iScience, Volume *25*

Supplemental information

Single-cell atlas unveils cellular heterogeneity and novel markers in human neonatal and adult intervertebral discs

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Supplemental Information. Figure S1

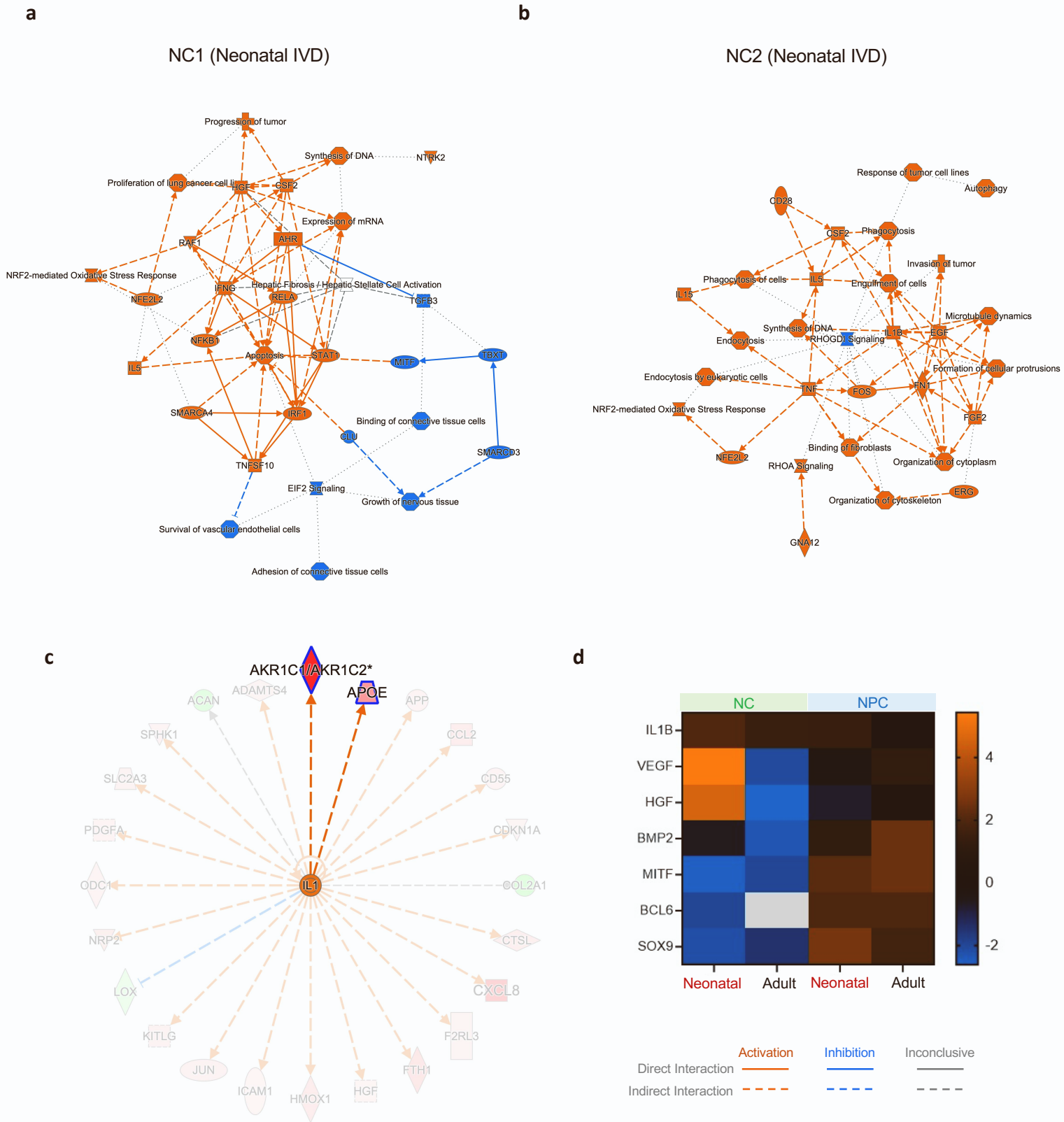


Figure S1. Additional Pathway and Network Analyses for NC Sub-Populations and Key Regulators in NC Populations Compared with NPC Populations in Neonatal and Adult IVD, Related to Figure 2. Pathway and network summary for **a)** NC1 and **b)** NC2 sub-populations in neonatal IVD. **c)** The IL1-regulated network involving *APOE* and *AKR1C1/AKR1C2.* **d)** Heatmap showing top regulators for NCs and NPCs in neonatal and adult IVD. Orange indicates activation, blue deactivation, and grey shows data that were either not detected or did not pass the filtering.

