Supplementary Table 1. Antibody list used in the experiments. *Related to Methods section.*

Antibody	Species	Dilution	Source
GAD 1	Rabbit	1:1,000	Millipore
Glutamate	Rabbit	1:15,000	Sigma Aldrich
PV	Rabbit	1:5,000	Swant
PV	Sheep	1:200	Thermo Fisher
PSD-95	Rabbit	1:1,000	Cell Signaling
Vglut1	Mouse	1:1,000	UC Davis
VGAT	Rabbit	1:1,000	Synaptic Systems
Gephyrin	Mouse	1:1,000	Synaptic Systems
Sox6	Rabbit	1:1,000	Millipore
ß-tubulin III	Mouse	1:2,000	Covance
Oct4	Rabbit	1:400	Cell Signaling
Tra-160	Mouse	1:500	Abcam
GFP	Chicken	1:1,000	Abcam
NCAM	Mouse	1:1,000	Santa Cruz Biotech
MEF2C	Rabbit	1:1,000	Cell Signaling
SST	Goat	1:1,000	Santa Cruz Biotech
Human Cytoplasm	Mouse	1:1,000	StemCells Inc
VIP	Rabbit	1:1,000	Immunostar
CCK	Rabbit	1:1,000	Sigma Aldrich
Calretinin	Goat	1:1,000	Swant
COUPTFII	Mouse	1:1,000	Perseus Proteomics
OLIG2	Rabbit	1:1,000	Millipore
GFAP	Mouse	1:1,000	UC Davis
ChAT	Goat	1:1,000	Chemicon
TH	Rabbit	1:1,000	Pel-Freez
5-HT	Rabbit	1:1,000	Immunostar

Supplementary Table 2. Primer list used in this study. *Related to Methods section.*

Gene	Sequence	
PCDHA2	Taqman assay ID: Hs00171012 (Thermo Fisher)	
PCDHA3	Forward	GTTTTCGCTAGAGGGCGCAT
	Reverse	CAACACGAGTCCAAGGGATTTA
PCDHA6	Forward	GGAAAGCAATGTCTGCTCCTC
	Reverse	CCTCCTCGGGTACGGAGTAG
PCDHA8	Forward	GTCCTGGTGAAGGATCATGGT
	Reverse	GCCTCGATGACGCTTTTGG
PCDHA-CR	Forward	CATTCTACGGGCTGGTCCAG
	Reverse	GGGTTGCCTGGTCCGTATTT
PCDHA-CR	Forward	AGCAGTGGCCAACAGTATCC
	Reverse	GGTCTCCTCCTTTTTGCCGA
PCDHG-CR	Forward	GGCCCAACAACCAGTTTGAC
	Reverse	CGTTGGTCAGTGTGGCATTG
PCDHG-CR	Forward	GGCCCAACAACCAGTTTGAC
	Reverse	CGTTGGTCAGTGTGGCATTG
NANOG	Forward	TTGGGACTGGTGGAAGAATC
	Reverse	GATTTGTGGGCCTGAAGAAA
PAX6	Forward	TCAGTTCCAGTTCAAGTTCCCG
	Reverse	CAGCCATTTTTCTTTCTTTCCTG
TBR1	Forward	ACAATTTTCCTGACTCCAAGGAC
	Reverse	ACTGTGACGAAGCTCAGAGAC
SLC17A7	Forward	CTGGGGCTACATTGTCACTCA
	Reverse	GCAAAGCCGAAAACTCTGTTG
GAD1	Forward	CTGCTCTTCTCTTACGCTCTCTGTC
	Reverse	TCTTCGGAAATGTTGCCTTAGG
LHX6	Forward	GGTCTATTCCTTGCGTGGATTATG
	Reverse	TCCGTGTGTGTGTTTTCCCC
NKX2-1	Forward	ACTGACACAAAGGAAGTGCCCC
	Reverse	GCCGCAAATACCAAACTGCC
SOX6	Forward	ATCTCTCATCCCGACCCAAGAC
	Reverse	TTCCCAGGCTTCCTCCAATG
GAPDH	Forward	GCTCAGACACCATGGGGAAGGT
	Reverse	GTGGTGCAGGAGGCATTG CTGA

