Supplemental Material, Table 1.

Table 1. Primer sets for sequencing the BTEB cDNA from fathead minnow.

Primer set	Primer name	Sequence (5' to 3')
Partial cDNA sequence	Forward primer	TGGACTTAAACCAGTGCATCCC
	Reverse primer	GGCTGTGGTAAAATATACGGCAAG
Full-length coding region sequence, outer nested primer set	Forward primer	CGATGTCCATGTGATGAGCAT
	Reverse primer	TCACGTAGTTGCTCAAACACCA
Full-length coding region sequence, inner nested primer set	Forward primer	CACTGCGCCCTGAGTTTTGTT
	Reverse primer	GCAGACATGTGATCATTGGAGC

Supplemental Material, Table 2.

Table 2. Primer and probe sequences for quantitative real-time RT-PCR assays.

Assay	Primer or probe	Sequence (5' to 3')	Amplicon size (bp)
TSH β-subunit	Forward primer	GGTGCAGCCTCTCTGAACCA	73
	Reverse primer	CTTCTGCTTCTCCAGGGACAGT	
	Probe	*6FAM*-AACGAGGACCCACCAACTCCTTCACA-*Tamra*	
GPH α-subunit	Forward primer	CACCCCTGAGGTCCAAGAAA	72
	Reverse primer	TGGCAACACAGCATGTAGCTT	
	Probe	*6FAM*-CCATGCTCGTTCCCAAAAATATCACATCA-*BHQ1*	
TH receptor α	Forward primer	TGCAGGCTGTACTCCTCATGA	83
	Reverse primer	CAGGTACGTCTCCTGACACTTCTC	
	Probe	*6FAM*-AGATCGTTCTGGACTGACATGTGTGGAAAAGAT-*BHQ1*	
TH receptor β	Forward primer	TTGCTCCAAGCCGTGATTCT	74
	Reverse primer	TGACAACGCTCTATCCGCTCTA	
	Probe	*6FAM*-CTTTCCTCTGATCGTCCAGGTTTAACGAGC-*BHQ1*	
BTEB	Forward primer	CAAACCGGCGTAAAGGAAAA	70
	Reverse primer	CATGCAGTCTGTCACAGTTCCA	
	probe	*6FAM*-CGGGAGAAATGCAGGGTGAAAAGGAC-*BHQ1*	

Supplemental Material, Table 3.

Table 3. Comparisons in body condition and liver somatic index (LSI) among PBDE 47 exposure groups.

		Body mass (g)	Fork length (mm)	Body condition factor	LSI
male	***Control***	3.23 ± 0.18	64.40 ± 1.14	5.43 ± 0.27	0.61 ± 0.02
	Low PBDE 47	3.42 ± 0.22	64.45 ± 1.13	5.58 ± 0.30	0.69 ± 0.06
	High PBDE 47	4.10 ± 0.28 *	67.45 ± 1.17	6.34 ± 0.38	0.84 ± 0.08 *
female	***Control***	1.27 ± 0.05	50.90 ± 0.55	2.64 ± 0.07	0.92 ± 0.05
	Low PBDE 47	1.13 ± 0.07	49.80 ± 0.87	2.55 ± 0.13	0.83 ± 0.08
	High PBDE 47	1.35 ± 0.05	52.11 ± 0.90	2.83 ± 0.05	1.07 ± 0.10

* $p < 0.05$ compared to control

Supplemental Material, Table 4.

