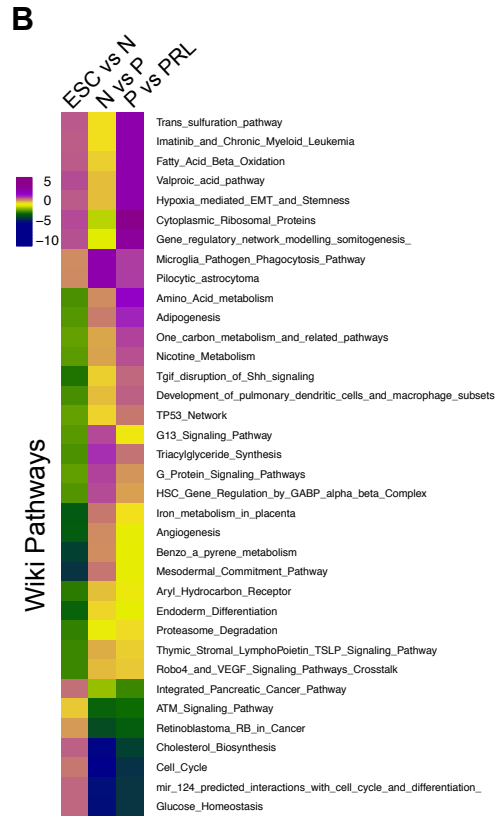
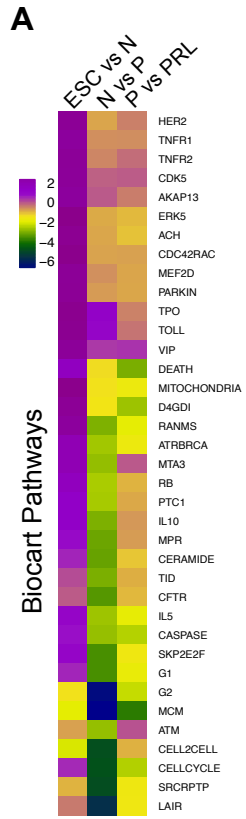
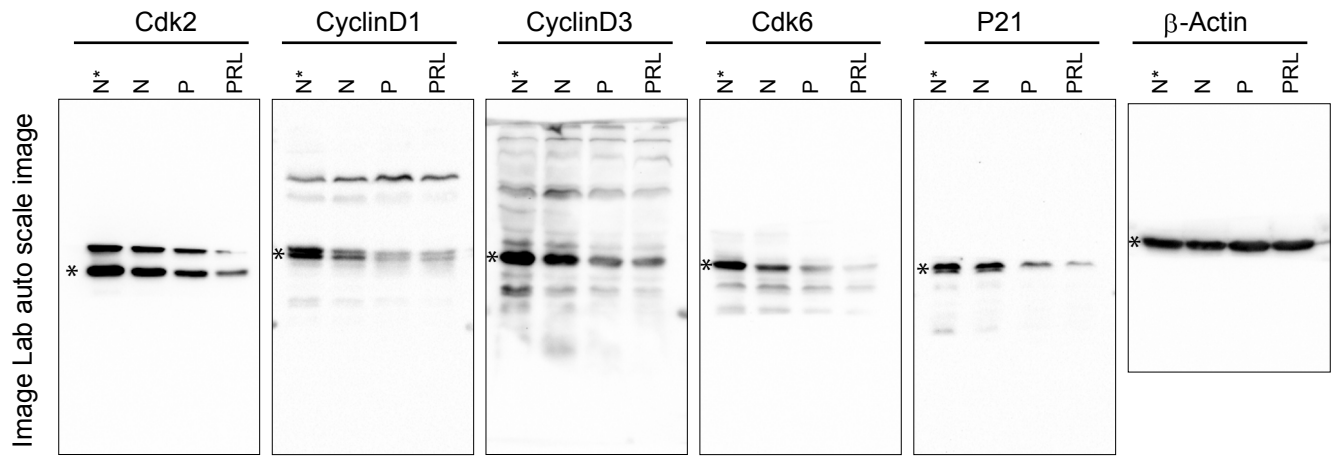
