Supplementary information for

Cognitive deficits and impaired hippocampal long-term potentiation in K_{ATP} -induced DEND syndrome

Shaul Yahil¹, David F. Wozniak^{2,4}, Zihan Yan¹, Steven Mennerick^{2,4} and Maria S. Remedi^{1,3}* ¹Department of Medicine, Division of Endocrinology, Metabolism, and Lipid Research, ²Department of Psychiatry, ³Department of Cell Biology and Physiology, ⁴Taylor Family Institute for Innovative Psychiatric Research, Washington University School of Medicine, 660 South Euclid Avenue, St. Louis, Missouri 63110, USA.

*Address all correspondence and reprint requests to MSR: Ph: (314) 362-6636, FAX: (314) 362-2244, email: <u>mremedi@wustl.edu</u>

Matherials and methods

<u>Animals</u> A Cre-inducible Kir6.2^[K185Q, Δ N30] GOF transgenic mouse line under the Rosa26 locus was previously generated (9). In this line, CAG-promoter dependent expression of Kir6.2^[K185Q, Δ N30] is prevented by a loxP-flanked Stop-cassette (Fig. S1A). Cre-mediated recombination excises the Stop-cassette and drives Kir6.2^[K185Q, Δ N30] expression in a tissue-specific manner along with soluble eGFP via an internal ribosomal entry site (IRES) (9). When crossed into appropriate promoter-Cre expressing mice this model allows selective induction of transgene expression, thereby modeling tissue-specific expression of K_{ATP}-GOF mutations.

<u>Behavioral tests</u> *One-hour locomotor activity and sensorimotor battery*- Mice were placed in transparent polystyrene enclosures (47.6x25.4x20.6cm) and movements were monitored using computerized photobeam instrumentation. In ledge and platform tests, mice were placed on an elevated Plexiglas ledge

(0.75cm wide) or small circular wooden platform (3.0cm diameter) elevated to 30 or 47cm, respectively, and the amount of time they remain on the platform was recorded. Screen tests were performed by placing mice head-oriented down in a wire mesh grid (16x10cm) elevated 47cm at 60° or 90°. The time taken to turn 180° and climb to the top of the wire-mesh was measured. Inverted screen tests began identically to screen tests, but the screens were then inverted 180° after ensuring the mouse had a secure grip. The time the mouse remain on the screen was measured. In the pole test, mice were oriented head-up with forepaws on top of a textured rod (8mmx55cm) and the time the mouse took to turn around and climb-down the pole was measured (a maximum score of 120s was assigned if the mouse fell off the pole). For walking initiation, mice were placed in the center of a 21x21cm square marked with tape, and the time mice took to leave the square was recorded. Each test lasted a maximum of 60s, except pole tests (120s).

MWM navigation- In cued trials, the escape platform was submerged beneath the water surface, but its location was denoted by a red tennis ball atop a rod, which was attached to the escape platform and served as a visual cue. To limit spatial learning during cued trials, the location of the platforms was varied across trials in the presence of very-few distal spatial cues. In place trials, the platform was hidden beneath the water surface and its location was kept constant across all trials, with several salient distal cues being present during testing. Mice were placed pseudorandomly into one of the four quadrants of the maze and had to learn the location of the submerged platform.

<u>RNA extraction, cDNA synthesis and qRT-PCR-</u> To address transcriptional levels of K_{ATP} channel expression, nK_{ATP} -GOF and hK_{ATP} -GOF brain tissues were subjected to reverse-transcriptase quantitative polymerase chain reaction (RT-qPCR). nK_{ATP} -GOF, hK_{ATP} -GOF, and littermate control mice were anesthetized with isofluorane prior to decapitation, then brains dissected into ice-cold PBS. Hippocampi were dissected and flash-frozen on liquid nitrogen. Total RNA was extracted from 25-30 mg of hippocampal tissue using RNeasy Mini-Kits (Qiagen) with an on-column DNase digestion step to remove genomic DNA. RNA concentration was measured using a NanoDrop One^C spectrophotometer (Thermo Scientific). 1000ng of RNA was reverse-transcribed in a 20µl final volume using a High Capacity cDNA

Reverse Transcription Kit (Applied Biosystems) alongside a no reverse-transcriptase (No-RT) control. *RT-qPCR* - cDNA samples were diluted to a concentration of $5ng/\mu l$ with nuclease-free water (Corning). Each RT-qPCR reaction consisted of $5\mu l$ cDNA (25ng total), 12.5 μl 2x PowerSybr Green I Master Mix (Applied Biosystems), 0.75 μl 10 μ M forward and reverse primers (300nM), and 6 μl nuclease-free water for a total reaction volume of 25 μl . Reactions were run in triplicate on an Applied Biosystems StepOnePlusTM Real-Time PCR System. Reaction cycle consisted of an initial denaturation for 10min at 95°C, followed by 40 cycles of 95°C for 15s; 60°C for 60s. Non-RT and non-DNA controls were included as negative controls in all plates. Primers were acquired either from previous publications (10) or the Harvard PrimerBank system, with ML32 run as a housekeeping gene (Table S7). *Data analysis and relative expression calculation*-StepOneTM Software (v2.3) was used to acquire RT-qPCR data and calculate cycle threshold (C_T) values. The delta C_T method was used to calculate relative expression levels for comparisons across genotypes, as follows:

 $K_{ATP}\text{-}GOF \text{ Expression} = 2^{-(K_{ATP}GOF(C_{T(Target Gene)} - C_{T(ML32)}) - K_{ATP}Control(C_{T(Target Gene)} - C_{T(ML32)}))}$

For littermate controls, C_T values were averaged, then subtracted from each triplicate value to produce average and standard deviation values for relative expression. Differences in gene expression between control littermates and K_{ATP} -GOF mice were assessed with unpaired Student's t-tests, with p<0.05 indicating statistically significant differences in expression. For eGFP expression we reported ΔC_T values with respect to ML32 since eGFP was not detected in control littermate mice, as expected by a Credependent construct. All analyses were performed on Microsoft Excel and Graphpad Prism.

<u>Glucose tolerance tests</u> Intraperitoneal Glucose Tolerance Tests were performed in 12hr fasted mice by injection of a bolus of glucose (1.5g/kg body weight). Tail blood was taken before (time 0) and at different times (15, 30, 45, 60, 90 and 120min) after glucose challenge and assayed for glucose content using the Glucometer Elite XL (Bayer Corp).

Immunofluorescence To address on-target recombination and transgene expression, anti-eGFP and anti-Cre immunofluorescence was performed in mouse frozen brain sections. nK_{ATP}-GOF, hK_{ATP}-GOF and littermate controls were perfused transcardially with Tyrode's-buffered saline (TBS) and fixative. TBS consisted of 0.85% NaCl and 25mM TRIZMA Base (Sigma), adjusted to pH=7.4 with HCl. Fixative consisted of 4% paraformaldehyde (PFA) and 0.1M monobasic monohydrate NaH₂PO₄, adjusted to pH=7.4 with NaOH. Brains were removed and placed for 4hrs in fixative before transfer to a sucrose gradient consisting of one overnight calibration in 15% sucrose in phosphate-buffered saline (PBS) followed by one overnight calibration in 30% sucrose in PBS. Whole brains were then frozen in blocks of Optimal Cutting Temperature (OCT) embedding medium over liquid nitrogen, sectioned sagittally or coronally at 7-10 μ m and plated onto Superfrost microscope slides for subsequent imaging. Cryosections were co-stained with anti-GFP (Abcam, Chk, ab13970, 1:500) and anti-Cre (Novagene; Rb, 69050, 1:1000) primary antibodies to detect K_{ATP} transgene (since eGFP was co-expressed with mutant K_{ATP}) and Cre expression. TruBlk quenching dye (1:20) was used to reduce background autofluorescence, and a secondary antibody concentration of 1:500 was applied.

Long-term potentiation

Hippocampal slice preparation- Sucrose-based slicing solutions were prepared as 87mM NaCl, 2.5mM KCl, 1.25mM anhydrous monobasic NaH₂PO₄, 25mM D-glucose, 75mM sucrose, and 25mM NaHCO₃. After 15min bubbling at room-temperature (RT) with 95% carbogen, 0.5mM CaCl₂ and 3mM MgCl₂ were added. Choline chloride-based solution was prepared as 92mM choline chloride, 2.5mM KCl, 1.2mM NaH₂PO₄, 25mM D-glucose, 5mM sodium ascorbate, 2mM thiourea, 3mM sodium pyruvate, 20mM HEPES, 30mM NaHCO₃). Recording aCSF consisted of 125mM NaCl, 2.5mM KCl, 1.25mM anhydrous-monobasic NaH₂PO₄, 3mM myo-inositol, 10mM D-glucose, 2mM sodium-pyruvate, and 25mM NaHCO₃. After 15min bubbling at RT with 95% carbogen, 2mM CaCl₂ and 1mM MgCl₂ were added. Slices were transferred to a choline chloride-based solution and allowed to recover at 32C in aCSF/95% carbogen for 30min before transfer to recording aCSF solutions at 30C. Slices were incubated at 30C in recording aCSF before transfer to a nylon-mesh recording chamber at 30C.

Measurement of fEPSP (electrophysiology)- Stimulating electrodes were placed at the interface of CA2 and CA1 in stratum radiatum, at the level of Schaffer Collateral fibers. Recording electrodes were placed distally into CA1 in both stratum radiatum and stratum pyramidale to capture synaptic events generated by action potentials traveling down the Schaffer collaterals and population spikes generated by CA1 pyramidal neurons, respectively. Internal solutions for recording pipettes consisted of aCSF. Recordings were performed on a MultiClamp 700B amplifier, digitized using a Digidata 1550 converter, and sampled at 20kHz at a filter bandwidth of 5kHz. The recording electrodes were borosilicate glass pipettes of ~one micron, granting an access resistance of 4-8MΩ. LTP were performed in current clamp-mode (Grass Instrument Co./Model-P511K pre-amplifier, Warner Instruments/Model-IE-210 electrometer, Digidata-1322A analog-to-digital converter) at 30C.

