**Supplemental File 1**: Describe in detail how the model makes decisions, with equations and include comprehensive sensitivity analysis

**Figure 1a.** Overview of model inputs to runCellSimulationFunction and output as pictures of cellular distributions colored according to where cells are in the cycle. **b.** Adaptation from Drasdo Holme of how the model works. **c.** Hierarchy of the model and what can be replaced.

**Figure 2** **a.** Multiple growth rates in boundary and no boundary (show every curve) **b.** Shows cap on density in unbounded case.

**Figure 3a.** Points which are the real data for experiments, lines which are the model fits at different cell lengths. Cell number vs time at different dosages. W/O synchronization. **b.** With synchronization.

**Figure 4**. **a.** Cartoon overview of how we simulate gene expression. **b.** Illustrating how the scaling varies between 0 to 1 for each pathway. **c.** Pick one dosage (10 um/mL) from **Figure 3** and plot each of the effective pathways vs time for that selection. Y-axis is % of pathway activity and all pathways can be plotted together. **d.** Comparison to real gene expression data (ELANA).

**Figure 5a** As Raymon is generating heatmap for 2 cell types w/o boundary. **b.** W/boundary. **c.** Varying mean of drug effect w/o boundary in a simulation where you would typically observe a balance in the cellular populations. **d.** Varying SD of drug effect w/o boundary where you would typically observe a balance in the cellular populations. Both **c** and **d** drug should have an effect which is a normal distribution on the population.

**Supplemental Figure 2** a. Similar figure to what Raymon is generating for 2 cell types w/ boundary & varying initial overall cellular density. **b.** As for Figure **5c** w/ boundary. **c.** As for Figure 5d w/ a boundary.

In a comparison of single cell relative to bulk RNA-sequencing data for multiple cell types we observed (**Figure 6**).