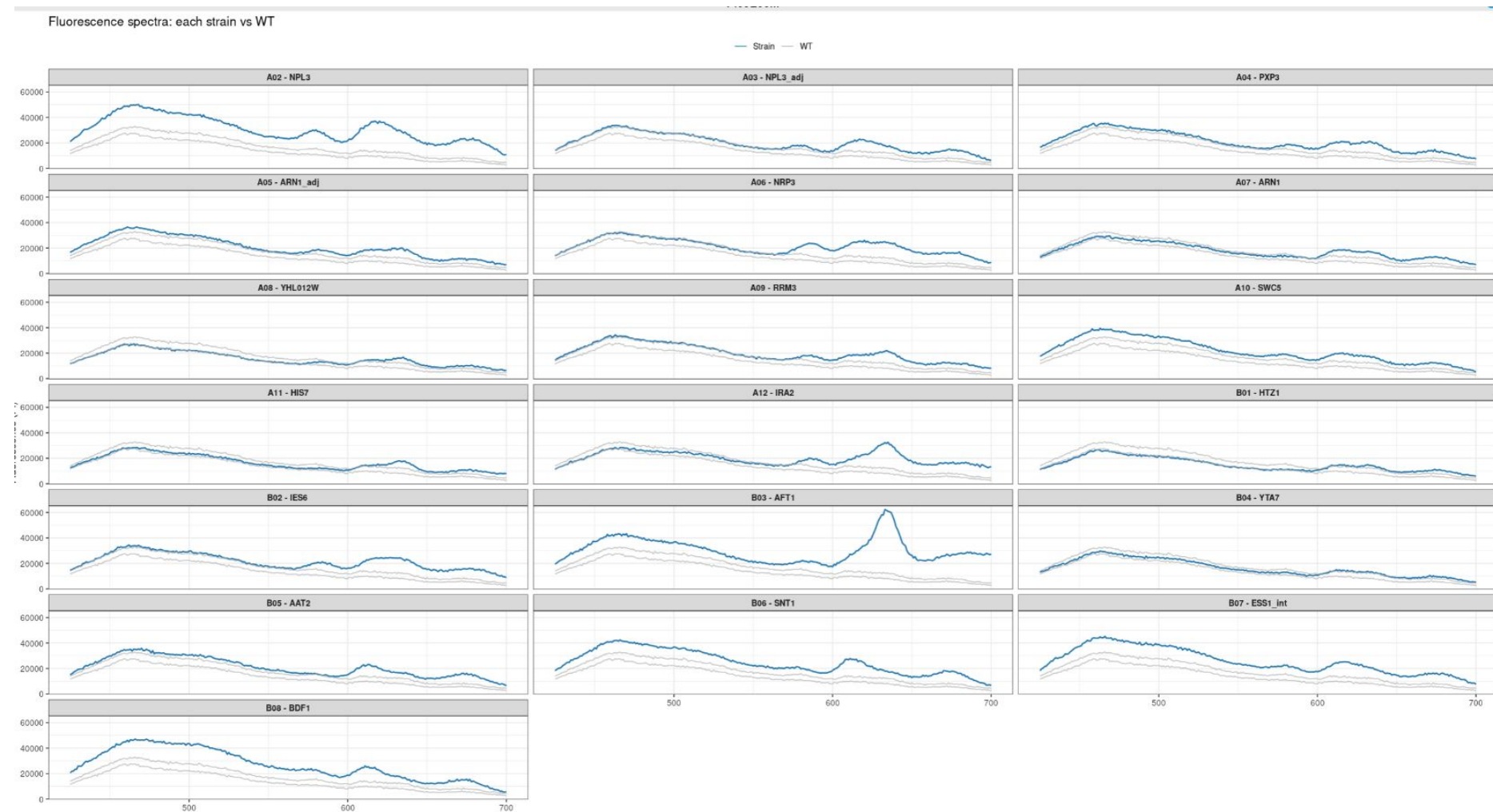
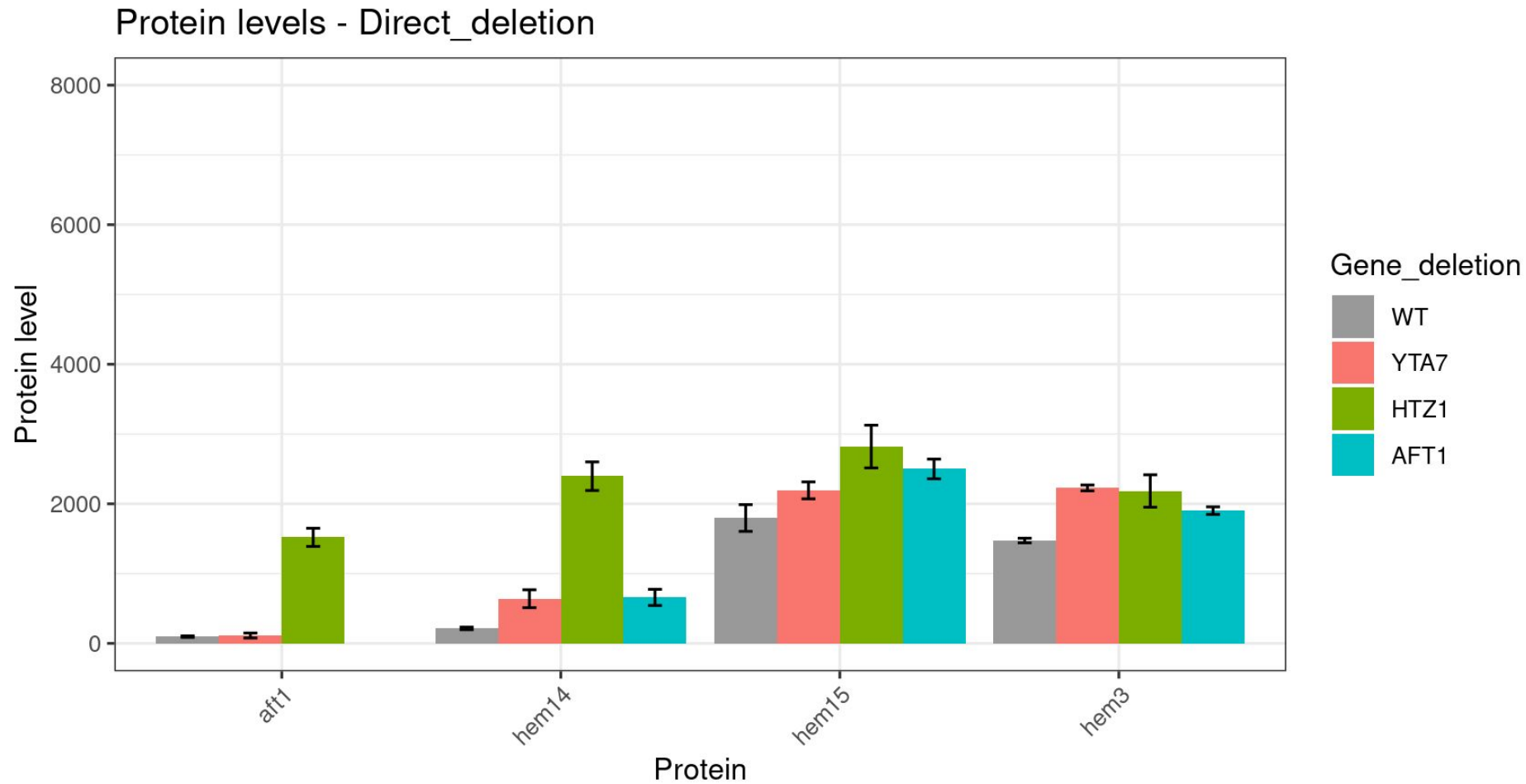


