# Porcine PBMC chromatin accessibility at single cell resolution

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Identifying cell type specific epigenomic regulatory network of porcine immune cells requires finding the cell type specific regions. We used scATACseq to profile the chromatin accessibility of PBMC cells collected from 2 founder pigs in the US Pig FAANG project. 17,230 nuclei passed quality filtering and a set of 110,444 common accessible peaks were found. We identified 36 clusters of cells with similar patterns of these peaks, using a shared nearest neighbor based clustering algorithm (Seurat/Signac). We identified 20,457 unique differentially accessible peaks (DAPs) that could potentially control cluster-specific gene expression. Gene activity profiles were generated by assigning fragments within 2000 bp of the annotated gene's TSS. Each cluster was classified in 2 ways: (1) by evaluating the predicted gene activity and the chromatin accessibility of DAPs close to genes with known expression in specific immune cell types, and (2) by integrating gene activity with our published PBMC scRNAseq data. We found these two methods have highly concordant annotation results. We found and annotated 14,092 cell type-specific DAPs. Further, GO analysis of genes with DAPs of each cell type identified significantly enriched GO terms highly related to immune functions of the corresponding cell type. Transcription factor (TF) binding motif enrichment analysis on the DAPs of each cell type was performed using HOMER. Our results demonstrate the power of scATAC to identify and annotate cell-type-specific regulatory elements in the porcine immune system. Co-accessibility networks for each cell type could be explored and thus help elucidate mechanisms regulating gene expression.