Human DRG (hDRG) sequencing data were downloaded as transcript-per-million (TPM) counts for Wangzhou et al (2020) and quantile normalized TPM (qnTPM) from Ray et al., 2023 (supplemental table 2, quantile normalized sheet). In line with published their published reports, only hDRG with clear neuronal enrichment were used from Ray et al., 2023. Ensembl IDs were mapped to gene symbols using biomaRt in R.

Visium data were accessed as a Seurat Object from Tavares-Ferreira et al. (2022). Single soma hDRG count data were downloaded from GEO (GSE249746) (Yu et al., 2024). Data were processed in line with their publication. Briefly, Seurat objects were created for individual donors (n=6) in R, and normalized (`NormalizeData(seurat\_obj) `. Variable features were calculated on the top 4500 features (`FindVariableFeatures(seurat\_obj, nfeatures = 4500) `). Integration anchors were calculated using FindIntegrationAnchors(object.list = seurat\_objects, scale=TRUE, normalization.method="LogNormalize", reduction="cca", l2.norm = TRUE, dims=1:30, k.anchor=5, k.filter=200, k.score=30, max.features=200, nn.method="annoy", n.trees=50, eps=0). Objects were then integrated using IntegrateData(ss.data, normalization.method="LogNormalize", features=NULL, features.to.integrate=NULL, dims=1:30, k.weight=80, weight.reduction=NULL, sd.weight=1, sample.tree=NULL, preserve.order=FALSE, eps=0). Data were then scaled (`ScaleData `) prior to dimensionality reduction (RunPCA(ss.data, npcs=50), RunUMAP(ss.data, reduction="pca", dims=1:25)). Clusters were then calculated using ` FindNeighbors(ss.data, reduction="pca", dims=1:25)` and `FindClusters(ss.data, resolution=3.4)` in line with published methods from Yu et al. (2024). Metadata were extracted from the project-associated github (taimeimiaole/NN\_hDRG-neuron-sequencing/Source\_code\_2/human\_meta\_final\_cluster.Rdata), with `cl.conserv\_final` set as Idents for plotting.

All plots were generated in R, using ggplot2 and/or Seurat.