Consortium
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APPENDIX. SUPPLEMENTARY DATA TO:

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Dysregulation of Long Intergenic Non-Coding RNA Expression
in the Schizophrenia Brain.

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Table S1. Examined brain regions

Number	Abbreviation	Region
1	CAUD	Caudate Nucleus
2	GP	Globus Pallidus
3	NACC	Nucleus Accumbens
4	PUT	Putamen
5	SN	Substantia Nigra
6	CB_GM	Cerebellar Gray Matter
7	CB_WM	Cerebellar White Matter
8	HYP	Hypothalamus
9	MDTH	Medial Dorsal Thalamus
10	BA4	Primary Motor Cortex
11	BA6a	Anterior Lateral Premotor Cortex
12	BA9	Dorsolateral Prefrontal Cortex
13	BA10m	Anterior Medial Prefrontal Cortex
14	BA11	Orbitofrontal Cortex
15	BA44	Ventrolateral Prefrontal Cortex - Broca
16	INSp	Posterior Insular Cortex
17	AMG	Amygdala
18	BA24	Ventral Anterior Cingulate Cortex
19	BA31	Posterior Cingulate Cortex
20	BA32	Dorsal Anterior Cingulate Cortex
21	CA3/DG	Hippocampus-CA3/Dentate Gyrus
22	ENTCTX	Entorhinal Cortex
23	BA17a	Primary Visual Cortex
24	BA18/19a	Secondary Visual Cortex
25	BA3/1/2	Primary Somatosensory Cortex
26	BA7m	Precuneus
27	BA40p	Posterior Supramarginal Gyrus
28	BA20a	Inferior Temporal Gyrus
29	BA21a	Middle Temporal Gyrus
30	BA22p	Superior Temporal Gyrus - Wernicke
31	BA38	Temporopolar Cortex
32	BA41/42	Primary Auditory Cortex
33	CCa	Anterior Corpus Callosum
34	CCp	Posterior Corpus Callosum
35	IC	Internal Capsule

Table S2. Brain donors’ information

Individual	Diagnosis	Gender	Age
HA	Healthy	M	62
HB	Healthy	F	61
HC	Healthy	F	34
HD	Healthy	M	34
X1	Paranoid Schizophrenia	M	36
X2	Paranoid Schizophrenia	M	74
X3	Paranoid Schizophrenia	F	57
X5	Paranoid Schizophrenia	M	62

Table S3. Differentially expressed lincRNAs

Ensembl ID	Gene Symbol	Region	Log$_2$ Fold Change	P-value (Tukey test)
ENSG00000214548	*MEG3*	CB_WM	2.869566	4.11E-11
ENSG00000259071	*RP11-247L20.4*	CB_WM	−2.56414	2.82E-05
ENSG00000259071	*RP11-247L20.4*	CB_GM	−2.51876	4.81E-05
ENSG00000247157	*LINC01252*	CB_WM	1.714425	7.92E-05
ENSG00000226380	*AC058791.1*	CB_WM	1.944861	0.000114
ENSG00000279278	*CH17-264L24.1*	CB_GM	−2.13513	0.000211
ENSG00000225746	*SNHG23*	CB_WM	1.752703	0.000212
ENSG00000277200	*RP11-74E22.8*	CB_WM	1.547006	0.000297
ENSG00000273492	*AP000230.1*	IC	−1.71486	0.000423
ENSG00000230417	*LINC00856*	CB_GM	−1.58385	0.000525
ENSG00000268120	*CTD-3193O13.11*	CB_WM	1.897773	0.000931
ENSG00000230606	*AC159540.1*	CB_WM	1.398952	0.001003
ENSG00000223403	*MEG9*	CB_WM	1.959656	0.001273
ENSG00000240875	*LINC00886*	CB_WM	1.717345	0.002263
ENSG00000232956	*SNHG15*	CCp	−1.07452	0.002283
ENSG00000225684	*FAM225B*	CCp	3.20662	0.002475
ENSG00000227640	*SOX21-AS1*	CCp	1.513218	0.003651
ENSG00000267651	*RP11-95O2.1*	CCp	−1.67407	0.004812
ENSG00000256982	*CTD-2555A7.2*	IC	−1.90171	0.007763
ENSG00000273084	*RP11-1275H24.3*	CCp	−1.52587	0.007846
ENSG00000277692	*RP11-358N2.2*	CB_WM	1.448069	0.008411
ENSG00000267575	*CTC-459F4.3*	CB_WM	0.708904	0.0094
ENSG00000231439	*WASIR2*	CB_WM	1.624409	0.011538
ENSG00000268601	*AC115522.3*	AMG	−1.68474	0.013271
ENSG00000273270	*RP11-212P7.2*	CCp	0.812451	0.014746
ENSG00000260804	*PKI55*	IC	−1.08373	0.018089
ENSG00000261402	*RP11-378I6.1*	NACC	−1.71707	0.019925
ENSG00000264247	*LINC00909*	GP	−0.66615	0.022133
ENSG00000251562	*MALAT1*	CB_WM	4.00427	0.022368
ENSG00000225746	*SNHG23*	CCa	1.403376	0.024082

