Supplementary Information

Inhibition of histone deacetylation rescues phenotype in a mouse model of Birk-Barel Intellectual Disability syndrome

Cooper et al.



Supplementary Figure 1: Deletion of *Kcnk9* does not affect anxiety and motor coordination of *Kcnk9*KO mice. No significant differences were observed in (a) the open-field-test between WT (n=12), *Kcnk9*KO^{mat} (n=16) and *Kcnk9*KO^{hom} (n=19) mice, (b) the elevated-plus-maze between WT (n=22), *Kcnk9*KO^{mat} (n=27) and *Kcnk9*KO^{hom} (n=35) mice, and (c) the rotarod-test between WT (n=15), *Kcnk9*KO^{mat} (n=12) and *Kcnk9*KO^{hom} (n=31) mice using One-way ANOVA and followed Bonferroni's multiple comparison post hoc test. Values are means \pm SEM. (a-c) Behavioral data are from biologically independent animals (n= number of mice). Statistical analyses and approaches are provided in Supplementary Table 1. Source data are provided as a Source Data file.



Supplementary Figure 2: Locus coeruleus expression analysis (a) Tyrosine hydroxylase (TH) RT-qPCR expression analysis. The TH expression was highly increased in locus coeruleus (LC, n=6) compared to cerebellum (n=5) and hippocampus (n=5) samples of WT mice. TH serves as a norepinephrine marker. (b) Coronal brain slice of an adult mouse; red arrows indicate tissue excision position of LC (top) schematic coronal section of the mouse brain at the position -5.4 relative to bregma¹; LC is depicted as a red triangle (bottom) (c) *Kcnk9* RT-qPCR expression analysis in LC samples of WT (n=3) compared to those of *Kcnk9*KO^{mat} (n=3) mice. (a,c) n= biologically independent samples from individual mice. Values are means \pm SEM. Source data are provided as a Source Data file.



Supplementary Figure 3: Epigenetic drug treatments in murine primary cortical neurons (mPCNs). (a) The compounds Zebularine and C646 show no effect on the *Kcnk9* expression in *Kcnk9*KO^{mat} mPCNs (Zebularine P=0.0667, C646 P=0.4727, Mann-Whitney-U test. (b) RT-qPCR expression analysis of known genes in the imprinting cluster on mouse chromosome 15. CI-994 treatment (20 μ M and 80 μ M CI-994) did not affect expression of *Trappc9, Peg13, Chrac1* and *Eif2c2* in mPCNs (n=2-3 cultures/group). (c) Evaluation of toxicity/viability in CI-994 treated mPCN compared to DMSO-treated controls. Cells were stained with Hoechst 33258 (nucleus) and NeuN (mature neurons) 3 days after treatment with either DMSO or CI-994. (d) Neuron density after CI-994 treatment. No significant difference in neuronal density was observed between DMSO (n=12), 10 μ M CI-994 (n=9) and 20 μ M CI-994 (n=9) treated mPCNs. Values are means ± SEM. Statistical analyses and approaches are provided in Supplementary Table 1. Source data are provided as a Source Data file.



Supplementary Figure 4: Allele-specific de-repression of *Kcnk9* **in the mouse brain (a)** Assay design and melt curve analysis for the allele-specific RT-qPCR (AS-RT-qPCR) of *Kcnk9*. Allele-specific primers bind to the strain-specific SNP at the 3'-end, allowing only the complementary primer to elongate (top). Agarose gel electrophoresis of PCR product (231 bp) loaded on 2% agarose gel using a 100 bp DNA ladder (middle). Melt curve analysis shows a primer-specific binding (bottom). **(b)** Analysis of expression levels using the C57BL/6 C and Cast/Ei T allele-specific primer and normalization with a reference gene revealed an increased expression of the paternal *Kcnk9* allele in the hippocampus in *Kcnk9*KO^{mat} hybrid mice treated with CI-994 (n= 4) compared to *Kcnk9*KO^{mat} DMSO controls (n= 8). No difference between the maternal *Kcnk9* allele expression comparing DMSO (n= 9) and CI-994 (n=4) treated mice (**c**) Gene expression of *Kcnk9* in WT mice treated with DMSO compared to CI-994 treated mice shows no significant differences in several analysed brain regions. WT cerebellum (DMSO n= 9, CI-994 n=12), hypothalamus (DMSO n= 9, CI-994 n= 11) and hippocampus (DMSO n=14, CI-994 n=4). Mann-Whitney U, Values are means ± SEM. Statistical analyses and approaches are provided in Supplementary Table 1. Source data are provided as a Source Data file. Components of this figure were created using Servier Medical Art templates, which are licensed under a Creative Commons Attribution 3.0 Unported License; https://smart.servier.com.



Supplementary Figure 5: No behavioural rescue of *Kcnk9*KO^{hom} mice after CI-994 treatment. (a) Y-maze percentage alternation analysis of DMSO-treated WT (n=27), DMSO-treated *Kcnk9*KO^{hom} (n=9) and CI994-treated *Kcnk9*KO^{hom} (n=9) treated mice. DMSO- and CI-994-treated *Kcnk9*KO^{hom} mice display a significant decrease in percentage alteration compared to WT mice. One-way ANOVA: F(2, 39) = 4.710, P = 0.0147; followed by Bonferroni's multiple comparison post hoc test, *P < 0.05. (b) Total locomotor activity in dark (12h) phase reveals no significant difference between DMSO-treated *Kcnk9*KO^{hom} (n=9) and CI-994-treated *Kcnk9*KO^{hom} (n=9) treated mice. A significant difference was observed by comparing DMSO-treated WT (n=24) and *Kcnk9*KO^{hom} mice. One-way ANOVA: F(2, 42) = 5.569, P = 0.0072; followed by Bonferroni's multiple comparison data are from biologically independent animals (n= number of mice). Values are means \pm SEM Statistical analyses and approaches are provided in Supplementary Table 1. Source data are provided as a Source Data file.



Supplementary Figure 6: CI-994 treatment of *Kcnk9*KO^{mat} mice does not interfere with DNA methylation at the *Peg13*-DMR. (a) Schematic presentation of the *Kcnk9* and *Peg13* loci on distal mouse chromosome 15. The *Peg13* differentially methylated region (*Peg13*-DMR) is analyzed in two separate assays. *Peg13*-DMR1 (green) and *Peg13*-DMR2 (violet). Individual CpGs analysed are depicted as lollipops. (b) The pyrogram shows the methylation status of the *Peg13*-DMRs in the hippocampus. The Y-axis shows the intensity of the light emission. The X-axis shows the dispensing order of the added nucleotides. The CpGs are highlighted in gray. In the blue box, the percentage of methylation is given. The bisulfite conversion control is highlighted in yellow. (c,d) CI-994 did not significantly alter the DNA methylation status of *Peg13*-DMR1 (CpGs 1-3) and *Peg13*-DMR2 (CpGs 17-22) in hippocampus, cerebellum or locus coeruleus measured using the bisulfite pyrosequencing method, n=3-5 DNA samples/ group, biologically independent animals. Values are means \pm SEM. Statistical analyses and approaches are provided in Supplementary Table 1. Source data are provided as a Source Data file.



Supplementary Figure 7: CI-994 treatment of *Kcnk9*KO^{mat} mice affects histone modifications at the *Kcnk9* locus. (a) Schematic presentation of *Kcnk9* on distal mouse chromosome 15. The murine *Kcnk9* gene is shown with the corresponding H3K27ac, H3K4me1 and H3K4me3 peaks (UCSC Genome Browser on Mouse July 2007 (NCBI37/mm9) Assembly). (b) TAF-ChIP-qPCR of H3K27ac marks at the promoter and intronic region of *Kcnk9* in the hippocampus of *Kcnk9*KO^{mat}animals following treatment with CI-994 (normalized to veh), *Kcnk9* promoter: P = 0.0342, and *Kcnk9* in the hippocampus of *Kcnk9*KO^{mat} animals following treatment at intergenic control region in the hippocampus of *Kcnk9*KO^{mat} animals following treatment with CI-994 (mormalized to veh). Related to figure 6b and suppl. (% of input). Related to figure 6b. (d) H3K27ac enrichment at intergenic control region in the hippocampus of *Kcnk9*KO^{mat} animals following treatment with CI-994 (normalized to veh). Related to figure 6b and suppl. figure 8c. (e) H3K27ac enrichment (norm to H3) at intergenic control region in the locus coeruleus of *Kcnk9*KO^{mat} animals following treatment with CI-994 (normalized to veh). Related to figure 6b. (f) TAF-ChIP-qPCR of H3K4me1 marks at the promoter and intronic region of *Kcnk9* in locus coeruleus of *Kcnk9*KO^{mat} animals following treatment with CI-994 (normalized to veh). Related to figure 6b. (f) TAF-ChIP-qPCR of H3K4me1 marks at the promoter and intronic region of *Kcnk9* in locus coeruleus of *Kcnk9*KO^{mat} animals following treatment with CI-994 (normalized to veh). Related to figure 6b. (f) TAF-ChIP-qPCR of H3K4me1 marks at the promoter and intronic region of *Kcnk9* in locus coeruleus of *Kcnk9*KO^{mat} animals following

treatment with CI-994 (normalized to veh). (g-h) Conventional ChIP-qPCR of H3K4me1 marks at the promoter and intronic region of *Kcnk9* in the hippocampus of *Kcnk9*KO^{mat} animals following treatment with CI-994 presented as (g) % of input and (h) normalized to veh. (i-j) Conventional ChIP-qPCR of H3K27ac marks at the promoter and intronic region of *Kcnk9* in the hippocampus of wildtype C57BL/6 animals following treatment with CI-994 presented as (i) % of input and (j) normalized to veh. (b-j) Values are means \pm SEM, Student's t-test; (n=3-4 animals/group). n= 3-4 samples/group, biologically independent animals. Data per plot was generated in 2 independent experiments. (k) Allele-specific ChIP-qPCR. The pyrogram shows the status of SNPS rs240891437 and rs47242380 in the intronic region of *Kcnk9* in the hippocampus. The Y-axis shows the intensity of the light emission. The X-axis shows the dispensing order of the added nucleotides. In the blue box, the percentage of the nucleotide arising from maternal and paternal allele is given. Statistical analyses and approaches are provided in Supplementary Table 1. Source data are provided as a Source Data file.

