

Fig. S1. Conserved epicardial development in *Xenopus*. (A-F') SEM images of ventral views of *Xenopus* epicardial development at (A) stage 39, pre-PEO attachment, (B) stage 41, (C) stage 42, (D) stage 43, (E) stage 44, (F) stage 46. Red arrowheads denote attached PEO (B,D) and the white dashed line the extent of epicardial sheet migration over the heart surface (C'-E'). A'-F' are magnified views of the ventricular surface. (G-J) ST-specific photoconversion of Kikume in stage 40 embryo (G) results in the migration of red fluorescent cells (white arrowheads) onto the myocardial surface at stage 43 (H-J); ventral view of cardiac region, hearts outlined with white dashed line. (K-P) Bmp2 expression detected by ISH. Lateral (K,L) and transverse (M-P) views of stage 45 embryos showing Bmp2 localized to the atrioventricular sulcus near the outflow tract (AVS/OFT) and the inflow tract-ventricular sulcus (IFT/VS). Hearts outlined with red dashed lines. e, eye; h, heart; gb, gall bladder; li/st, liver/septum transversum; oft, outflow tract; ven, ventricle. Scale bars: 1 mm in H,K,M; 250 μ m in G; 500 μ m in O.

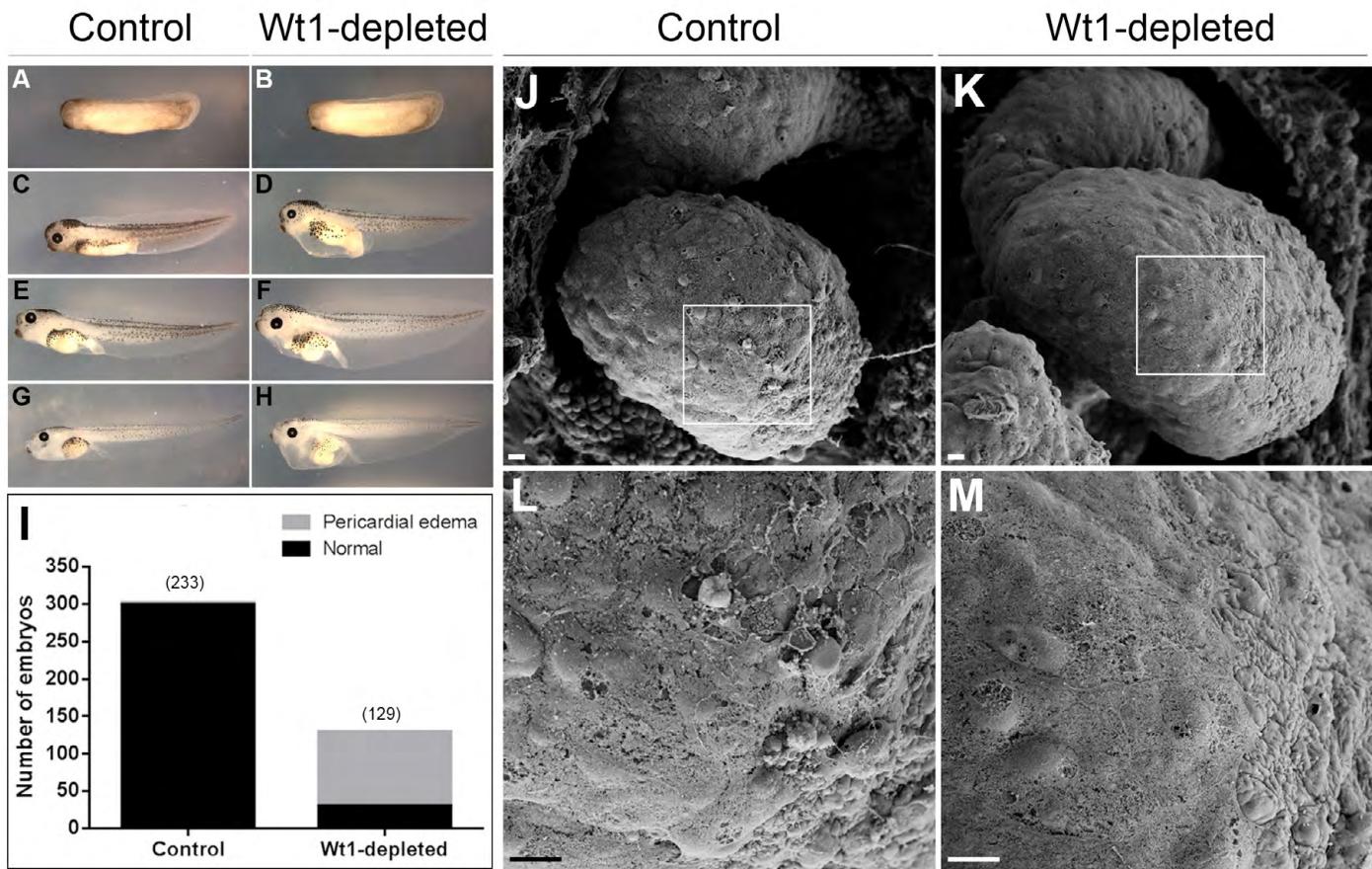


Fig. S2. Analysis of Wt1-depleted embryos. (A-H) Brightfield images of live embryos at (A,B) stage 28, (C,D) stage 40, (E,F) stage 43, (G,H) stage 46. (I) Quantification of pericardial edema observed in embryos at stages 44-46; total embryos in brackets, two independent experiments, $P<0.0001$ by two-tailed Fisher's exact test. Likelihood ratio χ^2 N=362, DF=1=259.856; $P<0.0001$, Pearson χ^2 N=362, DF=1=234.094; $P<0.0001$. (J-M) SEM images of stage 45 hearts depicting normal epicardial sheet migration over the heart in both (J,L) control and (K,M) Wt1-depleted embryos. Boxed areas indicate the regions of the ventricular surface magnified in L,M. Scale bar: 10 μ m.

