Cell Reports, Volume *42*

Supplemental information

Spiny projection neurons exhibit transcriptional signatures within subregions of the dorsal striatum

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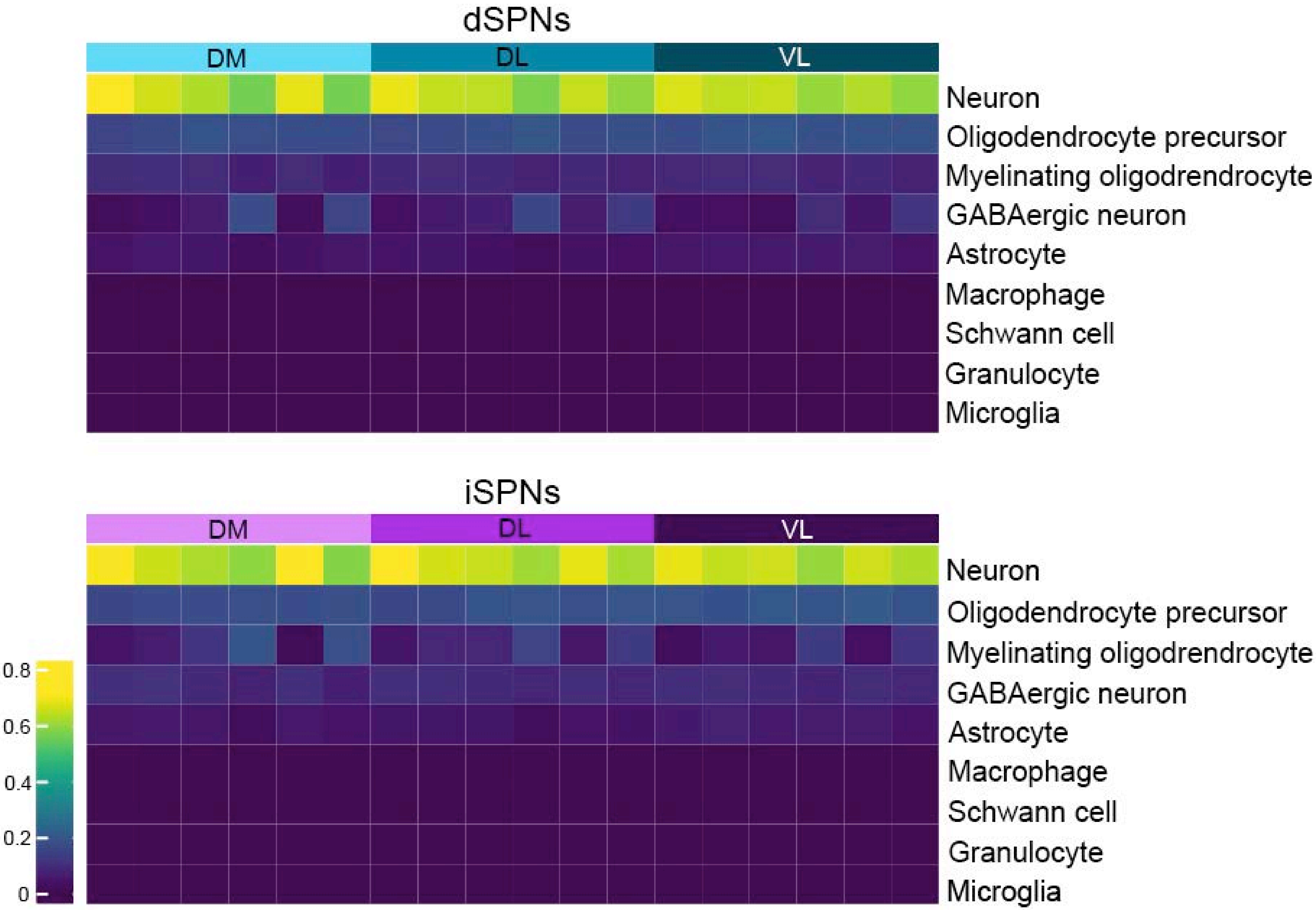

Figure S1. The majority of cells sampled were neuronal based on spatial deconvolution, related to Figure 1. Normalized gene expression data was used along with the Adult-Brain_MCA cell profile matrix as cell markers. Scale bar represents proportion of cells sampled. Abbreviations are: dorsomedial (DM), dorsolateral (DL) and ventrolateral (VL).