Table S3. Differentially expressed lincRNAs (continued)

Ensembl ID	Gene Symbol	Region	Log_2 Fold Change	P-value (Tukey test)
ENSG00000268798	*CTB-25B13.5*	BA4	1.249001	0.02615
ENSG00000260328	*RP11-416I2.1*	IC	−2.4147	0.027127
ENSG00000269893	*SNHG8*	CB_WM	−0.74012	0.03098
ENSG00000247157	*LINC01252*	CCp	1.298164	0.033168
ENSG00000234608	*MAPKAPK5-AS1*	CCp	−1.51999	0.033435
ENSG00000281332	*LINC00997*	BA21a	−0.80463	0.034155
ENSG00000261600	*RP11-575H3.1*	CCp	1.714837	0.037807
ENSG00000269893	*SNHG8*	CCp	−0.72933	0.038809
ENSG00000277476	*RP11-147L13.13*	AMG	0.584851	0.038993
ENSG00000276564	*CTA-276F8.1*	CB_WM	1.217344	0.040268
ENSG00000272316	*XXbac-BPGBPG55C20.2*	CCp	1.046699	0.043271

Note: Region information according to Table S1. Log2FC shows the base-two-logarithm transformed values of fold-change for the expression difference between SZ and HC samples in the listed region. P-value shows the outcome of post-hoc Tukey test for the listed region.

Table S4. Correlation of lincRNA expression differences with the ones reported by other studies

Region	# overlapping genes	Pearson		Spearman		Study
		r	p-value	ρ	p-value	
Amygdala	21	0.6964	0.00045	0.6052	0.004369	[31]
Amygdala	24	0.4235	0.03919	0.4453	0.02921	[33]
Dorsolateral PFC	36	0.1596	0.3526	0.1470	0.3909	[34]

