

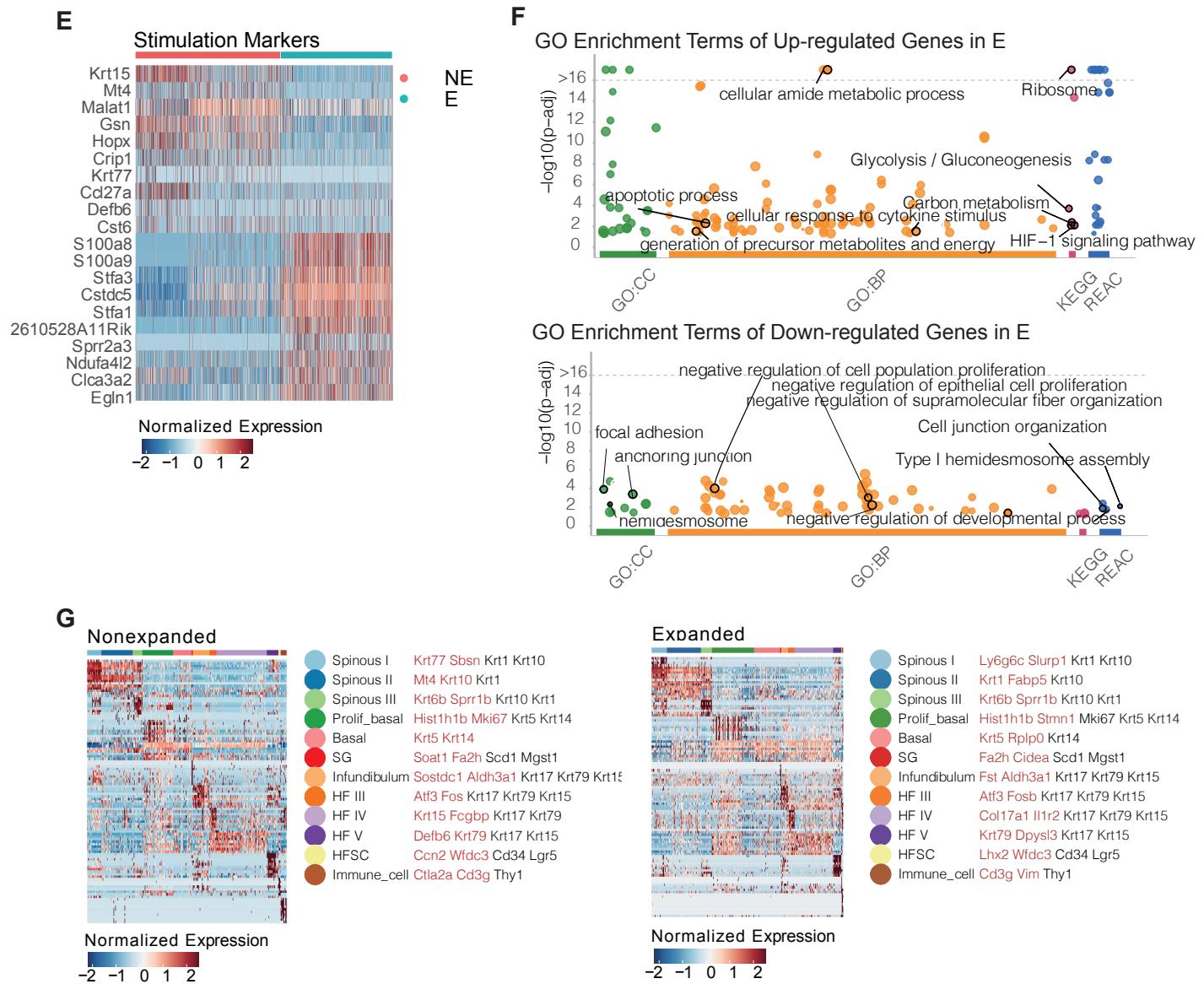
**Figure 1. scRNA-seq reveals different skin cell types and their change during skin expansion**

**A)** UMAP plot for full epidermal cells in NE and E showing 12 cell clusters (n<sub>NE</sub>=8,479, n<sub>E</sub>=6,570). Colors corresponding to cell types on the right.

**B)** Bar plot illustrating cell components in each sample. Chi-square test was performed (\*p < 0.05; \*\*p < 0.005; \*\*\*p < 0.0005).

**C)** Feature plot showing the expression level of established cell type markers used to identify cell clusters.

**D)** Bar plot illustrating cell phase constitution in each sample. Chi-square test was performed (\*p < 0.05; \*\*p < 0.005; \*\*\*p < 0.0005).