Supplemental Information. Figure S2

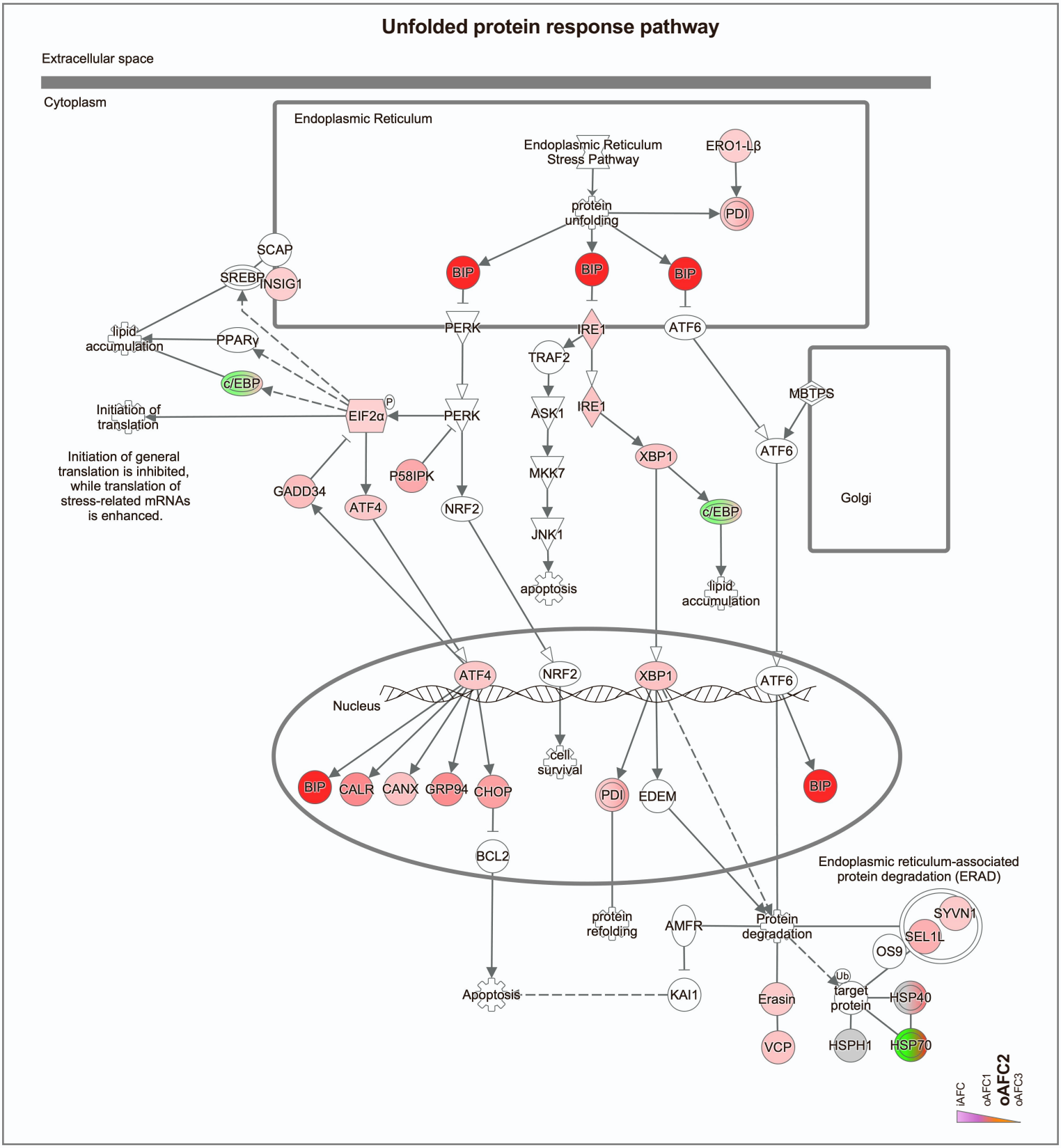


Figure S2. Gene Expression Projected on the Spatially Dependent Unfolded Protein Response Signaling Pathway for oAFC2 Sub-Populations in Neonatal IVD. Related to Figure 5.

