Supplementary Materials

Human iPSC glial mouse chimeras reveal glial contributions to schizophrenia

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SUPPLEMENTARY FIGURES

Figure S1 *(related to Figures 1, 2 and 4)*

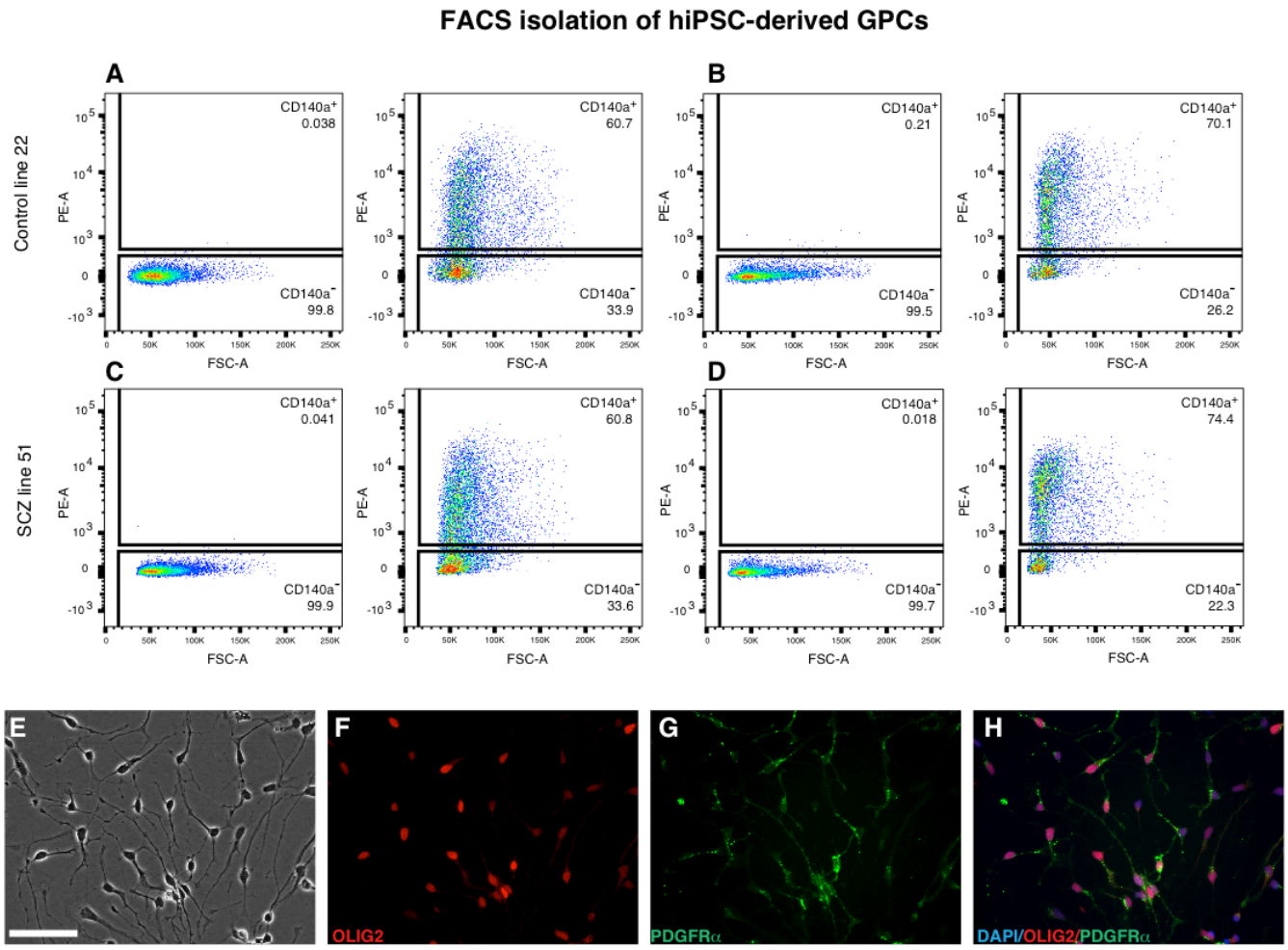


Figure S1

CD140a$^+$ glial progenitor cells could be efficiently produced from both SCZ and normal hiPSCs

Flow cytometry for CD140a/PDGFαR$^+$ glial progenitor cells (*right* plots, compared to unstained gating controls on *left*), reveals dominant proportions of CD140a-defined cells in both normal control patient-derived (*top*, **A-B**) and SCZ-derived (*bottom,* **C-D**) preparations. **A-C** and **B-D** were run as matched pairs; **A** and **C**, 177 and 168 days in vitro (DIV); **B** and **D**, 188 and 196 DIV. **E-H** show a representative post-FACS preparation of CD140a-sorted cells, as **E**, a phase image, immunostained for both olig2 (**F**, *red*) and PDGFRα (**G; H**, *merged*). These plots were typical of GPC cultures of both normal and SCZ-derived hiPSC lines. The sorted populations were used for genomics assessment, while both sorted and unsorted cells were used for transplantation, with no evident performance differences between the two.

