

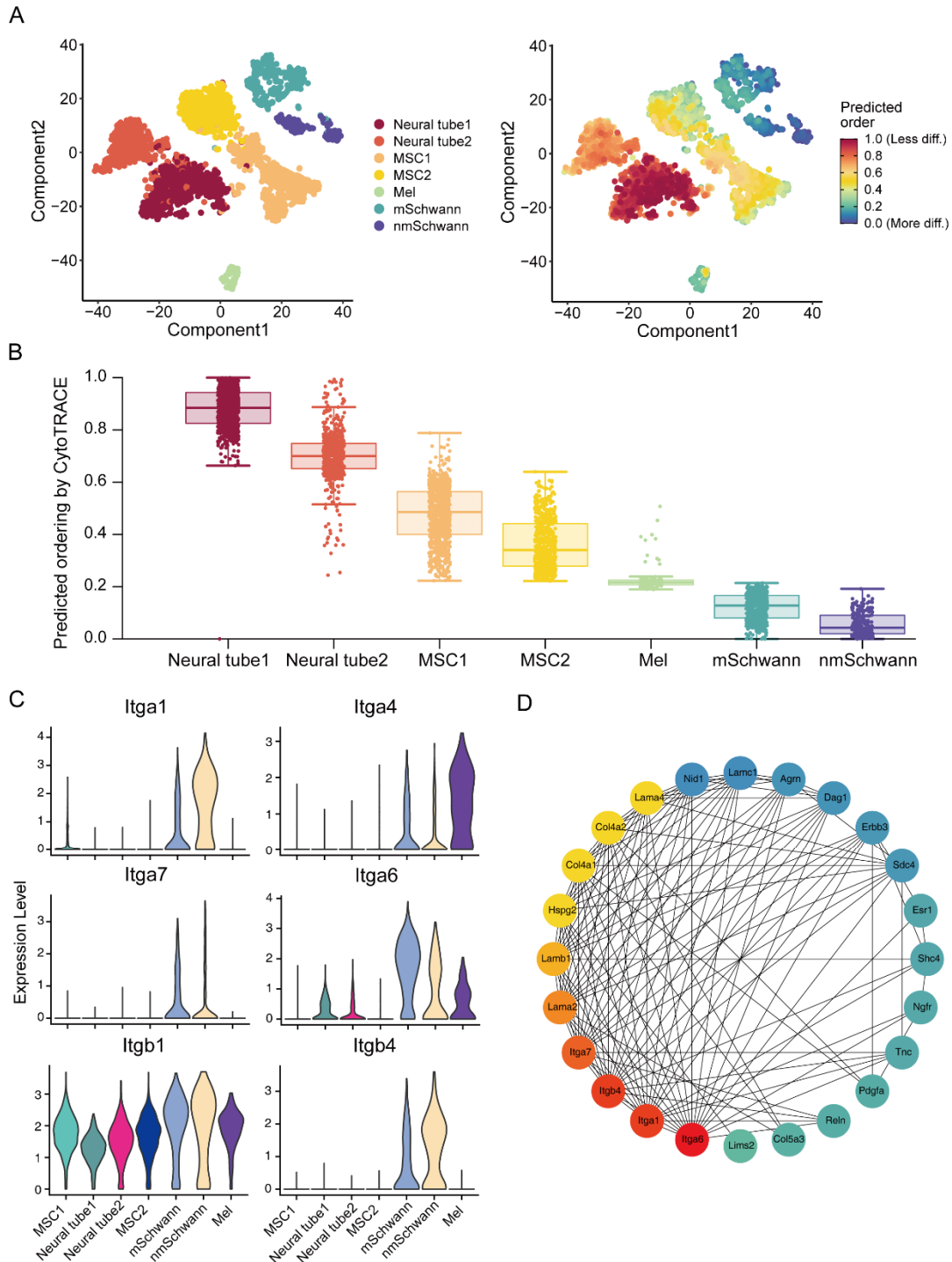
Supplementary Material

Developmentally Regulated Expression of Integrin Alpha-6 Distinguishes Neural Crest Derivatives in the Skin

