

# 1 Whole Genome and Embryo Transcriptome Analysis of Vertebrate Identifies *nxhl*

## 2 Controlling Angiogenesis by Targeting VE-PTP

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28 **ABSTRACT**

29 **BACKGROUND:** Angiogenesis is closely associated with angiogenesis-dependent diseases including  
30 cancers and ocular diseases. Anti-angiogenic therapeutics have been focusing on the (VEGF)/VEGFR  
31 signaling axis. However, the clinical resistance, high cost and frequent administration of anti-VEGF drugs  
32 make it urgent to discover novel angiogenic pathways. VE-PTP (*ptprb*) is a novel target with great anti-  
33 angiogenic potential. However, it is unclear whether upstream signaling pathways targeting VE-PTP exist in  
34 angiogenesis.

35 **METHODS:** Whole genome and embryo transcriptome sequencing were applied to discover the new gene  
36 *nxhl*. Transgenic zebrafish model, morpholino knockdown and small interfering RNA were used to explore  
37 the role of *nxhl* in angiogenesis both *in vitro* and *in vivo*. RNA pulldown, RIP and ChIRP-MS were used to  
38 identify interactions between RNA and protein.

39 **RESULTS:** We discovered a novel zebrafish gene *nxhl* which is a homologue of the conserved gene *nxh*  
40 that co-expressed with some key genes essential for embryo development in vertebrate. *Nxhl* deletion causes  
41 angiogenesis defects in embryo. Moreover, *nxhl* is essential to mediate effects of angiogenesis *in vivo* and *in*  
42 *vitro*, and *ptprb* depletion duplicates the phenotypes of *nxhl* deficiency. Importantly, *nxhl* acts upstream of  
43 *ptprb* and regulates many extreme important *ptprb*-linked angiogenic genes by targeting VE-PTP (*ptprb*)  
44 through interactions with NCL. Notably, *nxhl* deletion decreases the phosphorylation of NCL T76 and  
45 increases the acetylation of NCL K88, suggesting *nxhl* may regulate downstream VE-PTP signaling  
46 pathways by mediation of NCL posttranslational modification. This is the first description of the interaction  
47 between *nxhl* and NCL, NCL and VE-PTP (*ptprb*), uncovering a novel *nxhl*-NCL-VE-PTP signaling pathway  
48 on angiogenesis regulation.

49 **CONCLUSIONS:** Our study identifies *nxhl* controlling angiogenesis by targeting VE-PTP through  
50 interactions with NCL, uncovering novel upstream controllers of VE-PTP. This *nxhl*-NCL-VE-PTP pathway  
51 may be a therapeutic target in the treatment of angiogenesis-dependent diseases.

52 **Key Words:** Angiogenesis, *nxhl*, VE-PTP, *ptprb*, nucleolin, WGD, cancer.

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## 54 **Clinical Perspective**

### 55 **What Is New?**

- 56 • We report a novel *nxhl*-NCL-VE-PTP signaling pathway that controls angiogenesis.
- 57 • We for the first time demonstrate that *nxhl* interacts with NCL which simultaneously binds to VE-PTP  
58 that plays key roles on EC adherens junction, integrity and vascular homeostasis.
- 59 • *Nxhl* also controls some other crucial VE-PTP-linked downstream angiogenic genes (such as Tie2,  
60 VEGFaa, VEGFR2, Erbb2, S1pr1 and Hey2) which explain the phenotypes induced by the *nxhl*  
61 deficiency.
- 62 • Our study indicates the key role of *nxhl* on controlling angiogenesis as an upstream regulator of VE-PTP.

### 63 **What Are the Clinical Implications?**

- 64 • There are several ongoing researches investigating the utility of VE-PTP or NCL inhibitors on treatment  
65 of angiogenesis-dependent diseases including a range of cancers and nonneoplastic diseases, such as AMD,  
66 DME, RA and atherosclerosis.
- 67 • Targeting the *nxhl*-NCL-VE-PTP pathway may facilitate therapeutic angiogenesis in patients with cancers  
68 or ocular diseases such as DME.
- 69 • Our study highlights the great potential of *nxhl* on anti-angiogenic therapeutics by targeting VE-PTP.

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78 Angiogenesis is a process of new blood-vessel spreading that is orchestrated by various angiogenic factors.  
79 It plays critical roles in reproduction, organ development and wound repair. Pathologically, it is closely  
80 related to “angiogenesis-dependent diseases” including a range of tumors and nonneoplastic diseases, such  
81 as age-related macular degeneration (AMD) ,<sup>1</sup> diabetic macular edema (DME) ,<sup>2</sup> rheumatoid arthritis (RA)<sup>3</sup>  
82 and atherosclerosis.<sup>4</sup> Judah Folkman suggested to consider angiogenesis as an ‘organizing principle’ in  
83 biology.<sup>5</sup> This conception shifted therapeutic strategies from tumor cell-centered to anti-angiogenesis-  
84 centered.<sup>6</sup> In the past decades, milestone discoveries of anti-angiogenic therapeutics have been mainly  
85 focused on the vascular endothelial growth factor (VEGF)/VEGFR signaling axis. Various inhibitors of this  
86 axis, such as Ramucirumab, have been approved for several solid cancers by FDA.<sup>7</sup> Over 3000 anti-  
87 angiogenic drugs have been registered clinical trials for cancer treatment and ocular neovascular diseases,<sup>8</sup>  
88 highlighting the significant value of anti-angiogenic drugs for clinical applications. However, in the clinical  
89 setting, simply blocking the existing VEGF signaling pathway or other angiogenic pathways appears to be  
90 less effective for advanced cases and often causes treatment resistance.<sup>9</sup> High cost of currently used anti-  
91 VEGF drugs and their frequent dosing make new drugs targeting novel angiogenic pathways clinically  
92 necessary and highly desirable.

93 We specially concern the protein vascular endothelial protein tyrosine phosphatase (VE-PTP, namely  
94 *ptprb* in zebrafish) in endothelial cells (ECs), which determine the permeability and integrity of the blood  
95 vessel wall and thereby is essential for angiogenesis. VE-PTP is a member of the R3-subclass of R-PTPs  
96 and consists of 2251 amino acids with 18 domains.<sup>10</sup> It is indispensable during mouse vessel development<sup>11-</sup>  
97 <sup>13</sup> due to the overactivated Tie2 and increased vessel enlargement.<sup>11, 12, 14</sup> Evidence shows that VE-PTP plays  
98 crucial roles in angiogenesis, EC adherens junction, integrity and vascular homeostasis.<sup>12, 15-18</sup> It binds to  
99 VEGFR2, resulting in increase of VEGFR2 phosphorylation and activation.<sup>19</sup> It also binds to Tie2 and  
100 negatively controls Tie2-induced vascular remodeling and angiogenesis by dephosphorylation.<sup>14</sup>

101 Suppressing VE-PTP, either by genetic deletion or specific VE-PTP inhibitor (AKB-9778 or ARP-1536)  
102 activates Tie2 and thereby regulates EC permeability, integrity and angiogenesis.<sup>20, 21</sup> Its specific inhibitor  
103 AKB-9778 has been investigated in cancer<sup>22, 23</sup> and retinal neovascularization,<sup>24, 25</sup> such as breast cancer<sup>26</sup>  
104 and DME,<sup>28</sup> and has exhibited its great clinical potential. Logically, targeting the upstream genes that directly  
105 or indirectly interact with VE-PTP might be a promising strategy to overcome limitations of current anti-  
106 VEGF agents. However, few *in vivo* studies have been conducted to investigate how VE-PTP is regulated  
107 by its upstream regulators. Notably, such regulators are still unreported.

108 Nucleolin (NCL) is also a highly conserved gene that highly expressed in ECs.<sup>26, 27</sup> Cell surface NCL  
109 plays crucial roles in the regulation of angiogenesis and tumorigenesis via interactions with various ligands,  
110 such as VEGF,<sup>26</sup> EGFR,<sup>28</sup> endostatin,<sup>29</sup> and HER2 (ErbB2).<sup>30</sup> For instance, VEGF is required for NCL cell  
111 surface localization in ECs, which strengthens its contribution to the angiogenesis.<sup>31, 32</sup> In addition, inhibition  
112 of cell surface NCL in ECs significantly suppresses the EC migration and prevents capillary tubule  
113 formation.<sup>31</sup> Previous researches demonstrate that anti-NCL pseudopeptides N6L impairs angiogenesis both  
114 *in vitro* and *in vivo* by targeting ECs and tumor vessels.<sup>33, 34</sup> Increased NCL expression is related to worse  
115 prognosis of many cancers, such as diffuse large B-cell lymphoma<sup>35</sup> and pancreatic ductal cancer.<sup>34</sup> For now,  
116 a variety of aptamers or antibodies targeting NCL, such as AS1411, are under clinical investigation for  
117 anticancer treatment and demonstrating promising perspectives,<sup>36</sup> highlighting its potential as a therapeutic  
118 target for anti-cancer therapy.

119 Similar functions of VE-PTP and NCL on angiogenesis provide us clues for further study. So far, it is  
120 unclear whether both genes closely associate and thereby mediate angiogenesis process. This should be  
121 investigated in an advanced model that facilitates *in vivo* angiogenesis assay. Zebrafish is such a valuable  
122 model system for investigation of vascular development. Experimental evidences have indicated that  
123 developmental angiogenesis in the zebrafish embryo might be an useful tool for angiogenesis research in

124 vertebrate because of its high similarity vascular network formation and expression patterns of key genes  
125 with humans and other vertebrates.<sup>37, 38</sup> The transparency and external development of embryo and the  
126 ability to produce various transgenic germ line fish, as well as the small size and rapid development make  
127 vasculature manipulation in zebrafish feasible and more cost-effective.<sup>39</sup> Conserved angiogenic signaling  
128 pathways make zebrafish as an ideal system for human angiogenesis researches and anti-angiogenic or anti-  
129 cancer drug screening.<sup>40, 41</sup>

130 Herein, we identified a novel conserved gene *nxhl*, a homologue of *nxh* which is reserved after whole  
131 genome duplication (WGD) in a teleost embryo transcriptome, by combination genome and embryo  
132 transcriptome and zebrafish model. *Nxhl* strongly controls angiogenesis both *in vitro* and *in vivo*, and acts as  
133 a critical upstream regulator of VE-PTP through interactions with NCL that binds to VE-PTP. It is a potential  
134 therapeutic target for angiogenesis-dependent diseases.

135

## 136 **METHODS**

137 Materials and raw data that support the findings of this study are available upon request to the corresponding  
138 authors. A detailed description of genome sequencing associated Materials and Methods is available in the  
139 Supplemental information.

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### 141 **Zebrafish Care and Maintenance**

142 Adult wild-type AB strain zebrafish were maintained at 28.5°C on a 14 h light/10 h dark cycle.<sup>42</sup> Five to six  
143 pairs of zebrafish were set up for nature mating every time. On average, 200–300 embryos were generated.  
144 Embryos were maintained at 28.5°C in fish water (0.2% Instant Ocean Salt in deionized water). The embryos  
145 were washed and staged according to.<sup>43</sup> The establishment and characterization of the *TG (zlyz:EGFP)*  
146 transgenic lines have been described elsewhere.<sup>39, 44</sup> The zebrafish facility at SMOC (Shanghai Model

147 Organisms Center, Inc.) is accredited by the Association for Assessment and Accreditation of Laboratory  
148 Animal Care (AAALAC) International.

149

### 150 **Zebrafish Microinjections**

151 Gene Tools, LLC (<http://www.gene-tools.com/>) designed the morpholino (MO). Antisense MO (GeneTools)  
152 were microinjected into fertilized one-cell stage embryos according to standard protocols.<sup>39</sup> Translation-  
153 blocking (ATG-MO) and splice-blocking morpholinos of the *nxhl* (zgc:113227, NM\_001014319.2) and  
154 *ptprb* (NM\_001316727.1) were designed, respectively. The standard control morpholino was used as Control  
155 MO (Gene Tools). The amount of the MOs used for injection was as follows: Control MO, ATG-MO and  
156 splice-blocking -MO, 4 ng per embryo. Effectiveness of *nxhl* and *ptprb* knockdown was confirmed by qPCR  
157 (Quantitative Real-Time PCR). For the morpholinos and primers, see [Table S28](#).

158

### 159 **Zebrafish Angiogenesis Studies and Image Acquisition**

160 To evaluate blood vessel formation in zebrafish, fertilized one-cell *fli1a-EGFP* transgenic lines embryos  
161 were injected with 4 ng *nxhl-e1i1*-MO, *nxhl*-ATG-MO, control-MO, and *ptprb-e4i4*-MO, *ptprb*-ATG-MO,  
162 control-MO, respectively. At 52 phf (*nxhl* MO) and 2 dpf (*ptprb* MO), embryos were dechorionated,  
163 anesthetized with 0.016% MS-222 (tricaine methanesulfonate, Sigma-Aldrich, St. Louis, MO). Zebrafish  
164 were then oriented on the lateral side (anterior, left; posterior, right; dorsal, top), and mounted with 3%  
165 methylcellulose in a depression slide for observation by fluorescence microscopy. The phenotypes of  
166 complete intersegmental vessels (ISVs) (i.e., the number of ISVs that connect the DA to the DLAV),  
167 parachordal vessels (PAV) and caudal vein plexus (CVP) were analyzed. Embryos and larvae were  
168 analyzed with Nikon SMZ 1500 Fluorescence microscope and subsequently photographed with digital  
169 cameras. A subset of images was adjusted for levels, brightness, contrast, hue and saturation with Adobe

170 Photoshop 7.0 software (Adobe, San Jose, California) to visualize the expression patterns optimally.  
171 Quantitative image analyses processed using image based morphometric analysis (NIS-Elements D3.1,  
172 Japan) and ImageJ software (U.S. National Institutes of Health, Bethesda, MD, USA;  
173 <http://rsbweb.nih.gov/ij/>). Inverted fluorescent images were used for processing. Positive signals were  
174 defined by particle number using ImageJ. Ten animals for each treatment were quantified and the total signal  
175 per animal was averaged.

