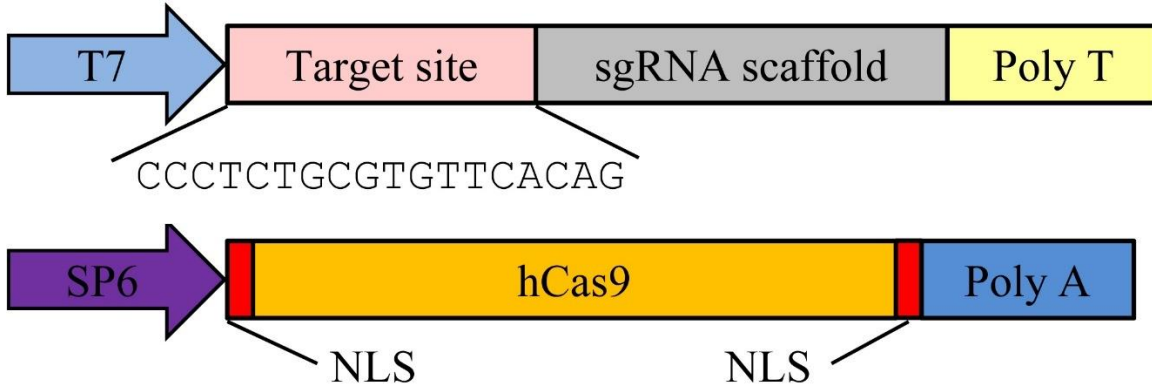


SUPPLEMENTARY DATA

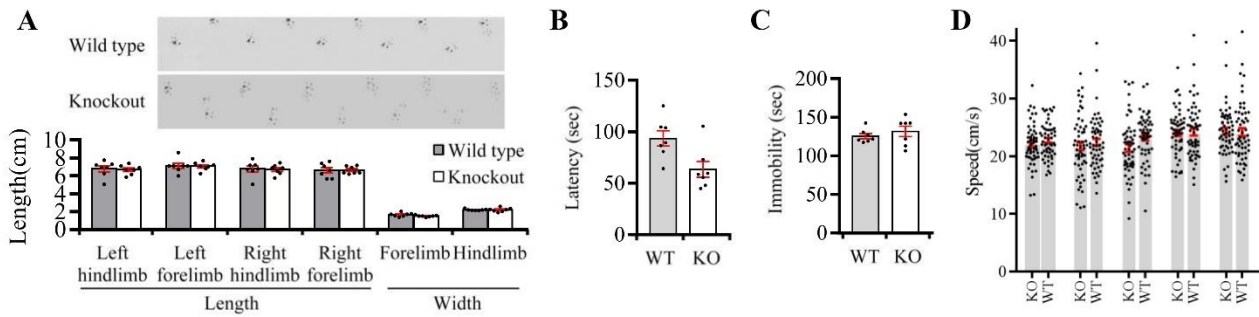
Age-related Loss of miR-124 Causes Cognitive Deficits *via* Derepressing RyR3 Expression

Kai Liu^{1,3,6}, Yongjia Yin², Yuan Le¹, Wen Ouyang¹, Aihua Pan⁴, Jufang Huang⁴, Zhongcong Xie⁵, Qubo Zhu^{2*}, Jianbin Tong^{1,3*}

