**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 (relatively more open in first group than second group, DEseq2 pval < 0.05).

(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).