

Figure S1
a

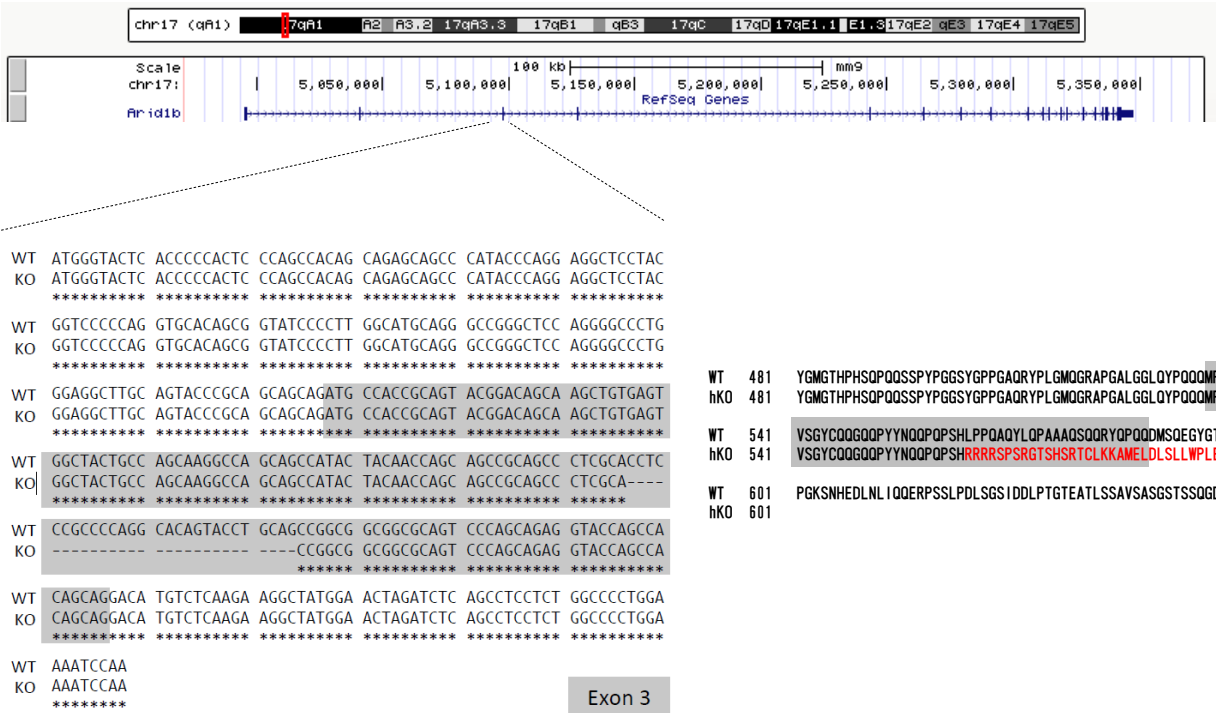


Figure S1. Generation of *Arid1b* hKO mice. (a) Deletion of the exon 3 region of the *Arid1b* gene results in premature termination. (b) Quantification of *Arid1b* mRNA in hKO mouse brains by RNA-Seq (left) and RT-PCR (right). (c) Quantification of ARID1B protein in hKO mouse brain by western assay. Data are expressed as the mean \pm SEM (WT, $n = 4$; *Arid1b* hKO, $n = 4$). p -values were calculated using Student's two-tailed t -test.

Figure S2

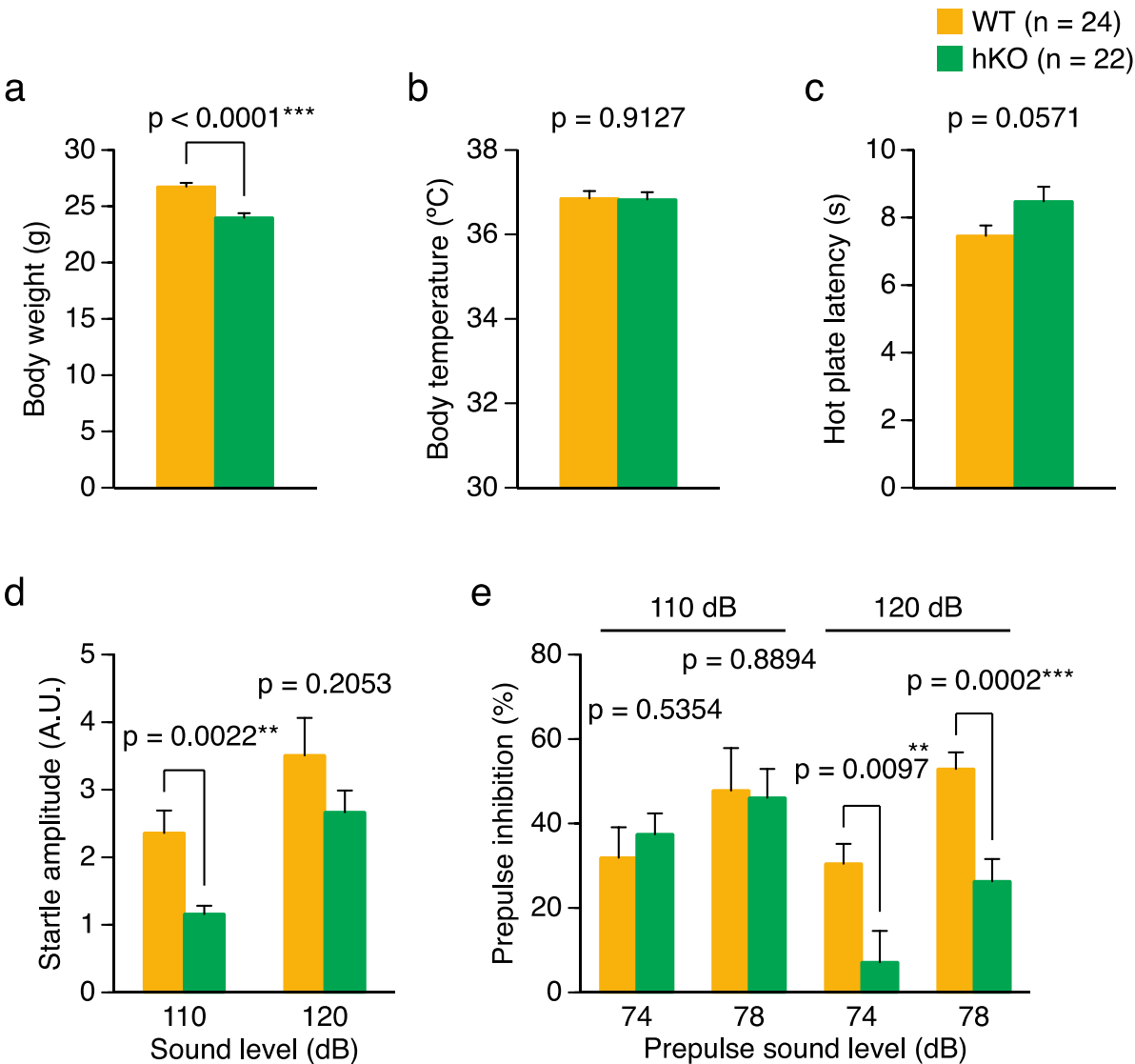


Figure S2. Physical characteristics and sensory functions in *Arid1b* hKO mice. (a) Body weight. (b) Body temperature. (c) Hot-plate latency. (d, e) Prepulse inhibition test. (d) Startle response amplitude. (e) Percentage of prepulse inhibition. Data are expressed as the mean \pm SEM (WT, $n = 24$; *Arid1b* hKO, $n = 22$). Significant differences between genotypes are indicated by $^{**} p < 0.01$ and $^{***} p < 0.001$, as determined by Student's two-tailed t -test.

