

Heterogeneity in old fibroblasts is linked to variability in reprogramming and wound healing

Nature. 2019 Oct;574(7779):553-558. doi: 10.1038/s41586-019-1658-5. Epub 2019 Oct 23.

Mahmoudi S1, Mancini E1, Xu L1,2, Moore A3,4, Jahanbani F1, Hebestreit K1, Srinivasan R4,5, Li X1, Devarajan K1, Prélôt L1, Ang CE4,6,7, Shibuya Y4,7, Benayoun BA1,8, Chang ALS9, Wernig M4,7, Wysocka J4,5, Longaker MT3,4, Snyder MP1, Brunet A10,11.

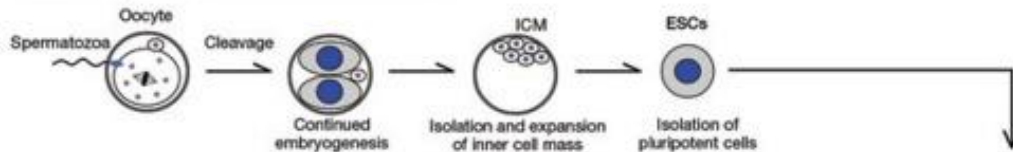
Methods

- C57/Bl6
- Young mice: 3 months
- Old mice: 28-29 months
- Mouse FBs: Primary FB isolation from young and old mice from skin, ears and lungs, isolated with Liberase
- Human FBs: Primary FBs from male volunteers of different ages with four biological grandparents of Ashkenazi Jewish descent; 4mm pre-auricular punch biopsy
- Cytokine profiling: 24h plating of cells in serum- and feeder-free medium; Luminex multi-analyte human and mouse assay
- Cellular reprogramming: lentiviral vector *OCT4*, *KLF4*, *SOX2*, *MYC*; Virus produced in human HEK293T-cells by PEI-transfection

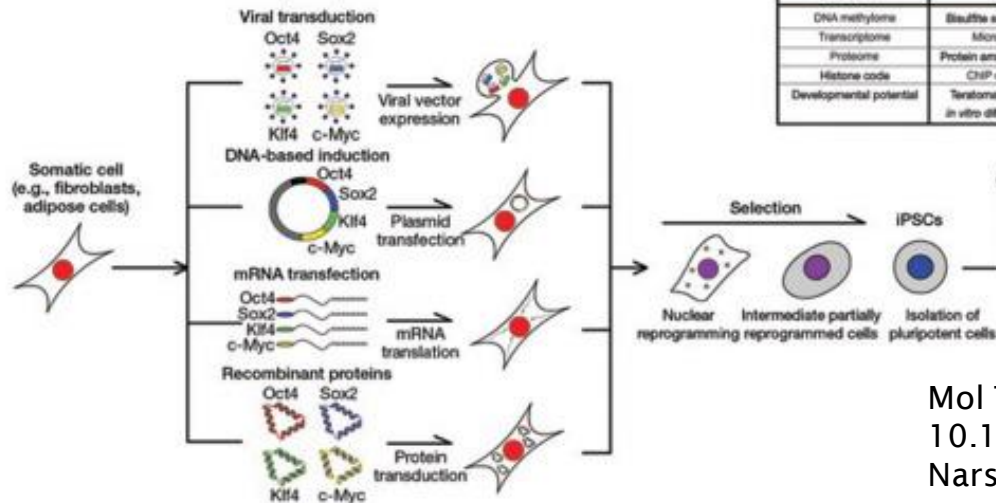
Methods: Reprogramming/ iPS-generation

- Takahashi, Yamanaka: Induction of Pluripotent Stem Cells from Mouse Embryonic and Adult Fibroblast Cultures by Defined Factors. Cell 2006
- “Yamanaka-Cocktail” = 4 transcription factors (TF) to reprogram cells into induced pluripotent stem cells: *OCT4*, *KLF4*, *SOX2*, *MYC*

a Embryonic stem cell derivation



b Methods of induced pluripotent stem cell derivation



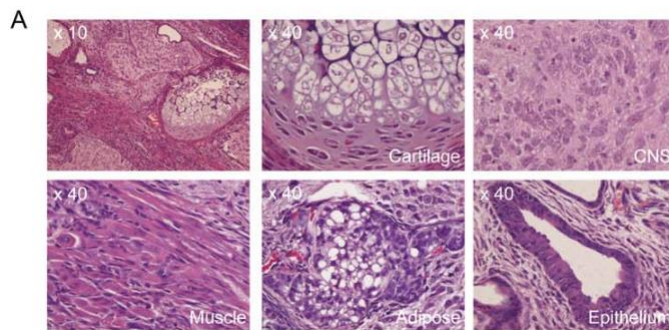
Techniques to compare and assess equivalence of ESCs and iPSCs	
Assessment	Test
DNA methylome	Bisulfite sequencing
Transcriptome	Microarray
Proteome	Protein array or 2D gel
Histone code	ChIP on chip
Developmental potential	Teratoma formation in vitro differentiation

Mol Ther. 2011 Apr;19(4):635-8. doi: 10.1038/mt.2011.41.
Narsinh KH1, Plews J, Wu JC.

Methods: Reprogramming/ iPS-generation

How to reprogram:

- Generate (e.g. in HEK-cells) or buy virus containing desired transcription factors
- Plate e.g. FBs, add virus + Polybrene (to enhance infection);
- plate cells with irradiated feeder cells
- Switch to embryonic stem cell medium
- After 13-15d, assess cells for distinct mES morphology, plate each iPS clone individually
- Assess for reprogramming efficiency: staining for AP and SSEA1 (markers for pluripotency)



Takashi, Yamanka, Cell 2006

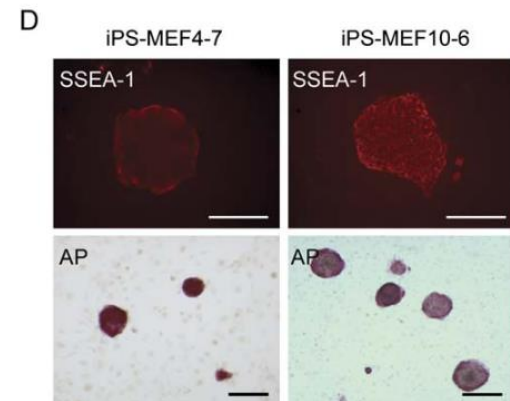


Fig. 1: Primary fibroblasts from old mice secrete inflammatory cytokines and show increased variability in reprogramming efficiency between mice.

Assessing reprogramming efficiency

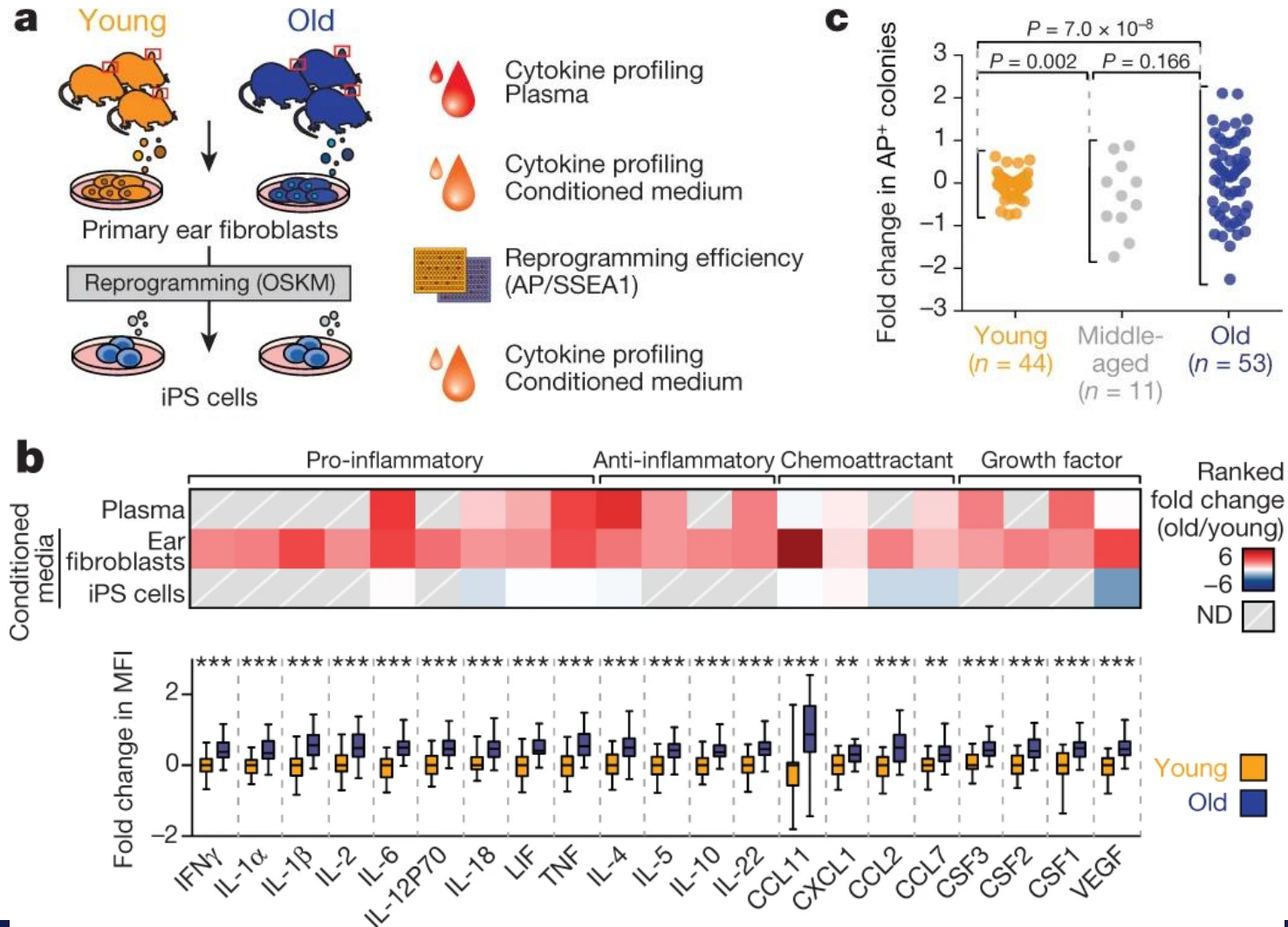


Fig. 2: Old fibroblast cultures exhibit a signature of an inflammatory activated state, which is associated with variability in reprogramming efficiency.

