging from 10-1000nM and mRNA ranging from 0.01 to 1nM, reflecting the
642 true abundances and ratios between each species.

643 **Cell culture and experimental interrogation** DLD1 colon carcinoma, MCF10A, and
644 HUVEC were acquired from the American Tissue Culture Collection (Manassas, VA).
645 Cells were grown in culture with RPMI 1640 medium with 10% fetal bovine serum and
646 1% penicillin/streptomycin for DLD1, EBM-2 supplemented with EGM-2, 5% fetal bovine
647 serum, and 1% penicillin/streptomycin for HUVEC, or MGEM 2 supplemented with insulin,
648 bovine pituitary extract, cholera toxin, hEGF, hydrocortisone, 5% horse serum, and 1%
649 penicillin/streptomycin for MCF10A. Cells were serum starved for 24 hours and removed
650 from all experimental conditions. Recombinant VEGFA165 was also removed from cul-
651 ture medium prior to experimentation. Recombinant human TGF- β 2 (R & D Systems,
652 Minneapolis, MN) was added to the culture medium at a concentration of 10 ng/ml and re-
653 combinant VEGFA165 at a concentration of (5ng/ml, 50ng/ml) for all relative experiments.
654 NFAT inhibitor (VIVIT peptide) (EMDBiosciences, Darmstadt, Germany), was added to
655 the culture medium at a concentration of 10 μ M for all relative experiments. Cells were
656 passaged 1:3 or 1:4 every 3-6 d and used between passages 4 and 8.

657 *VEGF treatment* DLD1 and MCF10A cells were suspended in culture media (with RPMI
658 1640 medium with 10% fetal bovine serum and 1% penicillin/streptomycin for DLD1 or
659 MGEM 2 supplemented with insulin, bovine pituitary extract, cholera toxin, hEGF, hydro-
660 cortisone, 5% horse serum, and 1% penicillin/streptomycin for MCF10A), and allowed to
661 aggregate overnight in hanging drop culture (20 μ L; 20,000 cells). The spherical aggre-
662 gates were placed on the surface of neutralized type I collagen hydrogels (1.5mg/mL)
663 and allowed to adhere. Cultures were then serum starved (1% serum) for 24 hours. Re-
664 combinant VEGFA165 was then added to the media (5ng/ml, 50ng/ml) and mRNA was
665 harvested after 3hr and 24hr timepoint.

666 *RT-PCR* RNA extractions were performed using a Qiagen total RNA purification kit (Qi-
667 agen, Valencia, CA) and RNA was reverse transcribed to cDNA using the SuperScript
668 III RT-PCR kit with oligo(dT) primer (Invitrogen). Sufficient quality RNA was determined
669 by an absorbance ratio A260/A280 of 1.8-2.1, while the quantity of RNA was determined
670 by measuring the absorbance at 260nm (A260). Real-time PCR experiments were con-
671 ducted using the SYBR Green PCR system (Biorad, Hercules, CA) on a Biorad CFX96
672 cycler, with 40 cycles per sample. Cycling temperatures were as follows: denaturing,
673 95C; annealing, 60C; and extension, 70C. Primers were designed to detect GAPDH, E-
674 cadherin, vimentin, Slug, Sp1, and NFATc1 in cDNA clones: Sp1 (F-TTG AAA AAG GAG
675 TTG GTG GC, R-TGC TGG TTC TGT AAG TTG GG, Accession NG030361.1), NFATc1
676 (F-GCA TCA CAG GGA AGA CCG TGT C, R-GAA GTT CAA TGT CGG AGT TTC TGA
677 G, Accession NG029226.1). GAPDH, E-cadherin, vimentin, and Slug primers were taken
678 from previously published literature (Medici *et al.*, 2008).

679 *Antibody Staining* Samples were fixed in 4% PFA overnight at 4C. Samples were then
680 washed for 15 minutes on a rocker 3 times with PBS, permeabilized with 0.2% Triton-X
681 100 (VWR International, Radnor, PA) for 10 minutes, and washed another 3 times with
682 PBS. Samples were incubated overnight at 4C in a 1% BSA (Rockland Immunochemi-
683 cals, Inc., Gilbertsville, PA) blocking solution followed by another 4C overnight incubation
684 with either rabbit anti-human E-cadherin 1:100 (Abcam, ab53033), mouse anti-human
685 phospho-Sp1 1:100 (Abcam, ab37707), mouse anti-human vimentin 1:100 (Invitrogen,
686 V9), and rabbit anti-human NFATc1 (Santa Cruz, sc-7294) 1:100. After 3 washes for 15
687 minutes with PBS, samples were exposed to Alexa Fluor 488 or 568 conjugated (Invit-
688 rogen), species specific secondary antibodies at 1:100 in 1% BSA for 2 hours at room
689 temperature. Three more washes with PBS for 15 minutes were followed by incubation
690 with either DRAQ5 far red nuclear stain (Enzo Life Sciences, Plymouth Meeting, PA) at
691 1:1000.

692 FACS Flow cytometry for E-cadherin 1:100 (Abcam) and vimentin 1:100 expressing cells
693 was performed. Briefly, cells were trypsinized, fixed with 4% PFA for 10 min and then pre-
694 served in 50% methanol/PBS. Cells were kept in the -20C until antibody staining was
695 preformed. Samples were divided into multiple aliquots in order to stain the proteins
696 separately and compensate for secondary antibody non-specific binding. Cells were in-
697 cubated for 24 hrs at 4 C in primary antibody diluted in either PBS (extracellular) or 0.2%
698 saponin-PBS (intracellular). Cells were then washed 3 times with PBS and incubated
699 with appropriate secondary antibodies and imaged using a Coulter Epics XL-MCL Flow
700 Cytometer (Coulter). All samples were compensated using appropriate background sub-
701 traction and all samples were normalized using 7500 cells per flow condition.

702 *Three-Dimensional Culture and Tubulogenesis Assays* For invasion/migration assays,
703 cells were resuspended in culture media, and allowed to aggregate overnight in hanging
704 drop culture (20 μ L; 20,000 cells). The spherical aggregates were placed on the surface of
705 neutralized type I collagen hydrogels (1.5mg/mL) and allowed to adhere for 2 hrs before
706 adding treatments. Cultures were maintained for 72 hrs, after which they were fixed in
707 4% PFA and slowly rehydrated using PBS. For compaction assays, cells were pelleted
708 via centrifugation and resuspended within a neutralized collagen hydrogel (1.5mg/mL)
709 solution at a density of 400,000 cells/mL. 250 μ L of gel was inoculated into culture wells,
710 which solidified after 60min. Treatments were then added within 800 μ L of the culture
711 medium without serum. Gels were liberated from the surfaces of the culture wells the
712 next day and cultured free floating for an additional 3-7 days, exchanging serum free
713 media with appropriate factors every 48 hrs.