176

### 177 **Quantitative Real-Time PCR**

178 Total RNA was extracted from 30 to 50 embryos per group in Trizol (Roche) according to the manufacturer's  
179 instructions. RNA was reverse transcribed using the PrimeScript RT reagent Kit with gDNA Eraser (Takara).  
180 Quantification of gene expression was performed in triplicates using Bio-rad iQ SYBR Green Supermix  
181 (Bio-rad) with detection on the Realplex system (Eppendorf). Relative gene expression quantification was  
182 based on the comparative threshold cycle method ( $2^{-\Delta\Delta Ct}$ ) using *efl $\alpha$*  as an endogenous control gene. qPCR  
183 on HUVECs were performed as similar procedures. All of the primers are listed in [Table S28](#).

184

### 185 **RNA-Seq**

186 Control MO-injected embryos and embryos injected with *nxf1* MO at 3 dpf were frozen for RNA-seq analysis.  
187 Three biological replicates of 30 embryos each were analyzed in each group. RNA was purified using  
188 RNAqueous Total RNA isolation kit (Thermo Fisher). Libraries were prepared with TruSeq RNA library  
189 Prep kit v2 (Illumina) according to the manufacturer's protocol. Libraries were sequenced at the CCHMC  
190 Core Facility using Illumina HiSeq 2500 device (Illumina) to generate 75 bp paired-end reads. Quality of  
191 the RNA-Seq reads was checked using Fastqc [<http://www.bioinformatics.babraham.ac.uk/projects/fastqc/>].  
192 All of the low-quality reads were trimmed using trimmomatic [<http://www.usadellab.org/cms/?page=trimmo>]



193 matic]. The trimmed RNA-Seq reads were mapped and quantified to latest Zebrafish genome assembly  
194 GRCz10 for each sample at default thresholds using RSEM [<http://deweylab.github.io/RSEM/>]. The mRNA  
195 levels were identified using TopHat v2.0.9 and Cufflinks and normalized by the Fragments Per Kilobase of  
196 exon model per Million mapped reads (FPKM). Differential expression was analyzed by using CSBB's  
197 [<https://github.com/skygenomics/CSBB-v1.0>]. Criteria of false discovery rate (FDR) <0.01 and fold changes  
198 <0.5 or >2.0 (<-1 or >1 log<sub>2</sub> ratio value, p value < 0.05) were used to identify differentially expressed genes.  
199 Gene Ontology (GO) annotation, domain annotation, Kyoto Encyclopedia of Genes and Genomes (KEGG)  
200 pathway annotation and enrichment were performed using ToppGene [<https://topgene.cchmc.org/>].

201

## 202 **Transwell Migration and Invasion Assays**

203 To examine the function of human Harbi1, the homologous gene of *nXH* and *nXHL*, siRNA targeting human  
204 Harbi1 gene (NM\_173811.4) was designed (see [Table S28](#)). HUVECs cells (ATCC, Manassas, Virginia,  
205 USA) were cultured in DMEM/F12 (Hyclone, USA) with 10% FBS (Gibco BRL, Co. Ltd.) and 1%  
206 penicillin-streptomycin (Sangon Biotech, China.) at 37°C in 5% CO<sub>2</sub> incubator. Three experimental groups  
207 HUVECs, HUVECs + si-Harbi1 NC and HUVECs+si-Harbi1 were set and 30 pmol si-Harbi1 per well in  
208 the 24-well plates (Corning-Costa) were transferred using 9 µl Lipofectamine RNAi MAX Reagent  
209 (Invitrogen, USA). The cell migration and invasion capacity of Harbi1 on HUVECs cells were determined  
210 by transwell insert chambers (Corning, NY, USA) covered with or without 50 µl of Matrigel (1:3 dilution,  
211 BD, NJ, USA). Cells were then harvested and dissociated into a single-cell suspension. 5×10<sup>4</sup> cells in serum-  
212 free medium were added to the upper chamber and 600 µl of 20% FBS-containing medium was added to the  
213 lower chamber. The chambers were then incubated for 72 h (5% CO<sub>2</sub>, 37 °C). Cells on the upper chamber  
214 were discarded, while cells on the lower chamber were fixed with 4% paraformaldehyde for 30 min and then  
215 stained with 0.1% crystal violet for 10 min. Cells that underwent migration or invasion were counted in  
216 triplicates in microscopic fields. The migration of nucleolin (NM\_005381.3) was also examined by similar

217 protocol above. The siRNA of NCL is listed in [Tale S28](#).

218

## 219 **Tube Formation Assay**

220 The HUVECs' culture conditions and experimental set were identical to the transwell migration and invasion  
221 assays. Thirty pmol si-Harbi1 or si-NCL per well of the 24-well plates (Corning-Costa) were transferred by  
222 using 9  $\mu$ l Lipofectamine RNAi MAX Reagent (Invitrogen, USA). Matrigel (250  $\mu$ l per well, BD  
223 Biosciences, USA) was added to the plates and cultured at 37 °C for 30 min. Then, a suspension containing  
224  $5 \times 10^4$  HUVECs was added to each well and cultured at 37°C in 5% CO<sub>2</sub> incubator. A final concentration of  
225 50  $\mu$ M Calcein-AM (Solarbio, China) per well was added to the plates and incubated for 30 min at 37°C. Six  
226 hours later, the tube formation was observed and counted under the fluorescence microscope. The number  
227 of formed tubes represented the tube forming capability of HUVECs.

228

## 229 **Comprehensive Identification of RNA-binding Proteins by Mass Spectrometry (ChIRP-MS)**

230 Zebrafish embryos (3 dpf) were collected and a total of  $2 \times 10^7$  cells were prepared and re-suspended in  
231 precooled PBS buffer followed by crosslinking with 3% formaldehyde for 30 min at 25°C. The reaction was  
232 stopped by incubation with 0.125 M glycine for 5 min. After centrifugation at 1,000 RCF for 3 min, the pre-  
233 binding probes (100 pmol per  $2 \times 10^7$  cells; probes see [Table S28](#)) were incubated with streptavidin beads  
234 for 30 min. The unbound probes were removed by washing three times. The beads with probes were  
235 incubated with the cell lysate and hybridized at 37°C overnight with shaking. All of the beads were washed  
236 3 times with pre-warmed wash buffer for 5 min. A small aliquot (1/20 of the beads) of post-ChIRP beads  
237 were reserved for RNA extraction and qPCR analysis. Then 100  $\mu$ L of elution buffer (12.5mM biotin, 7.5mM  
238 HEPES pH 7.5, 75mM NaCl, 1.5mM EDTA, 0.15% SDS, 0.075% sarkosyl, 0.02% Na-Deoxycholate, and

239 20 U benzonase) was added and the protein was eluted at 37°C for 1 h. The eluent was transferred to a fresh  
240 low-binding tube and the beads were eluted again with 100 µL of elution buffer. The two eluents were  
241 combined and the reverse-crosslinking was performed at 95°C for 30 min. The protein was precipitated with  
242 0.1% SDC and 10% TCA by centrifugation at 4°C for 2 h. The pellets were then washed with precooled 80%  
243 acetone three times before the proteins were used for mass spectrometry (MS) analysis. Then 5 µL peptides  
244 of each sample were collected and separated by nano-UPLC easy-nLC1200 liquid phase system before they  
245 were detected using an on-line mass spectrometer (Q-Exactive) at a solution of 70,000. All of the original  
246 MS data were queried against zebrafish protein database (UNIPROT\_zebrafish\_2016\_09). Only those  
247 proteins with an FDR < 0.01 and an adjusted *p*-value < 0.05 were considered differentially expressed. The  
248 identified proteins were then further examined using bioinformatics, including GO) and KEGG pathway  
249 annotations.

250

### 251 ***Nxhl* Protein Expression and Antibody Preparation**

252 Briefly, *nxhl* gene (zgc:113227, NM\_001014319.2) was synthesized and the expression plasmid pET-B2m-  
253 *nxhl*-His was constructed using the seamless cloning technology (Figure S13 and Figure S14). The plasmid  
254 was transferred into the *Escherichia coli* strain B21 (DH3) for protein expression and the resulting protein  
255 was purified by Ni-NTA chromatography column. The purified *nxhl* protein was used to immunize Japanese  
256 big ear rabbits to produce polyclonal antibody. The specificity of polyclonal antibody was detected by anti-  
257 His Western blotting and its immunity was verified by ELISA. We purified 6mg of fusion protein (62.0 kDa)  
258 with 85% purity. After immunization in rabbits, a *nxhl* polyclonal antibody with a titer of 1:256,000 was  
259 obtained. The concentration of the *nxhl* antibody purified by Protein G affinity chromatography column was  
260 10 mg/mL and the purity was 90%. The obtained *nxhl* antibody was used to perform Western blotting assays.

261

## 262 **Western Blotting Assays**

263 Zebrafish tissues from knock-down group and control were treated with 1 mL of tissue lysate (50 mmol/L  
264 Tris, 0.1% SDS, 150 mmol/L NaCl, 1% NP-40, 5 mmol/L EDTA, 5 µg/mL aprotinin and 2 mmol/L PMSF  
265 followed by lysis with protein lysate at 4°C for 30 min). All of the samples were centrifuged at 12,000 r/min  
266 at 4°C for 20 min and the supernatant was removed to detect the protein concentration using a bicinchoninic  
267 acid (BCA) kit (CW BIO. Co., Ltd., Shanghai, China). Samples were resolved by SDS-PAGE using a  
268 NuPAGE 4–12% gel (Life Technologies). Proteins were transferred onto a nitrocellulose filter (BioRad,  
269 Hercules, CA, USA) and sealed at 4°C overnight by 5% dried skimmed milk. The membranes were incubated  
270 with diluted primary rabbit polyclonal *ptprb* (VE-PTP)(PA5-68309, Invitrogen, USA) (1:1000), Hey2(PA5-  
271 72676, Invitrogen, USA) (1: 2000), Dot1L(ab72454, Abcam, UK) (1:2000) , S1pr1(PA5-72648, Invitrogen,  
272 USA) (1: 1000), HAND2 (PA5-68502, Invitrogen, USA) (1µg/mL) , Nucleolin (ab50279, Abcam, UK)  
273 (1:1000), Nucleolin (phosphor T76, ab168363, Abcam, UK) (1:1000), Nucleolin (phosphor T84, ab196338,  
274 Abcam, UK) (1:1000), Nucleolin (acetyl K88, ab196345, Abcam, UK) (1:1000), *nahl* (Lab made, 1:1000)  
275 and *ptprb* (Lab made, 1:1000) antibodies overnight at 4°C followed by washing with PBS at room  
276 temperature. The membranes were treated with goat-anti-rabbit, rabbit-anti-goat or goat-anti-mouse IgG-  
277 HRP secondary antibody (1: 2000, CWBiotech., Ltd., Beijing, China) and incubated at 37°C for 2 h. After  
278 washing with PBS, the membrane was soaked in enhanced chemiluminescence (ECL) kit (CW Biotech.,  
279 Ltd., Beijing, China) according to the manufacturer's protocols.

280

## 281 **RNA Binding Protein Immunoprecipitation Assay (RIP)**

282 To detect the interactions between *nahl* mRNA and nucleolin protein, and VE-PTP mRNA and nucleolin  
283 protein, RIP was conducted as follows: constructed *nahl*-pcDNA3.1 (pcDNA3.1 vector V79020, Invitrogen,

284 USA) was transferred into 293T cells and its overexpression was verified by qPCR. Then  $10^7$  293T cells  
285 were suspended and lysed for 20 mins with 1 ml RIPA lysis buffer (Thermo Fisher Scientific, USA)  
286 containing 1  $\mu$ l of protease inhibitor (Beyotime, China). Twenty  $\mu$ l of cell lysates were used as input, for the  
287 IgG and IP experimental group. Magnetic beads were pretreated with an anti-rabbit IgG (Beyotime, China;  
288 negative control) or anti-Nucleolin (ab50279, Abcam, UK) for 1 h at room temperature, and cell extracts  
289 were immunoprecipitated with the beads-antibody complexes at 4°C overnight. The retrieved RNA was  
290 purified by using the phenol-chloroform method and subjected to real-time qPCR and general reverse-  
291 transcription PCR for *nxhl* and VE-PTP analysis. Primers are list in [Table S28](#).

292

### 293 **RNA Pull-down Assay**

294 To detect the interactions between VE-PTP mRNA and nucleolin protein in 293T cells, and *ptprb* mRNA  
295 and nucleolin protein in zebrafish tissues, probes for VE-PTP (human) and *ptprb* (zebrafish) were designed  
296 and synthesized. Probes were list in [Table S28](#). Probes are labeled with 3  $\mu$ g biotin then heated at 95°C for 2  
297 min followed by standing at room temperature for 30 min. Magnetic beads were washed and resuspended in  
298 50  $\mu$ l RIP buffer, then the biotinylated and denatured probes were added and incubated for 1 h at room  
299 temperature. The nucleolin protein was extracted with 1 ml RIP buffer, sonicated, centrifuged at 12,000 rpm  
300 for 15 min, and the supernatant (nucleolin protein) was retained. A magnetic separator was used to remove  
301 the liquid and the protein solution was rinsed three times using RIP buffer. The protein solution was added  
302 to the magnetic bead-probe mixture, and RNase inhibitor was added to the lysate. The mixture was incubated  
303 at room temperature for 1 h and washed five times with 1 ml RIP buffer once. Then 2 $\times$ SDS loading buffer  
304 was added to the mixture, denatured at 95°C for 10 min, and used for subsequent Western blotting. The  
305 Western blotting was performed as described above. The antibody Nucleolin (ab50279, Abcam, UK) (1:1000)  
306 was used in the detection of VE-PTP (human) and *ptprb* (zebrafish) in 293T cells and zebrafish tissue.

