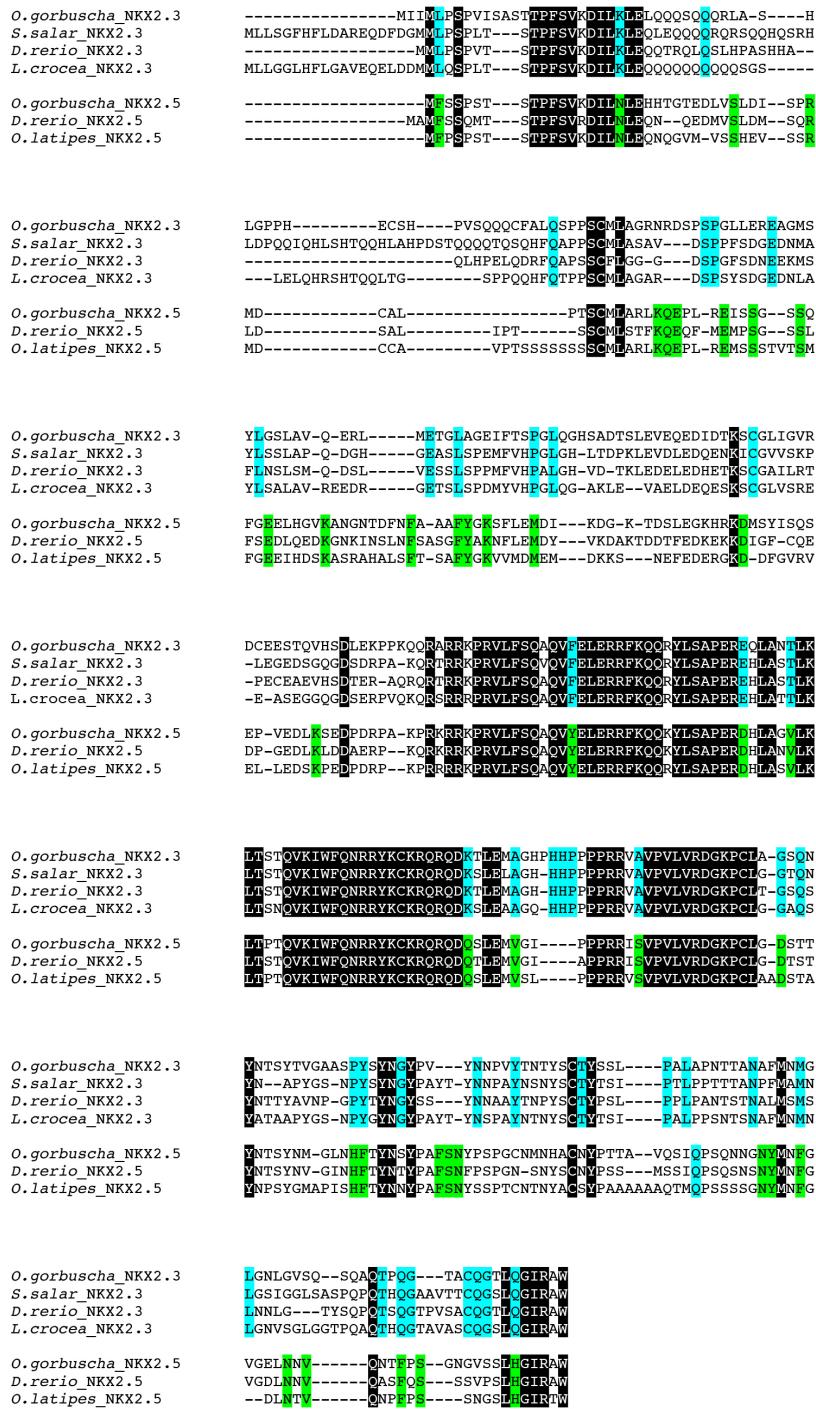


Figure S1. Distribution of ventricles with increased aspect ratio among pink salmon treatment groups. The absolute count (y-axis) and percent (above each bar) are given for ventricles at each given range of aspect ratio. Data are derived from experiments detailed previously (Incardona et al., 2015).

