

Esrrb Unlocks Silenced Enhancers for Reprogramming to Naive Pluripotency

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In our originally published article, input reads mapped to the mm9 rather than mm10 version of the mouse genome, which were prepared for a pilot analysis, were inadvertently used as controls for ChIP-seq peak calling. Those incorrect input files were used for peak calling to estimate background distribution, but they were not directly used for other downstream analysis, e.g., peak clustering. We have reanalyzed the data using the correct input reads aligned to mm10. This has reduced the number of significant peaks, mostly due to eliminating false positives (e.g., the cluster Esrrb c2 from the original version has disappeared), but it did not affect the overall results derived from the peak calling. We have now made changes to reflect this in Figures 2A, 2C–2E, S2F–S2I, S2L, and S2M; Table S3; the legend for Figure 2A (a corrected version of which also appears below the corrected version of the figure); and the processed mapping data deposited in ArrayExpress. Accordingly, a line of text in our Results section that formerly read, “The Esrrb binding sites (c1 and c3) were highly enriched for the cognate estrogen-related receptor (ERR) motif,” now reads, “The Esrrb binding sites (c1 and c2) were highly enriched for the cognate estrogen-related receptor (ERR) motif.” These changes do not affect the interpretation of the ChIP-seq results. We sincerely apologize for any confusion that this error may have caused.



