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The 16p11.2 homologs *fam57ba* and *doc2a* generate certain brain and body phenotypes

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**Abstract**

Deletion of the 16p11.2 CNV affects 25 core genes and is associated with multiple symptoms affecting brain and body, including seizures, hyperactivity, macrocephaly, and obesity. Available data suggest that most symptoms are controlled by haploinsufficiency of two or more 16p11.2 genes. To identify interacting 16p11.2 genes, we used a pairwise partial loss of function antisense screen for embryonic brain morphology, using the accessible zebrafish model. *fam57ba*, encoding a ceramide synthase, was identified as interacting with the *doc2a* gene, encoding a calcium-sensitive exocytosis regulator, a genetic interaction not previously described. Using genetic mutants, we demonstrated that *doc2a⁺/⁻ / fam57ba⁺/⁻* double heterozygotes show hyperactivity and increased seizure susceptibility relative to wild-type or single *doc2a⁺/⁻* or *fam57ba⁺/⁻* mutants. Additionally, *doc2a⁺/⁻ / fam57ba⁺/⁻* double heterozygotes demonstrate the increased body length and head size. Single *doc2a⁺/⁻* and *fam57ba⁺/⁻* heterozygotes do not show a body size increase; however, *fam57ba⁻⁻* homozygous mutants show a strongly increased head size and body length, suggesting a greater contribution from *fam57ba* to the haploinsufficient interaction between *doc2a* and *fam57ba*. The *doc2a⁺/⁻ / fam57ba⁺/⁻* interaction has not been reported before, nor has any 16p11.2 gene previously been linked to increased body size. These findings demonstrate that one pair of 16p11.2 homologs can regulate both brain and body phenotypes that are reflective of those in people with 16p11.2 deletion. Together, these findings suggest that dysregulation of ceramide pathways and calcium sensitive exocytosis underlies seizures and large body size associated with 16p11.2 homologs in zebrafish. The data inform consideration of mechanisms underlying human 16p11.2 deletion symptoms.

**Introduction**

Identifying multigenic contribution and relevant genetic interactions contributing to neurodevelopmental disorders is a huge challenge facing the field. In these disorders, physical comorbidities are frequently associated with mental health disorders and compound challenges faced by people with these diagnoses. Multigenic regions associated with neurodevelopmental disorders include copy number variants (CNVs). Loss of one copy of the 16p11.2 is the CNV is highly prevalent, occurring in 1 in 2000 people (1), and is linked to many symptoms affecting brain and body function, including autism spectrum disorders (ASDs), intellectual disability, developmental delay, language impairment, seizures, macrocephaly, obesity, hypotonia, motor impairment, and gastrointestinal problems (2–10).

The 16p11.2 CNV affects 25 core genes, and we considered four models to account for the connection between loss of function in core genes and specific phenotypes or symptoms. First, a single gene from 16p11.2 could be linked to all symptoms (Fig. 1A). This model is not supported by the extensive sequencing analysis that has been done for people with autism and intellectual disability and autism spectrum disorders (ASDs), intellectual disability, developmental delay, language impairment, seizures, macrocephaly, obesity, hypotonia, motor impairment, and gastrointestinal problems (2–10).

The 16p11.2 CNV affects 25 core genes, and we considered four models to account for the connection between loss of function in core genes and specific phenotypes or symptoms. First, a single gene from 16p11.2 could be linked to all symptoms (Fig. 1A). This model is not supported by the extensive sequencing analysis that has been done for people with autism and intellectual disability and autism spectrum disorders (ASDs), intellectual disability, developmental delay, language impairment, seizures, macrocephaly, obesity, hypotonia, motor impairment, and gastrointestinal problems (2–10).
solutions for gene-phenotype relationships in multi-symptomatic CNV disorders. (A) A single gene accounts for all of the associated symptoms. (B) The interaction of two or more genes accounts for all of the associated symptoms. (C) Single genes account for a single symptom each. (D) Two or more genes interact to affect one symptom each. These interacting genes can be in different and overlapping sets. There are also additional models that would be composites of the last two hypotheses.