307

## 308 **Statistical Analysis**

309 All data are presented as mean  $\pm$  SEM. Statistical analysis and graphical representation of the data were  
310 performed using GraphPad Prism 7.0 (GraphPad Software, San Diego, CA). Statistical evaluation was  
311 performed by using a Student's t test, ANOVA, or  $\chi^2$  test as appropriate.  $p$  value of less than 0.05 was  
312 considered statistically significant. Statistical significance is indicated by \* or  $p$  value. \* represents  $p < 0.05$ ,  
313 and \*\*\* indicates  $p < 0.0001$ . The results are representative of at least three independent experiments.

314

## 315 **RESULTS**

### 316 **WGD Drives Teleost Karyotypes Stability in Embryo**

317 We have been thinking that whether the reserved genes after WGD in vertebrate function in regulation of  
318 angiogenesis. We tried to find such gene conserved in vertebrate. We used a teleost golden pompano which  
319 underwent WGD as an experimental model. We firstly obtained a high-quality genome by *de novo*  
320 sequencing, assembling and annotation of this teleost (Figure S1, S2, S3; TableS1-S17). The genomic  
321 landscape of genes, repetitive sequences, genome map markers, Hi-C data, and GC content of the golden  
322 pompano genome is visualized by circos<sup>45</sup> in Figure 1A. Then, we reconstructed the evolutionary history of  
323 teleost fishes with spotted gar, zebrafish and other teleosts to examine the evolutionary position of the teleost  
324 in vertebrate (Figure 1B, Figure S4). Assuming a constant rate of distribution of silent substitutions (dS)<sup>46</sup>  
325 of  $1.5 \times 10^{-8}$ , we revealed the dates of WGD (Ts3R) and Ss4R at 350 Mya and 96 Mya, respectively (Figure  
326 1C). Genome collinearity comparison (Figure 1D, and Table S18) implied that teleost-ancestral karyotypes  
327 are considerably conserved in post-Ts3R rediploidization with large fissions, fusions or translocations  
328 (Figure 1E, and Table S19-S20). Next, we classified the Ts3R subgenomes according to the integrity of gene  
329 as belonging to the LF, MF, and Other subgenome.<sup>47</sup> The component of rediploidization-driven subgenomes

330 is unequally distributed among subgenomes (Figure 2A), suggesting an asymmetric retention of ancestral  
331 subgenomes in teleosts.<sup>48, 49</sup> For now, knowledge on the relationship between rediploidization process and  
332 embryo development stability is largely unclear. We then compared the genome-wide transcriptional levels  
333 of LF, MF, and Other karyotypes from whole-embryo development stages (OSP to YAPS) (Figure 2B).  
334 Karyotypes-retained regions (LF and MF) showed comparable expression levels during the embryo  
335 development, while karyotypes-loss regions (Other) were expressed at significantly lower levels (signed-  
336 rank sum test,  $P < 0.01$ ) (Figure 2B, Figure S5). The Ks/Ks values of karyotypes-retained regions are  
337 significantly lower than those of karyotypes-loss regions (Figure 2C). This observation indicated that  
338 karyotypes-loss genes evolved faster than did the karyotypes-retained regions. We propose that karyotypes-  
339 retained genes are crucial for retaining embryo development stability and that karyotypes-loss genes are  
340 more prone to contribute to genetic diversity. Detail descriptions about subgenome and evolution can be  
341 found in supplementary information.

342

### 343 ***Nxhl* Is A Conserved Homologue of *Nxh* Retained after WGD**

344 Then we analyzed the gene expression pattern of golden pompano embryo (Figure S6 and Table S21-  
345 S26), and found that all 57 of the samples were separated into two components (Figure S6). The first 33  
346 samples (from OSP to MGS) cluster into a clade and the residual 24 samples (from LGS to YAPS) cluster  
347 into another. The genes in the first clade were non-redundant reserved hub-genes and clearly “silenced”  
348 compared with those of the second clade, in which the gene levels show an explosive increase. We also  
349 noticed that before LGS, a group of genes in three stages, HBS, EGS, and MGS, are highly expressed in the  
350 first clade (Figure S6). We clustered these genes by using the WGCNA R package and found that most of  
351 them clustered into the purple\_module and are co-expressed in a close network, indicating regulatory roles  
352 for these genes (Figure 2 DE). Among them, EVM0008813 (designated as New XingHuo, *nxh*; Figure 2F)

353 is retained one copy after WGD and dominantly expresses in HBS, EGS and MGS stages. It is closely co-  
354 expressed with some key genes (Figure 2E), such as *eomesa*, *dkk2* and *mix11*, which play essential roles on  
355 embryo development.<sup>50-52</sup> We proposed that *nxh* could be a crucial controller that regulates key steps of  
356 embryo development. We found that *nxh* contains 3 exons with two introns and its expression (qPCR) in  
357 EGS, MGS and LGS is highly identical to our sequencing data (FPKM, Figure 2F). We noticed that *nxh* is a  
358 WGD-specific gene and belongs to the karyotypes-retained genes (MF), implicating its important conserve  
359 function during evolution. We then searched its homologue in NCBI database by BLASTp and only one  
360 gene *zgc:113227* (designated as New XingHuo-like; *nxhl*) shares 54.7% similarity to *nxh* at the amino acid  
361 level in zebrafish. Also, the collinear analysis confirmed *nxhl* as its homologue gene in zebrafish (Figure  
362 2G). We found that *nxh* and *nxhl* have the same functional domain DDE\_Tnp\_4 as the other seven genes in  
363 different species have (Figure 2H), suggesting they may have similar biological functions during embryo  
364 development. So, we asked what could the function of *nxhl* be?

365

### 366 ***Nxhl* Affects Angiogenic Phenotypes *In Vitro* and *In Vivo***

367 Firstly, we investigated whether loss of *nxhl* affects morphology development in zebrafish. We observed that  
368 both *nxhl*<sup>eli1</sup> and *nxhl*<sup>ATG</sup> morphants resulted in nearly identical phenotypes of pericardial oedema, body  
369 axis bending, and caudal fin defects (Figure 3A, Figure S7, and Figure S8) at 3 days post fertilization (dpf),  
370 confirming that the phenotype of *nxhl* knockdown is *nxhl*-specific (Figure 3A). Regarding the vascular  
371 system, embryos injected with *nxhl*<sup>eli1</sup> MO present thinner ISVs (yellow arrows) and ectopic sprouts  
372 (asterisk) of dorsal aorta compared with controls, and the *nxhl* knockdown prevents the parachordal vessel  
373 (PAV) formation, the precursor to the lymphatic system. Moreover, heartbeat and circulation in the caudal  
374 vein (CV) is visible in the control fish, but is abnormal in *nxhl*-MO-injected fish (Supplementary Movie1,  
375 2). Both *nxhl*<sup>eli1</sup> and *nxhl*<sup>ATG</sup> morphants dramatically disrupted normal splicing of *nxhl* (Figure 3A),



376 indicating high efficiency and specificity of the morpholino knockdown of *nxhl*. Consistent with this, *nxhl*  
377 morphants resulted in a high percentage of embryos with defects (81.55%, n=103 embryos in *nxhl*<sup>eli1</sup> MO  
378 and 100%, n=106 embryos in *nxhl*<sup>ATG</sup> MO) and low survival rate (45.78%, n=225 embryos in *nxhl*<sup>eli1</sup> MO  
379 and 17.68%, n=198 embryos in *nxhl*<sup>ATG</sup> MO) compared with controls (n=218 embryos) at 3 dpf (Figure 3A  
380 and Figure S7B). This confirmed that knockdown of *nxhl* certainly causes morphological defects in the heart  
381 and caudal fin in zebrafish.

382 We then used the *Tg(fli1a:EGFP)<sup>y1</sup>* zebrafish as a model to investigate the connections between the  
383 vascular system and these phenotypes. Embryos were injected with 4 ng control MO or *nxhl*<sup>eli1</sup> MO. We  
384 found that loss of *nxhl* caused intersegmental vessel (ISV) growth defect and disruption of the honeycomb  
385 structure in the CVP at 52 hpf (Figure 3B). Also, *nxhl*<sup>eli1</sup> morphant resulted in a thinner ISV growth and  
386 ectopic sprouts of dorsal aorta at the rear-somite with only 10% of complete ISVs (n=365 embryos)  
387 compared with 98% of complete ISVs in controls (n=335 embryos). We observed that the *nxhl* knockdown  
388 prevented the PAV formation (Figure 3B) and caused specific defects in CVP formation (Figure 3C).  
389 Quantification of loop formation and the area at CVP showed a 8.2-fold and 3-fold decrease in *nxhl*<sup>eli1</sup>  
390 morphants (n=10 embryos) at 52 hpf, respectively (Figure 3C). Our data indicate that *nxhl* plays a critical  
391 role in controlling PAV, ISV and CVP formation and vascular integrity during angiogenesis, which is an  
392 explanation strongly consistent with the heart and caudal fin phenotypes observed. What is the mechanism  
393 behind?

394 Endothelial cells (ECs) line the inner lumen of vessels and are the building elements of blood vessels,  
395 we then speculated that *nxhl* may affect angiogenesis via ECs. This is supported by the significant enrichment  
396 of the genes involved in blood vessel morphogenesis when *nxhl* was knocked down (Table S29). Since  
397 human Harbi1 gene shares DDE\_Tnp\_4 domain with *nxhl* (Figure 2E), it is supposed that both genes play  
398 similar roles. We used human umbilical vein endothelial cells (HUVECs) as a vascular epithelioid cells

399 model *in vitro*. Next, we designed siRNAs targeting human Harbi1, transferred siRNA into HUVECs and  
400 investigated their cell migration, invasion, and tube formation. Silence of Harbi1 significantly inhibited the  
401 tube formation and cell migration compared with controls (Figure 3D). Furthermore, the invasion abilities  
402 in Harbi1 defect cells are also significantly inhibited compared with controls (Figure 3D). Moreover, silence  
403 of Harbi1 significantly inhibited the angiogenesis of non-small cell lung cancer cell (A548) and human colon  
404 cancer cell (HCT116) *in vitro* (Figure S9). This highlights the pro-angiogenesis function of Harbi1 and  
405 indicates that *nxhl* like their human homolog Harbi1, play role in angiogenesis and anti-cancer process via  
406 ECs.

407

#### 408 ***Nxhl* Regulates *Ptprb* Expression and Angiogenic Networks**

409 To investigate how *nxhl* mediates angiogenesis, we firstly examined transcriptome sequencing (RNA-seq)  
410 data from zebrafish after injection of 4 ng *nxhl*<sup>eli1</sup> MO at 3 dpf. We found that loss of *nxhl* greatly changes  
411 the transcriptome with 1955 down-regulated and 698 up-regulated (Figure S10; Table S21). We noticed that  
412 in the KEGG pathways associated with angiogenesis development are significantly enriched in the *nxhl*-  
413 silenced group (Figure S11; Table S22-26). We speculated that the transcription of genes linked to  
414 angiogenesis development may also be significantly changed in the *nxhl*-silenced zebrafish. We then  
415 screened and examined the expression of 18 genes that previously documented to be closely related to heart  
416 defects and/ or angiogenesis.<sup>53-57</sup> Consistent with the RNA-seq data, we found that 13 of these genes (*ptprb*,  
417 *tie2*, *nr2f1a*, *s1pr1*, *hey2*, *dot1L*, *hand2*, *erbb2*, *klf2a*, *mef2cb*, *mef2aa*, *ephB2a* and *cx40.8*) were significantly  
418 decreased while two genes (*vegfaa* and *vegfr2*) increased sharply. *S1pr2*, *egfl7*, and *nrg2a* were kept  
419 unchanged (Figure 4A-D). Notably, the arterial marker *ephB2a* and venous marker *erbb2* were decreased in  
420 *nxhl* morphants compared to the wild-type (Figure 4D). Normally, the increase of *vegfaa* and *vegfr2* is linked  
421 to the enhancement of vascular system.<sup>58, 59</sup> However, in our study, both genes increased while others

422 decreased when *nxhl* was silenced. We speculated this is a consequence of a negative feedback regulation to  
423 avoid an excessive decrease in the vascular system. We found that *nxhl*<sup>e11</sup> morphants result in decrease of  
424 the *nxhl* at protein level. *Ptprb*, the most decreased gene at mRNA level, is also greatly reduced at the protein  
425 level. The *s1pr1*, *hand2*, *dot1L*, and *hey2* proteins were also downregulated compared with controls (Figure  
426 4E). As previously reported, *ptprb*, *tie2*, *nr2f1a*, *s1pr1*, *vegfaa* and *vegfr2* normally contribute to vascular  
427 development and deletion of each of them leads to defects on the vascular system during embryo  
428 development,<sup>14, 58-61</sup> while loss of *dot1L*, *hand2*, *erbb2*, *mef2cb*, *mef2aa*, *ephB2a* or *cx40.8* always results in  
429 angiogenesis system or heart development defects.<sup>55, 62-68</sup> *Hey2* and *klf2a* have been implicated in the  
430 regulation of both angiogenesis and heart development.<sup>69, 70</sup> Based on these reports, we built a schematic  
431 diagram of the network as shown in Figure 4F. This network demonstrates that silence of *nxhl* does  
432 downregulate the key genes that are essential for heart and /or vascular development. To this end, our results  
433 showed that loss of *nxhl* greatly affects the expression of these key genes in the network, suggesting that the  
434 heart and vascular phenotypes caused by *nxhl* deletion are greatly due to the regulation of these genes, and  
435 the expression profiles of these genes explain the *nxhl* deficient-induced phenotypes. Thus, we then asked  
436 how *nxhl* controls the angiogenesis and angiogenic networks.

