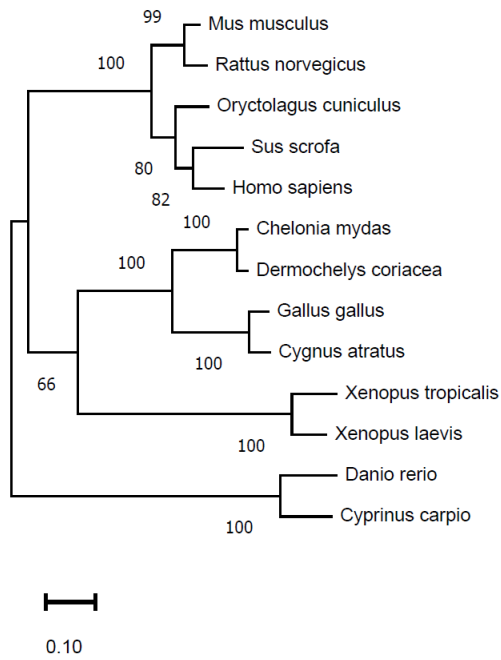


Supplementary materials

Supplementary Table S1.

List of primer sequences used in this study.

Sequences of primers used for cloning		
Name	Forward (5'->3')	Reverse (5'->3')
P2A-mTurquoise (<i>Stu</i> I and <i>Xba</i> I)	ATAGGCCT GGAAGCGGAGCTACTAACTTCAG	ATTCTAGA TTACTTGTACAGCTCGTCCATGC
<i>zc3h12a</i> _CDS (<i>Eco</i> RI and <i>Eco</i> RV)	ATGAATTC TCCATCCGGCATCAATATGCAG	ATGATATC GAAGAACTCTCCGCTGGATTGAG
Mcpip1_D112N	CCTATAGTTATTAATGGCAGCAATGTGG	CTTCAGGTCACTTTCAGCTTCAG
Sequences of primers used for qRT-PCR		
Gene	Forward (5'->3')	Reverse (5'->3')
<i>foxh1</i>	ATAAGTCCACAGGGATGGCG	ACAGAGTCCCTCCAGCCTTT
<i>nrarpa</i>	TTTTCTGCGAGAAGCCCCAT	CTGGAAACATCAGCAACGCC
<i>rasl11b</i>	CTAAGCGGTTTATCGGCGAC	GTGGTCAGTGCAGCTCAATC
<i>rhov</i>	GCTGATGGATACTGCTGGACA	TGTTGGGTTCAACCACACTGAA
<i>rps11</i>	TAAGAAATGCCCTTCACTG	GTCTCTTCTCAAAACGGTTG
<i>zc3h12a</i>	CCGAGGGCACCGAAATATCA	CATCAGGTGGCATGAACTTGTC
<i>eef1</i>	CTACCCTCCTCTTGGTCGCT	GGAACGGTGTGATTGAGGGAA
<i>actb2</i>	CATCCTCCGTCTGGACTTGG	CGCAAGATTCCATACCCAAGAA
<i>rpl13a</i>	TGGAGGACTGTAAGAGGTATGCT	GGACAACCATGCGCTTTCTC



[%]	<i>D. rerio</i>	<i>C. carpio</i>	<i>X. tropicalis</i>	<i>X. laevis</i>	<i>C. mydas</i>	<i>D. coriacea</i>	<i>G. gallus</i>	<i>C. atratus</i>	<i>M. musculus</i>	<i>R. norvegicus</i>	<i>O. cuniculus</i>	<i>S. scrofa</i>	<i>H. sapiens</i>
<i>D. rerio</i>	100												
<i>C. carpio</i>	82.90	100											
<i>X. tropicalis</i>	50.28	49.72	100										
<i>X. laevis</i>	51.20	51.43	86.72	100									
<i>C. mydas</i>	50.00	50.44	54.39	53.99	100								
<i>D. coriacea</i>	50.45	50.88	54.49	54.08	96.08	100							
<i>G. gallus</i>	50.72	51.17	53.44	54.00	76.93	76.28	100						
<i>C. atratus</i>	50.00	51.55	53.96	54.26	75.50	74.84	92.53	100					
<i>M. musculus</i>	50.19	50.37	54.34	54.70	59.76	59.86	59.30	59.58	100				
<i>R. norvegicus</i>	50.19	50.74	52.87	53.59	59.59	59.35	58.43	59.05	92.79	100			
<i>O. cuniculus</i>	51.58	51.01	53.79	53.78	60.07	60.51	58.93	58.84	83.56	82.72	100		
<i>S. scrofa</i>	49.44	49.45	54.03	54.53	61.69	62.15	61.03	61.37	81.00	81.87	84.36	100	
<i>H. sapiens</i>	50.28	50.46	53.05	53.41	60.07	59.83	58.58	58.67	82.55	82.89	86.31	86.25	100

Supplementary Figure S1. Phylogenetic trees based on the amino acid sequences of Mcpip1 of zebrafish (*D. rerio*) and selected representative species of other groups of vertebrates. For alignment, accession numbers are as follows: *D. rerio* - XP_021322483.1, *Cyprinus carpio* - XP_042596295.1, *Xenopus tropicalis* - XP_004911656.2, *X. laevis* - XP_018105042.1, *Chelonia mydas* - XP_043388107.1, *Dermochelys coriacea* - XP_038233907.1, *Gallus gallus* - XP_040545661.1, *Cygnus atratus* - XP_035417882.1, *Mus musculus* - NP_694799.1, *Rattus norvegicus* - NP_001071139.1, *Oryctolagus cuniculus* - XP_051688026.1, *Sus scrofa* - XP_020951625.1, *Homo sapiens* - NP_079355.2.

