

**The role of glutamate pyruvate transaminase 2
(GPT2) in neurometabolism and molecular
mechanisms of GPT2 Deficiency**

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INTRODUCTION

My thesis work has focused on the contribution of the mitochondrial enzyme glutamate pyruvate transaminase 2 (GPT2) to neurometabolism. The Introduction will begin with the advent of my work on GPT2 in the context of its associated neurological disease, GPT2 Deficiency. The following sections will introduce metabolic pathways related to GPT2 as well as concepts that I think are crucial to understanding the function of GPT2 in the physiology of the nervous system. The last section of the Introduction will briefly outline each chapter in the thesis.

In 2016, Dr. Eric M. Morrow's laboratory discovered autosomal recessive loss-of-function mutations in *GPT2* that cause postnatal microcephaly, intellectual disability and progressive spastic paraplegia in humans (Ouyang et al., 2016). *GPT2* encodes for mitochondrial glutamate pyruvate transaminase, also known as alanine aminotransferase 2, that reversibly transfers an amino group from glutamate to pyruvate forming alanine and alpha-ketoglutarate (Figure 1.1). Following the clinical presentation of one of the pedigrees by Rajab and colleagues (Rajab et al., 2006), Ouyang and co-workers presented two large kindreds with recent shared ancestry from Pakistan and Sultanate of Oman. The LOD scores linked the disease to 16q11.2 and Sanger sequencing of *GPT2* confirmed the mutation in the two pedigrees. Since then, several more kindreds with *GPT2* mutations have been identified (Baytas and Morrow, 2018; Binaafar et al., 2020; Celis et al., 2015; Hengel et al., 2018; Kaymakcalan et al., 2018; Lobo-Prada et al., 2017; Ouyang et al., 2019; Ruaud et al., 2021). The full list of mutations along the *GPT2* gene sequence is given in Figure 1.2. For a full detailed clinical presentation, please refer to the Results of Chapter 2.

Conceptually, our investigations on GPT2 and its role in neurometabolism starts with the human neurological developmental disease as these monogenic disorders have been very useful in elucidating basic mechanisms of growth and maintenance of the nervous system. While this may be viewed as reductionist given the vast metabolic networks with hundreds of enzymes, the specific contribution of GPT2 may underlie critical metabolic mechanisms of cellular growth and energetics that have been left undiscovered in the nervous system. This perspective is relevant to why we care about this particular metabolic enzyme especially when the golden age of biochemistry has produced so prolifically a vast literature on metabolism for decades. The answer, as in any translational science, comes two-fold. On one hand, the questions that arise with the function of this protein are of great importance to the health and maintenance of neuronal cells. For example, the question of how synaptic glutamate release is regulated is fundamental to proper functioning of the nervous system as it not only forms the basis of neurotransmission but also that of energy homeostasis in the cell. Glutamate is an excellent carbon source for tricarboxylic acid cycle intermediates (Hertz et al., 2007; Kovacevic, 1971; McKenna, 2007; Westergaard et al., 1995) and has one of the highest P/O ratios, that is the amount of esterification of inorganic phosphate (i.e. formation of ATP) per oxygen atom consumed (Case and Mc, 1951; Milstein et al., 1968). This suggests that glutamate is a major endogenous energy substrate. Metabolic processes that handle glutamate availability have not been studied closely with modern genetic tools and further investigation will allow for a better understanding of neurometabolism. On the other hand, we care about the GPT2 function because dysregulation of metabolic pathways related to GPT2, such as macromolecule synthesis and energy balance, have

been implicated in neurodegenerative diseases including Alzheimer's and amyotrophic lateral sclerosis (ALS). Studying the role of GPT2 in neurometabolism may probe into pathophysiology of not only GPT2 Deficiency but that of other more common neurodegenerative diseases.

Importantly, the metabolic investigations have only recently focused on the GPT2 protein. However, the focus has been centered on cancer or liver metabolism (Caiola et al., 2020; DeBerardinis et al., 2008; Hao et al., 2016; Kim et al., 2019; Tan et al., 2017) and has abandoned the nervous system and the relevance of GPT2 to neuronal growth and maintenance. In the following chapters, you will find questions posed regarding the role of GPT2 in neurometabolism along with their putative answers. Figure 1.4 gives a summary of the overarching questions asked in this work and the associated chapters wherein results are presented. The same figure of questions is available with overall answers in the Conclusion chapter.

The following sections in the Introduction provide background information and literature on GPT2 and the related metabolic pathways, particularly in the context of the nervous system.

GPT2 and transamination

GPT2 and its paralog GPT1 are part of the class I pyridoxal 6-phosphate-dependent aminotransferases which also include glutamate oxaloacetate aminotransferase (aspartate aminotransferase) among other transaminases. Transamination, the collective process for the chemical reaction of transferring an amino group, has seen much attention

since Krebs (Krebs, 1953), and has been shown to be critical for a variety of metabolic processes including synthesis and degradation of amino acids, replenishment of the tricarboxylic acid (TCA) cycle intermediates, nitrogen balance and glucose-alanine cycle. Transamination usually involves glutamate and alpha-ketoglutarate along with an amino acid and its corresponding alpha-keto acid. Historically, GPT enzymes have been studied as biomarkers of liver toxicity as damaged hepatocytes release GPT enzymes into the bloodstream (Karmen et al., 1955; Yang et al., 2009). Studies regarding their role in cellular growth particularly in the cancer field had to wait for decades.

***GPT2* and *GPT1*: where are they expressed?**

Humans and mice have two isozymes (isoforms of enzymes that carry out the same reaction), human *GPT2* on chromosome 16, mouse *Gpt2* on chr. 8 and human *GPT1* on chr. 8, mouse *Gpt1* on chr. 15 . Human *GPT2* is prominently expressed in muscle, fat, kidney, brain and liver and *GPT1* is expressed in kidney, liver and fat tissues (Yang et al., 2002). Murine expression patterns of *Gpt2* and *Gpt1* have been found to be similar to their human counterparts (Jadhao et al., 2004). *GPT2* protein contains a mitochondrial localization sequence and is carried to the mitochondria whereas *GPT1* lacks this signal and resides in the cytoplasm (Meton et al., 2004; Ouyang et al., 2016). Most important distinction between *GPT2* and *GPT1* in humans is that *GPT2* is present in the brain tissue and *GPT1* appears to be completely absent both at the level of protein (as determined by immunohistochemistry and western blotting) and mRNA (Hodge et al., 2019; Kang et al., 2011; Lindblom et al., 2007). However, expression patterns in different cell types either in the nervous system or other systems have not been studied.

Evolution of *GPT2* or *GPT1* genomic sequences have not been well studied; however the mutations in human *GPT2* that lead to GPT2 Deficiency disease were found to be in protein residues that have been well conserved in mammals (Celis et al., 2015; Ouyang et al., 2016). From *E. coli* to plants to humans, glutamate pyruvate transaminases have been shown to be important for alanine synthesis, nitrogen balance and regulation of glutamate, pyruvate and alpha-ketoglutarate (Escalera-Fanjul et al., 2017; Kim et al., 2010; Xu et al., 2017). Amusingly, recent evidence suggests that there is an upregulation of *Gpt2* in the evolution of venom glands of snakes (Barua and Mikheyev, 2021).

GPT2 in the tricarboxylic acid cycle metabolism

As can be seen immediately in the reaction, catalysis by GPT2 results in a net production of a tricarboxylic acid (TCA) cycle intermediate, alpha-ketoglutarate (Figure 1.1A). TCA cycle enzymes such as aconitase have the critical role of cycling TCA intermediates that produce reducing equivalents, NADH and FADH₂, which are used to make ATP via the electron transport chain. The same TCA cycle intermediates are also consumed to synthesize amino acids, fatty acids and nucleotides which in turn form macromolecules that help the cell grow. Therefore, there is always a need of external input toward the TCA cycle intermediates to ensure its continuity of the metabolic support for the cell. Hans Kornberg coined the term *anaplerotic reactions* to mean metabolic routes of carbon sources channeling into the TCA cycle (Kornberg, 1966). Kornberg used his term to mean pathways producing TCA cycle intermediates (e.g. pyruvate or acetate being a fuel source into the TCA cycle), and over time the term anaplerotic reaction came to mean a reaction resulting in the net synthesis or flux into the

TCA cycle (Owen et al., 2002). The following table lists of all known anaplerotic enzymes/processes (including preferred direction of the reaction, co-factors used, predominantly expressing cell types and any associated diseases) that I was able to curate (Table 1.1).

Deficiencies in almost all the anaplerotic reactions lead to neurological disorders with varying clinical features including psychomotor delay and intellectual disability. To date, much attention has been given to pyruvate carboxylase as the main anaplerotic enzyme in the mammalian brain. Pyruvate carboxylase is a biotin-dependent enzyme that fixes a CO₂ molecule to pyruvate yielding malate. In the mammalian brain, pyruvate carboxylase is expressed exclusively by glial cells (particularly astrocytes and oligodendrocytes) (Yu et al., 1983) and neither protein expression of this enzyme nor pyruvate carboxylation have been shown to occur in neurons. Astrocytes are known to give metabolic support for the neurons by releasing growth factors such as BDNF, GDNF and NGF as well as TCA cycle intermediates such as malate and citrate that are readily taken up by neurons (Westergaard et al., 1994). However, it is unlikely that neurons do not have indispensable intracellular mechanisms to replenish their own TCA cycle. Historically, the school of thought revolving around astrocytes as the main metabolic support for neurons may be responsible for downplaying the metabolic capabilities of neuronal cells. Only recently, metabolic flexibility in neurons has seen more attention and the role of anaplerotic processes in neurons have not been well studied (Divakaruni et al., 2017; Hohnholt et al., 2018).

The GPT2 reaction has indeed been studied in the context of the TCA cycle; however almost exclusively within the cancer field. GPT2 has been found to be critical

for tumorigenesis due to its anaplerotic ability of channeling glutamine into the TCA cycle. Yang and co-workers have shown that glutamine oxidation supports the TCA cycle and cell survival when mitochondrial pyruvate transport is blocked (Yang et al., 2014). While they do not look at GPT2 specifically, they attribute glutamine oxidation to transaminases. Hao and co-workers found that mutations in *PIK3CA* (phosphatidylinositol 3-kinase alpha) reprograms glutamine metabolism by upregulating GPT2 in colorectal cancer cells (Hao et al., 2016). These cells shift their metabolome to utilize glutamine more to resupply the TCA cycle intermediates due to upregulation of GPT2 protein with concomitant increases in alanine levels. Similarly, Smith and co-workers saw that in colon cancer cells, the GPT2 protein is upregulated to support glutamine oxidation into the TCA cycle and blocking *GPT2* translation by shRNAs makes the cancerous cells non-tumorigenic (Smith et al., 2016). Additionally, glutaminase, one of the major metabolic enzymes that convert glutamine into glutamate, allows for the first step for glutamine oxidation into the TCA cycle and when this enzyme is inhibited in HeLa cells, GPT2 protein is upregulated and increases cell viability (Kim et al., 2019). Overall, in the field of cancer, GPT2 has been found to be a major enzyme that replenishes TCA cycle intermediates and help the cells survive and grow.

There is other evidence that links GPT2 to the replenishment of the TCA cycle intermediates in several other biological entities. Strikingly, GPT2 forms 30% of all alpha-ketoglutarate in isolated rat liver mitochondria in State 4 respiration (in the absence of ADP) (Lenartowicz and Wojtczak, 1988). GPT2 has also been implicated in compensatory mechanisms to circumvent issues of TCA cycle metabolism. For example, the conditional knockout of pyruvate carboxylase in the mouse liver, alanine and alpha-

ketoglutarate levels increase and this has been attributed to GPT2 (Cappel et al., 2019). Interestingly, models of oxidative phosphorylation deficits induced by mitochondrial DNA mutations (Chen et al., 2018) and disrupted mitochondrial fusion dynamics (Motori et al., 2020) display increased levels of GPT2 and GPT1.

GPT2 and its role in replenishing the TCA have been not well studied in the context of the nervous system. More recently, McNair and co-workers find diminished entry of glutamate into the TCA cycle in synaptosomes (isolated nerve terminals) after deletion of glutamate transporter (GLT1) under the SynapsinI promoter (i.e. neuronal GLT1) and observe increased alanine levels. While they do not mention GPT2, they attribute this result to transaminases (McNair et al., 2019).

No other paper exists to this day that investigates the contributions of GPT2 to neurometabolism. To put GPT2 into the context of the nervous system, Figure 1.1B shows synaptosomes (isolated nerve terminals) and Figure 1.1C shows the metabolic interplay between glutamatergic, GABAergic neurons and astrocytes. (For a broader metabolic pathway map, refer to Figure 1.3). While currently the extent to which GPT2 is expressed in these cells is not known, GPT2 allows for glutamate oxidation into the TCA cycle along with other enzymes such as aspartate aminotransferase and glutamate dehydrogenase. Even though glutamate-glutamine cycle ensures that glutamine gets back into neurons to be made into glutamate again, glutamate itself can be used as a carbon source for all the three cell types shown in Figure 1.1C and one of the ways in which this may happen is via GPT2.

GPT2 in glutamate metabolism

Forty years ago (1980s), glutamate was finally accepted as the main excitatory neurotransmitter in the brain (Fonnum, 1984). To date, many enzymes and transporters have been identified and GPT2 has also seen attention with regard to glutamate metabolism. The role of GPT2 in glutamate metabolism in neuronal tissues has been the subject of study since Krebs's time (Haslam and Krebs, 1963). Haslam and Krebs found that in the presence of pyruvate, 90% of all amino nitrogen of glutamate is converted into alanine in guinea pig cerebral cortex slices *ex vivo* indicating that GPT2 reaction is a major route in glutamate oxidation into the TCA cycle.

However, since Krebs, many groups have given less role for GPT2 to play in synaptic glutamate availability. There are several lines of evidence that have led to this. Overall glutamate pyruvate transaminase activity (GPT1 and GPT2) doubles in the first three postnatal weeks in the developing rat brain, but it is still orders of magnitude lower compared to the activity of aspartate aminotransferase (Benuck et al., 1971; Wilbur and Patel, 1974). Glutaminase also shows higher activity than glutamate pyruvate transaminases in the rat brain (Salganicoff and Derobertis, 1965).

Since GPT2 is an equilibrium enzyme (i.e. the ratio of product to reactant concentrations is close to 1) (Krebs, 1953), alanine formation and glutamate formation are equally probable. However, due to relative concentrations and Michaelis constants of the substrates *in vivo*, the predicted direction of the GPT2 reaction is toward alanine formation (Erecinska and Silver, 1990; Miller et al., 1973; Ruscak et al., 1982). Furthermore, the velocity of ¹⁵N-alanine (heavy nitrogen labeled) formation from the precursor ¹⁵(amine)-N-glutamine was seven times higher than that of ¹⁵N-glutamate

formation from ^{15}N -alanine; indicating alanine formation is more likely in synaptosomes (Erecinska et al., 1994). GPT2 may still influence glutamate levels available for synaptic release, even though it may not play a direct role in its synthesis.

Nevertheless, new evidence may point to different directions in different cell types. Alpha-ketoglutarate is a very good precursor for glutamate (Peng et al., 1993; Peng et al., 1991; Shank et al., 1989) and loss of isocitrate dehydrogenase (which converts isocitrate into alpha-ketoglutarate) has been linked to defects in the TCA cycle and synaptic transmission (Ugur et al., 2017). Excitatory synaptic transmission continues even when the glutamate-glutamine cycle is inhibited in rat hippocampal slices (Kam and Nicoll, 2007). These results could be about transaminases, most likely aspartate aminotransferase and particularly hexose-phosphate amidotransferase as glucose is an excellent source of glutamate (Issop et al., 2018; Peng et al., 1993). It is yet unclear whether GPT2 plays a role in glutamate homeostasis at the synaptic site.

GPT2 in alanine metabolism

Another prominent pathway that GPT2 influences is alanine, a non-essential amino acid in mammals. Alanine is the second most frequent amino acid in the primary structure of proteins (Fasman, 1989) and may have been one of the first amino acids that formed in the primordial soup in the famous Muller-Urey experiment (Miller, 1953; Miller and Urey, 1959). So, what have we learned since the times of abiogenesis?

One of the most prominent physiological pathways involving alanine is the glucose-alanine cycle (Felig, 1973). Alanine is released into the bloodstream from all

over the body and reaches the liver to be made into pyruvate and therefrom into glucose via gluconeogenesis. Direct roles of GPT2 and GPT1 have been studied in connection with the glucose-alanine cycle. For instance, hepatic GPT2 protein is upregulated in gluconeogenic conditions including diabetes and downregulated by insulin (Honma et al., 2017; Qian et al., 2015). Recently, loss of mitochondrial pyruvate carrier 2 in the liver has been found to cause gluconeogenesis defects and the TCA cycle is compensated by pyruvate-alanine cycling via GPT2 (Bowman et al., 2016; McCommis et al., 2015).

More recently, alanine has been shown to activate AMP kinase, an important nutrient sensor in hepatic cells *in vitro* or *in vivo* (Adachi et al., 2018). Interestingly, Ron-Harel and co-workers found that T-cell activation depends on extracellular alanine and preferentially used for protein synthesis *in vitro*, possibly in agreement with activating AMP kinase to increase macromolecule synthesis (Ron-Harel et al., 2019). Finally, Rossiter and colleagues found that alanine deprivation in *GPT2*-null cancerous cell lines leads to reduced cell division and growth (Rossiter et al., 2021). These results put alanine in the forefront of protein synthesis and cellular growth in multiple systems.

In the context of the nervous system, alanine metabolism and transport have been studied in neurons and astrocytes. One of the most prominent findings is that alanine is preferentially released from neurons and taken up by astrocytes (Rae et al., 2003; Waagepetersen et al., 2000). This is consistent with the view that the predicted reaction is toward alanine formation given much higher concentrations of glutamate compared to alanine in neurons. One timely piece of caution regarding metabolism: no metabolite is isolated in biological contexts; every metabolite is linked to each other as nodes in a vast network. This may be why opposite findings regarding preferential release of alanine are

obtained from the same group in two papers that are seven years apart (Waagepetersen et al., 2000; Westergaard et al., 1993). It is also imperative that medium conditions are absolutely controlled since the metabolite compositions would have large impacts on the metabolome. However, whether alanine formation within neurons is critical for survival and growth of neurons is yet unexplored.

Brief Outline of Chapters in the thesis

Chapter 2 presents the neurological disease and the mouse model for the human GPT2 Deficiency that has been described and published for the first time (Ouyang et al., 2016). The autosomal recessive mutations in *GPT2* are shown to be loss-of-function in HeLa cells transfected with the constructs of the *GPT2* coding sequence bearing the mutation. Expression patterns of GPT2 via lacZ staining in the mouse brain are presented in Chapter 2 and differential expression of GPT2 and GPT1 in neurons and astrocytes *in vitro* is studied in Chapter 3. Mitochondrial and cytosolic localization of GPT2 and GPT1, respectively are confirmed in a variety of different cells and in subcellular fractionation of brain tissues in Chapters 2, 3,4 and 6.

To address metabolic mechanisms of GPT2 Deficiency, the consequences of GPT2 loss on the entire mouse brain metabolome are presented. Chapter 2 contains targeted metabolomics (the omics study of the metabolome) on the whole mouse brain and Chapter 3 investigates the progression of the altered metabolome across developmental timepoints. Following metabolomics, Chapter 2 investigates the effects of GPT2 loss on glutamine-dependent anaplerosis, i.e. replenishment of the TCA cycle

intermediates, in mouse embryonic fibroblasts *in vitro* and Chapter 3 expands that line of inquiry to neurons and astrocytes.

Chapter 3 continues with addressing the extent to which GPT2 is needed for neuronal growth and survival particularly as it relates to motor function and behavior. Specifically, we asked whether GPT2 is redundant in neurons or astrocytes. We investigate if cell specific deletions of *Gpt2* are sufficient to cause the phenotype using Cre drivers *in vivo*. In addition, as alanine formation is a critical function of GPT2, we ask whether alanine is a non-essential amino acid because of GPT2 and we perform deprivation assays in *Gpt2*-null neurons and astrocytes *in vitro*. Conversely, we test alanine supplementation *in vivo* for possible therapeutic effects in alleviating the *Gpt2*-null phenotype.

Chapters 3 and 5 explore various brain and spinal cord regions that may have specific vulnerability to the loss of GPT2. Pathological screening in the nervous system via immunohistochemistry to visualize cell counts, neurodegeneration markers and stains, and axonal projections may identify different neuronal circuits for which GPT2 function is essential. This in turn may explain the behavioral and motor phenotypes observed in the *Gpt2*-null mice and may be suggestive of the human phenotype. Chapter 3 explores mainly the spinal cord and cortical motor areas. Chapter 5 focuses on locus coeruleus (LC), the main noradrenergic supplier in the central nervous system implicated in the pathophysiology of Alzheimer's and Parkinson's Disease. We present evidence for a novel mechanism of neurodegeneration in LC.

Chapter 4 delineates the contribution of GPT2 to synaptic glutamate availability in the context of electrophysiology in hippocampal slices and synaptosomes, isolated

nerve terminals. Among a multitude of enzymes and reactions (44 reactions as curated from KEGG – Kyoto Encyclopedia of Genes and Genomes), the role of GPT2 in synaptic glutamate levels is unexplored and this investigation may identify a novel mechanism of regulation of the glutamate pool via a mitochondria-localized metabolic enzyme. This chapter also contains evidence for rescuing of metabolic defects associated with glutamate and TCA cycle metabolism in *Gpt2*-null mice by supplementing the TCA cycle.

Chapter 6 involves a cancerous cell line, KBM-7 based leukemia near-haploid cell lines, HAP1 cells, that carry *GPT2* mutations introduced by CRISPR (clustered regularly interspaced short palindromic repeats). This line of inquiry was pursued to determine if there are findings in cancerous cell lines that correlate with any of the phenotype seen with GPT2 Deficiency in other cell types and tissues. While the differences between the biological contexts are vast and unavoidable, this study may attribute a ubiquitous mechanism to the role of GPT2 in cellular growth.

Chapter 7, the Conclusion chapter, will attempt to give a summary and a broader picture of the results shown in the prior chapters.

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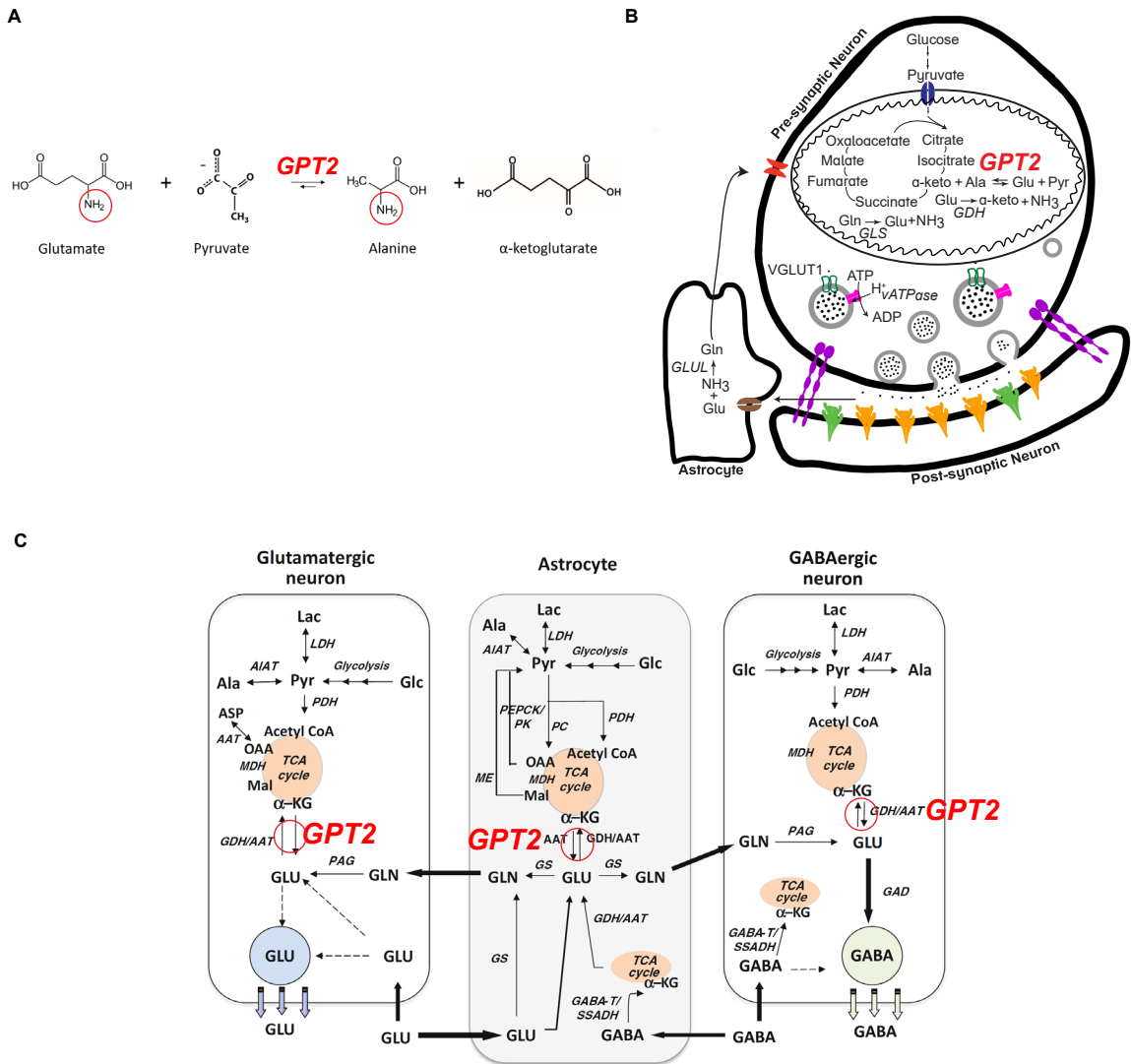


Figure 1.1 – Gpt2 and relevant metabolic pathways.

A. The reaction catalyzed by GPT2. It's a reversible reaction transferring an amino group (red circle) from glutamate to pyruvate yielding alanine and alpha-ketoglutarate. Note that the predicted direction of the reaction is toward alanine formation reflected in the arrow lengths.

B. Metabolic pathways relevant to Gpt2 and glutamate metabolism in synaptosomes (isolated nerve terminals) including pre-synaptic neuron, post-synaptic neuron and astrocytic components. GDH: glutamate dehydrogenase, GLS: glutaminase, GLUL: glutamine synthetase. **C.** Adapted from the first figure in (McKenna and Ferreira, 2016). GPT2 is added to the metabolic pathways along with GDH (glutamate dehydrogenase) and AAT (aspartate aminotransferase) noting the arrows in the reaction with a red circle. The authors omitted the mitochondrial isozyme of glutamate pyruvate transaminase but the cytosolic isozyme is denoted as A/AAT. Abbreviations: Ala: alanine, a-KG: alpha-ketoglutarate, ASP: aspartate, GABA-T: GABA aminotransferase, Glc: glucose, Glu: glutamate, GAD: glutamate decarboxylase, Gln: glutamine, GS: glutamine synthetase, Lac: lactate, LDH: lactate dehydrogenase, Mal: malate, MDH: malate dehydrogenase, OAA: oxaloacetate, PAG: phosphate-activated glutaminase, PEPCK: phosphoenolpyruvate carboxykinase, Pyr: pyruvate, PDH: pyruvate dehydrogenase, PK: pyruvate kinase, SSADH: succinic semialdehyde dehydrogenase. Copyright permission for panel C is granted from Elsevier.

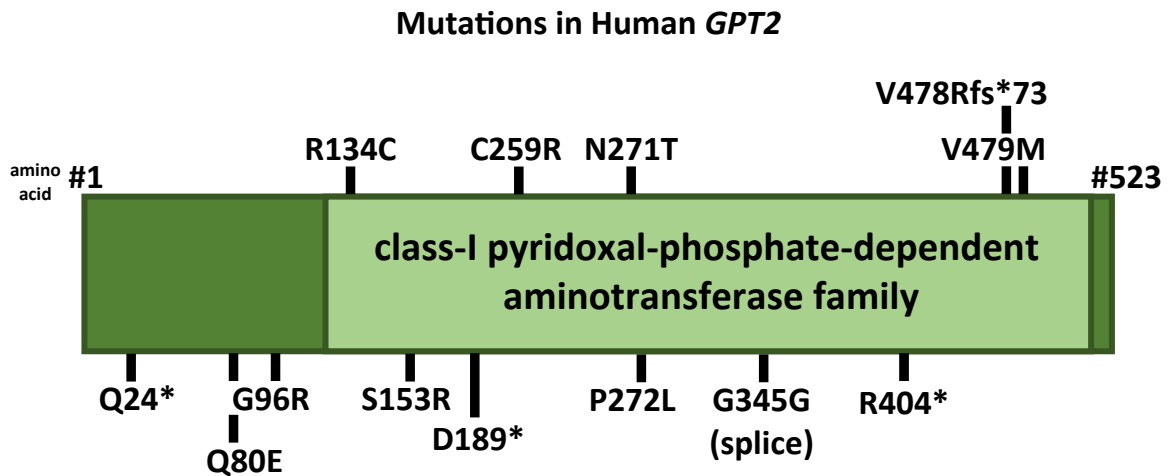


Figure 1.2 – Mutations in the human *GPT2* gene. Mutations in human *GPT2* gene. *Gpt2* belongs to the class-I pyridoxal-phosphate dependent aminotransferase enzyme family and the sequence that shows similarity within the members of the enzyme family is shown in lighter green. RefSeq number of *Gpt2*: NM_133443. Mutations are found in the following publications: S153R: (Celis et al. 2015); R404X, P272L: (Ouyang et al. 2016); R134C, V479M: (Kaymakcalan et al. 2018); Q24X: (Hengel et al. 2018); N271T, V478Rfs*73, C259R, G345G(splice), Q80E: (Ouyang et al. 2019); G96R: (Lobo-Prada et al. 2017), D189*: (Ruaud et al. 2021).

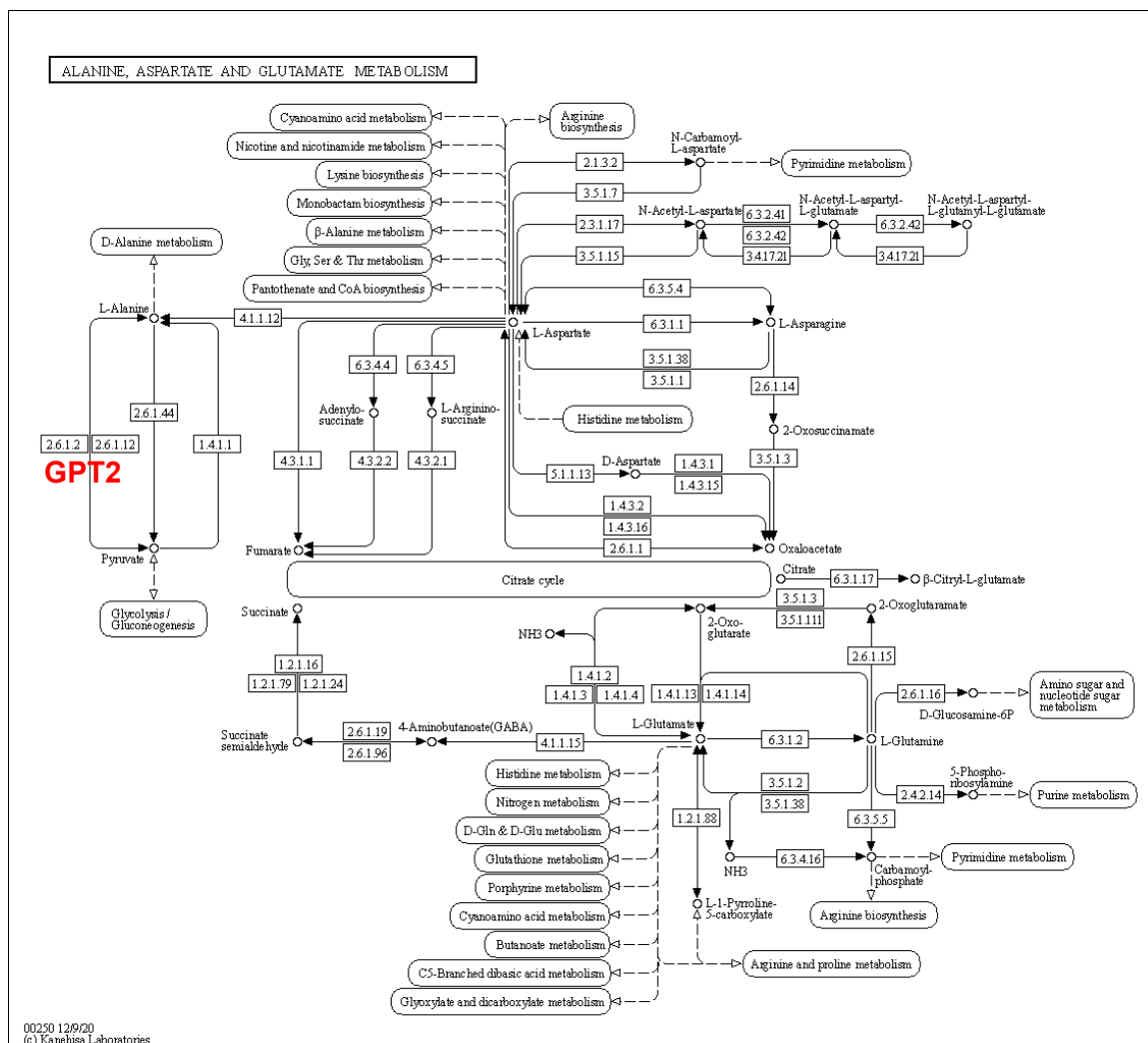


Figure 1.3 – KEGG: the Alanine, Aspartate and Glutamate Metabolism Pathway. **A.** Image taken from Kyoto Encyclopedia of Genes and Genomes (KEGG) (Kanehisa et al., 2020) showing Alanine, Aspartate and Glutamate metabolism and the related connections to other metabolic pathways (Pathway map no.: 00250). GPT2 is shown in red, the enzyme number: EC 2.6.1.2. Copyright permission granted from Kanehisa Laboratories.

ROLE OF GPT2 in NEUROMETABOLISM

GPT2 DEFICIENCY



Figure 1.4 – Questions asked regarding the role of Gpt2 in neurometabolism through the study of Gpt2 deficiency.

Table 1.1. – Reactions that result in net production of a TCA cycle intermediate – a list of Anaplerotic pathways.

Enzyme/Process	Reaction	Predicted preferred reaction	Additional Co-factors	Predominantly expressing Cell Type	Any Associated Diseases
Pyruvate carboxylase ¹	pyruvate + HCO ₃ ⁻ + ATP → oxaloacetate + ADP + Pi	forward	biotin, acetyl CoA, Mg ²⁺ , Mn ²⁺	glial	OMIM 266150: Pyruvate carboxylase deficiency (failure to thrive, intellectual disability, recurrent seizures, developmental delay, abnormal movements (spasticity, tremor, dyskinesia, hyperreflexia, Babinski sign))
Glutamate pyruvate transaminase 1/2/3	glutamate + pyruvate ↔ alanine + alpha-ketoglutarate	forward	pyridoxal 6-phosphate	???	OMIM 616281: GPT2 deficiency (postnatal microcephaly, intellectual disability, spastic paraplegia, hyperreflexia, hypertonia, wide-gait)
Glutamate dehydrogenase ³	glutamate + H ₂ O + NAD(P) ⁺ → alpha-ketoglutarate + NH ₃ + NAD(P)H + H ⁺	forward		neuronal/glial	OMIM 606762: Hyperactivation of GLUD1 (hypersaline hemolytic hypoglycemia, seizures)
Malic enzyme ^{4,5}	pyruvate + CO ₂ + NAD(P)H → malate + NAD(P) ⁺	reverse		neuronal (mitochondrial), glial (cytosolic)	
Phosphoenolpyruvate carboxylase ^{1,6}	phosphoenolpyruvate + HCO ₃ ⁻ → oxaloacetate + Pi	reverse	Co ²⁺ , Mg ²⁺ , Mn ²⁺	neuronal/glial	OMIM 261650: PCK deficiency (hypoglycemia, fatty liver, liver failure)
Adenylosuccinate lyase ⁷	adenylosuccinate → AMP + fumarate	forward		???	OMIM 103950: ADSL deficiency (failure to thrive, microcephaly, psychomotor delay, intellectual disability, autism, hyperreflexia, inability to walk, refractory seizures, spasticity, gait ataxia)
B-oxidation of fatty acids/cholesterol & Valine, isoleucine, threonine, methionine Degradation: methylmalonic acid mutase (final reaction) ⁸	→ → → → → → → → L-methylmalonyl CoA → succinyl CoA	forward	cobaltamide	neuronal	OMIM 251000: MMUT deficiency (failure to thrive, developmental delay, hypotonia, lethargy)
Phenylalanine, Tyrosine Degradation: fumaryl acetoacetase (final reaction) ⁹	→ → → → fumarylacetoacetate → fumarate + acetoacetate	forward	Ca ²⁺ , Mg ²⁺	glial (oligodendrocytes)	OMIM 276700: FAH deficiency (failure to thrive, episodic paralysis, episodic peripheral neuropathy)

¹ (Jitrapakdee et al., 2008), ² (Ouyang et al., 2016), ³ (Erecinska and Silver, 1990), ⁴ (Vogel et al., 1998), ⁵ (Hassel and Bråthe, 2000), ⁶ (Cruz et al., 1998), ⁷ (Spiegel et al., 2006), ⁸ (Ballhausen et al., 2009), ⁹ (Labelle et al., 1993).

Chapter 2: Mutations in mitochondrial enzyme GPT2 cause metabolic dysfunction and neurological disease with developmental and progressive features.

This Chapter contains the paper published in Proceedings of the National Academy of Sciences of the United States of America (PNAS) in 2016 by Qing Ouyang and co-workers. doi.org/10.1073/pnas.1609221113. My contributions were Figure 5 and supplementary figure 7, involving metabolomics in *Gpt2*-null whole brain and lacZ staining for *Gpt2* expression pattern in *Gpt2*-heterozygous mouse brains. The rest were conducted by Dr. Qing Ouyang in Dr. Eric Morrow's laboratory and Dr. Toko Nakayama, and clinicians involved in human patients with GPT2 Deficiency. For funding sources please refer to the Chapter.

Mutations in mitochondrial enzyme GPT2 cause metabolic dysfunction and neurological disease with developmental and progressive features

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Contributed by David E. Housman, June 22, 2016 (sent for review February 1, 2016); reviewed by Elizabeth M. C. Fisher and William C. Mobley

Mutations that cause neurological phenotypes are highly informative with regard to mechanisms governing human brain function and disease. We report autosomal recessive mutations in the enzyme glutamate pyruvate transaminase 2 (GPT2) in large kindreds initially ascertained for intellectual and developmental disability (IDD). GPT2 [also known as alanine transaminase 2 (ALT2)] is one of two related transaminases that catalyze the reversible addition of an amino group from glutamate to pyruvate, yielding alanine and α -ketoglutarate. In addition to IDD, all affected individuals show postnatal microcephaly and ~80% of those followed over time show progressive motor symptoms, a spastic paraplegia. Homozygous nonsense p.Arg404* and missense p.Pro272Leu mutations are shown biochemically to be loss of function. The GPT2 gene demonstrates increasing expression in brain in the early postnatal period, and GPT2 protein localizes to mitochondria. Akin to the human phenotype, Gpt2-null mice exhibit reduced brain growth. Through metabolomics and direct isotope tracing experiments, we find a number of metabolic abnormalities associated with loss of Gpt2. These include defects in amino acid metabolism such as low alanine levels and elevated essential amino acids. Also, we find defects in anaplerosis, the metabolic process involved in replenishing TCA cycle intermediates. Finally, mutant brains demonstrate misregulated metabolites in pathways implicated in neuroprotective mechanisms previously associated with neurodegenerative disorders. Overall, our data reveal an important role for the GPT2 enzyme in mitochondrial metabolism with relevance to developmental as well as potentially to neurodegenerative mechanisms.

GPT2 | intellectual and developmental disability | mitochondria | metabolomics | spastic paraplegia

Intellectual and developmental disabilities (IDDs) occur in 2% of people worldwide and rank first in the United States as a cause of lifelong disability (1). IDD can be accompanied by various associated features, including motor disability. Hereditary spastic paraplegia (HSP) is a unique form of motor disability that is characterized by progressive spasticity and weakness of the lower extremities (2). In addition, postnatal microcephaly may occur with IDD and complicated forms of HSP, and likely reflects failures in processes driving postnatal brain growth such as neuronal arborization, synaptogenesis, and gliogenesis (3).

In this study, we present the discovery of loss-of-function mutations in the gene encoding the enzyme glutamate pyruvate transaminase 2 (GPT2) in autosomal recessive IDD with postnatal microcephaly and motor findings consistent with progressive spastic

Significance

We report autosomal recessive mutations in the enzyme glutamate pyruvate transaminase 2 (GPT2) in a neurological syndrome involving intellectual disability, reduced brain growth, and progressive motor symptoms. We show that the mutations inactivate the enzyme. GPT2 catalyzes the reversible addition of an amino group from glutamate to pyruvate, yielding alanine and α -ketoglutarate. The GPT2 gene demonstrates expression in brain postnatally, and the protein localizes to mitochondria. As in humans, Gpt2-null mice exhibit reduced brain growth. Furthermore, mutant mouse brains show abnormal metabolite levels, including in pathways involving amino acid metabolism, the TCA cycle, and neuroprotective mechanisms. Our study identifies GPT2 as an important mitochondrial enzyme in disease that has general relevance to developmental and potentially to neurodegenerative mechanisms.

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The authors declare no conflict of interest.

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paraplegia. GPT2 [also known as alanine transaminase 2 (ALT2) or alanine aminotransferase 2 (ALAT2)] is one of two related enzymes that catalyze the reversible addition of an amino group from glutamate to pyruvate, yielding alanine and α -ketoglutarate. GPT2 and highly related GPT are among several transaminases that regulate critical metabolic processes, including amino acid metabolism and the tricarboxylic acid (TCA) cycle. Glutamate is also a substrate in the synthesis of glutathione, an important antioxidant in cells (4). We show that GPT2 is localized to mitochondria and is expressed at increasing levels in brain during early postnatal development corresponding to periods of circuit development.

Mitochondria play an essential role in neurons given the high energy demands of these cells, and mitochondria are particularly abundant at synapses, where they mediate synaptic growth, energetics, signaling, and protection (5). Mitochondrial dysfunction is involved in both human neurodevelopmental as well as neurodegenerative disease (6–8). The TCA cycle in mitochondria functions in both energy production as well as in biosynthetic processes. TCA cycle intermediates may be extracted for biosynthetic metabolism through a process termed cataplerosis, and TCA intermediates are replenished via anaplerosis (9).

In addition to identification of mutations in GPT2 in human neurological disease, we have developed a mouse model of *Gpt2* deficiency. Akin to the human phenotype, we see reduced brain growth in this mouse model. Metabolomics studies in *Gpt2*-null mouse brains reveal reduced TCA metabolites consistent with a defect in anaplerosis. We also identify metabolomic signatures reflecting abnormalities in amino acid metabolism, as well as in neuroprotective mechanisms previously implicated in neurodegenerative disease. Overall, our data support an important role for GPT2 in mitochondria-based metabolism and neurological disease with both developmental and progressive features.

Results

Clinical Analyses of Pedigrees with Intellectual Disability and Postnatal Microcephaly. As a contribution to understanding the genetic underpinnings of neurological disease, we have studied two large consanguineous kindreds with a neurodevelopmental condition. Affected members in families shown in Fig. 1A share a phenotype that includes intellectual disability with postnatal microcephaly and variable, progressive spasticity (see also ref. 10). In total, our studies included 14 affected individuals. All affected individuals

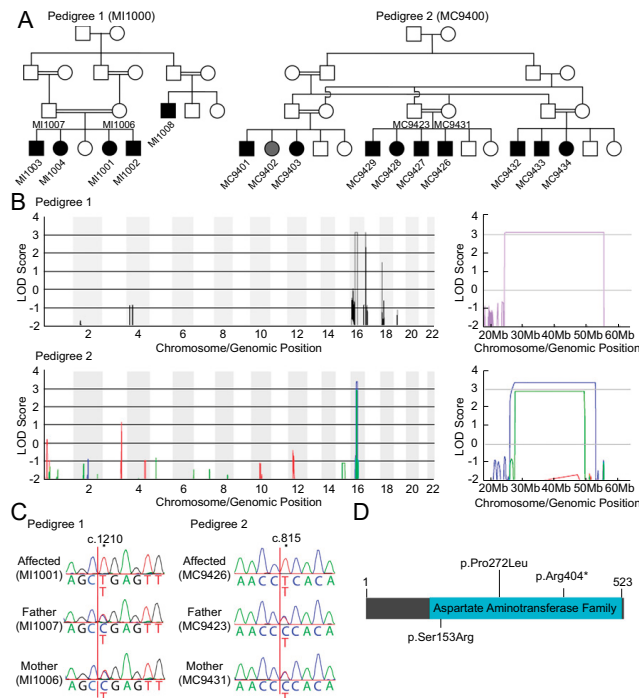


Fig. 1. Identification of *GPT2* mutations in large kindreds with recent shared ancestry affected by IDD with postnatal microcephaly. (A) Pedigree 1 (MI1000) is from Pakistan. Pedigree 2 (MC9400) is from the Sultanate of Oman. Filled symbols indicate affected individuals. Shaded symbol (MC9402) indicates a similarly affected individual, who was found not to have a homozygous *GPT2* mutation. We have described the clinical presentation of pedigree 2 (MC9400) in a prior publication (10). (B) Genome-wide LOD scores for pedigree 1 show a region of linkage on chromosome 16q11.2, with a maximum multipoint LOD score of 3.13. Linkage analysis of pedigree 2 was performed for each of the three branches. Branch 1 (red) did not show a region of statistically significant linkage given heterozygous individual MC9402 with phenocopy, whereas both branch 2 (blue) and branch 3 (green) indicate linkage to chromosome 16q11.2 with LOD scores of 3.38 and 2.90, respectively. Magnified LOD score graphs for chromosome 16q are shown on the *Right*. (C) Sanger sequencing of *GPT2* confirmed the identified mutations in pedigree 1 (c.1210C>T, p.Arg404*) and pedigree 2 (c.815C>T, p.Pro272Leu). Positions of mutations are according to NM_133443.3 (cDNA) and NP_597700.1 (protein). (D) Schematic diagram of conserved domains in *GPT2*. The positions of the mutations with a previously reported mutation (p.Ser153Arg) are shown (14).

were born after uneventful pregnancies without asphyxia. Head circumference was normal at birth for all seven individuals for whom data were available, but affected individuals subsequently developed microcephaly postnatally, ranging from 2.8 to 6.8 SDs below the mean (Table 1 and *SI Appendix, Table S1*). The majority (88%) of affected individuals were reported to be hypotonic during infancy. All 9 cases with data available (of 14 total cases) were able to walk by the age of 3 y. All had delayed speech and showed oral-motor dysfunction. Five (36%) had a history of seizures, with three (MC9426, MC9429, and MI1002) having been diagnosed with various types of epilepsy syndromes, including one with Lennox-Gastaut syndrome, and the other two individuals each reporting a single seizure episode. Full detailed clinical descriptions are provided in *SI Appendix, Table S1*.

The majority (83%) of the affected individuals showed subsequent difficulty in walking. Over time, motor examination was remarkable for hypertonia and hyperreflexia. In most cases (77%), lower extremities were more severely affected, thus presenting as spastic diplegia or spastic paraplegia. In some individuals, hand movements were clumsy, tremulous, and poorly coordinated. Results from brain imaging studies [computed tomography or magnetic resonance imaging (MRI)] were obtained for 10 individuals and showed no obvious structural malformation other than microcephaly, except for 1 individual who had reduced white matter volume and a thin corpus callosum (*SI Appendix, Fig. S1*).

Identifying *GPT2* Mutations by Linkage Mapping and Whole-Exome Sequencing. Pedigrees 1 and 2 showed strong linkage to a locus on chromosome 16q (Fig. 1*B*). In pedigree 1, genome-wide linkage analysis of the larger branch (affected individuals: MI1001, MI1002, MI1003, and MI1004) revealed a region of linkage on chromosome 16q with a maximum logarithm of odds (LOD) score of 3.13 (Fig. 1*B*). The region was delineated by SNP markers rs198188 to rs12917822 (chr16: 24,136,201–55,165,407). In pedigree 2, LOD scores were calculated for each of the three branches of the family separately due to complexity of the pedigree. Branches 2 and 3 showed evidence of linkage to the same region of chromosome 16q. The regions were delineated by SNP markers rs205162 to rs6498968 for branch 2 (chr16: 25,596,637–52,653,785) and rs17720179 to rs1567522 for branch 3 (chr16: 27,188,853–49,302,826), with maximum LOD scores of 3.38 and 2.91, respectively (Fig. 1*B*). In branch 1, two of the affected individuals (MC9401 and MC9403) showed linkage to this region.

Whole-exome sequencing (WES) of all affected individuals in pedigree 1 revealed a single shared homozygous, nonsense variant (c.1210C>T, p.Arg404*) in the *GPT2* gene (RefSeq NM_133443.3)

Table 1. Phenotypic features of 14 affected individuals with *GPT2* mutations

Phenotype	No. of positive cases	Frequency, %
Microcephaly	14/14	100
Postnatal microcephaly	7/7	100*
Intellectual disability	14/14	100
Hypotonia during infancy	7/8	88*
Oral-motor dysfunction	12/12	100*
Hyperreflexia	11/13	85*
Hypertonia	12/13	92*
Joint contractures	3/14	21
Ability to walk by age 3	9/9	100*
Subsequent deterioration in walking ability	10/12	83*
Spastic diplegia/paraplegia	10/13	77*
Seizures	5/14	36

*Based on cases with data available.

in the linkage interval. There were no other rare, loss-of-function mutations shared by all affected members of the pedigree in the interval or elsewhere in the genome. The homozygous *GPT2* gene variant was confirmed by Sanger sequencing and segregated with the disease in pedigree 1 (Fig. 1*C*). All members unaffected for microcephaly in the pedigree were heterozygous. The candidate variant was not present in the National Heart, Lung, and Blood Institute (NHLBI) Exome Variant Server or in dbSNP. In pedigree 2, using WES of three affected individuals (MC9401, MC9428, and MC9432), we identified a homozygous missense variant in the *GPT2* gene (c.815C>T, p.Pro272Leu) as the only shared candidate variant in the linkage interval (Fig. 1*C*). All affected individuals were homozygous, and no unaffected individuals were found to be homozygous. Individual MC9402, who showed a microcephalic phenotype, was heterozygous, and thereby likely represents a phenocopy. This p.Pro272Leu variant was not found in the NHLBI Exome Variant Server or in dbSNP, and was predicted to be damaging by PolyPhen-2 (11), SIFT (12), and Provean (13), suggesting its pathogenicity (*SI Appendix, Table S2*). Since our discovery of the mutations above, a single homozygous missense change in *GPT2* (c.459C>G, p.Ser153Arg) was reported in two siblings with a similar phenotype, including microcephaly and developmental delay (14) (Fig. 1*D*).

Human Mutations in *GPT2* Lead to Reduced Protein Levels and Enzyme Activity. We studied the protein stability and enzymatic activity of the identified human mutations, and our results are consistent with a loss-of-function mechanism. We expressed each of the three mutated transcripts in HeLa cells and studied protein levels using Western blotting with an antibody raised to the full-length *GPT2* (Fig. 2*A*). We detected a control, full-length protein at the predicted size of V5His-tagged *GPT2* (62.8 kDa, arrow). For the truncating mutation p.Arg404*, we detected a scant quantity of the predicted truncated protein (44.4 kDa, arrowhead), consistent with nonsense-mediated decay of the mRNA and/or an unstable protein. Less than 4% of control protein was detected (quantified in Fig. 2*B*). The missense mutations p.Ser153Arg and p.Pro272Leu were expressed at $37.6 \pm 6.3\%$ and $10 \pm 2.2\%$ of control levels, respectively, reflecting protein instability (Fig. 2*B*). Structural predictions for the missense changes also suggest deleterious effects (*SI Appendix, Fig. S2*).

To substantiate further the interpretation that these mutations lead to loss of enzyme function, we tested the enzymatic activity of mutant proteins directly. We expressed constructs for full-length *GPT2* protein, as well as for each of the three mutant alleles, in HeLa cells. We subsequently made protein extract from cells and tested *GPT2* enzyme activity. In the cell lines expressing each of the mutant alleles, including the missense mutations, enzyme activity relative to control was substantially diminished (to background levels) (Fig. 2*C*). Thus, the mutations in *GPT2* are associated with reductions or loss of protein as well as loss of enzyme activity. Even in the case of the missense mutations, wherein there was a small level of intact protein, the enzyme activity of protein with these missense mutations was not detectable above background levels.

***GPT2* Expression Increases in Postnatal Developing Brain.** To evaluate the role of *GPT2* in developing brain, we first measured protein and enzyme activity in developing mouse brains. In normal mice, we found highest levels of *Gpt2* protein in the early postnatal period using Western blotting (*SI Appendix, Fig. S3A*). Total *Gpt2* enzyme activity was detectable at postnatal day 1 (P1), yet enzyme activity was found to increase nearly 10-fold by P18 (*SI Appendix, Fig. S3B*), correlating with increases in *Gpt2* protein levels. In published RNA-seq data from cell lineages purified from mouse brain, *Gpt2* mRNA expression was threefold higher than that for the related enzyme *Gpt1* in neurons [8.9 vs. 3.0 fragments per kilobase of exons per million fragments mapped (FPKM), respectively] (*SI Appendix, Fig. S3C*) (15). *Gpt2* also has a

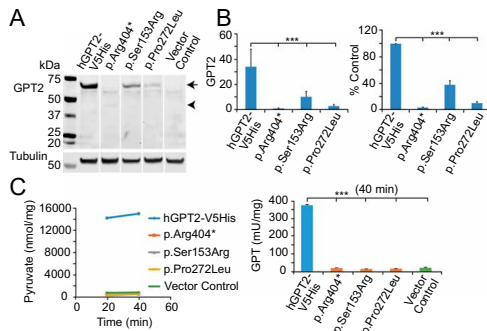


Fig. 2. Mutations in GPT2 lead to reduced protein levels and enzyme activity. (A) Western blot results of mutated GPT2 protein. Lysates of HeLa cells transfected with human control GPT2 (hGPT2-V5His), p.Arg404*, p.Ser153Arg, p.Pro272Leu, or vector-only constructs were probed with anti-GPT2 antibody. All of the three GPT2 mutants show reduced protein levels compared with control GPT2 (hGPT2-V5His). Arrow indicates the expected GPT2 protein band; arrowhead indicates the truncated GPT2 protein band. (B) Quantification of Western blots. (Left) Overexpressed GPT2 bands were normalized to tubulin. (Right) Overexpressed GPT2 level in each lane was normalized to the GPT2 control (hGPT2-V5His). $n = 6$ replicates. Data are presented as means \pm SEMs. $***P < 0.001$. (C) GPT enzyme functional assay indicated that mutations in GPT2 lead to loss of the enzyme activity. HeLa cells were transfected with human control GPT2 (hGPT2-V5His), p.Arg404*, p.Ser153Arg, p.Pro272Leu, or vector-only constructs. Lysates were used to analyze the GPT activity. (Left) GPT activity was measured by pyruvate production after either a 20- or 40-min incubation with substrate at 37 °C. All three GPT2 mutants had similar pyruvate production as the vector control. (Right) GPT activity was measured in cell lysate after incubating with substrate at 37 °C for 40 min and is represented as enzyme activity (in milliunits) per milligram of tested sample. Only the overexpressed GPT2 control protein showed significant high enzyme activity. $n = 4$ replicates. Data are presented as means \pm SEMs. $***P < 0.001$.

high level of expression (far exceeding *Gpt* expression) in oligodendrocyte precursor cells (137.7 vs. 4.8 FPKM, respectively) and newly formed oligodendrocytes (48.7 vs. 2.6 FPKM, respectively) (*SI Appendix, Fig. S3D*) (15).

In humans, through analyses of the Allen Institute's Developmental Transcriptome Dataset, we observed that *GPT2* mRNA is broadly expressed across all parts of the human brain throughout development and into adulthood, with highest levels in the early postnatal years (*SI Appendix, Fig. S4A*). Interestingly, although mRNA levels for *GPT2* and for *GPT* are correlated, *GPT2* mRNA levels are generally >20-fold higher than *GPT* levels in human brain (*SI Appendix, Fig. S4B*). Based on these data, peak levels of *GPT2* expression correlate with major periods of synaptogenesis and myelination in both mouse and human developing postnatal brain (16–19).

GPT2 Protein Is Localized to Mitochondria. GPT2 harbors a strong mitochondrial-localization sequence, which is not present in GPT (*SI Appendix, Fig. S5A*). None of the missense mutations appeared to interfere with the predicted mitochondrial localization using PSORT II predictions (20) (*SI Appendix, Fig. S5A*). Exogenously expressed GPT2 wild-type (WT) protein demonstrated a very high degree of costaining with mitochondrial markers, such as Mito-GFP (*Fig. 3A, Top*). By comparison, expression of the p.Arg404* mutant protein produced very little protein (*Fig. 3A, Bottom*); however, the small amount of protein that was discernible (by increasing the imaging parameters to maximal sensitivity) localized to mitochondria (*SI Appendix, Fig. S5B*). The exogenously expressed missense proteins, either the

p.Ser153Arg or p.Pro272Leu, both demonstrated higher levels of protein than the truncating mutation but reduced levels of staining relative to the control (*Fig. 3B*). This reduced amount of staining did colocalize with the mitochondrial stains, yet we expect these enzymes to be inactive, as shown previously (*Fig. 2C*).

Next, we established two GPT2-mutant HEK293FT cell lines using CRISPR-Cas9 genome editing (*Fig. 3C* and *SI Appendix, Table S3*). We introduced homozygous nonsense mutations (c.265G>T, p.Glu89*; and c.1210C>T, p.Arg404*), the latter of which is the same variant as we identified in pedigree 1. We confirmed by quantitative reverse transcription-PCR (qRT-PCR) that cells containing either of these two *GPT2* mutations showed significant decreases in *GPT2* mRNA compared with WT cells (*Fig. 3D*). Western blot analysis of fractionated lysates from WT and mutant HEK293FT cells revealed that endogenous GPT2 localized to the mitochondrial fraction in WT cells and was absent from the cytoplasmic fraction, whereas GPT2 was undetectable in either fraction in mutant cells (*Fig. 3E*).

Gpt2-Null Mice Demonstrate Reduced Postnatal Brain Growth. We generated mice with a germline disruption of the *Gpt2* gene (*SI Appendix, Fig. S6*) and observed decreases in postnatal brain growth akin to the human phenotype. Homozygous mutant mice were born in the expected Mendelian ratio (*SI Appendix, Table S4*). Western blotting of brain lysates demonstrated that Gpt2 protein was abolished in the mutant mice (*SI Appendix, Fig. S6C*). Also of note, postnatal brains of homozygous mutant mice at P18 showed significantly reduced total brain Gpt enzyme activity (*SI Appendix, Fig. S6D*). Homozygous mutant brain size was generally indistinguishable at birth, and, behaviorally, mutants were similar to control littermates for the first 2 wk postnatally. However, at approximately P18, homozygous mutant mice began to demonstrate reduced motor activity. Subsequent to the emergence of reduced motor behavior, homozygous mutant mice grew sickly and died generally between P18 and P26 (*SI Appendix, Table S4*). Given the expression of the β -galactosidase gene from the endogenous *Gpt2* promoter in the targeted allele, we were able to study the distribution of *Gpt2* expression in the heterozygous mouse brain. We found that, in P78 heterozygous mice, *Gpt2* expression was widely distributed throughout the brain (*SI Appendix, Fig. S7*). Staining was particularly apparent in the prefrontal cortex, striatum, hippocampus, and granular cell layer of the cerebellum.

We compared brain area between littermate homozygous mutant ($n = 12$) and WT animals ($n = 7$) at P18–P22 (*Fig. 4*). *Gpt2*-null brains showed a small but consistent and significant reduction in cortical area relative to control ($P < 0.03$) (*Fig. 4B*). Furthermore, analysis of areas and lengths of different brain regions showed a consistent and significant decrease in brain size in *Gpt2*-null animals compared with control animals (*Fig. 4 C* and *D*). For example, comparison of combined areas of cortex (CX), midbrain (MB), and cerebellum (CB) demonstrated a 13% decrease in area ($P < 0.0015$). We further observed that the number of SV2-positive puncta representing synapses were significantly reduced (30% less than WT; $P = 0.005$) at 10–14 d in vitro (*Fig. 4 E* and *F*). Based on these findings, we conclude that GPT2 has an important role in brain growth during postnatal development and potentially in synapse development.

Amino Acid Metabolism Is Defective in Gpt2-Null Mouse Brains. To identify metabolic defects in neural tissue in vivo, we investigated *Gpt2*-null mouse brains for derangements in metabolite levels. We analyzed 276 metabolites from P18 acute brain preparations from *Gpt2*-null and WT mice using targeted mass spectrometry (MS)-based metabolomics and metabolite set enrichment analysis (MSEA) (*Fig. 5A*). The top three pathways identified were as follows: protein biosynthesis [P value = 0.0000000644, false discovery rate (FDR) = 0.00000515] (largely reflecting changes in amino acid metabolism); citric acid cycle (P value = 0.00000733,

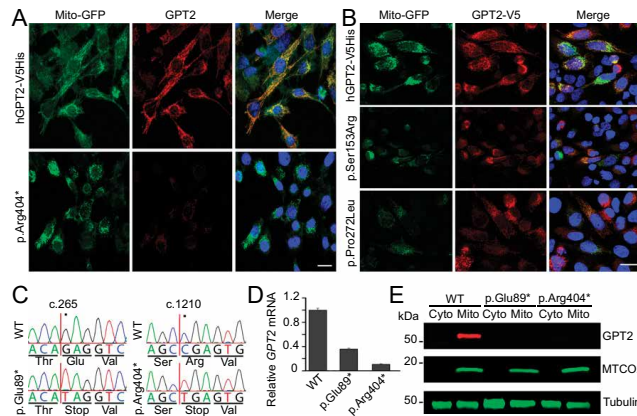


Fig. 3. GPT2 localizes to mitochondria. (A) HeLa cells coexpressing Mito-GFP (a mitochondrial marker, green) and either normal, human GPT2 (hGPT2-V5His) or human GPT2 with the p.Arg404* mutation were immunostained with anti-GPT2 antibody (red). Under the same imaging parameters, p.Arg404* showed a decrease in protein expression level. Immunostaining for GPT2 showed high colocalization with mitochondrial markers for control protein. (B) HeLa cells coexpressing Mito-GFP and C-terminal V5-tagged human GPT2 control (hGPT2-V5His) or mutations p.Ser153Arg or p.Pro272Leu were stained with anti-V5 antibody (red). Under the same imaging parameters as control, the images of cells expressing mutant GPT2 demonstrate reduced protein levels yet maintain mitochondrial localization in the residual signal. (Scale bar, 10 μ m.) (C–E) GPT2-mutant HEK293FT cells were generated by CRISPR-Cas9 genome editing. (C) Sanger sequencing traces of WT HEK293FT cells and the GPT2-mutant HEK293FT cell lines are shown. The mutant cell lines harbor homozygous nonsense mutations in the *GPT2* gene (c.265G>T, p.Glu89*; c.1210C>T, p.Arg404*). Positions of the variants are according to NM_133443.3 (cDNA) and NP_597700.1 (protein). (D) Graphed are the results of qRT-PCR analysis of WT HEK293FT cells and the two lines of GPT2-mutant cells (p.Glu89*, p.Arg404*). For all samples, GPT2 mRNA was normalized to 18S rRNA. (E) Immunoblot analysis of WT HEK293FT cells and the GPT2 mutant cells (p.Glu89*, p.Arg404*). In WT cells, GPT2 is absent from the cytosolic fraction (Cyto) and highly enriched in the mitochondrial fraction (Mito). In cells expressing either of the two mutants, GPT2 is absent from both fractions. Tubulin and MTCO2 (cytochrome c oxidase subunit II) are shown as a loading control marker and a mitochondrial marker, respectively.

FDR = 0.000293); and glutathione metabolism (P value = 0.0000142, FDR = 0.000379) (Fig. 5A and *SI Appendix*, Table S5).

At the level of primary metabolites in the GPT reversible reaction in *Gpt2*-null brains, alanine showed a strong decrease (fold change = 0.885, FDR = 0.008) (Fig. 5B and *SI Appendix*, Table S6). We corroborated these brain findings of alanine depletion by direct measure of alanine secretion and by isotope tracing experiments in *Gpt2*-null murine embryonic fibroblasts (MEFs) (Fig. 6). *Gpt2*-null MEFs exhibited near-complete loss of alanine secretion into the media (Fig. 6A). *Gpt2* deletion also substantially reduced transfer of ^{15}N from [α - ^{15}N]glutamine to alanine (Fig. 6B), as would be expected if *Gpt2* rather than *Gpt1* were the major isoform exchanging amino groups between glutamate and α -ketoglutarate. When cultured in medium supplemented with uniformly labeled [^{13}C]glucose, the *Gpt2*-null MEFs also had reduced ^{13}C labeling in alanine, whereas lactate labeling was conserved (Fig. 6C, two left panels). Therefore, taken together, metabolomic and direct isotope tracing measures indicate that *Gpt2* is the major *Gpt* isoform responsible for alanine production and secretion.

Although the alanine pool was depleted, several other amino acid pools were substantially elevated in P18 brain, particularly essential amino acids, including phenylalanine (fold change = 1.641, FDR = 0.024) (Fig. 5C and *SI Appendix*, Table S6). Notably urea was substantially decreased (fold change = 0.246, FDR = 0.017), which suggests a decrease in production of amine groups, consistent with dysregulation of total cellular aminotransferase activity and/or nitrogen disposal perhaps due to decreases in alanine secretion.

Additional Abnormal Metabolomics Signatures in *Gpt2*-Null Mouse Brains: Anaplerosis and Neuroprotective Mechanisms. In addition to defects in amino acid metabolism, P18 *Gpt2*-null mouse brains exhibit abnormal metabolomics signatures involving TCA cycle and neuroprotective mechanisms (Fig. 5A and *SI Appendix*, Table

S5). With regard to the TCA cycle, five of eight TCA cycle intermediates were substantially decreased (Fig. 5D and *SI Appendix*, Table S6), including the following: citrate (fold change = 0.655, P = 0.015), isocitrate (fold change = 0.868, P = 0.0064), succinate (fold change = 0.759, P = 0.009), fumarate (fold change = 0.881, P = 0.002), and malate (fold change = 0.735, P = 0.001). Surprisingly, ATP and GTP levels were somewhat elevated, as was acetyl-CoA.

Depletion of TCA cycle intermediates in brain is consistent with a defect in anaplerosis, the metabolic process involved in replenishing TCA cycle intermediates used during cellular anabolism and biosynthesis. Because *Gpt* enzyme activity converts glutamate to α -ketoglutarate, this function has been proposed to promote glutamine-dependent anaplerosis (21). Overall, labeling of TCA cycle intermediates from [^{13}C]glucose was enhanced by *Gpt2* deletion (Fig. 6C). Altered label distributions included enhanced malate m+3 and citrate m+5 fractions, which is consistent with suppressed glutamine-dependent anaplerosis and increased carboxylation of pyruvate (22). These altered labeling patterns are expected if reduced entry of glutamine-derived carbon into the TCA cycle via α -ketoglutarate is offset by an increased contribution of 4-carbon intermediates from glucose. Culture in [^{13}C]glutamine confirmed a reduced contribution of glutamine-dependent anaplerosis to TCA cycle intermediates in *Gpt2*-deficient cells (Fig. 6D).

Finally, we found in P18 *Gpt2*-null brains that several metabolites related to neuroprotective mechanisms are misregulated (Fig. 5E): glutathione (fold change = 0.715, FDR = 0.038), folate (fold change = 0.383, FDR = 0.024), and cysteine (fold change = 0.609, FDR = 0.083) levels were reduced; whereas cystathionine levels were substantially elevated (fold change = 2.409, FDR = 0.00036). Elevations of cystathionine were also found in newborn P0 mouse brain (fold change = 1.701, FDR = 0.029) (*SI Appendix*, Table S8). We conducted metabolomics analysis on newborn (P0) brain from

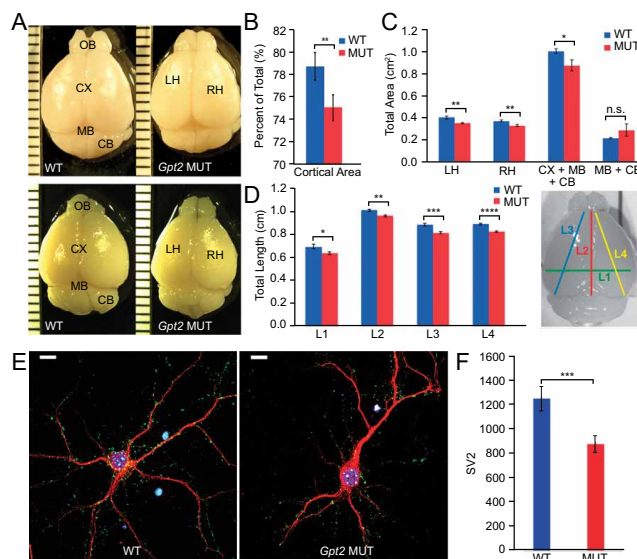


Fig. 4. *Gpt2* deficiency causes a reduction in brain size in mouse. (A) Panels depict two representative brain pairs from littermate animals for each genotype at P21 (Top) and P22 (Bottom). Left panels show WT perfused brains. Right panels show *Gpt2*-null brains (MUT). Measurements were taken of the cortex (CX), the midbrain (MB), the cerebellum (CB), the left hemisphere (LH), and the right hemisphere (RH). Ruler demarcations reflect 1-mm scale. (B) Cortical area presented as a percentage of total brain area is shown for WT animals and for *Gpt2*-null animals (MUT). ** $P < 0.03$. (C) Graphed is a comparison of area in square centimeters in four different brain regions: LH (** $P < 0.0025$), RH (** $P < 0.0015$), CX+MB+CB (* $P < 0.0015$), and MB+CB (n.s., $P < 0.1$). (D) Graphed is a comparison of length measurements between WT and *Gpt2*-null (MUT) animals. Measurements are depicted in the brain image on the Right. We found significant differences in width across two hemispheres (L1, green line) (* $P < 0.015$), in the midline anterior–posterior distance (L2, red line) (** $P < 0.0015$), in the diagonal length of the left hemisphere (L3, blue line) (** $P < 0.0002$), and in the right hemisphere (L4, yellow line) (**** $P < 0.000001$). $n = 7$ WT and 12 MUT animals for all brain size measurements. Data are presented as means \pm SEMs. Statistical analysis was conducted using Student's *t* test. (E) *Gpt2*-null hippocampal neurons show reduced synapses compared with neurons from WT littermates at 10 DIV, as visualized by SV2 staining (green). Neurons were immunostained with antibodies against SV2 and MAP2 (red). (Scale bar, 10 μ m.) (F) The graph depicts quantification of SV2 densities per 135- μ m² region of field of view in WT and MUT neurons. Data are presented as means \pm SEMs. $n = 4$ WT animals and 3 MUT animals across 3 litters. **** $P = 0.005$.

mutant animals compared with combined WT and heterozygous littermates. Although *Gpt2* protein expression undergoes substantial up-regulation in the postnatal period (SI Appendix, Fig. S34), we reasoned that analysis at this early time point could pinpoint the most proximal metabolic derangements resulting from loss of *Gpt2*. At P0, only four metabolites demonstrated misregulated levels adhering to a conservative FDR correction. Among these were two metabolites observed also at the P18 time point: alanine (fold change = 1.573, FDR = 0.000165), a primary metabolite in the *Gpt2* reaction, and also interestingly, cystathionine (fold change = 1.701, FDR = 0.029). Of note, alanine was up-regulated at P0, whereas by contrast it was significantly down-regulated at P18. The other two misregulated metabolites that withstood FDR correction were hydroxyproline (fold change = 1.767, FDR = 0.000335) and sarcosine (fold change = 1.337, FDR = 0.0153). Both of these metabolites are involved in amino acid metabolism. Overall, our data support a role for *Gpt2* in mitochondrial function and various metabolic pathways, including amino acid metabolism, anaplerotic processes involved in TCA cycle intermediates, and pathways implicated in neuroprotective mechanisms (e.g., pathways involving the metabolites cysteine, cystathionine, glutathione, and folate).

Discussion

In this study, we report rare, homozygous mutations in the gene encoding the enzyme *GPT2* in large consanguineous pedigrees segregating with a neurological phenotype involving IDD, postnatal mi-

crocephaly, and spastic paraplegia with progressive features. We present one extended kindred with a LOD score greater than 3.1 (pedigree 1, M11000) segregating a homozygous nonsense *GPT2* mutation (p.Arg404*). Another large extended kindred of three branches (pedigree 2, MC9400) segregates a deleterious, homozygous missense *GPT2* mutation (p.Pro272Leu) with LOD scores greater than 3.3 and 2.9 in branches 2 and 3, respectively. An individual of pedigree 2 (MC9402, branch 1), who similarly presented with microcephaly and IDD, was not homozygous for the *GPT2* variant. Because this family is highly consanguineous, it is likely that this individual has an additional genetic mutation. During the course of our work, a third homozygous, deleterious missense *GPT2* mutation (p.Ser153Arg) was reported in a large pedigree with recent shared ancestry and three affected individuals presenting with a similar phenotype (14).

In biochemical studies, we demonstrate that the human mutations are loss of function. For the p.Arg404* mutant protein, we demonstrate that the truncated *GPT2* protein is not made or is unstable in expression studies in cell lines. We also show here that the p.Pro272Leu and p.Ser153Arg proteins are unstable and, through structural predictions, likely have deleterious effects on protein folding (SI Appendix, Fig. S2). All mutant *GPT2* proteins, p.Arg404*, p.Pro272Leu, and p.Ser153Arg, are enzymatically inactive, consistent with loss-of-function, autosomal recessive mutations.

The clinical phenotype of the affected individuals associated with *GPT2* mutations presented herein is generally uniform. Postnatal microcephaly and IDD were noted in all affected

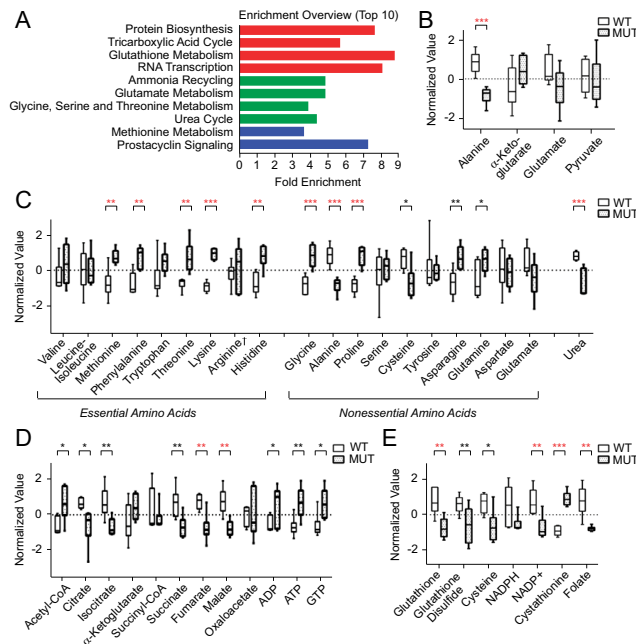


Fig. 5. Metabolomics profile of postnatal *Gpt2*-null mouse brain. (A) Overrepresentation analysis of metabolomics in brains from *Gpt2*-null (MUT) compared with WT *Gpt2* mice at P18. The reference library contained 88 metabolite sets for normal metabolic pathways. Metabolites showing significant increases or decreases (compared with control on Student's *t* test *P* value less than 0.05) were flagged. The hypergeometric test was used to determine whether flagged metabolites from specific pathways were significantly overrepresented. Red, $FDR < 0.01$; green, $0.01 < FDR < 0.03$; blue, $0.03 < FDR < 0.05$. (B–E) Box plots of metabolites, with whiskers representing minimum and maximum values. The peak intensity areas were normalized by a pooled reference sample from the WT *Gpt2* group (probabilistic quotient normalization), and auto (unit) scaling was performed whereby the data were mean-centered and divided by the SD of each group. Unpaired Student's *t* test was performed assuming equal group variance. The box plots in each of the panels show the following: (B) metabolites from the primary GPT enzyme reaction, (C) amino acids, (D) TCA cycle intermediates, and (E) metabolites involved in neuroprotective mechanisms. $n = 6$ WT animals and 6 MUT animals. * = $0.01 < \text{raw } P < 0.05$, ** = $0.001 < P < 0.01$, *** = $P < 0.001$. Red stars denote a corresponding FDR below 0.05. Also refer to *SI Appendix, Table S5*, for MSEA data; *SI Appendix, Table S6*, for full set of metabolite Student's *t* tests; and *SI Appendix, Table S7*, for raw data. [†]Arginine is a conditionally essential amino acid.

individuals, most had oral motor difficulties, and several had seizures. These clinical findings are highly consistent with those of the individuals reported in ref. 14. There is no clear difference in severity between individuals with truncating mutations and missense mutations, consistent with our biochemical data that all mutations lead to a severe or complete loss of GPT2 enzyme function.

An important aspect of our work is that we have had the opportunity to follow patients longitudinally. Thereby, we are able to extend the neurological phenotype, which appears to include progressive features in addition to developmental disease. With regard to motor findings, we find that hypotonia during infancy gives way to hypertonia more notably in the lower extremities (spastic diplegia or paraplegia). Among the 14 affected individuals studied herein, ~80% showed slowly progressive spastic diplegia or paraplegia with hyperreflexia and hypertonia as one of the major features. Although rapid regression is not noted, motor difficulties seem to be slowly progressive in many of the cases, consistent with our metabolomics studies that suggest abnormalities in neuroprotective mechanisms. Defects in such mechanisms have been previously implicated in hereditary spastic diplegia (23).

The acquisition of neurological features during early postnatal life indicates the brain's requirement for GPT2 during this critical period of brain development. Postnatal brain development is

characterized by the formation, refinement, and maintenance of circuitry involving neuronal arborization, synaptogenesis, oligodendrocyte expansion, and myelination (3). We find *GPT2* expression to increase in brain during the early postnatal period and to be expressed in both neurons and glia. Prior studies have indicated strong neuronal expression and weaker or absent glial expression in adult human brain (24); however, data presented here support a role for GPT2 in both neurons and glia, at least during early postnatal development (*SI Appendix, Fig. S3*). Our finding that *GPT2* expression reaches highest levels in the early postnatal period both in human and in mouse brain, concurrent with peaks in synaptogenesis (17, 18, 25), suggests a role in this process. We also observe decreases in brain growth postnatally both in human and in mouse. Our initial findings support defects in synapse formation (Fig. 4 *E* and *F*), again consistent with failures in synaptogenesis perhaps arising from mitochondrial dysfunction. Importantly, we demonstrate here that *GPT2* is localized to mitochondria. *GPT2* has a strong mitochondrial localization signal, whereas *GPT* does not. The two isoforms of GPTs, *GPT* and *GPT2*, show different spatial expression patterns. *GPT2* is highly expressed in the CNS. There is also a possibility that other defects in postnatal brain development are involved, including abnormal oligodendrocyte development. In humans, myelination increases rapidly between 6 and 24 mo

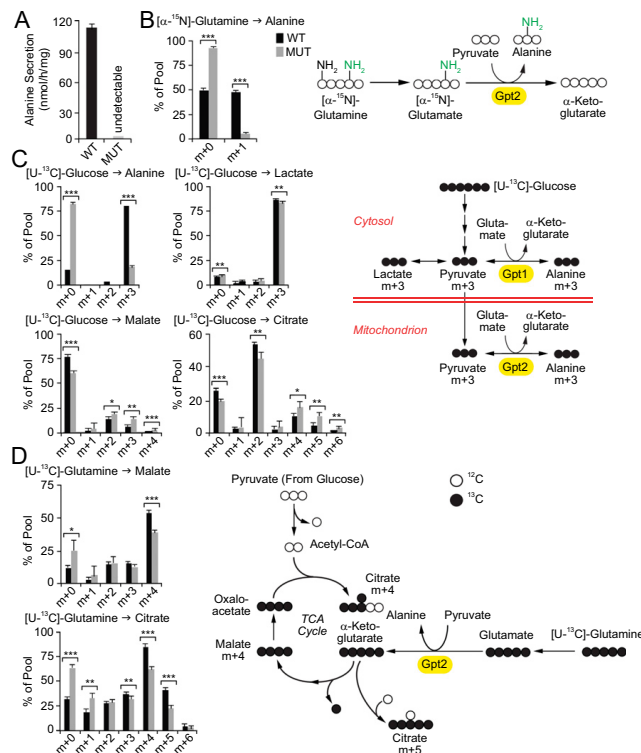


Fig. 6. Defective alanine production and glutamine-dependent anaplerosis in *Gpt2*-null cells. Immortalized MEF cell lines were prepared from WT and *Gpt2*-null mice (MUT) and investigated in culture. (A) Total alanine abundance in the medium was measured by HPLC. Alanine secretion in the MUT cells was scarcely detectable. (B) Graphed are fractional enrichments of extracellular alanine during culture with $[\alpha\text{-}^{15}\text{N}]$ glutamine. Levels of transfer of radioisotope from glutamine to alanine are substantially reduced in the *Gpt2*-null cells. (Schematic Right) ^{15}N (green) is transferred from $[\alpha\text{-}^{15}\text{N}]$ glutamine, via $[\alpha\text{-}^{15}\text{N}]$ glutamate, to $[\alpha\text{-}^{15}\text{N}]$ alanine. This pathway requires activity of a glutamate pyruvate transaminase, such as *Gpt2*. (C) Shown are mass isotopologue distributions for alanine, lactate, malate, and citrate after culture with $[\text{U}\text{-}^{13}\text{C}]$ glucose and unlabeled glutamine. Altered label distributions, including reduced alanine m+3, and enhanced malate m+3 and citrate m+3 fractions, are consistent with suppressed glutamine-dependent anaplerosis (22). (Schematic Right) $[\text{U}\text{-}^{13}\text{C}]$ glucose gives rise to $[\text{U}\text{-}^{13}\text{C}]$ pyruvate (pyruvate m+3) via the glycolytic pathway. This pyruvate can be converted to lactate m+3 or alanine m+3. Conversion of pyruvate to alanine involves the *Gpt1* (cytosol)- or *Gpt2* (mitochondrion)-dependent transfer of an amino group to pyruvate from glutamate. A large reduction of labeling of alanine from glucose in *Gpt2*-deficient cells implies that *Gpt2* is required for alanine synthesis. (D) Shown are mass isotopologue distributions for malate and citrate after culture with unlabeled glucose and $[\text{U}\text{-}^{13}\text{C}]$ glutamine. Reduced direct transfer of radioisotope from glutamine to malate and citrate demonstrates suppressed glutamine-dependent anaplerosis in *Gpt2*-null cells. (Schematic Right) $[\text{U}\text{-}^{13}\text{C}]$ glutamine generates fully labeled α -ketoglutarate via glutamate. The resulting α -ketoglutarate can proceed around the oxidative TCA cycle as shown, giving rise to malate m+4 and citrate m+4. In addition, α -ketoglutarate may become reductively carboxylated through the addition of one unlabeled carbon, resulting in citrate m+5 (49). Loss of *Gpt2*, which catalyzes the conversion of glutamate to α -ketoglutarate, is predicted to reduce labeling of metabolites downstream of α -ketoglutarate during culture with $[\text{U}\text{-}^{13}\text{C}]$ glutamine. It would also increase the contribution of glucose carbon to TCA cycle metabolites, as described in ref. 22. Data are presented as the means \pm SDs for three parallel cultures, with results shown for one representative experiment. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$ by unpaired, two-sample Student's *t* test.

postnatally and may increase more gradually into adolescence (16, 26). A minority of patients have shown a reduced white matter volume on brain MRI [participant MI1003; *SI Appendix, Table S1*; and also an affected individual in the study by Celis et al. (14)]. Interestingly, in mouse, we observe strong *Gpt2* expression in oligodendrocyte precursor cells that undergo rapid expansion in the early postnatal period (19, 27–29).

It is appealing to speculate that disease progression in the postnatal period may be prevented by intervention, particularly in the setting of abnormalities of amino acid metabolism. GPTs serve an important role in a variety of metabolic functions, including amino

acid metabolism, the urea cycle, and the TCA cycle, in addition to roles in neurotransmitter (both glutamate and GABA) synthesis. Glutamate, in turn, is also a substrate for the synthesis of glutathione, a key element in the cellular machinery to protect against oxidative damage and cell death (30, 31). Depletion of alanine levels is the strongest signal observed of the primary metabolites in the brain. Similarly, in patient cerebrospinal fluid, decreases in alanine were seen (14). Interestingly, we do not see strong changes in glutamate. Elevations of glutamate at the synapse would be predicted to be particularly excitotoxic (32); however, we do not see strong changes in total brain glutamate in newborn mice or at P18. Future studies

may examine specific cell types or tissue compartments (i.e., the synapse) more precisely for alterations in metabolites or damage. Given the lack of spatial resolution, our current experiments make it difficult to interpret a role for GPT2 in the glutamate–glutamine cycle at the synapse. Indeed, the GPT enzyme has been used experimentally and in therapeutic models to reduce excitotoxic glutamate levels through a proposed scavenging approach (33).

In the postnatal brain at P18, our experiments seem to indicate that Gpt2 serves to provide a source of alanine in the brain. Also, given the very low urea levels, Gpt2 activity may play an important role in nitrogen metabolism perhaps through generation of alanine. At P18, by contrast to decreases in alanine, *Gpt2*-null brains demonstrate elevations in several essential amino acids, including elevations in phenylalanine, which have been implicated in other encephalopathies, notably phenylketonuria, and may be modifiable by diet. We also observed elevations in glycine, which is also associated with progressive encephalopathy, intellectual disability, and seizures (34).

We also observe metabolic defects indicating abnormalities in glutamine-dependent anaplerosis of TCA cycle intermediates. GPT2 facilitates glutamine's ability to serve as an anaplerotic precursor by enabling the conversion of glutamate to α -ketoglutarate in the mitochondria. Our findings are similar to a previous study in which GPT activity was observed to be required for glutamine to stimulate both respiration and growth of KRAS-transformed cancer cells in culture (35). The importance of the role of GPT2 and anaplerosis in neurons and glia warrants further investigation.

Importantly, a metabolic signature previously associated with neurodegenerative disease was observed in *Gpt2*-null brain. Cystathionine elevation is among the strongest signals in the metabolomics dataset with statistically significant elevations at both P0 and P18. Recently, several studies have implicated the accumulation of this product, as well as decreases in cysteine, which are also observed in *Gpt2*-null brains, in neurodegenerative disease. More specifically, through deficiency in cystathionine γ -lyase and mechanisms involving both redox homeostasis and sulfhydrylation, this metabolic pathway has been pinpointed in both Huntington's disease (36, 37) and Parkinson's disease (38), as well as other neurological diseases with mitochondrial defects. Other statistically significant perturbations in P18 brain supporting abnormalities in neuroprotective mechanisms include reductions in glutathione and folate. In summary, we have identified mutations in the mitochondrial enzyme GPT2 in a human neurological disorder, wherein mutations lead to metabolic dysfunctions that have general relevance to developmental as well as potentially to neurodegenerative mechanisms and disease.

Subjects and Methods

Human Studies. Human subject research was conducted according to protocols approved by the institutional review boards of Boston Children's Hospital, Beth Israel Deaconess Medical Center, and Butler Hospital, and equivalent committees of the other participating institutions. Written informed consent was obtained from all participants or their legal guardians.

Genome-Wide SNP Genotyping, Linkage Analysis, and WES. DNA was genotyped using either Affymetrix Genome-Wide Human SNP Array 6.0 (MI1000) or Illumina HumanOmniExpress BeadChip array (MC9400). Affymetrix genotype calls were made using Birdsuite 1.5.5 (39) and Illumina calls by GenomeStudio version 2011.1 (Illumina). Genome-wide LOD scores were calculated using high-quality SNPs. PLINK, version 1.07 (40), was used to reduce linkage disequilibrium between markers. MERLIN, version 1.1.2 (41), was used to remove genotyping errors and to calculate LOD scores, assuming an autosomal recessive mode of inheritance with 100% penetrance and a disease allele prevalence of 0.0001. WES was performed using the Agilent Sure-Select Human All Exon or All Exon, version 5, capture array. Samples were sequenced on an Illumina HiSeq 2500. Sequence data were analyzed using GATK and variants annotated using ANNOVAR (42).

DNA Constructs and Antibodies. Human *GPT2* gene (GenBank: BC062555.1) was cloned into pcDNA3.1/V5-His-TOPO mammalian expression vector to generate C-terminal V5His-tagged pHGPT2-V5His. GPT2 mutants p.Arg404*,

p.Ser153Arg, and p.Pro272Leu were constructed using QuikChange site-directed mutagenesis (Agilent Technologies). The pTag GFP2-Mito vector was from Evrogen. Antibodies used were as follows: rabbit anti-C-terminal GPT2 antibody (SAB140991; Sigma-Aldrich), rabbit anti-full-length GPT2 antibody (16757-1-AP; Proteintech), mouse anti-V5 antibody (R960-25; Life Technologies), mouse anti-SV2 antibody (SV2-c; Developmental Studies Hybridoma Bank), chicken anti-MAP2 antibody (AB-15452; Millipore), mouse anti-Tubulin antibody (ab56676; Abcam), and rabbit anti-MTDCO2 antibody (ab109739; Abcam).

GPT Enzyme Activity Assay. GPT activity was analyzed using the alanine aminotransferase (ALT) Assay Kit (Abcam). Mouse brains or cells were homogenized in ice-cold ALT Assay buffer and centrifuged. Protein concentrations of supernatants were determined by bicinchoninic acid assay. GPT activity was detected using 30 μ g of brain extracts or 3.5 μ g of cell extracts.

Genome Editing of GPT2 in HEK293FT Cells. Genomic alterations in HEK293FT cells at the *GPT2* locus were made using the CRISPR-Cas9 system (43). Twenty nucleotide guide RNA (gRNA) sequences were designed to target double-stranded breaks at respective *GPT2* target loci. For each transfection, a 180-nt single-stranded oligonucleotide was cotransfected with gRNA and the CRISPR-Cas9 construct [pSpCas9(BB)-2A-GFP; Addgene] to create single base substitutions via nonhomologous recombination. At 48 h posttransfection, single cells were sorted with GFP signal by FACS. The targeted genomic region was sequenced (see *SI Appendix, Table S3*, for sequences used). *GPT2* mRNA level was quantified by qRT-PCR using primers (Hs0037287.m1; Life Technologies).

Generation of Gpt2-Null Mice. *Gpt2* cryopreserved mutant embryos were established through resources at the Knockout Mouse Project at University of California, Davis (Project ID CSD24977). The background of the embryos is C57BL/6N, and these mice were fully backcrossed into a C57BL/6J line. The targeting construct involved a gene trap (splice acceptor) and *LacZ*-Neo cassette (*SI Appendix, Fig. S6A*). Heterozygous males and heterozygous females were mated to produce offspring of both genders and all genotypes. Animals were genotyped by PCR with forward primer CSD-gene-F (5'-CTA ACT TGT CCT GCA TGG TGT CAG C-3') and reverse primer CSD-gene-tR (5'-CTA CAA ACA CTG GAC CCA AAC GTC C-3') for a WT band of 504 bp. Forward primer CSD-loxF (5'-GAG ATG GCG CAA CGC AAT TAA TG-3') and reverse primer CSD-gene-R (5'-GGC TTT CTA CCA GGA GGA ACA GAG G-3') yields a 283-bp mutant band (*SI Appendix, Fig. S6B, Left*). WT and mutant mRNA were detected using RT-PCR, with the forward primer Unitrap-F (5'-CTG AGG TAA TCC GAG CCA AC-3') and reverse primer Unitrap-wtR (5'-CGC TCG TTT CTT AGC GTC TT-3') detecting a WT band (114 bp) and the Unitrap-F primer and Unitrap-lacZ primer (5'-TGG CGA AAG GGG GAT GTG-3') detecting a 300-bp mutant band (*SI Appendix, Fig. S6B, Right*). *LacZ* staining was performed as described (44). All experiments involving mice were carried out in accordance with the National Institutes of Health *Guide for the Care and Use of Laboratory Animals* (45) under the protocols approved by the Brown University Institutional Animal Care and Use Committee.

Brain Size Measurement. Matched littermate pairs collected between P18 and P22 were transcardially perfused with 4% (wt/vol) paraformaldehyde and imaged using a Leica MZ16F. ImageJ analysis software was used to measure the area of the cortical hemispheres, midbrain, and cerebellum. Length measurements were done using four defined starting points.

Hippocampal Cultures. Hippocampal neurons were cultured as described (46). At 10–14 d in vitro (DIV), cells were immunostained with anti-SV2 and anti-MAP2 antibodies. MAP2-positive neurons were scored for SV2 puncta using ImageJ Particle Analysis.

Metabolomics. Craniotomies were performed on P0 and P18 litters from *Gpt2* heterozygous parents. Whole brains were used for metabolomics preparations performed as per Yuan et al. (47). Methanol extracts were dried and run by targeted tandem liquid chromatography (LC)-MS/MS. Briefly, samples were injected via hydrophilic interaction LC at high pH using HPLC coupled to a 5500 QTRAP mass spectrometer (AB/SCIEX). Metabolites were monitored using SRM mode for 300 transitions with positive/negative polarity switching. Peak areas for each detected metabolite were integrated using MultiQuant software (AB/SCIEX). The results were analyzed using MetaboAnalyst 3.0 (48).

Stable Isotope Tracing in MEFs. MEFs were maintained in DMEM with 10% (vol/vol) FCS and immortalized by SV40 T antigen. Experiments were performed between 5 and 15 passages. Stable isotope tracing experiments were performed as described previously (22). Briefly, cultures were overlaid with DMEM containing either 10 mM [13 C]glucose and 4 mM unlabeled glutamine,

or 10 mM unlabeled glucose and 4 mM [^{13}C]glutamine. After culturing for 6–8 h, the cells were rinsed in ice-cold normal saline and lysed with three freeze–thaw cycles in cold 50% (vol/vol) methanol. Lysates were centrifuged, and supernatants were evaporated and derivatized by *tert*-butyldimethylsilyl-methyltrifluoroacetamide (Sigma-Aldrich). One microliter of derivatized material was injected onto an Agilent 7890 gas chromatograph networked to an Agilent 5975 mass selective detector. For analysis of ^{15}N labeling in extracellular alanine, MEFs were incubated with medium containing 10 mM unlabeled glucose and 4 mM (α - ^{15}N)glutamine for 8 h. An aliquot of medium was passed over an AG50 column (Bio-Rad), and then amino acids were eluted with 4 mL of 4 N ammonium hydroxide. These samples were evaporated and processed as above. Total alanine abundance in medium was measured by HPLC (Hitachi L8900).

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SI Appendix

Ouyang et al. (2016). Mutations in mitochondrial enzyme GPT2 cause metabolic dysfunction and neurological disease with developmental and progressive features.

Supplemental data include 7 figures and 9 tables. Also provided are a list of web resources and additional acknowledgments.

Supplemental Figures:

Figure S1. Magnetic Resonance Imaging (MRI) findings in individuals with *GPT2* mutations.

Figure S2. Structural prediction of GPT2 missense mutations.

Figure S3. *Gpt2* gene and protein expression in developing mouse brain.

Figure S4. *GPT2* gene expression in developing human brain.

Figure S5. Data related to the mitochondrial localization of GPT2.

Figure S6. *Gpt2* targeted gene disruption in mouse.

Figure S7. LacZ staining of *Gpt2* wild-type and heterozygous brain sections.

Supplemental Tables:

Table S1. Detailed clinical summary of individuals with *GPT2* mutations.

Table S2. *In silico* prediction of the pathogenicity of identified *GPT2* variants.

Table S3. Targeted guide RNA sequences and primer sequences for CRISPR-Cas9 editing.

Table S4. Comparison of numbers of littermate offspring and age at time of death across wild-type and *Gpt2* mutant mice resulting from Het X Het parental cross.

Table S5. Metabolite set enrichment analysis of P18 *Gpt2* mutant mouse brain.

Table S6. Significantly changed metabolites in *Gpt2* mutant mouse brains (P18).

Table S7. Peak area intensities in *Gpt2* mutant mouse brains (P18).

Table S8. Significantly changed metabolites in *Gpt2* mutant mouse brains (P0).

Table S9. Peak area intensities in *Gpt2* mutant mouse brains (P0).

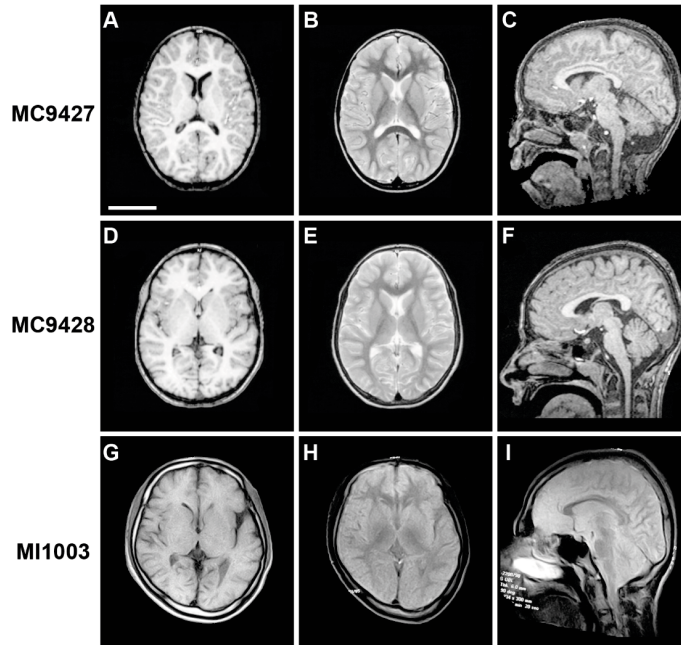


Fig. S1. Magnetic Resonance Imaging (MRI) findings in individuals with *GPT2* mutations. (A-I) Representative images of MRI scans from three affected individuals (MC9427, MC9428, and MI1003): T1-weighted axial images (A, D, and G), T2-weighted axial images (B and E), fluid-attenuated inversion recovery (FLAIR) axial image (H), T1-weighted sagittal images (C and F), and T2-weighted sagittal image (I). The ages at imaging were 13 years (MC9427), 10 years (MC9428), and 16 years (MI1003). Affected individuals MC9427 and MC9428 show microcephaly with normal brain architecture. Individual MI1003 shows reduced white matter volume and a thin corpus callosum. Scale bar, 10 cm.

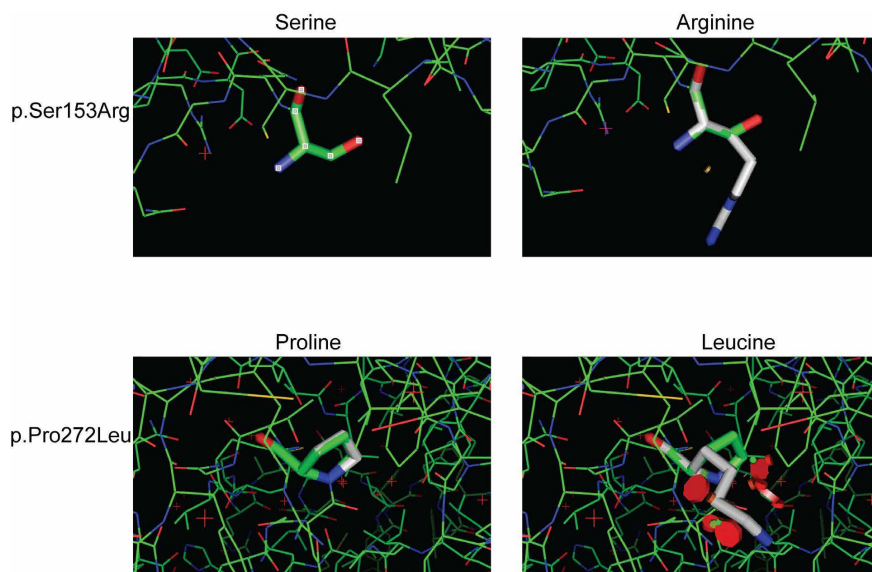


Fig. S2. Structural prediction of GPT2 missense mutations. Three-dimensional structural prediction of the two GPT2 missense mutations p.Ser153Arg and p.Pro272Leu as visualized by PyMOL software. Shown are predicted structures before (*Left*) and after (*Right*) the indicated amino acid substitutions. Both of the amino acid substitutions are non-conservative and are predicted to be deleterious to GPT2 protein structure.

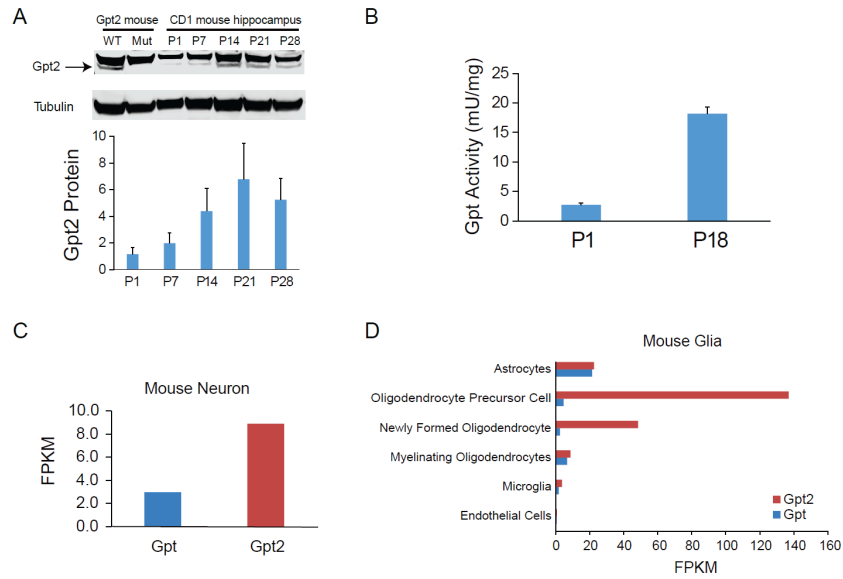


Fig. S3. *Gpt2* gene and protein expression in developing mouse brain. (A) Comparison of *Gpt2* protein expression levels in wild-type (WT) mouse hippocampus throughout development. *Top*, western blot analysis showing the presence and absence of *Gpt2* protein in WT and *Gpt2* null (Mut) mouse, respectively, and the developmental regulation of *Gpt2* protein in mouse hippocampus. Arrow indicates the expected band for endogenous *Gpt2* at 58 kDa. A nonspecific band is present at approximately 60 kDa. *Bottom*, quantification of western blots. *Gpt2* expression was normalized to tubulin throughout WT CD1 mouse hippocampal development at stages of postnatal day 1 (P1), P7, P14, P21, and P28. $n = 3$. Data are presented as means \pm SEMs (x 1000). (B) *Gpt* activity in brain lysate after incubating with substrate at 37 °C for 40 min and represented as enzyme activity (mU) per mg of tested sample. P1, $n = 7$; P18, $n = 5$. Data are presented as means \pm SEMs. (C) *Gpt2* and *Gpt* gene expression in neurons of mouse cerebral cortex. (D) *Gpt2* and *Gpt* gene expression in major glia cell types of mouse cerebral cortex. Units are in fragments per kilobase of exon per million fragments mapped (FPKM, x axis) (1).

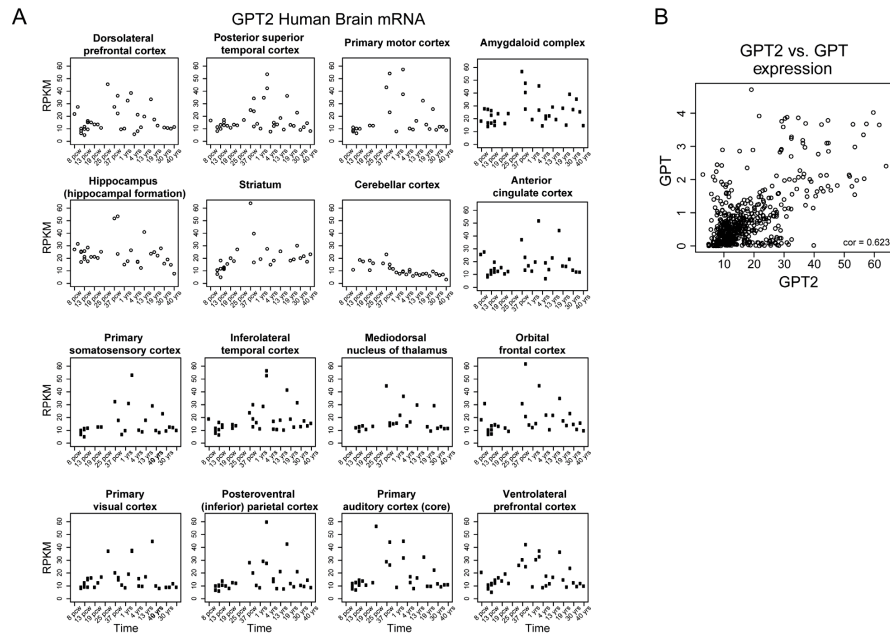


Fig. S4. *GPT2* gene expression in developing human brain. (A) *GPT2* gene expression in representative human brain regions across development. Gene expression data are from post-mortem human brain samples from the March 2014 version of the Allen Institute for Brain Science's BrainSpan (<http://developinghumanbrain.org>). BrainSpan's Developmental Transcriptome includes data generated by RNA sequencing, normalized to RPKM (reads per kilobase per million reads). Data were summarized to 21,392 unique Ensembl gene identifiers and consisted of 524 samples derived from 26 anatomic brain regions. Of those samples, 498 were derived from 16 brain regions. Donors were age 8 weeks post-conception to 40 years old. *GPT2* expression is generally highest in late fetal life and the first 5 years of life, except in cerebellar cortex. (B) *GPT2* and *GPT* expression in the BrainSpan transcriptome dataset plotted using all brain regions and time points. *GPT* and *GPT2* expression levels are correlated ($r = 0.623$), but *GPT2* expression is much higher overall, about 22-fold greater.

A

hGPT2 MQRAAALVRRGCGPRT PSSWGRS QSSAAAE 30
 hGPT MASSTGDRSQAVRHGLRAKVLTL DGMNPRV 30

PSORT II Prediction					
	Cytoplasmic	Nuclear	Mitochondrial	Vesicles of secretory system	Prediction
hGPT	34.8%	26.1%	26.1%	13.0%	Cytoplasmic
hGPT2		4.3%	95.7%		Mitochondrial
p.Arg404*		4.3%	95.7%		Mitochondrial
p.Ser153Arg		4.3%	95.7%		Mitochondrial
p.Pro272Leu		4.3%	95.7%		Mitochondrial

B

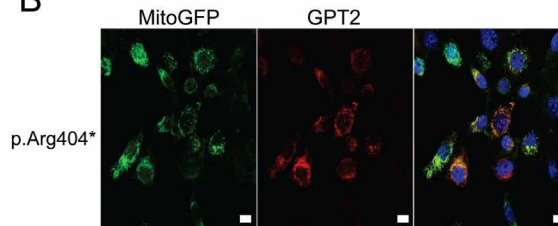


Fig. S5. Data related to the mitochondrial localization of GPT2. (A) N-terminal amino acid alignment of human GPT2 and GPT. On GPT2, the red line indicates the predicted cleavage site for the mitochondrial signal peptide sequence. GPT2 has a strong predicted mitochondrial localization signal, but GPT does not. None of the four mutations changes the PSORT II program's predicted mitochondrial localization for GPT2 (2). (B) Mitochondrial localization of the GPT2 truncation mutant p.Arg404* at increased imaging sensitivity parameters. The p.Arg404* GPT2 mutant shows little protein expression in studies involving transfection of cell lines (Main Text Fig. 3A). When microscopy parameters are altered to increase sensitivity substantially, the p.Arg404* protein becomes visible and, furthermore, shows a mitochondrial subcellular localization. This demonstrates that, although the protein expression level of this mutation is drastically reduced relative to control, the protein that is made continues to be localized to mitochondria. Scale bar, 10 μ m.

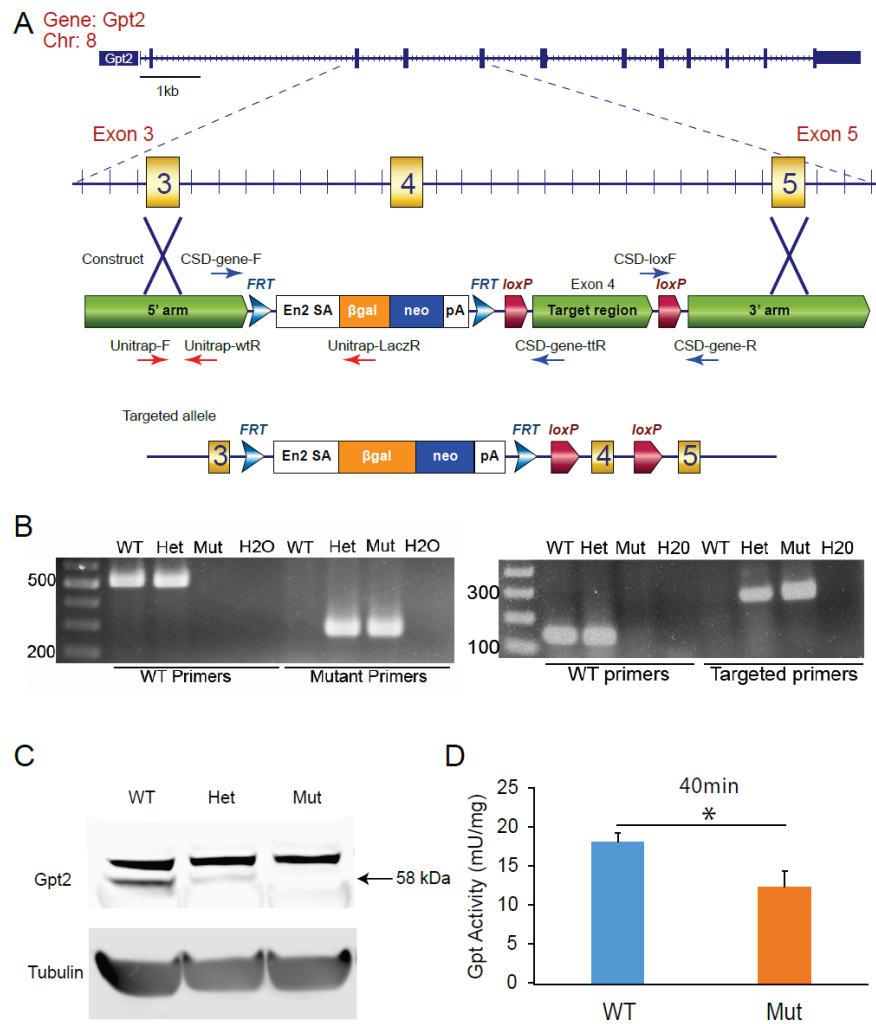


Fig. S6. *Gpt2* targeted gene disruption in mouse. (A) Diagrammatic representation of the *Gpt2* gene in the mouse genome. A mutant allele was generated by adding a gene trap (splice acceptor) and *LacZ-Neo* cassette before the targeted exon 4 of *Gpt2*. (B) PCR genotyping gels of wild-type (WT), heterozygous (Het), and homozygous mutant (Mut) mice. *Left*, representative PCR genotyping gel showing a 504 base pair (bp) band (primer pairs CSD-gene-F and CSD-gene-ttR) present in WT littermates and Het littermates, but not Mut littermates, and a 283 bp

7

band (primer pairs CSD-loxF and CSD-gene-R) present in Mut littermates and Het littermates, but not WT littermates. *Right*, RT-PCR gel showing that, when using primers specific for the WT *Gpt2* allele (Unitrap-F and Unitrap-wtR), the WT band (114 bp) cannot be amplified in Mut littermates; however, when using specific *LacZ*-targeted primers (Unitrap-F and Unitrap-LacZR), the *LacZ* band (300 bp) can be amplified in Mut littermates. (C) Western blot analysis of WT, Het, and Mut mouse brains. Gpt2 protein (58 kDa, *Arrow*) is not detected in brain lysates from *Gpt2* homozygous mutant (Mut) mice, but it is detected in WT and Het littermates. A nonspecific band is present at approximately 60 kDa. (D) Gpt activity in brain lysate after incubating with substrate at 37 °C for 40 min and represented as enzyme activity (mU) per mg of tested sample. WT, $n = 5$; Mut, $n = 3$. Data are presented as means \pm SEMs. $*P < 0.05$.

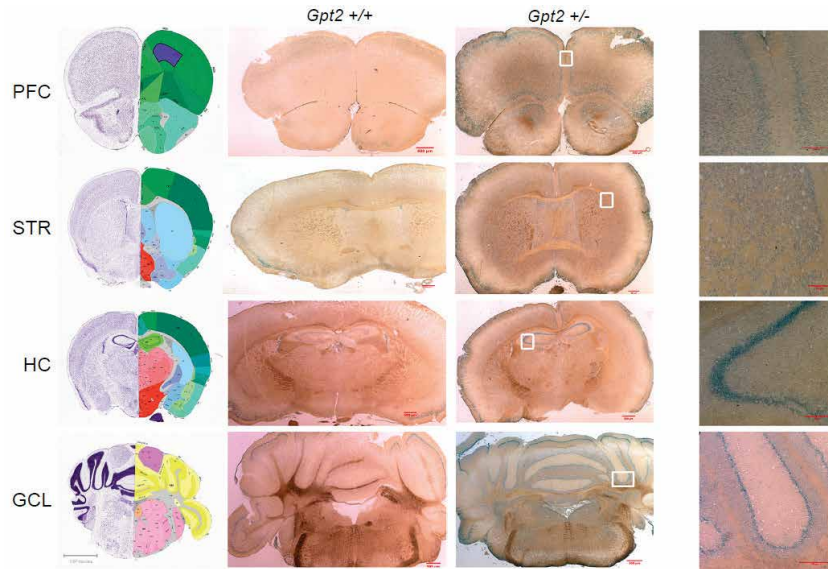


Fig. S7. LacZ staining of *Gpt2* wild-type and heterozygous brain sections. The coronal tissue sections from adult mouse brain were matched across genotypes with corresponding anatomical locations from Allen Brain Atlas images on the far left column. Lower magnification scale bar, 500 μm . The far right column shows higher magnification images of the *Gpt2* +/- tissue sections (within areas demarcated by the white boxes). Higher magnification scale bar, 200 μm . Regions of interest that showed considerable β -galactosidase activity were PFC, Prefrontal Cortex; Str, Striatum; HC, Hippocampus; and GCL, Granular Cell Layer.

Table S1. Detailed clinical summary of individuals with *GPT2* mutations.
(See attached.)

Table S2. *In silico* prediction of the pathogenicity of identified *GPT2* variants.

Amino acid change (Family)	p.Pro272Leu (Pedigree 2)
PolyPhen-2 score (prediction)	1.000 (probably damaging)
SIFT score (prediction)	0.001 (damaging)
PROVEAN score (prediction)	-9.48 (deleterious)

Table S3. Targeted guide RNA sequences and primer sequences for CRISPR-Cas9 editing.

Targeted sequences for CRISPR-Cas9 editing		
c.265G>T; p.Glu89*		GCTCGGATGACCTCTGTGAA
c.1210C>T; p.Arg404*		CACTCGGCTGAATTGCTCAA
Primers for verifying CRISPR-Cas9-engineered mutant cell lines		
c.265G>T; p.Glu89*	Forward	ACCCTTTAAGAGCCTTGATTCC
	Reverse	TCAGAAAGGCAGGAAGGAGG
c.1210C>T; p.Arg404*	Forward	GCTTTCGATTCTGGCTGTCC
	Reverse	CACACACTCACAGTCCTCCT

Table S4. Comparison of numbers of littermate offspring and age at time of death across wild-type and *Gpt2* mutant mice resulting from Het X Het parental cross.

Postnatal (P) Age	Mut	Het	WT
P0	9	15	5
P1	7	6	7
P2	5	9	13
P3	0	2	1
P4	0	1	0
P5	1	2	0
P6	1	0	1
P7	0	0	0
P8	0	0	0
P9	0	0	0
P10	0	0	0
P11	0	1	0
P12	0	2	0
P13	0	0	0
P14	0	0	0
P15	0	1	0
P16	1	0	0
P17	0	0	0
P18	2	0	0
P19	2	1	2
P20	7	0	0
P21	9	0	0
P22	10	0	0
P23	4	2	0
P24	2	0	0
P25	4	0	0
Death after 1st postnatal week ¹	41	7	2
Animals surviving to P26 ²	1/65	222/264	92/121
Total pups born (genotyped at P0) across all experiments³	193	445	243

¹“Death after 1st postnatal week” shows the total death number from P8–P25 in littermates of all genotypes resulting from matings from heterozygous parents. *Gpt2* null mice (Mut) had an unusually high occurrence of death in this period as compared to wild-type (WT) or heterozygous (Het) mice.

²“Animals born surviving to P26” is the number of animals alive at P26 as a proportion of the total number of animals born from heterozygous parents and allowed to grow to P26 (i.e., the total number is the sum of the number of animals that died from P0–P25 and the number of animals still surviving at P26). As shown, almost all *Gpt2* mutant mice (Mut) died before P26.

³“Total pups born (genotyped at P0) across all experiments” is the total number of littermates born of each indicated genotype from heterozygous matings. Genotypes reflect approximately the expected Mendelian ratio of Mut:Het:WT = 1:2:1 or a slight reduction in homozygous *Gpt2* null animals that was not statistically significant ($P = 0.25$).

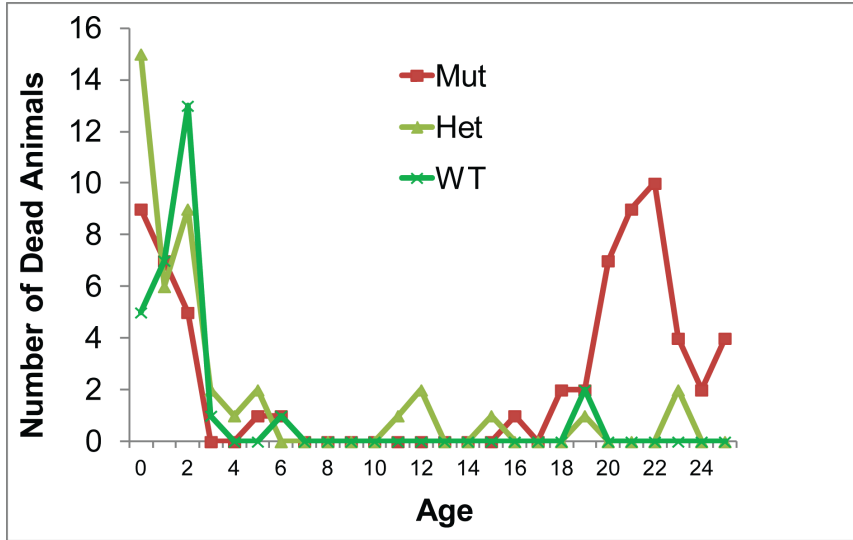


Table S5. Metabolite set enrichment analysis of P18 *Gpt2* mutant mouse brain.
(See attached.)

Over-representation analysis of metabolites (hits) that were significantly increased or decreased in *Gpt2* mutant P18 mouse brains in comparison to controls as per Student's *t*-test results. A normal metabolic pathway-associated library containing 88 metabolite sets was referenced [Small Molecule Pathway Database (SMPDB)]. Hypergeometric test was used to determine whether a metabolite set is represented more than expected by chance. One-tailed *P* value was adjusted for multiple testing using the Holm-Bonferroni method. Fold enrichment refers to the ratio of observed number of hits to expected number of hits. FDR = False discovery rate. The results were compiled and analyzed in MetaboAnalyst 3.0 (3).

Table S6. Significantly changed metabolites in *Gpt2* mutant mouse brains (P18). *P* values from two-sided Student's *t*-test (threshold *P* value = 0.05) and FDR values were calculated from the normalized data. The mean peak values are intensities; standard deviations and fold changes were calculated from the raw data. Negative and positive ion modes of mass spectrometry are denoted as "-nega" or "-posi", respectively. FDR = False Discovery Rate. The results were compiled and analyzed in MetaboAnalyst 3.0 (3).