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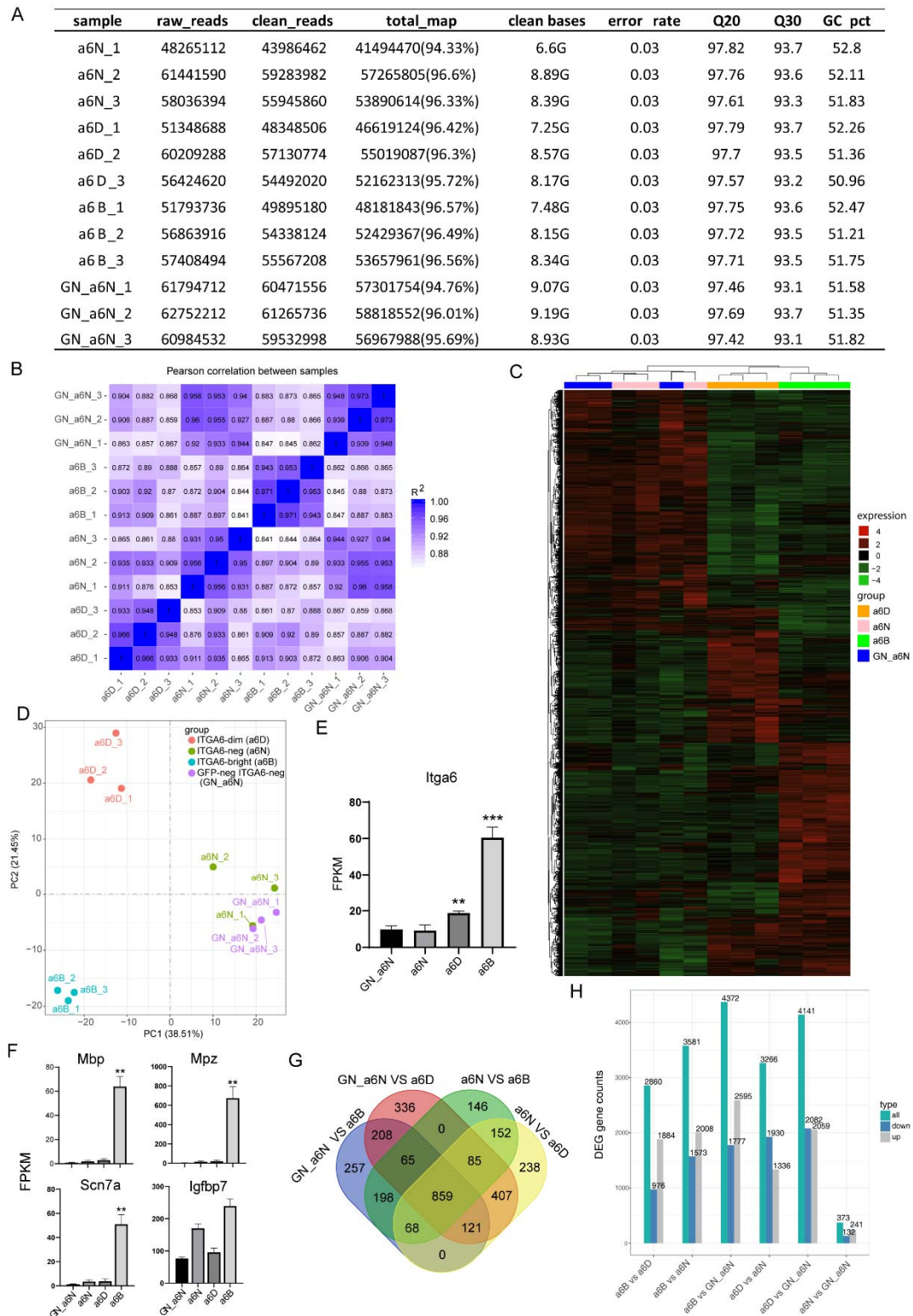
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Supplementary Figures



Supplement Figure 1. CytoTRACE analysis of cell state and expressions of Integrins among cell clusters.