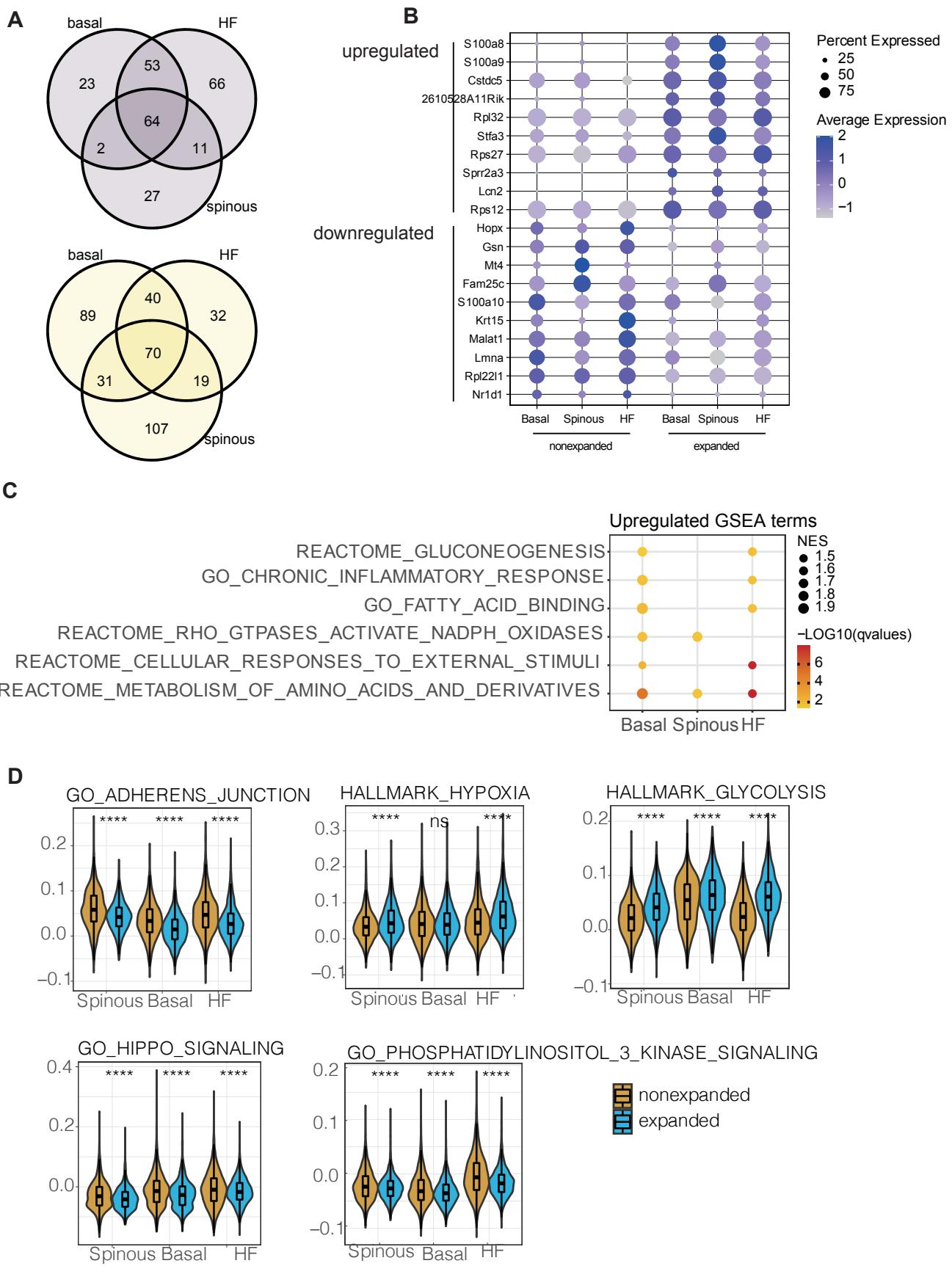


**Figure 1 (con'd). scRNA-seq reveals different skin cell types and their change during skin expansion**  
**E**) Heatmap for the top 10 condition feature gene in NE and E sample.

**F**) Manhattan plot highlighted the selected GO terms using top E up-regulated genes (up, 171 DEGs), and down-regulated genes (down, 77 DEGs).

**G**) Heatmaps for the top10 cluster feature genes (top10) in NE and E sample

Genes listed in black represent the top two marker genes for each cluster, whereas those in red represent the additional genes used in the final identification of the cluster cell type.