714 Tubulogenesis was defined as a typical nonmalignant acini structure. This includes a
715 polarized epithelial cell, hollow lumen, and the basal sides of the cell are surrounded by
716 ECM proteins (Fig. 6A, Controls or VEGF treated). Previous work has shown that change
717 in the morphological characteristics of nontumorigenic MCF10A epithelial acini occur over
718 time and exploiting them to growth in 3D culture can be quantified. For example, using

719 image segmentation, Chang et al. (Chang *et al.*, 2007) examined the elongation of the
720 MCF10A acini at 6, 12, and 96 hours after a particular treatment. Polizzotti et al. (Poliz-
721 zotti *et al.*, 2012) also suggested a computational method to quantify acini structure based
722 on morphological characteristics in nonmalignant, noninvasive, and invasive conditions.
723 Adapted from these approaches, we first fluorescently labeled our cultures and captured
724 the acini structures by 3D confocal microscopy. Next individual acini structures in the im-
725 ages were segmented by imageJ and labeled. We then extracted the number of ductal
726 branches. Ductal branching was defined as any elongated cell cluster extending away
727 from the total acini structure, which was manually segmented and counted using ImageJ.
728 A total of 5 images for each condition were used, and approximately 12 acini were ana-
729 lyzed in each image. Total branching was normalized to the amount of acini present, and
730 provides an overall general assessment to the extent of acini remodeling.

731 *Statistics* Results are expressed as mean \pm standard error, $n \geq 6$. Data was analyzed
732 with the GraphPad Prism version 4.00 for Windows (GraphPad Software, San Diego,
733 CA) and SAS (Statistical Analysis Software, Cary, NC). A one-way ANOVA with Tukey's
734 post hoc was used to compare differences between means and data was transformed
735 when necessary to obtain equal sample variances. Differences between means were
736 considered significant at $p < 0.05$.

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Extracellular

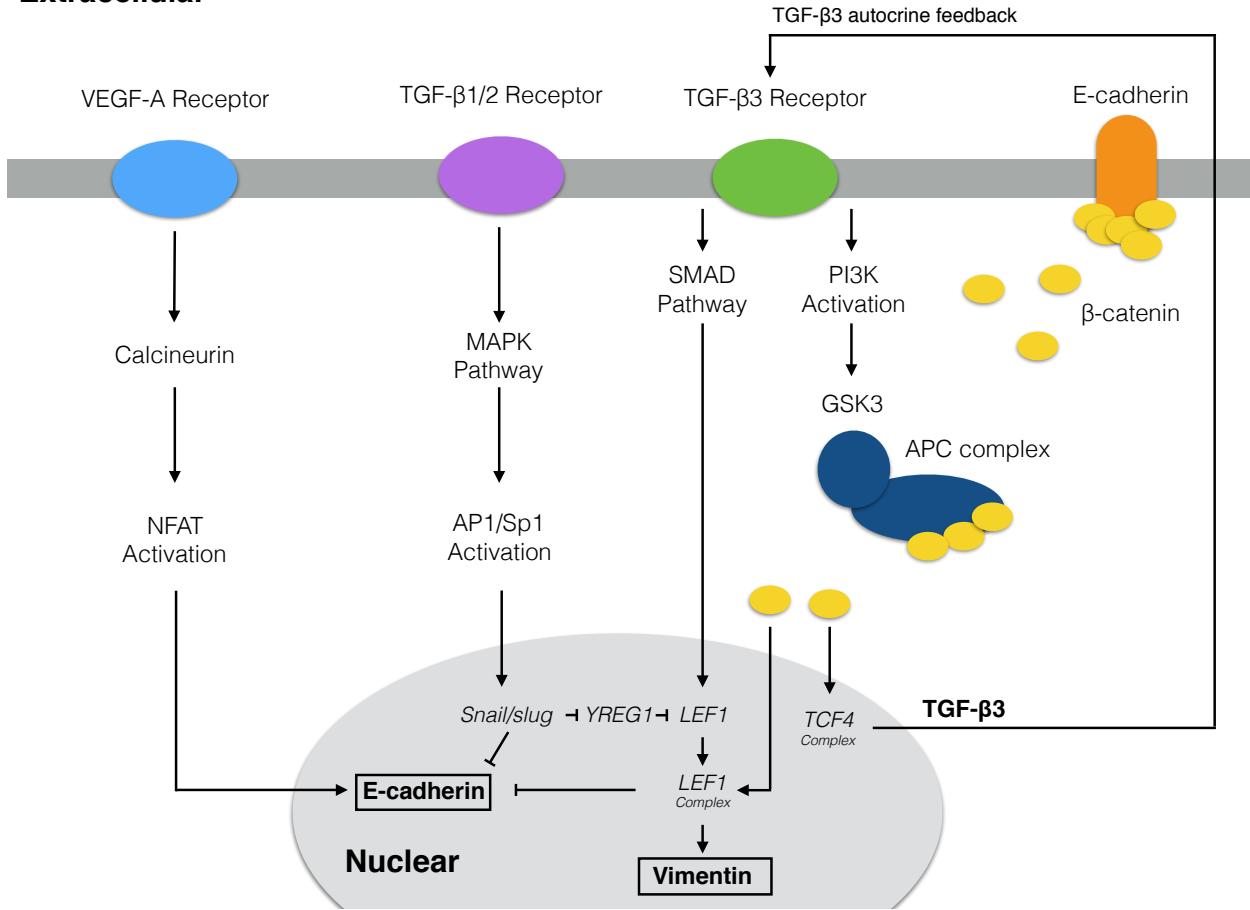


Fig. 1: Model connectivity recreates the core architecture during EMT. The EMT network contains 97 nodes (proteins, mRNA, and genes) interconnected by 169 interactions. Central to EMT induction, activation of the MAPK cascade occurs through TGF- β 1/2 binding which activates the AP-1/Sp1 transcriptional axis. AP-1/Sp1 drives an autocrine response of TGF- β 3, which activates the Smad cascade, leading to phenotypic change. Conversely, VEGF-A binding can stabilize an epithelial phenotype through NFAT activation. Downstream activation of β -catenin signaling due to E-cadherin loss and GSK3 inactivation of β -cateinin confinement is critical to the complete activation of the EMT program. The complete list of molecular interactions that comprise the model is given in the supplement.