Supplementary Table 3. Cell lines used for each experiment. *Related to Methods section.*

Group	Cell ID	Immunocytochemistry	Cell counting	pilot RNAseq	Glutaminergic differentiation	RNAseq on larger cohort	Real Time PCR	Electrophysiology *in vitro*	Electrophysiology *in vivo*	Arborization anlysis	GO6893 treatment	siRNA treatment	Synapse analysis after grafting
HC	317	√	√			√	√		√	√			
	PYAUM	√	√			√	√			√	√		√
	272	√	√	√	√	√	√	√		√	√		√
	190	√	√	√	√	√	√			√	√	√	√
	367	√	√	√	√	√	√	√		√	√	√	√
	292	√	√			√	√						
	365	√	√			√	√						
	226	√	√	√	√	√	√					√	
	M_139	√	√			√	√	√		√	√		√
	99	√	√			√	√			√	√		√
	107	√	√			√	√			√	√		√
	L5	√	√			√	√						
	L7	√	√			√	√	√		√	√		
	L9	√	√			√	√						
SCZ	67	√	√	√	√	√	√	√	√	√	√		√
	117	√	√			√	√	√		√	√		
	128	√	√	√	√	√	√		√	√		√	√
	212	√	√	√	√	√	√		√			√	
	162	√	√	√	√	√	√	√		√	√	√	
	58	√	√			√	√		√	√	√		
	282	√	√			√	√						√
	285	√	√			√	√	√		√	√		
	L8	√	√			√	√						
	L10	√	√			√	√						√
	1442	√	√			√	√						
	483	√	√			√	√			√	√		√
	689	√	√			√	√			√	√		√
	755	√	√			√	√		√	√	√		√

Supplementary Table 4. Break down data table of Fig. 3c (n= 3 differentiations per cell line).

	Group	HC cIN				SCZ cIN			
Gene	Cell ID	190	226	272	367	128	162	212	67
PCDHA2	Average	1.46	1.71	1.76	0.81	0.38	0.57	1.22	0.23
	SEM	0.11	0.78	0.33	0.15	0.04	0.13	0.39	0.06

Supplementary Table 5. Break down data table of Fig. 3f, Supplementary Fig. 8a, and 8f (n= 2 differentiations per cell line).

			PCDHA2		*PCDHA3*		*PCDHA6*		*PCDHA8*		*PCDHG-CR*		*PCDHA-CR*	
Sample	Group	Cell ID	Average	SEM	Average	SEM	Average	SEM	Average	SEM	Average	SEM	Average	SEM
Glutamatergic neuron	HC	190	1.01	0.37	1.10	0.26	0.81	0.12	1.05	0.14	0.78	0.04	1.26	0.04
		226	1.12	0.65	0.73	0.23	1.37	0.52	0.95	0.00	1.20	0.44	1.05	0.16
		272	1.65	1.35	1.55	1.05	4.48	1.12	2.27	0.46	1.37	0.75	2.03	0.67
		367	1.68	1.15	1.51	0.95	0.23	0.05	0.51	0.23	1.35	0.91	0.40	0.06
	SCZ	128	0.55	0.34	1.19	0.66	0.68	0.25	0.93	0.55	1.28	0.56	1.32	0.45
		162	1.12	0.43	0.75	0.12	0.82	0.14	1.13	0.18	1.75	0.53	2.60	0.59
		212	1.02	0.02	0.88	0.58	2.83	1.06	1.18	0.22	1.03	0.06	1.26	0.12
		67	0.55	0.26	0.62	0.48	0.64	0.36	0.65	0.25	1.32	0.83	1.00	0.60

Supplementary Table 6. Break down data table of Fig. 4c and Supplementary Fig. 8e (n= 2 differentiations per cell line)