	Mean Peak Area Intensity (WT)	Mean Peak Area Intensity (Mut)	Standard Deviation (WT)	Standard Deviation (Mut)	Fold Change (Mut/WT)	<i>P</i> value	(-log <i>P</i>)	FDR
lysine	803356.9333	1833545.117	152481.0854	270421.3016	2.282354257	8.12E-07	6.09	0.000199
cystathionine	547907.3	1320016.967	115697.8766	117903.0564	2.409197626	3.01E-06	5.521	0.000369
cholic acid	33105.94683	5314.160833	10497.15187	3375.28434	0.160519826	0.0001	3.904	0.0079908
proline	15475919	22428706.17	1329244.649	3164887.801	1.449264898	0.0001	3.848	0.0079908
alanine	17631392.5	15611829.17	762953.6881	1184463.913	0.885456391	0.0002	3.788	0.0079908
guanidoacetic acid	316621.8	445213.6833	66629.4731	45403.41862	1.406137175	0.0004	3.349	0.016581
glycine	2441.616167	6529.891833	1071.037025	1731.660534	2.674413744	0.0005	3.288	0.016581
2-keto-isovalerate	6931355.833	6067903.667	306813.5781	568595.4536	0.8754281	0.0006	3.211	0.016581
urea	1626969.735	400024.8083	226947.3301	524364.1094	0.245871082	0.0007	3.178	0.016581
deoxyribose-phosphate	156010.04	98624.67167	15201.34689	8289.089736	0.632168748	0.0007	3.17	0.016581
N-acetyl-glucosamine-1-phosphate	198716.0167	154847.1333	15196.24609	15077.2336	0.779238312	0.0008	3.071	0.018898
folate	98008.695	37548.31667	28771.46461	4640.057922	0.383112097	0.0012	2.925	0.023561
NADP+-nega	168018.315	67253.26667	51492.50621	23717.55948	0.400273427	0.0013	2.903	0.023561
malate	10470619.67	7700541.5	661844.1715	652751.5948	0.735442767	0.0014	2.867	0.023783
histidine	5510466.833	9870994.333	1564334.072	1396281.204	1.791317257	0.0015	2.833	0.023923
phenylalanine	2764123.167	4535573.333	852412.4465	820375.7523	1.640872371	0.0016	2.806	0.023923
fumarate	6453366.833	5686016.667	404988.2382	388485.7269	0.88109305	0.0022	2.654	0.031943
methionine	1285558.167	1879339.5	373058.3906	280172.5516	1.461886011	0.0025	2.606	0.033709
glutathione	14012643	10016342.33	2070523.752	1871473.958	0.714807502	0.0029	2.532	0.037849
threonine	4463144.5	6853462.167	568849.8393	1437858.811	1.535568066	0.0032	2.493	0.03898
dephospho-CoA-posi	49462.86167	124478.2683	19481.7889	45243.20567	2.51660062	0.0033	2.476	0.03898
hydroxyphenylpyruvate	41631.97333	30159.04167	3939.369415	7422.75454	0.724420181	0.0038	2.423	0.042066
NADP+-posi	199377.7683	94725.22	57191.16249	45194.65476	0.475104224	0.004	2.401	0.042295
dephospho-CoA-nega	27059.12	68188.84	13322.63876	25070.56369	2.519994737	0.0049	2.308	0.05023
methylmalonic acid	7567786.833	5705437.333	574682.4676	622323.7233	0.753910946	0.0055	2.257	0.052783
asparagine	799742.3667	1019191.617	85165.35657	91826.46778	1.274399931	0.0057	2.242	0.052783
pyroglutamic acid	132041.25	246045.8	29733.92463	81940.02195	1.863401021	0.0059	2.227	0.052783
UTP-nega	46838.85833	140972.6867	26117.64639	62769.55117	3.00973789	0.0061	2.214	0.052783
citrate-isocitrate	7921255.167	6877127.833	573904.6351	619933.245	0.868186631	0.0064	2.194	0.052783
glucosamine	137964.3183	81114.24667	32605.083	9449.288049	0.587936415	0.0065	2.19	0.052783
IMP	9235691.667	6869645.167	1615206.298	699879.7197	0.74381491	0.0076	2.122	0.058483
glutathione-nega	774181.5667	558013.2167	70706.01271	135519.4	0.720778227	0.0076	2.117	0.058483
ATP-nega	526053.2	1208106.35	254133.4215	463907.953	2.296547859	0.0084	2.076	0.062399
succinate	6104226.333	4632350.5	449631.9542	549639.4156	0.758875941	0.0095	2.024	0.065628

citraconic acid	327398.1333	725850.9	42156.96008	292604.0945	2.217028218	0.0095	2.022	0.065628
DL-pipecolic acid	68270150.83	76923811.67	7815936.201	6117821.015	1.126756141	0.0096	2.016	0.065628
trans, trans-farnesyl diphosphate	24560.80017	8587.927	9918.644297	4039.084121	0.349659903	0.0104	1.983	0.068792
homocysteine	81770.83833	63140.91167	10224.36149	8646.992739	0.772169064	0.0117	1.932	0.075475
cysteine	80887.08833	49257.67667	13389.49742	24897.01829	0.608968349	0.0133	1.877	0.083426
dGTP	572296.3833	1327639	240360.3648	572180.8785	2.319845169	0.0144	1.843	0.087925
maleic acid	6718346.5	6063339.167	280151.7174	633581.3479	0.902504681	0.0148	1.831	0.087925
acetyl-CoA-posi	16886.447	44016.03017	9332.737523	20092.08655	2.606589188	0.0153	1.816	0.087925
citrate	7099462.45	4653529.933	315287.6052	1887719.881	0.655476378	0.0154	1.812	0.087925
GTP-nega	23692.64933	73773.9435	25118.93136	34890.55861	3.113790377	0.0169	1.771	0.094309
O8P-O1P	15371.533	24820.4355	5174.16945	6048.999211	1.614701377	0.0181	1.742	0.098693
dCDP-nega	11139.37917	25371.15767	9161.169113	8006.167667	2.277609666	0.019	1.722	0.10095
ascorbic acid	27267959.67	23846210	1372067.637	2904782.378	0.874513909	0.0243	1.615	0.12661
GMP	12120754.83	9799956	1865185.158	1249335.112	0.808526873	0.0279	1.555	0.14234
ribose-phosphate	1460590.583	1018590.8	385200.6649	159073.9534	0.697382834	0.0297	1.527	0.14857
glutathione disulfide-nega	8982199.333	7006599	997146.645	1412732.04	0.780053831	0.0324	1.49	0.1568
cystine	32445.841	16897.46317	11347.30116	7284.471353	0.520789804	0.0328	1.485	0.1568
creatinine	5277095.667	4728426.5	588173.2638	608749.0511	0.896028194	0.0333	1.478	0.1568
N-carbamoyl-L-aspartate-nega	18208.46667	25464.065	3725.89318	6200.733923	1.398473878	0.0345	1.462	0.15947
guanine	99026.54633	233169.9418	73845.20487	101252.4476	2.354620558	0.0361	1.443	0.16357
OBP	46418.21	67602.865	15823.9628	14751.7061	1.456386728	0.0378	1.422	0.16846
dCMP	28319.545	19385.73167	5888.256613	5589.232082	0.684535421	0.0398	1.4	0.17417
glutamine	56321021	63188380.83	7868063.564	5154978.117	1.121932446	0.041	1.387	0.17642
pantothenate	1486.143833	4321.981167	969.7241714	2587.623957	2.908184975	0.0431	1.366	0.18139
fructose-6-phosphate	2526.723	7145.374167	1600.470659	4399.228125	2.827921449	0.0443	1.353	0.18139
hydroxyproline	379041.6	303953.5333	63605.58734	44461.86162	0.801900196	0.045	1.347	0.18139
4-aminobutyrate	9639418.5	8616305.833	1112532.086	849888.7394	0.893861578	0.0455	1.342	0.18139
UMP	678302.8833	511459.1667	138251.1972	94160.90048	0.754027705	0.0472	1.326	0.18139
ADP-nega	1659.808833	3923.48	872.1070656	2082.634948	2.363814387	0.048	1.319	0.18139
sarcosine	3824569.5	3510547.667	303820.4423	433722.8604	0.917893548	0.0488	1.311	0.18139
hexose-phosphate	668008.15	498977.5167	55006.01208	144936.0807	0.746963217	0.049	1.31	0.18139
carbamoyl phosphate	59255426.83	61509289	4426620.985	4602102.814	1.038036384	0.0499	1.302	0.18139

Table S7. Peak area intensities in *Gpt2* mutant mouse brains (P18).
(See attached.)

Columns contain different biological samples (*Gpt2* mutant and wild-type brains) and rows are analyzed metabolites.

Table S8. Significantly changed metabolites in *Gpt2* mutant mouse brains (P0).

Wild-type and heterozygote littermate brain samples were combined. *P* values from Student's *t*-test and FDR values were calculated from the normalized data. The mean peak values are intensities; standard deviations and fold changes were calculated from the raw data. Negative and positive ion modes of mass spectrometry are denoted as "-nega" or "-posi", respectively. FDR = False Discovery Rate. The results were compiled and analyzed in MetaboAnalyst 3.0 (3).

	Mean Peak Area Intensity (WT)	Mean Peak Area Intensity (Mut)	Standard Deviation (WT)	Standard Deviation (Mut)	Fold Change (Mut/WT)	<i>P</i> value	(-log <i>P</i>)	FDR
alanine	13573473	21346208	2074392	1988245	1.572642	6.25E-07	6.2043	0.000165
hydroxyproline	3623628	6403408	750493.7	1321084	1.767126	2.54E-06	5.5956	0.000335
sarcosine	2842840	3799557	573481.7	496537.2	1.336536	0.000173	3.7609	0.015259
cystathionine	616056.2	1047694	122304.9	314545.9	1.700647	0.000436	3.36	0.028808
anthranilate	13152.77	25941.14	7159.526	6575.875	1.972295	0.005587	2.2528	0.263
threonine	6499735	9971932	2547526	2754458	1.534206	0.00604	2.219	0.263
lysine	1288446	680140.4	441835.5	554968.2	0.527877	0.006974	2.1565	0.263
3-methylphenylacetic acid	10793.06	19526.2	5320.812	7036.357	1.809145	0.011704	1.9317	0.33095
citrulline	3736152	4712573	753161.1	529321.7	1.261344	0.012287	1.9106	0.33095
kynurenic acid	84407.48	129450.2	15280.7	34755.42	1.533634	0.012536	1.9018	0.33095
trans, trans-farnesyl diphosphate	45567.87	66091.31	17125.62	17798.62	1.450393	0.016342	1.7867	0.39222
N-carbamoyl-L-aspartate	21667.71	28648.35	5285.695	4586.656	1.322168	0.020742	1.6831	0.44767
histidine	2367147	3870416	1007695	1511573	1.635055	0.022044	1.6567	0.44767
myo-inositol	52450917	50668447	7628124	6402414	0.966016	0.027248	1.5647	0.51381
S-adenosyl-L-homocysteine-posi	168188.9	280300.7	66768.5	155909.4	1.666583	0.03479	1.4585	0.57404
hydroxyphenylacetic acid	39811.92	21733.41	12030.56	16485.57	0.545902	0.039253	1.4061	0.60957
allantoin	2477784	2917487	627221.1	494912.2	1.177458	0.048372	1.3154	0.70945

Table S9. Peak area intensities in *Gpt2* mutant mouse brains (P0).
(See attached.)

Columns contain different biological samples (*Gpt2* mutant and wild-type brains) and rows are analyzed metabolites. *Gpt2* heterozygote brain samples were labeled as wild-type to pool them with the wild-type brain samples in the analysis.

Web Resources

BrainSpan: Atlas of the Developing Human Brain, <http://developinghumanbrain.org>
1000 Genomes Project, <http://www.1000genomes.org/>
ANNOVAR, <http://www.openbioinformatics.org/annovar/>
Burrows-Wheeler Aligner, <http://bio-bwa.sourceforge.net>
Complete Genomics 69 Genomes Data, <http://www.completegenomics.com/public-data/69-Genomes/>
dbSNP, <http://www.ncbi.nlm.nih.gov/SNP/>
GATK, <http://www.broadinstitute.org/gatk/>
ImageJ, <http://imagej.nih.gov/ij/>
NHLBI Exome Sequencing Project (ESP) Exome Variant Server, <http://evs.gs.washington.edu/EVS/>
MetaboAnalyst 3.0, <http://www.metaboanalyst.ca/>
Online Mendelian Inheritance in Man (OMIM), <http://www.omim.org>
Picard, <http://broadinstitute.github.io/picard/>
PLINK, <http://pngu.mgh.harvard.edu/purcell/plink/>
Primer3, <http://primer3.ut.ee/>
PROVEAN, <http://provean.jcvi.org>
SAMtools, <http://samtools.sourceforge.net/>
SIFT, <http://sift.jcvi.org>
SMDPB, <http://smpdb.ca/>
PolyPhen-2, <http://genetics.bwh.harvard.edu/pph2/>
RefSeq, <http://www.ncbi.nlm.nih.gov/RefSeq>
Brain RNA-Seq, http://web.stanford.edu/group/barres_lab/brain_rnaseq.html

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Table S1. Detailed clinical summary of individuals with *GPT2* mutations.

Individual code Consanguinity (Parental relatedness)	Pedigree 1 (M11000)				Pedigree 2 (MC9400)			
	M11001	M11002	M11003	M11004	M11008	M11009	M11010	M11011
Gender	Female	Male	Male	Female	Male	Male	Female	Female
Age at examination	15y	19y	29y	25y	25y	17y	17y	19y
Head circumference at birth	N/A	N/A	N/A	N/A	N/A	33 cm (-1.72 SDs)	33 cm (-1.72 SDs)	33 cm (-1.6 SDs)
Length at birth	N/A	N/A	N/A	N/A	N/A	47 cm (-1.11 SDs)	47 cm (-1.11 SDs)	49 cm (-0.13 SDs)
Weight at birth	N/A	N/A	N/A	N/A	N/A	2.65 kg (-1.41 SDs)	2.65 kg (-1.41 SDs)	2.7 kg (-1.34 SDs)
Head circumference at examination	50.8 cm (+3.30 SDs)	49 cm (-4.10 SDs)	50 cm (-3.44 SDs)	49 cm (-5.01 SDs)	N/A	50 cm (-3.44 SDs)	50 cm (-3.44 SDs)	49 cm (-4.99 SDs)
Height at examination	48 kg (-1.69 SDs)	31 kg (-4.2 SDs)	48 kg (-2.5 SDs)	43 kg (-2.1 SDs)	N/A	46.5 kg (-5.04 SDs)	48 cm (-4.10 SDs)	153 cm (-1.42 SDs)
Motor development	hypotonia during infancy, head control at 6m	head control at 7m, sat at 8m	head control at 7m, sat at 8m	hypotonia during infancy, head control at 6m, sat at 7m	hypotonia during infancy, delayed development	hypotonia during infancy, walked at 2.5y	hypotonia during infancy, walked at 2.5y	delayed development, microcephaly noted at 6m
Age of being able to walk	N/A	2y	2y	2y	N/A	2.5y	2.5y	1.5y
Speech and cognition	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Speech and cognition	delayed speech, cognition at the level of 3-6y	delayed speech, limited to simple words, cognitive level of 1y	delayed speech, one word sentences at 8y	delayed speech	delayed speech	delayed speech, used to speak clearly, no speech at exam	delayed speech, used to speak clearly, no speech at exam	delayed speech, talking at the level of 1y
One-motor	dysarthria, drooling	dysarthria, drooling	dysarthria, drooling	N/A	N/A	dysarthria, drooling	dysarthria, drooling	drooling
Motor examination	N/A	hypertonia, spastic diplegia	hypertonia, spastic diplegia	hypertonia, spastic diplegia	N/A	hypertonia, spastic diplegia	hypertonia, spastic diplegia	hypertonia, spastic diplegia
Seizures/Epilepsy	No. EEG (19y): normal	febrile seizures at 6m, epilepsy with GTCs at 2.5y, EEG (19y): normal	febrile seizures at 3m, EEG (32y): normal	No	N/A	N/A	N/A	hypertonia, mild hyperreflexia, spastic diplegia
Imaging	CT (19y): normal	CT (10y): normal	MRI (16y): moderately diminished white matter	CT (29y): normal	N/A	N/A	N/A	40 kg (-2.0 SDs)
Remarks	persistent diarrhea during infancy, febrile seizures at 2y, progressive difficulty in walking	progressive difficulty in walking	progressive difficulty in walking	persistent diarrhea during infancy, progressive difficulty in walking	N/A	N/A	N/A	clumsy gait at exam
<i>GPT2</i> mutation	p.Arg404*	p.Arg404*	p.Arg404*	p.Arg404*	p.Arg404*	p.Arg404*	p.Arg404*	p.Arg404*

Individual code Consanguinity (Parental relatedness)	Pedigree 1 (M11000)				Pedigree 2 (MC9400)			
	MC9401	MC9403	MC9429	MC9428	MC9427	MC9426	MC9425	MC9424
Gender	Male	Female	Male	Female	Male	Male	Male	Male
Age at examination	3y	17y	29y	19y	17y	17y	17y	17y
Head circumference at birth	33 cm (-1.72 SDs)	33 cm (-1.6 SDs)	48 cm (-0.37 SDs)	33 cm (-1.72 SDs)	33 cm (-2.22 SDs)	33 cm (-2.22 SDs)	33 cm (-2.22 SDs)	33 cm (-1.6 SDs)
Length at birth	47 cm (-1.11 SDs)	48 cm (-1.11 SDs)	48 cm (-1.11 SDs)	48 cm (-1.11 SDs)	47 cm (-1.11 SDs)	47 cm (-1.11 SDs)	47 cm (-1.11 SDs)	49 cm (-0.13 SDs)
Weight at birth	2.85 kg (-1.09 SDs)	2.5 kg (-1.72 SDs)	N/A	N/A	2.65 kg (-1.41 SDs)	2.65 kg (-1.41 SDs)	2.65 kg (-1.41 SDs)	2.7 kg (-1.34 SDs)
Head circumference at examination	45 cm (-6.79 SDs)	46 cm (-5.40 SDs)	51 cm (-2.77 SDs)	48 cm (-5.93 SDs)	48 cm (-5.93 SDs)	48 cm (-5.93 SDs)	48 cm (-5.93 SDs)	49 cm (-4.99 SDs)
Height at examination	140 cm (-3.9 SDs)	115 cm (-4.15 SDs)	155 cm (-3.0 SDs) at 21y	138 cm (-1.76 SDs) at 12y	108 cm (-2.6 SDs) at 7y	102 cm (-0.05 SD) at 4y	175 cm (-0.22 SD)	179 cm (+0.79 SD)
Weight at examination	27 kg (4.0 SDs)	15 kg (-5.5 SDs)	48 kg (-2.5 SDs) at 21y	27 kg (-2.3 SDs) at 12y	15 kg (-0.77 SD) at 7y	15 kg (-0.77 SD) at 4y	49 kg (-2.4 SDs)	39 kg (-2.9 SDs)
Motor development	hypotonia during infancy	hypotonia during infancy	walked at 3y	better walking until 5y, afterwards unstable	hypotonia during infancy, walked at 2.5y	hypotonia during infancy, walked at 2.5y	noted clumsy gait in preschool	clumsy gait at exam
Age of being able to walk	3y	N/A	3y	N/A	2.5y	2.5y	3.5y	1.5y
Speech and cognition	Yes	N/A	Yes	Yes	Yes	Yes	Yes	No
Speech and cognition	delayed speech, limited to simple words, cognition at the level of 3y	delayed speech, limited to simple words, cognition at the level of 3y	simple words, cognition at the level of 3y	delayed speech, can read name at exam	delayed speech, used to speak clearly, no speech at exam	delayed speech, used to speak clearly, no speech at exam	delayed speech, can speak short sentences	N/A
One-motor	dysarthria, drooling	dysarthria, reduced facial expression	dysarthria, drooling	dysarthria, mild drooling	dysarthria, drooling	dysarthria, drooling	dysarthria, drooling	dysarthria, drooling
Motor examination	hypertonia, spastic diplegia (R>L)	hypertonia, spastic diplegia	hypertonia, spastic diplegia, contracture on left ankle	hypertonia, spastic diplegia	hypertonia, spastic diplegia	hypertonia, spastic diplegia, pronounced tremor of the lower limbs	hypertonia, spastic diplegia	mild hypotonia, hyperreflexia

Seizures/Epilepsy	No	No	epilepsy	No	No	No	No	No	Lemox-Gasaut syndrome. EEG showed bilateral slow waves with delta ranged slow waves	No	febrile seizures at the age of 2y for 9 days, no seizures afterwards	No
Imaging	MRI (16y): enlarged extracerebral fluid spaces	MRI (13y): normal	N/A	MRI (10y): normal	MRI (13y): normal	CT (4y): normal	N/A	N/A	patient history of prolonged hyperpyrexia at 3y	N/A	N/A	CT (3y): normal
Remarks	N/A	N/A	Fell from the roof at 7y, became wheelchair-bound, progressive difficulty in walking	progressive difficulty in walking	mild kyphoscoliosis							Fell from the roof at 3y, no bladder or bowel control
Genetic mutation	p.Pr0272L.eu	p.Pr0272L.eu		p.Pr0272L.eu	p.Pr0272L.eu							p.Pr0272L.eu
CT: computed tomography, EEG: electroencephalography, GTCs: generalized tonic clonic seizures, MRI: magnetic resonance imaging, N/A: not available												

quinolate	61401.0438	37094.60011	55279.04712	33780.75198	38608.28052	34882.73241	36935.63789	39566.82918	61678.14955
phosphoenolpyruvate	5300.160256	6752.745264	5588.13573	N/A	12384.86612	15059.54701	N/A	7832.654806	13591.29444
Uric acid	22080.9182	29007.00166	28776.72556	19383.25317	13189.17949	25955.92063	12905.95589	26276.28138	5209.022444
dihydroxy-acetone-phosphate	179192.4772	309885.3816	252203.7427	296260.281	212674.4156	325956.288	43708.49933	312950.5308	284.37614676
phosphoenolpyruvate	63331.13425	128948.8237	109303.1277	74110.02680	141132.3085	45110.84172	45785.63541	57056.48838	794.19.88787
phosphoenolpyruvate	3510501.344	10879415.318	5582640.365	7164501.165	8719437.818	6720410.691	6658957.86	63854.10.89	5968592.09
phosphoenolpyruvate	148193.7752	46266.47469	49226.47469	96049.8745	67428.51547	50170.254	11024.69372	109106.3585	109106.3585
shikimate	63861.87774	1201.33.0255	115094.6024	59822.72977	58519.16893	109406.21.08	129896.8825	141391.6237	109106.3585
ascorbate	39119.5965	46549.23449	46519.48949	52814.65019	46887.88864	39173.62606	51204.84226	50164.17937	58595.00365
ascorbic acid	21103214.83	28137.12177	25987383.54	25987383.54	25987383.54	25987383.54	25987383.54	25987383.54	25987383.54
2-hydroxybutyric acid	56019902.57	60083438.4	65095941.26	59513422.83	62171934.25	68303116.53	65700090.26	69436240.71	70755249.53
N-carbamoyl-L-aspartate	28737.38044	33890.88833	17249.74111	22480.49045	18335.31982	16249.74737	10977.28512	19866.86853	203.83.28379
Pyrophosphate	75793.47138	134847.4399	98312.17184	127542.3583	144260.9115	182423.1563	108722.9176	103487.1847	130716.8207
glucosyl-L-actone	6686.461956	11980.00222	6874.229954	9932.047308	3143.896773	5226.622246	5740.114012	8896.766276	10977.23272
myo-inositol	8899097.176	9984988.976	7303514.824	8471179.119	8232863.122	10877860.21	6586956.978	10096833.48	10343003.16
hydroxyphenylpyruvate	18379.23773	41815.06616	28220.74811	43387.3857	47583.48599	37114.13835	44388.27381	36546.46812	40772.08018
homocysteic acid	35014.90721	18304.69057	13256.75039	32052.3713	22349.70904	23811.29351	32384.78114	37471.80945	37471.80945
4-pyridoxic acid	27011.02586	28840.2178	18304.1908	18767.98678	15648.88515	24238.96227	27090.94528	30326.34036	20692.88128
3-phosphoglycerate	4517.67931	11595.87586	23526.34261	12218.31828	15152.54433	16374.47372	14762.60219	6284.29827	10854.33657
Indoleacrylic acid	6932.019916	10144.97567	7411.442383	N/A	15396.43884	N/A	11537.97548	8769.821313	N/A
Kynurenic acid	67433.32822	61276.0044	41443.89179	53756.4719	55014.11294	57601.55388	78624.37039	8505.666004	64963.90666
citrate-isocitrate	584710.023	74707.8189	7047997.203	8099287.292	7738533.155	816270.658	6865432.563	8777287.544	7888618.053
isocitrate	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
citrate	4432890.82	2612.997529	5866710.371	6836545.348	7283448.712	7200039.307	6867772.938	7637284.92	6871682.55
2-dehydro-D-gluconate	N/A	N/A	7840.971042	10454.68749	N/A	10992.24996	6272.356375	12546.98861	8365.997321
D-gluconate	4704.570484	8885.228845	3658.571461	12544.75196	21953.87387	38864.1641	15677.61452	24566.52555	18331.19043
D-xythiose-4-phosphate	41812.97886	23925.94287	25992.88622	15641.88181	N/A	N/A	N/A	N/A	N/A
Xanthurenic acid	12676.35338	5878.162388	6321.419546	7855.268521	N/A	N/A	31832.50897	7256.446672	17758.53976
lipate	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
D-glucarate	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
deoxyribose-phosphate	108418.9421	91063.09164	94721.78798	88587.43539	159306.4193	15097.63673	160053.974	157680.074	128355.8685
panthothenate	N/A	N/A	4169.265626	6800.15592	N/A	N/A	3654.513227	N/A	N/A
prepanthothenate	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
deoxyuridine	4698.321884	N/A	N/A	5235.939033	N/A	N/A	N/A	N/A	N/A
ribose-phosphate	932204.3438	1116454.228	777220.8726	1263385.48	1705318.333	1386143.325	1263516.316	1036820.852	1199721.48
thymidine	10976.93323	7318.920573	8360.979423	6794.98002	7318.769687	6885486491	5216.029911	9513.80663	9844.51844
uridine	7673.280243	N/A	N/A	N/A	N/A	9238.481788	8682.768037	N/A	6703.846724
deoxyinosine	3658.593528	4710.740222	4204.101773	5746.432755	N/A	N/A	N/A	N/A	6372.37709
shikimate-3-phosphate	6794.648983	4710.740222	4204.101773	32578.06243	33432.80038	14845.04424	14713.07446	10941.58183	21424.63983
D-glucosyl-L-actone-6-phosphate	20386.28509	38158.30233	23014.42871	48853.51139	65487.92541	20860.23564	35175.50866	N/A	22734.75417
hexose-1-phosphate	616946.2912	207616.9669	587155.0727	916477.7195	649288.3957	722959.9144	596813.4781	608253.6643	646591.1373
glucose-1-phosphate	5751.103845	9252.789884	9469.82933	5230.23031	10270.16026	4943.022061	5733.918519	9946.286248	5736.860034
glucose-6-phosphate	31357.40199	44408.53097	7320.64429	16205.25208	50133.80345	47136.65192	19335.088	35036.46554	7218.980461
fructose-6-phosphate	6897.07664	4704.963161	14635.14946	94103.11314	3856.995112	N/A	3136.698393	N/A	5210.0245
1,3-bisphosphoglycerate	19865.22746	59629.99214	28759.61471	22800.28106	29588.28759	62537.9056	52790.12112	45220.03478	52731.87395
2,3-Diphosphoglyceric acid	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
S-ribosyl-L-homocysteine	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
mega	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
inosine	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

6-phospho-D-gluconate	N/A	8366.004695	8365.205699	N/A	10453.03073	6274.205581	181418.6263	N/A	7316.826152
xanthosine	N/A	N/A	N/A	41399.77035	N/A	2104.940149	N/A	N/A	N/A
D-sedoheptulose-1,7-	N/A	27182.71738	29947.1452	71068.51648	61737.11694	5320.10813	41770.14273	34497.36899	57474.52899
N-acetylglucosamine-1-	132850.5735	13884.9151	169494.557	1682.192022	225772.7547	189666.0607	181418.6263	187535.3342	210754.3278
phosphate									
gluathione-nega	554062.6948	609953.0991	679675.9492	334806.5243	772763.8742	880232.8986	772270.4052	648506.7146	749011.1869
dUMP-nega	7324.06721	6796.315543	7320.308668	5750.401422	1704.504042	15681.40401	6794.872682	7318.442691	10971.06223
Geranyl-PP	30289.12553	51231.61088	86766.59182	61733.17337	3770.84534	40009.378	66908.92905	49636.00951	49636.00951
OMP-OP	20887.91059	17837.86491	30856.6094	94791.63427	13368.02036	16854.32474	15262.42003	25603.02777	8935.987291
dTMP-nega	22989.39229	41286.46243	40249.7891	31363.43323	31363.35622	21432.01678	26694.6789	36866.06414	40250.14418
cyclic-AMP	9909.670172	N/A	13851.02286	14217.09417	6397.332891	15133.57195	14113.74769	18529.67938	5352.812654
fructose-1,6-bisphosphate	60627.11876	49699.08987	50752.21301	32377.0253	54147.7604	73451.62697	26728.48097	35993.26803	40542.04727
trehalose-sucrose	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	5742.565077
Cellulose	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
orotidine-5-phosphate	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
SBP	14638.3724	6236.317999	12019.7131	7236.531125	10978.52723	7745.613865	9410.06429	12024.22673	12114.22944
trans, trans-farnesyl	5292.998861	4810.510412	7623.552608	8391.908095	17241.46238	18820.48587	26119.37956	33441.30043	11396.5056
diphosphate									
S-adenosyl-L-homocysteine	147948.0287	246696.3625	202717.2264	194989.4893	101920.3353	223746.0335	119199.0882	155273.7737	176666.4617
nega									
dCDP-nega	20909.16234	14732.287	31361.91585	36202.5146	18817.93293	N/A	8176.142469	572.966789	28228.97108
5-phosphoribosyl-1-	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
pyrophosphate									
Deoxycholic acid	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
OBP	46806.17667	73703.63786	61673.60875	52279.87091	89901.1561	25602.63431	39734.61335	32409.06196	71099.5985
dUDP-nega	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
CDP-nega	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
UDP-nega	113945.1804	116043.9284	300559.6481	2995.101638	201732.289	81571.7087	154715.4649	129618.2103	188167.6393
Cholic acid	9931.114991	N/A	7304.027863	7840.690001	4704.19181	42341.43527	44241.59404	28751.46874	17248.46289
trehalose-6-Phosphate	27705.91186	26494.74489	66763.17093	38996.85567	41821.52266	34518.54776	62979.85376	40396.54354	65088.61337
Thiamine pyrophosphate	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
adenosine 5-	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
phosphosulfate									
ADP-nega	6272.37349	5226.573501	4704.542781	N/A	N/A	N/A	N/A	N/A	3136.306336
dGDP-nega	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
IDP-nega	3414960.219	3275329.146	622541.6332	51691.52977	7857112.066	3482171.55	6195061.304	2602.21346	6273551.319
GDP-nega	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
CDP-ethanolamine	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
FMN	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
cholesterly sulfate	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
dCTP-nega	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
dUTP-nega	4705.998353	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
dTTP-nega	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
CTP-nega	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
UTP-nega	84118.14786	90428.65775	191763.4277	148939.0819	81547.33721	18816.51981	39729.32003	35541.12985	100948.3056
CDP-choline	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
dATP-nega	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
GATP-nega	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Taurodeoxycholic acid	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
ATP-nega	566906.7704	939754.689	1307561.242	2034456.446	1012397.859	195462.8462	512392.188	449695.3835	1037601.5703
dGTP	545005.9455	1005130.539	1459977.669	2338464.119	986396.8368	304227.881	599034.2944	446332.0437	1066509.375
GTP-nega	36888.33501	56451.2186	97182.97401	73178.13305	11463.95662	3847.003247	15122.88814	18361.16112	78924.13515
UDP-D-glucose	1546749.703	1551420.479	2356397.789	208819.337	2118077.213	1637193.018	2005176.184	177968.1912	2426349.974
UDP-D-glucuronate	106636.7162	108722.9927	129108.9701	180275.0097	140814.2532	148973.7321	157442.079	132768.9112	177721.64

ADP-D-glucose	1823.4041	9401.595659	1306.16939	9832.040548	1824.50612	10978.64339	22897.12047	13590.97491	11500.82081	16339.88474
gaseous 5-diphosphate, 3-diphosphate	13435.49653	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	10983.79326
UDP-N-acetyl-glucosamine	808653.6529	669607.526	866163.346	711397.8832	596862.7773	727824.4422	100447.502	665985.3895	594344.6727	917848.6509
glutathione disulfide-nega	6203309.855	6847751.978	560896.964	5591433.633	847981.188	10189389.86	1032906.08	837246.28	7526779.991	9014657.494
NAD-nega	239392.3938	920553.0609	891668.8753	1027594.771	591770.4461	1730154.308	1517379.559	1238701.62	819560.1015	1435916.653
NADPH-nega	10973.64741	138592.4359	183478.1206	88339.39126	98830.11313	294791.0162	189760.2007	212194.1775	220064.9557	223730.1064
dephospho-CoA-nega	58195.2184	26057.5063	102763.5961	842.22.0992	28739.40855	16253.52327	17030.70926	14573.04056	35947.94817	51810.08652
cyclic bis (3->5) dimeric GMP	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
NADP-nega	20907.75903	59068.38143	91988.53005	65861.70051	93038.87281	26087.44871	192867.053	159889.8638	136939.988	164678.16132
NADPH-nega	N/A	N/A	N/A	N/A	N/A	N/A	3136.21559	N/A	N/A	N/A
coenzyme A-nega	40687.88085	42338.0758	144798.2729	105080.1885	59608.56432	65868.67021	60635.33952	47112.36744	49134.60018	114014.3803
acetyl-CoA-nega	N/A	N/A	N/A	6590.011352	N/A	N/A	N/A	N/A	N/A	N/A
propionyl-CoA-nega	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
butyryl-CoA	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
acetoacetyl-CoA-nega	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
malonyl-CoA-nega	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3-hydroxybutyryl-CoA	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
succinyl-CoA-nega	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
methionyl-CoA-nega	N/A	N/A	N/A	3658.383397	N/A	N/A	N/A	N/A	N/A	N/A
3-hydroxy-3-methylglutaryl-CoA-nega	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2-hydroxyglutarate	796698.8583	817971.6843	109327.9166	777670.7896	856656.1598	1088314.802	1042684.228	819067.8629	865806.2535	875139.4176
2-deoxyglucose-6-phosphate	N/A	N/A	N/A	N/A	N/A	7180.026981	N/A	N/A	N/A	N/A
4-phosphopantoate	13665.60042	3623.883719	14835.10433	12021.71583	4430.361228	18292.93284	N/A	7840.895944	7809.723428	7824.785071
ethanolamine	26598.03081	11872.14585	1181.880143	25046.58609	1448991.521	2028396.594	1715474.956	1374243.531	1743407.561	1451754.25
glycine	9731.364576	N/A	N/A	9868.414889	8936.532513	N/A	9990.949486	N/A	N/A	N/A
alanine	4100.759615	6794.91616	9408.743991	7839.284959	2814.190639	3658.918923	N/A	3658.182111	N/A	11386.55533
betaine aldehyde	1561201.28	165127.242	17458470.74	1458169.4	17719106.36	18231286.93	17929002.83	15973496.15	18143361.71	2612.463542
choline	297101.2877	231442.3263	258133.0158	2581661.9973	318510.8151	256993.7142	274731.1108	270889.4271	245518.0234	17793082.31
4-aminovalerate	109902.0666	71282.23858	26721.38616	43041.15517	N/A	49289.03127	64402.74489	54905.44431	69656.33893	N/A
dimethylglycine	8714626.294	8120577.612	10432524.45	8389217.675	10711425.65	11189775.8	8826641.168	8018318.746	899568.399	10117690.58
serine	2748332.676	2434459.925	15916.00404	21489.20368	6559.288424	N/A	N/A	13536.22895	19875.5905	11482.01101
cysteine	108682.7543	169131.5825	3300387.933	2904177.561	3222319.741	2879542.451	285278.579	2435967.884	1539294.98	308478.01
creatine	4713066.138	4844040.61	4821007.338	3851688.794	74802.00523	60719.62331	59491.08431	63870.70709	60880.43273	60345.14861
proline	19957964.29	23431326.3	25892534.82	20193108.76	1625784.89	1625784.89	5828145.365	4312072.523	5255631.663	4879101.678
indole	119637.5956	104848.8702	88451.05906	112455.33053	184297.15	184297.15	13108590.82	14537931	17294412.63	19938800.03
biohane	6171488.405	7634578.259	7031479.514	6663044.229	56485.51406	183222.8248	41961.2015	47978.19033	55816.8231	79965.90453
valine	170364.9951	163482.7763	122808.0273	118010.1978	6787086.454	938320.773	6307022.387	7910265.254	7088983.414	5453515.525
threonine	5701872.058	7062709.005	7597306.731	4624190.885	6934939.227	139132.8213	140374.7004	102646.858	109160.2733	114737.5536
homoserine	21422.8686	23499.26351	28226.82956	33973.41729	33622.48523	4850881.323	4887992.54	4190889.805	4507828.321	4997149.445
purine	46218.08105	108318.764	98835.99286	108471.3544	48409.09681	31361.1692	19747.81378	22965.41501	13497.56233	12021.52128
cysteine	25265.31919	46894.69542	100490.6552	48919.85259	94430.35596	84689.14102	55486.66462	53388.91458	32147.14547	63604.98278
creatine	12672436.2	11678735.3	130642679.3	135198201	127788916.1	10300697.6	71275.68493	81707.0695	74235.46388	62431.10359
nicotinamide	100841663.1	84980345.94	77625767.88	11871109.2	10038977.3	33721490.6	11766075.6	11990959.1	113596491.1	114251995
imidazoleacetic acid	53755.34208	67973.38743	47632.41228	30839.47767	28163.35376	88305.02109	56652.54416	6096361.28	88116.54852	1800860.74
thymine	N/A	N/A	8570.947109	N/A	N/A	N/A	3889.417068	N/A	N/A	14073.98748
DL-Picolinic acid	67804919.28	77108245.43	85062655.26	75585042.15	65071590.82	81081445.15	6610211.9	56142713.77	74447714.35	6676228.53

sarcosine	3338865.644	3652798.28	3803528.714	2667400.786	3980328.449	3388374.482	3840177.27	4108508.789	4070676.961	3207886.874	3981710.558	3738455.078
putrescine	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	9307.600983	N/A	N/A
spermidine	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	186759.6494	N/A
spermine	N/A	N/A	N/A	N/A	N/A	N/A	N/A	2613.763884	N/A	N/A	N/A	N/A
N-acetyl spermine	N/A	N/A	N/A	N/A	13726.43797	N/A	N/A	N/A	20460.14331	N/A	N/A	N/A
N-acetyl spermidine	5442.3976	N/A	3918.256752	4231.248549	N/A	6389.922329	4708.464401	N/A	N/A	N/A	6246.323053	N/A

Table with 5 columns: Name, CAS No., Molecular Weight, SMILES, and InChI. Contains chemical data for various compounds including amino acids, vitamins, and pharmaceuticals.

Chapter 3: Mitochondrial enzyme GPT2 regulates metabolic mechanisms required for neuron growth and motor function *in vivo*.

This Chapter contains the paper published in Human Molecular Genetics in 2021, doi.10.1093/hmg/ddab269. I conducted all the experiments, Shawn M. Davidson ran LC-MS at Princeton. Ralph DeBerardinis contributed intellectually, and the project was performed under the supervision of Eric M. Morrow. For funding sources please refer to the Chapter.

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General Article

GENERAL ARTICLE

Mitochondrial enzyme GPT2 regulates metabolic mechanisms required for neuron growth and motor function *in vivo*

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Abstract

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The metabolic needs for postnatal growth of the human nervous system are vast. Recessive loss-of-function mutations in the mitochondrial enzyme glutamate pyruvate transaminase 2 (*GPT2*) in humans cause postnatal undergrowth of brain, and cognitive and motor disability. We demonstrate that *GPT2* governs critical metabolic mechanisms in neurons required for neuronal growth and survival. These metabolic processes include neuronal alanine synthesis and anaplerosis, the replenishment of tricarboxylic acid (TCA) cycle intermediates. We performed metabolomics across postnatal development in *Gpt2*-null mouse brain to identify the trajectory of dysregulated metabolic pathways: alterations in alanine occur earliest; followed by reduced TCA cycle intermediates and reduced pyruvate; followed by elevations in glycolytic intermediates and amino acids. Neuron-specific deletion of *GPT2* in mice is sufficient to cause motor abnormalities and death pre-weaning, a phenotype identical to the germline *Gpt2*-null mouse. Alanine biosynthesis is profoundly impeded in *Gpt2*-null neurons. Exogenous alanine is necessary for *Gpt2*-null neuronal survival *in vitro* but is not needed for *Gpt2*-null astrocytes. Dietary alanine supplementation in *Gpt2*-null mice enhances animal survival and improves the metabolic profile of *Gpt2*-null brain but does not alone appear to correct motor function. In surviving *Gpt2*-null animals, we observe smaller upper and lower motor neurons *in vivo*. We also observe selective death of lower motor neurons *in vivo* with worsening motor behavior with age. In conclusion, these studies of the pathophysiology of *GPT2* Deficiency have identified metabolic mechanisms required for neuronal growth and that potentially underlie selective neuronal vulnerabilities in motor neurons.

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Introduction

After birth, the human brain and spinal cord continue to increase dramatically in size, reaching near adult proportions by age 6 (1–5). Postnatal growth of the nervous system is largely driven by axonal, dendritic, and synaptic growth, as well as glial development, as processes such as neurogenesis are completed prior to birth. The biosynthetic needs for postnatal nervous system growth are vast, particularly for long-projecting neurons such as in the motor system. The metabolic mechanisms governing this growth have broad significance to nervous system development and disease.

Genetic diseases offer a powerful lens to investigate metabolism in the human brain. Childhood metabolic diseases may also be amenable to treatments via dietary restrictions or supplements (6). We have identified a new childhood neurometabolic disease caused by autosomal recessive, loss-of-function mutations in the mitochondrial enzyme glutamate pyruvate transaminase 2 (*GPT2*) (7). *GPT2* Deficiency is associated with undergrowth of the brain in the postnatal period (i.e. postnatal microcephaly), as well as cognitive and motor disability. Motor disability in *GPT2* Deficiency has been diagnosed as progressive spastic paraplegia, a condition preferentially affecting lower limbs and construed to be caused by selective vulnerabilities in long-projecting motor neurons (7,8). Spastic paraplegia has been linked to over 70 genetic loci; however, there are only a limited number of genes reflecting a mitochondrial process (8). Knowledge of *GPT2* function, therefore, may contribute uniquely to an understanding of metabolic mechanisms governing neuronal growth, as well as to selective neuronal vulnerabilities in large and long-projecting neurons, such as motor neurons.

GPT2 is one of two transaminases that catalyze the reversible addition of an amino group from glutamate, the major excitatory neurotransmitter in brain, to pyruvate, yielding alanine and α -ketoglutarate, a tricarboxylic acid (TCA) cycle intermediate (9). *GPT2*-mediated metabolism has been studied in the context of cancer, particularly the role of *GPT2* in supporting the TCA cycle (10–14). The TCA cycle enables fuel oxidation, as well as cataplerosis, the process wherein TCA cycle intermediates are consumed for synthesis of macromolecules for cell growth (15). Anaplerosis is the process whereby TCA cycle intermediates are replenished. Homeostatic regulation of anaplerosis and cataplerosis is crucial for times of high biosynthetic need, such as postnatal brain development during which there is a strong upregulation in *GPT2* expression (7).

In the current study, we discover *GPT2*-mediated metabolic processes critical for neuronal growth and motor function. Both germline and conditional pan-neuronal deletion of *GPT2* in mice result in motor abnormalities and premature death pre-weaning. Motor abnormalities include wide hind-limb gait, reminiscent of spastic paraplegia in humans. We demonstrate that *GPT2*-mediated metabolic fluxes into alanine and the TCA cycle are required preferentially for neurons, despite expression in both neurons and glia. We also find metabolic impairments in the *Gpt2*-null brain starting in the first postnatal week, including reduced levels of alanine and TCA cycle intermediates, followed by abnormalities in amino acid and glucose metabolism. Alanine, a non-essential amino acid, becomes essential for survival and growth of *Gpt2*-null neurons *in vitro*, but not for *Gpt2*-null astrocytes. Treatment of *Gpt2*-null animals with supplemental dietary alanine extends survival of mutant animals but does not ameliorate motor function. Lifespan extension of *Gpt2*-null animals on the high-alanine

diet permitted us to study the progression of neuropathology and to identify selective death of lower motor neurons in *Gpt2*-null spinal cords. Overall, our data point to alanine as a potential therapeutic supplement for human patients with *GPT2* Deficiency and identify a central role for *GPT2*-mediated mechanisms in neuronal growth, particularly in long-projecting neurons in motor circuitry.

Results

GPT2 activity is required in neurons *in vivo* for motor function and animal survival

We observed a motor phenotype in germline *Gpt2*-null mice, potentially akin to spastic paraplegia that is observed in patients with *GPT2* Deficiency. In order to study the neuronal requirements of *GPT2* as it may relate to this motor phenotype, we generated a neuron-specific deletion of *GPT2*. We mated mice carrying a conditional *Gpt2* allele, with loxP sites flanking exon 4 (Fig. 1A), to mice expressing Cre-recombinase driven by the rat Synapsin-I promoter, allowing for cell-specific deletion of *GPT2* in neurons starting at as early as embryonic day 12 (16). Of the tissues examined, excision of exon 4 by Synapsin-I-Cre-mediated recombination was observed only in the nervous tissue, brain and spinal cord (Fig. 1B). The excised allele was not present in the liver, kidney or hind-limb or fore-limb muscle. The neuronal specificity of the Synapsin-I-Cre line was further confirmed by an Ai14-tdTomato Cre reporter line (Supplementary Material, Fig. S1). We previously reported that *Gpt2*-null mice demonstrated premature death between postnatal day 18 (P18) and P28 (7). The pan-neuronal deletion of *GPT2* (the mice hence named SynI-cKO) resulted in a similar premature death phenotype as observed for *Gpt2*-null mice (Fig. 1C). All *Gpt2*-null mice ($n=56$) and SynI-cKO mice ($n=34$) died by P28. SynI-cKO mice also started showing weight loss at the same time as *Gpt2*-null mice, at approximately P18 (Fig. 1D).

Gpt2-null and SynI-cKO mice demonstrated a similar motor phenotype, involving motor weakness particularly of hind-limbs, beginning at approximately P18. To measure overall limb grip strength, we performed the wire hang test on *Gpt2*-null and SynI-cKO mice (Fig. 1E). Both groups displayed average and maximum hanging times less than 50% of their wild-type (WT) littermates' performances, indicating poor grip strength and weakness (average hanging time WT: 28.1 ± 2.3 , *Gpt2*-null: 12.52 ± 1.5 , SynI-cKO: 10.6 ± 0.9 seconds). Both *Gpt2*-null and SynI-cKO mice had hind-limb clasping reflex (Fig. 1F and Supplementary Material, Videos S1–S3). Furthermore, gait with a wide hind-limb stance was also present in both *Gpt2*-null and SynI-cKO mice as quantified by DigiGait, a ventral plane videography of rodent gait on a treadmill (Fig. 1G). Further, in the open field arena, animals could be seen dragging their hind-limbs, again reflecting weakness of the hind-limbs (Supplementary Material, Videos S4–S6). Overall, these data indicate the importance of the *GPT2* enzyme in motor function and mouse survival. Deletion of *GPT2* specifically in neuronal cells was sufficient to cause a similar behavioral phenotype as the germline *Gpt2*-null, emphasizing the requirement for *GPT2* enzyme activity in neurons.

Metabolomics across postnatal development in *Gpt2*-null brain identifies the trajectory of dysregulated metabolic pathways

In order to investigate the role of *GPT2* in postnatal brain growth and to observe the progression of metabolic perturbations

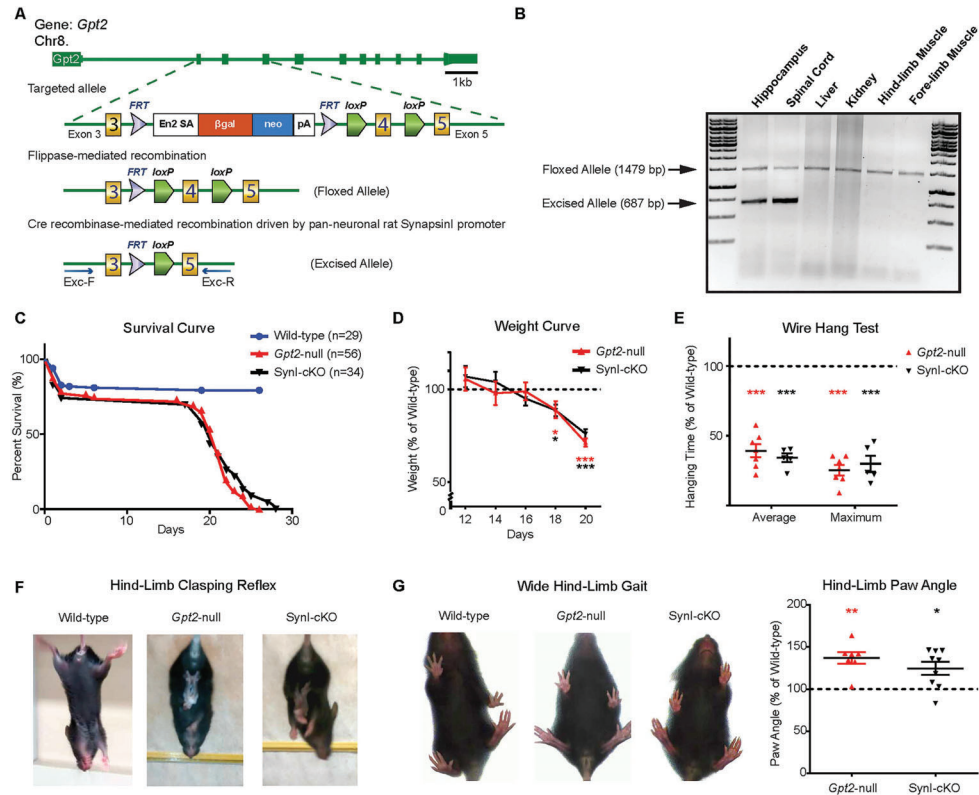


Figure 1. GPT2 activity is required in neurons *in vivo* for motor function and animal survival. (A) Schematic depicting disruption of the *Gpt2* gene at the mouse genomic locus, leading to the germline-null and conditional alleles. The targeted allele consists of flippase recognition sites (FRT) flanking a cassette containing a strong splicing acceptor site (Engrailed 2-SA), β -galactosidase gene, neomycin resistance gene and polyadenylation site between exon 3 and exon 4. After flippase-mediated recombination, the floxed *Gpt2*-allele is converted to a conditional construct with two loxP sites flanking exon 4 (the floxed allele). Prior to Cre recombinase-mediated excision by a tissue-specific promoter, the floxed allele produces a normal GPT2 protein. The excised allele is detected with primers Exc-F & Exc-R (see Materials and Methods). (B) Validation of the conditional allele *in vivo*. Cre recombinase driven by the rat Synapsin-I promoter excises exon 4 only in neuronal cells. In PCR genotyping, the floxed allele appears at 1479 bp and the excised allele at 687 bp. The excision of exon 4 is absent in non-neuronal tissues such as liver, kidney and muscle. (C) Similar timelines of postnatal death in germline *Gpt2*-null and Synapsin-I-Cre conditional mutant (Syn1-cKO) animals. Survival curves of wild-type (blue), germline *Gpt2*-null (red) and Syn1-cKO (black) mice. Wild-type $n=29$ mice, *Gpt2*-null $n=56$, Syn1-cKO $n=34$. Log-rank (Mantel-Cox) test was used to determine differences between the curves. $P < 0.0001$ (wild-type versus *Gpt2*-null), $P < 0.0001$ (wild-type versus Syn1-cKO), $P = 0.5777$ (*Gpt2*-null versus Syn1-cKO). (D) Reduction in weight gain in germline *Gpt2*-null and Syn1-cKO animals compared to wild-type. Weight curves of *Gpt2*-null (red) and Syn1-cKO (black) animals expressed as a percentage of their wild-type littermates ($n=7-11$). $*0.01 < P < 0.05$, $**0.001 < P < 0.01$, $***P < 0.001$. (E) Reduced performance on wire hang test by *Gpt2*-null (red) and Syn1-cKO (black) animals. Average and maximum hanging times are expressed as a percentage of their wild-type littermates. $***P < 0.001$. (F) *Gpt2*-null and Syn1-cKO mice demonstrate hind-limb clasping reflex. When suspended by the tail, the wild-type mice extend their hind-limbs but the *Gpt2*-null and Syn1-cKO mice bend their hind-limbs toward the body midline and clasp their hind paws. (G) *Gpt2*-null and Syn1-cKO mice stand in a wide stance with hind paws spread further apart. Representative images of wide hind-limb gait in *Gpt2*-null and Syn1-cKO mice and quantification of the absolute paw angle with respect to the midline, expressed as a percentage of their wild-type littermates; *Gpt2*-null: $136.9 \pm 6.8\%$ $P = 0.0017$, Syn1-cKO: $124.7 \pm 7.5\%$ $P = 0.011$. Data were collected and analyzed with DigiGait software.

during postnatal brain development in *Gpt2*-null mice, we conducted targeted polar metabolic profiling on acutely dissected hippocampus at P0, P7, P14 and P18 (Fig. 2 and Supplementary Material, Tables S1–S4). We chose hippocampus as the target tissue to monitor metabolic changes, given the high *Gpt2* gene expression (7). Notably, alanine was among the first metabolites in the entire metabolome in *Gpt2*-null hippocampus to show a significant fold change with respect to the WT littermate controls, evident as early as P0 (Fig. 2C and E). Alanine

levels were increased at P0, $134 \pm 7.9\%$ of WT ($P = 0.0035$), then gradually reduced to $89 \pm 1.7\%$ ($P = 0.0024$) at P7, then to $74 \pm 2.6\%$ ($P = 1.16 \times 10^{-6}$) at P14 and finally to $72 \pm 2.6\%$ of WT at P18 ($P = 3.20 \times 10^{-7}$). With regard to the other metabolites in the GPT2 reaction (Fig. 2C), pyruvate remained within the range of the WT levels at P0, P7 and P14 but reduced to $60.8 \pm 4.9\%$ of the WT at P18 ($P = 0.008$). Glutamate levels were slightly elevated in the *Gpt2*-null tissue at P7 ($112.3 \pm 2.1\%$, $P = 0.0103$) but then gradually decreased at P14 ($91.2 \pm 2.9\%$, $P = 0.0423$) and at P18 ($69.5 \pm 4.4\%$,

$P=0.0001$) in comparison to WT. Alpha-ketoglutarate levels in *Gpt2*-null tissue remained similar to WT levels at P0, P7 and P14 but increased at P18 ($134.7 \pm 10.6\%$, $P=0.011$).

To investigate how the global metabolic profile changes in the hippocampus during postnatal development, we plotted the 2-D scores of the principal component analysis (PCA) of the metabolomics data (Fig. 2D). The two groups, WT and *Gpt2*-null, did not separate well at ages P0 and P7. However, consistent with upregulation of the GPT2 protein in the brain postnatally (7), at P14 and P18, the metabolic profile of *Gpt2*-null hippocampus was distinctly different from WT. The indistinct metabolic profiles seen at P0 and P7 point out that any significant changes happening early during the first postnatal week, such as changes in alanine, likely reflect primary effects of GPT2 Deficiency.

For a more comprehensive view of the metabolome, volcano plots were graphed (Fig. 2E). At P0, alanine and kynurenic acid were elevated, whereas tryptophan and xanthurenic acid were decreased. At P7, the early decrease of alanine was accompanied by reductions in malate ($80.7 \pm 5.4\%$, $P=0.0126$) and fumarate ($86.5 \pm 5.4\%$, $P=0.0286$) levels, key metabolites of the TCA cycle, as well as a reduction in serine ($74.4 \pm 3.5\%$, $P=2.7 \times 10^{-4}$), a major interconvertible precursor of alanine (17).

Subsequent to decreases in alanine and TCA cycle intermediates, we noted elevations in several amino acids. At P14, alanine dropped to 74% of the WT value, along with reductions in TCA cycle intermediates including malate ($73.1 \pm 3.2\%$, $P=1.87 \times 10^{-6}$), fumarate ($78.7 \pm 2.2\%$, $P=1.55 \times 10^{-5}$) and succinate ($75.5 \pm 2\%$, $P=7.18 \times 10^{-6}$). At P14, although glutamate levels were at 91% of the WT, some of the other amino acids were elevated, such as valine, threonine, proline, arginine and leucine-isoleucine. Serine levels were still low in *Gpt2*-null hippocampus at P14 ($70.3 \pm 2.7\%$, $P=8.58 \times 10^{-4}$) (Fig. 2E).

At P18, 7 out of 10 essential amino acids had increased levels in the *Gpt2*-null hippocampus, including valine, leucine-isoleucine, phenylalanine, threonine, lysine and arginine (Fig. 2E). Methionine, tryptophan and histidine remained unchanged. On the other hand, from the non-essential amino acids, only proline showed an increase ($181.8 \pm 6.6\%$, $P=2.3 \times 10^{-5}$), whereas alanine ($72 \pm 2.6\%$, $P=3.2 \times 10^{-7}$), glutamate ($69.5 \pm 4.4\%$, $P=0.0332$), serine ($69.8 \pm 2.3\%$, $P=0.0003$) and cysteine ($67.3 \pm 9.9\%$, $P=0.0478$) showed a decrease. The GPT2 gene has been shown to be a target of the stress-induced transcription factor ATF4, which promotes transcription of metabolic enzymes and amino acid transporters at times of metabolic stress such as amino acid limitation (14,18,19). However, we found no increases of ATF4 protein levels in cortex, hippocampus or liver tissue of *Gpt2*-null mice at P18, suggesting the elevation of amino acids in the *Gpt2*-null metabolome was not caused by a compensatory increase of ATF4 (Supplementary Material, Fig. S2A).

The overall decline of TCA cycle intermediates at P18 was accompanied by dramatic increases in levels of almost all glycolytic intermediates except pyruvate, including glucose 6-phosphate ($380.3 \pm 25.8\%$, $P=7.64 \times 10^{-6}$), fructose 1,6-bisphosphate ($453.8 \pm 65\%$, $P=9.15 \times 10^{-5}$) and phosphoenolpyruvate ($244.1 \pm 29.6\%$, $P=0.0075$). We searched for protein level increases in glycolytic enzymes such as hexokinase I and pyruvate dehydrogenase, but these proteins were not increased in hippocampus (Supplementary Material, Fig. S2B). These data suggest that the increases in glycolytic intermediate metabolites may be due to regulation of enzyme activities at a substrate level, given that pyruvate levels are particularly reduced in *Gpt2*-null hippocampus at P18, which would directly promote glycolysis. Overall, the metabolomics data indicate that alanine synthesis

is one of the first metabolic pathways that was altered as a result of loss of GPT2 in postnatal brain development. The early decline in alanine levels was followed by reductions in TCA cycle intermediates and subsequent increases in amino acids and glycolytic intermediates in *Gpt2*-null hippocampus.

GPT2 is enriched in neurons as compared to astrocytes

Brain metabolomics studies indicated that alanine biosynthesis was altered early in postnatal development in the *Gpt2*-null brain (Fig. 2). One intriguing possibility of a mechanism for pathogenesis is that alanine, normally a non-essential amino acid, has become an essential amino acid in GPT2 Deficiency. Before investigating the role of GPT2 in alanine biosynthesis in neurons and astrocytes, we characterized GPT2 expression in these cells.

We initially confirmed mitochondrial localization of GPT2 in the mouse brain. After subcellular fractionation of the whole mouse brain at P18, GPT2 was enriched in the mitochondrial fraction, whereas the paralog of GPT2, GPT1, remained in the cytosolic fraction (Fig. 3A). Enzyme activity in the mitochondrial fractions of *Gpt2*-null whole mouse brains revealed almost zero alanine transaminase activity (Fig. 3B), confirming the localization of GPT2 to the mitochondria at the activity level and the absence of GPT1 in mitochondria based on enzyme activity.

GPT2 expression was more enriched in neurons than astrocytes. We separately cultured cortical neurons and astrocytes from brains of newborn mouse pups and examined GPT2 expression by western blotting. We observed both GPT2 and GPT1 in both cortical neuronal and astrocyte-enriched cultures; however, GPT1 appeared far less abundant in the neuronal culture (Fig. 3C). The ratio of GPT2 to GPT1 band intensities was significantly greater in cortical neuronal cultures (36.15 ± 7.7) than astrocyte cultures (5.98 ± 1.88). Notably, the *Gpt2*-null cortical neuronal cultures had significantly more reduction in total alanine aminotransferase activity ($35 \pm 1\%$ of WT) than *Gpt2*-null astrocytes ($52.3 \pm 3.1\%$ of WT) as compared to the corresponding WT cultures, confirming the enrichment of GPT2 in neurons (Fig. 3D). Confocal microscopy images of cortical neurons (days in vitro—DIV14) and astrocytes in culture revealed the presence of GPT2 in both cell types co-localizing with the mitochondrial marker MitoTracker Red (Fig. 3E). In addition, we analyzed *Gpt1* and *Gpt2* gene expression in the adult mouse hippocampus *in silico*. We curated the number of transcripts from the single-cell RNA sequencing data that are publicly available in DropViz (www.dropviz.org) (20) (Supplementary Material, Fig. S3). We found that mouse neurons preferentially express the *Gpt2* isozyme. *Gpt1* expression was virtually absent, whereas the astrocytes expressed both isozymes. Overall, these data suggest the enrichment of GPT2 in neuronal cells.

Alanine biosynthesis and glutamine-fueled anaplerosis are diminished in *Gpt2*-null neurons *in vitro*

To study alanine biosynthesis in *Gpt2*-null cells, we investigated the conversion of glutamine or glucose into alanine via isotope tracing experiments with [α - 15 N]-glutamine and [U - 13 C]-glucose in cortical neuronal and astrocyte-enriched cultures (Fig. 3F and G). After 24 h in Tyrode medium (artificial cerebrospinal fluid-like, see Materials and Methods), fractional enrichment of labeled alanine in the WT cortical neuronal culture was $28.3 \pm 1.9\%$ and $29.6 \pm 4.8\%$ with the [α - 15 N]-glutamine and [U - 13 C]-glucose precursor, respectively (Fig. 3G, top). In contrast, in *Gpt2*-null cortical neurons, neither [α - 15 N]-glutamine nor [U - 13 C]-glucose precursors resulted in labeling of

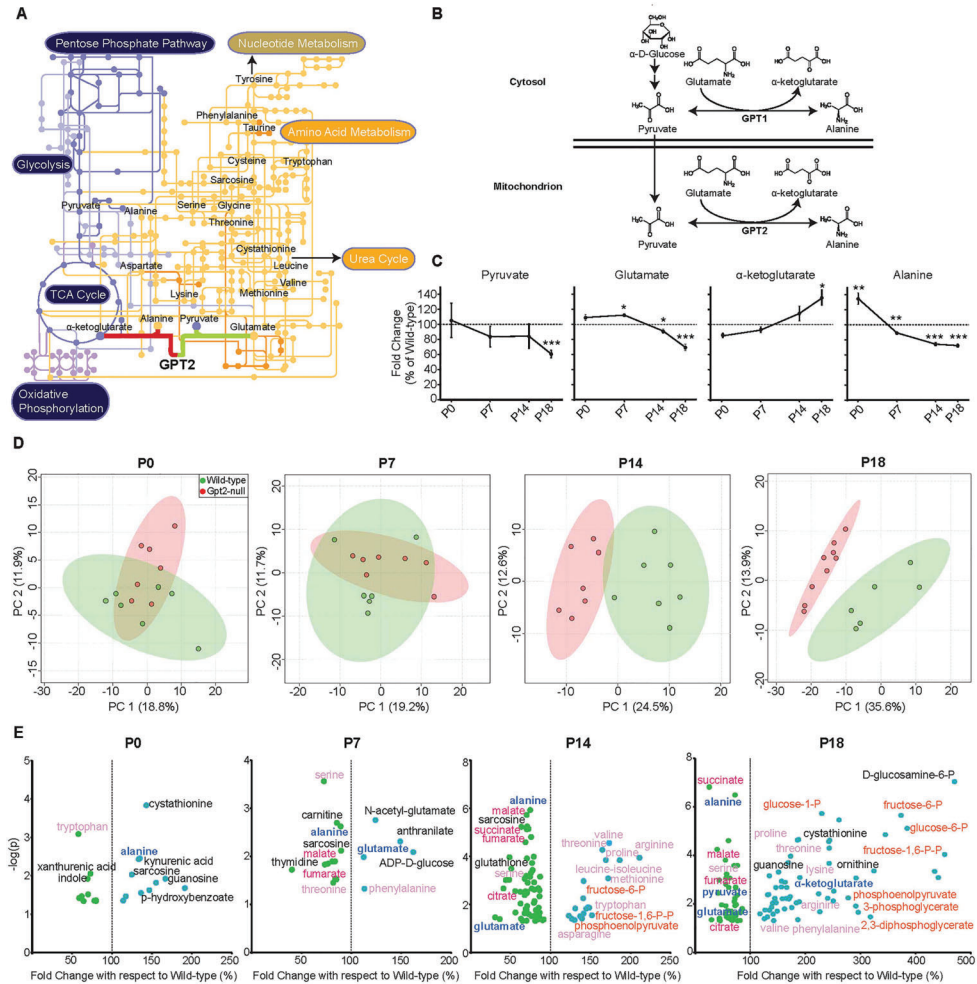


Figure 2. Metabolomics in *Gpt2*-null hippocampus across postnatal development reveals the trajectories of defective metabolic pathways. (A) GPT2 and the relevant metabolic pathways. The metabolic pathway map was modified from KEGG (Kyoto Encyclopedia of Genes and Genomes) (<https://www.kegg.jp/>) (48). GPT2 links amino acid metabolism (orange pathways and nodes) to the TCA cycle metabolism and glycolysis (dark purple pathways and nodes). The metabolic network illustrates the interconnection of pathways that GPT2 has an immediate influence on as well as more remote connections such as, nucleotide metabolism, pentose phosphate pathway and the urea cycle. (B) In the mitochondrion, the primary reaction of GPT2 involves a reversible transfer of an amino group from glutamate to pyruvate yielding alanine and α -ketoglutarate. The cytosolic paralog, GPT1, catalyzes the same transaminase reaction. (C) Fold changes of the metabolites in the GPT2 reaction in *Gpt2*-null hippocampus across postnatal development. The peak intensities obtained from targeted tandem liquid chromatography–mass spectrometry (LC–MS/MS) were normalized to the sample median. At each time point, *Gpt2*-null (P0: $n = 7$, P7: $n = 6$, P14: $n = 7$, P18: $n = 9$) was compared to the average of the wild-type (P0: $n = 7$, P7: $n = 7$, P14: $n = 7$, P18: $n = 6$). One sample t-test was run for each metabolite ($*0.01 < P < 0.05$, $**0.001 < P < 0.01$, $***P < 0.001$). (D) 2-D Score Plots of PCA in the *Gpt2*-null hippocampus. The peak intensities obtained from LC–MS/MS were normalized to the sample median and auto-scaled (mean-centered and divided by the standard deviation of each group). Analyses were performed in MetaboAnalyst 4.0 (<https://www.metaboanalyst.ca>). (E) Volcano plots of significantly changed metabolites in *Gpt2*-null hippocampus across postnatal development. The fold changes are expressed as a percentage of the wild-type average. Note the greater $-\log(P)$ value on the y-axis, the stronger the raw P-value is. The dashed line is positioned at 100% of wild-type, so that any metabolite (green dots) left of the line had a reduced level and any metabolite (blue dots) right of the line had an increased level in *Gpt2*-null hippocampus. Dark blue metabolites are the GPT2 primary reaction metabolites (alanine, α -ketoglutarate, pyruvate, glutamate), magenta metabolites are TCA cycle intermediates, pale pink metabolites are proteinogenic amino acids and orange metabolites are glycolysis intermediates. The entire metabolomics data sets along with false discovery rates for each metabolite can be found in Supplementary Material, Tables S1–S4.

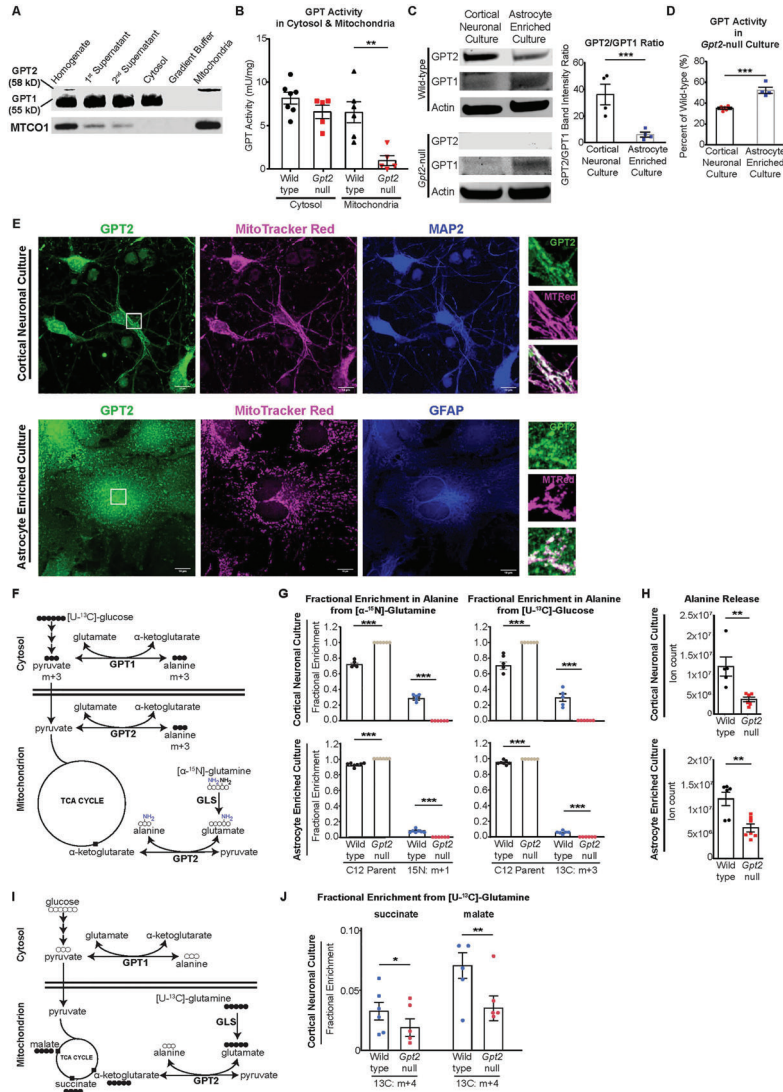


Figure 3. GPT2 is enriched in neurons and sustains alanine biosynthesis and the TCA cycle in neurons *in vitro*. (A) Western blotting of GPT2 and GPT1 in subcellular fractions of the mouse brain at P18. GPT2 (58 kDa) was present only in the total homogenate and mitochondrial fractions. GPT1 (55 kDa) was present in the homogenate and other intermediate fractions containing cytosol but not in the mitochondrial fraction. MTCO1: Mitochondrially encoded cytochrome c oxidase subunit 1. (B) GPT enzyme activity assay in the cytosolic and mitochondrial fractions extracted from wild-type and *Gpt2*-null mouse brain. Wild-type cytosol: 8.15 ± 0.68 mU/mg; *Gpt2*-null cytosol: 6.57 ± 0.77 mU/mg; wild-type mitochondria: 6.53 ± 1.21 mU/mg; *Gpt2*-null: 0.95 ± 0.58 mU/mg. $**P = 0.0038$. (C) GPT2 is enriched in neuronal cultures as compared to GPT1, which is more abundant in astrocytes. Representative images of western blotting of GPT2 and GPT1 in wild-type and *Gpt2*-null cortical neuronal and astrocyte-enriched cultures. Quantification of the ratio of GPT2 to GPT1 band intensity (right). $***P = 0.009$. (D) GPT enzyme activity assay in *Gpt2*-null cortical neuronal and astrocyte-enriched cultures expressed as percentage of their wild-type littermate cultures. $***P = 0.0006$. (E) Primary cortical neurons (top) and astrocyte-enriched cultures (bottom) from wild-type mice demonstrate localization of GPT2 to mitochondria. Confocal microscopy images of GPT2 (green), MitoTracker Red CMXRos (magenta) and MAP2 or GFAP (blue). Scale bar: 10 μ m. Regions boxed in white in the images on the left (GPT2) were magnified and are depicted in images on the right to demonstrate co-localization of GPT2 and MitoTracker Red. (F) Metabolic pathways that convert [13 C]-glucose and [15 N]-glutamine into alanine. GLS: Glutaminase. The filled circles refer to heavy isotope 13-carbon atoms. The heavy nitrogen isotope is highlighted blue. Molecules with heavy isotopes are designated as 'm + #' and the number refers to the number of heavy isotope atoms. (G) GPT2 is required for alanine synthesis from glucose or glutamine in both primary neurons and

alanine. In astrocyte-enriched WT cultures (Fig. 3G, bottom), fractional enrichment of labeled alanine was $8.3 \pm 0.9\%$ and $5.1 \pm 0.8\%$ with the [α - ^{15}N]-glutamine and [^{13}C]-glucose precursor, respectively, a far lower level of labeling than in WT neurons. As in *Gpt2*-null neurons, *Gpt2*-null astrocytes showed no labeling of alanine from either [α - ^{15}N]-glutamine or [^{13}C]-glucose. Alanine release into the Tyrode medium was also substantially reduced in *Gpt2*-null cortical neurons and astrocytes (Fig. 3H). Importantly, the reduction in alanine release was more pronounced in cortical neuronal cultures ($31.2 \pm 5.1\%$ of WT) than in astrocyte cultures ($51.2 \pm 6.5\%$ of WT). Thus, in the medium conditions tested, *Gpt2*-null cortical neurons and astrocytes lacked the ability to produce alanine from either glutamine or glucose. The lack of labeling of alanine in *Gpt2*-null cells, despite the expression of GPT1, indicates that GPT2 is mainly responsible for alanine synthesis. In addition, the greater enrichment of labeled alanine in cortical neuronal cultures compared to astrocyte cultures suggests that the GPT2 reaction is more engaged to synthesize alanine in neurons compared to astrocytes.

Our data indicate that GPT2 supports the TCA cycle in cortical neuronal cultures (Fig. 3I and J). In *Gpt2*-null neurons, fractional enrichment of TCA cycle intermediates from ^{13}C -glutamine was reduced by approximately 40–50%. Fractional enrichments in labeled succinate from [^{13}C]-glutamine precursor were $3.27 \pm 0.74\%$ and $1.89 \pm 0.72\%$ for the WT and *Gpt2*-null cortical neuronal cultures, respectively. Similarly, fractional enrichments in labeled malate from [^{13}C]-glutamine precursor were $7.91 \pm 1.2\%$ and $3.93 \pm 1.16\%$ for the WT and *Gpt2*-null cortical neuronal cultures, respectively. These data indicate that glutamine-fueled anaplerosis in *Gpt2*-null neurons is significantly diminished.

Exogenous alanine is required for survival of *Gpt2*-null animals *in vitro* and extends lifespan of *Gpt2*-null animals *in vivo*

Given the profound decrease in alanine biosynthesis, particularly in neurons, we tested the hypothesis that exogenous alanine may be essential for growth and survival of *Gpt2*-null cells. To test this hypothesis in neurons, we continuously monitored cell death in these cultures (Fig. 4A). *Gpt2*-null hippocampal cultures deprived of alanine showed significantly greater apoptotic cell death than *Gpt2*-null neurons with alanine or WT neurons, as measured by fluorescence of Annexin V Orange Reagent. We also measured neurite length (neurite phase confluence) in hippocampal neuronal cultures with alanine deprivation (Fig. 4B). Growth of neurites as measured by increases in neurite length using the InCuCyte S3 Live-Cell Analysis System came to a halt in *Gpt2*-null neuronal cultures without alanine. As expected, WT cultures grown in medium with or without alanine showed a similar growth pattern, confirming that alanine is a non-essential amino acid in WT cultures. In a complementary experiment using Opera Phenix High Content Screening Confocal Microscopy, neurons (NeuN+) and apoptotic cells (cleaved Caspase3+, Cas3+) were counted at DIV14 after alanine

deprivation in hippocampal neuronal cultures (Fig. 4C). NeuN+ counts for *Gpt2*-null cultures deprived of alanine were greatly reduced. *Gpt2*-null cultures with alanine had slightly reduced NeuN+ counts compared to WT cultures, albeit without statistical significance (with alanine, WT: 470 ± 78.5 versus *Gpt2*-null: 331 ± 59.7 , $P = 0.2093$). Cas3+ to NeuN+ count ratio was greater in *Gpt2*-null cultures deprived of alanine compared to WT cultures. Therefore, both live-cell analysis (InCuCyte) and high-content imaging (Opera Phenix) experiments showed independently that exogenous alanine needs to be supplied for the survival of *Gpt2*-null neurons *in vitro*. To test the reliance of synapse development on exogenous alanine *in vitro*, we stained *Gpt2*-null cultures for synaptic vesicle glycoprotein 2 (SV2) and imaged cells using Opera Phenix High Content Screening Confocal Microscopy (Supplementary Material, Fig. S4). Synapse counts (SV2 puncta) per nuclei were greatly reduced in *Gpt2*-null cultures deprived of alanine. Interestingly, *Gpt2*-null cultures grown with alanine also had modestly fewer SV2+ puncta compared to WT cultures, indicating loss of GPT2 leads to decreased synaptogenesis that is specifically enhanced by alanine deprivation.

In contrast to *Gpt2*-null neurons, which required exogenous alanine, *Gpt2*-null astrocytes deprived of alanine grew comparably to controls *in vitro* (Fig. 4D). The cell growth of *Gpt2*-null astrocytes over time, as determined by InCuCyte Live-Cell Analysis, was not impacted by alanine deprivation. It is important to note that WT and *Gpt2*-null astrocytes grew much better in astrocyte-plating medium (APM), which has regular fetal bovine serum, compared to the cultures that had custom-made media with dialyzed fetal bovine serum. We repeated the alanine deprivation experiment in astrocyte cultures using Opera Phenix High Content Screening Confocal Microscopy (Fig. 4E). Astrocytes were examined 14 days after alanine deprivation. GFAP+ cell count and Cas3+ count to GFAP+ count ratio were similar between WT and *Gpt2*-null astrocytes. Thus, unlike neurons, *Gpt2*-null astrocytes were able to grow in alanine-deficient media. To address the role of GPT2 in astrocytes *in vivo*, we used the GFAP-Cre 77.6 line (21) to delete GPT2 specifically in astrocytes in living animals. Unlike SynI-cKO and conventional germline *Gpt2*-null mice, GFAP-Cre conditional *Gpt2*-null mice survived past P30 and into adulthood, indicating that GPT2 expression in astrocytes is dispensable for animal survival (Supplementary Material, Fig. S5). Overall, the need for GPT2 was more apparent in neurons compared to astrocytes both *in vitro* and *in vivo*, and there is a requirement for exogenous alanine in *Gpt2*-null neurons *in vitro*.

Given the observation that exogenously supplied alanine is required for *Gpt2*-null neurons *in vitro*, we set out to test the hypothesis that supplemental dietary alanine would ameliorate the phenotype seen in *Gpt2*-null animals *in vivo* (Fig. 5). We increased the alanine content from 1.19% alanine (regular alanine diet, RA) to 5% alanine (high-alanine diet, HA) by weight in the rodent diet given *ad libitum*. We first investigated the extent to which alanine levels were affected in the serum of *Gpt2*-null mice. *Gpt2*-null mice fed RA diet showed substantial reductions in the serum alanine concentration at P18 [WT (RA) 0.776 ± 0.006 mM versus *Gpt2*-null (RA) 0.652 ± 0.025 mM, $P = 0.0007$] (Fig. 5A). Importantly, in the *Gpt2*-null animals, the

astrocytes. Fractional enrichment in alanine from [α - ^{15}N]-glutamine (left) or [^{13}C]-glucose (right) in wild-type and *Gpt2*-null cortical neuronal cultures (top) at DIV15 and astrocytes (bottom). The culture medium was replaced with Tyrode medium at DIV14 and samples were collected at DIV15. *** $P < 0.0001$. (H) Prominent decreases in alanine release from *Gpt2*-null neurons and astrocytes. Medium samples were collected at same time as the cell pellets in G. Neuronal culture: ** $P = 0.0057$; astrocyte culture: ** $P = 0.0031$. (I) Metabolic pathways that convert [^{13}C]-glutamine into alanine and the TCA cycle intermediates. (J) GPT2 sustains TCA cycle intermediates in cortical neuronal cultures. Fractional enrichment in succinate or malate from [^{13}C]-glutamine in cortical neuronal cultures as processed in G. Mixed model analysis was done to assess statistical significance with genotype as fixed factor and litters used for culture as random factor. * $P = 0.0139$ ** $P = 0.0044$.

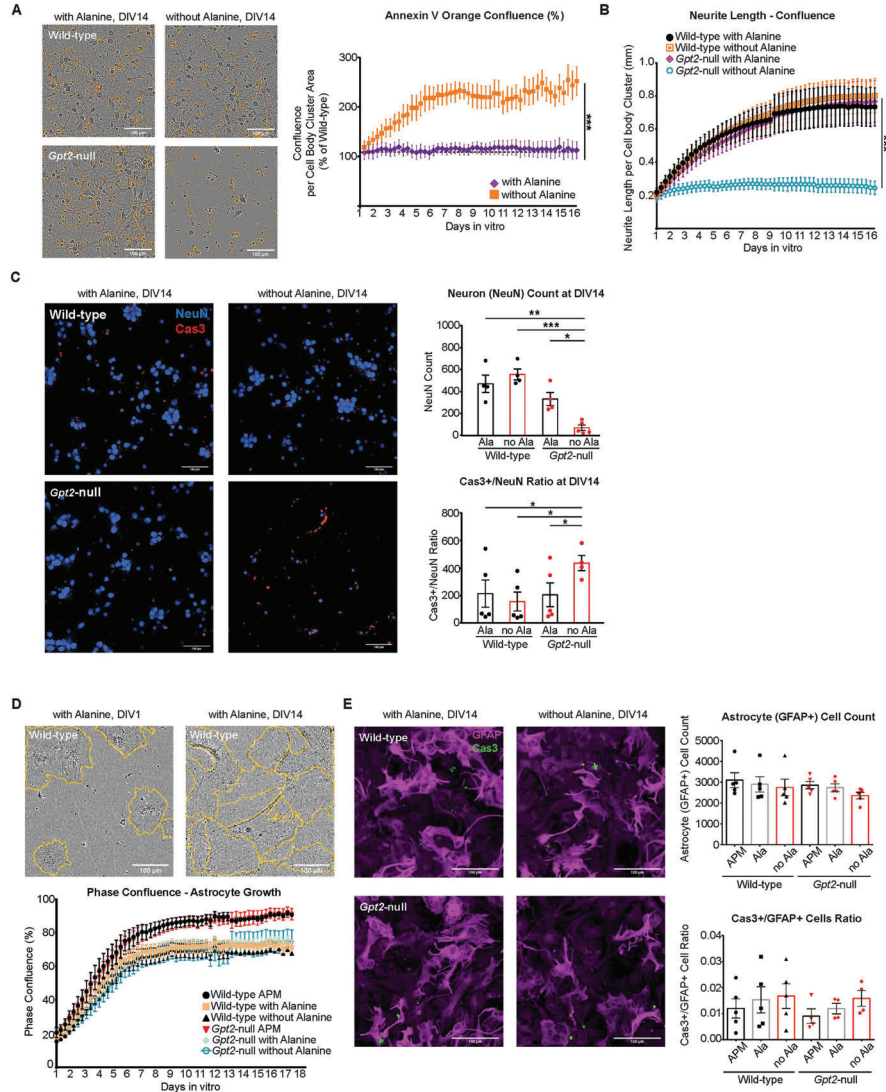


Figure 4. Exogenous alanine is required in *Gpt2*-null neurons for survival in vitro. (A) *Gpt2*-null culture deprived of alanine undergoes apoptosis. Representative images of Annexin V Orange Reagent staining in InCuCyte (left). Scale bar: 100 μ m. The orange confluence per Cell Body Cluster Area values for *Gpt2*-null cultures were expressed as a percentage of their wild-type littermate cultures (right). The curves were fit by non-linear regression (one-phase exponential association) and best-fit values were compared ($***P < 0.0001$). $n = 5$ cultures. (B) *Gpt2*-null neurons fail to arborize without exogenous alanine. Graphs based on InCuCyte S3 NeuroTrack continuous analysis of neurite length as detected by phase confluence. The curves were fit by non-linear regression (one-phase exponential association) and best-fit values were compared ($P < 0.0001$). $n = 5-7$ cultures. (C) Neuronal cell count is decreased and Cas3+ cell count is increased in *Gpt2*-null cultures deprived of alanine. Images from Opera Phenix High Content Screening Confocal Microscopy (left) and quantification of NeuN+ cell counts (top) and Cas3+/NeuN+ ratio (bottom). Scale bar: 100 μ m. The cells were fixed at DIV14 and the quantification represents the time point DIV14 only. $*P < 0.05$, $**P < 0.005$, $***P < 0.0005$. (D) *Gpt2*-null astrocytes do not need exogenous alanine to survive in vitro. InCuCyte S3 phase contrast images from a wild-type astrocyte-enriched culture grown with alanine, at DIV1 (left) and DIV14 (right). Orange lines delineate the cell perimeter. Scale bar: 100 μ m. Quantification of phase confluence over time (bottom). Refer to Materials and Methods for composition of Astrocyte Plating Medium (APM). Other media are similar to APM except they have dialyzed fetal bovine serum and 200 mM glutamine (instead of GlutaMAX) with or without 0.02 mM alanine. (E) Opera Phenix High Content Screening Confocal Microscopy (20 \times water objective) images of GFAP (magenta) and Caspase3 (Cas3, green) in wild-type and *Gpt2*-null astrocyte-enriched cultures and quantification of GFAP+ cell count (right, top), Cas3+/GFAP+ cell count ratio (right, bottom). Scale bar: 100 μ m. GFAP+ cell count for no alanine condition, wild-type: 2750 ± 398.6 versus *Gpt2*-null: 2362 ± 161.4 , $P = 0.3936$. Cas3+/GFAP+ cell count ratio for no alanine condition, wild-type: 0.0167 ± 0.0047 versus *Gpt2*-null: 0.0158 ± 0.003 , $P = 0.8855$.

HA diet normalized serum alanine (Fig. 5A). Overall, there was no statistically significant difference between *Gpt2*-null (HA) and WT (HA) serum alanine levels, albeit with a trend toward a decrease [WT (HA): 0.775 ± 0.004 mM versus *Gpt2*-null (HA): 0.687 ± 0.044 mM, $P = 0.0703$]. Interestingly, in WT mice given HA diet [WT (HA)], alanine levels did not change compared to alanine levels in WT (RA) mice, which is suggestive of normalizing effects due to hepatic metabolism [WT (RA): 0.775 ± 0.006 mM versus WT (HA) 0.775 ± 0.004 mM, $P = 0.8980$]. The alanine levels in *Gpt2*-null brain at P18 were also normalized by the HA diet as per targeted metabolomics (Fig. 5B). Importantly, we discovered that *Gpt2*-null mice fed the HA diet *ad libitum* have increased survival past P30 (Fig. 5C). Out of a total of 38 *Gpt2*-null animals fed HA diet, 13 (34%) were able to survive past P30, whereas none of the *Gpt2*-null mice fed the RA survived (Fig. 5C). WT mice showed no negative effect of HA diet on survival, suggesting good tolerability of high levels of alanine in the diet. However, despite encouraging improvements in survival, *Gpt2*-null mice on HA diet failed to thrive and stagnated in weight gain (Fig. 5D). Motor defects such as wide gait and clasp reflex in the hindlimbs were present in *Gpt2*-null (HA) mice at P18, similar to the *Gpt2*-null (RA) mice (Fig. 5E and Supplementary Material, Videos S7–S10). As *Gpt2*-null mice aged on HA diet, their walking progressively worsened as evidenced by Open Field Tests performed at P18, P30, P60 and P90 (Fig. 5E, Supplementary Material, Videos S11–S18). At around age P90, they tended to lose the ability to stand on their paws completely and displayed crawling behavior. To determine the extent to which the altered metabolome in the neural tissue was corrected by the HA diet, we performed targeted metabolomics on acutely dissected hippocampal tissue from WT (HA) and *Gpt2*-null (HA) mice at P18 (Supplementary Material, Fig. S6A–D, Supplementary Material, Tables S5 and S6). The HA diet resulted in marked improvements in the metabolic profile of *Gpt2*-null hippocampus, particularly for GPT2 reaction metabolites, TCA cycle intermediates and glucose metabolism (Supplementary Material, Fig. S6A–D, Supplementary Material, Tables S5 and S6). In summary, the supplemental dietary alanine improved survival of *Gpt2*-null mice and the metabolic profile of the *Gpt2*-null brain but failed to correct growth and motor abnormalities.

Surviving adult *Gpt2*-null mice on high-alanine diet reveal worsening hypoplasia of the central nervous system and death of lower motor neurons in the spinal cord

Rescue of survival on the HA diet permitted us to examine the progression of neuropathology in surviving *Gpt2*-null animals. Initially at P18, we examined gross anatomy abnormalities in *Gpt2*-null mice fed RA diet. From the two representative WT and *Gpt2*-null images (Fig. 6A), the overall decreased size of the *Gpt2*-null central nervous system was apparent. Thicknesses of the cervical and lumbar enlargements of the spinal cord in the *Gpt2*-null mice (RA) were decreased as well. Also at P18, we examined the spinal cord by immunohistochemistry in *Gpt2*-null (RA) mice. Neuronal numbers were similar; however, motor neurons in the ventral horn, stained for choline acetyltransferase (ChAT), were notably smaller in soma size in the *Gpt2*-null animals in both cervical and lumbar spinal cords (Fig. 6B and C). Reductions in soma size in *Gpt2*-null spinal cord appeared relatively selective for ChAT+ cells, as staining for NeuN, a pan-neuronal marker, in the dorsal horn of cervical and lumbar spinal cord yielded similar densities of NeuN+ soma (Fig. 6B and C) and similar soma size across both genotypes (Supplementary Material, Fig. S7A).

Calbindin+ interneuron counts in the dorsal horn were also similar between the two genotypes (Supplementary Material, Fig. S7C).

We subsequently investigated progressive neuropathology in surviving *Gpt2*-null animals on the HA diet at P90. Surviving adult *Gpt2*-null (HA) mice displayed progressive dysfunction in motor behavior (Fig. 5). The gross anatomy showed worsening on several measurements in the brain and spinal cord of *Gpt2*-null (HA) mice (Fig. 6D and Supplementary Material, Fig. S8A–G). At P90, there was pronounced difference in size of the enlargements in *Gpt2*-null (HA) and WT (HA) spinal cords. It is noteworthy that whereas the WT spinal cord had apparently grown from P18 to P90, the *Gpt2*-null mice stagnated in growth in the spinal cord.

Spinal cords from surviving *Gpt2*-null mice on the HA diet demonstrated reduced motor neuron count, as well as smaller soma sizes in both the cervical and lumbar spinal cord (Fig. 6E and F). This is in contrast to the spinal cords at P18, which only demonstrated reduced soma size, but not reduced soma count at this earlier time point. Loss of neurons at P90 was selective to ChAT+ motor neurons in the ventral horn, as the NeuN+ soma densities in the dorsal horn of both cervical and lumbar spinal cord were comparable (Fig. 6E and F), as was the soma size between the two genotypes (Supplementary Material, Fig. S7B). Also, Calbindin+ interneuron counts in the dorsal horn were similar between WT (HA) and *Gpt2*-null (HA) mice (Supplementary Material, Fig. S7D). We did not detect any microgliosis or positive Fluoro-Jade C staining in either *Gpt2*-null (RA) or *Gpt2*-null (HA) spinal cord (Supplementary Material, Fig. S9). However, in agreement with motor neuron death, in the *Gpt2*-null (HA) spinal cord, we observed astrogliosis with enhanced GFAP staining in the gray matter (Fig. 6G). We also examined for any pathology in the primary motor cortex, as dysfunction in upper motor neurons has been implicated in the etiology of hereditary spastic paraplegia (8). As in the lower motor neurons of the spinal cord, reduced soma size was also present in layer 5 neurons of the primary motor cortex of both *Gpt2*-null (RA) mice at P18 and *Gpt2*-null (HA) mice at P90 (Supplementary Material, Fig. S10). We did not detect any reduction in NeuN+ count, astrogliosis, microgliosis or positive Fluoro-Jade C staining in layer 5 of the primary motor cortex in either *Gpt2*-null (RA) mice at P18 or *Gpt2*-null (HA) mice at P90. Overall, these results indicate that GPT2 regulates processes involved in neuronal growth of both upper and lower motor neurons and that the ventral horn motor neurons in the spinal cord demonstrate selective vulnerability to the loss of GPT2, likely conferring progressive worsening of motor function with age in *Gpt2*-null animals.

Discussion

In this study, we identify metabolic mechanisms wherein the mitochondrial enzyme GPT2 governs neuronal growth. Evidence from both patients with progressive spastic paraplegia and from mouse here indicates that motor function is vulnerable to defects in GPT2-mediated metabolism. Metabolomics on developing postnatal *Gpt2*-null brain demonstrated an early defect in alanine synthesis and impairments in anaplerosis of the TCA cycle. Notably, through conditional deletion of GPT2 in neurons, corroborated by studies in primary cultures, our data support a prominent role for GPT2-mediated mechanisms within neurons, as opposed to in astrocytes. Therefore, these studies pinpoint fundamental metabolic processes required for neuronal growth, and that potentially underlie selective vulnerabilities in motor neuron disease.

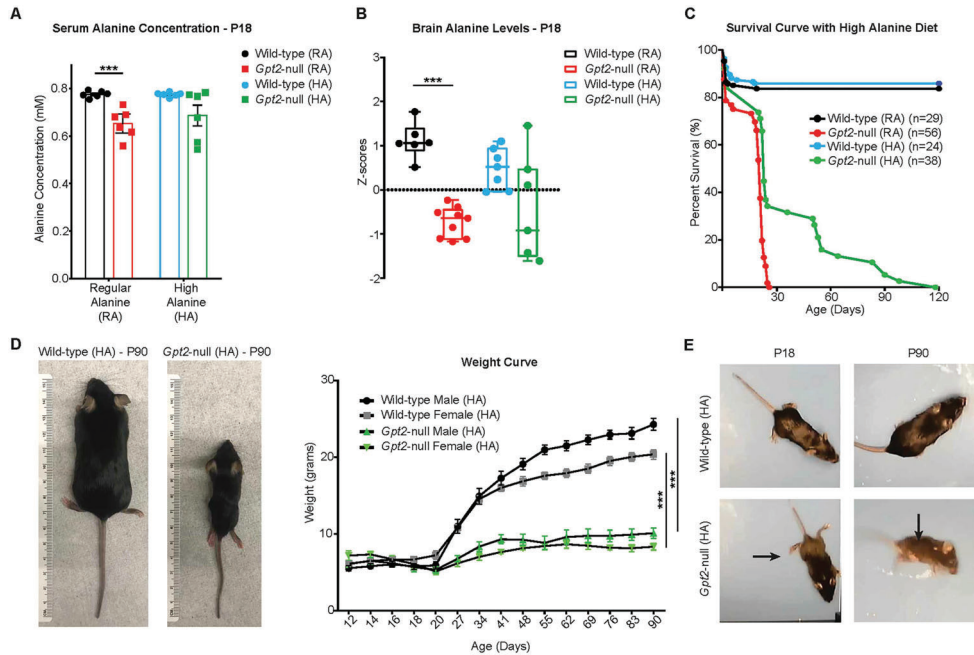


Figure 5. High-alanine diet improves survival and metabolomic profile in the hippocampus of *Gpt2*-null mice but does not alleviate body weight or motor deficits. (A) Serum alanine levels are normalized by the high-alanine (HA) diet in *Gpt2*-null mice at P18. Serum alanine concentrations of wild-type and *Gpt2*-null mice fed either RA or HA diet measured at P18. ****P* (wild-type (RA) versus *Gpt2*-null (RA) < 0.0001); *P* (wild-type (HA) versus *Gpt2*-null (HA) = 0.07). (B) Alanine levels are normalized by the HA diet in *Gpt2*-null hippocampus. Z-scores of alanine levels are shown in the box-and-whisker plot. The peak intensities obtained from targeted tandem liquid chromatography-mass spectrometry (LC-MS/MS) were normalized to the sample median as in Figure 2. ****P* < 0.001. (C) *Gpt2*-null mice on HA diet can survive up to P120. Survival curves of germline *Gpt2*-null mice and their wild-type littermates given RA diet (1.19% w/w) or HA diet (5% w/w). Log-rank (Mantel-Cox) test was used to determine significant differences between the curves, *P* (*Gpt2*-null (RA) versus *Gpt2*-null (HA)) < 0.0001, *P* (wild-type (HA) versus *Gpt2*-null (HA)) < 0.0001. (D) *Gpt2*-null mice that survive on HA diet do not gain body weight in a manner similar to wild-type mice. Representative images of wild-type (left) and *Gpt2*-null (right) mice at P90 fed HA diet. Weight curves of wild-type and *Gpt2*-null mice fed HA diet at ages from P12 to P90. The curves were fit to the Gompertz equation; *P* (wild-type male (HA) versus *Gpt2*-null male (HA)) < 0.0001, *P* (wild-type female (HA) versus *Gpt2*-null female (HA)) < 0.0001. *n* = 5–13 mice. (E) Adult *Gpt2*-null mice that survive on HA diet display worsening motor dysfunction. Pictures of wild-type (HA) (top) and *Gpt2*-null (HA) (bottom) mice at ages P18 (left) and P90 (right). Note the wide hind-limb gait (horizontal arrow) in the *Gpt2*-null (HA) mouse at P18 and the crawling behavior at P90 (vertical arrow). Also see Supplementary Material, Videos S11–S18.

Our experiments indicate that GPT2 is required particularly for neurons. While we do not know the exact cause of animal death, the neuron-specific deletion of GPT2 *in vivo* was sufficient to cause motor abnormalities and premature death similar to that seen in the germline *Gpt2*-null mice. This phenotype was not observed after astrocyte-specific deletion of GPT2. In further support of a role for GPT2 in neurons, our data demonstrated that GPT2 is enriched in neuronal cultures compared to GPT1, which is more abundant in astrocyte cultures. At the mRNA level, *Gpt2* is more abundant than *Gpt1* in mouse neurons, whereas in astrocytes, expression levels of *Gpt1* and *Gpt2* are comparable (22). In contrast to the mouse brain, GPT1 mRNA is virtually absent in the human cortex (23,24) wherein there is an abundance of GPT2 mRNA.

During the early postnatal period in which GPT2 expression is upregulated (7), dysregulation of alanine occurs earliest (at P0) shortly preceding reductions in TCA cycle intermediates (at P7). There is also reduced conversion of glutamine into TCA cycle intermediates via pyruvate transamination in *Gpt2*-null neuronal cultures. In the brain, studies have focused on pyruvate

carboxylase as the major anaplerotic enzyme, particularly in astrocytes (25,26). Human patients with deficiencies in mitochondrial pyruvate carboxylase and pyruvate dehydrogenase, enzymes that support the TCA cycle directly, have hyperalaninemia, most likely due to channeling of pyruvate with glutamate to alanine and α -ketoglutarate via GPT2 (27,28). Our study pinpoints the non-redundant function of GPT2 for neuronal TCA cycle maintenance and alanine synthesis.

Subsequent to reductions in TCA cycle intermediates in *Gpt2*-null brain, we observed prominent increases in almost all glycolytic intermediates, although pyruvate was decreased. Reduced pyruvate may cause decreased substrate inhibition of glycolytic enzymes. Flux analysis *in vivo* may also address the possibility of pyruvate being consumed more by pyruvate carboxylase to make oxaloacetate, which is one of the few TCA cycle intermediates that did not change in *Gpt2*-null brain. Surprisingly, α -ketoglutarate too is unchanged or increased in *Gpt2*-null brain. Metabolites including the TCA cycle intermediates can be efficiently managed by complexes of multiple enzymes (29). To date, the only enzyme that GPT2 is known to form

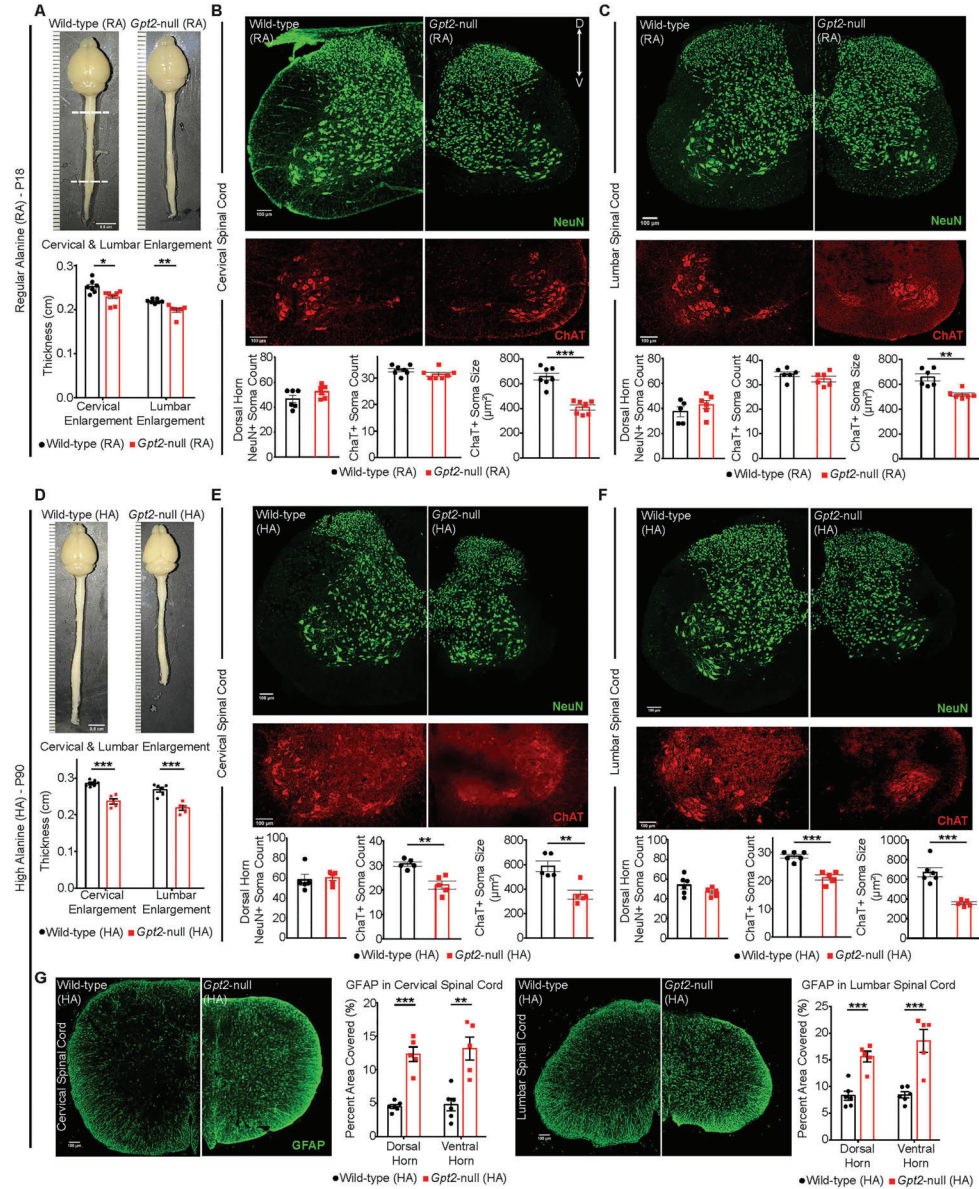


Figure 6. Surviving adult *Gpt2*-null mice fed high-alanine diet exhibit worsening hypoplasia in the central nervous system and selective death of lower motor neurons in the spinal cord. (A) Images of the gross anatomy of the central nervous system of P18 wild-type and *Gpt2*-null mice fed RA diet. Top and bottom dashed lines denote cervical and lumbar enlargement, respectively. Quantification of thickness is shown below the images. Scale bar: 0.5 cm. (B) Images of cervical spinal cord sections from wild-type (RA) and *Gpt2*-null (RA) mice at P18 stained for neurons (top, NeuN, green) and motor neurons (bottom, ChAT, red). Quantification of dorsal horn NeuN+ soma count, ChAT+ soma count and ChAT+ soma size is shown below the images. (C) Images of lumbar spinal cord sections from wild-type (RA) and *Gpt2*-null (RA) mice at P18 stained for neurons (top, NeuN, green) and motor neurons (bottom, ChAT, red). Quantification of dorsal horn NeuN+ soma count, ChAT+ soma count and ChAT+ soma size is shown below the images. (D) Images of the gross anatomy of the central nervous system of P90 wild-type and *Gpt2*-null mice fed HA diet. Cervical and lumbar enlargements were identified as in A. Quantification of thickness is shown below the images. Scale bar: 0.5 cm. (E) Images of cervical spinal cord sections

complexes with is glutamate dehydrogenase (30). Glutamate dehydrogenase is another major anaplerotic enzyme in the brain and may be acting in part to upregulate α -ketoglutarate levels in neurons (31).

Following defects in TCA cycle and alanine levels, we saw prominent increases in essential amino acids in the *Gpt2*-null brain. GPT2 links alanine synthesis and the TCA cycle, thereby supporting both energetics and biosynthesis of macromolecules, particularly proteins. Of note, alanine is the second most frequent amino acid in the primary structure of proteins overall across the domains of Bacteria and Eukarya (32). More studies *in vivo* are warranted to determine the possibilities of changes in specific transporter levels or increased protein breakdown in a compensatory attempt to support both alanine supply and also the TCA cycle. By removing alanine from medium at DIV1, we observed decline of neuronal arborization, as well as cell death in neurons but not in astrocytes. This indicates that alanine has become an essential amino acid and must be supplied exogenously to *Gpt2*-null neurons, whereas GPT2 is not required for astrocytes *in vitro* even without exogenous alanine.

Improvement of animal survival in *Gpt2*-null mice with HA diet re-asserts the conversion of alanine from being a non-essential amino acid to an essential amino acid and allowed us to observe progression of the motor dysfunction in *Gpt2*-null mice as they age. The phenotype of premature death in *Gpt2*-null mice was not completely abolished with HA diet. The variability of the rescue is most likely due to the *ad libitum* nature of the diet regimen and the *Gpt2*-null pup may survive better if alanine is continuously force-fed. Surviving *Gpt2*-null animals on HA diet almost completely lost their ability to walk at around P60 to P90. Neuropathology demonstrated reduced number and soma size of lower motor neurons in the spinal cord, but not of dorsal horn neurons; therefore, we conclude that *Gpt2*-null animals demonstrate selective loss of lower motor neurons. Smaller soma sizes and loss of spinal cord motor neurons have been observed in other neurological diseases, including amyotrophic lateral sclerosis (ALS) (33). Genetic mutations in *SPG11*, or *spatacsin*, a spastic paraplegia gene, also cause spinal cord motor neuron death (34).

Hereditary spastic paraplegia has been attributed to upper motor neuron degeneration due to requirements for long-range axonal projections (8). Although we did not observe any degeneration or cell loss in the primary motor cortex of *Gpt2*-null mice, the soma sizes of the layer 5 neurons were reduced, suggesting that GPT2 acts on similar mechanisms of neuronal growth in both upper and lower motor neurons. Importantly, a majority of mouse models of spastic paraplegia show motor disability without death of upper motor neurons (8,35). Whether the loss of lower motor neurons in *Gpt2*-null mice occurs cell autonomously or due to diminished connectivity from other circuits remains to be explored. Interestingly, one recent case report of a patient with GPT2 Deficiency has demonstrated motor neuropathy consistent with our findings of loss of lower motor neurons in the mouse model (36).

Our data suggest that dietary modifications may involve alanine as a potential therapeutic supplement for human patients with GPT2 Deficiency. Supplemental alanine has been shown to be well tolerated in humans (37–39). To date, the only biochemical finding in human patients with GPT2 Deficiency is decreased alanine levels in the plasma (40), a result which is supported by our data here in the *Gpt2*-null mouse. In our experiments, high alanine supplementation rescued survival and improved metabolic derangements in *Gpt2*-null brain; however, this dietary supplementation did not prevent progression of motor disability or improve weight gain. Alternative procedures to enhance alanine delivery may be warranted, or alanine supplementation in combination with additional dietary modifications may be needed.

In summary, these studies of GPT2 Deficiency have identified broadly significant metabolic mechanisms critical for neuronal growth and for motor circuitry, which contain some of the largest and longest projecting neurons in the nervous system. We present evidence that GPT2-mediated mechanisms are essential for neuronal alanine synthesis and anaplerotic support of the TCA cycle. We find that the loss of GPT2 *in vivo* causes selective vulnerability in lower motor neurons. Finally, our data permit evaluation of high alanine supplementation as a potential treatment for GPT2 Deficiency that may be rapidly implemented and has a favorable risk benefit profile in children.

Materials and Methods

Ethics statement

All experiments involving mice were done in accordance with the National Institutes of Health *Guide for the Care and Use of Laboratory Animals* (41) and approved by the Brown University Institutional Animal Care and Use Committee.

Animals

Gpt2-null animals were obtained as described previously [Knockout Mouse Project at University of California, Davis (MMRRC_047980-UCD)] (7). For generation of the conditional-null ready mouse, the sequence flanked by two FRT sites was excised by mating the *Gpt2*-heterozygous mouse with a mouse containing the flippase transgene (IMSR_JAX:003946). To obtain a pan-neuronal conditional-null mouse, the animal with *Gpt2*-flox allele was mated with a mouse having the Cre recombinase transgene driven by the rat Synapsin-I promoter (IMSR_JAX:003966). The excision of exon 4 by Cre recombinase was tested by PCR with the following primers: Exc-F (5'-CTAACTGTCTGCATGGTGTGACG-3') and Exc-R (5'-GGCTTTCTACCAGGAGGAACAGAGG-3'); the primers detect the floxed allele (1479 bp), the WT allele (1347 bp) and the excised allele (687 bp). To obtain an astrocyte-specific conditional-null mouse, the animal with *Gpt2*-flox allele was mated with the GFAP-Cre line 77.6 (IMSR_JAX:024098). For both Synapsin-I-Cre

from wild-type (HA) and *Gpt2*-null (HA) mice at P90 stained for neurons (top, NeuN, green) and motor neurons (bottom, ChAT, red). Quantification of dorsal horn NeuN+ soma count, ChAT+ soma count and ChAT+ soma size is shown below the images. (F) Images of lumbar spinal cord sections from wild-type (HA) and *Gpt2*-null (HA) mice at P90 stained for neurons (top, NeuN, green) and motor neurons (bottom, ChAT, red). Quantification of dorsal horn NeuN+ soma count, ChAT+ soma count and ChAT+ soma size is shown below the images. (G) Images of GFAP staining in cervical (left) and lumbar (right) spinal cord sections from wild-type (HA) and *Gpt2*-null (HA) mice at P90. Quantification is shown to the right of corresponding images and is represented as percent total area of the dorsal horn or ventral horn covered by GFAP staining. For B, C, E and F, dorsal horn NeuN+ soma were counted in a 100 × 100 μm^2 window. ChAT staining belongs to the same section as NeuN but images of the ventral horn were cropped and magnified to better visualize motor neurons. Soma size was measured by the surface area of the cell in the maximum intensity projection image. Scale bar: 100 μm . For all figures: *0.01 < P < 0.05; **0.001 < P < 0.01; ***P < 0.001.

and GFAP-Cre lines, only females possessing the Cre transgene were used to mate with male *Gpt2* flox/flox due to germline recombination observed in males. Every animal was checked for germline recombination by PCR genotyping in the tail. The Synapsin-I-Cre line was confirmed using a Cre reporter line, Ai14-R26-tdTomato (IMSR_JAX:007914). The background of all mice was C57BL6/J (IMSR_JAX:000664); the mice with a different strain of origin were backcrossed to C57BL6/J at least for six generations.

The mice were maintained under a 12-h light/dark cycle (lights on at 7 a.m./off at 7 p.m.) throughout the year. Feed and water were given *ad libitum*. Formulations for the RA diet (1.19% by weight, LabDiet) and HA diet (5% by weight, Envigo) can be found in Supplementary Material Table S7. The breeding pairs were set up when the *Gpt2*-heterozygous mice were two months old. As soon as they were set up for breeding, their diet was switched from RA diet to the HA diet and they were fed with the HA diet for the entire duration of collecting samples from their progeny.

Behavioral tests

Open field test. The mice were placed at the center of an empty solid mouse cage (31 cm × 31 cm) and the movement was recorded from an overhead camera.

Wire hang test. The mouse was allowed to grab onto a cage topper. The cage topper was inverted approximately 30 cm above the floor of the cage. The time elapsed before the mouse fell off into the cage was recorded. The inter-trial interval was 1 min with five trials in total. The trial was terminated if the hanging time exceeded 2 min.

Hind-limb clamping reflex. The mouse was suspended from the tail for 10 s and the clamping reflex was noted. Three trials were performed.

DigiGait. DigiGait (MouseSpecifics), a ventral plane videography high-throughput instrument with a treadmill, was used for capturing a variety of motor deficits. The lane length was adjusted to an appropriate length depending on the age (P18) and size of the animal to be tested (approximately 8 cm). The animal was placed on the DigiGait treadmill and allowed to walk or run freely as the belt moved at 8 cm/s. Five seconds of video was captured and analyzed by the DigiGait Analyzer software.

Metabolomics and isotope tracing

Metabolomics. Craniotomies on pups after decapitation or cervical dislocation at designated postnatal ages were performed. Hippocampi were dissected immediately on ice. Wet weight of the tissue was measured, and the tissue was flash frozen in liquid nitrogen to quench metabolism. The tissue was processed as previously described with minor modifications (42). The tissue was immersed in 500 μ l of 80% (vol/vol) high-performance liquid chromatography (HPLC)-grade methanol (cooled to -80°C). The tissue was ground with a Kimble pestle, vortexed for 1 min and incubated at -80°C for 4 h. To pellet debris, the sample was centrifuged at $14\,000 \times g$ for 10 min at 4°C . While the supernatant was kept at -80°C , 400 μ l of 80% (vol/vol) methanol (cooled to -80°C) was added to the pellet, which was then vortexed for 1 min, incubated at -80°C for 30 min and then centrifuged at $14\,000 \times g$ for 10 min at 4°C . The supernatants were combined and re-spun at $14\,000 \times g$ for 10 min at 4°C . The supernatants

were divided equally in 1.5-ml Eppendorf tubes and concentrated using a Savant SpeedVac vacuum concentrator (Thermo Scientific) at ambient temperature. Tandem mass spectrometry (MS) was done at Beth Israel Deaconess Medical Center Mass Spectrometry Facility. The samples were re-suspended in liquid chromatography (LC)/mass spectrometry (MS)-grade water and run in tandem LC-MS/MS. Samples were injected into hydrophilic interaction liquid chromatography (HILIC) at high pH using HPLC coupled to a 5500 QTRAP mass spectrometer (AB/SCIEX). Selected Reaction Monitoring (SRM) mode for 300 transitions with positive/negative polarity switching fragmented precursor ions and selected for product ions. Peak areas for each detected metabolite were integrated using MultiQuant software (AB/SCIEX). The statistical analyses and data visualization were done using MetaboAnalyst 4.0 (43) (RRID:SCR_015539). If half of data for a metabolite was not available, then that metabolite was omitted from analysis. All data were normalized by median normalization and auto-scaled (mean-centered and divided by standard deviation of each variable). Unpaired Student's *t*-test assuming equal variance was used to generate a *P*-value.

Isotope tracing. The cortical neuronal cultures at 14 days in vitro (DIV14) were incubated with Tyrode medium (140 mM NaCl, 4 mM KCl, 2 mM CaCl_2 , 2 mM MgCl_2 , 10 mM HEPES) with either 0.5 mM [α - ^{15}N]-glutamine (Sigma-Aldrich, 486809), 0.5 mM [^{13}C]-glutamine (Sigma-Aldrich, 605166) or 4 mM [^{13}C]-glucose (Cambridge Isotope Laboratories, CLM-1396-PK) for 24 h. LC-MS analysis for soluble metabolites was achieved on the Q Exactive PLUS Hybrid Quadrupole-Orbitrap Mass Spectrometer (Thermo Scientific) coupled with hydrophilic interaction chromatography (HILIC). To perform the LC separation of cultured cell samples, an XBridge BEH Amide column (150 mm × 2.1 mm, 2.5 μ m particle size, Waters, Milford, MA) was used with a gradient of solvent A (95%:5% H_2O : acetonitrile with 20 mM ammonium acetate, 20 mM ammonium hydroxide, pH 9.4), and solvent B (100% acetonitrile). The gradient was 0 min, 85% B; 2 min, 85% B; 3 min, 80% B; 5 min, 80% B; 6 min, 75% B; 7 min, 75% B; 8 min, 70% B; 9 min, 70% B; 10 min, 50% B; 12 min, 50% B; 13 min, 25% B; 16 min, 25% B; 18 min, 0% B; 23 min, 0% B; 24 min, 85% B; 30 min, 85% B. The flow rate was 150 μ l/min; the injection volume was 10 μ l; and the column temperature was 25°C . MS full scans were in negative ion mode with a resolution of 140 000 at *m/z* 200 and scan range of 75–1000 *m/z*. The automatic gain control (AGC) target was 1×10^6 .

Cell culture

Mouse primary hippocampal neuron culture. Hippocampal neurons were cultured as described previously (44). Hippocampi from pups aged P0-P1 were dissected in Hank's Balanced Salt Solution (HBSS) (Gibco, 14170-112) and placed in 500 μ l of 20 U/ml papain (Worthington, LK003176) in Earle's Balanced Salt Solution (EBSS) (Worthington, LK003188). The tube with hippocampi/papain was incubated at 37°C for 15 min. The tissue was triturated with a 1-ml pipette tip for 12 strokes. The tissue was further incubated at 37°C for 15 min and triturated. The remaining bits of tissue were allowed to settle and the overlying solution with dissociated cells was spun in a separate tube at 300 *g* for 5 min at room temperature. The cell pellet was dissolved gently in Inhibitor Solution (540 μ l EBSS, 60 μ l Ovomucoid Protease Inhibitor (Worthington Biochemical, LK003182), 30 μ l DNase (Worthington Biochemical, LK003170) per hippocampi) and filtered through a 70- μ m nylon mesh (Fisher Scientific, 22363548). The filtered cell suspension was layered on top of 1 ml Ovomucoid Protease Inhibitor and spun at 70 *g* for 10 min

at room temperature. The supernatant was discarded, and the cell pellet was re-suspended in Neurobasal A+ (NeuroBasal-A (Thermo Fisher Scientific, 10 888 022), 1× B27 Supplement (Thermo Fisher Scientific, 17 504 044), 2 mM GlutaMAX (Thermo Fisher Scientific, 35 050 061)). The full media was changed the next day followed by half media changes every 3 days.

Mouse primary astrocyte-enriched cultures. The culturing protocol was adapted from (45,46). Cortices from pups aged P0-P1 were dissected in HBSS, diced into 6 pieces and transferred to a 15-ml conical tube. The tissue was incubated in 0.25% Trypsin-EDTA in HBSS at 37°C for 30 min. The solution was removed carefully to leave the tissue pieces at the bottom, and 6 ml of Astrocyte Plating Medium (APM) (DMEM (Thermo Fisher Scientific, 10 569-010), 10% fetal bovine serum (Invitrogen, 16 000 044), 1% Penicillin/Streptomycin (Invitrogen, 15 140 122)) was added. The tissue was triturated for 15 strokes with a 10-ml pipette and then 5 strokes more with a 1-ml pipette. The cell suspension was filtered through 70-µm nylon mesh and seeded in a 25-cm² flask (Corning, 3289). After 2 days, the full medium was changed, and then half medium was changed every 3 days. When the astrocyte layer was confluent (~7 days), the flask was shaken at 225 rpm overnight at 37°C. The full medium was changed to APM with 20 µM cytosine arabinoside (Ara-C) to remove any other contaminating proliferative cell types. After two days, the full medium was changed to APM. The Ara-C treatment was repeated the next day. Mild trypsin (0.0675%) treatment was used to lift off the astrocyte layer as a whole and leave the remaining microglia at the bottom of the flask. The layer was incubated in 1 ml of Accutase (StemCellTechnologies, 07920) in a fresh tube at 37°C for 10 min. The layer was dissociated with a 1-ml pipette tip with five strokes. About 2 ml APM was added; the solution was mixed and filtered through a 70-µm nylon mesh. Cells were seeded to plates/dishes coated with 5 µg/ml laminin.

Alanine deprivation in vitro and custom-made cell culture medium. For neuronal cultures, the Neurobasal A+ composition can be found in Supplementary Material Table S7. The cells were incubated with custom-made Neurobasal A+ without alanine, along with 1× B27, 1% Penicillin/Streptomycin and 2 mM glutamine. Neurons were seeded in a 96-well plate (Corning 3596, coated with 100 µg/ml poly D-lysine) at a density of 25 000 cells per well. For alanine deprivation in astrocytes, instead of regular fetal bovine serum, dialyzed fetal bovine serum (Invitrogen, 26 400 044) was used to avoid extra alanine coming from the fetal bovine serum. The rest of the medium composition was the same as APM. Astrocytes were seeded in a 96-well plate (Corning, 3596) at a density of 2000 cells per well.

Continuous analysis of cellular growth and death in vitro

Mouse primary hippocampal neurons were seeded in a 96-well plate (Corning, 3596, coated with 100 µg/ml poly D-lysine) at a density of 25 000 cells per well. The plate was imaged continuously using an IncuCyte S3 Live-Cell Analysis System (Essen BioScience) with the 10× objective. The imaging was interrupted only at media changes every 3 days. The neurites were identified with the NeuroTrack module using phase contrast images. The neurites and cell bodies were segmented in the Brightness mode with an adjustment of 0.3. Any cell body cluster smaller than 100 µm² was excluded. Neurite sensitivity and width were set at 0.75 and 1 µm, respectively. Every data point for Neurite length and Neurite Branch Point was normalized to the cell

body cluster of the first time point in order to account for cell density variability. IncuCyte Annexin V Orange Reagent (Essen BioScience, 4759), a specific phosphatidylserine (PS) cyanine dye, was used to detect apoptotic cells over time. The orange fluorescence confluence was normalized to the cell body cluster area at each time point and expressed as a percentage of its paired WT culture. The orange fluorescence was segmented in adaptive mode with a threshold adjustment of 2. Edge Sensitivity was set at -15. Any orange dot with eccentricity greater than 0.95 was excluded or with a mean intensity lower than 4 was excluded. The acquisition time was 400 ms.

Astrocyte-enriched cultures were seeded in a 96-well plate (Corning, 3596) at a density of 2000 cells per well. The plate was imaged continuously using an IncuCyte S3 Live-Cell Analysis System (Essen BioScience) with the 10× objective. The imaging was interrupted only at media changes every 3 days. The phase confluence was determined using the BasicAnalyzer module with segmentation adjustment set at 2 and area filter at minimum 1 µm².

Immunofluorescence

Cultured cells. The cells were washed with 1× phosphate-buffered saline (PBS) (Fisher Scientific, BP3994) and fixed with 4% paraformaldehyde (PFA) at room temperature for 10 min. The following steps were performed in order: 3 × 5-min 1× PBS washes, 10-min permeabilization in PBS with 0.25% Triton X-100 (T8787, Sigma), 1-h blocking with 10% normal goat serum (NGS) (Jackson ImmunoResearch, 005-000-121) in PBS with 0.1% Triton X-100 (PBST), overnight incubation at 4°C with primary antibody in 2% NGS-PBST, 3 washes with PBST, 1-h incubation with secondary antibody in 2% NGS-PBST, 3 washes with PBST and counterstaining with 300 nM DAPI (Invitrogen, D1306). To visualize mitochondria *in vitro*, the cells were incubated with 100 nM MitoTracker Red CMXRos (Invitrogen, M7512) for 25 min at 37°C, 5% CO₂, prior to performing the immunofluorescence protocol. Coverslips were mounted onto slides with Fluoromount G (SouthernBiotech, 0100-01).