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H.s. ZC3H12A[NP_079355.2] -----VVIDGNSVAMSHGNKEVFSCRGILLAVNWFLERGHTDITVFVPSWRKEQPRP 189
D.r. Zc3h12a[XP_021322483.1] -----IVIDGNSVAMSHGNKEVFSCRGIELAVNYFLDRGHRNITVFVPSWRKEQPRP 160

H.s. ZC3H12B[NP_001010888.3] -----VVIDGNSVAMSHGNKEEFSCRGILAVDNWFLDKGHKIDITVFVPAWRKEQSRP 244
D.r. Zc3h12b[NP_001164500.1] -----IVIDGNSVAMSHGNKEVFSCRGILAVDNWFLDKGHKIDITVFVPAWRKEQSRP 216

H.s. N4BP1 [NP_694574.3] -----IVIDGNSVAITHGLKFFSCRGIAIAVEYFWKLGNRNITVFVPPQWRTR--R 668
D.r. N4bp1 [NP_956081.2] -----IIVIDGNSVAMAHGLRVFSCRGIAIAVEAFWRRGHREITVFVPPQWRQK--K 649

H.s. KHNYN [NP_056114.1] -----DLRHIVIDGNSVAMVHGLQHYFSSRGIAIAVQYFWDRGHRDITVFVPPQWRFS--K 488
D.r. Khnyn [XP_005166358.1] AKFSNTIPKAKPERGAVASVVTGPQRFLGLEKPKFSLQLSDQPGDAQLRHVIVIDGNSVAMSHGLGVFSCRGIALAVQHFVAEGHREIMVFPQWRQK--N 636
                          :*****: **      ** ** :*: *   *: :* *****

H.s. ZC3H12A[NP_079355.2]      DVPITDQHILRELEKKKILVFTPSRRVGGKRVVVCYDDRFIVKLAYESDGIIVSNDTYRDLQGERQEWRKFIEERLLMYS----- 268
D.r. Zc3h12a[XP_021322483.1] DVPISDQHILGELEKKKFLVFTPSRRVGGKRVVVCYDDRFIVKLAHDLGGIIVSNDTYRDLQSERPEWKRKFIEERLLMYS----- 239

H.s. ZC3H12B[NP_001010888.3] DAPIIDQDILRKLEKEKILVFTPSRRVQGRVVCYDDRFIVKLAFLDSGDIIVSNDNYRDLQVERPEWKKFIEERLLMYS----- 323
D.r. Zc3h12b[NP_001164500.1] DAPIIDQDILRKLEKEKILVFTPSRRVQGRVVCYDDRFIVKLACDSGDIIVSNDNYRDLQNERPEWKKFIEERLLMYS----- 295