SUPPLEMENTARY DATA

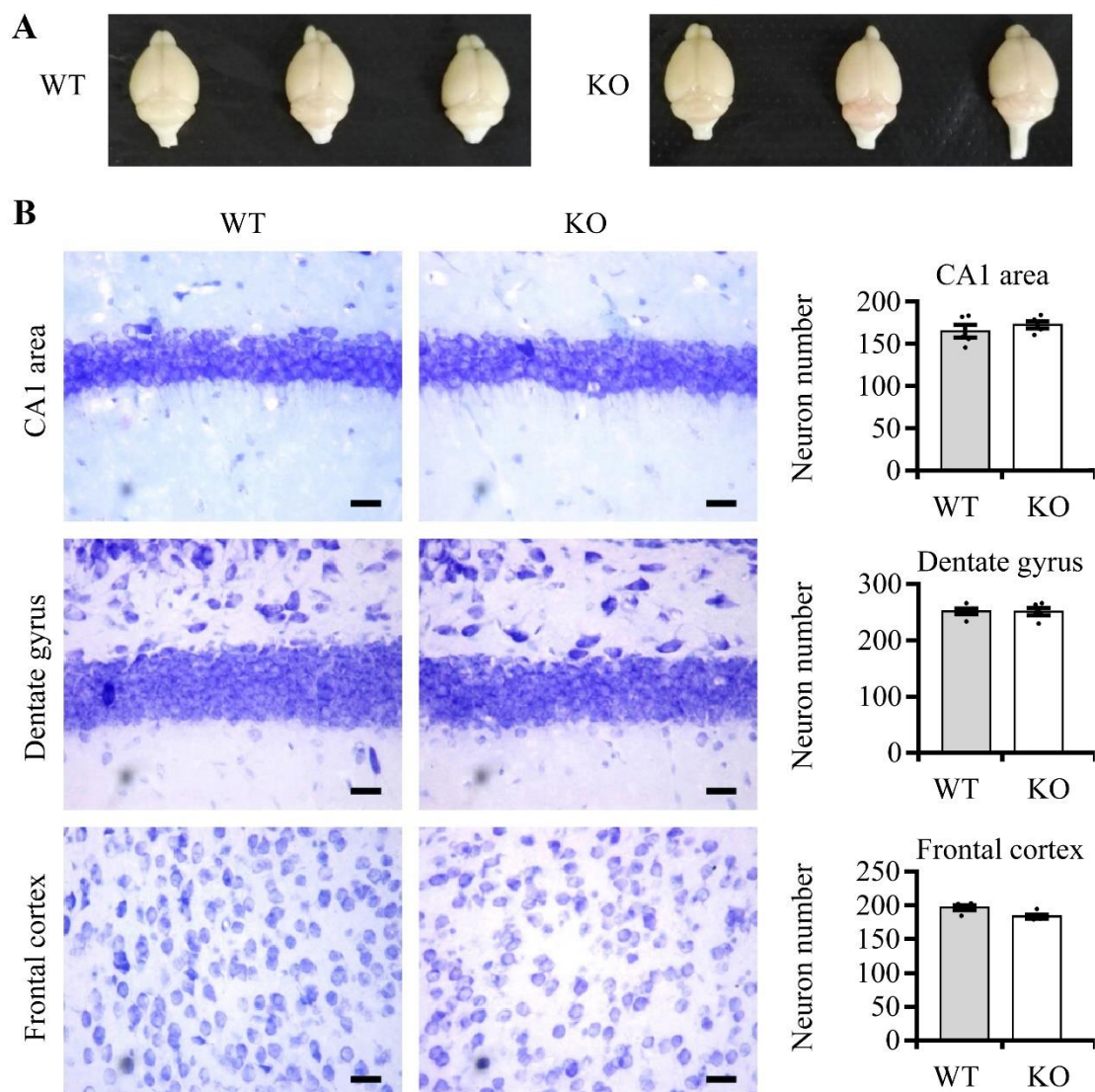


Supplementary Figure 1. RNA constructs of the Cas9/RNA system used in this study. T7, T7 promoter; SP6, SP6 promoter; NLS, nuclear localization signal.



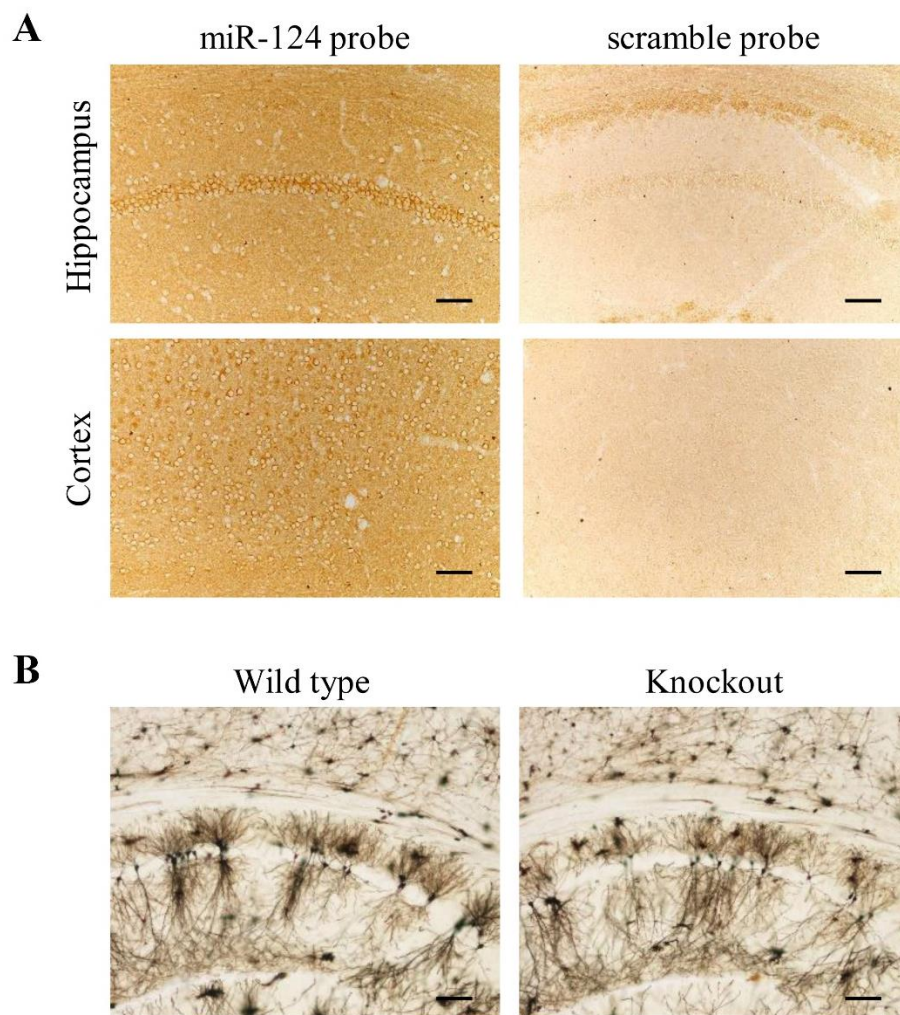
Supplementary Figure 2. Motor activity of wild-type (+/+) and homozygous (-/-) mice. (A) Footprints were recorded for the two types of mice. Stride lengths were measured for the left hindlimb, left forelimb, right hindlimb, and right forelimb; the forelimb and hindlimb stride widths were the same between the two genotypes. (N=7 mice per group. Two-sided Student's t-tests (left hindlimb: $t=0.102$, $P=0.9202$; left forelimb: $t=0.1405$, $P=0.8903$; right hindlimb: $t=0.4742$, $P=0.6427$; right forelimb: $t=0.8306$, $P=0.4201$; forelimb: $t=0.7966$, $P=0.4390$; hindlimb: $t=1.685$, $P=0.1142$) or Mann-Whitney U tests.). (B) In the rotarod tests, the latencies to fall from the rotated rods were similar for all genotypes (N=7 mice per group. latency: $t=2.564$, $P=0.0854$; Two-sided Student's t-tests). (C) In the forced swimming tests, the immobility durations of the two genotypes of mice were recorded to assess the depression-like moods of these mice. (N=7 animals per group, $t=1.04$, $P=0.112$, two-sided Student's t-tests) (D) Swimming speed of the two genotypes of mice for 5 days. (* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$)