			PCDHA2		*PCDHA3*		*PCDHA6*		*PCDHA8*		*PCDHG-CR*		*PCDHA-CR*	
Sample	Group	Cell ID	Average	SEM	Average	SEM	Average	SEM	Average	SEM	Average	SEM	Average	SEM
cIN	HC	226	3.84	0.84	2.11	1.33	1.19	0.55	4.76	1.63	2.53	1.94	2.96	2.11
		L9	0.22	0.17	0.45	0.05	0.62	0.25	2.52	1.23	4.05	2.48	1.38	0.40
		365	6.23	0.21	0.51	0.06	0.39	0.09	0.26	0.10	2.09	1.28	2.68	1.39
		L7	0.84	0.18	0.75	0.13	1.75	0.87	1.30	0.38	1.93	0.38	2.58	0.30
		292	1.60	0.31	2.11	0.18	2.07	0.27	2.11	0.04	0.85	0.01	0.72	0.14
		M_139	2.46	2.11	1.50	0.73	2.01	0.21	1.87	0.21	1.06	0.04	0.63	0.17
		367	1.10	0.47	1.89	0.57	1.84	0.25	0.66	0.25	0.12	0.02	0.36	0.09
		107	0.20	0.01	2.28	0.21	1.49	0.99	1.40	1.09	0.86	0.49	1.38	0.95
		190	2.20	0.82	1.62	1.30	2.06	1.39	1.72	1.55	1.59	0.82	1.63	0.84
		99	0.89	0.65	1.61	0.78	2.05	1.67	0.77	0.62	1.57	0.58	0.95	0.05
		272	3.06	1.69	1.56	1.37	1.27	0.40	2.18	1.61	2.38	1.55	0.83	0.12
		PYAUM	1.43	0.75	0.96	0.34	2.47	1.11	0.86	0.40	0.81	0.44	2.93	1.44
		317	0.54	0.35	1.04	0.54	1.13	0.06	0.98	0.42	0.39	0.07	0.52	0.05
		L5	0.63	0.16	0.41	0.12	0.16	0.14	0.49	0.09	0.86	0.05	0.29	0.01
	SCZ	285	0.45	0.23	0.46	0.22	0.57	0.55	0.16	0.03	0.38	0.08	0.79	0.06
		L8	0.16	0.08	0.88	0.04	0.39	0.04	0.43	0.10	1.31	0.05	1.00	0.14
		282	0.17	0.02	1.28	0.46	1.64	0.69	0.95	0.01	0.89	0.11	0.77	0.04
		755	0.60	0.48	0.44	0.12	0.84	0.11	0.67	0.23	0.82	0.01	0.75	0.09
		58	0.25	0.01	0.40	0.37	0.20	0.02	0.45	0.03	0.29	0.05	0.17	0.01
		689	0.38	0.10	0.47	0.02	0.96	0.39	0.13	0.01	0.23	0.22	0.27	0.23
		162	0.32	0.01	0.65	0.35	0.41	0.03	0.71	0.40	0.40	0.00	0.64	0.09
		483	1.07	0.90	0.91	0.39	1.12	0.43	0.49	0.38	0.32	0.07	0.59	0.04
		212	0.94	0.24	0.45	0.01	0.72	0.32	1.43	0.41	0.58	0.39	0.61	0.02
		L10	0.08	0.05	1.10	0.54	1.31	0.91	2.09	0.26	0.06	0.04	0.14	0.04
		128	0.36	0.01	0.41	0.06	0.43	0.38	0.87	0.50	0.33	0.11	0.56	0.10
		117	0.26	0.02	0.36	0.36	1.08	0.65	0.78	0.46	0.25	0.25	0.22	0.21
		67	0.21	0.03	0.46	0.02	0.65	0.18	0.79	0.49	0.41	0.15	0.49	0.40
		1442	0.60	0.39	0.28	0.00	0.22	0.18	0.11	0.06	0.33	0.09	0.30	0.04

Supplementary Table 7. Break down data table of Fig. 5a (n= 20 neurons per mouse).

