BIOACCUMULATION MODEL REPORT GREATER LOS ANGELES AND LONG BEACH HARBOR WATERS

In Support of

Final Dominguez Channel and Greater Los Angeles and Long Beach Harbor Waters Toxic Pollutants Total Maximum Daily Load

Prepared for

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LIST OF ACRONYMS AND ABBREVIATIONS

µg	microgram
AF	accumulation factor
ASDA	apparent specific dynamic action
Bight	Southern California Bight Regional Monitoring Program
BSAF	biota-sediment accumulation factor
cm	centimeter
CSM	conceptual site model
CSULB	California State University Long Beach
DCE	Dominguez Channel Estuary
DDX	dichlorodiphenyltrichloroethane and its derivatives
FMZ	fish movement zone
g	gram
Harbor	Greater Los Angeles and Long Beach Harbor Waters
Harbor Toxics TMDL	*Final Dominguez Channel and Greater Los Angeles and Long Beach Harbor Waters Toxic Pollutants Total Maximum Daily Load*
kg	kilogram
L	liter
LA	Los Angeles
LARE	Los Angeles River Estuary
LB	Long Beach
m	meter
mg	milligram
mm	millimeter
Montrose	Montrose Chemical Corporation
ng	nanogram
NRDA	Natural Resource Damage Assessment
OC	organic carbon

OEHHA	Office of Environmental Health Hazard Assessment
PCB	polychlorinated biphenyl
POC	particulate organic carbon
Ports	Ports of Long Beach and Los Angeles
PV Shelf	Palos Verdes Shelf
SQO	Sediment Quality Objective
SWAC	surface-weighted average concentration
TMDL	total maximum daily load
TP	trophic position
USEPA	U.S. Environmental Protection Agency
VPS	Vemco Positioning System
WRAP	Water Resources Action Plan

1 INTRODUCTION

Addressing indirect human health effects of sediment-borne contaminants due to the consumption of fish from the Los Angeles/Long Beach (LA/LB) Harbor is a critical component of the recent *Final Dominguez Channel and Greater Los Angeles and Long Beach Harbor Waters Toxic Pollutants Total Maximum Daily Load* (Harbor Toxics TMDL; RWQCB and USEPA 2011). To minimize human health risks associated with fish consumption, the Harbor Toxics TMDL sets annual contaminant limits in surface sediment, stormwater effluent, and fish tissues. These limits are concentration-based (typically generated from or referred to as numeric targets). Currently all of the sediments and fish tissue within the LA/LB Harbor exceed the sediment and/or fish tissue numeric targets for total polychlorinated biphenyls (PCBs)[1] and/or total dichlorodiphenyltrichloroethane and its derivatives (DDX)[1]; thus, compliance with the Harbor Toxics TMDL presents a challenge. The Ports of Long Beach and Los Angeles (together termed the Ports) are developing a bioaccumulation model as part of a Human Health (Indirect Effects) Sediment Quality Objective (SQO) assessment of the Greater Los Angeles and Long Beach Harbor Waters to better understand how compliance with the Harbor Toxics TMDL may be achieved. Specifically, the bioaccumulation model will be used to develop a scientifically defensible link between fish contaminant concentrations and contaminant sources and to provide the Ports with a tool for evaluating the effectiveness of different management alternatives at reducing fish tissue concentrations.

The next sections provide a description of the following:

- The Harbor Toxics TMDL and its purpose
- The key issue of concern regarding compliance with the Harbor Toxics TMDL
- The compliance approach the Ports are implementing to better understand the linkages between sources and receptors and how this information may be used to implement effective management strategies

[1] In this report, total PCB refers to total congener PCBs or total Aroclor PCBs; total DDX refers to the sum of the following constituents: 4,4'-DDT, 4,4'-DDE, 4,4'-DDD, 2,4'-DDT, 2,4'-DDE, and 2,4'-DDD.

1.1 Harbor Toxics TMDL

The Harbor Toxics TMDL (RWQCB and USEPA 2011) was adopted in 2011 by the Regional Water Quality Control Board and became effective on March 23, 2012. The Harbor Toxics TMDL and subsequent Basin Plan Amendment (RWQCB 2011) were established to address water quality impairments and provide a plan for restoring beneficial uses of the Harbor. Specifically, at the time the Harbor Toxics TMDL was developed, several TMDL-designated waterbodies within the Harbor had been on the State's Clean Water Act 303(d) list for more than a decade for one or more contaminants in one or more media (i.e., water, sediment, or fish tissue).

To restore sediment and water quality, protect marine life, and minimize human health risks from the consumption of fish, the Final Harbor Toxics TMDL allocates the load for each 303(d)-listed contaminant among non-point source (bed sediments) and point sources (waste load allocations; RWQCB and USEPA 2011). The Harbor Toxics TMDL requires that compliance be demonstrated by 2032 or 20 years after its effective date. For the bioaccumulative compounds, compliance may be demonstrated by any one of the following methods:

- Meeting final sediment load allocations or annual limits
- Meeting fish tissue targets for species resident in the Harbor
- Meeting sediment targets protective of fish tissue (over a 3-year averaging period)
- Demonstrating that the SQO is protective of human health and has been met in accordance with the *Water Quality Control Plan for Enclosed Bays and Estuaries* (SWRCB 2009), after it has been amended to include the process for assessment of the Human Health SQO

Despite the numerous mechanisms available, compliance with the TMDLs for bioaccumulative compounds remains the Ports' greatest compliance challenge for the following reasons:

- Currently, all of the Harbor is in exceedance of the sediment targets and/or the fish tissue targets for total PCBs and/or total DDX.
- At the time the Harbor Toxics TMDL was deemed effective, the *Water Quality Control Plan for Enclosed Bays and Estuaries* (SWRCB 2009) did not provide guidance on performing an assessment of the Human Health (Indirect Effects) SQO; thus, it was

unclear exactly how this could be applied to demonstrate compliance with the Harbor Toxics TMDL.

- The Harbor Toxics TMDL acknowledges that a site-specific linkage between sediments in the Harbor and fish tissue (for white croaker and other species) has not been established (Section 7.4 of RWQCB and USEPA 2011). Consequently, there is no guarantee that implementation of sediment remediation (recommended under the TMDL's phased implementation plan; Section 7.3 of RWQCB and USEPA 2011) will result in corresponding reductions in PCBs and DDX in fish tissue.
- The ongoing watershed sources of PCBs and DDX had not been fully characterized and controlled as of the effective date of the Harbor Toxics TMDL. Again, there is no guarantee that implementation of sediment remediation recommended in the implementation plan would be effective in reducing surface sediment and fish tissue concentrations if recontamination potential exists.

Since the Harbor Toxics TMDL's effective date, the State Water Resources Control Board staff have developed a Proposed Human Health SQO Indirect Effects Assessment document that describes the procedures that may be used to perform a Human Health (Indirect Effects) SQO Assessment (Beegan 2015). The document outlines the assessment process for the Human Health SQO, but some details are still under development. The draft SQO policy describes a tiered site assessment process for evaluating whether site sediments meet the Human Health SQO and are protective of human consumers of locally caught seafood. The first tier is a screening level assessment in which site data are examined to determine if further evaluation is needed. Tier 2 is a complete site assessment of sediment quality involving the evaluation of consumption risk and linkage between sediment bioaccumulatives and seafood tissue concentrations using a bioaccumulation model with some site-specific inputs. Tier 3 is a more complex and site-specific assessment which may be most applicable to complex sites with challenging site conditions, such as the Harbor. This report has been developed in support of such a Tier 3 assessment.

1.2 Approach for Achieving Compliance with Harbor Toxics TMDL

The Ports' approach for achieving compliance with the Harbor Toxics TMDL involves two steps. First, the Ports are undergoing a Tier 3 site assessment to more accurately assess linkage between sediment and fish tissue within the Human Health SQO policy. The Ports' Tier 3 site assessment involves developing and using a site-specific, calibrated bioaccumulation model of the Harbor to quantify the contribution of sediment and other sources of contaminants to fish tissue concentrations and then integrating these findings with an accurate evaluation of consumption risk. Second, after the site-specific bioaccumulation model has been calibrated and linked to the Water Resources Action Plan (WRAP) model, long-term model simulations will be performed to evaluate the effectiveness of different management alternatives at reducing fish tissue concentrations. Based on the results of the linked models, sediment management alternatives will be developed to support the prioritization of management actions based on their effectiveness at reducing fish tissue concentrations. This model-based approach to develop effective management actions is a standard practice used at numerous contaminated sediment sites throughout the United States under the Comprehensive Environmental Response, Compensation, and Liability Act (often referred to as Superfund or CERCLA) and the Resource Conservation and Recovery Act.

The Ports' Tier 3 assessment has been underway since 2012 and has involved numerous steps, including development of a conceptual site model (CSM; Anchor QEA 2014a; Anchor QEA and Everest 2015), completion of a data gap analysis to determine key data needs in support of modeling efforts (Anchor QEA 2013a, 2014a; Port of Long Beach and Port of Los Angeles 2013), implementation of special studies designed to fill key data needs (Anchor QEA 2013b, 2014b, 2014c, 2014d, 2014e), and quantitative model development and calibration. This report describes the development and calibration of the site-specific bioaccumulation model, which describes the transfer of PCBs and DDX from sediment and water into the Harbor food web, including the target fish species (white croaker [*Genyonemus lineatus*], California halibut [*Paralichthys californicus*], and surfperches [*Cymatogaster aggregata* and *Phanerodon furcatus*]). The development and calibration of the WRAP model (describing the hydrodynamic, sediment transport, and chemical fate mechanisms affecting PCBs and DDX) is discussed in a separate document (Everest 2017).

1.3 Study Area Description

The area named as the Greater Los Angeles and Long Beach Harbor Waters (Harbor) in the Harbor Toxics TMDL includes LA/LB Harbor, Eastern San Pedro Bay, and Los Angeles River

Estuary (LARE), Queensway Bay, and Dominguez Channel Estuary (DCE; Figure 1-1). Eastern San Pedro Bay, which lies to the east of Pier J, exchanges water, sediment, and fish with the Harbor through the opening south of Pier J, just inside the breakwater. The LA/LB Harbor and Eastern San Pedro Bay are bounded to the south by the federal breakwater, which stretches across most of San Pedro Bay in three distinct segments.

Three major freshwater inputs (Dominguez Channel, LA River, and San Gabriel River) from very large heavily urbanized watersheds in Los Angeles Basin drain into San Pedro Bay and define unique physical and chemical characteristics in different regions of the Bay. The LA/LB Harbor is the receiving waterbody for the Dominguez Channel Watershed, which encompasses more than 130 square miles that drain to the DCE and into the LA/LB Harbor through Consolidated Slip. Both the LA River Watershed and San Gabriel River Watershed discharge into Eastern San Pedro Bay through the LA and San Gabriel rivers, respectively. The Harbor is also directly influenced by nearshore watersheds inputs, which consist of the remaining drainage area that discharges directly into the LA/LB Harbor and Eastern San Pedro Bay.

While not included in the Harbor study area, Palos Verdes Shelf (PV Shelf) is included as an exposure area in the bioaccumulation model because of the observed migration of white croaker and California halibut between the Harbor and PV Shelf.[2] Likewise, the area outside of the Harbor that is included in the WRAP model grid is used as the outside Harbor exposure area. This area was also necessary to include due to the movement of both white croaker and California halibut to areas outside of the Harbor that are distinct from PV Shelf.

1.4 Report Organization

The report is organized as follows:

- Section 2 describes the CSM for the study area, and chemical and biological processes that affect the transport, migration, and potential impacts of PCBs and DDX to fish.
- Section 3 describes the bioaccumulation model, its prior use at contaminated sediment sites, and its governing equations.

[2] PV Shelf is an area off the coast of California that is known to have high concentrations of DDX, as well as some PCBs (CH2M Hill 2007). Hence, chemical exposure while fish reside on PV Shelf provides a potentially important contribution to their total body burden.

- Section 4 describes the model parameterization and application to the Harbor.
- Section 5 describes the calibration approach and results.
- Section 6 describes the sensitivity analysis results and uncertainty analysis approach.
- Section 7 provides a summary and the next steps for the model.
- Section 8 provides all citations.

2 CONCEPTUAL SITE MODEL

A CSM is a representation of physical, chemical, and biological processes that affect the transport, migration, and potential impacts of contamination to receptors within a specific waterbody or environment (USEPA 2005). To develop the CSM for the Harbor, representative food web species were selected and the pathways and sources of PCBs and DDX to those receptors were defined. Figure 2-1 is an illustration of the Harbor CSM and shows the physical processes that drive the fate and transport of PCBs and DDX, and their sources to the Harbor food web. The figure shows the relationship between the models used to simulate each process: the WRAP model simulates hydrodynamic, sediment transport, and chemical fate processes (Everest 2017), and the bioaccumulation model simulates accumulation of PCBs and DDX from sediment, water, and prey, to fish receptors.

2.1 Physical Conceptual Site Model

The relative importance of contaminant sources to the Harbor was investigated through the development of a chemical fate-specific CSM for the water column (Anchor QEA and Everest 2015). Specifically, a chemical mass balance evaluation of the total PCB and total DDX concentrations in the Harbor indicated that the flux of dissolved contaminants from surface sediments is an important process. The mass balance evaluation also showed that watershed loadings—particularly for inflows from the San Gabriel River, Los Angeles River, and Dominguez Channel—may also be an important source of contaminants to Harbor waters. Tidal exchange appears to be an important contaminant loss mechanism. Other mechanisms contributing to the gain or loss of PCBs and DDTs to the LA/LB Harbor were found to be less important; these include wet and dry atmospheric deposition, groundwater flow, and chemical degradation in the water column.

2.2 Biological Conceptual Site Model

The receptors of concern to the Harbor includes the white croaker, the only fish named in the Harbor Toxics TMDL, and two other fish that are subject to regional consumption advisories. To represent the Harbor food web, the bioaccumulation model includes fish receptors with a range of feeding strategies: California halibut, a sport fish that consumes pelagic and benthic fish; white croaker, which consumes a mixture of benthic invertebrates and prey fish; and representative prey fish, shiner, and white surfperches, which consume water column and benthic invertebrates. Two types of invertebrates, a representative deposit-feeder and a representative filter-feeder, have been included as well. The basis for selection of these representative species is described in Section 2.2.1. The degree to which the representative species are exposed to the various PCB and DDX sources to the Harbor is influenced by their habitat and movement patterns, as described in Section 2.2.2.

2.2.1 Representative Receptors of Concern

Figure 2-2 shows the representative Harbor food web and illustrates the sediment and water column sources of PCBs and DDX. As shown in Figure 2-2, the transfer of PCBs and DDX from sediments and the water column to receptors of concern occurs through both the benthic and pelagic food webs.

2.2.1.1 White Croaker

White croaker was selected as a representative species in support of the Harbor Toxics TMDL because Section 7.6.2 (RWQCB and USEPA 2011) requires compliance monitoring of this species. In addition, this species is representative of benthic-feeding fish, is abundant in the Harbor (MEC 1988, 2002; SAIC 2010), and is commonly caught and consumed by local anglers in the Cabrillo Pier area (SCCWRP and MBC 1994). The health advisory and safe eating guidelines developed by OEHHA (2009) suggest that white croaker caught from Ventura to San Mateo Point should not be eaten (regardless of age or gender) due to elevated total PCB and total DDX concentrations in croaker fillets, which historically exceed fish consumption advisory tissue levels. White croaker are found in nearshore habitats and are a bottom-dwelling species that primarily feed on benthic organisms, including polychaetes and clams. Consequently, it is likely that white croaker are indirectly exposed to sediment contaminants through the consumption of benthic organisms (Moore 1999) and possibly through incidental ingestion of sediment (Ware 1979). They are also directly exposed to contaminants in the water column through gill exchange.

2.2.1.2 California Halibut

California halibut was selected as a representative sport fish because halibut are commonly caught and consumed by anglers in the Harbor at Cabrillo Pier (SCCWRP and MBC 1994) and have been shown to be abundant in the Harbor during the biological surveys conducted in 2000, 2008, and 2013/14 (MEC 2002; SAIC 2010; MBC 2016). In addition, the State of California Office of Environmental Health Hazard Assessment (OEHHA) consumption advisories include halibut caught in the Harbor region due to elevated concentrations of total PCBs and total DDX (OEHHA 2009). Further, halibut were also selected because their large body cavity size was amenable to acoustic tags; therefore, their movement could be studied as part of a passive fish tracking study that has since been completed by California State University Long Beach (CSULB; Lowe et al. 2015b). Higher trophic level fish predators such as California halibut are indirectly exposed to PCBs through consumption of smaller benthic-feeding and prey fishes such as white croaker and surfperches. They are directly exposed to contaminants in the water column through gill exchange.

2.2.1.3 Surfperches

Shiner surfperch was initially selected as the representative prey species because they are abundant in the Harbor and surrounding waterways (SAIC 2010) and are likely prey for higher trophic level fishes, such as California halibut (CDFG 2001, 2002; Allen 1988; CDFW 2013). Shiner surfperch is also listed in OEHHA (2009) for reduced consumption or no consumption due to elevated total PCB and total DDX concentrations measured in tissue of surfperch from the region. As part of special studies conducted in support of modeling work, limited numbers of shiner surfperch were caught within the Harbor. Consequently, white surfperch data were collected and used along with shiner surfperch data to understand spatial and temporal contaminant patterns in surfperches and in model development. Shiner surfperch are representative of important prey fish, because the diet of this species is similar to other key prey fish in the Harbor, such as topsmelt. Both shiner surfperch and topsmelt have been shown to feed on zooplankton, algae, amphipods, polychaetes, and gastropods (Odenweller 1975; Sempier 2003; UC 2013). While white surfperches grow larger than shiner surfperches, they are known to have similar life histories (i.e., habitat, feeding strategies, diet, and mode of reproduction; CDFG 2002; CDFW 2003) and, therefore, were used together with shiner surfperches as representative prey fishes in the bioaccumulation model.

2.2.1.4 Invertebrates

The Harbor food web comprises a variety of organisms that have been described in previous Port biological surveys (SAIC 2010; MEC 2002). For the bioaccumulation model, two types of invertebrates with different feeding strategies were chosen to separately represent the benthic and pelagic food webs. Deposit-feeding invertebrates in sediment may be directly exposed to PCBs and DDX through ingestion of contaminated sediment or detritus, or through direct exposure through contact with sediments, porewater, or surface water. Within the water column, PCBs and DDX sorbed to particulate matter may be consumed by filter-feeding invertebrates and other water column invertebrates such as amphipods or mysids.

Bivalves were used to represent filter feeding organisms in the pelagic food web. Bivalves were selected because they are easy to collect and their diets are representative of other pelagic invertebrates (i.e., cumaceans and mysids) that feed in the upper portion of the water column and are consumed by perch (Arnot and Gobas 2004). Polychaetes, which are known to be abundant in LA/LB Harbor (Anchor QEA 2014a; MBC 2016) and are preyed upon by white croaker, were used to represent deposit-feeding benthic organisms.

2.2.2 Fish Movement Zones

In addition to the feeding strategies of representative organisms in the Harbor food web, habitat preferences and the range and magnitude of fish movement are also important to characterizing exposure sources. Thus, to define the exposure sources of migrating fish, the Harbor fish were split into subpopulations defined by their movement patterns. To support the division into subpopulations, the Harbor was divided into fish subpopulation areas, or fish movement zones (FMZs). These zones were developed with data and information regarding habit quality, including aquatic habitat data, benthic infaunal abundance data, and Harbor bathymetry (Anchor QEA 2014a). Additionally, the movement of two species, white croaker and California halibut—evaluated as part of regional fish tracking studies conducted by CSULB (Lowe et al. 2015a, 2015b)—was also considered.

A detailed description of FMZ development is provided in Appendix A. The FMZs developed for the Harbor and PV Shelf are shown in Figures 2-3 and 2-4, respectively, and are as follows:

- **DCE FMZ**: The 8.2-mile, unlined, estuarine portion of the Dominguez Channel.
- **Consolidated Slip FMZ**: The most upstream portion of LA/LB Harbor that first receives pollutant loads from the Dominguez Channel watershed.