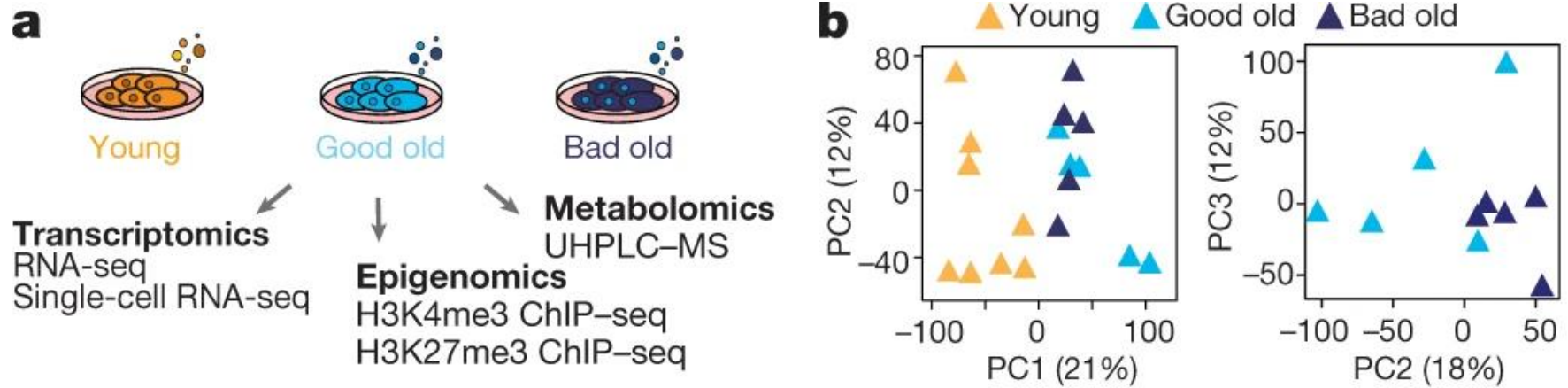
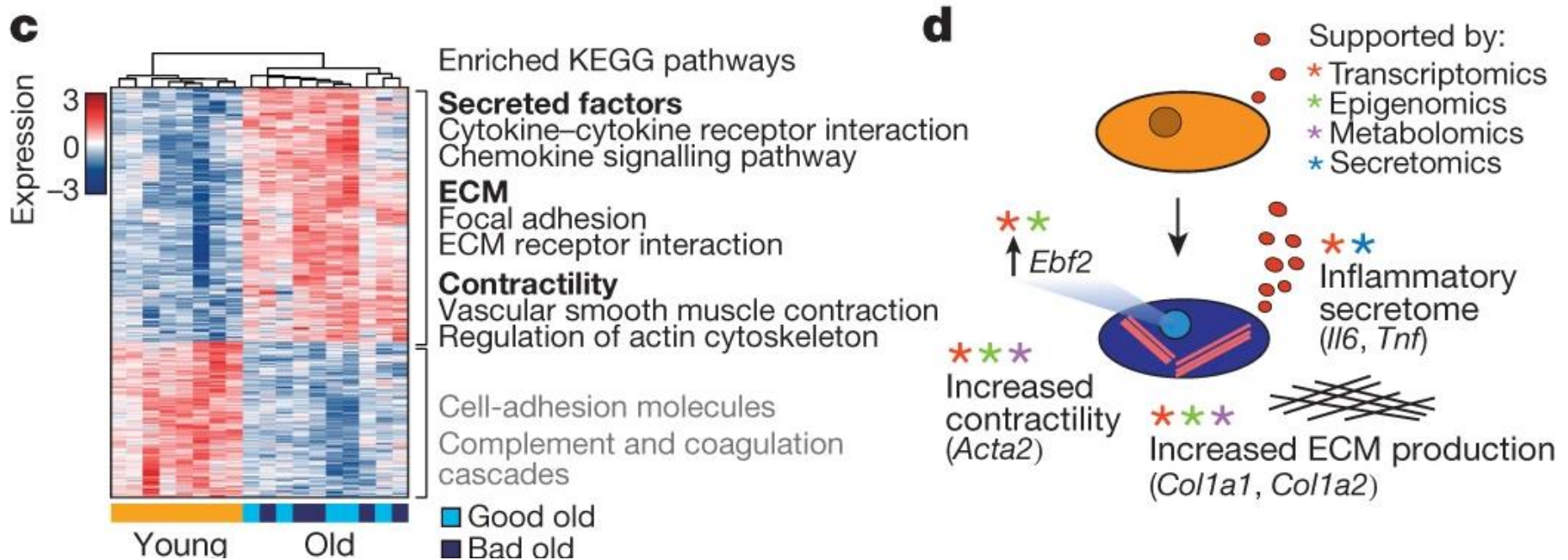


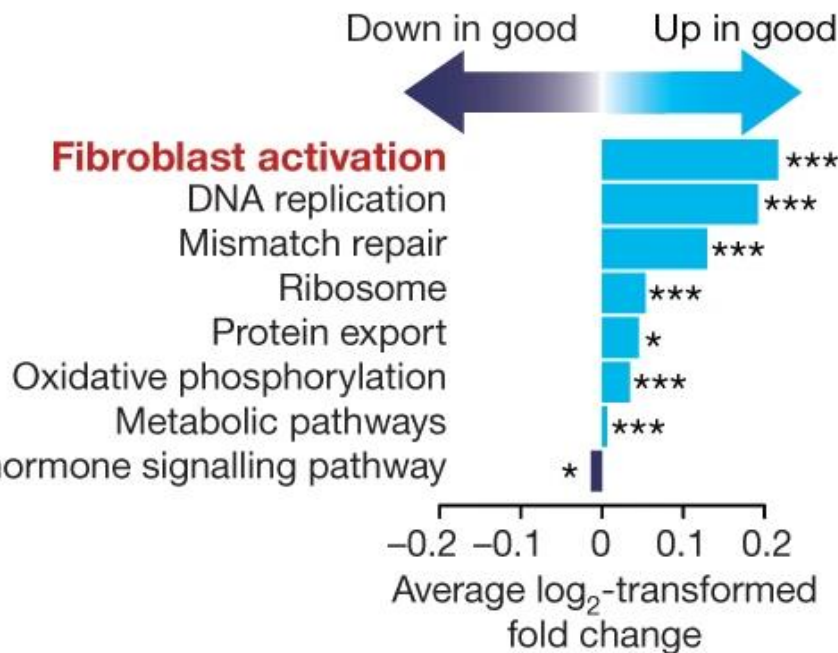
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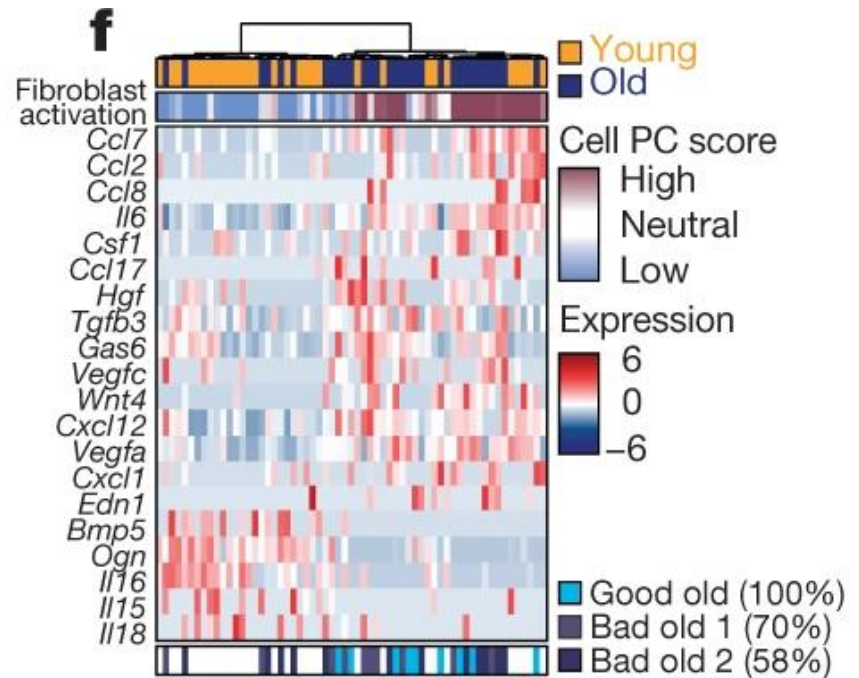
EBF2 = potential driver for FB activation

Fig. 2: Old fibroblast cultures exhibit a signature of an inflammatory activated state, which is associated with variability in reprogramming efficiency.

Pathway analysis of FBs with good or bad reprogramming



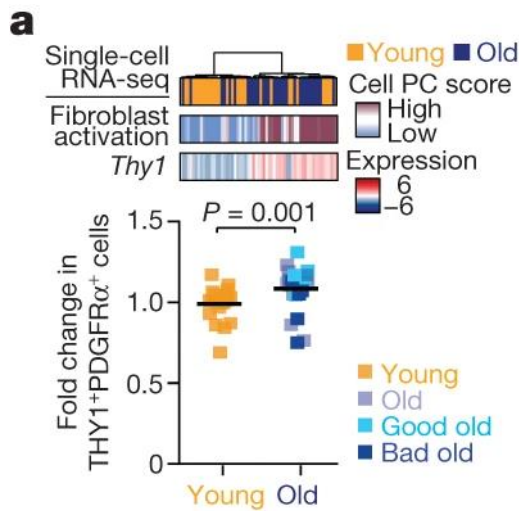
PAGODA-analysis of scRNAseq from young, good and bad old FBs



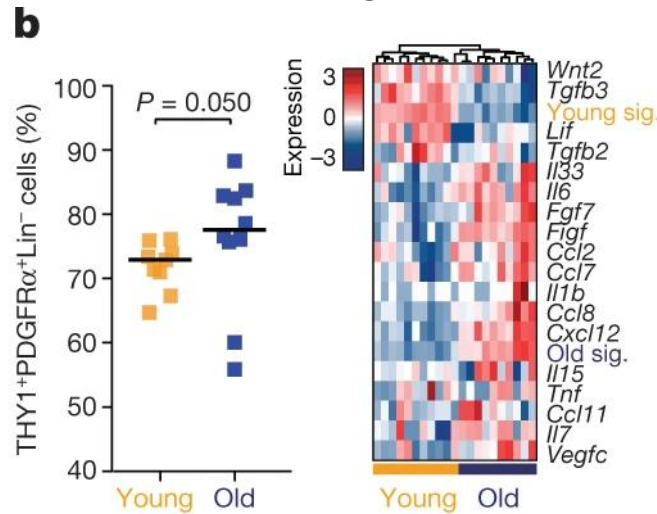
- Old FBs → more „activated FBs“
- Activated FBs = better reprogramming
- Activated FBs = myofibroblasts = profibrogenic
- Activated FBs = proliferate, no senescence markers (Figure E5b-e)

Figure 3: Age-associated increase in activated fibroblasts and the cytokines that they secrete drive part of the variability in reprogramming between mice.

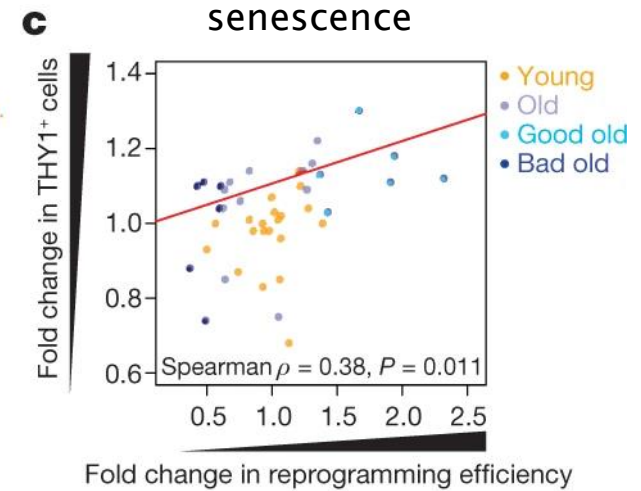
Old FBs contain more *Thy1*⁺ FBs, and express more *Ebf2*



More *Thy1*⁺ in ears of old mice and higher FB activation signature



Better reprogramming = more *THY1*⁺, more proliferation, less senescence



THY1 = activation marker,
PDGFR α = FB-marker

Figure 3: Age-associated increase in activated fibroblasts and the cytokines that they secrete drive part of the variability in reprogramming between mice.

Conditioned medium (CM) from activated (=THY1+) FB enhanced reprogramming

Swapping of CM reduces differences in reprogramming efficiency

IL6 enhances & TNF reduces reprogramming efficiency

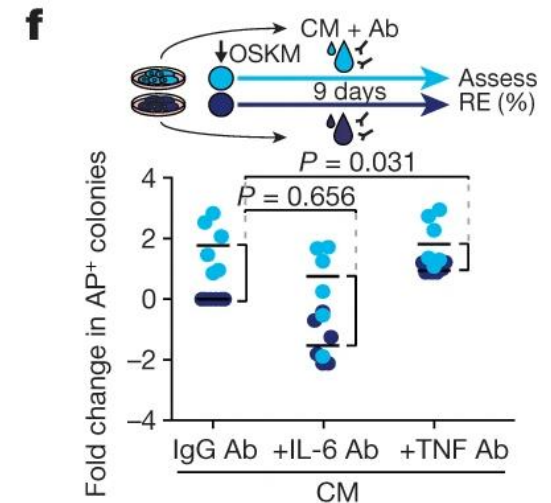
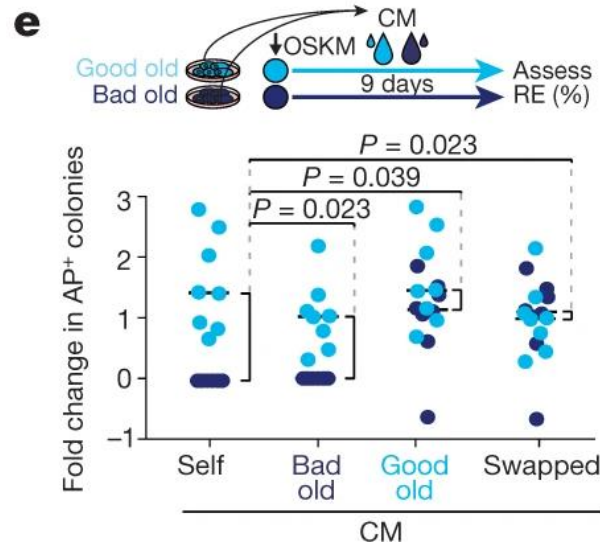
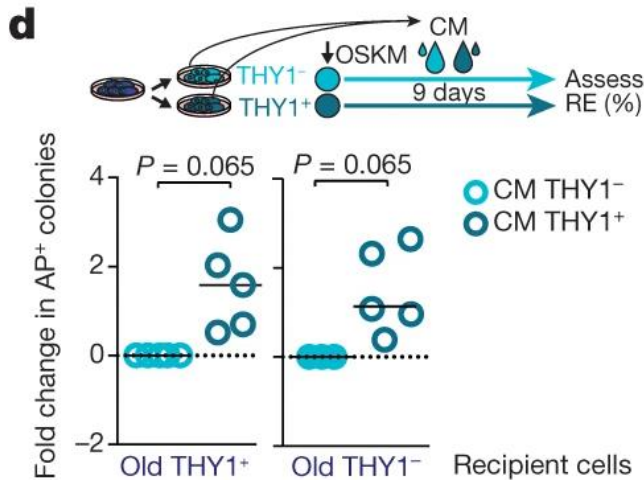


Figure 3: Age-associated increase in activated fibroblasts and the cytokines that they secrete drive part of the variability in reprogramming between mice.

