Appendices

The short-and long-term effects of genetically silencing deep-layer cortical glutamatergic projection neurons on GABAergic neurons

UNIVERSITY OF OXFORD

Florina Petra Szabó

St John's College

A thesis submitted for the degree of

Doctor of Philosophy

Appendix 1

CHAPTER 3

Transgenic strain	Mouse Genotype	Experimental Cohort	Timepoint	Nr of cells	Nr of sections	Measured features
Rbp4-Cre;Ai14;Snap25$^{fl/fl}$	Cre-;Ai14;Snap25$^{fl/fl}$ or Cre-;Ai14;Snap25$^{fl/+}$ (ctrl)	Developmental	P14	175	4	*Soma area* *Perimeter* *Circularity* *Roundness* *Solidity*
Rbp4-Cre;Ai14;Snap25$^{fl/fl}$	Cre+;Ai14;Snap25$^{fl/fl}$ (cKO)	Developmental	P14	131	4	
Rbp4-Cre;Ai14;Snap25$^{fl/fl}$	Cre-;Ai14;Snap25$^{fl/fl}$ or Cre-;Ai14;Snap25$^{fl/+}$ (ctrl)	Developmental	P21	180	4	
Rbp4-Cre;Ai14;Snap25$^{fl/fl}$	Cre+;Ai14;Snap25$^{fl/fl}$ (cKO)	Developmental	P21	236	4	
Rbp4-Cre;Ai14;Snap25$^{fl/fl}$	Cre-;Ai14;Snap25$^{fl/fl}$ or Cre-;Ai14;Snap25$^{fl/+}$ (ctrl)	Adult	12 weeks	168	3	
Rbp4-Cre;Ai14;Snap25$^{fl/fl}$	Cre+;Ai14;Snap25$^{fl/fl}$ (cKO)	Adult	12 weeks	171	3	
Both male and female mice were used throughout the experiments.						

Supplementary Table 1. Number of cells and number of sections used to perform morphometric analyses of various soma features of PV-positive neurons in the caudoputamen at each time point. The table shows the soma parameters selected for morphometric measurements.

Morphometrics			
Parvalbumin - *Genotype* effect			
Development			**Adult**
Parameters measured	**P14 ctrl - cKO**	**P21 ctrl - cKO**	**12 weeks ctrl - cKO**
Soma Area	ns	*	ns
Soma Perimeter	ns	ns	ns
Soma Circularity	ns	ns	ns
Soma Roundness	ns	**	ns
Soma Solidity	ns	ns	ns

Supplementary Table 2. Summary table showing the effect of genotype on the soma morphology of parvalbumin neurons in the caudoputamen. Morphometric analyses were performed to determine the short- and long-term impacts of chronically silencing L5 projection neurons on the soma morphology of PV interneurons.

Summary of results

Development

Genotype effect	**Density P14 - PV**	ROI	*M1*	ns	**Density P21 - PV**	ROI	*M1*	ns
			S1	ns			*S1*	ns
			CPu	ns			*CPu*	ns
			GPe	ns			*GPe*	ns
			MD	ns			*MD*	ns
			LP	ns			*LP*	ns
			SC	ns			*SC*	ns
Age effect	**Developmental trajectory P14- P21**	ctrl	*M1*	ns				
			S1	ns				
			CPu	ns				
			GPe	ns				
			MD	ns				
			LP	ns				
			SC	*				
		cKO	*M1*	ns				
			S1	ns				
			CPu	ns				
			GPe	ns				
			MD	ns				
			LP	ns				
			SC	ns				
Layer effect	**Laminar distribution P14 - PV**	M1	*Layer 1*	ns	**Laminar distribution P21 - PV**	M1	*Layer 1*	ns
			Layer 2/3	ns			*Layer 2/3*	ns
			Layer 5	ns			*Layer 5*	ns
			Layer 6	ns			*Layer 6*	ns
		S1	*Layer 1*	ns		S1	*Layer 1*	ns
			Layer 2/3	ns			*Layer 2/3*	ns
			Layer 4	ns			*Layer 4*	ns
			Layer 5	ns			*Layer 5*	ns
			Layer 6	ns			*Layer 6*	ns
Age & Layer effect	**Developmental trajectory P14 - P21**	M1 ctrl	*Layer 1*	ns				
			Layer 2/3	ns				
			Layer 5	ns				
			Layer 6	ns				
		M1 cKO	*Layer 1*	ns				
			Layer 2/3	ns				
			Layer 5	ns				
			Layer 6	ns				
		S1 ctrl	*Layer 1*	ns				
			Layer 2/3	ns				
			Layer 4	ns				
			Layer 5	ns				
			Layer 6	ns				
		S1 cKO	*Layer 1*	ns				
			Layer 2/3	ns				
			Layer 4	ns				
			Layer 5	ns				
			Layer 6	ns				

Summary of results

Adult

Density 3 months - PV	ROI - PV	*M1*	ns	VVA	*M1*	ns	PV+ VVA+	*M1*	ns
		S1	ns		*S1*	ns		*S1*	ns
		CPu	ns		*CPu*	ns		*CPu*	ns
		GPe	ns						
		MD	ns						
		LP	ns						
		SC	ns						
Developmental trajectory - PV P21 - 3 months	ctrl	*M1*	ns						
		S1	ns						
		CPu	ns						
		GPe	****						
		MD	ns						
		LP	ns						
		SC	ns						
	cKO	*M1*	ns						
		S1	ns						
		CPu	ns						
		GPe	****						
		MD	ns						
		LP	ns						
		SC	ns						
Laminar distribution 3 months	M1 - PV	*Layer 1*	ns	M1 - VVA	*Layer 1*	ns	M1 - PV+ VVA+	*Layer 1*	ns
		Layer 2/3	ns		*Layer 2/3*	**		*Layer 2/3*	ns
		Layer 5	ns		*Layer 5*	**		*Layer 5*	ns
		Layer 6a	ns		*Layer 6a*	ns		*Layer 6a*	ns
		Layer 6b	ns		*Layer 6b*	ns		*Layer 6b*	ns
	S1 - PV	*Layer 1*	ns	S1 - VVA	*Layer 1*	ns	S1 - PV+ VVA+	*Layer 1*	ns
		Layer 2/3	ns		*Layer 2/3*	ns		*Layer 2/3*	ns
		Layer 4	**		*Layer 4*	ns		*Layer 4*	**
		Layer 6a	ns		*Layer 6a*	ns		*Layer 6a*	ns
		Layer 6b	ns		*Layer 6b*	ns		*Layer 6b*	ns
	M1 - PV+ VVA-	*Layer 1*	ns	M1 - PV- VVA+	*Layer 1*	ns			
		Layer 2/3	ns		*Layer 2/3*	ns			
		Layer 5	**		*Layer 5*	*			
		Layer 6a	ns		*Layer 6a*	ns			
		Layer 6b	ns		*Layer 6b*	ns			
	S1 - PV+ VVA-	*Layer 1*	ns	S1 - PV- VVA+	*Layer 1*	ns			
		Layer 2/3	ns		*Layer 2/3*	ns			
		Layer 4	ns		*Layer 4*	ns			
		Layer 6a	ns		*Layer 6a*	ns			
		Layer 6b	ns		*Layer 6b*	ns			
Developmental trajectory P21 - 3 months	M1 ctrl - PV	*Layer 1*	ns						
		Layer 2/3	ns						
		Layer 5	ns						
		Layer 6	***						
	M1 cKO - PV	*Layer 1*	ns						
		Layer 2/3	ns						
		Layer 5	ns						
		Layer 6	ns						
	S1 ctrl - PV	*Layer 1*	ns						
		Layer 2/3	ns						
		Layer 4	*						
		Layer 5	ns						
		Layer 6	ns						
	S1 cKO - PV	*Layer 1*	ns						
		Layer 2/3	ns						
		Layer 4	ns						
		Layer 5	ns						
		Layer 6	ns						

Supplementary Table 3. Summary of the results of the density, laminar distribution, and trajectory of PV neurons and their different subpopulations (PV+ VVA+, PV+ VVA-, PV- VVA+) in the cortical and subcortical regions of interest at different postnatal stages and in adulthood.

CHAPTER 3

Figure	Analysis	Effect	Values	Statistical test	P value
Figure 3.3.f	PV interneuron *cell density* (mean ± SEM)	***Genotype*** (Local)	P14 M1 ctrl: 93.561 ± 3.589 P14 M1 cKO: 135.431 ± 40.920	two-way ANOVA with Šídák's multiple comparisons test	p=0.3679 (ns)
			P21 M1 ctrl: 105.176 ± 5.746 P21 M1 cKO: 129.017 ± 17.756	two-way ANOVA with Šídák's multiple comparisons test	p=0.6323 (ns)
Figure 3.3.g	PV interneuron *cell density* (mean ± SEM)	***Genotype*** (Local)	P14 S1 ctrl: 130.780 ± 13.257 P14 S1 cKO: 168.428 ± 47.865	two-way ANOVA with Šídák's multiple comparisons test	p=0.5806 (ns)
			P21 S1 ctrl: 139.705 ± 16.128 P21 S1 cKO: 158.262 ± 19.200	two-way ANOVA with Šídák's multiple comparisons test	p=0.8327 (ns)
Figure 3.3.h	PV interneuron cell density (mean ± SEM)	***Trajectory*** (Local)	P14 M1 ctrl: 93.561 ± 3.589 P21 M1 ctrl: 105.176 ± 5.746	two-way ANOVA with Šídák's multiple comparisons test	p=0.7467 (ns)
			P14 S1 ctrl: 130.780 ± 13.257 P21 S1 ctrl: 139.705 ± 16.128	two-way ANOVA with Šídák's multiple comparisons test	p= 0.8398 (ns)
Figure 3.3.i	PV interneuron cell density (mean ± SEM)	***Trajectory*** (Local)	P14 M1 cKO: 135.431 ± 40.920 P21 M1 cKO: 129.017 ± 17.756	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9868 (ns)
			P14 S1 cKO: 168.428 ± 47.865 P21 S1 cKO: 158.262 ± 19.200	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9671 (ns)
Figure 3.4.d	PV interneuron cell density (mean ± SEM)	***Genotype*** (Global)	P14 LP ctrl: 50.4 ± 5.9, P14 LP cKO: 64.4 ± 28	two-way ANOVA with Šídák's multiple comparisons test	p=0.999 (ns)
			P14 MD ctrl: 59.6 ± 4.6, P14 MD cKO: 48.0 ± 5.2	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			P14 CPu ctrl: 84.4 ± 6.6 P14 CPu cKO: 69.7 ± 3.4	two-way ANOVA with Šídák's multiple comparisons test	p=0.9998 (ns)
			P14 GPe ctrl: 381.1 ± 39.4 P14 GPe cKO: 420.3 ± 71.8	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9813 (ns)

			P14 SC ctrl: 246.6 ± 40.3 P14 SC cKO: 355.3 ± 106.8	two-way ANOVA with Šídák's multiple comparisons test	p= 0.4308 (ns)
Figure 3.4.d	PV interneuron cell density (mean ± SEM)	***Genotype*** (Global)	P21 LP ctrl: 50.2 ± 14.0 P21 LP cKO: 63.6 ± 10.0	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
	PV interneuron cell density (mean ± SEM)	***Genotype*** (Global)	P21 MD ctrl: 62.8 ± 1.6 P21 P21 MD cKO: 64.3 ± 10.2	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			P21 CPu ctrl: 86.3 ± 5.1 P21 CPu cKO: 85.3 ± 4.9	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			P21 GPe ctrl: 397.0 ± 50.8 P21 GPe cKO: 485.0 ± 117.4	two-way ANOVA with Šídák's multiple comparisons test	p= 0.7598 (ns)
			P21 SC ctrl: 438.7 ± 94.8 P21 SC cKO: 415.7 ± 45.9	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9992 (ns)
Figure 3.4.f	PV interneuron cell density (mean ± SEM)	***Trajectory*** (Global)	P14 LP ctrl: 50.4 ± 5.9 P21 LP ctrl : 50.2 ± 14.0	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			P14 MD ctrl: 59.6 ± 4.6 P21 MD ctrl: 62.8 ± 1.6	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			P14 CPu ctrl: 84.4 ± 6.6 P21 CPu ctrl: 87.0 ± 5.4	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			P14 GPe ctrl: 381.1 ± 39.4 P21 GPe ctrl: 397.0 ± 50.8	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9997 (ns)
			P14 SC ctrl: 246.6 ± 40.3 P21 SC ctrl: 438.7 ± 94.8	two-way ANOVA with Šídák's multiple comparisons test	p= 0.0217 (*)
Figure 3.4.g	PV interneuron cell density (mean ± SEM)	***Trajectory*** (Global)	P14 LP cKO: 64.4 ± 28.5 P21 LP cKO: 63.6 ± 10.0	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			P14 MD cKO: 48.0 ± 5.2 P21 MD cKO: 64.3 ± 10.2	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)

			P14 CPu cKO: 69.7 ± 3.4 P21 CPu cKO: 85.3 ± 4.9	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			P14 GPe cKO: 420.3 ± 71.8 P21 GPe cKO: 485.0 ± 117.3	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9474 (ns)
			P14 SC cKO: 355.3 ± 106.8 P21 SC cKO: 415.7 ± 45.9	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9605 (ns)
Figure 3.5.d	PV interneuron soma measurements (mean ± SEM)	***Genotype Morphology*** (Global)	*Soma Area* P14 CPu ctrl: 172.6 ± 5.5 P14 CPu cKO: 174.7 ± 6.4	unpaired student t-test with Welch's correction	p= 0.8085 (ns)
			Soma Perimeter P14 CPu ctrl: 58.6 ± 1.6 P14 CPu cKO: 60.5 ± 2.3	unpaired student t-test with Welch's correction	p= 0.5071 (ns)
			Soma Circularity P14 CPu ctrl: 0.663 ± 0.0 P14 CPu cKO: 0.656 ± 0.0	unpaired student t-test with Welch's correction	p= 0.7071 (ns)
			Soma Roundness P14 CPu ctrl: 0.695 ± 0.0 P14 CPu cKO: 0.712 ± 0.0	unpaired student t-test with Welch's correction	p= 0.2717 (ns)
			Soma Solidity P14 CPu ctrl: 0.865 ± 0.0 P14 CPu cKO: 0.851 ± 0.0	unpaired student t-test with Welch's correction	p= 0.2479 (ns)
Figure 3.5.f	PV interneuron soma measurements (mean ± SEM)	***Genotype Morphology*** (Global)	*Soma Area* P21 CPu ctrl: 161.7 ± 4.7 P21 CPu cKO: 147.1 ± 4.0	unpaired student t-test with Welch's correction	p= 0.0192 (*)
			Soma Perimeter P21 CPu ctrl: 57.9 ± 1.6 P21 CPu cKO: 55.3 ± 1.4	unpaired student t-test with Welch's correction	p= 0.2311 (ns)
			Soma Circularity P21 CPu ctrl: 0.648 ± 0.0 P21 CPu cKO: 0.647 ± 0.0	unpaired student t-test with Welch's correction	p= 0.9626 (ns)
			Soma Roundness P21 CPu ctrl: 0.701 ± 0.0 P21 CPu cKO: 0.661 ± 0.0	unpaired student t-test with Welch's correction	p= 0.0035 (**)
			Soma Solidity P21 CPu ctrl: 0.849 ± 0.0 P21 CPu cKO: 0.852 ± 0.0	unpaired student t-test with Welch's correction	p= 0.7592 (ns)
Figure 3.6.b	PV interneuron soma measurements (mean ± SEM)	***Trajectory Morphology*** (Global)	*Soma Area* P14 CPu ctrl: 172.6 ± 5.5 P21 CPu ctrl: 161.7 ± 4.7	unpaired student t-test with Welch's correction	p=0.1335 (ns)
			Soma Perimeter P14 CPu ctrl: 58.6 ± 1.6 P21 CPu ctrl: 57.9 ± 1.6	unpaired student t-test with Welch's correction	p=0.7445 (ns)
			Soma Circularity P14 CPu ctrl: 0.663 ± 0.0 P21 CPu ctrl: 0.648 ± 0.0	unpaired student t-test with Welch's correction	p=0.3908 (ns)

			Soma Roundness P14 CPu ctrl: 0.695 ± 0.0 P21 CPu ctrl: 0.701 ± 0.0	unpaired student t-test with Welch's correction	p=0.7074 (ns)
			Soma Solidity P14 CPu ctrl: 0.865 ± 0.0 P21 CPu ctrl: 0.849 ± 0.0	unpaired student t-test with Welch's correction	p=0.1297 (ns)
Figure 3.6.d	PV interneuron soma measurements (mean ± SEM)	***Trajectory Morphology*** (Global)	*Soma Area* P14 CPu cKO: 174.7 ± 6.4 P21 CPu cKO: 147.1 ± 4.0	unpaired student t-test with Welch's correction	p= 0.0003 (***)
			Soma Perimeter P14 CPu cKO: 60.5 ± 2.3 P21 CPu cKO: 55.3 ± 1.4	unpaired student t-test with Welch's correction	p= 0.0558 (ns)
			Soma Circularity P14 CPu cKO: 0.656 ± 0.0 P21 CPu cKO: 0.647 ± 0.0	unpaired student t-test with Welch's correction	p=0.6464 (ns)
			Soma Roundness P14 CPu cKO: 0.712 ± 0.0 P21 CPu cKO: 0.661 ± 0.0	unpaired student t-test with Welch's correction	p= 0.0003 (***)
			Soma Solidity P14 CPu cKO: 0.851 ± 0.0 P21 CPu cKO: 0.852 ± 0.0	unpaired student t-test with Welch's correction	p= 0.9262 (ns)
Figure 3.7.b	PV interneuron soma measurements (mean ± SEM)	***Genotype Morphology*** (Global)	*Soma Area* 12 weeks CPu ctrl: 121 ± 3.8 12 weeks CPu cKO: 129 ± 4.7	unpaired student t-test with Welch's correction	p= 0.2301 (ns)
			Soma Perimeter 12 weeks CPu ctrl: 56.8 ± 1.9 12 weeks CPu cKO: 56.6 ± 2.1	unpaired student t-test with Welch's correction	p= 0.9398 (ns)
			Soma Circularity 12 weeks CPu ctrl: 0.555 ± 0.0 12 weeks CPu cKO: 0.585 ± 0.0	unpaired student t-test with Welch's correction	p= 0.1721 (ns)
			Soma Roundness 12 weeks CPu ctrl: 0.656 ± 0.0 12 weeks CPu cKO: 0.669 ± 0.0	unpaired student t-test with Welch's correction	p= 0.4804 (ns)
			Soma Solidity 12 weeks CPu ctrl: 0.782 ± 0.0 12 weeks CPu cKO: 0.797 ± 0.0	unpaired student t-test with Welch's correction	p= 0.3412 (ns)
Figure 3.7.d	PV interneuron soma measurements (mean ± SEM)	***Trajectory Morphology*** (Global)	*Soma Area* P21 CPu ctrl: 161.7 ± 4.7 12 weeks CPu ctrl: 121 ± 3.8	unpaired student t-test with Welch's correction	p= <0.0001 (****)

			Soma Perimeter P21 CPu ctrl: 57.9 ± 1.6 12 weeks CPu ctrl: 56.8 ± 1.9	unpaired student t-test with Welch's correction	p= 0.6702 (ns)
			Soma Circularity P21 CPu ctrl: 0.648 ± 0.0 12 weeks CPu ctrl: 0.555 ± 0.0	unpaired student t-test with Welch's correction	p= <0.0001 (****)
			Soma Roundness P21 CPu ctrl: 0.701 ± 0.0 12 weeks CPu ctrl: 0.656 ± 0.0	unpaired student t-test with Welch's correction	p= 0.0050 (**)
			Soma Solidity P21 CPu ctrl: 0.849 ± 0.0 12 weeks CPu ctrl: 0.782 ± 0.0	unpaired student t-test with Welch's correction	p= <0.0001 (****)
Figure 3.7.e	PV interneuron soma measurements (mean ± SEM)	***Trajectory Morphology*** (Global)	*Soma Area* P21 CPu cKO: 147.1 ± 4.0 12 weeks CPu cKO: 129 ± 4.7	unpaired student t-test with Welch's correction	p= 0.0028 (**)
			Soma Perimeter P21 CPu cKO: 55.3 ± 1.4 12 weeks CPu cKO: 56.6 ± 2.1	unpaired student t-test with Welch's correction	p= 0.6048 (ns)
			Soma Circularity P21 CPu cKO: 0.647 ± 0.0 12 weeks CPu cKO: 0.585 ± 0.0	unpaired student t-test with Welch's correction	p= 0.0020 (**)
			Soma Roundness P21 CPu cKO: 0.661 ± 0.0 12 weeks CPu cKO: 0.669 ± 0.0	unpaired student t-test with Welch's correction	p= 0.6391 (ns)
			Soma Solidity P21 CPu cKO: 0.852 ± 0.0 12 weeks CPu cKO: 0.797 ± 0.0	unpaired student t-test with Welch's correction	p= <0.0001 (****)
Figure 3.11.c	PV interneuron distribution (mean ± SEM)	***Genotype Laminar Distribution*** (Local)	**P14 M1** L1: 0 ± 0 (ctrl), L1: 0 ± 0 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			L2/3: 106.8 ± 6.5 (ctrl), L2/3: 164.7 ± 52.9 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.5340 (ns)
			L5: 129.3 ± 5.6 (ctrl), L5: 174.7 ± 43.1 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.7345 (ns)
			L6: 59.0 ± 8.2 (ctrl), L6: 87.1 ± 42.8 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9370 (ns)

Figure 3.11.d	PV interneuron distribution (mean ± SEM)	***Genotype Laminar Distribution*** (Local)	**P21 M1** L1: 0 ± 0 (ctrl), L1: 0 ± 0 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			L2/3: 126.8 ± 9.7 (ctrl), L2/3: 150.3 ± 22.4 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.6876 (ns)
			L5: 145.2 ± 9.8 (ctrl), L5: 170.0 ± 25.1 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.6454 (ns)
			L6: 38.8 ± 10.6 (ctrl), L6: 68.7 ± 13.0 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.4757 (ns)
Figure 3.11.e	PV interneuron distribution (mean ± SEM)	***Trajectory Laminar Distribution*** (Local)	**P14-P21 M1** L1: 0 ± 0 (P14, ctrl), L1: 0 ± 0 (P21, ctrl)	two-way ANOVA with Šídák's multiple comparisons test	p=>0.9999 (ns)
			L2/3: 106.8 ± 6.5 (P14, ctrl), L2/3: 126.8 ± 9.7 (P21, ctrl)	two-way ANOVA with Šídák's multiple comparisons test	p=0.3337 (ns)
			L5: 129.3 ± 5.6 (P14, ctrl), L5: 145.2 ± 9.9 (P21, ctrl)	two-way ANOVA with Šídák's multiple comparisons test	p=0.5500 (ns)
			L6: 59.0 ± 8.2 (P14, ctrl), L6: 38.8 ± 10.6 (P21, ctrl)	two-way ANOVA with Šídák's multiple comparisons test	p=0.3260 (ns)
Figure 3.11.f	PV interneuron distribution (mean ± SEM)	***Trajectory Laminar Distribution*** (Local)	**P14-P21 M1** L1: 0 ± 0 (P14, cKO), L1: 0 ± 0 (P21, cKO)	two-way ANOVA with Šídák's multiple comparisons test	p=>0.9999 (ns)
			L2/3: 164.7 ± 52.9 (P14, cKO), L2/3: 150.3 ± 22.4 (P21, cKO)	two-way ANOVA with Šídák's multiple comparisons test	p=0.9939 (ns)
			L5: 174.7 ± 43.1 (P14, cKO), L5: 170.0 ± 25.1 (P21, cKO)	two-way ANOVA with Šídák's multiple comparisons test	p=>0.9999 (ns)
			L6: 87.1 ± 42.8 (P14, cKO), L6: 68.7 ± 13.0 (P21, cKO)	two-way ANOVA with Šídák's multiple comparisons test	p=0.9849 (ns)
Figure 3.11.i	PV interneuron distribution (mean ± SEM)	***Genotype Laminar Distribution*** (Local)	**P14 S1** L1: 0 ± 0 (ctrl), L1: 0 ± 0 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p=>0.9999 (ns)

			L2/3: 96.1 ± 19.0 (ctrl), L2/3: 93.3 ± 29.2 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p=>0.9999 (ns)
			L4: 336.1 ± 49.5 (ctrl), L4: 390.1 ± 130.4 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9541 (ns)
			L5: 186.3 ± 18.2 (ctrl), L5: 243.2 ± 63.0 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9434 (ns)
			L6: 63.2 ± 5.6 (ctrl), L6: 106.4 ± 26.9 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9824 (ns)
Figure 3.11.j	PV interneuron distribution (mean ± SEM)	***Genotype Laminar Distribution*** (Local)	**P21 S1** L1: 0 ± 0 (ctrl), L1: 0 ± 0 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p=>0.9999 (ns)
			L2/3: 122.3 ± 10.7 (ctrl), L2/3: 124.8 ± 13.7 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			L4: 352.6 ± 53.3 (ctrl), L4: 307.1 ± 26.9 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.6483 (ns)
			L5: 190.7 ± 21.1 (ctrl), L5: 214.5 ± 23.3 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9640 (ns)
			L6: 68.8 ± 19.8 (ctrl), L6: 99.4 ± 21.4 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9024 (ns)
Figure 3.11.k	PV interneuron distribution (mean ± SEM)	***Trajectory Laminar Distribution*** (Local)	**P14-P21 S1** L1: 0 ± 0 (P14, ctrl), L1: 0 ± 0 (P21, ctrl)	two-way ANOVA with Šídák's multiple comparisons test	p=>0.9999 (ns)
			L2/3: 96.1 ± 19.0 (P14, ctrl), L2/3: 122.3 ± 10.7 (P21, ctrl)	two-way ANOVA with Šídák's multiple comparisons test	p=0.9706 (ns)
			L4: 336.1 ± 49.5 (P14, ctrl), L4: 352.6 ± 53.3 (P21, ctrl)	two-way ANOVA with Šídák's multiple comparisons test	p=0.9964 (ns)
			L5: 186.3 ± 18.2 (P14, ctrl), L5: 190.7 ± 21.1 (P21, ctrl)	two-way ANOVA with Šídák's multiple comparisons test	p=>0.9999 (ns)

			L6: 63.2 ± 5.6 (P14, ctrl), L6: 68.8 ± 19.8 (P21, ctrl)	two-way ANOVA with Šídák's multiple comparisons test	p=>0.9999 (ns)
Figure 3.11.l	PV interneuron distribution (mean ± SEM)	***Trajectory Laminar Distribution*** (Local)	**P14-P21 S1** L1: 0 ± 0 (P14, cKO), L1: 0 ± 0 (P21, cKO)	two-way ANOVA with Šídák's multiple comparisons test	p=>0.9999 (ns)
Figure 3.11.l	PV interneuron distribution (mean ± SEM)	***Trajectory Laminar Distribution*** (Local)	L2/3: 93.3 ± 29.2 (P14, cKO), L2/3: 124.8 ± 13.7 (P21, cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9909 (ns)
			L4: 390.1 ± 130.4 (P14, cKO), L4: 307.1 ± 26.9 (P21, cKO)	two-way ANOVA with Šídák's multiple comparisons test	p=0.6379 (ns)
			L5: 243.2 ± 62.9 (P14, cKO), L5: 214.5 ± 23.3 (P21, cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9941 (ns)
			L6: 106.4 ± 26.9 (P14, cKO), L6: 99.4 ± 21.4 (P21, cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
Figure 3.12.e	PV interneuron density (mean ± SEM)	***Genotype*** (Local)	**Adult (12-week-old)** M1 ctrl: 109.3 ± 15.0 M1 cKO: 105.0 ± 6.4	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9700 (ns)
			S1 ctrl: 132.5 ± 14.6 S1 cKO: 161.0 ± 16.1	two-way ANOVA with Šídák's multiple comparisons test	p= 0.2887 (ns)
Figure 3.12.f	*Vicia villosa agglutinin (VVA)* density (mean ± SEM)	***Genotype*** (Local)	**Adult (12-week-old)** M1 ctrl: 147.7 ± 8.3 M1 cKO: 112.1 ± 5.5	two-way ANOVA with Šídák's multiple comparisons test	p= 0.0544 (ns)
			S1 ctrl: 220.4 ± 16.2 S1 cKO: 250.8 ± 6.3	two-way ANOVA with Šídák's multiple comparisons test	p= 0.1044 (ns)
Figure 3.12.g	PV+ VVA+ density (mean ± SEM)	***Genotype*** (Local)	**Adult (12-week-old)** M1 ctrl: 48.9 ± 7.2 M1 cKO: 36.4 ± 2.7	two-way ANOVA with Šídák's multiple comparisons test	p=0.4484 (ns)
			S1 ctrl: 71.4 ± 8.7 S1 cKO: 94.9 ± 9.7	two-way ANOVA with Šídák's multiple comparisons test	p= 0.0848 (ns)
Figure 3.12.g	PV+ VVA+ percentage (mean ± SEM)	***Genotype*** (Local)	**Adult (12-week-old)** M1 ctrl: : 44.6% ± 1.4 M1 cKO: 34.8% ± 2.3	two-way ANOVA with Šídák's multiple comparisons test	p= 0.0081 (**)