Subject	Figure	Genotype	Mean ± SEM	Factor	n	Statistics	Interaction F value	P value	post hoc	adjusted p-values
		WT	64.31 ± 1.619		23				Bonferroni's	
Y-maze	1b	Kcnk 9KO ^{mat}	56.62 ± 1.438		27	one way	F (2, 91) = 7.261	P=0.0012	multiple	**P<0.01
alteration		Kcnk 9KO ^{hom}	59.02 ± 1.020		44	ANOVA			comparisons test	*P<0.05
		WT	22685 ± 2059		13					(WT vs. Kcnk 9KO
		Kcnk 9KO ^{mat}	29678 ± 3623	Light phase	10	one way	F (2, 29) = 2,281	P = 0.1203	multiple	n s.
		Kcnk 9KO ^{hom}	30978 ± 3817	-8	9	ANOVA	. (-,,		comparisons test	
										*P<0.05
Circadian	1c	WT	38741 ± 2384		18					(WT vs. Kcnk 9KO ^{mat})
Rhythm		Kcnk 9KO ^{mat}	48170 ± 2457		13				Bonferroni's	****P<0.0001
				Dark phase		one way ANOVA	F (2, 43) = 22.70	P < 0.0001	multiple comparisons	(W1 vs. Kcnk 9KO)
		KenkaKOhom	61800 + 2627		15				test	(Kcnk9KO ^{mat} vs. Kcnk9KO ^{hom})
		KCIIK 9KU	01800 1 2027		15					
			96,12142 ± 0,171	Cerebellum	14					
			99,15 ± 0,298	Pons	10					
			96,225 ± 1,541	Olfactory bulb	12					
			93,22143 ± 0,334	Cortex	14					
		Maternal expression of	99,45715 ± 0,204	Hippocampus	14					
		(C57BL/6xCast/Ei)F1	98,43333 ± 0,358	Hypothalamus	9					
			95,28 ± 0,360 99,06 ± 0,434	Midbrain	5					
			98,38 ± 0,450	Medulla	5					
			86,5 ± 1,843	Locus coeruleus	4					
			3,939 ± 0,154	Cerebellum	14					
QUASEP	1d		0,850 ± 0,298	Pons	10					
			3,775 ± 1,541	Olfactory bulb	12					
			6,750 ± 0,314	Cortex	14					
			0.542 1 0.204	Hinnesomous	14					
		Paternal expression of	0,543 ± 0,204	hippocanipus	14					
		(C57BL/6xCast/Ei)F1	1,567 ± 0,358	Hypothalamus	9					
			4,720 ± 0,360	Striatum	5					
			0,940 ± 0,434	Midbrain	5					
			1,620 ± 0,450	Medulla	5					
			13,500 ± 1,843	Locus coeruleus	4					
		WT	14.00 ± 1.704		12				Ronferroni's	
Open field (percent in	Suppl. 1a	Kcnk 9KO ^{mat}	17.97 ± 1.895		16	one way	F (2, 44) = 0.3167	P = 0.7302	multiple	n.s.
center)		Kcnk 9KO ^{hom}	13.11 ± 1.361		19	ANOVA			test	
Elevated plus		WT	14.00 ± 1.704		22				Bonferroni's	
maze	Suppl. 1b	Kcnk 9KO ^{mat}	17.97 ± 1.895		27	one way	F (2, 81) = 2.568	F (2, 81) = 2.568 P = 0.0829	multiple	n.s.
(duration in open arms)		Kcnk 9K0 ^{hom}	13.11 ± 1.361		35	ANOVA			test	
		WT	240.5 ± 14.59		15				Denfermelle	
Rotarod (Latency to	Suppl. 1c	Kcnk 9KO ^{mat}	237.6 ± 15.72		12	one way	F (2, 55) = 0.0116	3 P = 0.9884	multiple	n.s.
fall)		Kcnk9KO ^{hom}	240.4 ± 10.49		31	ANOVA	. (2, 55) = 0.01108		comparisons test	
		shRNA 1	0,250		1					
		shRNA 2	0,080		1					
		shRNA 3	0,110		1					
relative		shRNA 4	0,070		1					
Kcnk9 expression	Fig. 2b	shRNA 6	0,030		1		Arithmetic means of Kcnk9 ex	pression of pre	sented IDs were	provided by Sirion Biotech
after knock- down		shRNA 7	0,060		1					
		shRNA 8 shRNA 9	0,040		1					
		shRNA 10	0,060		1					
		neagtive control	1,000		1					
		WT scrambled	1.000 ± 0.05220		8					
		WT kcnk9	1.031 ± 0.04726	PFC	4			n.s.		
Kcnk9	Fig 2c	knock-down WT scrambled	1.000 ± 0.08301		7	Mann-				
after knock-	left	control WT kcnk9	0.9579 ± 0.06216	Hippoccampus	4	Whitney U (Two-tailed)		n.s.		
down		knock-down WT scrambled	1.000 ± 0.1570		7					
		control WT kcnk9	0.2067 ± 0.08371	Locus coeruleus	4			P = 0,004		
		knock-down WT scrambled			-					
Tyrosine	Fig. 2c	control	1.148 ± 0.1343	Locus comulaus	7	Mann-				
nydroxylase expression	right	WT kcnk9	1,000 + 0 1702	Locus coeruleus	А	Whitney U (Two-tailed)		n.s.		
		knock-down	1.000 ± 0.1/03		4					

