

1 Wastewater treatment plant effluent alters pituitary gland gonadotropin mRNA levels in juvenile  
2 coho salmon (*Oncorhynchus kisutch*)

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4 Louisa B. Harding<sup>a</sup>, Irvin R. Schultz<sup>b</sup>, Denis A. M. da Silva<sup>c</sup>, Gina M. Ylitalo<sup>c</sup>, Dave Ragsdale<sup>d,1</sup>,  
5 Stephanie I. Harris<sup>d</sup>, Stephanie Bailey<sup>d</sup>, Barry V. Pepich<sup>d</sup>, and Penny Swanson<sup>c,e,\*</sup>

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7 <sup>a</sup> School of Aquatic and Fishery Sciences, University of Washington, Seattle, WA 98195, USA

8 <sup>b</sup> Pacific Northwest National Laboratory – Marine Sciences Laboratory, 1529 West Sequim Bay  
9 Road, Sequim, WA 98382, USA

10 <sup>c</sup> Northwest Fisheries Science Center, National Marine Fisheries Service, National Oceanic and  
11 Atmospheric Administration, 2725 Montlake Blvd E, Seattle, WA 98112, USA

12 <sup>d</sup> Manchester Environmental Laboratory, United States Environmental Protection Agency  
13 Region 10, 7411 Beach Drive E, Port Orchard, WA 98366, USA

14 <sup>e</sup> Center for Reproductive Biology, Washington State University, Pullman, WA 98164, USA

15

16 \*Corresponding author: Penny Swanson

17 Phone: +1 206-860-3282; Fax: +1 206-860-3467

18 *E-mail address:* penny.swanson@noaa.gov

19

20 <sup>1</sup> Current address: PO Box 88, Ophir, OR, 97464, USA

21

22 **Abstract:**

23 It is well known that endocrine disrupting compounds (EDCs) present in wastewater  
24 treatment plant (WWTP) effluents interfere with reproduction in fish, including altered gonad  
25 development and induction of vitellogenin (Vtg), a female-specific egg yolk protein precursor  
26 produced in the liver. As a result, studies have focused on the effects of EDC exposure on the  
27 gonad and liver. However, impacts of environmental EDC exposure at higher levels of the  
28 hypothalamic-pituitary-gonad axis are less well understood. The pituitary gonadotropins,  
29 follicle-stimulating hormone (Fsh) and luteinizing hormone (Lh) are involved in all aspects of  
30 gonad development and are subject to feedback from gonadal steroids making them a likely  
31 target of endocrine disruption. In this study, the effects of WWTP effluent exposure on pituitary  
32 gonadotropin mRNA expression were investigated to assess the utility of Lh beta-subunit (*lhb*)  
33 as a biomarker of estrogen exposure in juvenile coho salmon (*Oncorhynchus kisutch*). First, a  
34 controlled 72-hour exposure to 17 $\alpha$ -ethynylestradiol (EE2) and 17 $\beta$ -trenbolone (TREN) was  
35 performed to evaluate the response of juvenile coho salmon to EDC exposure. Second, juvenile  
36 coho salmon were exposed to 0, 20 or 100% effluent from eight WWTPs from the Puget Sound,  
37 WA region for 72 hours. Juvenile coho salmon exposed to 2 and 10 ng EE2 L<sup>-1</sup> had 17-fold and  
38 215-fold higher *lhb* mRNA levels relative to control fish. Hepatic *vtg* mRNA levels were  
39 dramatically increased 6,670-fold, but only in response to 10 ng EE2 L<sup>-1</sup> and Fsh beta-subunit  
40 (*fshb*) mRNA levels were not altered by any of the treatments. In the WWTP effluent exposures,  
41 *lhb* mRNA levels were significantly elevated in fish exposed to five of the WWTP effluents. In  
42 contrast, transcript levels of *vtg* were not affected by any of the WWTP effluent exposures. Mean  
43 levels of natural and synthetic estrogens in fish bile were consistent with pituitary *lhb* expression,  
44 suggesting that the observed *lhb* induction may be due to estrogenic activity of the WWTP  
45 effluents. These results suggest that *lhb* gene expression may be a sensitive index of acute  
46 exposure to estrogenic chemicals in juvenile coho salmon. Further work is needed to determine  
47 the kinetics and specificity of *lhb* induction to evaluate its utility as a potential indicator of  
48 estrogen exposure in immature fish.

49

50 **Keywords:** Endocrine disrupting compound; pituitary; gonadotropin; luteinizing hormone;  
51 follicle-stimulating hormone; vitellogenin; wastewater effluent

52

53 **1. Introduction:**

54 It is now well established that some chemicals in the environment are capable of  
55 disrupting normal endocrine function in humans and wildlife such as fish (Hotchkiss et al., 2008;  
56 León-Olea et al., 2014). These endocrine disrupting compounds (EDCs), including certain  
57 pharmaceuticals, pesticides, and a variety of industrial compounds, can act to mimic or block  
58 endogenous hormones by interfering with their synthesis, availability, or action (Crisp et al.,  
59 1998). EDC exposure has been associated with reduced fertility (Jobling et al., 2002), sex  
60 reversal (Jobling et al., 1998), and reproductive failure (Kidd et al., 2007; Nash et al., 2004) in a  
61 variety of aquatic organisms.

62 Municipal wastewater treatment plant (WWTP) effluents are one of the primary sources  
63 of EDCs into the aquatic environment. Fish collected downstream of some WWTPs exhibit  
64 symptoms of endocrine disruption and altered reproductive function including reduced gonad  
65 size, delayed maturation, and decreased steroidogenesis (Folmar et al., 2001; Vajda et al., 2011,  
66 2008; Woodling et al., 2006). In addition, feminization of male fish has been reported  
67 downstream of WWTPs including observations of intersex gonads or reduced primary and  
68 secondary male sex characteristics (Jobling et al., 1998; Purdom et al., 1994; Vajda et al., 2011,  
69 2008). Chemical analyses identified natural estrogens [estradiol (E2) and estrone (E1)] and  
70 synthetic estrogens [17 $\alpha$ -ethynylestradiol (EE2)] as the most likely feminizing agents in  
71 wastewater effluents (Desbrow et al., 1998; Rodgers-Gray et al., 2000). In addition, various  
72 anthropogenic compounds such as alkylphenols [nonylphenols (NP) and octylphenols (OP)] and  
73 bisphenol A (BPA) have also been identified as estrogen receptor (ER) agonists or antagonists  
74 and are present in wastewater effluent (Snyder et al., 2001).

75 Early studies on the effects of WWTP effluent exposure on fish reproduction found  
76 elevated expression of vitellogenin (Vtg) in male fish exposed to WWTP effluent (Folmar et al.,  
77 1996; Harries et al., 1997; Purdom et al., 1994). Vtg is an egg yolk protein precursor that is  
78 induced in maturing female fish in response to rising plasma E2 levels. Vtg synthesis can also be  
79 stimulated in male or juvenile fish of both sexes in response to exogenous estrogen exposure.  
80 Indeed, Vtg can be increased thousands fold in male fish in response to estrogens making it a  
81 widely used biomarker of estrogen exposure (Sumpter and Jobling, 1995; Thorpe et al., 2000).

82 As such, many studies of endocrine disruption or estrogen exposure have focused on the gonad  
83 and liver. However, reproduction is controlled by the hypothalamic-pituitary-gonad (HPG) axis  
84 and EDCs may exert their effects at higher levels of the HPG axis.

85 The pituitary gonadotropins (Gths), follicle stimulating hormone (Fsh) and luteinizing  
86 hormone (Lh), are heterodimeric glycoprotein hormones composed of a common alpha subunit  
87 and a hormone-specific beta subunit. The Gths are involved in all aspects of gonad development  
88 and function including steroidogenesis, gametogenesis, final gamete maturation, and gamete  
89 release (Levavi-Sivan et al., 2010; Swanson et al., 2003). The Gths are synthesized and released  
90 in response to a variety of factors from the brain, primarily gonadotropin-releasing hormone  
91 (GnRH) released from the hypothalamic neurons that directly innervate the fish pituitary gland.  
92 In addition, the Gths are regulated by positive and negative feedback from the gonad via steroid  
93 hormones and other gonadal peptides. For example, when immature trout or salmon are treated  
94 with estrogen or aromatizable androgens, pituitary and plasma Fsh levels decrease while  
95 pituitary Lh beta subunit (*lhb*) mRNA levels and pituitary Lh content increase (Breton et al.,  
96 1997; Dickey and Swanson, 1998; Saligaut et al., 1998), suggesting estrogens play an important  
97 role in regulating both gonadotropins. In support of this, estrogen response elements (EREs)  
98 have been identified in the *lhb* (Le Dréan et al., 1995; Liu et al., 1995; Sohn et al., 1999; Xiong  
99 et al., 1994) and Fsh beta subunit (*fshb*) (Rosenfeld et al., 2001; Sohn et al., 1998; Vischer, 2003)  
100 gene promoters of various fish species. Therefore, it is possible that Gths may be susceptible to  
101 endocrine disruption by estrogenic contaminants such as EE2 or WWTP effluent.

102 In salmonids, pituitary *fshb* and *lhb* mRNA and plasma Fsh and Lh expression profiles  
103 are well characterized (Breton et al., 1998; Campbell et al., 2006; Gomez et al., 1999; Prat et al.,  
104 1996; Swanson et al., 1991). In male and female coho salmon, pituitary *fshb* mRNA levels,  
105 pituitary Fsh content, and plasma Fsh levels begin to increase about one year prior to spawning  
106 (Campbell et al., 2006). In contrast, *lhb* mRNA levels and pituitary Lh content increase during  
107 late gametogenesis and final gamete maturation in response to increasing levels of estradiol or  
108 aromatizable androgens (Breton et al., 1998; Gomez et al., 1999; Prat et al., 1996; Swanson et  
109 al., 1991). However, similar to the case of Vtg, increased expression of *lhb* mRNA and  
110 accumulation of Lh protein content in the pituitary of immature fish can be induced in response  
111 to estrogen treatment. Studies have shown that mRNA levels for *lhb* are induced in response to

112 EE2 or other estrogenic contaminants (Harding et al., 2013; Harris et al., 2001; Johns et al.,  
113 2009; Maeng et al., 2005; Rhee et al., 2010; Yadetie and Male, 2002). Using high-throughput  
114 sequencing and RNA-Seq, we previously demonstrated that waterborne exposure of  
115 previtellogenic coho salmon to 12 ng L<sup>-1</sup> EE2 for up to 6 weeks had widespread effects on the  
116 pituitary transcriptome and dramatically altered Gth mRNA levels. At 6 weeks, *lhb* was induced  
117 395-fold and was the most significantly altered transcript, while *fshb* was downregulated -3.5  
118 fold (Harding et al., 2013). Alterations in plasma Gth levels have also been observed in response  
119 to EDC exposure (Brown et al., 2007; Golshan et al., 2014; Harris et al., 2001). Female rainbow  
120 trout (*Oncorhynchus mykiss*) exposed to 4-nonylphenol at 0.7, 8.3, or 85.6 µg L<sup>-1</sup> for 18 weeks  
121 during early secondary oocyte growth showed reduced *fshb* mRNA levels, pituitary Fsh content  
122 and plasma Fsh levels and increased plasma Lh and Vtg (Harris et al., 2001). These findings  
123 suggest that Gths may be sensitive targets of EDC exposure and may be involved in inhibited  
124 gonad growth and altered reproduction associated with endocrine disruption (Filby et al., 2006;  
125 Harris et al., 2001).

