a

Fluorescence Unit vs Length [bp]

b

Sequencing Saturation(%) vs Total Reads (*10^6)

Batch
1
2
3

c

Genes detected

Batch 1, Batch 2, Batch 3, Ho 2018, Gokce 2016

d

UMAP_2 vs UMAP_1

Neurons
Astrocytes
OPC
Oligo
Macrophages
Vascular

Oligo
Astrocytes
OPC
Vascular cells
Macrophages
Neurons

e

UMAP_2 vs UMAP_1

Batch 1
Batch 2
Batch 3
Gokce 2016
Ho 2018

f

UMAP_2 vs UMAP_1

Drd1-Ho   Drd2-Ho   Retro-labelled

g

Drd1

UMAP_2 vs UMAP_1

h

D1^{NAc-VM}
D1^{NAc-VP}

Arc **

Expression Level (Normalized TPM)

Klf5 **

Expression Level (Normalized TPM)

i

Retro-DIO-mCherry   NAc   Retro-DIO-EYFP

VM   *D1-Cre*   VP

j

Arc   *mCherry*   *EYFP*   Merge

Klf5   *mCherry*   *EYFP*   Merge

k

D1^{NAc-VM}
D1^{NAc-VP}

Arc **

Puncta number

Cumulative probability vs Puncta numbers / Arc$^+$

D1^{NAc-VM}
D1^{NAc-VP}

Klf5 *

Puncta number

Cumulative probability vs Puncta numbers / Klf5$^+$

Supplementary information, Fig. 7 Quality control of scRNA-Seq and correlation with previous RNA-Seq datasets of mouse striatum.

a, Representative example of PCR-amplified cDNA from one cell. **b,** Sequencing saturation plot from three batches of libraries prepared. The percentage of cumulative detected kmers from every 10k reads were plotted. **c,** Number of gene count distribution from each batch of samples, as well as striatal single cell data from Ho et al. (Ho 2018) and Gokce et al. (Gokce 2016). **d,** Distribution of data as colored by batch and origin. **e,** UMAP plot of combined single cell data from Ho *et al*. (Ho 2018) and Gokce *et al*. (Gokce 2016) and data we collected. **f,** Comparison of distribution of D1 and D2 cells from Ho *et al*. (Ho 2018) in neurons we collected. **g,** Distribution of D1-expressing cells in the neuronal population. **h,** Violin plot of *Arc* and *Klf5* expression in transcriptome analysis [Negative binomial generalized linear models, $D1^{NAc-VM}$ n = 120 cells, $D1^{NAc-VP}$ n = 182 cells, *Arc*: W = -2.743, $p = 0.007$; *Klf5*: W = 3.084, $p = 0.002$] **i,j,** Representative confocal images of smFISH of *EYFP* ($D1^{NAc-VP}$), *mCherry* ($D1^{NAc-VM}$) and *Arc* or *Klf5*   (white) in the NAc of D1-Cre mice with the injection of $AAV_{2/retro}$-*EF1α-DIO-EYFP* into the VP and $AAV_{2/retro}$-*EF1α-DIO-mCherry* in the VM. Scale bar: 25 μm. **k,** Quantification bar graph and cumulative frequency distribution of *Arc* and *Klf5* expression in $D1^{NAc-VM}$ (*EYFP*$^+$) and $D1^{NAc-VP}$ (*mCherry*$^+$) neurons. [VM: n = 3, VP: n = 3, Two-tail *Student's t*-test, *Arc* :$t(4) = -6.831$, $p = 0.0024$; *Klf5* :$t(4) = 3.423$, $p = 0.0267$] $^{***}p < 0.001$ $^{*}p < 0.05$, $^{**}p < 0.01$. Related to Figure 4.