

Figure S2

Sn-RNA-Seq run summaries

A

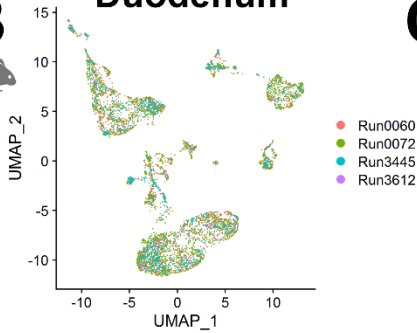


	Duodenum	Ileum	Colon	All
Approx. Nuclei Encapsulated	12884	24413	30551	67848
10X Total Runs	2	4	3	9
inDrop Total Runs	2	2	2	6
Total Runs	4	6	5	15
10x Total Nuclei	5394	8291	14271	27956
inDrop Total Nuclei	1756	3570	3328	8654
Total Nuclei Pre-cleaning	7150	11861	17599	36610
Total Nuclei Post-cleaning *	6217	8379	10612	25208
Total Reads 10x	7.8E+08	1.8E+09	9.5E+08	3.6E+09
Total Reads inDrop	1.7E+08	1.3E+08	2.5E+08	5.5E+08
Total Reads	9.4E+08	2.0E+09	1.2E+09	4.1E+09

B

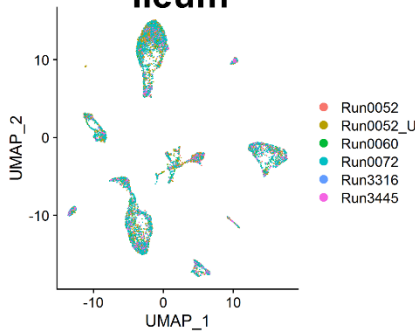


Duodenum



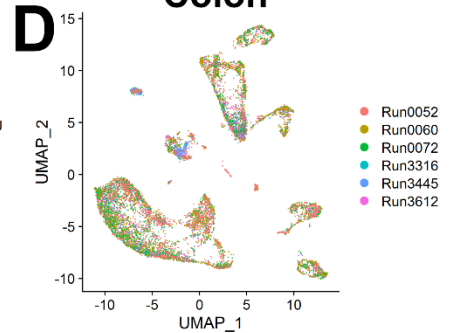
C

Ileum



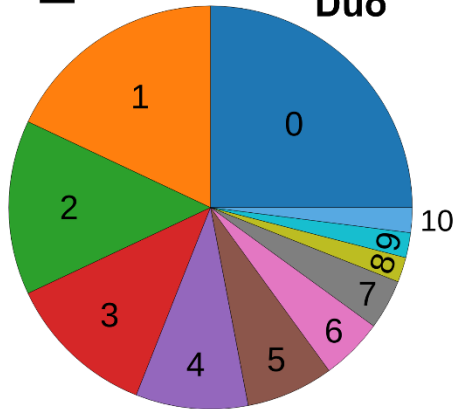
D

Colon



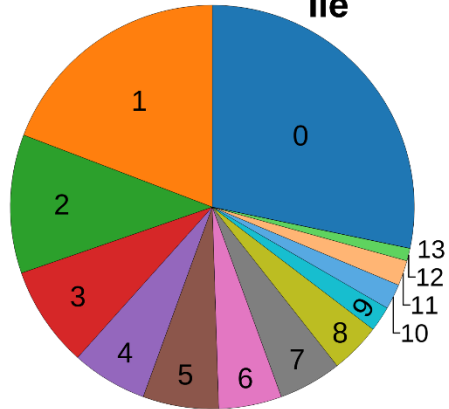
E

Duo



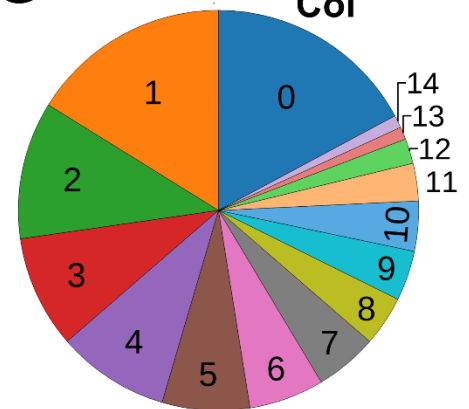
F

Ile



G

Col



H

Cluster composition (% Total)

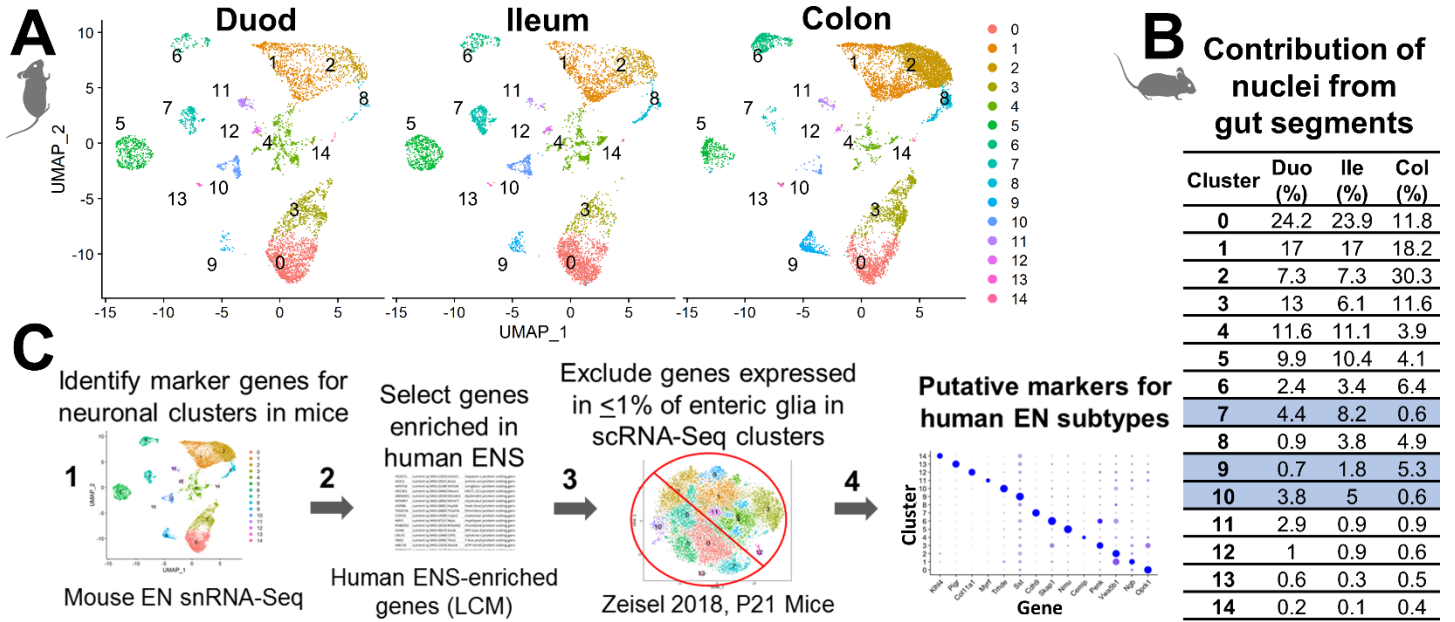
Cluster	Duodenum	Ileum	Colon
0	24.6%	28.5%	17.5%
1	18.2%	19.0%	16.2%
2	13.6%	11.4%	10.7%
3	11.8%	7.8%	9.2%
4	8.9%	6.4%	8.8%
5	7.2%	5.9%	7.1%
6	5.2%	5.1%	5.9%
7	4.3%	4.6%	5.1%
8	2.4%	4.4%	4.5%
9	2.3%	2.3%	4.3%
10	1.5%	1.8%	4.2%
11	-	1.7%	3.0%
12	-	0.6%	1.8%
13	-	0.4%	1.3%
14	-	-	0.6%