Figure S2. Sequence alignments of fish *nKX2.3* and *nKX2.5* orthologs, with pink salmon at top.

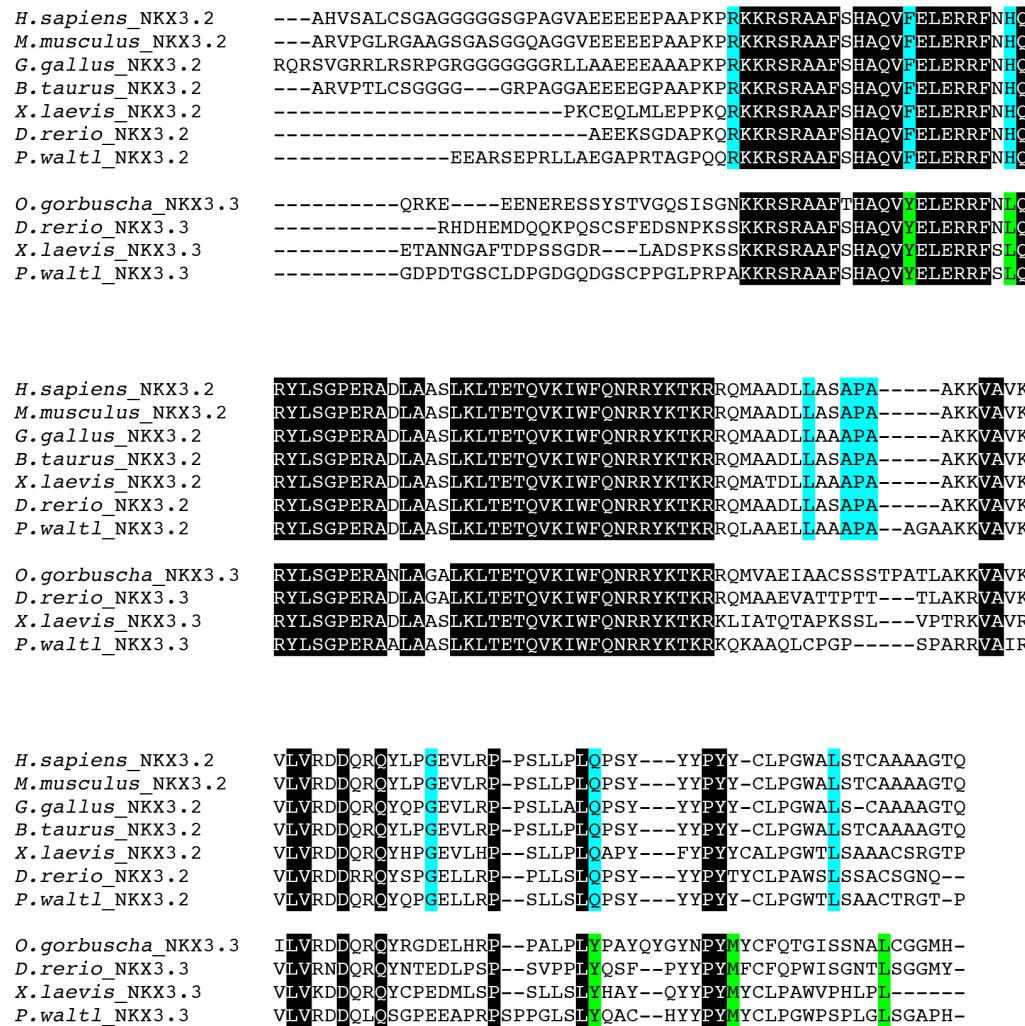


Figure S3. Sequence alignments of vertebrate *nkx3.2* and *nkx3.3* orthologs, with pink salmon at the top of *nkx3.3* alignments.

