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***In vivo* inhibition of the mitochondrial H<sup>+</sup>-ATP synthase in neurons promotes  
metabolic preconditioning**

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**Abstract.**

A key transducer in energy conservation and signaling cell death is the mitochondrial H<sup>+</sup>-ATP synthase. The expression of the ATPase Inhibitory Factor 1 (IF1) is a strategy used by cancer cells to inhibit the activity of the H<sup>+</sup>-ATP synthase to generate a ROS signal that switches on cellular programs of survival. We have generated a mouse model expressing a mutant of human IF1 in brain neurons to assess the role of the H<sup>+</sup>-ATP synthase in cell death *in vivo*. The expression of hIF1 inhibits the activity of oxidative phosphorylation and mediates the shift of neurons to an enhanced aerobic glycolysis. Metabolic reprogramming induces brain preconditioning affording protection against quinolinic acid-induced excitotoxicity. Mechanistically, preconditioning involves the activation of the Akt/p70S6K and PARP repair pathways and Bcl-xL protection from cell death. Overall, our findings provide the first *in vivo* evidence highlighting the H<sup>+</sup>-ATP synthase as a target to prevent neuronal cell death.

**Keywords:** Brain preconditioning / Energy metabolism / H<sup>+</sup>-ATP-synthase / Inhibitory Factor 1 (IF1) / Mitochondria.

## **Introduction.**

The H<sup>+</sup>-ATP synthase of the inner mitochondrial membrane is a master regulator of energy metabolism and cell fate. In oxidative phosphorylation (OXPHOS) the H<sup>+</sup>-ATP synthase utilizes the H<sup>+</sup> electrochemical gradient generated by the respiratory chain to synthesize most of the ATP that is required to sustain cellular activities of the differentiated aerobic cell. Many findings corroborate the molecular and functional integration of OXPHOS (Dey & Moraes, 2000; Tomiyama et al., 2006), and specifically of the H<sup>+</sup>-ATP synthase (Alavian et al., 2011; Chen et al., 2011; Matsuyama et al., 1998; Santamaria et al., 2006; Shchepina et al., 2002) with cell death. In fact, apoptosis has been shown to be strictly dependent upon subunits of the H<sup>+</sup>-ATP synthase in yeast, mammals and plants (Chivasa et al., 2011; Gross et al., 2000; Matsuyama et al., 1998). The point of no return in cell death is the permeabilization of the inner mitochondrial membrane to low molecular weight solutes, through opening of the so-called permeability transition pore (PTP) (Di Lisa et al., ; Galluzzi et al., 2009). Although the molecular composition of the PTP remains unknown recent findings support that the high-conductance channel is composed by dimers of the H<sup>+</sup>-ATP synthase (Giorgio et al., 2013), consistent with the finding that subunit c of the F<sub>0</sub>-channel of the H<sup>+</sup>-ATP synthase is required for the activity of the PTP (Bonora et al., 2013). Cyclophilin D that regulates the activity of the PTP also interacts and regulates the activity of the H<sup>+</sup>-ATP synthase (Giorgio et al., 2009).

Down-regulation of the H<sup>+</sup>-ATP synthase is functionally linked to resistance to chemotherapy in cancer cells (Hernlund et al., 2009; Li et al., 2010; Sanchez-Arago et al., 2013a; Shin et al., 2005) consistent with the emerging role of the mitochondrial synthase in the execution of cell death. More recently, cancer cells have been shown to escape from death by inhibiting the activity of the H<sup>+</sup>-ATP synthase by the

overexpression of the ATPase Inhibitory Factor 1 (IF1) (Faccenda et al., 2013; Formentini et al., 2012; Sanchez-Arago et al., 2013b), that mimics the inhibitory effect of oligomycin (OL) in apoptosis (Matsuyama et al., 1998; Santamaria et al., 2006; Shchepina et al., 2002). IF1 is the physiological inhibitor of the mitochondrial H<sup>+</sup>-ATP synthase (Gledhill et al., 2007). Mechanistically, cell survival results from rewiring of energy metabolism and nuclear reprogramming due to a reactive oxygen species (ROS) signal that is produced in mitochondria after the IF1-mediated inhibition of the H<sup>+</sup>-ATP synthase (Formentini et al., 2012; Sanchez-Arago et al., 2013b).

We present a mouse model expressing a mutant of human IF1 (hIF1) in neurons under the control of a doxycyclin-regulated promoter. The purpose of this model was to inhibit by the most effective way the activity of the H<sup>+</sup>-ATP synthase *in vivo*. Studies in total brain, isolated mitochondria and primary neuronal cultures demonstrate that overexpression of hIF1 partially inhibits oxidative phosphorylation triggering an adaptive metabolic response that results in increased aerobic glycolysis. The IF1-mediated metabolic reprogramming results in brain preconditioning and involves a mild oxidative stress that protects neurons from excitotoxic damage, enhancing motor behavior. Overall, our findings provide the first demonstration that links the inhibition of the H<sup>+</sup>-ATP synthase with protection from neuronal damage *in vivo*, highlighting the pivotal role that the engine of OXPHOS has as a cell death regulator.

## Results.

**A mouse model to inhibit the neuronal H<sup>+</sup>-ATP synthase *in vivo*.** To assess the role of OXPHOS in neurons we generated a transgenic mouse (H<sup>+</sup>) that integrates in its genome the mutant H49K of the human ATPase Inhibitory Factor 1 (hIF1) under a tetracycline regulated promoter (TRE-H49K) (Figure 1A). The H49K mutant has a higher binding affinity for the  $\beta$ -catalytic subunit of the H<sup>+</sup>-ATP synthase (Cabezon et al., 2000). Double-transgenic Tet Off mice (H<sup>+</sup>/T<sup>+</sup>) were generated by breeding H<sup>+</sup> animals with CamKII-tTA mice (T<sup>+</sup>) that express the tTA transgene (Figure 1A) in neurons. Western blots (Figure 1A) and immunohistochemistry of coronal brain slices (Figures 1B, S1 and S2) revealed that only the H<sup>+</sup>/T<sup>+</sup> genotype expresses hIF1 in mitochondria of neurons, resulting in ~3-fold increase in the total cellular content of IF1 (Figure 1A). The expression of hIF1 did not affect the expression of other mitochondrial proteins (Figures 1C and S3). However, the concentration of ATP was significantly diminished in the brain of H<sup>+</sup>/T<sup>+</sup> mice when compared to controls (Figure 1D). These changes were accompanied by an increased concentration of AMP (Figure 1D) and the concurrent phosphorylation of the metabolic sensor AMPK (Figure 1E) in the brain of H<sup>+</sup>/T<sup>+</sup> mice. Interestingly, a significant increase in the expression of the glycolytic enzymes GAPDH and LDH-A (Figure 1E) was observed in brain extracts of H<sup>+</sup>/T<sup>+</sup> mice. Despite these differences, H<sup>+</sup>/T<sup>+</sup> mice were born in the expected Mendelian ratios and were normal in appearance, home-cage behavior, reproduction and longevity up to one year follow up.

**hIF1 inhibits the H<sup>+</sup>-ATP synthase.** The hydrolytic activity of the H<sup>+</sup>-ATP synthase was significantly reduced in isolated brain mitochondria from H<sup>+</sup>/T<sup>+</sup> mice when compared to controls (Figure 1F). Consistently, TMRM<sup>+</sup> staining after the administration of antimycin A revealed a minor capacity of mitochondria from H<sup>+</sup>/T<sup>+</sup>

mice to sustain the membrane potential ( $\Delta\Psi_m$ ) (Figure 1G). Likewise, oxygen consumption rates revealed that both State 3 (ADP-stimulated), uncoupled (FCCP-induced) and OL sensitive respiration were significantly diminished when compared to controls (Figure 2A). The latter is consistent with the inhibition of the synthase activity of the ATP synthase by the expression of hIF1. No relevant differences were observed in  $\Delta\Psi_m$  in  $H^+/T^+$  mice when compared to controls (Figures 1G and 2B). However, the addition of ADP triggered a larger  $\Delta\Psi_m$  depolarization in mitochondria of wild type *versus*  $H^+/T^+$  mice (Figure 2B), also consistent with the partial inhibition of the synthase activity of the  $H^+$ -ATP synthase by hIF1. A mild increase in the carbonylation of specific proteins (Figure 2C) and in the basal levels of catalase, SOD1 and SOD2 (Figure 2D) was observed in the brain of  $H^+/T^+$  mice when compared to controls. However, no significant differences in GSH and GSH/GSSG ratio were observed (Figure 2E), showing that the oxidative stress induced by hIF1 expression is of mild intensity.

**hIF1 inhibits cytochrome *c* oxidase activity.** No relevant differences were noted in the content of native Complexes I, II, III and V in mitochondria between  $H^+/T^+$  mice and controls (Figure 2F). Interestingly, mitochondria of  $H^+/T^+$  mice showed no formation of supercomplex containing Complex IV (Figure 2F). In fact, most of Complex IV migrated as monomer (Figure 2F). Consistent with the role of supercomplexes in the rate of respiration (Acin-Perez et al., 2008; Lapuente-Brun et al., 2013), the enzymatic activity of Complex IV was significantly diminished in mitochondria of  $H^+/T^+$  mice (Figure 2G). No differences were noted in the activities of Complex I and Complex II+III between both phenotypes (Figure 2G).

**hIF1 promotes metabolic reprogramming and ROS signaling in cortical neurons.** Only primary cultures of cortical neurons (Figure S4) derived from  $H^+/T^+$

embryos expressed hIF1 (Figure 3A-C). Expression of hIF1 resulted in a significant decrease in the cellular content of ATP (Figure 3D) and in the activity of the H<sup>+</sup>-ATP synthase (Figure 3E). This effect was not observed in 4d cultures (Figure 3E), when neurons are not yet expressing hIF1 (Figure 3B). The expression of hIF1 resulted in a significant increase in aerobic glycolysis as assessed by the rate of lactate production (Figure 3F). OL induced aerobic glycolysis only in neurons derived from control animals (Figure 3F), supporting that hIF1 is stimulating aerobic glycolysis to its maximum rate (Figure 3F). Analysis of the expression of PK-M2, LDH-A and GAPDH confirmed the induction of glycolysis in H<sup>+</sup>/T<sup>+</sup> neurons when compared to wild type cultures (Figure 3G). Basal fluorescence did not show significant differences between H<sup>+</sup>/T<sup>+</sup> and controls (Figures 3H, S5 and S6), suggesting that there is no major difference in  $\Delta\Psi_m$ . Consistent with the inhibition of both the synthase and hydrolase activity of the H<sup>+</sup>-ATP synthase by hIF1, we observed that  $\Delta\Psi_m$  changes in response to OL were lower (Figure S5) whereas those to antimycin A were higher (Figure S6) in H<sup>+</sup>/T<sup>+</sup> cultures than in control. The production of superoxide radical was enhanced in H<sup>+</sup>/T<sup>+</sup> neurons when compared to wild type (Figure 3I). An increase in the carbonylation of specific neuronal proteins was observed (Figure 3J) consistent with a higher basal production of ROS in H<sup>+</sup>/T<sup>+</sup> neurons and with data in brain homogenates (Figure 2C).

**hIF1-mice are protected from quinolinic acid-induced brain damage.** To assess the role of H<sup>+</sup>-ATP synthase in cell death *in vivo*, one year old control and hIF1 expressing mice received an injection of quinolinic acid into the left striatal region of the brain (Martinez-Serrano & Bjorklund, 1996; Schwarcz et al., 2012). Weight loss after injury (Figure 4A), spleen volume contraction (Figure 4B), and enlargement of the ipsilateral ventricle (Figure 4C), which are respective indexes of general impairment of animal health, monocyte recruitment and tissue loss suggest that hIF1 expressing mice



are partially protected from excitotoxicity. Hematoxylin-eosin stained brain sections also revealed a significant ~50% reduction in the lesion area in  $H^+/T^+$  mice (Figure 4D). The reduced expression of the neuronal markers DARPP-32 (Figure 4E) and NeuN (Figure S7) in the brain of controls further support a higher neuronal protection in  $H^+/T^+$  mice. Quantification of microglia (Figure 4E, Iba-1, red staining and Figure S8) and phagocytes (Figure 4E, Ed-1, green staining and Figure S8) revealed a significant increase in gliosis in control when compared to  $H^+/T^+$  mice suggesting that hIF1 protects neurons from damage and hence from the subsequent local inflammation.

**Neurological evaluation indicates a better performance in hIF1 mice.** No differences in locomotor performance were observed between control and  $H^+/T^+$  mice before quinolinic acid administration (Figure S9A-F). However, three locomotor tests showed that  $H^+/T^+$  mice are partially protected from quinolinic acid-induced damage and maintained lower deviation from pre-surgical values than control animals (Figure S9 and Supplementary videos for control and hIF1 expressing mice). Paw usage contralateral to the brain lesion (right) was significantly diminished in control animals when compared to  $H^+/T^+$  mice (Figure S9A). No differences were noted in the use of the ipsilateral forelimb (left) (Figure S9B). Gate analysis revealed that control mice showed an increased stride length of the contralateral forelimb (Figure S9C) and in the coefficient of variation for base width of the hind limbs (Figure S9D) when compared to  $H^+/T^+$  mice in the “footprint” test (Carter et al., 1999). After lesion all animals showed an increase in the number of paw-slips in the grid test (Brooks & Dunnett, 2009) but as early as 4 days post-surgery  $H^+/T^+$  mice were able to walk through the grid with a significant lower number of paw slips (Figure S9E). The motility index of  $H^+/T^+$  mice was unaltered by lesion (Figure S9F). However, control mice were less prone to explore than  $H^+/T^+$  mice suggesting a severe motor impairment (Figure S9F) (Supplemental

videos for control and hIF1 expressing mice). Overall, H<sup>+</sup>/T<sup>+</sup> mice showed lower deviation from pre-surgical values than control animals.

**hIF1 protects from quinolinic acid-induced cell death.** FluoroJade B positive neurons both in the core and penumbra region of the lesion were significantly augmented in control when compared to H<sup>+</sup>/T<sup>+</sup> mice (Figure 5A). Analysis of apoptotic cell death by the determination of caspase 3 activation confirmed that hIF1 expressing neurons were protected from apoptosis in the penumbra (Figure 5B). Most of the toxic cascades stimulated by quinolinic acid implicate the formation of ROS (Schwarcz et al., 2012). Consistently, the GSH content in the damaged hemisphere was highly reduced when compared to the non-stressed tissue (compare Figure 5C versus Figure 2D). Remarkably, both the GSH content and the GSH/GSSG ratio were significantly higher in the affected hemisphere of hIF1 expressing mice than in controls (Figure 5C).