Figure S3

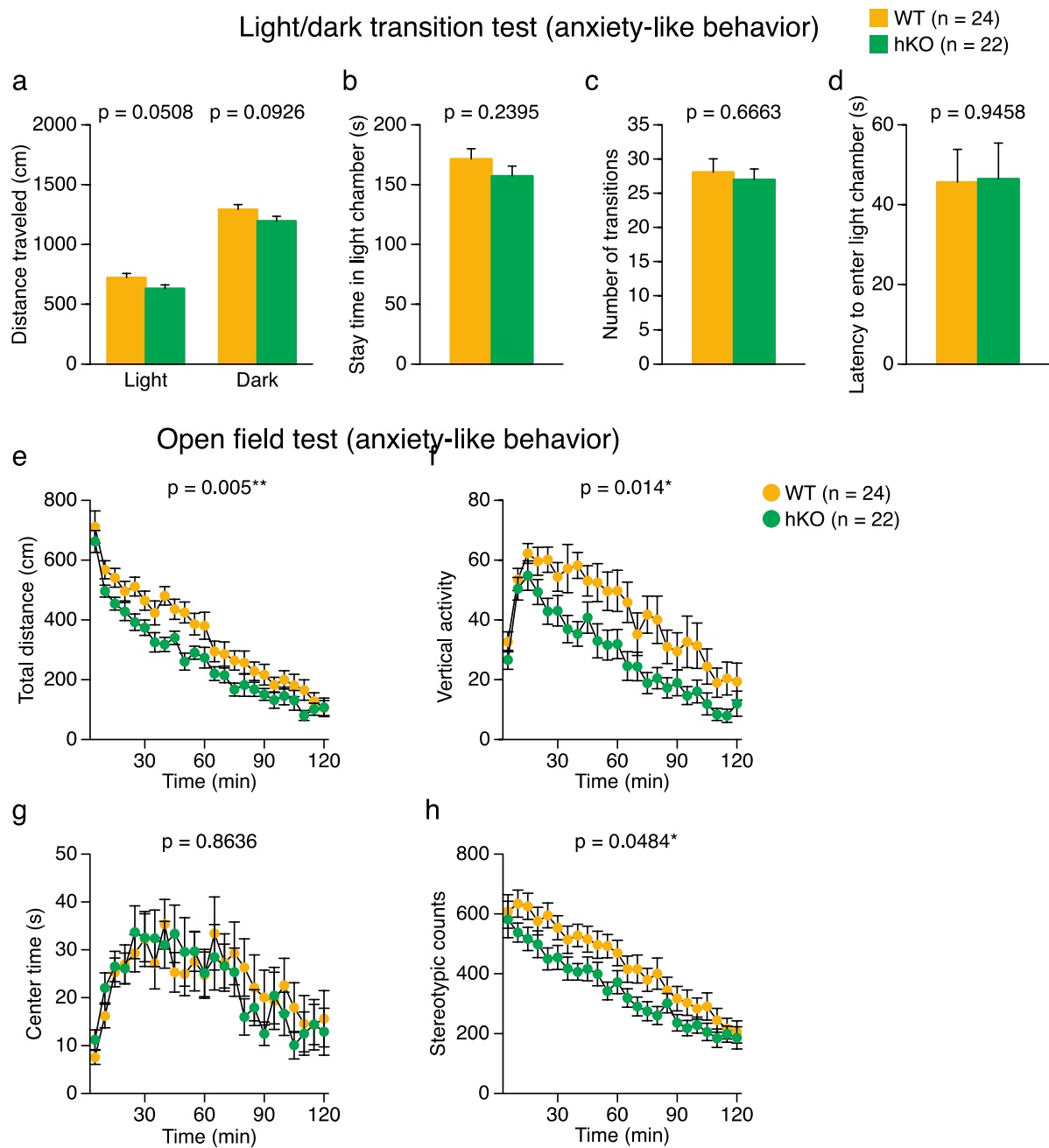


Figure S3. Locomotor activity and anxiety-like behavior in *Arid1b* hKO mice. (a–d) Light/dark transition test. (a) Distance traveled. (b) Stay time in the light chamber. (c) Number of transitions between light and dark chambers. (d) Latency of entering the light chamber. (e–h) Open field test. (e) Distance traveled. (f) Vertical activity. (g) Stay time in center area. (h) Stereotypic behavior counts. Data are expressed as the mean \pm SEM (WT, $n = 24$; *Arid1b* hKO, $n = 22$). Significant differences between genotypes are indicated by * $p < 0.05$ and ** $p < 0.01$, as determined by Student's two-tailed t -test (a–d) or two-way repeated-measures ANOVA (e–h).

Figure S4

Home cage social interaction test (social behavior)

● WT (n = 11 pairs)
● hKO (n = 9 pairs)

