

Supplementary Materials

1	MDWGT L QT I LGGVNKHSTS I GKIWLTVLF I FRI M	hCX26
1	MSWGALYAQLGGVNKHSTS L GK I WL S VLF I FRIC	zCx30.3
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35	I L V V A A K E V W G D E Q A D F V C N T L Q P G C K N V C Y D H Y	hCX26
35	I L V V A A E T V W G D E Q S D F T C N T Q Q P G C K N V C Y D H F	zCx30.3
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69	F P I S H I R L W A Q L Q I F V S T P A L L V A M H V A Y R R H E K	hCX26
69	F P V P H I R F W C L Q L I F V S T P A L L V A M H V A Y R K R N M	zCx30.3
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103	K R K F I K G E I K S E F K — D I E E E I K T Q K Q V R I E G S L W W	hCX26
103	K K K S I L A K R G G N G K G D D D L E S L K N R R L P I T G P L W W	zCx30.3
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135	T Y T T S S I F F R V I F E A A F M Y V F Y V M Y D G F S M Q R L V K	hCX26
137	T Y T T S S L F F R L L F E A G F M Y A L Y Y Y Y D G F Q M A R L V K	zCx30.3
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169	C N A W P C P N T V D C F V S R P T E K T V F T V F M I A V S G I C	hCX26
171	C E Q W P C P N K V D C F I S R P T E K T V F T I F M V G S S A I C	zCx30.3
	#	*
203	I L L L N V T E L C Y L L I R Y C S G K S K P V	hCX26
205	I T V L N V A E L A Y L L I V K A L R C S A R K G R R S F V H Q E K	zCx30.3
	#	*
227		hCX26
239	M S T T E K A H L Q N E K N A R L L S S A S D S S S N K T V	zCx30.3

Figure 1. The alignments of amino acid sequences between human CX26 and zebrafish Cx30.3. The gray shading highlights identical residues of the two sequences. The hashtag indicates human p.R184 or zebrafish p.R186, while the asterisks mark p.D46, p.E47, and p.Y65 with bonding connection to p.R184/p.R186 of adjacent or the same connexin. The positions of p.D46, p.E47, and p.Y65 are identical in human and zebrafish.

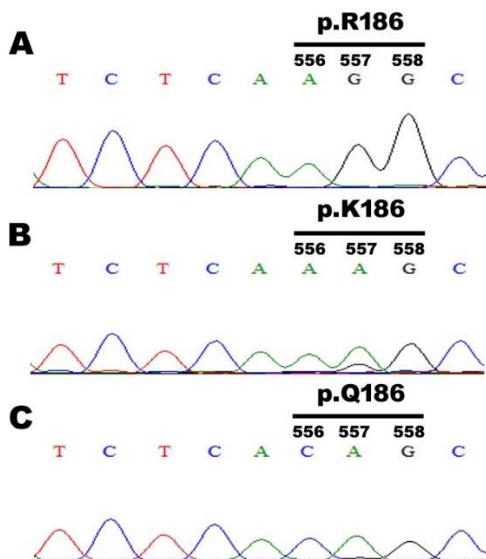


Figure 2. Confirmation of the genomic DNA sequences in (A) Tg(agr2:cx30.3-EGFP WT), (B) Tg(agr2:cx30.3-EGFP R186K) with 557G>A, and (C) Tg(agr2:cx30.3-EGFP R186Q) with 556A>C and 557G>A. The genomic DNA was obtained from the tissues of caudal fins. Polymerase chain reaction was conducted to amplify cx30.3 genes for DNA sequencing.

Table S1. Amino acid sequences of Cx30.3 variants.

Cx30.3 Variants	Amino Acid Sequences
Cx30.3 p.R186	MSWGALYAQLGGVNKHSTSLGKIWLSVLFIFRICILVIAAETVGDEQSDFTCNTQ QPGCKNVCYDHFFPVSHIRFWCLQLIFVSTPALLVAMHVAYRKRNMKKSILAKR GGNGKGDDESLKNRRLPITGPLWWTYTSSLFFRLLFEAGFMYALYYVYDGFQMA RLVKCEQWPCPNKVDCFIS R PTEKTVFTIFMVGSSAICIVLNVAELAYLIVKALLRCS ARAKGRRSFVHQEKMSTEKAHLQNEKNARLLSSASDSSSNKTV
Cx30.3 p.Q186	MSWGALYAQLGGVNKHSTSLGKIWLSVLFIFRICILVIAAETVGDEQSDFTCNTQ QPGCKNVCYDHFFPVSHIRFWCLQLIFVSTPALLVAMHVAYRKRNMKKSILAKR GGNGKGDDESLKNRRLPITGPLWWTYTSSLFFRLLFEAGFMYALYYVYDGFQMA RLVKCEQWPCPNKVDCFIS Q PTEKTVFTIFMVGSSAICIVLNVAELAYLIVKALLRCS ARAKGRRSFVHQEKMSTEKAHLQNEKNARLLSSASDSSSNKTV
Cx30.3 p.K186	MSWGALYAQLGGVNKHSTSLGKIWLSVLFIFRICILVIAAETVGDEQSDFTCNTQ QPGCKNVCYDHFFPVSHIRFWCLQLIFVSTPALLVAMHVAYRKRNMKKSILAKR GGNGKGDDESLKNRRLPITGPLWWTYTSSLFFRLLFEAGFMYALYYVYDGFQMA RLVKCEQWPCPNKVDCFIS K PTEKTVFTIFMVGSSAICIVLNVAELAYLIVKALLRCS ARAKGRRSFVHQEKMSTEKAHLQNEKNARLLSSASDSSSNKTV