APPENDIX C
FOOD WEB MODEL AND DIOXIN BSAF

EAST WATERWAY OPERABLE UNIT

SUPPLEMENTAL REMEDIAL INVESTIGATION/ FEASIBILITY STUDY

FINAL SUPPLEMENTAL REMEDIAL INVESTIGATION REPORT

APPENDIX C: FOOD WEB MODEL AND DIOXIN BSAF

For submittal to

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LIST OF ACRONYMS AND ABBREVIATIONS

DOC	dissolved organic carbon
Ecology	Washington State Department of Ecology
EM	edible meat
EPA	US Environmental Protection Agency
EPC	exposure point concentration
ERA	ecological risk assessment
EW	East Waterway
FS	feasibility study
FWM	food web model
HHRA	human health risk assessment
K_{OC}	organic carbon-normalized partition coefficient
K_{OW}	octanol-water partition coefficient
LDW	Lower Duwamish Waterway
LDWG	Lower Duwamish Waterway Group
MIS	multi-increment sampling
NLOC	non-lipid organic carbon
NLOM	non-lipid organic matter
NOAA	National Oceanic and Atmospheric Administration
NRS	nominal range sensitivity
OC	organic carbon
PCB	polychlorinated biphenyl
POC	particulate organic carbon
PSDDA	Puget Sound Dredged Disposal Analysis
RBTC	risk-based threshold concentration
r	correlation coefficient
RI	remedial investigation
RME	reasonable maximum exposure
ROC	receptor of concern
SD	standard deviation
SE	standard error
SPAF	species predictive accuracy factor
SRI	supplemental remedial investigation
SWAC	spatially weighted average concentration
TBT	tributyltin
TOC	total organic carbon
WB	whole body
ww	wet weight

C.1 INTRODUCTION

This appendix was prepared to provide detailed descriptions of the polychlorinated biphenyls (PCB) food web model (FWM) and the dioxin and furan biota-to-sediment accumulation factor (BSAF) calculations that were used to derive sediment risk-based threshold concentration (RBTC) values presented in Section 8 of the Supplemental Remedial Investigation (SRI) for East Waterway (EW). Section C.2 describes the FWM parameters and the structure of the FWM, and presents results of the sensitivity and uncertainty analyses that were conducted with the FWM. Section C.3 presents the calculation of BSAF values for selected dioxin and furan congeners, the process and specific methodology for deriving sediment RBTCs for dioxins and furans using the BSAF approach with selected congeners, and the uncertainties associated with the methodology. Evaluation of the regression relationships that were used to model bioaccumulation of cPAHs and TBT for the development of sediment RBTCs is provided in Section 8 of the SRI.

C.2 PCB FOOD WEB MODEL

This section describes the FWM for total PCBs developed for the EW. A comprehensive dataset of total polychlorinated biphenyl (PCB) concentrations in sediment and tissue collected in the EW was compiled for the SRI to evaluate the nature and extent of contamination and to conduct human health and ecological baseline risk assessments. The EW FWM was developed to estimate the relationship between total PCB concentrations in tissues of aquatic organisms and sediment in order to develop RBTCs for total PCBs in sediment for the SRI (see SRI Section 8). The FWM will also be used in the feasibility study (FS) to estimate residual risks from PCBs that may remain following various sediment cleanup alternatives in the EW.

The EW FWM was developed in consultation with the US Environmental Protection Agency (EPA) and is consistent in approach with the Lower Duwamish Waterway (LDW) FWM (Windward 2010). Model design, parameter selection, and model calibration generally followed the procedures used for the LDW. The LDW FWM was developed through consultation among the Lower Duwamish Waterway Group (LDWG), US Environmental Protection Agency (EPA) (both ORD and Region 10 staff), the Washington State Department of Ecology (Ecology), US Army Corps of Engineers, and the National Oceanic and Atmospheric Administration (NOAA). In addition, Jon Arnot, co-author of a refined version

of the model (Arnot and Gobas 2004a), was consulted regarding technical details for application of the model to the LDW.

Species that were important for development of human health and ecological RBTCs were selected for inclusion in the model. Important prey for these species were also modeled. The EW FWM was constructed and initially parameterized using literature-derived and site-specific data to select point estimates or develop distributions for all model parameters. The model was then calibrated to identify sets of parameter values (from the distributions) that best estimated empirical tissue concentration data collected from the EW. The calibration process does not necessarily identify the "true" value for each FWM parameter because numerous combinations of parameters can produce the same results. Nonetheless, the model calibration demonstrated its usefulness in predicting PCB concentrations in the tissue of EW species. Results of the calibrated FWM were subsequently used in the development of sediment RBTCs for PCBs, and may also serve as a tool to support future risk management decision-making for the site.

The parameterization and calibration of the FWM and its application to the EW are discussed in greater detail in the subsections that follow. Section C.2.1 describes the basic structure of the Arnot and Gobas FWM (Arnot and Gobas 2004a). Section C.2.2 describes the approach for applying the FWM to the EW. Section C.2.3 presents the model input parameters and describes how values were selected. Section C.2.4 presents empirical tissue concentration data from the EW for comparison to model predictions; Section C.2.5 presents methods and results of the calibration process; and Section C.2.6 presents methods and results of sensitivity and uncertainty analyses. Use of the FWM in the calculation of sediment RBTCs is discussed in Section C.2.7. A summary of these subsections is provided in Section C.2.8.

C.2.1 Description of Arnot and Gobas Food Web Model

To estimate the relationship between total PCB concentrations in tissue and sediment in the EW, an updated version (Arnot and Gobas 2004a) of the original Gobas model for predicting the uptake of organic chemicals in aquatic food webs (Gobas 1993) was used. This version of the model was developed and applied in the RI and FS of the LDW site. The original Gobas

model was a steady-state,[1] mass-balance bioaccumulation model that was originally developed to describe the bioaccumulation of PCBs in the Great Lakes food web. The Gobas model was later refined (Arnot and Gobas 2004a) to reflect a clearer understanding of bioaccumulation processes based on subsequent field and laboratory studies (Arnot and Gobas 2004b; Gobas and MacLean 2003; Gobas et al. 1999; Nichols et al. 2001; Roditi and Fisher 1999). New elements added by Arnot and Gobas (2004a) to refine the model included:

- A new model for partitioning chemicals into organisms that separates the organisms into three components: lipids, non-lipid organic matter (NLOM)[2] , and water
- Kinetic models for predicting chemical concentrations in algae, phytoplankton, and zooplankton were added[3]
- New allometric relationships for predicting gill ventilation rates in a wide range of aquatic species
- A mechanistic model for predicting changes in the concentration of organic chemicals in the gut contents of a range of species as the gut contents pass through their gastrointestinal tract

The Arnot and Gobas FWM (Arnot and Gobas 2004a) has five compartments: phytoplankton/algae, zooplankton, filter-feeding benthic invertebrates, scavenger/predator/ detritivore benthic invertebrates, and fish. The FWM estimates concentrations of hydrophobic organic chemicals for each compartment using equations that represent the biological processes involved in the uptake and loss of hydrophobic organic chemicals (Figure C.2-1). Thus, each compartment (e.g., fish) has its own unique set of equations. The model has three physical media: sediment, water column water, and sediment porewater.

[1] A steady-state assumption means that concentrations of chemicals in tissue are assumed to not change over time or that concentrations of chemicals in tissue maintain a state of relative equilibrium even after undergoing fluctuations or transformations. The steady-state assumption is reasonable for applications to field situations in which organisms have been exposed to hydrophobic organic chemicals over a long period of time particularly at sites with contaminated sediment. Concentrations in tissue fluctuate slowly compared with exposures, so the body burden – especially the average body burden in a population of individuals – tends to reflect the average concentration to which the population is exposed over time.

[2] For phytoplankton only, there is a non-lipid organic carbon (NLOC) compartment instead of NLOM.

[3] This is an update over statistical models which were previously used to describe these bioaccumulation steps.

Note that the version of the model used for the EW was a different version of the Arnot and Gobas model than was used for the LDW FWM; the AQUAWEB 1.1 version of the model was used for the EW FWM and AQUAWEB 1.2 (Gobas 2006) was used for the LDW FWM (Windward 2010).[4] The Arnot and Gobas model is based on several fundamental assumptions, including:

- Primary routes for the uptake of hydrophobic organic chemicals by zooplankton, benthic invertebrates, and fish are ventilation of sediment porewater or water column water, and ingestion of sediment particles or organisms.
- Primary routes for the loss of hydrophobic organic chemicals by zooplankton, benthic invertebrates, and fish are metabolism, growth dilution, ventilation of porewater or water column water, and fecal egestion.
- Chemicals are assumed to be homogeneously distributed within each tissue phase of the organism (i.e., lipids, water, and NLOM [e.g., proteins and carbohydrates] or NLOC[5]).
- Organisms are assumed to be single compartments that exchange chemicals with their surrounding environments.
- Chemical losses via egg deposition or sperm ejection are assumed to be negligible.

[4] The AQUAWEB 1.2 version of the model includes differentiation in the gut between non-lipid organic carbon (NLOC), from consumption of sediment and phytoplankton, and NLOM from consumption of all other organisms. NLOC and NLOM have different affinities for PCBs. AQUAWEB 1.2 also accounts for differences between lipid and water density in the organism (Gobas 2006).

[5] NLOC was used as the third phase for chemical partitioning in phytoplankton instead of NLOM, as discussed in Table C.2-1. For sediment, PCBs were assumed to partition into organic carbon.

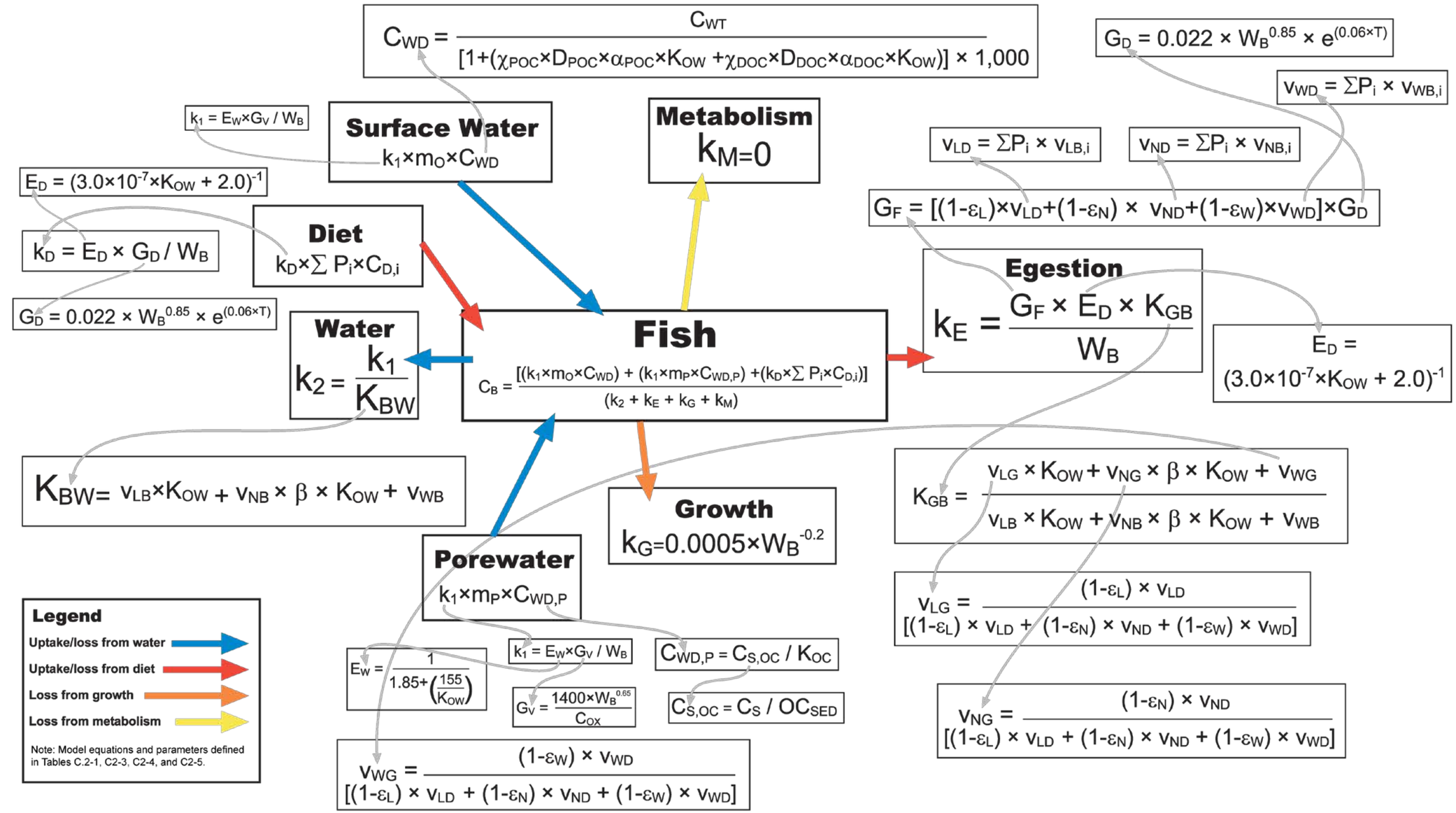


Figure C.2-1

Equations and Parameters Used to Estimate Total PCB Concentrations for Fish in the Arnot and Gobas Model

Justification for these assumptions is provided in Arnot and Gobas (2004a). The applicability of these assumptions to the EW is a significant uncertainty that should be considered when interpreting model output. The fact that the Arnot and Gobas model includes species-specific compartments, multiple pathways, and mechanistic equations makes the model more complicated than other available methods, such as the use of biota-sediment accumulation factors, which represent empirical relationships between few variables. The increased complexity of the Arnot and Gobas model does not necessarily increase the likelihood that the model estimates will be more accurate because the values used for certain parameters are derived from literature (rather than site-specific data). However, the model can be used as a tool to assess the relative importance of various pathways and mechanisms and can potentially be used to enable better estimates than other approaches under varying conditions. As shown in the following, the model has been found to reasonably predict PCB concentrations in EW media, and is deemed useful for the RI and FS.

Model equations are separated into biological equations that simulate the biological processes leading to the uptake and loss of chemicals by organisms (Figure C.2-1), environmental equations that simulate the partitioning of the chemical in the environment, and a single-chemical equation that derives a log organic carbon-normalized partition coefficient (K_{OC}) value from log octanol-water partition coefficient (K_{OW}). These model equations are identified under the biological, environmental, and total PCBs headings in Table C.2-1. Details on the model equations, including definitions for all model parameters, are presented in Arnot and Gobas (2004a). Model parameters for each equation are described in the following subsections.

Table C.2-1
Equations for the Arnot and Gobas Model

Parameter	Symbol	Unit	Equation	Notes	Source
Biological					
Chemical concentration in the modeled species	C_B	µg/kg ww	$C_B = [k_1 \times (m_O \times C_{WD} + m_P \times C_{WD,P}) + k_D \times \sum P_i \times C_{D,i}]/(k_2 + k_E + k_G + k_M)$		Arnot and Gobas (2004a)
Chemical concentration in prey item i	$C_{D,i}$	µg/kg ww	$C_{D,I} = C_B$ or $C_{D,I} = C_S$ (depending on diet)	chemical concentrations in prey items are represented by the equation for chemical concentration in the modeled species (C_B) for any organisms consumed or by the input value for concentration of total PCBs in sediment (C_S) for sediment consumed	Arnot and Gobas (2004a)
Fraction of water column water ventilated	m_O	fraction	$m_O = 1 - m_p$	Fraction of total water ventilated from water column water (i.e., water that is not directly in association with the sediment)	Arnot and Gobas (2004a)
Rate constant for aqueous uptake by fish, invertebrates, and zooplankton	k_1	L/kg·day	$k_1 = E_W \times G_V/W_B$	chemical uptake via the respiratory area (e.g., gills or other respiratory surface)	Gobas (1993); Gobas and MacKay (1987), as cited in Arnot and Gobas (2004a)
Rate constant for aqueous uptake by phytoplankton /algae	k_1	L/kg·day	$k_1 = (A + (B/K_{OW}))^{-1}$	chemical uptake across the cell wall	Arnot and Gobas (2004a)
Rate constant for chemical elimination via the respiratory area	k_2	day^{-1}	$k_2 = k_1/K_{BW}$	chemical loss via the respiratory surface (e.g., gills or cell wall)	Gobas (1993), as cited in Arnot and Gobas (2004a)
Rate constant for chemical uptake via the diet	k_D	kg food/kg organism·day	$k_D = E_D \times G_D/W_B$	For phytoplankton/algae, k_D is zero.	Gobas (1993), as cited in Arnot and Gobas (2004a)
Rate constant for chemical elimination via excretion into egested feces	k_E	day^{-1}	$k_E = G_F \times E_D \times K_{GB}/W_B$	For phytoplankton/algae, k_E is zero.	Gobas et al. (1993), as cited in Arnot and Gobas (2004a)

Table C.2-1

Equations for the Arnot and Gobas Model (cont.)

Parameter	Symbol	Unit	Equation	Notes	Source
Rate constant for growth of aquatic organisms	k_G	day^{-1}	$k_G = 0.000502 \times W_B^{-0.2}$	Regression relationship was established at temperatures around 10°C. (Mean water column temperatures in the EW were around 10°C.)	Thomann et al. (1992) as cited in Arnot and Gobas (2004a)
Dietary chemical transfer efficiency	E_D	%	$E_D = (3.0 \times 10^{-7} \times K_{OW} + 2.0)^{-1}$		Arnot and Gobas (2004a)
Respiratory surface chemical uptake efficiency	E_W	%	$E_W = (1.85 + (155/K_{OW}))^{-1}$		Gobas (1988), as cited in Arnot and Gobas (2004a)
Feeding rate – filter feeders (clams)	G_D	kg/d	$G_D = G_V \times Css \times \sigma$		Morrison et al. (1996), as cited in Arnot and Gobas (2004a)
Feeding rate – other species	G_D	kg/d	$G_D = 0.022 \times W_B^{0.85} \times e^{(0.06 \times T)}$	based on studies of feeding rates in cold-water fish (being used for zooplankton and aquatic invertebrate species as well)	Weiniger (1978), as cited in Arnot and Gobas (2004a)
Fecal egestion rate	G_F	kg/d	$G_F = [(1 - \varepsilon_L) \times v_{LD}) + (1 - \varepsilon_N) \times v_{ND} + (1 - \varepsilon_W) \times v_{WD}] \times G_D$		Arnot and Gobas (2004a)
Gill ventilation rate	G_V	L/d	$G_V = 1{,}400 \times W_B^{0.65}/C_{OX}$		Arnot and Gobas (2004a)
Organism-water partition coefficient on a wet weight basis	K_{BW}	L water/kg biota	$K_{BW} = k_1/k_2 = v_{LB} \times K_{OWL} + v_{NB} \times \beta \times K_{OW} + v_{WB}$		Arnot and Gobas (2004a)
NLOM content of organism	v_{NB}	%	$v_{NB} = 1 - (v_{LB} + v_{WB})$		Arnot and Gobas (2004a)
NLOC content of phytoplankton	v_{NP}	%	$v_{NP} = 1 - (v_{LP} + v_{WP})$		Arnot and Gobas (2004a)

Table C.2-1

Equations for the Arnot and Gobas Model (cont.)

Parameter	Symbol	Unit	Equation	Notes	Source
Phytoplankton/algae-water partition coefficient on a wet weight basis	K_{PW}	L water/kg phytoplankton/ algae	$K_{PW} = v_{LP} \times K_{OW}/\delta_L + \beta_{OC} \times v_{NP} \times K_{OW} + v_{WP}/\delta_W$		Arnot and Gobas (2004a)
Chemical partition coefficient between the contents of the gastrointestinal tract and the organism	K_{GB}	kg biota/kg digesta	$K_{GB} = (v_{LG} \times K_{OW} + v_{NG} \times \beta \times K_{OW} + v_{WG})/ (v_{LB} \times K_{OW} + v_{NB} \times \beta \times K_{OW} + v_{WB})$		Arnot and Gobas (2004a)
Lipid fraction of gut contents	v_{LG}	kg lipid/kg digesta ww	$v_{LG} = (1 - \varepsilon_L) \times v_{LD}/ [(1 - \varepsilon_L) \times v_{LD} + (1 - \varepsilon_N) \times v_{ND} + (1 - \varepsilon_W) \times v_{WD}]$		Arnot and Gobas (2004a)
NLOM fraction of gut contents	v_{NG}	kg NLOM/kg digesta ww	$v_{NG} = (1 - \varepsilon_N) \times v_{ND}/ [(1 - \varepsilon_L) \times v_{LD} + (1 - \varepsilon_N) \times v_{ND} + (1 - \varepsilon_W) \times v_{WD}]$		Arnot and Gobas (2004a)
Water fraction of gut contents	v_{WG}	kg water/kg digesta ww	$v_{WG} = (1 - \varepsilon_W) \times v_{WD}/ [(1 - \varepsilon_L) \times v_{LD} + (1 - \varepsilon_N) \times v_{ND} + (1 - \varepsilon_W) \times v_{WD}]$		Arnot and Gobas (2004a)
Overall lipid content of the diet	v_{LD}	kg lipid/kg food ww	$v_{LD} = \Sigma P_i \times v_{LB,i}$		Arnot and Gobas model spreadsheet (Gobas 2006)
Overall NLOM content of the diet	v_{ND}	kg NLOM/kg food ww	$v_{ND} = \Sigma P_i \times v_{NB,i}$		Arnot and Gobas model spreadsheet (Gobas 2006)
Overall water content of the diet	v_{WD}	kg water/kg food ww	$v_{WD} = \Sigma P_i \times v_{WB,i}$		Arnot and Gobas model spreadsheet (Gobas 2006)
Non-lipid organic carbon content of phytoplankton	v_{OCP}	kg NLOC/kg phytoplankton	$v_{OCP} = 1 - (v_{LP} + v_{WP})$		Arnot and Gobas (2004a)
Fraction of non-lipid organic matter in organism *i*	$v_{NB,i}$	kg NLOM/kg organism	$v_{NB,i} = 1 - (v_{LB,i} + v_{WB,i})$	B = biota	Arnot and Gobas (2004a)

Table C.2-1

Equations for the Arnot and Gobas Model (cont.)

Parameter	Symbol	Unit	Equation	Notes	Source
Environmental					
Freely dissolved chemical concentration in the porewater	$C_{WD,P}$	µg/L	$C_{WD,P} = C_{S,OC}/K_{OC}$		Kraaij et al. (2002), as cited in Arnot and Gobas (2004a)
Chemical concentration in the sediment, organic carbon normalized	$C_{S,OC}$	µg/kg	$C_{S,OC} = C_S/OC_{sed}$		Calculated using Phase 1 and Phase 2 sediment data
Freely dissolved chemical concentration in the water	C_{WD}	µg/L	$C_{WD} = (C_{WT} \times \phi)/1{,}000$	Simulates sequestering of chemical by DOC and POC in the water.	Arnot and Gobas (2004a)
Bioavailable solute fraction	□	unitless	$\phi = 1/(1 + \chi_{POC} \times D_{POC} \times \alpha_{POC} \times K_{OW} + \chi_{DOC} \times D_{DOC} \times \alpha_{DOC} \times K_{OW})$	Simulates sequestering of chemical by DOC and POC in the water.	Arnot and Gobas (2004a)
Total PCBs					
Organic carbon-water partition coefficient	K_{OC}	L/kg	$K_{OC} = 0.35 \times K_{OW}$	There are many different relationships established between K_{OW} and K_{OC}. This relationship was based on the analysis of a wide range of analytes (including PCB congeners) and soil/sediment matrices. The authors excluded data that may not have represented equilibrium conditions that can be very influential for high-molecular-weight PCBs. It is consistent with the commonly used approximation of $K_{OC} = 0.4\ K_{OW}$.	Seth et al. (1999)

C – centigrade
DOC – dissolved organic carbon
K_{OW} – octanol-water partition coefficient
LDW – Lower Duwamish Waterway
NLOC – non-lipid organic carbon
NLOM – non-lipid organic matter
PCB – polychlorinated biphenyl
POC – particulate organic carbon
ww – wet weight

Each species in the model has a master equation that combines chemical uptake and loss for that species (C_B). The master equation has two potential chemical uptake mechanisms and four potential chemical loss mechanisms. Chemical concentrations in phytoplankton are calculated assuming aqueous uptake across the cell wall ($k_1 \times m_o \times C_{WD}$), loss across the cell wall (k_2), and loss via growth dilution (k_G). Chemical concentrations in zooplankton, invertebrates, and fish are calculated assuming uptake from water (i.e., water column water and porewater) via the respiratory surface ($k_1 \times (m_o \times C_{WD} + m_p \times C_{WD,P})$) and uptake from the diet ($k_D \times \sum P_i \times C_{D,i}$). Chemical loss mechanisms for zooplankton, invertebrates, and fish include metabolism (k_M), growth dilution (k_G), loss to water via the respiratory surface (k_2), and fecal egestion (k_E). Because the Arnot and Gobas model (2004a) assumes steady-state conditions, it does not recognize short-term changes in rates of uptake or loss from short-term changes in biological or environmental conditions. For each model run, one value was calculated for each uptake or loss mechanism.

Water column water, porewater, and sediment are the three abiotic environmental media included in the FWM. Total PCB concentrations in the water column (C_{WT}) are entered as whole water total PCB concentrations. The dissolved fraction (C_{WD}) in water column water is calculated in the model by estimating the relative partitioning of PCBs among particulate organic carbon (POC), dissolved organic carbon (DOC), and the freely dissolved phase (Table C.2-1). Total PCB concentrations in porewater are estimated assuming equilibrium partitioning with the sediment particles (Table C.2-1). The equilibrium partitioning equation does not account for partitioning to colloidal carbon within the sediment matrix. Total PCB concentrations in sediment are entered as total dry-weight concentrations and converted to organic carbon (OC)-normalized concentrations for uptake and loss calculations. One sediment compartment represents both bottom sediment and suspended sediment; thus, sediment exposure is the same regardless of whether exposure occurs while sediment is settled at the bottom of the water column or suspended in the water column as particulate. Exposure through direct sediment contact via the dermis or integument is not explicitly modeled in the FWM.

Exposure routes for chemicals in sediment include diffusion to porewater and the ingestion of sediment particles. The exposure route for chemicals in the water column water and porewater is ventilation across the respiratory surface (e.g., gills) or cell wall.

C.2.2 Approach for Applying the Food Web Model in the East Waterway

In order to apply the Arnot and Gobas model (2004a) to the EW, each species or species assemblage to be modeled was assigned to a compartment (i.e., phytoplankton/algae, zooplankton, filter-feeding benthic invertebrates, scavenger/predator/detritivore benthic invertebrates, or fish). Even though all compartments share a master equation (see equation for C_B in Table C.2-1), they have different sub-models (e.g., equations for rate constants) and different parameters that define those sub-models. Thus, the selection of a compartment determines the parameters that need to be defined for each species or species assemblage.

Three species of adult fish, two species of adult crab, shrimp, and clams (species not specified) in the EW were modeled. These species are referred to as target species because they were either receptors of concern (ROCs) in the ecological risk assessment (ERA) or served as key prey species for other receptors in the ERA, or are seafood items consumed by people in the human health risk assessment (HHRA). The following organisms were modeled for the EW:

- Phytoplankton/algae
- Zooplankton
- Benthic invertebrates
- Clams
- Shrimp
- Juvenile fish
- Red rock crab
- Dungeness crab
- Shiner surfperch
- English sole
- Brown rockfish

Fish and crab were each modeled using a fish compartment. Crabs are large mobile invertebrates that eat other invertebrates and fish depending on crab species modeled. Crabs were modeled using fish equations instead of scavenger/predator/detritivore benthic

invertebrate equations because the majority of the species used to develop the scavenger/predator/detritivore benthic invertebrate equations and associated parameter values were benthic infauna filter feeders or detritivores, and judged to be less applicable to modeling crabs than the fish equations. In addition, it was determined early in the modeling process that using fish equations resulted in estimates of crab tissue concentrations of total PCBs that were more similar to site-specific empirical data for crab. Clams[6] were modeled using a filter-feeding benthic invertebrate compartment. Other prey species modeled included phytoplankton, zooplankton, benthic invertebrates, shrimp, and juvenile fish. Phytoplankton and zooplankton, and juvenile fish were modeled using phytoplankton/algae and zooplankton compartments, and juvenile fish were modeled using fish compartments. For the same reason that crabs were modeled using fish compartment equations, shrimp were also modeled using fish compartment equations. Benthic invertebrates, which make up a large portion of fish diets (see Section C.2.3.2.2), were modeled as a single assemblage using a scavenger/predator/detritivore benthic invertebrate compartment. These species were modeled to serve as prey, approximating the transfer of chemicals from environmental media through the food web.

The EW is approximately 1.5 miles long and was modeled as a single area to reflect the majority of the species compartments in the FWM which represent species that have home ranges as large as or larger than the EW. Tissue data were collected to characterize the area as a whole.

C.2.3 Model Parameters

The application of the Arnot and Gobas (2004a) FWM to the EW required the selection of values for over 100 input parameters (including dietary fractions). Because the Arnot and Gobas model was applied in the EW assuming steady-state conditions, it was most appropriate for parameter values to represent means of populations (as opposed to individuals) and means of physical conditions over several years (as opposed to shorter periods [e.g., 1 month]). Uncertainty regarding the estimates of mean values for parameters was represented quantitatively through the use of probability distributions. The model was

[6] The clam compartment was intended to represent multiple species collected and analyzed from the EW as part of the SRI: butter clam (*Saxidomus giganteus*), Eastern soft-shell *(Mya arenaria*), cockle (*Clinocardium nuttali*), and native littleneck (*Protothaca staminea*).

run and calibrated probabilistically in order to systematically explore all plausible parameter sets and their corresponding estimated total PCB concentrations in tissue. Probability distributions were developed for 102 parameters, and point estimates were used to characterize 20 parameters that had limited data, low variability, and/or low sensitivity (these are often labeled with "na" in the distribution column of the parameter tables).

To characterize a parameter distribution, several statistical descriptors (e.g., mean, mode, standard deviation [SD]) were required. Estimates of the population of values for each input parameter were represented by either a normal or triangular distribution, which was assumed to represent the uncertainty around the mean estimate. Parameter names, symbols, units, selected values (probability distributions or point estimates), comments, and source information are presented in tables in Sections C.2.3.1 to C.2.3.3.

According to the central limit theorem, with sufficient sample size, estimates of the mean approach a normal distribution. Parameters that had adequate site-specific empirical data or literature data to develop means and SDs were assigned a normal distribution. Triangular distributions were assumed for those parameters with more limited data. A triangular distribution requires selection of a mode (a most-likely value) and maximum and minimum values for the parameter (Warren-Hicks and Moore 1998). Both mode and mean values are presented for parameters with triangular distributions; means are only presented for comparison with calibrated values. The mean of the triangular distribution was calculated using the following equation:

$$\text{Mean} = \frac{(\text{mode} + \text{minimum} + \text{maximum})}{3} \qquad \text{(C-1)}$$

Values and statistical descriptors for each of the FWM parameters were derived from site-specific EW data, values developed for the LDW FWM (Windward 2010), data from the literature (including data from other models), and default values used in previous applications of the Arnot and Gobas model to the Great Lakes (Arnot and Gobas 2004a) or San Francisco Bay (Gobas and Arnot 2005). Many of the default values used in previous applications of the Arnot and Gobas model were also derived from the literature. The following sections present the parameters, estimates of relevant statistical descriptors, and the form of the probability distribution selected to represent each parameter, with parameters grouped under total PCBs-specific, general, and species-specific. These sections

also provide the rationale for selecting individual parameter values or distributions for the parameters.

C.2.3.1 Total PCBs-Specific Parameters

This section presents the model parameter values that are specific to total PCBs: sediment and water concentrations and Kow. Total PCBs-specific parameters are available site-specific data or values taken from the literature. Site-specific PCB data were available for water and sediment concentration inputs to the FWM.

As was done for the LDW FWM (2010), the Kow value for total PCBs was estimated as a congener concentration-weighted average log value using concentrations of individual PCB congeners in EW tissue samples and the log Kow values for those PCB congeners taken from the literature (Equation C-2). Only one Kow value is used in the FWM for application to all media in the model (including all the different species modeled). So it is necessary to develop one value that best represents the average partitioning of the congeners in the system. The literature PCB congener-specific log Kows were taken from Hawker and Connell (1988).

$$\text{Average } \log K_{OW} = \frac{\sum_{i=1}^{n} C_i \times \log K_{OWi}}{\sum C_i} \qquad \text{(C-2)}$$

Where:

C_i = Detected concentration of PCB congener i (µg/kg wet weight [ww])
Log K_{OWi} = log Kow of PCB congener i (L/kg)
n = number of detected PCB congeners

For the LDW modeling, the concentration-weighted average log Kow (6.6) was based on benthic invertebrate tissue data, which was decided in collaboration with EPA and NOAA. The mean and standard error (SE) of eight concentration-weighted log Kow values for benthic invertebrates were then used to define a normal distribution for log Kow for the LDW model.[7] For the LDW, the average log Kow derived using PCB congeners in all

[7] Consistent with the Central Limit Theorem, estimates of the mean are expected to approximate a normal distribution with the mean of the distribution defined by the mean of the raw data, and the standard deviation of the distribution defined by the standard error of the raw data.

available tissue types (i.e., fish, crab, shellfish, and invertebrates) was the same as the average derived using only benthic invertebrate samples.

However, for the EW, congener data were not available for benthic invertebrates. Since the LDW modeling found that the average log Kow was the same using either all available tissue types or only benthic invertebrate samples, values from other tissue types were explored for use in the EW modeling. Table C.2-2 presents the concentration-weighted log Kows for all EW tissue samples for which congener data were available. The average for each species group is also shown. The range (6.6 to 6.9) of concentration-weighted log Kows for individual EW tissue samples was fairly small. The average across all samples and the average of averages for the species groups were both 6.7. Because of the tight distribution of estimates based on empirical concentration data, a normal distribution was assumed for this model parameter with a mean equal to the average (6.7) and a standard deviation equal to the SE (0.042) of the averages for the species groups. The average of the concentration-weighted log Kows for the 13 subtidal surface composite sediment samples of the EW (a possible surrogate for benthic invertebrates) was also 6.7 with an SE of 0.021.