- **LA Inner Harbor FMZ**: The main channel of LA Harbor; connects Consolidated Slip with LB Inner Harbor and LA Outer Harbor.
- **Fish Harbor FMZ**: The inlet on the southwest portion of Terminal Island that was historically a hub for commercial fishing vessels and canneries.
- **Seaplane Lagoon FMZ**: The inlet in the middle of Terminal Island, which connects to LA Harbor via the channel that runs between Piers 300 and 400.
- **LA Outer Harbor FMZ**: Includes TMDL-designated areas: Outer Harbor (Port of Los Angeles side), Inner Cabrillo Beach, Cabrillo Marina, and the deep channel between Piers 300 and 400.
- **LB Inner Harbor North and South FMZ**: Includes the TMDL-designated area identified as Inner Harbor, within the jurisdiction of Port of Long Beach.
- **LB Outer Harbor FMZ:** Includes the Southeast Basin and Outer Harbor (Port of Long Beach side; Figure 1-1).
- **LARE FMZ:** Includes the TMDL-designated area identified as LARE (Queensway Bay; Figure 1-1).
- **Eastern San Pedro Bay FMZ:** Includes the entrance channel to Pier J and the TMDL-designated area identified as San Pedro Bay, inside the breakwater.
- **Outside Harbor Exposure Area**: The area immediately outside the Harbor gates that represents a portion of the WRAP model grid (Everest 2017).
- **PV Shelf FMZs:** Includes four FMZs that were established on PV Shelf based on the data collected by Wolfe and Lowe (2015), along with consideration of chemical contamination data and bathymetry described in Appendix A and shown in Figure 2-4.

2.3 Nature and Extent of PCB and DDX Contamination

Spatial and temporal patterns in the concentration and composition of PCBs and DDX in sediment and fish were evaluated to support our understanding of contaminant sources as well as fate and transport and bioaccumulation processes. Analyses included the geographic relationships between contaminant sources and contaminant distributions in sediments and fish. Historical trends in sediment and fish contaminant concentrations were analyzed to assess the potential for natural recovery. The extent to which the composition of PCBs and DDX in sediment, water, and biota varies throughout the Harbor was evaluated to support selection of chemicals to model (i.e., individual congeners versus compound class sums). This section describes the observed spatial, temporal, and compositional patterns.

2.3.1 Spatial

The spatial distributions of sediment and fish tissue total PCB and total DDX concentrations in each FMZ are provided in Figures 2-5 through 2-8[3]. Zone concentrations are plotted starting on the left of each figure with the Los Angeles Harbor FMZs from the most estuarine outward, Long Beach Harbor FMZs from the most estuarine outward, and Eastern San Pedro Bay. Outside Harbor and PV Shelf data are included on the right side of each figure for comparative purposes.

2.3.1.1 Sediment

The spatial distributions of total PCB and total DDX concentrations in surface sediments are shown in Figures 2-5 and 2-6, respectively, on both a dry-weight (top panel) and organic carbon (OC)-normalized basis (bottom panel).

Within the Harbor, the highest average and median sediment total PCB concentrations are found in Consolidated Slip, and concentrations generally decrease moving from the Inner to Outer Harbor. Concentrations in PV Shelf sediments are elevated, comparable to or greater than the more contaminated portions of the Harbor. Concentrations in Eastern San Pedro Bay fall generally within the range of concentrations measured in the Harbor, although at the lower end of the range. Carbon normalization tends to reduce variability among reaches of the Harbor (compare the two panels of Figure 2-5, noting the difference in number of log cycles on the vertical axes). This suggests that the distribution of PCBs in Harbor sediments is due in part to fate and transport processes (sorption to organic matter, transport, and deposition). Organic carbon normalization does not change the qualitative patterns, however.

Similar to total PCB, the highest total DDX concentrations are also found in Consolidated Slip; carbon normalization reduces these gradients but does not alter the qualitative picture.

[3] The box plots show median (horizontal central line), mean (diamonds), hinges (ends of boxes; 25 and 75 percentiles), whiskers (from hinges to 1.5 times distance between hinges and median), inner (stars), and outer (open circles) outliers.

Additionally, PV Shelf total DDX concentrations are more than an order of magnitude above concentrations in the LA/LB Harbor zones (on both dry weight and carbon normalized bases), whereas the total PCB distribution on PV Shelf overlaps with concentrations measured in the Harbor. In addition, total PCB concentrations exhibit a much steeper decline from the LA Inner Harbor to the Outer Harbor than total DDX, suggesting that elevated historical concentrations outside the Harbor may have played a greater role in the past for DDX than for PCBs.

2.3.1.2 Fish Tissue

The spatial distribution of total PCB and total DDX concentrations for four fish species (white croaker, queenfish, California halibut, and topsmelt) with data sufficient to evaluate are presented in Figures 2-7 and 2-8, respectively, on a wet-weight (top panel) and lipid (bottom panel) basis. The wet-weight-basis plots show total PCB and total DDX in fillet for all species except topsmelt, which shows whole body results, and the lipid-normalized basis plots include both fillet and whole body concentrations. Spatial patterns in fish total PCB concentrations show some similarities to sediment total PCB patterns. All four species exhibit the highest total PCB concentrations (on a lipid-normalized basis) in Consolidated Slip; the same pattern is seen on a wet-weight basis for all species except California halibut. However, on a wet-weight basis, the median total PCB concentrations in white croaker on PV Shelf are similar to those in Consolidated Slip fish, but lipid-normalized total PCBs in white croaker are higher in Consolidated Slip than in fish from PV Shelf and the rest of the Harbor FMZs. White croaker median total PCB concentrations in Fish Harbor are comparable to those in Consolidated Slip on a wet-weight basis and somewhat lower on a lipid basis, but still elevated relative to fish from other FMZs in the Harbor (Figure 2-7d). The spatial distribution of total PCB concentrations in queenfish and California halibut are similar to those in white croaker, although no data are available for PV Shelf and the sample sizes are smaller for these species (Figures 2-7a and b, respectively). Average topsmelt total PCB concentrations are similar throughout the Harbor, except for within Consolidated Slip; however, no samples are available from Fish Harbor (Figure 2-7c) for comparison.

The highest average total DDX concentrations in white croaker from the Harbor (more than 1,000 µg/kg wet weight) were found in fish collected from LA Inner FMZ (Figure 2-8d).

Average white croaker total DDX concentrations in the remainder of the LA/LB Harbor ranged from approximately 100 to 400 μg/kg wet weight (Figure 2-8d). As with sediment, average and median total DDX concentrations in PV Shelf white croaker are well above any white croaker DDX concentrations in the Harbor (Figure 2-8d). Average total DDX concentrations in the other fish species are generally lower than in white croaker, ranging between 2 to 300 μg/kg wet weight (Figures 2-8a, b, and c). No consistent spatial patterns in average total DDX concentrations are evident for queenfish, California halibut, or topsmelt; however, some of the highest concentrations measured for topsmelt were measured in fish from zones encompassing Outer Harbor (LA Outer, LB Outer, and Seaplane Lagoon FMZs). Currently, data are not available for queenfish, California halibut, and topsmelt from PV Shelf.

2.3.2 Temporal Trends

The evaluation of temporal trends in PCBs and DDX are limited to white croaker and bivalves because they are the only organisms with sufficient data. Temporal trends of PCBs and DDX for surface sediment are discussed in the Data Gaps Analysis Report (Anchor QEA 2014a).

2.3.2.1 Temporal Trends in White Croaker

Figures 2-9 through 2-12 show temporal trends in white croaker total PCB and DDX concentrations from the Harbor and PV Shelf. The trends are presented on a wet-weight (Figures 2-9 and 2-11) and lipid-normalized (Figures 2-10 and 2-12) basis. Total PCB and total DDX concentrations have declined from the 1990s to the present; more recently, since approximately 2000, the declines continue but at slower rates. Rates of decline from 2002 to present were calculated for subareas where sufficient data are available. PCB decline rates are based on congener data only.

Total PCB concentrations in white croaker demonstrate downward trends over time within LA Outer Harbor and Outside Harbor areas on both a wet-weight and lipid basis (Figures 2-9 and 2-10). Total PCBs in white croaker from PV Shelf and LA Outer Harbor exhibit downward trends; however, declines are significant for only PCBs on a lipid basis at PV Shelf ($p<0.01$).

Total DDX concentrations in white croaker show a decline in LA Outer Harbor, Outside Harbor areas, Eastern San Pedro Bay, and PV Shelf on both a wet-weight and lipid basis (Figures 2-11 and 2-12). Declines are only significant for total DDX on a wet-weight basis at LA Outer Harbor (p=0.05) and on a lipid basis at PV Shelf (p=0.01).

2.3.2.2 Temporal Trends in Bivalves

Figure 2-13 shows temporal trends in total PCB and total DDX concentrations in bivalves (i.e., white sand clams and mussels) at Cabrillo Pier and on PV Shelf. Total PCB and total DDX trends are presented on a dry-weight basis because much of the historical data were only present in this format. PCB congener trends were evaluated using the 18 congeners that were consistently measured as part of both State and NOAA Mussel Watch programs since the 1980s (Melwani et al. 2013). For each area evaluated, total PCBs and total DDX rates of decline were calculated.

Recent total PCB concentrations in clams collected in the vicinity of the Cabrillo Pier suggest a decline, but the variability in the data prevent calculation of a rate, unlike the bivalves from PV Shelf (p~0.06; Figure 2-13a). Total DDX concentrations in Cabrillo Pier and PV Shelf bivalves appear to have declined (although the P values associated with the slopes are greater than 0.05); the rates are similar (Figure 2-13b).

2.3.2.3 Summary of Temporal Trends

Overall, the historical data suggest that natural recovery is ongoing in the Harbor and on PV Shelf. The possible declines in DDX and PCBs reported here for bivalves are consistent with decreasing historical trends for these contaminants in mussels from other subareas of the Harbor and at many Southern California sites, as described by the State Water Resources Control Board (Melwani et al. 2013). Specifically, Melwani et al. (2013) demonstrated significant decreases in mussel total PCB and total DDX concentrations at two other sites in LA Harbor (Consolidated Slip and near former National Steel site), Newport Bay, Oceanside, and San Diego Bay. Similarly, data collected in white croaker since 2002 are suggestive of declines in Total PCB and Total DDX concentrations. Finally, while the evaluation of trends in surface sediment concentrations is confounded by limited data collected at variable depths, the weight of evidence supports ongoing declines (see Figure 5-3 in the Data Gaps

Analysis Report; Anchor QEA 2014a). Overall, considering sediment, fish, and bivalve data, total PCB and DDX concentrations appear to be recovering at a few percent per year.

2.3.3 PCB and DDX Composition

PCB compositions in sediment, fish, and mussels are generally consistent throughout the Harbor and are dominated by tetra- through hepta-PCBs (Figures 2-14 through 2-16). PCB composition in water column samples is dominated by tri- through hexa-PCBs (Figure 2-17). The predominance of homologs with lower chlorination levels in water is expected based on the greater solubility of the lower molecular weight PCB congeners and the generally greater bioaccumulation potential of higher homologs.

The composition of DDX is dominated by 4,4'-DDE in water, sediment, fish, and bivalves throughout the Harbor and on PV Shelf (Figures 2-18 through 2-21).

3 BIOACCUMULATION MODEL

The bioaccumulation model will be used in conjunction with the WRAP model to develop a scientifically defensible, site-specific link between PCB and DDX sources (i.e., water, sediment, and food) and fish PCB and DDX concentrations, and to provide the Ports with a tool for evaluating the effectiveness of various management alternatives for reducing fish tissue concentrations. This approach parallels similar efforts underway in San Francisco Bay, as part of the region's TMDL implementation process. A bioaccumulation model has already been developed for San Francisco Bay as a whole (Gobas and Arnot 2010), but as of 2012, the model had yet to be applied to subareas to establish site-specific linkages or provide time-dependent scenario modeling (Jones et al. 2012). A CSM of site-specific bioaccumulation for San Francisco Bay was recently completed (Melwani et al. 2012); it identifies temporal and spatial variation in exposure and bioaccumulation, and highlights the importance of site-specific linkages in the consideration of management decisions. The approach described for the Harbor is similar in that it will rely on a CSM that identifies Harbor contaminant sources and sinks, which will then be quantified using linked models of contaminant fate, transport, and bioaccumulation to determine effectiveness of various management alternatives.

The bioaccumulation model is based on the framework developed as part of the Montrose Chemical Corporation (Montrose) Natural Resource Damage Assessment (NRDA) project (HydroQual 1997) and used in the risk assessment conducted as part of the PV Shelf Remedial Investigation and Feasibility Study (CH2M Hill 2007) to develop sediment remediation goals (Glaser 2009). It has been modified to represent the Harbor food web structure for target fish species and fish migration among subareas of the Harbor and to and from PV Shelf. The bioaccumulation model relies on the AQFDCHN bioaccumulation model framework (i.e., computer code), a bioenergetic, mechanistic, dynamic modeling framework originally developed 30 years ago by Thomann and Connolly (1984) and subsequently updated and routinely applied to many projects (see Table 3-1). AQFDCHN simulates contaminant bioaccumulation from water column and sediment exposure, and accounts for site-specific growth rates of organisms throughout their lives, as well as seasonal and annual changes in diet and lipid content. Generally, there are two types of bioaccumulation models: those that rely on equilibrium-based distribution coefficients such as bioaccumulation factors or biota-sediment accumulation factors (BSAFs), and those that rely on process-based equations

(Barber 2008). AQFDCHN, similar to the BASS (Barber 2001), Ecofate (Gobas et al. 1988), and AQUATOX (USEPA 2000), is a process-based model and estimates chemical concentrations in fish as a function of aqueous and dietary exposure. Aqueous uptake occurs through diffusion across the gills, and dietary uptake occurs through ingestion of prey items, by assuming assimilation of a constant fraction of prey chemical concentrations. AQFDCHN, similar to Ecofate, is distinguished from models such as AQUATOX because chemical elimination is explicitly computed (Barber 2008).

The WRAP model is a three-dimensional hydrodynamic, sediment transport, and chemical fate model (Figure 2-1; Everest 2017). The bioaccumulation model processes are directly linked to the WRAP model processes; water column dissolved and particulate, and sediment concentrations estimated from WRAP model simulations provide inputs to AQFDCHN (Figure 2-1). Both models were calibrated to simulate the complex hydrodynamic, sediment transport, and PCB and DDX fate and bioaccumulation in the Harbor.

3.1 Governing Equations

Bioaccumulation is the net accumulation of chemicals by an organism through all exposure routes. AQFDCHN is a mathematical description of the transfer of PCBs within the food web (Figure 2-2). The food web includes the primary energy transfer pathways from the exposure sources to the species of interest. The generic model framework relies on a time-variable mechanistic simulation of organism bioenergetics and phase partitioning of contaminants. The site-specific component of the model includes the food web structure, species-specific bioenergetics and body composition, water temperature, PCB and DDX chemical properties, and contaminant exposure concentrations. This dynamic (i.e., time variable) PCB and DDX bioaccumulation model, based on principles of mass and energy conservation, computes the uptake and loss of PCBs and DDX in fish. Uptake occurs from the water-column dissolved phase through diffusion across gills and from water-column and sediment particulates through predation, while losses occur through diffusion across respiratory surfaces and growth. Uptake and loss rates are calculated from respiration, feeding, and empirically defined PCB- and DDX-transfer efficiencies. The bioaccumulation model relies on two basic sets of equations: 1) accumulation of invertebrates at the base of the food web; and 2) accumulation in fish.

3.1.1 Accumulation in Invertebrates

A BSAF is used to describe accumulation of PCBs and DDX in invertebrates feeding on particulate matter in the sediments (e.g., algae, detritus, or sediment) and a water-column accumulation factor (AF) is used to describe accumulation in invertebrates feeding on particulate matter in the water-column:

$$\nu_L = AF \times C_{oc} \tag{1}$$

where:

AF = accumulation factor. For invertebrates feeding on particulate matter in sediments, this value is the BSAF (kilogram [kg] organic carbon/kg lipid). For invertebrates feeding on particulate matter in the water column, this value is the water-column particulate AF (kg organic carbon/kg lipid).

ν_L = concentration of chemical in the invertebrate (milligrams per kilogram [mg/kg] lipid)

C_{OC} = concentration of chemical on sediment or water-column particulate matter (mg/kg organic carbon)

Accumulation in invertebrates is represented in the model as the same mix of trophic levels. Chemical concentrations on particulate matter are represented on an OC basis, because PCBs and DDX sorb to carbon within the sediment bed and the water-column, and carbon represents the food source of invertebrates.

3.1.2 Accumulation in Fish

Fish accumulate PCBs and DDX directly from the water-column dissolved phase through respiration, as well as indirectly through consumption of prey items, such as invertebrates and smaller fish that in turn accumulate from the water and diet. Fish accumulate PCBs and DDX indirectly from the sediment by consuming prey that in turn consume sediment, and in some cases directly through ingestion of sediment. Accumulation of PCBs and DDX in fish is calculated through time-variable mechanistic equations that are based on toxicokinetic and bioenergetic principles.

3.1.2.1 Basic Equation

The accumulation of PCBs and DDX in fish is described by the following equation:

$$\frac{dv_i}{dt} = K_{ui}c + \alpha_c \sum_{j=1}^{n} C_{ij}\, v_j - \left(K_{dep_i} + G_i\right)v_i \qquad (2)$$

where:

i and j	=	indices for predator and prey, respectively
v_i	=	concentration of chemical in species i (micrograms per gram wet weight [μg/g(w)])
K_{ui}	=	rate constant for respiratory chemical uptake by species i (liters per gram of wet weight per day [L/g(w)-d])
K_{dep_i}	=	chemical depuration rate constant by species i (d^{-1}[1/day])
α_c	=	chemical assimilation efficiency from prey
C_{ij}	=	predation or consumption rate of species i on species j (g(w)prey/g(w) predator-d)
G_i	=	growth rate of species i (g(w)/g(w)-d)
n	=	number of species (including different year classes of a single species) preyed upon by species i
c	=	dissolved concentration of chemical in water (μg/L)
v_j	=	concentration of chemical in prey j (μg/g(w))

The first term of Equation 2 represents the direct uptake (i.e., diffusion) across the gills of PCBs and DDX by the fish from water. The second term represents the flux of PCBs or DDX into the fish through feeding. The third term represents the loss of chemicals due to diffusion across the gill (depuration) and the change in concentration due to growth. The gill is assumed to be the major site of depuration. The fecal elimination rate is generally much less than the growth rate and is not included in the model. The dynamic bioaccumulation model is applied to each fish species, accounting for species-specific differences in growth, consumption, and elimination rates.

The individual processes within Equation 2 have been discussed in detail elsewhere (Connolly 1991; Connolly et al. 1992) and are summarized and updated below.

Chemical Mass Transfer at the Gill. The chemical uptake rate constant K_u is defined for a given species from a chemical mass transfer coefficient k_{gl} and the active gill surface area A_{gl}:

$$K_u = \frac{k_{gl} A_{gl}}{W} \tag{3}$$

where:

W = wet weight of the fish (g(w))

k_{gl} = chemical mass transfer coefficient (centimeter [cm]/d)

A_{gl} = active gill surface area (cm^2)

To help solve Equation 3, the oxygen uptake rate constant, K_{uO_2}, is used and is defined by the ratio of the fish respiration rate to the oxygen concentration of the water (c_{O_2}):

$$K_{uO_2} = \frac{R}{c_{O_2}} \tag{4}$$

where:

R = respiration rate (gO_2/g(w)-d)

c_{O_2} = oxygen concentration in the water (gO_2/L)

The oxygen uptake rate constant can also be described in terms of a mass transfer rate constant at the gill (k_{glO_2}).

$$K_{uO_2} = \frac{k_{glO_2} A_{gl}}{W} \tag{5}$$

Equations 4 and 5 may be equated and solved for A_{gl}. Substituting this expression for A_{gl} in Equation 3 shows that gill uptake (K_u) can be determined from the oxygen uptake rate constant, K_{uO_2}, and the ratio of the mass transfer coefficients of the chemical and oxygen.

$$K_u = \frac{k_{gl}}{k_{glO_2}} K_{uO_2} = \frac{k_{gl}}{k_{glO_2}} \frac{R}{c_{O_2}} \tag{6}$$

The bioenergetic component of the model computes the respiration rate. In the Harbor model, the concentration of oxygen in water is calculated assuming saturation, incorporating corrections for temperature and salinity (although any value for dissolved oxygen concentration can be incorporated as appropriate). The ratio of chemical to oxygen mass transfer rates (k_{gl}/k_{glO_2}, called "P ratio" in the model documentation) is estimated from experimental data (QEA 1999).