SUPPLEMENTARY DATA



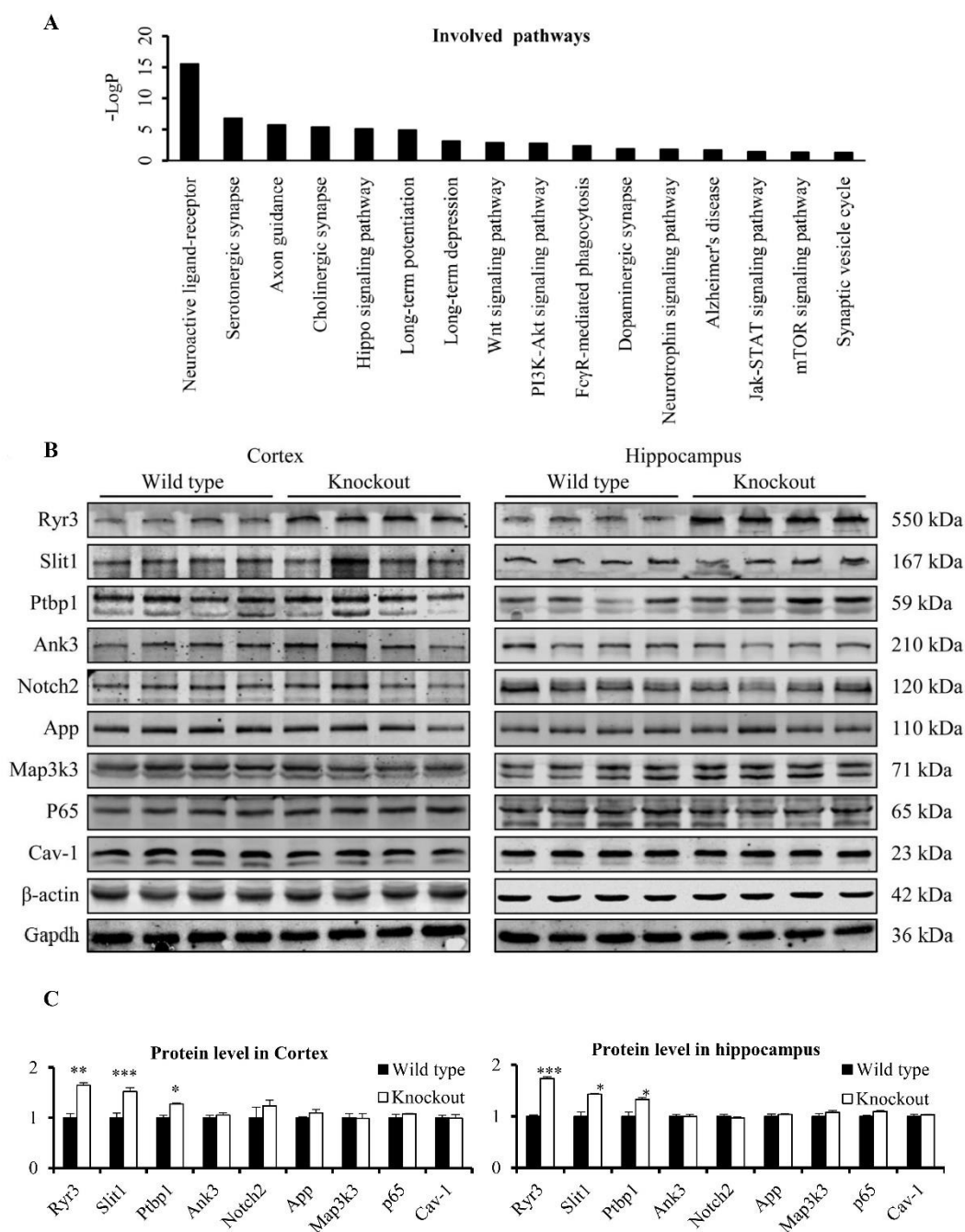
Supplementary Figure 3. Brain size and neuron number in the hippocampus and frontal cortex of wild-type and miR-124-3 (-/-) mice (3–4 months). (A) *Ex vivo* images of the brains revealed that the brain sizes of both the wild-type and miR-124-3(-/-) mice were similar. (B) Representative images of hippocampal sections stained with Nissl indicated that the neuron densities of the miR-124-3(-/-) mice and wild-type mice were the same. Scale bar, 40 μ m. Right panel shows the quantification analysis of the neuronal counts in the hippocampal CA1, dentate gyrus and frontal cortex regions (n=4 for each group. Results are mean \pm SEM values. The data were analyzed using Mann-Whitney U tests (CA1 area: $t=1.052$, $P=0.2982$; DG: $t=0.08838$, $P=0.9307$; FC: $t=2.08$, $P=0.0711$)).