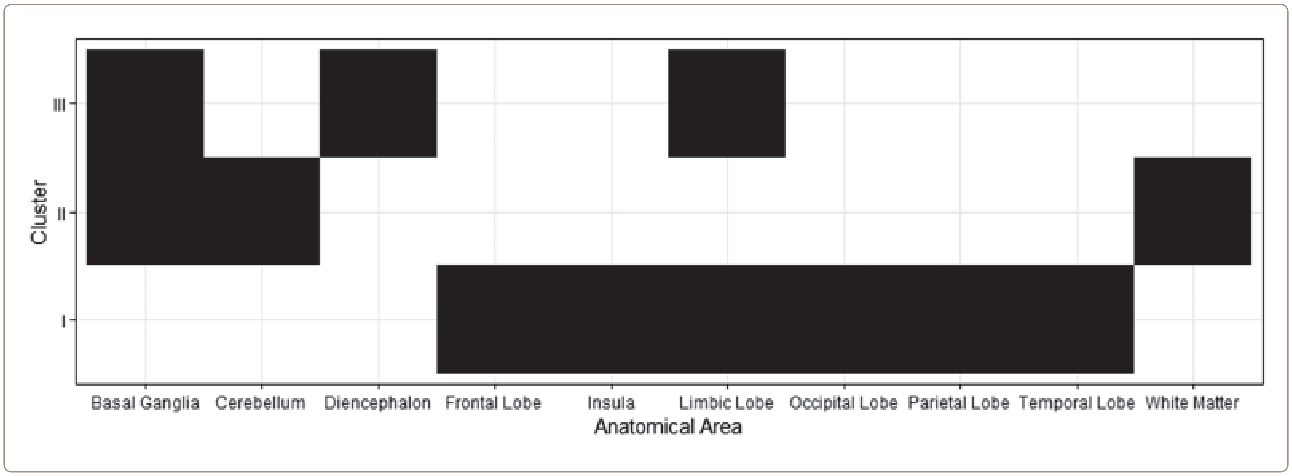

Figure S1. Intersection of lincRNA expression-based clusters and brain anatomical areas. Colored areas mark anatomical structures comprising lincRNA expression-based clusters depicted in Figure 2C.

