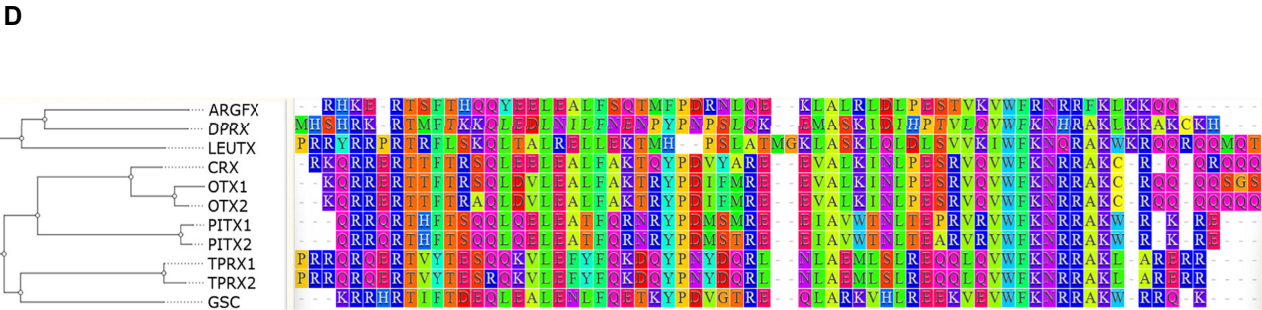
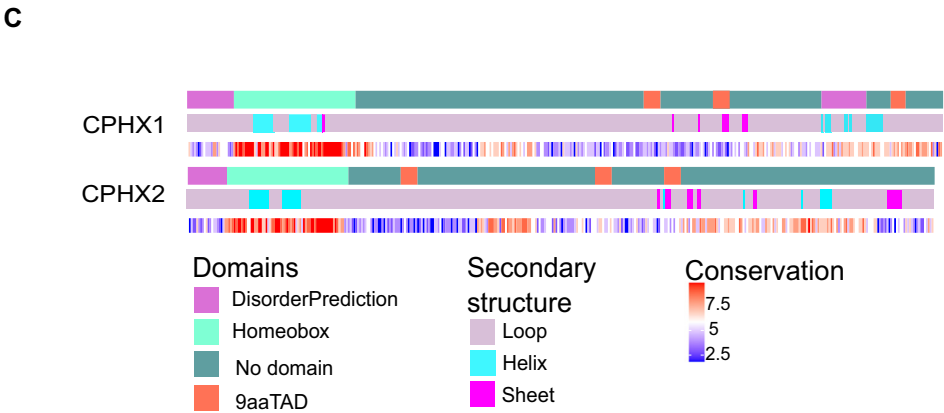