Tissue. The tissues from mice were dissected out after transcardial perfusion with 1× PBS and then with 4% PFA. The tissues were cryoprotected by serially incubating in sucrose solutions of 10%, 20% and 30% overnight at 4°C. The final solution was then changed to half by volume sucrose/OCT (Optimal Cutting Temperature, Fisher Scientific, 23-730-571) and gently shaken for 1 h at 4°C. The tissues were frozen in dry ice/methanol bath and stored at -80°C until the day of sectioning at the cryostat. The sections were cut at 30-µm thickness. The immunofluorescence protocol was as follows, in order: 3-min fixing with 4% PFA, 3 × 5-min 1× PBS washes, 2-h blocking in NGS or normal donkey serum (NDS, Jackson ImmunoResearch, 017-000-121) with 1% (w/v) bovine serum albumin (Fisher Scientific, BP1600) and 0.4% Triton X-100 (Sigma-Aldrich, T8787) (Note: if a mouse-raised antibody was used, a 1-h incubation with 20 µg/ml AffiniPure Fab Fragment Goat Anti-Mouse IgG (H+L) (AB_2338476) or AffiniPure Fab Fragment Donkey Anti-Mouse IgG (H+L) (AB_2307338) in blocking solution was performed), overnight incubation at 4°C with primary antibody in blocking solution, 2 × 4-min washes with blocking solution, 3 × 4-min washes with 0.4% Triton X-100 in PBS, 2-h incubation with secondary antibody in blocking solution, 2 × 4-min washes with blocking solution, 3 × 4-min washes with 0.4% Triton X-100 in PBS, 5-min incubation in DAPI (Invitrogen, D1306) and 3 × 5-min washes with PBS. Coverslips

were then mounted onto slides with Fluoromount G (Southern-Biotech, 0100-01). The list of antibodies can be found in the Key Resources Table.

Confocal microscopy. Imaging and quantification of cell death, cell count, synapse count and arborization were done using an Opera Phenix High Content Screening System and Harmony software (PerkinElmer, RRID:SCR_018809). Hippocampal neuronal cultures, astrocyte-enriched cultures or co-cultures were seeded on an Opera Phenix Ultra CellCarrier 96-well plate (PerkinElmer, 6055302), and at indicated times, different media conditions were tested. Immunofluorescence as described above was done at DIV14 for all plates. The wells were filled with 1× PBS and imaged immediately after. For confocal microscopy on tissues, Olympus FV3000 confocal laser scanning microscope and Fluoview software were used (RRID:SCR_017015). Images were processed and analyzed with ImageJ (RRID:SCR_003070).

Fluoro-Jade C staining

The tissue cryostat sections were mounted on Superfrost Plus microscope slides (Fisher Scientific, 22-230-892) and dried at 50°C for 30 min. The slides were immersed in the following solutions at room temperature in order: 0.2% NaOH in 80% ethanol for 5 min, 70% ethanol for 2 min, distilled water for 2 min, 0.06% potassium permanganate for 10 min, distilled water for 2 min, 0.0001% Fluoro-Jade C (Sigma-Aldrich, AG325) in 0.1% acetic acid for 10 min and 3 times distilled water for 1 min. The slides were dried at 50°C for 10 min, immersed in xylene for 1 min and coverslipped with DPX (Millipore Sigma 06522).

Subcellular fractionation of mouse brain

The protocol was adapted from (47). The brain was immediately removed after cervical dislocation and rinsed in ice-cold 1× brain homogenization buffer (0.320 M sucrose, 1 mM EDTA, 5 mM Tris base, pH 7.4). After decanting, fresh 10 ml/g 1× brain homogenization buffer was added, and the brain was cut into small chunks with surgical scissors. A Kimble pestle was used to homogenize the tissue with 12 strokes each lasting 4 s. The tube was spun at 1300 × g for 3 min at 4°C. The first supernatant was put aside on ice and the pellet was re-suspended in half starting volume with 1× brain homogenization buffer. The pellet was homogenized with a Kimble pestle with eight strokes each lasting 4 s. The tubes were spun at 1300 × g for 3 min at 4°C. The second supernatant was combined with the first and the sample was spun at 10 000 × g for 10 min at 4°C with a Sorvall RC6Plus centrifuge using the SS34 rotor. The pellet was re-suspended in 10 ml/g original tissue of 15% Percoll (Percoll, Cytiva 17089102 prepared in 1× brain homogenization buffer). The suspension was carefully layered onto a Percoll gradient (23–40%) and the tube was spun at 22 000 × g for 10 min at 4°C. The bottom layer was considered the mitochondrial fraction. After carefully removing the upper layers, the mitochondria were aspirated and re-spun with 4 volumes of 1× brain homogenization buffer, at 11 600 rpm for 10 min at 4°C. The supernatant was removed, and 4 volumes of Tyrode-like buffer (118 mM NaCl, 5 mM KCl, 1 mM MgCl₂, 1.2 mM CaCl₂, 0.1 mM Na₂HPO₄·H₂O, 20 mM HEPES, 10 mM glucose, pH 7.4) was added. The tube was spun at 18 000 × g for 10 min at 4°C. After carefully removing the supernatant, the mitochondria were re-suspended in 0.5 ml/g (of original tissue) fatty-acid free bovine serum albumin (10 mg/ml in 1× brain homogenization buffer). The final volume was brought to 3 ml/g (of original tissue) and tube was spun at 6900 × g for 10 min at 4°C

with a tabletop centrifuge. The final pellet was re-suspended in the appropriate buffer for the subsequent assay.

Western blotting

Cells were homogenized in NP40 Cell Lysis Buffer (Invitrogen, FNN0021), 1× PhosStop (Roche, 04906837001), 1× Protease inhibitor Cocktail (PIC, Roche 05892970001) and 0.1 mM PMSF (Sigma-Aldrich, 93482). Tissues were homogenized in RIPA buffer (50 mM Tris, 0.15 M NaCl, 1 mM EDTA, 1% Triton X-100, 0.5 g sodium deoxycholate, 0.1% SDS) with 1× PhosStop and 1× PIC. Twenty-µg protein samples were incubated in NuPage Sample buffer (Invitrogen, NP0007) and NuPage reducing agent (Invitrogen, NP0004) at 70°C for 10 min and immediately placed on ice. The samples were run in NuPage 4–12% Bis-Tris gel (Invitrogen, NP0321) at 175 V until the dye front was at the end of the gel. The gel was transferred to a nitrocellulose membrane (Invitrogen, LC2000) in NuPage Transfer Buffer with 20% methanol at 30 V for 1 h. The blot was blocked with Li-Cor Blocking Buffer (Li-Cor, 927–50000) for 30 min and then permeabilized for 5 min in TBST (Fisher Scientific, BP2411) with 0.05% Tween20 (Sigma-Aldrich, P7949). The blot was incubated in primary antibodies at 4°C overnight. The blot was washed 3 × 5 min with TBST, incubated with secondary antibodies for 1 h, washed with TBST and finally placed in TBS. The blot was imaged using the Li-Cor Odyssey CLx Imaging System (resolution: 84 µm, background subtraction: median) and analyzed using Image Studio Lite software (RRID:SCR_013715). Protein amount in each sample was determined using the bicinchoninic acid (BCA) assay (Thermo Scientific Pierce, PI23227).

GPT enzyme activity assay

GPT activity assay was performed using the Alanine Amino-transferase (ALT) Assay Kit (Sigma-Aldrich, MAK052) according to the manufacturer's manual. Five-µg protein sample of cytosolic or mitochondrial fractions were used. Protein amount in each sample was determined using the BCA assay (Thermo Scientific Pierce, PI23227). BioTek Cytation5 plate reader was used to detect fluorescence; Gen5 software was used to analyze the data (RRID:SCR_017317).

Serum alanine concentration

Blood samples were collected from mice by cardiac puncture, clotted in SST-Mini Gold Top tubes for 15 min, and spun at 2500 rpm with a tabletop minicentrifuge for 10 min. The serum samples were deproteinized with a 10-kDa molecular weight cutoff spin filter (Corning, 431481). Alanine concentration was determined using the Alanine Assay Kit according to the manufacturer's manual (Sigma-Aldrich, MAK001). BioTek Cytation5 plate reader was used to detect fluorescence; Gen5 software was used to analyze the data (RRID:SCR_017317).

In silico analysis of Gpt1 and Gpt2 gene expression

Gene expression profiles of the mouse hippocampus were extracted from DropViz (www.dropviz.org) (20). Data were visualized using JMP Pro 14 (RRID:SCR_014242).

Statistical analysis

All data presented in the figures and the Results section are presented as average ± standard error of the mean, unless otherwise noted. The statistical test for comparisons of two groups was unpaired two-tailed Student t-test unless otherwise noted

or when the data are presented as percentage of the WT average value, in which case one-sample t-test was performed with a hypothetical value of 100. All statistical analyses were compiled using GraphPad Prism software (RRID:SCR_002798). Mixed model analysis was done using JMP Pro 14 (RRID:SCR_014242).

Supplementary Material

Supplementary Data are available at HMGJ online.

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Conflict of Interest statement. The authors declare no competing interests.

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Author contributions

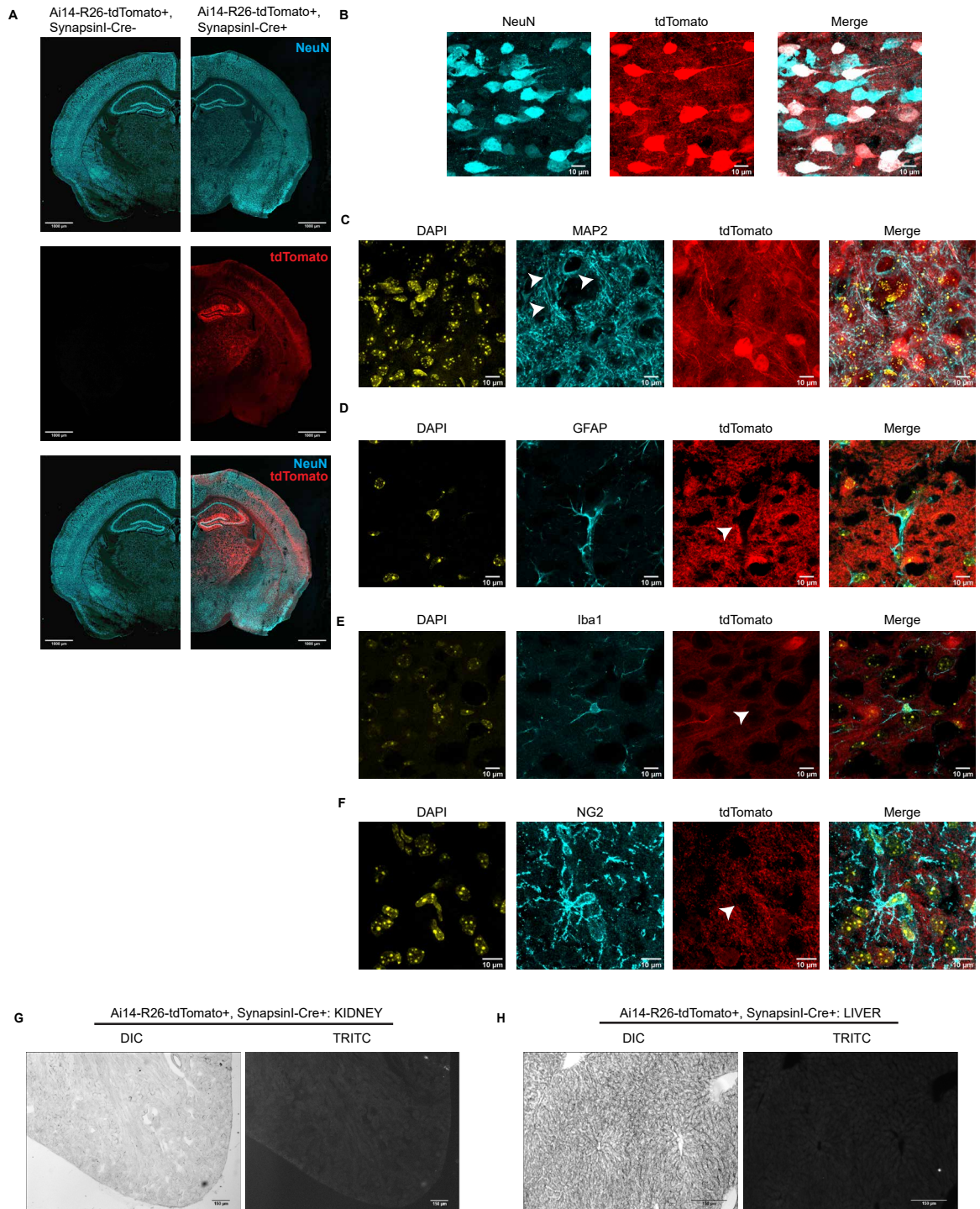
Conceptualization O.B. and E.M.M.; O.B. conducted all experiments; S.M.D. contributed to studies involving mass spectrometry for isotope tracing; Data Curation and Visualization O.B.; Experimental Design and Data Analysis O.B., S.M.D., R.J.D. and E.M.M.; Formal Analysis and Writing—Original Draft, O.B. and E.M.M.; Writing—Review & Editing, O.B., S.M.D. R.J.D. and E.M.M.; Supervision, Project Administration, and Funding Acquisition, E.M.M.

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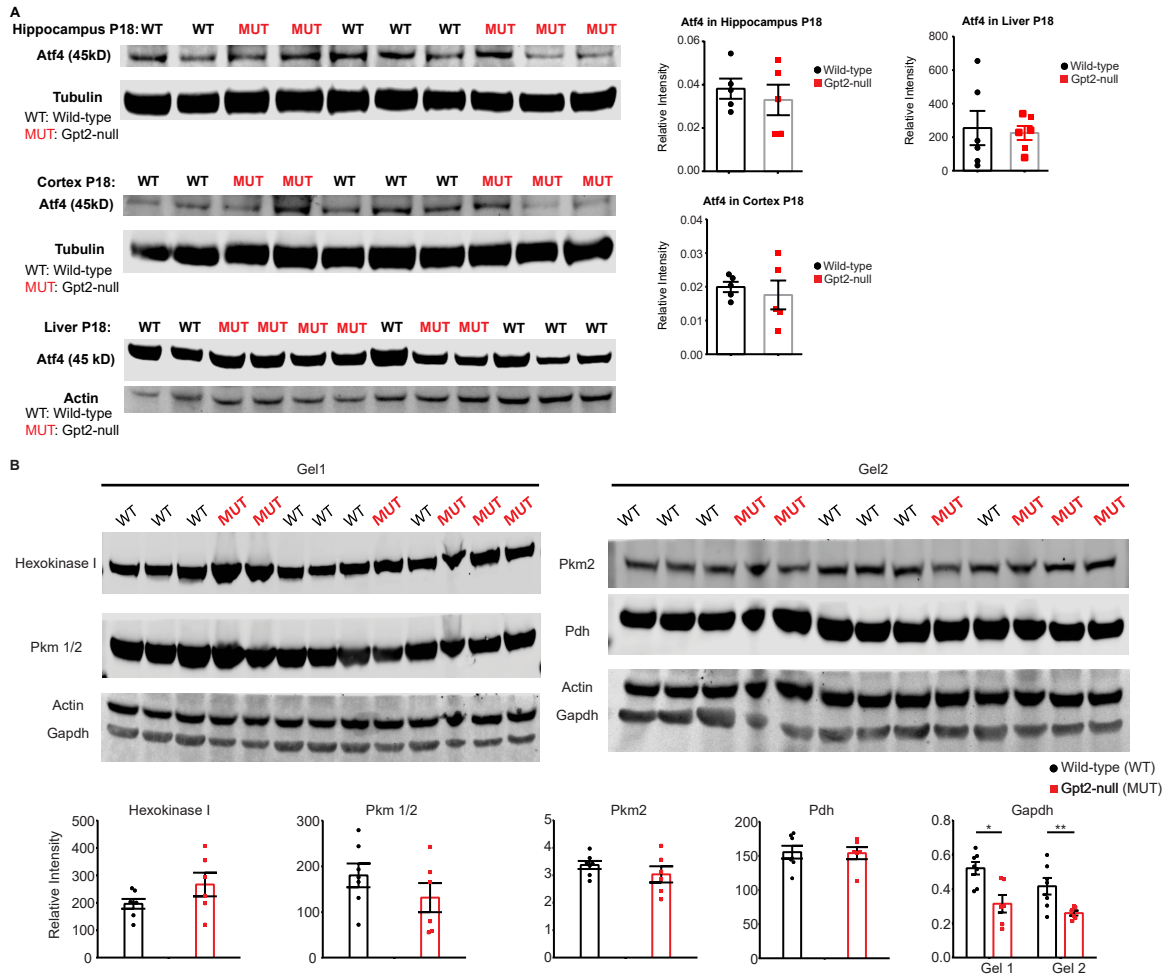
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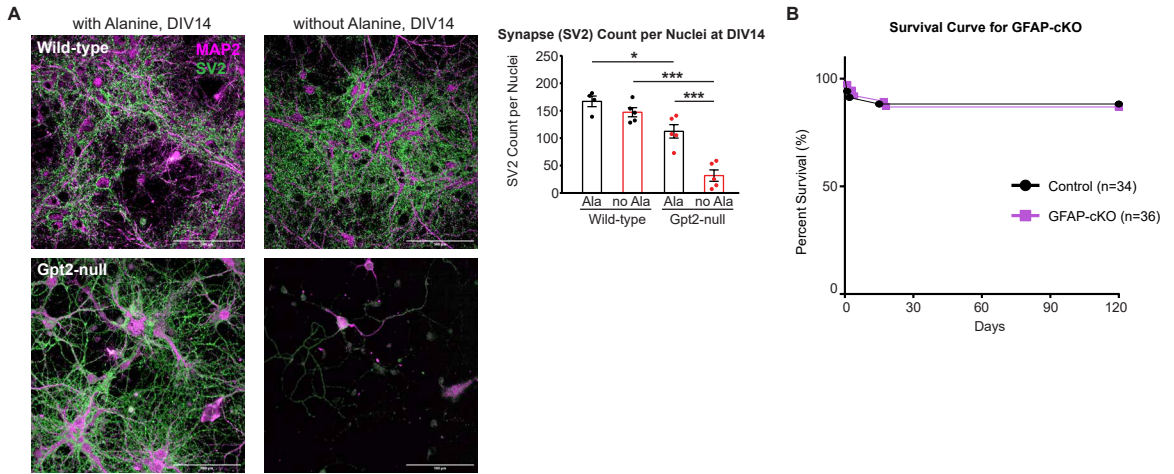
SUPPLEMENTARY FIGURE 1.



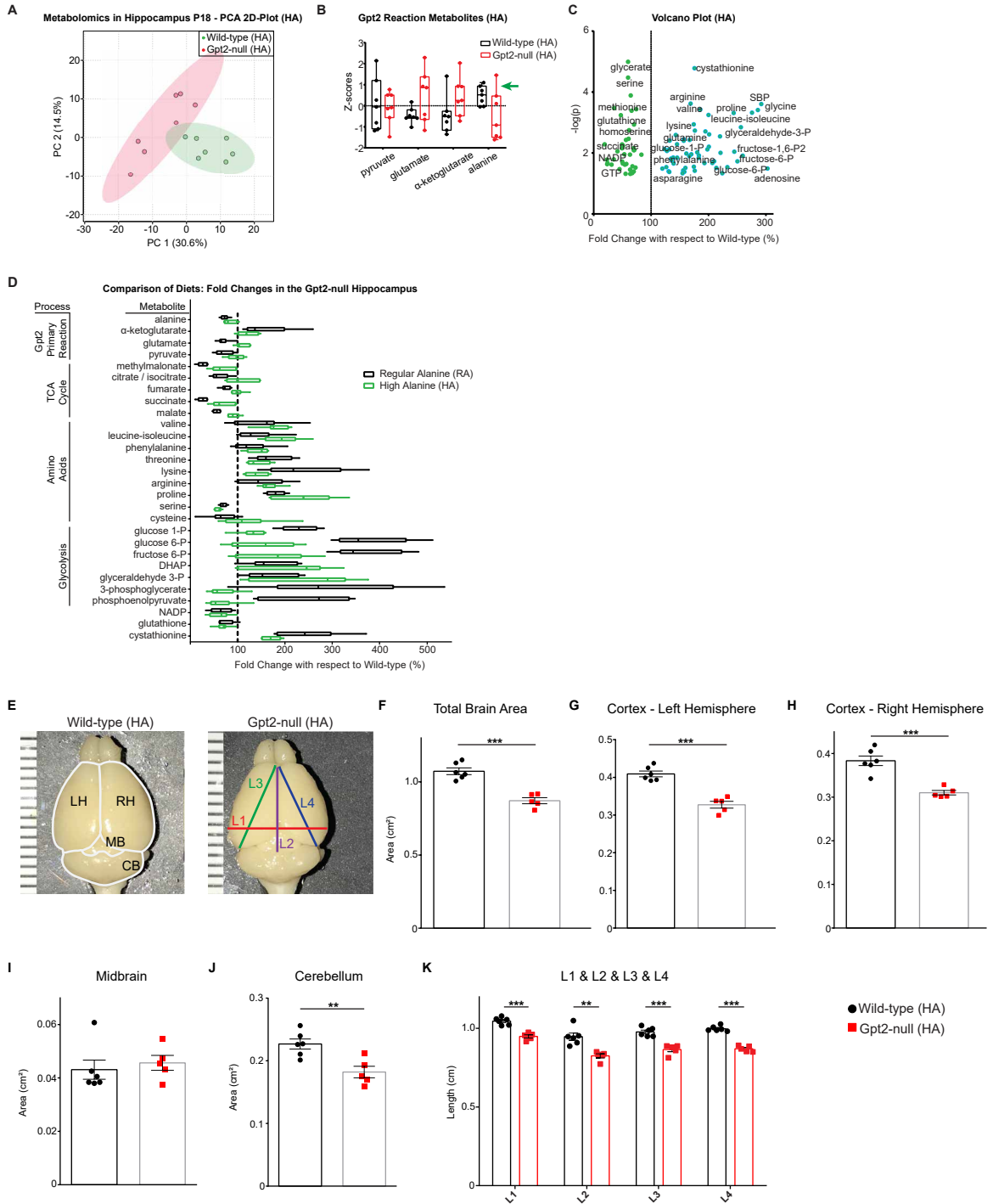
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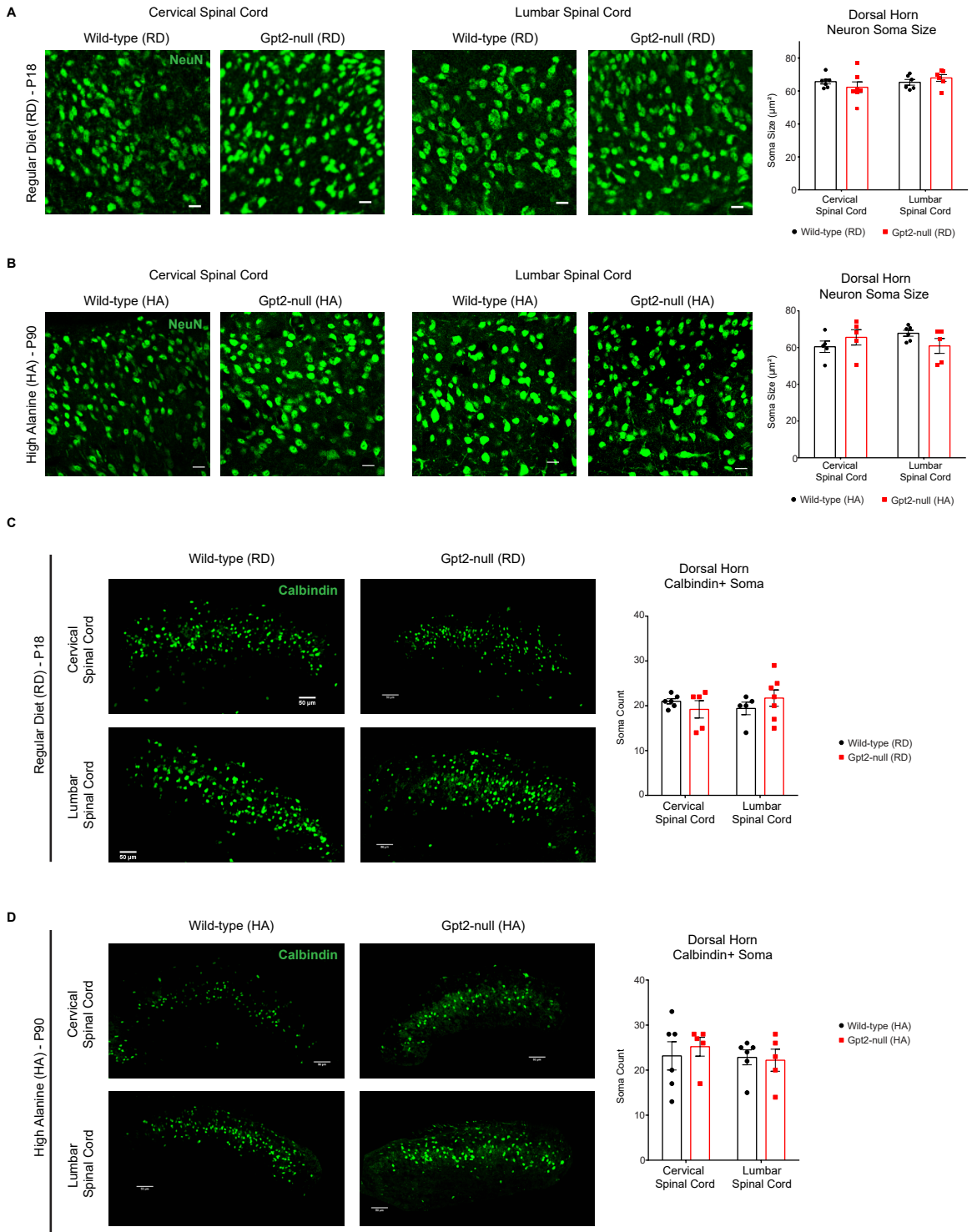
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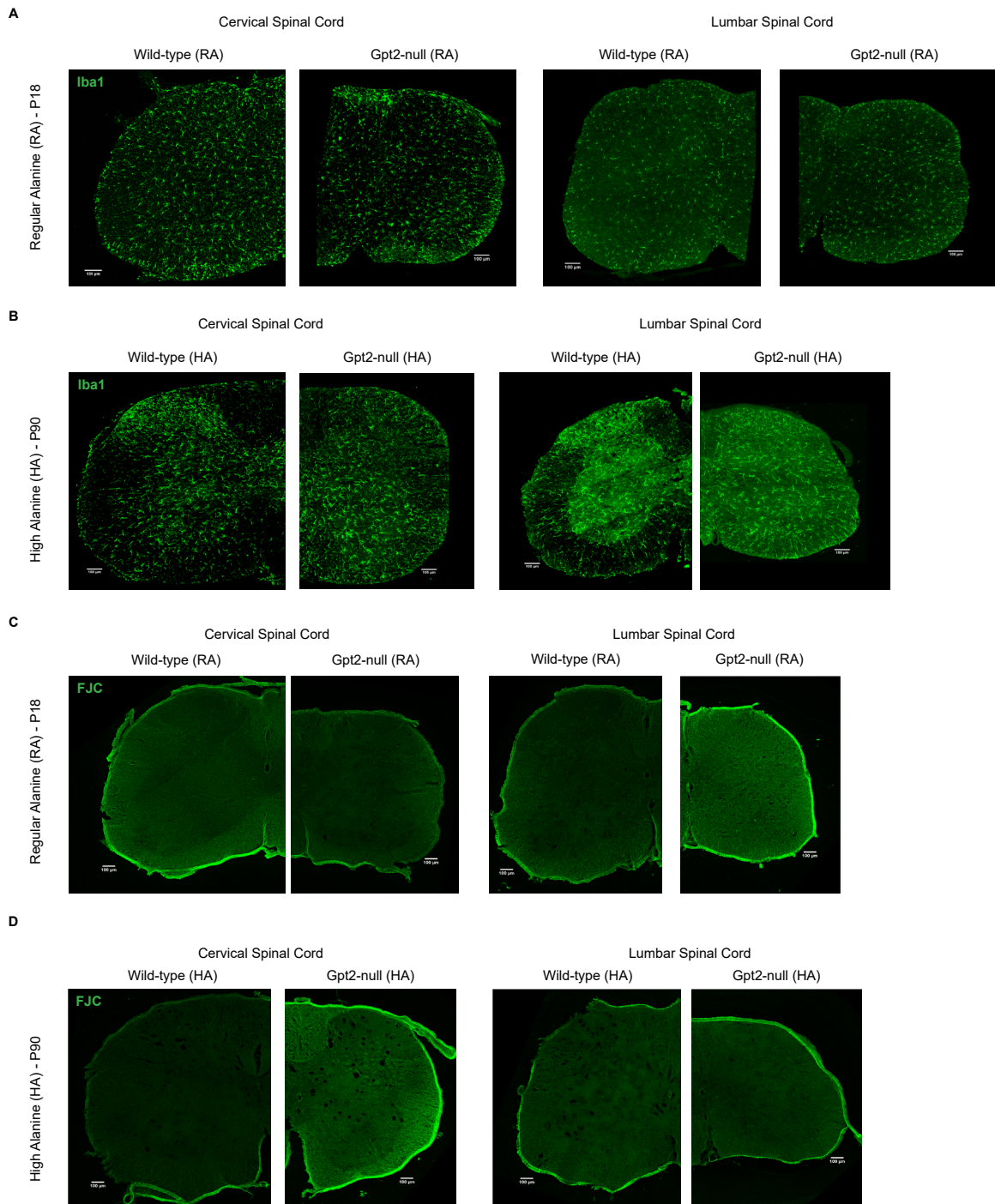
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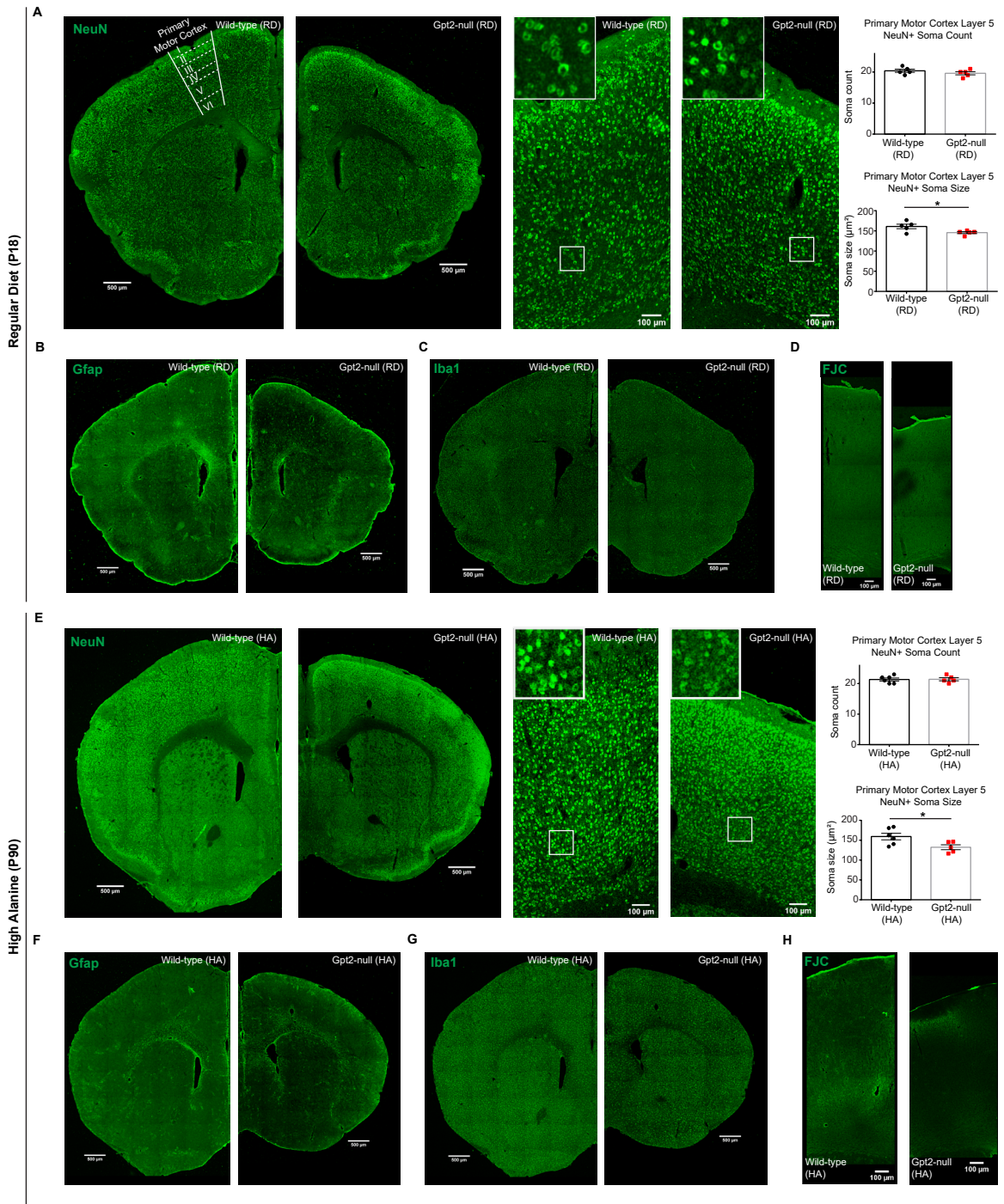
SUPPLEMENTARY FIGURE 5



SUPPLEMENTARY FIGURE 6



SUPPLEMENTARY FIGURE 7



SUPPLEMENTARY Data

Supplementary Figure Legends

Supplementary Figure S1. Confirmation of the SynapsinI-Cre mouse line with the Ai14-R26-tdTomato Cre reporter line.

A. Coronal brain section images of Ai14-R26-tdTomato Cre⁺/SynapsinI-Cre⁻ (left) and Ai14-R26-tdTomato Cre⁺/SynapsinI-Cre⁺ (right) animals at P50. Note the tdTomato (middle) is absent in the animal without the SynapsinI-Cre transgene. Overall tdTomato signal appears abundant near the neuronal soma (NeuN, cyan, top). Scale bar: 1000 μ m.

B. NeuN (cyan) and tdTomato (red) signals in images of somatosensory cortex (layer 3) from an Ai14-R26-tdTomato Cre⁺/SynapsinI-Cre⁺ animal, taken with a 63X objective. White color indicates co-localization of NeuN and tdTomato. Scale bar: 10 μ m.

C. MAP2 (cyan) and tdTomato (red) signals in images of somatosensory cortex (layer 3) from an Ai14-R26-tdTomato Cre⁺/SynapsinI-Cre⁺ animal, taken with a 63X objective. White color indicates co-localization of MAP2 and tdTomato. Arrow heads point toward example areas where co-localization of MAP2 and tdTomato is observed. Scale bar: 10 μ m.

D. GFAP (cyan) and tdTomato (red) signals in images of somatosensory cortex (layer 3) from an Ai14-R26-tdTomato Cre⁺/SynapsinI-Cre⁺ animal, taken with a 63X objective. Note that the GFAP signal is not present in cells positive for tdTomato signal (arrowhead). Scale bar: 10 μ m.

E. Iba1 (cyan) and tdTomato (red) signals in images of somatosensory cortex (layer 3) from an Ai14-R26-tdTomato Cre+/SynapsinI-Cre+ animal, taken with a 63X objective. Note that the Iba1 signal is not present in cells positive for tdTomato signal (arrowhead). Scale bar: 10 μ m.

F. NG2 (cyan) and tdTomato (red) signals in images of somatosensory cortex (layer 3) from an Ai14-R26-tdTomato Cre+/SynapsinI-Cre+ animal, taken with a 63X objective. Note that the NG2 signal is not present in cells positive for tdTomato signal (arrowhead). Scale bar: 10 μ m.

G. Differential interference contrast (DIC, left) microscopy image and the TRITC signal (tdTomato, right) in a corresponding fluorescence microscopy image of the kidney from an Ai14-R26-tdTomato Cre+/SynapsinI-Cre+ animal, taken with a 10X objective. Note the absence of fluorescence in the kidney tissue. Scale bar: 150 μ m.

H. Differential interference contrast (DIC, left) microscopy image and the TRITC signal (tdTomato, right) in a corresponding fluorescence microscopy image of the liver from an Ai14-R26-tdTomato Cre+/SynapsinI-Cre+ animal, taken with a 10X objective. Note the absence of fluorescence in the liver tissue. Scale bar: 150 μ m.

Supplementary Figure 2. Quantification of protein levels of the transcription factor Atf4 and enzymes involved in glycolysis in wild-type and Gpt2-null mice at P18 by Western blotting.

A. Western blotting for Atf4 (Entrez gene: 468) in hippocampus, cortex and liver protein lysates from wild-type and Gpt2-null mice at P18. There were no statistically significant changes in normalized band intensities (Hippocampus: WT: 0.038 ± 0.0047 vs. MUT:

0.033 ± 0.0070, $P = 0.5560$; Cortex: WT: 0.0199 ± 0.0015 vs. MUT: 0.0176 ± 0.0043, $P = 0.6172$; Liver: WT: 254.7 ± 102.1 vs. MUT: 225.2 ± 41.68, $P = 0.7947$). Each Atf4 band was normalized to its corresponding tubulin band. Each lane represents a protein lysate sample from a different animal.

B. Western blotting for hexokinase I, pyruvate kinase (Pkm1/2), pyruvate kinase (Pkm2), pyruvate dehydrogenase (Pdh) and glyceraldehyde 3-phosphate dehydrogenase (Gapdh) in hippocampus protein lysates from wild-type and Gpt2-null animals at P18. There were no statistically significant changes in normalized band intensities of hexokinase I (WT: 196.3 ± 17.8 vs. MUT: 266.8 ± 43.1, $P = 0.138$), Pkm 1/2 (WT: 180.3 ± 25.95 vs. MUT: 131.7 ± 31.84, $P = 0.2567$) or Pkm2 (WT: 3.37 ± 0.15 vs. MUT: 3.03 ± 0.29, $P = 0.3013$) between the wild-type and Gpt2-null samples. Gapdh was significantly reduced in the Gpt2-null hippocampus (Gel1: WT: 0.521 ± 0.036 vs. MUT: 0.314 ± 0.051, $P = 0.0063$; Gel2: WT: 0.416 ± 0.048 vs. MUT: 0.2594 ± 0.015, $P = 0.0148$). Each band was normalized to its corresponding actin band. Each lane represents a protein lysate sample from a different animal.

Supplementary Figure 3. Synaptogenesis in Gpt2-null hippocampal neurons in vitro and survival curve of GFAP-cKO animals *in vivo*.

A. Synapse count per neuron is decreased in Gpt2-null cultures and this phenotype is worsened by alanine deprivation. Images from Opera Phenix High Content Screening Confocal Microscopy of SV2 (green) and MAP2 (magenta) (left) and quantification of SV2 count per nuclei (right). The cells were processed as in panel C. Scale bar: 100 μm. * $P < 0.05$, ** $P < 0.005$, *** $P < 0.0005$.

B. Survival curve of GFAP-Cre conditional-null (GFAP-cKO) and control mice. Control (black) n=34, GFAP-cKO (magenta) n=36 animals. Log-rank (Mantel-Cox) test was used to determine significant differences between the curves. P (Control vs. GFAP-cKO) = 0.8937.

Supplementary Figure 4. Metabolic profile and gross anatomy measurements of wild-type and Gpt2-null brain at P90 on High Alanine diet.

A. 2-D Score Plots of PCA of the polar metabolic profile in the wild-type (HA) (green) and Gpt2-null (HA) (red) hippocampus at P18. Note that the confidence regions (95%) of the two groups intersect.

B. Z-scores of normalized peak intensities of metabolites in the Gpt2 reaction from wild-type (HA) (black) and Gpt2-null (HA) (red) hippocampus at P18. The green arrow points to the three Gpt2-null (HA) samples that were closest to the wild-type (HA) samples. All comparisons were statistically insignificant.

C. Volcano plots of significantly changed metabolites in the Gpt2-null (HA) hippocampus with respect to wild-type (HA) levels. The peak intensities were processed as in (Figure 2D). Wild-type (HA) n=7 mice, Gpt2-null (HA) n=7.

D. Comparison of fold changes of metabolites in hippocampal samples obtained at P18 from mice fed RA diet (black) or HA diet (green). Metabolites of interest were sorted according to processes, including Gpt2 reaction metabolites, TCA cycle metabolites, amino acids and glycolysis. In the box-and-whisker plots, the whiskers are minimum and maximum with the vertical line denoting the average. The entire metabolomics data sets along with false discovery rates for each metabolite can be found in Table S5.

E. Images of brains from a wild-type (HA, left) and Gpt2-null (HA, right) littermate pair at age P90 marked with the area and length measurements. Ruler demarcations are at 1-mm scale. LH: Left Hemisphere, RH: Right Hemisphere, MB: Midbrain, CB: Cerebellum.

F. Total brain area measurements of wild-type (HA, black) and Gpt2-null (HA, red) mice at P90. There was a statistically significant reduction in total brain area in Gpt2-null (HA) mice compared to wild-type (HA) mice at P90. Wild-type (HA): $1.072 \pm 0.023 \text{ cm}^2$ vs. Gpt2-null (HA): $0.8709 \pm 0.02 \text{ cm}^2$, $***P = 0.0001$. The measurements excluded the olfactory bulb.

G. Cortex - Left Hemisphere area measurements of wild-type (HA, black) and Gpt2-null (HA, red) mice at P90. There was a statistically significant reduction in the measured area in Gpt2-null (HA) mice compared to wild-type (HA) mice at P90. Wild-type (HA): $0.3834 \pm 0.01 \text{ cm}^2$ vs. Gpt2-null (HA): $0.3102 \pm 0.005 \text{ cm}^2$, $***P = 0.0003$.

H. Cortex - Right Hemisphere area measurements of wild-type (HA, black) and Gpt2-null (HA, red) mice at P90. There was a statistically significant reduction in the measured area in Gpt2-null (HA) mice compared to wild-type (HA) mice at P90. Wild-type (HA): $0.4091 \pm 0.0076 \text{ cm}^2$ vs. Gpt2-null (HA): $0.3274 \pm 0.009 \text{ cm}^2$, $***P < 0.0001$.

I. Midbrain area measurements of wild-type (HA, black) and Gpt2-null (HA, red) mice at P90. The Gpt2-null (HA) mice at P90 had similar midbrain area as their wild-type (HA) littermates. Wild-type (HA): $0.0431 \pm 0.0036 \text{ cm}^2$ vs. Gpt2-null (HA): $0.0456 \pm 0.0028 \text{ cm}^2$, $P = 0.6017$.

J. Cerebellum area measurements of wild-type (HA, black) and Gpt2-null (HA, red) mice at P90. There was a statistically significant reduction in the measured area in Gpt2-null

(HA) mice compared to wild-type (HA) mice at P90. Wild-type (HA): 0.2268 ± 0.008 cm² vs. Gpt2-null (HA): 0.1821 ± 0.009 cm², ** $P = 0.0051$.

K. L1, L2, L3 and L4 length measurements of wild-type (HA, black) and Gpt2-null (HA, red) mice at P90. There were statistically significant reductions in all four measured areas in Gpt2-null (HA) mice compared to wild-type (HA) mice at P90. L1, Wild-type (HA): 1.046 ± 0.0096 cm vs. Gpt2-null (HA): 0.949 ± 0.01 cm, *** $P < 0.0001$; L2, Wild-type (HA): 0.947 ± 0.023 cm vs. Gpt2-null (HA): 0.825 ± 0.013 cm, ** $P = 0.0018$; L3, Wild-type (HA): 0.977 ± 0.012 cm vs. Gpt2-null (HA): 0.865 ± 0.014 cm, *** $P = 0.00016$; L4, Wild-type (HA): 0.998 ± 0.0069 cm vs. Gpt2-null (HA): 0.8702 ± 0.008 cm, *** $P < 0.0001$.

Supplementary Figure S5. NeuN+ and Calbindin+ cell analyses in the spinal cord in wild-type and Gpt2-null mice on regular alanine diet at P18 or high alanine diet at P90.

A. Images of NeuN+ soma in cervical and lumbar spinal cord sections (100 μ m x 100 μ m) from wild-type and Gpt2-null mice on RA diet at P18. (Cervical spinal cord NeuN+ count, Wild-type (RA): 46.5 ± 2.99 vs. Gpt2-null (RA): 52.3 ± 2.12 , $P = 0.1425$; Lumbar spinal cord NeuN+ count, Wild-type (RA): 37.4 ± 4 vs. Gpt2-null (RA): 43 ± 3.36 , $P = 0.3073$.) Quantification of soma size for neurons of the dorsal horn is shown to the right. (Cervical spinal cord NeuN+ soma size, Wild-type (RA): 65.68 ± 1.41 μ m² vs. Gpt2-null (RA): 62.26 ± 3.25 μ m², $P = 0.3541$; Lumbar spinal cord NeuN+ soma size, Wild-type (RA): 65.26 ± 1.72 μ m² vs. Gpt2-null (RA): 67.89 ± 2.03 μ m², $P = 0.3457$.) Scale bar: 10 μ m.

B. Images of NeuN+ soma in cervical and lumbar spinal cord sections (100 μm x 100 μm) from wild-type and Gpt2-null mice on HA diet at P90. (Cervical spinal cord NeuN+ count, Wild-type (HA): 58.2 ± 5.36 vs. Gpt2-null (HA): 60.4 ± 2.94 , $P = 0.7283$; Lumbar spinal cord NeuN+ count, Wild-type (HA): 53.8 ± 3.86 vs. Gpt2-null: 46.6 ± 2.01 , $P = 0.1533$.) Quantification of soma size for neurons of the dorsal horn is shown to the right. (Cervical spinal cord NeuN+ soma size, Wild-type (HA): $60.45 \pm 3.1 \mu\text{m}^2$ vs. Gpt2-null: $65.54 \pm 4.18 \mu\text{m}^2$, $P = 0.3566$; Lumbar spinal cord NeuN+ soma Size, Wild-type (HA): $67.79 \pm 1.62 \mu\text{m}^2$ vs. Gpt2-null: $60.89 \pm 4.05 \mu\text{m}^2$, $P = 0.1245$.) Scale bar: 10 μm .

C. Images of Calbindin+ soma in cervical and lumbar spinal cord sections from wild-type and Gpt2-null mice on RA diet at P18 (stitched images taken with 20X objective). Quantification of Calbindin+ soma in the dorsal horn is shown to the right. (Cervical spinal cord Calbindin+ count, Wild-type (RA): 21 ± 0.58 vs. Gpt2-null (RA): 19.2 ± 1.93 , $P = 0.3581$; Lumbar spinal cord Calbindin+ count, Wild-type (RA): 19.4 ± 1.4 vs. Gpt2-null (RA): 21.7 ± 1.82 , $P = 0.3717$.) Scale bar: 50 μm .

D. Images of Calbindin+ soma in cervical and lumbar spinal cord sections from wild-type and Gpt2-null mice on HA diet at P90 (stitched images taken with 20X objective). Quantification of Calbindin+ soma in the dorsal horn is shown to the right. (Cervical spinal cord Calbindin+ count, Wild-type (HA): 23.17 ± 3.13 vs. Gpt2-null (HA): 25.2 ± 2.08 $P = 0.6185$; Lumbar spinal cord Calbindin+ count, Wild-type (HA): 22.83 ± 1.66 vs. Gpt2-null (HA): 22.2 ± 2.46 , $P = 0.8309$.) Scale bar: 50 μm .

Supplementary Figure S6. Iba1 and Fluoro-Jade C staining in spinal cord in wild-type and Gpt2-null mice on regular alanine diet at P18 or high alanine diet at P90.

A. Images of Iba1 staining in cervical and lumbar spinal cord sections from wild-type and Gpt2-null mice on RA diet at P18 (stitched images taken with 20X objective). Scale bar: 100 μm .

B. Images of Iba1 staining in cervical and lumbar spinal cord sections from wild-type and Gpt2-null mice on HA diet at P90 (stitched images taken with 20X objective). Scale bar: 100 μm .

C. Images of Fluoro-Jade C (FJC) fluorescence in cervical and lumbar spinal cord sections from wild-type and Gpt2-null mice on RA diet at P18 (stitched images taken with 20X objective). Scale bar: 100 μm .

D. Images of Fluoro-Jade C (FJC) fluorescence in cervical and lumbar spinal cord sections from wild-type and Gpt2-null mice on HA diet at P90 (stitched images taken with 20X objective). Scale bar: 100 μm .

Supplementary Figure S7. NeuN, Iba1, Gfap and Fluoro-Jade C staining in the primary motor cortex of Gpt2-null mice on regular alanine diet at P18 and high alanine diet at P90.

A. Images of NeuN staining in coronal sections containing primary motor cortex from wild-type (left) and Gpt2-null (right) mice on RA diet at P18 (stitched images taken with 20X objective). Cortical layers are demarcated, and the primary motor cortex is denoted. Scale bar: 500 μm . The primary motor cortex was cropped, and layer 5 neurons boxed in white were magnified and are shown in the inset in the upper left corner. Scale bar: 100 μm . Quantification of NeuN⁺ soma count and soma size are shown on the right. *0.01 < P < 0.05.

B. Images of Gfap staining in coronal sections containing the primary motor cortex from wild-type (left) and Gpt2-null (right) mice on RA diet at P18. Scale bar: 500 μm .

C. Images of Iba1 staining in coronal sections containing the primary motor cortex from wild-type (left) and Gpt2-null (right) mice on RA diet at P18. Scale bar: 500 μm .

D. Images of Fluoro-Jade C (FJC) staining in coronal sections containing the primary motor cortex from wild-type (left) and Gpt2-null (right) mice on RA diet at P18. Scale bar: 100 μm .

E. Images of NeuN staining in coronal sections containing primary motor cortex from wild-type (left) and Gpt2-null (right) mice on HA diet at P90 (stitched images taken with 20X objective). Scale bar: 500 μm . The primary motor cortex was cropped, and the layer 5 neurons boxed in white were magnified and are shown in the inset in the upper left corner. Scale bar: 100 μm . Quantification of NeuN⁺ soma count and soma size are shown on the right. *0.01 < P < 0.05.

F. Images of Gfap staining in coronal sections containing the primary motor cortex from wild-type (left) and Gpt2-null (right) mice on HA diet at P90. Scale bar: 500 μm .

G. Images of Iba1 staining in coronal sections containing the primary motor cortex from wild-type (left) and Gpt2-null (right) mice on HA diet at P90. Scale bar: 500 μm .

H. Images of Fluoro-Jade C (FJC) staining in coronal sections containing the primary motor cortex from wild-type (left) and Gpt2-null (right) mice on HA diet at P90. Scale bar: 100 μm .

For supplementary videos, refer to the Brown Thesis Repository.

Supplementary Video S1. Hind-limb clasp reflex of wild-type mouse at P18 raised on regular alanine diet.

Supplementary Video S2. Hind-limb clasp reflex of Gpt2-null mouse at P18 raised on regular alanine diet.

Supplementary Video S3. Hind-limb clasp reflex of SynapsinI-Cre Gpt2-cKO mouse at P18 raised on regular alanine diet.

Supplementary Video S4. Open Field Test of wild-type mouse at P18 raised on regular alanine diet.

Supplementary Video S5. Open Field Test of Gpt2-null mouse at P18 raised on regular alanine diet.

Supplementary Video S6. Open Field Test of SynapsinI-Cre Gpt2-cKO mouse at P18 raised on regular alanine diet.

Supplementary Video S7. Hind-limb clasp reflex of wild-type mouse at P18 raised on high alanine diet.

Supplementary Video S8. - Hind-limb clasping reflex of Gpt2-null mouse at P18 raised on high alanine diet.

Supplementary Video S9. Hind-limb clasping reflex of wild-type mouse at P90 raised on high alanine diet.

Supplementary Video S10. Hind-limb clasping reflex of Gpt2-null mouse at P90 raised on high alanine diet.

Supplementary Video S11. Open Field Test of wild-type mouse at P18 raised on high alanine diet.

Supplementary Video S12. Open Field Test of Gpt2-null mouse at P18 raised on high alanine diet.

Supplementary Video S13. Open Field Test of wild-type mouse at P30 raised on high alanine diet.

Supplementary Video S14. Open Field Test of Gpt2-null mouse at P30 raised on high alanine diet.

Supplementary Video S15. Open Field Test of wild-type mouse at P60 raised on high alanine diet.

Supplementary Video S16. Open Field Test of Gpt2-null mouse at P60 raised on high alanine diet.

Supplementary Video S17. Open Field Test of wild-type mouse at P90 raised on high alanine diet.

Supplementary Video S18. Open Field Test of Gpt2-null mouse at P90 raised on high alanine diet.

Supplementary Tables

Supplementary Table S1. Targeted polar metabolomics in hippocampal tissue from wild-type and Gpt2-null littermates at age P18 raised on regular alanine diet.

This dataset includes Original Data of Liquid Chromatography-Mass Spectrometry (LC-MS) Peak Intensities, Normalized Data (Original Data was normalized to the sample median and auto-scaled (z-score)) and T-test Results (t.stat, raw p-value, -log(raw p-value), False Discovery Rate (FDR) and Fold Change of Gpt2-null average with respect to the wild-type average).

Supplementary Table S2. Targeted polar metabolomics in hippocampal tissue from wild-type and Gpt2-null littermates at age P14 raised on regular alanine diet.

This dataset includes Original Data of Liquid Chromatography-Mass Spectrometry (LC-MS) Peak Intensities, Normalized Data (Original Data was normalized to the sample median and auto-scaled (z-score)) and T-test Results (t.stat, raw p-value, -log(raw p-value), False Discovery Rate (FDR) and Fold Change of Gpt2-null average with respect to the wild-type average).

Supplementary Table S3. Targeted polar metabolomics in hippocampal tissue from wild-type and Gpt2-null littermates at age P7 raised on regular alanine diet.

This dataset includes Original Data of Liquid Chromatography-Mass Spectrometry (LC-MS) Peak Intensities, Normalized Data (Original Data was normalized to the sample median and auto-scaled (z-score)) and T-test Results (t.stat, raw p-value, -log(raw p-

value), False Discovery Rate (FDR) and Fold Change of Gpt2-null average with respect to the wild-type average).

Supplementary Table S4. Targeted polar metabolomics in hippocampal tissue from wild-type and Gpt2-null littermates at age P0 raised on regular alanine diet.

This dataset includes Original Data of Liquid Chromatography-Mass Spectrometry (LC-MS) Peak Intensities, Normalized Data (Original Data was normalized to the sample median and auto-scaled (z-score)) and T-test Results (t.stat, raw p-value, -log(raw p-value), False Discovery Rate (FDR) and Fold Change of Gpt2-null average with respect to the wild-type average).

Supplementary Table S5. Targeted polar metabolomics in hippocampal tissue from wild-type and Gpt2-null littermates at age P18 raised on high alanine diet.

This dataset includes Original Data of Liquid Chromatography-Mass Spectrometry (LC-MS) Peak Intensities, Normalized Data (Original Data was normalized to the sample median and auto-scaled (z-score)) and T-test Results (t.stat, raw p-value, -log(raw p-value), False Discovery Rate (FDR) and Fold Change of Gpt2-null average with respect to the wild-type average).

Supplementary Table S6. Comparison of fold changes of Gpt2-null liquid chromatography-mass spectrometry average peak intensities between regular alanine diet and high alanine diet at P18.

The table involves metabolites in the main Figure 6H and includes RA diet raw p-values and False Discovery Rates (FDR) from wild-type vs. Gpt2-null comparison, HA diet raw p-values and FDR from wild-type vs. Gpt2-null comparison, fold changes of Gpt2-null average peak intensities with respect to wild-type average peak intensities in the RA diet, fold changes of Gpt2-null average peak intensities with respect to wild-type average peak intensities in the HA diet, and raw p-values for the comparison of fold changes between RA diet and HA diet. The raw LC-MS peak intensity data can be found in Supplementary Tables 1 and 5.

Supplementary Table S7. Composition of regular alanine diet (1.19% w/w), high alanine diet (5% w/w) and Neurobasal-A culture medium.

In the “Diet” sheet, all of the components of the two different diets are given side by side; N/A indicates non-applicable for components with no available information in the respective diet product sheet.

SUPPLEMENTARY TABLE 1. T-TEST RESULTS.

	t.stat	p.value	#NAME?	FDR	Fold Change with respect to Wild-type
D-glucosamine-6-phosphate	10.614	8.97E-08	7.047	1.38E-05	4.7053
succinate	-10.176	1.47E-07	6.8332	1.38E-05	0.25503
Methylmalonic acid	-10.142	1.53E-07	6.816	1.38E-05	0.25573
alanine	-9.5125	3.20E-07	6.4944	2.18E-05	0.72356
glucose-1-phosphate	8.136	1.86E-06	5.7308	0.000101	2.2966
fructose-6-phosphate	8.0051	2.22E-06	5.6535	0.000101	3.735
D-erythrose-4-phosphate	7.6933	3.42E-06	5.4658	0.000133	2.6093
glucose-6-phosphate	7.1358	7.64E-06	5.1171	0.00026	3.8465
acetylphosphate	6.7383	1.39E-05	4.8579	0.000419	3.451
D-sedoheptulose-1-7-phosphate	6.4386	2.21E-05	4.6565	0.000515	1.8756
proline	6.4046	2.33E-05	4.6333	0.000515	1.8561
cystathionine	6.4015	2.34E-05	4.6312	0.000515	2.4378
D-glucosamine-1-phosphate	-6.3686	2.46E-05	4.6087	0.000515	0.60301
SBP	6.3164	2.67E-05	4.5728	0.00052	2.4239
hexose-phosphate	5.9288	4.99E-05	4.3015	0.000906	2.4318
sn-glycerol-3-phosphate	-5.8579	5.61E-05	4.2509	0.000954	0.39787
fructose-1,6-bisphosphate	5.5651	9.15E-05	4.0387	0.001464	4.5254
threonine	5.4697	0.000108	3.9684	0.001625	1.7303
malate	-5.2508	0.000157	3.8051	0.002243	0.54869
dimethylglycine	5.1179	0.000197	3.7045	0.002686	1.6855
lysine	5.0761	0.000212	3.6727	0.002752	2.43
2-keto-isovalerate	-4.9633	0.000259	3.5863	0.003078	0.76705
serine	-4.9611	0.00026	3.5846	0.003078	0.70543
dephospho-CoA-nega	4.6724	0.000436	3.3601	0.004933	3.2447
6-phospho-D-gluconate	4.6513	0.000453	3.3435	0.004933	4.3435
guanosine	4.6165	0.000483	3.316	0.005053	1.5122
NADP_posi	-4.5115	0.000585	3.2329	0.005892	0.57027
citrulline	4.4176	0.000695	3.1582	0.006749	1.3455
CTP-nega	4.3298	0.000817	3.0878	0.007027	4.4112
acadesine	4.3284	0.000819	3.0867	0.007027	1.8972
glyoxylate	-4.3242	0.000825	3.0833	0.007027	0.56157
ornithine	4.3074	0.000851	3.0698	0.007027	2.9203
S-ribosyl-L-homocysteine-nega	-4.3067	0.000853	3.0693	0.007027	0.62762
propionyl-CoA-posi	-4.2028	0.001034	2.9854	0.008274	0.43477
a-ketoglutarate	4.1459	0.00115	2.9393	0.008937	1.5662
dTMP	4.0933	0.001269	2.8965	0.009588	1.6296
UTP-nega	-3.9822	0.001564	2.8058	0.011495	0.55752
Indoleacrylic acid	3.8532	0.001996	2.7	0.013616	1.5643
glutathione-nega	-3.8462	0.002022	2.6942	0.013616	0.73341
2-deoxyglucose-6-phosphate	3.8294	0.002088	2.6804	0.013616	1.6604
3-phospho-serine	-3.8274	0.002095	2.6787	0.013616	0.60835
Phenylpropionic acid	3.822	0.002117	2.6743	0.013616	1.4627
fumarate	-3.8133	0.002153	2.6671	0.013616	0.73379
guanosine 5-diphosphate,3-diphosphate	3.6447	0.002967	2.5277	0.018341	2.5147
putrescine	-3.5424	0.003609	2.4426	0.021813	0.41599
Ng,NG-dimethyl-L-arginine	3.5121	0.003824	2.4174	0.022614	2.2382
xanthine	3.4785	0.004079	2.3895	0.023605	1.3306
cholesterol	3.4619	0.004211	2.3757	0.023859	1.3149
Maleic acid	-3.4429	0.004367	2.3598	0.024241	0.76004
dihydroxy-acetone-phosphate	3.3694	0.00503	2.2984	0.027362	1.7218
cholesteryl sulfate	3.313	0.005606	2.2514	0.029638	2.7763
phenylpyruvate	3.2944	0.00581	2.2358	0.029638	2.4033
ribose-phosphate	3.2881	0.005881	2.2306	0.029638	1.4435
xanthosine	3.2815	0.005956	2.225	0.029638	1.6541
2-Hydroxy-2-methylbutanedioic acid	-3.2783	0.005993	2.2224	0.029638	0.71885
N1-Methyl-2_2-pyridone-3_5-carboximide	3.2656	0.006141	2.2117	0.02975	1.5805
D-glyceraldehyde-3-phosphate	3.2578	0.006234	2.2052	0.02975	1.6991
phosphoenolpyruvate	3.1606	0.007517	2.124	0.03525	2.5057

pyruvate	-3.1303	0.007968	2.0987	0.036732	0.71086
Pyroglutamic acid	3.1174	0.008169	2.0879	0.037031	1.8876
methylnicotinamide	3.0935	0.008553	2.0679	0.038136	1.4281
arginine	3.0732	0.008893	2.0509	0.038975	1.466
Imidazoleacetic acid	3.0655	0.009027	2.0444	0.038975	1.8355
leucine-isoleucine	3.0413	0.009456	2.0243	0.04019	1.4029
glutathione	-2.9783	0.010675	1.9716	0.044672	0.74152
creatine	-2.967	0.010909	1.9622	0.044959	0.47892
AMP	-2.9271	0.011778	1.9289	0.047817	0.72286
biotin	-2.9134	0.012092	1.9175	0.04833	0.55546
nicotinate	2.9062	0.01226	1.9115	0.04833	2.9146
OBP	2.8456	0.013773	1.861	0.05352	1.3879
Pyrophosphate	2.8314	0.014152	1.8492	0.054217	1.7528
2-hydroxygluterate	-2.7825	0.015543	1.8085	0.058718	0.8514
homocysteic acid	2.7626	0.016145	1.792	0.060156	1.6196
O8P-O1P	2.7075	0.017934	1.7463	0.065921	1.2672
Thiamine pyrophosphate	2.6968	0.018306	1.7374	0.06639	1.3478
FMN	-2.677	0.019009	1.721	0.068032	0.59108
CDP-choline	-2.6622	0.019554	1.7088	0.069075	0.64678
FAD	2.6523	0.019926	1.7006	0.069486	1.4878
uracil	2.6206	0.021163	1.6744	0.072863	2.2623
3-phosphoglycerate	2.5943	0.022246	1.6527	0.075637	2.9583
GMP	-2.5785	0.022921	1.6398	0.07697	0.82108
dGTP	-2.5459	0.024381	1.613	0.080872	0.74965
UMP	-2.5312	0.025066	1.6009	0.082144	0.73415
hypoxanthine	2.5177	0.025714	1.5898	0.082774	1.1749
inosine	-2.5146	0.025867	1.5873	0.082774	0.5485
Acetyllysine	2.5014	0.02652	1.5764	0.083878	1.4132
CDP-nega	-2.4364	0.029969	1.5233	0.093697	0.6711
2-oxobutanoate	-2.4242	0.030664	1.5134	0.094779	0.73572
citrate-isocitrate	-2.3877	0.03283	1.4837	0.10021	0.60868
glutamate	-2.3824	0.033157	1.4794	0.10021	0.6801
5-phosphoribosyl-1-pyrophosphate	-2.3686	0.034024	1.4682	0.10061	0.56668
2,3-Diphosphoglyceric acid	2.3641	0.034312	1.4645	0.10061	3.1795
homocysteine	2.3627	0.034401	1.4634	0.10061	1.3102
taurine	-2.3514	0.035137	1.4542	0.10167	0.66429
Acetylcarnitine DL	-2.3433	0.035669	1.4477	0.10213	0.65566
NADP_nega	-2.3217	0.03713	1.4303	0.1052	0.64732
2-Isopropylmalic acid	-2.2999	0.038668	1.4127	0.10768	0.60313
hydroxyproline	-2.2929	0.039174	1.407	0.10768	0.66867
Xanthurenic acid	-2.2926	0.039194	1.4068	0.10768	0.44059
phenylalanine	2.2695	0.040906	1.3882	0.11126	1.2551
carnitine	-2.2511	0.042319	1.3735	0.11397	0.68848
D-glucono--lactone-6-phosphate	2.2207	0.044758	1.3491	0.11763	1.8631
N-acetyl spermidine	-2.2207	0.044762	1.3491	0.11763	0.43676
thiamine	-2.2181	0.044976	1.347	0.11763	0.29626
spermidine	-2.2025	0.046282	1.3346	0.11989	0.65964
cysteine	-2.1845	0.04784	1.3202	0.12194	0.67508
N-acetyl-glucosamine	-2.183	0.047971	1.319	0.12194	0.81509
valine	2.1727	0.048886	1.3108	0.12202	1.4232
ATP-nega	-2.1691	0.049209	1.308	0.12202	0.76463
D-glucarate	-2.1676	0.049345	1.3068	0.12202	0.45083

SUPPLEMENTARY TABLE 2. T-TEST RESULTS.

	t.stat	p.value	#NAME?	FDR	Fold Change with respect to Wild-type
alanine	-8.9586	1.16E-06	5.9359	0.000266	0.74235
malate	-8.5599	1.87E-06	5.7285	0.000266	0.6994
sarcosine	-7.6894	5.63E-06	5.2498	0.00035	0.70529
biotin	-7.6594	5.85E-06	5.2326	0.00035	0.63282
succinate	-7.5058	7.18E-06	5.144	0.00035	0.72223
Methylmalonic acid	-7.4854	7.38E-06	5.1321	0.00035	0.7016
fumarate	-6.9453	1.55E-05	4.81	0.000631	0.75395
Glycerophosphocholine	-6.6006	2.54E-05	4.5959	0.000877	0.68414
valine	6.5401	2.77E-05	4.5576	0.000877	1.7315
threonine	6.099	5.34E-05	4.2721	0.001523	1.646
2-keto-isovalerate	-5.6809	0.000102	3.9907	0.002464	0.78756
glucosamine	-5.6429	0.000108	3.9646	0.002464	0.48409
arginine	5.6146	0.000113	3.9451	0.002464	2.111
myo-inositol	-5.574	0.000121	3.9171	0.002464	0.70177
leucine-isoleucine	5.4762	0.000142	3.849	0.002553	1.6904
proline	5.4685	0.000143	3.8437	0.002553	1.863
D-gluconate	-5.2988	0.000189	3.7242	0.003164	0.76608
glutathione-nega	-4.9785	0.000321	3.494	0.005077	0.50625
Maleic acid	-4.9052	0.000363	3.4404	0.005441	0.77185
carnitine	-4.8603	0.000391	3.4075	0.005577	0.7706
N-acetyl-L-aspartylglutamic acid	-4.7271	0.000491	3.309	0.006663	0.75036
glutathione disulfide-posit	-4.5701	0.000643	3.1915	0.008335	0.69533
taurine	-4.5214	0.0007	3.1548	0.008394	0.86689
glutathione disulfide-nega	-4.5159	0.000707	3.1507	0.008394	0.74114
glutathione	-4.4886	0.000741	3.1301	0.008449	0.36882
methionine	4.4312	0.000819	3.0865	0.008982	1.7187
serine	-4.4047	0.000858	3.0663	0.00906	0.67459
2-Isopropylmalic acid	-4.3506	0.000944	3.0251	0.009458	0.48015
coenzyme A-posit	-4.3396	0.000962	3.0167	0.009458	0.43719
fructose-6-phosphate	4.285	0.00106	2.9749	0.010066	1.4109
NAD_nega	-4.2132	0.001203	2.9196	0.011063	0.79157
allantoin	-4.1942	0.001245	2.9049	0.011085	0.71182
2-hydroxygluturate	-3.9	0.00211	2.6757	0.017822	0.84424
Ascorbic acid	-3.8871	0.00216	2.6656	0.017822	0.40859
dihydroorotate	-3.8798	0.002189	2.6598	0.017822	0.76155
Creatinine	-3.8255	0.002415	2.6171	0.01912	0.79601
creatine	-3.7895	0.002579	2.5886	0.019862	0.85906
hydroxyproline	-3.7429	0.002807	2.5517	0.020676	0.55569
dCDP-nega	-3.735	0.002848	2.5455	0.020676	0.68327
S-adenosyl-L-homocysteine-nega	-3.7216	0.002919	2.5348	0.020676	0.70452
2-oxo-4-methylthiobutanoate	-3.7112	0.002975	2.5266	0.020676	0.61806
homoserine	-3.6416	0.003378	2.4714	0.022921	0.70061
glycerate	-3.5405	0.004067	2.3907	0.026957	0.67399
4-aminobutyrate	-3.4775	0.004568	2.3403	0.029183	0.85947
N-Acetyl-L-alanine	-3.4727	0.004608	2.3365	0.029183	0.86117
D-glyceraldehyde-3-phosphate	3.3724	0.005545	2.2561	0.034356	1.4063
citrate	-3.2251	0.007285	2.1376	0.044174	0.79725
N-acetyl-glucosamine-1-phosphate	-3.1372	0.008577	2.0667	0.050925	0.78983
xanthine	-3.0991	0.009206	2.0359	0.053544	0.62281
5-methoxytryptophan	-2.9729	0.011639	1.9341	0.066344	0.70423
tryptophan	2.909	0.013105	1.8826	0.073231	1.4681
CMP	-2.8906	0.013561	1.8677	0.073483	0.84958
cystathionine	2.8865	0.013665	1.8644	0.073483	1.4823
uracil	2.8483	0.014668	1.8336	0.077417	1.307
phosphoenolpyruvate	2.8315	0.015134	1.82	0.077976	1.4453
Pyrophosphate	-2.8248	0.015322	1.8147	0.077976	0.6858
betaine aldehyde	-2.7642	0.017144	1.7659	0.084692	0.81423
phosphocreatine	-2.7614	0.017236	1.7636	0.084692	0.69579
S-adenosyl-L-methionine	-2.6352	0.021764	1.6623	0.10463	0.55863
2-ketohaxanoic acid	-2.6287	0.022027	1.657	0.10463	0.86036
aminoimidazole carboxamide ribonucleotide	-2.5957	0.02341	1.6306	0.10938	0.67308
fructose-1,6-bisphosphate	2.579	0.024142	1.6172	0.11098	1.411
dTDP-nega	-2.5389	0.02599	1.5852	0.11757	0.72885

dTTP-nega	2.4951	0.028168	1.5502	0.12544	1.5165
thymine	-2.4839	0.028753	1.5413	0.12607	0.80775
asparagine	2.4679	0.029609	1.5286	0.12786	1.2267
glucose-6-phosphate	2.4461	0.030813	1.5113	0.12972	1.3688
glyoxylate	-2.4436	0.030951	1.5093	0.12972	0.76083
deoxyadenosine	-2.3851	0.034443	1.4629	0.14227	0.30437
UMP	-2.3702	0.035388	1.4511	0.14408	0.86011
lysine	2.3158	0.039064	1.4082	0.15399	1.3916
histidine	2.3059	0.039768	1.4005	0.15399	1.2653
4-phosphopantothenate	-2.3055	0.039798	1.4001	0.15399	0.62868
allantoate	-2.303	0.039982	1.3981	0.15399	0.82509
malonyl-CoA-posi	-2.2926	0.040738	1.39	0.15481	0.36189
citrate-isocitrate	-2.2813	0.041578	1.3811	0.15592	0.84483
glutamate	-2.2714	0.04233	1.3734	0.15668	0.91185
3-phosphoglycerate	2.24	0.044797	1.3488	0.16324	1.2995
UDP-N-acetyl-glucosamine	-2.2344	0.04525	1.3444	0.16324	0.90039
trehalose-sucrose	-2.2074	0.047505	1.3233	0.16924	0.69607
6-phospho-D-gluconate	-2.1942	0.048643	1.313	0.16936	0.80539
trehalose-6-Phosphate	-2.1932	0.04873	1.3122	0.16936	0.64971
betaine	-2.1648	0.051268	1.2902	0.17535	0.83613
NADP_nega	-2.1449	0.053127	1.2747	0.17535	0.77668
adenine	2.1409	0.053502	1.2716	0.17535	1.3167
Methylcysteine	2.1409	0.053502	1.2716	0.17535	1.3167
NADP_posi	-2.1378	0.053798	1.2692	0.17535	0.73833
S-adenosyl-L-homoCysteine-posi	-2.1342	0.054145	1.2664	0.17535	0.81253
AMP	-2.1192	0.055618	1.2548	0.1781	0.8536
SBP	2.1104	0.056487	1.2481	0.17887	1.4184
3-hydroxybuterate	2.0516	0.062693	1.2028	0.19635	3.9369
ADP-nega	-2.0304	0.065083	1.1865	0.20162	0.87199
Pyroglutamic acid	-2.0181	0.066509	1.1771	0.2033	0.5319
D-glucosamine-1-phosphate	-2.0122	0.067198	1.1726	0.2033	0.73747
aconitate	-2.0074	0.067768	1.169	0.2033	0.89074
D-glucosamine-6-phosphate	1.9551	0.07426	1.1292	0.22046	1.1939
arginosuccinic acid	1.9266	0.078036	1.1077	0.22424	1.2244
Acetylcarnitine DL	-1.9233	0.078487	1.1052	0.22424	0.88592
NADPH	-1.9232	0.078506	1.1051	0.22424	0.77113
Phenylpropionic acid	-1.9219	0.078682	1.1041	0.22424	0.80977
IMP	-1.9099	0.080336	1.0951	0.22669	0.81602
tyrosine	1.8987	0.081901	1.0867	0.22884	1.4037
GMP	-1.8738	0.085503	1.068	0.23484	0.82377
D-sedoheptulose-1-7-phosphate	1.8725	0.085694	1.067	0.23484	1.2328
2-Hydroxy-2-methylbutanedioic acid	-1.8564	0.088102	1.055	0.23715	0.87354
orotate	-1.8558	0.088202	1.0545	0.23715	0.82138
Methionine sulfoxide	1.8424	0.090252	1.0445	0.24039	1.279
orotidine-5-phosphate	1.8243	0.093089	1.0311	0.24565	1.3658
Phenyllactic acid	1.791	0.098525	1.0065	0.25761	1.3795
Citraconic acid/itaconic acid	-1.7509	0.10546	0.97691	0.26843	
itaconic acid	-1.7509	0.10546	0.97691	0.26843	
NADH-nega	-1.7483	0.10592	0.97503	0.26843	
L-arginino-succinate	1.7455	0.10643	0.97294	0.26843	
Kynurenine	1.7369	0.10797	0.96668	0.26993	
glucono--lactone	-1.7188	0.11132	0.95342	0.27449	
Flavone	-1.7166	0.11172	0.95185	0.27449	
UDP-nega	-1.6847	0.11785	0.92869	0.28284	
oxaloacetate	1.6847	0.11785	0.92866	0.28284	
adenosine 5-phosphosulfate	-1.6771	0.11936	0.92314	0.28284	
indole	1.6763	0.11952	0.92254	0.28284	
homocysteine	1.6735	0.12008	0.92052	0.28284	

propionyl-CoA-posi	4923.62	9900.36	3306.524	2499.853	2477.648	2425.483	N/A	3302.719	8208.132	4906.727	N/A	2475.671	5005.93
acetoacetyl-CoA-posi	N/A	8233.963	7432.759	N/A	8287.981	4955.181	7432.771	7432.932	13215.56	5785.416	2425.623	8882.309	12387.76
malonyl-CoA-posi	N/A	8260.328	N/A	N/A	4130.261	5781.467	N/A	14038.13	8283.584	4130.114	7435.255	7398.504	6607.485
succinyl-CoA-posi	3331.685	10735.49	N/A	4955.232	4939.016	N/A	N/A	N/A	4127.033	N/A	N/A	4955.173	N/A
sarcosine	23622314	25076195	23261222	26965524	25695411	21504143	23855299	25864395	29684073	29629634	27212762	26936577	26900435
putrescine	11553.23	3880.415	20926.51	89357.55	51825.15	64498.7	95639.79	15279.43	18450.95	9560.998	57247.86	116323.5	97490.88
spermidine	60874.55	73592.36	190276.2	87650.25	165993.7	27243.6	125173.2	92912.24	129217.2	175754.9	130334.3	197297.5	60115.48
N-acetyl spermine	56871.88	19580.61	59763.52	58292.12	14783.7	52179.06	68566.39	61642.52	13226.93	19525.98	51720.19	67634.57	59198.16
N-acetyl spermidine	25581.39	38296.49	59313.18	50573.86	60028.07	63213.01	71620.67	9927.56	46467.83	51654.34	60544.32	4614.731	63300.32
Nicotinamide Riboside	N/A	9673.623	13937.68	5230.753	13105.31	16330.28	N/A	2475.125	7163.776	10436.56	4795.692	9798.261	15861.02
Adenylosuccinate	209770	203989.6	120576.7	92463.9	85062.68	88366.47	66070.28	246107	183343.3	104884.4	97452.09	71026.28	71852.96
cholesterol	184815.2	229592.8	237157.5	1818610	3845339	359627.2	3617547	196552.3	979483.7	254456.5	187467.7	199033.4	4022461
arginosuccinic acid	460061.7	359647.7	284373.5	593620.5	551415.9	367334.1	341900.7	457036.8	527858.3	592892.3	373842.2	411179.3	448498.7
phosphocreatine	4201208	3887395	5230796	3783003	3915016	2872636	6175433	3063237	5837287	5482801	6376827	4712822	3141131
retinoic acid	11113.45	3667.718	7397.434	8249.712	8095.305	6135.332	15591.85	3115.25	9280.8	5038.955	5084.168	N/A	6679.403
spermine	505398.2	648295.1	685354.3	524428.8	609125.7	670619.9	569115.8	652518.9	817302.4	697410.9	706445.7	627550.3	601115.5
HMG-CoA_pos	8258.033	3157.876	6859.825	8953.726	10587.59	3983.183	8724.883	6605.463	9238.367	4684.802	7360.329	13178.98	13960.43
N-acetyl-L-aspartic acid	9206557	7796160	9290669	7435841	8441058	7144562	8971049	7367402	10446932	9376917	6936283	6752714	8383097
N-acetyl-L-aspartylglutamic acid	35584665	37537107	41909591	40442547	36780592	35879567	29940807	39221282	43962993	39659002	35153655	39576045	34170060

N-acetyl spermidine	-0.992891	-0.524807	0.616535	0.017752	0.762419	0.956012	1.274267	-1.632782	-0.173377	0.160429	0.561157	-1.868385	0.843671
Nicotinamide Riboside	-1.329821	0.040627	0.991059	-0.64417	0.94042	1.583758	-1.311435	-1.06841	-0.343629	0.279439	-0.673372	0.155312	1.380222
Adenylosuccinate	1.334724	1.099912	0.001036	-0.654733	-0.575503	-0.489105	-0.945113	2.104598	0.80428	-0.371052	-0.487503	-0.964716	-0.856824
cholesterol	-0.671412	-0.650795	-0.63018	0.259346	1.731677	-0.540572	1.558984	-0.660099	-0.226091	-0.626836	-0.666083	-0.661054	1.783116
arginosuccinic acid	-0.020967	-1.176799	-1.562724	1.21721	1.582895	-0.435867	-0.823079	0.129428	0.507724	1.480232	-0.757061	-0.437443	0.29645
phosphocreatine	-0.398294	-0.771034	0.741189	-0.781568	-0.241737	-1.131005	1.711925	-1.20321	0.763004	0.736274	1.498333	0.074063	-0.997941
retinoic acid	0.924907	-0.927109	0.160331	0.191279	0.432972	-0.079522	2.443857	-0.995743	0.412765	-0.522313	-0.502355	-1.539301	0.000232
spermine	-1.865333	-0.525476	0.819628	-1.752261	0.191058	1.111267	-0.399854	0.119309	1.446552	0.562827	0.725926	-0.331682	-0.101962
HMG-CoA_pos	-0.071514	-1.561865	-0.316548	0.082102	0.965778	-1.131092	0.34074	-0.468518	0.132077	-1.052993	-0.254458	1.399436	1.936854
N-acetyl-L-aspartic acid	0.46509	-0.948708	1.13159	-1.092076	0.692995	-0.404153	1.096987	-0.803969	1.234593	0.818316	-1.197013	-1.444671	0.451018
N-acetyl-L-aspartylglutamic acid	-1.113392	-0.982284	1.797009	0.142533	0.625066	0.497123	-1.804469	0.454428	1.039102	0.453699	-0.87384	0.311868	-0.546842

SUPPLEMENTARY TABLE 3. T-TEST RESULTS.

	t.stat	p.value	#NAME?	FDR	Fold Change with respect to Wild-type
serine	-5.2562	0.00027	3.5687	0.077215	0.72498
N-acetyl-glutamate	4.1086	0.001734	2.761	0.16854	1.241
carnitine	-4.0278	0.00199	2.7012	0.16854	0.85477
alanine	-3.9287	0.002357	2.6276	0.16854	0.89179
anthranilate	3.5139	0.00485	2.3142	0.27744	1.4886
sarcosine	-3.2632	0.007556	2.1217	0.3312	0.89694
ADP-D-glucose	3.2236	0.008106	2.0912	0.3312	1.6195
glutamate	3.09	0.010286	1.9877	0.35051	1.1233
Maleic acid	-2.9755	0.01262	1.8989	0.35051	0.83563
malate	-2.9745	0.012643	1.8982	0.35051	0.80745
glycerate	-2.9139	0.014091	1.8511	0.35051	0.76458
thymidine	-2.89	0.014707	1.8325	0.35051	0.7343
malonyl-CoA-positi	-2.7501	0.018887	1.7238	0.41552	0.40459
fumarate	-2.5176	0.028595	1.5437	0.57153	0.83805
2-keto-isovalerate	-2.4911	0.029975	1.5232	0.57153	0.84802
threonine	-2.4016	0.035135	1.4543	0.62804	0.81845
phenylalanine	2.2366	0.046977	1.3281	0.79031	1.1304

Table with columns for chemical name and multiple columns of numerical values representing various data points for each compound.

NAD+_posi	2173499.801	2236996.905	2390609.287	2484417.748	1857078.773	1857480.913	1735626.37	2625957.241	2095622.206	1991614.282	1912899.078	2707030.4	1837546.12	2876606.255
NADH	95801.17033	72676.07123	175908.341	104883.1938	104061.0127	121407.1952	49551.34074	92538.51859	132136.8302	88568.25141	107560.7475	90023.291	92486.72184	86814.07553
dephospho-CoA-posi	12388.1221	N/A	6822.77704	N/A	N/A	N/A	3305.109939	9082.906912	9087.300042	6851.74831	10714.97056	3355.77124	9092.8183	8758.055333
NADP+_posi	176241.8383	178926.8495	239504.5072	266422.737	176445.9699	188306.9057	148682.7505	269130.0819	246160.784	188906.0968	226796.3551	184112.79	194910.7258	187566.854
NADPH	30557.36003	25601.83956	28906.56319	38836.17969	28079.09509	26426.12831	17342.89639	42942.93762	14810.6119	28080.91946	26428.43626	21471.392	23949.13101	28926.40816
coenzyme A-posi	35158.39825	29739.05167	32163.32008	39638.65623	5763.645034	14038.4441	10742.44462	28940.43722	44595.89659	22376.78683	14040.2660	17339.746	17318.93179	8259.838292
FAD	182519.3475	107363.4692	147021.1505	170949.0464	187470.9165	31378.83817	58636.81859	175927.191	180088.6073	131293.7431	173423.979	146176.57	112320.1297	143700.9715
acetyl-CoA-posi	24606.06706	20315.79252	21307.13281	28244.92814	19820.52564	20812.27537	6937.433586	12883.90385	22322.64671	18830.10944	23814.94493	28736.182	21893.34763	19901.75322
propionyl-CoA-posi	4133.84853	N/A	N/A	2477.559808	N/A	N/A	N/A	N/A	N/A	3280.311086	N/A	N/A	N/A	N/A
acetoacetyl-CoA-posi	3302.815683	N/A	N/A	4127.793599	N/A	N/A	4130.234365	3274.774318	3302.776368	N/A	3305.182424	N/A	N/A	3302.577063
malonyl-CoA-posi	N/A	4952.724177	N/A	4127.78683	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
succinyl-CoA-posi	N/A	N/A	N/A	N/A	3319.094957	N/A	N/A	N/A	N/A	4127.767869	N/A	N/A	N/A	5780.274518
serotone	18059366.23	15543373.68	17936790.12	12985413.11	14743476.18	13675561.61	11247031.62	18967909.67	12215084.66	9711514.846	13869700.56	15084913	11198265.93	11171291.45
putrescine	29451.80706	49422.48926	26128.98725	120098.7434	125654.2587	137670.854	161626.0075	42164.82887	13712.43472	N/A	35011.44774	213363.92	196639.410	186009.8832
spermidine	542650.1992	654370.0883	628926.2975	603417.378	770781.1689	1002578.568	1060505.864	788009.6742	847730.4069	624054.1929	751494.1012	978066.2	1312095.4	998763.4812
N-acetyl spermine	138807.2590	199267.4575	230195.6224	190611.4313	151337.3481	157045.374	226877.1064	154959.4878	163588.5621	253145.0973	203814.1224	172428.34	123564.0024	131311.0489
N-acetyl spermidine	36156.30144	29977.45415	11736.20409	5583.138484	8210.883169	13919.59311	26484.63821	30749.88949	23282.26053	70011.15026	15153.60388	10172.661	26429.06485	7141.40285
Nicotinamide Riboside	5491.194198	6450.737678	2461.851037	3496.822163	4878.615974	N/A	6256.751424	18309.62431	45135.26443	8063.931562	3736.101931	7034.4119	6969.132456	8847.816542
Adenylosuccinate	79283.5050	37163.95484	105710.5625	32209.57234	38814.38439	36339.6824	33862.10483	81761.9456	61112.25187	22298.44158	51205.55186	96623.951	21475.40203	33861.16902
cholesterol	373325.6755	270887.8624	81734.73779	875437.0153	64195.2144	84217.12993	67970.30108	592119.3629	447618.5329	72675.15361	60287.31427	68993.57	110715.2886	69557.45225
arginosuccinic acid	165207.4475	166615.1791	253995.2821	217769.3251	168985.6266	141515.3004	129779.5564	178487.7044	134348.7401	112930.5028	140741.3268	228403.02	336995.4948	231126.4076
phosphocreatine	1700467.391	2817446.101	2913102.331	2933919.845	3251974.979	2537982.893	1990425.121	3129745.615	3778327.828	2728212.122	2977436.986	273366.8	3037965.223	2571091.163
retinoic acid	17435.17383	6266.155978	3111.653254	4953.496725	N/A	N/A	N/A	N/A	4368.794763	4914.644343	N/A	4952.4333	3644.148464	N/A
spermine	680404.9321	815302.5903	733881.6556	578374.9840	725345.5902	733916.0955	840593.8718	800977.3302	510597.4353	565555.9776	677947.3028	564930.11	582716.5568	465411.6383
HMG-CoA_pos	4921.434224	6605.427453	10813.88772	7432.587675	13213.0361	9083.058999	2477.529225	5780.460184	5825.028855	7432.943982	N/A	14865.861	4127.78027	N/A
N-acetyl-L-aspartic acid	1276049.903	1615719.847	1597639.681	1088276.736	1156243.976	843194.7243	635602.7009	1585680.626	1471341.123	1127462.551	1114084.081	1478418.5	988376.1339	975872.8529
N-acetyl-L-aspartylglutamic acid	14056283.32	14240186.19	17856543.11	13508034.17	14260639.55	9203192.734	10233937.72	22499383.33	15384660.54	11007030.38	11869540.92	15372696	10368522.95	12750540.76

SUPPLEMENTARY TABLE 4. T-TEST RESULTS.

	t.stat	p.value	#NAME?	FDR	Fold Change with respect to Wild-type
cystathionine	5.4603	0.000145	3.8379	0.041247	1.4288
tryptophan	-4.4333	0.000816	3.0881	0.11592	0.5798
alanine	3.6209	0.003509	2.4549	0.26152	1.3483
Kynurenic acid	3.5944	0.003683	2.4338	0.26152	1.3339
Xanthurenic acid	-3.1259	0.008758	2.0576	0.42252	0.73046
sarcosine	3.0953	0.00927	2.0329	0.42252	1.2478
guanosine	2.961	0.011898	1.9245	0.42252	1.6672
indole	-2.9608	0.011902	1.9244	0.42252	0.69533
p-aminobenzoate	2.8331	0.015088	1.8214	0.47611	1.5513
quinolinate	2.6568	0.020914	1.6796	0.54334	1.9124
dehydroascorbic acid	2.6534	0.021045	1.6769	0.54334	11.581
p-hydroxybenzoate	2.5904	0.023638	1.6264	0.55908	1.4665
spermine	2.5008	0.027873	1.5548	0.55908	1.3629
deoxyguanosine	-2.4542	0.030358	1.5177	0.55908	0.70009
Cholic acid	2.4509	0.030541	1.5151	0.55908	4.0976
deoxyinosine	-2.392	0.034009	1.4684	0.55908	0.6206
2-hydroxygluterate	2.3904	0.034109	1.4671	0.55908	1.1728
Nicotinamide Riboside	-2.3329	0.037868	1.4217	0.55908	0.59065
N6-Acetyl-L-lysine	-2.2598	0.043224	1.3643	0.55908	0.79847
fructose-6-phosphate	2.2506	0.043953	1.357	0.55908	1.14
trehalose-6-Phosphate	-2.2469	0.04424	1.3542	0.55908	0.77888
Acetyllysine	-2.2367	0.045062	1.3462	0.55908	0.80026
OBP	-2.2341	0.045277	1.3441	0.55908	0.64391

cysteine sulfinate	N/A	1652.513	1652.512	1652.591	N/A	1652.591	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
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SUPPLEMENTARY TABLE 5. T-TEST RESULTS.

	t.stat	p.value	#NAME?	FDR	Fold Change with respect to Wild-type
glycerate	-7.2467	1.02E-05	4.9917	0.002382	0.59934
cystathionine	6.8987	1.65E-05	4.7815	0.002382	1.756
serine	-6.4074	3.37E-05	4.473	0.003231	0.59893
S-adenosyl-L-homocysteine-nega	-5.531	0.00013	3.8872	0.009335	0.6456
arginine	5.1544	0.000239	3.6212	0.010754	1.6884
D-glucono--lactone-6-phosphate	5.1337	0.000248	3.6063	0.010754	2.9197
NADH-nega	-4.9492	0.000337	3.4726	0.010754	0.35569
homocysteine	-4.8999	0.000366	3.4365	0.010754	0.7418
valine	4.8846	0.000376	3.4253	0.010754	1.8568
glycine	4.8625	0.00039	3.409	0.010754	2.86
glutathione-nega	-4.8318	0.000411	3.3864	0.010754	0.66039
SBP	4.7438	0.000477	3.3214	0.010809	2.7581
proline	4.7308	0.000488	3.3117	0.010809	2.4381
leucine-isoleucine	4.6449	0.000565	3.2476	0.0111	2.0011
methionine	-4.632	0.000578	3.238	0.0111	0.47253
L-arginino-succinate	4.2378	0.001152	2.9385	0.019719	1.7427
glutathione	-4.2319	0.001164	2.9341	0.019719	0.70268
D-glyceraldehyde-3-phosphate	4.1154	0.001432	2.844	0.022917	2.5645
CDP-nega	-3.9911	0.00179	2.7471	0.026541	0.61685
arginosuccinic acid	3.9749	0.001843	2.7344	0.026541	1.7624
citrulline	3.94	0.001963	2.7071	0.026918	1.9468
D-sedoheptulose-1-7-phosphate	3.818	0.002448	2.6112	0.032049	2.0116
lysine	3.7917	0.002568	2.5904	0.03216	1.4301
dihydroxy-acetone-phosphate	3.7349	0.002848	2.5454	0.034179	2.2005
homoserine	-3.635	0.003419	2.4661	0.038128	0.60759
Ng,NG-dimethyl-L-arginine	3.6102	0.003579	2.4463	0.038128	1.5687
6-phospho-D-gluconate	3.5857	0.003743	2.4268	0.038128	1.6706
UDP-nega	-3.5855	0.003744	2.4267	0.038128	0.56257
glutamine	3.5582	0.003937	2.4048	0.038128	1.3233
betaine	3.5534	0.003972	2.401	0.038128	1.5678
threonine	3.4095	0.005179	2.2858	0.045896	1.4523
dATP-nega	-3.4081	0.005191	2.2847	0.045896	0.19132
dGDP-nega	-3.4011	0.005259	2.2791	0.045896	0.49547
ADP-nega	-3.3534	0.005744	2.2408	0.048651	0.51019
ornithine	3.3074	0.006254	2.2038	0.051465	2.0062
hydroxyphenylpyruvate	3.2915	0.006442	2.191	0.051536	6.8436
Methylmalonic acid	-3.2467	0.006999	2.155	0.053183	0.69378
IDP-nega	-3.2453	0.007017	2.1538	0.053183	0.49359
hexose-phosphate	3.2135	0.007443	2.1282	0.053525	1.2375
glucose-1-phosphate	3.2033	0.007586	2.12	0.053525	1.3174
cysteine sulfinate	3.2009	0.00762	2.118	0.053525	1.9806
succinate	-3.1739	0.008011	2.0963	0.054486	0.7079
GDP-nega	-3.1656	0.008135	2.0896	0.054486	0.69803
lactate	3.1387	0.008552	2.0679	0.055979	1.2755
NADH	-3.1216	0.008829	2.0541	0.056505	0.41451
fructose-1,6-bisphosphate	3.1075	0.009062	2.0428	0.056736	2.4496
fructose-6-phosphate	3.0801	0.009536	2.0206	0.058435	1.8032
Uric acid	3.0612	0.009877	2.0054	0.059263	2.2095
homocysteic acid	3.0313	0.010441	1.9812	0.061369	1.6144
dCDP-nega	-3.0016	0.011034	1.9573	0.061903	0.53362
3-S-methylthiopropionate	3.0008	0.011051	1.9566	0.061903	1.7009
NADP_nega	-2.9872	0.011334	1.9456	0.061903	0.63235
N-acetyl-glutamate	-2.9844	0.011392	1.9434	0.061903	0.83082
4-phosphopantothenate	2.9546	0.012041	1.9193	0.064218	1.8328
acetyl-CoA-posi	2.9436	0.01229	1.9105	0.064354	2.5965

guanosine	2.9269	0.012677	1.897	0.065196	1.6667
inosine	2.869	0.014117	1.8503	0.070832	1.385
phenylalanine	2.8633	0.014265	1.8457	0.070832	1.4539
dTMP-nega	2.8532	0.014536	1.8376	0.070954	1.8303
O8P-O1P	2.8249	0.01532	1.8147	0.073536	1.348
dTTP-nega	-2.7951	0.01619	1.7907	0.07644	0.35175
UTP-nega	-2.782	0.016588	1.7802	0.077053	0.23091
orotidine-5-phosphate	2.7651	0.017116	1.7666	0.078244	1.3564
hypoxanthine	2.7154	0.018768	1.7266	0.083295	2.0986
trehalose-sucrose	2.7145	0.018799	1.7259	0.083295	2.5039
NAD_nega	-2.7036	0.01918	1.7172	0.083693	0.49777
anthranilate	2.6473	0.021286	1.6719	0.090101	2.0677
ribose-phosphate	2.6421	0.021492	1.6677	0.090101	1.9297
dGTP	-2.6358	0.021741	1.6627	0.090101	0.24142
choline	-2.625	0.022178	1.6541	0.090101	0.5075
GMP	2.6242	0.022212	1.6534	0.090101	1.3926
adenosine 5-phosphosulfate	-2.6072	0.022918	1.6398	0.091673	0.56891
ATP-nega	-2.598	0.02331	1.6325	0.091964	0.23462
1-Methyladenosine	-2.5793	0.024131	1.6174	0.092837	0.54323
GTP-nega	-2.5782	0.024176	1.6166	0.092837	0.31133
Glycerophosphocholine	-2.5115	0.02733	1.5634	0.10357	0.67541
IMP	2.4915	0.028354	1.5474	0.10605	1.7447
asparagine	2.4765	0.029145	1.5354	0.10642	1.2644
dephospho-CoA-posi	2.4756	0.029193	1.5347	0.10642	2.3286
coenzyme A-posi	-2.4589	0.030099	1.5214	0.10836	0.72882
p-aminobenzoate	2.4443	0.030912	1.5099	0.1087	2.1363
glucose-6-phosphate	2.4437	0.030948	1.5094	0.1087	1.5977
adenosine	2.4192	0.032364	1.4899	0.11133	3.028
creatine	2.4174	0.032471	1.4885	0.11133	1.1964
NAD_posi	-2.3924	0.033989	1.4687	0.11516	0.44918
2-deoxyglucose-6-phosphate	-2.3747	0.035098	1.4547	0.11754	0.63464
Kynurenine	2.3398	0.037397	1.4272	0.1238	1.5596
deoxyinosine	2.3275	0.038247	1.4174	0.12517	1.76
guanine	2.3032	0.039967	1.3983	0.12933	1.3063
5-phosphoribosyl-1-pyrophosphate	-2.2955	0.04053	1.3922	0.1297	0.69725
nicotinamide	2.2803	0.041657	1.3803	0.1314	1.579
UMP	2.2761	0.041974	1.377	0.1314	1.3173
S-adenosyl-L-homoCysteine-posi	-2.229	0.045689	1.3402	0.14101	0.67077
dUTP-nega	2.22	0.046441	1.3331	0.14101	2.2411
retinoic acid	2.2191	0.046512	1.3324	0.14101	1.5482
Methionine sulfoxide	-2.1977	0.048334	1.3157	0.14408	0.55589
hydroxyproline	-2.1955	0.048528	1.314	0.14408	0.63787

SUPPLEMENTARY TABLE 6.

Process	Metabolite	Regular Alanine diet raw p-value Wild-type vs. Gpt2-null	Regular Alanine diet FDR Wild-type vs. Gpt2-null	HighAlanine Diet raw p-value Wild-type vs. Gpt2-null	HighAlanine Diet FDR Wild-type vs. Gpt2-null	Regular Alanine diet Average Fold Change of Gpt2-null with respect to Wild-type	HighAlanine Diet Average Fold Change of Gpt2-null with respect to Wild-type	T-test raw p-value Regular Alanine diet Fold Change vs. HighAlanine Diet Fold Change
Gpt2 Primary Reaction	alanine	3.20E-07	2.18E-05	0.063088	0.16917	0.72356	0.840525514	0.0395784
	alpha-ketoglutarate	0.00115	0.0089368	0.095833	0.20905	1.5662	1.220052429	0.0658246
	glutamate	0.033157	0.10021	0.084423	0.20094	0.6801	1.093886	< 0.0001
	pyruvate	0.0079676	0.036732	0.81071	0.87777	0.71086	0.963193571	0.0228856
TCA Cycle	methylmalonate	1.5274E-07	0.000013849	0.0069988	0.053183	0.25573	0.69378	0.000371539
	citrate / isocitrate	0.03283	0.10021	0.39294	0.54147	0.60868	1.112621429	0.0025491
	fumarate	0.0021525	0.013616	0.77129	0.85861	0.73379	0.998334714	0.000732427
	succinate	1.4684E-07	0.000013849	0.0080114	0.054486	0.25503	0.7079	0.000181595
	malate	0.00015665	0.0022425	0.36458	0.5097	0.54869	0.914192571	< 0.0001
Amino Acids	valine	0.048886	0.12202	0.00037558	0.010754	1.4232	1.8568	0.156672
	leucine-isoleucine	0.0094564	0.04019	0.00056542	0.0111	1.4029	2.0011	0.0156494
	phenylalanine	0.049096	0.11126	0.014265	0.070832	1.2551	1.4539	0.387461
	threonine	0.00010754	0.0016251	0.0051785	0.045896	1.7303	1.4523	0.109879
	lysine	0.00021246	0.0027518	0.0025683	0.03216	2.43	1.4301	0.00902864
	arginine	0.0088934	0.038975	0.00023922	0.010754	1.466	1.6884	0.367231
	proline	0.000023263	0.0005152	0.0004879	0.010809	1.8561	2.4381	0.0285752
	serine	0.00026027	0.003078	0.00033653	0.0032307	0.70543	0.59893	0.00766536
	cysteine	0.04784	0.12194	0.47334	0.60858	0.67508	1.183571571	0.0431325
	Glycolysis	glucose 1-phosphate	1.8585E-06	0.00010066	0.0075861	0.053525	2.2966	1.3174
glucose 6-phosphate		7.6364E-06	0.00025964	0.030948	0.1087	3.8465	1.5977	< 0.0001
fructose 6-phosphate		2.2205E-06	0.00010066	0.0095363	0.058435	3.735	1.8032	0.000121749
DHAP		0.0050298	0.027362	0.0028482	0.034179	1.7218	2.2005	0.173065
Glyceraldehyde 3-phosphate		0.0062344	0.02975	0.0014323	0.022917	1.6991	2.5645	0.044075
3-phosphoglycerate		0.022246	0.075637	0.087256	0.20266	2.9583	0.711067857	0.00194799
phosphoenolpyruvate		0.0075166	0.03525	0.077768	0.19143	2.5057	0.673756	0.000213552
NADP		0.03713	0.1052	0.011334	0.061903	0.64732	0.63235	0.783583
glutathione		0.0020221	0.013616	0.00041074	0.010754	0.73341	0.66039	0.585811
cystathionine		0.00002338	0.0005152	0.00001654	0.0023817	2.4378	1.756	0.014917

SUPPLEMENTARY TABLE 7. DIET COMPOSITION

Regular Diet (RA) - PicoLab Rodent Diet 20 (5053)

High Alanine Diet (HA) - Envigo Teklad (TD. 190381)

Nutrient	Regular Diet (RA) - PicoLab Rodent Diet 20 (5053)	High Alanine Diet (HA) - Envigo Teklad (TD. 190381)
Protein, % (w/w)	21	19.9
Arginine, %	1.29	1.21
Cystine, %	0.36	0.35
Glycine, %	0.97	2.33
Histidine, %	0.53	0.45
Isoleucine, %	0.8	0.82
Leucine, %	1.57	1.11
Lysine, %	1.18	1.8
Methionine, %	0.62	0.82
Phenylalanine, %	0.91	0.75
Tyrosine, %	0.6	0.5
Threonine, %	0.78	0.82
Tryptophan, %	0.24	0.18
Valine, %	0.97	0.82
Serine, %	0.98	0.35
Aspartic acid, %	2.19	0.35
Glutamic acid, %	4.18	4
Alanine, %	1.19	5
Proline, %	1.31	3.5
Fat, % (w/w)	6.3	8
Soybean Oil %	N/A	8
Cholesterol, ppm	142	N/A
Linoleic Acid, %	2.12	N/A
Linolenic Acid, %	0.27	N/A
Arachidonic Acid, %	0.01	N/A
Omega-3 Fatty Acids, %	0.45	N/A
Total Saturated Fatty Acids, %	0.78	N/A
Total Monounsaturated Fatty Acids, %	0.96	N/A
Carbohydrates, % (w/w)	65.9	60.2
Fiber (Crude), %	4.6	N/A
Neutral Detergent Fiber, %	16	N/A
Acid Detergent Fiber, %	5.8	N/A
Nitrogen-Free Extract (by difference), %	53.4	N/A
Cellulose	N/A	30
Maltodextrin	N/A	15
Starch, %	28.2	15
Glucose, %	0.1	N/A
Fructose, %	0.24	N/A
Sucrose, %	3.25	N/A
Lactose, %	1.34	N/A
Sucrose, %	N/A	29.838
Total Digestible Nutrients, %	75.1	N/A
Gross Energy, kcal/gm	4.11	N/A
Physiological Fuel Value, kcal/gm	3.43	N/A
Metabolizable Energy, kcal/gm	3.03	N/A
Minerals	N/A	3.5 (AIN-93M-MX (94049))
Ash, %	5.9	N/A
Calcium, %	0.81	0.82
Phosphorus, %	0.64	N/A
Phosphorus (non-phytate), %	0.34	N/A
Potassium, %	1.1	N/A
Magnesium, %	0.22	N/A
Sulfur, %	0.33	N/A
Sodium, %	0.3	N/A
Chloride, %	0.52	N/A
Fluorine, ppm	9.3	N/A
Iron, ppm	185	N/A
Zinc, ppm	89	N/A
Manganese, ppm	84	N/A
Copper, ppm	14	N/A
Cobalt, ppm	0.71	N/A
Iodine, ppm	0.97	N/A
Chromium (added), ppm	0.01	N/A
Selenium, ppm	0.37	N/A
Vitamins	N/A	1.95 (AIN-93-VX (94047))
Carotene, ppm	1.5	N/A
Vitamin K, ppm	3.3	N/A
Thiamin, ppm	17	N/A
riboflavin, ppm	8	N/A
Niacin, ppm	85	N/A
Pantothenic Acid, ppm	17	N/A
Choline Chloride	2000 (ppm)	0.27 (%)
Folic Acid, ppm	3	N/A
Pyridoxine, ppm	9.6	N/A
Biotin, ppm	0.3	N/A
B12, mcg/kg	51	N/A
Vitamin A, IU/gm	15	N/A
Vitamin D3 (added), IU/gm	2.3	N/A
Vitamine E, IU/kg	99	N/A
Ascorbic Acid, mg/gm	0	N/A
TBHQ, antioxidant	N/A	0.002
Food Color	N/A	0.01
Calories provided by:		
Protein, %	24.517	20.3

Fat (ether extract), %	13.134	18.3
Carbohydrates, %	62.349	61.4
Gross Energy, kcal/gm	4.07	3.9

SUPPLEMENTARY TABLE 7. MEDIUM COMPOSITION

NEUROBASAL MEDIUM

Components	Molecular Weight	Concentration (mg/L)	mM
Amino Acids			
Glycine	75	30	0.4
L-Alanine	89	2	0.02247191
L-Arginine hydrochloride	211	84	0.39810428
L-Asparagine-H ₂ O	150	0.83	0.005533333
L-Cysteine	121	31.5	0.2603306
L-Histidine hydrochloride-H ₂ O	210	42	0.2
L-Isoleucine	131	105	0.8015267
L-Leucine	131	105	0.8015267
L-Lysine hydrochloride	183	146	0.7978142
L-Methionine	149	30	0.20134228
L-Phenylalanine	165	66	0.4
L-Proline	115	7.76	0.06747826
L-Serine	105	42	0.4
L-Threonine	119	95	0.79831934
L-Tryptophan	204	16	0.078431375
L-Tyrosine Sodium dihydrate	265.47	72	0.39779004
L-Valine	117	94	0.8034188
Vitamins			
Choline chloride	140	4	0.028571429
D-Calcium pantothenate	238.27	4	0.008385744
Folic Acid	441	4	0.009070295
Niacinamide	122	4	0.032786883
Pyridoxal hydrochloride	204	4	0.019607844
Riboflavin	376	0.4	0.00106383
Thiamine hydrochloride	337	4	0.011869436
Vitamin B12	1355	0.0068	5.02E-06
i-Inositol	180	7.2	0.04
Inorganic Salts			
Calcium Chloride (CaCl ₂) (anhyd.)	147	200	1.8018018
Ferric Nitrate (Fe(NO ₃) ₃ ·9H ₂ O)	404	0.1	2.48E-04
Magnesium Chloride (anhydrous)	203.3	77.3	0.8136842
Potassium Chloride (KCl)	75	400	5.3333335
Sodium Bicarbonate (NaHCO ₃)	84	2200	26.190475
Sodium Chloride (NaCl)	58	4000	68.965515
Sodium Phosphate monobasic (NaH ₂ PO ₄ ·H ₂ O)	138	125	0.9057971
Zinc sulfate (ZnSO ₄ ·7H ₂ O)	288	0.194	6.74E-04
Other Components			
D-Glucose (Dextrose)	180	4500	25
HEPES	238	2600	10.92437
Phenol Red	376.4	8.1	0.021519661
Sodium Pyruvate	110	25	0.22727273
Glutamine / Glutamax	146.14 / 203	292.28 / 406	2

Additional Components: 1% P/S and 1X B27 Supplement.

Chapter 4 : Loss of mitochondrial enzyme GPT2 causes degeneration in locus coeruleus.

I conducted all experiments. Erin Fingleton contributed to Figure 6.

Electrophysiology was investigated in Julie A. Kauer's laboratory and the project was performed under Eric M. Morrow's supervision. For funding sources please refer to the Chapter.

**Loss of mitochondrial enzyme GPT2
causes early neurodegeneration in locus coeruleus**

Short/running title: Loss of GPT2 causes degeneration in locus coeruleus

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selective vulnerability

Abstract

Background

Locus coeruleus (LC) is among the first brain areas to degenerate in Alzheimer's disease and Parkinson's disease; however, the underlying causes for the vulnerability of LC neurons are not well defined. Here we report a novel mechanism of degeneration of LC neurons caused by loss of the mitochondrial enzyme glutamate pyruvate transaminase 2 (GPT2). GPT2 Deficiency is a newly-recognized childhood neurometabolic disorder. The GPT2 enzyme regulates cell growth through replenishment of tricarboxylic acid (TCA) cycle intermediates.

Methods

We investigated neuropathology in GPT2-null mice. We examined projections of LC noradrenergic neurons via immunohistochemical staining for norepinephrine transporter (NET) and ELISA measurements of norepinephrine. Electrophysiological properties of GPT2-null LC neurons were studied using whole cell recordings.

Results

In GPT2-null mice, we observe an early and striking loss of tyrosine hydroxylase (TH) positive neurons in LC and reduced soma size at postnatal day 18. GPT2-null LC shows positive Fluoro-Jade C staining. Neuron loss is accompanied by selective, prominent microgliosis and astrogliosis in LC. We observe reduced noradrenergic projections to and norepinephrine levels in hippocampus and spinal cord. Whole cell recordings in GPT2-null LC slices show reduced soma size and abnormal firing and action potentials.

Conclusions

As compared to the few genetic animal models with selective LC degeneration, loss of LC neurons in GPT2-null mice is the earliest developmentally. Early neuron loss in LC in a model of human neurometabolic disease provides important clues regarding the metabolic vulnerability of LC and may lead to new therapeutic targets.

Introduction

Locus coeruleus (LC) is the main source of norepinephrine for virtually the entire central nervous system, serving a multitude of functions including modulation of arousal, sleep-wake states, motor function, inflammatory response, and metabolism (1-8). LC dysfunction has been noted in psychiatric disorders, including anxiety, depression, attention-deficit hyperactivity disorder and addiction (9-15). LC is also a particularly vulnerable brain area implicated in neurodegenerative diseases, including Alzheimer's disease (AD) and Parkinson's disease (PD), wherein LC is among the first brain regions to degenerate (16-21). In these degenerative diseases, the underlying causes for LC vulnerability are not clear and pinpointing these mechanisms may pave the way for therapeutic interventions.

Genetic mutations offer a powerful and unbiased approach to identify disease mechanisms; however, there are very few known genetic mutations in animal models that lead to selective neurodegeneration in LC. Such mutations may reveal mechanisms of selective vulnerability of LC neurons. Previously reported mouse mutations with LC neurodegeneration include models of Parkinson's Disease: the PARKIN null (22); the PINK1 null (23); and the LRRK1/2 double knockout (24). LC neuron loss is also seen in transgenic mouse models of Alzheimer's Disease (Tg2576) (25) and Down Syndrome (Ts65Dn) (26). In all of these models, neuron loss generally occurs after six months of age. The only model reported to date that has early dysfunction of LC neurons, at two months of age, is the MECP2-null mouse (27).

Here we report a novel mechanism of degeneration, gliosis, and neuron loss in LC in an animal model of Glutamate Pyruvate Transaminase 2 (GPT2) Deficiency. GPT2 is a

metabolic enzyme in the mitochondria, catalyzing a reversible transfer of an amino group from glutamate to pyruvate producing alanine and alpha-ketoglutarate (28). GPT2 is a major metabolic enzyme that links amino acid metabolism with the tricarboxylic acid (TCA) cycle. GPT2 supports cellular growth and energetics through replenishment of tricarboxylic acid (TCA) cycle intermediates (29-31). GPT2 also modulates levels of glutamate, the main excitatory neurotransmitter in the central nervous system (29-31). Importantly, human patients with recessive, loss-of-function mutations in GPT2 display postnatal microcephaly, intellectual disability, and motor abnormalities including spasticity and weakness in the lower limbs (spastic paraplegia) (28, 32). GPT2-null mice recapitulate the phenotype of postnatal microcephaly and motor dysfunction and prematurely die pre-weaning (28); however, LC neurodegeneration in the GPT2-null mouse has not been previously described. The degeneration and neuron loss in LC in a model of neurometabolic disease may provide important new clues regarding the underlying pathophysiology GPT2 Deficiency. These findings may also pinpoint novel metabolic mechanisms involved in neuronal vulnerability of LC in more common neurodegenerative diseases.

Methods and Materials

Ethics Statement

All experiments involving mice were done in accordance with the National Institutes of Health *Guide for the Care and Use of Laboratory Animals* (33) and approved by the Brown University Institutional Animal Care and Use Committee.

Animals

GPT2-null animals were obtained from Knockout Mouse Project at University of California, Davis as described previously (28). The background of all mice was C57BL/6J. The mice were maintained under a 12-hour light/dark cycle (lights on at 7am / off at 7pm) throughout the year. Feed and water were given ad libitum.

Immunofluorescence

The brains and spinal cord from mice were dissected out after transcardial perfusion with 1X PBS then with 4% PFA. The tissues were cryoprotected by serially incubating in sucrose solutions of 10%, 20% and 30% overnight at 4°C. The final solution was then changed to half by volume sucrose/OCT (Optimal Cutting Temperature, FisherScientific, 23-730-571) and gently shaken for 1 hr at 4°C. The tissues were frozen in dry ice/methanol bath and stored at -80°C until day of sectioning at the cryostat. The sections were cut at 30 µm thickness. The immunofluorescence protocol was as follows, in order: 3-min fixing with 4% PFA, 3 x 5-min 1X PBS washes, 2-hr blocking in normal goat serum (NGS, Jackson ImmunoResearch, 005-000-121) with 1% (w/v) bovine serum albumin (FisherScientific, BP1600) and 0.4% TritonX-100 (Sigma-Aldrich, T8787)

(Note: if a mouse-raised antibody was used, a 1-hr incubation with 20 $\mu\text{g}/\text{mL}$ AffiniPure Fab Fragment Goat Anti-Mouse IgG (H+L) (Jackson ImmunoResearch, 115-007-003) in blocking solution was performed), overnight incubation at 4°C with primary antibody in blocking solution, 2 x 4-min washes with blocking solution, 3 x 4-min washes with 0.4% TritonX-100 in PBS, 2-hr incubation with secondary antibody in blocking solution, 2 x 4-min washes with blocking solution, 3 x 4-min washes with 0.4% TritonX-100 in PBS, 5-min incubation in DAPI (Invitrogen, D1306) and 3 x 5-min washes with PBS. Coverslips were then mounted onto slides with Fluoromount G (SouthernBiotech, 0100-01). Primary antibodies used in this study: mouse anti-tyrosine hydroxylase (TH) (Millipore-Sigma MAB318, 1:300), rabbit anti-Iba1 (Wako Chemicals 019-19741, 1:500), mouse anti-norepinephrine transporter (NET, abcam, ab211463, 1:400), rat anti-CD68 (Abd Serotec (Bio-rad), MCA1957, 1:100), chicken anti-Gfap (Aves, Gfap, 1:400), chicken anti-beta-galactosidase (abcam, ab9361, 1:500). Secondary antibodies used in this study: Goat anti-mouse IgG (H+L) AlexaFluor 594 (Invitrogen, A-11032, 1:600), goat anti-rabbit IgG (H+L) AlexaFluor 488 (Invitrogen, A-11034, 1:600), goat anti-chicken IgY (H+L) AlexaFluor 647 (Invitrogen, A-32933, 1:600), goat anti-rat IgG (H+L) AlexaFluor 647 (Invitrogen, A-21247, 1:600).

For confocal microscopy on tissues, Olympus FV3000 confocal laser scanning microscope and FluoView software were used. Images were processed and analyzed with ImageJ.

Quantification of LC TH⁺ neurons. Every serial coronal section (30 μm) starting approximately from the section where cerebral aqueduct first appears were stained with tyrosine hydroxylase (TH) to prevent loss of sections containing LC. The sections with

LC proper, identified by the canonical “boomerang” shaped cluster of TH⁺ neurons were selected for counting, at least two sections 60 µm apart were blindly counted for each animal.

Fluoro-Jade C Staining

The tissue cryostat sections were mounted on Superfrost Plus microscope slides (FisherScientific, 22-230-892) and dried at 50°C for 30 min. The slides were immersed in the following solutions at room temperature in order: 0.2% NaOH in 80% ethanol for 5 min, 70% ethanol for 2 min, distilled water for 2 min, 0.06% potassium permanganate for 10 min, distilled water for 2 min, 0.0001% Fluoro-Jade C (Sigma-Aldrich, AG325) in 0.1% acetic acid for 10 min and 3 times distilled water for 1 min. The slides were dried at 50°C for 10 min, immersed in xylene for 1 min and coverslipped with DPX Mounting medium (Millipore Sigma 06522).

Hematoxylin & Eosin (H&E) Staining

10 µm sections obtained from paraffin embedded tissue were processed in the following steps in order: 2 x 10-min deparaffinization with xylene; 2 x 5-min rehydration in 100% ethanol; 2 min 95% ethanol and 2 min with 70% ethanol; wash in distilled water; 8 min stain in Mayer hematoxylin solution (Sigma-Aldrich MHS1); 10 min rinse in warm running tap water; wash in distilled water for 30 seconds; dip slides in 95% ethanol 10 times; stain in Eosin Y solution (Sigma-Aldrich HT110116) for 30 seconds; 95% ethanol 5 min; 100% ethanol 5 min each 2 times; clear in xylene 5 min each 2 times; mount with DPX Mounting medium (Millipore Sigma 06522).

Norepinephrine Enzyme-Linked immunosorbent Assay (ELISA)

Tissues were acutely dissected after cervical dislocation and weighed immediately before flash freezing in liquid nitrogen. The spinal cord and hippocampus tissues were homogenized in 300 μ l ddH₂O and cortex tissues in 500 μ l ddH₂O using a Kimble pestle and motor. The homogenate was spun at 5000 x g for 5 min and 200 μ l was extracted from each sample. The norepinephrine in tissues was detected using Norepinephrine ELISA Kit (Abnova, KA1891) according to the manufacturer's manual.

Brain Slice Preparation

Coronal slices (250 μ m) were prepared from anesthetized mice. The brain was immediately extracted and placed in a vibratome (Leica, VT1000). Slices were cut in ice-cold oxygenated artificial cerebrospinal fluid (ACSF, in mM): 119 NaCl, 2.5 KCl, 2.5 CaCl₂·2H₂O, 1.0 NaH₂PO₄·H₂O, 1.3 MgSO₄·7H₂O, 26.0 NaHCO₃, 11 glucose. Slices were recovered in the same oxygenated ACSF solution at room temperature for 1 hr and then transferred to a recording chamber where they were continuously submerged in ACSF at 28°C with a flow rate of 1-2 ml/min.

Electrophysiological Recordings

Locus coeruleus was recognized by its proximity to the fourth ventricle bordering lateral pons and all LC neurons had a characteristic pacemaking activity. Whole cell recordings were performed at current-clamp mode using a MultiClamp 700B Amplifier (Molecular Devices). Signals were low-pass filtered at 3kHz and digitized at 10kHz through Digidata

1550 digitizer (Molecular Devices). Patch electrodes were fabricated from borosilicate glass capillaries (Sutter Instruments) using a P-97 micropipette puller (Sutter Instruments). Patch pipettes had a resistance of 3-8 MOhm filled with patch pipette internal solution consisting of (in mM): 125.0 KCl, 2.8 NaCl, 10.0 HEPES, 2.0 MgCl₂, 2.37 ATP-Mg, 0.32 GTP-Na, 0.6 EGTA, (pH 7.23-7.28, 270-278 mOsm). Capacitance and membrane resistance were calculated from voltage response to an injection of -100 pA. For constructing averaged action potential, action potentials within pacemaking activity in each cell were detected and averaged. All electrophysiological recordings were analyzed using Clampfit software.

Statistical Analysis

All data presented in the Figures and the Results section are presented as average \pm standard error of the mean, unless otherwise noted. The statistical test for comparisons of two groups was unpaired two-tailed Student t-test unless otherwise noted. All statistical analyses were compiled using GraphPad Prism software. Mixed model analysis was done using JMP Pro 14.

Results

We observed prominent microgliosis in the LC of GPT2-null mice at postnatal day 18 (P18) (Fig.1). Screening in sagittal sections of GPT2-null mouse brains revealed selective microglial activation in a pontine region, later confirmed to be LC (Fig.1, Fig.S1A). The microgliosis in GPT2-null LC was already visible in images taken with a 2X objective, indicating the severity of microglial activation (Fig.1B, left). The zoomed-in images of the LC showed clustered microglia with increased fluorescence intensity for Ionized calcium binding adaptor molecule 1 (Iba1), a marker for microglia (Fig.1B, right). The microglia appeared more amoeboid in shape and clustered particularly around the ventral LC. Microglia were evenly distributed throughout the rest of the sagittal section of GPT2-null mouse brain indicating that there was a selective microgliosis in LC after loss of GPT2. The microglial response in the ventral LC was visible in the coronal sections (Fig.2B) and astrogliosis was also apparent (Fig.S2A). CD68, a lysosomal glycoprotein that is expressed in high levels in activated, phagocytic microglia (34), was also elevated in GPT2-null LC, detected as enlarged immunofluorescent puncta (Fig.S3). Absence of microgliosis was observed in coronal sections of other areas of the GPT2-null brain, including various regions of cortex, hippocampus, thalamus, hypothalamus, midbrain, cerebellum and medulla, confirming selective vulnerability of LC (Fig.S1B-E). Microgliosis and astrogliosis were absent with no apparent cell loss in LC of GPT2-null mice at P10 (Fig.S2B), suggesting that the damage in LC occurred later in postnatal development.

