

Supplementary Materials

Table S1. Sequences of the primers used for PCR.

Primer Name	Purpose	Sequence(5' to 3')
<i>nanos1a</i> -5' RACE-R1	RACE	AGCAGTCCAGGTGCCCCGCTCTCTCCAA
<i>nanos1a</i> -5' RACE-R2	RACE	ACGCCGGGGAATCGTCCAAGCCCAGG
<i>nanos1a</i> -5' RACE-R3	RACE	TCGGTGATGGAGTTGGGGTTCTGGGG
<i>nanos1a</i> -3' RACE-F1	RACE	TAATCGCGGGCAGCGTTGGAGA
<i>nanos1a</i> -3' RACE-F2	RACE	GTTTCTCGATACTGAGCCCCCTTC
<i>nanos1b</i> -5' RACE-R1	RACE	GTCCATGGAGAGCAGGTCTGAG
<i>nanos1b</i> -5' RACE-R2	RACE	GTGCTCGTACGGCCTGAGAAGAGA
<i>nanos1b</i> -3' RACE-F1	RACE	TAATTGGGCACGGCAGGGACA
<i>nanos1b</i> -3' RACE-F2	RACE	ACCCTTGGA CTGCTGCTGCGC
<i>nanos1b</i> -3' RACE-F3	RACE	CTCTCTTCTCAGGCCGTACGAGCAC
<i>nanos2</i> -5' RACE-R1	RACE	GTCCGAGAGGCTGGAGGGTGA
<i>nanos2</i> -5' RACE-R2	RACE	TGGGTGACATAGTCCCGGAGA
<i>nanos2</i> -3' RACE-F1	RACE	GGGACGAGTACACCTTTGACAGTG
<i>nanos2</i> -3' RACE-F2	RACE	CCTGTTAGGGACTAGTTCACCC
<i>nanos3</i> -5' RACE-R1	RACE	TCAGCACGGAAGGGGTCTGTAGCG
<i>nanos3</i> -5' RACE-R2	RACE	CGAGGTCGCCGCTTTGGCACA
<i>nanos3</i> -5' RACE-R3	RACE	GACAGTCCTATGTAGTCTCTCC
<i>nanos3</i> -3' RACE-F1	RACE	CGCTACAGACCCCTTCCGTGCTGA
<i>nanos3</i> -3' RACE-F2	RACE	AACCAGGCCGGGGATGTTCTG
<i>nanos1a</i> -F	RT-PCR	GACTTGAAGGAGCGTTTCTCGAT
<i>nanos1a</i> -R	RT-PCR	CTTTAATGGTCGCTGGGATGGC
<i>nanos1b</i> -F	RT-PCR	CGGTTTGCTCCTGCGTAATTGG
<i>nanos1b</i> -R	RT-PCR	CTTCAGGATGTGGGTGCCGTAA
<i>nanos2</i> -F	RT-PCR	ACTACCCTCTCCGGGACTATGT
<i>nanos2</i> -R	RT-PCR	GCGTCATCAGTCATTTCACTTTCCC
<i>nanos3</i> -F	RT-PCR	TGTGCCAAAGCGGCGACCTCG
<i>nanos3</i> -R	RT-PCR	CAGAACATCCCCGGCCTGGTT
β -actin-F	RT-PCR	GAAATCGCCGCACTGAGTTGTTG
β -actin-R	RT-PCR	ACCATCACTCCCTGATGCCT
<i>nanos1a</i> -probe-F	ISH	GCCAGGAGCTGATGGAGTTTGAGT
<i>nanos1a</i> -probe-R	ISH	TAATACGACTCACTATAGGAGACTTTGGAATG TCAGGCTTTTCAT
<i>nanos1b</i> -probe-F	ISH	GCCATCCCAGCGACCATTAAAG
<i>nanos1b</i> -probe-R	ISH	TAATACGACTCACTATAGGTCATCCCCTTTGC CAATGTCAG
<i>nanos2</i> -probe-F	ISH	GACGGGGAGTGCTTCGACATGT
<i>nanos2</i> -probe-R	ISH	TAATACGACTCACTATAGGGCGTCATCAGTCA TTTCACTTTCCC
<i>nanos3</i> -probe-F	ISH	CTGGAGAGACTACATAGGACTGTC
<i>nanos3</i> -probe-R	ISH	TAATACGACTCACTATAGGTGGCCCCCGTGGC TCCGCACA