126         The aim of this study was to examine the effects of WWTP effluents on pituitary Gths in  
127 14-18 month old juvenile coho salmon (*Oncorhynchus kisutch*) and to evaluate the utility of *lhb*  
128 as a potential biomarker of estrogen exposure. Based on the strong induction of *lhb* mRNA levels  
129 in response to EE2 and other ER agonists, we hypothesized that *lhb* mRNA levels would be  
130 increased in response to WWTP effluents containing estrogenic chemicals. Juvenile coho salmon  
131 were selected for this study because: 1) coho salmon are ecologically relevant species in the  
132 Pacific Northwest region of North America; 2) presmolts or smolts (14-18 month old, early  
133 gametogenesis) have low to non-detectable basal expression of hepatic *vtg* and pituitary *lhb* in  
134 both male and female fish at this stage; 3) primary oocyte growth and early stages of  
135 spermatogenesis occur at this life history stage and may be affected by contaminants in WWTP  
136 effluent; 4) the low body size (< 50 g body mass) at this stage makes them more practicable for  
137 waterborne exposure studies; and 5) salmon presmolts and smolts are residing in or migrating  
138 through urban waterways and potentially exposed to EDCs during these stages. To evaluate the  
139 response of juvenile coho salmon to EDC exposure, we first conducted a controlled 72-hr  
140 exposure to EE2 and 17β-trenbolone (TREN; a synthetic androgen used in cattle production).  
141 TREN and EE2 were selected as a model androgen and estrogen, respectively. Second, we

142 exposed coho salmon to 100% effluent, 20% effluent, or control water for 72 hrs. Effluent from  
143 eight WWTPs were selected to include a range of treatment processes (secondary and tertiary),  
144 which vary in their removal efficiency of steroid estrogens. In addition to pituitary Gth mRNA  
145 levels, we measured hepatic *vtg* mRNA levels as a positive control of estrogen exposure. Where  
146 possible, chemical analyses on exposure effluents and bile from exposed fish were conducted to  
147 quantify exposure to a variety of contaminants with estrogenic activity. Analysis of several  
148 selective serotonin reuptake inhibitors (SSRIs) in effluents was also performed because of high  
149 occurrence in WWTP effluent and in Puget Sound estuary waters (Hedgespeth et al., 2012;  
150 Meador et al., 2016; Verlicchi et al., 2012) and reported effects on Gth levels in fish (Prasad et  
151 al. 2015).

152

## 153 **2. Materials and methods**

### 154 *2.1 Chemicals for exposure and water chemistry*

155  $17\alpha$ -ethynylestradiol (CAS #: 57-63-6; purity > 99%),  $17\beta$ -trenbolone (CAS #: 10161-  
156 33-8; purity > 99%), methyl-N-trimethylsilyl-trifluoroacetamide (MSTFA),  
157 heptafluorobutyrylimidazole (HFBI), iodotrimethylsilane (ITS), and resublimed iodine were  
158 obtained from Sigma-Aldrich Chemical Co. (St Louis, MO). Fluoxetine hydrochloride (CAS #:  
159 56296-78-7; purity > 98%) was obtained from Spectrum chemicals (Gardena, CA).  
160 Norfluoxetine-oxalate was obtained from Cerilliant<sup>®</sup> Analytical Reference Standards (CAS #:  
161 107674-50-0; Sigma-Aldrich, St. Louis, MO). Sertraline hydrochloride (CAS #: 79559-97-0;  
162 purity > 98%) was obtained from Toronto Research Chemicals (Toronto, Ontario, CA).  
163 Citalopram hydrobromide (CAS #: 59729-32-7; purity > 98%) was obtained from TCI America  
164 (Portland, OR). [2,4,16,16]d4- $17\alpha$ -ethynylestradiol (EE2-d4, CAS #: 350820-06-3),  
165 [16,16,17]d3-estradiol (E2-d3, CAS #: 79037-37-9), [2,4,16,16]d4-estrone (E1-d4, CAS #:  
166 53866-34-5) and [16 $\alpha$ -Hydroxy- $17\beta$ -estradiol]d2-estriol (E3-d2, CAS #: 53866-32-3), all > 97%  
167 purity, were purchased from C/D/N isotopes (Pointe-Claire, Quebec, CA). Pentadeuterated  
168 fluoxetine (fluoxetine-d5, CAS #: 1173020-43-3, > 99% ring labeled) was obtained from Isotec  
169 (Sigma-Aldrich, St. Louis, MO). All other chemicals were of reagent grade or better and were  
170 obtained from standard sources.

171

172 *2.2 Fish maintenance*

173 Coho salmon eyed embryos were obtained from the Issaquah Hatchery in mid-December  
174 and incubated in Heath trays at 8 °C at the Northwest Fisheries Science Center hatchery facilities  
175 (Seattle, WA). After ponding, fish were reared in recirculated 10 – 10.5 °C fresh water under a  
176 simulated natural photoperiod. Lighting above the tanks was continually adjusted to match the  
177 natural photoperiod of Seattle, WA (47.6°N). Fish were fed a standard ration of BioDiet  
178 commercial feed (Bio-Oregon, Longview, WA) according to Bio-Oregon’s feed rate guidelines.  
179 On January 31, 2012, 300 coho salmon parr (~14 month old, ~20 g body weight) were  
180 transferred to Pacific Northwest National Laboratory – Marine Science Laboratory (PNNL-MSL,  
181 Sequim, WA). Fish were initially maintained in circular 1400 L fiberglass tanks. The holding  
182 tanks were maintained using a single-pass flow through system using fresh water obtained from  
183 MSL’s artesian well (440 ft depth), which was pre-aerated and added to tanks at a minimum flow  
184 rate of 12 L/min. After three weeks of acclimation, groups of fish were transferred to smaller,  
185 370 L circular fiberglass tanks (water inflow rate of 4 L/min). Water temperature, dissolved  
186 oxygen, and pH were monitored weekly throughout the acclimation and exposures with values  
187 ranging from 11.8 – 12.5 °C for temperature, 8.0 – 9.4 mg L<sup>-1</sup> for dissolved oxygen, and 7.75 –  
188 8.05 for pH. Fish were maintained under a simulated natural photoperiod regime for Sequim,  
189 WA (48.1°N) with artificial dusk and dawn and fed a standard ration of Bio-Oregon® soft moist  
190 pellets. All fish were maintained according to the guidelines established by the Institutional  
191 Animal Care and Use Committee of PNNL-MSL.

192

193 *2.3 EE2 and TREN Exposures*

194 Controlled exposures to EE2 and TREN were performed for comparison with WWTP  
195 effluent exposures. Seventy two-hour exposures to EE2 or TREN were conducted using a  
196 continuous flow-through protocol similar to previous studies (Schultz et al., 2013). Exposure  
197 water was prepared using a concentrated aqueous stock solution that was slowly added to the  
198 exposure tanks using a peristaltic pump. No organic co-solvents were used. All exposure tanks  
199 were allowed to equilibrate with the dosing system for three days prior to the addition of fish.  
200 Nominal exposure values were adjusted based on daily monitoring of water and stock solution

201 in-flow rates. Water samples from each tank were removed and analyzed for EE2 or TREN at the  
202 start and end of the exposure.

203 In February 2012, 14-month old, mixed sex coho salmon were randomly assigned to  
204 treatment tanks (2 tanks/treatment; 10 fish/tank) and exposed to nominal concentrations of 0, 2  
205 or 10 ng EE2 L<sup>-1</sup> (0.0074 or 0.037 nM EE2) or 20 or 200 ng TREN L<sup>-1</sup> (0.074 or 0.740 nM  
206 TREN) fresh water for 72 hours. At the end of 72 hours, fish were anesthetized in buffered  
207 tricaine methanesulfonate (0.05% MS-222; Argent Laboratories, Redmond, WA) and euthanized  
208 by decapitation. Fork length (nearest mm), body weight (nearest 0.1 g), gonad weight and liver  
209 weight (nearest mg) were recorded. Gonad and liver weights were used to calculate  
210 gonadosomatic index (GSI) and hepatosomatic index (HSI) respectively, according to the  
211 following equation: (tissue mass/body mass) X 100. The pituitary gland and a small piece (~50  
212 mg) of liver were dissected and flash frozen in liquid nitrogen and stored at -80 °C until RNA  
213 isolation.

214

#### 215 *2.4 WWTP Effluent Exposures*

216 In April and May, effluent grab samples were collected from eight WWTPs around Puget  
217 Sound (WWTP A – H), which were selected based on differences in treatment processes and  
218 effluent dilution factors (Table 1). Approximately 200 gallons (750 L) of effluent were collected  
219 from each WWTP in 55-gallon (208-L) Teflon<sup>®</sup>-lined drums. Wherever possible, samples were  
220 collected at treatment points after final filtration, but prior to chlorine disinfection. For WWTP E  
221 some mortality due to residual chlorine was observed. Therefore, for sites F-H, if samples were  
222 collected post chlorination, a minimum volume of anhydrous sodium thiosulfate solution was  
223 added to attain a concentration of 6.7 mg L<sup>-1</sup> in order to reduce the free available chlorine (FAC)  
224 based on guidance in EPA's *Methods for Measuring the Acute Toxicity of Effluents and*  
225 *Receiving Waters to Freshwater and Marine Organisms* (U.S. EPA, 2002). The effluent samples  
226 were refrigerated and transported to PNNL-MSL for exposure studies. Drums of effluent were  
227 stored in fiberglass tanks with running well water to maintain a temperature of ~12 °C. Effluents  
228 were chilled overnight with aeration to remove residual chlorine if present and exposures were  
229 initiated the following morning.



230 Exposures were conducted during April and May when fish were undergoing  
231 smoltification. At this stage, fish are sexually immature with ovaries containing perinucleolar  
232 stage oocytes (Campbell et al., 2006) and testes containing only Type A (undifferentiated)  
233 spermatogonia (Schulz et al., 2010). Juvenile 16- to 17-month old, mixed-sex coho salmon were  
234 randomly assigned to 0%, 20%, or 100% WWTP effluent treatment (2 tanks/treatment; 6  
235 fish/tank) and exposed under semi-static conditions with a 60% tank water replacement  
236 conducted daily in accordance with the EPA's *Methods for Measuring the Acute Toxicity of*  
237 *Effluents and Receiving Waters to Freshwater and Marine Organisms* (U.S. EPA, 2002).  
238 Exposure tanks were filled with 110 L of 0%, 20%, or 100% effluent. Every 24 hours,  
239 approximately 66 L of exposure water was removed and replaced by new exposure water  
240 previously chilled to 12 °C. Fish were fed up to the day before the experiment, and then were  
241 fasted during the exposure. After 72 hours, fish were euthanized in buffered MS-222 and  
242 decapitated. Fork length, body weight, gonad weight and liver weight, were recorded and GSI  
243 and HSI were calculated as described above. The pituitary gland and a small piece (~ 50 mg) of  
244 liver were dissected and placed in 0.75 mL RNAlater® (Life Technologies, Carlsbad, CA).  
245 Tissues were stored in RNAlater® at room temperature for up to a week and then stored at -20  
246 °C or -80 °C until RNA isolation. When possible, bile was collected from the gallbladder with a  
247 clean 1-mL syringe tipped with a 23 G needle. Bile was stored at -80 °C until analysis.