			S1 ctrl: 53.7% ± 1.5	two-way ANOVA with Šídák's multiple comparisons test	p= 0.1479 (ns)
			S1 cKO: 9.3% ± 2.8		
Figure 3.12.h	PV subtypes density (mean ± SEM)	***Genotype*** (Local)	**Adult (12-week-old)** **M1** PV+ VVA+: 48.9 ± 7.2 (ctrl), PV+ VVA+: 36.4 ± 2.7 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.3793 (ns)
			PV+ VVA-: 64.7 ± 8.8 (ctrl), PV+ VVA-: 72.6 ± 4.6 (cKO)		p= 0.7926 (ns)
			PV- VVA+: 100.2 ± 7.2 (ctrl), PV- VVA+: 73.2 ± 6.4 (cKO)		p= 0.0263 (*)
Figure 3.12.h	PV subtypes density (mean ± SEM)	***Genotype*** (Local)	**Adult (12-week-old)** **S1** PV+ VVA+: 71.4 ± 8.7 (ctrl), PV+ VVA+: 94.9 ± 9.7 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p=0.2707 (ns)
			PV+ VVA-: 67.0 ± 7.5 (ctrl), PV+ VVA-: 69.5 ± 10.8 (cKO)		p= 0.9978 (ns)
			PV- VVA+: 151.6 ± 15.8 (ctrl), PV- VVA+: 143.4 ± 8.1 (cKO)		p= 0.9343 (ns)
Figure 3.12.j	PV-VVA density (correlation coefficient)	***Genotype*** (Local)	**Adult (12-week-old)** r= 0.551 (M1 ctrl)	Pearson correlation	p=0.449 (ns)
Figure 3.12.k			r= -0.828 (M1 cKO)	Pearson correlation	p=0.172 (ns)
Figure 3.12.l			r= 0.422 (S1 ctrl)	Pearson correlation	p=0.578 (ns)
Figure 3.12.m			r= 0.077 (S1 cKO)	Pearson correlation	p=0.923 (ns)
Figure 3.13.c	PV interneuron distribution (mean ± SEM)	***Genotype Laminar Distribution*** (Local)	**Adult (12-week-old)** **PV M1** L1: 0 ± 0 (ctrl), L1: 0 ± 0 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			L2/3: 143.9 ± 15.8 (ctrl), L2/3: 125.3 ± 15.2 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p=0.8536 (ns)
			L5: 132.7 ± 21.6 (ctrl), L5: 170.6 ± 13.1 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p=0.2076 (ns)
			L6a: 93.2 ± 10.7 (ctrl), L6a: 91.3 ± 18.8 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			L6b: 26.5 ± 7.7 (ctrl), L6b: 18.6 ± 6.5 (cKO)	two-way ANOVA with Šídák's	p=0.9961 (ns)

				multiple comparisons test	
Figure 3.13.g	*Vicia villosa agglutinin* (VVA) distribution (mean ± SEM)	***Genotype Laminar Distribution*** (Local)	**Adult (12-week-old) VVA M1** L1: 0 ± 0 (ctrl), L1: 0 ± 0 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			L2/3: 205.1 ± 13.2 (ctrl), L2/3: 154.2 ± 15.3 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.0028 (**)
			L5: 214.6 ± 12.6 (ctrl), L5: 159.2 ± 12.4 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.0011 (**)
			L6a: 120.5 ± 10.8 (ctrl), L6a: 107.8 ± 5.1 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.8803 (ns)
			L6b: 2.0 ± 2.0 (ctrl), L6b: 0 ± 0 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
Figure 3.13.d	*PV subtypes (PV+ VVA+)* distribution (mean ± SEM)	***Genotype Laminar Distribution*** (Local)	**Adult (12-week-old) PV+ VVA+ M1** L1: 0 ± 0 (ctrl), L1: 0 ± 0 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			L2/3: 72.5 ± 9.8 (ctrl), L2/3: 48.8 ± 6.3 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.0562 (ns)
			L5: 56.6 ± 7.2 (ctrl), L5: 56.6 ± 10.2 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			L6a: 35.9 ± 5.7 (ctrl), L6a: 35.9 ± 7.9 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			L6b: 3.8 ± 3.8 (ctrl), L6b: 0 ± 0 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9962 (ns)
Figure 3.13.e	*PV subtypes (PV+ VVA-)* distribution (mean ± SEM)	***Genotype Laminar Distribution*** (Local)	**Adult (12-week-old) PV+ VVA- M1** L1: 0 ± 0 (ctrl), L1: 0 ± 0 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			L2/3: 77.1 ± 6.1 (ctrl), L2/3: 81.9 ± 11.2 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9984 (ns)
			L5: 82.1 ± 18.0 (ctrl), L5: 131.1 ± 6.6 (cKO)	two-way ANOVA with Šídák's	p= 0.0052 (**)

				multiple comparisons test	
			L6a: 58.6 ± 9.2 (ctrl), L6a: 59.4 ±13.4 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			L6b: 25.6 ± 9.9 (ctrl), L6b: 11.4 ± 5.6 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.7992 (ns)
Figure 3.13.f	*PV subtypes (PV- VVA+)* distribution (mean ± SEM)	***Genotype Laminar Distribution*** (Local)	**Adult (12-week-old) PV- VVA+ M1** L1: 0 ± 0 (ctrl), L1: 0 ± 0 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			L2/3: 127.7 ± 11.5 (ctrl), L2/3: 106.1 ± 19.0 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.5393 (ns)
			L5: 157.5 ± 11.5 (ctrl), L5: 109.7 ± 6.6 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.0119 (*)
			L6a: 81.1 ± 11.7 (ctrl), L6a: 71.2 ± 15.1 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9670 (ns)
			L6b: 2.0 ± 2.0 (ctrl), L6b: 0 ± 0 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
Figure 3.13.j	*PV interneuron* distribution (mean ± SEM)	***Genotype Laminar Distribution*** (Local)	**Adult (12-week-old) PV S1** L1: 0 ± 0 (ctrl), L1: 0 ± 0 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			L2/3: 110.4 ± 27.9 (ctrl), L2/3: 150.2 ± 16.7(cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.6969 (ns)
			L4: 234.6 ± 36.2 (ctrl), L4: 336.8 ± 34.3 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.0063 (**)
			L5: 196.6 ± 16.6 (ctrl), L5: 259.4 ± 28.4 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.2028 (ns)
			L6a: 97.9 ± 12.1 (ctrl), L6a: 110.5 ± 12.3 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9987 (ns)

			L6b: 48.8 ± 7.6 (ctrl), L6b: 42.4 ± 12.6 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
Figure 3.13.n	*Vicia villosa agglutinin* (VVA) distribution (mean ± SEM)	***Genotype Laminar Distribution*** (Local)	**Adult (12-week-old) VVA S1** L1: 0 ± 0 (ctrl), L1: 0 ± 0 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			L2/3: 193.8 ± 14.4 (ctrl), L2/3: 192.1 ± 9.9 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			L4: 605.6 ± 61.9 (ctrl), L4: 669.1 ± 27.4 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.2112 (ns)
			L5: 288.4 ± 7.9 (ctrl), L5: 350.7 ± 16.4 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.2282 (ns)
			L6a: 164.7 ± 12.5 (ctrl), L6a: 192.7 ± 5.6 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9252 (ns)
			L6b: 13.6 ± 2.6 (ctrl), L6b: 2.4 ± 2.4 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9994 (ns)
Figure 3.13.k	*PV subtypes (PV+ VVA+)* distribution (mean ± SEM)	***Genotype Laminar Distribution*** (Local)	**Adult (12-week-old) PV+ VVA+ S1** L1: 0 ± 0 (ctrl), L1: 0 ± 0 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			L2/3: 53.4 ± 15.4 (ctrl), L2/3: 60.9 ± 8.0 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9999 (ns)
			L4: 188.5 ± 43.0 (ctrl), L4: 289.9 ± 38.1 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.0023 (**)
			L5: 100.3 ± 9.8 (ctrl), L5: 147.5 ± 19.6 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.4017 (ns)
			L6a: 46.9 ± 8.4 (ctrl), L6a: 60.8 ± 6.1 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9961 (ns)
			L6b: 5.4 ± 2.2 (ctrl), L6b: 6.2 ± 6.2 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)

Figure 3.13.l	*PV subtypes (PV+ VVA-)* distribution (mean ± SEM)	***Genotype Laminar Distribution*** (Local)	**Adult (12-week-old)** **PV+ VVA- S1** L1: 0 ± 0 (ctrl), L1: 0 ± 0 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			L2/3: 74.4 ± 19.5 (ctrl), L2/3: 88.7 ± 10.3 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9740 (ns)
			L4: 48.1 ± 15.6 (ctrl), L4: 31.8 ± 8.1 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9510 (ns)
			L5: 93.2 ± 16.2 (ctrl), L5: 113.8 ± 26.7 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.8651 (ns)
			L6a: 55.2 ± 4.9 (ctrl), L6a: 53.6 ± 10.1 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			L6b: 51.9 ± 2.2 (ctrl), L6b: 39.8 ± 15.9 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9886 (ns)
Figure 3.13.m	*PV subtypes (PV- VVA+)* distribution (mean ± SEM)	***Genotype Laminar Distribution*** (Local)	**Adult (12-week-old)** **PV- VVA+ S1** L1: 0 ± 0 (ctrl), L1: 0 ± 0 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			L2/3: 138.1 ± 10.2 (ctrl), L2/3: 124.7 ± 13.4 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9958 (ns)
			L4: 393.4 ± 43.1 (ctrl), L4: 342.9 ± 27.3 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.2724 (ns)
			L5: 182.2 ± 8.0 (ctrl), L5: 187.7 ± 24.4 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			L6a: 118.5 ± 14.1 (ctrl), L6a: 129.0 ± 2.3 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9989 (ns)
			L6b: 9.5 ± 4.0 (ctrl), L6b: 2.4 ± 2.4 (cKO)	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9999 (ns)
Figure 3.14.c	*PV-VVA* density (correlation coefficient)	***Genotype*** (Local)	**Adult (12-week-old)** **M1** L2/3: r= 0.297 (ctrl)	Pearson correlation	p=0.703 (ns)
			L2/3: r= -0.351 (cKO)	Pearson correlation	p=0.649

					(ns)
			L5: r= 0.211 (ctrl)	Pearson correlation	p=0.789 (ns)
			L5: r= 0.386 (cKO)	Pearson correlation	p=0.614 (ns)
			L6a: r= 0.048 (ctrl)	Pearson correlation	p=0.952 (ns)
			L6a: r= -0.438 (cKO)	Pearson correlation	p=0.562 (ns)
			L6b: r= -0.549 (ctrl)	Pearson correlation	p=0.451 (ns)
Figure 3.14.d	*PV-VVA* density (correlation coefficient)	***Genotype*** (Local)	**Adult (12-week-old)** **S1** L2/3: r= -0.016 (ctrl)	Pearson correlation	p=0.984 (ns)
			L2/3: r= -0.672 (cKO)	Pearson correlation	p=0.328 (ns)
			L4: r= 0.038 (ctrl)	Pearson correlation	p=0.962 (ns)
			L4: r= -0.507 (cKO)	Pearson correlation	p=0.493 (ns)
			L5: r= -0.925 (ctrl)	Pearson correlation	p=0.075 (ns)
			L5: r= -0.108 (cKO)	Pearson correlation	p=0.892 (ns)
			L6a: r= 0.754 (ctrl)	Pearson correlation	p=0.246 (ns)
			L6a: r= 0.646 (cKO)	Pearson correlation	p=0.354 (ns)
			L6b: r= -0.533 (ctrl)	Pearson correlation	p=0.467 (ns)
			L6b: r= -0.475 (cKO)	Pearson correlation	p=0.525 (ns)
Figure 3.15.c	*PV interneuron* density (mean ± SEM)	***Genotype*** (Global)	**Adult (12-week-old)** CPu ctrl: 64.3 ± 11.9, CPu cKO: 65.8 ± 5.4	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			GPe ctrl: 180.8 ± 19.3, GPe cKO: 194.3 ± 14.9	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9989 (ns)
			LP ctrl: 24.0 ± 6.3, LP cKO: 24.5 ± 3.2	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			MD ctrl: 15.7 ± 4.0, MD cKO: 23.0 ± 5.5	two-way ANOVA with Šídák's multiple comparisons test	p= >0.9999 (ns)
			TRN ctrl: 765.0 ± 44.7, TRN cKO: 746.3 ± 47.8	two-way ANOVA with Šídák's	p= 0.9966 (ns)

				multiple comparisons test	
			SC ctrl: 341.0 ± 21.3, SC cKO: 327.3 ± 45.0	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9989 (ns)
Figure 3.15.d	*PV interneuron density* (mean ± SEM)	***Trajectory*** (Global)	**P21-12 weeks (ctrl)** P21 LP ctrl: 50.21 ± 14.0 12 weeks LP ctrl: 23.98 ± 6.3	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9957 (ns)
			P21 MD ctrl: 62.82 ± 1.6 12 weeks MD ctrl: 15.67 ± 4.0	two-way ANOVA with Šídák's multiple comparisons test	p=0.8648 (ns)
			P21 CPu ctrl: 86.31 ± 5.1 12 weeks CPu ctrl: 64.32 ± 11.9	two-way ANOVA with Šídák's multiple comparisons test	p=0.9980 (ns)
			P21 GPe ctrl: 397.0 ± 50.8 12 weeks GPe ctrl: 180.8 ± 19.3	two-way ANOVA with Šídák's multiple comparisons test	p=<0.0001 (****)
			P21 SC ctrl: 438.7 ± 94.8 12 weeks SC ctrl: 341.0 ± 21.3	two-way ANOVA with Šídák's multiple comparisons test	p=0.1271 (ns)
Figure 3.15.e	*PV interneuron density* (mean ± SEM)	***Trajectory*** (Global)	**P21-12 weeks (cKO)** P21 LP cKO: 63.6 ± 10.0 12 weeks LP cKO: 24.5 ± 3.2	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9796 (ns)
			P21 MD cKO: 64.3 ± 10.2 12 weeks MD cKO: 23.0 ± 5.5	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9794 (ns)
			P21 CPu cKO: 85.3 ± 4.9 12 weeks CPu cKO: 65.8 ± 5.4	two-way ANOVA with Šídák's multiple comparisons test	p= 0.9997 (ns)
			P21 GPe cKO: 485.0 ± 117.4 12 weeks GPe cKO: 194.3 ± 14.9	two-way ANOVA with Šídák's multiple comparisons test	p= <0.0001 (****)
			P21 SC cKO: 415.7 ± 45.9 12 weeks SC cKO: 327.4 ± 45.0	two-way ANOVA with Šídák's multiple comparisons test	p=0.4268 (ns)
Figure 3.15.f	*VVA subtypes density* (mean ± SEM)	***Genotype*** (Global)	**Adult (12-week-old)** CPu VVA+ ctrl: 61.1 ± 3.1 CPu VVA+ cKO: 50.4 ± 7.1	two-way ANOVA with Šídák's multiple comparisons test	p= 0.2743 (ns)
			CPu PV- VVA+ ctrl: 25.2 ± 5.6	two-way ANOVA with Šídák's	p=0.8362 (ns)

			CPu PV- VVA+ cKO: 21.4 ± 2.9	multiple comparisons test	
Figure 3.15.g	*PV subtypes* percentage	***Genotype*** (Global)	**Adult (12-week-old)** CPu PV+ VVA+ ctrl: 55.20% ± 5.5 CPu PV+ VVA+ cKO: 44.86% ± 8.3	two-way ANOVA with Šídák's multiple comparisons test	p=0.5326 (ns)
			CPu PV+ VVA- ctrl: 44.80 ± 5.5 CPu PV+ VVA- cKO: 55.13% ± 8.3	two-way ANOVA with Šídák's multiple comparisons test	p=0.5326 (ns)
Figure 3.15.h	*PV-VVA* density (correlation coefficient)	***Genotype*** (Global)	**Adult (12-week-old)** CPu ctrl: r= 0.840	Pearson correlation	p=0.075 (ns)
			CPu cKO: r= 0.095	Pearson correlation	p=0.879 (ns)

CHAPTER 3

Figure	Analysis	Effect	Values	Statistical test	P value
Figure 3.17.C	NPY interneuron *cell density* (mean ± SEM)	***Genotype*** (Local)	ACA ctrl: 19.667 ± 1.171 ACA cKO: 17.431 ± 2.494	two-way ANOVA with Šídák's multiple comparisons test	p=0.7420 (ns)
			M2 ctrl: 30.074 ± 2.645 M2 cKO: 19.036 ± 2.423	two-way ANOVA with Šídák's multiple comparisons test	p=0.0073 (**)
Figure 3.17.F	NPY interneuron *soma morphology* (mean ± SEM)	***Genotype*** (Local)	***soma area*** ACA ctrl: 56.08 ± 2.651 ACA cKO: 79.94 ± 4.819	unpaired two-tailed Mann-Whitney test	p<0.0001 (****)
			soma perimeter ACA ctrl: 35.87 ± 0.978 ACA cKO: 43.19 ± 1.349	unpaired two-tailed Mann-Whitney test	p<0.0001 (****)
			soma circularity ACA ctrl: 0.5483 ± 0.0138 ACA cKO: 0.5307 ± 0.0170	unpaired two-tailed Mann-Whitney test	p=0.4523 (ns)
			soma roundness ACA ctrl: 0.5882 ± 0.0125 ACA cKO: 0.5962 ± 0.0160	unpaired two-tailed Mann-Whitney test	p=0.8760
			soma solidity ACA ctrl: 0.7779 ± 0.0086 ACA cKO: 0.7760 ± 0.0111	unpaired two-tailed Mann-Whitney test	p=0.8375
Figure 3.17.G	NPY interneuron *soma morphology* (mean ± SEM)	***Genotype*** (Local)	***soma area*** M2 ctrl: 57.41 ± 1.928 M2 cKO: 59.78 ± 3.001	unpaired two-tailed Mann-Whitney test	p=0.8105 (ns)
			soma perimeter M2 ctrl: 35.15 ± 0.6387 M2 cKO: 37.13 ± 0.8330	unpaired two-tailed Mann-Whitney test	p=0.0979 (ns)

			soma circularity M2 ctrl: 0.5763 ± 0.0109 M2 cKO: 0.5317 ± 0.0155	unpaired two-tailed Mann-Whitney test	p=0.0147 (*)
			soma roundness M2 ctrl: 0.6184 ± 0.0112 M2 cKO: 0.5853 ± 0.0148	unpaired two-tailed Mann-Whitney test	p=0.1072 (ns)
			soma solidity M2 ctrl: 0.7902 ± 0.0065 M2 cKO: 0.7643 ± 0.0095	unpaired two-tailed Mann-Whitney test	p=0.0315 (*)
Figure 3.18.D	NPY interneuron *cell density* (mean ± SEM)	***Genotype*** (Local)	M1 ctrl: 85.19 ± 1.790 M1 cKO: 68.27 ± 4.075	unpaired two-tailed t-test with Welch's correction	p=0.0178 (*)
Figure 3.18.E	NPY interneuron *soma morphology* (mean ± SEM)	***Genotype*** (Local)	***soma area*** M1 ctrl: 65.75 ± 1.662 M1 cKO: 69.47 ± 1.864	unpaired two-tailed Mann-Whitney test	p=0.1694 (ns)
			soma perimeter M2 ctrl: 37.40 ± 0.5072 M2 cKO: 40.46 ± 0.6769	unpaired two-tailed Mann-Whitney test	p=0.0053 (**)
			soma circularity M2 ctrl: 0.5813 ± 0.0082 M2 cKO: 0.5473 ± 0.0097	unpaired two-tailed Mann-Whitney test	p=0.0029 (ns)
			soma roundness M2 ctrl: 0.6500 ± 0.0079 M2 cKO: 0.6393 ± 0.0090	unpaired two-tailed Mann-Whitney test	p=0.3415 (ns)
			soma solidity M2 ctrl: 0.8010 ± 0.0051 M2 cKO: 0.7809 ± 0.0059	unpaired two-tailed Mann-Whitney test	p=0.0056 (**)
Figure 3.19.D	NPY interneuron *cell density* (mean ± SEM)	***Genotype*** (Local)	S1 ctrl: 84.49 ± 6.572 S1 cKO: 70.03 ± 3.144	unpaired two-tailed t-test with Welch's correction	p=0.0966 (ns)
Figure 3.19.E	NPY interneuron *soma morphology* (mean ± SEM)	***Genotype*** (Local)	***soma area*** S1 ctrl: 80.05 ± 1.401 S1 cKO: 72.93 ± 1.403	unpaired two-tailed Mann-Whitney test	p=0.0003 (***)
			soma perimeter S1 ctrl: 42.20 ± 0.4474 S1 cKO: 41.53 ± 0.4916	unpaired two-tailed Mann-Whitney test	p=0.1431 (ns)
			soma circularity S1 ctrl: 0.5724 ± 0.0067 S1 cKO: 0.5440 ± 0.0071	unpaired two-tailed Mann-Whitney test	p=0.0038 (**)
			soma roundness S1 ctrl: 0.6604 ± 0.0061 S1 cKO: 0.6474 ± 0.0069	unpaired two-tailed Mann-Whitney test	p=0.3219 (ns)
			soma solidity S1 ctrl: 0.8036 ± 0.0039 S1 cKO: 0.7870 ± 0.0041	unpaired two-tailed Mann-Whitney test	p=0.0008 (***)
Figure 3.20.C	NPY interneuron	***Layer*** (Local)	**M1** L1, ctrl: 82.340 ± 3.526 L1, cKO: 38.901 ± 4.866	two-way ANOVA with Šídák's multiple comparisons test	p=0.0004 (***)

	laminar distribution (mean ± SEM)		L2/3, ctrl: 144.652 ± 6.203 L2/3, cKO: 107.665 ± 6.303	two-way ANOVA with Šídák's multiple comparisons test	p=0.0028 (**)
			L5, ctrl: 54.380 ± 2.158 L5, cKO: 65.652 ± 5.701	two-way ANOVA with Šídák's multiple comparisons test	p=0.8302 (ns)
			L6a, ctrl: 71.893 ± 7.001 L6a, cKO: 49.393 ± 9.269	two-way ANOVA with Šídák's multiple comparisons test	p=0.1271 (ns)
			L6b, ctrl: 54.672 ± 10.782 L6b, cKO: 44.626 ± 8.023	two-way ANOVA with Šídák's multiple comparisons test	p=0.8427 (ns)
Figure 3.20.D	NPY interneuron *soma morphology* (mean ± SEM)	***Layer*** (Local)	**M1** **soma area** L1, ctrl: 51.39 ± 3.750 L1, cKO: 56.66 ± 8.639	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)
			L2/3, ctrl: 60.04 ± 2.721 L2/3, cKO: 69.95 ± 2.732	Kruskal-Wallis test with Dunn’s multiple comparisons	p=0.0794 (ns)
			L5, ctrl: 79.12 ± 3.557 L5, cKO: 70.33 ± 3.163	Kruskal-Wallis test with Dunn’s multiple comparisons	p=0.4299 (ns)
			L6a, ctrl: 70.10 ± 3.314 L6a, cKO: 70.32 ± 3.944	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)
			L6b, ctrl: 57.22 ± 5.354 L6b, cKO: 77.05 ± 12.16	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)
Figure 3.20.D	NPY interneuron *soma morphology* (mean ± SEM)	***Layer*** (Local)	**M1** **soma perimeter** L1, ctrl: 34.07 ± 1.172 L1, cKO: 39.09 ± 3.403	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)
			L2/3, ctrl: 36.45 ± 0.9193 L2/3, cKO: 40.75 ± 1.048	Kruskal-Wallis test with Dunn’s multiple comparisons	p=0.0494 (*)
			L5, ctrl: 40.27 ± 0.9518 L5, cKO: 40.75 ± 1.320	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)
			L6a, ctrl: 38.00 ± 1.076 L6a, cKO: 39.54 ± 1.112	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)

			L6b, ctrl: 36.24 ± 2.099 L6b, cKO: 43.38 ± 3.928	Kruskal-Wallis test with Dunn’s multiple comparisons	p=0.3774 (ns)
Figure 3.20.D	NPY interneuron *soma morphology* (mean ± SEM)	***Layer*** (Local)	**M1** **soma circularity** L1, ctrl: 0.5379 ± 0.0205 L1, cKO: 0.4862 ± 0.0374	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)
			L2/3, ctrl: 0.5683 ± 0.0160 L2/3, cKO: 0.5482 ± 0.0179	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)
			L5, ctrl: 0.6047± 0.0160 L5, cKO: 0.5605 ± 0.0186	Kruskal-Wallis test with Dunn’s multiple comparisons	p=0.1837 (ns)
			L6a, ctrl: 0.6078 ± 0.0157 L6a, cKO: 0.5570 ± 0.0163	Kruskal-Wallis test with Dunn’s multiple comparisons	p=0.1676 (ns)
			L6b, ctrl: 0.5512 ± 0.0323 L6b, cKO: 0.5089 ± 0.040	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)
Figure 3.20.D	NPY interneuron *soma morphology* (mean ± SEM)	***Layer*** (Local)	**M1** **soma roundness** L1, ctrl: 0.6226 ± 0.0190 L1, cKO: 0.6121 ± 0.0370	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)
			L2/3, ctrl: 0.6768 ± 0.0162 L2/3, cKO: 0.6540 ± 0.0149	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)
			L5, ctrl: 0.6661 ± 0.0139 L5, cKO: 0.6516 ± 0.0164	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)
			L6a, ctrl: 0.6409 ± 0.0158 L6a, cKO: 0.6273 ± 0.0185	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)
			L6b, ctrl: 0.5773 ± 0.0326 L6b, cKO: 0.5696 ± 0.0340	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)
Figure 3.21.C	NPY interneuron *laminar distribution* (mean ± SEM)	***Layer*** (Local)	**S1** L1, ctrl: 78.011 ± 17.978 L1, cKO: 39.953 ± 10.990	two-way ANOVA with Šídák's multiple comparisons test	p=0.0823 (ns)
			L2/3, ctrl: 164.407 ± 15.120 L2/3, cKO: 125.086 ± 8.963	two-way ANOVA with Šídák's multiple comparisons test	p=0.0926 (ns)

			L4, ctrl: 67.600 ± 7.568 L4, cKO: 55.477 ± 6.161	two-way ANOVA with Šídák's multiple comparisons test	p=0.6926 (ns)
			L5, ctrl: 51.516 ± 5.038 L5, cKO: 60.198 ± 3.559	two-way ANOVA with Šídák's multiple comparisons test	p=0.9932 (ns)
			L6a, ctrl: 53.257 ± 5.279 L6a, cKO: 53.498 ± 4.144	two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			L6b, ctrl: 72.191 ± 16.683 L6b, cKO: 42.956 ± 11.506	two-way ANOVA with Šídák's multiple comparisons test	p=0.2943 (ns)
Figure 3.21.D	NPY interneuron *soma morphology* (mean ± SEM)	***Layer*** (Local)	**S1** **soma area** L1, ctrl: 56.97 ± 3.629 L1, cKO: 49.98 ± 4.240	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)
			L2/3, ctrl: 73.41 ± 1.860 L2/3, cKO: 69.28 ± 1.961	Kruskal-Wallis test with Dunn’s multiple comparisons	p=0.6717 (ns)
			L4, ctrl: 85.32 ± 4.141 L4, cKO: 80.35 ± 4.851	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)
			L5, ctrl: 103.9 ± 3.622 L5, cKO: 79.85 ± 2.791	Kruskal-Wallis test with Dunn’s multiple comparisons	p<0.0001 (****)
			L6a, ctrl: 82.93 ± 3.603 L6a, cKO: 73.10 ± 3.702	Kruskal-Wallis test with Dunn’s multiple comparisons	p=0.1540 (ns)
			L6b, ctrl: 76.16 ± 5.322 L6b, cKO: 83.78 ± 10.22	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)
Figure 3.21.D	NPY interneuron *soma morphology* (mean ± SEM)	***Layer*** (Local)	**S1** **soma perimeter** L1, ctrl: 38.18 ± 1.198 L1, cKO: 36.76 ± 1.925	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)
			L2/3, ctrl: 40.18 ± 0.6277 L2/3, cKO: 41.13 ± 0.7497	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)
			L4, ctrl: 42.09 ± 1.152 L4, cKO: 42.38 ± 1.259	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)

			L5, ctrl: 48.72 ± 1.287 L5, cKO: 42.88 ± 1.031	Kruskal-Wallis test with Dunn’s multiple comparisons	p=0.0018 (**)
			L6a, ctrl: 42.88 ± 1.086 L6a, cKO: 40.99 ± 1.211	Kruskal-Wallis test with Dunn’s multiple comparisons	p=0.6980 (ns)
			L6b, ctrl: 42.38 ± 1.831 L6b, cKO: 45.21 ± 3.575	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)
Figure 3.21.D	NPY interneuron *soma morphology* (mean ± SEM)	***Layer*** (Local)	**S1** **soma circularity** L1, ctrl: 0.4994 ± 0.0244 L1, cKO: 0.4977 ± 0.0297	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)
			L2/3, ctrl: 0.5806 ± 0.0099 L2/3, cKO: 0.5335 ± 0.0109	Kruskal-Wallis test with Dunn’s multiple comparisons	p=0.0140 (*)
			L4, ctrl: 0.6073 ± 0.020 L4, cKO: 0.5605 ± 0.0257	Kruskal-Wallis test with Dunn’s multiple comparisons	p=0.7654 (ns)
			L5, ctrl: 0.5705 ± 0.0168 L5, cKO: 0.5667 ± 0.0155	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)
			L6a, ctrl: 0.5757 ± 0.0168 L6a, cKO: 0.5496 ± 0.0155	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)
			L6b, ctrl: 0.5539 ± 0.0314 L6b, cKO: 0.5222 ± 0.0331	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)
Figure 3.21.D	NPY interneuron *soma morphology* (mean ± SEM)	***Layer*** (Local)	**S1** **soma roundness** L1, ctrl: 0.6432 ± 0.0218 L1, cKO: 0.6212 ± 0.0305	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)
			L2/3, ctrl: 0.6676 ± 0.00889 L2/3, cKO: 0.6505 ± 0.0101	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)
			L4, ctrl: 0.7078 ± 0.0183 L4, cKO: 0.6667 ± 0.0242	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)
			L5, ctrl: 0.6784 ± 0.0143 L5, cKO: 0.6454 ± 0.0150	Kruskal-Wallis test with Dunn’s multiple comparisons	p>0.9999 (ns)

			L6a, ctrl: 0.6368 ± 0.0151 L6a, cKO: 0.6438 ± 0.0169	Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
			L6b, ctrl: 0.5573 ± 0.0265 L6b, cKO: 0.6347 ± 0.0379	Kruskal-Wallis test with Dunn's multiple comparisons	p=0.6854 (ns)
Figure 3.22.B	NPY interneuron *cell density* (mean ± SEM)	***Genotype*** (Global)	CPu, ctrl: 42.56 ± 4.684 CPu, cKO: 32.02 ± 2.991	unpaired two-tailed t-test with Welch's correction	p=0.0923 (ns)
Figure 3.22.D	NPY interneuron *soma morphology* (mean ± SEM)	***Genotype*** (Global)	**soma area** CPu, ctrl: 82.43 ± 3.664 CPu, cKO: 80.85 ± 4.198	unpaired two-tailed Mann-Whitney test	p=0.7761 (ns)
			soma perimeter CPu, ctrl: 47.35 ± 1.349 CPu, cKO: 44.99 ± 1.362	unpaired two-tailed Mann-Whitney test	p=0.2188 (ns)
			soma circularity CPu, ctrl: 0.4753 ± 0.0149 CPu, cKO: 0.5137 ± 0.0174	unpaired two-tailed Mann-Whitney test	p=0.0491 (*)
			soma roundness CPu, ctrl: 0.5435 ± 0.0162 CPu, cKO: 0.5988 ± 0.0191	unpaired two-tailed Mann-Whitney test	p=0.0283 (*)
			soma solidity CPu, ctrl: 0.7469 ± 0.0097 CPu, cKO: 0.7769 ± 0.0100	unpaired two-tailed Mann-Whitney test	p=0.0286 (*)

Supplementary Table 4. Summary of data and statistical analyses related to each figure of **Chapter 3**. The table shows the related figure number, type of cell investigated, type of analysis done, related numerical values, and type of statistical tests conducted.

