Table S1 Primer pairs for qPCR on cDNA from primary hippocampal neurons and mouse brain.

Primer sequences and amplicon sizes are based on mouse sequences (accession numbers: NM_008084.2 (*gapdh*), NM_010408.3 (*hcn1*), NM_008226.2 (*hcn2*)). Amplicon sizes of *gapdh* fragments are indicated for cDNA (150bp) and genomic DNA (284bp).

protein	gene	primer	sequence (5‘ →3‘)	T_m	amplicon size
GAPDH	*gapdh*	forward	GGTATCGTGGAAGGACTCATG	62°C	150bp/284bp
		reverse	GCTGCCAAGGCTGTGGGC		
HCN1	*hcn1*	forward	ACTGTGGGCGAATCCCTGG	62°C	184bp
		reverse	CCACCAGCAGCTGTGCAGA		
HCN2	*hcn2*	forward	GGAGAATGCCATCATCCAGG	62°C	149bp
		reverse	CAGCAGGCTGTGGCCATGA		

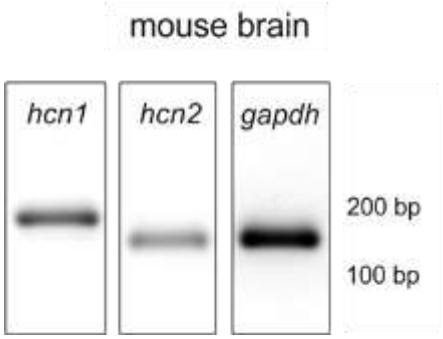

Fig. S1 Semi-quantitative PCR analysis.

Semi-quantitative PCR analysis of *hcn1*, *hcn2* and *gapdh* gene expression on mouse brain cDNA. Sizes of marker bands are indicated on the right. Primer pairs were tested for specificity and efficiency. Marker bands and their respective sizes are indicated on the right.

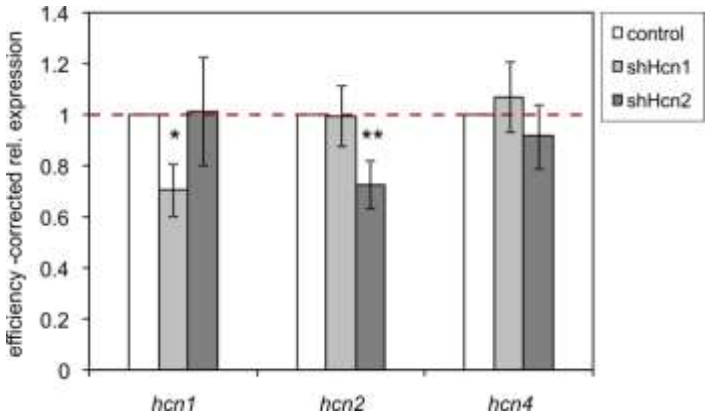

Fig. S2 Quantification of gene expression by real-time PCR.

Knockdown analyses for *hcn1*, *hcn2*, and *hcn4* in primary hippocampal neurons after 14 days in vitro are shown as the efficiency-corrected expression of *hcn* genes in relation to *gapdh*. Specificity and efficiency of knockdown was analyzed for *hcn1* (n=4) and *hcn2* (n=6) as well as *hcn4* (n=3) as an independent control gene and mean values are depicted for each target gene. Samples were treated for 12 d with rAAV9_CaMK2-eGFP_hU6-shHcn1, rAAV9_CaMK2-eGFP_hU6-shHcn1 or treated with vehicle as a control. Relative transcript expression of target genes was normalized to the vehicle-treated control. Error bars indicate s.e.m. and the level of significance is indicated (Student's *t* test: * $p< 0.03$; ** $p< 0.02$).