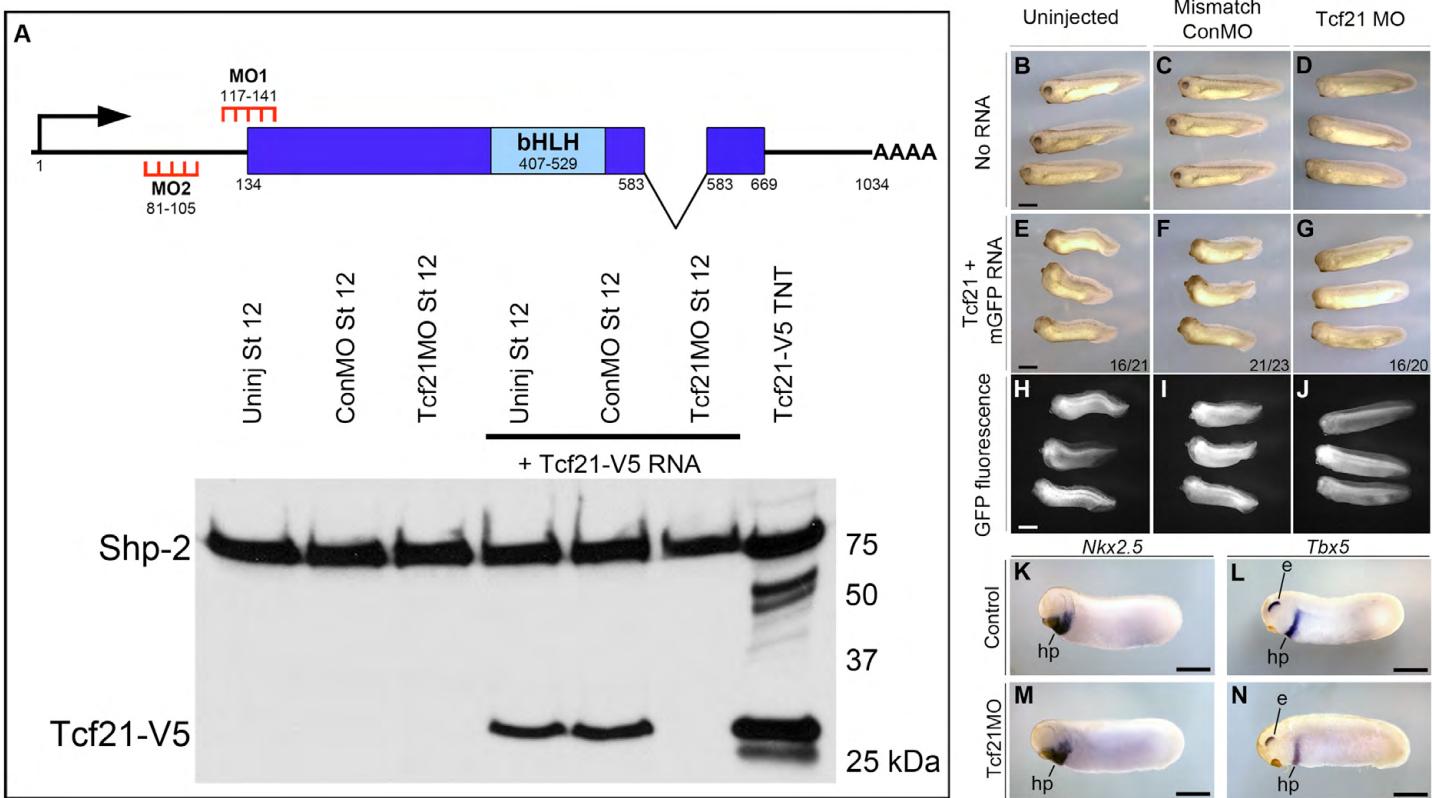


Fig. S3. Validation of Tcf21-MO specificity. (A) Schematic showing relative MO positioning on *Xenopus Tcf21* mRNA; numbers denote nucleotide base pair positions. Validation of MO-specific Tcf21 translation inhibition by V5 western blot on stage 12 embryos; representative blot from four independent experiments. Shp2 protein provided a loading control, *in vitro* translated Tcf21-V5 a positive control. Molecular weight standards are included to right of blot. (B–J) Rescue of embryonic Tcf21-overexpression phenotype (stunted AP axis development, membrane ruffling, reduced ocular development, prominent cement gland) by (D,G,J) Tcf21-MO injection relative to (C,F,I) control 5-base mismatch MO and (B,E,H) uninjected embryos; representative images from two independent experiments. mGFP RNA provided an RNA injection control (H–J); anterior to left of panel. (K–N) *In situ* hybridization on whole control and Tcf21-depleted embryos (stage 26–28) demonstrating correct specification of heart mesoderm by (K,M) *Nkx2.5* and (L,N) *Tbx5* expression. bHLH, basic helix-loop-helix domain; hp, heart primordium. Scale bars: 10 mm in H; 2 mm in K–N.

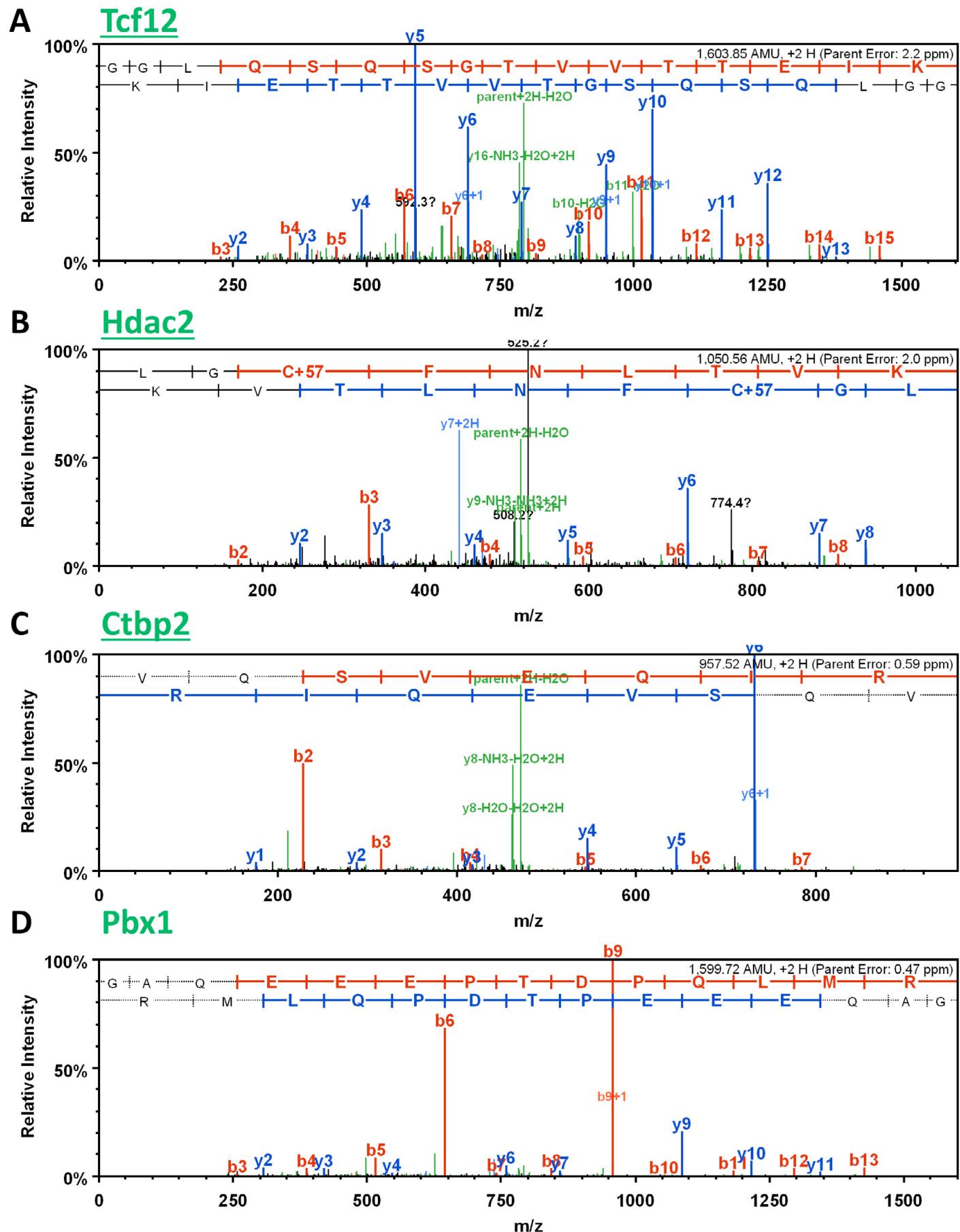


Fig. S4. Validation of Tcf21-Ctbp2 interaction and expression in *Xenopus* cardiac tissue. Identification of (A) Tcf12, (B) HDAC2, (C) Ctbp2 and (D) Pbx1 in the immuno-isolates of Tcf21, as shown by CID MS/MS analysis of representative peptides.

A

Tcf21 Modified Residue	Previously reported	Peptide Sequence	Xc	PEP	Z	ΔM , ppm	Phospho RSSite Probability
S37	No	(K)EFGISNDS*NEESSTCDNGSPK(K) (K)LDPNKEFGISNDS*NEESSTCDNGSPK(K) (K)LDPNKEFGISNDS*NEESSTCDNGSPK(K)	5.92 7.14 5.40	1.24 E-4 1.23 E-9 2.92 E-2	2 3 2	2.4 0.081 1.3	99.0 99.1 90.7
S48	No	(K)LDPNKEFGISNDSNEESSTCDNGS*PK(K)	7.49	5.06 E-10	3	2.9	100.0
S67	No	(K)KS*PLGTINQEGK(Q) (K)S*PLGTINQEGK(Q)	4.24 3.15	1.37 E-3 2.35 E-3	2 2	1.2 1.4	100.0 100.0

Xc , SEQUEST cross-correlation score; PEP, Proteome Discoverer posterior error probability; Z, charge state; ΔM ppm, actual minus calculated peptide mass parts per million; Phospho RSSite Probability, Phosphorylation site assignment score determined by Proteome Discoverer.

