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Translation Repression by Maternal RNA Binding Protein Zar1 is Essential for Early Oogenesis in Zebrafish

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Abstract

Large numbers of maternal RNAs are deposited in oocytes and are reserved for later development. Control of maternal RNA translation during oocyte maturation has been extensively investigated and its regulatory mechanisms are well documented. However, translational regulation of maternal RNAs in early oogenesis is largely unexplored. In this study, we generated zebrafish *zar1* mutants which result in early oocyte apoptosis and fully penetrant male development. Loss of p53 suppresses the apoptosis in *zar1* mutants and restores oocyte development. *zar1* immature ovaries show upregulation of proteins implicated in endoplasmic reticulum (ER) stress and the unfolded protein response (UPR). More importantly, loss of Zar1 causes markedly upregulation of zona pellucida (ZP) family proteins, while overexpression of ZP proteins in oocytes causes upregulation of stress related *activating transcription factor 3* (*atf3*), arguing that tightly controlled translation of ZP proteins is essential for ER homeostasis during early oogenesis. Furthermore, Zar1 binds to *zona pellucida* (*zp*) mRNAs and represses their translation. Together our results indicate that regulation of translational repression and de-repression are essential for precisely controlling protein expression during early oogenesis.

Key Words: Zar1; Zona pellucida; oogenesis; p53; zebrafish; translational control; ER stress; unfolded protein response; apoptosis; sex differentiation

Introduction

In contrast to spermatogenesis, oogenesis is associated with increasing cell volume and accumulating maternal molecules such as RNAs and proteins, which are essential for oogenesis itself and early embryogenesis. Maternal gene expression is temporally and spatially controlled (Becalska and Gavis, 2009; Curtis et al., 1995; Evans and Hunter, 2005; Li et al., 2010; Richter and Lasko, 2011). In most species, maternal RNAs play central roles during early embryogenesis due to the absence of zygotic transcription at initial embryonic stages. To accomplish their functions during early embryogenesis, some of the maternal RNAs are extensively regulated post-transcriptionally during oocyte maturation and early embryogenesis. For example, maternal mRNA translation can be regulated by cytoplasmic polyadenylation (Richter, 2007; Richter and Lasko, 2011). Maternal RNA stability can also be regulated by micro RNAs, 3'un-translated region (UTR) length, and even codon usage (Barckmann and Simonelig, 2013; Mishima and Tomari, 2016; Norbury, 2013), which can further temporally control protein expression.

In addition to cytoplasmic components, oocytes also maintain complex cell surface structures including glycoprotein containing zona pellucida, which surrounds oocyte plasma membrane and is vital for oocyte integrity. At fertilization in mouse, ZP proteins (such as ZP2 and ZP3) are required to bind to spermatozoa and to initiate acrosome reaction (Conner et al., 2005). In mouse, FIGalpha activates transcription of *Zp1*, *Zp2*, or *Zp3* through an E-box in their promoters (Liang et al., 1997; Soyal et al., 2000). In zebrafish, vitelline envelope (mammal zona pellucida equivalent) starts to form during stage IB follicles. ZP glycoproteins are encoded by multicopy *zp* genes whose expression is tightly regulated at transcriptional and translational levels, yet their regulators remain unclear (Mold et al., 2009). I

Zebrafish oocyte development is closely associated with sex determination (Liew and Orban, 2013). Adult zebrafish possess only testes or ovaries, but juveniles are initially bipotential. Undifferentiated gonads are ovary-like with early stage oocytes

(Maack and Segner, 2003; Takahashi, 1977). These early stage oocytes grow to full-size in females, but degenerate and are replaced by spermatogenesis in males (Uchida et al., 2002). Zebrafish without germ cells develop into male adults, indicating germ cells are essential for female development (Campbell et al., 2015; Draper et al., 2007; Houwing et al., 2007; Siegfried and Nusslein-Volhard, 2008; Slanchev et al., 2005). When oocytes are depleted in juveniles, zebrafish also develop into males (Dranow et al., 2013; Hartung et al., 2014; Houwing et al., 2008; Rodriguez-Mari et al., 2010; Rodriguez-Mari et al., 2011; Shive et al., 2010; White et al., 2011). Attenuating apoptosis pathways by loss of p53 restores ovarian development in otherwise all male *fancl* and *brca2* mutants (Rodriguez-Mari et al., 2010; Rodriguez-Mari et al., 2011; Shive et al., 2010). In addition, germ cells and oocytes are also required to maintain female phenotype in adult zebrafish (Dranow et al., 2016; Dranow et al., 2013). Separately, the estrogen pathway activation suppresses apoptosis in mouse and fish ovaries (Janz and Van Der Kraak, 1997; Kim et al., 2009). Estrogen is also essential for zebrafish female development (Dranow et al., 2016; Guiguen et al., 2010). Furthermore, juvenile fish exposed to estrogen are prone to become females (Larsen et al., 2009; Orn et al., 2003).

Maternal genes have been studied in a number of model organisms. *Zar1* (*zygotic arrest 1*) is initially identified as a maternal gene in mouse. *Zar1* null female mice generate fully grown oocytes and the eggs can be fertilized, but the resulting embryos fail to develop beyond 2-cell stage, suggesting that *Zar1* is required for very early embryogenesis (Wu et al., 2003a). The molecular regulatory mechanism of ZAR1 in oocytes is largely unknown, but in vitro results suggest that its *Xenopus* homolog may function as a RNA binding protein to regulate RNA translation (Yamamoto et al., 2013). ZAR1s are conserved in vertebrates and contain an atypical plant homeodomain (PHD) zinc finger (Znf) domain in C-terminus (Wu et al., 2003b). In this report, we reveal that Zar1 functions by repressing *zp* RNA translation thereby preventing overload of ZP proteins in early oocytes. Our results indicate that Zar1 is critically required for early oogenesis.

Results

Zebrafish *zar1* null mutants exclusively develop into adult males

To study Zar1 functions, we first examined *zar1* RNA expression. Zebrafish *zar1* is expressed in ovaries but absent in testes (Fig. 1A). *zar1* RNA is highly expressed in primary growth (Stage I) and cortical alveolus (Stage II) oocytes (oocyte staging according to Selman et al. (Selman et al., 1993)) (Fig. 1A). Zar1 protein was also detected in Stage I and II oocytes but not in Stage III oocytes (Fig. 1B). We generated *zar1* mutants by TALEN system (Fig. 1C-E) and CRISPR/Cas9 system (Fig. S1) (Chang et al., 2013; Huang et al., 2011; Li et al., 2011). Several mutant lines were obtained. We focused on the $zar1^{gd5}$ mutant line (Fig. 1E) and the $zar1^{gd6}$ mutant line (Fig. S1C). Immunoblotting results indicate that Zar1 protein is absent in both $zar1^{gd5/gd5}$ (Fig. 1F) and $zar1^{gd6/gd6}$ homozygotes (Fig. S1D).

We intercrossed $zar1^{gd5/+}$ heterozygotes to obtain $zar1^{gd5/gd5}$ homozygotes. No morphological difference was observed between $zar1^{gd5/gd5}$ homozygotes and siblings during embryonic and juvenile stages (data not shown). To our surprise, we could not detect adult female *zar1* homozygotes based on external morphology. In contrast, sex ratios in sibling wild-type and heterozygotes were normal (Fig. 2A). Furthermore, histological analysis of adult gonads indicated no ovary in *zar1* homozygotes (Fig. 2B-D). It should be noted that all $zar1^{gd5/gd5}$ homozygous males were fertile. There is no histological difference in testes between the homozygotes and siblings (Fig. 2C, D). Analysis of $zar1^{gd6/gd6}$ homozygotes further suggests that loss of Zar1 causes the all-male phenotype (Fig. S1E). Results in this study were generated using $zar1^{gd5}$, unless otherwise indicated.

To further confirm that the all-male phenotype was due to Zar1 deficiency, we used an oocyte-specific *zp3b* (*zpc*) promoter (Onichtchouk et al., 2003) to drive *zar1* transgene expression in oocytes. *EGFP* driven by the heart-specific *cmlc2* promoter was inserted into the transgenic construct *Tg(zp3b:zar1,cmlc2:EGFP)* to facilitate screening of transgenic zebrafish (Fig. 2E). EGFP positive embryos, indicating

embryos carrying *Tg(zp3b:zar1,cmlc2:EGFP)*, were selected at 48-72 hours post fertilization (Fig. S2A-A'). EGFP positive *zar1* homozygous males were crossed with EGFP positive *zar1* heterozygous females. As expected, all EGFP negative *zar1*$^{-/-}$ homozygotes were male. In contrast, females were recovered from EGFP positive *zar1*$^{-/-}$ homozygotes (Fig. 2F). Accordingly Zar1 expression, albeit at relatively low level, was detected in EGFP positive *zar1*$^{-/-}$ homozygotes (Fig. S2B). Ovaries of the rescued *zar1* homozygous females were morphologically similar to those of the heterozygous females (Fig. 2G, H). Together, these results confirm that the all-male phenotype results from Zar1 deficiency.

Loss of Zar1 results in female-to-male sex reversal

Two possibilities can account for the all-male phenotype of *zar1* mutants. *zar1* homozygous females died out during development; alternatively, *zar1* homozygous females reversed to males. To resolve this issue, we crossed *zar1* heterozygous females with *zar1* homozygous males. If the all-male phenotype is caused by female lethality, the number of homozygotes should be around 1/2 of the number of heterozygotes, assuming the allele segregated in a Mendelian manner. If it is caused by sex-reversal, the numbers of homozygotes and heterozygotes should be similar. The observed survival rate was 91.6% (174 out of 190), indicating the all-male phenotype in *zar1* mutants is not caused by female lethality. The number of *zar1* homozygotes was similar to that of *zar1* heterozygotes (Fig. 3A). Among heterozygotes, about 50% were female. As expected, no females were observed among *zar1* homozygotes (Fig. 3A). These results indicate that the all-male phenotype in *zar1* mutants is caused by female-to-male sex reversal.

To better understand the sex reversal process in *zar1* homozygotes, we examined their gonads at different developmental stages. Undifferentiated gonads in *zar1* homozygotes resembled those in control siblings (heterozygotes and wild-type) at 22 days post fertilization (dpf) (Fig. 3B, C). Only stage I oocytes were detected in these undifferentiated gonads. At 33 dpf, sex is determined, but gonads are immature

(Rodriguez-Mari et al., 2010). At 33 dpf, similar to the control gonads, *zar1* mutant gonads were either immature ovaries (Fig. 3D, E) or immature testes (Fig. 3F, G). From 22 dpf to 33 dpf, oocyte volume increased similarly both in *zar1* mutants and in control siblings. Most oocytes in *zar1* homozygotes resembled the control oocytes. However aberrant vesicles started to appear in *zar1* mutant oocytes (Fig. 3E, arrows), suggesting ovarian development defects occurred as early as 33 dpf. At 39 dpf, stage II oocytes appeared in *zar1* heterozygous ovaries and wild-type ovaries (Fig. 3H). In contrast, oocyte growth appeared arrested in the mutants (Fig. 3I) with obvious aberrant vesicles (Fig. 3I, arrows). The vesicles resemble cortical granules (CGs). To identify the nature of the vesicles, we used *Maclura pomifera* agglutinin (MPA) which recognizes CG contents (Becker and Hart, 1999). Indeed, the aberrant vesicles in the mutant oocytes were MPA positive (Fig. 3L), indicating they are CGs. The CGs in the mutants are larger than those in sibling controls. In addition, the CGs appear in smaller oocytes in the mutants, suggesting that they are prematurely accumulated. We also noticed that CG number in mutant oocytes is far less than that in sibling oocytes (Fig. 3M).

At 50 dpf, *zar1* mutant ovaries became ovotestis, containing both oocytes and spermatocytes (Fig. 3N, O). At 60 dpf, when oocytes reached stage III in control ovaries, spermatogenesis dominated in the *zar1* mutant ovotestis with a few residual stage I oocytes (Fig. 3P, Q). Testis development in *zar1* mutants resembled that in sibling controls (Figs. 3F, 3G, 3J, 3K, and S3). The percentage of immature ovaries at 33-41 dpf in *zar1* homozygotes (54.5%) is similar to that in *zar1* heterozygous controls (56.9%) (Fig. S4). These results further confirm that the all-male phenotype in *zar1* mutants is due to female-to-male sex reversal.

Apoptosis in *zar1* mutants is mediated through p53 pathway

We hypothesized that degeneration of *zar1* homozygous oocytes is mediated by apoptosis. To test this, we used the TUNEL assay to examine apoptosis in immature ovaries at 37-40 dpf. Few apoptotic cells could be seen in immature ovaries of *zar1*

heterozygotes but apoptosis was readily detected in *zar1* homozygous ovaries (Fig. 4A-C). p53 mediated germ cell apoptosis causes gonad transformation in several zebrafish mutants (Rodriguez-Mari et al., 2010; Rodriguez-Mari et al., 2011; Shive et al., 2010). To test whether apoptosis in *zar1* homozygotes is mediated by p53, we crossed $zar1^{-/-}$ males with $p53^{M214K/M214K}$ ($p53^{-/-}$) females and then crossed $p53^{+/-}$;$zar1^{+/-}$ F1 progenies. 8 out of 14 $p53^{-/-}$;$zar1^{-/-}$ double mutants were female while all the other 28 mutant siblings ($p53^{+/-}$;$zar1^{-/-}$ or $p53^{+/+}$;$zar1^{-/-}$) were male (Fig. 4D), suggesting oogenesis arrest in $zar1^{-/-}$ mutants was suppressed by p53 deficiency. $p53^{-/-}$;$zar1^{-/-}$ double mutant ovaries were indistinguishable from control ovaries histologically (Fig. 4E, F), but the chorions of $p53^{-/-}$;$zar1^{-/-}$ double mutant eggs failed to lift upon activation (Fig. S5). As expected, apoptosis was also blocked in $p53^{-/-}$;$zar1^{-/-}$ double mutant ovaries (Fig. 4G-J). Thus, p53 mediated apoptosis contributes to oocyte degeneration in the $zar1^{-/-}$ mutants.