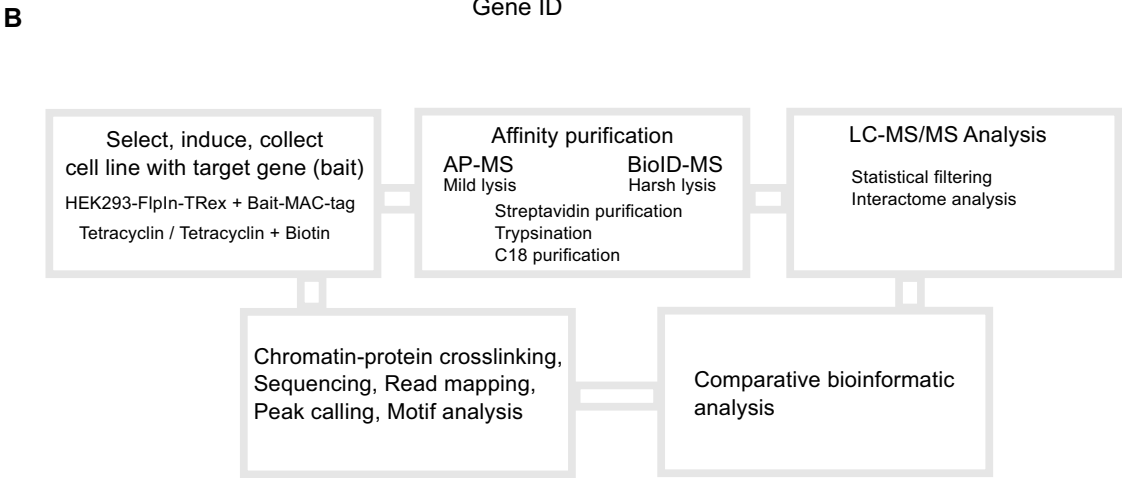
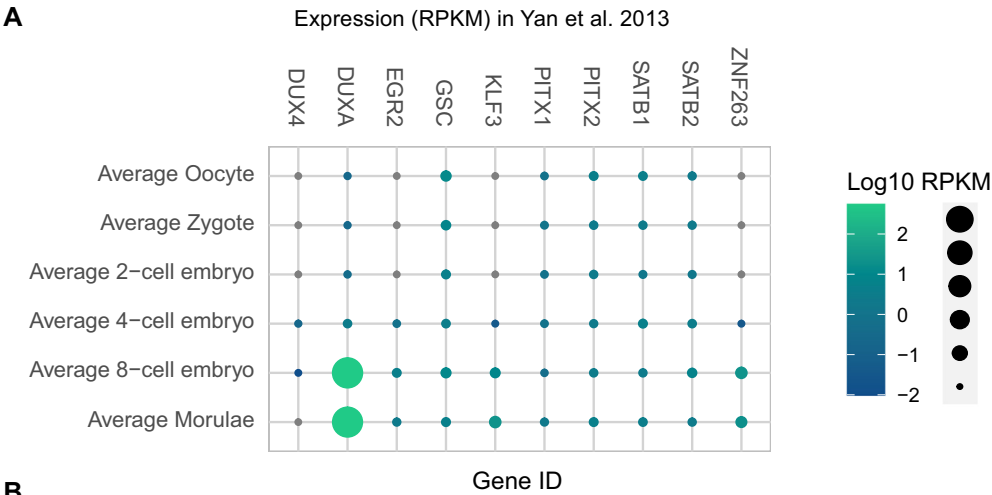
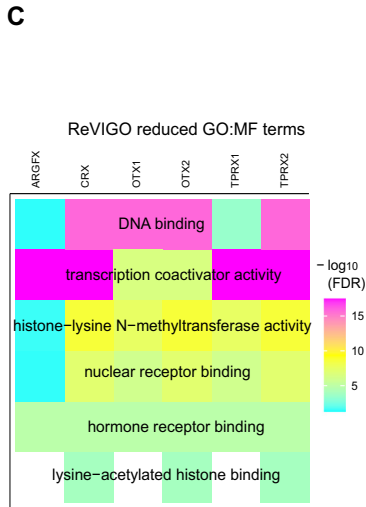