Supplementary Table 1: Summary of statistical analyses and approaches

Circadian	Fig. 2d	WT scrambled control	78517 ± 5343		Dark phase	9	Mann- Whitney U			P=0,0101			
, any can		WT kcnk9 knock-down	1059	984 ± 6	699		10	(Two-tailed)					
Y-maze	Fig. 2a	WT scrambled control	60.4	44 ± 2.3	52		9	Mann-			P=0.0707		
alteration	115.20	WT kcnk9 knock-down	53.3	20 ± 4.0	02		10	(Two-tailed)			1=0,0757		
			420,600	±	24,150	LC	6					Locus Coeruleus	vs. Cerebellum ****P < 0.0001
Tyrosine hydroxylase	Suppl. 2a	Kcnk 9KO ^{mat}	6,562	±	1,117	Cerebellum	5	one way		F (2, 13) = 242.0		Locus Coeruleus v	vs. Hippocampus ****P < 0.0001
expression			0,664	±	0.1037	Hippocampus	5					Cerebe	llum vs. Hippocampus
		Kcnk9KOmat	1,000	±	0,637		3	Mann-					
Kcnk9 expression	Suppl. 2c	WT	5.914	±	0.033	LC	3	Whitney U (Two-tailed)			P=0.1000		
		WT	2,383	±	0,153	day	46		Interaction	F (2, 192) = 4,42F	B = 0.0122		Light Phase:Kcnk9KOhom vs. Dark
		Kcnk 9KO ^{mat}	2,593	±	0,181	day	41		Interaction	F (2, 182) = 4.435	P = 0.0132	Bonferroni's	phase:Kcnk9KOhom **P<0.01
frequency	3d	WT	3,265	±	0,258	night	22	2-way- ANOVA	Phase	F (1, 182) = 16.93	P < 0.0001	comparisons	Dark phase:Kcnk9KOmat vs. Dark
		Kcnk 9KO ^{mat}	2,640 3.799	± ±	0,284 0.295	night	26 30		Genotype	F (2, 182) = 1.836	P = 0.1624	test	phase:Kcnk9KOhom *P<0.05
			.,		.,	5	Cultures						vs. DMSO
Cortical			1.00	00 ± 0.04	417 724	DMSO VPA	7	one way				Bonferroni's	****P < 0.0001
neurons all drugs	4c	Kcnk 9KO ^{mat}	5.30	07 ± 0.61	183	DZnep	3	ANOVA		F (4, 14) = 92.00	P < 0.0001	comparisons	*****P < 0.0001
			5.96	3 ± 0.18	874 760	SAHA CI-994	3					(CA	****P < 0.0001 ****P < 0.0001
							Cultures						Kcnk 9KO ^{mat}
			1.00	00 ± 0.06	656 351	DMSO	9					Bonferroni's	vs. DMSO
Cortical neurons	4d	u taua ^{mat}	3.64	12 ± 0.29	920	4 μΜ	4	one way		F (5, 22) = 75.51	P < 0.0001	multiple	****P < 0.0001
CI-994		Kcnk 9KO	4.34	9 ± 0.10	035	40 µM	4					test	*****P < 0.0001
			5.21	16 ± 0.22	264 824	80 μM WT DMSO	4						****P < 0.0001 ****P < 0.0001
						(3-5 wells/	sample)						
Duration of			1,000	±	0,104	day 1 DMSO	2 samples	Uppaired			1 day P=0,0297		
unsilencing in cortical	4e	Kcnk 9KO ^{mat}	2,738	± +	0,339	day 1 CI-994	3 samples	t-test (Two-					
neurons			2,619	+	0,265	day 10 CI-994	4 samples	tancay			10 days P=0.0001		
Cortical							Cultures				vs. DMSO		
Cortical neurons drugs no	Suppl. 3a	Kcnk 9KO ^{mat}	1.00	00 ± 0.04 01 ± 0.0	417	DMSO	Cultures 7 3	Mann- Whitney U (Two-tailed)			vs. DMSO P= 0.0667		
Cortical neurons drugs no effect	Suppl. 3a	Kcnk 9KO ^{mat}	1.00 0.90 0.54	00 ± 0.04 01 ± 0.0 48 ± 0.3	417 113 38	DMSO Zebularine C646	Cultures 7 3 4	Mann- Whitney U (Two-tailed)			vs. DMSO P= 0.0667 P =0.4727		
Cortical neurons drugs no effect	Suppl. 3a	Kcnk 9K0 ^{mat} Kcnk 9K0 ^{mat} Fif2c2	1.00 0.91 0.54		417 13 38	DMSO Zebularine C646	Cultures 7 3 4 Cultures 2	Mann- Whitney U (Two-tailed)			vs. DMSO P= 0.0667 P =0.4727		
Cortical neurons drugs no effect	Suppl. 3a	Kcnk 9KO ^{mat} Kcnk 9KO ^{mat} Elf2c2 Chrac1	1.00 0.9 0.5 1,050 0,646	00 ± 0.04 01 ± 0.0 48 ± 0.3 ± ±	417 113 38 0,014 0,014	DMSO Zebularine C646	Cultures 7 3 4 Cultures 2 3	Mann- Whitney U (Two-tailed)			vs. DMSO P= 0.0667 P =0.4727		
Cortical neurons drugs no effect RT-qPCR	Suppl. 3a	Kcnk 9KO ^{mat} Kcnk 9KO ^{mat} Eif2c2 Chrac1 Peg13 Trappc9	1.00 0.91 0.54 1,050 0,646 0,442 0,337	200 ± 0.04 01 ± 0.0 48 ± 0.3 ± ± ± ±	417 13 38 0,014 0,014 0,018 0,678	DMSO Zebularine C646 CI-994 20 µM	Cultures 7 3 4 Cultures 2 3 3 3 3	Mann- Whitney U (Two-tailed)			vs. DMSO P= 0.0667 P =0.4727		
Cortical neurons drugs no effect RT-qPCR analysis of cluster genes	Suppl. 3a Suppl. 3b	Kenk 9K0 ^{mat} Kenk 9K0 ^{mat} Elf2c2 Chrac1 Peg13 Trapp9 Kenk9 Elf2r2	1.00 0.91 0.50 0,646 0,442 0,337 6,448 2,718	- 00 ± 0.04 01 ± 0.0 48 ± 0.3 ± ± ± ±	417 13 38 0,014 0,014 0,018 0,678 0,016 0,024	DMSO Zebularine C646 CI-994 20 µM	Cultures 7 3 4 Cultures 2 3 3 3 3 2 2	Mann- Whitney U (Two-tailed) Mann- Whitney U			vs. DMSO P= 0.0667 P =0.4727		
Cortical neurons drugs no effect RT-qPCR analysis of cluster genes	Suppl. 3a Suppl. 3b	Kcnk9K0 ^{mat} Eij2c2 Chrac1 Peg13 Trappc9 Kcnk9 Eij2c2 Chrac1	1.00 0.9 0.5 1,050 0,646 0,442 0,337 6,448 2,718 1,084	20 ± 0.04 01 ± 0.0 48 ± 0.3 ± ± ± ± ± ± ±	417 113 38 0,014 0,014 0,018 0,678 0,016 0,024 0,024	DMSO Zebularine C646 CI-994 20 µM	Cultures 7 3 4 Cultures 2 3 3 3 2 3 2 2	Mann- Whitney U (Two-tailed) Mann- Whitney U			vs. DMSO P= 0.0667 P =0.4727		
Cortical neurons drugs no effect RT-qPCR analysis of duster genes	Suppl. 3a Suppl. 3b	Kenk 9K0 ^{mat} Kenk 9K0 ^{mat} Elf2c2 Chrac1 Peg13 Trappe9 Kenk9 Elf2c2 Chrac1 Peg13 Trappe9	1.00 0.9 0.5 1,050 0,646 0,442 0,337 6,448 2,718 1,084 1,084 1,060 0,965	200 ± 0.04 01 ± 0.0 48 ± 0.3 ± ± ± ± ± ± ± ±	417 113 38 0,014 0,014 0,018 0,078 0,016 0,024 0,024 0,024 0,024 0,024	DMSO Zebularine C646 Cl-994 20 µM Cl-994 80 µM	Cultures 7 3 4 Cultures 2 3 3 2 3 2 3 2 3 3 2 3 3 3 2 3 3 3 2 3 3 3 3 3 3 3 3 3 3 3 3 3	Mann- Whitney U (Two-tailed) Mann- Whitney U			vs. DMSO P= 0.0667 P =0.4727		
Cortical neurons drugs no effect RT-qPCR analysis of cluster genes	Suppl. 3a Suppl. 3b	Kenk 9KO ^{mat} Elf2c2 Chrac1 Peg13 Trappc9 Kenk9 Elf2c2 Chrac1 Peg13 Trappc9 Kenk9	1.00 0.90 0.50 0,646 0,442 0,337 6,448 2,718 1,084 1,060 0,965 20,870	+ + + + + + + + + + + + + + + + + + +	417 13 38 0,014 0,014 0,018 0,078 0,016 0,024 0,024 0,024 0,024 0,024 0,024 0,024	DMSO Zebularine C646 CI-994 20 µM CI-994 80 µM	Cultures 7 3 4 Cultures 2 3 3 3 2 3 2 3 3 2 3 3 2 3 3 2 3 3 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 3 3 2 3	Mann- Whitney U (Two-tailed) Mann- Whitney U			vs. DMSO P= 0.0667 P =0.4727		
Cortical neurons drugs no effect RT-qPCR analysis of cluster genes	Suppl. 3a Suppl. 3b	Kenk9K0 ^{mat} Elf2c2 Chrac1 Peg13 Trappe9 Kenk9 Elf2c2 Chrac1 Peg13 Trappe9 Kenk9	1.00 0.9 0.5 1,050 0,646 0,442 0,337 6,448 2,718 1,084 1,084 1,060 0,965 20,870 41,000	100 ± 0.04 001 ± 0.04 148 ± 0.3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	417 113 38 0,014 0,014 0,014 0,014 0,014 0,078 0,016 0,024 0,020000000000	DMSO Zebularine C646 CI-994 20 µM CI-994 80 µM	Cultures 7 3 4 Cultures 2 3 3 2 3 2 3 2 3 2 3 2 3 2 3 2 2 3 2 2 12	Mann- Whitney U (Two-tailed) Mann- Whitney U			vs. DMSO P= 0.0667 P =0.4727		
Cortical neurons drugs no effect RT-qPCR analysis of cluster genes Neuron density after CI-994	Suppl. 3a Suppl. 3b Suppl. 3d	Kenk 9K0 ^{mat} Eif2c2 Chrac1 Peg13 Trappc9 Kenk9 Eif2c2 Chrac1 Peg13 Trappc9 Kenk9 Kenk9K0 ^{mat}	1.00 0.9 0.5 1,050 0,646 0,442 0,337 6,448 2,718 1,084 1,084 1,084 1,084 1,084 1,084 1,085 20,870 41,000 34,580	2 00 ± 0.04 48 ± 0.3 2 ± ± ± ± ± ± ± ± ± ± ± ± ±	417 113 38 0,014 0,014 0,018 0,078 0,016 0,024 0,025 0,020000000000	DMSO Zebularine C646 Cl-994 20 µM Cl-994 80 µM DMSO Cl-994 10 µM	Cultures 7 3 4 Cultures 2 3 3 3 2 3 2 3 2 3 2 3 2 2 3 2 2 12 9	Mann- Whitney U Mann- Whitney U one way ANOVA		F (2, 27) = 0.8983	vs. DMSO P= 0.0667 P=0.4727		
Cortical neurons drugs no effect RT-qPCR analysis of duster genes Neuron density after CI-994 treatment	Suppl. 3a Suppl. 3b Suppl. 3d	Kenk 9KO ^{mat} Kenk 9KO ^{mat} Elf2c2 Chrac1 Peg13 Trappe9 Kenk9 Elf2c2 Chrac1 Peg13 Trappe9 Kenk9 Kenk9KO ^{mat}	1.00 0.9 0.5 0.646 0.442 0.337 6.448 2.718 1.084 1.060 0.965 20.870 41,000 34,580	200 ± 0.04 48 ± 0.3 ± ± ± ± ± ± ± ± ± ± ± ± ±	417 13 38 0,014 0,014 0,018 0,014 0,018 0,016 0,024 0,024 0,024 0,024 0,024 0,024 0,024 0,024 0,042 3,530	DMSO Zebularine C646 CI-994 20 µM CI-994 80 µM DMSO CI-994 10 µM CI-994 20 µM	Cultures 7 3 4 Cultures 2 3 3 2 3 3 2 3 3 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 3 2 2 3 3 3 2 2 3 3 3 2 3 3 3 2 3	Mann- Whitney U (Two-tailed) Mann- Whitney U one way ANOVA		F (2, 27) = 0.8983	vs. DMSO P= 0.0667 P=0.4727 P=0.4727		
Cortical neurons drugs no effect RT-qPCR analysis of cluster genes Neuron density after CI-934 treatment	Suppl. 3a Suppl. 3b	Kenk 9KO ^{mat} Elf2c2 Chrac1 Peg13 Trappc9 Kcnk9 Elf3c2 Chrac1 Peg13 Trappc9 Kenk9 Kenk9KO ^{mat}	1.00 0.90 0.50 1,050 0,646 0,442 0,337 6,448 2,718 1,084 1,084 1,084 1,084 1,084 1,084 1,084 1,084 34,580 34,580	2 00 ± 0.04 48 ± 0.3 2 ± ± ± ± ± ± ± ± ± ± ± ± ±	417 13 38 0,014 0,024 0,025 0,0	DMSO Zebularine C646 СI-994 20 µM СI-994 80 µM DMSO CI-994 10 µM CI-994 20 µM	Cultures 7 3 4 Cultures 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 9 9 9 9	Mann- Whitney U (Two-talled) Mann- Whitney U one way ANOVA		F (2, 27) = 0.8983	vs. DMSO P= 0.0667 P=0.4727 P=0.4191 P= 0.4191		
Cortical neurons drugs no effect RT-qPCR analysis of cluster genes cluster genes Neuron density after CI-994 treatment	Suppl. 3a Suppl. 3b	Kenk9K0 ^{mat} Eij2c2 Chrac1 Peg13 Trappe9 Kenk9 Eij2c2 Chrac1 Peg13 Trappe9 Kenk9 Kenk9	1.00 0.90 0.50 1,050 0,646 0,442 0,337 6,448 2,718 1,084 1,060 0,965 20,870 41,000 34,580 34,860		417 13 38 0,014 0,014 0,014 0,014 0,014 0,014 0,014 0,024 0,024 0,024 0,024 0,024 0,024 0,024 0,042 1,530 4,035 10 10 10 10 10 10 10 10 10 10	DMSO Zebularine C646 CI-994 20 µM CI-994 80 µM DMSO CI-994 10 µM CI-994 20 µM	Cultures 7 3 4 Cultures 2 3 3 2 3 2 3 3 2 3 3 2 3 3 2 3 3 2 3 3 2 9 9 9 DMSO: 12 CI-994: 13 DMSO: 5 2	Mann- Whitney U Mann- Whitney U one way ANOVA		F (2, 27) = 0.8983	vs. DMSO P= 0.0667 P=0.4727 P=0.4191 P = 0.4191		