SUPPLEMENTARY DATA



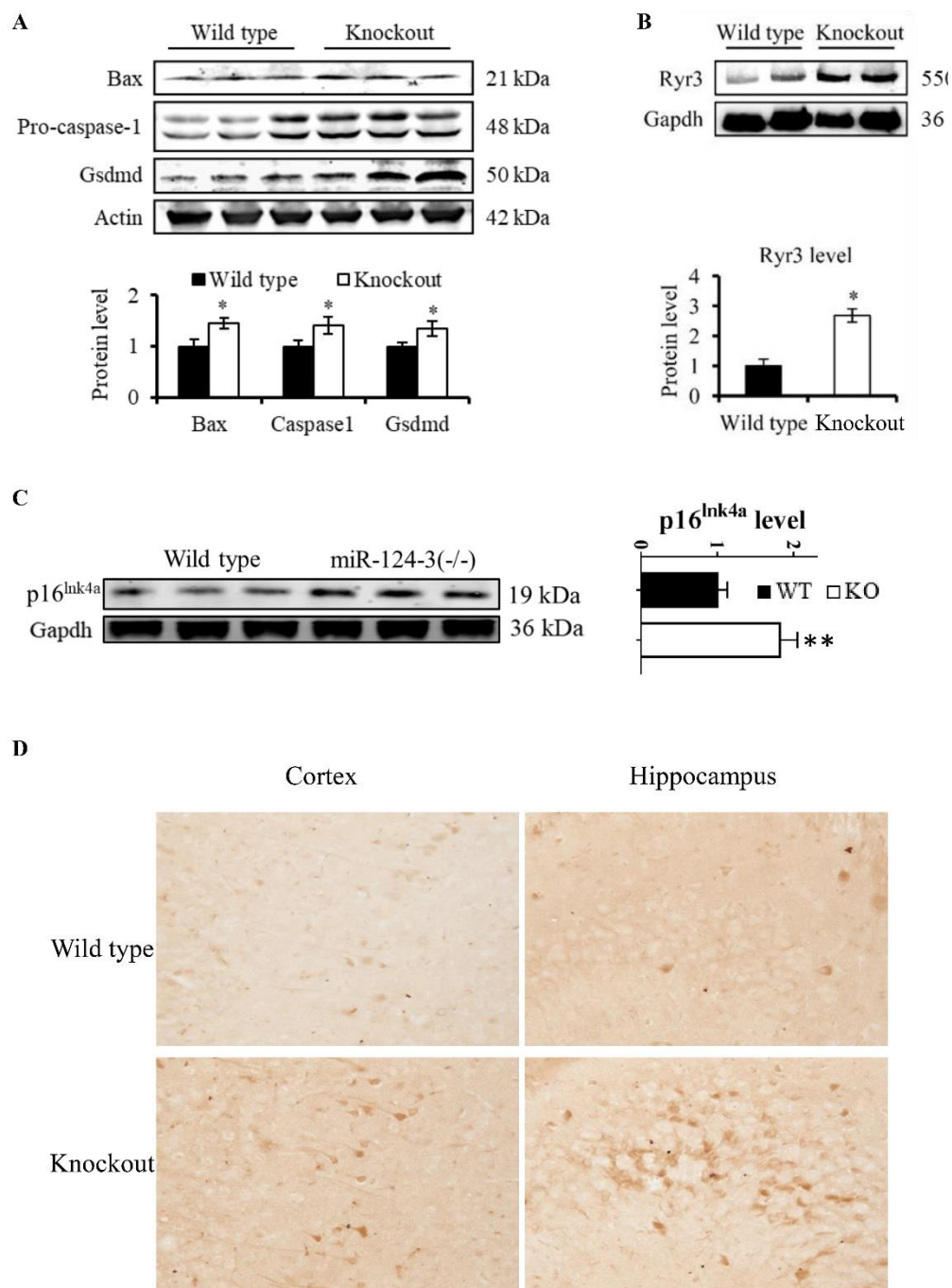
Supplementary Figure 4. *In situ hybridization* by scramble probe and miR-124 probe (Scale bar, 25 μ m) and Golgi staining of the CA1 of wild type and miR-124-3(-/-) mice (Scale bar, 80 μ m).

SUPPLEMENTARY DATA



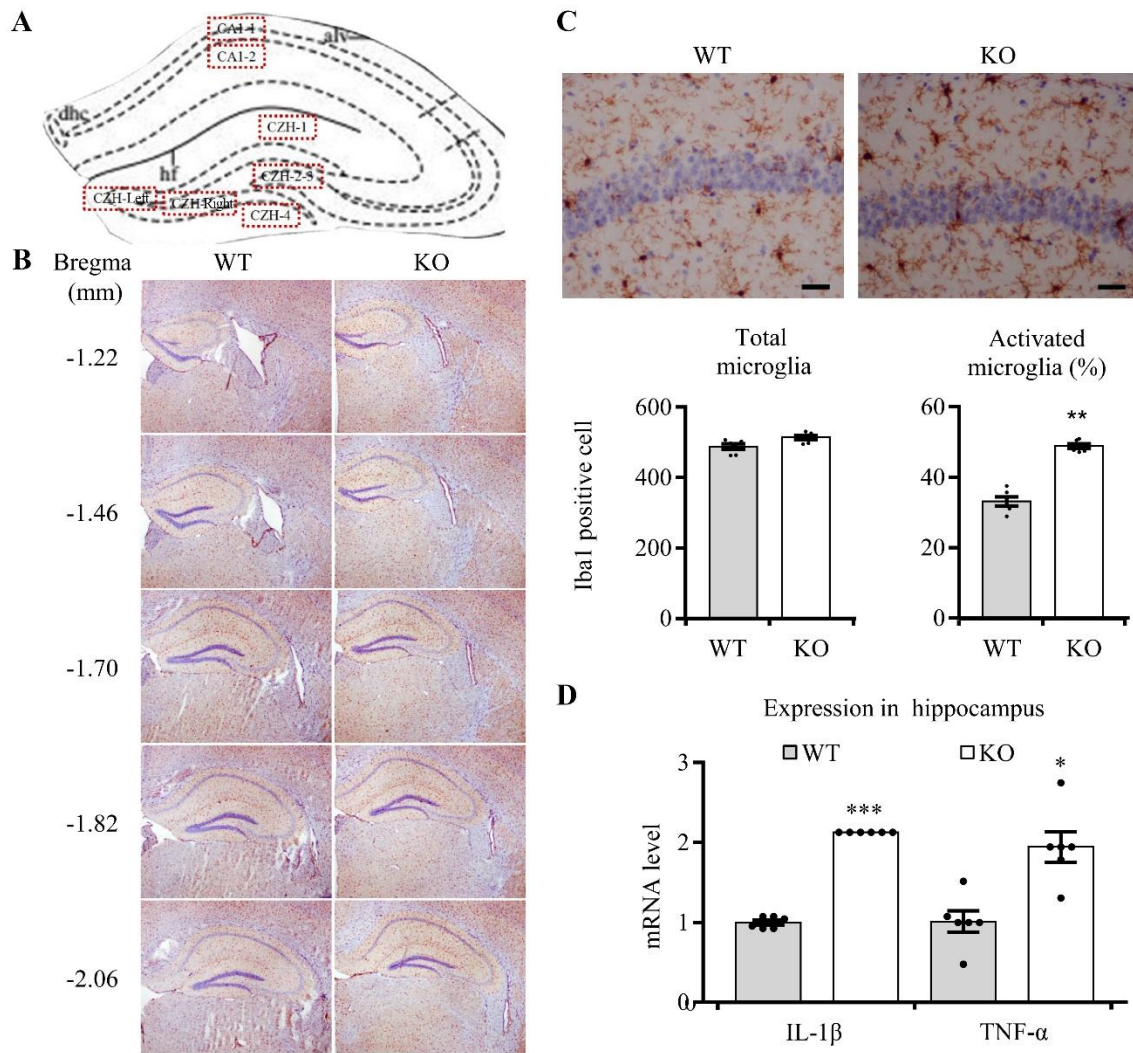
Supplementary Figure 5. (A) KEGG pathway analysis of significantly altered gene in the miR-124-3(-/-) mice compared to wild type mice. (B) Western blot and quantification of downstream gene proteins in hippocampus and parietal cortex of miR-124-3(-/-) and wild-type mice. β -actin and GAPDH was used as internal control (mean \pm SEM; n=4 mice per group; *P < 0.05, **P < 0.01, ***P < 0.001; Mann-Whitney U tests).

