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Richelle Reid, Emory University
Peng Jin, Emory University
Michael Epstein, Emory University
Tamara Caspary, Emory University
Stephen Warren, Emory University

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Argonaute2 Is Essential for Mammalian Gastrulation and Proper Mesoderm Formation

Reid S. Alisch1, Peng Jin1, Michael Epstein1, Tamara Caspary1, Stephen T. Warren1,2,3*

Introduction

Argonaute proteins comprise a highly conserved gene family necessary for a range of physiological and developmental processes. These proteins are defined by the presence of PAZ and PIWI domains, which modulate protein–protein interactions, nucleic acid binding, and, in some cases, mRNA cleavage [1–5]. Argonaute proteins serve as scaffolds for target-mRNA recognition by short regulatory guide RNAs during the process of RNA interference (RNAi) [6]. The Argonaute family was initially linked to RNAi-related phenomena through genetic studies in Caenorhabditis elegans [7] and has since been shown to play a gene-silencing role in plants, yeast, and flies [8–10]. Members of the mammalian Argonaute family associate with micro-RNAs in the RNA-induced silencing complex (RISC), indicating a post-transcriptional gene regulation role in mammals [6]. In the mouse, loss of a single Argonaute family member, eIF2C2 (Argonaute2 or Ago2), disrupts RISC activity and gives rise to several midgestational developmental abnormalities, including failed neural tube closure, mesodermal malformations [11]. These studies demonstrated that AGO2 plays an essential role in RNA-induced silencing complex (RISC), which induces the absence of full paralog redundancy. However, the specific role played by AGO2 during mammalian development remains unclear. To characterize this role, we investigated Ago2-null embryos during gastrulation and found that Ago2 is required for proper fibroblast growth factor (FGF) signaling and mesoderm formation. We further determine that Ago2 haploinsufficiency partially rescues the classic T/+ short-tail phenotype [12], which is consistent with Ago2 residing in a previously mapped interval shown to modify T [13]. Together, these data reveal a genetic interaction between Ago2 and T and indicate that AGO2 is essential to the formation of a mammalian germ layer.

Results/Discussion

We explored the role of AGO2 in early mammalian development using gene-trapped embryonic stem cells to generate a mouse line that transmits an interrupted Ago2 allele without an obvious heterozygous phenotype. The interrupted Ago2 allele was characterized, and primers were designed to distinguish wild-type from mutants by genotyping (Figure 1A and 1B). This disruption deletes most of the PIWI domain and results in an apparent functional null allele [11] (Figure 1A and 1C). Full-term litters from heterozygous intercrosses did not yield homozygous (Ago2+/–) offspring. At embryonic day 9.5 (e9.5), we observed two classes of null embryo: intact embryos with assorted morphological phenotypes, such as the neural tube and cardiac malformations that are consistent with the earlier findings of Liu and colleagues [11]; unpublished data), and embryonic remnants (Figure 1D). Unexpectedly, however, intact e9.5 null embryos were observed in numbers significantly lower than predicted based on genetic ratios (12/134; p < 0.0001; Table 1). Because intact null embryos were recovered in the appropriate genetic ratios during gastrulation (i.e., at e7.5; Table 1), Ago2 plays an important role at an earlier stage of development than previously reported [11].

Vertebrate gastrulation initiates at e6.5 and establishes the three germ layers of the developing embryo (reviewed in [14]). During gastrulation, embryonic ectoderm (epiblast) cells are recruited to a transient embryonic structure known as the primitive streak, located on the posterior side of the embryo. At the primitive streak, the epiblast cells undergo an
Author Summary

Gastrulation is a developmental phase that delineates the three embryonic germ layers: ectoderm, endoderm, and mesoderm. The gene Brachyury is essential for mesoderm development, and short-tail mice, which were later found to be carrying a Brachyury mutation, have been known since 1927. In this study, we found a genetic interaction between Brachyury and another gene in mouse, Argonaute2. We show that the loss of Argonaute2, a necessary component of a recently appreciated pathway of gene regulation called RNA interference, results in embryonic death during gastrulation, abnormal expression of Brachyury, and expansion of the mesoderm layer. This suggests that Argonaute2 is important in early development and in regulating Brachyury function. Consistent with this conclusion, we found that mice simultaneously carrying mutations in both Argonaute2 and Brachyury have significantly longer tails than mice with only a Brachyury mutation. A closer look at other genes involved in mesoderm development revealed that a disruption in fibroblast growth factor signaling may explain the mesoderm expansion in mice carrying the Argonaute2 mutation. Together this work demonstrates that a factor best known as a key component of RNA interference is required for the formation of a mammalian germ layer.

