



Figure 3: Trajectory inference in ionocyte and its two subtypes with differentially expressed genes analyzed in each trajectory. (A) Trajectory inference in all human airway cells: Two lineages (two curves in the plot after t-SNE dimension reduction) are identified with a shared trajectory traversing through basal cells and secretory cells. (B) Trajectory inference in all ionocytes: dots represent two estimated cell states, lines represent the global structure of the lineage. (C) Gene set enrichment analysis results for differentially expressed genes along the ionocyte pseudo-time trajectory. (D) Heatmap of differentially expressed genes along the ionocyte trajectories: The columns are ionocytes ordered by their estimated pseudotime in the ionocyte trajectory. CF/CO status is annotated on the top. (E) & (F) Trajectory inference in ionocyte subtype 0 & subtype 1. (G) & (H). Heatmap of differentially expressed genes along the ionocyte subtype 0 trajectory & subtype 1 trajectory.