Table C.2-2
Weighted Log K_{OW}s for EW Samples Analyzed for PCB Congeners

Sample Type[a]	Concentration Weighted Total PCB Log KOW for Sample	Average for Species Group
Rockfish		
Brown rockfish	6.8	6.8
Brown rockfish	6.9	
Brown rockfish	6.9	
Brown rockfish	6.8	
Brown rockfish	6.8	
Brown rockfish	6.8	
Clams		
Butter clam	6.6	6.6
Butter clam	6.6	
Cockle	6.6	
Crab		
Red rock and Dungeness crab	6.8	6.8
Red rock and Dungeness crab	6.8	
Red rock and Dungeness crab	6.8	
English Sole		
English sole	6.7	6.7

Sample Type[a]	Concentration Weighted Total PCB Log KOW for Sample	Average for Species Group
English sole	6.7	
English sole	6.7	
Perch		
Shiner surfperch	6.8	6.8
Shiner surfperch	6.8	
Shiner surfperch	6.8	
Average	**6.7**	**6.7**
Standard Error	0.021	0.042

[a] Rockfish samples were analyzed as individuals. All other samples were composite samples.

EW – East Waterway

K_{ow} – octanol water partition coefficient

PCB – polychlorinated biphenyl

Table C.2-3 provides total PCBs-specific model parameter values, consisting of the average concentration-weighted log Kow value for congeners, water concentration, sediment concentration, and metabolic rates for fish and invertebrates. Total PCBs water concentration data were available from events representing dry and wet seasons and one storm event(Windward 2009). The data were collected at 1 m above the bottom and 1 m below the surface throughout EW (SRI Map 4-7). Concentrations of total PCBs in water samples were calculated as the sum of detected PCB congeners. For each parameter, the nominal values, distribution type, and distribution values used for calibration (the nominal value for the distribution mean, and the standard deviation for normal distributions), and information sources are provided. The nominal values are initial best estimates for each parameter used as the distribution mean. Consistent with the LDW FWM (Windward 2010), no distribution was assigned to the average total PCB sediment concentration (i.e., the spatially weighted average concentration [SWAC]) because it was considered a decision variable (i.e., uncertainty in the current SWAC would be similar to uncertainty in the SWAC for alternative conditions assessed using the calibrated FWM, such as sediment RBTC values).

Table C.2-3

Total PCBs-Specific Parameters Used to Calibrate the EW FWM for Total PCBs

Parameter	Symbol	Unit	Nominal Value	Distribution Type	Distribution Value[a]	Source
K_{OW}[a]	K_{OW}	kg/L	6.7	normal	SD = 0.042	Based on EW fish and invertebrates (see Table C.2-2).
Water concentration-total (i.e., dissolved and particulate)[a]	C_{WT}	ng/L	1.31	normal	SD = 0.184	EW SRI/FS dataset, n = 57 near-surface and near-bottom samples
Sediment concentration (SWAC)	C_S	µg/kg	470	na	na	Nominal value is based on the area weighted average of the subtidal SWAC and the mean of the MIS intertidal samples from the EW SRI/FS dataset.
Fish metabolic rates	K_M	1/day	0	na	na	Assumed to be 0 for total PCBs.
Invertebrate metabolic rates	K_M	1/day	0	na	na	Assumed to be 0 for total PCBs.

[a] Consistent with the Central Limit Theorem, estimates of the mean are expected to approximate a normal distribution with the mean of the distribution defined by the mean of the raw data (nominal value in the fourth column), and the SD of the distribution defined by the SE of the raw data (value in the sixth column).

EW – East Waterway
FS – feasibility study
K_{OW} – octanol-water partition coefficient
MIS – multi-increment sampling
na – not applicable
PCB – polychlorinated biphenyl
SD – standard deviation
SE – standard error
SRI – remedial investigation
SWAC – spatially weighted average concentration (based on an inverse distance weighting approach as described in Section 4 of the SRI)

C.2.3.2 General Model Parameters

General model parameters were selected for the FWM based on available site-specific data or based on data available from the literature. Table C.2-4 presents general physical/chemical parameters, parameters for the bioavailable fractions from water, and biological parameters used in the model. The nominal values (i.e. the default values used before model calibration), distributions used for calibration (with the nominal value as the distribution mean and the standard deviation for normal distributions), and information sources are provided.

Table C.2-4
General Model Parameter Distributions and Selected Values Used to Calibrate the EW FWM

Parameter	Symbol	Unit	Nominal Value	Distribution Type	Distribution Value[a]	Source Notes
Physical/Chemical Parameters						
Organic carbon content of sediment	OC_{sed}	unitless	1.62%	normal	SD=0.12	Nominal value is based on the area-weighted average of the subtidal SWAC and the mean of the MIS intertidal samples from EW SRI/FS dataset. The intertidal portion of the EW is small (2.7% of the area). The subtidal samples were mostly of similar size. Therefore the SE of the OC for the 13 subtidal composite samples was selected as the SD for the distribution. The average of the 13 subtidal samples (1.66%) was similar to the spatially weighted average for the EW (i.e. a spatially weighted average of the13 subtidal samples and the average of the three MIS intertidal samples).
Mean water temperature	T	°C	10.3	normal	SD = 0.20	Data collected by King County (see EW ERA Map A.2-7 for location). Samples were collected monthly (2/25/08 to 8/15/11) at approximately 1 m below the surface and approximately 1 m above the bottom (n = 86). All values were averaged.
Concentration of suspended solids	C_{SS}	kg/L	2.9E-6	normal	SD = 5.3E-7	Data collected by King County (see EW ERA Map A.2-7 for location). Samples were collected monthly (2/25/08 to 9/19/11) at approximately 1 m below the surface and approximately 1 m above the bottom (n = 88). All values averaged. Non-detects were assumed to equal method detection limit. Concentrations were below the reported detection limit for 52% of the samples (i.e. 46 of the 88 samples).
Bioavailable Fraction Parameters						
POC concentration in water	D_{POC}	kg/L	1.4E-7	normal	SD = 1.8E-8	Data collected by King County (see EW ERA Map A.2-7 for location). Samples were collected monthly (2/25/08-9/19/11) at approximately 1 m below the surface and approximately 1 m above the bottom (n = 88). All values averaged. POC calculated as TOC minus DOC. When DOC > TOC, POC was assumed to equal 0. DOC>TOC for 26% of the samples.
POC proportionality constant	αPOC	unitless	0.35	na	na	Arnot and Gobas (2004a)
DOC concentration in water	D_{DOC}	kg/L	1.7E-6	normal	SD = 2.3E-8	Data collected by King County (see EW ERA Map A.2-7 for location). Samples were collected monthly (2/25/08 to 9/19/11) at approximately 1 m below the surface and approximately 1 m above the bottom (n = 88). All values averaged.

Parameter	Symbol	Unit	Nominal Value	Distribution Type	Distribution Value[a]	Source Notes
DOC proportionality constant	αDOC	unitless	0.08	na	na	Arnot and Gobas (2004a)
General Biological Parameters						
Uptake constant A for organism	A	unitless	6.0×10^{-5}	na	na	Gobas and Arnot (2005), Arnot and Gobas (2004a)
Uptake constant B for organism	B	unitless	5.50	na	na	Gobas and Arnot (2005), Arnot and Gobas (2004a)
Dietary transfer efficiency constant A	E_{DA}	unitless	3×10^{-7}	na	na	Arnot and Gobas (2004a)
Dietary transfer efficiency constant B	E_{DB}	unitless	2.0	na	na	Arnot and Gobas (2004a)
NLOM-octanol proportionality constant	β	unitless	0.035	na	na	Arnot and Gobas (2004a)
NLOC-octanol proportionality constant	γ	unitless	0.35	na	na	Arnot and Gobas (2004a)

[a] For normal distributions, the mean of the distribution (and the raw data) is provided as the nominal value in the third column of the table and the SE of the raw data defines the standard deviation of the distribution. Consistent with the Central Limit Theorem, estimates of the mean are expected to approximate a normal distribution with the mean of the distribution defined by the mean of the raw data, and the SD of the distribution defined by the SE of the raw data.

DOC – dissolved organic carbon
FS – feasibility study
MIS – multi- increment sampling
na – not analyzed
NLOC – non-lipid organic carbon
NLOM – non-lipid organic matter
OC – organic carbon
POC – particulate organic carbon
SD – standard deviation
SE – standard error
SRI – supplemental remedial investigation
SWAC – spatially weighted average concentration
TOC – total organic carbon

C.2.3.3 Species-Specific Parameters

Species-specific model parameters were selected for the FWM based on available site-specific data or based on data available from the literature. Table C.2-5 presents species-specific model values for parameters other than diets (presented later).

Table C.2-5

Species-Specific Parameter Distributions and Selected Values Used to Calibrate the EW FWM

Parameter		Unit	Nominal Value	Distribution Type	Distribution Values[a]	Source Notes
Phytoplankton/algae						
Lipid fraction of organism	v_{LB}	fraction	0.0012	normal	SD = 0.005	Mackintosh et al. (2004)
Water content fraction of organism	v_{WB}	fraction	0.956	normal	SD = 0.055	Mackintosh et al. (2004)
Fraction of pore water ventilated	m_p	unitless	0	na	na	Live in water column and are assumed to not be exposed to porewater.
Growth rate constant	k_G	1/day	0.08	na	na	Value from Swackhamer and Skoglund (1993) as cited in Arnot and Gobas (2004a). Only phytoplankton/algae has a growth rate constant (k_G) as an input number instead of an equation. This is a mean annual value based on empirical data in which slow-growth conditions (winter) were 0.03 day^{-1} and active-growth conditions (summer) were 0.13 day^{-1}.
Zooplankton						
Weight	w_B	kg	1.6×10^{-7}	normal	SD = 3.6×10^{-8}	Data from Giles and Cordell (1998). SD reported by Giles and Cordell (1998).
Lipid fraction of organism	v_{LB}	fraction	0.012	normal	SD = 0.003	Data from Kuroshima et al. (1987). SD of data reported in Kuroshima et al. (1987), assuming the data represented a distribution of mean values.
Water content fraction of organism	v_{WB}	fraction	0.9	normal	SD = 0.015	Data from Kuroshima et al. (1987). SD of data reported in Kuroshima et al. (1987), assuming the data represented a distribution of mean values.
Dietary absorption efficiency of lipid	ε_L	fraction	0.72	triangular	mode = 0.72 mean = 0.71 min = 0.55 max = 0.85	Data from Conover (1966) as cited in Arnot and Gobas (2004a). Study involved *Calanus hyperboreus* eating diatoms and flagellates from Gulf of Maine.

Table C.2-5

Species-Specific Parameter Distributions and Selected Values Used to Calibrate the EW FWM (cont.)

Parameter		Unit	Nominal Value	Distribution Type	Distribution Values[a]	Source Notes
Dietary absorption efficiency of NLOM	ε_N	fraction	0.71	triangular	mode = 0.72 mean = 0.71 min = 0.55 max = 0.85	Data from Conover (1966) as cited in Arnot and Gobas (2004a). Study involved *Calanus hyperboreus* eating diatoms and flagellates from Gulf of Maine.
Dietary absorption efficiency of water	ε_W	fraction	0.55	na	na	Value from Gobas and Arnot (2005)
Fraction of pore water ventilated	m_p	fraction	0	na	na	live in water column and are assumed to not be exposed to porewater
Invertebrate Absorption Efficiencies						
Dietary absorption efficiency of lipid	ε_L	fraction	0.75	triangular	mode = 0.75 mean = 0.62 min = 0.15 max = 0.96	Data from Roditi and Fisher (1999), Berge and Brevik (1996), Gordon (1966), Parkerton (1993) as cited in Arnot and Gobas (2004a). These studies involved zebra mussels from tidal freshwater section of the Hudson River and polychaetes from Cape Cod intertidal flats.
Dietary absorption efficiency of NLOM	ε_N	fraction	0.75	triangular	mode = 0.75 mean = 0.62 min = 0.15 max = 0.96	Data from Roditi and Fisher (1999), Berge and Brevik (1996), Gordon (1966), Parkerton (1993) as cited in Arnot and Gobas (2004a). These studies involved zebra mussels from the tidal freshwater section of the Hudson River and polychaetes from Cape Cod intertidal flats.
Dietary absorption efficiency of water	ε_W	fraction	0.55	na	na	Value from Gobas and Arnot (2005).
Fish Absorption Efficiencies						
Dietary absorption efficiency of lipid	ε_L	fraction	0.92	triangular	mode = 0.92 mean = 0.92 min = 0.90 max = 0.95	Data from Gobas et al. (1999) as cited in Arnot and Gobas (2004a). Based on 73-day laboratory test with adult rainbow trout (*Oncorhynchus mykiss*) and a field study of rock bass (*Ambloplites rupestris*).
Dietary absorption efficiency of NLOM	ε_N	fraction	0.60	triangular	mode = 0.60 mean = 0.58 min = 0.50 max = 0.65	Data from Nichols et al. (2001) as cited in Arnot and Gobas (2004a). Based on study with tetrachlorobiphenyl and rainbow trout.

Table C.2-5

Species-Specific Parameter Distributions and Selected Values Used to Calibrate the EW FWM (cont.)

Parameter		Unit	Nominal Value	Distribution Type	Distribution Values[a]	Source Notes
Dietary absorption efficiency of water	ε_W	fraction	0.55	na	na	Value from Gobas and Arnot (2005).
Benthic Invertebrates						
Weight	w_B	kg	5.1×10^{-5}	normal	SD = 2×10^{-5}	There were no organism counts or taxonomy for EW benthic invertebrate samples. Hence, these values are based on weight estimates for the LDW. Estimates of benthic invertebrate body weights in samples analyzed for PCBs for the LDW were based on abundances of major taxonomic groups (i.e., annelids, crustaceans, mollusks, and miscellaneous taxa) of benthic invertebrates in taxonomy samples collected in 2004 (Windward 2005). Based on comparison of photographs from the EW benthic invertebrate samples and taxonomy from the LDW benthic invertebrates, there appears to be significant overlap in the major taxa present as well a number of key species.
Lipid fraction of organism	v_{LB}	fraction	0.0062	normal	SD = 0.00047	EW SRI/FS dataset, n=8 composites
Water content fraction of organism	v_{WB}	fraction	0.76	normal	SD = 0.017	EW SRI/FS dataset, n=8 composites
Fraction of pore water ventilated	m_p	unitless	0.20	triangular	mode = 0.20 mean = 0.17 min = 0.05 max = 0.25	Used Winsor et al. (1990), Gobas and Wilcockson (2003), Gobas and Arnot (2005), and knowledge of organism behavior to develop values
Clams						
Weight	w_B	kg	0.023	triangular	mode = 0.023 mean = 0.021 min = 0.0032 max = 0.037	EW SRI/FS dataset, n=123 individuals, weights only available for multiple shelled individuals weighed together (n=11 composites), so variance could not be calculated. Min and max are for average individual weights estimated for the different composites (based on number of clams and total composite weight).
Lipid fraction of organism	v_{LB}	fraction	0.0065	normal	SD = 0.00057	EW SRI/FS dataset, n=10 composites

Table C.2-5

Species-Specific Parameter Distributions and Selected Values Used to Calibrate the EW FWM (cont.)

Parameter		Unit	Nominal Value	Distribution Type	Distribution Values[a]	Source Notes
Water content fraction of organism	v_{WB}	fraction	0.86	normal	SD = 0.0086	EW SRI/FS dataset. n=10 composites
Fraction of pore water ventilated	m_p	unitless	0.20	triangular	mode = 0.20 mean = 0.17 min = 0.05 max = 0.25	Used Winsor et al. (1990), Gobas and Wilcockson (2003), Gobas and Arnot (2005), and knowledge of organism behavior to develop values
Filter feeder (clam) scavenging efficiency	σ	unitless	1	na	na	Value from Arnot and Gobas (2004a). Used to calculate feeding rate for filter feeders.
Shrimp						
Weight	w_B	kg	0.0042	triangular	mode = 0.0042 mean = 0.0056 min = 0.00067 max = 0.012	EW SRI/FS dataset, weights available for 2 individuals plus multiple individuals weighed together (n=26 total individuals), so SE could not be calculated. Weight for heaviest individual sampled used as maximum. Smallest average individual weight for composites (based on number of shrimp and total composite weight) used as minimum..
Lipid fraction of organism	v_{LB}	fraction	0.0083	normal	0.00083	EW SRI/FS dataset, n=1 composite sample. Applied SD of 10%.
Water content fraction of organism	v_{WB}	fraction	0.76	normal	0.076	EW SRI/FS dataset, n=1 composite sample. Applied SD of 10%.
Fraction of pore water ventilated	m_p	unitless	0.02	triangular	mode = 0.02 mean = 0.02 min = 0.01 max = 0.03	Used Winsor et al. (1990), Gobas and Wilcockson (2003), Gobas and Arnot (2005), and knowledge of organism behavior to develop values
Juvenile Fish						
Weight	w_B	kg	0.006	normal	SD = 0.0007	No data available from the EW. Based on ≤ 80 mm shiner surfperch from the LDW and background locations sampled in 2004 and 2005 (n = 16) (Windward 2010).

Table C.2-5

Species-Specific Parameter Distributions and Selected Values Used to Calibrate the EW FWM (cont.)

Parameter		Unit	Nominal Value	Distribution Type	Distribution Values[a]	Source Notes
Lipid fraction of organism	v_{LB}	fraction	0.025	normal	SD = 0.006	Mean value based on mean lipid content of adult shiner surfperch and English sole collected from the LDW with a correction factor of 0.5 applied based on ratios of juvenile and adult fish lipids described in the literature (Gobas and Arnot 2005; Robards et al. 1999). Standard deviation estimated as 2 × SE of 19 lipid values (Windward 2010).
Water content fraction of organism	v_{WB}	fraction	0.739	normal	SD = 0.020	Based on LDWG Phase 2 data for adult shiner surfperch. Mean of all composite samples (n = 46) (Windward 2010).
Fraction of pore water ventilated	m_p	unitless	0.01	triangular	mode = 0.01 mean = 0.01 min = 0.005 max = 0.02	Used Winsor et al. (1990), Gobas and Wilcockson (2003), Gobas and Arnot (2005), and knowledge of organism behavior to develop values(Windward 2010).
Red Rock Crab						
Weight	w_B	kg	0.43	normal	SD = 0.072	EW SRI/FS dataset, n = 56 individuals in 8 composite samples, weight weighted weight approach for mean and SE
Lipid fraction of organism	v_{LB}	fraction	0.0086	normal	SD = 0.0016	EW SRI/FS dataset, n = 8 composites
Water content fraction of organism	v_{WB}	fraction	0.83	normal	SD = 0.0056	EW SRI/FS dataset, n = 8 composites
Fraction of pore water ventilated	m_p	unitless	0.02	triangular	mode = 0.02 mean = 0.02 min = 0.01 max = 0.03	Used Winsor et al. (1990), Gobas and Wilcockson (2003), Gobas and Arnot (2005), and knowledge of organism behavior to develop values
Dungeness Crab						
Weight	w_B	kg	0.51	normal	SD = 0.068	EW SRI/FS dataset, n = 7 individuals in one composite sample, body weight-weighted approach for mean, SE based on individuals included in the one composite analytical sample.
Lipid fraction of organism	v_{LB}	fraction	0.019	normal	SD = 0.0019	EW SRI/FS dataset, n = 1 composite sample. Applied SD of 10%.

Table C.2-5

Species-Specific Parameter Distributions and Selected Values Used to Calibrate the EW FWM (cont.)

Parameter		Unit	Nominal Value	Distribution Type	Distribution Values[a]	Source Notes
Water content fraction of organism	v_{WB}	fraction	0.81	normal	SD = 0.081	EW SRI/FS dataset, n = 1 composite sample. Applied SD of 10%.
Fraction of pore water ventilated	m_p	unitless	0.02	triangular	mode = 0.02 mean = 0.02 min = 0.01 max = 0.03	Used Winsor et al. (1990), Gobas and Wilcockson (2003), Gobas and Arnot (2005), and knowledge of organism behavior to develop values
Shiner Surfperch						
Weight	w_B	kg	0.019	normal	SD = 0.00077	EW SRI/FS dataset, n = 100 individuals in 11 composite samples, body weight-weighted approach for mean and SE
Lipid fraction of organism	v_{LB}	fraction	0.046	normal	SD = 0.0034	EW SRI/FS dataset, n = 11 composites
Water content fraction of organism	v_{WB}	fraction	0.73	normal	SD = 0.0063	EW SRI/FS dataset, n = 11 composites
Fraction of pore water ventilated	m_p	unitless	0.01	triangular	mode = 0.01 mean = 0.01 min = 0.005 max = 0.02	Used Winsor et al. (1990), Gobas and Wilcockson (2003), Gobas and Arnot (2005), and knowledge of organism behavior to develop values
English Sole						
Weight	w_B	kg	0.141	normal	SD = 0.0064	EW SRI/FS dataset, n = 65 individuals in 13 composite samples, body weight weighted approach for mean and SE
Lipid fraction of organism	v_{LB}	fraction	0.035	normal	SD = 0.0028	EW SRI/FS dataset, n = 13 composites
Water content fraction of organism	v_{WB}	fraction	0.78	normal	SD = 0.0045	EW SRI/FS dataset, n = 13 composites
Fraction of pore water ventilated	m_p	unitless	0.01	triangular	mode = 0.01 mean = 0.01 min = 0.005 max = 0.02	Used Winsor et al. (1990), Gobas and Wilcockson (2003), Gobas and Arnot (2005), and knowledge of organism behavior to develop values

Table C.2-5

Species-Specific Parameter Distributions and Selected Values Used to Calibrate the EW FWM (cont.)

Parameter		Unit	Nominal Value	Distribution Type	Distribution Values[a]	Source Notes
Rockfish						
Weight	w_B	kg	0.30	normal	SD = 0.033	EW SRI/FS dataset, n = 13 individuals (weights of 2 individuals analyzed were not reported)
Lipid fraction of organism	v_{LB}	fraction	.032	normal	SD = 0.0016	EW SRI/FS dataset, n = 15 individuals
Water content fraction of organism	v_{WB}	fraction	0.72	normal	SD = 0.0077	EW SRI/FS dataset, n = 15 individuals
Fraction of porewater ventilated	m_p	unitless	0.01	triangular	mode = 0.01 mean = 0.01 min = 0.005 max = 0.02	Used Winsor et al. (1990), Gobas and Wilcockson (2003), Gobas and Arnot (2005), and knowledge of organism behavior to develop values.

[a] For triangular distributions, the nominal value is the most likely value ("mode") and the range is defined by the maximum and minimum values. For normal distributions, the mean of the distribution (and the raw data) is provided as the nominal value in the fourth column of the table and the SE of the raw data defines the standard deviation of the distribution, unless otherwise specified in the source notes column (i.e. phytoplankton/algae and zooplankton values based on literature sources rather than EW SRI/FS data). Consistent with the Central Limit Theorem, estimates of the mean are expected to approximate a normal distribution with the mean of the distribution defined by the mean of the raw data, and the standard deviation of the distribution defined by the SE of the raw data.

BPJ – best professional judgment
EW – East Waterway
FS – feasibility study
LDW – Lower Duwamish Waterway
na – not applicable
SD – standard deviation
SE – standard error
SRI – remedial investigation

As was done for the LDW FWM, a body weight-weighted average approach was used to develop organism weights for the EW FWM. When weights for individuals included in composite samples were available (i.e., for Dungeness crab, red rock crab, English sole, and shiner surfperch), body weight-weighted averages were developed to account for differences in individual contributions to empirical chemistry data for the composite samples. For example, larger individuals might contribute more to the empirical PCB concentration in a composite sample than do smaller individuals because mass from all individuals was composited together. Mean and SE estimates for fish (except rockfish, which were analyzed as individuals not composites) and crab weights (W_B) were calculated based on the average whole-body weight of fish or crab included in composite samples (W_C). The average whole-body weight for each fish or crab composite sample was calculated as a body weight-weighted average to account for the fact that composite samples included fish (or crab) with different weights (kg), and thus some fish (or crab) contributed more tissue mass (kg) to the composite sample than did others. The body weight-weighted average for a given composite sample was calculated using (C-3).

$$W_C = \sum_{i-1}^{n} \left(W_i \times \left(\frac{W_i}{\sum W_{i....n}} \right) \right) \qquad \text{(C-3)}$$

Where:

W_C = body weight-weighted average for a given composite sample (kg)
W_i = individual fish or crab weight from a given composite sample (kg)
n = number of individual fish or crab included in a given composite sample

Mean weights of all composite samples were then calculated using the following equation:

$$W_B = \frac{\sum W_{C...n}}{n} \qquad \text{(C-4)}$$

Where:

W_B = mean wet weight for a given species of fish or crab (weight of biota) (kg)
W_C = body weight-weighted average for a given composite sample (kg)

n = number of fish or crab composite samples

The number of samples (individuals and composites) is indicated in the source notes column of Table C.2-5. As with earlier parameter tables, the initial nominal values, distribution used for calibration, and information sources are provided. The invertebrate absorption efficiencies were applied to all modeled invertebrates (other than plankton), and the fish absorption efficiencies were applied to modeled fish (Table C.2-5). EW data on juvenile fish, or a reasonable surrogate, were not available, so values developed for the LDW FWM were used for juvenile fish parameters.

The species-specific dietary fractions for the modeled species are presented in Table C.2-6. The sum of the nominal values for all dietary components for any given modeled species does not necessarily equal one. The dietary fractions for each species were normalized to one in the dietary matrix in the FWM.[8] For species that were also included in the LDW FWM (i.e., zooplankton, benthic invertebrates, juvenile fish, Dungeness crab, shiner surfperch, and English sole), the same initial dietary distributions were used for the EW FWM.

Table C.2-6
Species-Specific Dietary Fraction Distributions Used to Calibrate the EW FWM

Prey Item by Consumer	Distribution Type	Nominal Value (fraction)	Distribution Value (fraction)[a]	Rationale and Source[b]
Zooplankton				
Phytoplankton/ algae	na	1	na	Due to a lack of empirical information, best professional judgment was used. It was assumed that the portion of carnivorous zooplankton in the EW is insignificant as compared to planktivores.
Benthic Invertebrates				
Sediment solids	triangular	0.79	mode = 0.79 mean = 0.78 min = 0.62 max = 0.93	Barnes and Mann (1980); California Academy of Sciences (2002); Cruz-Rivera and Hay (2001); Fauchald and Jumars (1979); Harbo (2001); Jensen (1995); Kozloff (1983); MarLIN (2002, 2004, 2005); Museum Victoria (1996); Palaeos (2004); Ricketts et al. (1985); Shimek (2003, 2004); Word (1990)
Phytoplankton/ algae	triangular	0.16	mode = 0.16 mean = 0.14 min = 0.06 max = 0.21	

[8] During the filtering of model runs, model runs with normalized dietary fractions that fell outside the maximum and minimum values specified in Table C.2-6 were discarded.

Prey Item by Consumer	Distribution Type	Nominal Value (fraction)	Distribution Value (fraction)[a]	Rationale and Source[b]
Zooplankton	triangular	0.05	mode = 0.05 mean = 0.08 min = 0.01 max = 0.17	
Clams				
Sediment solids	triangular	0.15	mode = 0.15 mean = 0.23 min = 0.05 max = 0.50	Bivalves rely almost entirely on phytoplankton for their diet. Given that the dominant clams in EW were butter and littleneck (and softshell clam in one small area), the focus should be on the feeding behavior of the clams collected, which feed from the water column (i.e. they are filter feeders). Note that the ranges overlap with those used for the LDW for softshell clam. Barnes (1980); Schink (1983)
Phytoplankton/ algae	triangular	0.80	mode = 0.80 mean = 0.75 min = 0.50 max = 0.95	
Zooplankton	triangular	0.05	mode = 0.05 mean = 0.05 min = 0 max = 0.10	
Shrimp				
Sediment solids	triangular	0.05	mode = 0.05 mean = 0.1 min = 0.05 max = 0.20	The diet of *Pandalus danae* (coonstripe shrimp) is mostly benthic polychaetes, but they will consume remains from crab predation of clams. Shrimp may also consume large jellyfish on a seasonal basis, but jellyfish are assumed to not make a large contribution to their overall diet (Jensen 2011). ADF&G (1985)
Zooplankton	triangular	0.05	mode = 0.05 mean = 0.17 min = 0.05 max = 0.50	
Benthic invertebrates	triangular	0.80	mode = 0.80 mean = 0.33 min = 0.10 max = 0.80	
Clams		0.10	mode= 0.10 mean=0.27 min=0.10 max=0.60	
Juvenile Fish				
Sediment solids	triangular	0	mode = 0 mean =0 min = 0 max = 0.01	Fresh et al. (1979); Miller et al. (1977); Wingert et al. (1979)
Zooplankton	triangular	0.5	mode = 0.5 mean = 0.56 min = 0.30 max = 0.87	
Benthic invertebrates	triangular	0.5	mode = 0.5 mean = 0.44 min = 0.13 max = 0.70	

Prey Item by Consumer	Distribution Type	Nominal Value (fraction)	Distribution Value (fraction)[a]	Rationale and Source[b]
Red Rock Crab				
Sediment solids	triangular	0	mode = 0 mean = 0.02 min = 0 max = 0.05	Per Jensen (2011), red rock crab are voracious predators, feeding on clams, mussels, barnacles, juvenile crab. Orensanz and Galluci (1988) also claim that red rock crabs eat clams and polychaetes. Red rock crabs select rocky outcroppings and hard substrate (gravel, rock, shell, hard-packed sand), though crabs living under piers would consume mostly mussels. Note that mussels are not included in the model.
Zooplankton	triangular	0.04	mode = 0.04 mean = 0.05 min = 0 max = 0.10	
Benthic invertebrates	triangular	0.25	mode = 0.25 mean = 0.23 min = 0.05 max = 0.40	
Clams		0.70	mode = 0.70 mean = 0.68 min = 0.50 max = 0.85	
Juvenile fish	na	0.01	na	
Dungeness Crab				
Sediment solids	triangular	0	mode = 0 mean = 0.02 min = 0 max = 0.05	Stevens et al. (1982); Gotshall (1977)
Zooplankton	triangular	0.48	mode = 0.48 mean = 0.39 min = 0 max = 0.68	
Benthic invertebrates	triangular	0.16	mode = 0.16 mean = 0.39 min = 0.16 max = 0.84	
Juvenile fish	triangular	0.36	mode = 0.36 mean = 0.37 min = 0.16 max = 0.58	
Shiner Surfperch				
Sediment solids	triangular	0.01	mode = 0.01 mean = 0.01 min = 0 max = 0.01	Fresh et al. (1979); Miller et al. (1977); Wingert et al. (1979)
Zooplankton	triangular	0.35	mode = 0.35 mean = 0.41 min = 0.15 max = 0.72	
Benthic invertebrates	triangular	0.64	mode = 0.64 mean = 0.59 min = 0.28 max = 0.85	

Prey Item by Consumer	Distribution Type	Nominal Value (fraction)	Distribution Value (fraction)[a]	Rationale and Source[b]
English Sole				
Sediment solids	triangular	0.01	mode = 0.01 mean = 0.04 min = 0 max = 0.10	Fresh et al. (1979); Wingert et al. (1979)
Phytoplankton	triangular	0.06	mode = 0.06 mean = 0.07 min = 0.05 max = 0.10	
Zooplankton	triangular	0.05	mode = 0.05 mean = 0.05 min = 0 max = 0.09	
Benthic Invertebrates	triangular	0.88	mode = 0.88 mean = 0.88 min = 0.86 max = 0.90	
Brown Rockfish				
Sediment solids	triangular	0.01	mode = 0.01 mean = 0.007 min = 0 max = 0.01	Diet developed based on approximate averages for prey fractions from Wingert et al.(1979); Stein and Hassler (1989); Hueckel and Buckley (1987), and Washington et al. (1978). Also considered the size of the prey items in studies compared to modeled prey species size. More emphasis was placed on the shrimp portion of diet than crab, as shrimp were used as a surrogate for small crab since the EW modeled crab are probably larger than would be typically consumed by rockfish).
Benthic invertebrates	triangular	0.05	mode = 0.05 mean = 0.55 min = 0.019 max = 0.095	
Shrimp	triangular	0.45	mode = 0.45 mean = 0.34 min = 0.10 max = 0.47	
Juvenile fish	triangular	0.25	mode = 0.25 mean = 0.22 min = 0.024 max = 0.38	
Red rock crab	triangular	0.25	mode = 0.25 mean = 0.38 min = 0.045 max = 0.858	

[a] Triangular distributions were used for all dietary parameters in model calibration. The minimum, maximum and mode were determined based on rationale and sources in the fifth column. The mean was estimated from these values using the Equation C-1 in Section C.2.3.

[b] Preliminary dietary prey and portions were determined for calibration of the FWM based on site- and regional-specific data whenever possible; however, dietary prey and portions for use in the ecological risk assessment may be slightly different because the diets used for the ecological risk assessment are intended to be health protective and can only include prey for which empirical data are available.

ADF&G – Alaska Department of Fish and Game

EW– East Waterway

LDW – Lower Duwamish Waterway

na – not applicable

C.2.4 Calibration

Calibration is a process of deriving a set of parameter values that optimizes the ability of the FWM to estimate total PCB concentrations in tissue that match empirical data from the EW as closely as possible. This process is important because proper calibration will improve the FWM's performance in estimating RBTCs in sediment. However, improving the ability of the model to match empirical data does not necessarily mean that the "true" values for each parameter have been identified. Numerous combinations of parameters can result in similar estimates of tissue concentrations. The fact that a model has the ability to accurately estimate concentrations using the calibration dataset does not necessarily indicate that the model will accurately predict actual concentrations under all conditions.

C.2.4.1 Methods

The FWM was calibrated probabilistically in order to systematically explore the plausible combinations of parameter values and their ability to estimate empirical data. The calibration process involved three steps:

1. Monte Carlo simulation
2. Model performance filtering
3. Identification of the best-fit parameter set

Each step is discussed in detail in the following subsections.