Supplemental Information. Figure S3

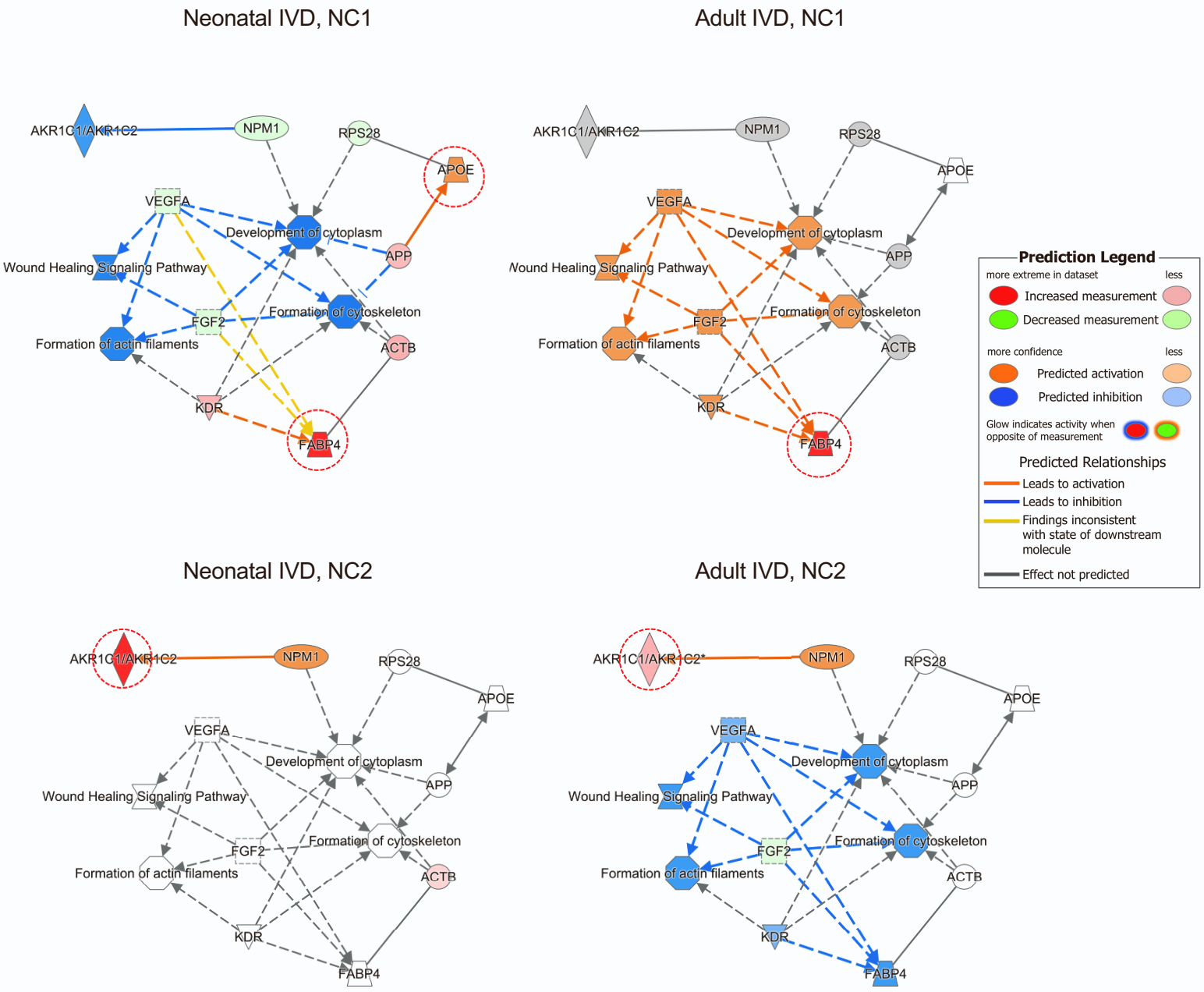


Figure S3. Regulatory networks showing novel NC markers (FABP4, APOE, AKR1C1) regulate NPC functions. Related to Figure 3.