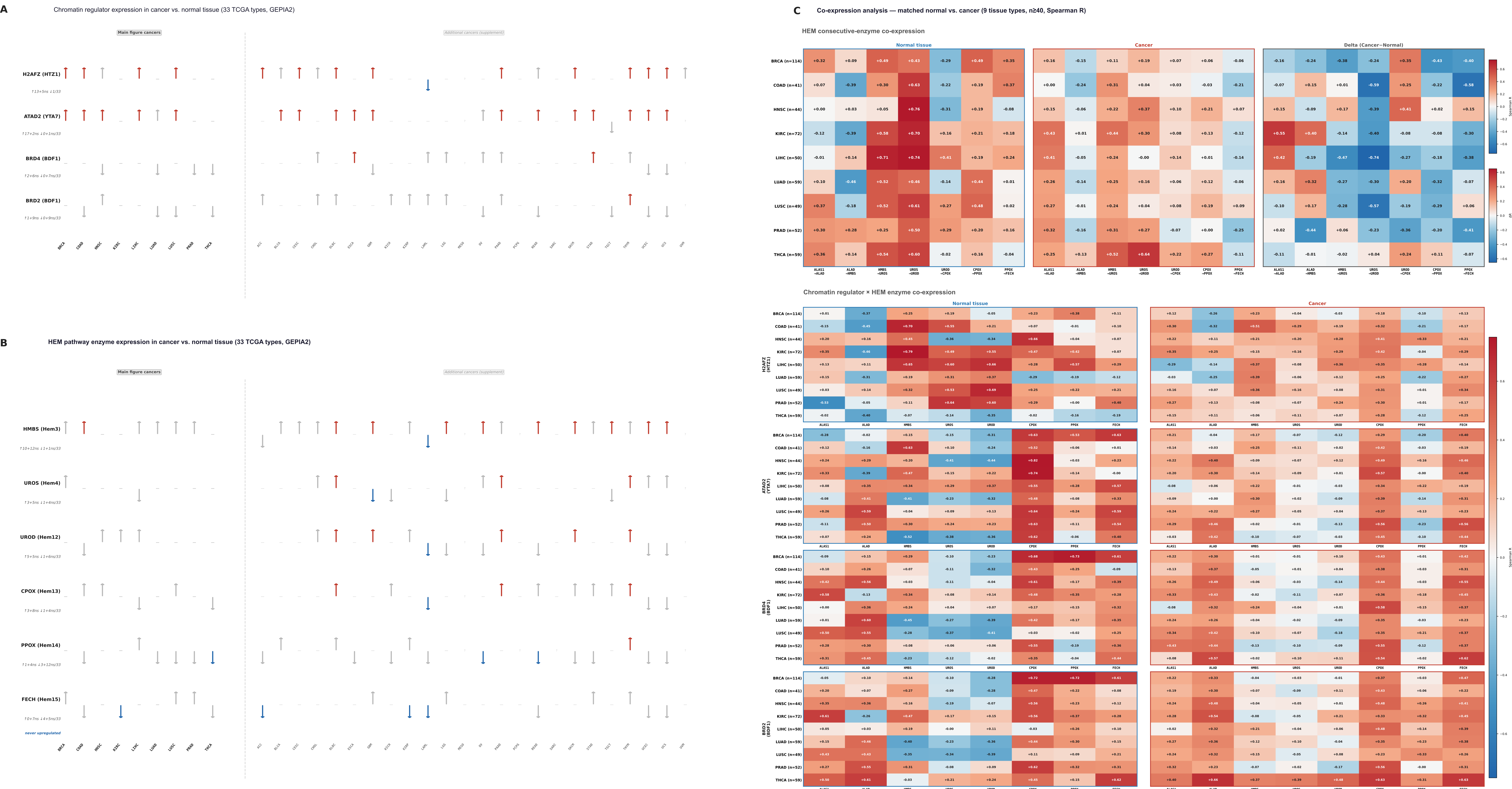


Supplemental figure 1. Fluorescence emission spectra at 400 nm excitation. Grey lines - wild type by4742 strain, Blue - deletion mutant spectrum



Supplemental fig 2 - Direct deletion of chromatin regulators and iron signalling gene affects level of GFP-tagged heme pathway genes (X axis). Protein level measured via flow cytometry of GFP abundance.