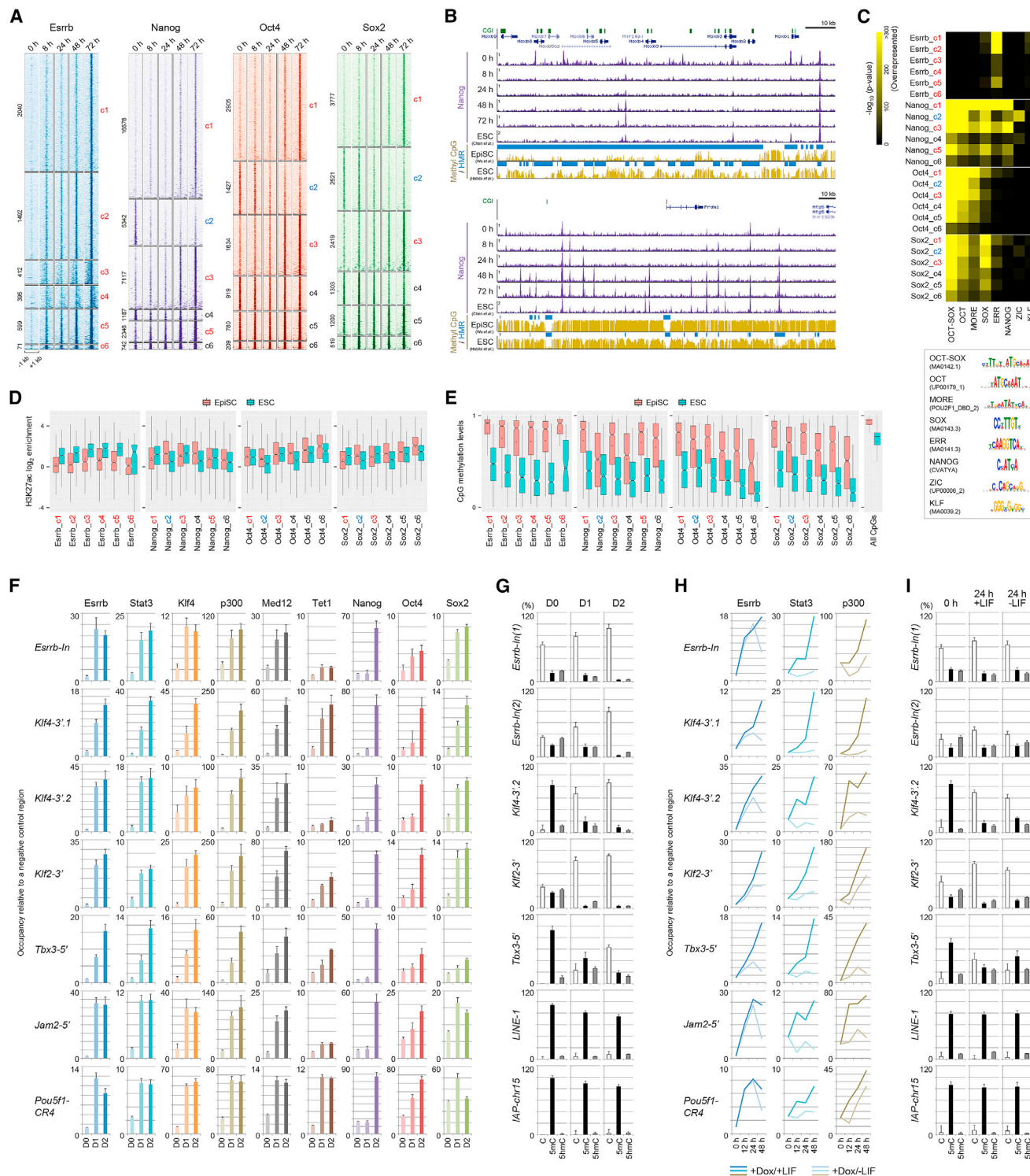
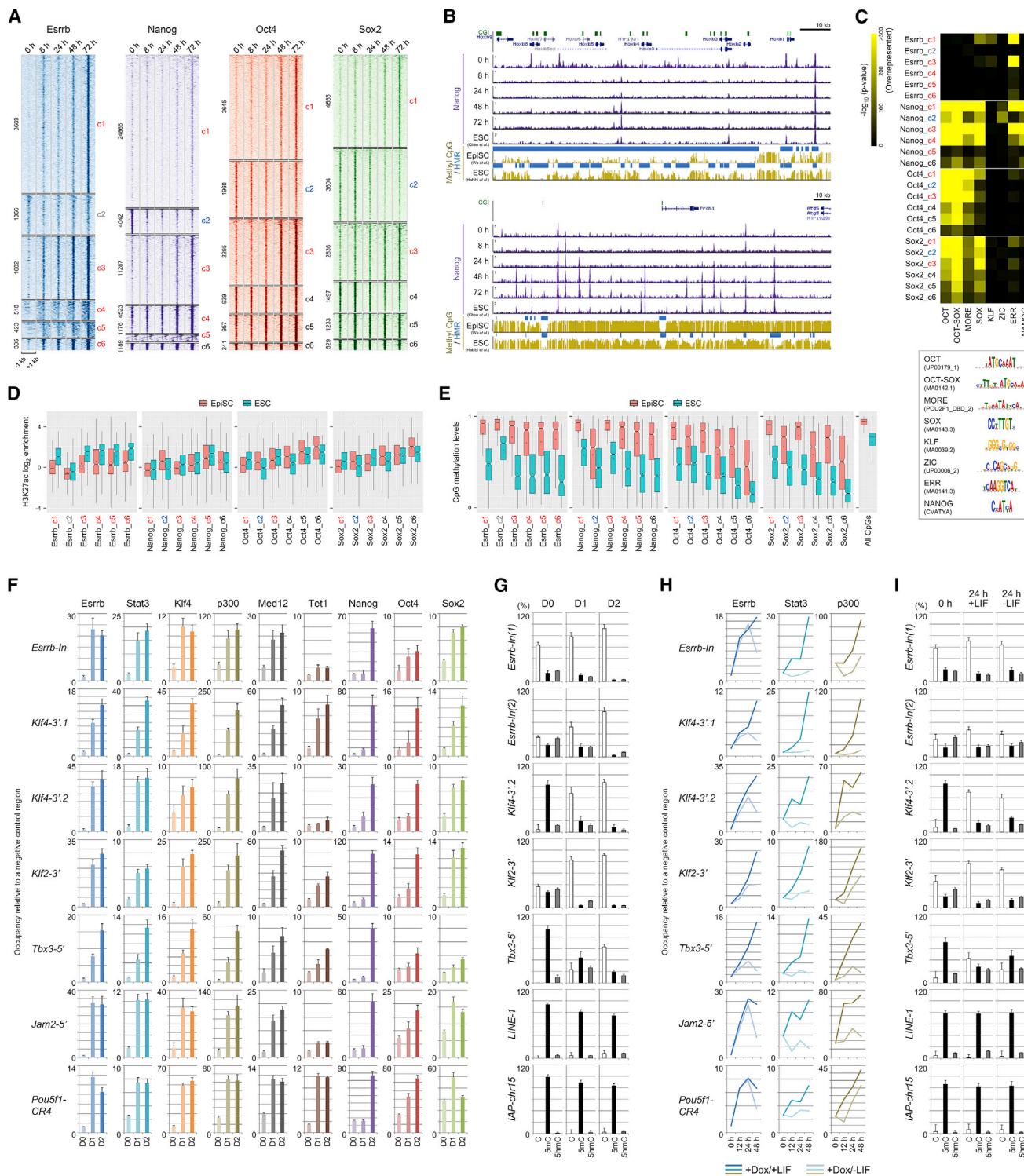