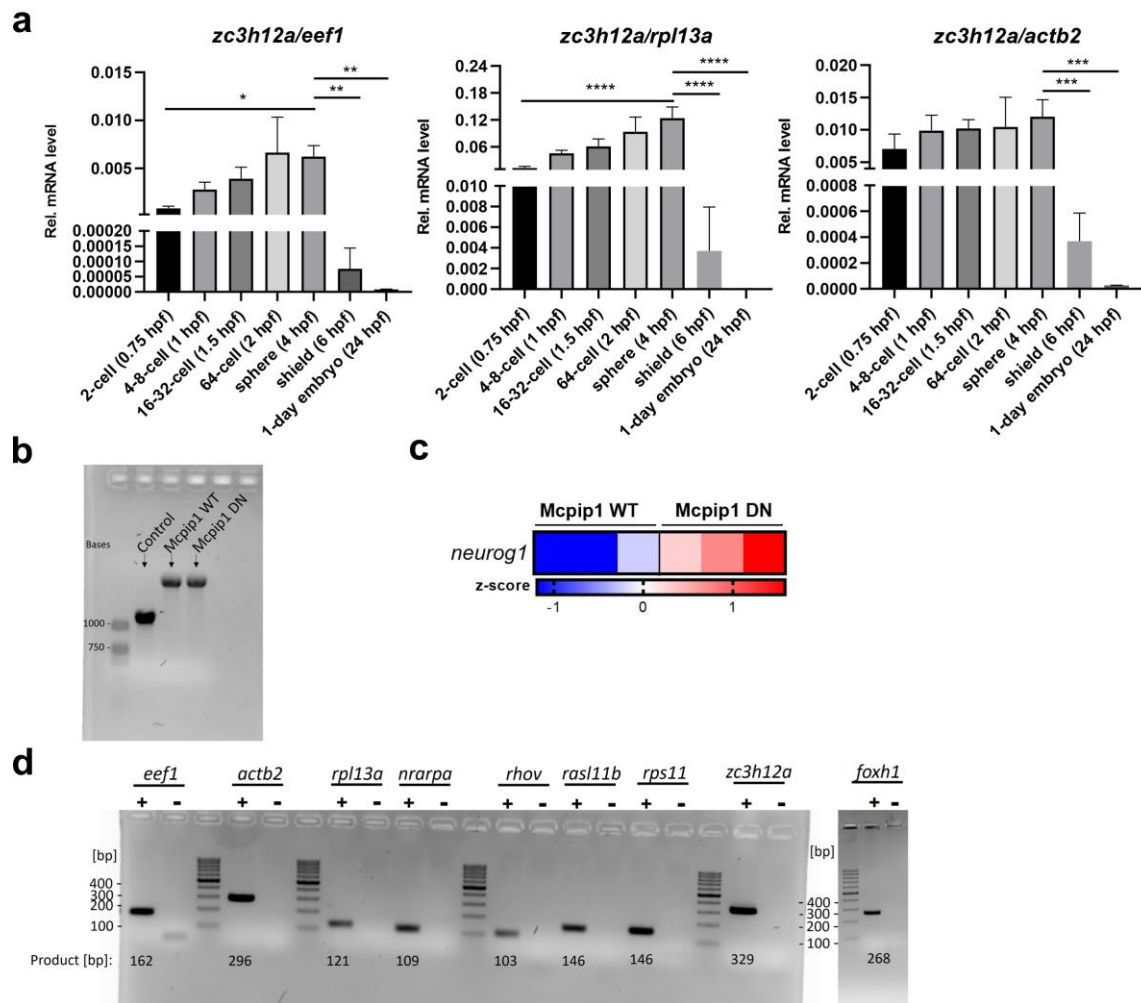
H.s. N4BP1 [NP_694574.3]      DPNVTEQHFLTQLQELGILSLTPARMVFGERIAASHDDRFLHLADKTGGIIVTNDNFREFVNESVSWREIITKRLQLY----- 746
D.r. N4bp1 [NP_956081.2]      DPNITEQHFLNQLNLRLLSFTPSREVCGRHISSHDDRFLHLAEKTGGIVTNDNLRDFVVSQSSEAWRIIHERLLQF----- 727

H.s. KHNYN [NP_056114.1]      DAKVRESHFLQKLYSLSLSLTSPSRVMDGKRISYDDRFMVKLAETDGIIVSNDQFRLAESESEKWMAIIRERLLPFTFVGNLFMVFPDDLGRNGPTLDE 589
D.r. Khnyn [XP_005166358.1] NSKIKERHYLNELHDLGLSYTPSREVEGKRITISYDDRFMLDLAQKTNGVIVTNDNLRDLVDESPAWRDIKKSLLQYVFAGDQFMLPDDPLGRGGPHLRD 690
                          : : :.. * :*      **:* :*,* :*****:..* .,*:*** *: : : * :* : * :

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[%]	H.s. ZC3H12A	D.r. Zc3h12a	H.s. ZC3H12B	D.r. Zc3h12b	H.s. N4BP1	D.r. N4bp1	H.s. KHNYN	D.r. Khnyn
H.s. ZC3H12A	100							
D.r. Zc3h12a	87.79	100						
H.s. ZC3H12B	83.21	80.15	100					
D.r. Zc3h12b	83.21	80.15	93.89	100				
H.s. N4BP1	48.82	51.18	49.61	49.61	100			
D.r. N4bp1	52.76	55.12	51.18	51.18	70.08	100		
H.s. KHNYN	54.69	57.03	54.69	53.91	59.84	63.78	100	
D.r. Khnyn	50.78	52.34	50.78	50.00	60.63	68.50	59.74	100

Supplementary Figure S2. Alignment of the PIN domain amino acid sequences of human and zebrafish PIN-domain-like superfamily members between *Homo sapiens* (*H.s.*) and *Danio rerio* (*D.r.*). Asterisk (*) denotes an identical residue, a colon (:) denotes conserved substitutions, and a period (.) denotes semiconserved substitutions.



Supplementary Figure S3. a. Real-time PCR analysis of *zc3h12a* mRNA level. *Eef1*, *rpl13a* and *actb2* were used as a reference genes. Data represent the mean $\pm$ SD, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$ by one-way ANOVA (only selected comparisons are shown). **b.** RNA denaturing agarose gel electrophoresis of ~ 300 ng synthesized mRNA. The Low Range ssRNA Ladder (New England BioLabs) was used. **c.** Heatmap presenting normalized (z-score) *neurog1* mRNA level with p value < 0.1 , based on RNA-seq data. **d.** DNA agarose gel electrophoresis of QRT-PCR products. Plus (+) means cDNA and minus (-) means water as a template. The 100 bp GeneRuler Ladder (New England BioLabs) was used.