B

IP 1

59% sequence coverage

MSTGSLSDVE	DFQDMEMLEC	DGIK <u>LDPNKE</u>	<u>FGISNDSNEE</u>	<u>SSTCDNGSPK</u>	<u>KGRGTSGKRR</u>
KASSKK <u>SPLG</u>	<u>TINQEGKQVQ</u>	<u>RNAANARERA</u>	RMRVLSKAFS	<u>RLKTTLPWVP</u>	<u>PDTKLSKLDT</u>
LR <u>LASSYIAH</u>	<u>LRQILANDKY</u>	<u>ENGYIHPVNL</u>	<u>TWPFMVAGKP</u>	<u>ENDLKEVVST</u>	<u>SRLCGPTAS</u>

S67- P

S37- P

S48- P

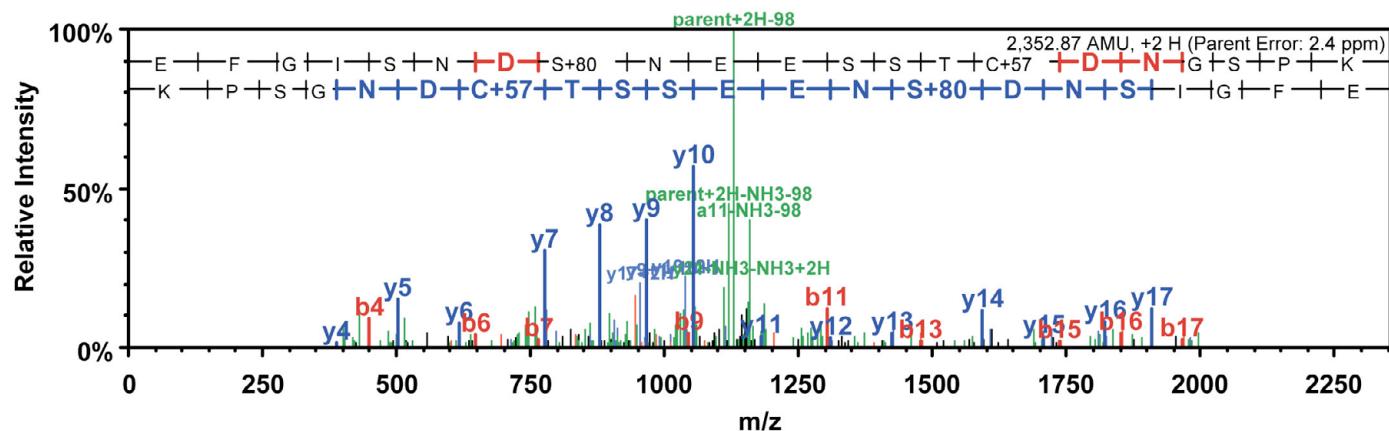
IP 2

54% sequence coverage

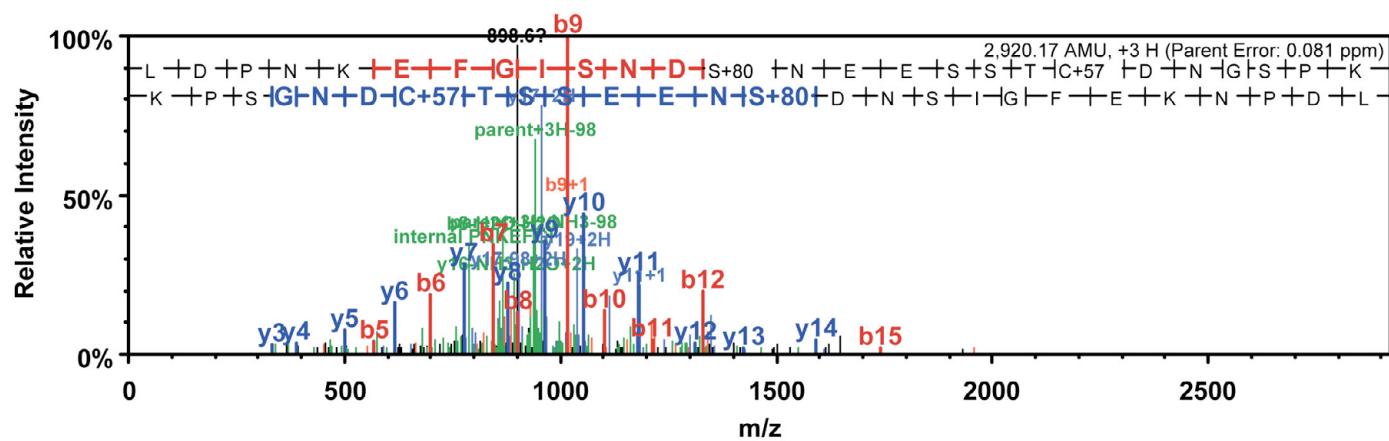
MSTGSLSDVE	D <u>FQDMEMLEC</u>	<u>DGIKLDPNKE</u>	<u>FGISNDSNEE</u>	<u>SSTCDNGSPK</u>	KGRGTSGKRR
K <u>ASSKKSPLG</u>	<u>TINQEGKQVQ</u>	<u>RNAANARERA</u>	RMRVLSKAFS	<u>RLKTTLPWVP</u>	<u>PDTKLSKLDT</u>
LR <u>LASSYIAH</u>	<u>LRQILANDKY</u>	<u>ENGYIHPVNL</u>	<u>TWPFMVAGKP</u>	<u>ENDLKEVVST</u>	<u>SRLCGPTAS</u>

C

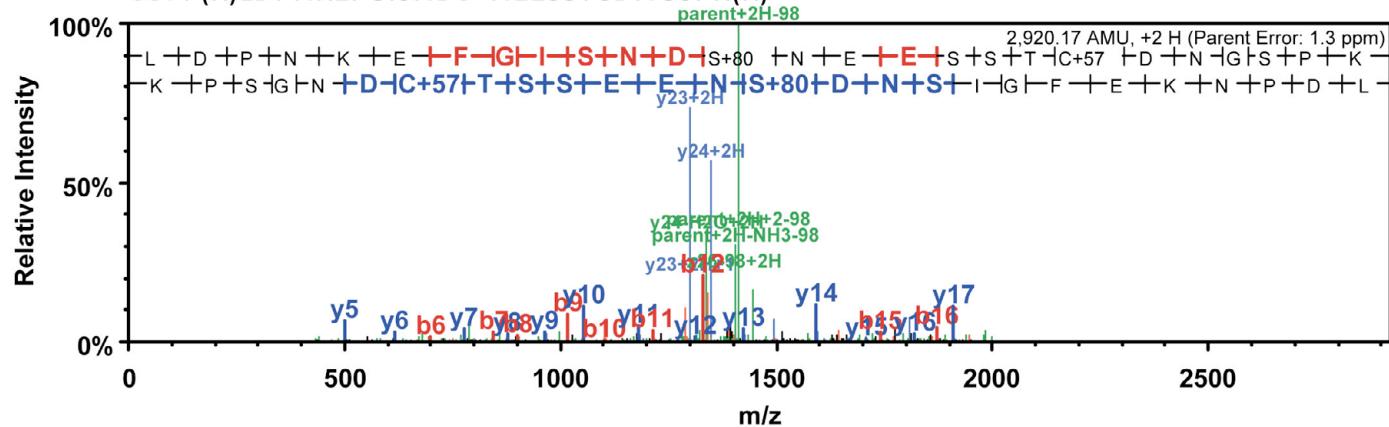
S37: (K)EFGISNDS*NEESSTCDNGSPK(K)

Tcf21 S37 Phosphorylation

S37: (K)LDPNKEFGISNDS*NEESSTCDNGSPK(K)



S37: (K)LDPNKEFGISNDS*NEESSTCDNGSPK(K)