Estrogen treatment restores oogenesis in *zar1* mutants

Estrogen is required for zebrafish female development (Dranow et al., 2016; Guiguen et al., 2010). Furthermore, juvenile fish exposed to 17α-ethinylestradiol (EE2), a synthetic estrogen agonist, are inclined to develop into females (Orn et al., 2003). To explore whether estrogen can affect *zar1* mutant ovarian development, we used EE2 (10 ng/L, 20 to 60 dpf) to treat *zar1* homozygous juveniles. Females were recovered from EE2 treated *zar1* homozygous mutants, although the female percentage in *zar1* homozygotes is not as high as that in *zar1* heterozygotes (Fig. 5A). No obvious histological difference could be detected between EE2 treated *zar1* mutant ovaries and control ovaries (Fig. 5B, C) yet the chorions of eggs from EE2 treated *zar1* mutants failed to lift properly upon activation (Fig. S6).

Estrogen treatment suppresses apoptosis in mouse and fish ovaries (Janz and Van Der Kraak, 1997; Kim et al., 2009). Separately, in breast cancer cells estrogen downregulates p53 target genes including *atf3*, *bgt2*, and *traf4*, which are involved in p53 mediated apoptosis (Bailey et al., 2012). At 33-34 dpf, *btg2* RNA was

downregulated while *traf4a* RNA had similar expression between *zar1* ovaries and control sibling ovaries (Fig. 5D). Only *atf3* was upregulated in *zar1* ovaries (Fig. 5E). Moreover, EE2 treatment was able to repress the *atf3* upregulation in *zar1* ovaries (Fig. 5E). These results suggest that estrogen may function through suppression of some stress-related genes to restore oogenesis.

Loss of Zar1 triggers ER stress and the unfolded protein response (UPR)

The ATF4-ATF3-CHOP cascade has been implicated in ER stress and the UPR (Jiang et al., 2004; Schroder and Kaufman, 2005). ER is involved in protein folding, posttranslational modification, and secretory activities. ER homeostasis is essential for normal cell functions (Wang and Kaufman, 2012). ER homeostasis can be disrupted by misfolded proteins and abnormally elevated secretory protein synthesis. Under ER stress, cells activate the UPR to alleviate ER burden by reducing protein translation, increasing protein degradation, and generating additional chaperones to assist protein folding. When the UPR fails to restore ER homeostasis, cells may undergo apoptosis (Breckenridge et al., 2003; Shore et al., 2011; Szegezdi et al., 2006). The UPR functions through three major pathways, initiated by three ER-localized transmembrane proteins, to restore ER homeostasis. One of them is initiated by protein kinase RNA like ER kinase (PERK). Activation of PERK contributes to the accumulation of activating transcription factor 4 (ATF4) (Bettigole and Glimcher, 2015; Sano and Reed, 2013), which upregulates ATF3 and CHOP expression. We checked expression level of CHOP encoding gene *ddit3* and found that, like *atf3*, *ddit3* was upregulated in *zar1* mutants (Fig. 6A). These results suggest that loss of Zar1 causes ER stress in ovaries.

Lack of specific antibodies against zebrafish antigens prevents us from using immunological methods to analyze ER stress and the UPR targets at protein level. To further study cellular stress in *zar1* mutant ovaries, we quantitatively compared proteomes of *zar1* homozygous ovaries to that of *zar1* heterozygous ones using isobaric tags for relative and absolute quantitation (iTRAQ) technology. We chose

ovaries at 33 dpf based on the following consideration: (i) Prior to 33 dpf, ovaries and testes are nearly indistinguishable morphologically; (ii) At 33 dpf, oocyte sizes are similar in both groups yet aberrant cortical granules start to appear in the mutants, indicating initial oocyte defects. Among more than 5300 proteins identified in ovaries from the two genotypes (Dataset S1), 325 proteins show differential expression ($P < 0.05$) (Dataset S2). 42 proteins were increased or decreased by more than two folds, with five proteins including Zar1 downregulated and 37 proteins upregulated in *zar1* homozygous ovaries (Dataset S2). We examined seven upregulated proteins and analyzed their mRNA expression (Fig. S7). Five of them were also transcriptionally upregulated. RNA levels of the other two were similar between the two groups, suggesting protein upregulation occurs at post-transcriptional level.

Among the 37 upregulated proteins, there are ER stress and the UPR related proteins such as Dnajc3a, Vapb, and Pdia4 (Fig. 6B and Table S1), indicating ER stress and the UPR occurred. If the PERK-ATF4-ATF3-CHOP UPR cascade is a major contributor for oogenesis arrest, we expect to restore female development by inhibiting PERK activity. To this end, we used PERK inhibitors (GSK2606414 and ISRIB) to treat *zar1* homozygous juveniles. In both treatments, females were recovered in *zar1* mutants (Fig. 6C, D), suggesting ER stress and the UPR play an important role in *zar1* oogenesis arrest.

Zar1 regulates translation of ZP proteins

In addition to the three upregulated ER stress related proteins (Fig. 6A and Table S1), there are another 34 upregulated proteins, among which 23 proteins have been annotated in various databases. 17 of them can be classified into two categories (Table S1). Seven proteins are ZP glycoproteins (Fig. 7A), and ten proteins have been implicated in immune regulation (Fig. S8). We speculated that upregulation of ER stress, the UPR, and immunity related proteins are secondary events. We hypothesize that overexpression of ZP glycoproteins in the *zar1* mutants may overwhelm translational and posttranslational machineries in early oocytes and cause ER stress

and the UPR. To test this hypothesis, we overexpressed Zp3b protein in zebrafish oocytes by injection of *zp3b-flag* RNA (Fig.7B). Indeed, *zp3b-flag* injected oocytes showed higher *atf3* expression compared to oocytes injected with control *rfp-flag* RNA (Fig.7C), suggesting ZP overexpression may cause the UPR possibly by overwhelming ER capacities.

We noticed that RNA levels of the seven corresponding *zp* RNAs were not upregulated in *zar1* homozygous mutants, with *zp2l1* transcript level actually downregulated (Fig. 7D) indicating that upregulation of ZP protein occurs post-transcriptionally. One possible role for Zar1 to fit into this model is to function as a translational repressor. As a first step to test the hypothesis, we examined whether Zar1 protein is associated with *zp* RNAs. We first confirmed that affinity purified Zar1 antibodies can specifically immunoprecipitate endogenous Zar1 in juvenile ovaries (Fig. 8A). We compared RNAs precipitated by the antibody between *zar1* mutants and heterozygous siblings. The results indicate that all seven *zp* RNAs are significantly enriched in Zar1 protein precipitate, while control RNAs (*ef1a* and *gapdh*) recovered similarly between the two lysates (Fig. 8B). Furthermore, in a yeast three-hybrid assay (Bernstein et al., 2002; Chen et al., 2014) Zar1 was shown to activate LacZ reporter expression in the presence of either z*p2l1* or z*p3b* RNAs (Fig. 8C, D), suggesting direct protein-RNA interaction. To check whether Zar1 Znf motif is required for the binding, we mutated all of the eight cysteines in the Znf domain to alanines (Fig. S9). Zar1 Znf domain mutant (Zar1-mu) failed to activate the reporter, suggesting the Znf domain is required for the binding (Fig.8C, D). Next, we tested whether Zar1 could repress *zp* mRNA translation in zebrafish oocytes. Using a ZP-luciferase reporter, we showed that wild type Zar1, but not Zar1-mu, downregulated *zp* translation (Fig.8E-G).

Next, using immunoprecipitation and Mass spectrometry (MS) we identified four Zar1 interacting candidates: vitellogenin 4 (Vtg4), Poly(A) binding protein, cytoplasmic 1-like (Pabpc1l/ePAB), eukaryotic translation initiation factor 4E transporter (4E-T), and cytoplasmic polyadenylation element-binding protein 1

(CPEB1) (Fig. S10 and Dataset S3). Results from STRING database search (Franceschini et al., 2013) indicate that Zar1, ePAB, 4E-T, and CPEB1 share an association network with Vtg4 outside of it (Fig. S10A). ePAB, 4E-T, and CPEB1 are all involved in translational regulation and ovarian development (Gray et al., 2000; Guzeloglu-Kayisli et al., 2012; Kamenska et al., 2014; Kasippillai et al., 2013; Voeltz et al., 2001). The interaction of Zar1 with CPEB and ePAB has been reported in *Xenopus* (Cook and Charlesworth, 2015). We confirmed the interaction between Zar1 and 4E-T both in vivo and in vitro (Fig. S10B-D). These results suggest that Zar1 likely interacts with translational regulatory factors to function in a common complex in regulating oogenesis.

Taken together, these results suggest that in early oocytes (stage I and II), Zar1 is required to negatively regulate ZP protein expression through direct Zar1-*zp* RNA interaction. The lack of Zar1 in early oocytes causes excess *zp* RNA translation and the resulting ZP proteins overwhelm ER capacities and cause the UPR and apoptosis (Fig. 8H).

Discussion

Maternal effect genes are relatively less studied compared to somatic genes in vertebrates. Previously, maternal ZAR1 was shown to be essential for early embryogenesis and was proposed to regulate protein translation (Wu et al., 2003a; Yamamoto et al., 2013). In this study, we reveal that zebrafish Zar1 is essential for very early oogenesis. Loss of Zar1 causes early oogenesis arrest and female-to-male sex reversal. Both genetic ablation of *p53* and estrogen treatment restore oogenesis and female fertility. Mechanistically, Zar1 binds to *zp* RNAs and represses their translation, while ZP protein overexpression in oocytes may cause ER stress and the UPR. Our results reveal previously unappreciated functions of Zar1 during early oogenesis.

Zar1 proteins are conserved in vertebrates, but their in vivo targets and molecular functions were largely unknown prior to this study. There are clear functional

differences between zebrafish Zar1 and its mouse homolog. In mouse, *Zar1* mutants develop normally, yet loss of maternal ZAR1 results in two-cell arrest (Wu et al., 2003a). In contrast, zebrafish *zar1* mutants show oogenesis arrest and female-to-male sex reversal. We also noticed that even very low level of *zar1* transgene expression in the homozygotes was sufficient to restore ovarian development. Like the *fancl* mutants, the z*ar1*mutants showed p53 mediated apoptosis and female-to-male sex reversal. In both *zar1* and *fancl* mutants, p53 deficiency can restore ovarian development. *zar1*$^{-/-}$;*p53*$^{-/-}$ double mutants also showed chorion elevation defect. In contrast, it is unknown whether similar chorion phenotype occurs in *fancl*$^{-/-}$;*p53*$^{-/-}$ double homozygous females. Oocyte clearing-out time is also different between *fancl* mutants (32 dpf) and *zar1* mutants (50 dpf). The difference may due to the requirement of Fancl in overall genome stability (Rodriguez-Mari et al., 2011), while Zar1 is involved in translational control of a limited numbers of RNAs.

Undifferentiated gonads in *zar1* homozygotes are indistinguishable from wild-type gonads, indicating that lack of Zar1 does not affect early gonad development prior to sex differentiation. In *zar1* homozygotes, oocyte size at 33 dpf is much larger than that at 22 dpf, indicating that loss of Zar1 does not impair initial gonad differentiation into ovaries. Furthermore, immature ovary to immature testis ratio (at 33-41 dpf) in *zar1* homozygotes is approximately 1:1, which is similar to that in *zar1* heterozygotes, suggesting that Zar1 is not required for initial sex differentiation. The appearance of aberrant cortical granules in *zar1* oocytes at 33 dpf is the initial sign of defective oogenesis, but the mutant oocytes could last more than two weeks before they are cleared out, suggesting that detrimental factors accumulate gradually in the oocytes. Several studies support the hypothesis that oocytes are essential for ovarian development and may suppress testis development (Dranow et al., 2016; Dranow et al., 2013; Hartung et al., 2014; Houwing et al., 2008; Rodriguez-Mari et al., 2010; Rodriguez-Mari et al., 2011; Shive et al., 2010; White et al., 2011). We hypothesize that gradual loss of oocytes leads to testis development in *zar1* homozygous females and eventually causes female-to-male sex reversal.

p53 mediated apoptosis is attributed to oocyte clearance in zebrafish *fancl* and *brca2* mutants (Rodriguez-Mari et al., 2010; Rodriguez-Mari and Postlethwait, 2011; Rodriguez-Mari et al., 2011; Shive et al., 2010). Apoptosis in *zar1* mutants is also mediated by p53 (Fig.4). In *zar1* mutant ovaries, upregulation of ER stress and the UPR related genes suggests that loss of Zar1 causes ER stress and the UPR. This hypothesis was partially supported by *atf3* upregulation upon overexpression of ZP proteins in oocytes (Fig.7C). Both EE2 treatment and p53 deficiency restore ovarian development and female development in *zar1* homozygous females. Previous studies suggest that in some organisms, estrogen can suppress oocyte apoptosis (Janz and Van Der Kraak, 1997; Kim et al., 2009). Hydroxysteroid (17-Beta) Dehydrogenase 1, an enzyme known to catalyze estrogen synthesis (Mindnich et al., 2004), is less abundant in *zar1* mutant ovaries (Dataset S2), suggesting that loss of Zar1 may affect estrogen synthesis. EE2 represses the upregulation of *atf3* in *zar1* mutants, suggesting some crosstalk between the UPR and the estrogen pathways, although additional functions of EE2 cannot be ruled out.