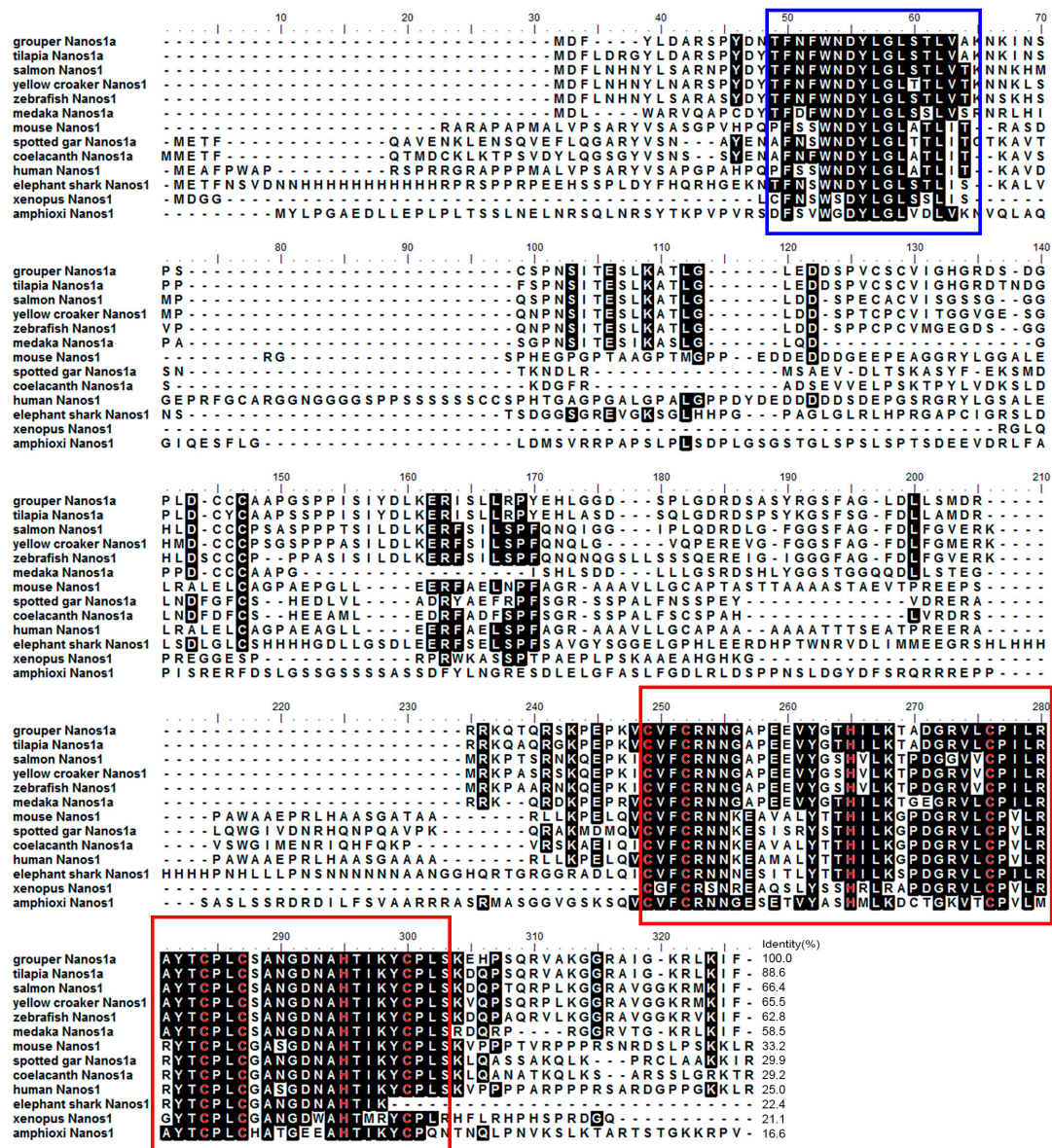


Figure S1. Amino acid alignments of *E. coioides* Nanos1A with the homologues from other vertebrates. The identities relative to *E. coioides* Nanos1A are exhibited at the end of each sequence. The blue frame indicates the conserved position of CCR4-NOT deadenylation interaction domain. The red frame indicates the conserved position of zf-domain. The 8 invariant cysteine and histidine residues in zf-domain were marked with red color.