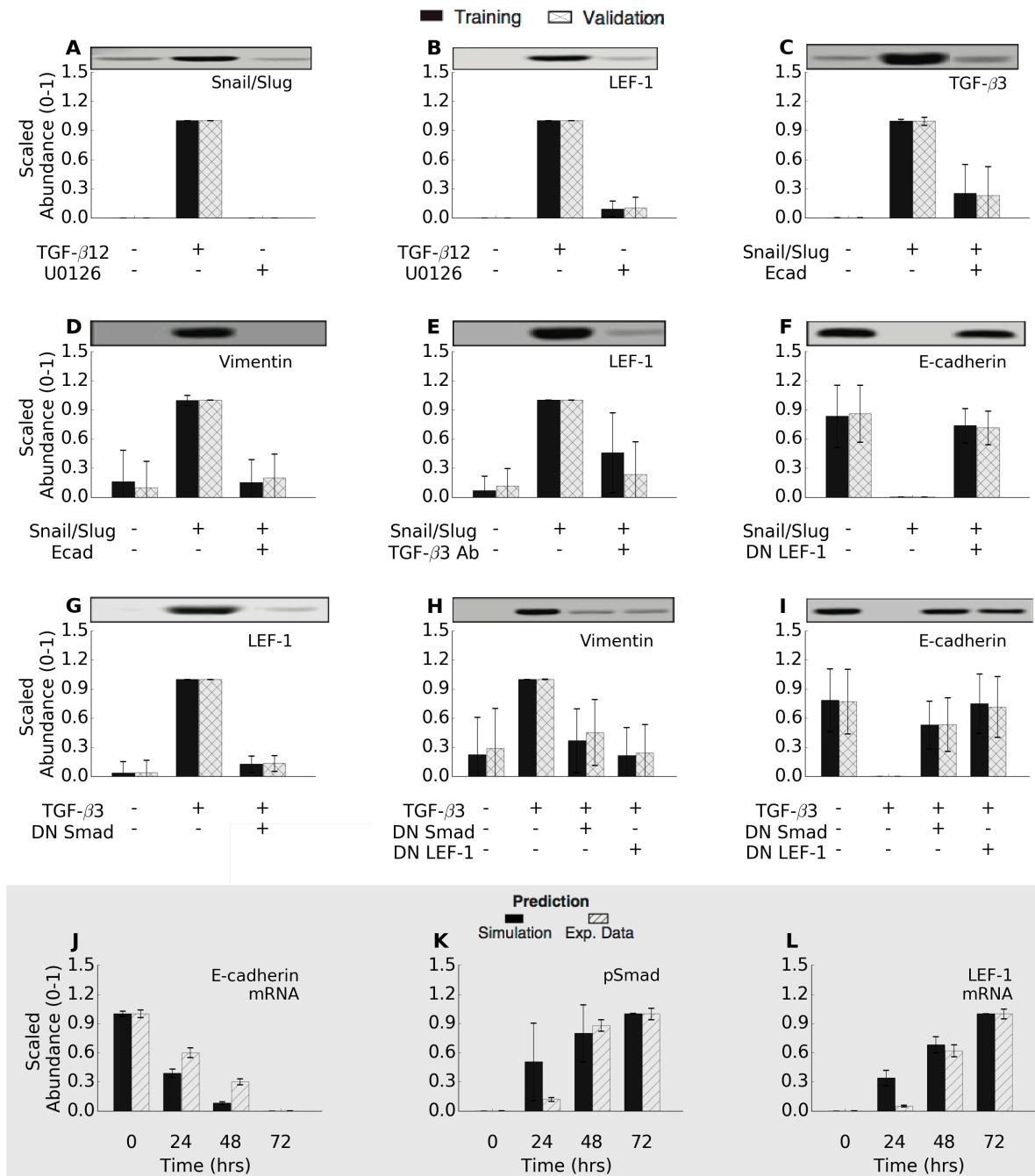


Fig. 2: Training and validation simulations. The population of EMT models qualitatively captured TGF- β -induced EMT signaling. (A-I) The population was generated using JuPOETs and trained using 11 different objective functions (41 data sets) taken from Medici *et al.* (Medici *et al.*, 2008). The model captured the simulated experiments for 72% of the cases. (J-L) The model populations were also compared against untrained temporal data to measure the effectiveness as a pure prediction.