Figure 2. Esrrb- and LIF-Dependent Remodeling of Core TF Occupancy during EpiSC Reprogramming (corrected)

(A) Heatmaps of ChIP-seq signals around the peaks that were grouped into six clusters (red, ESC-specific; blue, EpiSC-specific; black, common). The number of peaks in each cluster is shown to the left of each heatmap.



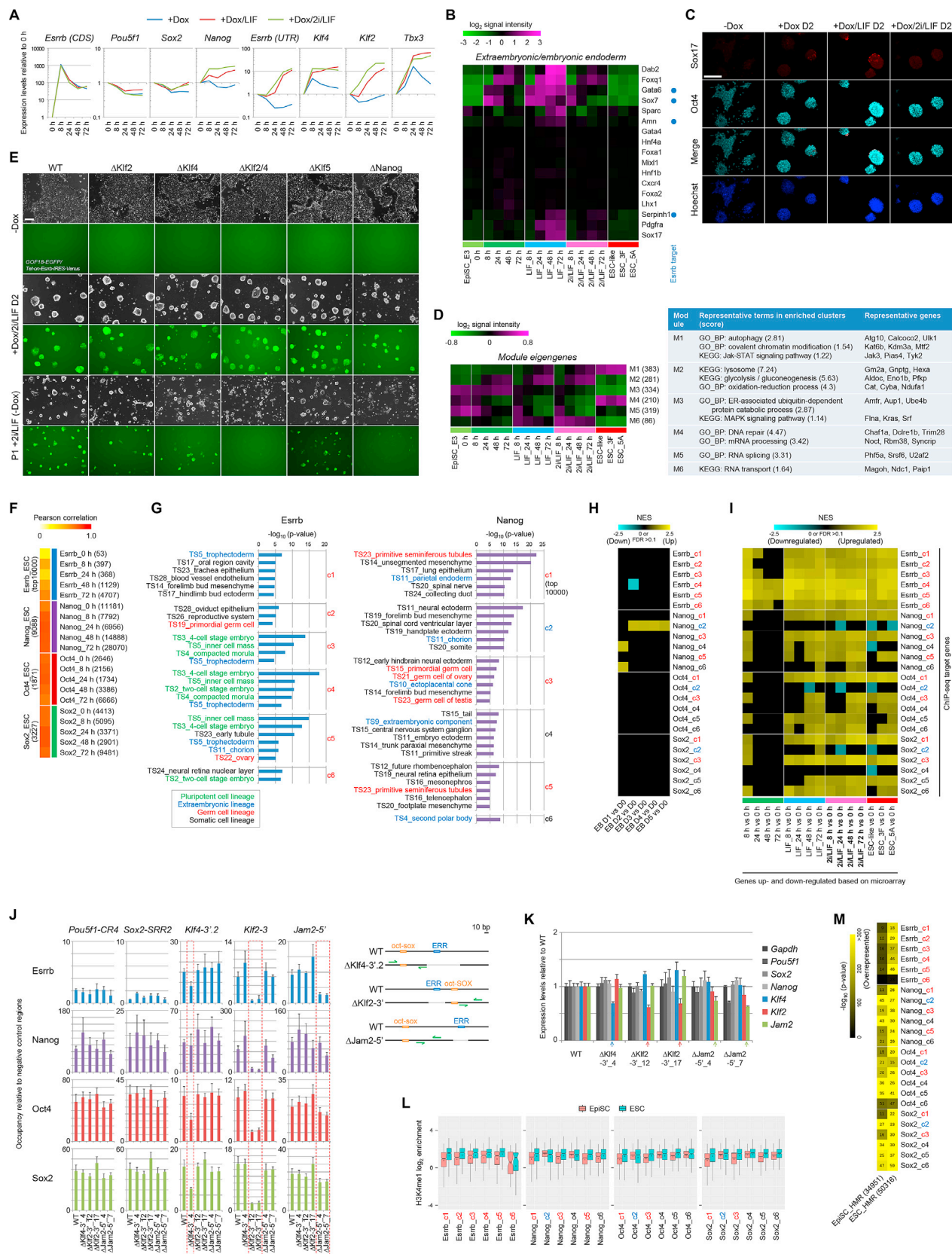


Figure S2. Esrrb and LIF Drive Remodeling of Core Transcriptional Networks, Related to Figures 1 and 2 and Tables S2-S4 (corrected)

