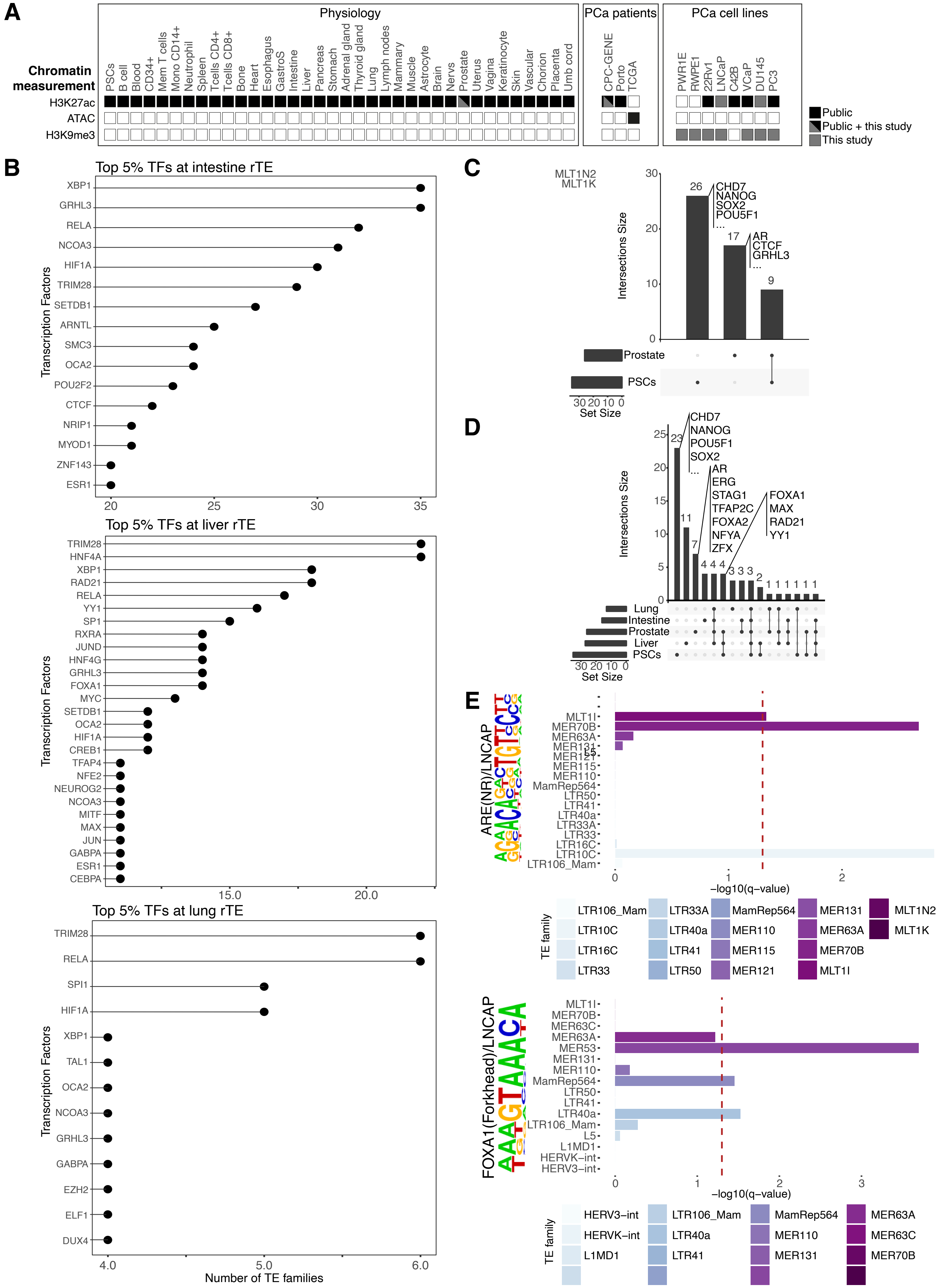
Supplementary Figure S1



Supplementary Figure S1

A. Data roadmap for the present study, showcasing the type of data used in this study.

B. Frequency plot of transcription factor cistromes (TF) enriched at regulatory transposable element families (rTE) enriched in intestine, liver or lung regulatory elements. The top 5% most frequently enriched transcription factor cistromes are shown.

C. UpSet plot showing the intersection of transcription factor cistromes found in the top 5% most frequent cistromes enriched in benign prostate or pluripotent stem cells (PSCs).

D. UpSet plot showing the intersection of transcription factor cistromes found in the top 5% most frequent cistromes enriched in benign prostate, lung, intestine, liver or pluripotent stem cells (PSCs).

E. Enrichment of AR and FOXA1 DNA recognition sequences within transposable element families showing enrichment of AR or FOXA1 cistromes (from Figure 2D). Bars represent $-\log10(\text{q-value})$ for each transposable element family for transcription factor DNA recognition sequences. The red dashed line corresponds to $-\log10(\text{q-value})=1.3$ (q-value=0.05) threshold. q-values correspond to Benjamini corrected p-values.