Whole-cell Patch Clamp Electrophysiology in Dissociated Hippocampal Neurons- Hippocampal tissue cultures (single-cell suspension onto collagen-coated tissue-culture plates) were incubated at least seven and up to fourteen days prior to patch-clamp recording. Low-potassium solutions (Na1, Na2) consisted of 2mM CaCl₂, 1mM MgCl₂, 10mM glucose, 135mM NaCl, 5mM KCl, 10mM HEPES, pH 7.2 w/ NaOH. Borosilicate pipettes were pulled to an access resistance between 4-8MΩ. Cells were first bathed in high sodium bath (identical to low-potassium solution) prior to local perfusion with experimental solutions, which were always applied in the following order: Low potassium 2 (Na1), high potassium 1 (K1), diazoxide (Dz), tolbutamide (Tol), high potassium 2 (K2), low potassium 2 (Na2). Low-potassium solutions (Na1, Na2) and the sodium bath were identical. High-potassium solutions (K1, K2) substituted 125 mM KCl and 5 mM NaCl for the concentrations in standard bath (pH with KOH). Diazoxide (Dz) and tolbutamide, respectively. All solutions also contained 1μM NBQX, 25μM APV, 10μM bicuculline, and 250nM TTX to isolate K_{ATP}-mediated currents (44). Internal solution consisted of K-gluconate with or without 0.5mM Mg-ATP and 2mM free MgCl₂.



Fig S1. Scheme of breeding strategy, glucose tolerance and K_{ATP} **gene expression** (**A**) schematic representation of Cre-dependent K_{ATP}-GOF mutation. The ROSA26 locus contains the loxP-flanked stop cassette, a pore-forming GOF mutation (Kir6.2^[K185Q,AN30]), and a GFP reporter under control of IRES (20). ROSA26-K_{ATP}-GOF mice were crossed with synapsin-Cre (Syn-Cre) (**B**), dopamine-receptor-D3-Cre (Drd3-Cre) (**C**) or tamoxifen-inducible pancreatic-homeobox1-Cre (Pdx-CreERTM (**D**) mice to generate pan-neuronal nK_{ATP}-GOF, hippocampal specific hK_{ATP}-GOF or pancreatic β-cell specific βK_{ATP}-GOF mice, respectively, alongside Cre-containing, ROSA26-containing, and wild-type littermates. Glucose tolerance tests in (**E**) nK_{ATP}-GOF mice (red, n=7) and littermate controls (grey, n=7), (**F**) hK_{ATP}-GOF mice (blue, n=11) and littermate controls (grey, n=12), and (**G**) βK_{ATP}-GOF mice (purple, n=8) and littermate controls (grey, n=8). All tests shown in this figure were acquired from the same cohort. (**H**) Hippocampal gene expression of Kir6.2 and SUR1 relative to ML32 (left) and ΔC_T for eGFP (right) in nK_{ATP}-GOF mice (red, n=3) and littermate controls (grey, n=3). (**I**) Hippocampal gene expression of Kir6.2 and SUR1 (left) and ΔC_T for eGFP (right) in hK_{ATP}-GOF mice (blue, n=3) and littermate controls (grey, n=3). *p<0.05 and ****p<0.0001. Non-significant differences are not indicated.



Fig. S2. Immunostaining of frozen brain sections in nK_{ATP} -GOF and hK_{ATP} -GOF mice. Anti-Cre (red) and anti-GFP (green) immunostaining in frozen sections of (A) nK_{ATP} -GOF and (B) hK_{ATP} -GOF. Control mice were used as negative control (C). DAPI nuclear staining in (blue).



Fig. S3. Sex effects in time on ledge and auditory cue tests for nK_{ATP} -GOF male and female mice. (A) Sensorimotor Battery test: time on ledge, (B) fear conditioning test: freezing during auditory cue. nK_{ATP} -GOF mice (red, n=7 males and n=7 females) and littermate control mice (gray, n=6 males and n=7 females). *p<0.05, **p<0.01, ***p<0.01****p<0.0001. All data in this figure were acquired from the same cohort.



Fig. S4. Baseline fEPSP slopes before LTP induction (**A**) Left: fEPSP slopes during baseline period in nK_{ATP} -GOF (red, n=7, 5 mice) and control littermates (grey, n=10, 6 mice); Right: average of baseline fEPSP slopes in left panel (**B**) Left: fEPSP slopes during baseline period in hK_{ATP} -GOF (blue, n=8, 3 mice) and control littermates (grey, n=12, 8 mice); Right: average of baseline fEPSP slopes in left panel. Non-significant differences are not indicated.



Fig. S5. Diabetic βK_{ATP} -GOF mice did not show most neurological features of DEND. Locomotor activity: (A) total ambulations, (B) vertical rears, (C) distance traveled in the periphery, (D) center entries and (E) time resting in βK_{ATP} -GOF mice (purple, n=12) and littermate controls (white, n=10). Sensorimotor battery: (F,G) climb to the top of the 60° and 90° inclined screen, (H) time on the ledge, (I) time to climb-down pole and (J) time on inverted screen. MWM cue trials: (K) escape path length, (L) latency. MWM place trials: (M) escape path length, (N) latency. MWM probe trials: (O) platform crossing and (P) time in target quadrant and spatial bias. Fear-conditioning: (Q) tone-shock baseline-training, (R) contextual fear and (S) auditory cue tests. *p<0.05, **p<0.01, ****p<0.0001. All data shown in this figure were acquired from the same cohort.

Variable (mean ± sd)	Overall Effects	F Statistics
Morris Water Maze (MWM)		
MWM Cued		
Escape Path Length (cm)	Genotype (Geno)	F(1,24) =10.83, p = 0.0031
	Session (S)	F(3,72) = 23.56, p < 0.00005
	Geno x S	F(3,72) = 4.702, p = 0.0047
Escape Path Latency (s)	Genotype	F(1,24) = 34.11, p < 0.00005
	Session (S)	F(3,72) = 20.10, p < 0.00005
Onimation and (and a)	Geno x S	ns
Swimming speed (cm/s)	Genotype	F(1,24) =114.1, p < 0.00005
	Copo x S	ns
MWM Place	Geno x S	115
Escape Path Length (cm)	Genotype	F(1.24) = 48.91 p < 0.00005
Escape i un Eengar (eni)	Session (S)	F(4.96) = 3.811 p = 0.0064
	Geno x S	F(4.96) = 5.960, p = 0.0003
Escape Path Latency (s)	Genotype	F(1,24) = 94.60, p < 0.00005
n de faite e	Session (S)	ns
	Geno x S	F(4,96) =4.217, p = 0.0034
Swimming speed (cm/s)	Genotype	F(1,24) = 39.19, p < 0.00005
01 03438 100 100 V04 10	Session (S)	F(4,96) = 11.85, p < 0.00005
0	Geno x S	F(4,96) = 2.751, p = 0.0325
MWM Probe		
Platform Crossings		
$(nK_{ATP}-GOF: 0.571 \pm 0.8516)$	Genotype	F(1,24) = 41.25, p < 0.00005
$(nK_{ATP}-control: 5.571 \pm 2.709)$		
Time in Target Quadrant (s)		
(nK _{ATP} -GOF: 11.86 ± 4.827)	Genotype	F(1,24) = 63.57, p < 0.00005
$(nK_{ATP}$ -control: 31 ± 7.282)		
Spatial Bias	T.1 (7)	5/1.01/2 11.0155
	Trials (T)	F(1,24) = 14.6155, p < 0.00005
Feer Conditioning		
Fear Conditioning		
Tone Shock Training		
Baseline Freezing Time (%)	Genotype	ns
December recording rand (70)	Session (S)	ns
	Geno x S	ns
Freezing Time in Training (%)	Genotype	F(1,24) = 7.578, p = 0.0111
	Session (S)	F(2.48) = 46.66, p < 0.00005
	Geno x S	F(2,48) = 7.450, p = 0.0028
Contextual Fearing		
Freezing in Previous Context (%)	Genotype	F(1,24) = 20.89, p = 0.0001
	Session (S)	F(7,168) = 5.4045, p = 0.0004
	Geno x S	F(7,168) = 5.4013, p = 0.0004
Auditory Cue		
Baseline Freezing Time (%)	Genotype	ns
	Session (S)	F(1,24) = 11.41, p = 0.0025
	Geno x S	ns
Freezing Time in Testing (%)	Genotype	F(1,24) = 28.63, p < 0.00005
	Session (S)	F(7,168) = 26.95, p < 0.00005
	Geno x S	F(1,168) = 4.68, p = 0.0002

Table S1. Means and ANOVA effects for locomotor activity assays, sensorimotor battery, and rotarod assays for nK_{ATP}-GOF and control mice

