

## Supplemental Information

### **Lrp13 is a novel vertebrate lipoprotein receptor that binds vitellogenins in teleost fishes**

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Abbreviated Title: Lrp13 is a novel vertebrate lipoprotein receptor

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**Table S1.** Primer names and sequences used in this study.

Primer	Nucleotide Sequence (5'-3')	Orientation	Oligo Position*
SB618 F	GCG AGT TCC AGT GGT CTT GTA AAT C	Forward	689-713
SB618 R	CCT CAG CCT TTC ATC TGT CCA GTA G	Reverse	1728-1704
WP618 R1 O†	CAG CAC GCT CTA TCT TCA CAA CG	Reverse	1615-1593
WP618 R1 N†	AAC GCT GTG GTC CAG TGA CTT C	Reverse	1509-1488
WP618 F1 O†	CTG TCA CCC AGG CTA CAT AAT GG	Forward	1116-1138
WP618 F2 N†	CAG GCT ACA TAA TGG AGG CAA GTG	Forward	1124-1147
WP618 F1 N†	TGG ACC AGA AGA CCA CAG GAA CTC	Forward	1349-1372
SB618 F0 O†	ACT TGT CCT CCC AGG GTC AGC TTC	Forward	2312-2335
WP618 F3 N†	AGA AGC GAG TGG TGC TGG CTG CTC	Forward	1844-1867
618For1	TGT GCA GGA GTG GTG GTC ATT G	Forward	3466-3487
618Rev1	TGC TTG CCC ATG AAT CTG CCT C	Reverse	‡
Rpl9For	GAC ACC AGC TCA ATG TCG TTA CC	Forward	--
Rpl9Rev	TCA AGG GAG TCA CTT TGG GTT TC	Reverse	--
SBLR8For	ATA CAA GTG CGA ATG CCA CAA CGG	Forward	--
SBLR8Rev	AAA GTC TGC ATC CAG AGC CAC TGT	Reverse	--
SBLRX+1For	TGT GTG TGT TCA CTC GGC TAC AGT	Forward	3373-3396
SBLRX+1Rev	ATC ACA GCA ATG ACC ACC ACT CCT	Reverse	‡
SB618ishF	TGC TTC AGA TGG GCA TTG AGA G	Forward	1946-1697
SB618ishR	CCT TCC TTT ATG AGA ACG GCA GTG	Reverse	2451-2474
CiLR13+1F§	<u>CAC GTG AAT TCG CTC</u> TGT ATT CTC TAC CAG CAT GTG	Forward	--
CiLR13+1R§	<u>AAT ATC ATC GAT CTC</u> ACA TTC TAA TGA ACA TGT CTC C	Reverse	--

\*Oligo positions are based on alignment to either the striped bass (SB) or white perch (WP) *lrp13* full-length open reading frame as indicated by the respective prefix of each primer.

‡This primer anneals within the 3' untranslated region of the *lrp13* gene transcript.

†The suffix 'O' indicates use as an outer primer and 'N' as an inner primer for nested PCR as defined in the FirstChoice RLM-RACE Kit protocol.

§Underlining indicates the 15 bp adaptor sequences corresponding to the pET302/NT-His expression vector (Invitrogen).

**Table S2.** Tryptic peptides identified by LC-ESI-MS/MS from protein-affinity purified white perch ovary Vtgrs corresponding to Lrp13 and Lr8-. Those peptides detected in all of the quadruplicate runs are shown. Alignment position is based on the full-length polypeptide sequences of white perch Lrp13 and Lr8-.

Peptides from Lr8-	Alignment Position
VINNVQTPVGIAVDWIYK	507-524
NLYWSDLGTK	525-534
GLKEPASIAVDPLSGFLYWSDWGEPAK	553-579
VLQSADYLAHPFALTVEFDR	636-655
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Peptides from Lrp13	
SDEESCTIAPACTTK	177-191
CIPTAWR	242-248
ITGEPFLLASIQTDLFLFGLR	388-408
KAILSLDYDWK	421-431
VFWVSLDTEGIR	435-446
WSSLDQK	447-453
ADSVAVDWLGR	464-474
NMYWIDGVNSQIVAIR	475-490
SLDHSVILDEDLDQPR	498-513
SLALLPQK	514-521
GLMFWTEIGNVVK	522-534
AIGSATLDGDDIQILQMK	577-594
IIHPLLQMGIESPCEK	645-660
MDCSHMCVLAPGPK	661-674
TLFLTDDGTTSLSSFK	751-766
LKDADLSSQGQLLK	767-780
DADLSSQGQLLK	769-780
VESIALHPPSGR	829-840