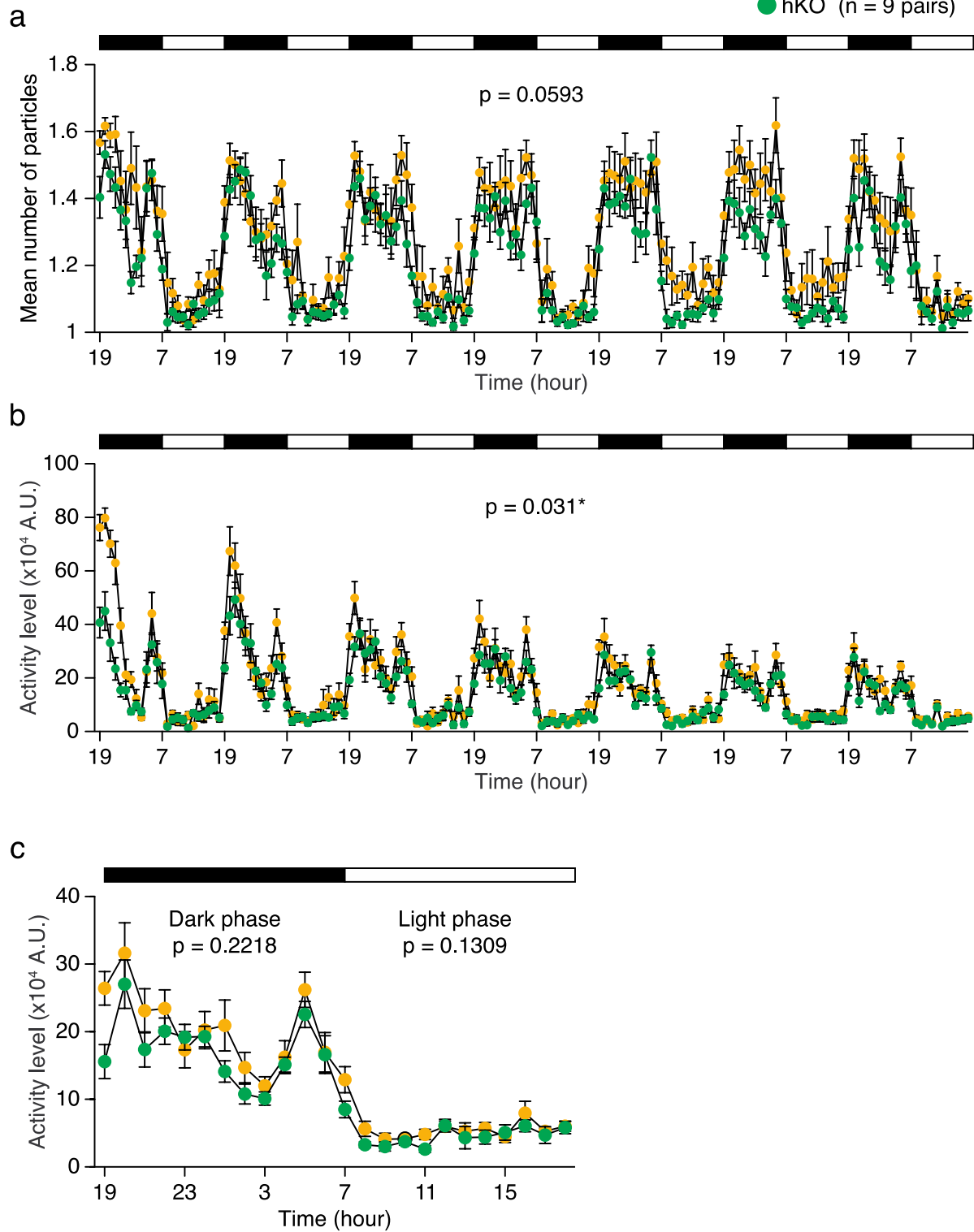


Figure S4. Locomotor activity and social behavior in a home cage in *Arid1b* hKO mice. (a–c) Home cage social interaction test. (a) Mean number of particles detected in the home cage during each hour of 1 week. Two particles indicate that the mice were not in contact with each other, and one particle indicates contact between the two mice. (b) Activity levels in pairs of mice. (c) Mean activity levels averaged over the last 3 days. Data are expressed as the mean \pm SEM (WT, $n = 11$; *Arid1b* hKO, $n = 9$). Significant differences between genotypes are indicated by $*p < 0.05$ and $**p < 0.01$, determined by two-way repeated-measures ANOVA.

Figure S5

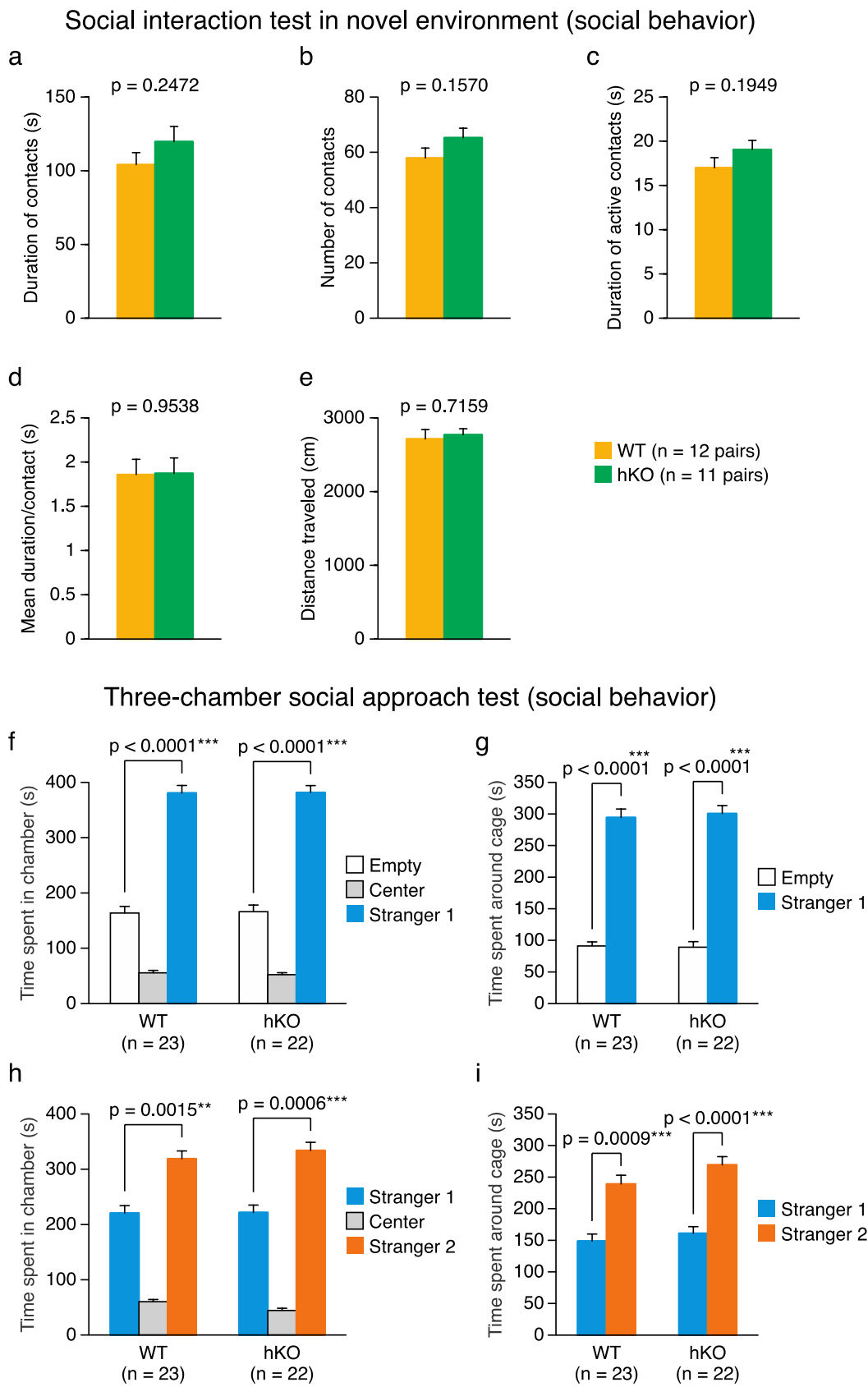


Figure S5. Social behavior of *Arid1b* hKO mice in the open field and in the three-chamber apparatus. (a–e) Social interaction test in a novel environment. (a) Duration of contacts. (b) Number of contacts. (c) Duration of active contacts. (d) Mean duration per contact. (e) Total distance traveled. (f–i) Three-chamber social approach test. (f) Time spent in chamber with an empty cage, center chamber, and chamber with a cage containing a stranger mouse (stranger 1). (g) Time spent around the empty cage and the cage with stranger 1. (h) Time spent in the chamber with the cage containing stranger 1, center chamber, and chamber with a cage containing a novel unfamiliar mouse (stranger 2). (i) Time spent around the cage containing stranger 1 and the cage containing stranger 2. Data from the social interaction test (WT, $n = 12$ pairs; *Arid1b* hKO, $n = 11$ pairs) and three-chamber social approach test (WT, $n = 23$; *Arid1b* hKO, $n = 22$) are expressed as the mean \pm SEM. Significant differences between genotypes are indicated with ** $p < 0.01$ and *** $p < 0.001$, as determined by Student's two-tailed t -test (a–e) or unpaired t -test (f–i).