CHAPTER 3

Effect	**Analysis**	**Region**	**Parameters**	**Layer 5-silenced** *(Rbp4-Cre;Ai14;Snap25$^{fl/fl}$)*
Genotype	**Soma morphology** *3 months*	**ACA**	*Area*	****↑
			Perimeter	****↑
			Circularity	ns
			Roundness	ns
			Solidity	ns
Genotype	**Soma morphology** *3 months*	**M2**	*Area*	ns
			Perimeter	ns
			Circularity	*↓
			Roundness	ns
			Solidity	*↓
Genotype	**Soma morphology** *3 months*	**M1**	*Area*	ns
			Perimeter	**↑
			Circularity	**↓
			Roundness	ns
			Solidity	**↓
Genotype	**Soma morphology** *3 months*	**S1**	*Area*	***↓
			Perimeter	ns
			Circularity	**↓
			Roundness	ns
			Solidity	***↓
Genotype	**Soma morphology** *3 months*	**CPu**	*Area*	ns
			Perimeter	ns
			Circularity	*↑
			Roundness	*↑
			Solidity	*↑
Layer	**Soma morphology** *3 months*	**M1** ***soma area***	*Layer 1*	ns
			Layer 2/3	ns
			Layer 5	ns
			Layer 6a	ns
			Layer 6b	ns
Layer	**Soma morphology** *3 months*	**M1** ***perimeter***	*Layer 1*	ns
			Layer 2/3	*↑
			Layer 5	ns
			Layer 6a	ns
			Layer 6b	ns
Layer	**Soma morphology** *3 months*	**M1** ***circularity***	*Layer 1*	ns
			Layer 2/3	ns
			Layer 5	ns

			Layer 6a	ns
			Layer 6b	ns
Layer	**Soma morphology** *3 months*	**M1** ***roundness***	*Layer 1*	ns
			Layer 2/3	ns
			Layer 5	ns
			Layer 6a	ns
			Layer 6b	ns
Layer	**Soma morphology** *3 months*	**M1** ***solidity***	*Layer 1*	ns
			Layer 2/3	ns
			Layer 5	ns
			Layer 6a	ns
			Layer 6b	ns
Layer	**Soma morphology** *3 months*	**S1** ***soma area***	*Layer 1*	ns
			Layer 2/3	ns
			Layer 4	ns
			Layer 5	****↓
			Layer 6a	ns
			Layer 6b	ns
Layer	**Soma morphology** *3 months*	**S1** ***perimeter***	*Layer 1*	ns
			Layer 2/3	ns
			Layer 4	ns
			Layer 5	**↓
			Layer 6a	ns
			Layer 6b	ns
Layer	**Soma morphology** *3 months*	**S1** ***circularity***	*Layer 1*	ns
			Layer 2/3	*↓
			Layer 4	ns
			Layer 5	ns
			Layer 6a	ns
			Layer 6b	ns
Layer	**Soma morphology** *3 months*	**S1** ***roundness***	*Layer 1*	ns
			Layer 2/3	ns
			Layer 4	ns
			Layer 5	ns
			Layer 6a	ns
			Layer 6b	ns
Layer	**Soma morphology** *3 months*	**S1** ***solidity***	*Layer 1*	ns
			Layer 2/3	*↓
			Layer 4	ns
			Layer 5	ns
			Layer 6a	ns
			Layer 6b	ns

Supplementary Table 5. Overview of the results of morphometric analyses of NPY+ interneurons in Chapter 3.

Appendix 2

Chapter 4

Figure	Analysis	Effect	Values	Statistical test	P value
DEVELOPMENTAL RESULTS					
Figure 4.5. B	Drd1a-Cre;Ai14; Snap25$^{fl/fl}$ *cell density* (mean ± SEM)	***Region***	P21 M1 cKO: 344.8 ± 38.48 P21 S1 cKO: 214.1 ± 39.00	Two-tailed unpaired student's t-test with Welch correction	p=0.0441 (*)
Figure 4.5. C	Drd1a-Cre;Ai14; Snap25$^{fl/fl}$ *Laminar distribution* (mean ± SEM)	***Layer*** *(Local)*	**P21** Layer 1 M1 cKO: 0.0 ± 0.0 Layer 1 S1 cKO: 0.0 ± 0.0	Two-way ANOVA with Šídák's multiple comparisons test	p>0.999 (ns)
			Layer 2/3 M1 cKO: 0.0 ± 0.0 Layer 2/3 S1 cKO: 0.0 ± 0.0	Two-way ANOVA with Šídák's multiple comparisons test	p>0.999 (ns)
			Layer 4 M1 cKO: 0.0 ± 0.0 Layer 4 S1 cKO: 0.0 ± 0.0	Two-way ANOVA with Šídák's multiple comparisons test	p>0.999 (ns)
			Layer 5 M1 cKO: 7.243 ± 2.745 Layer 5 S1 cKO: 4.962 ± 1.619	Two-way ANOVA with Šídák's multiple comparisons test	p>0.999 (ns)
			Layer 6a M1 cKO: 729.019 ± 100.640 Layer 6a S1 cKO: 498.980 ± 105.478	Two-way ANOVA with Šídák's multiple comparisons test	p=0.1256 (ns)
			Layer 6b M1 cKO: 2159.080 ± 131.293 Layer 6b S1 cKO: 1312.600 ± 135.148	Two-way ANOVA with Šídák's multiple comparisons test	p<0.0001 (****)
Figure 4.5. E	PV interneuron *Cell density* (mean ± SEM)	***Genotype*** (Local)	**P21** ACA ctrl: 213.237 ± 18.060 ACA cKO: 246.71 ± 21.564	Two-way ANOVA with Šídák's multiple comparisons test	p=0.4470 (ns)
			P21 M1 ctrl: 178.447 ± 21.526 M1 cKO: 184.694 ± 9.988	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9913 (ns)
			P21 S1 ctrl: 146.952 ± 11.329 S1 cKO: 186.913 ± 14.378	Two-way ANOVA with Šídák's multiple comparisons test	p=0.2834 (ns)
Figure 4.5. F	PV interneuron *Laminar distribution* (mean ± SEM)	***Layer*** (Local)	**P21 M1** Layer 1 ctrl: 4.533 ± 4.533 Layer 1 cKO: 2.891 ± 1.793	Two-way ANOVA with Šídák's multiple comparisons test	p>0.999 (ns)

			Layer 2/3 ctrl: 224.307 ± 35.168 Layer 2/3 cKO: 248.285 ± 15.902	Two-way ANOVA with Šídák's multiple comparisons test	p=0.8671 (ns)
			Layer 5 ctrl: 220.627 ± 24.448 Layer 5 cKO: 212.872 ± 19.220	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9991 (ns)
Figure 4.5. F	PV interneuron *Laminar distribution* (mean ± SEM)	***Layer*** (Local)	**P21 M1** Layer 6a ctrl: 178.639 ± 16.380 Layer 6a cKO: 179.950 ± 14.461	Two-way ANOVA with Šídák's multiple comparisons test	p>0.999 (ns)
			Layer 6b ctrl: 5.630 ± 1.890 Layer 6b cKO: 12.906 ± 4.612	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9993 (ns)
Figure 4.5. F	PV interneuron *Laminar distribution* (mean ± SEM)	***Layer*** (Local)	**P21 S1** Layer 1 ctrl: 0.00 ± 0.00 Layer 1 cKO: 3.034 ± 3.034	Two-way ANOVA with Šídák's multiple comparisons test	p>0.999 (ns)
			Layer 2/3 ctrl: 121.544 ± 10.342 Layer 2/3 cKO: 180.000 ± 23.426	Two-way ANOVA with Šídák's multiple comparisons test	p=0.4134 (ns)
			Layer 4 ctrl: 233.644 ± 26.331 Layer 4 cKO: 279.395 ± 31.549	Two-way ANOVA with Šídák's multiple comparisons test	p=0.6850 (ns)
			Layer 5 ctrl: 376.115 ± 56.953 Layer 5 cKO: 249. 859 ± 23.001	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0025 (**)
			Layer 6a ctrl: 132.024 ± 10.053 Layer 6a cKO: 163.017 ± 15.001	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9286 (ns)
			Layer 6b ctrl: 14.300 ± 10.708 Layer 6b cKO: 20.214 ± 8.016	Two-way ANOVA with Šídák's multiple comparisons test	p>0.999 (ns)
Figure 4.6. C	PV interneuron *soma morphology* (mean ± SEM)	***Genotype*** (Global)	**P21 Striatum** soma area: 111.4 ± 2.860 (ctrl)	Two-tailed unpaired Mann-Whitney test	p=0.0206 (*)
			soma area: 102.6 ± 2.332 (cKO)		
			soma perimeter: 44.22 ± 0.70 (ctrl)	Two-tailed unpaired Mann-Whitney test	p=0.0398 (*)
			soma perimeter: 43.13 ± 0.758 (cKO)		
			soma circularity: 0.716 ± 0.0099 (ctrl)	Two-tailed unpaired Mann-Whitney test	p=0.7316 (ns)

			soma circularity: 43.13 ± 0.0094 (cKO)		
			soma roundness: 0.698 ± 0.0097 (ctrl)	Two-tailed unpaired Mann-Whitney test	p=0.0261 (ns)
			soma roundness: 0.666 ± 0.0090 (cKO)		
			soma solidity: 0.888 ± 0.0048 (ctrl)	Two-tailed unpaired Mann-Whitney test	p=0.6597 (ns)
			soma solidity: 0.885 ± 0.0049 (cKO)		
Figure 4.6. F	PV interneuron *cell density* (mean ± SEM)	***Genotype*** (Global)	**P21** CPu ctrl: 72.940 ± 6.122	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9012 (ns)
			CPu cKO: 92.674 ± 5.267		
			GPe ctrl: 364.915 ± 9.956	Two-way ANOVA with Šídák's multiple comparisons test	p=0.7095 (ns)
			GPe cKO: 334.028 ± 13.083		
			TRN ctrl: 778.743 ± 57.386	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9967 (ns)
			TRN cKO: 785.444 ± 26.447		
Figure 4.7. C	GABA-B R1 *receptor density* (mean ± SEM)	***Genotype & Layer*** (Local)	**P21 M1** L5 GABA-B R1+: 917.965 ± 32.687 (ctrl)	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0119 (*)
			L5 GABA-B R1+: 730.941 ± 71.415 (cKO)		
			L5 PV+ GABA-B R1+: 38.065 ± 8.774 (ctrl)	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9972 (ns)
			L5 PV+ GABA-B R1+: 20.857 ± 1.799 (cKO)		
			L5 PV+ GABA-B R1-: 182.562 ± 23.972 (ctrl)	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9997 (ns)
			L5 PV+ GABA-B R1-: 192.015 ± 20.232 (cKO)		
			L5 PV- GABA-B R1+: 879.900 ± 33.696 (ctrl)	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0254 (*)
			L5 PV- GABA-B R1+: 710.084 ± 71.994 (cKO)		
Figure 4.7. D	GABA-B R1 *receptor density* (mean ± SEM)	***Genotype & Layer*** (Local)	**P21 S1** L5 GABA-B R1+: 925.765 ± 44.799 (ctrl)	Two-way ANOVA with Šídák's multiple comparisons test	p<0.0001 (****)
			L5 GABA-B R1+: 595.894 ± 25.488 (cKO)		
			L5 PV+ GABA-B R1+: 66.072 ± 11.451 (ctrl)	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9972 (ns)
			L5 PV+ GABA-B R1+: 54.401 ± 9.808 (cKO)		
			L5 PV+ GABA-B R1-: 159.936 ± 16.405 (ctrl)	Two-way ANOVA with Šídák's multiple comparisons test	p=0.8413 (ns)
			L5 PV+ GABA-B R1-: 195.458 ± 22.349 (cKO)		

			L5 PV- GABA-B R1+: 859.693 ± 45.355 (ctrl) L5 PV- GABA-B R1+: 547.967 ± 23.447 (cKO)	Two-way ANOVA with Šídák's multiple comparisons test	p<0.0001 (****)
Figure 4.7. G	GABA-B R1 *percentage* (mean ± SEM)	***Genotype & Region*** (Local)	**P21 M1** L5 PV+ GABA-B R1+: 17.776 ± 3.718 (ctrl) **P21 S1** L5 PV+ GABA-B R1+: 29.336 ± 3.636 (ctrl)	Two-way ANOVA with uncorrected Fisher's LSD test	p=0.0288 (*)
			P21 M1 L5 PV+ GABA-B R1+: 10.302 ± 1.644 (cKO) **P21 S1** L5 PV+ GABA-B R1+: 22.072 ± 4.069 (cKO)	Two-way ANOVA with uncorrected Fisher's LSD test	p=0.0264 (*)
Figure 4.8. C	GABA-A δ *receptor density* (mean ± SEM)	***Genotype & Region*** (Local)	**P21** **M1** ctrl: 896.740 ± 39.274 M1 cKO: 992.850 ± 34.779	Two-way ANOVA with Šídák's multiple comparisons test	p=0.1834 (ns)
			P21 **S1** ctrl: 1011.670 ± 32.398 S1 cKO: 1014.775 ± 46.017	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9980 (ns)
Figure 4.8. F	Drd1a-Cre;Ai14; Snap25$^{fl/fl}$ *cell density* (mean ± SEM)	***Region*** (Local)	**P21** M1 cKO: 988.1 ± 84.51 S1 cKO: 601.6 ± 79.45	Two-tailed unpaired student's t-test with Welch's corrections	p=0.0104 (*)
Figure 4.8. G	Drd1a-Cre+; GABA-A δ+ *cell density* (mean ± SEM)	***Region*** (Local)	**P21** M1 cKO: 187.0 ± 20.24 S1 cKO: 104.8 ± 18.55	Two-tailed unpaired student's t-test with Welch's corrections	p=0.0174 (*)
Figure 4.8. H	Drd1a-Cre+; GABA-A δ+ *cell density* (mean ± SEM)	***Region*** (Local)	**P21 M1** Drd1a-Cre+ cKO: 988.061 ± 84.512 Drd1a-Cre+;GABA-A δ+ cKO: 186.972 ± 20.235	Two-way ANOVA with Šídák's multiple comparisons test	p<0.0001 (****)
			P21 S1 Drd1a-Cre+ cKO: 601.649 ± 79.450 Drd1a-Cre+;GABA-A δ+ cKO: 104.809 ± 18.548	Two-way ANOVA with Šídák's multiple comparisons test	p<0.0001 (****)
Figure 4.12. D	Calretinin *cell density* (mean ± SEM)	***Genotype*** (Global)	**P21** CPu ctrl: 39.30 ± 6.669 CPu cKO: 39.56 ± 6.047	Two-tailed unpaired student's t-test with Welch correction	p=0.9777 (ns)
Figure 4.12. E	Somatostatin *cell density* (mean ± SEM)	***Genotype*** (Global)	CPu ctrl: 52.97 ± 6.228 CPu cKO: 44.37 ± 6.612	Two-tailed unpaired student's t-test with Welch correction	p=0.3716 (ns)

Figure 4.12. F	Calretinin *soma morphology* (mean ± SEM)	***Genotype*** (Global)	**P21 CPu** soma area: 60.67 ± 1.996 (ctrl) soma area: 68.43 ± 1.964 (cKO)	Two-tailed unpaired Mann-Whitney test	p=0.0027 (**)
			soma perimeter: 33.18 ± 0.898 (ctrl) soma perimeter: 36.55 ± 0.992 (cKO)	Two-tailed unpaired Mann-Whitney test	p=0.0041 (**)
			soma circularity: 0.725 ± 0.0152 (ctrl) soma circularity: 0.687 ± 0.017 (cKO)	Two-tailed unpaired Mann-Whitney test	p=0.0673 (ns)
			soma roundness: 0.679 ± 0.0145 (ctrl) soma roundness: 0.666 ± 0.016 (cKO)	Two-tailed unpaired Mann-Whitney test	p=0.5686 (ns)
			soma solidity: 0.872 ± 0.007 (ctrl) soma solidity: 0.666 ± 0.007 (cKO)	Two-tailed unpaired Mann-Whitney test	p=0.0878 (ns)
Figure 4.13. D	Calretinin *cell density* (mean ± SEM)	***Genotype*** (Global)	**P21** CA1 ctrl: 20.29 ± 2.333 CA1 cKO: 37.81 ± 1.543	Two-tailed unpaired student's t-test with Welch correction	p=0.0004 (***)
Figure 4.13. E	Somatostatin *cell density* (mean ± SEM)	***Genotype*** (Global)	**P21** CA1 ctrl: 50.54 ± 2.151 CA1 cKO: 42.79 ± 1.356	Two-tailed unpaired student's t-test with Welch correction	p=0.0195 (*)
Figure 4.9. B	Neuropeptide-Y *cell density* (mean ± SEM)	***Genotype*** (Local)	**P21** ACA ctrl: 22.05 ± 1.821 ACA cKO: 30.57 ± 2.953	Two-way ANOVA with Šídák's multiple comparisons test	p=0.2212 (ns)
			M2 ctrl: 34.228 ± 2.943 M2 cKO: 48.905 ± 5.507	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0262 (*)
Figure 4.9. E	Neuropeptide-Y *cell density* (mean ± SEM)	***Genotype*** (Local)	**P21** M1 ctrl: 102.0 ± 5.262 M1 cKO: 115.9 ± 2.448	Two-tailed unpaired student's t-test with Welch correction	p=0.0565 (ns)
Figure 4.9. F	Neuropeptide-Y *laminar distribution* (mean ± SEM)	***Genotype*** (Local)	**P21 M1** Layer 1 ctrl: 74.222 ± 16.589 Layer 1 cKO: 94.095 ± 5.337	Two-way ANOVA with Šídák's multiple comparisons test	p=0.4593 (ns)
			Layer 2/3 ctrl: 158.086 ± 10.538 Layer 2/3 cKO: 178.512 ± 9.205	Two-way ANOVA with Šídák's multiple comparisons test	p=0.4297 (ns)
			Layer 5 ctrl: 72.715 ± 5.541 Layer 5 cKO: 75.500 ± 10.288	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9998 (ns)
			Layer 6a ctrl: 82.143 ± 6.649		p=0.5755 (ns)

			Layer 6a cKO: 99.947 ± 4.714	Two-way ANOVA with Šídák's multiple comparisons test	
			Layer 6b ctrl: 78.223 ± 5.442	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 6b cKO: 79.748 ± 5.634		
Figure 4.9. G	Neuropeptide-Y *cell density* (mean ± SEM)	***Genotype*** (Local)	**P21** S1 ctrl: 94.97 ± 3.857	Two-tailed unpaired student's t-test with Welch correction	p=0.0828 (ns)
			S1 cKO: 113.0 ± 7.745		
Figure 4.9. H	Neuropeptide-Y *laminar distribution* (mean ± SEM)	***Genotype*** (Local)	**P21 S1** Layer 1 ctrl: 85.079 ± 10.164	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9659 (ns)
			Layer 1 cKO: 73.973 ± 11.011		
			Layer 2/3 ctrl: 191.102 ± 8.357	Two-way ANOVA with Šídák's multiple comparisons test	p=0.2248 (ns)
			Layer 2/3 cKO: 220.364 ± 19.531		
			Layer 4 ctrl: 67.555 ± 9.251	Two-way ANOVA with Šídák's multiple comparisons test	p=0.7237 (ns)
			Layer 4 cKO: 86.005 ± 9.693		
			Layer 5 ctrl: 46.186 ± 3.026	Two-way ANOVA with Šídák's multiple comparisons test	p=0.3238 (ns)
			Layer 5 cKO: 72.768 ± 8.739		
			Layer 6a ctrl: 83.052 ± 4.617	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 6a cKO: 82.890 ± 7.926		
			Layer 6b ctrl: 44.616 ± 11.748	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0199 (*)
			Layer 6b cKO: 87.777 ± 2.903		
Figure 4.10. C	Neuropeptide-Y *cell density* (mean ± SEM)	***Genotype*** (Global)	**P21** CPu ctrl: 59.24 ± 3.397	Two-tailed unpaired student's t-test with Welch correction	p=0.0328 (*)
			CPu cKO: 72.38 ± 3.787		
Figure 4.10. D	Neuropeptide-Y *soma morphology* (mean ± SEM)	***Genotype*** (Global)	**P21 CPu** soma area: 95.52 ± 3.196 (ctrl)	Two-tailed unpaired Mann-Whitney test	p=0.0092 (**)
			soma area: 107.2 ± 3.105 (cKO)		
			soma perimeter: 49.06 ± 1.006 (ctrl)	Two-tailed unpaired Mann-Whitney test	p=0.0064 (**)
			soma perimeter: 53.11 ± 1.075 (cKO)		
			soma circularity: 0.510 ± 0.0118 (ctrl)	Two-tailed unpaired Mann-Whitney test	p=0.4008 (ns)
			soma circularity: 0.497 ± 0.0116 (cKO)		

Figure 4.10. D	Neuropeptide-Y *soma morphology* (mean ± SEM)	***Genotype*** (Global)	soma roundness: 0.570 ± 0.013 (ctrl)	Two-tailed unpaired Mann-Whitney test	p=0.885 (ns)
			soma roundness: 0.574 ± 0.012		
			soma solidity: 0.781 ± 0.0078 (ctrl)	Two-tailed unpaired Mann-Whitney test	p=0.3851 (ns)
			soma solidity: 0.767 ± 0.0079 (cKO)		
Figure 4.11. B	Neuropeptide-Y *cell density* (mean ± SEM)	***Genotype*** (Global)	**P21** CA1 ctrl: 37.26 ± 2.502	Two-tailed unpaired student's t-test with Welch correction	p=0.0210 (*)
			CA1 cKO: 56.45 ± 5.491		
Figure 4.11. D	Neuropeptide-Y *cell density* (mean ± SEM)	***Genotype*** (Global)	**P21** CA3 ctrl: 34.68 ± 3.519	Two-tailed unpaired student's t-test with Welch correction	p=0.1850 (ns)
			CA3 cKO: 44.27 ± 5.472		
Figure 4.11. D	Neuropeptide-Y *cell density* (mean ± SEM)	***Genotype*** (Global)	**P21** DG ctrl: 71.02 ± 7.880	Two-tailed unpaired student's t-test with Welch correction	p=0.0615 (ns)
			DG cKO: 94.44 ± 7.341		

ADULT					
Figure	**Analysis**	**Effect**	**Values**	**Statistical test**	**P value**
Figure 4.15. B	Drd1a-Cre;Ai14; Snap25$^{fl/fl}$ *laminar distribution* (mean ± SEM)	***Layer + Region*** (Local)	**12 weeks** Layer 1 (S1 dense cKO): 0.00 ± 0.00 Layer 1 (S1 sparse cKO): 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 2/3 (S1 dense cKO): 0.00 ± 0.00 Layer 2/3 (S1 sparse cKO): 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 4 (S1 dense cKO): 0.00 ± 0.00 Layer 4 (S1 sparse cKO): 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 5 (S1 dense cKO): 6.761 ± 1.540 Layer 5 (S1 sparse cKO): 0.985 ± 0.985	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 6a (S1 dense cKO): 444.841 ± 53.902 Layer 6a (S1 sparse cKO): 160.038 ± 13.609	Two-way ANOVA with Šídák's multiple comparisons test	p<0.0001 (****)
			Layer 6b (S1 dense cKO): 1456.526 ± 90.450 Layer 6b (S1 sparse cKO): 841.574 ± 51.887	Two-way ANOVA with Šídák's multiple comparisons test	p<0.0001 (****)
Figure 4.15. C	Drd1a-Cre;Ai14; Snap25$^{fl/fl}$ *cell density* (mean ± SEM)	***Region*** (Local)	**12 weeks** S1 sparse cKO: 89.66 ± 7.296 S1 dense cKO: 203.7 ± 16.78	Two-tailed unpaired student's t-test with Welch correction	p=0.0011 (**)
Figure 4.15. F	Drd1a-Cre;Ai14; Snap25$^{fl/fl}$ *laminar distribution (trajectory)* (mean ± SEM)	***Layer + Region*** (Local)	**S1 dense** Layer 1 (P21 cKO): 0.00 ± 0.00 Layer 1 (12 wks cKO): 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 2/3 (P21 cKO): 0.00 ± 0.00 Layer 2/3 (12 wks cKO): 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 4 (P21 cKO): 0.00 ± 0.00 Layer 4 (12 wks cKO): 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 5 (P21 cKO): 4.962 ± 1.619		p>0.9999 (ns)

			Layer 5 (12 wks cKO): 6.761 ± 1.540	Two-way ANOVA with Šídák's multiple comparisons test	
			Layer 6a (P21 cKO): 498.980 ± 105.478	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9867 (ns)
			Layer 6a (12 wks cKO): 444.841 ± 53.902		
			Layer 6b (P21 cKO): 1312.600 ± 135.148	Two-way ANOVA with Šídák's multiple comparisons test	p=0.4175 (ns)
			Layer 6b (12 wks cKO): 1456.526 ± 90.450		
Figure 4.15. G	Drd1a-Cre;Ai14; Snap25$^{fl/fl}$ *cell density* (mean ± SEM)	***Region + Age*** (Local)	**S1 dense** P21 cKO: 241.1 ± 39.00	Two-tailed unpaired student's t-test with Welch correction	p=0.8152 (ns)
			12 wks cKO: 203.7 ± 16.78		
Figure 4.16. B	Parvalbumin *cell density* (mean ± SEM)	***Genotype*** (Local)	**12 weeks** ACA ctrl: 65.03 ± 3.456	Two-tailed unpaired student's t-test with Welch correction	p=0.2646 (ns)
			ACA cKO: 53.95 ± 8.199		
Figure 4.16. C	*Vicia villosa* agglutinin *cell density* (mean ± SEM)	***Genotype*** (Local)	**12 weeks** ACA ctrl: 73.43 ± 4.135	Two-tailed unpaired student's t-test with Welch correction	p=0.1871 (ns)
			ACA cKO: 61.41 ± 7.023		
Figure 4.16. D	Parvalbumin subclasses *cell density* (mean ± SEM)	***Genotype*** (Local)	**12 weeks, ACA** PV+ VVA+ ctrl: 47.926 ± 3.387	Two-way ANOVA with Šídák's multiple comparisons test	p=0.2145 (ns)
			PV+ VVA+ cKO: 37.638 ± 6.488		
			PV+ VVA- ctrl: 14.867 ± 3.893	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9917 (ns)
			PV+ VVA- cKO: 16.315 ± 2.676		
			PV- VVA+ ctrl: 23.188 ± 2.375	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9994 (ns)
			PV- VVA+ cKO: 23.776 ± 3.420		
Figure 4.16. F	Parvalbumin *cell density* (mean ± SEM)	***Genotype*** (Local)	**12 weeks** M1 ctrl: 213.0 ± 7.686 M1 cKO: 182.5 ± 17.13	Two-tailed unpaired student's t-test with Welch correction	p=0.1591 (ns)
Figure 4.16. G	*Vicia villosa* agglutinin *cell density* (mean ± SEM)	***Genotype*** (Local)	**12 weeks** M1 ctrl: 185.8 ± 4.718	Two-tailed unpaired student's t-test with Welch correction	p=0.4143 (ns)
			M1 cKO: 171.7 ± 15.03		
Figure 4.16. H	Parvalbumin subclasses *cell density* (mean ± SEM)	***Genotype*** (Local)	**12 weeks, M1** PV+ VVA+ ctrl: 147.105 ± 12.229	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0187 (*)
			PV+ VVA+ cKO: 109.594 ± 11.848		
			PV+ VVA- ctrl: 74.309 ± 7.539	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9673 (ns)
			PV+ VVA- cKO: 69.086 ± 6.872		