Figure S2 *(related to Figure 2)*

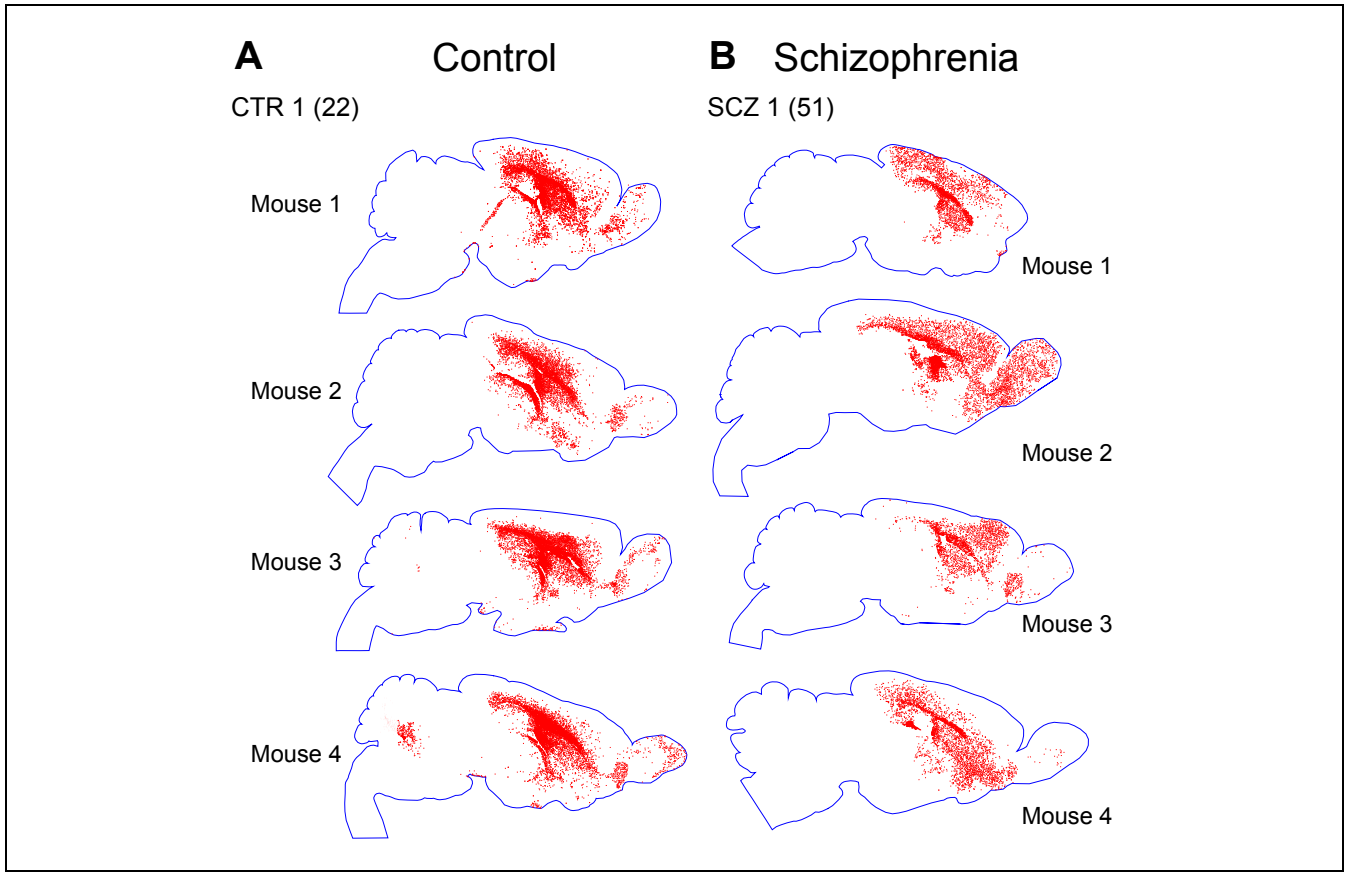


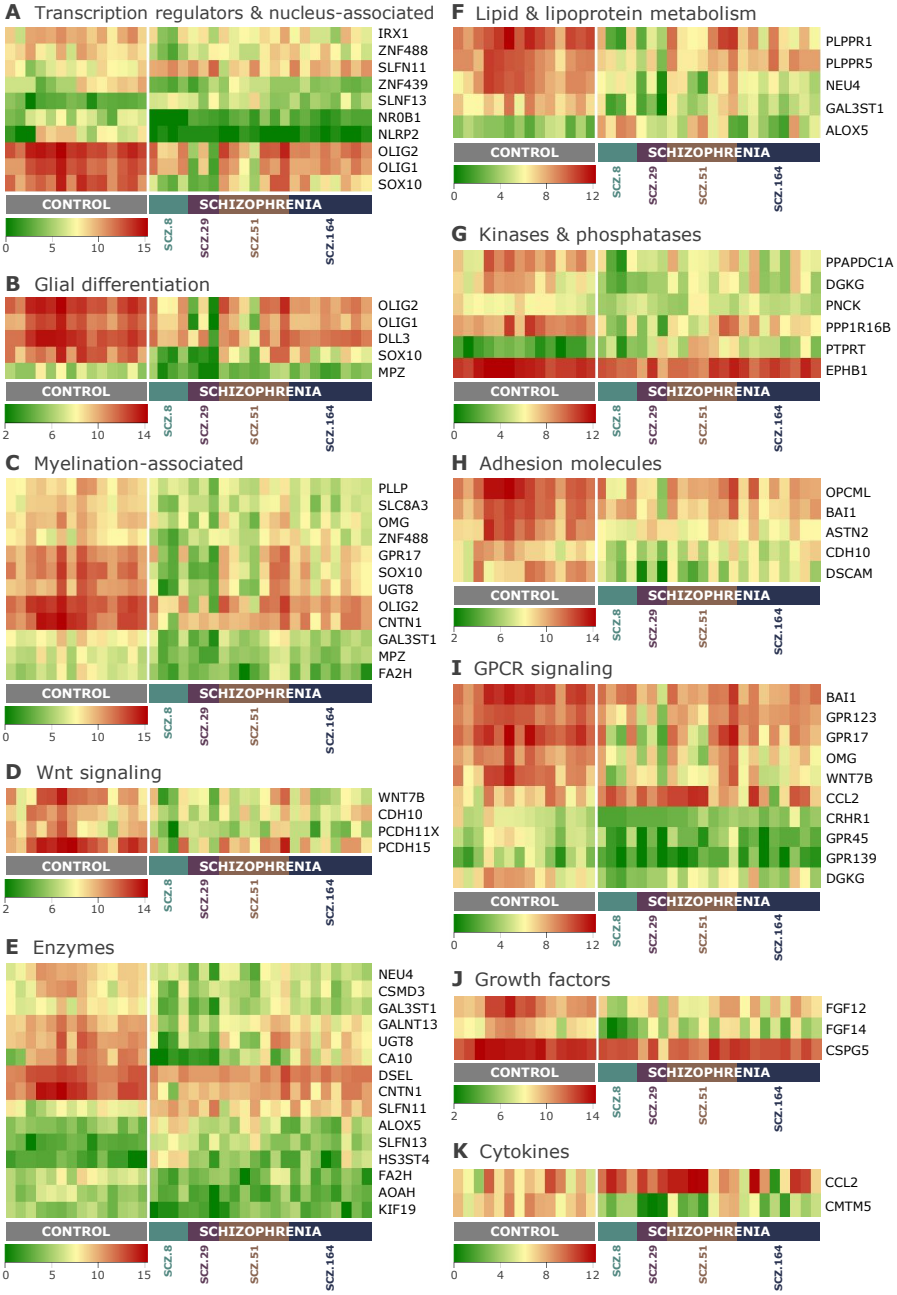
Figure S2

Schizophrenia-derived GPCs exhibit aberrant dispersal in vivo

The dispersal patterns of GPCs produced from SCZ patients typically differed from that of iPSC hGPCs derived from normal patients, in that SCZ GPCs did not remain and expand within the white matter before progressing to cortical infiltration, as was otherwise invariably the case with normal GPCs. A-B show 4 mice each implanted with either control subject-derived (line 22) or SCZ patient-derived (line 51) hGPCs. All