248

#### 249 2.5 Exposure chemical analyses

250 Exposure water from the control exposure was analyzed for the presence of EE2 or  
251 TREN. Separate aliquots were analyzed for TREN and EE2. WWTP effluents were analyzed for  
252 natural and synthetic estrogens including E1, E2, E3 (estriol) and EE2. Exposure water (100 mL)  
253 or WWTP effluent samples (850-900 mL) were fortified with deuterated internal standards (E2-  
254 d<sub>3</sub> for E2; EE2-d<sub>4</sub> for EE2; E1-d<sub>4</sub> for E1), spiked with NaCl (1 or 10 g; previously baked at 500  
255 °C for 12 hrs) and then extracted with either 15 or 150 mL of methyl-tert-butyl ether (MTBE).  
256 The ether extracts were evaporated under N<sub>2</sub> and the residue mixed with the appropriate  
257 derivatizing agent. For estrogens, 25 µL of MSTFA containing ITS (1000:4 v/v) as a catalyst  
258 was used and heated at 70 °C for 30 min prior to analysis (Schultz et al., 2001). For TREN, 25  
259 µL of MSTFA containing re-sublimed I<sub>2</sub> as the catalyst was used (Marchand et al., 2000). The

260 steroid-trimethylsilyl derivatives were then quantified using a gas chromatography-mass  
261 spectrometer (GC-MS) system (Agilent 6890 GC, 5973inert MS). The analytes were separated  
262 on a DB-5 column (J&W 30m, 0.25 mm I.D., 0.25  $\mu$ m film thickness) with splitless injection at  
263 90 °C with other oven conditions as described by Stanford and Weinberg (2007). The MS was  
264 operated in electron impact mode with selective ion monitoring (SIM) made for m/z 342, 346,  
265 416, 419, 425, 429, 442, 504 and 506 that were used for E1, E1-d4, E2, E2-d3, EE2, EE2-d4,  
266 TREN, E3 and E3-d2 quantification, respectively.

267 WWTP effluents were also analyzed for the presence of selective serotonin reuptake  
268 inhibitors (SSRIs) including fluoxetine (FLX), norfluoxetine (NFLX), citalopram (CIT), and  
269 sertraline (SER). Analyses of SSRIs were conducted using GC-MS using the method described  
270 by Wille (2008) and Wille et al. (2007). In brief, 0.8 L water samples were spiked with an  
271 internal standard (IS; d5-fluoxetine) adjusted to ~ pH 12 with 2 N NaOH and then extracted once  
272 with an excess volume of MTBE. The MTBE extract was evaporated to dryness (under N<sub>2</sub>) and  
273 the residue derivatized with 50  $\mu$ L heptafluorobutyrylimidazole (HFBI) at 80 °C for 30  
274 min. Afterwards, the samples were cooled, mixed first with 400  $\mu$ L deionized water to terminate  
275 the reaction, then mixed with 600  $\mu$ L toluene, vortexed and centrifuged. The toluene layer  
276 containing the HFBI derivatives was removed, volume reduced to 125  $\mu$ L under N<sub>2</sub> and then  
277 injected onto the GC-MS. Quantification was done using selected-ion monitoring with monitored  
278 ions (m/z): 117, 344 (FLX), 117, 340 (NFLX), 122, 349 (d5-fluoxetine [IS]) 274, 501 (SER) and  
279 58 (CIT). The retention times and spectra of all analytes were determined or confirmed from  
280 authentic standards.

281

## 282 *2.6 Bile sample preparation, enzymatic hydrolysis and solid-phase extraction (SPE)*

283 This method was modified from da Silva et al. (2013). Briefly, approximately 30  $\mu$ L of  
284 bile was diluted with 200  $\mu$ L of water, followed by the addition of 30  $\mu$ L of 2.5 ng/ $\mu$ L mixture of  
285 surrogate standard (S-std) containing BPA-d16, E1-d4, E2-d4, EE2-d4 and NP-d5. Acetone (2  
286 mL) was added and the sample was kept in -20 °C for 45 min for partial protein precipitation.  
287 The sample was then centrifuged at 4,000 rpm for 10 min and supernatant was transferred to a  
288 new glass tube. The acetone was evaporated under N<sub>2</sub> flow at 35 °C and 1 mL of 1 M acetate  
289 buffer pH 5 was added containing 2,000 U of  $\beta$ -glucuronidase/sulfatase. The mixture was kept in

290 an incubator for 2 h at 40 °C to ensure complete enzymatic hydrolysis of the glucuronide and  
291 sulfate conjugated metabolites of the EDCs. Glacial acetic acid (300 µL) was added and the final  
292 hydrolyzed bile mixture was loaded on to a solid phase extraction (SPE) cartridge packed with  
293 60 mg of polymeric reversed-phase sorbent (Strata X from Phenomenex Inc, Torrance, CA,  
294 USA) that had been previously conditioned with 2 mL of methanol and 2 mL of water. The  
295 cartridge was then washed with 1.5 mL of water, followed by 1.5 mL of methanol/water (60/40,  
296 v/v), and was dried under vacuum for 30 min. The analytes were eluted with 1.5 mL of methanol  
297 into vial containing 30 µL of 2.5 ng/µL BPA-d4 solution, used as recovery standard (Rec-std).  
298 An aliquot of the final methanolic extract was diluted 10 times in methanol prior to analyses.

299

### 300 *2.7 Bile analyses by liquid chromatography/tandem mass spectrometry (LC-MS/MS)*

301 Final bile extracts were analyzed by liquid chromatography (LC, Acquity system, Waters  
302 Co., Milford, MA, USA) coupled with a triple quadrupole tandem mass spectrometer (MS/MS,  
303 QTRAP 5500, AB Sciex, Framingham, MA, USA). For each sample, 10 µL of diluted extract  
304 was injected into the LC-MS/MS. The LC was equipped with a 0.2 µm pre-filter followed by a  
305 2.1 x 5.0 mm (1.7 µm particle size) C18 guard column and a 2.1 x 150 mm (1.7 µm particle size)  
306 reversed-phase column. Water (solvent A) and methanol (solvent B) were used as the mobile-  
307 phase. The total analysis time was 26 min using a linear gradient, as follows (solvent A/solvent  
308 B): initial gradient was 60/40 at 0.2 mL/min; 14 min to 20/80 at 0.2 mL/min; 1 min to 100% B at  
309 0.2 mL/min; 0.1 min to increase the flow up to 0.35 mL/min and held for 4.9 min; 0.1 min to  
310 reduce flow to 0.30 mL/min; 0.9 min to initial gradient 60/40 at 0.3 mL/min and held for 5 min.  
311 The column temperature was maintained at 45 °C. Electrospray ionization (ESI) mode was used  
312 for the ionization of all analytes. The MS/MS was operated in negative ion mode and the  
313 analytes were detected via multiple-reaction monitoring (MRM). The ion source was kept at 700  
314 °C and the capillary voltage was -4.5 kV. Declustering potential and entrance potential were set  
315 at -60 V and -10 V, respectively. Other details on the MRM parameters are given in the Table 2.  
316 The analytes were quantified by S-std and based on the calibration curve of each analyte. The  
317 recovery of each S-std was calculated by the Rec-std.

318

### 319 *2.8 Gene expression analyses*

320 Tissues were homogenized using either a Mini Beadbeater-96 (BioSpec Products Inc,  
321 Bartlesville, OK) or a TissueLyzer II homogenizer (QIAGEN, Valencia, CA). Total pituitary  
322 RNA and total liver RNA from male fish were isolated using RNeasy Plus Mini Kit® (QIAGEN)  
323 following the manufacturer's instructions for isolation of total RNA from animal tissues. Total  
324 liver RNA was isolated from female fish using Tri-Reagent (Molecular Research Center,  
325 Cincinnati, OH) according to the manufacturer's instructions. RNA degradation was observed in  
326 some liver samples from the EE2 and TREN exposure experiment due to issues with freezer  
327 temperature. Therefore, samples from subsequent experiments were collected in RNAlater® to  
328 reduce RNA degradation. RNA samples were run on 1% agarose gels to check for RNA quality.  
329 Only samples with distinct 28S and 18S ribosomal RNA bands at an approximately 2:1 ratio  
330 were used for qPCR analysis. High quality liver RNA samples were DNase treated using  
331 Ambion® TURBO DNA-free™ (Life Technologies). Briefly, a 23 µL reaction was composed of  
332 20 µL (3000 ng) total RNA, 2 µL DNase I Buffer and 1 µL TURBO DNase and incubated at 37  
333 °C for 1 h. DNase treatment was then inactivated with 2 µL inactivation reagent and vortexed at  
334 room temperature. RNA yield was quantified with a NanoDrop ND-1000 (Thermo Fisher  
335 Scientific, Waltham, MA). DNA-free samples (125 ng pituitary RNA or 250 ng liver RNA) were  
336 reverse transcribed with SuperScriptII (Life Technologies) in 10 µL reactions as described in  
337 Kitano et al. (2010). Quantitative real-time RT PCR (qPCR) assays were designed and  
338 performed as previously described (Harding et al., 2013). Briefly, qPCR assays were run using  
339 an ABI 7900HT Fast Real-Time PCR System (Life Technologies) in 384-well plates using  
340 standard cycling conditions. Reactions were 12.5 µL each and consisted of 1X Power SYBR  
341 Green PCR Master Mix (Life Technologies), 150 nM of the forward and reverse primer, and 0.5  
342 ng cDNA template. Four concentrations of standard curve samples generated from a serial  
343 dilution of cDNA (from pooled RNA) ranging from 0.05 to 5 ng cDNA were included in each  
344 plate in triplicate. When possible, samples of a given tissue from all exposure dates were run on  
345 a single 384-well qPCR plate to eliminate plate-to-plate variation between qPCR runs. In every  
346 case, all control and treated samples from a given exposure date were analyzed on a single plate.  
347 No template controls showed no detectable amplification over 40 cycles of PCR. For *vtg* and  
348 *fshb*, no amplification controls showed no detectable amplification within 35 cycles of PCR. For  
349 *lhb*, no amplification controls showed no detectable amplification within 34 cycles of PCR, any

350 samples amplifying after Ct 34 were considered below the level of quantitation. Samples that  
351 were below the level of quantitation were assigned the lowest measurable value. Data were  
352 expressed relative to the housekeeping gene, eukaryotic elongation factor-1 a (*eef1a*). *Eef1a* was  
353 selected as the housekeeping gene because it is stably expressed in both tissues and is not  
354 significantly affected by hormone treatment in this or previous studies (Harding et al., 2013;  
355 Luckenbach et al., 2010). Pituitary and liver *eef1a* mRNA levels were not significantly different  
356 in treated animals compared to controls (Supplemental Figure 1). To improve visualization,  
357 normalized qPCR values were divided by their control mean to set the control mean value to one.  
358 qPCR primers were previously reported (Harding et al., 2013).