437

### 438 **Loss of *Ptprb* Duplicates the Phenotypes of *Nxhl* Deficiency**

439 As described above, we noticed that *ptprb* is the most downregulated gene after silence of *nxhl* and is the  
440 one that closely linked to both vascular integrity and angiogenesis as well.<sup>11, 13, 19, 71-73</sup> To test whether there  
441 is a positive connection between *nxhl* and *ptprb*, we silenced *ptprb* by injection of 4 ng *ptprb*<sup>e4i4</sup> and *ptprb*  
442 <sup>ATG</sup> morphants designed (Figure S12, Table S30). Both *ptprb* morphants resulted in slight pericardial edema,  
443 shortened body axis and severe body axis bending in zebrafish (Figure 5A; Figure S12). Moreover, heartbeat  
444 and circulation in the caudal vein (CV) is visible in the control fish (Supplementary Movie 3,4), but is

445 abnormal in *ptprb*-MO-injected fish (Supplementary Movie 5-8). *Ptprb* morphants also resulted in a high  
446 percentage of embryos with defects (75.48%, n=208 embryos in *ptprb* MO and 0.94%, n=212 embryos in  
447 control) and lower survival rate compared with controls at 50 hpf (Figure 5A). Both *ptprb* morphants  
448 dramatically disrupted normal splicing of *ptprb* (Figure 5B-D), decreased the survival rate, but unchanged  
449 the *nxhl* expression, indicating high efficiency and specificity of the morpholino knockdown of *ptprb*. In the  
450 vascular system, loss of *ptprb* leads to an indefinite absence or deformity of DLAVs (blue arrowhead) and  
451 ISVs in the tail end (white and yellow arrowhead), and a decrease of PAV (red arrowhead) formation (Figure  
452 5E). Knockdown of *ptprb* caused significantly decrease of the mean diameter of ISVs compared with  
453 controls (Figure 5F). Also, *ptprb* morphants caused CVP sinus cavities defects (Figure 5G), and resulted in  
454 a 5.6-fold and 2.2-fold decrease of CVP loop formation and CVP area (n=83 embryos) at 50 hpf, respectively  
455 (Figure 5G). These data are to some extent consistent with previous reports<sup>57</sup> and strongly suggest that loss  
456 of *ptprb* phenocopies *nxhl* deficiency. Moreover, We found that most of the 15 genes in *ptprb*-knockdown  
457 experiment present an expression profile similar to that in *nxhl*-knockdown experiment, except *vegfaa* and  
458 *vegfr2* (Figure 5H). To this end, we logically concluded that knockdown of *ptprb* mimics phenotypes of *nxhl*  
459 deficiency, and both should act in the same signaling pathway. However, which one is downstream of the  
460 other is unclear. Therefore, we examined the *nxhl* expression after silence of *ptprb*, and we found that it was  
461 kept unchanged (Figure 5D), but we observed a significant decrease of *ptprb* expression after silence of *nxhl*.  
462 This confirms that *ptprb* acts at the downstream of *nxhl*.

463

#### 464 ***Nxhl* Regulates VE-PTP (*ptprb*) through Interactions with NCL**

465 As mentioned above, among the 18 genes associated with heart and vascular development, 15 genes were  
466 significantly changed by both *nxhl* and *ptprb* morphants. We suppose these genes may be part of a regulatory  
467 network of their own. We then built a schematic diagram of the network according to previous reports (Figure

468 4F). This network presents connections between most of these genes, suggesting a cooperative regulation  
469 mechanism on the heart and vascular development. As we already knew that *ptprb* acts downstream of *nxhl*,  
470 we next asked if *nxhl* directly interacts with *ptprb* to mediate these genes. Thus, we designed *nxhl* probes  
471 and conducted a ChIRP-MS experiment in zebrafish to find out those proteins binding to *nxhl*. Eleven  
472 proteins with change folds above 2 were discovered (Figure 6A). This indicates that the *nxhl* RNA may  
473 interact with these proteins. Unexpectedly, *ptprb* was not found in these proteins (Figure 6A). This suggests  
474 that proteins other than *ptprb* may interact with *nxhl*. We next focused on the proteins that are associated  
475 with the vascular system, and nucleolin (NCL) (Figure 6A) aroused our interest because of its molecular  
476 conservation and important functions on angiogenesis.<sup>31, 74</sup> Loss of NCL in zebrafish causes oedema and  
477 body axis bending,<sup>75</sup> as well as suppression of adhesion, proliferation and migration of HUVECs.<sup>76</sup> These  
478 phenotypes are identical to the phenotypes caused by *nxhl* depletion, suggesting NCL may associate with  
479 *nxhl*. To figure out whether *nxhl* interacts with NCL, we performed RNA Immunoprecipitation (RIP) using  
480 the NCL protein as bait protein in 293T cells (Figure S13, S14, S15) and then detected the *nxhl* RNA using  
481 qPCR. We found that *nxhl* RNA is significantly higher than that in IgG control in the RNAs pulled-down by  
482 the NCL protein (Figure 6B). The RNA pulled down was amplified and the sequencing results confirmed  
483 that it is *nxhl* mRNA. This indicates that the NCL protein reversely interacts with *nxhl* RNA. Therefore,  
484 these experiments prove that *nxhl* RNA and NCL protein interact physically.

485 However, still no evidence was found on the interaction between *nxhl* and *ptprb*. Could it be that NCL  
486 interacts with *ptprb*, thus bridging *nxhl* and *ptprb*? Such scenario was never proposed or documented before.  
487 However, a report showed that VEGF interacts with NCL.<sup>77</sup> As *nxhl* acts similarly to VEGF on angiogenesis  
488 development, we then supposed that NCL might also interact with *ptprb* or its human homologue VE-PTP,  
489 the key molecule in angiogenesis. To test this hypothesis, we detected VE-PTP mRNA using the same RNAs  
490 pulled-down by NCL protein, and we found that VE-PTP mRNA is significantly higher than that in IgG

491 control. The RNA pulled down was amplified and the sequencing results proved that it is VE-PTP mRNA.  
492 This confirms that the NCL protein can also interact with VE-PTP mRNA physically (Figure 6B). We next  
493 verified this interaction in 293T cells using the VE-PTP RNA pulldown experiment in the reverse way, and  
494 the result of western blotting against NCL protein supports the existence of interaction between VE-PTP and  
495 NCL (Figure 6C). However, whether this interaction occurs between NCL and *ptprb* in zebrafish is unclear.  
496 We next designed a zebrafish *ptprb* gene-specific probe to pull down the proteins that interact with *ptprb* in  
497 the juvenile zebrafish. We found that the NCL protein strongly binds with *ptprb* (Figure 6C). These results  
498 indicate that the NCL protein not only interacts with VEP-PTP in 293T cells but also with *ptprb* in zebrafish.

499 So far, we proved that *nxhl* and NCL, NCL and VEP-PTP (*ptprb*) interact physically. However, how  
500 *nxhl* regulates NCL and *ptprb* is unclear. To address this issue, we micro-injected 4 ng *nxhl*-e1i1-MO in one  
501 cell stage embryo, and found that resemble phenotypes were induced as that shown in Figure 3AB and Figure  
502 S16. Meanwhile, we found that loss of *nxhl* not only causes a significant decrease of NCL mRNA and total  
503 protein level but also leads to decrease of phosphorylated T76 and increase of the acetylated K88 of the NCL  
504 protein (Figure 6D). This suggests that knockdown of *nxhl* significantly affects the expression of NCL, which  
505 plays vital functions in angiogenesis,<sup>31</sup> although the impact of phosphorylation and acetylation of NCL  
506 protein on the heart and vascular development have not been deeply understood yet.<sup>74</sup> Then we investigated  
507 the expression of the downstream gene *ptprb*, and found that loss of *nxhl* also decreases *ptprb* at both mRNA  
508 and protein levels (Figure 6D). These results suggest that silence of *nxhl* leads to angiogenesis defects due  
509 to the downregulation of both NCL and *ptprb* via the interactions of *nxhl*-NCL and NCL-*ptprb*, which  
510 consequently mediates the angiogenesis-linked landmark gene network.

511

## 512 **NCL Regulates Angiogenesis and VE-PTP *in vitro***

513 Although the physical interactions between *nxhl* and NCL and NCL and *ptprb* (VE-PTP) and regulatory role

514 of *nxhl* on NCL and *ptprb* (VE-PTP) are confirmed in our study, whether NCL regulates *ptprb* (VE-PTP) is  
515 still unknown. We next examined the functions of NCL on angiogenesis and expression of VE-PTP by silence  
516 of NCL in HUVECs. As shown in Figure 7, silence of NCL not only significantly inhibited the tube formation  
517 but also the cell migration of HUVECs comparing with the controls. Notably, silence of NCL greatly  
518 decreased the expression of VE-PTP at both mRNA and protein levels, suggesting that NCL not only interacts  
519 with VE-PTP but also regulates its expression. This highlights the pro-angiogenesis function of NCL and its  
520 direct regulatory role on VE-PTP expression, and proves that the *nxhl*-NCL-VE-PTP (*ptprb*) signaling  
521 pathway is logical and reasonable for angiogenesis.

522

### 523 ***Nxhl* Controls Angiogenesis by Targeting VE-PTP (*ptprb*) and Linking Angiogenesis Regulatory Genes**

524 It is confirmed that loss of *nxhl* not only downregulates *ptprb* but the angiogenesis landmark genes (Figure  
525 4F), with the addition of finding that *nxhl* binds to NCL which interacts with VE-PTP (*ptprb*), we conclude  
526 that *nxhl* controls angiogenesis through *nxhl*-NCL-VE-PTP (*ptprb*)-linked angiogenesis regulatory genes.  
527 This, for the first time, uncovers the existence of upstream regulatory genes of VE-PTP (*ptprb*). Based on  
528 these data, we built a new schematic diagram based on the network in Figure 4F that shows the novel *nxhl*-  
529 NCL-VE-PTP (*ptprb*) signaling links to the keystone angiogenesis genes (Figure 8A vs. Figure 4F). We also  
530 made a schematic diagram to describe the possible mechanism underlying *nxhl*-induced phenotypes of  
531 pericardial oedema and vascular patterning defects (Figure 8B). Knockdown of *nxhl* significantly and  
532 broadly downregulates angiogenesis-associated landmark genes, including *dot1L*, *hand2*, *erbb2*, *mef2aa*,  
533 *n2rf1a*, *hey2*, *slpr1*, *tie2*, *ptprb*, *mef2cb*, *ephB2a*, *klf2a* and *cx40.8*, through *nxhl*-NCL-VE-PTP  
534 (*ptprb*) pathway, while *vegfr2* and *vegfaa* negative feedback control this downregulation. Moreover, loss of  
535 *nxhl* increases the phosphorylation of NCL(T76) and decreases the acetylation NCL (K88), indicating that  
536 *nxhl* may control angiogenesis by impacting NCL posttranslational modification to regulate downstream VE-  
537 PTP signaling pathways. This highlights the crucial role of *nxhl* on angiogenesis development via a hitherto

538 unreported *nxml*-NCL-VE-PTP (*ptprb*) pathway, which extends the upstream regulatory member of keystone  
539 gene VE-PTP (*ptprb*). We conclude that *nxml* controls angiogenesis by targeting VE-PTP (*ptprb*) through  
540 interaction with NCL and linking vascular keystone regulatory genes. Given the extreme importance of the  
541 angiogenesis development, and the broad connections with landmark genes, we believe the finding of this  
542 novel signaling pathway to be of considerable importance for the study of the angiogenesis development and  
543 angiogenesis-dependent diseases.

544

## 545 **DISCUSSION**

546 Previous studies showed that VE-PTP is a key player in regulation of angiogenesis and EC adherens  
547 junction,<sup>12-15</sup> and is a potential therapeutic target for angiogenesis-dependent diseases.<sup>7, 8</sup> It binds to some  
548 proteins, such as Tie2, VEGFR2, VE-cadherin and FGD5, that mediate angiogenic signaling pathways.<sup>18, 25-  
549 27, 29</sup> In the present study, we identified a novel zebrafish gene *nxml*. It controls angiogenic processes *in vitro*  
550 and *in vivo*. Deletion of *nxml* causes angiogenesis-associated phenotypes. Loss of VE-PTP duplicates the  
551 phenotypes caused by the upstream *nxml* deficiency, confirming both act in the same angiogenic signaling  
552 pathway. We for the first time show that *nxml* physically binds to NCL which interacts with VE-PTP and  
553 thereby controls angiogenesis. Our study defines a novel *nxml*-NCL-VE-PTP signaling pathway for  
554 angiogenesis regulation.

555 Anti-angiogenic drugs have been a focus of study and lots of inhibitors of angiogenesis are currently  
556 used as monotherapy or in combination with chemotherapy or cytokine treatment.<sup>78</sup> Previous studies showed  
557 that AKB-9778, a specific inhibitor of VE-PTP, has demonstrated promising clinic perspective for treatment  
558 of angiogenesis-dependent diseases, although it is still under clinical investigation.<sup>31-34</sup> This highlights the  
559 great value of VE-PTP on anti-angiogenic agents. Logically, targeting the upstream regulator of VE-PTP  
560 may achieve the same or better effects to that of AKB-9778, because its broader and stronger modulatory  
561 forces. However, few upstream regulation mechanisms of VE-PTP has been documented yet. In this study,



562 we identify *nxml* as a novel powerful upstream regulator of VE-PTP. We find that *nxml* plays a role in  
563 angiogenesis not only because it sharply decreases expressions of VE-PTP and other key angiogenic genes,  
564 but also the *nxml* deletion-caused angiogenesis phenotypes, such as pericardial oedema, defects of caudal fin,  
565 intersegmental vessel and caudal vein plexus, are duplicated by the VE-PTP deficiency. These phenotypes  
566 of VE-PTP knockdown are mostly identical to a previous study using different morphants to ours.<sup>57</sup>  
567 Additionally, no changes occur in *nxml* expression upon VE-PTP knockdown, but the expression of VE-PTP  
568 significantly decreases upon loss of *nxml*. This highly implicates that *nxml* regulates VE-PTP at its upstream  
569 and both act in a same signaling pathway. Importantly, the splice-blocking *nxml* MO displayed phenotypes  
570 which are totally overlapping with the translation-blocking MOs, confirming the specificity of phenotypes  
571 obtained by *nxml* injection rather than MO off-target effects. Moreover, *nxml* controls angiogenesis via ECs  
572 migration and tube formation, which is consists with the angiogenic characteristics of VE-PTP on EC  
573 adhesion and integrity,<sup>16-18</sup> confirming its angiogenesis controlling function acts via ECs. This is also  
574 strongly supported by our findings that silence of the highly conserve human homologue of *nxml* not only  
575 inhibits the HUVECs migration and tube formation but suppresses the migrations and invasions of cancer  
576 cell lines by inhibiting ECs (Figure S9). All these data suggest that *nxml* is a powerful upstream angiogenesis  
577 governor targeting VE-PTP.