Results

A subset of interacting 16p11.2 pairs affect early brain development and other phenotypes

We were particularly interested in genetic interactions, which are defined as a combination of two mutations that leads to a phenotype that cannot be predicted from the effects of either mutation alone (38). In other words, a genetic interaction between two gene products results from a non-additive effect of the single gene phenotypes. An additive phenotype resulting from summation of each single gene LOF would not be considered an interaction. To test the hypothesis that two genes from the 16p11.2 CNV interact to impact brain development, we compared the effects of partial LOF in individual zebrafish 16p11.2 CNVs to that of two homologs together.

...single genes to mediate 16p11.2 deletion phenotypes, of...
Figure 2. A subset of pairwise combinations of 16p11.2 homologs alter brain and ventricle morphology. (A) Definition of an interacting pair. Dorsal views of 24 hpf embryos with red dye injected into the ventricles. Single gene LOFs were induced to about ~50% normal RNA remaining (or a sub-phenotypic dose) and generally resembled control MO-injected embryos. If a pair of genes interacted, then suppressing them together resulted in abnormal brain and ventricle morphology. (B) Pie chart of all 162 pairwise combinations tested. (C) Map of interacting pairs of genes, with the lines drawn between two genes if they interact, and scaling the font size of the gene name according to the number of interactions it has.

Unlike our previous study, where we found phenotypes associated with 70–95% single gene knockdown for the majority of 16p11.2 homologs, the partial LOF used here for interaction analysis was ≤50% for each gene to more closely reflect the hemizygous state of people with 16p11.2 deletion CNVs. We defined interacting gene pairs as those that gave no or little phenotype for single partial LOF, but did affect the embryonic brain formation with double partial LOF (Fig. 2A). LOF was induced by injection of antisense morpholino-modified oligonucleotides (MOs) defined in our previous study (33), with the amount of MO titrated so approximately 50% normal RNA remained as determined by qPCR (splice-blocking MOs) or a sub-phenotypic dose (translation blocking MOs) (Supplementary Material, Table S1). We analysed interaction between all 162 possible pairwise combinations of 19 genes, by assaying early brain and ventricle morphology at 24 hours post fertilization (hpf). We chose this assay for two reasons. First, nervous system development is impacted by multiple signaling pathways and is sensitive to perturbations (39–41). Second, radiological examinations of people with 16p11.2 CNVs indicate changes in the volume of certain brain regions and associated brain ventricle size (5,42–44). However, zebrafish analyses are performed at the equivalent of first trimester human embryos, and human screening for 16p11.2 deletions at these stages has not been done.

Of the 162 gene pairs tested, 16 (10%) resulted in a ventricle phenotype after double partial LOF (Fig. 2B, Supplementary Material, Fig. S1). A pair of genes was scored as interacting if >50% of the double LOF embryos showed a brain morphology phenotype after normalization. To normalize numbers, background levels of a phenotype after single gene LOF were subtracted from the levels after double gene LOF. Most gene combinations (146, 90%) did not yield any phenotype, suggesting that interactions observed were specific. Additional controls for MO specificity included injection with a p53 MO, since activation of p53 has been associated with off target MO effects, and prevention of a phenotype by RNA injection (45). Furthermore, other 16p11.2 homolog expression levels were not affected by double LOF injections (Supplementary Material, Fig. S2).

We used these data to map a 16p11.2 homolog genetic interaction network with lines drawn between interacting genes and scaling the font size of the gene name relative to the number of interactions (Fig. 2C). Fourteen of nineteen genes screened were part of this interaction map. Six of these genes emerged as highly interactive in impacting early brain morphology: fam57ba and kif22 with four interactions each; and asphd1, hipr3, kctd13, and sez612 with three interactions each.

Because people with 16p11.2 CNV deletions exhibit multiple symptoms and because defects in early brain morphology may indicate additional nervous system involvement, we conducted a secondary screen for four additional phenotypes: neuronal specification using a NeuroD:GFP line, cranial motor neuron patterning using an islet1:GFP line, enteric neuron density, and muscle fiber organization. Of the 16 gene pairs identified from our initial screen, 11 LOF pairs impacted at least one secondary screen phenotype (Supplementary Materials, Fig. S3, Tables S2 and S3). Overall, there was enrichment for positive interactions, showing a linkage between brain and body phenotypes. Assaying gene pairs that did not interact with the primary screen gave no interactions for any of the secondary screen phenotypes, indicating the strength of brain and ventricle morphology as a first pass assay.