SUPPLEMENTARY DATA



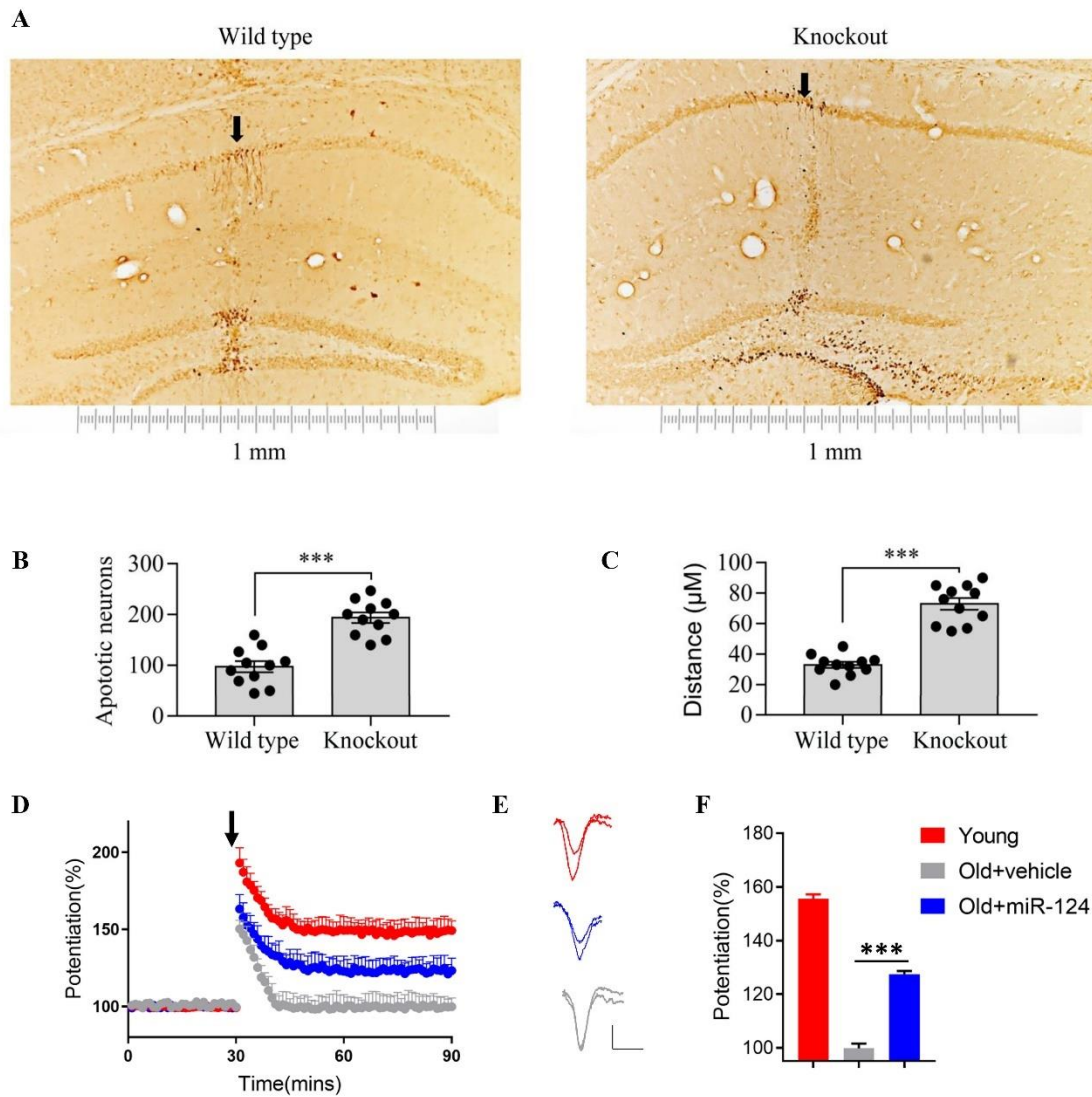
Supplementary Figure 6. Apoptosis and pyroptosis factors increased in miR-124-3(-/-) mice. (A) Protein levels of Bax, caspase-1, and gasdermin D (GSDMD) were detected using western blot; β -actin was used as an internal control. The statistical plot of the western blot bands, upper panel. (B) Protein levels of RyR3 (isolated using ultracentrifugation) on membranes and statistical plots of the western blot bands. (C) Protein levels of p16^{lnk4a} and statistical plots of the western blot bands. (D) Representative images of immunostaining for p16^{lnk4a}. (The results are mean \pm SEM values, data analyzed using Mann-Whitney U tests). (* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$).