In *Xenopus laevis,* Zar1 binds to Translational Control Sequence (TCS) of *Wee1* and *Mos* mRNAs and represses their translation in immature oocytes (Yamamoto et al., 2013). However, we did not recover Wee1 and Mos in iTRAQ analysis. This may due to the detection limitation of iTRAQ or that Wee1 and Mos may not express during early oogenesis in zebrafish. *zp* RNAs are highly enriched in Zar1 immunoprecipitate in early ovaries (Fig. 8B). Furthermore, Zar1 likely binds to *zp* RNAs directly as shown in the yeast three-hybrid assay (Fig. 8C). The finding that Znf domain mutated Zar1 failed to bind to *zp* RNAs and to repress *zp* RNA translation in oocytes, suggesting that the Znf domain mediates the binding of Zar1 to *zp* RNAs. The exact molecular mechanism that Zar1 represses *zp* RNA translation remains to be investigated. There are a number of means that RNA binding proteins can exert their translational inhibitory functions towards their RNA targets. In general, depolyadenylation is considered as a mechanism to repress mRNA translation, while polyadenylation is used to initiate and enhance translation (Richter, 2007). We notice

that all the 7 *zp* mRNAs have relatively short 5'UTR and 3' UTR (most of them are under 100 bp), suggesting Zar1 may not use *zp* RNA UTRs to regulate translation. However, there might be common binding motifs/secondary structures in *zp* RNAs for Zar1 binding. Bioinformatics and experimental analyses of *zp* RNA structures are warranted. More recently, Amon and colleagues showed that RNA binding protein Rim4 can forms amyloid-like aggregates that translationally repress its target RNAs in gametogenesis (Berchowitz et al., 2015). This mode of mRNA-specific translational repression may be used in zebrafish oogenesis. Zar1 contains a putative low complexity/disordered region, which is usually found in amyloid-like proteins or proteins capable of forming hydrogel (Courchaine et al., 2016; Kato et al., 2012). Whether Zar1 can form amyloid-like structure or hydrogel will be examined experimentally.

Zar1 was reported to be associated with known translation factors, such as CPEB and ePAB (Cook and Charlesworth, 2015). Similarly, we found that zebrafish Zar1 coimmunoprecipited with CPEB, ePAB, and 4E-T. ePAB and CPEB have been shown to control mRNA translation and oogenesis (Gray et al., 2000; Guzeloglu-Kayisli et al., 2012; Voeltz et al., 2001). Human 4E-T controls mRNA decay and represses translation of bound mRNAs (Kamenska et al., 2014). Moreover, 4E-T mutations are implicated in human primary ovarian insufficiency (Kasippillai et al., 2013). Previous studies in *Xenopus laevis* show that CPEB forms RNP complex and interacts with Pabpc1l and 4E-T (Kim and Richter, 2007; Minshall et al., 2007; Standart and Minshall, 2008). We propose that Zar1, as a component of a maternal translational complex, may recruit other translational regulators and repress *zp* mRNA translation in early oocytes. Future study will examine how the translational complex is regulated in zebrafish oocytes.

Materials and Methods

Zebrafish and maintenance

All animal studies in this report were approved by the Institutional Review Board of the Institute of Genetics and Developmental Biology, Chinese Academy of Sciences. Zebrafish husbandry and manipulations were performed as described (Westerfield, 2000). Genotyping for *p53* mutant was performed as reported (Berghmans et al., 2005).

Generation of *Tg(zp3:zar1,cmlc2:EGFP)* transgenic zebrafish

The 412bp promoter of zebrafish *zp3b* (*zpc*) (Onichtchouk et al., 2003) was amplified by PCR with reported primers and cloned in the upstream of *zar1* coding sequence. The *EGFP* sequence under the control of *cmlc2* promoter was cloned into *zar1* construct in different directions. The plasmid containing *cmlc2* promoter was reported previously (Chen et al., 2010). The transgene was introduced into zebrafish genome with the *Tol2* transposon system (Kawakami et al., 2004).

qRT-PCR and statistical analysis

Total RNA was extracted from the isolated gonads using TRIzol reagent (Thermo Fisher Scientific). 2 μg of total RNA was used to synthesize cDNA with M-MLV reverse transcriptase. qPCR was performed using SsoFast EvaGreen Supermix (Bio-Rad) in 10 μl reactions. *ef1a* and *gapdh* were amplified with reported primers (McCurley and Callard, 2008). Additional primers are listed (Table S2). Ovaries from at least six fish were analyzed for each genotype and treatment. Two-tailed unpaired *t*-test was used to determine whether the difference between two groups is significant.

RNA *in situ* hybridization on cryosections

Animals were sacrificed with standard operations (Westerfield, 2000). Ovaries and testes were isolated and fixed in 4% PFA overnight at 4 ^{o}C. Cryosection *in situ*

hybridization was performed as described (Simmons et al., 2007). The full-length *zar1* coding sequences were used to synthesize DIG-labeled probe (Roche).

Histology and TUNEL assay

For juveniles at 22-60 dpf, heads and tails were cut off. The middle parts containing gonads were fixed in Bouin's solution (Sigma) overnight at 4 °C. For adults, ovaries and testes were isolated and fixed in Bouin's solution overnight at 4 °C. Fixed tissues were embedded in paraffin and sectioned at 10 microns. Hematoxylin and eosin staining (H&E staining) was then performed on the sections. Samples for TUNEL assay (Roche, 12156792910) were fixed in 4% PFA.

RNA Immunoprecipitation (RIP)

Ovaries were homogenized and lysed with RIP buffer (20 mM Tris HCl pH 8.0, 137 mM NaCl, 10% glycerol, 0.5% NP-40, 2 mM EDTA, RNase inhibitor and protease inhibitors were added freshly) on ice for 30min. Antibodies were added to the supernatant and incubated for 4 hours with gentle rotation at 4°C. Protein A beads were then added and incubated for 1.5 hours. They were washed for 4 times (10 minutes each). The suspension was divided into two parts for protein and RNA preparation.

Juvenile treatment with EE2 and inhibitors

Working solution: EE2 (Sigma, E4876), GSK2606414 (Selleck, S7307) and ISRIB (Selleck, S7400) were diluted to working concentration with system water. 30 juveniles were put in a 10 liter tank containing the working solution. Fish water was renewed by dripping 20 liters of working solution per day. The juveniles were treated from 20 dpf or 22 dpf to 60 dpf and then transferred to zebrafish housing system and their gender was analyzed one month later.

Oocyte isolation and microinjection

Ovaries were isolated from adult females and transferred into fish oocyte culture media (OCM: 20 mM HEPES, 0.2 mg/ml of BSA, 75% L-15 medium, adjust to pH 7.5) (Mold et al., 2009). Oocytes were dissociated by gentle pipetting. Oocytes at desired stage were collected, microinjected, and cultured in OCM. Stage II oocytes were used to test the function of Zar1. As oocytes earlier than stage IV are easily stressed during in vitro manipulation, only healthy stage IV oocytes were used to test the relation between Zp overexpression and ER stress.

Luciferase assay

zp3b were cloned downstream of Firefly luciferase encoding sequences (*firefly*) in pCS2 vector. *firefly-zp3b*, *rfp-flag*, *zar1*, *zar1-mu* (Znf domain mutated) mRNAs were synthesized in vitro using SP6 Transcription Kit (Thermo, AM1340). *renilla* mRNAs were synthesized in vitro using T7 Transcription Kit (Thermo, AM1344). *firefly-zp3b* mRNAs (200 ng/μl) and *renilla* mRNAs (70 ng/μl) were mixed with *rfp-flag* mRNAs (210 ng/μl), *zar1* mRNAs (260 ng/μl) or *zar1-mu* mRNAs (260 ng/μl). The mixed mRNAs were injected into stage II oocytes (0.2 nl per oocyte). The injected oocytes were cultured in OCM for 4 hours. Luciferase assay was performed using Dual-Luciferase Reporter Assay System (Promega, E1910).

Quantitative proteomic analysis by iTRAQ

At 33 dpf, 10 ovaries for each genotype (*zar1*$^{-/-}$ and *zar1*$^{+/-}$) were pooled together and homogenized in a denaturing buffer (1%SDS, 1 mM sodium orthovanadate, 1 mM sodium fluoride, protease inhibitors) on ice. The iTRAQ analysis was performed as described (Bi et al., 2014; Udeshi et al., 2013) (see supplementary information for details). The UniProt proteome sequences for *Danio rerio* were used for the database searching.

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Author contributions

L.M. and J.Z. designed the experiments and wrote the paper; L.M., Y.Y., F.C., J.F., F.Z. W.M., Y.J., X.H. and L.S. performed the experiments; L.M., X.H., Y.W., D.C. and J.Z. analyzed the data.

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Figures

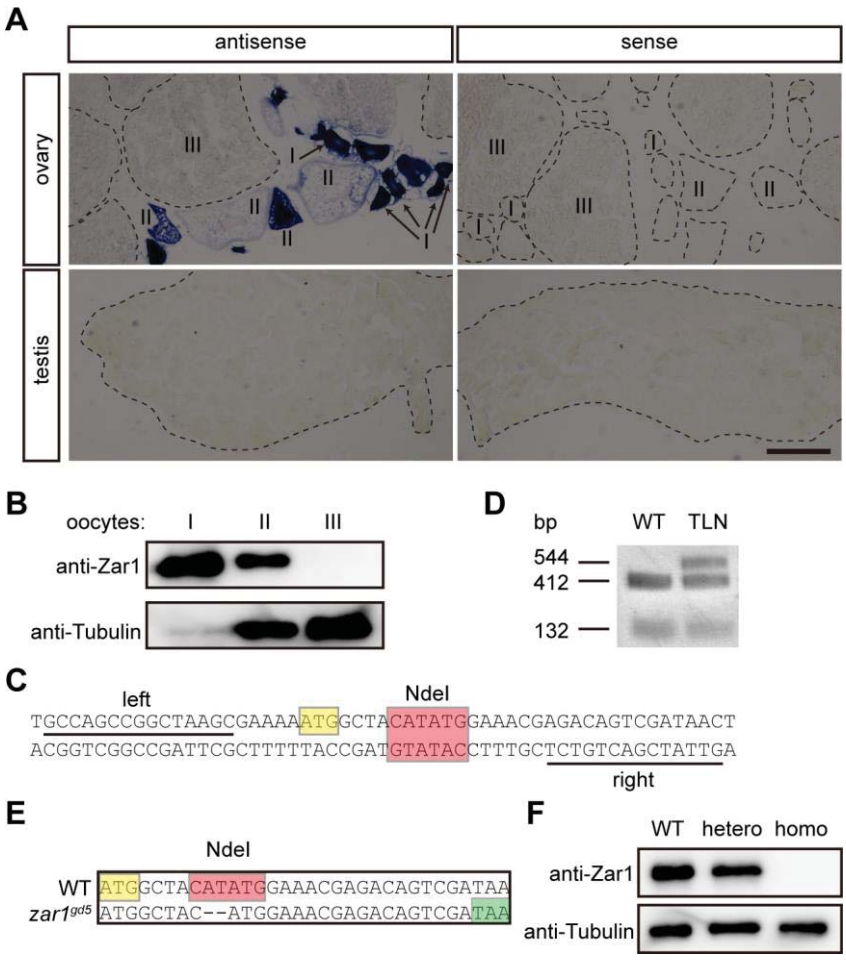

Fig. 1. Generation of a *zar1* mutant with TALENs in zebrafish.

(A) *In situ* hybridization on cryosections of wild-type gonads with *zar1* antisense probe and sense probe. Scale bar: 0.2 mm. (B) Immunoblotting to detect Zar1 protein level in stage I, stage II, and stage III oocytes. 10 oocytes were lysed for each stage. (C) The TALEN sequences for *zar1* mutant generation. (D) Digestion of PCR products from wild-type (WT) and *zar1* TALEN mRNA injected embryos with Nde1 restriction enzyme. (E) DNA sequences of the *zar1*^{gd5} mutant fish line. A premature stop codon was generated. (F) Western blot of Zar1 in gonads from WT, heterozygotes (hetero) and homozygotes (homo) at 25 dpf. DNA sequences highlighted in yellow are the start codon; red are Nde1 recognition sites; green are the premature stop codon.