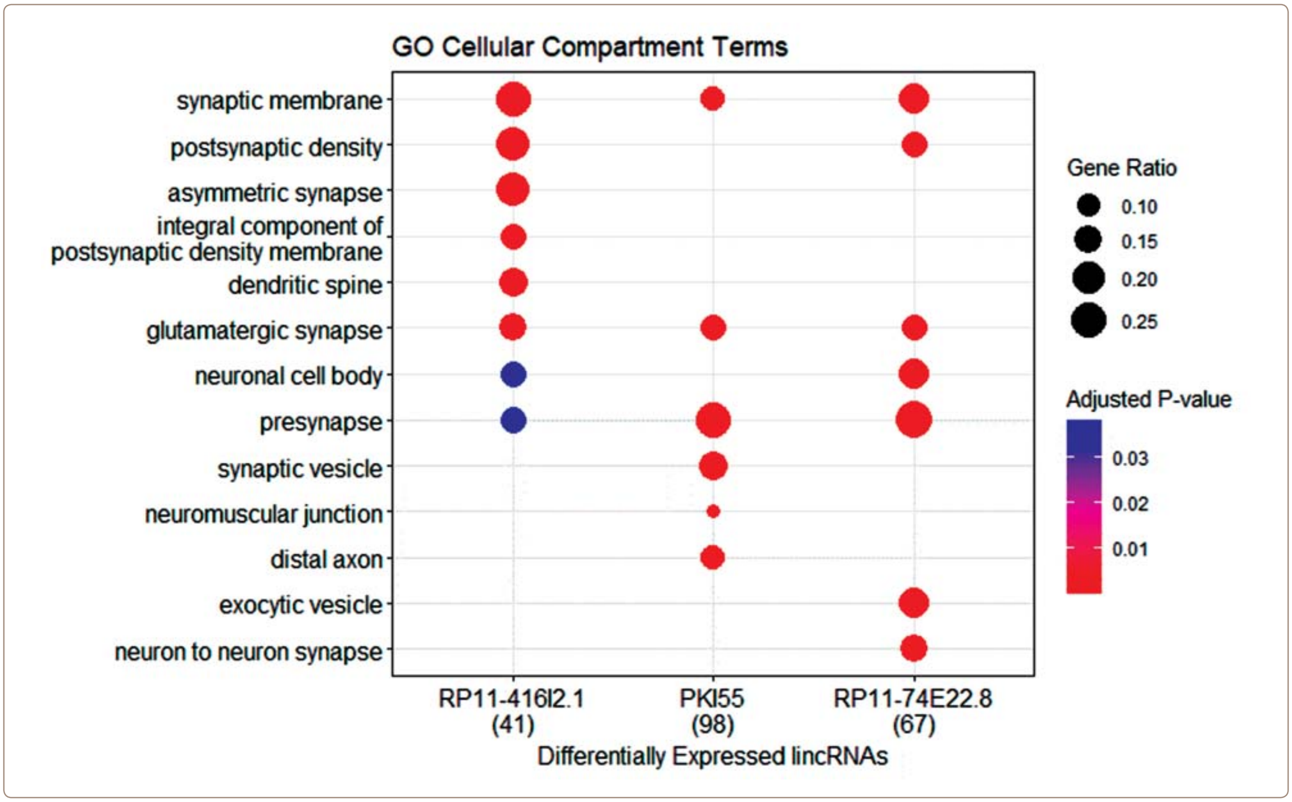

Figure S2A. Top GO "cellular compartment" terms enriched in the three target-rich DEL mRNA targets.