Figure S6

Comparisons of brain gene expression patterns

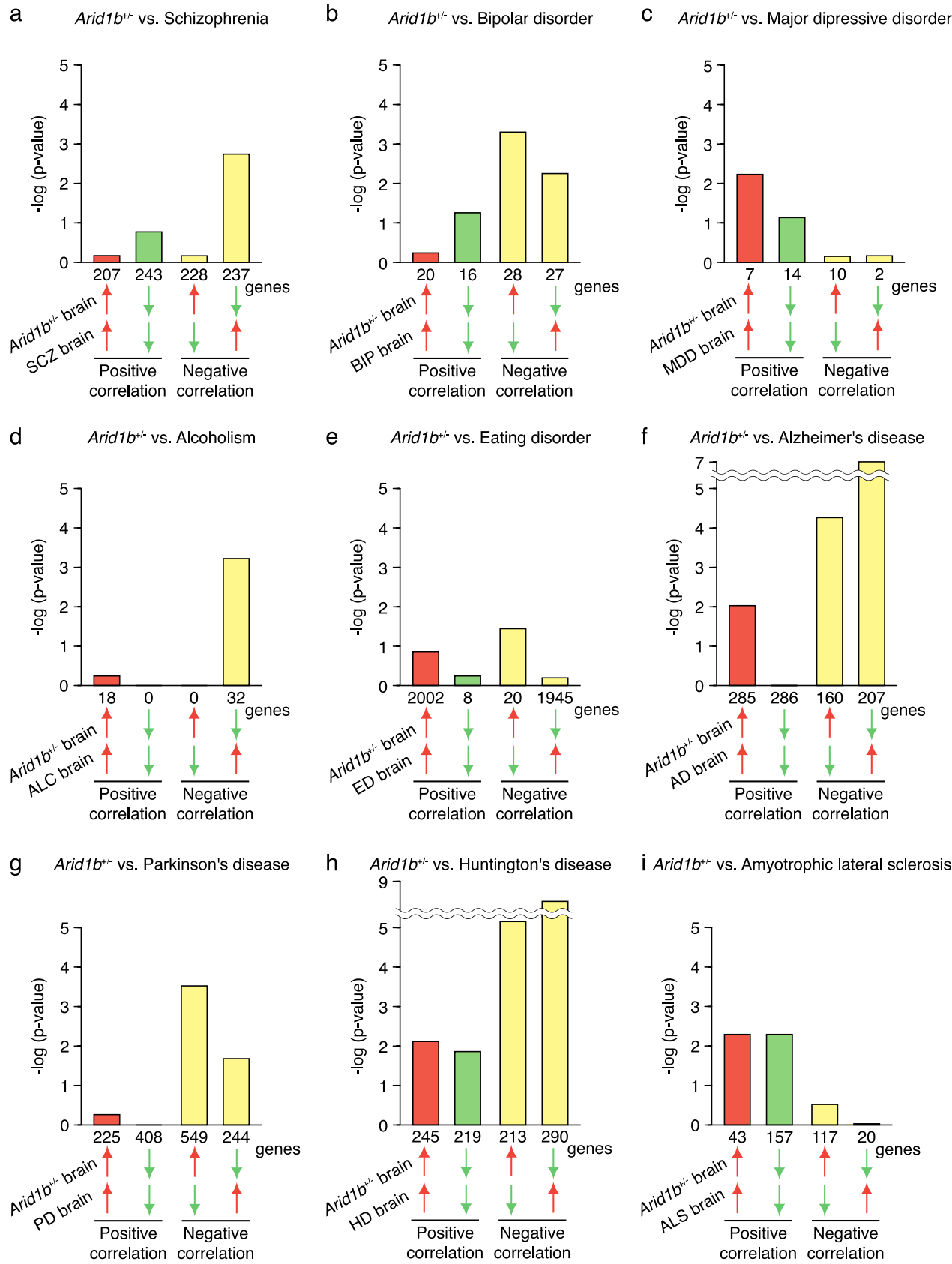


Figure S6. Comparison of brain gene expression patterns in *Arid1b* hKO mice with other genomic data. (a) Comparison of brain gene expression patterns in *Arid1b* hKO mice with those in schizophrenia, (b) bipolar disorder, (c) depressive disorder, (d) alcoholism, (e) eating disorder, (f) Alzheimer's disease, (g) Parkinson's disease, (h) Huntington's disease and (i) amyotrophic lateral sclerosis patients.

