

## Title

*Arx* expansion mutation perturbs cortical development by augmenting apoptosis without activating innate immunity in a mouse model of X-Linked Infantile Spasms Syndrome

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## Key words

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## Summary Statement

We found non-cell autonomous apoptosis and fewer *Arx*<sup>+</sup> interneurons in neonatal neocortex of an ISSX *Arx* expansion model. Early estradiol therapy rescued *Arx*<sup>+</sup> interneuron density, but did not prevent apoptosis.

## Abstract

X-linked infantile spasms (ISSX) is a clinically devastating developmental epileptic encephalopathy with life-long impact.  $Arx^{(GCG)10+7}$ , a mouse model of the most common triplet-repeat expansion mutation of *ARX*, exhibits neonatal spasms, electrographic phenotypes, and abnormal migration of GABAergic interneuron subtypes. Neonatal presymptomatic treatment with 17 $\beta$ -Estradiol (E2) in  $Arx^{(GCG)10+7}$  reduces spasms and modifies progression of epilepsy. Cortical pathology during this period, a crucial point for clinical intervention in ISSX has largely been unexplored, and the pathogenic cellular defects that are targeted by early interventions are unknown. In the first postnatal week, we identified a transient wave of elevated apoptosis in  $Arx^{(GCG)10+7}$  mouse cortex that is non-*Arx* cell autonomous, since mutant *Arx*-immunoreactive (*Arx*+) cells are not preferentially impacted by cell death. NeuN+ survival was also not impacted suggesting a vulnerable subpopulation in the immature  $Arx^{(GCG)10+7}$  cortex. Inflammatory processes during this period might explain this transient elevation in apoptosis, however, transcriptomic and immunohistochemical profiling of several markers of inflammation revealed no innate immune activation in  $Arx^{(GCG)10+7}$  cortex. Neither neonatal E2 hormone therapy, nor ACTH(1-24), the frontline clinical therapy for ISSX, diminished the augmented apoptosis in  $Arx^{(GCG)10+7}$ , but both rescued neocortical *Arx*+ cell density. Since early E2 treatment effectively prevents seizures in this model, enhanced apoptosis does not solely account for the seizure phenotype, but may contribute to other aberrant brain function in ISSX. However since both hormone therapies, E2 and ACTH(1-24), elevate the density of cortical *Arx*+-interneurons, their early therapeutic role in other neurological disorders hallmarked by interneuronopathy should be explored.

## Introduction

Early infantile epileptic encephalopathies (EIEE) include a heterogeneous class of genetic neuronal synchronization disorders hallmarked by their postnatal clinical appearance and complex neurodevelopmental phenotypes (Kalser and Cross, 2018). Mutations in over 20 genes have been identified for EIEE (Axeen and Olson, 2018; McTague et al., 2016), but most molecular details of how and when these single gene errors perturb the formation of critical brain circuits are not well understood. A clinical subset of EIEE, the so-called ‘catastrophic epilepsies’, are distinguished by the onset of infantile spasms (IS), developmental cognitive delay, and life-long pharmaco-resistant epilepsy (Howard and Baraban, 2017). One of the original and best studied genes in this subgroup is the X-linked transcription factor *Aristaless-related homeobox* gene (*ARX*) (Bienvenu et al., 2002; Colasante et al., 2008). *ARX* mutations are responsible for a rich spectrum of EIEE syndromes whose phenotypic severity often correlate with the degree of structural damage to the protein, and include X-linked infantile spasms (ISSX1), Ohtahara Syndrome, and severe dyskinetic disorders (Kato, 2015; Kato et al., 2004; Sherr, 2003; Shoubridge et al., 2010).

Within the forebrain, *Arx* is expressed in developing and mature GABAergic interneurons and is crucial for the migratory capacity of these cells to reach the cortical plate (Colombo et al., 2004; Poirier et al., 2004). This prototypical cell-specificity underlying *Arx* pathogenesis inspired the term ‘interneuronopathy’ (Kato and Dobyns, 2005). In addition to controlling migration, the absolute size of the cortical progenitor cell pool in the mouse brain is dependent on *Arx* (Colasante et al., 2015; Friocourt et al., 2008). Given the molecular complexity of *Arx* function which coordinates the transcription of dozens of known gene targets (Friocourt and Parnavelas, 2011; Fulp et al., 2008; Quille et al., 2011), much information on the specificity of the cellular pathogenesis underlying *Arx*-related pleiotropy is still missing. Aside from intrinsic deficits in proliferation and migration of *Arx*<sup>+</sup> progenitors in the embryonic forebrain, it is not well understood how mutations in *Arx* might impact postnatal processes extrinsic to *Arx*<sup>+</sup>

interneurons, such as synaptogenesis, cell death, and differentiation during early cortical development.

One of the most common mutations in *ARX* is a triplet repeat expansion in the first polyalanine tract (PA1) that expands this region from 10 to 17 alanines (Shoubridge et al., 2010). Patients with this mutation display a less severe phenotype than individuals with deletion or truncation mutations in *ARX* causing major brain malformations (Kato et al., 2004; Kitamura et al., 2002; Sherr, 2003). Expansion mutations in PA1 alter binding of *Arx* with transcriptional cofactors and impair transcription regulation, leading to a more subtle disturbance of interneurons (Mattiske et al., 2016; Nasrallah et al., 2012). Mouse models of this expansion have been developed and are viable compared to *Arx* knockout (KO) mice which show early lethality (Kitamura et al., 2009; Price et al., 2009). Mouse models of PA1 expansion display aberrant migration and loss of several GABAergic interneuron subtypes in the cortex, however, there are differences between models in identity, severity, and location of these cellular phenotypes (Beguin et al., 2013; Lee et al., 2017; Price et al., 2009). Mutant *Arx*<sup>(GCG)<sup>10+7</sup></sup> males recapitulate human ISSX phenotypes, including neonatal spasms, seizures, and behavioral comorbidities and thus facilitate isolation of *Arx* pathogenic mechanisms (Price et al., 2009). Studies in this model notably reveal interneuronopathy with a selective loss of calbindin+ and neuropeptide Y+ cells, but sparing parvalbumin+ cells (Olivetti et al., 2014; Price et al., 2009).

Complex dysregulation of the *Arx*-linked transcriptome on survival of distinct neuronal precursor populations remains to be explored. Interestingly, when the effects of *Arx* mutations were examined in pancreatic endocrine progenitors where *Arx* is expressed during early development, it was found that *Arx* deletion caused aberrant specification of glucagon-producing alpha cells into a beta islet cell identity, whereas *Arx* expansion mutation led to enhanced apoptosis of alpha cells during development (Wilcox et al., 2013a; Wilcox et al., 2013b). Since *Arx* expansion causes dysregulation of genes that are directly or indirectly involved in apoptosis (Mattiske et al., 2016), we examined the postnatal *Arx*<sup>(GCG)<sup>10+7</sup></sup> mouse brain

for inappropriate developmental cell death. Unexpectedly, we identified a transient wave of enhanced programmed cell death in neocortex at the end of the first week that affected only non-Arx+ cells. Although we have not positively identified the vulnerable cell type, the onset of this wave coincides with the onset of the spasms phenotype in  $Arx^{(GCG)10+7}$  mice. Since anti-inflammatory hormone treatment with adrenocorticotrophic hormone (ACTH) can be clinically effective in reducing infantile spasms (Song et al., 2017), we looked for evidence of cellular inflammation that might account for the enhanced neonatal cell death, but found none. We also determined that the antiepileptogenic efficacy of the neuroprotective hormone, 17 $\beta$ -estradiol in this model, as well as ACTH peptide fragment 1-24 (ACTH(1-24)), is likely due to rescue of Arx+ interneurons rather than mitigating the wave of elevated cortical apoptosis.

## Results

### **$Arx^{(GCG)10+7}$ mutants exhibit an enhanced wave of CC3-mediated apoptosis in the neocortex during the first postnatal week.**

To test the hypothesis that  $Arx^{(GCG)10+7}$  expansion mutation may alter patterns of apoptosis in the postnatal brain, we examined  $Arx^{(GCG)10+7}$  and wildtype (WT) littermates using a specific antibody against cleaved caspase-3 (CC3), a marker of the execution phase of apoptosis (Porter and Janicke, 1999). We profiled CC3-expressing cells at 5 time points during the first two weeks of life (P1, P4, P7, P9, and P14) across the rostro-caudal extent of the neocortex and hippocampus in parasagittal brain sections of mutant  $Arx^{(GCG)10+7}$  pups and WT littermates (Fig. 1A-E). Two-Way ANOVA analysis yielded a significant effect of genotype on CC3-immunoreactive (CC3+) levels in the neocortex ( $P=0.0025$ , Fig. 1F) and Bonferroni's multiple comparisons test yielded a significant, 25-35% increase in CC3+ cells in  $Arx^{(GCG)10+7}$  neocortex compared to WT littermates at P7 ( $P=0.0012$ , Fig. 1F). Binning analysis in the neocortex revealed that CC3+ cell localization did not differ between genotypes in terms of

laminar position (Fig. S1A). In contrast, CC3+ cells were rarely present in the hippocampus after P1; when found, they were typically in the CA1 region, however, there was no significant effect of genotype ( $P=0.2035$ , Two Way ANOVA) and no significant differences between genotypes at any age in the hippocampus (Fig. 1G). The elevated apoptosis in P7 neocortex was confirmed by TUNEL assay, which showed an overall increase in TUNEL-labeled cells at P7 in mutants ( $P=0.0051$ , Unpaired t test, Fig. 1H). Overall, these data demonstrate a transient increase in CC3+ cells in the neocortex of mutants, but not hippocampus, with the most robust difference occurring at P7.

### **Mutant Arx+ cortical interneurons do not exhibit altered apoptosis.**

We initially expected that the augmented cell death was likely cell-autonomous and that the  $Arx^{(GCG)10+7}$  mutation enhanced apoptosis in this interneuron population. During the first two postnatal weeks, GABAergic interneurons normally undergo a wave of apoptosis, reducing their population density by about 20-30%, with a peak in apoptosis at P7 (Priya et al., 2018; Southwell et al., 2012). We therefore predicted that the increase in CC3+ cells in the mutant is due to elevated death of a subpopulation of Arx-immunoreactive (Arx+) interneurons expressing the expansion mutation, similar to its effects in pancreas (Wilcox et al., 2013a). To test this, we profiled the developing cortex using parasagittal brain sections and specific antibodies against Arx and CC3 and looked for an increase in Arx+ cells that express CC3. However, at all ages profiled (P1, P4, P7, P9, and P14), counts of Arx+ and CC3+ co-labeled cells did not significantly differ between  $Arx^{(GCG)10+7}$  and WT littermate control brains ( $F(1,88)=0.2374$ ,  $P=0.6273$ , Two-Way ANOVA; Fig.1I). Since the  $Arx^{(GCG)10+7}$  neocortex exhibited a reduced Arx+ cell density (Fig. 1K and (Price et al., 2009)), there may be proportionally more Arx+ cells labeled with CC3 in  $Arx^{(GCG)10+7}$  mutants compared to WT. However, normalizing co-labeled Arx+ CC3+ cells to Arx+ density counts at each age did not reveal any significant differences between genotypes ( $F(1, 88)=0.01996$ ,  $p=0.8880$ , Fig. 1J). These data indicate that the

increased apoptosis present in  $Arx^{(GCG)10+7}$  mutant cortex is extrinsic, i.e. non-cell autonomous as it does not reflect a concomitant increase in  $Arx+$  cell death.

### **$Arx^{(GCG)10+7}$ does not impact survival of NeuN expressing cortical neurons**

Since  $Arx^{(GCG)10+7}$  does not affect the neonatal survival of  $Arx+$  interneurons, other cells must account for elevated neonatal CC3+ expression. During embryonic development,  $Arx$  is transiently expressed in neural progenitors that also give rise to cortical excitatory neurons, however, these neurons do not retain  $Arx$  expression upon exiting the subventricular niche (Colasante et al., 2008; Colombo et al., 2004; Friocourt et al., 2006). Therefore, we speculated that  $Arx^{(GCG)10+7}$  mutant protein might alter transcriptional networks in this progenitor subpopulation and affect their postnatal survival despite the absence of mutant  $Arx$ . If apoptosis within this population is increased at P7, we might expect to observe a concomitant reduction in cortical neuron density at a later age. To test this, we profiled neuronal survival one week later (P14) in the cortex of  $Arx^{(GCG)10+7}$  and WT littermates using NeuN and  $Arx$  antibodies. NeuN is a pan-neuronal marker whereas  $Arx$  is expressed in about 70-90% of GABAergic interneurons, depending on brain and cortical region (Colombo et al., 2004; Poirier et al., 2004). Therefore, a majority of NeuN neurons that do not express  $Arx$  (NeuN+  $Arx-$ ) are cortical excitatory neurons. We quantified the densities of NeuN+  $Arx-$  and total NeuN density in two neocortical regions: retrosplenial agranular cortex (RSA) and motor cortex in P14 parasagittal slices (Fig. 2A,B). We found no difference in the densities of NeuN+ neurons that do not express  $Arx$  (NeuN+  $Arx-$  /mm<sup>2</sup>) in the RSA ( $p=0.7575$ , Unpaired t test, Fig. 2C) or in motor cortex ( $p=0.8665$ , Mann Whitney test, Fig. 2D) at this age. We also profiled total NeuN density (NeuN+/mm<sup>2</sup>) and found no significant differences (RSA,  $p=0.6511$ , Unpaired t test, Fig. 2E); motor cortex,  $p=0.9551$ , Mann Whitney test, Fig. 2F). These results suggest that  $Arx^{(GCG)10+7}$  does not affect the survival of cortical non- $Arx$  expressing neurons.