SCZ hGPC-engrafted mice show disproportionate hGPC entry into the cortical and striatal gray matter, with less expansion and hence less net engraftment in the forebrain white matter tracts. This difference in hGPC dispersal pattern was noted consistently in all 4 SCZ lines assessed in vivo, each derived from a different patient, relative to their matched 4 control lines, similarly obtained from distinct patients (see **Figure 2**).

Figure S3 *(related to Figure 4)*

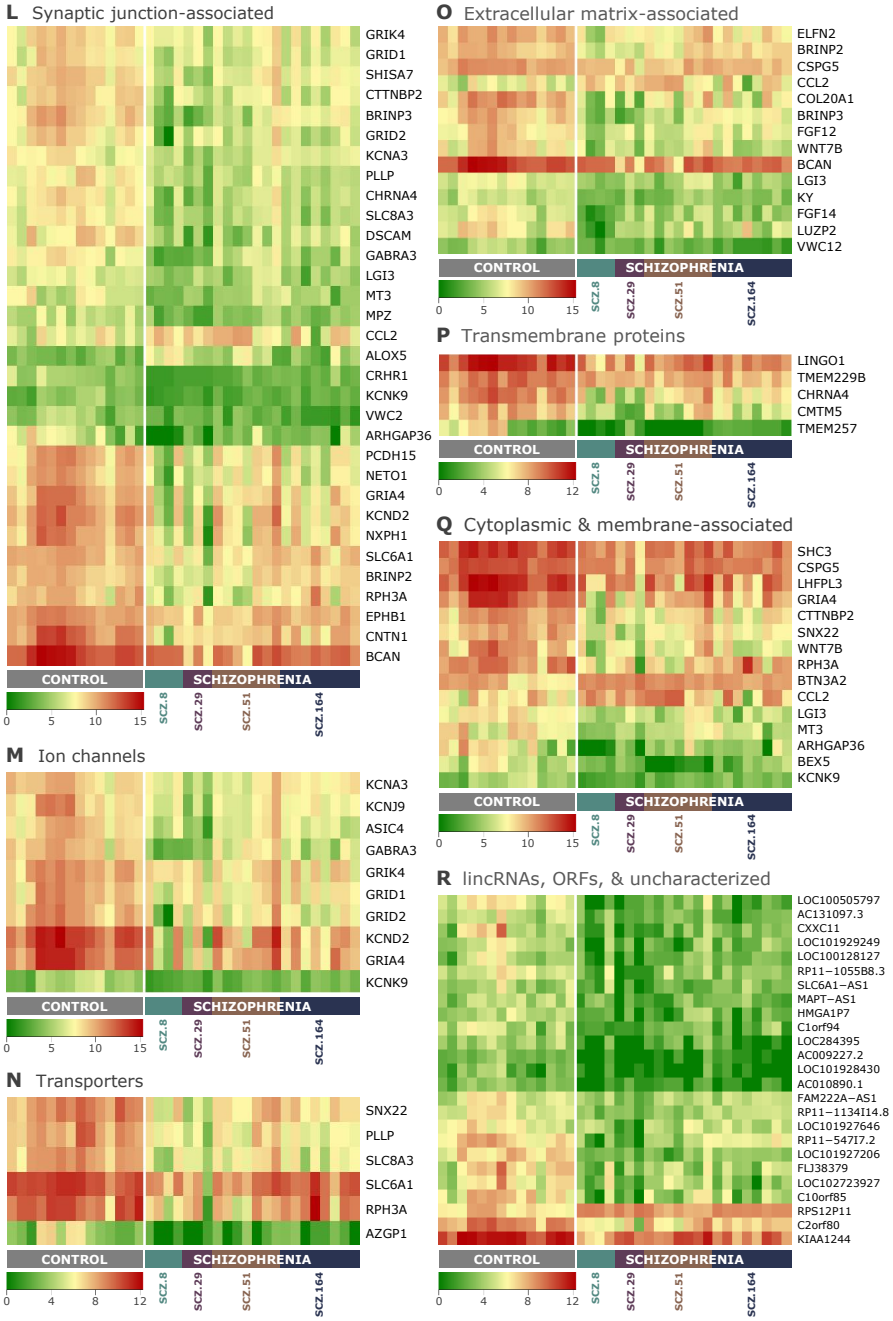
Heat maps of significantly dysregulated genes in schizophrenic relative to control hiPSC GPCs



