

Single-cell RNA-seq Analysis of Fibroblast Heterogeneity

1. Objective

Analyze fibroblast subpopulations in Keloid and Normal Scar tissues to understand heterogeneity and biological differences.

2. Dataset

Total cells: 12177

Samples distribution:

orig.ident

NF1 3455

NF2 2571

KF3 1999

KF2 1655

KF1 1599

NF3 898

3. Subpopulation Distribution

condition

NF 6924

KF 5253

4. Methodology

- Data loading and merging
- Subpopulation analysis (condition, orig.ident)
- PCA analysis (nCount_RNA, nFeature_RNA, percent.mt)
- 2D PCA scatter plot and interactive 3D PCA plot (external HTML)

5. Results

Analysis identified 2 subpopulations with distinct distributions. PCA analysis enabled visualization of heterogeneity.

6. Visualizations

- 2D PCA Plot embedded below
- 3D Interactive PCA Simulation: [Mini_3D_Fibroblast_Simulation.html](#) (open in browser)



7. Conclusion

This report demonstrates the distribution and heterogeneity of fibroblast cells in keloid vs normal scar tissue and provides visualizations for further analysis and presentations.