## Innate immune response does not account for enhanced neonatal apoptosis in

### *Arx*<sup>(GCG)10+7</sup> cortex

The increased CC3+ cell number in mutant neocortex is temporally confined to the first week of life and cannot be attributed to increased cell death of mutant Arx+ interneurons or reduced survival of Neun+ neurons. Acute and chronic inflammation in the immature brain can lead to apoptosis (Hagberg et al., 2015) and inflammation is a known cause of IS (Shandra et al., 2017). Thus, we speculated that an activated innate immune response in the postnatal *Arx*<sup>(GCG)10+7</sup> brain might contribute to increased cell death, and if so, could provide a basis for neuroactive hormone therapy. We therefore examined immunohistochemical markers of inflammation including astrogliosis and microgliosis and profiled inflammatory cytokine mRNA expression in cortical samples using Nanostring and qPCR. We found no significant differences between *Arx*<sup>(GCG)10+7</sup> and WT brain in astrogial activation via GFAP immunoreactivity at P7, the age of maximal CC3 expression (Fig. 3). Since this antibody was inadequate for accurate cell body counting, total GFAP antibody fluorescence was quantified in several brain regions at P7 and these regions did not exhibit any apparent microscopic differences in astrocyte morphology (Fig. 3A-H) nor any significant differences in mean GFAP fluorescence intensity (Fig. 3I-L). Regions profiled included the retrosplenial agranular (RSA) region of the neocortex ( $p=0.4686$ , unpaired T-test, Fig. 3I), white matter ( $p=0.6277$ , unpaired T-test, Fig. 3L), and the CA1 ( $p=0.7385$ , unpaired T-test, Fig. 3K) and dentate gyrus ( $p=0.2139$ , unpaired T-test, Fig. 3L) of the hippocampus.

Similarly, microglial activation was profiled using antibodies to IBA-1 and CD68 (Fig. 4A-F). IBA-1 is a microglial marker and CD68 is expressed by microglia that are actively phagocytic (Witcher et al., 2015). There were no significant differences in IBA-1+ CD68+ cell densities between genotypes in the motor cortex ( $p=0.3889$ , unpaired T-test) or hippocampus ( $p=0.3260$ , Mann Whitney test) (Fig. 4G-H), nor any significant difference in IBA-1+ cell densities in the motor cortex ( $p=0.2093$ , unpaired T-test) or hippocampus ( $p=0.3889$ , unpaired T-test) (Fig. 4I-



J), indicating no changes in the level of microglial activation and invasion between genotypes, respectively. This lack of evidence of cellular inflammatory activity was supported by cortical mRNA expression profiling studies which did not reveal any significant differences in cytokine mRNA levels according to Nanostring Pathway Scoring on a total of 50 cytokines and cytokine-related genes ( $p=0.9307$ , Mann Whitney test, Fig. 5A, see Table S1 for gene list). In addition, qPCR validation of canonical neuroinflammatory cytokines (*Il1b*, *Il6*, and *Tnf*) did not indicate changes in cortical mRNA expression between P7  $Arx^{(GCG)10+7}$  and WT littermates (Fig. 5B-D) (*Il1b*,  $p=0.0652$ , Mann Whitney test; *Il6*,  $p=0.1321$ , Mann Whitney test; *Tnf*,  $p=0.1513$ , Mann Whitney test). Taken together, these findings indicate that the transient increase in neonatal cortical apoptosis in  $Arx^{(GCG)10+7}$  mutants at P7 is unlikely to be driven by an inflammatory process.

### **Early hormone therapies modulate interneuron density but not apoptosis in neonatal $Arx^{(GCG)10+7}$ mice.**

We next sought to determine whether pretreatment with 17 $\beta$ -Estradiol (E2), a multifaceted, estrogen receptor-dependent (and independent) neuroactive hormone (Azcoitia et al., 2019), might ameliorate the elevated CC3-mediated cortical apoptosis in  $Arx^{(GCG)10+7}$ , thus providing a mechanism for its early protective effect. Previously, we showed that E2 treatment reduces neonatal spasms and aberrant electrographic phenotypes including seizures and interictal discharge in adults when administered daily during the first week of life, but not later in adult  $Arx^{(GCG)10+7}$  mutants (Olivetti et al., 2014). Thus, the increase we observed in CC3 expression at P7 overlaps with the effective time for E2 treatment (P3-10). We treated mutant cohorts with E2 (40 $\mu$ g/kg/day) or vehicle (sesame oil) daily from P3 to P7 and evaluated cortical cell death at P7. E2 had no effect on cortical CC3+ counts ( $p=0.6548$ ; Unpaired T Test, Fig. 6A). In addition, we quantified Arx+ cell density in two cortical areas, the retrosplenial agranular region (RSA) and motor cortex following treatment. E2 had no effect on P7 Arx+ cell density in

the RSA cortex ( $p=0.2804$ , Unpaired T Test, Fig. 6B); however, E2 significantly increased Arx+ cell density in the motor cortex ( $p=0.0004$ , Unpaired T Test, Fig. 6C). E2 rescued Arx+ densities similar to WT levels in the motor cortex with a mean of  $409.2\pm 59.60$  Arx+ cells/mm<sup>2</sup> in WT (Fig. 1K) and  $493.2\pm 38.8$  Arx+ cells/mm<sup>2</sup> in E2-treated *Arx*<sup>(GCG)10+7</sup> (Fig. 6C). We also determined that P3-7 E2 treatment did not affect the number of Arx+ cells undergoing apoptosis at P7, as the number of Arx+ cells that expressed the CC3 apoptotic marker was similar between hormone and vehicle treated controls ( $p=0.8177$ , Unpaired t test, Fig. 6D), suggesting that the mechanism by which E2 increases Arx+ cell density is not by improving their survival. Similarly, we examined the effect of ACTH(1-24), a widely-used clinical therapy for IS (Kelley and Knupp, 2018; Song et al., 2017). We first tested the efficacy of early ACTH(1-24) treatment on aberrant phenotypes in *Arx*<sup>(GCG)10+7</sup> and found that ACTH(1-24) was ineffective in this model at two different doses (Fig. S2 A-E). Interestingly, ACTH(1-24)-treated mutants exhibited an elevated number of cortical CC3+ cells compared to vehicle control (Fig. S2F), yet similar to E2 treatment, ACTH(1-24) increased Arx+ cell density in the motor cortex but not the RSA (Fig. S2 G-H).

## Discussion

Deletions or truncating mutations in *ARX* result in major human cortical malformations and early lethality in *Arx* mouse models (Kato et al., 2004; Kitamura et al., 2002). A more subtle disturbance of this transcription factor in both human and mouse models leads to serious neurodevelopmental disease with only microscopic evidence of interneuron migration failure (Kitamura et al., 2009; Lee et al., 2017; Price et al., 2009), which offers an opportunity to isolate early pathogenic mechanisms before misleading terminal stages. Studies of *Arx* have focused on identifying its transcriptional targets and their role in embryonic brain development and adult pathophysiology; however, less is known about their impact upon programmed cell death during the early neonatal period of cortical maturation, a point when detrimental phenotypes such as

infantile spasms appear and clinical intervention is crucial. In this study, we investigated how the  $Arx^{(GCG)10+7}$  expansion mutation, a humanized genetic model of ISSX with impaired cellular migration, disrupts programmed cell death and whether established treatments have an effect on this neonatal cellular endophenotype. We found an enhancement of extrinsic apoptosis in the early postnatal brain that may alter the balance of network excitability, thereby contributing to epilepsy and other developmental comorbidities. However, neither early E2 treatment, which is effective in preventing seizures in this model, nor ACTH, a clinically effective treatment in some cases of IS, mitigated elevated cell death, indicating these treatments have a complex relationship with the neurodevelopmental phenotype in  $Arx^{(GCG)10+7}$ .

### **Identity of non-cell autonomous apoptosis in $Arx^{(GCG)10+7}$**

In WT prenatal brain, *Arx* is expressed in immature interneurons of the subpallial ganglionic eminences (Colombo et al., 2004; Poirier et al., 2004). As these interneurons migrate to their correct position in the cortical plate, they predominantly retain an *Arx*+ identity (Colombo et al., 2004; Poirier et al., 2004). *Ex vivo* experiments have shown that poly-alanine mutations in *ARX* lead to nuclear inclusions and result in increased cell death in mutant-expressing cells, however, these results were obtained in heterologous expression systems that overexpressed *ARX*, and have not been corroborated *in vivo* (Nasrallah et al., 2004; Price et al., 2009). During the first two postnatal weeks, GABAergic interneurons normally undergo a wave of apoptosis, reducing their population density by about 20-30%, with a peak in apoptosis at P7 (Priya et al., 2018; Southwell et al., 2012). Unexpectedly however, we found that excess cell death in  $Arx^{(GCG)10+7}$  was non-cell autonomous, since mutant *Arx*+ neurons did not contribute to the increase in CC3+ cells. One possible explanation is that this cellular phenotype reflects a vulnerable subpopulation of cortical precursor neurons that had once expressed  $Arx^{(GCG)10+7}$  prior to the postnatal window we examined. In the embryonic brain, *Arx* is expressed in neural progenitor cells of the pallial subventricular zone, but with postnatal development and exit from

the subventricular niche, these neurons lose *Arx* expression (Colombo et al., 2004; Friocourt et al., 2008). However, we did not find reduced survival of NeuN+ neurons that did not express *Arx*. A study by Beguin and colleagues found no alterations in pyramidal neuron migration and cortical layering in a similar PA1 expansion model or in pyramidal progenitors electroporated with this PA1 expansion mutation, however, they did find aberrant excitatory activity and altered dendritic and synaptic arborization of hippocampal pyramidal neurons, demonstrating a non-cell autonomous structural defect (Beguin et al., 2013). Although we were unable to definitively identify this population, we speculated that progenitors that had once expressed the  $Arx^{(GCG)10+7}$  may enter aberrant transcriptional programs that later lead to premature cellular demise. To corroborate this, we profiled P7 cortical mRNA expression using Nanostring and the nCounter® mouse Neuropathology panel, but were unable to validate mRNA expression alterations identified in Nanostring analysis using qPCR, with the exception of *Npy* (Table S2, Fig. S3). Further studies are required to specifically determine if other cortical cells involved in cellular migration that undergo partial or complete apoptosis during postnatal cortical development, such as Cajal-Retzius cells or glia (Wong and Marin, 2019), exhibit altered apoptosis in  $Arx^{(GCG)10+7}$  mutants. However, it is unlikely that Cajal-Retzius cells are preferentially affected as they typically reside in Layer 1 and we found no preferential layer occupied by CC3+ cells in  $Arx^{(GCG)10+7}$  mutants (Fig. S1).

### **Etiology of elevated apoptosis and potential impact on neonatal cortical development**

Acute and chronic inflammation in the immature brain is associated with inappropriate apoptosis and is a risk factor for IS development (Hagberg et al., 2015; Pardo et al., 2014; Shandra et al., 2017). Moreover, the anti-inflammatory peptide hormone ACTH constitutes the frontline medical treatment for IS (Hani and Mikati, 2016). Therefore, we speculated that an innate immune response in the postnatal  $Arx^{(GCG)10+7}$  brain might contribute to increased apoptosis. However, we found no apparent cellular or molecular evidence of inflammation.

Interestingly, ACTH(1-24) had no therapeutic effect in  $Arx^{(GCG)10+7}$  mutant mice (Fig. S2A-F). Although the therapeutic action of ACTH may be due to decreasing inflammation in human cases of IS, our data suggest that  $Arx^{(GCG)10+7}$  may be a model of the many clinical cases of ACTH-unresponsive IS. Neither E2 nor ACTH(1-24) targeted exaggerated apoptosis, yet E2 had a therapeutic effect on spasms and electrographic phenotypes in these mice (Olivetti et al., 2014). Thus, the relevance of increased early apoptosis to the epilepsy phenotype, as well as other neurodevelopmental comorbidities in the ISSX syndrome remains uncertain.

### **Mechanisms of hormonal therapies in ISSX1 and interneuronopathy models**

Interestingly, E2 and ACTH(1-24) increased Arx+ density in the motor cortex to a similar degree in  $Arx^{(GCG)10+7}$ , and this effect was regional, since we saw no change of Arx+ cell density in the RSA cortex. However, the disparity in clinical efficacy between E2 and ACTH(1-24) suggests that increasing Arx+ cells in only some cortical regions is not sufficient to modify disease progression, and other mechanisms driving epileptogenesis, such as disinhibition from mislocalized interneurons, may prevail. The increase in Arx+ density could be due to different mechanisms, including upregulated *Arx* expression within an undetected subpopulation of interneurons, or enhanced migration of Arx+ cells in the neocortex. Data from *Arx* mouse models suggest that polyalanine expansions in PA1 cause both a decrease in protein levels and affect the ability of *Arx*-expressing interneurons to migrate to the cortex (Lee et al., 2017; Lee et al., 2014; Olivetti and Noebels, 2012). It remains unclear whether this decrease is due to loss of *Arx* interneurons or reduction of *Arx* protein by other mechanisms. Previous data from our lab showed that neonatal E2 treatment does not affect brain expression of *Arx* mRNA (Olivetti et al., 2014). As E2 treatment has implications for potential clinical trials of ACTH-resistant IS, future work should also determine the effects of upregulating mutant forms of *Arx* such as  $Arx^{(GCG)10+7}$  and whether E2 simply upregulates gene expression or improves outcomes of  $Arx^{(GCG)10+7}$ -expressing cells.

