

**Supplementary Fig 1. Spatial transcriptomics of LPC lesions show that fibroblasts are distinct from cells expressing *Rgs5* or *Tagln* genes; Ligand – receptor (L-R) interactions between cells in day 14 LPC lesions.** a, b: Spatial transcriptomic analyses reveal that the fibroblast cluster contains minimally *Rgs5* which is enriched in pericytes, or *Tagln*. c, e. Number of significant ligand-receptor interactions between any pair of two cell populations shown as (c) circle plot and (e) heatmap. d, f. Interaction strength between ligand-receptor of any pair of two cell populations shown as (d) circle plot and (f) heatmap. In the circle plots, the circle sizes are proportional to the number of cells in each group; edge weights are proportional to the interaction strength. g. Scatter plot of incoming and outgoing interaction strength showing fibroblasts as major outgoing signaling source. Dot size is proportional to the number of inferred links (outgoing and incoming) associated with each cell group. h, i. Chord plot showing L-R interactions with fibroblasts as source (h) or receiver (i) of signal.

**Supplementary Fig 2. Incoming and outgoing fibroblast L-R interactions in day 14 LPC lesions.** a, b. Bubble plot delineating L-R interactions from one cell group (i.e. sender) to another (i.e. target) as indicated in the plot.

**Supplementary Fig 3. Cell contributions to communication networks.** a, b. Dot plots indicating cell type contribution to (a) outgoing and (b) incoming communication patterns.

**Supplementary Fig 4. Inferred Incoming and outgoing signaling patterns between fibroblasts, OPCs and macrophages in day 14 LPC lesions.** Heatmap of (a) inferred outgoing and (b) incoming signaling pathways as assessed for the 3 cell groups. Color bar in the heatmap represents the relative signaling strength of a pathway across all cell groups (values are row-scaled). Top colored bar plot shows the total signaling strength of a cell group by summarizing all pathways displayed in the heatmap. The right grey bar plot shows the total signaling strength of a pathway by summarizing all cell groups displayed in the heatmap. Heatmap of (c) outgoing and (e) incoming signaling pathways that contribute to each communication pattern. River plots showing the cell source for (d) outgoing and (f) incoming communication patterns and the pathways associated with them. The thickness of the flow indicates contribution of cell group or signaling pathway to each pattern.

**Supplementary Fig 5. Axon densities are unchanged in fibroblast occupied regions.** a. Representative image of a day 21 LPC lesion stained for DAPI, NFH, and PDGFR $\beta$ . b. Quantification comparing NFH positive axon density in fibroblast occupied areas with the rest of the LPC lesion. Sample sizes  $n = 7$  across two experiments. Two-tailed, unpaired t-test comparing groups. Data are the mean  $\pm$  s.d.

**Supplementary Fig 6. Main cell types as assessed in MS lesions.** a. Heatmap of top 5 differentially expressed genes across annotated cell groups.