I

Cluster composition (Total Nuclei)

Cluster	Duodenum	Ileum	Colon
0	1531	2388	1856
1	1132	1594	1714
2	848	959	1133
3	731	650	972
4	553	534	936
5	445	491	756
6	321	429	626
7	265	386	536
8	151	367	475
9	144	195	452
10	96	155	447
11	-	142	320
12	-	54	189
13	-	35	141
14	-	-	59

Figure S3



D Putative subtype identities and top cluster markers

Cluster	Proposed Subtype	Known Markers	Top 3 Mouse	Top 3 Human-Match	% Tot. (Lit)	% Obs.
0	Excitatory longitudinal MMN	Calb2/Chat/ Tac1+/-	Brinp2/Fbxw15/Specp1	Oprk1/Brinp2/Tmem132c	13% (1)	18.7%
1	Inhibitory longitudinal MMN	Nos1/Vip	Ass1/Cygb/Col25a1	Ngb/Gsg1/Col25a1	3% (1)	~8.2% ^E
2	Inhibitory circular MMN	Nos1/Vip/Npy+/-	Gm4876/Gm16083/Dsc2	Vwa5b1/Sv2b/Oprd1	23% (1)	~26.5% ^E
3	Excitatory circular MMN	Chat/Tac1/Calb2+/-	Tac1/Necab2/Htr2b	Penk/Sncb/Olfm3	21% (1)	7.7%
3s	Ascending IN	Chat/Tac1/Calb2+/-	Kctd16/Unc5d [^]	Kctd16/Unc5d [^]	4% (1)	~2.6% ^E
4	Unassigned	-	Slc24a3/Myh11/Carmn	Cemip/Kcnp1	-	8.1%
5	IPAN	Calcb/Calb2+/-	Nmu/Pcdh10/Cysltr2	Nmu/Pcdh10/Cbln2	~9%** (1)	7.5%
6	IPAN	Nefl/Calb1[sparse]	Nxph2/Cckar/Eif3h	Skap1/Nefl/Nxph2	~9%** (1)	4.0%
6s	Serotonergic (Descend. IN)	Nefl/5-HT	Slc6a4/Carpt/Grp [^]	Slc6a4/Carpt/Grp [^]	1% (1)	0.5%
7	Type I/'simple'	Nefl	Cdh9/Zim1/B230209E15Rik	Cdh9/Mgat4c/Klhl1	~9%** (1,2)	3.5%
7s	Intestinofugal***	Chat +/-Cck/Grp	Slc24a3/Carmn [^]	Slc24a3/Carmn [^]	~0.25% ^G (1,3)	0.3%
8	Unassigned	Nos1/Gal/Sst(low)	*No highly-selective markers	*No selective markers	-	3.6%
9	Descending IN (Filamentous)	Sst/Calb2/Th	Adamts1/Gm30382/Irf1	Sst/Galnt5/Pantr1	4% ^F (1)	3.0%
10	Descending IN (Type I)	Chat/Nos1/Gad2	Neurod6/AI593442/Bcr	Trhde/Bean1/Neurod6	3% (1)	2.8%
11	Unassigned	-	C3/Igfbp6/Upk3b	Myrf/Nkain4/Cldn15	-	1.4%
12	Unassigned	-	Cdh19/Apoe/Col11a1	Col11a1/Tmprss5/Car12	-	0.82%
13	Unassigned	-	Reg3b/Pigr/Epcam	Pigr/Klf5/Cdh1	-	0.45%
14	Unassigned	-	Ccl21a/Mmnr1/Pecam1	Klhl4/Arap3/Radil	-	0.03%