IL6:TNF correlates with RE

Activated:non-activated FB and their cytokines drive variability between FB cultures in old mice

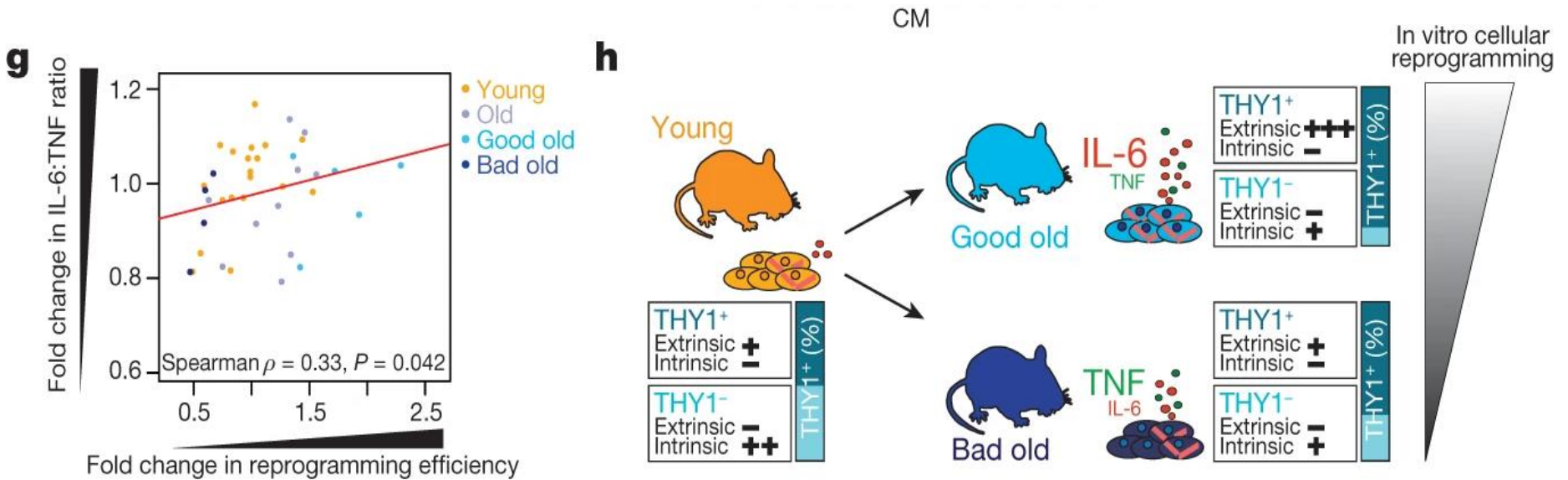
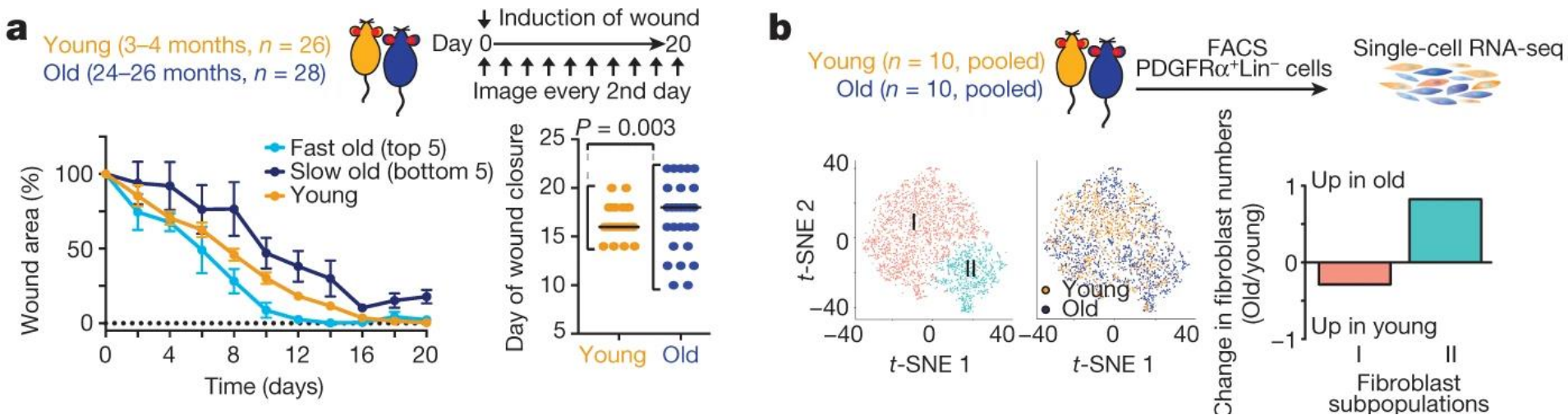
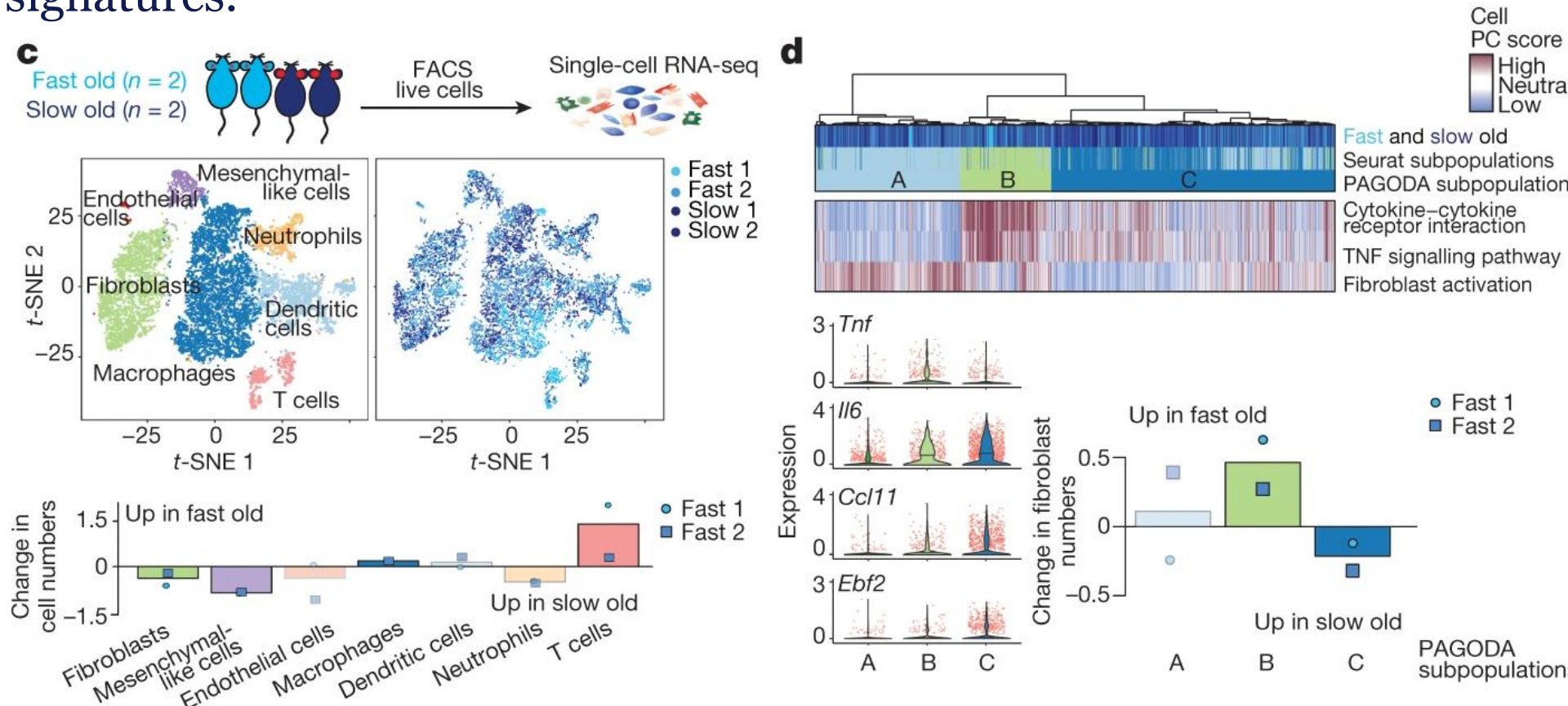


Figure 4: Wound healing rate is variable between old mice and correlates with fibroblast subpopulations with distinct cytokine signatures.



Increased variability
in wound healing rate
old vs young

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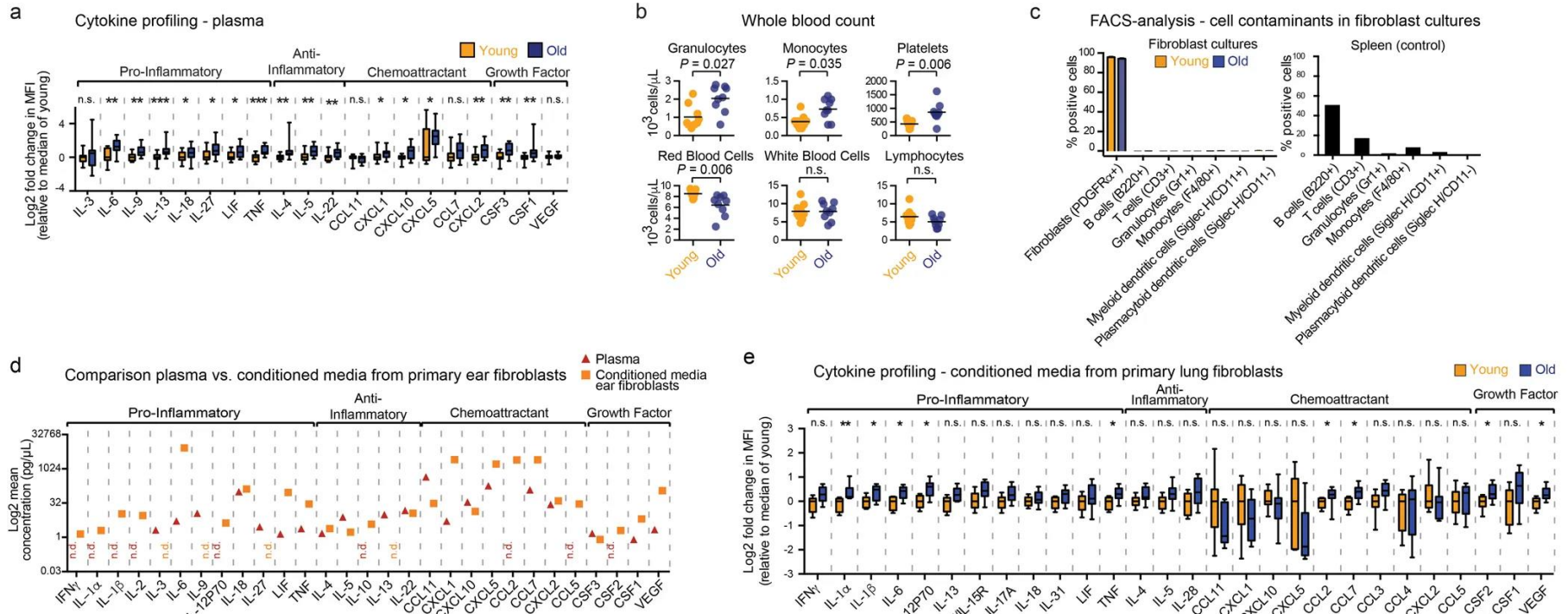
- B more abundant in fast healing old,
- Increased cytokine expression: TNF up →
- TNF associated with fast wound healing + bad reprogramming