			PV- VVA+ ctrl: 54.094 ± 6.689 PV- VVA+ cKO: 58.318 ± 5.630	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9822 (ns)
Figure 4.16. I	Parvalbumin *laminar distribution* (mean ± SEM)	***Layer + Region*** (Local)	**M1 (12 weeks)** Layer 1 ctrl: 0.00 ± 0.00 Layer 1 cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 2/3 ctrl: 282.143 ± 21.920 Layer 2/3 cKO: 259.431 ± 17.106	Two-way ANOVA with Šídák's multiple comparisons test	p=0.8169 (ns)
			Layer 5 ctrl: 283.329 ± 16.530 Layer 5 cKO: 224.865 ± 25.368	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0752 (ns)
			Layer 6 ctrl: 168.790 ± 18.228 Layer 6 cKO: 139.256 ± 15.222	Two-way ANOVA with Šídák's multiple comparisons test	p=0.6345 (ns)
Figure 4.16. J	Parvalbumin subclasses *laminar distribution* (mean ± SEM)	***Layer + Cell type*** (Local)	**M1 (12 weeks)** **PV+ VVA+** Layer 1 ctrl: 0.00 ± 0.00 Layer 1 cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 2/3 ctrl: 198.572 ± 26.979 Layer 2/3 cKO: 177.088 ± 21.133	Two-way ANOVA with Šídák's multiple comparisons test	p=0.8041 (ns)
			Layer 5 ctrl: 215.529 ± 22.497 Layer 5 cKO: 135.360 ± 11.913	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0036 (**)
			Layer 6 ctrl: 103.680 ± 6.216 Layer 6 cKO: 75.655 ± 7.947	Two-way ANOVA with Šídák's multiple comparisons test	p=0.6115 (ns)
Figure 4.16. K	Parvalbumin subclasses *laminar distribution* (mean ± SEM)	***Layer + Cell type*** (Local)	**M1 (12 weeks)** **PV+ VVA-** Layer 1 ctrl: 0.00 ± 0.00 Layer 1 cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 2/3 ctrl: 103.087 ± 11.297 Layer 2/3 cKO: 82.342 ± 7.767	Two-way ANOVA with Šídák's multiple comparisons test	p=0.5770 (ns)
			Layer 5 ctrl: 88.489 ± 15.284 Layer 5 cKO: 89.505 ± 18.212	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 6 ctrl: 83.195 ± 10.449		p=0.6274 (ns)

			Layer 6 cKO: 63.601 ± 8.953	Two-way ANOVA with Šídák's multiple comparisons test	
Figure 4.16. L	*Vicia villosa* agglutinin *laminar distribution* (mean ± SEM)	***Layer*** (Local)	**M1 (12 weeks)** **VVA+** Layer 1 ctrl: 0.00 ± 0.00 Layer 1 cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 2/3 ctrl: 258.938 ± 4.453 Layer 2/3 cKO: 246.004 ± 26.690	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9222 (ns)
			Layer 5 ctrl: 260.593 ± 10.198 Layer 5 cKO: 231.913 ± 17.633	Two-way ANOVA with Šídák's multiple comparisons test	p=0.3902 (ns)
			Layer 6 ctrl: 119.083 ± 9.544 Layer 6 cKO: 112.075 ± 4.948	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9914 (ns)
Figure 4.16. M	Vicia villosa agglutinin *laminar distribution* (mean ± SEM)	***Layer + Cell type*** (Local)	**M1 (12 weeks)** **PV- VVA+** Layer 1 ctrl: 0.00 ± 0.00 Layer 1 cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 2/3 ctrl: 89.527 ± 17.535 Layer 2/3 cKO: 68.915 ± 7.537	Two-way ANOVA with Šídák's multiple comparisons test	p=0.4108 (ns)
			Layer 5 ctrl: 72.900 ± 13.275 Layer 5 cKO: 96.553 ± 12.096	Two-way ANOVA with Šídák's multiple comparisons test	p=0.2816 (ns)
			Layer 6 ctrl: 20.892 ± 5.282 Layer 6 cKO: 36.420 ± 5.923	Two-way ANOVA with Šídák's multiple comparisons test	p=0.6702 (ns)
Figure 4.16. N	Parvalbumin *developmental trajectory* ctrl (mean ± SEM)	***Layer + Age*** (Local)	**M1 ctrl** **P21 – 12 weeks** P21, Layer 1 ctrl: 4.533 ± 4.533 12 wks, Layer 1 ctrl: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p=0.997 (ns)
			P21, Layer 2/3 ctrl: 224.307 ± 35.168 12 wks, Layer 2/3 ctrl: 282.143 ± 21.920	Two-way ANOVA with Šídák's multiple comparisons test	p=0.1775 (ns)
			P21, Layer 5 ctrl: 220.627 ± 24.448 12 wks, Layer 5 ctrl: 283.329 ± 16.530	Two-way ANOVA with Šídák's multiple comparisons test	p=0.1246 (ns)

			P21, Layer 6 ctrl: 184.269 ± 14.642 12 wks, Layer 6 ctrl: 168.790 ± 18.228	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9704 (ns)
Figure 4.16. O	Parvalbumin developmental trajectory cKO (mean ± SEM)	***Layer + Age*** (Local)	**M1 cKO** **P21 – 12 weeks** P21, Layer 1 cKO: 2.891 ± 1.793 12 wks, Layer 1 cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			P21, Layer 2/3 cKO: 248.285 ± 15.902 12 wks, Layer 2/3 cKO: 259.431 ± 17.106	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9803 (ns)
			P21, Layer 5 cKO: 212.872 ± 19.220 12 wks, Layer 5 cKO: 224.865 ± 25.368	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9743 (ns)
			P21, Layer 6 cKO: 192.855 ± 15.879 12 wks, Layer 6 cKO: 139.256 ± 15.222	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0925 (ns)
Figure 4.17. C	Parvalbumin *cell density* (mean ± SEM)	***Genotype + Region*** (Local)	**S1 dense** 12 wks, ctrl: 188.999 ± 11.631 12 wks, cKO: 176.705 ± 8.737	Two-way ANOVA with uncorrected Fisher's LSD test	p=0.5090 (ns)
			S1 sparse 12 wks, ctrl: 154.876 ± 18.672 12 wks, cKO: 135.708 ± 10.114	Two-way ANOVA with uncorrected Fisher's LSD test	p=0.3079 (ns)
			ctrl S1 dense: 188.999 ± 11.631 S1 sparse: 154.876 ± 18.672	Two-way ANOVA with uncorrected Fisher's LSD test	p=0.0792 (ns)
			cKO S1 dense: 176.705 ± 8.737 S1 sparse: 135.708 ± 10.114	Two-way ANOVA with uncorrected Fisher's LSD test	p=0.0387 (*)
Figure 4.17. D	*Vicia villosa* agglutinin *cell density* (mean ± SEM)	***Genotype + Region*** (Local)	**S1 dense** 12 wks, ctrl: 220.841 ±7.873 12 wks, cKO: 202.763 ± 7.151	Two-way ANOVA with uncorrected Fisher's LSD test	p=0.2775 (ns)
			S1 sparse 12 wks, ctrl: 249.186 ± 11.088	Two-way ANOVA with uncorrected Fisher's LSD test	p=0.7978 (ns)

			12 wks, cKO: 253.374 ± 16.765		
			ctrl S1 dense: 220.841 ±7.873	Two-way ANOVA with uncorrected Fisher's LSD test	p=0.0970 (ns)
			S1 sparse: 249.186 ± 11.088		
			cKO S1 dense: 202.763 ± 7.151	Two-way ANOVA with uncorrected Fisher's LSD test	p=0.0062 (**)
			S1 sparse: 253.374 ± 16.765		
Figure 4.17. E	Parvalbumin subclasses *cell density* (mean ± SEM)	***Genotype + Cell type*** (Local)	**S1 dense (12 weeks)** PV+ VVA+, ctrl: 125.259 ± 11.565	Two-way ANOVA with Šídák's multiple comparisons test	p=0.6906 (ns)
			PV+ VVA+, cKO: 112.087 ± 1.999		
			PV+ VVA-, ctrl: 63.740 ± 4.102	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9998 (ns)
			PV+ VVA-, cKO: 64.751 ± 7.655		
			PV- VVA+, ctrl: 100.146 ± 15.717	Two-way ANOVA with Šídák's multiple comparisons test	p=0.8452 (ns)
			PV- VVA+, cKO: 90.397 ± 7.236		
Figure 4.17. F	Parvalbumin subclasses *cell density* (mean ± SEM)	***Genotype + Cell type*** (Local)	**S1 sparse (12 weeks)** PV+ VVA+, ctrl: 132.003 ± 15.031	Two-way ANOVA with Šídák's multiple comparisons test	p=0.1547 (ns)
			PV+ VVA+, cKO: 98.249 ± 7.390		
			PV+ VVA-, ctrl: 23.013 ± 5.788	Two-way ANOVA with Šídák's multiple comparisons test	p=0.7621 (ns)
			PV+ VVA-, cKO: 37.933 ± 11.100		
			PV- VVA+, ctrl: 111.803 ± 15.233	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0321 (*)
			PV- VVA+, cKO: 157.933 ± 12.921		
Figure 4.17. G	Parvalbumin *laminar distribution* (mean ± SEM)	***Genotype + Layer*** (Local)	**S1 dense (12 weeks)** Layer 1, ctrl: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 1, cKO: 0.00 ± 0.00		
			Layer 2/3, ctrl: 175.376 ± 21.937	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 2/3, cKO: 178.270 ± 13.497		
			Layer 4, ctrl: 361.609 ± 17.871	Two-way ANOVA with Šídák's multiple comparisons test	p=0.5744 (ns)
			Layer 4, cKO:394.611 ± 5.047		
			Layer 5, ctrl: 255.468 ± 19.957		p=0.2145 (ns)

			Layer 5, cKO: 209.785 ± 29.260	Two-way ANOVA with Šídák's multiple comparisons test	
			Layer 6a, ctrl: 183.100 ± 13.394 Layer 6a, cKO: 137.766 ± 10.069	Two-way ANOVA with Šídák's multiple comparisons test	p=0.2217 (ns)
			Layer 6b, ctrl: 26.926 ± 5.444 Layer 6b, cKO: 27.889 ± 14.862	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
Figure 4.17. G’	Parvalbumin *laminar distribution* (mean ± SEM)	***Genotype + Layer*** (Local)	**S1 sparse (12 weeks)** Layer 1, ctrl: 0.00 ± 0.00 Layer 1, cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 2/3, ctrl: 144.908 ± 34.614 Layer 2/3, cKO: 143.943 ± 16.430	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 4, ctrl: 278.962 ± 34.058 Layer 4, cKO: 239.900 ± 27.162	Two-way ANOVA with Šídák's multiple comparisons test	p=0.6730 (ns)
			Layer 5, ctrl: 214.095 ±22.079 Layer 5, cKO: 198.403 ± 16.842	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9944 (ns)
			Layer 6a, ctrl: 133.439 ± 16.659 Layer 6a, cKO: 90.831 ± 14.088	Two-way ANOVA with Šídák's multiple comparisons test	p=0.5815 (ns)
			Layer 6b, ctrl: 20.270 ±5.384 Layer 6b, cKO: 27.685 ± 8.628	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
Figure 4.17. H	*Vicia villosa agglutinin laminar distribution* (mean ± SEM)	***Genotype + Layer*** (Local)	**S1 dense (12 weeks)** Layer 1, ctrl: 0.00 ± 0.00 Layer 1, cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 2/3, ctrl: 163.300 ± 14.455 Layer 2/3, cKO: 128.276 ± 4.168	Two-way ANOVA with Šídák's multiple comparisons test	p=0.8341 (ns)
			Layer 4, ctrl: 527.824 64.386 Layer 4, cKO: 624.624 ± 29.163	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0163 (*)
			Layer 5, ctrl: 323.277 ± 6.692 Layer 5, cKO: 257.738 ± 10.265	Two-way ANOVA with Šídák's multiple comparisons test	p=0.2053 (ns)
			Layer 6a, ctrl: 184.622 ± 11.198		p=0.7734 (ns)

			Layer 6a, cKO: 146.470 ± 9.811	Two-way ANOVA with Šídák's multiple comparisons test	
			Layer 6b, ctrl: 7.038 ± 5.015	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 6b, cKO: 3.866 ± 3.866		
Figure 4.17. H’	*Vicia villosa agglutinin laminar distribution* (mean ± SEM)	***Genotype + Layer*** (Local)	**S1 sparse (12 weeks)** Layer 1, ctrl: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 1, cKO: 0.00 ± 0.00		
			Layer 2/3, ctrl: 206.685 ± 18.532	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 2/3, cKO: 214.256 ± 19.742		
			Layer 4, ctrl: 541.546 ± 44.867	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 4, cKO: 544.992 ± 43.377		
			Layer 5, ctrl: 378.177 ± 19.933	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9989 (ns)
			Layer 5, cKO: 365.040 ± 28.201		
			Layer 6a, ctrl: 154.145 ± 6.912	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 6a, cKO: 155.320 ± 11.872		
			Layer 6b, ctrl: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 6b, cKO: 2.425 ± 2.425		
Figure 4.17. I	Parvalbumin subtypes *laminar distribution* (mean ± SEM)	***Genotype + Layer*** (Local)	**S1 dense (12 weeks)** **PV+ VVA+** Layer 1, ctrl: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 1, cKO: 0.00 ± 0.00		
			Layer 2/3, ctrl: 85.022 ± 8.080	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 2/3, cKO: 80.336 ± 5.800		
			Layer 4, ctrl: 289.056 ± 40.828	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0806 (ns)
			Layer 4, cKO: 343.111 ± 9.367		
			Layer 5, ctrl: 161.058 ± 19.265	Two-way ANOVA with Šídák's multiple comparisons test	p=0.1886 (ns)
			Layer 5, cKO: 114.918 ± 14.535		
			Layer 6a, ctrl: 135.850 ± 12.013	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0751 (ns)
			Layer 6a, cKO: 81.187 ± 8.281		
			Layer 6b, ctrl: 7.038 ± 5.015		p>0.9999 (ns)

			Layer 6b, cKO: 3.886 ±3.886	Two-way ANOVA with Šídák's multiple comparisons test	
Figure 4.17. I’	Parvalbumin subtypes *laminar distribution* (mean ± SEM)	***Genotype + Layer*** (Local)	**S1 sparse (12 weeks)** **PV+ VVA+** Layer 1, ctrl: 0.00 ± 0.00 Layer 1, cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 2/3, ctrl: 108.668 ± 27.802 Layer 2/3, cKO: 87.286 10.492	Two-way ANOVA with Šídák's multiple comparisons test	p=0.8976 (ns)
			Layer 4, ctrl: 253.123 ± 17.944 Layer 4, cKO: 230.830 ± 26.262	Two-way ANOVA with Šídák's multiple comparisons test	p=0.8762 (ns)
			Layer 5, ctrl: 191.414 ± 19.118 Layer 5, cKO: 141.247 ± 13.279	Two-way ANOVA with Šídák's multiple comparisons test	p=0.1220 (ns)
			Layer 6a, ctrl: 104.409 ± 12.128 Layer 6a, cKO: 54.592 ± 8.023	Two-way ANOVA with Šídák's multiple comparisons test	p=0.1267 (ns)
			Layer 6b, ctrl: 5.611 ± 3.708 Layer 6b, cKO: 5.004 ± 3.067	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
Figure 4.17. J	*Vicia villosa agglutinin laminar distribution* (mean ± SEM)	***Genotype + Layer*** (Local)	**S1 dense (12 weeks)** **PV- VVA+** Layer 1, ctrl: 0.00 ± 0.00 Layer 1, cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 2/3, ctrl: 65.040 ± 19.768 Layer 2/3, cKO: 47.940 ± 2.636	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9872 (ns)
			Layer 4, ctrl: 280.540 ± 47.516 Layer 4, cKO: 281.513 ± 21.002	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 5, ctrl: 162.219 ± 24.926 Layer 5, cKO: 122.981 ± 15.410	Two-way ANOVA with Šídák's multiple comparisons test	p=0.5955 (ns)
			Layer 6a, ctrl: 49.339 ± 10.478 Layer 6a, cKO: 65.283 ± 6.103	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9911 (ns)
			Layer 6b, ctrl: 0.00 ± 0.00 Layer 6b, cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)

Figure 4.17. J’	Vicia villosa agglutinin *laminar distribution* (mean ± SEM)	***Genotype + Layer*** (Local)	**S1 sparse (12 weeks)** **PV- VVA+** Layer 1, ctrl: 0.00 ± 0.00 Layer 1, cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 2/3, ctrl: 93.161 ± 29.712 Layer 2/3, cKO: 126.970 ± 14.811	Two-way ANOVA with Šídák's multiple comparisons test	p=0.5824 (ns)
			Layer 4, ctrl: 279.464 ± 29.689 Layer 4, cKO: 354.438 ± 10.859	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0090 (**)
			Layer 5, ctrl: 186.762 ± 20.603 Layer 5, cKO: 223.793 ± 18.233	Two-way ANOVA with Šídák's multiple comparisons test	p=0.4784 (ns)
			Layer 6a, ctrl: 49.736 ± 8.826 Layer 6a, cKO: 87.653 ± 6.162	Two-way ANOVA with Šídák's multiple comparisons test	p=0.4507 (ns)
			Layer 6b, ctrl: 0.00 ± 0.00 Layer 6b, cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
Figure 4.17. K	Parvalbumin subtypes *laminar distribution* (mean ± SEM)	***Genotype + Layer*** (Local)	**S1 dense (12 weeks)** **PV+ VVA-** Layer 1, ctrl: 0.00 ± 0.00 Layer 1, cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 2/3, ctrl: 76.540 ± 18.828 Layer 2/3, cKO: 97.934 ± 7.793	Two-way ANOVA with Šídák's multiple comparisons test	p=0.7483 (ns)
			Layer 4, ctrl: 60.325 ± 17.819 Layer 4, cKO: 52.852 ± 5.511	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9983 (ns)
			Layer 5, ctrl: 94.410 ± 7.244 Layer 5, cKO: 77.007 ± 19.806	Two-way ANOVA with Šídák's multiple comparisons test	p=0.8839 (ns)
			Layer 6a, ctrl: 47.818 ± 12.387 Layer 6a, cKO: 64.773 ± 7.649	Two-way ANOVA with Šídák's multiple comparisons test	p=0.8959 (ns)
			Layer 6b, ctrl: 19.887 ± 5.897 Layer 6b, cKO: 24.003 ± 14.552	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
Figure 4.17. K’	Parvalbumin subtypes	***Genotype + Layer*** (Local)	**S1 sparse (12 weeks)** **PV+ VVA-** Layer 1, ctrl: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)

	laminar distribution (mean ± SEM)		Layer 1, cKO: 0.00 ± 0.00		
			Layer 2/3, ctrl: 36.239 ± 9.016 Layer 2/3, cKO: 56.657 ± 14.237	Two-way ANOVA with Šídák's multiple comparisons test	p=0.5424 (ns)
			Layer 4, ctrl: 2.443 ± 2.443 Layer 4, cKO: 9.070 4.712	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9966 (ns)
			Layer 5, ctrl: 22.732 ± 7.477 Layer 5, cKO: 57.156 ± 19.477	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0630 (ns)
			Layer 6a, ctrl: 29.518 ± 10.315 Layer 6a, cKO: 39.063 ± 9.348	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9767 (ns)
			Layer 6b, ctrl: 20.270 ± 5.384 Layer 6b, cKO: 25.260 ± 6.325	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9993 (ns)
Figure 4.21. C	Parvalbumin *cell density* (mean ± SEM)	***Genotype*** (Global)	**Striatum** 12 wks, ctrl: 83.82 ± 12.28 12 wks, cKO: 70.97 ± 5.179	Two-tailed unpaired student's t-test with Welch correction	p=0.3756 (ns)
Figure 4.21. D	Parvalbumin *soma morphology* (mean ± SEM)	***Genotype*** (Global)	**Striatum (12 weeks)** soma area, ctrl: 111.7 ± 2.604 soma area, cKO: 107.3 ± 2.625	Two-tailed unpaired Mann-Whitney test	p=0.2876 (ns)
			soma perimeter, ctrl: 45.61 ± 1.077 soma perimeter, cKO: 43.79 ± 0.758	Two-tailed unpaired Mann-Whitney test	p=0.3423 (ns)
			soma circularity, ctrl: 0.709 ± 0.0097 soma circularity, cKO: 0.712 ± 0.0097	Two-tailed unpaired Mann-Whitney test	p=0.7508 (ns)
			soma roundness, ctrl: 0.710 ± 0.0082 soma roundness, cKO: 0.689 ± 0.0086	Two-tailed unpaired Mann-Whitney test	p=0.0933 (ns)
			soma solidity, ctrl: 0.879 ± 0.0054 soma solidity, cKO: 0.881 ± 0.0051	Two-tailed unpaired Mann-Whitney test	p=0.5893 (ns)
Figure 4.21. F	Parvalbumin *developmental trajectory (ctrl)*	***Age*** (Global)	**Striatum** P21, ctrl: 72.94 ± 6.122 12 wks, ctrl: 83.82 ± 12.28	Two-tailed unpaired student's t-test with Welch correction	p=0.4587 (ns)

	(mean ± SEM)				
Figure 4.21. G	Parvalbumin *developmental trajectory (cKO)* (mean ± SEM)	***Age*** (Global)	**Striatum** P21, cKO: 92.67 ± 5.267 12 wks, cKO: 70.97 ± 5.179	Two-tailed unpaired student’s t-test with Welch correction	p=0.0188 (*)
Figure 4.21. H	Parvalbumin *developmental trajectory (ctrl)* (mean ± SEM)	***Age*** (Global)	**Striatum** **soma area** P21, ctrl: 111.4 ± 2.860 12 wks, ctrl: 111.7 ± 2.604	Two-tailed unpaired Mann-Whitney test	p=0.9941 (ns)
			soma perimeter P21, ctrl: 44.22 ± 0.70 12 wks, ctrl: 44.93 ± 0.837	Two-tailed unpaired Mann-Whitney test	p=0.9629 (ns)
			soma circularity P21, ctrl: 0.716 ± 0.0099 12 wks, ctrl: 0.709 ± 0.0097	Two-tailed unpaired Mann-Whitney test	p=0.7986 (ns)
			soma roundness P21, ctrl: 0.698 ± 0.0099 12 wks, ctrl: 0.709 ± 0.0081	Two-tailed unpaired Mann-Whitney test	p=0.4329 (ns)
			soma solidity P21, ctrl: 0.888 ± 0.0048 12 wks, ctrl: 0.879 ± 0.0054	Two-tailed unpaired Mann-Whitney test	p=0.2035 (ns)
Figure 4.21. I	Parvalbumin *developmental trajectory (cKO)* (mean ± SEM)	***Age*** (Global)	**Striatum** **soma area** P21, cKO: 102.6 ± 2.33 12 wks, cKO: 107.3 ± 2.63	Two-tailed unpaired Mann-Whitney test	p=0.1748 (ns)
			soma perimeter P21, cKO: 43.13 ± 0.758 12 wks, cKO: 43.79 ± 0.758	Two-tailed unpaired Mann-Whitney test	p=0.2892 (ns)
			soma circularity P21, cK0: 0.709 ± 0.0094 12 wks, cKO: 0.712 ± 0.0097	Two-tailed unpaired Mann-Whitney test	p=0.6789 (ns)
			soma roundness P21, cK0: 0.666 ± 0.0090 12 wks, cKO: 0.689 ± 0.0086	Two-tailed unpaired Mann-Whitney test	p=0.0882 (ns)
			soma solidity P21, cK0: 0.885 ± 0.0049 12 wks, cKO: 0.881 ± 0.0050	Two-tailed unpaired Mann-Whitney test	p=0.7284 (ns)
Figure 4.22. C	Parvalbumin *cell density* (mean ± SEM)	***Genotype*** (Global)	**12 weeks** GPe, ctrl: 206.828 ± 15.748	Two-way ANOVA with Šídák's multiple comparisons test	p=0.7458 (ns)

			GPe, cKO: 532.538 ± 54.483		
			TRN, ctrl: 206.828 ± 15.748	Two-way ANOVA with Šídák's multiple comparisons test	p=0.7658 (ns)
			TRN, cKO: 571.742 ± 59.148		
Figure 4.22. F	Parvalbumin *developmental trajectory (ctrl)* (mean ± SEM)	***Age*** (Global)	**GPe** P21, ctrl: 364.915 ± 9.956	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0188 (*)
			12 wks, ctrl: 206.828 ± 15.748		
			TRN P21, ctrl: 778.743 ± 57.386	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0011 (**)
			12 wks, ctrl: 532.538 ± 54.483		
Figure 4.22. G	Parvalbumin *developmental trajectory (cKO)* (mean ± SEM)	***Age*** (Global)	**GPe** P21, cKO: 334.028 ± 13.083 12 wks, cKO: 245.874 ± 23.493	Two-way ANOVA with Šídák's multiple comparisons test	p=0.1160 (ns)
			TRN P21, ctrl: 785.444 ± 26.447	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0011 (**)
			12 wks, cKO: 571.742 ± 59.148		
Figure 4.25. C	Somatostatin *cell density* (mean ± SEM)	***Genotype*** (Global)	**12 weeks** CA1, ctrl: 47.960 ± 2.543	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9891 (ns)
			CA1, cKO: 45.746 ± 4.533		
			CA3, ctrl: 56.445 ± 6.537	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9967 (ns)
			CA3, cKO: 57.921 ± 4.796		
			DG, ctrl: 82.270 ± 7.415	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0020 (**)
			DG, cKO: 49.804 ± 6.565		
Figure 4.25. G	Somatostatin *cell density* (mean ± SEM)	***Genotype*** (Global)	**12 weeks** CPu, ctrl: 43.35 ± 6.152	Two-tailed unpaired student's t-test with Welch correction	p=0.3575 (ns)
			CPu, cKO: 35.77 ± 4.684		
Figure 4.25. H	Somatostatin & Vicia villosa agglutinin *cell density* (mean ± SEM)	***Genotype*** (Global)	**12 weeks** **SST+ VVA+** CA3, ctrl: 19.553 ± 3.008	Two-tailed unpaired student's t-test with Welch correction	p=0.0429 (*)
			CA3, cKO: 28.776 ± 2.304		
Figure 4.25. I	Somatostatin & Vicia villosa agglutinin *percentage* (mean ± SEM)	***Genotype*** (Global)	**12 weeks** **SST+ VVA+** CA3, ctrl: 34.88% ± 3.957	Two-tailed unpaired student's t-test with Welch correction	p=0.0431 (*)
			CA3, cKO: 50.98 ± 5.288		
Figure 4.25. J	Somatostatin *developmental trajectory (ctrl)*	***Age*** (Global)	**Striatum** P21, ctrl: 52.970 ± 6.228	Two-way ANOVA with Šídák's multiple comparisons test	p=0.3037 (ns)
			12 wks, ctrl: 43.348 ± 6.152		

	(mean ± SEM)		**CA1** P21, ctrl: 50.542 ± 2.151 12 wks, ctrl: 47.960 ± 2.543	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9110 (ns)
Figure 4.25. K	Somatostatin *developmental trajectory (cKO)* (mean ± SEM)	***Age*** (Global)	**Striatum** P21, cKO: 44.372 ± 6.612 12 wks, cKO: 35.766 ± 4.684	Two-way ANOVA with Šídák's multiple comparisons test	p=0.3807 (ns)
			CA1 P21, cKO: 42.795 ± 1.356 12 wks, cKO: 45.746 ± 4.533	Two-way ANOVA with Šídák's multiple comparisons test	p=0.8860 (ns)
Figure 4.18. B	Neuropeptide-Y *cell density* (mean ± SEM)	***Genotype*** (Local)	**12 weeks** ACA, ctrl: 17.678 ± 2.162 ACA, cKO: 20.815 ± 2.129	Two-way ANOVA with Šídák's multiple comparisons test	p=0.6432 (ns)
			M2, ctrl: 30.855 ± 3.601 M2, cKO: 27.353 ± 2.113	Two-way ANOVA with Šídák's multiple comparisons test	p=0.5794 (ns)
Figure 4.18. C	Neuropeptide-Y *developmental trajectory (ctrl)* (mean ± SEM)	***Age*** (Local)	**ACA** P21, ctrl: 22.051 ± 1.821 12 wks, ctrl: 17.678 ± 2.162	Two-way ANOVA with Šídák's multiple comparisons test	p=0.4989 (ns)
			M2 P21, ctrl: 34.228 ± 2.943 12 wks, ctrl: 30.855 ± 3.601	Two-way ANOVA with Šídák's multiple comparisons test	p=0.6550 (ns)
Figure 4.18. D	Neuropeptide-Y *developmental trajectory (cKO)* (mean ± SEM)	***Age*** (Local)	ACA P21, cKO: 30.570 ± 2.953 12 wks, cKO: 20.815 ± 2.129	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0990 (ns)
			P21, cKO: 48.905 ± 5.507 12 wks, cKO: 27.353 ± 2.113	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0007 (***)
Figure 4.18. F	Neuropeptide-Y *soma morphology* (mean ± SEM)	***Genotype*** (Local)	**12 weeks** **soma area** ACA, ctrl: 54.18 ± 2.711 ACA, cKO: 59.79 ± 2.858	Two-tailed unpaired Mann-Whitney test	p=0.3239 (ns)
			soma perimeter ACA, ctrl: 35.30 ± 0.924 ACA, cKO: 35.93 ± 0.961	Two-tailed unpaired Mann-Whitney test	p=0.8417 (ns)
			soma circularity ACA, ctrl: 0.535 ± 0.0137 ACA, cKO: 0.566 ± 0.0123	Two-tailed unpaired Mann-Whitney test	p=0.0827 (ns)
			soma roundness ACA, ctrl: 0.598 ± 0.0131 ACA, cKO: 0.604 ± 0.0129	Two-tailed unpaired Mann-Whitney test	p=0.8502 (ns)
			soma solidity ACA, ctrl: 0.761 ± 0.0092 ACA, cKO: 0.788 ± 0.0071	Two-tailed unpaired Mann-Whitney test	p=0.0384 (*)
			12 weeks **soma area**	Two-tailed unpaired Mann-Whitney test	p=0.2267 (ns)

