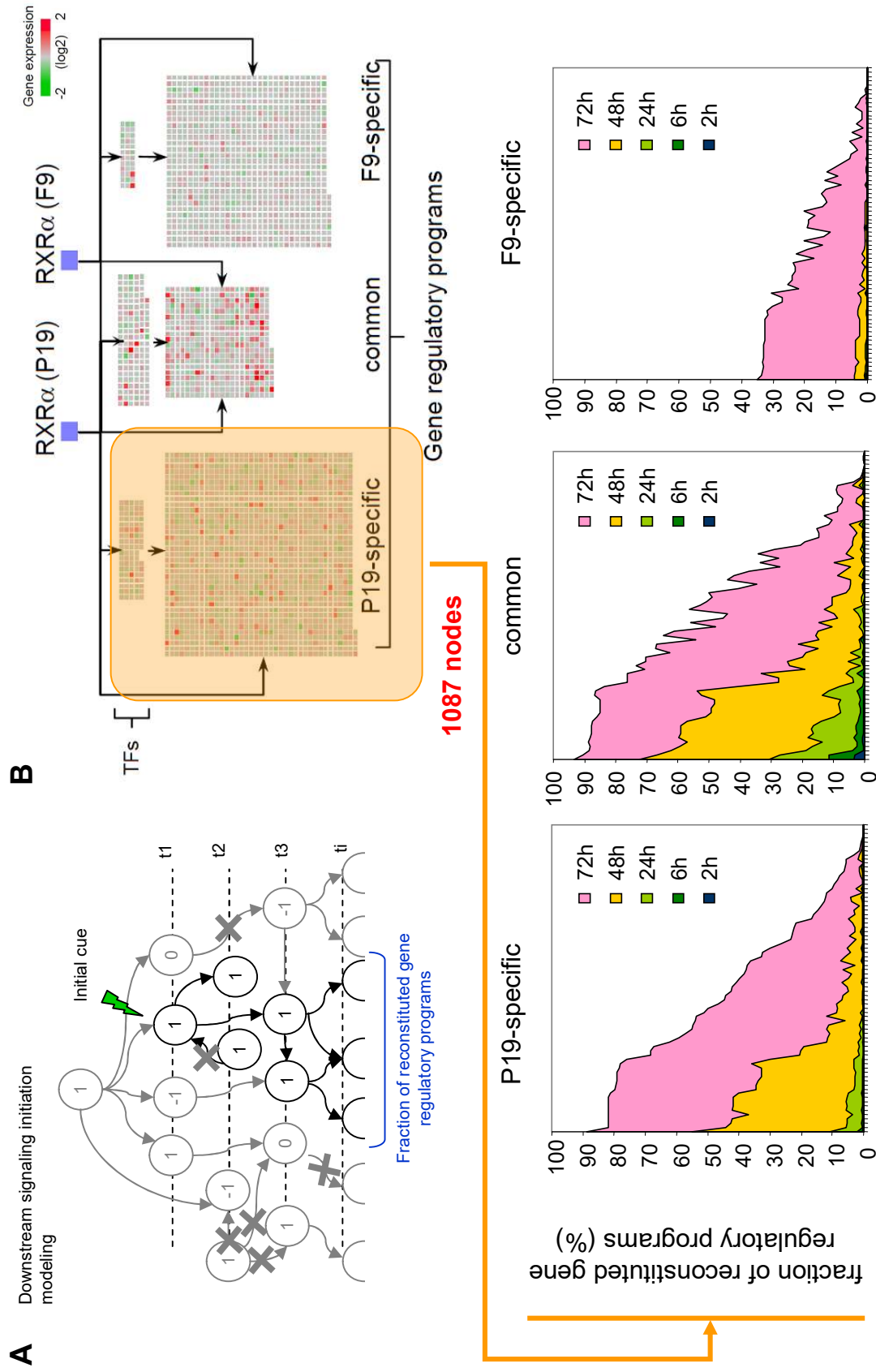




P19-specific nodes (top 75 (~7%) ranked on the basis of their P19-specific response at 72h)

Supplemental Fig. S13. Signal propagation approach for identifying key TFs involved in cell fate acquisition. (A) Schematic illustration of the signal propagation model when the initiation occurs at a downstream node ("initial cue", green flash) in the reconstructed GRN; forbidden connections are indicated by an "X". **(B)** The reconstructed RXR α /RAR signal transduction GRN is used as template to evaluate the potential of each of the P19-specific nodes to reconstitute partially or entirely the gene regulatory program. **(Bottom left)** Ranking of the 1087 nodes comprising the P19-specific GRP along the X-axis based on their capacity to reconstitute a fraction (Y-axis) of the P19-specific program. The corresponding readouts are also shown for the reconstitution of the common (**middle panel**) and F9-specific (**right panel**) GRPs (same ranking than in the P19-specific program).