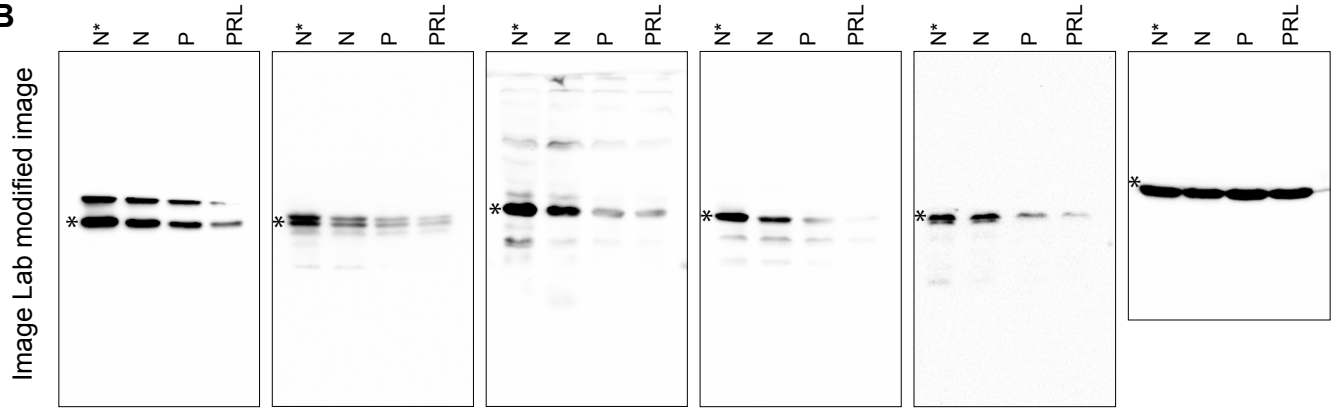
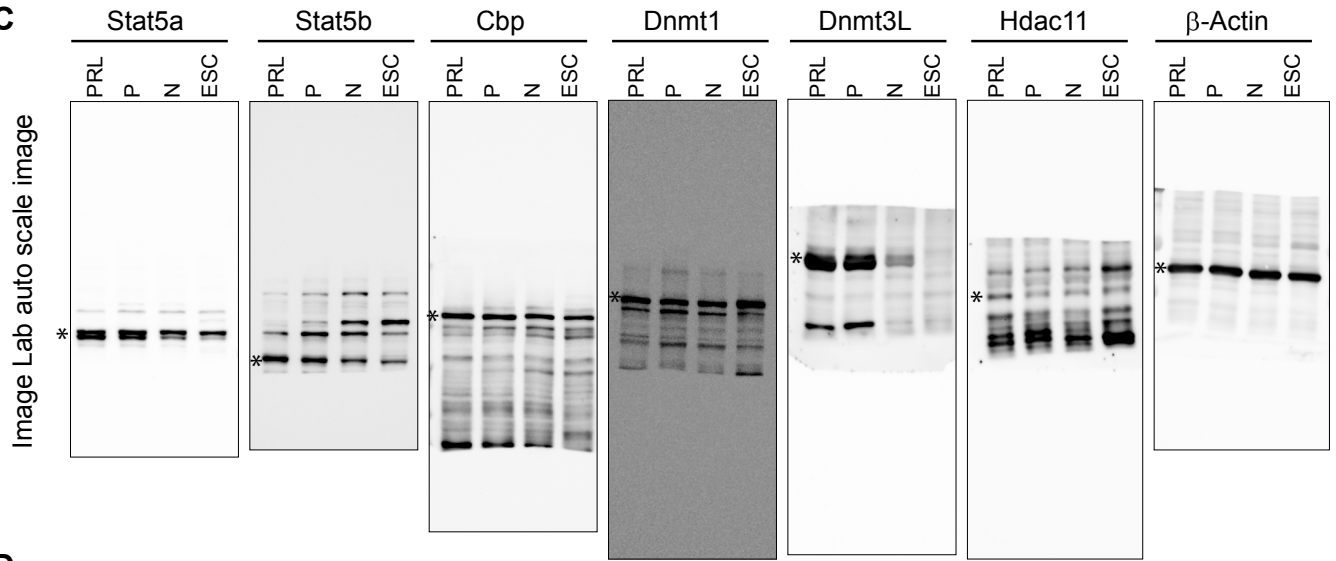
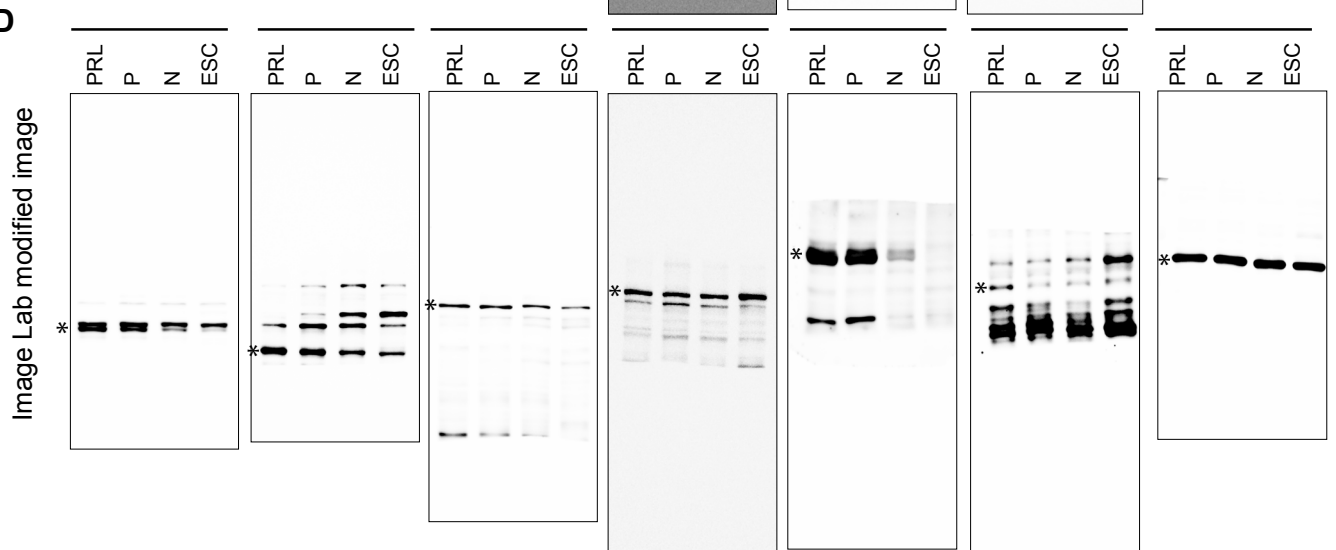