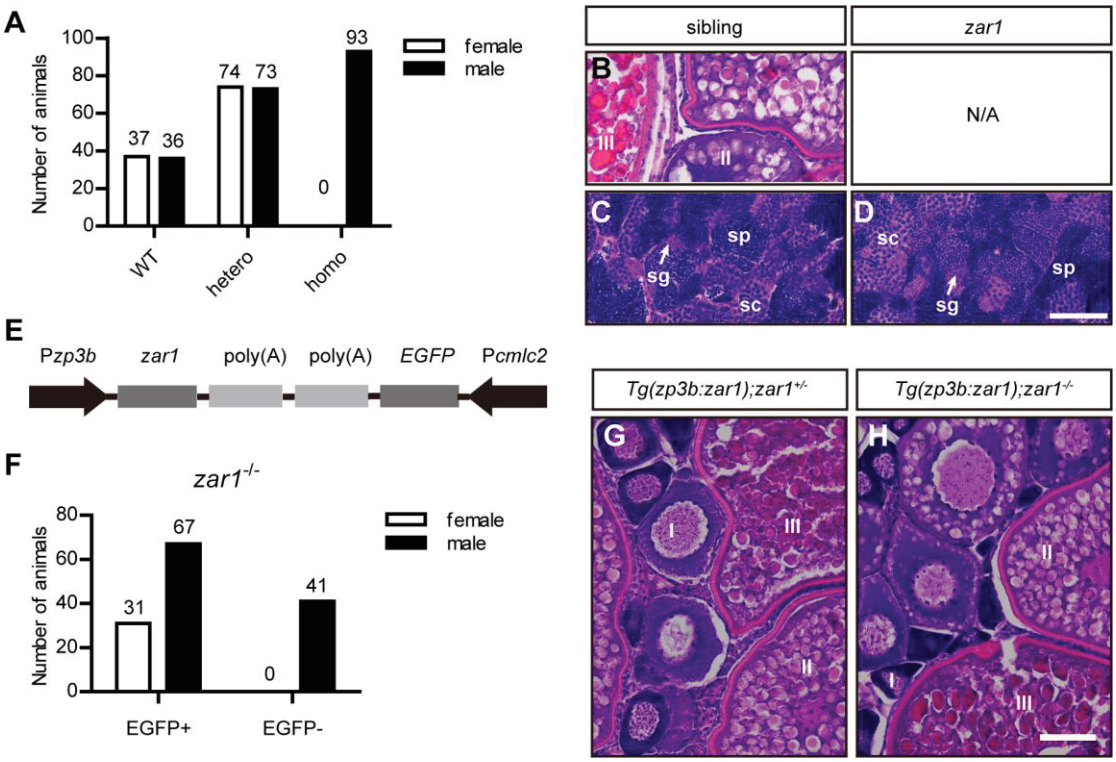

Fig. 2. Loss of Zar1 causes all-male phenotype in zebrafish.

(A) Analysis of genders of *zar1* homozygotes (homo), heterozygotes (hetero), and wild-type siblings. (B-D) Histological analysis of gonads of *zar1* homozygotes and sibling controls by H&E staining. About half of the gonads (20/37) from wild-type and *zar1* heterozygotes were ovaries (B) while the other half (17/37) were testes (C). All the 13 gonads from *zar1* homozygotes were testes (D). (E) Schematic diagram of the *Tg(zp3b:zar1)* transgenic construct. *EGFP* coding sequences were put under *cmlc2* promoter to help visually identify transgenic fish. (F) Gender analysis of $zar1^{-/-}$ homozygotes with or without EGFP signal, indicating *Tg(zp3b:zar1)* transgene. Females were recovered only from $zar1^{-/-}$ homozygotes with the *Tg(zp3b:zar1)* transgene. (G-H) H&E staining of ovaries of $zar1^{+/-}$ heterozygotes and $zar1^{-/-}$ homozygotes on the *Tg(zp3b:zar1)* transgenic backgrounds. Ovaries from the *Tg(zp3b:zar1)* transgene rescued $zar1^{-/-}$ homozygotes are normal histologically. *Tg(zp3b:zar1)*: *Tg(zp3b:zar1,cmlc2:EGFP)*; sg: spermatogonia; sc: spermatocytes; sp: sperm; Scale bar: 0.04 mm.

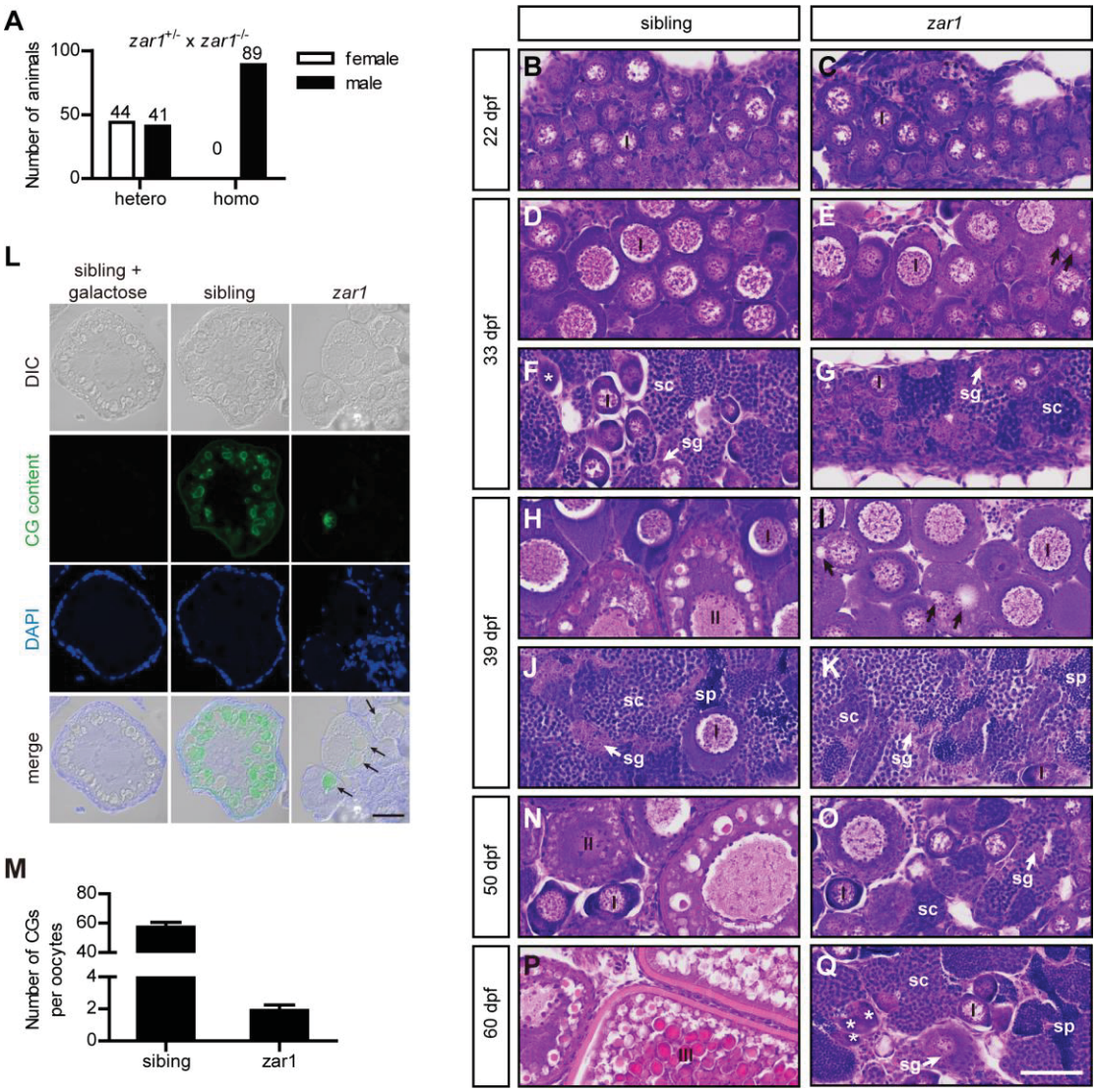

Fig. 3. Zar1 deficiency caused all-male phenotype is due to female-to-male sex reversal.

(A) Analysis of genders of *zar1* homozygotes (homo) and heterozygous siblings (hetero). *zar1*$^{+/-}$ heterozygous females were crossed with *zar1*$^{-/-}$ homozygous males and genders of their progenies were analyzed. (B-K, N-Q) Gonad development of *zar1* homozygotes and control siblings was analyzed by H&E staining. At 22 dpf, zebrafish gonads were undifferentiated. Gonads of *zar1* homozygotes and control siblings were indistinguishable histologically (B-C). At 33 dpf, WT gonads differentiated into immature ovaries and immature testes. Minor developmental abnormality was

observed in *zar1* homozygotes. Oocytes in *zar1* homozygotes were similar to those in wild-type in size and morphology, but aberrant vesicles (arrow indicated) were observed in ooplasm of a few *zar1* homozygous oocytes (D-E). Testis development in *zar1* homozygotes was normal compared to that in control siblings (F-G). At 39 dpf, ovarian developmental abnormality in *zar1* homozygotes became more pronounced (H-I), while testis development in *zar1* homozygotes was similar to the controls (J-K). Immature ovaries in control siblings contained stage I and stage II oocytes (H) while oocytes in *zar1* homozygotes resembled stage I oocytes, indicating oogenesis arrest in *zar1* homozygotes. In addition, aberrant vesicles (arrow indicated) in *zar1* homozygotes increased significantly in size and numbers. (L) MPA (*Maclura pomifera* agglutinin) staining of ovary sections. Juveniles at 37-40 dpf fixed with 4% PFA were embedded in paraffin. Sections (10 μm) were stained with MPA. 0.5 M D-galactose inhibited MPA staining. MPA specifically stains CGs in control siblings. The aberrant vesicles in *zar1* mutant ovaries are MPA positive (arrows). (M) Comparison of CG numbers between *zar1* mutants and siblings. At 50 dpf, stage II oocytes were observed in heterozygous and wild-type ovaries (N), but large numbers of oocytes underwent atresia in *zar1* homozygotes, and spermatogonia and spermatocytes appeared among oocytes, indicating the appearance of transitional ovaries (ovotestis) (O). At 60 dpf, stage III oocytes were seen in the control ovaries (P), in contrast, very few oocytes were left in ovotestis of *zar1* mutants and spermatogenesis further processed (Q). At 22 dpf, six juveniles were analyzed for each genotype. At 33 dpf, 39 dpf, 50 dpf, and 60 dpf, 20 juveniles per stage were analyzed for each genotype. Stars indicate degenerating oocytes. sg: spermatogonia; sc: spermatocytes; sp: sperm; Scale bar: 0.04 mm.

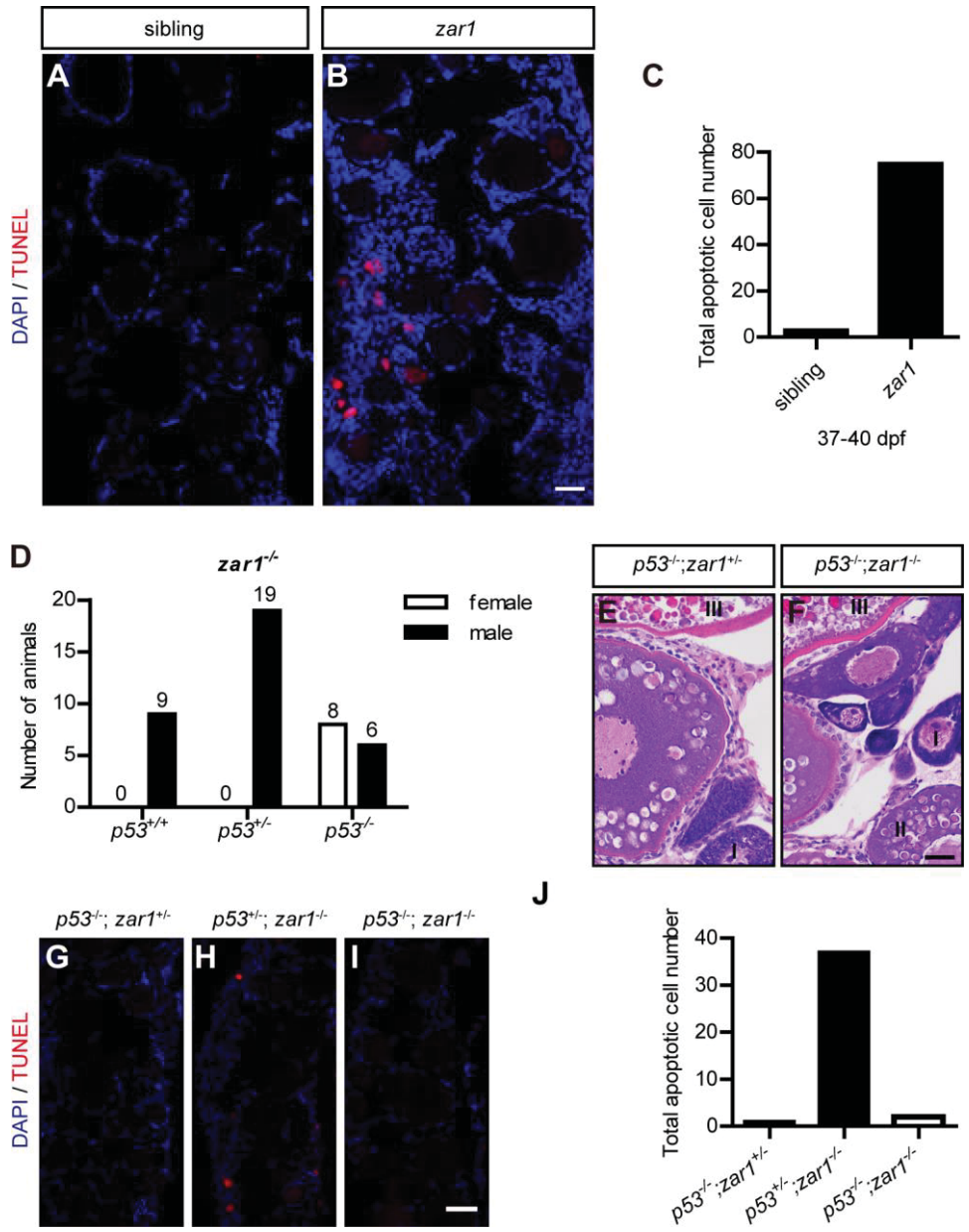

Fig. 4. Zar1 deficiency caused all-male phenotype is due to p53-mediated apoptosis.

