## **Supplementary Information**

## Supplementary Figure Legends

Supplemental Figure 1. Comparison of genes across datasets and cell types. Comparison of detected genes across (A) individual datasets and (B) striatal cell types visualized by violin plots. (C) Stacked bar plot showing the contribution of cells from individual datasets across the 35 clusters and accompanied by violin plots showing the number of detected genes across striatal cell type clusters. (D) Scaled expression of marker genes for each cell type.

**Supplemental Figure 2. cellAlign analysis of dSPNs and iSPNs. (A)** Datasets plotted over pseudotime for SPNs, dSPNs (top), iSPNs (bottom) using C17 cells as root populations. **(B)** Datasets plotted over pseudotime for SPNs, dSPNs (top), iSPNs (bottom) using P9 cells as root populations. **(C)** Dissimilarity matrix and global alignment of pseudotime trajectories between iSPNs and dSPNs using cells from the P9 dataset as root.

**Supplemental Figure 3. Uncropped Western blots of Figure 5E.** Western blot results using antibodies for MOBP and TUJ1. Samples are imaged using an Odyssey infrared imaging system.



























Ppp1r1b









Figure S2

С





Pseudotime Shift Abs. Sign 0 0.5 -0+

Scaled Distance

0

iSPNs dSPNs

## Figure S3

Marker

(kDa)



M= protein marker  $1-3=Foxp1^{CTL}$  samples  $4-6=Foxp1^{D1}$  samples  $7-9=Foxp1^{D2}$  samples  $10-12=Foxp1^{DD}$  samples