Supplementary Materials for Modeling the competing effects of the immune system and EMT on epithelial cancers

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Contents

1 Model Description

1.1 Tissue cell fate

During each cell cycle, every cell randomly is assigned a cell fate from the following options:

- proliferation

- apoptosis
- immune clearance (by NKs or CTLs)
- rest in G_0

For each cell, a weight is chosen for each option and these are normalized to probabilities which then are used to randomly determine what each cell does during the cell cycle.

1.1.1 Proliferation

There are four factors that contribute to the weight of a cell to proliferate. The first is a base proliferation rate that all cells have, p. Second, if the cell has a mutation in the proliferation pathway ($\delta_P = 1$), then the weight for proliferation is proportionally increased by Δ_P. Third, if the cell is mesenchymal ($\zeta = 1$), then the weight for proliferation is proportionally decreased by Δ_{MGA}, which stands for mesenchymal growth arrest. This lost proliferation for mesenchymal cells will later be used to increase their chance of resting. Fourth, there is a negative feedback of the cells on their own proliferation which is quantified by a Hill factor as a function of the tissue cell population, N_C, with EC50 term K_0. In total, the weight for proliferation is given by

$$\rho_P = p(1 + \delta_P \Delta_P)(1 - \zeta \Delta_{\text{MGA}}) \frac{K_0}{K_0 + N_C} \tag{2.1}$$

1.1.2 Apoptosis

There are two factors that contribute to a cell's weight for undergoing apoptosis. There is a basal apoptosis rate that all cells experience, d_C for death. Second, if the cell has a mutation in the apoptosis pathway ($\delta_A = 1$), then the weight for undergoing apoptosis is proportionally decreased by Δ_A. In total, the weight for apoptosis is given by

$$\rho_A = d_C(1 - \delta_A \Delta_A) \tag{2.2}$$

1.1.3 Immune Clearance

For both NK clearance and CTL clearance, the weights are built with the same factors but have different parameter values for NK and CTLs. First of all, the cell needs to be malignant ($\delta_{\text{MUT}} = 1$). Second, there is a Hill factor that captures the probability of an immune cell finding and interacting with the given tissue cell with EC50 term K_1. Third, NKs and CTLs have their own efficacy parameters, E_{NK} and E_{CTL}, which can be understood as the rate of immune clearance given an immune cell has found the mutated cell.

Fourth, there is a decreasing Hill factor based on the number of Treg cells present with EC50 term K_2. Finally, there are two factors that proportionally decrease the weight of immune clearance depending on if the cell has an immune evasion mutation ($\delta_{\text{IE}} = 1$) or if it is mesenchymal ($\zeta = 1$) with respective decreases Δ_{IE} and Δ_{MIE}. In total, the weight of NK clearance is given by

$$\rho_{\text{NK}} = \delta_{\text{MUT}} \frac{N_{\text{NK}}}{N_C/K_1 + N_{\text{NK}}} \frac{E_{\text{NK}}}{1 + N_{\text{Treg}}/K_2} (1 - \delta_{\text{IE}}\Delta_{\text{IE}})(1 - \zeta\Delta_{\text{MIE}}) \quad (2.3)$$

A similar formula holds for CTLs with only the number of CTLs and their efficacy being different from the above equation.

1.1.4 Rest in G_0

The weight associated with rest is taken as 1 except in the case of mesenchymal cells. Recall that mesenchymal cells had their proliferation rate decreased by $1 - \zeta\Delta_{\text{MGA}}$ (see Eq. 2.1). The biological assumption here is that mesenchymal cells instead of proliferating will instead rest, so this lost proliferation weight is added to the resting weight. Hence, the weight of rest is given by

$$\rho_R = 1 + \zeta p(1 + \delta_P\Delta_P)\Delta_{\text{MGA}} \frac{K_0}{K_0 + N_C} \quad (2.4)$$

Again, the reason for adding that term is due to the understanding that overall mesenchymal cells proliferate less as individual cells rest longer in the G_0 phase.

1.1.5 Completing the Cell Cycle

After the cell fates are determined and the results reflected in the system, there are a few things that happen before the system moves on to a new cell cycle. First, the NK and CTL populations are reduced by the number of mutated cells they cleared. This represents the fact that individual immune cells lose efficacy as they carry out their effector functions. Second, all proliferating cells have a cell-specific probability of undergoing a driver mutation in one of the three pathways. If they do, one is randomly chosen among the three pathways and the pathway in that cell becomes altered. If the cell does not undergo a mutation, then its probability of mutation during subsequent cell cycles increases.