(A-C) TUNEL staining of ovary sections of *zar1* homozygotes and control siblings at 37-40 dpf. Obvious apoptotic cells were observed in immature ovaries in *zar1* homozygotes (A), but not in sibling controls (B). (C) Quantification of apoptotic cells. 18 sections from 6 juveniles were counted for each genotype. (D) Gender analysis of *zar1*$^{-/-}$ homozygotes on different *p53* genotype backgrounds (*p53*$^{+/+}$, *p53*$^{+/-}$ *and p53*$^{-/-}$).

Females were only observed in *p53*$^{-/-}$;*zar1*$^{-/-}$ double homozygous mutants. (E-F) H&E staining of sections of *p53*$^{-/-}$;*zar1*$^{+/-}$ and *p53*$^{-/-}$;*zar1*$^{-/-}$ adult ovaries. *p53*$^{-/-}$;*zar1*$^{-/-}$ ovaries were morphologically normal. (G-J) TUNEL staining of ovary sections of *p53*$^{-/-}$;*zar1*$^{-/-}$ ovaries at 37-40 dpf with *p53*$^{-/-}$;*zar1*$^{+/-}$ and *p53*$^{+/-}$;*zar1*$^{-/-}$ ovaries as controls. (J) Quantification of apoptotic cells. 9 sections from 3 juveniles were counted for each genotype. Scale bar: 0.02 mm.

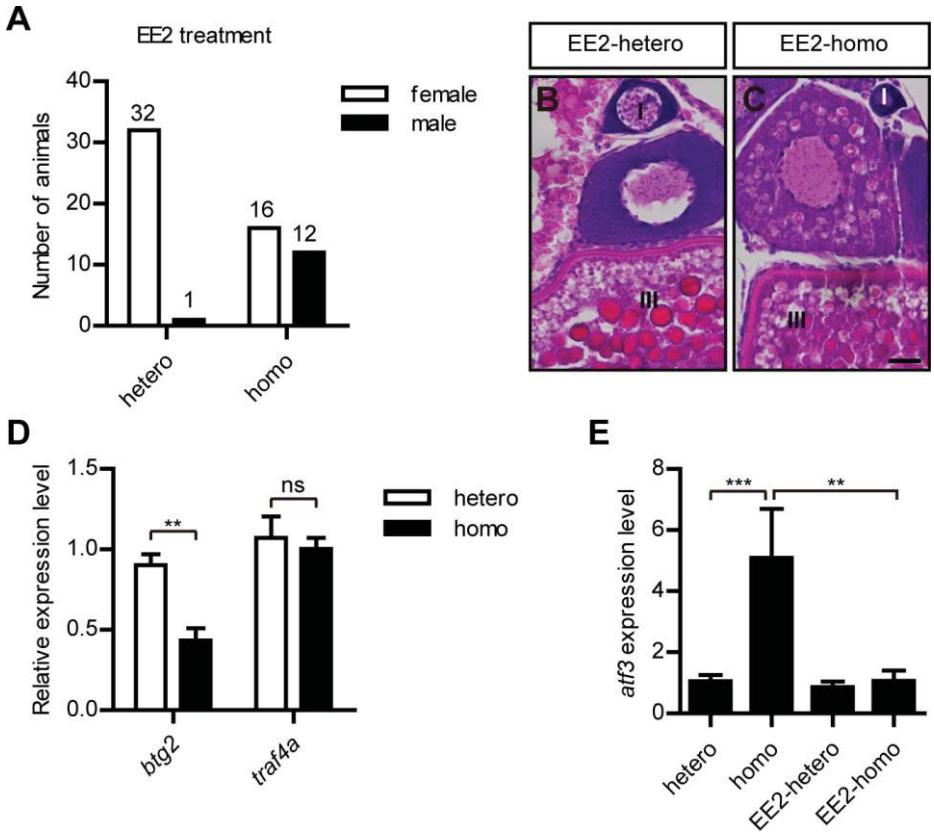

Fig. 5. EE2 treatment restores ovarian development in *zar1* homozygous mutant.

(A)Statistics for sex ratio of *zar1* homozygous and heterozygous mutants under EE2 treatment. (B-C) H&E staining of ovarian tissue in EE2 treated *zar1* homozygotes and heterozygotes. Similar to *zar1* heterozygous ovaries, the treated homozygous mutant ovaries possessed all stages of oocytes. (D) *btg2* and *traf4a* expression analyzed by qPCR in *zar1* homozygotes and heterozygotes. (E) *atf3* expression analyzed by qPCR in *zar1* homozygotes and heterozygotes with or without EE2 treatment. Gene expression was normalized to expression of *elongation factor 1 alpha (ef1a)*. hetero: *zar1* heterozygotes; homo: *zar1* homozygotes; EE2-hetero: EE2 treated *zar1* heterozygotes; EE2-homo: EE2 treated *zar1* homozygotes; ns: not significant; **: $P < 0.01$. Scale bar: 0.02 mm.

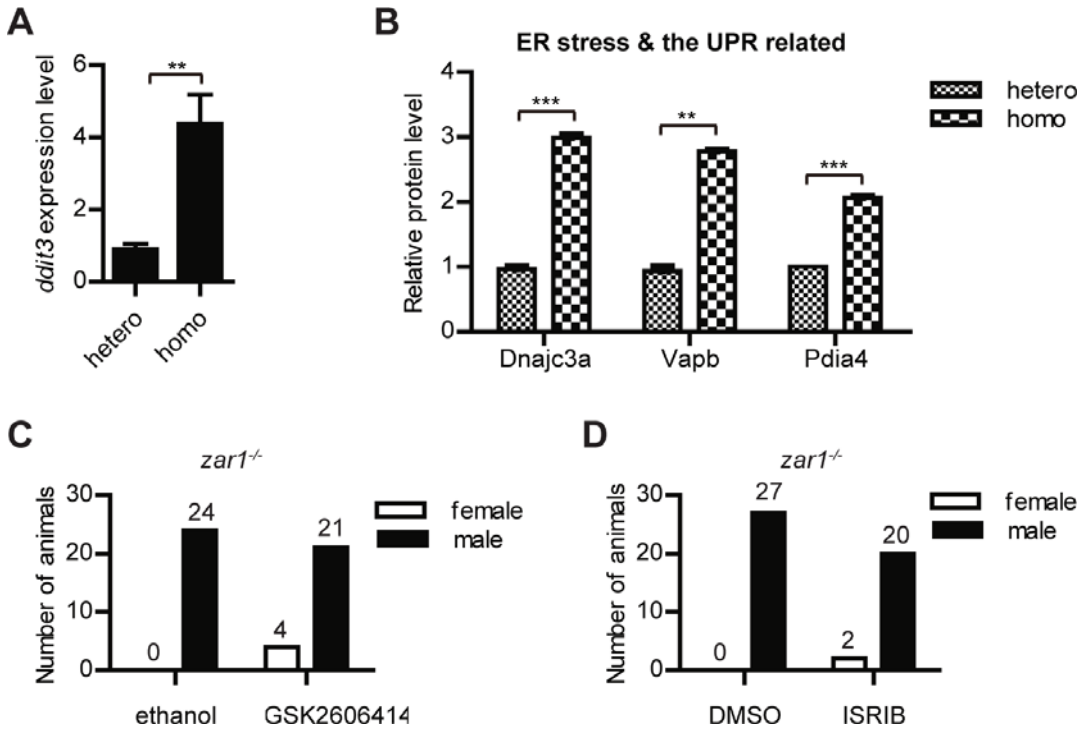

Fig. 6. ER stress and the UPR may be responsible for deprivation of female development of zar1 homozygous mutants.

(A) Transcriptional upregulation of *ddit3*, examined with qPCR, in mutant ovaries at 33-34 dpf. Internal control: *ef1a*. (B) ER stress and the UPR related proteins were upregulated in *zar1* homozygous (homo) ovaries compared to heterozygous (hetero) ovaries at 33-34 dpf determined by iTRAQ. (C-D) PERK inhibitor treatment restored female development in zar1 homozygous mutants. Juveniles were treated with two PERK inhibitors from 22 dpf to 60 dpf. Final concentration: GSK2606414, 6 nM; ISRIB, 50 nM. **: $P < 0.01$; ***: $P < 0.001$.

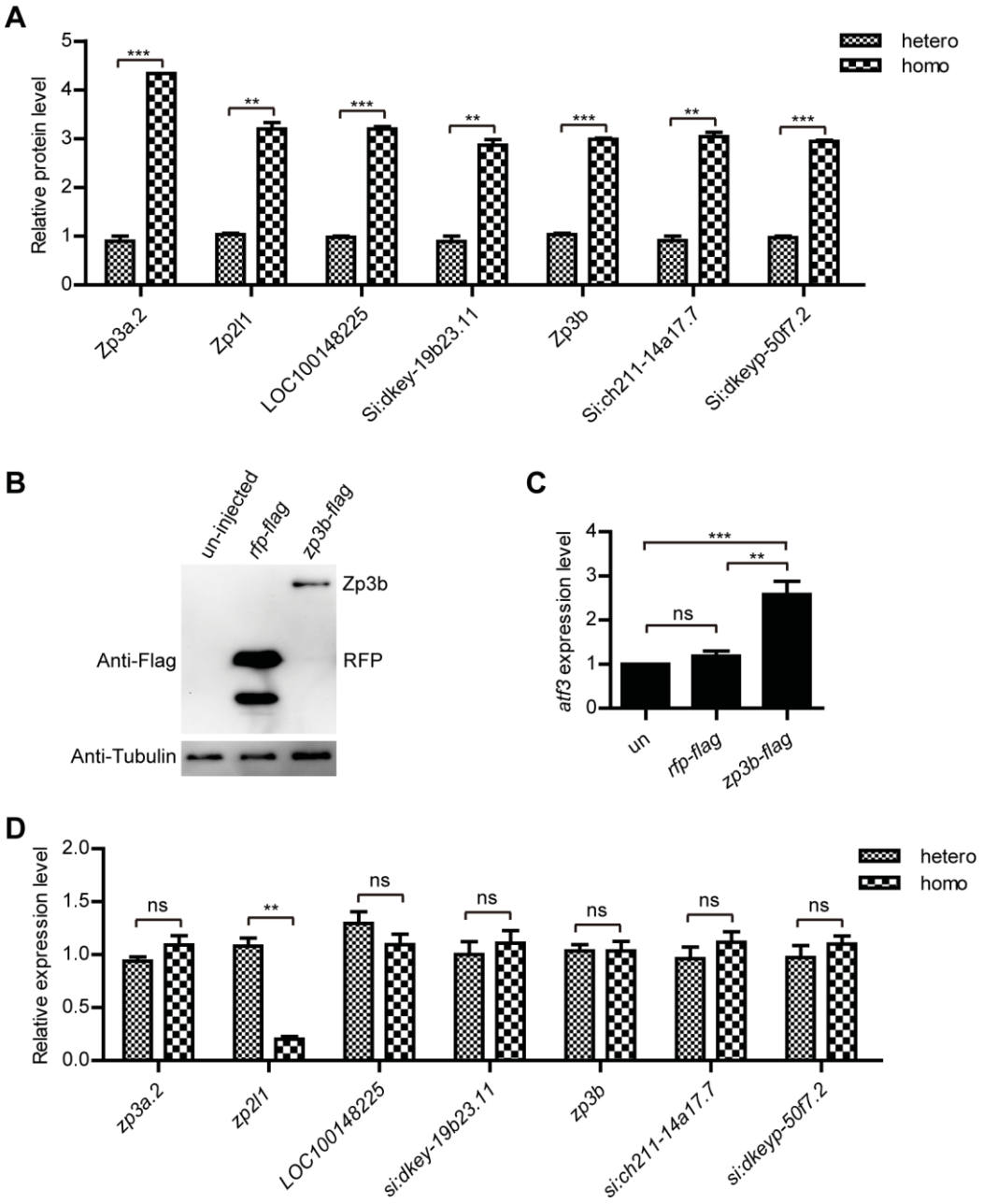

Fig. 7. Translational upregulation of zona pellucida proteins may cause ER stress.