Figure S7

Malformed brain in 5% of *Arid1b* hKO mice

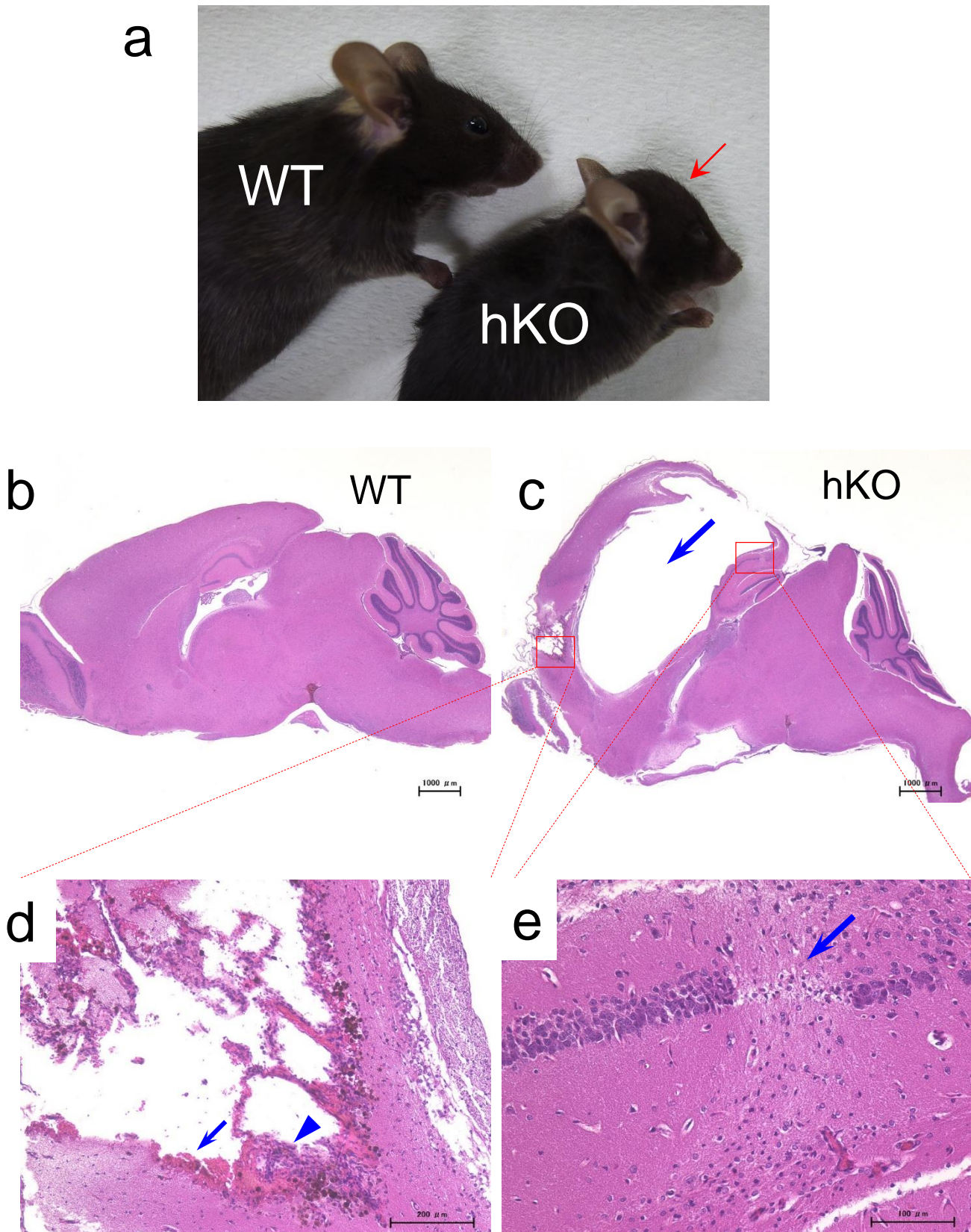


Figure S7. Appearance of *Arid1b* hKO mouse with malformed brain and wild type mouse with normal brain. (a) A mouse with an inflated head (right, red arrow) and a normal littermate (left) are *Arid1b* hKO and wild type, respectively. (b) Wild-type mouse brain (sagittal section) stained with hematoxylin–eosin. (c) Section of *Arid1b* hKO brain. Enlarged lateral ventricle (arrow) and some malformations (red frames) are indicated. (d) Enlargement of the left-hand framed portion of (c), showing an abnormal cavity (arrow) and new vascularization (arrow head). (e) Enlargement of the right-hand framed portion of (c), showing corruption in the pyramidal cell layer of the hippocampus (arrow).

Table S1: A behavioral test battery in Arid1b hKO mice.

Order	Test	Age (weeks)	Figure
1	General health and neurological screen	10-13	Figure 2a, b and S2a-c
2	Light/dark transition test	10-13	Figure S3a-d
3	Open field test	11-13	Figure S3e-h
4	Elevated plus maze test	11-14	Figure 1a-d
5	Hot plate test	12-14	Figure S2c
6	Social interaction test	12-14	Figure S5a-e
7	Rotarod test	12-15	Figure 1c
8	Three-chamber social approach test	13-15	Figure S5f-i
9	Prepulse inhibition test	13-16	Figure S2d, e
10	Porsolt forced swim test	13-16	Figure 3g, h
11	Beam test	16-19	Figure 2d-h
12	Barnes maze test	16-23	Figure 1g, h
13	Fear conditioning test	33-40	Figure 3a-f
14	Home cage social interaction test	39-42	Figure 1e, f and S4a-c

Supplementary Table S2. Microarray and RNA-seq datasets used in the brain gene expression pattern analysis.

Dataset	Accession number	Brain sample	Figure
Autism spectrum disorder	GSE38322	Occipital lobe of autistic patients	Figure 4a
Chd8 heterozygous knockout mice	DRA003116	Whole brain of adult male Chd8 heterozygous knockout mice	Figure 4b
Fast-spiking interneurons in neonatal mouse brain	GSE17806	Fast-spiking interneurons isolated from the somatosensory cortex of mice at 7 days old	Figure 4c
Schizophrenia (SCZ)	GSE53987	Prefrontal cortex (BA46) tissues of female schizophrenia patients	Supplementary figure 6a
Bipolar disorder (BIP)	GSE35978	Parietal cortex of patients with bipolar disorder	Supplementary figure 6b
Major depressive disorder (MDD)	GSE54575	Orbital ventral prefrontal cortices of major depressive disorder patients	Supplementary figure 6c
Alcoholism (ALC)	GSE49376	Prefrontal cortex of patients with alcoholism	Supplementary figure 6d
Eating disorder (ED)	GSE60190	Prefrontal cortex of patients with eating disorder	Supplementary figure 6e
Obsessive-compulsive disorder	No data available		
Panic disorder	No data available		
Anxiety disorder	No data available		
Posttraumatic stress disorder	No data available		
Alzheimer's disease (AD)	GSE48350	Post central gyri of Alzheimer's disease patients	Supplementary figure 6f
Parkinson's disease (PD)	GSE8397	Superior frontal gyrus of Parkinson's disease patients	Supplementary figure 6g
Huntington's disease (HD)	GSE79666	Motor cortices of patients with Huntington's disease	Supplementary figure 6h
Amyotrophic lateral sclerosis (ALS)	GSE67196	Frontal cortices of patients with amyotrophic lateral sclerosis	Supplementary figure 6i
Spinocerebellar disease	No data available		
Multiple system atrophy	No data available		
Progressive supranuclear ophthalmoplegia	No data available		

Supplementary Table S3. Statistical analyses of behavioral data.