**hIF1 signals the activation of neuroprotection pathways.** Phosphorylation of Akt is part of the survival signaling pathway induced in cells confronted with mitochondrial respiration defects and/or mild oxidative stress (Leslie, 2006; Pelicano et al., 2006). Consistently, the phosphorylation of Akt was significantly augmented in both brain hemispheres of mice expressing hIF1 (Figure 5D). We also observed an enhanced phosphorylation of the pro-survival p70S6K in both brain hemispheres (Figure 5D) and enhanced expression of *c-fos* in the damaged area of H<sup>+</sup>/T<sup>+</sup> mice (Figure 5E). Moreover, the content of IκBα, which is the negative regulator of NFκB transcription factor, was significantly diminished in the damaged hemisphere of H<sup>+</sup>/T<sup>+</sup> mice (Figure 5D). Changes in IκBα expression were paralleled by opposite changes in the expression of Bcl-xL, a downstream target of NFκB that is involved in preventing cell death (Figure 5D). In contrast, the expression of the antiapoptotic Bcl-2 was not affected by hIF1 expression or by quinolinic acid administration (Figure 5D). Remarkably, the ATP and

ADP content in the damaged area of the left hemisphere was much lower in  $H^+/T^+$  mice (Figure 6A). In contrast, the AMP content was significantly increased (Figure 6A). The larger drop in ATP content of  $H^+/T^+$  mice can be explained by the enforced hIF1-mediated inhibition of the synthase activity of the  $H^+$ -ATP synthase, but could also result from higher activation of ATP consuming reactions following activation of repair mechanisms. This is consistent with a higher basal PARP activity in the brain of  $H^+/T^+$  mice (Figure 6B), a difference that was magnified after hemispheric damage (Figure 6B).

**ROS are involved in cell death.** Consistent with the role of ROS in mediating neuronal excitotoxicity (Schwarcz et al., 2012) we observed that quenching ROS after glutamate induced cell-death significantly arrested cell death in primary neuronal cultures of control mice (Figure 6C). The cell death response to glutamate was much less in neurons of hIF1 expressing mice (Figure 6C). In fact, cell death was essentially the same as that of control neurons treated with the antioxidant mito Q (Figure 6C), presumably because the hIF1-mediated activation of the pro-survival signaling pathways (Figures 5D and 6B) confers a more resistant phenotype against ROS mediated cell-death.

**Bcl-xL participates in hIF1-mediated protection of neuronal death.** Blue-native gels confirmed the interaction of Bcl-xL with the  $H^+$ -ATP synthase (Figure 6D) in agreement with recent findings (Alavian et al., 2011; Chen et al., 2011). However, and to our surprise, we found that Bcl-xL preferentially interacts with a native protein complex that migrates with Complex I of the respiratory chain (Figure 6D). Remarkably, silencing of Bcl-xL in neurons restored the glutamate or hypoxia-driven cell death in pre-conditioned neurons of  $H^+/T^+$  mice (Figure 6E), further supporting the

role of the anti-apoptotic Bcl-xL in neuroprotection and eventually its cross-talk with the activity of the H<sup>+</sup>-ATP synthase.

## Discussion

Herein, we demonstrate that the expression of hIF1 partially inhibits the H<sup>+</sup>-ATP synthase activity promoting rewiring of neuronal metabolism to an enhanced aerobic glycolysis. Inhibition of the H<sup>+</sup>-ATP synthase activates pathways to prevent apoptotic cell death. In other words, expression of hIF1 induces a state of preconditioning that prevents neuronal death after excitotoxic damage as assessed both *in vivo* and in primary cultures. These findings provide the first *in vivo* account highlighting the relevance of rewiring energy metabolism in brain preconditioning, and stress the potential value of the H<sup>+</sup>-ATP synthase as a target for therapeutic intervention. Moreover, the transgenic H<sup>+</sup> mouse developed offers a valuable tool to investigate the relevance of OXPHOS impairments in mammalian tissues *in vivo*. Until recently, IF1 was considered an inhibitor of the hydrolase activity of the ATP synthase that helps to preserve cellular ATP during hypoxia or ischemia (Faccenda et al., 2013; Gledhill et al., 2007). However, previous *in vitro* studies (Husain & Harris, 1983; Lippe et al., 1988) and more recent findings *in vivo* (Formentini et al., 2012; Sanchez-Arago et al., 2013b; Sanchez-Cenizo et al., 2010; Shen et al., 2009) have stressed the role of IF1 as an inhibitor of the synthase activity of the H<sup>+</sup>-ATP synthase. The results in this study demonstrate the *in vivo* function of hIF1 as an inhibitor of the ATP synthase and of cell death.

Since we also observed a down-regulation of respiration and of the activity and assembly of Complex IV, it can be argued that hIF1 exerts neuroprotection by its effect on the activity of the respiratory chain rather than on the ATP synthase. However, this explanation seems unlikely because the impairment of the respiratory chain is detrimental for cell survival. In fact, very recent findings (Cogliati et al., 2013) have highlighted that the disassembly of respiratory chain supercomplexes leads to an

increase and not to a decrease in cell death, in agreement with our observation. Hence, we suggest that the effects of hIF1 on respiration result from feedback regulation of Complex IV activity/assembly by the inhibition of the ATP synthase, although the mechanism involved deserves further investigation. However, we cannot rule out that hIF1 might be controlling the execution of cell death by regulating *cristae* remodeling (Cogliati et al., 2013; Faccenda et al., 2013) (Figure 7G). It is well established that dimers of the H<sup>+</sup>-ATP synthase promote the high local curvature of the inner membrane at *cristae* ridges (Davies et al., 2012; Davies et al., 2011; Paumard et al., 2002). Recently, the genetic disruption of *cristae* shape morphology has been shown to favor apoptosis (Cogliati et al., 2013), providing a link between mitochondrial morphology and cell death. In this regard, it has been suggested that IF1 regulates the oligomeric state of the H<sup>+</sup>-ATP synthase increasing the density of *cristae* and the formation of dimeric ATP synthase complexes (Bisetto et al., 2013; Campanella et al., 2008; Garcia et al., 2006; Minauro-Sanmiguel et al., 2005). Although this suggestion has been questioned (Fujikawa et al., 2012; Tomasetig et al., 2002; Wittig & Schagger, 2009), it is possible that the over-expression of hIF1 might contribute to stabilize *cristae* structure hence upgrading, at the structural level, the threshold for cell death (Figure 7G).

Energy metabolism in neurons is highly dependent on OXPHOS. Unexpectedly, H<sup>+</sup>/T<sup>+</sup> mice revealed no symptoms of neurological dysfunction. It is likely that the energy deficit triggered by a limited OXPHOS promotes the activation of the metabolic stress sensor AMPK (Mihaylova & Shaw, 2011) and the subsequent activation of aerobic glycolysis to partially compensate ATP provision in these neurons. It is really intriguing to find that tissues that have a very high energy demand such as heart, liver and kidney are those that express higher levels of IF1 (Sanchez-Arago et al., 2013b;

Sanchez-Cenizo et al., 2010). Mouse (Figure 7A) and human neurons of the brain and cerebellum (Figure 7B-F and Figure S10) are not an exception showing a very high expression of IF1 when compared to astrocytes. Therefore, we suggest that the actual physiological function of IF1 in normal energy demanding tissues is to ameliorate apoptosis geared by the activity of the  $H^+$ -ATP synthase under cellular stressful conditions. This hypothesis is supported by previous findings in different cancer cells (Faccenda et al., 2013; Formentini et al., 2012; Sanchez-Arago et al., 2013b; Sanchez-Cenizo et al., 2010). Obviously, this idea further supports that in addition to the well characterized pH regulated binding of IF1 to the  $H^+$ -ATP synthase under depolarization conditions (Cabezón et al., 2000), the activity of IF1 is regulated in these tissues by additional mechanisms that could involve the interaction of IF1 with other proteins (Lopez-Mediavilla et al., 1993) (Figure 7G) and/or tissue-specific post-translational modifications (Zhao et al., 2011).

Inhibition of the synthase activity of the  $H^+$ -ATP synthase by IF1 is known to promote a mild ROS signal (Formentini et al., 2012; Sanchez-Arago et al., 2013b), which is consistent with the observed inhibition of the  $H^+$ -ATP synthase, the enhanced production of ROS in neuronal cultures and the increased carbonylation of brain and neuronal proteins in hIF1 expressing mice (Figure 7G). ROS are known activators of several of the pro-survival signaling pathways that we have shown to be activated in the brain of  $H^+/T^+$  mice such as Akt/p70S6K (Datta et al., 1997; Harada et al., 2001) and NF $\kappa$ B (Karin, 2006; Ravati et al., 2001). The persistent mild oxidative stress in the brain of these animals could represent an additional mechanism involved in preconditioning (Iadecola & Anrather, 2011) by raising, at the functional level, the threshold at which a toxic insult will normally unleashed the molecular events that trigger cell death (Figure 7G). Indeed, we have observed that quenching ROS largely

inhibits glutamate induced neuronal cell death only in non-preconditioned cultures. The finding that IF1 protects cancer cells from chemotherapy induced apoptosis via ROS-mediated signaling (Formentini et al., 2012; Sanchez-Arago et al., 2013b) further supports this idea.

Importantly, our data show that hIF1 expressing neurons in the injured area are partially protected from cell death when compared to controls despite showing remarkably less ATP and ADP concentrations. Hence, we suggest that either the set-point of ATP availability for triggering cell death has not been reached (Galluzzi et al., 2012) or that the flux at which ATP is being produced by the stimulation of aerobic glycolysis is enough to preserve cellular functions. An enhanced activity of ATP-consuming reactions such as the induction of protein synthesis revealed by the activation of p70S6K and of repair pathways by the activation of PARP in hIF1 expressing neurons might also contribute to the depletion of the phosphorylated nucleotides in these animals. Taken as a whole, our findings indicate that a sustained partial inhibition of OXPHOS mediates the activation of protein synthesis, the induction of repair mechanisms and the prevention of apoptosis. Three behavioral locomotor tests confirm that hIF1 expressing mice show milder neurological impairment after injury.

Under conditions of cellular stress induced by different chemotherapeutic agents the mitochondrial  $H^+$ -ATP synthase generates a high intensity ROS signal that triggers apoptotic cell death (Johnson et al., 2005; Santamaria et al., 2006; Wondrak, 2009). Recent findings indicate that the  $H^+$ -ATP synthase forms part of the PTP (Bonora et al., 2013; Giorgio et al., 2013) stressing previous functional reports on the relevance of this complex of OXPHOS in cell death (Matsuyama et al., 1998; Santamaria et al., 2006; Shchepina et al., 2002) and the tangled circuitry of energy metabolism and apoptosis (Andersen & Kornbluth, 2013). Bcl-xL is the prevailing anti-apoptotic protein in the



brain (Alavian et al., 2011; Michels et al., 2013). We suggest that the over-expression of Bcl-xL after induced excitotoxicity in the brain *in vivo* mediates the prevention of cell death, consistent with previous findings in cancer cells (Formentini et al., 2012; Sanchez-Arago et al., 2013b) and with the fact that the silencing of Bcl-xL reverted the protection afforded by IF1 over-expression. Moreover, Bcl-xL is also localized at the inner mitochondrial membrane where it interacts with the H<sup>+</sup>-ATP synthase to enhance its activity by reducing futile ion cycling (Alavian et al., 2011; Chen et al., 2011). Herein, we have confirmed this interaction. We suggest that Bcl-xL might act as an additional regulator of the PTP, acting as the molecular bridge that links events at the inner and outer mitochondrial membranes. In fact, the silencing of Bcl-xL abrogates the pro-survival effect of the inhibition of the H<sup>+</sup>-ATP synthase mediated by hIF1. Moreover, the finding that Bcl-xL also interacts with other complexes of the respiratory chain, presumably Complex I, broadens the biological relevance of this anti-apoptotic protein in the regulation of mitochondrial physiology and cellular metabolism.

CryoEM studies of the macromolecular organization of the inner membrane reveal no interaction between Complex I and the H<sup>+</sup>-ATP synthase (Davies et al., 2011). However, cyclophilin D that favors PTP opening, binds to and regulates the activity of the H<sup>+</sup>-ATP synthase (Giorgio et al., 2009) and affects modulation of PTP by rotenone (Li et al., 2012). These findings suggest that the metabolic and/or the structural preconditioning mediated by hIF1 increases the threshold of PTP opening by preventing the channel formation capacity of the H<sup>+</sup>-ATP synthase (Giorgio et al., 2013) (Figure 7G). Overall, our data provide the first *in vivo* demonstration that the activity of the H<sup>+</sup>-ATP synthase is necessary for the efficient execution of cell death. Hence, the H<sup>+</sup>-ATP synthase not only functions as the power plant of the cell but also as a pivotal regulator of cell death.

## **Materials and methods.**

**Transgenic animals.** The pCMV-SPORT6-H49K plasmid (Sanchez-Cenizo et al., 2010) containing the H49K mutant version of human IF1 was PCR amplified and the PCR product assembled into the pTRE2hyg vector (Clontech Laboratories Inc.) into the BamHI and NotI restriction sites. The TRE2hyg-H49K plasmid was digested with SexAI/BsrBI (New England Biolabs) and the 2.5Kb DNA fragment of interest purified with Elu-Quik kit (Shleicher & Schuell). Transgenic mice (TRE-H49K-25, H<sup>+</sup>) were obtained by pronuclear microinjection of the construct by the Servicio de Transgenesis of the CNB/CBMSO (UAM, Madrid, Spain), using standard protocols. Integration of the construct was confirmed by PCR (forward, 5'-CACAGAGTAGAGAACAACACTG-3'; reverse, 5'-GTTAGTAGCACACAGACAAA-3'). The Bl6-Tg(Camk2a-tTa)1Mmay/J mice (T<sup>+</sup>), expressing the transactivator tTA in neurons (Mayford et al., 1996) were used. The Tet-Off double transgenic animals (H<sup>+</sup>/T<sup>+</sup>) were obtained by breeding H<sup>+</sup> and T<sup>+</sup> mice. Animals were maintained on the C57/Bl6 genetic background. To turn off the expression of hIF1, double transgenic mice were administered doxycycline (2mg/mL) in the drinking water during 15 days. Animal experiments were carried out after approval of the Institutional Review Board (Ethical Committee of the UAM, CEI-24-571) in compliance with animal policies and ethical guidelines of the European Community.

**Brain mitochondria.** Adult mice brain mitochondria were prepared after the permeabilization of synaptosomes with 100  $\mu$ M digitonine. The purity of mitochondrial preparations was assessed by western blotting. Oxygen consumption rates in isolated mitochondria (200  $\mu$ g protein) were determined in a Clark-type electrode. Glutamate plus malate (10 mM) were used as respiratory substrates in the presence or absence of 0.5 mM ADP, 6  $\mu$ M OL, 5  $\mu$ M FCCP and 1  $\mu$ M antimycin A. The composition of the

respiration buffer is 75 mM manitol, 25 mM sucrose, 20 mM Tris-HCl, 5 mM phosphate, 0.3 mM EGTA, 0.5 mM EDTA, 100 mM KCl, 0.1% BSA, pH 7.4.

For the determination of the mitochondrial membrane potential, ~100  $\mu\text{g}$  of mitochondria were charged with 100 nM TMRM<sup>+</sup> (Life Technologies). Changes in fluorescence were recorded using an Aminco-Bowman Series 2 Luminescence Spectrometer after addition of the following compounds (final concentration): 10 mM succinate, 1 mM ADP, 6  $\mu\text{M}$  OL, 5  $\mu\text{M}$  FCCP, 2  $\mu\text{M}$  rotenone and 1  $\mu\text{M}$  antimycin A.