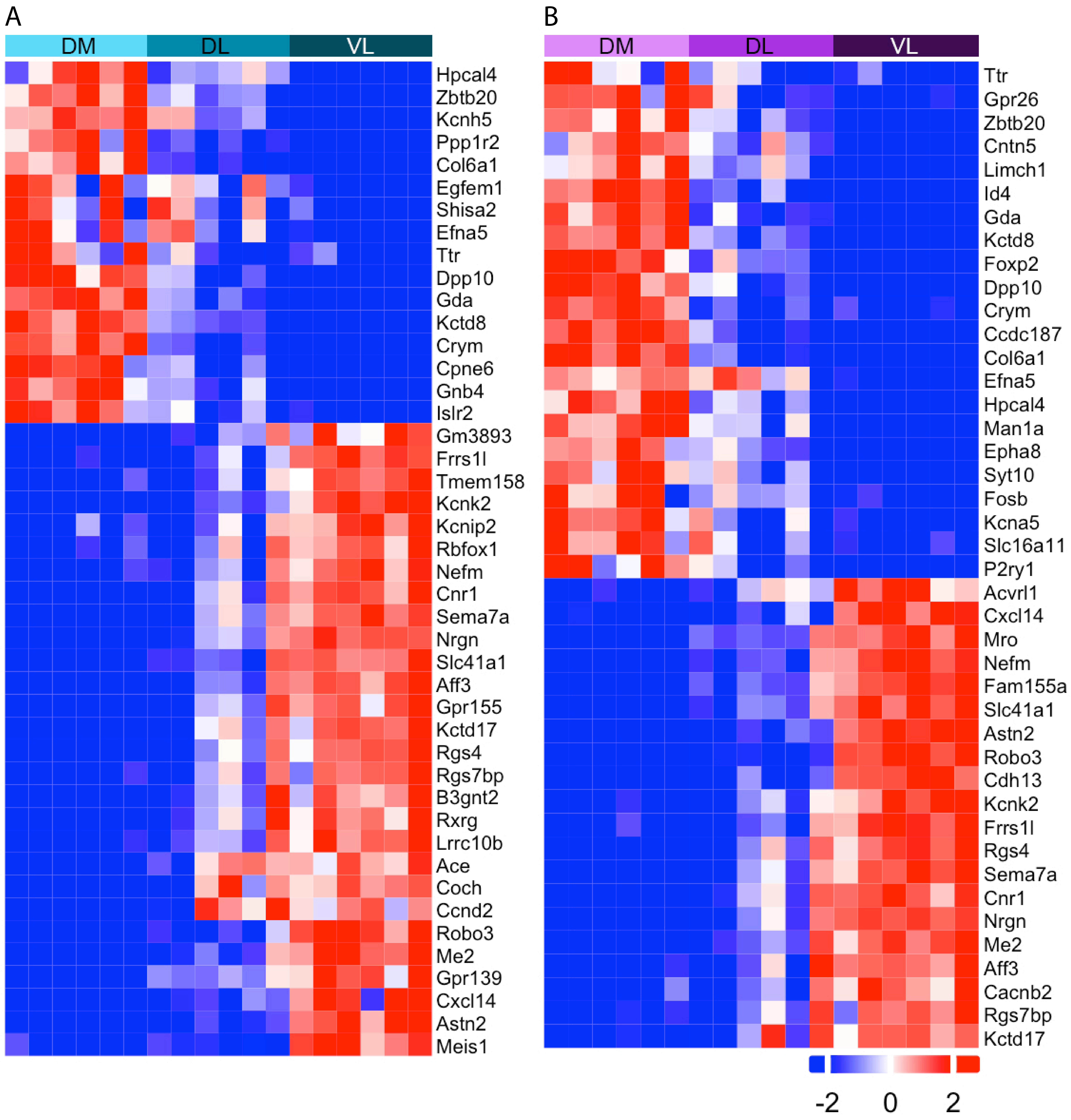

Figure S2. Heatmaps illustrating gradients of gene expression in dorsomedial (DM), dorsolateral (DL) and ventrolateral (VL) striatum in dSPNs (A) and iSPNs (B), related to Figure 3. Genes with > 2-fold change in gene expression between DM and VL are included. Each column within a region represents an individual animal (n=6); gene expression was assessed in every region and each SPN subtype for all mice. The order of animals is consistent across regions and cell types.

Table S1. Genes with >2-fold difference in expression between dorsomedial and ventrolateral striatum in dSPNs and/or iSPNs (p-adj < 0.01), Related to Figure 2

Gene	**Gene product**	**|Fold-change|**	
Genes enriched in dorsomedial striatum		**dSPNs**	**iSPNs**
Ccdc187	Coiled-coil domain containing 187	1.664	2.337
Cntn5	contactin 5	1.892	2.075
Col6a1	collagen, type VI alpha 1	6.431	5.320
Cpne6	copine VI	2.143	1.845
Crym	crystallin mu	3.331	2.650
Dpp10	dipeptidyl peptidase 10	2.708	2.692
Efna5	ephrin A5	2.053	2.280
Egfem1	EGF-like and EMI domain containing 1	2.102	1.732
Epha8	EPH receptor A8	1.923	2.183
Fosb	FosB proto-oncogene	1.776	2.206
Foxp2	forkhead box P2	1.222	2.016