The gill depuration rate is computed by assuming equilibration between lipid and water:

$$K_{dep} = K_u \left(\frac{1}{f_a + K_{fw} f_L}\right) v \tag{7}$$

where:

f_L	=	lipid fraction of the fish
f_a	=	aqueous fraction of the fish
K_{fw}	=	fish lipid-water partition coefficient

Bioenergetics. An important characteristic of the model is that all of these key bioaccumulation processes are quantitatively linked by the bioenergetic component of the model. Growth and respiration rates are used to calculate the total energy requirement, which is used to calculate the rate of consumption of contaminated prey (Equation 2). In addition, the respiration rate is used to calculate the rate of diffusion of chemicals across the gill surface (Equation 6). Finally, the growth rate is used to calculate the dilution of chemicals within the body of the organism (Equation 2).

The model computes growth rates based upon a species-specific relationship between age and weight:

$$G = \frac{1}{W}\frac{dW}{dt} \tag{8}$$

The respiration model is:

$$R = \beta W^{\gamma} e^{\rho T} c_{act} \tag{9}$$

where:

T = temperature (degrees Celsius [°C])

c_{act} = activity multiplier

β, γ, ρ = empirical coefficients determined by experiment

The model accounts for standard metabolism (i.e., metabolism in the absence of feeding and activity) and the added impact of swimming. In addition, effects of apparent specific dynamic action (ASDA) are incorporated. The ASDA consists of the heat produced during digestion and the energy required for absorption, digestion, transportation, and deposition of food materials.

The rate of consumption of food, $\Sigma_j(C_{ij})$, is calculated from the rate of energy usage. Energy usage is estimated from the sum of the rates of production and metabolism. The rate of metabolism is computed from the respiration rate at time t (R_t, gO_2/g(w)-d) by stoichiometrically converting respiration to units of kJ/g(w)-d using a conversion factor λ_o = 13.7 kJ/g O_2 (Brett and Groves 1979). The rate of energy usage for production of body tissue is determined from the growth in mass and the energy density of the fish tissue (λ_t, kJ/g(w)):

$$\lambda = 39.5 f_L + 20.08 f_P \tag{10}$$

where:

f_P = fraction protein = f_D - f_L

f_D = fraction dry weight (g(d)/g(w))

f_L = fraction of lipid of the fish (g lipid (d)/g(w))

The energy usage rate at time t (P_i, kJ/g(w)-day), is then:

$$P_i = \lambda_o R_t + \left(\frac{W_{t+1}\lambda_{t+1} - W_t \lambda_t}{W_t}\right) \tag{11}$$

where:

W_{t+1} = weight at time t+1 (g(w))

The model computes P_i based upon field measurements of lipid content and weight/age relationships.

4 APPLICATION TO THE GREATER LOS ANGELES AND LONG BEACH HARBOR WATERS

This section provides a description of how the AQFDCHN bioaccumulation model was parameterized with data and information to develop a site-specific food web model for the Harbor. A description of the site-specific food web structure, bioenergetics parameters, contaminant mass transfer, growth, diet, and characterization of exposure concentrations that have been used to parameterize the bioaccumulation model are described below.

4.1 Diet and Food Web Structure

The model food web is a simplification of the Harbor ecological food web, designed to capture the key trophic levels and exposure sources (surface sediment and surface water) to the species of primary interest. Toward that end, the model food web includes the following components:

- Mussels and oysters represent filter-feeding organisms whose diet is based on consumption of plankton for the most part, with a limited contribution from sediment/detritus.
- Worms represent deposit-feeding benthic organisms whose diet is primarily sediment/detritus.
- Shiner and white surfperches represent pelagic fishes with opportunistic feeding on the benthos.
- White croaker represent benthic-feeding fish whose feeding strategy may include consumption of some filter-feeding organisms or smaller fishes.
- Adult halibut (greater than 500 millimeters [mm]) represent piscivorous fish whose diet primarily consists of fishes such as surfperches and smaller croaker.

Model species' diets were based on the literature; a summary of the diet information is summarized in the following subsections for each model species. A specific diet was selected for each representative species (and size class in some cases) based on a weight of evidence evaluation, taking into account the characteristics of each study, including proximity to the Harbor, application of the diet information in prior bioaccumulation models, recentness of the study, and consistency among studies. To determine whether the selected diets accurately represented the trophic positions (TPs) of each species, selected diets were compared with site-specific stable nitrogen isotope data collected as part of the Ports' 2014

Harbor food web sampling program (Anchor QEA 2014b; AMEC Foster Wheeler 2015) and a 2014 Sediment and Polychaete Special Study (Anchor QEA 2014c; Environ 2015).

4.1.1 California Halibut

Information from the literature indicated that the diet of California halibut varies by age (Table 4-1). Juvenile California halibut (less than 20 mm) from Alamitos Bay were found to consume primarily zooplankton and crustaceans. Slightly larger juvenile halibut (20 to 150 mm) consume larger crustaceans and also prey on small fish such as gobies (Allen 1988). Plummer et al. (1983) found that larger halibut (124 to 476 mm) off the coast of Northern San Diego County primarily consume small fish such as anchovies. Similar findings were reported by Haaker (1975) for California halibut from Anaheim Bay. At larger sizes, adult halibut (greater than 500 mm) consume a greater proportion of larger fish such as white croaker (Wertz and Domeier 1997).

4.1.2 White Croaker

White croaker are benthic foragers whose diets are primarily composed of polychaetes and crustaceans found within soft sediment habitats (Allen 1982, 1985, 2001). Younger white croaker (less than 200 mm) from LA Outer Harbor incorporate zooplankton into their diet in addition to polychaetes and crustaceans; nominal amounts of fish such as anchovy are also consumed by young croaker (101 to 200 mm; Ware 1979; Table 4-2). In a study of the diet of juvenile and adult white croaker (125 to 300 mm) collected along the Southern California Coast and embayments, Malins et al. (1987) found that LA/LB Harbor white croaker primarily consume polychaetes and crustaceans, whereas mussels and deposit-feeders are the key prey of Dana Point white croaker (Table 4-2). A small proportion of fish were found in the white croaker diets in all areas. San Francisco Bay white croaker (210 to 340 mm total length) were found to have a more diverse diet, including zooplankton, worms, benthic shrimp and other crustaceans, bivalves, and small fish (Gobas and Arnot 2010).

4.1.3 Shiner Surfperch[4]

Diets for shiner surfperch reported in literature are summarized in Table 4-3. Most studies on shiner surfperch have demonstrated that their diet largely consists of zooplankton and/or crustaceans such as shrimp, amphipods, and isopods (Odenweller 1975; Bane and Robinson 1970; Jahn 2008; Woods 2010). Shiner surfperch have also been shown to consume some detritus, phytoplankton, crustaceans, mussels, and worms. Variation in shiner surfperch diets described in the literature is likely related to age, location, and season. Odenweller (1975) found that shiner surfperch from Anaheim Bay switch their diet between seasons and consume more zooplankton and less sediment and detritus-dwelling organisms in summer and fall than in winter and spring.

In a bioaccumulation model developed for San Francisco Bay, shiner surfperch diets were primarily based on crustaceans and plankton (Gobas and Arnot 2010). In contrast, juvenile shiner surfperch were assumed to consume a diet primarily comprised of phytoplankton (60%) and zooplankton (25%) in the Mackintosh et al. (2004) bioaccumulation model of False Creek Harbour near Vancouver, British Columbia.

4.1.4 Invertebrate Diets

For the purpose of quantifying PCB and DDX transfer from sediment and water-column sources to fish, invertebrates are distinguished by their primary exposure source (water column *via* algae or freshly deposited detritus versus sediment *via* deposit feeding) and degree of bioaccumulation. The relative proportion of particulate material ingested by the representative invertebrate prey deriving from the water column versus the sediment bed is based on literature and site-specific data.

Mussels are representative of filter-feeding organisms, including clams, oysters, some amphipods, brachiopods, and other pelagic organisms that derive most of their food from the water-column particulates. Given that these organisms filter water just above the sediment surface, a small amount of detritus deriving from the sediment may also be ingested

[4] White surfperch are known to have similar feeding strategies and diets to those of shiner surfperch (CDFG 2002; CDFW 2003). Carbon and nitrogen stable isotope data from the Ports' special studies also indicate similar diets and TPs for the two surfperch species (Section 4.1.1.5).

incidentally (Mackintosh et al. 2004; Gobas and Arnot 2010). Crustaceans represent scavengers such as amphipods. The crustacean group primarily consumes recently deposited detritus deriving from the water column (Gobas and Arnot 2010).

Worms are representative of deposit-feeding organisms, including polychaete and other annelid worms. These organisms primarily consume sediment detritus.

To characterize bioaccumulation in water-column invertebrates, the Ports collected mussels and measured tissue concentrations of PCBs and DDX as part of the Ports' 2014 Food Web Study (Anchor QEA 2014b; AMEC Foster Wheeler 2015). Mussels were targeted at four locations; however, mussels were not available in Consolidated Slip, so oysters were collected as a surrogate (Figure 4-1).

AFs for the water-column invertebrates were calculated from the 2014 mussel and oyster data and water-column particulate concentrations measured at the closest location; results for total PCB and DDX are shown in Table 4-4. These values are high compared with literature and ranged from 8.74 to 15.6 for total PCBs and 5.91 to 15.3 for total DDX. AFs ranged from 3 to 4 based on data measured in Green Bay as part of the Green Bay Mass Balance Study (Connolly et al. 1992) and are within the range of values reported for the Hudson River (Lamoureux et al. 2011). The higher water-column particulate AF values for algae/detritus compared with sediment is consistent with greater bioavailability of PCBs associated with recently generated water-column particulates compared with aged sediments (Hatzinger and Alexander 1995). However, because the values measured in the Harbor were generally higher than the literature, the minimum values of 8.74 and 5.91 measured in LA Outer Harbor for total PCB and total DDX, respectively, were used in the model for all areas in the Harbor.

To characterize bioaccumulation in benthic invertebrates, the Ports collected polychaetes and mixed benthic invertebrate samples that were co-located with sediment samples as part of the paired 2014 Sediment and Polychaete Special Study (Anchor QEA 2014c; Environ 2015). Polychaetes were the target benthic invertebrate, but in some areas of the Harbor, insufficient mass of polychaetes was collected; consequently, in those areas tissue chemical analyses include mixed benthic infaunal organisms. The paired polychaete/benthic infaunal and surface sediment sampling locations (stations labels as benthic organisms) are shown in Figure 4-1.

BSAF values for total PCB and total DDX were calculated from the paired polychaete/benthic infaunal and surface sediment samples available for each location, taking an average of the BSAFs from samples collected from the same location (Table 4-5). Whole Harbor values were derived from log-log regressions of concentrations of total PCBs in benthic organisms and paired sediments (Figure 4-2). BSAF values for total PCBs are within the range reported in the literature (i.e., Wong et al. 2001). However, many of the total DDX BSAF values measured in polychaetes are low compared with literature. Evaluation of laboratory quality assurance information indicated that there were quality concerns with the DDX data for the benthic organisms. Therefore, a subset (Consolidated Slip, LA Inner Harbor, and LA Outer Harbor) of locations with sufficient sample mass were reanalyzed for total DDX using a more precise method with lower detection limits (i.e., Method 1699 [USEPA 2007b]). Total DDX BSAFs calculated from the reanalyzed samples were two to ninefold higher than those calculated from the original total DDX results. Given the more precise method used for the reanalysis and that the resulting BSAFs for these samples were closer to literature values, the resulting BSAFs based on the reanalyzed benthic tissue samples were used where available, and DDX BSAF values based on the original benthic samples that were less than the median BSAF reanalysis value of 0.56 were set at that value.

4.1.5 Validation of the Model Diets and Food Web Structure

A summary of the diet of each target species or group that provides the basis for the diets used in the bioaccumulation model is shown in Table 4-6. To validate this food web structure, stable nitrogen isotope data were collected from each species as part of the Ports' 2014 Food Web Study (Anchor QEA 2014b; AMEC Foster Wheeler 2015) and 2014 Sediment and Polychaete Special Study (Anchor QEA 2014c; Environ 2015). Nitrogen isotope composition (symbolized as $\delta^{15}N$[5]) is known to provide an indication of TP (Adams et al. 1983); values increase with each trophic level. To perform the validation, $\delta^{15}N$ data were

5 $\delta^{15}N$ is the concentration ratio of $^{15}N/^{14}N$ stable isotopes, expressed relative to a standard (i.e., $\delta^{15}N$), with units of parts per thousand (‰).

compared with the TP of each species as calculated using the selected diets and knowledge of their ecological role, based on the Adams et al. 1983 model as shown in Equation 12.

$$TP_{target\ species} = \left(\sum_{i=1}^{n} TP_{prey\ i}\ x\ p_{prey\ i} \right) + 1 \qquad (12)$$

where:

TP_{prey_i} = trophic position of each prey item i

p_{prey_i} = proportion of each prey item i in the diet

The nitrogen content ($\delta^{15}N$) of each species correlates favorably ($R^2 = 0.80$, $p = 0.02$) with the TP based on Adams et al. (1983), indicating that the selected diets represented by the TP model reflect the TPs determined based on $\delta^{15}N$ data for each species (Figure 4-3).

Results of the nitrogen and carbon stable isotope analyses are presented in Figure 4-4. Distinct clusters of organisms with similar carbon and nitrogen ratios indicate several different trophic levels are present in the representative Harbor food web. These findings suggest that the model species and their model diets are representative of the key trophic levels within the Harbor.

4.2 Bioenergetics

Site-specific and literature-based information concerning bioenergetics, toxicokinetics, and body composition was used to parameterize the bioaccumulation model, including growth and respiration rates, contaminant mass transfer at the gill, contaminant mass transfer at the gut, and body lipid contents. The sources of these parameters are described in the following subsections.

4.2.1 Growth Rates

Model growth rates are calculated from weight versus age relationships (see Equation 8). Species-specific weight-at-age relationships for target species were determined using both weight-at-age data collected as part of the Ports' 2014 Food Web Study (Anchor QEA 2014b; AMEC Foster Wheeler 2015) and published literature, as cited in the sections below.

In the Ports' 2014 Food Web Study, age was determined using either fish scales or otoliths (i.e., the inner ear structure), both of which exhibit annual rings. Additional details are provided in the following subsections.

4.2.1.1 California Halibut

The California halibut growth rate used in the model is based on length-at-age relationships and weight-at-length relationships from MacNair et al. (2001) and Hammann and Ramirez-Gonzalez (1990), respectively, and with consideration of weight-at-age data from halibut collected as part of the Ports' 2014 Food Web Study (AMEC Foster Wheeler 2015). A comprehensive study of growth of California halibut along the Southern California coast (i.e., from the United States-Mexico Border to Point Conception, California) conducted by MacNair et al. (2001) provided the length-at-age relationships for females and males. Length-at-age data were converted to weight-at-age by averaging the female and male lengths at each age and then converting total lengths to weights using the weight-at-length function established by Hammann and Ramirez-Gonzalez (1990) for California halibut in Todos Santos Bay, Baja, California. Figure 4-5 shows the California halibut growth rate (plotted as weight-at-age) used in the model overlaid with the site-specific weight-at-age based on otolith annuli collected as part of the Ports' 2014 Food Web Study (AMEC Foster Wheeler 2015).

The growth rate for California halibut used in the model shows a good fit to weight-at-age data for halibut caught in the Harbor as part of the Ports' 2014 Food Web Study (AMEC Foster Wheeler 2015) for fish ages 1 through 4. The model growth rate overestimates the weight of halibut at age 4 or older; this is likely due to limited weight-at-age data for halibut older than age 4 from the Harbor as part of the Ports' 2014 Food Web Study (AMEC Foster Wheeler 2015). Additional California halibut size data collected throughout LA/LB Harbor as part of the Ports' Biological Survey from 2013/14 (MBC 2016) include size data for halibut ages 4 and older and compare well with the literature-based growth rate used in the model including fish ages 4 through 7. Uncertainty in the halibut growth rate is further evaluated and discussed in Section 5.

4.2.1.2 White Croaker

White croaker growth rates used in the bioaccumulation model rely on length-at-age relationships and weight-at-length relationships from Moore (1999) and the Ports' Biological Survey from 2013/14 (MBC 2016), respectively. Length-at-age relationships from Moore (1999) were established for white croaker from PV Shelf and are consistent with other studies of croaker growth in the region (Love et al. 1984; Isaacson 1964). Length-at-age data were converted to weight-at-age by averaging the female and male lengths at each age and then converting total lengths to weights using a weight-at-length function established using Harbor white croaker weight and age data as part of the Ports' Biological Survey (MBC 2016). Figure 4-6 shows the white croaker growth rate (plotted as weight-at-age) used in the model overlaid with the site-specific weight-at-age based on otolith annuli collected as part of the Ports' 2014 Food Web Study (AMEC Foster Wheeler 2015).

The growth rate for white croaker used in the model shows a good fit to weight-at-age data for white croaker caught in the Harbor as part of the Ports' 2014 Food Web Study (AMEC Foster Wheeler 2015). Uncertainty in the croaker growth rate is further evaluated and discussed in Section 5.

4.2.1.3 Surfperches

The weight-at-age relationship for surfperches used in the model was determined using weight- and scale-based age data from shiner perch and white surfperch collected as part of the Ports' 2014 Food Web Study (AMEC Foster Wheeler 2015). The weights were plotted against the ages for each individual fish in which both measurements were taken. A growth function (i.e., power regression model) was fit to the data and used to represent the growth rate of surfperches in the model. Figure 4-7 shows that the growth rate used in the model compares well with the site-specific weight-at-age based on otolith annuli collected as part of the Ports' 2014 Food Web Study (AMEC Foster Wheeler 2015).

4.2.2 Respiration

Respiration is calculated in the bioaccumulation model as a function of weight, water temperature, an activity multiplier, and empirical coefficients (see Equation 9). The weight of the fish is specified by growth rates, and the temperature profile was obtained from data collected by the Port of Los Angeles from three stations throughout the LA Harbor and data collected as part of the low detection limit water-column study of the Harbor (Anchor QEA 2013b, 2014d; Ramboll Environ and Weston 2015). For white croaker, the activity multiplier and empirical coefficients used in the Montrose NRDA bioaccumulation model (HydroQual 1997) were used (Table 4-7); the HydroQual (1997) respiration model was based on Hemmingsen (1960). Respiration coefficients for shiner surfperch (Table 4-7) were based on respiration rates for surfperch measured by Webb (1975) and Gordon et al. (1989). Similarly, respiration coefficients for California halibut (Table 4-7) were based on respiration rates for halibut measured by Merino et al. (2009, 2011).

4.2.3 Lipid Contents

Average lipid contents used in the model were calculated with samples collected from 2002 through 2014 (AMEC Foster Wheeler 2015; Environ 2015; see the Data Gaps Analysis Report [Anchor QEA 2014a] for a complete listing of historical programs). Average lipid contents of California halibut and white croaker were calculated from fillet[6] samples and those of surfperches were calculated from whole body samples (Table 4-8). In the model, lipid values for California halibut and white croaker fillets were converted to whole body values by applying whole body to fillet ratios derived from fish collected in 2014 within the Harbor, through the Coastal Marine Fish Contaminant Survey data from PV Shelf (NOAA and USEPA 2007), and as part of the Bioaccumulation of Contaminants in Recreational and Forage Fish in Newport Bay (Allen et al. 2004) (Table 4-9).

4.2.4 Contaminant Mass Transfer at the Gill

Computation of the contaminant depuration rates requires the estimation of the partitioning of contaminants between fish lipid and aqueous phases (K_{fw}; Equation 7). For the analyte group sums (i.e., total PCBs and total DDX), the K_{fw} value reflects the congener or chemical composition in the modeled species.

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[6] The majority of fillet samples were skin-off fillets. However, for a few samples, there was no documentation of the type of fillet that was collected. Because contaminant concentrations and lipid contents were consistent with other data, these were included in the dataset and assumed to be skin-off fillet samples.