Figure 4.18. H	Neuropeptide-Y *soma morphology* (mean ± SEM)	***Genotype*** (Local)	M2, ctrl: 56.94 ± 1.878		
			M2, cKO: 53.57 ± 1.914		
			soma perimeter M2, ctrl: 35.93 ± 0.671	Two-tailed unpaired Mann-Whitney test	p=0.2749 (ns)
			M2, cKO: 35.03 ± 0.796		
			soma circularity M2, ctrl: 0.546 ± 0.0096	Two-tailed unpaired Mann-Whitney test	p=0.5817 (ns)
			M2, cKO: 0.560 ± 0.0113		
			soma roundness M2, ctrl: 0.603 ± 0.0101	Two-tailed unpaired Mann-Whitney test	p=0.9080 (ns)
			M2, cKO: 0.605 ± 0.0103		
			soma solidity M2, ctrl: 0.777 ± 0.0061	Two-tailed unpaired Mann-Whitney test	p=0.9446 (ns)
			M2, cKO: 0.775 ± 0.0066		
Figure 4.19. C	Neuropeptide-Y *cell density* (mean ± SEM)	***Genotype*** (Local)	**12 weeks** M1, ctrl: 87.949 ± 3.060	Two-way ANOVA with Šídák's multiple comparisons test	p=0.5104 (ns)
			M1, cKO: 80.560 ± 4.664		
			S1, ctrl: 86.490 ± 3.800	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9690 (ns)
			S1, cKO: 88.050 ± 7.052		
Figure 4.19. D	Neuropeptide-Y *cell trajectory (ctrl)* (mean ± SEM)	***Age*** (Local)	**M1** P21, ctrl: 101.994 ± 5.262	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0529 (ns)
			12 wks, ctrl: 87.949 ± 3.060		
			S1 P21, ctrl: 94.973 ± 3.857	Two-way ANOVA with Šídák's multiple comparisons test	p=0.2949 (ns)
			12 wks, ctrl: 86.490 ± 3.800		
Figure 4.19 E	Neuropeptide-Y *cell trajectory (cKO)* (mean ± SEM)	***Age*** (Local)	**M1** P21, cKO: 115.869 ± 2.448	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0012 (**)
			12 wks, cKO: 80.560 ± 4.664		
			S1 P21, cKO: 113.042 ± 7.745	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0164 (*)
			12 wks, cKO: 88.050 ± 7.052		
Figure 4.19. F	Neuropeptide-Y *laminar distribution* (mean ± SEM)	***Genotype & Layers*** (Local)	**M1** Layer 1, ctrl: 78.676 ± 7.911	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9995 (ns)
			Layer 1, cKO: 81.669 ± 9.743		
			Layer 2/3, ctrl: 138.565 ± 5.853	Two-way ANOVA with Šídák's multiple comparisons test	p=0.2677 (ns)
			Layer 2/3, cKO: 117.806 ± 7.648		
			Layer 5, ctrl: 67.796 ± 3.968		p>0.9999 (ns)

			Layer 5, cKO: 68.824 ± 3.329	Two-way ANOVA with Šídák's multiple comparisons test	
			Layer 6a, ctrl: 67.450 ± 5.102 Layer 6a, cKO: 59.466 ± 4.904	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9548 (ns)
			Layer 6b, ctrl: 71.844 ± 12.313 Layer 6b, cKO: 54.787 ± 9.910	Two-way ANOVA with Šídák's multiple comparisons test	p=0.4729 (ns)
Figure 4.19. G	Neuropeptide-Y *laminar distribution* (mean ± SEM)	***Genotype & Layers*** (Local)	**S1** Layer 1, ctrl: 78.515 ± 14.782 Layer 1, cKO: 71.623 ± 12.190	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9981 (ns)
			Layer 2/3, ctrl: 169.229 ± 8.764 Layer 2/3, cKO: 145.067 ± 6.203	Two-way ANOVA with Šídák's multiple comparisons test	p=0.5173 (ns)
			Layer 4, ctrl: 57.281 ± 13.089 Layer 4, cKO: 85.240 ± 14.349	Two-way ANOVA with Šídák's multiple comparisons test	p=0.3482 (ns)
			Layer 5, ctrl: 59.907 ± 5.985 Layer 5, cKO: 70.370 ± 8.851	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9823 (ns)
			Layer 6a, ctrl: 60.667 ± 5.345 Layer 6a, cKO: 70.049 ± 8.866	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9899 (ns)
			Layer 6b, ctrl: 81.902 ± 14.402 Layer 6b, cKO: 52.628 ± 8.107	Two-way ANOVA with Šídák's multiple comparisons test	p=0.2977 (ns)
Figure 4.19. J	Neuropeptide-Y *cell trajectory (ctrl)* (mean ± SEM)	***Age & Layers*** (Local)	**M1 ctrl** **Layer 1** P21, ctrl: 74.222 ± 16.589 12 wks, ctrl: 78.676 ± 7.911	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9984 (ns)
			Layer 2/3 P21, ctrl: 158.086 ± 10.538 12 wks, ctrl: 138.565 ± 5.853	Two-way ANOVA with Šídák's multiple comparisons test	p=0.4906 (ns)
			Layer 5 P21, ctrl: 72.715 ± 5.541 12 wks, ctrl: 67.796 ± 3.968	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9974 (ns)
			Layer 6a		p=0.7574

			P21, ctrl: 82.143 ± 6.649 12 wks, ctrl: 67.450 ± 5.102	Two-way ANOVA with Šídák's multiple comparisons test	(ns)
			Layer 6b P21, ctrl: 78.223 ± 5.442 12 wks, ctrl: 71.844 ± 12.313	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9913 (ns)
Figure 4.19. K	Neuropeptide-Y *cell trajectory (ctrl)* (mean ± SEM)	***Age & Layers*** (Local)	**M1 cKO** **Layer 1** P21, cKO: 94.095 ± 5.337 12 wks, cKO: 81.669 ± 9.743	Two-way ANOVA with Šídák's multiple comparisons test	p=0.7582 (ns)
			Layer 2/3 P21, cKO: 178.512 ± 9.205 12 wks, cKO: 117.806 ± 7.648	Two-way ANOVA with Šídák's multiple comparisons test	p<0.0001 (****)
			Layer 5 P21, cKO: 75.500 ± 10.288 12 wks, cKO: 68.824 ± 3.329	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9775 (ns)
			Layer 6a P21, cKO: 99.947 ± 4.714 12 wks, cKO: 59.466 ± 4.904	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0022 (**)
			Layer 6b P21, cKO: 79.748 ± 4.714 12 wks, cKO: 54.787 ± 9.910	Two-way ANOVA with Šídák's multiple comparisons test	p=0.1112 (ns)
Figure 4.19. L	Neuropeptide-Y *cell trajectory (ctrl)* (mean ± SEM)	***Age & Layers*** (Local)	**S1 ctrl** **Layer 1** P21, ctrl: 85.079 ± 10.164 12 wks, ctrl: 78.515 ± 14.782	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9978 (ns)
			Layer 2/3 P21, ctrl: 191.102 ± 8.357 12 wks, ctrl: 169.229 ± 8.764	Two-way ANOVA with Šídák's multiple comparisons test	p=0.5455 (ns)
			Layer 4 P21, ctrl: 67.555 ± 9.251 12 wks, ctrl: 57.281 ± 13.089	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9765 (ns)
			Layer 5 P21, ctrl: 46.186 ± 3.026 12 wks, ctrl: 59.907 ± 5.985	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9094 (ns)
			Layer 6a P21, ctrl: 83.052 ± 4.617 12 wks, ctrl: 60.667 ± 5.345	Two-way ANOVA with Šídák's multiple comparisons test	p=0.5190 (ns)

			Layer 6b P21, ctrl: 44.616 ± 11.748 12 wks, ctrl: 81.902 ± 14.402	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0596 (ns)
Figure 4.19. M	Neuropeptide-Y *cell trajectory (cKO)* (mean ± SEM)	***Age & Layers*** (Local)	**S1 cKO** **Layer 1** P21, cKO: 73.973 ± 11.011 12 wks, cKO: 71.623 ± 12.190	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 2/3 P21, cKO: 220.364 ± 19.531 12 wks, cKO: 145.067 ± 6.203	Two-way ANOVA with Šídák's multiple comparisons test	p<0.0001 (****)
			Layer 4 P21, cKO: 86.005 ± 9.693 12 wks, cKO: 85.240 ± 14.349	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 5 P21, cKO: 72.768 ± 8.739 12 wks, cKO: 70.370 ± 8.851	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 6a P21, cKO: 82.890 ± 7.926 12 wks, cKO: 70.049 ± 8.866	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9524 (ns)
			Layer 6b P21, cKO: 87.777 ± 2.903 12 wks, cKO: 52.628 ± 8.107	Two-way ANOVA with Šídák's multiple comparisons test	p=0.1345 (ns)
Figure 4.20. B	Neuropeptide-Y *soma morphology* (mean ± SEM)	***Genotype*** (Local)	**12 wks** **Soma area** M1, ctrl: 66.57 ± 1.385 M1, cKO: 72.11 ± 1.358	Two-tailed unpaired Mann-Whitney test	p=0.0002 (***)
			Soma perimeter M1, ctrl: 39.51 ± 0.4531 M1, cKO: 39.75 ± 0.4180	Two-tailed unpaired Mann-Whitney test	p=0.1497 (ns)
			Soma circularity M1, ctrl: 0.548 ± 0.0061 M1, cKO: 0.558 ± 0.0065	Two-tailed unpaired Mann-Whitney test	p=0.2626 (ns)
			Soma roundness M1, ctrl: 0.625 ± 0.0066 M1, cKO: 0.645 ± 0.0069	Two-tailed unpaired Mann-Whitney test	p=0.0259 (*)
Figure 4.20. C	Neuropeptide-Y *soma morphology* (mean ± SEM)	***Genotype & Layer*** (Local)	**M1** **Soma area** Layer 1, ctrl: 34.70 ± 2.96 Layer 1, cKO: 52.81 ± 3.21	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p=0.0042 (**)
			Layer 2/3, ctrl: 64.32 ± 1.81	One-way ANOVA Kruskal-Wallis test	p=0.0028 (**)

			Layer 2/3, cKO: 73.38 ± 1.99	with Dunn's multiple comparisons	
			Layer 5, ctrl: 80.43 ± 3.22 Layer 5, cKO: 80.75 ± 3.01	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
			Layer 6a, ctrl: 68.34 ± 3.05 Layer 6a, cKO: 72.11 ± 3.16	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
			Layer 6b, ctrl: 69.45 ± 6.75 Layer 6b, cKO: 70.25 ± 5.64	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
Figure 4.20. C	Neuropeptide-Y *soma morphology* (mean ± SEM)	***Genotype & Layer*** (Local)	**M1** **Perimeter** Layer 1, ctrl: 28.27 ± 1.39 Layer 1, cKO: 34.54 ± 1.19	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p=0.0149 (*)
			Layer 2/3, ctrl: 38.40 ± 0.58 Layer 2/3, cKO: 40.65 ± 0.67	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p=0.0380 (*)
			Layer 5, ctrl: 42.74 ± 1.00 Layer 5, cKO: 40.45 ± 0.81	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
			Layer 6a, ctrl: 42.74 ± 1.00 Layer 6a, cKO: 40.47 ± 0.91	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
			Layer 6b, ctrl: 38.74 ± 2.06 Layer 6b, cKO: 39.29 ± 2.10	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
Figure 4.20. C	Neuropeptide-Y *soma morphology* (mean ± SEM)	***Genotype & Layer*** (Local)	**M1** **Circularity** Layer 1, ctrl: 0.546 ± 0.0212 Layer 1, cKO: 0.547 ± 0.0179	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
			Layer 2/3, ctrl: 0.542 ± 0.0090 Layer 2/3, cKO: 0.560 ± 0.0099	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p=0.9986 (ns)
			Layer 5, ctrl: 0.557 ± 0.0136 Layer 5, cKO: 0.551 ± 0.0136	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
			Layer 6a, ctrl: 0.545 ± 0.0134	One-way ANOVA Kruskal-Wallis test	p>0.9999 (ns)

			Layer 6a, cKO: 0.564 ± 0.0153	with Dunn's multiple comparisons	
			Layer 6b, ctrl: 0.570 ± 0.0244	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
			Layer 6b, cKO: 0.587 ± 0.0343		
Figure 4.20. C	Neuropeptide-Y *soma morphology* (mean ± SEM)	***Genotype & Layer*** (Local)	**M1** **Roundness** Layer 1, ctrl: 0.535 ± 0.0232	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p=0.1117 (ns)
			Layer 1, cKO: 0.608 ± 0.0186		
			Layer 2/3, ctrl: 0.626 ± 0.0098	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p=0.2242 (ns)
			Layer 2/3, cKO: 0.656 ± 0.0102		
			Layer 5, ctrl: 0.647 ± 0.0133	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
			Layer 5, cKO: 0.631 ± 0.0147		
			Layer 6a, ctrl: 0.649 ± 0.0146	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
			Layer 6a, cKO: 0.672 ± 0.0167		
			Layer 6b, ctrl: 0.585 ± 0.0266	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p=0.1369 (ns)
			Layer 6b, cKO: 0.689 ± 0.0297		
Figure 4.20. E	Neuropeptide-Y *soma morphology* (mean ± SEM)	***Genotype*** (Local)	**12 wks** **Soma area** S1, ctrl: 75.32 ± 1.454 S1, cKO: 69.92 ± 1.404	Two-tailed unpaired Mann-Whitney test	p=0.0052 (**)
			Soma perimeter S1, ctrl: 41.05 ± 0.4520	Two-tailed unpaired Mann-Whitney test	p=0.344 (*)
			S1, cKO: 39.71 ± 0.4691		
			Soma circularity S1, ctrl: 0.558 ± 0.0061	Two-tailed unpaired Mann-Whitney test	p=0.7053 (ns)
			S1, cKO: 0.556 ± 0.0063		
			Soma roundness S1, ctrl: 0.640 ± 0.0065	Two-tailed unpaired Mann-Whitney test	p=0.2813 (ns)
			S1, cKO: 0.632 ± 0.0060		
Figure 4.20. F	Neuropeptide-Y *soma morphology* (mean ± SEM)	***Genotype & Layer*** (Local)	**S1** **Soma area** Layer 1, ctrl: 48.7 ± 5.65	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
			Layer 1, cKO: 46.6 ± 3.81		
			Layer 2/3, ctrl: 66.8 ± 1.79	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
			Layer 2/3, cKO: 64.4 ± 2.13		
			Layer 4, ctrl: 85.8 ± 4.12	One-way ANOVA Kruskal-Wallis test	p=0.1221 (ns)
			Layer 4, cKO: 72.9 ± 3.86		

				with Dunn's multiple comparisons	
			Layer 5, ctrl: 93.6 ± 3.74 Layer 5, cKO: 86.7 ± 3.38	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
			Layer 6a, ctrl: 82.2 ± 3.58 Layer 6a, cKO: 67.2 ± 2.89	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p=0.0084 (**)
			Layer 6a, ctrl: 71.3 ± 6.14 Layer 6a, cKO: 83.0 ± 9.03	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
Figure 4.20. F	Neuropeptide-Y *soma morphology* (mean ± SEM)	***Genotype & Layer*** (Local)	**S1** **Perimeter** Layer 1, ctrl: 33.72 ± 2.21 Layer 1, cKO: 32.09 ± 1.42	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
			Layer 2/3, ctrl: 39.70 ± 0.652 Layer 2/3, cKO: 38.42 ± 0.779	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
			Layer 4, ctrl: 42.50 ± 1.104 Layer 4, cKO: 40.37 ± 1.89	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
			Layer 5, ctrl: 44.66 ± 1.040 Layer 5, cKO: 43.37 ± 0.962	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
			Layer 6a, ctrl: 42.73 ± 1.031 Layer 6a, cKO: 39.82 ± 1.082	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p=0.1156 (ns)
			Layer 6b, ctrl: 39.74 ± 2.070 Layer 6b, cKO: 44.47 ± 2.863	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p=0.9534 (ns)
Figure 4.20. F	Neuropeptide-Y *soma morphology* (mean ± SEM)	***Genotype & Layer*** (Local)	**S1** **Circularity** Layer 1, ctrl: 0.533 ± 0.223 Layer 1, cKO: 0.568 ± 0.266	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
			Layer 2/3, ctrl: 0.541 ± 0.0097 Layer 2/3, cKO: 0.553 ± 0.0105	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
			Layer 4, ctrl: 0.602 ± 0.0225	One-way ANOVA Kruskal-Wallis test	p=0.6149 (ns)

			Layer 4, cKO: 0.562 ± 0.0193	with Dunn's multiple comparisons	
			Layer 5, ctrl: 0.580 ± 0.0128	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
			Layer 5, cKO: 0.576 ± 0.0129		
			Layer 6a, ctrl: 0.558 ± 0.0144	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
			Layer 6a, cKO: 0.540 ± 0.0135		
			Layer 6b, ctrl: 0.572 ± 0.0250	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
			Layer 6b, cKO: 0.524 ± 0.0334		
Figure 4.20. F	Neuropeptide-Y *soma morphology* (mean ± SEM)	***Genotype & Layer*** (Local)	**S1** **Roundness** Layer 1, ctrl: 0.631 ± 0.0255	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
			Layer 1, cKO: 0.614 ± 0.0242		
			Layer 2/3, ctrl: 0.638 ± 0.010	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
			Layer 2/3, cKO: 0.629 ± 0.010		
			Layer 4, ctrl: 0.689 ± 0.020	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p=0.5671 (ns)
			Layer 4, cKO: 0.640 ± 0.016		
			Layer 5, ctrl: 0.654 ± 0.016	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
			Layer 5, cKO: 0.667 ± 0.013		
			Layer 6a, ctrl: 0.639 ± 0.014	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
			Layer 6a, cKO: 0.613 ± 0.013		
			Layer 6b, ctrl: 0.565 ± 0.026	One-way ANOVA Kruskal-Wallis test with Dunn's multiple comparisons	p>0.9999 (ns)
			Layer 6b, cKO: 0.570 ± 0.033		
Figure 4.23. C	Neuropeptide-Y *cell density* (mean ± SEM)	***Genotype*** (Local)	12 weeks CPu, ctrl: 39.90 ± 2.56	Two-tailed unpaired student's t-test with Welch correction	p=0.0654 (ns)
			CPu, cKO: 33.39 ± 1.39		
Figure 4.23. C	Neuropeptide-Y *trajectory (ctrl)* (mean ± SEM)	***Age*** (Local)	**CPu** P21, ctrl: 59.24 ± 3.39	Two-tailed unpaired student's t-test with Welch correction	p=0.0023 (**)
			12 wks, ctrl: 39.90 ± 2.56		
Figure 4.23. C	Neuropeptide-Y *trajectory (cKO)*	***Age*** (Local)	**CPu** P21, cKO: 72.38 ± 3.79	Two-tailed unpaired student's t-test with Welch correction	p=0.0002 (***)
			12 wks, ctrl: 33.39 ± 1.39		

	(mean ± SEM)				
Figure 4.23. E	Neuropeptide-Y *soma morphology* (mean ± SEM)	***Genotype*** (Local)	**CPu** **Soma area** CPu, ctrl: 77.37 ± 3.72 CPU, cKO: 74.19 ± 4.20	Two-tailed unpaired Mann-Whitney test	p=0.5445 (ns)
			Soma perimeter CPu, ctrl: 45.93 ± 1.34 CPu, cKO: 42.29 ± 1.30	Two-tailed unpaired Mann-Whitney test	p=0.1727 (ns)
			Soma circularity CPu, ctrl: 0.477 ± 0.0166 CPU, cKO: 0.519 ± 0.170	Two-tailed unpaired Mann-Whitney test	p=0.0809 (ns)
			Soma roundness CPu, ctrl: 0.569 ± 0.0174 CPu, cKO: 0.554 ± 0.0191	Two-tailed unpaired Mann-Whitney test	p=0.6480 (ns)
			Soma solidity CPu, ctrl: 0.746 ± 0.0115 CPu, cKO: 0.764 ± 0.0114	Two-tailed unpaired Mann-Whitney test	p=0.3050 (ns)
Figure 4.24. B	Neuropeptide-Y *cell density* (mean ± SEM)	***Genotype*** (Local)	**12 weeks** CA1, ctrl: 28.038 ± 4.342 CA1, cKO: 26.562 ± 2.893	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9981 (ns)
			CA3, ctrl: 33.664 ± 3.315 CA3, cKO: 33.572 ± 4.100	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			DG, ctrl: 80.056 ± 7.574 DG, cKO: 71.202 ± 11.849	Two-way ANOVA with Šídák's multiple comparisons test	p=0.7263 (ns)
Figure 4.24. D	Neuropeptide-Y *cell trajectory (ctrl)* (mean ± SEM)	***Age*** (Local)	**CA1** P21, ctrl: 37.261 ± 2.502 12 wks, ctrl: 28.038 ± 4.342	Two-way ANOVA with Šídák's multiple comparisons test	p=0.5502 (ns)
			CA3 P21, ctrl: 34.679 ± 3.519 12 wks, ctrl: 33.664 ± 3.315	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9990 (ns)
			DG P21, ctrl: 71.017 ± 7.880 12 wks, ctrl: 80.056 ± 7.574	Two-way ANOVA with Šídák's multiple comparisons test	p=0.5662 (ns)
Figure 4.24. D	Neuropeptide-Y *cell trajectory (cKO)* (mean ± SEM)	***Age*** (Local)	**CA1** P21, cKO: 56.445 ± 5.491 12 wks, cKO: 26.652 ± 2.893	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0147 (*)
			CA3 P21, cKO: 44.271 ± 5.472 12 wks, cKO: 33.572 ± 4.100	Two-way ANOVA with Šídák's multiple comparisons test	p=0.6247 (ns)
			DG P21, cKO: 94.444 ± 7.341 12 wks, cKO: 71.202 ± 11.849	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0706 (ns)

Appendix 3

Chapter 5

Figure	Analysis	Effect	Values	Statistical test	P value
ADULT					
Figure 5.11. B	**Drd1a-Cre** *cell density* (mean ± SEM)	***Genotype***	M1 ctrl: 246.4 ± 14.94	Two-tailed unpaired student's t-test with Welch correction	p=0.5909 (ns)
			M1 cKO: 236.0 ± 10.52		
Figure 5.11. C	**Drd1a-Cre** *cell number* (mean ± SEM)	***Genotype***	M1 ctrl: 122.6 ± 3.787	Two-tailed unpaired student's t-test with Welch correction	p=0.5295 (ns)
			M1 cKO: 117.6 ± 6.350		
Figure 5.11. D	**Drd1a-Cre** *cell density* (mean ± SEM)	***Region***	M1, ctrl: 246.442 ± 14.942	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0007 (***)
			S1 dense, ctrl: 168.150 ± 5.885		
			M1, cKO: 236.005 ± 10.518	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0015 (**)
			S1, cKO: 164.884 ± 11.498		
Figure 5.11. F	**Drd1a-Cre** *laminar distribution* (mean ± SEM)	***Layer***	Layer 1, ctrl: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 1, cKO: 0.00 ± 0.00		
			Layer 2/3, ctrl: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 2/3, cKO: 0.00 ± 0.00		
			Layer 5, ctrl: 1.875 ± 1.188	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 5, cKO: 1.238 ± 1.238		
			Layer 6a, ctrl: 478.840 ± 60.785	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9973 (ns)
			Layer 6a, cKO: 460.994 ± 36.487		
			Layer 6b, ctrl: 1939.812 ± 37.840	Two-way ANOVA with Šídák's multiple comparisons test	p<0.0001 (****)
			Layer 6b, cKO: 1649.568 ± 60.235		
Figure 5.12. C	**Drd1a-Cre** *cell density* (mean ± SEM)	***Genotype***	S1 total, ctrl: 238.0 ± 11.61	Two-tailed unpaired student's t-test with Welch correction	p=0.9350 (ns)
			S1 total, cKO: 239.9 ± 18.88		
Figure 5.12. D	**Drd1a-Cre** *cell number* (mean ± SEM)	***Genotype***	S1 total, ctrl: 121.2 ± 7.155	Two-tailed unpaired student's t-test with Welch correction	p=0.9734 (ns)
			S1 total, cKO: 121.6 ± 9.581		
Figure 5.12. E	**Drd1a-Cre**	***Region***	S1 *dense*, ctrl: 168.150 ± 5.885		p<0.0001 (****)

	cell density (mean ± SEM)		S1 *sparse*, ctrl: 69.877 ± 6.690	Two-way ANOVA with Šídák's multiple comparisons test	p<0.0001 (****)
Figure 5.12. F	**Drd1a-Cre** *cell density* (mean ± SEM)	***Genotype***	S1 *dense*, ctrl: 168.150 ± 5.885 S1 *dense*, cKO: 164.884 ± 11.498	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9532 (ns)
			S1 *sparse*, ctrl: 69.877 ± 6.690 S1 *sparse*, cKO: 75.042 ± 7.657	Two-way ANOVA with Šídák's multiple comparisons test	p=0.8876 (ns)
Figure 5.12. G	**Drd1a-Cre** *cell number* (mean ± SEM)	***Genotype***	S1 *dense*, ctrl: 84.750 ± 3.362 S1 *dense*, cKO: 83.167 ± 5.742	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9602 (ns)
			S1 *sparse*, ctrl: 36.417 ± 3.914 S1 *sparse*, cKO: 38.417 ± 3.933	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9374 (ns)
Figure 5.12. J	**Drd1a-Cre** *laminar distribution* (mean ± SEM)	***Layer***	**S1 *dense*** Layer 1, ctrl: 0.00 ± 0.00 Layer 1, cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 2/3, ctrl: 0.588 ± 0.588 Layer 2/3, cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 4, ctrl: 0.00 ± 0.00 Layer 4, cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 5, ctrl: 2.172 ± 1.360 Layer 5, cKO: 7.589 ± 3.513	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 6a, ctrl: 285.910 ± 25.592 Layer 6a, cKO: 329.405 ± 27.063	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9895 (ns)
			Layer 6b, ctrl: 1580.335 ± 145.506 Layer 6b, cKO: 1191.824 ± 77.380	Two-way ANOVA with Šídák's multiple comparisons test	p<0.0001 (****)
Figure 5.12. K	**Drd1a-Cre** *laminar distribution* (mean ± SEM)	***Layer***	**S1 *sparse*** Layer 1, ctrl: 0.00 ± 0.00 Layer 1, cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 2/3, ctrl: 0.729 ± 0.729 Layer 2/3, cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)

			Layer 4, ctrl: 0.00 ± 0.00 Layer 4, cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 5, ctrl: 1.332 ± 1.332 Layer 5, cKO: 0.747 ± 0.747	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 6a, ctrl: 115.667 ± 14.269 Layer 6a, cKO: 106.218 ± 21.191	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 6b, ctrl: 704.579 ± 45.827 Layer 6b, cKO: 873.054 ± 78.984	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0006 (***)
Figure 5.12. L	**Drd1a-Cre** *laminar distribution* (mean ± SEM)	***Layer + Region***	S1 *dense*, Layer 1, cKO: 0.00 ± 0.00 S1 *sparse*, Layer 1, cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			S1 *dense*, Layer 2/3, cKO: 0.00 ± 0.00 S1 *sparse*, Layer 2/3, cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			S1 *dense*, Layer 4, cKO: 0.00 ± 0.00 S1 *sparse*, Layer 4, cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			S1 *dense*, Layer 5, cKO: 7.589 ± 3.513 S1 *sparse*, Layer 5, cKO: 0.747 ± 0.747	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			S1 *dense*, Layer 6a, cKO: 329.405 ± 27.063 S1 *sparse*, Layer 6a, cKO: 106.218 ± 21.191	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0002 (***)
			S1 *dense*, Layer 6b, cKO: 1191.824 ± 77.380 S1 *sparse*, Layer 6b, cKO: 873.054 ± 78.984	Two-way ANOVA with Šídák's multiple comparisons test	p<0.0001 (****)
Figure 5.12. M	**Drd1a-Cre** *laminar distribution* (mean ± SEM)	***Layer + Region***	S1 *dense*, Layer 1, ctrl: 0.00 ± 0.00 S1 *sparse*, Layer 1, ctrl: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			S1 *dense*, Layer 2/3, ctrl: 0.588 ± 0.588 S1 *sparse*, Layer 2/3, ctrl: 0.729 ± 0.729	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			S1 *dense*, Layer 4, ctrl: 0.00 ± 0.00		p>0.9999 (ns)

			S1 *sparse*, Layer 4, ctrl: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	
			S1 *dense*, Layer 5, ctrl: 2.172 ± 1.360	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			S1 *sparse*, Layer 5, ctrl: 1.332 ± 1.332		
			S1 *dense*, Layer 6a, ctrl: 285.910 ± 25.592	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0637 (ns)
			S1 *sparse*, Layer 6a, ctrl: 115.667 ± 14.269		
			S1 *dense*, Layer 6b, ctrl: 1580.335 ± 145.506	Two-way ANOVA with Šídák's multiple comparisons test	p<0.0001 (****)
			S1 *sparse*, Layer 6b, ctrl: 704.579 ± 45.827		
Parvalbumin					
Figure 5.14. C	**Parvalbumin** *cell density* (mean ± SEM)	***Genotype***	ACA, ctrl: 112.184 ± 6.527	Two-way ANOVA with Šídák's multiple comparisons test	p=0.5870 (ns)
			ACA, cKO: 97.086 ± 14.009		
			M1, ctrl: 177.063 ± 15.911	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9728 (ns)
			M1, cKO: 180.418 ± 2.356		
Figure 5.14. D	***Vicia villosa* agglutinin** *cell density* (mean ± SEM)	***Genotype***	ACA, ctrl: 98.173 ± 4.365	Two-way ANOVA with Šídák's multiple comparisons test	p=0.8798 (ns)
			ACA, cKO: 91.559 ± 4.651		
			M1, ctrl: 185.017 ± 10.678	Two-way ANOVA with Šídák's multiple comparisons test	p=0.3979 (ns)
			M1, cKO: 203.424 ± 16.048		
Figure 5.14. E	**Parvalbumin ‘subtypes’** *cell density* (mean ± SEM)	***Genotype + Cell type***	**ACA** PV+ VVA+, ctrl: 64.417 ± 1.782	Two-way ANOVA with Šídák's multiple comparisons test	p=0.7799 (ns)
			PV+ VVA+, cKO: 55.087 ± 8.594		
			PV+ VVA-, ctrl: 48.284 ± 9.134	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9180 (ns)
			PV+ VVA-, cKO: 41.999 ± 5.445		
			PV- VVA+, ctrl: 33.164 ± 7.571	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9864 (ns)
			PV- VVA+, cKO: 36.472 ± 9.917		
Figure 5.14. F	**Parvalbumin ‘subtypes’** *cell density* (mean ± SEM)	***Genotype + Cell type***	**M1** PV+ VVA+, ctrl: 80.605 ± 9.285	Two-way ANOVA with Šídák's multiple comparisons test	p=0.5292 (ns)
			PV+ VVA+, cKO: 95.056 ± 7.066		