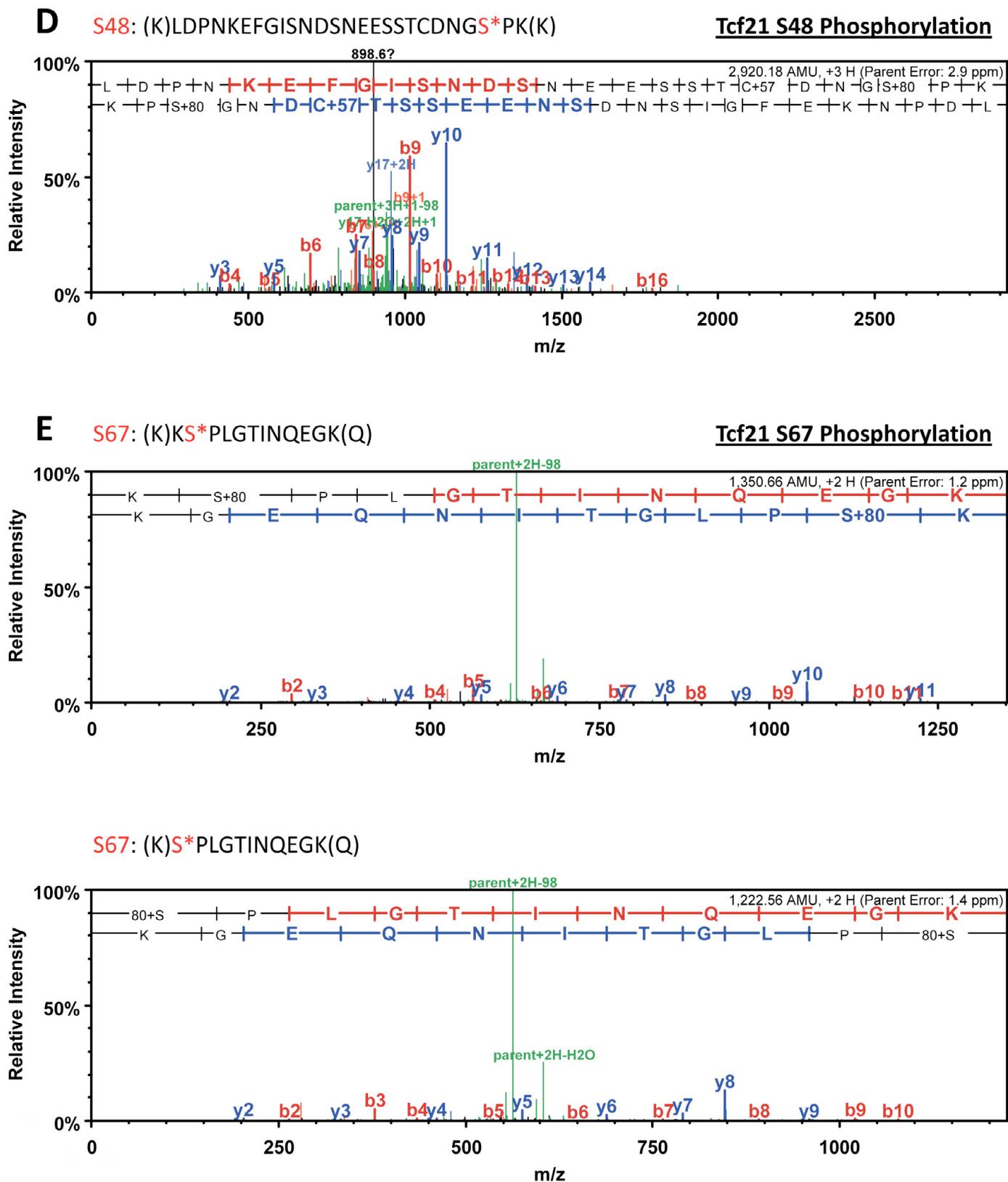


Fig. S5. Mass spectrometry identification of phosphorylation sites on Tcf21. (A) Summary of identified phosphorylation peptides and confidence scores. (B) Sequence coverage of isolated Tcf21 from two biological replicates (IP1 and IP2) as highlighted in green. Red labels indicate the location of the three Tcf21 phosphorylations. (C-E) Representative CID MS/MS spectra of Tcf21 phosphorylated peptides: S37 (C), S48 (D) and S67 (E).

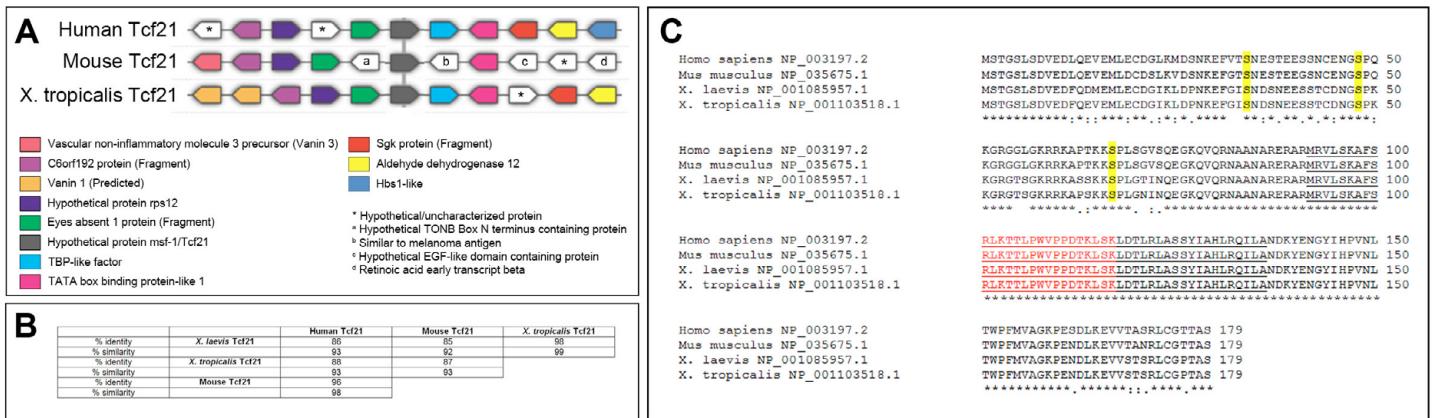


Fig. S6. Genomic and protein conservation of Tcf21. (A) Synteny of Tcf21 loci in human, mouse and *X. tropicalis* genomes (Metazome). (B) Tcf21 protein conservation highlighting percentage of identity and similarity between *X. laevis*, *X. tropicalis*, mouse and human. (C) Protein alignments of Tcf21 between human, mouse and *Xenopus* (ClustalW). Highlights represent post-translational modifications observed in *X. laevis* Tcf21 residues by mass spectrometry analysis and conservation of residues across the species; yellow, phosphorylation; red text, putative nuclear localization sequence (Trausch-Azar et al., 2004); underlined residues mark the conserved basic helix-loop-helix DNA-binding domain.