578 On the other hand, the effects of *nxml* controlling angiogenesis depend on its binding with NCL, which  
579 simultaneously bridges *nxml* and VE-PTP. To our best knowledge, this is the first description on the  
580 interactions between *nxml* and NCL, NCL and VE-PTP, uncovering a novel angiogenesis signaling complex  
581 at the upstream of VE-PTP. NCL expresses broadly in all cells in a proliferation-dependent manner<sup>79</sup> and  
582 almost all compartments of cells. Like VEP-TP, NCL also associates both cancer and other angiogenic  
583 diseases. However, this function is more likely related to the cell surface NCL rather than that in other  
584 compartments. The cell surface NCL is clustered and highly expressed in ECs of angiogenic blood vessels

585 during angiogenesis,<sup>26, 27, 80</sup> suggesting that NCL functions as an angiogenic gene. Also, it expresses at the  
586 surface of tumor cells, including tumor cells and tumor vasculature. This allows the targeting of different  
587 cellular compartments of solid tumors. Additionally, cell surface NCL has been identified in cancer stem  
588 cells (CSCs) from different breast cancer cells lines.<sup>81</sup> Since CSCs are highly tumorigenic,<sup>82, 83</sup> the  
589 association of NCL with the stemness highlights the value of NCL as a potential therapeutic target.<sup>84</sup>  
590 Importantly, dysregulation of NCL associates with higher risk of recurrence or poorer overall survival for  
591 some cancers.<sup>85</sup> These define NCL as both prognostic marker and therapeutic target, highlighting its great  
592 value on development of anti-angiogenic drugs.<sup>31, 74</sup> In this study, we identified the direct interactions  
593 between *nxhl* and NCL, and NCL and VE-PTP (*ptprb*) in both zebrafish and 293T cells by ChIRP, RNA  
594 Immunoprecipitation and RNA pulldown methods, although we did not yet figure out which subset of NCL  
595 (surface, nucleolar or cytoplasmic NCL) participates in this interaction. Importantly, we proved that silence  
596 of NCL inhibits angiogenesis of HUVECs and expression of VE-PTP at both mRNA and protein levels. This  
597 further supports that NCL plays key roles on angiogenesis by directly controlling downstream VE-PTP.  
598 Moreover, deletion of *nxhl* causes a significant decrease of NCL at both mRNA and total protein levels,  
599 suggesting that *nxhl* significantly affects and regulates the NCL. This is further supported by the decrease of  
600 the phosphorylated T76 and increase of the acetylated K88 of NCL protein upon the *nxhl* knockdown (Figure  
601 6D). Previous study suggested that NCL phosphorylation status heavily affects its cellular  
602 compartmentalization.<sup>86</sup> It promotes EGFR phosphorylation, dimerization and cell growth.<sup>28, 87</sup> It also  
603 promotes HER2 (namely Erbb2) phosphorylation and subsequent MAPK/ Erk pathway activation.<sup>30</sup>  
604 Clinically, combination treatment with NCL and HER2 inhibitors exhibited superior efficacy compared with  
605 single treatment in the invasion capacity of breast cancer cells.<sup>88</sup> Except EGF and HER2, NCL also binds to  
606 VEGF,<sup>26</sup> whose receptor VEGFR2 is tightly associated with VE-PTP resulting in increase of VEGFR2  
607 phosphorylation and activation.<sup>19</sup> Since EGFR, HER2 and VE-PTP/VEGFR2 have been tightly associated

608 with angiogenesis, we consider *nxhl* may control angiogenesis by affecting NCL phosphorylation which  
609 regulates downstream EGFR, HER2 or VE-PTP/VEGFR2 signaling pathways. Notably, in our study,  
610 expressions of VEGFR2 and Erbb2 are significantly affected by *nxhl* knockdown, partially supporting this  
611 point of view. However, this needs to be investigated in our future works. In addition, NCL acetylation at  
612 K88 was previously described *in vivo* and *in vitro*, and this post-translational modification sharply changes  
613 its cellular localization. Previous study suggested that NCL may be involved in pre-mRNA synthesis or  
614 metabolism because of the presence of NCL-K88ac in nuclear speckles.<sup>89</sup> However, the characterization and  
615 functional significance of NCL acetylation in angiogenesis are still unclear. What the consequences of NCL-  
616 K88ac increase on *nxhl* or VE-PTP and subsequent pathways needs further investigation. Taken together,  
617 our data enabled us to conclude that *nxhl* regulates the angiogenesis via the *nxhl*-NCL-VE-PTP (*ptprb*)  
618 pathway.

619 The strong power of *nxhl* on angiogenesis controlling also relies on the effects of some other crucial  
620 downstream angiogenic genes (such as Tie2, VEGFaa, VEGFR2, S1pr1 and Hey2) which broadly associate  
621 VE-PTP signaling (Figure 4, Figure 8). What needs to be stressed is that the expressions of these genes  
622 explain the phenotypes induced by the *nxhl* deficiency. They all play irreplaceable roles in multiple aspects  
623 of angiogenesis development. For instance, Hand2 is vital in heart development in zebrafish and mouse.<sup>90</sup>  
624 <sup>91</sup> It has been identified as a specifier of outflow tract cells in the mouse by single cell sequencing.<sup>92</sup> Hey2  
625 mediates the dynamics of cardiac progenitor cells addition to the zebrafish heart.<sup>69</sup> It is identified as a  
626 component of the NKX2-5 cardiac transcriptional network regulating the early stage of the human heart  
627 development.<sup>93</sup> The Dot1L,<sup>63</sup> Mef2aa,<sup>64</sup> Mef2cb,<sup>65</sup> Erbb2,<sup>66</sup> Klf2a<sup>70</sup> and EphB2a<sup>94</sup> also play key roles in the  
628 growth of the chamber, cardiomyocyte differentiation, myocardial cell addition, cardiac trabeculation, atrial  
629 fibrillation, gap junction, valvulogenesis and myocardial trabeculation during heart development.  
630 Importantly, the heart and vascular development are always linked. Previous studies showed that silence of

631 zebrafish *S1pr1* not only leads to global and pericardial edema, lack of blood circulation, altered posterior  
632 cardinal vein structure, reduced vascularization in ISVs and CVPs,<sup>61</sup> but also regulates the endothelial barrier  
633 integrity via the *S1pr1*/VE-cadherin/*EphB4a* pathway.<sup>95</sup> Similar phenotypes can be induced by the  
634 knockdown of *Nr2f1a* in zebrafish due to the decrease of cell proliferation and migration instead of cell death  
635 in ECs.<sup>60</sup> Moreover, mutation of *Nr2f1a* results in smaller atria due to a specific reduction in the atrial  
636 cardiomyocyte number and an increase of the rate of atrial cardiomyocyte differentiation.<sup>96</sup> Another key gene,  
637 *Tie2*, is essentially required for ISV growth, sprouting, migration, and proliferation of tip cells and acts  
638 coordinately with VEGF signaling to control angiogenesis *in vivo*.<sup>97</sup> Loss of *Tie2* leads to death at E10.5 due  
639 to vessel remodeling defects and lack of trabeculation.<sup>98</sup> Notably, Ang-*Tie2* system is indispensable for  
640 vascular and lymphatic development.<sup>99</sup> The anti-angiogenic effects of VE-PTP inhibitor, AKB-9778, likely  
641 rely on the Ang-*Tie2* pathway.<sup>17</sup> In our study, *nxml* deletion leads to significant decrease of *Tie2*, suggesting  
642 it regulates not only VE-PTP but also Ang-*Tie2* system, which crosstalk with VE-PTP. From this point of  
643 review, *nxml* is a multifunctional master of angiogenesis process. This explains our findings that the  
644 phenotypes induced by *nxml* knockdown mostly resemble the phenotypes caused by deletion of these genes  
645 associate with VE-PTP. Although the specific mechanisms underlying need further elucidation, given the  
646 extreme importance of these genes in angiogenesis development, we consider the phenotypes caused by *nxml*  
647 morphants as direct or indirect consequences of the down-regulation of VE-PTP and these key genes. We  
648 believe the fire-new *nxml*-NCL-VE-PTP signaling pathway is a highlight for vertebrate angiogenesis  
649 development regulation.

650 In conclusion, we clearly demonstrate that a novel gene *nxml* controls angiogenesis by targeting VE-  
651 PTP through interaction with NCL whose posttranslational modification (phosphorylation and acetylation)  
652 may affect downstream VE-PTP signaling pathways. Furthermore, we have elucidated some of the crucial  
653 downstream pathways that may be implicated in regulating the angiogenesis. This study reveals a fire-new

654 *nxhl*-NCL-VE-PTP signaling pathway governing vertebrate angiogenesis development, implicating its great  
655 potential as therapeutic target for angiogenesis-dependent diseases.

656  
657

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668

## 669 **Author contributions**

670 H.L.L and X.H.C designed the scientific objectives and oversaw the project. H.L.L., X.H.C., Y.Z.Z., J.X.P.,  
671 and Y.L discussed the primary ideas of the article. Y.D.Z, J.X.P., Y.L., Y.H., Q.Y.L., P.P.H., C.L.Y., P.Y.W.,  
672 X.L.C., and P.F.F. collected samples for sequencing DNA and RNA. C.M.J. and their colleagues performed  
673 genome sequencing, assembly and annotation. C.M.J. and H.Y.Y performed phylogenomic and whole  
674 genome duplication evolution analysis. C.M.J. H.Y.Y., H.L.L., and Y.D.Z performed RNA-seq analysis.  
675 H.L.L and Y.D.Z performed functional assay of zebrafish *nxhl* gene and Harbi1 gene. C.M.J, H.Y.Y., H.L.L.,  
676 and Y.D.Z prepared the supplemental data and method. C.M.J. and H.L.L prepared the draft manuscript with  
677 input from all other authors. H.L.L., X.H.C., Y.L., and H.K.Z. discussed and revised the manuscript.

678

## 679 **Data availability**

680 The authors declare that all data reported in this study are fully and freely available from the date of  
681 publication. This Whole Genome Shotgun project has been deposited at DDBJ/ENA/GenBank under the  
682 accession WOFJ000000000. The version described in this paper is version WOFJ01000000. The draft genome  
683 data (genome assembling and annotations) and RNA-Seq data of the embryo are available under BioProject  
684 PRJNA574895. Transcriptome (Illumina) data of *nxml* silence are available in the Sequence Read Archive  
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686