Variable (mean ± sd)	Overall Effects	F Statistics
Morris Water Maze (MWM)		
7		
MWM Cued		
Escape Path Length (cm)	Genotype (Geno)	F(1,24) = 10.83, p = 0.0031
	Blocks of Trials (BT)	F(3,72) = 23.56, p < 0.00005
	Geno x BI	F(3,72) = 4.702, p = 0.0047
Escape Path Latency (s)	Genotype	F(1,24) = 34.11, p < 0.00005
	BIOCKS OF TRIAIS (BT)	F(3,72) = 20.10, p < 0.00005
Curioranian anneal (ann(a)		ns
Swimming speed (cm/s)	Blooks of Trials (PT)	P(1,24) = 114.1, p < 0.00005
	Cono x PT	115
MW/M Place	Geno X D1	115
Eccane Dath Length (cm)	Capatura	E(1.24) = 48.91 p < 0.00005
Liscape Faul Length (cm)	Blocks of Trials (BT)	F(1,24) = 40.51, p < 0.00005
	Cono y BT	F(4,96) = 5.061, p = 0.0004
Econo Dath Latancy (c)	Genetype	F(1,24) = 94.60 p < 0.00005
Escape Fail Latency (3)	Blocks of Trials (BT)	ns
	Geno x BT	F(4.96) = 4.217 n = 0.0034
Swimming speed (cm/s)	Genotype	F(1,24) = 39,19 p < 0,00005
Chilling opeca (child)	Blocks of Trials (BT)	F(4.96) = 11.85 p < 0.00005
	Geno x BT	F(4.96) = 2.751 p = 0.0325
MWM Probe		(,,ee)
Platform Crossings		
(nKATP-GOF: 0.571 ± 0.8516)	Genotype	F(1,24) = 41,25, p < 0.00005
(nKATP-control: 5.571 ±		
2.709)		
Time in Target Quadrant (s)		
(nKATP-GOF: 11.86 ± 4.827)	Genotype	F(1,24) = 63.57, p < 0.00005
(nKATP-control: 31 ± 7.282)		
Spatial Bias		
	Trials (T)	F(1,24) = 14.6155, p < 0.00005
	200	
Fear Conditioning		
Tone-Shock Training		
Baseline Freezing Time (%)	Genotype	ns
	Minutes (M)	ns
	Geno x M	ns
Freezing Time in Training	Genotype	F(1,24) = 7.578, p = 0.0111
(%)		5/0.40 40.00 0.00005
	Minutes (M)	F(2,48) = 46.66, p < 0.00005
Contractual Examina	Geno XIVI	F(2,48) = 7.450, p = 0.0028
Contextual Fearing	Canabuna	E(1.24) = 20.80 = = 0.0001
(%)	Genotype	P(1,24) = 20.69, p = 0.0001
	Minutes (M)	F(7,168) = 5.4045, p = 0.0004
	Geno x M	F(7,168) = 5.4013, p = 0.0004
Auditory Cue		
Baseline Freezing Time (%)	Genotype	ns
	Minutes (M)	F(1,24) = 11.41, p = 0.0025
	Geno x M	ns
Freezing Time in Testing (%)	Genotype	F(1,24) = 28.63, p < 0.00005
	Minutes (M)	F(7,168) = 26.95, p < 0.00005
	Geno x M	F(7,168) = 4.68, p = 0.0002

Table S2. Means and ANOVA effects for Morris Water Maze and fear conditioning assays in nKATP-

GOF and control mice

Variable (mean ± sd)	Overall Effects	F Statistics
Morris Water Maze (MWM)		
MWM Cued	0	F(4.04) = 40.02 = = 0.0024
Escape Path Length (cm)	Genotype (Geno)	F(1,24) = 10.83, p = 0.0031
	Blocks of Trials (BT)	F(3,72) = 23.56, p < 0.00005
Concern Dath Later and (a)	Geno X BI	F(3,72) = 4.702, p = 0.0047
Escape Path Latency (s)	Genotype Blooks of Trials (PT)	F(1,24) = 34.11, p < 0.00005
	Gone v BT	r(3,12) = 20.10, p < 0.00005
Swimming speed (cm/s)	Genotype	F(1, 24) = 114, 1, p < 0,00005
Swimming speed (crivs)	Blocks of Trials (BT)	ns
	Geno x BT	ns
MWM Place	0000 XD1	
Escape Path Length (cm)	Genotype	F(1.24) = 48.91 p < 0.00005
zooupo i un zongin (oni)	Blocks of Trials (BT)	F(4.96) = 3.811 p = 0.0064
	Geno x BT	F(4.96) = 5.960, p = 0.0003
Escape Path Latency (s)	Genotype	F(1,24) = 94.60, p < 0.00005
	Blocks of Trials (BT)	ns
	Geno x BT	F(4,96) =4.217, p = 0.0034
Swimming speed (cm/s)	Genotype	F(1,24) = 39.19, p < 0.00005
	Blocks of Trials (BT)	F(4,96) = 11.85, p < 0.00005
	Geno x BT	F(4,96) = 2.751, p = 0.0325
MWM Probe		
Platform Crossings		
$(nK_{ATP}-GOF: 0.571 \pm 0.8516)$	Genotype	F(1,24) = 41.25, p < 0.00005
$(nK_{ATP}-control: 5.571 \pm 0.700)$	1.1000.05	
Time in Target Quadrant (a)		
$(pK_{res}, COE: 11.86 \pm 4.827)$	Genetype	F(1,24) = 63.57 p < 0.00005
$(nK_{arp}-control: 31 + 7.282)$	Genotype	1 (1,24) = 03.31, p < 0.00003
Snatial Bias		
oputur bius	Trials (T)	F(1.24) = 14.6155 p < 0.00005
Fear Conditioning		
Tone-Shock Training		
Baseline Freezing Time (%)	Genotype	ns
	Minutes (M)	ns
	Geno x M	ns
Freezing Time in Training (%)	Genotype	F(1,24) = 7.578, p = 0.0111
	Minutes (M)	F(2,48) = 46.66, p < 0.00005
	Geno x M	F(2,48) = 7.450, p = 0.0028
Contextual Fearing		
Freezing in Previous Context (%)	Genotype	F(1,24) = 20.89, p = 0.0001
	Minutes (M)	F(7,168) = 5.4045, p = 0.0004
	Geno x M	F(7,168) = 5.4013, p = 0.0004
Auditory Cue		
Baseline Freezing Time (%)	Genotype	ns
	Minutes (M)	F(1,24) = 11.41, p = 0.0025
	Geno x M	ns
Freezing Time in Testing (%)	Genotype	F(1,24) = 28.63, p < 0.00005
	Minutes (M)	F(7,168) = 26.95, p < 0.00005
	Geno x M	F(1,168) = 4.68, p = 0.0002
	1	

Table S3. Means and ANOVA effects for locomotor activity assays, sensorimotor battery, and rotarod assays for hK_{ATP}-GOF and control mice