epithelial-to-mesenchymal transition (EMT), before migrating away from the streak and being specified as either the mesoderm or the definitive endoderm germ layers [15,16]. By e7.5, a complete mesoderm layer is formed. Brachyury (T), a T-box transcription factor, is expressed in the primitive streak and in the epiblast cells near the primitive streak [17,18]. To determine whether a proper primitive streak is formed in the Ago2 mutants, we examined the expression of T in Ago2 null embryos by whole-mount in situ hybridization. We found that homozygous disruption of Ago2 results in expanded expression of T compared to its expression in wild-type e7.5 embryos, indicating an abnormal primitive streak in Ago2 mutants (Figure 2A and 2B and insets). Notably, the Ago2 mutants exhibit a variability in the expansion of T expression (Figure S1B and S1C), which may account for the ability of some Ago2 mutants to escape gastrulation arrest and develop until midgestation [11]. Also consistent with previous studies is the reduced extraembryonic region in the e7.5 Ago2 mutant embryos; this finding further suggests embryos that survive to later stages have generalized nutritional deficiencies caused by yolk sac and placental defects [11].

Previous experiments have shown that ectopic expression of T is sufficient to induce mesoderm formation [19], leading us to hypothesize that Ago2 plays a role in mesoderm development. To explore this possibility, we assessed the expression pattern of another known mesoderm marker, Tbx6 [20], and found that homozygous disruption of Ago2 also results in an expansion of Tbx6 expression compared with its expression in wild-type e7.5 embryos (Figure S2A and S2B). These findings, paired with the expanded T expression, argue for an Ago2 function in mesoderm development.

To determine the spatial localization of Ago2 during gastrulation, we examined its wild-type expression pattern in sectioned heterozygous Ago2 e7.5 embryos by using antibodies against β-galactosidase (from the gene trap’s lacZ insertion driven by the endogenous Ago2 promoter) and BRACHURY. We found that wild-type Ago2 expression is restricted to the apical side of the epithelial cell layer and does not overlap with T in the mesenchymal cells of the primitive streak (Figure 2C, 2E, and 2G). Coupled with the fact that homozygous loss of Ago2 results in expanded T

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**Figure 1. Characterization of the Ago2 Disruption in ES Cell Clone RRE192**

(A) Insertion of the gene-trap vector into intron 12 of the mouse Ago2 locus. Exons 1, 12, and 18 are labeled. Exons encoding the PAZ domain are shown in yellow, and exons encoding the PIWI domain are shown in orange. The insertion cassette contains a splice acceptor (SA), a fusion of the β-galactosidase and neomycin phosphotransferase coding sequences (β-gal), and a polyadenylation signal (pA). FRT and loxP sites are denoted as black triangles. The relative location of primers used for genotyping are shown as half-arrows and are labeled a, b, and c.

(B) The genotypes of embryos from heterozygous intercrosses. Shown is a gel displaying PCR products using primers a and b, identifying the normal allele, and primers a and c, identifying the normal allele, and primers a and b, identifying the uninterrupted allele. The PCR loaded into the water lane lacked template DNA and acts as a negative control. +/- represents wild-type; +/– represents Ago2 heterozygote; +/- represents Ago2 homozygous mutant.

(C) Western blot analysis of AGO2 in e7.5 wild-type ( +/-) and Ago2 homozygous mutant (+/-) embryos. EIF4E was used as a loading control.

(D) Variable phenotype of Ago2 homozygous (Ago2–/–) mutant embryos at e9.5. Shown here are three littersmates. The variable Ago2–/–phenotypes included decidua containing only embryonic remnants (ii and iii). This phenotype also was variable as either remnants of embryoid structures (ii) or as cell masses lacking obvious embryonic development (iii). Note the size magnification of the embryonic remnants, as they are much smaller than the wild-type (WT) littermate (i).
expression into the epithelial cell layer (Figure 2F and 2H), these data suggest that Ago2 could play a role in defining the primitive streak. The attenuation of Ago2 expression as cells enter the primitive streak also raises the possibility that AGO2 plays a role in EMT. Indeed, failure to undergo proper EMT is a phenotype observed in embryos with defects in mesoderm development [21]. By contrast, because T is expressed throughout the epiblast of the Ago2 mutants (Figure 2B [inset], 2F, and 2H), these mutants likely exhibit aberrant EMT because an excess of epithelial cells are being fated to become mesoderm, which ultimately could result in expanded mesoderm at the expense of the epithelial cell layer.