Recent data also suggests that E2 may have neuroprotective effects in interneurons and interneuronopathy models. We previously reported that E2 can increase the density of Parvalbumin and Neuropeptide Y interneuron subtypes in the somatosensory cortex of *Arx<sup>(GCG)10+7</sup>* (Olivetti et al., 2014). E2 has also been shown to have neuroprotective effects in interneuronopathy models and across species. E2 increases GAD-67+ GABAergic interneurons in a rat model of IS (Chachua et al., 2016), and elevates PV expression in a *Pvalb* KO model of autism with rescue of aberrant phenotypes (Filice et al., 2018). Additionally, premature rabbit neonates treated with E2 exhibited increased cortical Arx and PV cell densities, upregulation of *Arx* mRNA expression, and increased expression of the *Arx* target *Shox2* (Panda et al., 2018). These studies, along with our own, indicate that early treatment with E2 may have a conserved role in elevating Arx+ cells and other GABAergic subtypes. However, to our knowledge, ACTH(1-24) has not yet been shown to have this effect on GABAergic subtypes. Together, these data suggest there may be shared mechanisms of action between E2 and ACTH and that both hormones may be candidate therapies for interneuronopathies characterized by loss or ectopia of GABAergic interneuron subtypes.

In summary, we have shown a transient increase in developmental brain apoptosis in *Arx<sup>(GCG)10+7</sup>* as indicated by increases in CC3 expression and TUNEL assay in P7 neocortex. Although the cellular identity of this vulnerable population is unknown, we found that augmented apoptosis in Arx+ mutant interneurons is not the cause, indicating enhanced cell death in *Arx<sup>(GCG)10+7</sup>* neonates is non-cell autonomous. We have also shown that elevated apoptosis is not a result of activation of inflammatory pathways, as we did not find any evidence of astroglial activation, microglial activation or invasion, or elevated cytokine expression in *Arx<sup>(GCG)10+7</sup>* neonates. In addition, ACTH(1-24), a known anti-inflammatory drug and front-line therapy in IS, showed no convincing efficacy in reducing spasms and seizures in *Arx<sup>(GCG)10+7</sup>* mutant mice. However, both ACTH(1-24) and E2 increased Arx+ densities in the neocortex, suggesting these

hormones may act on similar pathways in  $Arx^{(GCG)10+7}$ . We conclude that the efficacy of early hormone stimulation in this ISSX1 model is likely due to direct neuroprotective actions rather than anti-inflammatory activity in immature brain.

## **Materials and Methods**

### $Arx^{(GCG)10+7}$ mice

$Arx^{(GCG)10+7}$  mice (*Mus musculus*) were developed previously and described in Price et al., 2009 and maintained on an inbred C57BL/6/129S5/SvEvBrd background (Olivetti et al., 2014; Price et al., 2009). As *Arx* gene is located on the X-chromosome, only hemizygous  $Arx^{(GCG)10+7}$  male mice and WT male littermates were used in this study. Mice were housed in groups of 2-5 animals in climate controlled conditions with 12hour light/dark cycles and allowed access to water and food ad libitum. All animal studies conformed to the National Institutes of Health (NIH) Guide for the Care and Use of Laboratory Animals and were approved by the Baylor College of Medicine Institutional Animal Care and Use Committee.

### E2 Treatment

17 $\beta$ -Estradiol (E2, Sigma-Aldrich, E2257) was administered to neonatal mice daily from P3 to P7. E2 administration is described in Olivetti et al., 2014. 40 $\mu$ g/kg/day E2 in sterile sesame oil (Sigma-Aldrich, S3547) or sterile sesame oil as control was administered by daily subcutaneous injection at the same time each day. For treatment at P7, animals were euthanized 2 hours after treatment and brains were collected. Litters were treated separately with drug or vehicle and non-littermate controls were used due to drug crossover from mothers to other pups in the litter or skin-to-skin contact between pups.

### Immunohistochemistry and TUNEL assay

Neonatal pups were decapitated at the specified age and brain tissue was fixed overnight at 4°C in 4% paraformaldehyde and cryoprotected in 30% sucrose. Immunohistochemistry (IHC) was performed on sagittal 20µm sections taken starting 200µm from the brain midline. For IHC Cleaved Caspase-3 (CC3)/Arx studies, six non-consecutive 20µm sections were used. All other assays utilized 3 or 4 non-consecutive 20µm sections taken starting 200µm from the brain midline: IBA1/CD68 IHC utilized 3 slices, GFAP IHC utilized 4 slices, and NeuN utilized 3 slices. IHC was performed as described in Olivetti, et al., 2014(Olivetti et al., 2014). Slices were blocked using 10% bovine serum albumin in 0.1% Triton-X100, incubated with primary antibody overnight at room temperature, washed then incubated in fluorophore-conjugated secondary antibody for 1 hour. Negative controls were performed by omitting primary antibody. The primary antibodies and concentrations used to perform these experiments include anti-Arx (1:500, UC Davis/NIH Neuromab clone N411/51), anti-CC3 (1:1000, Cell Signaling Technology Cat. #9661), anti-NeuN (1:1000, EMD Millipore #ABN78), anti-GFAP (1:500, UC Davis/NIH Neuromab clone N206A/8), anti-IBA-1 (1:1000, Wako #019-19741), and anti-CD68 (1:250, Biorad MCA1957). Secondary antibodies include Alexa-Fluor™ 594 anti-mouse IgG1 (1:1000, Invitrogen A21125), Alexa-Fluor™ 488 anti-Rabbit IgG (1:1000, Invitrogen A11070), Alexa-Fluor™ 594 anti-Rabbit (1:1000, Invitrogen A11072), and Alexa-Fluor™ 594 anti-Mouse IgG2a (1:1000, Invitrogen A21135). Slides were mounted with VECTASHIELD® Hardset™ Antifade Mounting Medium with DAPI (H-1500). TUNEL assay was performed on fixed 20µm sections using the In Situ Cell death detection kit (Roche, cat. 11-684-795-910). 4 non-consecutive 20 µm slices starting 200µm from the brain midline were used for TUNEL assay. Positive controls for TUNEL assay were performed by incubation with 50U/mL DNase I (Zymo E1010) for 10 minutes. Negative controls were performed by omitting terminal transferase enzyme.



### Microscopy and image analysis

All microscopy was performed using a Nikon inverted epifluorescent microscope with an Andor Zyla 4.2 PLUS camera. Nikon NIS Elements Pro software was used to analyze images. All image analysis was done by an observer blinded to genotype and/or treatment using numerical identifiers. If one or more slices exhibited significant damage, the sample was excluded from analysis. For most experiments, cells were individually counted using the NIS Elements Taxonomy tool. For CC3/Arx IHC, total cells across the entire neocortical plate were quantified. For Arx density analysis, a section 400 $\mu$ m in width and the depth of the cortical plate were taken from the retrosplenial agranular cortex (RSA) and the motor cortex of the neocortex. For NeuN analysis, two regions located in the RSA and motor cortex of the neocortex were used. Quantitative analysis was done with automated cell counting on FIJI (ImageJ version 1.52, JAVA version 1.8.0) by converting images to binary and using the Measure Particles plugin. For GFAP quantification, integrated density of selected regions (RSA cortex, White matter, Dentate Gyrus, and CA1 of hippocampus) was quantified using FIJI. Background integrated density multiplied by the area of section was subtracted from the integrated density of the area of interest to obtain a value for each slice. 4 slices were averaged to obtain a mean corrected total fluorescence for each sample. For IBA-1/CD68 IHC, densities of IBA-1+ and IBA-1/CD68+ co-labeled cells were quantified from RSA (not shown) cortex, motor cortex, and hippocampus. For all assays, counts and densities were averaged between 6, 4, or 3 slices (see previous methods section) to obtain an average for one 20 $\mu$ m slice. For CC3 bin analysis and quantification of cortical depth and area, Image J (FIJI version 1.52p) was used to generate 6 equal bins across the neocortical plate. Values from each bin were averaged between four non-consecutive parasagittal slices between 200 and 400 $\mu$ m from the brain midline to obtain one bin value per sample. Using Image J (FIJI version 1.52p), the same four parasagittal slices were also used to measure sagittal area and cortical depth in the retrosplenial agranular region (RSA) and motor cortex (see Fig. S1). Four slices were averaged to obtain one area or depth value per sample.

### mRNA expression profiling using Nanostring and qPCR

Nanostring mRNA expression profiling was conducted using nCounter® mouse Neuropathology Plus Panel which contains probe sets to query the expression of 800 unique mRNA's (<https://www.nanostring.com/products/gene-expression-panels/ncounter-neuropathology-panels>). Table S3 contains a list of 29 additional probes that were designed to profile mRNA from Arx targets, and other factors found to be dysregulated in the  $Arx^{(GCG)7/Y}$  model (Kitamura et al., 2009; Mattiske et al., 2016). RNA was extracted from P7 cortical (neocortex and hippocampus) from the left hemisphere using Qiagen RNeasy Plus kit with gDNA eliminator column (Cat. 74134). Cortices from  $Arx^{(GCG)10+7}$  and WT male littermates were used (6 WT and 6  $Arx^{(GCG)10+7}$ ). The BCM Genome and RNA Profiling Core performed the assay on an nCounter MAX 5s and RNA quality control using a NanoDrop One and Agilent 2100 Bioanalyzer. Only RNA samples that met strict quality and purity criteria (RIN >8 and no anomalies in Bioanalyzer spectrograph) were submitted for analysis. Output data was analyzed, and quality controlled using Nanostring NSolver software (version 4.0.70). Differential expression between genotypes was conducted using a linear regression model in the Advanced Analysis software (version 2.0.115) in nSolver and corrected for batch and litter effects (see <https://www.nanostring.com/products/analysis-software/advanced-analysis> for more information). mRNAs that were below the detection limit of nCounter MAX 5s were excluded from analysis. Pathway scoring analysis for cytokines (see Table S1 for list of genes) was also performed in Advanced Analysis software (version 2.0.115) in nSolver which uses the first principal component of expression data to determine pathway-level information from a group of genes (Tomfohr et al., 2005).

### Quantitative PCR of mRNA expression

Quantitative PCR (qPCR) was used to validate changes shown in Nanostring analyses for and cytokine mRNA expression. qPCR was performed using 20ng RNA from separate biological replicate P7 cortices. RNA was extracted and quality was assessed as described above. Real time qPCR assays were performed on an AppliedBiosystems Quantstudio 3 using TaqMan Fast Advanced Master Mix (Thermofisher, cat. 4444963) and TaqMan assays (Thermofisher, see Table S4). Data was analyzed using AppliedBiosystems Quantstudio Design & Analysis software. Table S4 contains the list of TaqMan probes used for qPCR. qPCR data was analyzed using the  $2^{-\Delta\Delta CT}$  method.

### ACTH 1-24 treatment:

Adrenocorticotrophic hormone fragment 1-24 (ACTH(1-24), Sigma-Aldrich, A0298) was administered to neonatal mice daily from P3 to P7 or P10. Mice treated from P3-7 were used for immunohistochemical studies and those treated from P3-10 underwent spasms behavioral monitoring or EEG surgery and video-EEG monitoring. As handling pups and time away from mother during spasms monitoring could influence pup development, separate cohorts were treated for EEG experiments. 2IU/kg/day or 4IU/kg/day ACTH(1-24) in sterile saline or sterile saline as control was administered by daily subcutaneous injection at the same time each day. ACTH(1-24) injections were administered after spasms recordings at ages P7-10. For immunohistochemical studies, spasms, and EEG studies, litters were treated separately with drug or vehicle and non-littermate controls were used due to potential for drug crossover from mothers to other pups in the litter or skin-to-skin contact between pups.

### Behavioral Spasms Monitoring and Quantification

Spasms were monitored similarly as described in Olivetti et al., 2014. Pups treated with ACTH(1-24) from P3-10 were placed in a warmed, compartmentalized container. Each chamber of the container contained a number which allowed the experimenter to be blinded to treatment.

A single pup was placed in a chamber measuring 5.5 × 7 cm and allowed to habituate for 10 minutes. Following habituation, pups were recorded with a HD digital video recorder for 50 minutes. Spasms were monitored daily from P7 to P11 in the light cycle between 5 and 7pm (when pups exhibited wakefulness). ACTH(1-24) subcutaneous injections (P7-10) were done after spasms monitoring. Spasm behavioral movements were quantified by a blinded experimenter as previously described in Olivetti et al., 2014. Movements consisting of major truncal flexion, abdominal contractions, and bowing or axial twisting of the body that resulted in pups lying supine were quantified.

#### Video electroencephalography

Video electroencephalography (VEEG) was conducted as previously described in Olivetti et al., 2014. Silver wires measuring 2mm in diameter were implanted in the epidural space to monitor cortical EEG while simultaneously recording video (VEEG). Mice treated with ACTH(1-24) daily from P3-P10 were anesthetized using isoflurane and surgically implanted at P35. VEEG was recorded weekly in 24-hour blocks from P45-72 in freely moving mice. Total recording time was an average of 89 hours per mouse, with at least 72 hours of total recording time. Electrographic seizures were quantified by a blinded experimenter as previously described in Olivetti et al., 2014 and seizure frequency was averaged over the total recording time for each mouse. Interictal spikes were quantified from EEG by a blinded experimenter from 4 x 1 hour intervals on different recording days between 3:00- 5:00pm. To obtain an average interictal spike frequency, counts from the 4 hours were averaged.