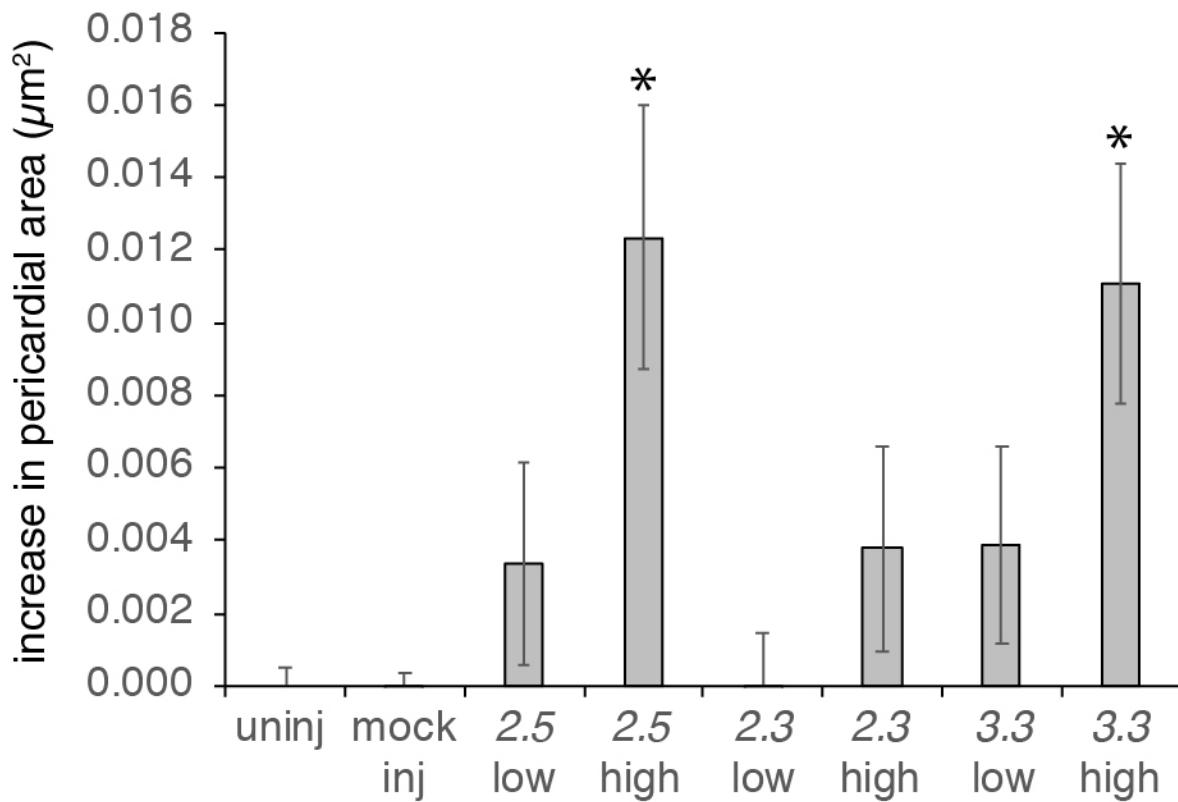


Figure S4. Quantification of edema accumulation in larvae following injection of *nRx* gene mRNAs. Pericardial area was measured in lateral views. Mean value of mock-injected controls was subtracted from each measured value to produce an “edema area” or elevation above control area. Values represent means  $\pm$  s.e.m. from 30 embryos for each treatment (10 each from 3 replicate growth dishes); asterisks indicate groups statistically different from control determined by one-way ANOVA and post-hoc Dunnett’s test. Low is 10 pg injection, high is 100 pg injection.