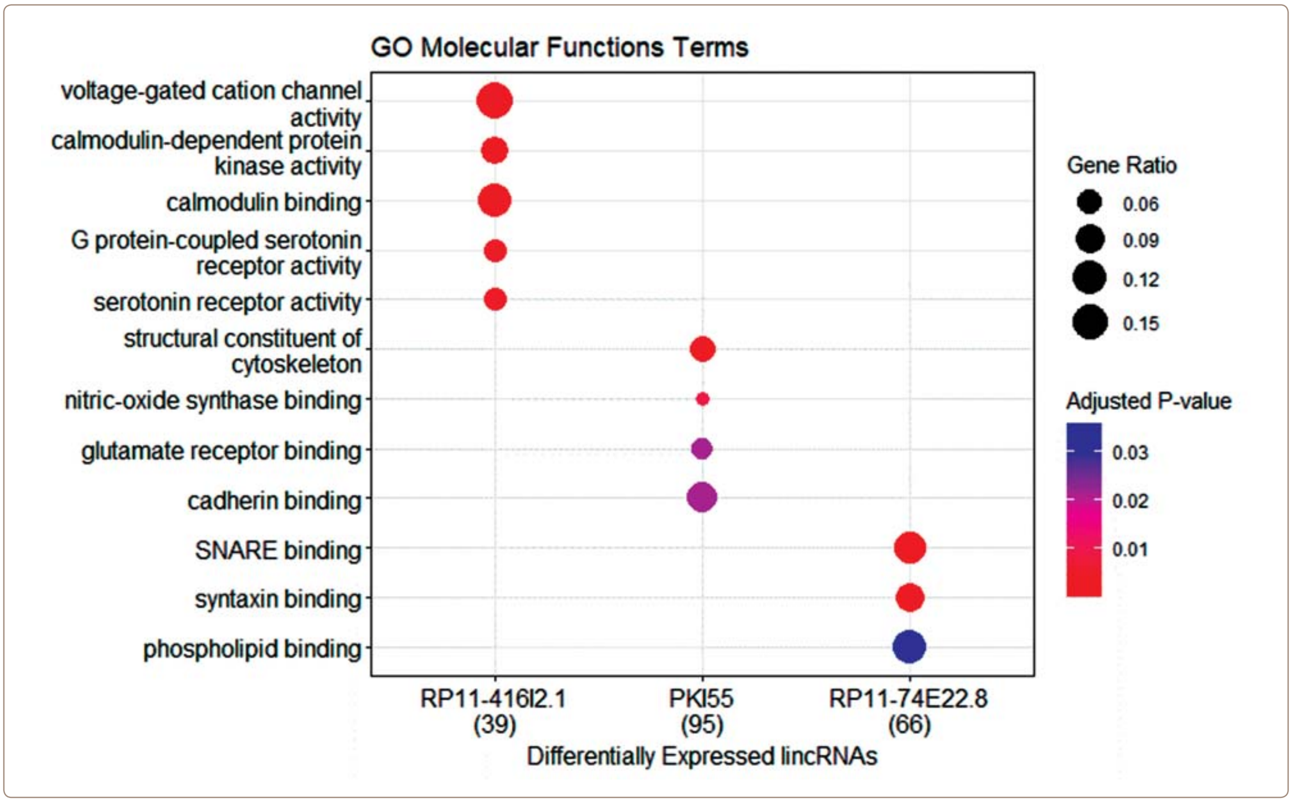

Figure S2B. Top GO "molecular function" terms enriched in the three target-rich DEL mRNA targets.

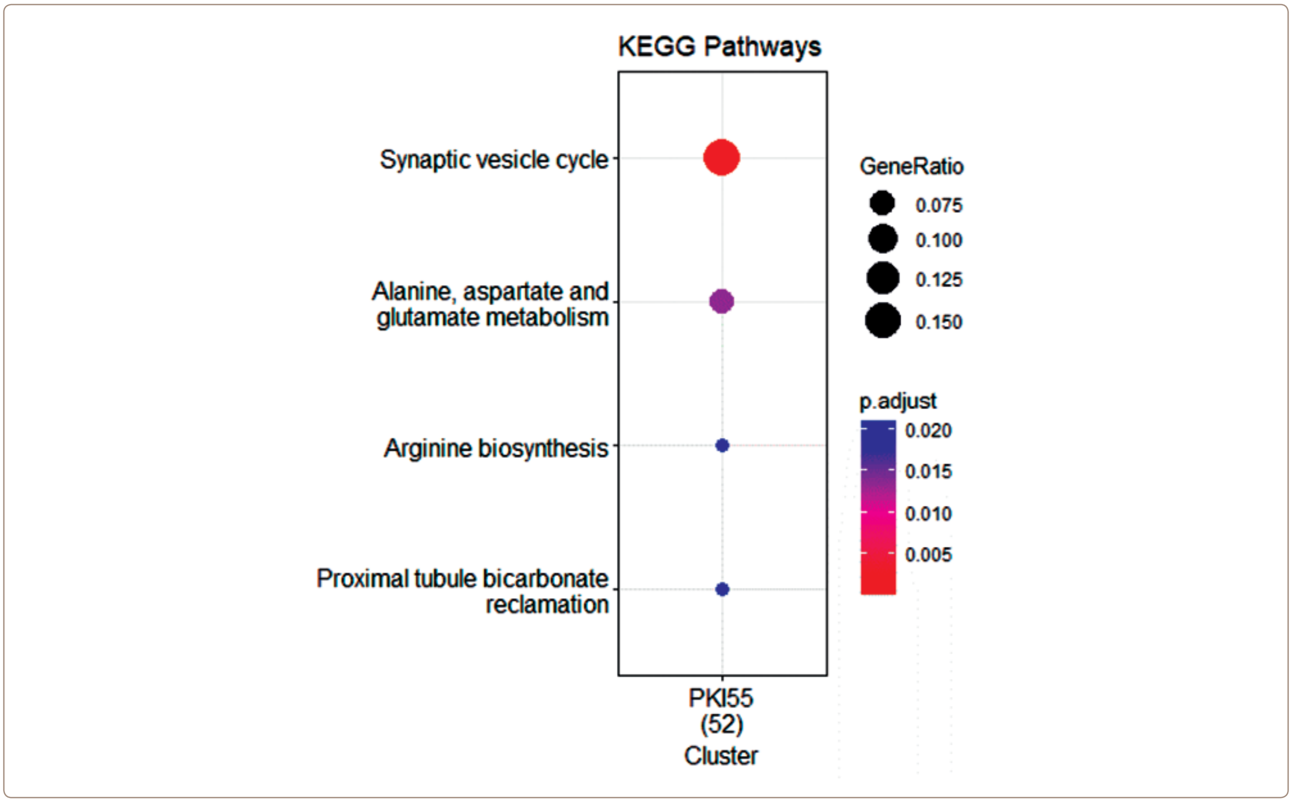

Figure S2C. Top KEGG pathways enriched in the three target-rich DEL mRNA targets.