		Neurite number from soma		Branch number		Neurite length	
Group	Mouse ID	Average	SEM	Average	SEM	Average	SEM
WT	1	5.25	0.30	9.60	0.42	552.34	20.93
	2	4.65	0.29	8.00	0.54	486.92	27.17
	3	5.05	0.30	9.30	0.89	498.73	48.29
	4	4.90	0.24	10.30	0.37	510.30	18.57
	5	4.80	0.30	12.40	0.93	484.07	36.69
KO	1	3.80	0.22	5.90	0.30	321.15	17.14
	2	4.65	0.22	7.90	0.49	444.79	27.32
	3	4.15	0.22	7.00	0.48	345.25	24.99
	4	4.45	0.32	8.85	0.80	349.05	33.81
	5	3.55	0.22	6.15	0.35	278.45	33.63

Supplementary Table 8. Break down data table of Fig. 5b and 5c (n= five 116 µm x 116 µm images per mouse).

		Inhibitory synaptic puncta per 100 µm²		Excitatory synaptic puncta per 100 µm²	
Group	Mouse ID	Average	SEM	Average	SEM
WT	1	38.17	1.77	23.27	5.65
	2	49.50	10.15	26.83	8.85
	3	46.64	7.63	31.60	1.71
	4	27.68	1.78	26.88	6.49
	5	41.39	2.96	41.04	4.17
KO	1	18.38	2.43	36.24	7.21
	2	22.51	3.25	21.98	6.07
	3	27.85	3.57	32.47	3.69
	4	15.11	1.27	54.29	5.68
	5	20.13	1.09	42.07	8.44

Supplementary Table 9. Break down data table of Fig. 6a (n= 20 neurons per cell line).

		Neurite number from soma		Branch number		Neurite length	
Group	Cell ID	Average	SEM	Average	SEM	Average	SEM
HC	272	4.10	0.35	8.80	0.88	1200.55	129.33
	190	3.65	0.23	7.55	0.41	894.11	48.41
	PYAUM	4.05	0.34	10.90	1.41	895.11	109.07
	107	4.45	0.39	8.50	0.78	1638.23	146.48
	99	4.50	0.31	8.90	0.87	1190.18	184.62
	317	4.80	0.43	12.05	1.41	2132.73	238.49
	M_139	5.45	0.58	9.20	1.13	1003.60	125.11
	L7	5.75	0.36	14.45	1.04	1909.93	132.82
	367	5.65	0.28	14.60	1.24	1827.86	141.92
SCZ	128	2.85	0.35	4.45	0.43	548.54	62.05
	67	2.15	0.13	3.45	0.25	319.89	27.77
	755	4.25	0.43	6.60	0.92	634.22	48.01
	117	3.80	0.48	8.35	1.02	1193.97	156.04
	689	4.05	0.33	8.30	1.00	1201.41	133.90
	483	4.35	0.27	7.70	0.54	1001.38	75.02
	285	3.15	0.27	6.30	0.60	833.89	90.13
	162	4.15	0.22	13.15	0.97	1147.54	66.83
	58	3.75	0.39	7.45	0.96	1127.62	156.48

Supplementary Table 10. Break down data table of Fig. 6b (n= 20 neurons per cell line).

