Supplementary information, Figure S5

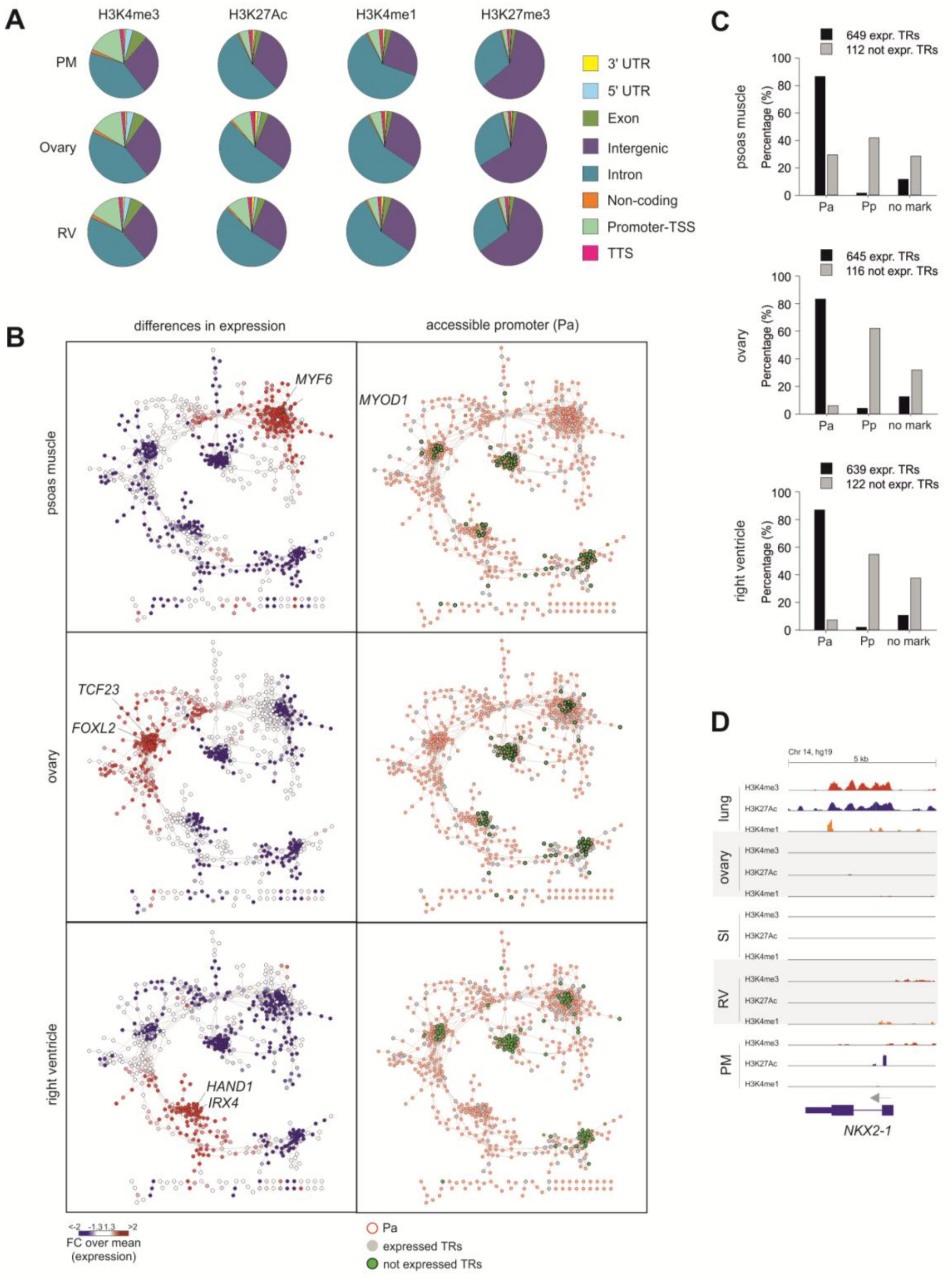

Figure S5: Human tissue-related TR networks show a differential epigenetic regulation of TR loci

(A) Distribution of the histone modifications H3K4me3, H3K27Ac, H3K4me1 and H3K27me3 to genomic regions calculated for each human tissue separately. **(B)** Human tissue-related TR network for psoas muscle, ovary and right ventricle overlaid with information on fold-changes (FC) over the mean expression value (left panel) and promoter status (right panel). Red border: accessible promoters; grey nodes: expressed TRs (cut off for expression ≥10); green: not expressed TRs. **(C)** Bar charts for the distribution of TRs belonging to the tissue-related TR network grouped into expressed (black) and not expressed TRs (grey) with accessible or poised promoter marks. **(D)** Tissue-specific promoter marks for the TF NKX2-1. Consolidated RNA-seq and ChIP-seq data (n=1) of the Road map consortium [5].