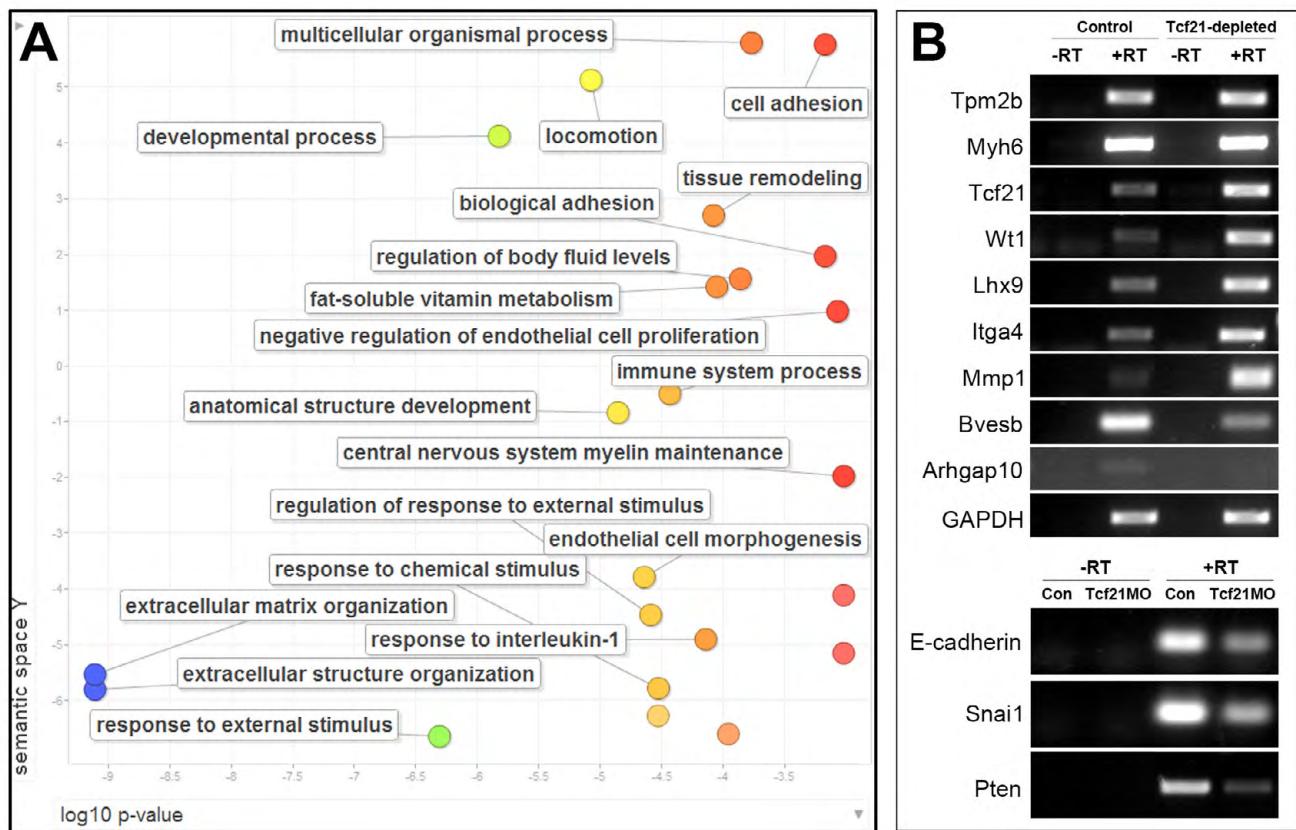


Fig. S7. RNA-seq validation of cardiac transcriptome by RT-PCR. (A) Gene Ontology (GO) term analysis on Tcf21-depleted upregulated RNA-seq dataset ≥ 1.8 fold (GORilla and ReviGO). (B) RT-PCR of stage 45 cardiac cDNA from control and Tcf21-depleted embryos from independent experiments to validate RNA-seq candidates. -RT, PCR control lane.

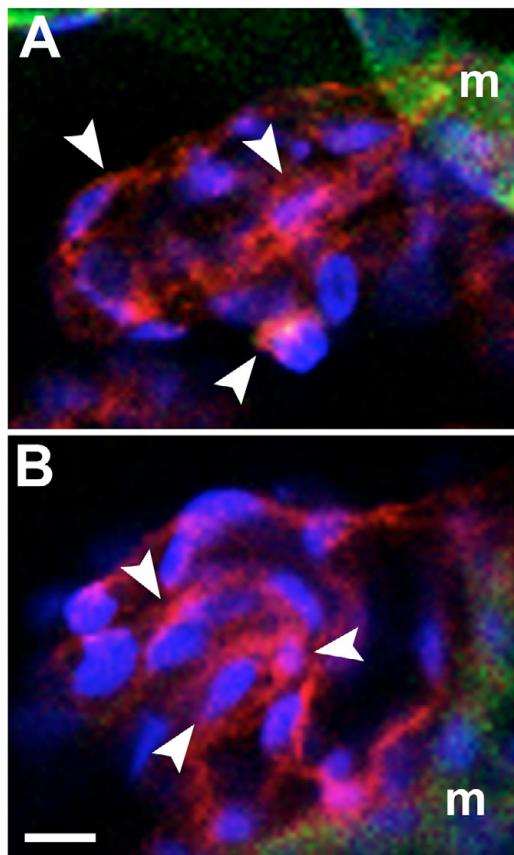


Fig. S8. Distribution of aPKC in the PEO resembles that in Tcf21-depleted epicardial cells. Immunohistochemical staining of transverse cardiac sections showing that staining of aPKC and its accumulation in the cytosol of attached PEO cells (arrowheads) in (A) control embryos resembles that in (B) Tcf21-depleted PEO cells and Tcf21-depleted migrating epicardial cells (see Fig. 5B''). m, myocardium. Scale bar: 10 μ m.

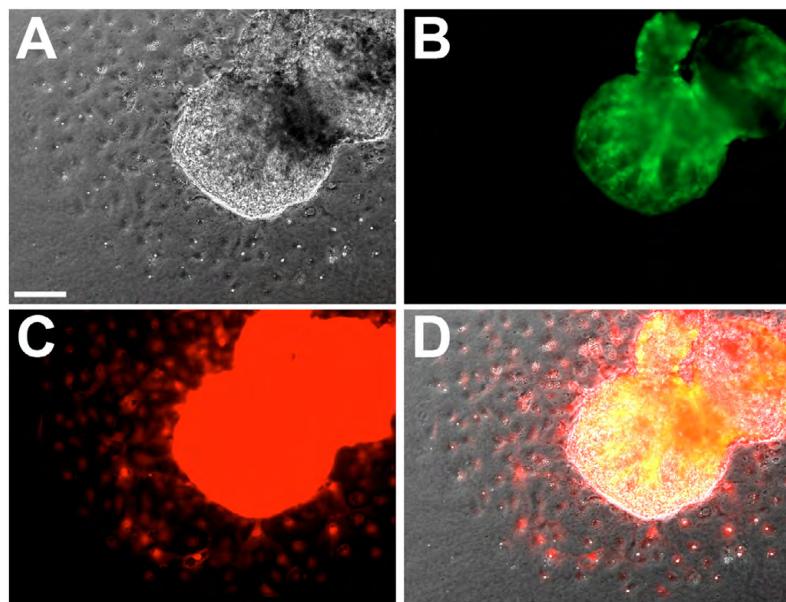


Fig. S9. Double-transgenic hearts used in epicardial migration assay. Cardiac explants were taken from double CA:eGFP and CMV:dsRED embryos to conduct epicardial migration live assays for more accurate tracking by Imaris software. (A) Brightfield, (B) GFP, (C) dsRED and (D) overlay. Confirmation that migrating cells are not cardiomyocytes is by the absence of GFP expression (B). Scale bar: 100 μ m.