359

## 360 2.9 Statistical analyses

361 Statistical analyses were performed using Prism 6 for Mac OSX (GraphPad Software, La  
362 Jolla, CA). Differences in morphometric data between duplicate tanks were analyzed by 2-way  
363 ANOVA (data not shown). Because no significant differences were found ( $p > 0.05$ ); duplicate  
364 tanks were pooled in further analyses. For qPCR data, outliers were identified by Grubb's outlier  
365 test at a threshold of  $p < 0.05$  and were removed from analyses. Data were log-transformed  
366 where necessary to meet parametric test criteria. Initial analyses, using a 2-way ANOVA, found  
367 no evidence of a sex effect, therefore male and female samples were pooled for subsequent  
368 analyses. Significant differences between treatments were determined by One-way ANOVA  
369 followed by Tukey's multiple comparison test with a significance threshold of  $p < 0.05$ . Data are  
370 expressed as mean  $\pm$  SEM. Total SSRI concentrations and combined estradiol equivalent (EEQ)  
371 were calculated from water and bile analytical chemistry data using the calculations below. Total  
372 SSRI concentration was calculated by summing the individual SSRI and SSRI metabolites.

$$373 \quad \text{Total SSRI} = [\text{FLX}] + [\text{NF}] + [\text{SER}] + [\text{CIT}]$$

374 EEQ was calculated using the equation by Young et al., (2004).

$$375 \quad \text{EEQ} = (\text{E1} \times 0.3) + (\text{E2} \times 1) + (\text{EE2} \times 10)$$

376

## 377 3. Results:

### 378 3.1 Control EE2 and TREN Exposures

#### 379 3.1.1 Chemical Analyses

380 Levels of EE2 and TREN in exposure water for respective chemicals were measured in  
381 each of the duplicate exposure tanks at the start and end of the 72-hour exposure. Exposures  
382 were designed to be approximately 2 and 10 ng L<sup>-1</sup> for EE2 and 20 and 200 ng L<sup>-1</sup> for TREN.  
383 Mean EE2 exposure levels in duplicate treatment tanks were 2.89 and 2.11 ng L<sup>-1</sup> for the 2 ng L<sup>-1</sup>  
384 nominal treatment and 11.65 and 11.89 ng L<sup>-1</sup> for the 10 ng L<sup>-1</sup> nominal treatment. Mean TREN  
385 exposure levels in duplicate tanks were 27.4 and 15.0 ng L<sup>-1</sup> for the 20 ng L<sup>-1</sup> nominal  
386 concentration and 192.6 and 175.5 ng L<sup>-1</sup> for the 200 ng L<sup>-1</sup> nominal concentration. Hereafter,  
387 nominal concentrations (2 and 10 ng L<sup>-1</sup>) and TREN (20 and 200 ng L<sup>-1</sup>) will be used to indicate  
388 treatment exposure levels.

389

### 390 3.1.2 Survival and morphometric data

391 Fish fork length ( $118 \pm 1$  mm), body weight ( $20.9 \pm 0.7$  g), GSI ( $0.336 \pm 0.010$  for  
392 females and  $0.022 \pm 0.001$  for males) and HSI ( $1.151 \pm 0.049$  for females and  $1.070 \pm 0.029$  for  
393 males) were not significantly affected by EE2 or TREN exposure (Supplemental Figure 2). No  
394 mortalities were observed over the 72-hour exposure.

395

### 396 3.1.3 Tissue mRNA levels

397 In the control EE2 and TREN exposure, pituitary *lhb* mRNA levels were significantly  
398 increased 17-fold and 215-fold relative to controls in fish exposed to 2 or 10 ng EE2 L<sup>-1</sup>,  
399 respectively (Figure 1b). TREN, on the other hand, did not significantly affect pituitary *lhb*  
400 mRNA levels in exposed fish. Pituitary *fshb* mRNA levels were not significantly affected by  
401 either the EE2 or TREN exposure (Figure 1c). Liver *vtg* mRNA levels were increased 6,670-fold  
402 in fish exposed to 10 ng L<sup>-1</sup> EE2 for 72 hours (Figure 1a). However, liver *vtg* mRNA levels were  
403 not affected by exposure to 2 ng EE2 L<sup>-1</sup> or either TREN dose.

404

## 405 3.2 WWTP Effluent Exposures:

### 406 3.2.1 Chemical Analyses in Effluent

407 Samples of undiluted effluent from all sites except E were analyzed for estrogens, 3  
408 selective serotonin reuptake inhibitors (SSRIs) and one SSRI metabolite, NFLX (Tables 3 and  
409 4). WWTP E effluent was not analyzed due to acute lethality during the exposure. For the

410 estrogens, E2 was detected in every effluent that was analyzed with levels reaching up to 2.6 ng  
411 L<sup>-1</sup> in effluent from site H. Low levels of E1 were detected in two of the effluents, but were  
412 below the level of quantitation (~ 0.5 ng L<sup>-1</sup>) in both cases. E3 was not detected in any effluent  
413 that was analyzed. EE2 was detected in 2 effluents with up to 0.8 ng L<sup>-1</sup> in site G effluent. SSRIs  
414 were much more prevalent in WWTP effluent samples; all measured SSRIs were detected in  
415 100% of the effluent samples. Average concentrations of SSRIs were 18.5 ng L<sup>-1</sup>, 73.3 ng L<sup>-1</sup>,  
416 75.7 ng L<sup>-1</sup> and 504.6 ng L<sup>-1</sup> for NFLX, SER, FLX, and CIT, respectively. FLX and SER were  
417 present in WWTP effluent at similar concentrations, while CIT was, on average, an order of  
418 magnitude higher in concentration. Combined, the total SSRI load ranged from a low of 77.5 ng  
419 L<sup>-1</sup> at site H to 1672.7 ng L<sup>-1</sup> at site G.

420

### 421 3.2.2 Survival and morphometric data

422 Mean ( $\pm$  SEM) fish fork-length ( $138 \pm 1$  mm), body weight ( $30.9 \pm 0.5$  g), GSI ( $0.349 \pm$   
423  $0.019$  for females and  $0.027 \pm 0.005$  for males), and HSI ( $0.866 \pm 0.009$  for females and  $0.868 \pm$   
424  $0.023$  for males) were not significantly different between tanks, so duplicate tanks were  
425 subsequently pooled. No mortalities were observed in response to effluent from WWTP A, B, C,  
426 D, F, or G over the 72-hour exposure. However, in the 100% WWTP E effluent exposure, 92%  
427 mortality was observed in the first 24 hours. This was attributed to residual chlorine exposure.  
428 After the water change at 24 hours, new fish were added to the tanks. Of these, there was 50%  
429 mortality within 24 hours of being added to the tanks, again presumably due to residual chlorine  
430 exposure. Therefore, the remaining fish from the 100% WWTP E effluent exposure were  
431 exposed to effluent for 48 hours, rather than the 72 hours used in other tests.

432

### 433 3.2.3 Tissue mRNA levels

434 Fish exposed to effluent from sites A, B, D, E, and F had significantly higher *lhb* mRNA  
435 than their respective controls (Figure 2). Fish exposed to 20% and 100% effluent from WWTP B  
436 had 9- and 42-fold higher *lhb* mRNA levels relative to controls, respectively. Similarly, fish  
437 exposed to 20% and 100% effluent from WWTP F had 16- and 491-fold increases in *lhb* mRNA  
438 levels as compared to controls. The mean level of *lhb* induction in fish exposed to 20% and  
439 100% WWTP F are similar in magnitude to those observed in fish exposed to 2 and 10 ng EE2

440 L<sup>-1</sup> in the control exposure. Although *fshb* mRNA levels were unaffected by EE2 and TREN  
441 exposure, *fshb* mRNA levels increased in a dose-dependent manner when exposed to effluent  
442 from WWTP B (Figure 3B). In contrast, liver *vtg* mRNA levels were not significantly altered by  
443 any of the WWTP effluent exposures (Figure 4).

444

#### 445 3.2.4 Chemical analyses in bile

446 Bile samples were analyzed for natural and synthetic steroidal estrogens, and the weakly  
447 estrogenic chemical, bisphenol-A (BPA), which is a component of polycarbonate plastic and  
448 epoxy resins and commonly found in WWTP effluent and the aquatic environment (Table 5).  
449 BPA was the most commonly detected chemical in bile from fish used in this study with  
450 concentrations ranging from 44.5 ng mL<sup>-1</sup> to 3900 ng mL<sup>-1</sup>. Natural steroidal estrogens, E1 and  
451 E2, were also frequently detected in bile samples from effluent exposed animals, but were not  
452 detected in any of the control bile samples. Mean E1 and E2 levels were as high as 71.7 and 50.7  
453 ng mL<sup>-1</sup>, respectively, in bile from WWTP F. EE2 was detected in bile from fish exposed to  
454 effluent from WWTP sites C, D, and F, with concentrations of > 10 ng mL<sup>-1</sup> in bile from fish  
455 exposed to WWTP C and F effluents. Considering steroidal estrogens (reported as EEQ) and  
456 BPA together, bile from fish exposed to WWTP H effluent showed the least amount of  
457 estrogenic chemicals. In contrast, bile from fish exposed to WWTP F effluent showed the highest  
458 occurrence and highest concentrations of estrogenic chemicals, including E1, E2, E3, and BPA.  
459 Bile from fish exposed to WWTP B effluent had the highest levels and highest occurrence of  
460 EE2.

461

#### 462 4. Discussion:

463 In this study, juvenile coho salmon, a native species in Puget Sound, were exposed to  
464 eight different WWTP effluents from the Puget Sound region and effects on pituitary *fshb* and  
465 *lhb*, and hepatic *vtg* mRNAs were evaluated. The advantage of using juvenile salmon is that both  
466 sexes are prepubertal, have low endogenous steroid levels (Campbell et al., 2006; Patiño and  
467 Schreck, 1986; Sower et al., 1992), and low or non-detectable expression of both *lhb* and *vtg*.  
468 However, both of these gene transcripts can be increased with exogenous estrogens in juvenile  
469 males and females (Crim et al., 1981; Thorpe et al., 2000). We found that acute (72-hour)



470 exposure of juvenile salmon to effluents from five WWTPs increased expression of pituitary *lhb*,  
471 but none of the effluents altered hepatic *vtg* expression and only one increased *fshb*. Fish exposed  
472 to effluents that induced the highest *lhb* levels also had the highest levels of estrogenic chemicals  
473 in bile. Acute exposures of juvenile coho salmon to low concentrations of EE2, a synthetic  
474 estrogen commonly found in WWTP effluent, indicated that pituitary *lhb* transcripts increased at  
475 lower exposure concentrations of EE2 than hepatic *vtg*, while exposure to an androgen, TREN,  
476 had no effect on any of the measured mRNAs. To our knowledge this is the first time that altered  
477 *lhb* mRNA levels have been reported in fish exposed to WWTP effluent. Further, our results  
478 suggest that *lhb* gene expression may be a sensitive indicator of acute exposure to estrogenic  
479 chemicals in juvenile coho salmon.

480

#### 481 *4.1 EE2 and TREN exposure*

482 In the current study, a controlled 72-hour exposure experiment demonstrated that  
483 pituitary *fshb* mRNA levels were not significantly altered in juvenile coho salmon exposed to  
484 EE2 or TREN. Previous studies examining the effects of sex steroids on Fsh regulation have  
485 shown that E2 suppresses *fshb* mRNA levels, pituitary Fsh content and plasma Fsh levels  
486 (Breton et al., 1997; Dickey and Swanson, 1998; Kobayashi et al., 2000; Saligaut et al., 1998).  
487 Further, female rainbow trout exposed to the estrogenic contaminant, 4-nonylphenol (NP), for 18  
488 weeks had significantly decreased pituitary *fshb* mRNA levels, pituitary Fsh content and plasma  
489 Fsh levels (Harris et al., 2001). Harris and colleagues found that plasma Fsh and pituitary *fshb*  
490 mRNA levels were the most sensitive endpoint assessed, being downregulated at the lowest NP  
491 concentrations tested. However, in coho salmon exposed to 12 ng EE2 L<sup>-1</sup>, significant declines in  
492 *fshb* mRNA levels were observed at 6 weeks, but not after 1 week (Harding et al., 2013). These  
493 results suggest that while *fshb* mRNA levels may be suppressed by exposure to estrogenic  
494 chemicals, longer duration exposures may be necessary to observe significant decreases in *fshb*  
495 mRNA levels.