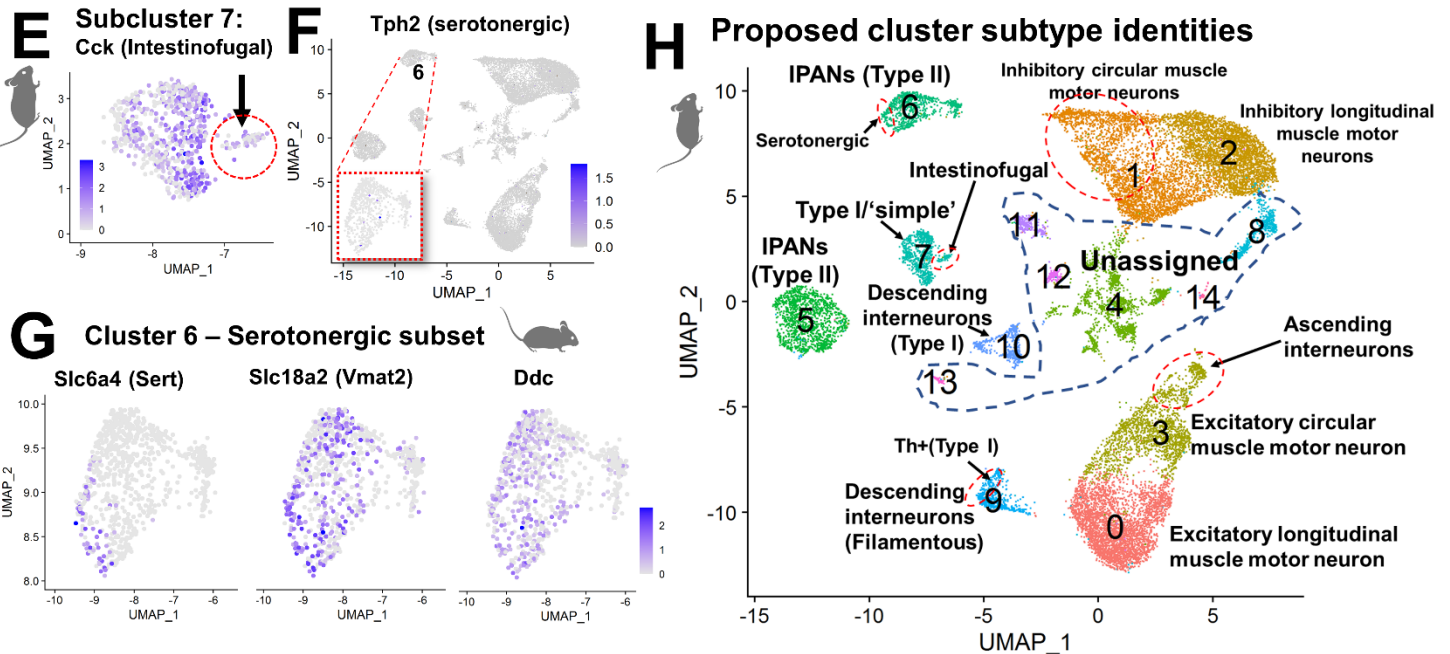


Figure S4

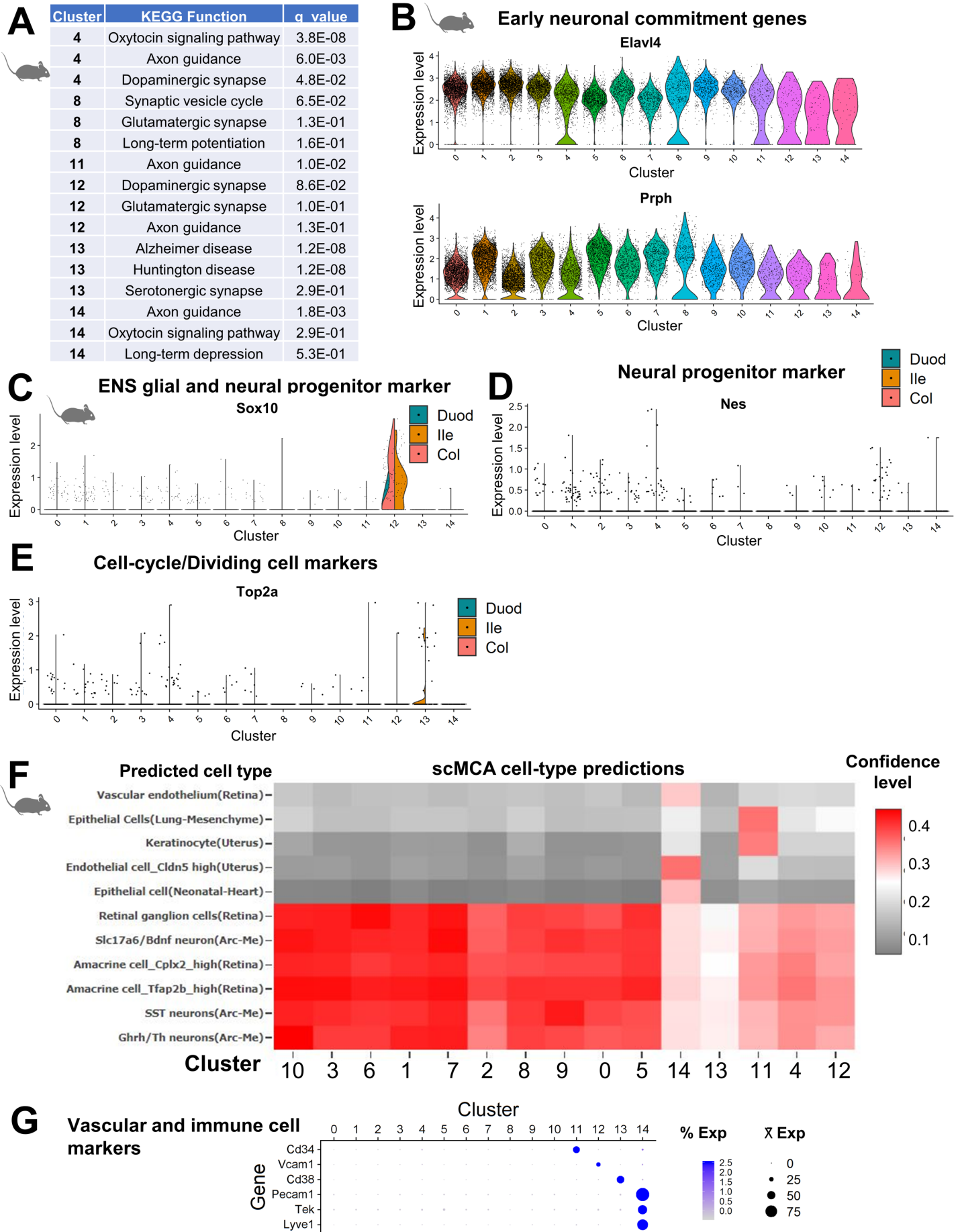