C.2.4.1.1 Monte Carlo simulation

The FWM was run probabilistically in Excel® with Crystal Ball® software. For each of the thousands of Monte Carlo simulations, parameter values were randomly selected from the parameter probability distributions described in Section C.2.3. The resulting set of parameter values selected in each model run is termed a "parameter set."[9] Each parameter set yielded an estimate of total PCB concentrations in the tissue of the modeled species.

During the Monte Carlo simulation, the probability distributions of dietary items for each species were treated as independent random variables, which meant that the sum of the

[9] Point estimates were assigned for some parameters so that the same value was selected for that parameter for each Monte Carlo simulation.

dietary fractions had to be normalized (because dietary fractions must sum to 1). Dietary fractions for each species in the FWM were normalized by dividing each dietary fraction by the sum of all dietary fractions for a given species. Treating the dietary fractions as independent random variables greatly simplified the Monte Carlo simulation. However, as a consequence, the normalized dietary fractions for some parameter sets fell outside of their specified probability distributions. The easiest way to address this issue was to apply a diet filter. Therefore, the last action taken in the Monte Carlo simulation step was to discard parameter sets if any of the normalized dietary fractions fell outside of their assigned ranges as defined in Table C.2-6. This step was a bookkeeping step, the only effect of which was to correct for an artifact of the way dietary fractions were defined.

C.2.4.1.2 Model performance filtering

Model performance filtering is a two step process of comparing estimated total PCB concentrations in tissue with available empirical data (i.e., total PCB concentrations detected in species collected in the EW). Typically FWM are considered to be performing well if the predictions are within a factor of three to five of the empirical data. However, because the EW FWM was performing better than this for all target tissues except clams, a difference great than a factor of two or less was selected for all target tissues except clams, which were targeted at three or less. Therefore, in the first filtering step, the parameter sets that resulted in estimated concentrations that were outside specified bounds for empirical data (i.e., a difference greater than a factor of two[10]) were rejected. The remaining parameter sets were retained for use in the second step of filtering and also in the sensitivity and uncertainty analyses. The total PCB mean concentration and standard deviation as well as sample size of the empirical dataset for PCB concentrations in EW tissues for each target species used in model calibration are presented in Table C.2-7. Additional details on these datasets can be found in Section 4 of the SRI.

[10] This criterion was applied to all species except clams. For clams, performance within a factor of 3 was considered acceptable.

Table C.2-7
Empirical Tissue Concentrations of Total PCBs in Target Species

Species	Mean Concentration (µg/kg ww)	Standard Deviation (µg/kg ww)	Sample Size
Benthic invertebrates	210	82	13 composites
Clams	56	24	11 composites
Shrimp	460	na	1 composite
Red rock crab	240	38	8 composites
Dungeness crab	860	na	1 composite
Shiner surfperch	1,500	1,400	11 composites
English sole	3,200	1,700	13 composites
Brown rockfish	2,000	1,700	15 individuals

PCB – polychlorinated biphenyl
ww – wet weight

Model estimates were compared with mean concentrations of total PCBs from composite samples of target species collected from the EW. Mean total PCB tissue concentrations were used rather than single composite sample values because the biological compartments in the FWM were assumed to represent populations, not individual organisms. No empirical data existed for phytoplankton, zooplankton, or juvenile fish, so the model was not calibrated for those species.

A species predictive accuracy factor (SPAF) was selected as the metric for model performance evaluation (i.e., to quantitatively compare model estimates and empirical data). The SPAF is the ratio of estimated to empirical total PCB concentrations in tissue for a given species, or the inverse of that ratio, whichever is greater (i.e., the SPAF will always be a number greater than 1). Accordingly, if the estimated concentration was greater than the empirical concentration, Equation C-5 was used to calculate the SPAF:

$$SPAF = \frac{C_M}{C_E} \qquad \text{(C-5)}$$

Where:

CM = model-estimated total PCB concentration in tissue (µg/kg ww)
CE = mean empirical total PCB concentration in tissue (µg/kg ww)

If the estimated concentration was less than empirical concentration, the reciprocal ratio (Equation C-6) was used:

$$SPAF = \frac{C_E}{C_M} \quad \text{(C-6)}$$

A perfect correlation between model-estimated and mean empirical concentrations would result in a SPAF of 1. Any difference between the model-estimated and mean empirical tissue concentrations would result in a SPAF > 1.

To meet the selected model performance criterion, SPAFs had to be < 2 for all species except clams. For clams, SPAFs < 3 were considered acceptable. If the SPAF of any species was > 2 (or > 3 for clams), the corresponding parameter set was rejected. The criteria applied to EW FWM performance were similar to that used for the LDW FWM (i.e., a SPAF < 2 for all species). The SPAF for clams was different because EW PCB concentrations in clams were much lower than those for other modeled EW species and because clams contribute a small portion to the overall risk associated with the consumption of seafood. Also, as discussed previously, model performance within a factor of three is considered good.

In order to understand a model performance assessment, it is important to understand the metric used. If a model run has a SPAF of X, the model's estimate differs from the empirical data with which it is being compared by a factor of X. Thus, model estimates with equal distance but opposite direction from an empirical data point (e.g., ±100 µg/kg ww from a mean concentration) will have different SPAFs, with the overestimate always having a higher SPAF. For example, if the mean empirical total PCB concentration in shiner surfperch tissue is 1,500 µg/kg ww, and for one parameter set the model estimate is 2,000 µg/kg ww (i.e., 500 µg/kg ww greater than the mean empirical concentration) and for another parameter set the model estimate is 1,000 µg/kg ww (i.e., 500 µg/kg ww less than the mean empirical concentration), the percent difference of both model estimates from the mean empirical tissue chemical concentration is 33.3%, but the SPAFs are 1.33 and 1.5, respectively. SPAF and percent difference metrics are both useful tools for assessing model performance.

In the second filtering step, parameter sets that met the model performance criterion (SPAF ≤ 2 for all species except clam) were visually checked to filter relationships among

parameters not expected to be found in nature. Such combinations could occur by chance during Monte Carlo sampling. None of the parameter sets that met the model performance criterion were excluded based on this review.

C.2.4.1.3 Identification of the best-fit parameter set

The final step in the FWM calibration was to identify the parameter set that produced estimates most similar to the empirical data (i.e., mean total PCB concentrations in tissue). To identify this parameter set, the average SPAF across species was calculated for each parameter set that passed the model performance filter. Parameter sets were then sorted by average SPAF across species, and the sets with the 10 lowest average SPAFs were identified. Of these, the run that had the fewest underpredictions (by species) and had the lowest SPAFs for the species contributing the most to risk (English sole, perch, and crabs) was selected as the "best–fit" calibrated model.

C.2.4.2 Results

The calibration process identified FWM parameter sets in Table C.2-8 that estimated total PCB concentrations for all species within a factor of 2 of empirical data (i.e., SPAF ≤ 2 except for clams). The mean SPAF across species for parameter sets that passed the model performance criterion was 1.7. The SPAF for the selected best-fit parameter set was 1.4 (i.e. the lowest average SPAF associated with a single set of model parameters), with more species overpredicted than underpredicted. Empirical data were not available for total PCB concentrations in phytoplankton, zooplankton, and juvenile fish tissue and, hence, these species were not included in the tabulated summary of model performance.

Table C.2-8
Summary of Model Performance

Species	SPAFs from Parameter Sets that Passed the Model Performance Filter				LDW Calibrated Model SPAFb,c
	Closest to Empirical (by species)[a]	Greatest Underprediction (by species)[a]	Greatest Overprediction (by species)[a]	Best Fit[b] (for all species)	
Benthic invertebrate	1.2	na	1.7	1.6	1.5
Clams	1.5	na	3.0	2.1	na[d]
Shrimp	1.0	**1.8**	1.9	1.3	na
Red rock crab	1.0	**1.3**	2.0	1.0	na
Dungeness crab	1.0	**1.8**	2.0	1.0	1.1

Species	SPAFs from Parameter Sets that Passed the Model Performance Filter				LDW Calibrated Model SPAFb,c
	Closest to Empirical (by species)[a]	Greatest Underprediction (by species)[a]	Greatest Overprediction (by species)[a]	Best Fit[b] (for all species)	
Shiner surf perch	1.0	**1.5**	1.2	1.0	**1.2**
English sole	1.6	**2.0**	na	**1.6**	1.1
Brown rockfish	1.0	**1.1**	1.8	1.3	na
Average SPAF[e]	1.2	**1.6**	1.9	1.4	1.2

[a] The values in these columns (except the average SPAFs) are based on the set of model parameters which yielded the closest to empirical, greatest underprediction, or greatest overprediction of the empirical average for each species (i.e. each column contains SPAFs based on multiple sets of model parameters; these are not based on single model runs).

[b] All the values in this column (including the average across species) are based model predictions from the same set of model parameters.

[c] LDW FWM (Windward 2010).

[d] Clams were included in the LDW FWM, but no SPAF was reported.

[e] The average SPAF listed here is the average of the values listed above. Therefore only the values in "Best Fit" and "LDW Calibrated Model" columns are calculated based on model predictions from a single set of model parameters. Averages (except minimum underprediction and maximum overprediction averages) are based on averages of over- and underpredictions.

na – not applicable

SPAF – species predictive accuracy factor

Bold indicates an underprediction.

Overall, the SPAFs indicate the FWM performed very well with most average tissue predictions being within a factor of two of the empirical mean concentrations. Estimated total PCB concentrations in fish and crab tissue associated with the best-fit parameter set were generally similar to mean empirical data for each species (Figure C.2-2). FWM estimates for English sole had the greatest differences from the mean empirical data compared to other fish and crab species (e.g. SPAF of 1.6 in Table C.2-8). Using a best-fit parameter set, PCB concentrations in English sole were underpredicted compared with empirical data; they also showed the highest underprediction of all species (Table C.2-8). Possible reasons for the underprediction of English sole PCB concentrations are discussed in Section C.2.5.2. Most of the benthic invertebrate and clam tissue concentrations estimated by the FWM were higher than the mean empirical benthic invertebrate and clam tissue concentrations (Figure C.2-3). The possible reasons for these differences are discussed in Section 4.5.2 of the SRI.

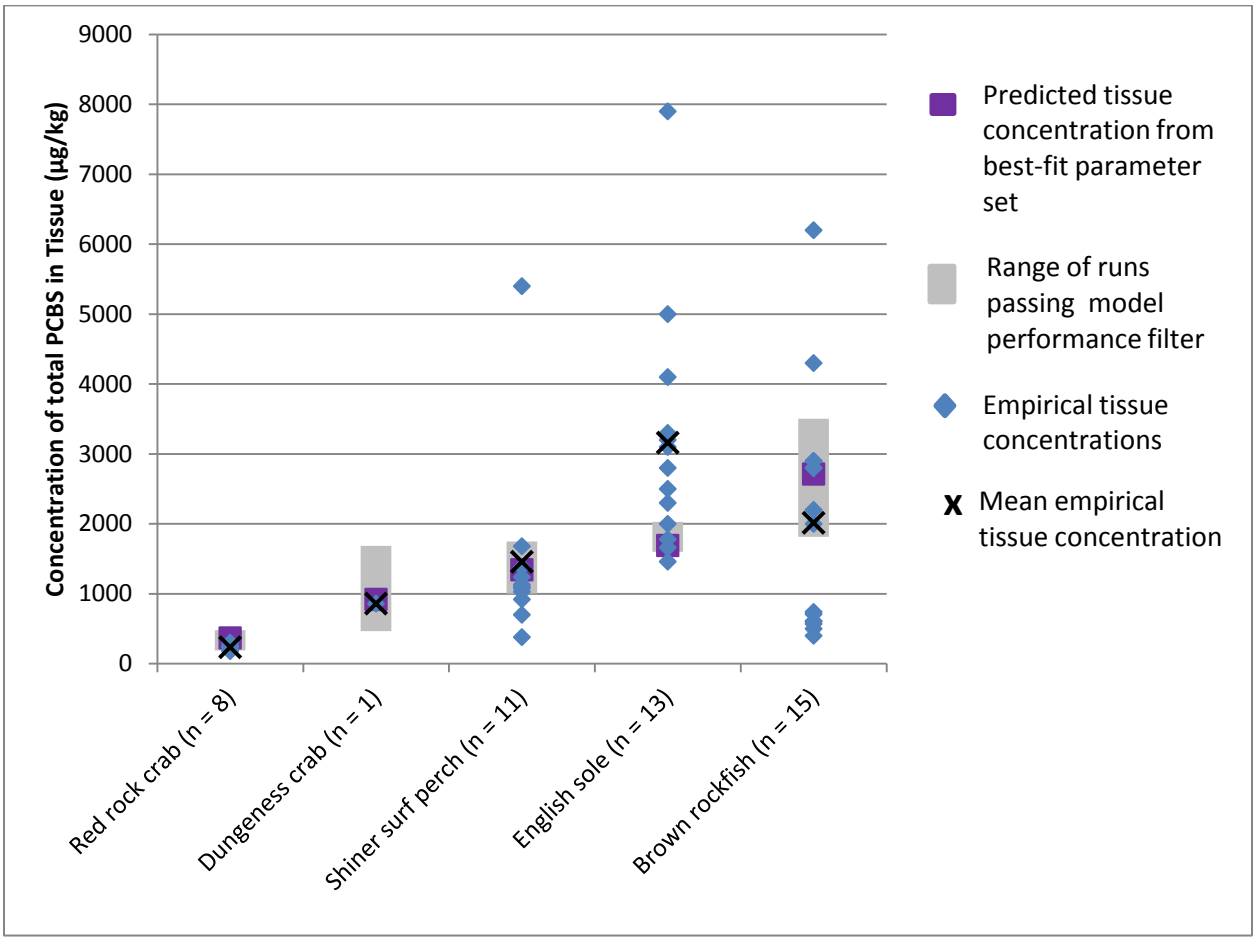


Figure C.2-2

Estimated Total PCB Concentrations in Tissues of Adult Fish and Crab Species for Parameter Sets that Passed the Model Performance Filter in the Best-Fit Model Parameter Set Relative to Empirical Data

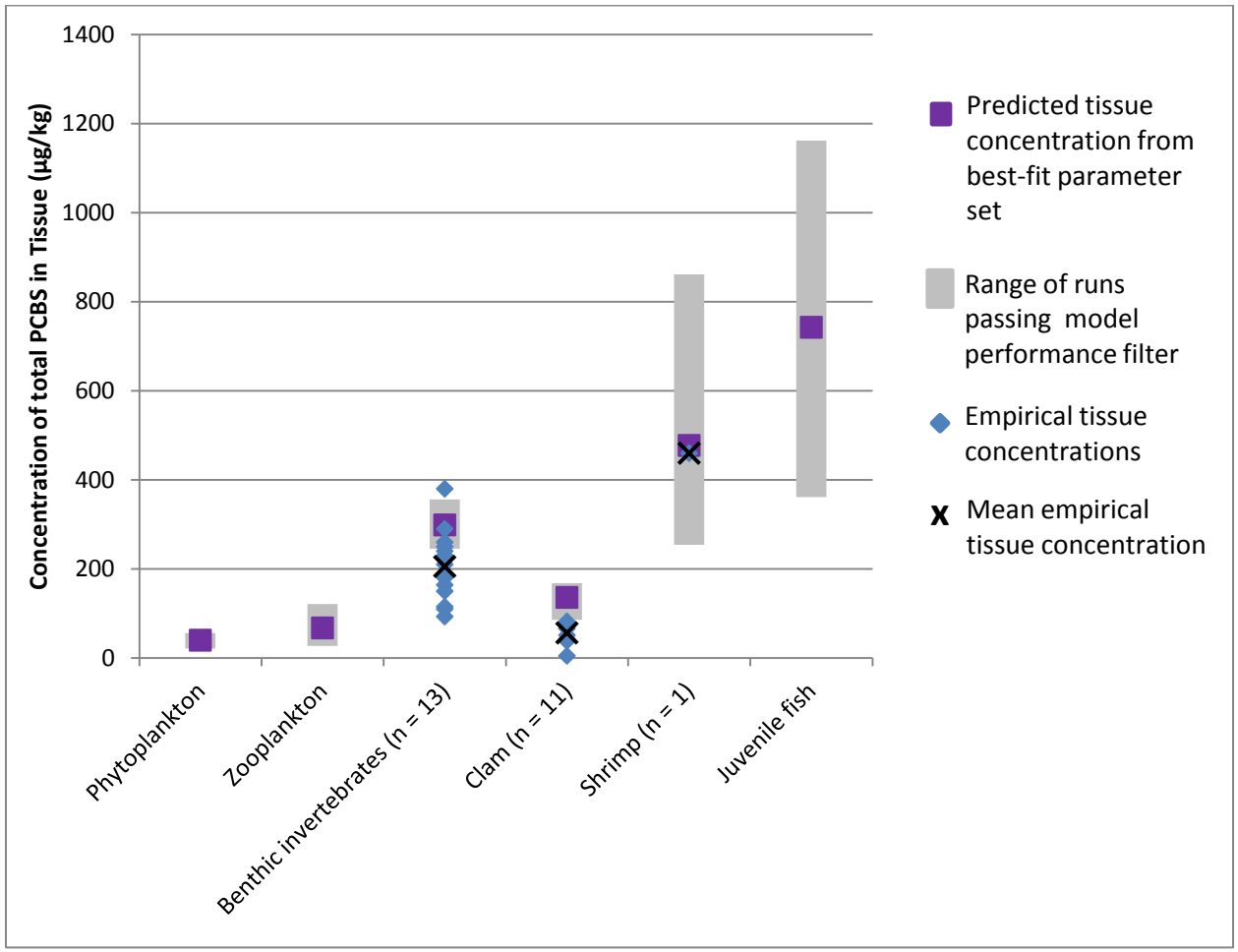


Figure C.2-3
Estimated Total PCB Concentrations in Tissues of Clam and Prey Species for Parameter Sets that Passed the Model Performance Filter in the Best-Fit Model Parameter Set Relative to Empirical Data

The calibration process rejected parameter sets that resulted in estimated tissue concentrations greater than a factor of 2 from empirical values for any species (or a factor of 3 for clams). Therefore, as part of the calibration process, parameter sets were selected (from all the parameters sets generated from the Monte Carlo model runs that provided predictions closest to empirical total PCB data.

Table C.2-9 shows the best-fit parameter values for the calibrated EW FWM. This table also presents the best-fit values from the LDW FWM (Windward 2010) for those parameters common to both models. Many of the differences in calibrated parameter values between the two models are the result of the differences in empirical data used for calibration (e.g., water

temperature, English sole weights, Kow). It is noteworthy that the total PCB concentration in sediment, which was not calibrated, was higher for the EW (470 µg/kg dw) than for the LDW (380 µg/kg dw). Mean empirical tissue concentrations were higher in the EW than LDW for some species (i.e., clams and English sole) and higher in the LDW than EW for others species (i.e., Dungeness crab and shiner surfperch) (Windward 2010). The EW FWM was also calibrated for four additional species (clams, shrimp, rockfish, and red rock crab in the EW instead of slender crab in the LDW FWM).

Table C.2-9
Best-Fit Parameter Set for the Calibrated Model

Parameter Description	Unit	EW Best-Fit Parameter Set	LDW Best-Fit Parameter Set[a]
Environmental Parameters			
Concentration of total PCBs in the water column	ng/L	1.16	1.22
Concentration of POC in the water column	kg/L	1.2×10^{-7}	2.3×10^{-7}
Concentration of DOC in the water column	kg/L	1.7×10^{-6}	2.2×10^{-6}
Mean water temperature	°C	10.1	11.0
Concentration of total suspended solids in the water column	kg/L	3.6×10^{-6}	5.4×10^{-6}
Concentration of total PCBs in sediment[b]	µg/kg dw	470	380
Sediment total organic carbon	unitless	0.014	0.0191
Chemical Parameters			
Octanol-water partition coefficient for total PCBs (log Kow)	kg/L	6.7	6.5
Biological Parameters			
Proportionality constant expressing the sorption capacity of NLOM relative to that of octanol (β)	unitless	0.035	0.031
Resistance to chemical uptake through aqueous phase for phytoplankton/ algae (A)	unitless	6×10^{-5}	6×10^{-5}
Resistance to chemical uptake through organic phase for phytoplankton/ algae (B)	unitless	5.5	6.2
Phytoplankton			
Lipid content of organism	fraction	0.0009	0.0014
Water content of organism	fraction	0.96	0.96
Zooplankton			
Organism weight	kg	1.2×10^{-7}	2.2×10^{-7}
Lipid content	fraction	0.011	0.014
Water content of organism	fraction	0.88	0.92
Dietary absorption efficiency of lipids (ε_L)	unitless	0.61	0.66

Parameter Description	Unit	EW Best-Fit Parameter Set	LDW Best-Fit Parameter Set[a]
Dietary absorption efficiency of NLOM (εN)	unitless	0.76	0.72
Dietary absorption efficiency of water	unitless	0.55	na
Benthic Invertebrates			
Organism weight	kg	6.9×10^{-5}	4.1×10^{-5}
Lipid content	fraction	0.0062	0.0083
Water content of organism	fraction	0.75	0.82
Relative fraction of porewater ventilated	unitless	0.21	0.13
Dietary absorption efficiency of lipids (εL)	unitless	0.74	0.30
Dietary absorption efficiency of NLOM (εN)	unitless	0.77	0.56
Dietary absorption efficiency of water	unitless	0.55	na
Benthic Invertebrate Filter Feeder (clam)			
Organism weight	kg	0.014	na
Lipid content	fraction	0.0059	na
Water content of organism	fraction	0.86	na
Relative fraction of porewater ventilated	unitless	0.10	na
Dietary absorption efficiency of lipids (εL)	unitless	0.45	na
Dietary absorption efficiency of NLOM (εN)	unitless	0.37	na
Dietary absorption efficiency of water	unitless	0.55	na
Shrimp			
Organism weight	kg	0.0058	na
Lipid content	fraction	0.0079	na
Water content of organism	fraction	0.70	na
Relative fraction of porewater ventilated	unitless	0.017	na
Dietary absorption efficiency of lipids (εL)	unitless	0.63	na
Dietary absorption efficiency of NLOM (εN)	unitless	0.95	na
Dietary absorption efficiency of water	unitless	0.55	na
Juvenile Fish			
Organism weight	kg	0.0048	0.006
Lipid content	fraction	0.030	0.015
Water content of organism	fraction	0.75	0.74
Relative fraction of porewater ventilated	unitless	0.013	0.01
Dietary absorption efficiency of lipids (εL)	unitless	0.91	0.92
Dietary absorption efficiency of NLOM (εN)	unitless	0.56	0.54
Dietary absorption efficiency of water	unitless	0.55	na
Red Rock Crab			
Organism weight	kg	0.41	na

Parameter Description	Unit	EW Best-Fit Parameter Set	LDW Best-Fit Parameter Set[a]
Lipid content	fraction	0.0081	na
Water content of organism	fraction	0.83	na
Relative fraction of porewater ventilated	unitless	0.021	na
Dietary absorption efficiency of lipids (εL)	unitless	0.26	na
Dietary absorption efficiency of NLOM (εN)	unitless	0.39	na
Dietary absorption efficiency of water	unitless	0.55	na
Dungeness Crab			
Organism weight	kg	0.45	0.653
Lipid content	fraction	0.018	0.034
Water content of organism	fraction	0.90	0.81
Relative fraction of porewater ventilated	unitless	0.027	0.02
Dietary absorption efficiency of lipids (εL)	unitless	0.67	0.71
Dietary absorption efficiency of NLOM (εN)	unitless	0.74	0.59
Dietary absorption efficiency of water	unitless	0.55	na
Shiner Surfperch			
Organism weight	kg	0.019	0.019
Lipid content	fraction	0.046	0.046
Water content of organism	fraction	0.73	0.74
Relative fraction of porewater ventilated	unitless	0.011	0.02
Dietary absorption efficiency of lipids (εL)	unitless	0.92	0.94
Dietary absorption efficiency of NLOM (εN)	unitless	0.58	0.56
Dietary absorption efficiency of water	unitless	0.55	na
English Sole			
Organism weight	kg	0.14	0.246
Lipid content	fraction	0.037	0.055
Water content of organism	fraction	0.78	0.75
Relative fraction of porewater ventilated	unitless	0.016	0.1
Dietary absorption efficiency of lipids (εL)	unitless	0.93	0.92
Dietary absorption efficiency of NLOM (εN)	unitless	0.64	0.59
Dietary absorption efficiency of water	unitless	0.55	na
Brown Rockfish			
Organism weight	kg	0.27	na
Lipid content	fraction	0.032	na
Water content of organism	fraction	0.72	na
Relative fraction of porewater ventilated	unitless	0.011	na
Dietary absorption efficiency of lipids (εL)	unitless	0.93	na

Parameter Description	Unit	EW Best-Fit Parameter Set	LDW Best-Fit Parameter Set[a]
Dietary absorption efficiency of NLOM (εN)	unitless	0.56	na
Dietary absorption efficiency of water	unitless	0.55	na
Dietary Fraction			
Benthic Invertebrates			
Sediment	fraction	0.88	0.70
Phytoplankton	fraction	0.074	0.18
Zooplankton	fraction	0.044	0.12
Benthic Invertebrate Filter Feeders (clams)			
Sediment	fraction	0.16	na
Phytoplankton	fraction	0.77	na
Zooplankton	fraction	0.073	na
Shrimp			
Sediment	fraction	0.14	na
Zooplankton	fraction	0.29	na
Benthic invertebrates	fraction	0.34	na
Benthic invertebrate filter feeders (clams)	fraction	0.23	na
Juvenile Fish			
Sediment	fraction	0.0015	0.00
Zooplankton	fraction	0.61	0.53
Benthic invertebrates	fraction	0.39	0.47
Red Rock Crab			
Sediment	fraction	0.029	na
Zooplankton	fraction	0.021	na
Benthic invertebrates	fraction	0.18	na
Benthic invertebrate filter feeders(clams)	fraction	0.76	na
Juvenile fish	fraction	0.010	na
Dungeness Crab			
Sediment	fraction	0.015	0.00
Zooplankton	fraction	0.41	0.37
Benthic invertebrates	fraction	0.33	0.24
Juvenile fish	fraction	0.24	0.39
Shiner Surfperch			
Sediment	fraction	0.0080	0.00
Zooplankton	fraction	0.35	0.23
Benthic invertebrates	fraction	0.64	0.76

Parameter Description	Unit	EW Best-Fit Parameter Set	LDW Best-Fit Parameter Set[a]
English Sole			
Sediment	fraction	0.033	0.04
Phytoplankton	fraction	0.061	0.05
Zooplankton	fraction	0.032	0.05
Benthic invertebrates	fraction	0.87	0.86
Brown Rockfish			
Sediment	fraction	0.0052	na
Benthic invertebrates	fraction	0.076	na
Shrimp	fraction	0.23	na
Juvenile fish	fraction	0.32	na
Red rock crab	fraction	0.36	na

[a] As reported in Appendix D of the LDW RI (Windward 2010). Parameter set is shown for information purposes only (not used in EW FWM).

[b] Value based on surface weighted average concentration of empirical data and is not calibrated in the model.

DOC – dissolved organic carbon
dw – dry weight
LDW – Lower Duwamish Waterway
NLOM – non-lipid organic matter
PCB – polychlorinated biphenyl
POC – particulate organic carbon
RI – remedial investigation

C.2.5 Sensitivity and Uncertainty Analyses

Sensitivity and uncertainty analyses were performed to assess the sensitivity of the FWM to individual input parameters in combination with the uncertainty in the estimates of those parameters. These analyses provide insight into uncertainties in the application of FWM results.

An uncertainty analysis is an evaluation of how uncertainties in model parameters affect the reliability of the model's output both qualitatively and quantitatively. Uncertainties can be reducible (i.e., they can be eliminated by gathering more information and/or considering available information differently) or irreducible (i.e., they cannot be eliminated because there is an element of either chance or variability in the parameter's distribution, such as variability across individuals in a population or within an individual over time).

A sensitivity analysis is an evaluation of how model estimates respond to changes in input values. The greater the response to a particular change (or set of changes), the higher the sensitivity to that parameter or parameters. A sensitivity analysis can thus provide

information regarding the relative importance of uncertainties by examining their potential influence on model output.

All models are simplifications of the processes and parameters that they describe. The calibrated FWM is designed to represent, to the extent possible, the complicated relationship between sediment and tissue, including aquatic organism life histories and foraging strategies across the food web. It is important to assess potential uncertainties in the FWM so that these uncertainties can be acknowledged in the model's application. The following two sensitivity and uncertainty analyses were conducted using the best-fit parameter set and are described in this section:

- Correlation coefficient analysis
- Nominal range sensitivity (NRS) analysis

These two types of sensitivity analysis were also performed for the LDW FWM (Windward 2010).

Because the SWAC for total PCBs in sediment of the EW was not varied in the calibration (i.e., it was treated deterministically as described in Sections C.2.3.1 and C.2.5), the influence of sediment concentration on model predictions was not examined as part of the correlation coefficient and NRS analyses.

Because the SWAC is an influential input parameter and was treated deterministically, any error in the point estimate of the SWAC used in the calibration was countered by offsetting adjustments in other FWM parameters. Thus, the parameter sets identified through the calibration process were highly influenced by the SWAC. For these reasons, which underlie the importance of this parameter to FWM calibration and predictions, the sensitivity of the FWM to total PCB concentrations in sediment was investigated (see Section C.2.5.3). This same type of analysis was also performed for the LDW FWM (Windward 2010).

C.2.5.1 Correlation Coefficient Analysis

Pearson product-moment correlation coefficients (r-values) were calculated to characterize the strength of the correlations between each FWM parameter and estimated total PCB concentrations in tissues. For each parameter, the absolute values of the correlation coefficients were averaged across all species in the FWM to provide a general sense of the

degree of covariance between a given parameter and predicted total PCB concentrations in the tissue of all species combined. The 20 parameters that correlated most strongly with tissue concentration estimates (i.e., had the highest average absolute r-values) were carried forward into the NRS analysis. Parameters for which correlations were lower were not evaluated further because they had a relatively low influence on model estimates.

Because the correlation coefficient analysis used output from the Monte Carlo runs, it accounted for parameter interactions as opposed to univariate analyses, which hold all other parameter values constant while changing the value for one parameter at a time. The NRS (Section C.2.5.2) is a univariate analysis. Because the correlation analysis incorporated parameter interactions, it was the most suitable analysis for identifying the 20 most important parameters.

The 20 parameters with the highest average absolute value correlation coefficients across species are presented in Table C.2-10. A positive correlation indicates that an increase in a parameter value led to an increase in estimated total PCB concentrations in tissue for a given species. A negative correlation indicates that an increase in a parameter value led to a decrease in the estimated concentrations for a given species. In general, parameter values that most strongly correlated with estimates for at least one tissue type included those that:

- Affected the uptake of total PCBs by benthic invertebrates (e.g., porewater ventilation) (important for several fish species which consume benthic invertebrates)
- Affected PCB exposure in the water column, particularly the concentration of total PCBs (important for phytoplankton and zooplankton which are consumed by many other species)
- Contributed to the uptake of total PCBs, including dietary absorption efficiencies (important for crab) and lipid and moisture content (important for various species)

In general, the parameters identified through this analysis and their relative importance for the EW FWM are similar to those identified for the LDW FWM (Windward 2010).

Table C.2-10
Parameters Most Strongly Correlated with Estimated Total PCB Concentrations in Tissue

Parameter	Correlation Coefficient (r)												
	Max	Mean (absolute value)	Phyto-plankton	Zoo-plankton	Benthic Inverte-brates	Clams	Shrimp	Juvenile Fish	Red Rock Crab	Dungeness Crab	Shiner Surf Perch	English Sole	Brown Rockfish
Benthic invertebrate porewater ventilation	0.87	0.39	-0.01	-0.01	**0.87**	-0.01	0.31	0.50	0.19	0.32	0.75	0.84	0.47
Concentration in water (ng/L)	0.83	0.26	**0.83**	0.58	0.10	0.13	0.09	0.26	0.11	0.14	0.25	0.13	0.21
Sediment OC	-0.28	0.18	-0.01	-0.01	-0.27	**-0.28**	-0.15	-0.16	-0.18	-0.11	-0.24	-0.26	-0.25
Clam porewater ventilation	0.91	0.16	0.00	0.00	0.00	**0.91**	0.12	0.00	0.36	0.02	0.01	0.00	0.28
Zooplankton lipids	0.76	0.10	0.01	**0.76**	-0.05	-0.01	-0.04	0.11	-0.04	-0.03	0.06	-0.04	0.00
Juvenile fish lipids	0.67	0.10	0.02	0.01	0.02	0.00	0.02	**0.67**	0.03	0.09	0.02	0.02	0.18
Red rock crab lipid absorption efficiency	0.58	0.09	-0.01	-0.02	0.01	-0.01	0.00	0.01	**0.58**	0.00	0.00	0.01	0.37
Red rock crab NLOM absorption efficiency	0.47	0.08	0.00	0.01	0.02	-0.01	0.01	0.02	**0.47**	0.00	0.02	0.02	0.30
Benthic invertebrate lipids	0.27	0.08	-0.01	0.00	**0.27**	0.00	0.04	0.10	0.02	0.05	0.15	0.12	0.06
Benthic invertebrate moisture	-0.29	0.07	0.01	0.01	**-0.29**	0.01	-0.04	-0.10	-0.02	-0.05	-0.15	-0.10	-0.06
K_{OW}	0.20	0.07	0.11	**0.20**	0.01	-0.03	0.07	0.10	0.02	0.05	0.06	0.03	0.09
Phytoplankton moisture	-0.53	0.07	**-0.53**	-0.11	0.01	0.01	0.00	-0.04	0.01	0.00	-0.02	0.01	-0.01
Conc suspended solids	0.13	0.07	-0.01	-0.01	**0.13**	0.07	0.06	0.06	0.04	0.04	0.10	0.13	0.08
Dungeness crab lipid absorption efficiency	0.66	0.07	-0.02	-0.02	0.00	0.01	0.00	0.00	0.00	**0.66**	-0.01	0.00	0.01
Shrimp lipid absorption efficiency	0.45	0.07	-0.01	0.00	-0.01	0.01	**0.45**	0.00	0.01	0.00	-0.01	-0.01	0.20
Juvenile fish moisture	-0.45	0.06	-0.02	-0.01	-0.01	0.01	-0.01	**-0.45**	-0.01	-0.06	-0.01	-0.01	-0.09

Parameter	Correlation Coefficient (r)												
	Max	Mean (absolute value)	Phyto-plankton	Zoo-plankton	Benthic Inverte-brates	Clams	Shrimp	Juvenile Fish	Red Rock Crab	Dungeness Crab	Shiner Surf Perch	English Sole	Brown Rockfish
Juvenile fish consumption of zooplankton	-0.32	0.06	0.01	0.02	0.01	0.01	0.00	**-0.32**	-0.01	-0.13	0.01	0.01	-0.12
Juvenile fish consumption of benthic invertebrates	0.32	0.06	-0.01	-0.02	-0.01	-0.01	0.00	**0.32**	0.01	0.13	-0.01	-0.01	0.12
Shrimp NLOM absorption efficiency	0.40	0.06	0.00	0.01	0.01	0.01	**0.40**	0.01	0.00	0.00	0.01	0.01	0.18
Red rock crab lipids	0.38	0.06	0.01	0.00	0.00	0.02	0.00	0.00	**0.38**	0.01	0.01	0.00	0.19

NLOM – non-lipid organic matter
K_{OW} – octanol-water partition coefficient
r – correlation coefficient
OC – organic carbon
PCB – polychlorinated biphenyl
Bold identifies the maximum correlation for each parameter.