			PV+ VVA-, ctrl: 95.968 ± 7.128 PV+ VVA-, cKO: 85.199 ± 5.190	Two-way ANOVA with Šídák's multiple comparisons test	p=0.7358 (ns)
			PV- VVA+, ctrl: 104.586 ± 4.871 PV- VVA+, cKO: 108.368 ± 12.408	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9833 (ns)
Figure 5.14. H	**Parvalbumin** *soma morphology* (mean ± SEM)	***Genotype***	**soma area** M1, ctrl: 101.3 ± 1.379 M1, cKO: 104.6 ± 1.345	unpaired two-tailed Mann-Whitney t-test	p=0.0302 (*)
			soma perimeter M1, ctrl: 43.25 ± 0.439 M1, cKO: 43.64 ± 0.440	unpaired two-tailed Mann-Whitney t-test	p=0.2040 (ns)
			soma circularity M1, ctrl: 0.7089 ± 0.0054 M1, cKO: 0.7209 ± 0.0053	unpaired two-tailed Mann-Whitney t-test	p=0.0719 (ns)
			soma roundness M1, ctrl: 0.6957 ± 0.0048 M1, cKO: 0.7027 ± 0.0047	unpaired two-tailed Mann-Whitney t-test	p=0.2477 (ns)
			soma solidity M1, ctrl: 0.8738 ± 0.0029 M1, cKO: 0.8798 ± 0.0028	unpaired two-tailed Mann-Whitney t-test	p=0.0939 (ns)
Figure 5.15. B	**Parvalbumin** *laminar distribution* (mean ± SEM)	***Layer***	**M1** Layer 1, ctrl: 3.335 ± 3.335 Layer 1, cKO: 1.622 ± 1.622	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 2/3, ctrl: 215.424 ± 21.152 Layer 2/3, cKO: 226.351 ± 8.236	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9856 (ns)
			Layer 5, ctrl: 221.817 ± 18.701 Layer 5, cKO: 250.724 ± 13.566	Two-way ANOVA with Šídák's multiple comparisons test	p=0.5313 (ns)
			Layer 6a, ctrl: 181.517 ± 19.233 Layer 6a, cKO: 166.393 ± 13.471	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9423 (ns)
			Layer 6b, ctrl: 37.951 ± 12.617 Layer 6b, cKO: 26.700 ± 7.121	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9836 (ns)
Figure 5.15. C	**PV+ VVA-**	***Layer***	**M1** Layer 1, ctrl: 0.00 ± 0.00 Layer 1, cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)

	laminar distribution (mean ± SEM)		Layer 2/3, ctrl: 76.444 ± 12.004	Two-way ANOVA with Šídák's multiple comparisons test	p=0.1273 (ns)
			Layer 2/3, cKO: 110.264 ± 14.338		
			Layer 5, ctrl: 151.535 ± 14.810	Two-way ANOVA with Šídák's multiple comparisons test	p=0.2587 (ns)
			Layer 5, cKO: 122.911 ± 10.770		
			Layer 6a, ctrl: 82.256 ± 4.590	Two-way ANOVA with Šídák's multiple comparisons test	p=0.6848 (ns)
			Layer 6a, cKO: 101.029 ± 8.875		
			Layer 6b, ctrl: 26.700 ± 7.121	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9860 (ns)
			Layer 6b, cKO: 34.959 ± 14.381		
Figure 5.15. D	**PV+ VVA+** *laminar distribution* (mean ± SEM)	***Layer***	**M1** Layer 1, ctrl: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 1, cKO: 0.00 ± 0.00		
			Layer 2/3, ctrl: 105.159 ± 10.819	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0027 (**)
			Layer 2/3, cKO: 149.907 ± 10.422		
			Layer 5, ctrl: 98.906 ± 13.009	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 5, cKO: 99.189 ± 5.976		
			Layer 6a, ctrl: 80.487 ± 10.999	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9991 (ns)
			Layer 6a, cKO: 84.136 ± 10.816		
			Layer 6b, ctrl: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 6b, cKO: 0.00 ± 0.00		
Figure 5.15. E	***Vicia villosa* agglutinin** *laminar distribution* (mean ± SEM)	***Layer***	**M1** Layer 1, ctrl: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 1, cKO: 0.00 ± 0.00		
			Layer 2/3, ctrl: 262.451 ± 16.019	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0361 (*)
			Layer 2/3, cKO: 311.440 ± 19.443		
			Layer 5, ctrl: 225.687 ± 9.201	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9339 (ns)
			Layer 5, cKO: 239.635 ± 19.848		
			Layer 6a, ctrl: 162.733 ± 9.634	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9998 (ns)
			Layer 6a, cKO: 166.818 ± 15.594		
			Layer 6b, ctrl: 0.00 ± 0.00		p>0.9999

			Layer 6b, cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	(ns)
Figure 5.15. F	**PV- VVA+** *laminar distribution* (mean ± SEM)	***Layer***	**M1** Layer 1, ctrl: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 1, cKO: 0.00 ± 0.00		
			Layer 2/3, ctrl: 157.831 ± 7.929	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9996 (ns)
			Layer 2/3, cKO: 161.533 ± 11.357		
			Layer 5, ctrl: 126.781 ± 7.386	Two-way ANOVA with Šídák's multiple comparisons test	p=0.8732 (ns)
			Layer 5, cKO: 140.446 ± 23.677		
			Layer 6a, ctrl: 82.245 ± 7.822	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 6a, cKO: 82.681 ± 10.861		
			Layer 6b, ctrl: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 6b, cKO: 0.00 ± 0.00		
Figure 5.16. C	**Parvalbumin** *cell density* (mean ± SEM)	***Genotype***	S1 dense, ctrl: 191.3 ± 15.43	Two-tailed unpaired student's t-test with Welch correction	p=0.5227 (ns)
			S1 dense, cKO: 202.6 ± 3.822		
Figure 5.16. D	***Vicia villosa*** agglutinin *cell density* (mean ± SEM)	***Genotype***	S1 dense, ctrl: 220.7 ± 2.528	Two-tailed unpaired student's t-test with Welch correction	p=0.2862 (ns)
			S1 dense, cKO: 212.0 ± 6.609		
Figure 5.16. E	**Parvalbumin 'subtypes'** *cell density* (mean ± SEM)	***Genotype***	**PV+ VVA+** S1 dense, ctrl: 96.165 ± 6.728	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9980 (ns)
			S1 dense, cKO: 97.838 ± 4.633		
			PV+ VVA- S1 dense, ctrl: 95.143 ± 8.734	Two-way ANOVA with Šídák's multiple comparisons test	p=0.7472 (ns)
			S1 dense, cKO: 104.783 ± 6.323		
			PV- VVA+ S1 dense, ctrl: 124.576 ± 4.715	Two-way ANOVA with Šídák's multiple comparisons test	p=0.7006 (ns)
			S1 dense, cKO: 114.153 ± 11.101		
Figure 5.16. F	**Parvalbumin** *laminar distribution* (mean ± SEM)	***Layer***	**S1 *dense*** **PV+** Layer 1, ctrl: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 1, cKO: 0.00 ± 0.00		
			Layer 2/3, ctrl: 184.237± 11.856		p=0.9795 (ns)

			Layer 2/3, cKO: 167.280 ± 6.744	Two-way ANOVA with Šídák's multiple comparisons test	
			Layer 4, ctrl: 326.756 ± 32.507	Two-way ANOVA with Šídák's multiple comparisons test	p=0.5180 (ns)
			Layer 4, cKO: 364.897 ± 22.198		
			Layer 5, ctrl: 279.410 ± 27.164	Two-way ANOVA with Šídák's multiple comparisons test	p=0.5800 (ns)
			Layer 5, cKO: 315.497 ± 14.954		
			Layer 6a, ctrl: 162.491 ± 19.061	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9856 (ns)
			Layer 6a, cKO: 178.305 ± 7.987		
			Layer 6b, ctrl: 28.417 ± 14.079	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9996 (ns)
			Layer 6b, cKO: 20.230 ± 3.616		
Figure 5.16. G	**PV+ VVA-** *laminar distribution* (mean ± SEM)	***Layer***	**S1 *dense* PV+ VVA-** Layer 1, ctrl: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 1, cKO: 0.00 ± 0.00		
			Layer 2/3, ctrl: 110.424 ± 8.859	Two-way ANOVA with Šídák's multiple comparisons test	p=0.8138 (ns)
			Layer 2/3, cKO: 91.266 ± 8.573		
			Layer 4, ctrl: 68.136 ± 12.280	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9027 (ns)
			Layer 4, cKO: 84.393 ± 21.626		
			Layer 5, ctrl: 153.585 ± 12.292	Two-way ANOVA with Šídák's multiple comparisons test	p=0.4815 (ns)
			Layer 5, cKO: 180.606 ± 18.902		
			Layer 6a, ctrl: 89.025 ± 11.849	Two-way ANOVA with Šídák's multiple comparisons test	p=0.6605 (ns)
			Layer 6a, cKO: 111.977 ± 4.492		
			Layer 6b, ctrl: 17.587 ± 10.376	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 6b, cKO: 17.527 ± 4.707		
Figure 5.16. H	**PV+ VVA+** *laminar distribution* (mean ± SEM)	***Layer***	**S1 *dense* PV+ VVA+** Layer 1, ctrl: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 1, cKO: 0.00 ± 0.00		
			Layer 2/3, ctrl: 73.814 ± 3.763		p>0.9999 (ns)

			Layer 2/3, cKO: 76.013 ± 7.544	Two-way ANOVA with Šídák's multiple comparisons test	
			Layer 4, ctrl: 258.629 ± 26.959	Two-way ANOVA with Šídák's multiple comparisons test	p=0.4577 (ns)
			Layer 4, cKO: 285.542 ± 7.661		
			Layer 5, ctrl: 125.825 ± 17.992	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9936 (ns)
			Layer 5, cKO: 134.891 ± 12.020		
			Layer 6a, ctrl: 73.466 ± 7.469	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9983 (ns)
			Layer 6a, cKO: 66.328 ± 7.362		
			Layer 6b, ctrl: 10.830 ± 7.376	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9965 (ns)
			Layer 6b, cKO: 2.703 ± 2.703		
Figure 5.16. I	**VVA+** *laminar distribution* (mean ± SEM)	***Layer***	**S1 *dense*** **VVA+** Layer 1, ctrl: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 1, cKO: 0.00 ± 0.00		
			Layer 2/3, ctrl: 173.445 ± 6.323	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9986 (ns)
			Layer 2/3, cKO: 182.263 ± 7.911		
			Layer 4, ctrl: 568.228 ± 33.806	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 4, cKO: 569.856 ± 19.972		
			Layer 5, ctrl: 311.225 ± 19.908	Two-way ANOVA with Šídák's multiple comparisons test	p=0.2880 (ns)
			Layer 5, cKO: 271.164 ± 11.042		
			Layer 6a, ctrl: 160.285 ± 7.151	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 6a, cKO: 159.674 ± 9.367		
			Layer 6b, ctrl: 10.830 ± 7.376	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 6b, cKO: 6.416 ± 6.416		
Figure 5.16. J	**PV- VVA+** *laminar distribution* (mean ± SEM)	***Layer***	**S1 *dense*** **PV- VVA+** Layer 1, ctrl: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 1, cKO: 0.00 ± 0.00		
			Layer 2/3, ctrl: 99.631 ± 6.552		p=0.9992 (ns)

			Layer 2/3, cKO: 106.249 ± 13.863	Two-way ANOVA with Šídák's multiple comparisons test	
			Layer 4, ctrl: 309.599 ± 22.306	Two-way ANOVA with Šídák's multiple comparisons test	p=0.8071 (ns)
			Layer 4, cKO: 289.352 ± 19.501		
			Layer 5, ctrl: 185.401 ± 6.251	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0374 (*)
			Layer 5, cKO: 136.272 ± 20.760		
			Layer 6a, ctrl: 86.818 ± 9.332	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9993 (ns)
			Layer 6a, cKO: 93.346 ± 6.892		
			Layer 6b, ctrl: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 6b, cKO: 2.109 ± 2.109		
Figure 5.17. B	**Parvalbumin** *soma morphology* (mean ± SEM)	***Genotype***	**soma area** S1 dense, ctrl: 109.4 ± 1.614	unpaired two-tailed Mann-Whitney t-test	p=0.0654 (ns)
			S1 dense, cKO: 111.9 ± 1.488		
			soma perimeter S1 dense, ctrl: 47.47 ± 0.543	unpaired two-tailed Mann-Whitney t-test	p=0.7945 (ns)
			S1 dense, cKO: 47.18 ± 0.496		
			soma circularity S1 dense, ctrl: 0.6607 ± 0.0058	unpaired two-tailed Mann-Whitney t-test	p=0.2658 (ns)
			S1 dense, cKO: 0.6715 ± 0.0055		
			soma roundness S1 dense, ctrl: 0.6653 ± 0.0048	unpaired two-tailed Mann-Whitney t-test	p=0.5595 (ns)
			S1 dense, cKO: 0.6707 ± 0.0045		
			soma solidity S1 dense, ctrl: 0.8517 ± 0.0032	unpaired two-tailed Mann-Whitney t-test	p=0.1567 (ns)
			S1 dense, cKO: 0.8589 ± 0.0030		
Figure 5.18. C	**Parvalbumin** *cell density* (mean ± SEM)	***Genotype***	S1 sparse, ctrl: 179.4 ± 18.04	Two-tailed unpaired student's t-test with Welch correction	p=0.4113 (ns)
			S1 sparse, cKO: 199.0 ± 12.49		
Figure 5.18. D	***Vicia villosa*** agglutinin	***Genotype***	S1 sparse, ctrl: 252.7 ± 19.93		p=0.7874 (ns)

	cell density (mean ± SEM)		S1 sparse, cKO: 258.8 ± 7.184	Two-tailed unpaired student’s t-test with Welch correction	
Figure 5.18. E	**Parvalbumin ‘subtypes’** *cell density* (mean ± SEM)	***Genotype + Cell type***	**PV+ VVA+** S1 sparse, ctrl: 80.605 ± 9.285	Two-way ANOVA with Šídák's multiple comparisons test	p=0.5566 (ns)
			S1 sparse, cKO: 95.056 ± 7.066		
			PV+ VVA- S1 sparse, ctrl: 52.674 ± 8.713	Two-way ANOVA with Šídák's multiple comparisons test	p=0.6388 (ns)
			S1 sparse, cKO: 65.624 ± 5.452		
			PV- VVA+ S1 sparse, ctrl: 104.586 ± 4.871	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9849 (ns)
			S1 sparse, cKO: 108.368 ± 12.408		
Figure 5.18. F	**Parvalbumin** *laminar distribution* (mean ± SEM)	***Layer***	**S1 *sparse*** **PV+** Layer 1, ctrl: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 1, cKO: 2.620 ± 2.620		
			Layer 2/3, ctrl: 142.545 ± 15.165	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9989 (ns)
			Layer 2/3, cKO: 152.832 ± 11.105		
			Layer 4, ctrl: 294.627 ± 36.202	Two-way ANOVA with Šídák's multiple comparisons test	p=0.3583 (ns)
			Layer 4, cKO: 340.133 ± 18.645		
			Layer 5, ctrl: 286.548 ± 26.249	Two-way ANOVA with Šídák's multiple comparisons test	p=0.3598 (ns)
			Layer 5, cKO: 331.995 ± 20.034		
			Layer 6a, ctrl: 140.358 ± 15.775	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9997 (ns)
			Layer 6a, cKO: 148.262 ± 13.283		
			Layer 6b, ctrl: 12.646 ± 7.353	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 6b, cKO: 14.656 ± 2.945		
Figure 5.18. G	**PV+ VVA-** *laminar distribution* (mean ± SEM)	***Layer***	**S1 *sparse*** **PV+ VVA-** Layer 1, ctrl: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 1, cKO: 0.00 ± 0.00		
			Layer 2/3, ctrl: 53.060 ± 39.633		p=0.8963 (ns)

			Layer 2/3, cKO: 39.633 ± 2.845	Two-way ANOVA with Šídák's multiple comparisons test	
			Layer 4, ctrl: 13.955 ± 5.844	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9992 (ns)
			Layer 4, cKO: 19.128 ± 3.770		
			Layer 5, ctrl: 99.227 ± 20.255	Two-way ANOVA with Šídák's multiple comparisons test	p<0.0001 (****)
			Layer 5, cKO: 166.591 ± 19.778		
			Layer 6a, ctrl: 57.667 ± 6.453	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9999 (ns)
			Layer 6a, cKO: 54.011 ± 7.306		
			Layer 6b, ctrl: 4.570 ± 4.570	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9719 (ns)
			Layer 6b, cKO: 14.656 ± 2.945		
Figure 5.18. H	**PV+ VVA+** *laminar distribution* (mean ± SEM)	***Layer***	**S1 *sparse*** **PV+ VVA+** Layer 1, ctrl: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 1, cKO: 0.00 ± 0.00		
			Layer 2/3, ctrl: 89.485 ± 8.972	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 2/3, cKO: 88.199 ± 30.835		
			Layer 4, ctrl: 280.672 ± 35.998	Two-way ANOVA with Šídák's multiple comparisons test	p=0.4846 (ns)
			Layer 4, cKO: 321.005 ± 19.937		
			Layer 5, ctrl: 187.322 ± 19.386	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9999 (ns)
			Layer 5, cKO: 180.647 ± 14.911		
			Layer 6a, ctrl: 82.691 ± 11.985	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9997 (ns)
			Layer 6a, cKO: 94.251 ± 7.358		
			Layer 6b, ctrl: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 6b, cKO: 0.00 ± 0.00		
Figure 5.18. I	***Vicia villosa*** agglutinin *laminar distribution* (mean ± SEM)	***Layer***	**S1 *sparse*** **VVA+** Layer 1, ctrl: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 1, cKO: 0.00 ± 0.00		
			Layer 2/3, ctrl: 197.322 ± 16.983	Two-way ANOVA with Šídák's multiple comparisons test	p=0.6138 (ns)
			Layer 2/3, cKO: 241.126 ± 23.796		

			Layer 4, ctrl: 486.092 ± 35.002 Layer 4, cKO: 515.010 ± 14.390	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9127 (ns)
			Layer 5, ctrl: 376.004 ± 25.554 Layer 5, cKO: 320.825 ± 42.499	Two-way ANOVA with Šídák's multiple comparisons test	p=0.3522 (ns)
			Layer 6a, ctrl: 188.385 ± 19.961 Layer 6a, cKO: 184.323 ± 9.368	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 6b, ctrl: 0.00 ± 0.00 Layer 6b, cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
Figure 5.18. J	**PV- VVA+** *laminar distribution* (mean ± SEM)	***Layer***	**S1 *sparse* PV- VVA+** Layer 1, ctrl: 0.00 ± 0.00 Layer 1, cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 2/3, ctrl: 107.837 ± 11.525 Layer 2/3, cKO: 127.927 ± 11.480	Two-way ANOVA with Šídák's multiple comparisons test	p=0.7547 (ns)
			Layer 4, ctrl: 199.291 ± 7.448 Layer 4, cKO: 194.005 ± 12.630	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9997 (ns)
			Layer 5, ctrl: 186.436 ± 20.536 Layer 5, cKO: 176.513 ± 17.721	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9894 (ns)
			Layer 6a, ctrl: 105.694 ± 8.807 Layer 6a, cKO: 96.391 ± 13.623	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9925 (ns)
			Layer 6b, ctrl: 0.00 ± 0.00 Layer 6b, cKO: 0.00 ± 0.00	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
Figure 5.19. C	**Parvalbumin** *cell density* (mean ± SEM)	***Genotype***	CPu, ctrl: 93.43 ± 12.56 CPu, cKO: 81.58 ± 3.109	Two-tailed unpaired student's t-test with Welch correction	p=0.4205 (ns)
Figure 5.19. D	**Parvalbumin** *soma morphology* (mean ± SEM)	***Genotype***	**soma area** CPu, ctrl: 97.15 ± 2.620 CPu, cKO: 94.73 ± 2.796	unpaired two-tailed Mann-Whitney t-test	p=0.5543 (ns)
			soma perimeter CPu, ctrl: 46.20 ± 1.280 CPu, cKO: 41.47 ± 0.825	unpaired two-tailed Mann-Whitney t-test	p=0.0427 (*)
			soma circularity CPu, ctrl: 0.640 ± 0.0147 CPu, cKO: 0.701 ± 0.0115	unpaired two-tailed Mann-Whitney t-test	p=0.0171 (*)

			soma roundness CPu, ctrl: 0.626 ± 0.011 CPu, cKO: 0.661 ± 0.010	unpaired two-tailed Mann-Whitney t-test	p=0.0224 (*)
Figure 5.19. G	**Parvalbumin** *cell density* (mean ± SEM)	***Genotype***	GPe, ctrl: 301.8 ± 29.09 GPe, cKO: 391.9 ± 9.760	unpaired two-tailed t-test with Welch's correction	p=0.0474 (*)
Figure 5.19. G	**Parvalbumin** *cell density* (mean ± SEM)	***Genotype***	TRN, ctrl: 609.4 ± 28.88 TRN, cKO: 599.6 ± 33.00	unpaired two-tailed t-test with Welch's correction	p=0.8306 (ns)

Figure	Analysis	Effect	Values	Statistical test	P value
NEUROPEPTIDE-Y					
Figure 5.20. C	**Neuropeptide-Y** *cell density* (mean ± SEM)	*Genotype*	ACA, ctrl: 34.626 ± 3.058 ACA, cKO: 36.449 ± 2.229	Two-way ANOVA with Šídák's multiple comparisons test	p=0.8900 (ns)
			M2, ctrl: 53.821 ± 3.637 M2, cKO: 46.866 ± 2.630	Two-way ANOVA with Šídák's multiple comparisons test	p=0.2251 (ns)
Figure 5.20. D	**Neuropeptide-Y** *soma morphology* (mean ± SEM)	***Genotype***	**soma area** ACA, ctrl: 52.14 ± 2.012 ACA, cKO: 54.20 ± 2.132	unpaired two-tailed Mann-Whitney test	p=0.6667 (ns)
			soma perimeter ACA, ctrl: 31.73 ± 0.666 ACA, cKO: 32.04 ± 0.654	unpaired two-tailed Mann-Whitney test	p=0.6000 (ns)
			soma circularity ACA, ctrl: 0.619 ± 0.0097 ACA, cKO: 0.620 ± 0.0103	unpaired two-tailed Mann-Whitney test	p=0.8529 (ns)
			soma roundness ACA, ctrl: 0.600 ± 0.0095 ACA, cKO: 0.616 ± 0.0094	unpaired two-tailed Mann-Whitney test	p=0.2507 (ns)
Figure 5.20. E	**Neuropeptide-Y** *soma morphology* (mean ± SEM)	***Genotype***	**soma area** M2, ctrl: 50.00 ± 1.790 M2, cKO: 56.19 ± 2.125	unpaired two-tailed Mann-Whitney test	p=0.0353 (*)
			soma perimeter M2, ctrl: 31.28 ± 0.636 M2, cKO: 32.26 ± 0.699	unpaired two-tailed Mann-Whitney test	p=0.1585 (ns)
			soma circularity M2, ctrl: 0.615 ± 0.0094 M2, cKO: 0.638 ± 0.0106	unpaired two-tailed Mann-Whitney test	p=0.0817 (ns)
			soma roundness M2, ctrl: 0.607 ± 0.0093 M2, cKO: 0.615 ± 0.0107	unpaired two-tailed Mann-Whitney test	p=0.4505 (ns)
			soma solidity M2, ctrl: 0.808 ± 0.0056 M2, cKO: 0.821 ± 0.0062	unpaired two-tailed Mann-Whitney test	p=0.0400 (*)
Figure 5.21. C	**Neuropeptide-Y** *cell density* (mean ± SEM)	***Genotype***	M1, ctrl: 104.789 ± 8.875 M1, cKO: 95.217 ± 6.587	Two-way ANOVA with Šídák's multiple comparisons test	p=0.5606 (ns)
			S1, ctrl: 118.426 ± 6.728 S1, cKO: 105.307 ± 3.982	Two-way ANOVA with Šídák's multiple comparisons test	p=0.3530 (ns)
Figure 5.21. D	**Neuropeptide-Y** *laminar distribution* (mean ± SEM)	***Layer***	**M1** Layer 1, ctrl: 69.680 ± 5.455 Layer 1, cKO: 82.550 ± 10.791	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9687 (ns)
			Layer 2/3, ctrl: 157.394 15.416	Two-way ANOVA with Šídák's	p=0.9977 (ns)

			Layer 2/3, cKO: 150.117 ± 7.237	multiple comparisons test	
			Layer 5, ctrl: 81.194 7.876	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9814 (ns)
			Layer 5, cKO: 69.773 ± 8.039		
			Layer 6a, ctrl: 79.521 ± 11.707	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 6a, cKO: 77.096 ± 7.710		
			Layer 6b, ctrl: 102.547 ± 31.617	Two-way ANOVA with Šídák's multiple comparisons test	p=0.3564 (ns)
			Layer 6b, cKO: 68.901 ± 4.162		
Figure 5.21. E	**Neuropeptide-Y** *laminar distribution* (mean ± SEM)	***Layer***	**S1** Layer 1, ctrl: 92.920 ± 6.116	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9999 (ns)
			Layer 1, cKO: 98.093 ± 12.658		
			Layer 2/3, ctrl: 181.503 17.943	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9946 (ns)
			Layer 2/3, cKO: 171.284 ± 11.566		
			Layer 4, ctrl: 111.639 ± 8.085	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 4, cKO: 113.998 ± 12.874		
			Layer 5, ctrl: 87.680 ± 8.805	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 5, cKO: 87.079 ± 11.404		
			Layer 6a, ctrl: 103.815 ± 10.983	Two-way ANOVA with Šídák's multiple comparisons test	p=0.5188 (ns)
			Layer 6a, cKO: 74.194 ± 6.082		
			Layer 6b, ctrl: 92.582 ± 25.588	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9093 (ns)
			Layer 6b, cKO: 74.471 ± 10.539		
Figure 5.21. F	**Neuropeptide-Y** *soma morphology* (mean ± SEM)	***Genotype***	**soma area** M1, ctrl: 73.97 ± 1.468	unpaired two-tailed Mann-Whitney test	p=0.0105 (*)
			M1, cKO: 78.66 ± 1.560		
			soma perimeter M1, ctrl: 38.60 ± 0.446	unpaired two-tailed Mann-Whitney test	p=0.1200 (ns)
			M1, cKO: 39.33 ± 0.460		
			soma circularity M1, ctrl: 0.618 ± 0.0065	unpaired two-tailed Mann-Whitney test	p=0.1686 (ns)
			M1, cKO: 0.630 ± 0.0069		
			soma roundness M1, ctrl: 0.641 ± 0.0062	unpaired two-tailed Mann-Whitney test	p=0.0818 (ns)
			M1, cKO: 0.657 ± 0.0068		
			soma solidity M1, ctrl: 0.825 ± 0.0037	unpaired two-tailed Mann-Whitney test	p=0.1010 (ns)