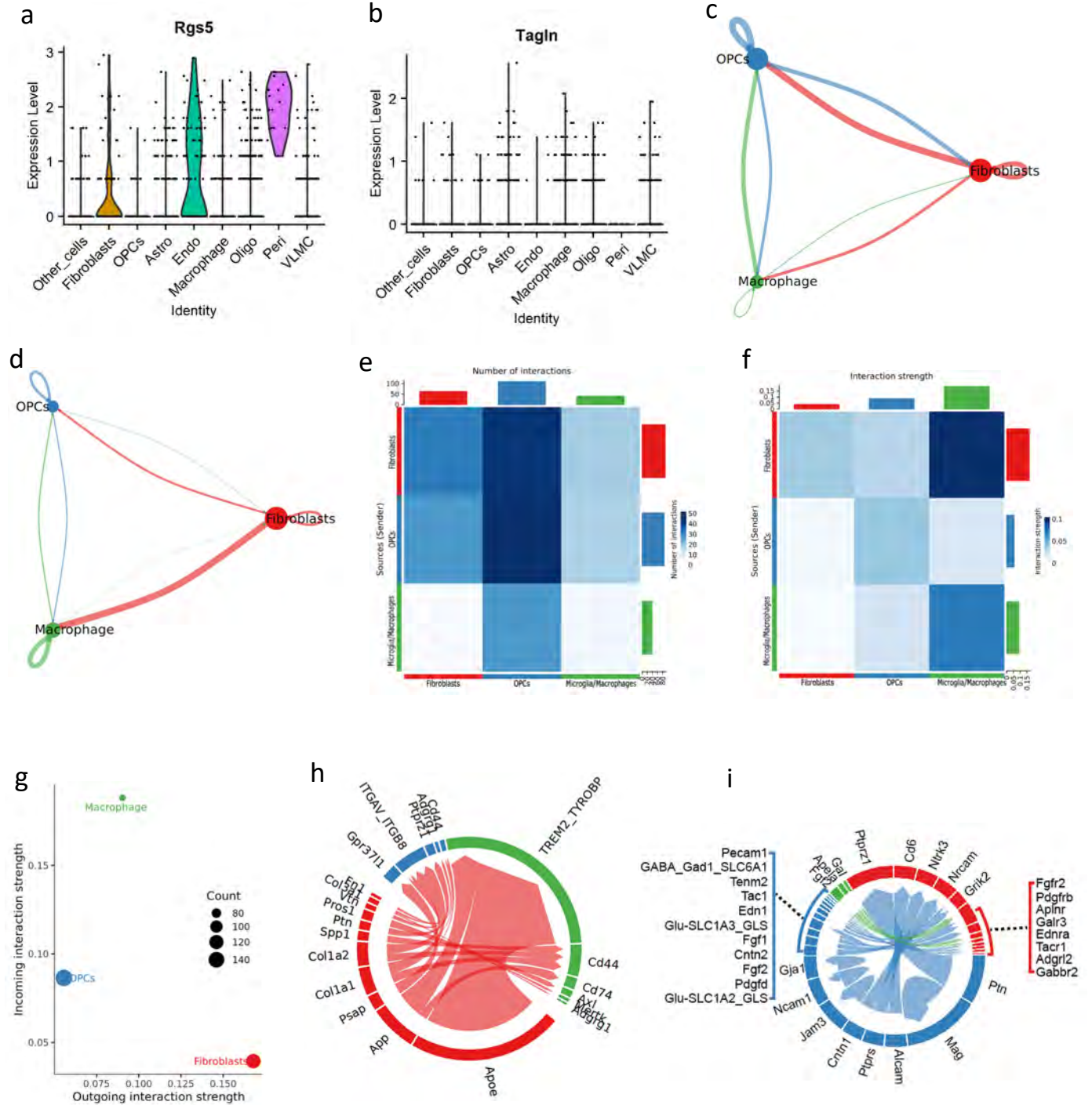
**Supplementary Fig 7. Non-fibroblast related marker expression across cell clusters assessed in MS lesions.** a. Violin plots of TAGLN and RGS5 normalised gene expression in snRNAseq dataset. b, c. String-db plot of DEG between fibroblast (b) subcluster 0, and (c) subclusters 1.

**Supplementary Fig 8. L-R interactions between fibroblasts, M/M and OPCs in MS lesions.** a, c. Number of significant ligand-receptor between any pair of two cell populations shown as (a) circle plot and (c) heatmap. b, d. Interaction strength between ligand-receptor any pair of two cell populations shown as (b) circle plot and (d) heatmap. In the circle plots, the circle sizes are proportional to the number of