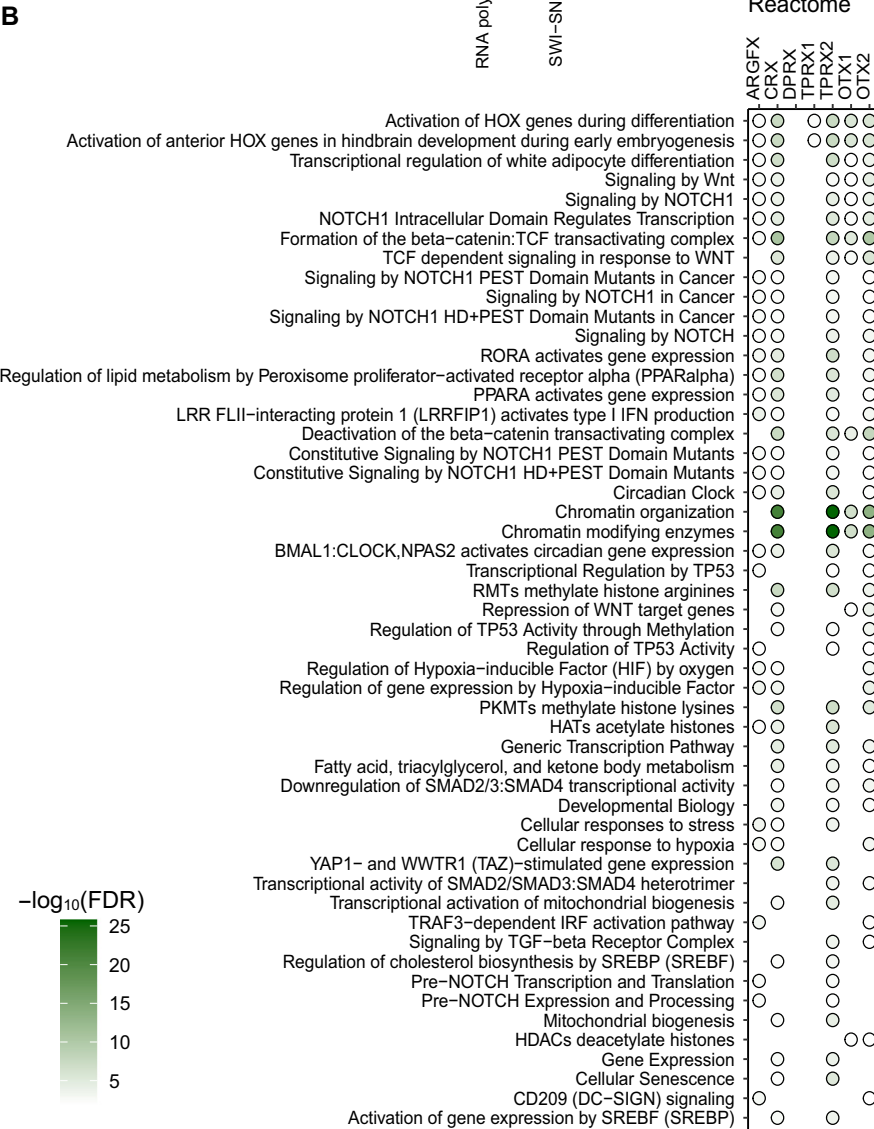
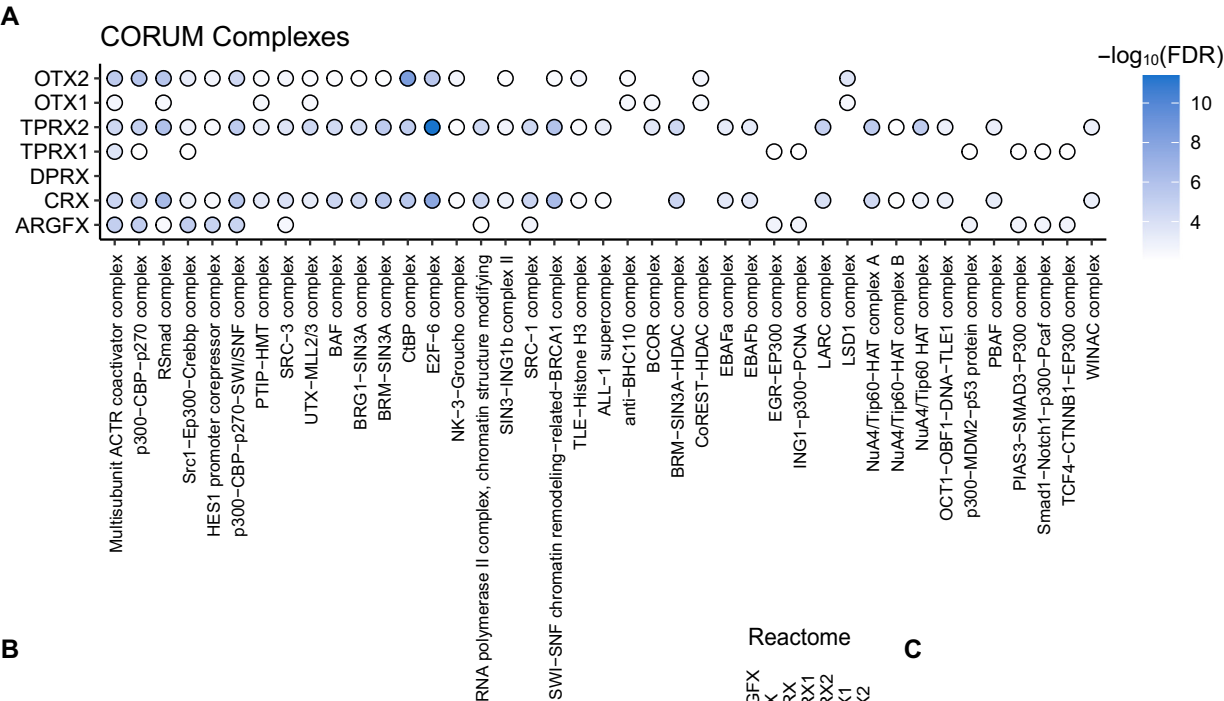