## Statistical Methods

All statistical analyses were done using GraphPad Prism 8 (version 8.1.1) software. For all analyses, N's represent individual biological replicates. Outliers were pre-defined as having means greater than 3 standard deviations from the group mean and were excluded from analyses. Data exclusion of outliers only applied to immunohistochemical analyses. To verify that studies had sufficient sample sizes to detect statistical differences between means, power analyses were conducted with a power of 80% for all analyses. If studies were deemed to be underpowered based on power analyses, additional cohort(s) were added to increase N. Prior to applying all parametric statistical tests that assume Gaussian distribution, the Shapiro-Wilk normality test was conducted to statistically determine if data distributed on a normal curve. If data failed this normality test, the appropriate non-parametric statistical analyses were used. Unless otherwise noted, all graphs are displayed as the genotype mean  $\pm$  SEM. For analyses that include multiple comparisons, appropriate post-hoc analyses were used that incorporate P-value corrections for multiple hypotheses testing. Statistical analyses and post-hoc analyses used in each assay are described in figure legends.

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## **Competing interests**

No competing interests declared.

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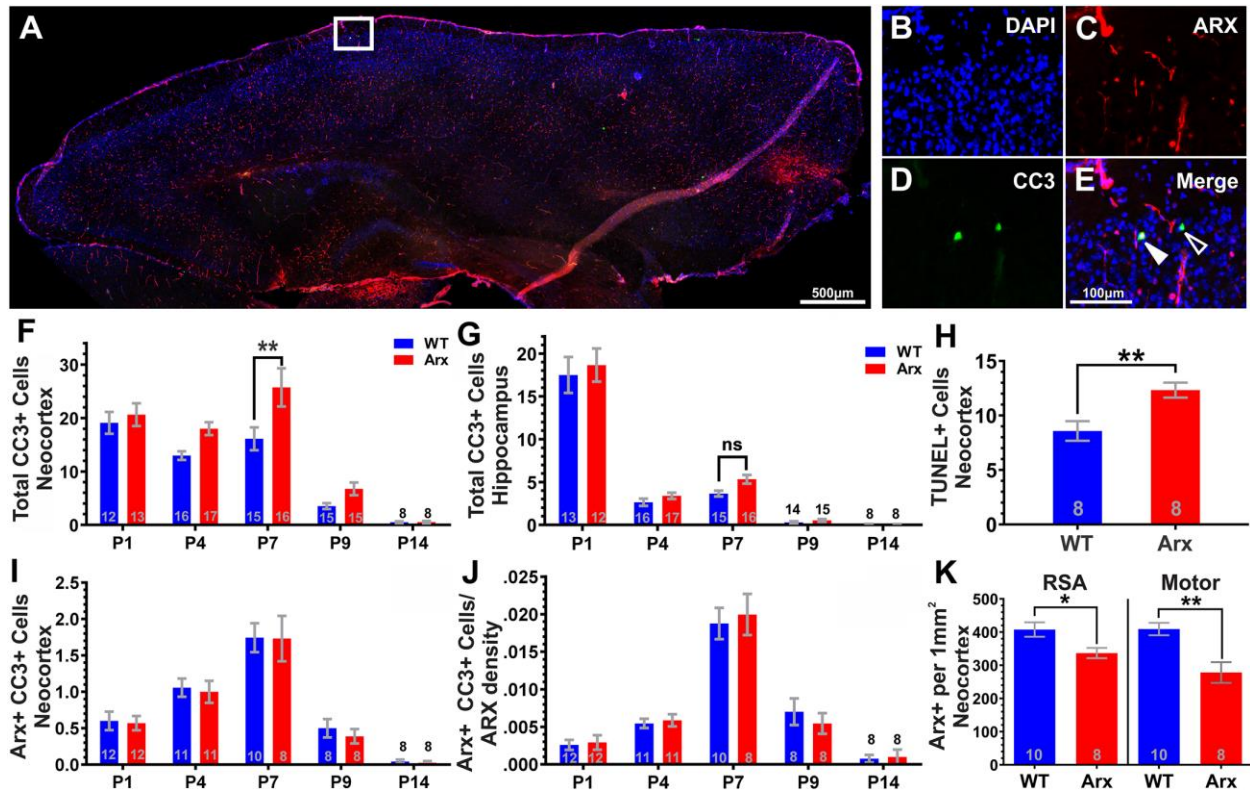
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## Figures



### Fig. 1. *Arx*<sup>(GCG)10+7</sup> expansion mutants exhibit age-dependent increase in non-cell

**autonomous apoptosis.** (A-E) Representative images of a parasagittal cortical section of P7

*Arx*<sup>(GCG)10+7</sup> showing CC3-immunoreactive (CC3+) (green) and Arx-immunoreactive (Arx+) (red)

cells in the neocortex. (B-E) Enlarged image of white box in A showing (B) DAPI, (C) Arx, (D)

CC3, and (E) merged immunostaining. (E) Arrowheads show CC3+ cells and closed arrowhead

shows CC3+ cells with Arx+ nuclei. (F-G) Histograms comparing mean CC3+ cells at P1, 4, 7,

9, and 14 from cortices of WT and *Arx*<sup>(GCG)10+7</sup> littermates (N=8-15 WT, N=8-16 mutant) in (F)

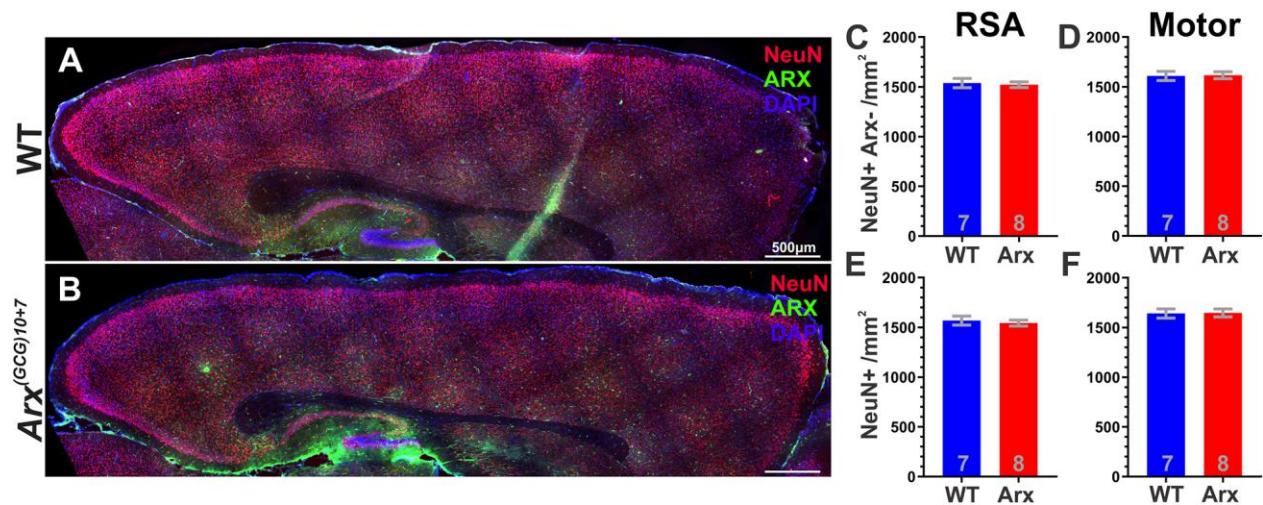
neocortex and (G) hippocampus. (F) In neocortex, Two-Way ANOVA yields an effect of

genotype (F(1,119)=5.338, p=0.0025) (G) In hippocampus, Two-Way ANOVA yields no effect of

genotype (F(1,72)=0.9080, P=0.2035). (H) Mean FITC+ cells (TUNEL+) in neocortex from

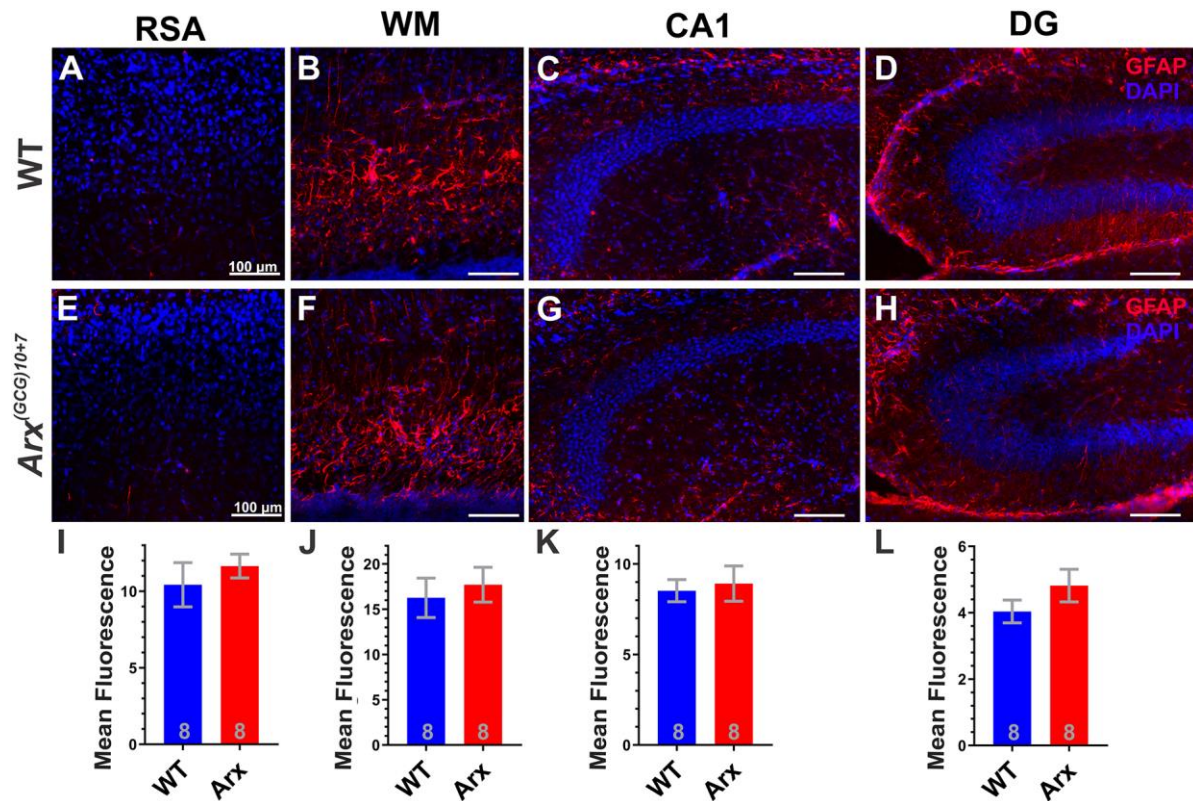
TUNEL assay at P7 (p=0.0051, Unpaired T Test, N=8 WT, 8 Arx). (I) Histograms comparing

mean CC3+ cells that co-express Arx (Arx+ CC3+). Two-Way ANOVA yields no effect of genotype ( $F(1,88)=0.2374$ ,  $p=0.6273$ ) (N=8-12 WT, 8-12 mutant). (J) Histograms comparing mean colabeled (CC3+ Arx+) cells normalized to Arx+ density. Two-Way ANOVA yields no effect of genotype ( $F(1,88)=0.01996$ ,  $p=0.8880$ ). (N=8-12 WT, 8-12 mutant) (K) Mean Arx+ density (Arx+ cells/mm<sup>2</sup>) at P7 in the retrosplenial agranular region (RSA) ( $p=0.0225$ ) and motor cortex ( $p=0.0017$ ) (Unpaired T-test) of *Arx*<sup>(GCG)<sup>10+7</sup></sup> mutants compared to WT. F-G and I-J utilized Two-Way ANOVA with Bonferroni's multiple comparisons test. Scale bar 500µm in (A) and (B-E) scale bar is 100µm with images scaled similarly. Means and SEMs are displayed for all graphs with exact N's displayed on bar graphs.\*P<0.05, \*\*P<0.01



**Fig. 2. *Arx<sup>(GCG)10+7</sup>* expansion mutants do not exhibit loss of Arx- cortical neurons at P14.**

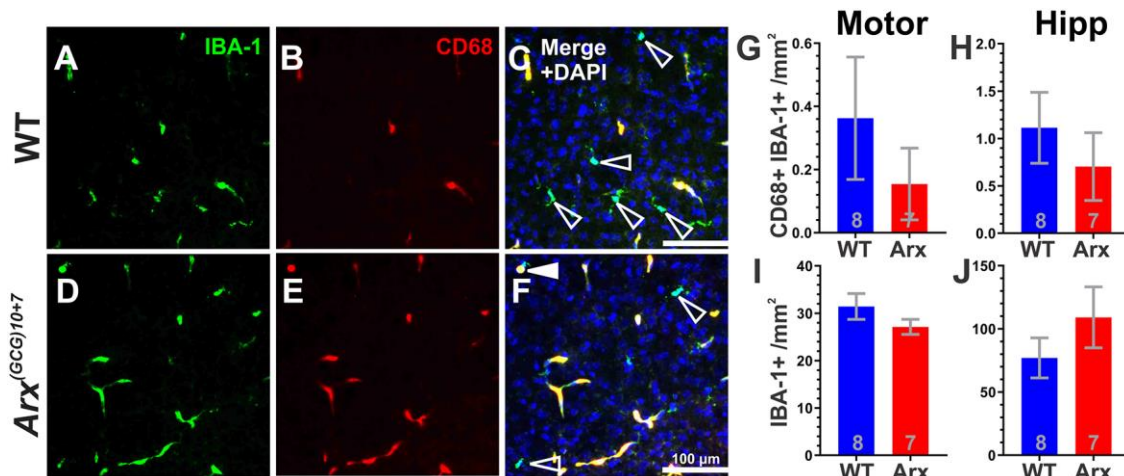
(A-B) Representative images of (A) WT and (B) *Arx<sup>(GCG)10+7</sup>* parasagittal sections showing NeuN and Arx-immunoreactive cells. (C-D) Mean density of NeuN+ cells that do not express Arx (NeuN+ Arx-/mm<sup>2</sup>) in two neocortical regions: (C) retrosplenial agranular region (RSA) ( $p=0.7575$ , Unpaired t test) and (D) motor cortex ( $p=0.8665$ , Mann Whitney test). (E-F) Mean total NeuN density (NeuN+ cells/mm<sup>2</sup>) of two neocortical regions (E) retrosplenial agranular region (RSA) ( $p=0.6511$ , Unpaired t test) and (F) Motor cortex ( $P=0.9551$ , Mann Whitney test). Scale bar is 500μm in A and B. Mean and SEMs are displayed. Exact N's are displayed on graph.