Figure S5

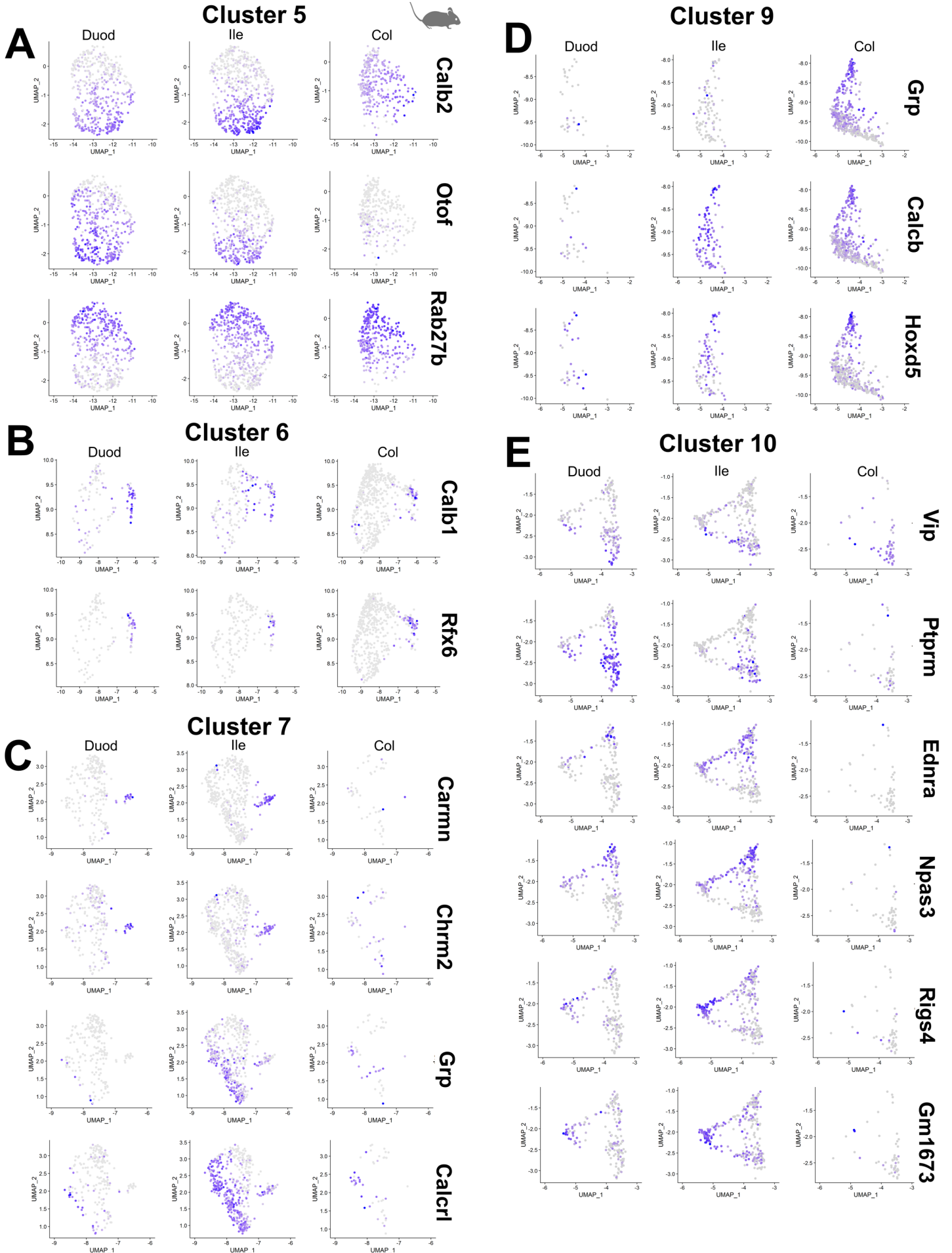


Figure S6

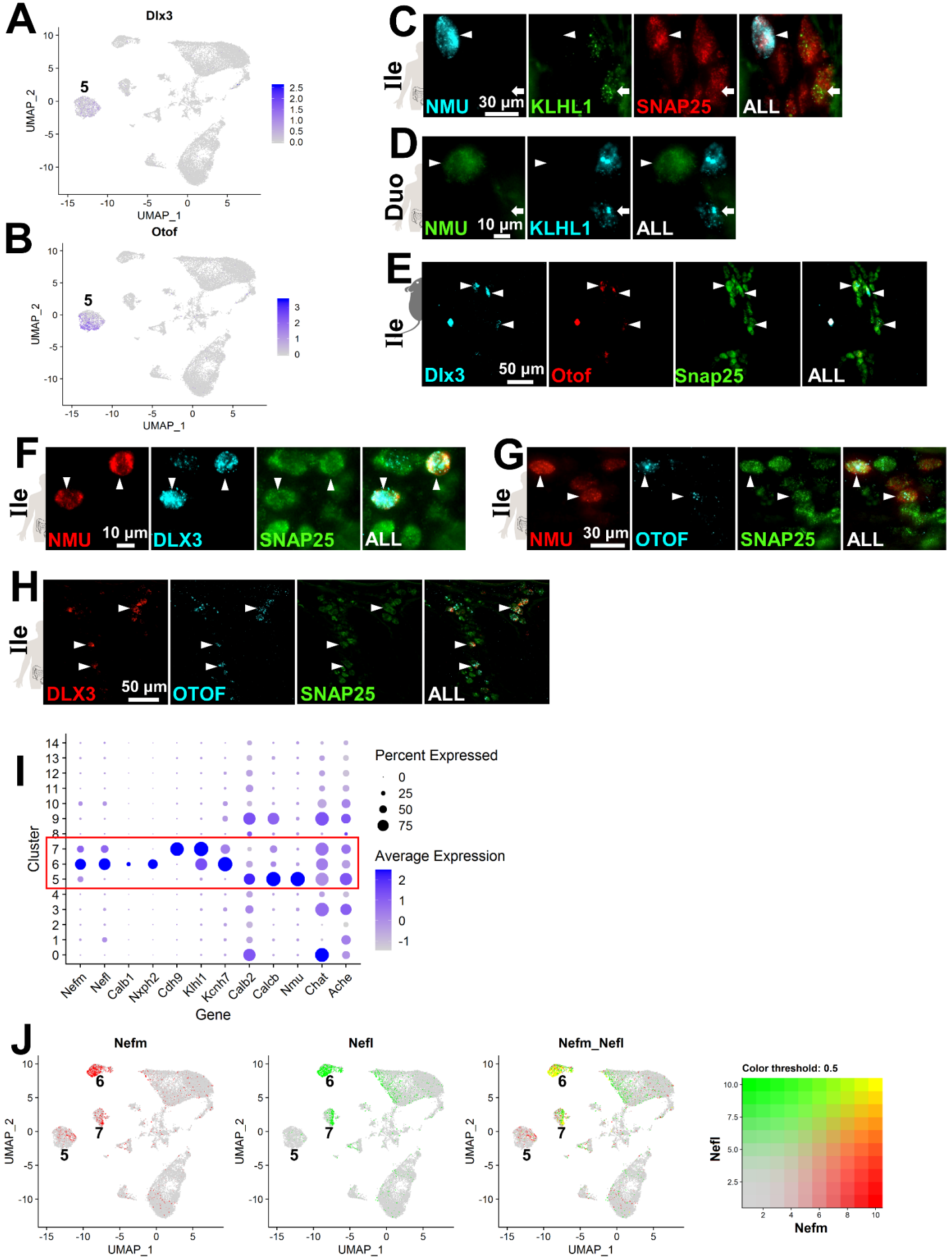