496 In the EE2 and TREN exposure experiment, levels of pituitary *lhb* mRNA were  
497 significantly induced by 2 and 10 ng L<sup>-1</sup> EE2 exposure compared to control and TREN-exposed  
498 fish. In agreement with these results, immature coho salmon exposed to 12 ng EE2 L<sup>-1</sup> for 1 or 6  
499 weeks increased *lhb* mRNA levels 241- and 395-fold, respectively, relative to controls (Harding

500 et al., 2013). Fathead minnow (*Pimephales promelas*) embryos exposed to 2, 10, or 50 ng EE2 L<sup>-1</sup>  
501 from fertilization until swim up (~7 days) had significantly elevated *lhb* mRNA levels (Johns et  
502 al., 2009). In other studies, weak estrogens increased *lhb* mRNA in exposed fish (Johns et al.,  
503 2009; Maeng et al., 2005; Rhee et al., 2010; Yadetie and Male, 2002). These data suggest that  
504 *lhb* mRNA levels are increased in immature fish in response to exogenous estrogens even at  
505 environmentally relevant concentrations.

506 While *lhb* mRNA levels were significantly increased in response to EE2 exposure, *lhb*  
507 mRNA levels were not altered by exposure to TREN, a nonaromatizable androgen. This is in  
508 agreement with previous studies that showed no change in *lhb* mRNA levels or pituitary Lh  
509 content in fish treated with nonaromatizable androgens (Aroua et al., 2007; Cavaco et al., 2001;  
510 Kobayashi et al., 2000). In salmonids, treatment with nonaromatizable androgens has been  
511 shown to cause small increases in *lhb* mRNA or Lh protein levels *in vivo*, but to a much lesser  
512 extent than E2 or testosterone (Antonopoulou et al., 1999; Borg et al., 1998; Crim et al., 1981;  
513 Melo et al., 2015). Additionally, in castrated Atlantic salmon (*Salmo salar*) parr, testosterone  
514 treatment dramatically increased pituitary Lh content and this effect was significantly attenuated  
515 by treatment with testosterone combined with an aromatase inhibitor (Antonopoulou et al.,  
516 1999). Therefore, our results and the results of previous studies suggest that positive regulation  
517 of *lhb* by androgens is aromatase dependent and nonaromatizable androgens have little, if any  
518 effect on *lhb* induction in salmonids.

519 In contrast to the *lhb* response, only the high concentration of EE2 resulted in elevated  
520 *vtg* expression in the liver. Previous work in juvenile brown trout (*Salmo trutta*), showed that  
521 hepatic *vtg* mRNA levels are significantly induced 24 hours after a 6-hour 320 ng E2 L<sup>-1</sup>  
522 exposure (Knudsen et al., 2011). These results indicate that *vtg* mRNA levels can be rapidly  
523 induced in juvenile salmonids in response to high levels of E2. In immature rainbow trout,  
524 exposure to levels as low as 1.0 ng EE2 L<sup>-1</sup> or 14 ng E2 L<sup>-1</sup> elevated *vtg* after 14 days (Thomas-  
525 Jones et al., 2003). Additionally the hepatic *vtg* mRNA levels were induced in immature rainbow  
526 trout exposed to 9.7 ng E2 L<sup>-1</sup> after 4 days, but not after 2 days (Thomas-Jones et al., 2003).  
527 These results suggest that hepatic *vtg* can also be induced in response to low estrogens, but in a  
528 time-dependent manner. Indeed, hepatic *vtg* mRNA levels increased for up to 2 weeks in male  
529 rainbow trout injected once with E2 (Pakdel et al., 1991). Unfortunately, in salmonids there is

530 little information on Vtg protein or mRNA induction in response to both short term (< 14 days)  
531 and low dose (< 5 ng L<sup>-1</sup>) EE2 exposure experiments, raising the possibility that 72-hour  
532 exposure duration is too short to observe *vtg* induction at low exposure levels. In fathead  
533 minnow, lowest-observed-effect concentrations (LOEC) of 2.2 and 5 ng EE2 L<sup>-1</sup> have been  
534 reported for *vtg* mRNA induction at 48 hours (Biales et al., 2007; Flick et al., 2014; Reddy et al.,  
535 2015). Similarly, in fathead minnow embryo and larvae exposed to 0, 18, or 1800 ng L<sup>-1</sup> E1, *vtg*  
536 mRNA levels were significantly induced at 6 days, but not at 3 days of exposure although the  
537 other estrogen responsive genes (estrogen receptor  $\alpha$  and cytochrome P450-aromatase-B) were  
538 already significantly induced at 3 days (Cavallin et al., 2015). Cavallin and colleagues suggested  
539 that the delayed induction of *vtg* may reflect the time required to upregulate a functional estrogen  
540 receptor in the liver. These data suggest that the 3-day exposure used in the current study may be  
541 insufficient to observe *vtg* induction in juvenile coho salmon in response to low concentrations of  
542 estrogens in exposure water.

543

#### 544 4.2 WWTP effluent exposures

545 In the current study, effluents collected from WWTPs in South Puget Sound were  
546 analyzed for the presence of steroidal estrogens and SSRIs. Due to the method of effluent  
547 sampling (grab samples rather than time-weighted sampling), it is not possible to draw firm  
548 conclusions about the effect of alternate wastewater treatment technologies on the removal of  
549 steroids or pharmaceuticals from WWTP effluents. However, steroidal estrogen and SSRI levels  
550 are still useful for understanding the biological responses of exposed animals. In addition, all  
551 sample collections occurred at the same time of day, and within a narrow seasonal time frame  
552 limiting time-dependent differences between WWTP effluent collections. Additionally, previous  
553 studies have shown that trickling filter WWTPs or trickling filters with activated sludge  
554 treatment have lower removal efficiencies of pharmaceuticals and personal care products  
555 including steroidal estrogens than tertiary treatment processes (Bartelt-Hunt et al., 2009; Janex-  
556 Habibi et al., 2009; Kasprzyk-Hordern et al., 2009). Measured concentrations of steroidal  
557 estrogens were in the low ng L<sup>-1</sup> range (<3 ng L<sup>-1</sup>) for all WWTP effluents at the beginning of the  
558 semi-static exposure and may have decreased over time due to degradation. Of the steroidal  
559 estrogens, E2 was the most prevalent and was detected in every effluent. E2 was also found in

560 the highest concentration (2.6 ng L<sup>-1</sup>) of any of the measured steroidal estrogens. In general, the  
561 levels of steroidal estrogens in effluent observed in this study are low compared to previous  
562 studies. For example, analyses of two WWTP effluents from Puget Sound identified estrone  
563 concentrations of 4.5 to 58 ng L<sup>-1</sup> (Meador et al., 2016). Elsewhere in North America, natural  
564 estrogens have been measured in wastewater effluents with concentrations ranging from 6-14  
565 (E1), <5 (E2) and <10-33 ng L<sup>-1</sup> (E3) (Huang and Sedlak, 2001; Lee and Peart, 1998; Snyder et  
566 al., 1999). Reported EE2 concentrations in WWTP effluents can vary widely, but also typically  
567 fall in the low ng L<sup>-1</sup> range (Young et al., 2004). In the United States, WWTP effluents had EE2  
568 concentrations ranging from <0.05-2.42 ng L<sup>-1</sup> (Huang and Sedlak, 2001; Snyder et al., 1999),  
569 however EE2 has been measured in streams at levels up to 273 ng L<sup>-1</sup>, with median measured  
570 concentrations below 10 ng L<sup>-1</sup> (Kolpin et al., 2002). Similarly, in Canadian WWTP effluents,  
571 EE2 concentrations reached 42 ng L<sup>-1</sup>, with median concentration of 9 ng L<sup>-1</sup> (Ternes et al.,  
572 1999).

573 We also measured a variety of SSRIs in the effluents due to their high occurrence in  
574 WWTP effluents (Hedgespeth et al., 2012; Meador et al., 2016; Verlicchi et al., 2012) due to  
575 incomplete removal during wastewater treatment (Lubliner et al., 2010). In addition, SSRIs  
576 bioaccumulate in tissues of fish exposed to WWTP effluent (Lajeunesse et al., 2011; Schultz et  
577 al., 2010) and are capable of altering Gth mRNA levels in fish. For example, a 2-week exposure  
578 of male zebrafish to CIT, decreased mRNA levels of GnRH 3 (*gnrhr3*), *fshb*, and *lhb* (Prasad et  
579 al., 2015). These data suggest that SSRIs could accumulate in fish brain tissues and potentially  
580 alter the brain-pituitary axis, including Gth mRNA expression.

581 In the present study, all of the SSRIs measured were detected in WWTP effluents  
582 typically in the 10 to 100 ng L<sup>-1</sup> range. These levels are consistent with concentrations of SSRIs  
583 previously measured in WWTP effluents from Puget Sound and are in the 95<sup>th</sup> to 99<sup>th</sup> percentile  
584 relative to what is seen elsewhere in the United States (Meador et al., 2016). CIT was present at  
585 the highest concentration in effluent from all WWTP effluents, except WWTP H. This is in  
586 agreement with a previous study that found measured CIT concentrations were, on average, an  
587 order of magnitude greater than SER or FLX in two effluent impacted streams (Schultz et al.,  
588 2010). The total SSRI concentrations were lowest in effluent from WWTP H (77.5 ng L<sup>-1</sup>),  
589 intermediate (480 – 770 ng L<sup>-1</sup>) for WWTP A, B, C, D, and F effluents, and highest in WWTP G

590 effluent (1672.7 ng L<sup>-1</sup>). There was no clear relationship between CIT or total SSRI  
591 concentrations in the effluents and any of the biological measurements. This may reflect varying  
592 kinetics of accumulation or bioconcentration for different SSRIs. Previous work suggests that  
593 particular SSRIs are selectively taken up in fish tissues. The main SSRIs measured in white  
594 sucker (*Catostomus commersonii*) brain tissues were FLX, SER and their metabolites (NFLX  
595 and N-desmethylsertraline), despite higher environmental levels of CIT (Schultz et al., 2010).  
596 Additionally, previously reported effects of SSRIs on Gth mRNA levels in fish were observed  
597 after 2 weeks of exposure (Prasad et al. 2015) whereas in the current study juvenile coho were  
598 only exposed to SSRIs via WWTP effluent for 3 days. Therefore, a longer exposure period may  
599 be required to observe effects of SSRIs on Gth expression.

600 In the WWTP effluent exposures, *lhb* mRNA levels were significantly elevated in fish  
601 exposed to 100% effluent from five of the eight WWTPs. Fish exposed to effluent from WWTP  
602 F, had the highest *lhb* induction. While in most cases, fish would not be expected to be exposed  
603 to 100% effluent, the acute dilution factor for several of the WWTPs is between 2 and 4 resulting  
604 in effluent concentrations of 25 to 50% (Table 1). In addition, it is expected that fish may be  
605 exposed for much longer than 72 hours resulting in increased *lhb* induction over time.