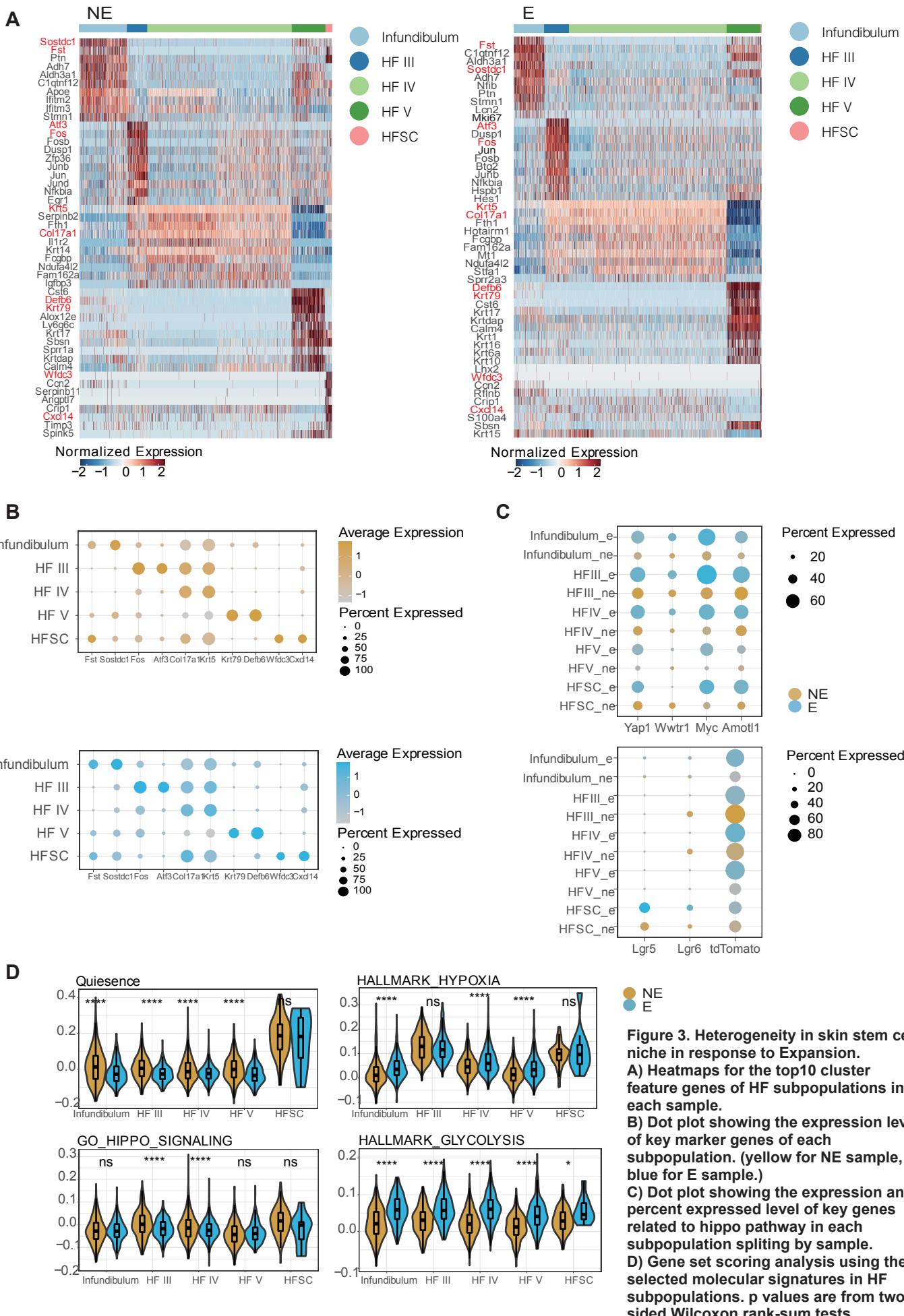
**Figure 2. Deconstruction expansion state in epithelial cell clusters.**

A) Venn plot displaying the number of shared upregulated (up) and downregulated (down) DEGs (DEGs,  $|avg\_logFC| > 0.25$  and  $p\_val\_adj < 0.05$ ) between epithelial main cell types.

B) Dot plot highlighted the top 10 shared feature genes between DEGs (DEGs,  $|avg\_logFC| > 0.25$  and  $p\_val\_adj < 0.05$ ) between epithelial main cell types.

C) Representative shared GO terms of expansion-associated DEGs in epithelial main cell types. “NES” indicates the normalized enrichment score. The color bar from yellow to red indicate the range of -log q values.

D) Gene set scoring analysis using the selected molecular signatures in main epithelial cell type. p values are from two-sided Wilcoxon rank-sum tests.