Figure S7

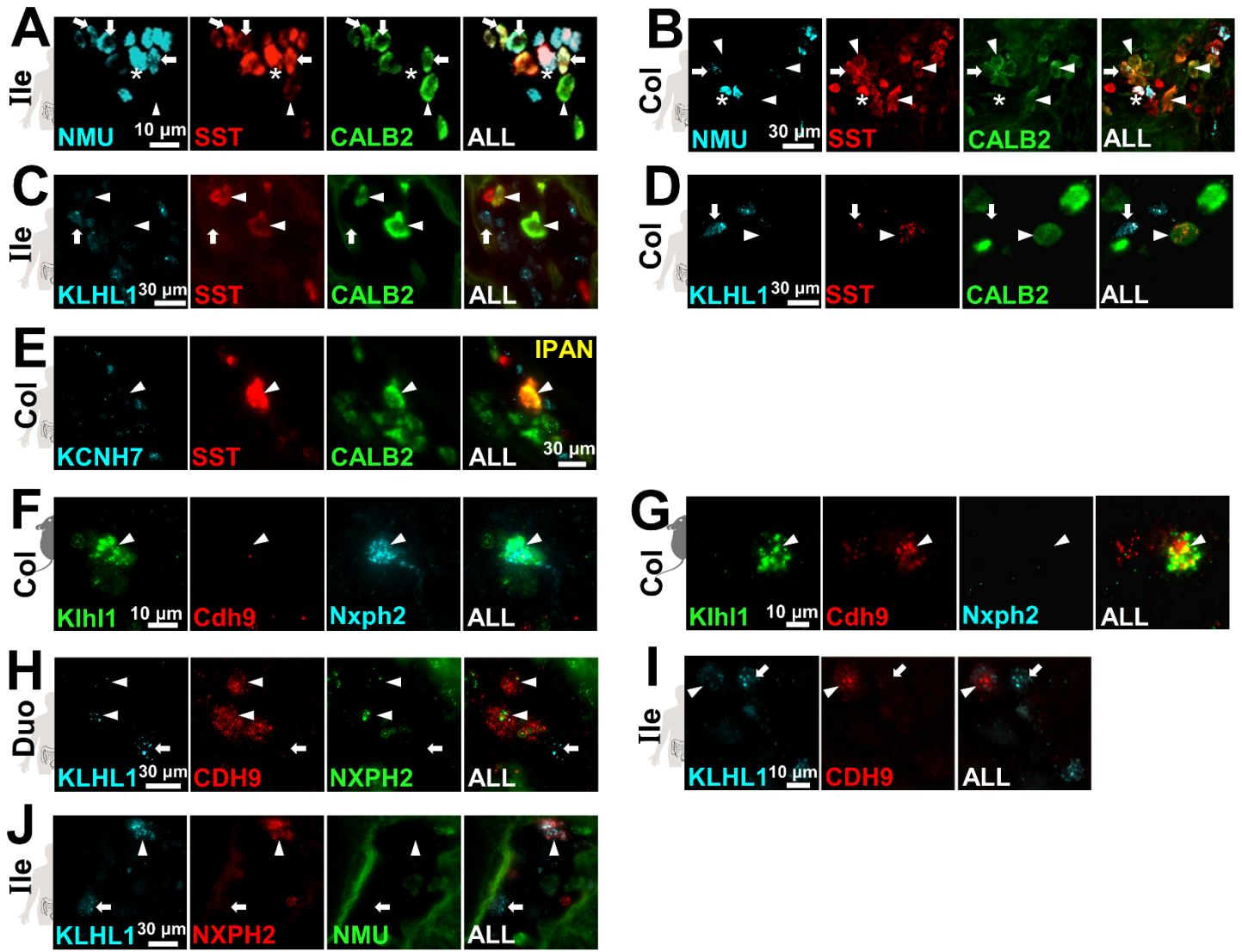


Figure S8

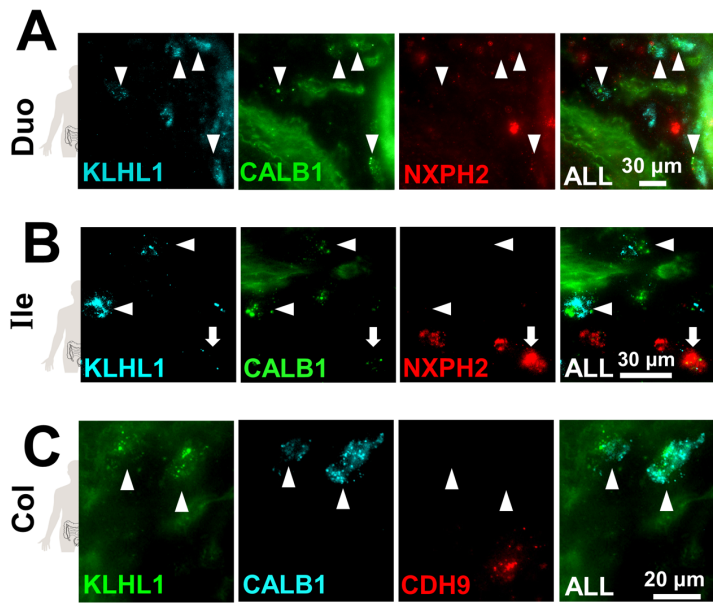