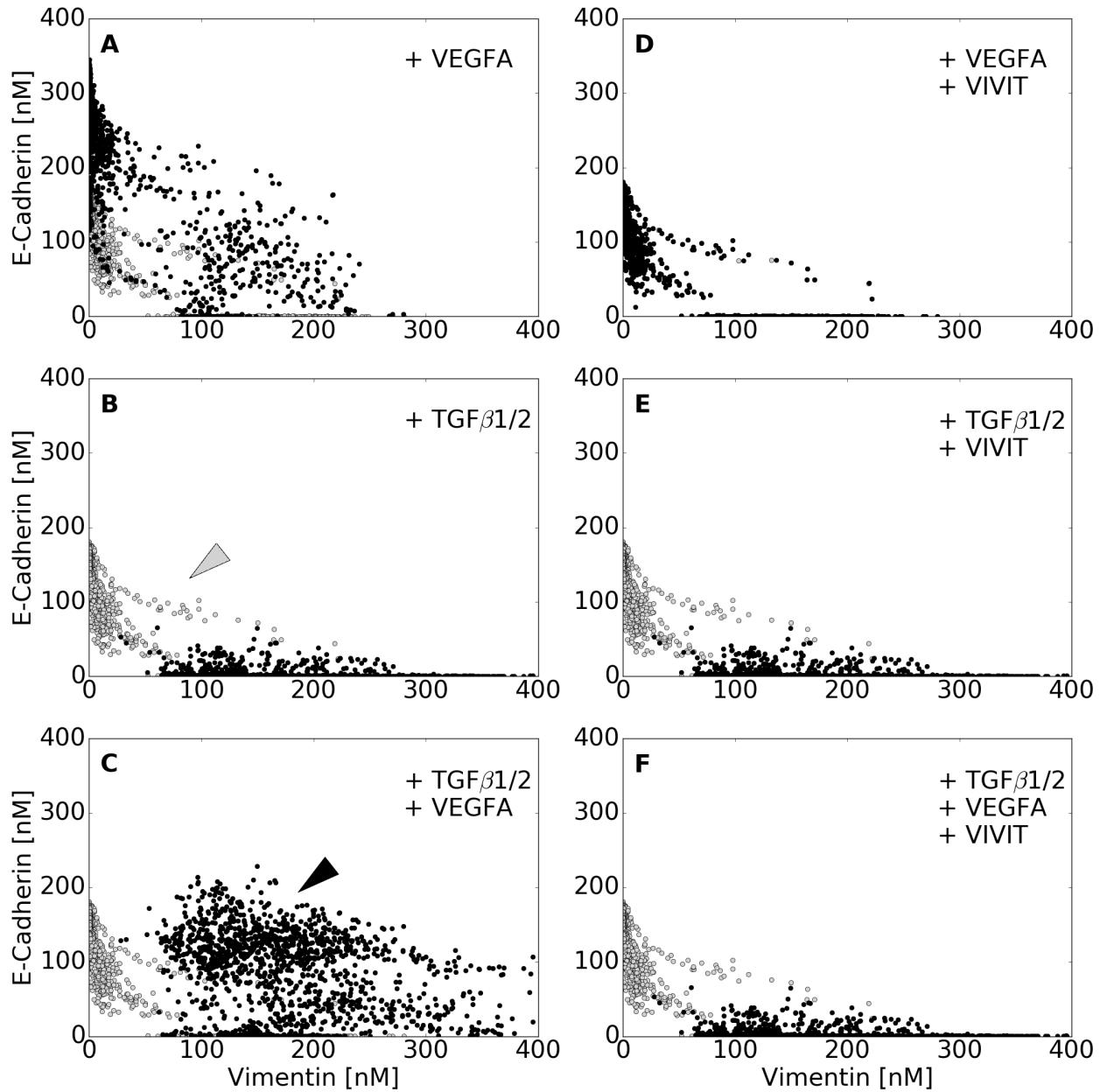


Fig. 3: Simulated VEGF-A and TGF- β 1/2 exposure promoted phenotype heterogeneity. Simulated response to TGF- β 1/2 and VEGF-A exposure with and without axis specific inhibitors. Vimentin and E-cadherin abundances (in nM) were used to quantify the shift in population at 48 hrs. (A-C) VEGF-A (50 a.u.) treatment resulted in a population with enhanced epithelial properties. This was contrary to the addition of TGF- β 2 (10 a.u.), which shifted the population towards a mesenchymal phenotype. Interestingly, the combined effects of TGF- β 2 and VEGFA was found to increase both ecadherin and vimentin levels, creating a heterogeneous population (black arrow), which can also be seen in a minority of untreated cells (gray arrow). (D-F) To isolate the effect of NFAT, we inhibited NFAT de-phosphorylation in combination with VEGFA. This negated the increase in ecadherin expression and shifted the population towards a mesenchymal phenotype (Q1,Q3). Likewise, combining NFAT inhibition with TGF- β mitigated all VEGF enhanced ecadherin expression. Lastly, combination of TGF- β 2, VEGFA, and NFAT inhibition nearly mitigated all effects of VEGFA, shifting the heterogeneous population towards a mesenchymal phenotype. In whole, high levels of phosphorylated-Sp1 correlated with vimentin expression, while NFAT was responsible for maintaining E-cadherin expression, although neither were mutually exclusive.

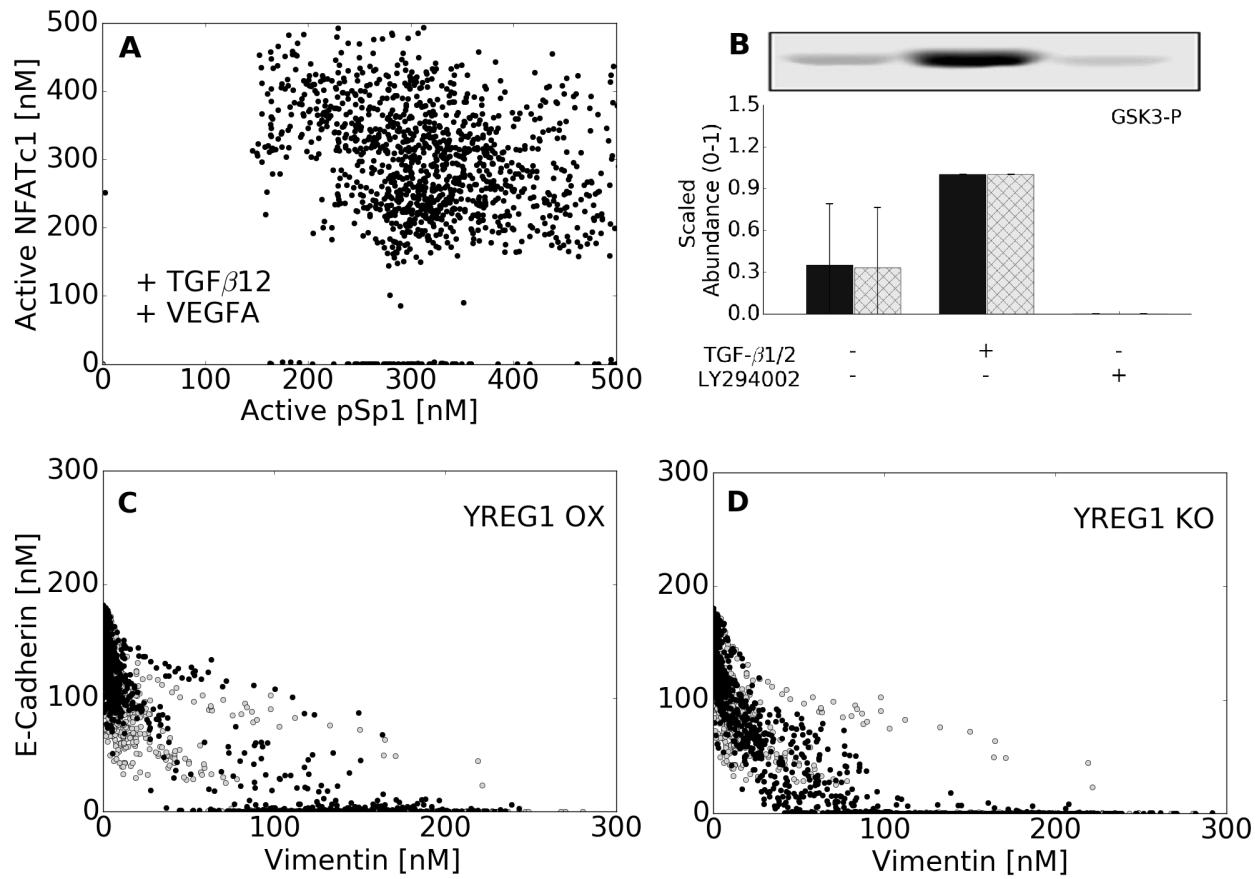


Fig. 4: Analysis of underlying signaling responses. (A) We examined the distribution of NFATc1 and AP1/SP1 in cells containing the hybrid phenotype (VEGF-A + TGF- β 2 case), showing the potential for cells to express both SP1 and NFATc1 in a non exclusive manner. (B) We were able to show a fit to an additional objective demonstrating the activation of GSK3 through PI3K. Our model captures this activation through TGF- β 3 signaling. LY294002 is a PI3K inhibitor. (C) We identified a novel regulator of LEF1 called YREG1 that allows Snail/Slug to emulate an inducer by repressing YREG1, which was required to stabilize the untreated population. YREG1 overexpression revealed an enhanced epithelial phenotype, while some inherently transformed cells moved towards a hybrid phenotype. (D) In the absence of YREG1, most of the population failed to consistently retain a stable epithelial state.