## 687 **Disclosures**

688 The authors declare no competing financial interests.

689

## 690 **Supplemental material**

691 Supplemental Information (Notes and Methods)

692 Supplemental Figures (Figure S1-S16)

693 Supplemental Tables (Table S1-S28)

694 Supplemental videos (Movie 1-8)

695

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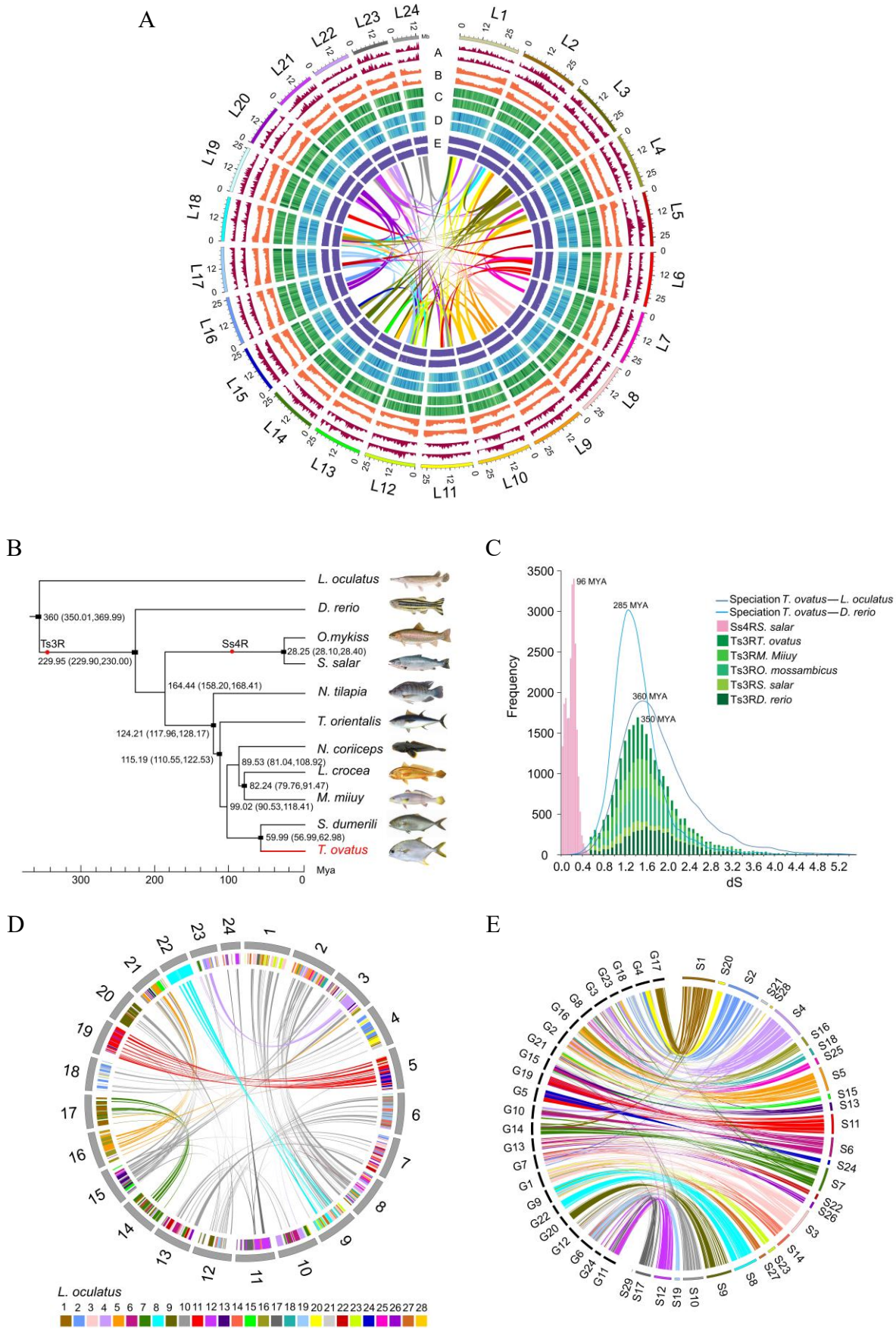
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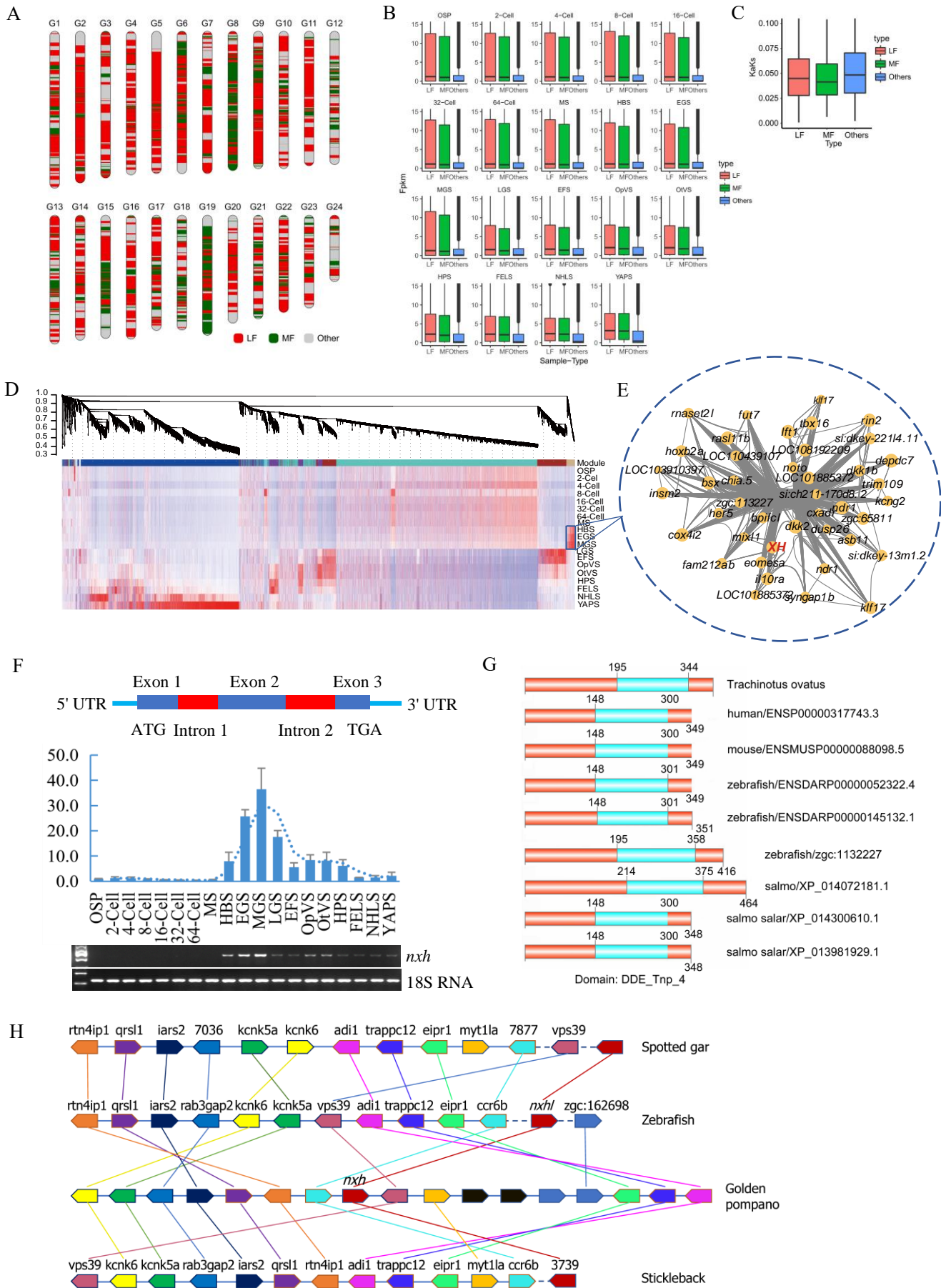
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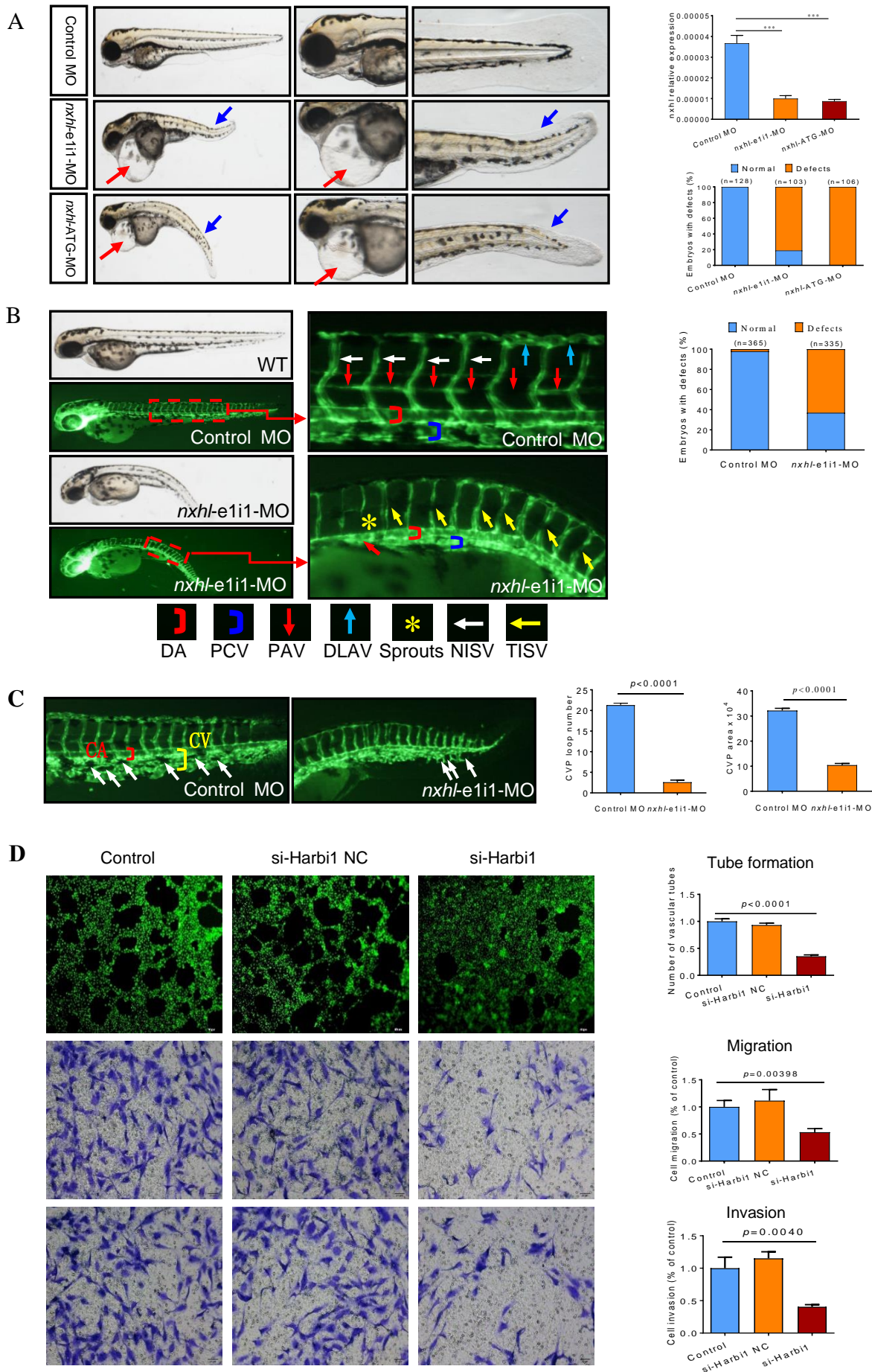
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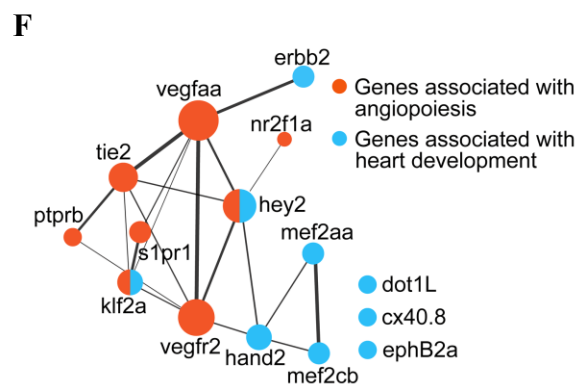
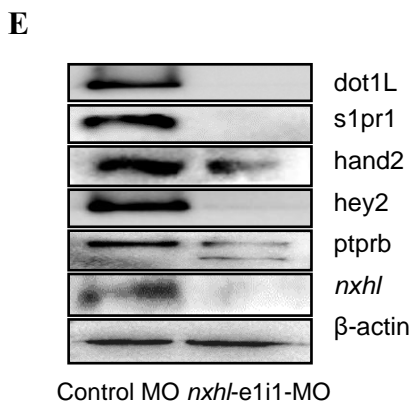
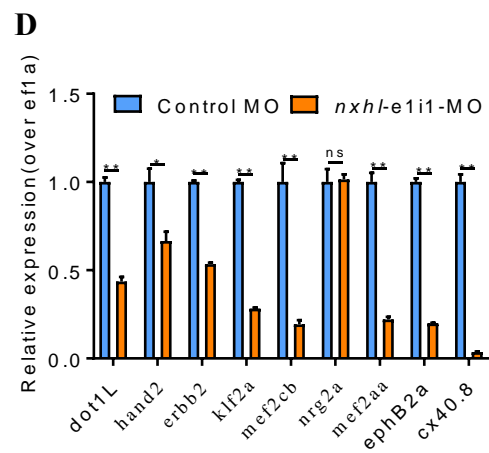
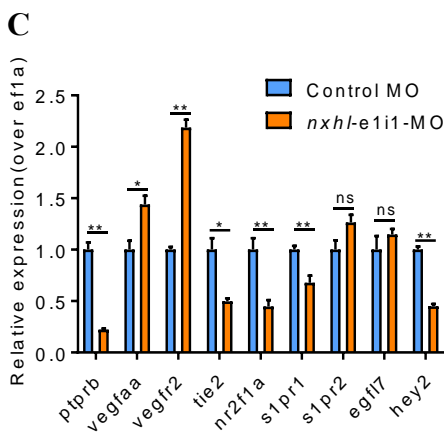
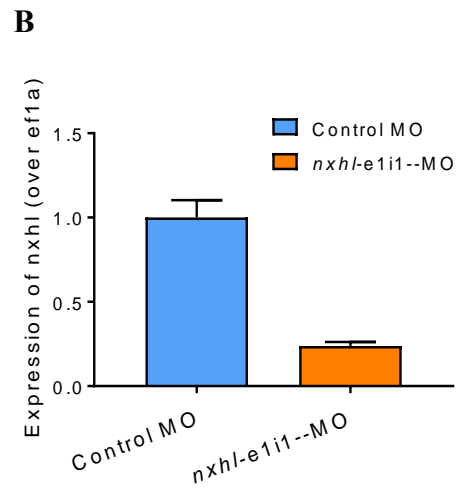
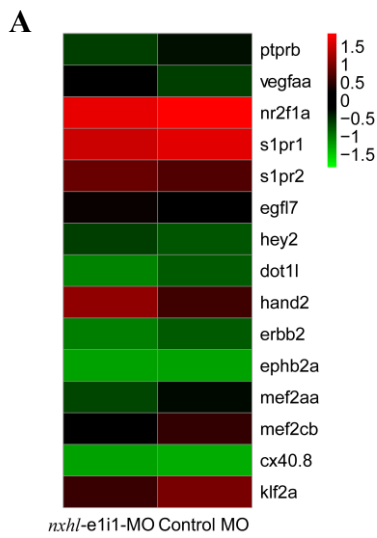


