Supplementary Information



Figure S1. Endoderm markers *SOX17* and *CER1* at day 4 of differentiation under high and low PI3K. The fold change is calculated over undifferentiated hESCs (number of repeats = 3).



Figure S2. Experimental dynamics for each repeat under high PI3K signaling. The levels of each molecule have been normalized by the maximum value for that molecule. The experimental time points presented here are 0.5, 1, 1.5, 2, 3, 6, 12, 18 and 24 h which were used for DBN analysis.



Figure S3. Experimental dynamics for each repeat under low PI3K signaling. The levels of each molecule have been normalized by the maximum value for that molecule. The experimental time points presented here are 0.5, 1, 1.5, 2, 3, 6, 12, 18 and 24 h which were used for DBN analysis.



Figure S4. Convergence characteristics for DBN analysis of entire time series (A,B) Log likelihood score for each repeat of high PI3K and low PI3K. (C,D) Marginal edge probabilities for selected nodes in the two conditions for each successive Gibbs sampling step. The marginal edge probability at a given step was calculated by using later half of the samples until that step. It is evident from the edges presented in this plot (as well as those not shown here) that the probabilities converge to the mean value by 250 steps.



Figure S5. DBNs for individual repeats in high PI3K condition over the entire time series data.



Figure S6. DBNs for individual repeats in low PI3K condition over the entire time series data.



Figure S7. Consensus DBNs for the early and late phases for increased number of time points in the high PI3K condition. The number of time points in each zone is 9, some of which are obtained by linear interpolation of the data in Figure 1. The time zones are defined in Figure 4.



Figure S8. Consensus DBNs for the early and late phases for increased number of time points in the low PI3K condition. Details are same as Figure S7.