- C more in slow healing old, higher in other cytokines, e.g. *Ccl11*
- Higher in TF *Ebf2*

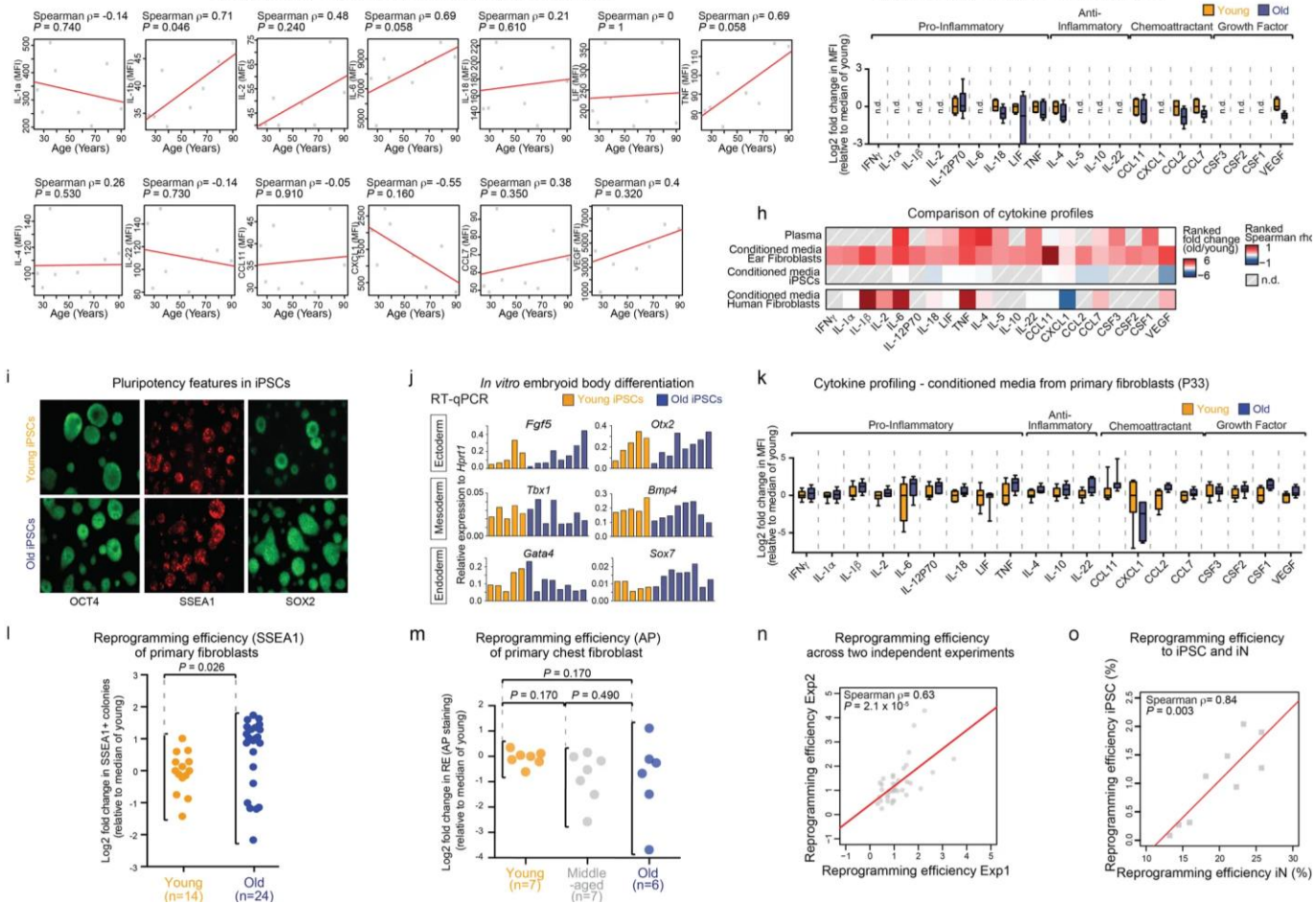
Discussion

- Conclusive story?
- Relevance?
 - There is no iPS-induction (?)/reprogramming in vivo?!
 - Only technical relevance?
- Would you rather have fibrosis or senescence?

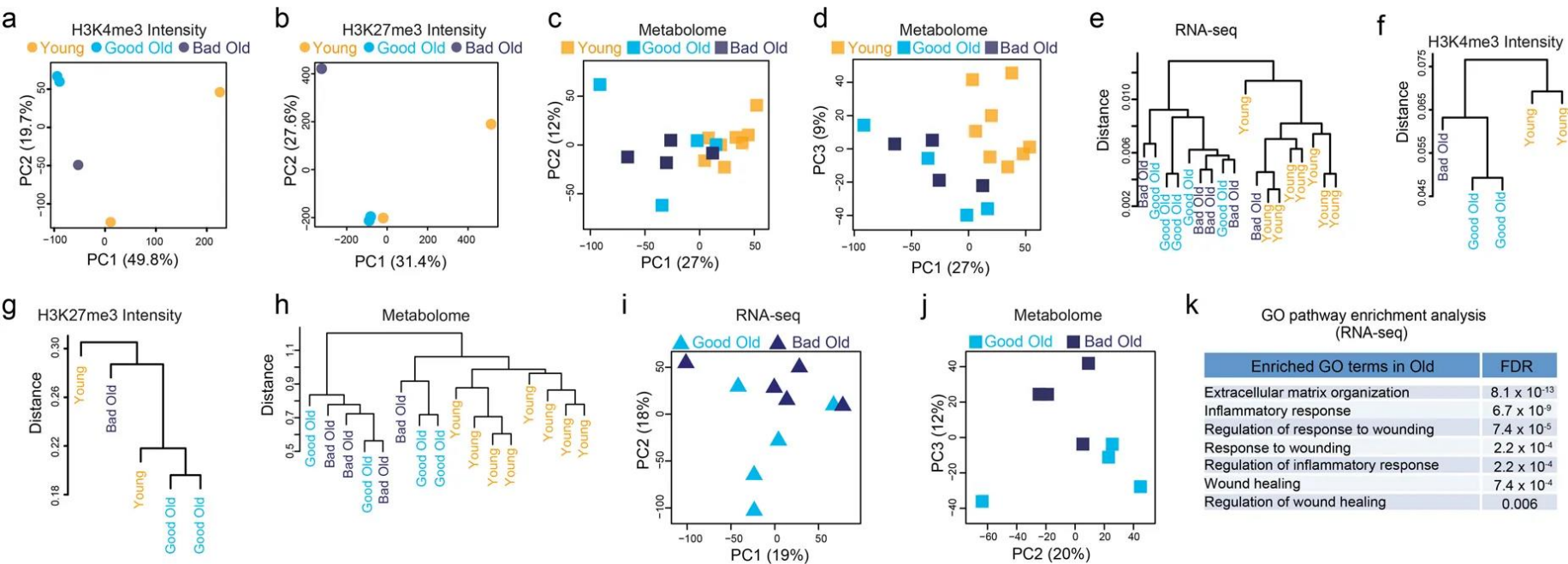
Extended Data 1: Extended Data Fig. 1 Primary old fibroblasts from mouse ear, mouse lungs and human skin secrete high levels of inflammatory cytokines, and the ability of individual cultures from ear fibroblasts to reprogram is stereotypical.



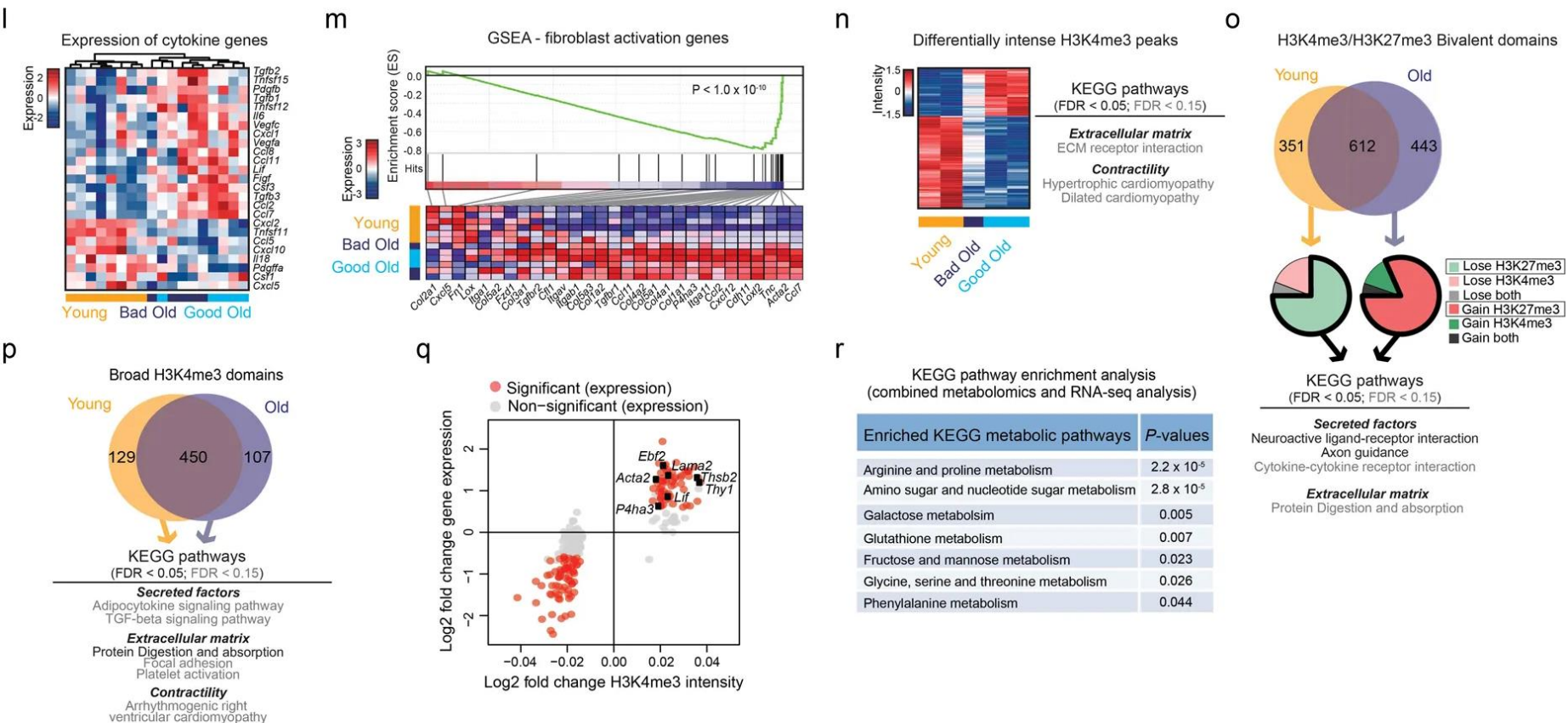
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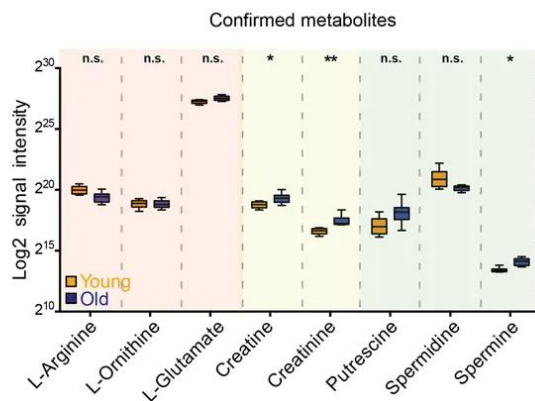


Extended Data Fig. 2 Old fibroblasts exhibit distinct transcriptomic, epigenomic and metabolomics profiles compared to young fibroblasts.