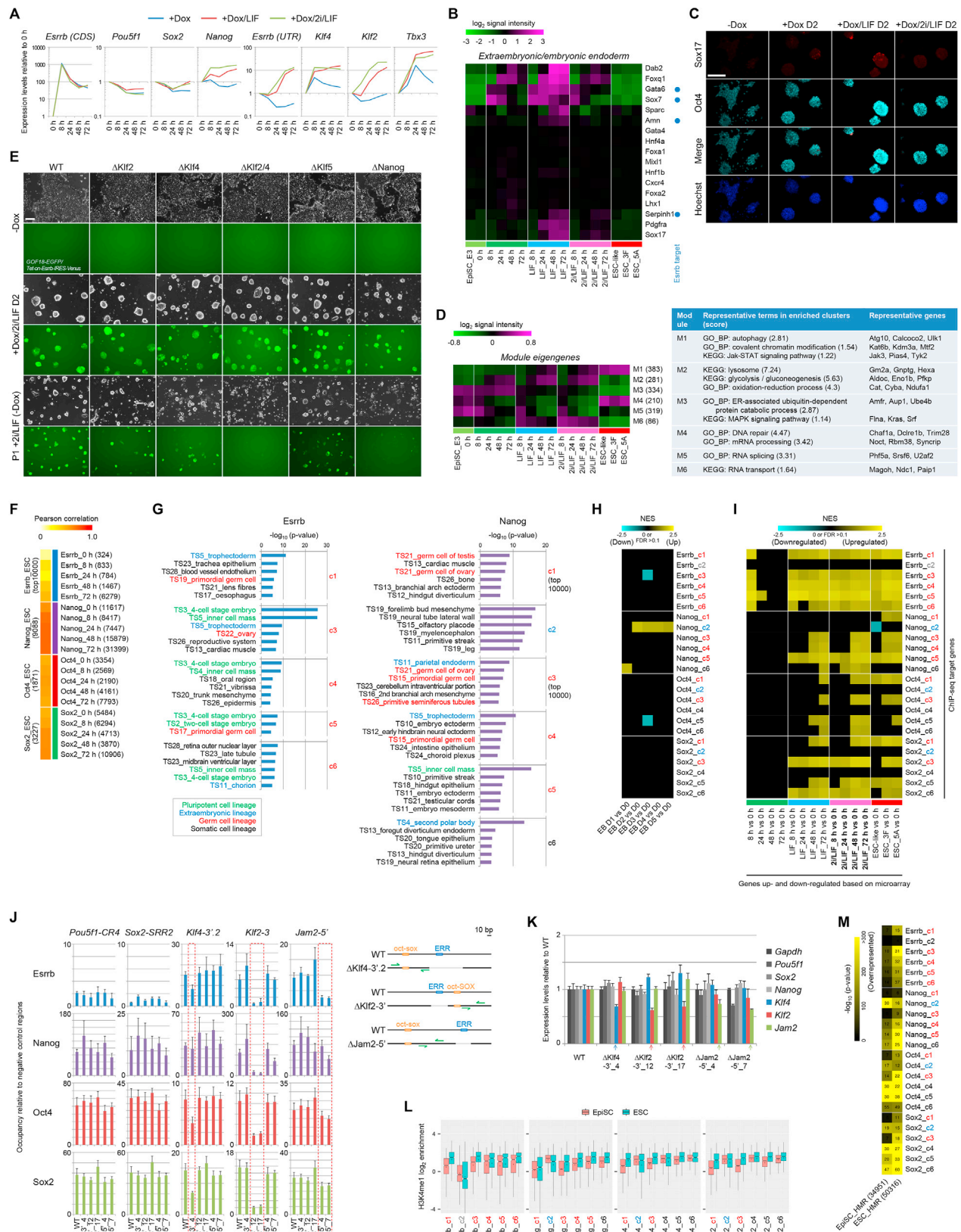


Figure S2. Esrrb and LIF Drive Remodeling of Core Transcriptional Networks, Related to Figures 1 and 2 and Tables S2–S4 (original)