There was significant degeneration and neuron loss in GPT2-null LC. Given the strong microgliosis phenotype, we tested for loss of neurons in GPT2-null LC. We

quantified the tyrosine hydroxylase (TH)⁺ cell count in the LC proper and there was a significant loss in TH⁺ cells in GPT2-null LC (Fig.3C). The soma size of the remaining GPT2-null TH⁺ cells in LC was also greatly reduced. Consistent with microglial activation, average Iba1 relative fluorescence intensity in GPT2-null LC was increased. Interestingly, the average TH relative fluorescence intensity was also increased in the GPT2-null LC. To further investigate the pathology, we stained the LC with Fluoro-Jade C (FJC), a fluorescein derivative that is selectively taken up by degenerating neurons (35). There were FJC⁺ cells in GPT2-null LC, particularly on the ventral side (Fig.4B). We also did H&E stains on GPT2-null LC and observed hypereosinophilic and necrotic neurons, consistent with neurodegeneration (Fig.4D).

In order to characterize the selective degeneration of LC in GPT2-null mice further, we quantified noradrenergic projections by staining coronal mouse brain sections for norepinephrine transporter (NET) (Fig.5). Coronal sections that contained hippocampus proper and surrounding cortical and subcortical areas showed overall reductions of NET staining in GPT2-null mice (Fig.5B). We quantified the noradrenergic innervation in the hippocampus CA1 region and the retrosplenial cortex (RSC) (Fig.5C&D). The RSC was chosen due to the easy identification of its anatomical location with respect to the hippocampus proper. A trend toward a decrease of NET staining in GPT2-null RSC was observed but it did not reach statistical significance (Fig.5C). In the GPT2-null hippocampus CA1 area, there was a significant reduction in NET staining (Fig.5D).

We found severe denervation of noradrenergic projections in GPT2-null spinal cord. The degeneration of the ventral LC may be exacerbated due to its long-range

projections to the spinal cord (1, 36). We hypothesized that NET staining in the cervical and lumbar enlargements of GPT2-null mice would be reduced. We examined the spinal cord in four anatomical areas for quantification: dorsolateral (DL), dorsomedial (DM), ventrolateral (VL) and ventromedial (VM) areas corresponding to approximately lateral spinal nucleus, laminae 3-4 of the dorsal horn, lamina 9 of the ventral horn and laminae 7-8 of the ventral horn, respectively (Fig.6). There were significant reductions of NET staining in both cervical and lumbar spinal cord of GPT2-null mice (Fig.6C&D). There were no significant differences of NET staining in the dorsolateral area of either cervical or lumbar enlargements albeit with trend toward a decrease in GPT2-null mice.

Norepinephrine levels were profoundly decreased in GPT2-null mice. We tested for alterations of norepinephrine levels in acutely dissected cortex, hippocampus, cervical and lumbar spinal cord of GPT2-null mice by an enzyme-linked immunosorbent assay (ELISA) (Fig.7). Consistent with the NET staining results from above (Fig.6), there was a significant reduction in norepinephrine levels of GPT2-null hippocampus, cervical and lumbar spinal cord but not of cortex (Fig.7A). Decreased norepinephrine levels were also observed at P14 but not at P7 (Fig.7B&C), suggesting that the denervation occurs after P7 in postnatal development. Reduction in norepinephrine levels was particularly profound in the spinal cord, consistent with the observation of selective degeneration in ventral LC, which preferentially projects to the spinal cord (36, 37). Overall, these data suggest a dramatic decrease in noradrenergic inputs into various regions of the central nervous system of GPT2-null mice.

Given the selective vulnerability of LC and decreased noradrenergic innervation in central nervous system, we hypothesized that performing whole-cell recordings in

GPT2-null LC neurons at P18 may capture alterations in electrophysiological properties associated with the decay in noradrenergic inputs (Fig.8). GPT2-null LC neurons had lower capacitance, consistent with a decreased soma size (Fig.8B), which corroborates our findings of decreased cell area as quantified by immunohistochemistry (Fig.3C). This finding also fits with a proposed function of GPT2 in cell growth (28). We also observe an increased membrane resistance (Fig.8C). Interestingly, there was a slightly increased pacemaking frequency in the GPT2-null LC neurons (Fig.8D), as apparent in the representative recordings (Fig.8A). This may be due to decreased autoinhibition caused by reduced norepinephrine levels and innervation (Fig.7) (38). Averaged action potential was plotted to visualize abnormalities in the overall shape of the spikes (Fig.8E). Several parameters were significantly changed. Peak amplitude of GPT2-null LC neuron spikes was increased (Fig.8F). Time to decay to half of the peak amplitude in GPT2-null spikes was reduced, indicating faster action potential kinetics (Fig.8G). Hyperpolarization peak amplitude of GPT2-null LC neurons was also increased (Fig.8H). Overall, the electrophysiological characterization of GPT2-null LC neurons indicated intrinsic cell properties consistent with reduced neuron size and altered action potential parameters that may in part underlie the deficiencies in norepinephrine supply in GPT2-null mice.

Discussion

LC has been shown to be one of the first brain areas that degenerate in AD and PD (18, 20, 21, 39, 40). The underlying causes for the vulnerability of LC have not been clearly defined, particularly in sporadic forms of AD and PD. One intriguing possibility is the distinct metabolic enzyme and metabolome profile of LC. To our knowledge, our study is the first to provide a strong phenotype of early microgliosis and degeneration in LC in an animal model of a neurometabolic disease.

One of the major clinical features of GPT2 Deficiency is postnatal microcephaly along with intellectual disability (ID), general in the range of moderate ID (28). LC has been shown to consolidate memory (41, 42) and synchronous LC neuron firing has been correlated with improved performance at cognitive tasks (43). Furthermore, stimulating the LC restores reversal learning in a rat model of Alzheimer's Disease (44). Reductions in norepinephrine levels in the GPT2-null mouse hippocampus (Fig.7), may suggest involvement of norepinephrine dysregulation in the etiology of ID seen in patients with GPT2 Deficiency. Interestingly, the GPT2-null mouse cortex did not show decreased norepinephrine levels, however different cortical areas may have been affected locally.

Among the diseases with LC dysfunction, the neurodevelopmental disorder Rett Syndrome has clinical features that are the most similar to GPT2 Deficiency. In Rett Syndrome, females with *MECP2* mutations display cognitive and motor abnormalities, including ID, loss of speech, spasticity, ataxia as well as postnatal microcephaly and seizures (45, 46). The Rett Syndrome mouse model (*MECP2*-null) displays reduced cell size and hyperexcitability of LC neurons, similar to our data in GPT2-null mice (Fig.8) as well as decreased norepinephrine levels in the pons and cingulate cortex (47, 48). While

the MECP2-null mouse has early dysfunction of LC neurons, no clear evidence of neurodegeneration or gliosis has been demonstrated in the MECP2-null LC. Rett Syndrome and GPT2 Deficiency may have commonalities regarding the role of LC dysfunction in their pathophysiology.

Human patients with GPT2 Deficiency display cognitive as well as motor abnormalities including spastic paraplegia (28). Motor deficits in the lower limbs seen in spastic paraplegia have been attributed to high energetic and biosynthetic costs of maintaining long-range projecting neurons (49). Locus coeruleus projects to virtually the entire central nervous system and descending noradrenergic tracts have been shown to influence motor function (1, 5, 50-53). LC neurons that project to the cortex are spread out along the dorsal-ventral axis of LC and those that project to the hippocampus remain dorsally whereas the spinal cord-projecting LC neurons reside at the ventral most region of LC (3, 37, 50, 54). Given the strong gliosis phenotype seen in the ventral LC and greatest reduction of norepinephrine levels in the spinal cord, it is possible that the LC neurons projecting to the spinal cord are particularly affected in GPT2-null mice.

An intriguing connection between GPT2 Deficiency in human patients and LC metabolism has recently emerged, where Ruaud and co-workers found reduced amount of pterins and homovanilic acid in the cerebrospinal fluid of patients with GPT2 Deficiency (55). A decreased level of homovanilic acid, a metabolite of tyrosine metabolism in dopaminergic and noradrenergic neurons, may reflect a secondary consequence of LC dysfunction in human patients with GPT2 Deficiency. A pterin derivative, tetrahydrobiopterin (BH₄) is used as a co-enzyme for nitric oxide synthase, the activity of which has been shown to modulate oxidative stress in LC (56). Increased pacemaking

activity (Fig.8) may also lead to increases in Ca^{2+} levels leading to more oxidative stress and possibly apoptosis.

GPT2 catalyzes a reaction that results in a net production of a tricarboxylic acid cycle intermediate and the replenishment of the TCA cycle is collectively named anaplerosis. Our data suggest that this reaction may have particular importance in maintaining the health of LC neurons and that the underlying pathophysiology may be influenced by dysregulation in metabolic pathways related to the TCA cycle. These pathways have not seen much attention in the context of LC (56, 57), but recently, dysfunction of oxidative phosphorylation which relies on the continuity of the TCA cycle, has been proposed to explain selective neuron loss seen in Alzheimer's Disease (58). Empirical data in favor of this proposal is not extensive, however LC dysfunction in the GPT2-null animal model may provide novel insights as to the significance of dysregulated pathways of energetics in the degenerating brain.

Two isoforms of glutamate pyruvate transaminase exist, a cytosolic, GPT1, and a mitochondrial isoform, GPT2 (59, 60). In a recent study of transcriptomic profiling by translating ribosome affinity purification (TRAP) in LC neurons (61), GPT2 expression turned out to be almost 4 times the expression of GPT1, suggesting GPT2 is the primary glutamate pyruvate transaminase in LC neurons. GPT2 expression was confirmed by β -galactosidase staining (a marker for GPT2 promoter activity in the GPT2-null allele) that co-localized with tyrosine hydroxylase in LC neurons of GPT2-het mice (Fig.S4). Other cells including astrocytes also express GPT2 (62). However, whether the degeneration of LC in GPT2-null mice occur cell or non-cell autonomously needs to be clarified by future experiments.

In summary, our results identify a novel metabolic mechanism of neurodegeneration in LC. The neuronal death in LC is caused by loss of GPT2, an enzyme that replenishes the TCA cycle. This process is critical for both energetics and biosynthetic pathways, and LC degeneration in GPT2-null mice may be a consequence of defects in these pathways. Studies of GPT2-mediated metabolism in LC may allow us to deepen our understanding of metabolic mechanisms involved in selective vulnerability in LC. This knowledge may lead to new therapeutic targets with benefit to a wide range of neurological and psychiatric diseases.

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Author contributions

Conceptualization O.B. and E.M.M.; O.B. conducted all experiments; Data curation and Visualization O.B.; Experimental Design and Data Analysis O.B, J.A.K. and E.M.M.; Formal analysis and Writing – Original Draft, O.B. and E.M.M.; Writing – Review & Editing, O.B., J.A.K. and E.M.M.; Supervision, Project Administration and Funding Acquisition, E.M.M.

Disclosures

The authors declare no competing interests.

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Figure Legends

Figure 1. GPT2 Deficiency leads to selective gliosis and neuron loss in locus coeruleus.

Selective microgliosis in GPT2-null LC in sagittal brain sections at P18. Images of tyrosine hydroxylase (TH, magenta), Iba1 (green) staining in wild-type (a) and GPT2-null (b) sagittal sections. D: Dorsal V: Ventral. Low magnification images taken with a 2X objective (are shown on the left, (scale bar: 500 μm), high magnification images taken with a 60X objective are on the right (scale bar: 100 μm).

Figure 2. Selective microgliosis in GPT2-null LC in coronal brain sections at P18.

Images of tyrosine hydroxylase (TH, magenta), Iba1 (green) staining in wild-type (a) and GPT2-null (b) coronal sections containing LC. D: Dorsal, V: Ventral, M: Medial, L: Lateral. Scale bar: 200 μm .

Figure 3. Smaller TH⁺ neurons and loss of TH⁺ in GPT2-null LC at P18.

High magnification images of microgliosis in GPT2-null LC at P18. Tyrosine hydroxylase (TH, magenta) and Iba1 (green) staining in wild-type (a) and GPT2-null (b) LC. (c) Quantification of TH⁺ cell count, TH⁺ soma area, TH average relative fluorescence intensity and Iba1 average relative fluorescence intensity are given below (wild-type: black, GPT2-null: red). Scale bar: 50 μm . ****0.001 < P < 0.01.**

Figure 4. Degeneration of LC neurons in GPT2-null LC.

Fluoro-Jade C staining at P18, wildtype (a), GPT2-null (b). Arrows point to degenerating cells and arrowheads point to normal cells. The asterisk denotes the 4th ventricle. Scale bar: 100 μ m. Eosinophilic and necrotic neurons are present in GPT2-null LC at P18.

Images of H&E staining in wild-type (c) and GPT2-null (d) LC (Scale bar: 100 μ m). The top arrow points to a necrotic neuron and the bottom arrow points to a hypereosinophilic neuron in GPT2-null LC, both visualized with higher magnification on the right (Scale bar: 5 μ m). The arrowhead points to a healthy neuron of the motor nucleus of the trigeminal nerve bordering the LC laterally. The asterisk denotes the LC.

Figure 5. Noradrenergic innervation in hippocampus is reduced in GPT2-null mice.

Noradrenergic innervation in hippocampus of GPT2-null mice at P18 is reduced. Images of

norepinephrine transporter (NET, green) staining in coronal sections containing hippocampus of

wild-type (a) and GPT2-null (b) mice (scale bar: 500 μ m). The white boxes indicate example areas of CA1 of hippocampus and retrosplenial cortex (RSC) where the staining was quantified.

Representative images of higher magnification are shown on the right for RSC (c) and hippocampus (d) (scale bar: 100 μ m). Quantification of NET staining as a fraction of the total

field of view is shown for cortex (c, right) and hippocampus (d, right) (wild-type: black, GPT2-null: red). SR: stratum radiatum, SP: stratum pyramidale, SO: stratum oriens.

**0.001 < P < 0.01.

Figure 6. Noradrenergic innervation in spinal cord of GPT2-null mice at P18 is reduced.

Images of norepinephrine transporter (NET, green) staining in coronal sections of cervical and

lumbar spinal cord of wild-type (a) and GPT2-null (b) mice (scale bar: 200 μ m). The white boxes

indicate example areas where the staining was quantified for cervical spinal cord (c) and lumbar spinal cord (d) (DL: dorsolateral, DM: dorsomedial, VL: ventrolateral, VM: ventromedial).

Quantification of NET staining as a fraction of the total field of view is shown (wild-type: black,

GPT2-null: red). *0.01 < P < 0.05; **0.001 < P < 0.01; *** P < 0.001.

Figure 7. Norepinephrine levels in hippocampus and spinal cord of GPT2-null mice are reduced at postnatal day 18 (P18) and P14 but not at P7.

Norepinephrine levels in hippocampus and spinal cord of GPT2-null mice at P18 (a) and P14 (b)

are reduced but not at P7 (c). Quantification of norepinephrine levels per wet weight of tissue

(pmol/g) in cortex, hippocampus, cervical and lumbar spinal cord of wild-type (black) and GPT2-null (red) mice as detected by enzyme-linked immunosorbent assay (ELISA) is shown. $*0.01 < P < 0.05$; $**0.001 < P < 0.01$.

Figure 8. Electrophysiological characterization of LC in GPT2-null mice reveals changes in intrinsic cell properties and action potential parameters.

(a) Representative image of LC with a patch pipette (left) and representative traces of recordings in LC neurons of wild-type (black) and GPT2-null (red) mice at P18. (b) Capacitance of GPT2-null LC neurons at P18 is reduced. Wild-type: black, GPT2-null: red. Each dot represents a different cell. $*0.01 < P < 0.05$. (c) Membrane resistance of GPT2-null LC neurons at P18 is increased. Wild-type: black, GPT2-null: red. Each dot represents a different cell. $***0.001 < P < 0.01$. (d) Pacemaking frequency of GPT2-null LC neurons at P18 is slightly increased. Wild-type: black, GPT2-null: red. Each dot represents a different cell. $*P = 0.0318$. Mixed model analysis was employed here with fixed effects: genotype, presence of hyperpolarization in resting membrane potential toward the end of recording and whether the pacemaking activity was retained throughout the recording, random effects: day of recording. (e) Shape of the averaged action potential from the pacemaking activity of wild-type (black, n=11 cells) and GPT2-null (red, n=11 cells) LC neurons at P18. (f) Peak amplitude of GPT2-null LC neuron action potential at P18 is increased. Wildtype: black, GPT2-null: red. Each dot represents a different cell. $*0.01 < P < 0.05$. (g) Time to decay to half amplitude of GPT2-null LC

neuron action potential at P18 is decreased. Wild-type: black, GPT2-null: red. Each dot represents a different cell. $**0.001 < P < 0.01$. (h) Hyperpolarization peak amplitude of GPT2-null LC neuron action potential at P18 is increased. Wild-type: black, GPT2-null: red. Each dot represents a different cell. $*0.01 < P < 0.05$.

SUPPLEMENTAL INFORMATION

Supplemental Figure Legends

Supplemental Figure 1. Selective microgliosis is observed in a pontine region in GPT2-null mice at P18.

a. Images of Iba1 (green) staining in GPT2-null sagittal sections at P18. Each section is separated by approximately 500 μm and succeeded medially from top to bottom. The arrowhead notes the pontine nucleus where clustered activated microglia are present. Note the absence of gliosis in other brain regions. The tile images taken with a 20X objective were stitched. Scale bar: 500 μm .

b. Images of Iba1 (green) staining in wild-type (left) and GPT2-null (right) coronal sections containing various brain regions including motor cortex and somatosensory areas, caudoputamen, nucleus accumbens. Note the absence of microgliosis throughout the brain section. Scale bar: 500 μm .

c. Images of Iba1 (green) staining in wild-type (left) and GPT2-null (right) coronal sections containing various brain regions including hippocampus, thalamus, hypothalamus, amygdala. Note the absence of microgliosis throughout the brain section. Scale bar: 500 μm .

d. Images of Iba1 (green) staining in wild-type (left) and GPT2-null (right) coronal sections containing various brain regions including cortical visual and entorhinal areas, midbrain. Note the absence of microgliosis throughout the brain section. Scale bar: 500 μm .

e. Images of Iba1 (green) staining in wild-type (left) and GPT2-null (right) coronal sections containing various brain regions including cerebellum and medulla oblongata.

Note the absence of microgliosis throughout the brain section. Scale bar: 500 μm .

Supplemental Figure 2. Microgliosis and astrogliosis is present in GPT2-null mice at P18 but not at P10.

a. Images of Gfap (cyan), Iba1 (yellow), tyrosine hydroxylase (TH, magenta) staining in wild-type and GPT2-null coronal sections at P18. Note the increase in Gfap staining in GPT2-null LC and clustering of microglia particularly around the ventral LC. Scale bar: 100 μm .

b. Images of Gfap (cyan), Iba1 (yellow), tyrosine hydroxylase (TH, magenta) staining in wild-type and GPT2-null coronal sections at P10. Note the absence of either microgliosis or astrogliosis in GPT2-null LC at P10. Scale bar: 100 μm .

Supplemental Figure 3. CD68 staining in reactive microglia in GPT2-null LC at P18.

a. Images of CD68 (cyan), Iba1 (yellow), tyrosine hydroxylase (TH, magenta) staining in wild-type and GPT2-null coronal sections at P18, taken with a 20X objective.

Arrowheads point to the increased size of CD68 puncta within the reactive microglia in GPT2-null LC. Scale bar: 100 μm .

b. Images of CD68 (cyan), Iba1 (yellow), tyrosine hydroxylase (TH, magenta) staining in wild-type and GPT2-null coronal sections at P18, taken with a 60X objective. Note the

enlarged CD68 puncta within the reactive microglia in GPT2-null LC. Scale bar: 100 μm .

Supplemental Figure 4. GPT2 is expressed in LC neurons.

a. Target allele construct that results in a GPT2-null allele. The targeted allele consists of flippase recognition sites (FRT) flanking a strong splicing acceptor site (Engrailed 2-SA), β -galactosidase (β -gal, an enzymatic reporter), neomycin (a selective marker for embryonic cells) and a polyadenylation site.

b. Immunofluorescence of β -galactosidase in CA3 area of hippocampus of a GPT2-heterozygous (GPT2-het) mouse at P18. Note the pattern of the β -gal (cyan) puncta aligning with the nuclei (DAPI, yellow) the stratum pyramidale of CA3, indicating strong expression in neurons and validity of the β -gal reporter. Scale bar: 100 μm .

c. Images of β -gal (cyan) and tyrosine hydroxylase (TH, magenta) staining in LC of GPT2-het mouse at P5 (top) and P18 (bottom). Note the stronger staining at P18 indicating increased expression of GPT2 at this timepoint compared to P5. Scale bar: 50 μm .

d. High magnification images of β -gal (cyan) and tyrosine hydroxylase (TH, magenta) staining in representative neurons in LC of GPT2-het mouse at P5 (top) and P18 (bottom). Note the larger puncta of β -gal at P18 indicating increased expression of GPT2 at this timepoint compared to P5. Scale bar: 5 μm .

FIGURE 1

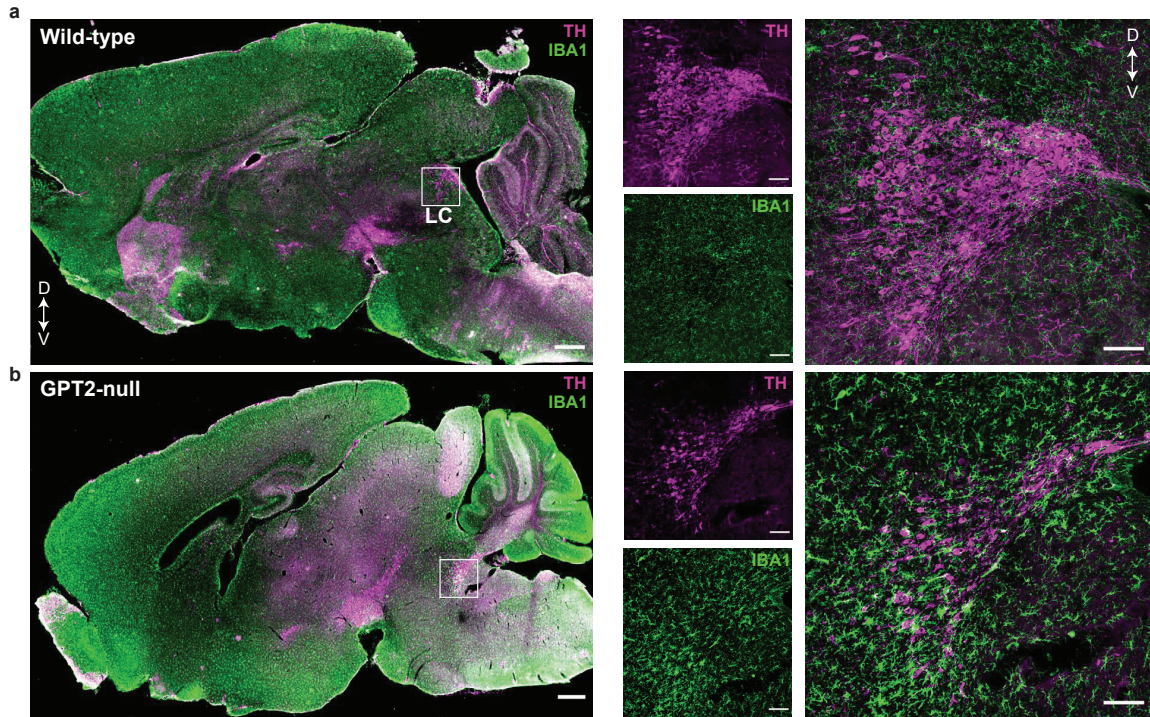


FIGURE 2

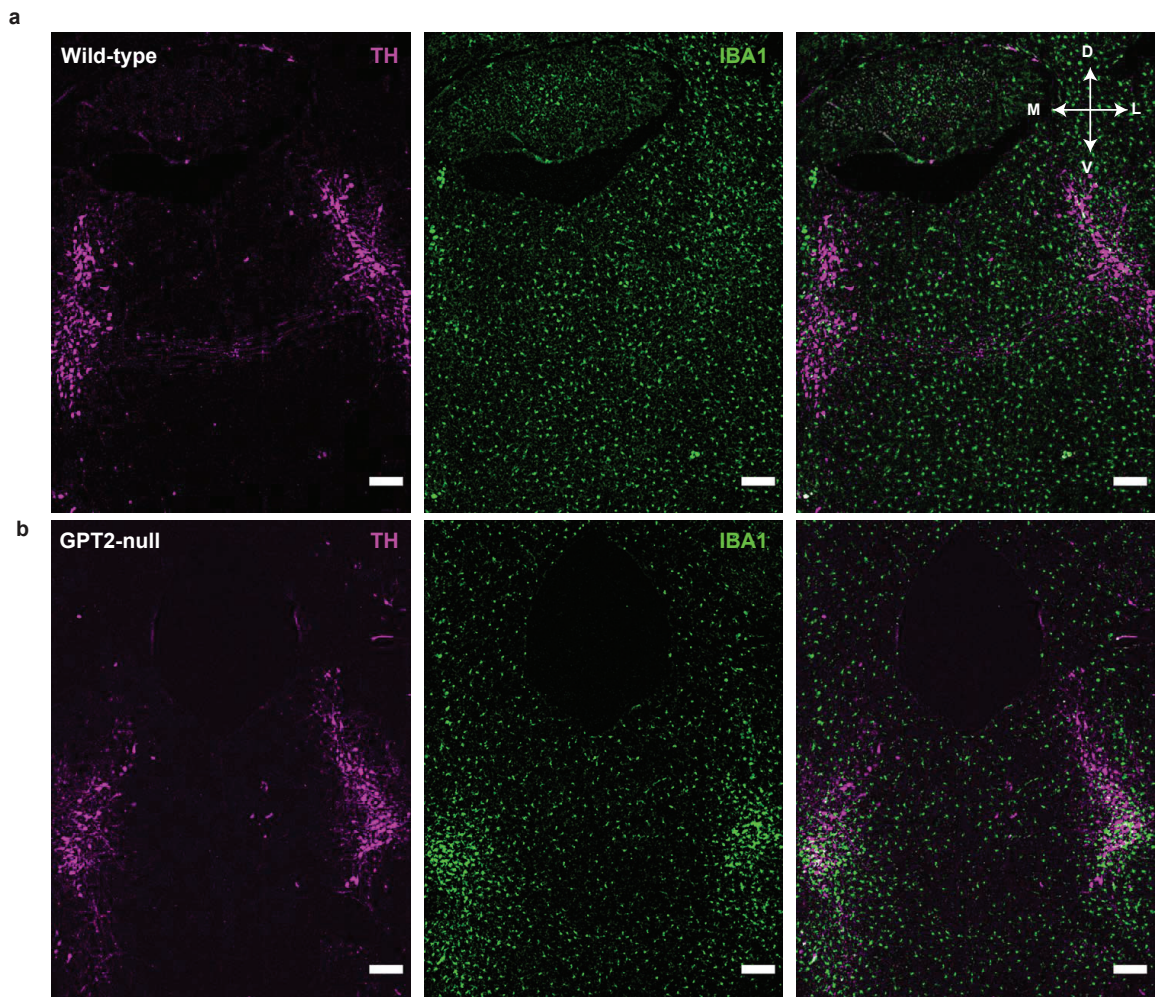


FIGURE 3

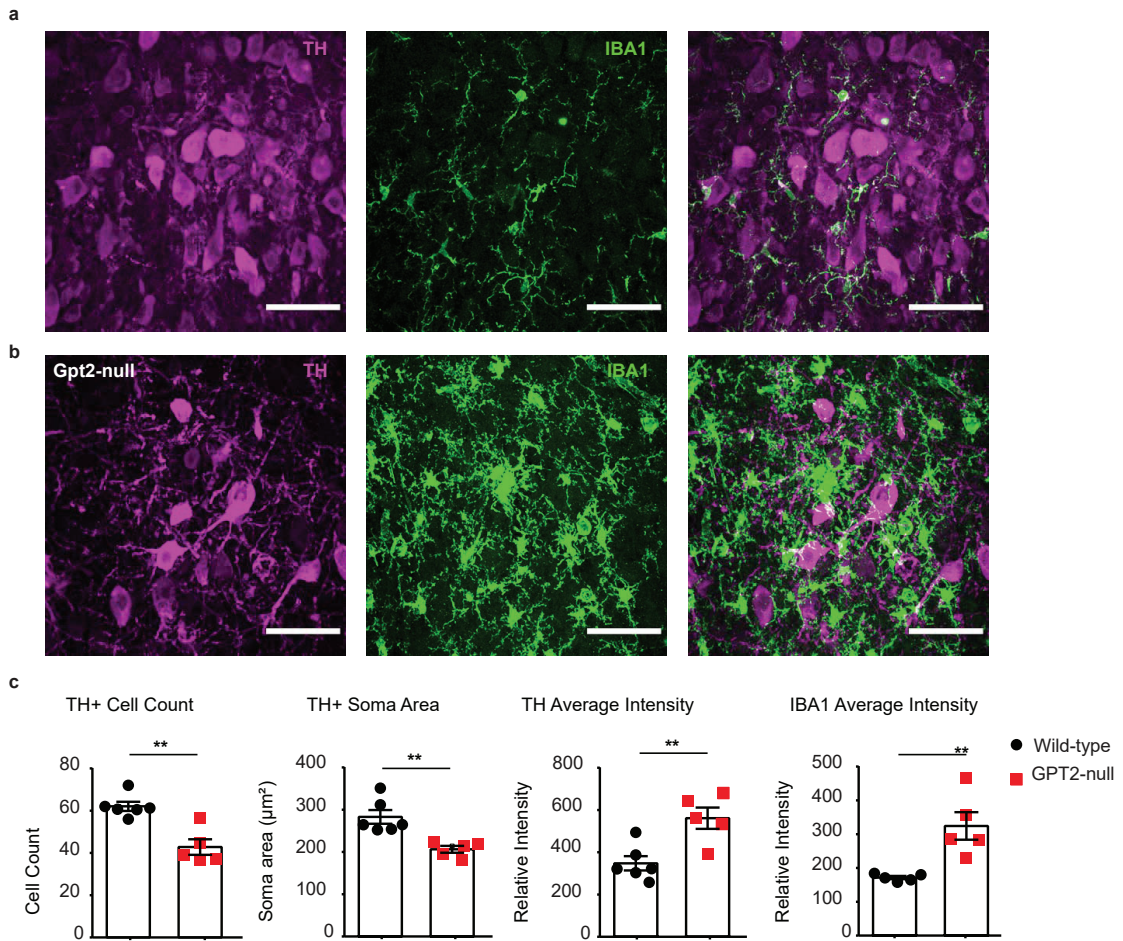


FIGURE 4

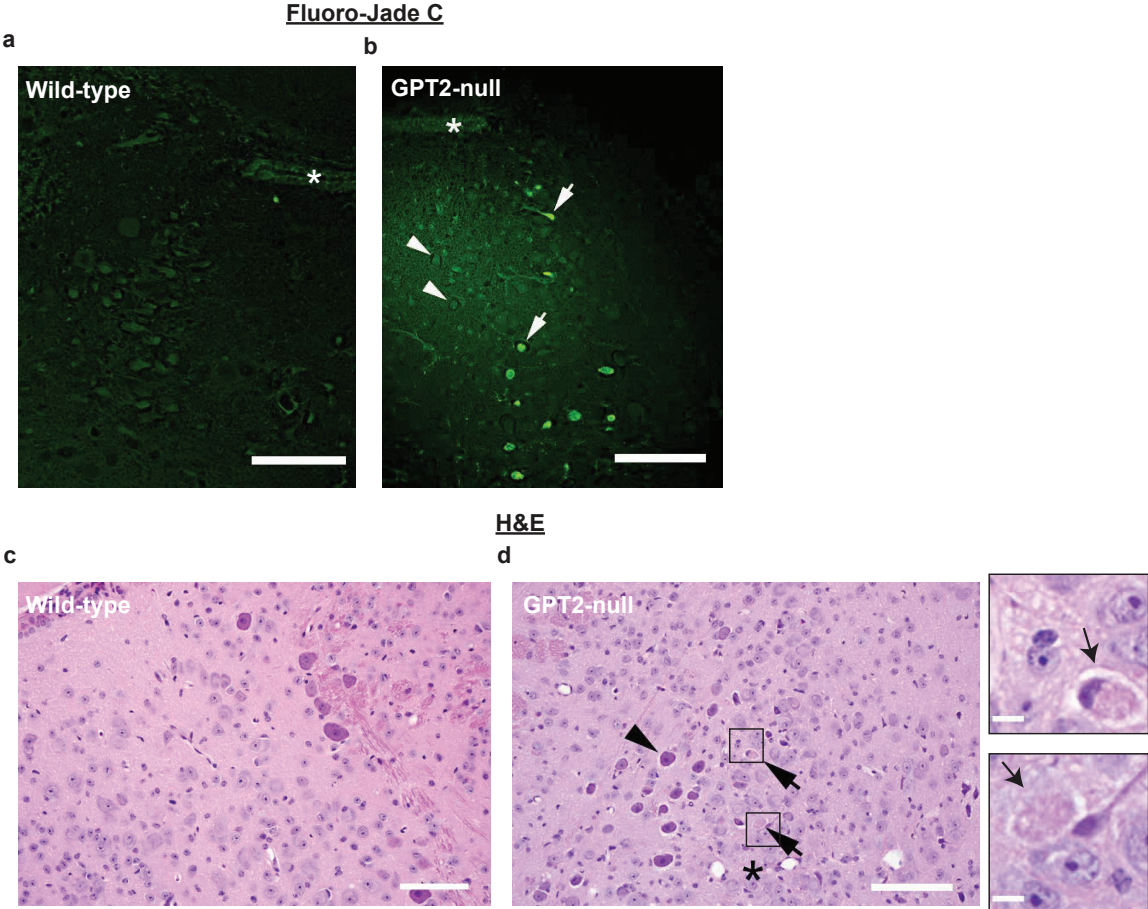


FIGURE 5

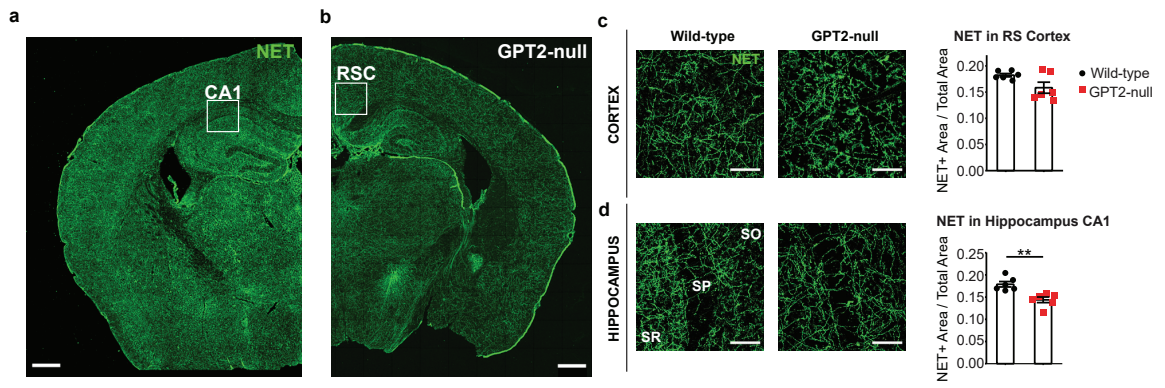


FIGURE 6

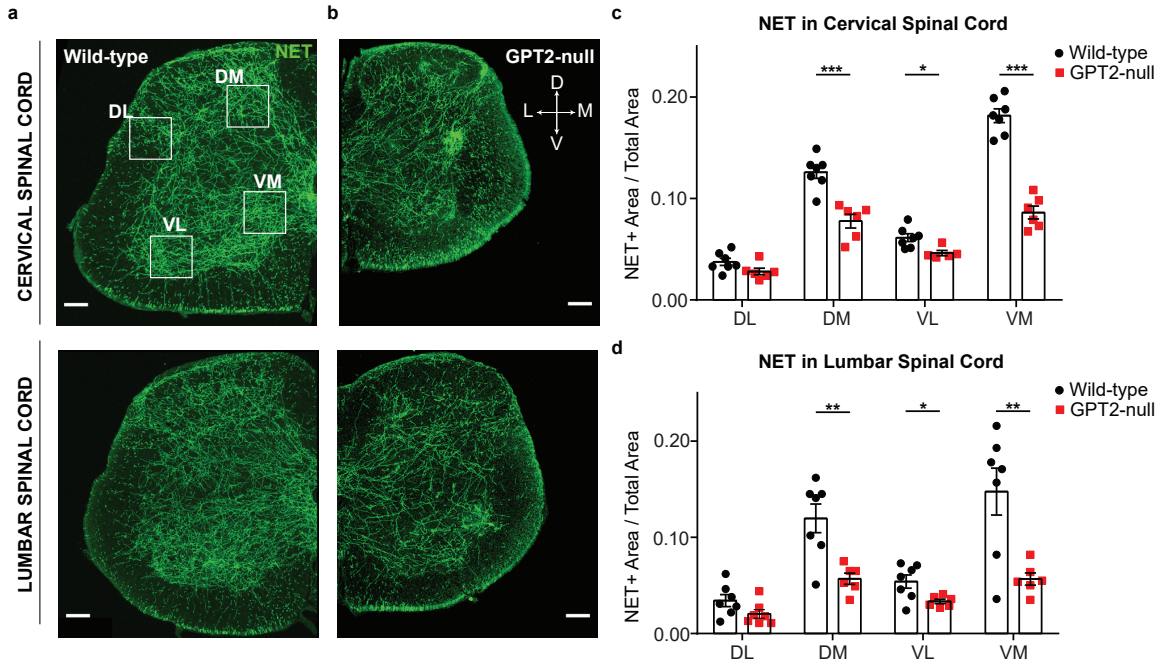


FIGURE 7

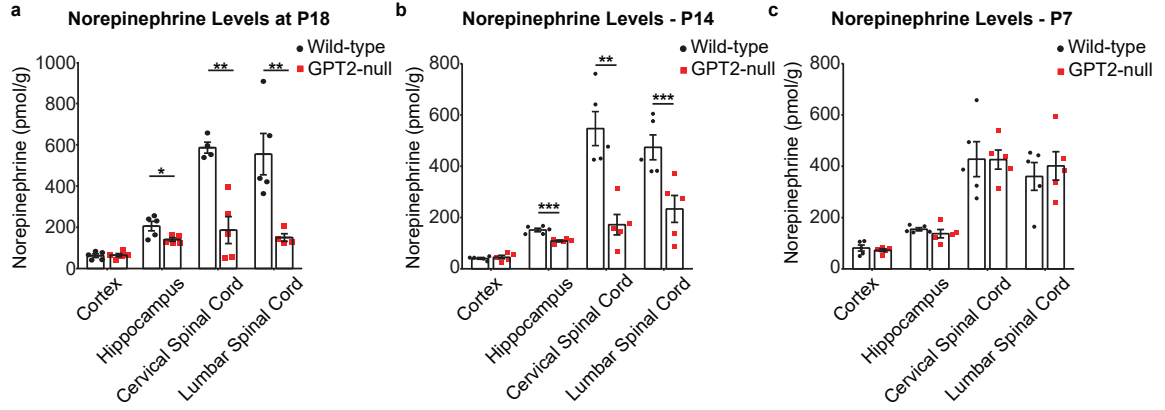


FIGURE 8

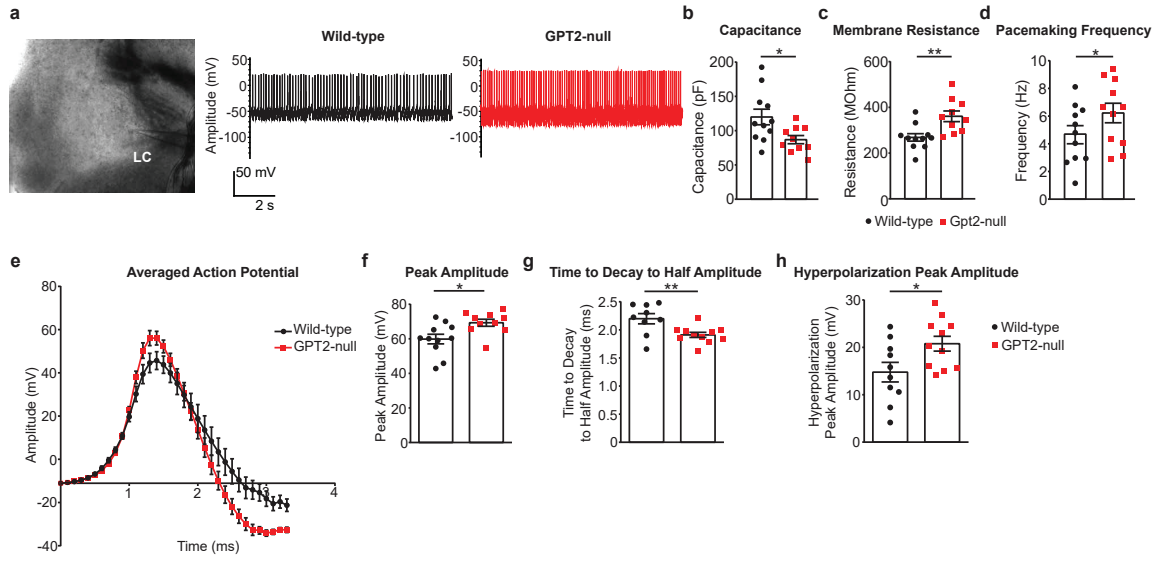


FIGURE S1

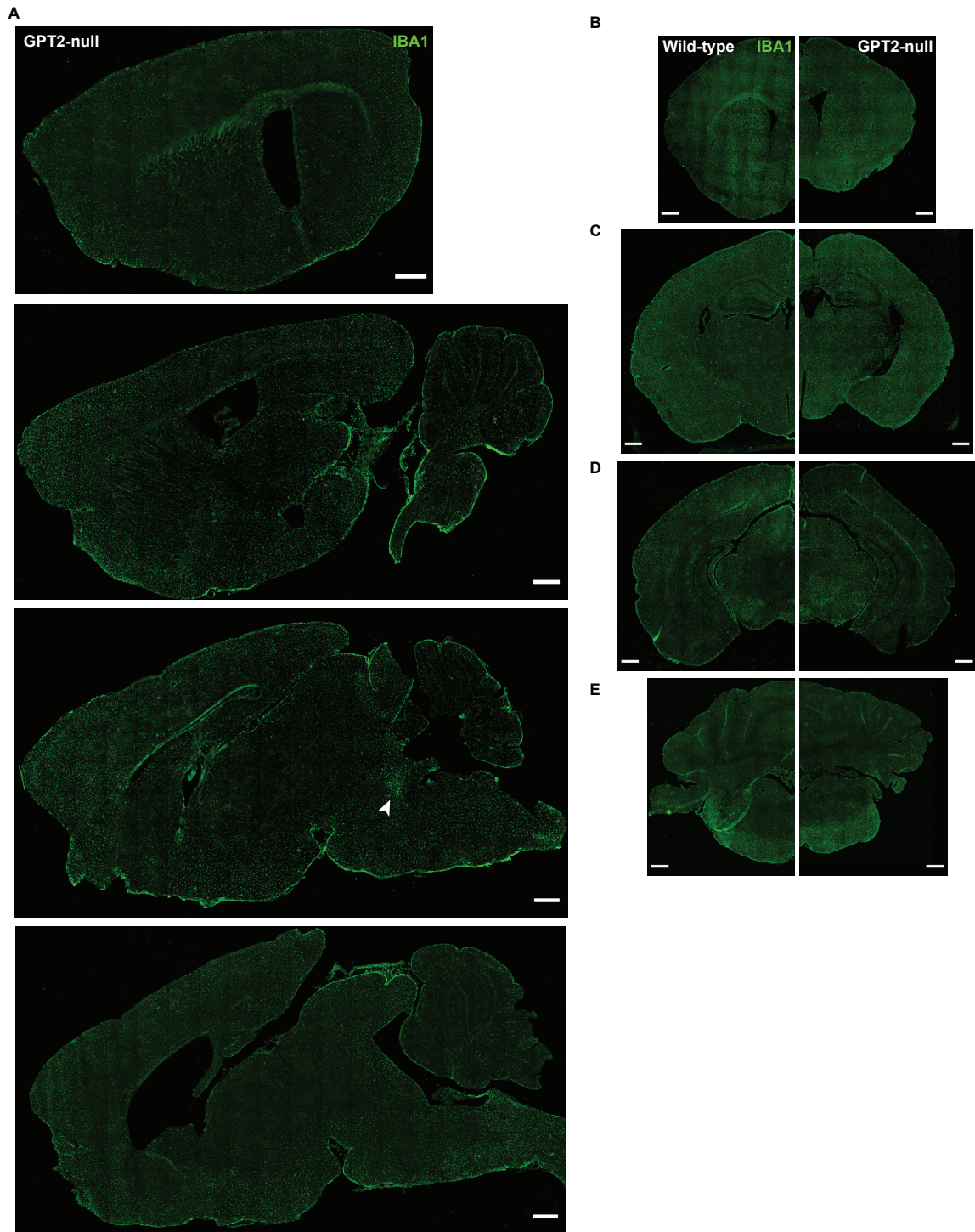


FIGURE S2

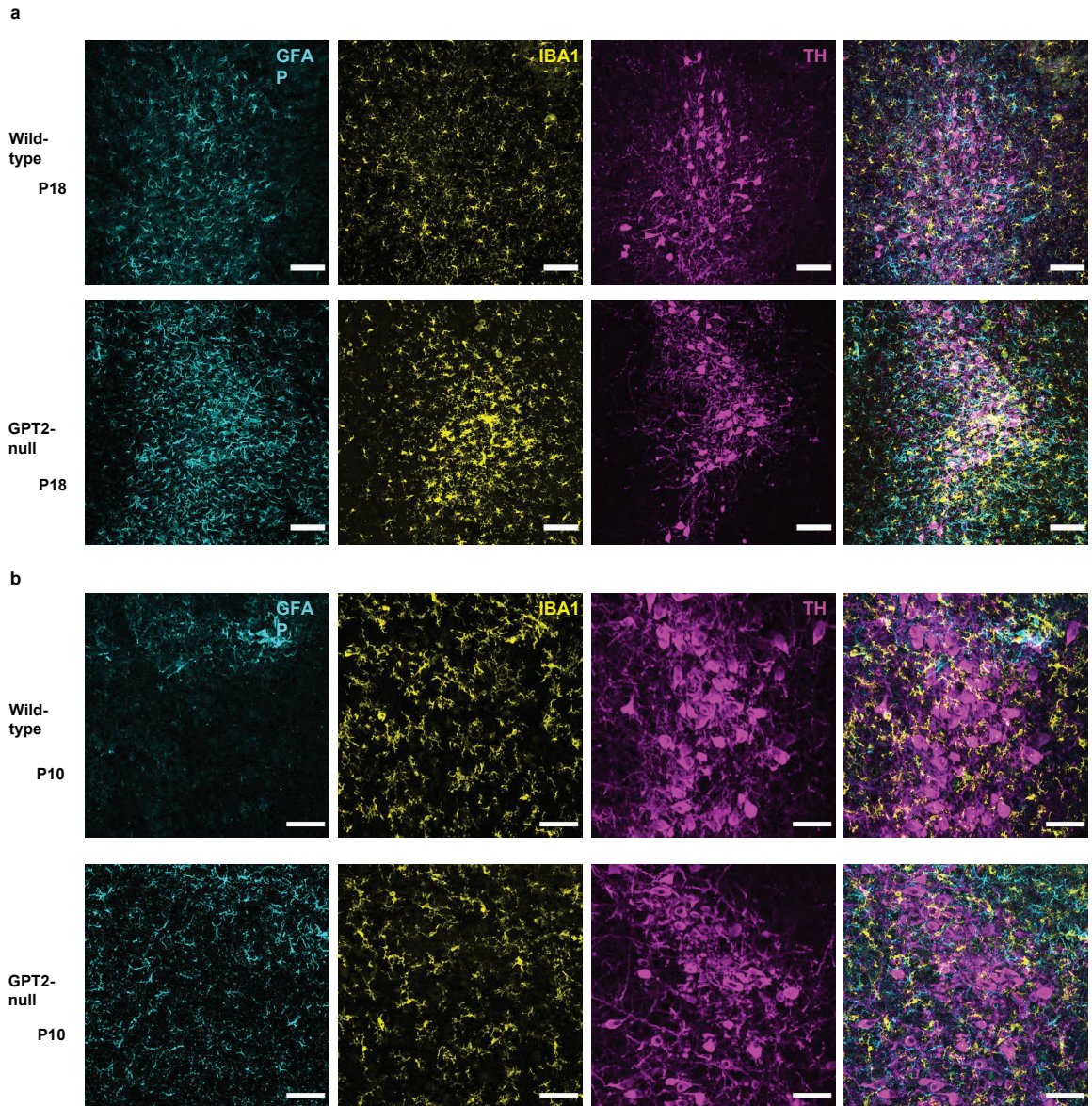


FIGURE S3

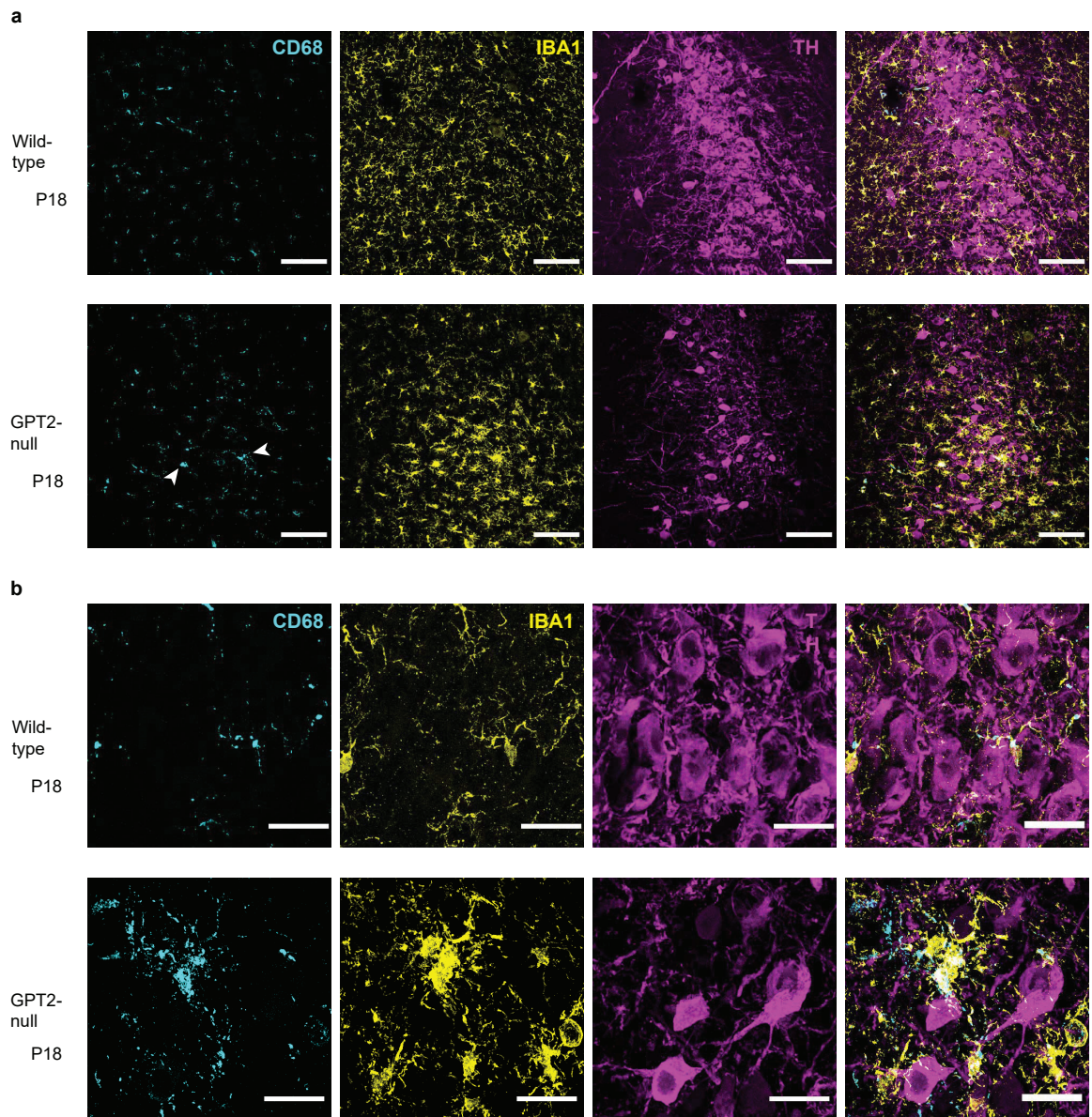
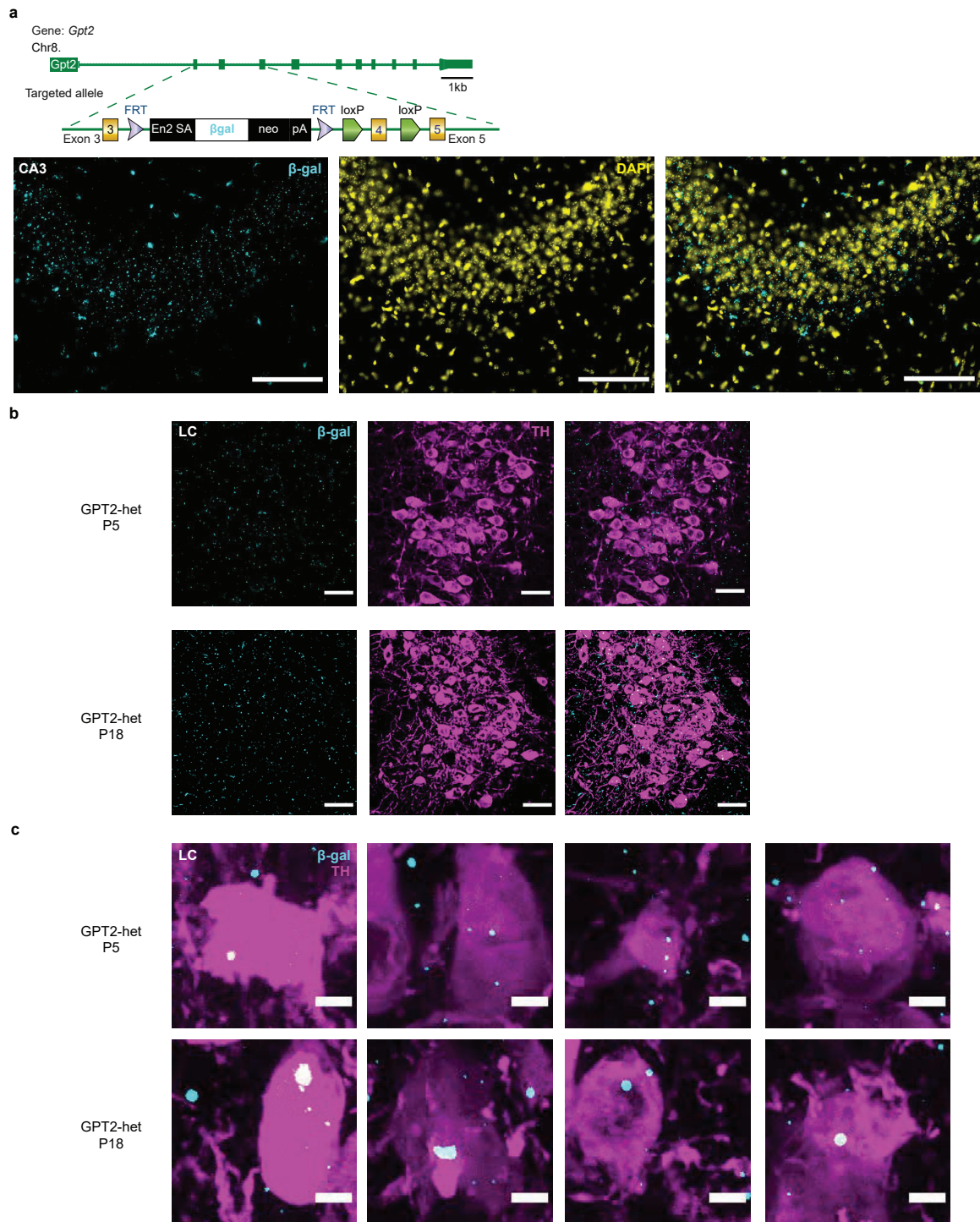


FIGURE S4



Chapter 5: Loss of mitochondrial enzyme GPT2 leads to reprogramming of synaptic glutamate metabolism.

I conducted all experiments. Shawn M. Davidson ran LC-MS at Princeton. The project was performed under the supervision of Julie A. Kauer and Eric M. Morrow. For funding sources please refer to the Chapter.

Loss of mitochondrial enzyme GPT2 leads to reprogramming of synaptic glutamate metabolism

Abbreviated Title: Loss of GPT2 rewires synaptic glutamate metabolism

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Abstract

Glutamate metabolism is tightly regulated by a multitude of metabolic enzymes to sustain both excitatory neurotransmission and energetics. Previously, we reported loss-of-function mutations in mitochondrial enzyme glutamate pyruvate transaminase 2 (*GPT2*) in humans that cause postnatal microcephaly, intellectual disability and motor abnormalities. Here we report that Gpt2 is enriched in isolated synaptic terminals and the loss of Gpt2 leads to a reprogramming of glutamate metabolism in male and female mice. Gpt2 governs a reversible reaction that may synthesize glutamate using alanine and alpha-ketoglutarate and mediate conversion of glutamine into alanine. Glutamatergic synaptic transmission in Gpt2-null CA1 hippocampal slices is impaired in a fashion consistent with decreased pre-synaptic glutamate levels. Glutamate levels released from Gpt2-null synaptosomes are reduced but restored to wild-type levels by alpha-ketoglutarate. Through isotope labeling studies, we observe that fractional enrichment of double heavy nitrogen labeled glutamine in Gpt2-null synaptosomes is increased but rescued by alpha-ketoglutarate. Gpt2 loss results in changes in levels of synaptic proteins involved in glutamate metabolism, particularly increases in glutamate dehydrogenase and glutamine synthetase. We find deficits in the tricarboxylic acid (TCA) cycle in Gpt2-null synaptosomes, but glutamine entry into the TCA cycle was intact. In conclusion, Gpt2 is a mitochondrial enzyme in synaptic terminals that links glutamate metabolism to alanine and TCA cycle metabolism, and in the absence of Gpt2, regulatory enzymatic mechanisms appear to be reprogrammed to partly maintain functioning of the glutamatergic synaptic transmission.

Significance Statement

Investigation of neurometabolism have recently implemented genetic approaches, furthering our understanding of metabolic pathways that sustain glutamatergic neurotransmission. Here we investigate the contributions of glutamate pyruvate transaminase 2 (Gpt2) to glutamate metabolism and the consequences of Gpt2 deficiency on synaptic transmission. Gpt2 deficiency in humans causes microcephaly and intellectual disability and understanding the function of Gpt2 may help delineate the metabolic mechanisms that support brain and cognitive development. In the absence of Gpt2, glutamate transmission is impaired but rescued by alpha-ketoglutarate supplementation. Gpt2 deficiency leads to compensatory upregulation of enzymes and transporters involved in glutamate metabolism. Our results emphasize the use of glutamate for replenishing the tricarboxylic acid cycle and the role of Gpt2 in sustaining energetics and neurotransmitter availability.

Introduction

Glutamate, the main excitatory neurotransmitter in the central nervous system (Fonnum, 1984; Villa and Nedivi, 2016), is crucial for neurotransmission as well as the tricarboxylic acid (TCA) cycle (Kovacevic, 1971; Westergaard et al., 1995), nitrogen balance (Cooper and Jeitner, 2016; Kurmi and Haigis, 2020), synthesis of proteins (Young and Ajami, 2000), glutathione (Sedlak et al., 2019), and gamma-aminobutyric acid synthesis (Sonnewald and McKenna, 2002). Glutamate metabolism has been studied widely using measurement of enzyme activities, concentrations, and labeling patterns of metabolites with heavy isotope or radioisotope labeled precursors (Erecinska and Silver, 1990b). Genetic approaches have since followed, furthering our understanding of the intricate metabolic pathways of glutamate metabolism that sustain neurotransmission.

Previously, we reported recessive loss-of-function mutations in the gene glutamate pyruvate transaminase 2 (*GPT2*) (also known as alanine aminotransferase) that lead to a neurodevelopmental disorder involving microcephaly, intellectual disability, and motor abnormalities (Ouyang et al., 2016). *Gpt2* is an alanine aminotransferase that catalyzes a reversible transamination, transferring an amino group from glutamate to pyruvate synthesizing alanine and alpha-ketoglutarate. *Gpt2* resides in the mitochondria while its paralog, *Gpt1* catalyzes the same reaction in the cytoplasm (Lindblom et al., 2007; Ouyang et al., 2016). *Gpt2* has been widely studied in the context of cancer and liver metabolism (Jin et al., 2015; Kim et al., 2019; McCommis et al., 2015; Smith et al., 2016); however, its role as a metabolic enzyme modulating glutamate levels in the

nervous system remains unknown. Genetic ablation of Gpt2 in mice has allowed us to study the extent to which Gpt2 regulates glutamate availability.

In this study, we report that Gpt2 is enriched in the mitochondria of isolated synaptic terminals (synaptosomes) and the loss of Gpt2 leads to a reprogramming of glutamate metabolism. Gpt2 may produce glutamate with alanine and alpha-ketoglutarate as precursors and mediate conversion of glutamine into alanine. Glutamatergic transmission in mouse brain slices is impaired evidenced by decreased miniature postsynaptic excitatory currents and faster decline of postsynaptic response in CA1 pyramidal neurons to repeated CA3 Schaffer collateral stimulation. Glutamate levels released upon membrane depolarization are reduced in Gpt2-null synaptosomes. Through isotope labeling studies, we observe that fractional enrichment of double heavy nitrogen labeled glutamine is increased. Alpha-ketoglutarate was able to raise glutamate and decrease fractional enrichment of double-labeled glutamine in Gpt2-null synaptosomes back to wild-type levels. We find increased protein levels of glutamate dehydrogenase and glutamine synthetase in Gpt2-null synaptosomes, two metabolic enzymes that mediate glutamate oxidation and ammonia fixation, respectively. We also find deficits in the TCA cycle in Gpt2-null synaptosomes although glutamine entry into the TCA cycle remains intact. Our results indicate that Gpt2 plays a role in sustaining energetics and neurotransmitter availability, and in the absence of Gpt2, these processes appear to be partly compensated by upregulation of metabolic enzymes and transporters involved in glutamate metabolism.

Results

Gpt2 is the primary glutamate-pyruvate transaminase in isolated nerve terminals.

To understand the contribution of Gpt2 to glutamate metabolism at the synapse, we first investigated Gpt2 protein expression in synaptosomes. Synaptosomes are isolated nerve terminals that form during homogenization and medium-speed centrifugation of mouse nervous tissues in a sucrose-based solution (Figure 1A) (Dunkley et al., 2008). Gpt2 was enriched both in synaptosomes and mitochondria (Figure 1C). Gpt1, the cytosolic paralog of Gpt2, was enriched in the cytosolic fraction but virtually absent in both synaptosomal and mitochondrial fractions. In Western blotting of the different subcellular fractions, we also confirmed the presence of some of the proteins involved in glutamate/glutamine metabolism at synaptic terminals (Figure 1B,C). We fractionated synaptosomes further into synaptic membranes, cytosol and vesicles and Gpt2 was not enriched in any of these fractions indicating that Gpt2 is enriched in the mitochondria situated in synaptic terminals (Figure 1D).

In agreement with the exclusive expression of Gpt2 in synaptosomes, we found only residual Gpt enzyme activity in Gpt2-null synaptosomes compared to the wild-type controls (Figure 1E). To further confirm absence of Gpt activity in Gpt2-null synaptosomes and assess the function of metabolic pathways that utilize Gpt2, we conducted isotope labeling experiments with heavy isotope labeled tracers (Figure 1F). From amine nitrogen-labeled glutamine ($[\alpha\text{-}^{15}\text{N}]$ -glutamine), alanine was not labeled at all in Gpt2-null synaptosome pellets or medium indicating that glutamine could not act as a precursor for alanine in the absence of Gpt2. Interestingly, the alanine pool that was released from wild-

type synaptosomes into the medium originated from [α - ^{15}N]-glutamine more than the alanine pool that remained in the pellet (Figure 1F, left).

Akin to a Gpt enzyme activity assay, an excess supply of heavy nitrogen labeled alanine (1.6 mM) and unlabeled alpha-ketoglutarate (1.6 mM) resulted in 41.7 ± 2.4 % labeling in glutamate of wild-type synaptosomal pellets as well as in 47.2 ± 2.3 % of the glutamate pool released into the medium, suggesting that alanine along with alpha-ketoglutarate can be used as substrates for glutamate in our wild-type synaptosome preparations (Figure 1F, right). On the other hand, Gpt2-null synaptosomal pellet or medium showed residual heavy nitrogen labeling in glutamate (5.1 ± 0.4 % in pellet; 4.9 ± 0.4 % in medium). Thus, we conclude that Gpt2 is the main alanine aminotransferase in synaptic terminals.

Electrophysiological recordings suggest decreased glutamatergic transmission in Gpt2-null hippocampus.

To assess the role of Gpt2 in synaptic transmission and modulation of glutamate, we conducted whole-cell patch-clamp recording experiments in pyramidal neurons of CA1 hippocampal slices (Figure 2A). We first characterized the electrophysiological properties of the Gpt2-null pyramidal neurons. The resting membrane potential of Gpt2-null pyramidal neurons was slightly depolarized (Wild-type: -63.8 ± 1.9 mV vs Gpt2-null: -59.8 ± 1.0 mV) (Figure 2B). The capacitance was reduced, and the membrane resistance was increased in Gpt2-null pyramidal neurons suggesting that Gpt2-null CA1 pyramidal neurons are smaller in soma size (Wild-type: 121.7 ± 6.7 pF vs Gpt2-null: 92.7 ± 4.8 pF; Wild-type: 122.7 ± 7.3 MOhm vs Gpt2-null: 160.5 ± 9.5 MOhm, respectively) (Figure 2C).

Slight depolarization and increased membrane resistance in Gpt2-null pyramidal neurons are visible in the representative traces in Figure 2A. Overall, the electrophysiological properties of Gpt2-null neurons were significantly altered.

Miniature post-synaptic currents are indirect measures of neurotransmitter levels in synaptic quanta, individual synaptic vesicles (Fatt and Katz, 1952; Ropert et al., 1990). To test whether absence of Gpt2 affected glutamate pools in synaptic vesicles, we recorded miniature post-synaptic excitatory currents (mEPSCs) from Gpt2-null CA1 pyramidal neurons voltage-clamped at -80mV. The mEPSC frequency was unchanged (Figure 2F, Wild-type: 0.12 ± 0.01 Hz vs Gpt2-null: 0.13 ± 0.01 Hz); however, the mEPSC peak amplitude was slightly decreased in Gpt2-null pyramidal neurons (Figure 2E&G, Wild-type: 13.7 ± 0.5 pA vs Gpt2-null: 11.6 ± 0.3 pA). The cumulative probability histogram of mEPSC peak amplitudes of all miniature excitatory events was shifted to the left in a representative Gpt2-null pyramidal neuron compared to its wild-type control (Figure 2H, Kolmogorov-Smirnov D value: 0.2386). Overall, these results suggest that glutamate levels were reduced in synaptic vesicles of excitatory afferents on Gpt2-null CA1 pyramidal neurons.

To test whether the GABAergic input onto Gpt2 pyramidal neurons was similarly affected, we recorded miniature post-synaptic inhibitory currents (mIPSCs) from Gpt2-null CA1 pyramidal neurons voltage-clamped at -80mV (Figure 2I-K). Both mIPSC frequency (Figure 2J) and peak amplitude (Figure 2K) were unchanged in Gpt2-null CA1 pyramidal neurons (Wild-type: 4.04 ± 1.03 Hz vs Gpt2-null: 3.3 ± 0.65 Hz; Wild-type: 35.5 ± 3.0 pA vs Gpt2-null: 33.1 ± 1.9 pA, respectively). The cumulative probability histogram of mIPSC peak amplitudes had a distribution similar to the wild-type control (Figure 2L). Overall,

these results suggest that GABA levels remained the same in synaptic vesicles at inhibitory synapses on Gpt2-null CA1 pyramidal neurons.

Protein levels of AMPAR, NMDAR and SV2 are reduced in Gpt2-null hippocampus.

The decreased glutamatergic transmission could be explained by alterations in cell properties and receptor protein levels of the post-synaptic neuron as well as in glutamate levels in the pre-synaptic neuron. To investigate levels of proteins involved in glutamatergic transmission, we did Western blotting in acutely dissected hippocampus tissues of wild-type and Gpt2-null mice at P18 (Figure 3A). There were significant decreases in AMPA receptor subunit 1 (AMPA, Gria1), synaptic vesicle protein 2 (SV2), and NMDA receptor (NMDAR, GluN1) in Gpt2-null hippocampus. Interestingly, there was also a modest increase in Psd95 protein levels in Gpt2-null hippocampus. There were no differences in the neuronal or astrocytic alanine/glutamine transporters, Snat1 and Asct1, respectively. The levels of astrocytic glutamate transporter, Glt1, essential for glutamate clearing from the synaptic cleft (Genda et al., 2011), remained unchanged in Gpt2-null hippocampus. Two metabolic enzymes, glutamine synthetase and glutamate dehydrogenase, crucial for glutamine/glutamate cycle (Hertz, 2013) and glutamate oxidation (McKenna et al., 2000), respectively, were unaltered in expression. There were no differences in vesicular glutamate (Vglut1, 2) or GABA (Vgat) transporters, suggesting that the decreased glutamate transmission was not due to a deficiency in vesicular transporter levels. The Gpt2-null cortex tissue was spared of any changes but Glt1 was significantly increased (Figure 3B).

We qualitatively assessed AMPAR and SV2 staining in Gpt2-null hippocampus by immunohistochemistry. Puncta patterns of AMPAR and SV2 in CA1 areas of wild-type and Gpt2-null hippocampus appeared to be similar (Figure 4A&B). There may be reductions of AMPAR particularly in dentate gyrus granular layer and reductions of SV2 particularly in CA3 stratum oriens, as assessed qualitatively in the images. AMPAR and SV2 puncta appeared to be morphologically intact in Gpt2-null CA1 hippocampus suggesting that decreases in AMPAR is unlikely to explain decreased glutamatergic transmission in Gpt2-null CA1.

Spines and synaptic vesicles were morphologically intact in Gpt2-null CA1 stratum radiatum.

We examined the ultrastructural properties of Gpt2-null CA1 stratum radiatum by electron microscopy (Figure 5&6). Spine counts as well as mitochondria counts per image taken at 21000X magnification were unchanged in Gpt2-null CA1 stratum radiatum (Figure 5B&C). Number of synaptic vesicles per spine and post-synaptic density length were also similar to the wild-type controls. Interestingly, we observed an increase in synaptic vesicle area suggesting increased vesicular size in Gpt2-null CA1 spines. Overall, the electron micrographs indicate that the ultrastructural morphology in Gpt2-null CA1 stratum radiatum was intact.

More rapid decline of glutamatergic synaptic transmission with electrical stimulation of Schaffer collaterals to CA1 in Gpt2-null hippocampus.

We reasoned that if overall glutamate levels in synaptic vesicles were reduced, the vesicular pool of glutamate would be depleted faster during a high frequency stimulus train of excitatory inputs to the CA1 pyramidal neurons. To test this, we stimulated the Schaffer collaterals (Figure 7A). The paired pulse facilitation remained the same in Gpt2 pyramidal neurons (Figure 7B, Wild-type: 1.41 ± 0.05 vs Gpt2-null: 1.51 ± 0.05) suggesting that the synaptic release probability is unchanged. The train response at 10 Hz yielded modest reductions in half-life of the fit curve in the Gpt2-null pyramidal neurons, as can be seen in the representative wild-type (black) and Gpt2-null (red) examples (the averaged peak amplitudes are normalized to the first peak amplitude) (Figure 7C, nonlinear regression with one-phase decay fit $F = 8.126$ (3,2594); Wild-type half-life 39.79 with 95% confidence interval of 31.07 to 55.31 vs Gpt2-null half-life 31.63 with 95% confidence interval of 25.45 to 41.78). The train response at 20 Hz for 10 seconds (200 pulses) resulted in greater reduction in half-life of the fit curve suggesting a more rapid depletion of glutamate levels in the Gpt2-null pyramidal neurons. (Figure 7D, nonlinear regression with one-phase decay fit $F = 95.48$ (3,5387); Wild-type half-life 45.34 with 95% confidence interval of 40.51 to 51.47 vs Gpt2-null half-life 31.70 with 95% confidence interval of 28.87 to 35.15). Overall, these data indicate that decreases in glutamatergic synaptic transmission in Gpt2-null hippocampus can be explained partly by decreases in vesicular glutamate levels in pre-synaptic neuron.

Released glutamate levels are reduced in Gpt2-null synaptosomes but rescued by alpha-ketoglutarate.

To determine whether vesicular glutamate levels were decreased, we detected glutamate release from synaptosomes upon depolarization by liquid chromatography/mass spectrometry (LC/MS). We initially confirmed the viability of our synaptosome preparations by observing increased levels of glutamate released after depolarization with 50 mM KCl in Krebs-like buffer compared to the release at baseline (Figure 8A). Overall glutamate levels in the cytosolic fraction of the Gpt2-null forebrain obtained during synaptosome preparation were significantly reduced as determined by enzymatic detection (Figure 8B), in agreement with the reduced glutamatergic transmission in Gpt2-null hippocampal slices (Figure 2). We then tested glutamate release and discovered that levels of glutamate released from Gpt2-null synaptosomes were reduced (Figure 8C). In contrast, released GABA levels were unchanged (Figure 8D) which agrees with the unchanged mIPSC amplitudes in CA1 hippocampal slices (Figure 2K).

Gpt2 catalyzes a reaction that results in a net production of a TCA intermediate (i.e. anaplerosis). TCA cycle intermediates, particularly, alpha-ketoglutarate have been shown to be precursors for synaptic glutamate (Peng et al., 1993; Peng et al., 1991; Shank et al., 1989; Shank and Bennett, 1993). We hypothesized that with the absence of the Gpt2 reaction, deficits of the TCA cycle may reduce the availability of synaptic glutamate. Therefore, we sought to rescue the decreases in synaptic glutamate levels by supplementing the synaptosomes with alpha-ketoglutarate.

When supplemented with alpha-ketoglutarate, released glutamate levels of Gpt2-null synaptosomes were restored to the wild-type levels (Figure 9A). However, alanine, another major product of the Gpt2 reaction, failed to correct the synaptic glutamate levels (Figure

9B). Alpha-ketoglutarate combined with alanine also corrected the glutamate levels in Gpt2-null synaptosomes (Figure 9C). In contrast, released GABA levels in Gpt2-null synaptosomes were unchanged with or without alpha-ketoglutarate or alanine supplementation (Figure 9D-F). We also demonstrated that alanine and alpha-ketoglutarate readily enter synaptosomes (Figure 9G-J). Notably, baseline alpha-ketoglutarate levels were unchanged but alanine levels were reduced in Gpt2-null synaptosomes (Figure 9G-J) in corroboration of our previous finding that alanine levels in the whole Gpt2-null brain were reduced (Ouyang et al., 2016). Overall, these results indicate that alpha-ketoglutarate was able to rescue glutamate levels and that a metabolic intervention was sufficient to correct glutamatergic deficiencies in Gpt2-null synaptosomes.

Glutamine metabolism is altered in Gpt2-null synaptosomes but rescued by alpha-ketoglutarate.

Glutamate is replenished in neurons primarily by glutamate-glutamine cycle at the tripartite synapse, formed by pre-synaptic neuron, post-synaptic neuron and astrocyte compartments (Ventura and Harris, 1999) (Figure 10A). We investigated changes in glutamine metabolism in Gpt2-null synaptosomes and discovered an increased fraction of double heavy nitrogen labeled glutamine, that is glutamine with a heavy nitrogen in both amine and amide groups (Figure 10B, left). This increase was reduced by supplementing the synaptosomes with alpha-ketoglutarate but not by alanine.

Glutamine levels at baseline without supplement are increased in Gpt2-null synaptosomes (Figure 10C). Glutamine entry into synaptosomes was not affected by alpha-ketoglutarate as evident in unchanged glutamine levels (Figure 10D) as well as in

unchanged fractional enrichments of single heavy nitrogen labeled glutamine (Figure 10E) and glutamate (Figure 10F) compared to the no supplement condition. This suggests that the action of alpha-ketoglutarate in decreasing the fractional enrichment of double-labeled glutamine was not caused by decreases in glutamine entry but by changes in glutamine metabolism.

In contrast, alanine decreased overall glutamine levels approximately by 50% in both wild-type and Gpt2-null synaptosomes (Figure 10D). While glutamine entry may be affected by alanine, as they compete for the same neutral amino acid transporters (Leke and Schousboe, 2016), this led to only modest decreases in the fractional enrichment of single heavy nitrogen labeled glutamine (Figure 10E) and glutamate (Figure 10F). This is also reflected by the observation that glutamate levels were unchanged with alanine supplementation (Figure 9B). Furthermore, alanine supplement did not result in any changes in fractional enrichment of double labeled glutamine in Gpt2-null synaptosomes (Figure 10B). Overall, these results suggest the reductions in double-labeled glutamine are feasible by alpha-ketoglutarate and not alanine.

Double-labeled glutamine can be formed by the concerted actions of glutamate dehydrogenase and glutamine synthetase (Figure 10A). We hypothesized that expression of these metabolic enzymes could be up-regulated in Gpt2-null synaptosomes and that this upregulation can explain the increases in fractional enrichment of double-labeled glutamine in Gpt2-null synaptosomes. We performed Western blotting in synaptosomes (Figure 11) for these metabolic enzymes and the synaptic proteins tested for earlier (Figure 3). We find increases of glutamate dehydrogenase and glutamine synthetase in Gpt2-null synaptosomes as well as increases in astrocytic glutamate transporter, Glt1, neuronal and

astrocytic neutral amino acid transporter (Snat1 and Asct1), vesicular glutamate (Vglut1) and GABA transporters. We also observed decreases in AMPA receptor (Gria1) and modest decreases in Psd95. These results suggest that increased levels of glutamate dehydrogenase and glutamine synthetase may lead to increases in double-labeled glutamine and that there is an up-regulation of proteins related to glutamate metabolism and transport in Gpt2-null synaptosomes.

TCA cycle has deficits but glutamine entry into the TCA cycle is intact in Gpt2-null synaptosomes.

Gpt2 and glutamate dehydrogenase not only modulate glutamate levels but also replenish the tricarboxylic acid (TCA) cycle by augmenting alpha-ketoglutarate (Erecinska and Silver, 1990b). Loss of Gpt2 leads to major deficits in the TCA cycle intermediates in the mouse brain and the process of replenishment of these intermediates, collectively called anaplerosis (Ouyang et al., 2016; Owen et al., 2002). We investigated whether the same TCA cycle deficits were present in Gpt2-null synaptosomes (Figure 12). We observed decreases in baseline levels of malate and fumarate but not succinate/methylmalonate (Figure 10A, left). In a separate experiment, we tested whether alpha-ketoglutarate along with glutamine would be able to rescue these deficits (Figure 10A, right). Malate levels were still decreased with glutamine but corrected by alpha-ketoglutarate in Gpt2-null synaptosomes. Fumarate levels remained the same as wild-type suggesting that glutamine alone had sufficient increases in overall fumarate levels. Succinate/methylmalonate levels remained the same as wild-type but augmented by alpha-ketoglutarate in Gpt2-null synaptosomes.

We also tested for glutamine as a precursor for the TCA cycle intermediates in Gpt2-null synaptosomes (Figure 10B). Given the loss of Gpt2, a decreased fractional enrichment of labeled TCA cycle intermediates using [U-¹³C]-glutamine as precursor was expected (Figure 6B, left). However, the fractional enrichments for all the TCA cycle intermediate measured were unchanged in Gpt2-null synaptosomes. This does not agree with the finding that glutamine cannot be used as a precursor to make alanine in Gpt2-null synaptosomes (Figure 1). This is also in stark contrast to decreased labeling of TCA cycle intermediates from ¹³C-glutamine in Gpt2-null fibroblasts as we reported previously (Ouyang et al., 2016). These results indicate that glutamine can be used by Gpt2-null synaptosomes to supplement the TCA cycle. We also tested for other metrics of energetics such as ATP levels, energy charge, as well as NAD to NADH and NADP to NADPH ratios. All remained unchanged in Gpt2-null synaptosomes albeit with a trending decrease in the energy charge. These results suggest that in the measures tested, the TCA cycle had deficits but was being supported by up-regulation of metabolic enzymes and of substrate transporters related to glutamate metabolism in isolated Gpt2-null synaptic terminals.

FIGURE 1

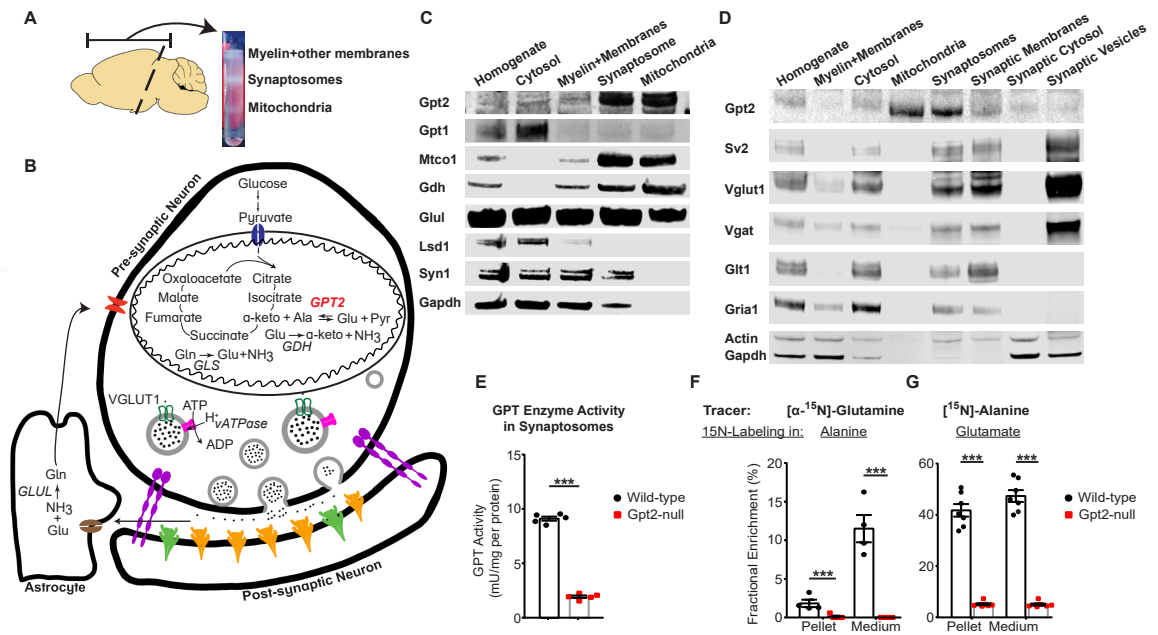


FIGURE 2

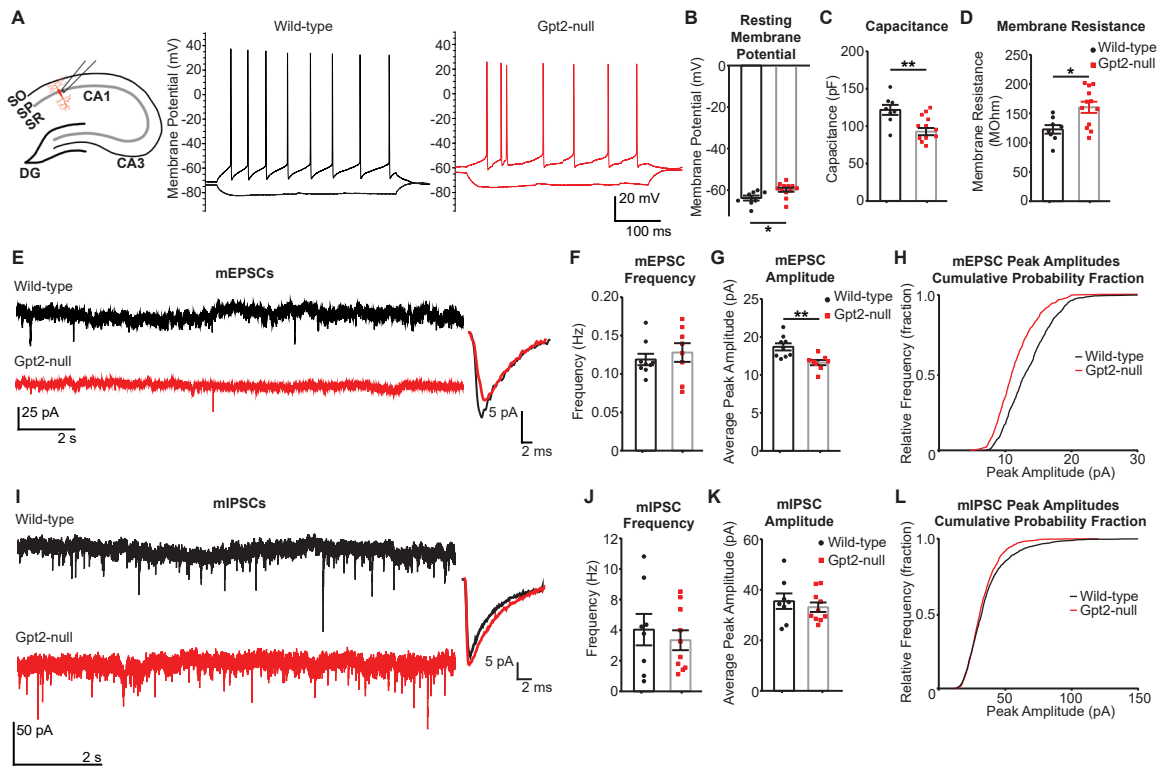


FIGURE 3

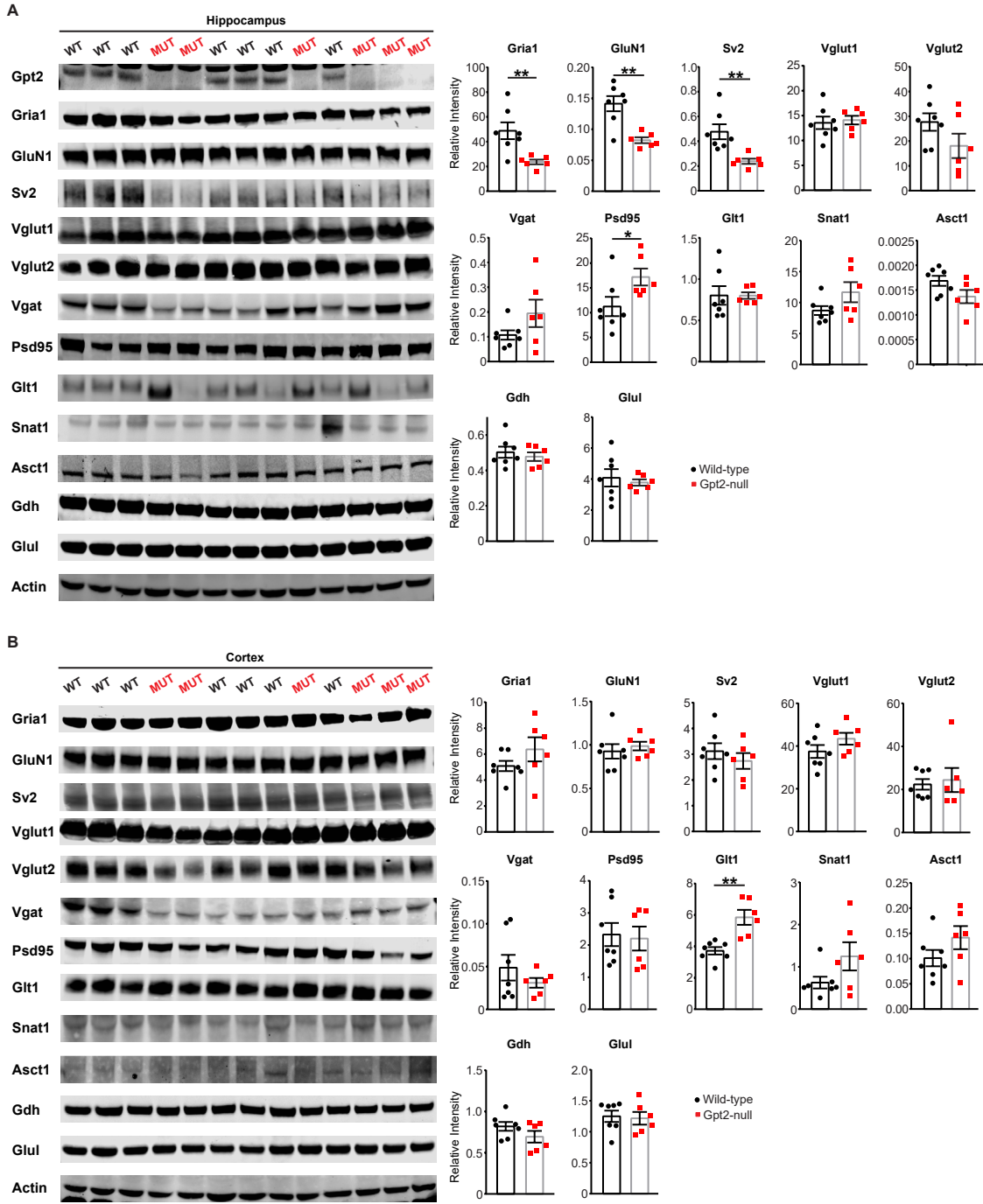


FIGURE 4

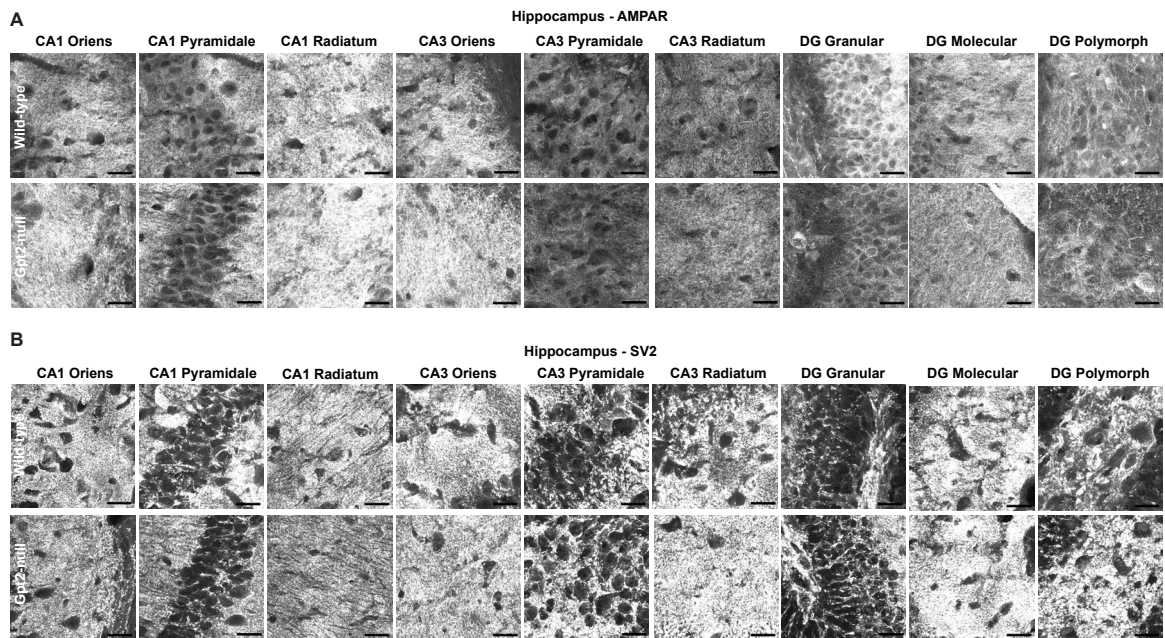
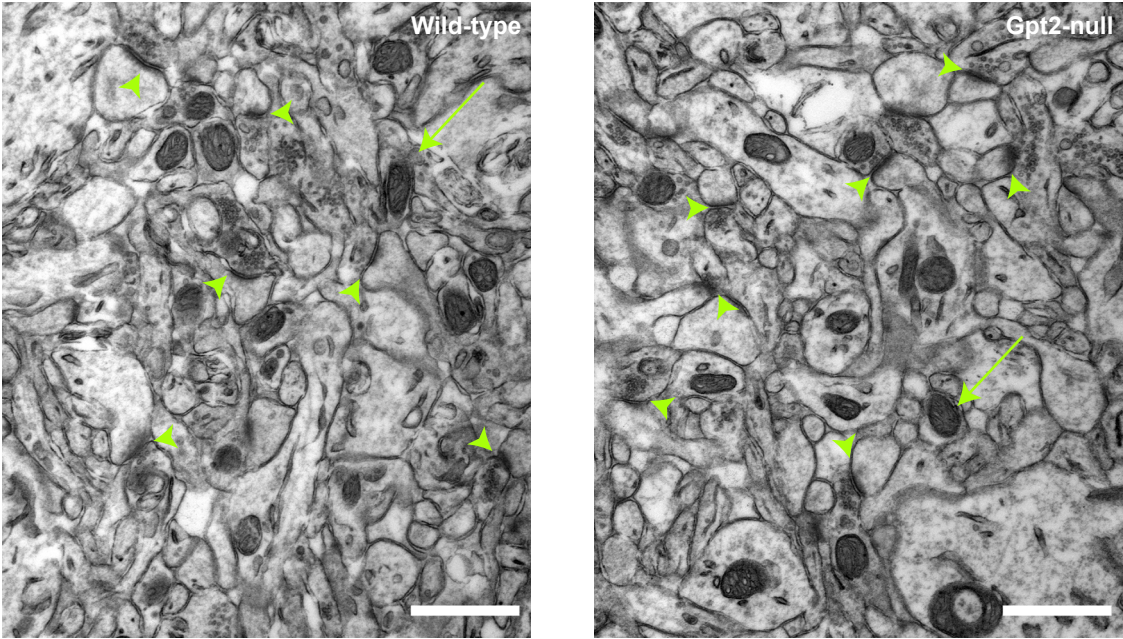
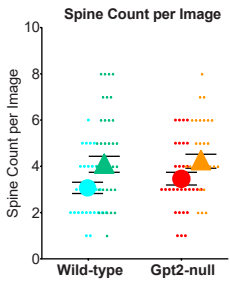


FIGURE 5

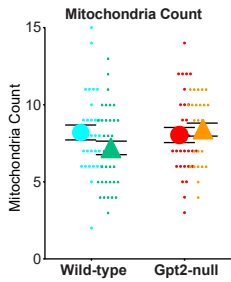
A



B



C



- Wild-type 1
- ▲ Wild-type 2
- Gpt2-null 1
- ▲ Gpt2-null 2

FIGURE 6

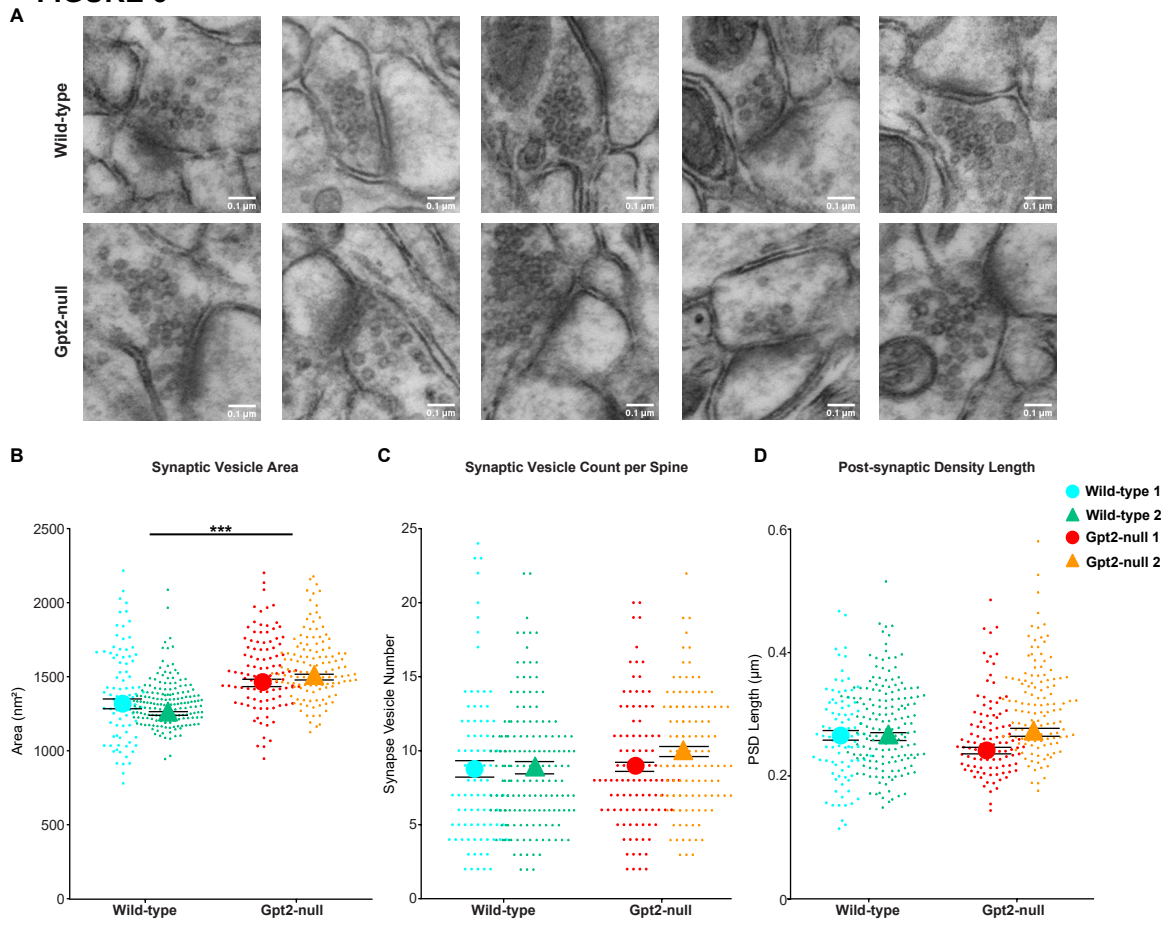


FIGURE 7

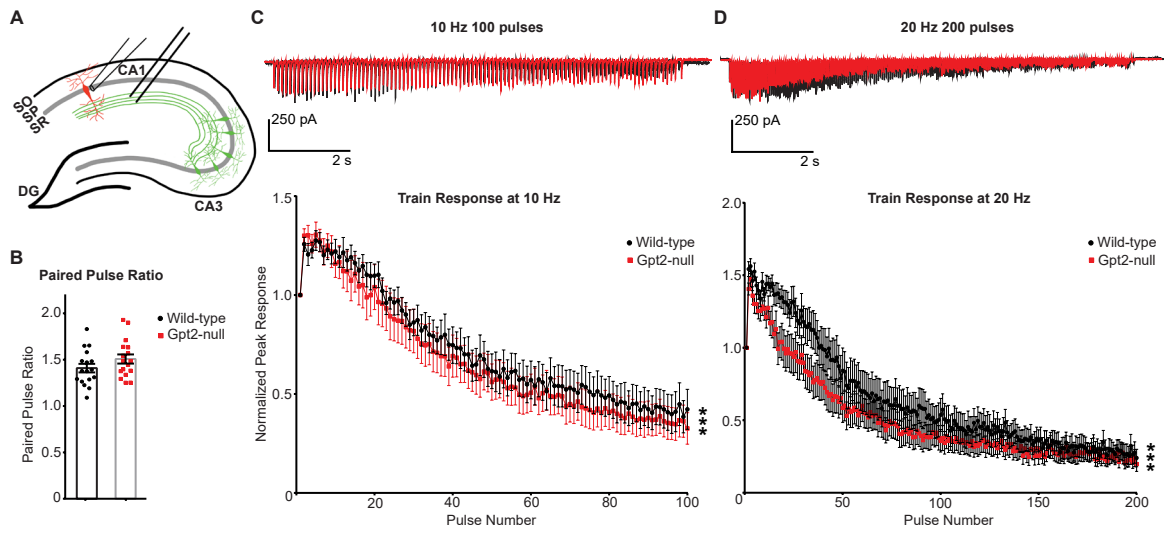


FIGURE 8

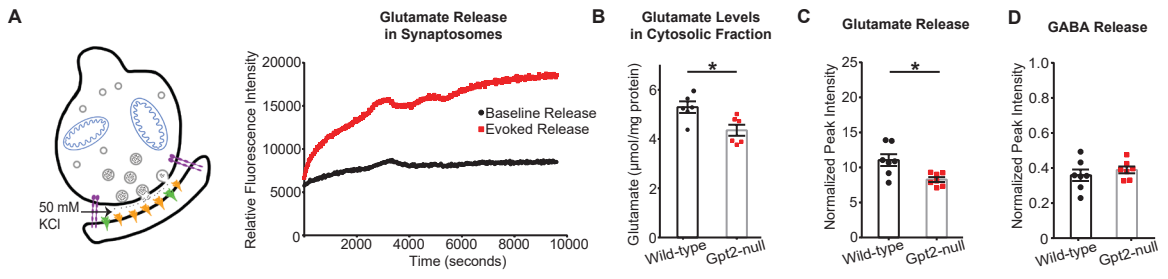


FIGURE 9

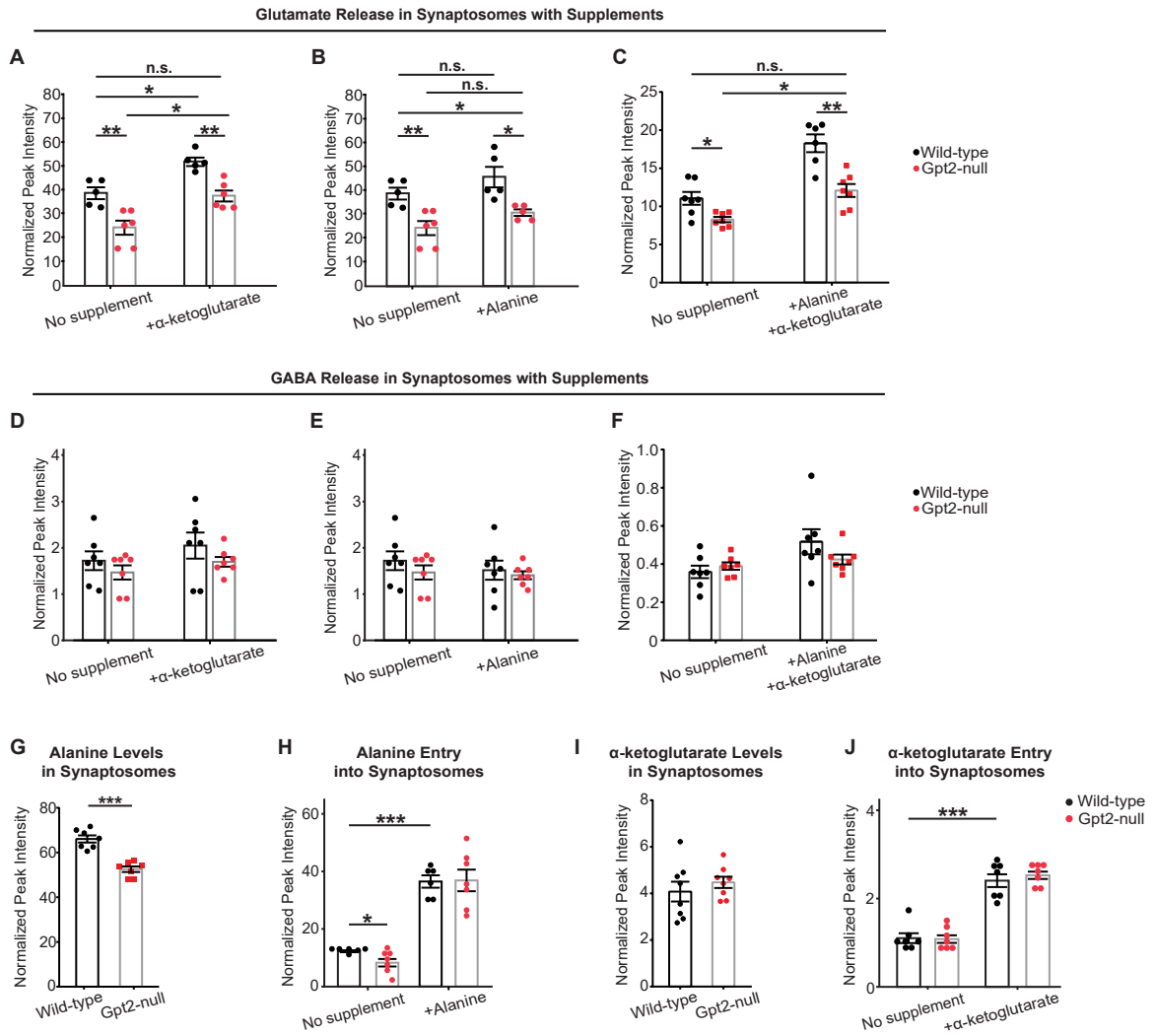


FIGURE 10

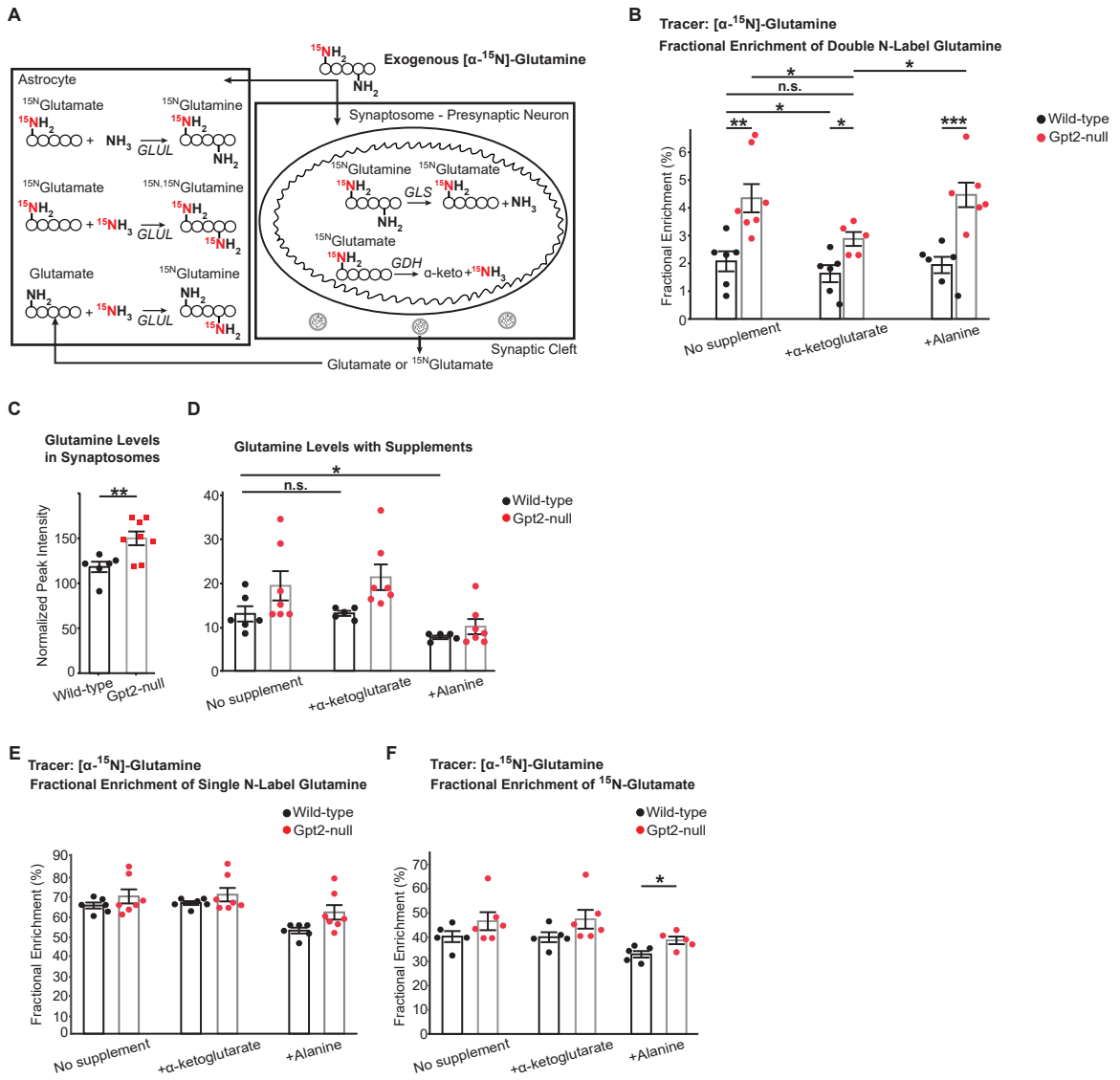


FIGURE 11

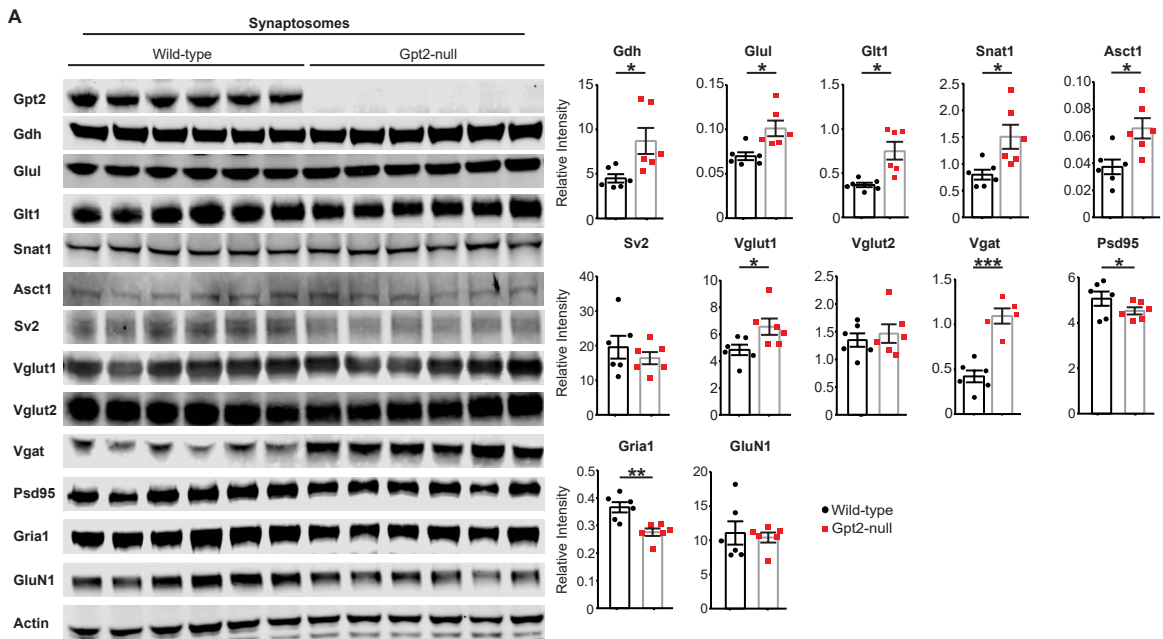


FIGURE 12

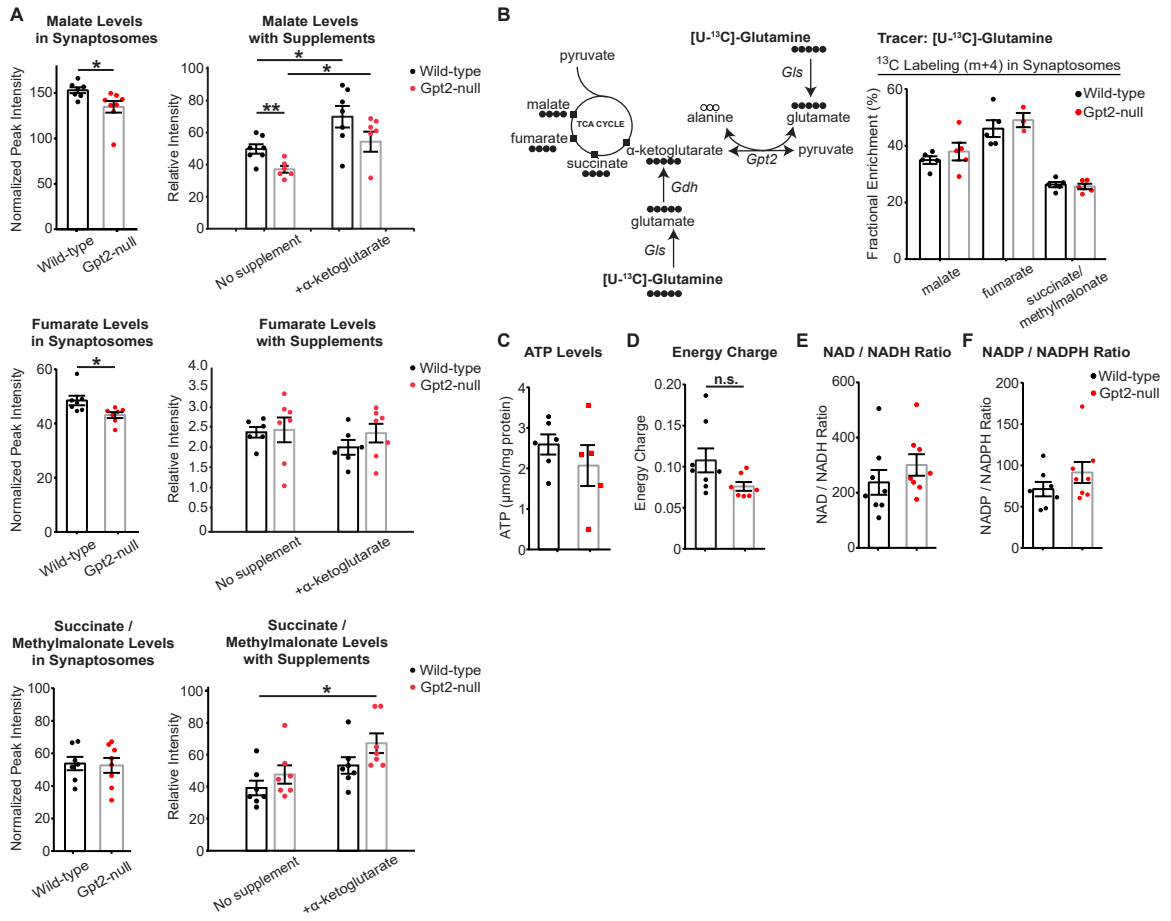


Figure Legends

Figure 1. Gpt2 is the primary glutamate pyruvate transaminase in synaptic terminals.

A. Fractionation of the mouse brain into fractions containing myelin and other membranes, synaptosomes (isolated nerve terminals) and mitochondria. Note that the synaptosomes are extracted from brain tissue containing only the forebrain, excluding olfactory bulb, midbrain and the brain stem.

B. Metabolic pathways relevant to Gpt2 and glutamate metabolism in synaptosomes including pre-synaptic neuron, post-synaptic neuron and astrocytic components. Ala: alanine, a-keto: alpha-ketoglutarate, Glu: glutamate, Gln: glutamine, Pyr: pyruvate, *GDH*: glutamate dehydrogenase, *GLS*: glutaminase, *GLUL*: glutamine synthetase.

C. Gpt2 is enriched in synaptosomes and mitochondria. Western blotting of the homogenate, cytosolic, myelin and membranes, synaptosomes and mitochondria fractions obtained from a wild-type mouse at postnatal day 18 (P18) for Gpt2, Gpt1, Mtc01 (mitochondrial marker, subunit 1 of complex IV cytochrome c oxidase), Gdh (glutamate dehydrogenase), Glul (glutamine synthetase), Lsd1 (nuclear marker, lysine-specific demethylase 1), Syn1 (synapsin I) and Gapdh (cytosolic marker, glyceraldehyde 3-phosphate dehydrogenase).

D. Gpt2 is enriched in mitochondria of synaptosomes. Western blotting of synaptosomes that were fractionated further into synaptic membrane, synaptic cytosol and synaptic vesicles obtained from a wild-type mouse at P18 for Gpt2, Sv2 (synaptic vesicle protein 2), Vglut1 (vesicular glutamate transporter 1), Vgat (vesicular GABA transporter), Glt1 (glutamate transporter 1, astrocytic), Gria1 (AMPA receptor subunit 1), Actin, Gapdh.

E. Overall Gpt enzyme activity in Gpt2-null is greatly reduced in Gpt2-null synaptosomes at P18. Each dot represents the total enzymatic activities of Gpt2 and Gpt1 in synaptosome

samples obtained from different wild-type (black) or Gpt2-null (red) mice. The enzymatic activities are expressed as mU/mg per protein. $P < 0.0001$.

F. Glutamine can not be used as a precursor for alanine in Gpt2-null synaptosomes at P18. Isotope tracing in wild-type (black) and Gpt2-null (red) synaptosomes at P18 using glutamine labeled with heavy nitrogen at the amine position. Each dot represents fractional enrichment of labeled pool of alanine in synaptosome from a different animal, expressed as percentage of total alanine pool. For pellet, $**P = 0.006$ and for medium, $***P = 0.00016$.

G. Alanine and alpha-ketoglutarate can be used as precursors for glutamate in wild-type but not in Gpt2-null synaptosomes at P18. Isotope tracing in wild-type (black) and Gpt2-null (red) synaptosomes at P18 using heavy nitrogen labeled alanine. Each dot represents fractional enrichment of labeled pool of glutamate in synaptosome from a different animal, expressed as percentage of total glutamate pool. For pellet and medium, $***P < 0.0001$.

Figure 2. Glutamatergic transmission is diminished in Gpt2-null CA1 hippocampus pyramidal neurons.

A. Schematic of the hippocampal slice preparation and a CA1 pyramidal neuron (red) and recording pipette. The representative whole-cell recordings of wild-type (left, black) and Gpt2-null (right, red) CA1 pyramidal neurons in current clamp mode at postnatal day 18 (P18). Current steps of 20 pA were used to depolarize or hyperpolarize the neuron.

B. Resting membrane potentials of Gpt2-null CA1 pyramidal neurons are slightly depolarized. The resting membrane potential of CA1 neurons from wild-type (black) and

Gpt2-null (red) mice at P18 was obtained immediately after breaking into the cell in current clamp mode. n = 4-5 mice/4-5 slices/8-12 cells. * $P = 0.019$.

C. Gpt2-null pyramidal neurons have lower capacitance. Each dot represents a different cell recording from wild-type (black) and Gpt2-null (red) mice at P18. ** $P = 0.002$.

D. Gpt2-null CA1 pyramidal neurons have greater membrane input resistance. Each dot represents a different cell recording from wild-type (black) and Gpt2-null (red) mice at P18. n = 4-5 mice/4-5 slices/8-12 cells. * $P = 0.01$.

E. Representative traces of miniature excitatory synaptic currents (mEPSC) from whole-cell recordings in CA1 pyramidal neurons of wild-type (top, black) and Gpt2-null (bottom, red) mice at P18. Averaged mEPSCs from one representative cell from wild-type (black) and Gpt2-null (red) cells at P18 are shown on the right.

F. mEPSC frequency is not changed in Gpt2-null CA1 pyramidal neurons. Each dot represents a different cell recording from wild-type (black) and Gpt2-null (red) mice at P18. n = 4-6 mice/4-6 slices/8-9 cells. $P = 0.52$.

G. mEPSC peak amplitude is reduced in Gpt2-null CA1 pyramidal neurons. Each dot represents a different cell recording from wild-type (black) and Gpt2-null (red) mice at P18. n = 4-5 mice/4-5 slices/8-12 cells. ** $P = 0.0035$.

H. Cumulative probability histogram of mEPSC peak amplitudes from representative wild-type (black) and Gpt2-null (red) CA1 pyramidal neurons at P18. Kolmogorov-Smirnov test was conducted, 4 neurons from each genotype were used to construct the curves; total mEPSC events, wild-type: 799 and Gpt2-null: 793. *** $P < 0.0001$; $d = 0.2386$.

I. Representative traces of miniature inhibitory synaptic currents (mIPSC) from whole-cell recordings in CA1 pyramidal neurons of wild-type (top, black) and Gpt2-null (bottom, red) mice at P18. Averaged mIPSCs from one representative cell from wild-type (black) and Gpt2-null (red) CA1 pyramidal neurons at P18 are shown on the right.

J. mIPSC frequency is not changed in Gpt2-null CA1 pyramidal neurons. Each dot represents a different cell recording from wild-type (black) and Gpt2-null (red) mice at P18. $n = 4-6$ mice/ $4-6$ slices/ $8-9$ cells. $P = 0.5614$.

K. mIPSC peak amplitude is not changed in Gpt2-null CA1 pyramidal neurons. Each dot represents a different cell recording from wild-type (black) and Gpt2-null (red) mice at P18. $n = 4-6$ mice/ $4-6$ slices/ $8-9$ cells. $P = 0.4999$

L. Cumulative probability histogram of mIPSC peak amplitudes from representative wild-type (black) and Gpt2-null (red) CA1 pyramidal neurons at P18. Kolmogorov-Smirnov test was conducted, 4 neurons from each genotype were used to construct the curves; total mEPSC events, wild-type: 800 and Gpt2-null: 800. $P = 0.1960$; $D = 0.0539$.

Figure 3. AMPAR, NMDAR and SV2 protein levels are reduced in Gpt2-null hippocampus.