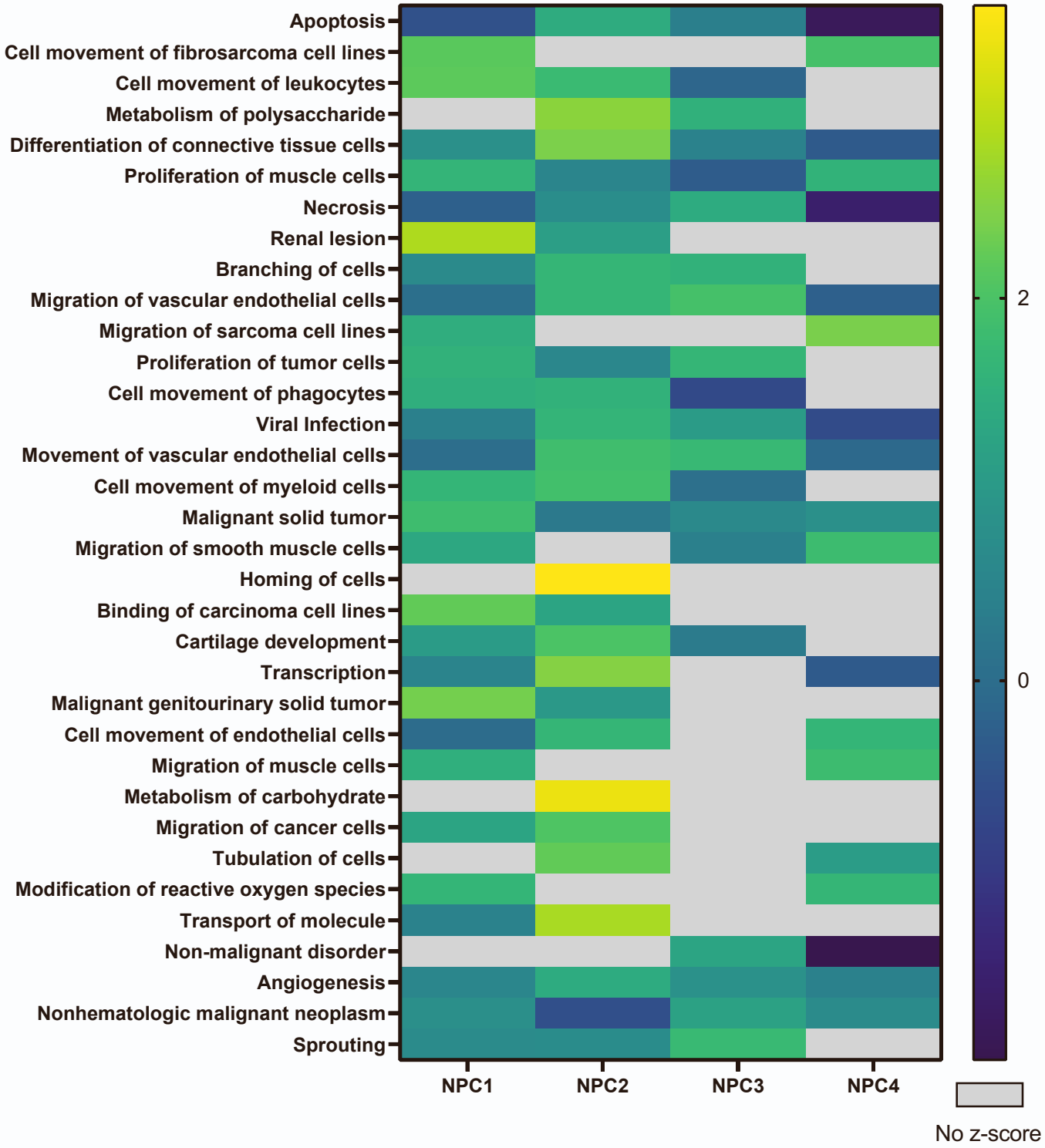


Figure S4. Distinct Enriched Functions for Four Different NPC Sub-Populations. Related to Figure 4.

Supplemental Information. Figure S5