Expression patterns for shared genes differentially expressed by hiPSC GPCs derived from 4 schizophrenic patients, relative to the pooled gene expression pattern of hGPCs derived from 3 control-derived iPSCs (log2 fold change >1.0, FDR 5%, 118 genes total). The dysregulated genes were manually annotated and grouped into relevant sets based on their function and cellular localization. Each heat map visualizes UQ-normalized, log2-transformed counts of genes grouped into the following functional categories, comprising genes encoding: **(A)** transcription regulators, zinc finger proteins, and other nucleus-associated proteins; **(B)** glial differentiation-associated proteins; **(C)** myelin-related genes and transcription factors; **(D)** Wnt pathway effectors; **(E)** metabolic enzymes; **(F)** lipid and lipoprotein metabolism; **(G)** kinases and phosphatases; **(H)** adhesion molecules, cadherins; and astrotactins; **(I)** GPCR signal intermediates; **(J)** growth factors; and **(K)** cytokines.

Figure S4 *(related to Figure 4)*

Additional heat maps of significantly dysregulated genes in SCZ relative to control hGPCs

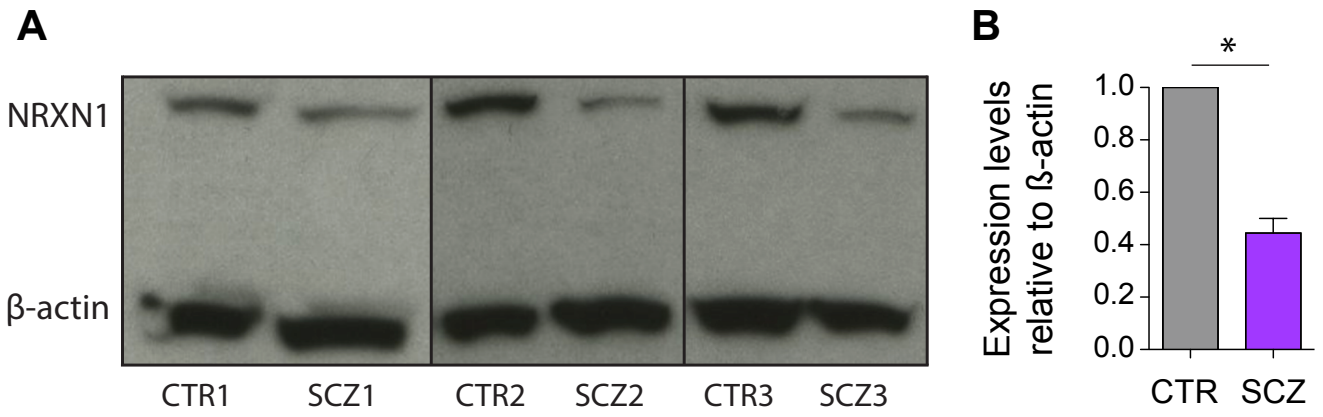


Additional heat maps of significantly dysregulated genes in SCZ relative to control hGPCs

As in **Figure S3**, expression patterns for genes differentially expressed by hiPSC GPCs derived from 4 SCZ patients, relative to the pooled gene expression pattern of hGPCs derived from 3 control-derived iPSCs (log2-fold change >1.0, FDR 5%, 118 genes total). As in **Figure S3**, which is derived from the same data set, each heat map visualizes UQ-normalized, log2-transformed counts of differentially expressed genes. These are grouped into the following functional categories, which follow those listed in **Figure S3**: **(L)** cell signaling and synaptic proteins; **(M)** ion channels; **(N)** transporters; **(O)** extracellular matrix constituents; **(P)** other transmembrane proteins; **(Q)** other cytoplasmic and membrane-bound proteins; and **(R)** unannotated genes, open reading frames, and long intergenic non-coding RNAs.

Figure S5 *(related to Figure 5)*

Neurexin-1 expression was suppressed in SCZ hiPSC GPCs



A, Western blots revealed that neurexin-1 protein was abundantly expressed by human GPCs purified by CD140a-directed FACS, and that neurexin-1 levels were lower in otherwise matched SCZ hGPCs (line 51 SCZ hGPCs vs. line 22 CTRL hGPCs). **B,** Quantitative densitometry revealed the significant decrease in neurexin1 protein expression by SCZ hGPCs relative to their CTR hGPCs. *p<0.05, Student's t-test.