			Neurite number from soma		Branch number		Neurite length	
Group	Condition	Cell ID	Average	SEM	Average	SEM	Average	SEM
HC	VEH	190	3.65	0.23	7.55	0.41	522.87	28.31
		L7	5.00	0.34	15.50	1.29	1137.92	85.95
		367	5.35	0.27	21.40	1.86	1545.45	142.76
		PYAUM	4.45	0.27	13.60	1.09	1002.77	79.26
		99	4.80	0.31	17.45	1.32	1206.03	121.12
		107	5.30	0.46	27.60	3.37	1702.06	152.33
		M_139	4.85	0.39	19.30	1.75	1332.62	87.85
		272	6.40	0.41	20.80	1.67	1303.70	70.48
	GO6893	190	4.25	0.19	9.55	0.63	702.13	55.49
		L7	4.35	0.32	14.05	1.45	1125.22	114.50
		367	4.80	0.28	14.80	0.81	1147.60	70.42
		PYAUM	5.25	0.30	18.80	1.44	1183.03	117.32
		99	5.15	0.43	25.65	2.67	1546.61	103.28
		107	4.70	0.30	22.75	2.36	1519.27	126.78
		M_139	4.30	0.33	17.65	2.15	1127.31	76.19
		272	6.45	0.36	17.80	1.35	1360.84	75.89
SCZ	VEH	689	3.95	0.35	6.80	0.52	520.37	39.13
		67	3.65	0.24	6.75	0.66	463.66	46.65
		162	4.45	0.29	13.30	0.94	892.94	47.69
		117	3.90	0.29	10.35	1.02	765.52	68.56
		285	4.35	0.22	12.20	0.83	905.22	95.19
		58	3.95	0.31	15.25	1.55	1178.94	97.86
		755	4.15	0.39	14.80	1.32	1354.89	123.34
		483	3.90	0.24	10.75	0.91	921.64	85.74
	GO6893	689	4.65	0.30	9.25	0.52	674.04	49.36
		67	4.50	0.25	10.25	0.78	740.41	58.12
		162	4.55	0.17	17.35	1.54	1079.18	88.45
		117	4.90	0.40	11.40	1.08	1001.52	84.61
		285	4.70	0.26	13.15	1.22	927.88	49.91
		58	4.90	0.34	17.05	1.27	1633.03	152.35
		755	6.30	0.67	20.55	2.50	1823.33	127.84
		483	4.15	0.32	20.55	2.21	1508.22	155.09

Supplementary Table 11. Break down data table of Fig. 6c (n= 20 neurons per cell line).

Group	siRNA condition	Cell ID	Neurite number from soma		Branch number		Neurite length	
			Average	SEM	Average	SEM	Average	SEM
HC	Negative control	190	3.95	0.26	14.55	1.24	852.71	57.52
		226	3.70	0.26	15.65	1.08	998.63	97.99
		367	3.05	0.26	8.00	0.63	1095.07	127.50
	PCDHA	190	3.05	0.22	8.85	1.07	403.37	41.10
		226	3.45	0.29	11.80	0.89	589.60	40.73
		367	2.00	0.21	4.90	0.33	360.85	43.70
	PCDHG	190	2.35	0.18	5.25	0.49	284.73	19.29
		226	2.40	0.27	8.00	1.03	353.69	50.46
		367	2.50	0.22	5.20	0.44	384.65	55.68
	PCDHA+G	190	2.90	0.29	9.80	0.96	428.82	47.14
		226	3.65	0.17	12.95	1.08	503.98	36.03
		367	2.40	0.21	4.70	0.39	372.70	45.96
SCZ	Negative control	212	3.30	0.19	10.05	0.69	705.96	49.39
		128	2.90	0.28	6.95	0.43	418.60	24.80
		162	3.25	0.27	7.85	0.73	418.16	39.15
	PCDHA	212	3.15	0.21	7.30	0.65	379.02	36.71
		128	3.30	0.22	7.30	0.46	370.26	24.83
		162	2.85	0.23	5.65	0.51	317.71	27.88
	PCDHG	212	3.05	0.17	6.90	0.59	326.73	35.67
		128	2.80	0.22	6.00	0.40	264.42	16.30
		162	2.45	0.21	4.15	0.33	178.22	15.15
	PCDHA+G	212	2.20	0.26	5.90	0.77	303.41	31.05
		128	3.00	0.21	6.55	0.41	295.64	18.77
		162	2.25	0.22	4.40	0.34	214.78	12.64

Supplementary Table 12. Break down data table of Fig. 7f and g (n= two 116 µm x 116 µm images per cell line).

