

The rows of data in Table 2 in “Glutamatergic Gene Expression Is Specifically Reduced in Thalamocortical Projecting Relay Neurons in Schizophrenia” by Sodhi *et al.*, published in *Biological Psychiatry* (2011: 70:646–654), were formatted and printed out

of alignment. The corrected version of Table 2 is printed here.

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Table 2. Analyses of Transcript Abundance in Medial Dorsal Thalamus Cell Populations of Schizophrenia Cases and the Comparison Group

Transcript	Diagnosis	n	Large Cells				Small Cells		
			Mean	SEM	t	df	p	Mean	SEM
GLUR1	NC	19	2.68	1.06	1.25	30	.22	1.34	.64
	SCZ	13	1.04	.29				1.12	.96
GLUR2	NC	19	3.97	.77	1.47	30	.15	1.68	.53
	SCZ	13	2.50	.43				1.27	.30
GLUR3	NC	19	3.45	.60	2.08	30	.046 ^a	1.17	.24
	SCZ	13	1.74	.46				.76	.26
GLUR4	NC	19	1.77	.59	.96	30	.34	.24	.05
	SCZ	13	1.06	.20				.18	.04
GLUR5	NC	19	3.93	.61	1.56	30	.13	1.22	.24
	SCZ	13	2.44	.73				.67	.24
GLUR6	NC	19	5.27	.73	2.83	30	.0083 ^a	2.05	.85
	SCZ	13	2.33	.65				1.37	.75
GLUR7	NC	19	5.80	.76	2.93	30	.0064 ^a	.64	.19
	SCZ	13	2.84	.50				.50	.17
KA1	NC	19	3.38	.67	.97	30	.34	1.48	.37
	SCZ	13	2.44	.63				1.05	.33
KA2	NC	19	3.39	.51	1.31	30	.20	1.80	.32
	SCZ	13	2.23	.77				11.95	11.26
NR1	NC	19	6.34	1.57	1.50	30	.15	1.98	.62
	SCZ	13	3.25	.94				.85	.17
NR2A	NC	19	5.18	1.20	1.85	30	.075	1.15	.64
	SCZ	13	2.15	.93				.55	.22
NR2B	NC	19	3.93	1.09	−.34	30	.74	.71	.32
	SCZ	13	4.86	2.95				.91	.62
NR2C	NC	19	4.36	.92	1.75	29.4	.091	1.47	.23
	SCZ	13	2.40	.65				1.02	.20
NR2D	NC	19	9.15	1.94	2.60	27.2	.015 ^a	2.28	1.16
	SCZ	13	3.36	1.10				1.28	.61
NR3A	NC	19	4.08	1.18	1.66	21.4	.11	1.27	.31
	SCZ	13	2.03	.37				1.14	.34
mGluR1	NC	20	1.19	.17	.18	30	.86	.80	.16
	SCZ	12	1.13	.28				.64	.46
mGluR2	NC	20	1.96	.41	1.99	27.1	.057	.39	.08
	SCZ	12	1.04	.21				.49	.13
mGluR3	NC	20	.98	.10	1.14	30	.26	1.08	.34
	SCZ	12	.79	.14				.91	.22
mGluR4	NC	20	1.69	.16	.41	30	.69	.44	.06
	SCZ	12	1.56	.32				.76	.32
mGluR5	NC	20	1.04	.10	.67	30	.51	1.11	.23
	SCZ	12	.94	.10				.65	.24
mGluR7	NC	20	1.67	.15	.07	16.2	.95	1.90	.27
	SCZ	12	1.65	.30				1.15	.23
mGluR8	NC	20	.39	.19	−1.46	11.2	.17	—	—
	SCZ	12	3.22	1.93				—	—
NFL	NC	19	6.60	1.46	.40	30	.69	2.17	.43
	SCZ	13	5.41	2.88				1.35	.51
PICK1	NC	19	6.87	2.61	1.42	30	.17	1.24	.34
	SCZ	13	2.29	.69				.87	.27
SHANK2	NC	20	1.77	.35	1.37	30	.18	.98	.12
	SCZ	12	1.12	.19				1.02	.26
Stargazin	NC	19	9.22	1.39	1.95	30	.06	3.23	.47
	SCZ	13	5.03	1.63				2.25	.62
SYNGAP1	NC	19	5.91	.94	3.81	25.8	.00077 ^a	1.23	.25
	SCZ	13	1.90	.47				1.88	1.00

Table 2. (continued)

Transcript	Diagnosis	<i>n</i>	Large Cells					Small Cells	
			Mean	SEM	<i>t</i>	df	<i>p</i>	Mean	SEM
<i>SAP97</i>	NC	19	2.78	.47	.72	30	.48	.66	.20
	SCZ	13	2.22	.63				.40	.08
<i>SAP102</i>	NC	19	3.93	.93	.39	30	.70	1.05	.28
	SCZ	13	3.25	1.61				1.29	.92
<i>PSD95</i>	NC	19	3.32	.52	1.22	30	.23	.35	.07
	SCZ	13	2.39	.52				.37	.18
<i>GRIP1</i>	NC	19	4.08	1.10	2.84	19.6	.01 ^a	9.35	7.86
	SCZ	13	.89	.23				.52	.17
<i>HOMER1</i>	NC	20	1.16	.11	.88	30	.38	1.22	.15
	SCZ	12	.98	.19				1.21	.25
<i>HOMER2</i>	NC	20	1.84	.27	1.21	30	.24	.98	.11
	SCZ	12	1.38	.20				1.19	.28
<i>HOMER3</i>	NC	20	.86	.21	−.69	30	.49	2.08	.78
	SCZ	12	1.10	.27				1.86	.27

Mean gene expression (ratio of measured transcript level to the geometric mean of the measurements for three housekeeping genes) are tabulated for glutamatergic transcripts within each subject group. The large cell population is enriched with glutamatergic relay neurons and the small cells are enriched with GABAergic neurons and astroglia.

NC, comparison group; SCZ, schizophrenia subjects; SEM, standard error of the mean.

^aPost hoc tests were performed for the large cell population, and statistically significant differences ($p < .05$) in transcript abundance between SCZ and the NC are indicated.