SUPPLEMENTARY TABLES

Table S1 (*related to Figure 1*)

Patients and cell lines used in this study

Subject number	hiPSC Line(s)	Age of subject	Gender	Ethnicity	RNA-Seq of CD140a^{+} GPCs	Anatomic assessment N=shiverer mice	Behavioral assessment N=myelin w/t mice
	Control Subjects						
Cntrl 1	**19, 22**	26	M	C	√	√	√
Cntrl 2	**37**	32	F	AA	√	√	√
Cntrl 3	**205**	25	M	C	√	√	√
Cntrl 4	**C27**	NA	NA	NA	√	√	
	Schizophrenic Subjects						
SCZ 1	**8**	10	F	C	√	√	
SCZ 2	**51, 52**	16	M	C	√	√	√
SCZ 3	**29, 31**	12	M	C	√		√
SCZ 4	**164**	14	F	AA	√	√	
SCZ 5	**193**	15	F	NA		√	√

A total of 11 new independent iPS cell lines were derived from 8 subjects; 5 juvenile-onset schizophrenic patients and 3 healthy controls; an established control line (C27) from an additional normal subject was published previously (Chambers et al., 2009; Wang et al., 2013), and graciously provided by L. Studer. hGPCs derived from these cells were assigned to individual experiments as noted. C, Caucasian; AA, African-American; NA, not available.

Table S2 (*related to Figure 4*)

Significantly dysregulated genes in schizophrenic relative to control GPCs

These tables list shared genes differentially expressed by hiPSC GPCs derived from 4 SCZ patients, relative to the pooled gene expression pattern of hGPCs from 3 control-derived iPSCs (log2 fold change >1.0, FDR 5%, 116 genes total, *red*, upregulated in SCZ vs CTRL; *green*, downregulated in SCZ GPCs). The fold- changes (FC) and FDR-adjusted *p* values shown here were derived from the comparison of the pooled SCZ-derived GPC lines to the pooled control-derived GPC lines. Dysregulated genes were grouped into functional sets by their cellular roles and localizations.

Gene ID	*Log2 FC*	*P Value*	*Entrez Gene Name*
Transcription regulators, & nucleus-associated (10 genes)			
SLFN13	2.832	2.18E-13	schlafen family member 13
SLFN11	2.193	6.47E-09	schlafen family member 11
NLRP2	-7.208	4.24E-58	NLR family, pyrin domain containing 2
SOX10	-4.448	8.37E-19	SRY-box 10
NR0B1	-3.321	5.92E-27	nuclear receptor subfamily 0 group B member 1
OLIG2	-3.196	4.23E-19	oligodendrocyte lineage transcription factor 2
OLIG1	-3.146	5.72E-22	oligodendrocyte transcription factor 1
ZNF439	-2.139	6.14E-08	zinc finger protein 439
IRX1	-1.815	5.52E-06	iroquois homeobox 1
ZNF488	-1.464	4.44E-07	zinc finger protein 488
Glial differentiation (5 genes)			
SOX10	-4.448	8.37E-19	SRY-box 10
OLIG2	-3.196	4.23E-19	oligodendrocyte lineage transcription factor 2
OLIG1	-3.146	5.72E-22	oligodendrocyte transcription factor 1
DLL3	-2.352	2.09E-24	delta-like 3 (Drosophila)
MPZ	-2.105	7.66E-13	myelin protein zero
Myelination-associated (12 genes)			
SOX10	-4.448	8.37E-19	SRY-box 10
GPR17	-3.357	1.94E-10	G protein-coupled receptor 17
UGT8	-3.250	4.36E-09	UDP glycosyltransferase 8
OLIG2	-3.196	4.23E-19	oligodendrocyte lineage transcription factor 2
GAL3ST1	-2.681	4.01E-12	galactose-3-O-sulfotransferase 1
CNTN1	-2.675	5.65E-15	contactin 1
PLLP	-2.581	1.21E-24	plasmolipin
OMG	-2.561	5.09E-12	oligodendrocyte myelin glycoprotein
FA2H	-2.440	4.45E-08	fatty acid 2-hydroxylase
SLC8A3	-2.224	2.00E-12	solute carrier family 8 (sodium/calcium exchanger), member 3
MPZ	-2.105	7.66E-13	myelin protein zero
ZNF488	-1.464	4.44E-07	zinc finger protein 488
Wnt signaling (4 genes)			
WNT7B	-2.626	1.46E-07	wingless-type MMTV integration site family member 7B
PCDH15	-2.530	1.42E-10	protocadherin-related 15
PCDH11X	-2.364	1.25E-08	protocadherin 11 X-linked
CDH10	-1.646	9.33E-07	cadherin 10
Enzymes (15 genes)			
SLFN13	2.832	2.18E-13	schlafen family member 13
SLFN11	2.193	6.47E-09	schlafen family member 11
HS3ST4	2.149	1.44E-04	heparan sulfate-glucosamine 3-sulfotransferase 4
ALOX5	1.777	2.35E-05	arachidonate 5-lipoxygenase
CA10	-3.550	3.07E-08	carbonic anhydrase X
NEU4	-3.361	8.31E-40	neuraminidase 4 (sialidase)
UGT8	-3.250	4.36E-09	UDP glycosyltransferase 8
GAL3ST1	-2.681	4.01E-12	galactose-3-O-sulfotransferase 1
CNTN1	-2.675	5.65E-15	contactin 1
CSMD3	-2.560	5.78E-10	CUB and Sushi multiple domains 3
GALNT13	-2.467	2.80E-11	polypeptide N-acetylgalactosaminyltransferase 13
FA2H	-2.440	4.45E-08	fatty acid 2-hydroxylase
AOAH	-2.271	2.99E-12	acyloxyacyl hydrolase
KIF19	-1.644	5.10E-06	kinesin family member 19
DSEL	-1.151	1.35E-10	dermatan sulfate epimerase-like
Lipid & lipoprotein metabolism (5 genes)			
ALOX5	1.777	2.35E-05	arachidonate 5-lipoxygenase
NEU4	-3.361	8.31E-40	neuraminidase 4 (sialidase)
GAL3ST1	-2.681	4.01E-12	galactose-3-O-sulfotransferase 1
PLPPR1	-2.652	1.16E-09	phospholipid phosphatase related 1
PLPPR5	-1.573	1.69E-09	phospholipid phosphatase related 5