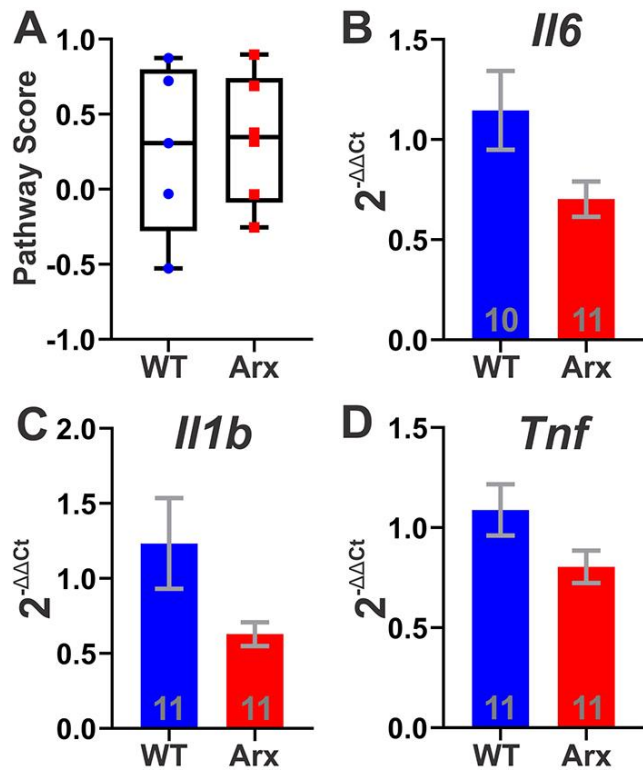
**Fig. 3. *Arx*<sup>(GCG)10+7</sup> expansion mutants do not exhibit an astrocytic response at P7. (A-H)**

Representative images from parasagittal slices showing GFAP immunohistochemistry (red) and DAPI nuclei (blue) from WT (A-D) and *Arx*<sup>(GCG)10+7</sup> (E-H) littermates. Images show each region quantified: retrosplenial agranular region of the neocortex (RSA, A&E), white matter (WM, B&F), CA1 of the hippocampus (C&G), and dentate gyrus of the hippocampus (DG, D&H). (I-L) Mean fluorescence quantified from each region specified and graphs display average values for each genotype in (I) Retrosplenial agranular (RSA) region of the neocortex ( $p=0.4686$ , Unpaired T Test), (J) White matter (WM,  $p=0.6277$ , Unpaired T Test), (K) CA1 of hippocampus (CA1,  $p=0.7385$ , Unpaired T Test), or (L) Dentate gyrus (DG,  $p=0.2139$ , Unpaired T Test).  $N=8$  WT, 8 mutant. Scale bar is  $100\mu\text{m}$  in A-H. Means and SEMs are displayed with N's displayed on bar graphs.

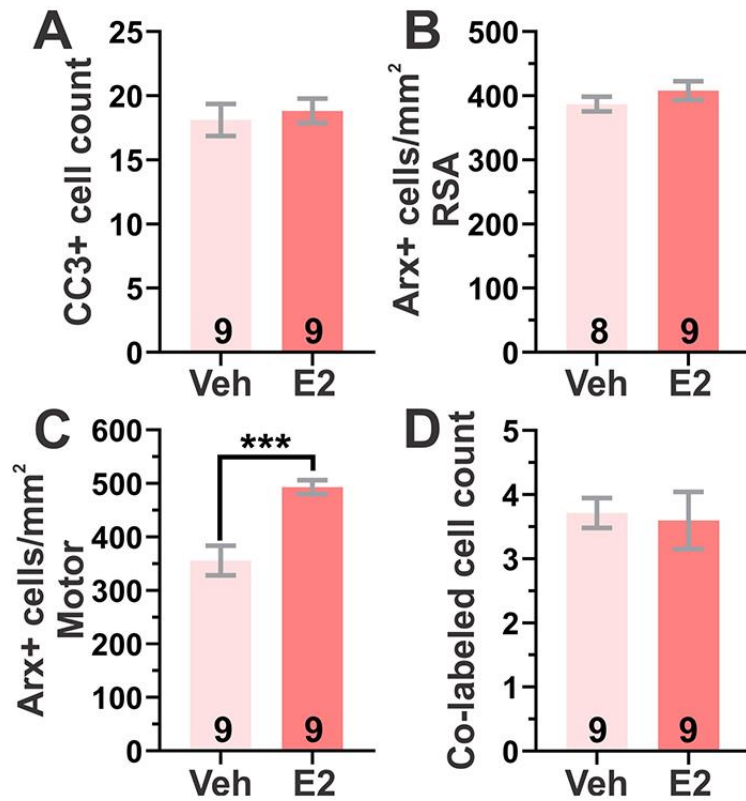




**Fig. 4. *Arx*<sup>(GCG)10+7</sup> expansion mutants do not exhibit microglial invasion or activation in the forebrain at P7. (A-F)** Representative images (A-C) of WT and (D-F) *Arx*<sup>(GCG)10+7</sup> neocortex at P7 showing (A&D) IBA-1 and (B&E) CD68 immunoreactivity, and (C&F) merged image plus DAPI. Open arrows indicate IBA-1+ cells and closed arrows indicate IBA-1+ cells with CD68+ nuclei. **(G-H)** Mean IBA-1+ cells that are CD68 immunoreactive per mm<sup>2</sup> in the (G) motor cortex (Motor) (p=0.5562, Mann Whitney test) and (H) hippocampus (Hipp) (p=0.3260, Mann Whitney test). **(I-J)** Mean IBA-1+ cells per mm<sup>2</sup> in the (I) motor cortex (Motor) (p=0.2093, Unpaired T Test) and (J) hippocampus (Hipp) (p=0.2748, Unpaired T Test). N=8 WT, 7 *Arx*<sup>(GCG)10+7</sup>. A-F are scaled similarly; scale bar is 100μm. Means and SEMs are displayed, exact N's are displayed on graphs.

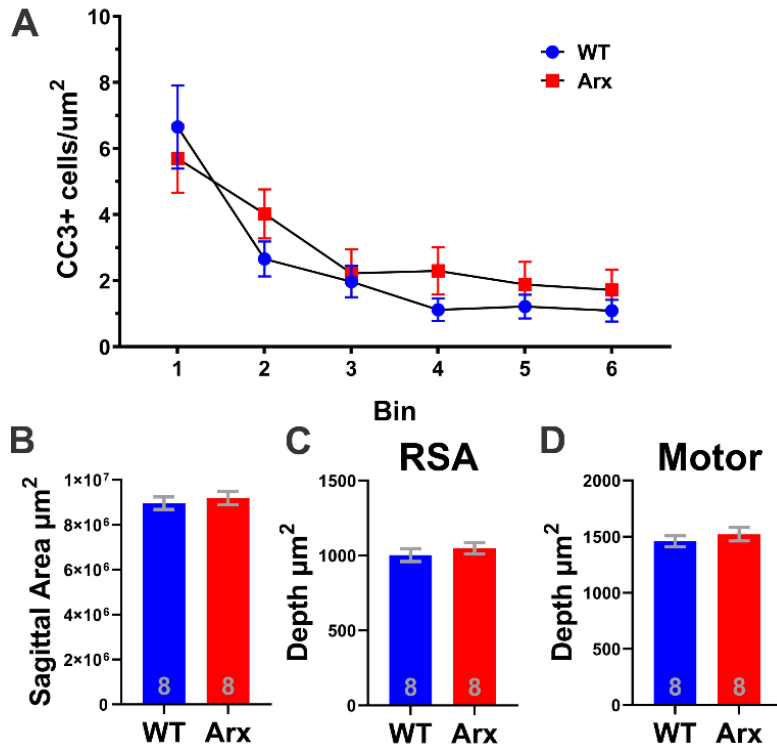


**Fig. 5. *Arx*<sup>(GCG)10+7</sup> mutation does not affect brain cytokine mRNA expression.** (A) Boxplot of cytokine pathway scores from Nanostring mRNA analysis ( $p=0.3095$ , Mann Whitney test;  $N=5$  WT, 6 Arx). (B-D) Average  $2^{-\Delta\Delta Ct}$  for mRNA expression of cytokines of *Il6*, *Il1b*, and *Tnf* at P7 using *Lars* expression for normalization (B) *Il6* ( $p=0.1321$ , Mann Whitney Test), (C) *Il1b* ( $p=0.0652$ , Mann Whitney Test), and (D) *Tnf* ( $p=0.1513$ , Mann Whitney Test). Means and SEMs are displayed, N's are displayed on graph.

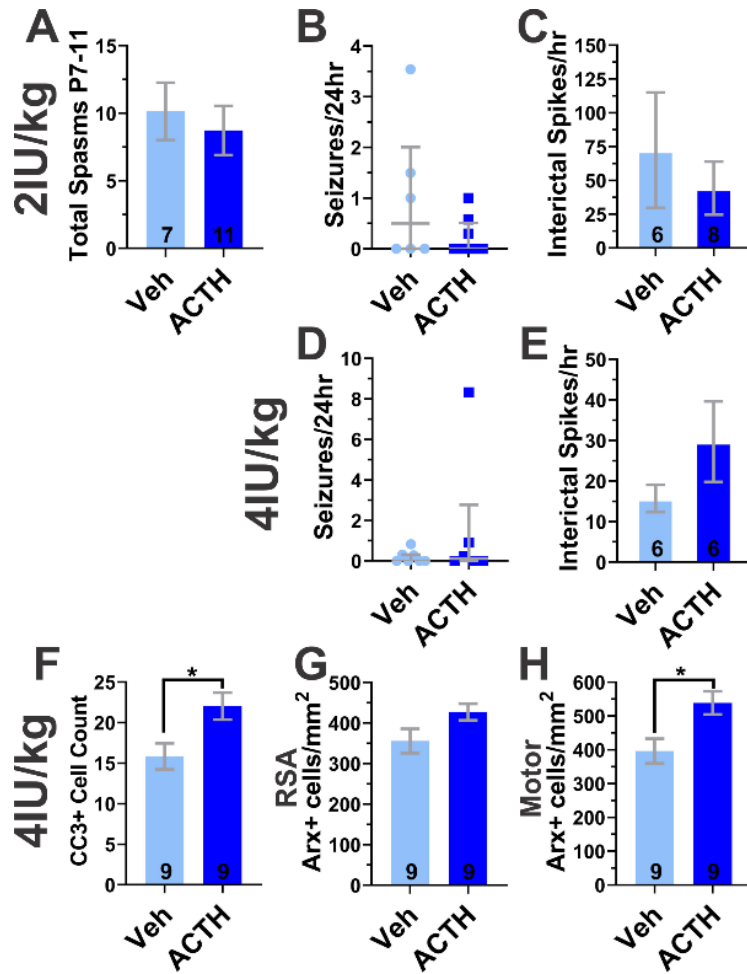


**Fig. 6. E2 treatment modifies neonatal cellular pathology in  $Arx^{(GCG)10+7}$ .** (A-C) Effect of P3-7 40 $\mu$ g/kg/day E2 treatment compared to vehicle (Veh) treatment (sesame oil) on CC3+ cell counts and Arx+ cell density in  $Arx^{(GCG)10+7}$  at P7. (A) Mean CC3+ counts in neocortex with E2 treatment (p=0.6548; Unpaired T Test) (B-C) Mean Arx+ cell density with E2 treatment in (B) retrosplenial agranular (RSA) region (p=0.2804, Unpaired T Test) and (C) motor cortex (p=0.0004, Unpaired T Test). (D) Mean neocortical Arx+ CC3+ colabeled cell counts with E2 treatment (p=0.8177, Unpaired t test). \*\*\*p<0.001. Mean and SEM are displayed. All Ns are displayed on graph.