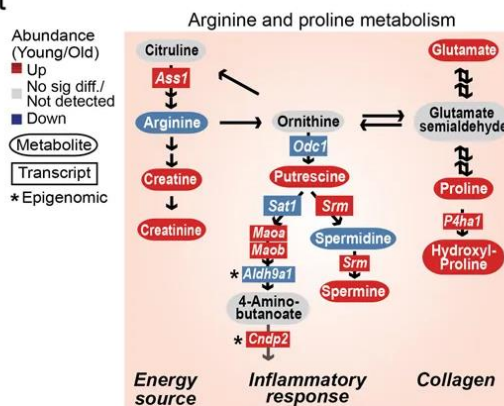


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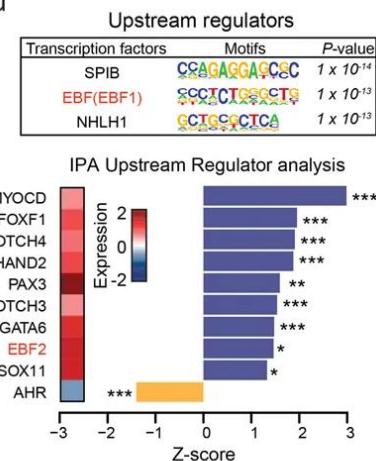
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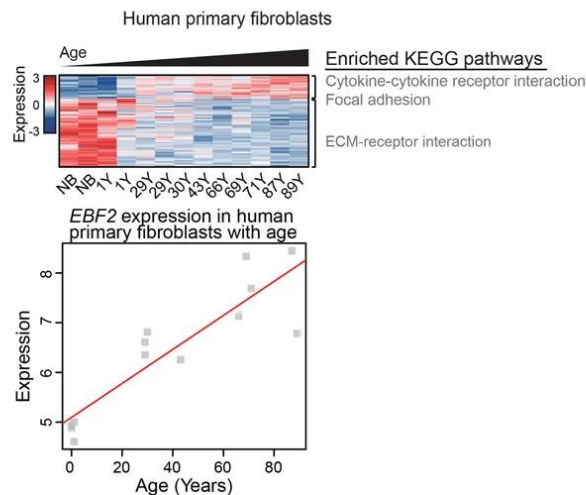
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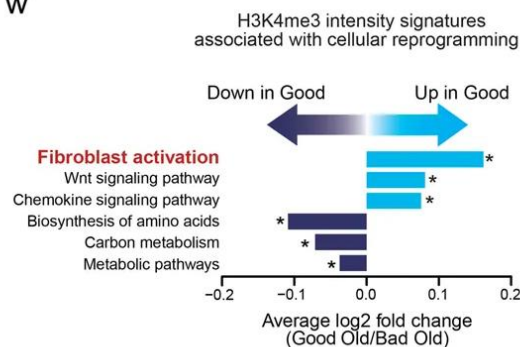
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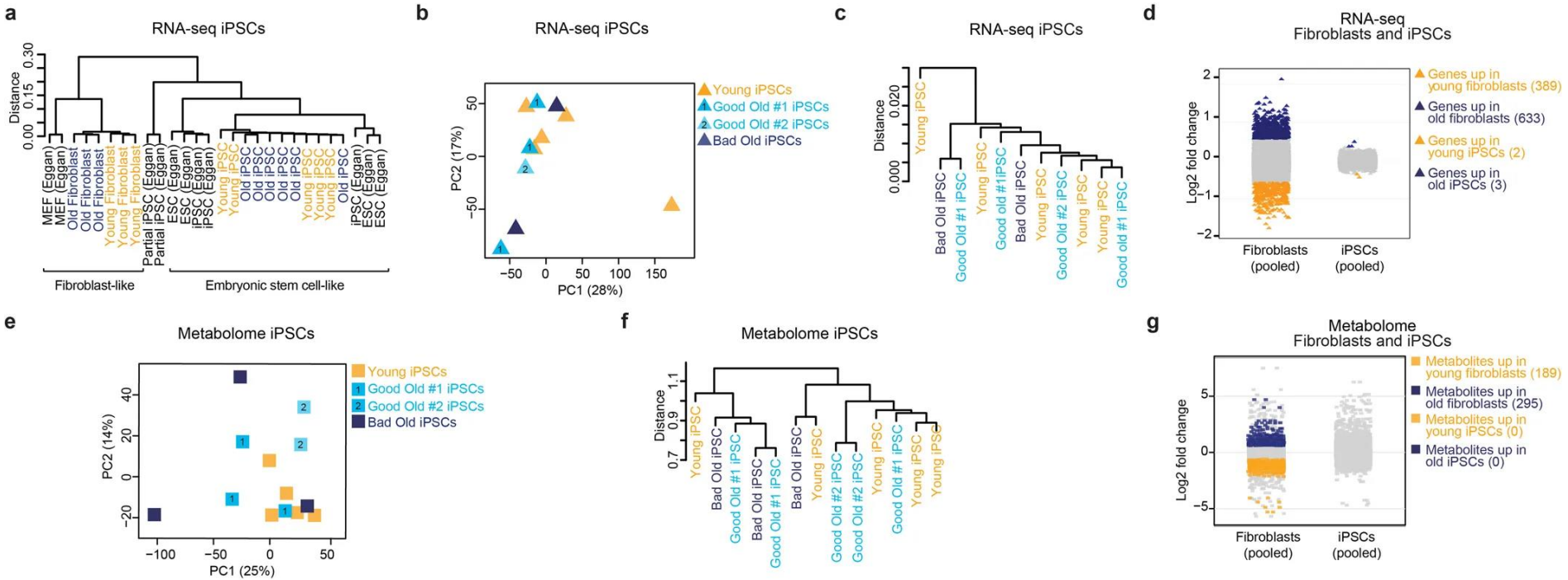
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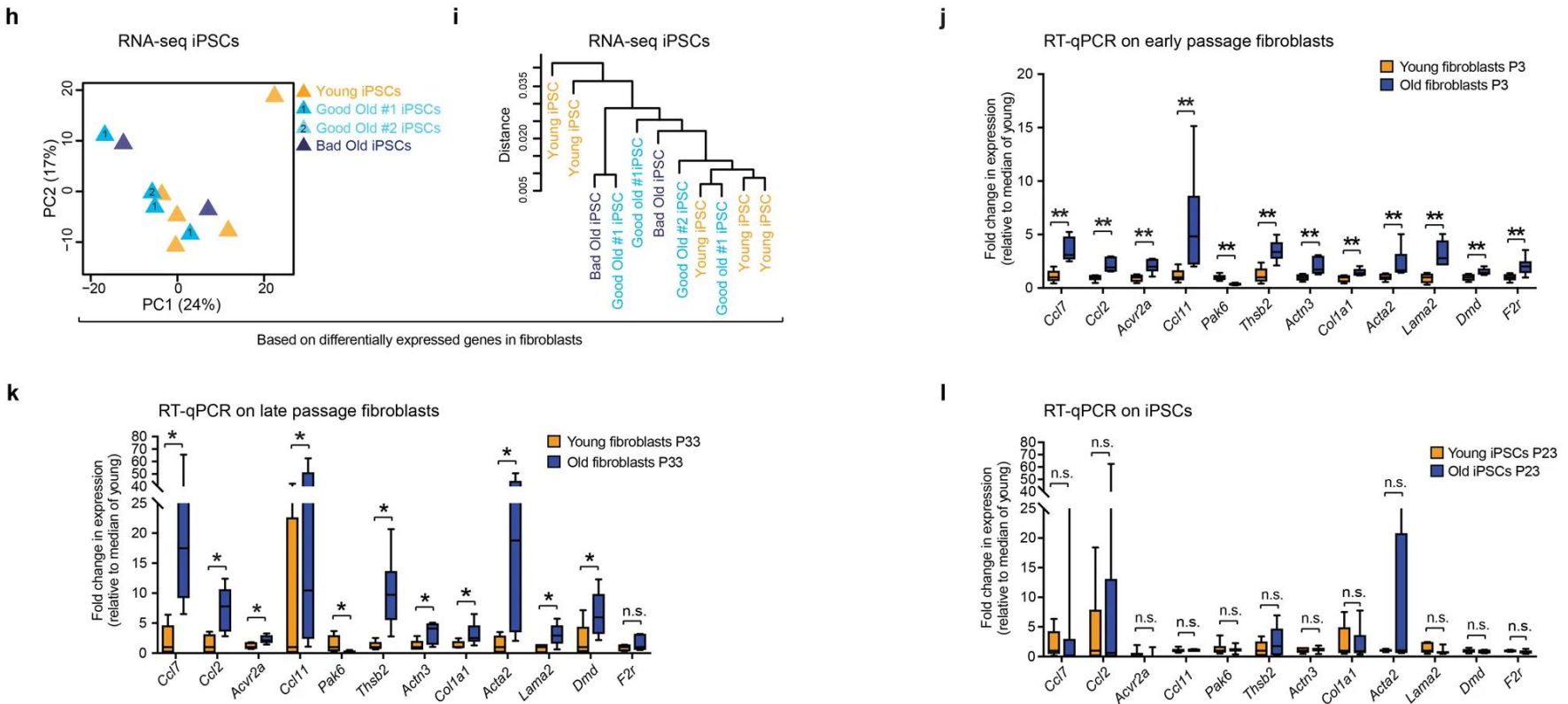
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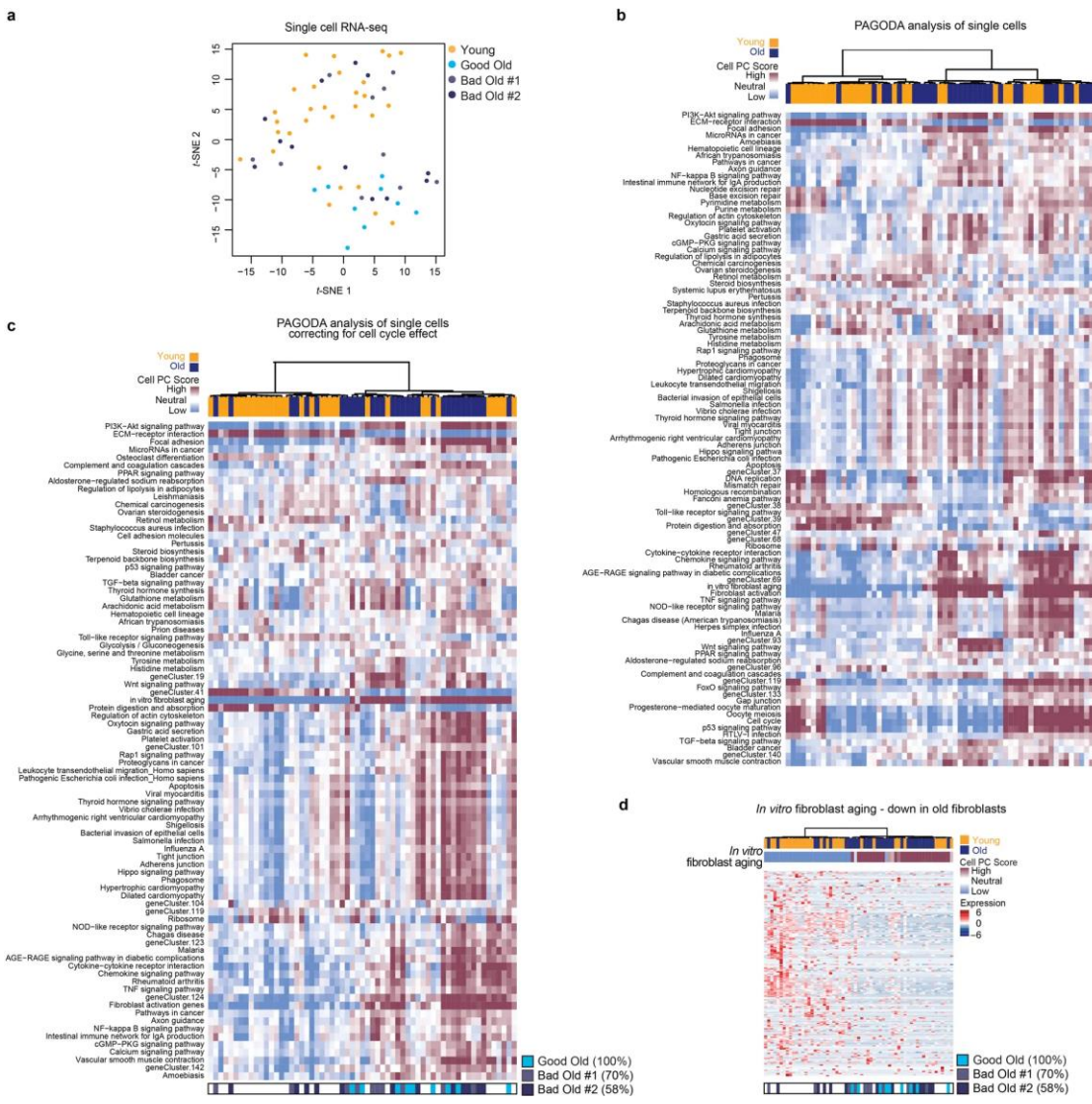
Extended Data Fig. 3 Reprogramming erases features of inflammaging and variability between mice.