Expanded View Figures

Figure EV1. Additional info and methods used in this study.

(A) Expression of other baits in the bait set in the embryonic transcriptomics dataset Yan et al (2013). (B) Overview of the methods used in this study. We first produced a stable cell line containing the protein of interest (bait), and then performed affinity purification mass spectrometry using two methods and chromatin immunoprecipitation sequencing in the same HEK293 cell line. We combined the produced data and performed bioinformatic analysis. (C) Domain prediction for CPHX1 and CPHX2. (D) Homeodomain alignment of all homeodomain proteins in the dataset.

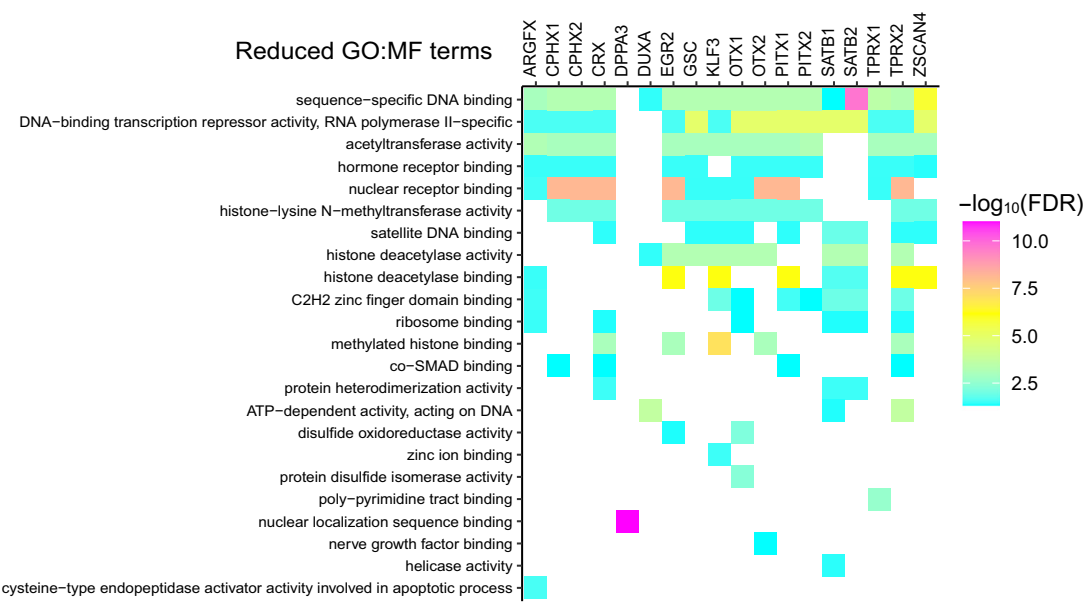