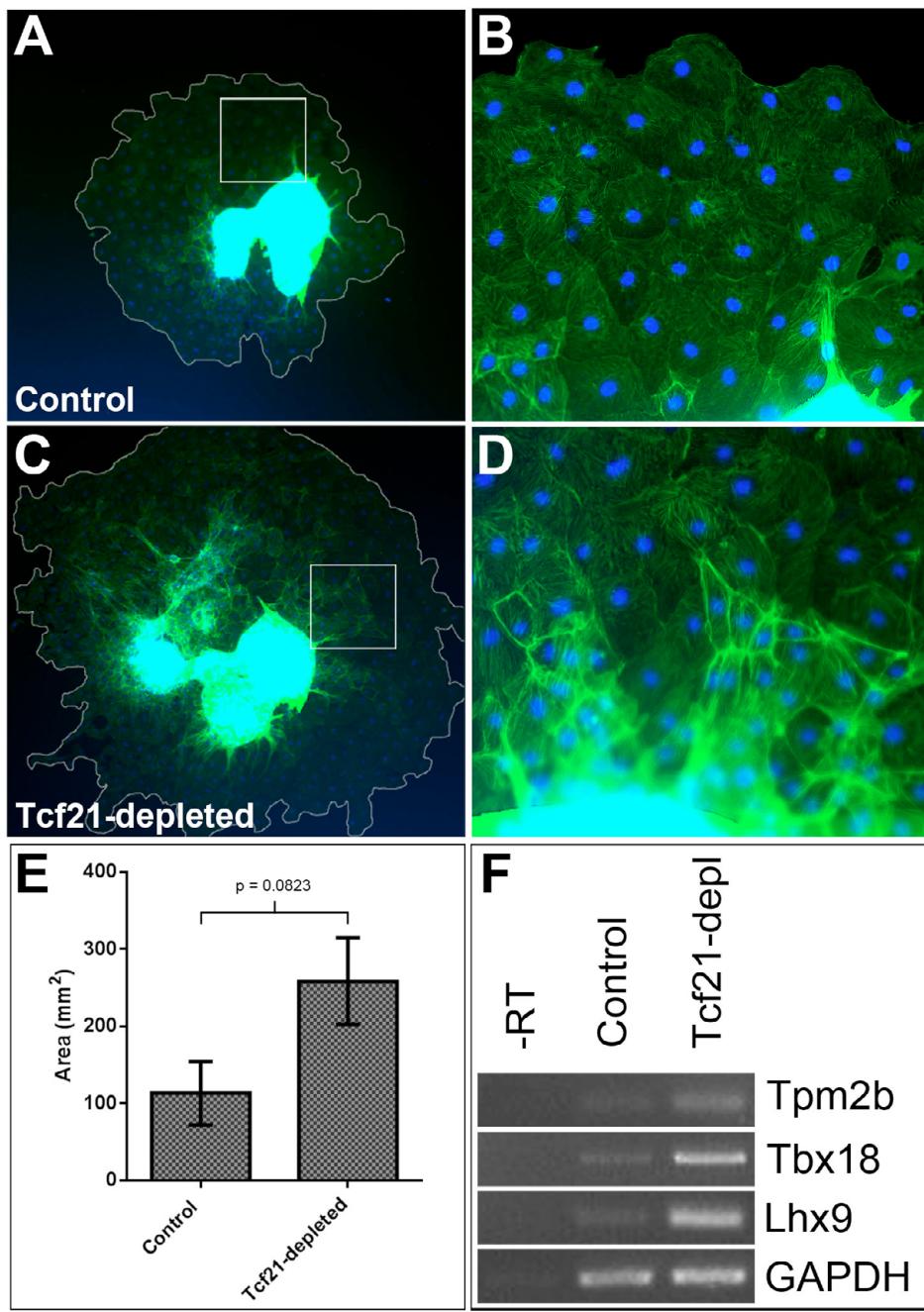
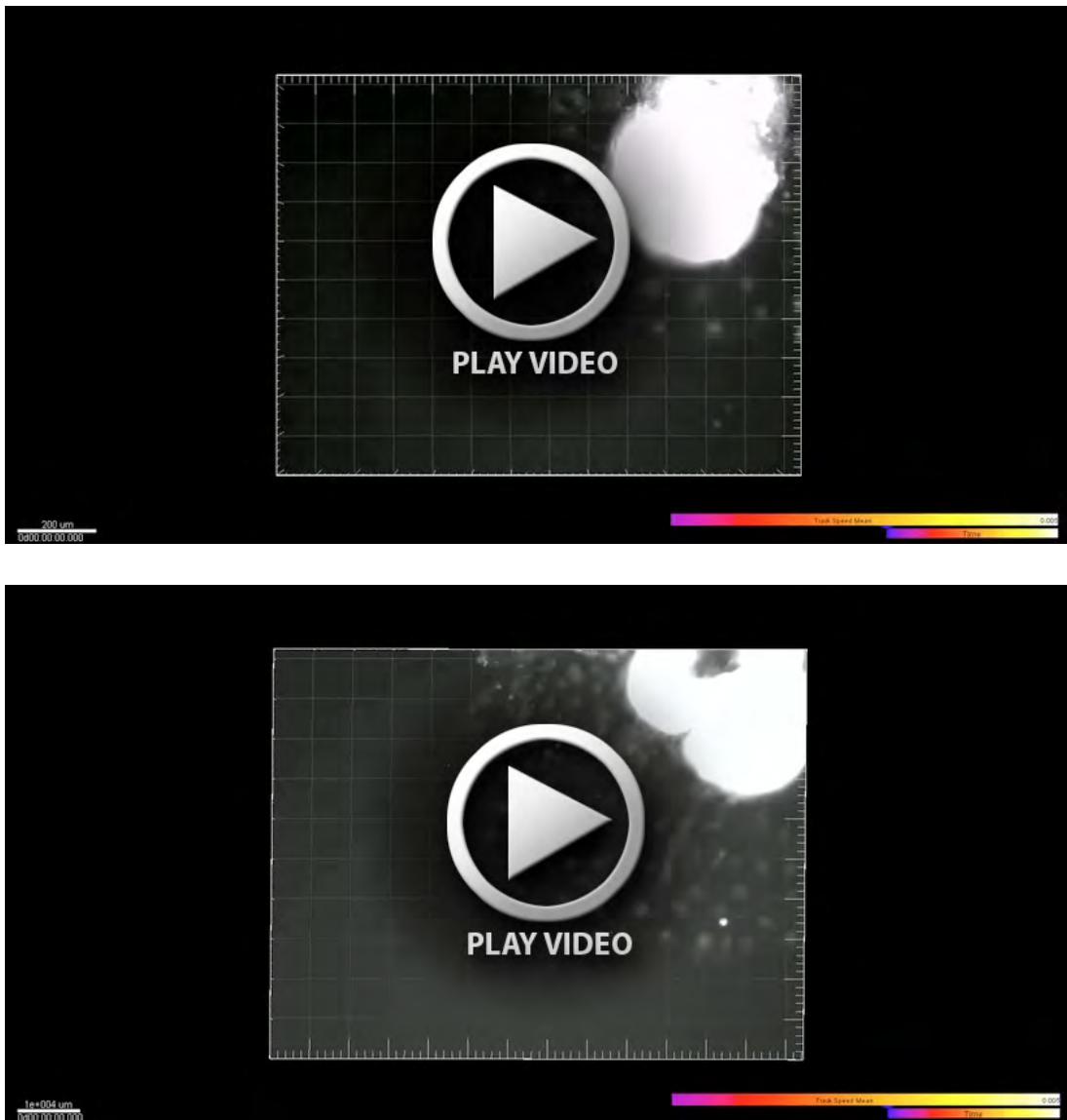


Fig. S10. F-actin stress fiber enrichment in migrating epicardial explant cultures. (A-D) Phalloidin staining of epicardial cells in cardiac explant cultures from control (A,B) and Tcf21-depleted (C,D) embryos. White outline depicts extent of epicardial migration after 48 hours. Magnified images of boxed views (B,D). (E) Two-tailed unpaired non-parametric Mann-Whitney statistical test analysis showing increased phalloidin-enriched epicardial area between control and Tcf21-depleted explant cultures, $P=0.0823$. (F) RT-PCR from explant cultures after removal of the heart, confirming that migrating cells express known epicardial genes *Tbx18* and *Lhx9* in both control and Tcf21-depleted cultures.



Movies 1 and 2. Live imaging of epicardial cell migration in control (Movie 1) and Tcf21-depleted (Movie 2) hearts. Imaris analysis dragon trails represent the average speed (mean, $\mu\text{m}/\text{second}$) of individual cells tracked, with lighter trails indicating faster migration. One frame per 30 minutes; movie is repeated after first 26 hours of culture.