Comprehensive profiling of transcriptional networks specific for lactogenic differentiation of mammary epithelial stem-like cells

Trinadha Rao Sornapudi¹, Rakhee Nayak¹, Prashanth Kumar Guthikonda¹, Anil Kumar Pasupulati³, Srinivas Kethavath¹, Vanita Uppada¹, Sukalpa Mondal¹, Sailu Yellaboina², and Sreenivasulu Kurukuti^{1*}

1. Department of Animal Biology, School of Life Sciences, University of Hyderabad, Hyderabad-500046, India.
2. CR Rao Advanced Institute of Mathematics, statistics and computer sciences, University of Hyderabad campus, Gachibowli, Hyderabad-500046, India
3. Department of Biochemistry, School of Life Sciences, University of Hyderabad, Hyderabad-500046, India.



A**B****C****D**

Supplementary Figure Legends:

Supplementary Fig.S1. Comparative pathway analysis of differentially expressed genes between ESC and HC11 cell-types. Heatmap showing enrichment score (Z-score) of up or downregulated genes using **(A)** BioCarta and **(B)** Wiki pathway tools between ESC vs. N, N vs. P and P vs. PRL treated HC11 cells. Z-score >2 denote significantly upregulated and <2 denotes significantly downregulated.

Supplementary Fig.S2. Full-length immunoblotting images of respective protein markers **(A)** and contrast adjusted images **(B)** of cell cycle regulators. Similarly, differentially expressed TFs and ERs in auto scale **(C)** and contrast adjusted images **(D)**. The molecular weight (kDa) of a marker is highlighted in asterisk (*).