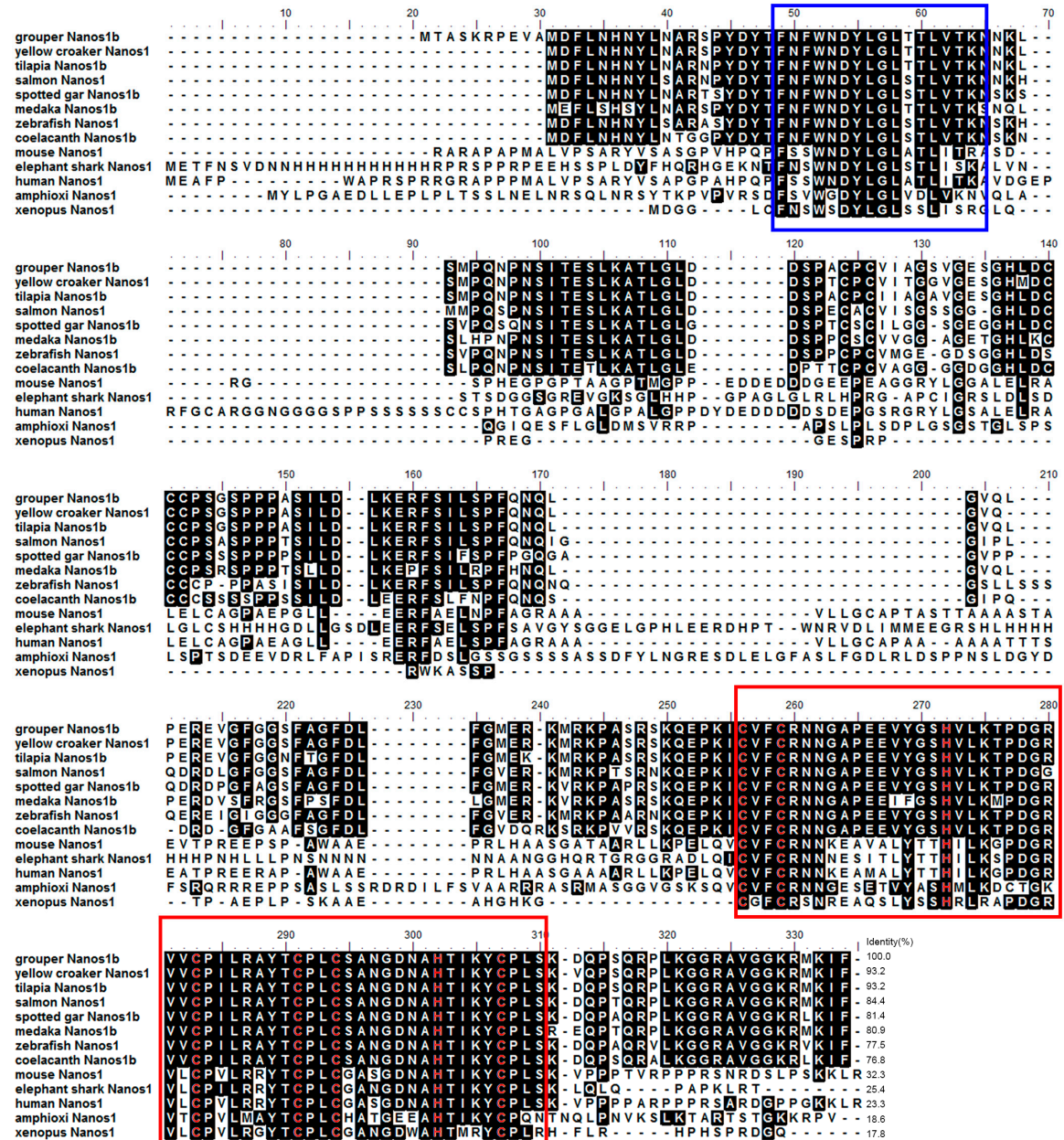


Figure S2. Amino acid alignments of *E. coioides* Nanos1B with the homologues from other vertebrates. The identities relative to *E. coioides* Nanos1B are exhibited at the end of each sequence. The blue frame indicates the conserved position of CCR4-NOT deadenylation domain. The red frame indicates the conserved position of zf-domain. The 8 invariant cysteine and histidine residues in zf-domain were marked with red color.

