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Appendix Table S1. Summary of behavioral analyses of *Ldb2* KO mouse

Test	Results	Validity as a schizophrenia model
Open field test	Hyperactivity*	Positive symptom-related.
Home cage activity	Hyperactivity	Positive symptom-related.
Elevated plus maze	Normal	
Light dark transition	Normal	
Tail suspension	Normal	
Prepulse inhibition	No reduction	
Social interaction (Encounter method)	No reduction	
Rotarod test	Normal in motor coordination	
Y maze test	Alternation reduced (tendency)	Working memory deficits.
Hot plate test	Normal	
Fear conditioning (contextual test)	Deduced freezing*	Cognitive deficits.
Fear conditioning (cued test)	Deduced freezing*	Cognitive deficits.
Barnes maze	Normal	
8-Arm radial maze	Normal	
Morris water maze	Moving speed reduced day-by-day	Abnormal mood control
Locomotor activity by dopamine agonist	Exaggerated locomotor activity by methyphenidate	Positive symptom-related
Locomotor activity by NMDA antagonist	Exaggerated locomotor activity by MK-801	Positive symptom-related
Neurogenesis in the dentate gyrus	Significantly reduced	Yes

* These phenotypes were ameliorated by the treatment with antipsychotics or lithium salt.

Appendix Table S2. Summary of the sequencing data used for the ChIP-seq analysis

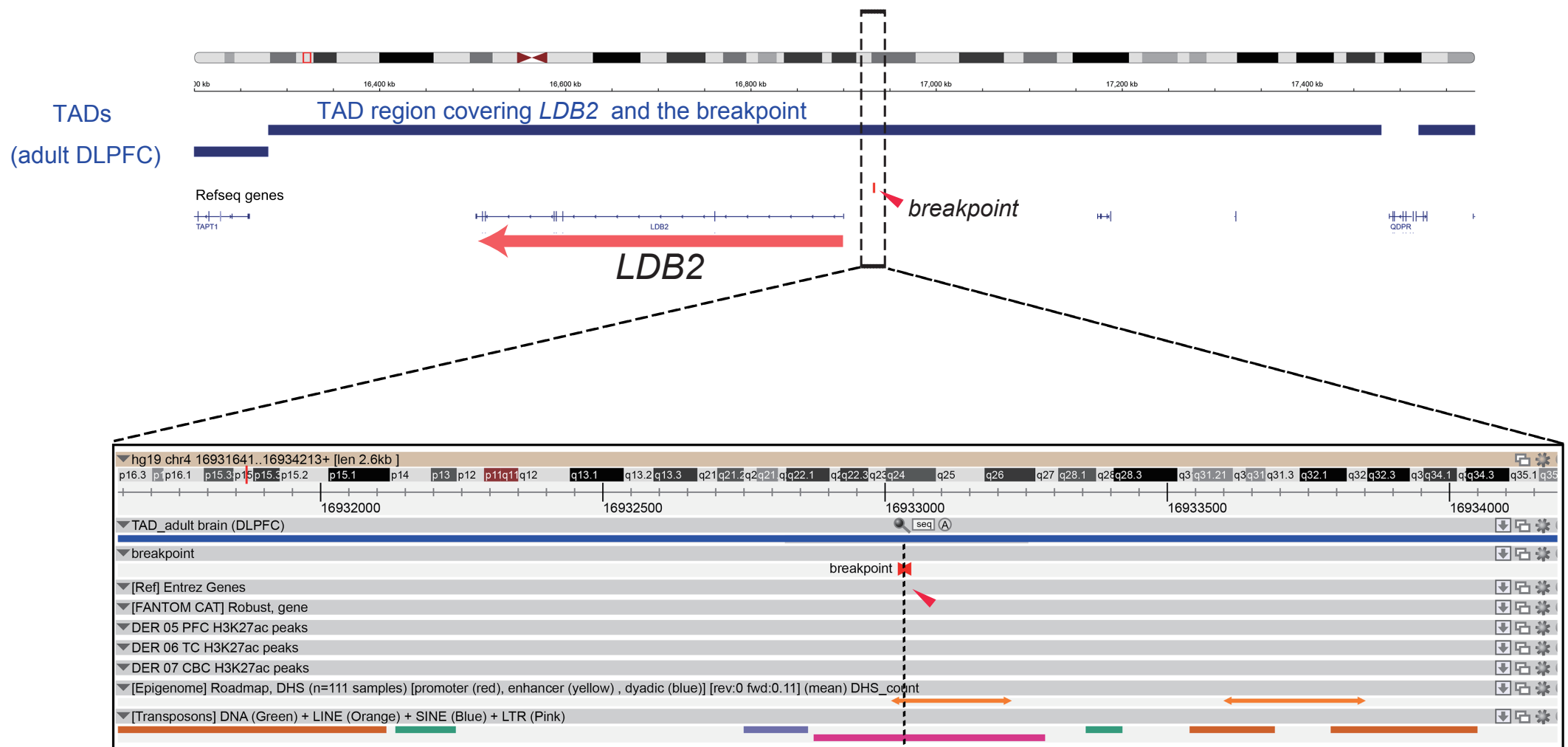
Cells	Read category	Accession	# Raw reads	# Reads after trimming	# Uniquely mapped reads	# Peaks called by MACS2
Neuroshere	input	DRA010493 (this study)	25,917,604	25,910,873	22,615,308	14,545
	ChIP	DRA010493 (this study)	15,742,990	15,623,377	13,304,886	
ECC1	input	SRR577960, SRR577961	69,068,747	65,833,683	50,654,757	12,661
	ChIP	SRR577989, SRR577990	61,928,846	57,924,494	45,639,854	
H1ES	input	SRR577840, SRR577841	83,500,187	71,558,442	58,119,276	12,727
	ChIP	SRR351691, SRR351692	58,088,393	49,544,038	39,135,817	
HCT116	input	SRR577956, SRR577957	68,496,387	62,739,879	50,210,480	10,144
	ChIP	SRR577901, SRR577902	46,895,186	40,520,593	32,029,919	
K562	input	SRR578001, SRR578002, SRR578003, SRR578004	176,829,940	145,526,245	115,798,395	59,385
	ChIP	SRR351661, SRR351662	70,572,446	60,927,720	48,494,406	