C.2.5.2 Nominal Range Sensitivity Analysis

In the NRS analysis, the input values for each of the top 20 parameters from Table C.2-10 were varied, one at a time, from their minimum to their maximum values, while all other FWM parameters were held at their best-fit values.[11] Minimum and maximum parameter values were identified in the sets that passed the model performance filter for each of the top 20 parameters (Table C.2-11). In general, the tighter the range in Table C.2-11, the more sensitive the model is to a given parameter.

Table C.2-11
Minimum and Maximum Values for Each Parameter Evaluated in the NRS

Parameter	Unit	Value from Parameter Sets that Passed Model Performance Filter[a]	
		Minimum	Maximum
Benthic invertebrate porewater ventilation	unitless	0.150	0.250
Concentration of PCBs in water	ng/L	0.852	1.773
Sediment OC content	unitless	0.0128	0.0191
Clam porewater ventilation	unitless	0.057	0.219
Zooplankton lipids	fraction	0.0037	0.0201
Juvenile fish lipids	fraction	0.0091	0.0441
Red rock crab lipid absorption efficiency	fraction	0.16	0.94
Red rock crab NLOM absorption efficiency	fraction	0.18	0.93
Benthic invertebrate lipids	fraction	0.0052	0.0075
Benthic invertebrate moisture	fraction	0.703	0.801
K_{OW}	kg/L	6.586	6.798
Phytoplankton moisture content	fraction	0.94334	0.97342
Concentration of PCBs in suspended solids	kg/L	1.3×10^{-6}	4.5×10^{-6}
Dungeness crab lipid absorption efficiency	fraction	0.17	0.91

[11] Nominal range sensitivity analysis is conventional terminology, but this analysis can also be referred to as an uncertainty analysis because it provides information about how uncertainties in model parameters affect the reliability of the model's output. The term "sensitivity" was adopted for this section to emphasize the comparative nature of the analysis.

Parameter	Unit	Value from Parameter Sets that Passed Model Performance Filter[a]	
		Minimum	Maximum
Shrimp lipid absorption efficiency	fraction	0.22	0.93
Juvenile fish moisture	fraction	0.668	0.794
Juvenile fish consumption of zooplankton	fraction	0.36	0.82
Juvenile fish consumption of benthic invertebrates	fraction	0.18	0.63
Shrimp NLOM absorption efficiency	fraction	0.17	0.95
Red rock crab lipids	fraction	0.0034	0.0125

[a] Performance filter: SPAF ≤ 2 for all species except clams (clam SPAF ≤ 3).

K_{OW} – octanol-water partition coefficient
NLOM – non-lipid organic matter
NRS – nominal range sensitivity
OC – organic carbon
PCB – polychlorinated biphenyl

Each of the minimum and maximum values was substituted, in turn, into the best-fit parameter set, yielding 40 new estimates of total PCB concentrations in each species' tissue. For each of the 20 parameters, NRS was calculated for each species as:

$$NRS = \left|\left(C_{Max} - C_{Min}\right)\right| \qquad \text{(C-7)}$$

Where:

C_{Max} = estimated total PCB concentration in tissue when the maximum value for the parameter being tested was substituted into the best-fit parameter set

C_{Min} = estimated total PCB concentration in tissue when the minimum value for the parameter being tested was substituted into the best-fit parameter set

A parameter's NRS value is a measure of the relative influence that parameter has on the uncertainty of FWM tissue estimates for each species. NRS values for each parameter for each species are presented in Table C.2-12. NRS values ranked by maximum NRS value across species indicate the relative potential effect of a given parameter on the uncertainty of FWM estimates. In order to understand the importance of a parameter, it is necessary to compare the NRS value to the estimated total PCB concentration for each modeled species (see bottom of Table C.2-12). This comparison provides a sense of the magnitude of the uncertainty associated with a specific parameter relative to the estimate. For example,

although the NRS value for concentration of PCBs in water is smaller in phytoplankton (26 µg/kg ww) than for Shiner surfperch (235 µg/kg ww), this parameter is proportionally more important for phytoplankton (FWM estimated total PCB concentration = 33 µg/kg ww) than Shiner surfperch (FWM estimated total PCB concentration = 1,494 µg/kg ww); the correlation coefficient for PCBs in water for phytoplankton is 0.83, while the correlation coefficient for PCBs in water for Shiner surfperch is 0.25 (Table C.2-10).

Table C.2-12
NRS Values for the Top 20 Parameters

Parameter	NRS (µg/kg ww)										
	Phyto-plankton	Zoo-plankton	Benthic Invertebrates	Clams	Shrimp	Juvenile Fish	Red Rock	Dungeness Crab	Shiner Surfperch	English Sole	Brown Rockfish
Benthic invertebrate porewater ventilation	0	0	115	0	99	188	31	205	437	**618**	539
Concentration of PCBs in water	26	48	26	22	91	201	38	196	235	183	**549**
Sediment organic carbon content	0	0	94	30	102	160	59	174	362	510	**542**
Clam porewater ventilation	0	0	0	127	73	0	134	0	0	0	**341**
Zooplankton lipids	0	61	6	0	**111**	81	5	103	40	30	11
Juvenile fish lipids	0	0	0	0	0	555	1	79	0	0	**740**
Red rock crab lipid absorption efficiency	0	0	0	0	0	0	196	0	0	0	**370**
Red rock crab NLOM absorption efficiency	0	0	0	0	0	0	127	0	0	0	**239**
Benthic invertebrate lipids	0	0	45	0	14	67	5	52	154	**207**	153
Benthic invertebrate moisture	0	0	70	0	55	63	9	65	112	74	**177**
K_{OW}	4	16	2	1	70	85	8	84	64	32	**258**
Phytoplankton moisture	17	8	0	1	6	20	1	19	15	1	**42**
Concentration of suspended solids	0	0	48	7	45	78	20	84	181	**255**	241
Dungeness crab lipid absorption efficiency	0	0	0	0	0	0	0	**892**	0	0	0

Parameter	NRS (µg/kg ww)										
	Phyto-plankton	Zoo-plankton	Benthic Invertebrates	Clams	Shrimp	Juvenile Fish	Red Rock	Dungeness Crab	Shiner Surfperch	English Sole	Brown Rockfish
Shrimp lipid absorption efficiency	0	0	0	0	411	0	0	0	0	0	**500**
Juvenile fish moisture	0	0	0	0	0	68	0	13	0	0	**98**
Juvenile fish consumption of zooplankton	0	0	0	0	0	463	7	272	0	0	**788**
Juvenile fish consumption of benthic invertebrates	0	0	0	0	0	454	7	266	0	0	**772**
Shrimp NLOM absorption efficiency	0	0	0	0	216	0	0	0	0	0	**263**
Red rock crab lipids	0	0	0	0	0	0	149	0	0	0	**221**
FWM-estimated total PCB concentrations in tissue (for reference)	**33**	**61**	**337**	**116**	**601**	**773**	**247**	**827**	**1,494**	**1,981**	**2,669**

Kow – octanol-water partition coefficient
NLOM – non-lipid organic matter
NRS – nominal range sensitivity
PCB – polychlorinated biphenyl
ww – wet weight
Bold indicates maximum NRS for that parameter.

Parameters that influenced estimates for all species were concentration of total PCBs in the water column and log K_{OW} (Table C.2-12). All three benthic invertebrate parameters (i.e., porewater ventilation, lipids and moisture content) had an effect on all species except phytoplankton, zooplankton, and clams, inasmuch as all other species eat benthic invertebrates. Parameters specific to an adult fish or crab species (e.g., dietary absorption efficiency of lipids (ε_L) for Dungeness crab) influenced tissue estimates only for that species, with the exception of red rock crab parameters, which also influenced rockfish, which eat red rock crab. Parameters specific to shrimp only influenced shrimp and rockfish, which also eat shrimp.

The results of the correlation coefficient analysis (Table C.2-11) and the NRS analysis (Table C.2-12) are different. These differences can be partly explained by the fact that correlation coefficients take parameter interaction into account, whereas NRS values are based on the effect of changing one parameter value at a time while all other values are held constant.

NRS values for benthic invertebrates, juvenile fish, and fish and crab species are presented graphically in Figures C.2-4 through C.2-12. Estimated correlation coefficients from the correlation analysis discussed in Section C.2.5.1 are also included for reference. Parameters with NRS values of zero are not shown on figures for individual species.

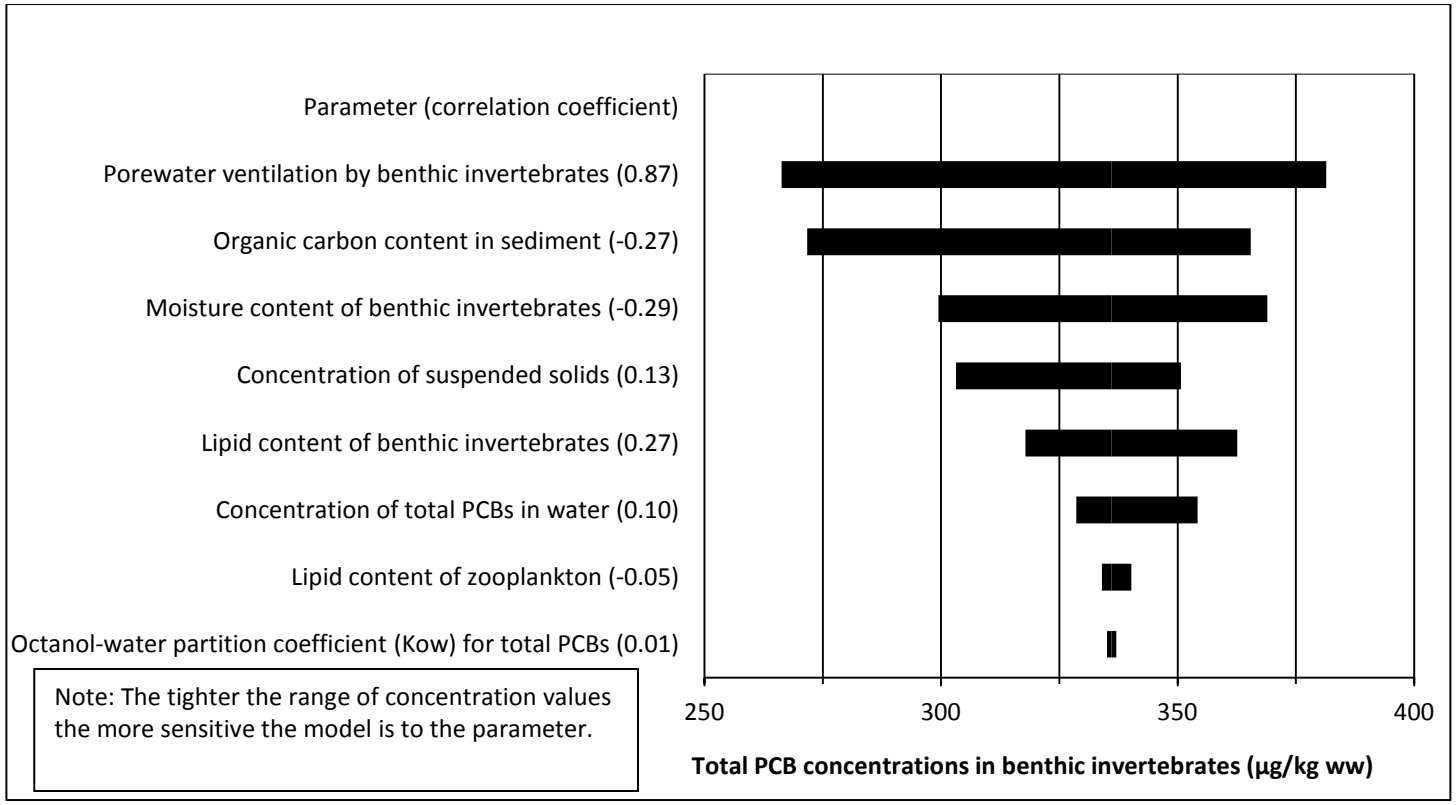


Figure C.2-4

Results of the NRS Analysis for Benthic Invertebrates

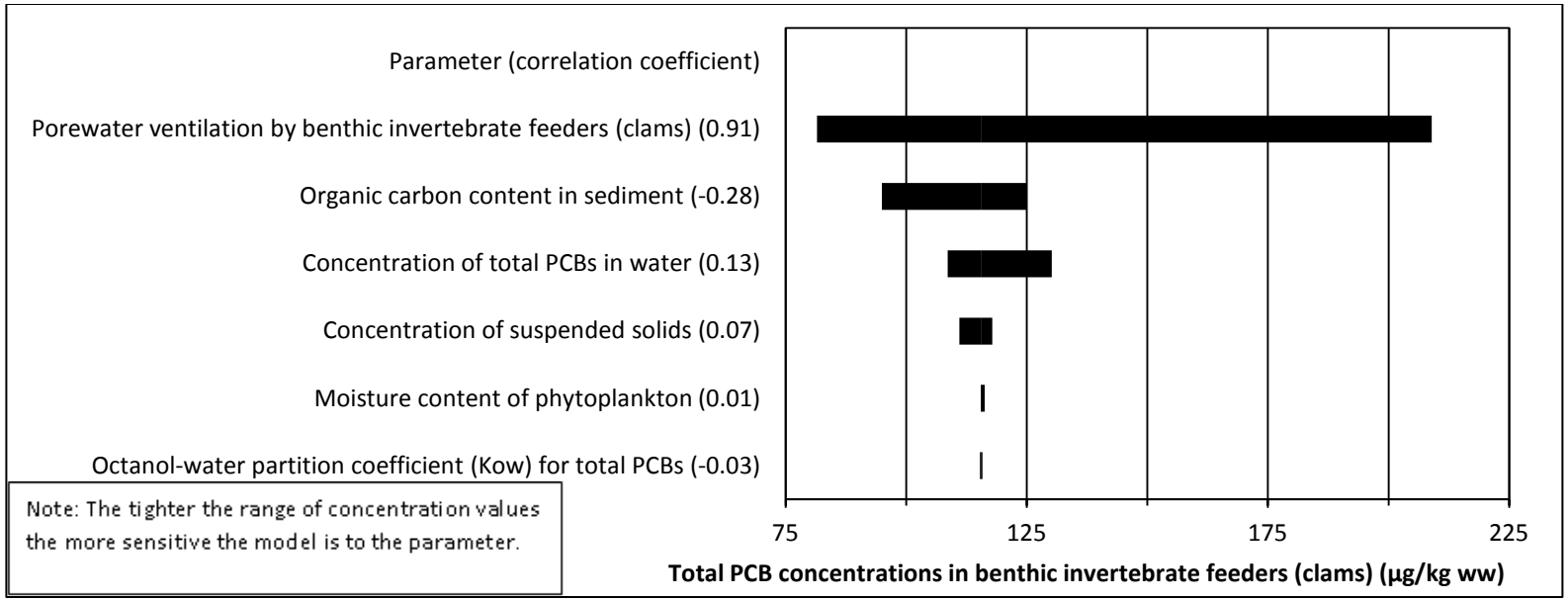


Figure C.2-5

Results of the NRS Analysis for Benthic Invertebrate Feeders (Clams)