Finally, the EMT values for each cell is updated. This depends on the cells current EMT score and how much TGF-β is currently in the system. The amount of TGF-β absorbed by all cells is given by an increasing Hill function in terms of the TGF-β in the TME. The saturation effect is to limit

the amount of TGF-β a cell can absorb in a given time interval. This quantity is then divided up randomly among the N_C living cells via a normally distributed noise term to determine how much exogenous TGF-β each cell receives during this cell cycle. Should this value, τ_i in Eq. 2.5, be negative, we interpret this as the cell losing TGF-β to the TME and thus being more likely to undergo MET.

$$\tau_i = \frac{\tau_{\max}}{N_C} \frac{\tau/K_3}{1+\tau/K_3} + X_i, \quad X_i \sim N(0, \sigma^2) \tag{2.5}$$

We then combine τ_i with the current EMT score of the cell, as a proxy for the endogenous TGF-β. Finally, if this quantity is large enough, the EMT score of the cell increases towards 1; otherwise, it decreases towards 0. Each cell then is relabeled as either epithelial or mesenchymal depending on its new EMT score and whether it is below or above the mesenchymal threshold. Thus, there are two main factors that determine if a cell will end a cell cycle as mesenchymal: concentration of TGF-β in the system and the current EMT score of the cell.

Next, the amount of TGF-β for the next cell cycle is determined by the number of mutated cells, N_{MUT}, and the number of Treg cells, N_{Treg}, each one producing a fixed amount of TGF-β. It is given by

$$\tau = \tau_{\text{MUT}} N_{\text{MUT}} + \tau_{\text{Treg}} N_{\text{Treg}} \tag{2.6}$$

Finally, the immune populations are updated. For the NKs, they obey the following differential equation:

$$N'_{\text{NK}} = \sigma_{\text{NK}} - d_{\text{NK}} N_{\text{NK}} \tag{2.7}$$

which is discretized to

$$N_{\text{NK}}(k+1) = \left(N_{\text{NK}}(k) - \frac{\sigma_{\text{NK}}}{d_{\text{NK}}} \right) \exp(-d_{\text{NK}} \Delta t) + \frac{\sigma_{\text{NK}}}{d_{\text{NK}}} \tag{2.8}$$

For CTLs and Tregs, they rely on malignant cells being cleared before they can be activated. Let $N^*_{\text{MUT}}(k)$ represent the number of malignant cells cleared by the immune system during cell cycle k. In addition, Treg recruitment is upregulated by TGF-β, which will be incorporated via a Hill function with EC50 term K_4. We choose the following differential equations to govern the CTL and Treg populations:

$$\begin{aligned} N'_{\text{CTL}} &= \sigma_{\text{CTL}} N^*_{\text{MUT}} - d_{\text{CTL}} N_{\text{CTL}} \\ N'_{\text{Treg}} &= \sigma_{\text{Treg}} N^*_{\text{MUT}} \frac{\tau}{1+\tau/K_4} - d_{\text{Treg}} N_{\text{Treg}} \end{aligned} \tag{2.9}$$

Discretized, these are:

$$
\begin{aligned}
N_{\mathrm{CTL}}(k+1) &= (N_{\mathrm{CTL}}(k) - \sigma_{\mathrm{CTL}} N^*_{\mathrm{MUT}}(k)/d_{\mathrm{CTL}}) \exp(-d_{\mathrm{CTL}}\Delta t) + \sigma_{\mathrm{CTL}} N^*_{\mathrm{MUT}}(k)/d_{\mathrm{CTL}} \\
N_{\mathrm{Treg}}(k+1) &= \left(N_{\mathrm{Treg}}(k) - \frac{\sigma_{\mathrm{Treg}} N^*_{\mathrm{MUT}}(k)}{d_{\mathrm{Treg}}} \frac{\tau(k)}{1+\tau(k)/K_4} \right) \exp(-d_{\mathrm{Treg}}\Delta t) \\
&\quad + \frac{\sigma_{\mathrm{Treg}} N^*_{\mathrm{MUT}}(k)}{d_{\mathrm{Treg}}} \frac{\tau(k)}{1+\tau(k)/K_4}
\end{aligned}
\tag{2.10}
$$