Cortical neurons drugs no effect RT-qPCR analysis of duster genes Neuron density after CI-994 treatment	Suppl. 3a Suppl. 3b	Kenk 9K0 ^{mat} Elf2c2 Chraci Peg13 Trappc9 Kenk9 Elf2c2 Chrac1 Peg13 Trappc9 Kenk9 Kenk9K0 ^{mat}	1.00 0.9 0.5 1.050 0.646 0.442 0.337 6.448 2.718 1.084 1.060 0.965 20.870 41,000 34,580 34,580 2.4 1,7	2 00 ± 0.04 48 ± 0.3 2 2 2 2 2 2 2 2 2 2 2 2 2	417 13 38 0,014 0,018 0,018 0,016 0,024 0,025 0,0	DMSO Zebularine C646 CI-994 20 µM CI-994 80 µM DMSO CI-994 10 µM CI-994 10 µM CI-994 20 µM	Cultures 7 3 4 Cultures 2 3 3 2 3 3 2 3 3 2 3 3 2 3 3 2 3 3 2 9 9 9 9	Mann- Whitney U (Two-tailed) Mann- Whitney U one way ANOVA		F (2, 27) = 0.8983	vs. DMSO P= 0.0667 P=0.4727 P=0.4727 P=0.4191 P= 0.4191 P= 0.3251		
Cortical neurons drugs no effect RT-qPCR analysis of duster genes Neuron density after CI-994 treatment	Suppl. 3a Suppl. 3b	Kenk 9KO ^{mat} Elf2c2 Chrac1 Peg13 Trappc9 Kcnk9 Elf2c2 Chrac1 Peg13 Trappc9 Kcnk9 Kcnk9KO ^{mat}	1.00 0.90 0.50 1,055 0,646 0,442 0,337 6,448 2,718 1,084 1,060 0,965 20,870 41,000 34,580 34,860 2.8 1,:	2 00 ± 0.04 48 ± 0.3 2 2 2 2 2 2 2 2 2 2 2 2 2	417 13 38 0,014 0,018 0,018 0,018 0,014 0,018 0,014 0,018 0,014 0,014 0,018 0,014 0,015 0,024 0,025 1,0	DMSO Zebularine C646 CI-994 20 µM CI-994 80 µM DMSO CI-994 10 µM CI-994 20 µM CI-994 20 µM CI-994 20 µM	Cultures 7 3 4 Cultures 2 3 3 2 3 3 2 3 3 2 3 3 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 3 2 2 9 9 9 9	Mann- Whitney U (Two-tailed) Mann- Whitney U one way ANOVA		F (2, 27) = 0.8983	vs. DMSO P= 0.0667 P=0.4727 P=0.4727 P=0.4191 P= 0.4191 P= 0.3251 P= 0.0003		
Cortical neurons drugs no effect RT-qPCR analysis of cluster genes cluster genes Neuron density after CI-994 treatment	Suppl. 3a	Kenk 9KO ^{mat} Elf2c2 Chrac1 Peg13 Trappe9 Kenk9 Elf2c2 Chrac1 Peg13 Trappe9 Kenk9 Kenk9KO ^{mat}	1.00 0.90 0.50 0.646 0.442 0.337 6.448 2.718 1.084 1.060 0.965 20.870 41,000 34,580 34,580 34,580 2.1 1. 2.1	2 00 ± 0.04 448 ± 0.3 ± ± ± ± ± ± ± ± ± ± ± ± ± ± ± ± 10,20	417 13 38 0,014 0,014 0,018 0,016 0,024 0,025 1,0	DMSO Zebularine C646 СI-994 20 µМ СI-994 80 µМ DMSO CI-994 10 µМ CI-994 20 µМ CI-994 20 µМ CI-994 20 µМ	Cultures 7 3 4 Cultures 2 3 3 2 3 3 2 3 3 2 3 3 2 3 3 2 3 3 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 3 3 3 2 2 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 2 2 2 2 3 3 2 2 2 2 2 2 3 3 2 2 2 2 2 3 3 2 2 2 2 2 2 2 2 3 3 2	Mann- Whitney U Mann- Whitney U one way ANOVA		F (2, 27) = 0.8983	vs. DMSO P= 0.0667 P=0.4727 P=0.4727 P=0.4727 P=0.4191 P= 0.3251 P= 0.0003		
Cortical neurons drugs no effect RT-qPCR analysis of cluster genes Neuron density after CI-934 treatment	Suppl. 3a	Kenk 9K0 ^{mat} Eij2c2 Chrac1 Peg13 Trappe9 Kenk9 Eij2c2 Chrac1 Peg13 Trappe9 Kenk9 Kenk9	1.00 0.90 0.50 1,050 0,646 0,442 0,337 6,448 2,718 1,084 1,060 0,965 20,870 41,000 34,580 34,580 34,860 2,8 1,; 2,1		417 13 38 0,014 0,024 0,024 0,024 0,024 0,024 0,024 0,024 0,024 0,024 0,024 0,024 0,024 0,024 0,025 1,024 0,025 1,024 0,024 0,024 0,025 1,024 0,025 1,0	DMSO Zebularine C646 CI-994 20 µM CI-994 20 µM DMSO CI-994 10 µM CI-994 20 µM CI-994 20 µM CI-994 20 µM CI-994 20 µM	Cultures 7 3 4 Cultures 2 3 3 2 3 3 2 3 3 2 3 3 2 3 3 2 3 3 2 3 3 2 3 3 2 3 3 2 3 3 2 3 3 2 3 3 2 5 3 3 2 5 3 5 2 5 3 5 2 5 3 5 2 5 3 5 2 5 5 5 5	Mann- Whitney U Mann- Whitney U one way ANOVA		F (2, 27) = 0.8983	vs. DMSO P= 0.0667 P=0.4727 P=0.4797 P= 0.4191 P= 0.4191 P= 0.3251 P= 0.0003 P= 0.0002		
Cortical neurons drugs no effect RT-qPCR analysis of duster genes Neuron density after CI-994 treatment	Suppl. 3a	Kenk 9K0 ^{mat} Elf2c2 Chrac1 Peg13 Trappc9 Kenk9 Elf2c2 Chrac1 Peg13 Trappc9 Kenk9 Kenk9K0 ^{mat}	1.00 0.90 0.50 1,050 0,646 0,442 0,337 6,442 0,337 6,442 1,060 0,965 2,718 1,084 1,060 0,965 2,0,870 41,000 34,580 34,860 2,8 1,; 2,2	- 00 ± 0.04 48 ± 0.3 ± ± ± ± ± ± ± ± ± ± ± ±	417 13 38 0,014 0,014 0,018 0,016 0,014 0,014 0,014 0,024 0,055 5 5	DMSO Zebularine C646 CI-994 20 µM CI-994 80 µM DMSO CI-994 10 µM CI-994 10 µM CI-994 20 µM Cerebellum Cortex Hippocampus Pons	Cultures 7 3 4 Cultures 2 3 3 3 2 3 2 3 2 3 2 3 2 3 3 2 2 3 3 3 2 2 3 3 3 2 2 3 3 3 2 2 3 3 2 2 3 3 3 2 2 3 3 3 2 2 3 3 2 2 3 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 3 2 2 3 3 3 2 2 3 3 2 2 3 3 3 2 2 3 3 2 2 3 3 3 2 2 3 3 2 2 3 3 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 2 2 2 3 3 3 2 2 2 2 3 3 3 2 2 2 2 3 3 3 2 2 2 3 3 2 2 2 2 3 3 2 2 2 2 3 3 2 2 2 2 3 3 2 2 2 2 3 3 2	Mann- Whitney U (Two-tailed) Mann- Whitney U one way ANOVA		F (2, 27) = 0.8983	vs. DMSO P= 0.0667 P=0.4727 P=0.4727 P=0.4191 P= 0.4191 P= 0.3251 P= 0.0003 P= 0.0002		
Cortical neurons drugs no effect RT-qPCR analysis of duster genes Neuron density after CI-994 treatment	Suppl. 3a Suppl. 3b	Kenk 9KO ^{mat} Elf2c2 Chrac1 Peg13 Trappc9 Kenk9 Elf3c2 Chrac1 Peg13 Trappc9 Kenk9 Kenk9KO ^{mat}	1.00 0.9 0.5 1,055 0,646 0,442 0,337 6,448 2,718 1,084 1,060 0,965 20,870 41,000 34,580 34,580 34,860 2.8 1,: 2,:		417 13 38 0,014 0,018 0,018 0,016 0,014 0,018 0,014 0,018 0,014 0,025 13 13 13 13 13 13 13 13 13 13	DMSO Zebularine C646 CI-994 20 µM CI-994 20 µM DMSO CI-994 10 µM CI-994 20 µM CI-994 20 µM CI-994 20 µM CI-994 20 µM Hippocampus Pons Hypothalamus	Cultures 7 3 4 Cultures 2 3 3 2 3 3 2 3 3 2 3 3 2 3 3 2 3 3 2 3 3 2 2 3 3 3 2 2 2 3 3 3 2 2 3 3 3 2 2 3 3 3 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 3 3 3 2 2 2 3 3 3 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 2 2 2 3 3 2 2 2 3 2 2 3 2 2 3 2 2 3 2 2 3 2 2 3 2 2 3 2 2 3 2 2 3 2 2 3 2 2 3 2 2 3 2 2 2 2 3 2 2 2 2 3 2	Mann- Whitney U (Two-tailed) Mann- Whitney U one way ANOVA		F (2, 27) = 0.8983	vs. DMSO P= 0.0667 P=0.4727 P=0.4727 P= 0.4791 P= 0.4191 P= 0.251 P= 0.0003 P= 0.0002 P= 0.0003		
Cortical neurons drugs no effect RT-qPCR analysis of cluster genes Uster genes Neuron density after CI-994 treatment	Suppl. 3a	Kenk 9KO ^{mat} Eif2c2 Chrac1 Peg13 Trapp9 Kenk9 Eif7c2 Chrac1 Peg13 Trapp9 Kenk9 Kenk9KO ^{mat}	1.00 0.90 0.50 0.646 0.442 0.337 6.448 2.718 1.084 1.060 0.965 20.870 41,000 34,580 34,580 34,580 2.4 1, 2,2 2,7	- 00 ± 0.04 48 ± 0.3 ± ± ± ± ± ± ± ± ± ± ± ± ±	417 13 38 0,014 0,014 0,018 0,016 0,024 0,025 1,0	DMSO Zebularine C646 CI-994 20 µM CI-994 20 µM DMSO CI-994 10 µM CI-994 20 µM CI-994 20 µM CI-994 20 µM Hippocampus Pons Hypothalamus	Cultures 7 3 4 Cultures 2 3 3 3 2 3 3 2 3 3 2 3 3 3 2 3 3 2 3 3 2 3 3 3 2 3 3 3 2 3 3 3 2 3 3 3 2 3 3 3 2 3 3 3 2 3 3 3 2 3 3 3 2 3 3 3 2 3 3 3 2 3 3 3 2 3 3 3 2 3 3 3 2 3 3 3 2 5 3 3 2 3 3 3 2 5 3 3 3 2 5 3 3 2 5 5 5 5	Mann- Whitney U Mann- Whitney U one way ANOVA		F (2, 27) = 0.8983	vs. DMSO P= 0.0667 P=0.4727 P=0.4727 P=0.4191 P= 0.4191 P= 0.3251 P= 0.0003 P= 0.0002 P= 0.0003		
Cortical neurons drugs no effect RT-qPCR analysis of cluster genes cluster genes RT-qPCR Konk9 expression in expression in	Suppl. 3a Suppl. 3b Suppl. 3d	Kenk 9KO ^{mat} Eij2c2 Chrac1 Peg13 Trappe9 Kenk9 Eij2c2 Chrac1 Peg13 Trappe9 Kenk9 Kenk9KO ^{mat}	1.00 0.90 0.50 1.050 0.646 0.442 0.337 6.448 2.718 1.084 1.060 0.965 20.870 41,000 34,580 34,580 34,580 2.6 1; 2,7 2,7 2,7		417 13 38 0,014 0,024 0,024 0,024 0,024 0,024 0,024 0,024 0,024 0,024 0,024 0,024 1,024 1,025 1,0	DMSO Zebularine C646 CI-994 20 µM CI-994 20 µM DMSO CI-994 10 µM CI-994 20 µM CI-994 20 µM CI-994 20 µM CI-994 20 µM Hippocampus Hippocampus Huppothalamus Medulla	Cultures 7 3 4 Cultures 2 3 3 2 3 2 3 3 3 2 3 3 3 2 3 3 2 3 3 2 3 3 2 3 3 2 3 3 2 3 3 3 2 3 3 2 3 3 2 3 3 2 5 3 3 2 5 5 5 5	Mann- Whitney U Mann- Whitney U one way ANOVA		F (2, 27) = 0.8983	vs. DMSO P= 0.0667 P=0.4727 P=0.4191 P= 0.4191 P= 0.3251 P= 0.0003 P= 0.0003 P= 0.3961		
Cortical neurons drugs no effect RT-qPCR analysis of cluster genes density after CI-994 treatment RT-qPCR <i>Konis</i> 0 in several brain regions	Suppl. 3a Suppl. 3b Suppl. 3d	Kenk 9K0 ^{mat} Elf2c2 Chrac1 Peg13 Trappe9 Kenk9 Elf2c2 Chrac1 Peg13 Trappe9 Kenk9 Kenk9K0 ^{mat}	1.00 0.90 0.55 1,055 0,646 0,442 0,337 6,442 0,337 6,442 1,084 1,084 1,084 1,084 1,080 34,580 34,580 34,860 2.8 1,' 2,2 2,2 2,5	- 50 ± 0.04 48 ± 0.3 ± ± ± ± ± ± ± ± ± ± ± ± ±	417 13 38 0,014 0,014 0,014 0,014 0,014 0,014 0,024 0,0	DMSO Zebularine C646 CI-994 20 µM CI-994 20 µM CI-994 80 µM DMSO CI-994 10 µM CI-994 10 µM CI-994 20 µM CI-994 20 µM Cerebellum Cortex Hippocampus Pons Hypothalamus Medulla Prefrontal	Cultures 7 3 4 Cultures 2 3 3 2 3 2 3 2 3 2 3 2 3 3 2 3 2 3 3 2 2 2 3 3 2 2 3 3 2 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 2 3 3 2 2 3 3 2 2 2 3 3 2 2 2 3 3 2 2 2 3 3 2 2 2 3 3 2 2 2 3 3 2 2 2 3 3 2 2 2 3 3 3 2 2 2 3 3 2 2 2 3 3 2 2 2 3 3 2 2 2 3 3 2 2 2 2 3 3 3 2 2 2 3 3 2 2 2 3 3 2 2 2 3 3 2 2 2 2 2 3 3 2 2 2 2 3 3 2 2 2 2 2 3 3 2	Mann- Whitney U (Two-tailed) Mann- Whitney U Mann- Whitney U (Two-tailed)		F (2, 27) = 0.8983	vs. DMSO P= 0.0667 P=0.4727 P=0.4727 P= 0.4791 P= 0.4191 P= 0.3251 P= 0.0003 P= 0.0002 P= 0.0003 P= 0.3961		
Cortical neurons drugs no effect RT-qPCR analysis of cluster genes Neuron density after CI-994 treatment RT-qPCR <i>Konk9</i> expression in several brain regions	Suppl. 3a Suppl. 3b Suppl. 3d	Kenk 9KO ^{mat} Eff2c2 Chrac1 Peg13 Trapp9 Kenk9 Eff2c2 Chrac1 Peg13 Trapp9 Kenk9 Kenk9KO ^{mat}	1.00 0.90 0.50 0.646 0.442 0.337 6.448 2.718 1.084 1.060 0.965 20.870 41,000 34,580 34,580 34,580 2.4 1, 2.7 2,7 2,7 2,7 2,0 0,5	- 00 ± 0.04 48 ± 0.3 ± ± ± ± ± ± ± ± ± ± ± ± ±	417 13 38 0,014 0,014 0,018 0,016 0,014 0,014 0,018 0,014 0,025 0,026 0,0	DMSO Zebularine C646 CI-994 20 µM CI-994 20 µM CI-994 80 µM DMSO CI-994 10 µM CI-994 10 µM CI-994 20 µM CI-994 20 µM CI-994 20 µM Hippocampus Pons Hippocampus Pons Hypothalamus Medulla	Cultures 7 3 4 Cultures 2 3 3 2 2 3 3 3 2 2 2 3 3 3 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 2 3 3 3 2 2 2 2 3 3 2 2 2 2 3 3 2 2 2 2 3 3 2 2 2 2 2 3 2 2 2 2 3 2 2 2 2 3 2	Mann- Whitney U Mann- Whitney U one way ANOVA		F (2, 27) = 0.8983	vs. DMSO P= 0.0667 P=0.4727 P=0.4727 P= 0.4791 P= 0.4191 P= 0.3251 P= 0.0003 P= 0.0003 P= 0.0003 P= 0.3961 P= 0.7319		