Test	Measure	Figure	t-test	ANOVA		
				Genotype	Trial/Time/Block/Session	Genotype × Trial/Time/Block/Session
Physical characteristics and neurological screen	Body weight (g)	Figure	$t_{44} = 5.44, p < 0.0001$			
	Body temperature (°C)	Figure	$t_{44} = 0.11, p = 0.9127$			
	Grip strength (N)	Figure	$t_{44} = 2.21, p = 0.0325$			
	Wire hang latency (s)	Figure	$t_{44} = 3.16, p = 0.0029$			
Hot plate test	Hot plate latency (s)	Figure	$t_{44} = 1.95, p = 0.0571$			
Rotarod test	Rotarod latency (s)	Figure		$F_{1,44} = 20.58, p < 0.0001$	$F_{3,320} = 20.39, p < 0.0001$	$F_{3,320} = 0.65, p = 0.6630$
Beam test	Moving speed (cm/s) on wide beam	Figure		$F_{1,21} = 9.94, p = 0.0048$	$F_{3,305} = 23.76, p < 0.0001$	$F_{3,305} = 0.66, p = 0.6553$
	Moving speed (cm/s) on narrow beam	Figure		$F_{1,21} = 11.22, p = 0.0030$	$F_{3,305} = 4.37, p = 0.0012$	$F_{3,305} = 1.32, p = 0.2604$
	Number of movements on wide beam	Figure		$F_{1,21} = 0.27, p = 0.6077$	$F_{3,305} = 2.36, p = 0.0453$	$F_{3,305} = 0.34, p = 0.8877$
	Number of movements on narrow beam	Figure		$F_{1,21} = 5.68, p = 0.0267$	$F_{3,305} = 1.84, p = 0.1106$	$F_{3,305} = 0.54, p = 0.7445$
	Total duration of movements (s) on wide beam	Figure		$F_{1,21} = 13.11, p = 0.0016$	$F_{3,305} = 23.43, p < 0.0001$	$F_{3,305} = 0.28, p = 0.9215$
	Total duration of movements (s) on narrow beam	Figure		$F_{1,21} = 14.77, p = 0.0009$	$F_{3,305} = 5.06, p = 0.0003$	$F_{3,305} = 1.37, p = 0.2433$
	Latency (s) on wide beam	Figure		$F_{1,21} = 5.43, p = 0.0299$	$F_{3,305} = 3.45, p = 0.0063$	$F_{3,305} = 0.59, p = 0.7059$
	Latency (s) on narrow beam	Figure		$F_{1,21} = 2.13, p = 0.1591$	$F_{3,305} = 2.21, p = 0.0587$	$F_{3,305} = 0.16, p = 0.9763$
	Number of slips on wide beam	Figure		$F_{1,21} = 11.98, p = 0.0023$	$F_{3,305} = 4.39, p = 0.0011$	$F_{3,305} = 2.24, p = 0.0557$
	Number of slips on narrow beam	Figure		$F_{1,21} = 20.65, p = 0.0002$	$F_{3,305} = 1.64, p = 0.1551$	$F_{3,305} = 1.14, p = 0.3433$
Open field test	Distance traveled (cm)	Figure		$F_{1,44} = 8.74, p = 0.0050$	$F_{23,1002} = 70.66, p < 0.0001$	$F_{23,3002} = 1.05, p = 0.4036$
	Vertical activity	Figure		$F_{1,44} = 6.54, p = 0.0140$	$F_{23,1002} = 29.84, p < 0.0001$	$F_{23,3002} = 1.20, p = 0.2358$
	Center time (s)	Figure		$F_{1,44} = 0.03, p = 0.8636$	$F_{23,1002} = 5.98, p < 0.0001$	$F_{23,3002} = 0.70, p = 0.8530$
	Stereotypic counts	Figure		$F_{1,44} = 4.12, p = 0.0484$	$F_{23,1002} = 49.56, p < 0.0001$	$F_{23,3002} = 1.04, p = 0.4144$
Light/dark transition test	Distance traveled (cm) in light chamber	Figure	$t_{44} = 2.01, p = 0.0508$			
	Distance traveled (cm) in dark chamber	Figure	$t_{44} = 1.72, p = 0.0926$			
	Latency to light chamber (s)	Figure	$t_{44} = 0.28, p = 0.7827$			
	Time spent in light chamber (s)	Figure	$t_{44} = 1.19, p = 0.2395$			
Elevated plus maze test	Number of transitions	Figure	$t_{44} = 0.43, p = 0.6663$			
	Distance traveled (cm)	Figure	$t_{44} = 2.09, p = 0.0429$			
	Number of entries	Figure	$t_{44} = 2.36, p = 0.0231$			
	Entries into open arms (%)	Figure	$t_{44} = 2.82, p = 0.0072$			
Social interaction test	Time on open arms (%)	Figure	$t_{44} = 2.31, p = 0.0259$			
	Distance traveled (cm)	Figure	$t_{21} = 0.37, p = 0.7159$			
	Number of contacts	Figure	$t_{21} = 1.47, p = 0.1570$			
	Total duration of contacts (s)	Figure	$t_{21} = 1.19, p = 0.2472$			
Three-chamber social approach test (Sociability test)	Total duration of active contacts (s)	Figure	$t_{21} = 1.34, p = 0.1949$			
	Mean duration of contact (s)	Figure	$t_{21} = 0.06, p = 0.9538$			
	Time spent in chamber (s) in WT	Figure	$t_{21} = 8.62, p < 0.0001$			
	Time spent in chamber (s) in hKO	Figure	$t_{21} = 8.93, p < 0.0001$			
Three-chamber social approach test (Social novelty preference test)	Time spent around cage (s) in WT	Figure	$t_{21} = 11.63, p < 0.0001$			
	Time spent around cage (s) in hKO	Figure	$t_{21} = 10.77, p < 0.0001$			
	Time spent in chamber (s) in WT	Figure	$t_{21} = 3.62, p = 0.0015$			
	Time spent in chamber (s) in hKO	Figure	$t_{21} = 4.05, p = 0.0006$			
Home cage social interaction test	Time spent around cage (s) in WT	Figure	$t_{21} = 3.82, p = 0.0009$			
	Time spent around cage (s) in hKO	Figure	$t_{21} = 4.84, p < 0.0001$			
	Activity level (A.U.)	Figure		$F_{1,18} = 5.48, p = 0.0310$	$F_{167,3006} = 28.95, p < 0.0001$	$F_{167,3006} = 2.52, p < 0.0001$
	Average activity level (A.U.) during the last 3 days (light phase)	Figure		$F_{1,18} = 2.50, p = 0.1309$	$F_{11,198} = 8.33, p < 0.0001$	$F_{11,198} = 1.00, p = 0.4433$
	Average activity level (A.U.) during the last 3 days (dark phase)	Figure		$F_{1,18} = 1.60, p = 0.2218$	$F_{11,198} = 13.47, p < 0.0001$	$F_{11,198} = 1.56, p = 0.1146$
	Number of particles	Figure		$F_{1,18} = 4.05, p = 0.0593$	$F_{167,3006} = 17.71, p < 0.0001$	$F_{167,3006} = 0.89, p = 0.8278$
	Average number of particles during the last 3 days (light phase)	Figure		$F_{1,18} = 6.17, p = 0.0231$	$F_{11,198} = 4.08, p < 0.0001$	$F_{11,198} = 0.44, p = 0.9367$
	Average number of particles during the last 3 days (dark phase)	Figure		$F_{1,18} = 3.11, p = 0.0949$	$F_{11,198} = 6.20, p < 0.0001$	$F_{11,198} = 0.61, p = 0.8188$
Startle response test	Startle response (110 dB)	Figure	$t_{44} = 3.26, p = 0.0022$			
	Startle response (120 dB)	Figure	$t_{44} = 1.29, p = 0.2053$			
Prepulse inhibition test	PPI (74-110 dB)	Figure	$t_{44} = 0.62, p = 0.5354$			
	PPI (78-110 dB)	Figure	$t_{44} = 0.14, p = 0.8894$			
	PPI (74-120 dB)	Figure	$t_{44} = 2.70, p = 0.0097$			
	PPI (78-120 dB)	Figure	$t_{44} = 4.09, p = 0.0002$			
Porsolt forced swim test	Immobility (%) on Day 1	Figure		$F_{1,42} = 3.90, p = 0.0550$	$F_{9,378} = 132.35, p < 0.0001$	$F_{9,378} = 2.29, p = 0.0164$
	Immobility (%) on Day 2	Figure		$F_{1,42} = 4.13, p = 0.0484$	$F_{9,378} = 21.21, p < 0.0001$	$F_{9,378} = 2.22, p = 0.0200$
	Distance traveled (cm) on Day 1	Figure		$F_{1,42} = 4.13, p = 0.0485$	$F_{9,378} = 188.60, p < 0.0001$	$F_{9,378} = 2.67, p = 0.0051$
	Distance traveled (cm) on Day 2	Figure		$F_{1,42} = 0.93, p = 0.3404$	$F_{9,378} = 23.29, p < 0.0001$	$F_{9,378} = 1.77, p = 0.0716$
Barnes maze test (acquisition)	Latency to target (s)	Figure		$F_{1,40} = 2.87, p = 0.0980$	$F_{6,320} = 20.89, p < 0.0001$	$F_{6,320} = 0.23, p = 0.9842$
Barnes maze test (reversal)	Latency to target (s)	Figure		$F_{1,40} = 4.78, p = 0.0347$	$F_{6,320} = 49.51, p < 0.0001$	$F_{6,320} = 2.16, p = 0.0595$
Barnes maze test (probe trial)	Time spent around target hole (s)	Figure	$t_{40} = 2.28, p = 0.0279$			
Fear conditioning test (Conditioning)	Freezing (%)	Figure		$F_{1,40} = 9.23, p = 0.0042$	$F_{7,280} = 17.65, p < 0.0001$	$F_{7,280} = 6.01, p < 0.0001$
Fear conditioning test (Context test 1 day after conditioning)	Freezing (%)	Figure		$F_{1,40} = 0.57, p = 0.4565$	$F_{4,160} = 5.04, p = 0.0007$	$F_{4,160} = 0.55, p = 0.6999$
Fear conditioning test (Cued test 1 day after conditioning, Pre-CS)	Freezing (%)	Figure		$F_{1,40} = 6.76, p = 0.0130$	$F_{2,80} = 29.40, p < 0.0001$	$F_{2,80} = 1.59, p = 0.2101$
Fear conditioning test (Cued test 1 day after conditioning, CS)	Freezing (%)	Figure		$F_{1,40} = 2.71, p = 0.1076$	$F_{2,80} = 21.31, p < 0.0001$	$F_{2,80} = 0.22, p = 0.8031$
Fear conditioning test (Context test 30 days after conditioning)	Freezing (%)	Figure		$F_{1,40} = 0.03, p = 0.8576$	$F_{4,160} = 4.15, p = 0.0032$	$F_{4,160} = 0.75, p = 0.5568$
Fear conditioning test (Cued test 30 days after conditioning, Pre-CS)	Freezing (%)	Figure		$F_{1,40} = 2.77, p = 0.1036$	$F_{2,80} = 9.46, p = 0.0002$	$F_{2,80} = 1.66, p = 0.1972$
Fear conditioning test (Cued test 30 days after conditioning, CS)	Freezing (%)	Figure		$F_{1,40} = 5.97, p = 0.0191$	$F_{2,80} = 12.92, p < 0.0001$	$F_{2,80} = 0.23, p = 0.7970$
Fear conditioning test (footshock 1)	Distance traveled (cm)	Figure		$F_{1,40} = 0.62, p = 0.4373$	$F_{14,560} = 40.72, p < 0.0001$	$F_{14,560} = 1.48, p = 0.1146$
Fear conditioning test (footshock 2)	Distance traveled (cm)	Figure		$F_{1,40} = 1.95, p = 0.1705$	$F_{14,560} = 44.01, p < 0.0001$	$F_{14,560} = 1.63, p = 0.0658$
Fear conditioning test (footshock 3)	Distance traveled (cm)	Figure		$F_{1,40} = 6.08, p = 0.0181$	$F_{14,560} = 46.07, p < 0.0001$	$F_{14,560} = 1.22, p = 0.2585$