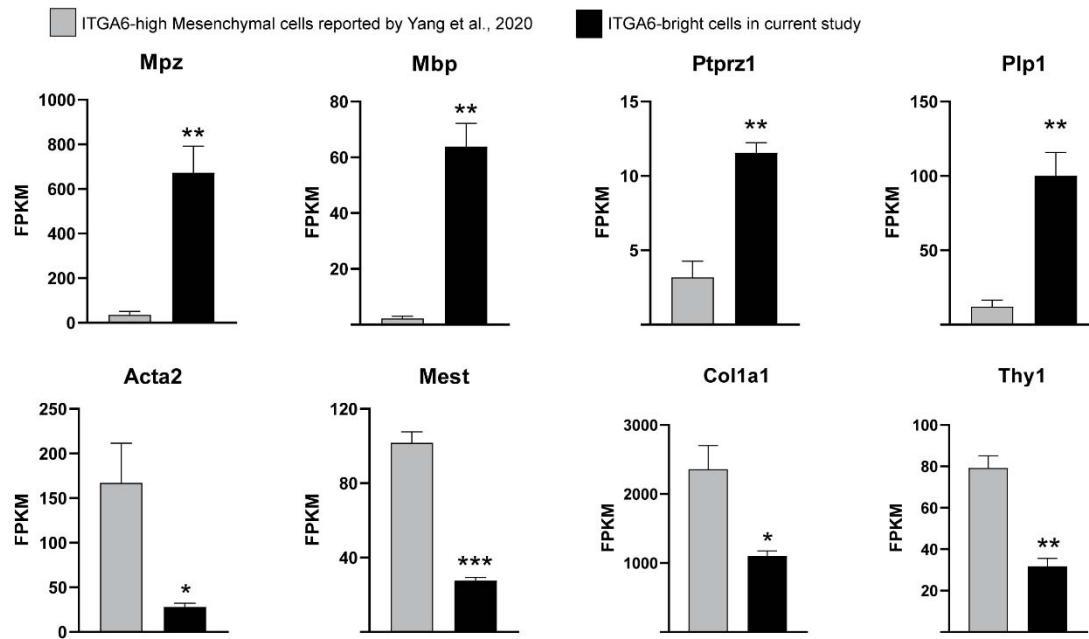
A, CytoTRACE analysis to predict the differentiation status of the seven cell clusters. In the architecture, highly differentiated cells have low transcriptional diversity and low CytoTRACE scores, while less differentiated cells have high transcriptional diversity and high scores. B, Boxplot showing the progressively decreasing differentiation ordering predicted by CytoTRACE. C, Violin plots showing the expression levels of integrins that dynamically changed during pseudotime analysis. D, PPI network of ECM-receptor interaction related genes. The colors ranging from red to yellow indicate the ten most significant hub genes with degree measurement from high to low among these molecules.



Supplement Figure 2. Overview of RNA-seq data.

A, Summary of the sequence quality, reads number and mapping results for transcriptomic analysis of ITGA6^{bright}, ITGA6^{dim}, ITGA6^{neg}, and GFP^{neg}ITGA6^{neg} cells subpopulations. B, Heatmap of Pearson's correlation coefficient for gene expression profiles of the 4 subpopulations. C&D, Hierarchical clustering and PCA

analysis showing the distinctive features of these subpopulations. E, FPKM values of *Itga6* in different cell subpopulations; *, compared with a6N, **p < 0.01; ***p < 0.001. F, FPKM values of *Mbp*, *Mpz*, *Scn7a*, *Igfbp7* in different cell subpopulations; *, compared with a6N, **p < 0.01. G, Venn diagram showing the numbers of common DEGs among the four different comparison groups. H, Bar graphs showing the numbers of DEGs between different groups of cells.



Supplement Figure 3. Differential gene expressions between ITGA6-high mesenchymal cells (Yang et al., 2020) and Wnt1-lineage derived ITGA6-bright cells.