Kinases & phosphatases (6 genes)

PTPRT	4.410	1.69E-17	protein tyrosine phosphatase, receptor type T
PPP1R16B	-2.665	1.29E-09	protein phosphatase 1 regulatory subunit 16B
PPAPDC1A	-2.357	6.76E-09	phospholipid phosphatase 4
DGKG	-2.306	9.29E-12	diacylglycerol kinase gamma
EPHB1	-1.344	3.89E-17	EPH receptor B1
PNCK	-1.226	4.25E-08	pregnancy up-regulated nonubiquitous CaM kinase

Adhesion molecules (5 genes)

DSCAM	-3.148	1.58E-12	Down syndrome cell adhesion molecule
ASTN2	-2.242	4.70E-21	astrotactin 2
OPCML	-2.099	7.87E-10	opioid binding protein/cell adhesion molecule-like
BAI1	-2.000	1.31E-12	adhesion G protein-coupled receptor B1
CDH10	-1.646	9.33E-07	cadherin 10

GPCR signaling (10 genes)

CCL2	1.832	1.97E-07	chemokine (C-C motif) ligand 2
GPR17	-3.357	1.94E-10	G protein-coupled receptor 17
GPR45	-2.895	2.95E-14	G protein-coupled receptor 45
WNT7B	-2.626	1.46E-07	wingless-type MMTV integration site family member 7B
GPR139	-2.589	1.32E-08	G protein-coupled receptor 139
OMG	-2.561	5.09E-12	oligodendrocyte myelin glycoprotein
CRHR1	-2.382	5.81E-12	corticotropin releasing hormone receptor 1
DGKG	-2.306	9.29E-12	diacylglycerol kinase gamma
BAI1	-2.000	1.31E-12	adhesion G protein-coupled receptor B1
GPR123	-1.807	1.76E-18	adhesion G protein-coupled receptor A1

Growth factors (3 genes)

FGF14	-2.021	5.14E-07	fibroblast growth factor 14
FGF12	-1.988	5.47E-09	fibroblast growth factor 12
CSPG5	-1.285	6.38E-17	chondroitin sulfate proteoglycan 5

Cytokines (2 genes)

CCL2	1.832	1.97E-07	chemokine (C-C motif) ligand 2
CMTM5	-3.023	3.69E-15	CKLF-like MARVEL transmembrane domain containing 5

Synaptic-junction associated (32 genes)

CCL2	1.832	1.97E-07	chemokine (C-C motif) ligand 2
ALOX5	1.777	2.35E-05	arachidonate 5-lipoxygenase
BRINP3	-3.433	4.70E-22	bone morphogenetic protein/retinoic acid inducible neural-specific 3
DSCAM	-3.148	1.58E-12	Down syndrome cell adhesion molecule
KCND2	-3.145	5.67E-11	potassium channel, voltage gated Shal related subfamily D, member 2
NXPH1	-2.892	3.11E-15	neurexophilin 1
CHRNA4	-2.755	4.45E-14	cholinergic receptor, nicotinic alpha 4
ARHGAP36	-2.686	1.21E-05	Rho GTPase activating protein 36
CNTN1	-2.675	5.65E-15	contactin 1
NETO1	-2.633	2.52E-12	neuropilin and tolloid like 1
PLLP	-2.581	1.21E-24	plasmolipin
PCDH15	-2.530	1.42E-10	protocadherin-related 15
GRIA4	-2.519	1.84E-09	glutamate receptor, ionotropic, AMPA 4
BCAN	-2.473	7.35E-32	brevican
GABRA3	-2.450	1.08E-12	gamma-aminobutyric acid (GABA) A receptor, alpha 3
CRHR1	-2.382	5.81E-12	corticotropin releasing hormone receptor 1
SHISA7	-2.302	1.43E-14	shisa family member 7
SLC8A3	-2.224	2.00E-12	solute carrier family 8 (sodium/calcium exchanger), member 3
MPZ	-2.105	7.66E-13	myelin protein zero
GRID2	-2.055	3.65E-06	glutamate receptor, ionotropic, delta 2
RPH3A	-2.014	1.01E-06	rabphilin 3A
VWC2	-2.003	9.67E-13	von Willebrand factor C domain containing 2
CTTNBP2	-1.904	7.21E-08	cortactin binding protein 2
MT3	-1.795	5.27E-09	metallothionein 3
KCNA3	-1.719	3.03E-12	potassium channel, voltage gated shaker related subfamily A, member 3
BRINP2	-1.625	2.03E-12	bone morphogenetic protein/retinoic acid inducible neural-specific 2
LGI3	-1.614	4.07E-08	leucine-rich repeat LGI family member 3
SLC6A1	-1.596	5.52E-11	solute carrier family 6 (neurotransmitter transporter), member 1
GRID1	-1.562	7.61E-07	glutamate receptor, ionotropic, delta 1
GRIK4	-1.547	2.73E-07	glutamate receptor, ionotropic, kainate 4
KCNK9	-1.460	4.40E-06	potassium channel, two pore domain subfamily K, member 9
EPHB1	-1.344	3.89E-17	EPH receptor B1

Ion channels (10 genes)