## Supplemental Information



**Fig. S1. *Arx*<sup>(GCG)10+7</sup> mutants do not exhibit differences in CC3 distribution or neocortical size compared to WT littermates at P7.** (A) Distribution of CC3+ density in Arx mutants and WT littermates in 6 laminar bins (1 most superficial, 6 most deep bin). There was no difference between genotypes ( $F(1,96)=1.681$ ,  $P=0.1979$ ), a significant effect of bin ( $F(5,96)=13.81$ ,  $P<0.0001$ ), but no interaction between bin and genotype ( $F(5,96)=0.7028$ ,  $P=0.6226$ ) (Two Way ANOVA).  $N=10$  WT, 8 Arx. Mean and SEM are displayed. (B) Area ( $\mu\text{m}^2$ ) of WT and *Arx*<sup>(GCG)10+7</sup> mutant sagittal slices ( $P=0.5812$ , Unpaired t test). (C-D) Depth ( $\mu\text{m}$ ) of two different cortical regions showing no difference between genotypes: (C) RSA cortex ( $P=0.4316$ , Unpaired t test) and (D) Motor cortex ( $P=0.4321$ , Unpaired t test) cortex.  $N=8$  WT, 8 Arx. Mean and SEM are displayed.



**Fig. S2. Neonatal ACTH(1-24) treatment modifies cellular pathology but has no effect on neonatal spasms and electrographic phenotypes in adult  $Arx^{(GCG)10+7}$ .** Effect of daily P3-10 ACTH(1-24) treatment at (A-C) 2IU/kg/day and (D-H) 4IU/kg/day compared to saline vehicle (Veh) control injections. (A) Average cumulative P7-11 spasms ( $p=0.6253$ , Unpaired T Test). (B&D) Average daily seizure frequency (seizures/24hr) from weekly P45-72 (average of 89 hours of total recording per mouse) video EEG recordings following neonatal 2IU/kg/day or 4IU/kg/day ACTH(1-24) treatment. (B) 2IU/kg/day ACTH(1-24) treatment ( $p=0.3287$ , Mann Whitney Test) (N=6 Veh, 8 ACTH(1-24)). (D) 4IU/kg/day ACTH(1-24) treatment ( $p=0.8701$ , Mann Whitney Test) (N=6 Veh, 6 ACTH(1-24)). (C&E) Average interictal spike frequency (interictal spikes/hr) following neonatal 2IU/kg/day or 4IU/kg/day ACTH(1-24) treatment. (C)

2IU/kg/day ACTH(1-24) treatment ( $p=0.4908$ , Mann Whitney Test). (E) 4IU/kg/day ACTH(1-24) treatment ( $p=0.3939$ , Mann Whitney Test). **(F-H)** Effect of P3-7 4IU/kg/day ACTH(1-24) treatment compared to vehicle (Veh) treatment (saline) on CC3+ cell counts and Arx+ cell density in Arx<sup>(GCG)10+7</sup> at P7. **(F)** Mean CC3+ counts in neocortex with ACTH(1-24) treatment ( $p=0.0166$ , Unpaired T Test) **(G-H)** Mean Arx+ cell density (Arx+ cells/mm<sup>2</sup>) with ACTH(1-24) treatment in (G) retrosplenial agranular (RSA) region ( $p=0.0673$ , Unpaired T Test) and (H) motor cortex ( $p=0.0117$ , Unpaired T Test). Mean and SEM are displayed. With the exception of B&D, all Ns are displayed on graph.

<i>Ccl12</i>	<i>Cx3cr1</i>	<i>Fasl</i>	<i>Il4ra</i>	<i>Prl</i>
<i>Ccl5</i>	<i>Cxcl10</i>	<i>Flt1</i>	<i>Il6</i>	<i>Tgfb1</i>
<i>Ccr2</i>	<i>Cxcl11</i>	<i>Flt4</i>	<i>Il6ra</i>	<i>Tgfb2</i>
<i>Ccr5</i>	<i>Cxcl12</i>	<i>Hgf</i>	<i>Inhbb</i>	<i>Tnf</i>
<i>Cd40</i>	<i>Cxcl16</i>	<i>Il10</i>	<i>Lif</i>	<i>Tnfrsf10b</i>
<i>Cntf</i>	<i>Cxcr4</i>	<i>Il10ra</i>	<i>Ltbr</i>	<i>Tnfrsf11b</i>
<i>Csf1</i>	<i>Egf</i>	<i>Il13ra1</i>	<i>Ngfr</i>	<i>Tnfrsf12a</i>
<i>Csf1r</i>	<i>Egfr</i>	<i>Il15ra</i>	<i>Osmr</i>	<i>Tnfrsf1a</i>
<i>Csf2rb</i>	<i>Epo</i>	<i>Il1b</i>	<i>Pdgfrb</i>	<i>Tnfrsf1b</i>
<i>Cx3cl1</i>	<i>Fas</i>	<i>Il1r1</i>	<i>Plekho2</i>	<i>Vegfa</i>

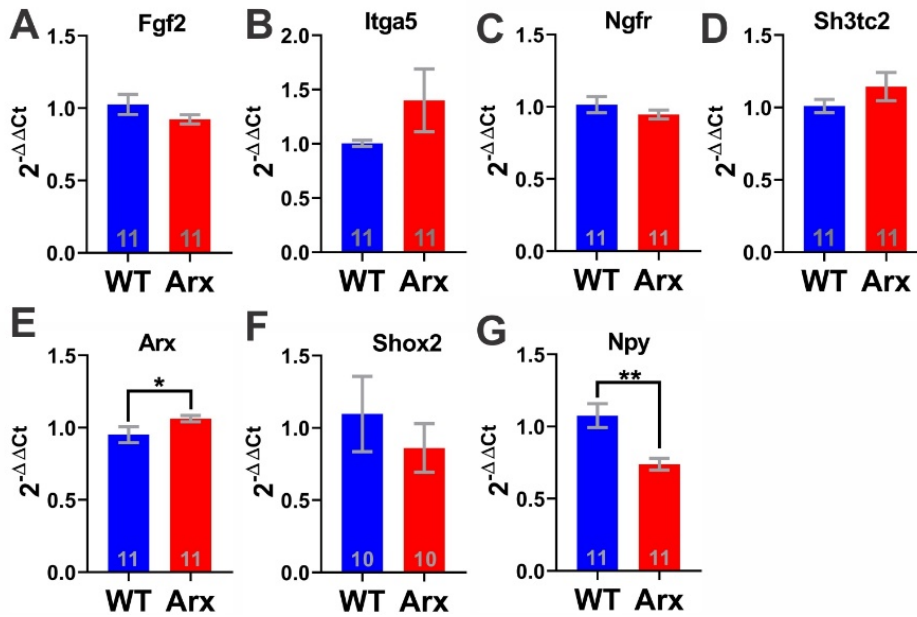
**Table S1.**

List of 50 cytokines and cytokine-related mRNA's from NCounter mouse Neuropathology panel used in Nanostring pathway analysis (See Fig. 5A).

mRNA	Correction Set	Uncorrected P-value	Corrected P-Value	Log2 fold change	Linear fold change
Ngfr-mRNA	Overlapping	0.00138	1	-1.110	0.465
Sh3tc2-mRNA	Overlapping	0.00707	1	-0.628	0.647
Fgf2-mRNA	Litter Correction	0.00454	1	-0.325	0.798
Itga5-mRNA	Overlapping	0.00205	1	-0.319	0.801
Hdac7-mRNA	Overlapping	0.00135	1	-0.173	0.887
Npy-mRNA	Batch Correction	0.00462	1	-0.171	0.888
Sirt1-mRNA	Batch Correction	0.00681	1	-0.162	0.894
Vegfa-mRNA	Overlapping	0.00583	1	-0.141	0.907
Atf4-mRNA	Overlapping	0.00878	1	-0.118	0.921
Htr1a-mRNA	Batch Correction	0.00797	1	-0.115	0.923
Acaa1a-mRNA	Batch Correction	0.00493	1	-0.093	0.937
Pnkd-mRNA	Batch Correction	0.00945	1	-0.094	0.937
Ran-mRNA	Overlapping	0.00594	1	-0.092	0.938
Ap4s1-mRNA	Overlapping	0.00354	1	-0.081	0.945
Ikbkb-mRNA	Batch Correction	0.00959	1	0.080	1.06

**Table S2. Differentially expressed mRNA candidates between WT and  $Arx^{(GCG)10+7}$  using Nanostring.** Data was corrected for batch and litter effects and 15 differentially expressed candidates were chosen based on uncorrected P-value less than 0.01. Highlighted candidates were chosen for validation by qRT-PCR.





**Fig. S3. Validation of Nanostring candidates using qPCR did not reveal mRNA expression changes in *Fgf2*, *Itga5*, *Ngfr*, *Sh3tc2*, and *Shox2* but did reveal changes in *Arx* and *Npy* expression in *Arx*<sup>(GCG)10+7</sup> P7 cortex compared to WT littermates. (A-G) Average expression ( $2^{-\Delta\Delta Ct}$ ) of each mRNA candidate is displayed. (A) *Fgf2* ( $p=0.1330$ , Mann Whitney Test) (B) *Itga5* ( $p=0.4385$ , Mann Whitney Test) (C) *Ngfr* ( $p=0.3316$ , Mann Whitney Test) (D) *Sh3tc2* ( $p=0.3653$ , Mann Whitney Test) (E) *Arx* ( $p=0.0400$ , Mann Whitney Test) (F) *Shox2* ( $p=0.6842$ , Mann Whitney Test) (G) *Npy* ( $p=0.0019$ , Mann Whitney Test). Mean and SEMs are displayed. Ns are displayed on graph.**

Gene Name	Accession ID	Probe Target Sequence
<b>Arx</b>	NM_007492.3	TACTGAAAATAACCCGGGAGGGTTCTCCCAATA TGCTTAGTATTGAAGTTTAAAAATTAAGCCCAAC CTTCTCTTCTCCGGATACCCCACTTAGC
<b>Birc6</b>	NM_007566.3	TCGGCGCTCAGCGCTAAACCAGGTGGACAGGTGA AATGTCAGTATATTTCTGCTGTGGATAAAGTGATAT TTGTGGATGATTACGCCGTGGGCTGTAGGA
<b>Csrnp3</b>	NM_178634.2	AAAGGACTTTGGGTTTGTTCATGCTATTGAAAGCAGT AATGGGGGCTGACTACTCCTTTTGGTTGACCGGTG GGGCTAATCTGGTGGGAATTCTGTGGTAA
<b>Cxcr5</b>	NM_007551.2	ACCGTGCCTTTCTCTTAACCAAGCAGAAAGCTGAAA CCGATCTACTTTAGGTAGCTGTCTGGTTCCAACCTA ACCAGCATTGGGTGAGCCCATGTTACT
<b>Drap1</b>	NM_024176.1	TGCCAAAACCATGACCACGTCCCACCTGAAGCAGT GCATTGAACTCGAGCAGCAGTTTGACTTCTTGA GACTTGGTGGCATCAGTGCCTGACATGCAG
<b>Ebf1</b>	NM_007897.2	CATAGGGGACAATTTCTTTGATGGGTTACAGGTCAT ATTCGGTACCATGCTGGTCTGGAGTGAGTTGATAA CTCCTCATGCCATCCGAGTTCAGACACCT
<b>Endog</b>	NM_007931.1	GGAACAACCTTGAGAGGTACAGCCGCAGCTTGACG CGAATTACAAAATGTCTATGTCTGCACGGGGCC GCTTTTCTGCCAGGACCGAGGCTGATGG
<b>Erbp4</b>	NM_010154.1	TCCTGGTGATCATGGCTTTGACATTTGCTGTCTATG TCAGAAGAAAGAGCATCAAAAAGAAACGTGCTTTG AGGAGATTCTGGAGACAGAGCTGGTAGA
<b>Esr1</b>	NM_007956.4	ACTCGCTACTGTGCCGTGTGCAATGACTATGCCTC TGGCTACCATTATGGGGTCTGGTCTGCGAAGGCT GCAAGGCTTTCTTAAAGAGAAGCATTCAAG
<b>Esr2</b>	NM_010157.3	TGCTTCTTATAACTGTAGCCAGTCCATCCTACCCTT GGAGCATGGTCCCATCTATATCCCTTCTCCTATGT AGAGAGCCGTCACGAATACTCAGCCATG
<b>Ghrh</b>	NM_010285.2	GGATGCAGCGACACGTAGATGCCATCTTCACCACC AACTACAGGAACTCCTGAGCCAGCTGTATGCCCG GAAAGTGATCCAGGACATCATGAACAAGCA
<b>Gnmt</b>	NM_010321.1	GGGTCATTGAAGAAGCCAACTGGTTGACGCTGGAC AAAGATGTGCTTTCAGGAGATGGCTTTGATGCTGT CATCTGCCTTGGGAACAGTTTTGCTCACTT
<b>Hdac4</b>	NM_207225.1	AGACGCTGAGTACTTGGCAGCCTCAGAACGGTGG TTATGCCTATCGCAAATGAGTTTGCCCCAGATGTG GTACTGGTGTTCATCGGGCTTCGATGCTGTG
<b>Hipk2</b>	NM_010433.2	AGGAAGCAAGAAAGTACATTTTCAACTGTTTGGATG ATATGGCCCAGGTGAACATGACAACAGATTTGGAA GGGAGTGACATGTTAGTAGAGAAGGCAGA
<b>Kcnma1</b>	NM_001253361.1	CGCATGTGGTGGGCTTTCTTGGCCTCCTCCATGGT GACTTTCTTCGGGGCCTTTCATCATCTTGCTCTG GCGGACGCTCAAGTACCTGTGGACCGTTT
<b>Kif26b</b>	NM_001161665.1	CATGATCGGAAGGGACGACTCTATGCAGAACCTGG GCATTATTCCATGTGCTATTTCTTGGCTGTTCAAGC TTATCAATGAGCGCAAAGAGAAGACGGGG