cells in each group; edge weights are proportional to the interaction strength. e. Schematic indicating inferred outgoing and incoming fibroblast signals and their distribution across signaling databases. f, g. Chord plot showing L-R interactions with fibroblasts as (f) source of signals, and (g) receiver of signals.

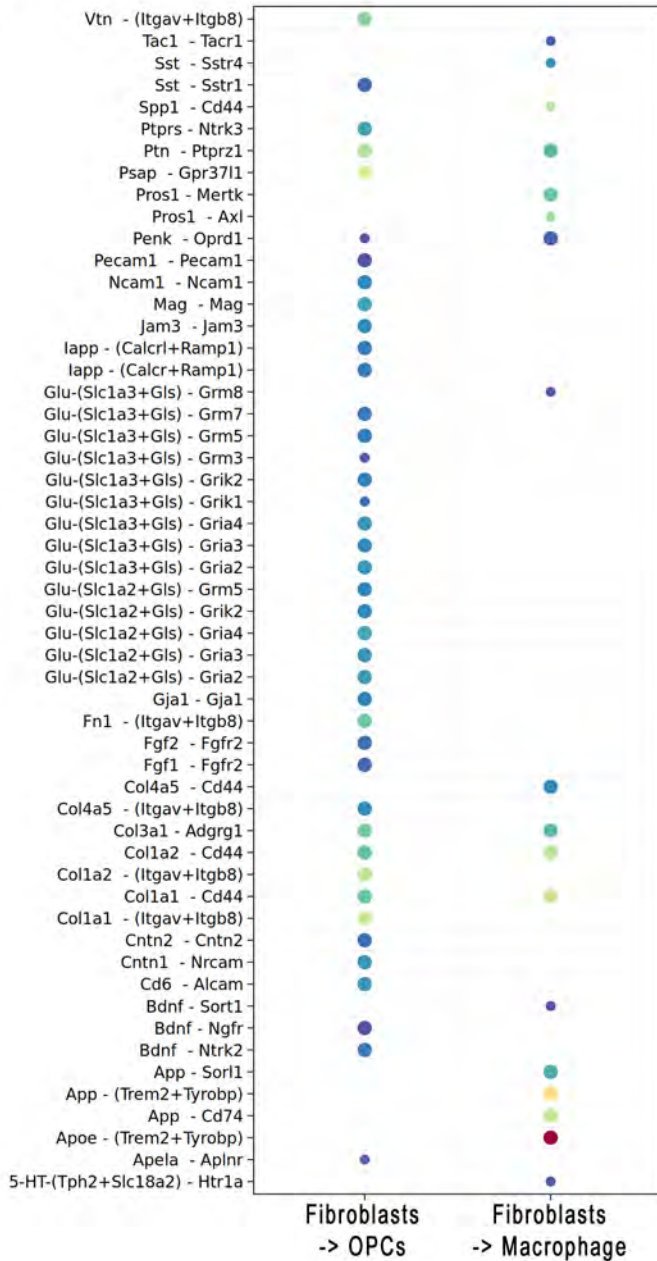
**Supplementary Fig 9. Inferred Fibroblast communication patterns in MS.** a, b. Bubble plots delineating L-R interactions from one cell group (i.e. sender) to another (i.e. target) as assessed with different signaling databases indicated in the plot (a) ECM-receptor and (b) secreted signaling databases. c, d. Dot plots of (c) outgoing and (d) incoming communication patterns.