In sum, these initial assays identified pairs of interacting genes in zebrafish, which were associated with phenotypes that could be reflective of symptoms in people with 16p11.2 deletion CNVs. None of these gene interactions has been previously described and could not have been predicted from database analysis, demonstrating the importance of functional studies for discovery of genetic interactions.

**doc2a<sup>−/−</sup>–fam57ba<sup>−/−</sup> double heterozygotes show hyperactivity and increased seizure propensity**

Mutants allow examination of gene function in older fish when MOs would be less effective. We generated TALEN mutant lines for some of the more interactive genes uncovered in our initial antisense screen, including fam57ba and doc2a. Zebrafish have two copies of the fam57ba gene, and previous analysis has supported the fam57ba copy as most active (33). Mouse Fam57b encodes a ceramide synthase (46) and Doc2a encodes a calcium sensor that primes vesicles for exocytosis (47,48). While there are strong indications of synaptic defects in the literature for some of the associated 16p11.2 CNV symptoms, particularly epilepsy (49,50) and ASD (51), as well as links to metabolic defects (52), there is little about ceramides in particular (53,54). Therefore, this seemed an intriguing gene combination to analyse further. There are reported roles for calcium and ceramide signaling at the synapse (55–57), and because attention deficit-hyperactivity disorder (ADHD) and seizures are prevalent among people with 16p11.2 deletion CNVs (2,6,8,10,58,59), we analysed mutant zebrafish larvae for their baseline movement level and seizure propensity.

Despite evolutionary distance, zebrafish have been a valuable tool for studying human epilepsies. Several assays have been used to validate the fish as a model for human epilepsies. Electrophysiological recordings of larval brain activity after PTZ treatment show epileptiform discharges of brief interictal bursts and long duration bursts similar to those seen in humans (60). The more easily measured increased swimming speed after PTZ treatment is directly correlated to seizure electrophysiology. Swimming velocity can be readily measured in an automated, high throughput system. Both swimming speed and electrophysiological recordings show attenuated response to human
anti-epileptic drugs (60,61). Zebrfish epilepsy models have led to identification of anti-convulsant compounds for drug-resistant Dravet syndrome (62), and of other novel anti-convulsants (63–68). Zebrfish have also been widely used to provide functional confirmation for gene candidates linked to seizures in people (69–74).

Movement of seven days post fertilization (dpf), the standard age at which these assays are conducted (60,75), wild-type and doc2a+/− fam57ba−/− larvae was analysed, comparing average velocity as an output of brain activity, with and without the seizure-inducing GABA-A antagonist pentylentetrazol (PTZ). Across four independent experiments, doc2a+/− fam57ba−/− larvae exhibited higher baseline movement levels as well as increased velocity with a minimal PTZ treatment relative to wild-type. The increased PTZ sensitivity was significant even with normalization to account for the increased baseline movement present in double heterozygotes (Fig. 3A–D). This normalization was done by subtracting the baseline velocity from the PTZ-induced velocity for each larva.

To determine the individual contributions of doc2a and fam57ba to this interaction, we examined a spectrum of doc2a and fam57ba genotypes, including doc2a+/− and fam57ba+/− single homozygous mutants (Table 1). fam57ba−/− mutants displayed higher baseline movement and PTZ sensitivity, but not to the same degree as double heterozygote doc2a+/− fam57ba−/− larvae (Fig. 3E–H). The double heterozygotes showed significantly higher activity than wild-type after a minimal 0.3 mM PTZ dose, which is far below the established dosing range of 2.5 to 25 mM required to induce seizures in wild-type fish (60,76).