Table S4. Down regulated genes in *Arid1b* hKO mice brain (fold change < -2, p < 0.05)

fold change	Gene Symbol	Description
-8.785834	Hoxb2	homeobox B2
-7.0651803	Prl	prolactin
-5.208952	Tg	thyroglobulin
-4.509183	9330111N05Rik	RIKEN cDNA 9330111N05 gene
-4.284863	Podnl1	podocan-like 1
-4.2418866	Pth2	parathyroid hormone 2
-4.225615	Igf2bp1	insulin-like growth factor 2 mRNA binding protein 1
-4.1967397	Gm2990	predicted gene 2990
-4.1946692	1700023A16Rik	RIKEN cDNA 1700023A16 gene
-4.0916605	Ccl3	chemokine (C-C motif) ligand 3
-3.8462672	LOC100503966	uncharacterized LOC100503966
-3.5904546	Cryaa	crystallin, alpha A
-3.5482562	Gm20199	predicted gene, 20199
-3.510942	Lin28a	lin-28 homolog A (C. elegans)
-3.320444	Abcb11	ATP-binding cassette, sub-family B (MDR/TAP), member 11
-3.3167024	C1qtnf3	C1q and tumor necrosis factor related protein 3
-3.2939663	Hoxd3	homeobox D3
-3.2942612	4932411G14Rik	RIKEN cDNA 4932411G14 gene
-3.276335	Pax8	paired box gene 8
-3.2846475	Gm5665	predicted gene 5665
-3.2428174	Hbq1b	hemoglobin, theta 1B
-3.2238915	Gm20337	predicted gene, 20337
-3.135054	4933405L10Rik	RIKEN cDNA 4933405L10 gene
-3.0332363	B230208H11Rik	RIKEN cDNA B230208H11 gene
-3.0280447	Gm19673	predicted gene, 19673
-2.99006	Agrp	agouti related protein
-2.9797118	Gm15941	predicted gene 15941
-2.9233184	4833417C18Rik	RIKEN cDNA 4833417C18 gene
-2.8478506	Acmsd	amino carboxymuconate semialdehyde decarboxylase
-2.8263907	Guca1a	guanylate cyclase activator 1a (retina)
-2.8012562	Ptk6	PTK6 protein tyrosine kinase 6
-2.7921495	Ppyr1	pancreatic polypeptide receptor 1
-2.7751737	Cdca3	cell division cycle associated 3
-2.7706063	Vgll2	vestigial like 2 homolog (Drosophila)
-2.7611718	Lipm	lipase, family member M
-2.7061338	Zfp345	zinc finger protein 345
-2.6982725	Mboat4	membrane bound O-acyltransferase domain containing 4
-2.6775281	Naa11	N(alpha)-acetyltransferase 11, NatA catalytic subunit
-2.6551392	Neurog1	neurogenin 1
-2.5700898	Tc2n	tandem C2 domains, nuclear
-2.5540054	Has2as	HAS2 antisense RNA (non-protein coding)
-2.4242957	Gm9725	predicted gene 9725
-2.406591	Cyp2d26	cytochrome P450, family 2, subfamily d, polypeptide 26
-2.3968318	Snora75	small nucleolar RNA, H/ACA box 75
-2.3988662	Irx6	Iroquois related homeobox 6 (Drosophila)
-2.3923612	Synb	syncytin b
-2.3772993	E130218I03Rik	RIKEN cDNA E130218I03 gene
-2.364054	Clic3	chloride intracellular channel 3
-2.337002	Hgfac	hepatocyte growth factor activator
-2.3373454	Npm2	nucleophosmin/nucleoplasmin 2
-2.3313246	Mir23b	microRNA 23b
-2.2768116	Gm13154	predicted gene 13154
-2.2683592	Slc5a4a	solute carrier family 5, member 4a
-2.2600186	Tusc5	tumor suppressor candidate 5
-2.203397	Wfdc3	WAP four-disulfide core domain 3
-2.1879494	Napsa	napsin A aspartic peptidase
-2.1738834	Gm19557	predicted gene, 19557
-2.1692603	Il27	interleukin 27
-2.1598554	Rhoh	ras homolog gene family, member H
-2.1567962	Epb4.2	erythrocyte protein band 4.2
-2.1499667	Best3	bestrophin 3
-2.1152246	Sbk2	SH3-binding domain kinase family, member 2
-2.120248	Ccdc63	coiled-coil domain containing 63
-2.1180272	Ccdc152	coiled-coil domain containing 152
-2.1040165	Tepp	testis, prostate and placenta expressed
-2.0983396	Muc1	mucin 1, transmembrane
-2.0994968	Fabp4	fatty acid binding protein 4, adipocyte
-2.0862854	Fam159b	family with sequence similarity 159, member B
-2.0938795	Ly9	lymphocyte antigen 9
-2.0866616	Igsf6	immunoglobulin superfamily, member 6