High-resolution PCB and DDX data from the Harbor food web and compliance monitoring sampling programs in 2014, as well as octanol-water partition coefficients (K_{ow})[7] values, were used to develop site-specific and species-specific weighted-harmonic mean K_{fw} values. Total PCBs and total DDXs, the modeled chemicals, are composed of individual congeners with varying bioaccumulation characteristics (i.e., K_{ow} values). As described in Section 2.3.3, the congener composition of the PCBs and DDX, and therefore the overall bioaccumulation characteristics of total PCBs and total DDX, are fairly uniform in Harbor invertebrates and fish. To capture their composition, the measured congener compositions were used to estimate representative K_{fw} values for total PCBs and total DDX for each species in each FMZ. For zones without fish samples, average K_{fw} results for all zones within the Harbor were used. Table 4-10 summarizes the log K_{fw} values per species and FMZ. Given that the composition of Total DDX is greater than 78% DDE, the K_{fw} values calculated for the Harbor fish are representative of the fate and transport and bioaccumulation characteristics of DDX in the Harbor food web. However, the composition of PCBs in the Harbor food web includes a wide range of congeners that have variable fate and transport and bioaccumulation characteristics. By using K_{fw} values that are weighted means of the individual congener values, the model is representative of the actual congener composition of the Harbor fish. To evaluate how the model behaves for individual PCB congeners, a sensitivity is included in Section 6, which evaluates model results for three individual PCB congeners.

The rate of contaminant exchange between water and the organism is also controlled by the efficiency with which the contaminant is absorbed from the water. The chemical uptake efficiency (P-ratio; k_{gl}/k_{glO_2}, where k_{gl} is the chemical mass transfer coefficient and k_{glO_2} is the oxygen mass transfer coefficient; Equation 6) can be approximated by the ratio of contaminant to oxygen exchange efficiency. Connolly et al. (1992) summarized the results of multiple experimental measurements of gill exchange, concluding that P-ratio values generally lie between 0.1 to 1.0 for PCBs in fish, and vary as a function of K_{ow}. A P-ratio of 0.54 was selected for both PCBs and DDX based on the average K_{fw} of the 2014 fish data.

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7 Slow-stir, or equivalent, K_{ow} values were used (de Bruijn et al. 1989). For PCB congeners not measured by de Bruijn et al. (1989), values measured by Hawker and Connell (1988) were used, adjusted based on a regression with de Bruijn et al. 1989 data. DDX-specific K_{ow} values were based on de Bruijn et al. 1989, Estimation Programs Interface (EPI) Suite's KOWWIN program, and the ClogP model.

4.2.5 Contaminant Mass Transfer at the Gut

The dose of contaminant that a fish receives from its prey (α_c) is modified by the assimilation efficiency of the contaminant (Equation 1). Based on the analyses presented in the Southern California Bight Damage Assessment Food Web/Pathways Study (HydroQual 1997), the assimilation efficiency for both total PCB and DDX was set equal to 0.8.

4.3 Exposure Characterization

Fish can acquire PCBs and DDX from both water-column and sediment sources. Fish movement data collected as part of fish tracking studies described above were quantified for purposes of determining sediment and water column exposures in the model as described in Section 2. The exposure concentrations for these media are discussed in Section 4.3.3.

4.3.1 Quantification of Fish Movement

Fish movement data collected as part of the Harbor and PV Shelf tracking studies described in Section 2.2 were quantified for each subpopulation of white croaker and California halibut to determine the proportional exposure to PCBs and DDX in each FMZ to which the fish migrate. Surfperches' movements were not included in either tracking study because it is not possible to surgically implant and tag small fishes or those with small body cavities with acoustic transmitters.

Movement patterns of white croaker were quantified by calculating the average proportion of days fish were detected at receivers in each FMZ for each separate subpopulation to determine the proportion of exposure that each subpopulation receives from each FMZ. A similar approach was used to evaluate California halibut movement patterns in the Harbor and white croaker movements on PV Shelf.

A summary of the average proportion of time white croaker and halibut spend in each FMZ is provided below for each subpopulation, along with supplemental movement information based on the literature that is relevant to halibut and surfperches. Additional details about fish movement analysis are discussed in Appendix A.

4.3.2 Subpopulation Migration

The average proportion of time the different subpopulations of white croaker and halibut spend in each FMZ is shown in Figures 4-8 and 4-9 and Tables 4-11 and 4-12. The Harbor tracking study results maps (Figures 4-8 and 4-9) are based solely on fish movement data and include pie charts that indicate the average proportion of days fish (croaker or halibut) subpopulations were detected in each FMZ. Similarly, the PV Shelf tracking study results map (Figure 4-10) includes a pie chart of the average proportion of detects per white croaker within each PV Shelf FMZ (based on Wolfe and Lowe 2015).

For white croaker, an estimate of the amount of time spent in different FMZs for subpopulations where fish were not caught and tagged (i.e., DCE, LA Inner Harbor, Seaplane Lagoon, and LB Inner Harbor South) is also included in Table 4-11. Assumptions for estimated FMZ exposure proportions are described in Appendix A.

4.3.2.1 White Croaker

Figure 4-8 shows that subpopulations of white croaker in Consolidated Slip, Outer LA Harbor, Fish Harbor, Eastern San Pedro Bay, and LB Inner Harbor North displayed some site fidelity to those areas; each subpopulation spent more time within their respective FMZ (i.e., Consolidated Slip, Outer LA Harbor, Fish Harbor, Eastern San Pedro Bay, and LB Inner Harbour North, respectively) than other FMZs. LB Outer Harbor white croaker showed no site fidelity to that area; however, only four of 25 fish tagged in LB Outer Harbor were detected at any point after tagging, and there were limited receivers in this FMZ. While site fidelity is uncertain in this area, it is possible that fish from this subarea spend more time in the LB Outer Harbor than the limited data indicate. A small proportion (less than 1%) of white croaker from some FMZs (e.g., Outer LA Harbor and Fish Harbor) spent time at the Harbor gates and were detected along the corridor to PV Shelf, indicating that some exposure is occurring outside of the Harbor and on PV Shelf.

Additional support for movement of croaker between the Harbor and PV Shelf was provided as part of the PV Shelf tracking study (Wolfe and Lowe 2015). As shown in Figure 4-10 and Table 4-13, an average 5% of all detections of PV Shelf croaker were at the Harbor gates. In addition, during the period of overlap between the PV Shelf and Phase 1 Harbor tracking studies (Appendix B), Wolfe and Lowe (2015) found that 47% of the fish tagged on PV Shelf were observed at Angel's Gate or Queen's Gate and 4% of all croaker tagged (i.e., four fish) were detected at one or more receivers in the LA main channel. Together, these findings suggest that a small proportion of fish caught in the Harbor have been exposed to sediment on PV Shelf; however, due to the lack of complete overlap between the tracking studies, the proportion of PV Shelf exposure for Harbor fish is uncertain. This was considered further during model calibration (see Section 5.1.3) and sensitivity analysis (Section 6.1.1.6).

4.3.2.2 California Halibut

Figure 4-9 and Table 4-12 show the movement patterns for two specific FMZs, LA Outer Harbor and Eastern San Pedro Bay, in which there were sufficient data to quantify movements. Due to the limited information available in the remaining FMZs, estimates of movement patterns were not determined in other areas. However, a whole Harbor exposure estimate was calculated using all halibut passive tracking data to provide an estimate for adult halibut that migrate into the Harbor seasonally, as described below, and potentially use the whole Harbor as habitat during this time.

The LA Outer Harbor and Eastern San Pedro halibut subpopulations showed strong site fidelity to their respective FMZs on an average basis (Figure 4-9, Table 4-12). However, individual fish within each subpopulation and within the Harbor as a whole showed a wide range of movements. Some individuals were shown to reside in an FMZ for as little as 2 days before moving on while others stayed in an FMZ for over a year. More than 50% of the tagged halibut were detected at the Harbor gates, and almost 20% of the halibut were detected on route to PV Shelf; these results indicated that movement of halibut out of the Harbor was common. It should also be noted that most of the California halibut that were caught and tagged in this study were caught in the Outer LA Harbor FMZ despite considerable efforts to catch subadult and adult halibut in all other Harbor areas (Lowe et al. 2015b).

A literature review was conducted on migration of California halibut in the region, and supporting movement information from the literature was then used in conjunction with movement data presented here to establish migration assumptions needed for fish exposures in the model.

Studies reviewed indicated that along the California coast, the movement of California halibut varies by age. California halibut have been shown to spawn in nearshore areas, and newly hatched larvae are transported into embayments and estuaries where they settle and often spend the next several years of their life (Valle et al. 1999; Kramer 1991; Hammann and Ramirez-Gonzalez 1990; CDFG 2001). As halibut mature, they migrate out of bays and estuaries (CDFG 2001) and move longer distances (Domeier and Chun 1995). The exact age at which migration out of embayments occurs is unclear and may vary by location and sex. While this information was not determined as part of the Harbor tracking study (Lowe et al. 2015b), the Ports' latest biological survey data (MBC 2016) show that juveniles ranging in total length from 100 to 500 mm are much more abundant in LA/LB Harbor than adults (greater than 500 mm). These data support the understanding that adults migrate to a greater extent between the Harbor and outside Harbor areas than juveniles. These findings are supported by Domeier and Chun (1995), who demonstrated that California halibut larger than 500 mm (total length) migrated significantly longer distances than juveniles as part of a 40-year California Department of Fish and Game conventional tagging study along the Southern California Bight (Southern California Bight Regional Monitoring Program; including embayments). Adult halibut are known to migrate to nearshore areas to spawn in the spring through late summer and to a lesser extent in the fall (CDFG 2001); halibut move off shore during the winter (Haaker 1975). These seasonal movements may not only be related to spawning but also may be related to seasonal movements of prey such as California grunion (*Leuresthes tenuis*; CDFG 2001).

4.3.2.3 Surfperches

As described above, neither tracking study attempted to evaluate the movements of surfperches. Consequently, a literature review was conducted on migration of surfperches (i.e., white surfperch and shiner surfperch) in the region and a summary is provided below. Studies of surfperches (shiner and white surfperches) indicate that these fish are residential and exhibit site fidelity to localized areas (CDFW 2013). Both surfperch species are abundant throughout the year in shallow water areas and near eelgrass beds and piers and pilings (CDFW 2013; Eschmeyer et al. 1983). Regional studies have shown that surfperches of varying size classes are commonly found throughout the year in LA/LB Harbor (Ports' Biological Surveys [SAIC 2010; MBC 2016]) and all of San Pedro Bay (NOAA 1990).

Based on this information, surfperches will be modeled as non-migratory, and the chemical exposure of each subpopulation will depend on the sole FMZ in which they reside, with the exception of DCE and LARE; all fish migrate out of the estuaries for much of the year due to unfavorable conditions (see Appendix A for a description of the migration assumptions for these areas).

4.3.3 Harbor Sediment and Water Exposure Concentrations

WRAP model outputs for each FMZ and the outside Harbor exposure area (Figure 2-3) were used as exposure inputs to the bioaccumulation model (Everest 2016). The outputs included freely dissolved water-column concentrations and water-column and surface sediment particulate concentrations on a carbon-normalized basis.

The WRAP model was developed based on available and qualified water-column and sediment data. Sediment data from 2002 through 2014 were used to characterize PCB and DDX concentrations in the sediment bed within the Harbor and the ocean; a cutoff year of 2002 retained most of the compiled dataset while excluding older data that do not reflect current conditions in the LA/LB Harbor. Surface sediment was assumed to be the top 16 cm, as this depth cutoff allows for retention of the majority of available data and provides a reasonable and likely conservative estimate of bioavailable sediment concentrations (Anchor QEA 2014a). Data were processed as follows:

- Total PCB and total DDX concentrations were calculated as the sum of individual PCB congeners or DDX related compounds.
- For individual PCB congeners or DDX related compounds, non-detect values were set to zero prior to summation. If all were non-detect, then half the maximum detection limit was used.
- Duplicate results were averaged with parent sample results.
- Aroclor results were excluded for samples with paired congener results.
- Low-resolution PCB results were excluded for samples with paired high-resolution PCB results.

Additional data processing has been previously described in detail (Anchor QEA 2013a, 2014a; Port of Long Beach and Port of Los Angeles 2013).

Thiessen polygons were then generated for the entire Harbor, followed by manual adjustments as needed (e.g., to eliminate the influence of data points across land during the process of assigning concentrations to grid cells in the WRAP model; for additional details, see Everest 2016). Figures 4-11a, 4-11b, and 4-11c show the Thiessen polygons for total PCBs for the Harbor, DCE, and LARE, respectively. Figures 4-12a, 4-12b, and 4-12c show them for total DDX for the same areas. These polygons were used to assign dry-weight surface sediment concentrations to each cell of the WRAP model grid.

The area covering the WRAP model grid outside of the breakwater was split into east and west portions based on the observed gradient in sediment PCB and DDT concentrations (Figures 4-11d and 4-12d). Arithmetic averages of dry-weight surface sediment data were assigned to each portion and subsequently assigned to corresponding WRAP model grid cells. These data provided the initial WRAP model surface sediment conditions.

WRAP model water-column initial conditions were specified based on calibrated ocean boundary conditions, based on an average of data from the Ports' 2014 and 2015 low-detection limit water-column study, whose sampling locations are shown in Figure 4-13. Appendix C provides details associated with the calculation of particulate water column PCB and DDX concentrations based on solid-phase micro-extraction (SPME) freely dissolved concentrations and site-specific partition coefficients.

Daily WRAP model-computed total PCB and total DDX concentrations in the surface sediment and water column for each FMZ were averaged over the simulation period (2014 through mid-2015, following a 2-year equilibration period). These averages are compared with data-based average concentrations in Figures 4-14 and 4-15 for PCB and DDX, respectively. In these figures, the data-based water-column concentrations were calculated from data from the Ports' 2014 and 2015 low-detection limit water-column study; with the exception of DCE and LARE, data-based surface sediment concentration were calculated as surface-weighted average concentrations (SWACs) based on Thiessen polygons (Figures 4-11a and 4-12a). Note that the model-computed water-column concentrations shown in Figures 4-14 and 4-15 represent averages over the entire FMZ, whereas the data were collected from specific locations. Nevertheless, except for water-column concentrations in Consolidated Slip and LARE, the WRAP model-computed concentrations are similar to the measured values. The higher

WRAP model water-column chemical concentrations in Consolidated Slip included multiple rain events at the end of 2014, whereas data were collected over a shorter period. As shown, the WRAP model-computed sediment concentrations compare well with the data. These model outputs were used as inputs to the bioaccumulation model (Table 4-14).

4.3.4 Palos Verdes Shelf Exposure Concentrations

PV Shelf exposure concentrations were based on carbon-normalized surface sediment data collected from 2005[8] through 2014. For areas without data, total PCB and total DDX concentrations were estimated using Inverse Distance Weighted interpolation via GIS software (Figures 4-16 and 4-17). SWACs were then calculated for each PV Shelf FMZ[9]. Finally, a weighted average concentration for PV Shelf was determined for PCBs and DDX separately by multiplying the SWAC for each of the four PV Shelf FMZs by the proportional detection frequencies for white croaker (Table 4-13) in each zone and then summing together.

[8] The starting year was selected as 2005 because PCB concentrations in PV Shelf sediment in prior years were measured on an Aroclor—not congener—basis.

[9] For PVS4, the area overlapping the WRAP model grid was excluded because exposure to that area was already accounted for in the WRAP model outside the Harbor area.

5 MODEL CALIBRATION

A steady-state calibration of the bioaccumulation model was performed, exposing the food web to WRAP model water-column and sediment concentrations averaged over the simulation period (1.5 years), and comparing computed tissue concentrations with average total PCB and DDX concentrations in fish collected between 2002 to 2014.

5.1 Calibration Approach

The bioaccumulation model was calibrated to surfperch, white croaker, and California halibut data collected between 2002 and 2014 and averaged by FMZ; sampling locations are shown in Figure 4-1, and the data sources are described in the Data Gaps Analysis Report (Anchor QEA 2014a). To achieve a robust data set for model calibration, it is necessary to balance the benefits of increased sample size against the uncertainty that may be caused by including data collected over several years. As discussed in Section 2.3.2, temporal trends in bivalve, fish, and mussel data suggest natural recovery is occurring but variability confound attempts to accurately characterize the rate. However, rates are consistent with rates of a few percent per year measured in mussels from other subareas of the Harbor and at many Southern California sites, as described by the State Water Resources Control Board (Melwani et al. 2013). Based on this level of decline, variability in total PCB and total DDX concentrations over the 2002 to 2014 period should be less than 25 to 50%, which is within the noise of within-year variability.

The model calibration relied on the growth, bioenergetic, and mass transfer parameters described in Section 4. For the calibration, the diet was simplified as described below in Section 5.1.1. Accumulation at the base of the food web (i.e., BSAFs) and the white croaker and California halibut migration patterns parameters adjusted during calibration are compared below in Sections 5.1.2 and 5.1.3, respectively. All adjustments to parameters made during the calibration process maintained consistency with the field data and the published literature upon which model parameters were based.

Model results and data are presented on a wet-weight and lipid-normalized basis. Wet-weight model results and data are presented on a fillet basis for white croaker and California halibut using whole body to fillet ratios derived from 2014 data and literature (Table 4-8) and on a whole-body basis for surfperches. Model results are averaged over the last year of simulation after the model has come to steady-state, and then weighted according to the size distribution of the fish data (Tables 5-1, 5-2, and 5-3 for surfperches, white croaker, and California halibut, respectively). Error bars show the range over the age classes that contribute to the average for model results and +/- two standard errors of the mean for data.

5.1.1 Fish Diets

The diets for California halibut, white croaker, and surfperches described in Section 4.1.1 formed the basis for the diets used in the model. Simplifications were made during the calibration process as described below.

The literature supports a California halibut diet of primarily water-column invertebrates (represented by mussels in the model) at the earliest life stage, incorporation of more crustaceans/scavengers and small fish at the intermediate life stages, and then diets of entirely fish as adults (Table 4-1). Thus, the model halibut diet transitions from 90 to 40% water-column invertebrates from ages 0 through 4, and fish are introduced at age 2. By age 5, halibut feed entirely on the representative water-column feeder (surfperches) and benthic feeder (white croaker; Table 5-4). Based on the literature for white croaker, diet is limited to invertebrates for ages 0 through 2, and fish are introduced at age 3 (Table 4-2). All studies identified white croaker's preference for deposit-feeding over water-column invertebrates and fish; thus, their model diet includes a higher proportion of deposit-feeders for both juveniles and adults (Table 5-5). For both white croaker and halibut, prey proportions were adjusted slightly, compared with literature values, to improve model fit and to account for the age (and size) of the prey items with increasing age (Tables 5-4 and 5-5).

The model surfperch diet consists of water-column and deposit-feeding invertebrates. The majority of the literature indicated a strong preference for water-column invertebrates (Table 4-3), and through calibration it was determined that 75% provided the best model fit (Table 5-6).

5.1.2 Benthic Invertebrate Bioaccumulation Factors

During the calibration process, model performance was assessed using two alternative approaches to BSAF values: zone-specific BSAF values and single overall best estimate calculated using all of the Harbor data (derived from log-log regressions of concentrations of total PCB in benthic organisms and paired sediments; Figure 4-2). Model results for fish based on whole Harbor BSAF values are compared with results based on BSAFs from the individual FMZs in Figure 5-1. As shown, the whole Harbor BSAF values degrade the calibration in many areas of the Harbor, particularly for PCBs in white croaker. Therefore, zone-specific BSAF values were used. The regression-based BSAF for total PCBs was used in zones where zone-specific measurements were not available (see Table 4-5). For total DDX, the median BSAF reanalysis value was used, as the regression was affected by the low BSAFs measured in some locations. Additional values are explored in the sensitivity and uncertainty evaluation (Section 6).

5.1.3 Fish Movement

Movement patterns for California halibut and white croaker were characterized initially using the fish tracking data and published literature (Section 4.3.3). This initial characterization was then modified during calibration; a detailed description of the migration calibration process is provided in Appendix D. The final characterization of fish movement in the model provided the best match with the chemical concentration data for fish for both total PCBs and total DDX in all fish zones, and both migrating species, while honoring the tracking study and published literature (shown in Appendix D). Only minor adjustments to fish movement patterns presented in Appendix A were made during the calibration process.