		Inhibitory synaptic puncta per 100 µm²		Excitatory synaptic puncta per 100 µm²	
Group	Cell ID	Average	SEM	Average	SEM
HC	99	18.30	2.60	30.78	1.94
	107	7.90	2.40	13.54	2.86
	190	19.65	3.06	22.63	3.80
	272	10.90	3.05	34.75	3.50
	317	6.75	1.40	41.89	2.80
	PYAUM	14.89	1.36	40.82	6.18
	M_139	16.10	0.20	20.63	1.97
SCZ	67	6.41	0.78	35.00	3.63
	128	8.64	0.99	49.43	13.79
	282	6.48	1.08	20.58	2.66
	483	6.08	1.44	32.58	6.26
	689	10.63	0.41	15.70	0.76
	755	9.33	1.33	42.99	2.93
	L10	12.00	0.74	40.73	3.18

Supplementary Table 13. Break down data table of Fig. 8b (n= 20 neurons per subject).

		Neurite number from soma		Branch number		Neurite length	
Group	Subject ID	Average	SEM	Average	SEM	Average	SEM
HC	10040	4.80	0.22	17.35	0.75	413.07	12.80
	10477	5.20	0.26	13.55	0.55	397.84	12.54
	16799	5.65	0.23	12.60	0.34	379.76	17.63
	8536	6.75	0.30	15.40	0.61	473.15	16.72
	6325	4.30	0.19	16.40	0.87	724.22	25.32
	4228	4.55	0.20	16.30	0.58	448.35	15.24
	5723	4.60	0.22	16.20	0.58	408.49	17.61
	13237	5.20	0.26	18.70	0.86	455.27	14.43
SCZ	10963	3.70	0.23	11.85	0.60	253.99	12.61
	853	3.40	0.21	10.20	0.52	212.52	10.94
	3019	3.50	0.22	7.55	0.54	165.05	13.26
	12413	3.60	0.23	12.50	0.37	336.44	9.36
	10308	3.70	0.21	12.95	0.58	497.91	22.81
	13097	4.40	0.22	16.40	0.56	361.83	23.59
	1545	3.85	0.20	15.55	0.81	402.64	22.85
	2464	3.65	0.18	13.80	0.56	347.35	12.85

Supplementary Table 14. Break down data table of Fig. 8c and d (n= four 116 µm x 116 µm images per subject).

		Inhibitory synaptic puncta per 100 µm²		Excitatory synaptic puncta per 100 µm²	
Group	Subject ID	Average	SEM	Average	SEM
HC	10040	26.74	5.62	16.94	2.27
	10477	16.54	1.80	15.50	3.08
	16799	30.48	0.90	20.05	1.72
	8536	23.85	2.25	22.18	0.46
	6325	32.45	1.78	22.77	1.43
	4228	12.12	0.85	42.53	1.34
	5723	21.52	1.40	35.93	1.74
	13237	24.95	2.47	14.77	0.81
SCZ	10963	15.36	3.51	9.03	1.51
	853	17.69	2.30	15.18	2.43
	3019	18.93	0.46	17.19	1.29
	12413	20.90	0.28	14.71	2.11
	10308	12.67	3.64	15.72	2.68
	13097	13.41	0.66	16.97	1.76
	1545	15.51	2.00	12.88	0.54
	2464	12.81	1.11	16.94	1.20

Supplementary Table 15. Summary of statistical analysis of electrophysiological data. *Related to Figure 2 and Supplementary Fig. 3 and 5.*

Response variable	n (cells)		Shapiro-Wilk test (p-value)	Data transformation	Test used (two-sided)	p-value
	HC	SCZ				
Membrane resistance	22	24	0.0001	log-transformed	Linear Mixed Effect Model	0.6462
Membrane capacitance	22	24	0.0001	log-transformed	Linear Mixed Effect Model	0.8979
K+ current density	12	12	0.2864	untransformed	Linear Mixed Effect Model	0.2587
Na+ current density	12	10	0.4591	untransformed	Linear Mixed Effect Model	0.1051
Resting membrane potential	18	20	0.0046	log-transformed	Linear Mixed Effect Model	0.0465
Afterhyperpolarization	14	18	0.6403	untransformed	Linear Mixed Effect Model	0.7822
AP threshold	14	18	0.8151	untransformed	Linear Mixed Effect Model	0.5417
AP half-width	9	13	0.1390	untransformed	Linear Mixed Effect Model	0.9117
sAP frequency	14	13	0.0011	log-transformed	Linear Mixed Effect Model	0.3358
sEPSC frequency	12	14	0.0001	log-transformed	Linear Mixed Effect Model	0.7657
sEPSC amplitude	12	14	0.1613	log-transformed	Linear Mixed Effect Model	0.3737
IPSC amplitude	15	13	0.0003	log-transformed	Linear Mixed Effect Model	0.3734