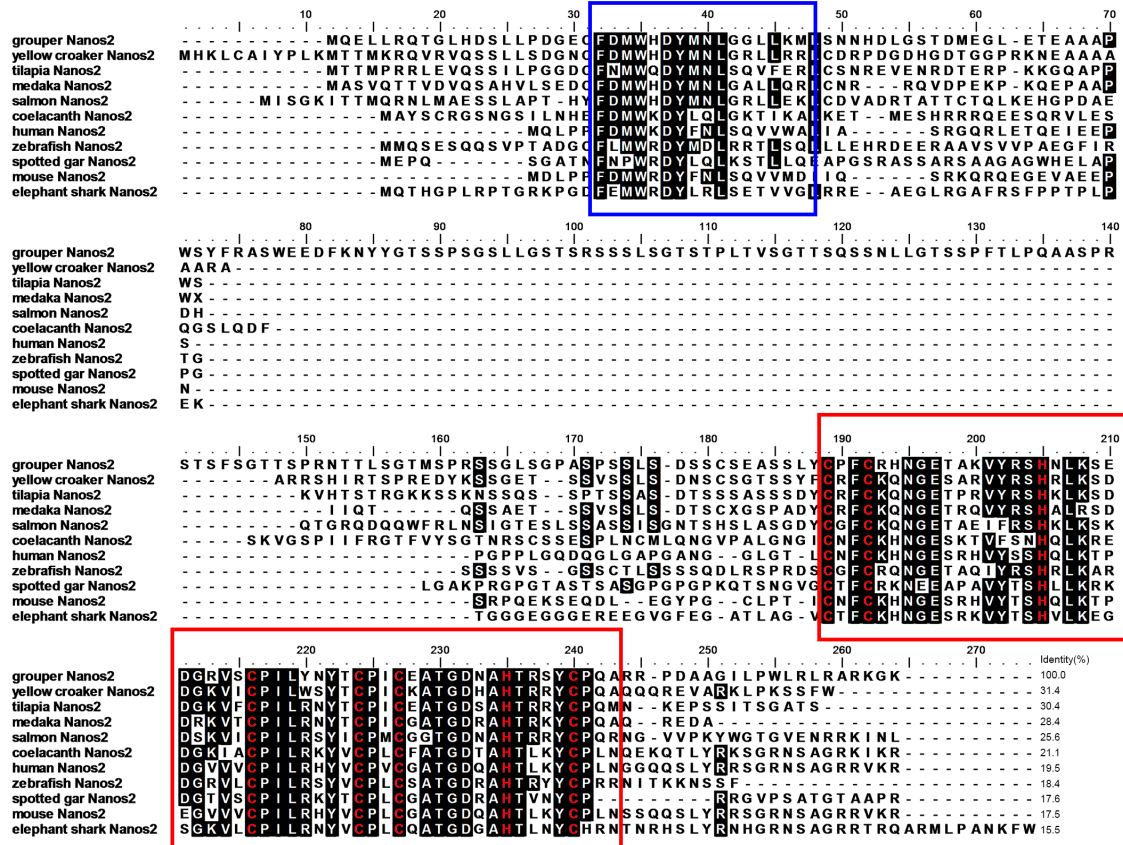


Figure S3. Amino acid alignments of *E. coioides* Nanos2 with the homologues from other vertebrates. The identities relative to *E. coioides* Nanos2 are exhibited at the end of each sequence. The blue frame indicates the conserved position of CCR4-NOT deadenylation interaction domain. The red frame indicates the conserved position of zf-domain. The 8 invariant cysteine and histidine residues in zf-domain were marked with red color.