606 The primary known factor stimulating *lhb* transcription in fish is E2 (Yaron et al., 2003).  
607 Based on the estrogenic nature of most WWTP effluents, it is tempting to speculate that the  
608 increased *lhb* mRNA levels observed in effluent exposed fish are due to estrogenic activity of  
609 those effluents. However, we were unable to demonstrate relationships between effluent steroid  
610 concentrations and *lhb* mRNA levels because of limited ability to measure steroidal estrogens in  
611 effluent samples using the methods we employed. It is possible that additional estrogenic  
612 chemicals are present in the effluents that were not measured. Additionally, the possibility that  
613 other non-estrogenic chemicals are able to induce *lhb* mRNA levels cannot be ruled out.

614 To further investigate the hypothesis that *lhb* mRNA levels are increased in effluent  
615 exposed fish due to exogenous estrogens, we measured steroidal estrogens in bile of fish exposed  
616 to wastewater effluents where possible. Analysis of bile fluid can provide an indication of the  
617 internal exposure level to estrogenic chemicals including steroidal estrogens, NP, and BPA  
618 (Larsson et al., 1999; Pettersson et al., 2006; Vermeirssen et al., 2005). Additionally, due to the  
619 accumulation of some estrogenic chemicals, bile analysis can be used to measure estrogenic

620 chemicals that are below the limit of detection in WWTP effluent (Gibson et al., 2005). In fish  
621 exposed to WWTP effluent, the highest steroid hormone levels were detected in effluent B and  
622 effluent F with 161 and 187 ng L<sup>-1</sup> EEQ respectively (see Table 5). These EEQ levels were, in  
623 large part, due to relatively high (>10 ng mL<sup>-1</sup>) bile concentrations of EE2. Interestingly, these  
624 results correspond well with the *lhb* induction we observed in fish exposed to effluents from  
625 WWTP B and F. Additionally, bile EEQ concentrations were highest in WWTP F, a trickling  
626 filter treatment plant which is known to be less efficient in removing pharmaceuticals including  
627 steroidal estrogens (Bartelt-Hunt et al., 2009; Kasprzyk-Hordern et al., 2009). These data support  
628 the hypothesis that induction of *lhb* expression in effluent-exposed juvenile coho is due to  
629 exposure to estrogenic chemicals in WWTP effluent.

630 Consistent with the lack of change observed in the control EE2 exposure, *fshb* mRNA  
631 levels were generally unaffected in fish exposed to WWTP effluent. However, *fshb* mRNA  
632 levels were significantly increased following exposure to WWTP B effluent. As mentioned  
633 above, E2 and estrogen mimics such as NP tend to suppress *fshb* expression or Fsh protein via  
634 negative feedback, but these effects generally occur after long-term exposure or treatment with  
635 estrogens. Given the exposure used was only 3 days, it is possible that the lack of negative effect  
636 on *fshb* was due to duration of exposure. The factors in WWTP B effluent that caused an  
637 increase in steady state levels in *fshb* are unknown, but could act by either antagonizing factors  
638 that reduce *fshb* levels, or stimulating those that increase *fshb* levels such as, gonadotropin-  
639 releasing hormone (GnRH) and kisspeptin from the brain and activin from the ovary (Levavi-  
640 Sivan et al., 2010; Yaron et al., 2003). Since Fsh plays a key role in regulating early stages of  
641 gametogenesis (Levavi-Sivan et al., 2010; Swanson et al., 2003), prolonged disruption of *fshb*  
642 production might impact plasma Fsh levels and ultimately alter age or seasonal timing of gonad  
643 growth, fecundity and gamete quality. Further research is needed to determine what chemicals  
644 present in WWTP effluents may elevate *fshb* levels, and whether prolonged exposure results in  
645 downstream effects on plasma Fsh and gametogenesis.

646 In the current study, liver *vtg* mRNA levels were not significantly elevated in fish  
647 exposed to effluents from any of the WWTPs tested. This is consistent with the lack of *vtg*  
648 induction observed in the low EE2 exposure in our control EE2 and TREN exposure. However,  
649 this is in contrast to previous studies that have shown *vtg* induction in fish exposed to WWTP or

650 in wild fish sampled downstream of WWTPs (Barber et al., 2007, 2011; Folmar et al., 2001,  
651 1996; Harries et al., 1999, 1997; Ings et al., 2011). These results suggest that the effluents tested  
652 had low estrogenic activity that was insufficient to stimulate *vtg* mRNA levels within the 72-hr  
653 period of exposure. Indeed, the steroidal estrogen levels measured in effluents in the current  
654 study are lower, on average, than previously reported levels (Huang and Sedlak, 2001; Lee and  
655 Peart, 1998; Snyder et al., 1999; Ternes et al., 1999). Further, the current experiment was shorter  
656 in duration than previous studies showing *vtg* mRNA induction in response to WWTP effluent  
657 exposure (14-28 days; Barber et al., 2007, 2011; Folmar et al., 2001, 1996; Harries et al., 1999,  
658 1997; Ings et al., 2011). Therefore, longer exposure duration may be necessary to induce *vtg*  
659 mRNA levels in response to estrogenic WWTP effluent. Because of the static renewal system we  
660 used and our limited ability to store large volumes of chilled WWTP effluent required for  
661 exposures, it was not possible to increase the duration of exposure in the current study.

662

## 663 **5. Conclusion:**

664 Pituitary *lhb* mRNA levels were significantly increased in juvenile coho salmon during  
665 an acute (72-hour) low EE2 (2 ng L<sup>-1</sup>) exposure. Similarly, *lhb* mRNA levels were induced 42-  
666 fold and 491-fold respectively above control in immature coho salmon exposed to 100% effluent  
667 from WWTP B and F for 72 hrs, Interestingly, fish exposed to 100% effluent from WWTP B and  
668 F also had the highest EEQ levels in their bile. These results suggest that *lhb* mRNA induction is  
669 a sensitive indicator of exposure to EDCs with estrogenic activity in juvenile coho salmon.  
670 However, due to the complex mixture of WWTP effluent, it is possible that other chemicals  
671 (other steroid hormones, pharmaceuticals, industrial compounds) may be contributing to the  
672 induction of *lhb* mRNA levels. In contrast, hepatic *vtg* transcripts were not significantly altered  
673 in response to 72-hour exposure to 2 ng EE2 L<sup>-1</sup> or any of the WWTP effluents tested. As a  
674 result, further work on the kinetics and specificity of the pituitary *lhb* response compared to  
675 hepatic *vtg* in this species and life history stage is needed. The results of this study emphasize the  
676 importance of measuring multiple biological endpoints to detect endocrine disruption, and raise  
677 the possibility that one mechanism whereby WWTP effluents may alter reproductive function in  
678 fish is via disrupted gonadotropin synthesis. Further work is needed to determine whether or to  
679 what extent altered Gth expression may affect reproductive function in EDC-exposed fish.

680

681 **Conflict of Interest:**

682 No competing financial interest is declared.

683

684 **Author contributions:**

685 LBH contributed to the design of the study, performed sampling of fish after the exposure,  
686 conducted RNA isolations and gene expression analyses, performed all statistical analyses of  
687 data, wrote the manuscript and generated all figures. IRS conducted the waterborne exposures  
688 and water chemical analyses, advised on the experimental design and set-up, wrote methods  
689 sections associated with the exposure chemical analyses, and provided valuable comments to the  
690 other sections of the manuscript. DAMS conducted the bile chemical analyses and wrote  
691 methods sections associated with the bile chemical analyses. DAMS and GMY assisted with data  
692 interpretation and manuscript revision. DR contributed to the design of the study, WWTP  
693 selection, and effluent collection. SIH and SB assisted with RNA isolations and manuscript  
694 preparation. BVP provided assistance with manuscript preparation and revisions. PS contributed  
695 to the study design, assisted with sampling of fish and data interpretation, and assisted LBH in  
696 writing and editing the manuscript. All co-authors have contributed to reviewing the manuscript  
697 and have approved the final submitted manuscript.

698

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709



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1013

1014

1015 Table 1. Types of waste water treatment processes at each collection site. Effluent was collected  
 1016 after the final filtration step at all WWTPs.

WWTP Site	Site Treatment Type	Waterbody Type	Acute Mixing Zone <sup>a</sup>	Chronic Mixing Zone <sup>a</sup>	Acute Dilution Factor <sup>b</sup>	Chronic Dilution Factor <sup>b</sup>
A	Activated sludge with ultraviolet (UV) disinfection	Marine	30 ft plus horizontal length of diffuser downstream, 10 ft upstream, 25% of river width	300 ft plus horizontal length of diffuser downstream, 100 ft upstream, 25% of river width	1.9	13.6
B	Oxidation ditch with chlorine disinfection	Fresh	10 ft. upstream, 30 ft. downstream, 26.75 ft width	100 ft. upstream, 300 ft. downstream, 26.75 ft width	2.62	11.35
C	Secondary sequencing batch reactor with UV disinfection	Marine	30 ft downstream	300 ft downstream, 17.7 ft from left bank.	3.9	19.7
D	Activated sludge with biological (Bardenpho process) nutrient removal and UV disinfection	Marine	21.4 ft from the ends of the diffuser and 21.5 feet from the centerline of the diffuser pipe	213.5 ft from the last discharge point at both ends of the diffuser section and 215 feet from the centerline of the diffuser section	22	22
E	Reclaimed water (Class A Reuse) from Collection Site D	No discharge to surface waters	NA	NA	NA	NA
F	Trickling filter with chlorine disinfection	Marine	27 ft x 67 ft	271 ft x 670 ft	53	88
G	STEP collection followed by secondary treatment (SBRs), and coagulation and flocculation with filtration to meet Class A reclaimed water requirements and chlorine disinfection	Fresh	19.7 feet wide, extends 30.15 feet downstream and 10.0 feet upstream.	19.7 feet wide, extends 301.5 feet downstream and 100.0 feet upstream	6.5	20
H	Activated sludge with membrane filtration and chlorine disinfection	No discharge to surface waters	NA	NA	NA	NA

1017 <sup>a</sup>Acute and chronic mixing zones: the area near the outfall where water quality standards for acute and chronic  
 1018 aquatic life criteria may exceed standards as authorized in a national pollutant discharge elimination system  
 1019 (NPDES) permit (McGowan, 2015).

1020 <sup>b</sup>Acute and chronic dilution factors: the lowest dilution achieved at the edge of the acute and chronic mixing zones  
 1021 (McGowan, 2015).



1022 Table 2: Individual multiple-reaction  
 1023 monitoring (MRM) parameters of target  
 1024 EDCs and deuterated standards

EDCs	ions (m/z)		CE (V)	CXP (V)
	Precursor	Product <sup>a</sup>		
E3	287.04	171.0	-50	-13
		(145.1)	-52	-9
BPA	226.91	212.1	-24	-7
		(133.1)	-34	-7
E1	269.16	144.9	-50	-5
		(142.8)	-64	-11
E2	271.06	145.1	-50	-7
		(182.9)	-54	-7
EE2	295.08	144.9	-54	-7
		(143.0)	-62	-11
OP	205.05	105.9	-26	-17
		(177.0)	-26	-13
NP	219.10	105.9	-28	-3
		(82.8)	-22	-13
BPA-d16	242.06	142.2	-36	-9
		(224.1)	-26	-9
BPA-d4	231.04	216.0	-24	-9
		(135.0)	-40	-15
E1-d4	273.04	147.1	-52	-7
		(145.1)	-68	-7
E2-d4	274.90	147.0	-54	-7
		(187.1)	-56	-7
EE2-d4	299.08	147.1	-48	-7
		(145.1)	-72	-7
NP-d5	224.10	110.6	-28	-9
		(110.0)	-28	-5

1025  
 1026 <sup>a</sup> Product ions in parenthesis were used for helping  
 1027 identifying the analytes only. CE = collision  
 1028 energy; CXP = collision cell exit potential.