Variable (mean ± sd)	Overall Effects	F Statistics
Morris Water Maze (MWW)		
MW/M Cued		
Ecoape Dath Length (cm)	Ganativas (Gana)	E(1.10) = 4.650 $p = 0.0441$
Escape Patri Lengtri (cm)	Blocks of Trials (BT)	F(1, 15) = 4.050, p = 0.0441 F(3, 57) = 39.62, p < 0.00005
	Geno y BT	ne
Escape Path Latency (s)	Genotype (Geno)	F(1.19) = 11.61 p = 0.003
Escape rain calency (3)	Blocks of Trials (BT)	F(3,57) = 40.62 p < 0.0005
	Geno x BT	ns
Swimming speed (cm/s)	Genotype (Geno)	$F(1 \ 19) = 9 \ 0.32 \ p = 0 \ 0.073$
owning speed (enroy	Blocks of Trials (BT)	F(3,57) = 4,588 p = 0,0087
22	Geno x BT	ns
MWM Place		
Escape Path Length (cm)	Genotype (Geno)	ns
Looopo i ani Longin (oni)	Blocks of Trials (BT)	F(4,76) = 3,501 p = 0,0112
	Geno x BT	ns
Escape Path Latency (s)	Genotype (Geno)	F(1,19) = 9,280, p = 0.0066
	Blocks of Trials (BT)	ns
	Geno x BT	ns
Swimming speed (cm/s)	Genotype (Geno)	F(1,19) = 10.18, p = 0.0048
	Blocks of Trials (BT)	F(4,76) =8.068, p < 0.00005
	Geno x BT	ns
MWM Probe		
Platform Crossings		
(hKATP-GOF: 1.000 ± 1.342)	Genotype	F(1,19) = 33.45, p < 0.00005
(hKATP-control: 4.750 ± 1.765)		
Time in Target Quadrant (s)		
(hK _{ATP} -GOF: 16.93 ± 6.535)	Genotype	F(1,19) = 4.700, p = 0.0431
(hK _{ATP} -control: 23.6 ± 7.409)		
Spatial Bias		
	Trials (T)	F(1,19) = 8.545, p = 0.0004
Fear Conditioning		
2	<i>k</i>	
Tone-Shock Training		
Baseline Freezing Time (%)	Genotype	ns
~~~~	Minutes (M)	ns
	Geno x M	ns
Freezing Time in Training (%)	Genotype	F(1,19) = 9.565, p = 0.006
-	Minutes (M)	F(2,38) = 38.03, p < 0.00005
	Geno x M	ns
Contextual Fearing		
(%)	Genotype	ns
000 - 00	Minutes (M)	ns
	Geno x M	F(7,133) = 2.519, p = 0.0360
Auditory Cue		
Baseline Freezing Time (%)	Genotype	ns
	Minutes (M)	ns
	Geno x M	ns
Freezing Time in Testing (%)	Genotype	ns
	Minutes (M)	F(7,133) = 7.827, p < 0.00005
	Geno x M	ns

Table S4. Means and ANOVA effects for Morris Water Maze and fear conditioning assays in

 $hK_{\mbox{\scriptsize ATP}}\mbox{-}{\rm GOF}$  and control mice

Variable (mean ± sd)	Overall Effects	F Statistics
Locomotor Activity		
Total Ambulations	Genotype (Geno)	ns
(Glib-nK _{ATP} -GOF: 5557 ± 3069)	Time Blocks (TB)	F(5,90) = 41.36, p < 0.00005
(Glib-nK _{ATP} -control: 3584 ± 1012)	Geno x TB	ns
Vertical Rears	Genotype (Geno)	ns
(Glib-nK _{ATP} -GOF: 586.8 ± 423.7)	Time Blocks (TB)	F(5,90) = 41.29, p < 0.00005
(Glib-nK _{ATP} -control: $531.1 \pm 168$ )	Geno x TB	ns
Entries into Center		
(Glib-nK _{ATP} -GOF: 278.5 ± 176.4)	Genotype	ns
(Glib-nK _{ATP} -control: $194.8 \pm 70.20$ )		
Distance in Periphery (cm)		
(Glib-nK _{ATP} -GOF: 13874 ± 5989)	Genotype	F(1,18) = 4.644, p = 0.0450
(Glib-nK _{ATP} -control: 9534 ± 1943)		
Sensorimeter Betten		
Climb Down Time on Dale (a)		
(Clin b Down Time on Pole (s) (Clib $pK_{res}$ COE: 47.72 + 35.84)	Ganatura	
(Glib-fit( $ATP$ -GOT : 47.72 ± 55.04)	Genotype	115
$\frac{(GIID-IIK_{ATP}-COIIIIOI. 27.07 \pm 11.50)}{Time to Top of 90% Screen$		
(Glib pK GOE: 19.83 ± 10.53)	Ganatypa	E(1.18) = 4.593 $p = 0.046$
(Glib nK == control: $34.28 \pm 17.18$ )	Genotype	1 (1,10) = 4.555, p = 0.040
(Gais in Approvintion, 54.20 ± 17.10)		
Morris Water Maze (MWM)		
MWM Cued		
Escape Path Length (cm)	Genotype (Geno)	ns
Loodpo i dai Longai (oni)	Blocks of Trials (BT)	F(3.54) = 32.20 n < 0.00005
	Geno x BT	ns
Escape Path Latency (s)	Genotype (Geno)	F(1.18) = 7.137 p = 0.0156
Escupe i un cateriey (s)	Blocks of Trials (BT)	F(3.54) = 38.94 p < 0.00005
8	Geno x BT	ns
Swimming speed (cm/s)	Genotype (Geno)	F(1,18) =12.71, p < 0.0022
()	Blocks of Trials (BT)	F(3.54) = 7.268, p < 0.0004
	Geno x BT	ns
MWM Place		
Escape Path Length (cm)	Genotype (Geno)	F(1,18) = 20.01, p = 0.0003
	Blocks of Trials (BT)	F(4,72) = 4.691, p = 0.002
20	Geno x BT	F(4,72) = 4.514, p = 0.0026
Escape Path Latency (s)	Genotype (Geno)	F(1,18) = 36.68, p = 0.00001
n (1991)	Blocks of Trials (BT)	ns
	Geno x BT	F(4,72) = 3.732, p = 0.0081
Swimming speed (cm/s)	Genotype (Geno)	F(1,18) = 11.29, p = 0.0035
	Blocks of Trials (BT)	F(4,72) = 6.708, p = 0.0001
	Geno x BT	ns
MWM Probe		
Time in Target Quadrant (s)		
(Glib-nK _{ATP} -GOF: 15.04 ± 6.878)	Genotype	F(1,18) = 38.87, p < 0.00005
(Glib-nK _{ATP} -control: $30.46 \pm 3.786$ )		
Spatial Bias		
	Trials (T)	F(3,54) = 14.03, p < 0.00005
Fear Conditioning		
Contextual Fearing		F(1 10) 00 00 0 0000
Freezing in Previous Context (%)	Genotype	F(1,18) = 20.69, p = 0.0002
	Minutes (M)	F(1, 126) = 4.741, p = 0.0003
A 112 C	Geno x M	ns
Auditory Cue		
Baseline Freezing Time (%)	Genotype	ns
	Winutes (W)	ns
	Geno x IVI	ns
Freezing Time in Lesting (%)	Genotype	F(1,18) = 7.567, p = 0.0131
×	I WINUTES (IVI)	r(1, 126) = 5.109, p = 0.0005
	Geno XIVI	ns

Table S5. Means and ANOVA effects for locomotor activity assays, sensorimotor battery, Morris

Water Maze, and fear conditioning assays in  $nK_{ATP}$ -Glib-GOF and control mice

Locomotor Activity         Fig. 3295         Example to the second secon	Variable (mean ± sd)	Overall Effects	F or T Statistics
Locomotor Activity         F(1,18)         F(2,59)         F(2,50)         F(2,50)         F(2,50) <td></td> <td></td> <td></td>			
Total Ambulations         Genotype (Geno) $F(1, 18) = 6.845, p = 0.0175$ $[BK_{ATP}-COF: 329 \pm 560, g < 0.00005$ $F(5, 90) = 59.69, p < 0.00005$ $[BK_{ATP}-COF: 1202 \pm 150, g          Geno x TB         ns           Distance in Penphery (cm)         Geno x TB         ns           [BK_{ATP}-COF: 1202 \pm 150, g          Genotype         F(1, 18) = 9.048, p = 0.0076 [BK_{ATP}-Control: 1223 \pm 190, g          Genotype         ns           Time Resting (s)         Genotype         ns           [BK_{ATP}-Control: 1233 \pm 17.7)         Genotype         T(1, 20) = 2.770, p = 0.0188 [BK_{ATP}-Control: 1852 \pm 374.1)         Time Resting (s)         Genotype [GK_{ATP}-Control: 36.4 \pm 31.50]         Time to Top of 60° Screen         F(1, 18) = 8.274, p = 0.0100 [BK_{ATP}-Control: 36.4 \pm 31.50]         Time to Top of Inverted Screen         F(1, 18) = 8.274, p = 0.0100 [BK_{ATP}-Control: 36.4 \pm 2.31.60]         Genotype         ns           [BK_{ATP}-Control: 54.63 \pm 12.25]         Time on Ledge (s)           [BK_{ATP}-Control: 54.63 \pm 12.25]         ns           Time on Ledge (s)         Genotype         ns           [BK_{ATP}-Control: 54.63 \pm 12.25]         ns           Moris Water Maze (MWM)         F(3,54) = 30.01, p < 0.0$	Locomotor Activity		
(BK _{ATP} -GOF: 3295 ± 36 2)         Time Blocks (TB) $F(5,90) = 58,99, p < 0.00005$ (BK _{ATP} -control: 4140 ±952 8)         Geno x TB         ns           Distance in Perphery (cm)         Geno x TB         ns           (BK _{ATP} -COT: 1283 ± 1306)         Entresi in Center         F(1,18) = 9.048, $p = 0.0076$ (BK _{ATP} -COT: 1283 ± 1306)         Genotype         ns           (BK _{ATP} -Cotrol: 243.6 ± 75.17)         Time Blocks (TB)         F(1,20) = 2.770, $p = 0.0188$ (BK _{ATP} -Cotrol: 1408 ± 217.7)         Genotype         ns           (BK _{ATP} -Cotrol: 1652 ± 374.1)         Genotype         ns           Sensorimotor Battery         Entresi To 50 60%         Sensorimotor Battery           Climb Down Time on Pole (s)         Genotype         ns           (BK _{ATP} -Cotrol: 36.05 ± 7.097)         Genotype         ns           Time to Top of Inverted Screen         F(1,18) = 8.274, $p = 0.0100$ (BK _{ATP} -cotrol: 36.63 ± 122.5)         Genotype         ns           Time to Top of Inverted Screen         F(3,54) = 29.57, $p < 0.00005$ (BK _{ATP} -cotrol: 36.74 ± 22.6)         Genotype (Geno)         ns           Time to Top of Inverted Screen         F(3,54) = 29.57, $p < 0.00005$ (BK _{ATP} -cotrol: 36.74 ± 22.6)         Ins         Screap Path Length (cm)<	Total Ambulations	Genotype (Geno)	$F(1 \ 18) = 6 \ 845 \ \alpha = 0 \ 0175$