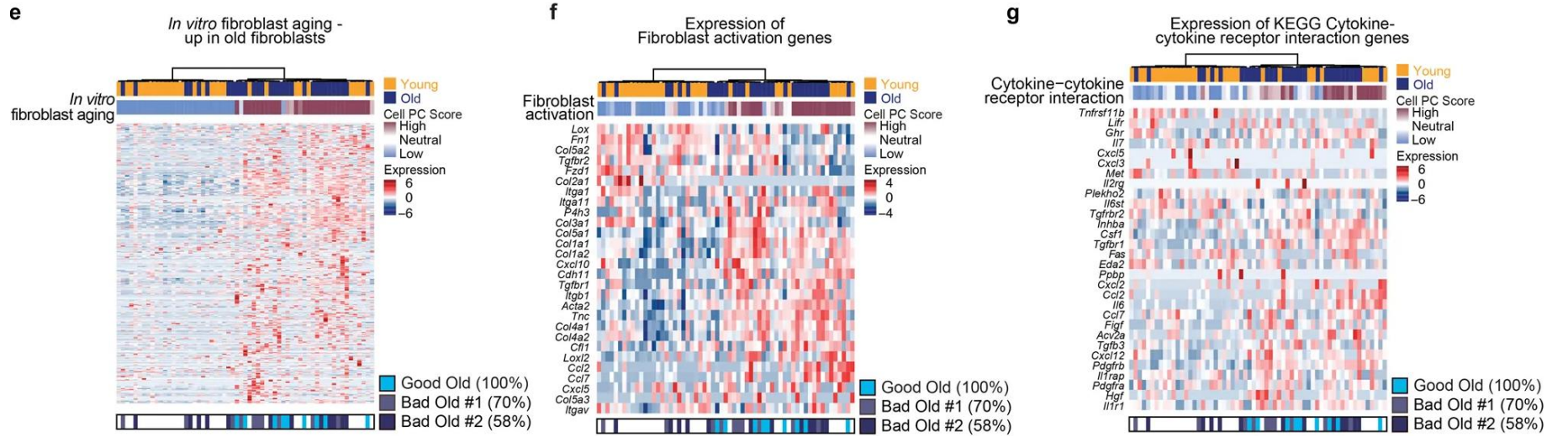
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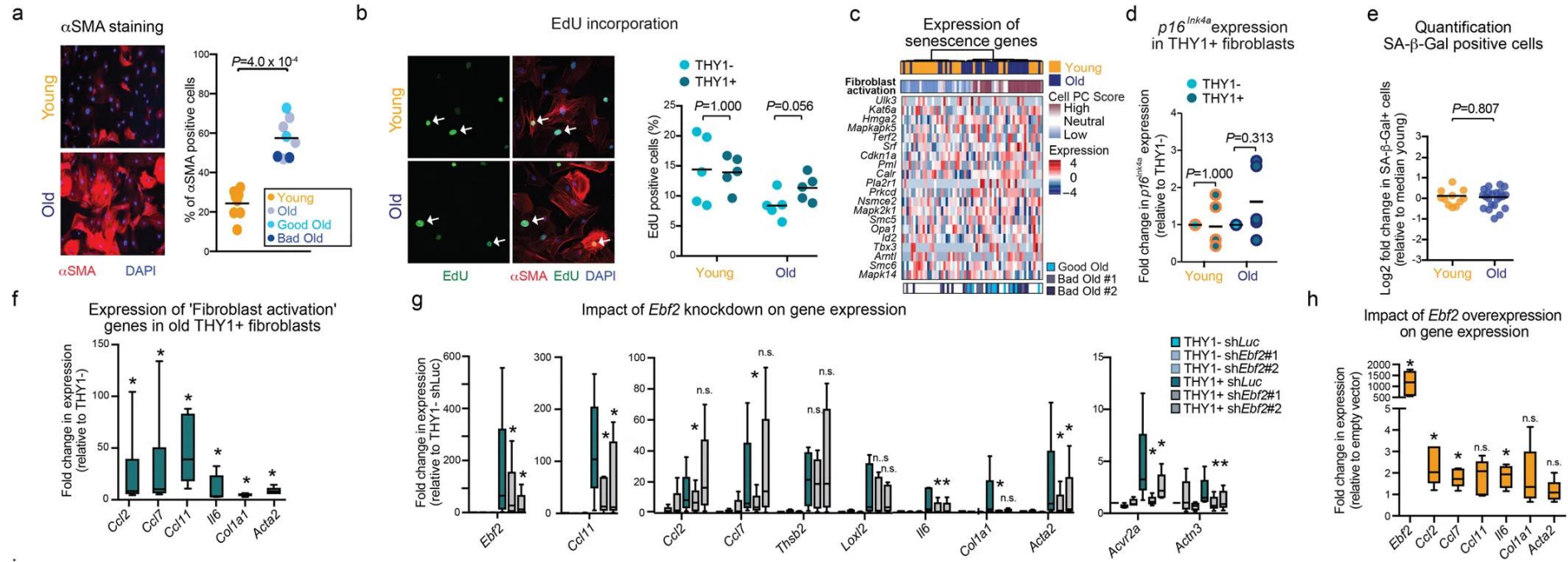
Extended Data Fig. 4: Correlation between the fibroblast activation signature and reprogramming efficiency in single-cell RNA-seq data.



