



Fig.S2 Quality control metrics of single cell RNA-sequencing data from human skin epidermal cells. **a, e** Pruning of cells with abnormal gene numbers ($350 > \text{genes}/\text{cell} < 5,000$; high mitochondrial gene percentage ($< 10\%$)) and outliers. Demarcated blue and red lines mark cut-offs for abnormal gene numbers and high mitochondrial gene percentage. Outliers are represented as red circles falling outside of fitted quadratic model. Valid cells were used for downstream analyses. **b, f** Violin plots showing distribution of features and counts expression levels, and mitochondrial gene percentage in valid cells used for downstream analyses. **c, g** Correlation plot between features and counts in valid cells. **d, h** Frequency distribution of Log-transformed features in valid cells.