	1		2,00	,-		01102201 7 0010	1				0,0022		
							CI-994: 6						
							DMSO: 7						
			2,90	0 ± 0,9	92	Locus coeruleus	CI-994: 8				P= 0.0401		
			2,25	5 ± 0,6	59	Caudal Pontine Reticular	DMSO: 7						
						Formation	CI-994: 4				P= 0,1409		
			5.337	7±0.1	.65	DMSO	9		Interaction	F (1, 42) = 26.16	P < 0.0001		
Cerebellum after CI-994 treatment		WT	5 445 + 0.422		22	C1 004	12		T	5 (4 42) 24 02	B - 0 0001	Bonferroni's	
	5c		5.445 ± 0.125		CI-994	12	2-way-	rreatment	r (1, 42) - 54.92	P < 0.0001	multiple	****P<0.0001 (all comparisons except DMSO: WT vs CL-994: WT)	
		Kenk 9KO ^{mat}	1.000 ± 0.125		.25	DMSO	12 ANOVA	Genotype	F (1, 42) = 719.1	P < 0.0001	test	DMSO: W1 vs CI-994: W1)	
			2.497	7 ± 0.1	.33	CI-994	13						
		Kcnk 9KO ^{mat}					Hippocampus						
		Eif2c2	1,000	±	0,016		5						
		Pea13	1,000	± ±	0,044	DMSO	5						
		Trappc9	1,000	±	0,054	51150	5				Kcnk9 Cl-		
analysis of	5d	Kcnk9	1,000	±	0,091		5	Mann-			994 vs.		
cluster genes		Eif2c2	1,000	±	0,156		5	whitney U			P=0.0079		
		Chrac1	0,982	±	0,088	C1994	5						
		Trappc9	1,210	±	0,105	(30mg/kg)	5						
		Kcnk9	2,313	±	0,423		5						
			64 627	72 + 1	290	DMSO	20		Interaction	E (1 96) - 2 700	R = 0.0574		**P<0.01
		WT	64.027			014130	20		-	r (1, 50) = 5.700			(WT:DMSO vs. Kcnk 9KO ^{mat} :DMSO) **P<0.01
Ymaze alteration			64.779	955 ±1	.014	CI-994	18	2-way-	Treatment	F (1, 96) = 4.096	P = 0.0458	Tukey multiple	(WT:CI-994 vs. Kcnk9KOmat :DMSO)
after CI-994	5e		57.1799	977 ± 1	1.584	DMSO	21	ANOVA		F (1, 96) = 8.992	8.992 P = 0.0035	comparisons test	*P<0.05
treatment		Kcnk 9KO ^{mat}	62 15 2	00 ± 1	402	CL 004	24		Genotype				(Kcnk9KOmat: CI-994 vs. Kcnk9KOmat :DMSO)
			03.132	00 I I	495	CI-994	24						
			17562,000	±	999,600	DMSO	20		Interaction	F (1, 43) = 0.5104	P = 0.0018		
Circadian		WT						2-way-		F (1, 43) =		Bonferroni's multiple	
Rhythm light phase CI-994	5f		16754,000	±	1061,000	CI-994	10	ANOVA	Treatment	0.006126	P = 0.0366	comparisons	n.s.
		Kcnk 9KO ^{mat}	15950,000	±	1073,000	DMSO	8		Genotype	F (1, 43) = 0.3064	P = 0.1763	test	
			16958,000	±	1557,000	CI-994	9						**D-0.01
		wt	35719,000	±	1874,000	DMSO	24		Interaction	F (1, 60) = 10.68	P = 0.0031		(WT:DMSO vs. Kcnk 9KO ^{mat} :DMSO)
Circadian Rhythm dark			38601,000	±	2630,000	CI-994	15	2-way-	Treatment	F (1, 60) = 4.571	P = 0.0518	multiple comparisons	
phase	51		47535.000	+	3016.000	DMSO	12	ANOVA					**R<0.01
CI-554		Kcnk 9KO ^{mat}	22758 000	-	3795.000	CL 004	12		Genotype	F (1, 60) = 1.872	P = 0.1960	test	(Kcnk9 KOmat: CI-994 vs. Kcnk9 KOmat
-			33758,000	Ŧ	2785,000	CI-994	13						:DMSO)
			1,000	±	0,185	maternal DMSO	8				B 0 0000		
Allele-specific			1,296	±	0,314	maternal	4	Mann.			P=0,6828		
expression of Kcnk9	Suppl. 4b	WT hippocampus	4 000		0.200	CI-994	0	Whitney U					
			1,000	Ŧ	0,200	naternal	9				P=0,2601		
			3,583	±	1,626	CI-994	4						
		WT cerebellum	1,000	±	0,128	DMSO	9				P=0 3368		
			1,054	±	0,076	CI-994	12				,		
Kcnk9			1,000	±	0,054	DMSO	9	Mann					
after CI-994	Suppl. 4c	WT hypothalamus	1 127	+	0 104	CI-994	11	Whitney U			P=0,1726		
treatment			-,	-									
		WT hippocampus	1,000	±	0,078	DMSO	14				P=0,8778		
			1,103	±	0,274	CI-994	4						
Y-maze		WT	64,630	±	1,291	DMSO	27	one way				Bonferroni's multiple	*P<0.05
alteration	Suppl.5a	Kcnk9KO ^{hom}	58,740	±	1,465	DMSO	9	ANOVA		F (2, 39) = 4.710	P = 0.0147	comparisons	(WT DMSO vs. Kcnk 9KO ^{ma} DMSO)
		Kcnk 9KO ^{hom}	58,200	±	1,775	CI-994	9					test	
		WT	35719,000	±	1874,000	DMSO	24					Bonferroni's	
Circadian	Suppl. 5b	Kcnk9KO ^{hom}	48275,000	±	5271,000	DMSO	9	one way ANOVA		F (2, 42) = 5.569	P = 0.0072	multiple comparisons	*P<0.05
Rhythm		KankaKohom	43338 000	+	2422.000	CI-004	9					test	(WT DMSO vs. Kcnk 9KO""DMSO) *P<0.05
		KEIK SKO	45550,000	-	5455,000	0.554	, in the second s						(WT DMSO vs. Kcnk 9KO ^{ma} CI-994
			1 000	*	0.147		DMCC						
		H3K27ac fold	1,000	Ŧ	0,147	kcnk9 prom	DIVI30. 9				P = 0.0001		
Conventional		enrichment in	2,137	±	0,1687		CI-994: 9						
ChIP H3K27ac		(Normalized to Veh)	1.000	+	0.232		DMSO: 8						
			,			kcnk9 intron		Chudont's t			P = 0.0270		
	6b		2,097	±	0,3791		CI-994: 8	test (Two-					
			1.000	± 0.12	245		DMSO: 4	tailed)					
		H3K27ac/H3 binding	2.288	± 0.49	945	kcnk9 prom	CI-994: 4				P = 0.0450		
Low-input ChIP H3K27ac		in LC (Fold Change to Veh)			205								
		5	1.000	± 0.23	305	kcnk9 intron	DMSO: 4				P =0.0202		
			2.414	± 0.38	838		CI-994: 3						
			72	2,990			WT DMSO=3				P 02		
			63	3,942			WT CI-994=4				r =0,2		