2 Definition of parameters specifying the model

Name	Description
p	proliferation rate of tissue cells
d_C	death rate of tissue cells
Δ_{MIE}	mesenchymal immune evasion
Δ_{MGA}	mesenchymal growth arrest
Δ_A	mutant cells decreased apoptosis
Δ_{IE}	mutant cells increased immune evasion
Δ_P	mutant cells increased proliferation
K_0	EC50 term for negative feedback of tissue cells on own proliferation
K_1	EC50 term for probability of NK cell finding mutant cell
K_2	EC50 term for Treg inhibition of cytotoxic functions
K_3	EC50 term for how much TGF-β each cell has
K_4	EC50 term for TGF-β activation of Tregs
E_{NK}	rate of NKs clearing mutants
E_{CTL}	rate of CTLs clearing mutants
σ_{NK}	NK source rate
σ_{CTL}	CTL source rate per cleared mutant cell
σ_{Treg}	Treg source rate per cleared mutant cell
d_{NK}	NK death rate
d_{CTL}	CTL death rate
d_{Treg}	Treg death rate
k_{EMT}	EMT/MET rate
σ	standard deviation of noise in TGF-β each cell receives
$\tau_{\max}$	max amount of TGF-β any cell can receive
τ_{MUT}	rate of TGF-β production by mutant cells
τ_{Treg}	rate of TGF-β production by Treg

Table S1: The model parameter names and descriptions. Note that many of these values are affected by the inflammation state of the system.

3 Parameter values used for simulation

Name	Description	INFL Low Value	INFL High Value
p	weight of proliferation for tissue cells	0.28	
d_C	weight of apoptosis for tissue cells	0.14	
Δ_{MIE}	MIE	0.6	
Δ_{MGA}	MGA	0.2	
Δ_A	proportional decrease to weight of apoptosis for cells with mutated apoptosis pathway	0.3	
Δ_{IE}	proportional increase to weight of immune evasion for cells with mutated immune evasion pathway	0.48	
Δ_P	proportional increase to weight of proliferation for cells with mutated proliferation pathway	0.36	
K_0	EC50 term for negative feedback of tissue cells on own proliferation	80 cells	
K_1	EC50 term for probability of NK cell finding mutant cell	8 cells	
K_2	EC50 term for Treg inhibition of cytotoxic functions	5 cells / volume	0.025 cells / volume
K_3	EC50 term for cumulative absorption of TGF-β	200 amount / volume	
K_4	EC50 term for TGF-β activation of Tregs	50 amount / volume	
E_{NK}	weight of NKs clearing mutants	10	30
E_{CTL}	weight of CTLs clearing mutants	200	600
σ_{NK}	NK source rate	1.3 cells / cycle	
σ_{CTL}	CTL source rate per cleared mutant cell	100 cells / (cleared mutants $\times$ cycles)	

σ_{Treg}	Treg source rate per cleared mutant cell	200 cells / (cleared mutants × concentration of TGF-β × cycles)	
d_{NK}	NK death rate	0.13 / cycle	
d_{CTL}	CTL death rate	0.0260 / cycle	
d_{Treg}	Treg death rate	0.0260 / cycle	
k_{EMT}	EMT/MET rate	0.01 / concentration of TGF-β	
σ	standard deviation of noise in TGF-β each cell receives	6 concentration of TGF-β	
τ_{max}	max amount of TGF-β any cell can receive	500 concentration of TGF-β	
τ_{MUT}	rate of TGF-β production by mutant cells	0.05 concentration of TGF-β / cell / cycle	
τ_{Treg}	rate of TGF-β production by Treg	0.5 concentration of TGF-β / cell / cycle	
	RP Cancer Line	0.5	
	INFL High Duration	30 cycles	
	INFL Low Duration	30 cycles	
	Mes Threshold	0.7	
	maximum initial mutation damage after warmup	0.01	
	increase in probability to mutate for non-mutating proliferating cells	0.0001	

Table S2: The model parameter names, descriptions, and values during both low and high inflammation. Parameters with only one value do not change with the inflammatory state.