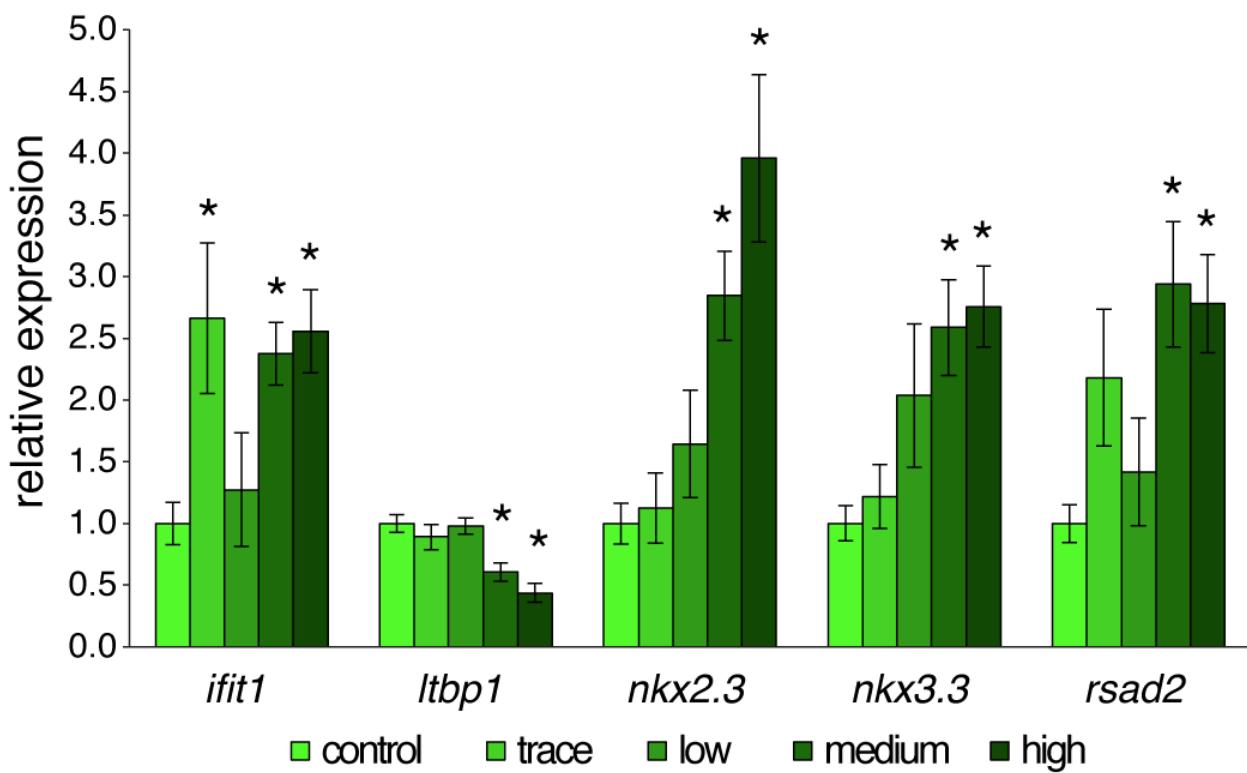


Figure S5. Validation of RNA-seq read count data by QPCR. QPCR was carried out for the indicated genes in the original RNA samples, as described in the Methods. Data represent mean  $\pm$  s.e.m. for  $N = 8$  (control, low, medium, high) and  $N = 5$  (trace). Asterisks indicate groups statistically different from control as determined by one-way ANOVA followed by Tukey-Kramer HSD post-hoc test.

**Table S1.** Complete list of differentially expressed genes.

[Click here to Download Table S1](#)

**Table S2.** Genes and primers used for RT-qPCR, RT-PCR, and for anti-sense and sense templates for *in situ* probes, 5' to 3'