In contrast, fam57ba−/− mutants needed 5 mM PTZ to show a nominally significant increase in velocity compared to wild-type. Single heterozygous doc2a+/− and fam57ba+/− fish did not show differences in baseline activity or 0.3 mM PTZ sensitivity compared to wild-type, indicating an interaction in the double heterozygote (Fig. 3I–P). doc2a+/− mutants alone did not exhibit changes in baseline movement or seizure susceptibility relative to wild-type at 0.3 mM (data not shown) or 5 mM PTZ (Fig. 3Q–T). Single heterozygotes were also tested at the higher 5 mM PTZ dose, but no significant differences were observed (data not shown). All genotypes tested except for fam57ba−/− larvae did not show changes in baseline activity or 0.3 mM PTZ sensitivity compared to wild-type larvae at 12 dpf (Fig. 5).

doc2a+/− fam57ba−/− fish showed slight increases in a subset of the dimensions, while fam57ba−/− larvae showed significant changes in all measurements, indicating that losing both copies of fam57ba has the more powerful effect on head size as well as body size. Single heterozygous doc2a+/− and fam57ba+/− larvae did not show changes in head size in any dimension, while doc2a+/− larvae showed a decrease in inter-eye width and an increase in two other dimensions (Fig. 5). If increased head dimensions are normalized by dividing by the body length of doc2a+/− fam57ba−/− and fam57ba−/− larvae, then no significant differences from wild-type are observed (not shown). Therefore, we predict DOC2A and in particular FAM57B contribute to general growth patterns, rather than specifically to head size, although species differences may play into the results.

These data demonstrate that doc2a+/− fam57ba−/− heterozygotes and fam57ba−/− mutants show increased body and head size

Since large body size, macrocephaly and obesity are significant symptoms among people with the 16p11.2 deletion, we next examined body size and head size in doc2a+/− fam57ba−/− larvae and other doc2a and fam57ba genotypes. In people with the 16p11.2 deletion, incidence of obesity increases with age, becoming significantly different from non-carriers by 3.5 years. There is also a correlated increase in pre-pubertal height above the population average, but only in obese 16p11.2 CNV deletion carriers. The occurrence of increased head circumference is also positively correlated with age and with obesity (10). With these considerations, head and body size of fish about halfway through the larval period (12 dpf) were assayed to assess a later developmental time point, perhaps more relevant to onset of human phenotypes.

A significant increase in body length was found in doc2a+/− fam57ba−/− larvae at 12 dpf (Fig. 4A–C). To analyse lipid content, larvae were stained with the lipid-binding dye Oil Red O (ORO), and the ORO was then extracted and quantified. While ORO concentrations were significantly elevated in doc2a+/− fam57ba−/− double heterozygotes (Fig. 4D), this difference was not seen after accounting for body length (Fig. 4E). In analysis of additional genotypes, we found that fam57ba−/− larvae displayed a much greater increase in body length versus wild-type (Fig. 4F–H). These fish also showed a significant increase in lipid content, even after normalizing to body length (Fig. 4I–J). Since doc2a+/−, fam57ba−/−, and doc2a−/− larvae did not show changes in body size or lipid content (Fig. 4K–Y), we conclude that with regard to body size, there is an interaction in the double heterozygote for body size but not normalized lipid content.

To assess head size, various measurements of mutants were made relative to wild-type larvae at 12 dpf (Fig. 5). doc2a+/− fam57ba−/− fish showed slight increases in a subset of the dimensions, while fam57ba−/− larvae showed significant changes in all dimensions measured, indicating that losing both copies of fam57ba has the more powerful effect on head size as well as body size. Single heterozygous doc2a+/− and fam57ba+/− larvae did not show changes in head size in any dimension, while doc2a−/− larvae showed a decrease in inter-eye width and an increase in two other dimensions (Fig. 5). If increased head dimensions are normalized by dividing by the body length of doc2a+/− fam57ba−/− and fam57ba−/− larvae, then no significant differences from wild-type are observed (not shown). Therefore, we predict DOC2A and in particular FAM57B contribute to general growth patterns, rather than specifically to head size, although species differences may play into the results.

These data demonstrate that doc2a+/− fam57ba−/− heterozygotes and fam57ba−/− mutants show increased head size, body size, and lipid content – phenotypes that are consistent with obesity.

