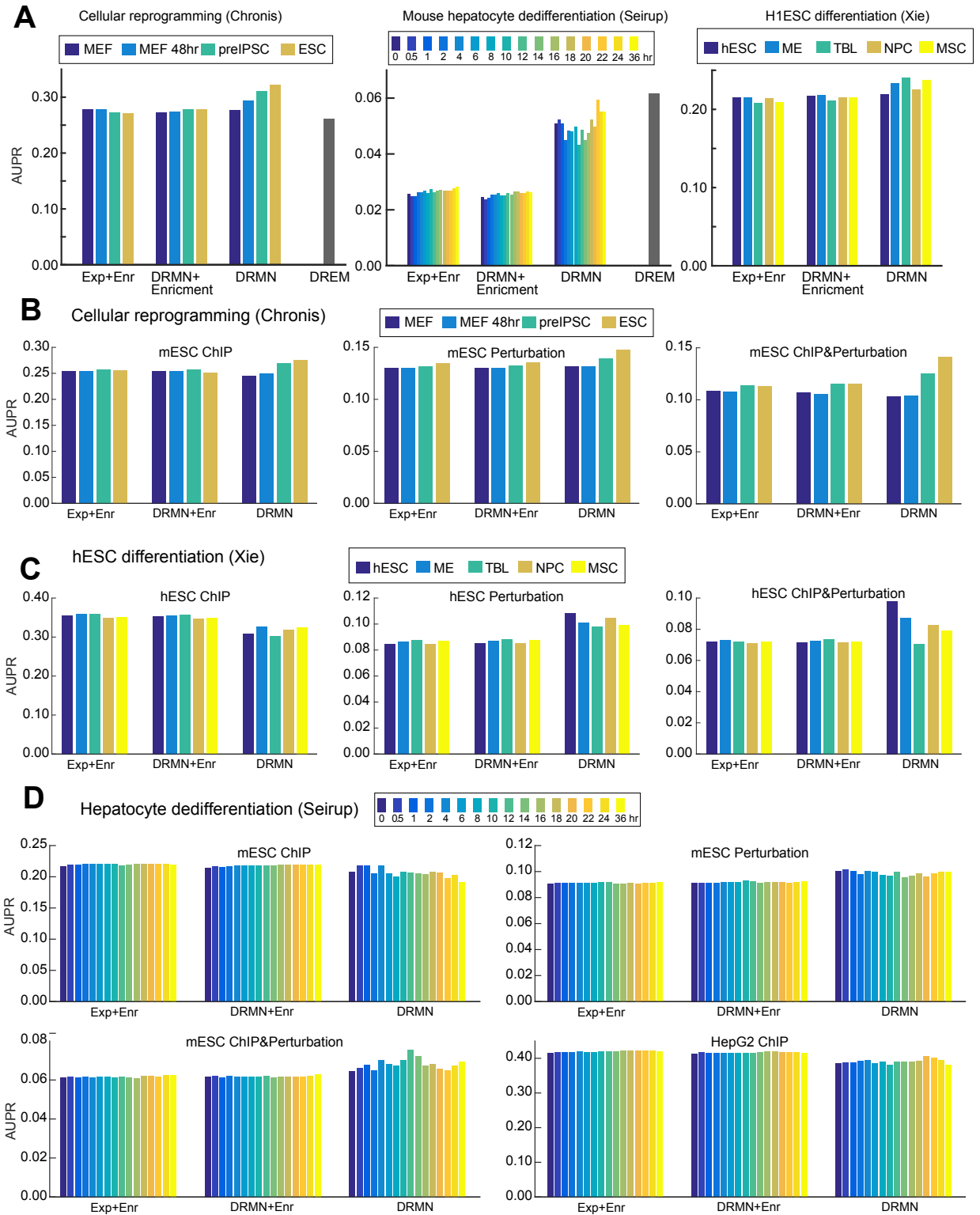




Supplemental Figure S6. **A.** The AUPR of regulator ranking with different strategies for cellular reprogramming, mouse hepatocyte dedifferentiation, and H1ESC differentiation. Each plot shows regulator enrichment of expression based modules (Exp+Enr), regulator enrichment of DRMN modules (DRMN+Enr), regulator ranking based on inferred DRMN networks (DRMN), and regulator ranking from DREM (when applicable). **B.** AUPR comparing inferred networks and baseline networks for cellular reprogramming, when compared to ChIP-based, Perturbation-based, and intersection of the ChIP and Perturbation-based gold standards in mESC. **C.** AUPR comparing inferred networks and baseline networks for H1ESC differentiation, when compared to ChIP-based, Perturbation-based, and intersection of the ChIP and Perturbation-based gold standards in hESC. **D.** AUPR comparing inferred networks and baseline networks for mouse hepatocyte dedifferentiation, when compared to ChIP-based, Perturbation-based, and intersection of the ChIP and Perturbation-based gold standards for mESC, and ChIP-based gold standard from HepG2 cell line. In each panel, we show the baseline networks from regulator enrichment of expression based modules (Exp+Enr), regulator enrichment of DRMN modules (DRMN+Enr), and inferred networks with edges scored by input feature multiplied by estimated regression coefficients (DRMN).