1029  
 1030

1031 Table 3: Steroid levels (E1 = estrone, E2 = 17 $\beta$ -estradiol, E3 = estriol, EE2 = 17 $\alpha$ -  
 1032 ethynylestradiol) in 100% WWTP effluent measured by GC-MS. NA = not assayed, nd = not  
 1033 detected, trace = detected, but below quantifiable detection by GC-MS.  
 1034

WWTP	Sample volume (L)	E1 (ng L <sup>-1</sup> )	E2 (ng L <sup>-1</sup> )	E3 (ng L <sup>-1</sup> )	EE2 (ng L <sup>-1</sup> )
A	0.863	trace	0.65	ND	ND
B	0.845	ND	1.89	ND	ND
C	0.854	ND	trace	ND	ND
D	0.885	ND	0.92	ND	ND
E	NA	NA	NA	NA	NA
F	0.872	ND	trace	ND	trace
G	0.844	ND	0.95	ND	0.83
H	0.836	trace	2.60	ND	ND

1035  
 1036  
 1037

1038 Table 4: Selective serotonin reuptake inhibitor (SSRI) levels in undiluted WWTP effluent  
 1039 measured by GC-MS. (FLX = fluoxetine, NF = norfluoxetine, SER = sertraline, CIT =  
 1040 citalopram, ND = not detected, NA = not assayed).

<b>WWTP</b>	<b>Sample volume (L)</b>	<b>FLX (ng L<sup>-1</sup>)</b>	<b>NF (ng L<sup>-1</sup>)</b>	<b>SER (ng L<sup>-1</sup>)</b>	<b>CIT (ng L<sup>-1</sup>)</b>	<b>Total SSRIs (ng L<sup>-1</sup>)</b>
A	0.804	37.9	4.7	44.8	467.0	554.5
B	0.861	26.5	4.1	43.1	408.3	482.1
C	0.86	51.6	7.7	52.9	389.1	501.3
D	0.857	91.1	5.9	71.6	600.6	769.2
E	NA	NA	NA	NA	NA	NA
F	0.843	67.2	56.4	186.5	336.6	646.8
G	0.822	209.0	47.1	87.6	1328.9	1672.7
H	0.837	46.3	3.5	26.2	1.5	77.5

1041

Table 5: Mean detected concentration (ng mL<sup>-1</sup>) and percent of samples above the limit of detection for steroidal estrogens [estrone (E1), 17β-estradiol (E2), estriol (E3), and 17α-ethynylestradiol (EE2)] and bisphenol A (BPA) in bile from control and WWTP effluent-exposed juvenile fish (mixed sex) as measured by LC-MS/MS. (ND = not detected, NA = not assayed).

<b>Treatment</b>	<i>N</i>	<b>BPA</b> ng mL <sup>-1</sup>	<b>% BPA</b>	<b>E1</b> ng mL <sup>-1</sup>	<b>% E1</b>	<b>E2</b> ng mL <sup>-1</sup>	<b>% E2</b>	<b>E3</b> ng mL <sup>-1</sup>	<b>% E3</b>	<b>EE2</b> ng mL <sup>-1</sup>	<b>% EE2</b>	<b>EEQ</b>
Composite control	9	76.5	22	ND	0	0	0	ND	0	ND	0	0
A	6	114	100	8.3	100	5.5	67	ND	0	ND	0	8.0
B	7	152	100	5.2	71	6.1	71	ND	0	15.3	86	161
C	3	1120	100	2.3	33	2.0	33	1.6	33	2.9	33	31.7
D	2	2050	100	ND	0	ND	0	ND	0	ND	0	0
E*	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
F	3	3900	100	71.7	100	50.7	100	44.0	100	11.5	67	187
G*	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
H	3	44.5	33	ND	0	ND	0	ND	0	ND	0	0

\* Not analyzed because bile was not collected or bile volume was not adequate.

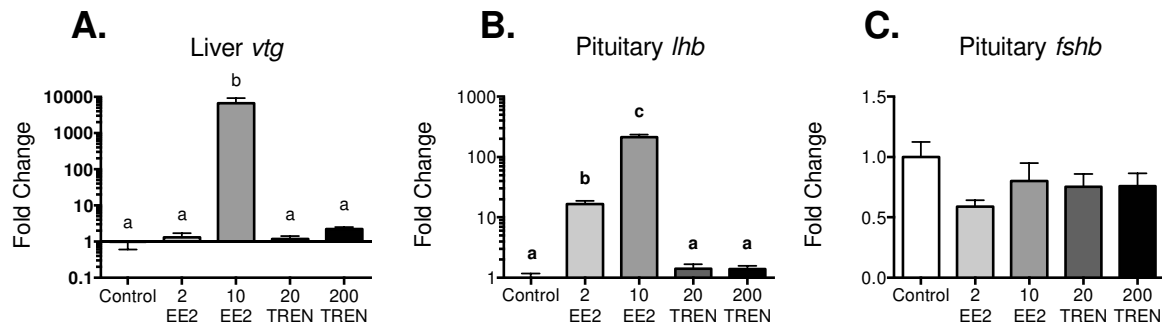


Figure 1. Relative levels of mRNAs for liver *vtg*, pituitary *lhb*, and pituitary *fshb* in juvenile coho salmon exposed to water containing 0, 2, or 10 ng L<sup>-1</sup> EE2 or 20 or 200 ng L<sup>-1</sup> TREN for 72 hrs. qPCR data were normalized to *ef1a* levels and then divided by control mean mRNA level for improved visualization of relative expression. The data are expressed as the mean  $\pm$  SEM ( $n = 5-8$  for liver, 19-20 for pituitary). Data were log transformed when necessary to conform to normality and were analyzed by one-way ANOVA followed by Tukey's multiple comparison test. Different letters indicate significant differences between treatments.

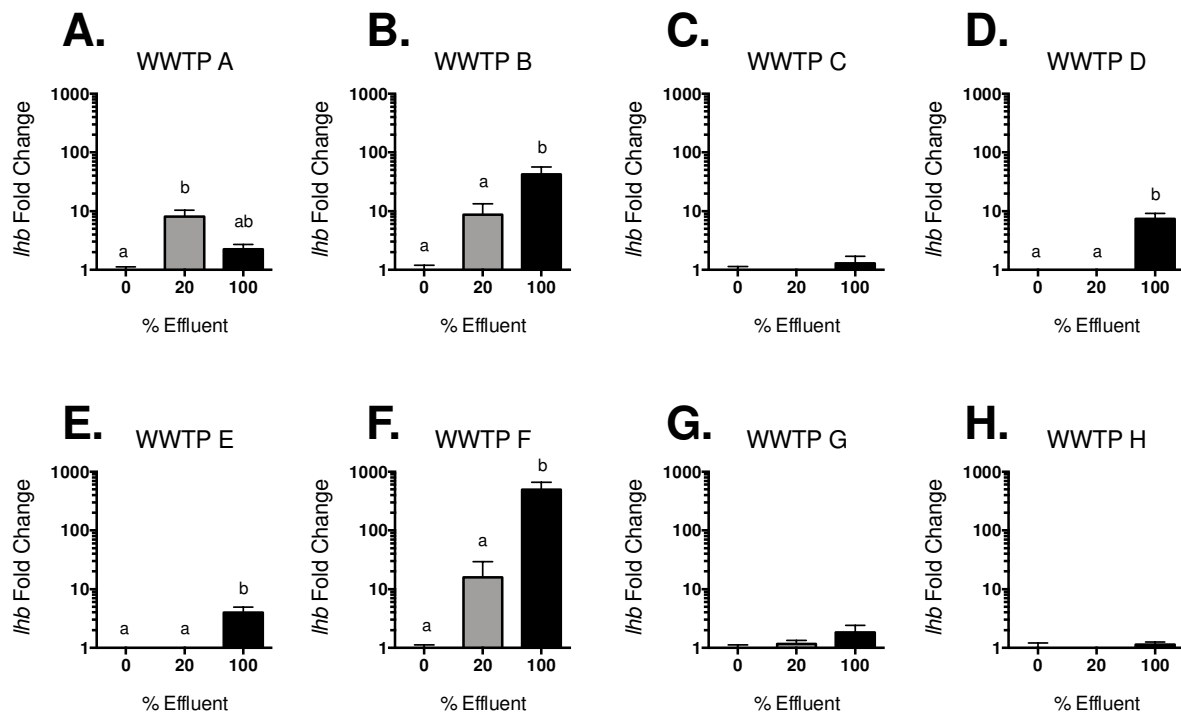


Figure 2. Relative levels of pituitary luteinizing hormone beta subunit (*lhb*) in juvenile coho salmon exposed to WWTP effluent for 72 hrs. The qPCR data were normalized to *eef1a* levels and then divided by the control mean mRNA level for improved visualization of relative expression. The data are expressed as the mean  $\pm$  SEM ( $n = 6-12$ ). Data were log transformed to conform to normality and were analyzed by one-way ANOVA followed by Tukey's multiple comparison test. Different letters indicate significant differences between treatments ( $p < 0.05$ ).

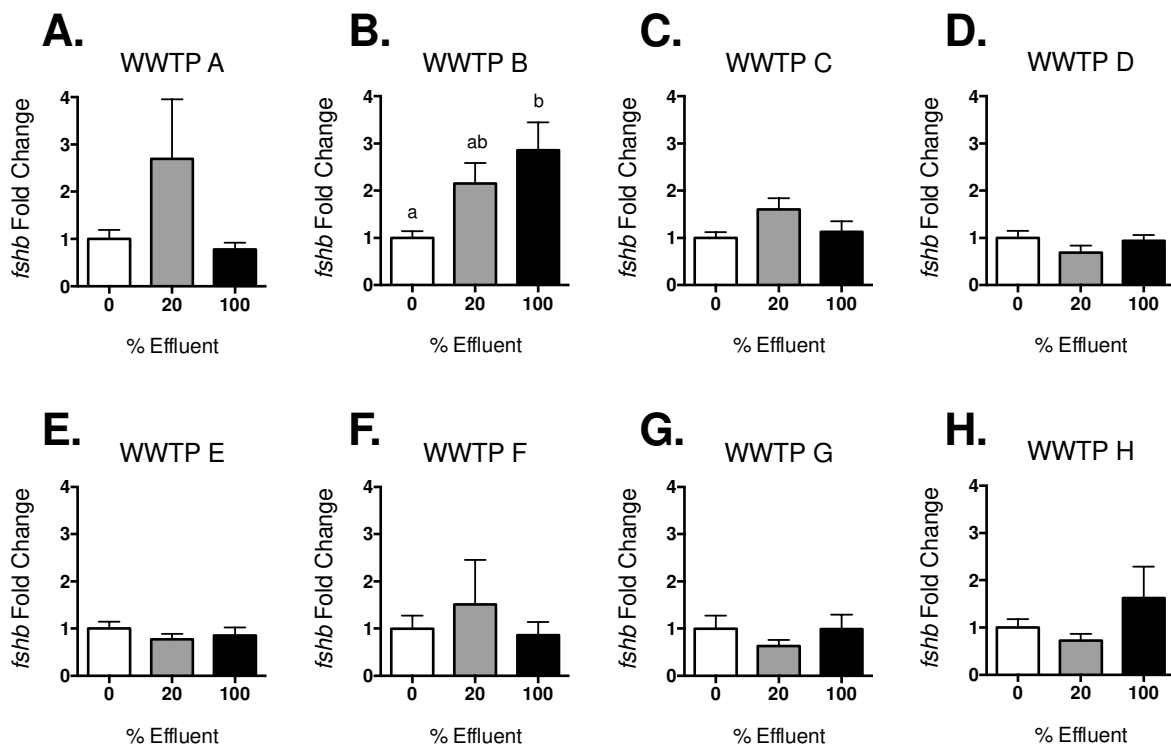


Figure 3. Relative levels of pituitary follicle stimulating hormone beta subunit (*fshb*) mRNA in juvenile coho salmon exposed to WWTP effluent for 72 hrs. qPCR data were normalized to *eef1a* levels and then divided by control mean mRNA level for improved visualization of relative expression. The data are expressed as the mean  $\pm$  SEM ( $n = 6-12$ ). Data were log transformed when necessary to conform to normality and were analyzed by one-way ANOVA followed by Tukey's multiple comparison test. Different letters indicate significant differences between treatments ( $p < 0.05$ ).