KCND2	-3.145	5.67E-11	potassium channel, voltage gated Shal related subfamily D, member 2
GRIA4	-2.519	1.84E-09	glutamate receptor, ionotropic, AMPA 4
GABRA3	-2.450	1.08E-12	gamma-aminobutyric acid (GABA) A receptor, alpha 3
ASIC4	-2.321	4.13E-14	acid sensing ion channel subunit family member 4
KCNJ9	-2.187	2.85E-21	potassium channel, inwardly rectifying subfamily J, member 9
GRID2	-2.055	3.65E-06	glutamate receptor, ionotropic, delta 2
KCNA3	-1.719	3.03E-12	potassium channel, voltage gated shaker related subfamily A, member 3
GRID1	-1.562	7.61E-07	glutamate receptor, ionotropic, delta 1
GRIK4	-1.547	2.73E-07	glutamate receptor, ionotropic, kainate 4
KCNK9	-1.460	4.40E-06	potassium channel, two pore domain subfamily K, member 9

Transporters (6 genes)

AZGP1	-3.323	1.66E-08	alpha-2-glycoprotein 1, zinc-binding
PLLP	-2.581	1.21E-24	plasmolipin
SNX22	-2.297	3.53E-20	sorting nexin 22
SLC8A3	-2.224	2.00E-12	solute carrier family 8 (sodium/calcium exchanger), member 3
RPH3A	-2.014	1.01E-06	rabphilin 3A
SLC6A1	-1.596	5.52E-11	solute carrier family 6 (neurotransmitter transporter), member 1

Extracellular matrix-associated (14 genes)

CCL2	1.832	1.97E-07	chemokine (C-C motif) ligand 2
COL20A1	-3.476	7.33E-14	collagen, type XX, alpha 1
BRINP3	-3.433	4.70E-22	bone morphogenetic protein/retinoic acid inducible neural-specific 3
WNT7B	-2.626	1.46E-07	wingless-type MMTV integration site family member 7B
BCAN	-2.473	7.35E-32	brevican
FGF14	-2.021	5.14E-07	fibroblast growth factor 14
VWC2	-2.003	9.67E-13	von Willebrand factor C domain containing 2
FGF12	-1.988	5.47E-09	fibroblast growth factor 12
LUZP2	-1.948	7.22E-06	leucine zipper protein 2
ELFN2	-1.943	1.47E-06	extracellular Leu-rich repeat and fibronectin type III domain containing 2
KY	-1.873	2.41E-13	kyphoscoliosis peptidase
BRINP2	-1.625	2.03E-12	bone morphogenetic protein/retinoic acid inducible neural-specific 2
LGI3	-1.614	4.07E-08	leucine-rich repeat LGI family member 3
CSPG5	-1.285	6.38E-17	chondroitin sulfate proteoglycan 5

Transmembrane proteins (5 genes)

TMEM257	-4.018	5.58E-23	transmembrane protein 257
CMTM5	-3.023	3.69E-15	CKLF-like MARVEL transmembrane domain containing 5
CHRNA4	-2.755	4.45E-14	cholinergic receptor, nicotinic alpha 4
LINGO1	-2.139	3.56E-14	leucine-rich repeat and Ig domain containing 1
TMEM229B	-1.187	7.76E-06	transmembrane protein 229B

Cytoplasmic & membrane-associated (15 genes)

CCL2	1.832	1.97E-07	chemokine (C-C motif) ligand 2
BTN3A2	1.355	8.10E-20	butyrophilin subfamily 3 member A2
BEX5	-3.885	2.55E-21	brain expressed X-linked 5
ARHGAP36	-2.686	1.21E-05	Rho GTPase activating protein 36
WNT7B	-2.626	1.46E-07	wingless-type MMTV integration site family member 7B
GRIA4	-2.519	1.84E-09	glutamate receptor, ionotropic, AMPA 4
SNX22	-2.297	3.53E-20	sorting nexin 22
LHFPL3	-2.250	1.71E-07	lipoma HMGIC fusion partner-like 3
RPH3A	-2.014	1.01E-06	rabphilin 3A
CTTNBP2	-1.904	7.21E-08	cortactin binding protein 2
SHC3	-1.830	7.88E-19	SHC (Src homology 2 domain containing) transforming protein 3
MT3	-1.795	5.27E-09	metallothionein 3
LGI3	-1.614	4.07E-08	leucine-rich repeat LGI family member 3
KCNK9	-1.460	4.40E-06	potassium channel, two pore domain subfamily K, member 9
CSPG5	-1.285	6.38E-17	chondroitin sulfate proteoglycan 5

lincRNAs, ORFs, & uncharacterized (25 genes)

RPS12P11	1.647	9.02E-30	not available
LOC101927206	-3.592	2.74E-63	not available
LOC100505797	-3.266	3.10E-27	myosin heavy chain IB-like
C10orf85	-3.081	3.52E-10	long intergenic non-protein coding RNA 1561
CXXC11	-2.814	7.70E-19	receptor (chemosensory) transporter protein 5 (putative)
LOC284395	-2.792	1.20E-10	uncharacterized LOC284395
RP11-547I7.2	-2.779	4.81E-34	not available
AC009227.2	-2.758	3.05E-13	not available
LOC101928430	-2.691	5.56E-10	not available
FLJ38379	-2.389	1.25E-15	not available
LOC102723927	-2.363	7.74E-21	uncharacterized LOC102723927
RP11-1055B8.3	-2.336	1.02E-16	not available
AC131097.3	-2.180	5.80E-16	not available
C1orf94	-2.077	7.03E-11	chromosome 1 open reading frame 94
HMGA1P7	-2.057	4.49E-09	high mobility group AT-hook 1 pseudogene 7
LOC101929249	-2.003	1.52E-06	uncharacterized LOC101929249
LOC101927646	-2.001	1.22E-10	uncharacterized LOC101927646
AC010890.1	-1.937	3.53E-10	not available
C2orf80	-1.924	6.74E-18	chromosome 2 open reading frame 80
MAPT-AS1	-1.844	5.40E-07	MAPT antisense RNA 1
LOC100128127	-1.814	1.43E-09	not available
RP11-1134I14.8	-1.783	5.72E-22	not available
SLC6A1-AS1	-1.706	1.31E-09	SLC6A1 antisense RNA 1
KIAA1244	-1.643	1.63E-10	ARFGEF family member 3
FAM222A-AS1	-1.297	1.10E-11	FAM222A antisense RNA 1