		Maternal H3K27ac enrichment in the	6	8,505		rs 240891437	Kcnk 9KO ^{mat}		
			6	51.894			Kcnk 9KO ^{mat}		P =0.4476
			-	-,			:CI-994=4	Student's t-	
		hippocampus (C57BI /6xCast/Ei)E1	6	51,180			WT DMSO=3	test (Two- tailed)	P =0.0571
			5	51,170			WT CI-994=4		
			5	7 820		rs 47242380	Kcnk 9KO ^{mat}		
				,020			:DMSO=6		P =0.0476
Allele-specific	6c		5	51,360			Kcnk 9KO ^{mat} :CI-994=4		
ChIP			2	27,010			WT DMSO=3		P =0,2
			3	86,058			WT CI-994=4		
			3	81,495		15 240891437	:DMSO=6		P =0 4476
		Paternal H3K27ac	3	88,106			Kcnk 9KO ^{mat} :CI-994=4		
		enrichment in the	3	8,800			WT DMSO=3	Student's t- test (Two-	
		(C57BL/6xCast/Ei)F1		0 020				tailed)	P =0.0571
				10,050		rs 47242380	WT CI-594-4		
			4	12,183			Kcnk 9KO ^{mat} :DMSO=6		D_0.0476
			4	8,640			Kcnk 9KO ^{mat}		1-0.070
							:CI-994=4		
			49,37	±	0,65	CrCc 1.3	DMSO: 3		D-0 1249
		Hippocampus	50,71	±	0,59	CP05 1-5	CI-994: 3		r= 0.1340
			39,36 37.87	± +	1,34	CpGs 17-22	DMSO: 3		P= 0.2744
			50,05	±	0,71		DMSO: 4		
Methylation		Coroballum	49,61	±	0,51	CpGs 1-3	CI-994: 3	RM 2-way- ANOVA	P= 0.6190
of Peg13- DMR	Suppl. 6	Cerebellulli	39,77	±	0,36	CpGs 17-22	DMSO: 4	treated vs	P= 0.9366
			39,72	±	0,70	•	CI-994: 3	non-u eateu	
			53,47	±	0,81	CpGs 1-3	DMSO: 5		P= 0.7135
		LC	36,40	±	1,30		DMSO: 5		
						CnGs 17-22			P= 0.1840
			38,73	±	1,18	op 00 - 1 - 1 -	CI-994: 5		
			38,73	± 0 ± 0.2	1,18 726		CI-994: 5 DMSO: 4		
TAF-ChIP	Sumal 7h	H3K27ac/H3 binding (normalized to veh)	38,73 1.000 2.369	± 0 ± 0.2 9 ± 0.4	1,18 726 146	kcnk9 prom	CI-994: 5 DMSO: 4 CI-994: 3	Student's t-	P = 0.0342
TAF-ChIP H3K27ac	Suppl. 7b	H3K27ac/H3 binding (normalized to veh) in hippocampus of Kcnk 9K0 ^{mat}	38,73 1.000 2.369 1.000	± 0 ± 0.2 9 ± 0.4 0 ± 0.3	1,18 726 146 419	kcnk9 prom	CI-994: 5 DMSO: 4 CI-994: 3 DMSO: 4	Student's t- test	P = 0.0342
TAF-ChiP H3K27ac	Suppl. 7b	H3K27ac/H3 binding (normalized to veh) in hippocampus of Kcnk 9K0 ^{mat}	38,73 1.000 2.369 1.000 1.787	± 0±0.2 9±0.4 0±0.3 7±0.1	1,18 726 146 419 179	kcnk9 prom	CI-994: 5 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3	Student's t- test	P = 0.0342 P = 0.1172
TAF-ChiP H3K27ac	Suppl. 7b	H3K27ac/H3 binding (normalized to veh) in hippocampus of Kcnk 9K0 ^{mat}	38,73 1.000 2.369 1.000 1.787 0,4436	± 0±0.2 9±0.4 0±0.3 7±0.1 ±	1,18 726 146 419 179 0,07741	kcnk9 prom kcnk9 intron	CI-994: 5 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 CI-994: 3	Student's t- test	P = 0.0342 P = 0.1172 P = 0.0648
TAF-ChiP H3K27ac	Suppl. 7b	H3K27ac/H3 binding (normalized to veh) in hippocampus of Kcnk 9K0 ^{mst} H3K27ac fold change enrichment	38,73 1.000 2.369 1.000 1.787 0,4436 0,2074	± 0 ± 0.2 9 ± 0.4 0 ± 0.3 7 ± 0.1 ± ±	1,18 726 146 419 179 0,07741 0,07044	kcnk9 prom kcnk9 intron kcnk9 prom	CI-994: 5 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 CI-994: 4 DMSO: 4	Student's t- test Student's t-	P = 0.0342 P = 0.1172 P =0.0648
TAF-ChiP H3K27ac Convent. ChiP H3K27ac	Suppl. 7b Suppl. 7c	H3K27ac/H3 binding (normalized to veh) in hippocampus of Kcnk 9K0 ^{mat} H3K27ac fold change enrichment (Normalized to input)	38,73 1.000 2.365 1.000 1.787 0,4436 0,2074 0,3834	\pm 0 ± 0.2 9 ± 0.4 0 ± 0.3 7 ± 0.1 \pm \pm \pm \pm \pm	1,18 726 146 419 0,07741 0,07044 0,1338	kcnk9 prom kcnk9 intron kcnk9 prom kcnk9 intron	CI-994: 5 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 CI-994: 4 DMSO: 4 CI-994: 4	Student's t- test Student's t- test (Two- tailed)	P = 0.0342 P = 0.1172 P = 0.0648 P = 0.2130
TAF-ChiP H3K27ac Convent. ChiP H3K27ac	Suppl. 7b Suppl. 7c	H3X27ac/H3 binding (normalized to veh) in hippocampus of Kcnk 9KO ^{mat} H3K27ac fold change enrichment (Normalized to input) in hippocampus of Kcnk 9KO ^{mat}	38,73 1.000 2.369 1.000 1.787 0,4436 0,2074 0,3834 0,176 0,0796	\pm 0 ± 0.2 9 ± 0.4 0 ± 0.3 7 ± 0.1 \pm \pm \pm \pm \pm \pm	1,18 726 146 419 179 0,07741 0,07044 0,1338 0,0652 0,01726	kcnk9 prom kcnk9 intron kcnk9 prom kcnk9 intron	CI-994: 5 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4	Student's t- test Student's t- test (Two- tailed)	P = 0.0342 P = 0.1172 P = 0.0648 P = 0.2130
TAF-ChiP H3K27ac Convent. ChiP H3K27ac	Suppl. 7b Suppl. 7c	H3K27ac/H3 binding (normalized to veh) in hippocampus of Kcnk 9KO ^{mat} H3K27ac fold change enrichment (Normalized to input) in hippocampus of Kcnk 9KO ^{mat}	38,73 1.000 2.369 1.000 1.787 0,4436 0,2074 0,3834 0,176 0,0796 0,03558	± 0 ± 0.2 9 ± 0.4 0 ± 0.3 7 ± 0.1 ± ± ± ± ± ± ±	1,18 726 146 419 179 0,07741 0,07044 0,0338 0,0652 0,01726 0,009545	kcnk9 prom kcnk9 intron kcnk9 prom kcnk9 intron lg3	CI-994: 5 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 CI-994: 3 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4	Student's t- test Student's t- test (Two- tailed)	P = 0.0342 P = 0.1172 P = 0.0648 P = 0.2130 P = 0.0671
TAF-ChiP H3K27ac Convent. ChiP H3K27ac	Suppl. 7b Suppl. 7c	H3K27ac/H3 binding (normalized to veh) in hippocampus of Kcnk 9K0 ^{mat} H3K27ac fold change enrichment (Normalized to input) in hippocampus of Kcnk 9K0 ^{mat}	38,73 1.000 2.365 1.000 1.787 0,4436 0,2074 0,3834 0,176 0,0796 0,03558 2,237	±) ± 0.2) ± 0.4) ± 0.3 t ± ± ± ± ± ± ± ± ± ±	1,18 726 419 0,07741 0,07044 0,1338 0,0652 0,01726 0,009545 0,485	kcnk9 prom kcnk9 intron kcnk9 intron kcnk9 intron lg3	CI-994: 5 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4	Student's t- test Student's t- test (Two- tailed) Student's t-	P = 0.0342 P = 0.1172 P = 0.0648 P = 0.2130 P = 0.0671
TAF-ChiP H3K27ac Convent. ChiP H3K27ac Convent. ChiP H3K27ac	Suppl. 7b Suppl. 7c Suppl. 7d	H3X27ac/H3 binding (normalized to veh) in hippocampus of Kcnk 9K0 ^{mat} H3K27ac fold change enrichment (Normalized to input) in hippocampus of Kcnk 9K0 ^{mat} H3K27ac fold change enrichment (normalized to veh)	38,73 1.000 2.365 1.000 1.787 0,4436 0,2074 0,3834 0,176 0,0796 0,03558 2,237 1,000	±) ± 0.2;) ± 0.4;) ± 0.3; t ± ± ± ± ± ± ± ± ± ± ± ± ±	1,18 726 419 179 0,07741 0,07044 0,1338 0,0652 0,01726 0,009545 0,485 0,268	kenk9 prom kenk9 intron kenk9 intron kenk9 intron lg3	CI-994: 5 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4	Student's t- test Student's t- test (Two- tailed) Student's t- test (Two- tailed)	P = 0.0342 P = 0.1172 P = 0.0648 P = 0.2130 P = 0.0671 P=0.0671
TAF-ChIP H3K27ac Convent. ChIP H3K27ac Convent. ChIP H3K27ac	Suppl. 7b Suppl. 7c Suppl. 7d	H3X27ac/H3 binding (normalized to veh) in hippocampus of Kcnk 9K0 ^{mat} H3K27ac fold change enrichment (Normalized to input) in hippocampus of Kcnk 9K0 ^{mat} H3K27ac fold change enrichment (normalized to veh) in hippocampus	38,73 1.000 2.369 1.000 1.787 0,4436 0,2074 0,3834 0,176 0,0796 0,03558 2,237 1,000	±) ± 0.2) ± 0.4) ± 0.3 7 ± 0.1 ± ± ± ± ± ± ± ± ± ± ±	1,18 726 146 419 0,07741 0,07044 0,1338 0,0652 0,01726 0,009545 0,485 0,268	kenk9 prom kenk9 intron kenk9 intron kenk9 intron lg3 lg3	CI-994: 5 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4	Student's t- test Student's t- test (Two- tailed) Student's t- test (Two- tailed)	P = 0.0342 P = 0.1172 P = 0.0648 P = 0.2130 P = 0.0671 P=0.0671
TAF-ChIP H3K27ac Convent. ChIP H3K27ac Convent. ChIP H3K27ac	Suppl. 7b Suppl. 7c Suppl. 7d	H3K27ac/H3 binding (normalized to veh) in hippocampus of Kcnk 9K0 ^{mst} H3K27ac fold change enrichment (Normalized to input) in hippocampus of Kcnk 9K0 ^{mst} H3K27ac fold change enrichment (normalized to veh) in hippocampus H3K27ac/H3 binding	38,73 1.000 2.369 1.000 1.787 0,4436 0,2074 0,3834 0,176 0,0796 0,03558 2,237 1,000 0,869	± D ± 0.2: 9 ± 0.4: 0 ± 0.3: ± ± ± ± ± ± ± ± ± ±	1,18 726 146 419 179 0,07741 0,07044 0,1338 0,0652 0,01726 0,009545 0,485 0,268	kcnk9 prom kcnk9 intron kcnk9 prom kcnk9 intron lg3	CI-994: 5 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4	Student's t- test Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t-	P = 0.0342 P = 0.1172 P = 0.0648 P = 0.2130 P = 0.0671 P=0.0671
TAF-ChiP H3K27ac Convent. ChiP H3K27ac TAF-ChiP H3K27ac	Suppl. 7b Suppl. 7c Suppl. 7d Suppl. 7e	H3K27ac/H3 binding (normalized to veh) in hippocampus of Kcnk 9KO ^{mat} H3K27ac fold change enrichment (Normalized to input) in hippocampus of Kcnk 9KO ^{mat} H3K27ac fold change enrichment (normalized to veh) in hippocampus	38,73 1.000 2.365 1.000 0,4436 0,2074 0,4436 0,2074 0,3834 0,0796 0,0796 0,03558 2,237 1,000 0,869 1,000	±) + 0.2:) + 0.4:) + 0.3: (7 + 0.1: ± ± ± ± ± ± ± ± ± ± ± ± ±	1,18 726 146 419 179 0,07741 0,07741 0,07044 0,0388 0,0652 0,01726 0,01726 0,01726 0,01726 0,0268	kcnk9 prom kcnk9 intron kcnk9 intron kcnk9 intron lg3 lg3	CI-994: 5 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4	Student's t- test Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t-	P = 0.0342 P = 0.1172 P = 0.0648 P = 0.2130 P = 0.0671 P=0.0671 P=0.0671
TAF-ChiP H3K27ac Convent. ChiP H3K27ac TAF-ChiP H3K27ac	Suppl. 7b Suppl. 7c Suppl. 7d	H3X27ac/H3 binding (normalized to veh) in hippocampus of Kcnk 9KO ^{mat} H3K27ac fold change enrichment (Normalized to input) in hippocampus of Kcnk 9KO ^{mat} H3K27ac fold change enrichment (normalized to veh) in hippocampus	38,73 1.000 2.365 1.000 0,4436 0,2074 0,3834 0,176 0,0796 0,03558 2,237 1,000 0,869 1,000	± 2) ± 0.2: 2) ± 0.4: 2) ± 0.3: 7 ± 0.1: 2 ± ± ± ± ± ± ± ± ± ± ± ±	1,18 726 146 419 179 0,07741 0,07741 0,07044 0,0652 0,0752 0,01726 0,009545 0,248 0,268 0,248	kcnk9 prom kcnk9 intron kcnk9 intron lg3 lg3 lg3	CI-994: 5 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 3 DMSO: 4	Student's t- test Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed)	P = 0.0342 P = 0.1172 P = 0.0648 P = 0.2130 P = 0.0671 P=0.0671 P=0.0671
TAF-ChIP H3K27ac Convent. ChIP H3K27ac TAF-ChIP H3K27ac	Suppl. 7b Suppl. 7c Suppl. 7d	H3X27ac/H3 binding (normalized to veh) in hippocampus of Kcnk 9K0 ^{mat} H3K27ac fold change enrichment (Normalized to input) in hippocampus of Kcnk 9K0 ^{mat} H3K27ac fold change enrichment (normalized to veh) in hippocampus	38,73 1.000 2.365 1.000 0,4436 0,2074 0,3834 0,176 0,0796 0,0796 0,03558 2,237 1,000 0,869 1,000 1,656 1,000	± ± 0.2: 0 ± 0.2: 0 ± 0.3: 7 ± 0.1: ± ± ± ± ± ± ± ± ± ± ± ±	1,18 726 146 419 179 0,07741 0,07044 0,0652 0,0745 0,01726 0,00545 0,248 0,248 0,248 0,248 0,212	kcnk9 prom kcnk9 intron kcnk9 intron lg3 lg3 lg3 kcnk9 prom	CI-994: 5 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3	Student's t- test Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed)	P = 0.0342 P = 0.1172 P = 0.0648 P = 0.2130 P = 0.0671 P=0.0671 P=0.7046 P = 0.1118
TAF-ChIP H3K27ac Convent. ChIP H3K27ac TAF-ChIP H3K27ac Low-input	Suppl. 7b Suppl. 7c Suppl. 7d	H3K27ac/H3 binding (normalized to veh) in hippocampus of Kcnk 9KO ^{mat} H3K27ac fold change enrichment (Normalized to input) in hippocampus of Kcnk 9KO ^{mat} H3K27ac fold change enrichment (normalized to veh) in hippocampus H3K27ac/H3 binding (normalized to veh) in LC	38,73 1.000 2.365 1.000 0,4336 0,2074 0,3834 0,2074 0,3834 0,2074 0,0796 0,0796 0,0796 0,03558 2,237 1,000 0,869 1,000 1,656 1,000 1,88	± 2) ± 0.2: 2) ± 0.4: 2) ± 0.3: 7 ± 0.1: 2 ± ± ± ± ± ± ± ± ± ± ± ± ±	1,18 726 146 419 179 0,07741 0,07044 0,0338 0,0652 0,01726 0,00545 0,268 0,268 0,248 0,248 0,248 0,212	kcnk9 prom kcnk9 intron kcnk9 intron lg3 lg3 lg3 kcnk9 prom kcnk9 prom	CI-994: 5 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3	Student's t- test Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t-	P = 0.0342 P = 0.1172 P = 0.0648 P = 0.2130 P = 0.0671 P = 0.0671 P = 0.0671 P = 0.7046 P = 0.1118 P = 0.7092
TAF-ChIP H3K27ac Convent. ChIP H3K27ac Convent. ChIP H3K27ac Low-input ChIP H3K47mac	Suppl. 7b Suppl. 7c Suppl. 7d Suppl. 7f	H3K27ac/H3 binding (normalized to veh) in hippocampus of Kcnk 9K0 ^{mat} H3K27ac fold change enrichment (Normalized to input) in hippocampus of Kcnk 9K0 ^{mat} H3K27ac fold change enrichment (normalized to veh) in hippocampus H3K27ac/H3 binding (normalized to veh) in LC H3K4me1/H3 binding (normalized to veh)	38,73 1.000 2.365 1.000 0,4336 0,2074 0,3834 0,176 0,0796 0,03558 2,237 1,000 0,869 1,000 1,656 1,000 1,188 1 1,219	± 0 ± 0.2 0 ± 0.3 7 ± 0.3 1 ± ± ± ± ± ± ± ± ± ± ± ± ±	1,18 726 146 419 179 0,07741 0,07044 0,0338 0,0652 0,01726 0,01726 0,00545 0,248 0,248 0,248 0,212 0,248 0,212	kcnk9 prom kcnk9 intron kcnk9 intron lg3 lg3 lg3 kcnk9 prom kcnk9 prom	CI-994: 5 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3	Student's t- test Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed)	P = 0.0342 P = 0.1172 P = 0.0648 P = 0.2130 P = 0.0671 P = 0.0671 P = 0.0671 P = 0.7046 P = 0.1118 P = 0.7092
TAF-ChIP H3K27ac Convent. ChIP H3K27ac Convent. ChIP H3K27ac Low-input ChIP H3K4me1	Suppl. 7b Suppl. 7c Suppl. 7d Suppl. 7f	H3K27ac/H3 binding (normalized to veh) in hippocampus of Kcnk 9K0 ^{mat} H3K27ac fold change enrichment (Normalized to input) in hippocampus of Kcnk 9K0 ^{mat} H3K27ac fold change enrichment (normalized to veh) in hippocampus H3K27ac/H3 binding (normalized to veh) in LC H3K4me1/H3 binding (normalized to veh) in LC of Kcnk 9K0 ^{mat}	38,73 1.000 2.365 1.000 0,436 0,0774 0,3834 0,176 0,0796 0,0796 2,237 1,000 0,869 1,000 1,656 1,000 1,888 1 1,219 1,	± 0 ± 0.2 0 ± 0.3 0 ± 0.3 ± ± ± ± ± ± ± ± ± ± ± ± ±	1,18 726 146 419 179 0,07741 0,07044 0,1338 0,0652 0,01726 0,005545 0,268 0,248 0,212 0,212 0,212	kcnk9 prom kcnk9 intron kcnk9 intron lg3 lg3 lg3 kcnk9 prom kcnk9 intron lg3	CI-994: 5 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4	Student's t- test Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed)	P = 0.0342 P = 0.1172 P = 0.0648 P = 0.2130 P = 0.0671 P = 0.0671 P = 0.0671 P = 0.1118 P = 0.7046 P = 0.7092 P = 0.7226
TAF-ChIP H3K27ac Convent. ChIP H3K27ac Convent. ChIP H3K27ac Low-input ChIP H3K4me1	Suppl. 7b Suppl. 7c Suppl. 7d Suppl. 7f	H3K27ac/H3 binding (normalized to veh) in hippocampus of Kcnk 9K0 ^{mat} H3K27ac fold change enrichment (Normalized to input) in hippocampus of Kcnk 9K0 ^{mat} H3K27ac fold change enrichment (normalized to veh) in hippocampus H3K27ac/H3 binding (normalized to veh) in LC H3K4me1/H3 binding (normalized to veh) in LC of Kcnk 9K0 ^{mat}	38,73 1.000 2.365 1.000 0,436 0,2074 0,3834 0,176 0,0796 0,03558 2,237 1,000 0,869 1,000 1,656 1,000 1,188 1,219 1 0,014	± 0 ± 0.2 0 ± 0.2 0 ± 0.3 1 ± ± ± ± ± ± ± ± ± ± ± ± ± ±	1,18 726 146 419 179 0,07741 0,07044 0,1338 0,0652 0,00545 0,01726 0,00545 0,268 0,248 0,212 0,248 0,212	kcnk9 prom kcnk9 intron kcnk9 intron lg3 lg3 lg3 kcnk9 prom kcnk9 intron lg3	CI-994: 5 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 3 DMSO: 4	Student's t- test Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed)	P = 0.0342 P = 0.1172 P = 0.0648 P = 0.2130 P = 0.0671 P = 0.0671 P = 0.0671 P = 0.1118 P = 0.7046 P = 0.7092 P = 0.7226