***Primary cultures of cortical neurons.*** Cerebral cortices were dissected from fetal mice at 16-17 days of gestation in Neurobasal Medium (NB) using the Papain Dissociation System kit (Worthington). Disrupted cortices were resuspended in NB supplemented with 10% HS and 2 mM glutamine. After 4–5 days in culture, non-neuronal cell division was halted by the addition of 3 mM cytosine arabioside for 24 h. Neurons were identified evaluating their morphology and positive immunoreactivity to Neu-N antibody (Chemicon International Inc.; 1:1000) and studied at 9-11 days of culture. Lack of staining with an anti-glial fibrillary acidic protein GFAP (Dako Cytomation; 1:1000) revealed the absence of astrocytes in cell cultures.

The rates of lactate production and of oxygen consumption (XF24 Extracellular Flux Analyzer, Seahorse Bioscience) were determined (Sanchez-Cenizo et al., 2010). The final concentration and order of injected substances was 6  $\mu\text{M}$  OL, 0.75 mM dinitrophenol (DNP), 1  $\mu\text{M}$  rotenone and 1  $\mu\text{M}$  antimycin A.

For the determination of the  $\Delta\Psi_m$  and ROS levels, 100 nM TMRM<sup>+</sup> or 2.5  $\mu\text{M}$  MitoSOX™ (Life Technologies) were respectively used in “redistribution mode” (Duchen et al., 2003). The fluorescence was analyzed by confocal microscopy using a Biorad Radiance 2000 Zeiss Axiovert S100TV using red (590/617 nm) excitation/emission wave lengths and quantified using ImageJ software. Fluorescence

intensity was quantified by removing background signal and measuring the mean fluorescence intensity in the pixels containing mitochondria in approximately the same number of cells and at least in 15 different fields per condition tested. 6  $\mu\text{M}$  OL, 2  $\mu\text{M}$  rotenone, 1  $\mu\text{M}$  antimycin A and 5  $\mu\text{M}$  FCCP were used.

Neuron transfection was done using Effectene Transfection Reagent (Quiagen) with control or Bcl-xL plasmid (Switchgear Genomics Inc.). For the determination of cell death, neurons were treated with 25  $\mu\text{M}$  glutamate (Sigma-Aldrich) during 5 min or deprived of oxygen for 1h (1%  $\text{O}_2$ ) in a Hypoxic Workstation H35 (Don Whitley Scientific). Neurons were incubated for 24h in the absence or presence of 20 nM Mito Q and after processed by confocal microscopy *in vivo* at 37°C and 5%  $\text{CO}_2$  using an Axioskop2-plus vertical microscope (Zeiss) coupled to a ccd color camera. Propidium iodide (2  $\mu\text{M}$ ) and calcein (1  $\mu\text{M}$ ) were utilized to determine cell death and viability, respectively. The number of cells was quantified in 20 fields per treatment using ImageJ software.

***Adenine nucleotides.*** Adenine nucleotides were extracted from frozen brain powder with a 6% perchloric acid solution. Determination of ATP, ADP and AMP in frozen brain powder was carried out by standard enzymatic procedures. The ATP concentration in primary cultures was determined using the ATP Bioluminescence Assay Kit CLS II (Roche).

***Protein electrophoresis, western blotting and protein carbonylation.*** Protein samples from brain and cellular extracts were fractionated on SDS-PAGE. Details of the antibodies used in western blots are provided in Supplementary Information. For the determination of protein carbonylation the Oxyblot Oxidized Protein Detection kit (Chemicon International Inc.) was used.

**Blue native (BN)-PAGE.** Protein extracts (250 µg) from control or H<sup>+</sup>/T<sup>+</sup> mice brain mitochondria were solubilized in BN-loading buffer. 1g of n-dodecyl β-D-maltoside / g protein was added to the samples and protein complexes were fractionated in BN-gels after addition of 2.5 µl of the Coomassie dye suspension. Electrophoresis was performed in “deep blue” cathode buffer B at constant voltage of 70 V until one-third of the whole electrophoresis run. Buffer B was then exchanged with the buffer “light blue”. Electrophoresis was performed for other 12 h at 70 V and then 3 h at 200V. BN-loading buffer: 50 mM NaCl, 1 mM EDTA, 5 mM 6-aminocaproic acid, 2% PMSF, 50 mM imidazole/HCl pH 7.0. BN-gels: acrylamide:bisacrylamide ratio ranging from 3% to 13% w/v; 0.5 M 6-Aminocaproic acid and 25 mM imidazole. Coomassie dye suspension (5% SBG-dye in 500 mM aminocaproic acid). Anode buffer: 25 mM imidazole, pH 7.0. “Deep blue” cathode buffer B: 50 mM tricine, 7.5 mM imidazole, 0.02% Serva Blue G (SBG), pH 7.5. “Light blue” cathode buffer B/10: the cathode buffer B with a ten times lower dye concentration (0.002% SBG).

**Determination of enzyme activities.** Brain mitochondria resuspended in respiration buffer containing 1% Triton X-100 were used for the spectrophotometric determination of complex I, II+III, IV and V activities as described (Barrientos et al., 2009).

**Glutathion determination.** The brain GSH and GSSG concentrations were determined using the Glutathione Assay Kit (BioVision Inc.).

**Animal surgery and histology.** One year old control (n = 10) and H<sup>+</sup>/T<sup>+</sup> (n = 10) male mice were used for surgery. To induce excitotoxic damage all animals received a single 0.5 µl dose of 20 nmol of quinolinic acid by stereotaxical injection into the left striatum. Coordinates (mm) AP (anteroposterior from bregma) = +0.25, ML = 2.75, D-V (vertical from dura) = -2.5 at a speed of 1µl/minute. The right hemisphere did not

receive any surgery and served as histological control. Twenty days after the lesion mice were sacrificed, transcardially perfused with 3% paraformaldehyde and cryoprotected with 30% sucrose. Sections (30  $\mu$ m thick) were taken in the coronal plane, stained with hematoxylin-eosin and processed for immunohistochemistry.

***Evaluation of animal behavior.*** Animal behavior was evaluated by footprint, grid and cylinder tests in a blinded way before surgery and every three days post-surgery until day of sacrifice (21<sup>th</sup> day). Gait abnormalities were detected by analysis of motor coordination and synchrony using the “footprint” test (Carter et al., 1999). Briefly fore and hind paws were dipped into water soluble ink of different colors and animals were left free to walk over absorbent paper in a straight line. Analysis included measurement of stride length, width of the base of support for the hind limbs and paw angle (fore and hind). Gait variability was studied using the coefficient of variation (CV) calculated from the equation  $100 \times \text{standard deviation}/\text{mean value}$ . For the grid test: Mice were left free to walk across a horizontal grid (size: 20x30cm, 10mm wire mesh). The number of ipsilateral and contralateral paw slips through the grid were counted and the motility index was calculated from the equation:  $\text{percentage of the time spent moving}/(\text{number of foot faults} + \text{number of stops})$  (Brooks & Dunnett, 2009). For the cylinder test: mice were placed in a perspex cylinder (9 cm diameter, 15cm tall) for 5 minutes and recorded with a videocamera. Paw usage was studied by measuring the number of forelimb wall contacts made with each paw when rearing (Brooks & Dunnett, 2009). Data is presented as number of contacts per minute for left, right and both forepaws simultaneously.

***Immunofluorescence/confocal microscopy and immunohistochemistry.*** Free-floating brain slices were incubated with blocking buffer (3% BSA and 0.1% Triton X-

100 in PBS) for 1 h at RT and then incubated overnight at 4°C with the primary antibodies specified.

The primary antibodies used were: anti-NeuN (1:100) and Fluoro Jade B (0.001%) from Millipore Bioscience Research Reagents; anti-GFAP (1:1000) from Dako Cytomation; anti-Iba-1 (1:500) from Wako; anti-Ed-1 (1:100) and anti-c-fos (1:100) from Santa Cruz Biotechnology, Inc.; anti-DARP-32 (1:500) from Chemicon International Inc. and anti-caspase-3 (1:100) from Cell Signaling Technology Inc. Secondary Cy-3/Cy-5/Cy-2-conjugated antibodies were used (Millipore Bioscience Research Reagents). Cellular fluorescence was analyzed by confocal microscopy using a Biorad Radiance 2000 Zeiss Axiovert S100TV using green (498/516 nm), red (590/617 nm) or blue (642/661 nm) excitation/emission wave lengths. The area and intensity of fluorescence were quantified by ImageJ software.

Mice brain slices were incubated in 3% H<sub>2</sub>O<sub>2</sub> in methanol for 10 min at room temperature to block the endogenous peroxidase activity. Antigens were retrieved by incubation in Dako Retrieval Solution (Dako Cytomation) for 2 min at 98°C. The anti-IF1 (1:200) and anti-β-F1-ATPase (1:20,000) were used for immunohistochemistry using the peroxidase based EnVision™ FLEX Mini kit High pH (Dako Cytomation). Specimens were then incubated with diaminobenzidine chromogenic substrate (Dako Cytomation) for 5 min at room temperature. To assess the expression of IF1 in human brain, 3 μm paraffin sections obtained from post mortem CNS specimens from a patient with no neurologic disease were processed for immunocytochemistry. Sections were automatically deparaffinised and immunostained with an Autostainer Link instrument from Dako (Carpinteria). Antigenic retrieval was performed at low pH, incubated with anti-IF1 at 1/100 dilution during 30 minutes and visualized with EnVision Flex system

from Dako (Carpinteria). Sections were observed with a Leica DMRE light microscope.

***Statistical Analysis.*** Statistical analyses were performed using a two-tailed Student's t-test. ANOVA with post hoc Dunnett's test were used for multiple comparisons to the control, using the SPSS 17.0 software package. The results shown are means  $\pm$  SEM. A  $p < 0.05$  was considered statistically significant.



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## **Author contributions**

LF and JMC designed research; LF, MPP, LSC, FS, JIL and CN performed research; LF, MPP, CN, AMS and JMC analyzed data; LF and JMC wrote the paper.

## **Conflict of Interest**

The authors declare no conflict of interests.

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## Figure legends.

**Figure 1.** Mice expressing hIF1 in neurons. **(A)** PCR analysis for the H49K variant of hIF1 and tTA constructs in wild type (wt), tTA ( $T^+$ ), H49K ( $H^+$ ) or double transgenic ( $H^+/T^+$ ) mice is shown. Western blots reveal the expression of hIF1 and IF1 (12 kDa) in total brain extracts. hIF1 is only expressed in  $H^+/T^+$  mice.  $\beta$ -actin expression is shown as loading control. **(B)** Immunohistochemistry (mitochondrial staining) for hIF1 and  $\beta$ -F1 ATPase ( $\beta$ -F1) in brain cortex of control (wt) and  $H^+/T^+$  mice. Magnification 63x. **(C)** Representative blots of the expression of hIF1, heat-shock protein 60 (HSP60), and mitochondrial complexes I (NADH9), II (SDH), III (Core II), IV (COXI and COX IV) and V ( $\beta$ -F1) in total brain extracts of wt and  $H^+/T^+$  mice. Two different samples per condition tested are shown. **(D)** Content of adenine nucleotides in brain extracts of control (wt, closed bars) and  $H^+/T^+$  mice (open bars). **(E)** Western blots show the hIF1 dependent phosphorylation of AMPK (p-AMPK) and the concurrent increase in glycolytic proteins lactate dehydrogenase A (LDH-A) and glyceraldehyde-3-phosphate dehydrogenase (GAPDH) in brain extracts (see histograms to the right). Two different samples per condition tested are shown.  $\beta$ -F1 and HSP60 expressions are shown as loading controls. **(F)** Hydrolytic activity of the  $H^+$ -ATP synthase in isolated mitochondria from brain of control (wt, black trace) and  $H^+/T^+$  (gray trace) mice. Where indicated, 10 $\mu$ M oligomycin (OL) was added. **(G)** Variation in the membrane potential (TMRM $^+$  staining) of isolated mitochondria from control (black trace) and  $H^+/T^+$  animals (gray trace) charged with 100 nM TMRM $^+$ . The effect of 1  $\mu$ M antimycin A in the presence of 10 mM ATP is shown. **(D,E,F)** Bars are the mean $\pm$ S.E.M. of six different samples. \*,  $P < 0.05$  when compared to control by Student's t test. See also Figures S1, S2 and S3.

**Figure 2.** hIF1 impairs oxidative phosphorylation. **(A)** Polarographic profiles of isolated mitochondria from control (lower trace) and  $H^+/T^+$  animals (upper trace). The effect of 10mM glutamate/malate, 0.5 mM ADP, 5  $\mu$ M oligomycin (OL), 5  $\mu$ M FCCP and 1  $\mu$ M antimycin A (Ant) is shown. Histograms reveal a reduction in State III (StIII) and uncoupled (FCCP) respiration in mitochondria of  $H^+/T^+$  mice (open bars) when compared to controls (wt, closed bars). OL-sensitive ATP synthase activity is also shown as a percentage of maximal respiration. **(B)** Variation in the membrane potential (TMRM<sup>+</sup> staining) of isolated mitochondria from control (black trace) and  $H^+/T^+$  animals (gray trace) charged with 100 nM TMRM<sup>+</sup>. The effect of 5 mM succinate, 1 mM ADP, 5  $\mu$ M OL and 5  $\mu$ M FCCP 1 is shown. Histograms show a larger reduction in  $\Delta\Psi_m$  after ADP administration in controls (wt, closed bars) when compared to hIF1 expressing mice ( $H^+/T^+$ , open bars). **(C)** Representative blot of the extent of carbonylation of total brain proteins. Two different samples per condition tested are shown. Tubulin was used as loading control. The migration of molecular mass markers is indicated to the right. Arrows (to the left) identify the migration of the two proteins used in the quantification of protein carbonylation (histograms). **(D)** Representative blots of catalase (cat), superoxide dismutase 1 and 2 (SOD1 and SOD2) expression in control (wt, closed bars) and hIF1 expressing ( $H^+/T^+$ , open bars) mice. **(E)** Cellular glutathione (GSH) and GSH/GSSG ratio in total brain. **(F)** Blue-native immunoblot analysis of mitochondrial membrane proteins visualized with antibodies against mitochondrial complexes I (NADH9), II (SDH), III (Core II), IV (COX IV) and V ( $\beta$ -F1-ATPase). The migration of monomers (Mon), dimers (Dim), supercomplex (SC), F1-ATPase (F1),  $H^+$ -ATP synthase (F0F1) and molecular mass markers is indicated. **(G)** Enzymatic activity of mitochondrial complex I, II+III and IV in isolated brain mitochondria of control (wt, closed bars) and  $H^+/T^+$  (open bars) mice. **(A-G)** Bars are



the mean  $\pm$  SEM of three (**A, B, D**), four (**C**) or six (**E, F**) determinations. \*,  $P < 0.05$  when compared to controls by Student's t test.