Table 4. Mean distribution for staging (% observed) of spermatogenesis and oogenesis in the testis and ovary of PBDE 47 exposed minnows

Male	Spermatogonia	1° spermatocytes	2° spermatocytes	Spermatids	Mature spermatozoa
Control	3.6 ± 0.9	8.8 ± 1.1	21.9 ± 2.8	16.6 ± 1.1	49.1 ± 4.3
Low PBDE 47	5.1 ± 1.9	12.7 ± 2.6	20.5 ± 2.0	29.3 ± 2.2 *	32.5 ± 5.7
High PBDE 47	11.9 ± 2.4	20.2 ± 2.2 *	22.3 ± 3.1	26.1 ± 1.4 *	19.5 ± 3.8 *

Female	Oogonia	Cortical alveola	Early vitellogenic	Late vitellogenic
Control	14.5 ± 3.2	44.6 ± 2.7	14.0 ± 1.6	26.9 ± 3.0
Low PBDE 47	23.8 ± 4.9	42.2 ± 4.5	9.4 ± 2.5	24.5 ± 4.6
High PBDE 47	13.2 ± 3.3	43.3 ± 3.2	18.1 ± 3.3	25.3 ± 2.6

* $p < 0.005$ compared to control

Supplemental Material, Figure 1.

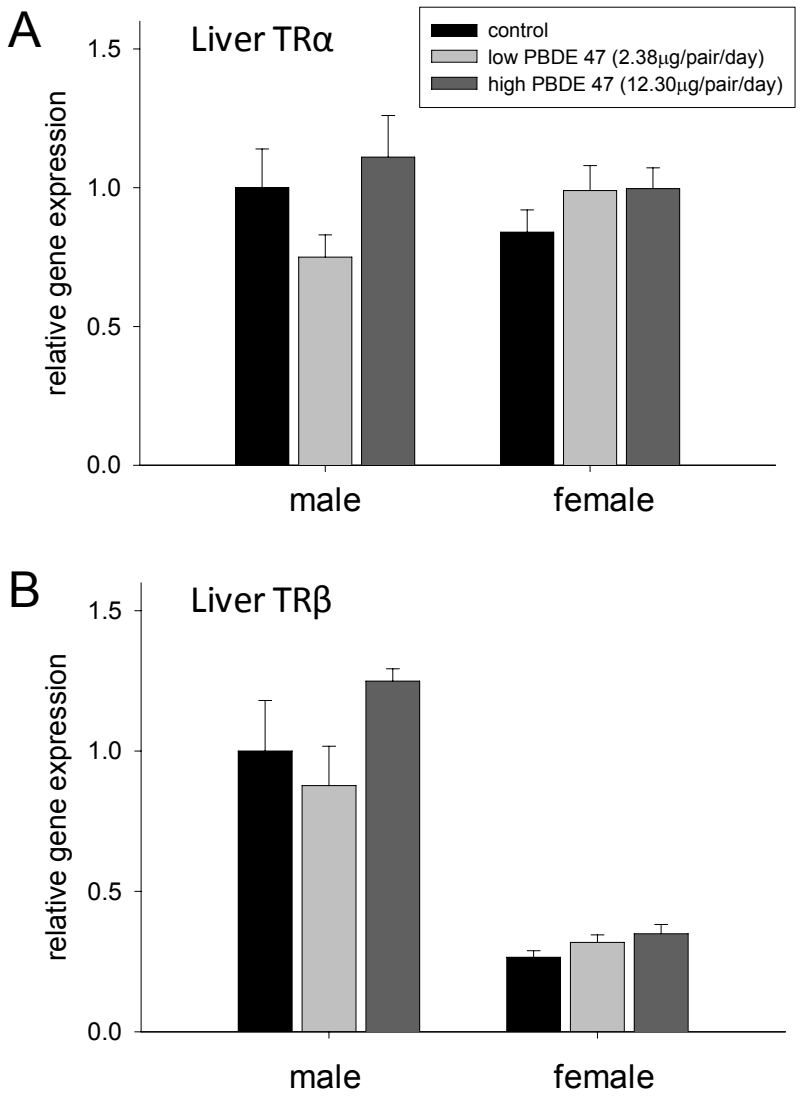

Figure 1. Relative gene expression for *thyroid hormone receptor (TR) α* and *β* in the liver of adult fathead minnows. Dietary exposure to PBDE 47 did not affect gene transcripts for *TRα* (**A**) or *TRβ* (**B**) in the liver. Male minnows did, however, have significantly greater levels of transcript for *TRβ* in the liver than females. Transcript levels are expressed relative to template RNA levels.