A. Western blotting of wild-type and Gpt2-null hippocampus protein lysates collected at P18. Note that Gpt2 is absent in Gpt2-null (MUT) but present in wild-type (WT) protein lysates. Each dot represents a different protein lysate sample from wild-type (black) or Gpt2-null (red) mice. $**P$ (Gria1, AMPAR, AMPA receptor subunit 1) = 0.0068; $**P$ (GluN1, NMDA receptor, subunit 1) = 0.0014; $**P$ (Sv2, synaptic vesicle protein 2) = 0.0052; P (Vglut1, vesicular glutamate transporter 1) = 0.7385; P (Vglut2, vesicular

glutamate transporter 2) = 0.1329; P (Vgat, vesicular GABA transporter) = 0.1388; * P (Psd95, post-synaptic density protein 95) = 0.0454; P (Glt1, glutamate transporter 1, astrocytic) = 0.9902; P (Snat1, sodium-coupled neutral amino acid transporter 1) = 0.1065; P (Asct1, alanine/serine/cysteine transporter 1) = 0.0809; P (Gdh, glutamate dehydrogenase) = 0.5524; P (Glul, glutamine synthetase) = 0.646. Each protein band is normalized to its corresponding intensity of the actin band.

B. Western blotting of wild-type and Gpt2-null cortex protein lysates collected at P18.

Each dot represents a different protein lysate sample from wild-type (black) or Gpt2-null (red) mice. P (Gria1) = 0.2058; P (GluN1) = 0.5595; P (Sv2) = 0.4032; P (Vglut1) = 0.1789; P (Vglut2) = 0.7331; P (Vgat) = 0.3243; P (Psd95) = 0.8146; ** P (Glt1) = 0.0015; P (Snat1) = 0.0963; P (Asct1) = 0.1671; P (Gdh) = 0.1784; P (Glul) = 0.8154. Each protein band is normalized to its corresponding intensity of the actin band.

Figure 4. AMPAR and SV2 staining patterns appear unchanged in the Gpt2-null CA1 hippocampus.

A. Representative images of AMPA receptor (AMPA) staining in wild-type (top) and Gpt2-null (bottom) hippocampus at P18. Various regions of the CA1, CA3 and dentate gyrus (DG) are shown. Scale bar: 20 μ m.

B. Representative images of SV2 staining in wild-type (top) and Gpt2-null (bottom) hippocampus at P18. Various regions of the CA1, CA3 and dentate gyrus (DG) are shown. Scale bar: 20 μ m.

Figure 5. Spine and mitochondria counts are unchanged in electron micrographs of CA1 stratum radiatum of Gpt2-null hippocampus.

A. Representative electron micrographs of wild-type (left) and Gpt2-null (right) CA1 stratum radiatum of the hippocampus at P18. Green arrowheads point to the spines, arrows point to the mitochondria. Scale bar: 1 μm .

B. Quantification of spines per image (21000X magnification). More than 25 micrographs from each animal were analyzed. Spine count: P (1st pair: 0.2833, 2nd pair: 0.9177).

C. Quantification of mitochondria per image (21000X magnification). More than 25 micrographs from each animal were analyzed. Mitochondria count: P (1st pair: 0.8094, 2nd pair: 0.0629).

Figure 6. Number of synaptic vesicles per spine remains unchanged and synaptic vesicle area is increased in Gpt2-null CA1 stratum radiatum.

A. Representative images of spines in wild-type (top) and Gpt2-null (bottom) CA1 stratum radiatum at P18. Scale bar: 0.1 μm .

B. Quantification of the area of synaptic vesicles. Each dot represents the area of synaptic vesicles averaged for each spine. P (1st pair: 0.0006, 2nd pair: <0.0001).

C. Quantification of the number of synaptic vesicles per spine. P (1st pair: 0.9051, 2nd pair: 0.0257).

D. Quantification of the post-synaptic density length. Each dot represents a spine. P (1st pair: 0.8426, 2nd pair: 0.0004).

*** denotes statistical significance in differences between both animal pairs.

Figure 7. More rapid decline of glutamatergic synaptic transmission with electrical stimulation of Schaffer collaterals to CA1 in Gpt2-null hippocampus.

A. Schematic of the hippocampal slice, a CA1 pyramidal neuron (red) and recording pipette, CA3 pyramidal neurons and Schaffer collaterals are shown in green. The stimulating electrode was placed approximately 200 microns away from each recorded CA1 pyramidal neuron.

B. Paired pulse ratios were unchanged as recorded in Gpt2-null CA1 pyramidal neurons at P18. Each dot represents a different cell recording from wild-type (black) and Gpt2-null (red) mice at P18. $n = 7-9$ mice/17 slices/17 cells. $P = 0.157$

C. A modest reduction in half-life of the fitted curve in the Gpt2-null pyramidal neurons during a 10 Hz stimulus train. Representative wild-type (black) and Gpt2-null (red) traces are shown on the top. The averaged peak amplitudes normalized to the first peak amplitude plotted by pulse number are shown on the bottom. Nonlinear regression with one-phase decay fit was performed; $F = 8.126$ (3,2594); wild-type half-life = 39.79 with 95% confidence interval of 31.07 to 55.31 vs Gpt2-null half-life = 31.63 with 95% confidence interval of 25.45 to 41.78. $n = 7-9$ mice/11-15 slices/11-15 cells. *** $P < 0.0001$.

D. A greater reduction is seen in the half-life of the fitted curve in the Gpt2-null pyramidal neurons during a 20 Hz stimulus train. Representative wild-type (black) and Gpt2-null (red) traces are shown on the top. The averaged peak amplitudes normalized to the first peak amplitude plotted by pulse number are shown on the bottom. Nonlinear regression with one-phase decay fit was performed; $F=95.48$ (3,5387); Wild-type half-life

45.34 with 95% confidence interval of 40.51 to 51.47 vs Gpt2-null half-life 31.70 with 95% confidence interval of 28.87 to 35.15. $n = 7-9$ mice/13-14 slices/13-14 cells. *** $P < 0.0001$.

Figure 8. Glutamate amount released upon depolarization is reduced in Gpt2-null synaptosomes.

A. Schematic of the synaptosomes and evoking glutamate release from synaptic vesicles with 50 mM KCl. Viability of synaptosomes was confirmed by adding 50 mM KCl to synaptosomes and comparing baseline (black) and evoked (red) glutamate levels in wild-type synaptosomes obtained at postnatal day 18 (P18).

B. Overall glutamate levels in the cytosolic fraction are reduced in Gpt2-null mice. Cytosol fraction of the forebrain was obtained by separating the supernatant from the crude synaptosomal pellet. Glutamate was detected by enzymatic method and expressed as $\mu\text{mol per mg}$ of protein. Each dot represents a different synaptosome sample obtained from wild-type (black) or Gpt2-null (red) mice at P18. * $P = 0.0161$.

C. Glutamate levels released upon depolarization are reduced in Gpt2-null synaptosomes. Each dot represents a different synaptosome sample obtained from wild-type (black) or Gpt2-null (red) mice at P18. * $P = 0.0106$.

D. Released GABA levels were unchanged in Gpt2-null synaptosomes. Each dot represents a different synaptosome sample obtained from wild-type (black) or Gpt2-null (red) mice at P18. $P = 0.4385$.

Figure 9. Decreases in released glutamate are restored by alpha-ketoglutarate in Gpt2-null synaptosomes.

A. Glutamate levels are restored by alpha-ketoglutarate in Gpt2-null synaptosomes. Each dot represents a different synaptosome sample obtained from wild-type (black) or Gpt2-null (red) mice at P18. Wild-type vs. Gpt2-null no supplement: $**P = 0.00533$; +alpha-ketoglutarate: $**P = 0.001$. Wild-type no supplement vs. Gpt2-null +alpha-ketoglutarate: $P = 0.7272$. Wild-type no supplement vs. wild-type +alpha-ketoglutarate: $P = 0.002$. Wild-type vs. Gpt2-null +alpha-ketoglutarate: $P = 0.001$. n.s. = statistically non-significant.

B. Glutamate levels are not restored by alanine in Gpt2-null synaptosomes. Each dot represents a different synaptosome sample obtained from wild-type (black) or Gpt2-null (red) mice at P18. Wild-type vs. Gpt2-null no supplement: $**P = 0.00533$; +alanine: $*P = 0.0109$. Wild-type no supplement vs. Gpt2-null +alanine: $*P = 0.0212$. Wild-type no supplement vs. alanine: $P = 0.211$. Gpt2-null no supplement vs. alanine: $P = 0.104$. n.s. = statistically non-significant.

C. Glutamate levels are restored by alanine and alpha-ketoglutarate combined supplementation in Gpt2-null synaptosomes. Each dot represents a different synaptosome sample obtained from wild-type (black) or Gpt2-null (red) mice at P18. Wild-type vs. Gpt2-null no supplement: $*P = 0.0106$. Wild-type vs. Gpt2-null +alanine +alpha-ketoglutarate: $**P = 0.0011$. Wildtype no supplement vs. Gpt2-null +alanine +alpha-ketoglutarate: $P = 0.4109$. Wild-type no supplement vs. +alanine+alpha-ketoglutarate: $***P = 0.0003$. Gpt2-null no supplement vs. +alanine+alpha-ketoglutarate: $P = 0.001$. n.s. = statistically non-significant.

D. Released GABA levels were unchanged with or without alpha-ketoglutarate in Gpt2-null synaptosomes. Each dot represents a different synaptosome sample obtained from wild-type (black) or Gpt2-null (red) mice at P18. Wild-type vs. Gpt2-null no supplement: $P = 0.4385$. Wild-type vs. Gpt2-null +alpha-ketoglutarate: $P = 0.2652$.

E. Released GABA levels with or without alanine. Each dot represents a different synaptosome sample obtained from wild-type (black) or Gpt2-null (red) mice at P18. Wild-type vs. Gpt2-null no supplement: $P = 0.4385$. Wild-type vs. Gpt2-null +alanine +alpha-ketoglutarate $P = 0.634$.

F. Released GABA levels with or without alanine and alpha-ketoglutarate combined supplementation. Each dot represents a different synaptosome sample obtained from wild-type (black) or Gpt2-null (red) mice at P18. Wild-type vs. Gpt2-null no supplement: 0.3395 . Wild-type vs. Gpt2-null +alanine +alpha-ketoglutarate $P = 0.2119$.

G. Alanine levels are reduced in Gpt2-null synaptosomes. Each dot represents a different synaptosome sample obtained from wild-type (black) or Gpt2-null (red) mice at P18. *** $P < 0.0001$.

H. Alanine can readily enter the synaptosomes. Each dot represents a different synaptosome sample obtained from wild-type (black) or Gpt2-null (red) mice at P18. No supplement: wild-type vs. Gpt2-null * $P = 0.019$. Wild-type no supplement vs. wild-type +alanine: *** $P < 0.0001$. +alanine: wild-type vs. Gpt2-null $P = 0.9356$.

I. Alpha-ketoglutarate levels are not changed in Gpt2-null synaptosomes. Each dot represents a different synaptosome sample obtained from wild-type (black) or Gpt2-null (red) mice at P18. $P = 0.4291$.

J. Alpha-ketoglutarate can readily enter the synaptosomes. Each dot represents a different synaptosome sample obtained from wild-type (black) or Gpt2-null (red) mice at P18.

Wild-type no supplement vs. wild-type +alpha-ketoglutarate: *** $P < 0.0001$.

Figure 10. Glutamine metabolism is altered in Gpt2-null synaptosomes and rescued by alpha-ketoglutarate.

A. Metabolic pathways relevant to glutamate/glutamine metabolism and isotope labeling patterns originating from exogenous amine nitrogen labeled glutamine in synaptosomes.

GLS: glutaminase, *GDH*: glutamate dehydrogenase. *GLUL*: glutamine synthetase.

B. Fractional enrichment of double-labeled glutamine is increased in Gpt2-null synaptosomes and restored by alpha-ketoglutarate. Each dot represents a different synaptosome sample obtained from wild-type (black) or Gpt2-null (red) mice at P18.

Wild-type vs. Gpt2-null no supplement: $P = **0.0047$; +alpha-ketoglutarate: $*P = 0.0135$; +alanine: *** $P = 0.0008$. Gpt2-null no supplement vs. Gpt2-null +alpha-ketoglutarate: $*P = 0.0457$. Gpt2-null +alanine vs. Gpt2-null +alpha-ketoglutarate: $*P = 0.0162$. Wild-type no supplement vs. Gpt2-null +alpha-ketoglutarate: $P = 0.1135$. Wild-type no supplement vs. alpha-ketoglutarate: $*P$ (paired Student's t-test) = 0.0007.

C. Baseline glutamine levels are increased in Gpt2-null synaptosomes. Each dot represents synaptosome samples obtained from different wild-type (black) or Gpt2-null (red) mice at P18. Wild-type vs. Gpt2-null *** $P = 0.0088$.

D. Entry of glutamine is unaffected by alpha-ketoglutarate. Each dot represents synaptosome samples obtained from different wild-type (black) or Gpt2-null (red) mice

at P18. Wild-type no supplement vs. +alanine: $*P = 0.0232$; Wild-type no supplement vs. +alpha-ketoglutarate: $P = 0.953$.

E. Exogenous amine labeled glutamine labels the majority of glutamine pool in synaptosome. Each dot represents synaptosome samples obtained from different wild-type (black) or Gpt2-null (red) mice at P18. Wild-type vs. Gpt2-null no supplement: $P = 0.287$; +alanine: $P = 0.0513$; +alpha-ketoglutarate: $P = 0.2885$.

F. Fractional enrichment of labeled glutamate with the amine heavy nitrogen labeled glutamine precursor. Each dot represents synaptosome samples obtained from different wild-type (black) or Gpt2-null (red) mice at P18. Wild-type vs. Gpt2-null no supplement: $P = 0.2$; +alanine: $*P = 0.023$; +alpha-ketoglutarate: $P = 0.147$.

Figure 11. Upregulation of proteins related to glutamate metabolism and transport in Gpt2-null synaptosomes.

A. Western blotting of wild-type and Gpt2-null synaptosome protein lysates collected at P18. Note that Gpt2 is absent in Gpt2-null (MUT) but present in wild-type (WT) protein lysates. Each dot represents a different protein lysate sample from wild-type (black) or Gpt2-null (red) mice. Wild-type vs. Gpt2-null: $*P$ (Gdh, glutamate dehydrogenase) = 0.0211; $*P$ (Glul, glutamine synthetase) = 0.01; $*P$ (Glt1, glutamate transporter 1, astrocytic) = 0.0305; $*P$ (Snat1, sodium-coupled neutral amino acid transporter 1) = 0.0155; $*P$ (Asct1, alanine/serine/cysteine transporter 1) = 0.0177; P (Sv2, synaptic vesicle protein 2) = 0.4176; $*P$ (Vglut1, vesicular glutamate transporter 1) = 0.0378; P (Vglut2, vesicular glutamate transporter 2) = 0.5829; $***P$ (Vgat, vesicular GABA transporter) = 0.0001; $*P$ (Psd95, post-synaptic density protein 95) = 0.0343; $**P$ (Gria1,

AMPA receptor subunit 1) = 0.0028; P (GluN1, NMDA receptor, subunit 1) = 0.7273.

Each protein band is normalized to its corresponding intensity of the actin band.

Figure 12. The TCA cycle has deficits but glutamine entry into the TCA cycle is intact in Gpt2-null synaptosomes.

A. Baseline malate and fumarate levels are reduced in Gpt2-null synaptosomes. Each dot represents a different sample from wild-type (black) or Gpt2-null (red) mice at P18.

Baseline wild-type vs. Gpt2-null malate: $*P = 0.0298$; fumarate: $*P = 0.0298$; succinate:

$P = 0.8557$. Malate wild-type vs. Gpt2-null no supplement: $**P = 0.006$; +alpha-

ketoglutarate: $P = 0.116$. Malate wild-type no supplement vs. +alpha-ketoglutarate: $*P =$

0.0178 . Malate Gpt2-null no supplement vs. +alpha-ketoglutarate: $P = 0.033$. Fumarate

wild-type vs. Gpt2-null no supplement: $P = 0.868$; +alpha-ketoglutarate: $P = 0.269$.

Succinate/methylmalonate wild-type vs. Gpt2-null no supplement: $P = 0.273$; +alpha-

ketoglutarate: $P = 0.109$. Succinate/methylmalonate Gpt2-null no supplement vs +alpha-

ketoglutarate: $*P = 0.038$.

B. Fractional enrichments of carbon labeled TCA cycle intermediates with the uniformly carbon labeled [U- ^{13}C]-Glutamine precursor is unchanged in Gpt2-null synaptosomes.

Each dot represents synaptosome samples obtained from different wild-type (black) or

Gpt2-null (red) mice at P18. Wild-type vs. Gpt2-null malate: $P = 0.402$;

succinate/methylmalonate: $P = 0.634$; fumarate: $P = 0.513$.

C. ATP levels are unchanged in Gpt2-null synaptosomes. Each dot represents

synaptosome samples obtained from different wild-type (black) or Gpt2-null (red) mice

at P18. ATP levels were enzymatically determined. Wild-type vs. Gpt2-null: $P = 0.3533$.

D. Energy charge is unchanged in Gpt2-null synaptosomes. Each dot represents synaptosome samples obtained from different wild-type (black) or Gpt2-null (red) mice at P18. Energy charge is calculated as: $[(ATP+0.5*ADP) / (ATP + ADP + AMP)]$. Wild-type vs. Gpt2-null: $P = 0.0761$.

E. NAD to NADH ratio is unchanged in Gpt2-null synaptosomes. Each dot represents synaptosome samples obtained from different wild-type (black) or Gpt2-null (red) mice at P18. Wild-type vs. Gpt2-null: $P = 0.3071$.

F. NADP to NADPH ratio is unchanged in Gpt2-null synaptosomes. Each dot represents synaptosome samples obtained from different wild-type (black) or Gpt2-null (red) mice at P18. Wild-type vs. Gpt2-null: $P = 0.2254$.

Discussion

Glutamate metabolism is maintained and tightly regulated by a multitude of metabolic enzymes and substrate transporters (Anderson and Swanson, 2000; Erecinska and Silver, 1990b; Haslam and Krebs, 1963; Schousboe et al., 1993; Yudkoff et al., 1993). An imbalance of substrates or proteins involved in glutamate metabolism often leads to a compensatory mechanism that takes advantage of alternative metabolic pathways (Alkan et al., 2018; Chen et al., 2018; Hohnholt et al., 2018; Motori et al., 2020; Yang et al., 2014). This flexibility of the metabolome related to glutamate is realized by 44 distinct enzymes that consume or produce glutamate, as curated in Kyoto Encyclopedia of Genes and Genomes (KEGG) (Kanehisa et al., 2020). Here, we report that loss of glutamate pyruvate transaminase 2 (Gpt2) causes reprogramming of glutamate metabolism which channels the use of glutamate to sustain the tricarboxylic acid (TCA) cycle in synaptic terminals.

The enzymes that produce or consume glutamate are many, but glutaminase and aspartate aminotransferase have been the focus of vast literature on glutamate synthesis (Erecinska and Silver, 1990a; Kovacevic, 1971; Masson et al., 2006; McKenna and Ferreira, 2016). Gpt2 has seen very little attention in the nervous system, particularly within the context of glutamate metabolism. This is most likely due to the observations that enzymatic activity of aspartate aminotransferase (also known as glutamate oxaloacetate transaminase, Got) has been found to be up to 100-fold greater than that of glutamate pyruvate transaminase in brain homogenates (Benuck et al., 1971; Salganicoff and Derobertis, 1965; Wilbur and Patel, 1974). Glutaminase and glutamate dehydrogenase have been shown to have higher enzymatic rates as well. Therefore, it is

unlikely that glutamate production is driven considerably by Gpt2. However, biochemical studies of enzyme activity rates have usually included both cytosolic and mitochondrial isoforms of glutamate pyruvate transaminase. Our study is the first to determine the effects of genetic ablation of Gpt2 on glutamate metabolism. Our results confirm the expectation that glutamate pyruvate transaminase does not produce or regulate glutamate to a great extent, evident in modest changes in our slice electrophysiology and synaptosome studies. However, as others have reported (Erecinska et al., 1994; Peng et al., 1993; Peng et al., 1991; Yudkoff et al., 1990), our studies also show that sufficient quantities of alanine and alpha-ketoglutarate can be used to make glutamate via transamination. Precedence of enzymes such as glutaminase, aspartate aminotransferase or glutamine synthetase in the regulation of glutamate metabolism is also reflected in the observation that genetic ablation of these enzymes lead to embryonic lethality in mice (Dickinson et al., 2016; He et al., 2007; Masson et al., 2006) whereas the loss of Gpt2 causes premature death, but only around weaning age (P21) (Ouyang et al., 2016).

Gpt2 is an equilibrium enzyme, that is it will try to balance the concentrations of both sides of the reaction (Krebs, 1953). Given K_m values and relative concentrations of its substrates in neurons, Gpt2 has been predicted to work in the direction of alanine and alpha-ketoglutarate formation *in vivo* (Bak et al., 2006; Erecinska et al., 1994; Lenartowicz and Wojtczak, 1988; Miller et al., 1973; Waagepetersen et al., 2000). Therefore, it might be initially expected that glutamate levels would be increased in Gpt2-null brain tissue; however, we observe decreases both electrophysiologically and biochemically. If we think along the lines of functional implications of the Gpt2 reaction in physiological conditions, that is production of alanine and alpha-ketoglutarate,

reduction of glutamate levels may not be as surprising. Glutamate, the major excitatory neurotransmitter, is an excellent source of carbon for the TCA cycle (therefore energy) in mitochondria (Hertz et al., 2007; Kovacevic, 1971; McKenna, 2007; Westergaard et al., 1995). Gpt2 contributes to glutamate oxidation in mitochondria and loss of Gpt2 may lead to upregulation of other metabolic enzymes that allow for glutamate oxidation into the TCA cycle, a crucial part of anaplerotic processes (replenishment of the TCA cycle). We find increases of glutamate dehydrogenase levels in Gpt2-null synaptic terminals that may be carrying out this task, along with increases in glutamine synthetase that allows for efficient ammonia fixation. Glutamate dehydrogenase catalyzes practically an irreversible reaction that favors glutamate deamination, and thus once glutamate is consumed by this enzyme, it is fixed to its keto acid, alpha-ketoglutarate (Hohnholt et al., 2018; McKenna et al., 2000; Westergaard et al., 1996) and may provide an explanation as to why glutamate levels tend to decrease in Gpt2-null brain tissue.

We find deficits in the TCA cycle of synaptosomes, such as decreases in malate and fumarate levels, but glutamine can still be efficiently used as a precursor to the TCA cycle intermediates. There are anaplerotic pathways, other than glutamate dehydrogenase and Gpt2, that may support the TCA cycle in the absence of Gpt2 such as pyruvate carboxylase and other aminotransferases that yield alpha-ketoglutarate from glutamate including branched-chain amino acid aminotransferases (Hutson, 2001; Morken et al., 2014). All these processes likely contribute to sustain the TCA cycle in Gpt2-null brain as long as they are able; however, each have certain complications. For example, pyruvate carboxylase exists mainly in astrocytes and utilizes ATP to make oxaloacetate (Hertz et al., 2007; Yu et al., 1983). Glutamate dehydrogenase is found both in neurons

and astrocytes but depends on NADP availability (Aoki et al., 1987). Aminotransferases that degrade essential amino acids usually work in the direction of producing glutamate and not alpha-ketoglutarate (Conway and Hutson, 2016). In contrast, Gpt2 depends neither on ATP nor NADP availability, thereby conferring a unique anaplerotic ability to the cell. Levels of Gpt2 and Gpt1 protein have been shown to increase in models of oxidative phosphorylation deficits induced by mitochondrial DNA mutations (Chen et al., 2018) and disrupted mitochondrial fusion dynamics (Motori et al., 2020). Gpt2's unique support of the TCA cycle may enhance both biosynthesis and energetics to sustain cell growth and this is also evident in smaller soma sizes and slightly depolarized CA1 pyramidal neurons (Figure 2) as well as microcephaly seen in both mice and human patients with Gpt2 mutations (Ouyang et al., 2016).

Alpha-ketoglutarate rescues glutamate levels and augments the TCA cycle intermediates. It is yet unclear whether alpha-ketoglutarate exerts its effects through other transaminases or by blocking glutamate dehydrogenase, or both. Nevertheless, by a metabolic intervention, i.e. alpha-ketoglutarate supplementation, it was possible to correct both glutamate levels and alterations in the glutamine metabolism in Gpt2-null synaptic terminals. This puts emphasis on the changes in the metabolome on top of the changes we observed in electrophysiological properties of Gpt2-null CA1 pyramidal neurons (decreased membrane potential, decreased capacitance, increase membrane resistance) or levels of synaptic proteins.

Alanine on the other hand had minimal effect on glutamate levels and glutamine metabolism. It is possible that there was a modest effect of alanine supplementation on glutamate levels in synaptosomes with a modest significance p-value (0.109). This is

possible through the residual Gpt1 in synaptosomes, however alanine failed to increase glutamate levels above wild-type levels and it failed to correct double-labeled glutamine unlike alpha-ketoglutarate. Reduction in fraction of double-labeled glutamine most likely occurs through inhibition of glutamate dehydrogenase by alpha-ketoglutarate as previously demonstrated as substrate inhibition (Engel and Chen, 1975).

Released GABA levels do not change in Gpt2-null synaptosomes and are not elevated by alpha-ketoglutarate. Glutamine has been shown to be a much better precursor than alpha-ketoglutarate which preferentially is converted into glutamate (Peng et al., 1993; Shank and Campbell, 1982, 1984). Our synaptosomes preparations contain not only glutamatergic but GABAergic nerve terminals and presence of glutamate decarboxylase which irreversibly converts glutamate into GABA (Roberts and Eidelberg, 1960) and possibly account for the unchanged GABA levels in Gpt2-null synaptosomes.

Synaptosomes, isolated nerve terminals, are artificial organelles that normally do not exist *in vivo* and, in most preparations, may reflect both neuronal metabolism and astrocytic metabolism (Dunkley et al., 2008). Tripartite synapses (presynaptic terminals, postsynaptic spines and associated astrocyte components) exist only in approximately 50% of all spines in the stratum radiatum of the CA1 hippocampus (Ventura and Harris, 1999). It is yet unclear whether Gpt2 would have more profound effects on glutamatergic synapses that do not rely on astrocytic processes. Given our data, Gpt2 may provide additional contributions to the TCA cycle at non-tripartite synapses *in vivo*.

Gpt2 belongs to the protein family of pyridoxal phosphate (PLP)-dependent aspartate aminotransferase superfamily (Yang et al., 2002). Aspartate aminotransferase 2 has been found to localize in both mitochondria and synaptic vesicles (Takeda and Ueda,

2017). Localization to synaptic vesicles has been proposed as a mechanism to locally synthesize glutamate to be loaded to synaptic vesicles (Takeda et al., 2012). Gpt2 however does not appear in synaptic vesicles and thus modulates glutamate levels from within mitochondria.

Electrophysiological and biochemical interpretations of glutamate levels may have been impacted by decreases in AMPA receptor subunit (Gria1) and SV2 in the hippocampus and increases in astrocytic glutamate transporter (Glt1) in synaptic terminals. While none of our experiments can conclude that the glutamate pool is decreased specifically in neurons, there is a reduction in overall glutamate levels (Figure 4). Gpt2 in mice is expressed in both neurons and astrocytes (Zhang et al., 2016). Further experiments are needed to identify changes in glutamate levels and enzymes in different cell types.

All processes related to glutamate metabolism have major differences across species. Most notably, Gpt1 seems to be absent in the human brain and Gpt2 is the sole alanine aminotransferase detected (Hodge et al., 2019; Kang et al., 2011). Another notable example is glutamate dehydrogenase; the *GDH* gene has seen a recent duplication event in humans and non-human primates, that is absent in rodents (Li et al., 2016). Therefore, caution must be taken when extrapolating interpretations of metabolic changes across species.

In conclusion, here we report the contributions of Gpt2 to glutamate metabolism and the functional consequences of Gpt2 loss. Gpt2 can be used to make vesicular glutamate if alanine and alpha-ketoglutarate are sufficiently supplied. Gpt2 loss results in changes in both synaptic protein composition and metabolism which can partly be

alleviated by alpha-ketoglutarate. Compensatory mechanisms including upregulation of metabolic enzymes and transporters may act in lieu of Gpt2 to sustain energetics and neurotransmitter availability. In sum, we find that Gpt2 is a metabolic enzyme enriched in synaptic terminals linking glutamate metabolism to alanine and TCA cycle metabolism that maintains proper functioning of the glutamatergic synaptic transmission.

Materials and Methods

Ethics Statement

All experiments that involved mice were done in accordance with the National Institutes of Health *Guide for the Care and Use of Laboratory Animals* (Council, 2011) and approved by the Brown University Institutional Animal Care and Use Committee.

Animals

Gpt2-null animals were obtained from Knockout Mouse Project at University of California, Davis (RRID: MMRRC_047980-UCD), genotyped and maintained as described previously (Ouyang et al., 2016). The background of all mice was C57B6/J (Jackson Laboratory Strain No. 664, RRID: IMSR_JAX:000664). The mice were maintained under a 12-hour light/dark cycle (lights on at 7 am and off at 7 pm). The mice had ad libitum access to feed and water. All experiments were conducted on mice at postnatal day 18 (P18).

Synaptosome Preparation

The protocol was adapted from (Sims and Anderson, 2008) and (Dunkley et al., 2008). Immediately after cervical dislocation, the brain was removed at an angle with double-

ended surgical spatula so that the midbrain, pons, medulla, and cerebellum were excluded (Figure 1A). Olfactory bulb was also excluded. The tissue was rinsed in ice-cold 1X brain homogenization buffer (0.32 M sucrose, 1 mM EDTA, 5 mM Tris, pH 7.4). Fresh 1X brain homogenization buffer (10 mL/g) was added, and the brain was cut into small pieces with surgical scissors. A Kimble pestle was used to homogenize the tissue with 12 strokes (each 4 sec). The tube was spun at 1300 x g for 3 min at 4°C. The first supernatant was stored on ice and the pellet was re-suspended in half starting volume with 1X brain homogenization buffer. The pellet was homogenized with a Kimble pestle with 8 strokes (each 4 sec). The tubes were spun at 1300 x g for 3 min at 4°C. The first and second supernatants were combined, and the sample was spun at 10000 x g for 10 min at 4°C with a Sorvall RC6Plus centrifuge using the SS34 rotor. The pellet was re-suspended in 10 mL per gram of original tissue with 15% Percoll (Percoll, Cytiva 17089102, prepared in 1X brain homogenization buffer). The suspension was carefully layered onto a Percoll gradient (23%-40%) and the tube was spun at 22000 x g for 10 min at 4°C. The top layer contains myelin and associated membranes, the middle layer contains synaptosomes and associated membranes and the bottom layer contains the mitochondrial fraction. After carefully removing the upper layer, the synaptosomes were aspirated and re-spun with 4 volumes of 1X brain homogenization buffer, at 16000 x g for 10 min at 4°C. The supernatant was carefully removed, and 4 volumes of Krebs-like buffer (118 mM NaCl, 5 mM KCl, 1 mM MgCl₂, 1.2 mM CaCl₂, 0.1 mM Na₂HPO₄·H₂O, 20 mM HEPES, 10 mM glucose, pH 7.4) was added. The tube was spun at 18000 x g for 10 min at 4°C. The final pellet was flash frozen in liquid nitrogen for experiments in which baseline metabolite levels were determined. For all other experiments, the final

pellet was re-suspended in the Krebs-like buffer with 0.5 mM glutamine (Invitrogen, 25030081).

For isolation of synaptic vesicles, after the synaptosomes were washed with 4 volumes of Krebs-like buffer, the pellet was re-suspended in 450 μ l ice-cold ddH₂O. The pellet was homogenized by pipetting. 4.95 μ l 1M HEPES (pH7.4, with NaOH) was immediately added and the mixture was incubated on ice for 30 min. The mixture was spun at 43,100 x g with SS-34 rotor at 4°C for 15 min. The supernatant was distributed equally to TLA 120.1 (Beckman Coulter) rotor thick-walled polycarbonate tubes (Beckman Coulter, 343776). The tubes were spun at 165,000 x g at 4°C for 1 hour. The pellet was re-suspended in 30 μ l RIPA buffer (50 mM Tris, 0.15 M NaCl, 1 mM EDTA, 1% TritonX-100, 0.5% (w/v) sodium deoxycholate, 0.1% SDS) with 1X PhosStop and 1X PIC for Western blotting.

Western Blotting

Tissues were homogenized in RIPA buffer (50 mM Tris, 0.15 M NaCl, 1 mM EDTA, 1% TritonX-100, 0.5% (w/v) sodium deoxycholate, 0.1% SDS) with 1X PhosStop and 1X PIC. Protein samples (20 μ g) were incubated in 1X NuPage Sample buffer (Invitrogen, NP0007) and 1X NuPage reducing agent (Invitrogen, NP0004) at 70°C for 10 min and immediately placed on ice. The samples were run in NuPage 4-12% Bis-Tris gel (Invitrogen, NP0321) at 170 V until the dye front was at the end of the gel. The gel was transferred to a nitrocellulose membrane (Invitrogen, LC2000) in 1X FisherScientific Pierce Western Blot Transfer Buffer (35040) with 20% methanol at 30 V for 1 hour. The blot was blocked with Li-Cor Blocking Buffer (Li-Cor Biosciences, 927-50000) for 30

min and permeabilized for 5 min in TBST (FisherScientific, BP2411) with 0.05% Tween20 (Sigma-Aldrich, P7949). The blot was incubated with primary antibodies in Li-Cor Intercept Antibody Diluent (Li-cor Biosciences, 927-65001) at 4°C overnight. The blot was washed 3 x 5 min with TBST, incubated with secondary antibodies diluted in TBST for 1 hour, washed with TBST and finally placed in TBS. The blot was imaged using the Li-Cor Odyssey CLx Imaging System (resolution: 84 µm, background subtraction: median) and analyzed using Image Studio Lite software (RRID:SCR_013715). Protein amount in each sample was determined using the bicinchoninic acid (BCA) assay (ThermoScientific Pierce, PI23227). Primary antibodies used in the study: mouse anti-Actin (Sigma, A3853, RRID:AB_262137, 42 kDa, 1:2000), rabbit anti-Asct1 (Alomone, ANT081, RRID:AB_2756719, 80 kDa, 1:250), mouse anti-Gapdh (Sigma, G8795, RRID:AB_1078991, 37 kDa, 1:40,000), rabbit anti-Gdh (Invitrogen, PA5-29492, RRID:AB_2546968, 55 kDa, 1:2000), mouse anti-Glt1 (Millipore, MAB2262, RRID:AB_10615610, 62 kDa, 1:1000), mouse anti-Glul (BD Biosciences, 610517, RRID:AB_397879, 42 kDa, 1:2000), mouse anti-GluN1 (SynapticSystems, 114001, RRID:AB_887749, 100 kDa, 1:1000), mouse anti-Gpt1 (Sigma, SAB1412234, RRID:AB_2885183, 55 kDa, 1:1000), rabbit anti-Gpt2 (Proteintech, 16757-1-AP, RRID:AB_2112098, 58 kDa, 1:600), rabbit anti-Gria1 (abcam, ab31232, RRID:AB_2113447, 100 kDa, 1:1000), rabbit anti-Lsd1 (CellSignaling, 2184, RRID:AB_2070132, 110 kDa, 1:1000), mouse anti-Mtco1 (abcam, ab14705, RRID:AB_2084810, 40 kDa, 1:2000), mouse anti-Psd95 (Pierce, ma1-046, RRID:AB_2092361, 95 kDa, 1:2000), mouse anti-Snat1 (Millipore, MABN502, RRID:AB_2716561, 50 kDa, 1:500), mouse anti-Sv2 (DSHB, SV2, RRID:AB_2315387,

90 kDa, 1:1000), rabbit anti-SynapsinI (Millipore, AB1543P, RRID:AB_90757, 77&80 kDa, 1:1000), guinea pig anti-Vgat (SynapticSystems, 131004, RRID:AB_887873, 50 kDa, 1:1000), guinea pig anti-Vglut1 (SynapticSystems, 135304, RRID:AB_887878, 50 kDa, 1:1000), guinea pig anti-Vglut2 (SynapticSystems, 135404, RRID:AB_887884, 55 kDa, 1:1000). Secondary antibodies used in the study: goat anti-Rabbit IRDye 680RD (Li-Cor Biosciences, 926-68071, RRID:AB_10956166, 1:20,000), goat anti-Rabbit IRDye 800CW (Li-Cor Biosciences, 925-32211, RRID:AB_2651127, 1:20,000), goat anti-Mouse IRDye 680RD (Li-Cor Biosciences, 925-68070, RRID:AB_2651128, 1:20,000), goat anti-Mouse IRDye 800CW (Li-Cor Biosciences, 926-32210, RRID:AB_621842, 1:20,000), donkey anti-Guinea pig IRDye 680RD (Li-Cor Biosciences, 925-68077, RRID:AB_2814914, 1:20,000), donkey anti-Guinea pig IRDye 800CW (Li-Cor Biosciences, 925-32411, RRID:AB_2814905, 1:20,000).

GPT Enzyme Activity Assay

GPT activity assay was performed using the Alanine Aminotransferase (ALT) Assay Kit (Sigma-Aldrich, MAK052) according to the manufacturer's manual. Synaptosomes were resuspended in 1X ALT Assay buffer. 5 µg protein sample was used. Protein amount in each sample was determined using the BCA assay (ThermoScientific Pierce, PI23227). BioTek Cytation5 plate reader was used to detect fluorescence; Gen5 software was used to analyze the data (RRID:SCR_017317).

Metabolite detection by Liquid Chromatography - Mass Spectrometry (LC-MS)

For all experiments in which metabolites were detected in synaptosomes without any additional supplements, synaptosomes were collected as above and the final pellet was flash frozen in liquid nitrogen. The pellet was homogenized in 400 μ L of 80% (vol/vol) methanol cooled to -80°C with Kimble pestle and motor, then vortexed for 1 min, incubated at -80°C for 4 hours. The samples were spun at $14000 \times g$ for 10 min at 4°C and the pellet was resuspended in 400 μ L of 80% methanol while the supernatant was stored at -80°C . The suspension was incubated at -80°C for 30 min and then spun at $14000 \times g$ for 10 min at 4°C . The supernatants were combined and re-spun at $14000 \times g$ for 10 min at 4°C . The supernatants were concentrated using a Savant SpeedVac vacuum concentrator (Thermo Scientific) at ambient temperature in 1.5-mL Eppendorf tubes. Liquid chromatography with tandem mass spectrometry (MS) was done at Beth Israel Deaconess Medical Center Mass Spectrometry Facility. The samples were re-suspended in liquid chromatography (LC) / mass spectrometry (MS)-grade water and run-in tandem LC-MS/MS. Samples were injected into hydrophilic interaction liquid chromatography (HILIC) at high pH using HPLC coupled to a 5500 QTRAP mass spectrometer (AB/SCIEX). Selected Reaction Monitoring (SRM) mode for 300 transitions with positive/negative polarity switching fragmented precursor ions and selected for product ions. Peak areas for each detected metabolite were integrated using MultiQuant software (AB/SCIEX). All data were normalized by median normalization of at least 100 metabolite peaks. Unpaired Student's t-test assuming equal variance was used to generate a p-value.

For all experiments that involve additional supplement with 1.6 mM alanine (Sigma, A7627) and 1.6 mM alpha-ketoglutarate (Sigma, 75890), synaptosomes in all conditions

were incubated in Krebs-like buffer with 0.5 mM glutamine for 15 min at 37°C. For evoked glutamate release, a final concentration of 50 mM KCl was added, and the suspension was incubated for 1 min at 37°C. The pellet was spun immediately after at 16000 x g at 4°C for 1 min. LC-MS analysis for soluble metabolites was achieved on the Q Exactive PLUS hybrid quadrupole-orbitrap mass spectrometer (Thermo Scientific) coupled with hydrophilic interaction chromatography (HILIC). To perform the LC separation, an XBridge BEH Amide column (150 mm × 2.1 mm, 2.5 μM particle size, Waters, Milford, MA) was used with a gradient of solvent A (95%:5% H₂O: acetonitrile with 20 mM ammonium acetate, 20 mM ammonium hydroxide, pH 9.4), and solvent B (100% acetonitrile). The gradient was 0 min, 85% B; 2 min, 85% B; 3 min, 80% B; 5 min, 80% B; 6 min, 75% B; 7 min, 75% B; 8 min, 70% B; 9 min, 70% B; 10 min, 50% B; 12 min, 50% B; 13 min, 25% B; 16 min, 25% B; 18 min, 0% B; 23 min, 0% B; 24 min, 85% B; 30 min, 85% B. The flow rate was 150 μL/min; the injection volume was 10 μL; the column temperature was 25°C. MS full scans were in negative ion mode with a resolution of 140,000 at m/z 200 and scan range of 75-1000 m/z. The automatic gain control (AGC) target was 1 × 10⁶.

Isotope Labeling in Synaptosomes. Synaptosome metabolite pool was labeled with 0.5 mM [α -¹⁵N]-glutamine (Sigma-Aldrich, 486809), 0.5 mM [U-¹³C]-glutamine (Sigma-Aldrich, 605166) or 1.6 mM [α -¹⁵N]-alanine (Cambridge Isotope Laboratories, NLM-454) for 15 min at 37°C. All conditions had labeled or unlabeled 0.5 mM glutamine in Krebs-like buffer.

Brain slice preparation

Coronal slices (250 μm) were prepared from anesthetized mice at postnatal day 18, as described previously (Brown et al., 2013). Briefly, the brain was immediately extracted and placed in a vibratome (Leica, VT1000). Slices were cut in ice-cold oxygenated artificial cerebrospinal fluid (ACSF, in mM): 119 NaCl, 2.5 KCl, 2.5 CaCl₂·2H₂O, 1.0 NaH₂PO₄·H₂O, 1.3 MgSO₄·7H₂O, 26.0 NaHCO₃, 11 glucose. Slices were recovered in the same oxygenated ACSF solution at room temperature for 1 hour and then transferred to a recording chamber where they were continuously submerged in ACSF at 28°C with a flow rate of 1-2 ml/min.

Electrophysiological recordings

Whole cell recordings of CA1 pyramidal neurons were performed using a MultiClamp 700B Amplifier (Molecular Devices). Signals were low-pass filtered at 3 kHz and digitized at 10 kHz via a Digidata 1550 digitizer (Molecular Devices). Patch electrodes were fabricated from borosilicate glass capillaries (Sutter Instruments) using a P-97 micropipette puller (Sutter Instruments). Patch pipettes had a resistance of 3-8 MOhm. For determining intrinsic cell properties, the patch pipette internal solution consisted of (in mM): 125.0 KCl, 2.8 NaCl, 10.0 HEPES, 2.0 MgCl₂, 2.37 ATP-Mg, 0.32 GTP-Na, 0.6 EGTA, (pH 7.23-7.28, 270-278 mOsm). Capacitance and membrane resistance were calculated from voltage response during injection of -100 pA.

For measuring miniature synaptic currents, the patch pipette internal solution consisted of (in mM): 125.0 CsCl, 2.8 NaCl, 10.0 HEPES, 2.0 MgCl₂, 2.37 ATP-Mg, 0.32 GTP-Na, 0.6 EGTA, (pH 7.23-7.28, 270-278 mOsm). At least 80 events were detected in ASCF with 1 μM TTX (Tocris, 1078) and 33 μM Bicuculline (Tocris, 0130) for miniature

excitatory synaptic currents or with 1 μ M TTX and 10 μ M DNQX (Sigma, D0540) for miniature inhibitory synaptic currents, while the cell was voltage-clamped at -80mV. The series resistance was monitored throughout the recording and the cell was excluded from analysis if it changed by 20%. Miniature events with multiple consecutive peaks or “shoulders” were counted for frequency but excluded from amplitude calculations. For miniature excitatory currents only: the traces were low-pass (Gaussian) filtered with a -3dB cutoff frequency of 1000 Hz for better visualization of miniature events with smaller amplitudes. The miniature events were detected using a template compiled from each recording individually in Clampfit software (SCR_011323).

For train analysis, the patch pipette internal solution consisted of (in mM): 125.0 KCl, 2.8 NaCl, 10.0 HEPES, 2.0 MgCl₂, 2.37 ATP-Mg, 0.32 GTP-Na, 0.6 EGTA, 5 mM QX-314 (Tocris, 2313) (pH 7.23-7.28, 270-278 mOsm). The external solution consisted of ASCF with 50 μ M d-APV (Tocris, 0106) and 100 μ M picrotoxin (Sigma, P1675). CA3 was surgically removed from the slice to minimize epileptic activity. To stimulate Schaffer collaterals, bipolar stainless steel microelectrodes with 2-5 MOhm impedance (FHC, UESMEGSEKNNM) were gently placed approximately 200 μ m away from the recorded pyramidal neuron. Paired pulses, 50 msec apart, were used to achieve a stable current response of approximately 150 - 300 pA. Trains were applied at 10 Hz for 10 seconds. Paired pulses were used to achieve the stable response and the process was repeated a total of 2-3 times. If the current response was able to recover to the original baseline response, then the trains were repeated with 20 Hz stimulation for 10 seconds. Cells with at least two rounds of trains were used for analysis. Paired pulse ratio was calculated by

dividing the peak amplitude of the second response to that of the first. All electrophysiological recordings were analyzed using Clampfit software.

Electron Microscopy

The animals were perfused with 1X PBS and then 2.5% glutaraldehyde, 2% paraformaldehyde, 2 mM calcium chloride in 0.15 M sodium cacodylate buffer. The 100 μ m thick tissue sections were obtained using a vibratome and fixed in glutaraldehyde/paraformaldehyde/calcium chloride/sodium cacodylate buffer for 3 hours at 4°C. The sections were washed in cold 0.15 M sodium cacodylate with 2 mM calcium chloride for 3 minutes, 5 times and then in filtered ddH₂O for 3 minutes, 5 times. The sections were placed in filtered thiocarbohydrazide (TCH) solution (10 mg/ml in ddH₂O) for 20 minutes. The sections were rinsed with ddH₂O for 3 minutes, 5 times. The sections were treated with 2% osmium oxide for 30 minutes and then washed with ddH₂O for 3 minutes, 5 times. The sections were placed in 1% (w/v) uranyl acetate at 4°C overnight. The tissue was washed with ddH₂O for 3 minutes, 5 times and then placed in lead aspartate solution (6.6 mg/ml, pH 5.5) at 60°C for 30 minutes. The tissues were washed in ddH₂O for 3 minutes, 5 times and then dehydrated in increasing concentration of ethanol (70%, 90%, 95%, 20 minutes once each and then 100% for 10 minutes, 3 times.). Epon embedding was performed with Embed-812 (Electron Microscopy Sciences, 14120), Araldite 502 (Electron Microscopy Sciences, 13900), DDSA (Electron Microscopy Sciences, 13700), DMP-30 (Electron Microscopy Sciences, 13600) in Chien molds and the tissues were left to polymerase overnight at 60°C overnight. The electron micrographs were obtained using Philips EM 410 transmission electron microscope.

Glutamate Detection by Enzymatic Method

Free glutamate levels in the cytosolic fraction, that is the supernatant obtained along with the pellet that was re-suspended in Percoll, were determined by enzymatic method using glutamate dehydrogenase. Protein concentration was quantified by the bicinchoninic acid (BCA) assay (ThermoScientific Pierce, PI23227). 100 µg of each sample was added to their respective wells in a black clear-bottom 96-well plate (Greiner Bio-One, 655090) and the final volume was completed to 200 µl with Krebs-like buffer. NADP⁺ (Sigma, N5755) at a final concentration of 1 mM was added to each well. After 6 minutes of equilibration, five units of glutamate dehydrogenase (Sigma, G2626) was added to each well. The excitation and emission filters were 340 and 460 nm, respectively. All readings were taken at 37°C. Glutamate standard (Sigma, G1251) was used for calibration.

To validate the viability of synaptosomes, 50 mM KCl was added to synaptosomes immediately after the glutamate dehydrogenase epoch reached a plateau. The readings were taken the parameters outlined above.

ATP Assay in Synaptosomes

In addition to LC-MS/MS, ATP levels in wild-type and Gpt2-null synaptosomes at P18 were quantified with ATP Assay Kit (abcam, 83355, lot: GR3299138) according to the manufacturer's instructions. The samples were deproteinized by PCA/KOH method as recommended by the manual. Protein amount in each sample was determined using the BCA assay (ThermoScientific Pierce, PI23227).

Experimental Design and Statistical Analyses

All data in the Figures and the Results section are presented as average \pm standard error of the mean, unless otherwise noted. The statistical test for comparisons of two groups was unpaired two-tailed Student t-test unless otherwise noted. All statistical analyses were compiled using GraphPad Prism software (RRID:SCR_002798).

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Chapter 6: Loss of GPT2 leads to reduced cellular growth and altered metabolome in near-haploid HAP1 cancerous cell lines.

I conducted all experiments; Tara Srivinas performed experiments in Figures 1E, 2, 3, 4, 5A&B, 6. The project was done under the supervision of Eric M. Morrow. For funding sources, please refer to the Funding information in Chapters 2, 3, 4 and 5.

Loss of GPT2 leads to reduced cellular growth and altered metabolome in HAP1 cells.

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ABSTRACT

Glutamate pyruvate transaminase 2 (GPT2) plays a central role in cellular growth and energetics by linking amino acid metabolism to the tricarboxylic acid cycle. Here we model the loss of GPT2 in two clones of near-haploid HAP1 cell lines. The loss of GPT2 is confirmed by Sanger sequencing, Western blotting, enzymatic activity and confocal microscopy. GPT2 loss in HAP1 cells causes decreases in cell size. Various medium conditions are employed including alanine deprivation and glutaminase inhibition to expose metabolic vulnerabilities of GPT2 loss *in vitro*. Proliferation rates of GPT2-null cells are reduced in medium deprived of alanine. We find decreases in cell proliferation rate with glutaminase inhibition only in Clone 2 GPT2-null cells. We do not find increases in apoptosis in either clone with or without alanine deprivation or glutaminase inhibition. We find no differences in mitochondrial membrane potential and reactive oxygen species as measured by confocal microscopy between the wild-type and mutant clones. Only Clone 2 GPT2-null cells displayed abnormal mitochondrial respiration. We discover alterations in the metabolic profiles of both GPT2-null clones particularly in the tricarboxylic cycle, alanine metabolism and overall amino acid metabolism. We conclude that HAP1 cells may be used to model cellular and biochemical alterations that result from loss of GPT2 and reveal fundamental mechanisms of cellular growth.

INTRODUCTION

Glutamate pyruvate transaminase 2 (GPT2), also known as alanine transaminase 2 (ALT2) or alanine aminotransferase 2 (ALAT2), plays a critical role in cellular growth and energetics by catalyzing the reversible transamination between alanine and α -ketoglutarate to produce pyruvate and glutamate (Glinghammar et al., 2009; Ouyang et al., 2016). Previously we had reported that loss-of-function mutations in *GPT2* cause a rare neurodevelopmental disorder that is characterized by microcephaly, intellectual disability, and motor abnormalities in humans (Baytas and Morrow, 2018; Ouyang et al., 2019; Ouyang et al., 2016). The products of the GPT2 reaction can be utilized to support ATP, protein synthesis and neurotransmitter production, all integral to neurodevelopmental processes. GPT2 has been shown to augment the biosynthetic capacity of not only neuronal cells but also of cancerous cells thereby granting them the ability of tumorigenesis (Kim et al., 2019; Smith et al., 2016). Understanding the precise role of the GPT2 protein may elucidate mechanisms for cellular growth that are commonly employed in a variety of biological contexts.

Unlike its cytosolic counterpart, GPT1, GPT2 localizes to the mitochondria and regulates metabolic processes such as alanine metabolism and the tricarboxylic acid (TCA) cycle (DeRosa and Swick, 1975; Lindblom et al., 2007). *GPT2* expression increases during the early postnatal stage in the brain, corresponding to high synaptogenic activity and a period of neural circuit development (Kang et al., 2011; Ouyang et al., 2016). As mitochondria are actively recruited to the presynaptic terminal to provide neurons with the energy required for synaptic growth and signaling (Devine and Kittler, 2018), and mitochondrial transport is tightly regulated during neuronal development (Morris and

Hollenbeck, 1993; Ruthel and Hollenbeck, 2003), dysfunction of mitochondrial processes could lead to substantial cellular impairments with neurological implications.

In mitochondria, glutamine is metabolized to glutamate by glutaminase, where it can be further converted to α -ketoglutarate, a TCA cycle intermediate (McKenna and Ferreira, 2016). The integration of α -ketoglutarate into the TCA cycle through glutamine metabolism is a key anaplerotic step in proliferating cells (DeBerardinis et al., 2007). Specifically, cancer cells exhibit a dependence on glutamine as the primary mitochondrial substrate for maintaining not only proliferation but also mitochondrial membrane potential and integrity, redox control, and macromolecular synthesis essential for cell survival (Wise and Thompson, 2010). GPT2 activity is critical to cancer cell proliferation but otherwise dispensable in non-malignant cells (Smith et al., 2016), pointing to a specific metabolic vulnerability associated with cancer cell progression that is regulated by GPT2.

We had previously generated Gpt2-null mice to assess morphological and metabolic phenotypes *in vivo* (Ouyang et al., 2016). Gpt2-null mice demonstrated significant reductions in brain size, weight and motor activity beginning at P18. Targeted metabolomics using coupled liquid chromatography and mass spectrometry (LC-MS/MS) performed using P18 Gpt2-null mouse brain samples revealed reductions in alanine and TCA cycle intermediates. Gpt2-null mouse embryonic fibroblasts exhibited almost complete loss of alanine secretion and nitrogen transfer from [α - ^{15}N]-glutamine to alanine and diminished carbon transfer from [U- ^{13}C]-glutamine to TCA cycle intermediates as measured by isotope tracing, confirming the importance of GPT2 in alanine and TCA cycle metabolism.

Here we modeled the loss of GPT2 in two clones of near-haploid HAP1 cell lines achieved with the CRISPR/Cas9 technique, derived from cells of a human patient with malignant chronic myeloid leukemia (Kotecki et al., 1999). As they are derived from a cancer cell lineage, HAP1 cells divide without cell cycle arrest and thus continuously face with profound metabolic needs. With increased metabolic demand and abundant cell counts, the HAP1 cell lines provide robust sampling for experimental design and analysis to assess the role of GPT2 in cellular growth. Given that GPT2 function is critical for cancer progression, we hypothesized that loss-of-function mutations in GPT2 would result in decreased cell proliferation and survival, altered metabolome and dysregulated mitochondrial mechanisms including changes in mitochondrial membrane potential and respiration. We further tested if alanine deprivation or glutaminase inhibition would expose or exacerbate any metabolic vulnerabilities in the absence of GPT2.

The loss of GPT2 in HAP1 cells is confirmed by Sanger sequencing, Western blotting, enzymatic activity and confocal microscopy. GPT2 loss in HAP1 cells causes decreases in cell size. Proliferation rates of GPT2-null cells are reduced in medium deprived of alanine. We find decreases in cell proliferation rate with glutaminase inhibition only in Clone 2 GPT2-null cells. We do not find increases in number of apoptotic cells in either clone with or without alanine deprivation or glutaminase inhibition. Assays measuring mitochondrial membrane potential and reactive oxygen species yield no differences between the wild-type and mutant clones. Seahorse XF Mito Stress Test measuring mitochondrial respiration results in varying findings across the two clones tested and overall only Clone 2 GPT2-null cells display abnormalities in respiration. We discover alterations in the metabolic profiles of both GPT2-null clones particularly in the TCA

cycle, alanine metabolism and overall amino acid metabolism. In addition to elucidating the biosynthetic mechanisms mediated by GPT2 important for cancer cell metabolism and cellular growth, this study provides a resource to study metabolic pathways that may have substantial implications for neurodevelopment.

RESULTS

Confirmation of loss of GPT2 in HAP1 cells

To confirm that the deletions in the *GPT2* gene in HAP1 cell lines were successfully introduced by CRISPR/Cas9 system, we performed Sanger sequencing of two clones. The sequences along exon 6 of the coding region confirmed an 11-base pair deletion starting at position 607 and a 20-base pair deletion starting at position 609 in the NM_133443 transcript in clone 1 (starting at position 183 in the Sanger sequence) and clone 2 (starting at position 184 in the Sanger sequence), respectively (Figure 1A). Both deletions resulted in loss of protein as evidenced by Western blotting (Figure 1B). The overall GPT enzyme activity assay, which would include activities of both GPT2 and GPT1, showed approximately 50% reduction in both clones indicating that the deletion mutations were loss-of-function.

Localization of GPT2 in mitochondria of HAP1 cells

We confirmed the mitochondrial localization of the GPT2 protein to mitochondria by both structural illumination microscopy (SIM) and confocal microscopy. In the SIM images the GPT2 puncta were enclosed by the MitoTracker Red puncta (Figure 1D). In the confocal microscopy, nearly all MitoTracker Red puncta appeared to be overlapped by the GPT2 puncta (Figure 1E). GPT2 fluorescence in the GPT2-null clones was much dimmer

compared to their wild-type clones and not appreciably greater than the background (Figure 1E).

Diminished cell size and proliferation in GPT2-null HAP1 cells.

Given the role of GPT2 in alanine biosynthesis, we hypothesized that alanine may become an essential amino acid in the absence of GPT2 and that alanine deprivation may decrease cell proliferation and survival. To this end, we continuously charted the growth of GPT2-null HAP1 cells in customized alanine-free Iscove's Modified Dulbecco's Medium (IMDM)-based media with dialyzed fetal bovine serum (dFBS) using the IncuCyte live-cell imaging system (Figure 2A). Alanine deprivation did cause a decrease in growth rate in both clones, however Clone 2 already had a decreased growth rate in the regular IMDM medium (Figure 2B). These results were particularly visible when the growth rates in mutant clones were expressed as a percentage of their respective wild-type clones (Figure 2B). Overall in all conditions, the cell areas of the GPT2-null clones were reduced compared to their wild-type clones suggesting a defect in overall growth of the cell (Figure 2C). Alanine deprivation failed to exacerbate this result; the overall cell size was already profoundly affected by the loss of GPT2. Clone 2 GPT2-null cells had smaller cell area compared to the other clones albeit with some variability across medium conditions (Figure 2C).

Given the role of GPT2 in using glutamate as a substrate to replenish the TCA cycle (anaplerosis) and the role of glutamine in cancer progression, we hypothesized that inhibition of the direct conversion of glutamine into glutamate may also cause decreases in cell proliferation and cell size (Figure 2D-E). To achieve this, we inhibited glutaminase, a mitochondrial enzyme that deaminates glutamine and produces glutamate, by a

glutaminase inhibitor bis-2-(5-phenyl acetamido-1,3,4-thiadiazol-2-yl) ethyl sulfide, BPTES. While BPTES caused decreases in growth rate in all wild-type and GPT2-null clones, only Clone 2 GPT2-null cells had a combined effect of genotype and BPTES (Figure 2D). BPTES also caused decreases in cell area in all wild-type and GPT2-null clones but the decrease was more profound in Clone 2 GPT2-null cells (Figure 2E). Glutaminase inhibition did not have the specific effect of alanine deprivation in GPT2-null clones but an overall effect on HAP1 cells. These results suggest that HAP1 cells are very susceptible to glutaminase inhibition but this is not exacerbated by the absence of GPT2.

To determine whether differences in cell proliferation are partly due to increased cell death, we continuously detected apoptotic cells in wild-type and GPT2-null clones using the IncuCyte live-cell imaging system (Figure 3A). Apoptosis was detected by the fluorescent Annexin V Orange Reagent which binds to phosphatidylserine residues that vertically flip to the outer plasma membrane during early apoptosis. There were no differences in number of apoptotic cell counts over time with or without alanine deprivation (Figure 3B) or glutaminase inhibition (Figure 3C). This suggests that decreases in growth rate in GPT2-null cells likely reflect a decrease in proliferative capacity rather than an increase in cell death.

Mitochondrial membrane potential, ROS levels and mitochondrial respiration in GPT2-null HAP1 cells.

As GPT2 localized to mitochondria and replenishes the TCA cycle, we investigated whether defects in growth rate and size in GPT2-null HAP1 cells are due to mitochondrial mechanisms. One of the major roles of the TCA cycle is to produce NADH and FADH₂, electron donors for the electron transport chain. With continuous supply of substrates and

co-factors, the electron transport chain produces and utilizes the hyperpolarized membrane potential in order to produce ATP. Mitochondrial membrane potential can be indirectly assessed by the fluorescence emitted by positively charged dyes that locate to the hyperpolarized mitochondrial membrane, such as tetramethylrhodamine, ethyl ester (TMRE). We determined whether absence of GPT2 in HAP1 cells may have an effect on the mitochondrial membrane potential that may underlie the observed growth defects. We could not find any differences between the fluorescence intensities of wild-type and GPT2-null cells with or without alanine deprivation (Figure 4B) or glutaminase inhibition (Figure 4D). We also quantified the mitochondrial footprint per cell as a measure of mitochondrial mass using the TMRE staining through the Mitochondrial Network Analysis toolkit in ImageJ. We failed to find any differences in mitochondrial footprint across all media conditions with or without alanine deprivation (Figure 4C) or glutaminase inhibition (Figure 4E). These results indicate that mitochondrial membrane potential and mass appear to be intact in GPT2-null HAP1 cells.

Mitochondrial superoxide production is a major source of oxidative stress. We evaluated the levels of mitochondrial superoxide by using MitoSOX which locates to mitochondria with its positively charged residues and fluoresces red when oxidized by superoxide (Figure 5A). We failed to find any changes in the fluorescence intensity of MitoSOX in GPT2-null cells with or without alanine deprivation or glutaminase inhibition (Figure 5B). To corroborate this finding, we performed a 2',7'-dichlorodihydrofluorescein diacetate (DCFDA) assay to indirectly quantify overall levels of reactive oxygen species (ROS) in HAP1 cells with tert-butyl hydroperoxide (TBHP) as a control oxidant. Similarly,

there were no changes in the fluorescence intensity of DCFDA in GPT2-null HAP1 cells. We conclude that overall ROS levels are unchanged in GPT2-null HAP1 cells.

Mitochondrial dysfunction may manifest in abnormal mitochondrial respiration. We performed Seahorse XFe96 Mito Stress Test on GPT2-null HAP1 clones (Figure 6). Mito Stress Test sequentially injects compounds to inhibit different complexes of the electron transport chain to assess oxygen consumption associated with each complex. First oligomycin which inhibits ATP synthase (Complex V), then Carbonyl cyanide-p-trifluoromethoxyphenylhydrazone (FCCP), an uncoupling agent, which collapses the proton gradient and allows for a free flow of protons through Complex IV for maximum possible respiration, and finally Rotenone/Antimycin A which inhibit Complexes I and III respectively to shut down mitochondrial respiration. This serves as a way to examine various aspects of mitochondrial respiration, including basal and maximal respiration, proton leak, spare respiratory capacity, ATP production and non-mitochondrial oxygen consumption. Oxygen consumption rate (OCR) normalized by cell count plotted over time revealed no changes between Clone 1 wild-type and GPT2-null HAP1 cells (Figure 6A). However, the overall respiration of the Clone 2 GPT2-null cells was lower compared to all other clones. Extracellular acidification rates (ECAR) plotted over time were similar across all clones with trending decreases in Clone 2 GPT2-null cells (Figure 6A). We also plotted OCR to ECAR ratio to assess whether the cells relied more on either oxidative phosphorylation or glycolysis (Figure 6B). The ratios were unchanged across all clones with trending decreases in Clone 2 GPT2-null cells. In all Mito Stress Test assay parameters, only Clone 2 GPT2-null cells showed decreases in oxygen consumption associated with basal respiration, maximal respiration, spare respiratory capacity, and ATP

production (Figure 6C). Clone 2 GPT2-null also showed trending decreases in spare respiratory capacity expressed as percentage of basal respiration, and respiratory control ratio (maximal respiration divided by proton leak) which represents maximum respiration achievable relative to the respiration spent to balance the proton leak (Brand and Nicholls, 2011).

Mito Stress Test may be performed after glutaminase inhibition with BPTES to expose any mitochondrial vulnerability to blockage of glutamine utilization as a substrate. (Figure 6D). We did not observe any major changes with glutaminase inhibition and Clone 2 GPT2-null cells showed diminished OCR levels throughout the assay. ECAR values were unchanged (Figure 6D) and OCR to ECAR ratios were similar across all clones (Figure 6E). In all Mito Stress Test assay parameters, similar to the test without any previous inhibition, only Clone 2 GPT2-null cells had decreased maximal respiration and a very slight but statistically significant decrease in non-mitochondrial oxygen consumption along with trending decreases in basal respiration, proton leak, spare respiratory capacity and ATP production (Figure 6F). Acute response to BPTES had trending decreases in Clone 1 GPT2-null, Clone 2 wild-type and GPT2-null cells compared to Clone 1 wild-type. Overall, we did not observe major changes in mitochondrial respiration or the associated parameters as measured by Seahorse Extracellular Flux Analyzer in Clone 1 GPT2-null cells but Clone 2 GPT2-null cells displayed abnormal mitochondrial respiration characteristics.

Altered metabolic profiles in GPT2-null HAP1 Cells.

To investigate the metabolic mechanisms behind the decreased proliferative capacity and reduced cell size of GPT2-null clones, we performed targeted metabolomics by liquid chromatography coupled to mass spectrometry (LC-MS/MS) (Figure 7,

Supplementary Table 1). The 2D Score plots of principal component analysis (PCA) showed that the two GPT2-null clones separated well from their respective wild-type clones although Clone 1 mutants overall appeared to separate better than Clone 2 mutants (Figure 7A). We plotted the metabolites with statistically significant fold changes with respect to their wild-type clones in a volcano plot (Figure 7B). Both clones exhibited major decreases in the TCA cycle intermediates, including fumarate, malate and isocitrate. Interestingly, we observed increases in kynurenine and xanthurenic acid related to tryptophan degradation pathway of which alanine is an end product (Phillips, 2014). A decrease in alanine, previously reported to occur in Gpt2-null mouse brain tissues (Ouyang et al., 2016), was found only in Clone 1 GPT2-null HAP1 cells. We also constructed a heat map consisting of top most significantly changed 25 metabolites (by raw p-value) (Figure 7C). To identify significantly changed processes, we performed an over-representation analysis and showed top 25 processes ordered by raw p-value (Figure 7D). Among the most significantly changed processes in the comparison of Clone 1 wild-type and GPT2-null cells were Alanine metabolism, Urea cycle, Glycine, Serine, Purine, Arginine and Proline metabolism, TCA cycle and Aspartate metabolism, all with false discovery rates less than 0.05. Clone 2 GPT2-null significantly changed processes were Urea cycle, Arginine, Proline, Aspartate and Purine Metabolism, Spermidine and Spermine Biosynthesis, TCA cycle and Pantothenate and CoA Biosynthesis although none were with false discovery rates less than 0.05. While the two GPT2-null clones shared similar metabolic signatures, Clone 1 GPT2-null appeared to result in a more robust alteration of the metabolome. The overall altered metabolic profile indicates dysregulation of alanine metabolism, the TCA cycle and amino acid metabolism in GPT2-null HAP1 cells.

FIGURE 1

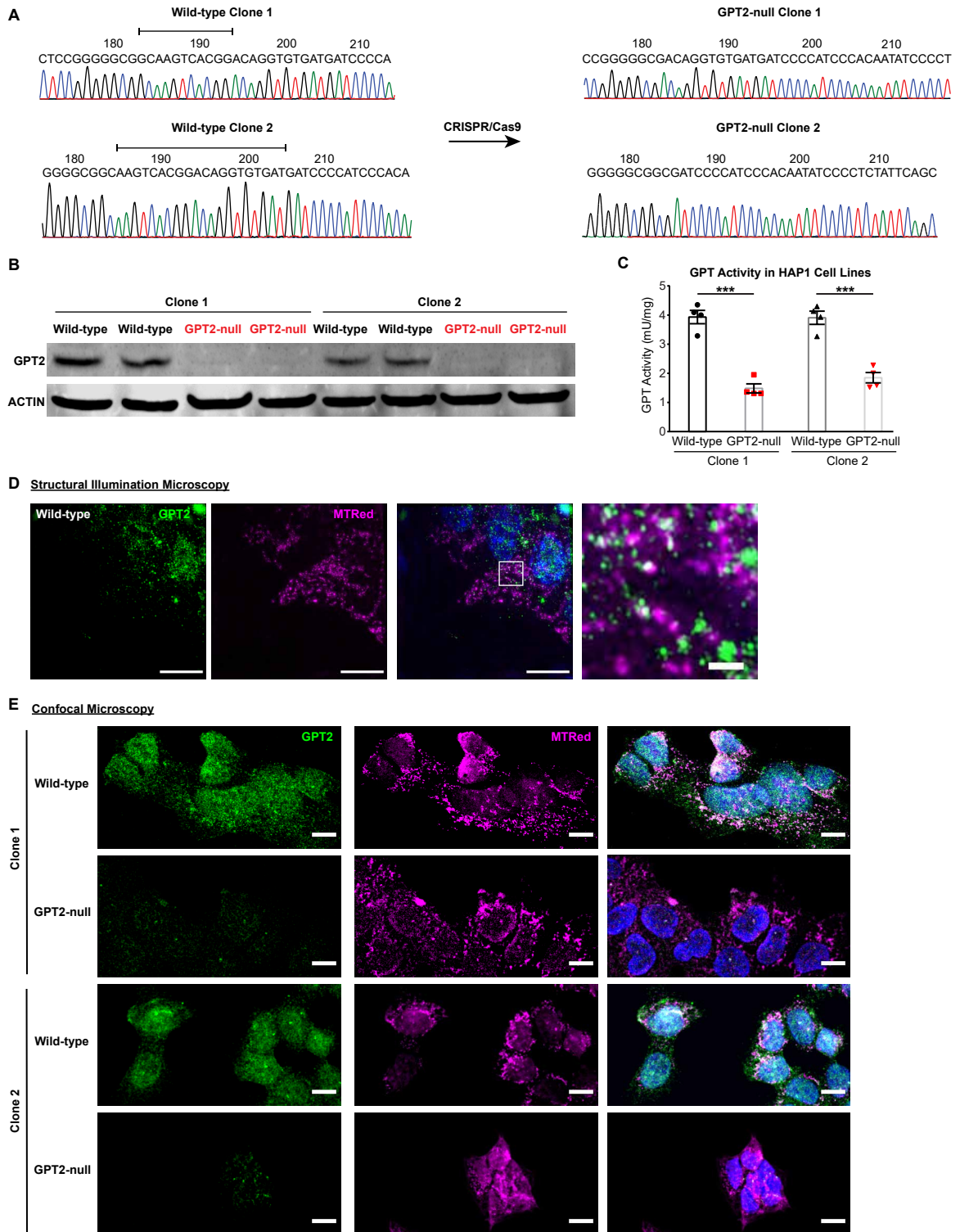


FIGURE 2

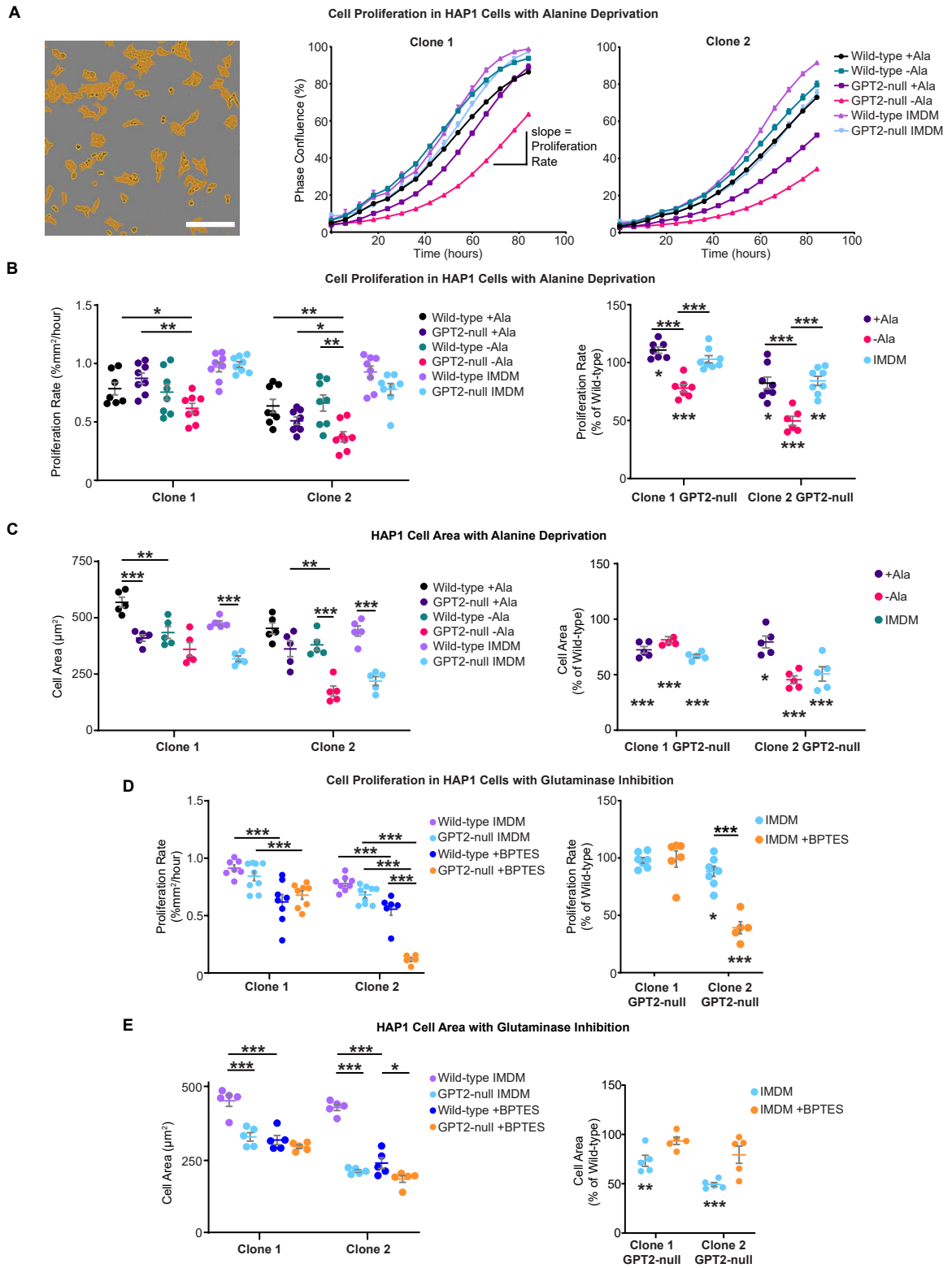


FIGURE 3

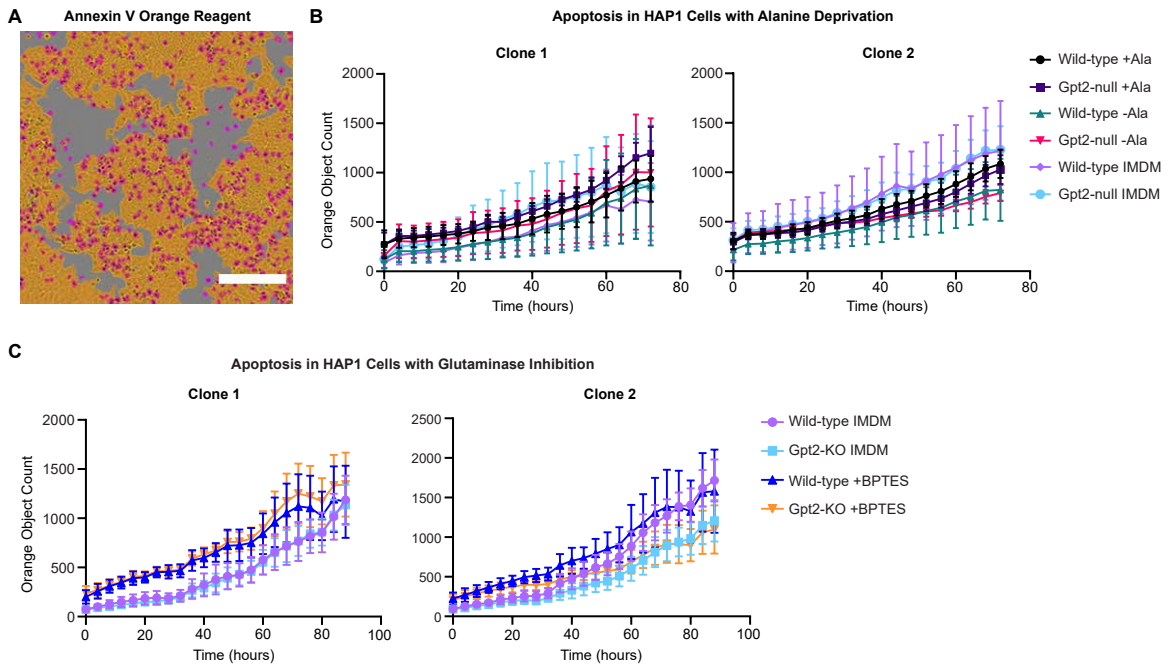


FIGURE 4

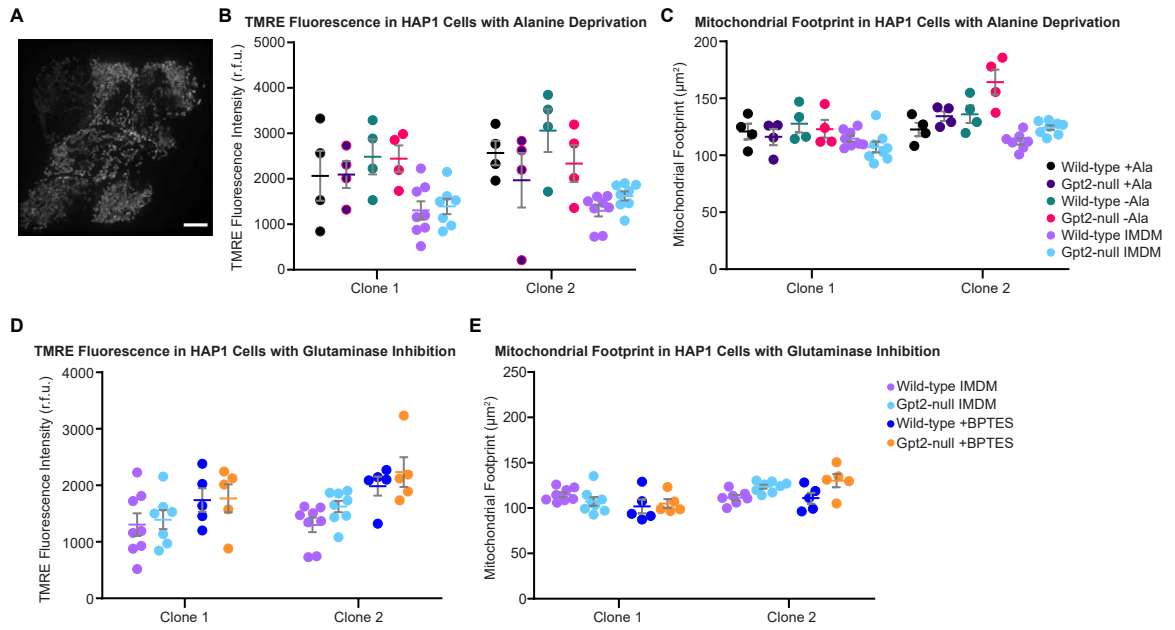


FIGURE 5

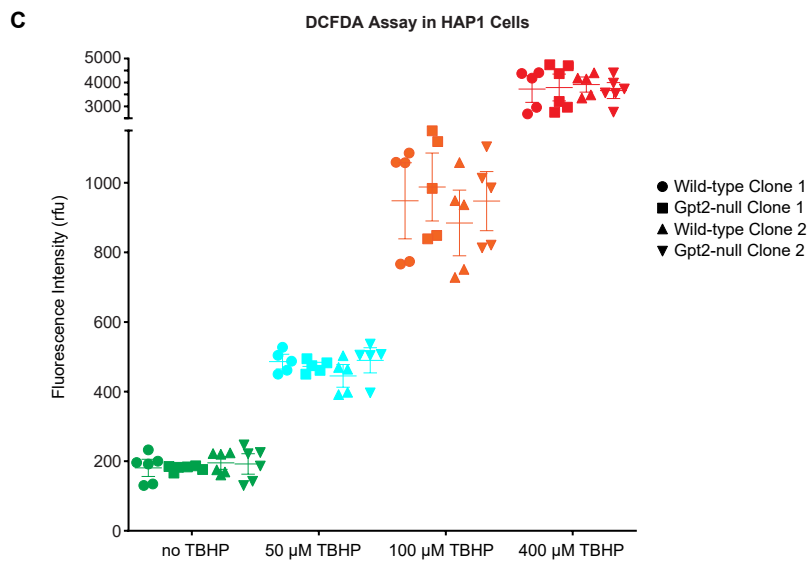
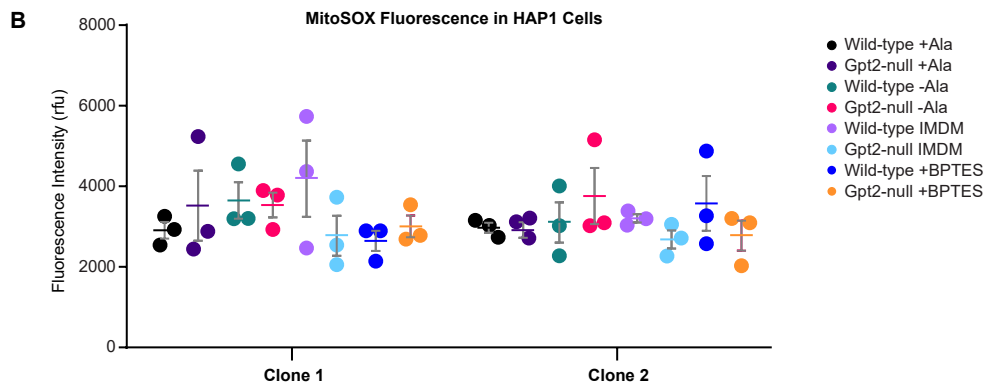
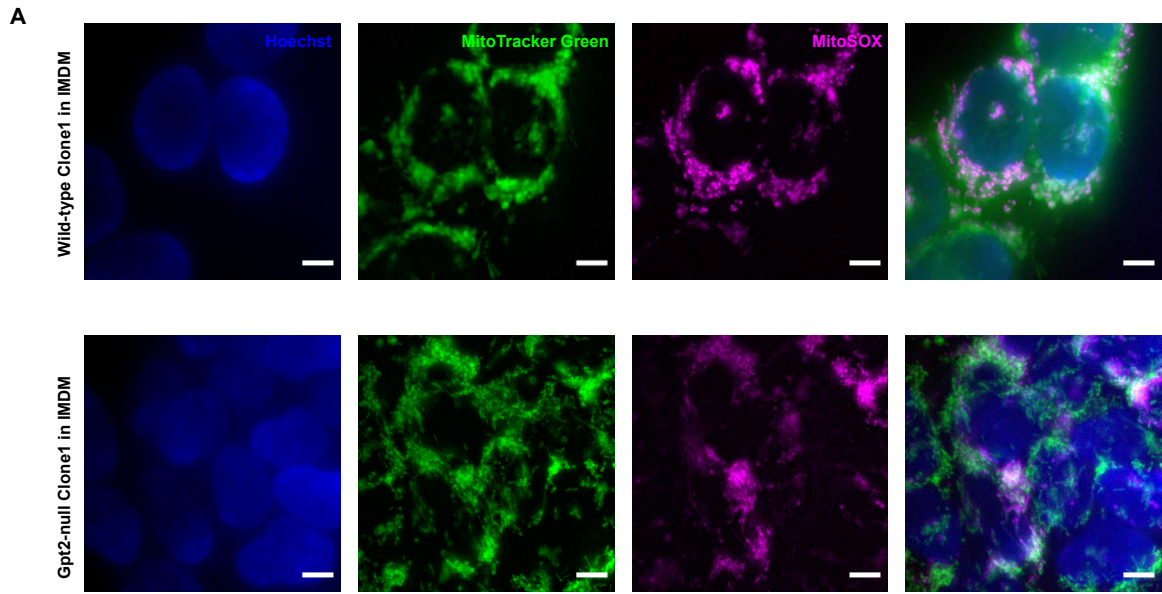


FIGURE 6

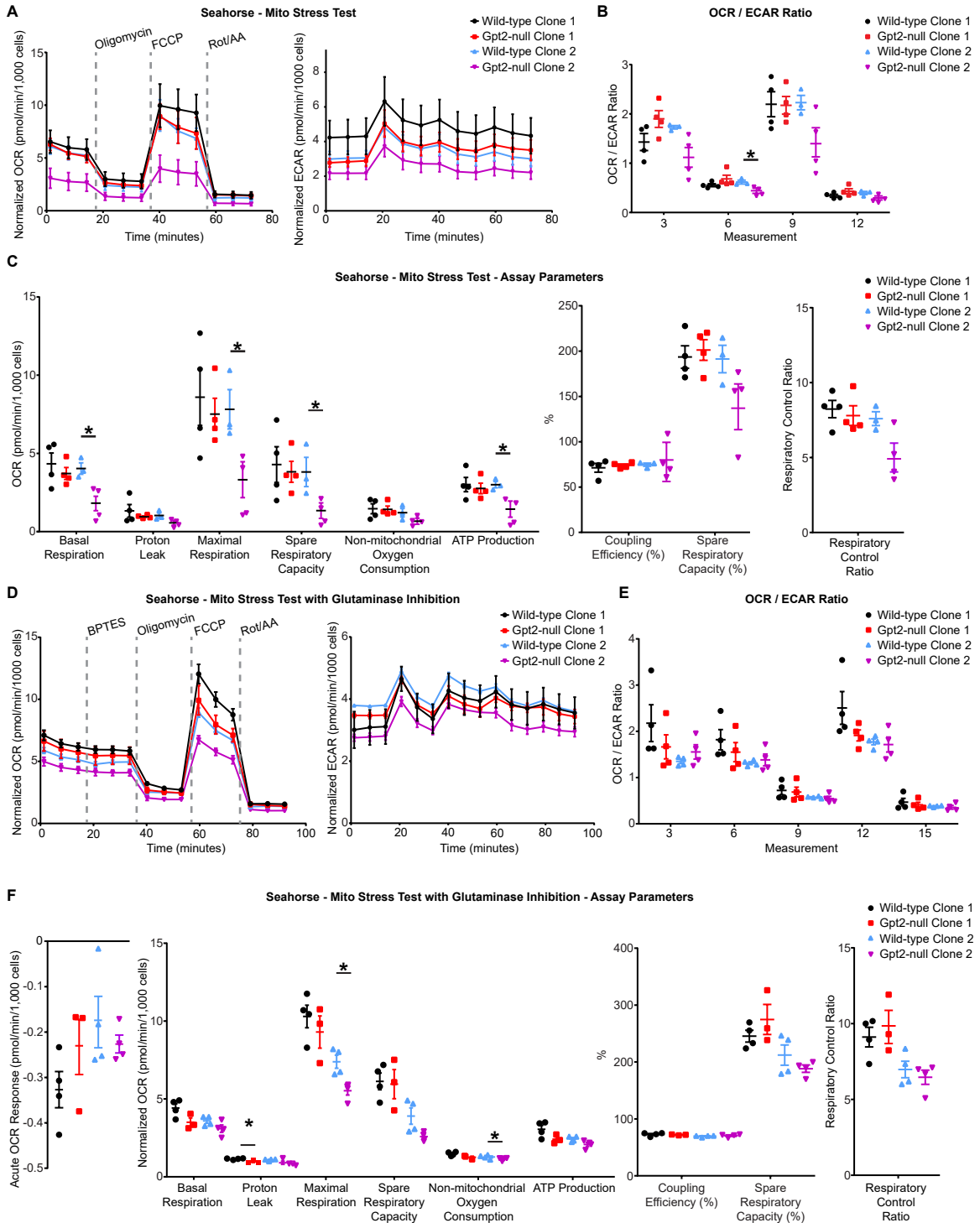


FIGURE 7

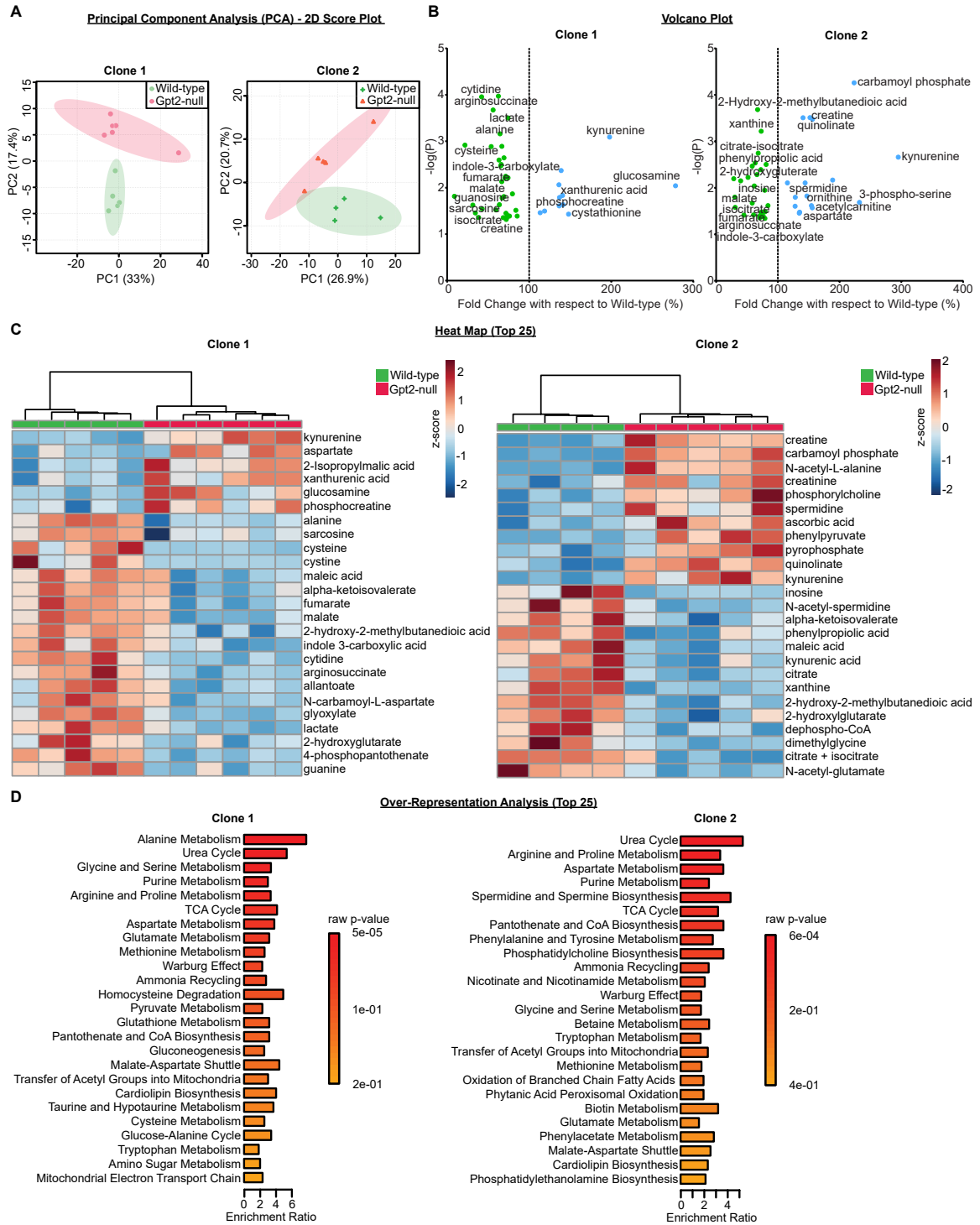


FIGURE LEGENDS

Figure 1. Cellular localization and deletion of GPT2 in HAP1 cell lines.

A. Deletions are successfully introduced to *GPT2* by CRISPR/Cas9 in HAP1 cells. Sanger sequencing around exon 6 of the human *GPT2* transcript NM_133443. The deleted sequences are noted with double-ended lines above the wild-type sequences (left) and the resulting mutant clones are shown on the right.

B. GPT2 protein is absent in both GPT2-null clones. Western blots of the two wild-type and GPT2-null clones with two replicates of each, GPT2 appears at the predicted size of 58 kDa. Actin (42 kDa) is stained for confirming protein loading in each lane.

C. Overall GPT activity is profoundly reduced in GPT2-null clones. This enzyme assay would include both GPT1 and GPT2 enzyme activities. *** $P < 0.001$.

D. Structural illumination microscopy shows GPT2 puncta enclosed by mitochondria. The images are taken using Clone 1 wild-type cells. GPT2 is shown in green and mitochondria are labeled with MitoTracker Red (magenta). Scale bar: 10 μm . The white box in the merged image encloses the area of the zoomed-in image on the far right, scale bar: 1 μm .

E. Confocal microscopy confirms the absence of GPT2 protein in GPT2-null clones and localization of GPT2 to mitochondria. GPT2 in green and MitoTracker Red in magenta, with Hoechst 33342 in blue in the merged image on the far right. Scale bar: 10 μm . Inset scale bar: 5 μm .

Figure 2. Cell size and proliferation rate are decreased in GPT2-null HAP1 cells.

A. Masking of HAP1 cells using IncuCyte live-cell imaging system and an example experiment showing the progression of the phase confluence (%) of the culture plotted over time with or without alanine deprivation. The proliferation rate is calculated from the slope of the linear phase. +Ala and -Ala refer to custom-made IMDM-based media (+dialyzed fetal bovine serum, dFBS) with or without alanine, respectively. IMDM refers to the regular medium with normal FBS. Scale bar: 250 μ m.

B. Both GPT2-null clones proliferate at a slower rate with alanine deprivation. Proliferation rate is expressed as percent confluence per hour. Proliferation of GPT2-null clones with alanine deprivation expressed as a percentage of their wild-type clones is given on the right. The asterisks above the data refer to the p-value obtained from two-tailed t-test between groups. The asterisks below the data refer to the p-value obtained from two-tailed one-sample t-test.

C. GPT2-null cells in both clones are smaller than their wild-type clones regardless of alanine deprivation. Cell area of GPT2-null clones expressed as a percentage of their wild-type clones in media with or without alanine is given on the right. The asterisks below the data refer to the p-value obtained from two-tailed one-sample t-test.

D. Glutaminase inhibition affects proliferation of all wild-type and GPT2-null clones. The cells were treated with 3 μ M BPTES for the entire duration of imaging. Proliferation rate of Clone 2 GPT2-null cells is particularly affected with glutaminase inhibition. The proliferation rate of the mutant clones expressed as a percentage of wild-type clones is given on the right. The asterisks above the data refer to the p-value obtained from two-tailed t-test comparison between media conditions. The asterisks below the data refer to

the p-value obtained from one-sample two-tailed t-test comparison to a hypothetical mean value of 100.

E. Glutaminase inhibition affects cell size of all wild-type and GPT2-null clones. Cell area of GPT2-null clones expressed as a percentage of their wild-type clones in media with or without glutaminase inhibition is given on the right. The asterisks below the data refer to the p-value obtained from one-sample two-tailed t-test comparison to a hypothetical mean value of 100.

* $0.01 < P < 0.05$, ** $0.001 < P < 0.01$, *** $P < 0.001$.

Figure 3. Apoptotic cell counts are unchanged in GPT2-null HAP1 cells.

A. Masking and detection of Annexin V Orange reagent (magenta) in HAP1 cells using IncuCyte live-cell imaging system. Scale bar: 250 μm .

B. Orange object counts plotted over time with or without alanine deprivation. +Ala and -Ala refer to custom-made IMDM-based media (+dFBS) with or without alanine, respectively. IMDM refers to the regular medium with normal FBS. n = 4 vials per group.

C. Orange object counts plotted over time with or without glutaminase inhibition. The cells were treated with 3 μM BPTES for the entire duration of imaging. n = 4 vials per group.

* $0.01 < P < 0.05$, ** $0.001 < P < 0.01$, *** $P < 0.001$.

Figure 4. Mitochondrial membrane potential and footprint are unchanged in GPT2-null HAP1 cells.

- A.** Example image of TMRE staining in HAP1 cells. Scale bar: 5 μ m.
- B.** Fluorescent intensities of TMRE in HAP1 cells with or without alanine deprivation. +Ala and -Ala refer to custom-made IMDM-based media (+dFBS) with or without alanine, respectively. IMDM refers to the regular medium with normal FBS. r.f.u.: relative fluorescence unit.
- C.** Mitochondrial footprint per cell measured as area covered by TMRE staining in HAP1 cells with or without alanine deprivation.
- D.** Fluorescent intensities of TMRE in HAP1 cells with or without glutaminase deprivation. The cells were treated with 3 μ M BPTES for the entire duration of imaging.
- E.** Mitochondrial footprint per cell measured as area covered by TMRE staining in HAP1 cells with or without glutaminase inhibition.

Figure 5. MitoSOX staining and DCFDA assay in HAP1 cells.

- A.** MitoSOX staining in Clone 1 wild-type (top) and GPT2-null (bottom) cells. Mitochondria were stained with MitoTracker green, MitoSOX shown in magenta and cell nuclei stained with Hoechst 33342 in blue. Scale bar: 5 μ m.
- B.** Fluorescence intensity of MitoSOX in HAP1 cells with or without alanine deprivation or glutaminase inhibition. +Ala and -Ala refer to custom-made IMDM-based media (+dFBS) with or without alanine, respectively. IMDM refers to the regular medium with normal FBS. For glutaminase inhibition, the cells were treated with 3 μ M BPTES for the entire duration of imaging. r.f.u: relative fluorescence unit.

C. DCFDA assay with varying concentrations of THBP in HAP1 cells in complete IMDM medium.

Figure 6. Seahorse Mito Stress Test in GPT2-null HAP1 cells.

A. Mitochondrial respiration as measured by Seahorse XFe96 Flux Analyzer in HAP1 cells. Mito Stress Test is shown; oxygen consumption rate per 1,000 cells (OCR, left) and extracellular acidification rate (ECAR, right) plotted over time. The baseline respiration epoch is followed by oligomycin, FCCP and Rotenone/Antimycin A (Rot/AA) epochs each starting after the dashed gray line, each epoch contains three consecutive measurements. n = 3-4 vials per group.

B. OCR to ECAR ratios calculated from the Mito Stress Test. The third, sixth and ninth measurements are immediately taken before oligomycin, FCCP and Rot/AA injections and the twelfth measurement is the last reading of the test.

C. Assay parameters of the Seahorse Mito Stress Test in HAP1 cells. Assay parameters include normalized OCR values associated with basal respiration, proton leak, maximal respiration, spare respiratory capacity, non-mitochondrial oxygen consumption, ATP production, coupling efficiency as a percentage, spare respiratory capacity as a percentage and respiratory control ratio.

D. Mito Stress Test performed with glutaminase inhibition after acute injection of BPTES. Normalized OCR (left) and ECAR (right) values plotted over time are shown. The baseline respiration epoch is followed by BPTES, oligomycin, FCCP and Rot/AA epochs each

starting after the dashed gray line; each epoch contains three consecutive measurements. n = 3-4 vials per group.

E. OCR to ECAR ratios calculated from the Mito Stress Test with glutaminase inhibition. The third, sixth, ninth and twelfth measurements are immediately taken before BPTES, oligomycin, FCCP and Rot/AA injections and the fifteenth measurement is the last reading of the test.

F. Assay parameters of the Seahorse Mito Stress Test with glutaminase inhibition in HAP1 cells. Assay parameters include normalized OCR values associated with acute response to BPTES, basal respiration, proton leak, maximal respiration, spare respiratory capacity, non-mitochondrial oxygen consumption, ATP production, coupling efficiency as a percentage, spare respiratory capacity as a percentage and respiratory control ratio.

* $0.01 < P < 0.05$.

Figure 7. Targeted metabolomics reveals altered metabolic profiles in GPT2-null HAP1 cells.

A. 2D Score plots of principal component analysis (PCA) of targeted metabolomics in HAP1 cells. The peak intensities obtained from liquid chromatography coupled to mass spectrometry (LC-MS/MS) were normalized to the sample median and auto-scaled (mean-centered and divided by the standard deviation of each group). Analyses were performed in MetaboAnalyst 4.0 (<https://www.metaboanalyst.ca>). Both clones of wild-type (green) and GPT2-null (red) HAP1 cell groups were well separated.

B. Volcano plots of targeted metabolomics in HAP1 cells. The fold changes were plotted on the x-axis, as percentage of the wild-type average peak intensity values. The y-axis is $-\log(\text{raw p-value})$ where the higher value indicates more statistically significant difference is between wild-type and GPT2-null clones. The dashed line denotes 100% of the wild-type; any metabolite left side of the line has a decreased value (green dots) and any metabolite right side of the line has an increased value (blue dots) compared to the wild-type. Raw data along with results of all statistical analyses can be found in [Supplementary Table 1](#).

C. Heat map clustering of the most significantly changed metabolites in GPT2-null HAP1 cells. The z-scores color scale is given on the right. The top 25 metabolites with lowest raw p-values are listed. Green samples are wild-type, red are GPT2-null.

D. Alanine, TCA cycle, and amino acid metabolism are altered in GPT2-null HAP1 cells. Over-representation analysis of significantly changed metabolites associated with metabolic pathways. The raw p-value color scale is given on the right. Enrichment ratio is the number of observed hits divided by hits expected by chance in a given metabolite pathway set. Metabolites included in each metabolic pathway set and related statistical analyses can be found in [Supplementary Table 1](#).

DISCUSSION

This study identifies glutamate pyruvate transaminase 2 (GPT2) as a critical metabolic enzyme in determining cell size and proliferation of human cancerous HAP1 cell lines. The loss of GPT2 in HAP1 cells causes decreases in cell size and with alanine deprivation GPT2-null cells divide at a slower rate. We performed various assays investigating possible mitochondrial mechanisms, such as mitochondrial membrane potential, reactive oxygen species, respiration which resulted in varying findings across the two clones tested. We discover alterations in the metabolic profiles of the GPT2-null clones particularly in the TCA cycle, alanine metabolism and overall amino acid metabolism. Our study in HAP1 cell lines provide a tenable biological resource for studying the GPT2 enzyme and its role in mitochondrial mechanisms underlying cellular growth.

We characterize the successful deletion of the GPT2 gene and consequently the protein in HAP1 cells (Figure 1). However, the overall GPT enzyme activity is only halved. Relative contributions of the two proteins to cell size and proliferation have not been studied simultaneously. Although GPT1 and GPT2 catalyze the same reaction in cytosolic and mitochondrial compartments respectively, the two enzymes may act upon different processes. For example, with inhibition of pyruvate entry into the mitochondria, alanine incorporation into lipids depends on GPT2 but not GPT1 in HEK293T cells (Bowman et al., 2016). Future studies are warranted to investigate if loss of GPT1 results in a similar growth defect.

GPT2 has been found to be necessary for survival and proliferation upon glutamine inhibition in HeLa cells (Kim et al., 2019). Our data support this view only for

Clone 2 GPT2-null HAP1 cells. Proliferation rates of Clone 1 wild-type and GPT2-null cells were similarly affected by glutaminase inhibition with BPTES. Clone 2 GPT2-null cells overall behaved abnormally; they did not proliferate or respire at the same rate as the wild-type cells even with complete medium. It is possible that Clone 2 may have acquired genomic changes other than deletion in GPT2 during the CRISPR/Cas9 technique. This discrepancy between our results and those of Kim and co-workers is possibly due to the differences between shRNA and CRISPR/Cas9 techniques. Other inherent differences in cell lines may also be partly responsible; variable expression levels of GPT2 may explain variabilities in resistance to glutaminase inhibition in certain non-small-cell lung cancer cell lines (Caiola et al., 2020).

Decreased cell size and proliferation particularly when alanine is removed from the medium may be linked to autophagy. Transamination is crucial for the mechanistic target of rapamycin (mTOR) activation and cellular growth; alanine and leucine in combination are sufficient to inhibit autophagy (Meijer et al., 2015). Loss of GPT2 has been shown to induce autophagy in a breast cancer cell line (Mitra et al., 2021) and possibly in mouse embryonic fibroblasts (Tan et al., 2017). A comprehensive study into autophagy markers with or without alanine deprivation may reveal mechanisms that underlie defects in cellular growth.

The tricarboxylic acid (TCA) cycle and the replenishment of its intermediates (anaplerosis) are instrumental in cellular growth and energetics as well as tumorigenesis (DeBerardinis et al., 2008). We observe significant decreases in TCA cycle intermediates including fumarate, malate, citrate/isocitrate in both GPT2-null clones, confirming the role of GPT2 as an anaplerotic enzyme in HAP1 cells. GPT2 has been shown to be

upregulated in cell lines with mutations in phosphatidylinositol 3-kinase α (PIK3C α) associated with colorectal cancer (Hao et al., 2016). With increased GPT2 levels, Hao and co-workers found increased glutamine flux into the TCA cycle with concomitant increases in alanine levels. Maintaining the TCA cycle is fundamental for biosynthesis and energetics and further studies can be performed to test whether exogenously supplied TCA cycle intermediates that readily enter the plasma membrane (e.g. citrate) may correct the decreases cell area or proliferation.

Loss-of-function mutations in GPT2 cause microcephaly, intellectual disability, and motor abnormalities in humans (Ouyang et al., 2016). The results in this study of cancerous HAP1 cell line may have implications for growth of neuronal and glial cells as well. Previously we had reported reduced glutamine entry into the TCA cycle in Gpt2-null mouse embryonic fibroblasts and reduced alanine and TCA cycle metabolism in the Gpt2-null brain. We also found that Gpt2-null mouse brains were smaller than their wild-type controls. These findings suggest parallels between the mechanisms regulated by GPT2 in HAP1 cells and the central nervous system despite the major differences in the two biological contexts. Thus, we conclude that HAP1 cells may be used to model cellular and biochemical alterations that result from loss of GPT2 and reveal fundamental mechanisms of cellular growth.

METHODS

Cell Culture

Human HAP1 wild-type and CRISPR-Cas9 GPT2-deleted cell lines were purchased from Horizon Discovery (Vienna, Austria). Cells were grown in Iscove's Modified Dulbecco's

Medium (IMDM, Thermo Fisher, 12440-053) supplemented with 10% fetal bovine serum (FBS, Thermo Fisher, 16000044) and 1% Penicillin-Streptomycin (P/S, Thermo Fisher, 15140122). Cells were collected using 0.25% Trypsin-EDTA solution (Invitrogen, 25200072) for assays as needed. Unless otherwise noted, cultures were maintained at 37°C in a humidified atmosphere of 5% CO₂. Full medium was replaced one day after cell thawing and once every three days thereafter. Cells were allowed to grow to approximately 80% confluency before passaging.

Alanine-free IMDM medium was custom-made according to commercial IMDM formulation (Thermo Fisher, 12440053) with 10% dialyzed fetal bovine serum (dFBS, Thermo Fisher, 26400044) and 1% Penicillin/Streptomycin (P/S, Invitrogen, 15140122).

For glutaminase inhibition, the cells were incubated with 3 µM BPTES both for acute response and continuous administration (Robinson et al., 2007).

PCR and Sanger Sequencing

HAP1 cells were trypsinized at 37°C for 5 min and 15 µL pellet volume was collected. Samples were vortexed for 15 sec in 50 µL Lucigen QuickExtraction buffer (Lucigen, QE09050), then transferred to 65°C heat block for 6 min. Extracts were then vortexed for 15 sec and heat-inactivated at 98°C for 2 min, after which DNA was amplified by touchdown PCR reaction. Primer sequences used to detect the wild-type GPT2 band were as follows: forward primer CSD-GPT2-F (5'-CTA ACT TGT CCT GCA TGG TGT CAG C-3') and reverse primer CSD-GPT2-R (5'-GGC TTT CTA CCA GGA GGA ACA GAG G-3') for a wild-type band of 504 bp. The Clone 1 mutant band was 493 bp and the Clone 2 mutant band was 484 bp. DNA amplicons were detected through DNA agarose gel

separation. Amplified products were sent for Sanger sequencing at GENEWIZ facilities (South Plainfield, NJ). Each sample was tested in duplicate. PCR reaction was executed as follows: 5' 95oC, 10 x (30'' 95oC, 30'' 65oC*, 45'' 72oC), 25 x (30'' 95oC, 45'' 55oC, 45'' 72oC), 5' 72oC. *Temperature decreased by 1oC per cycle (touchdown).

Western Blotting

HAP1 cells were lysed using NP40 Cell Lysis Buffer (Thermo Fisher, FNN0021) with 100 μ M PMSF (Sigma, 93482), 1X PhosSTOP (Roche, 4986845001), and 1X Protease Inhibitor Cocktail (PIC, Roche, 5892791001). During lysis, cells were kept on ice for 30 min and vortexed at 10 min intervals, then transferred to microcentrifuge tubes and spun at 13,000 rpm for 10 min at 4°C. Total protein was quantified using BCA Protein Assay Kit according to the manufacturer's instructions (Thermo Fisher, 23225) and absorbance was measured using Cytation 5 Plate Reader. Lysates were heated at 90oC for 5 min in 1X NuPage LDS sample buffer (Invitrogen, NP0007) with 1X NuPage sample reducing agent (Invitrogen, NP0009). Protein samples were run on 4–12% Bis-Tris precast polyacrylamide gel (Invitrogen, NP0321) and transferred to nitrocellulose membranes (Invitrogen LC2000) in NuPage Transfer Buffer (Thermo Fisher, NP0006) with 20% methanol (v/v) at 30V for 1 hour. The membrane was then blocked for 30 min at room temperature using TBS blocking buffer (Li-cor Biosciences, 927-50000), washed for 5 min in TBS-Tween (0.05% Tween-20 in 1X TBS), and incubated with primary antibodies overnight at 4oC. The membrane was subsequently washed thrice with TBS-Tween for 5 min per wash and incubated for 1 hour at room temperature in secondary antibody diluted in TBS-Tween. Following three washes with TBS-Tween for 5 min per wash, the

membrane was scanned with the Odyssey CLx Infrared Imaging System (Li-cor Biosciences). The primary antibodies used were rabbit anti-GPT2 (Proteintech, 16757-1-AP, 1:600) and mouse anti-actin (Sigma, A3853, 1:1000). The secondary antibodies used were goat anti-rabbit IRDye680 (Li-cor Biosciences, 926-32221, 1:20,000) and goat anti-mouse IRDye800 (Li-cor Biosciences, 926-32210, 1:20,000).

GPT Enzyme Activity Assay

GPT activity assay was performed using the alanine aminotransferase (ALT) assay kit (Sigma, MAK052) according to the manufacturer's manual. 5 µg protein sample of cell lysates were used. Protein amount in each sample was determined by the bicinchoninic acid (BCA) assay (ThermoScientific Pierce, PI23227). BioTek Cytation5 plate reader was used to detect fluorescence; Gen5 software used to analyze the data.

Immunocytochemistry, Confocal & Structural Illumination Microscopy

HAP1 cells were grown at 20,000 cells/well in Millicell EZ Slide (Thermo Fisher, PEZGS0816) for 48 hours. Cells were then incubated with MitoTracker Red CMXRos (Thermo Fisher, M7512) at a working concentration of 100 nM in IMDM medium for 25 min prior to fixation. Slides were rinsed with 1X PBS and fixed in 4% (w/v) paraformaldehyde for 15 min, after which they were washed thrice with 1X PBS for 5 min each and permeabilized with 0.25% (v/v) Triton X-100 in 1X PBS for 10 min at room temperature. Thereafter, cells were blocked with 10% normal goat serum in 1X PBS + 0.1% Triton X-100 (PBST) for 1 hour at room temperature and incubated

overnight at 4°C with rabbit anti-GPT2 primary antibody (Proteintech, 16757-1-AP, 1:800) in PBST containing 2% normal goat serum. After washing thrice in PBST for 5 min each, cells were incubated for 1 hour at room temperature with AlexaFluor 488 secondary antibody diluted 1:600 in PBST containing 2% normal goat serum. Nuclei were counterstained using 300 nM DAPI (Invitrogen, D1306) for 5 min at room temperature, and cells were subsequently washed thrice with 1X PBS for 5 min per wash. Slides were mounted using Fluoromount-G (SouthernBiotech, 0100-01).

Structured illumination microscopy (SIM) was performed on slides using the DeltaVision OMX SR microscope (GE Healthcare Life Sciences). Z-stack images were obtained using the 60X oil objective (refractive index immersion oil-1.516) and light path-SI under sequential acquisition mode. Z-series images were processed by OMX SI reconstruction, alignment, and maximal projection sequentially using softWoRx software. Slides were also visualized by confocal microscopy using 60X oil objective using FV3000 microscope (Olympus). The laser settings (e.g. laser power, light offset) were kept consistent across conditions and genotypes.

Proliferation and Cell Death Assays

Cell proliferation and death were monitored using the IncuCyte S3 Live-Cell Imaging system (Essen BioScience, v2018B). Cells were seeded at 5,000 cells/well in complete IMDM, custom-made alanine-free medium, custom-made alanine-supplemented IMDM, or complete IMDM treated with 3 μ M BPTES (bis-2-(5-phenyl acetamido-1,3,4-thiadiazol-2-yl) ethyl sulfide) (Cayman Technologies, 19284) for glutaminase inhibition.

Proliferation rate was calculated as the slope of the graph plotting phase confluence (%) vs. time (hours).

Apoptosis was measured in real time using IncuCyte Annexin V Orange Reagent (Essen BioScience, 4759), which marks apoptotic cells. The vial containing Annexin V was solubilized in 100 μ L 1X PBS and the working dilution of Annexin V in media was 1:200. The total medium volume per well was 200 μ l. The cells were treated with Annexin V starting a day after they were seeded in 96-well plates. Cells were seeded in triplicate or quadruplicate wells. Immediately after seeding, cells were incubated in the IncuCyte machine for 30 min to equilibrate. Brightfield and fluorescent images were captured using the 10X objective at 4-hour intervals for 96 hours total. IncuCyte integrated analysis software was employed to measure cell confluence through high-definition phase-contrast imaging, which calculates the density of cells in each imaging field. Artifacts were excluded based on morphological characteristics using cell area thresholding (between 120 and 250 μ m², where needed) and phase mask edge sensitivity (0 to 1) adjustments.

Cell Size

Cells seeded for IncuCyte assays were imaged using brightfield microscopy with the 10X objective. Brightfield images taken 24 hours after IncuCyte initiation were collected and analyzed blindly. 10 cells per image were manually circled using ImageJ. 10 images per experimental sample were analyzed. Each dot in Figures 2C&E represents the cell area

averaged across all cells of the images for each experimental sample. Each sample represents cells that had been thawed from different cryovials.

Mitochondrial Membrane Potential and Morphology

Cells were seeded at 20,000 cells/dish in single 35mm CellVis glass bottom dishes (Fisher Scientific, NC0794151) and allowed to grow for 48 hours until 80% confluent. Cells were subsequently incubated with tetramethylrhodamine, ethyl ester (TMRE) (Sigma, 87917), at working concentration of 500 nM for 20 min and imaged live using the 60X oil objective (refractive index immersion oil 1.526) and conventional light path (568 nm excitation) of the DeltaVision OMX SR microscope (GE Healthcare Life Sciences). Processing of binary-converted images was conducted using Mitochondrial Network Analysis toolkit (MiNA, macro code freely available on Github) (Valente et al., 2017) to ascertain fluorescence intensity of mitochondrial membranes and mitochondrial footprint.

Mitochondrial Respiration Assays

Cells were seeded at 40,000 cells/well in Seahorse XFe96 V3 PS Cell Culture Microplates (Seahorse Biosciences, 101085-004) and allowed to settle for 4 hours at 37°C in a 5% CO₂ humidified atmosphere. Cells were subsequently washed with DMEM XF assay medium at pH 7.4 (Seahorse Biosciences, 103575-100) supplemented with 10 mM glucose (Seahorse Biosciences, 103577-100), 2 mM glutamine (Seahorse Biosciences, 103579-100), and 1 mM sodium pyruvate (Seahorse Biosciences, S8636)

and incubated for 1 hour at 37°C in a non-CO₂ incubator. Oxygen consumption rate (OCR) and extracellular acidification rate (ECAR) were subsequently measured using Seahorse Extracellular Flux (Seahorse Biosciences, XFe96) analyzer. Working concentrations of 1.5 µM oligomycin, 1 µM FCCP, 0.5 µM rotenone and 0.5 µM antimycin A were loaded into the injection ports in the XFe96 sensor cartridge in sequence and the Mito Stress Test was performed. For Mito Stress Test with glutaminase inhibition, 3 µM BPTES was injected before oligomycin followed by FCCP, rotenone and antimycin A. Mito Stress Test Assay parameters were calculated automatically using Wave software (Seahorse Biosciences).

Following the assay, cells were rinsed gently with 1X PBS and fixed in 4% (w/v) paraformaldehyde for 10 min, after which they were washed twice for 5 min each wash with 1X PBS at room temperature. Nuclei were counterstained using 300 nM DAPI for 5 min at room temperature, and cells were subsequently washed thrice with 1X PBS for 5 min per wash. Cell density per well was measured using the Cytation 5 Plate Reader (Biotek Instruments, Winooski, VT) by imaging wells at 405nm and measures of respiration were normalized to cell density per well.

Mitochondrial ROS Measurements

HAP1 cells were seeded at 20,000 cells/dish in CellVis 35mm glass bottom dishes and incubated for 48 hours at 37°C, 5% CO₂. Cells were subsequently treated with 0.2 µM MitoSOX Red (Thermo Fisher, M26008), 0.125 µM MitoTracker Green (Thermo Fisher,

M7514), and 90 μ M Hoechst (Thermo Fisher, H3570) at 37°C, 5% CO₂ for 10 min.

Cells were then imaged live using the 60X oil objective (refractive index immersion oil 1.526) and conventional light path of the DeltaVision OMX SR microscope (GE Healthcare Life Sciences). Mitochondrial superoxide levels were measured by fluorescence intensity of puncta using ImageJ.

DCFDA – Cellular Reactive Oxygen Species Detection Assay

HAP1 cells (25,000 cells per well) were seeded on 96-well black Greiner clear-bottom microplates (Greiner Bio-One, 655090, allowed to settle in complete IMDM medium for 4 hours and stained with 2',7'-dichlorodihydrofluorescein diacetate (DCFDA). The assay performed according to the manufacturer's manual (abcam, ab113851). For a positive control, the cells were treated with varying concentrations of tert-butyl hydroperoxide (TBHP).

Metabolomics

HAP1 cells were grown in complete IMDM until approximately 80% confluence in 10 cm dishes. The cells were quickly washed with 1X PBS at room temperature and then immediately the metabolism was quenched with 500 μ l 80% (v/v) methanol (cooled to -80°C). The mixture was vortexed for 1 min and incubated at -80°C for 4 hours. To pellet debris, the sample was spun at 14,000 x g for 10 min at 4°C. While the supernatant was kept at -80°C, 400 μ l of 80% methanol (cooled to -80°C) was added to the pellet, which was then vortexed for 1 min, incubated at -80°C for 30 min and then spun at 14,000 x g

for 10 minutes at 4°C. The supernatants were combined and re-spun at 14,000 x g for 10 min 4°C. The supernatants were concentrated in 1.5 ml Eppendorf tubes with SpeedVac at ambient temperature. Tandem mass spectrometry was done at Beth Israel Deaconess Medical Center Mass Spectrometry Facility. The samples were re-suspended in liquid chromatography (LC)/mass spectrometry (MS)-grade water and run in tandem LC-MS/MS. Samples were injected into hydrophilic interaction liquid chromatography (HILIC) at high pH using HPLC coupled to a 5500 QTRAP mass spectrometer (AB/SCIEX). Selected Reaction Monitoring (SRM) mode for 300 transitions with positive/negative polarity switching fragmented precursor ions and select for product ions. Peak areas for each detected metabolite were integrated using MultiQuant software (AB/SCIEX). The statistical analyses and data visualization including PCA plot, volcano plot, heat map and over-representation analysis were done using MetaboAnalyst 4.0 (Chong et al., 2019). If half of data for a metabolite is not available than that metabolite was omitted from analysis. All data was normalized by median normalization and auto-scaled (mean-centered and divided by standard deviation of each variable). For over-representation analysis, we used Small Molecule Pathway Database (SMPDB) metabolite pathway sets (Supplementary Table 1). Unpaired Student's two-tailed t-test assuming equal variance was used to generate a raw p-value.

Statistics

All statistical tests indicated in the text were performed using GraphPad Prism (GraphPad Software, San Diego, CA) unless otherwise noted. Each dot in the graphs represents an average of technical replicates from cell clones that had been thawed from different

cryovials. Two-tailed t-tests were performed to find significant differences between groups unless otherwise noted. One-sample t-test was used to determine statistically significant difference with the hypothetical mean of 100 to compare GPT2-null values when expressed as a percentage of the averaged wild-type value. Raw P values were considered significant below 0.05 and error bars represent standard error of the mean unless otherwise noted.