**Figure 3.** hIF1 induced metabolic reprogramming and ROS signaling in cortical neurons. (**A**) *In vivo* phase contrast images of 9 d cultures of cortical neurons obtained from control and  $H^+/T^+$  embryos. Magnification 40x. Representative western blot (**B**) and immunocytochemistry (**C**) show the expression of hIF1 only in 9 d neurons of  $H^+/T^+$  mice.  $\beta$ -F1-ATPase ( $\beta$ -F1) is used as loading control. DAPI (4',6-diamidino-2-phenylindole) staining is also shown. Magnification 40x. (**D**) The cellular ATP content was determined in control (wt, closed bar) and  $H^+/T^+$  (open bar) neuronal cultures. (**E**) Shows the oligomycin sensitive respiration (OSR) and maximal respiration in 4d and 9d neuronal cultures from control (wt, closed bar) and  $H^+/T^+$  (open bar) embryos. (**F**) Rates of aerobic glycolysis in the absence or presence of 5  $\mu$ M oligomycin (OL). (**G**) Representative blots of the expression of pyruvate kinase M2 (PKM2), lactate dehydrogenase A (LDH-A), glyceraldehyde-3-phosphate dehydrogenase (GAPDH) and heat-shock protein 60 (HSP60) in control (wt, closed bars) and hIF1 expressing ( $H^+/T^+$ , open bars) neurons (**H,I**) *In vivo* staining of TMRM<sup>+</sup> (**H**,  $\Delta\Psi_m$ ) or MitoSOX (**I**, ROS) charged mitochondria from 10d primary cultures of cortical neurons. Magnification 40x. (**J**) Representative experiment of carbonylation of proteins in primary neuronal cultures derived from control (wt) and  $H^+/T^+$  mice. Tubulin is shown as loading control. The migration of molecular mass markers is indicated to the right. Histograms show the quantification of p35 and p29 proteins. (**D-J**) The data shown are mean  $\pm$  SEM of three (**D-F, H-I**) or four (**G, J**) cultures per condition. \*,  $P < 0.05$  when compared to control by Student's t test. See also Figures S4, S5 and S6.

**Figure 4.** hIF1 protects from quinolinic acid-induced brain damage. Animal weight loss (**A**) and spleen weight (**B**) in control (wt, closed squares) and  $H^+/T^+$  (open squares) mice at the indicated time after surgery (**A**) or at time of sacrifice (21 day) (**B-E**). (**C**) Representative ventricular symmetry in sections of the brain from control (wt, closed bar) and  $H^+/T^+$  (open bar) mice. Magnification 2.5x. The percentage increase in ventricle area is shown. (**D**) Brain sections stained with hematoxylin-eosin. Four different animals per condition tested are presented. The area of the lesion is indicated. Magnification 20x. Histograms show a reduction in the lesion area in  $H^+/T^+$  mice (open bar) when compared to control (wt, closed bar) mice. Bars are the mean  $\pm$  SEM. of five animals. D, dorsal; M, medial. (**E**) Representative staining of nuclei (DAPI, blue), protein phosphatase 1 (DARPP-32, white), microglia (Iba-1, red), macrophage/monocyte (Ed-1, green) antibodies the left hemisphere. Magnification 5x. Histograms show the quantification of fluorescence in controls (wt, closed bar) and  $H^+/T^+$  (open bar) mice. (**A-E**) Bars are the mean  $\pm$  SEM. of five (**C-E**) or ten (**A-B**) animals. Where indicated, numbers correspond to the identification code of the mouse. \*,  $P < 0.05$  when compared to control by Student's t test. See also Figures S7, S8, S9 and Supplementary Videos.

**Figure 5.** The inhibition of the  $H^+$ -ATP synthase protects neurons from apoptosis. (**A**) Fluorochrome B staining in degenerating neurons in the core and penumbra of the striatal lesion. Three different images of animals identified by numbers are presented. Magnification 20x. Histograms show a reduction of the fluorochrome B positive area in  $H^+/T^+$  (open bar) when compared to control (wt, closed bar) mice. (**B**) Activated caspase 3 staining in the penumbra of the striatal lesion in control (wt, closed bars) and hIF1 ( $H^+/T^+$ , open bars) expressing mice. Magnification 20x. Histograms show a reduction in the apoptotic area in  $H^+/T^+$  mice. (**C**) Brain glutathione (GSH) content and GSH/GSSG

ratio in the injured area of control (wt, closed bar) and  $H^+/T^+$  (open bar) mice. **(D)** Representative blots of the expression of protein kinase B (p-AKT, AKT), phospho p70 S6 kinase (p-P70S6), IkappaB alpha ( $I\kappa B\alpha$ ), B-cell lymphoma-extra large (Bcl-xL) and B-cell lymphoma 2 (Bcl-2) in the right (R) and left (L) hemispheres of wt and  $H^+/T^+$  mice. One control and two different  $H^+/T^+$  animals are shown. **(E)** DAPI (blue), c-Fos (green) and glial fibrillary acidic protein (GFAP, red) staining of brain slices of the left hemisphere after three weeks post-surgery. Magnification 5x. Histograms show the quantification of fluorescence in control (wt, closed bar) and  $H^+/T^+$  (open bar) mice. D, dorsal; M, medial. **(A-E)** Determinations were carried out at 21 day post-surgery. Bars are the mean  $\pm$  SEM. of three **(E)**, four **(D)** or five **(A-C)** animals. \* and #,  $P < 0.05$  when compared to the right or left hemisphere of controls, respectively.

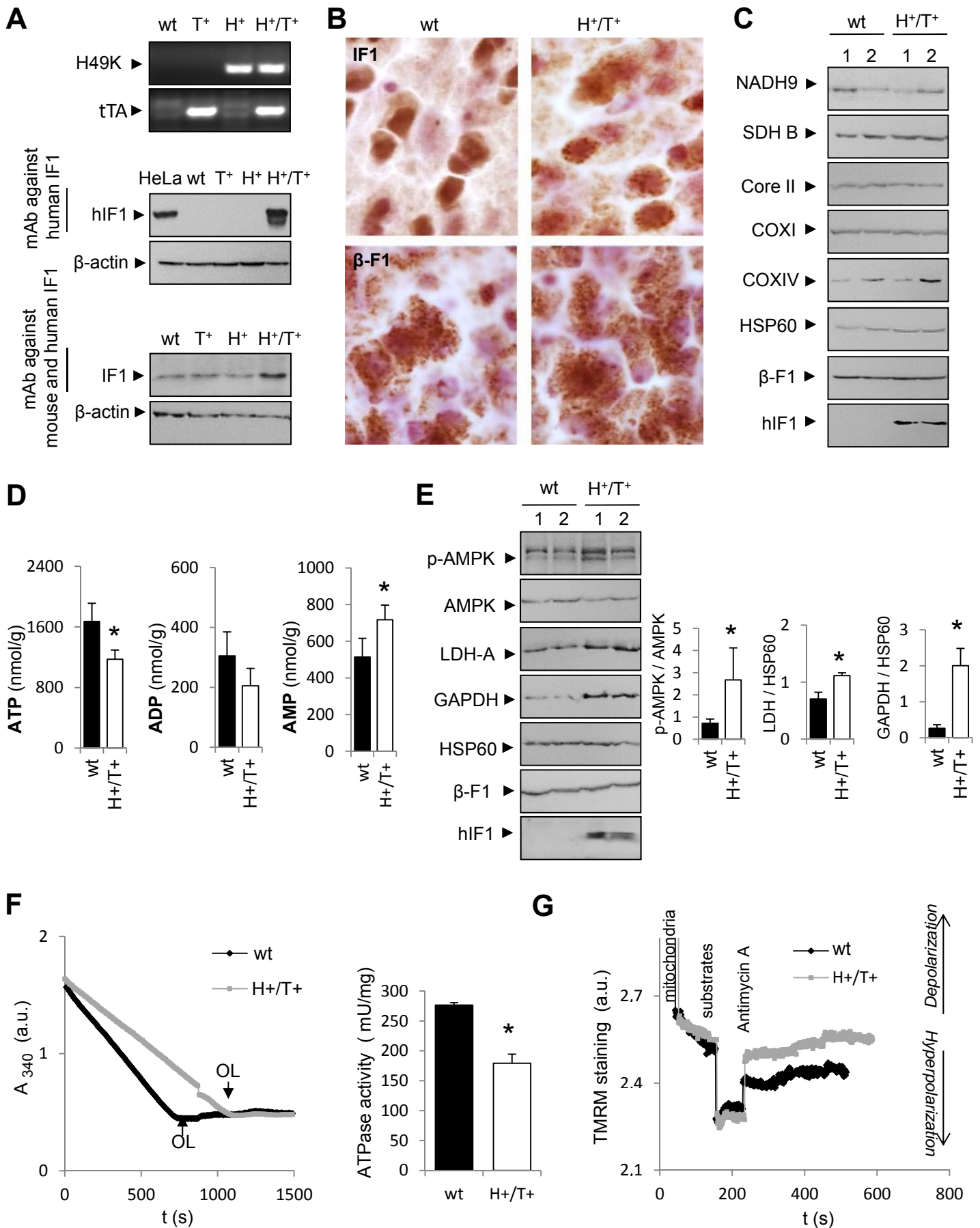
**Figure 6.** Bcl-xL is involved in hIF1-mediated protection of neurons. **(A)** Content of adenine nucleotides in the injured area of the left hemisphere of control (wt, closed bars) and hIF1 expressing ( $H^+/T^+$ , open bars) mice. \*,  $P < 0.05$  when compared to control (wt) by Student's t test. **(B)** Representative blots of the polymer poly-ADP-ribose (PAR), the product of poly-ADP-ribose polymerase-1 (PARP-1) activity, in right (R) and left (L) hemispheres of control (wt, closed bars) and  $H^+/T^+$  (open bars) mice. One control and two  $H^+/T^+$  mice are shown.  $\beta$ -F1-ATPase expression is shown as loading control. Histograms show the quantification of PAR/ $\beta$ -F1 ratio. \* and #,  $P < 0.05$  when compared to the right or left hemisphere of controls, respectively. **(C)** Effect of ROS scavenging (20 nM mito Q, mQ) on glutamate primed cell death in neurons derived from control (wt, closed bars) and  $H^+/T^+$  (open bar) mice. **(D)** Blue-native immunoblot analysis of Bcl-xL immunoreactivity associated to complexes of mitochondrial OXPHOS. The migration of complex I (CI, NADH9), F0F1-ATPase (CV,  $\beta$ -F1-

ATPase) and Bcl-xL in control (wt) and  $H^+/T^+$  mice is indicated. The migration of molecular mass markers is indicated to the right. **(E)** Effect of glutamate and 1 h hypoxia on cell death in primary cultures of cortical neurons derived from control (wt, closed bars) and  $H^+/T^+$  (open bar) mice. The silencing of Bcl-xL (siBcl-xL) using  $\beta$ -actin as loading control is illustrated. **(A, B, C, E)** Bars are the mean  $\pm$  SEM of three **(B, C, E)** or five **(A)** experiments. \* and #,  $P < 0.05$  when compared to control (wt) or to silencing control ( $H^+/T^+$ , siCRL).

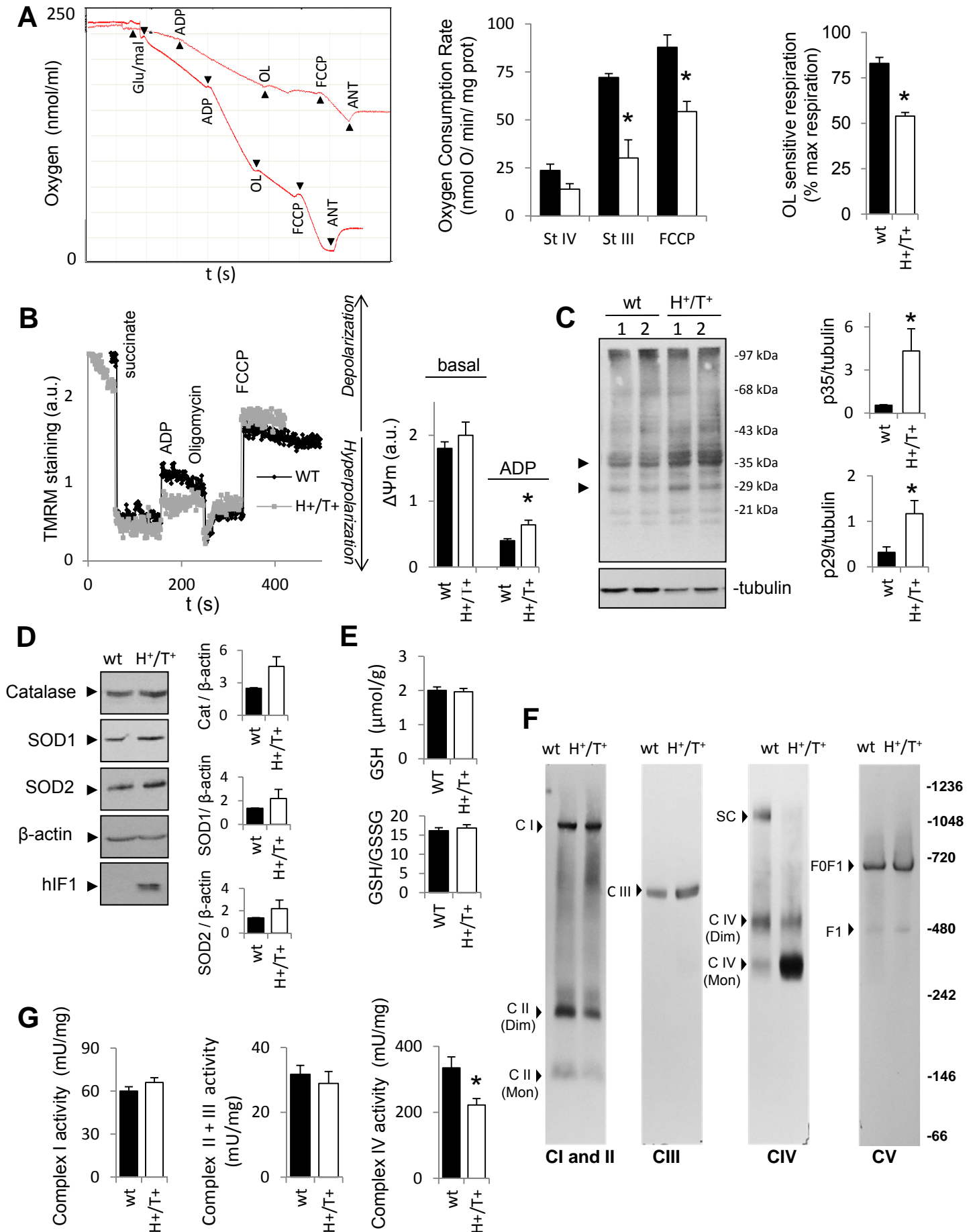
**Figure 7.** IF1 expression in human brain. **(A)** Western blots of the expression of IF1 in fractionated proteins from mice neurons and astrocytes using the commercial anti-mouse IF1.  $\beta$ -F1-ATPase ( $\beta$ -F1) expression is shown as loading control. Histograms show the quantification of IF1/ $\beta$ -F1 ratio. The data shown are mean  $\pm$  SEM of 3-4 preparations. **(B,C)** Immunocytochemistry of hIF1 in human cerebral cortex. Note IF1 immunolabelling in cortical neurons of the parieto-occipital cortex and the negative labeling of astrocytes. Magnification 20x **(B)** and 63x **(C)**. **(D-F)** Immunocytochemistry for IF1 in human cerebellar sections. **(D, E)**: positive immunolabelling for hIF1 in Purkinje cells, granular neurons and Golgi type II neurons. Magnification 20x **(D)** and 63x **(E)**. **(F)**: Strong hIF1 immunolabelling in neurons of the cerebellar dentate nucleus. Magnification 20x. **(G)** The schematic illustrates the role of the over-expression of hIF1 in preconditioning of the brain. In normal mice the IF1 present is non-functional as relevant repressor of the synthetic activity of the  $H^+$ -ATP synthase either by its binding to a putative receptor (BP) and/or because of covalent modifications of the protein. The over-expression of hIF1 with higher affinity for  $\beta$ -F1-ATPase partially interferes with OXPHOS and promotes an enhanced glycolysis and a mild ROS signal that activates in the nucleus pathways of survival and repair enhancing the threshold level required to

execute cell death. In addition, hIF1 overexpression might affect the dimerization of the  $H^+$ -ATP synthase that is involved in PTP formation. The metabolic (red arrows) and structural (violet arrow) pathways of brain preconditioning are highlighted. Upon administration of a death stimuli hIF1 inhibits more effectively the synthase activity of the  $H^+$ -ATP synthase than endogenous IF1. By a mechanism that remains to be discovered IF1 prevents PTP opening and extensive neuronal cell death. See also Figure S10.