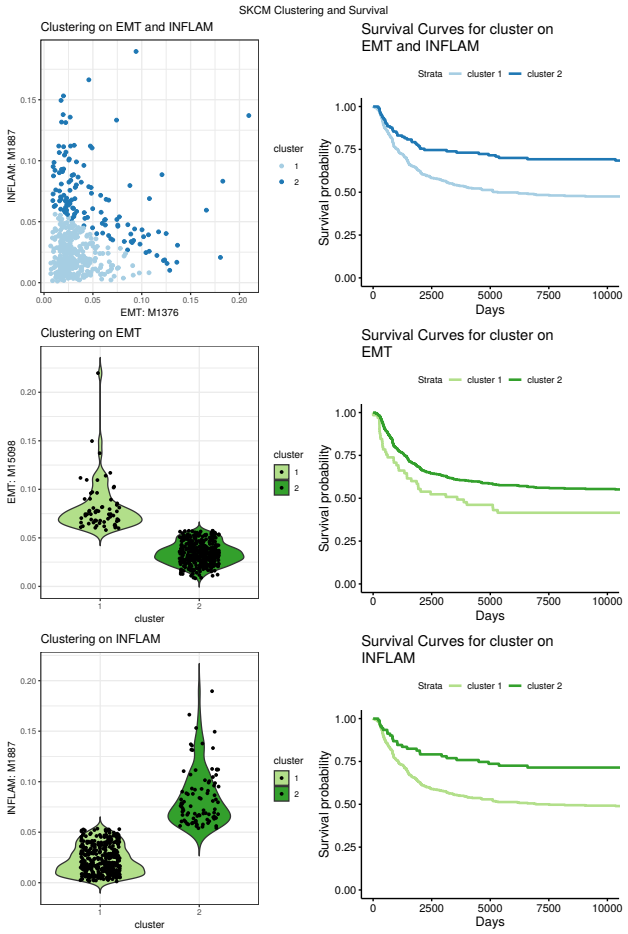

Figure S1: A. K-means clustering of SKCM using gene ontology terms indicative of EMT and inflammation signatures ($k = 2$). B. Survival plots corresponding to the clustering on EMT and inflammation. C. K-means clustering of SKCM using gene ontology terms indicative of an EMT signature ($k = 2$). D. Survival plots corresponding to the clustering on EMT. E. K-means clustering of SKCM using gene ontology terms indicative of inflammation ($k = 2$). F. Survival plots corresponding to the clustering on inflammation.

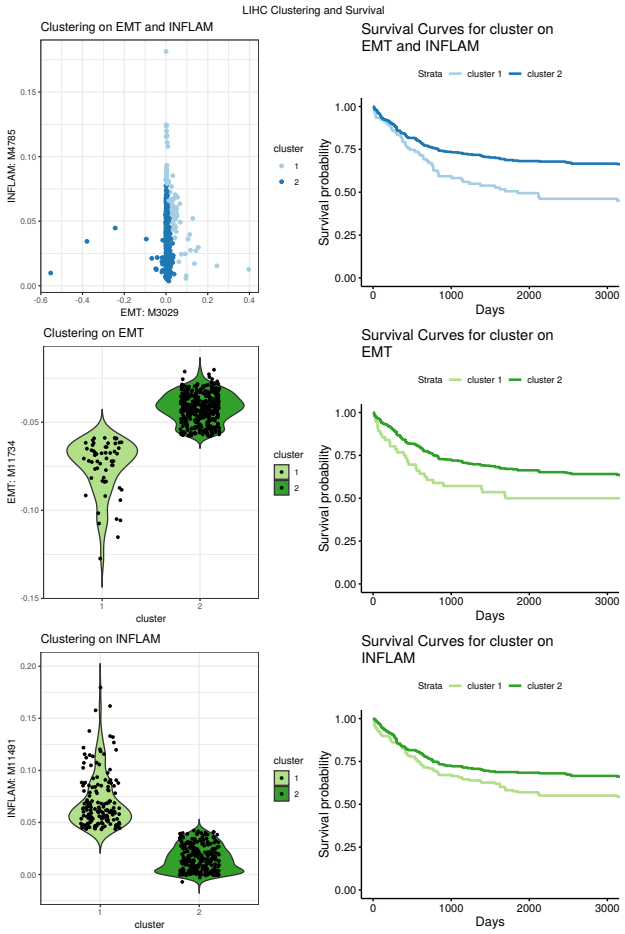

Figure S2: A. K-means clustering of LIHC using gene ontology terms indicative of EMT and inflammation signatures ($k = 2$). B. Survival plots corresponding to the clustering on EMT and inflammation. C. K-means clustering of LIHC using gene ontology terms indicative of an EMT signature ($k = 2$). D. Survival plots corresponding to the clustering on EMT. E. K-means clustering of LIHC using gene ontology terms indicative of inflammation ($k = 2$). F. Survival plots corresponding to the clustering on inflammation.