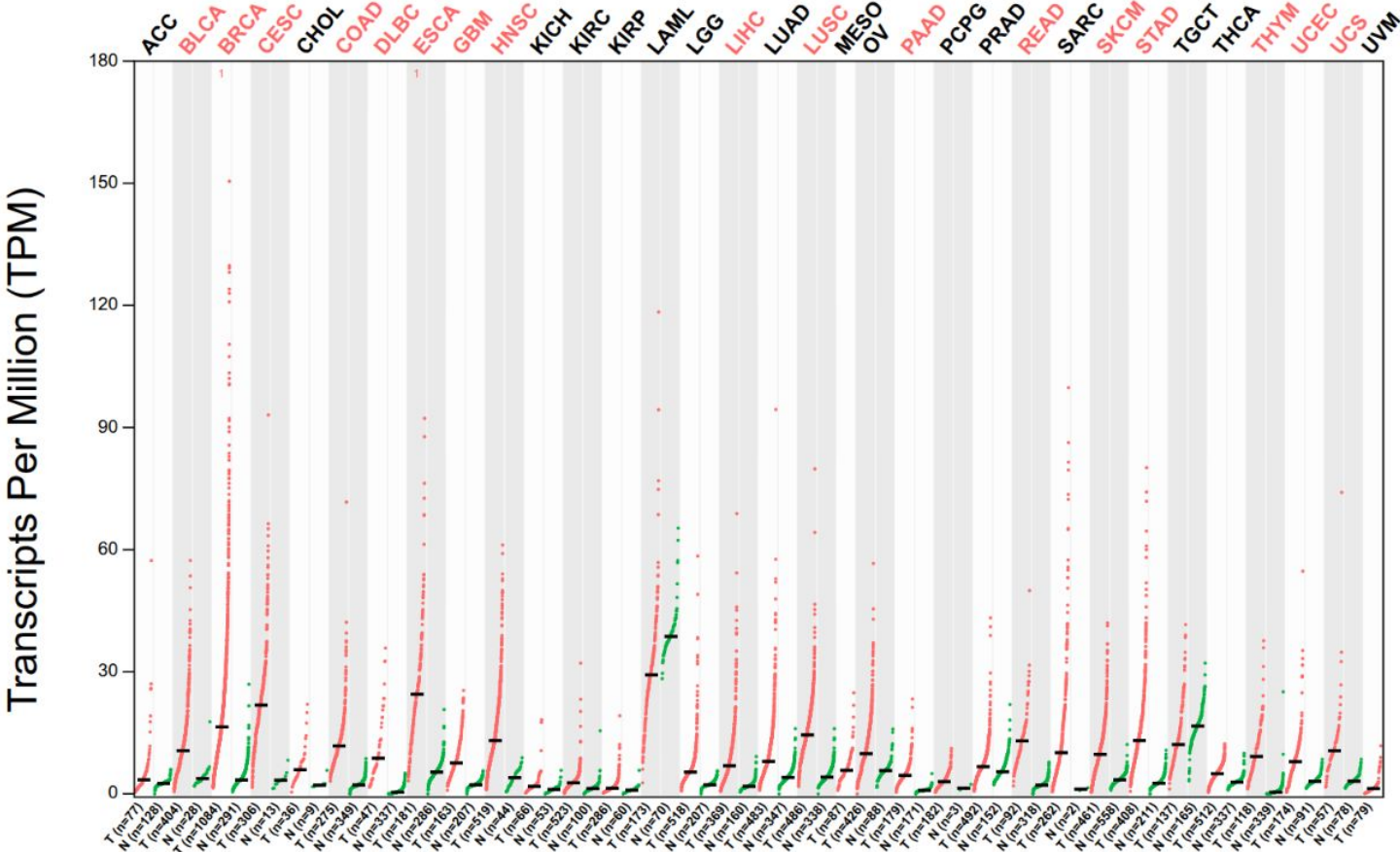
Chromatin dysregulation and heme pathway imbalance in cancer



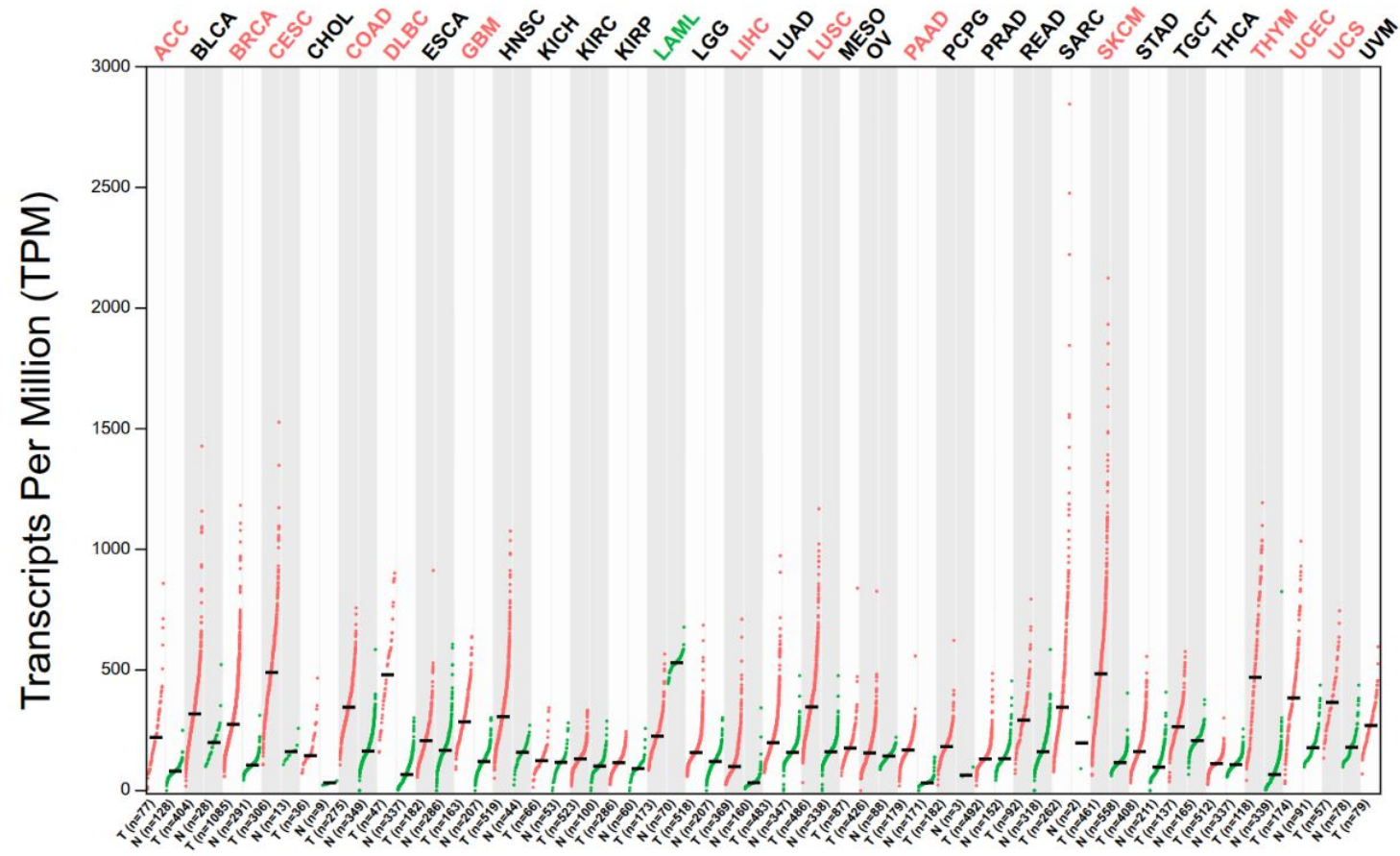
Supplemental fig 3 - Effects of cancer transformation on levels (A,B) and mutual correlation (D) of chromatin regulators and heme biosynthesis genes, as well as intrapathway correlation of adjacent enzymes (C). (A) Expression level changes across cancer types were visualized directly from GEPIA2 output plots and summarized in tabular form indicating significant upregulation/downregulation (colored arrows), or a insignificant but noticeable change (grey arrows) for each gene-cancer combination.