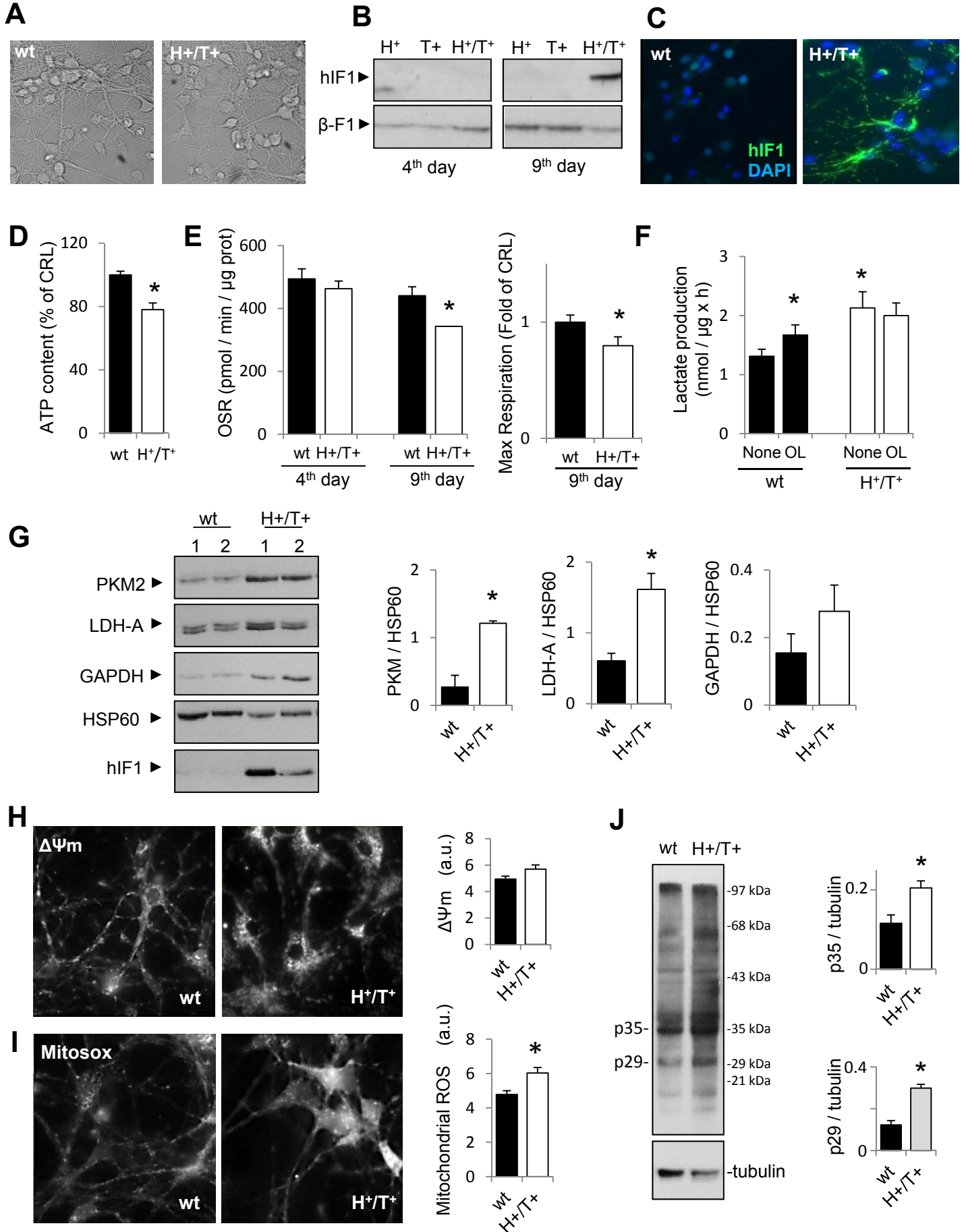
**Figure 1**



**Figure 2**

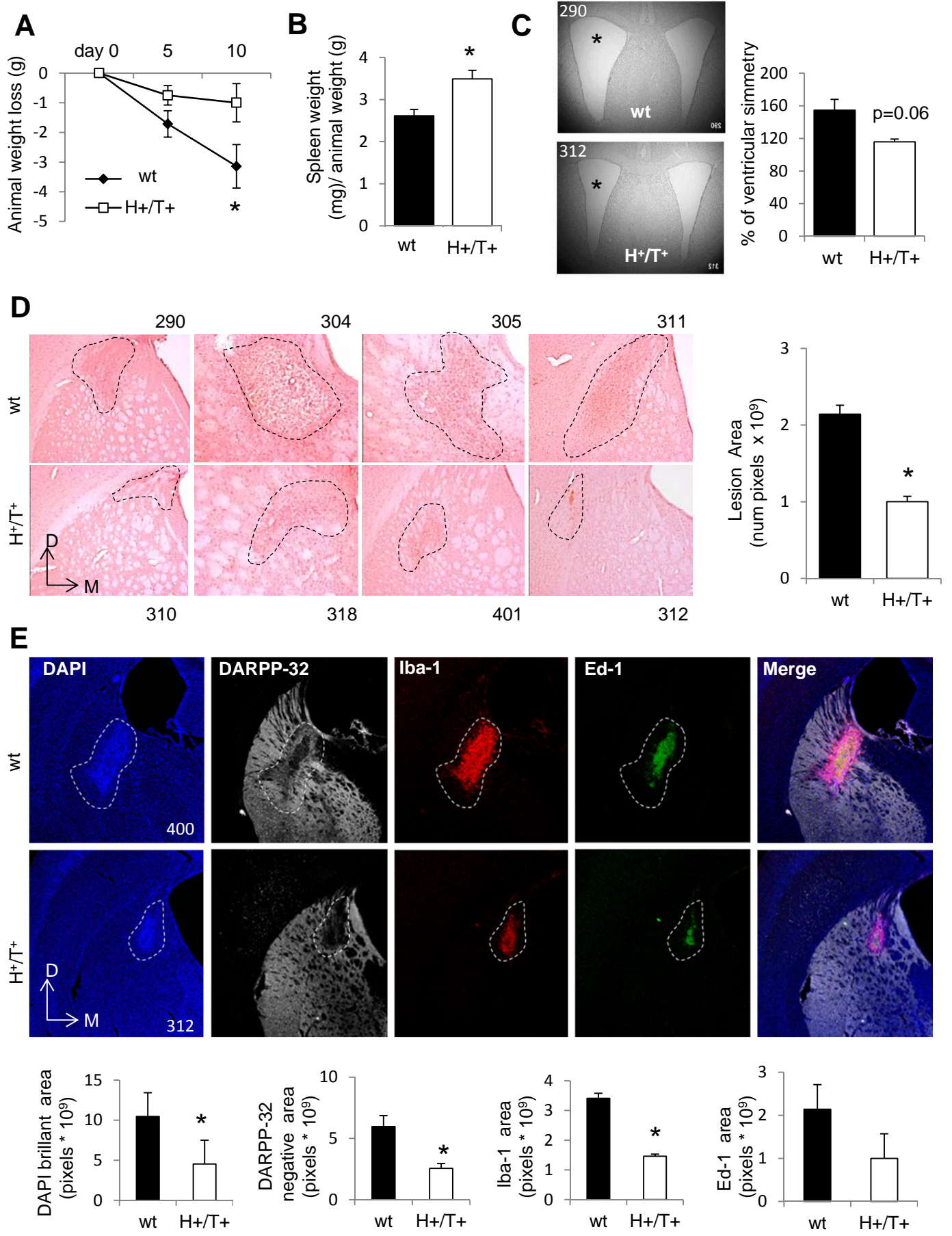


**Figure 3**

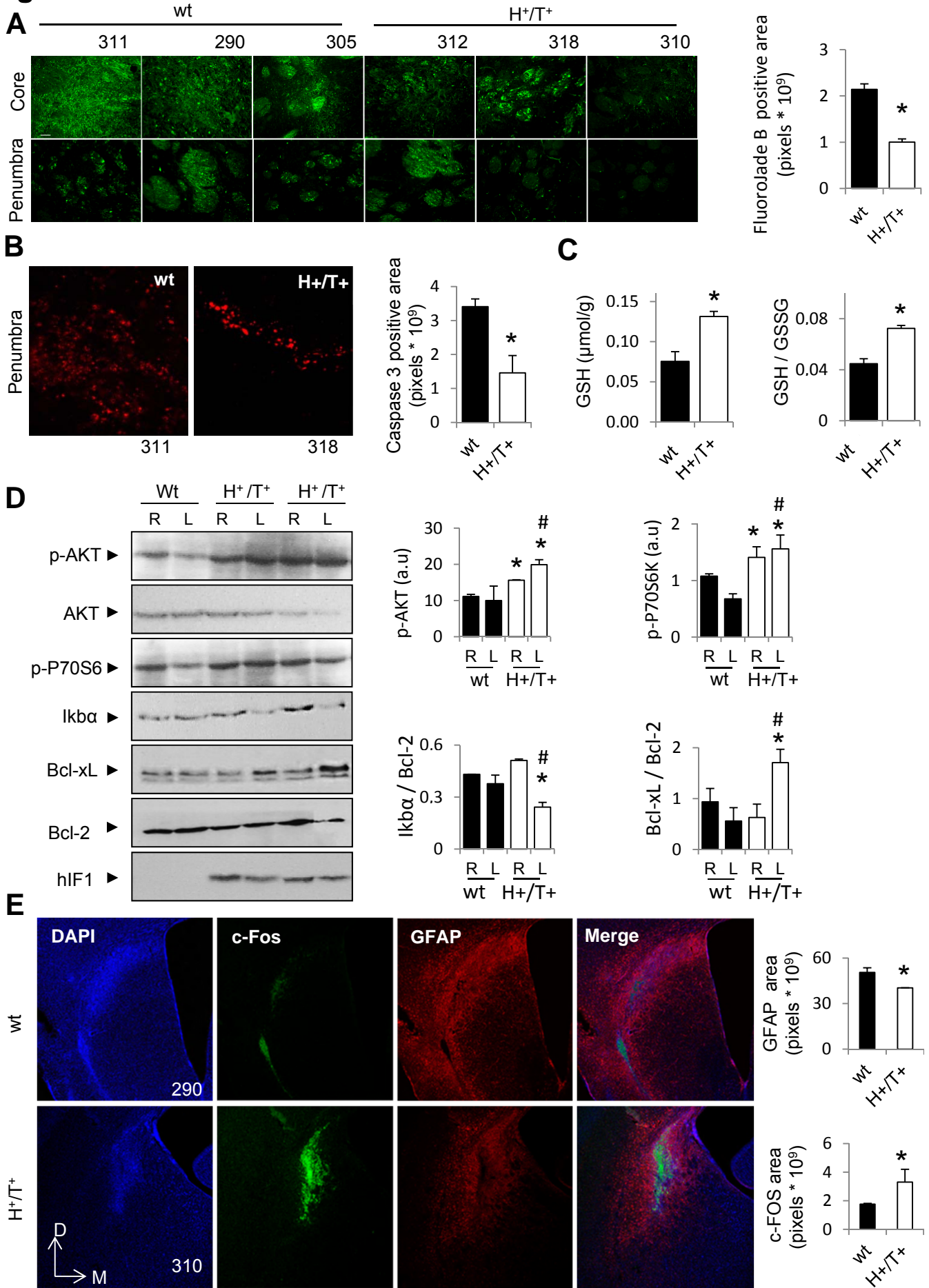




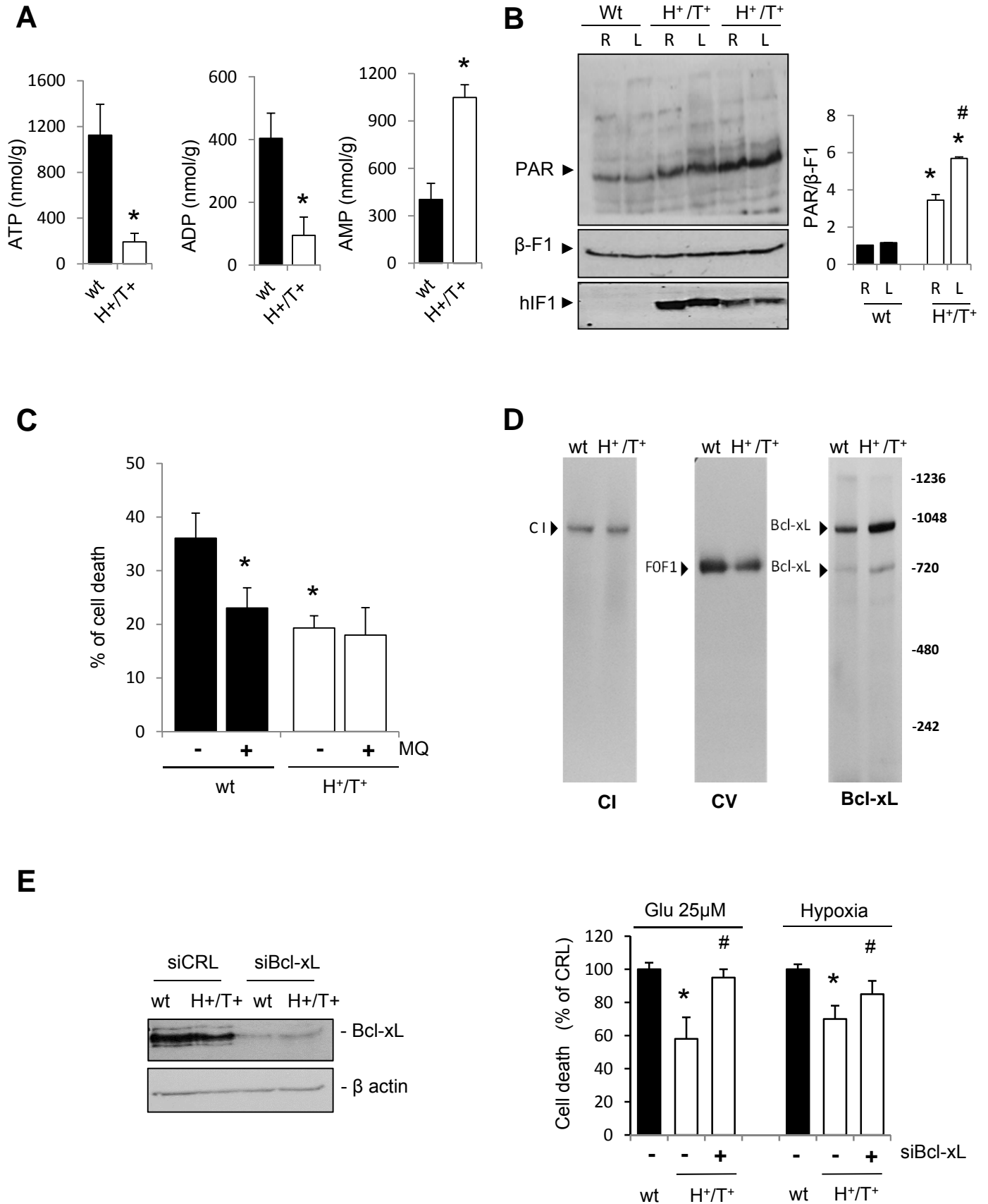
**Figure 4**



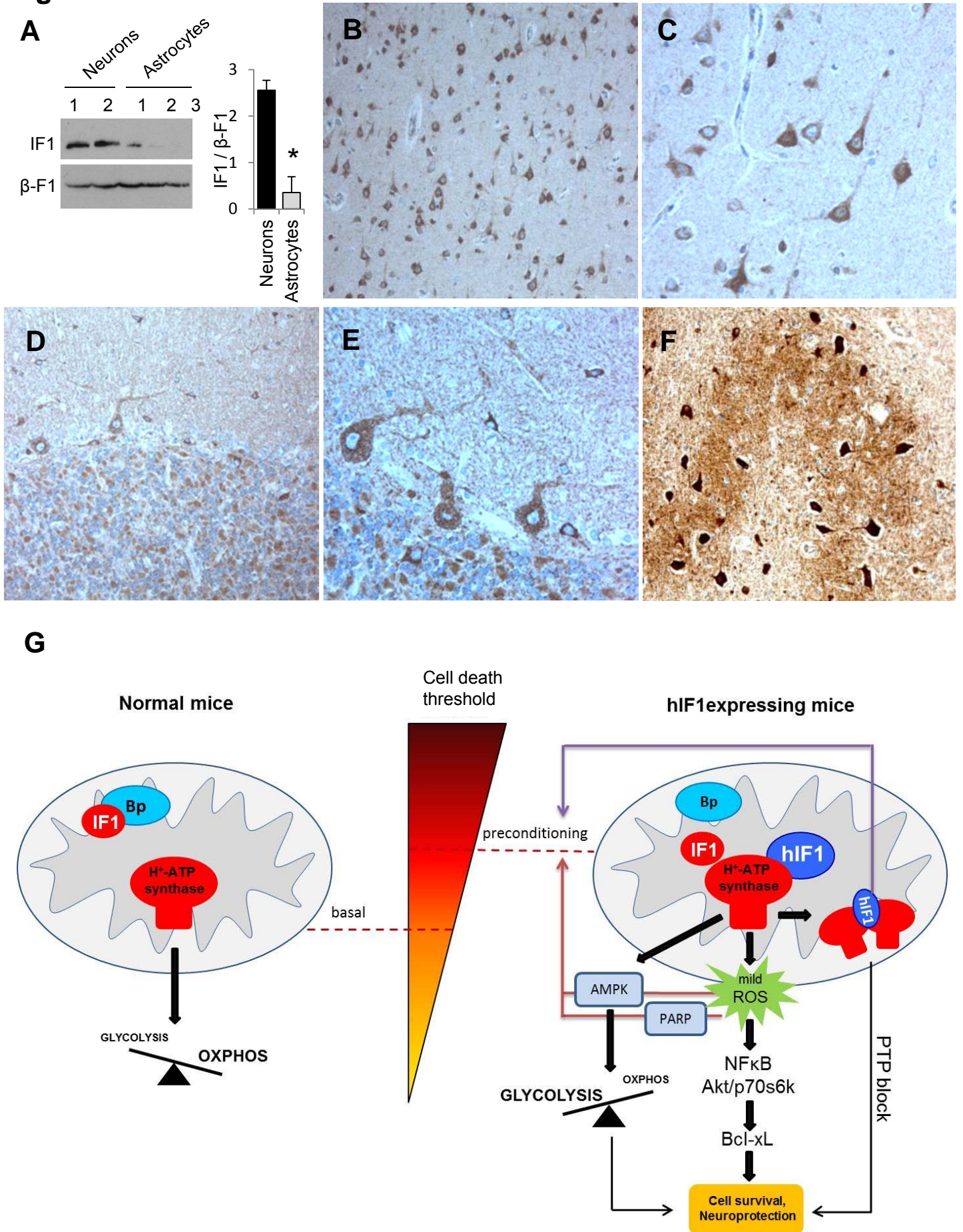