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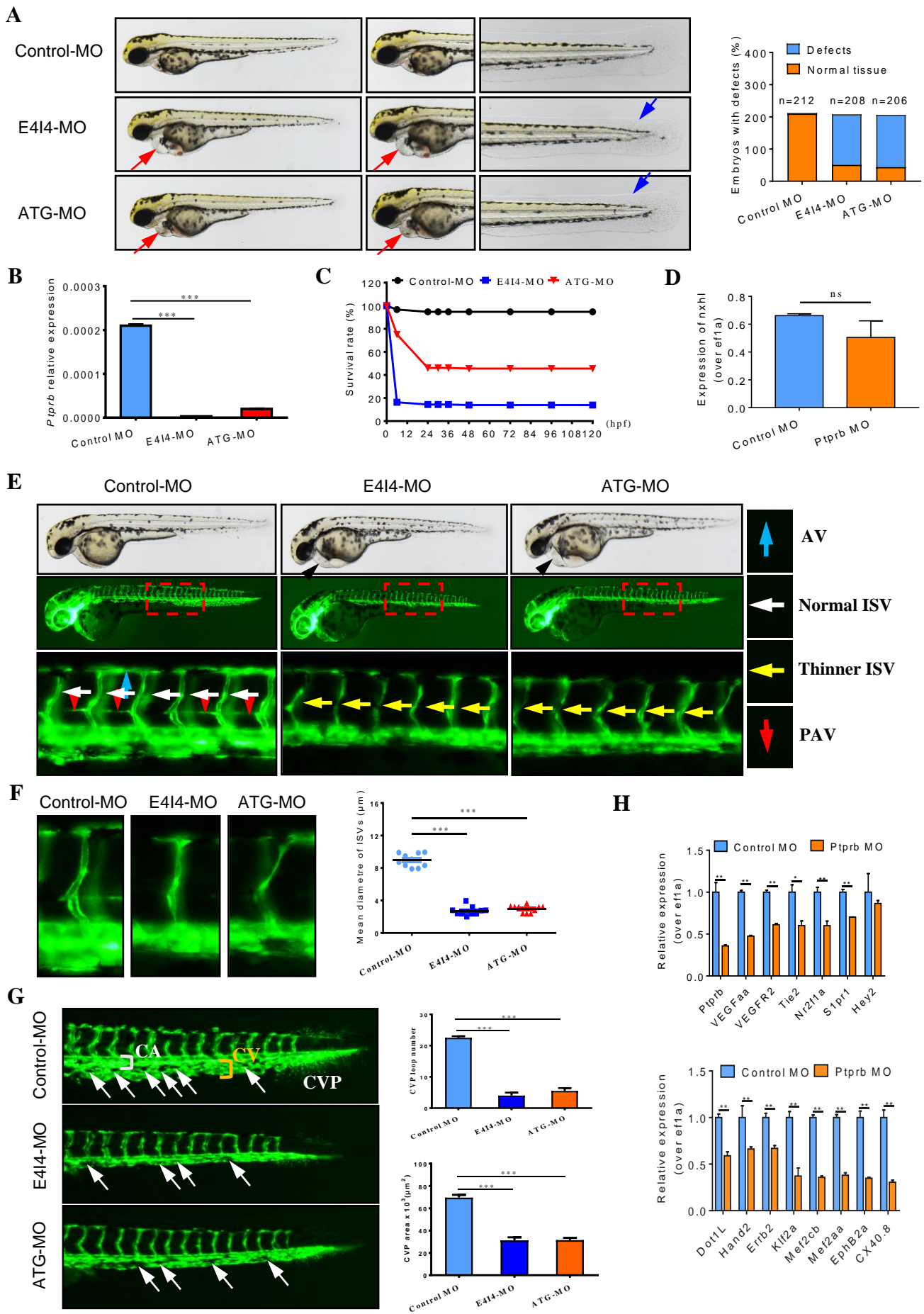
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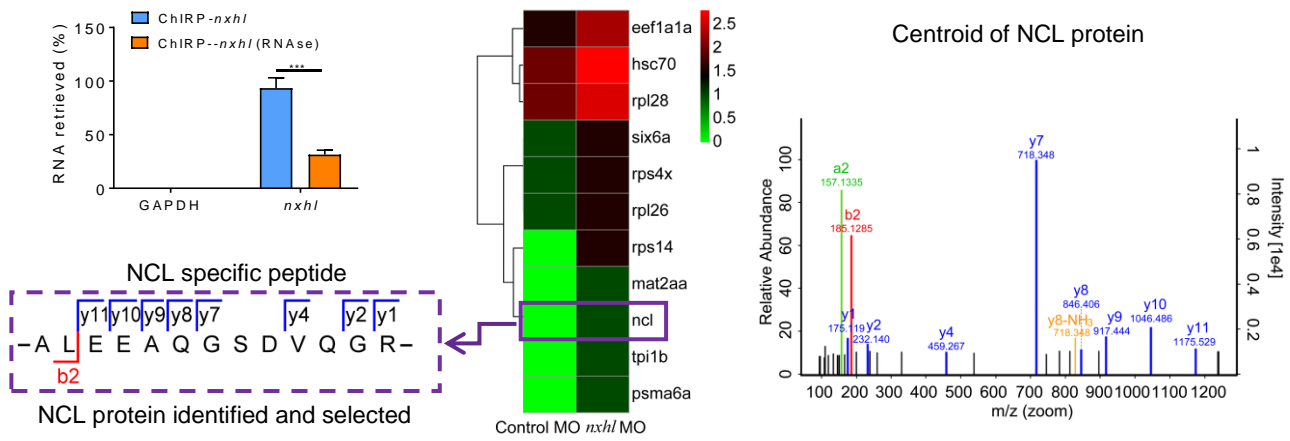
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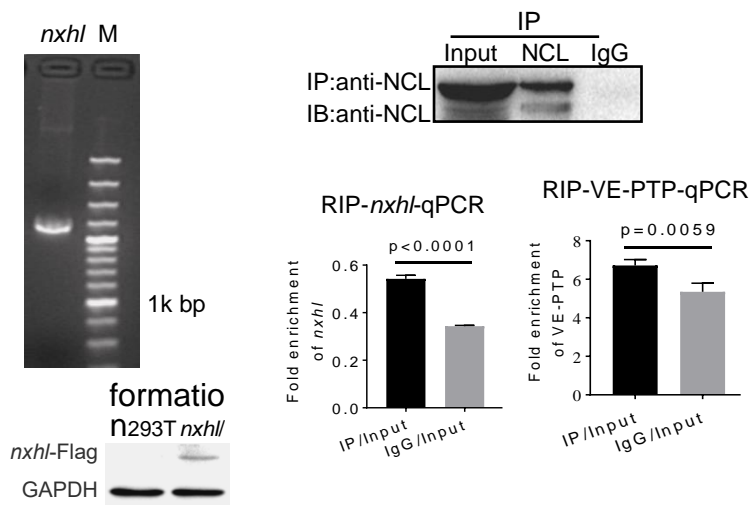




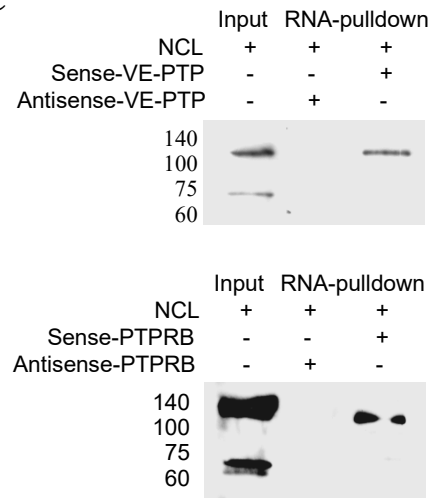
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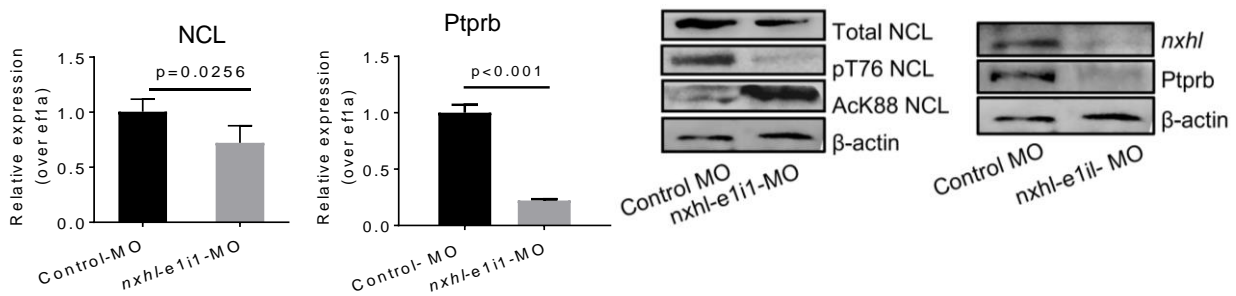
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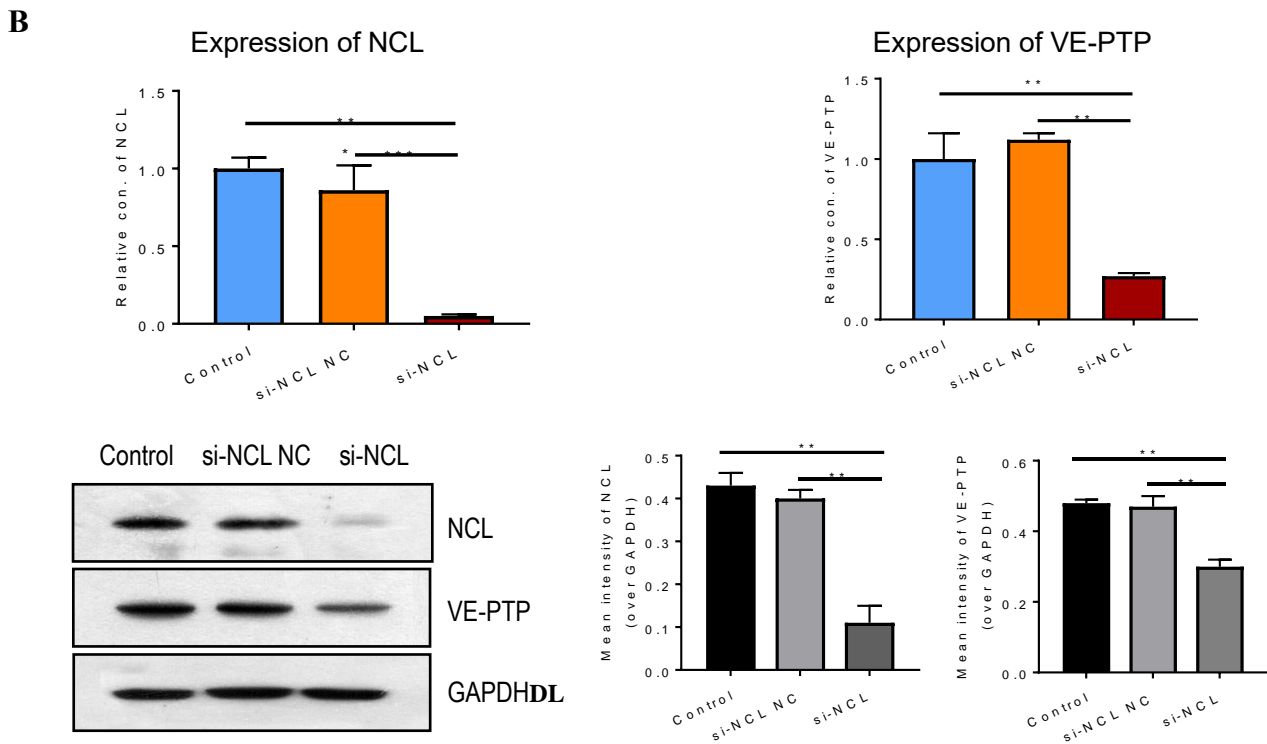
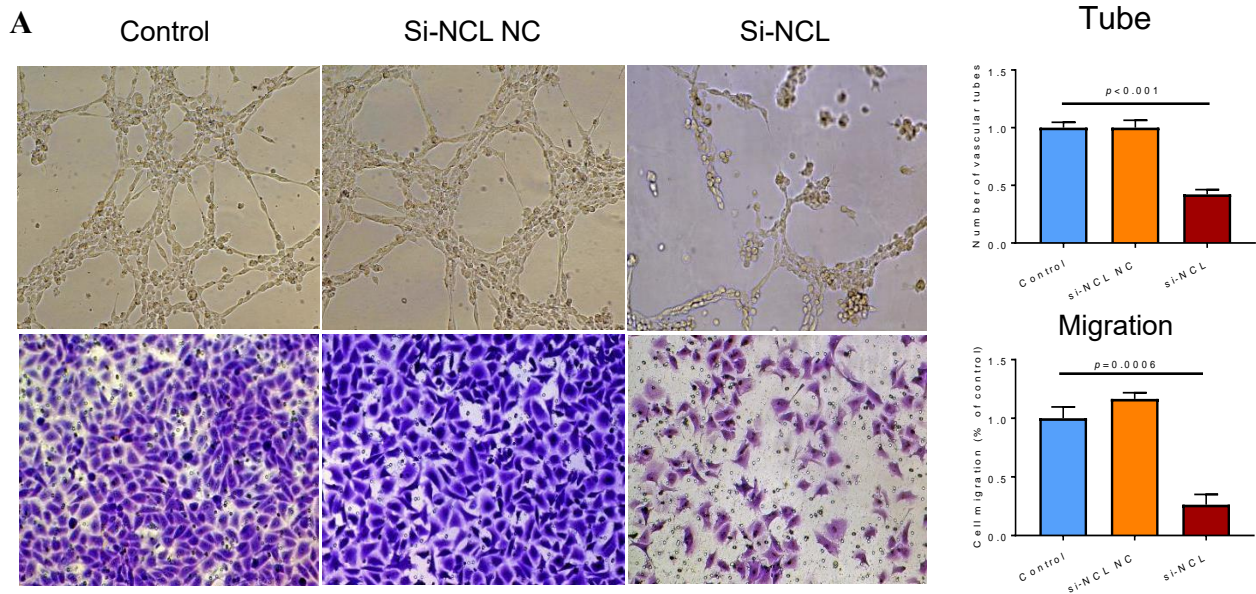
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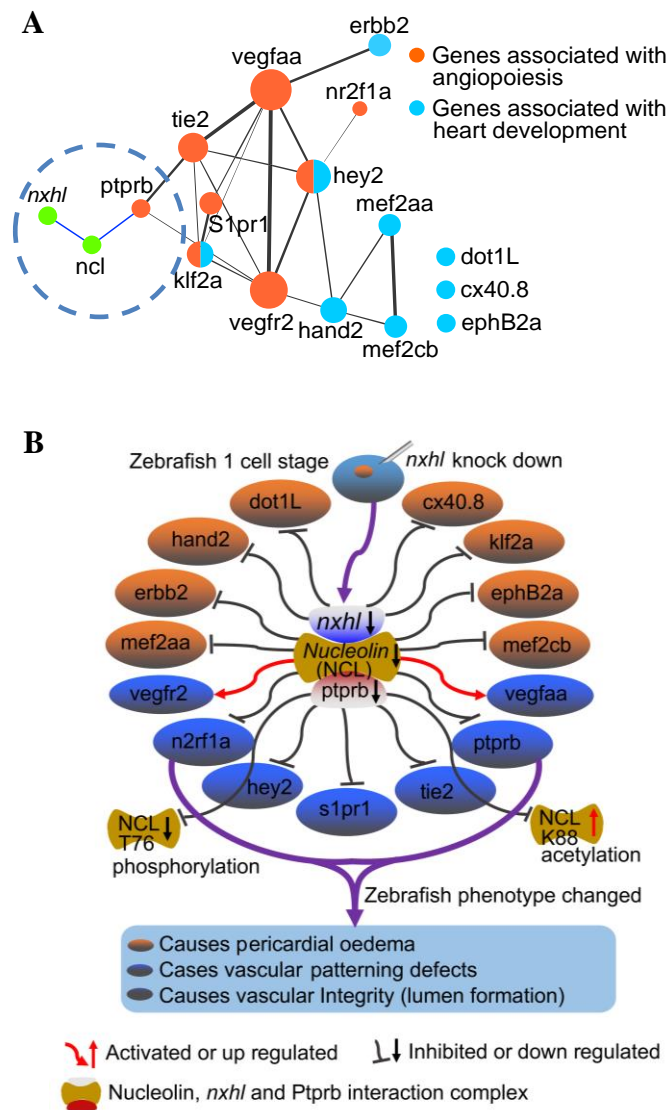
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## FIGURE LEGENDS