TAF-ChIP H3K27ac Convent. ChIP H3K27ac Convent. ChIP H3K27ac Low-input ChIP H3K4me1	Suppl. 7b Suppl. 7c Suppl. 7d Suppl. 7f	H3X27ac/H3 binding (normalized to veh) in hippocampus of Kcnk 9K0 ^{mat} H3K27ac fold change enrichment (Normalized to input) in hippocampus of Kcnk 9K0 ^{mat} H3K27ac fold change enrichment (normalized to veh) in hippocampus H3K27ac/H3 binding (normalized to veh) in LC H3K4me1/H3 binding (normalized to veh) in LC of Kcnk 9K0 ^{mat}	38,73 1.000 2.365 1.000 0,4336 0,2074 0,3834 0,176 0,0796 0,03558 2,237 1,000 0,869 1,000 1,656 1,000 1,188 1 1,219 1 0,014 0,014 0,005	± 2) ± 0.2 2) ± 0.4 2) ± 0.3 7 ± 0.1 ± ± ± ± ± ± ± ± ± ± ± ± ±	1,18 726 146 419 0,07741 0,0704 0,1338 0,0652 0,00545 0,268 0,268 0,248 0,212 0,248 0,212 0,248 0,212	kcnk9 prom kcnk9 intron kcnk9 intron lg3 lg3 lg3 kcnk9 intron kcnk9 intron kcnk9 intron lg3 kcnk9 prom	CI-994: 5 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4	Student's t- test Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t-	P = 0.0342 P = 0.1172 P = 0.0648 P = 0.2130 P = 0.0671 P = 0.0671 P = 0.0671 P = 0.1118 P = 0.7092 P = 0.7226 P = 0.1115
TAF-ChIP H3K27ac Convent. ChIP H3K27ac Convent. ChIP H3K27ac Low-input ChIP H3K4me1	Suppl. 7b Suppl. 7c Suppl. 7d Suppl. 7f Suppl. 7f	H3X27ac/H3 binding (normalized to veh) in hippocampus of Kcnk 9K0 ^{mat} H3K27ac fold change enrichment (Normalized to lnput) in hippocampus of Kcnk 9K0 ^{mat} H3K27ac fold change enrichment (normalized to veh) in hippocampus H3K27ac/H3 binding (normalized to veh) in LC H3K4me1/H3 binding (normalized to veh) in LC of Kcnk 9K0 ^{mat} H3K4me1 fold change enrichment (Normalized to input) in Kcnk 9K0 ^{mat}	38,73 1.000 2.365 1.000 0,4336 0,2074 0,3834 0,176 0,0796 0,03558 2,237 1,000 0,869 1,000 1,656 1,000 1,656 1,000 1,188 1 1,219 1 0,014 0,005 0,019 0,0084	±	1,18 726 146 419 0,07741 0,07044 0,1338 0,0652 0,01726 0,09545 0,268 0,268 0,248 0,212 0,248 0,212 0,248 0,212 0,248 0,212	kcnk9 prom kcnk9 intron kcnk9 intron lg3 lg3 lg3 kcnk9 prom kcnk9 intron lg3 kcnk9 prom kcnk9 prom kcnk9 prom	CI-994: 5 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4	Student's t- test Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed)	P = 0.0342 P = 0.1172 P = 0.0648 P = 0.2130 P = 0.0671 P = 0.0671 P = 0.0671 P = 0.7046 P = 0.1118 P = 0.7092 P = 0.7226 P = 0.1115 P = 0.1299
TAF-ChIP H3K27ac Convent. ChIP H3K27ac Convent. ChIP H3K27ac TAF-ChIP H3K27ac Low-input ChIP H3K4me1	Suppl. 7b Suppl. 7c Suppl. 7d Suppl. 7f Suppl. 7f	H3X27ac/H3 binding (normalized to veh) in hippocampus of Kcnk 9K0 ^{mat} H3K27ac fold change enrichment (Normalized to lnput) in hippocampus of Kcnk 9K0 ^{mat} H3K27ac fold change enrichment (normalized to veh) in hippocampus H3K27ac/H3 binding (normalized to veh) in LC H3K4me1/H3 binding (normalized to veh) in LC of Kcnk 9K0 ^{mat} H3K4me1 fold change enrichment (Normalized to input) in Kcnk 9K0 ^{mat}	38,73 1.000 2.365 1.000 0,4336 0,2074 0,3834 0,176 0,0796 0,03558 2,237 1,000 0,869 1,000 1,656 1,000 1,656 1,000 1,656 1,000 1,656 1,000 1,014 0,005 0,0143 1,019 0,0046 0,002	± 0 ± 0.2: 0 ± 0.4: 0 ± 0.3: 7 ± 0.1: ± ± ± ± ± ± ± ± ± ± ± ± ±	1,18 726 146 419 0,07741 0,07044 0,1338 0,0652 0,00553 0,268 0,268 0,268 0,248 0,212 0,248 0,212 0,248 0,212	kcnk9 prom kcnk9 intron kcnk9 intron lg3 lg3 lg3 kcnk9 intron kcnk9 intron lg3 kcnk9 intron lg3	CI-994: 5 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 3 DMSO: 4	Student's t- test Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed)	P = 0.0342 P = 0.1172 P = 0.0648 P = 0.2130 P = 0.0671 P = 0.0671 P = 0.0671 P = 0.7046 P = 0.1118 P = 0.7092 P = 0.7092 P = 0.7226 P = 0.1115 P = 0.1299 P = 0.9485
TAF-ChIP H3K27ac Convent. ChIP H3K27ac Convent. ChIP H3K27ac TAF-ChIP H3K27ac Low-input ChIP H3K4me1	Suppl. 7b Suppl. 7c Suppl. 7d Suppl. 7f	H3X27ac/H3 binding (normalized to veh) in hippocampus of Kcnk 9K0 ^{mat} H3K27ac fold change enrichment (Normalized to input) in hippocampus of Kcnk 9K0 ^{mat} H3K27ac fold change enrichment (normalized to veh) in hippocampus H3K27ac/H3 binding (normalized to veh) in LC H3K4me1/H3 binding (normalized to veh) in LC of Kcnk 9K0 ^{mat} H3K4me1 fold change enrichment (Normalized to input) in Kcnk 9K0 ^{mat}	38,73 1.000 2.365 1.000 0,2074 0,3834 0,176 0,0796 0,03558 2,237 1,000 0,869 1,000 1,656 1,000 1,656 1,000 1,656 1,000 1,656 1,000 1,656 1,000 1,219 1,000 0,0144 0,005 0,001843 0,002 0,001843 2,930	± 0 ± 0.2' 0 ± 0.4: 1 ± 0.4: 1 ± 1 ± 1 ± 1 ± 1 ± 1 ± 1 ± 1 ± 1 ± 1 ±	1,18 726 146 419 0,07741 0,07044 0,1338 0,0652 0,01726 0,00545 0,268 0,268 0,248 0,248 0,248 0,248 0,212 0,248 0,212 0,313 0,268 0,212 0,248 0,212 0,248 0,212 0,248 0,212	kcnk9 prom kcnk9 intron kcnk9 intron lg3 lg3 lg3 kcnk9 prom kcnk9 intron lg3 kcnk9 intron lg3 kcnk9 intron kcnk9 intron kcnk9 intron	CL-994: 5 DMSO: 4 CL-994: 3 DMSO: 4 CL-994: 3 DMSO: 4 CL-994: 4 DMSO: 4 CL-994: 4 DMSO: 4 CL-994: 4 DMSO: 4 CL-994: 3 DMSO: 4 CL-994: 3 DMSO: 4 CL-994: 3 DMSO: 4 CL-994: 3 DMSO: 4 CL-994: 4 DMSO: 4 CL-994: 9 CL-994: 4 DMSO: 4 CL-994: 9 CL-994: 9 CL-994: 4 DMSO: 4 CL-994: 9 CL-994: 9 CL-994: 4 DMSO: 4 CL-994: 9 CL-994: 4 DMSO: 4 CL-994: 4 DMSO: 4 CL-994	Student's t- test Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed)	P = 0.0342 P = 0.1172 P = 0.0648 P = 0.2130 P = 0.0671 P = 0.0671 P = 0.0671 P = 0.1118 P = 0.7092 P = 0.7226 P = 0.1115 P = 0.1115 P = 0.1115 P = 0.1115 P = 0.1115 P = 0.1115 P = 0.1115
TAF-ChIP H3K27ac Convent. ChIP H3K27ac Convent. ChIP H3K27ac Low-input ChIP H3K4me1 Convent. ChIP	Suppl. 7b Suppl. 7c Suppl. 7d Suppl. 7f Suppl. 7f Suppl. 7f	H3K27ac/H3 binding (normalized to veh) in hippocampus of Kcnk 9K0 ^{mat} H3K27ac fold change enrichment (Normalized to input) in hippocampus of Kcnk 9K0 ^{mat} H3K27ac fold change enrichment (normalized to veh) in hippocampus H3K27ac/H3 binding (normalized to veh) in LC H3K4me1/H3 binding (normalized to veh) in LC of Kcnk 9K0 ^{mat} H3K4me1 fold change enrichment (Normalized to veh) in kipocampus H3K4me1 fold change enrichment (Normalized to veh)	38,73 1.000 2.365 1.000 0,2074 0,3834 0,176 0,0796 0,03558 2,237 1,000 0,869 1,000 1,656 1,000 1,656 1,000 1,656 1,000 1,656 1,000 1,219 1,0014 0,005 4,005 1,000 0,001843 2,930 1,000 2,217	± 0 ± 0.2: 0 ± 0.4: ± ± ± ± ± ± ± ± ± ± ± ± ±	1,18 726 146 419 0,07741 0,07044 0,1338 0,0652 0,00545 0,268 0,268 0,248	kcnk9 prom kcnk9 intron kcnk9 intron lg3 lg3 lg3 lg3 kcnk9 prom kcnk9 intron lg3 kcnk9 intron lg3 kcnk9 intron kcnk9 intron kcnk9 intron	CI-994: 5 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DM	Student's t- test Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t-	P = 0.0342 P = 0.1172 P = 0.0648 P = 0.2130 P = 0.0671 P = 0.0671 P = 0.0671 P = 0.7046 P = 0.1118 P = 0.7092 P = 0.7226 P = 0.1115 P = 0.1299 P = 0.1115 P = 0.1129
TAF-ChIP H3K27ac Convent. ChIP H3K27ac Convent. ChIP H3K27ac Low-input ChIP H3K4me1 Convent. ChIP H3K4me1	Suppl. 7b Suppl. 7c Suppl. 7d Suppl. 7f Suppl. 7g Suppl. 7f	H3&27ac/H3 binding (normalized to veh) in hippocampus of Kcnk 9KO ^{mat} H3&27ac fold change enrichment (Normalized to input) in hippocampus of Kcnk 9KO ^{mat} H3&27ac/H3 binding (normalized to veh) in hippocampus H3&27ac/H3 binding (normalized to veh) in LC H3&4me1/H3 binding (normalized to veh) in LC H3&4me1/H3 binding (normalized to veh) in LC of Kcnk 9KO ^{mat} H3&4me1 fold change enrichment (Normalized to veh) in hippocampus H3&4me1 fold change enrichment (Normalized to veh) in hippocampus	38,73 1.000 2.365 1.000 0,433 0,2074 0,3834 0,176 0,0796 0,03558 2,237 1,000 0,869 1,000 1,656 1,000 1,188 1 1,219 1,000 1,655 1,000 1,188 1 1,219 1,000 1,656 1,000 1,188 1 1,219 1,000 1,219 1,000 1,188 1 1,219	± ± 0 ± 0.2' 0 ± 0.4' ±	1,18 726 146 419 0,07741 0,07044 0,0338 0,0652 0,01726 0,01726 0,01726 0,0485 0,248 0,248 0,248 0,248 0,248 0,242 0,248 0,0480 0,0560 0,0560 0,0560 0,0560 0,0560 0,0560 0,0560 0,0560 0,0560 0,0560 0,0560 0,0000000000	kcnk9 prom kcnk9 intron kcnk9 intron lg3 lg3 lg3 kcnk9 prom kcnk9 intron lg3 kcnk9 prom kcnk9 intron lg3 kcnk9 prom kcnk9 intron lg3	CI-994: 5 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 3 CI-994: 4 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DM	Student's t- test Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed)	P = 0.0342 P = 0.1172 P = 0.0648 P = 0.2130 P = 0.0671 P = 0.0671 P = 0.0671 P = 0.7046 P = 0.1118 P = 0.7092 P = 0.7092 P = 0.7226 P = 0.1115 P = 0.1129 P = 0.1129 P = 0.1129 P = 0.1129
TAF-ChIP H3K27ac Convent. ChIP H3K27ac Convent. ChIP H3K27ac Low-input ChIP H3K4me1 Convent. ChIP H3K4me1	Suppl. 7b Suppl. 7c Suppl. 7d Suppl. 7f Suppl. 7f Suppl. 7f	H3&27ac/H3 binding (normalized to veh) in hippocampus of Kcnk 9KO ^{mat} H3&27ac fold change enrichment (Normalized to input) in hippocampus of Kcnk 9KO ^{mat} H3&27ac/H3 binding (normalized to veh) in hippocampus H3&27ac/H3 binding (normalized to veh) in LC H3&4me1/H3 binding (normalized to veh) in LC of Kcnk 9KO ^{mat} H3&4me1 fold change enrichment (Normalized to input) <i>in Kcnk</i> 9KO ^{mat} hippocampus H3&4me1 fold change enrichment (Normalized to veh) in hippocampus of Kcnk 9KO ^{mat}	38,73 1.000 2.365 1.000 0,433 0,2074 0,3334 0,176 0,0796 0,03558 2,237 1,000 0,869 1,000 1,656 1,000 1,108 1 1,219 1 0,014 0,014 0,001843 2,930 1,000 0,001843 2,930 1,003 0,01843 2,930 1,003 0,01843 1,001 0,014 0,014 0,014 0,014 0,014 0,014 0,014 0,014 0,014 0,014 0,014 0,014 0,014 0,014 0,014 0,000 0,014 0,000 0,014 0,014 0,014 0,000 0,000 0,000 1,000 0,000 0,014 0,014 0,000 0,	± 0 ± 0.2' 0 ± 0.4' ±	1,18 726 146 419 0,07741 0,07044 0,0338 0,0652 0,01726 0,01726 0,01726 0,0248 0,046 0,005 0,00000000	kcnk9 prom kcnk9 intron kcnk9 intron lg3 lg3 lg3 lg3 kcnk9 prom kcnk9 intron lg3 kcnk9 prom kcnk9 intron lg3 kcnk9 prom kcnk9 intron lg3	CI-994: 5 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DM	Student's t- test Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed)	P = 0.0342 P = 0.1172 P = 0.0648 P = 0.2130 P = 0.0671 P = 0.0671 P = 0.0671 P = 0.7046 P = 0.1118 P = 0.7092 P = 0.7226 P = 0.1115 P = 0.1129 P = 0.1129 P = 0.1129 P = 0.1299 P = 0.1299 P = 0.1299 P = 0.1299 P = 0.1299 P = 0.1299 P = 0.485
TAF-ChIP H3K27ac Convent. ChIP H3K27ac Convent. ChIP H3K27ac Low-input ChIP H3K4me1 Convent. ChIP H3K4me1	Suppl. 7b Suppl. 7c Suppl. 7d Suppl. 7f Suppl. 7f Suppl. 7f	H3K27ac/H3 binding (normalized to veh) in hippocampus of Kcnk 9KO ^{mat} H3K27ac fold change enrichment (Normalized to input) in hippocampus of Kcnk 9KO ^{mat} H3K27ac/H3 binding (normalized to veh) in hippocampus H3K4me1/H3 binding (normalized to veh) in LC H3K4me1/H3 binding (normalized to veh) in L C of Kcnk 9KO ^{mat} H3K4me1 fold change enrichment (Normalized to input) <i>in Kcnk</i> 9KO ^{mat} hippocampus H3K4me1 fold change enrichment (Normalized to veh) in hippocampus H3K4me1 fold change enrichment (Normalized to veh) in hippocampus H3K4me1 fold change enrichment (Normalized to veh) in hippocampus of Kcnk 9KO ^{mat}	38,73 1.000 2.365 1.000 0,433 0,274 0,3334 0,176 0,0796 0,03558 2,237 1,000 0,869 1,000 1,000 1,000 1,656 1,000 1,188 1 1,219 1 0,014 0,014 3,2930 1,000 2,217 1 1,035 0,01843 2,930 1,003 1,00446 1,000 1,005 0,019 0,00466 0,001843 2,930 1,005 0,01403 2,930 1,005 0,01403 2,035 1,000 1,005 1,000 1,0	± ± 0 ± 0.2 0 ± 0.4 ± <	1,18 726 146 419 0,07741 0,07044 0,0338 0,0652 0,01726 0,01726 0,035 0,0268 0,248 0,248 0,212 0,248 0,212 0,248 0,212 0,248 0,212 0,248 0,212 0,313 0,268 0,212 0,212 0,313 0,268 0,212 0,005 0,212 0,005 0,212 0,005 0,000 0,005 0,00000000	kcnk9 prom kcnk9 intron kcnk9 intron kcnk9 intron lg3 lg3 lg3 kcnk9 prom kcnk9 intron lg3 kcnk9 prom kcnk9 intron lg3 kcnk9 prom kcnk9 intron lg3 kcnk9 prom kcnk9 intron lg3 kcnk9 prom	CI-994: 5 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DM	Student's t- test Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t-	P = 0.0342 P = 0.1172 P = 0.0648 P = 0.2130 P = 0.0671 P = 0.0671 P = 0.0671 P = 0.7046 P = 0.1118 P = 0.7092 P = 0.7092 P = 0.7226 P = 0.1115 P = 0.1129 P = 0.1129 P = 0.1129 P = 0.1129 P = 0.1129 P = 0.1129 P = 0.1299 P = 0.485 P = 0.2312
TAF-ChIP H3K27ac Convent. ChIP H3K27ac Convent. ChIP H3K27ac Low-input ChIP H3K47ac Convent. ChIP H3K4me1 Convent. ChIP	Suppl. 7b Suppl. 7c Suppl. 7d Suppl. 7f Suppl. 7f Suppl. 7f	H3K27ac/H3 binding (normalized to veh) in hippocampus of Kcnk 9K0 ^{mat} H3K27ac fold change enrichment (Normalized to input) in hippocampus of Kcnk 9K0 ^{mat} H3K27ac/H3 binding (normalized to veh) in hippocampus H3K4me1/H3 binding (normalized to veh) in LC H3K4me1/H3 binding (normalized to veh) in LC of Kcnk 9K0 ^{mat} H3K4me1 fold change enrichment (Normalized to input) <i>in Kcnk</i> 9K0 ^{mat} H3K4me1 fold change enrichment (Normalized to veh) in hippocampus H3K4me1 fold change enrichment (Normalized to veh) in hippocampus H3K4me1 fold change enrichment (Normalized to veh) in hippocampus of Kcnk 9K0 ^{mat}	38,73 1.000 2.365 1.000 0,433 0,274 0,3334 0,176 0,0796 0,03558 2,237 1,000 0,869 1,000 1,000 1,000 1,656 1,000 1,188 1 1,219 1 0,014 0,014 3,2930 1,000 2,217 1,035 0,01843 2,930 1,003 0,01843 2,930 1,003 0,01843 2,930 1,003 0,01843 2,930 1,003 0,01843 2,930 1,003 1,003 0,01843 1,005 0,001843 2,035 1,000 0,001843 2,035 1,000 1,005 0,001843 1,000 1,005 0,001843 1,000 1,005 0,001843 1,000 0,001843 1,000 0,001843 1,000 0,001843 1,000 1,003 0,001843 1,000 0,001843 1,000 0,001843 0,000 1,003 0,001843 0,000 1,003 0,001843 0,000 0,001843 0,000 0,001843 0,000 0,00	± ± 0 ± 0.2: ±<	1,18 726 146 419 0,07741 0,07044 0,0338 0,0652 0,01726 0,003545 0,248 0,248 0,248 0,212 0,248 0,212 0,248 0,212 0,248 0,212 0,248 0,212 0,313 0,162 0,313 0,162 0,313 0,162 0,313 0,268 0,212 0,000 0,005 0,000 0,005 0,000 0,005 0,000 0,005 0,000 0,005 0,000000	kcnk9 prom kcnk9 intron kcnk9 intron kcnk9 intron lg3 lg3 kcnk9 intron kcnk9 intron lg3 kcnk9 prom kcnk9 intron lg3 kcnk9 prom kcnk9 intron lg3 kcnk9 prom kcnk9 intron	CI-994: 5 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 3 DMSO: 4 CI-994: 4 DMSO: 4 CI-994: 4 DM	Student's t- test Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed) Student's t- test (Two- tailed)	P = 0.0342 P = 0.1172 P = 0.0648 P = 0.2130 P = 0.0671 P = 0.0671 P = 0.0671 P = 0.7046 P = 0.1118 P = 0.7092 P = 0.7092 P = 0.7226 P = 0.1115 P = 0.1129 P = 0.115 P = 0.129 P = 0.129 P = 0.2312 P = 0.231