Among the mesoderm cell types induced by T expression are the axial and paraxial mesoderms, both of which derive the skeletal tissues that contribute to tail development in vertebrates (reviewed in [22]). In fact, the level of T expression correlates directly with tail length, as evidenced by the short-tail phenotype long recognized in heterozygous T (T+/+) mice [12]. Remarkably, previous mapping of T modifier loci defined a small interval on chromosome 15 that includes the Ago2 locus [13]. In order to genetically test whether Ago2 could be the gene responsible for modifying the tail length in T/+ mice, we crossed mice heterozygous for the T deletion with mice heterozygous for the Ago2 disruption (Ago2+/–). We plotted the ratio of tail length to body length for a quantitative comparison of heterozygous mice with double heterozygotes (Figure 3A). While the average tail-to-body ratio in both wild-type and Ago2+/– mice is approximately

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**Table 1. Full-term and Embryonic Litter Numbers From Ago2 Heterozygous Crosses**

<table>
<thead>
<tr>
<th>Stage</th>
<th>Wild-Type</th>
<th>Heterozygote</th>
<th>Homozygote</th>
<th>p-Value</th>
</tr>
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<td>17</td>
<td>33</td>
<td>0</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>e7.5 Embryo</td>
<td>17</td>
<td>48</td>
<td>15</td>
<td>0.192</td>
</tr>
<tr>
<td>e9.5 Embryo</td>
<td>27</td>
<td>82</td>
<td>12</td>
<td>0.0001*</td>
</tr>
</tbody>
</table>

*Indicates this p-value was calculated without the addition of the embryonic remnants.

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**Figure 2.** The Homozygous Disruption of Ago2 Results in an Expansion of T Expression and Mesoderm Formation

(A, B) Whole-mount in situ hybridization using an antisense probe against T on e7.5 wild-type (A) and Ago2−/− (B) embryo littermates. The Ago2−/− embryos exhibit an expansion of the primitive streak (block-arrow). Note that Ago2−/− e7.5 embryos are smaller and rounder than wild-type, suggesting aberrant growth. The scale bar represents 200 μm. (A, B, insets) Sections from whole-mount in situ hybridized e7.5 embryos. Shown are representative wild-type (A, inset) and Ago2−/− embryos (B, inset). The scale bar represents 50 μm.

(C–H) Paraffin sections from Ago2+/– (C, D, G) and Ago2−/− (D, F, H) e7.5 embryos were stained with antibodies against β-galactosidase (C, D, G; blue) and BRACHYURY (E, F, G; red). Coexpression of the proteins will appear yellow (G, H; merge). At this stage, wild-type Ago2 expression is restricted to the epithelial cell layer, and it does not overlap with BRACHYURY in the primitive streak. The scale bar represents 50 μm. The arrows denote the relative location of the primitive streak. The brackets indicate the approximate region of the mesoderm layer and/or the epithelial cell layer. m = mesoderm layer; ec = epithelial cell layer.

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Dicer expressed in the epithelial cell layer. However, in micro-RNA pathway [11] to cleave and degrade T (upper) quartiles of the scatter plot data. The of the notches are located at the median confidence intervals. The extreme endpoints of the notched-box plot represent the 25% (lower) and the 75% (upper) quartiles of the scatter plot data. The x-axis shows each genotype name, and n is the number of mice. The y-axis shows the ratio of tail-to-body length. The asterisks denote that the double heterozygotes had significantly greater tail-to-body length ratios relative to single T heterozygotes (p = 0.007).

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Figure 3. The Distribution of Tail Length for Each Genotype
(A) Shown are four mice from the same litter. While the tail lengths are indistinguishable between wild-type (WT) and Ago2 heterozygote (Ago2+/−) mice, the T heterozygote (T+/−) tail is reduced to approximately 30% of wild-type. In contrast, double heterozygous (Ago2+/− T+/−) mice have tail lengths that are approximately 60% of wild-type.

(B) Shown are the raw data (vertical scatterplot) overlaid with a notched-box plot. The center of the notched-box plot is the median, and the endpoints of the notches are located at the median confidence intervals. The extreme endpoints of the notched-box plot represent the 25% (lower) and the 75% (upper) percentiles of the scatter plot data. The x-axis shows each genotype name, and n is the number of mice. The y-axis shows the ratio of tail-to-body length. The asterisks denote that the double heterozygotes had significantly greater tail-to-body length ratios relative to single T heterozygotes (p = 0.007).