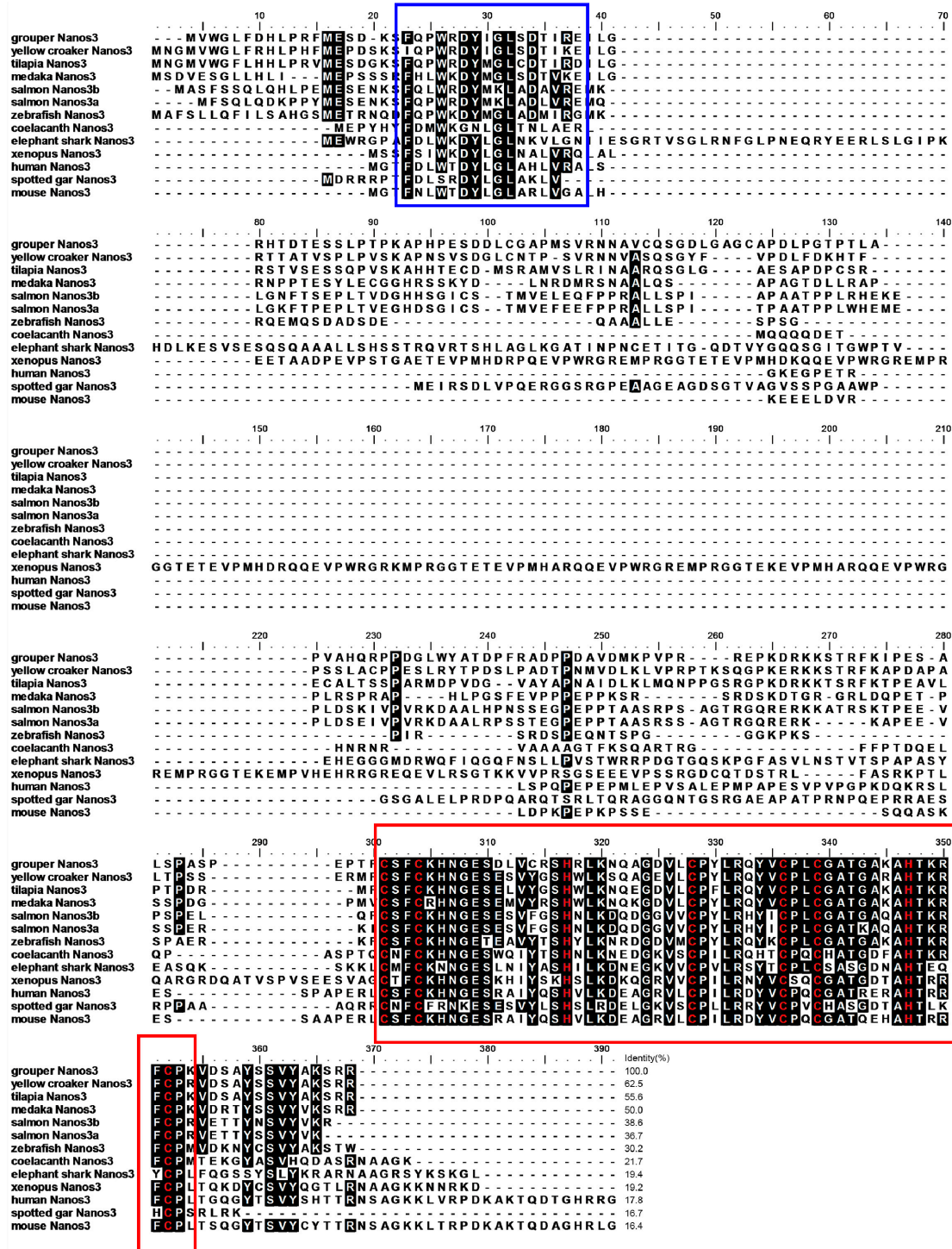


Figure S4. Amino acid alignments of *E. coioides* Nanos3 with the homologues from other vertebrates. The identities relative to *E. coioides* Nanos3 are exhibited at the end of each sequence. The blue frame indicates the conserved position of CCR4-NOT deadenylation interaction domain. The red frame indicates the conserved position of zf-domain. The 8 invariant cysteine and histidine residues in zf-domain were marked with red color.