Table S5. Up regulated genes in *Arid1b* hKO mice brain (fold change < -2, p < 0.05)

fold change	Gene Symbol	Description
6.911925	Areg	amphiregulin
5.0602455	Gbp8	guanylate-binding protein 8
4.7839174	Klri2	killer cell lectin-like receptor family I member 2
4.435064	Zp2	zona pellucida glycoprotein 2
4.392006	A730018C14Rik	RIKEN cDNA A730018C14 gene
4.384695	F630028O10Rik	RIKEN cDNA F630028O10 gene
4.1315637	Gdf7	growth differentiation factor 7
4.08308	Gm12408	predicted gene 12408
4.00279	Bpifa1	BPI fold containing family A, member 1
3.9308658	Klf14	Kruppel-like factor 14
3.7878077	Fgfr4	fibroblast growth factor receptor 4
3.7767737	Gm2518	interferon induced transmembrane protein 2 pseudogene
3.6329799	Otop3	otopetrin 3
3.5988166	1700123I01Rik	RIKEN cDNA 1700123I01 gene
3.5129895	Mesp2	mesoderm posterior 2
3.5110056	Emilin3	elastin microfibril interfacer 3
3.5066862	Gm14492	predicted gene 14492
3.4818408	Tmem45b	transmembrane protein 45b
3.40611	Mogat1	monoacylglycerol O-acyltransferase 1
3.383388	Fbxo43	F-box protein 43
3.3563833	Gpr84	G protein-coupled receptor 84
3.3490303	Krt83	keratin 83
3.3343937	Myo15b	myosin XVB
3.3041756	Usp50	ubiquitin specific peptidase 50
3.2955153	Gm11961	predicted gene 11961
3.289348	Pax5	paired box gene 5
3.2450645	Slc6a14	solute carrier family 6 (neurotransmitter transporter), member 14
3.222701	2010001M09Rik	RIKEN cDNA 2010001M09 gene
3.2140906	Ffar3	free fatty acid receptor 3
3.1673195	Mmp8	matrix metalloproteinase 8
3.1610575	Cyp24a1	cytochrome P450, family 24, subfamily a, polypeptide 1
3.147995	Aqp2	aquaporin 2
3.0993717	1700120B22Rik	RIKEN cDNA 1700120B22 gene
3.084226	Slc25a31	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 31
3.0516515	Fbp1	fructose biphosphatase 1
3.0512648	Cyp2c44	cytochrome P450, family 2, subfamily c, polypeptide 44
2.9070935	4930519F16Rik	RIKEN cDNA 4930519F16 gene
2.9061913	Slc16a5	solute carrier family 16 (monocarboxylic acid transporters), member 5
2.8569329	A830012C17Rik	RIKEN cDNA A830012C17 gene
2.835883	Ces1f	carboxylesterase 1F
2.7937973	Olfir464	olfactory receptor 464
2.7877383	Cd244	CD244 natural killer cell receptor 2B4
2.787456	Hp	haptoglobin
2.7588398	BC024582	cDNA sequence BC024582
2.745353	1600010M07Rik	RIKEN cDNA 1600010M07 gene
2.7137992	Ifi272b	interferon, alpha-inducible protein 27 like 2B
2.7046108	Gm12676	predicted gene 12676
2.6633875	Serpib10-ps	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 10, pseudogene
2.6597853	Clec2i	C-type lectin domain family 2, member i
2.6458151	Tssk6	testis-specific serine kinase 6
2.6296997	Gm13403	predicted gene 13403
2.6193464	Gad1l	glutamate decarboxylase-like 1
2.5904422	Tmprss2	transmembrane protease, serine 2
2.5618844	Col9a1	collagen, type IX, alpha 1
2.5561414	Cilp	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase
2.511111	Insm2	insulinoma-associated 2
2.5058055	Ceacam15	carcinoembryonic antigen-related cell adhesion molecule 15
2.4807065	Abp1	amiloride binding protein 1 (amine oxidase, copper-containing)
2.4807065	2310002J15Rik	RIKEN cDNA 2310002J15 gene
2.473039	Cldn22	claudin 22
2.4644089	Gm10334	predicted gene 10334
2.4634347	Plac8	placenta-specific 8
2.4587035	P2rx3	purinergic receptor P2X, ligand-gated ion channel, 3
2.4282923	Xirp1	xin actin-binding repeat containing 1
2.415078	Lif	leukemia inhibitory factor
2.3905227	Ttc22	tetratricopeptide repeat domain 22
2.256361	Ccr10	chemokine (C-C motif) receptor 10
2.2426867	Gm15104	predicted gene 15104
2.2286832	C1qtnf7	C1q and tumor necrosis factor related protein 7
2.2283084	Adamts7	a disintegrin-like and metalloproteinase (reprolysin type) with thrombospondin type 1 motif, 7
2.2056947	1810064F22Rik	RIKEN cDNA 1810064F22 gene
2.181652	Prss55	protease, serine, 55
2.1674907	Klrb1f	killer cell lectin-like receptor subfamily B member 1F
2.1520178	Gylt1b	glycosyltransferase-like 1B
2.1451557	Gm16497	predicted gene 16497
2.1422753	Atp6v1e2	ATPase, H ⁺ transporting, lysosomal V1 subunit E2
2.1388183	LOC100503361	transmembrane protein 95-like
2.11306	Timp1	tissue inhibitor of metalloproteinase 1
2.090713	Fam154a	family with sequence similarity 154, member A
2.0536246	Gm17281	predicted gene, 17281
2.0510998	Lpcat2b	lysophosphatidylcholine acyltransferase 2B
2.048164	Idi2	isopentenyl-diphosphate delta isomerase 2
2.046321	ORF63	open reading frame 63
2.044373	Pabpc4l	poly(A) binding protein, cytoplasmic 4-like
2.0441408	Fgf23	fibroblast growth factor 23
2.0098748	Gm9836	predicted pseudogene 9836