



Using mESC dataset, we plotted the changes in regulatory strength over time between key TFs and their target genes in the dynamic network inferred by MTGRN. The red curve represents the regulatory strength over time, while the blue curve shows the expression of the regulatory gene over time. We can see that the trend in regulatory gene expression aligns with the trend in its regulatory strength on the target gene (both are decreasing), indicating that the dynamic GRN inferred by MTGRN is accurate. (*Nanog*, *Esrrb*, *Nr0b1*, and *Utf1* are all key transcription factors in the development of mouse embryonic stem cells.)