Gene	Primer Pair
<i>ifit</i>	
RT-qPCR	F: AGAACATGGCAGAGTTGATAGTGC R: GTTCACAATTCTCGCTCTG
anti-sense	F: AGAACATGGCAGAGTTGATAGTGC R: TAATACGACTCACTATAAGGGAGAGTCACAATTCTCGCTCTG
sense	F: ATTAGGTGACACTATAGAGAACATGGCAGAGTTGATAGTGC R: GTTCACAATTCTCGCTCTG
<i>ltbp1</i>	
RT-qPCR	F: GGAAGAGTGTGGCATTCTGAAC R: TCCCTGGCCACACAGTAGTTAG
anti-sense	F: CTTTGCCCCCTGAAGAACAC R: TAATACGACTCACTATAAGGGAGATCGTACCGATCTCCTCATC
sense	F: ATTAGGTGACACTATAGCTTGCCCCCTGAAGAACAC R: TCGTACCGCGATCTCCTCATC
<i>nkx2.3</i>	
RT-qPCR	F: GCCCCTATAGTTATAATGGCTACC R: AGGCGTTAGCAGTAGTGTGTTGG
anti-sense	F: GCCCCTATAGTTATAATGGCTACC R: TAATACGACTCACTATAAGGGAGAAGGGCGTTAGCAGTAGTGTGTTGG
sense	F: ATTAGGTGACACTATAGGCCCTATAGTTATAATGGCTACC R: AGGCGTTAGCAGTAGTGTGTTGG
<i>rsad2</i>	
RT-qPCR	F: GAATGCTGGGGAGAACAGTC R: GCATGTCAGCTTGCTCCAC
anti-sense	F: CATTCTGGCCATTCTCTGTG R: TAATACGACTCACTATAAGGGAGAACAGTC
sense	F: ATTAGGTGACACTATAGCATTCTGGCCATTCTGTG R: AGACTGTTCTCCCCAGCATT
<i>nkx3.3</i>	
RT-qPCR	F: GGGCCAATCCATATCTGGTAAC R: GATCTTCACCGCCACTTTCTTAG
anti-sense	F: CCAGGTGAAAATCTGGTTCC R: TAATACGACTCACTATAAGGGAGACACAAAGCGCATTGCTAGAG
sense	F: ATTAGGTGACACTATAGCCAGGTGAAAATCTGGTTCC R: CACAAAGCGCATTGCTAGAG

<i>wdtc1</i>	
RT-qPCR	F: GACAAAAGGGCAACAGCTC R: GGAGCCGCTCACAAATGTACT
<i>eif1</i> □	
RT-qPCR	F: CCCCTGGACACAGAGATTCATC R: AGAGTCACACC GTTGGCGTTAC
<i>nkx2.3</i>	
RT-PCR	F: CCTCCAACAAAACAGAAACTGC R: AGCATAGGCCATT CACATCC
<i>nkx2.5</i>	
RT-PCR	F: CAAAAGGCGTGTGACCC R: CCCACTGAAGTAATAACCTGCATC
zebrafish <i>nkx2.3</i>	
RT-qPCR	F: TACCCCAGTCTCCTCCTCTAC R: CGAGGTTGTTCAAACCTCATGC
zebrafish <i>nkx2.5</i>	
RT-qPCR	F: AGCCTCGAGTTCTCTCTCA R: GTTCTGGAACCAGATCTTCACC
zebrafish <i>nkx3.3</i>	
RT-qPCR	F: CATGCGAGGAAGAAC AACA R: CTGCCCGAGATCTT CTTG
anti-sense 1	F: GAATAACCGAACCTCCTTT R: TAATACGACTCACTATAGGGAGATATTGCCTTGTCATTCT
sense 1	F: ATTTAGGTGACACTATAGGAATAACCGAACCTCCTTT R: TATTGCCTTGTCATTCT
anti-sense 2	F: ATTTAGGTGACACTATAGTATCATCAGACCAGCATTCA R: TAATACGACTCACTATAGGGAGAGCCTCAAATTAAAGTGTGC
sense 2	F: TATCATCAGACCAGCATTCA R: GCCTCAAATTAAAGTGTGC

F = forward primer; R = reverse primer

**Dataset 1:** Statistics associated with sequencing reads, mapping and read count comparisons

[Click here to Download Dataset 1](#)

**Dataset 2.** Fully annotated pink salmon cardiac transcriptome and output of BLAST search for viral-related genes.

[Click here to Download Dataset 2](#)