

Supplementary Figures

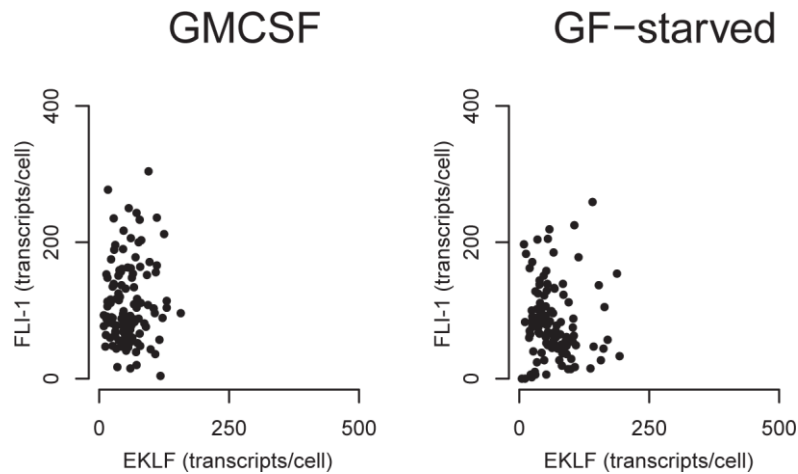


Figure S1. Correlation between EKL and FLI-1 levels before treatment

UT-7/GM cells maintained in GMCSF were growth-factor starved for 18 hours. Cells were fixed before and after starvation and the mRNA FISH method was used to obtain transcript counts for EKL and FLI-1 in individual cells. Phase plots show the degree of correlation between transcription factors before treatment with cytokines.

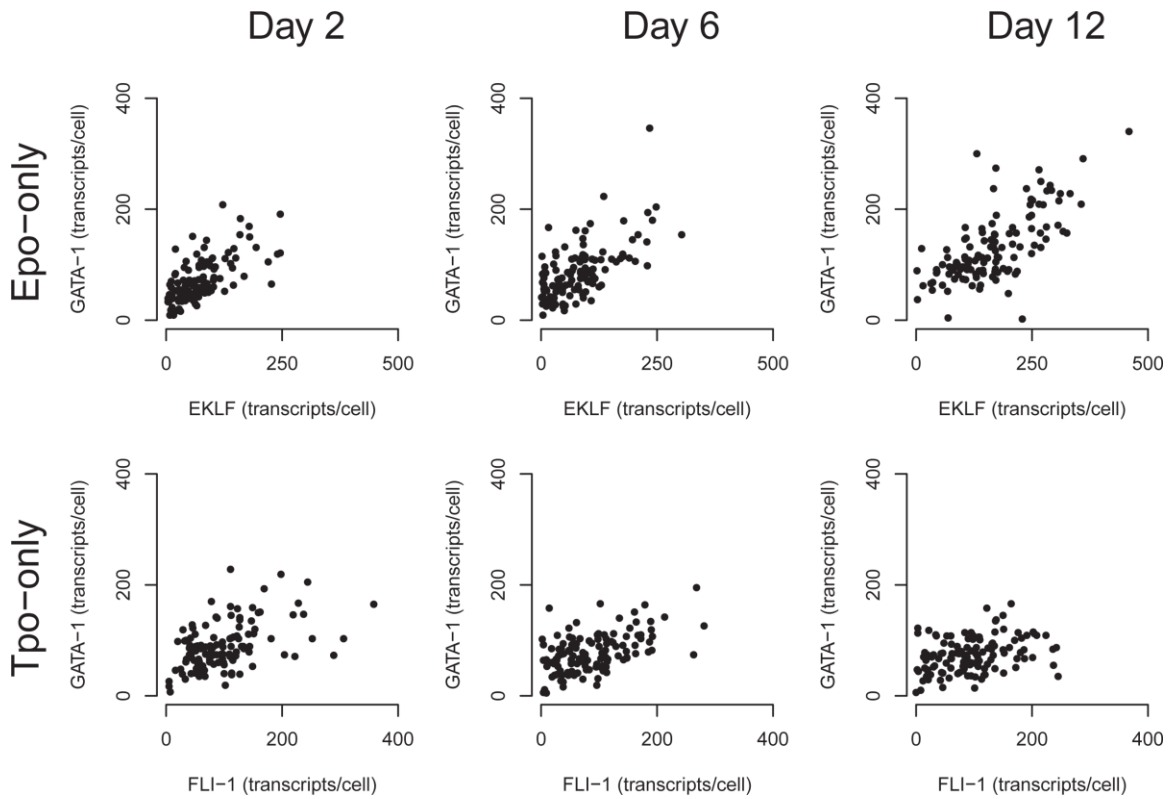


Figure S2. Correlation of GATA-1 levels with EKL and FLI-1 under Epo and Tpo treatment

UT-7/GM cells maintained in GMCSF were growth-factor starved for 18 hours, and subsequently passaged into medium containing only Epo or only Tpo. mRNA FISH was used to obtain transcript counts for GATA-1, EKL, and FLI-1 in individual cells. Phase plots show the degree of correlation between transcription factors.