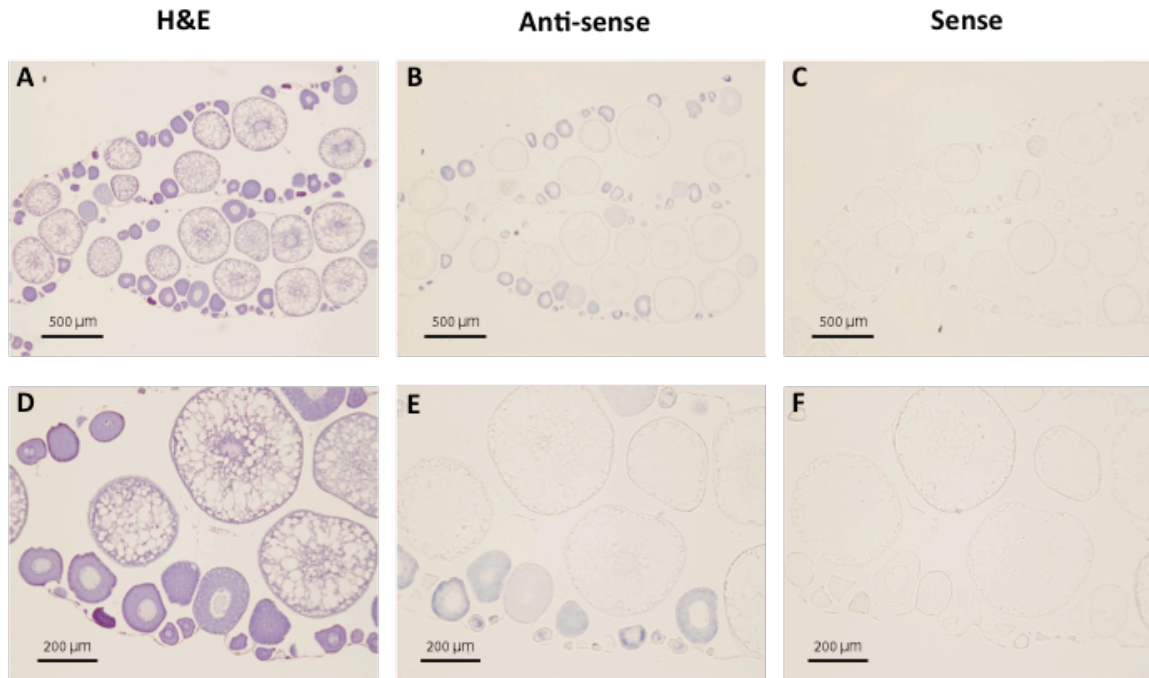


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sbLrp13      882 SLVFSSNGDKIYWADTGLGTIGSIQLDGSYRELKTGDGLVAVALSDDTL 931
sbLrp13      932 LWMTVSDKTRLWYRDEQQESKLWFEVGTENVSLKAFSNSSQTGSNQC TDN 981
sbLrp13      982 GNCQHLCLATPGGRTCKCAHDHILVHDTYCNPEQRCPSGTRPCLDELSCQ 1031
sbLrp13     1032 PVEKFCNRHIDCYDHSDENCVSVKQWSEAKVPALTWAHNSPPPTFPPLPGL 1081
sbLrp13     1082 SGVSGPNTTLNESSQLRNLTAQDCSQKHCSGNGRCVKNNGNSACVCSLGY 1131
sbLrp13     1132 SGDSCQDHLLKTMQGPVIVYGAAGLCAGVVVIAVMAVVVKRRKSANGRRAR 1181
sbLrp13     1182 PAAVKETSMTDLENKAETTPSKQPSVDTDKPEEVASSVD 1221

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**Figure S1.** ClustalW alignment of striped bass Lrp13 (sbLrp13) and white perch Lr8– (wpLr8–) polypeptide sequences. Amino acid positions are indicated by the numbers to the left and right. Asterisks (\*) and dots (.) under each residue pair indicate identical and chemically similar residues, respectively, in the aligned sequences. Domain demarcations are shown above the sequences and predicted signal peptides are indicated in boldfaced text. Conserved cysteine [C] residues in LDLa and EGF precursor domains are shown by shaded boxes. Conserved DxSDE and YWxD motifs and NPxY and YxxØ endocytosis signals are underlined. Residues shown in boldfaced italics correspond to peptides identified by ESI-LC/MS/MS of ligand-affinity purified Vtgrs (see: **Table S2** above). Black boxes containing white letters indicate conserved isoleucine [I], leucine [L], valine [V] or methionine [M], residues that typically proceed the medial [C] in each LDLa.



**Figure S2.** *In situ* hybridization of *lrp13* in striped bass ovary. (**A** and **D**) Hematoxylin-eosin stain; (**B** and **E**) adjacent sections probed with anti-sense *lrp13*; (**C** and **F**) adjacent sections probed with sense *lrp13*. Blue signal in **B** and **E** represents *lrp13* localization and this signal is absent in **C** and **F**.