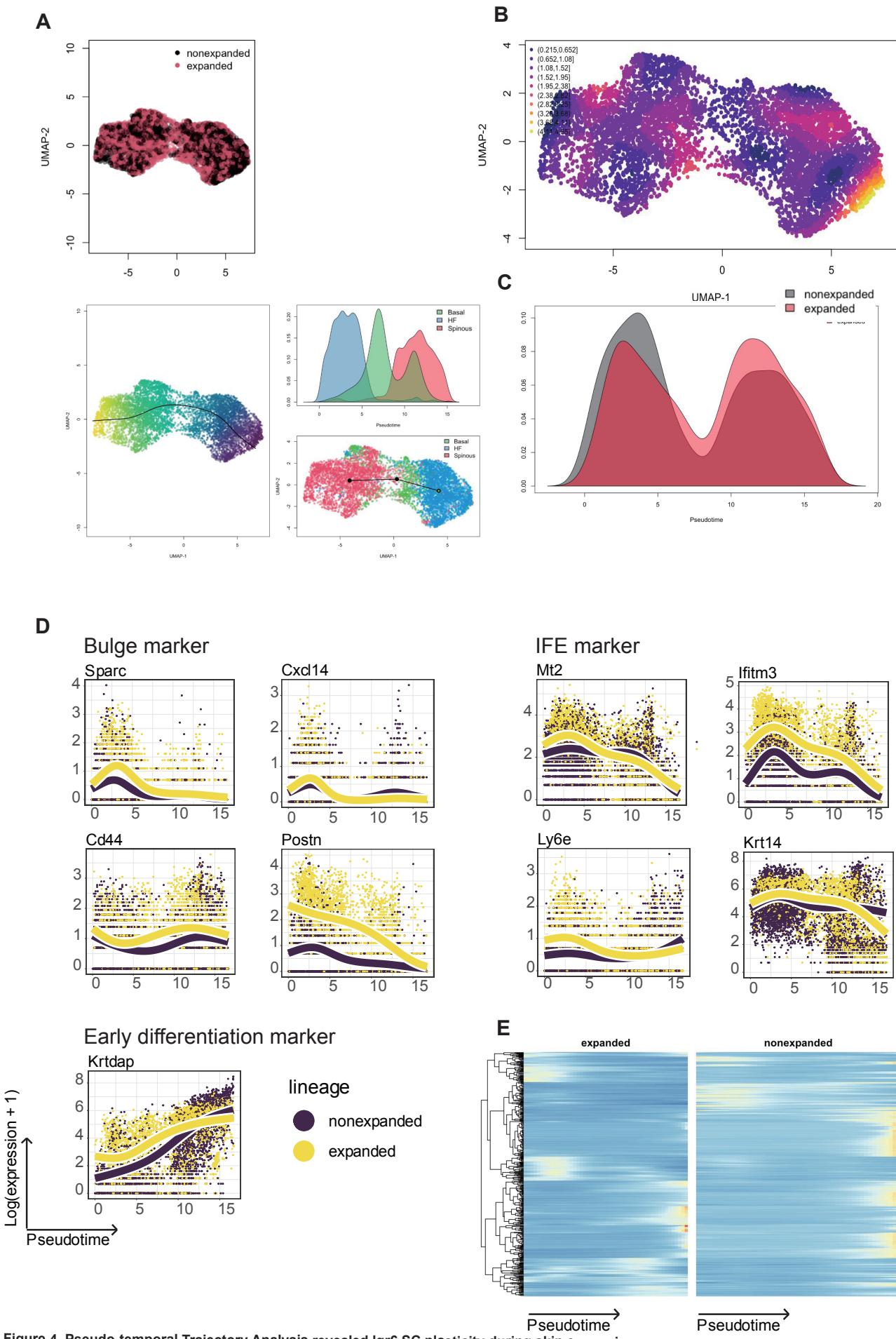


Figure 4. Pseudo-temporal Trajectory Analysis revealed Igr6 SC plasticity during skin expansion.

A) Distribution of Igr6 progenitor and Igr6 progenies on UMAP colored by condition/cell type. Distribution of cells along the inferred trajectory.

B) Distribution of Imbalance score on UMAP, showing the balancedness on the global development path.

C) Density estimation of Igr6 progenitor and Igr6 progenies along the inferred pseudo-time.

D) Expression pattern of selected bulge/IFE/differentiation markers in Igr6 progenitor and Igr6 progenies cells with trajectory.

E) heatmaps of the genes DE between conditions. The DE genes are ordered according to hierarchical clustering on the E condition.