Table S3 (*related to Figure 5*)

Significantly dysregulated synaptic genes in SCZ GPCs

	SCZ.08 vs. Pooled CTR		*SCZ.29 vs. Pooled CTR*		*SCZ.51 vs. Pooled CTR*		*SCZ.164 vs. Pooled CTR*		*SCZ.08+29+51+164 vs. Pooled CTR*	
Gene ID	*Log2 FC*	*P Value*	*Log2 FC*	*P Value*	*Log2 FC*	*P Value*	*Log2 FC*	*P Value*	*Log2 FC*	*P Value*
DSCAML1	-1.971	8.83E-07	-2.968	1.31E-04	-1.089	8.32E-05	NS	NS	-0.982	5.34E-08
LINGO1	-2.320	3.29E-04	-2.885	2.26E-04	-1.452	3.36E-06	-2.523	9.19E-12	-2.139	3.56E-14
NLGN1	-1.249	3.37E-04	-1.014	4.32E-02	NS	NS	-0.545	3.88E-02	-0.625	3.15E-04
NLGN2	NS	NS	-0.767	1.74E-02	-0.384	3.01E-03	-0.408	1.47E-02	-0.452	3.37E-06
NLGN3	-0.563	3.98E-02	-1.669	3.07E-03	-1.011	1.63E-09	-0.958	3.67E-05	-1.143	1.61E-19
NRP1	-1.362	1.15E-03	1.409	5.00E-04	NS	NS	NS	NS	NS	NS
NRP2	NS	NS	1.548	2.07E-03	NS	NS	-0.733	3.65E-02	NS	NS
NRXN1	-3.259	5.93E-06	-2.984	5.55E-03	-1.176	1.35E-02	NS	NS	-1.161	2.04E-04
NRXN2	NS	NS	-2.179	9.04E-06	-1.252	2.71E-11	-0.720	3.33E-03	-1.102	6.82E-17
NRXN3	1.874	1.60E-04	NS	NS	NS	NS	1.198	1.20E-02	0.909	6.89E-04
NTNG2	-0.874	7.99E-03	-1.814	3.51E-04	NS	NS	NS	NS	NS	NS
NXPE3	NS	NS	NS	NS	NS	NS	0.410	1.74E-02	0.248	2.79E-02
NXPH1	-3.019	3.98E-07	-3.666	1.84E-03	-1.338	1.06E-02	-2.317	2.46E-09	-2.892	3.11E-15
NXPH2	-2.288	5.62E-04	NS	NS	NS	NS	NS	NS	NS	NS
NXPH3	NS	NS	-2.225	1.49E-03	-1.084	7.92E-03	NS	NS	-0.675	2.66E-02
NXPH4	-2.186	5.96E-03	4.095	4.08E-14	NS	NS	-1.560	1.09E-02	NS	NS
PTPRZ1	NS	NS	-2.967	2.60E-05	-0.792	4.13E-03	-0.870	5.38E-03	-1.296	2.41E-11
RGS4	-1.982	6.80E-05	2.184	3.97E-04	1.105	7.04E-04	-1.419	2.64E-03	NS	NS
SLITRK2	-6.812	1.35E-04	NS	NS	-7.307	7.51E-25	-9.321	5.54E-06	-6.138	5.52E-14
SLITRK3	-2.958	2.68E-03	NS	NS	-1.698	6.37E-04	-3.490	1.61E-11	-2.502	6.76E-07
SLITRK4	-4.157	7.12E-05	NS	NS	-3.713	5.02E-05	-2.678	1.20E-02	-2.457	5.86E-05
SLITRK5	-2.047	3.87E-07	NS	NS	-1.184	1.54E-06	-1.734	9.31E-08	-1.152	1.05E-08
SPARCL1	-2.314	6.14E-06	NS	NS	NS	NS	-0.843	3.87E-02	NS	NS
TNR	-3.082	8.83E-06	-5.108	1.89E-07	-2.227	8.81E-13	NS	NS	-2.137	5.56E-12

Genomic analysis of SCZ-derived hGPCs from 4 different patients revealed the significant and shared down-regulation in these cells of a number of synaptic genes, including neuroligin-3, neuroexophilin-1, LINGO1 and DSCAML1, relative to their normal controls (*red*, upregulated in SCZ vs CTRL; *green*, downregulated in SCZ GPCs; color intensity proportionate to differential dysregulation). Other synapse-associated genes, such as the SLITRKs 2-5, were significantly and sharply downregulated in GPCs derived from 3 of the 4 patients (lines 8, 51 and 164).

Lines 08, 29, 51 and 164: schizophrenia-derived, different patients; pooled controls, 3 lines, each from a different patient. Individual SCZ line data shown as well as pooled SCZ data, to highlight both commonalities and distinctions between SCZ GPCs derived from different patients. Log2FC: $\log_2$ fold-change in expression. NS: not significant.