**Figure 5**



**Figure 6**

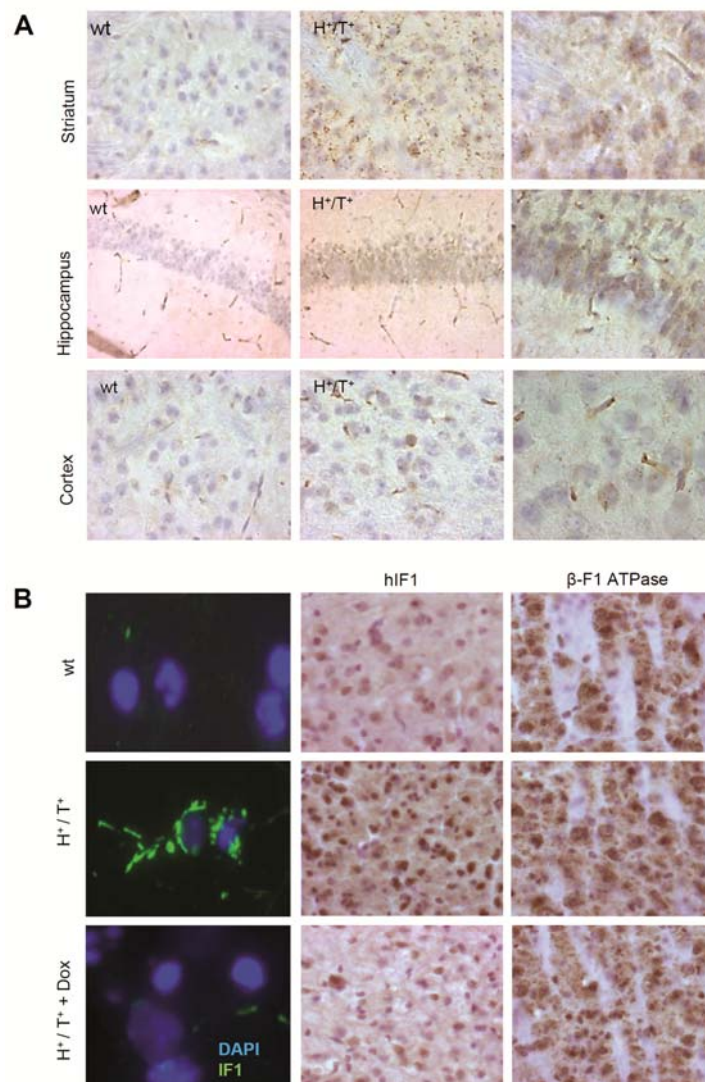


**Figure 7**

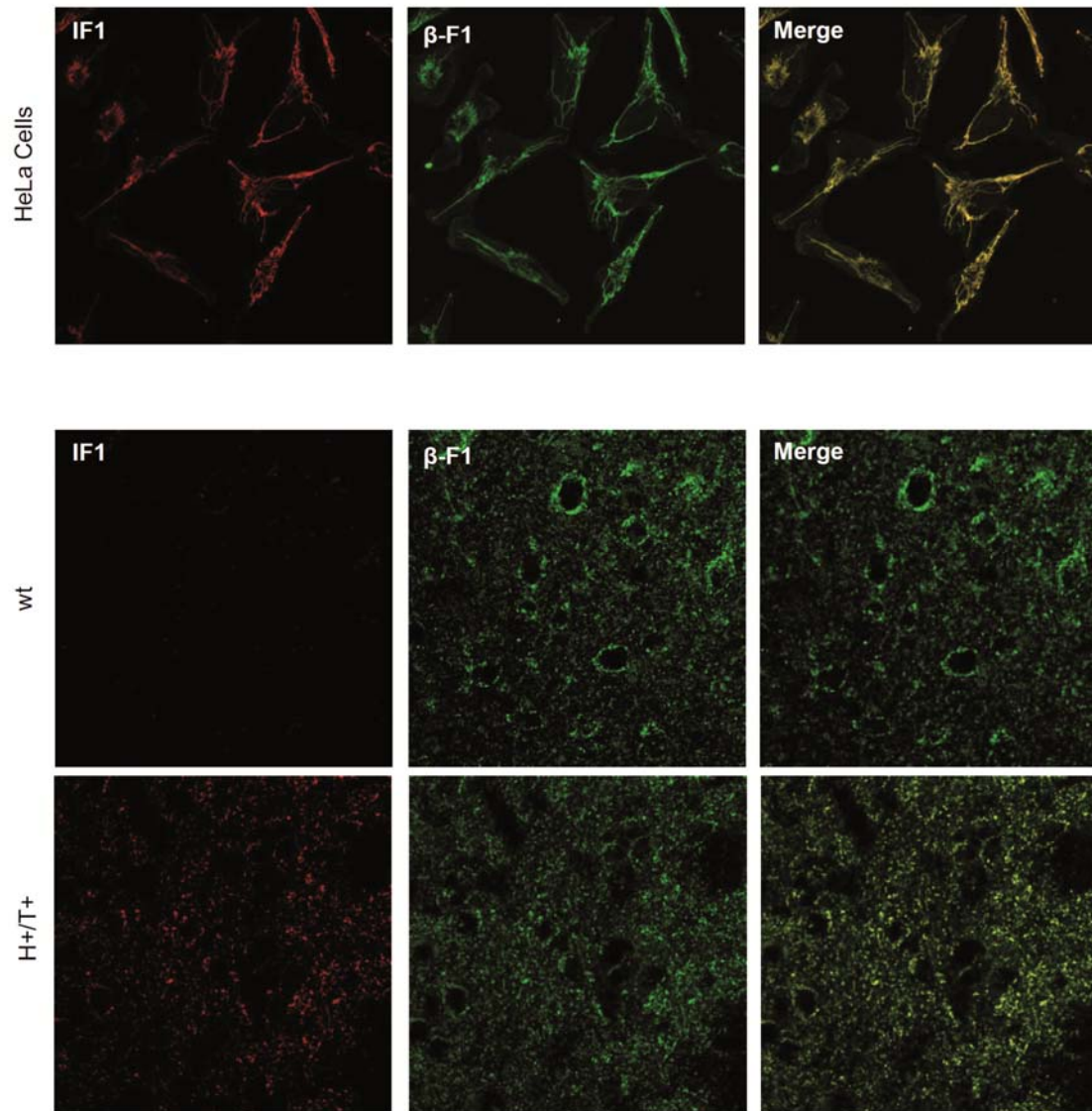


## Supplementary Information.

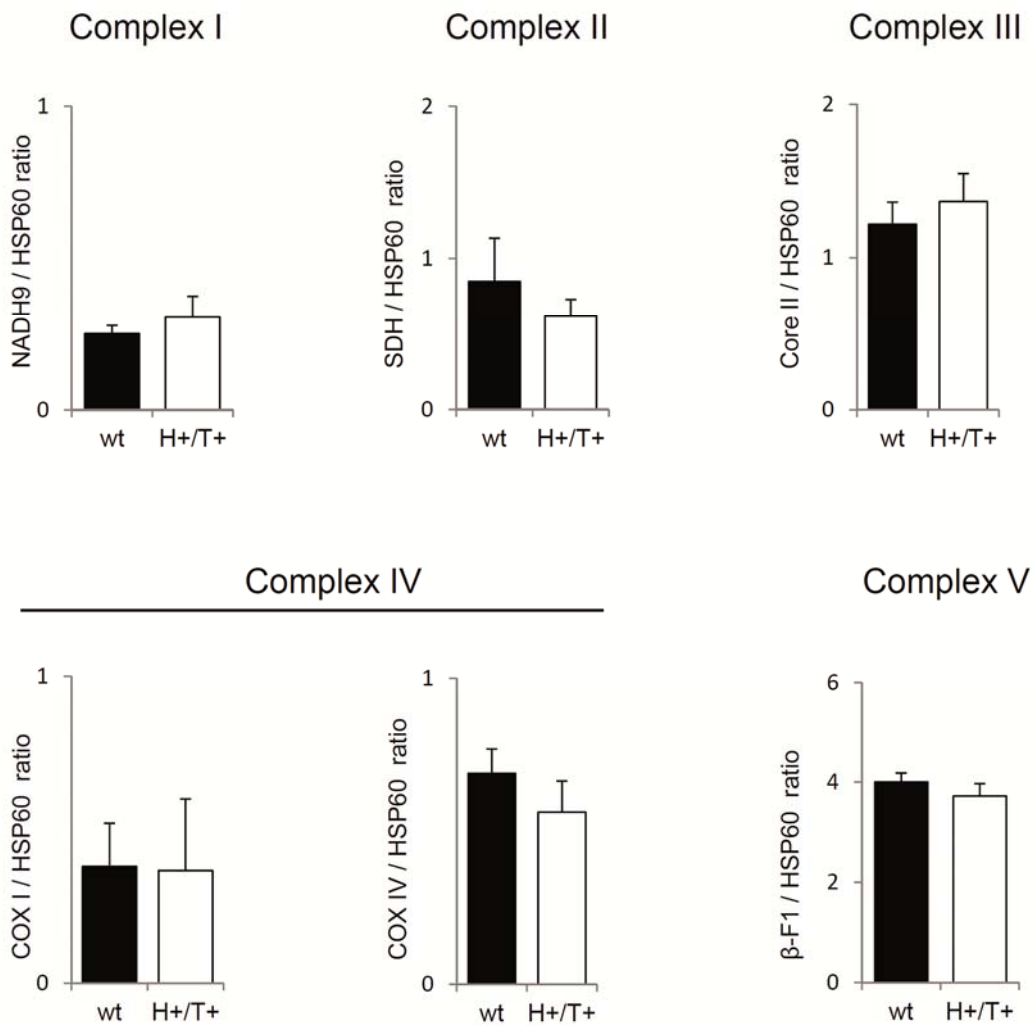
### Supplementary Figures.