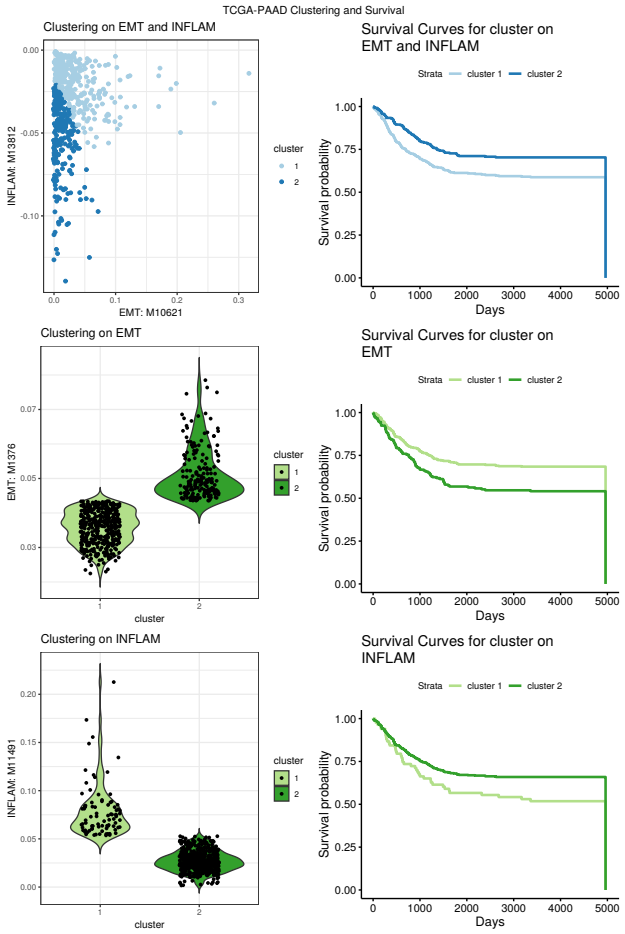

Figure S3: A. K-means clustering of LUAD using gene ontology terms indicative of EMT and inflammation signatures ($k = 2$). B. Survival plots corresponding to the clustering on EMT and inflammation. C. K-means clustering of LUAD using gene ontology terms indicative of an EMT signature ($k = 2$). D. Survival plots corresponding to the clustering on EMT. E. K-means clustering of LUAD using gene ontology terms indicative of inflammation ($k = 2$). F. Survival plots corresponding to the clustering on inflammation.

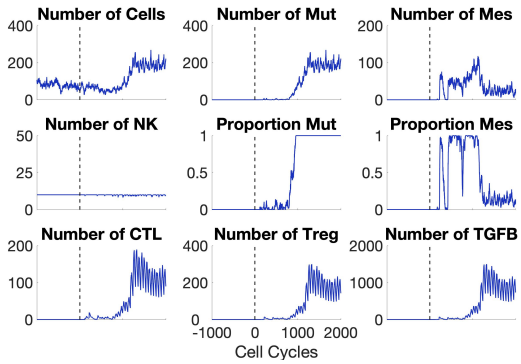

Figure S4: Single patient trajectory without immune cells targeting premalignant cells. Compare to Fig. 1B.

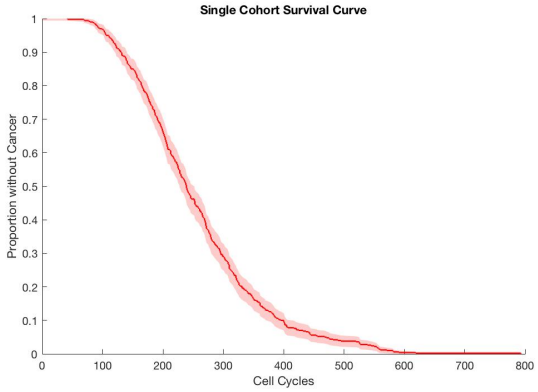

Figure S5: Sample cohort survival curve without immune cells targeting premalignant cells. Compare to Fig. 1C.