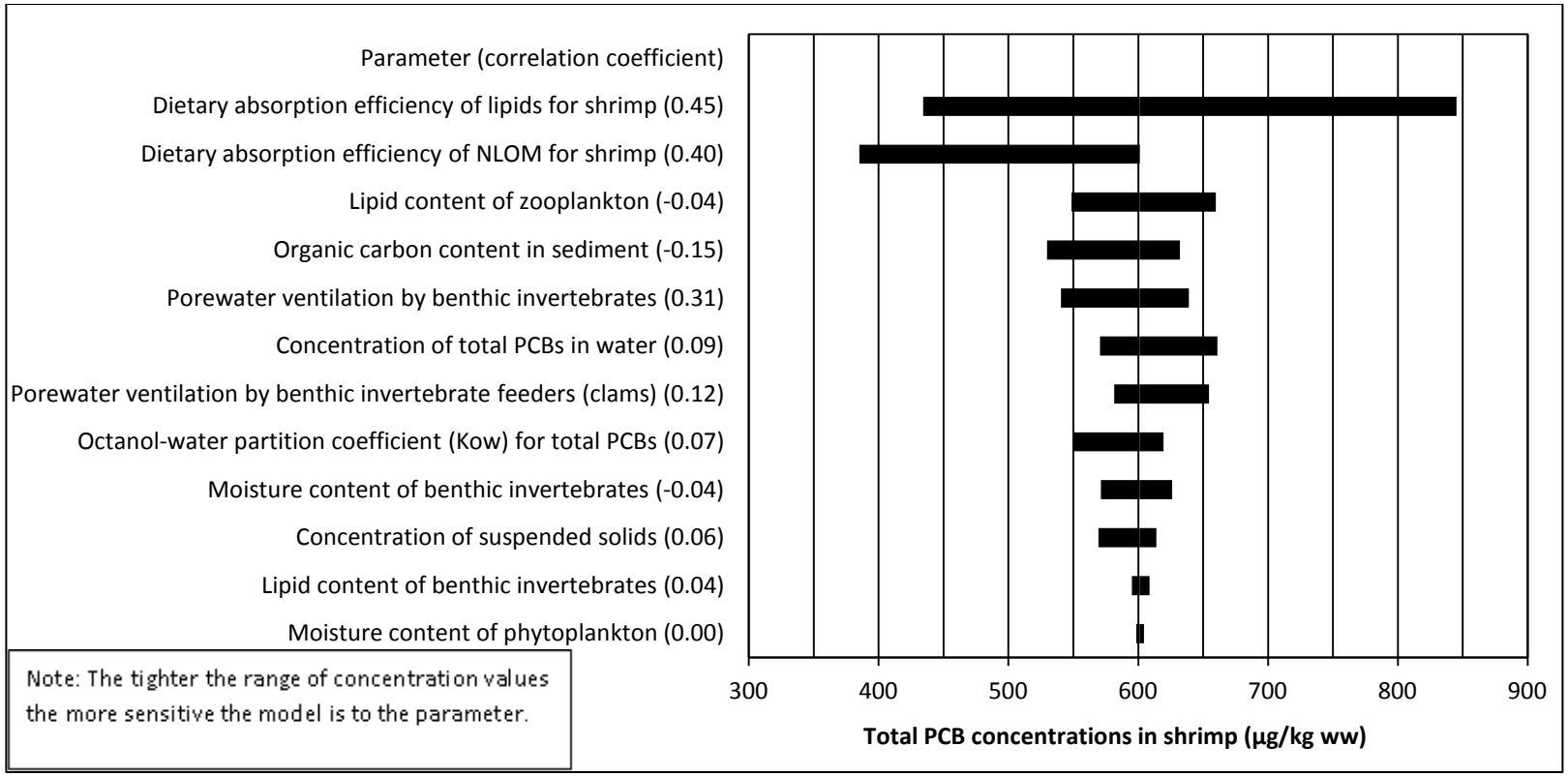


Figure C.2-6
Results of the NRS Analysis for Shrimp

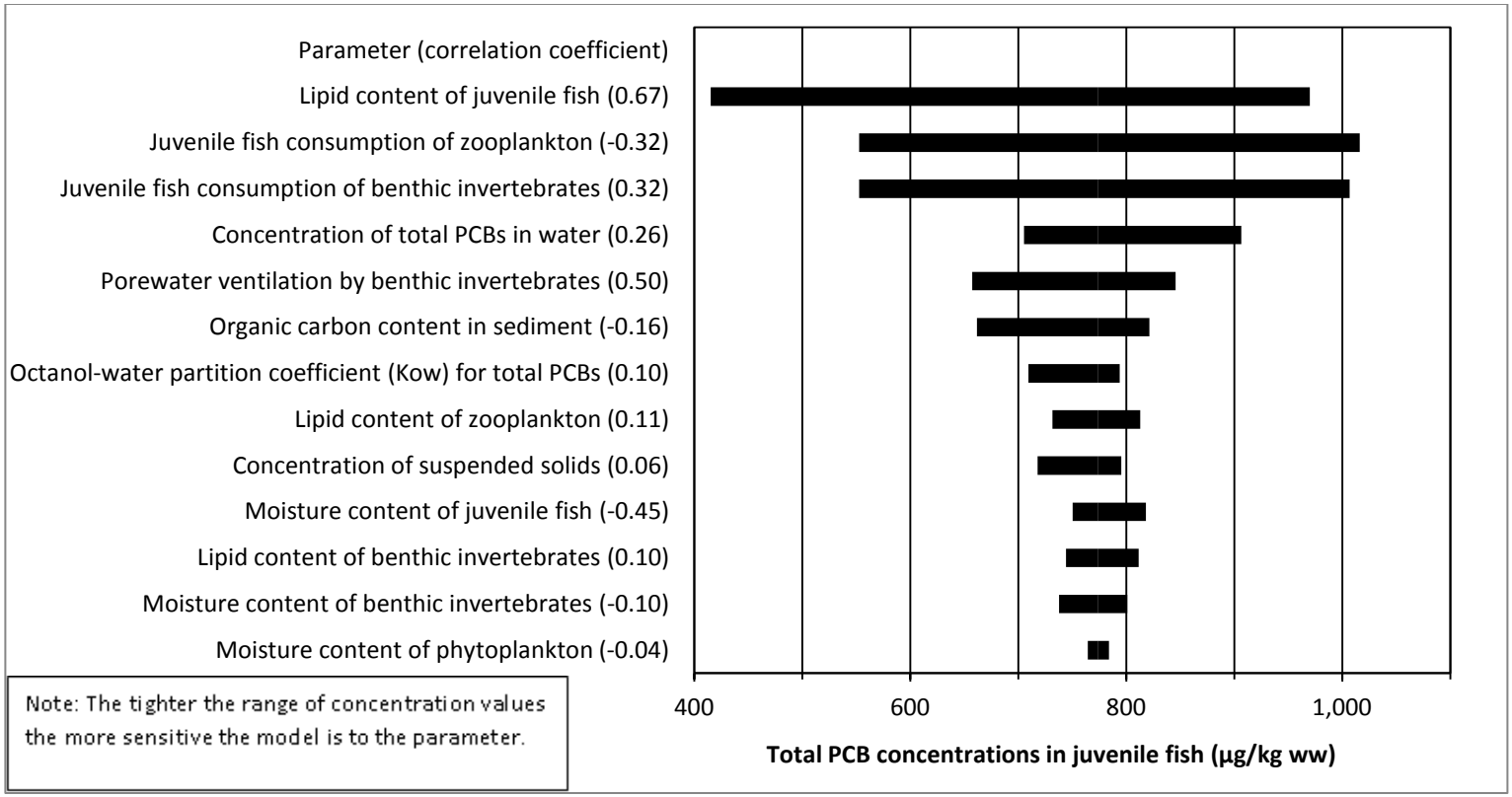


Figure C.2-7

Results of the NRS Analysis for Juvenile Fish

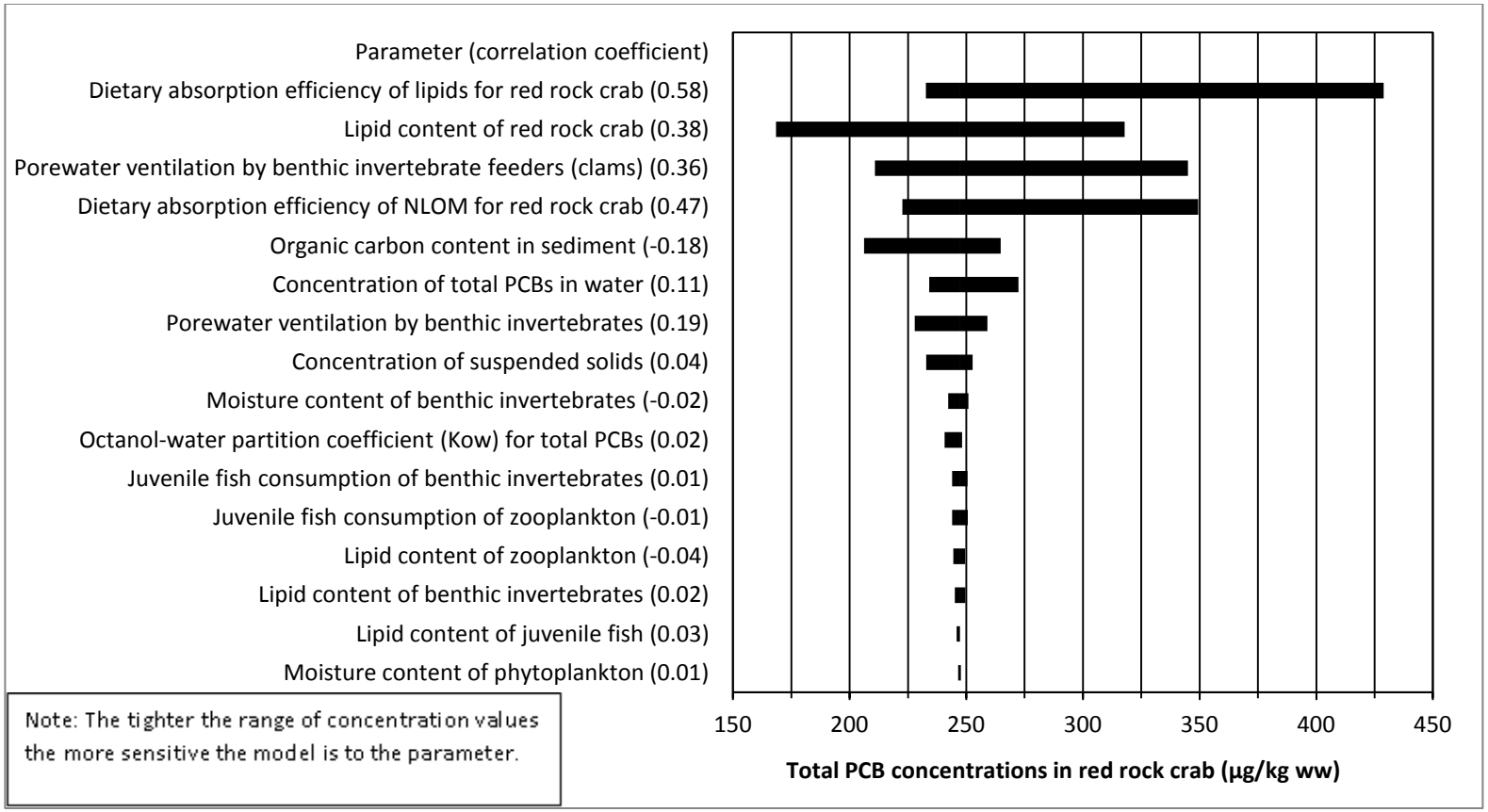


Figure C.2-8
Results of the NRS Analysis for Red Rock Crab

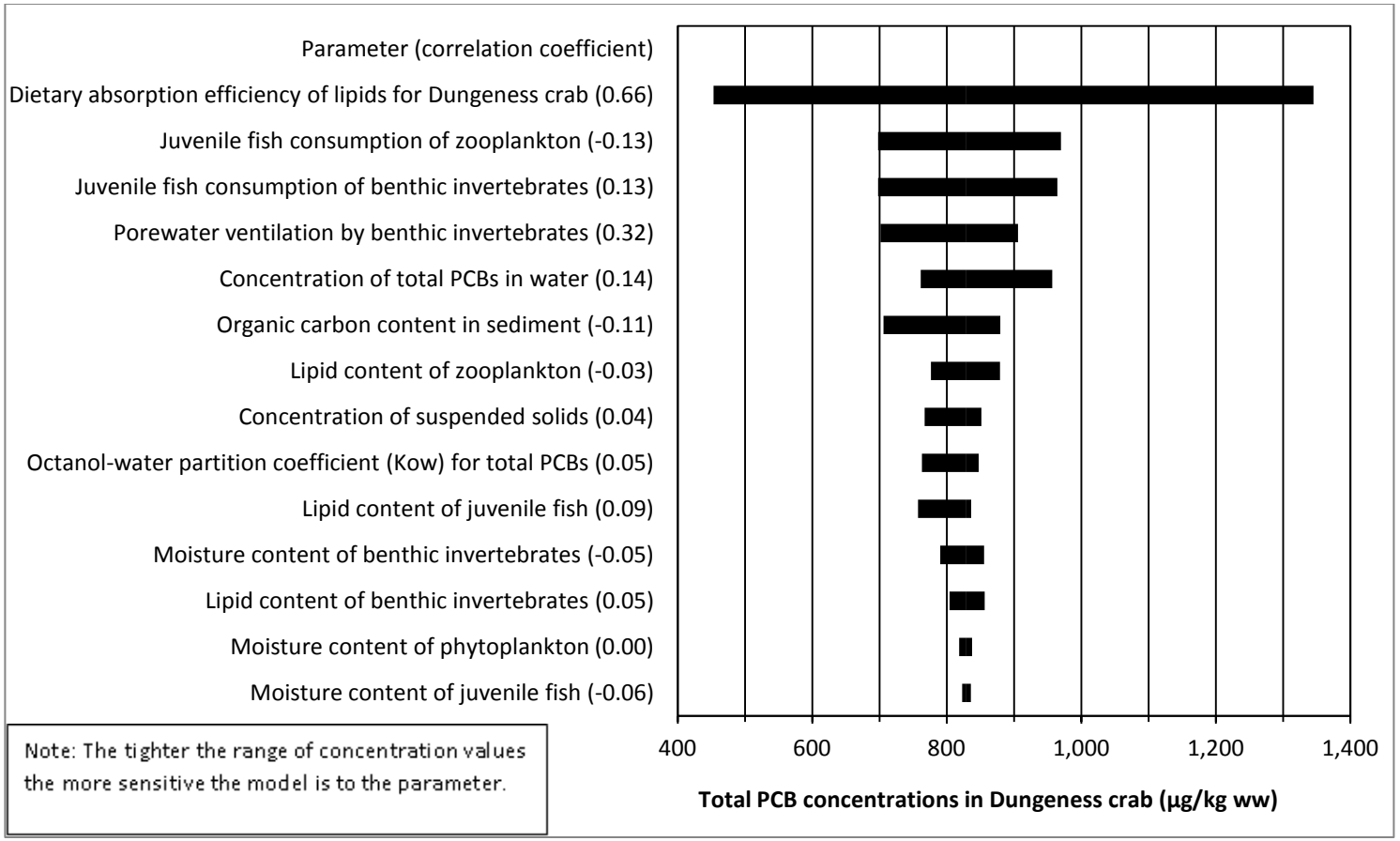


Figure C.2-9

Results of the NRS Analysis for Dungeness Crab

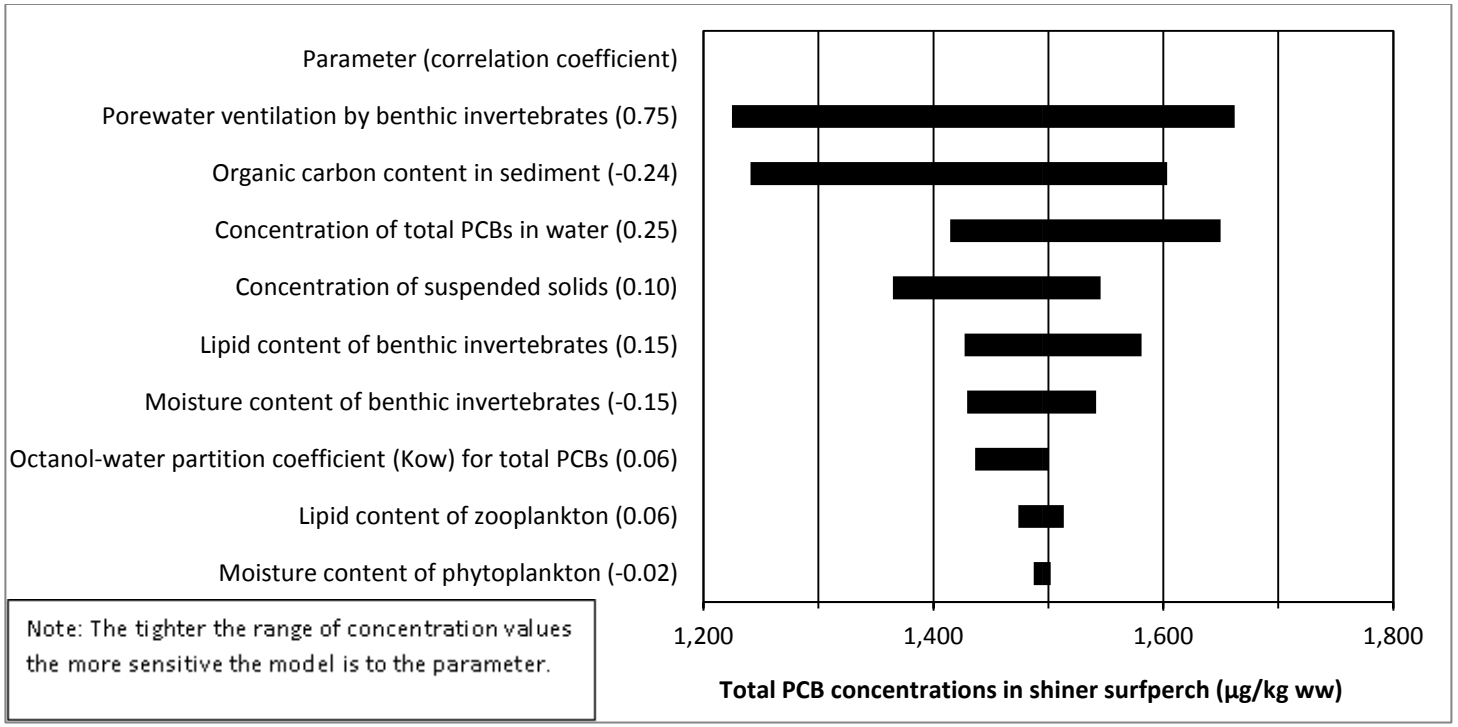


Figure C.2-10
Results of the NRS Analysis for Shiner Surfperch

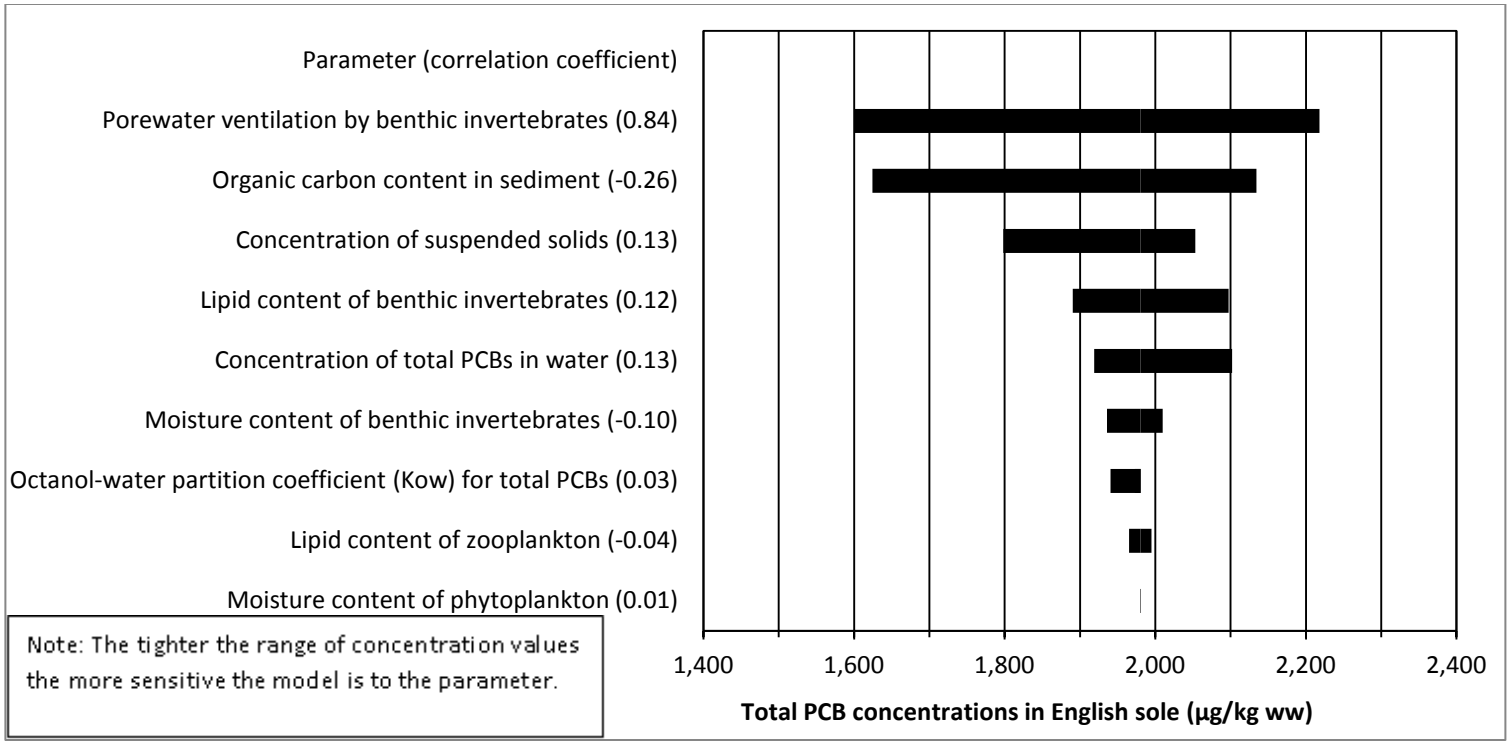


Figure C.2-11

Results of the NRS Analysis for English Sole

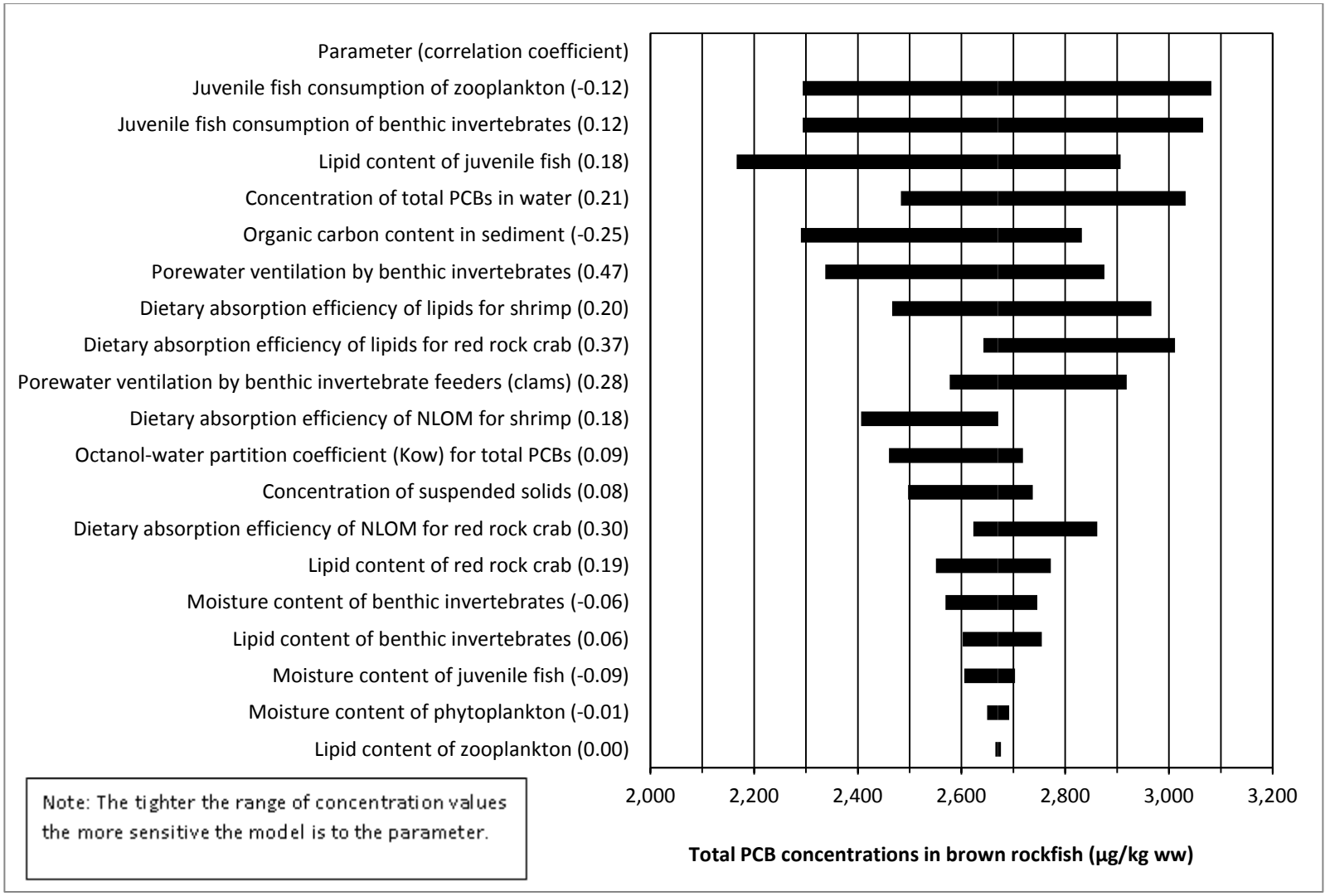


Figure C.2-12

Results of the NRS Analysis for Brown Rockfish

The total PCB concentrations in tissue shown in bold on the figures are the estimated concentrations that resulted from the best-fit parameter set for Calibration 1. The bars range from C_{Max} (the estimated concentration in tissue that results when the maximum value for a given parameter is used) to C_{Min} (the estimated concentration in tissue that results when the minimum value for a given parameter is used) (see Table C.2-11). NRS is the absolute value of the difference between C_{Max} and C_{Min} (Equation C-7).

Log K_{OW} influenced estimates of total PCBs in tissue for all species (see Figures C.2-4 to C.2 12). Log K_{OW} is a key parameter for total PCB uptake and loss in tissues in the FWM. The range of possible input values for this parameter is high, which may contribute to the high NRS values.

Several benthic invertebrate-specific parameters had a relatively significant influence on model estimates for many species. All target fish and crab species modeled were assumed to consume benthic invertebrates as a significant component of their diet. Benthic invertebrate lipid content, moisture content, and porewater ventilation influenced the FWM estimates for many species. . Benthic invertebrate lipid and moisture content also influenced the FWM estimates for many species.

Total PCB concentrations in the water column had a significant influence on estimated total PCB concentrations in phytoplankton and zooplankton (no figures are presented for these species). Most other species were affected by the total PCB concentration in water as well, for some (shiner surfperch, juvenile fish, Dungeness crab, and clams) because phytoplankton or zooplankton constitute a considerable portion (i.e., at least 25%) of their diets. In addition, because juvenile fish and shrimp were assumed to consume significant amounts of zooplankton (61 and 29% of their diets), estimated tissue total PCB concentrations in species that consume juvenile fish and/or shrimp (e.g., Dungeness crab and rockfish) had additional sensitivity to this parameter.

Estimated total PCB concentrations in shrimp and crab were highly influenced by dietary absorption efficiencies (Figures C.2-6, C.2-8, and C.2-9). Dietary absorption efficiencies for invertebrates had broad ranges of defined mean values (i.e., both NLOM and lipid dietary

absorption efficiencies ranged from 16 to 96%),[12] which may explain the significant influence of these parameters.

Benthic invertebrates make up the majority of the diets of English sole and shiner surfperch. Consequently, estimated total PCB concentrations in English sole and shiner surfperch were heavily influenced by benthic invertebrate-specific parameters (Figures C.2-10 and C.2-11). In addition, both these species were also influenced by sediment OC. Sediment OC affects PCB uptake by benthic invertebrates because the majority of the benthic invertebrate diet is sediment.

Brown rockfish PCB concentrations were influenced by a large number of parameters. This was expected inasmuch as rockfish was the highest-trophic-level species modeled and hence were affected by the parameters that influenced PCB uptake by their prey and the diets of their prey. Overall, NRS values are also higher for brown rockfish than for other species, but the FWM predicted concentration of PCBs in rockfish is also higher than for any other modeled species (Table C.2-12, Figures C.2-3 to C.2-12).

The NRS analysis provided a sense of which parameters had the greatest potential to influence FWM estimates. It is not surprising that the parameters identified as the "most sensitive" through the NRS analysis were generally the same parameters that were adjusted through calibration (Section C.2.4). The NRS also provides insight as to why calibration resulted in slighter higher SPAFs for some species (i.e., English sole, clams, and benthic invertebrates). For benthic invertebrates, for which tissue concentrations of total PCBs were overpredicted, only a few parameters influenced predicted concentrations. The diet for benthic invertebrates was defined as primarily sediment (calibration range defined the diet as 62 to 93% sediment), and the most important parameter based on the highest correlation coefficient (0.87) and highest NRS value was porewater ventilation (Table C.2-12, Figure C.2-4). Although the calibration range for porewater ventilation was larger for benthic invertebrates (5 to 25%) than for other species, this range was still not very broad. The two parameters with the next highest NRS values for benthic invertebrates (organic carbon content in sediment and moisture content of benthic invertebrates) also had narrow

[12] For comparison, the dietary absorption efficiency ranges for fish were 50 to 65% for NLOM and 90 to 95% for lipids.

calibration ranges (see Tables C.2-4 and C.2-5). Thus, the tools to improve prediction of benthic invertebrates were limited. Likewise, clam tissue concentrations were also overpredicted. Clams had only a few dietary items and were influenced heavily by their porewater ventilation (Figure C.2-5), which also had a limited range. In contrast, English sole tissue concentrations were underpredicted. There were fewer parameters available to influence predicted PCB concentrations for English sole (Figure C.2-11) than for other species (e.g. rockfish [Figure C.2-12]). The English sole diet is almost entirely benthic invertebrates and the calibration range for this dietary parameter was small (86 to 90% of the English sole diet), so English sole was influenced heavily by benthic invertebrate parameters. Most changes in parameters that would increase (i.e., improve) English sole predictions would lead to even higher (i.e., worse) predictions for benthic invertebrates, which the model already overpredicts. It may be more likely that English sole have important exposures to PCBs from outside the EW (their home range may be larger than the EW), and/or their uptake of PCBs from water is more important than is characterized by the model.

In general, the parameters that had the greatest influence on model uncertainty were those with values that had been derived from the literature (i.e. not those with empirical data from the EW) and had broad ranges. In addition, the parameters evaluated and their relative importance in the NRS (e.g., the influence of Kow, concentration of total PCBs in water, benthic invertebrate porewater ventilation, and dietary absorption efficiencies on tissue concentrations) were similar for the EW and LDW FWMs (Windward 2010).

C.2.5.3 SWAC Sensitivity and Uncertainty Analysis

The EW total PCB SWAC was not evaluated in the correlation coefficient or NRS analyses (Sections C.2.5.1 and C.2.5.2) because the SWAC is a decision variable, consistent with Morgan and Henrion (1990), and thus had only one value for calibration. The results of an analysis of the sensitivity of the FWM to the SWAC and the potential influence of the SWAC on the uncertainty of FWM estimates are presented in this section. A similar evaluation was also performed for the LDW FWM (Windward 2010).

As discussed in Section C.2.4.2, the FWM tended to overestimate total PCB concentrations in tissue (Figures C.2-2 and C.2-3). The following assumptions made in defining the SWAC for the FWM could have contributed to the model's tendency to overestimate tissue concentrations for target species in the EW.

- The interpolation method used to generate the SWAC (i.e., inverse distance weighting) has uncertainties.
- The SWAC used in the FWM assumed that fish and crab species in the EW use all areas of the EW equally. In reality, some or all of the fish and crab species may preferentially use some areas of the EW with more suitable habitat (e.g., better food sources or refuge from predators); any such differential use patterns are not represented by the SWAC.

The SWAC used in the FWM assumed that all modeled species use the EW 100% of the time, whereas English sole and crabs are known to have home ranges larger than the EW. No site use factors were applied nor were exposure differences applied for species that may move out of the EW periodically or for part of the year[13].To explore the effects of SWAC uncertainty on FWM estimates and on the tendency of the FWM to overestimate concentrations of total PCBs in tissue more than underestimate them (Section C.2.4.2), the best-fit parameter set was run an additional eight times, each time with a different SWAC than the initial estimate of 470 µg/kg dw. Model estimates were compared with empirical data to determine which SWAC resulted in the best fit for the FWM. The water PCB concentration was held constant in order to illustrate the impact of the sediment PCB concentration on model estimates.

The initial run used a SWAC of 470 µg/kg dw, which was the SWAC for the calibrated model. Two model runs were made with slightly higher SWACs, and six runs used a lower SWAC. Six lower SWACs were investigated because the FWM overestimated tissue concentrations for most species at 470 µg/kg dw. Table C.2-13 shows the predicted tissue concentrations in various tissues associated with the eight SWACs.

[13] This site use assumption applies to some other exposure parameters, such as total PCB concentrations in water, since it was assumed that modeled organisms are exposed only to EW water.

Table C.2-13
Sensitivity of FWM Estimates to the SWAC

Species	Mean Empirical Total PCB Concentration in Tissue (µg/kg ww)	Estimated Total PCB Concentration in Tissue for Selected SWACs (µg/kg ww)[a]								
		500	480	470	450	400	350	300	200	100
Benthic invertebrates	210	357	344	337	324	292	259	**227**	162	97
Clams	56	122	118	116	112	103	93	84	**65**	46
Shrimp	460	632	612	601	580	529	**447**	425	322	218
Red rock crab	240	260	251	247	**239**	217	196	175	133	91
Dungeness crab	860	**864**	839	827	802	741	679	617	494	371
Shiner surfperch	1,500	1,571	1,520	**1,494**	1,443	1,316	1,189	1,061	807	552
English sole	3,200	**2,093**	2,018	1,981	1,906	1,720	1,534	1,348	976	604
Brown rockfish	2,000	2,795	2,711	2,669	2,585	2,375	2,165	**1,955**	1,534	1,114

[a] Best-fit parameter set was used for model runs.

FWM – food web model
PCB – polychlorinated biphenyl
SWAC – spatially weighted average concentration
ww – wet weight

Bold identifies the estimates closest to mean empirical tissue data for that species.

The SWAC that produced the lowest average SPAF across species for the best-fit parameter set was 400 µg/kg dw (Table C.2-14), although average SPAFs were very similar (between 450 and 350 µg/kg dw). The SWAC of 400 µg/kg dw was the only tested value that produced SPAFs that were less than 2 for each individual species.

Table C.2-14
Effects of SWAC on FWM Performance

Species	SPAF Based on FWM Runs that Used Selected SWACs (µg/kg ww)[a]								
	500	480	470	450	400	350	300	200	100
Benthic invertebrates	1.70	1.64	1.61	1.54	1.39	1.24	**1.08**	1.30	2.16
Clams	2.17	2.10	2.07	2.00	1.83	1.67	1.50	**1.16**	1.21
Shrimp	1.37	1.33	1.31	1.26	1.15	**1.04**	1.08	1.43	2.11
Red rock crab	1.08	1.05	1.03	**1.01**	1.10	1.22	1.37	1.81	2.65
Dungeness crab	**1.00**	1.02	1.04	1.07	1.16	1.27	1.39	1.74	2.32
Shiner surfperch	1.05	1.01	**1.00**	1.04	1.14	1.26	1.41	1.86	2.72
English sole	**1.53**	1.59	1.62	1.68	1.86	2.09	2.37	3.28	5.30
Brown rockfish	1.40	1.36	1.33	1.29	1.19	1.08	**1.02**	1.30	1.80
Average SPAF	1.41	1.39	1.38	1.36	**1.35**	1.36	1.40	1.73	2.53

[a] Best-fit parameter set was used for model runs.

dw – dry weight
FWM – food web model
SPAF – species predictive accuracy factor
SWAC – spatially weighted average concentration
ww – wet weight

Bold identifies the best-fit estimate for a species as compared with empirical tissue data.
Underlined values are SPAFs calculated from underestimated tissue concentrations.

When total PCB concentrations in sediment were reduced from 470 to 200 µg/kg dw, a change of 57%, the average change in tissue concentrations across all species was 46%. This indicates that the average of FWM estimates across species responds in a relatively proportional manner to changes in total PCB concentrations in sediment when the concentration of total PCBs in water is held constant.

C.2.5.4 Uncertainty in Other Input Parameters

A number of uncertainties in EW FWM parameters were not evaluated in the sensitivity and uncertainty analyses presented above. Many of these are the same as those identified for the LDW FWM (Windward 2010). These uncertainties include the following (discussed below):

- Characterizing the true uptake and depuration processes with FWM equations
- Applicability of basic assumptions of the Arnot and Gobas FWM (Arnot and Gobas 2004a) to EW organisms and conditions (i.e., primary routes of chemical uptake, homogeneous distribution of chemicals within organisms, assumptions about equilibrium between organisms and the environment)
- Mean of the empirical data as an estimate of true mean tissue total PCB concentrations in the EW
- Appropriateness of the spatial scale for modeled species

The model's quantitative description of the uptake and depuration processes is an important uncertainty. Biological processes are highly complex and were necessarily simplified for the creation of the model. The degree to which this simplification appropriately captures the critical elements of these processes for predicting current and particularly future conditions is unknown. With regard to current conditions, the model reasonably estimates current PCB tissue concentrations, providing some confidence in its design.

The degree to which the model is appropriate for the EW organisms and conditions is another source of uncertainty. The Gobas model (Gobas 1993) was originally developed for a

freshwater lake very different from the EW. The model has since been applied to a variety of freshwater and marine environments (deBruyn et al. 2004; Gobas and Arnot 2005). However, each system is unique, and the model assumptions related to primary routes of chemical uptake, homogeneous distribution of chemicals within organisms, and equilibrium between organisms and the environment (Arnot and Gobas 2004b) are violated to some degree in any system.

Empirical data for each species tended to be highly variable; minimum and maximum total PCB concentrations in the tissue of different species ranged from 10-fold lower to 3 times higher than the species' mean tissue concentrations. Factors that contribute to the variance in tissue concentrations include laboratory protocols,, age of the organisms sampled, and time and spatial heterogeneity. In addition, for clams, there were different species in different composite samples. The variability in the empirical dataset reflects uncertainties that carry over into the calibration process. Although empirical data represent the best approximation of tissue concentrations in the EW, the variability in the data suggest the potential for uncertainty in estimates of the mean.

The FWM was applied to the entire EW. However, the EW is about 1.5 miles in length, and several species may have larger home ranges and/or seasonally migrate in and out of the EW (into Elliott Bay and/or the LDW). Data are available regionally, particularly from the LDW, for several of the modeled species. English sole are believed to maintain migration patterns throughout their lives (Day 1976). Home range estimates of approximately 3 km^2 (1.2 square miles) have been developed for English sole through the use of acoustic tracking (O'Neill et al. 2005) and an empirical relationship between sediment PAH concentrations and lesion prevalence (Stern et al. 2003). Home range estimates of approximately 9 km^2 (3.5 square miles) for English sole were reported in the Puget Sound Dredged Disposal Analysis (PSDDA) report based on best professional judgment (PSDDA 1988). Information available on shiner surfperch from the LDW[14] suggests that the LDW likely supports resident juveniles and first-year adults in addition to second- and third-year adults that migrate from Puget Sound during summer mating and parturition. February to October monthly beach seine sampling data from locations throughout the LDW and into Elliott Bay indicate that shiner surfperch are rare in the LDW from February through April and abundant from May

[14] Information specific to EW is not available.

through October (Shannon 2006). Shiner surfperch abundance in the LDW peaks in the summer, when they bear their young (Miller et al. 1975; Shannon 2006). Results from a quarterly survey of the LDW indicate that the abundance of Dungeness crab may not vary substantially throughout the year (Windward 2004), although it is not known if Dungeness crab are year-round residents. In California, female Dungeness crab were reported to have annual home ranges less than 2 km (1.25 miles) (Diamond and Hankin 1985, as cited in Pauley et al. 1986). A separate report (CDFG 2002) stated that most migrations in California waters were less than 10 miles, but some individuals moved up to 100 miles, with males moving farther than females. WDFW (2002) reported that Dungeness crab seasonally move between estuaries and offshore waters.

The EW FWM presented here does not account for exposure that may occur outside of the EW. However, if species are using areas outside of the EW that have lower sediment PCB concentrations for part of their lives, this would contribute to an overestimation by the FWM, which assumes exclusive use of the EW.

C.2.6 Application of the FWM to Calculate Sediment RBTCs

RBTCs represent the concentrations of a COC that correspond to specific thresholds of risk in sediment or tissue.[15] In Section 8 of the SRI, RBTCs were estimated for various human and ecological exposure pathways for risk driver COCs identified in the baseline risk assessments (Appendices A and B). The FWM was used to generate sediment RBTCs for total PCBs based on human health exposure through the consumption of seafood and for two fish receptors, English sole and brown rockfish, based on exposure to total PCBs in sediment, water, and contaminated prey and the resulting risk to the fish in the ERA.

This use of the FWM carries an implicit assumption that risks associated with tissue concentrations of PCBs are a predictable function of sediment PCB concentrations and that risks from PCBs can thus be predictably reduced by lowering sediment concentrations.

This section describes the four main steps of the process used to generate estimates of sediment RBTCs for total PCBs at the EW site. Briefly, sediment and water input parameters

[15] For example, a 1×10^{-6} RBTC is the tissue concentration (or the associated sediment concentration) at which the excess cancer risk equals 1×10^{-6} for a specific human exposure scenario.

for total PCBs were selected, and then the model was run iteratively to estimate the tissue concentrations of total PCBs that corresponded to each set of input parameters. The estimated tissue concentrations were then used in the human health risk equations, and through multiple iterations of those steps the sediment concentrations associated with particular risk thresholds were identified. Details on each of these steps are discussed below. The process described here is the same process that was used for the calculation of LDW RBTCs using the LDW FWM (Windward 2010).

Step 1. Estimate Total PCB Concentrations in Surface Sediment and in Overlying Water in the Water Column

To estimate sediment RBTCs, the FWM required paired inputs of total PCB concentrations in surface sediment and surface water; both of these input parameters are important for the model. RBTCs are developed for PCB sediment concentrations lower than current average concentrations reflecting assumed future conditions, and lower sediment concentrations would be expected to be associated with lower water column concentrations. For current conditions, the surface sediment concentration was represented by the SWAC for the EW, which has been estimated to be 470 µg/kg dw. The EW-wide mean total PCB concentration in water was 1.31 ng/L, and the calibrated value was 1.16 ng/L.

In the future, total PCB concentrations in sediment and water are expected to be lower following sediment remediation and source control actions within the EW. Because these concentrations are not yet known, the FWM was run with total PCB concentrations in sediment ranging from 0 to 470 µg/kg dw. Total PCB concentrations in sediment are not expected to reach 0 µg/kg dw under assumed future conditions of the EW because of background sources of PCBs to the system. The low end of the range (approaching zero PCBs in sediment) was modeled to estimate total PCB concentrations in tissue at very low concentrations in sediment.

In order to estimate future tissue concentrations, assumption about water concentrations relative to sediment were made. Future total PCB concentrations in the water column were divided into three groupings corresponding to general ranges of sediment concentrations, with single values of water concentrations for each sediment range. For total PCB concentrations in surface sediment between 250 and 470 µg/kg dw, a water concentration of 1.2 ng/L was assumed based on the best-fit parameter set (Table C.2-15). This concentration

is slightly below the present EW-wide mean concentration of 1.31 ng/L (Table C.2-3). For the lower sediment ranges, total PCB concentrations in water were assumed to be (roughly) proportionately lower (Table C.2-15). The porewater concentration parameter (estimated by the model) provides a mechanism for the FWM to account for the potentially higher concentrations of PCBs within the sediment-water interface.

Table C.2-15
Assumed Relationships Between Total PCB Concentrations in Sediment and Surface Water for the Calculation of RBTCs in Sediment

Range of Total PCB Concentrations in Sediment (µg/kg dw)	Assumed Total PCB Concentrations in the Water Column (ng/L)
0 – 100	0.6
100 – 250	0.9
250 – 470	1.2

dw – dry weight
PCB – polychlorinated biphenyl
RBTC – risk-based threshold concentration

The assumptions in Table C.2-15 are consistent with those used in the LDW FWM for RBTC development (Windward 2010). However there are differences in the flow regimes and inputs for the two waterways (e.g., the Green River is contiguous with the LDW, the EW is contiguous with Elliott Bay, and the residence time of water is longer in the LDW than the EW). Hence, there is uncertainty in applying the assumptions about the relationship between PCBs in water and sediment developed for the LDW to the EW. Following the assumptions in Table C.2-15, at low sediment concentrations, water will be the overwhelming contributor to FWM predicted tissue concentration. However, water concentrations associated with post-remedial EW sediment concentrations (e.g. >20 µg/kg dw) might be lower than 0.6 ng/L, in which case some FWM estimated sediment RBTCs would be lower than necessary to achieve the tissue RBTCs. The assumptions in Table C.2-15 in combination with the FWM are simplifications of the complex relationship of three matrices (water, sediment, and tissue) which have been made for estimation of RBTCs. The uncertainties inherent in these assumptions should be considered when interpreting RBTC estimates.

Step 2. Run the Model Probabilistically Using Monte Carlo Simulation

The FWM was run probabilistically as a Monte Carlo simulation using Crystal Ball® software, allowing numerous model runs for small incremental changes in total PCB concentrations in sediment, with concentrations ranging from 0 to 470 µg/kg dw. The total PCB concentration in water for each of these runs also varied, per the relationship described in Table C.2-15.

Results of these model runs (i.e., estimates of total PCB concentrations in tissue) using the best-fit (for all species combined) parameter set are displayed graphically in Figure C.2-13, with numerical results presented in Table C.2-16. The "steps" in estimated total PCB concentrations in tissue occurred at total PCB concentrations in sediment that corresponded with the three sediment/water intervals defined in Step 1.

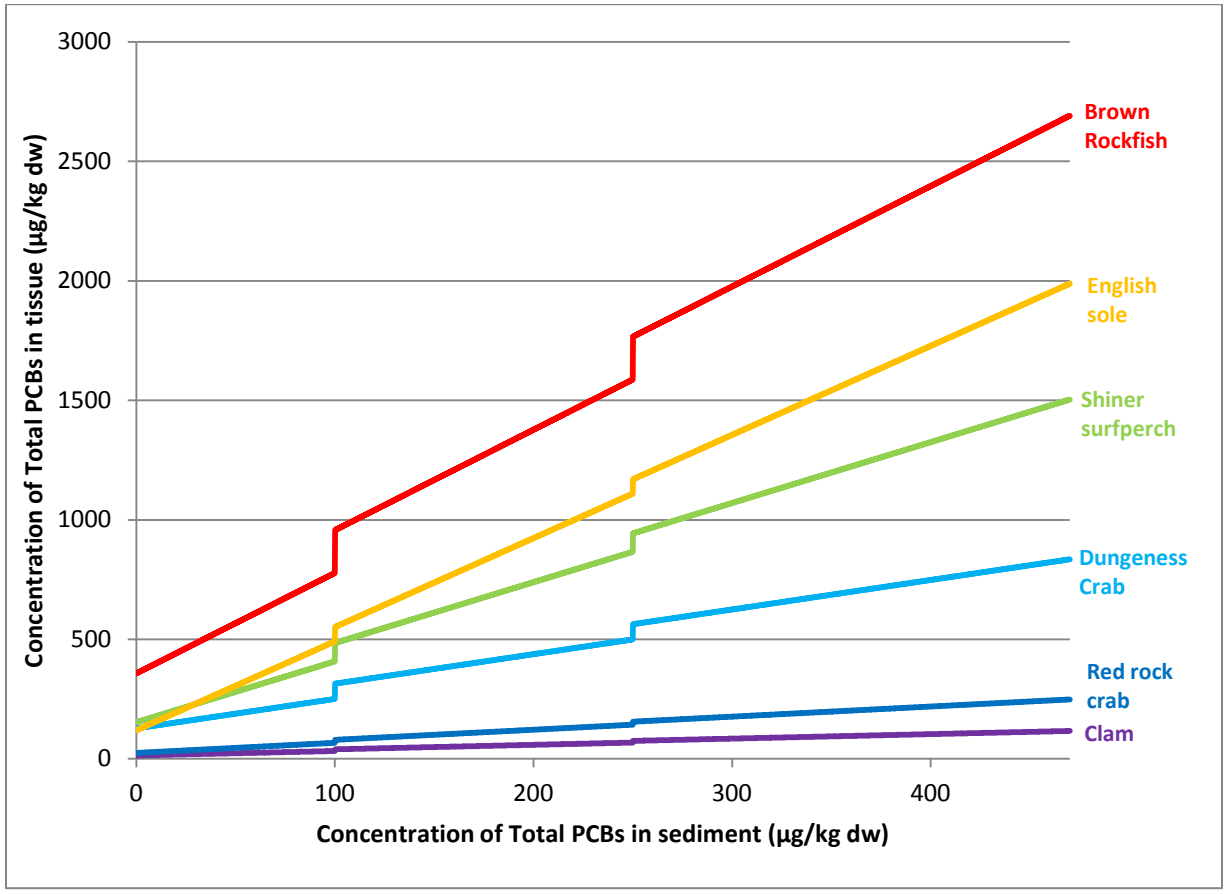


Figure C.2-13
Total PCB Concentrations in Whole-body Tissue of Seafood Species as a Function of Total PCB Concentrations in Sediment

Table C.2-16
Excess Cancer Risk Levels for Two Human Health Seafood Consumption Scenarios that Corresponded to Total PCB Concentrations in Sediment

Total PCB Concentration Used as Input Values		FWM-Predicted Total PCB Concentrations (µg/kg ww)										Excess Cancer Risk Estimates Based on FWM Output	
Sediment (µg/kg dw)	Water (ng/L)	Benthic Inverte-brates	Clam	Red Rock Crab (WB)	Red Rock Crab (EM)	Dungeness Crab (WB)	Dungeness Crab (EM)	Shiner Surfperch (WB)	English Sole (WB)	English Sole (Fillet)	Brown Rockfish (WB)	Adult Tribal RME (Tulalip Data)	Child Tribal RME (Tulalip Data)
0	0.6	17	14	25	11	127	26	153	120	70	358	9.7E-05	1.8E-05
1	0.6	17	14	25	11	129	27	156	123	72	362	9.9E-05	1.8E-05
2	0.6	18	14	26	11	130	27	158	127	74	366	**1.0E-04**	1.8E-05
10	0.6	23	16	29	12	140	29	179	157	91	400	1.1E-04	2.1E-05
20	0.6	30	18	33	14	152	31	204	194	113	442	1.3E-04	2.3E-05
50	0.6	49	24	46	19	189	39	281	306	178	568	1.7E-04	3.2E-05
75	0.6	65	28	57	24	220	45	344	399	232	673	2.1E-04	3.9E-05
100	0.6	82	33	67	28	251	52	408	492	286	778	2.5E-04	4.6E-05
120	0.9	103	44	88	37	339	70	535	626	364	1,041	3.3E-04	6.1E-05
160	0.9	129	51	105	44	389	80	637	775	451	1,209	3.9E-04	7.2E-05
200	0.9	155	59	122	52	438	90	739	924	537	1,377	4.6E-04	8.4E-05
250	0.9	187	68	143	61	500	103	867	1,110	646	1,587	5.4E-04	**9.8E-05**
250.1	1.2	196	75	156	66	564	116	943	1,170	681	1,766	5.8E-04	1.1E-04
275	1.2	212	80	166	70	594	122	1,007	1,262	735	1,871	6.2E-04	1.1E-04
300	1.2	228	85	177	75	625	129	1,070	1,355	789	1,976	6.6E-04	1.2E-04
350	1.2	260	94	198	84	687	141	1,198	1,541	897	2,186	7.4E-04	1.4E-04
400	1.2	293	104	219	93	748	154	1,325	1,728	1,005	2,396	8.2E-04	1.5E-04
470	1.2	338	117	249	105	835	172	1,503	1,988	1,157	2,691	9.3E-04	1.7E-04

dw – dry weight
EM – edible meat
FWM – food web model
PCB – polychlorinated biphenyl
RME – reasonable maximum exposure
WB – whole body

Bold identifies value closest to 1E-4 excess cancer risk.

