

Supplementary Material: Vitellogenesis in the Blue Gourami is Accompanied by Brain Transcriptome Changes

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Table S1. Genes differentially expressed in PVTL/HVTL (as in Figure 2A) and their putative functions.

Upregulated in HVTL		
Gene ID	Gene Name	GenBank Function
RL36	ribosomal protein 36 60S large ribosomal subunit	Component of the large ribosomal subunit
YWHAE (1433E)	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon	1. Monooxygenase activity 2. Protein domain specific binding
TSN8	Tetraspanin-8	integrin binding
TMEM59L	Transmembrane protein 59 like	Modulates the O-glycosylation and complex N-glycosylation steps occurring during the Golgi maturation of APP. Inhibits APP transport to the cell surface and further shedding GTPase-activating protein (GAP) that stimulates the GTPase activity of Rho-type GTPases. Thereby, controls Rho-type GTPases cycling between their active GTP-bound and inactive GDP-bound states.
RHG44	rho GTPase-activating protein 44-like	Microtubule minus-end binding protein that acts as a regulator of non-centrosomal microtubule dynamics and organization. Specifically required for the biogenesis and maintenance of zonula adherens by anchoring the minus-end of microtubules to zonula adherens and by recruiting the kinesin KIFC3 to those junctional sites.
CAMP3	Calmodulin-regulated spectrin-associated protein 3	Involved in cell growth regulation. May be involved in the regulation of mitogenic signals and control of cell proliferation. Involved in the internalization of ligand-inducible receptors of the receptor tyrosine kinase (RTK) type, in particular EGFR.
EPS15	Epidermal growth factor receptor pathway substrate 15	Binds to F-actin and exhibits pH-sensitive F-actin depolymerizing activity. Regulates actin cytoskeleton dynamics. Important for normal progress through mitosis and normal cytokinesis.
COF1	Cofilin	RNA polymerase II core promoter proximal region sequence-specific DNA binding; RNA polymerase II transcription factor activity, sequence-specific DNA binding; Transcription coactivator activity, transcription factor binding
JUNB	JunB proto-oncogene, AP-1 transcription factor subunit	Recognizes and binds the palindromic sequence 5'-TTGGCNNNNNGCCAA-3' present in viral and cellular promoters and in the origin of replication of adenovirus type 2. These proteins are individually capable of activating transcription and replication.
NFIC	Nuclear factor I C	DNA binding, Protein heterodimerization activity
H2B1	Histone H2B-like	RNA binding
STAU2	Staufen double-stranded RNA binding protein 2	
EFNA3	Ephrin A3	Binds promiscuously Eph receptors residing on adjacent cells, leading to contact-dependent bidirectional signaling into neighboring cells.
RGRF1	Ras Protein Specific Guanine Nucleotide Releasing Factor 1	Promotes the exchange of Ras-bound GDP by GTP.
Upregulated in PVTL		
CERS6	Ceramide synthase 6	DNA binding
CERS5	Ceramide synthase 5	Dihydroceramide synthase. Catalyzes the acylation of sphingosine to form dihydroceramide.
Rtn4rl1	Reticulon-4 receptor-like 2	Cell surface receptor. Plays a functionally redundant role in postnatal brain development and in regulating axon regeneration in the adult central nervous system. Contributes to normal axon migration across the brain midline and normal formation of the corpus callosum. Protects motoneurons against apoptosis.
ARX	Aristaless related homeobox	Appears to be indispensable for central nervous system development. May play a role in the neuronal differentiation of the ganglionic eminence and ventral thalamus. May also be involved in axonal guidance in the floor plate.
UNC80	unc-80 homolog, NALCN activator	Component of the NALCN sodium channel complex, required for channel regulation. UNC80 is essential for NALCN sensitivity to extracellular calcium.
PHOP1	Probable phosphatase phospho1	Probable phosphatase, involved in bone mineralization
ATP1B2	ATPase Na ⁺ /K ⁺ Transporting Subunit Beta 2	This is the non-catalytic component of the active enzyme, which catalyzes the hydrolysis of ATP coupled with the exchange of Na ⁺ and K ⁺ ions across the plasma membrane. The exact function of the beta-2 subunit is not known.