Supplementary Table 16. Summary of statistical analysis of gene expression data. *Related to Figure 3, 4 and Supplementary Fig. 8.*

Sample	Gene name	n (differentiations)	Shapiro-Wilk's test (p-value)	data transformation	Test used (two sided)	p-value
cIN	*PCDHA2*	12	0.0100	log-transformed	Linear Mixed Effect Model	0.0179
glutamatergic neuron	*PCDHA2*	8	0.0133	log-transformed	Linear Mixed Effect Model	0.3663
glutamatergic neuron	*PCDHA3*	8	0.0520	untransformed	Linear Mixed Effect Model	0.3524
glutamatergic neuron	*PCDHA6*	8	0.0010	log-transformed	Linear Mixed Effect Model	0.9039
glutamatergic neuron	*PCDHA8*	8	0.0586	untransformed	Linear Mixed Effect Model	0.5903
glutamatergic neuron	*PCDHA-CR*	8	0.0280	log-transformed	Linear Mixed Effect Model	0.5607
glutamatergic neuron	*PCDHG-CR*	8	0.1824	untransformed	Linear Mixed Effect Model	0.4847
cIN	*PCDHA2*	28	0.0001	log-transformed	Linear Mixed Effect Model	0.0009
cIN	*PCDHA3*	28	0.0001	log-transformed	Linear Mixed Effect Model	0.0085
cIN	*PCDHA6*	28	0.0001	log-transformed	Linear Mixed Effect Model	0.0362
cIN	*PCDHA8*	28	0.0001	log-transformed	Linear Mixed Effect Model	0.0234
cIN	*PCDHA-CR*	28	0.0001	log-transformed	Linear Mixed Effect Model	0.0016
cIN	*PCDHG-CR*	28	0.0001	log-transformed	Linear Mixed Effect Model	0.0021

Supplementary Table 17. Summary of statistical analysis of phenotype data. *Related to Figure 5-8.*

Data	Experiment	n	Shapiro-Wilk's test (p-value)	Data transformation	Test used (two sided)	p-value
Fig. 5a	Neurite length	100 neurons	0.0000	untransformed	Linear Mixed Effect Model	0.0001
Fig. 5a	Branch number	100 neurons			Mixed Effect Log-Linear Model	0.001
Fig. 5a	Neurite number from soma	100 neurons			Mixed Effect Log-Linear Model	0.008
Fig. 5b	Inhibitory synaptic puncta	25 images	0.0000	untransformed	Linear Mixed Effect Model	0.0001
Fig. 5c	Excitatory synaptic puncta	25 images	0.0840	untransformed	Linear Mixed Effect Model	0.2316
Fig. 6a	Neurite length	180 neurons	0.0001	log-transformed	Linear Mixed Effect Model	0.0088
Fig. 6a	Branch number	180 neurons			Mixed Effect Log-Linear Model	0.0049
Fig. 6a	Neurite number from soma	180 neurons			Mixed Effect Log-Linear Model	0.0013
Fig. 6b	Neurite length of HC	160 neurons	0.0001	log-transformed	Two-Level Hierarchical Linear Mixed Effect Model	0.7024
Fig. 6b	Neurite length of SCZ	160 neurons	0.0001	log-transformed	Two-Level Hierarchical Linear Mixed Effect Model	0.0001
Fig. 6b	Branch number of HC	160 neurons			Two-Level Hierarchical Mixed Effect Log-Linear Model	0.8293
Fig. 6b	Branch number of SCZ	160 neurons			Two-Level Hierarchical Mixed Effect Log-Linear Model	0.0001
Fig. 6b	Neurite number from soma of HC	160 neurons			Two-Level Hierarchical Mixed Effect Log-Linear Model	0.6545
Fig. 6b	Neurite number from soma of SCZ	160 neurons			Two-Level Hierarchical Mixed Effect Log-Linear Model	0.0001
Fig. 7f	Inhibitory synaptic puncta	14 images	0.0540	untransformed	Linear Mixed Effect Model	0.0324
Fig. 7g	Excitatory synaptic puncta	14 images	0.4561	untransformed	Linear Mixed Effect Model	0.4679
Fig. 8b	Neurite length	160 neurons	0.0001	log-transformed	Linear Mixed Effect Model	0.0050
Fig. 8b	Branch number	160 neurons			Mixed Effect Log-Linear Model	0.0077
Fig. 8b	Neurite number from soma	160 neurons			Mixed Effect Log-Linear Model	0.0001
Fig. 8c	Inhibitory synaptic puncta	32 images	0.0430	log-transformed	Linear Mixed Effect Model	0.0073
Fig. 8d	Excitatory synaptic puncta	32 images	0.0001	log-transformed	Linear Mixed Effect Model	0.0086