Gda	guanine deaminase	2.196	2.159
Gnb4	G protein subunit beta 4	2.146	1.432
Gpr26	G protein-coupled receptor 26	1.906	2.362
Hpcal4	hippocalcin like 4	2.196	2.510
Id4	inhibitor of DNA binding 4	1.777	2.205
Islr2	immunoglobulin superfamily containing leucine rich repeat 2	2.271	1.973
Kcna5	potassium voltage-gated channel subfamily A member 5	1.863	2.037
Kcnh5	potassium voltage-gated channel subfamily H member 5	2.070	1.843
Kctd8	potassium channel tetramerisation domain containing 8	2.527	3.261
Limch1	LIM and calponin homology domains 1	1.619	2.342
Man1a	mannosidase 1, alpha	1.537	2.140
P2ry1	purinergic receptor P2Y1	1.016	2.005
Ppp1r2	protein phosphatase 1 regulatory inhibitor subunit 2	2.145	1.804
Shisa2	shisa family member 2	2.017	1.770
Slc16a11	solute carrier family 16 member 11	1.381	2.068
Syt10	synaptotagmin 10	1.634	2.413
Ttr	transthyretin	2.380	2.459
Zbtb20	zinc finger and BTB domain containing 20	2.321	2.087
Genes enriched in ventrolateral striatum			
Ace	angiotensin 1 converting enzyme	2.123	1.820
Acvrl1	activin A receptor like type 1	1.881	2.151
Aff3	ALF transcription elongation factor 3	2.424	2.131
Astn2	astrotactin 2	3.926	4.830
B3gnt2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	2.091	1.759

