**Figure 6** **Integrated analysis reveals multiple important Bcl6 target TF candidates**

(A) Schematic of the integrated analytical approach

(B) Schematic of the SMARTA cell transfer system used for ATAC-seq analysis. Representative flow cytometry of TFH, TH1, TFH-like, and TH1-like subsets.

(C) tSNE analysis of differential ATAC-seq chromatin accessibility

(D) Genome-browser tracks depict ATAC-seq chromatin accessibility, TF occupancy, and corresponding gene expression.

(E) Heatmap plots the frequencies of the most enriched TF motifs in differentially accessible regions.

(F) TF footprints derived from ATAC-seq reads over representative TF motifs within accessible ATAC-seq regions.

(G) Genome-browser tracks depict ATAC-seq chromatin accessibility and TF occupancy.

(H) Gene expression from RNA-seq data (see Fig 4).

(I) Genome-browser tracks depict ChIP-Seq peaks.

(J) Gene expression from RNA-seq data (see Fig 4).