Supplemental Material, Figure 2.

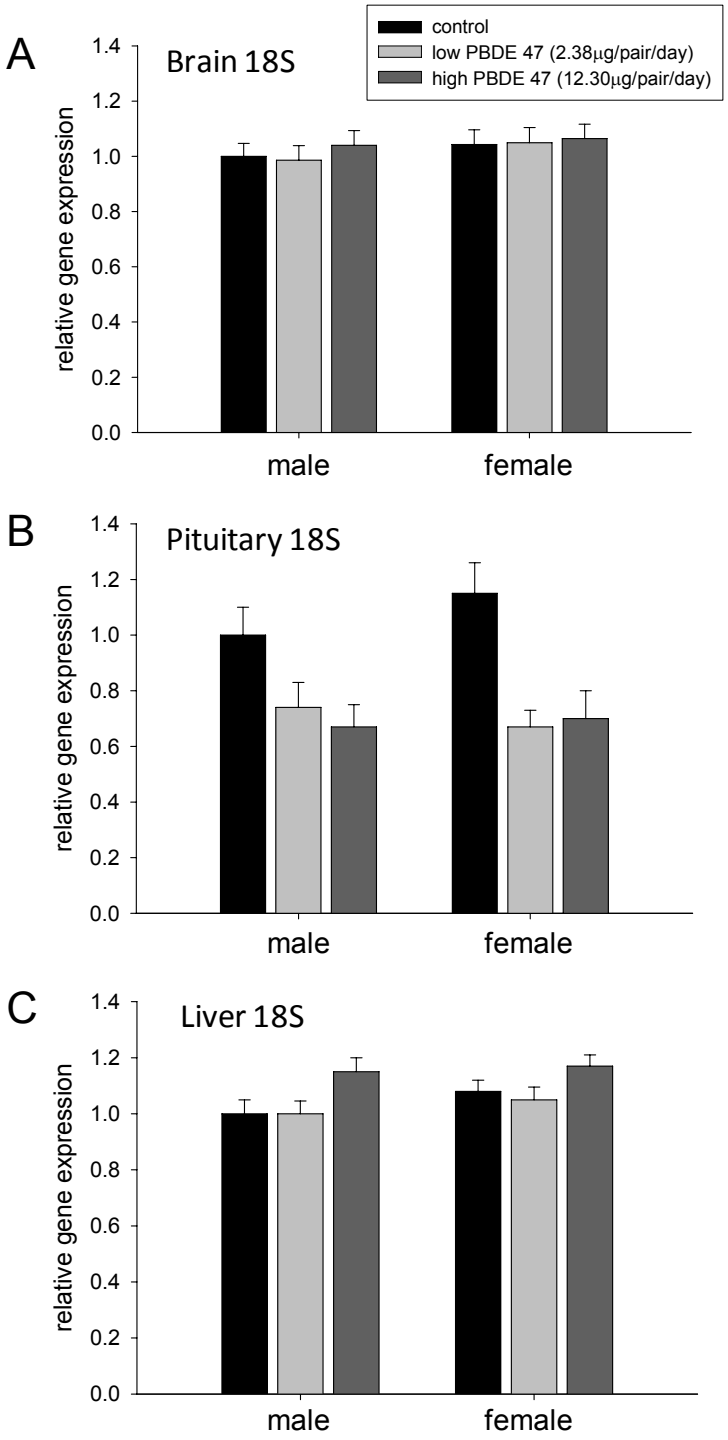

Figure 2. Relative gene expression for the housekeeper gene *18S*. Dietary exposure to PBDE 47 did not affect transcripts for *18S* in the brain (**A**), but caused significant reductions in *18S* mRNA levels in the pituitary gland (**B**), and elevated *18S* transcript in the liver at the high PBDE 47 dose.