$\begin{array}{c   c  } \hline   c   \\   c   \\$	$(\beta K_{ATP}-GOF; 3295 \pm 546.2)$	Time Blocks (TB)	F(5.90) = 59.69, p < 0.00005
Distance in Periphery (cm)         Image: constraint of the second	(βK _{ATP} -control: 4140 ±952.8)	Geno x TB	ns
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	Distance in Periphery (cm)		
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	(βK _{ATP} -GOF: 7829 ± 1560)	Genotype	F(1,18) = 9.048, p = 0.0076
Entres into Center ( $BK_{ATP}$ -COF: 202 2 = 5.05) Genotype ins ( $BK_{ATP}$ -COF: 1498 ± 217.7) Genotype $T(1.20) = 2.770, p = 0.0188$ ( $BK_{ATP}$ -Control: 1852 ± 374.1) Sensorimotor Battery Climb Down Time on Pole (s) ( $BK_{ATP}$ -Control: 35.04 ± 31.58) Time to Top of GoS Creen (BK_{ATP}-CoF: 17.58 ± 9.831) ( $BK_{ATP}$ -Cof: 17.58 ± 9.831) Genotype $F(1.18) = 8.274, p = 0.0100$ ( $BK_{ATP}$ -CoF: 77.58 ± 9.831) Genotype $F(1.18) = 8.274, p = 0.0100$ ( $BK_{ATP}$ -CoF: 77.58 ± 9.831) Genotype $F(1.18) = 8.274, p = 0.0100$ ( $BK_{ATP}$ -CoF: 77.68 ± 4.840) Genotype $F(1.18) = 8.274, p = 0.0100$ ( $BK_{ATP}$ -CoF: 36.74 ± 23.16) Genotype $F(1.18) = 8.274, p = 0.0100$ ( $BK_{ATP}$ -CoF: 36.74 ± 23.16) Genotype $F(3.54) = 30.01, p < 0.00005$ Geno x BT $F(3.54) = 30.01, p < 0.00005$ Geno x BT $F(3.54) = 29.57, p < 0.00005$ Escape Path Latency (s) Genotype (Geno) ns Elocks of Trials (BT) $F(3.54) = 29.57, p < 0.00005$ Geno x BT $F(3.54) = 29.57, p < 0.00005$ F(4.72) = 27.08, p < 0.00005 F(4.72) = 27.08, p < 0.00005 F(5.54) = 11.49, (Genotype (Geno) ns F(7.126) = 0.625, p = 0.0100 Fear Conditioning $F(7.126) = 9.453, p < 0.00005Fear Conditioning$ $F(7.126) = 0.625, p = 0.0191Fear Conditioning$ $F(7.126) = 0.0191$ $F(7.126) = 7.037, p < 0.0005Fear Conditioning$ $F(7.126) = 7.037, p < 0.0005Fear Conditioning$ $F(7.126) = 7.037, p < 0.0005Fear Conditioning$ $F(7.126) = 7.$	(βK _{ATP} -control: 10283 ± 1906)	-	
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	Entries into Center	0	
$ \begin{array}{c} (prk_{\rm PCOIND.} (24.30 \pm 10.17) \\ (BK_{\rm ATP}-COIND.} (24.30 \pm 217.7) \\ (BK_{\rm ATP}-COIND.} (14.98 \pm 21.58) \\ (BK_{\rm ATP}-COIND.} (14.58 \pm 31.49) \\ (BK_{\rm ATP}-COIND.} (14.58 $	$(\beta K_{ATP}-GOF: 202.2 \pm 50.50)$	Genotype	ns
Intervention         Title Section           INVEXTP-Control:         1852 ± 374.1)           Sensorimotor Battery         Intervention           Climb Down Time on Pole (s)         Genotype           (BKATP-COTTIC):         35.04 ± 31.58)           Time to Top of 60° Screen         F(1.18) = 8.274, $p = 0.0100$ (BKATP-Control:         35.04 ± 31.58)           Time to Top of 60° Screen         F(1.18) = 8.274, $p = 0.0100$ (BKATP-COTIC):         56.05 ± 7.097)           Time to Top of lowerted Screen         F(1.18) = 8.274, $p = 0.0100$ (BKATP-COTIC):         56.03 ± 12.25)           Time on Ledge (s)         Genotype         ns           (BKATP-COTIC):         56.20 ± 20.65)           Morris Water Maze (MWM)         Notris Water Maze (MWM)           Blocks of Trials (BT)         F(3.54) = 30.01, $p < 0.00005$ Geno x BT         ns           Escape Path Length (cm)         Genotype (Geno)         ns           Blocks of Trials (BT)         F(3.54) = 29.57, $p < 0.00005$ Geno x BT         ns         Secape Path Length (cm)         Genotype (Geno)           Escape Path Length (cm)         Genotype (Geno)         ns         Secape NBT           Blocks of Trials (BT)         F(3.54) = 24.89, $p $	Time Resting (s)	-	
(BKATP-Control: 1852 = 374.1)Check pSensorimotor BatteryImage: Control: 1852 = 374.1)Climb Down Time on Pole (s)Genotype(BKATP-COT: 41.06 = 17.01)Genotype(BKATP-COT: 55.04 = 31.59)Time to Top of 60° Screen(BKATP-COT: 17.95 = 9.831)Genotype(BKATP-COT: 57.68 ± 4.840)Genotype(BKATP-Cotrol: 56.04 = 31.59)Time to Top of Inverted Screen(BKATP-Cotrol: 56.75.78 ± 4.840)(BKATP-Cotrol: 36.74 ± 23.16)(BKATP-Cotrol: 36.20 ± 20.65)Morris Water Maze (MWM)MWM CuedEscape Path Length (cm)Genotype (Geno)Blocks of Trials (BT)F(3.54) = 30.01, p < 0.00005	$(\beta K_{ATP}-GOF: 1498 \pm 217.7)$	Genotype	T(1.20) = 2.770, $p = 0.0188$
Sensorimotor BatteryImage: sensorimotor BatteryClimb Down Time on Pole (s) ( $\beta K_{ATP}$ -GOF: 41.06 ± 17.01) ( $\beta K_{ATP}$ -GOF: 41.06 ± 17.01) ( $\beta K_{ATP}$ -GOF: 17.95 ± 9.831) ( $\beta K_{ATP}$ -GOF: 17.95 ± 9.831) ( $\beta K_{ATP}$ -Cortic: 8.605 ± 7.097)Time to Top of Inverted Screen ( $\beta K_{ATP}$ -Cortic: 8.605 ± 7.097)( $\beta K_{ATP}$ -Cortic: 8.605 ± 7.097)Time to Top of Inverted Screen ( $\beta K_{ATP}$ -Cortic: 36.63 ± 12.25)Time on Ledge (s) ( $\beta K_{ATP}$ -Cortic: 36.63 ± 12.25)Morris Water Maze (MWM)MWM Cued Escape Path Length (cm)Genotype (Geno) Geno x BTScape Path Latency (s)Genotype (Geno) Blocks of Trials (BT)F(3.54) = 29.57, p < 0.00005 Geno x BTMVM PlaceEscape Path Latency (s)Genotype (Geno) Blocks of Trials (BT)F(4,72) = 27.08, p < 0.00005 Geno x BTMWM PlaceEscape Path Latency (s)Genotype (Geno) Blocks of Trials (BT)F(4,72) = 27.08, p < 0.00005 Geno x BTMWM PlaceEscape Path Latency (s)Genotype (Geno) Blocks of Trials (BT)F(4,72) = 22.52, p < 0.00005 Geno x BTMWM Probe Blocks of Trials (BT)F(4,72) = 22.52, p < 0.00005 Geno x BTFear ConditioningFreezing Im Previous Context (%)Geno x MF(7,126) = 9.453, p < 0.00005 Geno x MFreezing Time (%)GenotypeResenting Freezing Time (%)Geno x MF(7,126) = 7.937, p < 0.0005 Geno x MFreezing Time in Testing (%)Geno x MF(7,1	(βK _{ATP} -control: 1852 ± 374.1)		
Sensorimotor BatteryImage: constraint of the sensor of the s			
Sensorimotor BatteryImage: Climb Down Time on Pole (s)Climb Down Time on Pole (s)Genotype(BK_ATP-GOF: 41.06 ± 17.01)GenotypeTime to Top of 60° Screen(BK_ATP-Control: 3.04 ± 31.58)Time to Top of for Screen(BK_ATP-Control: 8.05 ± 7.097)Time to Top of Inverted Screen(BK_ATP-CONTROL 8.40 ± 7.097)Time to Top of Inverted Screen(BK_ATP-CONTROL 8.40 ± 2.25)Time on Ledge (s)Genotype(BK_ATP-Control: 36.74 ± 23.16)(BKATP-Control: 36.74 ± 23.16)(BKATP-Control: 36.74 ± 23.16)(BKATP-Control: 36.74 ± 23.16)(BKATP-Control: 36.70 ± 20.65)Image: Control: 36.74 ± 23.16)MWM CuedEscape Path Length (cm)Genotype (Geno)Escape Path Length (cm)Genotype (Geno)Blocks of Trials (ET) $F(3.54) = 30.01, p < 0.00005$ Escape Path Latency (s)Genotype (Geno)Blocks of Trials (ET) $F(3.54) = 29.57, p < 0.00005$ MWM PlaceImage: Clicks of Trials (ET)Escape Path Length (cm)Genotype (Geno)Blocks of Trials (ET) $F(4.72) = 27.08, p < 0.00005$ Geno x BTnsEscape Path Latency (s)GenotypeGeno x BTnsImage: Clicks of Trials (ET) $F(4.72) = 27.08, p < 0.00005$ Geno x BTnsImage: Clicks of Trials (ET) $F(4.72) = 22.52, p < 0.00005$ Geno x BTnsImage: Clicks of Trials (ET) $F(4.72) = 22.52, p < 0.00005$ Geno x BTnsImage: Clicks of Trials (ET) $F(7.126) = 9.453, p < 0.00005$ Geno x BT </td <td></td> <td>8</td> <td></td>		8	
Climb Down Time on Pole (s)         Image: control 35.04 $\pm$ 31.58)           (BK_ATP-GOF: 41.06 $\pm$ 17.01)         Genotype         ns           (BK_ATP-Control 35.04 $\pm$ 31.58)         Image: control 35.04 $\pm$ 31.58)         Image: control 35.04 $\pm$ 31.58)           Time to Top of 60° Screen         F(1,18) = 8.274, $p = 0.0100$ (BK_ATP-GOF: 17.95 $\pm$ 9.831)         Genotype           Time to Top of Inverted Screen         Image: control 36.05 $\pm$ 7.097)         Image: control 36.05 $\pm$ 7.097)         Image: control 36.05 $\pm$ 7.097)           Time on Ledge (s)         Genotype         ns         Image: control 36.02 $\pm$ 20.65)           Image: control 36.20 $\pm$ 20.65)         Image: control 36.20 $\pm$ 20.65)         Image: control 36.20 $\pm$ 20.65)           Morris Water Maze (MWM)         Image: control 36.20 $\pm$ 20.65)         Image: control 36.20 $\pm$ 20.65)           Blocks of Trials (BT)         F(3,54) $\pm$ 30.01, $p < 0.00005$ Geno x BT           Escape Path Length (cm)         Genotype (Geno)         ns           Blocks of Trials (BT)         F(3,54) $=$ 20.01, $p < 0.00005$ Geno x BT           Escape Path Length (cm)         Genotype (Geno)         ns           Escape Path Length (cm)         Genotype (Geno)         ns           Escape Path Length (cm)         Genotype (0no)         ns           Escape Path Length (cm) <td< td=""><td>Sensorimotor Battery</td><td></td><td></td></td<>	Sensorimotor Battery		