The FWM was also used to estimate a range of total PCB concentrations in each tissue type. Parameter sets that passed the model performance criterion (SPAF ≤ 2 for all species except clam; SPAF of ≤ 3 for clams) were reviewed to determine which set produced the highest and lowest estimated total PCB concentrations across the species contributing the most to RME human health risk.

The same parameter sets for maximum, minimum, and best fit were used for the development of RBTCs for all multi-species human health consumption scenarios (i.e., the RBTC and lower bound and upper bound values for the adult tribal RME, child tribal RME, adult API RME, adult Suquamish, adult tribal CT, child tribal CT, adult API CT scenarios). The "best fit" model was used for calculating the RBTCs for one-meal-per month scenarios for human health and English sole and rockfish tissue concentrations for ecological risks. However, the parameter sets that led to the highest and lowest human health risks for multi-species seafood diets did not necessarily have the highest and lowest concentrations for each individual species. For the evaluation of risk scenarios involving PCB concentrations for a single species (i.e., the one-meal-per-month scenarios for human health risk and English sole and rockfish tissue concentrations for ecological risks), the parameter sets with the maximum and minimum concentrations for each species within the SPAF bounds (SPAF ≤ 2 for all species except SPAF ≤ 3 for clams) were selected for bounding purposes. For example, a different parameter set was selected for the development of the lower-bound (RBTC) estimates for rockfish consumption under the one-meal-per-month scenario than was selected for the development of the lower-bound (RBTC) estimates for clam consumption under the one-meal-per-month scenario.

By way of example, Figures C.2-14 and C.2-15 present the results for shiner surfperch and rockfish, respectively. The red lines represent the FWM estimates using the best-fit parameter set (used for all RBTCs). The yellow and orange lines are the lower- and upper-bound estimates used for human health seafood consumption (with a multispecies diet) exposure scenarios. However, these parameter sets were not used for upper and lower bound (RBTC) estimates for the one-meal-per-month scenarios for human health risk and English sole and rockfish tissue concentrations for ecological risks; species-specific parameters sets were used for the upper and lower bound values for those scenarios.

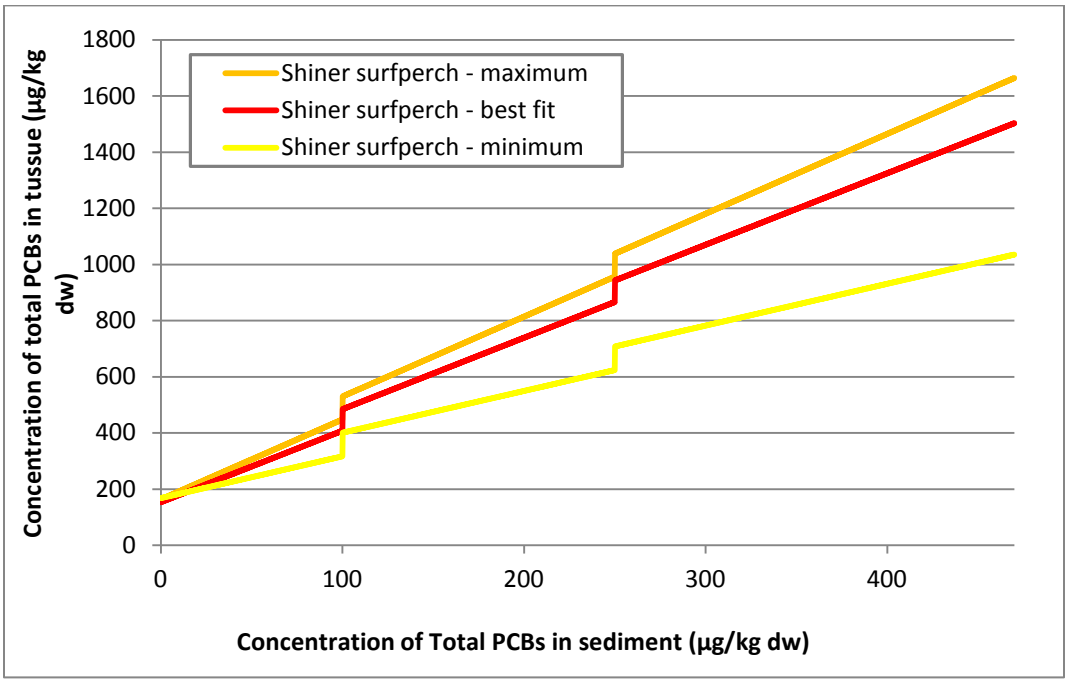


Figure C.2-14

Estimated Total PCB Concentrations in Shiner Surfperch Using Best-Fit, Maximum, or Minimum Parameter Sets as a Function of Total PCB Concentration in Sediment

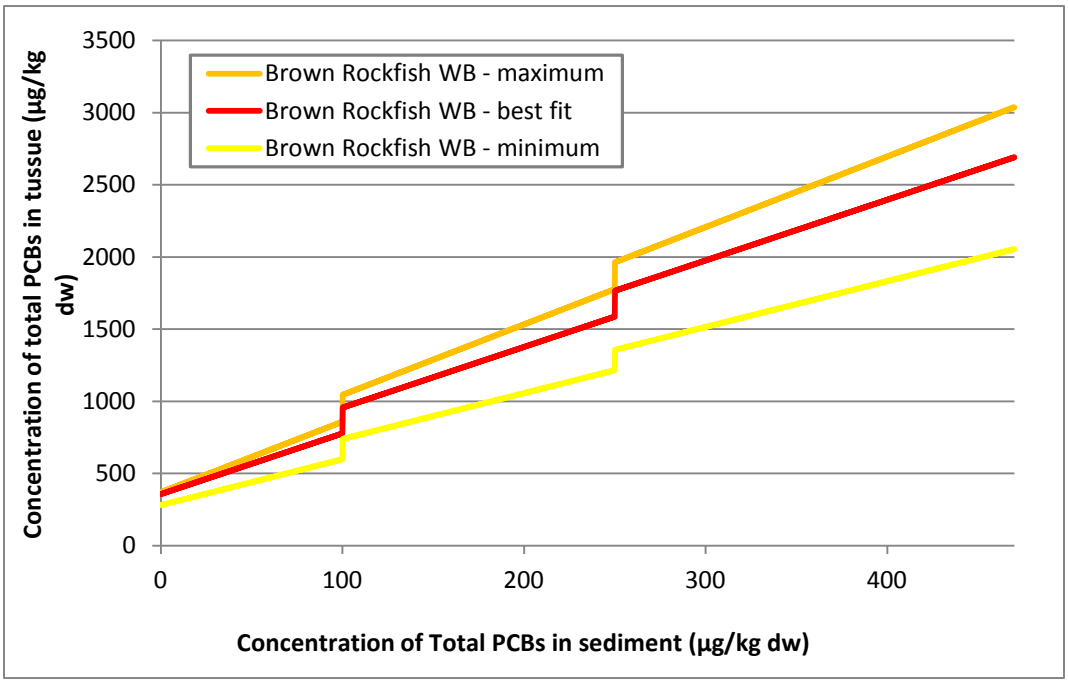


Figure C.2-15

Estimated Total PCB Concentrations in Rockfish Using Best-Fit, Maximum, or Minimum Parameter Sets as a Function of Total PCB Concentration in Sediment

The upper-bound estimates were more similar to the best-fit estimates for Shiner surfperch and rockfish because of the model's precalibration tendency to underpredict for these species. The upper- and lower-bound estimates are not upper and lower confidence intervals and do not reflect a statistical measure of uncertainty. Instead, the upper and lower bounds reflect some of the variability in FWM estimates, which was constrained by the model performance SPAF of ≤ 2 for all species except clam (SPAF ≤ 3). The upper and lower bounds do not include consideration of sediment variance (or uncertainty in the SWAC) because the sediment concentration was considered to be a decision variable. Analyses of model sensitivity and uncertainty associated with the SWAC were presented in Section C.2.5.3.

Step 3. Calculate Risk Estimates Using the Output Generated by Each FWM Run

The estimated total PCB concentrations in tissue for the modeled species,[16] which corresponded to each of the thousands of FWM runs associated with incremental steps in total PCB concentration in sediment, were entered into the human health and ecological receptor risk equations. These estimated tissue concentrations were used in the risk equations in the same way that exposure point concentrations (EPCs) were used in the risk assessments.

Excess cancer risks and non-cancer hazards were estimated using these estimates for each of the seafood ingestion scenarios evaluated in the HHRA (Appendix B) and for HQs equal to 1.0 for English sole and rockfish, two fish receptors in the ERA (Appendix A). Risks were calculated using the best-fit, maximum, and minimum estimates over the full range of paired total PCB concentrations in sediment and water.

Step 4. Identify the Sediment RBTC Associated with a Given Risk Threshold

Because of the large number of tissue predictions and risks generated for each of the human health and ecological exposure scenarios, it was necessary to devise a method for organizing

[16] The FWM estimated total PCB concentrations in whole-body organisms. In the HHRA, some of the seafood ingestion scenarios included the consumption of edible meat (crabs) or fillet (English sole). Therefore, conversion factors were developed. The conversion factors used to convert total PCB concentrations in whole-body organisms to lower concentrations in edible meat or fillet concentrations were 0.42 for red rock crabs, 0.21 for Dungeness crabs, and 0.58 for English sole. These conversion factors were based on the ratio of whole-body to edible-meat concentrations detected in individual EW fish tissue samples and detected in composite crab edible meat and hepatopancreas samples collected as part of the EW SRI/FS.

the data so that RBTCs could be efficiently identified for any of the risk thresholds of interest (i.e., cancer risks of 1×10^{-4}, 1×10^{-5}, and 1×10^{-6}). Thus, the risk estimates described in Step 3 were compiled in a table to facilitate the identification of the total PCB concentration in sediment that corresponded to a selected excess cancer risk threshold (1×10^{-4}, 1×10^{-5}, or 1×10^{-6}) or a non-cancer hazard (hazard quotient = 1) for each of the exposure scenarios.

Table C.2-16 demonstrates the manner in which sediment RBTCs were identified for two of the seafood consumption scenarios, and presents 18 of the many model runs that were conducted. The right-hand columns show excess cancer risk for the adult and child tribal RME seafood consumption scenarios, and the bold cells identify specific excess cancer risk levels (1×10^{-4} for the adult and child Tulalip RME). Their corresponding sediment concentrations using the best-fit model parameters can be found in the left column; these sediment concentrations are the RBTCs for those scenarios for the cancer risk threshold of 1×10^{-4}. Thus, for the adult tribal RME scenario based on Tulalip data, a sediment RBTC of 2 µg/kg dw total PCBs was associated with the 1×10^{-4} excess risk level; for the child tribal RME scenario based on Tulalip data, a sediment RBTC of 250 µg/kg dw total PCBs was associated with the 1×10^{-4} excess risk level. Note that the apparent jump in tissue concentrations and risk estimates between 250 µg/kg and 250.1 µg/kg is the result of a change in the assumed water contribution (see Table C.2-15) from 0.9 ng/L to 1.2 ng/L. Sediment RBTCs as well as upper and lower bounds for other risk scenarios and risk thresholds are presented in Section 8 in the main body of the SRI. The full table of all of the seafood consumption scenarios evaluated in the HHRA (Appendix B) is too large to reproduce in this format.

In total, three sediment values were identified for each risk scenario/risk threshold: the RBTC (based on the best-fit parameter set) and upper and lower bounds. These sediment RBTCs and upper and lower bounds are presented in Section 8 in the main body of the SRI. Note that the water concentration associated with any given sediment RBTC (or upper or lower bound) concentration is as indicated in Table C.2-15. For example, a sediment RBTC of 50 µg/kg dw would have an assumed water concentration of 0.6 ng/L, while a sediment RBTC of 280 µg/kg dw would have an assumed water concentration of 1.2 ng/L.

At extremely low sediment PCB concentrations, the PCB concentration in water alone is sufficient to result in estimates of tissue concentrations that correspond to excess cancer risk

estimates greater than 1×10^{-5} for people who consume seafood (for all RME consumption scenarios). Thus, it was not possible to calculate sediment RBTCs at the lower risk threshold levels, such as 1×10^{-6} and 1×10^{-5}. This exercise indicates that the assumption implicit in RBTC calculations that tissue concentrations (and therefore risk estimates) are predictable functions of PCB concentrations in sediment alone may be tenuous, particularly at very low sediment concentrations.

C.2.7 Summary

The FWM was developed to estimate the relationship between total PCB concentrations in tissue and sediment in order to estimate RBTCs in sediment for the EW SRI/FS. The FWM will also be used in the FS to assess residual risks that may remain following various sediment cleanup alternatives with resultant reduced total PCB sediment concentrations.

The structure of the EW FWM, like the LDW FWM, was based on the Arnot and Gobas model (Arnot and Gobas 2004a), a steady-state bioaccumulation model. The EW FWM provides estimates of total PCB concentrations in the tissue of 11 species or species groups, based on bioaccumulation of total PCBs from sediment and the water column. Many of the species included in the FWM were ecological receptors, prey for ecological receptors, or consumed by humans, as described in the risk assessments (Appendices A and B).

Input parameter values and distributions for the model were based on literature-derived and site-specific environmental data. The model was calibrated to identify sets of parameter values that best estimated empirical tissue total PCB concentration data. For many model input parameters, distributions of estimates of mean values were developed to reflect uncertainty in their values. Calibration was performed using a probabilistic approach in order to systematically explore all combinations of plausible parameter sets and their corresponding estimated total PCB concentrations in tissue.

Through the calibration process, a best-fit parameter set that estimated total PCB concentrations for all modeled target species within a factor of 2, except clams, which were within a factor of 3, of empirical data was identified. The average factor for all species was 1.4. A FWM that predicts average tissue concentrations to within 3 to 5 of the average empirical dataset is considered to be performing well.

To better understand the strengths and limitations of the model, model sensitivities and uncertainties were evaluated. The parameters that most influenced model uncertainty were those that affected the uptake of total PCBs by benthic invertebrates (e.g., porewater ventilation), affected PCB exposure from the water column (e.g., water concentration), and contributed to the uptake of total PCBs, including dietary absorption efficiencies (for crab) and lipid and moisture content (for various species). In general, the parameters that most influenced model uncertainty had broad ranges of values derived from the literature.

The FWM was used to develop sediment RBTCs for total PCBs. Following a four-step process, sediment RBTCs associated with various risk thresholds for various human health seafood ingestion scenarios and for two fish receptors were identified. Best-fit sediment RBTCs, as well as upper- and lower-bound RBTCs, were identified. Upper and lower bounds were developed based on the model performance criteria and do not reflect the total range of uncertainty in the sediment RBTCs. Sediment RBTCs are presented in Section 8 in the main body of the SRI.

C.3 DIOXINS AND FURANS RBTCs

The dataset for dioxins and furans in EW includes sediment and tissue data. However, no dioxin and furan data are available for water samples or benthic invertebrate tissue which precluded the use of a FWM to develop RBTCs for dioxins and furans. In addition, the FWM was not used for dioxins and furans because application of the model to a toxicity equivalent mixture of compounds is complicated, and would have required certain input parameters that are not readily available (such as a K_{OW} value weighted to account for differences in toxicity of the various dioxin and congeners). Also, the FWM was not calibrated for dioxin and furan compounds. Instead, sediment dioxin and furan RBTCs were developed from tissue RBTCs using a BSAF approach. Available EW tissue and sediment data were used to calculate site-specific BSAFs which were then used with the tissue RBTCs to calculate sediment RBTCs presented in Section 8 of the SRI.

The first step in developing RBTCs for dioxins and furans was to evaluate the consistency of the dioxin and furan patterns in tissue and sediment samples (Section C.3.1). This analysis also identified the dioxin and furan congeners that contributed the most to the dioxin and furan TEQ for each sample. The calculation of the BSAF values is discussed in Section C.3.2, the calculation of species-specific tissue RBTCs is discussed in Section C.3.3, and the

calculation of sediment RBTCs from the tissue RBTCs is detailed in Section C.3.4. Finally, the uncertainties associated with these calculations are discussed in Section C.3.5.

C.3.1 Dioxin and Furan Pattern Analysis

To evaluate the consistency of the dioxin and furan patterns in the available tissue and sediment samples the percent contribution of each of the 17 dioxin and furan TEQ congeners to the sum of the concentrations of these congeners was calculated. The detection frequency for each dioxin and furan congener and tissue type is provided in Table C.3-1. It should be noted that there were very low detection frequencies for clam and geoduck tissues which results in considerable uncertainty with regard to the dioxin and furan patterns which are primarily based on reporting limits for specific dioxin and furan congeners.

Table C.3-1
EW Fish Tissue Summary for Dioxins/Furans

Chemical	Detection Frequency					
	Shiner Surfperch	English Sole	Brown Rockfish	Crab	Clam	Geoduck
2,3,7,8-TCDD	2/3	3/3	4/6	6/6	0/3	0/4
1,2,3,7,8-PeCDD	2/3	2/3	3/6	5/6	0/3	0/4
1,2,3,4,7,8-HxCDD	1/3	2/3	0/6	4/6	0/3	1/4
1,2,3,6,7,8-HxCDD	2/3	3/3	6/6	6/6	0/3	1/4
1,2,3,7,8,9-HxCDD	0/3	1/3	2/6	4/6	0/3	1/4
1,2,3,4,6,7,8-HpCDD	2/3	3/3	6/6	6/6	3/3	1/4
OCDD	3/3	3/3	6/6	6/6	3/3	4/4
2,3,7,8-TCDF	3/3	3/3	6/6	6/6	1/3	3/4
1,2,3,7,8-PeCDF	2/3	3/3	5/6	6/6	0/3	0/4
2,3,4,7,8-PeCDF	3/3	3/3	4/6	5/6	1/3	0/4
1,2,3,4,7,8-HxCDF	0/3	0/3	5/6	0/6	0/3	1/4
1,2,3,6,7,8-HxCDF	2/3	3/3	2/6	5/6	0/3	0/4
1,2,3,7,8,9-HxCDF	0/3	0/3	2/6	5/6	0/3	0/4
2,3,4,6,7,8-HxCDF	2/3	3/3	4/6	4/6	0/3	0/4
1,2,3,4,6,7,8-HpCDF	0/3	0/3	6/6	0/6	2/3	3/4
1,2,3,4,7,8,9-HpCDF	0/3	1/3	0/6	1/6	0/3	0/4
OCDF	2/3	3/3	2/6	4/6	3/3	1/4

EW – East Waterway
HpCDD – heptachlorodibenzo-*p*-dioxin
HpCDF – heptachlorodibenzofuran
HxCDD – hexachlorodibenzo-*p*-dioxin
HxCDF – hexachlorodibenzofuran
OCDD – octachlorodibenzo-*p*-dioxin
OCDF – octachlorodibenzofuran
PeCDD – pentachlorodibenzo-*p*-dioxin
PeCDF – pentachlorodibenzofuran
TCDD – tetrachlorodibenzo-*p*-dioxin
TCDF – tetrachlorodibenzofuran

The English sole, shiner surfperch and crab tissue samples analyzed for dioxins and furans were three supercomposite samples which were created by compositing an equal portion of all existing composite samples to create one sample for each species and sample type. Three replicate composite samples were created for each tissue type. The dioxin patterns for these tissue samples are very similar within each tissue type, as expected because the three samples are replicates of one another. The predominant compound in the English sole whole body samples was OCDD which represented 51 to 59% of the total dioxin and furan concentrations (Figure C.3-1). In the shiner surfperch whole body samples, OCDD represented 31 to 35% of the total dioxin and furan concentration with 2,3,7,8-TCDF contributing 31 to 38%. Finally, the predominant congeners in the crab tissue samples (edible meat and hepatopancreas) were OCDD (26 to 50%) and 2,3,7,8-TCDF (17 to 22%).

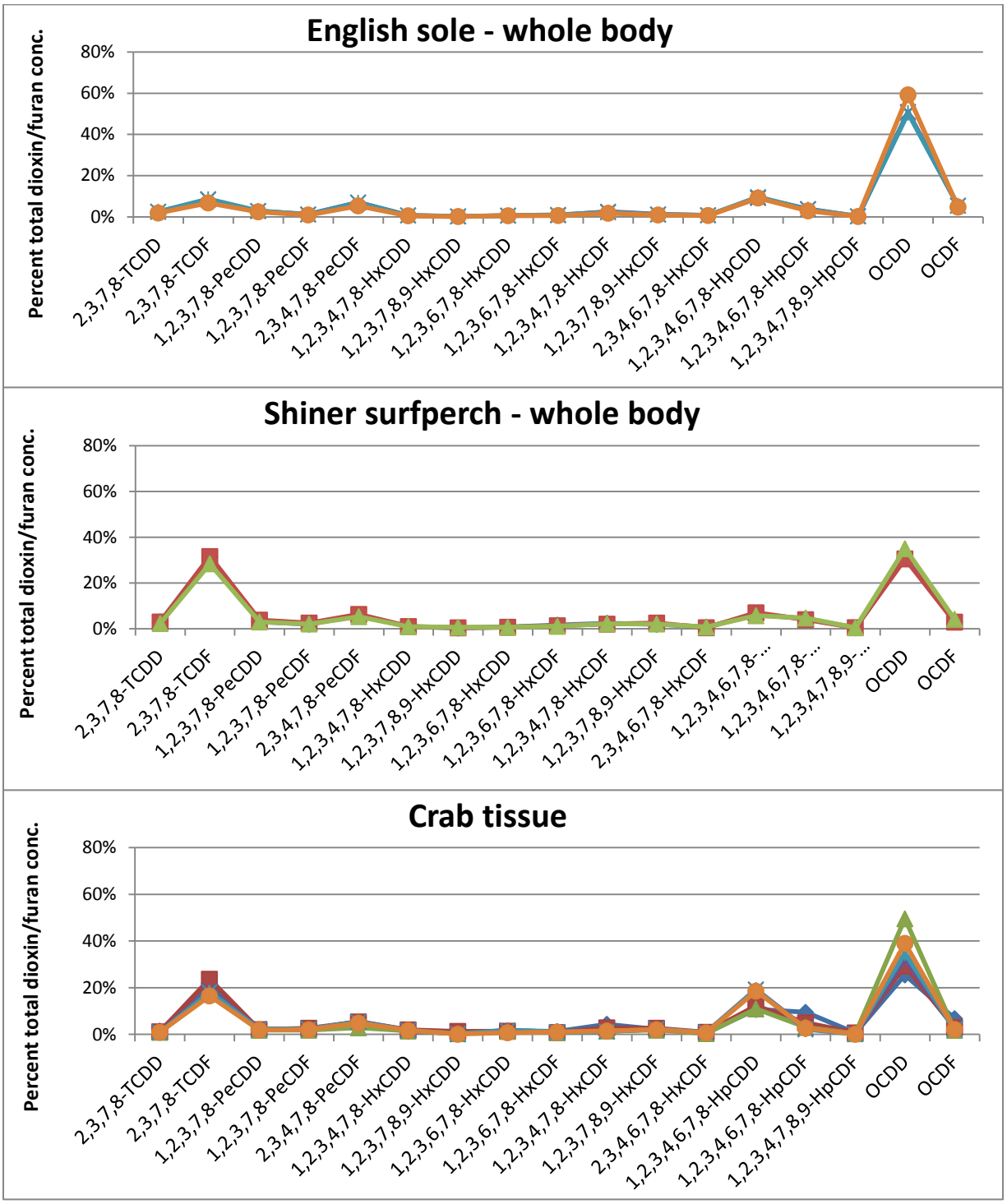


Figure C.3-1

Dioxin and Furan Composition Plot for English Sole (n =3), Shiner Surfperch (n=3), and Crab edible meat (n=3) and hepatopancreas (n =3), the individual samples are represented by unique colors in each plot

Intertidal clam species (i.e., butter, cockle, little neck and Eastern softshell), geoducks, and brown rockfish were not analyzed as supercomposite samples. Intertidal clams were analyzed as composites created for each species and location from which they were collected and geoducks were analyzed as individuals for the analysis of edible meat and as composites for gut balls. Brown rockfish were analyzed as individual fish rather than composites because of the small home ranges for this species. The dioxin and furan composition profiles for these species are provided in Figure C.3-2. The patterns associated with these tissue types were more variable than the results for the supercomposite tissue samples due to the fact that the samples represent either individual organisms and locations (e.g. rockfish) or composites that represent specific, unique organisms and locations (e.g. intertidal clams) with their inherent variability.

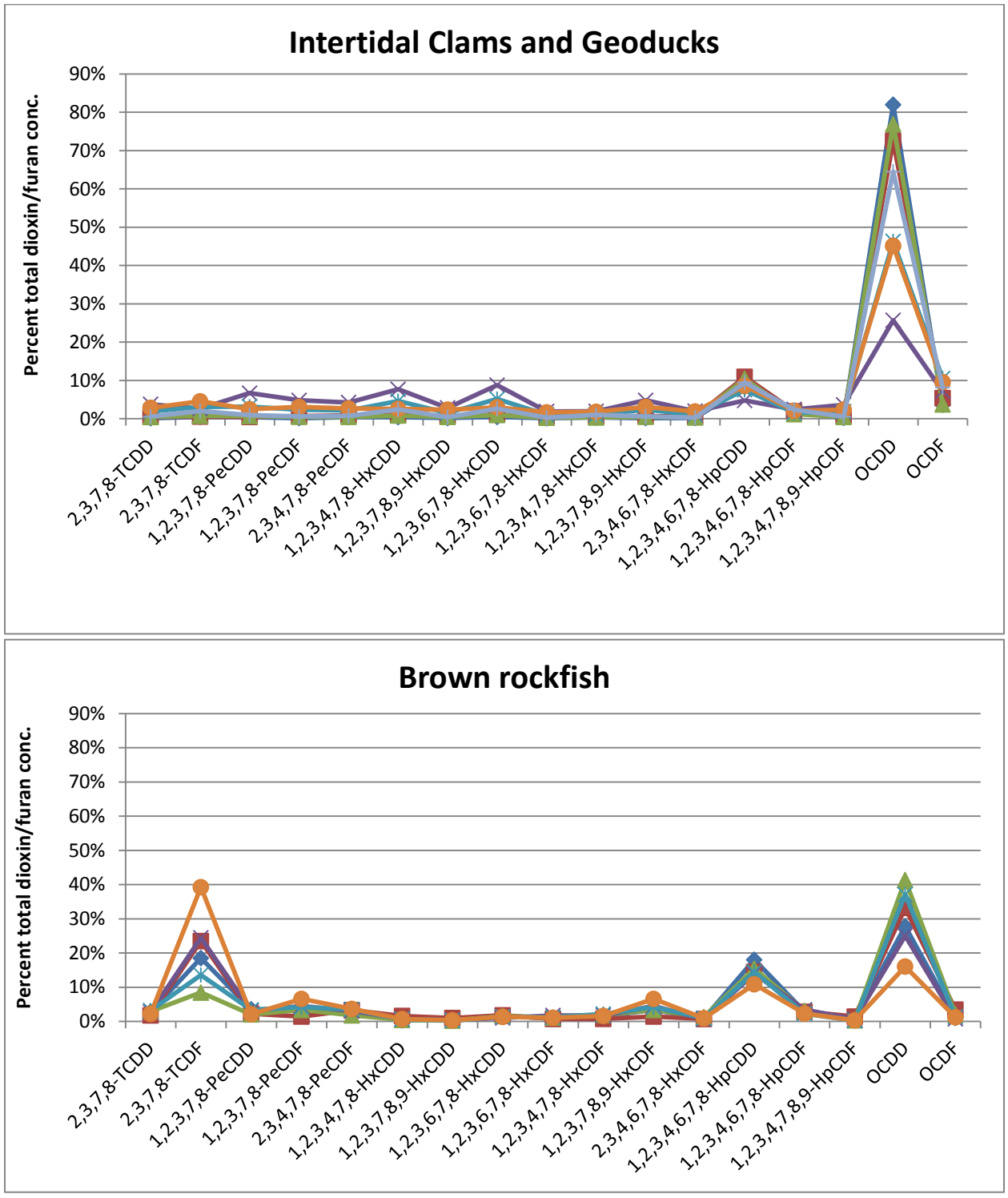


Figure C.3-2

Dioxin and Furan Composition Plot for Intertidal Clams (n=4), Geoducks edible meat (n=3) and gutballs (n=2) and Brown Rockfish (n=6) the individual samples are represented by unique colors in each plot

For intertidal clams and geoduck tissues, the predominant congener was OCDD which contributed 25 to 82% of the total dioxin and furan concentration. There were a significant number of non-detected dioxin and furan congeners in the intertidal clam and geoduck tissues (7 of 17 dioxin and furan congeners were never detected) compared to the other tissue types (1 of 17 dioxin and furan congeners were never detected) which resulted in similar contributions for the non-detected congeners based on reporting limits. The patterns with the larger OCDD contributions were associated with the intertidal clam tissues (77 to 82%) compared to the geoduck tissues (45 to 65%). For brown rockfish, OCDD, 1,2,3,4,6,7,8-HpCDD, and 2,3,7,8-TCDF were the predominant congeners, with OCDD contributing 16 to 41% of the total dioxin and furan concentration, 1,2,3,4,6,7,8-HpCDD contributing 11 to 18% of the total dioxin and furan concentration, and 2,3,7,8-TCDF contributing 8 to 39% of the total dioxin and furan concentration. The dioxin patterns without OCDD were also examined (Figure C.3-3). The variance that is observed for intertidal clams and geoducks is primarily a result of the low detection frequencies for the clam and geoduck samples. The variance in the brown rockfish reflects the fact that these samples were analyzed as individual fish rather than composites.

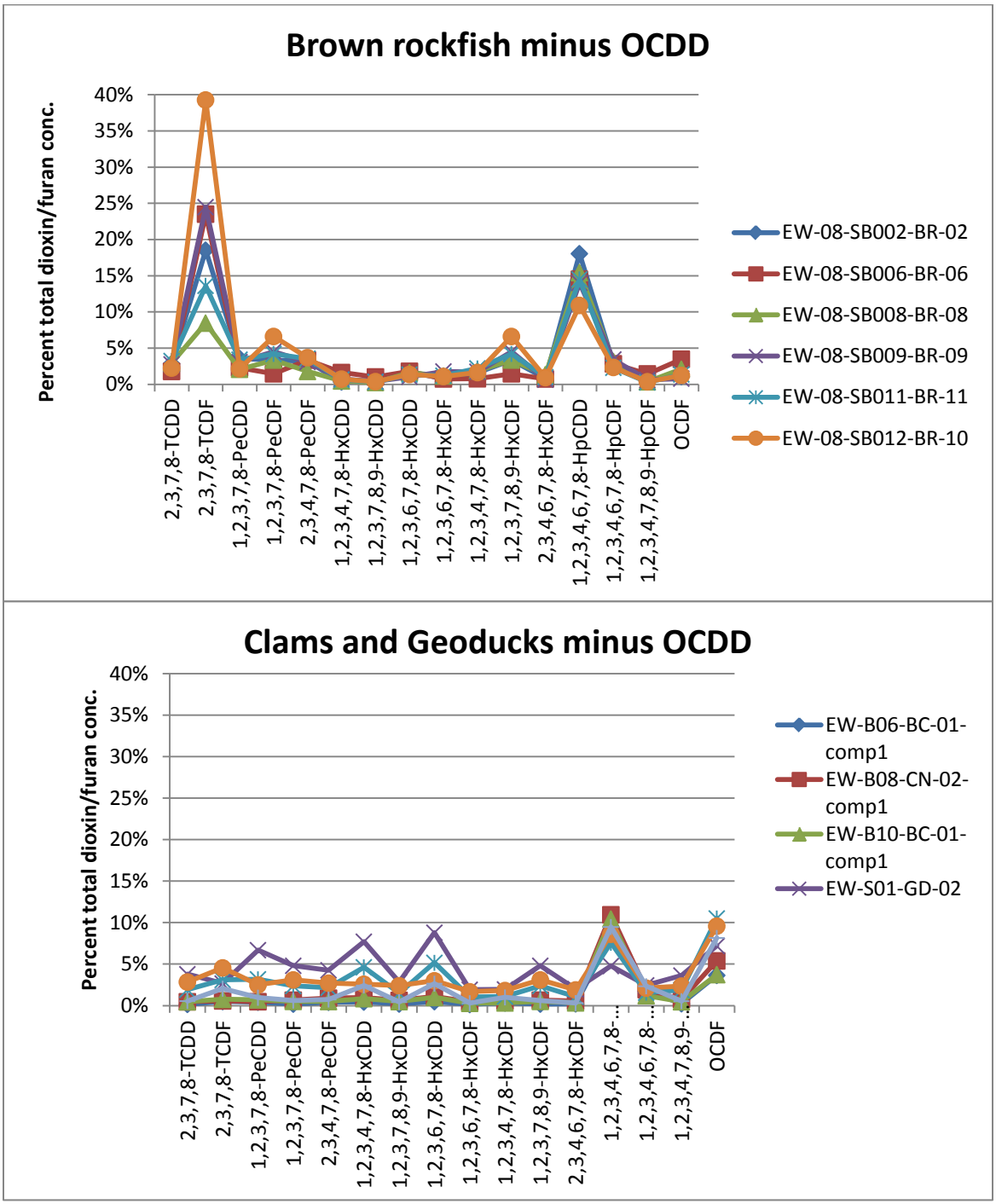


Figure C.3-3

Dioxin and Furan Composition Plot for Intertidal Clams, Geoducks and Brown Rockfish minus the contribution from OCDD

Finally, the dioxin and furan composition patterns for the sediment samples are provided in Figure C.3-4. Thirteen subtidal composite surface sediment samples were analyzed for dioxins and furans and each composite sample represents a specific area within the waterway and 4 intertidal MIS samples (Figure C.3-5) (Map 4-2). The dioxin and furan composition patterns in all the sediment composite samples were similar (Figure C.3-4). The predominant compound was OCDD which contributed 77 to 85% of the total dioxin and furan concentration.