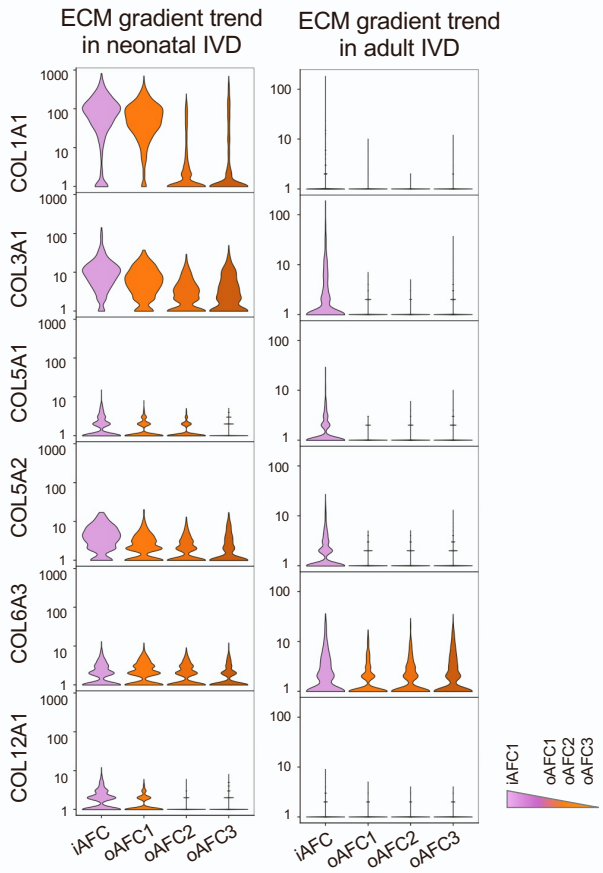


Figure S5. Comparison of the Spatially Dependent Trend of Expression Levels for Collagen-Relevant Genes in Neonatal and Adult IVD. Related to Figure 5.