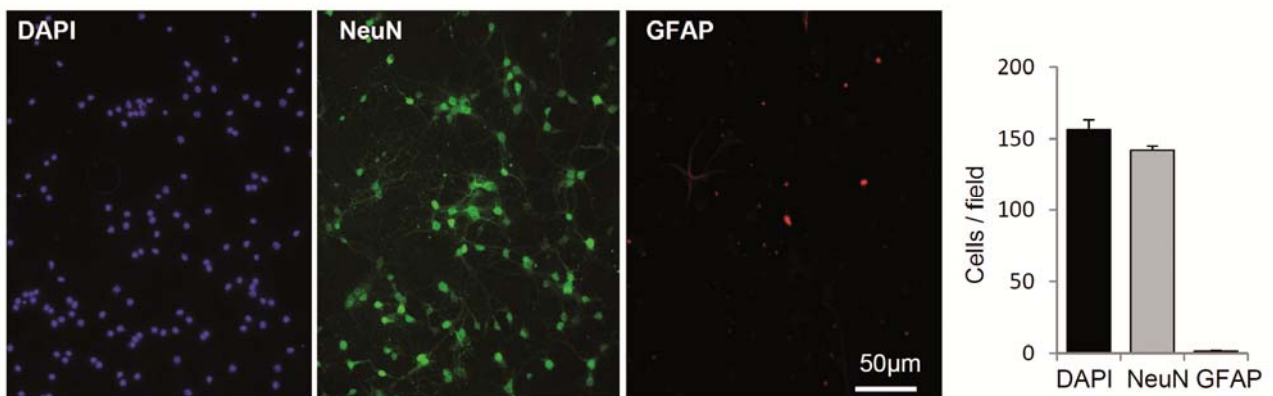
**Figure S1.** (A) Immunohistochemistry of hIF1 in brain striatum, hippocampus and cortex of control (wt) and hIF1 expressing (H<sup>+</sup>/T<sup>+</sup>) mice. Magnification 40x (first and second columns) and 63x (third column). (B) Immunofluorescence (first column) and immunohistochemistry of hIF1 and  $\beta$ -F1-ATPase in the brain of control (wt) and hIF1 expressing (H<sup>+</sup>/T<sup>+</sup>) mice. Note that the oral administration of doxycycline abrogates the expression of hIF1 in H<sup>+</sup>/T<sup>+</sup> mice. Magnification 63x (first column) and 40x (second and third columns).



**Figure S2.** hIF1 is localized in mitochondria. Upper panels, HeLa cells were transfected with the pCMV-SPOR6-H49K plasmid and processed for immunofluorescence microscopy for hIF1 (red) and  $\beta$ -F1-ATPase ( $\beta$ -F1, green). Immunohistochemistry for hIF1 (red) and  $\beta$ -F1-ATPase ( $\beta$ -F1, green) in brain cortex of control (wt, middle panel) and H<sup>+</sup>/T<sup>+</sup> (lower panel) mice. Magnification 40x (upper panel) and 20x (middle and lower panel). Note that hIF1 is only expressed in neurons of H<sup>+</sup>/T<sup>+</sup> mice whereas  $\beta$ -F1-ATPase is present in glia and neurons of both phenotypes.

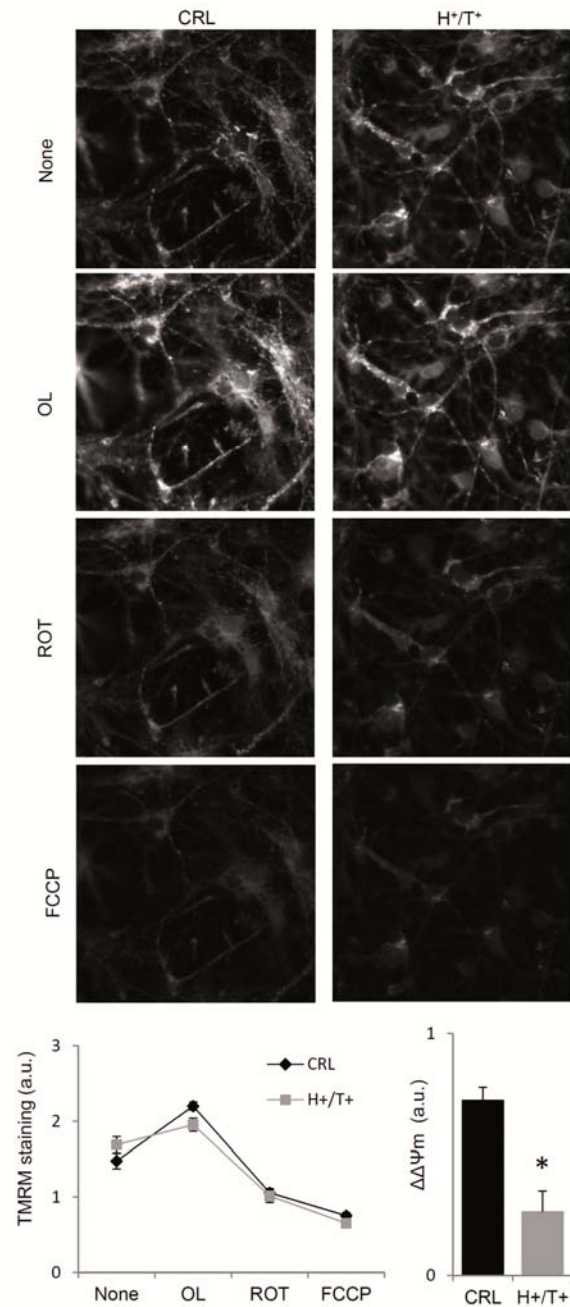


**Figure S3.** Quantification of the expression of OXPHOS proteins. Fractionated proteins were blotted against heat-shock protein 60 (HSP60), and mitochondrial complexes I (NADH9), II (SDH), III (Core II), IV (COXI and COX IV) and V ( $\beta$ -F1) in total brain extracts of wt and H+/T+ mice as shown in Fig. 1C. The data shown are mean  $\pm$  SEM of 3 experiments assayed in duplicate.

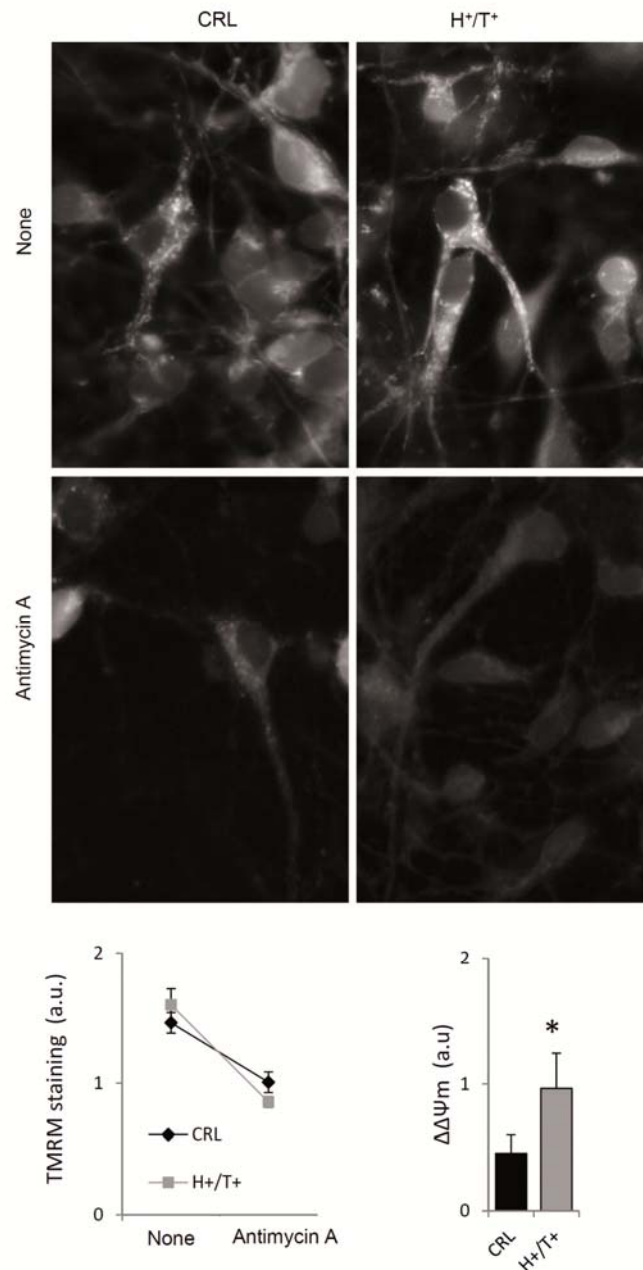


**Figure S4.** Nine days after seeding, the cultures revealed that they were mainly composed of neurons. Immunocytochemistry for the neuronal marker NeuN (green) and the astrocyte marker GFAP (red) in primary cultures of cortical neurons. The nuclei were stained with DAPI (blue). Histograms show the quantification of the number of each cell type per field. Magnification 10x. The data shown are mean  $\pm$  SEM of 7 fields.