Figure S9

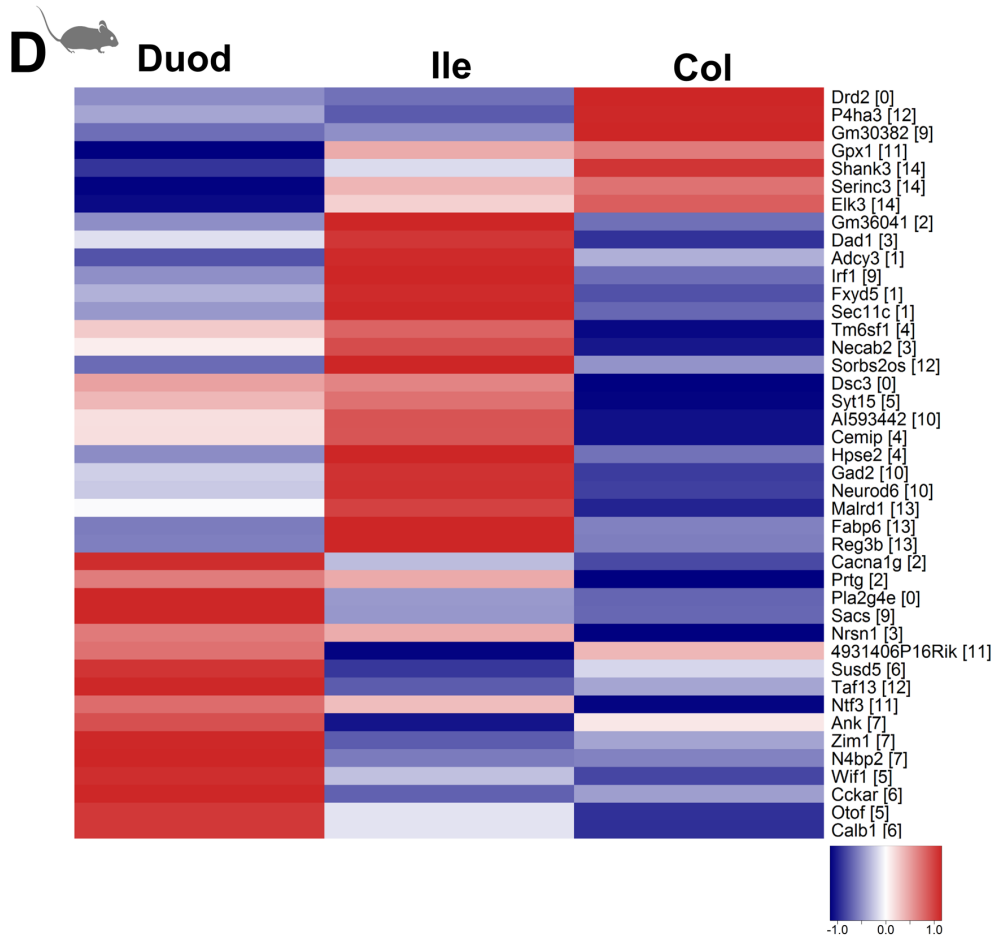
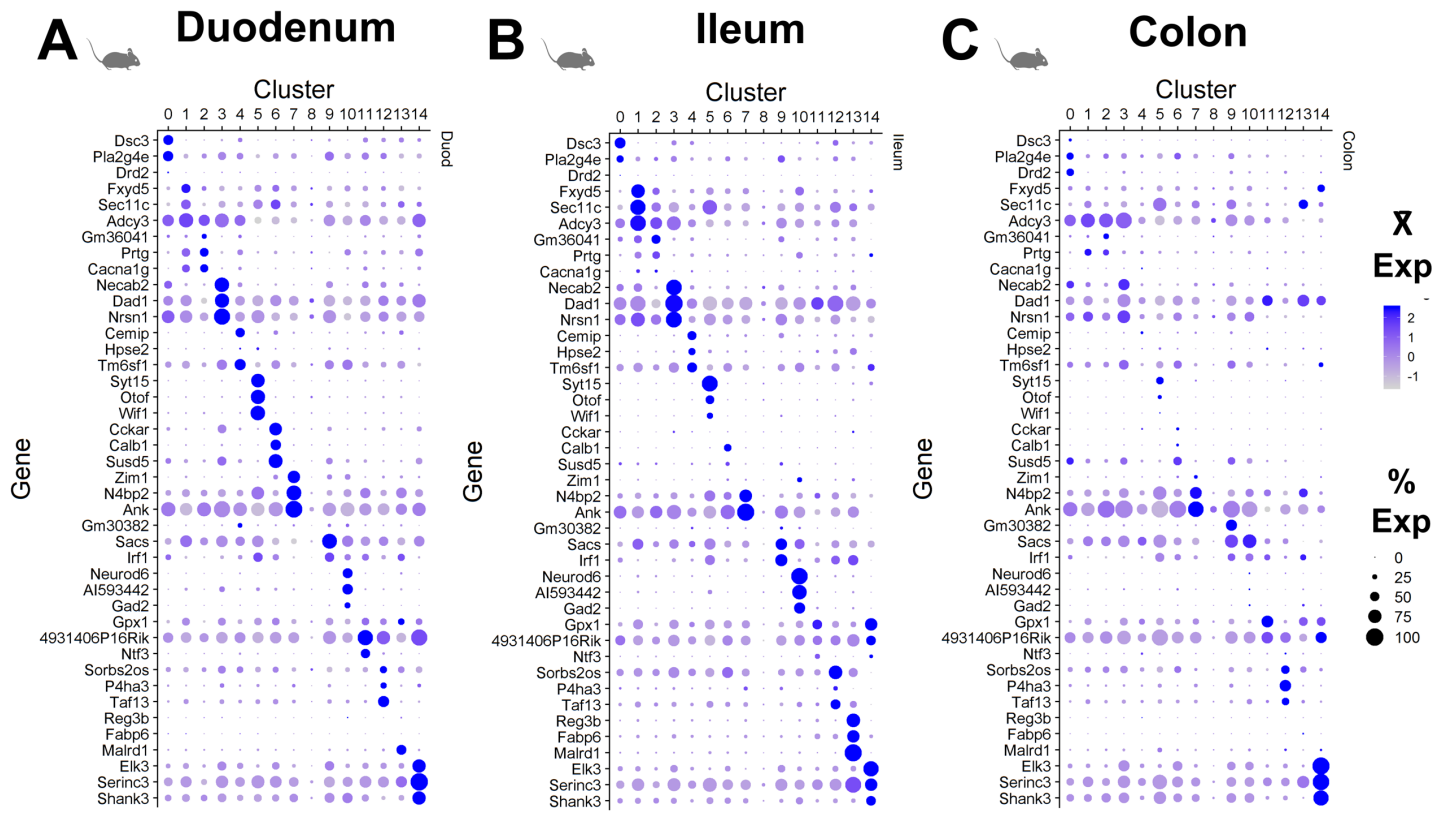