The final model movement patterns are presented in Tables 5-7 and 5-8 for white croaker and California halibut, respectively. These tables indicate whether the proportions were increased or decreased compared with the movement patterns for white croaker and California halibut characterized based on the fish tracking data (Tables 4-10 and 4-11, respectively); for all of the Harbor areas that did not have specific tracking study proportions for California halibut (all FMZs except LA Outer Harbor and Eastern San Pedro Bay), the changes were compared with the proportions determined for the whole Harbor.

Migration in the model is accomplished by "migrating" the fish to the FMZs for the average proportion of time the subpopulations spend in each zone indicated in Tables 5-7 and 5-8. "Migration" occurs by exposing the fish subpopulations to the water, sediment, and prey concentrations for each FMZ they migrate to, according to the fish tracking data, for the average proportion of time (days of the year) that they spend in that FMZ.

Model results without migration, with migration based solely on the fish tracking data, and the adjusted migration are compared in Figure 5-2. As shown, the differences in model-estimated total PCB and total DDX concentrations are generally similar across the three migration scenarios, but the adjusted migration improves the calibration for total DDX for both white croaker and California halibut.

5.2 Calibration Results

Final model-data comparisons of total PCB and total DDX concentrations in surfperches, white croaker, and California halibut for each FMZ are shown in Figures 5-3 through 5-8. In Figure 5-6, the average concentrations observed in white croaker from LA Inner Harbor are shown with (purple bar) and without (blue bar) the one fish sample with DDX concentrations that are an order of magnitude higher than the mean concentrations in the Harbor (compare outlier to mean in Zone 2 of Figure 4-6d in the Data Gaps Analysis Report [Anchor QEA 2014a]). Given the anomalous DDX concentration in this fish, the source of this exposure is evaluated separately and discussed in Section 4.2.1.

The model provides a reasonable match to the observed total PCB and total DDX concentrations. Model-estimated average total PCBs in surfperches are generally within a factor of two of the data, with the exception of LB Inner Harbor South (Figure 5-9a). For LB Inner Harbor South, this could be due to more localized exposure to higher sediment concentrations compared with the FMZ average. The model also underpredicts total DDX in surfperches in LB Inner Harbor South and Fish Harbor (Figure 5-10a). Again, this could be due to more localized exposure; given that surfperches are non-migratory, their exposure may reflect specific habitat areas within each FMZ, rather than exposure spread evenly throughout the FMZ, or there could be localized variations in their diet (i.e., could be feeding on a higher proportion of benthic compared with water-column invertebrates).

Average total PCB concentrations computed by the model for white croaker are within or close to a factor of two of the data for all areas (Figure 5-9b).

Model estimates for white croaker total DDX concentrations are close to or within a factor of two of data in all areas and certainly within a factor of three (Figure 5-10b). The wide range of lipid contents in the fish collected from these zones is likely the reason for the lipid-based model underestimates as the model is based on the average lipid content of the data.

Average wet-weight and lipid-based total PCB concentrations are over-estimated by the model for California halibut LB Outer Harbor and LARE and underestimated for LB Inner Harbor South on a lipid basis (Figure 5-9c). This is likely due to the uncertainty associated with migration to other Harbor subareas for the California halibut, given the limited tracking information for fish from these FMZs as well as small, variable sample sizes of the lipid data used as inputs to the model. Average total DDX concentrations estimated by the model for California halibut are generally within a factor of two for all areas on a lipid-basis but are over-estimated by the model (although within a factor of four) for a wet-weight basis for several areas of the Harbor (Figure 5-10c). Again, this is likely to due to uncertainty in the tracking data and variability in lipid contents.

5.2.1 Simulation of LA Inner Harbor White Croaker with Elevated DDX

As discussed in Section 5.2, one white croaker sample from LA Inner Harbor demonstrated a total DDX concentration that was an order of magnitude higher than other fish from this FMZ. Lipid content and size of this fish was not unusual, and its total PCB concentration is within the range of other LA Harbor croaker. Given that DDX exposure concentrations in the Harbor are not high enough to support the DDX concentrations measured in this fish, and that the fish tracking study found that white croaker migrate between the Harbor—particularly LA Harbor—and PV Shelf (Section 4.3), a likely scenario is that the elevated DDX white croaker sample was initially exposed to the higher DDX concentrations on PV Shelf and then migrated into the Harbor. This would be consistent with the results of the PV Shelf tracking study (Wolfe and Lowe 2015). To evaluate this scenario, a simulation was conducted in which a white croaker spent its first 5 years on PV Shelf and then moved into the Harbor for the next year (the fish falls within a weight range that is consistent with a

6-year-old fish). The results of this simulation are shown in Figure 5-11; the model total DDX results for each age class are shown as different colored lines, and the measured total DDX concentration in this fish is shown as a black dot. This simulation supports the scenario that a subset of Harbor croaker are exposed to PV Shelf sediments for extended periods.

6 SENSITIVITY AND UNCERTAINTY

The utility of the bioaccumulation model as a predictive tool depends on: 1) its ability to reproduce PCB and DDX levels measured in the fish during the calibration period; and 2) the extent to which it provides an accurate estimate of the relative importance of surface sediment and water-column PCBs and DDXs to the biota. The former defines predictive ability under current conditions, whereas the latter affects predictive ability associated with future conditions and remedial activities. The goal of the sensitivity analysis is to identify the model input parameters to which the model results are the most sensitive and, thus, can have the greatest impact on 1 and 2 above. The uncertainty analysis then builds on the sensitivity analysis by developing alternate predictions produced when taking into account model sensitivity and uncertainty for each of the key parameter values. The sensitivity analysis is discussed in Section 6.1, and the approach to the uncertainty analysis is presented in Section 6.2.

6.1 Model Sensitivity

The sensitivity of the model was evaluated for the parameters to which the model is most sensitive and for which there is some uncertainty associated with their true values. The selection of parameters for evaluation, and the range of values used for those parameters, were based on the results of multiple model simulations and professional judgment, maintaining consistency with published literature and site data. Parameters include growth, diet, accumulation at the base of the food web (BSAF and the water-column particulate AF), and migration. Additionally, the sensitivity of the bioaccumulation model to the WRAP model sensitivity results was evaluated. The values of the parameters used in the sensitivity analysis are discussed in Section 5.1.1, and the results are presented in Section 5.1.2.

6.1.1 Sensitivity Parameter Values

6.1.1.1 Growth Rates

In general, faster growth rates lead to lower chemical concentrations because of the phenomenon of growth dilution. Model simulations to evaluate sensitivity were performed using both lower bound and upper bound growth rates. Alternative growth rates were determined using alternate fits to the 2014 weight-at-age relationships described in Section 4.2.1. The surfperch growth rate used in the model was developed from the weight-at-age data for both shiner and white surfperch (Section 4.2.1.3). Alternative growth rates were developed by fitting separate rates to the white surfperch and shiner surfperch (Figure 6-1), which results in faster and slower growth, respectively. The white croaker growth rate used in the model was based on length-at-age data from Moore (1999) that were converted to a weight-at-age relationship using the weight-at-length function based on the Ports' Biological Survey data (MBC 2016); weight-at-age data from the Ports' 2014 Food Web Study were also considered (AMEC Foster Wheeler 2015). An alternative (slower) growth rate was established by using the weight-at-length function published by Moore (1999) to convert length-at-age data to weight-at-age (Figure 6-2). The California halibut growth rate used in the model was based on length-at-age relationships and weight-at-length relationships from MacNair et al. (2001) and Hammann and Ramirez-Gonzalez (1990), respectively, and with consideration of weight-at-age data from halibut collected as part of the Ports' 2014 Food Web Study (AMEC Foster Wheeler 2015). Alternative growth rates were established by using separate male and female length-at-age relationships (MacNair et al. 2001) along with the same weight-at-length relationship (Hammann and Ramirez-Gonzalez 1990), which resulted in slower and faster growth rates, respectively (Figure 6-3).

6.1.1.2 Diet

Diet affects bioaccumulation because contaminant concentrations in prey items vary. For example, eating at higher trophic levels leads to higher predicted fish tissue concentrations. One simulation for each species was performed to evaluate the effects of changes in diet. Alternative diets for target species were determined for surfperches, croaker, and halibut by slightly modifying the diet in a way that improved the relationship with $\delta^{15}N$ but maintained consistency with the range of diets observed in the literature (Section 4.1.1.5. Figure 6-4 illustrates how the TP changes based on alternative diets for surfperches, croaker, and halibut in relationship to $\delta^{15}N$. Alternative diets by age of each species are presented in Tables 6-1, 6-2, and 6-3 for surfperches, croaker, and halibut, respectively.

6.1.1.3 Invertebrate Bioaccumulation

The diet of benthic invertebrates is represented by the BSAF; the BSAF directly affects contaminant concentrations throughout the portion of the food web that includes benthic invertebrates. Two simulations, using the individual minimum and maximum total PCB and

DDX BSAFs as alternative values measured in the 2014 Sediment and Polychaete Special Study (Anchor QEA 2014c; Environ 2015), were run. For total DDX, the minimum BSAF value was set at the minimum reanalysis value of 0.10.

As noted in Section 4.1.1, the water-column particulate AFs determined from the 2014 bivalve study and the low detection limits study water-column particulate concentrations, were high relative to the literature. Thus, the lower-bound value for the sensitivity was taken from the literature (4.0; Connolly et al. 1992), and the upper-bound values were based on the maximum values based on the site data (see Section 4.1.1). Total PCB and DDX maximum water-column particulate accumulation values determined from the 2014 bivalve data and the low-detection limit Special Study water-column particulate concentrations are shown in Table 4-4.

6.1.1.4 PCB Congeners

The bioaccumulation model was evaluated for a range of PCB congeners that represent a wide range of fate and transport and bioaccumulation properties. These congeners were selected by reviewing the PCB homolog and congener composition of sediment and fish data collected within the FMZs (Figures 2-14 and 2-15 and 2-19 and 2-20, respectively) and on PV Shelf. Tetra through hepta-PCB homologues account for the majority of total PCBs in Harbor sediment and fish. Given that the log K_{fw} values for the fish are about 6.8, a value in line with a penta-PCB homolog, representative congeners were selected from tetra-, hexa-, and hepta-PCB homologs. From these homologue groups, congeners with the highest concentrations (and minimum number of non-detects) across data sets were selected, avoiding co-eluting congeners to simplify the creation of model inputs and model-data comparisons among media. The three individual PCB congeners selected were PCB-074, PCB-153, and PCB-180, whose log K_{ow} values are 6.59, 7.32, and 7.76, respectively.

For each of the three individual PCB congeners selected, sediment and water column exposure concentrations were developed from the same data, and with the same methods used to develop the initial conditions for the WRAP model, described in Section 4.3.3; for this sensitivity, the data-based concentrations for the congeners were used directly, as the WRAP model was not run for the individual congeners. Sediment exposure concentrations of carbon-normalized PCB concentrations were computed by calculating SWACs for each Harbor FMZ that is outside the Harbor and PV Shelf (see Section 4.3.3).

Water column exposure concentrations were calculated from freely dissolved PCB data collected during low-detection limit events 1, 2, and 3 using the same approach described in Section 4.3.3. Water-column accumulation factors and BSAFs were computed using the same approach described in Section 4.1.1.4 and the K_{ow} values were used directly as surrogates for the K_{fw} values. The chemical uptake efficiency (P-ratio) values were set to 0.8, 0.5, and 0.35 for PCB-074, PCB-153, and PCB-180, respectfully. All other model input parameters were kept the same as for the total PCB calibration.

6.1.1.5 Migration

Alternative migration patterns were established by individually adjusting white croaker and adult halibut migration to the three areas with the highest sediment PCB concentrations (Fish Harbor and Consolidated Slip) and DDX concentrations (PV Shelf) and the lowest overall concentrations (the Outside Harbor area). Changes in migration to these areas have the greatest potential to affect the sediment contribution estimates and, consequently, the selection of future management alternatives. The following three alternative migration patterns were evaluated separately for white croaker (Tables 6-4 to 6-6) and California halibut (Tables 6-7 to 6-9):

- Reduced migration for all fish subpopulations exposed to Fish Harbor and increased migration to PV Shelf (Tables 6-4 and 6-7)
- Reduced migration for all fish subpopulations exposed to Consolidated Slip and increased migration to PV Shelf (Tables 6-5 and 6-8)
- Replaced migration to PV Shelf for fish subpopulations exposed to PV Shelf in the calibration with migration to the outside Harbor area (Tables 6-8 and 6-9)

6.1.1.6 WRAP Model

In parallel with the sensitivity testing performed on bioaccumulation model-specific parameters, the sensitivity of the WRAP model was separately evaluated for the parameters to which the model was most sensitive and for which there is uncertainty associated with their true values. The most sensitive and uncertain WRAP model parameters include ocean boundary (high and low estimates), sediment bed concentration (double and half the bed organic concentration), and watershed loading (high and low estimates). The average sediment and water particulate concentrations for each FMZ predicted by the WRAP model base calibration and sensitivity analyses (i.e., the inputs used in the bioaccumulation to evaluate sensitivity) are shown in Table 6-10.

Table 6-11 provides a summary of the low and high ranges of all parameters evaluated as part of the sensitivity analyses and a description of the basis for these ranges. Parameter ranges for the examination of model sensitivity were based upon a combination of the data, literature, and professional judgment.

6.1.2 Sensitivity Analysis Approach

The sensitivity of the model to these parameters was evaluated by running the model unchanged except for the parameter of interest, one at a time. Results were evaluated using the proportional change in mean wet-weight- and lipid-based total PCB and total DDX concentrations in all three fish species resulting from running the model at the low and high end of each parameter range. The sensitivity evaluation metric used was change relative to calibration result:

$$Change\ Relative\ to\ Calibration = \frac{(Sensitivity\ Result - Calibration\ Result)}{Calibration\ Result}$$

6.1.3 Sensitivity Analysis Results

Figure 6-5 compares the average wet-weight-based sensitivity results, based on the alternative values provided above, for each species, for all tested model parameters. The bars for each model parameter represent the average of the ratios of the difference between the model results for the sensitivity and calibration, divided by the calibration result, for all the FMZs. Minimum and maximum model parameter values result in ratios that are above or below the line, respectively. Surfperch DDX and PCB tissue concentrations are most sensitive to the alternative water-column particulate AF and sediment bed concentration. Surfperch DDX and PCB tissue concentrations were relatively sensitive to growth rate. Both total PCB and DDX white croaker tissue concentrations are most sensitive to BSAF and sediment bed concentration, and white croaker total DDX tissue concentrations are most sensitive to increased and decreased PV Shelf migration. California halibut total DDX concentrations are most sensitive to increased and decreased migration to PV Shelf. California halibut also are relatively sensitive to sediment bed concentration, the water-column particulate AF, and BSAF. Total DDX halibut and surfperch tissue concentrations are also relatively sensitive to the ocean boundary.

Figures 6-6 through 6-15 compare the sensitivity results for each species for the following parameters: growth, diet, BSAF, water-column particulate AF, alternate Fish Harbor migration, alternate Consolidated Slip migration, replacement of PV Shelf migration, ocean boundary, sediment bed, and watershed loadings, respectively, for each FMZ. The bars for each model parameter represent the ratios of the difference between the model results for the sensitivity and calibration, divided by the calibration result. Minimum and maximum model parameter values result in ratios that are above or below the line, respectively. The same general conclusions can be drawn from these figures as for the average sensitivity results shown in Figure 6-9. In addition, these sensitivity evaluations enable comparison of the results between the various areas of the Harbor. Halibut and surfperch tissue concentrations show a greater response to the alternate growth rates in areas of the Harbor with relatively lower exposure concentrations (Figure 6-10). There is little difference in model response to the alternate diets between Harbor areas (Figure 6-11). As would be expected, model response to the alternative BSAF sensitivity is most pronounced in the Harbor areas where the upper- and lower-bound alternate value differs most from the value used in the calibration (e.g., LB Inner Harbor South where the alternate upper-bound was 2.71 and 1.47 for total PCB and total DDX, respectively, compared with 0.61 for total PCB and 0.56 for total DDX [Figure 6-12]). The spatial trend in the water-column particulate concentrations results is also a function of the difference in the alternate values used in the sensitivity and the calibration values (Figure 6-13). The model response is also more sensitive to alternate BSAF and the water-column particulate AFs in areas with higher sediment and water-column concentrations, respectively (Figures 6-12 and 6-13). Also, as would be expected, replacing migration to Harbor areas with relatively higher total PCB and total DDX levels with migration to PV Shelf results in higher total DDX fish tissue concentrations and slightly lower total PCB concentrations (Figures 6-14 and 6-15). Likewise, replacing migration to PV Shelf with migration to just outside the Harbor results in lower total DDX concentrations (Figure 6-17). Areas of the Harbor closest to the ocean boundary are the most sensitive to changes in the ocean boundary sensitivity values (Figure 6-17), while the opposite spatial trend is seen for the watershed loading sensitivity (Figure 6-19). Model sensitivity to the alternative sediment bed concentrations is a complex function of the differences in BSAF and sediment concentrations among Harbor areas (Figure 6-18). For example, LB Inner Harbor South relies on a lower total PCB and total DDX BSAF compared with that for LB Outer Harbor (Table 4-5), but the total PCB sediment exposure concentrations are higher in LB Inner Harbor South compared with LB Outer Harbor (Table 4-12), so the response is similar for total PCB tissue concentrations between locations. However, total DDX sediment exposure concentrations are the same in both of these Harbor areas, so LB Outer Harbor has a greater response (Figure 6-18).

In summary, when values of the above-mentioned parameters are varied within ranges that are reasonable in light of site-specific data and published literature, the computed tissue concentrations are almost always within a factor of approximately two (a factor of two on Figures 6-10 through 6-19 is represented by bars that reach to 1 or -1). Most results lie within approximately 50% (bars that reach to 0.5 or -0.5). The impacts of parameter uncertainty on the relationship between model and data are shown in Figures 6-20 through 6-25. In most cases, the sensitivity analysis does not materially impact the relationship of model result to data; that is, for specific chemicals, species and zones, the fit may be better or worse, but generally with overlapping error bars. This provides a qualitative picture of the overall uncertainty associated with the bioaccumulation model.

6.1.3.1 PCB Congeners

Model-data comparisons of PCB-74, PCB-153, and PCB-180 for each FMZ are shown in Figures 6-26, 6-27, and 6-28, respectively. As shown, the congener calibrations are reasonable for all species.

To evaluate model bias across congeners measured and model-estimated BSAF values are compared in Figure 6-29a. A similar plot for total PCB and total DDX is provided for comparison (Figure 6-29b). While there is deviation from the 1:1 line, the majority are within a factor of two, and with the exception of a few comparisons, are generally within a factor of ten. Additionally, there is no consistent bias for individual congeners or chemicals, suggesting that variability is due to variability in the data and not due to model performance for the individual congeners.

6.2 Uncertainty Analysis

Model uncertainty is evaluated in the context of the questions the model is being asked to address. The bioaccumulation model will be used to evaluate the relative benefits of alternative contaminant management plans, which may include upland source reduction (addressing contaminants entering the Harbor from the major tributaries) or sediment remediation (which may include dredging, capping, or amendments). Thus, for each species in each FMZ, the critical uncertainty is the extent to which contaminant concentrations in fish tissues might be affected by reductions in local sediment concentrations within the FMZ. Therefore, the goal of the uncertainty analysis is to develop reasonable alternative versions of the model (termed alternative calibrations) that still match the tissue data reasonably well, honor the available site data and published literature, and yet produce upper and lower bound representation of the influence of local sediments on local tissues.

To develop uncertainty bounds, simulations in model parameters were varied to produce upper- and lower-bound estimates of the sediment contribution to the fish tissue.