Table S1. Gene Ontology (GORilla) analysis of Tcf21-depleted upregulated (≥ 1.8 -fold) dataset

[Download Table S1](#)

Table S2. Gene Ontology (GORilla) analysis of Tcf21-depleted downregulated (≥ 1.8 -fold) dataset

[Download Table S2](#)

Table S3. RNA-seq read analysis

[Download Table S3](#)

Table S4. RT-PCR primers used to validate RNA-seq data

Primer	Sequence (5'-3')
GAPDH RTPCR F	TTGAAGGGAGGTGCCAAG
GAPDH RTPCR R	GATGACCTTGCAGAGAGGAG
Myh6 RTPCR F	AGTCACAGTCGCCTCCATTG
Myh6 RTPCR R	GTCCCCTCTGGTTCTGCTTG
Tpm2b RTPCR F	CTCAGGAGAACGCTGGAGATG
Tpm2b RTPCR R	CGGTCCAACCTCTCCTCTAC
Tcf21 RTPCR F	CATAGCTCACCTGCGTCAA
Tcf21 RTPCR R	GGACCACACAATCGGCTAGT
Wt1 RTPCR F	CCATTCTTCAAACATGAGG
Wt1 RTPCR R	GCTCCCGTACAAGTGTCA
Lhx9 RTPCR F	TGGAGAGGAGGTCAAAGTCG
Lhx9 RTPCR R	GCACAGTGTAGGCTCTCAGG
Itga4 RTPCR F	GAGCAATCCTGGTGTATCC
Itga4 RTPCR R	CACCCAGCCACTGGTTATCT
MMP1 RTPCR F	CTTCCCCGCAGATAAACAAAG
MMP1 RTPCR R	TCTGCTGGAGCTTCAGTG
Bvesb RTPCR F	GCAGGACTCGTTATTCCAAG
Bvesb RTPCR R	TCCAAAGCACATCGGAAGAG
Arhgap10 RTPCR F	ATAGCGAAGAGTGGGAGGTG
Arhgap10 RTPCR R	TGGCGAGGTTGATGAAGTG
Pten RTPCR F	CCCCTGCTCTCGCTCGCTGG
Pten RTPCR R	TAACCTCTCTGCTCGCTGG
Rac1 RTPCR F	TGGGTAAAACATGCTTGCTG
Rac1 RTPCR R	TCCACCATAACATTGGCAGA
Cdc42 RTPCR F	ACTCCAGAGACAGCCGAGAA
Cdc42 RTPCR R	GGCCAATATCGCTTCATCA
E-cadherin RTPCR F	AACTCCACAGCAAGGACACC
E-cadherin RTPCR R	TCTGGAAAAGTCAGCACTGG
Snai1 RTPCR F	GCAAGAAGCCCAACTACAGC
Snai1 RTPCR R	TGTCCCAGACAAGAGGTGTG

Table S5. Morpholino oligonucleotides

Morpholino	Sequence (5'-3')
Tcf21-MO1	GTGGACATGATCTGTTATGCTGCTC
Tcf21-MO2	GATCAAGGTGTGACTGAATGCAATA
Control-MO	GAT <u>GAA</u> CGT <u>CT</u> GACT <u>CA</u> AT <u>CC</u> AATA
Wt1-ex2Donor	CTAACACAGCAGTTACCTAGAGAGGT
Wt1-ex3Acceptor	CTGTAGGAACATCACATCACATTAA

Underlining indicates the five mismatches in Control-MO compared with Tcf21-MO2.

Table S6. Primers used to clone *Xenopus* cDNA fragments for *in situ* hybridization constructs

Primer	Sequence (5'-3')
xl.ndrg4b.F.ish	GCG CTCGAG CACAATGGAGGTTCCCTGCT
xl.ndrg4b.R.ish	GCG GAATTCAACAATCCCCAGCTTTCAT
xl.inta4.F.ish	GCG CTCGAG GAGTTCCCAAGAACCCACA
xl.inta4.R.ish	GCG GAATTGCACACAGCCACTTGTGAGAA
xl.lhx9.F.ish	GCG CTCGAG CTACAACCACGCTTGCAAAA
xl.lhx9.R.ish	GCG GAATTGCAGCTGGAGTAATTGCACA
xl.arhgap10.F.ish	GCG CTCGAG ACGCAATACTCCGAAGCTGT
xl.arhgap10.R.ish	GCG AAGCTT ACGTCAGAGTAGGGGTGTGG
xl.bmp2a.F.ish	GCG CTCGAG TCTACACGGAGGTTGGAG
xl.bmp2a.R.ish	GCG GAATTACAAAGCAATGCACACTGGA
xl.ephrinb2.F.ish	GCG CTCGAG TTTTATCTGCAGGGCACCTAT
xl.ephrinb2.R.ish	GCG GAATTACGCACTGTGGACCAGGAGAT
xl.dact1.F.ish	GCG CTCGAG AGGCATCGCACAACCTAAAG
xl.dact1.R.ish	GCG GAATTCTGGAAAAGCTCAGGATGGAC
xl.pdgfra.F.ish2	GCG CTCGAG CTCGAAATGCCACTACAGA
xl.pdgfra.R.ish2	GCG GAATTCCACAAAGGTGTCATTGTTGC
xl.ficolinb.F.ish2	GCG CTCGAG GCGTGGACCTGACAGATTTC
xl.ficolinb.R.ish2	GCG GAATTCTGGTTCCGTCCCAGAAG
xl.bmp7.ishF	GCG CTCGAG CGACCAACCATTGTATGCAC
xl.bmp7.ishR	GCG GAATTCCAGCTCAGAGGCACATTCA
xl.cops2.ishF	GCG CTCGAG TTGGTTGGTGTGTCCCTGAA
xl.cops2.ishR	GCG GAATTCCGCTGCACTGTTATTTGC
xl.ccdc69.ishF	GCG CTCGAG CAACGCAAATGAACATTGG
xl.ccdc69.ishR	GCG GAATTCAATGGGTCGTAGCCCTTTT
xl.xbp1.ishF	GCG CTCGAG GCTTGCCTATGAAGGAGCAC
xl.xbp1.ishR	GCG GAATTCCGGTCAGAGTTCAGAGGAG
xl.nes.ishF	GCG CTCGAG CCATGTCAAGAGCGAAAAGT
xl.nes.ishR	GCG GAATTCTGCAGTGAAGGCAGTGATT
xl.txnip.ishF	GCG CTCGAG ATTGGATGGAGCCTGTGAC
xl.txnip.ishR	GCG GAATTCTCTGGCGGGATTGTATAGC
xl.tcf3.ishF	GCG CTCGAG GTTGTGGGAAGCAAGGATA
xl.tcf3.ishR	GCG GAATTCTTGGAAATAACCCACCCAAAA
xl.mmp9.ishF	GCG CTCGAG TGGGAAAGGAGTAGTGCAT
xl.mmp9.ishR	GCG AAGCTT AGCCATCCCTGCAAAGTGT
xl.pcdh1.ishF	GCG CTCGAG GCTAAACCACCGATTCCAA
xl.pcdh1.ishR	GCG GAATTCTGCACATGCCCTTATATT