Figure S10

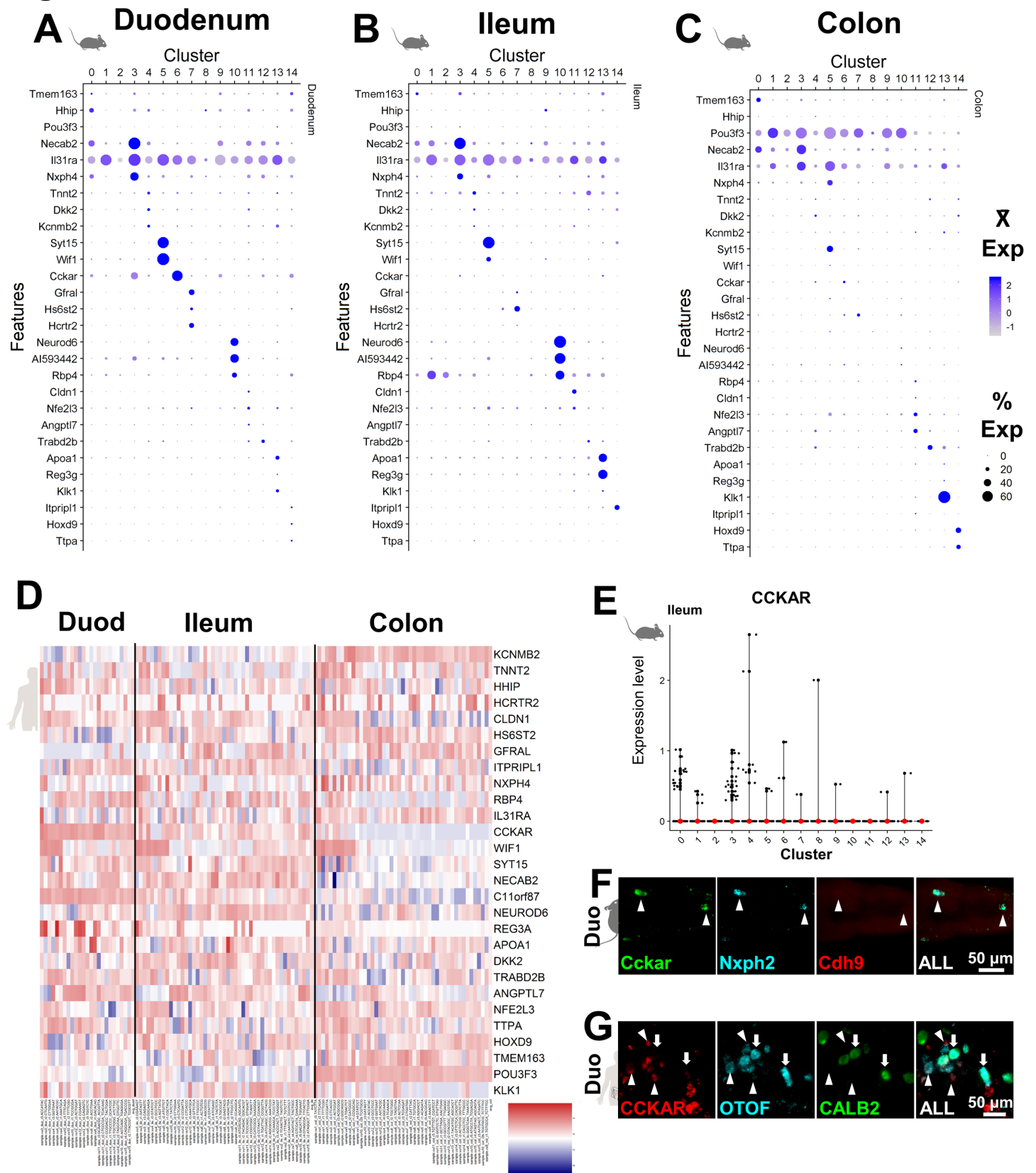
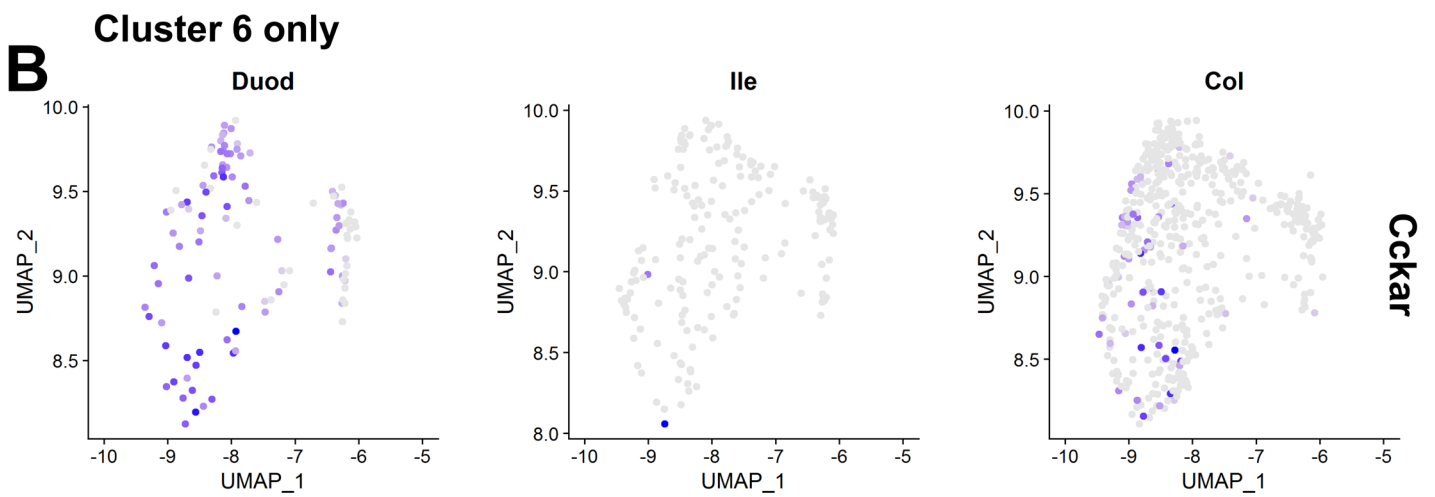
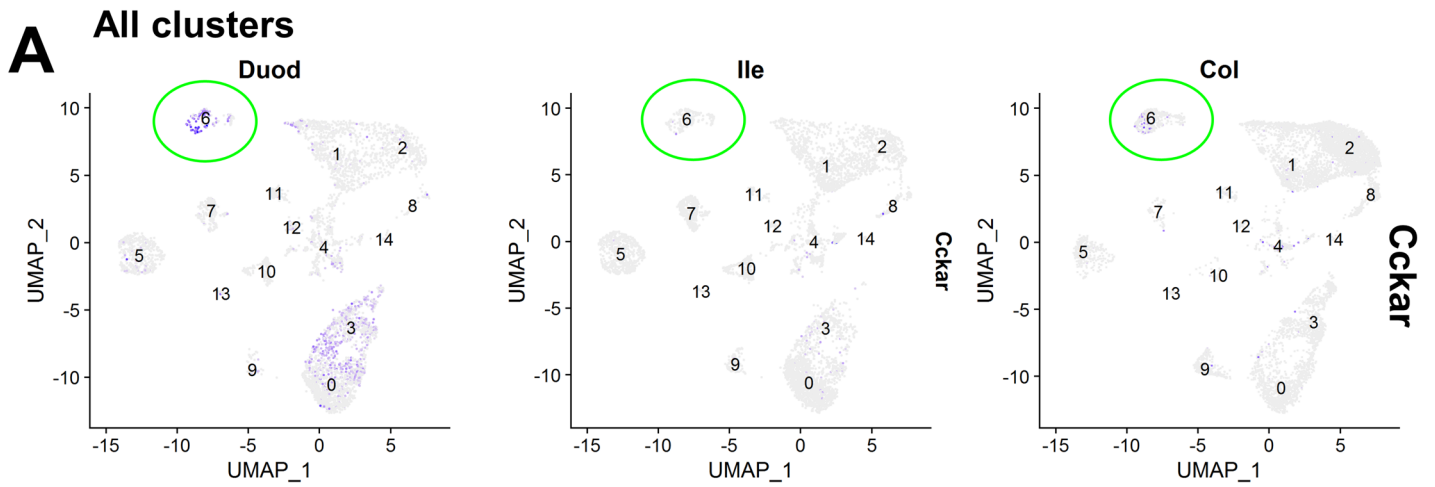