Upregulated in HVTL		
Gene ID	Gene Name	GenBank Function
IQEC3	IQ Motif and Sec7 Domain 3	Acts as a guanine nucleotide exchange factor (GEF) for ARF1
ROBO2	Roundabout guidance receptor 2	Anterior/posterior axon guidance; Central nervous system projection neuron axonogenesis; Negative regulation of axon extension involved in axon guidance
MBNL1	Muscleblind like splicing regulator 1	Metal ion binding
CRY1	Cryptochrome-1	Transcriptional repressor that forms a core component of the circadian clock
RGRF2	Ras guanine nucleotide exchange factor 2	Functions as a calcium-regulated nucleotide exchange factor activating both Ras and rac1 through the exchange of bound GDP for GTP. May function in synaptic plasticity.
DLX5	Distal-less homeobox 5	Transcriptional factor involved in bone development. Acts as an immediate early BMP-responsive transcriptional activator essential for osteoblast differentiation.
ZEP1	Zeaxanthin epoxidase	Converts zeaxanthin into antheraxanthin and subsequently violaxanthin.
CLSTN3	Calsyntenin 3	May modulate calcium-mediated postsynaptic signals. Complex formation with APBA2 and APP, stabilizes APP metabolism and enhances APBA2-mediated suppression of beta-APP40 secretion, due to the retardation of intracellular APP maturation/
AHSG	(FETUA) alpha 2-HS glycoprotein	Probably involved in differentiation.
AAK1	AP2 associated kinase 1	Regulates clathrin-mediated endocytosis by phosphorylating the AP2M1/mu2 subunit of the adaptor protein complex 2 (AP-2). which ensures high affinity binding of AP-2 to cargo membrane proteins during the initial stages of endocytosis
EOMES	Eomesodermin	Functions as a transcriptional activator playing a crucial role during development. Functions in gastrulation, regulating mesoderm differentiation. Activates wnt8, t/bra, chrd and mix-A/mix.1 expression.

Table S2. Blue gourami receptor gene sequences.

Gene name	Trichogaster trichopterus sequences
Gonadotropin-releasing hormone II receptor (GnRHR)	TTTCACTCAGTGTGCCACTCATGGCAGCTTCAGCCGCCGCTGGCAGGAGACTCTTTACAACATGT TTTACTTCACCACGCTGTATGTTGTTCCCTGCTGGTGATGAGCTGCTGCTACAGCCGCATCCTGC TGCACATCCACAAGCAGCACCTGAGGAACAAAGCGGGCGAGTCTTACCTGCGCCGCAGCGGCA CTGATATTATCCCAAAGGCCCGGATGAAGACCCTGAAGATGACGGTGGTCATCGTGCTTTCCTTT CTGGTTTGTGGACTCCTTACTACCTTCTGGGAATCTGGTACTGGTTCAGCCCCGACATGCTGCGC ATCACACCCGAGTATGTGCACCACGCCCTCTTTGTGTTGGGAACCTGAACACCTGCTAAC
Membrane progesterin receptor epsilon (mPR)	TTTACATCCCGAGCGCTTGTGTTGTAGCAATCATCTGTGCTCTGCTGCTGCAACACTCGCCAGA AGTGGAGGCAGCATCGGTACATTATCCGGACCCTGGTTTCTCTCCCGTTCCTCATTTCCTCCA CGCCCGTGTCTACCGCTCCTAACAGATCGCCTTATTCCACCACCTCGTCTCTCTTGCCGCAT CCACTGCCATGTCCACGTTTTTTATCGCCACTGCTTCTGGCTGCTGGTTTCAGCTGTCTTTAACAT CAGCAAAGTGCCTGAGCGGCTGGCCCCAGTGCCTTTGACATCTGGGGGCACAGCCACCAGTGG TTCCACTGCTGCACATTTCTGTCCATCCTGGATGAACCTCACATGATCAAGAGTGAGGTGAGAGC CATCCTGCTCAGCTCGACTCTGCTGCTGCCCCCGCCACCCTCTCTGCTGCTGCTGACCTACCAT AGCTTCCACCTACGGGGTGATGCTGCTCCTCCAGACTACCATCATCTCCATCATTATGTGGTTTCG CATGGTGTGCCAACTGCATCTACGGACCTCAGATTGATCAGCTAGCAAAGGAACACCCCAAAA AATACCTGAAGTGTCACACAT
G-protein coupled receptor 54 (GPCR)	TGCTTGTGCGACTCGTGGGCAATTCCTGGTTATCTATGTCATCTCCAAACACAGGCAATGAGG ACGGCCACCAACTTCTACATAGCAAACCTGGCTGCCACCGACATCATCTTCTTGGTGTGCTGCGT CCCCTTACCGCCACCCCTCTATCCCTCCCTGGATGGATCTTTGGCAATTTTCATGTGCAAATTTGT CGCCTTTTACAGCAGGTAACACCGTGATTCATGTATCTGCTATC

Table S3. Blue gourami receptor gene primer sequences.

Short Name	Gene Name	Direction	Sequence
GPCR	G-protein coupled receptor 54	Forward	CATCTTCTTGGTGTGCTGCG
		Reverse	TGATACAGGTGGCTTGGACG
mPR	Membrane progesterone receptor epsilon(mPR)	Forward	GGAGGCAGCATCGGTACATT
		Reverse	ACGAGGTGGTGAATAAGGC
GnRHR	Gonadotropin releasing hormone receptor	Forward	CGCTGTATGTTGTTCCCTG
		Reverse	GCAGCCACCTCTTACCTTTG