Climb Down Time on Pole (s) [ $BK_{ATP}=CORTIOL 35.04 \pm 31.58$ ] Time to Top of 60° Screen [ $BK_{ATP}=Control: 35.04 \pm 31.58$ ] Time to Top of 60° Screen [ $BK_{ATP}=Control: 8.605 \pm 7.097$ ] Time to Top of Inverted Screen [ $BK_{ATP}=Control: 54.63 \pm 12.25$ ] Time on Ledge (s) [ $BK_{ATP}=Control: 54.63 \pm 12.25$ ] Time on Ledge (s) [ $BK_{ATP}=Control: 54.63 \pm 12.25$ ] <b>Morris Water Maze (MWM)</b> <b>MVM Cued</b> Escape Path Length (cm) Blocks of Trials (BT) Escape Path Latency (s) Genotype (Geno) Blocks of Trials (BT) Escape Path Length (cm) Blocks of Trials (BT) F(3,54) = 29.57, p < 0.00005 Geno x BT ns Escape Path Length (cm) Blocks of Trials (BT) F(4,72) = 27.08, p < 0.00005 Geno x BT ns Escape Path Latency (s) Blocks of Trials (BT) F(4,72) = 22.08, p < 0.00005 Geno x BT ns Escape Path Latency (s) Blocks of Trials (BT) F(4,72) = 22.52, p < 0.00005 Geno x BT ns Escape Path Latency (s) Blocks of Trials (BT) F(4,72) = 22.52, p < 0.00005 Geno x BT ns Escape Path Latency (s) Blocks of Trials (BT) F(4,72) = 22.52, p < 0.00005 Geno x BT ns <b>MVM Probe</b> Time in Target Quadrant (s) [ $BK_{ATP}-COT: 28.63 \pm 11.49$ ] ( $BK_{ATP}-COT: 28.63 \pm 31.49$ ] Spatial Bias Freezing in Previous Context (%) Minutes (M) F(7,126) = 9.453, p < 0.00005 Fear Conditioning Contextual Fearing Freezing in Previous Context (%) Minutes (M) F(7,126) = 9.453, p < 0.00005 Freezing Time in Testing (%) Genotype ns Minutes (M) F(7,126) = 7.224, p = 0.01101 Auditory Cue Baseline Freezing Time (%) Genotype ns Minutes (M) F(7,126) = 7.237, p < 0.00005 Geno x M ns State Part Part Part Part Part Part Part Part	01		
$\begin{array}{c   l } \label{eq:constraint} \end{tabular} \end{tabuar} \end{tabular} \end{tabular} \end{tabular} tabula$	GIIIID DOWN TIME on Pole (s)	Genetyre	ne
$ \begin{array}{c c c } (prA_{11}-control: 30.94 \pm 31.30) \\ \hline \mbox{Time to Top 6 60° Screen} \\ (BA_{TP}-GOF: 17.95 \pm 9.831) \\ \hline \mbox{Gentype} \\ (BA_{TP}-Control: 8.605 \pm 7.097) \\ \hline \mbox{Time to Top of Inverted Screen} \\ (BA_{TP}-GOF: 57.68 \pm 4.840) \\ \hline \mbox{Gentype} \\ (BA_{TP}-control: 54.63 \pm 12.25) \\ \hline \mbox{Time on Ledge (s)} \\ (BA_{TP}-COTF) \\ (BA$	$(\beta K_{4TP} - GOT + 41.00 \pm 11.01)$	Genotype	115
$(\beta K_{ATT}-GOF: 17.95 \pm 9.831)$ Genotype $F(1,18) = 8.274, p = 0.0100$ $(\beta K_{ATT}-control: 8.605 \pm 7.097)$ Image to the second of inverted Screen         Image to the second of inverted Screen $(\beta K_{ATT}-control: 54.63 \pm 12.25)$ Image to the second of inverted Screen         Image to the second of inverted Screen $(\beta K_{ATTP}-control: 54.63 \pm 12.25)$ Image to the second of inverted Screen         Image to the second of inverted Screen $(\beta K_{ATTP}-control: 36.20 \pm 20.65)$ Image to the second of inverted Screen         Image to the second of inverted Screen $(\beta K_{ATTP}-control: 36.20 \pm 20.65)$ Image to the second of inverted Screen         Image to the second of inverted Screen $(\beta K_{ATTP}-control: 36.20 \pm 20.65)$ Image to the second of inverted Screen         Image to the second of inverted Screen $(\beta K_{ATTP}-Control: 36.20 \pm 20.65)$ Image to the second of inverted Screen         Image to the second of inverted Screen $(\beta K_{ATTP}-Control: Screen ST         Image to the second of inverted Screen ST         Image to the second of inverted Screen ST           (\beta K_{ATTP}-Control: Screen ST         Image to the second ST         Image to the second ST         Image to the second ST           (\beta K_{ATTP}-Control: Screen ST         Image to the second ST         Image to the second ST         Image to the second ST           (\beta K_{ATTP}-Contr$	Time to Top of 60° Screen		
$(\beta K_{ATP}-control: 8.605 \pm 7.097)$ $D$ Time to Top of Inverted ScreenGenotype $(\beta K_{ATP}-Control: 54.63 \pm 12.25)$ nsTime on Ledge (s)Genotype $(\beta K_{ATP}-Control: 36.74 \pm 23.16)$ Genotype $(\beta K_{ATP}-Control: 36.74 \pm 23.16)$ ( $\beta K_{ATP}-Control: 36.20 \pm 20.65)$ Morris Water Maze (MWM)Image: Control: 36.20 \pm 20.65)Morris Water Maze (MWM)Image: Control: 36.20 \pm 20.65)Morris Water Maze (MWM)Image: Control: 36.20 \pm 20.65)Blocks of Trials (BT)F(3.54) = 30.01, p < 0.00005	$(\beta K_{ATP}-GOF: 17.95 \pm 9.831)$	Genotype	F(1,18) = 8.274, p = 0.0100
Time to Top of Inverted Screen ( $[BX_{ATP}-GOF: 57.68 \pm 4.840)$ ( $GRA_{TP}-Control: 54.63 \pm 12.25)$ Send to the temp main of the temp main of temp( $BX_{ATP}-GOF: 36.74 \pm 23.16)$ ( $BX_{ATP}-Control: 36.74 \pm 23.16)$ ( $BX_{ATP}-Control: 36.74 \pm 23.16)$ Send temp main of temp main of tempMorris Water Maze (MWM)Image: Context (Context)Morris Water Maze (MWM)Image: Context (Context)Morris Water Maze (MWM)Image: Context (Context)Morris Water Maze (MWM)Image: Context (Context)Blocks of Trials (BT)F(3.54) = 30.01, p < 0.00005	(βK _{ATP} -control: 8.605 ± 7.097)		
( $\beta$ K _{ATP} -GOF: 57.68 ± 4.840)         Genotype         ns           ( $\beta$ K _{ATP} -control: 54.63 ± 12.25)         Imme on Ledge (s)         Genotype         ns           ( $\beta$ K _{ATP} -GOF: 36.74 ± 23.16)         ( $\beta$ K _{ATP} -Control: 36.20 ± 20.65)         Imme on Ledge (s)         Genotype           Morris Water Maze (MWM)         Imme on Ledge (s)         Genotype (Geno)         ns           MWM Cued         Escape Path Length (cm)         Genotype (Geno)         ns           Escape Path Latency (s)         Genotype (Geno)         ns           Blocks of Trials (BT) $F(3,54) = 30.01, p < 0.00005$ Geno x BT         ns           Blocks of Trials (BT) $F(3,54) = 29.57, p < 0.00005$ Geno x BT         ns           Blocks of Trials (BT) $F(4,72) = 27.08, p < 0.00005$ Geno x BT         ns           Escape Path Latency (s)         Genotype (Geno)           Blocks of Trials (BT) $F(4,72) = 22.52, p < 0.00005$ Geno x BT         ns           Blocks of Trials (BT) $F(4,72) = 22.52, p < 0.00005$ Geno x BT         ns           ( $\beta$ K _{ATP} -COF: 26.08 ± 11.49)         Genotype           ( $\beta$ K _{ATP} -Control: 28.63 ± 3.409)         Spatial Bias           Freezing in Previous Context </td <td>Time to Top of Inverted Screen</td> <td></td> <td></td>	Time to Top of Inverted Screen		
$\begin{array}{c   l   l   l   l   l   l   l   l   l  $	(βK _{ATP} -GOF: 57.68 ± 4.840)	Genotype	ns
Inne on Ledge (s)Genotypens $(\beta K_{ATP}-GOF: 36.74 \pm 23.16)$ $(\beta K_{ATP}-GOF: 36.74 \pm 23.16)$ $(\beta K_{ATP}-GOF: 36.74 \pm 23.16)$ Morris Water Maze (MWM) $(M = 100000000000000000000000000000000000$	$(\beta K_{ATP}-control: 54.63 \pm 12.25)$		
$\begin{array}{c   l   l   l   l   l   l   l   l   l  $	Time on Ledge (s)	Genotype	ns
Image: product set of the s	$(\beta K_{ATP}-GOF: 36.74 \pm 23.16)$		
Morris Water Maze (MWM)Image: Constraint of the system of th	(prarp-control: 56.20 ± 20.65)		