The combination of values that were used to develop alternative calibrations with upper- and lower-bound sediment contributions is provided in Table 6-12. These include the parameters where the model was most sensitive, based on the sensitivity analysis results presented in Section 6.1.3; BSAF, water column particulate AF, and the ocean boundary. Alternate values of the sediment bed concentrations were not included in this example because the alternate BSAF values achieve the same result, effectively. These alternative model input parameters were combined to maximize and minimize the sediment contribution to the fish tissue concentration while still producing reasonable comparisons with the data. For the upper-bound sediment contribution, 2 standard errors of the mean FMZ BSAF values were added to the calibration value for each zone, and were combined with the water column particulate AFs that had 2 standard errors of the mean water column particulate AF values subtracted from the calibration value. Additionally, the minimum ocean boundary WRAP model scenario was combined for the upper-bound sediment contribution calibration. The lower-bound sediment concentration used the similar lower-bound BSAF values and upper-bound water column AF and ocean boundary WRAP model scenario.

The results are compared with the base calibration for each FMZ in Figure 6-30. As shown, results vary by species. In Consolidated Slip, the lower-bound sediment contribution calibration produces higher total PCB and DDX concentrations compared with the base calibration for surfperch, while the upper-bound sediment contribution calibration results in lower concentrations for this species (Figure 6-30b). This is due to the stronger water column tie for this species. The opposite results are seen for total PCB in white croaker; the lower-bound sediment contribution results in concentrations that are lower compared with the base calibration, and the upper-bound calibration produced higher concentrations due to the stronger sediment tie for this species. Lower- and upper-bound sediment contribution calibrations produce Total DDX concentrations in white croaker that are about the same, suggesting that the water column is a more important source of DDX compared with PCBs. For California halibut, lower- and upper-bound sediment contribution calibrations produce concentrations of both chemicals that are similar to the base calibration, given the mixed diet of this species. Similar results for surfperch are seen for all FMZs (Figure 6-30); the lower-bound sediment contribution produces higher, and the upper-bound sediment contribution produces lower total PCB and DDX concentrations. However, for white croaker, the results are variable across FMZs; in LA Inner Harbor, the results are similar to those in Consolidated Slip for total PCBs, while the upper- and lower-bound sediment contributions produce concentrations similar to the base calibration in most of the other FMZs. For California halibut, the results for most of the FMZs are similar to surfperch; the lower-bound sediment contribution produces higher, and the upper-bound sediment contribution produces lower total PCB and DDX concentrations, except for LA Inner Harbor and LB Inner Harbor South, where concentrations for all three calibrations are about the same. For all species and chemicals in each FMZ, the alternative calibrations produce reasonable matches to the data and, thus, will be carried forward in the evaluation of scenarios, to capture the uncertainty in the most sensitive model input parameters that have the greatest impact on the relative contribution of contaminant sources.

7 SUMMARY AND NEXT STEPS

This report describes the development and calibration of a site-specific, bioenergetics-based bioaccumulation model that predicts the transfer of PCBs and DDX within the Harbor food web to fish species of interest. The bioaccumulation model relies on the AQFDCHN model framework and has been modified to represent the Harbor food web structure for target fish species and migration of fish among subareas of the Harbor and to and from PV Shelf. In addition to fish movement and food web structure, this model accounts for site-specific diet, lipid content, and growth rates of organisms. The bioaccumulation model was successfully linked to the WRAP model, which simulates the hydrodynamics, sediment transport, and chemical fate in the Harbor and predicts sediment and water-column particulate and dissolved concentrations of PCBs and DDX; these values were used as exposure inputs in the bioaccumulation model. The model was also successfully calibrated using site data collected as part of Ports' special studies and literature-based values.

7.1 Modeling of PCBs

The model provides a reasonable match to the observed total PCB concentrations for surfperches, white croaker, and California halibut, both on a wet-weight and lipid-normalized basis. Key findings were as follows:

- Model-estimated average total PCB concentrations in surfperches are generally within a factor of two of the data, with the exception of LB Inner Harbor South, possibly due to more localized exposure of these residential fishes to higher sediment concentrations as compared with the FMZ average.
- For white croaker, average total PCB concentrations estimated by the model are within or close to a factor of two of the data for all areas.
- California halibut average total PCB concentrations are over-estimated by the model for LB Outer Harbor and LARE and underestimated for LB Inner Harbor South on a lipid-basis. This is likely due to the uncertainty associated with migration to other Harbor subareas and variable lipid contents.

7.2 Modeling of DDX

The model also provides a reasonable match to the observed total DDX concentrations for surfperches, white croaker, and California halibut, both on a wet-weight and lipid-normalized basis. Key findings were as follows:

- Model-estimated average total DDX concentrations in surfperches are generally within a factor of two of the data, with the exception of underestimates of total DDX in LB Inner Harbor South and Fish Harbor. These model-data differences could be due to more localized exposure in these FMZs, as surfperches' exposure may reflect specific habitat areas within each FMZ, rather than exposure spread evenly throughout the FMZ.
- For white croaker, model estimates of total DDX were within or close to a factor of two and well within a factor a three of data in all areas. The wide range of lipid contents of the fish data in these zones is likely the reason lipid-based model under-estimates.
- California halibut average total DDX concentrations are generally within a factor of two for all areas on a lipid basis but are over-estimated by the model (although within a factor of four) on a wet-weight basis for several areas of the Harbor. Again, this is likely to due to uncertainty in the tracking data and variability in lipid contents.

7.3 Sensitivity and Uncertainty Analyses

The sensitivity of the model was evaluated for the parameters to which the model is most sensitive, and for which there is some uncertainty associated with their true values. The selection of parameters for evaluation, and the range of values used for those parameters, was based on the results of multiple model simulations and professional judgment, maintaining consistency with published literature and site data. The sensitivity analysis identified the model parameters to which the estimated fish tissue concentrations are the most sensitive. Sensitivity results are as follows:

- Surfperch DDX and PCB tissue concentrations were most sensitive to the water-column particulate AF and sediment bed concentration and relatively sensitive to growth rate.

- White croaker total PCB and DDX concentrations were most sensitive to BSAF and sediment bed concentration, and croaker total DDX tissue concentrations were sensitive to increases and decreases in migration to PV Shelf.
- California halibut total DDX concentrations were most sensitive to increased and decreased migration to PV Shelf and halibut total DDX and total PCBs were relatively sensitive to sediment bed concentration and the water-column particulate AF.
- Total DDX halibut and surfperch tissue concentrations were also relatively sensitive to the ocean boundary.

The uncertainty analysis builds on the sensitivity analysis to produce alternate calibrations that maximize and minimize the predicted sediment contribution to fish tissue concentrations. These alternate calibrations provide uncertainty bounds on the calibration and be presented along with the baseline and management scenarios.

Results of this study demonstrate that the bioaccumulation model can be used to accurately simulate the relationship between sediment and water bioaccumulative concentrations and those in target fish species. Future plans include using the linked WRAP and bioaccumulation model to evaluate the effectiveness of various management alternatives at reducing Harbor fish tissue concentrations; uncertainties associated with the modeling will be incorporated when applying the tool for this purpose. In addition, the data collected within this program and the linked model results will be used to provide the technical basis for modifications to the TMDL at the reconsideration. Specifically, special study data and model results will be used to:

- Demonstrate scientifically defensible linkages between all PCB and DDX sources (i.e., ongoing watershed inputs, Harbor sediment, and off-site sediment) and fish tissue impairments that can be used to update the linkage analysis in the Harbor Toxics TMDL.
- Identify the most effective management actions for reducing fish tissue impairments and incorporate results into a revised implementation plan.

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TABLES

Table 3-1

Previous Applications of AQFDCHN Model at Project Sites Across the United States

Application/Project	Modeled Species	Reference
Neal's Landfill (Conard's Branch and Richland Creek), Indiana	Creek chub	QEA 2007 and USEPA 2007a
Grasse River, New York	Smallmouth bass	Alcoa Inc. 2012
Fox River PCBs Site, Wisconsin	Walleye, rainbow smelt, alewife, and gizzard shad	QEA 2001
Upper Hudson River PCBs Site, New York	Largemouth bass, brown bullhead, and pumpkinseed	QEA 1999
Southern California Bight	White croaker, kelp bass, and dover sole	HydroQual 1997
Green Bay Mass Balance Study	Walleye and brown trout	Connolly et al. 1992
New Bedford Harbor	Winter flounder and lobster	Connolly 1991
Lake Michigan	Lake trout	Thomann and Connolly 1984

Table 4-1
Food Web Structure and Diet of California Halibut

Species[1]	Zooplankton	Mussels/ Filter Feeders	Crustaceans/ Scavengers	Worms/ Deposit Feeders	Fish 1: Prey Fish (e.g., Surfperches)	Fish 2: Benthic-Feeding Fish (e.g., White Croaker)	Source
California Halibut SL< 20 mm	0.80		0.19	0.01			Allen 1988
California Halibut 20 mm < SL < 150 mm	0.11		0.88	0.01			Allen 1988
California Halibut 120-510 mm SL		0.02	0.3		0.45	0.23	Haaker 1975
California Halibut 124-476 mm SL		0.02	0.08		0.74	0.16	Plummer et al. 1983
California Halibut > 500 mm					0.5	0.5	Wertz and Domeier 1997

Notes:

[1]Species listed are representative of the group of prey items and not necessarily the species identified in the referenced study.

mm = millimeter

SL = standard length

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Table 4-2
Food Web Structure and Diet of White Croaker

Species[1]	Sediment/ Detritus	Phytoplankton (including algae)	Zooplankton	Mussels/ Filter Feeders	Crustaceans/ Scavengers	Worms/ Deposit Feeders	Fish 1: Prey Fish (e.g., Surfperches)	Source
White Croaker age 0	0.05	0.05	0.2	0.1	0.3	0.3		Gobas and Arnot 2010
White Croaker age > 0	0.05				0.55	0.4		Gobas and Arnot 2010
White Croaker		0.03	0.01	0.09	0.11	0.48	0.28	Jahn 2008
White Croaker LA/LB				0.04	0.28	0.61	0.07	Malins et al. 1987
White Croaker Dana Point				0.36	0.12	0.47	0.05	Malins et al. 1987
White Croaker 18-50 mm	0.05		0.54		0.24	0.17		Ware 1979
White Croaker 51-100 mm	0.05		0.12		0.76	0.07		Ware 1979
White Croaker 101-150 mm	0.05		0.12		0.66	0.17		Ware 1979
White Croaker 151-200 mm	0.05		0.01		0.35	0.59		Ware 1979
White Croaker 201-250 mm	0.05				0.73	0.22		Ware 1979
White Croaker 251-300 mm	0.05				0.475	0.475		Ware 1979

Notes:

[1]Species listed are representative of the group of prey items and not necessarily the species identified in the referenced study.

LA/LB = Los Angeles/Long Beach
mm = millimeter

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Table 4-3
Food Web Structure and Diet of Shiner Surfperch

Species	Sediment/ Detritus	Phytoplankton (including algae)	Zooplankton	Mussels/ Filter Feeders	Crustaceans/ Scavengers	Worms/ Deposit Feeders	Source
Shiner Perch Summer/Fall (juveniles and adults)	0.18	0.08	0.66		0.06	0.02	Odenweller 1975
Shiner Perch Winter/Spring (juveniles and adults)	0.31	0.11	0.37	0.04	0.11	0.06	Odenweller 1975
Shiner Perch (juveniles and adults)	0.25	0.3	0.03	0.05	0.22	0.15	Bane and Robinson 1970
Shiner Perch (90-140 mm)		0.1	0.1	0.1	0.43	0.27	Jahn 2008
Shiner Perch (29-73 mm)		0.15	0.1	0.1	0.5	0.15	Woods 2010
Other surfperch species (adults)		0.15	0.58	0.15		0.12	Mackintosh et al. 2004, Supplemental Information Table 2
Shiner Perch (juveniles)	0.1	0.6	0.25			0.05	Mackintosh et al. 2004, Supplemental Information Table 2
Shiner Perch age 0	0.05	0.1	0.2		0.55	0.1	Gobas and Arnot 2010
Shiner Perch age > 0	0.05	0.1	0.1		0.55	0.2	Gobas and Arnot 2010

Notes:

mm = millimeter

Odenweller, D.B., 1975. The life history of the shiner surfperch Cymatogaster aggregata Gibbons. *Fish Bulletin* 165:107-115.

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Table 4-4
Water Column Particulate Accumulation Factor

Fish Movement Zone	% Lipids	Water Column Particulate Accumulation Factor (g OC/g lipid)	
		Total PCB	Total DDX
Consolidated Slip	1.01	11.9	10.9
Los Angeles Inner Harbor	1.15	15.6	15.3
Los Angeles Outer Harbor	1.45	8.74	5.91
Long Beach Inner Harbor South	1.47	10.8	7.23

Notes:
Water Column Particulate Accumulation Factors calculated for Los Angeles Outer Harbor were used in the bioaccumulation model for all the Fish Movement Zones.
Mussel and oyster data are from 2002 to 2014.
Water particulate concentrations were calculated from solid-phase microextraction data from the Low Detection Limit Water Column Study (Events 1 and 2 in 2014) using site-specific partition coefficients. Average of Long Beach Inner Harbor North and Long Beach Outer Harbor samples were used for Long Beach Inner Harbor South.
DDX = dichlorodiphenyltrichloroethane-related compounds (4,4'-DDT, 4,4'-DDE, 4,4'-DDD, 2,4'-DDT, 2,4'-DDE, and 2,4'-DDD)
g = gram
OC = organic carbon
PCB = polychlorinated biphenyl

Table 4-5
Biota Sediment Accumulation Factor

Fish Movement Zone	% Lipid	Biota Sediment Accumulation Factor (g OC/g lipid)		
		Total PCB	Total DDX	Total DDX Re-Analysis
Dominguez Channel Estuary	NA	NA	NA	NA
Consolidated Slip	1.56	0.59	0.20	0.10(1)
Los Angeles Inner Harbor	2.18	0.58	0.08	0.56
Fish Harbor	0.15	2.71	1.50	NA
Seaplane Lagoon	0.56	2.55	1.47	NA
Los Angeles Outer Harbor	1.34	0.65	0.14	0.81(1)
Long Beach Inner Harbor North	0.93	1.61	0.18	NA
Long Beach Inner Harbor South	1.29	0.61	0.22	NA
Long Beach Outer Harbor	1.27	1.76	0.28	NA
Los Angeles River Estuary	NA	NA	NA	NA
Eastern San Pedro Bay	NA	NA	NA	NA
Whole Harbor	1.22	2.54	0.52	NA

Notes:
(1) The re-analysis was limited to one of the duplicate samples in this zone; initial values for Consolidated Slip and Los Angeles Outer Harbor were 0.06 and 0.09 for these samples, respectively.
Biota sediment accumulation factors calculated for total PCB were used in the bioaccumulation model for both total PCB and total DDX for each specific fish movement zone in which they were calculated. Duplicate polychaete/benthic organism were collected in Los Angeles Outer Harbor, Consolidated Slip, and Long Beach Outer Harbor; BSAF values are the average of duplicate BSAF values for these zones.
Factors calculated from the regression on all paired polychaete/benthic organism sediment samples (Figure 4-2).
Paired sediment and polychaete/benthic organism data were collected in 2014.
DDX = dichlorodiphenyltrichloroethane-related compounds (4,4'-DDT, 4,4'-DDE, 4,4'-DDD, 2,4'-DDT, 2,4'-DDE, and 2,4'-DDD)
g = gram
NA = not available. For these entries, values used in the model were based on Biota Sediment Accumulation.
OC = organic carbon
PCB = polychlorinated biphenyl

Table 4-6
Trophic Position of Target Species in the Greater Harbor Waters Based on a Trophic Position Model

Trophic Position	Species	Sediment	Phytoplankton	Zooplankton	Polychaetes	Bivalve	Surfperches	Croaker(s)	Source
2.23	Polychaetes/Deposit Feeders	0.90	0.05	0.05	--	--	--	--	Gobas and Arnot 2010
2.11	Bivalves/Filter Feeders	0.30	0.65	0.05	--	--	--	--	Gobas and Arnot 2010
2.97	Surfperches	0.05	0.10	0.10	0.20	0.55	--	--	Gobas and Arnot 2010
3.26	White Croaker LA/LB	--	--	--	0.76	0.17	0.07	0.00	Malins et al. 1987
3.80	CA Halibut 120-510 mm	--	--	--	0.30	0.02	0.45	0.23	Haaker 1975
4.11	CA Halibut > 500 mm	--	--	--	--	--	0.50	0.50	Wertz and Domeier 1997

Notes:

Trophic position values at the base of the food chain (sediment and phytoplankton) were assigned according to Vander Zanden and Rasmussen (1996).

The trophic position model used to estimate trophic position of all other organisms was based on Adams et al. (1983).

Diets used to predict trophic position were simplified based on the sources provided.

CA = California

LA/LB = Los Angeles/Long Beach

mm = millimeter

Adams, S.M., B.L. Kimmel, and G.R. Ploskey, 1983. Sources of organic matter for reservoir fish production: a trophic-dynamics analysis. *Canadian Journal of Fisheries and Aquatic Sciences* 40:1480-1495.

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Wertz, S. and M. Domeier, 1997. Relative importance of prey items to California halibut. *California Fish and Game* 88.1:21-29.

Table 4-7
Bioenergetic Parameters

	β	γ	ρ	Activity Multiplier (C_{act})
Surfperch	0.022	0.269	0.059	1.16
White Croaker	0.025	0.249	0.051	2.00
California Halibut	0.136	0.255	0.062	2.00

Notes:

β,γ,ρ are empirical coefficients determined by experiment; C_{act} is the activity multiplier (see Equation 9).

Surfperch bioenergetic parameters based on:

Gordon, M.S., H.G. Chin, and M. Vojkovich, 1989. Energetics of swimming in fishes using different methods of locomotion: I. Labriform swimmers. *Fish physiology and Biochemistry* 6:341-352.

White Croaker parameters based on the respiration model of Hemmingsen, A.M., 1960. Energy metabolism as related to body size and respiratory surfaces, and its evolution. *Reports of the Steno Memorial Hospital and Nordinsk Insulin Laboratorium* 9:6-110.

California Halibut parameters estimated from:

Merino, G.E., R.H. Piedrahita, and D.E. Conklin, 2009. Routine oxygen consumption rates of California halibut (Paralichthys californicus) juveniles under farm-like conditions. Aquacultural Engineering 41:166-175.

Merino, G.E., D.E. Conklin, and P.H. Piedrahita, 2011. Diel rhythms of oxygen consumption rates of California halibut (Paralichthys californicus) under culture in a recirculating system. Aquacultural Engineering 45:28-34.

Table 4-8
Fish Lipid Contents

Fish Movement Zone	Average Lipid (%)		
	California Halibut	White Croaker	Surfperch[1]
Dominguez Channel Estuary	NA	NA	NA
Consolidated Slip	0.06	1.19	6.66
Los Angeles Inner Harbor	NA	1.07	NA
Fish Harbor	0.08	2.35	4.70
Seaplane Lagoon	0.25	1.25	NA
Los Angeles Outer Harbor	0.26	1.75	2.35
Long Beach Inner Harbor North	0.23	0.82	NA
Long Beach Inner Harbor South	0.12	1.21	4.19
Long Beach Outer Harbor	0.45	1.63	5.33
Los Angeles River Estuary	0.32	1.77	NA
Eastern San Pedro Bay	0.46	2.13	NA
All Harbor Zones[2]	0.25	1.59	4.39

Notes:

1 = Surfperch includes white surfperch and shiner surfperch.

2 = All Harbor Zones include Fish Movement Zones within the Harbor except Dominguez Channel Estuary and Los Angeles River Estuary.

California halibut and white croaker lipids (fillet) were measured from 2002 through 2014. Surfperch lipids (whole body) were measured in 2014 as no previously measured lipid data were available.

Five non-detect values for California halibut in 2014 were replaced with the method detection limit.

DDX = dichlorodiphenyltrichloroethane-related compounds (4,4'-DDT, 4,4'-DDE, 4,4'-DDD, 2,4'-DDT, 2,4'-DDE, and 2,4'-DDD)

NA = Zones without fish samples. Lipid results from "All Harbor Zones" were used in the model for these zones except for Dominguez Channel Estuary, which used Consolidated Slip values.