**Supplementary Fig 10. Fibroblast interactions in MS lesions.** a, b. Heatmap and river plots indicating cell and signaling pathways associated with outgoing and incoming communication patterns in MS lesions. The thickness of the flow indicates contribution of cell group or signaling pathway to each pattern. c, d. Venn diagrams of (l) outgoing and (m) incoming signaling pathways comparing MS and LPC lesions.

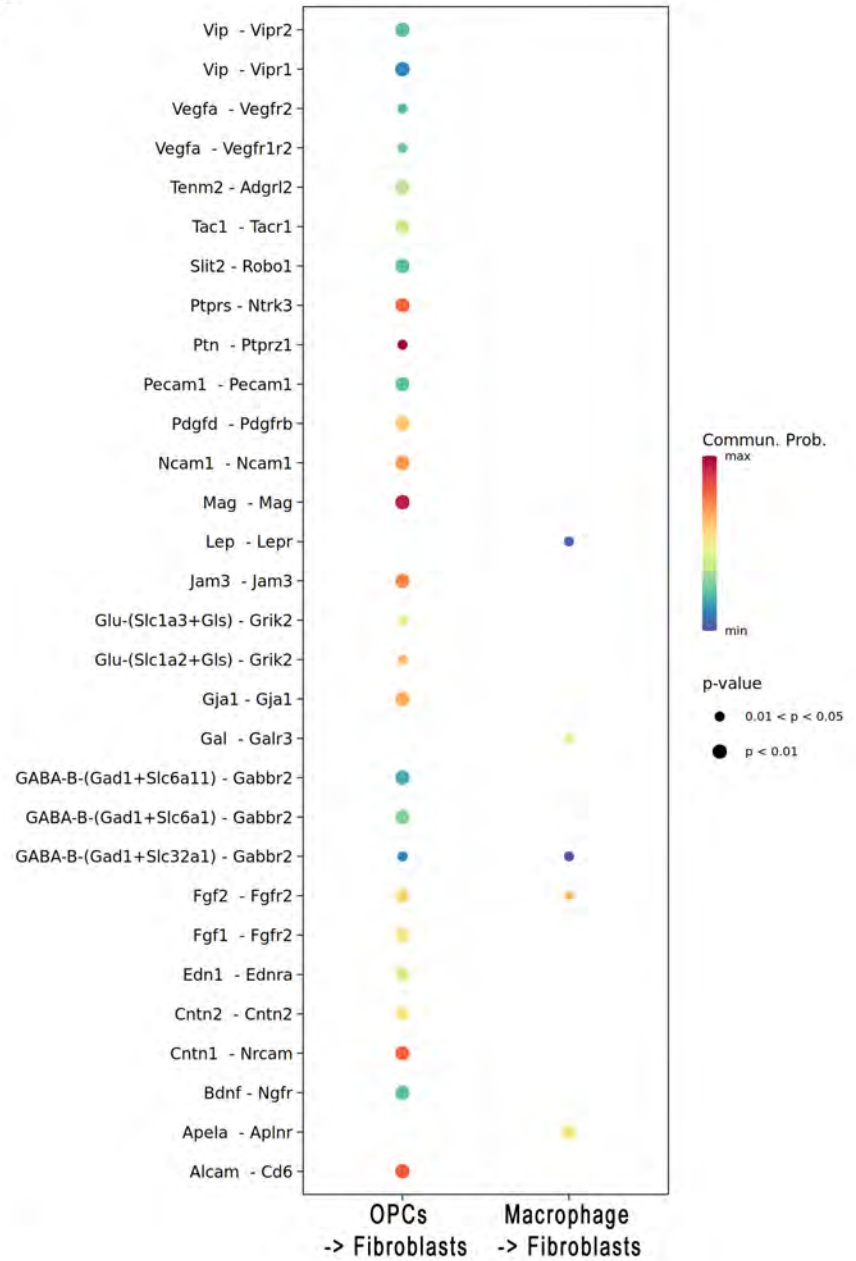
**Supplementary Fig 11. Inferred Communication pattern contributions in MS lesions.** a, b. Heatmap of (a) inferred outgoing and (b) incoming signaling pathways as assessed for the 3 cell groups. Colour bar in the heatmap represents the relative signaling strength of a pathway across all cell groups (values are row-scaled). Top colored bar plot shows the total signaling strength of a cell group by summarizing all pathways displayed in the heatmap. The right grey bar plot shows the total signaling strength of a pathway by summarizing all cell groups displayed in the heatmap. c, d. Venn-diagrams comparing LPC (CosMx) and MS (snRNAseq) (c) outgoing and (d) incoming fibroblast L-R interactions.