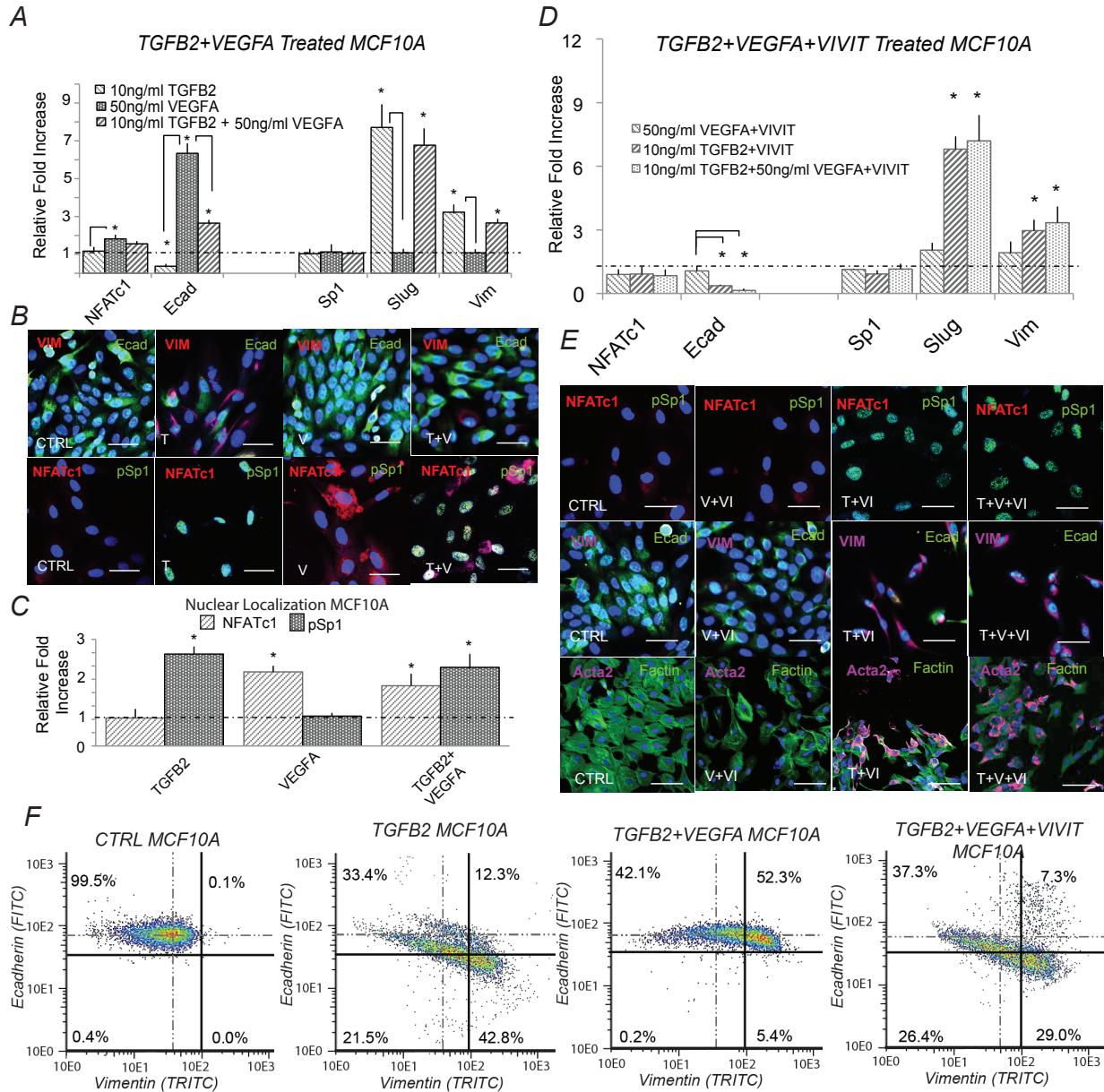


Fig. 5: Simultaneous TGF- β 1/2 and VEGF-A treatment induced phenotype heterogeneity and is dependent upon NFAT activity *in-vitro*. (A) In MCF10A, treatment with (10ng/ml) TGF- β 2 increased Slug and vimentin, while ecadherin expression was inhibited at both the gene and protein level at 48 hrs. Conversely, VEGFA alone increased both NFATc1 and ecadherin gene expression. Simultaneous TGF- β 2 (10ng/ml) and VEGFA (50ng/ml) treatment increased Slug, NFATc1, and vimentin expression, while also increasing ecadherin levels via qPCR. (B-C) Immunofluorescence confirmed these results and nuclear co-localization of both phospho-Sp1 and NFAT were found dependent upon TGF- β 2 and VEGFA, respectively. (D) To isolate the effect of NFAT, treatment of VEGFA (50ng/ml) and VIVIT (10 μ M) reduced ecadherin expression at 48hrs (control-dashed line). Similarly, combined TGF- β 2, VEGFA and VIVIT treatment increased Slug and vimentin expression, while inhibiting ecadherin levels via qPCR. (E) These findings were confirmed via immunofluorescence as the VIVIT peptide inhibited ecadherin and nuclear localization of NFATc1 in all three cases. (F) Quantitative flow cytometry also confirmed this trend. Similar experiments in DLD1 followed a similar trend (supplement). Magnification, 40x. Scale bars: 50 μ m. C=Control, T=TGF- β 2 , V=VEGFA, VI= NFAT inhibitor (VIVIT). Asterisks signify statistical differences from each other according to a one-way ANOVA with Tukey's post hoc ($p < 0.05$).