(A) ZP proteins were upregulated in *zar1* homozygous (homo) ovaries compared to heterozygous (hetero) ovaries at 33-34 dpf determined by iTRAQ.

(B-C) Overexpression of *zp3b* in oocytes caused upregulation of *atf3*. Stage IV oocytes were injected with 600 pg of *rfp* or *zp3b* mRNAs. Injected oocytes were

cultured in OCM for 4 hours and collected for RNA and protein extraction with TRIzol reagent. (B) Western blot to confirm the translation of injected mRNAs.
(C) qPCR to detect *atf3* expression in injected oocytes. (D) qPCR to detect *zp* gene transcription. Internal control: *ef1a*. ns: not significant; **: $P < 0.01$; ***: $P < 0.001$.

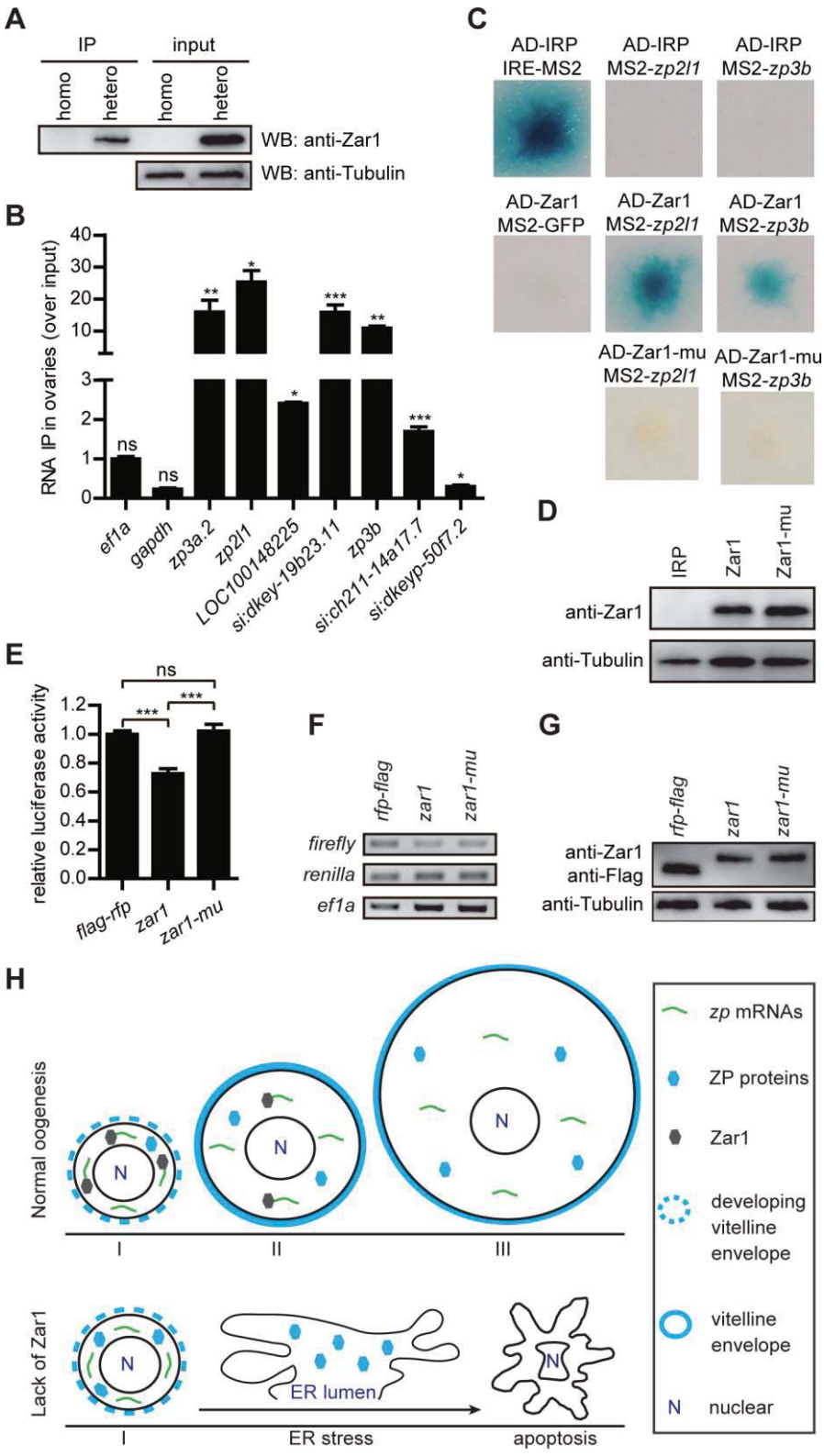

Fig. 8. Zar1 represses translation of ZP proteins in zebrafish oocytes.

(A-D) Zar1 binds to *zp* mRNAs. (A-B) RNA immunoprecipitation with anti-Zar1 antibody from *zar1* homozygous ovaries (homo) and heterozygous ovaries (hetero) at 33-34 dpf. (A) Zar1 protein was precipitated by anti-Zar1 antibody in heterozygous ovaries. (B) qPCR analysis of *zona pellucida* (*zp*) mRNAs immunoprecipitated from heterozygous ovaries with anti-Zar1 antibodies. Relative level of immunoprecipitated ef1a mRNA compared to the input ef1a mRNA was assigned as 1. (C) Analyzing interaction of zebrafish Zar1 and *zp* mRNAs with a yeast three-hybrid system. (D) Western blot analysis indicates expression of Zar1 and Zar1-mu in yeast. (E-G) Zar1 represses translation of Zp proteins in oocytes. (E) Statistics of relative luciferase activity. *zar1* mRNA injection repressed Zp3b translation. Mutation of Zar1 Znf domain abolished its translational repression activity. (F) RT-PCR of injected RNA reporters. (G) Western blot analysis shows expression of RFP-Flag, Zar1, and Zar1-mu. (H) A model of translational regulation of *zp* mRNAs. In early oocytes (stage I and II), Zar1 binds to *zp* mRNAs and negatively regulates their translation. Later, Zar1 proteins are gradually degraded and the translational repression of *zp* mRNAs is removed allowing enough ZP proteins to be used in the vitelline membrane development. The lack of Zar1 in early oocytes causes excess *zp* RNA translation and the resulting ZP proteins overwhelm ER, which cause the UPR and apoptosis. ns: not significant; *: $P < 0.05$; **: $P < 0.01$; ***: $P < 0.001$.

Supplementary information

Translation Repression by Maternal RNA Binding Protein Zar1 is Essential for Early Oogenesis in Zebrafish

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Materials and Methods

Mutant generation and genotyping

The zebrafish *zar1* mutants were generated using the Tübingen strain with TALEN system or CRISPR/Cas9 system. The following primers were used to identify *zar1* mutants generated with TALEN system: for mutant screening a pair of primers (forward primer: 5'-CTTTCCCAAACCTCGAAAATCGT-3'; reverse primer: 5'-GGGGTGAGATTTGGGTTGATCTG-3') were used; for *zar1*^{gd5} mutant line specific genotyping two forward primers (5'-GCGAAAAATGGCTACATAT-3' to detect the WT allele and 5'-GCGAAAAATGGCTACATGG-3' to detect the mutant allele) and a reverse primer (5'-TCCGGGATTCTACTGGGGAGTAA-3') were used

Antibodies

Zar1 antibody was generated with full-length recombinant Zar1 protein purified from *E.coli* by immunizing rabbits and affinity purified with SulfoLink Immobilization Trial Kit (Thermo, 20325). Zar1 antibody was diluted 1:1000. Other antibodies and beads were purchased: 4E-T antibody (Abcam, ab6034, 1:500); tubulin antibody (Sigma, T6074, 1:4000); FLAG antibody (Sigma, F3165, 1:2000); anti-FLAG M2 affinity gel (Sigma, A2220); and protein A beads (Millipore, 16-156).

Quantitative proteomic analysis by iTRAQ

The ovary lysates were boiled for 10 min and centrifuged (12000 rpm, 10 min). The supernatant (100 μg protein / sample) were reduced (10 mM DTT, 37^{o}C, 1 h), alkylated (55 mM iodoacetamide, room temperature, 1 h, in the dark), and transferred to the Microcon YM-30 centrifugal filter units (EMD Millipore Corporation) where the lysis buffer was replaced with iTRAQ dissolution buffer. Samples were digested with trypsin (sequencing grade, 1:50, 37 ^{o}C, overnight). The resulting peptides were labeled, according to the manufacturer's manual with slight modifications, with iTRAQ Reagents (AB Sciex Inc.). Briefly, the peptides were incubated with the ethanol-dissolved iTRAQ reagents (2 h, room temperature), and then terminated by adding H_2O to 30% of the total reaction volume. The labeled samples were mixed together with equal ratios in amount and fractioned by reverse phase HPLC. The mixed peptides were resuspended in 0.5 ml of RP-HPLC solvent A (2% ACN, 5 mM ammonium formate, pH 10), and separated into 10 fractions using the Gemini-NX 5u c18 110A (P/No: 00G-4454-Y0 3*250 mm length, 5 m particle size, Phenomenex) on a Waters e2695 separations module system with a flow rate of 0.4 ml/min. A 97 min basic RP LC method was utilized for offline fractionation. The gradient consisted of an initial increase to 8% solvent B (1.1%B/min) (90% ACN/5 mM ammonium formate, pH 10) followed by a 38 min linear gradient (0.5% B/min) from 8% solvent B to 27% B and successive ramps to 31% B (1%B/min), 39% B (0.5%B/min), and 60% B (3%B/min). The separated peptides were further desalted with C18 StageTips, concentrated with a SpeedVac, resuspended with 0.1% formic acid.

Figures

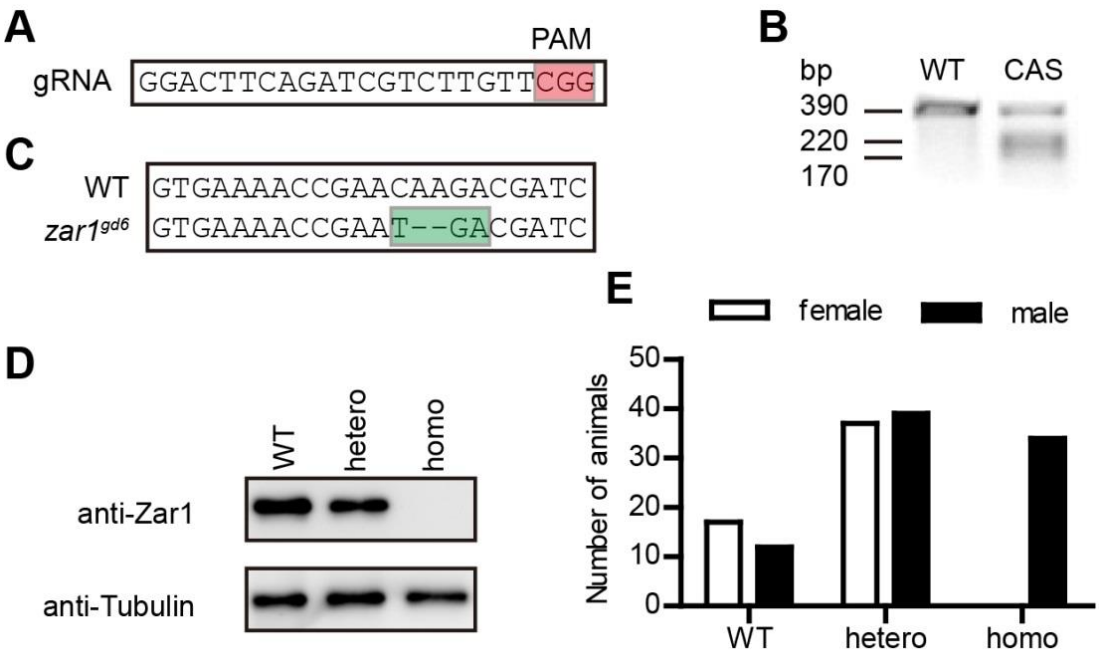

Fig. S1. *zar1* mutant generation with CRISPR/Cas9 system

(A) Selected gRNA sequence. DNA sequences highlighted in red are the protospacer-adjacent motif (PAM). (B) PCR fragments (amplified with the following primers: primer-F: 5'-AGGTCACAGAGACGGTTGACAGC-3' and primer-R: 5'-ACTTTCCCACCGTAGGTTGCAGT-3') were digested with T7 endonuclease I to test the gRNA. (C) DNA sequences of the *zar1*^{gd6} mutant line. Green highlighted DNA sequences are the premature stop codon. Two *zar1*^{gd6} mutant line specific forward primers (5'-CCAGTGAAAACCGAACAA-3' to detect the WT allele and 5'-CCAGTGAAAACCGAATGA-3' to detect the mutant allele) were used together with the reverse primer (primer-R) mentioned above to do genotyping. (D) Western blot of Zar1 in gonads at 25 dpf from wild-type (WT), *zar1*$^{gd6/+}$ heterozygotes (hetero) and *zar1*$^{gd6/gd6}$ homozygotes (homo). Gonads from 8 fish were mixed together and lysed for each genotype. (E) Analysis of the gender of *zar1*$^{gd6/gd6}$ homozygotes (homo), *zar1*$^{gd6/+}$ heterozygotes (hetero) and WT siblings.

