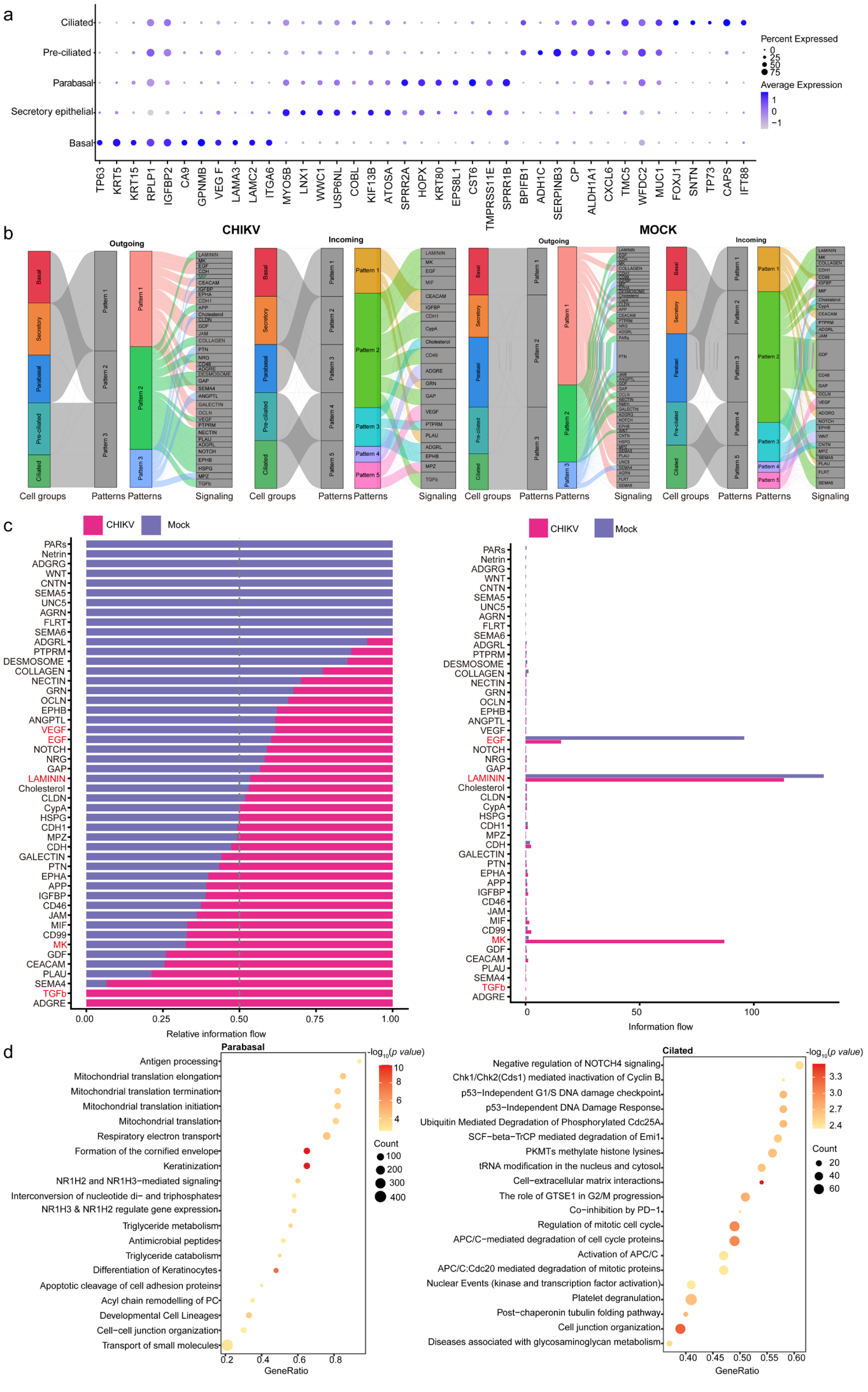
Extended Data Fig. 4



Extended Data Fig. 4 | Validation of epithelial cell identity and perturbation of intercellular communication networks. a, Dot plot visualizing the expression of canonical lineage-specific marker genes defining the five distinct epithelial clusters (Basal, Secretory, Parabasal, Pre-ciliated, and Ciliated) identified in the snRNA-seq dataset. The dot size represents the percentage of cells expressing the marker while the color intensity indicates the average scaled expression level. **b,** Alluvial diagrams comparing the intercellular communication patterns between CHIKV-infected (left) and Mock-infected (right) conditions that map cell groups to their dominant outgoing (secretion) and incoming (reception) signaling patterns and associated pathways using CellChat analysis. **c,** Assessment of global signaling pathway alterations in which the left panel shows the relative information flow (stacked bars) for significant signaling pathways (CHIKV-enriched pathways in pink; Mock-enriched pathways in purple). The right panel displays the absolute information flow strength for selected pathways highlighting the loss of homeostatic signals (such as EGF, WNT, and LAMININ) and the emergence of stress-associated signals (including MK, TGF-β, and SEMA4) upon infection. **d,** Dot plots showing the functional enrichment analysis (KEGG) for Parabasal (left) and Ciliated (right) cell populations. The analysis highlights metabolic and structural perturbations in parabasal cells and DNA damage response pathways in ciliated cells. Dot size indicates the gene count and the color gradient represents statistical significance (−log10 P value).