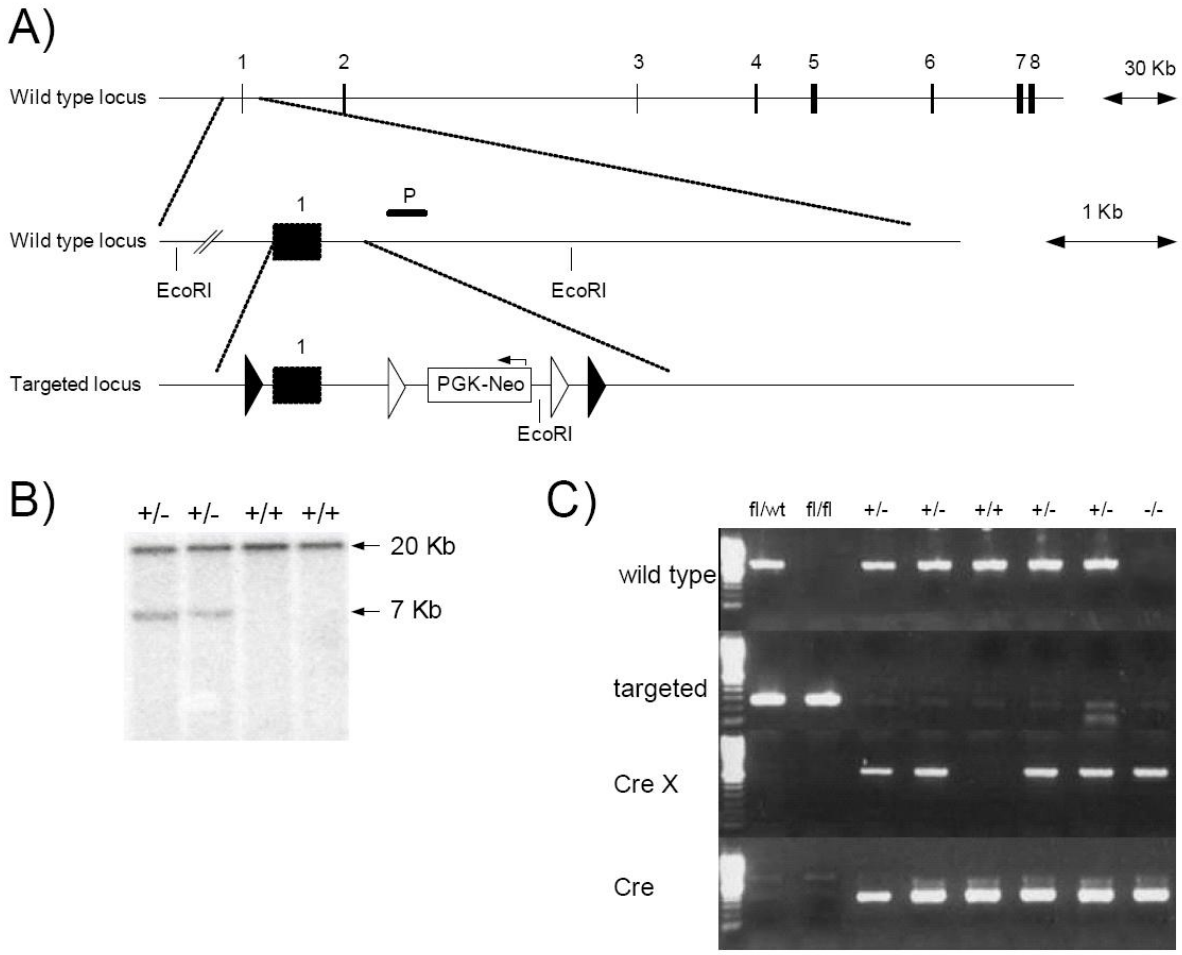

Figure S1. Disruption of the HCN1 gene. **(A)** Map of HCN1 genomic region. Rectangles represent the coding areas of the HCN1 locus. Closed arrows represent loxP sites, open arrows FRT sites. P marks the location of the 3' external probe. **(B)** Southern blot **(C)** Genomic DNA PCR. Four PCR reactions are needed to determine the genotype of HCN1 mice: a *wild-type* PCR to amplify the wild-type allele, *targeted* for the flox allele, *Cre X* to detect the Cre recombined knockout allele and *Cre* to determine if the Cre transgene is present.

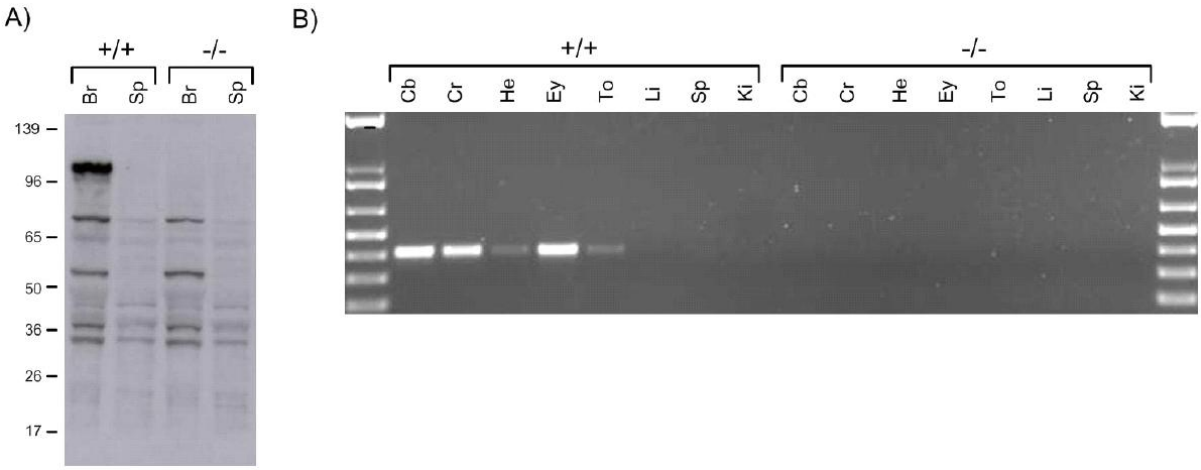

Figure S2. Expression of the HCN1 gene in $HCN1^{+/+}$ and $HCN1^{-/-}$ mice. **(A)** Western blot analysis of tissues from $HCN1^{+/+}$ and $HCN1^{-/-}$ mice. Br, brain; Sp, spleen. **(B)** RT-PCR analysis of tissues from $HCN1^{+/+}$ and $HCN1^{-/-}$ mice. Cb, cerebellum; Cr, cerebrum; He, heart; Ey, eye; To, tongue; Li, liver; Sp, spleen; Ki, kidney.