**Figure 1. WGD of golden pompano notifies vertebrate karyotypes evolution.** **A**, Overview of golden pompano (*Trachinotus ovatus*). Numbers on the circumference are at the megabase scale. **a** Gene density of female *T. ovatus* (window size = 500 Kb). **b** TE content density of female *T. ovatus* (window size = 500 Kb). **c** Genome markers (optical) density of female *T. ovatus* (window size = 500 Kb). **d** Hi-C depth of female *T. ovatus* (window size = 500 Kb). **e** GC content of female *T. ovatus* (window size = 500 Kb). **f** Color bands in the middle of the Circos plot connect segmental duplication (minimum five gene pairs) from Teleost-specific

1016 whole genome duplication (Ts3R) events. **B**, Phylogenetic relationship of Perciformes and relevant teleost  
1017 lineages. The position of golden pompano is highlighted in red. Red circles represent the Teleost specific  
1018 whole genome duplication (Ts3R), Salmonid-specific whole genome duplication (Ss4R), respectively. The  
1019 divergence time was estimated using the nodes with calibration times derived from the Time Tree database,  
1020 which were marked by a black rectangle. **C**, Inspection of whole genome duplication events based on  
1021 synonymous mutation rate (Ks) distribution. The x axis shows the synonymous distance until a Ks cut-off  
1022 of 5.2. **D**, Internal genome synteny of golden pompano. Double-conserved synteny between the golden  
1023 pompano and spot gar genomes. Only genes anchored to chromosomes are represented. **E**, Macro-synteny  
1024 comparison between spotted gar and golden pompano shows the overall one-to-two double-conserved  
1025 synteny relationship between spotted gar to a post-Ts3R teleost genome.

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1028 **Figure 2. *Nxhl* is a conserved homologue of *nxh* retained after WGD.** **A**, Component of less fragment  
1029 (LF) and major fragment (MF) subgenomes within golden pompano genome. **B**, Boxplot of expression level  
1030 of LF, MF and Other gene sets. **C**, Selection bias associated with ancestral subgenomes fragmentation. The  
1031  $K_a/K_s$  values were calculated by orthologous pairs between golden pompano and spotted gar which is  
1032 outgroup species without Ts3R genome duplication events. **D**, WGCNA analysis of embryonic development  
1033 stages revealed gene-network modules enriched. **E**, Hub-gene network of the purple module. Size of the dots  
1034 represents hubness. Color of the dots represents the increasing expression level from low to high. Bold text  
1035 highlights the genes known for *nxh* (EVM0008813) gene. **F**, Validation of expression level for *nxh* by QPCR  
1036 technology. 18s RNA was considered as internal marker. Gene structure of *nxh* was showed at upper region.  
1037 **G**, Micro-synteny analysis of *nxh* locus among spotted gar, zebrafish, gold pompano and stickleback. Two  
1038 inversions and one insertion occurred in *nxh* locus region of golden pompano genomes. **H**, Domains of *nxh*  
1039 and other homologous protein. The domains were identified in SMART database (<http://smart.embl.de/>).

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1041 **Figure 3. *Nxhl* affects angiogenic phenotypes *in vivo* and *in vitro*.** **A**, Gross morphology at 3 dpf in wild-  
1042 type AB strain. Knock down *nxhl* present pericardial oedema (red arrow) and caudal fin defects (blue arrow).  
1043 The bar graph shows the validation of MO against *nxhl*, and the percentage of embryos with development  
1044 defects after knockdown of *nxhl* with *el11*-MO and ATG-MO. **B**, knockdown of *nxhl* causes angiogenic  
1045 defects in *Tg(fli1a:EGFP)<sup>y1</sup>* zebrafish. Images represent bright field and fluorescent field of  
1046 *Tg(fli1a:EGFP)<sup>y1</sup>* embryos at 52 hpf, with the angiogenic structures visualized by GFP fluorescence and  
1047 labelled ISV and DLAV. The bar graph shows the percentage of embryos with angiogenic defects after  
1048 knockdown of *nxhl* with *nxhl-el11*-MO. **C**, *nxhl* knockdown impairs formation of the CVP in zebrafish.  
1049 Quantification of loop formation and area at CVP at 52 hpf. CA, caudal artery; CV, caudal vein. NISV, normal  
1050 intersegmental vessel; TISV, thinner intersegmental vessel. **D**, Silence of *Harbi1* inhibits angiogenic  
1051 development *in vitro*. The tube formation, cell migration and invasion potential of HUVECs treated with si-  
1052 *Harbi1* was determined by using transwell chambers as described in the “Materials and methods” section.  
1053 Scale bars, 50  $\mu$ m. Representative images of cells stained in si-*Harbi1* treated HUVEC cells. The data  
1054 represent as mean $\pm$ SEM from three independent experiments. \* $p$ <0.05  $p$ <0.05, \*\* $p$ < 0.001 represents  
1055 statistically significant.

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1057 **Figure 4. *Nxhl* modulates *ptprb* expression and angiogenic networks.** **A**, Heatmap of the 15 selected genes  
1058 from zebrafishes after injection of 4ng *nxhl<sup>el11</sup>* MO at 3 dpf examined by RNA-seq. **B**, Expression of *nxhl*  
1059 post injection of *nxhl<sup>el11</sup>* MO 3 dpf. **C**, Expression of genes associated with angiopoiesis post injection of  
1060 *nxhl<sup>el11</sup>* MO 3 dpf using QPCR. **D**, Expression of genes associated with heart development post injection of  
1061 *nxhl<sup>el11</sup>* MO 3 dpf using QPCR. **E**, Networks of the genes previously reported to be associated with  
1062 angiopoiesis and heart development. Cytoscape V3.6.1 was used to build this network. **F**, Protein levels of  
1063 the selected genes associated with angiopoiesis and heart development post injection of *nxhl<sup>el11</sup>* MO 3 dpf

1064 by using Western blotting.  $\beta$ -actin antibody was used as internal control. The data above represent as  
1065 mean $\pm$ SEM from three independent experiments. \* $p$ <0.05  $p$ <0.05, \*\* $p$ < 0.001 represents statistically  
1066 significant.

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1068 **Figure 5. Loss of *ptprb* phenocopies *nxhl* deficiency.** **A**, Gross morphology at 3 dpf. Knock down *ptprb*  
1069 present pericardial oedema (red arrow) and caudal fin defects (blue arrow). The bar graph shows the  
1070 percentage of embryos with development defects after knockdown of *ptprb*. **B**, Endogenous *ptprb* in control  
1071 and *ptprb* morphants were assessed by qPCR. **C**, A time-course plot of percent survival in control and *ptprb*  
1072 morphants for 3 days. dpf, days post fertilization. **D**, Expression of *nxhl* post injection of *ptprb* MO 3 dpf.  
1073 **E**, Morpholino knockdown of *ptprb* causes angiogenic defects. Representative bright field and fluorescent  
1074 images of *Tg(fli1a:EGFP)<sup>yl</sup>* embryos at 50 hpf with the vascular structures visualized by eGFP fluorescence  
1075 and labelled ISV and DLAV. The boxed regions are shown at higher magnification in the bottom panels. **F**,  
1076 Quantification of the mean diametre of ISVs shows significantly decrease in *ptprb*-MO injected embryos.  
1077 Columns, mean; SEM (n=10; ANOVA;) DLAV, dorsal longitudinal anastomotic vessels; ISV, intersegmental  
1078 vessel. **G**, *ptprb* knockdown impairs formation of the CVP in zebrafish. Bars show the quantification of loop  
1079 formation and area at CVP. CA, caudal artery; CV, caudal vein. **H**, Expression of genes associated with  
1080 angiopoiesis (above) and heart development (down) post injection of *ptprb* MO 50 hpf using QPCR. The  
1081 data represent as mean $\pm$ SEM from three independent experiments. \* $p$ <0.05  $p$ <0.05, \*\* $p$ < 0.001 represents  
1082 statistically significant.

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1084 **Figure 6. *Nxhl* regulates VE-PTP (*ptprb*) through interactions with NCL.** **A**, ChIRP-MS identification  
1085 of *nxhl* RNA binding proteins. qPCR identification of *nxhl* RNA in the eluted RNAs. Graph shows more  
1086 than 90% *nxhl* RNA was retrieved, and no GAPDH was detected. Heat map shows major proteins are

1087 enriched and significantly (change fold >2 and  $p < 0.05$ ) retrieved by *nxhl* and control probes, analyzed by  
1088 LC/MS-MS. NCL protein (purple boxed) was selected as candidate for follow-up study. The Centroid of  
1089 NCL protein shows that NCL protein is pull down and identified by LC/MS-MS. The specific peptide  
1090 identifies NCL protein. **B**, RIP-qPCR assay to detect the interaction between *nxhl*, VE-PTP mRNA and NCL  
1091 protein. The mRNA expression of *nxhl* was determined by qPCR and Western blotting against Flag antibody  
1092 was performed to identify the successful expression of pcDNA3.1- Flag-*nxhl* plasmid in 293T cells. Bars  
1093 show the interaction between *nxhl* mRNA and NCL protein. The interaction between VE-PTP mRNA and  
1094 NCL protein is shown too, and qPCR shows the detection for VE-PTP mRNA expression in the NCL-pulled  
1095 down RNA. **C**, Pull down assay to detect the interaction between *nxhl*, VE-PTP mRNA and NCL protein.  
1096 Gels show the interaction between VE-PTP mRNA and NCL protein. Western blotting was performed to  
1097 detect NCL protein in the VE-PTP-biotin probe -pulled down proteins in 293T cells. The interaction between  
1098 *ptprb* mRNA and NCL protein is shown too. **D**, Loss of *nxhl* affects the expression of NCL at both mRNA  
1099 and protein levels. The mRNA expression of NCL and *ptpr* were determined by qPCR. The total NCL protein,  
1100 phosphorylated NCL, acetylated NCL, total *nxhl* and *ptprb* protein were detected by Western blotting using  
1101 specific NCL antibodies. The mRNA expression of *ptprb* was determined by qPCR. The data represent as  
1102 mean $\pm$ SEM from three independent experiments. \* $p < 0.05$ ,  $p < 0.05$ , \*\* $p < 0.001$  represents statistically  
1103 significant.

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1105 **Figure 7. Silence of NCL inhibits angiogenesis and expression of VE-PTP *in vitro*.** **A**, Silence of NCL  
1106 inhibits angiogenesis of HUVECs *in vitro*. The tube formation and cell migration potential of HUVECs  
1107 treated with si-NCL was determined by using transwell chambers as described in the “Materials and methods”  
1108 section. Scale bars, 20  $\mu$ m. Representative images of cells stained in si-NCL treated HUVEC cells. The data  
1109 represent as mean $\pm$ SEM from three independent experiments. \* $p < 0.05$   $p < 0.05$ , \*\* $p < 0.001$  represents

1110 statistically significant. **B**, Silence of NCL inhibits the expression of VE-PTP at both mRNA and protein  
1111 levels. The expression of NCL and VE-PTP was quantified by qPCR. Protein levels of NCL and VE-PTP  
1112 were examined by using Western blotting post silence of NCL. GAPDH antibody was used as internal  
1113 control. The gray intensities of the WB images were calculated and present as mean±SEM from three  
1114 independent experiments. \* $p < 0.05$ , \*\* $p < 0.001$  represents statistically significant.

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1116 **Figure 8. *Nxhl* controls angiogenesis by targeting VE-PTP (*ptprb*)-related angiogenic genes. A,**  
1117 Schematic model illustrating the mechanism of *nxhl* in zebrafish angiogenesis and heart development. The  
1118 interactions between *nxhl* mRNA and NCL protein, NCL protein and *ptprb* mRNA are new-found  
1119 interactions in this study. **B**, Possible mechanism of *nxhl* in zebrafish angiogenesis and heart development.  
1120 Knockdown of *nxhl* may downregulate the *nxhl*-NCL-*ptprb* complex, subsequently regulate the proteins  
1121 associated with angiogenesis and heart development, and finally result in heart pericardial oedema,  
1122 vascular patterning and integrity defects.