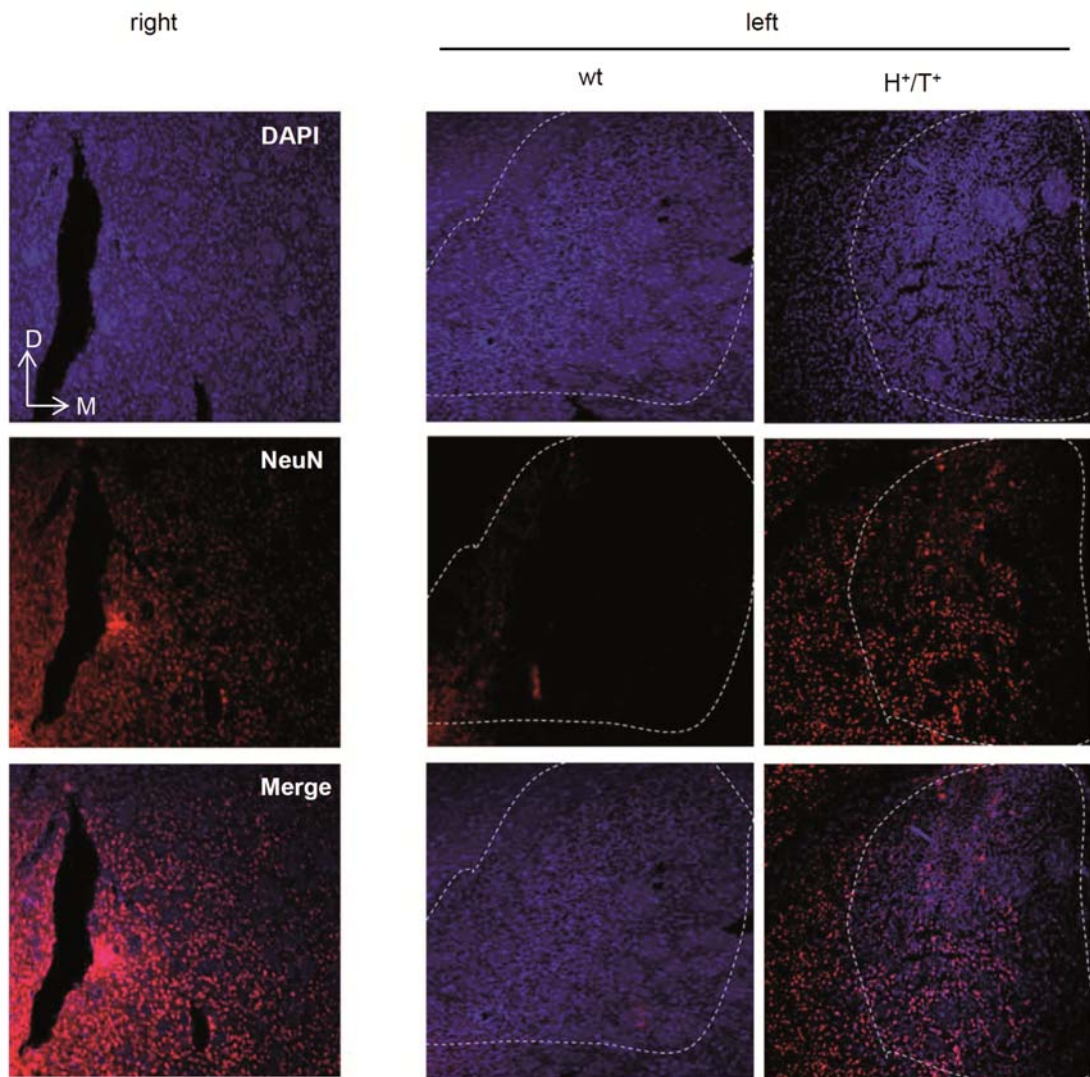




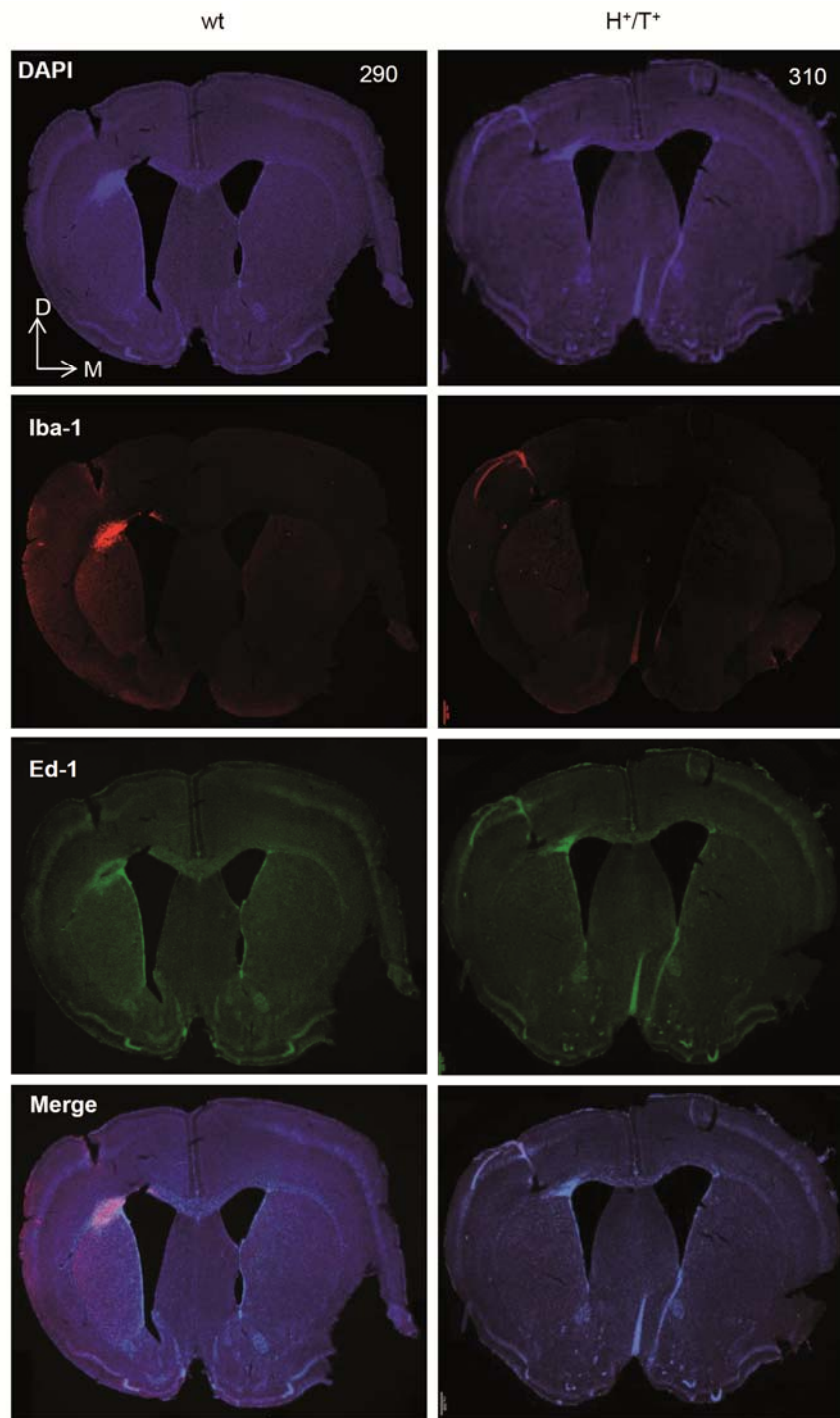
**Figure S5.** *In vivo* staining of TMRM<sup>+</sup> charged mitochondria from 9-10d primary cultures of cortical neurons derived from control (CRL) and H<sup>+</sup>/T<sup>+</sup> embryos. Images and graph represent the sequential cytofluorometric measurements of mitochondrial membrane potential (TMRM staining,  $\Delta\Psi_m$ ) in basal condition (None), after addition of 6 $\mu$ M oligomycin (OL), 1 $\mu$ M rotenone (ROT) and finally 5 $\mu$ M FCCP in the same field. Histograms show the quantification of  $\Delta\Psi_m$  differences between OL treated cells and basal condition. Magnification 40x. The data shown are mean  $\pm$  SEM of 15 fields per condition. \*,  $p < 0.05$  when compared to control by Student's t test.



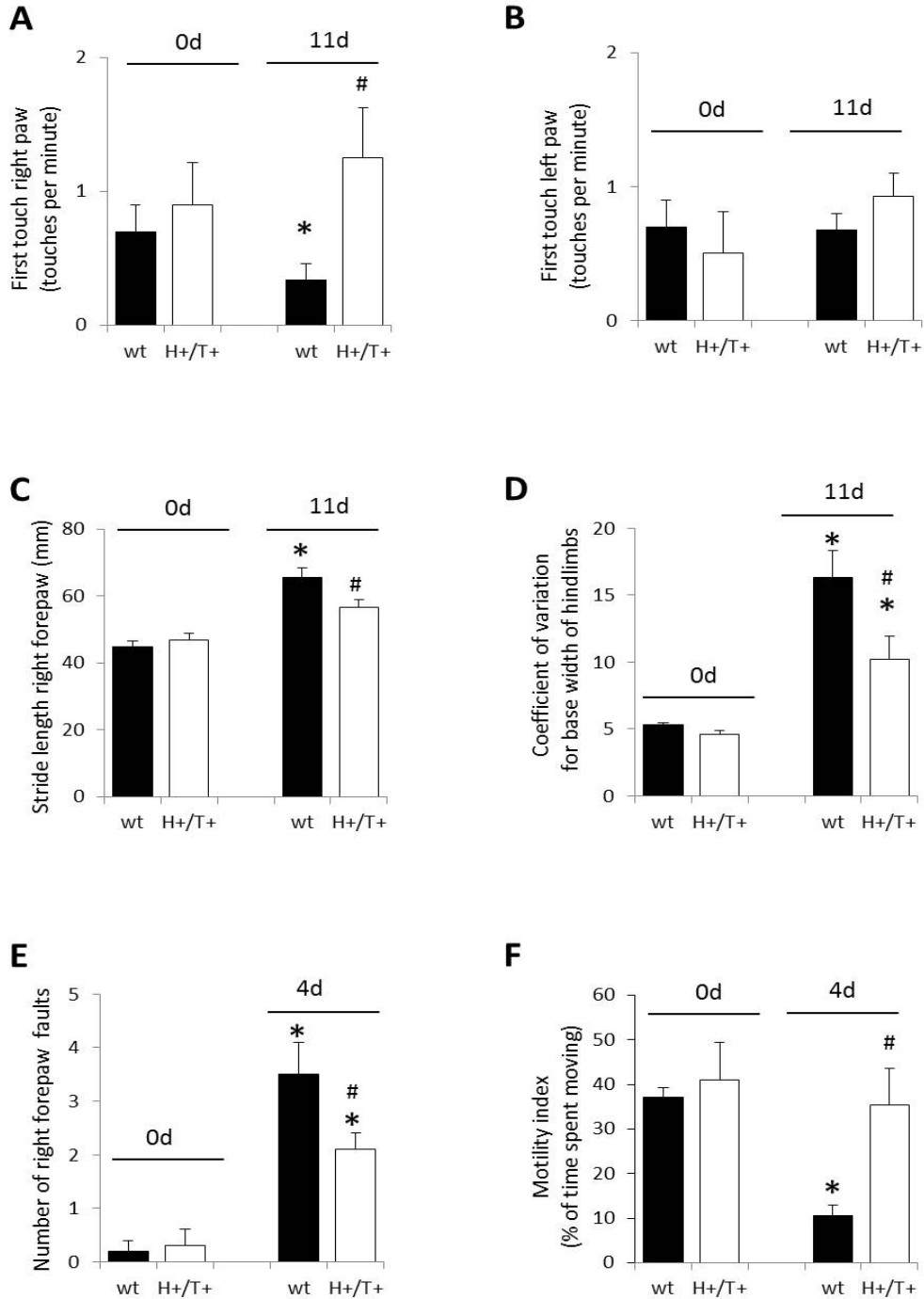
**Figure S6.** *In vivo* staining of TMRM<sup>+</sup> charged mitochondria from 9-10d primary cultures of cortical neurons derived from control (CRL) and  $H^+/T^+$  embryos. Images and graph represent the sequential cytofluorometric measurements of mitochondrial membrane potential (TMRM staining,  $\Delta\Psi_m$ ) in basal condition (None) and after the addition of 1 $\mu$ M antimycin A. Histograms show the quantification of  $\Delta\Psi_m$  differences between basal condition and antimycin treated cells. Magnification 40x. The data shown are mean  $\pm$  SEM of 15 fields per condition. \*,  $p < 0.05$  when compared to control by Student's t test.



**Figure S7.** Immunohistochemistry for the neuronal marker NeuN (red) in right (non-damaged) and left (damaged) brain hemispheres of control (wt) and hIF1 expressing ( $H^+/T^+$ ) mice. The nuclei have been stained with DAPI (blue). Magnification 10x. Note that at 20 days after surgery the striatum has already started to degenerate and the left hemisphere of control mice showed no NeuN expression in the focus of the lesion. In contrast, visible NeuN-staining was observed in  $H^+/T^+$  mice indicating the partial protection from cell death exerted by hIF1. D, dorsal; M, medial.

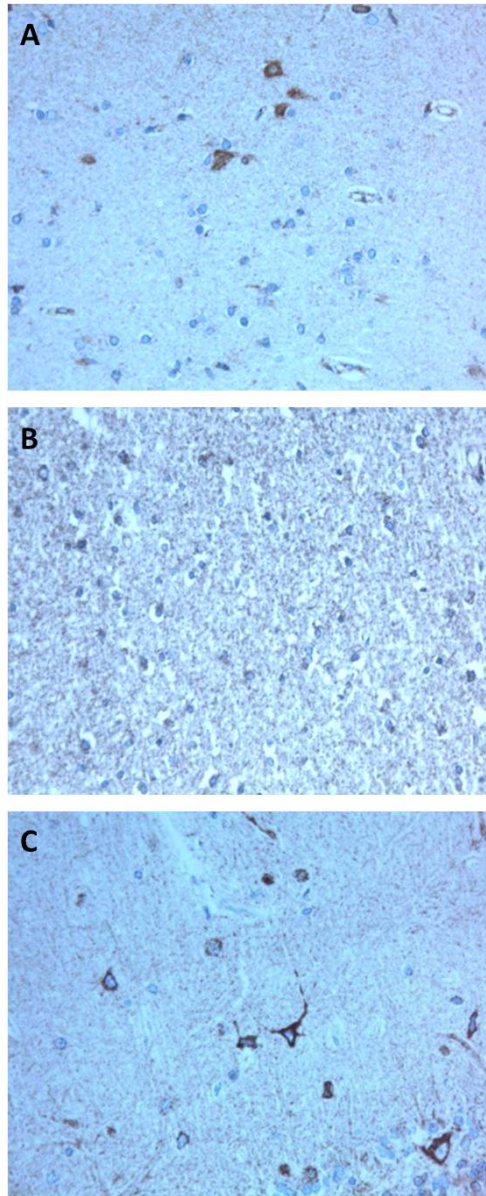


**Figure S8.** Representative staining of DAPI (nucleus, blue), Iba-1 (microglia, red) and Ed-1 (macrophage, green) antibodies in coronal slices of the brain in control (wt) and H<sup>+</sup>/T<sup>+</sup> mice three weeks after surgery. Magnification 2.5x. Note the minor recruitment of inflammatory cells in the brain of hIF1 expressing mice.



**Figure S9.** Locomotor evaluation indicates better performance in hIF1 expressing mice. Neurological evaluation in control (wt, closed bars) and hIF1 expressing ( $H^{+}/T^{+}$ , open bars) mice is shown. Cylinder test (**A** and **B**), foot print analysis (**C** and **D**) and grid test (**E** and **F**) before (0 d) and after four or eleven days (4 d, 11 d) post-surgery. Bars are the mean  $\pm$  SEM. of ten animals. (**A**) Represents the number of the “first touch” per minute using the right paw, which is contralateral to the brain lesion while (**B**) shows

the touches of the “first touch” per minute using the ipsilateral paw. **(C)** Stride length right forepaw is reduced after lesion in  $H^+/T^+$  mice when compared to control (wt) animals. **(D)** Gait variability for base width of hindlimbs studied using the coefficient of variation. **(E)** Number of contralateral paw slips through the grid is shown at 4 days post-surgery. **(F)** Motility index was strongly diminished in control (wt) animals. **(A-F)** \*,  $P < 0.05$  when compared to control at day 0. #,  $P < 0.05$  when compared to control at day 4 or 11 post-surgery.



**Figure S10.** Immunocytochemistry of hIF1 in human cerebral cortex (**A**, **B**) and cerebellum (**C**) sections. (**A**) Cortico-subcortical area showing positive neurons and negative astrocytes. (**B**) White matter. Negative immunolabelling for astrocytes and oligodendrocytes. (**C**) Positive immunostaining in basket cells of the molecular layer. Magnification 63x. Other hIF1 positive neuronal types are: neurons from the diencephalic, thalamic, hypothalamic and mesencephalic nuclei, lateral and medial corpus geniculatum, motor and sensitive brain-stem nuclei, inferior olives, Clarke columns and motor and sensitive neurons from the spinal cord (data no shown).

**Supplementary Videos 1, 2, 3 and 4.** Grid test in control mice 9, 290, 304 and 305 at 11 days post-surgery.

**Supplementary Videos 5, 6, 7 and 8.** Grid test in hIF1 expressing mice 296, 312, 345 and 346 at 11 days post-surgery.



## **Supplementary Materials and Methods.**

**Western Blot and Protein carbonylation antibodies.** The primary monoclonal antibodies developed in our lab and used in this study were: anti-HSP60 (1:5,000), anti-NADH-9 (1:1,000), anti- $\beta$ -F1-ATPase (1:20,000), anti-LDH-A (1:1,000), anti-GAPDH (1:20,000) and anti-PKM2 (1:1,000) (Acebo et al., 2009). The monoclonal antibody specifically recognizing the human (Sanchez-Cenizo et al., 2010) and mouse (Molecular Probes) IF1 proteins were used at 1:200 dilution. Other antibodies used were: anti- $\beta$ -actin (1:20,000), anti-tubulin (1:5,000) and anti-catalase (1:5,000) from Sigma-Aldrich; anti-SDH (1:1000) from Life Technologies; anti-Complex III subunit Core 2 (1:1,000), anti-COXI (1:1,000), anti-COXIV (1:1,000) and anti-SOD1 (1:1,000) from Abcam; anti-SOD2 (1:5,000) from Santa Cruz Biotechnology, Inc.; anti-PAR (1:1000) from Enzo Life Science Inc.; anti-I $\kappa$ B $\alpha$  (1:1,000), anti-Akt (1:1,000), anti-p-Akt (1:1,000), anti-p-p70S6K (1:1,000), anti-Bcl-xL (1:1,000) and anti-Bcl-2 (1:1,000) from Cell Signaling Technology Inc. Peroxidase-conjugated anti-mouse, anti-goat or anti-rabbit IgGs (Nordic Immunology; 1:3,000) were used as secondary antibodies.

For the determination of protein carbonylation, dinitrophenylhydrazine (DNPH) derivatization was carried out on 20  $\mu$ g of proteins derived from brain or neuronal extracts. Samples were fractionated on SDS–12% PAGE. The antibodies used were rabbit anti-DNP (1:150) and goat anti-rabbit IgGs (1:300). The blots were revealed using the ECL<sup>®</sup> reagent (Amersham Pharmacia Biotech). The intensity of the bands was quantified using a Kodak DC120 digital camera and the Kodak 1D Analysis Software.

## **Supplementary References.**

Acebo, P., Giner, D., Calvo, P., Blanco-Rivero, A., Ortega, A.D., Fernandez, P.L., Roncador, G., Fernandez-Malave, E., Chamorro, M., and Cuezva, J.M. (2009) Cancer abolishes the tissue type-specific differences in the phenotype of energetic metabolism. *Transl Oncol* **2**: 138-145.

Sanchez-Cenizo L, Formentini L, Aldea M, Ortega AD, Garcia-Huerta P, Sanchez-Arago M, Cuezva JM (2010) Up-regulation of the ATPase inhibitory factor 1 (IF1) of the mitochondrial H<sup>+</sup>-ATP synthase in human tumors mediates the metabolic shift of cancer cells to a Warburg phenotype. *J Biol Chem* 285: 25308-25313