SUPPLEMENTARY DATA



Supplementary Figure 7. Neuroinflammation was enhanced in the brains of miR-124-3(-/-) mice. (A) Schematic diagram of seven selected areas in the hippocampal CA1 and dentate gyrus regions. (B) Images of regions of the hippocampus were taken at the levels of -1.22, -1.46, -1.70, -1.82, and -2.06 mm, relative to the bregma; all were taken at the same magnification (40 \times objective lens). (C) Upper panel, representative images showing immunostaining for Iba1 in the hippocampus. A quantitative analysis (lower panel) found that activated microglia was significantly increased in the miR-124-3(-/-) mice. (D) qPCR analysis of proinflammatory cytokine mRNA levels for TNF- α and IL-1 β in the hippocampus between two groups; β -actin was used as an internal control. (The results were presented as mean \pm standard deviation values. N=6. Total microglia: $t=1.662$, $P=0.1719$; active microglia: $t=7.186$, $P=0.002$; mRNA level: IL-1 β : $t=26.85$, $P<0.0001$; TNF- α : $t=2.876$, $P=0.0452$). (* $P<0.05$, ** $P<0.01$, *** $P<0.001$)

SUPPLEMENTARY DATA



Supplementary Figure 8. A β 1-42 induced more serious neuron apoptosis in the hippocampus of miR-124-3(-/-) mice. (A) Representative images of hippocampal neuron apoptosis of wild-type (WT) and miR-124-3(-/-) (KO) mice 3 days after exogenous A β 1-42 injection. Arrow meant needle track. (B) Quantification of apoptotic cells in the hippocampus of wild-type (WT) and miR-124-3(-/-) (KO) mice 3 days after exogenous A β 1-42 injection (mean \pm SEM; n=11 sections from 4 mice per genotypes; *** $P < 0.001$; Mann-Whitney U tests). (C) The farthest distance from needle track to apoptotic cells disappearance in the hippocampus of wild-type (WT) and miR-124-3(-/-) (KO) mice 3 days after exogenous A β 1-42 injection (mean \pm SEM; n=11 sections from 4 mice per genotypes; *** $P < 0.001$; Mann-Whitney U tests). (D) Summary plots of mean normalized field EPSP slope (Arrow meant LTP induction), example traces (E) and quantitative analysis of long-term potentiation (LTP) (F) in hippocampus slices of Young (3 month), Old (20 month) +Vehicle and Old (20 month) +MiR-124 group. (Scale bars=10 ms, 1 mV; mean \pm SEM; n=10 slices from 3 mice per group; *** $P < 0.001$; Mann-Whitney U tests).

SUPPLEMENTARY DATA

Supplementary Table 1. Sequences of PCR primer sets used in this study.

Primer name	Access number	Primer sequence (direction 5'–3')
miR-124-3 Wild-type	NC_000068.7	Forward: CTCTGCGTGTTACACGCG Reverse: CCTTCTCGTGACGTCCTAGG
miR-124-3 Knock-out	NC_000068.7	Forward: GCCCTCTGCGTGTTCTATA Reverse: ATGTTCCGCCGATTTGTCC
miR-124		RT-Primer: GTCGTATCCAGTGCAGGGTCCGAGGTATTCCGACTGGATAC GACGGCATT Forward: ATAATTCGGTAAGGCACGCGGTG Reverse: ATCCAGTGCAGGGTCCGAGG
Mmu-pre-miR-124-3	NC_000068.7	Forward: TGCGTGTTACACAGCGGAC Reverse: CGCGTGCCTTAATTGTATAGACA
Mmu-pre-miR-124-1		Forward: AGGCCTCTCTCCGTGTTT Reverse: CCCATTCTTGGCATTACC
Mmu-pre-miR-124-2		Forward: AGACTCTGCTCTCCGTGTTT Reverse: CGTAGGCTCCGCTCTTGG
Mmu-U6	NM_001191004.1	Forward: GGCAGGAACATGGCAGCATC Reverse: GCGTGGGCTTTAGCTTGTCC
Mmu-IL-1 β	NM_008361.4	Forward: GCCCATCCTCTGTGACTCAT Reverse: AGGCCACAGGTATTTTGTCTG
Mmu-TNF- α	NM_013693.3	Forward: ATGCACCACCATCAAGGACTCAA Reverse: ACCACTCTCCCTTTGCAGAACTC
Rat-U6	NM_001126085.1	Forward: CTCAGGTTTCTGCCTCCCA Reverse: CCTCGGTAATCCACGCCAGA
Hsa-U6	NM_007080.2	Forward: AAAGCAAATCATCGGACGACC Reverse: GTACAACACATTGTTTCTCGGA

Supplementary Table 2. Detailed information about the statistical analyses associated with each Figure.

Fig. #	Compare (group size; n)	Passed normality test (Yes/No)	Statistical method	P-value	T-value	F-value
Fig. 1C	n =6,8 and 9 for >60, 50-60 and <50 group	Yes	one-way ANOVA followed by Tukey <i>post hoc</i> Test	$P < 0.0001$		$F_{(2, 21)} = 29.15$
Fig. 1E	<i>in situ</i> hybridization of miR-124 in the cortex and hippocampus of different ages of rats.	Yes	one-way ANOVA followed by Tukey <i>post hoc</i> test.	$P < 0.0001$		Cortex: $F_{(3, 28)} = 279.7$
	2months vs 12months			$P < 0.001$		
	12months vs 24months			$P = 0.0235$		
	24months vs 33months			$P = 0.0023$		
				$P < 0.0001$		Hippocampus CA1: $F_{(3, 32)} = 594.4$
	2months vs 12months			$P < 0.001$		
	12months vs 24months			$P = 0.0003$		
	24months vs 33months			$P = 0.0053$		
Fig. 1F	miR-124 in the cortex and hippocampus of rats (n=6 for each age-group)	Yes	one-way ANOVA followed by Tukey <i>post hoc</i> Test	$P < 0.0001$		Cortex: $F_{(3, 20)} = 34.83$
	2months vs 12months			$P = 0.0012$		
	12months vs 24months			$P = 0.0401$		
	24months vs 33months			$P = 0.0020$		
				$P < 0.0001$		Hippocampus: $F_{(3, 28)} = 211.9$
	2months vs 12months			$P = 0.0016$		