Supplementary Table 18. Summary of statistical analysis of phenotype data after siRNA transfection. *Related to Figure 6c.*

Experiment	n (neurons)	Comparison	Shapiro-Wilk's test (p-value)	Data transformation	Test used (two sided)	Adj. p-value
Neurite length of HC	60	Overall	0.0001	log-transformed	Two-Level Hierarchical Linear Mixed Effect Model	0.0001
		Negative Cont. vs. PCDHA			Dunnett's multiple comparison test	0.0001
		Negative Cont. vs. PCDHG			Dunnett's multiple comparison test	0.0001
		Negative Cont. vs. PCDHA+G			Dunnett's multiple comparison test	0.0001
Branch number of HC	60	Overall			Two-Level Hierarchical Mixed Effect Log-Linear Model	0.0001
		Negative Cont. vs. PCDHA			Dunnett's multiple comparison test	0.0001
		Negative Cont. vs. PCDHG			Dunnett's multiple comparison test	0.0001
		Negative Cont. vs. PCDHA+G			Dunnett's multiple comparison test	0.0001
Neurite number from soma of HC	60	Overall			Two-Level Hierarchical Mixed Effect Log-Linear Model	0.0039
		Negative Cont. vs. PCDHA			Dunnett's multiple comparison test	0.0698
		Negative Cont. vs. PCDHG			Dunnett's multiple comparison test	0.0011
		Negative Cont. vs. PCDHA+G			Dunnett's multiple comparison test	0.1976
Neurite length of SCZ	60	Overall	0.0001	log-transformed	Two-Level Hierarchical Linear Mixed Effect Model	0.0001
		Negative Cont. vs. PCDHA			Dunnett's multiple comparison test	0.0001
		Negative Cont. vs. PCDHG			Dunnett's multiple comparison test	0.0001
		Negative Cont. vs. PCDHA+G			Dunnett's multiple comparison test	0.0001
Branch number of SCZ	60	Overall			Two-Level Hierarchical Mixed Effect Log-Linear Model	0.0001
		Negative Cont. vs. PCDHA			Dunnett's multiple comparison test	0.0072
		Negative Cont. vs. PCDHG			Dunnett's multiple comparison test	0.0001
		Negative Cont. vs. PCDHA+G			Dunnett's multiple comparison test	0.0001
Neurite number from soma of SCZ	60	Overall			Two-Level Hierarchical Mixed Effect Log-Linear Model	0.1118
		Negative Cont. vs. PCDHA			Dunnett's multiple comparison test	0.9975
		Negative Cont. vs. PCDHG			Dunnett's multiple comparison test	0.4811
		Negative Cont. vs. PCDHA+G			Dunnett's multiple comparison test	0.0812