

File name: Supplementary Data 1

Description: Sample metadata for each species and smFISH experiments.

File name: Supplementary Data 2

Description: Summary of neuronal proportions across species and tissues, including scCODA results for neuron-to-glia and neuron-to-glia subtype comparisons across species and tissues.

File name: Supplementary Data 3

Description: scCODA results for interneuron proportions across species in the putamen.

File name: Supplementary Data 4

Description: Interneuron proportions across samples, species, and tissues, including scCODA results comparing primates and non-primates across tissues.

File name: Supplementary Data 5

Description: Differential gene expression analysis results of *LMO3* (*BAT*) interneurons compared to other interneurons within the bat putamen. Significantly upregulated and downregulated genes were identified using a two-sided Wilcoxon rank-sum test with Bonferroni adjustment ($P < 0.05$; $\log_2FC > 0.6$ for upregulated genes and $\log_2FC < -0.6$ for downregulated genes).

File name: Supplementary Data 6

Description: Differential gene expression analysis results of *FOXP2* *TSHZ2* (*BAT*) interneurons compared to other interneurons within the bat putamen. Significantly upregulated and downregulated genes were identified using a two-sided Wilcoxon rank-sum test with Bonferroni adjustment ($P < 0.05$; $\log_2FC > 0.6$ for upregulated genes and $\log_2FC < -0.6$ for downregulated genes).

File name: Supplementary Data 7

Description: Gene ontology enrichment analysis of WGCNA results for bat cell types was performed using a one-sided hypergeometric test. Terms with $FDR < 0.01$ were considered significant.

File name: Supplementary Data 8

Description: scCODA results for interneuron proportions across species in the caudate nucleus, with human as the reference.

File name: Supplementary Data 9

Description: scCODA results for interneuron proportions across species in the putamen, with human as the reference.

File name: Supplementary Data 10

Description: Gene ontology enrichment analysis of WGCNA results for human cell types was performed using a one-sided hypergeometric test. Terms with $FDR < 0.01$ were considered significant.