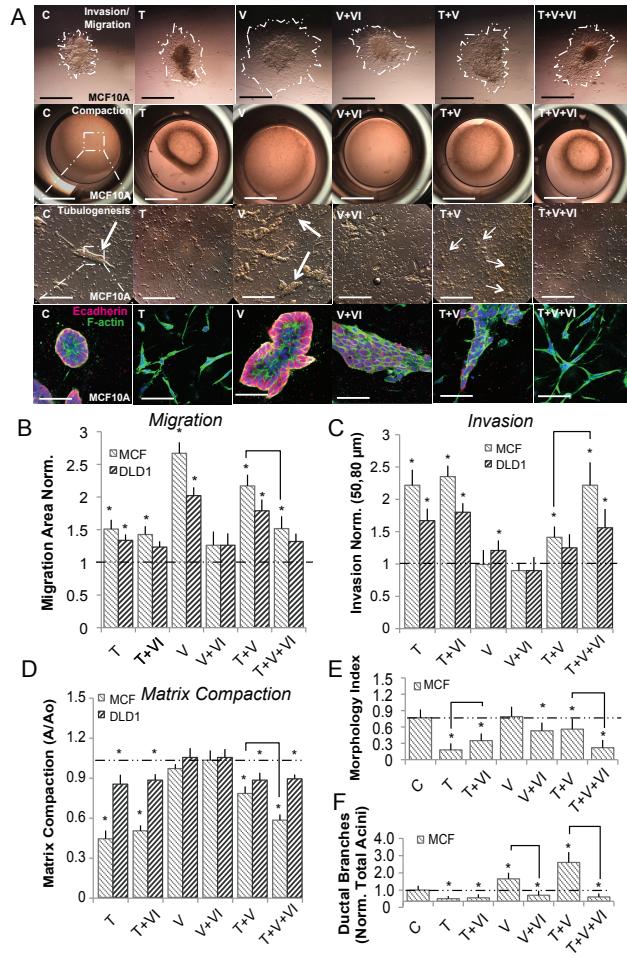


Fig. 6: Ductal branching is dependent upon phenotype heterogeneity within MCF10A in 3-D culture. MCF10A and DLD1 were formed into spheroids overnight and explanted to a collagen gel for 72 hrs. For compaction and tubular assays, cells were embedded into collagen gels for 72 hrs, and the extent of tubulogenesis was measured at 7 days. (A-D) Within MCF10A, TGF- β 2 (10ng/ml) enhanced invasion and contractile properties while, VEGFA (50ng/ml) promoted increased migration. TGF- β 2 with VEGFA significantly increased migration, while limiting with compaction. VIVIT (10 μ M) in combination with VEGFA and TGF- β 2 decreased migration and compaction, while increasing invasion. (D) Likewise, cell morphology (circularity index) correlated with both invasion and compaction in MCF10A. (E-F) The size of tubular structures (acini) also increased significantly upon addition of VEGFA, while the number of ductal branches was most significant upon simultaneous TGF- β 2 and VEGFA treatment (Red-Ecadherin, Green-Factin, Blue-Nuclear). DLD1 cells followed a similar trend, although the degree of migration, invasion, and compaction was less significant. In addition, no tubular structures were identified during the 7 day tubulogenesis endpoints. Scale bars: 500 μ m, 1000 μ m, 250 μ m, and 80 μ m, respectively. C=Control, T=TGF- β 2 , V=VEGFA, VI= NFAT inhibitor (VIVIT). Asterisks signify statistical differences from each other according to a one-way ANOVA with Tukey's post hoc ($p < 0.05$). Boxes in the left-most panel identify regions identified by arrows that were then imaged in greater zoom in the panel immediately below. The box diagram was not repeated for arrows in the other panels for clarity, but the same method was applied.

983 **Supplemental Materials and Methods**

984 **Estimation and cross-validation of EMT model parameters.** We used the Pareto Opt-
985 imal Ensemble Technique (POETs) multiobjective optimization framework in combina-
986 tion with leave-one-out cross-validation to estimate an ensemble of TGF- β /EMT models.
987 Cross-validation was used to calculate both training and prediction error during the pa-
988 rameter estimation procedure (Kohavi, 1995). The 41 intracellular protein and mRNA
989 data-sets used for identification were organized into 11 objective functions. These 11
990 objective functions were then partitioned, where each partition contained ten training ob-
991 jectives and one validation objective. POETs integrates standard search strategies e.g.,
992 Simulated Annealing (SA) or Pattern Search (PS) with a Pareto-rank fitness assignment
993 (Bassen *et al.*, 2016, Song *et al.*, 2010). Denote a candidate parameter set at iteration
994 $i + 1$ as \mathbf{k}_{i+1} . The squared error for \mathbf{k}_{i+1} for training set j was defined as:

$$E_j(\mathbf{k}) = \sum_{i=1}^{\mathcal{T}_j} \left(\hat{\mathcal{M}}_{ij} - \hat{y}_{ij}(\mathbf{k}) \right)^2 \quad (\text{S1})$$

995 The symbol $\hat{\mathcal{M}}_{ij}$ denotes scaled experimental observations (from training set j) while
996 \hat{y}_{ij} denotes the scaled simulation output (from training set j). The quantity i denotes
997 the sampled time-index and \mathcal{T}_j denotes the number of time points for experiment j . In
998 this study, the experimental data used for model training was typically the band intensity
999 from Western or Northern blots. Band intensity was estimated using the ImageJ software
1000 package Abramoff *et al.* (2004). The scaled measurement for species x at time $i =$
1001 $\{t_1, t_2, \dots, t_n\}$ in condition j is given by:

$$\hat{\mathcal{M}}_{ij} = \frac{\mathcal{M}_{ij} - \min_i \mathcal{M}_{ij}}{\max_i \mathcal{M}_{ij} - \min_i \mathcal{M}_{ij}} \quad (\text{S2})$$

1002 Under this scaling, the lowest intensity band equaled zero while the highest intensity
1003 band equaled one. A similar scaling was defined for the simulation output. By doing this
1004 scaling, we trained the model on the relative change in blot intensity, over conditions or

O#	Species (protein)	Cell Type	Training	Prediction	Random
O1	LEF1	DLD1 CC,MDCKII,A375 MC	0.54 ± 0.167	0.505 ± 0.175	1.765 ± 0.223
O2	Vimentin	DLD1 CC,MDCKII,A375 MC	1.044 ± 0.668	0.783 ± 0.666	2.098 ± 0.784
O3	TGF β 3	DLD1 CC,MDCKII,A375 MC	0.119 ± 0.262	0.225 ± 0.418	1.408 ± 0.732
O4	E-cadherin	DLD1 CC,MDCKII,A375 MC	2.299 ± 0.449	2.154 ± 0.625	3.459 ± 0.643
O5	β -catenin	DLD1 CC,MDCKII,A375 MC	0.752 ± 0.38	0.514 ± 0.351	1.025 ± 0.0
O6	TGF β 3	DLD1 CC,MDCKII,A375 MC	1.662 ± 0.55	1.54 ± 0.677	3.328 ± 0.981
O7	GSK3-P	DLD1 CC,MDCKII,A375 MC	0.19 ± 0.291	0.203 ± 0.292	0.756 ± 0.309
O8	LEF1	DLD1 CC,MDCKII,A375 MC	0.023 ± 0.078	0.03 ± 0.11	0.937 ± 0.298
O9	E-Cadherin	DLD1 CC,MDCKII,A375 MC	1.092 ± 1.228	1.412 ± 1.348	2.652 ± 1.435
O10	Snail/Slug	DLD1 CC,MDCKII,A375 MC	0.019 ± 0.0	0.019 ± 0.0	1.111 ± 0.744
O11	LEF1	DLD1 CC,MDCKII,A375 MC	0.005 ± 0.015	0.013 ± 0.06	0.797 ± 0.431

Fig. S1: Training and prediction values as a function of condition for the 11 TGF- β objective functions versus a random parameter control.