Supplemental Information. Figure S6

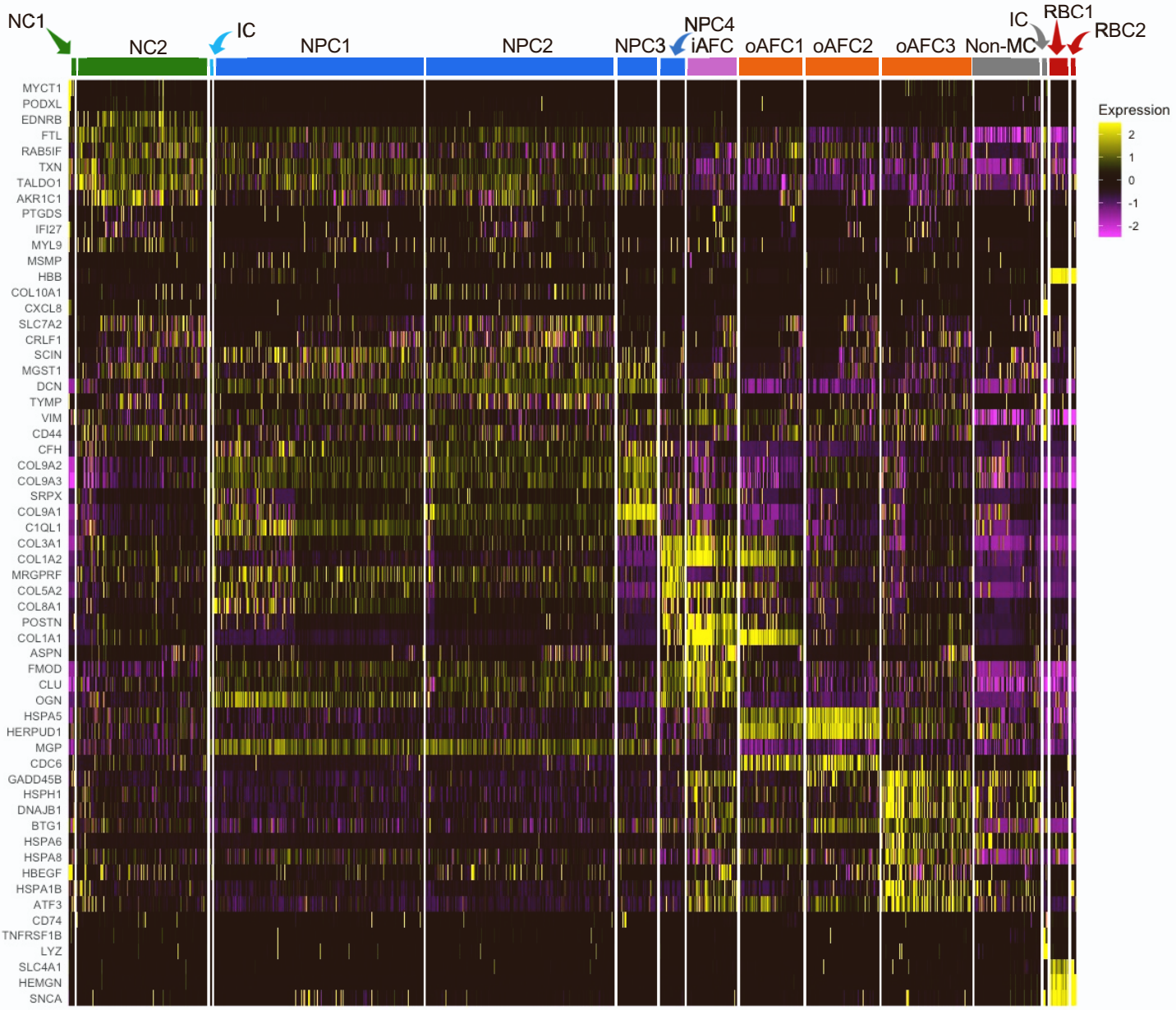
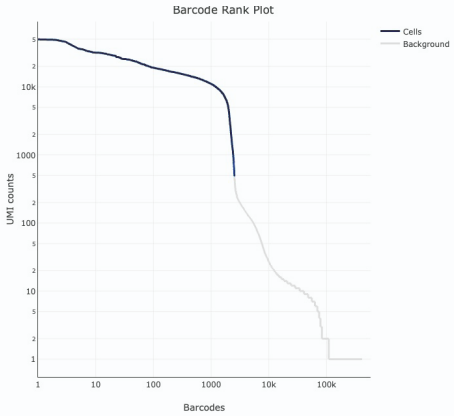


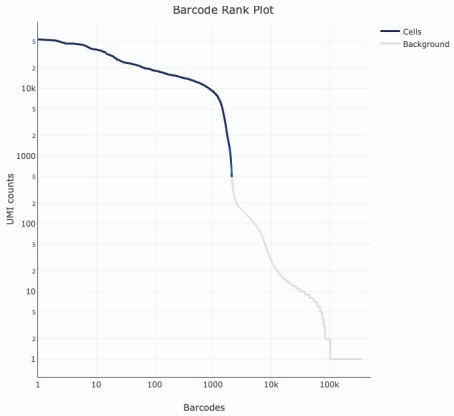
Figure S6. Heatmap Showing the Transcriptomes of Top Differentially Expressed Genes for All Sub-Populations Identified in Human IVD. Data include both neonatal and adult IVD. Related to 6