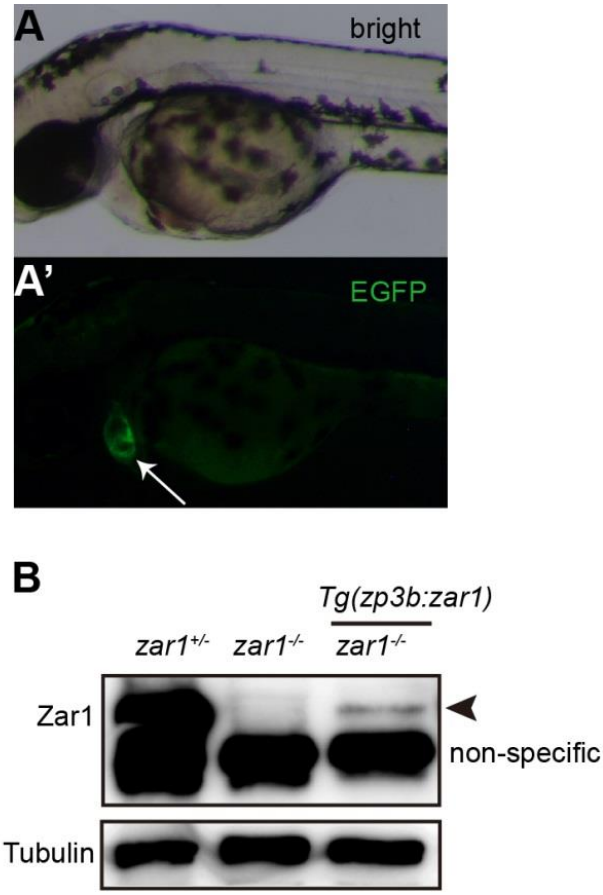

Fig. S2. Zar1 is expressed in *zar1* homozygous females with the *Tg(zp3b:zar1,cmlc2:EGFP)* transgene.

(A, A') Heart specific EGPF signal (arrow) seen in transgenic embryos. (B) Western blot to detect Zar1 protein in adult ovaries. Zar1 was expressed in the transgene rescued adult *zar1* homozygous ovaries (arrowhead). Compared with Zar1 expression level in *zar1* heterozygous mutant ovaries (hetero), Zar1 expression level in transgene rescued *zar1* homozygous (homo) mutant ovaries was low. The smaller bands are non-specific.

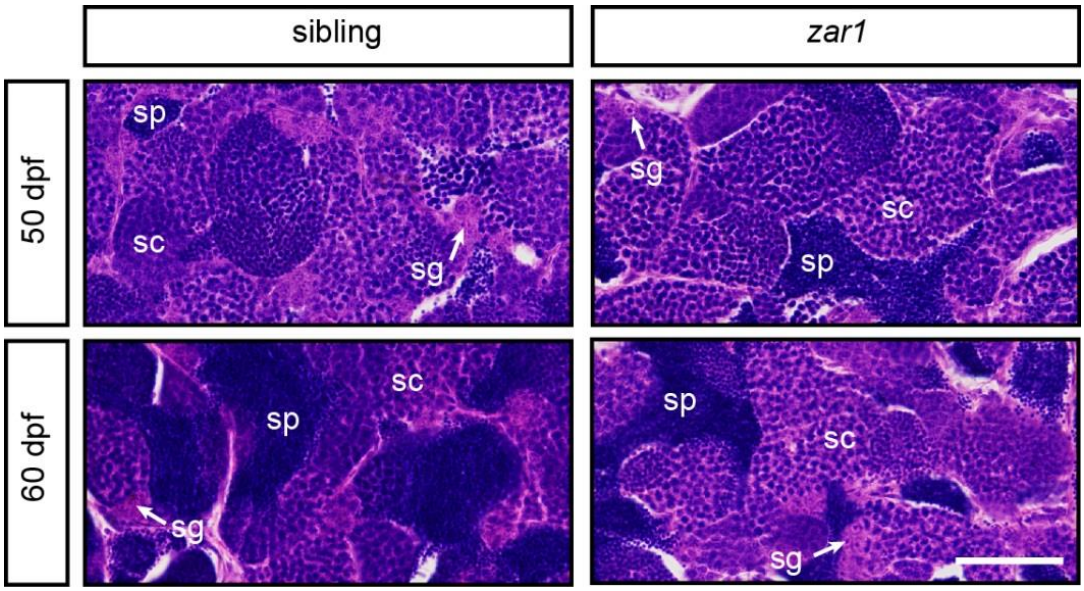

Fig. S3. Spermatogenesis is not affected in *zar1* mutant males.

Histology analysis of testes of *zar1* homozygous males and control siblings at 50 dpf and 60 dpf. Spermatogenesis in *zar1* homozygous males resembles that in control siblings. sg: spermatogonia; sc: spermatocytes; sp: sperm; Scale bar: 0.04 mm.

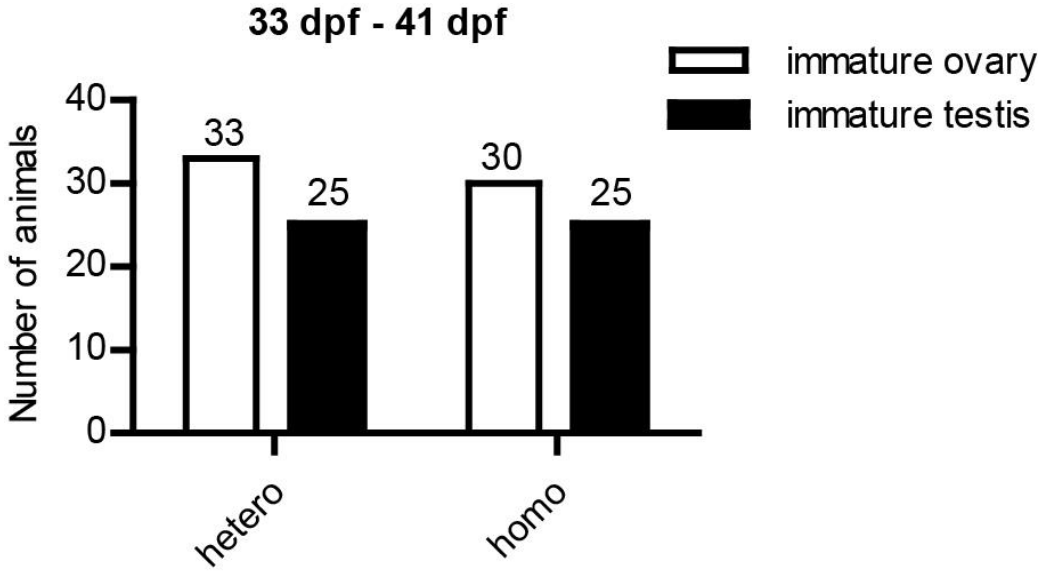

Fig. S4. Sex ratio in juveniles at 33-41 dpf is not affected in *zar1* mutants.

Sex ratios in *zar1* homozygotes (homo) and *zar1* heterozygotes (hetero) at 33 dpf-41 dpf. Sex of *zar1* homozygotes and *zar1* heterozygotes was determined at 33-41 dpf according to H&E staining results.

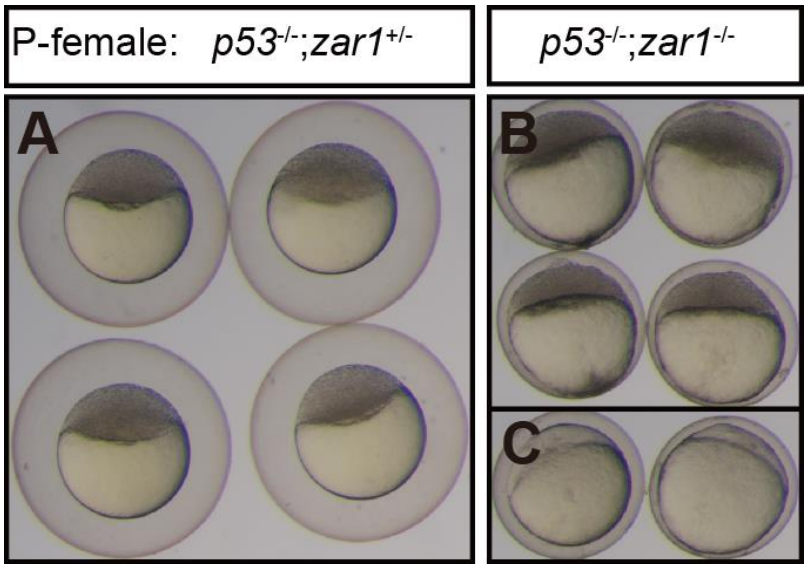

Fig. S5. The chorions of eggs from *p53*$^{-/-}$;*zar1*$^{-/-}$ failed to elevate normally.

Five *p53*$^{-/-}$;*zar1*$^{+/-}$ females and five *p53*$^{-/-}$;*zar1*$^{-/-}$ females were crossed with wild-type males. The chorions of eggs from *p53*$^{-/-}$;*zar1*$^{+/-}$ lifted normally (A). The chorions of eggs from *p53*$^{-/-}$;*zar1*$^{-/-}$ failed to lift. Cleaved embryos (B) and uncleaved embryos (C); P-female: genotypes of the mothers

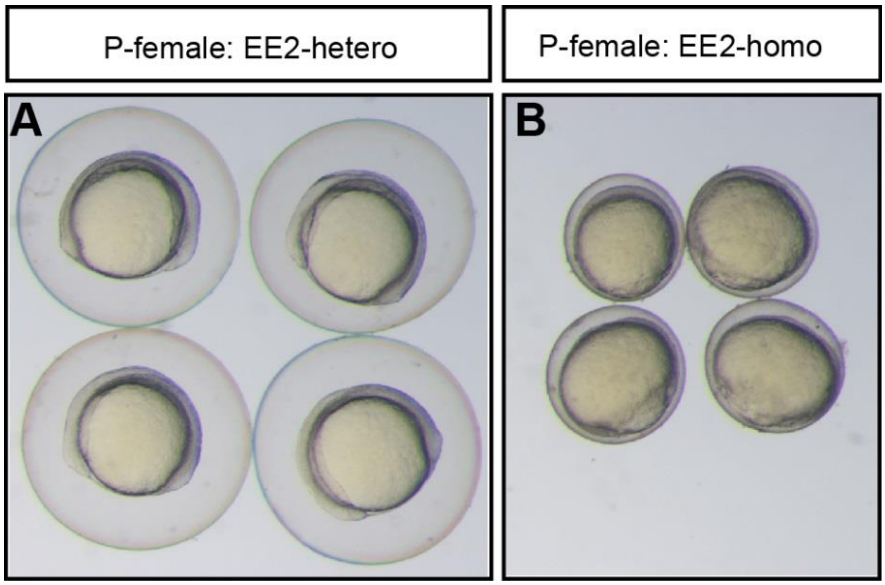

Fig. S6. The chorions of *zar1* mutant eggs failed to elevate normally.

EE2 treated females were crossed with wild-type males. Embryos from 6 heterozygous females (EE2-hetero) and 6 homozygous females (EE2-homo) were analyzed. The chorions of *zar1* homozygotes failed to lift properly compared with those of *zar1* heterozygotes. P-female: genotypes of the mothers.

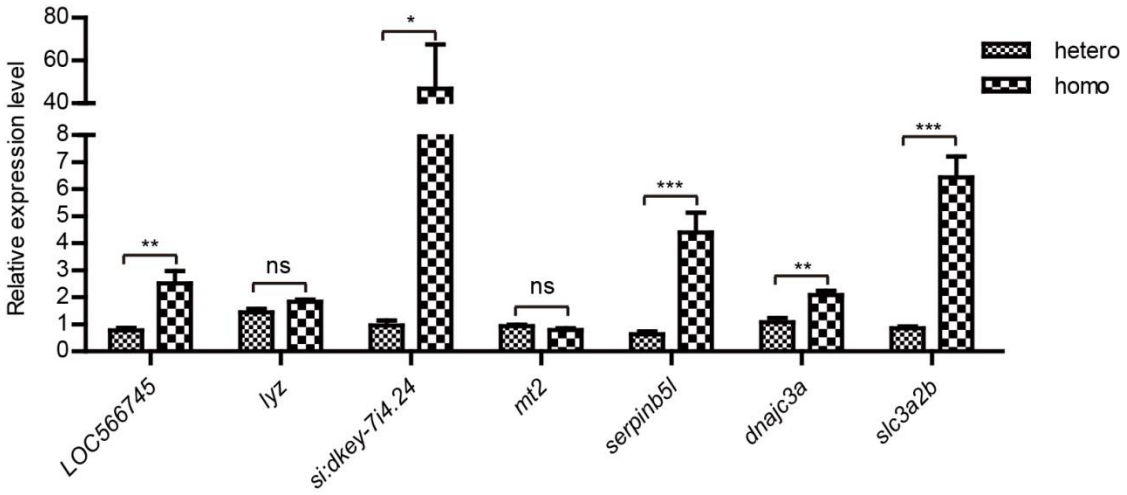

Fig. S7. qPCR to confirm the iTRAQ result.