1005 time (depending upon the experiment). Thus, when using multiple data sets (possibly from
 1006 different sources) that were qualitatively similar but quantitatively different e.g., slightly
 1007 different blot intensities over time or condition, we captured the underlying trends in the
 1008 scaled data.

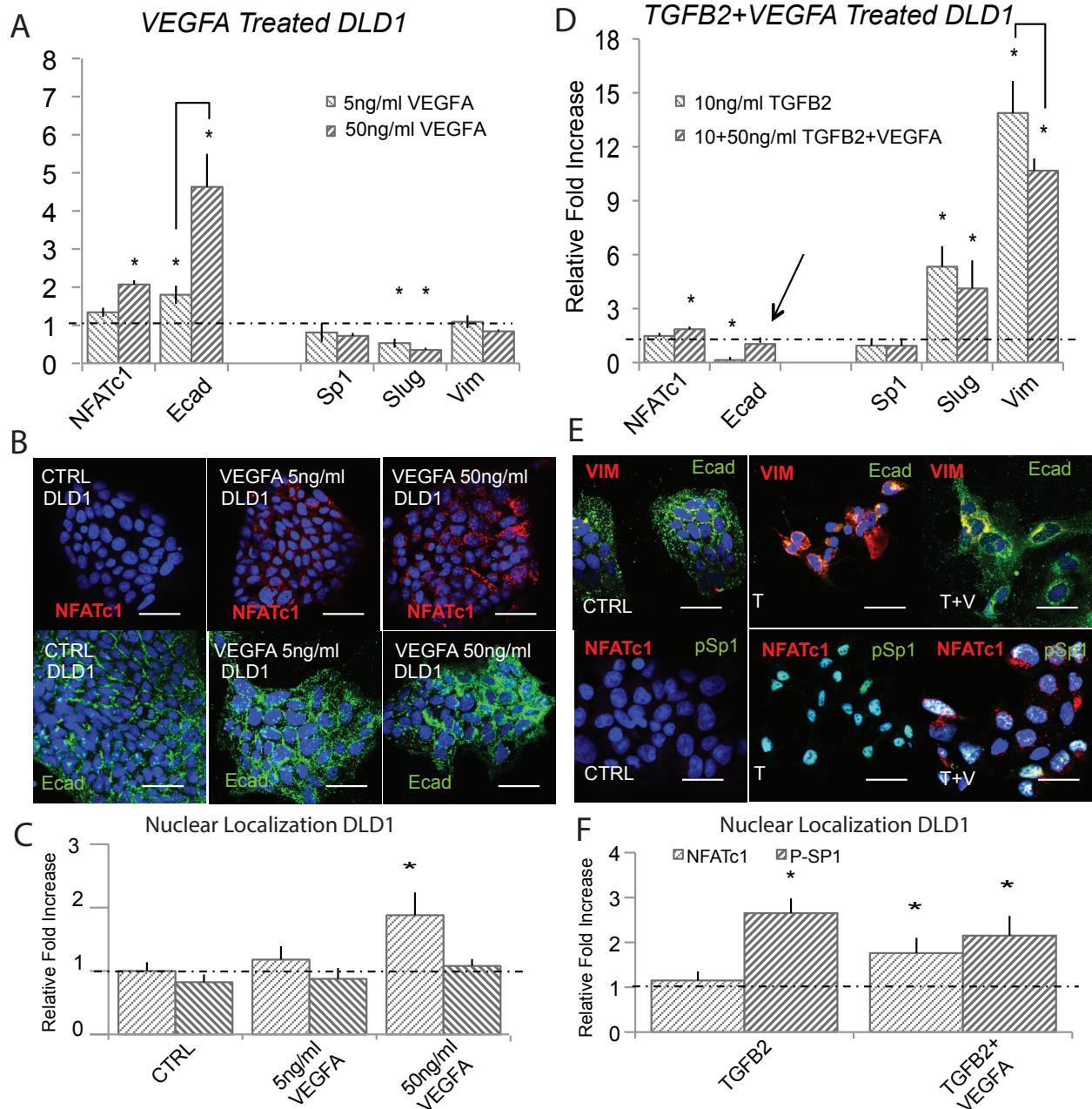


Fig. S2: VEGF-A attenuates TGF- β 1/2 to induce phenotype heterogeneity in DLD1. (A) In DLD1, we found that 5ng/ml of VEGFA increased NFATc1 and E-cadherin gene expression via qPCR and 50ng/ml potentiated this effect at 48 hrs. (B - C) These findings were confirmed at the protein level via immunofluorescence, as ecadherin levels and nuclear localization of NFATc1 increased. (D) Treatment with (10ng/ml) TGF β 2 resulted in mesenchymal transformation as measured via qPCR against target genes Slug, ecadherin, vimentin, Sp1, and NFATc1. (E - F) Immunofluorescence and nuclear localization revealed a strong presence of phospho-Sp1. (G) Combination of VEGFA (50ng/ml) and TGF β 2 (10ng/ml) treatment resulted in increased Slug, NFATc1, and vimentin expression, while also increasing ecadherin levels compared to control. (H) Immunofluorescence confirmed these results, as both ecadherin and vimentin levels were elevated. (I) A significant increase in nuclear localization of both NFATc1 and phospho-Sp1 were also found. Magnification, 40x. Scale bars: 50 μ m. C=Control, T=TGF β 2 , V=VEGFA, VI=NFAT inhibitor (VIVIT). Asterisks signify statistical differences from each other according to a one-way ANOVA with Tukey's post hoc ($p < 0.05$).