xl.fst.ishF	GCG CTCGAG AAAGGTTCACTGTGCGGAAT
xl.fst.ishR	GCG GAATTG GCTCGGGTAAGTCGTGTTGT
xl.s100a11.ishF	GCG CTCGAG TCCGAGCTCTGCTCTTCTC
xl.s100a11.ishR	GCG AAGCTT AGGGGTCACTCAGGGTTCT
xl.mmp1.ishF	ATGCTGTCACCACCATGAGA
xl.mmp1.ishR	AGCTTGGGTCCGTCTTATT
xl.npx1.ishF	TCTTGGTGCTGAAGTGAACG
xl.npx1.ishR	AGACTGCCAAGCTGGACTA
xl.clu.ishF	GTGCAATGAGACCATGTTGG
xl.clu.ishR	AGCGACTCAAAGTTCCCAGA
xl.col18a1.ishF	GGAAGCTAGGGGTGCTAAG
xl.col18a1.ishR	GCAAGGAGTCAGCGGTAGAA
xl.col1a2.ishF	GAAGAAGGCCATCTGCTAC
xl.col1a2.ishR	GATTGAGAGTCCTCCTTGG
xl.plp1a.ishF	CTGGGCAGAGGCAGAAATAG
xl.plp1a.ishR	CACCTGCTCAACCCATTAC
xl.gpr84.ishF	ATCATGTCGCTGGCATTAACT
xl.gpr84.ishR	CAACTGCAACCAGCTCATTAAC
xl.mmp13.ishF	TCAGCCAACCTAACGATTT
xl.mmp13.ishR	GGCGCACACAAAATAAGGT
xl.serP.ishF	GGGAAACAGCTGCAGAGAAC
xl.serP.ishR	TGTACTGGCTGGGTCTTC
xl.prom1.ishF	GCCTCTGCTGCTTGTAC
xl.prom1.ishR	TCTGGGTCTGCTTGTAC
xl.plat.ishF	GGGTATTGGCTGTGGAAAGA
xl.plat.ishR	CCCTGGTATCAGCCACACTT
xl.kcp.ishF	GCTCTCTAACGCCCTCAGGT
xl.kcp.ishR	TGGTGTGTGGCGAAAATAAA
xl.fgl1.ishF	ATGGCATGGATGGTGGTATT
xl.fgl1.ishR	TGCATCCAGGGTCATAACAA
xl.rfx5.ishF	CCACAGCATCACATTCAAAC
xl.rfx5.ishR	TGTCAGGGCTGTAGTGCAAG
xl.rarres1.ishF	TGGCTGTCCCCCTACTACTG
xl.rarres1.ishR	AGAATGGGGAAAGAAGTGCT
xl.anxa2.ishF	GCCAGGAAGAAGGAAGTGTG
xl.anxa2.ishR	CCTTTGTGTCTGCCAAT

Table S7. Antibodies and stains

Antibody	Description	Use	Source	Dilution
Anti-Atypical protein kinase C (PKC ζ)	Rabbit poly	IF	SC-216, Santa Cruz	1:100
Anti-Cytokeratin	Mouse IgG1	IF	1h5, DHSB	1:100
Anti-Green fluorescent protein (GFP)	Rabbit poly	IF	A-11122, Molecular Probes, Invitrogen	1:150
Anti-GFP (JL8)	Mouse IgG2	WB	632381, Clontech	1:10,000
Anti-HA 1.1	Mouse IgG1	WB	MMS-101P, Covance	1:2000
Anti-Laminin	Rabbit poly	IF	L9393, Sigma	1:100
Phalloidin-488 (F-actin)	–	IF	A12379, Molecular Probes, Invitrogen	1:250
Anti-Shp2 (PTP1D)	Mouse IgG1	WB	610622, BD Transduction	1:2500
Anti-Tropomyosin	Mouse IgG1	IF	CH1, DHSB	1:10
Anti-V5	Mouse IgG	WB	46-1157, Invitrogen	1:5000
Anti-Vimentin	Mouse IgG1	IF	14h7, DHSB	1:100
Alexa-488/546/647 (secondary)	–	IF	Molecular Probes, Invitrogen	1:750

IF, immunofluorescence; WB, western blot.

Table S8. Enriched and prominent Tcf21 interaction partners identified by mass spectrometry analysis

Protein	Gene	Accession number	MW (kDa)	Unweighted spectrum counts								% Sequence coverage IP1	% Sequence coverage IP2		
				Tcf21-EGFP		Tcf21-EGFP		Number of peptides IP1	Number of peptides IP2						
				IP1	IP2	IP1	IP2								
Transcription factor 21	<i>TCF21</i>	Q6GNB7	20	154	266	0	0	13	12	59	54				
								Unmodified: 9	Unmodified: 7						
								Modified: 4	Modified: 5						
Transcription factor 12	<i>TCF12</i>	Q99081	73	3	2	0	0	3	2	7	5				
Histone deacetylase 2	<i>HDAC2</i>	P70288	55	4	14	0	0	2	6	8	17				
C-terminal-binding protein 2	<i>CTBP2</i>	P56545	49	3	6	1	0	3	4	2	12				
Pre-B-cell leukemia transcription factor 1	<i>PBX1</i>	P40424	47	17	4	0	0	9	2	29	6				
DNA mismatch repair protein Msh6	<i>MSH6</i>	P52701	153	2	36	0	0	2	17	2	15				
ATP-dependent DNA helicase Q1	<i>RECQL</i>	P46063	73	5	17	0	0	5	6	9	9				
DNA ligase 3	<i>LIG3</i>	P49916	113	4	14	0	0	4	2	4	9				
E3 ubiquitin-protein ligase HUWE1	<i>HUWE1</i>	Q7Z6Z7	482	18	11	0	0	17	10	5	4				
Chloride intracellular channel protein 4	<i>CLIC4</i>	Q9QYB1	29	3	6	1	0	2	6	6	33				
Cleavage and polyadenylation specificity factor subunit 6	<i>CPSF6</i>	Q16630	59	3	13	1	0	2	4	2	10				
Poly(A)-specific ribonuclease PARN	<i>PARN</i>	O95453	73	2	7	0	0	2	4	4	10				
Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1	<i>PIN1</i>	Q13526	18	2	6	0	0	2	5	18	52				

Shown are the most enriched and prominent Tcf21 interaction partners isolated from HEK293 cells in two biological replicates (IP1 and IP2) and characterized by mass spectrometry analysis.

Table S9. RNA-seq validation by cardiac RT-PCR

Gene	Fold change relative to controls	RNA-seq validation?
<i>Tcf21</i>	2.93095368	Yes
<i>Wt1</i>	2.332362741	Yes
<i>Lhx9</i>	3.768277666	Yes
<i>Itga4</i>	2.785567683	Yes
<i>Mmp1</i>	22.28987494	Yes
<i>BvesB</i>	0.614366083	Yes
<i>Arhgap10</i>	0.585936231	Yes
<i>Pten</i>	0.7558539	Yes
<i>Cdh1</i>	0.87530691	Yes
<i>Snai1</i>	0.894567689	Yes

Table S10. RNA-seq validation by whole-embryo *in situ* hybridization

Gene	Tcf21-depleted fold change relative to controls	Expressed in cardiac region	Expressed in PEO/epicardium	RNA-seq validated	Expressed in early PEO
<i>Tcf21</i>	2.29396358	Yes	Yes	Yes	Yes
<i>Tbx18</i>	–	Yes	Yes	Yes	Yes
<i>Itga4</i>	2.180174615	Yes	Yes	Yes	Yes
<i>Lhx9</i>	2.949310248	Yes	Yes	Yes	Yes
<i>S100a11</i>	1.975934966	Yes	Yes	Yes	No
<i>Plat</i>	2.17920842	Yes	Yes	Yes	Yes
<i>Kcp</i>	2.155748912	Yes	Yes	Yes	Yes
<i>Fgl1</i>	2.096563801	Yes	Yes	Yes	Yes
<i>Mpz</i>	3.108780309	Yes	Yes	Yes	Yes
<i>Col1a2</i>	1.959802918	Yes	Yes	Yes	No
<i>Col18a1</i>	1.908395677	Yes	Weak expression	Yes	Yes
<i>Txnip</i>	1.99692408	Yes	Weak expression	Yes	–
<i>Rarres1</i>	1.825228651	Yes	Yes	Yes	–
<i>Clu</i>	3.018690068	Yes	Yes	Yes	–
<i>Serpine1</i>	2.762411644	Yes	Weak expression	Yes	–
<i>Anxa1</i>	1.824081683	Yes	Weak expression	Yes	–
<i>Gpr84</i>	10.53169439	No	No	No	–
<i>Plp1a</i>	15.75437891	No	No	No	–
<i>Pdgfra</i>	0.393522958	Yes	Yes	Yes	–
<i>Ndrg4b</i>	0.581342148	Yes	Weak expression	Yes	–
<i>Bmp2a</i>	0.436356976	Yes	No	Yes	–
<i>EphrinB2</i>	0.487155026	Yes	No	Yes	–
<i>Dact1</i>	0.346196019	Yes	No	Yes	–
<i>Pcdh1</i>	0.427475387	Yes	Weak expression	Yes	–
<i>EpoR</i>	0.446220369	Yes	No	Yes	–