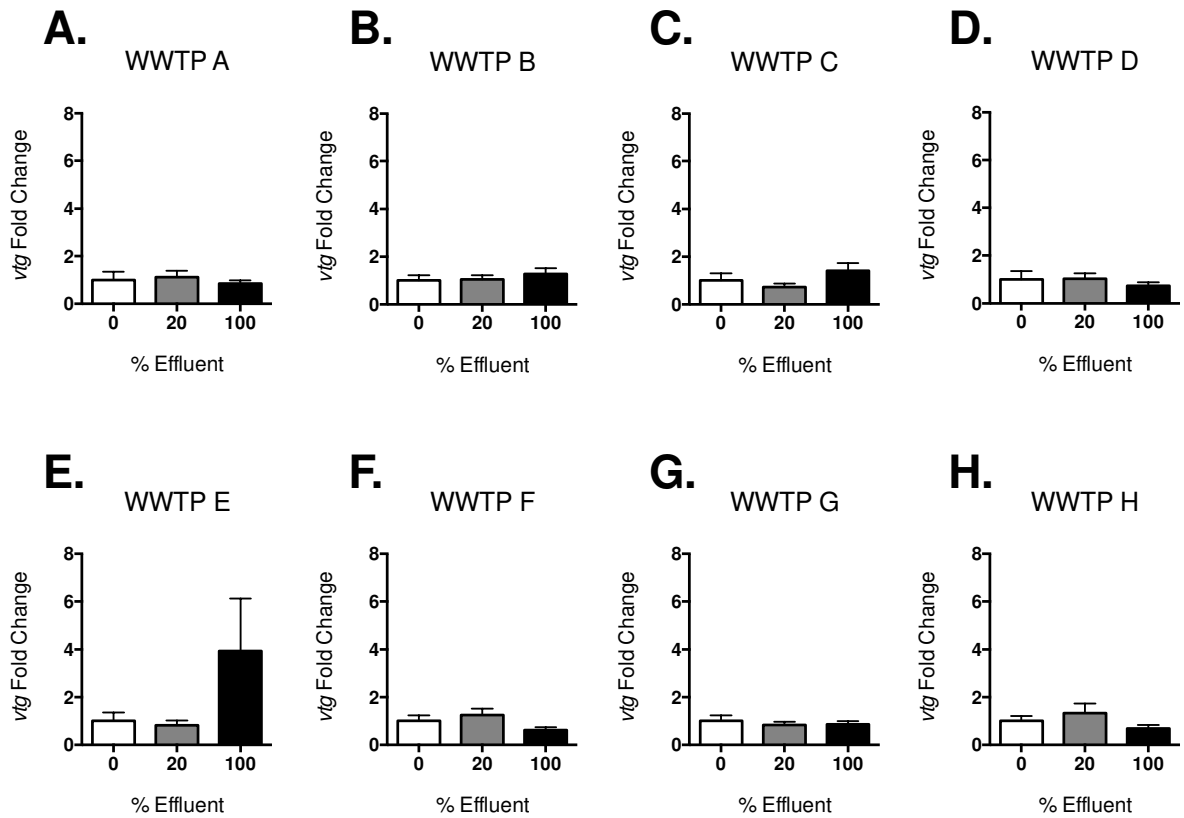
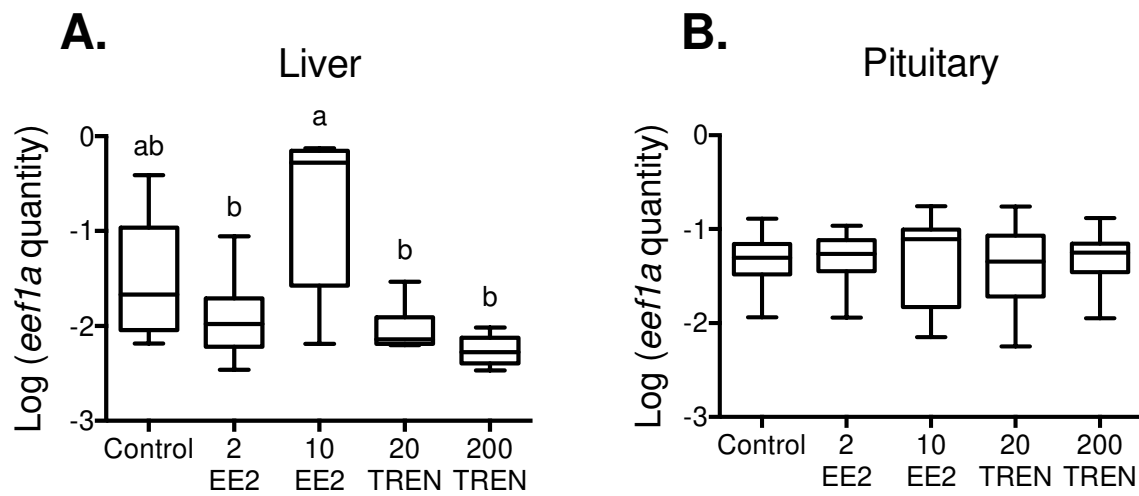
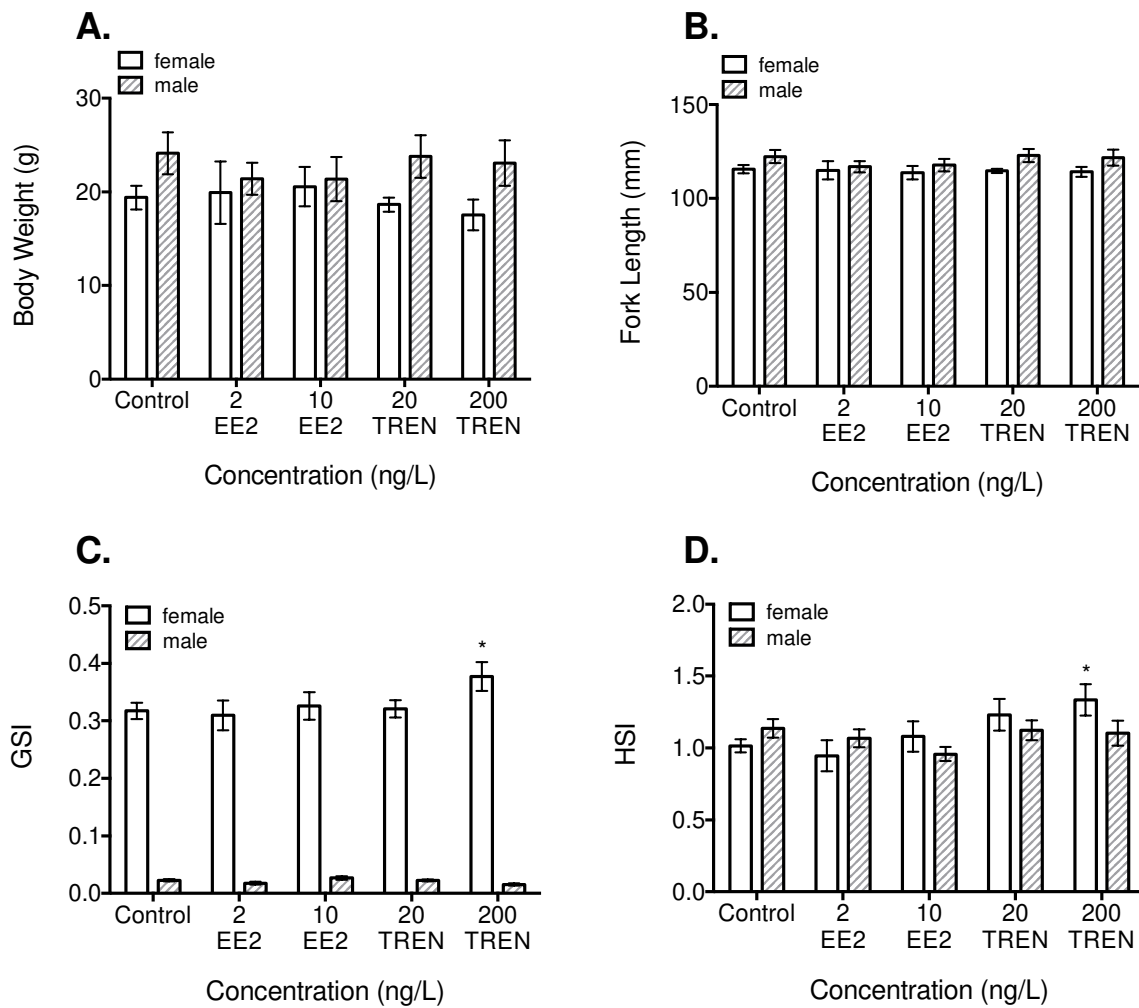


Figure 4. Relative levels of vitellogenin (*vtg*) mRNA in juvenile coho salmon exposed to WWTP effluent for 72 hrs. qPCR data were normalized to *eef1a* levels and the divided by the control mean mRNA level for improved visualization of relative expression. The data are expressed as the mean  $\pm$  SEM ( $n = 6-12$ ). Data were log transformed to conform to normality and were analyzed by one-way ANOVA followed by Tukey's multiple comparison test. Different letters indicate significant differences between treatments ( $p < 0.05$ ).





Supplemental Figure 1: Log levels of mRNA for *eef1a* measured by qPCR in (A) liver or (B) pituitary of fish exposed to 0 ng L<sup>-1</sup>, 2 ngEE2 L<sup>-1</sup>, 10 ng EE2 L<sup>-1</sup>, 20 ng TREN L<sup>-1</sup> or 200 ng TREN L<sup>-1</sup> for 72 hrs. *eef1a* levels were used to normalize hepatic *vtg* and pituitary *lhb* and *fshb* mRNA levels. No significant differences were observed between control and EE2 or TREN-exposed samples. (1-way ANOVA followed by Tukey's multiple comparisons test). The data are expressed as mean ± SEM ( $n = 5 - 8$  for liver and 20 for pituitary).



Supplemental Figure 2: Morphometric data from control EE2 and TREN exposure. Body weight (A) and fork length (B) did not significantly differ between tanks or treatments (2-way ANOVA,  $p > 0.05$ ). Gonadosomatic index (GSI) significantly differed between male (C) and female (D) fish (2-way ANOVA,  $p < 0.0001$ ), but did not significantly differ between tanks (2-way ANOVA,  $p > 0.05$ ). Hepatosomatic index (HSI) was not significantly different based on sex or tank. The data are expressed as mean  $\pm$  SEM (A and B;  $n = 10$ ; C – D;  $n = 2 - 9$ ).