This repository contains 74 files.

* ReplicateFigures.R—R script for replicating the main figures present in the manuscript, including visualizing Visium sections colored according to spatial transcriptomic phenotype, uniform manifold approximation and projection (UMAP) plots, raw spatial transcriptomic gene expression counts shown in the context of the tissue, kernel density estimates of mean protein intensity level, bar plots of proportions of neurons, as well as violin plots, heat maps, boxplots, and scatterplots of relative expression.
* ReplicateFigures\_Supplemental.R—R script for replicating the supplemental figures present in the manuscript.
* SingleCell\_TranscriptomicData—folder containing all transcriptomic data necessary to replicate the figures.
  + LCM-qPCR\_Negddct.txt—Negddct HT-qPCR data on 41 DMV neurons and 40 NAmb neurons (20 cardiac-projecting (FB) from either brain region; 20 from the left side of either brain region).
  + LCMseq\_SeuratObject.rds—scaled and normalized (as well as raw count) data on 227 DMV neurons (115 cardiac-projecting; 113 from left; 77 from caudal; 75 from intermediate and rostral).
  + 10xsc\_SeuratObject.rds—scaled and normalized (as well as raw count) data on 3,195 single cells from the dorsal brainstem (1,796 from left).
  + 10xsc\_NeuronalSubset\_SeuratObject.rds—scaled and normalized (as well as raw count) data on 2,446 single cells annotated as clusters 1-4 in 10xsc\_SeuratObject.rds.
* Spatial\_Transcriptomics—folder containing spatial transcriptomics data files necessary to replicate the figures.
  + S1-S8—folders corresponding to individual sections from which data was obtained.
    - clusters.csv—file for reading in the clusters
    - filtered\_feature\_bc\_matrix.h5—gene expression count data in Hierarchical Data Format
    - aligned\_fiducials.jpg.gz—aligned fiducials of the tissue image
    - detected\_tissue\_image.jpg.gz—image of tissue and spots
    - scalefactors\_json.json.gz—scale factors in json format
    - tissue\_hires\_image.png.gz—hi-res image of tissue
    - tissue\_lowres\_image.png.gz—low-res image of tissue
    - tissue\_positions\_list.csv.gz—list of spatial barcodes and the coordinates specifying spots
* Annotations—folder containing all annotation files necessary to replicate the figures.
  + 10xsc-Sample\_Annotations.txt—sample annotations for the 10x genomics single cell RNAseq data stored in 10xsc\_SeuratObject.rds.
  + LCM-qPCR\_Gene\_Annotations.txt—gene annotations for the HT-qPCR data, LCM-qPCR\_Negddct.txt.
  + LCM-qPCR\_Sample\_Annotations.txt—sample annotations for the HT-qPCR data, LCM-qPCR\_Negddct.txt.
  + LCMseq-Sample\_Annotations.txt—sample annotations for the LCM-RNAseq data stored in LCMseq\_SeuratObject.rds.