



Figure S6. Ensemble and comparison of learned networks from single cell datasets

(A-B) Ensembles of learned networks. Learning was achieved using the (A) CCE single cell data and (B) Nanog-rescue single cell data. Light cyan nodes represent genes; gray squares represent learned regulatory logic transition functions. Links from upstream parent nodes appearing in more than 90% of equally well-fitted Boolean functions are colored in green (activation) and red (repression). Other links are not shown. (C) Overlap among four ensemble networks learned from the serum/LIF, 2i/LIF, CCE and Nanog-rescue single cell dataset, respectively. Links that are consistent across all four models are shown.