			M1, cKO: 0.831 ± 0.0040		
Figure 5.21. G	**Neuropeptide-Y** *soma morphology* (mean ± SEM)	***Genotype***	**soma area** S1, ctrl: 71.38 ± 1.334	unpaired two-tailed Mann-Whitney test	p<0.0001 (****)
			S1, cKO: 81.91 ± 1.620		
			soma perimeter S1, ctrl: 37.46 ± 0.428	unpaired two-tailed Mann-Whitney test	p=0.0001 (***)
			S1, cKO: 39.75 ± 0.438		
			soma circularity S1, ctrl: 0.628 ± 0.0060	unpaired two-tailed Mann-Whitney test	p=0.3931 (ns)
			S1, cKO: 0.634 ± 0.0067		
			soma roundness S1, ctrl: 0.640 ± 0.0056	unpaired two-tailed Mann-Whitney test	p=0.0239 (*)
			S1, cKO: 0.659 ± 0.0064		
			soma roundness S1, ctrl: 0.825 ± 0.0036	unpaired two-tailed Mann-Whitney test	p=0.1740 (ns)
			S1, cKO: 0.831 ± 0.0039		
			L6b, cKO: 91.87 ± 9.212		
			L6b, cKO: 44.24 ± 2.804		
			L6b, cKO: 0.8153 ± 0.0161		
Figure 5.22. B	**Neuropeptide-Y** *soma morphology* (mean ± SEM)	***Layer***	**S1** **soma area** L1, ctrl: 38.19 ± 3.185	Kruskal-Wallis test with Dunn's multiple comparisons test	p=0.1745 (ns)
			L1, cKO: 54.36 ± 5.269		
			L2/3, ctrl: 71.98 ± 2.289	Kruskal-Wallis test with Dunn's multiple comparisons test	p=0.0005 (***)
			L2/3, cKO: 84.98 ± 2.466		
			L4, ctrl: 67.08 ± 3.401	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
			L4, cKO: 74.01 ± 4.019		
			L5, ctrl: 86.99 ± 3.278	Kruskal-Wallis test with Dunn's multiple comparisons test	p=0.6712 (ns)
			L5, cKO: 97.18 ± 3.876		
			L6a, ctrl: 67.81 ± 2.404	Kruskal-Wallis test with Dunn's multiple comparisons test	p=0.2256 (ns)
			L6a, cKO: 76.58 ± 3.546		
			L6b, ctrl: 79.93 ± 6.570	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
			L6b, cKO: 72.93 ± 7.614		
Figure 5.22. B	**Neuropeptide-Y** *soma morphology* (mean ± SEM)	***Layer***	**S1** **soma perimeter** L1, ctrl: 27.37 ± 1.256	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
			L1, cKO: 30.36 ± 1.422		
			L2/3, ctrl: 37.85 ± 0.806	Kruskal-Wallis test with Dunn's multiple comparisons test	p=0.0253 (*)
			L2/3, cKO: 40.87 ± 0.852		
			L4, ctrl: 36.86 ± 1.010	Kruskal-Wallis test with Dunn's	p>0.9999 (ns)
			L4, cKO: 37.49 ± 1.006		

				multiple comparisons test	
			L5, ctrl: 41.63 ± 0.9444	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
			L5, cKO: 44.52 ± 1.226		
			L6a, ctrl: 36.24 ± 0.738	Kruskal-Wallis test with Dunn's multiple comparisons test	p=0.0431 (*)
			L6a, cKO: 39.28 ± 1.042		
			L6b, ctrl: 40.20 ± 2.149	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
			L6b, cKO: 38.41 ± 2.053		
Figure 5.22. B	**Neuropeptide-Y** *soma morphology* (mean ± SEM)	***Layer***	**S1** **soma circularity** L1, ctrl: 0.6299 ± 0.0271	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
			L1, cKO: 0.6517 ± 0.0283		
			L2/3, ctrl: 0.6314 ± 0.0105	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
			L2/3, cKO: 0.6520 ± 0.0116		
			L4, ctrl: 0.6109 ± 0.0198	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
			L4, cKO: 0.6312 ± 0.0193		
			L5, ctrl: 0.6243 ± 0.0129	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
			L5, cKO: 0.6193 ± 0.0136		
			L6a, ctrl: 0.6397 ± 0.0113	Kruskal-Wallis test with Dunn's multiple comparisons test	p=0.9994 (ns)
			L6a, cKO: 0.6106 ± 0.0147		
			L6b, ctrl: 0.5885 ± 0.0241	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
			L6b, cKO: 0.6454 ± 0.0254		
Figure 5.22. B	**Neuropeptide-Y** *soma morphology* (mean ± SEM)	***Layer***	**S1** **soma roundness** L1, ctrl: 0.6294 ± 0.0255	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
			L1, cKO: 0.6477 ± 0.0217		
			L2/3, ctrl: 0.6486 ± 0.0093	Kruskal-Wallis test with Dunn's multiple comparisons test	p=0079 (**)
			L2/3, cKO: 0.6948 ± 0.0103		
			L4, ctrl: 0.6690 ± 0.0156	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
			L4, cKO: 0.6624 ± 0.0174		
			L5, ctrl: 0.6377 ± 0.0129	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
			L5, cKO: 0.6412 ± 0.0142		
			L6a, ctrl: 0.6283 ± 0.0111		p>0.9999

			L6a, cKO: 0.6227 ± 0.0152	Kruskal-Wallis test with Dunn’s multiple comparisons test	(ns)
			L6b, ctrl: 0.5864 ± 0.0260 L6b, cKO: 0.6312 ± 0.0315	Kruskal-Wallis test with Dunn’s multiple comparisons test	p>0.9999 (ns)
Figure 5.22. B	**Neuropeptide-Y** *soma morphology* (mean ± SEM)	***Layer***	**S1** **soma solidity** L1, ctrl: 0.7929 ± 0.0179 L1, cKO: 0.8147 ± 0.0182	Kruskal-Wallis test with Dunn’s multiple comparisons test	p=0.6389 (ns)
			L2/3, ctrl: 0.8267 ± 0.0064 L2/3, cKO: 0.8425 ± 0.0064	Kruskal-Wallis test with Dunn’s multiple comparisons test	p=0.3543 (ns)
			L4, ctrl: 0.8129 ± 0.0121 L4, cKO: 0.8194 ± 0.0122	Kruskal-Wallis test with Dunn’s multiple comparisons test	p>0.9999 (ns)
			L5, ctrl: 0.8305 ± 0.0078 L5, cKO: 0.8337 ± 0.0072	Kruskal-Wallis test with Dunn’s multiple comparisons test	p>0.9999 (ns)
			L6a, ctrl: 0.8346 ± 0.0064 L6a, cKO: 0.8173 ± 0.0086	Kruskal-Wallis test with Dunn’s multiple comparisons test	p=0.8370 (ns)
			L6b, ctrl: 0.8164 ± 0.0160 L6b, cKO: 0.8438 ± 0.0157	Kruskal-Wallis test with Dunn’s multiple comparisons test	p>0.9999 (ns)
Figure 5.23. B	**Neuropeptide-Y** *cell density* (mean ± SEM)	***Genotype***	CA1, ctrl: 45.193 ± 7.698 CA1, cKO: 59.028 ± 10.159	Two-way ANOVA with Šídák's multiple comparisons test	p=0.7005 (ns)
			CA3, ctrl: 43.348 ± 5.244 CA3, cKO: 46.576 ± 9.080	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9925 (ns)
			DG, ctrl: 115.749 ± 10.170 DG, cKO: 89.464 ± 11.823	Two-way ANOVA with Šídák's multiple comparisons test	p=0.1579 (ns)
Figure 5.23. C	**Neuropeptide-Y** *soma morphology* (mean ± SEM)	***Genotype***	**soma area** CA3, ctrl: 85.60 ± 5.822 CA3, cKO: 67.50 ± 4.766	unpaired two-tailed Mann-Whitney test	p=0.0123 (*)
			soma perimeter CA3, ctrl: 47.10 ± 1.849 CA3, cKO: 44.57 ± 2.013	unpaired two-tailed Mann-Whitney test	p=0.1498 (ns)
			soma circularity CA3, ctrl: 0.4862 ± 0.0168	unpaired two-tailed Mann-Whitney test	p=0.1431 (ns)

			CA3, cKO: 0.4528 ± 0.0172		
			soma roundness CA3, ctrl: 0.5424 ± 0.0144	unpaired two-tailed Mann-Whitney test	p=0.8218 (ns)
			CA3, cKO: 0.5475 ± 0.0176		
			soma solidity CA3, ctrl: 0.7526 ± 0.0112	unpaired two-tailed Mann-Whitney test	p=0.0668 (ns)
			CA3, cKO: 0.7213 ± 0.0118		
Figure 5.23. D	**Neuropeptide-Y** *soma morphology* (mean ± SEM)	***Genotype***	**soma area** DG, ctrl: 94.41 ± 3.818	unpaired two-tailed Mann-Whitney test	p=0.4986 (ns)
			DG, cKO: 95.52 ± 3.913		
			soma perimeter DG, ctrl: 45.39 ± 1.091	unpaired two-tailed Mann-Whitney test	p=0.3485 (ns)
			DG, cKO: 46.54 ± 1.203		
			soma circularity DG, ctrl: 0.5598 ± 0.0103	unpaired two-tailed Mann-Whitney test	p=0.5503 (ns)
			DG, cKO: 0.5506 ± 0.0122		
			soma roundness DG, ctrl: 0.5622 ± 0.0102	unpaired two-tailed Mann-Whitney test	p=0.6547 (ns)
			DG, cKO: 0.5538 ± 0.0112		
			soma solidity DG, ctrl: 0.8046 ± 0.0065	unpaired two-tailed Mann-Whitney test	p=0.4373 (ns)
			DG, cKO: 0.7965 ± 0.0077		
Figure 5.23. F	**Neuropeptide-Y** *cell density* (mean ± SEM)	***Genotype***	CPu, ctrl: 56.46 ± 3.866	unpaired two-tailed t-test with Welch's correction	p=0.2786 (ns)
			CPu, cKO: 64.64 ± 5.582		
Figure 5.23. G	**Neuropeptide-Y** *soma morphology* (mean ± SEM)	***Genotype***	**soma area** CPu, ctrl: 86.99 ± 3.651	unpaired two-tailed Mann-Whitney test	p=0.7563 (ns)
			CPu, cKO: 90.14 ± 3.815		
			soma perimeter CPu, ctrl: 44.63 ± 1.282	unpaired two-tailed Mann-Whitney test	p=0.1732 (ns)
			CPu, cKO: 47.52 ± 1.330		
			soma circularity CPu, ctrl: 0.5577 ± 0.0155	unpaired two-tailed Mann-Whitney test	p=0.0449 (*)
			CPu, cKO: 0.5151 ± 0.0154		
			soma roundness CPu, ctrl: 0.5717 ± 0.0159	unpaired two-tailed Mann-Whitney test	p=0.3469 (ns)
			CPu, cKO: 0.5512 ± 0.0156		
			soma solidity CPu, ctrl: 0.8009 ± 0.0093	unpaired two-tailed Mann-Whitney test	p=0.1501 (ns)
			CPu, cKO: 0.7787 ± 0.0098		

Results **NPY**					
ADULT – Morphometrics – Layer 6-specific strains					
Effect	**Analysis**	**ROIs**	**Features**	**Layer 6b-silenced** *(Drd1a-Cre;Ai9;$Snap25^{fl/fl}$)*	**Layer 6b-enhanced** *(Drd1a-Cre;Ai9;$Pten^{fl/fl}$)*
Genotype	**Soma morphology** *3 months*	**ACA**	*Area*	ns	ns
			Perimeter	ns	ns
			Circularity	ns	ns
			Roundness	ns	ns
			Solidity	*↑	ns
Genotype	**Soma morphology** *3 months*	**M2**	*Area*	ns	*↑
			Perimeter	ns	ns
			Circularity	ns	ns
			Roundness	ns	ns
			Solidity	ns	*↑
Genotype	**Soma morphology** *3 months*	**M1**	*Area*	***↑	*↑
			Perimeter	ns	ns
			Circularity	ns	ns
			Roundness	*↑	ns
			Solidity	ns	ns
Genotype	**Soma morphology** *3 months*	**S1**	*Area*	**↓	****↑
			Perimeter	*↓	***↑
			Circularity	ns	ns
			Roundness	ns	*↑
			Solidity	ns	ns
Genotype	**Soma morphology** *3 months*	**CPu**	*Area*	ns	ns
			Perimeter	ns	ns
			Circularity	ns	*↓
			Roundness	ns	ns
			Solidity	ns	ns
Genotype	**Soma morphology** *3 months*	**CA3**	*Area*	ns	*↓
			Perimeter	ns	ns
			Circularity	ns	ns
			Roundness	ns	ns
			Solidity	ns	ns
Genotype	**Soma morphology** *3 months*	**DG**	*Area*	*↓	ns
			Perimeter	ns	ns
			Circularity	ns	ns

				Roundness	ns	ns
				Solidity	ns	ns
Layer	**Soma morphology** *3 months*	**M1**	*Area*	*Layer 1*	**↑	ns
				Layer 2/3	**↑	ns
				Layer 5	ns	ns
				Layer 6a	ns	ns
				Layer 6b	ns	ns
Layer	**Soma morphology** *3 months*	**M1**	*Perimeter*	*Layer 1*	*↑	ns
				Layer 2/3	*↑	ns
				Layer 5	ns	ns
				Layer 6a	ns	ns
				Layer 6b	ns	ns
Layer	**Soma morphology** *3 months*	**M1**	*Circularity*	*Layer 1*	ns	ns
				Layer 2/3	ns	ns
				Layer 5	ns	ns
				Layer 6a	ns	ns
				Layer 6b	ns	ns
Layer	**Soma morphology** *3 months*	**M1**	*Roundness*	*Layer 1*	ns	ns
				Layer 2/3	ns	ns
				Layer 5	ns	ns
				Layer 6a	ns	ns
				Layer 6b	ns	ns
Layer	**Soma morphology** *3 months*	**M1**	*Solidity*	*Layer 1*	ns	ns
				Layer 2/3	ns	ns
				Layer 5	ns	ns
				Layer 6a	ns	ns
				Layer 6b	ns	ns
Layer	**Soma morphology** *3 months*	**S1**	*Area*	*Layer 1*	ns	ns
				Layer 2/3	ns	***↑
				Layer 4	ns	ns
				Layer 5	ns	ns
				Layer 6a	**↓	ns
				Layer 6b	ns	ns
Layer	**Soma morphology** *3 months*	**S1**	*Perimeter*	*Layer 1*	ns	ns
				Layer 2/3	ns	*↑
				Layer 4	ns	ns
				Layer 5	ns	ns
				Layer 6a	ns	*↑
				Layer 6b	ns	ns
Layer		**S1**	*Circularity*	*Layer 1*	ns	ns

	Soma morphology *3 months*			*Layer 2/3*	ns	ns
				Layer 4	ns	ns
				Layer 5	ns	ns
				Layer 6a	ns	ns
				Layer 6b	ns	ns
Layer	**Soma morphology** *3 months*	**S1**	*Roundness*	*Layer 1*	ns	ns
				Layer 2/3	ns	**↑
				Layer 4	ns	ns
				Layer 5	ns	ns
				Layer 6a	ns	ns
				Layer 6b	ns	ns
Layer	**Soma morphology** *3 months*	**S1**	*Solidity*	*Layer 1*	ns	ns
				Layer 2/3	ns	ns
				Layer 4	ns	ns
				Layer 5	ns	ns
				Layer 6a	ns	ns
				Layer 6b	ns	ns

Figure	Analysis	Effect	Values	Statistical test	P value
SOMATOSTATIN					
Figure 5.24. B	**Somatostatin** *cell density* (mean ± SEM)	***Genotype***	ACA, ctrl: 62.16 ± 7.565	Two-tailed unpaired student's t-test with Welch's correction	p=0.6850 (ns)
			ACA, cKO: 58.40 ± 4.316		
Figure 5.24. E	**Somatostatin** *cell density* (mean ± SEM)	***Genotype***	M1, ctrl: 166.242 ± 13.695	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0581 (ns)
			M1, cKO: 121.167 ± 6.073		
			S1, ctrl: 152.298 ± 16.191	Two-way ANOVA with Šídák's multiple comparisons test	p=0.3439 (ns)
			S1, cKO: 126.949 ± 13.390		
Figure 5.24. F	**Somatostatin** *laminar distribution* (mean ± SEM)	***Layer***	**M1** Layer 1, ctrl: 25.246 ± 10.157	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9974 (ns)
			Layer 1, cKO: 17.600 ± 2.722		
			Layer 2/3, ctrl: 172.111 ± 14.521	Two-way ANOVA with Šídák's multiple comparisons test	p=0.5986 (ns)
			Layer 2/3, cKO: 144.752 ± 10.105		
			Layer 5, ctrl: 233.663 ± 28.773	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0053 (**)
			Layer 5, cKO: 163.725 ± 9.506		
			Layer 6a, ctrl: 158.761 ± 14.724	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0745 (ns)
			Layer 6a, cKO: 109.123 ± 11.367		
			Layer 6b, ctrl: 113.873 ± 10.408	Two-way ANOVA with Šídák's multiple comparisons test	p=0.0177 (*)
			Layer 6b, cKO: 52.801 ± 8.280		
Figure 5.24. G	**Somatostatin** *laminar distribution* (mean ± SEM)	***Layer***	**S1** Layer 1, ctrl: 5.612 ± 3.500	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 1, cKO: 1.744 ± 1.744		
			Layer 2/3, ctrl: 127.567 ± 19.928	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 2/3, cKO: 119.885 ± 11.409		
			Layer 4, ctrl: 170.665 ± 50.859	Two-way ANOVA with Šídák's multiple comparisons test	p=0.7878 (ns)
			Layer 4, cKO: 135.277 ± 24.369		
			Layer 5, ctrl: 212.690 ± 9.544		p=0.4728 (ns)

			Layer 5, cKO: 164.188 ± 11.249	Two-way ANOVA with Šídák's multiple comparisons test	
			Layer 6a, ctrl: 170.783 ± 14.695	Two-way ANOVA with Šídák's multiple comparisons test	p=0.8109 (ns)
			Layer 6a, cKO: 136.512 ± 20.697		
			Layer 6b, ctrl: 91.334 ± 8.944	Two-way ANOVA with Šídák's multiple comparisons test	p>0.9999 (ns)
			Layer 6b, cKO: 87.383 ± 17.981		
Figure 5.25. B	**Somatostatin** *soma morphology* (mean ± SEM)	***Genotype***	**soma area** M1, ctrl: 36.77 ± 0.768	unpaired two-tailed Mann-Whitney test	p=0.9648 (ns)
			M1, cKO: 37.47 ± 0.954		
			soma perimeter M1, ctrl: 27.67 ± 0.336	unpaired two-tailed Mann-Whitney test	p=0.1836 (ns)
			M1, cKO: 28.39 ± 0.404		
			soma circularity M1, ctrl: 0.596 ± 0.0052	unpaired two-tailed Mann-Whitney test	p=0.0003 (***)
			M1, cKO: 0.568 ± 0.0057		
			soma roundness M1, ctrl: 0.550 ± 0.0059	unpaired two-tailed Mann-Whitney test	p=0.0139 (*)
			M1, cKO: 0.528 ± 0.0064		
			soma solidity M1, ctrl: 0.789 ± 0.0030	unpaired two-tailed Mann-Whitney test	p=0.0003 (***)
			M1, cKO: 0.773 ± 0.0036		
Figure 5.25. C	**Somatostatin** *soma morphology* (mean ± SEM)	***Genotype***	**soma area** S1, ctrl: 42.56 ± 0.966	unpaired two-tailed Mann-Whitney test	p<0.0001 (****)
			S1, cKO: 35.54 ± 0.881		
			soma perimeter S1, ctrl: 30.10 ± 0.368	unpaired two-tailed Mann-Whitney test	p<0.0001 (****)
			S1, cKO: 27.84 ± 0.395		
			soma circularity S1, ctrl: 0.572 ± 0.0056	unpaired two-tailed Mann-Whitney test	p=0.9630 (ns)
			S1, cKO: 0.572 ± 0.0059		
			soma roundness S1, ctrl: 0.547 ± 0.0056	unpaired two-tailed Mann-Whitney test	p=0.0376 (*)
			S1, cKO: 0.530 ± 0.0059		
			soma solidity S1, ctrl: 0.777 ± 0.0034	unpaired two-tailed Mann-Whitney test	p=0.2252 (ns)
			S1, cKO: 0.771 ± 0.0036		
Figure 5.25. D	**Somatostatin** *soma morphology* (mean ± SEM)	***Layer***	**M1** **soma area** L1, ctrl: 37.6 ± 9.19	Kruskal-Wallis test with Dunn’s multiple comparisons test	p>0.9999 (ns)
			L1, cKO: 42.0 ± 10.4		
			L2/3, ctrl: 39.2 ± 1.30	Kruskal-Wallis test with Dunn’s multiple comparisons test	p=0.9306 (ns)
			L2/3, cKO: 37.4 ± 1.51		
			L5, ctrl: 31.7 ± 1.16		p>0.9999

			L5, cKO: 32.8 ± 1.53	Kruskal-Wallis test with Dunn’s multiple comparisons test	(ns)
			L6a, ctrl: 39.9 ± 1.63 L6a, cKO: 44.0 ± 1.94	Kruskal-Wallis test with Dunn’s multiple comparisons test	p=0.0918 (ns)
			L6b, ctrl: 47.6 ± 3.54 L6b, cKO: 50.4 ± 7.19	Kruskal-Wallis test with Dunn’s multiple comparisons test	p>0.9999 (ns)
Figure 5.25. D	**Somatostatin** *soma morphology* (mean ± SEM)	***Layer***	**M1** **soma perimeter** L1, ctrl: 29.17 ± 5.583 L1, cKO: 29.61 ± 4.355	Kruskal-Wallis test with Dunn’s multiple comparisons test	p>0.9999 (ns)
			L2/3, ctrl: 29.47 ± 0.576 L2/3, cKO: 29.25 ± 0.703	Kruskal-Wallis test with Dunn’s multiple comparisons test	p>0.9999 (ns)
			L5, ctrl: 25.56 ± 0.526 L5, cKO: 25.94 ± 0.614	Kruskal-Wallis test with Dunn’s multiple comparisons test	p>0.9999 (ns)
			L6a, ctrl: 28.07 ± 0.640 L6a, cKO: 30.91 ± 0.812	Kruskal-Wallis test with Dunn’s multiple comparisons test	p=0.0200 (*)
			L6b, ctrl: 32.52 ± 1.698 L6b, cKO: 32.13 ± 2.645	Kruskal-Wallis test with Dunn’s multiple comparisons test	p>0.9999 (ns)
Figure 5.25.D	**Somatostatin** *soma morphology* (mean ± SEM)	***Layer***	**M1** **soma circularity** L1, ctrl: 0.626 ± 0.0614 L1, cKO: 0.579 ± 0.0600	Kruskal-Wallis test with Dunn’s multiple comparisons test	p>0.9999 (ns)
			L2/3, ctrl: 0.564 ± 0.0091 L2/3, cKO: 0.549 ± 0.0102	Kruskal-Wallis test with Dunn’s multiple comparisons test	p>0.9999 (ns)
			L5, ctrl: 0.606 ± 0.0086 L5, cKO: 0.580 ± 0.0091	Kruskal-Wallis test with Dunn’s multiple comparisons test	p=0.2387 (ns)
			L6a, ctrl: 0.614 ± 0.0098 L6a, cKO: 0.568 ± 0.0112	Kruskal-Wallis test with Dunn’s multiple comparisons test	p=0.0163 (*)
			L6b, ctrl: 0.583 ± 0.0278 L6b, cKO: 0.591 ± 0.0399	Kruskal-Wallis test with Dunn’s multiple comparisons test	p>0.9999 (ns)
Figure 5.25. D	**Somatostatin** *soma morphology* (mean ± SEM)	***Layer***	**M1** **soma roundness** L1, ctrl: 0.581 ± 0.0520 L1, cKO: 0.578 ± 0.0630	Kruskal-Wallis test with Dunn’s multiple comparisons test	p>0.9999 (ns)
			L2/3, ctrl: 0.561 ± 0.0106 L2/3, cKO: 0.530 ± 0.0109	Kruskal-Wallis test with Dunn’s multiple comparisons test	p=0.3069 (ns)

			L5, ctrl: 0.541 ± 0.0095 L5, cKO: 0.516 ± 0.0102	Kruskal-Wallis test with Dunn's multiple comparisons test	p=0.3001 (ns)
			L6a, ctrl: 0.541 ± 0.0115 L6a, cKO: 0.534 ± 0.0129	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
			L6b, ctrl: 0.600 ± 0.0339 L6b, cKO: 0.626 ± 0.0442	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
Figure 5.25. D	**Somatostatin** *soma morphology* (mean ± SEM)	***Layer***	**M1** **soma solidity** L1, ctrl: 0.786 ± 0.0390 L1, cKO: 0.762 ± 0.0343	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
			L2/3, ctrl: 0.771 ± 0.0056 L2/3, cKO: 0.761 ± 0.0065	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
			L5, ctrl: 0.789 ± 0.0049 L5, cKO: 0.776 ± 0.0056	Kruskal-Wallis test with Dunn's multiple comparisons test	p=0.1680 (ns)
			L6a, ctrl: 0.806 ± 0.0053 L6a, cKO: 0.783 ± 0.0069	Kruskal-Wallis test with Dunn's multiple comparisons test	p=0.0373 (*)
			L6b, ctrl: 0.780 ± 0.0171 L6b, cKO: 0.791 ± 0.0238	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
Figure 5.25. E	**Somatostatin** *soma morphology* (mean ± SEM)	***Layer***	**S1** **soma area** L1, ctrl: 23.90 ± 3.558 L1, cKO: 43.49 ± 0.00	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
			L2/3, ctrl: 48.95 ± 2.088 L2/3, cKO: 39.87 ± 2.002	Kruskal-Wallis test with Dunn's multiple comparisons test	p=0.0152 (*)
			L4, ctrl: 39.04 ± 2.515 L4, cKO: 24.90 ± 1.577	Kruskal-Wallis test with Dunn's multiple comparisons test	p<0.0001 (****)
			L5, ctrl: 33.79 ± 1.547 L5, cKO: 31.07 ± 1.323	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
			L6a, ctrl: 47.99 ± 1.798 L6a, cKO: 39.25 ± 1.639	Kruskal-Wallis test with Dunn's multiple comparisons test	p=0.0089 (**)
			L6b, ctrl: 64.02 ± 5.988 L6b, cKO: 56.69 ± 5.545	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
Figure 5.25. E	**Somatostatin** *soma morphology* (mean ± SEM)	***Layer***	**S1** **soma perimeter** L1, ctrl: 27.49 ± 4.364 L1, cKO: 27.31 ± 0.00	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
			L2/3, ctrl: 32.44 ± 0.8046		p=0.1154 (ns)

			L2/3, cKO: 30.10 ± 0.9694	Kruskal-Wallis test with Dunn's multiple comparisons test	
			L4, ctrl: 29.45 ± 0.9174	Kruskal-Wallis test with Dunn's multiple comparisons test	p<0.0001 (****)
			L4, cKO: 23.65 ± 0.8725		
			L5, ctrl: 26.58 ± 0.5994	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
			L5, cKO: 26.06 ± 0.6058		
			L6a, ctrl: 32.24 ± 0.6865	Kruskal-Wallis test with Dunn's multiple comparisons test	p=0.0043 (**)
			L6a, cKO: 28.88 ± 0.7176		
			L6b, ctrl: 36.74 ± 2.170	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
			L6a, cKO: 37.16 ± 2.377		
Figure 5.25. E	**Somatostatin** *soma morphology* (mean ± SEM)	***Layer***	**S1** **soma circularity** L1, ctrl: 0.420 ± 0.0684	Kruskal-Wallis test with Dunn's multiple comparisons test	p=0.5227 (ns)
			L1, cKO: 0.733 ± 0.00		
			L2/3, ctrl: 0.581 ± 0.0127	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
			L2/3, cKO: 0.558 ± 0.0125		
			L4, ctrl: 0.543 ± 0.0166	Kruskal-Wallis test with Dunn's multiple comparisons test	p=0.8357 (ns)
			L4, cKO: 0.574 ± 0.0175		
			L5, ctrl: 0.581 ± 0.0095	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
			L5, cKO: 0.572 ± 0.0104		
			L6a, ctrl: 0.569 ± 0.0098	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
			L6a, cKO: 0.584 ± 0.0103		
			L6b, ctrl: 0.594 ± 0.0297	Kruskal-Wallis test with Dunn's multiple comparisons test	p=0.9312 (ns)
			L6a, cKO: 0.535 ± 0.0346		
Figure 5.25. E	**Somatostatin** *soma morphology* (mean ± SEM)	***Layer***	**S1** **soma roundness** L1, ctrl: 0.442 ± 0.0836	Kruskal-Wallis test with Dunn's multiple comparisons test	p=0.8996 (ns)
			L1, cKO: 0.697 ± 0.00		
			L2/3, ctrl: 0.576 ± 0.0115	Kruskal-Wallis test with Dunn's multiple comparisons test	p=0.2260 (ns)
			L2/3, cKO: 0.541 ± 0.0122		
			L4, ctrl: 0.535 ± 0.0170	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
			L4, cKO: 0.521 ± 0.0164		
			L5, ctrl: 0.525 ± 0.0094	Kruskal-Wallis test with Dunn's multiple comparisons test	p>0.9999 (ns)
			L5, cKO: 0.520 ± 0.0101		
			L6a, ctrl: 0.557 ± 0.0104		p=0.5730