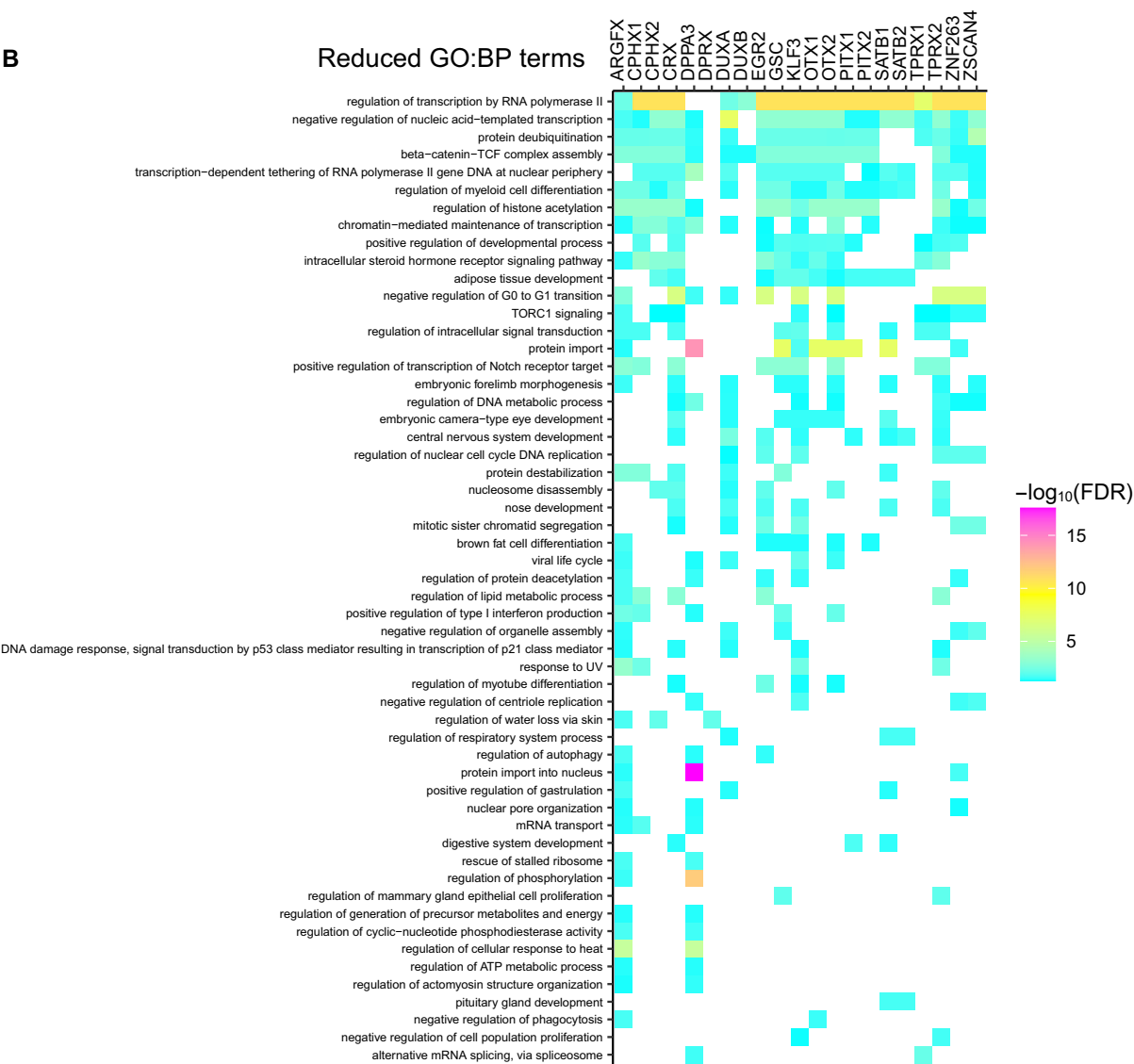
**Figure EV2. Enrichment analysis of PRDL bait interactomes.**

(A) CORUM complex enrichment analysis for PRDL bait interactomes, color indicates inverse significant enrichment of complex ($-\log_{10}$ (FDR)). Cutoff for image FDR < 0.05, Fishers Exact Test. (B) Reactome pathway enrichment analysis for PRDL bait interactomes, color indicates inverse significant enrichment of pathways ($-\log_{10}$ (FDR)). Cutoff for image FDR < 0.05, Fishers Exact Test. (C) Gene ontology molecular function enrichment analysis of PRDL bait interactomes, color indicates inverse significant enrichment of pathways ($-\log_{10}$ (FDR)). Cutoff for image FDR < 0.05, Fishers Exact Test.