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MWM CuedGenotype (Geno)nsEscape Path Length (cm)Genotype (Geno)nsBlocks of Trials (BT) $F(3,54) = 30.01, p < 0.00005$ Geno x BTnsEscape Path Latency (s)Genotype (Geno)Blocks of Trials (BT) $F(3,54) = 29.57, p < 0.00005$ Geno x BTnsBlocks of Trials (BT) $F(3,54) = 29.57, p < 0.00005$ Geno x BTnsEscape Path Length (cm)Genotype (Geno)Blocks of Trials (BT) $F(4,72) = 27.08, p < 0.00005$ Geno x BTnsEscape Path Latency (s)Genotype (Geno)Blocks of Trials (BT) $F(4,72) = 22.52, p < 0.00005$ Geno x BTnsBlocks of Trials (BT) $F(4,72) = 22.52, p < 0.00005$ Geno x BTnsBlocks of Trials (BT) $F(4,72) = 22.52, p < 0.00005$ Geno x BTns( $\beta K_{ATP}$ -GOF: 26.08 ± 11.49)Genotype( $\beta K_{ATP}$ -GOT: 28.63 ± 3.409)Spatial BiasTrials (T) $F(3,54) = 24.89, p < 0.00005$ Fear ConditioningFreezing in Previous Context( $\%$ )Minutes (M) $F(7,126) = 9.453, p < 0.00005$ Geno x M $F(7,126) = 3.060, p = 0.0100$ Auditory CuensBaseline Freezing Time (%)GenotypeGeno x M $F(7,126) = 7.224, p = 0.0150$ Freezing Time in Testing (%)GenotypeRenotypensMinutes (M) $F(7,126) = 7.937, p < 0.0005$ Geno x Mns			
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Blocks of Trials (BT) $F(3,54) = 30.01, p < 0.00005$ Geno x BT         ns           Escape Path Latency (s)         Genotype (Geno)           Blocks of Trials (BT) $F(3,54) = 29.57, p < 0.00005$ Geno x BT         ns           MWM Place         ns           Escape Path Length (cm)         Genotype (Geno)         ns           Blocks of Trials (BT) $F(4,72) = 27.08, p < 0.00005$ Geno x BT         ns           Escape Path Latency (s)         Genotype (Geno)         ns           Blocks of Trials (BT) $F(4,72) = 22.52, p < 0.00005$ Geno x BT           Time in Target Quadrant (s)         ms         (βK _{ATP} -GOF: 26.08 ± 11.49)         Genotype           Spatial Bias         Trials (T) $F(3,54) = 24.89, p < 0.00005$ Fear Conditioning         Geno x M         F(7,126) = 9.453, p < 0.00005           Geno x M         Geno x M $F(7,126) = 3.060, p = 0.0100$ Auditory Cue         Minutes (M) $F(7,126) = 3.060, p = 0.0190$	Escape Path Length (cm)	Genotype (Geno)	ns
Geno x B1         ns           Escape Path Latency (s)         Genotype (Geno)         ns           Blocks of Trials (BT) $F(3,54) = 29.57, p < 0.00005$ Geno x BT         ns           MWM Place         ns           Escape Path Length (cm)         Genotype (Geno)         ns           Blocks of Trials (BT) $F(4,72) = 27.08, p < 0.00005$ Geno x BT           Escape Path Latency (s)         Genotype (Geno)         ns           Escape Path Latency (s)         Genotype (Geno)         ns           Blocks of Trials (BT) $F(4,72) = 22.52, p < 0.00005$ Geno x BT         ns           MWM Probe         ns           Time in Target Quadrant (s)         Genotype $(\beta K_{ATP}$ -GOF: $26.08 \pm 11.49)$ Genotype           Spatial Bias         Trials (T)           F(3,54) = 24.89, p < 0.00005		Blocks of Trials (BT)	F(3,54) = 30.01, p < 0.00005
Escape Path Latency (s)Genotype (Geno)nsBlocks of Trials (BT) $F(3,54) = 29.57, p < 0.00005$ Geno x BTnsMWM PlaceBlocks of Trials (BT)Escape Path Length (cm)Genotype (Geno)Blocks of Trials (BT) $F(4,72) = 27.08, p < 0.00005$ Geno x BTnsEscape Path Latency (s)Genotype (Geno)Blocks of Trials (BT) $F(4,72) = 22.52, p < 0.00005$ Geno x BTnsMWM ProbensTime in Target Quadrant (s)(Genotype( $\beta K_{ATP}$ -Cortrol: 28.63 $\pm$ 11.49)GenotypeSpatial BiasTrials (T)Freezing in Previous ContextGenotype(%)Minutes (M)F(7,126) = 9.453, p < 0.00005		Geno x BI	ns
Didoks of Trials (Df) $F(3,34) = 23.97$ , $p < 0.00003$ Geno x BT         ns           MWM Place         ns           Escape Path Length (cm)         Genotype (Geno)         ns           Blocks of Trials (BT) $F(4,72) = 27.08$ , $p < 0.00005$ Geno x BT         ns           Escape Path Latency (s)         Genotype (Geno)         ns           Blocks of Trials (BT) $F(4,72) = 22.52$ , $p < 0.00005$ Geno x BT         ns           MWM Probe         ns           Time in Target Quadrant (s)         (Genotype $(\beta K_{ATP}$ -Control: 28.63 ± 11.49)         Genotype           Spatial Bias         Trials (T)           Freezing in Previous Context         Genotype           (%)         Minutes (M)           F(7,126) = 9.453, $p < 0.00005$ Geno x M $F(7,126) = 3.060, p = 0.0100$ Auditory Cue         Seno x M           Baseline Freezing Time (%)         Genotype         ns           Minutes (M) $F(7,126) = 6.625, p = 0.0191$ Geno x M $F(7,126) = 7.937, p < 0.0005$	Escape Path Latency (s)	Blocks of Trials (BT)	ns E(3.54) = 29.57, p < 0.00005
WWM Place         Instruct           Escape Path Length (cm)         Genotype (Geno)         ns           Blocks of Trials (BT) $F(4,72) = 27.08, p < 0.00005$ Geno x BT           Escape Path Latency (s)         Genotype (Geno)         ns           Escape Path Latency (s)         Blocks of Trials (BT) $F(4,72) = 22.52, p < 0.00005$ Geno x BT         ns           MWM Probe         ns           Time in Target Quadrant (s)         (gKATP-GOF: 26.08 ± 11.49)           (gKATP-control: 28.63 ± 3.409)         Genotype           Spatial Bias         Trials (T)           Freezing in Previous Context         Genotype           (%)         Minutes (M)           F(7,126) = 9.453, p < 0.00005		Geno x BT	ns
Escape Path Length (cm)Genotype (Geno)nsBlocks of Trials (BT) $F(4,72) = 27.08, p < 0.00005$ Geno x BTnsEscape Path Latency (s)Genotype (Geno)Blocks of Trials (BT) $F(4,72) = 22.52, p < 0.00005$ Geno x BTnsMWM ProbensTime in Target Quadrant (s) $(\beta K_{ATP}$ -GOF: 26.08 ± 11.49)Genotypens $(\beta K_{ATP}$ -control: 28.63 ± 3.409) $(\beta K_{ATP}$ -control: 28.63 ± 3.409)Spatial BiasTrials (T)Fear ConditioningContextual FearingFreezing in Previous ContextGenotypeGeno x M $F(7,126) = 9.453, p < 0.00005$ Geno x M $F(7,126) = 3.060, p = 0.0100$ Auditory CuensBaseline Freezing Time (%)GenotypeGeno x M $F(7,126) = 6.625, p = 0.0191$ Geno x M $F(7,126) = 7.224, p = 0.0150$ Freezing Time in Testing (%)GenotypeReno x M $F(7,126) = 7.937, p < 0.0005$	MWM Place		
Blocks of Trials (BT) $F(4,72) = 27.08, p < 0.00005$ Geno x BT         ns           Escape Path Latency (s)         Genotype (Geno)         ns           Blocks of Trials (BT) $F(4,72) = 22.52, p < 0.00005$ Geno x BT         ns           MWM Probe         ns           Time in Target Quadrant (s)         ( $\beta K_{ATP}$ -GOF: 26.08 ± 11.49)         Genotype $(\beta K_{ATP}$ -control: 28.63 ± 3.409)         Spatial Bias         rs           Spatial Bias         Trials (T) $F(3,54) = 24.89, p < 0.00005$ Fear Conditioning         Trials (T) $F(7,126) = 9.453, p < 0.00005$ Geno x M $F(7,126) = 3.060, p = 0.0100$ Geno x M           Auditory Cue         ns         Ninutes (M) $F(7,126) = 6.625, p = 0.0191$ Baseline Freezing Time (%)         Genotype         ns         Ninutes (M)           F(7,126) = 7.224, p = 0.0150         Freezing Time in Testing (%)         Geno x M $F(7,126) = 7.937, p < 0.0005$	Escape Path Length (cm)	Genotype (Geno)	ns
Geno x BT         ns           Escape Path Latency (s)         Genotype (Geno)         ns           Blocks of Trials (BT) $F(4,72) = 22.52, p < 0.00005$ Geno x BT         ns           MWM Probe         ns           Time in Target Quadrant (s)         ( $\beta K_{ATP}$ -GOF: 26.08 ± 11.49)         Genotype           ( $\beta K_{ATP}$ -control: 28.63 ± 3.409)         rs         ( $\beta K_{ATP}$ -control: 28.63 ± 3.409)           Spatial Bias         Trials (T) $F(3,54) = 24.89, p < 0.00005$ Fear Conditioning		Blocks of Trials (BT)	F(4,72) = 27.08, p < 0.00005