			0,006498	±	0,002042	-	DMSO: 4		
		H3K27ac fold change	1,606 1,000	± ±	0,351 0,290	kcnk9 prom	CI-994: 4 DMSO: 4	Student's t- test (Two-	P =0,2312
Convent. ChIP H3K27ac	Suppl. 7j	(Normalized to veh)	1,094 1	± ±	0,210 0,2851	kcnk9 intron	CI-994: 4 DMSO: 4		P =0.7998
		WT	1,331 1	± ±	0,325 0,3143	lg3	CI-994: 4 DMSO: 4	talled)	P = 0.7092

Abbreviations: n, number of samples/mice; n.s., not significant

Supplementary Table 2: Primers used for PCR and pyrosequencing analyses

Primer			Sequence (5' – 3')
TASK3-P3	F	Genotyping	TGCGAGCTTCAGAGAGGATG
TASK3-P4	R	Genotyping	ATGCTCTAATCTCCAGTCTG
Kcnk9 Exon2	F	Genotyping	CACCACGCCATGTACTTCCT
Kcnk9 Exon2	R	Genotyping	GGACCGGAAGTAGGTGTTCC
Kcnk9-SNP	F	Allele-specific RT qPCR	CACAACTATCGGATATGGACATGC
Kcnk9-SNP	R	Allele-specific RT qPCR	TGCCGCGGTGTTCGAT
Kcnk477	F	QUASEP	GCCTGTACCTTCACCTAC
Kcnk477	R	QUASEP	CACAACTATCGGATATGGACATGC
Kcnk477_S	Seq	QUASEP	TGCCGCGGTGTTC
kcnk9-283/284	F	RT-qPCR	ACTATCGGATATGGACATGCTGC
kcnk9-283/284	R	RT-qPCR	GCCCAGGCTCTGGAACATAA
Bant	F	RI-qPCR	ATCCACTGAGCAAAGCCGAA
	R C		
Impa2	Г D		
Impaz Konkû promotor			
Konk9 promoter	P		
Kenk9 intron	F		
Kenk9 intron	R	ChIP-gPCR	
	_	Methylation	
mPeg13-CpG 1-9	F	analysis	TTGGATGAGTTATTATATAAGGTTTAAAA
mPeg13-CpG 1-9	R	Methylation analysis	ACAACTACCTACATTCCAAATCT
mPeg13-CpG_1-9	Seq	Methylation analysis	AAATTTTAATAAGATGGGTTAAT
mPeg13-CpG 17-22	F	Methylation analysis	AGATTTGGAATGTAGGTAGTTGTGA
mPeg13-CpG 17-22	R	Methylation analysis	ССТСААТААААССАТТСТААТСААСТАТ
mPeg13-CpG 17-22	Seq	Methylation analysis	GGTAATTTGTTAGGTGGAGATATA
Ago2_F	F	Cluster gene analysis	CGACAACATCACCCATCCCA
Ago2_R	R	Cluster gene analysis	TTTGATTGTTCTCCCGGTGGT
Chrac1_F	F	Cluster gene analysis	AAGAGCTCTCCCGAGGTGTC
Chrac1-R	R	Cluster gene analysis	TACTGAACAAAGAGCTCCGTGGC
Peg13_F	F	Cluster gene analysis	AAGATCCGCGGCCTTTACTC
Peg13_R	R	Cluster gene analysis	TTTTGCCCATTCCTCGGTCA
Trappc9_F	F	Cluster gene analysis	TGGGGCTGAAAAGACACTACAA
Trappc9_R	R	Cluster gene analysis	TGGTAGTGTACCAGGGCGT
Kcnk9-SNP_EP-C_F	F	AS-RT-qPCR	TGCCGCGGTGTTCGAC
Kcnk9-SNP_EP_R	R	AS-RT-qPCR	GCATGTCCATATCCGATAGTTGTG
Kcnk9-SNP_EP-T_F	F	AS-RT-qPCR	TGCCGCGGTGTTCGAT
KCNK9-AS-ChIP-F	F	AS-CHIP	AAATTCGCCGGTTCCTTCTAC
KCNK9-AS-ChIP-R	R	AS-CHIP	gagatgtagcgcacacgaagc
KCNK9-AS-ChIP-S	Seq	AS-CHIP	aaggaatgggtgtgc

Abbreviations: F, forward primer; R, reverse primer; Seq, pyrosequencing primer

Supplementary References

1. Paxinos, G. & Franklin, K. B. J. The Mouse Brain in Stereotaxic Coordinates (Academic Press, 2008).