Cacnb2	calcium voltage-gated channel auxiliary subunit beta 2	1.886	2.018
Ccnd2	cyclin D2	2.211	1.796
Cdh13	cadherin 13	1.529	2.118
Cnr1	cannabinoid receptor 1	5.711	5.048
Coch	cochlin	2.041	1.764
Cxcl14	C-X-C motif chemokine ligand 14	2.953	2.522
Fam155a	Family with sequence similarity 155 member A	1.691	2.067
Frrs1l	ferric-chelate reductase 1 like	2.236	2.114
Gm3893	predicted gene 3893	2.086	1.813
Gpr139	G protein-coupled receptor 139	2.352	1.231
Gpr155	G protein-coupled receptor 155	3.734	1.998
Kcnip2	potassium voltage-gated channel interacting protein 2	2.066	1.808
Kcnk2	potassium two pore domain channel subfamily K member 2	2.952	2.336
Kctd17	potassium channel tetramerisation domain containing 17	2.577	2.245
Lrrc10b	leucine rich repeat containing 10B	2.140	1.986
Me2	malic enzyme 2	2.820	2.608
Meis1	meis homeobox 1	2.416	1.550
Mro	maestro	1.837	2.605
Nefm	neurofilament medium polypeptide	2.558	3.331
Nrgn	neurogranin	3.546	3.054
Rbfox1	RNA binding protein fox-1 homolog 1	2.013	1.926
Rgs4	regulator of G protein signaling 4	2.609	2.501
Rgs7bp	regulator of G protein signaling 7 binding protein	2.078	2.027
Robo3	roundabout guidance receptor 3	3.461	6.118
Rxrg	retinoid X receptor gamma	2.012	1.999
Sema7a	semaphorin 7A	2.758	2.766
Slc41a1	solute carrier family 41 member 1	2.177	2.156
Tmem158	transmembrane protein 158	2.109	1.818

Protein names obtained from the National Library of Medicine, National Center for Biotechnology Information.

Table S2. Genes with region-dependent expression in either dSPNs or iSPNs. Related to Figure 3

Gene	Factor	F (df1, df2)	P value
Ano3	Region x cell type	F (2, 20) = 24.32	P<0.0001
Atp6ap1l	Region x cell type	F (2, 20) = 8.012	P=0.0028
Baiap3	Region x cell type	F (2, 20) = 5.588	P=0.0118
Ceacam10	Region x cell type	F (2, 20) = 5.391	P=0.0134
Cfap77	Region x cell type	F (2, 20) = 3.533	P=0.0485
Chrm4	Region x cell type	F (2, 20) = 25.54	P<0.0001
Cntnap3	Region x cell type	F (2, 20) = 8.040	P=0.0027
Foxp2	Region x cell type	F (2, 20) = 6.123	P=0.0084
Galnt18	Region x cell type	F (2, 20) = 9.322	P=0.0014
Galr1	Region x cell type	F (2, 20) = 4.006	P=0.0344
Gm5741	Region x cell type	F (2, 20) = 3.606	P=0.0460
Gpr139	Region x cell type	F (2, 20) = 16.63	P<0.0001
Kcng1	Region x cell type	F (2, 20) = 12.89	P=0.0003
Mfsd10	Region x cell type	F (2, 20) = 4.258	P=0.0288
Myo5c	Region x cell type	F (2, 20) = 9.366	P=0.0013
Necab1	Region x cell type	F (2, 20) = 118.8	P<0.0001
Nt5e	Region x cell type	F (2, 20) = 16.44	P<0.0001
P2ry1	Region x cell type	F (2, 20) = 7.551	P=0.0036
Plxnd1	Region x cell type	F (2, 20) = 4.890	P=0.0187
Rbp1	Region x cell type	F (2, 20) = 4.161	P=0.0308
Serpine2	Region x cell type	F (2, 20) = 18.01	P<0.0001
Stum	Region x cell type	F (2, 20) = 3.912	P=0.0368
Synpr	Region x cell type	F (2, 20) = 7.762	P=0.0032
Zfp512	Region x cell type	F (2, 20) = 10.01	P=0.0010

Results from two-way repeated measures ANOVAs with region as the repeated measure