Discussion

A major challenge in human genetics is the definition of how multigenic copy number variant regions connect to multiple associated symptoms. Deletion of the 16p11.2 CNV is paradigmatic of this challenge, presenting a global burden for four million affected people. We used the tractable zebrafish system and a functional screen to uncover genotype/phenotype connections amongst 16p11.2 homologs, reaching three major conclusions. 1) A subset of 16p11.2 genes interact after partial loss of function and define a functional network, the doc2a and fam57ba genes interact to regulate hyperactivity and seizure susceptibility.
These conclusions add new understanding to the mechanism underlying 16p11.2 deletion phenotypes, and further suggest previously undescribed correlations between brain and body health.

Gene interactions among the 16p11.2 interval do not converge on functional networks predicted by gene-set enrichment.
analysis (79). Furthermore, no evidence for physical interactions between 16p11.2 genes has been found (80). These findings imply indirect mechanisms of gene interaction, which could only be uncovered by functional assays. Genetic interaction data do not indicate mechanism, but are invaluable in focusing subsequent molecular or cellular assays.

The subset of highly interactive 16p11.2 zebrafish homologs that our pairwise assays reveal have diverse predicted functions, and include asph1d, fam57ba, hirip3, kud13, klf22 and sze62 (Table 2). The initial hypothesis that each pair of genes would be sufficient to regulate a specific 16p11.2 phenotype may be too simple, as suggested by the network of interactions uncovered that affect a single phenotype. Rather, each 16p11.2 deletion symptom may depend on haploinsufficiency of multiple genes (Fig. 1). It is possible that even if multiple 16p11.2 genes regulate each symptom, these converge functionally on a few common biochemical or cell biological targets.

The interaction of doc2a and fam57ba in genetic mutants suggests a mechanism by which brain activity is regulated. Although both genes are expressed predominantly in the head of larval zebrafish (Supplementary Material, Fig. S6) and are apparently co-expressed in the adult mouse brain (81) and the pre-natal human brain (82), it is unclear whether they function in the same cells. The Doc2a gene encodes a calcium sensor that interacts with the docking machinery to prime vesicles for exocytosis (47,48,83), including at the synapse (57). Mutations in other synaptic vesicle docking components are associated with ADHD and epilepsy (72,84,85).

Fam57b has a Tran-Lag1-Cln8 (TLC) domain associated with ceramide synthases (86), and is capable of ceramide synthesis in vitro (46). Based on this ceramide synthase activity, we predict that there is a change in the ceramide cohort in fam57ba mutant fish, and possibly in people with 16p11.2 CNVs. Serum levels of particular sphingomyelins, a ceramide derivative, have been shown to be decreased in people with ADHD (87). Mice treated with fumonisin B1, a general ceramide synthase inhibitor, are sensitized to PTZ-induced seizures (88), and mutations in two ceramide synthase genes in humans are associated with progressive myoclonus epilepsy (54,89).

Dysregulated ceramides could interact with DOC2A to impact synaptic signaling in several ways (Fig. 6). Ceramides are critical structural components of cell membranes and dysregulation could affect vesicle fusion and endocytic recycling. In
possible contribution from premature adipocyte differentiation in fam57ba−/− mutants, but we did not observe significant differences in white adipose tissue depots at 12 dpf (data not shown).

The effects of mutating fam57ba and doc2a in zebrafish are more similar to increased body and head size in people with 16p11.2 deletions than phenotypes seen in mouse models. Instead, mouse 16p11.2 deletion models exhibit reduced body and head size as well as decreased adiposity and do not recapitulate this human phenotype (30–32). Mouse models do recapitulate other aspects of human symptoms, including hyperactivity, impaired learning, and social deficits (30–32,99), illustrating the utility of using multiple animal models to address human gene function.