PCB = polychlorinated biphenyl

Table 4-9
Whole Body to Fillet Ratios

Species	Ratio		
	Lipid	Total PCB	Total DDX
California Halibut	15	15	15
White Croaker	4	4	4

Notes:

Estimated from:

AMEC Foster Wheeler. *Draft Report. Harbor Toxics TMDL Special Study - Food Web Sampling.* 2014 Food Web Study data. Prepared for Port of Los Angeles and Port of Long Beach. July 2015.

NOAA and USEPA. *2002 – 2004 Southern California Coastal Marine Fish Contaminants Survey* . Coastal Marine Fish Contaminant Survey Data for the Palos Verdes Shelf. June 2007.

Allen, M.J., D.W. Diehl, and E.Y. Zeng. *Bioaccumulation of Contaminants in Recreational and Forage Fish in Newport Bay, California in 2000 – 2002* . Southern California Coastal Water Research Project Technical Report 436. June 2004.

Whole body concentrations were estimated as weighted-averages of fillet and carcass concentrations.

DDX = dichlorodiphenyltrichloroethane-related compounds (4,4'-DDT, 4,4'-DDE, 4,4'-DDD, 2,4'-DDT, 2,4'-DDE, and 2,4'-DDD)

PCB = polychlorinated biphenyl

Table 4-10
Fish Lipid-Water Partition Coefficients

Fish Movement Zone	Total PCB (Log K_{fw})			Total DDX (Log K_{fw})		
	California Halibut	White Croaker	Surfperch[1]	California Halibut	White Croaker	Surfperch[1]
Dominguez Channel Estuary	NA	NA	NA	NA	NA	NA
Consolidated Slip	6.86	NA	6.79	6.85	6.85	6.70
Los Angeles Inner Harbor	NA	NA	NA	NA	NA	NA
Fish Harbor	6.81	6.75	6.84	6.96	6.93	6.94
Seaplane Lagoon	NA	6.79	NA	NA	6.92	NA
Los Angeles Outer Harbor	6.84	6.76	6.88	6.94	6.93	6.93
Long Beach Inner Harbor North	NA	NA	NA	NA	NA	NA
Long Beach Inner Harbor South	6.77	6.85	6.92	6.95	6.92	6.93
Long Beach Outer Harbor	NA	NA	NA	6.90	6.93	6.93
Los Angeles River Estuary	NA	NA	NA	NA	NA	NA
Eastern San Pedro Bay	NA	NA	NA	6.91	6.87	NA
All Harbor Zones*	6.83	6.79	6.86	6.92	6.92	6.89

Notes:

1 = Surfperch includes white surfperch and shiner surfperch.

* All Harbor Zones include Fish Movement Zones within the Harbor, with the exception of Dominguez Channel Estuary and Los Angeles River Estuary.

Values are averages of the weighted-harmonic means of individual fish within each fish movement zone.

Non-detect congener values were set to zero.

DDX = dichlorodiphenyltrichloroethane-related compounds (4,4'-DDT, 4,4'-DDE, 4,4'-DDD, 2,4'-DDT, 2,4'-DDE, and 2,4'-DDD)

K_{fw} = fish lipid-water partition coefficient

NA = Zones without fish samples. K_{fw} results from "All Harbor Zones" were used in the model except for Dominguez Channel Estuary, which used Consolidated Slip values where available, and Los Angeles River Estuary, which used Eastern San Pedro Bay values where available.

PCB = polychlorinated biphenyl

Table 4-11
Average Proportion of Days Detected for Each White Croaker Subpopulation by Zone (Phase 2)

White Croaker Subpopulation	Fish Movement Zone Where Fish Were Detected												
	Dominguez Channel Estuary	Consolidated Slip	Los Angeles Inner Harbor	Fish Harbor	Seaplane Lagoon	Los Angeles Outer Harbor	Long Beach Inner Harbor North	Long Beach Inner Harbor South	Long Beach Outer Harbor	Los Angeles River Estuary	Eastern San Pedro Bay	Outside Harbor	Palos Verdes Shelf
Dominguez Channel Estuary*	0.20	0.48	0.29	--	--	--	0.03	--	--	--	--	--	--
Consolidated Slip	--	0.61	0.36	--	--	0.00	0.03	0.001	--	--	--	0.0010	0.001
Los Angeles Inner Harbor*	--	0.29	0.21	--	--	0.44	0.01	0.001	--	--	--	0.04	0.003
Fish Harbor	--	--	0.00	0.82	0.01	0.05	0.003	0.002	--	--	--	0.11	0.01
Seaplane Lagoon*	--	0.01	0.04	0.002	--	0.90	--	--	--	--	--	0.05	0.002
Los Angeles Outer Harbor	--	0.01	0.04	0.002	--	0.90	--	--	--	--	--	0.05	0.002
Long Beach Inner Harbor North	--	0.01	0.06	0.02	0.001	0.01	0.72	0.14	0.02	--	0.0010	0.01	0.002
Long Beach Inner Harbor South*	--	0.01	0.06	0.02	0.001	0.01	0.72	0.14	0.02	--	0.0010	0.01	0.002
Long Beach Outer Harbor	--	--	--	--	0.01	--	0.17	0.58	--	--	--	0.25	--
Los Angeles River Estuary*	--	--	--	--	--	--	--	--	0.01	0.20	0.76	0.03	--
Eastern San Pedro Bay	--	--	--	--	--	--	--	--	0.01	--	0.96	0.03	--

Notes:
-- = not detected
*For completeness, this table includes estimated movement patterns for subpopulations for which there were no tracking data available (i.e., fish movement zones in which fish movement data were not collected as part of the Harbor tracking study) for the mod

Table 4-12
Average Proportion of Days Detected for Each California Halibut Subpopulation by Zone

California Halibut Subpopulation		Fish Movement Zone Where Fish Were Detected											
	Dominguez Channel Estuary	Consolidated Slip	Los Angeles Inner Harbor	Fish Harbor	Seaplane Lagoon	Los Angeles Outer Harbor	Long Beach Inner Harbor North	Long Beach Inner Harbor South	Long Beach Outer Harbor	Los Angeles River Estuary	Eastern San Pedro Bay	Outside Harbor	Palos Verdes Shelf
Dominguez Channel Estuary*	0.20	0.26	0.01	0.04	0.01	0.10	0.02	0.02	0.01	--	0.08	0.23	0.02
Los Angeles Outer Harbor	--	--	--	0.03	0.02	0.91	--	--	--	--	--	0.03	0.01
Los Angeles River Estuary*	--	--	--	--	--	0.02	--	--	0.02	0.20	0.51	0.25	--
Eastern San Pedro Bay	--	--	--	--	--	0.05	--	--	0.02	--	0.90	0.02	0.01
Whole Harbor**	--	0.04	0.01	0.07	0.01	0.60	0.04	0.03	0.01	--	0.14	0.05	0.01

Notes:

-- = not detected

*For completeness, this table includes estimated movement patterns for Dominguez Channel Estuary and Los Angeles River Estuary subpopulations for which there were no tracking data collected as part of the Harbor tracking study.

**The Whole Harbor fish movement pattern, which is based on all California halibut movement data collected as part of the Phase 2 Harbor Tracking Study, was used to estimate movements for adult halibut subpopulations from the following fish movement zones in which insufficient (sample size ≤ 3) or no fish movement data were collected: Consolidated Slip, Los Angeles Inner Harbor, Fish Harbor, Seaplane Lagoon, Long Beach Inner Harbor North, Long Beach Inner Harbor South, and Long Beach Outer Harbor.

Table 4-13
Average Proportion of Detections per White Croaker within Each Palos Verdes Shelf Zone

Zone	Average Detects per Fish per Zone (Including Movement to Gates)	Average Detects per Fish per Zone (Excluding Movement to Gates)
PVS1	0.50	0.52
PVS2	0.27	0.28
PVS3	0.08	0.09
PVS4	0.10	0.11
Gates	0.05	NA

Note:
Gates refer to Angels and Queens Gates.

Table 4-14
Sediment and Water Exposure Concentrations Based on WRAP Model Results Averaged over Simulation Period

Fish Movement Zone/Area	Total PCB			Total DDX		
	Water Column, Dissolved (ng/L)	Water Column, Particulate (µg/g OC)	Sediment (µg/g OC)	Water Column, Dissolved (ng/L)	Water Column, Particulate (µg/g OC)	Sediment (µg/g OC)
Dominguez Channel Estuary	11.95	13.75	12.88	11.60	16.81	6.15
Consolidated Slip	1.80	2.07	15.63	1.42	2.06	3.99
Los Angeles Inner Harbor	0.51	0.59	4.07	0.46	0.67	3.93
Fish Harbor	0.60	0.70	8.87	0.29	0.42	5.28
Seaplane Lagoon	0.32	0.37	2.34	0.33	0.47	2.29
Los Angeles Outer Harbor	0.26	0.29	1.45	0.29	0.43	3.59
Long Beach Inner Harbor North	0.47	0.54	2.87	0.43	0.62	1.34
Long Beach Inner Harbor South	0.33	0.38	5.56	0.30	0.44	2.96
Long Beach Outer Harbor	0.24	0.28	1.20	0.27	0.40	2.75
Los Angeles River Estuary	1.34	1.54	3.32	0.86	1.24	0.78
Eastern San Pedro Bay	0.35	0.40	1.84	0.32	0.47	1.37
Ocean	0.18	0.20	0.38	0.21	0.30	8.69
Palos Verdes Shelf*	0.14	0.11	13.28	0.48	0.49	334.57

Notes:

* Water column values were calculated from data from Fernandez et al. 2012 and the project database (Anchor QEA 2014). Sediment values are surface-weighted average concentrations of surface data from 2005 and 2014 multiplied by detection frequencies of white croaker (Section 3.2.2).

µg = microgram

DDX = dichlorodiphenyltrichloroethane-related compounds (4,4'-DDT, 4,4'-DDE, 4,4'-DDD, 2,4'-DDT, 2,4'-DDE, and 2,4'-DDD)

g = gram
kg = kilogram
L = liter
ng = nanogram
OC = organic carbon
PCB = polychlorinated biphenyl
WRAP = Water Resources Action Plan

Anchor QEA, 2014. *Data Gaps Analysis for Bioaccumulation Model Development.* Prepared for Ports of Long Beach and Los Angeles. August 2014.

Fernandez, L.A, W. Lao, K.A. Maruya, C. White, and R.M Burgess, 2012. Passive sampling to measure baseline dissolved persistent organic pollutant concentrations in the water column of the Palos Verdes Shelf Superfund site. *Environmental Science and Technology* 46: 11937-11947.

Table 5-1
Size Distribution of Surfperch

Age Class	Weight (grams)	Proportion
1	79	0.23
2	103	0.27
3	121	0.32
4	135	0.09
5	147	0.09
6	157	-
7	167	-

Table 5-2
Size Distribution of White Croaker

Age Class	Weight (grams)	Proportion
1	55	0.01
2	69	0.00
3	85	0.01
4	101	0.03
5	120	0.16
6	139	0.13
7	159	0.21
8	181	0.20
9	203	0.11
10	227	0.07
11	251	0.03
12	276	0.04

Table 5-3
Size Distribution of California Halibut

Age Class	Weight (grams)	Proportion
1	87	-
2	223	0.03
3	440	0.13
4	743	0.33
5	1,129	0.19
6	1,593	0.03
7	2,126	0.05
8	2,718	0.08
9	3,358	0.08
10	4,035	0.04
11	4,740	0.05
12	5,463	0.01
13	6,195	-
14	6,929	-
15	7,628	-

Table 5-4
Diet Proportions for California Halibut Used in Model Calibration

California Halibut Age	Diet Proportions															
	Water-Column Invertebrates	Deposit-Feeding Invertebrates	Surfperch							White Croaker						
			Age 1	Age 2	Age 3	Age 4	Age 5	Age 6	Age 7	Age 1	Age 2	Age 3	Age 4	Age 5	Age 6	Age 7
Age 1	0.90	0.10	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Age 2	0.80	0.20	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Age 3	0.60	0.20	0.20	---	---	---	---	---	---		---	---	---	---	---	---
Age 4	0.50	0.20	0.20	---	---	---	---	---	---	0.10	---	---	---	---	---	---
Age 5	0.40	0.20		0.30	---	---	---	---	---	---	0.10	---	---	---	---	---
Age 6	---	---	---	---	0.60	---	---	---	---	---	---	0.40	---	---	---	---
Age 7	---	---	---	---	0.60	---	---	---	---	---	---	0.40	---	---	---	---
Age 8	---	---	---	---	---	0.60	---	---	---	---	---	---	0.40	---	---	---
Age 9	---	---	---	---	---	0.60	---	---	---	---	---	---	0.40	---	---	---
Age 10	---	---	---	---	---	---	0.50	---	---	---	---	---	---	0.50	---	---
Age 11	---	---	---	---	---	---	0.50	---	---	---	---	---	---	0.50	---	---
Age 12	---	---	---	---	---	---	---	0.50	---	---	---	---	---	---	0.50	---
Age 13	---	---	---	---	---	---	---	0.50	---	---	---	---	---	---	0.50	---
Age 14	---	---	---	---	---	---	---	---	0.50	---	---	---	---	---	---	0.50
Age 15	---	---	---	---	---	---	---	---	0.50	---	---	---	---	---	---	0.50

Note:

--- = not applicable

Table 5-5
Diet Proportions for White Croaker Used in Model Calibration

White Croaker Age	Diet Proportions						
	Water-Column Invertebrates	Deposit-Feeding Invertebrates	Surfperch				
			Age 1	Age 2	Age 3	Age 4	Age 5
Age 1	0.25	0.75	---	---	---	---	---
Age 2	0.25	0.75	---	---	---	---	---
Age 3	0.25	0.75	---	---	---	---	---
Age 4	0.17	0.76	0.07	---	---	---	---
Age 5	0.17	0.76	---	0.07	---	---	---
Age 6	0.17	0.76	---	0.07	---	---	---
Age 7	0.17	0.76	---	---	0.07	---	---
Age 8	0.17	0.76	---	---	0.07	---	---
Age 9	0.17	0.76	---	---	---	0.07	---
Age 10	0.17	0.76	---	---	---	---	0.07
Age 11	0.17	0.76	---	---	---	---	0.07
Age 12	0.17	0.76	---	---	---	---	0.07

Note:

--- = not applicable

Table 5-6
Diet Proportions for Surfperch Used in Model Calibration

Surfperch Age	Diet Proportions	
	Water-Column Invertebrates	Deposit-Feeding Invertebrates
Age 1	0.75	0.25
Age 2	0.75	0.25
Age 3	0.75	0.25
Age 4	0.75	0.25
Age 5	0.75	0.25
Age 6	0.75	0.25
Age 7	0.75	0.25

Table 5-7
Model Calibration Exposure Proportions for White Croaker

White Croaker Subpopulation	FMZ Exposure Proportion*												
	Dominguez Channel Estuary	Consolidated Slip	Los Angeles Inner Harbor	Fish Harbor	Seaplane Lagoon	Los Angeles Outer Harbor	Long Beach Inner Harbor North	Long Beach Inner Harbor South	Long Beach Outer Harbor	Los Angeles River Estuary	Eastern San Pedro Bay	Outside Harbor	Palos Verdes Shelf
Dominguez Channel Estuary	0.2	0.48	0.29	0	0	0	0.03	0	0	0	0	0	0
Consolidated Slip	0	0.61	0.36	0	0	0 (0.001)	0.03	0 (0.001)	0	0	0	0 (0.001)	0 (0.001)
Los Angeles Inner Harbor	0	0.24 (0.29)	0.23 (0.36)	0	0	0.44	0.01	0 (0.001)	0	0	0	0.04	0.04 (0.003)
Fish Harbor	0	0	0	0.83 (0.82)	0.01	0.05	0 (0.003)	0 (0.002)	0	0	0	0.1 (0.11)	0.01
Seaplane Lagoon	0	0.01	0.04	0 (0.002)	0.01 (0.0)	0.89 (0.90)	0	0	0	0	0	0.05	0 (0.002)
Los Angeles Outer Harbor	0	0.01	0.04	0 (0.002)	0	0.9	0	0	0	0	0	0.04 (0.05)	0.01 (0.002)
Long Beach Inner Harbor North	0	0.01	0.06	0.02	0 (0.001)	0.01	0.63 (0.72)	0.14	0.02	0	0 (0.001)	0.10 (0.01)	0.01 (0.002)
Long Beach Inner Harbor South	0	0.01	0.06	0.02	0 (0.001)	0.01	0.72	0.14	0.02	0	0 (0.001)	0.01	0.01 (0.002)
Long Beach Outer Harbor	0	0	0	0	0.01	0	0.16 (0.17)	0.3 (0.58)	0.23 (0.0)	0	0	0.30 (0.25)	0
Los Angeles River Estuary	0	0	0	0	0	0	0	0	0.01	0.2	0.76	0.03	0
Eastern San Pedro Bay	0	0	0	0	0	0	0	0	0.01	0	0.96	0.03	0

Note:

* Exposure proportions are fractions of a year that fish reside in a specific FMZ.

() Values in parentheses are average proportions from the tracking study; values only provided for proportion adjustments.

In the model, fish migrate from the starting FMZ to other FMZs in the column order from left to right and reside there for the proportion of time indicated. Exceptions are as follows:

Fish in Seaplane Lagoon migrate to Los Angeles Outer Harbor before migrating in the order above.

Fish in Long Beach Inner Harbor North migrate to Long Beach Inner Harbor South before migrating in the order above.

Fish in Long Beach Outer Harbor migrate to Long Beach Inner Harbor South and Long Beach Inner Harbor North before migrating in the order above.

Exposure proportions were adjusted compared to Table 3-2 and are shown as color-coded cells:

Increase

Decrease

FMZ = fish movement zone

Table 5-8
Model Calibration Adjusted Exposure Proportions for California Halibut

California Halibut Subpopulation	Age Class*	FMZ Exposure Proportion**												
		Dominguez Channel Estuary	Consolidated Slip	Los Angeles Inner Harbor	Fish Harbor	Seaplane Lagoon	Los Angeles Outer Harbor	Long Beach Inner Harbor North	Long Beach Inner Harbor South	Long Beach Outer Harbor	Los Angeles River Estuary	Eastern San Pedro Bay	Outside Harbor	Palos Verdes Shelf
Dominguez Channel Estuary	Juveniles	0.2	0.8	0	0	0	0	0	0	0	0	0	0	0
	Adults	0.2	0.26	0.01	0.04	0.01	0.1	0.02	0.02	0.01	0	0.08	0.23	0.02
Consolidated Slip	Adults	0	0.33 (0.04)	0.01	0.05 (0.07)	0.01	0.13 (0.6)	0.03 (0.04)	0.03	0.01	0	0.1 (0.14)	0.27 (0.05)	0.03 (0.01)
Los Angeles Inner Harbor	Adults	0	0.03 (0.04)	0.02 (0.01)	0.05 (0.07)	0.01	0.42 (0.6)	0.03 (0.04)	0.03	0.01	0	0.1 (0.14)	0.29 (0.05)	0.01
Fish Harbor	Adults	0	0.03 (0.04)	0.01	0.08 (0.07)	0.01	0.4 (0.6)	0.03 (0.04)	0.03	0.01	0	0.1 (0.14)	0.3 (0.05)	0 (0.01)
Seaplane Lagoon	Adults	0	0.03 (0.04)	0.01	0 (0.07)	0.45 (0.01)	0.04 (0.6)	0.03 (0.04)	0.03	0.01	0	0.1 (0.14)	0.3 (0.05)	0 (0.01)
Los Angeles Outer Harbor	Adults	0	0	0	0.03	0.22 (0.02)	0.45 (0.91)	0	0	0 (0.02)	0	0	0.3 (0.03)	0.01
Long Beach Inner Harbor North	Adults	0	0.03 (0.04)	0.01	0 (0.07)	0.01	0.43 (0.6)	0.08 (0)	0.03	0.01	0	0.1 (0.14)	0.3 (0.05)	0 (0.01)
Long Beach Inner Harbor South	Adults	0	0.03 (0.04)	0.01	0.05 (0.07)	0.01	0.38 (0.6)	0.03 (0.04)	0.08	0.01	0	0.1 (0.14)	0.27 (0.05)	0.03 (0.01)
Long Beach Outer Harbor	Adults	0	0 (0.04)	0.01	0 (0.07)	0.01	0.06 (0.6)	0.03 (0.04)	0.03	0.46 (0.01)	0	0.1 (0.14)	0.3 (0.05)	0 (0.01)
Los Angeles River Estuary	Juveniles	0	0	0	0	0	0	0	0	0	0.2	0.8	0	0
	Adults	0	0	0	0	0	0.02	0	0	0.02	0.2	0.51	0.25	0
Eastern San Pedro Bay	Adults	0	0	0	0	0	0.03 (0.05)	0	0	0.03 (0.01)	0	0.64 (0.9)	0.3 (0.02)	0 (0.01)

Note:

*Juveniles and adults are age classes 1 to 5 and 6 to 15, respectively. California halibut juveniles are resident except at Dominguez Channel Estuary and Los Angeles River Estuary.

