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## Reporting Summary

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Statistic				
For all statis	l analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods sec	tion.		
n/a Confirm	a Confirmed			
☐ X The	The exact sample size ( $n$ ) for each experimental group/condition, given as a discrete number and unit of measurement			
☐ X A S	A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly			
□ X The	atistical test(s) used AND whether they are one- or two-sided mmon tests should be described solely by name; describe more complex techniques in the Methods section.			
∑ A c	A description of all covariates tested			
A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons				
IVIII	description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regressariation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)	sion coefficient)		
	Il hypothesis testing, the test statistic (e.g. $F$ , $t$ , $r$ ) with confidence intervals, effect sizes, degrees of freedom and $P$ values as exact values whenever suitable.	alue noted		
∑ Foi	yesian analysis, information on the choice of priors and Markov chain Monte Carlo settings			
∑ Foi	erarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes			
∑	ites of effect sizes (e.g. Cohen's $d$ , Pearson's $r$ ), indicating how they were calculated			
·	Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.			
Softwar	and code			
Policy inforn	on about <u>availability of computer code</u>			
Data colle	n All Illumina sequencing data in this study were collected by the manufacturer's software following the manufacturer's pig	peline.		
Data analy	R statistical language(version 3.6) and GraphPad Prism 7 were used for data analysis.			
	izing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to age code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further informations.			
Data				
All manusc - Accessio - A list of	on about <u>availability of data</u> s must include a <u>data availability statement</u> . This statement should provide the following information, where applica odes, unique identifiers, or web links for publicly available datasets res that have associated raw data n of any restrictions on data availability	ble:		
	ata generated during this study can be accessed at NCBI SRA database under Bioproject accession number PRJNA565584.(www.nct A565584). All data are available from the corresponding author at request on reasonable request.	oi.nlm.nih.gov/		
Field-	pecific reporting			
Please selec	e one below that is the best fit for your research. If you are not sure, read the appropriate sections before making yo	our selection.		
X Life scien	☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences			

## Life sciences study design

LITE SCIET	1662.2	tudy design		
All studies must dis	sclose on the	ese points even when the disclosure is negative.		
Sample size	Sample size was indicated in the figure legends and source data of each experiment. For gene expression, about 30 embryos of wild-type and mutant at each stage were used. 5 wild-type adult zebrafish were used for gene expression in tissues. 5 adult zebrafish in wild-type and mutant were used for sections and H&E staining of ovary. About 30 eggs and embryos were collected in each group to prepare for RNA-seq. No less than 1000 zebrafish embryos were prepared for RIP.			
Data exclusions	No data wer	re excluded from the analyses.		
Replication	All attempts	pts at replication were successful.		
Randomization	Sample alloc	ocation into groups was random.		
Blinding	There is no b	plinding in the study, because the phenotypes are distinct between the mutant and control embryos.		
We require informati	ion from autho	specific materials, systems and methods  ors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.		
Materials & ex	perimenta	l systems Methods		
n/a Involved in th	-	n/a Involved in the study		
Antibodies	5	∑ ChIP-seq		
Eukaryotic		Flow cytometry		
Palaeontol		MRI-based neuroimaging		
	nd other organ			
	search particip	ants		
Clinical dat	la			
Antibodies				
Antibodies used		All antibodies used are commercially available.		
		rabbit Monoclonal to HA-tag, catalogue #3724, lot #8, Cell Signaling Technology. rabbit polyclonal to β-Catenin, catalogue # ab16051, Abcam.		
		IgG control, catalogue # NI01, lot #3010039, Merck Millipore.		
		anti-Rabbit IgG Alexa Fluor® Plus 488-conjugated secondary antibody, catalogue # A32731, lot #SE250296, Invitrogen. anti-β-actin antibody, AC026,ABclonal.		
Validation		All experimental antibodies in this study are commercially available and are validated for the species and technique, and the validation data is accessible from vendor's website.		
Animals and	l other o	organisms		
		es involving animals; ARRIVE guidelines recommended for reporting animal research		
Laboratory anima		Zebrafish embryos were all used between 0 and 26 hours post fertilization and the adult zebrafish were about 90 day post fertilization.		
Wild animals		N/A		
Field-collected sa	amples	N/A		
Ethics oversight		All experiments involving zebrafish were approved and in compliance with the requirements of the IACUC of Huazhong Agricultural University (HZAUFI-2015-006).		

Note that full information on the approval of the study protocol must also be provided in the manuscript.