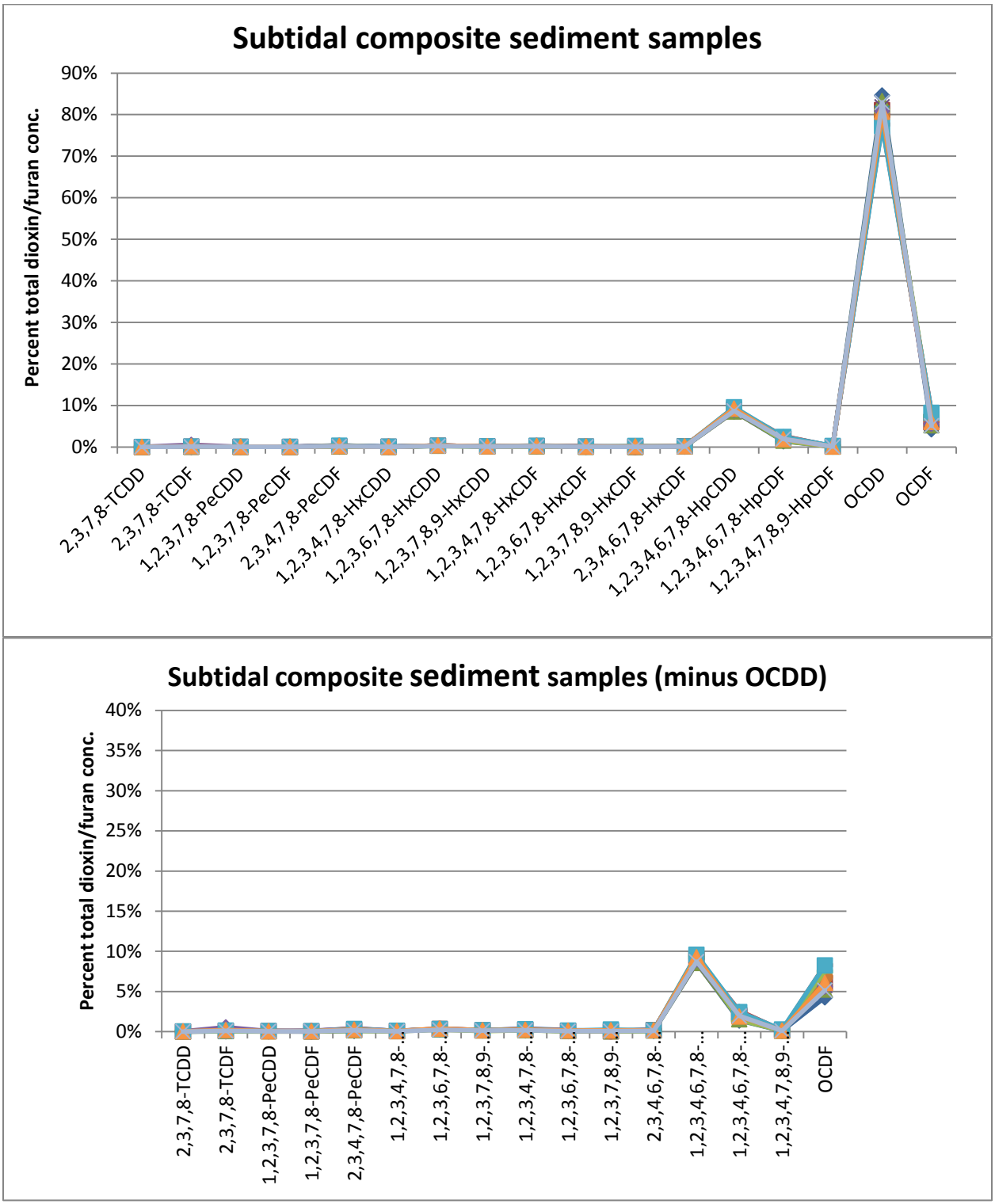
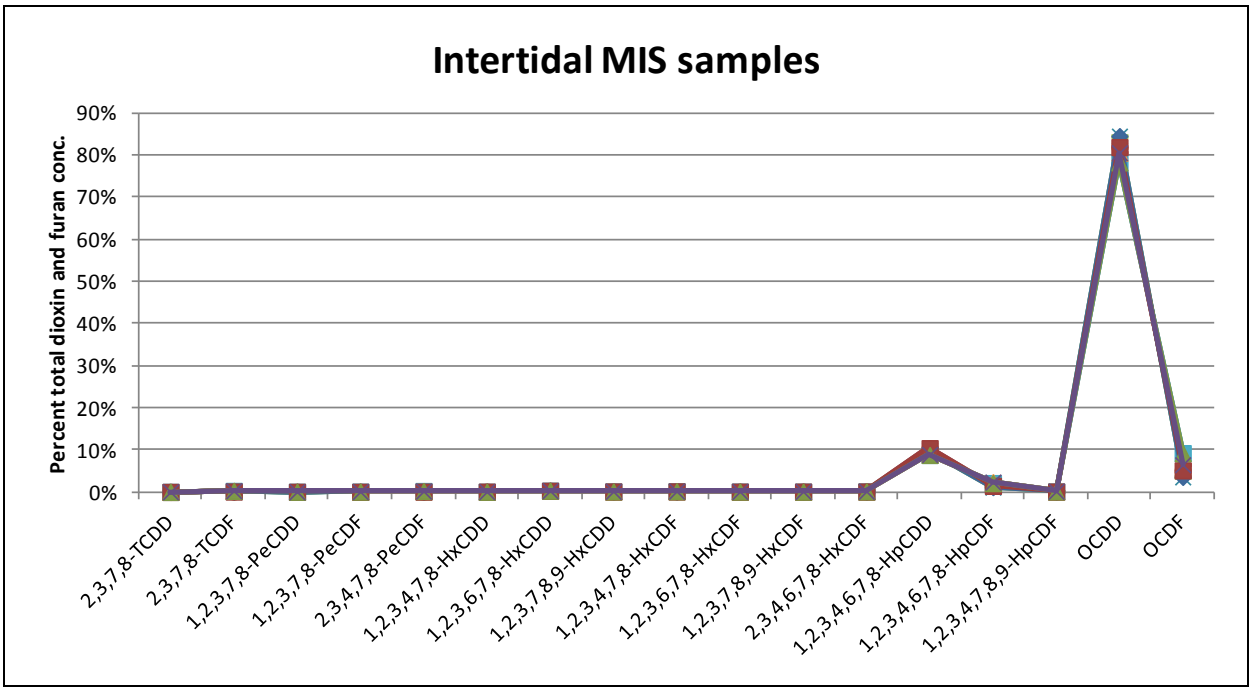


Figure C.3-4

Dioxin and Furan Composition Plot for Subtidal Composite Sediment Samples (n = 13) the individual samples are represented by unique colors in each plot.



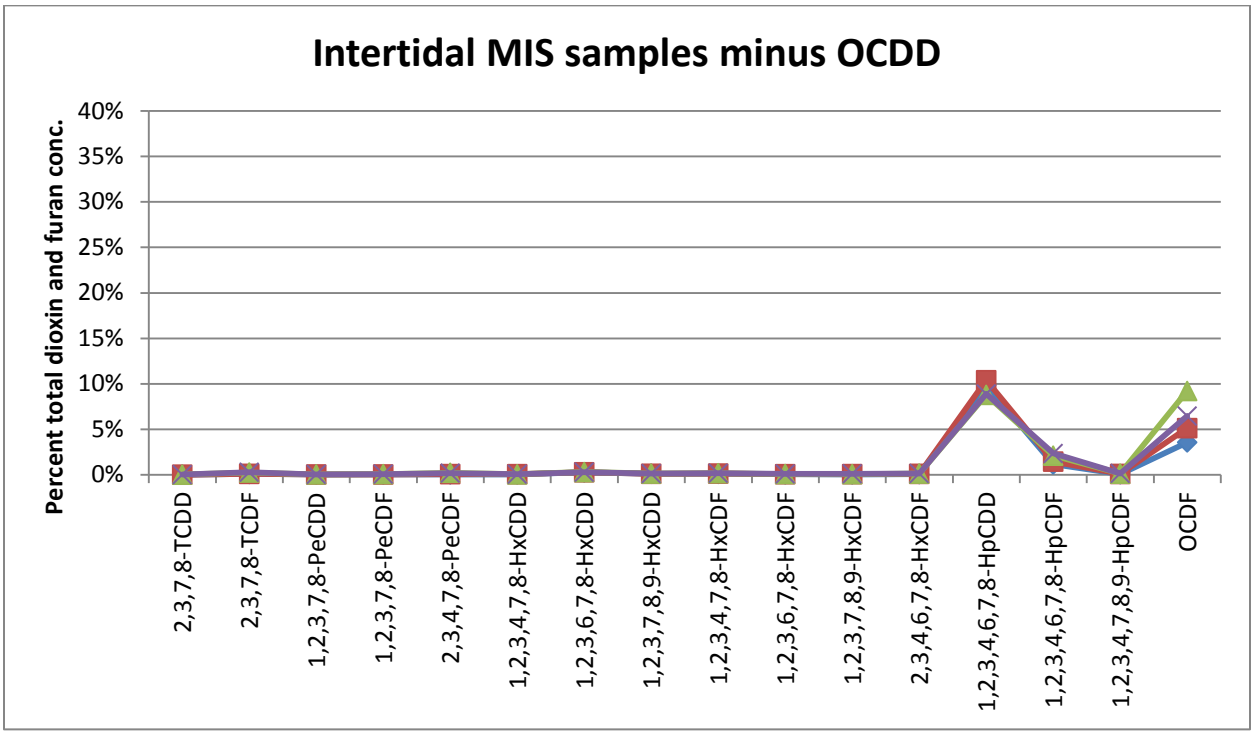


Figure C.3-5

Dioxin and Furan Composition Plot for Intertidal MIS Sediment Samples (n =4) the individual samples are represented by unique colors in each plot.

In addition to comparing the dioxin and furan congener patterns on the basis of concentration, it is also important to examine the contribution of each of the 17 dioxin and furan TEQ congeners to the calculated dioxin TEQ for each sample because the tissue and sediment RBTC values are based on TEQs, rather than on dioxin and furan congener concentrations. The calculation of dioxin TEQs are discussed in Appendix D. For the purposes of the pattern evaluation, the dioxin TEQ values were calculated based on the mammalian TEF values (WHO 2005). In Figures C.3-6, C.3-7 and C.3-8 the TEQ contribution from each of the dioxin and furan congeners is presented as the percentage of the total dioxin TEQ for the sample. In general the patterns are consistent for the tissues analyzed as super composite samples. The greatest variability is seen for clams, geoducks and brown rockfish. It is important to note that for the intertidal clam and geoduck tissues, 7 of the 17 dioxin and furan congeners were never detected and therefore the contributions for these congeners are based on reporting limits. The brown rockfish were analyzed as individual fish and therefore, more variance would be expected between samples.

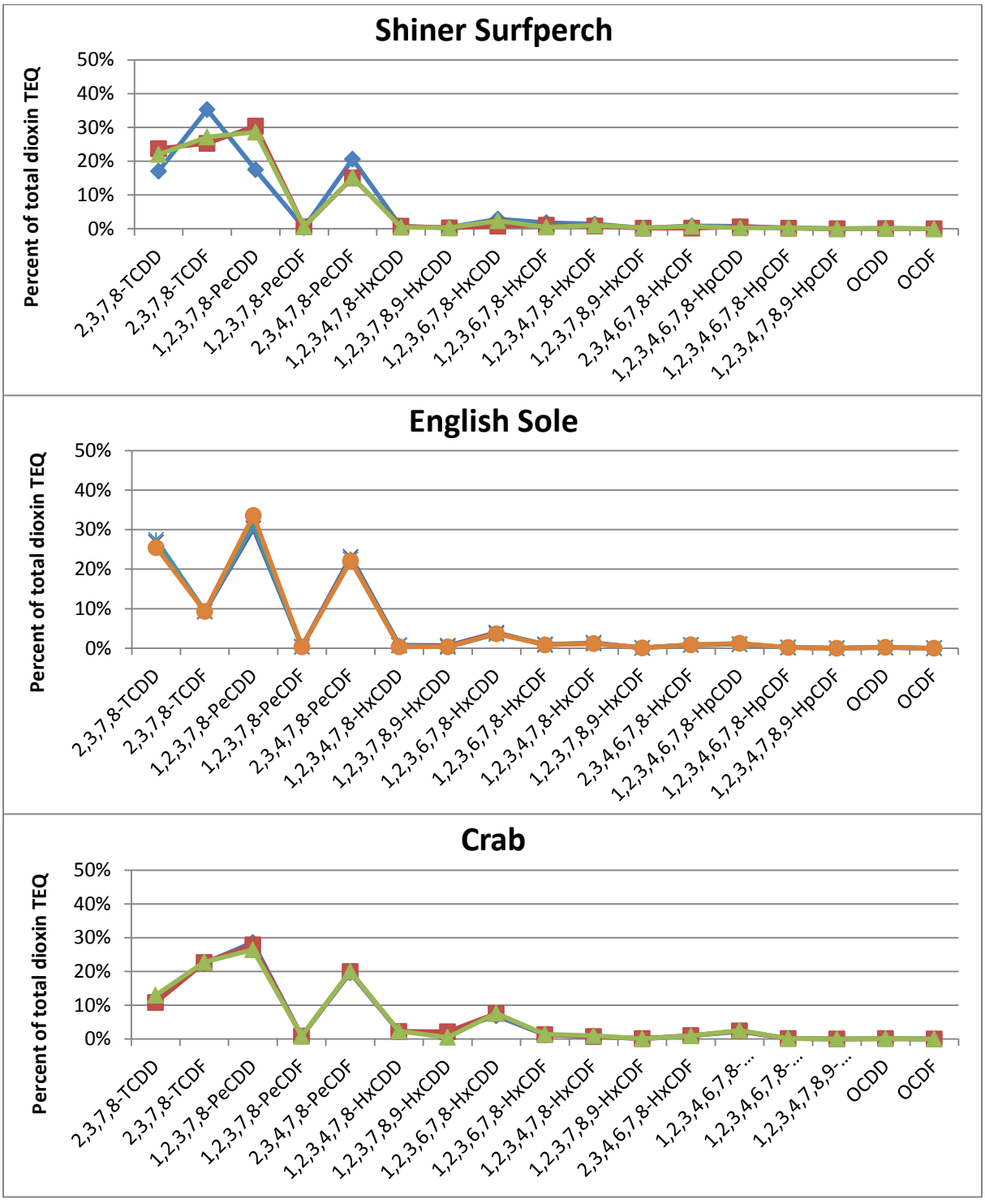


Figure C.3-6

TEQ-Based Dioxin and Furan Composition Patterns for English Sole (n =3), Shiner Surfperch (n=3), and Crab Tissues (n=6) the individual samples are represented by unique colors in each plot.

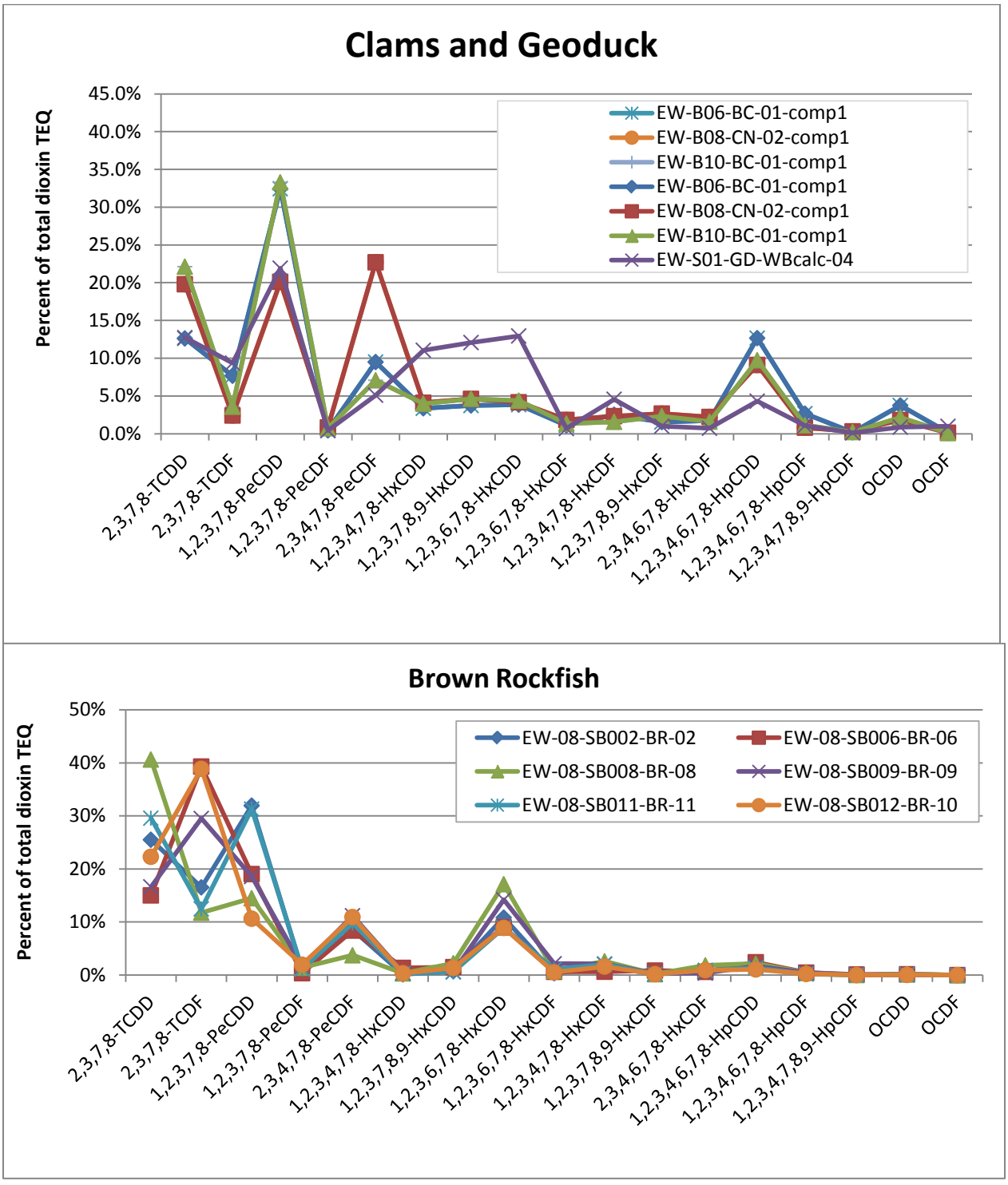


Figure C.3-7

TEQ-Based Dioxin and Furan Composition Patterns for Intertidal Clams, Geoducks, and Brown Rockfish

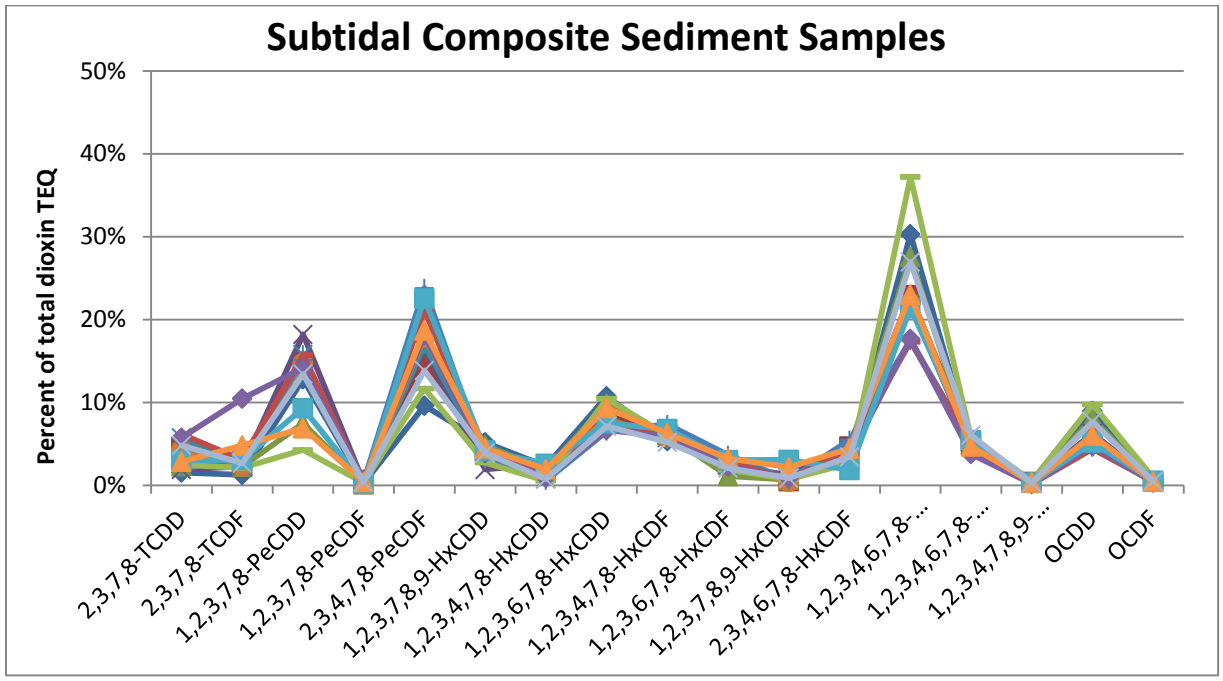


Figure C.3-8

TEQ-Based Dioxin and Furan Composition Patterns for Subtidal Composite Sediment Samples (n=13) the individual samples are represented by unique colors in each plot.

The analysis of the dioxin and furan patterns in tissue showed that the dioxin and furan patterns were generally consistent within each of the sample types and between sample types both in terms of the concentration patterns and the TEQ patterns. Similarly, the sediment patterns were similar to one another. One consistent difference between sediment and tissue patterns was the contribution of 1,2,3,4,6,7,8-HpCDD, which was a significant contributor to the TEQ in sediment samples and not in tissues. The fact that the tissue patterns and sediment patterns are internally consistent is important to the calculation of a TEQ-based BSAF. The BSAFs were calculated for individual congeners and then converted to dioxin and furan TEQ values based on the measured TEQ composition patterns. Variability in the patterns in tissue or sediment would increase the uncertainty in the results considerably.

The dioxin and furan congeners that contributed the greatest percentage to the sample TEQ values were identified for use in the calculation of BSAFs (Table C.3-1). These congeners were selected because they were frequently detected in the tissue samples and they represent toxicologically important congeners due to the contribution to the TEQ. The sum of the TEQ contributions from these four dioxin and furan congeners represent 68 to 93% of the dioxin

TEQ in the tissue samples and 37% of the dioxin TEQ in the sediment samples (mainly due to the absence of 1,2,3,4,6,7,8-HpCDD which does not contribute significantly to the tissue TEQ). The congeners were frequently detected in all tissue types and sediment with the exception of the clam and geoduck tissue samples where 2,3,7,8-TCDD and 1,2,3,7,8-PeCDD were never detected, 2,3,7,8-TCDF was detected four out of seven samples, and 2,3,4,7,8-PeCDF was detected in one out of seven samples. BSAFs should not be calculated based on non-detected results because the reporting limit is an analytical artifact and does not reflect the concentration of these congeners. Therefore, BSAFs were calculated for all tissue types except the clam and geoduck tissue because of the low detection frequencies of the congeners in these tissues and because there were no sediment samples specific to the clam and geoduck sampling areas analyzed for dioxins and furans that could be used to calculate the BSAFs.

C.3.2 BSAF Calculation

BSAFs for dioxins and furans are calculated as the ratio of the lipid normalized tissue concentration to the organic carbon normalized sediment concentration (Equation C-8):

$$BSAF = \frac{\text{tissue conc.} / \text{fraction lipid}}{\text{sediment conc.} / \text{foc}} \qquad \text{(C-8)}$$

BSAFs were calculated for the four dioxin and furan congeners that were identified as the primary contributors to the dioxin TEQ values for tissues (Table C.3-2).

Table C.3-2
Percent TEQ for Dioxin and Furan Congeners with Greatest Contribution to the Dioxin TEQ

Sample	2,3,7,8-TCDD Mean Percent TEQ (range of values)	2,3,7,8-TCDF Mean Percent TEQ (range of values)	1,2,3,7,8-PeCDD Mean Percent TEQ (range of values)	2,3,4,7,8-PeCDF Mean Percent TEQ (range of values)	Sum
English sole – whole body	27 (26 – 28)	9 (no range)	32 (30 – 34)	23 (22 – 23)	91
Shiner surfperch – whole body	21 (17 – 24)	29 (25 – 35)	26 (18 – 30)	17 (15 – 20)	93
Crab tissue	12 (11 – 13)	23 (no range)	28 (27 – 29)	20 (no range)	83
Clams and geoducks	21[a] (13 – 32)	6[b] (2 – 10)	31[a] (20 – 43)	10[c] (5 – 23)	68

Sample	2,3,7,8-TCDD Mean Percent TEQ (range of values)	2,3,7,8-TCDF Mean Percent TEQ (range of values)	1,2,3,7,8-PeCDD Mean Percent TEQ (range of values)	2,3,4,7,8-PeCDF Mean Percent TEQ (range of values)	Sum
Brown rockfish	25 (15 – 40)	25 (12 – 39)	21 (11 – 31)	9 (4 – 11)	80
Subtidal composite surface sediment	4 (2 – 6)	3 (1 – 10)	13 (4 – 18)	17 (10 – 24)	37

[a] 2,3,7,8-TCDD and 1,2,3,7,8-PeCDD were never detected in clam and geoduck tissue samples. The TEQs are based on TEFs multiplied by half the reporting limits for these congeners.

[b] 2,3,7,8-TCDF was not detected in 3 out of 7 clam and geoduck tissue samples. The TEQs are based on reporting limits when these congeners are not detected.

[c] 2,3,4,7,8-PeCDF was not detected in 6 out of 7 clam and geoduck tissue samples. The TEQs are based on reporting limits when these congeners are not detected.

PeCDD – pentachlorodibenzo-*p*-dioxin
PeCDF – pentachlorodibenzofuran
TCDD – tetrachlorodibenzo-*p*-dioxin
TCDF – tetrachlorodibenzofuran
TEQ – toxic equivalent

The BSAFs calculated for each of the four tissue types are provided in Table C.3-3. The sediment values used for all calculations were the area-weighted average, organic carbon-normalized sediment concentrations for each congener from the 13 subtidal composite samples. The English sole, shiner surfperch and crab tissues were all composited on an EW-wide basis. The brown rockfish samples were analyzed as individual fish. The relationship between the brown rockfish tissue concentrations and the sediment concentration in the composite sample collected closest to the brown rockfish sampling location was investigated and no relationship was observed ($r^2 = 0.08$). BSAF values were calculated for brown rockfish using both the area-wide sediment concentration as well as the sediment concentration from the nearest sediment composite sample (Table C.3-3). Because of this apparent lack of relationship with sediment, the BSAFs calculated for the individual rockfish are more variable than the BSAFs calculated for English sole, shiner surfperch, and crab tissues. There were no consistent differences between the brown rockfish BSAFs calculated using the EW-wide mean OC-normalized sediment concentrations and the BSAFs calculated using the nearest sediment value (Table C.3-3). The mean rockfish BSAF based on the EW-wide mean sediment concentration was used in the calculation of sediment RBTCs because the results were less variable than using data from proximate composite sediments with data from individual rockfish samples, and because no relationship was seen between concentrations in rockfish tissue concentrations and proximate composite sediment sample concentrations.

Table C.3-3

BSAF Values

Species	Sample ID	2,3,7,8-TCDD BSAF	2,3,7,8-TCDF BSAF	1,2,3,7,8-PeCDD BSAF	2,3,4,7,8-PeCDF BSAF
English sole – whole body	EW08-ES-WB-SUPCOMP1	0.41	0.20	0.15	0.09
	EW08-ES-WB-SUPCOMP2	0.47	0.22	0.17	0.10
	EW08-ES-WB-SUPCOMP3	0.43	0.22	0.18	0.10
Shiner surfperch – whole body	EW08-SS-WB-SUPCOMP1	0.16	0.23	0.05	0.03
	EW08-SS-WB-SUPCOMP2	0.16	0.23	0.06	0.03
	EW08-SS-WB-SUPCOMP3	0.14	0.24	0.06	0.03
Crab – soft tissues	EW08-RRDC-WBcalc-SUPCOMP1	0.39	1.03	0.30	0.17
	EW08-RRDC-WBcalc-SUPCOMP2	0.37	1.08	0.30	0.18
	EW08-RRDC-WBcalc-SUPCOMP3	0.41	1.01	0.27	0.17
Brown rockfish	EW-08-SB006-BR-06	0.59 (0.80)[a]	0.53 (0.60)[a]	0.24 (0.29)[a]	0.05 (0.06)[a]
	EW-08-SB009-BR-09	0.15 (0.26)[a]	0.27 (0.85)[a]	0.06 (0.08)[a]	0.02 (0.05)[a]
	EW-08-SB012-BR-10	0.80 (1.1)[a]	0.32 (0.36)[a]	0.18 (0.31)[a]	0.04 (0.06)[a]
	EW-08-SB008-BR-08	0.53 (0.79)[a]	0.65 (1.2)[a]	0.19 (0.19)[a]	0.05 (0.06)[a]
	EW-08-SB011-BR-11	0.85 (1.1)[a]	0.50 (0.83)[a]	0.29 (0.33)[a]	0.07 (0.08)[a]
	EW-08-SB002-BR-02	0.26 (0.23)[a]	0.63 (0.83)[a]	0.08 (0.07)[a]	0.03 (0.03)[a]
	Mean Rockfish BSAF[b]	0.53	0.48	0.17	0.04

[a] BSAF calculated based on the nearest sediment composite sample.

[b] Mean rockfish BSAF is the mean of the BSAF calculated for individual fish based on the area-wide average sediment concentration.

BSAF – biota-sediment accumulation factor

BSAF – biota-sediment accumulation factor
PeCDD – pentachlorodibenzo-*p*-dioxin
PeCDF – pentachlorodibenzofuran
TCDD – tetrachlorodibenzo-*p*-dioxin
TCDF – tetrachlorodibenzofuran
TEQ – toxic equivalent

The relationship between the sediment concentrations and BSAF values cannot be evaluated because all the tissues (except rockfish) were analyzed as site-wide composite samples. The variability in the individual rockfish tissues does not correlate with sediment concentrations.

C.3.3 Species-specific Tissue RBTC Calculations

The starting point for calculating dioxin and furan sediment RBTCs for RME seafood consumption scenarios presented in the HHRA was the tissue RBTCs presented in Section 8.2.2. These tissue RBTCs represent the ingestion-weighted average concentration in

tissue that corresponds to a certain risk level for each scenario. In order to calculate sediment RBTCs using the dioxin/furan BSAFs, it was necessary to calculate species-specific tissue RBTCs. The main assumptions required for these calculations were:

1) The relative ingestion rates for the various items in the market basket diet (i.e., the percentages of various seafood types that people eat)
2) The relative tissue contaminant concentrations among the food items

Because both of these factors may change in the future, it is important to recognize that there is considerable uncertainty associated with the dioxin/furan sediment RBTCs based on these species-specific tissue RBTCs.

The species-specific tissue RBTCs are presented in Table C.3-4. This table shows species-specific tissue RBTCs for all species in the market basket used to assess risks in the HHRA (Appendix B), although it was only possible to develop dioxin and furan BSAFs for benthic fish (English sole), perch, crab, and rockfish (see Section C.3.2). BSAFs for other species could not be developed, and the tissue RBTCs are presented here for informational purposes only.

Table C.3-4
Dioxin and Furan Species-Specific Tissue RBTCs

	Dioxin/Furan Tissue RBTCs at Various Risk Levels (ng TEQ/kg ww)								
	Adult Tribal RME (Tulalip data)			Adult Tribal RME (Tulalip data)			Adult API RME		
RBTC Type	**10^{-6}**	**10^{-5}**	**10^{-4}**	**10^{-6}**	**10^{-5}**	**10^{-4}**	**10^{-6}**	**10^{-5}**	**10^{-4}**
Overall RBTC	**0.0056**	**0.056**	**0.56**	**0.030**	**0.30**	**3.0**	**0.019**	**0.19**	**1.9**
Benthic fish, fillet[a]	0.0072	0.072	0.72	0.039	0.39	3.9	0.020	0.20	2.0
Benthic fish, whole body	na	na	na	na	na	na	0.048	0.48	4.8
Clams[b]	0.0035	0.035	0.35	0.019	0.19	1.9	0.0096	0.096	0.96
Crab, edible meat[b]	0.0045	0.045	0.45	0.024	0.24	2.4	0.012	0.12	1.2
Crab, whole body	0.012	0.12	1.2	0.064	0.64	6.4	0.033	0.33	3.3
Geoduck, edible meat[b]	0.0023	0.023	0.23	0.012	0.12	1.2	na	na	na
Geoduck, whole body[b]	0.0018	0.018	0.18	0.0098	0.098	0.98	na	na	na
Pelagic fish, perch	0.013	0.13	1.3	0.069	0.69	6.9	0.035	0.35	3.5
Pelagic fish, rockfish	0.026	0.26	2.6	0.14	1.4	14	0.071	0.71	7.1

[a] Benthic fish fillet RBTCs were converted to whole body tissue concentrations using a fillet-to-whole body conversion factor (fillet RBTCs were divided by the factor of 0.582 to calculate the whole body concentration).