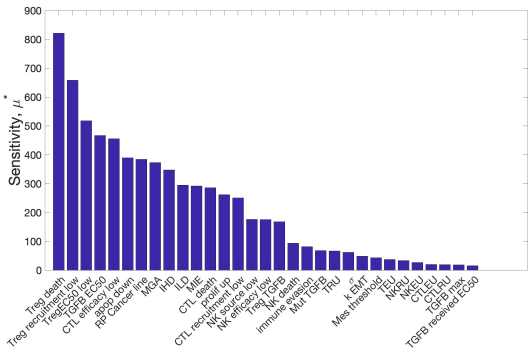

Figure S6: Morris-OAT global sensitivity without immune cells targeting premalignant cells. Compare to Fig. 2.

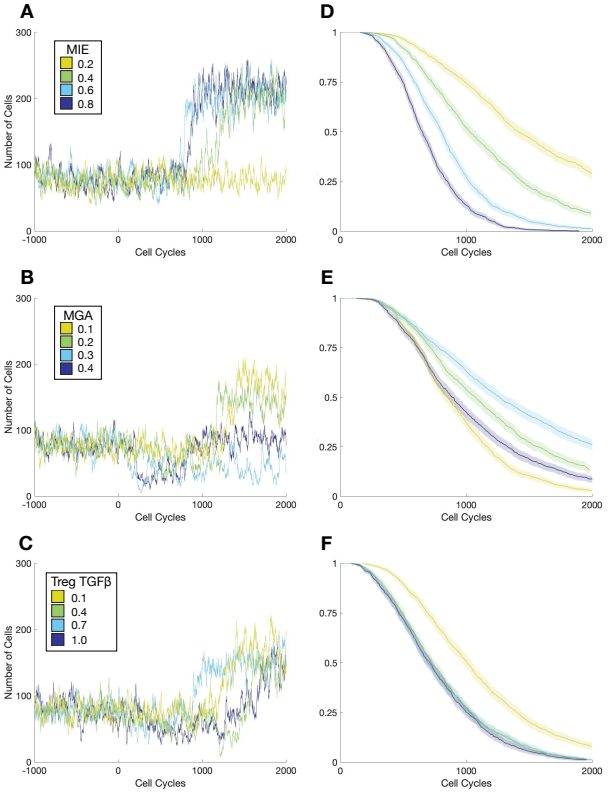

Figure S7: Effects of mesenchymal tumor cell properties on the Time to Cancer without immune cells targeting premalignant cells. Compare to Fig. 3.

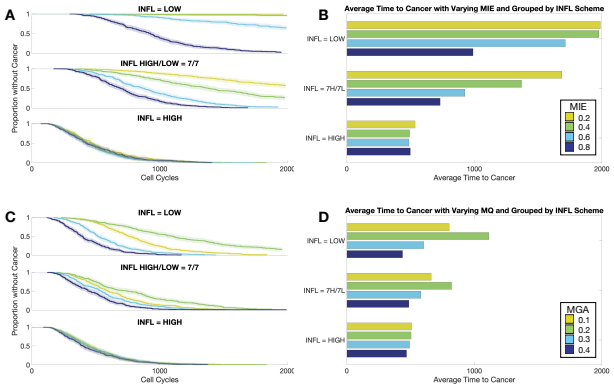

Figure S8: Effects of inflammation on the Time to Cancer without immune cells targeting premalignant cells. Compare to Fig. 4.

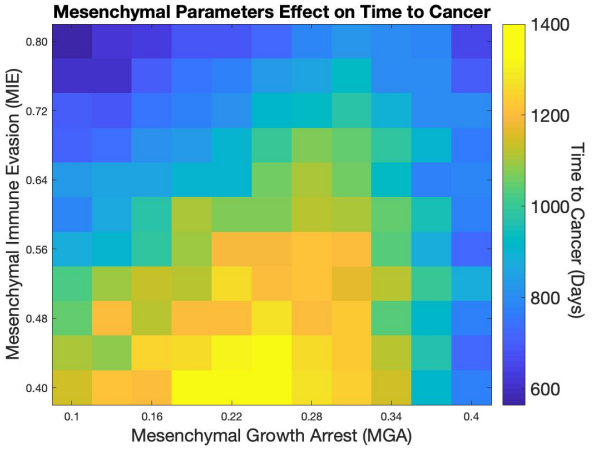

Figure S9: Summary of the contrasting effects of MIE and MGA on Time to Cancer without immune cells targeting premalignant cells. Compare to Fig. 5.