SUPPLEMENTARY DATA

	12months vs 24months			$P=0.0027$		
	24months vs 33months			$P=0.0031$		
Fig. 2D	miR-124 level between WT and KO (n=9 for each group)	Yes	two-sided Student's <i>t</i> -test			
	MiR-124-1 HPC	Yes		$P=0.5661$	$t=0.654$	
	MiR-124-1 BC	Yes		$P=0.3985$	$t=0.46$	
	MiR-124-2 HPC	Yes		$P=0.6632$	$t=0.383$	
	MiR-124-2 BC	Yes		$P=0.7752$	$t=0.9108$	
	MiR-124-3 HPC	Yes		$P < 0.0001$	$t=22.059$	
	MiR-124-3 BC	Yes		$P < 0.0001$	$t=34.438$	
	MiR-124 HPC	Yes		$P < 0.0001$	$t=19.66$	
	MiR-124 BC	Yes		$P < 0.0001$	$t=21.851$	
Fig. 2E	mRNA level of Bhlhe23 and the Ythdf1 between WT and KO (n=4 for each group)	Yes	two-sided Student's <i>t</i> -test			
	Bhlhe23	Yes		$P=0.2247$	$t=1.294$	
	Pri-miR-124-3	Yes		$P < 0.0001$	$t=20.11$	
	Ythdf1	Yes		$P=0.7808$	$t=0.29$	
Fig. 3B	Time savings for different ITIs between WT and KO (n=16 for each group)	Yes	two-sided Student's <i>t</i> -test			
	5sec	Yes		$P=0.0011$	$t=3.364$	
	20min	Yes		$P < 0.001$	$t=4.898$	
	2h	Yes		$P=0.0011$	$t=3.377$	
	4h	Yes		$P=0.0041$	$t=2.946$	
	Length savings for different ITIs between WT and KO (n=16 for each group)	Yes	two-sided Student's <i>t</i> -test			
	5sec	Yes		$P=0.0016$	$t=3.265$	
	20min	Yes		$P < 0.001$	$t=4.591$	
	2h	Yes		$P=0.0003$	$t=3.765$	
	4h	Yes		$P=0.0016$	$t=3.266$	
Fig. 3D	Time to find the hidden platform between WT and KO (n=11 for each group)	Yes	two-way ANOVA followed by Tukey <i>post hoc</i> test			Time: $F_{(3,21)} = 39.53$, $P < 0.0001$; Group: $F_{(1,7)} = 23.82$, $P = 0.0018$; Interaction: $F_{(3,21)} = 0.9221$, $P = 0.4473$.
Fig. 3E	<i>left panel</i>	Yes	two-sided Student's <i>t</i> -test	$P=0.018$	$t=2.99$	
	<i>medial panel</i>	Yes	two-sided Student's <i>t</i> -test	$P=0.0435$	$t=2.219$	
	<i>right panel</i>	Yes	two-sided Student's <i>t</i> -test	$P=0.002$	$t=3.787$	
Fig. 3F	Total time	Yes	two-sided Student's <i>t</i> -test	$P=0.6478$	$t=0.4642$	
	Preference for novel object	Yes	two-sided Student's <i>t</i> -test	$P=0.0037$	$t=3.328$	
Fig. 4A	LTP at SC-CA1 synapses in the hippocampus (n = 9 slices from 3 mice for both genotypes)	No	the Mann-Whitney U test	$P < 0.0001$		
Fig. 4B	LTD at SC-CA1 synapses in the hippocampus (n = 10 slices from 4 mice for both genotypes)	No	the Mann-Whitney U test	$P < 0.0001$		
Fig. 4C	Spine density of basal and apical dendrites of CA1 neurons (n=5 for each group)	No	the Mann-Whitney U test			
	DG outer layer	No		$P=0.1449$		
	CA1 basal	No		$P=0.0136$		
	CA1 apical	No		$P < 0.0001$		
Fig. 4D	Protein levels of Syp and Psd95 in hippocampus (n=3)	No	the Mann-Whitney U test			

SUPPLEMENTARY DATA

	Syn	No		$P=0.01$		
	Psd95	No		$P=0.0145$		
Fig. 5C		Yes	two-tailed Student's t-test (n=6 for each group)			
	Cortex					
	RyR3	Yes		$P=0.0021$		
	Hippocampus					
	RyR3	Yes		$P=0.00145$		
Fig. 5D (UPPER)	Luciferase assay	Yes	one-way ANOVA followed by Tukey <i>post hoc</i> test.	$P=0.0001$		$F_{(3,8)} = 30.33$
	0nM vs 5nM	Yes		$P>0.9999$		
	0nM vs 10nM	Yes		$P=0.007$		
	0nM vs 15nM	Yes		$P=0.002$		
	RyR3mutant	Yes		$P=0.6052$		$F_{(3,8)}=0.6493$
	pmirGLO	Yes		$P=0.6631$		$F_{(3,8)}= 0.5484$
Fig. 5D (LOWER)	Luciferase assay of miR-124-3 inhibitor	Yes	two-sided Student's t-test			
	RyR3	Yes		$P=0.0017$	$t=4.02$	
	mutant	Yes		$P=0.3924$	$t=0.51$	
	pmirGLO	Yes		$P=0.6896$	$t=0.32$	
Fig. 6B	RyR3 protein level	Yes	one-way ANOVA followed by Tukey <i>post hoc</i> test	$P<0.0001$		$F_{(2,15)} = 166.4$
	WT+vehicle vs KO+vehicle	Yes		$P<0.0001$		
	KO+vehicle vs KO+shRNA	Yes		$P<0.0001$		
Fig. 6C	Time to find the hidden platform between WT and KO (n=13, 19 and 16 mice for WT+vehicle, KO+vehicle and KO+ShRyr3 group, respectively)	Yes	two-way ANOVA followed by Tukey <i>post hoc</i> test	$P<0.0001$		Grouped: $F_{(2,225)}=33.07$
				$P<0.0001$		Time: $F_{(4,225)} = 61.19$
				$P=0.4563$		Interaction: $F_{(8,225)} = 0.925$
Fig. 6D	Parameters for assessing acquired memory (n=13, 19 and 16 mice for WT+vehicle, KO+vehicle and KO+ShRyr3 group, respectively)	Yes	one-way ANOVA followed by Tukey <i>post hoc</i> test			
	Platform crossing	Yes		$P=0.0241$		$F_{(2,45)}=4.054$
	Time in the quadrant (%)	Yes		$P=0.0111$		$F_{(2,45)}=4.982$
	Latency to target	Yes		$P=0.0216$		$F_{(2,45)}=4.179$
Fig. 6E	LTP at SC-CA1 synapses in the hippocampus (n=14 slices from 6 mice per genotypes)	Yes	one-way ANOVA followed by Tukey <i>post hoc</i> test	$P<0.0001$		$F_{(2,90)}=4674$
	Wild-type+Vehicle vs KO+Vehicle	Yes		$P<0.0001$		
	Wild-type+Vehicle vs KO+RyR3	Yes		$P<0.0001$		
	KO+Vehicle vs KO+RyR3	Yes		$P<0.0001$		
Fig. 6f	LTD at SC-CA1 synapses in the hippocampus (n=13 slices from 6 mice per genotypes)	Yes	one-way ANOVA followed by Tukey <i>post hoc</i> test	$P<0.0001$		$F_{(1,798,53.95)}=2832$
	Wild-type+Vehicle vs KO+Vehicle	Yes		$P<0.0001$		
	Wild-type+Vehicle vs KO+RyR3	Yes		$P<0.0001$		
	KO+Vehicle vs KO+RyR3	Yes		$P<0.0001$		
Fig. 6G	Calcium fluorescence (n= 8 slices from 4 mice per group)	Yes	two-way ANOVA followed by Tukey <i>post hoc</i> test	$P=0.0014$		Interaction: $F_{(2,24)} = 8.777$
		Yes		$P=0.0002$		Treatment: $F_{(1,24)} = 19.26$
		Yes		$P<0.0001$		Group: $F_{(2,24)} = 132.3$
	WT+ Vehicle (Before Glutamate) vs. WT+vehicle (After Glutamate)	Yes		$P<0.0001$		
	KO+Vehicle (Before Glutamate) vs KO+Vehicle (After Glutamate)	Yes		$P=0.9942$		
	KO + shRyR3(Before Glutamate) vs KO + shRyR3(After Glutamate)	Yes		$P=0.0002$		