			L6a, cKO: 0.533 ± 0.0114	Kruskal-Wallis test with Dunn’s multiple comparisons test	(ns)
			L6b, ctrl: 0.570 ± 0.0340	Kruskal-Wallis test with Dunn’s multiple comparisons test	p>0.9999 (ns)
			L6a, cKO: 0.558 ± 0.0290		
Figure 5.26. B	**Somatostatin** *cell density* (mean ± SEM)	***Genotype***	CPu, ctrl: 70.67 ± 7.542	unpaired two-tailed t-test with Welch’s correction	p=0.6232 (ns)
			CPu, cKO: 63.82 ± 10.79		
Figure 5.26. D	**Somatostatin** *soma morphology* (mean ± SEM)	***Genotype***	**soma area** CPu, ctrl: 75.28 ± 2.910	unpaired two-tailed Mann-Whitney test	p=0.6894 (ns)
			CPu, cKO: 73.42 ± 2.721		
			soma perimeter CPu, ctrl: 44.47 ± 1.242	unpaired two-tailed Mann-Whitney test	p=0.7611 (ns)
			CPu, cKO: 43.86 ± 1.065		
			soma circularity CPu, ctrl: 0.505 ± 0.0147	unpaired two-tailed Mann-Whitney test	p=0.7046 (ns)
			CPu, cKO: 0.495 ± 0.0140		
			soma roundness CPu, ctrl: 0.536 ± 0.0141	unpaired two-tailed Mann-Whitney test	p=0.2094 (ns)
			CPu, cKO: 0.509 ± 0.0149		
Figure 5.27. B	**SST+ VVA+** *cell density* (mean ± SEM)	***Genotype***	CA1, ctrl: 14.757 ± 4.193	Two-way ANOVA with Šídák's multiple comparisons test	p=0.8166 (ns)
			CA1, cKO: 11.990 ± 1.597		
			CA3, ctrl: 22.596 ± 4.081	Two-way ANOVA with Šídák's multiple comparisons test	p=0.7603 (ns)
			CA3, cKO: 25.825 ± 2.917		
Figure 5.27. C	**SST+ VVA+** *percentage* (mean ± SEM)	***Genotype***	CA1, ctrl: 36.21 ± 9.982	Two-way ANOVA with Šídák's multiple comparisons test	p=0.6682 (ns)
			CA1, cKO: 28.87 ± 4.903		
			CA3, ctrl: 40.84 ± 3.661	Two-way ANOVA with Šídák's multiple comparisons test	p=0.8757 (ns)
			CA3, cKO: 45.00 ± 4.495		
Figure 5.27. D	**SST+ VVA-** *cell density* (mean ± SEM)	***Genotype***	CA1, ctrl: 24.902 ± 3.239	Two-way ANOVA with Šídák's multiple comparisons test	p=0.4071 (ns)
			CA1, cKO: 30.897 ± 4.218		
			CA3, ctrl: 31.358 ± 1.065	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9942 (ns)
			CA3, cKO: 31.820 ± 3.940		
Figure 5.27. E	**SST+ VVA-** *percentage* (mean ± SEM)	***Genotype***	CA1, ctrl: 63.793 ± 9.982	Two-way ANOVA with Šídák's multiple comparisons test	p=0.6682 (ns)
			CA1, cKO: 71.133 ± 4.903		
			CA3, ctrl: 59.163 ± 3.661	Two-way ANOVA with Šídák's multiple comparisons test	p=0.8757 (ns)
			CA3, cKO: 55.003 ± 4.495		
Figure 5.27. F	**Somatostatin** *cell density* (mean ± SEM)	***Genotype***	CA1, ctrl: 39.659 ± 2.440	Two-way ANOVA with Šídák's multiple comparisons test	p=0.9131 (ns)
			CA1, cKO: 42.887 ± 3.482		

			CA3, ctrl: 53.955 ± 5.128 CA3, cKO: 57.644 ± 4.011	Two-way ANOVA with Šídák's multiple comparisons test	p=0.8771 (ns)
			DG, ctrl: 77.474 ± 4.518 DG, cKO: 66.867 ± 2.540	Two-way ANOVA with Šídák's multiple comparisons test	p=0.1824 (ns)
Figure 5.28. B	**Somatostatin** *soma morphology* (mean ± SEM)	***Genotype***	**soma area** CA1, ctrl: 88.92 ± 4.286 CA1, cKO: 75.99 ± 3.758	unpaired two-tailed Mann-Whitney test	p=0.0284 (*)
			soma perimeter CA1, ctrl: 45.44 ± 1.534 CA1, cKO: 39.66 ± 1.242	unpaired two-tailed Mann-Whitney test	p=0.0079 (**)
			soma circularity CA1, ctrl: 0.554 ± 0.0162 CA1, cKO: 0.610 ± 0.0171	unpaired two-tailed Mann-Whitney test	p=0.0217 (*)
			soma roundness CA1, ctrl: 0.558 ± 0.0175 CA1, cKO: 0.614 ± 0.0177	unpaired two-tailed Mann-Whitney test	p=0.0255 (*)
Figure 5.28. D	**Somatostatin** *soma morphology* (mean ± SEM)	***Genotype***	**soma area** CA3, ctrl: 54.38 ± 2.706 CA3, cKO: 61.47 ± 3.139	unpaired two-tailed Mann-Whitney test	p=0.1771 (ns)
			soma perimeter CA3, ctrl: 39.18 ± 1.339 CA3, cKO: 41.41 ± 1.253	unpaired two-tailed Mann-Whitney test	p=0.2234 (ns)
			soma circularity CA3, ctrl: 0.474 ± 0.0161 CA3, cKO: 0.467 ± 0.0146	unpaired two-tailed Mann-Whitney test	p=0.7534 (ns)
			soma roundness CA3, ctrl: 0.535 ± 0.0157 CA3, cKO: 0.507 ± 0.0137	unpaired two-tailed Mann-Whitney test	p=0.1714 (ns)
Figure 5.28. F	**Somatostatin** *soma morphology* (mean ± SEM)	***Genotype***	**soma area** DG, ctrl: 84.34 ± 3.720 DG, cKO: 73.43 ± 3.415	unpaired two-tailed Mann-Whitney test	p=0.0658 (ns)
			soma perimeter DG, ctrl: 46.43 ± 1.269 DG, cKO: 43.49 ± 1.353	unpaired two-tailed Mann-Whitney test	p=0.0557 (ns)
			soma circularity DG, ctrl: 0.496 ± 0.0141 DG, cKO: 0.506 ± 0.0170	unpaired two-tailed Mann-Whitney test	p=0.7115 (ns)
			soma roundness DG, ctrl: 0.556 ± 0.0146 DG, cKO: 0.514 ± 0.0169	unpaired two-tailed Mann-Whitney test	p=0.0810 (ns)

Summary of conditional deletion of *Pten* in different brain regions and cell types

Loss Of *Pten* Function Experiments

MOUSE MODEL	Experimental strategy	Type & time of deletion	Targeted cells	Region of deletion	Behavioural phenotype	Anatomical & physiological alterations	Reference
$PTEN^{-/-}$	gene targeting techniques in the mouse germ line and mouse ES cells (inactivation *via* homologue recombination)	homozygous deletion; embryonic	somatic	whole-body knockout	embryonic lethality at days 3.5 and 9.5	impaired ability of ES cells to differentiate into endodermal, ectodermal and mesodermal derivatives; hyperplastic-dysplastic changes in the intestinal mucosa, testis atrophy, skin hyperkeratosis spontaneous development of germ cell, gonadostromal thyroid, and colon tumours	Di Cristofano et al. 1998
$PTEN^{+/-}$	gene targeting (deletion of PTEN into exon 5 - most frequently mutated exon in the germline)	heterozygous deletion; embryonic	germline	whole-body knockout	N/A (embryonic lethality in Pten-/- mice occurs by day 6.5)	variety of different tumours including lymphomas, dysplastic intestinal polyps, endometrial complex atypical hyperplasia, prostatic intraepithelial neoplasia, and thyroid neoplasms	Podsypanina et al. 1999
$PTEN^{+/-}$	crossing $Pten^{tm1Rps/+}$ ($Pten^{+/-}$) mice with wild-type ($Pten^{+/+}$) mice	heterozygous deletion; embryonic	germline	no tissue-specificity	both sexes showed social impairments; (no social or social novelty preference); males showed abnormalities related to repetitive behaviour (marble burying) and mood/anxiety; females exhibited circadian activity and emotional learning phenotypes	brain overgrowth	Clipperton-Allen and Page 2014; Clipperton-Allen and Page 2015)
$PTEN^{+/-}$	backcrossing B6.129-$Pten^{tm1Rps}$ ($Pten^{+/-}$) to C57BL/6J mice	heterozygous deletion; embryonic	germline	no tissue-specificity	selective impairments in ASD-relevant behaviours, particularly social behaviour (deficits in the three-chamber	macrocephaly, increased axonal branching and connectivity, increased activity in the	(Huang et al. 2016)

					social approach test in adult females)	BLA in response to social stimuli, hyperactivity of the mPFC–BLA circuitry, subcortical-projecting layer V neurons are hypertrophic, have greater soma size and dendritic complexity than callosal-projecting neurons, elevated pS6 levels in Ctip2+ layer V neurons during early postnatal development (P4-P14)	
Gfap-Cre; Pten$^{fl/fl}$	Cre-*loxP* system (homozygous *Pten flox* mice (*Pten*$^{loxP/loxP}$) crossed with *Gfap-Cre* transgenic mice)	tissue-specific deletion; conditional knockout (homozygous), by P0-P14	deletion targeted to glial cells, but Pten loss limited to neuronal cells instead of astrocytes	granule cells of the dentate gyrus and the cerebellum (extent of Pten loss greater in the dentate gyrus), plus some cortical neurons	neurological defects including seizures and ataxia developed by 9 weeks of age, status epilepticus	macrocephaly, cell-autonomous increase in soma size, increased phosphorylation of Akt, thickened cerebellar folia, dysplasia of granule cells, dysplastic Purkinje cells, hypertrophied glial cells and oligodendrocytes with aberrant myelination, homozygous mice display hallmark symptoms of Lhermitte-Duclos disease (LDD)	(Backman et al. 2001)
Gfap-Cre; Pten$^{fl/fl}$	Cre-*loxP* system (homozygous *Pten flox* mice (*Pten*$^{loxP/loxP}$) crossed with *Gfap-Cre* transgenic mice)	tissue-specific deletion, conditional knockout (homozygous), by P14	astrocytes, 80–90% of hippocampal neurons and cerebellar granule neurons, 50–80% of pyramidal neurons	astrocytes throughout the brain, dentate gyrus, cerebellum, and the cerebral cortex	seizures, ataxia, premature death	altered morphology and neuronal hypertrophy including enlarged somata and nucleoli, increased ribosome density, enlarged dendritic processes, increased spine density, myelination defects, enlarged presynaptic terminals,	(Fraser et al. 2008; Fraser et al. 2004)

						marked decreased synaptic transmission, increased astrocyte proliferation	
Emx1-Cre; Pten$^{fl/+}$	Cre-*loxP* system (*Pten*$^{loxP/loxP}$) crossed with *Emx1*$^{tm1(cre)Krj}$ (*Emx1-Cre)* transgenic mice)	tissue-specific deletion, conditional knockout (heterozygous); *Emx1-Cre*$^{+}$; *Pten*$^{loxP/loxP}$ mice not viable after P10.	cortical neural progenitor cells and their descendants, including pyramidal neurons, astrocytes, and oligodendrocytes, plus a subset of cells in the olfactory bulb	cerebral cortex (no region-specificity)	social behavioural deficits	overgrowth of the cerebral cortex, increased total brain mass and cerebral cortex mass, excess neurons at birth and excess glia in adulthood	(Chen et al. 2015)
Emx1-Cre^{+}; Pten$^{loxP/+}$; Ctnnb1$^{loxP/+}$	*Pten*$^{loxP/+}$; *Ctnnb1*$^{loxP/+}$ male mice mated with *Emx1-Cre*$^{+}$; *Pten*$^{loxP/+}$;*Ctnnb1*$^{loxP/+}$ female mice	tissue-specific deletion, conditional knockout (heterozygous)	cortical neural progenitors and descendants	cerebral cortex (no region-specificity)	not tested	elevated β-catenin activity significantly reduced cortex mass in mutants decreased number of total nuclei in the cerebral cortex, reduced hyperplasia, haploinsufficiency for *Ctnnb1*, but not *Mtor* or *Rptor*	(Chen et al. 2015)
Nex-Cre, Pten$^{loxP/+}$; **Nex-Cre, Pten$^{loxP/loxP}$**	crossing homozygous NEX-*Cre* knock-in mice with Cre-negative conditional neuron subset-specific *Pten*(NS-*Pten*) knockout mice (Pten$^{loxP/loxP}$)	tissue-specific deletion, conditional knockout (homozygous (NEX-Cre+;Pten$^{loxP/loxP}$*)* knockout mice die within 1 week after birth	excitatory neurons immediately after they become postmitotic	all forebrain (no region-specificity)	premature lethality of homozygous Pten knockout mice	macrocephaly and neuronal hypertrophy NEX-Cre+;Pten$^{loxP/loxP}$ mice, intact migration but over migration into the marginal zone and distortion of cortical cellular layers MAP2 upregulation, higher levels of the NMDA receptor subunits 2A and 2B	(Kazdoba et al. 2012)
Pten x tdTomato	breeding mice with lox-P flanked exon 5 of the PTEN gene to mice with a lox-P flanked STOP cassette in the ROSA locus preventing expression of tandem dimer tomato (tdTomato)	double transgenic mice; tissue-specific deletion by viral injection (unilateral intracortical injections of AAV-Cre recombinase at 8 or more weeks of age); adulthood	adult cortical neurons	sensorimotor cortex	no overt neurological symptoms, absence of seizures, mixed effects on motor function as assessed by the rotarod and cylinder tasks, unilateral Pten deletion led to slight rotarod	progressive increase in cell bodies, dendrites, and axons of cortical neurons, persistent activation of mTORC1, elevated levels of pS6 proteins in cortical motoneurons,	(Gallent and Steward 2018)

					impairments, while bilateral Pten deletion enhanced rotarod performance (motor coordination and learning)	layer V pyramidal neurons displaying the highest levels of pS6	
Pten$^{fl/fl}$	Transgenic mice with a floxed exon 5 of the *PTEN* gene (*PTEN*$^{fl/fl}$)	tissue-specific deletion by viral injection (intracortical injections of AAV-Cre recombinase at P1); neonatal	cortical motoneurons	sensorimotor cortex (*PTEN* deletion affecting neurons in all cortical layers, though *PTEN* expression reported to be maintained in layer III-IV cortical neurons in some instances)	trend for enhanced rotarod performance (not statistically significant), normal open field activity	increased cortical thickness and massive hypertrophy of layer V cortical motoneurons, no evidence of tumour formation or other neuropathology, focally increased ratio of neuropil to cell bodies at deletion site, elevated mTOR activity	(Gutilla et al. 2016; Gutilla and Steward 2016)
Pten$^{fl/fl}$	*loxP* sites flanking exon 5 of the phosphatase and tensin homolog gene	retroviral deletion (co-injection of retroviruses encoding only one fluorescent protein with retroviruses encoding a distinct fluorescent protein-T2A-Cre, into the dentate gyrus of P7 Pten$^{fl/fl}$ mice); neonatal	newborn granule cells	dentate gyrus	not tested (previous research showing the emergence of seizures following the deletion of Pten from postnatally generated granule neurons, (Pun et al. 2012))	hypertrophy, hyperexcitability of KO neurons, increased neuronal activity, increased synaptic depolarisation, increased dendritic filopodia density, excess excitatory synaptogenesis, increases in excitatory drive to KO neurons, altered action potential threshold	(Williams et al. 2015)
Pten$^{loxP/loxP}$	homozygous mutant mice (*PTEN*$^{loxP/loxP}$) in which *PTEN* exons 4 and 5 are flanked by *loxP* sites	Cre recombination; conditional deletion by injection of an AAV expressing GFP-IRES-Cre into the left auditory cortex of *PTEN*$^{loxP/loxP}$ mice between P18 and P21; early development	sparse subset of auditory cortical neurons	left auditory cortex	not tested	altered connectivity, increase in the strength of both long-range and local excitatory inputs; PTEN-cKO neurons in the auditory cortex receiving stronger inputs from both the contralateral auditory cortex and the thalamus; outgrowth of dendrites and spines;	(Xiong et al. 2012)

						increased mEPSC frequency; increase in mEPSC amplitude	
Nse-Cre; $Pten^{loxP/loxP}$	both alleles of the *Pten* gene contain loxP sites and *Cre* is expressed under the neuron-specific enolase promoter	conditional knockout mouse, tissue-specific deletion; late-onset model	granule cell, pyramidal neurons in the CA3, select populations of postmitotic neurons in the cortex	hippocampal dentate gyrus, CA3, and the entorhinal cortex	autism-relevant behaviours, spontaneous seizures and deficits in hippocampus-based social and cognitive behaviours, hypersensitivity to sensory stimuli, and anxiety	macrocephaly of the dentate gyrus and the overlying neocortex, compression of the CA1 pyramidal cell layer and the deeper layers of entorhinal cortex, reduced dendritic arborization of DG neurons, overactivation of mTOR in DGCs and CA3 pyramidal neurons, neuronal hypertrophy, enhanced LTP, impaired LTD	(Takeuchi et al. 2013)
Nse-Cre; $Pten^{loxP/loxP}$	*Neuron-specific enolase* (*Nse*) promoter-driven *Cre* transgenic mouse line	conditional knockout mouse, tissue-specific deletion; by 4 weeks of age	subsets of differentiated neurons in the cortex and hippocampus (30-60% of forebrain neurons by 4 weeks of age)	layers III to V of the cerebral cortex and in the CA3, dentate gyrus granular layer (GL), and polymorphic layer (PML) of the hippocampal formation	ASD phenotype including exaggerated reaction to sensory stimuli, anxiety-like behaviours, seizures, decreased learning; deficits in nest formation, less interaction with the novel target mouse, defects in maternal care	macrocephaly, neuronal hypertrophy, axonal and dendritic growth, ectopic positioning of dentate axons, increased spine density, altered polarity of neuronal processes	(Kwon et al. 2006)
Gli1-$CreER^{T2}$:: $Pten^{flox/flox}$	Gli1-$CreER^{T2}$ hemizygous:: $PTEN^{wt/flox}$ mice crossed to $PTEN^{wt/flox}$ mice to generate Gli1-$CreER^{T2}$ hemizygous::$PTEN^{flox/flox}$ mice	conditional, Cre-inducible knockout; tissue-specific deletion, injection of tamoxifen at P14	a subset of granule cells (deletion of Pten from ~27% of hippocampal granule cells)	hippocampus	epilepsy	increased intrinsic excitability of Pten-deficient cells, lower input resistance, tendency towards burst firing (fire doublets and triplets), longer dendrites with more branches, overlapping dendritic branches, impaired excitation/inhibition balance, increased sEPSC frequency,	(Santos et al. 2017)

						sexual dimorphism, females (both control and KOs) receiving more sEPSCs and sIPSCs	
Gli1-CreER^{T2} **hemizygous, PTEN$^{flox/flox}$, green fluorescent protein (GFP) reporter$^{+/-}$**	Gli1-CreERT2 hemizygous, PTEN$^{flox/wt}$ mice crossed to GFP reporter heterozygous (+/-) or homozygous (+/+), PTEN$^{flox/wt}$ mice	conditional knockout; Cre inducible transgenic mouse, tamoxifen treatment at P14, postnatal deletion (selective deletion of *PTEN* gene from neural progenitor cells beginning 14 days after birth)	restricted subset of granule cells: ≥9% of granule cells (9%–25% of the entire population); (selective deletion of *PTEN* from a small number of glial cells; mostly protoplasmic astrocytes as well, but astrocytes minimally affected)	hippocampal dentate gyrus	epilepsy, spontaneous seizures, but no tumours	hyperactivation of the mTOR pathway, hypertrophy, de novo appearance of basal dendrites, increased dendritic spine density, and ectopically located somata, hallmark Pathologies of Temporal Lobe Epilepsy, minimal reactive gliosis, mossy fiber sprouting	(Pun et al. 2012)
Slc6a3-Cre (DAT-Cre) x Pten$^{flox/flox}$	Cre-loxP system, Slc6a3-Cre - dopamine transporter (DAT) promoter-driven Cre transgenic mouse line; Slc6a3-Cre crossed to Pten^{loxP} mice	knockin, tissue-specific ablation; Cre expression driven by the DAT promoter and mediates deletion of exon 5 of the Pten gene approximately at embryonic day 15	postmitotic mesencephalic dopaminergic neurons (lesser expression of DAT levels present in the olfactory bulb and hypothalamic areas as well)	ventral midbrain (substantia nigra pars compacta (SNc) and ventral tegmental area (VTA) a))	locomotor response to a novel environment unchanged	neuronal hypertrophy, increase in SNc and VTA total volume, increased number of TH+ neurons, increased DRD1 and prodynorphin mRNA levels in striatonigral projecting neurons, intact extracellular dopamine dynamics, protection against neurotoxic insults	(Diaz-Ruiz et al. 2009)
hGFAP-Cre$^{+/-}$/ Pten^{loxp}	Cre-loxP system; hGFAP-Cre line crossed to PTEN$^{loxp/loxp}$ mice, hGFAP-Cre$^{+/-}$/PTEN$^{loxp/loxp}$ and hGFAP-Cre$^{+/-}$/PTEN$^{loxp/-}$	compound mice, conditional knockout, cell type-specific deletion (hGFAP promoter directed PTEN deletion)	astroglia, but Pten deletion also in radial glial-derived neuronal cells	central nervous system (no region-specificity)	not tested (mouse GFAP promoter-directed conditional deletion of PTEN from cerebellar, cortical, and hippocampal neurons leads to seizures and ataxia)	defects in neuronal layering and patterning, accelerated radial glial proliferation and scaffold formation in the hippocampus, cortex, and cerebellum, misguided neuronal profileration,	(Wen et al. 2013)

						migration defects, increased neuronal progenitor population	
CamKII-Cre$^{+/-}$; Pten$^{loxp/loxp}$ Thy1-GFP	Mice with a Pten$^{loxp/loxp}$ allele flanking exon 5 crossed with mice carrying both an αCamKII-driven Cre transgene and a Thy1-driven green fluorescent protein	conditional knockout; tissue-specific deletion (*Camk2a*) promoter driving Cre recombinase expression in the forebrain, including CA1 pyramidal neurons in the hippocampus; mature mice	excitatory forebrain neurons	cerebral cortex and hippocampus, no region-specificity	not tested	laminar-specific, large-scale growth of apical dendrites in *Pten*$^{-/-}$ mice; longer apical dendrites detected only in layer 2/3 pyramidal neurons (layer 5 pyramidal neurons' dendritic length unchanged), no effect on basal dendritic length, unaltered spine density, mature cortical neurons exhibit constitutively active growth-promoting pathways	(Chow et al. 2009); (Sperow et al. 2012)
Nkx2.1-Cre × Pten$^{flox/flox}$	crossing *Pten*^{Flox} mice to *Nkx2.1-Cre* mice; *Ai14* Cre-dependent reporter line used to label Cre-expressing cells	conditional knockout; tissue-specific deletion (*Nkx2.1-Cre* BAC transgenic line drives Cre expression in the ventricular zone (VZ) of the MGE and POA (beginning on embryonic day ~9.5)	interneuron progenitors in the ventricular zone; MGE-and POA-derived GABAergic interneurons	ventricular zone	deficits in social interaction, reduced social behaviour, but normal levels of exploratory activity, locomotion, and anxiety	increased AKT signaling; differential impact on SST^{+} and PV^{+} interneurons; reduced interneuron numbers, increased PV^{+}/SST^{+} ratio, and ectopic PV^{+} processes in layer 1; increased inhibition onto neocortical pyramidal neurons (increase in sIPSCs); reduced gamma rhythms at rest	(Vogt et al. 2015)
PV-Cre × Pten$^{flox/flox}$ **SST-Cre × Pten$^{flox/flox}$**	Pten$^{fl/fl}$ mice crossed to Sst-Cre$^{+/+}$ mice to generate Sst-Cre$^{+/+}$/Pten$^{fl/+}$ mice; three types of experimental mice generated by crossing Sst-Cre$^{+/+}$/*Pten*$^{fl/+}$ breeders, 1) Sst-Cre$^{+/+}$/*Pten*$^{+/+;}$ 2) Sst-Cre$^{+/+}$/*Pten*$^{fl/+;}$ and 3) Sst-Cre$^{+/+}$/*Pten*$^{fl/fl}$;	Cre/loxP recombination system; conditional knockout; cell type-specific deletion	parvalbumin and somatostatin interneurons	no region specificity	autism-like symptoms (reduced social novelty preference and the presence of repetitive behaviours – increased self-grooming); PV-Pten-KO mice exhibiting hyperactivity,	not tested	(Shin et al. 2021)

	same breeding strategy applied to breed PV-Cre$^{+/+}$/Pten$^{fl/+}$breeders and their offspring				impairment in motor coordination/learning, and anxiolytic-like behaviors; Sst-Pten-KO displaying anxiety-like behaviors		
L7-Cre × Pten$^{flox/flox}$	crossing L7-Cre transgenic mice with mice Pten^{flox} mice	conditional knockout; deletion by Cre-loxP recombination system; Cre expression is driven by the Purkinje cell-specific promoter L7	Purkinje cells (L7 promoter is also expressed in retinal bipolar neurons, but only a few of them were labelled)	cerebellum	ASD-related behavioural symptoms include severe impairments in social interaction; repetitive behaviour (stereotyped jumping), decreased self-grooming; impaired motor learning (rotarod test); normal performance in all cognitive test	aberrant Purkinje cell morphology and hypertrophy (overgrowth of all PC compartments, axonal and dendritic swellings, abnormal dendritic branching, accumulation of cytoskeletal components); reduced firing frequency and input resistance observed in Pten-deleted Purkinje cells; increased amplitude of EPSCs; deficits in PC spontaneous and evoked firing activity	(Cupolillo et al. 2016)

Morphometric analyses

Chapter 3

(Rbp4-Cre;Ai14;Snap25$^{fl/fl}$)

Figure	Interneuron	Region	Genotype	Number of cells
3.17. F	Neuropeptide-Y	ACA	ctrl	176
			cKO	106
3.17. G	Neuropeptide-Y	M2	ctrl	250
			cKO	142
3.18. E	Neuropeptide-Y	M1	ctrl	357
			cKO	291
3.19. E	Neuropeptide-Y	S1	ctrl	610
			cKO	513
3.20. D	Neuropeptide-Y	M1 L1	ctrl	57
			cKO	23
		M1 L2/3	ctrl	95
			cKO	92
		M1 L5	ctrl	89
			cKO	91
		M1 L6a	ctrl	90
			cKO	70
		M1 L6b	ctrl	26
			cKO	15
3.21. D	Neuropeptide-Y	S1 L1	ctrl	52
			cKO	25
		S1 L2/3	ctrl	261
			cKO	215
		S1 L4	ctrl	61
			cKO	44
		S1 L5	ctrl	103
			cKO	117
		S1 L6a	ctrl	100
			cKO	93
		S1 L6b	ctrl	33
			cKO	19
3.22. D	Neuropeptide-Y	CPu	ctrl	110
			cKO	87

Morphometric analyses

Chapter 4

(Drd1a-Cre;Ai14;Snap25$^{fl/fl}$*)*

Figure	Interneuron	Region	Genotype	Number of cells
DEVELOPMENT				
4.6. C	Parvalbumin	CPu	ctrl	193
			cKO	246
4.10. D	Neuropeptide-Y	CPu	ctrl	158
			cKO	190
4.12. F	Calretinin	CPu	ctrl	109
			cKO	106
ADULT				
4.18. F	Neuropeptide-Y	ACA	ctrl	150
			cKO	185
4.18. F	Neuropeptide-Y	M2	ctrl	265
			cKO	232
4.20. B	Neuropeptide-Y	M1	ctrl	642
			cKO	565
4.20. C	Neuropeptide-Y	M1 L1	ctrl	54
			cKO	74
		M1 L2/3	ctrl	279
			cKO	234
		M1 L5	ctrl	146
			cKO	136
		M1 L6a	ctrl	129
			cKO	112
		M1 L6b	ctrl	34
			cKO	23
4.20. E	Neuropeptide-Y	S1	ctrl	632
			cKO	655
4.20. F	Neuropeptide-Y	S1 L1	ctrl	37
			cKO	46
		S1 L2/3	ctrl	274
			cKO	243
		S1 L4	ctrl	46
			cKO	79
		S1 L5	ctrl	121
			cKO	132
		S1 L6a	ctrl	114
			cKO	133
		S1 L6b	ctrl	40
			cKO	22
4.21. C	Parvalbumin	CPu	ctrl	237
			cKO	229
4.21. H	Parvalbumin	CPu, P21	ctrl	193
		CPu, 12 wks	ctrl	237

4.21. I	Parvalbumin	CPu, P21	cKO	246
		CPu, 12 wks	cKO	229
4.23. E	Neuropeptide-Y	CPu	ctrl	103
			cKO	88

Morphometric analyses

Chapter 5

(Drd1a-Cre;Ai14;Pten$^{fl/fl}$)

Figure	Interneuron	Region	Genotype	Number of cells
5.14. H	Parvalbumin	M1	ctrl	1056
			cKO	1083
5.17. B	Parvalbumin	S1 dense	ctrl	1137
			cKO	1221
5.19. D	Parvalbumin	CPu	ctrl	184
			cKO	155
5.20. D	Neuropeptide-Y	ACA	ctrl	300
			cKO	306
5.20. E	Neuropeptide-Y	M2	ctrl	311
			cKO	273
5.21. F	Neuropeptide-Y	M1	ctrl	645
			cKO	593
5.21. G	Neuropeptide-Y	S1	ctrl	755
			cKO	641
5.22. B	Neuropeptide-Y	S1 L1	ctrl	47
			cKO	50
		S1 L2/3	ctrl	263
			cKO	222
		S1 L4	ctrl	85
			cKO	82
		S1 L5	ctrl	135
			cKO	143
		S1 L6a	ctrl	187
			cKO	125
		S1 L6b	ctrl	38
			cKO	19
5.23. C	Neuropeptide-Y	CA3	ctrl	94
			cKO	100
5.23. D	Neuropeptide-Y	DG	ctrl	251
			cKO	193
5.23. G	Neuropeptide-Y	CPu	ctrl	121
			cKO	133
5.25. B	Somatostatin	M1	ctrl	1026
			cKO	735
5.25. C	Somatostatin	S1	ctrl	957

			cKO	773
5.25. D	Somatostatin	M1 L1	ctrl	15
			cKO	12
		M1 L2/3	ctrl	288
			cKO	234
		M1 L5	ctrl	401
			cKO	296
		M1 L6a	ctrl	281
			cKO	175
		M1 L6b	ctrl	40
			cKO	18
5.25. E	Somatostatin	S1 L1	ctrl	3
			cKO	1
		S1 L2/3	ctrl	188
			cKO	165
		S1 L4	ctrl	124
			cKO	99
		S1 L5	ctrl	326
			cKO	252
		S1 L6a	ctrl	289
			cKO	229
		S1 L6b	ctrl	27
			cKO	27
5.26. D	Somatostatin	CPu	ctrl	152
			cKO	136
5.28. B	Somatostatin	CA1	ctrl	85
			cKO	93
5.28. D	Somatostatin	CA3	ctrl	111
			cKO	128
5.28. F	Somatostatin	DG	ctrl	116
			cKO	96