<b>Mef2c</b>	NM_001170 537.1	TTCTACTACTAAAGGTATCAATGGAACATGAAGACG AGTATTTAGGCAGAAGCAAACAGGAAACCATCCTT ACAAACATGCTTACCTGCACATCTGTTT
<b>Msx2</b>	NM_013601. 2	CTACCCCTTCCATAGACCTGTGCTCCCCATCCCGC CTGTTGGACTCTATGCCACGCCGGTTGGATATGGC ATGTACCATCTATCCTAAGGAAGACCAGAT
<b>Myt1l</b>	NM_001093 775.1	ATCAGTGACAGAAGTTATGCTGAGGGGATGTCACA GCAGGACAGTAGAAATATGAACTATGTCATGCTAG GGAAGCCCATGAACAATGGACTCATGGAGA
<b>Ndufa1 3</b>	NM_023312. 2	CAGATTCTCCGGGAAAACCTGGAGGAGGAAGCCAT CATCATGAAGGATGTGCCCAACTGGAAGGTGGGC GAGTCTGTGTTCCATACCACACGATGGGTGC
<b>Pcdhg a5</b>	NM_033588. 4	CAGTACTTTCGAGCACCGTCCATATCAGCGTGACC GTTCTTGATGCAAACGATAACGCACCCTTGTTTACC CAAAGCGAATATAGGGTGAGTGTTCCGGA
<b>Pde3a</b>	NM_018779. 1	ATATAGGAAGAAAATGTGGCCGTATTCTGAGCCAG GTATCATACAGACTGTTTGAAGACATGGGGCTCTTT GAAGCCTTTAAATCCCGGTTAGGGAGTT
<b>Perp</b>	NM_022032. 4	CTTCACGATAACCCTGCTGTTAATTACATCTATAAC TGGGCCTATGGCTTCGGATGGGCGGCCACCATCAT CTTGATTGGTTGTTCCCTTCTTCTTCTGCT
<b>Prdx5</b>	NM_012021. 2	AAAGAAGGTGAACTTGGCAGAGCTGTTCAAGGGCA AGAAAGGTGTTTTGTTTGGAGTCCCTGGGGCATT ACACCTGGCTGTTCTAAGACCCACCTGCCT
<b>Samd5</b>	NM_177271. 3	GATGAGATGCGGAAGACTGGAAAGGGGCGTATTTA GGACCTTCTTTCACAAAGGGAAGTGGATGGTGACT CTGCAAACACTTATCAGCTTAACGTTTTCT
<b>Sfn</b>	NM_018754. 2	AATCTGATTTGGTAATCCAAGACGCTCCTGCAATGC AGCCAGCCCTGAACTGCAGGGGGCAGTCTGGAGC CGAAAGGTGCCTTTGCAGGTGGGACCTGCG
<b>Shox2</b>	NM_013665. 1	ATTTTACCCTGGAACAACCTCAACGAGCTGGAGAGG CTTTTCGATGAGACCCACTATCCAGACGCTTTCATG CGCGAGGAATTGAGCCAGCGACTGGGGCT
<b>Twist1</b>	NM_011658. 2	AATGGACAGTCTAGAGACTCTGGAGCTGGATAACT AAAAATAAATCTATATGACAAAGATTTTCATGGAAAT TAGAAGAGCAGAGACCAAATTCACAAGA
<b>Zfp369</b>	NM_178364. 5	GTTACAAGGTTTCATCTGCACAAAATCACCAGATGG GGTCTAGGGCAGGAAGAGCCAGGGACAACAGCAT CTTAACACATGTAAAAATTCACCAGAAAGGC

**Table S3**

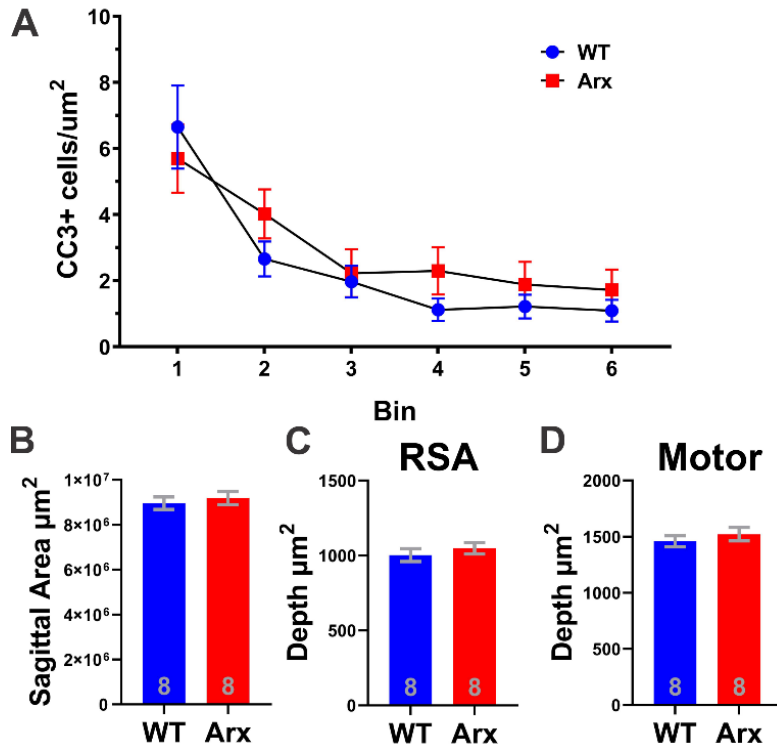
List of 29 additional mRNA probes added to the Nanostring Mouse Neuropathology panel.

Probe	TaqMan™ Assay ID	Use
<i>Lars</i>	Mm00506560_m1	Normalizer/Housekeeping
<i>Tnf</i>	Mm00443258_m1	Target
<i>Il6</i>	Mm00446190_m1	Target
<i>Il1b</i>	Mm00434228_m1	Target
<i>Fgf2</i>	Mm00433287_m1	Target
<i>Itga5</i>	Mm00439797_m1	Target
<i>Ngfr</i>	Mm00446294_m1	Target
<i>Sh3tc2</i>	Mm01261770_m1	Target
<i>Arx</i>	Mm00545903_m1	Target
<i>Shox2</i>	Mm00443183_m1	Target
<i>Npy</i>	Mm00445771_m1	Target

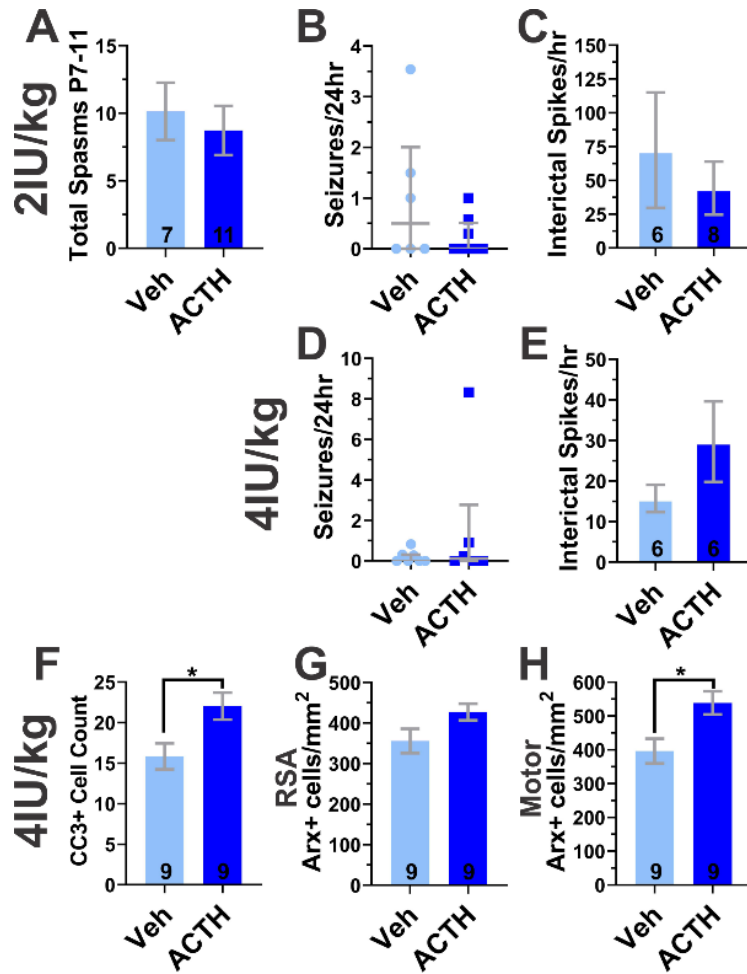
**Table S4**

TaqMan™ Gene Expression Assay ID's used for qPCR validation. *Lars* mRNA expression was used as a normalization/housekeeping gene as it was computationally identified by Nanostring assay as having adequate expression and low variability between samples.

## Supplemental Information

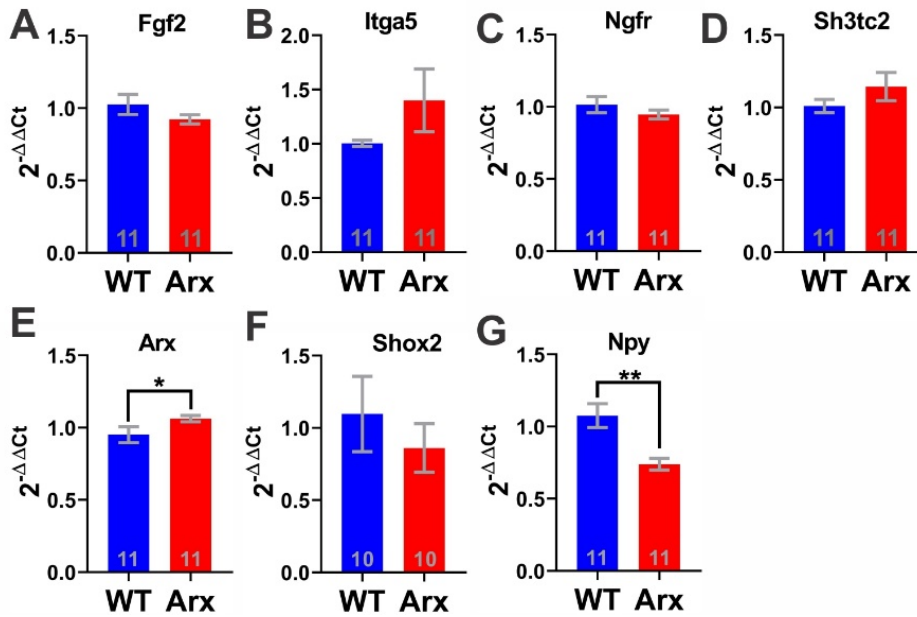


**Fig. S1. *Arx*<sup>(GCG)10+7</sup> mutants do not exhibit differences in CC3 distribution or neocortical size compared to WT littermates at P7.** (A) Distribution of CC3+ density in Arx mutants and WT littermates in 6 laminar bins (1 most superficial, 6 most deep bin). There was no difference between genotypes ( $F(1,96)=1.681$ ,  $P=0.1979$ ), a significant effect of bin ( $F(5,96)=13.81$ ,  $P<0.0001$ ), but no interaction between bin and genotype ( $F(5,96)=0.7028$ ,  $P=0.6226$ ) (Two Way ANOVA).  $N=10$  WT, 8 Arx. Mean and SEM are displayed. (B) Area ( $\mu\text{m}^2$ ) of WT and *Arx*<sup>(GCG)10+7</sup> mutant sagittal slices ( $P=0.5812$ , Unpaired t test). (C-D) Depth ( $\mu\text{m}$ ) of two different cortical regions showing no difference between genotypes: (C) RSA cortex ( $P=0.4316$ , Unpaired t test) and (D) Motor cortex ( $P=0.4321$ , Unpaired t test) cortex.  $N=8$  WT, 8 Arx. Mean and SEM are displayed.



**Fig. S2. Neonatal ACTH(1-24) treatment modifies cellular pathology but has no effect on neonatal spasms and electrographic phenotypes in adult *Arx<sup>(GCG)10+7</sup>*.** Effect of daily P3-10 ACTH(1-24) treatment at (A-C) 2IU/kg/day and (D-H) 4IU/kg/day compared to saline vehicle (Veh) control injections. (A) Average cumulative P7-11 spasms ( $p=0.6253$ , Unpaired T Test). (B&D) Average daily seizure frequency (seizures/24hr) from weekly P45-72 (average of 89 hours of total recording per mouse) video EEG recordings following neonatal 2IU/kg/day or 4IU/kg/day ACTH(1-24) treatment. (B) 2IU/kg/day ACTH(1-24) treatment ( $p=0.3287$ , Mann Whitney Test) (N=6 Veh, 8 ACTH(1-24)). (D) 4IU/kg/day ACTH(1-24) treatment ( $p=0.8701$ , Mann Whitney Test) (N=6 Veh, 6 ACTH(1-24)). (C&E) Average interictal spike frequency (interictal spikes/hr) following neonatal 2IU/kg/day or 4IU/kg/day ACTH(1-24) treatment. (C)

2IU/kg/day ACTH(1-24) treatment ( $p=0.4908$ , Mann Whitney Test). (E) 4IU/kg/day ACTH(1-24) treatment ( $p=0.3939$ , Mann Whitney Test). **(F-H)** Effect of P3-7 4IU/kg/day ACTH(1-24) treatment compared to vehicle (Veh) treatment (saline) on CC3+ cell counts and Arx+ cell density in Arx<sup>(GCG)<sup>10+7</sup></sup> at P7. **(F)** Mean CC3+ counts in neocortex with ACTH(1-24) treatment ( $p=0.0166$ , Unpaired T Test) **(G-H)** Mean Arx+ cell density (Arx+ cells/mm<sup>2</sup>) with ACTH(1-24) treatment in (G) retrosplenial agranular (RSA) region ( $p=0.0673$ , Unpaired T Test) and (H) motor cortex ( $p=0.0117$ , Unpaired T Test). Mean and SEM are displayed. With the exception of B&D, all Ns are displayed on graph.