Figure S4 - output of GEPIA database on expression of chromatin regulators and heme biosynthesis genes in cancer and normal tissues

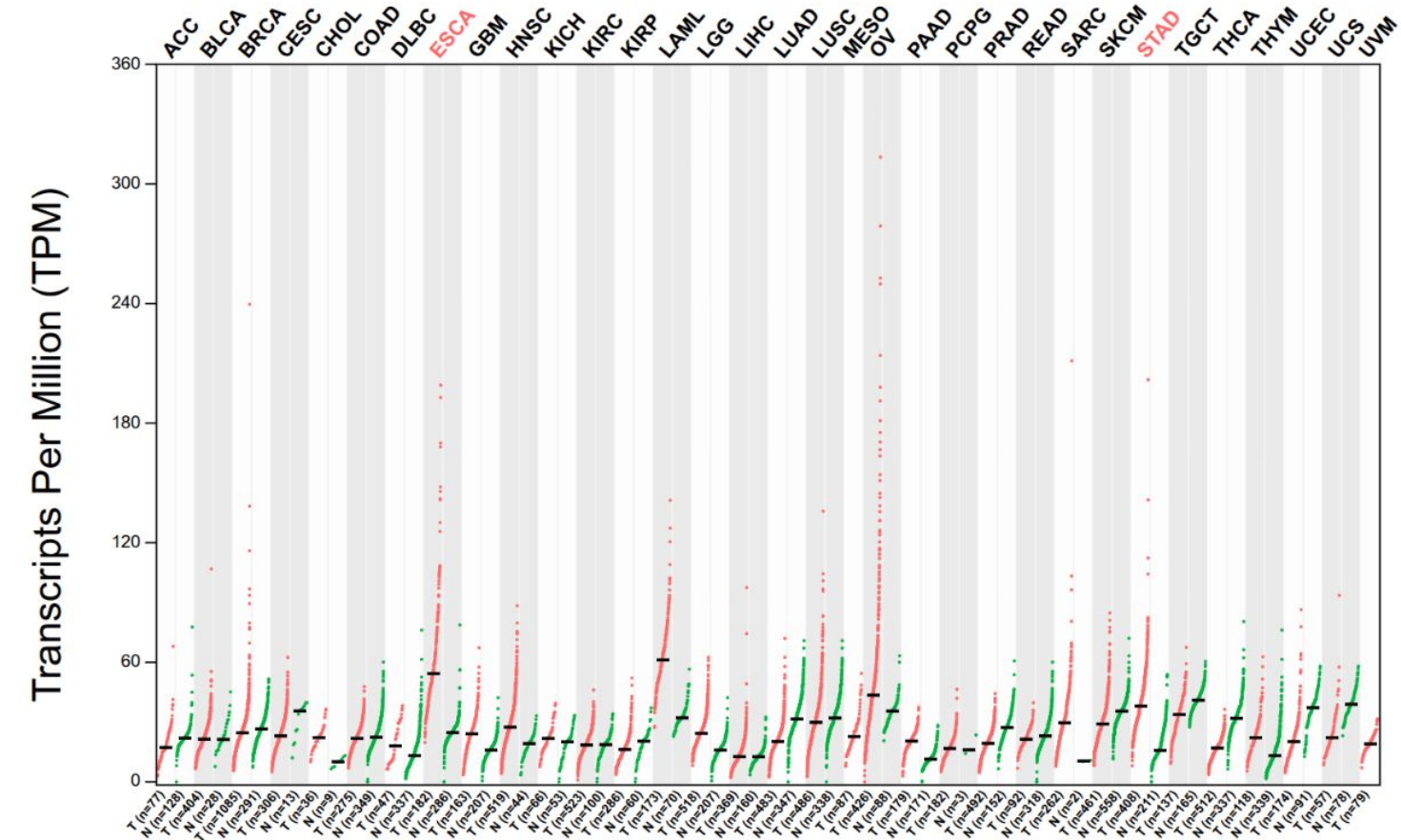
ATAD2



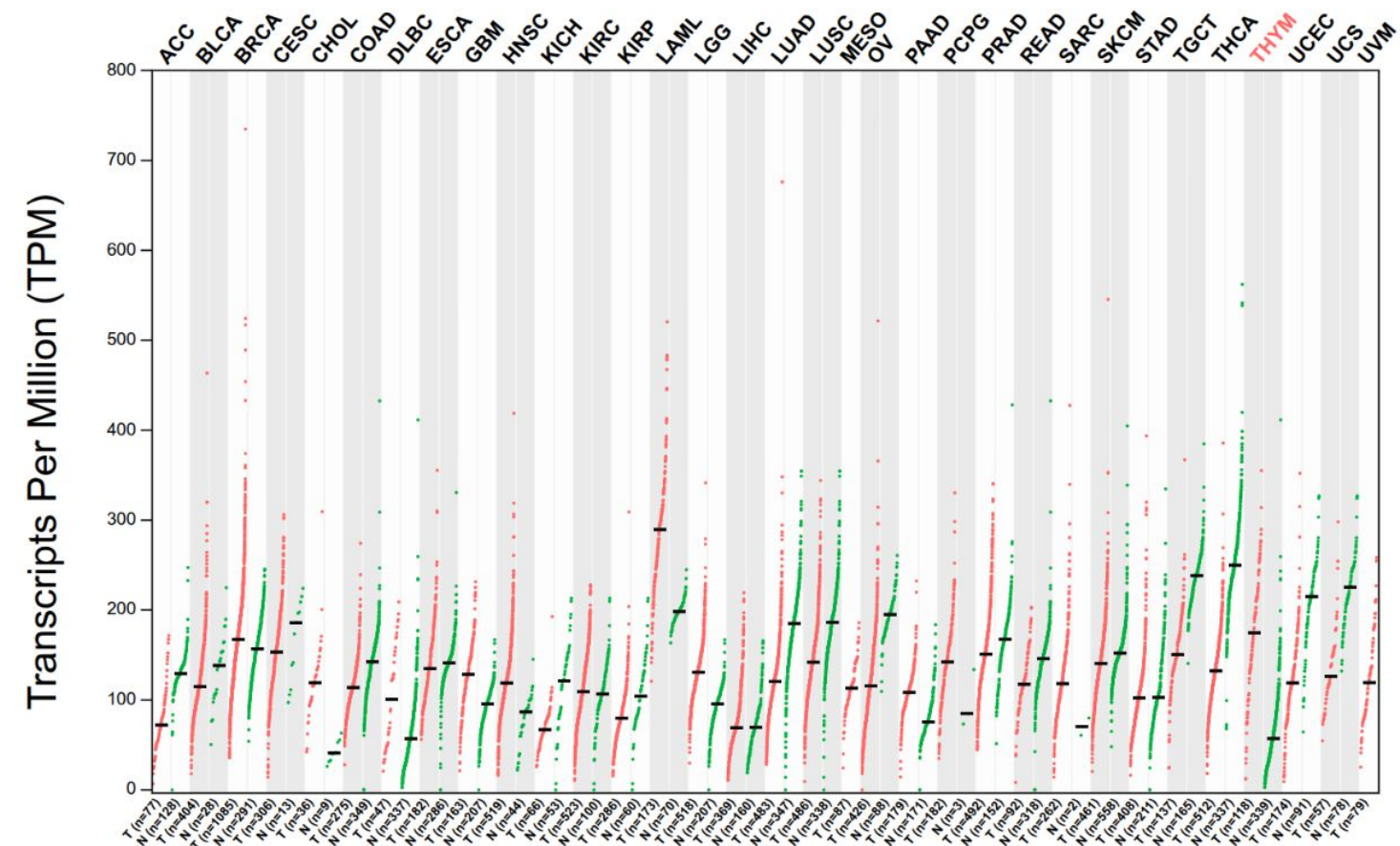
H2AZ



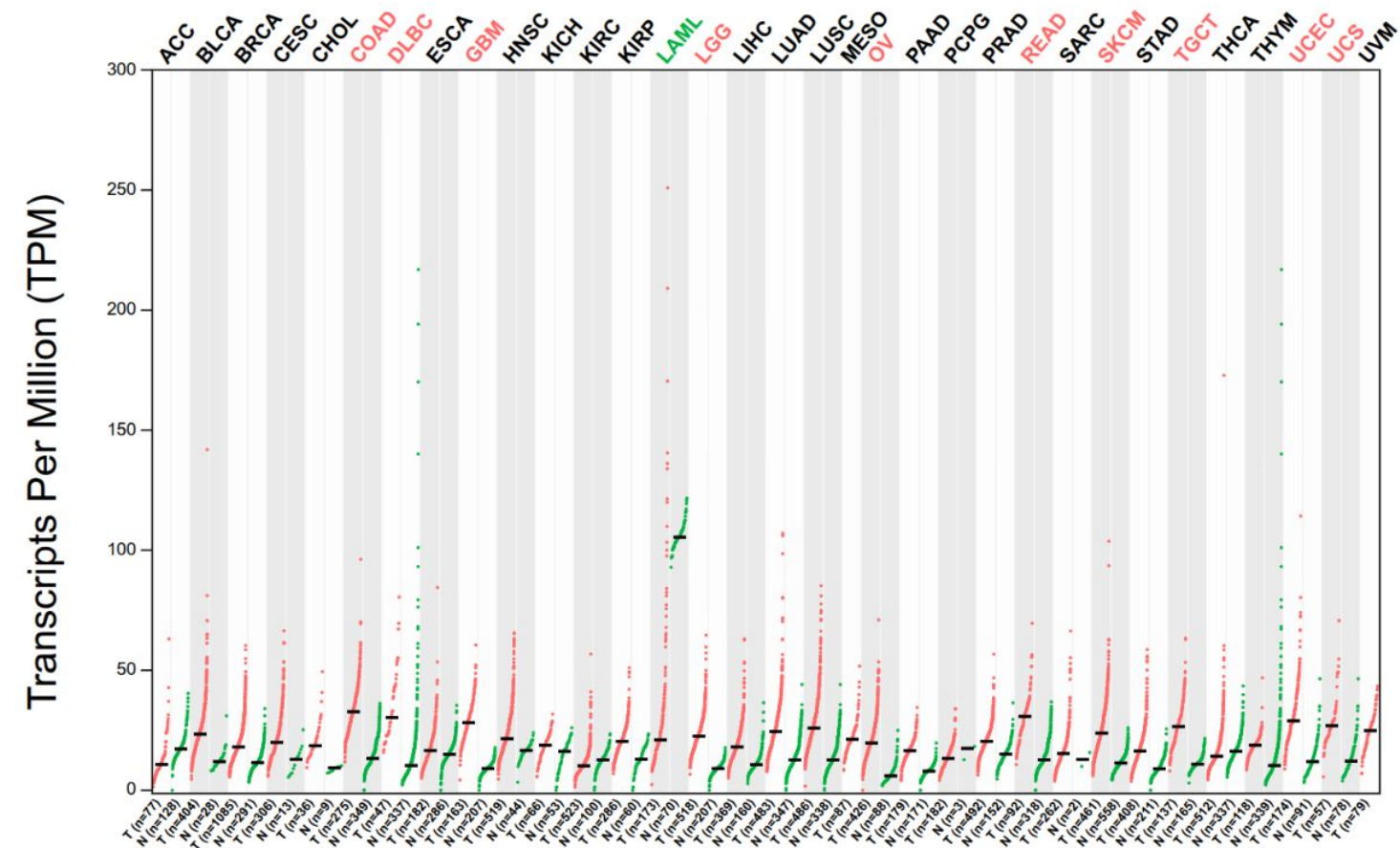