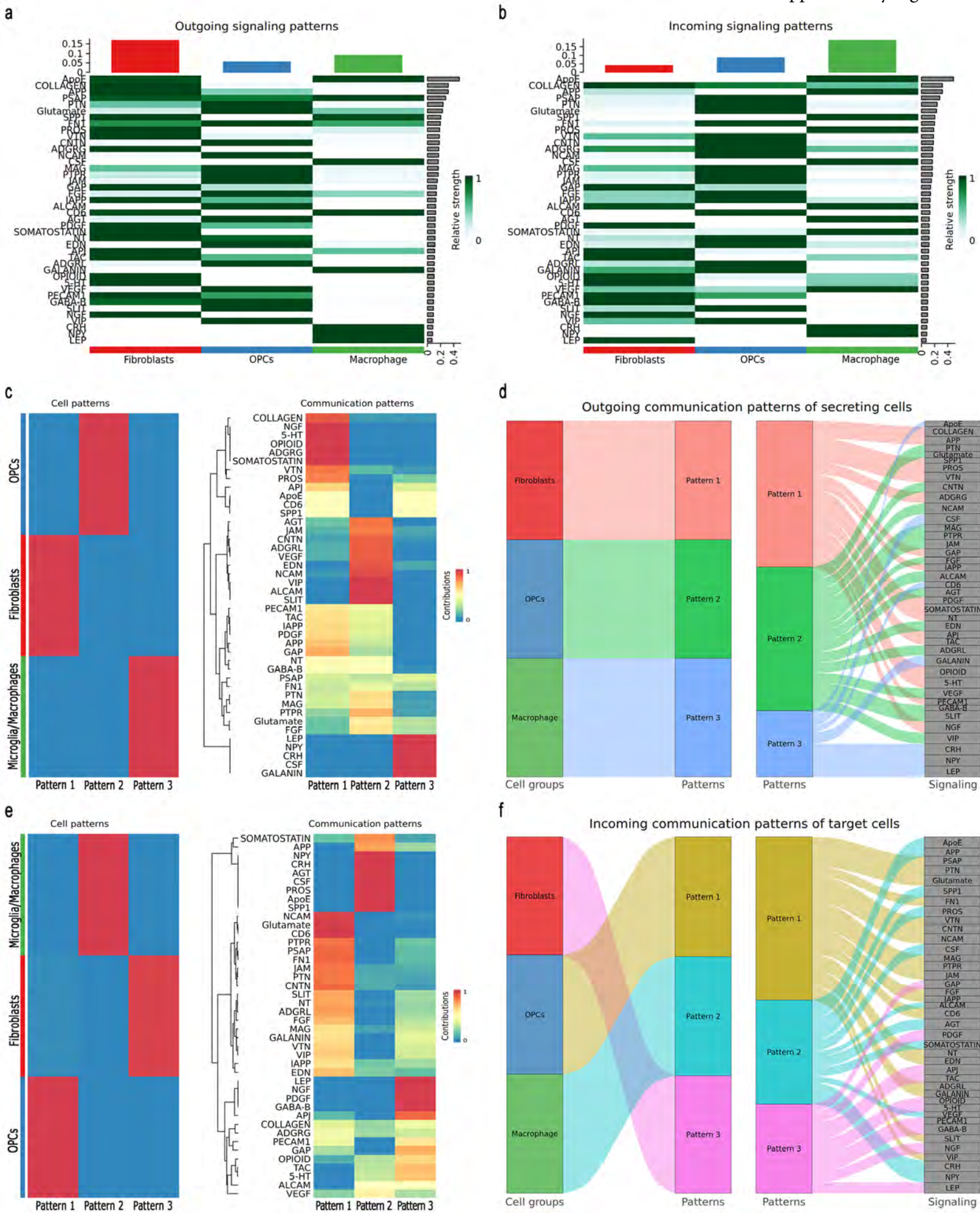
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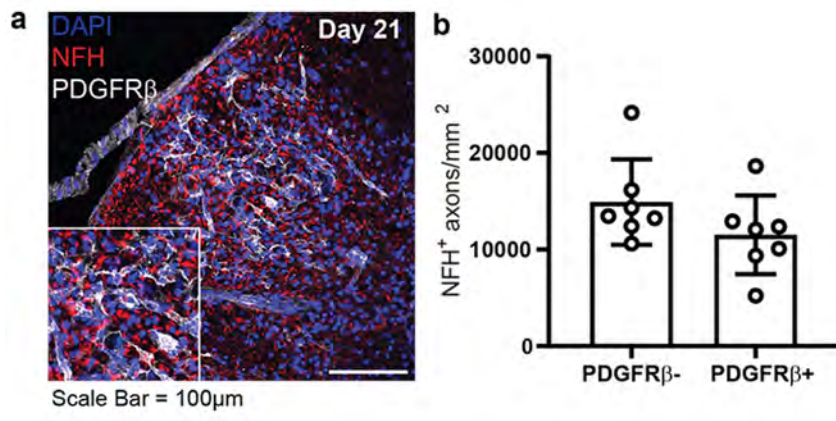