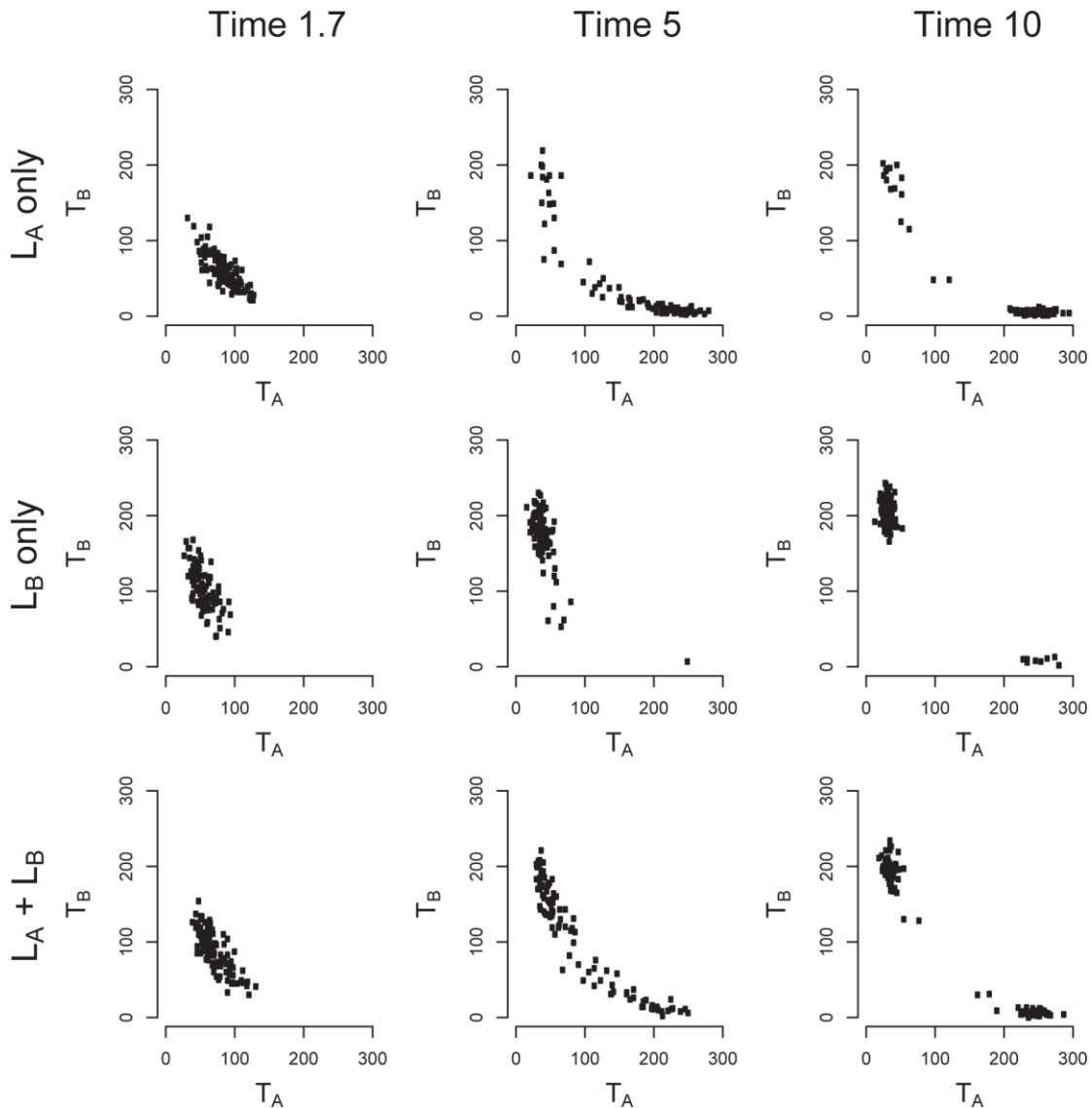


Figure S3. Simulated master transcription factor dynamics under different treatment regimes

The ECAA model was stochastically simulated under different ligand concentrations: L_A only ($L_A = 1000$, $L_B = 0$), L_B only ($L_A = 0$, $L_B = 1000$), and $L_A + L_B$ ($L_A = 1000$, $L_B = 1000$). For each treatment condition, 100 separate simulations were performed, yielding 100 trajectories. Plots show snapshots of trajectories at different times. Each simulation was started in the bipotent state ($T_A = 60$, $T_B = 70$). Simulation results show that under the given parameters, the ECAA model yields discrete decisions, which can be influenced by extrinsic cues.

Table S1

[Click here to Download Table S1](#)