BRD4



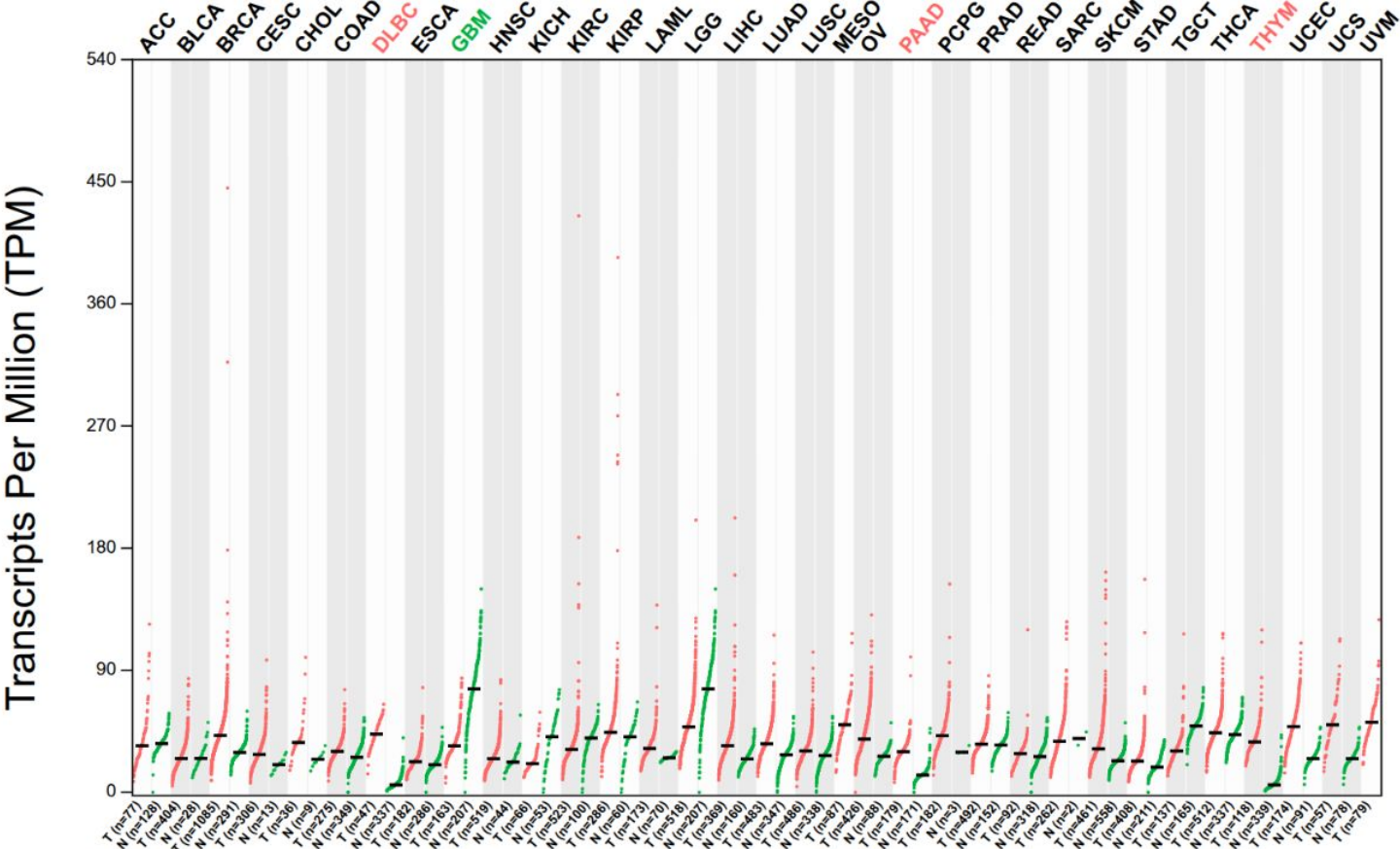
BRD2



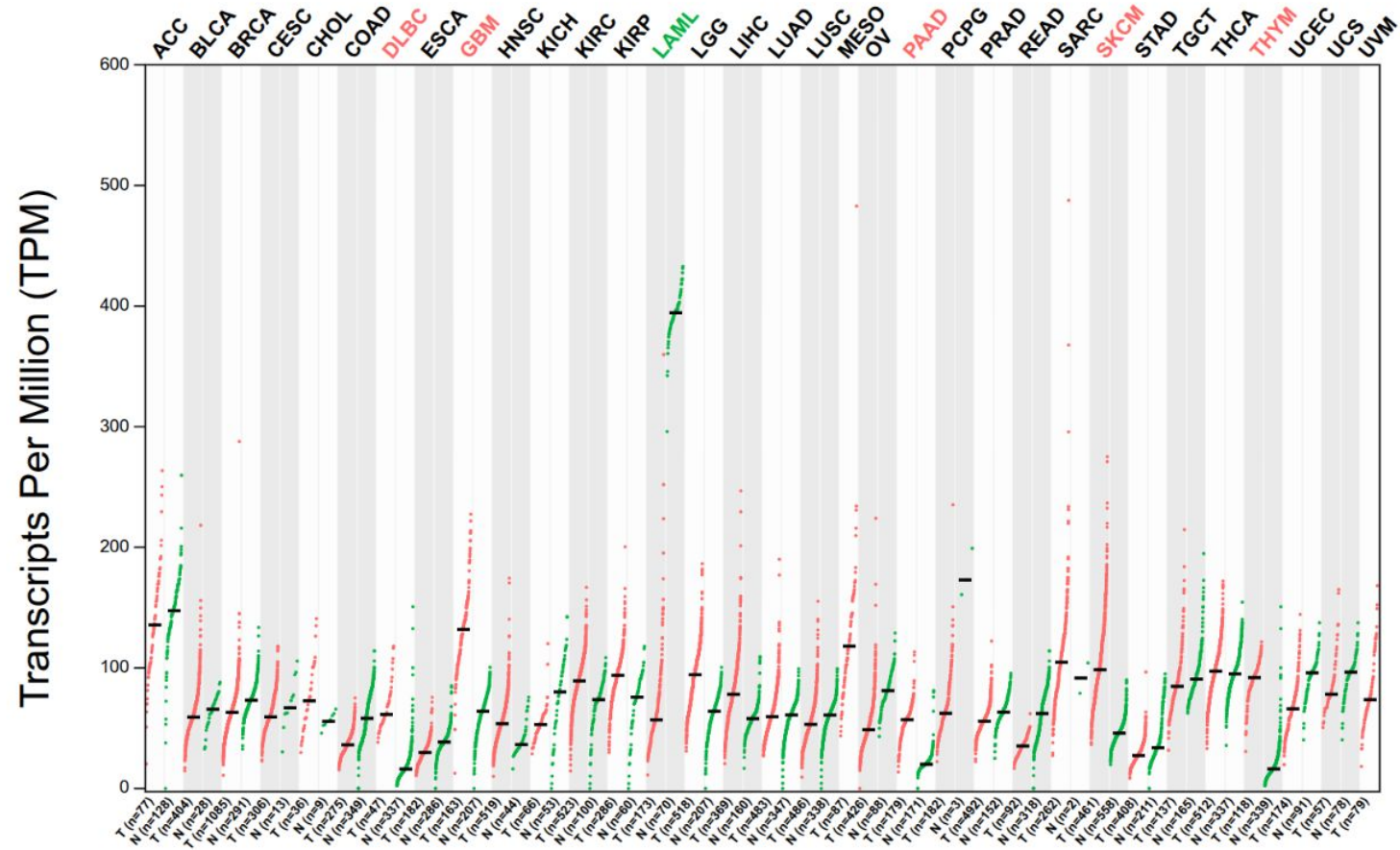
HMBS (Hem3)