0.85, the average ratio in T/+ mice is 0.35 (Figure 3B). By contrast, the average tail-to-body ratio in double heterozygote mice is 0.58; the double heterozygotes have significantly longer tails than the T/+ mice (p < 0.01). Thus, haploinsufficiency of Ago2 results in a partial rescue of the short-tail T/+ phenotype, demonstrating that Ago2 is a genetic modifier of T expression. As an initial investigation to determine whether Ago2 is one of the previously mapped modifiers of T expression [13], we searched the entire Ago2 genomic locus (approximately 80 kb) for single nucleotide polymorphisms (SNPs) [23] and analyzed Ago2 expression between the previously reported background strains. Remarkably, we found only one intronic SNP and that the Ago2 expression levels are indistinguishable between the strains (unpublished data). While this might be interpreted to rule out Ago2 as one of the previously mapped modifiers, this is a gross analysis of Ago2 expression in whole embryos and at only a single stage of development. Indeed, our genetic data clearly show that Ago2 is a modifier of T expression.

These studies reveal a genetic interaction between Ago2 and T and demonstrate that Ago2 mediates mesoderm development. The loss of Ago2 is known to disrupt RISC activity [11], suggesting AGO2 influences T expression via the microRNA pathway. Because the homozygous loss of Ago2 results in expanded T expression into the epithelial cell layer (Figure 2F and 2H), AGO2 may utilize its "slicser" activity within the micro-RNA pathway [11] to cleave and degrade T transcripts expressed in the epithelial cell layer. However, in Dicer−/− mutants, RISC activity is disrupted upstream of Ago2, and these mice do not express T at all [24], indicating that either Ago2 is more restricted than Dicer for RISC activity or the other Argonaute protein family members might retain a low level of functional redundancy to partially compensate for the loss of AGO2. Alternatively, AGO2 might regulate upstream inducers of T, such as Bmp4, Eomesodermin, Fgfr1, or Wnt3a [25–28]. Studies conducted in Xenopus laevis have demonstrated that both transforming growth factor α and FGF signaling are required to initiate T expression as gastrulation commences [18,29,30]. In mice, mutational analysis of the known FGF genes established that only Fgfr4 and Fgf8 are required during gastrulation [31,32]. Fgfr4 and Fgf8 are coexpressed throughout the primitive streak in an opposing gradient, with Fgf8 expression highest at the posterior end of the streak and barely detectable at the anterior end. Subsequent genetic studies determined that FGF receptor 1 (Fgfr1) is required for the initiation of T expression in the posterior end of the primitive streak, suggesting that Fgf8 is the likely ligand in this region [33]. We examined the expression of Fgf8 in Ago2 null embryos by whole-mount in situ hybridization and found that homozygous disruption of Ago2 results in expanded expression of Fgf8 compared to its expression in wild-type c7.5 embryos (Figure 4A and 4B), reminiscent of the expanded T expression pattern (Figure 2A and 2B). These data suggest abnormal FGF signaling causes the expanded T expression in Ago2−/− embryos.

In the mouse, direct upstream inducers of Fgf8 are not precisely characterized, but the homozygous loss of either Bmp4 or Eomesodermin (Eomes) results in failure to express both Fgf8 and T [27,28]. We therefore examined the expression of Bmp4 and Eomes in Ago2-null embryos by whole-mount in situ hybridization and found that homozygous disruption of Ago2 results in expanded expression of Eomes compared to its expression in wild-type c7.5 embryos (Figure 4C and 4D), which is consistent with previous data suggesting that Eomes and Fgf8 function similarly during gastrulation [28,34].
contrast, despite the morphological differences, the localization of Bmp4 expression is indistinguishable between Ago2 mutants and their wild-type littermates, in that Bmp4 expression in Ago2 mutants remains restricted to the extraembryonic ectoderm and the proximal embryonic tissue (Figure 4E and 4F). Taken together, these data suggest that Eomes is an upstream inducer of Fgf8 and that Bmp4 is either upstream of Eomes or in a parallel pathway to induce Fgf8 and T gene expression. Finally, as with T, the expansion of both Fgf8 and Eomes expression in the Ago2 mutants is varied, which again suggests a plausible explanation for those Ago2 mutants that escape gastrulation arrest and develop until midgestation ([11]; unpublished data).