A

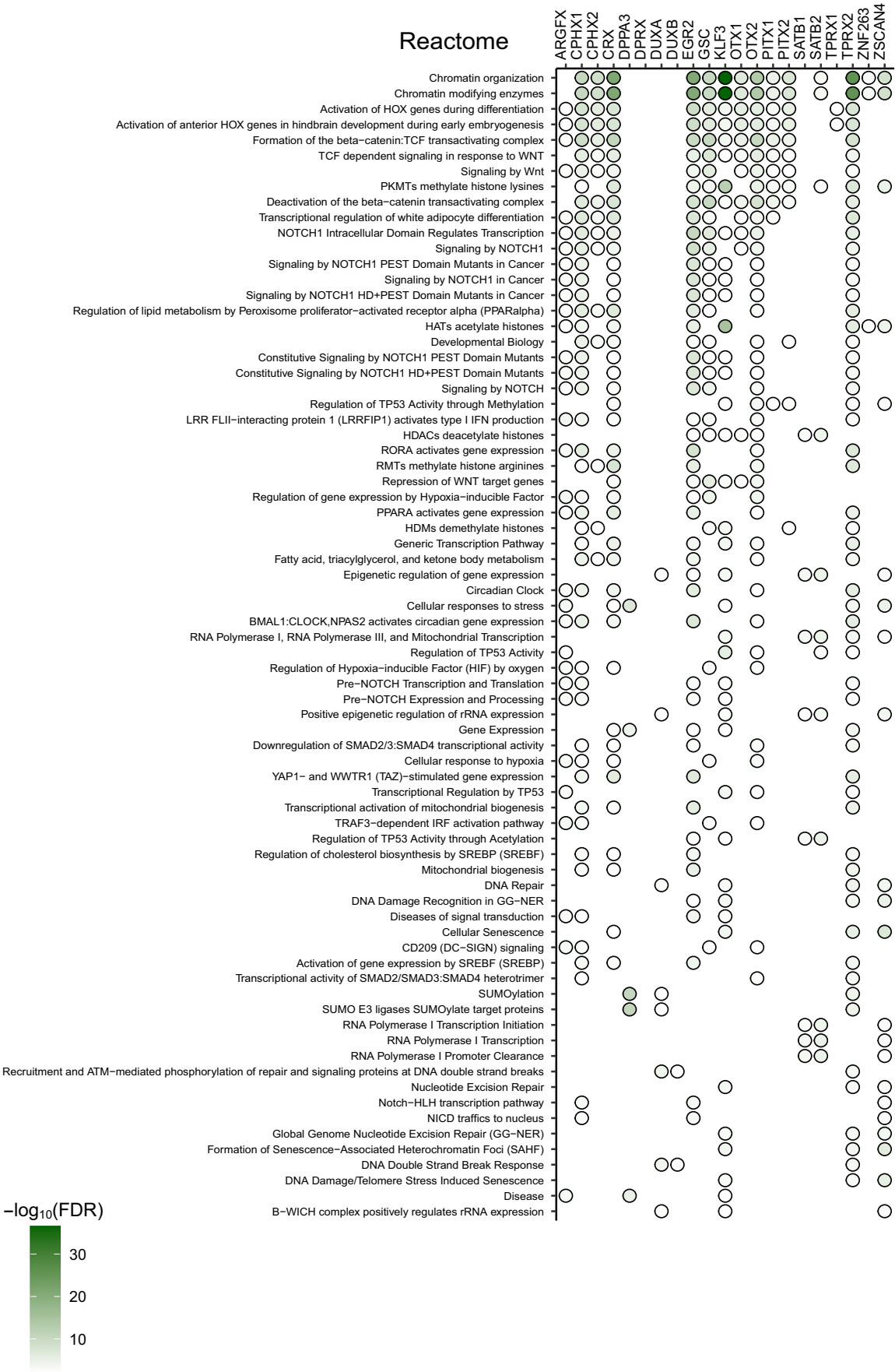


B



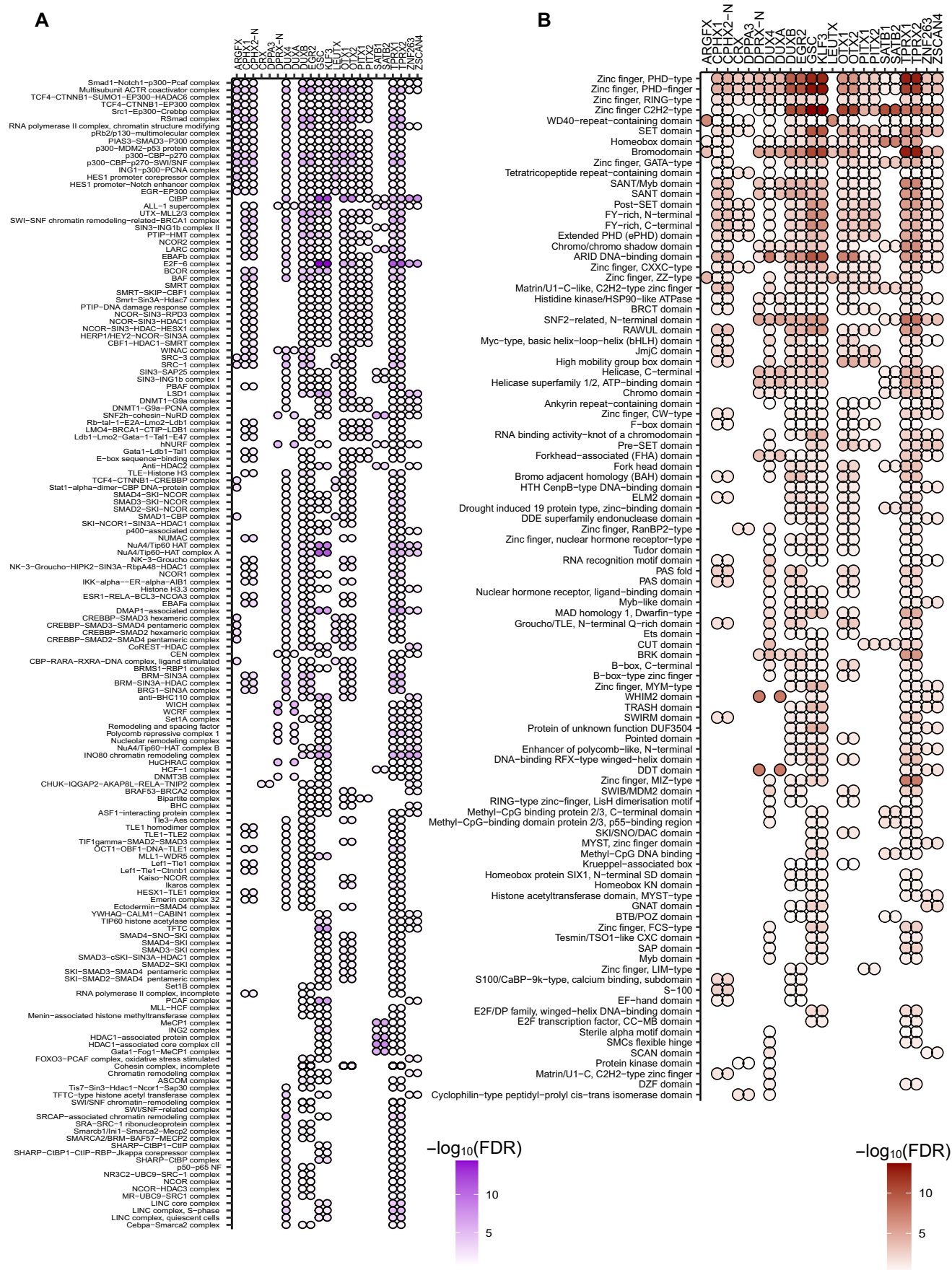
**Figure EV3. Gene ontology enrichment analysis of BioID-MS HCIs.**

(A) Gene ontology molecular function enrichment analysis of all BioID-MS HCIs, color indicates inverse significant enrichment of pathways ($-\log_{10}$ (FDR)). Cutoff for image FDR < 0.05, Fishers Exact Test. (B) Gene ontology biological process enrichment analysis of all BioID-MS HCIs, color indicates inverse significant enrichment of pathways ($-\log_{10}$ (FDR)). Cutoff for image FDR < 0.05, Fishers Exact Test.



**Figure EV4. Reactome pathway and ChIP-seq peak overlap analysis.**

Reactome pathway enrichment analysis of all bait interactomes, color indicates inverse significant enrichment of pathways ($-\log_{10}(\text{FDR})$). Cutoff for image FDR < 0.05, Fishers Exact Test.



**Figure EV5. Enrichment analysis of expanded BioID-MS dataset.**

(A) Significantly enriched (Fishers Exact Test, $FDR < 0.01$) protein complexes in the interactomes of each bait. Protein complexes were obtained from the CORUM database. Only complexes enriched in more than two baits are drawn. Increased blue color indicates inverse statistical significance ($-\log_{10}(FDR)$). Complexes are ordered by frequency. (B) Statistically significant enriched InterPro domains ($FDR < 0.01$) in the interactome of each bait, indicated by the number of shared baits. Color indicates $-\log_{10}(FDR)$ of enrichment analysis. Domains are ordered by $-\log_{10}(FDR)$ and frequency.