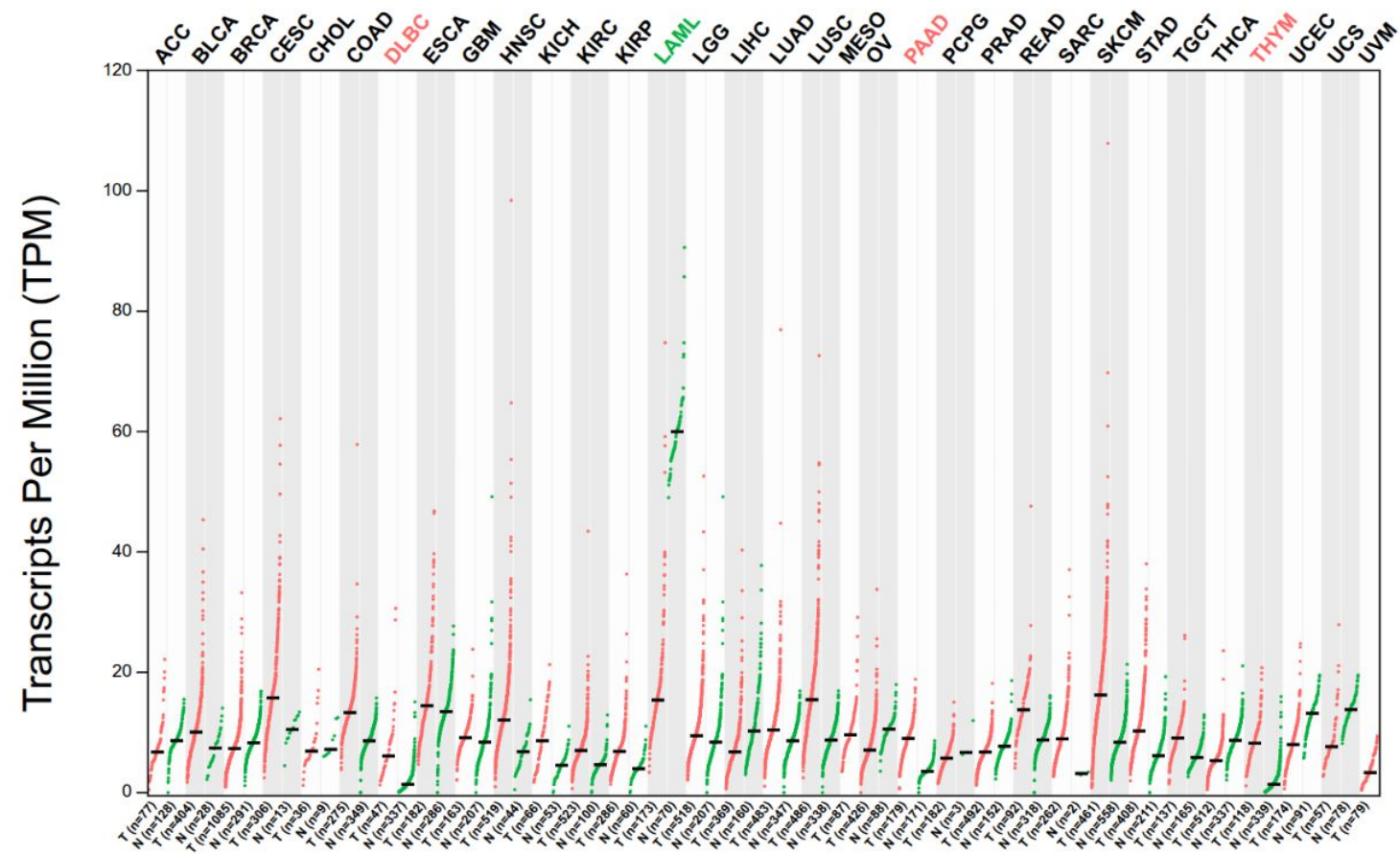
UROS (Hem4)