The induction of T expression has been studied extensively in the 15 years since the gene was cloned. These studies attribute the restricted initiation of T expression to morphogenetic movements and cell signaling cascades by showing that disruption of these processes ultimately results in aberrant T expression and mesoderm development [27,28]. Coupled with earlier work in X. laevis demonstrating that Bmp4 induces Eomes transcription [35], our data suggest a T induction working model in which Bmp4 is also an upstream inducer of Eomes in mouse (Figure 5). At the commencement of gastrulation in wild-type embryos, Ago2 may regulate the proper level of Eomes gene expression, which ultimately induces the downstream expression of Fgf8 and T. In the absence of Ago2, Eomes may not be regulated properly, leading to its overexpression and a resultant downstream overinduction of Fgf8 and T. Alternatively, Ago2 may regulate an as-yet-unknown upstream inducer of Eomes, or Ago2 may simultaneously have a direct influence on Fgf8 and T gene expression. Because AGO2 is best known to associate with micro-RNA, it might be notable that we find computational algorithms have predicted micro-RNA binding sites in Eomesodermin, Fgf8, and T [http://microrna.sanger.ac.uk/targets/v3/], suggesting the modifying influence of Ago2 is mediated by the micro-RNA pathway, although experimental validation of these micro-RNA binding sites awaits further study. In this case, AGO2 may utilize its “slicer” activity within the micro-RNA pathway [11] to cleave and degrade Eomesodermin, Fgf8, and/or T transcripts expressed outside the primitive streak. Distinguishing among these models will

Figure 4. The Homozygous Disruption of Ago2 Results in a Disruption of FGF Signaling

(A–F) Whole-mount in situ hybridization using an antisense probe against Fgf8, Eomesodermin, or Bmp4 on e7.5 wild-type (A, C, E) and Ago2+/− (B, D, F) embryo littermates. The Ago2+/− embryos exhibit a lateral expansion of Fgf8 and Eomesodermin expression away from the primitive streak (B, D; block-arrow). In contrast, the localization of Bmp4 expression is indistinguishable between wild-type (E) and Ago2+/− (F) embryo littermates.

(E, F) Embryos imaged with reflective and transmitted light. The scale bar represents 200 μm.

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require further analysis of Ago2-null mice that are also null for potential upstream inducers of T. These possibilities notwithstanding, our findings demonstrate that AGO2 is a key factor both in the regulation of T expression and in mesoderm formation, placing a known component of the RNAi machinery in mammalian germ layer development.

Materials and Methods

Genotype and phenotype analysis. Genomic DNA from tail or ear tissue was isolated according to standard procedures. Embryonic and full-term litters were genotyped for the Ago2 disruption via a standard PCR procedure and the following primers: (a) 5'-CAGTGGCTCCAGATGAAAGCG-3'; (b) 5'-CCAGGAGAGATGA CAGGTGTTG-3'; and (c) 5'-GTGTTCCAGTCAGGCGTTG-3'.

The heterozygous T mice (B10:1Fla-ala T (b+) / f) were purchased from The Jackson Laboratory. The Ago2 (0.25) mice are on a congenic C57Bl/6 background, as all the mice used have been backcrossed at least ten generations onto a C57Bl/6 background. While it has been demonstrated that the background strain can affect the heterozygous T tail phenotype, this phenotype is not affected in strains on C57Bl/6 background (e.g., C57Bl/10 and C57Bl/16; [13]). Heterozygote crosses (T(b+) × Ago2 (b+)) were set up, and the offspring (on a mix of C57Bl/6 and C57Bl/10 backgrounds) were aged 6 to 8 wk to allow for the completion of tail development. At this time, ear tissue was taken, to provide a DNA source, and each animal was subjected to a measurement of tail length as a fraction of body length. Offspring were genotyped for the T deletion using SYBR Green in a standard quantitative PCR procedure and the following primers: (d) 5'-CCGGTGCTGTAAGGTAAATGT-3' and (e) 5'-CCTCCATT GAGCTGTGTGGT-3'.

The resultant PCR products were quantified using the iQ5 software package and normalized against a known biallelic locus.

Western blot analysis. Embryos were first dissected free from the yolk sac, which was reserved for DNA extraction, then individually boiled in 30 μl of 2x Laemmli buffer before undergoing SDS 10%–PAGE. After transfer to nitrocellulose membrane, the membranes were blocked with 1% milk in PBS–0.1% Tween 20 (Blotto) and incubated with antibodies against Ago2 (Abnova) and EIF4E (BD Biosciences) for 1 h at room temperature in Blotto. Membranes were washed in Blotto and incubated with horseradish peroxidase–conjugated anti-mouse antibodies (Sigma) for 1 h at room temperature in Blotto. Membranes were washed in Blotto and visualized by chemiluminescence in accordance with the manufacturer’s (New England Nuclear) protocol.