Escape Path Latency (s)         Genotype (Geno)         ns           Blocks of Trials (BT) $F(4,72) = 22.52, p < 0.00005$ Geno x BT         ns           MWM Probe         ns           Time in Target Quadrant (s)         ( $\beta K_{ATP}$ -GOF: 26.08 ± 11.49)         Genotype $(\beta K_{ATP}$ -control: 28.63 ± 3.409)         Spatial Bias         ns           Spatial Bias         Trials (T) $F(3,54) = 24.89, p < 0.00005$ Fear Conditioning         ns         No           Contextual Fearing         Freezing in Previous Context         Genotype           Freezing in Previous Context         Genotype         ns           (%)         Minutes (M) $F(7,126) = 9.453, p < 0.00005$ Geno x M $F(7,126) = 3.060, p = 0.0100$ Auditory Cue         Ninutes (M) $F(7,126) = 6.625, p = 0.0191$ Geno x M $F(7,126) = 7.224, p = 0.0150$ Freezing Time in Testing (%)           Geno x M $F(7,126) = 7.937, p < 0.0005$		Geno x BT	ns
Blocks of Trials (BT) $F(4,72) = 22.52, p < 0.00005$ Geno x BT         ns           Time in Target Quadrant (s)         ns $[\beta K_{ATP}$ -GOF: 26.08 ± 11.49)         Genotype $[\beta K_{ATP}$ -control: 28.63 ± 3.409)         ns           Spatial Bias         rials (T)           Fear Conditioning         F(3,54) = 24.89, p < 0.00005	Escape Path Latency (s)	Genotype (Geno)	ns
Geno x B1         ns           MWM Probe         ns           Time in Target Quadrant (s)         ( $\beta K_{ATP}$ -GOF: 26.08 ± 11.49)         Genotype           ( $\beta K_{ATP}$ -control: 28.63 ± 3.409)         ( $\beta K_{ATP}$ -control: 28.63 ± 3.409)         ( $\beta K_{ATP}$ -control: 28.63 ± 3.409)           Spatial Bias         Trials (T) $F(3,54) = 24.89, p < 0.00005$ Fear Conditioning		Blocks of Trials (BT)	F(4,72) = 22.52, p < 0.00005
Time in Target Quadrant (s)           [ßK _{ATP} -COF: 26.08 ± 11.49)         Genotype         ns           [ßK _{ATP} -control: 28.63 ± 3.409)	MW/M Probo	Geno X BI	ns
Image: Contextual Fearing       Genotype       ns         Spatial Bias       Trials (T) $F(3,54) = 24.89, p < 0.00005$ Fear Conditioning       Trials (T) $F(3,54) = 24.89, p < 0.00005$ Freezing in Previous Context       Genotype       ns         (%)       Minutes (M) $F(7,126) = 9.453, p < 0.00005$ Geno x M $F(7,126) = 3.060, p = 0.0100$ Auditory Cue       Minutes (M) $F(7,126) = 6.625, p = 0.0191$ Baseline Freezing Time (%)       Genotype       ns         Minutes (M) $F(7,126) = 7.224, p = 0.0150$ Freezing Time in Testing (%)         Geno x M $F(7,126) = 7.937, p < 0.0005$ Seno x M $F(7,126) = 7.937, p < 0.0005$	Time in Target Quadrant (s)		
Image: Spatial Bias       Trials (T) $F(3,54) = 24.89, p < 0.00005$ Spatial Bias       Trials (T) $F(3,54) = 24.89, p < 0.00005$ Fear Conditioning       Freezing in Previous Context       Genotype         (%)       Minutes (M) $F(7,126) = 9.453, p < 0.00005$ Geno x M $F(7,126) = 3.060, p = 0.0100$ Auditory Cue       Minutes (M)         Baseline Freezing Time (%)       Genotype         Minutes (M) $F(7,126) = 6.625, p = 0.0191$ Geno x M $F(7,126) = 7.224, p = 0.0150$ Freezing Time in Testing (%)       Genotype         Geno x M $F(7,126) = 7.937, p < 0.0005$	$(\beta K_{ATP}-GOF: 26.08 \pm 11.49)$	Genotype	ns
Spatial Bias         Trials (T)         F(3,54) = 24.89, p < 0.00005           Fear Conditioning         Fear Conditioning         Fear Conditioning           Contextual Fearing         Freezing in Previous Context         Genotype           (%)         Minutes (M)         F(7,126) = 9.453, p < 0.00005	(βK _{ATP} -control: 28.63 ± 3.409)		
Trials (T) $F(3,54) = 24.89, p < 0.00005$ Fear Conditioning       Fill         Contextual Fearing       Second Seco	Spatial Bias		
Fear Conditioning         Fearing           Contextual Fearing         Freezing in Previous Context           (%)         Genotype           Minutes (M)         F(7,126) = 9.453, p < 0.00005		Trials (T)	F(3,54) = 24.89, p < 0.00005
Fear Conditioning         Contextual Fearing           Contextual Fearing         ns           Freezing in Previous Context         Genotype         ns           (%)         Minutes (M)         F(7,126) = 9.453, p < 0.00005		- N-5110	
Contextual Fearing         ns           Freezing in Previous Context         Genotype         ns           (%)         Minutes (M)         F(7,126) = 9.453, p < 0.00005	Fear Conditioning		
Contextual realing         Genotype         ns           (%)         Minutes (M)         F(7,126) = 9.453, p < 0.00005	Contextual Feering		
Minutes (M)         F(7,126) = 9.453, p < 0.00005           Geno x M         F(7,126) = 3.060, p = 0.0100           Auditory Cue         ns           Baseline Freezing Time (%)         Genotype           Minutes (M)         F(7,126) = 6.625, p = 0.0191           Geno x M         F(7,126) = 7.224, p = 0.0150           Freezing Time in Testing (%)         Genotype           Minutes (M)         F(7,126) = 7.937, p < 0.0005	Freezing in Previous Context	Genotype	ns
Minutes (M)         F(7,126) = 9.453, p < 0.00005           Geno x M         F(7,126) = 3.060, p = 0.0100           Auditory Cue         ns           Baseline Freezing Time (%)         Genotype           Minutes (M)         F(7,126) = 6.625, p = 0.0191           Geno x M         F(7,126) = 7.224, p = 0.0150           Freezing Time in Testing (%)         Genotype         ns           Minutes (M)         F(7,126) = 7.937, p < 0.0005	(%)	Controlype	
Geno x M         F(7,126) = 3.060, p = 0.0100           Auditory Cue         ns           Baseline Freezing Time (%)         Genotype           Minutes (M)         F(7,126) = 6.625, p = 0.0191           Geno x M         F(7,126) = 7.224, p = 0.0150           Freezing Time in Testing (%)         Genotype           Minutes (M)         F(7,126) = 7.937, p < 0.0005		Minutes (M)	F(7,126) = 9.453, p < 0.00005
Auditory Cue         ns           Baseline Freezing Time (%)         Genotype         ns           Minutes (M)         F(7,126) = 6.625, p = 0.0191           Geno x M         F(7,126) = 7.224, p = 0.0150           Freezing Time in Testing (%)         Genotype           Minutes (M)         F(7,126) = 7.937, p < 0.0005		Geno x M	F(7,126) = 3.060, p = 0.0100
Baseline Freezing Time (%)         Genotype         ns           Minutes (M)         F(7,126) = 6.625, p = 0.0191         Geno x M           Geno x M         F(7,126) = 7.224, p = 0.0150           Freezing Time in Testing (%)         Genotype         ns           Minutes (M)         F(7,126) = 7.937, p < 0.0005	Auditory Cue		
Minutes (M)         F(7,126) = 6.625, p = 0.0191           Geno x M         F(7,126) = 7.224, p = 0.0150           Freezing Time in Testing (%)         Genotype         ns           Minutes (M)         F(7,126) = 7.937, p < 0.0005	Baseline Freezing Time (%)	Genotype	ns
Geno x M         F(7,126) = 7.224, p = 0.0150           Freezing Time in Testing (%)         Genotype         ns           Minutes (M)         F(7,126) = 7.937, p < 0.0005		Minutes (M)	F(7, 126) = 6.625, p = 0.0191
Integring time in testing (%)         Genotype         ns           Minutes (M)         F(7,126) = 7.937, p < 0.0005	Freezing Time in Testing (0/)	Geno x M	r(1, 126) = 1.224, p = 0.0150
Geno x M ns	Freezing time in testing (%)	Minutes (M)	F(7, 126) = 7.937 p < 0.0005
	1 ⁰	Geno x M	ns

Table S6. Means and ANOVA effects for locomotor activity assays, sensorimotor battery, Morris Water Maze, and fear conditioning assays in  $\beta K_{ATP}$ -GOF and control mice.

Short name	Primer	Sequence (5'-3')
Kir6.2	fwd	CGG GCG CAT GGT GAC AGA GG
	rev	CGA TGG GCC TGG GCC GTT TT
SUR1	fwd	TGA GCA TTG GAA GAC CCT CAT
	rev	CAG CAC CGA AGA TAA GTT GTC A
GFP	fwd	AAG GGC ATC GAC TTC AAG G
	rev	TGC TTG TCG GCC ATG ATA TAG
ML32	fwd	TTC CTG GTC CAC AAT GTC AA
	rev	GGC TTT TCG GTT CTT AGA GGA

Table S7. Primers for RT-qPCR