Supplemental Information. Figure S7

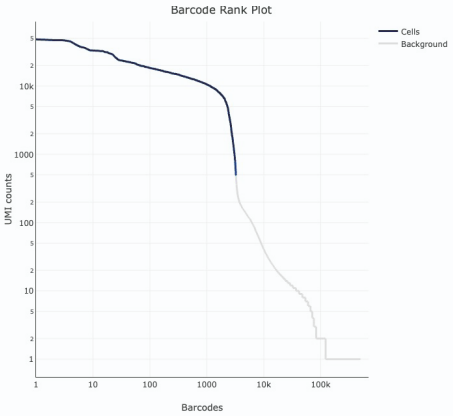
Sample 1
Neonatal IVD



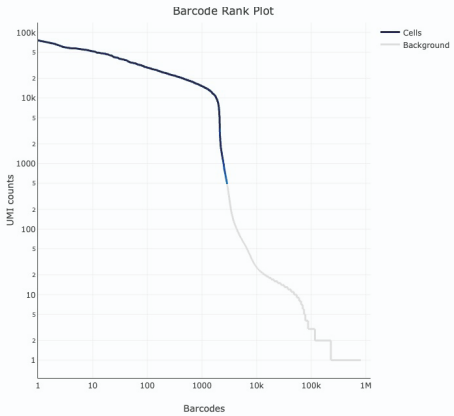
Sample 2
Neonatal IVD



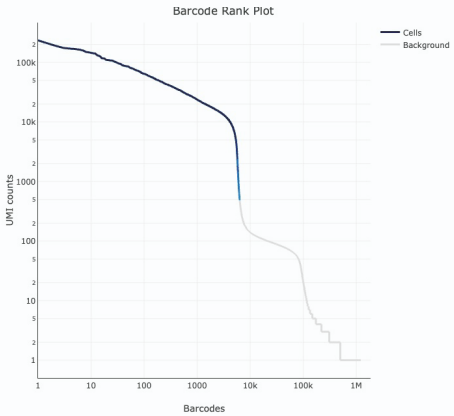
Sample 3
Neonatal IVD



Sample 4
Adult IVD



Sample 5
Adult IVD



Sample 6
Adult IVD

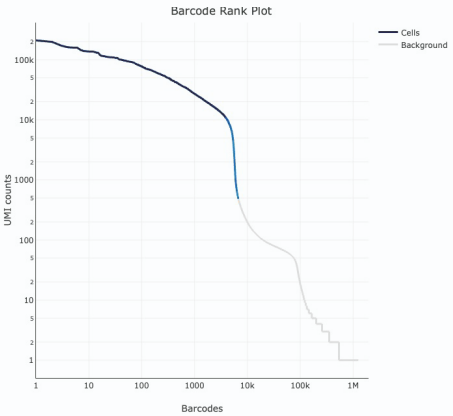


Figure S7. Barcode Rank Plot Showing the Filtered UMI Distribution over Barcodes. Related to STAR Methods.

Supplemental Information. Table S1

Table S1. The basic information of samples, human subjects, and single cell RNA sequencing.
(Raw data is available at Gene Expression Omnibus, the series accession number is GSE189916)

Samples	1	2	3	4	5	6
Human Subjects	Neonatal NDRI, ND18842 (L1-L5)	Neonatal NDRI, ND18842 (L1-L5)	Neonatal NDRI, ND18842 (L1-L5)	Cedars-Sinai Biobank (L2-L3)	Cedars-Sinai Biobank (L1-L4)	Cedars-Sinai Biobank (L2-L5)
Ages	0	0	0	76	57	66
Back pain history?	No	No	No	No	No	No
Group Assignment	Neonatal IVD	Neonatal IVD	Neonatal IVD	Adult IVD	Adult IVD	Adult IVD
Number of cells sequenced	2501	2063	3210	2722	5990	5523
Mean reads per cell	132317	166578	95322	73328	97823	114588
Median genes per cell	2601	2519	2376	3231	3592	3618
Median UMI counts per cells	9727	8836	8173	13124	13648	14672