SUPPLEMENTARY DATA

	WT + Vehicle(Before Glutamate) vs KO + Vehicle(Before Glutamate)	Yes		$P<0.0001$		
	KO+shRyr3(Before Glutamate) vs KO + Vehicle(Before Glutamate)	Yes		$P=0.003$		
	KO + Vehicle(Before Glutamate) vs WT + Vehicle(Before Glutamate)	Yes		$P<0.0001$		
Fig. 7B	Apoptotic neuron counting	Yes	two-sided Student's t-test	$P=0.0021$	$t=4.755$	
Fig. 7C	Apoptotic neuron range	Yes	two-sided Student's t-test	$P<0.0001$	$t=14.56$	

Supplementary Table 3. Chromosomal locations and precursor sequences of different miR-124 family members¹

	Pre-microRNA sequence	Location
Hsa-Pre-miR-124-1	AGGCCUCUCUCUCGUGUUCACAGCGGACCUUGA UUUAAAUGUCCAUACAAUUAAGGCACGCGGUGAA <u>UGCCAAGAAUGGGGCGUG</u>	chr8(-): 9903388-9903472
Hsa-Pre-miR-124-2	AUCAAGAUAAGAGGCUCUCUCGUGUUCACA GCGGACCUUGAUUUAAUGUCAUACAAUUAAGGCA <u>CGCGGUGAAUGCCAAGAGCGGAGCCUACGGCUGCA</u> CUUGAA	chr8(+): 64379149-64379257
Hsa-Pre-miR-124-3	UGAGGGCCCCUCUGCGUGUUCACAGCGGACCUUG AUUUAAUGUCUAUACAAUUAAGGCACGCGGUGAA <u>UGCCAAGAGAGGGCGCCUCC</u>	chr20(+): 63178500-63178586
Mmu-Pre-miR-124-1	AGGCCUCUCUCUCGUGUUCACAGCGGACCUUGA UUUAAAUGUCCAUACAAUUAAGGCACGCGGUGAA <u>UGCCAAGAAUGGGGCGUG</u>	chr14(+): 64590657-64590741
Mmu-Pre-miR-124-2	AUCAAGAUCAGAGACUCUCUCGUGUUCACA GCGGACCUUGAUUUAAUGUCAUACAAUUAAGGCA <u>CGCGGUGAAUGCCAAGAGCGGAGCCUACGGCUGCACUUGAA</u>	chr3(+): 17795662-17795770
Mmu-Pre-miR-124-3	CUCUGCGUGUUCACAGCGGACCUUGAUUUAAUGU CUAUACAAUUAAGGCACGCGGUGAAUGCCAAGAG	chr2(+): 180894040-180894107

¹The sequences underline are mature miR-124 sequence.

Supplementary Table 4. Information of primary antibodies for western blots.

Target	Dilution ratio	Source	Product code	Country
Syp	1:1000	Proteintech	17785-1-AP	China
Psd95	1:1000	Cell Signaling Technology	3409	USA
RyR3	1:1000	MilliporeSigma	AB9082	USA
Slit1	1:1000	ABclonal	A16430	China
Ptbp1	1:1000	ABclonal	A1831	China
Ank3	1:1000	Proteintech	27980-1-AP	China
Notch2	1:1000	ABclonal	A0560	China
App	1:1000	ABclonal	A11019	China
Map3k3	1:1000	ABclonal	A16058	China
P65	1:1000	Proteintech	10745-1-AP	China
Cav-1	1:1000	Proteintech	16447-1-AP	China
beta-actin	1:1000	Proteintech	60008-1-Ig	China
Bax	1:1000	Proteintech	50599-2-Ig	China
Caspase1	1:1000	Abcam	ab1872	USA
GSDMD	1:1000	Abcam	ab209845	USA
p16Ink4a	1:1000	Abcam	ab211542	USA
GAPDH	1:1000	Proteintech	60004-1-Ig	China