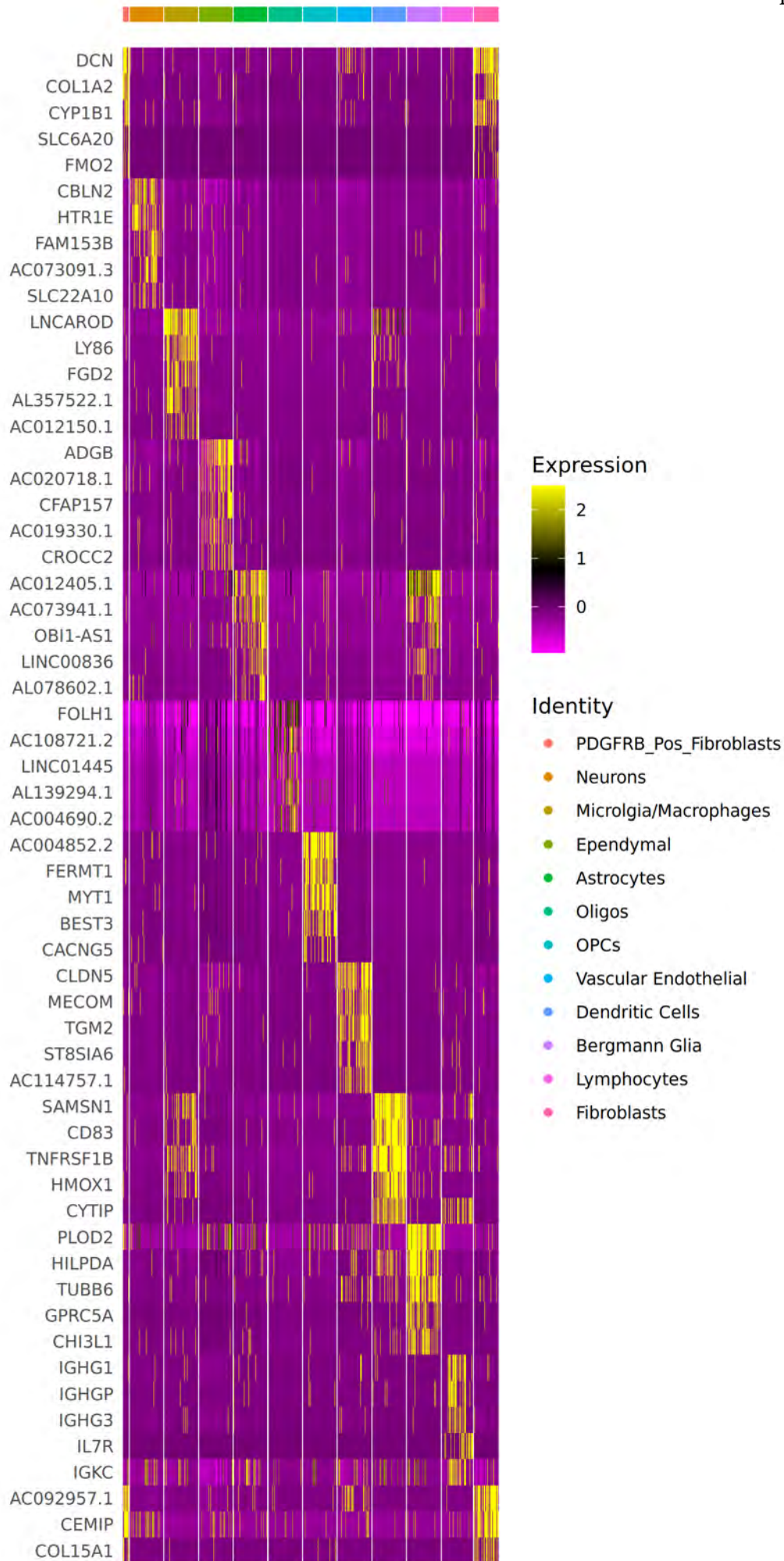
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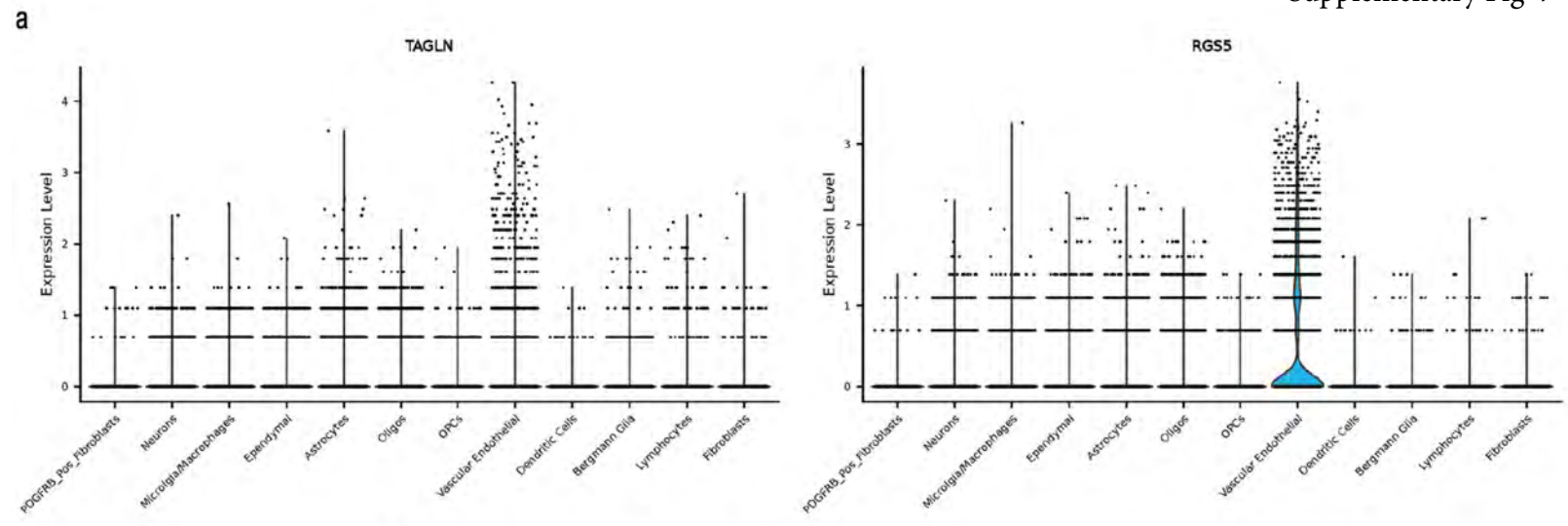