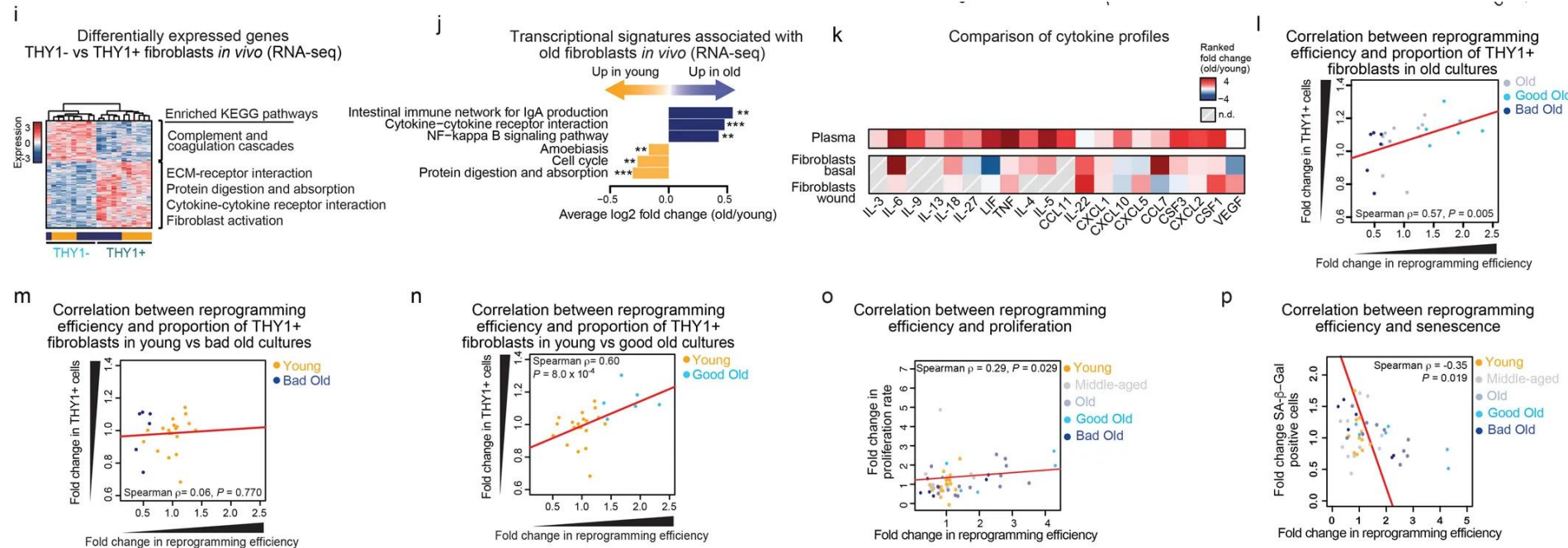
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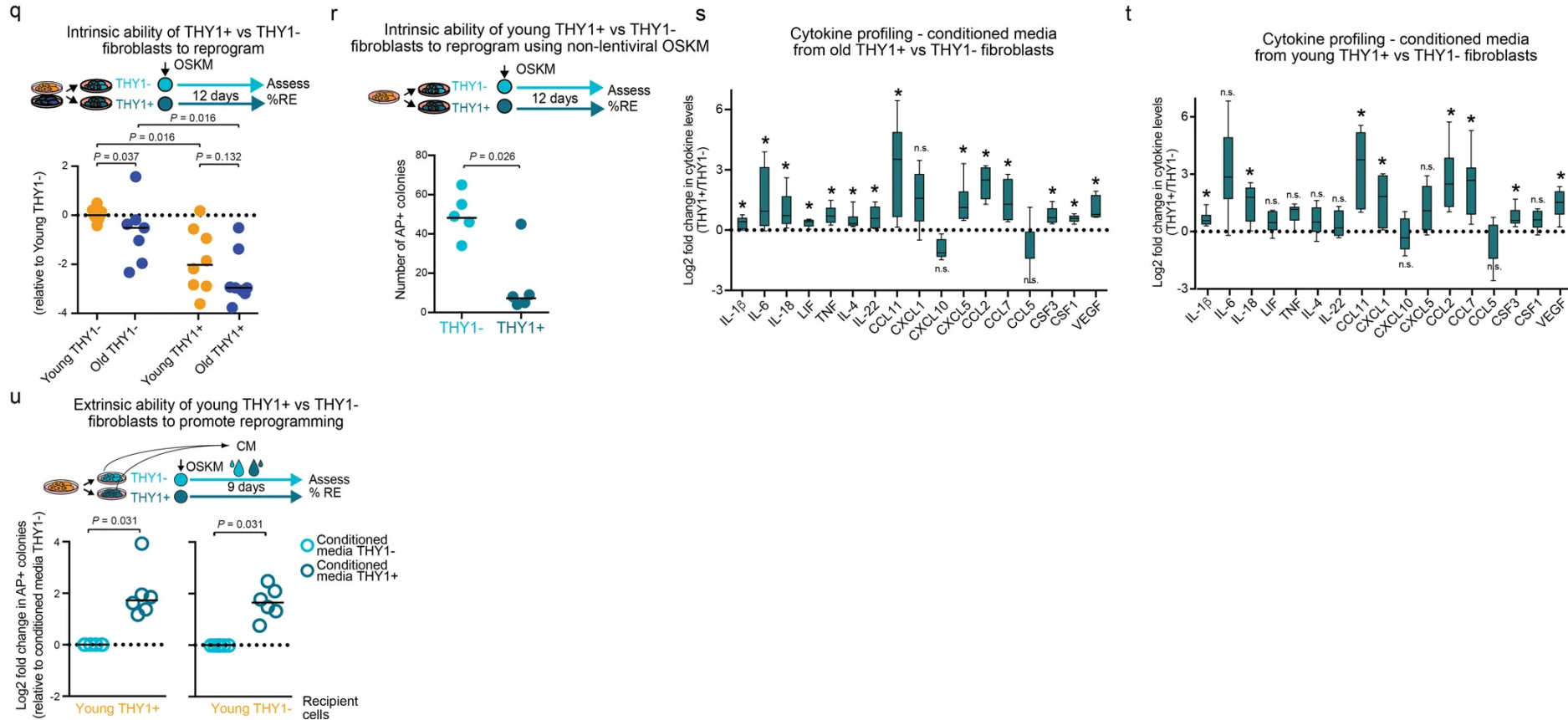
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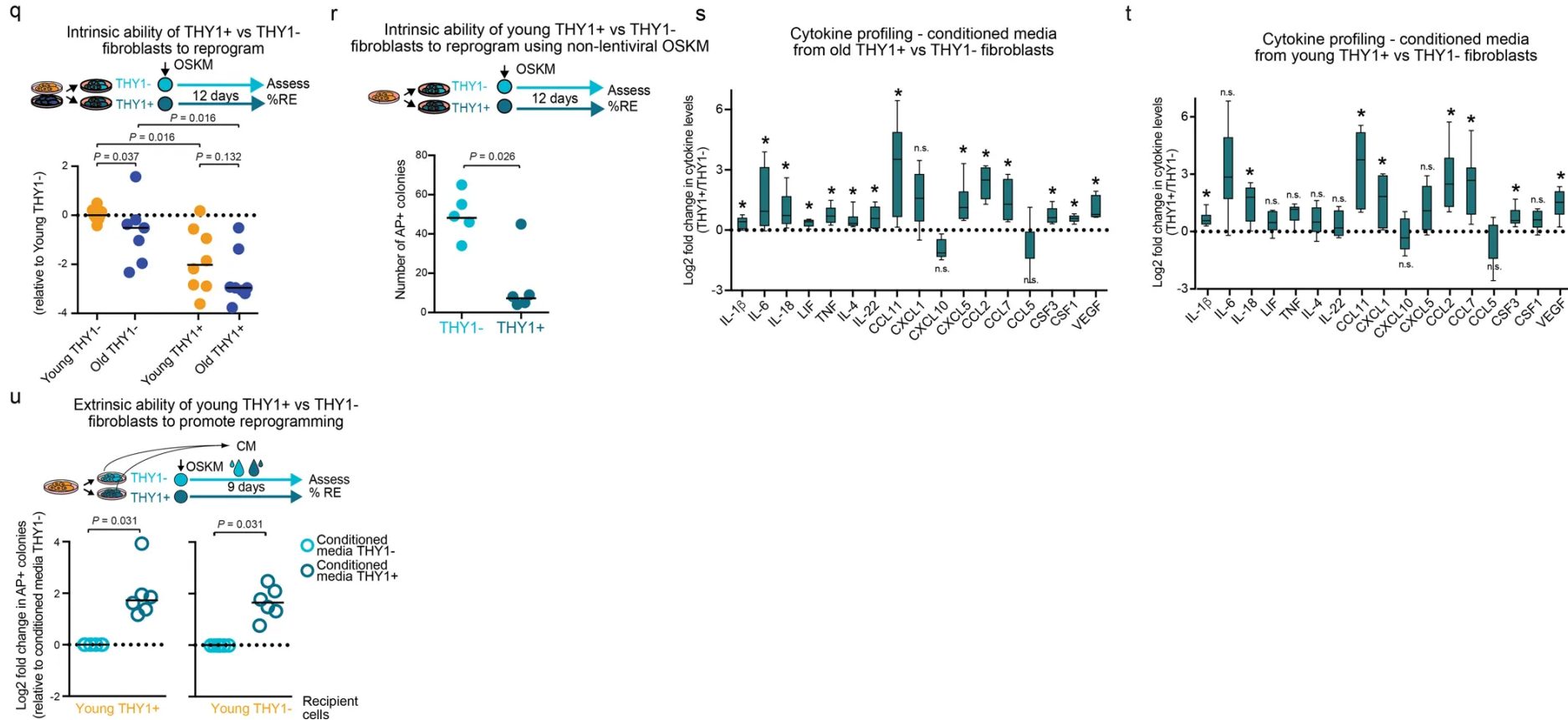
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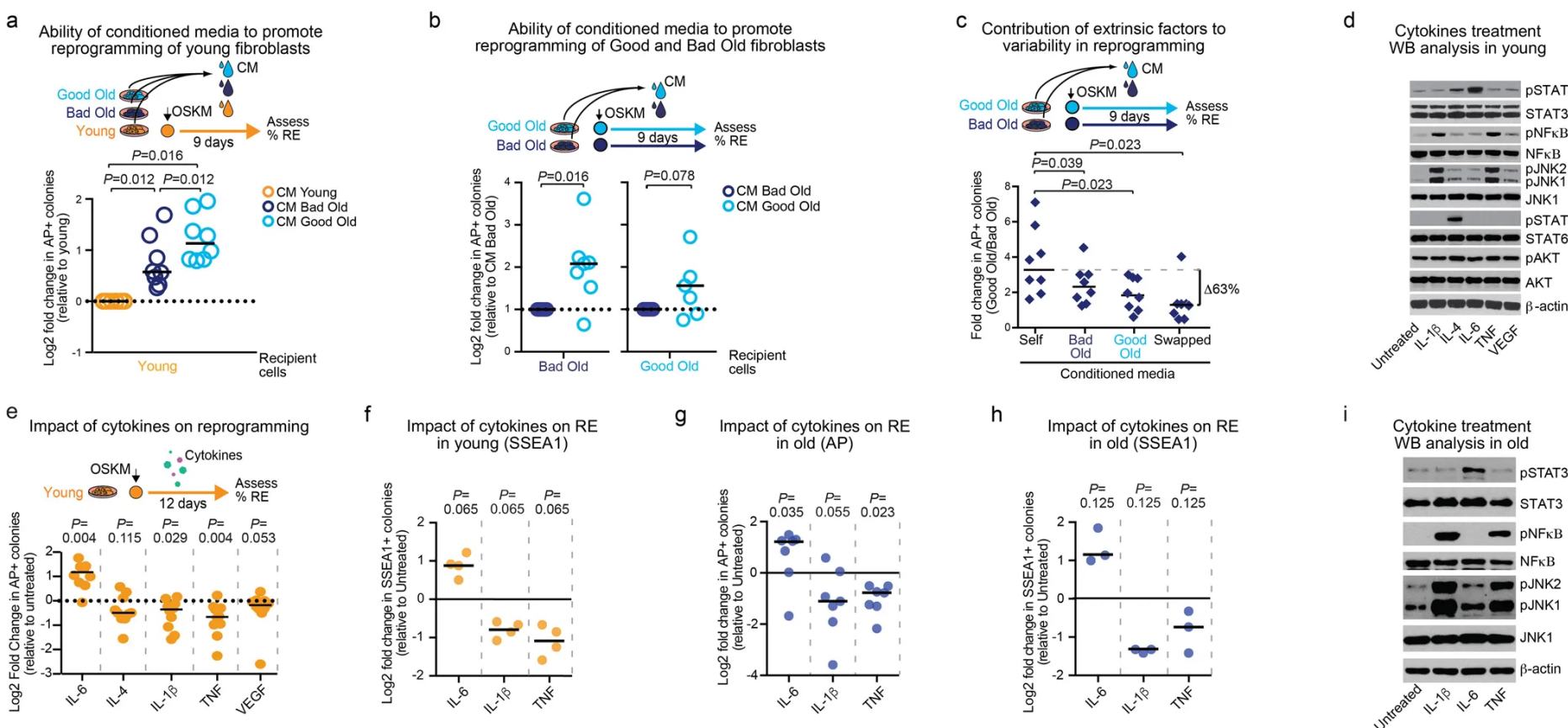
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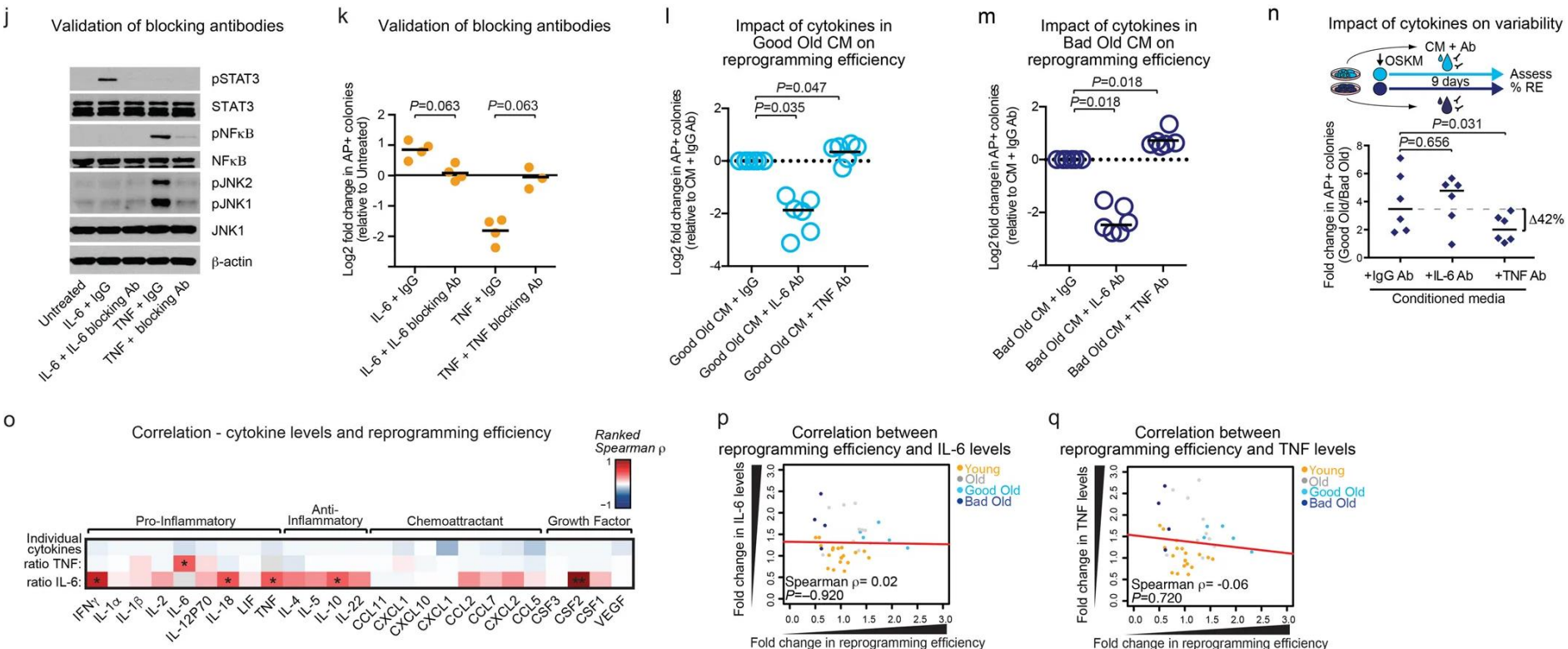
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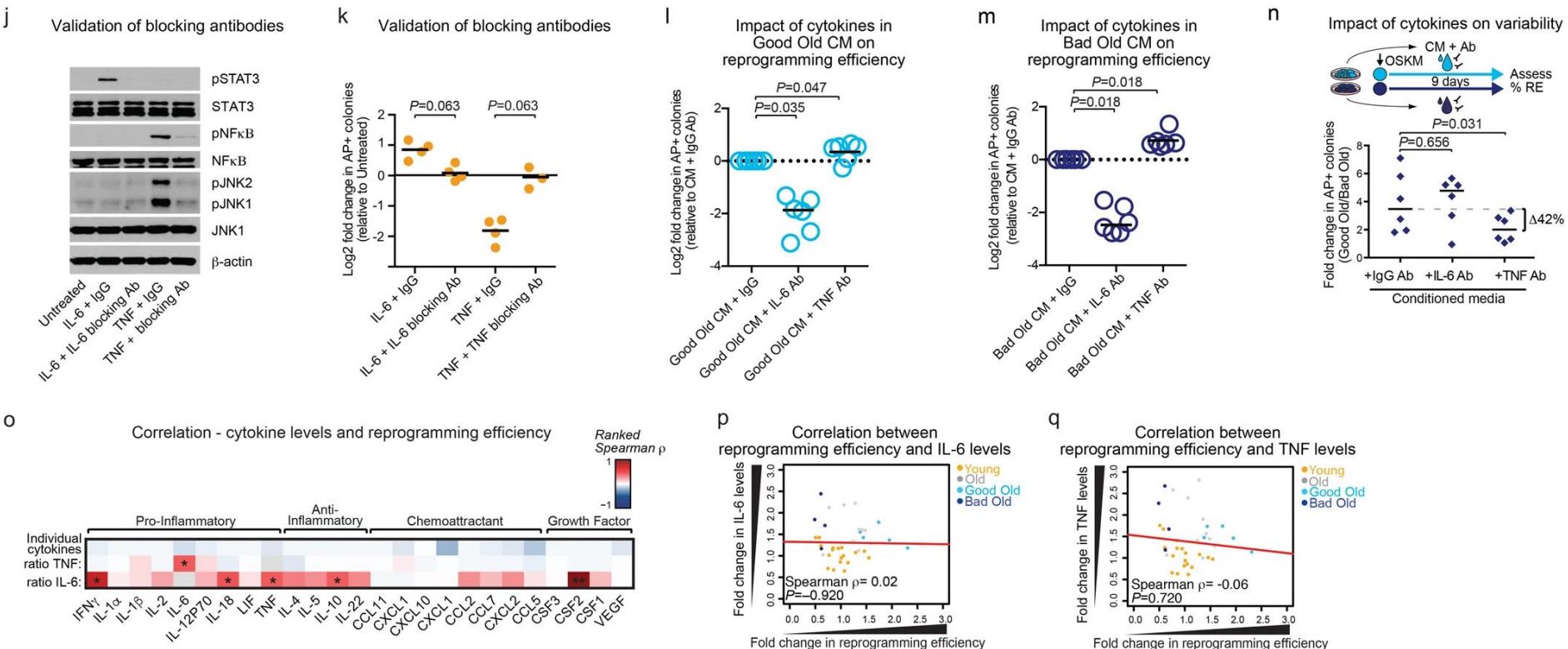
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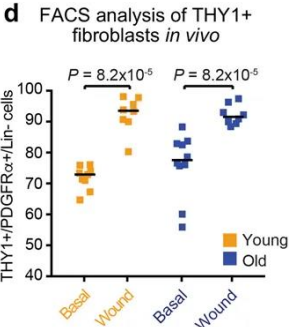
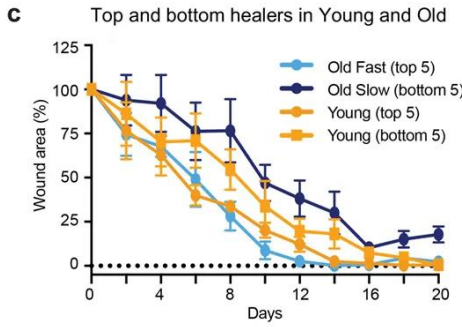
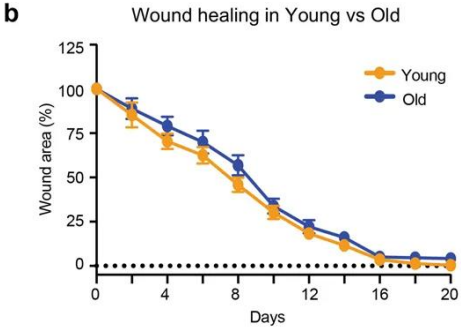
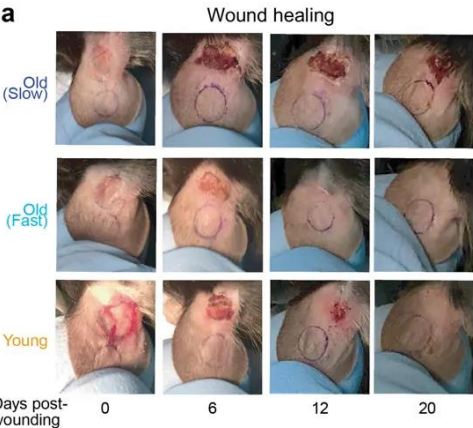
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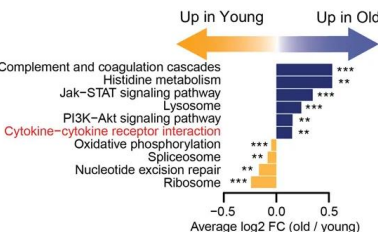