Statistical analysis of mRNA levels of upregulated genes in *zar1* homozygotes (homo), according to iTRAQ result. Ovaries were isolated from *zar1* homozygotes (homo) and *zar1* heterozygotes (hetero) at 33 dpf. Seven out of the first 25 upregulated genes were tested. Internal control: *ef1a*; ns: not significant; *: P < 0.05; **: P < 0.01; ***: P < 0.001.

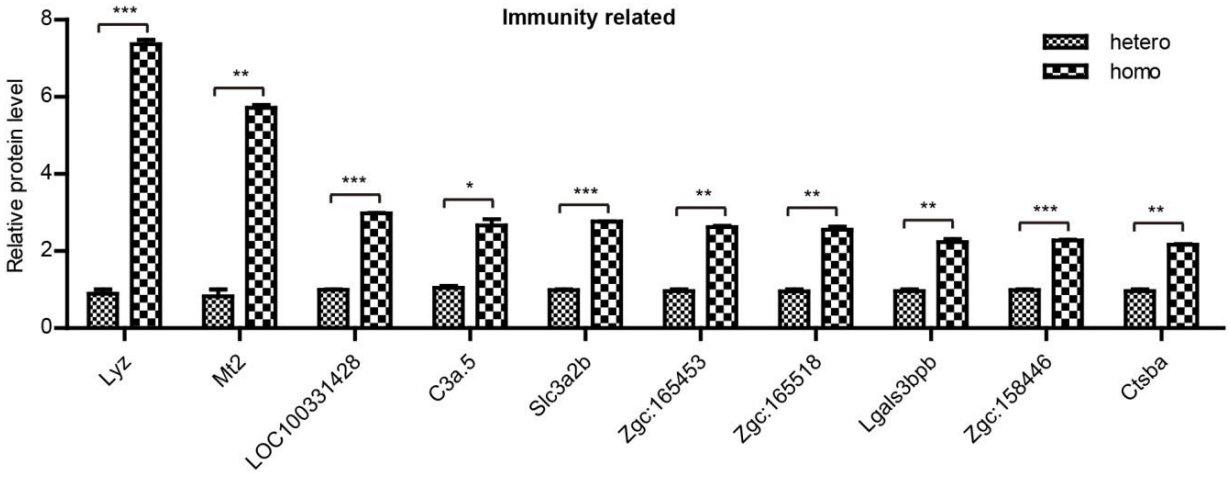

Fig. S8. Immunity related proteins are upregulated in *zar1* mutants.

Statistical analysis of immune related proteins upregulated in *zar1* homozygotes (homo) compared to heterozygotes (hetero) determined by iTRAQ. *: P < 0.05; **: P < 0.01; ***: P < 0.001.

Fig. S9. Mutation of the Zar1 Znf domain.

The 8 cysteines in Zar1 Znf domain are mutated to alanines.

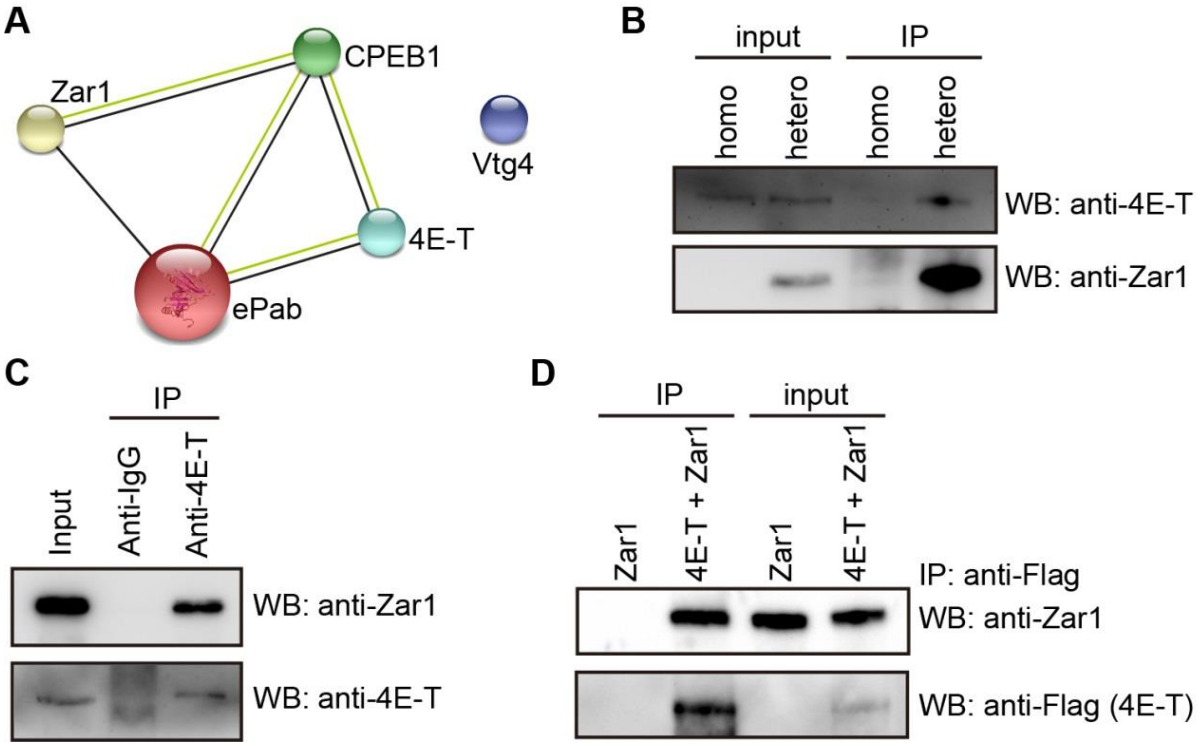

Fig. S10. Interaction between Zar1 and translation initiation factor 4E transporter.

(A) Association analysis of Zar1 with the immunoprecipitated proteins by searching STING database (evidence view). (B) 4E-T was immunoprecipitated by the Zar1 antibody from *zar1* heterozygous ovaries (hetero, $p53^{-/-};zar1^{+/-}$) but not from *zar1* homozygous ovaries (homo, $p53^{-/-};zar1^{-/-}$). (C) Zar1 was immunoprecipitated from ovaries by a 4E-T antibody but not by a control antibody. (D) Zar1 was immunoprecipitated by the Flag antibody from HEK293 cells co-transfected with *zar1* and *eif4enif1-flag* plasmids but not from cells transfected with *zar1* plasmid alone.

Tables

Table S1. The three categories of upregulated proteins (> 2 fold over controls) in *zar1* mutants

Category	Accession	Protein Name	Gene symbol
ER stress & the UPR related	Q6P0U6	DnaJ (Hsp40) homolog, subfamily C, member 3a	*dnajc3a*
	Q6P2B0	Vesicle-associated membrane protein-associated protein B/C	*vapb*
	Q6P3I1	Protein disulfide-isomerase A4	*pdia4*
Zona pellucida proteins	Q5TYP2	Zona pellucida glycoprotein 3a, tandem duplicate 2	*zp3a.2*
	A7MBW8	Zona pellucida glycoprotein 2, like 1	*zp2l1*
	A8WG31	pellucida sperm-binding protein 3	*LOC100148225*
	F1R4N4	Egg envelope glycoprotein-like	*si:dkey-19b23.11*
	A7MBS3	Zona pellucida glycoprotein 3b	*zp3b*
	B0R0H4	ZPC domain containing protein 1	*si:ch211-14a17.7*
	Q5TYX2	ZPA domain containing protein	*si:dkeyp-50f7.2*
Immunity related	Q24JW2	Lysozyme	*lyz*
	Q1LV07	Metallothionein	*mt2*
	F1QYN0	Complement C3-like	*LOC100331428*
	F1QLN6	Complement component c3a, duplicate 5	*c3a.5*
	Q803G1	Solute carrier family 3, member 2b	*slc3a2b*
	E7FCS3	Alpha-2-macroglobulin-liked, duplicate 1	*a2m1*
	F1QF63	Alpha-2-macroglobulin-liked, duplicate 2	*a2m2*
	F1Q6K5	Lectin, galactoside-binding, soluble, 3 binding protein b	*lgals3bpb*
	A2VD28	Complement factor B	*cfb*
	Q6PH75	Cathepsin B	*ctsba*

Table S2. Sequences of primers used in qPCR and RT-PCR.

gene	primers
atf3	F: 5'-TCAATGGCTACTGAATTCCAACTG-3'
	R: 5'-TTCTTGTGGCATGTTATGTGGAC-3'
ddit3	F: 5'-AGTTGGAGGCGTGGTATGAAGAC-3'
	R: 5'-GTCAACCAGGTGAGCGAACAG-3'
btg2	F: 5'-CATTAGAAACCAGACAAATCCTCGT-3'
	R: 5'-GGAGCGGTGCTGTGGTTAAG-3'
traf4a	F: 5'-GAACTCTGGACTCGACATGCTCA-3'
	R: 5'-ATTGCACAAGGCTCATCTTCCTC-3'
LOC566745	F: 5'- GAGTTGCAACTTGAGAAGCTCTTC-3'
	R: 5'-TCCTCCAACCCAAACCCAGATC-3'
lyz	F: 5'-AGAATTTGTGCAAAGTGGCCTGT-3'
	R: 5'-AAGAATCCCAGGTTTCCCATGAT-3'
si:dkey-7i4.24	F: 5'-CCGCTCTGAAACAAAAGCAGTGG-3'
	R: 5'-CGCTTAGATGGATGGGGTCAGGT-3'
mt2	F: 5'-GACTGGAACTTGCAACTGTGGTG-3'
	R: 5'-GGGCAGCAAGAACAACAACTCTT-3'
serpinb5	F: 5'-TGATACAGGCAATGGTGGAGTTG-3'
	R: 5'-CTGTCGAGGAATCTGCTCCTAGC-3'
zp2l1	F: 5'-TTTCTGACTTTGGGTCGTTGTTG-3'
	R: 5'-GGGAACAAAGTGGTCAGGTAACG-3'
LOC100148225	F: 5'-GCCTTCATGTTCCAGGATACACC-3'
	R: 5'-CCCAGTAAGTTGGCCTTCAACAC-3'
dnajc3a	F: 5'-AGACAACTTCCAGGATGCAGAGG-3'
	R: 5'-GTCCAGAACCAAACGGATTGAAC-3'
zp3b	F: 5'-TTGTGTTCATCGACTGGTGTGTG-3'

	R: 5'-ACTCCTGCTATCTGCAAGACATC-3'
Slc3a2b	F: 5'-GGAGTGATGTCGTAGCCCTCATT-3'
	R: 5'-GAGGAGCAAGTCCACACCAGTTT-3'
zp3a.2	F: 5'-ACCCAGGACTGCATTCACTGC-3'
	R: 5'-ACAAGTTCAGGAGAACTCTAATC-3'
si:dkey-19b23.11	F: 5'-TATTCCTCTGACGCAAAGCCAGT-3'
	R: 5'-GTCCACTGAAAGGGTTTCAAGGT-3'
si:ch211-14a17.7	F: 5'-GCAGTGTTTCATGCTGAATTTGG-3'
	R: 5'-GAGACCACTCTTTTGGCCTTTCA-3'
si:dkeyp-50f7.2	F: 5'-CAGGCCTAAATTCAGCAATGACC-3'
	R: 5'-GCGGTTGTGAGGTAAACGAAATC-3'
firefly	F: 5'-GTTGACCGCCTGAAGTCTCTGAT-3'
	R: 5'-CCACGATCTCTTTTTCCGTCATC-3'
renilla	F: 5'-ATTGAATCGGACCCAGGATTCTT-3'
	R: 5'-TTTCATCAGGTGCATCTTCTTGC-3'

Table S3. Proteomic comparison between *zar1* homozygotes and *zar1* heterozygotes.

Proteomic analysis with iTRAQ to compare *zar1* homozygous ovaries (homo) with *zar1* heterozygous ovaries (hetero). 10 ovaries for each genotype were isolated at 33 dpf and analyzed with iTRAQ. Two replicates were performed for each genotype. The UniProt proteome sequences for Danio rerio were used for the database searching.

Click here to Download Table S3

Table S4. Summary of differentially expressed proteins based on the iTRAQ result.

Analysis of differentially expressed proteins between *zar1* homozygous ovaries (homo) and *zar1* heterozygous ovaries (hetero) determined by iTRAQ. 325 proteins show differential expression ($P < 0.05$). 42 proteins changed by more than 2 folds, among which 37 proteins were upregulated and 5 proteins were down-regulated in homozygous ovaries compared with the control ovaries.

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Table S5. Mass Spectrometry (MS) analysis of proteins precipitated by the Zar1 antibody.

MS analysis of immunoprecipitated proteins from *zar1* heterozygotes and *zar1* homozygotes. Immunoprecipitation with the Zar1 antibody was performed using *zar1* heterozygous mutant ovaries ($p53^{-/-}$;$zar1^{+/-}$) and *zar1* homozygous mutant ovaries ($p53^{-/-}$;$zar1^{-/-}$) followed by MS analysis. 59 proteins from *zar1* heterozygous ovaries and 44 proteins from *zar1* homozygous ovaries were precipitated.

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