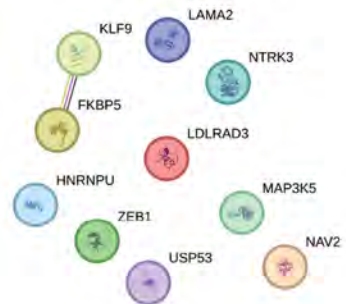






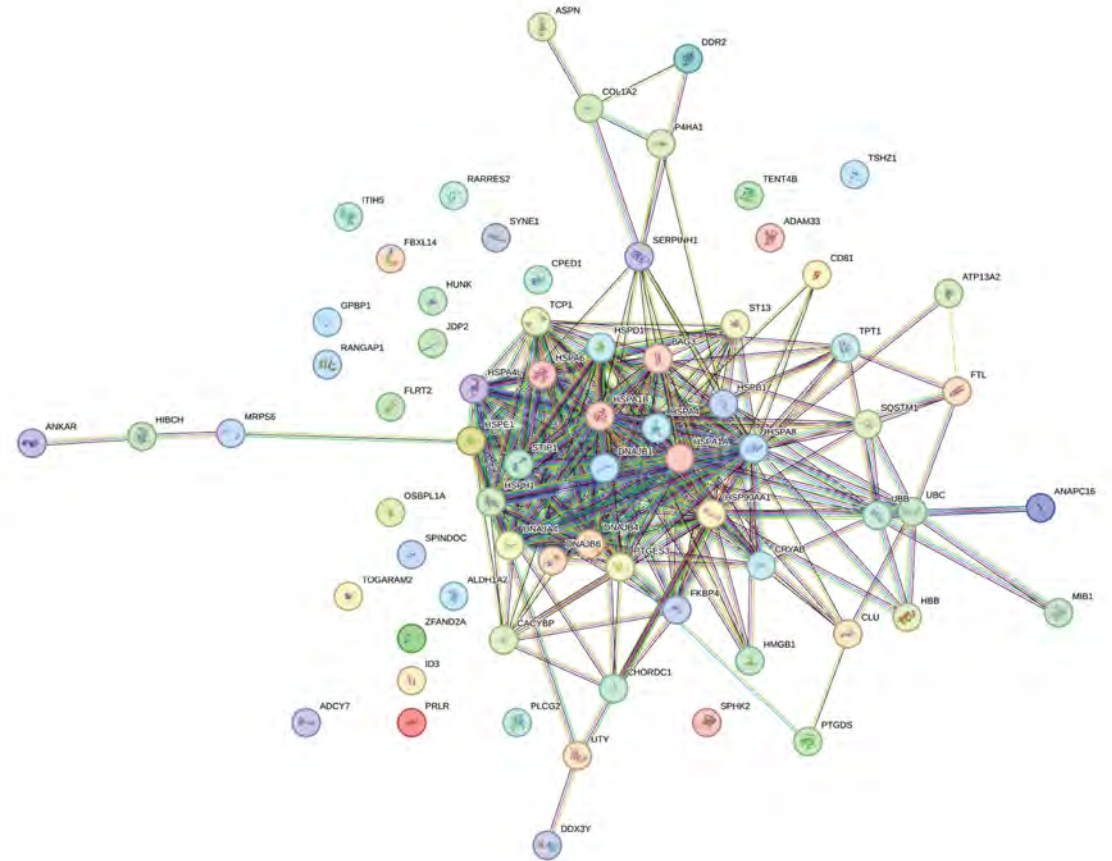
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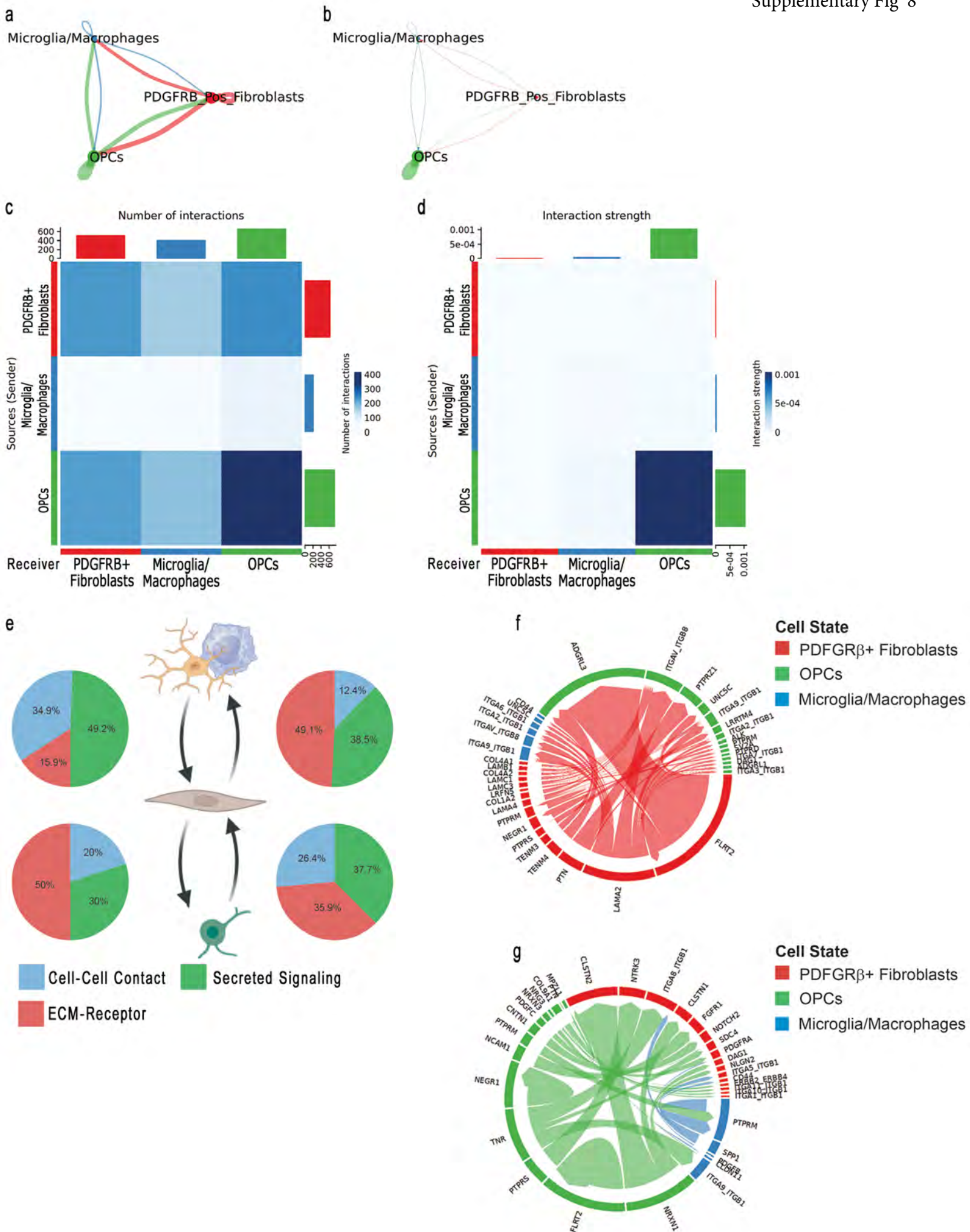
### Subcluster 0