Extended Data Fig. 7: Ageing is associated with an increased variability in wound healing between old mice, and old fibroblasts in wounds are distinct from primary fibroblasts derived from healthy ear skin.

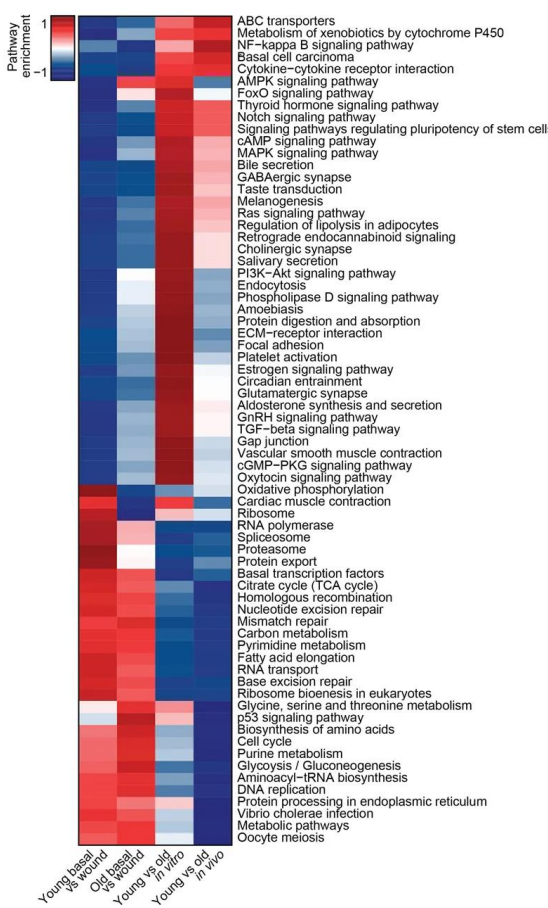


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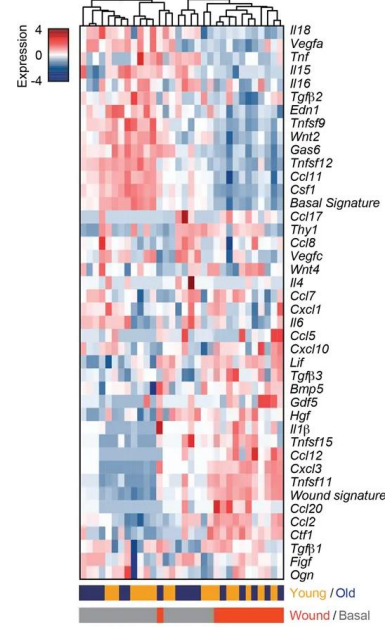
e Transcriptional signatures associated with old fibroblasts in wounds (RNA-seq)



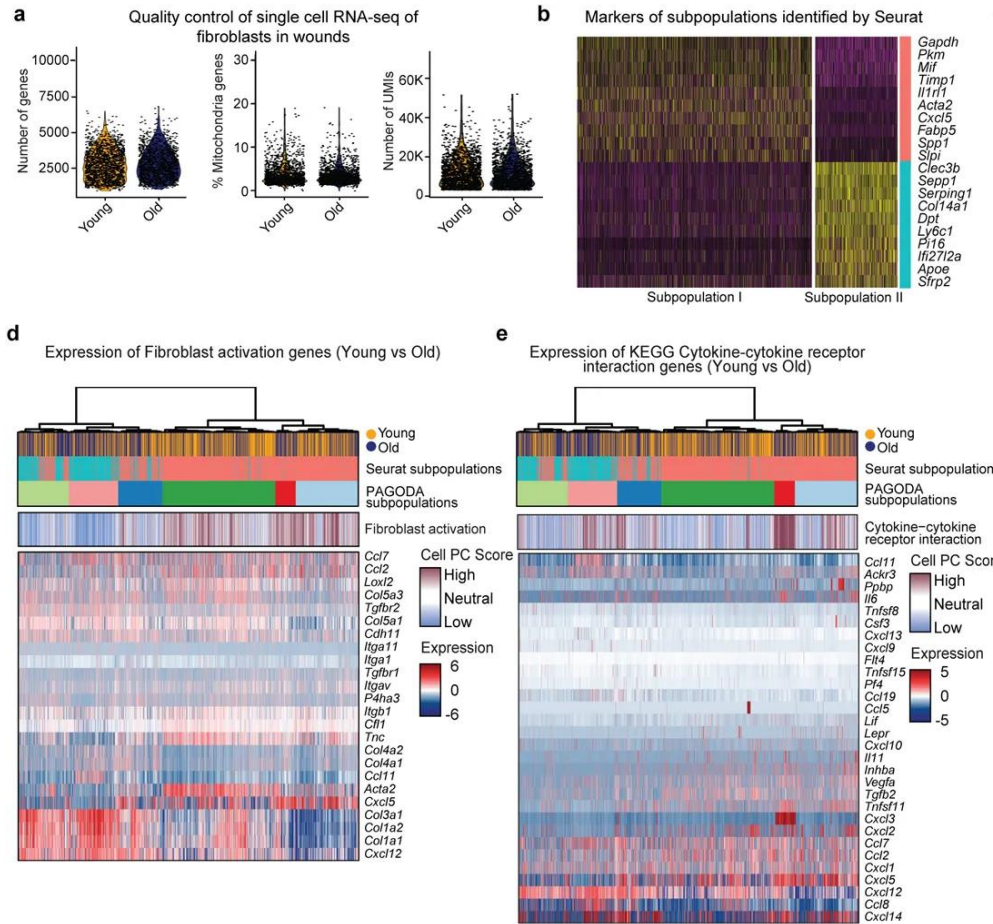
f Enrichment of KEGG pathways with age or wounding (RNA-seq)



g Cytokines genes in vivo Basal vs Wound (RNA-seq)

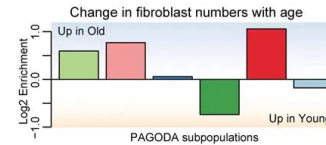
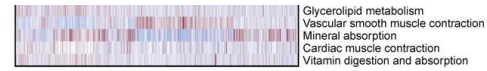
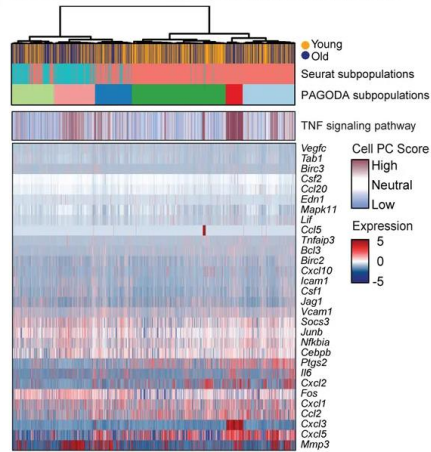


Extended Data Fig. 8: Single-cell RNA-seq analysis of fibroblasts in wounds from young and old mice and single-cell RNA-seq analysis of entire wounds from old slow- and fast-healing mice at day 7.



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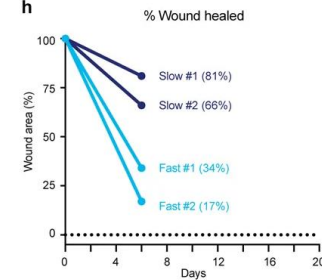
f Expression of KEGG TNF signaling pathway genes (Young vs Old)



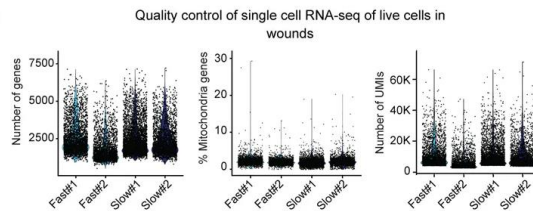
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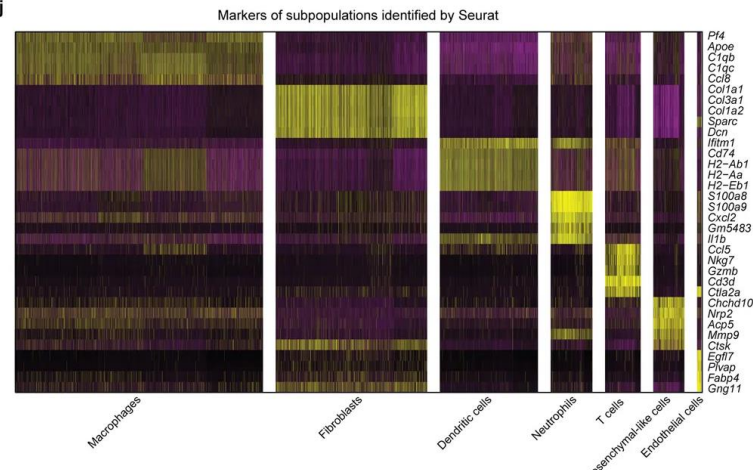
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Extended Data Fig. 9: Seurat and PAGODA single-cell RNA-seq analyses of fibroblasts identify distinct fibroblast subpopulations associated with fast- or slow-healing trajectories.