Figure S11



Regional expression of Cckar in neuronal cluster 6 in mice

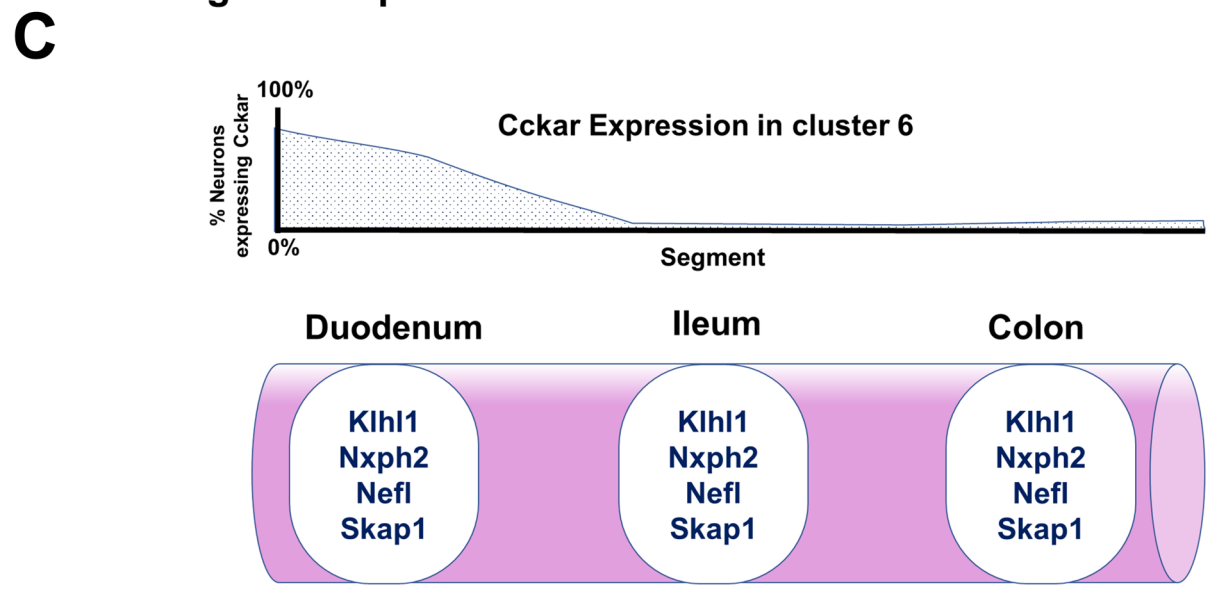


Figure S12

A



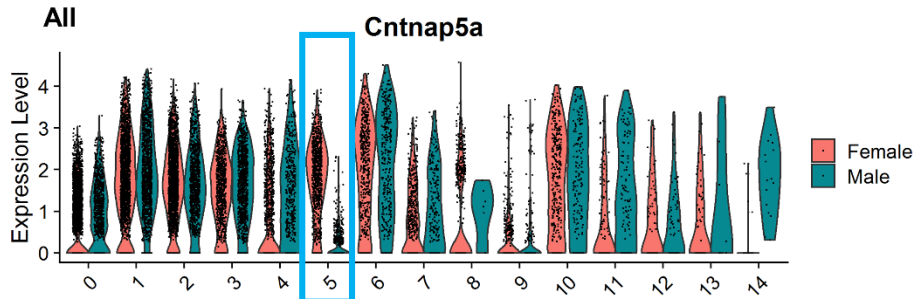
Gene	Sex	logFC	Segment(s)
<i>XIST</i>	Female	5.5, 5.0, 4.7	Col, Ile, Duo
<i>AC005332.2</i>	Female	5.1	Duo
<i>SLC6A14</i>	Female	1.3	Col
<i>TACSTD2</i>	Female	1.2	Col
<i>LINC02529</i>	Female	1.2	Col
<i>MUC5B</i>	Female	1.1	Col
<i>ZNF516</i>	Female	1.1	Col
<i>PLXNB3</i>	Female	1.1	Col
<i>RPTOR</i>	Female	1	Col
<i>RN7SL2</i>	Female	1	Col
<i>RPS4Y1</i>	Male	-12.0, -10.9, -10.3	Ile, Col, Duo
<i>EIF1AY</i>	Male	-11.1, -10.4, -10.3	Ile, Col, Duo
<i>DDX3Y</i>	Male	-10.0, -9.6	Ile, Col, Duo
<i>NLGN4Y</i>	Male	-9.3, -9.1, -8.7	Ile, Duo, Col
<i>UTY</i>	Male	-8.5, -7.8, -7.6	Ile, Duo, Col
<i>ZFY</i>	Male	-8.3, -7.7, -7.6	Ile, Col, Duo
<i>KDM5D</i>	Male	-7.6, -7.4, -6.7	Ile, Duo, Col
<i>USP9Y</i>	Male	-7.1, -7.0, -6.8	Duo, Ile, Col
<i>TMSB4Y</i>	Male	-6.7, -6.3	Ile, Col, Duo
<i>TTY14</i>	Male	-6.3, -6.0, -5.2	Ile, Col, Duo

B

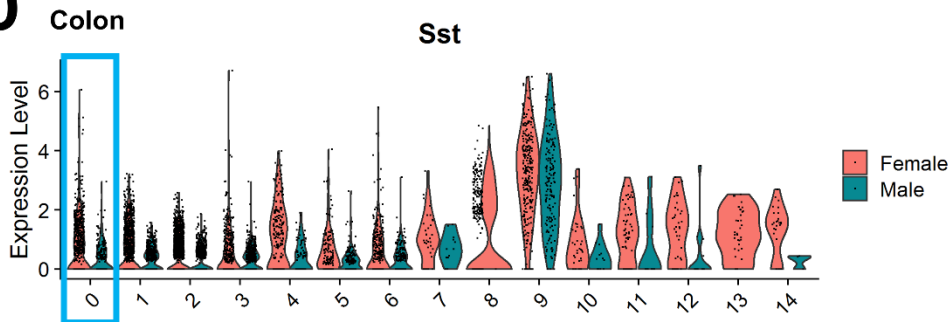


Gene	Sex	Avg logFC	Cluster(s)	Segment(s)	% Cell Exp Diff
<i>Xist</i>	Female	2.4	ALL	Col, Ile, Duo	98%
<i>Tsix</i>	Female	1	ALL	Ile, Duo, Col	81%
<i>Sst</i>	Female	1	0	Col	10%
<i>Cntnap5a</i>	Female	1.7	5	Duo, Ile, Col	47%
<i>Uty</i>	Male	-1.1	ALL	Col, Duo, Ile	-89%
<i>Eif2s3y</i>	Male	-0.8	ALL	Ile, Duo, Col	-77%
<i>Ddx3y</i>	Male	-0.5	ALL	Duo, Ile, Col	-68%
<i>Kdm5d</i>	Male	-0.3	5, 10	Col, Duo	-62%

C



D



E

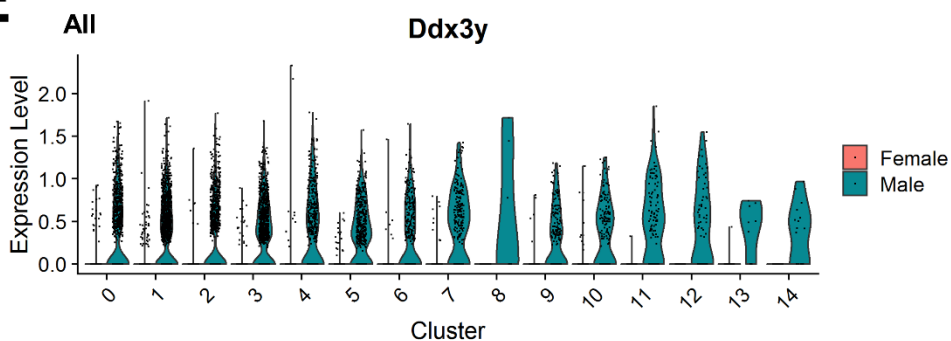
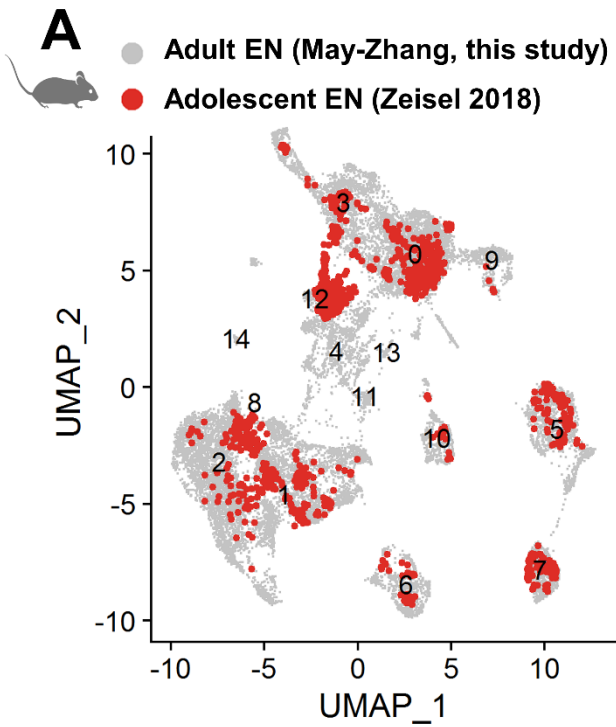



Figure S13



B



Cluster	Proposed Identity	Adult EN (% Total)	Juvenile EN (% Total)
0	Excitatory longitudinal muscle motor neurons	18.6%	21.6%
1	Inhibitory longitudinal muscle motor neurons	17.5%	19.3%
2	Inhibitory circular muscle motor neurons	17.4%	10.9%
3	Excitatory circular muscle motor neurons	10.3%	8.4%
4	Unassigned	8.1%	8.0%
5	IPAN	7.5%	7.1%
6	IPAN	4.5%	6.8%
7	(Type I/'simple')	3.8%	6.7%
8	Unassigned	3.5%	5.9%
9	Descending interneurons (Filamentous)	3.0%	3.1%
10	Descending interneurons (Type I)	2.8%	2.3%
11	Unassigned	1.4%	0.0%
12	Unassigned	0.8%	0.0%
13	Unassigned	0.4%	0.0%
14	Unassigned	0.3%	0.0%