TMEM59 FAM190B SLC2A3 GPR137C STX4 MIR636 RRAS RBCK1 PLCD1 GUCY1B3 GCIC TUSC3
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P4RS2 P4RS2 ERO1L STX4 MIR636 RRAS RBCK1 PLCD1 GUCY1B3 GCIC TUSC3
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SASS6 NANOS1 C10orf132 PTPN21 MTS1L MTS1L MTS1L MTS1L MTS1L MTS1L
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Appendix Table S4.

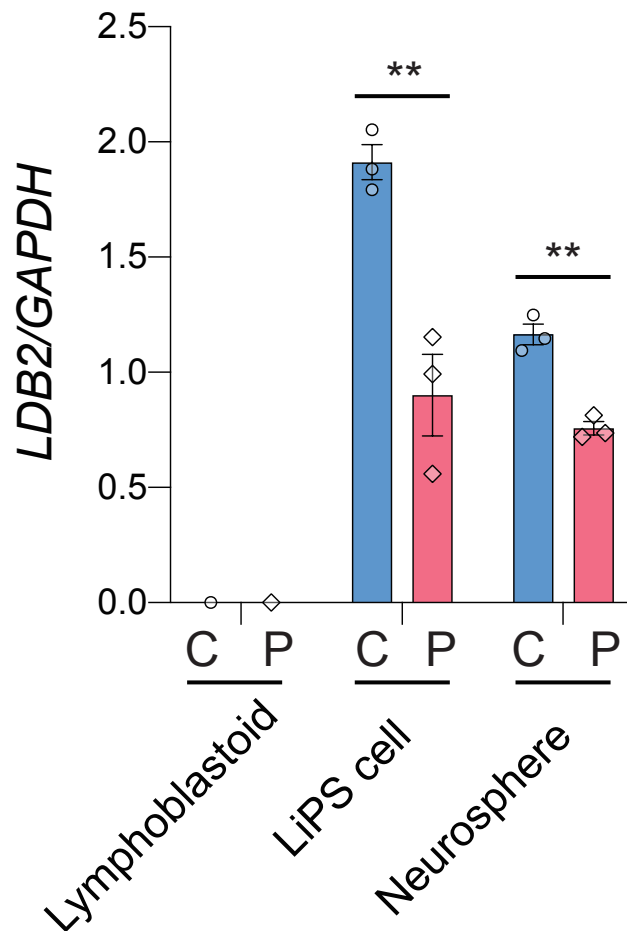
Twenty five genes that were contained in the biological process ‘Regulation of dendrite spine morphogenesis’ and detected in both LDB2 and EGR1 ChIP analyses