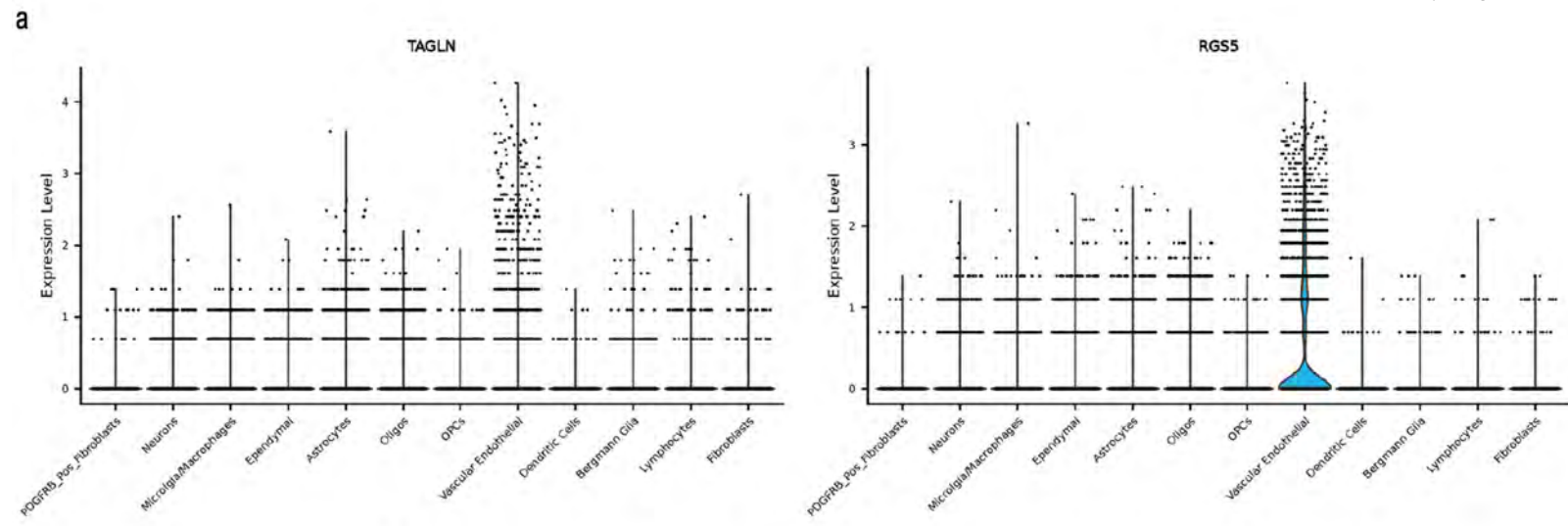


**c**

### Subcluster 1

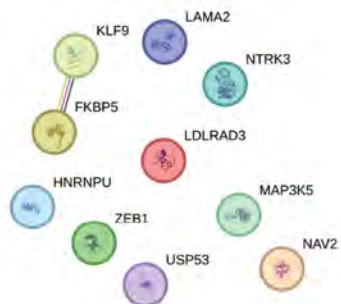






**b**

### Subcluster 0



**c**

### Subcluster 1

