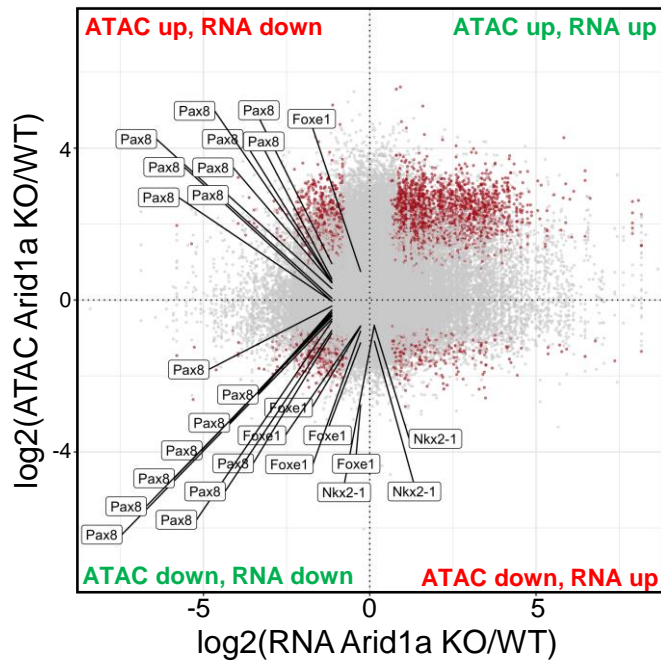
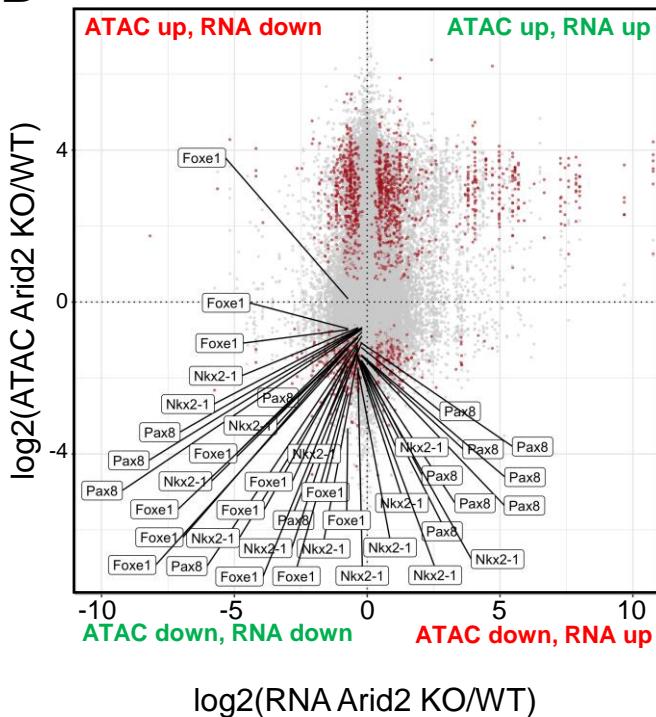
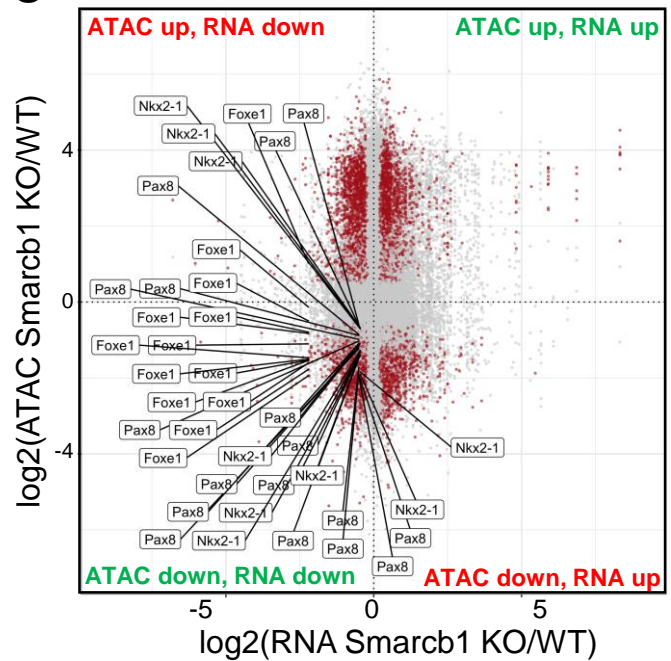


**A****B****C**

**Supplementary Figure S5: Impact of *Arid1a*, *Arid2* and *Smarcb1* loss on thyroid lineage TF expression and chromatin accessibility.** (A) Intersection of RNA-seq and ATAC-seq in YFP-sorted *Arid1a* thyroid cells compared to WT plotted as log<sub>2</sub>-fold change. Each point represents a peak-gene relationship. ATAC peaks with fold-change > 1.5 and FDR adjusted p-value < 0.05 and RNA FDR adjusted p-value < 0.05 are indicated as red dots. Thyroid lineage TFs with RNA-seq or ATAC-seq fold change > 1.5 are highlighted. (B-C) Intersection of RNA-seq and ATAC-seq in *Arid2* KO (B) and *Smarcb1* KO (C) thyroids compared to WT plotted as log<sub>2</sub>-fold change. Scatter plots are labeled as in (A).