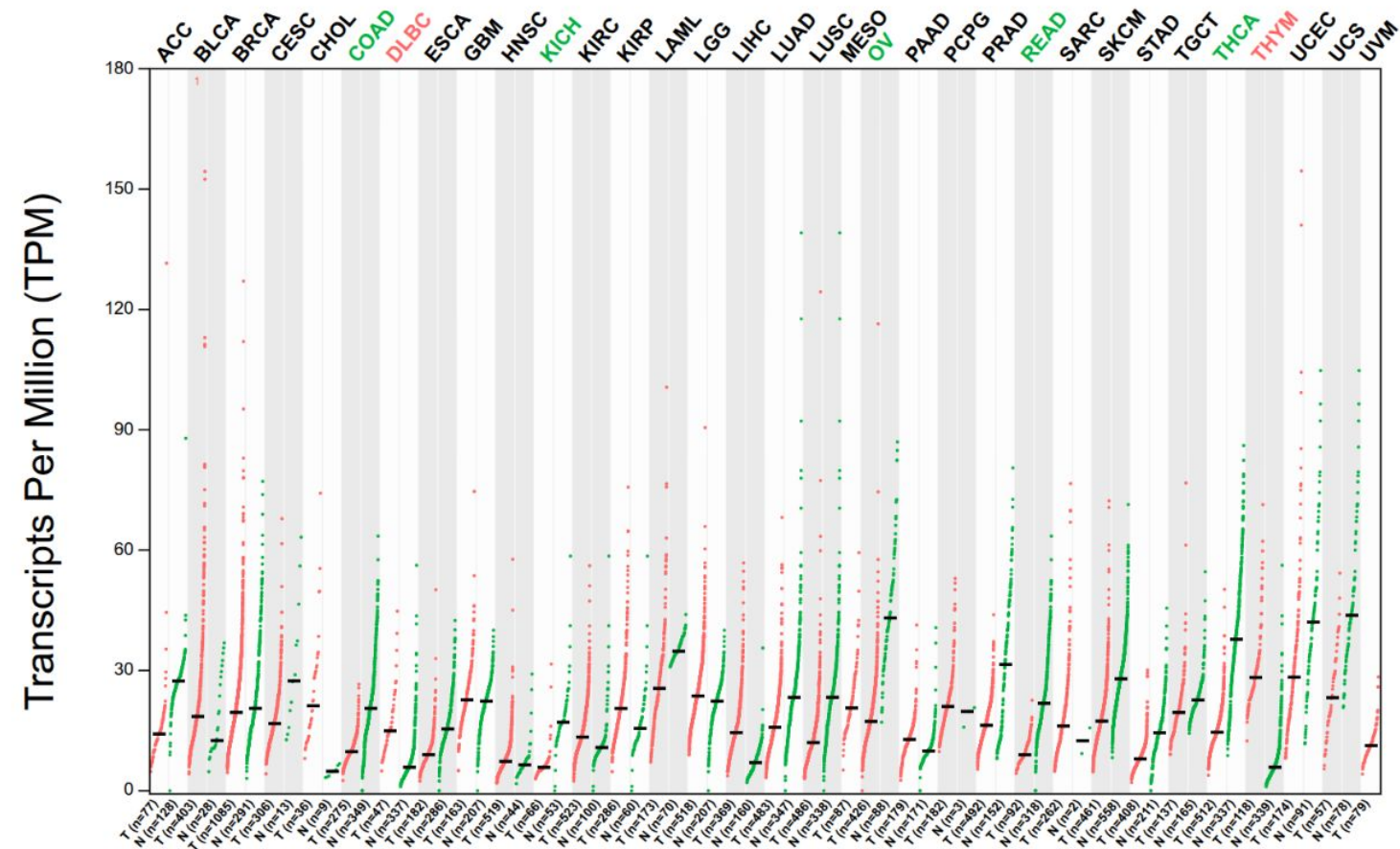
UROD Hem12



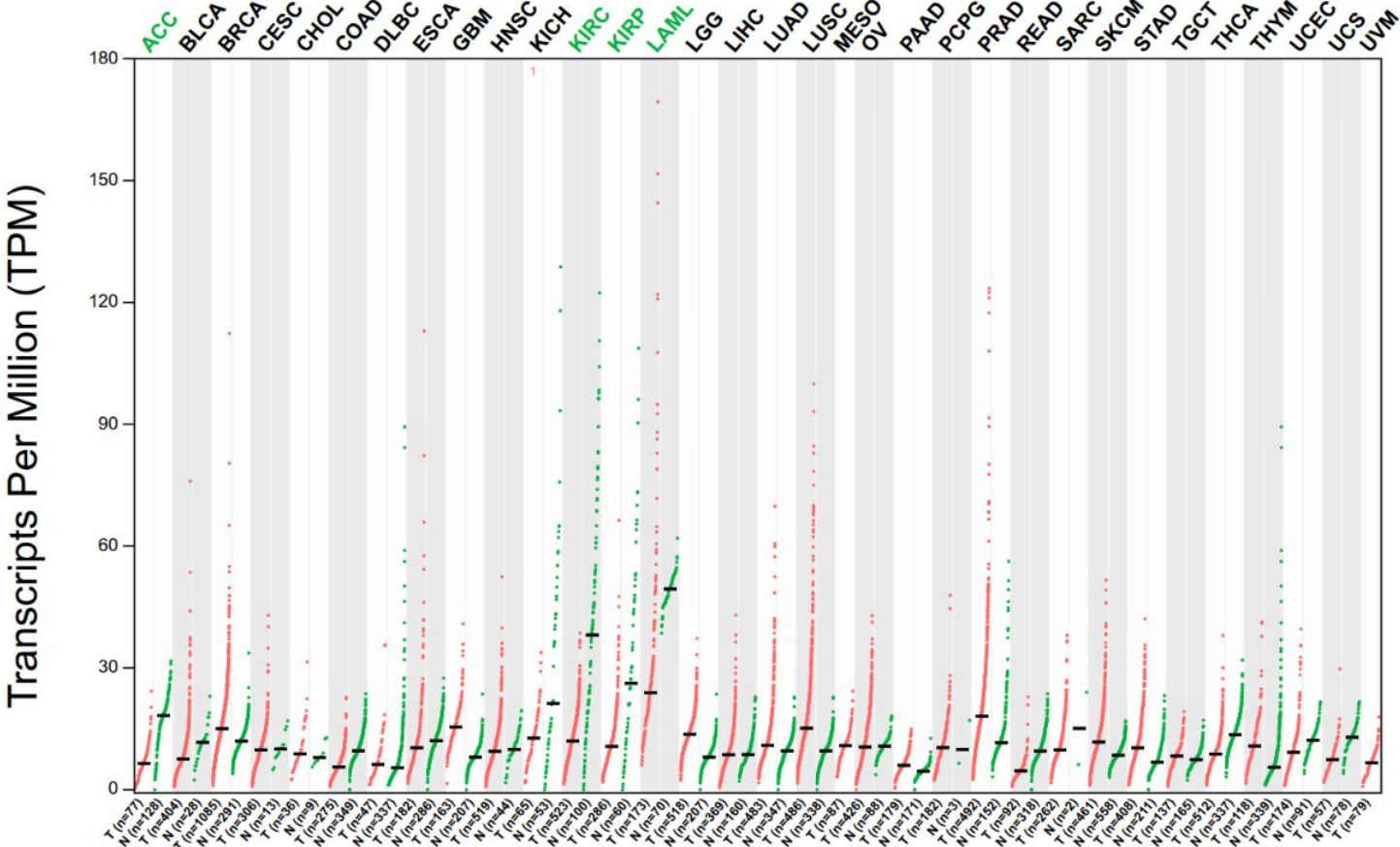
CPOX - Hem13



PPOX (Hem 14)



FECH (Hem15)



Supplemental fig 5. Comparison of intra-pathway enzyme expression correlation in cancer vs normal tissues for the heme and fatty acid biosynthesis pathways.