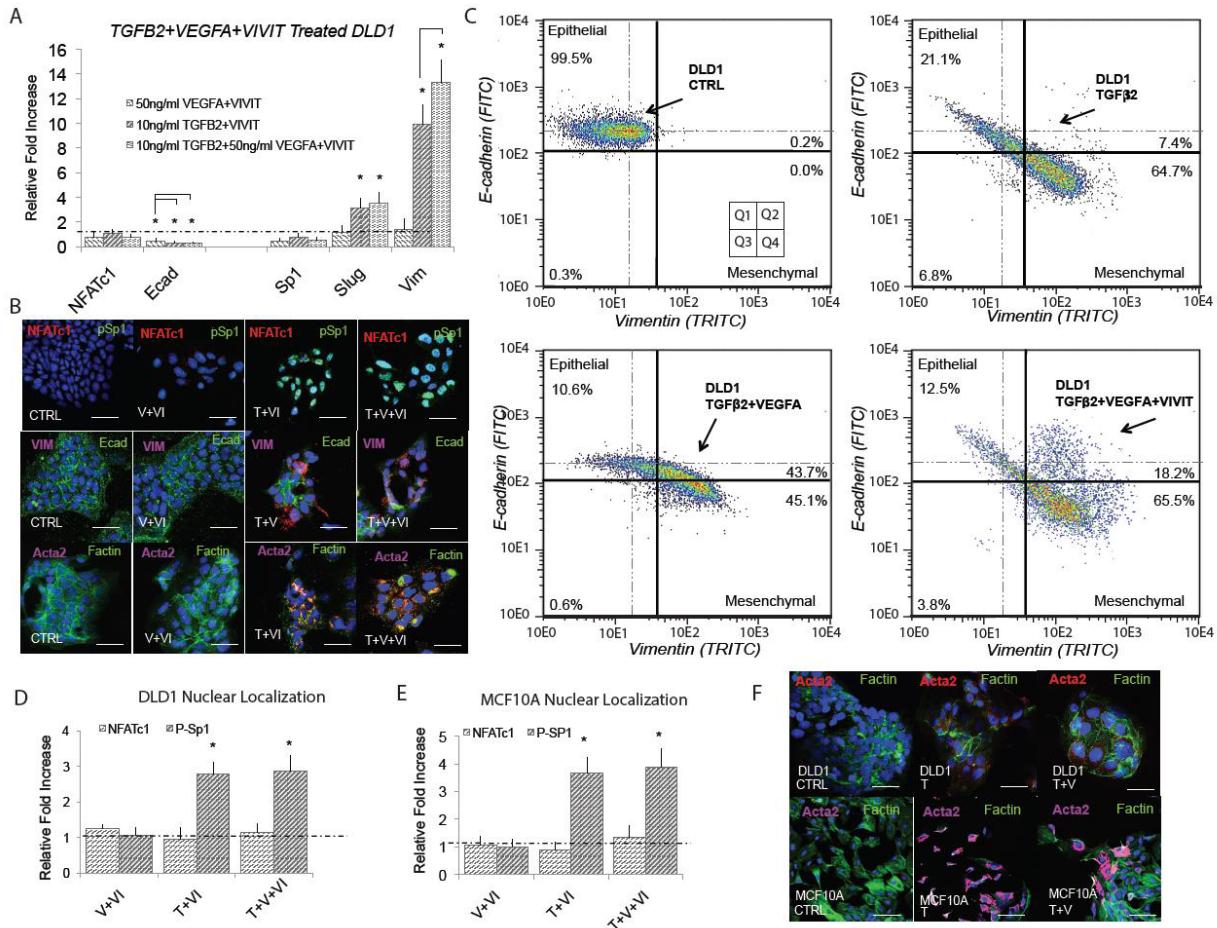


Fig. S3: E-cadherin expression is dependent upon NFAT activity in DLD1. (A) Treatment with VEGFA (50ng/ml) and NFAT inhibitory peptide VIVIT (10μM) resulted in significantly reduced ecadherin expression (qRT-PCR at 48hrs). Addition of TGF β 2 (10ng/ml) and VIVIT resulted in increased Slug and vimentin expression, while inhibiting ecadherin levels. Combined TGF β 2, VEGFA, and VIVIT treatment resulted in target genes Slug and vimentin expression increased, while inhibiting ecadherin levels. No change in Sp1 or NFATc1 expression was found. (B) These findings were confirmed via immunofluorescence as the VIVIT inhibitors was shown to inhibit ecadherin levels in all three cases. We also found no change in gene or nuclear localization of NFATc1 in all three cases, while phospho-Sp1 was found to increase in both TGF β conditions. (C) Quantitative flow cytometry also confirmed this trend. (D,E) TGF β 2, VEGFA and VIVIT treatment in DLD1 and MCF10A resulted in no change of Sp1 expression or NFATc1 expression. (F) Likewise, no change in nuclear localization of NFAT in all three cases, however phospho-Sp1 was found to increase in both TGF β conditions. Magnification, 40x. Scale bars: 50μm. C=Control, T=TGF β 2 , V=VEGFA, VI= NFAT inhibitor (VIVIT). Asterisks signify statistical differences from each other according to a one-way ANOVA with Tukey's post hoc ($p < 0.05$).

PRELIMINARY DATA USED TO HANDFIT RESPONSE OF VEGFA WITHIN SYSTEM

MCF10A								
VEGFA		Relative mRNA			Normalized			
		Ecad	Slug	Vim	Ecad	Slug	Vim	
5ng/ml	3HR	1.31	1.04	0.93	0.00	1.00	1.00	
	48 HR	3.60	1.03	0.91	0.45	0.94	0.88	
50ng/ml	3HR	1.37	0.92	0.88	0.01	0.25	0.71	
	48 HR	6.34	0.88	0.76	1.00	0.00	0.00	
Standard Deviation								
VEGFA		Relative mRNA			Normalized			
		Ecad	Slug	Vim	Ecad	Slug	Vim	
		0.89	0.03	0.02	0.00	0.03	0.02	
5ng/ml	48 HR	0.78	0.03	0.27	0.10	0.03	0.26	
	50ng/ml	0.11	0.10	0.53	0.00	0.03	0.43	
		0.53	0.21	0.19	0.08	0.00	0.00	
DLD1								
VEGFA		Relative mRNA			Normalized			
		Ecad	Slug	Vim	Ecad	Slug	Vim	
5ng/ml	3HR	1.21	0.76	1.03	0.00	1.00	0.76	
	48 HR	1.80	0.53	1.09	0.17	0.44	1.00	
50ng/ml	3HR	1.54	0.46	1.03	0.10	0.27	0.76	
	48 HR	4.63	0.35	0.84	1.00	0.00	0.00	
Standard Deviation								
VEGFA		Relative mRNA			Normalized			
		Ecad	Slug	Vim	Ecad	Slug	Vim	
5ng/ml	3HR	0.80	0.10	0.18	0.00	0.13	0.13	
	48 HR	0.24	0.12	0.17	0.02	0.10	0.16	
50ng/ml	3HR	0.89	0.19	0.45	0.06	0.11	0.33	
	48 HR	0.87	0.06	0.05	0.19	0.00	0.00	
Computer ENSEMBLE mRNA								
VEGFA		Absolute mRNA			Normalized			
		Ecad	Slug	Vim	Ecad	Slug	Vim	
5ng/ml	3HR	0.94	88.12	10.23	0.00	1.00	1.00	
	48 HR	2.10	55.64	5.45	0.40	0.41	0.40	
50ng/ml	3HR	1.44	64.10	8.43	0.17	0.56	0.77	
	48 HR	3.85	33.40	2.32	1.00	0.00	0.00	
Standard Deviation								
VEGFA		Absolute mRNA			Normalized			
		Ecad	Slug	Vim	Ecad	Slug	Vim	
5ng/ml	3HR	0.21	22.34	2.45	0.00	0.25	0.24	
	48 HR	0.45	15.55	1.12	0.09	0.11	0.08	
50ng/ml	3HR	0.38	17.87	2.23	0.05	0.16	0.20	
	48 HR	1.30	9.46	0.45	0.34	0.00	0.00	

Fig. S4: Fill me in.