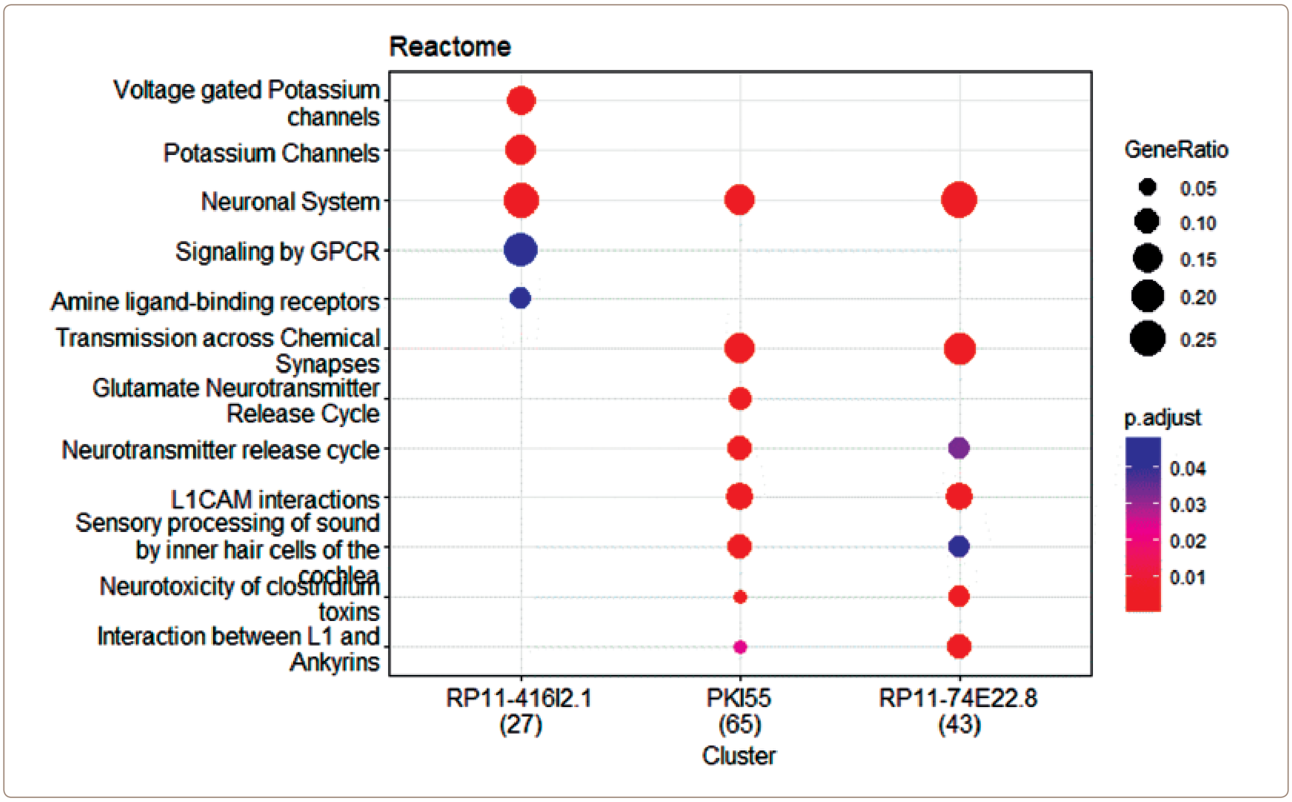

Figure S2D. Top Reactome entries enriched in the three target-rich DEL mRNA targets.