The conversion factor is the mean of the ratios of measured fillet to whole body dioxin and furan TEQ values for EW English sole.

[b] BSAFs for these species-tissue type combinations could not be developed. Species-specific RBTCs are presented for informational purposes only.

API – Asian and Pacific Islander
BSAF – biota to sediment accumulation factor
RBTC – risk-based threshold concentration
RME – reasonable maximum exposure
TEQ – toxic equivalent
ww – wet weight

The following describes in detail the steps that were used to calculate the species-specific tissue RBTCs presented in Table C.3-4. To clarify the process for species-specific tissue RBTC derivation, an example calculation is also discussed in each step, using the RBTC for dioxin/furan TEQ at the 1×10^{-6} risk level for the adult tribal RME scenario based on Tulalip data.

1. **Overall tissue RBTC**: The starting point for calculating a species-specific tissue RBTC is the ingestion-weighted tissue RBTC (as presented in Section 8.2.2 of the RI). These ingestion-weighted tissue RBTCs, which are also referred to as "overall tissue RBTCs," are calculated based on the overall seafood ingestion rate (IR) and other scenario-specific parameters (e.g., body weight and exposure duration). The overall tissue RBTC dioxin/furan TEQ at the 1×10^{-6} risk level for the adult tribal RME scenario based on Tulalip data is 0.0056 ng/kg wet weight (ww) (Table C.3-4).

2. **Ingestion-weighted average concentration equation**: To calculate species-specific tissue RBTCs, the ingestion-weighted tissue RBTC must be broken down into its component pieces, which represent all the components of the diet (Equation C-9).

$$C_{ingestion.weighted} = (IR\%_{clam} \times C_{clam}) + (IR\%_{crabEM} \times C_{crabEM}) + (IR\%_{crabWB} \times C_{crabWB}) + (IR\%_{geoEM} \times C_{geoEM}) + (IR\%_{geoWB} \times C_{geoWB}) + (IR\%_{perch} \times C_{perch}) + (IR\%_{rockfish} \times C_{rockfish}) +.(IR\%_{ES-WB} \times C_{ES-WB}) + (IR\%_{ES-fil} \times C_{ES-fil}) \quad \text{(C-9)}$$

   Where IR% is the species-specific percentage of the total seafood ingestion rate; C is the species-specific tissue contaminant concentration; and $C_{ingestion\text{-}weighted}$ is the ingestion-weighted average contaminant concentration discussed in Step 1.

   For the adult tribal RME scenario based on Tulalip data, Equation C-10 presents the same equation but with the actual ingestion rate percentages and the overall tissue RBTC of 0.0056 ng /kg ww substituted, as appropriate.

$$0.0056 = (40.6\% \times C_{clam}) + (27.0\% \times C_{crabEM}) + (8.6\% \times C_{crabWB}) + (6.7\% \times C_{geoEM}) + (0.9\% \times C_{geoWB}) + (1.0\% \times C_{rockfish}) + (7.4\% \times C_{perch}) + (0\% \times C_{ES-WB}) + (7.8\% \times C_{ES-fil}) \quad \text{(C-10)}$$

As was done in the HHRA, in cases where there were no data for an individual COPC in mussel tissue (as is the case for dioxins and furans), the percentage of the consumption rate attributed to mussels was distributed proportionally to the other consumption groups (see Table B-13). At the ingestion-weighted tissue RBTC of 0.0056 ng/kg ww (i.e., the overall tissue RBTC), the "C" for each species is equal to the species-specific dioxin/furan TEQ tissue RBTC for the 1×10^{-6} risk level for the adult tribal RME scenario based on Tulalip data.

3. **Species-to-species relationship**: As shown in Equation C-10, nine different variables (i.e., the concentrations of the different consumption categories) remain once all the ingestion rates have been substituted. This equation cannot be solved for a single species concentration (i.e., single variable) unless the concentration relationships among the various species are known and are assumed to be constant over time. The relationship among species (represented by ratios, as shown in Equation C-11) can be approximated based on empirical dioxin and furan data from the EW. In this example, relationships among the concentrations in various species were derived based on the HHRA tissue dataset for the EW. Thus, to calculate the concentration of a single species (e.g., perch) in the market basket, it is necessary to use the ratio of the average concentration for that species to the ingestion-weighted average concentration (which is calculated as shown in Step 4).

4. **Solving the equation for species-specific tissue RBTCs**: Based on the assumptions in Step 3, Equation C-10 can be simplified to Equation C-11 and solved for a single species (in this example, perch).

$$C_{perch} = \frac{RBTC_{overall} \times EPC_{perch}}{C_{ingestion.weighted}} \quad \text{(C-11)}$$

In this example, the overall RBTC is equal to 0.0056 ng/kg ww, and based on the empirical dataset used for the HHRA, the perch concentration used in the HHRA (i.e., the EPC) is equal to 1.4 ng/kg ww, and the ingestion-weighted tissue concentration is equal to 0.61 ng/kg ww. Note that the ingestion-weighted concentration of 0.61 ng/kg ww was calculated by substituting the empirical tissue concentrations from the HHRA dataset into Equation C-9, as shown in Equation C-12.

$$C_{ingestionweighted} = 0.61 = (40.6\% \times 0.38) + (27.0\% \times 0.49) + (8.6\% \times 1.3) + (6.7\% \times 0.25) + (0.9\% \times 0.2) + (1.0\% \times 2.8) + (7.4\% \times 1.4) + (0\% \times 1.9) + (7.8\% \times 0.79) \quad \text{(C-12)}$$

To calculate the perch tissue RBTC, these values are substituted into Equation C-11, as shown in Equation C-13.

$$C_{perch} = RBTC_{perch} = \frac{RBTC_{overall} \times EPC_{perch}}{Average_{ingestion.weighted}} = \frac{0.0056 \times 1.4}{0.61} = 0.013 \quad \text{(C-13)}$$

This proportionality calculation is then repeated for the other tissue types that comprise the diet.

As noted above, this approach assumes that relative contaminant concentrations among the species remain the same even when conditions change. Different species-to-species relationships could be calculated if multiple empirical datasets were available, which in turn would result in different tissue RBTCs.

C.3.4 Sediment RBTC Calculations

As discussed in Section C.3.3, species-specific tissue RBTCs were calculated for the four species for which dioxin and furan BSAFs were available. The species-specific tissue RBTCs are based on the cancer risk threshold of 10^{-6} and are back-calculated from the threshold following the HHRA procedures for each of the RME scenarios; results are provided in Table C.3-5. The tissue RBTCs are for total dioxin and furan TEQ, which are the chemical forms for which risks are calculated in the HHRA.

Table C.3-5
Species-Specific Dioxin/Furan Tissue RBTCs (ng TEQ/kg ww)

Scenario	Risk Level	Dioxin and Furan	English Sole	Shiner Surfperch	Crab[a]	Brown Rockfish
Adult Tribal RME (Tulalip data)	10^{-6}	**Dioxin and Furan**	**0.017**[b]	**0.013**	**0.012**	**0.026**
		2,3,7,8-TCDD	0.005[b]	0.003	0.001	0.006
		2,3,7,8-TCDF	0.002[b]	0.004	0.003	0.006
		1,2,3,7,9-PeCDD	0.005[b]	0.003	0.003	0.005
		2,3,4,7,8-PeCDF	0.004[b]	0.002	0.002	0.002

Scenario	Risk Level	Dioxin and Furan	English Sole	Shiner Surfperch	Crab[a]	Brown Rockfish
Child Tribal RME (Tulalip data)	10^{-6}	**Dioxin and Furan**	**0.092** [b]	**0.069**	**0.064**	**0.14**
		2,3,7,8-TCDD	0.024 [b]	0.014	0.008	0.034
		2,3,7,8-TCDF	0.0085 [b]	0.020	0.015	0.034
		1,2,3,7,9-PeCDD	0.029 [b]	0.018	0.018	0.029
		2,3,4,7,8-PeCDF	0.021 [b]	0.012	0.043	0.012
Adult API RME	10^{-6}	**Dioxin and Furan**	**0.048**	**0.035**	**0.033**	**0.071**
		2,3,7,8-TCDD	0.013	0.007	0.004	0.018
		2,3,7,8-TCDF	0.004	0.010	0.007	0.018
		1,2,3,7,9-PeCDD	0.015	0.009	0.009	0.015
		2,3,4,7,8-PeCDF	0.010	0.006	0.007	0.006

[a] Crab whole body concentrations

[b] English sole fillet RBTCs were converted to whole body tissue concentrations using a fillet-to-whole body conversion factor (fillet RBTCs were divided by the factor of 0.582 to calculate the whole body concentration).

API – Asian and Pacific Islander
RBTC – risk-based threshold concentration
RME – reasonable maximum exposure
TEQ – toxic equivalent
ww – wet weight

The process for the calculation of sediment RBTCs from the tissue RBTCs is described in detail below and illustrated in Figure C.3-9. The following is a brief summary of the process. The total TEQ tissue RBTCs are first converted to individual congener TEQs for the four individual congeners for which sufficient data were available to develop BSAFs. These four tissue congener TEQs are then converted to tissue concentrations, which are then converted to sediment concentrations using the BSAFs developed above. The sediment concentrations for the four congeners are then converted to four sediment TEQs, and the four sediment congener TEQs are then related to total dioxin/furan TEQ in sediment, which becomes the sediment RBTC for total TEQs.

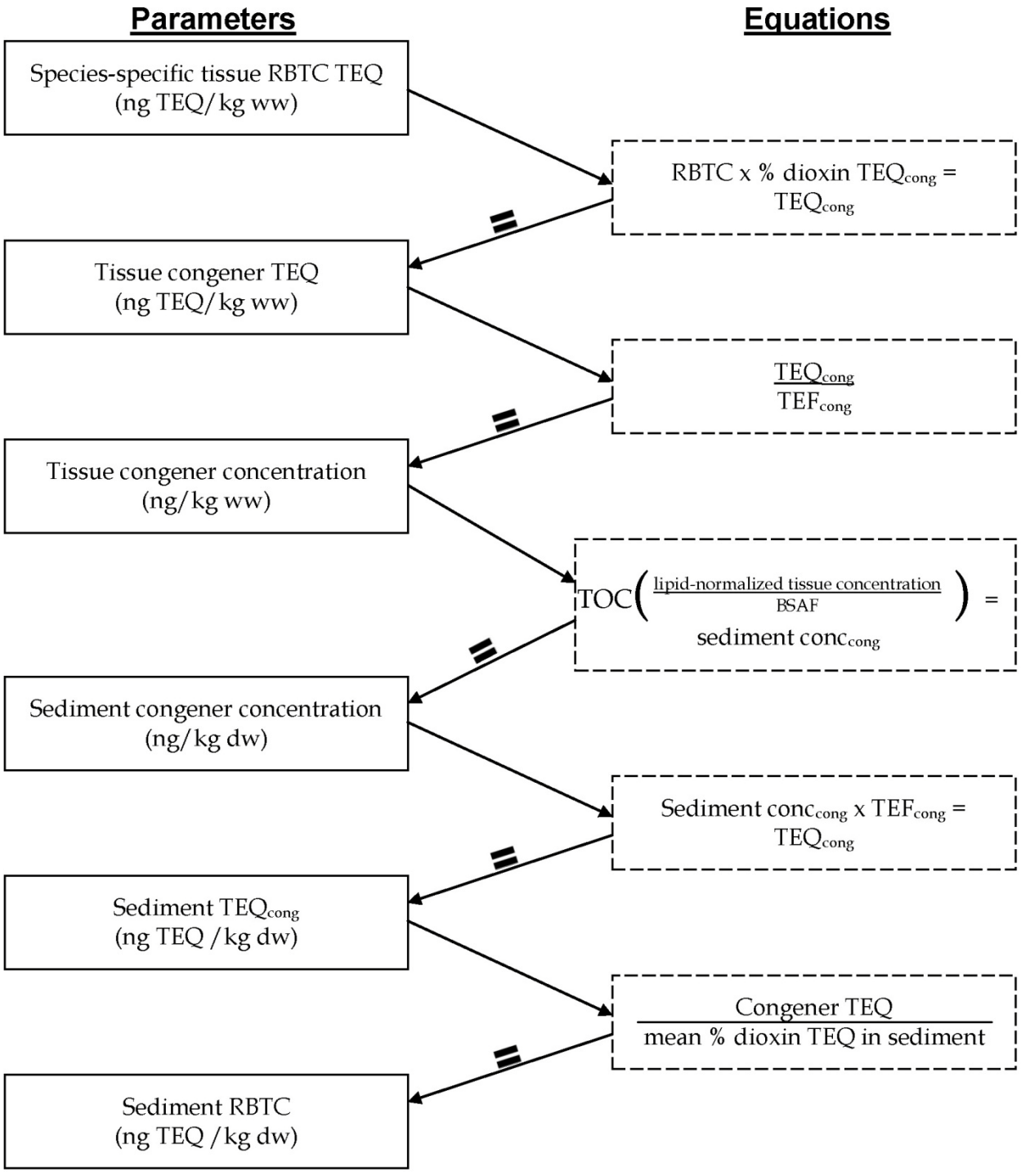


Figure C.3-9

Flow Diagram for Dioxin and Furan Sediment RBTC Calculation

As shown in the first box of Figure C.3-9, the RBTC values are risk-based concentrations of the dioxin/furan TEQ in tissue. The tissue congener TEQ value for each of the four congeners were calculated based on the fraction of the total TEQ represented by the congener in the tissue samples. The tissue congener TEQ concentration was then converted to a tissue congener concentration by dividing the TEQ by the congener TEF value.

The congener tissue concentrations (on a wet weight basis) were lipid-normalized and then used to calculate the corresponding organic carbon normalized sediment concentration based on the BSAF for the specific congener and tissue type using Equation C-14.

$$\text{sediment conc (OC – normalized)} = \frac{\text{tissue conc (lipid – normalized)}}{\text{BSAF}} \qquad \text{(C-14)}$$

The species- specific tissue lipid values and sediment organic carbon values were calculated based on the mean of the measured species-specific lipid values and sediment organic carbon values. The organic carbon normalized sediment concentration of each of the congeners was converted to a dry weight concentration and then converted into a TEQ value using the congener TEF value. The congener TEQ sediment concentration was finally converted into dioxin /furan TEQ concentration based on the mean contribution of the congener to the sediment dioxin/furan TEQ in the sediment composite samples (Table C.3-2). The resultant values are the sediment RBTCs for dioxins and furans based on total TEQ. The sediment dioxin/furan RBTC values calculated for each dioxin and furan congener for the human health RME seafood ingestion scenarios are provided in Table C.3-6. The four congener-specific values calculated for each tissue type are very consistent within the tissue type and across the four tissue types. Because all of the values were calculated based on the presumption of consistent congener patterns in both tissues and sediments, each of the congeners functions as a surrogate of the others. The mean of the four congener-specific sediment RBTCs within each scenario can be considered the sediment RBTC for total dioxin/furan TEQ for the specified tissue type.

Table C.3-6
Dioxin/furan Sediment RBTCs (ng TEQ/kg dw)

Scenario	Risk Level	Dioxin and Furan	English sole	Shiner surfperch	Crab	Brown Rockfish
Adult Tribal RME (Tulalip data)	10^{-6}	2,3,7,8-TCDD	0.20	0.21	0.18	0.21
		2,3,7,8-TCDF	0.16	0.17	0.18	0.24
		1,2,3,7,9-PeCDD	0.18	0.19	0.16	0.19
		2,3,4,7,8-PeCDF	0.15	0.17	0.18	0.16
		Mean	**0.17**	**0.19**	**0.18**	**0.18**
Child Tribal RME (Tulalip data)	10^{-6}	2,3,7,8-TCDD	1.05	0.97	1.15	1.11
		2,3,7,8-TCDF	0.85	0.98	0.92	1.29
		1,2,3,7,9-PeCDD	0.95	0.87	1.04	0.84
		2,3,4,7,8-PeCDF	0.82	0.97	0.90	0.96
		Mean	**0.92**	**0.95**	**1.00**	**1.05**
Adult API RME	10^{-6}	2,3,7,8-TCDD	0.55	0.50	0.59	0.57
		2,3,7,8-TCDF	0.44	0.50	0.47	0.66
		1,2,3,7,9-PeCDD	0.49	0.44	0.53	0.43
		2,3,4,7,8-PeCDF	0.43	0.50	0.46	0.49
		Mean	**0.48**	**0.48**	**0.51**	**0.54**

API – Asian and Pacific Islander
dw – dry weight
RBTC – risk-based threshold concentration
RME – reasonable maximum exposure
TEQ – toxic equivalent

C.3.5 Uncertainties

There are several sources of uncertainty in the use of the BSAF approach to develop sediment RBTCs for dioxin:

- The dataset that was used to develop the BSAFs is limited. Specifically, the only data available for English sole, shiner surfperch, and crab tissues are supercomposite samples which were designed to provide a robust assessment of the mean dioxin TEQ concentration. However, the variability of the TEQ concentrations and the dioxin and furan patterns cannot be assessed based on these samples.

- The use of the BSAF approach is based on the assumption that the observed tissue dioxin TEQ composition patterns within each species are consistent throughout the populations and will be consistent in the future.
- The sediment dioxin TEQ composition patterns are also assumed to be consistent throughout the site and remain consistent in the future.
- The derivation of the species-specific dioxin and furan tissue RBTCs is based on the proportion of these species in the diets evaluated in the HHRA. If there were changes in the relative proportions in the diet then different tissue RBTCs would be derived.
- In addition, this approach assumes that relative contaminant concentrations among the species remain the same even when conditions change. Different species-to-species relationships could be calculated if multiple empirical datasets were available, which in turn would result in different RBTCs.

Analysis of variability associated with the brown rockfish samples was conducted. All of the other tissue types were analyzed as supercomposite samples for dioxins and furans so it is not possible to examine the variance associated with these tissue types. In addition, because of the limited home range of brown rockfish, BSAFs were calculated based on the dioxin concentration in the sediment sample closest to the location of the rockfish sample.

First, the uncertainty associated with the variance of the BSAFs calculated for individual fish was investigated. The minimum and maximum BSAFs calculated for the individual rockfish based on the nearest sediment sample were used to calculate RBTC values for the Adult Tribal RME at 10^{-6} risk level. The sediment RBTC calculated with the mean BSAFs for each dioxin and furan congener based on the site-wide sediment average dioxin concentration was 0.18 ng TEQ/ kg dw. When the sediment RBTC was calculated with the minimum BSAF value for each dioxin congener the RBTC was 0.33 ng TEQ/kg dw. When the sediment RBTC was calculated with the maximum BSAF value for each dioxin congener the sediment RBTC was 0.11 ng TEQ/kg dw.

The variance in the dioxin patterns in the individual rock fish samples was also examined. The sediment RBTC calculated based on the mean rockfish dioxin patter for the Adult Tribal RME at 10^{-6} risk level was 0.18 ng TEQ /kg dw. When the dioxin congener patterns for each

of the individual fish were used to calculate sediment RBTC values, the values ranged from 0.12 to 0.21 ng TEQ/kg dw.

Based on this limited dataset, it appears that the variability associated with the BSAF and the dioxin pattern in the individual rockfish samples are a potential source of uncertainty in the calculation of sediment RBTCs for dioxins and furans.

C.4 TBT TISSUE AND SEDIMENT RBTCS FOR BENTHIC INVERTEBRATES

Tributyl tin (TBT) was identified as a risk driver for benthic invertebrates in the EW ERA. The tissue RBTC for benthic invertebrates is equal to the TBT tissue TRV used in the ERA: 120 µg/kg ww. This tissue TRV is based on sterilization of female gastropods due to imposex after chronic exposure to TBT in water (Gibbs et al. 1988). In order to develop a sediment TBT RBTC for benthic invertebrates, the relationship between benthic invertebrate tissue TBT concentrations and the TBT concentrations in the co-located sediment samples was investigated.

Two EW datasets were considered in developing a sediment RBTC based on the tissue TRV. The first dataset was based on field-collected tissue samples. TBT concentrations were measured in 12 composite samples of benthic invertebrates collected (Map 4-2) throughout the EW as part of the SRI. These samples were created from the mixture of benthic invertebrate species collected from grab samples and represent a wide range of marine species (e.g., polychaetes, harpacticoid copepods, gammarid amphipods and clams [< 1 cm]). Each tissue composite sample represents the available tissue obtained from 5 to 11 grab samples collected within a sampling area. Equal aliquots from all the sediment grab samples within a sampling area were combined into a composite sediment sample that corresponded to each composite tissue sample. It should be noted that the tissue samples were created using all available tissue and due to the variation in the amount of tissue present in each of the individual grab samples, the individual grab samples were not equally represented on a mass basis in the composite tissue sample. By contrast, the sediment composite samples were created using an equal volume of sediment from each grab sample. The use of unequal tissue mass from different species in each composite sample adds some uncertainty to the comparison of tissue concentrations to sediment concentrations among the 12 areas.

The second dataset was based on tissue and sediment samples that were analyzed as part of laboratory bioaccumulation testing conducted in with two different EW sediment samples and two test organisms. The two test organisms were marine polychaetes, *Nephtys caecoides* and *Armandia brevis* (Windward 2003*). Nephtys* is a standard test organism that is commonly used in bioaccumulation testing and *Armandia* has been shown to be sensitive to TBT exposure (Meador and Rice 2001). The tests were conducted under both static and flow-through conditions for each organism with two EW sediment samples that contained two concentrations of sediment TBT; results from both conditions are used in the present analysis.

TBT is an organo-metallic compound that exhibits properties associated with both charged ionic chemicals and organic chemicals (Berg et al. 2001). For example,the bioavailability of sediment-associated TBT has been shown to be related to the the organic carbon content of sediment (Meador et al. 1997; Meador 2000), similar to nonpolar organic chemicals. However, the lipid content in tissues does not appear to affect TBT bioaccumulation (Meador 2000; Meador et al. 2002), similar to ionic chemicals. Therefore, the relationship between dry-weight tissue concentrations and organic carbon-normalized sediment concentrations was used as the basis for developing the sediment RBTC.

The first step in developing an RBTC for TBT was to evaluate the relationships in the SRI data through regression analysis. The initial regression relationship based on the SRI EW composite benthic invertebrate tissue and co-located sediment data is shown in FigureC.4-1). The regression relationship had an r^2 of 0.3, and p value of 0.07. This regression relationship was not useful for determining a RBTC value because of the lack of significance in the regression.

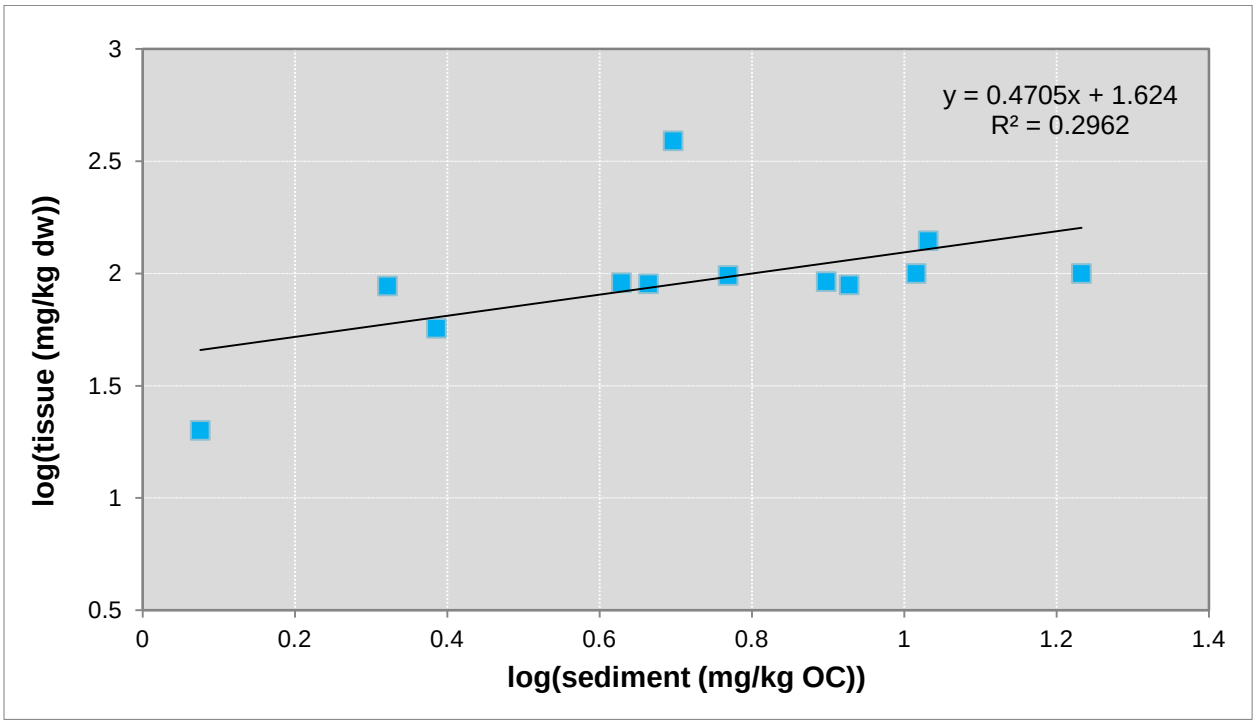


Figure C.4-1
Regression Relationship between Concentrations of TBT in Tissue and Concentrations of TBT in Sediment

Rather than using the regression relationship in Figure C.4-1, the TBT RBTC was developed based on a bioaccumulation factor (BAF) approach consistent with the approach used by Meador et al. 2002. The BAF approach was used with both datasets (i.e., the SRI data and the bioaccumulation test data). A BAF value was calculated for each tissue and sediment sample based on the dry weight tissue concentration and the organic carbon normalized sediment concentration (Equation C-15). The BAF values calculated for each sample are provided in Table C.4-1. It is important to note that there is considerable uncertainty associated with the calculation of the BAF values due to the lack of correlation between the tissue and sediment concentrations for both the SRI and the bioaccumulation test datasets.

$$BAF = \frac{\text{dry weight tissue TBT concentration}}{\text{OC} - \text{normalized sediment concentration}} \quad \text{(C-15)}$$

Table C.4-1

Tissue and Sediment TBT Concentrations Used to Calculate Sample-Specific BAF Values

Sample	Tissue TBT Concentrations (mg/kg dw)[a]	Sediment TBT Concentrations (mg/kg OC)	BAF
EW Field-Collected Benthic Ttissues			
EW08-BI02W	0.10	1.19	0.08
EW08-BI05	1.95	4.97	0.39
EW08-BI06	0.455	4.25	0.11
EW08-BI09	0.44	2.10	0.21
EW09-BI03N	0.70	10.75	0.07
EW09-BI03S	0.445	8.47	0.05
EW09-BI04N	0.50	10.37	0.05
EW09-BI04S	0.45	4.62	0.10
EW09-BI08N	0.50	17.08	0.03
EW09-BI08S	0.46	7.90	0.06
EW09-BI10N	0.285	2.43	0.12
EW09-BI10S	0.49	5.87	0.08
EW Bioaccumulation Test Ttissues			
B2 - N-FT[b]	0.144	7.04	0.02
B2 - A-FT[c]	0.303	7.04	0.04
B2 -A-S[c]	0.515	7.04	0.07
B6- N-FT[b]	0.361	11.61	0.03
B6 -A-FT[c]	0.744	11.61	0.06
B6-A-S[c]	1.450	11.61	0.12

[a] Wet weight tissue concentrations were converted to dry weight based on 20% solids fraction which is consistent with the measured values for these samples which ranged from 16.2-28.9% with a mean of 23.5%.

[b] Bioaccumulation test conducted with *Nephtys caecoides* under flow-through conditions for 45 days.

[c] Bioaccumulation test conducted with *Armandia brevis* under flow –through and static conditions for 45 days.

BAF – bioaccumulation factor
dw – dry weight
EW – East Waterway
OC – organic carbon
TBT – tributyltin

The sample-specific BAF values for the field-collected tissue samples ranged from 0.03 to 0.39 with eight of the 12 values less than or equal to 0.10. In order to develop a sediment TBT RBTC, the central tendency of the BAF dataset was estimated using both the arithmetic mean (mean TBT BAF = 0.11) and the median (median TBT BAF = 0.08) of the BAF values. The mean value is higher than the median because it is more influenced by the highest BAF

concentration (0.39) associated with the highest tissue TBT concentration (Figure C.4-2). The bioaccumulation test results resulted in BAF values similar to those seen for the field-collected tissues (Figure C.4-2). The lowest BAF values (0.02 and 0.03) were calculated for the Neanthes tissues which were run under flow-through conditions. The BAF values for Armandia ranged from 0.04 to 0.12. The Armandia tests were run under both flow-through and static conditions. The Armandia BAFs based on flow-through conditions were approximately half the BAF for the static conditions based on the same test sediment.

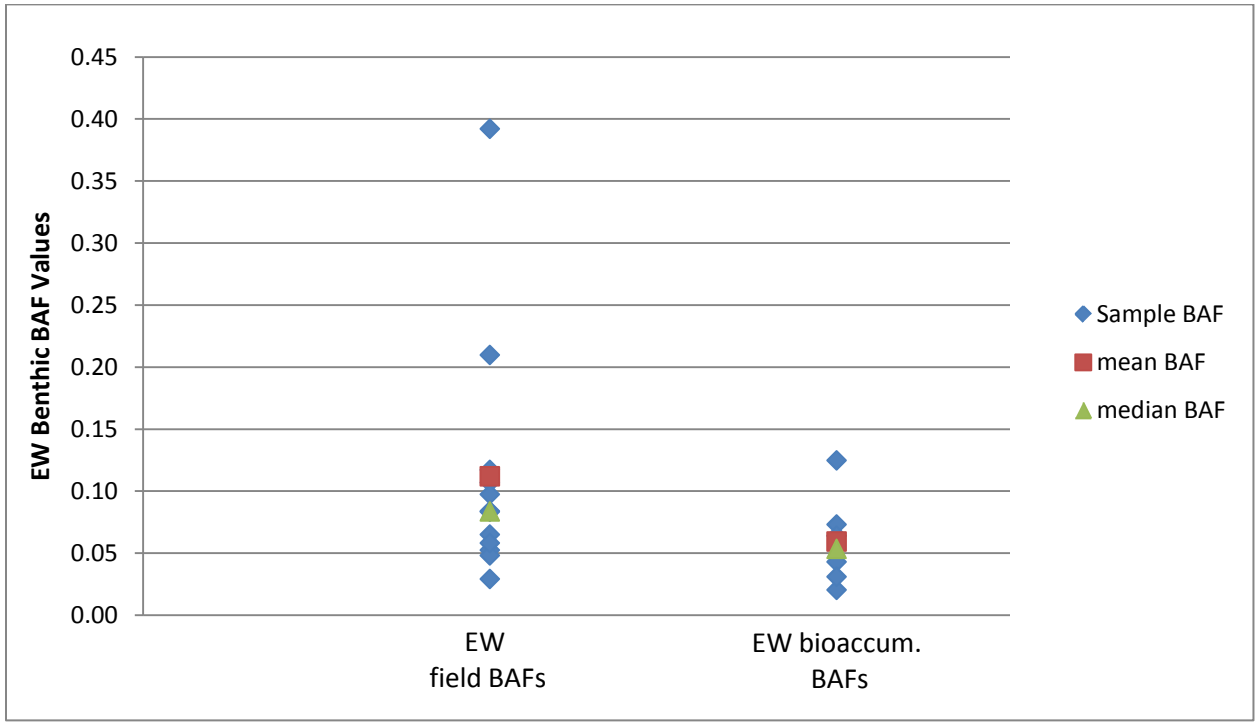


Figure C.4-2
Distribution of EW BAF Values for TBT

Using Equation C-16) to develop sediment TBT RBTC values, the mean and median TBT BAF values were used to estimate sediment concentrations that correspond to the TBT tissue TRV used in the ERA. RBTCs were calculated separately for the SRI dataset and the bioaccumulation test dataset using all the data, the *Armandia* data as a subset of the bioaccumulation data.

$$\text{Sediment RBTC}(\text{mg/kgOC}) = \frac{\text{dry weight tissue TBT TRV}}{\text{BAF}} \qquad \text{(C-16)}$$

The ranges of estimated sediment RBTC values are presented in Table C.4-2.

Table C.4-2
Estimated TBT Sediment RBTCs for Benthic Invertebrates

Dataset	Count	BAF Type	BAF	Tissue TRV (mg/kg dw)	Sediment RBTC (mg/kg OC)
EW benthic invertebrate tissue	12	mean TBT BAF	0.11	0.60	5.5
		median TBT BAF	0.08	0.60	7.5
EW bioaccumulation (*Neanthes* and *Armandia*)	6	mean TBT BAF	0.06	0.60	10
		median TBT BAF	0.05	0.60	12
EW bioaccumulation (*Armandia* only)	4	mean TBT BAF	0.08	0.60	7.5
		median TBT BAF	0.07	0.60	8.5

BAF – bioaccumulation factor
dw – dry weight
OC – organic carbon
RBTC – risk-based threshold concentration
TBT – tributyltin

The sediment RBTC values range from of 5.5 to 12 mg/kg OC and represent dry weight concentrations in sediment ranging from 88.0 and 192 µg/kg TBT dw at a TOC concentration of 1.6% dw, which is the site-wide mean TOC concentration for EW surface sediments.

The sediment RBTC value for TBT is 7.5 mg/kg OC based on the median BAF value for the field collected benthic invertebrate dataset. This value was selected because the field dataset is the largest dataset and represents the benthic organisms present in East Waterway and the range of sediment TBT concentrations present throughout the waterway. The median BAF (BAF = 0.08) provides the best estimate of the central tendency of the dataset. This value is consistent with the results of the bioaccumulation test results for EW sediments that were conducted with an organism that has been demonstrated to effectively accumulate TBT (*Armandia brevis*).

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