Our results indicate for the first time that FAM57B functions in both brain and body health, through interaction with DOC2A and perhaps together with other, as yet unidentified genes (summarized in Fig. 6). Together, these data suggest that in people with 16p11.2 deletions, ceramide dysregulation and altered exocytosis may be mechanisms underlying seizures and obesity. The identification of a potential lipid mechanism underlying pathology suggests a role for metabolic regulation of the 16p11.2-related phenotypes addressed. Because we focused on this single interaction for further analysis, there is nothing to

Figure 4. Body size and lipid amounts are affected by doc2a and fam57ba. A representative experiment is shown from the 5 conducted. (A,B) 12 dpf larvae stained with Oil Red O (ORO) are shown for wild-type and doc2a+/− fam57ba+/−. (C) A significant increase in body length as measured from the tip of the nose to the end of the tail is found for doc2a+/− fam57ba+/− larvae (n = 19) compared to wild-type (n = 19). (D) ORO was extracted back out of the stained larvae and quantified, showing a significant increase in the concentration of lipids in the double heterozygotes (yellow bar) compared to wild-type (blue bar). (E) After accounting for length, there is no longer a significant increase in ORO concentration in doc2a+/− fam57ba+/− larvae (F,G) Wild-type and fam57ba−/− larvae stained with ORO. (H) A significant increase in body length was found comparing fam57ba−/− larvae (n = 30) to wild-type (n = 30). (I) ORO quantification showed a significant increase in the concentration of lipids for fam57ba−/− homozygotes (purple bar) compared to wild-type (blue bar). (J) When accounting for length, ORO concentration is still significantly elevated in fam57ba−/− fish. (K–Y) No significant changes in size or ORO concentration were observed for fam57ba+/+ (n = 29), doc2a+/− (n = 26), and doc2a+/− (n = 36) larvae compared to their respective wild-type controls. **P < 0.01, ***P < 0.001, ****P < 0.0001. Scale bar = 500 μm.
rule out that other 16p11.2 genes also contribute to seizure propensity and body size, as well as other phenotypes. Future directions include molecular analysis of \textit{fam57ba} and \textit{doc2a} interaction, assessment of whether function of these genes is dysregulated in human 16p11.2 deletion cells, and exploring interactions of additional 16p11.2 homologs with \textit{doc2a} and/or \textit{fam57ba} related phenotypes.

**Materials and Methods**

**Fish lines and maintenance**

Adult zebrafish of the wild-type AB strain were maintained at 28°C on 12h/12h light/dark cycle. Embryos were obtained from natural spawnings and staged as previously described by Kimmel et al. (1995). The transgenic lines used, islet1:GFP and NeuroD:GFP, have been previously characterized (100,101). Due to the polygenic nature of sex determination and timing of gonadal development in zebrafish (102,103), we are unable to determine the sexes of the embryos and larvae for our experiments. Table 2. Diverse predicted functions for most interactive 16p11.2 genes. Little is known about ASPHD1 function, although it contains an aspartate beta-hydroxylase domain, and aspartate beta-hydroxylase is important for regulating calcium homeostasis (112). FAM57B is a ceramide synthase that regulates adipogenesis in mouse tissue culture cells (46). HIRIP3 may be part of a complex involved in chromatin and histone metabolism (113). KCTD13 encodes a ubiquitin ligase adaptor (114) that is reported to have reciprocal effects on zebrafish head size with gain- and loss-of-function (35). KIF22 is a kinesin-like protein that links chromosomes to the mitotic spindle (115,116), and is necessary for proper embryonic chromosome segregation (118) and synaptic development (34). SEZ6L2 is a seizure-related protein that modulates neurite outgrowth (117).

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<td>(112)</td>
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<tr>
<td>FAM57B</td>
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<td>HIRIP3</td>
<td>Chromatin and histone metabolism</td>
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<td>KCTD13</td>
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<td>KIF22</td>
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<td>(115,116)</td>
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<td>SEZ6L2</td>
<td>Modulates neurite outgrowth</td>
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Neuronal specification and cranial motor neuron patterning were analysed at 2 dpf using transgenic lines. Embryos were scored in 2–4 independent experiments, with the combined number of embryos scored across experiments shown in the figures.