Gene Symbol	Protein
<i>CAPRIN1</i>	Caprin-1
<i>CAMK2B</i>	Calcium/calmodulin-dependent protein kinase type II subunit beta
<i>ARC</i>	Activity-regulated cytoskeleton-associated protein
<i>CAPRIN2</i>	Caprin-2
<i>SRCIN1</i>	SRC kinase signaling inhibitor 1
<i>SHANK3</i>	SH3 and multiple ankyrin repeat domains protein 3
<i>ARHGAP33</i>	Rho GTPase-activating protein 33
<i>OPA1</i>	Dynamin-like 120 kDa protein, mitochondrial
<i>PDLIM5</i>	PDZ and LIM domain protein 5
<i>DBN1</i>	Drebrin
<i>PTEN</i>	Phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN
<i>PAFAH1B1</i>	Platelet-activating factor acetylhydrolase IB subunit alpha
<i>ITPKA</i>	Inositol-trisphosphate 3-kinase A
<i>CFL1</i>	Cofilin-1
<i>KALRN</i>	Kalirin
<i>LRRK2</i>	Leucine-rich repeat serine/threonine-protein kinase 2
<i>BAIAP2</i>	Brain-specific angiogenesis inhibitor 1-associated protein 2
<i>PPP1R9A</i>	Neurabin-1
<i>LRP8</i>	Low-density lipoprotein receptor-related protein 8
<i>CTTN</i>	Src substrate cortactin
<i>DNM3</i>	Dynamin-3
<i>NLGN1</i>	Neurologin-1
<i>CDK5R1</i>	Cyclin-dependent kinase 5 activator 1
<i>ABI2</i>	Abl interactor 2
<i>UBE3A</i>	Ubiquitin-protein ligase E3A