Ecnanos3 3'UTR

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ACCAGCAGGTGGCAGGTAGCAAAAAGACACAGAGGGCTGAAACTTCCTT
TTATTGAGTGTGGTTTTGTTTTATTATCACGTGTGTGTGTGTGTAGTTTG
GGTTTTATTTGCATGCTTTGSCACGTTTGCCTTGTAGCCTTCTCTAAAGC
TGATTGGAGTTATTTCCAGCTGGTCTTTTACGGCCCTTGCTTTCTCTAA
CAGTGTCCCTTTGGGGGTTTTCATTTTGTATTGTTCTTTCAATAACGACTG
CCAGATATGTTTGGGAGGAGAAAAAATAAAGACAATGTAAGTTTTATTT
TTTTTAAATGAAACATTTTTTAACATGGCCACTTAATATCATACCTCCTGC
CCATGCATTAAAGGATCATCACACTGTCACACCTTTCTCTGAAGACCTAT
CAGTAATAACTTTAATACACCATGTAAACATCAAGTGACCATGTCAGCATT
TTAAATTATTTATTTAATTAATATATGAGTGAGGTGTTCTTGTTCGTAC
CTGTTCTGAGGCATGTTTGTGTTTTATTTCAATATTGTACATGTGGCTCTT
CTAAAATGCCGCAAAAGCTCTTCTCACTCTGAGAAAAGAAATGTGTGAAT
TAATCTGTGTGAATATTATTGTATGCCAGAATATACATAGTGAACCAAAA
AAAAAAAAAAAAAAAAAAAAA

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Figure S5. The sequence of *Ecnanos3* 3'-UTR. U-rich motifs are marked with gray shadow and the putative miR-430 binding site is indicated with frame where the different nucleotide against canonical seed sequence of miR-430 is marked by red.

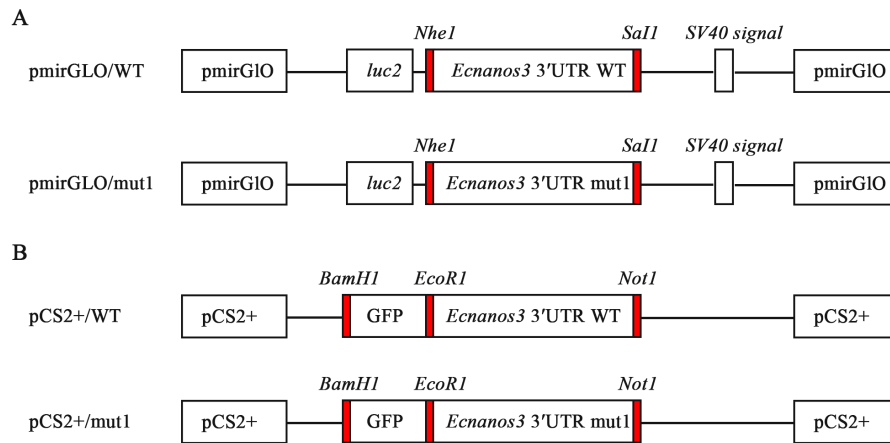


Figure S6. Schematic of the luciferase constructs and GFP constructs. (A) Schematic of the luciferase constructs. (B) Schematic of the GFP constructs.

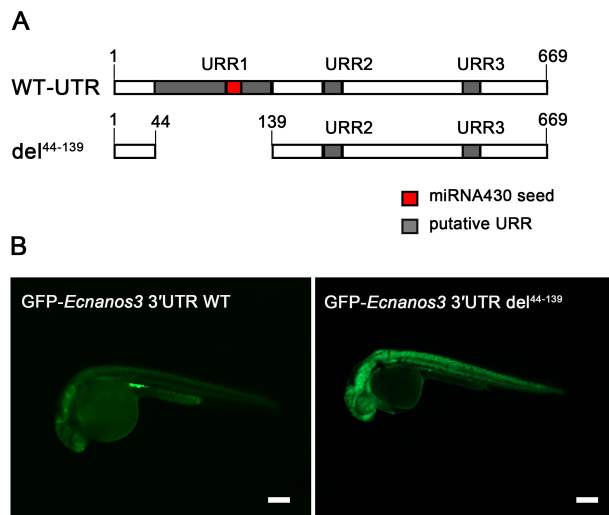


Figure S7. Schematic representation of *Ecnanos3* 3'-UTR del44-139 and function of URR1 in *Ecnanos3* 3'-UTR. (A) Schematic representation of *Ecnanos3* 3'-UTR del44-139; (B) PGCs visualization at 26 hpf by using GFP fused *Ecnanos3* 3'-UTR WT and *Ecnanos3* 3'-UTR del44-139, respectively. Bar: 250 μ m.