Microscopy
Bright-field and fluorescent images were captured on a Zeiss Stereo Discovery V8 microscope with an AxioCam MRc digital camera using ZEN software (Zeiss). Confocal imaging was performed on an inverted Zeiss LSM710 laser-scanning microscope with a 25X (0.8 NA) LD LCI Plan Apochromat oil-immersion objective.

Immunohistochemistry
Embryos and larvae were fixed in 4% PFA. Anti-HuC/D monoclonal antibody (Invitrogen) was used at 1:500, znp1 (anti-SYT2, Abcam) monoclonal antibody was used at 1:200, and Alexa Fluor 488 secondary antibody (Jackson) was used at 1:400. Alexa Fluor 635 phalloidin (Invitrogen) was used at 1:40. Cell counting was done in Imaris (Bitplane) with manual threshold adjustment.

TALEN generation and identification of TALEN mutants
Target sites for TALENs were identified using Mojo Hand (106) and TALE-NT 2.0 (107). All sites chosen had a restriction enzyme site at the cut site to be used for genotyping (Supplementary Material, Table S4). TALENs were cloned and injected into one-cell zebrafish embryos as previously described (108,109). F0 fish with high germline transmission rates were identified by loss of restriction site, sequenced, and outcrossed. The resulting heterozygous F1 fish were in-crossed if they carried the same mutation to generate wild-type, heterozygous, and mutant siblings. These F2 fish were bred to generate embryos and larvae used in the experiments described below.

Seizure assays
Wild-type and doc2a−/− fam57ba−/− double heterozygous cousin embryos were obtained from separate crosses of sibling wild-type and single homozygous mutant fish, respectively. Single heterozygous fish were generated by crossing homozygous to wild-type fish. At 7 dpf, larvae were pipetted into 96-well plates in 200 μl E3 media, allowed to acclimate to the plate for 15 min, and then moved to the Noldus Daniovision for another 10 min habituation period. Baseline activity was then recorded for 10 min. Following this, 100 μl E3 was removed from each well, and replaced with 100 μl of varying concentrations of PTZ to test a range of doses. Plates were immediately placed back on the Daniovision system for a 10-min habituation period, followed by another 10- min recording. Average velocity was calculated using the Ethovision XT 11 software from Noldus. The numbers shown in the figures are combined from 2 to 5 independent experiments. Even though there may not necessarily be a correlation between baseline movement and velocity after PTZ addition, we still accounted for this possibility by normalization via subtracting the baseline velocity from the PTZ-induced velocity for each larva.
Anti-epileptic drug treatments

Human anti-epileptic drugs were added to larvae for 15 min before PTZ addition and seizures were assayed as above. Valproic acid (Sigma) was used at 3 mM and carbamazepine (Sigma) was used at 100 μM.

Oil red O staining and quantification

To control for variable growth rates, bowl larval density was checked daily to ensure equal numbers of wild-type and test genotype larvae within experiments. Larvae were fixed at 12 dpf in 4% FFA and washed in PBS. Pigment was bleached with 1% KOH/3% H₂O₂ solution. The 0.5% stock Oil Red O (Sigma) solution was made in isopropanol. Immediately before use, a working 0.3% solution was made with dH₂O, allowed to stand for 10 min after mixing, and then filtered. Larvae were incubated in the fresh working solution for 30 min to 2 h, rinsed quickly twice in 60% isopropanol, and rinsed again in PBS (110,111). To quantify ORO amount, ORO was extracted back out of 15–25 stained larvae per genotype by soaking 2–4 fish in 300 μl isopropanol for at least 60 min with occasional agitation until larvae appeared white in appearance. The supernatant from these 6–8 pools per genotype was removed, split in triplicate, and absorbance was measured at 492 nm (averaged from 10 readings per well). Average concentration was calculated per larva by comparison to a standard curve analysed on the same plate.

Statistical analysis

Exact binomial tests were used for statistical analysis comparing qualitative phenotypes. Unpaired nonparametric t-tests were used for statistical analysis comparing quantitative phenotypes. Unless noted otherwise, error bars on bar graphs reflect standard error, while error bars on scatter plots show standard deviation.

Supplementary Material

Supplementary Material is available at HMG online.

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Conflict of Interest statement. None declared.

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