In situ hybridization. Immediately following dissection, embryos were fixed overnight in 4% paraformaldehyde (Electron Microscopy Sciences) at 4 °C. Fixed embryos were washed three times in PBS, dehydrated through a methanol series (25%, 50%, 75%, 2x 100%), and stored at −20 °C. In situ hybridizations were performed on whole-mount embryos, as described [36,37]. Antisense riboprobes were synthesized from Brachury, Fgf8, Eomesodermin, and Bmp4 cDNA-containing plasmids using a digoxigenin-UTP labeling kit (Roche). Digoxigenin-labeled compounds were detected using alkaline phosphatase–conjugated antidigoxigenin (Roche). Whole-embryo images were captured using a dissection scope (Zeiss Stemi) with attached camera (Zeiss AxiosCam MRC). Following in situ hybridization, embryos were paraffin embedded using a standard protocol. Then 10-μm sections were dried to positively charged slides (Surgipath). Dried sections were deparaffinized and hydrated by standard procedures. Sections were imaged using a Zeiss Axioscope with attached camera (SPOT, Diagnostic Instruments, Inc.).

Immunohistochemistry. Immediately following dissection, embryos were fixed for 2 to 3 h in a 6:3:1 ratio of 100% EtOH/37% formaldehyde (Fisher)/100% acetic acid (Fisher) at 4 °C. Fixed embryos were washed 3x in PBS and were paraffin embedded using a standard protocol. Then 10-μm sections were dried to positively charged slides (Surgipath). Dried sections were deparaffinized and hydrated by standard procedures, before blocking endogenous peroxidases in 100% methanol/3% hydrogen peroxide for 10 min at room temperature. Sections were then rinsed with water and PBS prior to antigen retrieval using a standard procedure (Dako). Following PBS washes, sections were blocked in 5% donkey serum/2% BSA for 1 h at room temperature. Blocked sections were incubated overnight with primary antibodies against T (Santa Cruz) and β-galactosidase (Cappel) at 4 °C. Sections were then rinsed in PBS and incubated for 1 h with the corresponding secondary antibodies (Invitrogen) at room temperature. Sections were rinsed in PBS and coverslips were mounted with n-propyl gallate (Sigma). Confocal imaging was performed using the ×20 objective lens and a Zeiss LSM 510 confocal microscope system (Figure 2).

Statistical analysis. We initially applied a Shapiro-Wilk test to our data to determine whether tail-to-body length ratios followed a normal distribution. When results indicated that the distribution was not normally distributed (p = 0.0043), we applied a nonparametric test of independent samples (Wilcoxon rank-sum) to assess differences in the tail-to-body length ratios between single heterozygotes and double (T+/Ago2–/–; n = 33) heterozygotes. The double heterozygotes were found to have significantly greater tail-to-body length ratios compared with single heterozygotes (p = 0.007). The endpoints of notches on the notched-box plot are located at the median ± 1.58 (IQR/√n) squared root of n, where IQR represents the interquartile range and n is the subgroup sample size [38].

Supporting Information

Figure S1. The Homozygous Disruption of Ago2 Results in a Variable Expansion of T Expression

(A–C) Whole-mount in situ hybridization using an antisense probe against T on e7.5 wild-type (A) and Ago2–/– (B, C) embryos. The Ago2–/– embryos exhibit an expansion of the primitive streak (block–arrow). The expansion can be classified as either partial ([B]; 9/17 Ago2–/– mutants) or profound ([C]; 8/17 Ago2–/– mutants). The scale bar represents 200 μm.

Found at doi:10.1371/journal.pgen.0030227.sg001 (1.4 MB PDF).

Figure S2. The Homozygous Disruption of Ago2 Results in an Expansion of Th6c Expression

(A, B) Whole-mount in situ hybridization using an antisense probe against Th6c on e7.5 wild-type (A) and Ago2–/– (B) embryos. The Ago2–/– embryos exhibit an expansion throughout the embryo. The scale bar represents 150 μm.

Found at doi:10.1371/journal.pgen.0030227.sg002 (57 KB PDF).

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Author contributions. RSA, PJ, and TC conceived and designed the experiments. RSA performed the experiments. RSA, ME, TC, and STW analyzed the data. RSA and STW contributed reagents/materials/analysis tools. RSA, TC, and STW wrote the paper.

References


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