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Supplementary Table 1 contains raw data and statistical analysis of targeted metabolomics obtained from Clone 1 and Clone 2 wild-type and GPT2-null HAP1 C

Sheets: RAW DATA, T-TEST, MSEA - ORA (Metabolite Set Enrichment Analysis - Over-representation Analysis)

CLONE 1						CLONE 2					
Metabolite	Fold Change (FC)	log2(FC)	raw P value	-LOG10(P)	False Discovery Rate (FDR)	Metabolite	Fold Change (FC)	log2(FC)	raw P value	-LOG10(P)	False Discovery Rate (FDR)
L-arginino-succinate	0.62407	-0.6781	0.000107	3.9708	0.015944	Carbamoyl phosphate	2.225	1.1633	5.925e-05	4.258	0.015446
cytidine	0.4204	-1.2502	0.0001107	3.9558	0.015944	2-Hydroxy-2-methylbutanedioic acid	0.67221	-0.573	0.0002076	3.8827	0.018762
glyoxylate	0.5609	-0.8342	0.0002123	3.6732	0.020376	N-Acetyl-L-alanine	1.5207	0.60473	0.0003095	3.5094	0.018762
lactate	0.74233	-0.4299	0.0003154	3.5011	0.022712	creatine	1.4078	0.49346	0.0003108	3.5075	0.018762
alanine	0.64451	-0.6337	0.000392	3.1599	0.039007	quinolate	1.5616	0.64303	0.000335	3.4749	0.018762
Kynurenine	1.9794	0.9851	0.0008127	3.0901	0.039007	xanthine	0.73068	-0.4527	0.0006059	3.2176	0.028274
cysteine	0.2172	-2.2029	0.0012088	2.9177	0.041576	citrate-isocitrate	0.68121	-0.5538	0.0017968	2.7455	0.07187
arginosuccinic acid	0.6673	-0.5836	0.0012851	2.8911	0.041576	Kynurenine	2.9505	1.561	0.0021884	2.6599	0.076592
4-phosphopantothenate	0.53752	-0.8656	0.0012993	2.8683	0.041576	N-acetyl-glutamate	0.63301	-0.6507	0.0029155	2.5353	0.086739
fumarate	0.69303	-0.529	0.0022765	2.6427	0.065562	Malic acid	0.8096	-0.3047	0.0031436	2.5026	0.086739
2-Hydroxy-2-methylbutanedioic aci	0.63227	-0.6614	0.0025369	2.5957	0.066422	Phenylpropiolic acid	0.58489	-0.7738	0.0034076	2.4676	0.086739
Indole-3-carboxylic acid	0.65921	-0.6012	0.0031587	2.5005	0.07513	2-hydroxyglutarate	0.72472	-0.4645	0.0040561	2.3917	0.09469
malate	0.6541	-0.6124	0.0033913	2.4696	0.07513	Kynurenic acid	0.66064	-0.5981	0.0051956	2.2844	0.10967
2-Isopropylmalic acid	1.3895	0.4746	0.0042681	2.3698	0.087801	citrate	0.51654	-0.9531	0.0059715	2.2239	0.10967
Malic acid	0.71395	-0.4861	0.0056827	2.2454	0.10373	dephospho-CoA-posi	0.2852	-1.8099	0.0063788	2.1953	0.10967
2-keto-isovalerate	0.70481	-0.5047	0.0061166	2.2135	0.10373	Ascorbic acid	1.8874	0.91643	0.0068134	2.1666	0.10967
allantoin	0.74228	-0.43	0.0061228	2.2131	0.10373	phenylpyruvate	11.29	3.497	0.0068273	2.1658	0.10967
N-carbamoyl-L-aspartate-nega	0.6653	-0.5879	0.0074148	2.1299	0.11864	N-acetyl spermidine	0.39769	-1.3303	0.0070572	2.1514	0.10967
Xanthurenic acid	1.3625	0.44621	0.0086568	2.0626	0.13074	Pyrophosphate	1.4415	0.52757	0.0078238	2.1066	0.10967
glucosamine	2.7826	1.4764	0.0090791	2.042	0.13074	Phosphorylcholine	1.1552	0.20818	0.0078335	2.106	0.10967
2-hydroxyglutarate	0.79602	-0.3291	0.013557	1.8678	0.1836	dimethylglycine	0.61831	-0.6936	0.0091233	2.0398	0.12164
aspartate	1.4066	0.4922	0.014682	1.8332	0.1836	2-keto-isovalerate	0.78726	-0.3451	0.011278	1.9478	0.14354
Cytidine	0.088847	-3.4925	0.015298	1.8154	0.1836	Creatinine	1.4709	0.55669	0.015014	1.8235	0.17876
sarcosine	0.69164	-0.5319	0.015515	1.8093	0.1836	inosine	0.30357	-1.7199	0.015833	1.8004	0.17876
phosphocreatine	1.3694	0.45354	0.016198	1.7905	0.1836	spermidine	1.2819	0.35833	0.015961	1.797	0.17876
guanine	0.67042	-0.5769	0.016575	1.7805	0.1836	3-phospho-serine	2.321	1.2148	0.020556	1.6871	0.22102
aconitate	0.63699	-0.6507	0.023196	1.6351	0.23479	L-arginino-succinate	0.58552	-0.7722	0.021312	1.6714	0.22102
cystathionine	1.4128	0.49856	0.023175	1.635	0.23479	DL-Pipecolic acid	0.83965	-0.2521	0.024121	1.6176	0.23184
guanosine	0.31339	-1.6739	0.023642	1.6263	0.23479	ornithine	1.5435	0.62616	0.024122	1.6176	0.23184
betaine aldehyde	1.3653	0.44919	0.024681	1.608	0.23874	2-Isopropylmalic acid	1.2793	0.35531	0.02484	1.6048	0.23184
inosine	0.4258	-1.2284	0.028432	1.5462	0.26414	aminimidazole carboxamide ribonucleotid	0.30878	-1.6954	0.026326	1.5796	0.23582
deoxyinosine	0.59618	-0.7496	0.030353	1.5221	0.26756	Acetylcarnitine DL	1.5967	0.63651	0.026951	1.5694	0.23582
sn-glycerol-3-phosphate	0.83762	-0.2556	0.030658	1.5135	0.26756	pantothenate	0.79297	-0.3347	0.032581	1.487	0.26245
glucose-1-phosphate	1.1876	0.24804	0.031831	1.4972	0.26962	fumarate	0.75991	-0.3961	0.032982	1.4817	0.26245
taurine	1.1332	0.18043	0.034575	1.4612	0.27637	cholesterol	1.3521	0.43521	0.033408	1.4762	0.26245
deoxyguanosine	0.34427	-1.5384	0.034966	1.4576	0.27637	malate	0.72995	-0.4601	0.033744	1.4718	0.26245
pyruvate	0.71701	-0.4799	0.035506	1.4497	0.27637	aspartate	1.3471	0.42985	0.035094	1.4548	0.26558
trehalose-6-Phosphate	1.4799	0.5655	0.037109	1.4305	0.2802	arginosuccinic acid	0.60624	-0.722	0.03815	1.4185	0.27704
oxaloacetate	0.73649	-0.4413	0.039807	1.4022	0.2802	methylnicotinamide	0.44588	-1.1524	0.038588	1.4135	0.27704
quinolinate	0.73953	-0.4353	0.039964	1.3983	0.2802	ribose-3-phosphate	0.70734	-0.4995	0.040395	1.3937	0.27888
glycine	0.76011	-0.3957	0.040851	1.3888	0.2802	Indole-3-carboxylic acid	0.76271	-0.3908	0.040836	1.389	0.27888
creatine	0.65385	-0.2279	0.040963	1.3887	0.2802	isocitrate	0.70599	-0.5023	0.044	1.3565	0.29333
hypoxanthine	0.38365	-1.3821	0.043716	1.3594	0.28655	D-gluconate	0.79023	-0.3397	0.045508	1.3419	0.29633
isocitrate	0.68391	-0.5481	0.044074	1.3558	0.28655						
Pyrophosphate	0.72537	-0.4632	0.044773	1.349	0.28655						
Flavone	4.3242	2.1124	0.046807	1.3297	0.29305						
Aminoadipic acid	0.72041	-0.4731	0.048205	1.3169	0.29538						

CLONE 1					CLONE 2									
Metabolic Pathway	Total	Expected Hits	Row P value	Hitin P value	FDR	Metabolic Pathway Set	Metabolic Hits	Total	Expected Hits	Row P value	Hitin P value	FDR	Metabolic Pathway Set	Metabolic Hits
Metabolic Pathway	19	1784	0.042	0.006	0.004	0.004	0.004	26	113	0.002	0.002	0.002	0.002	0.002
Urea Cycle	28	13	0.0071	0.006	0.004	0.004	0.004	53	217	7	0.0020	0.004	0.002	0.002
Fatty Metabolism	36	150	0.0071	0.002	0.002	0.002	0.002	20	33	2	0.0020	0.004	0.002	0.002
Amino and Protein Metabolism	74	332	0.0071	0.008	0.002	0.002	0.002	18	870	3	0.002	0.002	0.002	0.002
Cofactor Cycle	32	144	0.0071	0.005	0.002	0.002	0.002	32	125	4	0.0020	0.002	0.002	0.002
Apoptosis Metabolism	35	137	0.0071	0.020	0.002	0.002	0.002	21	862	2	0.0020	0.002	0.002	0.002
Glycolysis Metabolism	44	232	0.0071	0.002	0.002	0.002	0.002	58	130	2	0.0020	0.002	0.002	0.002
Metabolic Intermediates	18	107	0.0071	0.002	0.002	0.002	0.002	18	120	3	0.0020	0.002	0.002	0.002
Metabolic Signaling	38	241	0.0071	0.002	0.002	0.002	0.002	33	120	3	0.0020	0.002	0.002	0.002
Anticancer Metabolism	36	184	0.0071	0.002	0.002	0.002	0.002	37	120	3	0.0020	0.002	0.002	0.002
Immune System Regulation	8	404	0.0071	0.002	0.002	0.002	0.002	38	221	4	0.0020	0.002	0.002	0.002
Pyruvate Metabolism	48	235	0.0071	0.002	0.002	0.002	0.002	38	221	4	0.0020	0.002	0.002	0.002
Glutamine Metabolism	32	160	0.0071	0.002	0.002	0.002	0.002	31	162	2	0.0020	0.002	0.002	0.002
Paracetamol and Cofactor Metabolism	31	160	0.0071	0.002	0.002	0.002	0.002	31	162	2	0.0020	0.002	0.002	0.002
Glutathione Metabolism	10	127	0.0071	0.002	0.002	0.002	0.002	22	160	2	0.0020	0.002	0.002	0.002
Fatty Acid Metabolism	10	846	0.0071	0.002	0.002	0.002	0.002	10	846	0	0.0020	0.002	0.002	0.002
Transfer of Fatty Groups into Mitochondria	20	846	0.0071	0.002	0.002	0.002	0.002	26	112	2	0.0020	0.002	0.002	0.002
Cardiac Energetics	11	446	0.0071	0.002	0.002	0.002	0.002	26	112	2	0.0020	0.002	0.002	0.002
Fatty and Lipid Metabolism	13	626	0.0071	0.002	0.002	0.002	0.002	8	820	1	0.0020	0.002	0.002	0.002
Glucose Metabolism	34	137	0.0071	0.002	0.002	0.002	0.002	46	130	3	0.0020	0.002	0.002	0.002
Glucose Metabolism	12	624	0.0071	0.002	0.002	0.002	0.002	6	626	1	0.0020	0.002	0.002	0.002
Tryptophan Metabolism	60	217	0.0071	0.002	0.002	0.002	0.002	10	301	1	0.0020	0.002	0.002	0.002
Indole Signaling Metabolism	33	140	0.0071	0.002	0.002	0.002	0.002	11	145	1	0.0020	0.002	0.002	0.002
Mitochondrial Electron Transport Chain	19	854	0.0071	0.002	0.002	0.002	0.002	12	848	1	0.0020	0.002	0.002	0.002

CONCLUSION

Figure 7.1 shows the questions introduced in Chapter 1 (outlined in Figure 1.4) and their summarized answers as obtained in this work. This section summarizes the main findings of the chapters, proposes future directions and extends the discussion that I could not fit in previously.

Does GPT2 confer the ability to synthesize alanine in the cells, i.e. non-essentiality of alanine? Would alanine supplementation alleviate/prevent metabolic or behavioral defects, i.e. may it be a therapeutic target?

We observe decreases in alanine and TCA cycle intermediates followed by increases in amino acid and glycolytic intermediates in the *Gpt2*-null hippocampus over the course of the first three postnatal weeks. By our data mining for the metabolites in the GPT2 reaction in KEGG (Kyoto Encyclopedia of Genes and Genomes) (Kanehisa et al., 2020), pyruvate has 22, glutamate 44, alpha-ketoglutarate 43 and alanine has 14 biochemical reactions that occur in both humans and mice. One may expect that any perturbations in level or function of GPT2 may affect alanine first. This expectation was justified in our previous report where reduction in alanine levels in the *Gpt2*-null whole brain and complete absence of alanine release into the medium by *Gpt2*-null mouse embryonic fibroblasts were observed (Ouyang et al., 2016). Strikingly, in human patients with GPT2 Deficiency, the biochemical panel in the blood plasma was within range of control levels except reduced alanine (Celis et al., 2015).

It may be puzzling to initially find *increases* in *Gpt2*-null brain alanine levels at P0 when at other timepoints there is a prominent decrease. Developmentally, free alanine

levels decrease in the rodent brain from infancy into adulthood while free glutamate levels increase (Levi et al., 1967; Morken et al., 2014). On the other hand, pyruvate and alpha-ketoglutarate concentrations in the brain remain relatively unchanged (Miller et al., 1973). *Gpt2* expression is present at P0 in the mouse brain and it increases during the first three weeks (Ouyang et al., 2016) as does *GPT2* expression in the first nine years of human postnatal brain development (Kang et al., 2011). Whether an increase in alanine levels at P0 is caused by differences in the direction of the GPT2 reaction across development or by a probable influence of the fetal nutrient composition supplied by the *Gpt2*-heterozygous mother is yet unclear. At P0, in addition to alanine, metabolites of the tryptophan-kynurenic acid degradation pathway of which alanine is an end product (Phillips, 2014), are significantly changed in *Gpt2*-null brain, such as kynurenic acid and tryptophan. These metabolites are not changed at other time-points including P7, P14 and P18 supporting the idea of the early fetal effects on *Gpt2*-null pups.

Reduced alanine levels seen in *Gpt2*-null mice brain was also expected given the function of normalizing levels of metabolites in the GPT2 reaction. Glutamate represents a larger pool of the brain metabolome (~10 $\mu\text{mol}/\text{gr}$) (Levi et al., 1967) compared to alanine which is the second most abundant proteinogenic amino acid in the plasma (Cynober, 2002) but is present in much lower concentration in the brain (~0.5 $\mu\text{mol}/\text{gr}$) (Levi et al., 1967). If glutamate and pyruvate constitute a larger pool than alanine and alpha-ketoglutarate, then GPT2, being an equilibrium enzyme (Krebs, 1953), will catalyze the reaction in favor of alanine production. In addition, given higher K_m values for alanine in the brain compared to the other primary reaction metabolites, alanine formation has been predicted to be favored *in vivo* (Lysiak et al., 1974) (Miller et al.,

1973). The current study identifies alanine as one of the first metabolites that is altered in the *Gpt2*-null brain, confirming the idea that alanine levels are sustained significantly by GPT2.

Survival and growth of *Gpt2*-null neuronal cultures is severely affected by alanine deprivation in the medium. Conversely, by adding extra alanine in the diet, it was possible to increase chances of survival in *Gpt2*-null mice. These results suggest that alanine became a conditionally essential amino acid; i.e. it has to be supplied exogenously for the organism to function normally. However, not all *Gpt2*-null mice survived under the high alanine diet regimen and this reduced penetrance of alanine supplementation is most likely due to the ad libitum nature of the diet administration. The wild-type mice on high alanine did not show increased alanine levels in the blood, meaning that it is very likely that the *Gpt2*-heterozygous mother on high alanine did not help raise alanine levels in the *Gpt2*-null pup via milk and the *Gpt2*-null pup that obtained more solid food had better chances of receiving extra alanine. The inability of the mother in passing on the extra alanine to its pup may be due to the first-pass metabolism of alanine in the liver and this is also likely to cause SynapsinI-Cre conditional *Gpt2*-null mice to die even on high alanine diet because there is GPT2 in the liver thereby decreasing free available alanine levels in the blood.

Of course, several follow-up questions are immediately raised. If exogenous alanine is critical to *Gpt2*-null mice, and we assume that alanine decreases are not merely a by-product of the absence of GPT2 reaction, what does alanine deprivation contribute in terms of lethality in mice? What does it mean to have reduced free alanine levels in the brain tissue and serum? What altered process does alanine supplementation reverse in the

body? Naturally, the overarching question would be: why do *Gpt2*-null mice die? The answers to these questions are yet unknown. My thesis work does not provide clear answers to these; however it can provide several lines of thought.

First, we know that SynapsinI-Cre conditional null mice die, and that a critical region in the nervous system is most likely responsible for the premature death. Such a region is likely to localize to the brainstem, possibly controlling autonomous functions such as CO₂, pH regulation on the blood, heart rate, breathing etc. Failure in any of these would lead to eventual death. The fact that the animals are dying close to weaning age (P21) most likely has to do with the increasing *Gpt2* expression pattern in the first two weeks of life and accumulating metabolic damage over time. It is unlikely that any of the motor systems that control gross body movements (fore/hind limbs) are behind the premature death. It is possible that the noradrenergic system, particularly the vagus nerve dysfunction (if any) may be responsible, at least in part, the death of *Gpt2*-null mice. Alanine supplementation may be providing the metabolic support for the brain region in question.

Second, how does extra alanine exert its influence over the system? Does it increase protein synthesis or does it correct gluconeogenesis in the liver thereby helping the body maintain its glucose balance (alanine-glucose cycle)? We do not find major differences in blood glucose (see Appendix for Chapter 3) so this would not work in favor of this hypothesis. However, it would be remiss to dismiss this idea because even if the blood glucose may not be relevant to the pathophysiology, extra alanine in the liver may help with other aspects of hepatic metabolism such as the TCA cycle (McCommis et al., 2015).

Alanine in protein synthesis could be of importance. Two papers have found that extracellular alanine is important for T-cell activation and protein synthesis in cancerous cell lines *in vitro* (Ron-Harel et al., 2019; Rossiter et al., 2021). Alanine is a proteinogenic amino acid and decreases in free alanine levels may slow down translation and in turn other biosynthetic pathways. Decreases in alanine or serine (a precursor for alanine) may also contribute to promiscuity in tRNA synthetases and cause misfolding and degradation in proteins. Mutations in alanyl tRNA-synthetase have been shown to incorporate serine instead of alanine and cause neurodegeneration in the cerebellar Purkinje cells (Vo et al., 2018). It might prove useful to perform stable isotope labeling by amino acids *in vitro* (SILAC) or *in vivo* (SILAM); the rate with which amino acids are incorporated into proteins may tell us the rate of nascent protein synthesis. Other techniques can be done including labeling nascent polypeptides with O-propargyl-puromycin (Forester et al., 2018) or other labels (Dieterich et al., 2010; Iwasaki and Ingolia, 2017).

Slowed down protein synthesis may be coupled to protein or cellular degradation. Alanine and leucine in combination at near-physiological concentrations have been shown to inhibit autophagy *in vitro* and alanine's contribution is transaminase dependent; i.e. autophagy continues in the presence of a transaminase inhibitor, aminooxyacetate (Meijer et al., 2015). Furthermore, inhibition of GPT2 impairs glutamine-mediated mTORC1 reactivation during amino acid starvation (Tan et al., 2017). Autophagy or other proteolytic pathways (ubiquitin-proteasome pathway) may also explain the increase in essential amino acids in *Gpt2*-null brain.

Our data suggest that dietary modifications may involve alanine as a potential therapeutic supplement for human patients with GPT2 Deficiency. Supplemental alanine has been shown to be well tolerated in humans (Bodamer et al., 2000; Carlin et al., 1987; Genuth and Castro, 1974). To date, the only biochemical finding in human patients with GPT2 Deficiency is decreased alanine levels in the plasma (Celis et al., 2015), a result which is supported by our data here in the *Gpt2*-null mouse. This data is very hopeful for a clinical trial involving alanine in people with GPT2 Deficiency.

Is the TCA cycle affected after the loss of GPT2? If so, does it occur in neurons or astrocytes or both? Would TCA cycle supplementation alleviate/prevent metabolic or behavioral defects, may it be a therapeutic target?

In our studies of the metabolome, we also observe prominent increases in glycolytic intermediates, preceded by an undermined TCA cycle in *Gpt2*-null brain. Is glycolysis being used more as ATP source given the deficits in the TCA cycle? While it has yet to be demonstrated, it is highly probable. The increased glycolytic intermediates may also be a result of reduced pyruvate levels which may cause decreased substrate inhibition of glycolytic enzymes. Indeed, glycolysis is regulated not only by pyruvate at the substrate level but also by alanine, which is an allosteric inhibitor of pyruvate kinase (Carbonell et al., 1973). We find no changes in glucose uptake in hippocampal neurons and astrocytes *in vitro* or in glycolytic enzyme protein levels that could have reflected changes in metabolite levels. Glucose uptake and flux analysis *in vivo* may further dissect out the mechanisms behind the increase in glycolytic metabolites.

Amino acids and the TCA cycle are closely linked. We observe increased levels in an intriguingly high number of amino acids in *Gpt2*-null brain. Increased amino acid profile (particularly essential amino acids) in the *Gpt2*-null brain may stem from increased transporter expression driven by the transcription factor ATF4, one of whose targets is GPT2, as the system is predicted to be in need of alanine (Hao et al., 2016; Salgado et al., 2014). However, this was not the case. More studies *in vivo* are warranted to determine the possibilities of changes in specific transporter levels or increased protein breakdown to support both alanine supply and the TCA cycle as free amino acids can readily be converted into TCA cycle intermediates.

The TCA cycle metabolism was profoundly affected in the absence of GPT2. We find decreases in glutamine-dependent anaplerosis (replenishment of the TCA cycle intermediates) in both neurons and astrocytes *in vitro*. Please refer to the Appendix for Chapter 3 for the data on astrocytes; as we had only the data for ¹³C labeling in alpha-ketoglutarate, I left it for the Appendix. Glutamine entry into the TCA cycle is affected in both cell types, and this is also evident in concomitant decreases in alanine release in both cell types. However, given all the data on survival *in vitro*, astrocytes may be able to utilize other metabolic pathways to support their TCA cycle such as pyruvate carboxylation which is exclusive to astrocytes. This is evident in metabolomics performed in wild-type and *Gpt2*-null astrocytes *in vitro*; no tangible differences in any of the metabolites were found (Appendix for Chapter 3).

We also find deficits in the TCA cycle in *Gpt2*-null synaptosomes (isolated nerve terminals), such as decreases in malate and fumarate levels, but glutamine can still be efficiently used as a precursor to the TCA cycle intermediates. There are anaplerotic

pathways, other than glutamate dehydrogenase and GPT2, that may support the TCA cycle in the absence of GPT2 such as pyruvate carboxylase and other aminotransferases that yield alpha-ketoglutarate from glutamate including branched-chain amino acid aminotransferases (Hutson, 2001; Morken et al., 2014). All these processes likely contribute to sustain the TCA cycle in *Gpt2*-null brain as long as they are able; however, each have certain complications. For example, pyruvate carboxylase exists mainly in astrocytes and consumes ATP to make oxaloacetate (Hertz et al., 2007; Yu et al., 1983). Glutamate dehydrogenase is found both in neurons and astrocytes but depends on NADP availability (Aoki et al., 1987). Aminotransferases that degrade essential amino acids usually work in the direction of producing glutamate and not alpha-ketoglutarate (Conway and Hutson, 2016). In contrast, GPT2 depends neither on ATP nor NADP availability, thereby conferring a unique anaplerotic ability to the cell. Levels of GPT2 and GPT1 protein have been shown to increase in models of oxidative phosphorylation deficits induced by mitochondrial DNA mutations (Chen et al., 2018) and disrupted mitochondrial fusion dynamics (Motori et al., 2020). GPT2's unique support of the TCA cycle may enhance both energetics and biosynthesis to sustain cell growth and this is also evident in smaller neuron soma sizes (e.g. CA1 pyramidal neurons, motor neurons in the spinal cord and motor cortex, noradrenergic neurons) as well as microcephaly seen in both mice and human patients with *GPT2* mutations (Ouyang et al., 2016).

Alpha-ketoglutarate was able to reverse the glutamate deficits in *Gpt2*-null synaptosomes and raise glutamate levels back to that of the wild-type. While it may prove useful to try alpha-ketoglutarate in hippocampal slices to see if glutamate transmission in electrophysiology is rescued, the entry and metabolism of alpha-

ketoglutarate are presumed to be different compared to synaptosomes. Other TCA cycle constituents, such as citrate may be tried as it is readily taken up by neurons and astrocytes (Yodoya et al., 2006).

TCA cycle supplementation *in vivo* is one of the future directions both in terms of rescuing glutamate deficits and also other metabolic derangements. So far, Triheptanoin, the triglyceride of heptanoic acid that can be fed into the TCA cycle via propionyl-CoA, has been tried but failed to rescue survival *in vivo*, however this was most likely due to unpalatability of the diet as it led to decreases in weight in the parents, smaller litter size and smaller stature of the pups. Alpha-ketoglutarate is an option and has been shown to increase lifespan of mice (Asadi Shahmirzadi et al., 2020). As always, first-pass metabolism in the liver is a key complicating problem and the *Gpt2*-null pups have to receive the supplementation early and continuously as the metabolic defects are already apparent at postnatal day 7. Forced feeding is not a practical option, osmotic pumps may be tried but the pups are very young and the procedure may lead to maternal negligence.

Is GPT2 metabolism redundant or essential in neurons?

Given that alanine deprivation leads to death of hippocampal *Gpt2*-null neurons *in vitro* and that SynapsinI-cre conditional *Gpt2*-null mice die the same way as the germline *Gpt2*-null mice, we can safely conclude that GPT2 function in neurons is essential. Astrocytes do not share this dependency on GPT2 as their growth and survival are not impaired in the absence of GPT2 *in vitro* and GFAP-cre conditional astrocyte-specific deletion of *Gpt2*-null mice does not lead to premature death *in vivo*.

Most likely, the functions of GPT2 and GPT1 are not redundant and their individual importance arise from differential expression in various cell types and not so much from compartmentation within different subcellular locations in the same cell. While such compartmentation is crucial for metabolic enzymes such as cytosolic and mitochondrial aspartate aminotransferases within the malate-aspartate shuttle (Berkich et al., 2007; Borst, 2020), no such shuttling has been reported for alanine within the cell, nor any emphasis on presence of the two GPT isoforms in the same cell. This joining of forces of GPT2 and GPT1 may exist in astrocytes (Figure 3) and recently, a candidate gene for a mitochondrial serine/alanine transporter has been published (Kory et al., 2018).

How is the animal behavior affected after GPT2 loss? Are there specific regions in the central nervous system with selective vulnerability to GPT2 loss?

As most humans with *GPT2* mutations suffer from progressive spastic paraplegia, wide gait, and hyperreflexia, we were expecting that *Gpt2*-null mice would re-capitulate the motor abnormalities. Indeed, *Gpt2*-null mice display wide gait and clasping reflex in the hind limbs, however, studies of any progressive nature in motor dysfunction would not be possible because all *Gpt2*-null mice die before post-natal day 30. High Alanine diet allows us to observe progression of the motor dysfunction in *Gpt2*-null mice as they age. At around two to three months, they almost completely lose their ability to walk on all four paws. Motor defects also manifest in neuropathology as reduced number and soma size of motor neurons in the spinal cord, along with a prominent astrogliosis in the gray matter. The observation that extra alanine in the diet improved survival but not the

motor function points at a possible need of extra TCA cycle support in the lower motor neurons, given prominent defects in the TCA cycle found both *in vivo* and *in vitro* experiments (Ouyang et al., 2016). The underlying causes of specific vulnerability of motor neurons in the spinal cord to the metabolic damage caused by absence of GPT2 are yet unknown. It is interesting that only a few mutations in mitochondrial proteins have been reported to cause spastic paraplegia (Blackstone, 2018). This study identifies GPT2 as a key metabolic mitochondrial protein in a mouse model of spastic paraplegia with motor abnormalities.

Smaller soma sizes and loss of spinal cord motor neurons have been observed in other neurological diseases including amyotrophic lateral sclerosis (ALS) (Taylor et al., 2016). Indeed, genetic mutations in SPG11, or Spatacsin, a spastic paraplegia gene, also cause spinal cord motor neuron death (Stevanin et al., 2008). Hereditary spastic paraplegia has been attributed to upper motor neuron degeneration due to greater energetic and biosynthetic demand of long-ranging axons (Blackstone, 2018). While we do not observe any degeneration or cell loss in primary motor cortex of *Gpt2*-null mice, the soma sizes of the layer 5 neurons are reduced, suggesting that GPT2 acts on similar mechanisms of neuronal growth in both upper and lower motor neurons. More in-depth analysis of upper motor neurons is warranted. Whether the loss of lower motor neurons in *Gpt2*-null mice occurs cell-autonomously or whether any other circuitry in the brain is as affected in the *Gpt2*-null mice remain to be explored. Importantly, a majority of mouse models of spastic paraplegia show motor disability without death of upper motor neurons (Blackstone, 2018; Salinas et al., 2008). Interestingly, one recent case report of a patient

with GPT2 Deficiency has demonstrated motor neuropathy consistent with our findings of loss of lower motor neurons in the mouse model (Ruaud et al., 2021).

We see damage in another area of the nervous system in *Gpt2*-null mice, locus coeruleus (LC). Since LC is implicated in Alzheimer's and Parkinson's Disease, much work has been done in humans and disease models; however the exact mechanisms by which this locus degenerates are unknown. This should not be said lightly; there is no consensus on how the LC neurons die, whether it be regarding the neuromelanin levels, oxidative stress or relative metal compositions. GPT2 Deficiency may provide a mechanistic venue for studying metabolic damage in LC and in doing so may help with therapeutics in Alzheimer's and Parkinson's Disease.

Since GPT2 is closely linked to motor function, one might ask whether there is any causality between LC damage in *Gpt2*-null mice and the motor abnormalities. Locus coeruleus projects to virtually the entire central nervous system and descending noradrenergic tracts have been shown to influence motor function (Amaral and Sinnamon, 1977; Foote et al., 1983; Harro et al., 2008; Kwasniewska et al., 2020; Loughlin et al., 1986; Rekling et al., 2000). Examples of motor abnormalities have been correlated with LC. Norepinephrine loss has been found to cause stronger motor deficits than MPTP treatment (resulting in almost complete loss of substantia nigra dopaminergic neurons) on its own (Rommelfanger et al., 2007). KIF5a deficiency, a type of spastic paraplegia (SPG10), presents with decreases in cerebrospinal fluid levels of 3-methoxy-4-hydroxyphenylglycol, a noradrenergic metabolite (Andreasson et al., 2019). More mechanistic studies are warranted to determine whether motor deficits seen in GPT2 Deficiency are linked primarily to defects of noradrenergic transmission.

One intriguing possibility for the selective vulnerability of LC is the distinct metabolic enzyme and metabolome profile of LC. An intriguing connection between GPT2 Deficiency in human patients and LC metabolism has recently emerged, where Ruaud and co-workers found reduced amount of pterins and homovanilic acid in the cerebrospinal fluid (Ruaud et al., 2021). A decreased level of homovanilic acid, a metabolite of tyrosine metabolism in dopaminergic and noradrenergic neurons, may reflect a secondary consequence of LC dysfunction. A pterin derivative, tetrahydrobiopterin (BH4) acts as a co-enzyme for tyrosine hydroxylase, which is essential for catecholamine synthesis (Ichinose et al., 2013). BH4 is made from dihydrobiopterin by dihydrobiopterin reductase consuming NADPH which is mainly synthesized via the pentose phosphate pathway. NADPH is readily made from glucose 6-phosphate dehydrogenase which is shown to have strong activity in LC of the rat (Amaral and Sinnamon, 1977). The vulnerability in LC may also originate from defective cellular energetics. Biosynthesis of macromolecules using NADPH as co-enzymes depend on a functioning tricarboxylic acid (TCA) cycle (Martinez-Reyes and Chandel, 2020). We have shown previously that TCA cycle intermediates are profoundly diminished in *Gpt2*-null brain. Metabolic studies in LC may allow us to explore the extent of metabolic mechanisms implicated by loss of GPT2.

BH4 is also used as a co-enzyme for nitric oxide synthase, the activity of which has been shown to modulate oxidative stress in LC (Higgins and Gross, 2010; Sanchez-Padilla et al., 2014). In the absence of BH4, electron transport from NADPH to heme, normally facilitated by BH4 in nitric oxide synthase, may be uncoupled leading to an increase in leakage to molecular oxygen causing an increase in superoxide anion.

Increased pacemaking activity may also lead to increases in Ca^{2+} levels leading to more oxidative stress and possibly apoptosis. Oxidative stress has been studied in LC vulnerability particularly in the context of neuromelanin and heavy metals (Zecca et al., 2004a; Zecca et al., 2004b). Detailed studies of metabolic pathways involved in oxidative stress in LC are warranted.

There have been other studies in animal models of Alzheimer's, Parkinson's, Rett syndrome and Down syndrome in addition to a study that involves genetic ablation of the mitochondrial sirtuin T3 that have been shown to cause degeneration, cell loss or gliosis in LC, however, these studies do not give a clearly defined degeneration of LC. To our knowledge, our study is the first to provide strong microgliosis and degeneration in LC in an animal model of a metabolic disease. Studies of GPT2 Deficiency and the link to deficits in LC may provide us clues as to why this locus is vulnerable and eventually lead to a therapeutic target that may be beneficial to a wide range of neurological diseases.

Does GPT2 have major contributions to synaptic glutamate availability?

Overall, our data suggests that GPT2 does not have a major influence on synaptic glutamate availability as evidenced by slight decreases in glutamate levels which may be explained by compensatory upregulation of other enzymes involved in glutamate metabolism. We report that GPT2 is enriched in the mitochondria of isolated synaptic terminals (synaptosomes) and the loss of GPT2 leads to a re-wiring of glutamate metabolism. GPT2 can be used to produce glutamate with alanine and alpha-ketoglutarate as precursors and to control conversion of glutamine into alanine. According to our data, approximately 40% of the glutamate pool released upon depolarization may come from

alanine in isolated synaptic terminals. It should be noted that “can” is not the same as “does” in a physiological setting. It is possible that GPT2 may reverse the reaction in favor of glutamate formation when enough substrates are available, however given that there are modest decrease in glutamate, GPT2 is unlikely to play a major rate-determining enzyme for synaptic glutamate synthesis.

The impaired glutamatergic transmission in mouse brain slices is evident in miniature excitatory current amplitude and faster decline of amplitude response in CA1 pyramidal neurons to repeated stimulation of CA3 Schaffer collaterals. The rest of Chapter 4 provides evidence that reprogramming of glutamate metabolism to support the TCA cycle is most likely the culprit behind decreases in glutamate. It is crucial to keep in mind that different types of synapses may rely on GPT2 differently (e.g. tripartite synapses).

Do any of the findings with GPT2 Deficiency in mice correlate with any phenotype in a cancerous cell line? i.e. is there a ubiquitous mechanism of cellular growth?

Gpt2-null HAP1 cells have smaller cell sizes and their rate of division is reduced with alanine deprivation. Their metabolomic profile contains similarities with those of *Gpt2*-null whole brain and hippocampus tissues, particularly in alanine, TCA cycle intermediates, and several of the amino acids. Therefore, HAP1 cell line may provide a useful and fast way for biochemical assays *in vitro*. Overall, it appears that GPT2 has a ubiquitous function across different cell types in controlling cellular growth and maintenance.

In summary

Recessive loss-of-function mutations in the mitochondrial enzyme glutamate pyruvate transaminase 2 (*GPT2*) in humans cause reduced postnatal brain growth, and cognitive and motor disability. *GPT2* catalyzes the reversible addition of an amino group from glutamate to pyruvate, yielding alanine and alpha-ketoglutarate. We demonstrate that *GPT2* governs critical metabolic mechanisms in neurons required for neuronal growth and survival in a mouse model of *GPT2* Deficiency. These metabolic processes include neuronal alanine synthesis and anaplerosis, the replenishment of tricarboxylic acid (TCA) cycle intermediates. By targeted metabolomics, we find alterations in alanine levels to occur earliest, followed by reduced TCA cycle intermediates and reduced pyruvate. Neuron-specific deletion of *Gpt2* in mice is sufficient to cause motor abnormalities and death pre-weaning, a phenotype identical to the germ-line *Gpt2*-null mouse. Alanine biosynthesis is profoundly impeded in *Gpt2*-null neurons. Exogenous alanine is necessary for *Gpt2*-null neuronal survival *in vitro* but is not needed for *Gpt2*-null astrocytes. Dietary alanine supplementation in *Gpt2*-null mice enhances animal survival. In surviving *Gpt2*-null animals, we observe smaller upper and lower motor neurons *in vivo*. We observe selective death of lower motor neurons *in vivo* with worsening motor behavior with age. *GPT2* Deficiency also involves a novel mechanism of degeneration, gliosis, and neuron loss in locus coeruleus with reduced noradrenergic projections to and norepinephrine levels in hippocampus and spinal cord in *Gpt2*-null mice. We report that *GPT2* is enriched in isolated synaptic terminals and *GPT2* loss leads to reprogramming of glutamate metabolism. Glutamatergic transmission in *Gpt2*-null CA1 hippocampal slices is impaired. Glutamate levels released from *Gpt2*-null isolated nerve terminals are reduced but restored to wild-type levels by alpha-ketoglutarate. These

studies of the pathophysiology of GPT2 Deficiency have identified metabolic mechanisms that are required for neuronal growth and that may underlie selective vulnerabilities in specific neuronal circuits. Alanine or TCA cycle supplementation may also prove useful as therapeutic targets in patients with GPT2 Deficiency.

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ROLE OF GPT2 in NEUROMETABOLISM

GPT2 DEFICIENCY

How does the pathogenic metabolome progress over time?

- Alanine & TCA cycle metabolism defects followed by increases in amino acids metabolism and glycolytic intermediates

How is the animal behavior affected after Gpt2 loss?

- Premature death by weaning, failure to thrive, wide hind-limb gait, hind-limb clasp reflexes.

Does Gpt2 confer the ability to synthesize alanine in the cells, i.e. non-essentiality of alanine?

- In neurons yes; alanine deprivation causes neuronal death in vitro.
- In astrocytes, alanine deprivation does not cause death in vitro.
- In vivo supplementation increases chances of animal survival.

Is Gpt2 metabolism redundant or essential in neurons?

- Essential. Animal behavioral and motor phenotype are present in Synapsin1-cre conditional Gpt2-null mouse.
- In vitro assays shows increased neuronal death after alanine deprivation.

Is the TCA cycle affected after the loss of Gpt2? If so, does it occur in neurons or astrocytes or both?

- Glutamine-dependent anaplerosis in Gpt2-null neurons and astrocytes is diminished.

Are there specific regions in the central nervous system with selective vulnerability to Gpt2 loss?

- Death of motor neurons in the spinal cord at P90
- Death of locus coeruleus neurons at P18

Would either alanine or TCA cycle supplementation alleviate/prevent metabolic or behavioral defects, i.e. may they be rescue strategies?

- In vivo alanine supplementation increases chances of animal survival.
- Alpha-ketoglutarate rescues glutamate defects in synaptosomes.

Does Gpt2 have major contributions to synaptic glutamate availability?

- Modest decreases in synaptic glutamate.
- Reprogramming of glutamate metabolism.

Chapter 2&3

Chapter 4

Chapter 5

Chapter 6

Do any of the findings with Gpt2 deficiency in mice correlate with any phenotype in a cancerous cell line? i.e. is there a ubiquitous mechanism of cellular growth?

- Smaller cell size.
- Similar metabolic profile.
- Reduced division rate with alanine deprivation.

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Appendix 3.1. Chemical panel of Gpt2-null serum at P18.

Introduction

We performed a chemical panel on the serum of Gpt2-null mice at postnatal day 18 (P18) to identify any pathological biomarkers present in the blood. The serum chemical panel included:

- a) aspartate aminotransferase (AST) and alanine aminotransferase (ALT), both have been used as indicator of liver damage.
- b) total protein
- c) creatine kinase, as an indicator of muscle damage
- d) blood nitrogen urea (BUN)
- e) cholesterol
- f) glucose
- g) bicarbonate (Total CO₂)
- h) triglycerides

Results/Key Points

- No major differences in any metric, except for a decrease in cholesterol levels in Gpt2-null serum at P18. There is also a modest decrease in triglycerides though statistically non-significant ($P = 0.188$).

Discussion

The difference in cholesterol is slight but could reflect decreases in lipid synthesis in Gpt2-null mice. The origin of this deficit is yet unclear.

Method

The serum was collected terminally by cardiac puncture after injection of sodium pentobarbital. The blood was collected in mini-SST gold tubes (IDEXX) with clot activator and gel barrier. The blood was inverted 10 times, incubated for 20 minutes, and spun at 2500 x g for 12 minutes. The serum was collected in a separate tube and stored at -80°C until day of shipment. The chemical panel was performed at IDEXX BioResearch (North Grafton, MA).

Figure Legends

Figure – Serum chemical panel in Gpt2-null mice at postnatal day 18.

A. Different measures in the chemical panel in wild-type (black) and Gpt2-null (red) mice at P18. AST: aspartate aminotransferase, ALT: alanine aminotransferase, BUN: blood nitrogen urea. n=4 wild-type (3 females, 1 male), n=6 Gpt2-null (4 females, 2 males).

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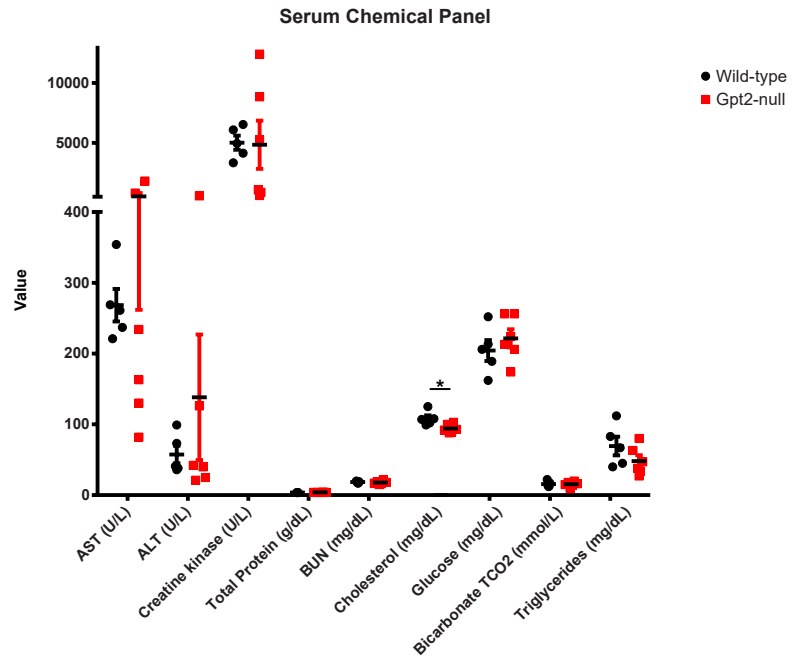


Figure A3.1 – Serum chemical panel in Gpt2-null mice at postnatal day 18.

Appendix 3.2. H&E stains in Gpt2-null muscle tissue at P18.

Introduction

Gpt2 is expressed in brain tissue as well as in skeletal muscle (Lindblom et al., 2007). Gpt2-null mice display motor abnormalities with abnormal wide hind-limb gait and smaller stature. It is possible that there is muscle wasting. The H&E stains in gastrocnemius and soleus muscle of the hind-limb of wild-type and Gpt2-null at postnatal day 18 (P18) are presented here.

Results/Key Points

- No major differences in the staining in either gastrocnemius or soleus muscle of the hind-limb in Gpt2-null mice at P18.

Discussion

It is still possible that there is decreased innervation on the muscle originating from the spinal cord, investigation of the neuromuscular junction may address this possibility.

Method

The mice were transcardially perfused with 1X PBS and then 4% paraformaldehyde. Paraffin sections were obtained of the muscle tissue and standard H&E staining was performed by Charles River Laboratories (Shrewsbury, MA).

Figure Legends

Figure A3.2. – H&E stains in gastrocnemius and soleus muscle of the hind-limb in wild-type and Gpt2-null mice at P18.

A. H&E stains in gastrocnemius (top) and soleus (bottom) muscle of the hind-limb in wild-type

(left) and Gpt2-null (right) mice at P18.

References

Lindblom, P., Rafter, I., Copley, C., Andersson, U., Hedberg, J.J., Berg, A.L., Samuelsson, A., Hellmold, H., Cotgreave, I., and Glinghammar, B. (2007). Isoforms of alanine aminotransferases in human tissues and serum--differential tissue expression using novel antibodies. *Arch Biochem Biophys* 466, 66-77.

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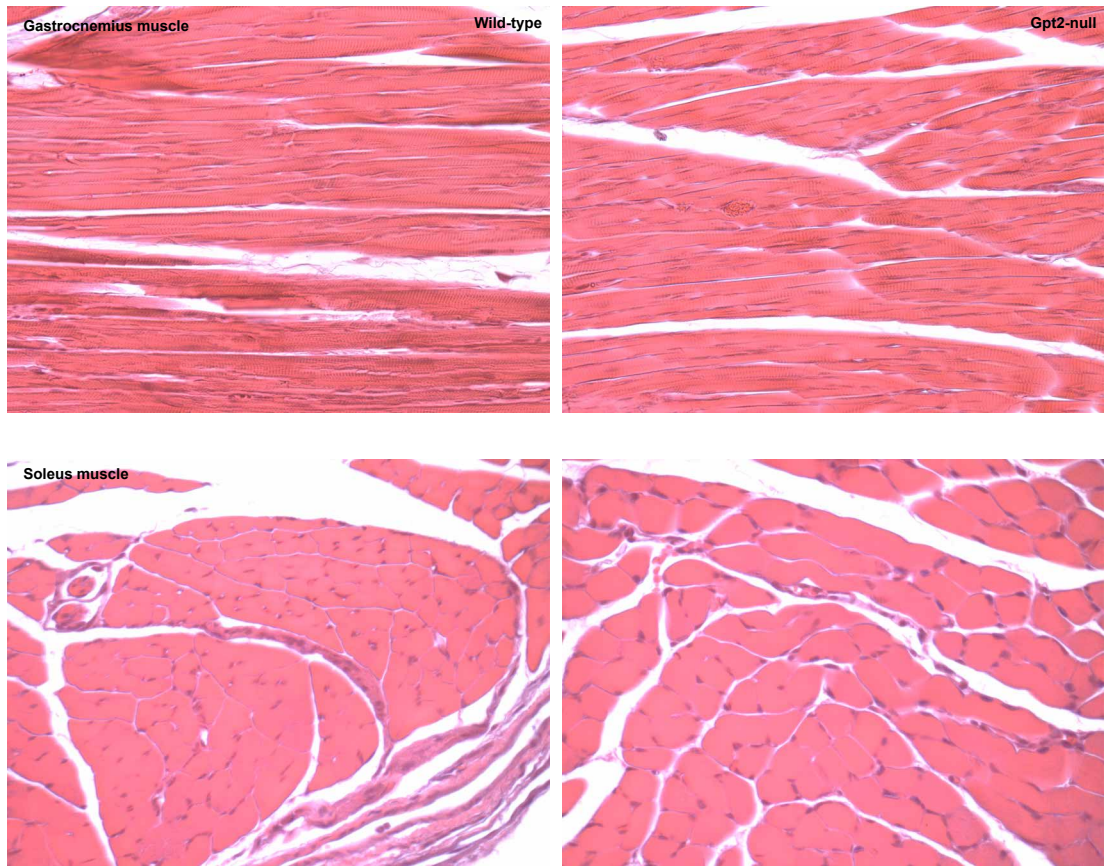


Figure A3.2 – H&E stains in gastrocnemius and soleus muscle of the hind-limb in wild-type and Gpt2-null mice at P18.

Appendix A3.3. Survival and behavior data on additional conditional deletion lines.

Introduction

I tested for phenotypic effects of other conditional deletion (cko) of Gpt2 in specific cell types in vivo. The aims of trying different Cre driver lines to delete Gpt2 in specific cells are to determine if Gpt2-cko mice survive past weaning age and to identify circuits that are most vulnerable to Gpt2 deficiency. As Gpt2-null and SynapsinI-Cre cko mice die just before weaning (postnatal day 21), it would be pertinent to pinpoint exactly in which neuron circuit the Gpt2 deletion leads to premature death. The selective vulnerabilities of different circuits may underlie the pathophysiology of Gpt2 deficiency.

The following Cre driver lines are used:

- 1) **CamKII-Cre** (Jax Strain No.: 005359): Allows for deletion of Gpt2 in excitatory pyramidal neurons mostly in the forebrain. As SynapsinI-Cre was pan-neuronal, CamKII-Cre can answer the question of whether the excitatory neurons in the forebrain are responsible for the premature death phenotype.
- 2) **Rbp4-Cre** (MMRRC Strain No.: 037128): Allows for deletion of Gpt2 in layer 5 pyramidal neurons. This is particularly useful in investigating whether Gpt2 deficiency specifically in motor neurons in the cortex would lead to motor abnormalities.
- 3) **Gfap-Cre** (Jax Strain No.: 024098): Allows for deletion of Gpt2 in astrocytes. This may provide contrast between the necessities for Gpt2 function in neurons versus astrocytes within the context of animal survival and motor behavior.

4) **Rosa26-CreERT2** (Jax Strain No.: 008463): Allows for tamoxifen-inducible time-controlled deletion of Gpt2 in the body. This may answer the question of whether Gpt2 is needed only developmentally or in the adult body as well.

Results/Key Points

- All tested strains of conditional Gpt2-null mice survived past weaning age with no overt abnormalities (motor, gross body anatomy). All mice have been observed until 6 months of age.

Available Data (not shown):

1. CamKII-Cre: Agarose gel electrophoresis showing genomic excision in the cortex, hippocampus (to a lesser degree, spinal cord tissues) and absence of excision in hind-limb muscle, liver, kidney and tail; Open Field Tests; Videos showing absence of Hind-limb clasping reflex; Number of mice that survived.
2. Rbp4-Cre: Agarose gel electrophoresis showing genomic excision in the cortex, hippocampus and liver and absence of excision in spinal cord, hind-limb and fore-limb muscle, tail; Open Field Tests; Number of mice that survived.
3. Gfap-Cre: Number of mice that survived.
4. Rosa26-CreERT2: Agarose gel electrophoresis showing genomic excision in the cortex, hippocampus, liver, kidney and tail. Western Blotting for Hippocampus and Cortex

Discussion

Interpretation of the results from each of the strains (with the associated complications):

1. CamKII-Cre: The expression starts around P4 and later increases to adult levels within first three weeks of life [1] whereas Synapsin-I Cre expression starts at embryonic day 12.5 [2]. Therefore one cannot rule out the possibility of the influence of the developmental timeframe on the effects of the Gpt2 deletion in excitatory neurons. More likely is the interpretation that the Gpt2 deletion in excitatory pyramidal neurons is not sufficient to cause premature death or motor abnormalities.
2. Rbp4-Cre: The expression starts around embryonic day 16.5. However, Rbp4 promoter is present in the brain and the liver (as evident in the PCR results showing genomic excision). Gpt2 is expressed in the liver and most likely this would have contributed to the phenotype. However, the conditional Gpt2-null mice had no phenotype, suggesting Gpt2 deletion in neither the liver nor layer 5 pyramidal neurons is sufficient to cause premature death or motor abnormalities.
3. Gfap-Cre: The expression has not been observed embryonically and only postnatally [3] so the possibility of the influence of the developmental timeframe cannot be ruled out. More likely is the interpretation that the Gpt2 deletion in astrocytes is not sufficient to cause premature death or motor abnormalities.
4. Rosa26-CreERT2: While all tested tissues had genomic excision, it was not 100% (i.e. the floxed allele was still detected. It is not feasible to determine to what extent the excision occurred, in which cell types or brain regions.

One technical complication for all conditional null models is that we lack the antibody for Gpt2 that works in mouse brain tissues. This prevents us from detecting absence of the protein in specific cell types.

Method

Genomic excision – PCR.

The excision of Exon 4 by Cre recombinase was tested by PCR with the following primers: ExcF (5'-CTAACTTGTCCTGCATGGTGTCAGC-3') and ExcR (5'-GGCTTTCTACCAGGAGGAACAGAGG-3') detecting the floxed allele (1479bp), the wild-type allele (1347bp) or the excised allele (687bp).

References

1. Tsien, J.Z., D.F. Chen, D. Gerber, C. Tom, E.H. Mercer, D.J. Anderson, M. Mayford, E.R. Kandel, and S. Tonegawa, *Subregion- and Cell Type–Restricted Gene Knockout in Mouse Brain*. *Cell*, 1996. **87**(7): p. 1317-1326.
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3. Gregorian, C., J. Nakashima, J. Le Belle, J. Ohab, R. Kim, A. Liu, K.B. Smith, M. Groszer, A.D. Garcia, M.V. Sofroniew, et al., *Pten deletion in adult neural stem/progenitor cells enhances constitutive neurogenesis*. *J Neurosci*, 2009. **29**(6): p. 1874-86.

Appendix 3.4. Data on additional diets and survival of SynapsinI-Cre conditional mice on high alanine diet.

I have tested other diets to improve the phenotype in Gpt2-null mice:

- 1. High Fat & High Alanine Diet (w/w 19% Lard, 5% Alanine TD.200002):** High fat diet may allow the pups to gain weight more easily (the diet induces obesity). While the Gpt2-null mice can survive past P30, they still failed to thrive and had motor abnormalities. I observed ten mice, only three survived up to two months, a fraction that is similar to that obtained from High Alanine diet (TD.190381). TD.200002 is a modified version of TD.06415. I terminated this experiment as it yielded unsatisfactory results and the breeding pair would get fatter and the progeny yield would decrease over time.
- 2. Triheptanoin Diet (w/w 23%Triheptanoin, TD.190870):** Triheptanoin is a triglyceride of heptanoic acid. Triheptanoin is metabolized in the liver and results in heptanoic acid (odd-carbon chain fatty acid that is converted into propionic acid) which may be used to replenish the TCA cycle (i.e. an anaplerotic supplement). It has been used in treatment of fatty acid oxidation disorders, glucose transporter 1 deficiency and pyruvate carboxylase deficiency. However, the mice did not tolerate this diet well. Their litter sizes were very low (2-4 pups per litter) and even the wild-type pups looked skinnier than the pups on the Regular diet. There were 5 Gpt2-null mice observed and none survived past weaning age. I terminated this experiment thereafter. TD.190870 is a modified version of TD.99366.
- 3. Triheptanoin with High Alanine (w/w 23%Triheptanoin, 5% Alanine, TD.190871):** I tested the combination of the two supplements. The results were similar to those of TD.190870.

4. **High Alanine (w/w 5 %) diet on SynapsinI-Cre mouse (TD.190381):** SynapsinI-Cre conditional Gpt2-null mouse would have absence of Gpt2 protein in neuronal cells and nowhere else. I tested whether this would improve survival fraction along with High Alanine diet. This was not the case. 12 out of 12 conditional Gpt2-null mice did not survive past weaning age. This is most likely due to metabolism of alanine in the liver as Gpt2 is present in the liver.

The breeding pairs on the special diets were started when the mice were two months old and the diet was given ad libitum. The strain background is C57B6/J (Jax Strain No 664).

Appendix 3.5. Immunohistochemistry in Spinal cord for various stains in Gpt2-null mice at P90 (high alanine diet): Cleaved Caspase3 (CC3), myelin basic protein (MBP), protein kinase C γ (PKC γ), neurofilament H (NFH), NG2, Olig2, SV2, VGLUT1, VGLUT2, VGAT, MTCO1, glutamate dehydrogenase (GDH), glutamine synthetase (GLUL), glucose transporter 1 (GLUT1).

Introduction

Immunohistochemical analysis in Gpt2-null spinal cord at postnatal day 90 (fed High Alanine diet, 5% w/w). The following proteins are tested, and the corresponding processes or hypotheses are listed:

Cleaved Caspase 3 (CC3): Cell death by apoptosis; death of motor neurons may explain dysfunction in the motor behavior seen in Gpt2-null mice.

Myelin Basic Protein (MBP): deficits in myelination or ascending/descending tracts.

Protein Kinase C γ (PKC γ): Specifically expressed in descending corticospinal tracts and the dorsal horn. Long projections of corticospinal tracts may be more vulnerable to damage.

Neurofilament H (NFH): General assessment of neuronal processes, particularly axons.

NG2: A marker for oligodendrocyte precursor cells. Oligodendrocyte precursor cells appear to have the highest number of fragments per kilobase of transcript per million

mapped reads (FPKM) as per the RNA-sequencing data done by (Zhang et al., 2014). It is possible that these cells may be particularly vulnerable to Gpt2 loss.

Olig2: A marker for oligodendrocytes. This would exclude the possible involvement of any problems in the number of oligodendrocytes.

SV2: A general marker for synaptic vesicles. We see reductions in SV2 puncta in Gpt2-null hippocampal neurons in vitro.

VGLUT1: An isoform of vesicular glutamate transporter on synaptic vesicles. We observe a slight upregulation of VGLUT1 in Gpt2-null synaptosomes; this may occur in spinal cord tissue as well. Both ascending and descending tracts in the spinal cord contain VGLUT1, any major absences of VGLUT1 puncta may indicate damage to those tracts or neurons that give rise thereto.

VGLUT2: An isoform of vesicular glutamate transporter on synaptic vesicles. Similar to VGLUT1, both ascending and descending tracts in the spinal cord contain VGLUT2, however differences in staining patterns with VGLUT1, may localize any potential abnormalities to a specific tract or nucleus in the spinal cord.

VGAT: A marker for synaptic vesicles containing 4-aminobutyric acid (GABA). We observe three-fold increases in protein levels in Gpt2-null synaptosomes. While we do

not know how this increase occurs, it may uniformly occur across the central nervous system in Gpt2-null mice.

MTCO1: Cytochrome c oxidase subunit 1, a marker of mitochondria. This may reveal problems of mitochondrial biogenesis. As Gpt2 loss results in deficits in the TCA cycle, mitochondrial biogenesis or shape (fission/fusion) may be altered and this may partly contribute to the pathological phenotype.

Glutamate dehydrogenase (GDH): A mitochondrial enzyme that converts glutamate into alpha-ketoglutarate and ammonia. GDH is an anaplerotic enzyme, meaning that it catalyzes a reaction that results in a net production of a TCA cycle intermediate. In the absence of Gpt2, GDH may be upregulated as a compensatory mechanism to support the TCA cycle, this is seen in Gpt2-null synaptosomes.

Glutamine Synthetase (GLUL): A cytosolic enzyme located mainly in astrocytes, that converts glutamate into glutamine. Up-regulation of this enzyme has been seen in animal models of epilepsy and in our data, in Gpt2-null synaptosomes.

Glucose Transporter 1 (GLUT1): A glucose transporter located mainly in endothelial cells that constitute the blood brain barrier. TCA cycle deficits in the Gpt2-null tissue can lead to upregulation of glucose uptake to support cellular energetics, through increased levels of GLUT1.

Results/Key Points

Table. Proteins stained via immunohistochemistry in Gpt2-null spinal cords at P90.
 “QL”: qualitatively assessed. “-”: no difference.

Marker	Gpt2-null with respect to Wild-type
CC3 (QL)	Positivity in Ventral Horn of Cervical&Lumbar
MBP (QL)	-
NFH	-
PKCγ	Decrease Total Area in Cervical&Lumbar. Worsened phenotype compared to P18 RegDiet.
SV2	Trending decrease in Cervical and Lumbar Dorsal horn, Lumbar Ventral Horn
VGLUT1	-
VGLUT2	Increases in Lumbar Dorsal&Lateral Horn
VGAT	Decrease in Cervical Dorsal Horn. Trending decreases in Lumbar Dorsal Horn
MTCO1	-
NG2 (QL)	-
GLUT1 (QL)	-
GLUL (QL)	-
GLUD	Trending Increase in Lumbar Lateral Horn.
Olig2	Increase in Lumbar Lateral Horn.

Discussion

The most prominent result here is the decreases in PKC γ staining that was also seen in Gpt2-null mice at postnatal day 18 on Regular Diet. This adds credibility to the result. While it is hard to tease the rescuing effects of High Alanine diet, since Gpt2-null mice at P90 have worsened motor abnormalities, a worsened phenotype in all the measures is expected. The reduction in percent area covered by PKC γ is worsened at P90 as a measure of percentage of wild-type. There was no difference between percent areas covered in Gpt2-null P18 and P90, suggesting that most likely the tracts were already severely affected and were not rescued by the diet. However we do not have data on spinal cord taken at an earlier timepoint such as P7 or P14 to deduce whether the tracts formed and then degenerated or did not form properly. It is interesting that the wild-type

cervical PKCg area grew in size at P90 compared to P18 whereas the lumbar PKCg area remained the same. While the two wild-types are at a different age, this suggests that the corticospinal tracts continues to develop during that period (most likely primarily in its myelin sheath).

Cleaved Caspase3 staining did show some positivity in the ventral horn at both cervical and lumbar spinal cord levels in Gpt2-null mice at P90; however the Cleaved Caspase3 signal did not localize with any DAPI signal therefore we are unable to categorize this as a true signal. While almost all animals tested showed similar patterns, we cannot verify the staining completely. We also failed to find any good CC3 staining in the literature for comparison. Furthermore, Fluoro-Jade C staining (another marker for neurodegeneration) failed to show any positivity.

While there are similarities in the results of SV2, VGAT and VGLUT2 staining at P90 compared to Gpt2-null mice at P18 on Regular diet, the results obtained with High alanine diet are relatively less striking or simply not statistically significant. The differences found at P18 on Regular diet were very slight and not as compelling as PKCg so the unremarkable results found in Gpt2-null mice fed High Alanine at P90 are not surprising.

Method

The animals received High Alanine diet (5% w/w) (Diet no. 190381) ad libitum.

Immunofluorescence – Tissue. The tissues from mice were dissected out after transcardial perfusion with 1X PBS – 4% PFA. The tissues were cryoprotected serially with 10%, 20% and 30% sucrose, each incubating overnight at 4°C. The solution was then changed to half by volume sucrose/OCT (Optimal Cutting Temperature, FisherScientific 23-730-571) and gently shaken for 1 hour at 4°C. The tissues were frozen in dry ice/methanol bath and stored at -80°C until day of sectioning at the cryostat. The sections were cut at 30µm thickness. The immunofluorescence protocol was as follows, in order: 3-minute fixing with 4% PFA, 3 5-minute 1X PBS washes, 2-hour blocking in Normal Goat or Donkey Serum (NDS, JacksonImmunoResearch, 017-000-121) with 1% (w/v) Bovine Serum Albumin (FisherScientific BP1600), 0.4% TritonX-100 (Sigma-Aldrich T8787), (if mouse-raised antibody is used: 1-hour incubation with 20 µg/ml AffiniPure Fab Fragment Goat Anti-Mouse IgG (H+L) (AB_2338476) or AffiniPure Fab Fragment Donkey Anti-Mouse IgG (H+L) (AB_2307338) in blocking solution), primary antibody in blocking solution incubation overnight at 4°C, 2 4-minute washes with blocking solution, 3 4-minute washes with 0.4% TritonX-100 in PBS, 2-hour secondary antibody in blocking solution incubation, 2 4-minute washes with blocking solution, 3 4-minute washes with 0.4% TritonX-100 in PBS, 5-minute incubation in DAPI (Invitrogen D1306), 3 5-minute washes with PBS and mounted with Fluoromount G (SouthernBiotech 0100-01). Images were processed and analyzed with ImageJ.

Confocal Microscopy. Olympus FV3000 confocal laser scanning microscope and FluoView software were used (RRID:SCR_017015). Maximum intensity projection of the images was used for the final analysis.

The following macro was used to detect puncta:

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“
run("Z Project...", "projection=[Max Intensity]");
run("Subtract Background...", "rolling=1 disable stack");
run("Enhance Contrast...", "saturated=0.3");
//run("Threshold...");
setAutoThreshold("Moments dark");
run("Convert to Mask", "method=Moments background=dark calculate");
run("Analyze Particles...", "size=0.15-150 circularity=0.50-1.00 display exclude summarize add stack");
dir = getDirectory("image");
name = getTitle();
index = lastIndexOf(name, ".");
if (index!=-1) name = substring(name, 0, index);
name = name + ".xls";
saveAs("Results", dir+name);
saveAs("Measurements", dir+name);
print(dir+name);
“

```

Table. Primary antibodies used in this study.

Antibody	Host Species	Company	Catalog No	Dilution
Neurofilament H	Ch	Millipore	AB5539	1:3200
SV2	Ms	DSHB	SV2-c	1:500
VGAT	Gp	SynapticSystems	131004	1:400
VGLUT1	Gp	Millipore	AB5905	1:1000
Olig2	Rb	abcam	ab109186	1:200
VGLUT2	Gp	SynapticSystems	135404	1:1600
GLUT1	Rb	abcam	ab652	1:250
CCas3	Rb	CellSignaling	9661	1:200
MTCO1	Ms	abcam	ab14705	1:400
GLUD	Rb	Invitrogen	PA5-29492	1:1600
NG2	Rb	Millipore	AB5320	1:200
Glutamine Synthetase	Rb	abcam	ab73593	1:800
MBP	Rat	Novus Biologicals	nb600-717	1:50
ChaT	Gt	Phosphosolutions	315-CHAT	1:400

PKC γ	Rb	abcam	109539	1:400
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Figure Legends

Figure A3.4. Cleaved Caspase 3 staining in spinal cord of Gpt2-null mice at P90 on high alanine diet.

A. Images of cleaved caspase 3 staining in wild-type (left) and Gpt2-null (right) cervical (top) and lumbar (bottom) spinal cords. Scale bar: 100 μ m.

B. Images of cleaved caspase 3 (green), DAPI (cyan), ChaT (choline acetyltransferase, red), NeuN (blue) in Gpt2-null lumbar spinal cord at P90. Scale bar: 50 μ m.

Figure A3.5. Myelin Basic Protein and Protein Kinase C γ staining in spinal cord of Gpt2-null mice at P90 on high alanine diet.

A. Images of myelin basic protein (MBP) staining in wild-type (left) and Gpt2-null (right) cervical (top) and lumbar (bottom) spinal cords. Scale bar: 100 μ m.

B. Images of protein kinase c γ (PKC γ) staining in wild-type (left) and Gpt2-null (right) cervical (top) and lumbar (bottom) spinal cords. Scale bar: 100 μ m. Quantification is given at the bottom. $**0.001 < P < 0.01$.

Figure A3.6. MTCO1 staining in spinal cord of Gpt2-null mice at P90 on high alanine diet..

A. Images of MTCO1 staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Dorsal, lateral and ventral horns are shown. Scale bar: 100 μ m. The quantification is given on the right.

Figure A3.7. Neurofilament H staining in spinal cord of Gpt2-null mice at P90 on high alanine diet.

A. Images of neurofilament H (NFH) staining in wild-type (left) and Gpt2-null (right) cervical (top) and lumbar (bottom) spinal cords. Scale bar: 100 μ m.

B. White boxes placed over to identify different areas of the spinal cord. Box 1: Corticospinal tract 2: laminae 1,2,3 of spinal gray 3: ventral funiculus 4: rubrospinal tract 5: lateral funiculus 6: laminae 10 of spinal gray. Quantification of NFH is given below.

C. Images of the different areas outlined in B.

Figure A3.8. NG2 and Olig2 staining in spinal cord of Gpt2-null mice at P90 on high alanine diet.

A. Images of NG2 staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Dorsal, lateral and ventral horns are shown. Scale bar: 100 μ m.

B. Images of Olig2 staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Scale bar: 100 μ m. The quantification of Olig⁺ cell counts is given at the bottom. *0.01 < *P* < 0.05.

Figure A3.9. SV2 staining in spinal cord of Gpt2-null mice at P90 on high alanine diet.

A. Images of SV2 staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Dorsal, lateral and ventral horns are shown. Scale bar: 100 μ m. The quantification is given on the right.

Figure A3.10. VGAT staining in spinal cord of Gpt2-null mice at P90 on high alanine diet.

A. Images of VGAT staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Dorsal, lateral and ventral horns are shown. Scale bar: 100 μm . The quantification is given on the right. $*0.01 < P < 0.05$.

Figure A3.11. VGLUT1 staining in spinal cord of Gpt2-null mice at P90 on high alanine diet.

A. Images of VGLUT1 staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Scale bar: 100 μm .

Figure A3.12. VGLUT2 staining in spinal cord of Gpt2-null mice at P90 on high alanine diet.

A. Images of VGLUT2 staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Scale bar: 100 μm . The quantification is given on the right. $*0.01 < P < 0.05$.

Figure A3.13. Glutamate dehydrogenase and Glutamine synthetase staining in spinal cord of Gpt2-null mice at P90 on high alanine diet.

A. Images of glutamate dehydrogenase (GLUD) staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Dorsal, lateral and ventral horns are shown. Scale bar: 100 μm . The quantification is given on the right.

B. Images of glutamine synthetase (GLUL) staining in wild-type (left) and Gpt2-null (right) cervical (top) and lumbar (bottom) spinal cords. Scale bar: 100 μ m.

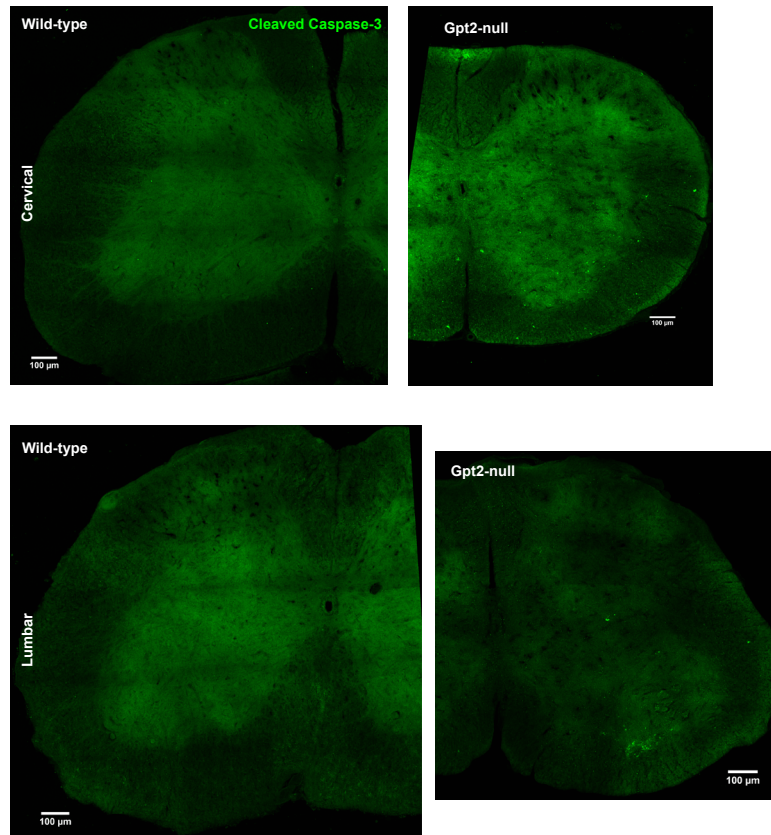
Figure A3.14. Glucose transporter 1 staining in spinal cord of Gpt2-null mice at P90 on high alanine diet.

A. Images of glucose transporter (GLUT1) staining in wild-type (left) and Gpt2-null (right) cervical (top) and lumbar (bottom) spinal cords. Scale bar: 100 μ m.

References

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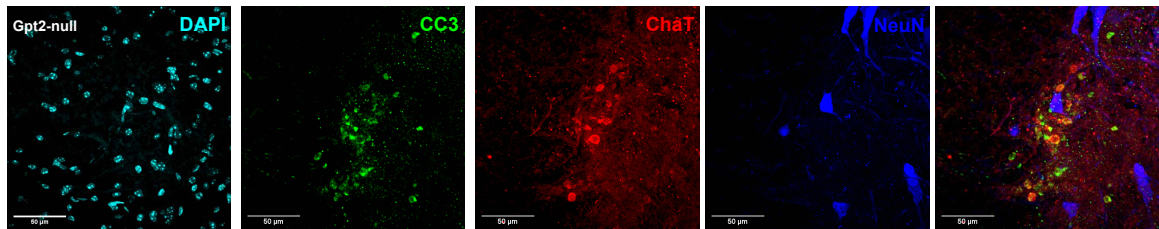


Figure A3.4. Cleaved Caspase 3 staining in spinal cord of Gpt2-null mice at P90 on high alanine diet. A. Images of cleaved caspase 3 staining in wild-type (left) and Gpt2-null (right) cervical (top) and lumbar (bottom) spinal cords. Scale bar: 100 μm. B. Images of cleaved caspase 3 (green), DAPI (cyan), ChaT (choline acetyltransferase, red), NeuN (blue) in Gpt2-null lumbar spinal cord at P90. Scale bar: 50 μm.

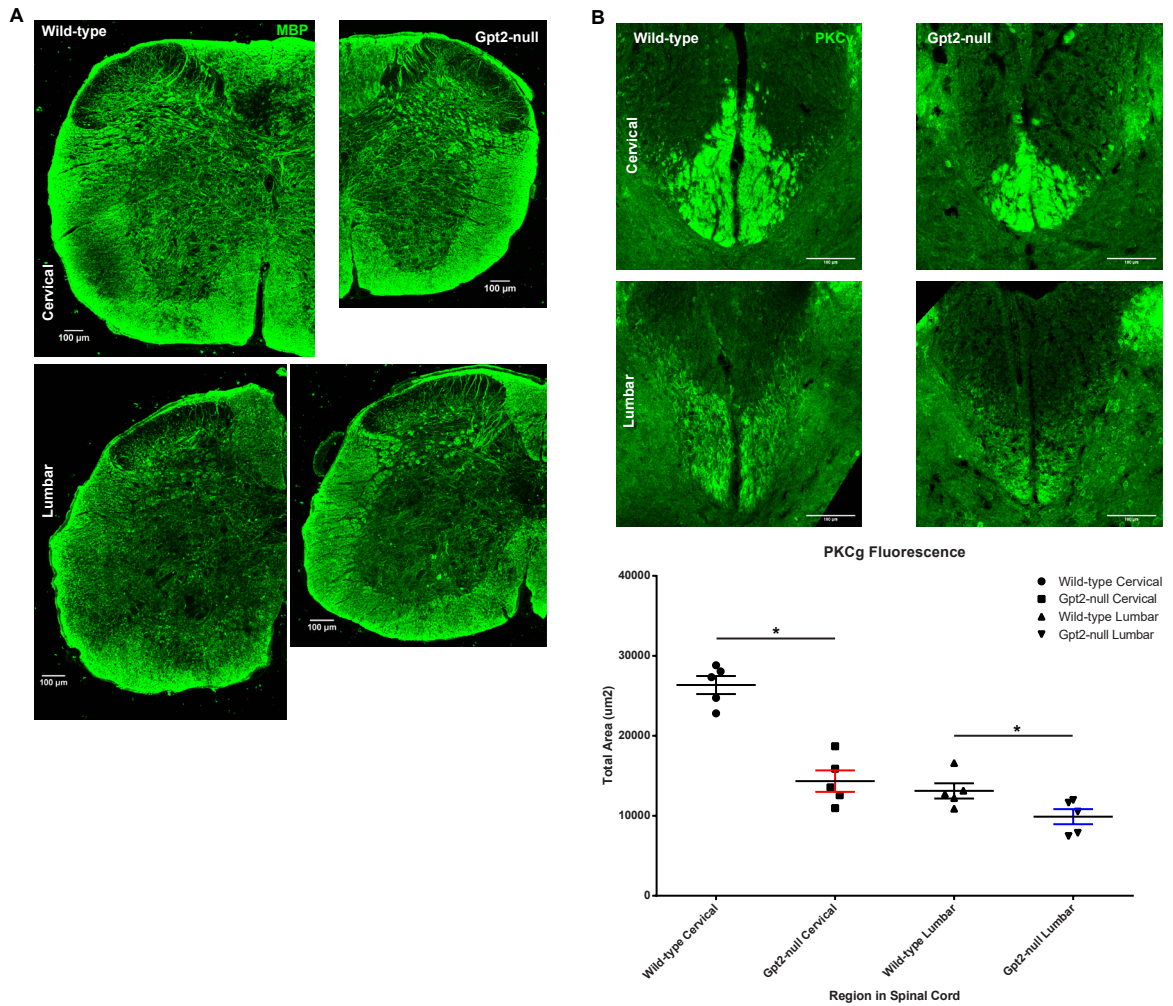


Figure A3.5. Myelin Basic Protein and Protein Kinase C γ staining in spinal cord of Gpt2-null mice at P90 on high alanine diet. A. Images of myelin basic protein (MBP) staining in wild-type (left) and Gpt2-null (right) cervical (top) and lumbar (bottom) spinal cords. Scale bar: 100 μ m. B. Images of protein kinase c γ (PKC γ) staining in wild-type (left) and Gpt2-null (right) cervical (top) and lumbar (bottom) spinal cords. Scale bar: 100 μ m. Quantification is given at the bottom. ****0.001 < P < 0.01.**

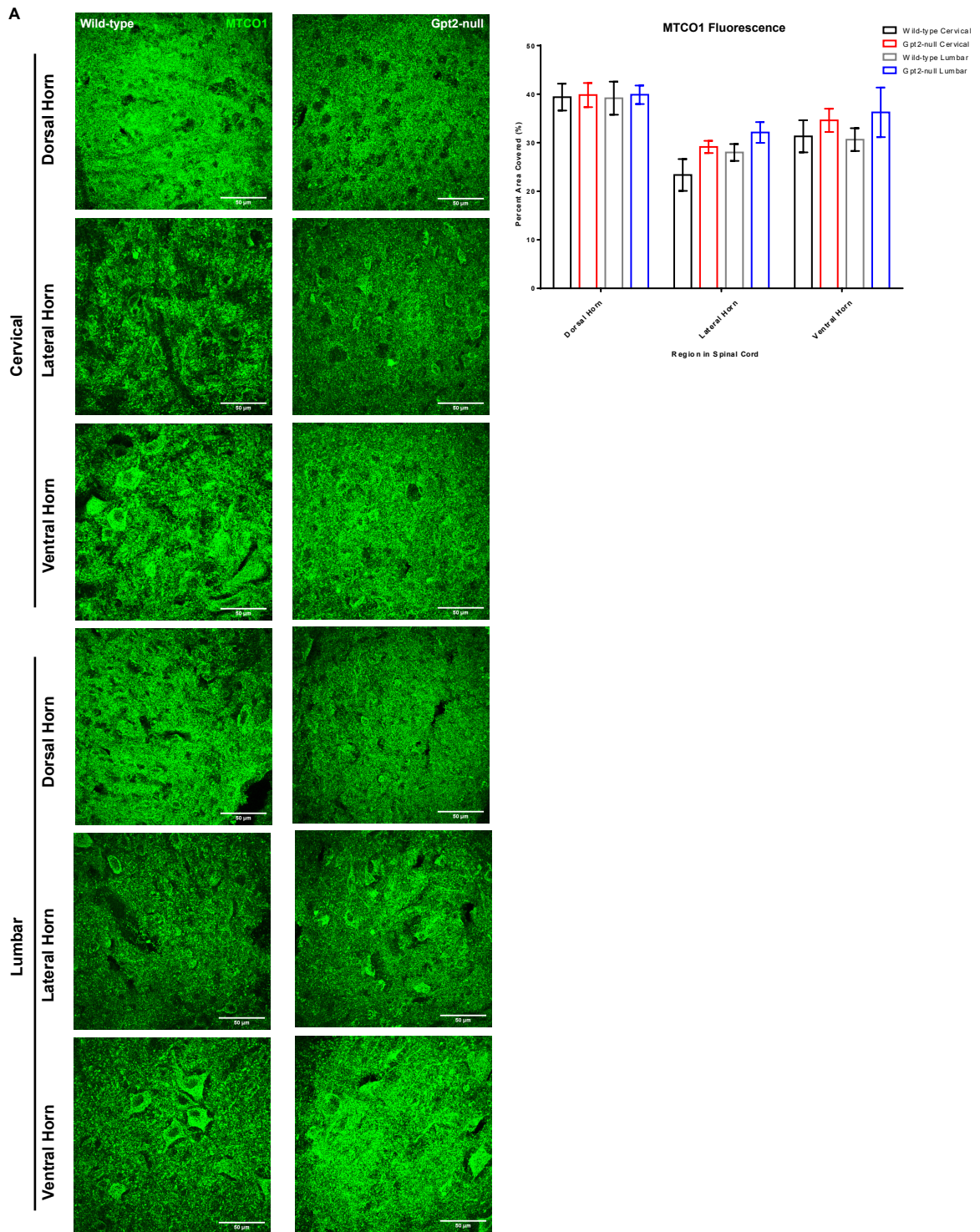


Figure A3.6. MTCO1 staining in spinal cord of Gpt2-null mice at P90 on high alanine diet. A. Images of MTCO1 staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Dorsal, lateral and ventral horns are shown. Scale bar: 100 μ m. The quantification is given on the right.

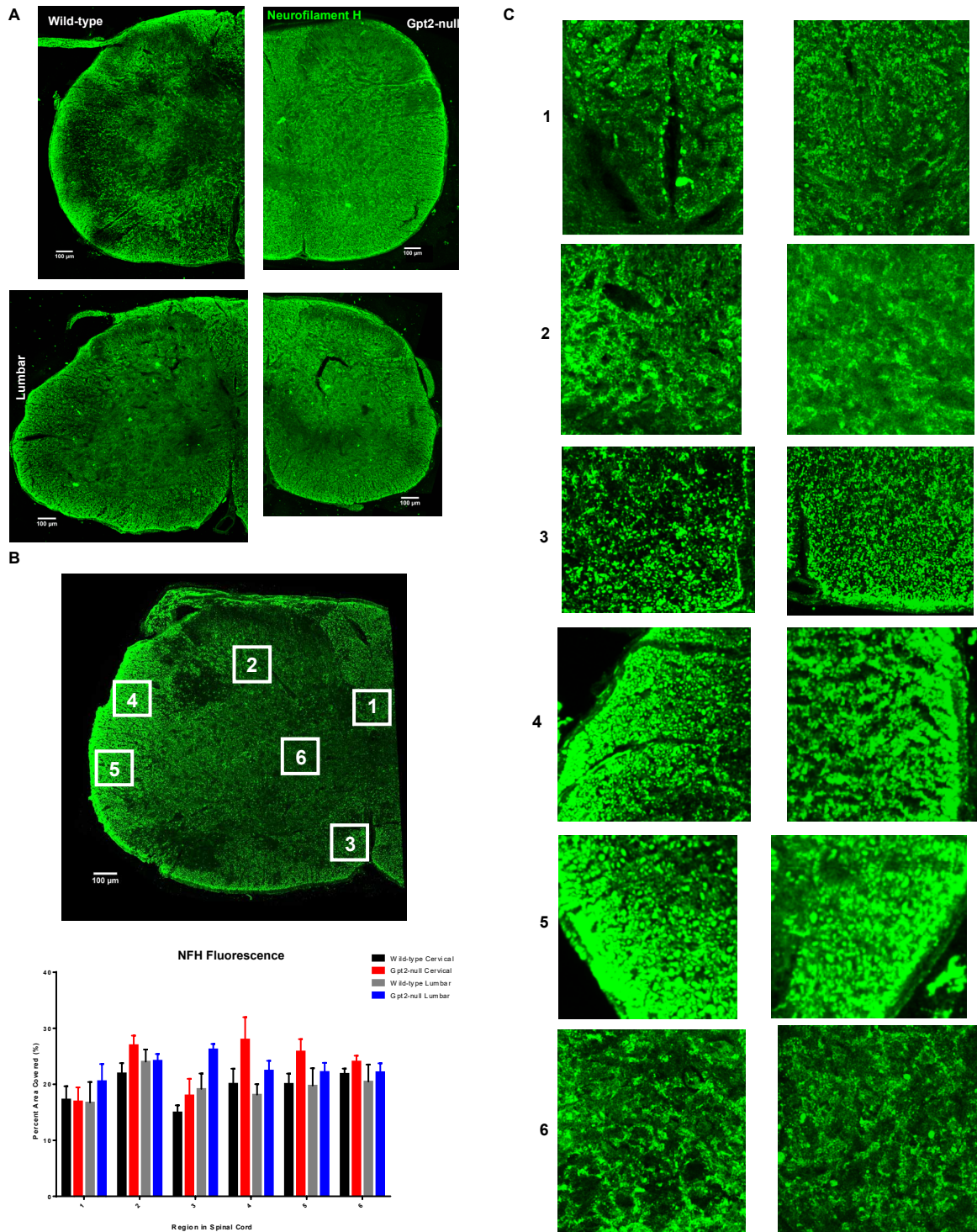


Figure A3.7. Neurofilament H staining in spinal cord of Gpt2-null mice at P90 on high alanine diet.

A. Images of neurofilament H (NFH) staining in wild-type (left) and Gpt2-null (right) cervical (top) and lumbar (bottom) spinal cords. Scale bar: 100 μ m.

B. White boxes placed over to identify different areas of the spinal cord. Box 1: Corticospinal tract
2: laminae 1,2,3 of spinal gray 3: ventral funiculus 4: rubrospinal tract 5: lateral funiculus
6: laminae 10 of spinal gray. Quantification of NFH is given below.

C. Images of the different areas outlined in B.

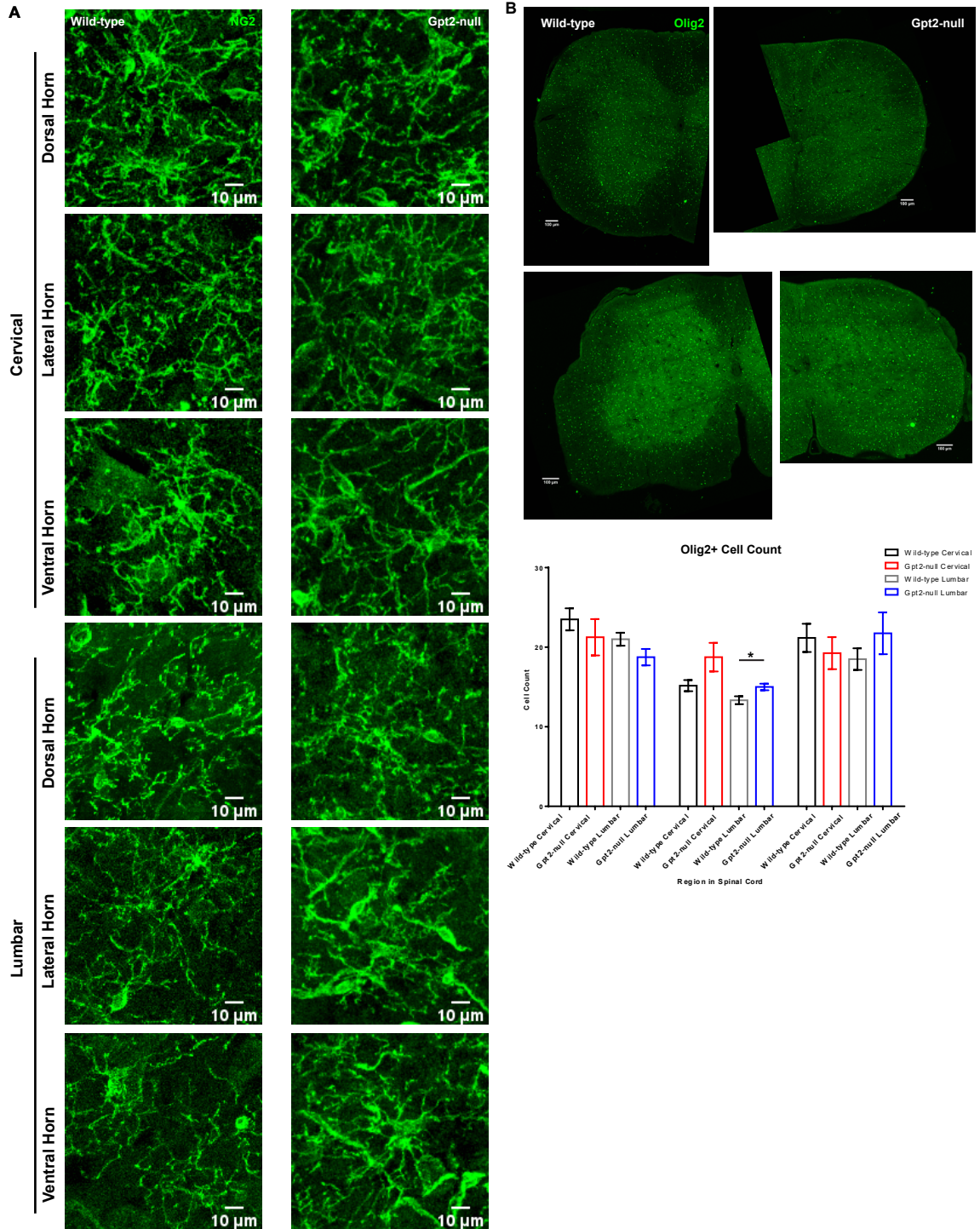


Figure A3.8. NG2 and Olig2 staining in spinal cord of Gpt2-null mice at P90 on high alanine diet.

A. Images of NG2 staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Dorsal, lateral and ventral horns are shown. Scale bar: 100 µm. B. Images of Olig2 staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Scale bar: 100 µm. The quantification of Olig+ cell counts is given at the bottom. *0.01 < P < 0.05.

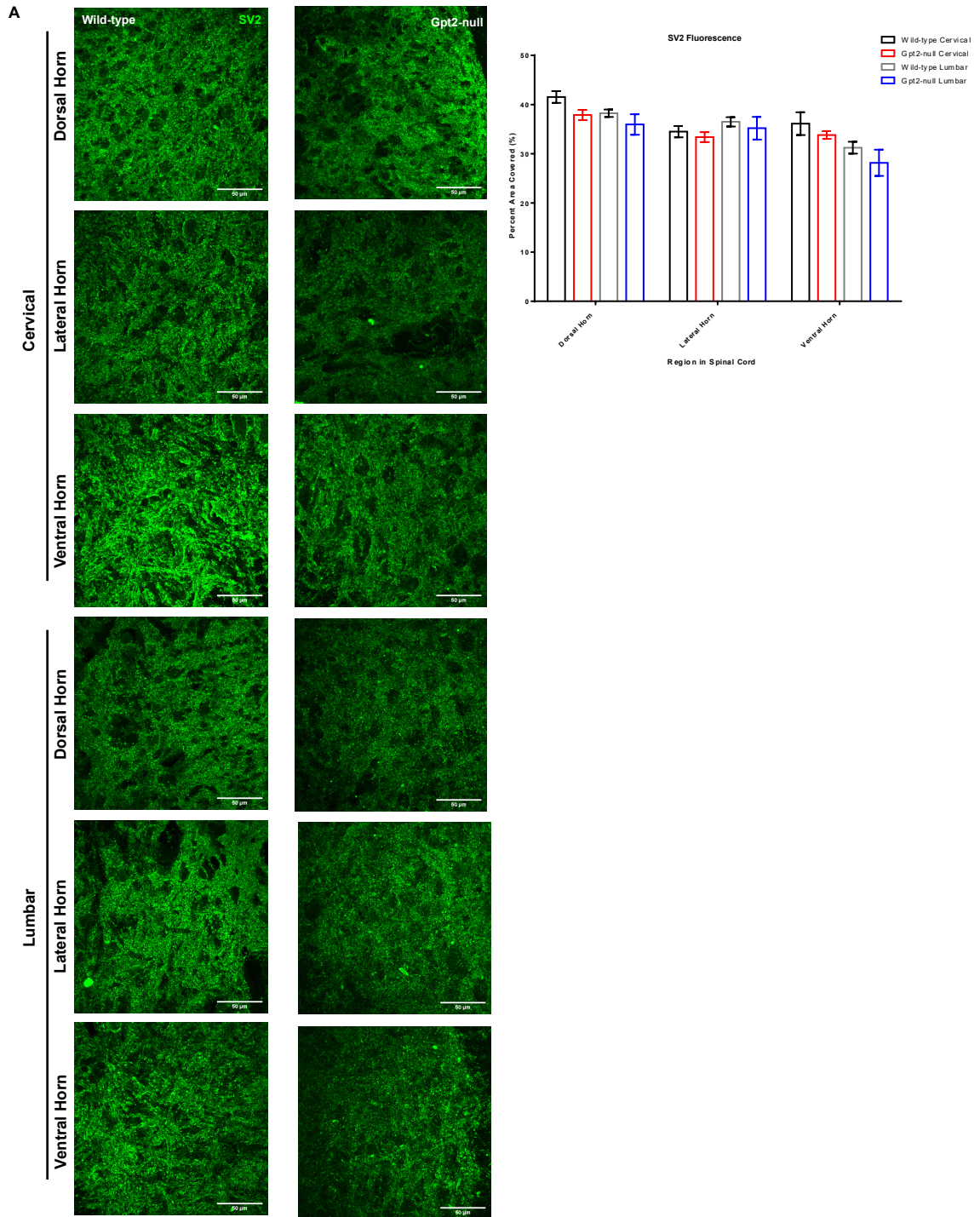


Figure A3.9. SV2 staining in spinal cord of Gpt2-null mice at P90 on high alanine diet. A. Images of SV2 staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Dorsal, lateral and ventral horns are shown. Scale bar: 100 µm. The quantification is given on the right.

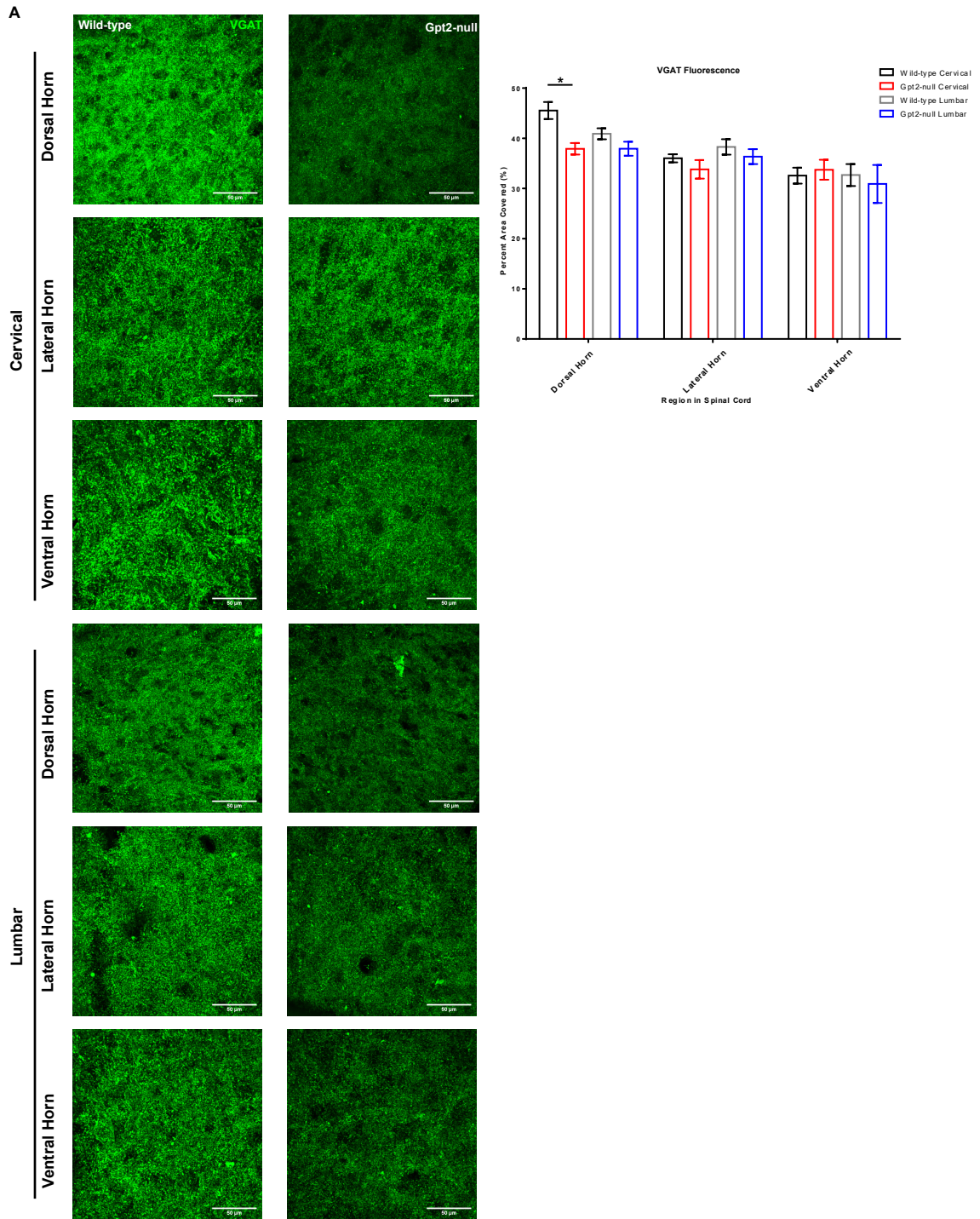


Figure A3.10. VGAT staining in spinal cord of Gpt2-null mice at P90 on high alanine diet.

A. Images of VGAT staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Dorsal, lateral and ventral horns are shown. Scale bar: 100 μ m. The quantification is given on the right. *0.01 < P < 0.05.

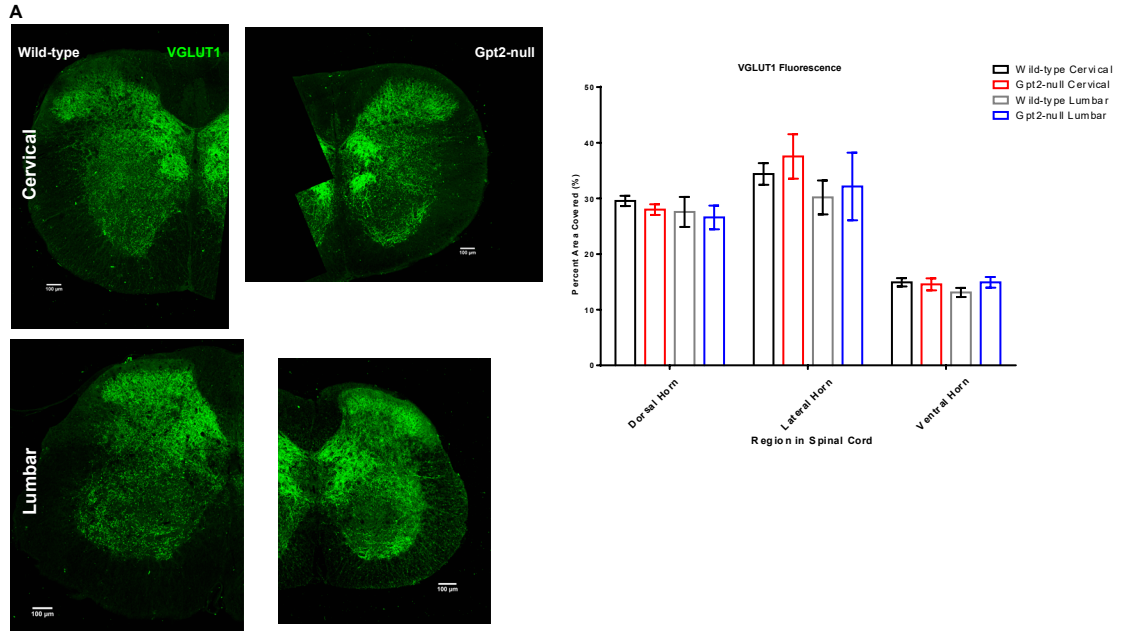


Figure A3.11. VGLUT1 staining in spinal cord of Gpt2-null mice at P90 on high alanine diet.

A. Images of VGLUT1 staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Scale bar: 100 μ m.

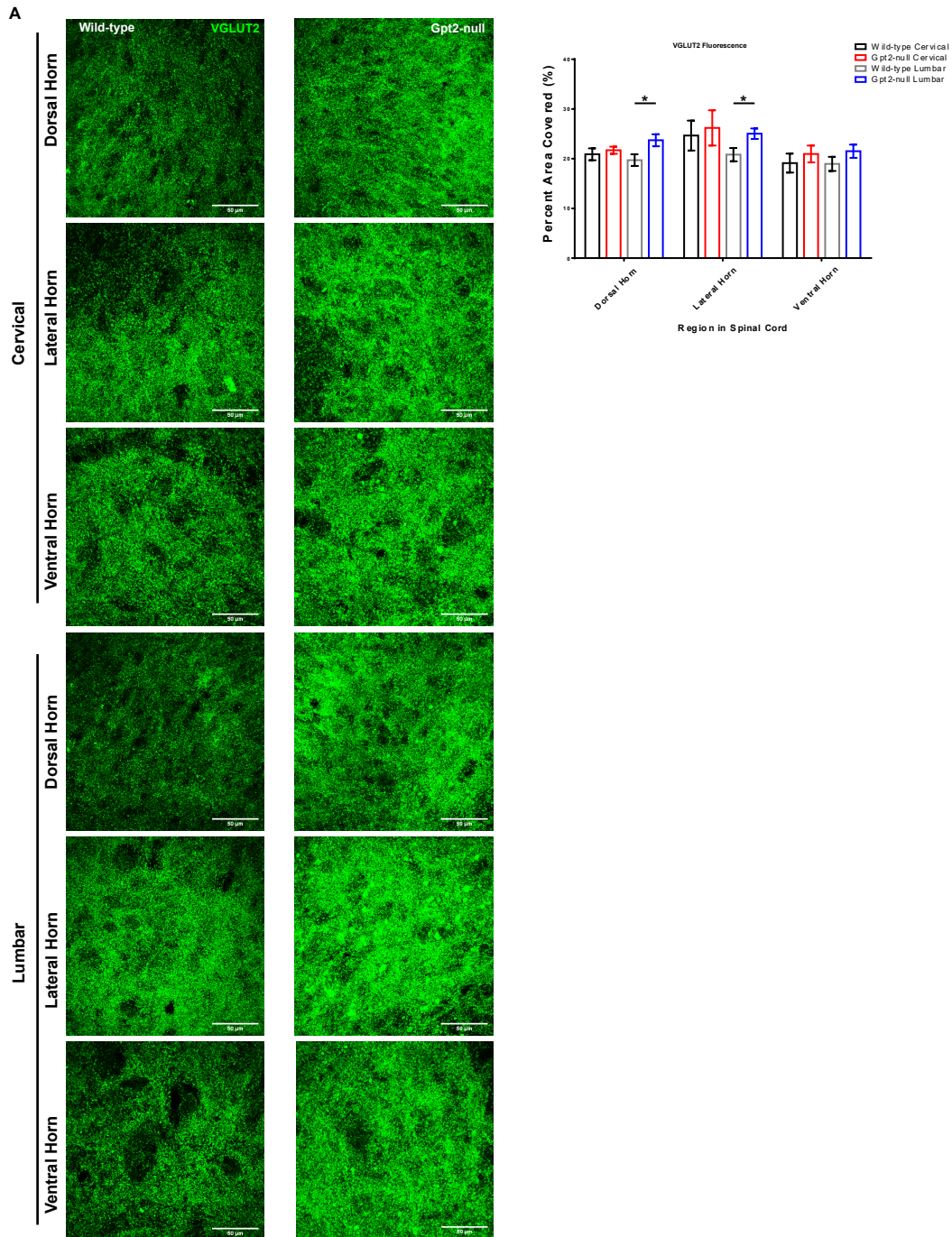


Figure A3.12. VGLUT2 staining in spinal cord of Gpt2-null mice at P90 on high alanine diet.

A. Images of VGLUT2 staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords.

Scale bar: 100 µm. The quantification is given on the right.

*0.01<P<0.05.

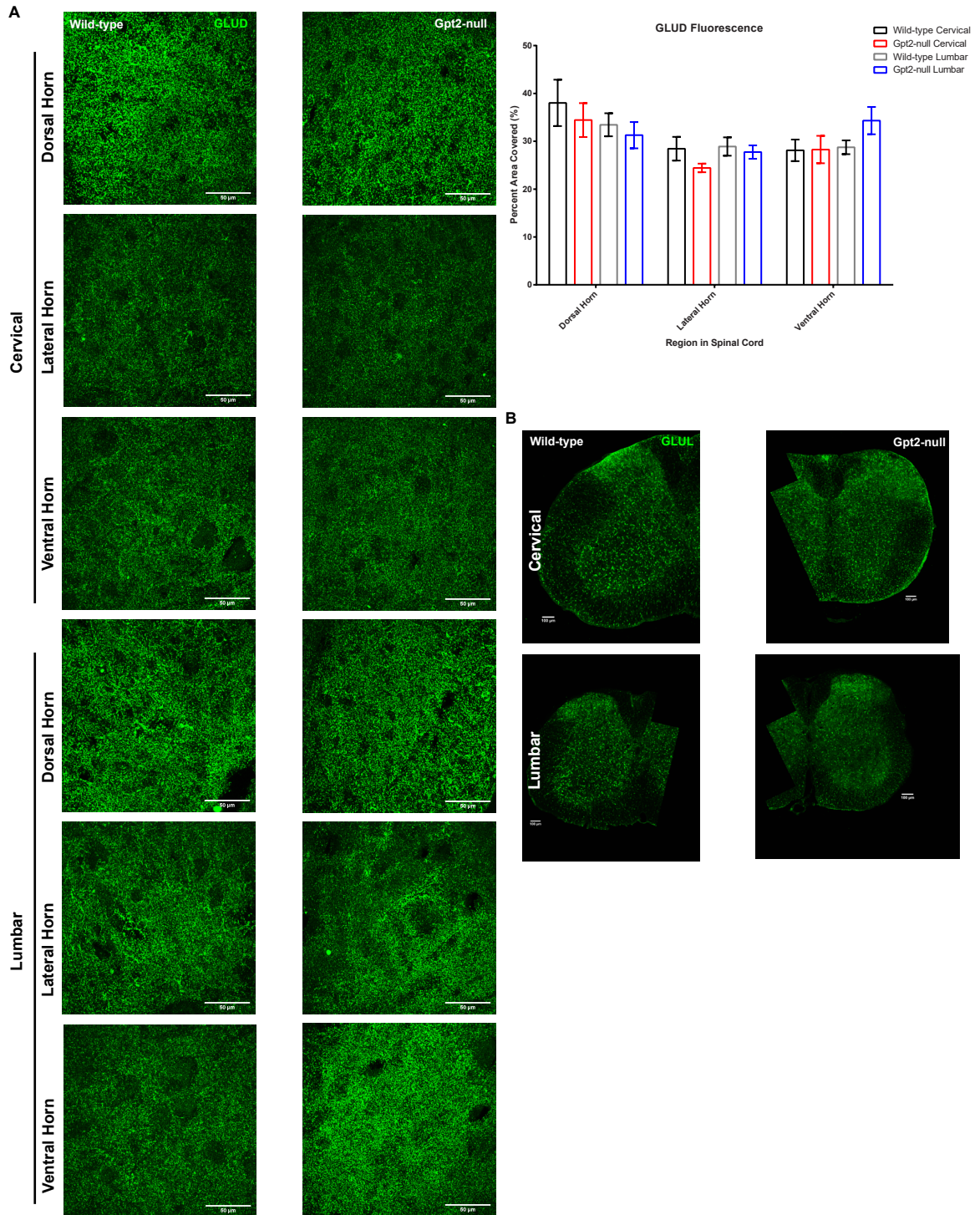


Figure A3.13. Glutamate dehydrogenase and Glutamine synthetase staining in spinal cord of Gpt2-null mice at P90 on high alanine diet.

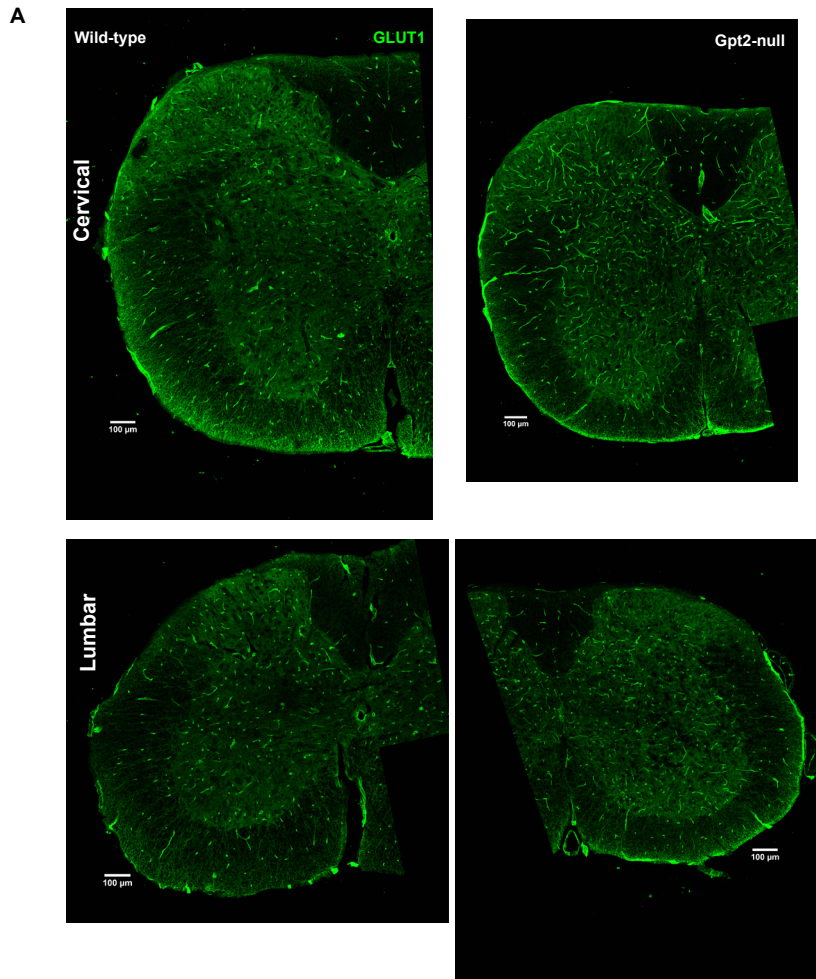


Figure A3.14. Glucose transporter 1 staining in spinal cord of Gpt2-null mice at P90 on high alanine diet. A. Images of glucose transporter (GLUT1) staining in wild-type (left) and Gpt2-null (right) cervical (top) and lumbar (bottom) spinal cords. Scale bar: 100 µm.

Appendix 3.6. Immunohistochemistry in Spinal cord for various stains in Gpt2-null mice at P18 (regular diet): Cleaved Caspase3 (CC3), myelin basic protein (MBP), protein kinase C γ (PKC γ), neurofilament H (NFH), NG2, Olig2, SV2, VGLUT1, VGLUT2, VGAT, MTCO1, glutamate dehydrogenase (GDH), glutamine synthetase (GLUL), glucose transporter 1 (GLUT1).

Introduction

Immunohistochemical analysis in Gpt2-null spinal cord at postnatal day 18 (fed Regular Diet). The following proteins are tested, and the corresponding processes or hypotheses are listed:

Cleaved Caspase 3 (CC3): Cell death by apoptosis; death of motor neurons may explain dysfunction in the motor behavior seen in Gpt2-null mice.

Myelin Basic Protein (MBP): deficits in myelination or ascending/descending tracts.

Protein Kinase C γ (PKC γ): Specifically expressed in descending corticospinal tracts and the dorsal horn. Long projections of corticospinal tracts may be more vulnerable to damage.

Neurofilament H (NFH): General assessment of neuronal processes, particularly axons.

NG2: A marker for oligodendrocyte precursor cells. Oligodendrocyte precursor cells appear to have the highest number of fragments per kilobase pf transcript per million

mapped reads (FPKM) as per the RNA-sequencing data done by (Zhang et al., 2014). It is possible that these cells may be particularly vulnerable to Gpt2 loss.

Olig2: A marker for oligodendrocytes. This would exclude the possible involvement of any problems in the number of oligodendrocytes.

SV2: A general marker for synaptic vesicles. We see reductions in SV2 puncta in Gpt2-null hippocampal neurons in vitro.

VGLUT1: An isoform of vesicular glutamate transporter on synaptic vesicles. We observe a slight upregulation of VGLUT1 in Gpt2-null synaptosomes; this may occur in spinal cord tissue as well. Both ascending and descending tracts in the spinal cord contain VGLUT1, any major absences of VGLUT1 puncta may indicate damage to those tracts or neurons that give rise thereto.

VGLUT2: An isoform of vesicular glutamate transporter on synaptic vesicles. Similar to VGLUT1, both ascending and descending tracts in the spinal cord contain VGLUT2, however differences in staining patterns with VGLUT1, may localize any potential abnormalities to a specific tract or nucleus in the spinal cord.

VGAT: A marker for synaptic vesicles containing 4-aminobutyric acid (GABA). We observe three-fold increases in protein levels in Gpt2-null synaptosomes. While we do

not know how this increase occurs, it may uniformly occur across the central nervous system in Gpt2-null mice.

MTCO1: Cytochrome c oxidase subunit 1, a marker of mitochondria. This may reveal problems of mitochondrial biogenesis. As Gpt2 loss results in deficits in the TCA cycle, mitochondrial biogenesis or shape (fission/fusion) may be altered and this may partly contribute to the pathological phenotype.

Glutamate dehydrogenase (GDH): A mitochondrial enzyme that converts glutamate into alpha-ketoglutarate and ammonia. GDH is an anaplerotic enzyme, meaning that it catalyzes a reaction that results in a net production of a TCA cycle intermediate. In the absence of Gpt2, GDH may be upregulated as a compensatory mechanism to support the TCA cycle, this is seen in Gpt2-null synaptosomes.

Glutamine Synthetase (GLUL): A cytosolic enzyme located mainly in astrocytes, that converts glutamate into glutamine. Up-regulation of this enzyme has been seen in animal models of epilepsy and in our data, in Gpt2-null synaptosomes.

Glucose Transporter 1 (GLUT1): A glucose transporter located mainly in endothelial cells that constitute the blood brain barrier. TCA cycle deficits in the Gpt2-null tissue can lead to upregulation of glucose uptake to support cellular energetics, through increased levels of GLUT1.

Results/Key Points

Table. Proteins stained via immunohistochemistry in Gpt2-null spinal cords at P18.
“QL”: qualitatively assessed. “-”: no difference.

Marker	Gpt2-null with respect to Wild-type
CC3 (QL)	
MBP (QL)	-
NFH	-
PKCγ	Decrease Total Area in Cervical&Lumbar.
SV2	Decrease in Lumbar Dorsal Horn. Trending Decrease in Lumbar Ventral Horn
VGLUT1	-
VGLUT2	Decrease in Lumbar Lateral Horn. Trending Decrease in Cervical&Lumbar Dorsal Horn
VGAT	Decrease in Cervical&Lumbar Dorsal Horn
MTCO1	Trending Decreases in Cervical Ventral Horn.
NG2 (QL)	-
GLUT1 (QL)	-
GLUL (QL)	-
GLUD	Decrease in Cervical Lateral&Ventral Horn. Trending Decrease in Lumbar Lateral Horn.
Olig2	-

Discussion

There were no major differences in cell death or structural differences in MBP or NFH suggesting that the tracts overall have developmentally formed. However, there was a significant decrease in the area covered by PKC γ , indicating a possible decrease in corticospinal tract projections. The total area covered by the staining may not be a very reliable measure because the animal and the spinal cord itself as a whole are smaller than the wild-type. We do not exactly know why this occurs or whether the tissues are uniformly smaller or parts of it are smaller. From the general overview of MBP or NFH staining, it appears that the Gpt2-null spinal cord sections are uniformly smaller. It is possible to prevent the confound of general smaller tissue size by dividing the area of the PKC γ staining by the total area of dorsal column assuming the “shrinkage” of the tissue

happens uniformly. The result of PKCg has to be considered as preliminary and needs to be validated by other methodologies. It would be more prudent to trace individual tracts to address the question of whether the corticospinal tract is degenerating. This may be achieved by either viral injection to the cortex (most pertinently motor cortex – although in mice, fine motor behavior may be coordinated mostly at the cervical level by the corticospinal tract ([Moreno-Lopez et al., 2020](#))) or mice that encode GFP in sparse neuronal populations (e.g. THY1-YFP). Electron microscopy may also identify individual axons and detect other morphological changes (e.g. myelin thickness, mitochondria number and shape).

SV2 seems to be significantly reduced in dorsal horn of the Gpt2-null lumbar spinal cord although there are trending decreases in the rest of the areas. This may reflect either reduced projections to the spinal cord, reduced SV2 production or reduced synaptic vesicle counts. Only VGAT and VGLUT2 seem to be affected in the same direction as SV2 particularly in the dorsal horn. NeuN+ or Calbindin+ cell counts were not changed so the reductions in VGAT/SV2/VGLUT2 are not due to dorsal horn neuron loss. While the differences are slight, these may point to emerging deficits in the afferent projections. This would not be surprising since if we hypothesize that neurons with long-projections are vulnerable primarily due to the long length of their processes, then this category of neurons includes afferent sensory neurons as well as motor neurons.

GLUD levels were significantly reduced however the background for these staining seems to be slightly different as the images did not show major qualitative differences.

This technical consideration is valid for the other stainings as well. Despite that the image analysis included background correction, this does not work perfectly and the manual counting of puncta was not preferred to prevent experimenter bias.

Another technical consideration could be that although there were at least 5 animals and 2 sections per staining, the sections from all animals were stained for the same protein on the same day to exclude variation within groups. It is possible to repeat the experiment once more for some of the proteins to validate the first experiment's results.

Method

Immunofluorescence – Tissue. The tissues from mice were dissected out after transcardial perfusion with 1X PBS – 4% PFA. The tissues were cryoprotected serially with 10%, 20% and 30% sucrose, each incubating overnight at 4°C. The solution was then changed to half by volume sucrose/OCT (Optimal Cutting Temperature, FisherScientific 23-730-571) and gently shaken for 1 hour at 4°C. The tissues were frozen in dry ice/methanol bath and stored at -80°C until day of sectioning at the cryostat. The sections were cut at 30µm thickness. The immunofluorescence protocol was as follows, in order: 3-minute fixing with 4% PFA, 3 5-minute 1X PBS washes, 2-hour blocking in Normal Goat or Donkey Serum (NDS, JacksonImmunoResearch, 017-000-121) with 1% (w/v) Bovine Serum Albumin (FisherScientific BP1600), 0.4% TritonX-100 (Sigma-Aldrich T8787), (if mouse-raised antibody is used: 1-hour incubation with 20 µg/ml AffiniPure Fab Fragment Goat Anti-Mouse IgG (H+L) (AB_2338476) or AffiniPure Fab Fragment

Donkey Anti-Mouse IgG (H+L) (AB_2307338) in blocking solution), primary antibody in blocking solution incubation overnight at 4°C, 2 4-minute washes with blocking solution, 3 4-minute washes with 0.4% TritonX-100 in PBS, 2-hour secondary antibody in blocking solution incubation, 2 4-minute washes with blocking solution, 3 4-minute washes with 0.4% TritonX-100 in PBS, 5-minute incubation in DAPI (Invitrogen D1306), 3 5-minute washes with PBS and mounted with Fluoromount G (SouthernBiotech 0100-01). Images were processed and analyzed with ImageJ.

Confocal Microscopy. Olympus FV3000 confocal laser scanning microscope and FluoView software were used (RRID:SCR_017015). Maximum intensity projection of the images was used for the final analysis.

The following macro was used to detect puncta:

```

“
run("Z Project...", "projection=[Max Intensity]");
run("Subtract Background...", "rolling=1 disable stack");
run("Enhance Contrast...", "saturated=0.3");
//run("Threshold...");
setAutoThreshold("Moments dark");
run("Convert to Mask", "method=Moments background=dark calculate");
run("Analyze Particles...", "size=0.15-150 circularity=0.50-1.00 display exclude summarize add stack");
dir = getDirectory("image");
name = getTitle();
index = lastIndexOf(name, ".");
if (index!=-1) name = substring(name, 0, index);
name = name + ".xls";
saveAs("Results", dir+name);
saveAs("Measurements", dir+name);
print(dir+name);
“

```

Table. Primary antibodies used in this study.

Antibody	Host Species	Company	Catalog No	Dilution
Neurofilament H	Ch	Millipore	AB5539	1:3200
SV2	Ms	DSHB	SV2-c	1:500

VGAT	Gp	SynapticSystems	131004	1:400
VGLUT1	Gp	Millipore	AB5905	1:1000
Olig2	Rb	abcam	ab109186	1:200
VGLUT2	Gp	SynapticSystems	135404	1:1600
GLUT1	Rb	abcam	ab652	1:250
CCas3	Rb	CellSignaling	9661	1:200
MTCO1	Ms	abcam	ab14705	1:400
GLUD	Rb	Invitrogen	PA5-29492	1:1600
NG2	Rb	Millipore	AB5320	1:200
Glutamine Synthetase	Rb	abcam	ab73593	1:800
MBP	Rat	Novus Biologicals	nb600-717	1:50
PKCg	Rb	abcam	109539	1:400

Figure Legends

Figure A3.15. Cleaved Caspase 3 staining in spinal cord of Gpt2-null mice at P18 on regular alanine diet.

A. Images of cleaved caspase 3 staining in wild-type (left) and Gpt2-null (right) cervical (top) and lumbar (bottom) spinal cords. Scale bar: 100 μ m.

Figure A3.16. Myelin Basic Protein and Protein Kinase C γ staining in spinal cord of Gpt2-null mice at P18 on regular alanine diet.

A. Images of myelin basic protein (MBP) staining in wild-type (left) and Gpt2-null (right) cervical (top) and lumbar (bottom) spinal cords. Scale bar: 100 μ m.

B. Images of protein kinase c γ (PKC γ) staining in wild-type (left) and Gpt2-null (right) cervical (top) and lumbar (bottom) spinal cords. Scale bar: 100 μ m. Quantification is given at the bottom. $**0.001 < P < 0.01$.

Figure A3.17. MTCO1 staining in spinal cord of Gpt2-null mice at P18 on regular alanine diet.

A. Images of MTCO1 staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Dorsal, lateral and ventral horns are shown. Scale bar: 100 μ m. The quantification is given on the right.

Figure A3.18. Neurofilament H staining in spinal cord of Gpt2-null mice at P18 on regular alanine diet.

A. Images of neurofilament H (NFH) staining in wild-type (left) and Gpt2-null (right) cervical (top) and lumbar (bottom) spinal cords. Scale bar: 100 μ m.

B. White boxes placed over to identify different areas of the spinal cord. Box 1: Corticospinal tract 2: laminae 1,2,3 of spinal gray 3: ventral funiculus 4: rubrospinal tract 5: lateral funiculus 6: laminae 10 of spinal gray. Quantification of NFH is given below.

C. Images of the different areas outlined in B.

Figure A3.19. NG2 and Olig2 staining in spinal cord of Gpt2-null mice at P18 on regular alanine diet.

A. Images of NG2 staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Dorsal, lateral and ventral horns are shown. Scale bar: 100 μ m.

B. Images of Olig2 staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Scale bar: 100 μ m. The quantification of Olig⁺ cell counts is given at the bottom.

Figure A3.20. SV2 staining in spinal cord of Gpt2-null mice at P18 on regular alanine diet.

A. Images of SV2 staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Dorsal, lateral and ventral horns are shown. Scale bar: 100 μ m. The quantification is given on the right. $*0.01 < P < 0.05$.

Figure A3.21. VGAT staining in spinal cord of Gpt2-null mice at P18 on regular alanine diet.

A. Images of VGAT staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Dorsal, lateral and ventral horns are shown. Scale bar: 100 μ m. The quantification is given on the right. $*0.01 < P < 0.05$.

Figure A3.22. VGLUT1 staining in spinal cord of Gpt2-null mice at P18 on regular alanine diet.

A. Images of VGLUT1 staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Scale bar: 100 μ m.

Figure A3.23. VGLUT2 staining in spinal cord of Gpt2-null mice at P18 on regular alanine diet.

A. Images of VGLUT2 staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Scale bar: 100 μ m. The quantification is given on the right.

Figure A3.24. Glutamate dehydrogenase and Glutamine synthetase staining in spinal cord of Gpt2-null mice at P18 on regular alanine diet.

A. Images of glutamate dehydrogenase (GLUD) staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Dorsal, lateral and ventral horns are shown.

Scale bar: 100 μ m. The quantification is given on the right. *0.01<P<0.05.

B. Images of glutamine synthetase (GLUL) staining in wild-type (left) and Gpt2-null (right) cervical (top) and lumbar (bottom) spinal cords. Scale bar: 100 μ m.

Figure A3.24. Glucose transporter 1 staining in spinal cord of Gpt2-null mice at P18 on regular alanine diet.

A. Images of glucose transporter (GLUT1) staining in wild-type (left) and Gpt2-null (right) cervical (top) and lumbar (bottom) spinal cords. Scale bar: 100 μ m.

Moreno-Lopez, Y., Bichara, C., Isope, P., and Cordero-Erausquin, M. (2020). Lumbar corticospinal tract in rodents modulates sensory inputs but does not convey motor command.

Zhang, Y., Chen, K., Sloan, S.A., Bennett, M.L., Scholze, A.R., O'Keefe, S., Phatnani, H.P., Guarnieri, P., Caneda, C., Ruderisch, N., *et al.* (2014). An RNA-sequencing transcriptome and splicing database of glia, neurons, and vascular cells of the cerebral cortex. *J Neurosci* 34, 11929-11947.

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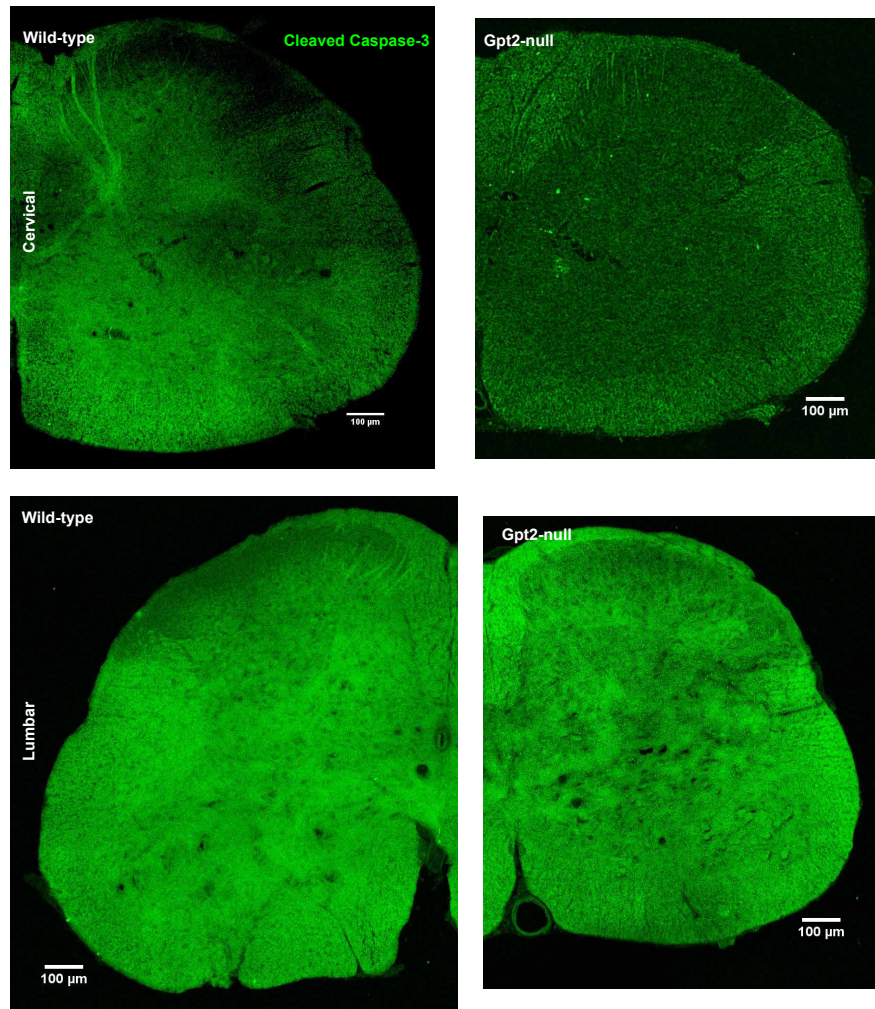


Figure A3.15. Cleaved Caspase 3 staining in spinal cord of Gpt2-null mice at P18 on regular alanine diet. A. Images of cleaved caspase 3 staining in wild-type (left) and Gpt2-null (right) cervical (top) and lumbar (bottom) spinal cords. Scale bar: 100 μm.

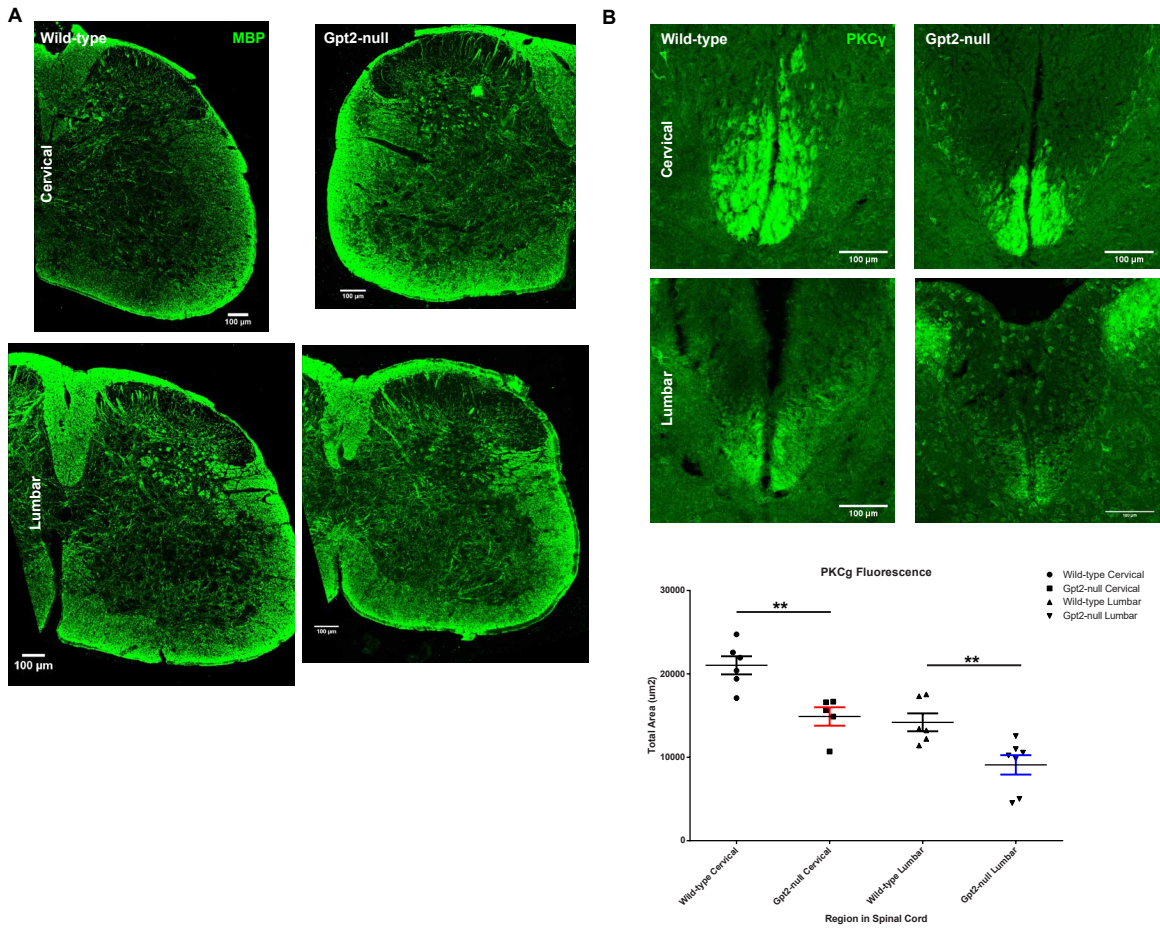


Figure A3.16. Myelin Basic Protein and Protein Kinase C γ staining in spinal cord of Gpt2-null mice at P18 on regular alanine diet.

A. Images of myelin basic protein (MBP) staining in wild-type (left) and Gpt2-null (right) cervical (top) and lumbar (bottom) spinal cords. Scale bar: 100 μ m.

B. Images of protein kinase c γ (PKC γ) staining in wild-type (left) and Gpt2-null (right) cervical (top) and lumbar (bottom) spinal cords.

Scale bar: 100 μ m. Quantification is given at the bottom. ******0.001<P<0.01.

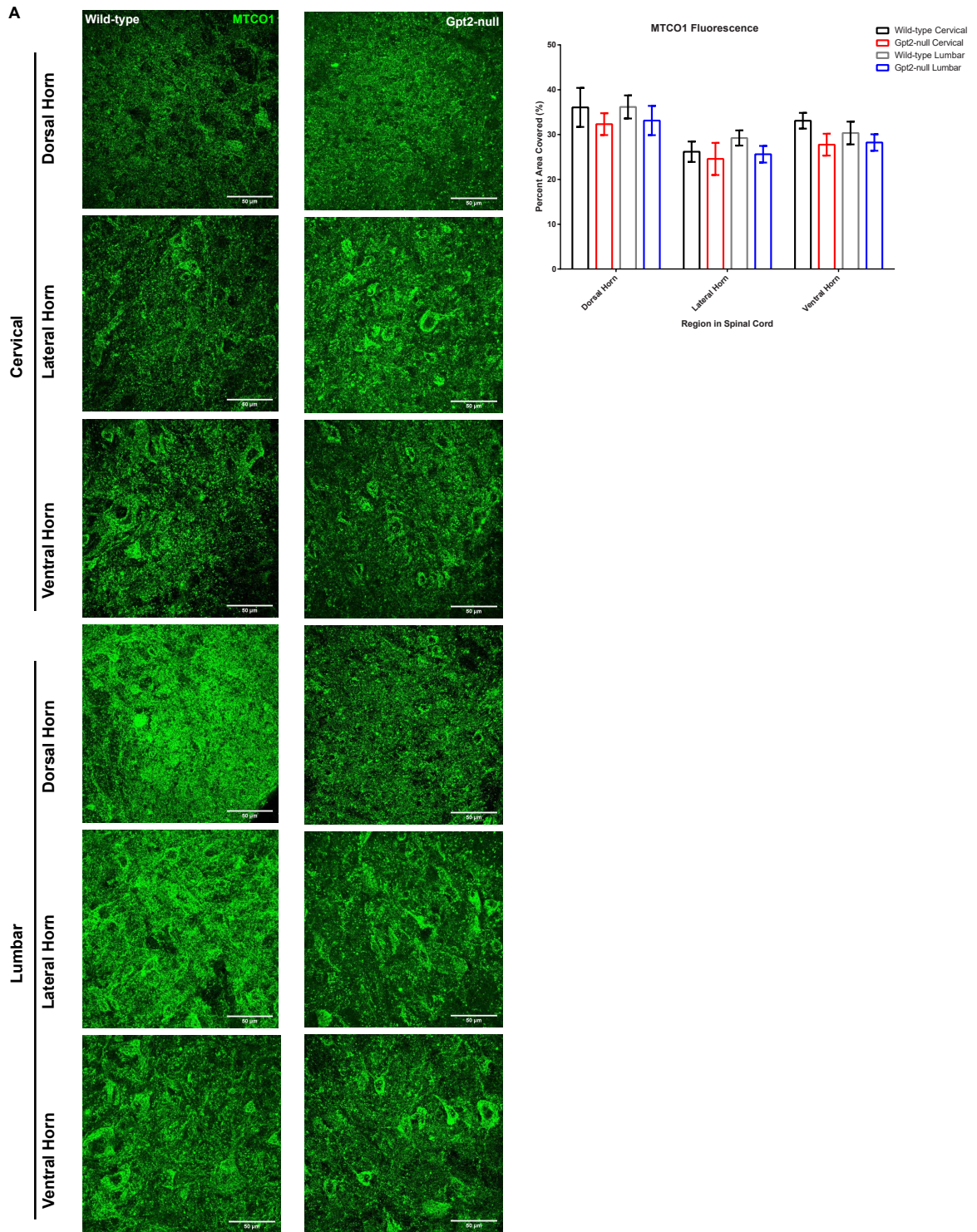


Figure A3.17. MTCO1 staining in spinal cord of Gpt2-null mice at P18 on regular alanine diet.
 A. Images of MTCO1 staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Dorsal, lateral and ventral horns are shown. Scale bar: 100 µm.
 The quantification is given on the right.

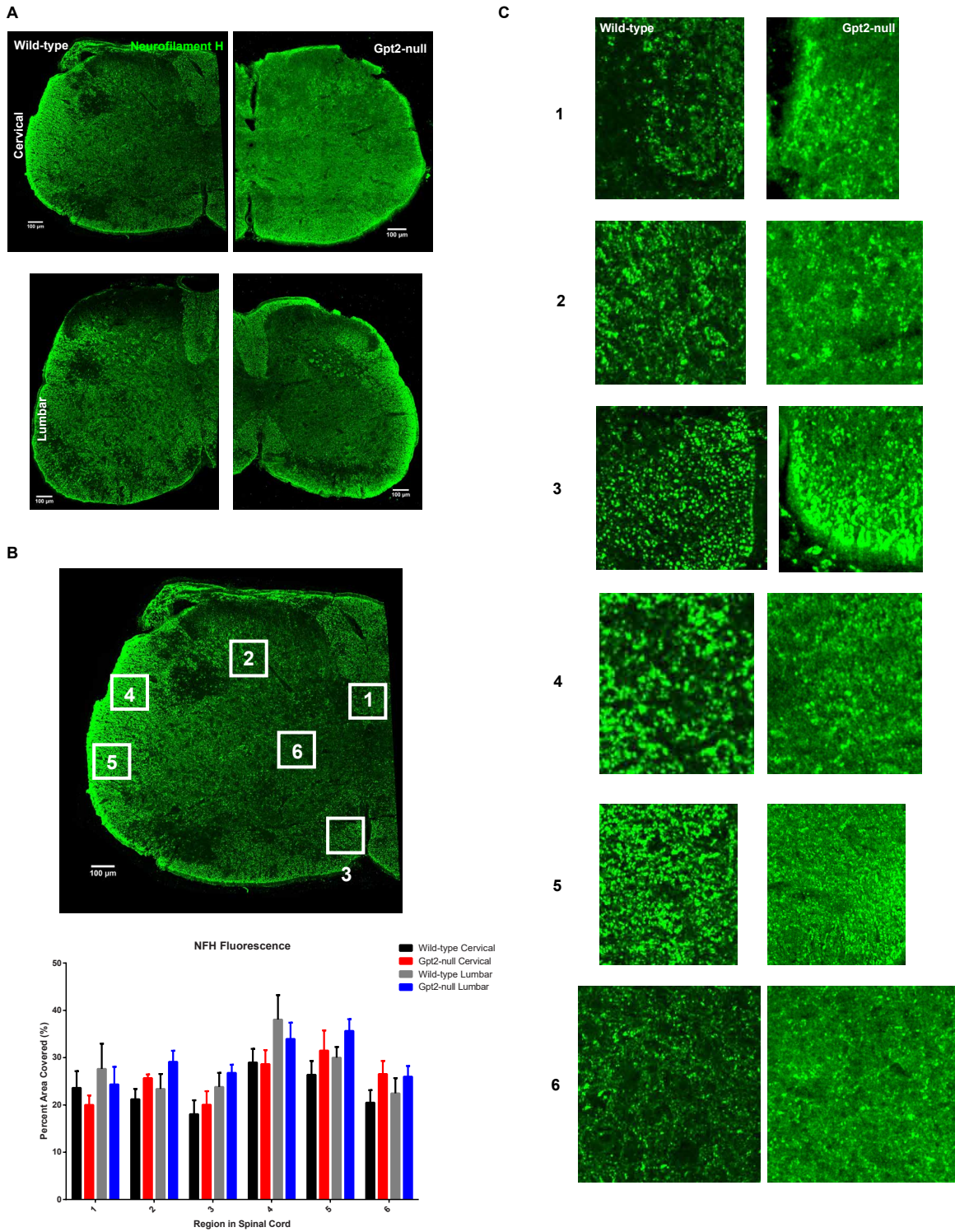


Figure A3.18. Neurofilament H staining in spinal cord of Gpt2-null mice at P18 on regular alanine diet. A. Images of neurofilament H (NFH) staining in wild-type (left) and Gpt2-null (right) cervical (top) and lumbar (bottom) spinal cords. Scale bar: 100 μ m. B. White boxes placed over to identify different areas of the spinal cord. Box 1: Corticospinal tract 2: laminae 1,2,3 of spinal gray 3: ventral funiculus 4: rubrospinal tract 5: lateral funiculus 6: laminae 10 of spinal gray. Quantification of NFH is given below. C. Images of the different areas outlined in B.

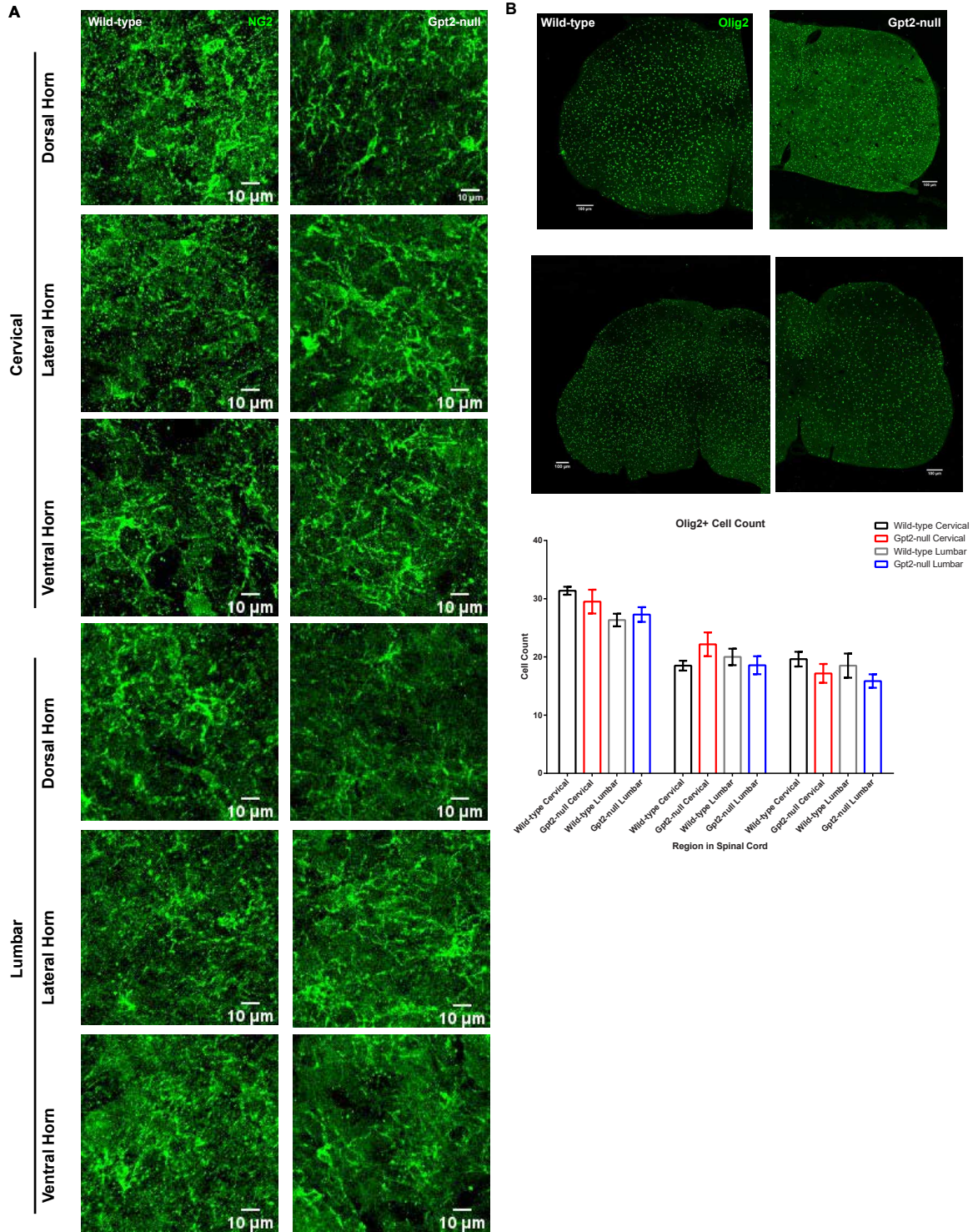


Figure A3.19. NG2 and Olig2 staining in spinal cord of Gpt2-null mice at P18 on regular alanine diet. A. Images of NG2 staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Dorsal, lateral and ventral horns are shown. Scale bar: 100 µm. B. Images of Olig2 staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Scale bar: 100 µm. The quantification of Olig2+ cell counts is given at the bottom.

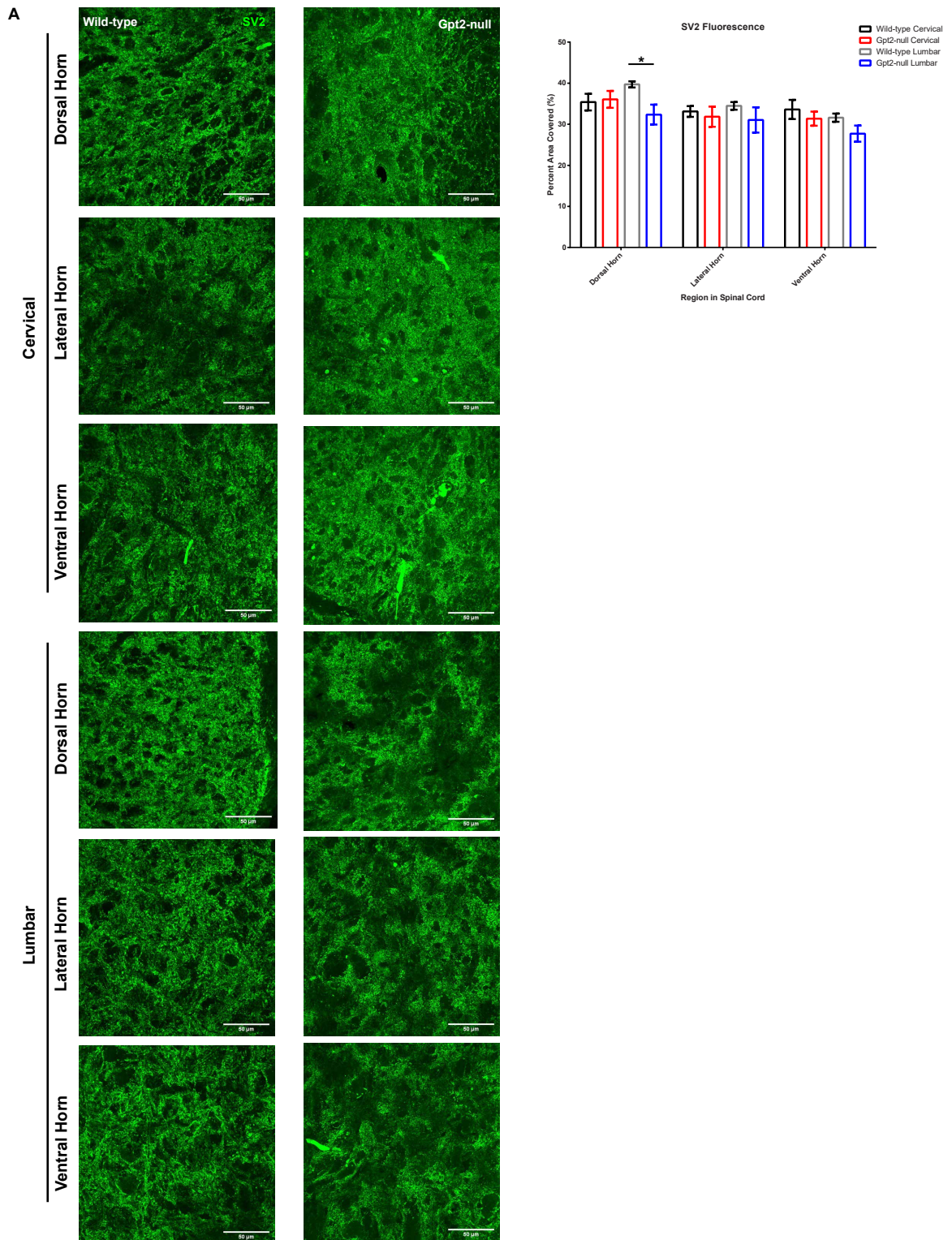


Figure A3.20. SV2 staining in spinal cord of Gpt2-null mice at P18 on regular alanine diet.
 A. Images of SV2 staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Dorsal, lateral and ventral horns are shown. Scale bar: 100 µm.
 The quantification is given on the right. *0.01<P<0.05.

A

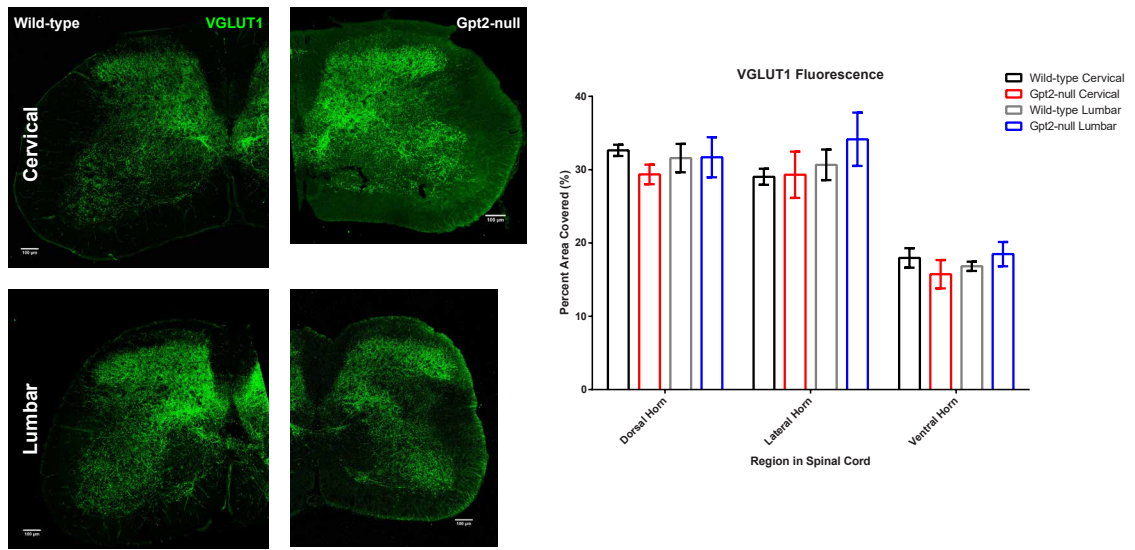


Figure A3.22. VGLUT1 staining in spinal cord of Gpt2-null mice at P18 on regular alanine diet. A. Images of VGLUT1 staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Scale bar: 100 µm.

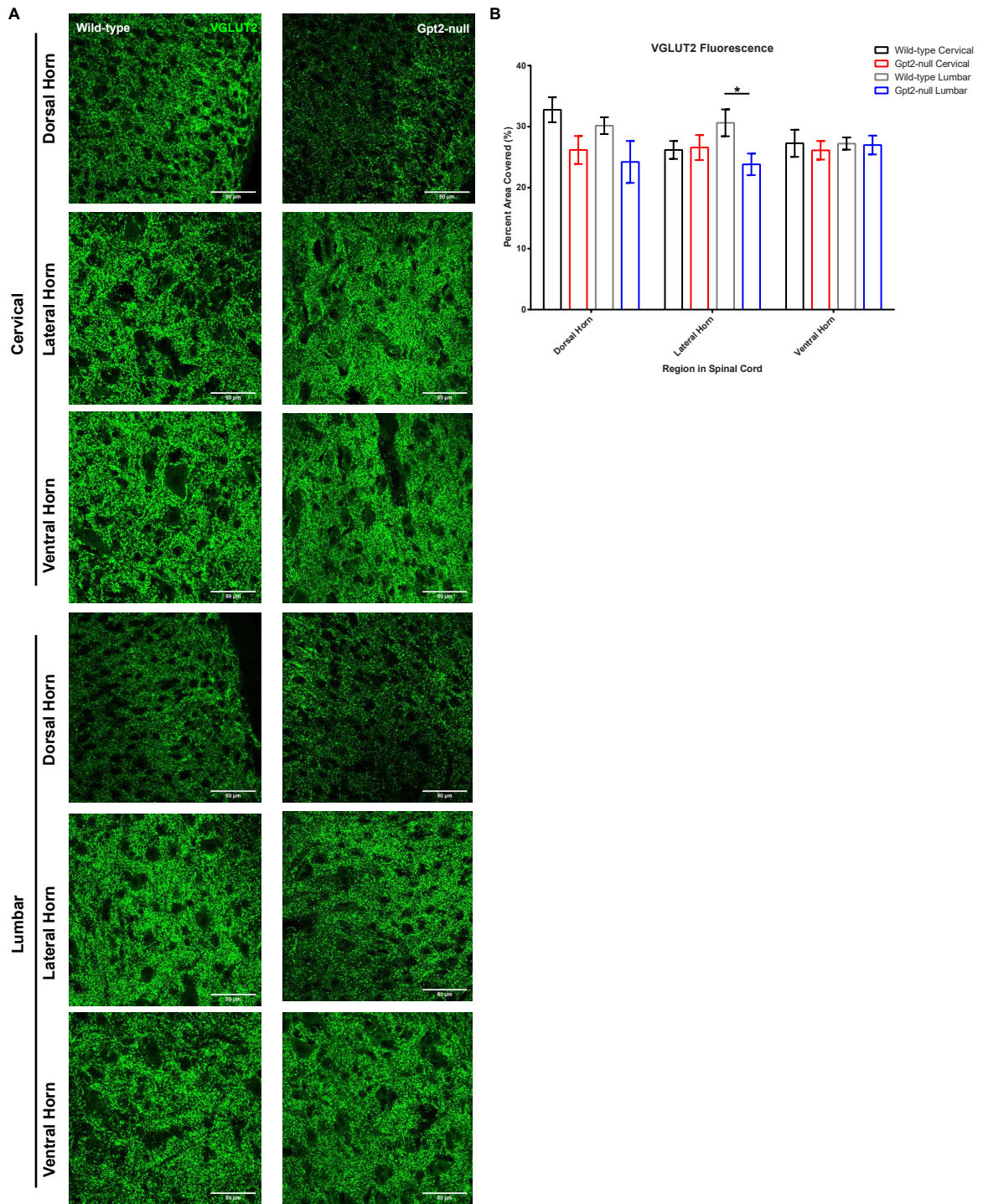


Figure A3.23. VGLUT2 staining in spinal cord of Gpt2-null mice at P18 on regular alanine diet.
 A. Images of VGLUT2 staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Scale bar: 100 µm. The quantification is given on the right.

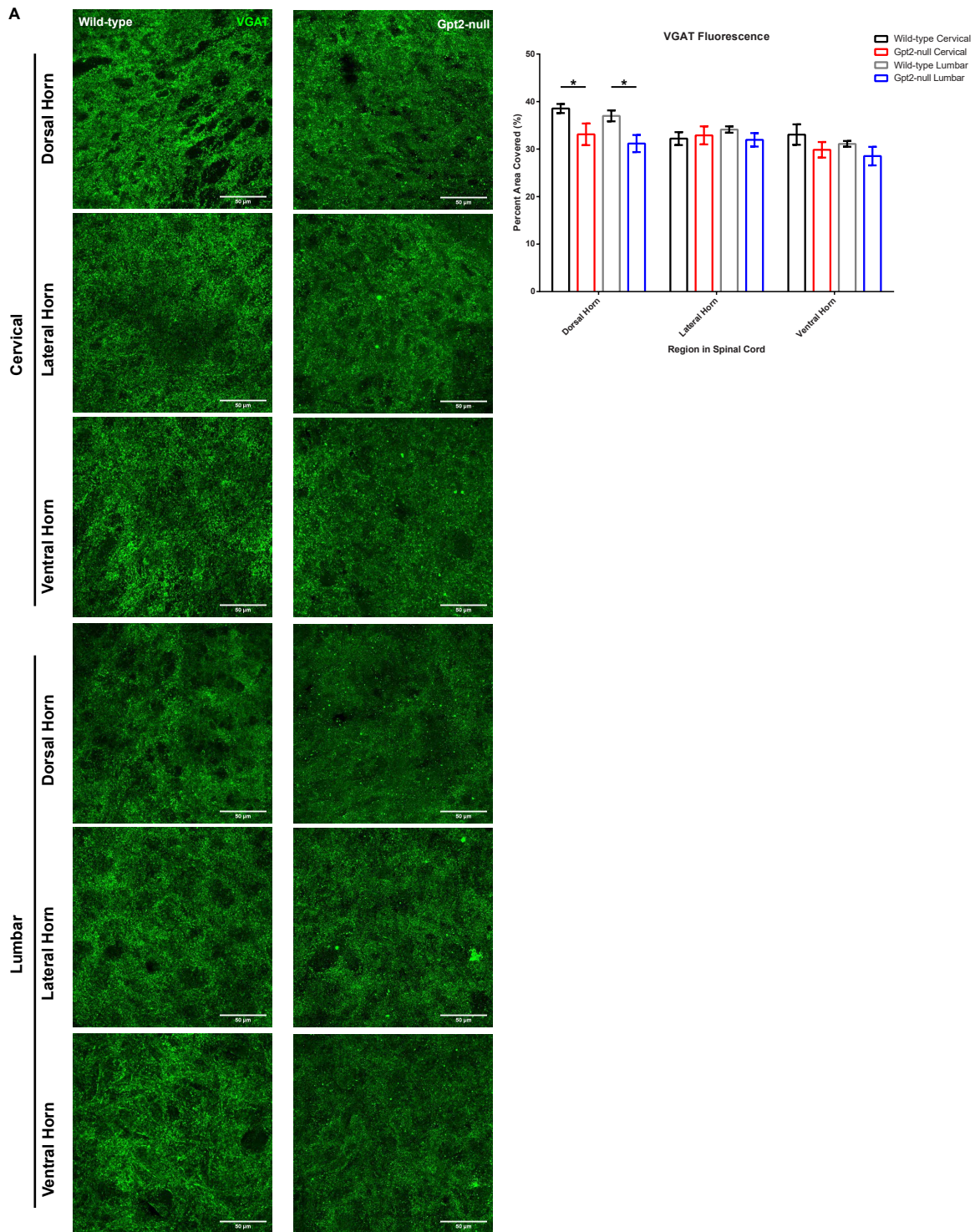
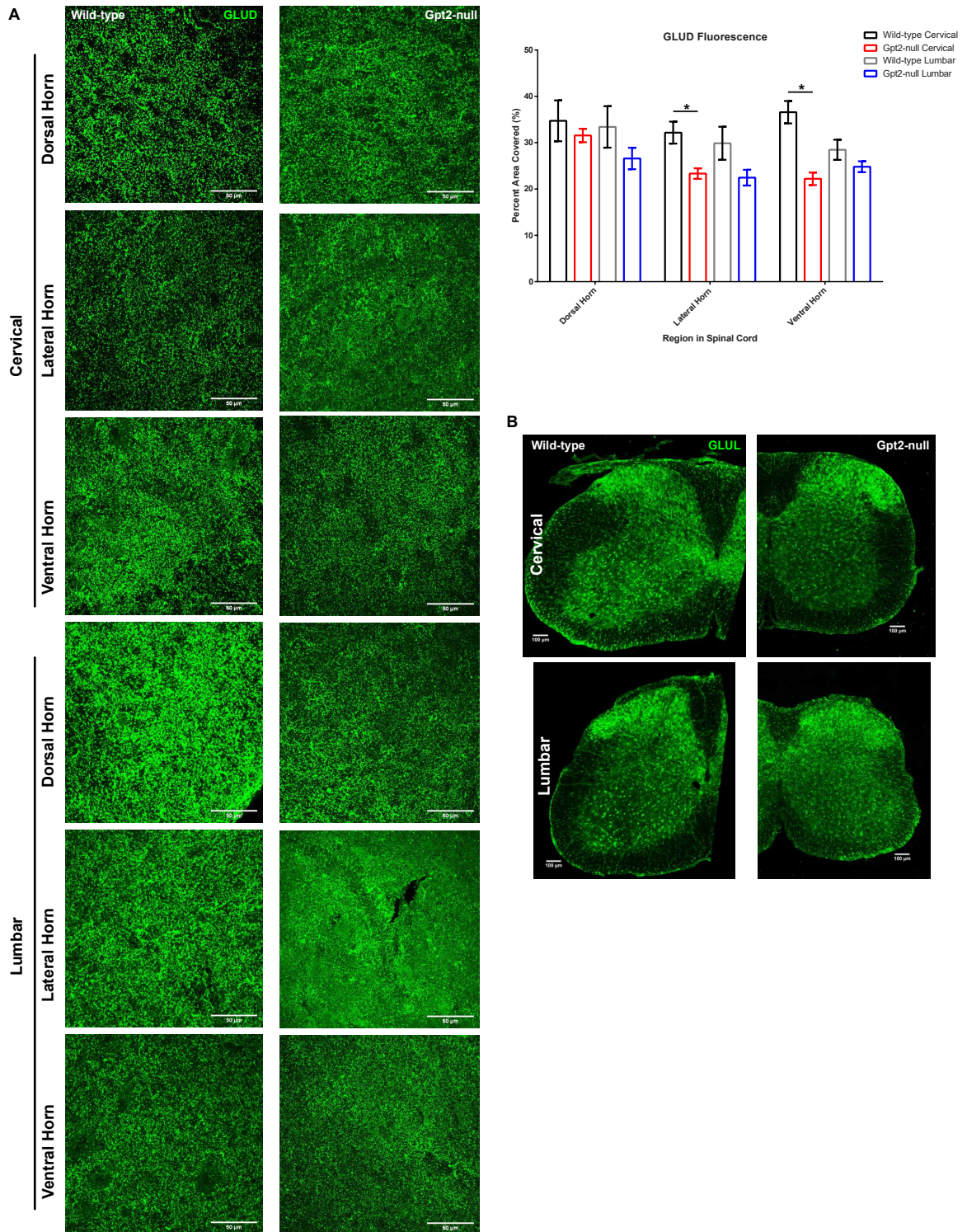


Figure A3.21. VGAT staining in spinal cord of Gpt2-null mice at P18 on regular alanine diet. A. Images of VGAT staining in wild-type (left) and Gpt2-null (right) cervical and lumbar spinal cords. Dorsal, lateral and ventral horns are shown. Scale bar: 100 µm. The quantification is given on the right. *0.01<P<0.05.



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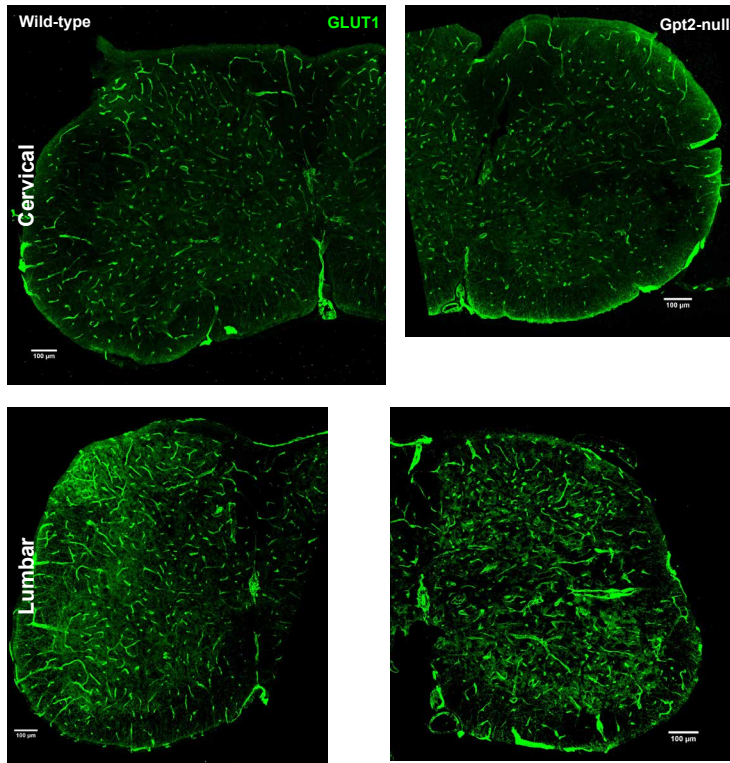


Figure A3.24. Glucose transporter 1 staining in spinal cord of Gpt2-null mice at P18 on regular alanine diet. A. Images of glucose transporter (GLUT1) staining in wild-type (left) and Gpt2-null (right) cervical (top) and lumbar (bottom) spinal cords. Scale bar: 100 µm.

Appendix A3.7. Oligodendrocyte specific protein in staining density in Gpt2-null mouse brains at P18 on regular diet.

Introduction

We investigated whether there are any global changes in the white matter of the Gpt2-null brain. We performed oligodendrocyte specific protein (Claudin-11) staining in coronal Gpt2-null brain sections (age postnatal day 18).

Key Points / Results

- No major differences in corpus callosum, striatum, cingulum bundle in Gpt2-null brains.

Discussion

Naturally the experiment could be expanded to other areas, however there were no major structural abnormalities in the areas tested. There can be subtle differences such as in the striatum, on the background near the nerve bundles, the wild-type seems to have more staining compared to the Gpt2-null image.

Method

Immunofluorescence – Tissue. The tissues from mice were dissected out after transcardial perfusion with 1X PBS – 4% PFA. The tissues were cryoprotected serially with 10%, 20% and 30% sucrose, each incubating overnight at 4°C. The solution was then changed to half by volume sucrose/OCT (Optimal Cutting Temperature, FisherScientific 23-730-571) and gently shaken for 1 hour at 4°C. The tissues were frozen in dry ice/methanol bath and stored at -80°C until day of sectioning at the cryostat. The sections were cut at 30µm thickness. The immunofluorescence protocol was as follows, in order: 3-minute fixing with 4% PFA, 3 5-minute 1X PBS washes, 2-hour blocking in Normal Goat or Donkey Serum (NDS, JacksonImmunoResearch, 017-000-121) with 1% (w/v) Bovine Serum Albumin (FisherScientific BP1600), 0.4% TritonX-100 (Sigma-Aldrich T8787), (if mouse-raised antibody is used: 1-hour incubation with 20 µg/ml AffiniPure Fab Fragment Goat Anti-Mouse IgG (H+L) (AB_2338476) or AffiniPure Fab Fragment Donkey Anti-Mouse IgG (H+L) (AB_2307338) in blocking solution), primary antibody in blocking solution incubation overnight at 4°C, 2 4-minute washes with blocking solution, 3 4-minute washes with 0.4% TritonX-100 in PBS, 2-hour secondary antibody in blocking solution incubation, 2 4-minute washes with blocking solution, 3 4-minute washes with 0.4% TritonX-100 in PBS, 5-minute incubation in DAPI (Invitrogen D1306), 3 5-minute washes with PBS and mounted with Fluoromount G (SouthernBiotech 0100-01). Images were processed and analyzed with ImageJ.

Confocal Microscopy. Imaging and quantification of cell death, cell count, synapse count, arborization were done with Opera Phenix High-Content Quantification System and Harmony software (PerkinElmer, RRID:SCR_018809). The hippocampal neuronal, astrocyte-enriched cultures or co-cultures were seeded on an OperaPhenix Ultra

CellCarrier 96-well plate (PerkinElmer, 6055302) and at indicated times, different media conditions were tested. Immunofluorescence as described above was done at 14 days in vitro (DIV14) for all plates. The wells were filled with 1X PBS and imaged immediately after. For confocal microscopy on tissues, Olympus FV3000 confocal laser scanning microscope and FluoView software were used (RRID:SCR_017015).

Primary antibody: Oligodendrocyte Specific Protein (abcam, ab53041) 1:200 dilution.

Figure Legends

Figure A.3.25. Oligodendrocyte Specific Protein staining in Gpt2-null coronal brain section at postnatal day 18.

- A.** Images of oligodendrocyte specific protein (green) in wild-type (left) and Gpt2-null (right) sections containing anterior forceps of corpus callosum, corpus callosum, striatum and cingulum bundle. Quantification of the percent area covered by the staining is given at the bottom. Scale bar: 50 μ m.

A

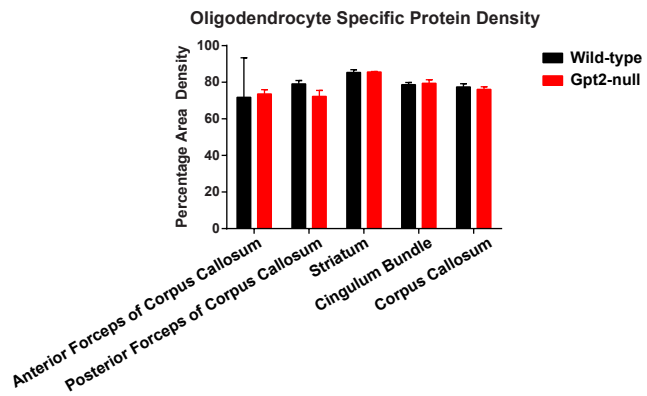
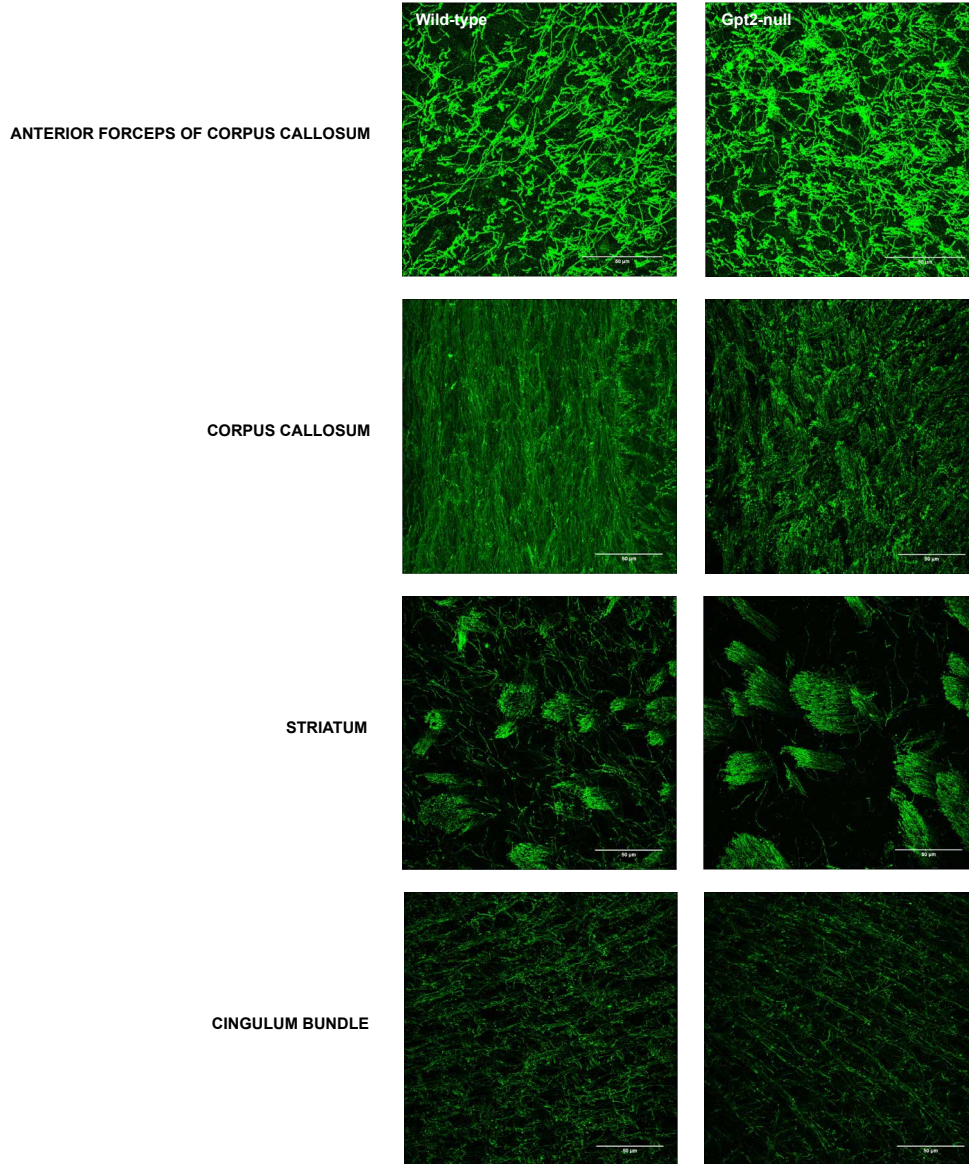


Figure A.3.25. Oligodendrocyte Specific Protein staining in Gpt2-null coronal brain section at postnatal day 18.

Appendix A.3.8. Ng2 & Gpt2 & MitotrackerRed staining in oligodendrocyte precursor cell culture.

Introduction

I characterized GPT2 staining in mouse microglia and oligodendrocyte precursor cells in vitro. GPT2 expression in these cell types has not been studied previously except in some RNA sequencing studies [1, 2].

Results/Key Points

GPT2 is expressed in microglia and oligodendrocyte precursor cells.

Discussion

GPT2 seems to be expressed in multiple cell types in the nervous system, including neurons, astrocytes, microglia and oligodendrocyte precursor cells. It seems to be a ubiquitously expressed protein. This may also be important in the pathophysiology of GPT2 deficiency.

Available data (not analyzed):

- CD68 staining in microglia is available. NG2 staining is also available however I am not sure if it worked.

Method

Cell Culture

A. Mouse Brain Dissection and Primary Mixed Glial Culturing

1. Spray the pup head with 70% ethanol and clean away with Kimwipe. Decapitate P0-P2 mouse. Make a midline incision to the scalp to expose the cranium and incise the cranium from neck to nose. Using forceps, the cranial flaps are gently pulled to the sides and the brain is removed using the flat side of the forceps. Place it in a dissecting dish containing ice-cold HBSS.
2. With the brain dorsal side up, make a shallow incision mid-sagittally. The incision should only pass through the meningeal layer.
3. Peel off the meninges using forceps in a lateral fashion. Make sure the meninges are removed and the brain is undamaged.
4. Gently pry the cortices away from the diencephalon in a lateral fashion. Remove hippocampus and cut the remaining connections with the diencephalon.
5. Dice each cortex into 6 pieces using sharp blade and gently transfer to a 15ml conical tube. Add HBSS to a total volume of 5.625 ml.
6. Add 625 ul of 2.5% Trypsin-EDTA. Mix by inverting and incubate the tissue in the water bath at 37°C for 30 min. Mix by occasional shaking by hand in a circling motion every 10 min.
7. Centrifuge for 5 min at 300g to pellet cortex tissue pieces.
8. Carefully remove supernatant by decantation into an empty dissecting dish¹. To avoid losing the tissue pellet you may mechanically retain it using a pipette. Dissociate the tissue into a single cell suspension by adding 3 ml astrocyte plating medium (APM) and vigorous pipetting using a 10ml plastic pipette until tissue pieces are dissociated into single cells (~30 times). Triturate slowly at first, and

¹ And not the liquid trash container as it may lead to contamination.

gradually increase speed as pieces dissociate. Don't introduce bubbles. Adjust volume to 6 ml using APM.

9. Use a 70um nylon mesh to separate chunks of tissue.
10. You can prove the dissociation of the cortex tissue into single cells by counting using a hemacytometer. Transfer 10 ul of cell suspension to 40ul Trypan Blue. One preparation of 1 mouse pup cortices should yield $2.5-3.745 \times 10^6$ dissociated single cells.
11. Transfer the cell suspension to the PDL-coated T25 flask.

B. Plating Astrocyte-enriched Culture

1. Do not disturb the culture for 2 days. After 2 days, gently remove the flask from the incubator, stand upright and change the medium completely. At later feedings, you don't need to be this careful. Change 2/3 of the media every 3 days thereafter (aspirate 4 ml and add 4 ml fresh medium). Neurons will wither and die without the proper supplements in media after DIV1.
2. On late day 5, add APM supplemented with insulin such that final concentration in the flask will be 5ug/ml. (aspirate 3 ml and add 3 ml of APM + 10ug/ml Insulin)
3. By day 6, an astrocyte monolayer should clearly be visible.
4. Astrocytes grown to confluency are identifiable as a monolayer of large, flat cells in a "brick wall" arrangement. After 7 to 8 days, when astrocytes are confluent and overlaying microglia sit exposed on the astrocyte layer or are already detached from the astrocyte layer, shake the T25 flask at 50 rpm for 45 min on an orbital shaker to remove loosely attached microglia. Don't disturb the astrocyte

layer, stand the flask upright. Discard the supernatant containing microglia or if you wish to culture and examine microglia, spin it down and plate for culture.

This will yield highly enriched microglial population. Put APM+Insulin (5ug/ml) in 5%CO₂ incubator for 6 hours.

5. Add 6 ml fresh APM+Insulin (5ug/ml) and continue by shaking the flask at 220 rpm for 18-21 hr to remove oligodendrocyte precursor cells (OPC). Discard the supernatant or spin it down and plate, if you wish to culture OPCs...
6. Add 120 ul of 1 mM Cytosine Arabinofuranoside to 6 ml astrocyte plating medium. (working concentration of Ara-C : 20uM)
7. Incubate in 8.5%CO₂ for 48 hours.
8. Refresh medium and allow cells to recover for 24 hours.
9. Repeat steps 6,7,8 (2nd cytosine arabinoside treatment).
10. Rinse the remaining confluent astrocyte layer twice with PBS, aspirate the PBS, add warm 3 ml 0.25% trypsin-EDTA and incubate in the CO₂ incubator at 37 °C. Check detachment of astrocytes every 5 min and enforce detachment of astrocytes by hitting the flask on the sides (2-3 times).
11. After astrocytes are detached from the culture flask, add 4 ml of astrocyte culture medium, spin cells at 180 x g for 5 min, aspirate supernatant and add 12 ml fresh astrocyte plating medium. One T25 tissue culture flask should yield around 2.5x10⁵ cells after the first cell split. Plate cells in two T25 culture flasks and incubate at 37 °C in the CO₂ incubator. Change the medium every 2 to 3 days. Alternatively seed directly on coverslips for ICC.
12. You can passage a couple more times.

C. Plating Microglia-enriched Culture

Population 1

1. After obtaining microglial suspension, filter it with 70um nylon mesh, then transfer it to a 15 ml Falcon tube and spin at 300g, 5min.
2. Careful! The pellet is very loose, aspirate supernatant carefully. Re-suspend pellet with 500 ul microglia plating medium (DMEM + 10% FES + 1% Penicillin/Streptomycin).
3. Count cell density by hemocytometer and bring it to 2×10^5 cells/ml with microglia plating medium.
4. Plate appropriate amount to the PDL-coated coverslips or wells/dishes. Allow microglia to adhere overnight. Use microglia in experiments after 2 days.

Population 2

1. After the overnight shake (step A5) and differential adhesion step (D2), add 1 ml 0.25% Trypsin-EDTA and add 4 ml of microglial plating medium as soon as you observe the cells detach.
2. Pellet cells at 300g, 5min.
3. Count and plate as in Population1. There might be residual astrocytes in this population.

D. Plating Oligodendrocyte Precursor Cells-enriched Culture

1. Equilibrate empty untreated Petri dishes in 5% CO₂ incubator for 30 min.
2. Transfer cell suspension with OPCs to the untreated Petri dishes (OPCs tend to attach to dishes treated for tissue culture) for 45 minutes at 37°C in 5% CO₂ incubator. Differential adhesion of microglia and astrocytes will separate them from OPCs.
3. Once the incubation is complete, examine the dishes under bright field. OPCs are identified as small cell clumps, typically of 3-5 cells but sometimes form large aggregates resembling neurospheres. Gently swirl the plates to detach any loosely adhered OPCs, and transfer the cell suspension from each plate into a 15mL conical tube.
4. Spin down cells at 300g, 5min.
5. Resuspend the pellet in 500ul of OPC medium with a P1000 pipette tip, followed by resuspension with a P200 pipette tip. (OPCs tend to grow in clumps).
6. Count the cells with a hemocytometer. Add appropriate amount of OPC medium so that the density is $2-5 \times 10^4$ cells/ml. Change half of the medium every other day.
7. Plate the cell suspension on poly-ornithine-coated plates for OPC proliferation with OPC medium.
8. For differentiation of OPCs into oligodendrocytes, change the medium to Oligodendrocyte differentiation medium. After 48 hours, oligodendrocyte-specific markers will appear.
9. Co-cultures of oligodendrocytes and neurons can also be achieved.

Immunofluorescence

To visualize mitochondria *in vitro*, the cells were incubated with 100 nM MitoTracker Red CMXRos (Invitrogen M7512) for 25 minutes at 37°C, 5% CO₂, then proceeded with the Immunofluorescence protocol. The cells were washed with 1X PBS (FisherScientific BP3994) and fixed with 4% paraformaldehyde (PFA) at room temperature for 10 minutes. Following steps were done in order: 3 5-minute 1X PBS washes, 10-minute permeabilization in PBS with 0.25% TritonX-100 (T8787, Sigma); 1-hour blocking with 10% Normal Goat Serum (NGS, JacksonImmunoResearch, 005-000-121) in PBS with 0.1% TritonX-100 (PBST); overnight incubation with primary antibody in 2% NGS-PBST; three washes with PBST; 1-hour incubation with secondary antibody; three washes with PBST; counterstaining with DAPI. Zeiss LSM800 confocal microscope was used. Images were processed and analyzed with ImageJ (RRID:SCR_003070).

Figure Legends

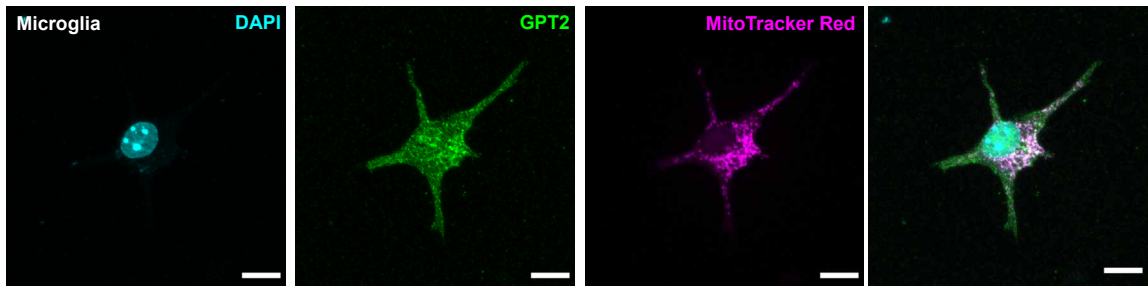
Figure A3.26. GPT2 staining in oligodendrocyte precursor cells and microglia in vitro.

A. GPT2 staining in microglia. DAPI (cyan), GPT2 (green), MitoTracker Red (magenta) and the merged imaged on the far right. Scale bar: 10 μ m.

B. GPT2 staining in oligodendrocyte precursor cells (OPCs). DAPI (cyan), GPT2 (green), MitoTracker Red (magenta) and the merged imaged on the far right. Scale bar: 10 μ m.

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2. Marques, S., D. van Bruggen, D.P. Vanichkina, E.M. Floriddia, H. Munguba, L. Varemo, S. Giacomello, A.M. Falcao, M. Meijer, A.K. Bjorklund, et al., *Transcriptional Convergence of Oligodendrocyte Lineage Progenitors during Development*. Dev Cell, 2018. **46**(4): p. 504-517 e7.

A



B

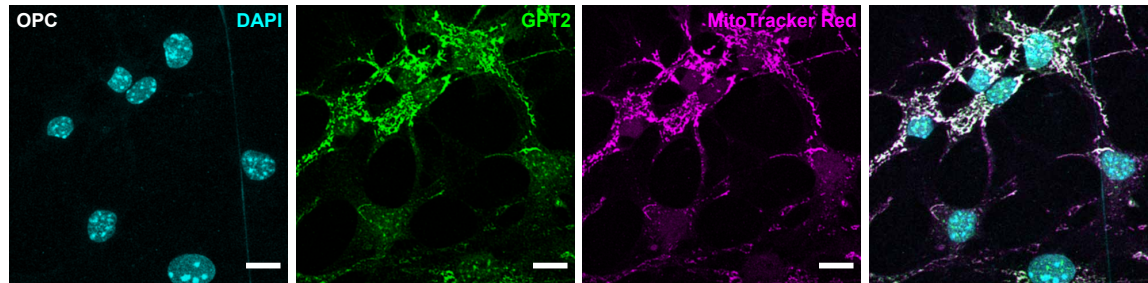


Figure A3.26. GPT2 staining in oligodendrocyte precursor cells and microglia in vitro.

Appendix A.3.9. Metabolomics in isolated mitochondria and cytosol fractions of Gpt2-null forebrains at P19.

Introduction

I performed metabolomics on cytosolic and mitochondrial fractions obtained from homogenization of wild-type and Gpt2-null whole mouse brains at postnatal day 18. This would allow us to observe differences in changes of metabolite pools in different cellular compartments. For example, glutamate concentration in neurons is much greater than that of alanine, pyruvate or alpha-ketoglutarate and this may be the reason why the predicted direction of the Gpt2 reaction is alanine production. Therefore, with the absence of Gpt2, glutamate levels in the mitochondria may increase and the cytosolic glutamate levels may not change. This prediction is not supported by the metabolomics data obtained from the whole hippocampus tissue where the Gpt2-null samples had a decreased glutamate level.

Results / Key Points

- Mitochondrial data has similar trends in phosphoenolpyruvate, 2-hydroxyglutarate, glutathione, fumarate, proline, malate, maleic acid, 2-ketoisovalerate as in whole brain and hippocampus tissue data.
- Cytosol data has similar trends in lysine, glucose-6-phosphate, glucose-1-phosphate, fructose-6-phosphate, maleic acid, SBP, threonine, glutathione, proline, fumarate, fructose-1,6-bisphosphate, sn-glycerol-3-phosphate, carnitine, 2-hydroxyglutarate, glutamine, ornithine, succinate as in whole brain and hippocampus tissue data.
- Alanine was decreased though with considerably more variability.

- Glutamate levels were trending toward a decrease in both cytosolic and mitochondrial fractions but no statistical significance was reached.

Discussion

It was very surprising to find that data for alanine had so much variability; in the whole tissue metabolomics data alanine significance had the one of the lowest raw p-values, if not the lowest, of all the data. This may be a variability inherent to fractionation of the whole brain or simply variation within this particular experiment. The inherent variability of fractionation consists of heterogeneity of the whole brain, the time taken to obtain the different fractions (1.5 hours for mitochondria, 0.5 hours for the cytosol fraction). The time spent in sucrose-based homogenization solution may cause washing away or decay of metabolites. Another important consideration is that mitochondria used for metabolomics originate from extra-synaptosomal mitochondria, i.e. the soma. Synaptosomes, isolated synaptic terminals, form during homogenization of brain tissue in sucrose-based solutions and contain copious amount of mitochondria. There are ways to extract the mitochondria (e.g. with digitonin) but it would further introduce chemical intervention and change the metabolome even further.

There are novel and fast ways to extract mitochondria *in vivo* under 12 minutes [1]. Mito-tag mice allow for conditional expression of the tag which allows for mitochondrial extraction from specific cell types. It would be very interesting to try extracting mitochondria belonging to different cell types (glutamatergic neurons vs. GABAergic

neurons) in Gpt2-null mice; this may pinpoint the differential mechanisms in the pathophysiology of Gpt2 deficiency.

Available Data (not shown): a) all heat maps and tables associated with the metabolomics data.

Method

Subcellular Fractionation of the mouse brain

The protocol was adapted from [2]. The whole brain including cerebellum was immediately removed after cervical dislocation and rinsed in ice-cold 1X Brain homogenization buffer (0.320 M Sucrose, EDTA 1mM, Tris base 5 mM, pH 7.4). After decanting, fresh 10ml/gr 1X Brain homogenization buffer was added, and the brain was cut into small chunks with surgical scissors. A Kimble pestle and motor were used to homogenize the tissue with 12 strokes each lasting 4 seconds. The tube was spun at 1300g for 3 minutes at 4°C. The 1st supernatant was put aside on ice and the pellet was re-suspended in half starting volume with 1X Brain homogenization buffer. The pellet was homogenized with a Kimble pestle and motor with 8 strokes each lasting 4 seconds. The tubes were spun at 1300g for 3 minutes at 4°C. This 2nd supernatant was combined with the first and the sample was spun at 10000g for 10 minutes at 4°C with Sorvall RC6Plus using the SS34 rotor. The supernatant is the cytosolic fraction. The pellet was re-suspended in 10m/gr original tissue of 15% Percoll (Percoll, Cytiva 17089102 prepared in 1X Brain homogenization buffer). The suspension was carefully layered onto a Percoll gradient (23% - 40%) and the tube was spun at 22000g for 10 minutes at 4°C.

The bottom layer is the mitochondria. After carefully removing the upper layers, the mitochondria were aspirated and re-spun with 4 volumes of 1X Brain homogenization buffer, at 11600rpm for 10 minutes at 4°C. The supernatant was removed, and 4 volumes of Tyrode-like buffer (118mM NaCl, 5mM KCl, 1mM MgCl₂, 1.2mM CaCl₂, 0.1 mM Na₂HPO₄.H₂O, 20mM HEPES, 10mM Glucose, pH7.4) was added. The tube was spun at 18000g for 10 minutes at 4°C. After carefully removing the supernatant, the mitochondria were resuspended in 0.5 ml/gr (of original tissue) fatty-acid free bovine serum albumin (BSA) (10mg/ml in 1X Brain homogenization buffer). The final volume was brought to 3ml/gr (of original tissue) and tube was spun at 6900g for 10 minutes at 4°C with a tabletop centrifuge. The final pellet was re-suspended in 80% (v/v) methanol (cooled to -80°C).

Metabolomics. Done as described with minor modifications [3]. The mitochondria fraction was immersed in 500µL of 80% (v/v) high-performance liquid chromatography (HPLC)-grade methanol (cooled to -80°C), vortexed for 1 minute and incubated at -80°C for 4 hours. To pellet debris, the sample was centrifuged at 14000g for 10 min at 4°C. While the supernatant was kept at -80°C, 400 ul of 80% (vol/vol) methanol (cooled to -80°C) was added to the pellet, which was then vortexed for 1 minute, incubated at -80°C for 30 minutes and then centrifuged at 14000g for 10 minutes at 4°C. The supernatants were combined and re-spun at 14000g for 10 minutes 4°C. The supernatants were concentrated with SpeedVac at ambient temperature. The cytosolic fraction was centrifuged at 14,000 g for 10 minutes at 4°C. Methanol (cooled to -80°C) was added to the supernatant so that the final solution is 80% (v/v) methanol and incubated at -80°C for 7 hours. The mixture was centrifuged at 14000 g for 10 minutes at 4°C. The supernatants

were concentrated with SpeedVac at ambient temperature. The dried pellets were kept at -80°C until the day of mass spectrometry.

Tandem mass spectrometry was done at Beth Israel Deaconess Medical Center Mass Spectrometry Facility. The samples were re-suspended in liquid chromatography (LC)/mass spectrometry (MS)-grade water and run in tandem LC-MS/MS. Samples were injected into hydrophilic interaction liquid chromatography (HILIC) at high pH using HPLC coupled to a 5500 QTRAP mass spectrometer (AB/SCIEX). Selected Reaction Monitoring (SRM) mode for 300 transitions with positive/negative polarity switching fragmented precursor ions and select for product ions. Peak areas for each detected metabolite were integrated using MultiQuant software (AB/SCIEX). The statistical analyses and data visualization were done using MetaboAnalyst 4.0 [4] (RRID:SCR_015539). If half of data for a metabolite is not available than that metabolite was omitted from analysis. All data was normalized by median normalization and auto-scaled (mean-centered and divided by standard deviation of each variable). Unpaired Student's t-test assuming equal variance was used to generate a p-value.

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Appendix A.3.10. Metabolomics in Gpt2-null hippocampus on zero alanine diet P18.

Introduction

We investigated changes of the metabolome in the hippocampus obtained from Gpt2-null mice fed with No Alanine diet (0% w/w) ad libitum at P18. It is possible that decreased alanine levels in the diet may exacerbate or quicken the phenotype in Gpt2-null mice.

Key Points

- The metabolic profile of the Gpt2-null hippocampus on No Alanine (0% w/w) at P18 very closely resembles the profile obtained from mice on Regular Diet P18.

Results

The principal component analysis shows that the metabolic profiles of wild-type and Gpt2-null groups were well separated. The list of metabolites that were significantly changed along with the fold changes resemble very closely with the results obtained from mice on Regular Diet at P18.

Discussion

Total alanine that is received by the pups cannot be empirically controlled as the mother gives alanine in the milk, however no alanine in the diet could have worsen the phenotype. To my knowledge, there is no specific way of blocking alanine entry into the brain either, the transporters that carry alanine also carry other neutral amino acids such as serine and glutamine. While it is not possible to eliminate alanine altogether, it is possible to deliver nutrients intraperitoneally or intracranially using an osmotic pump, however this is technically challenging. Other methods such as oral gavage or i.p. injections would have to be done

continuously throughout the day (and night) to ensure high levels of the nutrient in the circulation and this is both stressful to the mice and technically challenging.

Method

As performed in Chapter 3 – Metabolomics.

Figure A.3.27. Metabolomics in Gpt2-null hippocampus at P14 from mice on High Alanine diet.

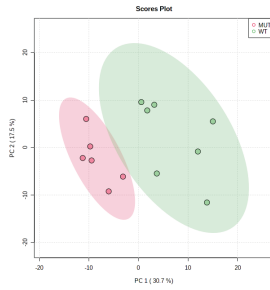
A. 2D-score plot of Principal Component Analysis. Wild-type (green), Gpt2-null (red).

B. List of significantly changed metabolites in Gpt2-null hippocampus on High Alanine diet at P14.

The metabolites were ordered according to their raw P value. FDR: False discovery rate. Fold changes are given as fraction of the averaged wild-type peak intensity value. The “trend” column refers to the comparison of results obtained from Regular diet and High Alanine diet; if there was a significant change in the same direction for that metabolite in both diets, it is named as “Same”; if there was an opposite trend, then “Opposite”. For example, alanine was significantly decreased in the Gpt2-null hippocampus compared to wild-type on High Alanine diet and similarly alanine was significantly decreased in the Gpt2-null hippocampus compared to wild-type on Regular Diet (hence “Same”).

A

Principal Component Analysis



B

	Fold Change	raw p value	FDR	Trend		Fold Change	raw p value	FDR	Trend		Fold Change	raw p value	FDR	Trend
fructose-1,6-bisphosphate	2.1107	1.71E-08	4.90E-06	Same	S-adenosyl-L-methionine	2.7405	0.003315	0.02495		cystathionine	1.2778	0.019097	0.07282	Same
serine	0.51333	4.94E-08	7.06E-06	Same	creatine	0.7761	0.003581	0.02626	Same	adenine	0.81393	0.020479	0.07707	
proline	1.6873	3.99E-06	0.00029	Same	xanthosine	0.64211	0.00397	0.02838	Opposite	L-arginino-succinate	1.5159	0.02084	0.07741	
dTMP	1.9196	4.01E-06	0.00029	Same	aconitate	0.48629	0.004448	0.03028		Methionine sulfoxide	0.51161	0.021432	0.07858	
homoserine	0.38865	9.03E-06	0.00052		1-Methyladenosine	0.7384	0.004521	0.03028		GDP	0.693	0.022244	0.08053	
D-glyceraldehyde-3-phosphate	1.7966	2.23E-05	0.00107	Same	D-glucosamine-6-phosphate	1.7257	0.004552	0.03028	Same	purine	1.4078	0.02391	0.08548	
glycerate	0.44716	5.08E-05	0.00208		dAMP	0.74125	0.005031	0.0327		betaine aldehyde	0.81006	0.026007	0.09183	
glutathione disulfide	0.67554	0.000133	0.00477		taurine	0.76611	0.005238	0.03329	Same	D-glucono- γ -lactone-6-phosphate	1.7122	0.026534	0.09254	Same
glucose-6-phosphate	2.4204	0.000212	0.00674	Same	sarcosine	0.77451	0.005466	0.03392		dGMP	0.80711	0.029148	0.10044	
1-Methyl-Histidine	2.4413	0.000326	0.00933		dGDP	0.69491	0.005864	0.03392		Glycerophosphocholine	0.71607	0.030432	0.10266	
fructose-6-phosphate	2.4874	0.000377	0.00955	Same	succinate	0.68891	0.005948	0.03392	Same	acetoacetyl-CoA	1.9568	0.030511	0.10266	
malate	0.65137	0.000401	0.00955	Same	Carbamoyl phosphate	0.78131	0.006079	0.03392		deoxyadenosine	0.12209	0.031165	0.10279	
valine	1.5929	0.00053	0.01083	Same	acetylphosphate	1.2148	0.006168	0.03392	Same	methionine	0.52598	0.03142	0.10279	
dephospho-CoA	1.7114	0.000573	0.01089	Same	ADP	0.6598	0.006607	0.03515		glyoxylate	0.51123	0.032054	0.10279	Same
myo-inositol	0.68088	0.00062	0.01109		4-aminobutyrate	0.8103	0.006787	0.03515		Pyrophosphate	0.80408	0.032347	0.10279	Opposite
D-glucuronate	0.76556	0.000888	0.01423		acadesine	0.50094	0.006856	0.03515	Opposite	hydroxyproline	0.70783	0.033901	0.10526	Same
CMP	0.80244	0.000914	0.01423		arginosuccinic acid	1.5429	0.006882	0.03515		N-acetyl-L-ornithine	0.38954	0.034158	0.10526	
alanine	0.76443	0.001051	0.01423	Same	IDP	0.69676	0.007717	0.03872		glycolate	0.67437	0.034404	0.10526	
AMP	0.80963	0.001058	0.01423	Same	glutathione	0.76442	0.008054	0.03971	Same	phosphocreatine	1.5958	0.034668	0.10526	
O-acetyl-L-serine	0.41926	0.001071	0.01423		hydroxyphenylpyruvate	0.65941	0.00885	0.0429		Urea	0.67147	0.035249	0.10526	
leucine-isoleucine	1.494	0.001094	0.01423	Same	S-adenosyl-L-homocysteine	0.74101	0.009558	0.04487		α -ketoglutarate	1.1701	0.035331	0.10526	Same
4-Pyridoxic acid	0.59833	0.001433	0.01665		D-erythrose-4-phosphate	1.5329	0.00957	0.04487	Same	xanthosine-5-phosphate	0.54002	0.049203	0.13327	
IMP	0.75453	0.001455	0.01665		Methylmalonic acid	0.72966	0.009756	0.04501	Same	thymine	0.77027	0.04942	0.13327	
N-acetyl-L-alanine	0.75971	0.001544	0.01699		Ng,NG-dimethyl-L-arginine	1.3425	0.011563	0.05249	Same	S-ribosyl-L-homocysteine	0.72185	0.0373	0.10998	Same
D-sedoheptulose-1-7-phosphate	1.4856	0.001721	0.01823	Same	fumarate	0.81983	0.013426	0.06	Same	dTTP	2.2683	0.03934	0.1133	
citruiline	1.7379	0.001896	0.01937	Same	Kynurenine	1.7308	0.015494	0.06724		N-acetyl-glutamine	0.77846	0.039425	0.1133	
cysteine	0.42511	0.002034	0.01985	Same	adenosine 5-phosphosulfate	0.70695	0.015773	0.06724		thymidine	0.68615	0.039819	0.1133	
arginine	1.7545	0.002082	0.01985	Same	dihydroxy-acetone-phosphate	1.4361	0.015907	0.06724	Same	3-hydroxybuterate	0.68684	0.040011	0.1133	
2-keto-isovalerate	0.79313	0.002168	0.02	Same	N-acetyl-aspartylglutamic acid	0.77936	0.015986	0.06724		O8P-O1P	1.25	0.043703	0.12254	Same
trehalose-6-Phosphate	0.71357	0.002444	0.02164		phosphoenolpyruvate	1.5227	0.016634	0.06895	Same	NADH	0.61834	0.047177	0.131	
Maleic acid	0.8044	0.002497	0.02164	Same	aminoimidazole carboxamide					uridine	0.73572	0.049114	0.13327	
indole	1.6595	0.002916	0.02396		ribonucleotide	0.64278	0.017352	0.07089						
tryptophan	1.6235	0.002932	0.02396		Citraconic acid	0.53767	0.01801	0.07157						
					Methylcysteine	0.80616	0.018106	0.07157						
					N-acetylglucosamine-1-phosphate	0.72423	0.018269	0.07157						
dCMP	0.75774	0.003234	0.02495		phosphate	0.72423	0.018269	0.07157						
N-acetyl-glutamate	0.8066	0.003261	0.02495		dimethylglycine	0.65552	0.019088	0.07282	Opposite					

Figure A.3.27. Metabolomics in Gpt2-null hippocampus at P14 from mice on High Alanine diet.

A. 2D-score plot of Principal Component Analysis. Wild-type (green), Gpt2-null (red).

B. List of significantly changed metabolites in Gpt2-null hippocampus on High Alanine diet at P14.

The metabolites were ordered according to their raw P value. FDR: False discovery rate.

Fold changes are given as fraction of the averaged wild-type peak intensity value.

The “trend” column refers to the comparison of results obtained from Regular diet and

High Alanine diet; if there was a significant change in the same direction for that metabolite in both diets,

it is named as “Same”; if there was an opposite trend, then “Opposite”. For example, alanine was

significantly decreased in the Gpt2-null hippocampus compared to wild-type on High Alanine diet and

similarly alanine was significantly decreased in the Gpt2-null hippocampus compared to wild-type on

Regular Diet (hence “Same”).

Appendix A3.11. Metabolomics in Gpt2-null hippocampus on high alanine diet P14.

Introduction

We investigated changes of the metabolome in the hippocampus obtained from Gpt2-null mice fed with High Alanine diet (5% w/w) ad libitum at P14. Differences with the results obtained from mice on Regular Diet (1% w/w) may lead to different interpretations. If at P14, the metabolic profile of the Gpt2-null hippocampus is better than the profile obtained from mice fed with Regular Diet, most likely Gpt2-null pups benefit from the mother, despite the first-pass metabolism (particularly in the liver) as at P14 the main source of nourishment for the pups is still the mother's milk. If at P14, the results are the same as Regular Diet, then we can conclude that the pups do not majorly benefit from the mother's milk at this time and the changes seen at P18 can be attributable to the pup's newly acquired ability to feed on solid chow. This is particularly important for alanine, if alanine levels do not improve at P14 then we are safe to assume that the pups do not benefit from the milk at this time.

Key Points

- The metabolic profile of the Gpt2-null hippocampus on High Alanine (5% w/w) at P14 very closely resembles the profile obtained from mice on Regular Diet P14.

Results

The principal component analysis shows that the metabolic profiles of wild-type and Gpt2-null groups were well separated. The list of metabolites that were significantly changed along with the fold changes resemble very closely with the results obtained from

mice on Regular Diet at P14. The most notable difference was that glutamate levels were not significantly changed in Gpt2-null hippocampus on High Alanine diet at P14 whereas there was a slight decrease (~10%) in mice on Regular Diet.

Discussion

Most likely the mother metabolizes the extra alanine and does not pass on supplementary alanine to the pup. Currently, we do not know if serum alanine levels in Gpt2-heterozygous mice are increased after ingestion of High Alanine diet, as serum alanine levels most likely have the biggest influence on the mother's milk composition.

Method

Metabolomics was performed as in Chapter 3.

Figure Legends

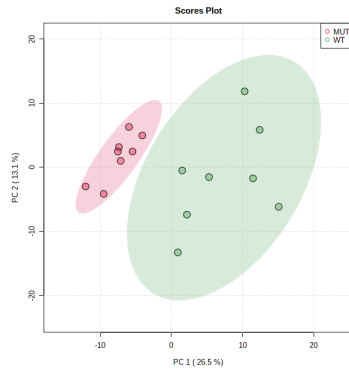
Figure A.3.28. Metabolomics in Gpt2-null hippocampus at P14 from mice on High Alanine diet.

A. 2D-score plot of Principal Component Analysis. Wild-type (green), Gpt2-null (red).

B. List of significantly changed metabolites in Gpt2-null hippocampus on High Alanine diet at P14. The metabolites were ordered according to their raw P value. FDR: False discovery rate. Fold changes are given as fraction of the averaged wild-type peak intensity value. The “trend” column refers to the comparison of results obtained from Regular diet and High Alanine diet; if there was a significant change in the same direction for that metabolite in both diets, it is named as “Same”; if there was an opposite trend, then “Opposite”. For example, alanine was significantly decreased in the Gpt2-null

hippocampus compared to wild-type on High Alanine diet and similarly alanine was significantly decreased in the Gpt2-null hippocampus compared to wild-type on Regular Diet (hence “Same”).

A Principal Component Analysis



	Fold Change	raw p-value	FDR	Trend		FC	p-value	FDR	Trend
cystathionine	2.0344	3.73E-09	1.07E-06	Same	CMP	0.8745	0.00299	0.01636	Same
glutathione disulfide	0.66257	2.58E-06	0.00026	Same	lactate	0.8577	0.00303	0.01636	Same
serine	0.66979	2.71E-06	0.00026	Same	4-aminobutyrate	0.8611	0.00318	0.01685	Same
glutathione	0.69301	5.66E-06	0.00035	Same	2-Aminooctanoic acid	0.6394	0.00338	0.01758	Same
myo-inositol	0.74261	6.41E-06	0.00035	Same	2-keto-isovalerate	0.8542	0.00493	0.02519	Same
valine	1.4053	7.73E-06	0.00035	Same	Creatinine	0.8592	0.00667	0.03348	Same
proline	1.4856	8.55E-06	0.00035	Same	Nicotinamide Riboside	0.7069	0.00707	0.03485	Same
sarcosine	0.79492	1.27E-05	0.00039	Same	2-ketohexanoic acid	0.8062	0.00729	0.03534	Same
lysine	1.6335	1.39E-05	0.00039	Same	thymidine	0.7072	0.01068	0.05068	Same
glycerate	0.55017	1.47E-05	0.00039	Same	D-erythrose-4-phosphate	1.218	0.01081	0.05068	Same
N-acetyl-glutamate	0.76016	1.51E-05	0.00039	Same	2-Isopropylmalic acid	0.5886	0.01177	0.05363	Same
Glycerophosphocholine	0.68235	2.72E-05	0.00063	Same	Ascorbic acid	0.5739	0.01195	0.05363	Same
glutathione disulfide	0.68381	2.87E-05	0.00063	Same	cytidine	0.6965	0.012	0.05363	Same
Pyrophosphate	0.82546	5.95E-05	0.0012	Same	Acetylcarnitine DL	0.8831	0.01219	0.05365	Same
fructose-1,6-bisphosphate	1.4465	6.31E-05	0.0012	Same	Hydroxyphenylacetic acid	0.7049	0.01265	0.0548	Same
N-acetyl-L-alanine	0.83936	9.18E-05	0.00164	Same	CDP	0.7367	0.01304	0.05566	Same
alanine	0.811	0.00015	0.00255	Same	ribose-phosphate	0.6987	0.01347	0.05664	Same
hydroxyphenylpyruvate	0.75995	0.00016	0.00255	Same	asparagine	1.1528	0.01388	0.05683	Same
fructose-6-phosphate	1.6959	0.00018	0.00275	Same	Thiamine pyrophosphate	0.3253	0.01391	0.05683	Same
succinate	0.71283	0.00023	0.00327	Same	dCDP	1.6918	0.01427	0.05746	Opposite
hydroxyproline	0.53947	0.00028	0.00385	Same	Kynurenine	2.063	0.01446	0.05746	Opposite
histidinol	0.65753	0.00051	0.00638	Same	xanthine	0.8172	0.01534	0.06012	Same
Methylmalonic acid	0.70086	0.00054	0.00638	Same	AMP	0.8592	0.01609	0.0622	Same
GDP	0.61099	0.00062	0.00684	Same	N-acetyl-L-aspartic acid	0.877	0.01662	0.06337	Same
D-sedoheptulose-1-7-phosphate	1.3631	0.00064	0.00684	Same	spermidine	1.6078	0.01984	0.07397	Same
glucose-6-phosphate	1.8325	0.00068	0.00684	Same	cytosine	0.8041	0.01991	0.07397	Same
ornithine	1.4066	0.00068	0.00684	Same	putrescine	0.3749	0.02023	0.07416	Same
Carbamoyl phosphate	0.7976	0.00069	0.00684	Same	uracil	0.4962	0.02198	0.07871	Opposite
Pyroglutamic acid	1.2792	0.00081	0.00747	Opposite	leucine-isoleucine	1.2821	0.02217	0.07871	Same
allantoin	0.74271	0.00081	0.00747	Same	dihydroxy-acetone-phosphate	1.7505	0.02229	0.07871	Same
CDP-ethanolamine	0.77771	0.00096	0.00851	Same	S-adenosyl-L-homocysteine	0.8304	0.02274	0.0793	Same
homoserine	0.66922	0.00099	0.00851	Same	uridine	0.7321	0.02502	0.08562	Same
citrulline	1.2604	0.00101	0.00851	Same	diphosphate	0.733	0.02515	0.08562	Same
dTMP	1.5429	0.0011	0.009	Same	adenine	0.8537	0.02617	0.08806	Opposite
arginine	1.2814	0.00125	0.0099	Same	deoxyadenosine	0.5936	0.0283	0.09413	Same
glucosamine	0.5482	0.00142	0.01086	Same	4-phosphopantothenate	0.7898	0.029	0.09534	Same
S-adenosyl-L-homocysteine	0.74829	0.00147	0.01086	Same	inosine	0.7415	0.03056	0.09931	Same
dephospho-CoA	1.4808	0.00148	0.01086	Same	2,3-dihydroxybenzoic acid	0.607	0.0319	0.10252	Same
glutathione	0.71577	0.00167	0.01165	Same	S-adenosyl-L-methionine	1.2343	0.03353	0.10655	Opposite
betaine	0.66677	0.00167	0.01165	Same	methionine	1.1835	0.03425	0.10764	Same
creatine	0.8568	0.0018	0.01228	Same	Taurodeoxycholic acid	0.5925	0.03545	0.10923	Same
2-hydroxygluturate	0.85984	0.00185	0.01231	Same	Phosphorylcholine	0.8632	0.03552	0.10923	Same
threonine	1.2374	0.00196	0.01245	Same	S-methyl-5-thioadenosine	2.0477	0.03789	0.11529	Same
UMP	0.86347	0.002	0.01245	Same	N-carbamoyl-L-aspartate	0.8519	0.03938	0.11854	Same
Maleic acid	0.85285	0.002	0.01245	Same	dTDP	0.6649	0.04012	0.11952	Same
cyclic-AMP	0.69201	0.00217	0.01321	Same	D-glyceraldehyde-3-phosphate	2.0442	0.0409	0.1206	Same
citrate-isocitrate	0.64446	0.00244	0.01454	Same	N-acetyl-glucosamine	0.7894	0.04444	0.1297	Same
fumarate	0.87589	0.0027	0.01527	Same	IMP	0.8419	0.04731	0.13581	Same
citrate	0.65362	0.0027	0.01527	Same	1-Methyladenosine	0.7249	0.04749	0.13581	Same
N-acetyl-glucosamine-1-phosphate	0.80588	0.00272	0.01527	Same	isocitrate	0.7028	0.0494	0.13987	Same

Figure A.3.28. Metabolomics in Gpt2-null hippocampus at P14 from mice on High Alanine diet. A. 2D-score plot of Principal Component Analysis. Wild-type (green), Gpt2-null (red). B. List of significantly changed metabolites in Gpt2-null hippocampus on High Alanine diet at P14. The metabolites were ordered according to their raw P value. FDR: False discovery rate. Fold changes are given as fraction of the averaged wild-type peak intensity value. The “trend” column refers to the comparison of results obtained from Regular diet and High Alanine diet; if there was a significant change in the same direction for that metabolite in both diets, it is named as “Same”; if there was an opposite trend, then “Opposite”. For example, alanine was significantly decreased in the Gpt2-null hippocampus compared to wild-type on High Alanine diet and similarly alanine was significantly decreased in the Gpt2-null hippocampus compared to wild-type on Regular Diet (hence “Same”).

Appendix 3.12. ¹³C labeling in alpha-ketoglutarate using U-¹³C-glutamine precursor in Gpt2-null astrocytes in vitro.

Introduction

This section contains data for U-¹³C-Glutamine labeling of alpha-ketoglutarate in astrocytic cultures.

Results/Key Points

- Reduced fractional enrichment of ¹³C labeled alpha-ketoglutarate in Gpt2-null astrocytes in vitro.

Discussion

There is decrease in glutamine-fueled anaplerosis (replenishment of the TCA cycle). We currently lack the labeling data for other TCA cycle intermediates malate, fumarate and succinate but they would be reinforcing the observed result with alpha-ketoglutarate.

Method

See Chapter 3 Methods for Isotope Tracing.

Figure Legends

Figure A.3.29. Decreased ¹³C labeling in alpha-ketoglutarate using U-¹³C-glutamine in Gpt2-null astrocytes.

A. Fractional enrichment of ¹³C labeling in alpha-ketoglutarate in wild-type (blue) and Gpt2-null (red) astrocytes in vitro. The raw p-value of the Student's t-test wild-type vs. Gpt2-null comparison are given on the figure. n (wild-type) = 6, n (Gpt2-null) = 5.

A

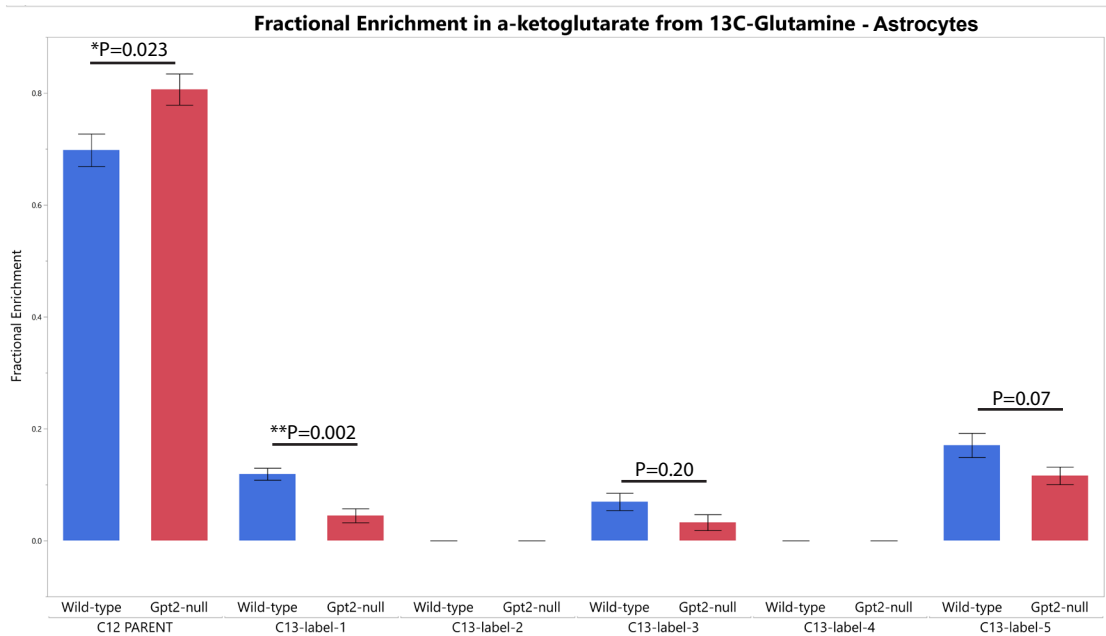


Figure A.3.29. Decreased ^{13}C labeling in α -ketoglutarate using U- ^{13}C -glutamine in Gpt2-null astrocytes. A. Fractional enrichment of ^{13}C labeling in α -ketoglutarate in wild-type (blue) and Gpt2-null (red) astrocytes in vitro. The raw p-value of the Student's t-test wild-type vs. Gpt2-null comparison are given on the figure. n (wild-type) = 6, n (Gpt2-null) = 5.

Appendix A.3.13. TMRE & DHE (dihydroethidium) & MitoSOX in Gpt2-null hippocampal neurons and astrocytes in vitro.

Introduction

Here we investigated changes in the mitochondrial membrane potential and oxidative stress in Gpt2-null hippocampal neurons and astrocytes in vitro. Mitochondrial membrane potential is formed by the electron transport chain that uses electrons resulting from substrate oxidation forming the proton gradient that constitutes the potential between the intermembrane space and the mitochondrial matrix. Gpt2 catalyzes a reaction that feeds into the TCA cycle thereby contributing to the substrate availability. Any deficits in this supply chain may result in deficits in mitochondrial membrane potential which may underlie the pathological phenotype seen in both mice and humans with Gpt2 deficiency. The mitochondrial membrane potential can be indirectly measured by tetramethylrhodamine, ethyl ester (TMRE), a cationic dye that localizes to hyperpolarized mitochondria. TMRE staining in vitro also allows for indirect quantification of mitochondrial mass or mitochondrial footprint, the area covered by the TMRE signal per cell.

Oxidative stress may also partly underlie the neurodegeneration seen in vivo thereby contributing to the phenotype seen in mice and humans. Gpt2 modulates glutamate levels and the loss of Gpt2 may have an influence on the glutamate pool that is used to make glutathione, one of the cell's main antioxidant defenses. Glutathione levels were reduced in Gpt2-null mouse brain and we found trending increases in non-mitochondrial oxygen consumption in Gpt2-null hippocampal neurons and astrocytes in vitro by using Seahorse

Extracellular Flux Analyzer, which may indicate increased levels of reactive oxygen species (ROS). To investigate oxidative stress, we stained the cells with MitoSOX, a mitochondrial superoxide anion indicator and dihydroethidium, which reacts with ROS in the cytoplasm and locates to the nucleus.

Key Points

- No differences in TMRE fluorescence intensity or mitochondrial footprint in Gpt2-null hippocampal neurons and astrocytes in vitro.
- No differences in DHE in Gpt2-null hippocampal neurons or astrocytes in vitro.
- Increased MitoSOX intensity in Gpt2-null hippocampal neurons but no differences in astrocytes in vitro.

Results

We first validated the correlation between the TMRE signal and mitochondrial membrane potential by observing the fluorescence intensity of the TMRE signal with 2 μ M FCCP, an uncoupler of the mitochondrial membrane potential. Within twenty minutes the TMRE fluorescence intensity dimmed whereas MitoTracker Green, which fluoresces independently of the mitochondrial membrane potential ([Pendergrass et al., 2004](#)) remained the same throughout. This indicates that TMRE is a valid method to indirectly measure mitochondrial membrane potential.

The TMRE fluorescence intensity did not change in either Gpt2-null hippocampal neurons grown to 14 days in vitro or astrocytes. The mitochondrial footprint, the area occupied by the TMRE staining per cell remained the same as the wild-type controls as well.

We tested for oxidative stress in Gpt2-null hippocampal neurons and astrocytes by using MitoSOX and DHE. We observe increased fluorescence intensity of MitoSOX in Gpt2-null hippocampal neurons in vitro. This increase was not apparent in the DHE staining. Gpt2-null astrocytes did not show any differences in either MitoSOX or DHE. These results indicate that there may be an increase of ROS specifically localized in the mitochondria of Gpt2-null hippocampal neurons in vitro.

Discussion

We fail to see any changes in mitochondrial membrane potential as measured by TMRE in Gpt2-null hippocampal neurons or astrocytes. These results seem to align with the Seahorse Extracellular Flux Analyzer data where there were no major differences in basal or maximal respiration. Two cautionary notes: fluorescence intensity of TMRE alone is not a direct way of assessing the absolute potential ([Gerencser et al., 2016](#)) and these values belong to mitochondria confined to the neuron soma, the mitochondria in the processes might be affected differently. It is also possible to assess the shape and connectivity of the mitochondria in these cells by the TMRE staining; however the results can be unclear. Unless there is a more obvious abnormality in the image, it is difficult to conclude whether there is a pathological shape in mitochondria in these cells. Severe fragmentation may indicate damage, while fusion of mitochondria may also indicate damage and indicate a way in which mitochondria try to share the restricted amount of metabolites. Electron microscopy in vitro or in vivo may help address these questions more quantitatively.

There was a trending increase in non-mitochondrial oxygen consumption in the Gpt2-null hippocampal neurons and astrocytes as measured by Seahorse Extracellular Flux

Analyzer (Refer to Appendix to Chapter 3). This may result from oxidases or ROS that may or may not be in the mitochondria. The increased MitoSOX signal in Gpt2-null hippocampal neurons may be in agreement with the Seahorse findings, even though we fail to see an increase in astrocytes. It must be noted that both MitoSOX and DHE are poor indicators of superoxide anion specifically (Zielonka and Kalyanaraman, 2010) and must be regarded as indirect ways to look at ROS in culture.

Method

Cell Culture

Mouse primary hippocampal neuron culture. Hippocampal neurons were cultured as described previously (Ouyang et al., 2013): Hippocampi from P0-1 pup were dissected in Hank's Balanced Salt Solution (HBSS) (Gibco 14170-112) and placed in 500µl of 20U/ml papain (Worthington LK003176, in Earle's Balanced Salt Solution (EBSS), Worthington, LK003188). The tube with hippocampi/papain was incubated at 37°C for 15 minutes. The tissue was triturated with 1ml pipette tip for 12 strokes. The tissue was further incubated at 37°C for 15 minutes and triturated. The remaining bits of tissue sunk and the solution with dissociated cells was spun in a separate tube at 300g, 5 minutes, at RT. The cell pellet was dissolved gently in Inhibitor Solution (540µl EBSS, 60µl Ovomuroid Protease Inhibitor (Worthington Biochemical, LK003182), 30µl DNase (Worthington Biochemical, LK003170) per hippocampi) and filtered through a 70µm nylon mesh (FisherScientific, 22363548). The filtered cell suspension was layered on top of 1ml Ovomuroid Protease Inhibitor and spun at 70g, 10 minutes, at RT. The supernatant was discarded, and the cell pellet was resuspended in Neurobasal A+ (NeuroBasal A (10888022), 1X B27 Supplement (ThermoFisher Scientific, 17504044), 2

mM GlutaMAX (ThermoFisher Scientific, 35050061). The full media was changed the next day and then half media every 3 days.

Mouse primary astrocyte-enriched cultures. The culturing protocol was adapted from (Albuquerque et al., 2009; Schildge et al., 2013): Cortices from P0-1 pup were dissected in HBSS, diced into 6 pieces and transferred to a 15ml conical tube. The tissue is incubated in 0.25% Trypsin-EDTA in HBSS at 37°C for 30 minutes. The solution is removed carefully to leave the tissue pieces at the bottom, 6ml Astrocyte Plating Medium (APM: DMEM (10569-010), 10% FBS (Invitrogen 16000044), 1% P/S (Invitrogen 15140122)) was added. The tissue is triturated for 15 strokes with 10ml pipette and then 5 strokes more with 1ml pipette. The cell suspension was filtered through 70 µm nylon mesh and seeded in a 25 cm²-flask (Corning 3289). After 2 days, the full medium was changed, then every 3 days. When the astrocyte layer was confluent (~7 days), the flask was shaken at 225 rpm overnight at 37°C. The full medium was changed to APM with 20 µM cytosine arabinoside (Ara-C) to remove any other contaminated proliferative cell types. After two days, the full medium was changed to APM. The Ara-C treatment was repeated the next day. Mild trypsin (0.0675%) treatment was used to lift off the astrocyte layer as a whole and leave the remaining microglia at the bottom of the flask. The layer was incubated in 1ml of Accutase (StemCellTechnologies, 07920) in a fresh tube at 37°C for 10 minutes. The layer was dissociated with 1ml pipette tip with 5 strokes. 2 ml APM was added; the solution was mixed and filtered through a 70 µm nylon mesh.

Mitochondrial Membrane Potential and Footprint

Hippocampal neurons were seeded at a density of 90,000 cells/dish in single 35mm CellVis glass bottom dishes (Fisher Scientific, NC0794151) and allowed to grow for 14 days in

vitro. Astrocytes were seeded at a density of 30,000 cells/dish. Cells were incubated with tetramethylrhodamine, ethyl ester (TMRE) (Sigma, 87917), at working concentration of 500 nM along with 0.125 μ M MitoTracker Green (Thermo Fisher, M7514) and 90 μ M Hoechst (Thermo Fisher, H3570) for 20 min and live imaged using the 60x oil objective (refractive index immersion oil 1.526) and conventional light path (568 nm excitation) of the DeltaVision OMX SR microscope (GE Healthcare Life Sciences). Processing of binary-converted images was conducted using Mitochondrial Network Analysis toolkit (MiNA, macro code freely available on Github) (Valente et al., 2017) to ascertain fluorescence intensity of mitochondrial membranes and mitochondrial footprint (area covered by the staining per cell). The brightest plane was imaged.

Mitochondrial ROS Measurements

Hippocampal neurons and astrocytes were seeded as above. Cells were treated with 0.2 μ M MitoSOX Red (Thermo Fisher, M26008), 0.125 μ M MitoTracker Green, and 90 μ M Hoechst at 37°C, 5% CO₂ for 10 min. Cells were then live imaged using the 60X oil objective (refractive index immersion oil 1.526) and conventional light path of the DeltaVision OMX SR microscope (GE Healthcare Life Sciences). Mitochondrial superoxide levels were measured by fluorescence intensity of puncta using ImageJ. Staining and quantification of DHE (working concentration: 10 μ M) was performed the same way as MitoSOX.

Figure Legends

Figure A.3.30 – Mitochondrial Membrane Potential as determined by TMRE

Fluorescence in Gpt2-null hippocampal neurons and astrocytes in vitro.

A. TMRE (magenta) and MitoTracker Green staining in wild-type (top) and Gpt2-null (bottom) hippocampal neurons at 14 days in vitro. Mitochondrial footprint is measured as area covered by MitoTracker Green fluorescence per cell. Each dot on the graph represents an average of at least 10 cells of a primary culture obtained from a different mouse pup. Scale bar: 10 μm .

B. TMRE (magenta) and MitoTracker Green staining in wild-type (top) and Gpt2-null (bottom) astrocytes at 14 days in vitro. Mitochondrial footprint is measured as area covered by MitoTracker Green fluorescence per cell. Each dot on the graph represents an average of at least 10 cells of a primary culture obtained from a different mouse pup. Scale bar: 10 μm .

Figure A.3.31. MitoSOX and DHE staining in Gpt2-null hippocampal neurons and astrocytes in vitro.

A. MitoSOX (magenta) and MitoTracker Green staining in wild-type (top) and Gpt2-null (bottom) hippocampal neurons at 14 days in vitro. MitoSOX intensities were measured from circling puncta that overlapped with MitoTracker Green staining. Each dot on the graph represents an average of at least 10 cells of a primary culture obtained from a different mouse pup. Scale bar: 10 μm . $*P = 0.0346$.

B. MitoSOX (magenta) and MitoTracker Green staining in wild-type (top) and Gpt2-null (bottom) astrocytes. MitoSOX intensities were measured from circling puncta that overlapped with MitoTracker Green staining. Each dot on the graph represents an average of at least 10 cells of a primary culture obtained from a different mouse pup. Scale bar: 10 μm .

C. DHE staining in the nuclei of wild-type (left) and Gpt2-null (right) hippocampal neurons at 14 days in vitro. Each dot on the graph represents an average of at least 10 cells of a primary culture obtained from a different mouse pup. Scale bar: 10 μ m.

D. DHE staining in the nuclei of wild-type (left) and Gpt2-null (right) astrocytes. Each dot on the graph represents an average of at least 10 cells of a primary culture obtained from a different mouse pup. Scale bar: 10 μ m.

Figure A.3.32. TMRE fluorescence over time in astrocytes with FCCP in vitro.

A. Images of TMRE (top) and MitoTracker Green (bottom) fluorescence in wild-type astrocytes treated with 2 μ M FCCP. Images are taken at 0, 20, 30, 40, 50, 60 minutes. Scale bar: 10 μ m.

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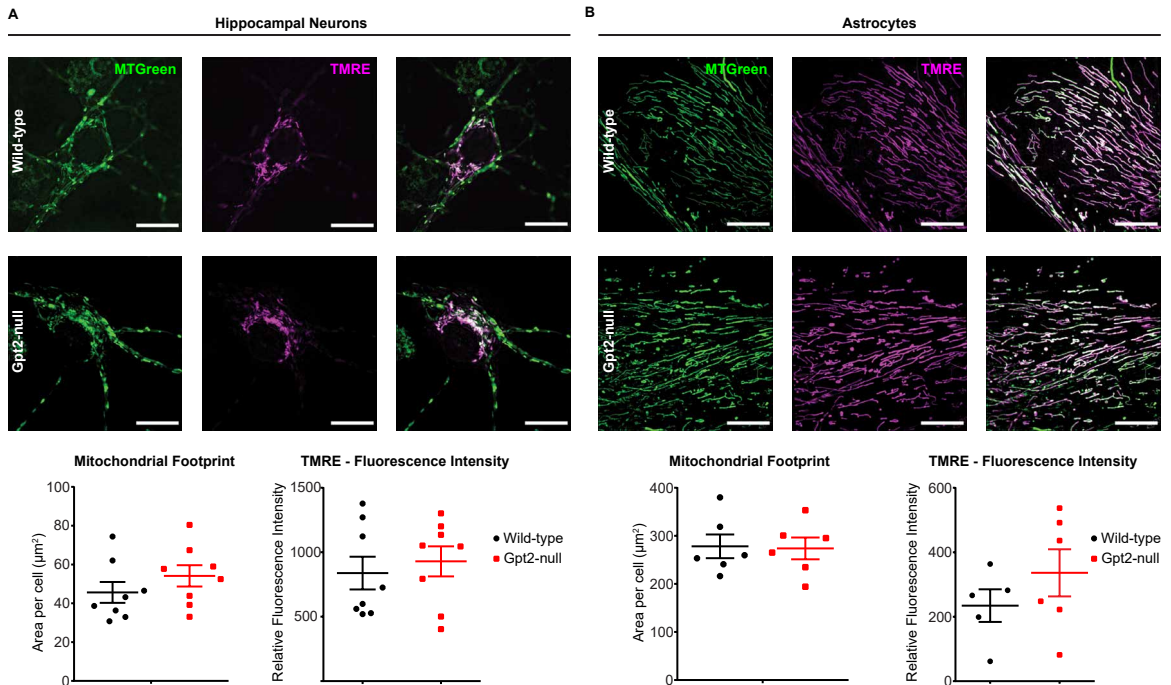


Figure A.3.30 – Mitochondrial Membrane Potential as determined by TMRE Fluorescence in *Gpt2*-null hippocampal neurons and astrocytes *in vitro*. A. TMRE (magenta) and MitoTracker Green staining in wild-type (top) and *Gpt2*-null (bottom) hippocampal neurons at 14 days *in vitro*. Mitochondrial footprint is measured as area covered by MitoTracker Green fluorescence per cell. Each dot on the graph represents an average of at least 10 cells of a primary culture obtained from a different mouse pup. Scale bar: 10 μm . B. TMRE (magenta) and MitoTracker Green staining in wild-type (top) and *Gpt2*-null (bottom) astrocytes at 14 days *in vitro*. Mitochondrial footprint is measured as area covered by MitoTracker Green fluorescence per cell. Each dot on the graph represents an average of at least 10 cells of a primary culture obtained from a different mouse pup. Scale bar: 10 μm .

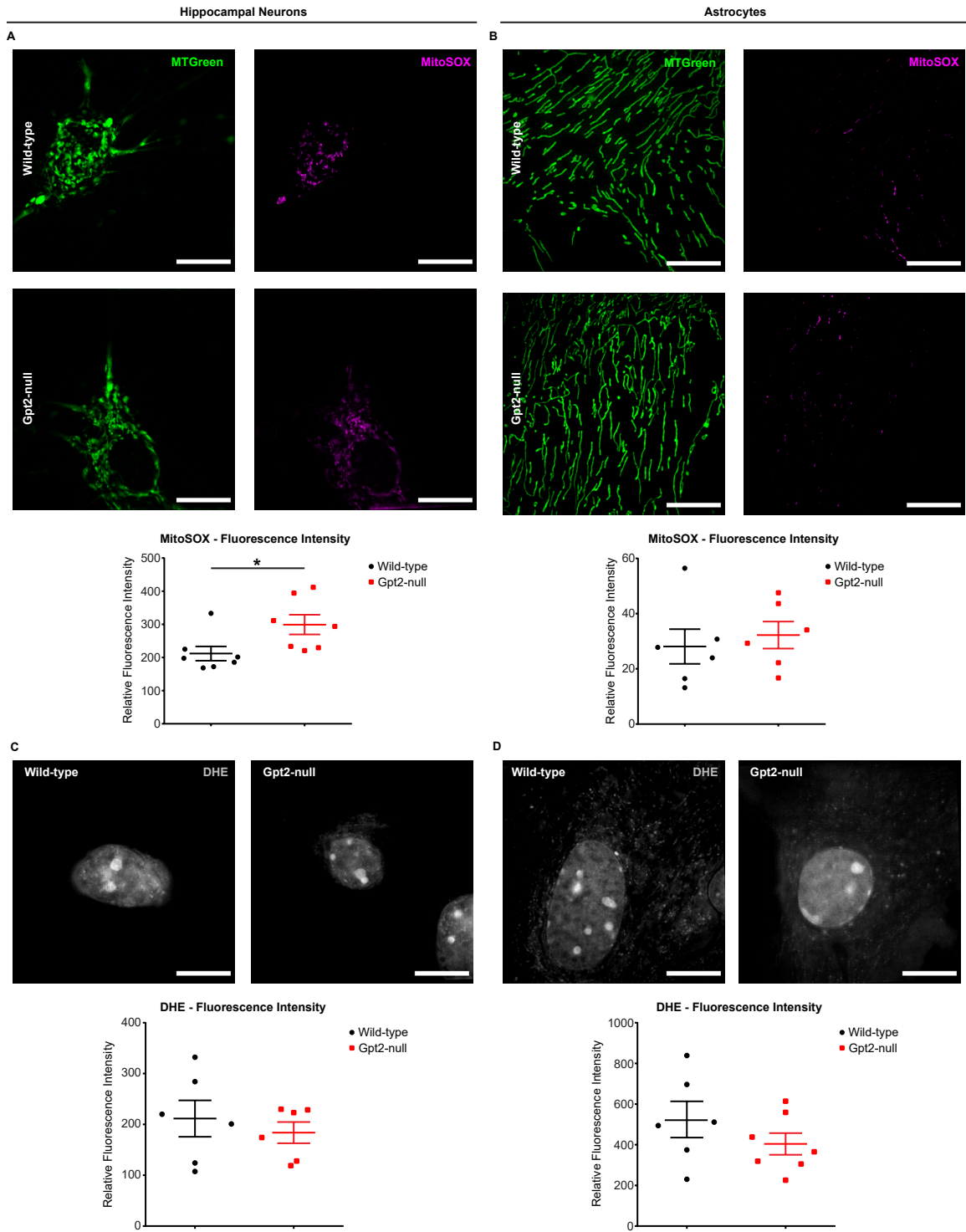


Figure A.3.31. MitoSOX and DHE staining in Gpt2-null hippocampal neurons and astrocytes in vitro.
 A. MitoSOX (magenta) and MitoTracker Green staining in wild-type (top) and Gpt2-null (bottom) hippocampal neurons at 14 days in vitro. MitoSOX intensities were measured from circling puncta that overlapped with MitoTracker Green staining. Each dot on the graph represents an average of at least 10 cells of a primary culture obtained from a different mouse pup. Scale bar: 10 μ m. * $P = 0.0346$.
 B. MitoSOX (magenta) and MitoTracker Green staining in wild-type (top) and Gpt2-null (bottom) astrocytes. MitoSOX intensities were measured from circling puncta that overlapped with MitoTracker Green staining. Each dot on the graph represents an average of at least 10 cells of a primary culture obtained from a different mouse pup. Scale bar: 10 μ m.
 C. DHE staining in the nuclei of wild-type (left) and Gpt2-null (right) hippocampal neurons at 14 days in vitro. Each dot on the graph represents an average of at least 10 cells of a primary culture obtained from a different mouse pup. Scale bar: 10 μ m.
 D. DHE staining in the nuclei of wild-type (left) and Gpt2-null (right) astrocytes. Each dot on the graph represents an average of at least 10 cells of a primary culture obtained from a different mouse pup. Scale bar: 10 μ m.

A

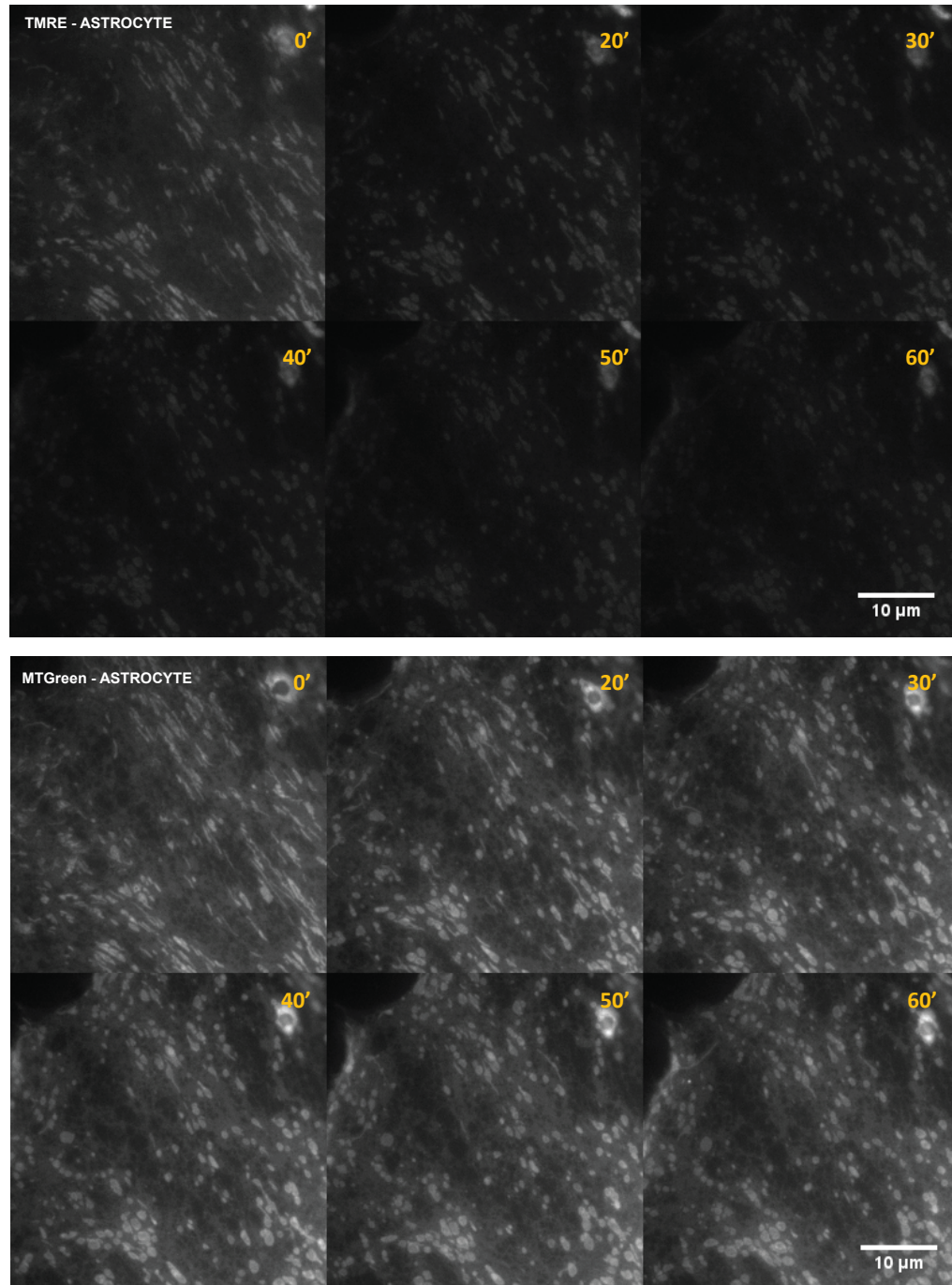


Figure A.3.32. TMRE fluorescence over time in astrocytes with FCCP in vitro.
A. Images of TMRE (top) and MitoTracker Green (bottom) fluorescence in wild-type astrocytes treated with 2 μ M FCCP. Images are taken at 0, 20, 30, 40, 50, 60 minutes. Scale bar: 10 μ m.

Appendix 3.14. Mitochondrial respiration using Seahorse Extracellular Flux Analyzer in Gpt2-null hippocampal neurons and astrocytes.

Introduction

Gpt2 links metabolism of pyruvate, the end product of glycolysis to the TCA cycle and amino acid metabolism. Gpt2 is an anaplerotic enzyme meaning that the reaction Gpt2 catalyzes will result in a net production of a TCA cycle intermediate. Given the influence of Gpt2 on the TCA cycle, we set out to test whether there are any alterations in mitochondrial respiration or glycolysis in Gpt2-null hippocampal neurons and astrocytes in vitro, which may partly contribute to the neurodevelopmental phenotype in Gpt2-null mice and humans. We addressed this question by using the Seahorse Extracellular Flux Analyzer that employs a real-time fluorescence-based detection of oxygen and proton levels. Oxygen consumption rate (OCR) and extracellular acidification rate (ECAR) can be used to assess oxidative phosphorylation and glycolysis, respectively. We hypothesized that there would be defects in respiration or glycolytic activity at baseline or with additional metabolic stress in Gpt2-null hippocampal neurons and astrocytes in vitro. Metabolic assays tested in this study include Mito Stress Test, Mito Stress Test with inhibition of glutaminase, mitochondrial pyruvate carrier or carnitine palmitoyltransferase, KCl depolarization, Flex Fuel Test and Glycolysis Stress Test.

Key Points

- Respiratory Control Ratio (maximal respiration divided by proton leak) is increased in the Gpt2-null hippocampal neurons in vitro.

- Spare respiratory capacity after glutaminase inhibition is decreased in Gpt2-null hippocampal neurons in vitro.
- Increase in extracellular acidification rate is delayed in response to UK5099 in Gpt2-null hippocampal neurons in vitro.
- Glycolytic reserve is increased in Gpt2-null hippocampal neurons in vitro.
- Gpt2-null astrocytes do not show abnormalities in any of the metrics obtained expect for a slightly increased non-mitochondrial oxygen consumption in vitro.

Results

To determine the extent to which mitochondrial respiration and extracellular acidification rely on Gpt2, we performed various respiration assays in cultured hippocampal neurons and astrocytes using Seahorse Extracellular Flux Analyzer. Mito Stress Test inhibits components of the electron transport chain to expose various metrics of mitochondrial respiration by sequentially injecting inhibitory compounds. Overall oxygen consumption rates (OCR) in Gpt2-null hippocampal neurons grown to 14 days in vitro were unchanged over the course of the assay. The extracellular acidification rates (ECAR) in Gpt2-null neurons were slightly elevated at baseline and when oligomycin was added. Various parameters of the Mito Stress Test including basal respiration, maximal respiration, spare respiratory capacity, ATP production, coupling efficiency, proton leak and non-mitochondrial oxygen consumption were unchanged in Gp2-null hippocampal neurons. There were slight trending increases in maximal respiration and in non-mitochondrial oxygen consumption as well as trending decreases in proton leak although these did not

reach statistical significance. However, there was a significant increase in respiratory control ratio (maximal respiration divided by proton leak) in Gpt2-null hippocampal neurons. In astrocytes, no changes were observed except an increased non-mitochondrial oxygen consumption. In both cell types, OCR to ECAR ratios were unchanged.

Gpt2 confers to the cell a pathway to replenish as the TCA cycle intermediates with the loss of Gpt2 the cell may not be able to sustain itself at times of high ATP demand. We tested if depolarization of neurons by KCl, a process that increases respiration to produce the ATP needed, would expose any vulnerabilities of Gpt2-null hippocampal neurons. We do not find any differences in either percent increase of OCR or ECAR following depolarization suggesting that Gpt2-null hippocampal neurons respire the same amount as wild-type controls after induction of neuronal firing.

Gpt2 provides one of the ways in which glutamate oxidation fuels the TCA cycle and therefore provides substrates for oxidative phosphorylation. We hypothesized that if various fuel sources are prevented from contributing to substrate pool for oxidative phosphorylation. Gpt2-null cells would present with reduced mitochondrial respiration and possible other defects associated thereof. When we inhibited pyruvate entry into mitochondria using UK5099, a potent inhibitor of mitochondrial pyruvate carrier (MPC), we did not observe any changes in the various metrics of mitochondrial respiration in Gpt2-null hippocampal neurons or astrocytes. It is of note that both wild-type and Gpt2-null maximal respiration in hippocampal neurons is severely affected in UK5099 compared to astrocytes. The acute response to UK5099 in neurons was also greater compared to astrocytes suggesting a general susceptibility to alterations of pyruvate entry into mitochondria in neurons.

When we inhibited glutaminase which converts glutamine into glutamate in the mitochondria, Gpt2-null hippocampal neurons displayed decreased spare respiratory capacity and spare respiratory capacity expressed as percentage of basal respiration. Even though it is a slight decrease (~10%), this change in Gpt2-null hippocampal neurons may suggest that glutamine may not be able to contribute to the maximal respiration that mitochondria can attain. Gpt2-null astrocytes did not display any differences compared to their wild-type controls.

We were also able to perform Mito Stress Test in the presence of etomoxir, an inhibitor of mitochondrial carnitine palmitoyltransferase in wild-type and Gpt2-null astrocytes. We do not observe any changes in any of the mitochondrial respiration in Gpt2-null astrocytes. Overall the results suggest that Gpt2-null hippocampal neurons may have mitochondrial respiration deficits with glutaminase inhibition but Gpt2-null astrocytes do not show major abnormalities in any of the metrics of the Mito Stress Test with or without inhibition of the glucose, glutamine or fatty acid pathways.

We also performed Flex Fuel Test where the extent to which the cells depend on or can utilize the three metabolic pathways of glucose, glutamine and fatty acids is tested. We do not observe any differences in fuel dependency or capacity of the three metabolic pathways between wild-type and Gpt2-null hippocampal neurons or astrocytes. However, we observed a delayed increase of ECAR in response to UK5099 in Gpt2-null hippocampal neurons but not astrocytes. This trend was observed regardless of whether UK5099 was administered alone or in combination with Etomoxir or BPTES. These results suggest that Gpt2-null neurons did not respond to blockage of pyruvate entry into the mitochondria as fast as their wild-type controls.