**Fig. S3. Validation of Nanostring candidates using qPCR did not reveal mRNA expression changes in *Fgf2*, *Itga5*, *Ngfr*, *Sh3tc2*, and *Shox2* but did reveal changes in *Arx* and *Npy* expression in *Arx*<sup>(GCG)10+7</sup> P7 cortex compared to WT littermates. (A-G) Average expression ( $2^{-\Delta\Delta Ct}$ ) of each mRNA candidate is displayed. (A) *Fgf2* ( $p=0.1330$ , Mann Whitney Test) (B) *Itga5* ( $p=0.4385$ , Mann Whitney Test) (C) *Ngfr* ( $p=0.3316$ , Mann Whitney Test) (D) *Sh3tc2* ( $p=0.3653$ , Mann Whitney Test) (E) *Arx* ( $p=0.0400$ , Mann Whitney Test) (F) *Shox2* ( $p=0.6842$ , Mann Whitney Test) (G) *Npy* ( $p=0.0019$ , Mann Whitney Test). Mean and SEMs are displayed. Ns are displayed on graph.**



<i>Ccl12</i>	<i>Cx3cr1</i>	<i>Fasl</i>	<i>Il4ra</i>	<i>Prl</i>
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<i>Ccr2</i>	<i>Cxcl11</i>	<i>Flt4</i>	<i>Il6ra</i>	<i>Tgfb2</i>
<i>Ccr5</i>	<i>Cxcl12</i>	<i>Hgf</i>	<i>Inhbb</i>	<i>Tnf</i>
<i>Cd40</i>	<i>Cxcl16</i>	<i>Il10</i>	<i>Lif</i>	<i>Tnfrsf10b</i>
<i>Cntf</i>	<i>Cxcr4</i>	<i>Il10ra</i>	<i>Ltbr</i>	<i>Tnfrsf11b</i>
<i>Csf1</i>	<i>Egf</i>	<i>Il13ra1</i>	<i>Ngfr</i>	<i>Tnfrsf12a</i>
<i>Csf1r</i>	<i>Egfr</i>	<i>Il15ra</i>	<i>Osmr</i>	<i>Tnfrsf1a</i>
<i>Csf2rb</i>	<i>Epo</i>	<i>Il1b</i>	<i>Pdgfrb</i>	<i>Tnfrsf1b</i>
<i>Cx3cl1</i>	<i>Fas</i>	<i>Il1r1</i>	<i>Plekho2</i>	<i>Vegfa</i>

**Table S1.**

List of 50 cytokines and cytokine-related mRNA's from NCounter mouse Neuropathology panel used in Nanostring pathway analysis (See Fig. 5A).

mRNA	Correction Set	Uncorrected P-value	Corrected P-Value	Log2 fold change	Linear fold change
Ngfr-mRNA	Overlapping	0.00138	1	-1.110	0.465
Sh3tc2-mRNA	Overlapping	0.00707	1	-0.628	0.647
Fgf2-mRNA	Litter Correction	0.00454	1	-0.325	0.798
Itga5-mRNA	Overlapping	0.00205	1	-0.319	0.801
Hdac7-mRNA	Overlapping	0.00135	1	-0.173	0.887
Npy-mRNA	Batch Correction	0.00462	1	-0.171	0.888
Sirt1-mRNA	Batch Correction	0.00681	1	-0.162	0.894
Vegfa-mRNA	Overlapping	0.00583	1	-0.141	0.907
Atf4-mRNA	Overlapping	0.00878	1	-0.118	0.921
Htr1a-mRNA	Batch Correction	0.00797	1	-0.115	0.923
Acaa1a-mRNA	Batch Correction	0.00493	1	-0.093	0.937
Pnkd-mRNA	Batch Correction	0.00945	1	-0.094	0.937
Ran-mRNA	Overlapping	0.00594	1	-0.092	0.938
Ap4s1-mRNA	Overlapping	0.00354	1	-0.081	0.945
Ikbkb-mRNA	Batch Correction	0.00959	1	0.080	1.06

**Table S2. Differentially expressed mRNA candidates between WT and  $Arx^{(GCG)10+7}$  using Nanostring.** Data was corrected for batch and litter effects and 15 differentially expressed candidates were chosen based on uncorrected P-value less than 0.01. Highlighted candidates were chosen for validation by qRT-PCR.

Gene Name	Accession ID	Probe Target Sequence
<b>Arx</b>	NM_007492.3	TACTGAAAATAACCCGGGAGGGGTTCTCCCAATA TGCTTAGTATTGAAGTTTAAAAATTAAGCCCAAC CTTCTCTTCCCTCCGGATACCCCACTTAGC
<b>Birc6</b>	NM_007566.3	TCGGCGCTCAGCGCTAAACCAGGTGGACAGGTGA AATGTCAGTATATTTCTGCTGTGGATAAAGTGATAT TTGTGGATGATTACGCCGTGGGCTGTAGGA
<b>Csrnp3</b>	NM_178634.2	AAAGGACTTTGGGTTTGTTCATGCTATTGAAAGCAGT AATGGGGGCTGACTACTCCTTTTGGTTGACCGGTG GGGCTAATCTGGTGGGAATTCTGTGGTAA
<b>Cxcr5</b>	NM_007551.2	ACCGTGCCTTTCTCTTAACCAAGCAGAAAGCTGAAA CCGATCTACTTTAGGTAGCTGTCTGGTTCCAACCTA ACCAGCATTGGGTGAGCCCATGTTACT
<b>Drap1</b>	NM_024176.1	TGCCAAAACCATGACCACGTCCCACCTGAAGCAGT GCATTGAACTCGAGCAGCAGTTTGACTTCTTGA GACTTGGTGGCATCAGTGCCTGACATGCAG
<b>Ebf1</b>	NM_007897.2	CATAGGGGACAATTTCTTTGATGGGTTACAGGTCAT ATTCGGTACCATGCTGGTCTGGAGTGAGTTGATAA CTCCTCATGCCATCCGAGTTCAGACACCT
<b>Endog</b>	NM_007931.1	GGAAACAACCTTGAGAGGTACAGCCGCAGCTTGACG CGAACTTACAAAATGTCTATGTCTGCACGGGGCC GCTTTTCTGCCCAGGACCGAGGCTGATGG
<b>Erbp4</b>	NM_010154.1	TCCTGGTGATCATGGCTTTGACATTTGCTGTCTATG TCAGAAGAAAGAGCATCAAAAAGAAACGTGCTTTG AGGAGATTCTGGAGACAGAGCTGGTAGA
<b>Esr1</b>	NM_007956.4	ACTCGCTACTGTGCCGTGTGCAATGACTATGCCTC TGGCTACCATTATGGGGTCTGGTCTGCGAAGGCT GCAAGGCTTTCTTAAAGAGAAGCATTCAAG
<b>Esr2</b>	NM_010157.3	TGCTTCTTATAACTGTAGCCAGTCCATCCTACCCTT GGAGCATGGTCCCATCTATATCCCTTCTCCTATGT AGAGAGCCGTCACGAATACTCAGCCATG
<b>Ghrh</b>	NM_010285.2	GGATGCAGCGACACGTAGATGCCATCTTACCACC AACTACAGGAACTCCTGAGCCAGCTGTATGCCCG GAAAGTGATCCAGGACATCATGAACAAGCA
<b>Gnmt</b>	NM_010321.1	GGGTCATTGAAGAAGCCAACTGGTTGACGCTGGAC AAAGATGTGCTTTCAGGAGATGGCTTTGATGCTGT CATCTGCCTTGGGAACAGTTTTGCTCACTT
<b>Hdac4</b>	NM_207225.1	AGACGCTGAGTACTTGGCAGCCTTCCAGAACGGTGG TTATGCCTATCGCAAATGAGTTTGCCCCAGATGTG GTACTGGTGTTCATCGGGCTTCGATGCTGTG
<b>Hipk2</b>	NM_010433.2	AGGAAGCAAGAAAGTACATTTTCAACTGTTTGGATG ATATGGCCCAGGTGAACATGACAACAGATTTGGAA GGGAGTGACATGTTAGTAGAGAAGGCAGA
<b>Kcnma1</b>	NM_001253361.1	CGCATGTGGTGGGCTTTCTTGGCCTCCTCCATGGT GACTTTCTTCGGGGGCTTTCATCATCTTGCTCTG GCGGACGCTCAAGTACCTGTGGACCGTTT
<b>Kif26b</b>	NM_001161665.1	CATGATCGGAAGGGACGACTCTATGCAGAACCTGG GCATTATTCCATGTGCTATTTCTTGGCTGTTCAAGC TTATCAATGAGCGCAAAGAGAAGACGGGG

<b>Mef2c</b>	NM_001170 537.1	TTCTACTACTAAAGGTATCAATGGAACATGAAGACG AGTATTTAGGCAGAAGCAAACAGGAAACCATCCTT ACAAACATGCTTACCTGCACATCTGTTT
<b>Msx2</b>	NM_013601. 2	CTACCCCTTCCATAGACCTGTGCTCCCCATCCCGC CTGTTGGACTCTATGCCACGCCGTTGGATATGGC ATGTACCATCTATCCTAAGGAAGACCAGAT
<b>Myt1l</b>	NM_001093 775.1	ATCAGTGACAGAAGTTATGCTGAGGGGATGTCACA GCAGGACAGTAGAAATATGAACTATGTCATGCTAG GGAAGCCCATGAACAATGGACTCATGGAGA
<b>Ndufa1 3</b>	NM_023312. 2	CAGATTCTCCGGGAAAACCTGGAGGAGGAAGCCAT CATCATGAAGGATGTGCCCAACTGGAAGGTGGGC GAGTCTGTGTTCCATACCACACGATGGGTGC
<b>Pcdhg a5</b>	NM_033588. 4	CAGACTTTTCGAGCACCGTCCATATCAGCGTGACC GTTCTTGATGCAAACGATAACGCACCCTTGTTTACC CAAAGCGAATATAGGGTGAGTGTTCCGGA
<b>Pde3a</b>	NM_018779. 1	ATATAGGAAGAAAATGTGGCCGTATTCTGAGCCAG GTATCATACAGACTGTTTGAAGACATGGGGCTCTTT GAAGCCTTTAAATCCCGGTTAGGGAGTT
<b>Perp</b>	NM_022032. 4	CTTCACGATAACCCTGCTGTTAATTACATCTATAAC TGGGCCTATGGCTTCGGATGGGCGGCCACCATCAT CTTGATTGGTTGTTCCCTTCTTCTTCTGCT
<b>Prdx5</b>	NM_012021. 2	AAAGAAGGTGAACTTGGCAGAGCTGTTCAAGGGCA AGAAAGGTGTTTTGTTTGGAGTCCCTGGGGCATT ACACCTGGCTGTTCTAAGACCCACCTGCCT
<b>Samd5</b>	NM_177271. 3	GATGAGATGCGGAAGACTGGAAAGGGGCGTATTTA GGACCTTCTTTCACAAAGGGAAGTGGATGGTGACT CTGCAAACACTTATCAGCTTAACGTTTTCT
<b>Sfn</b>	NM_018754. 2	AATCTGATTTGGTAATCCAAGACGCTCCTGCAATGC AGCCAGCCCTGAACTGCAGGGGGCAGTCTGGAGC CGAAAGGTGCCTTTGCAGGTGGGACCTGCG
<b>Shox2</b>	NM_013665. 1	ATTTTACCCTGGAACAACCAACGAGCTGGAGAGG CTTTTCGATGAGACCCACTATCCAGACGCTTTCATG CGCGAGGAATTGAGCCAGCGACTGGGGCT
<b>Twist1</b>	NM_011658. 2	AATGGACAGTCTAGAGACTCTGGAGCTGGATAACT AAAAATAAATCTATATGACAAAGATTTTCATGGAAAT TAGAAGAGCAGAGACCAAATTCACAAGA
<b>Zfp369</b>	NM_178364. 5	GTTACAAGGTTTCATCTGCACAAAATCACCAGATGG GGTCTAGGGCAGGAAGAGCCAGGGACAACAGCAT CTTAACACATGTAAAAATTCACCAGAAAGGC

**Table S3**

List of 29 additional mRNA probes added to the Nanostring Mouse Neuropathology panel.

Probe	TaqMan™ Assay ID	Use
<i>Lars</i>	Mm00506560_m1	Normalizer/Housekeeping
<i>Tnf</i>	Mm00443258_m1	Target
<i>Il6</i>	Mm00446190_m1	Target
<i>Il1b</i>	Mm00434228_m1	Target
<i>Fgf2</i>	Mm00433287_m1	Target
<i>Itga5</i>	Mm00439797_m1	Target
<i>Ngfr</i>	Mm00446294_m1	Target
<i>Sh3tc2</i>	Mm01261770_m1	Target
<i>Arx</i>	Mm00545903_m1	Target
<i>Shox2</i>	Mm00443183_m1	Target
<i>Npy</i>	Mm00445771_m1	Target

**Table S4**

TaqMan™ Gene Expression Assay ID's used for qPCR validation. *Lars* mRNA expression was used as a normalization/housekeeping gene as it was computationally identified by Nanostring assay as having adequate expression and low variability between samples.