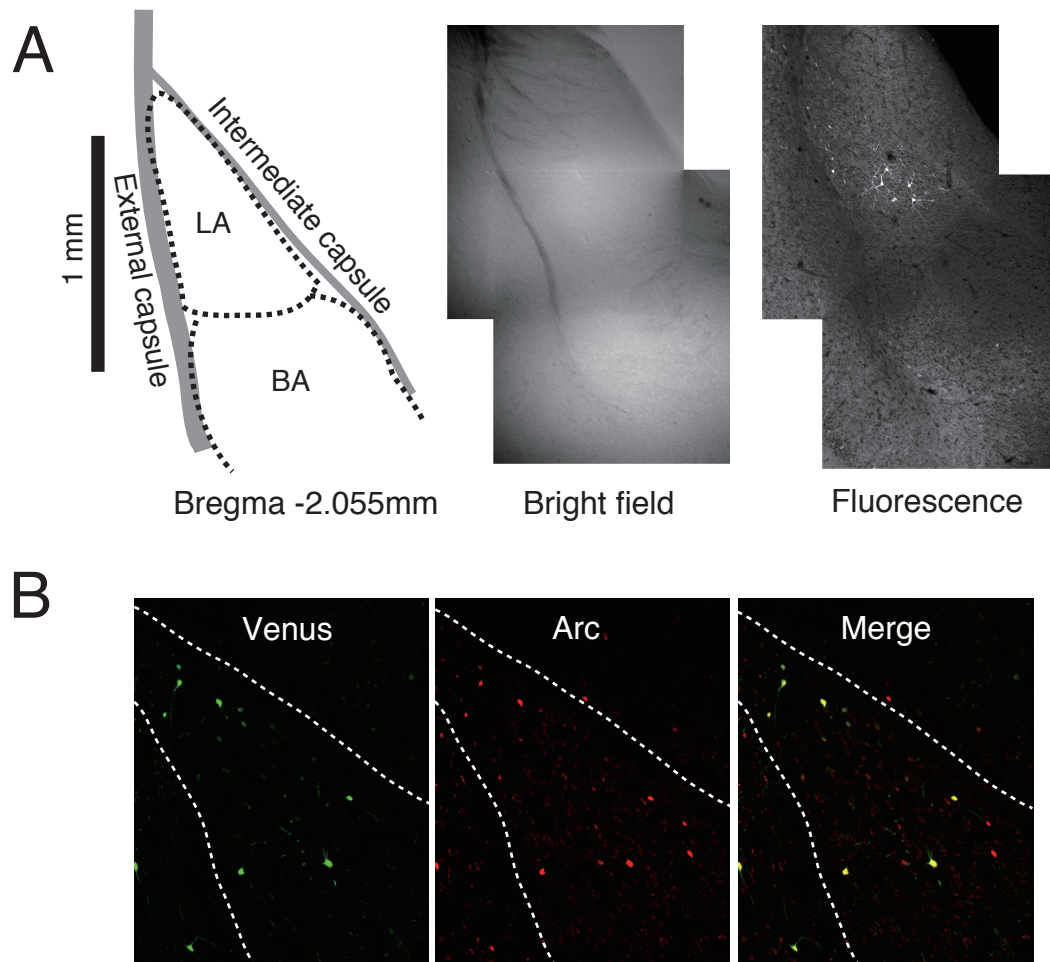
Appendix Figure S1: TAD map

TAD (topologically associating domain) structure around the chromosome 4 breakpoint of the proband is shown. The red arrowhead indicates the position of the breakpoint. Note that the breakpoint in chromosome 13 is within so-called ‘gene desert’.



Appendix Figure S2: Reduced *LDB2* expression in the patient derived cells

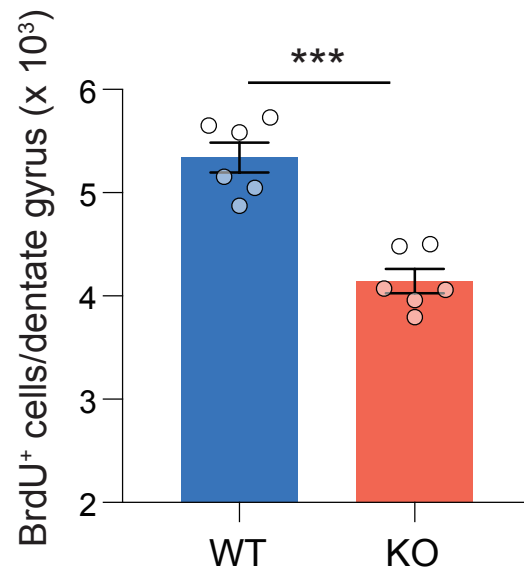
Quantitative RT-PCR detected *LDB2* expression in the patient's lymphoblastoid cell-derived iPS (LiPS) cells and neurospheres differentiated from the LiPS cells. Three independent LiPS clones each from the patient (P) and a healthy control (C; 39 years old, male) were examined. **: $p < 0.01$ (t -test). Data are shown as means $\pm$ S.E.M ($n = 3$ each, lymphoblastoid and neurosphere). There are no biological replicates in lymphoblastoid cells.



Appendix Figure S3: Analysis of neuronal activity in the Arc-Venus mouse

A. A schematic image of the basolateral complex of the amygdala (left), and bright-field (middle) and Venus-fluorescence (right) images in the corresponding area.

B. Venus fluorescence (green) counterstained immunohistochemically by an anti-Arc antibody (red) in the LA.



Appendix Figure S4: Abnormality of neurogenesis in the hippocampus of *Ldb2* KO animals

Neurogenesis in the hippocampal dentate gyrus was evaluated by the incorporation of BrdU. BrdU-positive cells from three animals for each genotype were separately counted. Data were shown as means with error bars representing SE. ***, $P < 0.001$, Student t -test ($n = 6$ for each genotype, 3 animals x both sides).