Given the slow response to UK5099 in neurons, we performed Glycolysis Stress Test on Gpt2-null hippocampal neurons and astrocytes. Glycolysis Stress Test measures how well the cells can respire without glucose and how much they can increase glycolytic activity to meet high ATP demand. The glycolytic reserve in Gpt2-null hippocampal neurons was profoundly increased compared to their wild-type controls. While there were trending decreases in glycolysis and trending increases in glycolytic capacity in Gpt2-null hippocampal neurons, they did not reach statistical significance. Accordingly, the OCR to ECAR ratio had trending decreases in Gpt2-null neurons, particularly after oligomycin injection. Astrocytes, however, did not show any differences in any of the Glycolysis Stress Test metrics. These results suggest that Gpt2-null hippocampal neurons have altered regulation of glycolysis. This is in agreement with profound increases of glycolytic intermediates in Gpt2-null hippocampus at P18 in vivo.

An increased glycolytic reserve may result from increased glycolytic enzyme content or increased glucose uptake. We tested for uptake of 2-NBDG (a fluorescent analog of glucose) in Gpt2-null hippocampal neurons and astrocytes in vitro and did not find any differences. There were no increased glycolytic enzyme content in Gpt2-null hippocampus in vivo. These results suggest that the altered regulation of glycolysis in Gpt2-null neurons is not caused by changes in glycolytic enzyme content or glucose uptake.

Discussion

Gpt2 loss did not lead to major respiration deficits in either hippocampal neurons or astrocytes in vitro. This is likely due to other metabolic enzymes present in the cell supporting the TCA cycle such as pyruvate dehydrogenase, glutamate dehydrogenase and

pyruvate carboxylase (expressed mainly in astrocytes). Given the TCA cycle deficits seen in multiple contexts including mouse embryonic fibroblasts, hippocampal neurons in vitro and brain tissues, we expected altered mitochondrial respiration and glycolytic activity. Paradoxically, however, Gpt2-null neurons exhibited higher respiratory control ratio in which decreases may indicate mitochondrial dysfunction. The nature of the dysfunction may include multiple factors such as deficits in electron transport chain enzymes, substrate oxidation and transporters, substrate availability and dysregulated mechanisms that act on proton leak. It is of importance that the OCR response to FCCP decline immediately after maximal OCR response which may mean either FCCP concentration was too high or our culture system in the media tested are respiring at an already high rate so that the spare capacity is reduced promptly. There were trending increases in maximal respiration (and in spare respiratory capacity) and trending decreases in proton leak in Gpt2-null hippocampal neurons and the resulting increase in respiratory control ratio was statistically significant. While it is unclear which factor is more prominently affecting this result, Gpt2-null neurons clearly showed normal respiration if not apparently better maximal respiration.

Gpt2-null neurons also displayed higher glycolytic reserve and a slow ECAR response to UK5099. We do not see changes in glucose uptake in Gpt2-null hippocampal neurons or greater glycolytic enzyme content in Gpt2-null hippocampus in vivo. Along with these data, the observation that the delayed ECAR response to acute application of UK5099 occurs within ten minutes and the response eventually catches up to the wild-type levels suggest that this altered regulation is at the substrate level. While the reasons are unclear, it is possible that pyruvate levels in Gpt2-null mitochondria may be elevated and may

allow keeping the glycolytic activity in the reserve and delay the increases in ECAR. This may happen particularly because Gpt2 is predicted to catalyze in the direction of alanine and alpha-ketoglutarate production. More studies are warranted to determine changes in the mitochondrial metabolome of Gpt2-null cells.

There was a slight, albeit statistically significant, decrease in spare respiratory capacity in Gpt2-null hippocampal neurons when glutaminase is inhibited. While the effect is not great, glutaminase inhibition may rob the Gpt2-null cells of the glutamate pool that may otherwise enter the TCA cycle. In the Flex Fuel Test, however, glutaminase inhibition affects mitochondrial respiration only slightly, if at all, whereas UK5099 has a profound effect on both wild-type and Gpt2-null hippocampal neurons meaning that glutamine may not play as a big role as glucose in mitochondrial respiration in neurons in the conditions tested.

It is noteworthy that Gpt2-null astrocytes do not show any differences in mitochondrial respiration or glycolytic activity. This is possibly due to the fact that Gpt1, the cytosolic paralog of Gpt2, is more abundantly expressed in mouse astrocytes than in neurons.

There was a significant increase in non-mitochondrial oxygen consumption in Gpt2-null astrocytes. Non-mitochondrial oxygen consumption has been attributed to oxidative stress and plasma membrane oxidases such as NADPH oxidase. While none of the other respiration metrics showed any differences, increased non-mitochondrial oxygen consumption could be due to changes in a metabolic pathway related to Gpt2 that is unexplored in astrocytes.

Method

Cell Culture

Mouse primary hippocampal neuron culture. Hippocampal neurons were cultured as described previously (Ouyang et al., 2013): Hippocampi from P0-1 pup were dissected in Hank's Balanced Salt Solution (HBSS) (Gibco 14170-112) and placed in 500µl of 20U/ml papain (Worthington LK003176, in Earle's Balanced Salt Solution (EBSS), Worthington, LK003188). The tube with hippocampi/papain was incubated at 37°C for 15 minutes. The tissue was triturated with 1ml pipette tip for 12 strokes. The tissue was further incubated at 37°C for 15 minutes and triturated. The remaining bits of tissue sunk and the solution with dissociated cells was spun in a separate tube at 300g, 5 minutes, at RT. The cell pellet was dissolved gently in Inhibitor Solution (540µl EBSS, 60µl Ovomuroid Protease Inhibitor (Worthington Biochemical, LK003182), 30µl DNase (Worthington Biochemical, LK003170) per hippocampi) and filtered through a 70µm nylon mesh (FisherScientific, 22363548). The filtered cell suspension was layered on top of 1ml Ovomuroid Protease Inhibitor and spun at 70g, 10 minutes, at RT. The supernatant was discarded, and the cell pellet was resuspended in Neurobasal A+ (NeuroBasal A (10888022), 1X B27 Supplement (ThermoFisher Scientific, 17504044), 2mM GlutaMAX (ThermoFisher Scientific, 35050061). The full media was changed the next day and then half media every 3 days.

Mouse primary astrocyte-enriched cultures. The culturing protocol was adapted from (Schildge et al., 2013, Albuquerque et al., 2009): Cortices from P0-1 pup were dissected in HBSS, diced into 6 pieces and transferred to a 15ml conical tube. The tissue is incubated in 0.25% Trypsin-EDTA in HBSS at 37°C for 30 minutes. The solution is removed carefully to leave the tissue pieces at the bottom, 6ml Astrocyte Plating Medium

(APM: DMEM (10569-010), 10% FBS (Invitrogen 16000044), 1% P/S (Invitrogen 15140122)) was added. The tissue is triturated for 15 strokes with 10ml pipette and then 5 strokes more with 1ml pipette. The cell suspension was filtered through 70 μ m nylon mesh and seeded in a 25cm²-flask (Corning 3289). After 2 days, the full medium was changed, then every 3 days. When the astrocyte layer was confluent (~7 days), the flask was shaken at 225 rpm overnight at 37°C. The full medium was changed to APM with 20 μ M cytosine arabinoside (Ara-C) to remove any other contaminated proliferative cell types. After two days, the full medium was changed to APM. The Ara-C treatment was repeated the next day. Mild trypsin (0.0675%) treatment was used to lift off the astrocyte layer as a whole and leave the remaining microglia at the bottom of the flask. The layer was incubated in 1ml of Accutase (StemCellTechnologies, 07920) in a fresh tube at 37°C for 10 minutes. The layer was dissociated with 1ml pipette tip with 5 strokes. 2ml APM was added; the solution was mixed and filtered through a 70 μ m nylon mesh.

Mitochondrial Respiration Assays

Mouse hippocampal neurons were seeded at a density of 90,000 cells/well in Seahorse XF24 V7 PS Cell Culture Microplates (Seahorse Biosciences, 100777-004) and allowed to grow in Neurobasal A+ medium for 14 days at 37°C in a 5% CO₂ humidified atmosphere. Astrocytes were seeded at a density of 25,000 cells/well before the day of the assay. On the day of the assay, cells were subsequently washed with DMEM XF assay medium at pH 7.4 (Seahorse Biosciences, 103575-100) supplemented with 10 mM glucose (Seahorse Biosciences, 103577-100), 2 mM glutamine (Seahorse Biosciences, 103579-100), and 1 mM sodium pyruvate (Seahorse Biosciences, S8636) and incubated for 1 hour at 37°C in a

non-CO₂ incubator for all assays except Glycolysis Stress Test which excludes glucose and pyruvate from the medium. Oxygen consumption rate (OCR) and extracellular acidification rate (ECAR) were subsequently measured using Seahorse Extracellular Flux (Seahorse Biosciences, XFe24) analyzer. For Mito Stress test, final concentrations of 1 μ M oligomycin (Sigma, 75351), 2 μ M FCCP (Sigma, C2920), 0.5 μ M antimycin A (Sigma, A8674), and 0.5 μ M rotenone (Sigma, R8875) were loaded into the injection ports in the XFe24 sensor cartridge in sequence. For Mito Stress Test with blocked pyruvate entry into mitochondria, 2 μ M UK5099 (Cayman, 16980) was injected before oligomycin followed by FCCP, rotenone and antimycin A. For Mito Stress Test with glutaminase inhibition, 3 μ M BPTES (Cayman, 19284) was injected before oligomycin followed by FCCP, rotenone and antimycin A. For Mito Stress Test with blocked palmitate entry into mitochondria, 4 μ M Etomoxir (Cayman, 11969-5) was injected before oligomycin followed by FCCP, rotenone and antimycin A. For Glycolysis Stress Test, 10 mM glucose was injected followed by oligomycin and 50 mM 2-deoxy-glucose (Cayman, 14325). For Flex Fuel Test for the glucose pathway (dependency), UK5099 injection was followed by Etomoxir/BPTES. Glucose pathway (capacity): Etomoxir/BPTES + UK5099. Glutamine pathway (dependency): BPTES + Etomoxir/UK5099. Glutamine pathway (capacity): Etomoxir/UK5099 + BPTES. Fatty acid pathway (dependency): Etomoxir + BPTES/UK5099. Fatty acid pathway (capacity): BPTES/UK5099 + Etomoxir. For depolarization, a final concentration of 50 mM KCl was added to the wells and the percent increase in OCR was calculated by dividing the last measurement before injection to the one immediately after KCl injection.

Mito Stress Test Assay parameters were calculated automatically using Wave software (Seahorse Biosciences). The parameters are calculated as follows: Non-mitochondrial oxygen consumption: Minimum rate measurement after Rot/AA injection. Basal respiration: (last rate measurement before first injection) – (non-mitochondrial oxygen consumption). Maximal Respiration: (Maximum rate measurement after FCCP injection) – (non-mitochondrial oxygen consumption). Proton leak: (Minimum rate measurement after oligomycin injection) – (non-mitochondrial oxygen consumption). ATP Production: (Last rate measurement after oligomycin injection) – (minimum rate measurement after oligomycin injection). Spare Respiratory Capacity: (Maximal respiration) – (Basal respiration). Spare Respiratory Capacity as a %: (Maximal Respiration) / (Basal Respiration) x 100. Acute Response to BPTES, UK5099 or Etomoxir: (Last rate measurement before oligomycin injection) – (Last rate measurement before acute injection). Coupling efficiency: ATP Production / Basal respiration x 100.

Glycolysis Stress Test Assay parameters were calculated automatically using Wave software (Seahorse Biosciences). The parameters are calculated as follows: Glycolysis: (Maximum rate measurement before oligomycin injection) – (Last rate measurement before glucose injection). Glycolytic capacity: (Maximum rate measurement after oligomycin injection) – (last rate measurement before glucose injection). Glycolytic Reserve: Glycolytic capacity – glycolysis. Glycolytic Reserve as a %: Glycolytic Capacity / Glycolysis x 100. Non-glycolytic acidification: last rate measurement before glucose injection.

Following the assay, cells were rinsed gently with 1X PBS and fixed in 4% (w/v) paraformaldehyde for 10 min, after which they were washed twice for 5 min each wash

with 1X PBS at room temperature. Nuclei were counterstained using 300 nM DAPI for 5 min at room temperature, and cells were subsequently washed thrice with 1X PBS for 5 min per wash. Cell density per well was measured using the Cytation 5 Plate Reader (Biotek Instruments, Winooski, VT) by imaging wells at 405nm and measures of respiration were normalized to cell density per well.

Figure Legends

Figure A 3.33. Seahorse Mito Stress Test in Gpt2-null hippocampal neurons and astrocytes.

A. Oxygen consumption (OCR) and extracellular acidification rates (ECAR) measured at baseline and after sequential injections of oligomycin (Oligo), FCCP, rotenone and antimycin A (Rot/AA) in wild-type (black) and Gpt2-null (red) hippocampal neurons at 14 days in vitro. OCR and ECAR values were normalized to cell count and expressed as pmol per minute per 1,000 cells. n=6 litters. **0.001<P<0.01, *0.01<P<0.05.

B. Mitochondrial respiration parameters obtained from Mito Stress Test in wild-type (black) and Gpt2-null (red) hippocampal neurons at 14 days in vitro. Baseline OCR/ECAR ratio was calculated using the last baseline measurement. *0.01<P<0.05.

C. Oxygen consumption (OCR) and extracellular acidification rates (ECAR) measured at baseline and after sequential injections of oligomycin (Oligo), FCCP, rotenone and antimycin A (Rot/AA) in wild-type (black) and Gpt2-null (red) astrocytes in vitro. OCR and ECAR values were normalized to cell count and expressed as pmol per minute per 1,000 cells. n=5 litters.

D. Mitochondrial respiration parameters obtained from Mito Stress Test in wild-type (black) and Gpt2-null (red) astrocytes. Baseline OCR/ECAR ratio was calculated using the last baseline measurement. * $0.01 < P < 0.05$.

Figure A 3.34. Seahorse Glyco Stress Test in Gpt2-null hippocampal neurons and astrocytes.

A. Oxygen consumption (OCR) and extracellular acidification rates (ECAR) measured at baseline and after sequential injections of glucose, oligomycin (Oligo), 2-deoxyglucose (2-DG) in wild-type (black) and Gpt2-null (red) hippocampal neurons at 14 days in vitro. OCR and ECAR values were normalized to cell count and expressed as pmol per minute per 1,000 cells. n=6-7 litters.

B. Mitochondrial respiration parameters obtained from Glyco Stress Test in wild-type (black) and Gpt2-null (red) hippocampal neurons at 14 days in vitro. Baseline OCR/ECAR ratio was calculated using the last measurement of each epoch. ** $0.001 < P < 0.01$, * $0.01 < P < 0.05$.

C. Oxygen consumption (OCR) and extracellular acidification rates (ECAR) measured at baseline and after sequential injections of glucose, oligomycin (Oligo), 2-deoxyglucose (2-DG) in wild-type (black) and Gpt2-null (red) astrocytes in vitro. OCR and ECAR values were normalized to cell count and expressed as pmol per minute per 1,000 cells. n=5 litters.

D. Mitochondrial respiration parameters obtained from Mito Stress Test in wild-type (black) and Gpt2-null (red) astrocytes. Baseline OCR/ECAR ratio was calculated using the last measurement of each epoch. * $0.01 < P < 0.05$.

Figure 3 A 3.35. Seahorse Mito Stress Test with UK5099 in Gpt2-null hippocampal neurons and astrocytes.

A. Oxygen consumption (OCR) and extracellular acidification rates (ECAR) measured at baseline and after sequential injections of UK5099, oligomycin (Oligo), FCCP, rotenone and antimycin A (Rot/AA) in wild-type (black) and Gpt2-null (red) hippocampal neurons at 14 days in vitro. OCR and ECAR values were normalized to cell count and expressed as pmol per minute per 1,000 cells. n=3 litters.

B. Mitochondrial respiration parameters obtained from Mito Stress Test with UK5099 in wild-type (black) and Gpt2-null (red) hippocampal neurons at 14 days in vitro.

C. Oxygen consumption (OCR) and extracellular acidification rates (ECAR) measured at baseline and after sequential injections of UK5099, oligomycin (Oligo), FCCP, rotenone and antimycin A (Rot/AA) in wild-type (black) and Gpt2-null (red) astrocytes in vitro. OCR and ECAR values were normalized to cell count and expressed as pmol per minute per 1,000 cells. n=5 litters.

D. Mitochondrial respiration parameters obtained from Mito Stress Test with UK5099 in wild-type (black) and Gpt2-null (red) astrocytes.

Figure A 3.36. Seahorse Mito Stress Test with BPTES in Gpt2-null hippocampal neurons and astrocytes.

A. Oxygen consumption (OCR) and extracellular acidification rates (ECAR) measured at baseline and after sequential injections of BPTES, oligomycin (Oligo), FCCP, rotenone and antimycin A (Rot/AA) in wild-type (black) and Gpt2-null (red) hippocampal neurons

at 14 days in vitro. OCR and ECAR values were normalized to cell count and expressed as pmol per minute per 1,000 cells. n=4 litters.

B. Mitochondrial respiration parameters obtained from Mito Stress Test with BPTES in wild-type (black) and Gpt2-null (red) hippocampal neurons at 14 days in vitro.

*0.01<P<0.05.

C. Oxygen consumption (OCR) and extracellular acidification rates (ECAR) measured at baseline and after sequential injections of BPTES, oligomycin (Oligo), FCCP, rotenone and antimycin A (Rot/AA) in wild-type (black) and Gpt2-null (red) astrocytes in vitro. OCR and ECAR values were normalized to cell count and expressed as pmol per minute per 1,000 cells. n=4 litters.

D. Mitochondrial respiration parameters obtained from Mito Stress Test with BPTES in wild-type (black) and Gpt2-null (red) astrocytes.

Figure A 3.37. Seahorse Mito Stress Test with Etomoxir in Gpt2-null astrocytes.

A. Oxygen consumption (OCR) and extracellular acidification rates (ECAR) measured at baseline and after sequential injections of Etomoxir (Eto), oligomycin (Oligo), FCCP, rotenone and antimycin A (Rot/AA) in wild-type (black) and Gpt2-null (red) astrocytes in vitro. OCR and ECAR values were normalized to cell count and expressed as pmol per minute per 1,000 cells. n=3 litters.

B. Mitochondrial respiration parameters obtained from Mito Stress Test with Etomoxir in wild-type (black) and Gpt2-null (red) astrocytes.

Figure A 3.38. Seahorse Flex Fuel Test in Gpt2-null hippocampal neurons and astrocytes.

A. Dependency (top) and capacity (bottom) of the Glucose pathway in wild-type (black, green) and Gpt2-null (red, magenta) hippocampal neurons at 14 days in vitro (left) and astrocytes (right) *in vitro*. To determine dependency on the glucose pathway, UK5099 was injected alone, followed by ETO and BPTES. To determine capacity of the glucose pathway, first ETO and BPTES were injected, followed by UK5099. OCR and ECAR values were expressed as percentage of the last baseline measurement n=6-8 litters.

*0.01<P<0.05.

B. Dependency (top) and capacity (bottom) of the Glutamine pathway in wild-type (black, green) and Gpt2-null (red, magenta) hippocampal neurons at 14 days in vitro (left) and astrocytes (right) *in vitro*. To determine dependency on the glutamine pathway, BPTES was injected alone, followed by ETO and UK5099. To determine capacity of the glutamine pathway, ETO and UK5099 were injected, followed by BPTES. OCR and ECAR values were expressed as percentage of the last baseline measurement n=6-8 litters. *0.01<P<0.05.

C. Dependency (top) and capacity (bottom) of the Fatty Acid pathway in wild-type (black, green) and Gpt2-null (red, magenta) hippocampal neurons at 14 days in vitro (left) and astrocytes (right) *in vitro*. To determine dependency on the glucose pathway, ETO was injected alone, followed by UK5099 and BPTES. To determine capacity of the glucose pathway, UK5099 and BPTES were injected, followed by ETO. OCR and ECAR values were expressed as percentage of the last baseline measurement n=5-8 litters.

*0.01<P<0.05.

Figure A 3.39. Aggregate dependency and capacity values of Seahorse Flex Fuel Test in Gpt2-null hippocampal neurons and astrocytes.

A. The three metabolic pathways tested in the Seahorse Flex Fuel Test. The glucose pathway is probed by preventing pyruvate entry into mitochondria with the inhibition of the mitochondrial pyruvate carrier (MPC) by UK5099. The glutamine pathway is probed by preventing the conversion of glutamine into glutamate (glu) with the inhibition of glutaminase (GLS) by BPTES. The fatty acid pathway is probed by preventing the palmitate entry into mitochondria with the inhibition of carnitine palmitoyltransferase 1 (CPT1) by Etomoxir (ETO). The GPT2 reaction is shown next to the tricarboxylic acid (TCA) cycle with the primary reaction metabolites, alpha-ketoglutarate, alanine (ala), glutamate (glu) and pyruvate (pyr).

B. Dependency and capacity of the three metabolic pathways in wild-type (black) and Gpt2-null (red) hippocampal neurons (top) at 14 days *in vitro* and astrocytes (bottom) *in vitro*. For detailed calculations, refer to Methods. n=6-8 litters.

Figure A 3.40. Oxygen consumption after depolarization with KCl in Gpt2-null hippocampal neurons.

A. Oxygen consumption (OCR, left) and extracellular acidification (ECAR, right) rates after KCl depolarization in wild-type (black) and Gpt2-null (red) hippocampal neurons at 14 days *in vitro*. OCR and ECAR values measured immediately after the addition of 50 mM KCl were divided by the last baseline measurement and expressed as a percentage.

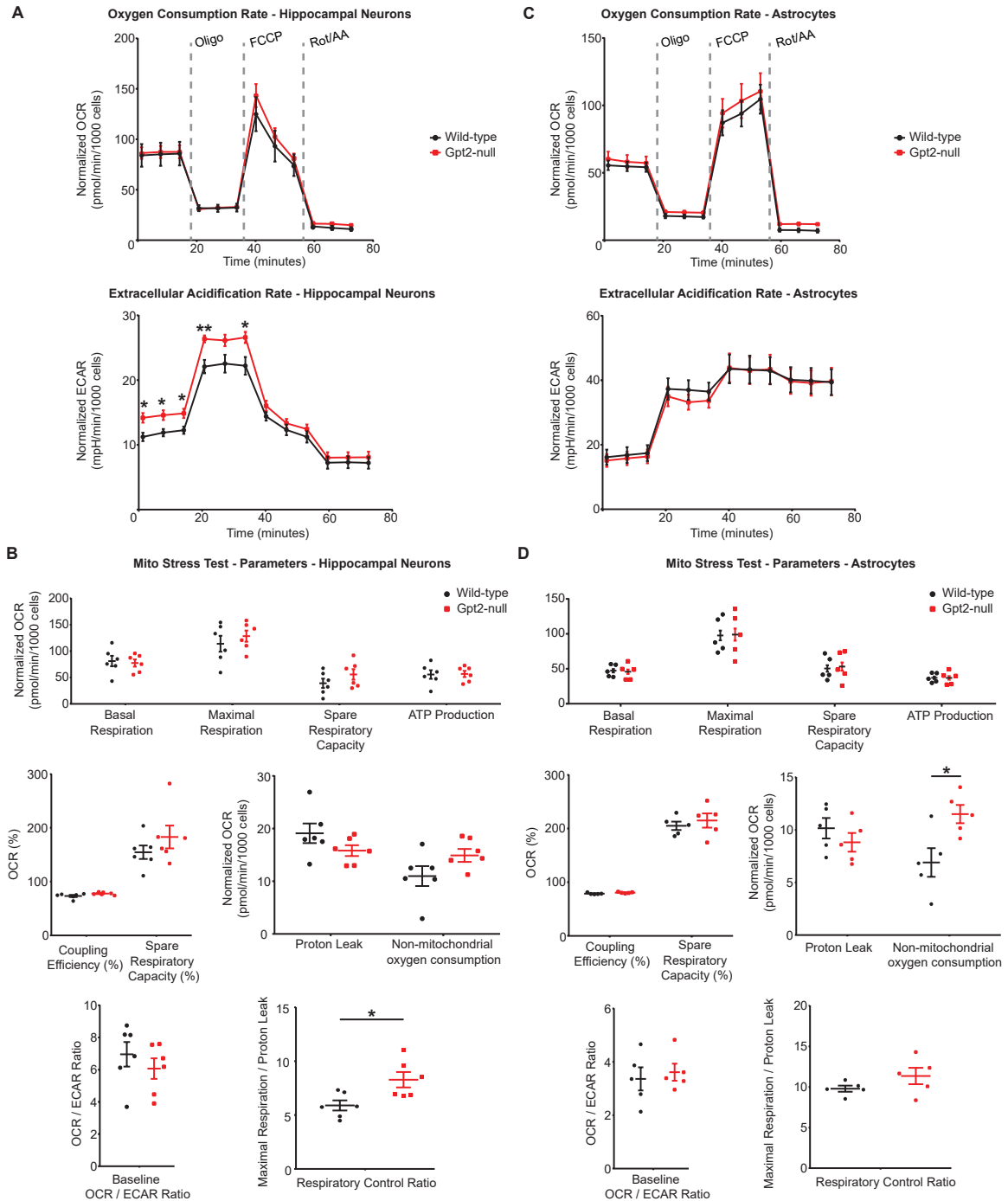


Figure A 3.33. Seahorse Mito Stress Test in Gpt2-null hippocampal neurons and astrocytes.

A. Oxygen consumption (OCR) and extracellular acidification rates (ECAR) measured at baseline and after sequential injections of oligomycin (Oligo), FCCP, rotenone and antimycin A (Rot/AA) in wild-type (black) and Gpt2-null (red) hippocampal neurons at 14 days in vitro. OCR and ECAR values were normalized to cell count and expressed as pmol per minute per 1,000 cells. n=6 litters. $^{**}0.001 < P < 0.01$, $^{*}0.01 < P < 0.05$. B. Mitochondrial respiration parameters obtained from Mito Stress Test in wild-type (black) and Gpt2-null (red) hippocampal neurons at 14 days in vitro. Baseline OCR/ECAR ratio was calculated using the last baseline measurement. $^{*}0.01 < P < 0.05$. C. Oxygen consumption (OCR) and extracellular acidification rates (ECAR) measured at baseline and after sequential injections of oligomycin (Oligo), FCCP, rotenone and antimycin A (Rot/AA) in wild-type (black) and Gpt2-null (red) astrocytes in vitro. OCR and ECAR values were normalized to cell count and expressed as pmol per minute per 1,000 cells. n=5 litters. D. Mitochondrial respiration parameters obtained from Mito Stress Test in wild-type (black) and Gpt2-null (red) astrocytes. Baseline OCR/ECAR ratio was calculated using the last baseline measurement. $^{*}0.01 < P < 0.05$.

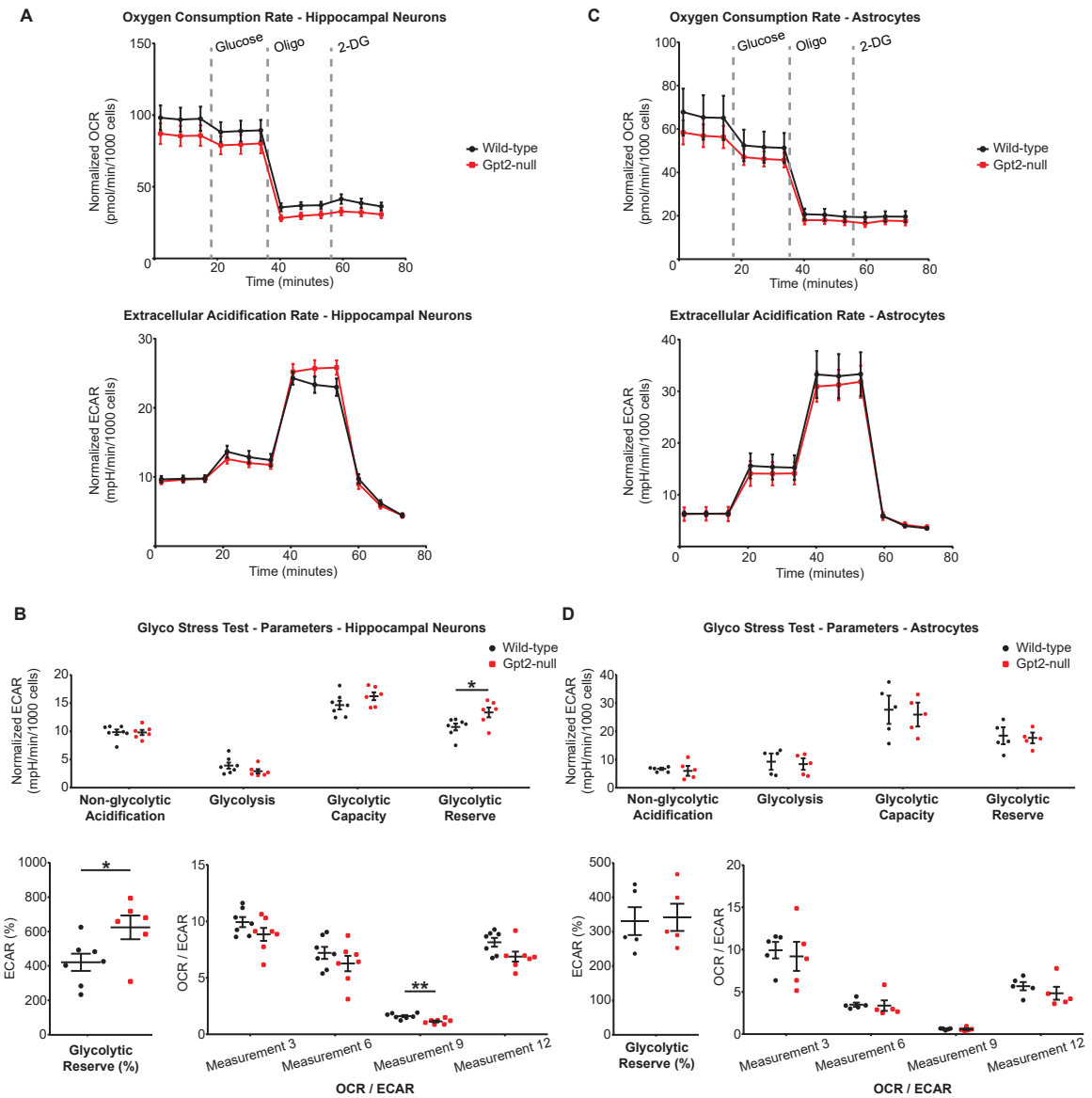


Figure A 3.34. Seahorse Glyco Stress Test in Gpt2-null hippocampal neurons and astrocytes.
 A. Oxygen consumption (OCR) and extracellular acidification rates (ECAR) measured at baseline and after sequential injections of glucose, oligomycin (Oligo), 2-deoxyglucose (2-DG) in wild-type (black) and Gpt2-null (red) hippocampal neurons at 14 days in vitro. OCR and ECAR values were normalized to cell count and expressed as pmol per minute per 1,000 cells. n=6-7 litters.
 B. Mitochondrial respiration parameters obtained from Glyco Stress Test in wild-type (black) and Gpt2-null (red) hippocampal neurons at 14 days in vitro. Baseline OCR/ECAR ratio was calculated using the last measurement of each epoch. **0.001<P<0.01, *0.01<P<0.05. C. Oxygen consumption (OCR) and extracellular acidification rates (ECAR) measured at baseline and after sequential injections of glucose, oligomycin (Oligo), 2-deoxyglucose (2-DG) in wild-type (black) and Gpt2-null (red) astrocytes in vitro. OCR and ECAR values were normalized to cell count and expressed as pmol per minute per 1,000 cells. n=5 litters. D. Mitochondrial respiration parameters obtained from Mito Stress Test in wild-type (black) and Gpt2-null (red) astrocytes. Baseline OCR/ECAR ratio was calculated using the last measurement of each epoch. *0.01<P<0.05.

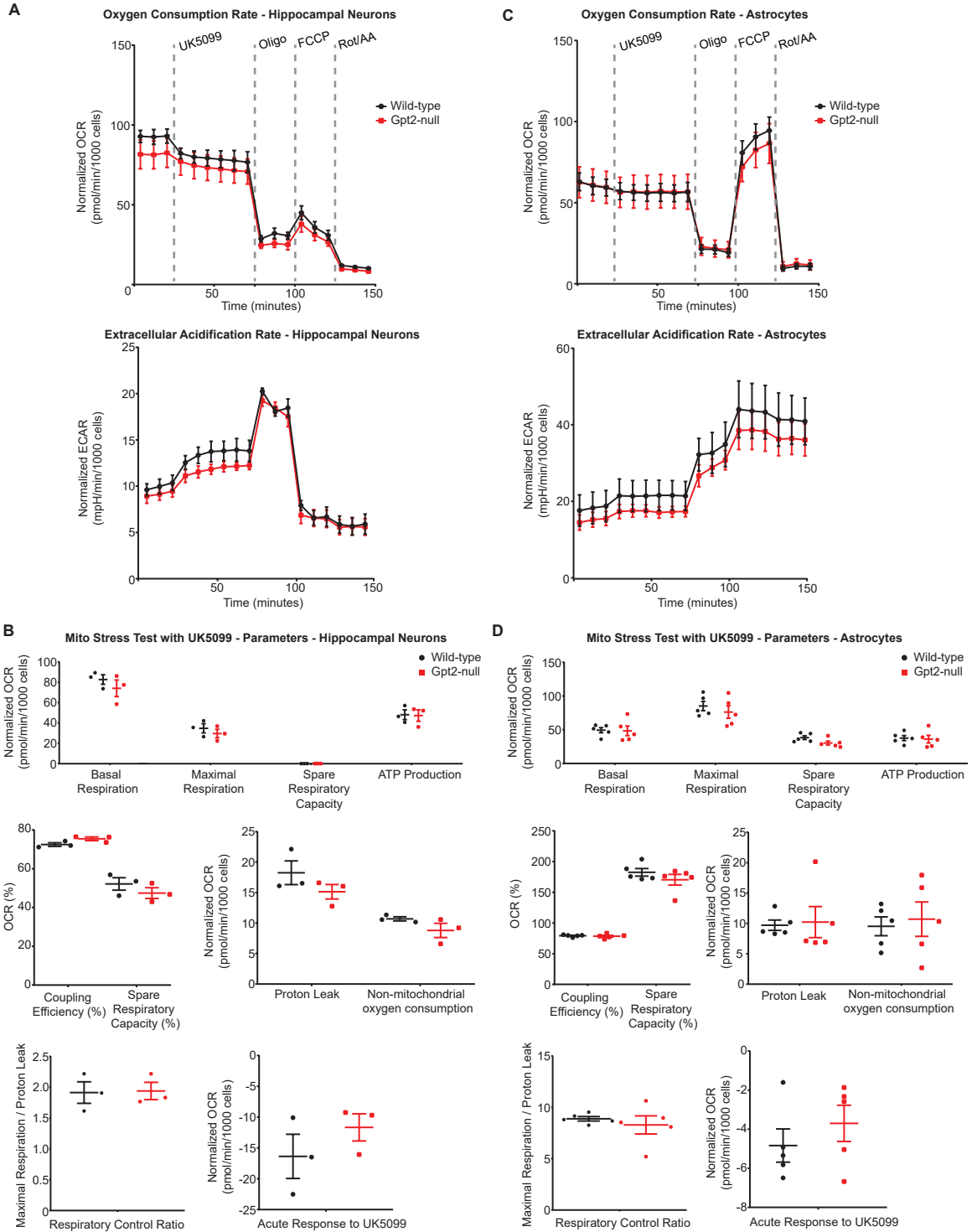


Figure 3 A 3.35. Seahorse Mito Stress Test with UK5099 in Gpt2-null hippocampal neurons and astrocytes.
 A. Oxygen consumption (OCR) and extracellular acidification rates (ECAR) measured at baseline and after sequential injections of UK5099, oligomycin (Oligo), FCCP, rotenone and antimycin A (Rot/AA) in wild-type (black) and Gpt2-null (red) hippocampal neurons at 14 days in vitro. OCR and ECAR values were normalized to cell count and expressed as pmol per minute per 1,000 cells. n=3 litters. B. Mitochondrial respiration parameters obtained from Mito Stress Test with UK5099 in wild-type (black) and Gpt2-null (red) hippocampal neurons at 14 days in vitro. C. Oxygen consumption (OCR) and extracellular acidification rates (ECAR) measured at baseline and after sequential injections of UK5099, oligomycin (Oligo), FCCP, rotenone and antimycin A (Rot/AA) in wild-type (black) and Gpt2-null (red) astrocytes in vitro. OCR and ECAR values were normalized to cell count and expressed as pmol per minute per 1,000 cells. n=5 litters. D. Mitochondrial respiration parameters obtained from Mito Stress Test with UK5099 in wild-type (black) and Gpt2-null (red) astrocytes.

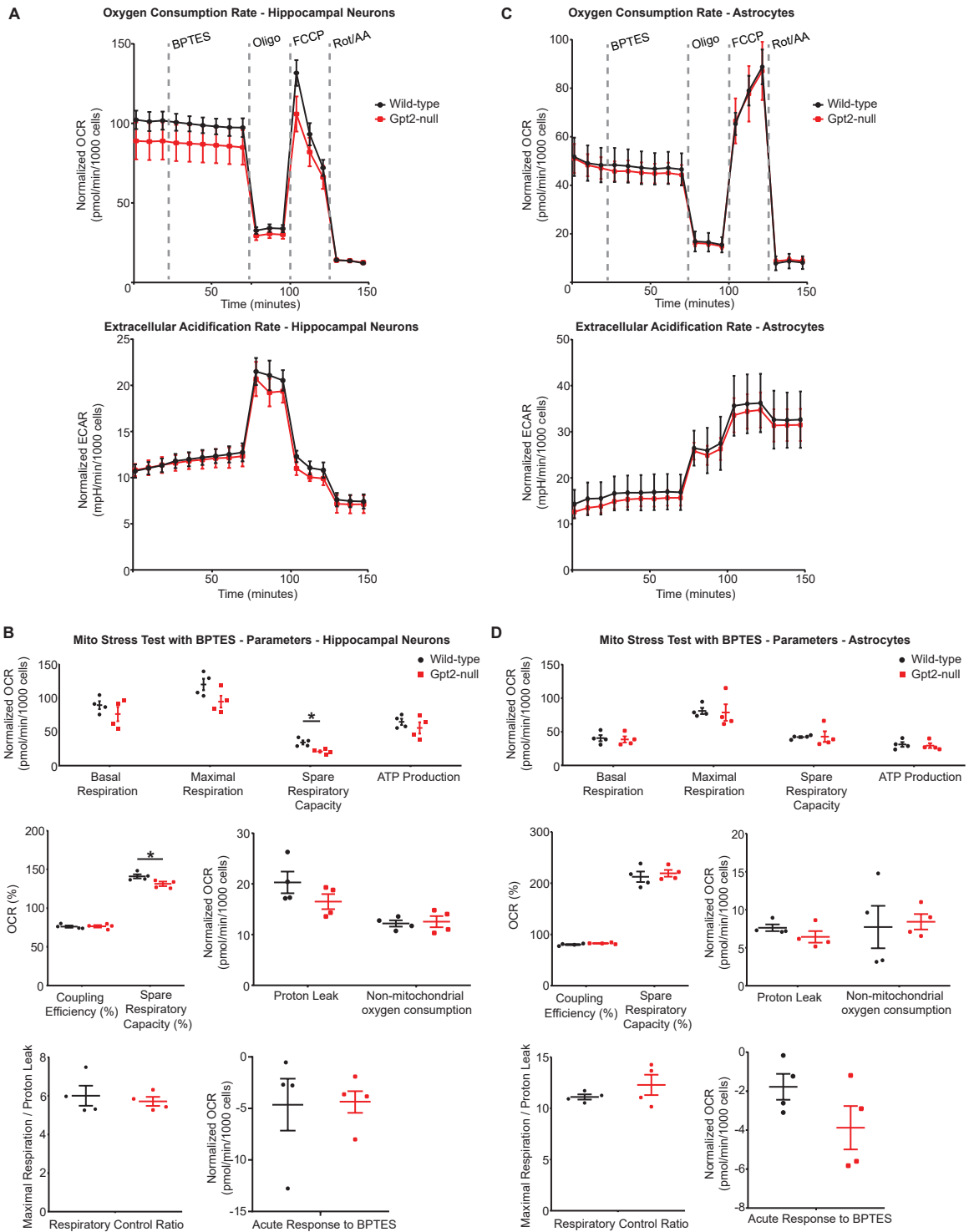
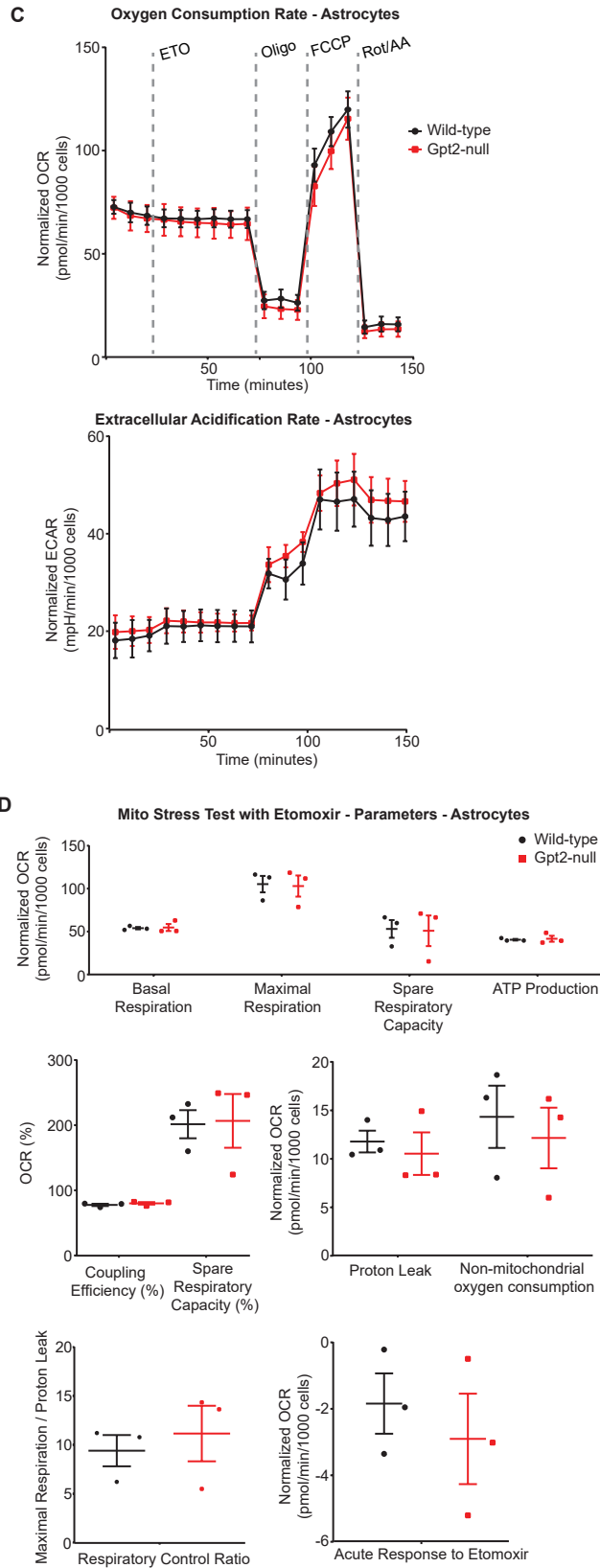


Figure A 3.36. Seahorse Mito Stress Test with BPTES in Gpt2-null hippocampal neurons and astrocytes.

A. Oxygen consumption (OCR) and extracellular acidification rates (ECAR) measured at baseline and after sequential injections of BPTES, oligomycin (Oligo), FCCP, rotenone and antimycin A (Rot/AA) in wild-type (black) and Gpt2-null (red) hippocampal neurons at 14 days in vitro. OCR and ECAR values were normalized to cell count and expressed as pmol per minute per 1,000 cells. n=4 litters.

B. Mitochondrial respiration parameters obtained from Mito Stress Test with BPTES in wild-type (black) and Gpt2-null (red) hippocampal neurons at 14 days in vitro. *0.01<P<0.05. C. Oxygen consumption (OCR) and extracellular acidification rates (ECAR) measured at baseline and after sequential injections of BPTES, oligomycin (Oligo), FCCP, rotenone and antimycin A (Rot/AA) in wild-type (black) and Gpt2-null (red) astrocytes in vitro. OCR and ECAR values were normalized to cell count and expressed as pmol per minute per 1,000 cells. n=4 litters. D. Mitochondrial respiration parameters obtained from Mito Stress Test with BPTES in wild-type (black) and Gpt2-null (red) astrocytes.



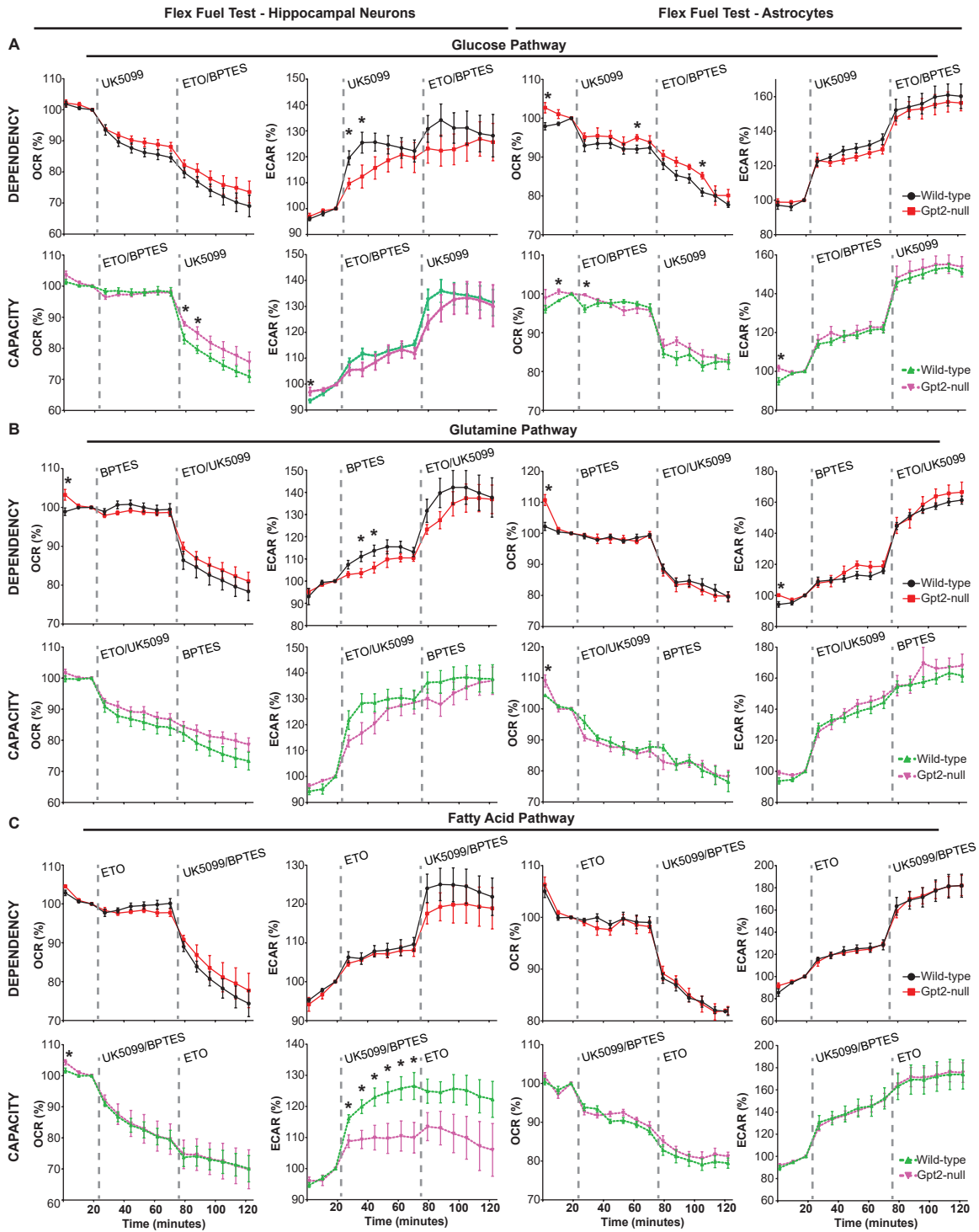


Figure A 3.38. Seahorse Flex Fuel Test in Gpt2-null hippocampal neurons and astrocytes.

A. Dependency (top) and capacity (bottom) of the Glucose pathway in wild-type (black, green) and Gpt2-null (red, magenta) hippocampal neurons at 14 days in vitro (left) and astrocytes (right) in vitro. To determine dependency on the glucose pathway, UK5099 was injected alone, followed by ETO and BPTES. To determine capacity of the glucose pathway, first ETO and BPTES were injected, followed by UK5099. OCR and ECAR values were expressed as percentage of the last baseline measurement n=6-8 litters. *0.01<P<0.05. B. Dependency (top) and capacity (bottom) of the Glutamine pathway in wild-type (black, green) and Gpt2-null (red, magenta) hippocampal neurons at 14 days in vitro (left) and astrocytes (right) in vitro. To determine dependency on the glutamine pathway, BPTES was injected alone, followed by ETO and UK5099. To determine capacity of the glutamine pathway, ETO and UK5099 were injected, followed by BPTES. OCR and ECAR values were expressed as percentage of the last baseline measurement n=6-8 litters. *0.01<P<0.05. C. Dependency (top) and capacity (bottom) of the Fatty Acid pathway in wild-type (black, green) and Gpt2-null (red, magenta) hippocampal neurons at 14 days in vitro (left) and astrocytes (right) in vitro. To determine dependency on the glucose pathway, ETO was injected alone, followed by UK5099 and BPTES. To determine capacity of the glucose pathway, UK5099 and BPTES were injected, followed by ETO. OCR and ECAR values were expressed as percentage of the last baseline measurement n=5-8 litters. *0.01<P<0.05.

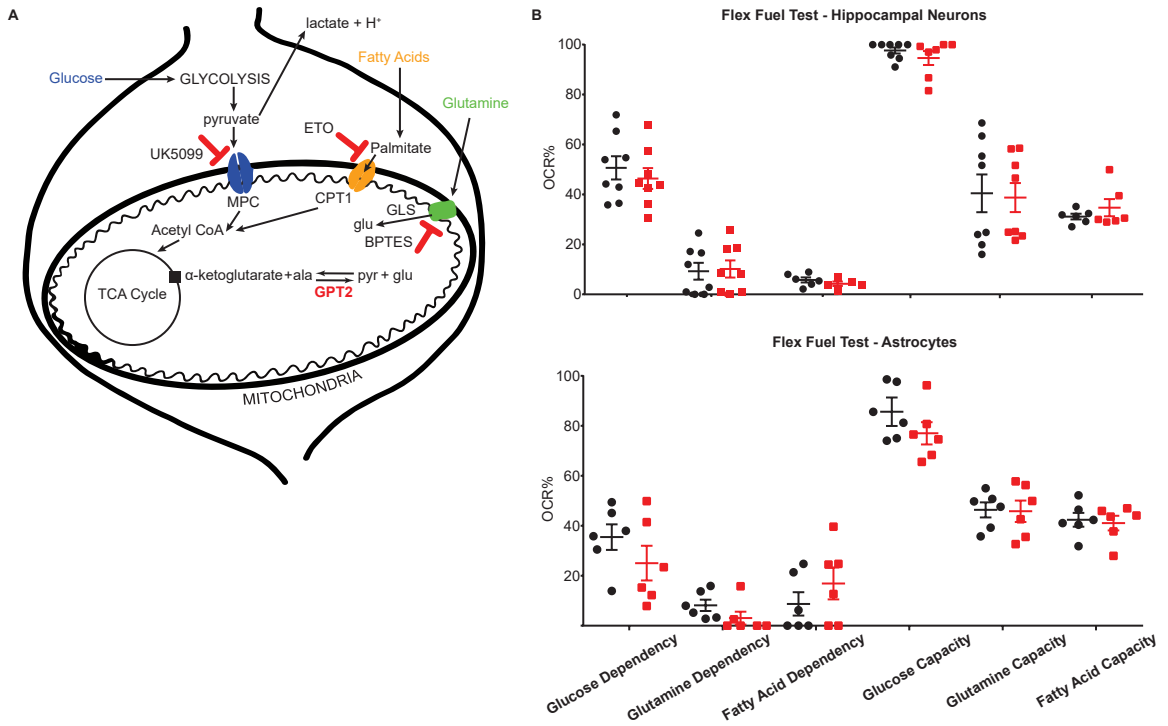


Figure A 3.39. Aggregate dependency and capacity values of Seahorse Flex Fuel Test in *Gpt2*-null hippocampal neurons and astrocytes. A. The three metabolic pathways tested in the Seahorse Flex Fuel Test. The glucose pathway is probed by preventing pyruvate entry into mitochondria with the inhibition of the mitochondrial pyruvate carrier (MPC) by UK5099. The glutamine pathway is probed by preventing the conversion of glutamine into glutamate (glu) with the inhibition of glutaminase (GLS) by BPTES. The fatty acid pathway is probed by preventing the palmitate entry into mitochondria with the inhibition of carnitine palmitoyltransferase 1 (CPT1) by Etomoxir (ETO). The GPT2 reaction is shown next to the tricarboxylic acid (TCA) cycle with the primary reaction metabolites, alpha-ketoglutarate, alanine (ala), glutamate (glu) and pyruvate (pyr). B. Dependency and capacity of the three metabolic pathways in wild-type (black) and *Gpt2*-null (red) hippocampal neurons (top) at 14 days in vitro and astrocytes (bottom) in vitro. For detailed calculations, refer to Methods. n=6-8 litters.

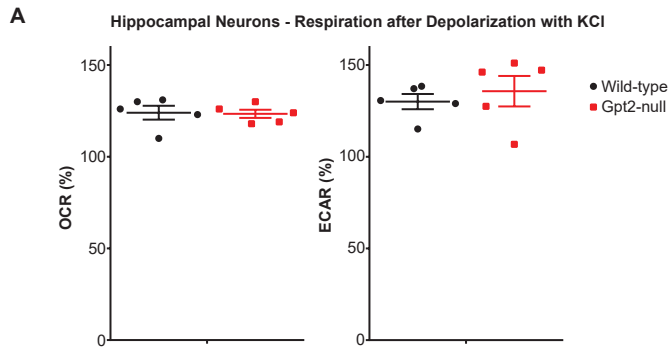


Figure A 3.40. Oxygen consumption after depolarization with KCl in Gpt2-null hippocampal neurons. A. Oxygen consumption (OCR, left) and extracellular acidification (ECAR, right) rates after KCl depolarization in wild-type (black) and Gpt2-null (red) hippocampal neurons at 14 days in vitro. OCR and ECAR values measured immediately after the addition of 50 mM KCl were divided by the last baseline measurement and expressed as a percentage.

Appendix 3.15. Determination of glycogen levels in Gpt2-null whole cortex and hippocampus at P18.

Introduction

We observe increased levels of almost all glycolytic intermediates in Gpt2-null hippocampus by targeted metabolomics at postnatal day 18 (P18). It is possible that the Gpt2-null cells are trying to upregulate glycolysis in order to support their energy supply. I hypothesized that glycogen in astrocytes may be mobilized, i.e. broken down to glucose for metabolic support of the neurons. I quantified glycogen levels in the Gpt2-null cortex and hippocampus.

Results/Key Points

- No changes in glycogen concentration in gpt2-null hippocampus or cortex at P18.

Discussion

The increase of the glycolytic intermediates is unlikely to be caused by glycogen mobilization. Pyruvate, the end product of glycolysis, is the only glycolytic intermediate that has decreased levels in Gpt2-null hippocampus. It is likely that there is decreased substrate inhibition by pyruvate on the upstream glycolytic enzymes. It is also possible that decreased levels of alanine, an allosteric inhibitor of pyruvate kinase, leads to disinhibition of pyruvate kinase thereby increased glycolytic flux into pyruvate (Carbonell et al., 1973). Experiments involving isotope tracing experiments using labeled glucose and glucose uptake in vivo may pinpoint the origin of the increase in glycolytic intermediates.

Method

The hippocampus and cortex tissues of wild-type and Gpt2-null mice were acutely dissected at P18 and weighed. The glycogen assay (Cayman Chemical, 700480) was performed according to the manufacturer's instructions.

Figure Legends

Figure A.3.41. Glycogen concentrations in hippocampus and cortex of wild-type and Gpt2-null mice at P18.

A. Glycogen concentrations normalized to protein content of hippocampus (left) and cortex (right) tissues in wild-type (black) and Gpt2-null (red) mice at P18.

Carbonell, J., Feliu, J.E., Marco, R., and Sols, A. (1973). Pyruvate kinase. Classes of regulatory isoenzymes in mammalian tissues. *Eur J Biochem* 37, 148-156.

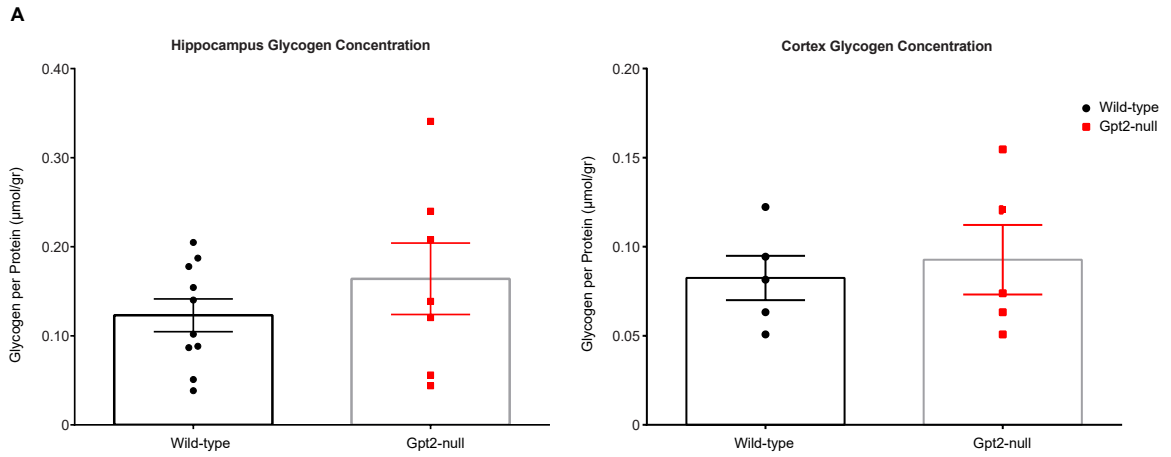


Figure A.3.41. Glycogen concentrations in hippocampus and cortex of wild-type and Gpt2-null mice at P18. A. Glycogen concentrations normalized to protein content of hippocampus (left) and cortex (right) tissues in wild-type (black) and Gpt2-null (red) mice at P18.

Appendix 3.16. Troubleshooting with antibodies for Gpt2.

Introduction

I tried various antibodies for Gpt2 on mouse brain sections. Immunohistochemistry for Gpt2 would be instrumental in:

- 1) determining differential expression of Gpt2 across different cell types and regions in the central nervous system
- 2) confirming conditional Gpt2-null mice models (absence of the protein in specific cell types)
- 3) confirming mitochondrial localization in mouse tissues.

Key methodological parameters tried were as follows:

- 1) Heat-induced epitope retrieval (HIER) in citrate buffer
- 2) Incubation of antibodies with Gpt2-null cortical protein (preadsorption that would precipitate) or Mouse GPT protein (Prospec, ENZ-1030) with different weight ratios (10:1, 20:1 or 40:1 ratio of cortical protein or GPT protein to GPT2 antibody)
- 3) Paraffin (6 μm) or frozen sections (10 μm)
- 4) Primary antibody concentrations (1:10, 1:20, 1:50, 1:100, 1:200, 1:400, 1:800, 1:1600)
- 5) Primary antibodies: a) Novus Biologicals NBP2-14072 Rabbit (immunogen: human C-terminus) b) Abcepta AP18028a Rabbit (immunogen: human N-terminus, 15-44 amino acids) c) ProteinTech 16757-1-AP Rabbit (immunogen: human full protein) d) elabscience E-AB-19961 Rabbit (immunogen: human C-terminus: 396-408).

6) Secondary antibodies: anti-rabbit 488 (Invitrogen, A11034) or anti-rabbit 594 (Invitrogen, A11037) AlexaFluor.

7) Negative control without primary antibody

Results / Key Points

1) None of the antibodies in any of the conditions tested worked. All primary antibodies had distinctive puncta in both wild-type and Gpt2-null brain tissue (hippocampus/cortex). Negative control shows no staining.

Discussion

There are homology differences between the immunogen sequences and mouse Gpt2 or Gpt1 sequences. For example, the immunogen for Novus Biological NBP2-14072, “PVSQAAMDIVVNPPVAGEESFEQFSREKESVLGNLA” has 92% homology with mouse Gpt2 and 76% homology with mouse Gpt1. Any homology greater than 50% is considered to have enough similarities for possible antibody binding. That is why the preadsorption was tried. However, it did not work. It is possible that the Gpt2 protein is still expressed in the Gpt2-null tissue. In the gene trap mouse with the Gpt2 null allele, there is a frameshift after Exon 4 leading to a premature stop codon. This would allow the C-terminus antibodies to not detect the protein made in Gpt2-null if it is made at all. However, both antibodies that targeted the C-terminus detected the protein.

In Western blotting, the protein is not detected at 58kDa in Gpt2-null brain samples by the Proteintech antibody and this is inferred by comparing the samples with their wild-type counterparts. However the antibody detects many different bands, some much higher in intensity compared to the Gpt2 band and these may either non-specific bands, Gpt2

proteins that result from different transcripts, polymerization, post-translation modification or proteins that are bound to Gpt2. In the matter of transcripts, humans have 2 transcripts for Gpt2. In humans, the truncated transcript has been shown to have no catalytic activity [1]. In mice, there appear to be 1 RefSeq RNA transcript (NM.173866) and 6 transcripts (those that cover almost the entire RefSeq transcript region) from GenBank. It is not known how the gene trap cassette affected those other transcripts or whether they have any catalytic activity.

A protein that is tagged with V5 or GFP may be made with genomic insertion. While this may itself affect the GPT2 function, it would have the potential to address the three aims listed in the Introduction.

Available Data (not shown):

- Images for Novus Biological and Proteintech antibodies.

Method

Heat-induced epitope retrieval was achieved by immersing the slides in 10 mM sodium citrate buffer (pH6 with 0.05% Tween 20) at 98°C for 10 minutes. After the slides cooled down, the immunohistochemistry proceeded as previously described in Chapter 3.

The preadsorption was done for 2 hours at room temperature in blocking solution.

1. Glinghammar, B., I. Rafter, A.K. Lindstrom, J.J. Hedberg, H.B. Andersson, P. Lindblom, A.L. Berg, and I. Cotgreave, *Detection of the mitochondrial and catalytically active alanine aminotransferase in human tissues and plasma*. Int J Mol Med, 2009. **23**(5): p. 621-31.

For Appendices 3.17, .18, .19, .20, .21, I will list my brief observations and more data is available upon request.

Appendix 3.17. Homing/righting reflex and open field test data on Gpt2-null mice at P18.

Homing reflex (the time it takes for the neonate pups to reach the cage bedding from a distance) and right reflexes (the time it takes for the neonate pup to right itself after it has been turned on its back) were normal in Gpt2-null mice. Open Field Test data shows that Gpt2-null mice at P18 tended to move around the open arena less. At around weaning age, they appeared lethargic and eventually died.

Appendix 3.18. Gpt2 expression in SynapsinI-Cre conditional Gpt2-null liver at P18.

The SynapsinI-Cre conditional Gpt2-null shows increased Gpt2 expression in the liver; presumable as a compensatory mechanism to upregulate the TCA cycle in the liver.

Appendix 3.19. Metabolomics in Gpt2-null serum on regular diet at P18.

In the serum taken from Gpt2-null mice by cardiac puncture (as in the serum chemical panel), we performed metabolomics and found decreases in glutathione, serine, alanine, citrate/isocitrate. Almost all metabolites with a significant raw p-value had decreased levels. However, PCA plots were unable to distinguish the wild-type and Gpt2-null groups suggesting that overall the serum metabolites are similar.

Appendix 3.20. Metabolomics in Gpt2-null astrocytes in vitro.

We performed metabolomics in Gpt2-null astrocytes in vitro and found no appreciable differences. This is most likely due to their growth medium which had all the metabolites necessary for their functioning metabolome.

Appendix 3.21. Lipidomics in Gpt2-null brain/spinal cord at P18.

We performed lipidomics on brain/spinal cords of Gpt2-null mice at P18 to determine if their lipid profiles had alterations. The most consistent results was increases in Cholesteryl ester in Gpt2-null brain and spinal cord. Increases have been associated with Huntington disease, Multiple sclerosis, Alzheimer's disease. I was expecting an overall decrease in levels given potential problem in macromolecule synthesis but relative quantification of lipidomics failed to reveal decreases in a particular lipid class. Absolute quantification of lipids may reveal further derangements in lipid synthesis or better still isotope tracing involving metabolite incorporation into lipids (e.g. citrate, acetate)

Appendix 4.1. Labeling of locus coeruleus with the NAT-EGFP-Rpl10a line and Western blotting in Gpt2-null locus coeruleus protein samples.

Introduction

In order to investigate the mechanisms behind the degeneration in Locus coeruleus (LC), it is imperative to extract the tissue specifically for metabolic, biochemical and transcriptomic assays. LC is a small nucleus only spanning approximately 400 μm in the anterior/posterior axis and in the dorsal/caudal axis. It is bordered by the motor nuclei of the trigeminal nerve laterally and Barrington's nucleus medially. By specifically labeling LC neurons, it is possible to pinpoint LC exactly and minimize the contamination from the surrounding nuclei. To this end, I crossed the Gpt2 line (Knockout Mouse Project-KOMP 4363039) with the EGFP/Rpl10a line (Jax Strain no.: 031150). EGFP/Rpl10a protein is a ribosomal fusion protein expressed under the control of Slc6a2 (norepinephrine transporter) promoter. It is possible to identify LC neurons by the presence of EGFP and the line also allows for isolation of polysomes and translating mRNAs from LC neurons.

I validated and characterized this line via my LC tissue collection technique by Western blotting. I compared tyrosine hydroxylase (TH), p62, ubiquitin, pmTOR levels.

b) decreases in overall TH levels indicating TH⁺ neuron loss

c) changes in overall levels of ubiquitinated proteins

d) changes in pmTOR levels that may indicate autophagy

Results/Key Points

Increases in p62 & decreases in TH levels in Gpt2-null LC.

No apparent changes in levels of overall ubiquitinated protein (75-150 kDa) or pmTOR.

Discussion

It is imperative to assess Iba1 or CD68 levels in western blotting to ensure that the method has more validity. However, so far, my western blotting failed to detect a band. It may have to do with reductive conditions in the western blotting. Other antibodies may be tried.

Other markers of degeneration or autophagy may be tried in the Western blotting to pinpoint a possible mechanism of neurodegeneration.

Transcriptomics or metabolomics experiments may be helpful to generate hypotheses as to how Gpt2-null LC neurons degenerate. Particularly transcriptomics may be achieved by pulling down the samples probed to GFP and detect mRNA from LC neurons specifically. Currently, the Western blotting described here includes neurons and glia present in the LC.

Available data (not shown)

Data for pS6: The levels of phosphorylated ribosomal protein S6 has been correlated to protein translation and neuronal activity and we see decreases in LC. since pS6 is prominently expressed in neurons, the decreased levels may reflect decreases of neuron count in of Gpt2-null LC.

Method

The Gpt2 line was crossed to NAT-EGFP/Rpl10a (Jax Strain no. 031150). The brains were flash frozen and stored at -80°C until sectioning. 150 µm thick cryosections were mounted on slides and LC was visualized with 488 nm LED of an inverted microscope. The LC was dissected with an insulin syringe and forceps and placed in RIPA buffer (0.05 M Tris pH7.4, 0.15 M NaCl, 1 mM EDTA, 1% Triton X-100, 0.01 g/ml sodium deoxycholate, 0.1% SDS, 1X Protease Inhibitor Cocktail (Roche, 11697498001), 1X PhosSTOP (Roche, 4906845001)). Protein concentration was determined by bicinchoninic acid (BCA) Assay (Thermo Scientific, 23225).

Primary antibodies used in Western blotting: GFP Rb CellSignaling 2956 (1:1000), Tubulin Ms Sigma T6074 (1:1000), TH Ms MAB318 MilliporeSigma (1:1000), pmTOR Rb Cellsignaling 5536S (1:1000), Ubiquitin Ms Invitrogen 13-1600 (1:500).

Figure Legends

Figure A4.1. Characterization of NAT-EGFP/Rpl10a line and Western blotting for TH, p62, ubiquitin, pmTOR in Gpt2-null LC.

A. Image of GFP signal in LC (left, scale bar:250 µm) and Western blotting characterization of the NAT-EGFP/Rpl10a line (right). EGFP/Rpl10a was detected with an antibody for GFP. The hippocampus (HPC) samples obtained from the same mice as NAT-GFP do not show a major band for EGFP/Rpl10a. Tyrosine hydroxylase (TH) is enriched in locus coeruleus samples. For comparison, the LC was also extracted from mice without GFP expression based on the anatomical hallmarks (LC is lateral to the fourth ventricle). Note that the enrichment of TH is less than the GFP-LC samples indicating the GFP line increased the enrichment of LC in sample collection. The

EGFP/Rpl10a and TH appear at the 50 and 60 kDa bands, respectively. D:dorsal, V:ventral, M:medial, L:lateral.

B. Western blotting for p62, TH, pmTOR, ubiquitin (75-150 kDa) in wildtype and Gpt2-null mice at postnatal day 18. Quantification is given below. For p62 $*P=0.0273$, for TH $**P=0.0062$.

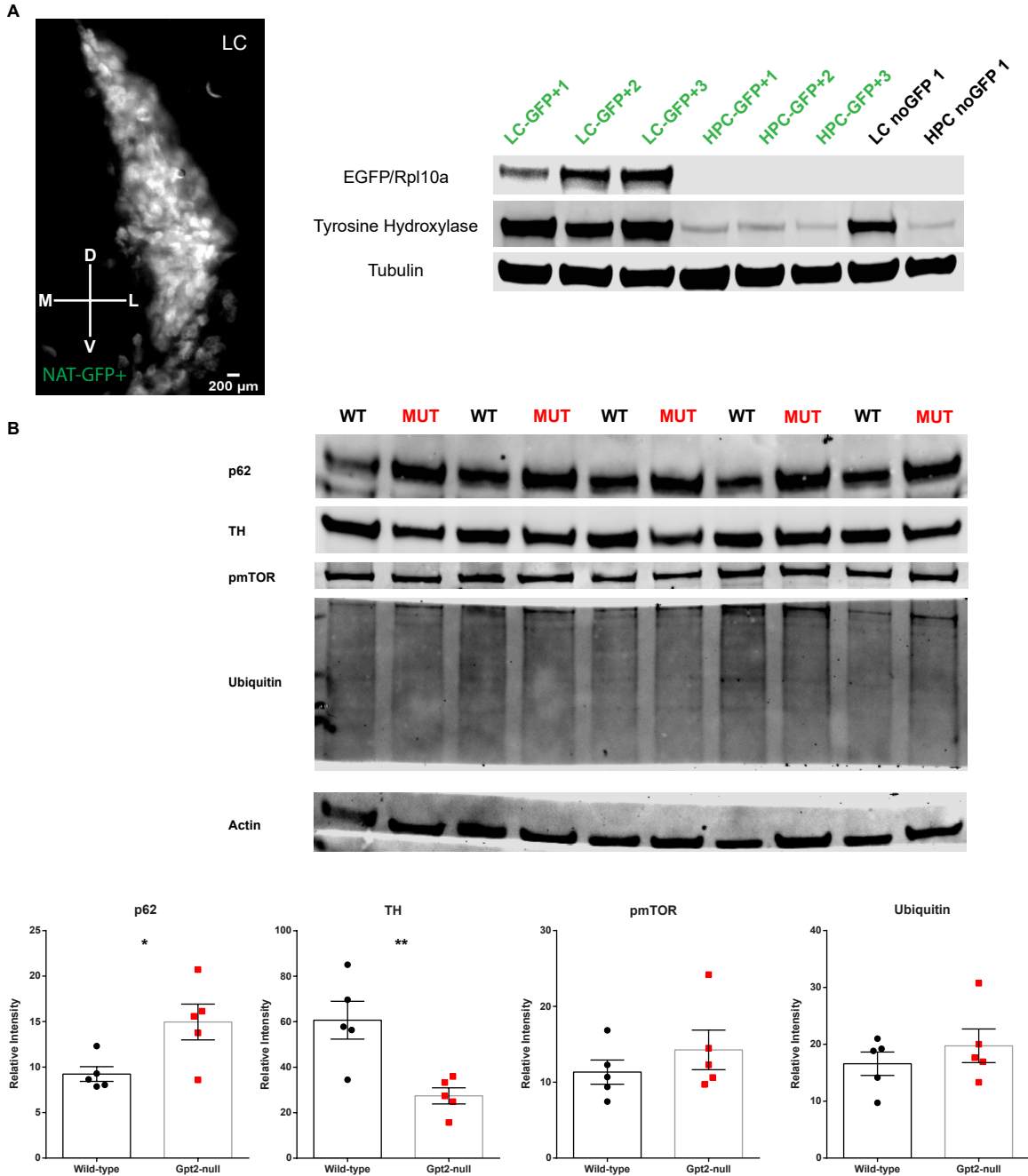


Figure A4.1. Characterization of NAT-EGFP/Rpl10a line and Western blotting for TH, p62, ubiquitin, pmTOR in Gpt2-null LC.

A. Image of GFP signal in LC (left, scale bar:250 μ m) and Western blotting characterization of the NAT-EGFP/Rpl10a line (right). EGFP/Rpl10a was detected with an antibody for GFP. The hippocampus (HPC) samples obtained from the same mice as NAT-GFP do not show a major band for EGFP/Rpl10a. Tyrosine hydroxylase (TH) is enriched in locus coeruleus samples. For comparison, the LC was also extracted from mice without GFP expression based on the anatomical hallmarks (LC is lateral to the fourth ventricle). Note that the enrichment of TH is less than the GFP-LC samples indicating the GFP line increased the enrichment of LC in sample collection. The EGFP/Rpl10a and TH appear at the 50 and 60 kDa bands, respectively. D:dorsal, V:ventral, M:medial, L:lateral. B. Western blotting for p62, TH, pmTOR, ubiquitin (75-150 kDa) in wildtype and Gpt2-null mice at postnatal day 18. Quantification is given below. For p62 *P=0.0273, for TH **P=0.0062.

Appendix 4.2. Tyrosine hydroxylase and Iba1 staining in locus coeruleus of Slc25a12-null and Acc1-het mice.

Introduction

I tested whether there is a degeneration or gliosis in locus coeruleus in other models of metabolism that were available in Dr. Morrow's laboratory. I used two models: a) Slc25a12 deficiency, Slc25a12 is a glutamate/aspartate exchanger in the mitochondria and deficiencies in this protein lead to developmental delay, seizures in humans as well as motor abnormalities and death pre-weaning in mutant mice. b) Acc1 deficiency, acetyl-CoA carboxylase 1 catalyzes the irreversible carboxylation of acetyl-CoA into malonyl-CoA, the initial step in de novo synthesis of fatty acids and homozygous deletion of Acc1 causes embryonic lethality in mice. I stained for tyrosine hydroxylase (TH) that stains for noradrenergic neurons in locus coeruleus and Iba1, a marker for microglia.

Results / Key Points

There is no apparent neuron loss or gliosis in locus coeruleus of Slc25a12-null (postnatal day 18, P18) and Acc1-heterozygous (P60) mice.

Discussion

The most relevant finding that can come out of this study is that locus coeruleus degeneration in Gpt2-null mice seem to be specific to Gpt2 deficiency and do not occur in the other two models of metabolic deficiencies. It is not entirely inconceivable that Slc25a12 deficiency would show degeneration in locus coeruleus since the protein is

involved in glutamate metabolism as well as malate-aspartate shuttle which is responsible for NADH transport into the mitochondria. If there had been a positive result, it would have been an interesting line of inquiry.

Method

Immunohistochemistry (Refer to Chapter) done as previously described. Primary antibodies: rabbit anti-Iba1 Wako Chemicals 019-19741 (1:500), mouse anti-tyrosine hydroxylase Millipore MAB318 (1:300). Secondary antibodies: Goat anti-Rabbit IgG (H+L) AlexaFluor488 Invitrogen A11034 (1:600); Goat anti-Mouse IgG (H+L) AlexaFluor594 Invitrogen A11032 (1:600).

Figure Legends

Figure A4.2. Iba1 and Th staining in locus coeruleus of Slc25a12-null and Acc1-heterozygous mice.

A. Images of Iba1 (green) and TH (red) in wild-type (left) and Slc25a12-null (right) mice at postnatal day 18. Scale bar: 100 μ m.

B. Images of Iba1 (green) and TH (red) in wild-type (left) and Acc1-heterozygous (right) mice at postnatal day 60. Scale bar: 100 μ m.

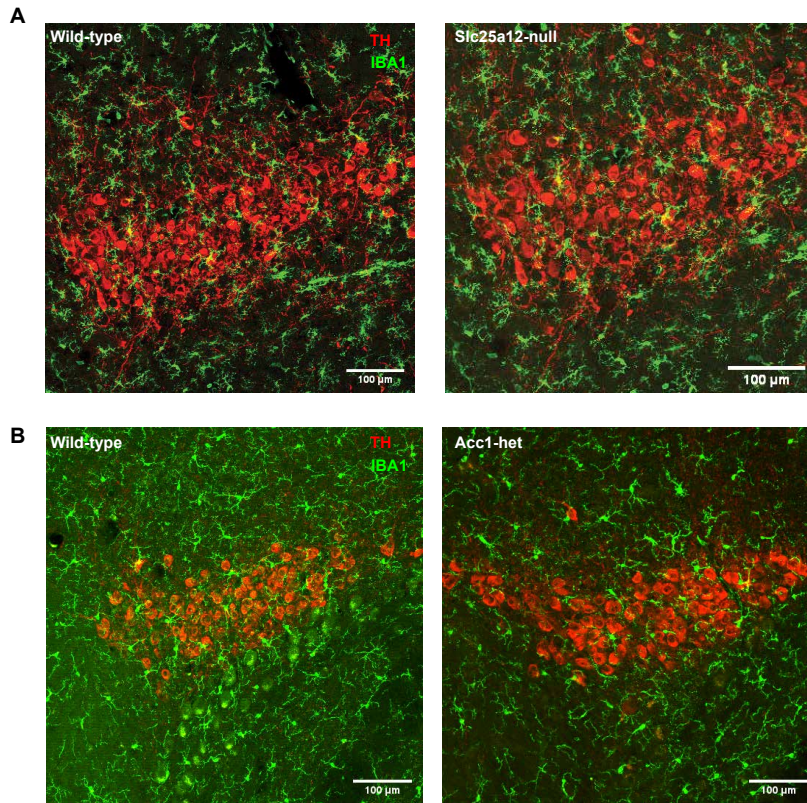


Figure A4.2. Iba1 and Th staining in locus coeruleus of *Slc25a12*-null and *Acc1*-heterozygous mice. A. Images of Iba1 (green) and TH (red) in wild-type (left) and *Slc25a12*-null (right) mice at postnatal day 18. Scale bar: 100 μ m. B. Images of Iba1 (green) and TH (red) in wild-type (left) and *Acc1*-heterozygous (right) mice at postnatal day 60. Scale bar: 100 μ m.

Appendix 4.3. Effects of sleep deprivation in locus coeruleus of Gpt2-heterozygous mice at P56.

This experiment was performed by Jimin Shin (Brown Neuroscience undergraduate, 2020).

Introduction

Locus coeruleus (LC) neurons have been shown to degenerate and die after three days of sleep deprivation in mice [1]. We hypothesized that Gpt2-heterozygous animals would show increased metabolic vulnerability in LC to sleep deprivation compared to their wild-type littermates thereby increasing the severity of neuron death.

Results/Key Points

- Confirmed validity of the 3-day sleep deprivation paradigm in wild-type mice at 8 weeks: there is decreased number of tyrosine hydroxylase (TH)+ neurons after sleep deprivation.
- Gpt2-heterozygous mice have more neuron death compared to wild-type mice after sleep deprivation.

Discussion

Although the reasons for why sleep deprivation causes rapid neuron loss in LC are unclear, it appears that even loss of one copy of Gpt2 allele is enough to cause worsening of neuron loss. It is best if the experiment is validated by another trial with increased number of animals and/or better still, by another laboratory.

Available Data (not shown):

- Images of LC for each group/condition.

- TH+ neuron counts for individual animal.
- Videos of animals using the toys that sleep deprivation paradigm is based on.

Method

The sleep deprivation paradigm was performed as described by Zhang and co-workers [1]. Control animals were left undisturbed, “short” sleep deprivation involved 3 hours in an enriched environment and “extended” sleep deprivation involved 8 hours in an enriched environment. Wild-type and Gpt2-heterozygous mice were subjected to sleep deprivation at 8 weeks of age. The toys involved, wheels, ladders, wooden maze and a paper hut. If the mouse were not moving for more than a minute, a gentle nudge was administered or one of the toys was moved to always keep the mouse vigilant. At the end of the experiment, the mice were transcardially perfused with 4% paraformaldehyde. 30 μ m thick cryosections of the LC were mounted on slides.

Figure Legends

Figure A4.3. Worsened LC neuron loss after sleep deprivation in Gpt2-heterozygous mice at 8 weeks of age.

A. Tyrosine hydroxylase+ neuron counts in Trial 1 involving only wild-type mice at postnatal day 56 (P56). n(control)=3, n(short)=4, n(extended)=2 mice. *** P <0.001.

B. Tyrosine hydroxylase+ neuron counts in Trial 2 involving only wild-type mice at P56. n(control)=2, n(short)=2, n(extended)=3 mice. *** P <0.001.

C. Tyrosine hydroxylase+ neuron count data from Trial 1&2 combined. *** P <0.001.

D. Tyrosine hydroxylase⁺ neuron counts of wild-type and Gpt2-heterozygous mice after extended sleep deprivation. n(wild-type)=5 , n(Gpt2-het)=3 mice.

E. Representative images of LC from wild-type and Gpt2-heterozygous mice after normal sleep or extended sleep deprivation. TH is shown in magenta. Scale bar: 50 μ m.

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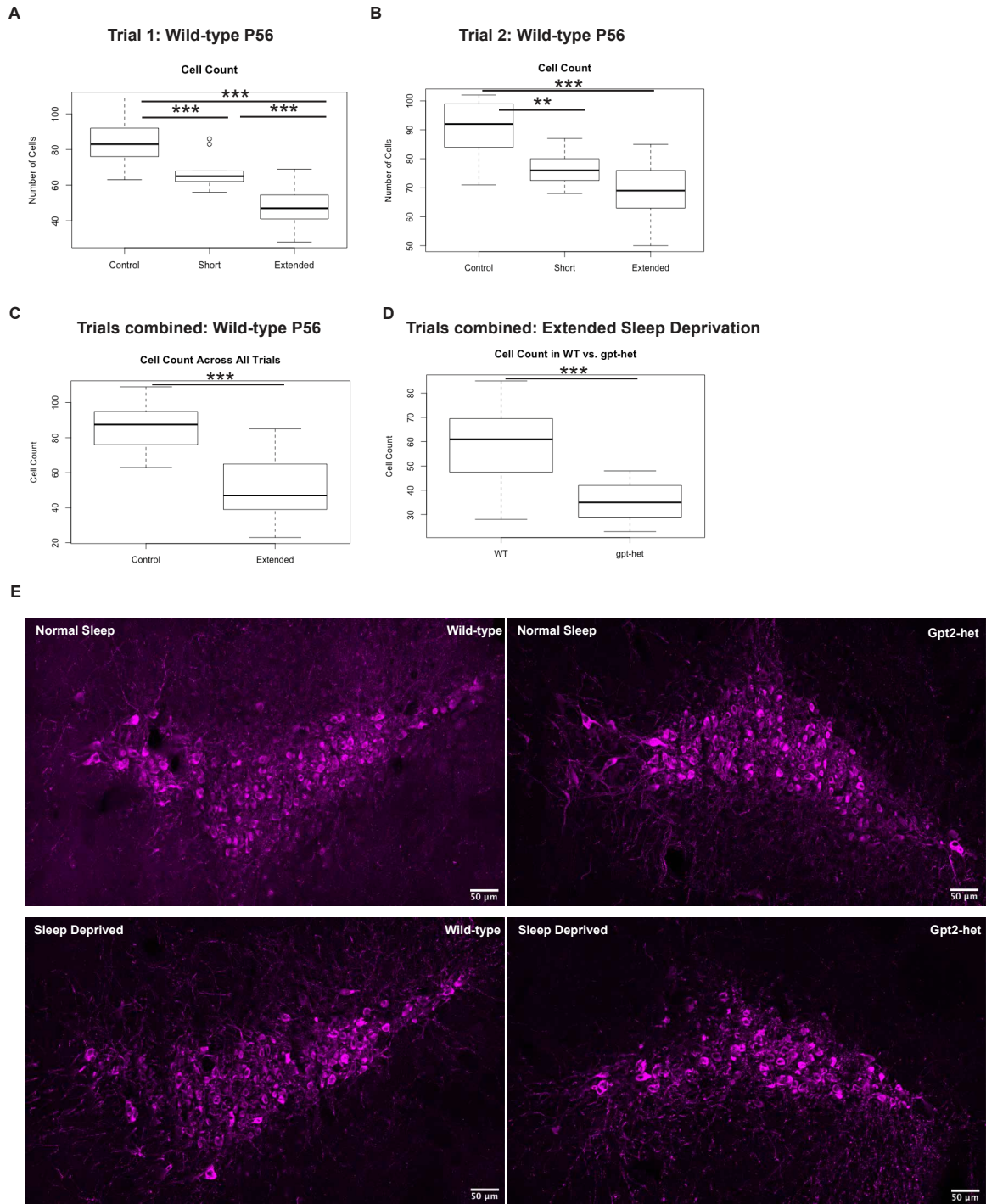


Figure A4.3. Worsened LC neuron loss after sleep deprivation in Gpt2-heterozygous mice at 8 weeks of age. A. Tyrosine hydroxylase+ neuron counts in Trial 1 involving only wild-type mice at postnatal day 56 (P56). n(control)=3, n(short)=4, n(extended)=2 mice. ***P<0.001. B. Tyrosine hydroxylase+ neuron counts in Trial 2 involving only wild-type mice at P56. n(control)=2, n(short)=2, n(extended)=3 mice. ***P<0.001. C. Tyrosine hydroxylase+ neuron count data from Trial 1&2 combined. ***P<0.001. D. Tyrosine hydroxylase+ neuron counts of wild-type and Gpt2-heterozygous mice after extended sleep deprivation. n(wild-type)=5, n(Gpt2-het)=3 mice. E. Representative images of LC from wild-type and Gpt2-heterozygous mice after normal sleep or extended sleep deprivation. TH is shown in magenta. Scale bar: 50 μm.

For Appendices 5.1, .2, I will list my brief observations and more data is available upon request.

Appendix 5.1. Additional data on ¹⁵N-glutamine and ¹⁵N-alanine labeling in Gpt2-null synaptosomes.

Fractional enrichments of N-labeling in aspartate and GABA from ¹⁵N-glutamine precursor were slightly increased in the Gpt2-null synaptosomes. Glutathione & serine levels showed major decreases. No major changes in levels of phenylalanine, fumarate, succinate, threonine, tryptophan, tyrosine, valine, leucine/isoleucine, NAD, phosphoenolpyruvate.

No N labeling in aspartate or GABA was observed using ¹⁵N-alanine as precursor in Gpt2-null synaptosomes.

Appendix 5.2. Additional data on metabolomics in Gpt2-null synaptosomes.

Metabolomics with Gpt2-null synaptosomes at P18 showed increases in cystathionine, proline, lysine, fructose 6-P and decreases in glutathione and serine (in agreement with metabolomics in whole brain and hippocampus tissues – Chapter 2&3). Compared to the whole brain and hippocampus tissue data, the PCA plots did not resolve the wild-type and Gpt2-null as well, this is most likely due alteration of the metabolome during the chemical procedure of obtaining synaptosomes.

Appendix 5.3. Network firing of cortical Gpt2-null neurons using Microelectrode Arrays (MEA).

Introduction

To investigate whether glutamatergic transmission is impacted in Gpt2-null neurons and whether there are developmental deficits in network firing properties in vitro, I used a multi-well microelectrode array (MEA) system, Axion Maestro Edge. It is an in vitro system and fails to capture the in vivo physiology; for example short periods of network firing followed by long periods of pause as seen in the MEAs does not occur in vivo cortical networks [1]. However, MEA system allows for a continuous monitoring of development of network firing in a controlled environment over time in the same wells and gives high-throughput put data with multiple relevant firing parameters such as firing rate, network burst frequency and duration, and coefficient of variation of inter-burst intervals (a measure of firing regularity). The multi-well arrangement also allows for use of multiple drug interventions on cells cultured from the same pup decreasing between pup variability.

Several experiments involved medium composition changes and interfering with the glutamine entry or metabolism to reveal possible vulnerabilities in Gpt2-null cortical neurons in vitro. The experiments and corresponding hypotheses are as follows:

1. Culture development over time in regular Neurobasal Medium: The continuous monitoring (day 4-15 in Neurobasal A medium (NBA)) may reveal delays in network firing in Gpt2-null cells.

2. Firing in Tyrode Medium (artificial cerebrospinal fluid): Medium deprivation in Gpt2-null cells (at day 14, for 24 hours) may cause further/faster decline of firing over time.
3. Firing in Glutaminase inhibition or Glutamine deprivation: Further decreases in glutamate by inhibiting glutaminase (converts glutamine into glutamate) with N,N'-[thiobis(2,1-ethanediyl-1,3,4-thiadiazole-5,2-diyl)]bis-benzeneacetamide (BPTES) or depriving the cultures of glutamine may reveal inability to compensate for glutamate availability in Gpt2-null cells (at day 14, for 24 hours in NBA).
4. Firing in Tyrode Medium with MeAIB: N-methyl-aminoisobutyric acid (MeAIB) inhibits Na-dependent amino acid transport system A transporters (ATA1 and ATA2). By blocking glutamine entry into neurons, we may block glutamine flux into glutamate that may otherwise occur via other metabolic enzymes such as glutamine fructose 6-phosphate aminotransferase (at day 14, for 24 hours in Tyrode).
5. Firing in Co-cultures: I tried four combinations, wild-type neuron&wild-type astrocyte, wild-type neuron&Gpt2-null astrocyte, Gpt2-null neuron & wild-type astrocyte and Gpt2-null neuron & Gpt2-null astrocyte. Contrary to the primary function of normal astrocytes, Gpt2-null astrocytes may dampen the resources available for neurons thereby causing deficits in the development of the neuronal culture (days 4-16 in NBA, then at day 16, for 24 hours in Tyrode).

Parameters of the MEA include: a) Mean Firing Rate b) Burst Frequency c) Burst Duration d) Inter-Burst Interval Coefficient of Variation e) Network Burst Frequency f) Network Burst Duration g) Network Inter-Burst Interval Coefficient of Variation.

Results / Key Points

1. No major differences in the development of firing patterns in Gpt2-null cortical neuronal cultures.
2. Slight decreases in electrode burst and network burst frequency in Gpt2-null neurons in the Tyrode medium toward the end of the 24-hour period.
3. No differences in firing after glutaminase inhibition or glutamine deprivation.
4. Glutamine deprivation allowed for a higher increase in firing compared to glutaminase inhibition in both wild-type and Gpt2-null neurons.
5. Blocking of glutamine entry into the cells by MeAIB did not cause any changes in firing pattern.
6. All four combinations of co-cultures developed in NBA and responded to Tyrode medium similarly.

Discussion

The experiments with multielectrode arrays using Gpt2-null neuronal cultures did not yield any significant results. Electrophysiology in Gpt2-null hippocampal slices showed slight decreases in glutamatergic transmission and upregulation of various proteins related to glutamate metabolism may account for that decrease. Altogether, Gpt2 does not appear to be a primary enzyme that chiefly contributes to glutamatergic transmission. Additional metabolic stresses such as nutrient deprivation (Tyrode medium), glutamine deprivation, glutaminase inhibition, blocking entry of glutamine into the cell did not reveal any vulnerabilities in Gpt2-null cortical neuronal cultures. While expressing the data as the percentage of the value obtained at the first time point may reduce within well and within culture variability, it would capture small significant changes if at all.

There were slight decreases in electrode burst and network burst frequencies in Gpt2-null cortical neurons in the Tyrode medium toward the end of the 24-hour period. The conditions were later repeated when MeAIB was introduced with reduced sample size, and the slight differences were not statistically significant.

The cortical neuronal cultures also contain an appreciable number of astrocytes (10%) and the neuronal firing is most likely supported by astrocytes. The starting astrocytes in the co-cultures would still override the astrocytes that accompany the neuronal culture as the starting astrocytes cover the entire well and the neurons are plated on top. There was no difference among the four co-culture combinations, suggesting that Gpt2-null astrocytes do not confer an additional metabolic burden on the neurons. This is perhaps not surprising since mouse Gpt2 astrocytes express Gpt1 and therefore may be able to adequately contribute to the glutamate metabolism in vitro. Human neurons or astrocytes do not express Gpt1 [2] and induced pluripotent stem cell derived neurons may be able to capture any deficiencies in network connectivity and activity in vitro.

It is possible that mouse hippocampal neurons can be used instead of cortical neurons but their cell yield is lower and does not always allow for using all the available wells. It is unlikely that hippocampal neurons have firing deficits given the absence of phenotype in cortical neurons though the raw data for hippocampal neurons grown in NBA from day 4 to day 16 is available.

It is worth considering if the different medium interventions properly worked. Medium deprivation as performed by using Tyrode medium or NBA without glutamine likely worked as intended even though the cells still contained glutamine and other substrates prior to the deprivation. 24 hours is likely to be enough to capture differences between

the wild-type and Gpt2-null cultures. On the other hand, the drug application is complicated by their efficiency and mechanism of action. MeAIB acts on sodium-dependent glutamine transporters but not on sodium-independent glutamine transporters which have been shown to be expressed in neurons or astrocytes [3]. BPTES is a specific inhibitor of glutaminase and likely inhibited the enzyme fully in our preparation but we did not specifically test for this. However experiments involving both MeAIB and BPTES are complemented by glutamine deprivation, and none of them showed any significant changes suggesting that Gpt2-null neurons are able to fire similarly to the wild-type cultures without depending on glutamine at all.

Another pathway worth investigating is glucose, as it is a major precursor for glutamate. While I have not conducted any experiments with either glucose deprivation or blocking pyruvate entry into the mitochondria, my expectation is that it will not reveal any deficits. The in vitro system does not seem to constitute the developmental and compensatory changes seen in vivo and these processes are likely the reason for why we observe decreases in glutamate levels and glutamatergic transmission in vivo. This idea is reinforced by the observation that Gpt2 normally catalyzes the reaction in the favor of alanine and alpha-ketoglutarate production not glutamate, likely to be the result of differences in concentration and K_m values for each substrate in neuronal cells. The expectation that would follow from these observations is an increase of glutamate at least in the mitochondria, contrary to what we observe in vivo. Refer to Chapter 2 for evidence that may suggest why a decrease in glutamate in Gpt2-null brain is observed.

Available data (not analyzed):

- Raw data for wild-type and Gpt2-null hippocampal neurons (75,000 per well) grown in NBA from day 4 to day 16.
- Other metrics from the MEA system (e.g. Inter-quartile range of normalized burst durations, measure of synchrony)

Method

Cell Culture

Mouse primary hippocampal neuron culture. Hippocampal neurons were cultured as described previously [4]: Hippocampi from P0-1 pup were dissected in Hank's Balanced Salt Solution (HBSS) (Gibco 14170-112) and placed in 500µl of 20U/ml papain (Worthington LK003176, in Earle's Balanced Salt Solution (EBSS), Worthington, LK003188). The tube with hippocampi/papain was incubated at 37°C for 15 minutes. The tissue was triturated with 1ml pipette tip for 12 strokes. The tissue was further incubated at 37°C for 15 minutes and triturated. The remaining bits of tissue sunk and the solution with dissociated cells was spun in a separate tube at 300g, 5 minutes, at RT. The cell pellet was dissolved gently in Inhibitor Solution (540µl EBSS, 60µl Ovomuroid Protease Inhibitor (Worthington Biochemical, LK003182), 30µl DNase (Worthington Biochemical, LK003170) per hippocampi) and filtered through a 70µm nylon mesh (FisherScientific, 22363548). The filtered cell suspension was layered on top of 1ml Ovomuroid Protease Inhibitor and spun at 70g, 10 minutes, at RT. The supernatant was discarded, and the cell pellet was resuspended in Neurobasal A+ (NeuroBasal A (10888022), 1X B27 Supplement (ThermoFisher Scientific, 17504044), 2mM GlutaMAX (ThermoFisher Scientific, 35050061). The full media was changed the next day and then half media every 3 days. Tyrode medium consisted of 140mM NaCl, 4mM KCl, 2mM

CaCl₂, 2mM MgCl₂, 10mM HEPES. The concentrations of BPTES and MeAIB were 3 μM and 10 μM respectively.

Mouse primary astrocyte-enriched cultures. The culturing protocol was adapted from [5, 6]: Cortices from P0-1 pup were dissected in HBSS, diced into 6 pieces and transferred to a 15ml conical tube. The tissue is incubated in 0.25% Trypsin-EDTA in HBSS at 37°C for 30 minutes. The solution is removed carefully to leave the tissue pieces at the bottom, 6ml Astrocyte Plating Medium (APM: DMEM (10569-010), 10% FBS (Invitrogen 16000044), 1% P/S (Invitrogen 15140122)) was added. The tissue is triturated for 15 strokes with 10ml pipette and then 5 strokes more with 1ml pipette. The cell suspension was filtered through 70μm nylon mesh and seeded in a 25cm²-flask (Corning 3289). After 2 days, the full medium was changed, then every 3 days. When the astrocyte layer was confluent (~7 days), the flask was shaken at 225 rpm overnight at 37°C. The full medium was changed to APM with 20μM cytosine arabinoside (Ara-C) to remove any other contaminated proliferative cell types. After two days, the full medium was changed to APM. The Ara-C treatment was repeated the next day. Mild trypsin (0.0675%) treatment was used to lift off the astrocyte layer as a whole and leave the remaining microglia at the bottom of the flask. The layer was incubated in 1ml of Accutase (StemCellTechnologies, 07920) in a fresh tube at 37°C for 10 minutes. The layer was dissociated with 1ml pipette tip with 5 strokes. 2ml APM was added; the solution was mixed and filtered through a 70 μm nylon mesh. 25,000 cells per well were seeded and maintained until seeding of neurons.

Microelectrode Array (MEA) Recordings

The microelectrode array plate used in the study was M384-tMEA-24W (Axion Biosystems) with 16 poly(3,4-ethylenedioxythiophene) (PEDOT) microelectrodes in each well. The electrodes were coated with 20 $\mu\text{g}/\text{ml}$ laminin (10 μl per well) for 2 hours prior to cell seeding. The neurons were seeded in a dotting method at a density of 150,000 cells per well in 10 μl and kept in the incubator for 1 hour before filling the well with medium (400 μl each). Six wells were designated for each experimental group.

The electrical activity was measured by Maestro Edge (Axion Biosystems). Any wells that had less than or equal to 13 active electrodes were excluded (minimum spike rate for active electrode selection criteria: 5 spikes / minute). Single electrode bursts are detected using Inter-Spike Interval (ISI) Threshold parameters, including a maximum of 100 ms inter-spike interval and a minimum of 5 of spikes. Network burst criteria included a maximum of 100 ms inter-spike interval, a minimum of 50 number of spikes and a minimum of 35% participating electrodes. Mean Firing Rate estimation detection window was 10 seconds.

Figure Legends

Figure A 5.1. MEA cortical neuronal culture firing in Neurobasal Medium

A. Images of Spike Amplitude seen in 24 wells of the MEA plate (left) and waveforms of 16 electrodes in a given well during a network burst activity.

B. MEA parameters of mean firing rate, burst frequency, burst duration, inter-burst interval coefficient of variation, network burst frequency, network burst duration and network inter-burst interval coefficient of variation. Wild-type (black), Gpt2-null (red), n=8 cultures. NBA: Neurobasal A medium.

Figure A 5.2 MEA cortical neuronal culture firing Tyrode Medium

A. MEA parameters of mean firing rate, burst frequency, burst duration, inter-burst interval coefficient of variation, network burst frequency, network burst duration and network inter-burst interval coefficient of variation. Wild-type (black), Gpt2-null (red), n=5 cultures. NBA: Neurobasal A medium. The linear regression was performed for the data of the linear phase in the plot (readings 7-26). Slope were compared. * $0.01 < P < 0.05$, ** $0.001 < P < 0.01$, *** $P < 0.001$.

Figure A 5.3. MEA cortical neuronal culture firing after glutamine deprivation or glutaminase inhibition.

A. MEA parameters of mean firing rate, burst frequency, burst duration, inter-burst interval coefficient of variation, network burst frequency, network burst duration and network inter-burst interval coefficient of variation. Wild-type with 3 μ M BPTES (black), Gpt2-null with 3 μ M BPTES (red), Wild-type without Glutamine (green), Gpt2-null without Glutamine (blue) n=5 cultures. NBA: Neurobasal A medium; NBA – Gln: Neurobasal A medium without Glutamine.

Figure A 5.4. MEA cortical neuronal culture firing after glutamine transport inhibition

A. MEA parameters of mean firing rate, burst frequency, burst duration, inter-burst interval coefficient of variation, network burst frequency, network burst duration and network inter-burst interval coefficient of variation. Wild-type with Tyrode (black),

Gpt2-null with Tyrode (red), Wild-type with 10 μ M MeAIB (green), Gpt2-null with 10 μ M MeAIB (blue) n=5 cultures. NBA: Neurobasal A medium.

Figure A 5.5. MEA cortical neuronal firing in co-cultures with astrocytes

A. MEA parameters of mean firing rate, burst frequency, burst duration, inter-burst interval coefficient of variation, network burst frequency, network burst duration and network inter-burst interval coefficient of variation. Wild-type neuron & wild-type astrocyte (black), wild-type neuron & Gpt2-null astrocytes (red), Gpt2-null neuron & wild-type astrocytes (green), Gpt2-null neuron & Gpt2-null astrocyte (blue), n=4 cultures. NBA: Neurobasal A medium.

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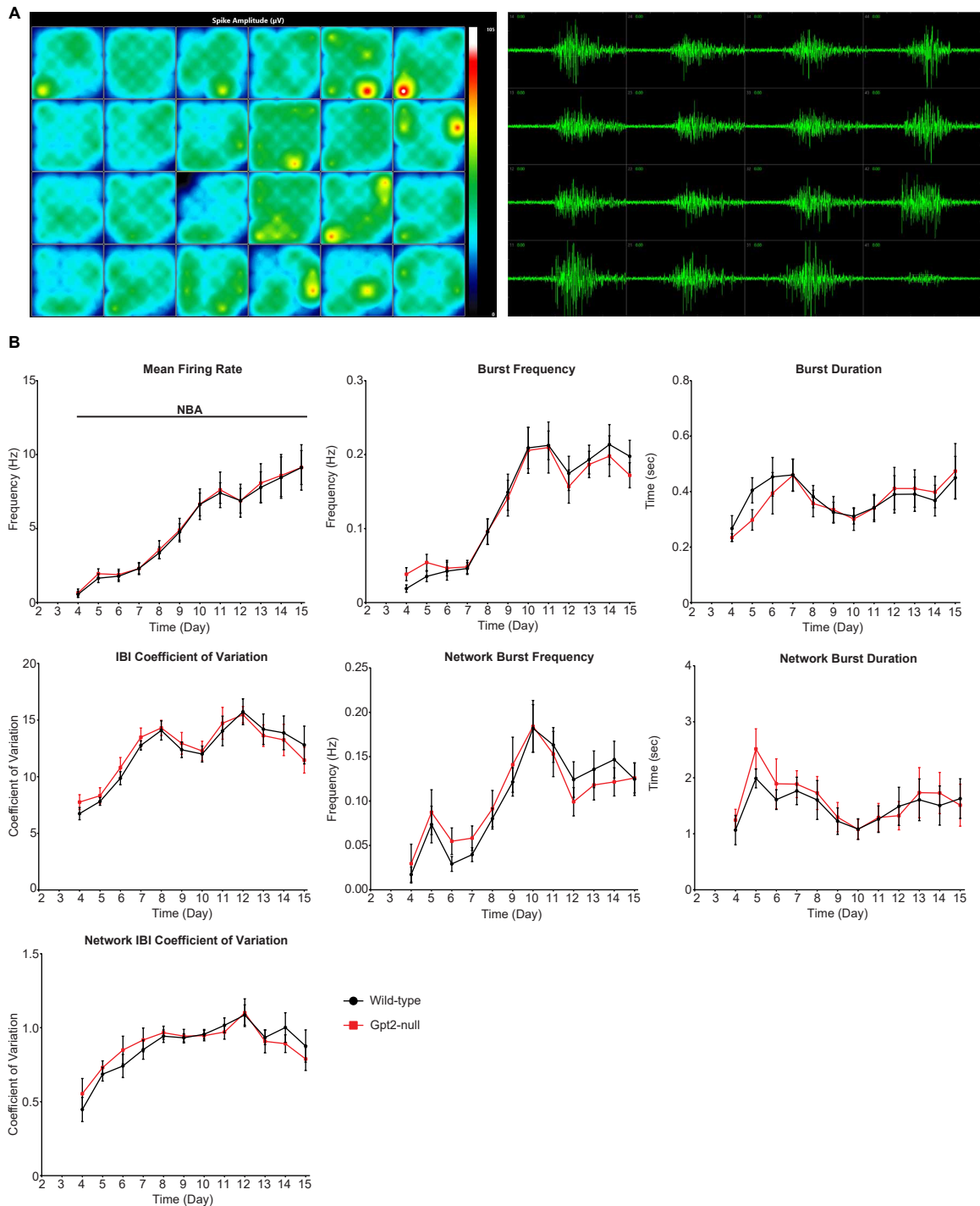


Figure A 5.1. MEA cortical neuronal culture firing in Neurobasal Medium

A. Images of Spike Amplitude seen in 24 wells of the MEA plate (left) and waveforms of 16 electrodes in a given well during a network burst activity. B. MEA parameters of mean firing rate, burst frequency, burst duration, inter-burst interval coefficient of variation, network burst frequency, network burst duration and network inter-burst interval coefficient of variation. Wild-type (black), Gpt2-null (red), n=8 cultures. NBA: Neurobasal A medium.

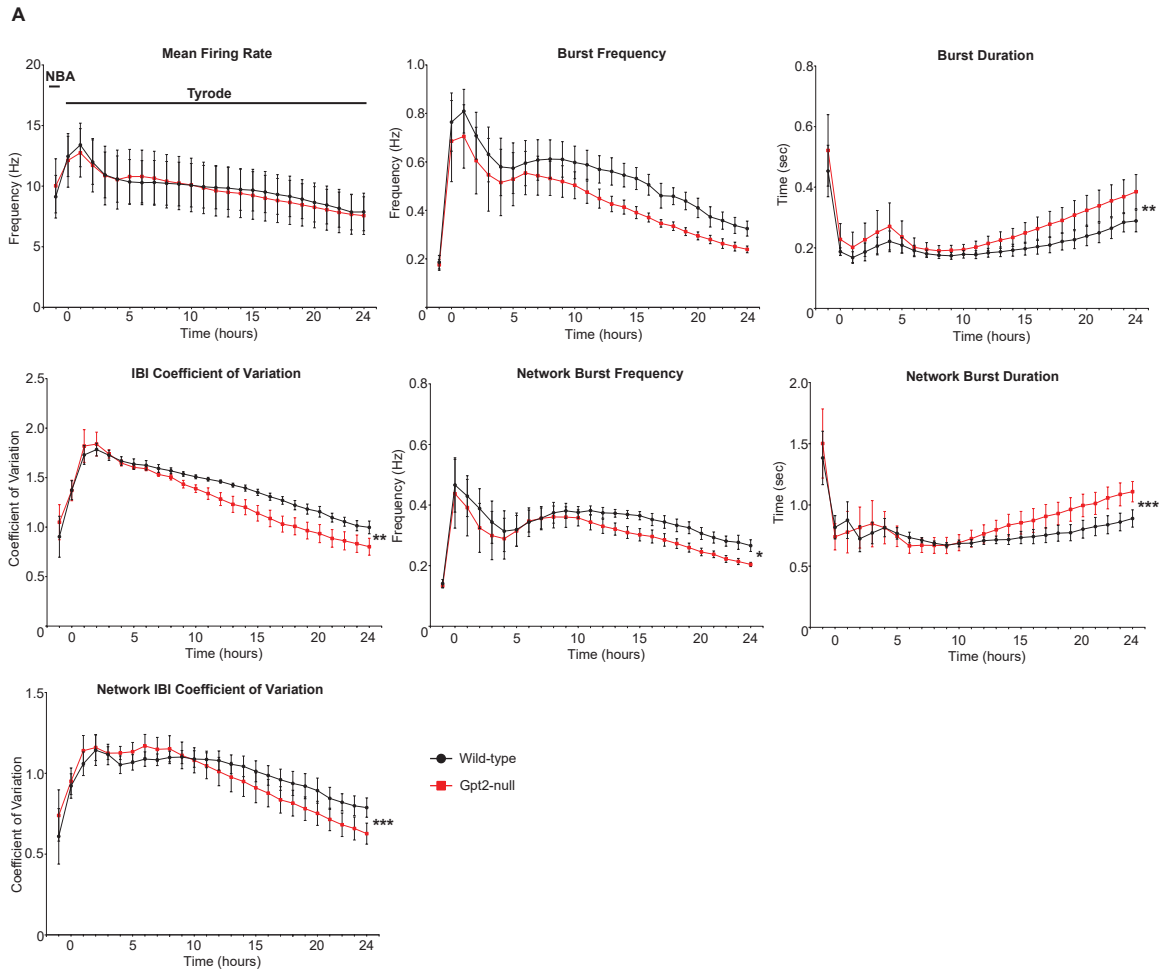


Figure A 5.2 MEA cortical neuronal culture firing Tyrode Medium

A. MEA parameters of mean firing rate, burst frequency, burst duration, inter-burst interval coefficient of variation, network burst frequency, network burst duration and network inter-burst interval coefficient of variation. Wild-type (black), Gpt2-null (red), n=5 cultures. NBA: Neurobasal A medium. The linear regression was performed for the data of the linear phase in the plot (readings 7-26). Slope were compared. *0.01<P<0.05, **0.001<P<0.01, ***P<0.001.

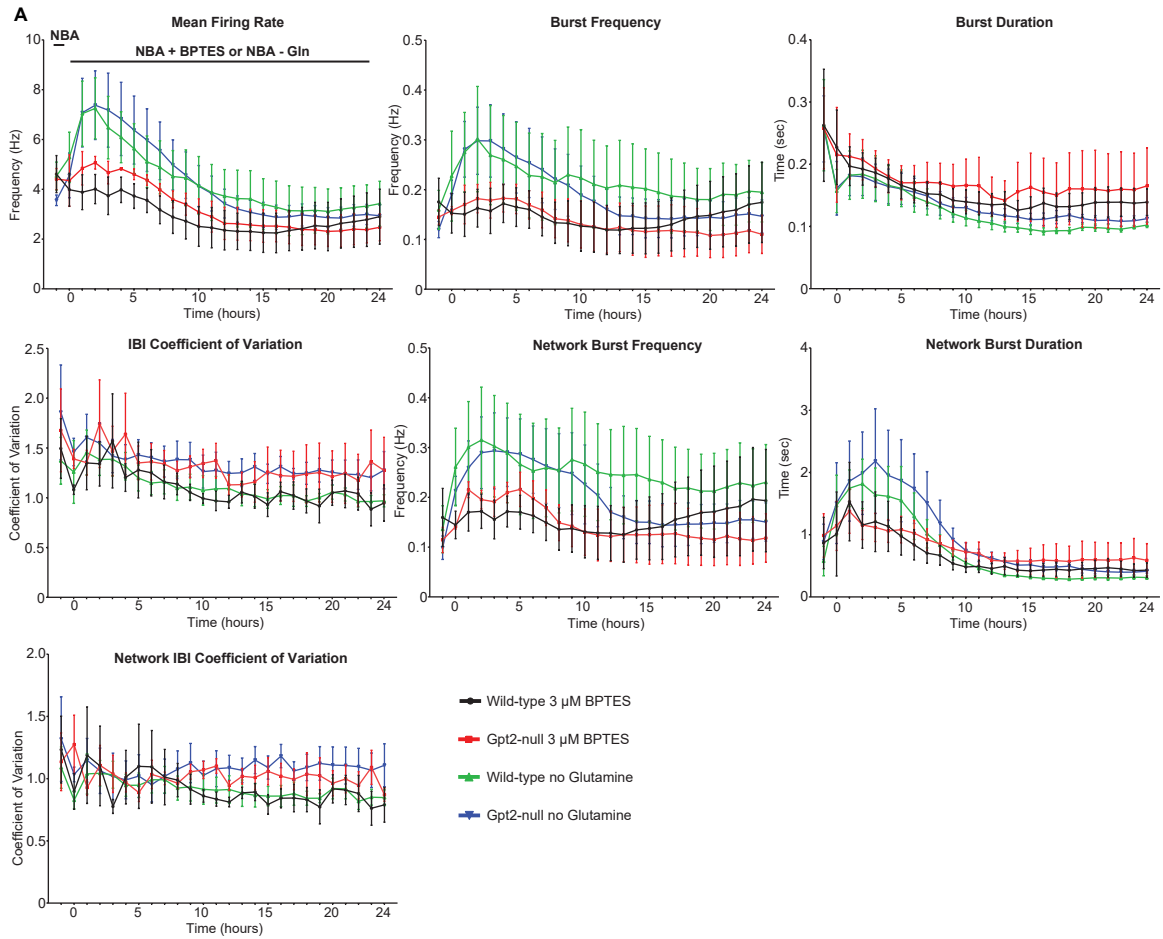


Figure A 5.3. MEA cortical neuronal culture firing after glutamine deprivation or glutaminase inhibition. A. MEA parameters of mean firing rate, burst frequency, burst duration, inter-burst interval coefficient of variation, network burst frequency, network burst duration and network inter-burst interval coefficient of variation. Wild-type with 3 μ M BPTES (black), Gpt2-null with 3 μ M BPTES (red), Wild-type without Glutamine (green), Gpt2-null without Glutamine (blue) n=5 cultures. NBA: Neurobasal A medium; NBA – Gln: Neurobasal A medium without Glutamine.

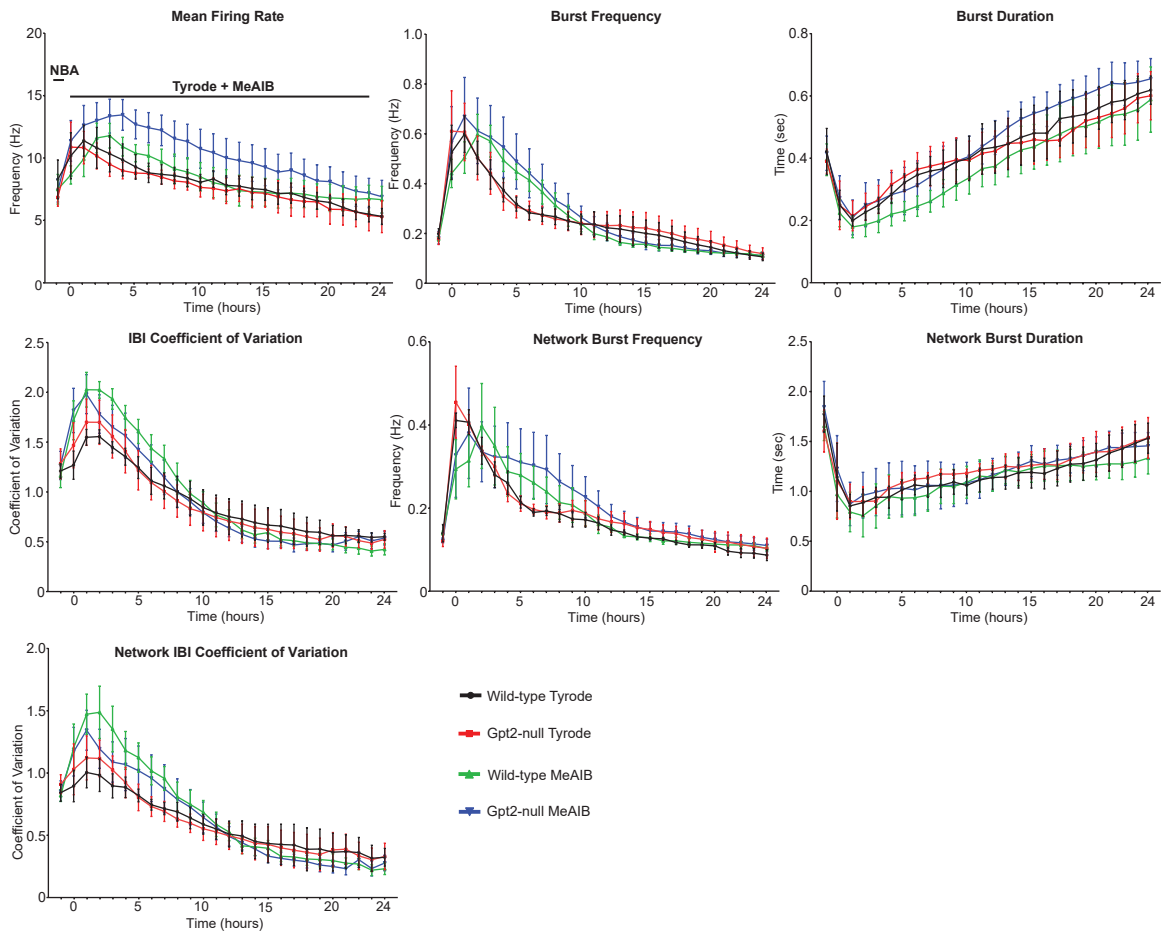


Figure A 5.4. MEA cortical neuronal culture firing after glutamine transport inhibition A. MEA parameters of mean firing rate, burst frequency, burst duration, inter-burst interval coefficient of variation, network burst frequency, network burst duration and network inter-burst interval coefficient of variation. Wild-type with Tyrode (black), Gpt2-null with Tyrode (red), Wild-type with 10 μ M MeAIB (green), Gpt2-null with 10 μ M MeAIB (blue) n=5 cultures. NBA: Neurobasal A medium.

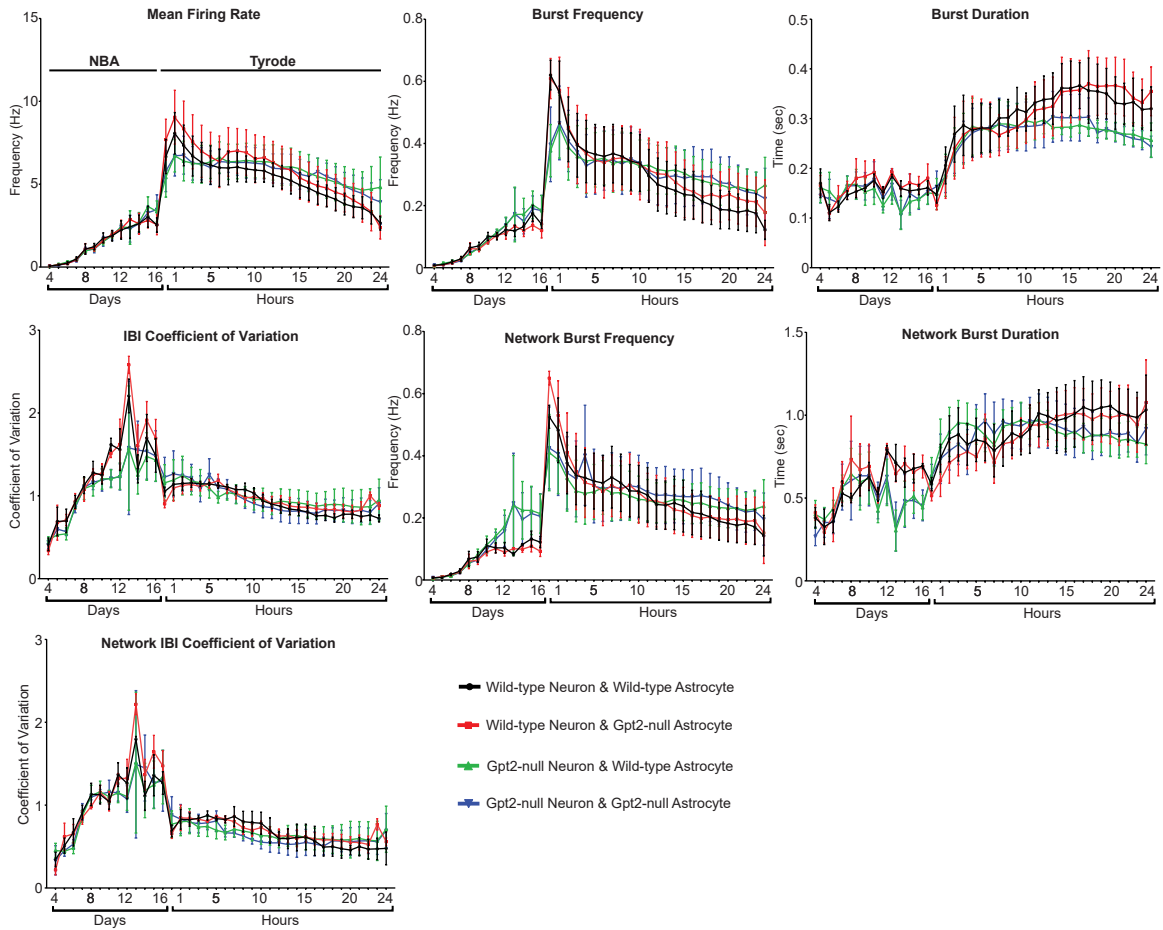


Figure A 5.5. MEA cortical neuronal firing in co-cultures with astrocytes

A. MEA parameters of mean firing rate, burst frequency, burst duration, inter-burst interval coefficient of variation, network burst frequency, network burst duration and network inter-burst interval coefficient of variation. Wild-type neuron & wild-type astrocyte (black), wild-type neuron & Gpt2-null astrocytes (red), Gpt2-null neuron & wild-type astrocytes (green), Gpt2-null neuron & Gpt2-null astrocyte (blue), n=4 cultures. NBA: Neurobasal A medium.