

## **Supplementary Data legends**

**Supplementary Data 1. Gene expression in each cell cluster identified by Seurat in healthy human skin.** Table indicating the most representative genes of each cluster, identified by comparing the gene expression of each cluster against all others in the integrated skin dataset (n=5). Only genes with a p-value < 0.05 and a fold-change > 1.25 are included.

**Supplementary Data 2. Genes expressed by the four fibroblast subpopulations in young samples.** Table indicating the most representative genes of each fibroblast subpopulation, identified by comparing the gene expression of each subpopulation against all the other clusters in the young dataset (n=2). Only genes with a p-value < 0.05 and a fold-change > 1.25 are included.

**Supplementary Data 3. Genes expressed by fibroblast subpopulations (second-level analysis) in young samples.** Table indicating the most representative genes of each fibroblast subpopulation, identified by comparing the gene expression of each cluster against all the other clusters present in the second-level analysis of young fibroblasts. Only genes with a p-value < 0.05 and a fold-change > 1.25 are included.

**Supplementary Data 4. Genes expressed by the four fibroblast subpopulations in old samples.** Table indicating the most representative genes of each fibroblast subpopulation, identified by comparing the gene expression of each subpopulation against all other clusters in the old skin dataset (n=3). Only genes with a p-value < 0.05 and a fold-change > 1.25 are included.

**Supplementary Data 5. Genes with age-related differential expression in each fibroblast subpopulation.** Table indicating the up- and down-regulated genes in each fibroblast subpopulation upon aging. Gene lists were determined by comparing the gene expression between young and old fibroblasts from each subpopulation. Only genes with a p-value < 0.05 and a fold-change > 1.25 are included.