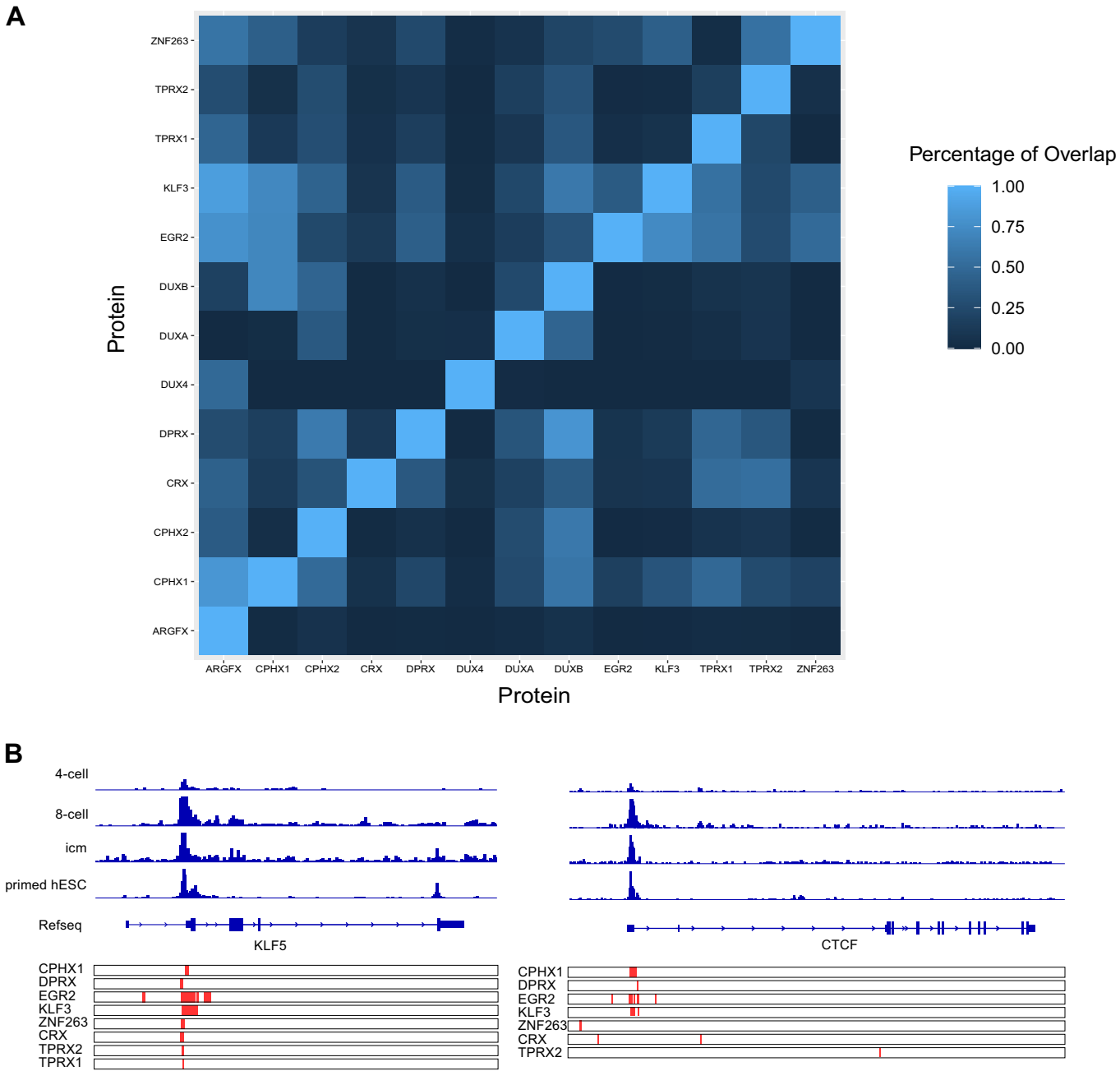


Figure EV6. ChIP-Seq Peaks over key EGA genes.

(A) Percentage overlap of identified ChIP-seq peaks. Overlaps were identified using bedtools closest and are shown as percentages from 0 to 1. (B) The embryonic ATAC-seq data from Wu et al (2018) from 4-cell, 8-cell, and ICM embryos and primed hESCs over key gene regions identified through our datasets. Genomic locations of differential ChIP-seq peaks are shown in red, relative to their position to key genes (RefSeq annotation).