** Exposure proportions are fractions of a year that fish reside in a specific FMZ.

In the model, fish migrate from the starting FMZ to other FMZs in the column order from left to right and reside there for the proportion of time indicated. Exceptions are as follows:

Fish in Seaplane Lagoon migrate to Los Angeles Outer Harbor before migrating in the order above.

Fish in Long Beach Inner Harbor North migrate to Long Beach Inner Harbor South before migrating in the order above.

Fish in Long Beach Outer Harbor migrate to Long Beach Inner Harbor South and Long Beach Inner Harbor North before migrating in the order above.

Exposure proportions were adjusted compared to Table 3-3 and are shown as color-coded cells:

Increase

Decrease

FMZ = fish movement zone

Table 6-1
Alternative Diet Proportions for Surfperch Used to Evaluate Model Sensitivity

Surfperch Age	Diet Proportions	
	Water-Column Invertebrates	Deposit-Feeding Invertebrates
Age 1	0.90	0.10
Age 2	0.90	0.10
Age 3	0.90	0.10
Age 4	0.90	0.10
Age 5	0.90	0.10
Age 6	0.90	0.10
Age 7	0.90	0.10

Table 6-2
Alternative Diet Proportions for White Croaker Used to Evaluate Model Sensitivity

White Croaker Age	Diet Proportions						
	Water-Column Invertebrates	Deposit-Feeding Invertebrates	Surfperch				
			Age 1	Age 2	Age 3	Age 4	Age 5
Age 1	0.50	0.50	---	---	---	---	---
Age 2	0.20	0.80	---	---	---	---	---
Age 3	0.10	0.80	0.10	---	---	---	---
Age 4	---	0.90	---	0.10	---	---	---
Age 5	---	0.90	---	0.10	---	---	---
Age 6	---	0.90	---	---	0.10	---	---
Age 7	---	0.90	---	---	0.10	---	---
Age 8	---	0.90	---	---	---	0.10	---
Age 9	---	0.90	---	---	---	---	0.10
Age 10	---	0.90	---	---	---	---	0.10
Age 11	---	0.90	---	---	---	---	0.10
Age 12	---	0.90	---	---	---	---	0.10

Note:
--- = not applicable

Table 6-3
Alternative Diet Proportions for California Halibut Used to Evaluate Model Sensitivity

California Halibut Age	Diet Proportions															
	Water-Column Invertebrates	Deposit-Feeding Invertebrates	Surfperch							White Croaker						
			Age 1	Age 2	Age 3	Age 4	Age 5	Age 6	Age 7	Age 1	Age 2	Age 3	Age 4	Age 5	Age 6	Age 7
Age 1	0.90	0.10	1.00	2.00	3.00	4.00	5.00	6.00	7.00	8.00	9.00	10.00	11.00	12.00	13.00	14.00
Age 2	0.80	0.20	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Age 3	0.60	0.20	0.20	---	---	---	---	---	---	---	---	---	---	---	---	---
Age 4	0.50	0.20	0.20	---	---	---	---	---	---	0.10	---	---	---	---	---	---
Age 5	0.40	0.20	---	0.30	---	---	---	---	---	---	0.10	---	---	---	---	---
Age 6	---	---	---	---	0.75	---	---	---	---	---	---	0.25	---	---	---	---
Age 7	---	---	---	---	0.75	---	---	---	---	---	---	0.25	---	---	---	---
Age 8	---	---	---	---	---	0.75	---	---	---	---	---	---	0.25	---	---	---
Age 9	---	---	---	---	---	0.75	---	---	---	---	---	---	0.25	---	---	---
Age 10	---	---	---	---	---	---	0.75	---	---	---	---	---	---	0.25	---	---
Age 11	---	---	---	---	---	---	0.75	---	---	---	---	---	---	0.25	---	---
Age 12	---	---	---	---	---	---	---	0.75	---	---	---	---	---	---	0.25	---
Age 13	---	---	---	---	---	---	---	0.75	---	---	---	---	---	---	0.25	---
Age 14	---	---	---	---	---	---	---	---	0.75	---	---	---	---	---	---	0.25
Age 15	---	---	---	---	---	---	---	---	0.75	---	---	---	---	---	---	0.25

Note:
--- = not applicable

Table 6-4
Exposure Proportions for White Croaker Used to Evaluate Model Sensitivity – Fish Harbor Alternative

Starting FMZ	FMZ Exposure Proportion*												
	Dominguez Channel Estuary	Consolidated Slip	Los Angeles Inner Harbor	Fish Harbor	Seaplane Lagoon	Los Angeles Outer Harbor	Long Beach Inner Harbor South	Long Beach Inner Harbor North	Long Beach Outer Harbor	Los Angeles River Estuary	Eastern San Pedro Bay	Outside Harbor	Palos Verdes Shelf
Dominguez Channel Estuary	0.2	0.48	0.29	0	0	0	0	0.03	0	0	0	0	0
Consolidated Slip	0	0.61	0.36	0	0	0	0	0.03	0	0	0	0	0
Los Angeles Inner Harbor	0	0.24	0.23	0	0	0.44	0	0.01	0	0	0	0.04	0.04
Fish Harbor	0	0	0	0.81	0.01	0.05	0	0	0	0	0	0.1	0.03
Seaplane Lagoon	0	0.01	0.04	0	0.01	0.89	0	0	0	0	0	0.05	0
Los Angeles Outer Harbor	0	0.01	0.04	0	0	0.9	0	0	0	0	0	0.04	0.01
Long Beach Inner Harbor North	0	0.01	0.06	0	0	0.01	0.14	0.72	0.02	0	0	0.01	0.03
Long Beach Inner Harbor South	0	0.01	0.06	0	0	0.01	0.14	0.72	0.02	0	0	0.01	0.03
Long Beach Outer Harbor	0	0	0	0	0.01	0	0.4	0.16	0.18	0	0	0.25	0
Los Angeles River Estuary	0	0	0	0	0	0	0	0	0.01	0.2	0.76	0.03	0
Eastern San Pedro Bay	0	0	0	0	0	0	0	0	0.01	0	0.96	0.03	0

Note:
* Exposure proportions are fractions of a year that fish reside in a specific FMZ.
In the model, fish migrate from the starting FMZ to other FMZs in the column order from left to right and reside there for the proportion of time indicated. Exceptions are as follows:
Fish in Seaplane Lagoon migrate to Los Angeles Outer Harbor before migrating in the order above.
Fish in Long Beach Inner Harbor North migrate to Long Beach Inner Harbor South before migrating in the order above.
Fish in Long Beach Outer Harbor migrate to Long Beach Inner Harbor South and Long Beach Inner Harbor North before migrating in the order above.
FMZ = fish movement zone

Table 6-5
Exposure Proportions for White Croaker Used to Evaluate Model Sensitivity – Consolidated Slip Alternative

	FMZ Exposure Proportion*												
Starting FMZ	**Dominguez Channel Estuary**	**Consolidated Slip**	**Los Angeles Inner Harbor**	**Fish Harbor**	**Seaplane Lagoon**	**Los Angeles Outer Harbor**	**Long Beach Inner Harbor South**	**Long Beach Inner Harbor North**	**Long Beach Outer Harbor**	**Los Angeles River Estuary**	**Eastern San Pedro Bay**	**Outside Harbor**	**Palos Verdes Shelf**
Dominguez Channel Estuary	0.2	0.46	0.29	0	0	0	0	0.03	0	0	0	0	0.02
Consolidated Slip	0	0.59	0.36	0	0	0	0	0.03	0	0	0	0	0.02
Los Angeles Inner Harbor	0	0.22	0.23	0	0	0.44	0	0.01	0	0	0	0.04	0.06
Fish Harbor	0	0	0	0.83	0.01	0.05	0	0	0	0	0	0.1	0.01
Seaplane Lagoon	0	0	0.04	0	0.01	0.89	0	0	0	0	0	0.05	0.01
Los Angeles Outer Harbor	0	0	0.04	0	0	0.9	0	0	0	0	0	0.04	0.02
Long Beach Inner Harbor North	0	0	0.06	0.02	0	0.01	0.14	0.72	0.02	0	0	0.01	0.02
Long Beach Inner Harbor South	0	0	0.06	0.02	0	0.01	0.14	0.72	0.02	0	0	0.01	0.02
Long Beach Outer Harbor	0	0	0	0	0.01	0	0.4	0.16	0.18	0	0	0.25	0
Los Angeles River Estuary	0	0	0	0	0	0	0	0	0.01	0.2	0.76	0.03	0
Eastern San Pedro Bay	0	0	0	0	0	0	0	0	0.01	0	0.96	0.03	0

Note:
* Exposure proportions are fractions of a year that fish reside in a specific FMZ.
In the model, fish migrate from the starting FMZ to other FMZs in the column order from left to right and reside there for the proportion of time indicated. Exceptions are as follows:
Fish in Seaplane Lagoon migrate to Los Angeles Outer Harbor before migrating in the order above.
Fish in Long Beach Inner Harbor North migrate to Long Beach Inner Harbor South before migrating in the order above.
Fish in Long Beach Outer Harbor migrate to Long Beach Inner Harbor South and Long Beach Inner Harbor North before migrating in the order above.
FMZ = fish movement zone

Table 6-6
Exposure Proportions for White Croaker Used to Evaluate Model Sensitivity – No Palos Verdes Shelf Migration

Starting FMZ	FMZ Exposure Proportion*												
	Dominguez Channel Estuary	Consolidated Slip	Los Angeles Inner Harbor	Fish Harbor	Seaplane Lagoon	Los Angeles Outer Harbor	Long Beach Inner Harbor South	Long Beach Inner Harbor North	Long Beach Outer Harbor	Los Angeles River Estuary	Eastern San Pedro Bay	Outside Harbor	Palos Verdes Shelf
Dominguez Channel Estuary	0.2	0.48	0.29	0	0	0	0	0.03	0	0	0	0	0
Consolidated Slip	0	0.61	0.36	0	0	0	0	0.03	0	0	0	0	0
Los Angeles Inner Harbor	0	0.24	0.23	0	0	0.44	0	0.01	0	0	0	0.08	0
Fish Harbor	0	0	0	0.83	0.01	0.05	0	0	0	0	0	0.11	0
Seaplane Lagoon	0	0.01	0.04	0	0.01	0.89	0	0	0	0	0	0.05	0
Los Angeles Outer Harbor	0	0.01	0.04	0	0	0.9	0	0	0	0	0	0.05	0
Long Beach Inner Harbor North	0	0.01	0.06	0.02	0	0.01	0.14	0.72	0.02	0	0	0.02	0
Long Beach Inner Harbor South	0	0.01	0.06	0.02	0	0.01	0.14	0.72	0.02	0	0	0.02	0
Long Beach Outer Harbor	0	0	0	0	0.01	0	0.4	0.16	0.18	0	0	0.25	0
Los Angeles River Estuary	0	0	0	0	0	0	0	0	0.01	0.2	0.76	0.03	0
Eastern San Pedro Bay	0	0	0	0	0	0	0	0	0.01	0	0.96	0.03	0

Note:
* Exposure proportions are fractions of a year that fish reside in a specific FMZ.
In the model, fish migrate from the starting FMZ to other FMZs in the column order from left to right and reside there for the proportion of time indicated. Exceptions are as follows:
Fish in Seaplane Lagoon migrate to Los Angeles Outer Harbor before migrating in the order above.
Fish in Long Beach Inner Harbor North migrate to Long Beach Inner Harbor South before migrating in the order above.
Fish in Long Beach Outer Harbor migrate to Long Beach Inner Harbor South and Long Beach Inner Harbor North before migrating in the order above.
FMZ = fish movement zone

Table 6-7
Exposure Proportions For California Halibut Used to Evaluate Model Sensitivity – Fish Harbor Alternative

Starting FMZ	Age Class*	FMZ Exposure Proportion **												
		Dominguez Channel Estuary	Consolidated Slip	Los Angeles Inner Harbor	Fish Harbor	Seaplane Lagoon	Los Angeles Outer Harbor	Long Beach Inner Harbor South	Long Beach Inner Harbor North	Long Beach Outer Harbor	Los Angeles River Estuary	Eastern San Pedro Bay	Outside Harbor	Palos Verdes Shelf
Dominguez Channel Estuary	Juveniles	0.2	0.8	0	0	0	0	0	0	0	0	0	0	0
	Adults	0.2	0.26	0.01	0	0.01	0.1	0.02	0.02	0.01	0	0.08	0.23	0.06
Consolidated Slip	Adults	0	0.33	0.01	0	0.01	0.13	0.03	0.03	0.01	0	0.1	0.27	0.08
Los Angeles Inner Harbor	Adults	0	0.03	0.02	0	0.01	0.42	0.03	0.03	0.01	0	0.1	0.29	0.06
Fish Harbor	Adults	0	0.03	0.01	0	0.01	0.4	0.03	0.03	0.01	0	0.1	0.3	0.08
Seaplane Lagoon	Adults	0	0.03	0.01	0	0.45	0.04	0.03	0.03	0.01	0	0.1	0.3	0
Los Angeles Outer Harbor	Adults	0	0	0	0	0.22	0.45	0	0	0	0	0	0.3	0.03
Long Beach Inner Harbor North	Adults	0	0.03	0.01	0	0.01	0.43	0.03	0.08	0.01	0	0.1	0.3	0
Long Beach Inner Harbor South	Adults	0	0.03	0.01	0	0.01	0.38	0.08	0.03	0.01	0	0.1	0.27	0.08
Long Beach Outer Harbor	Adults	0	0	0.01	0	0.01	0.06	0.03	0.03	0.46	0	0.1	0.3	0
Los Angeles River Estuary	Juveniles	0	0	0	0	0	0	0	0	0	0.2	0.8	0	0
	Adults	0	0	0	0	0	0.02	0	0	0.02	0.2	0.51	0.25	0
Eastern San Pedro Bay	Adults	0	0	0	0	0	0.03	0	0	0.03	0	0.64	0.3	0

Notes:

* Juveniles and adults are age classes 1 to 5 and 6 to 15, respectively. California halibut juveniles are resident except at Dominguez Channel Estuary and Los Angeles River Estuary.

** Exposure proportions are fractions of a year that fish reside in a specific FMZ.

In the model, fish migrate from the starting FMZ to other FMZs in the column order from left to right and reside there for the proportion of time indicated. Exceptions are as follows:

Fish in Seaplane Lagoon migrate to Los Angeles Outer Harbor before migrating in the order above.

Fish in Long Beach Inner Harbor North migrate to Long Beach Inner Harbor South before migrating in the order above.

Fish in Long Beach Outer Harbor migrate to Long Beach Inner Harbor South and Long Beach Inner Harbor North before migrating in the order above.

FMZ = fish movement zone

Table 6-8

Exposure Proportions for California Halibut Used to Evaluate Model Sensitivity – Consolidated Slip Alternative

Starting FMZ	Age Class*	FMZ Exposure Proportion**												
		Dominguez Channel Estuary	Consolidated Slip	Los Angeles Inner Harbor	Fish Harbor	Seaplane Lagoon	Los Angeles Outer Harbor	Long Beach Inner Harbor South	Long Beach Inner Harbor North	Long Beach Outer Harbor	Los Angeles River Estuary	Eastern San Pedro Bay	Outside Harbor	Palos Verdes Shelf
Dominguez Channel Estuary	Juveniles	0.2	0.8	0	0	0	0	0	0	0	0	0	0	0
	Adults	0.2	0.23	0.01	0.04	0.01	0.1	0.02	0.02	0.01	0	0.08	0.23	0.05
Consolidated Slip	Adults	0	0.3	0.01	0.05	0.01	0.13	0.03	0.03	0.01	0	0.1	0.27	0.06
Los Angeles Inner Harbor	Adults	0	0	0.02	0.05	0.01	0.42	0.03	0.03	0.01	0	0.1	0.29	0.04
Fish Harbor	Adults	0	0	0.01	0.08	0.01	0.4	0.03	0.03	0.01	0	0.1	0.3	0.03
Seaplane Lagoon	Adults	0	0	0.01	0	0.45	0.04	0.03	0.03	0.01	0	0.1	0.3	0.03
Los Angeles Outer Harbor	Adults	0	0	0	0.03	0.22	0.45	0	0	0	0	0	0.3	0
Long Beach Inner Harbor North	Adults	0	0	0.01	0	0.01	0.43	0.03	0.08	0.01	0	0.1	0.3	0.03
Long Beach Inner Harbor South	Adults	0	0	0.01	0.05	0.01	0.38	0.08	0.03	0.01	0	0.1	0.27	0.06
Long Beach Outer Harbor	Adults	0	0	0.01	0	0.01	0.06	0.03	0.03	0.46	0	0.1	0.3	0
Los Angeles River Estuary	Juveniles	0	0	0	0	0	0	0	0	0	0.2	0.8	0	0
	Adults	0	0	0	0	0	0.02	0	0	0.02	0.2	0.51	0.25	0
Eastern San Pedro Bay	Adults	0	0	0	0	0	0.03	0	0	0.03	0	0.64	0.3	0

Notes:

* Juveniles and adults are age classes 1 to 5 and 6 to 15, respectively. California halibut juveniles are resident except at Dominguez Channel Estuary and Los Angeles River Estuary.

** Exposure proportions are fractions of a year that fish reside in a specific FMZ.

In the model, fish migrate from the starting FMZ to other FMZs in the column order from left to right and reside there for the proportion of time indicated. Exceptions are as follows:

Fish in Seaplane Lagoon migrate to Los Angeles Outer Harbor before migrating in the order above.

Fish in Long Beach Inner Harbor North migrate to Long Beach Inner Harbor South before migrating in the order above.

Fish in Long Beach Outer Harbor migrate to Long Beach Inner Harbor South and Long Beach Inner Harbor North before migrating in the order above.

FMZ = fish movement zone

Table 6-9
Exposure Proportions for California Halibut Used to Evaluate Model Sensitivity – No Palos Verdes Shelf Migration Alternative

Starting FMZ	Age Class*	FMZ Exposure Proportion **												
		Dominguez Channel Estuary	Consolidated Slip	Los Angeles Inner Harbor	Fish Harbor	Seaplane Lagoon	Los Angeles Outer Harbor	Long Beach Inner Harbor South	Long Beach Inner Harbor North	Long Beach Outer Harbor	Los Angeles River Estuary	Eastern San Pedro Bay	Outside Harbor	Palos Verdes Shelf
Dominguez Channel Estuary	Juveniles	0.2	0.8	0	0	0	0	0	0	0	0	0	0	0
	Adults	0.2	0.26	0.01	0.04	0.01	0.1	0.02	0.02	0.01	0	0.08	0.25	0
Consolidated Slip	Adults	0	0.33	0.01	0.05	0.01	0.13	0.03	0.03	0.01	0	0.1	0.3	0
Los Angeles Inner Harbor	Adults	0	0.03	0.02	0.05	0.01	0.42	0.03	0.03	0.01	0	0.1	0.3	0
Fish Harbor	Adults	0	0.03	0.01	0.08	0.01	0.4	0.03	0.03	0.01	0	0.1	0.3	0
Seaplane Lagoon	Adults	0	0.03	0.01	0	0.45	0.04	0.03	0.03	0.01	0	0.1	0.3	0
Los Angeles Outer Harbor	Adults	0	0	0	0.03	0.22	0.45	0	0	0	0	0	0.3	0
Long Beach Inner Harbor North	Adults	0	0.03	0.01	0	0.01	0.43	0.03	0.08	0.01	0	0.1	0.3	0
Long Beach Inner Harbor South	Adults	0	0.03	0.01	0.05	0.01	0.38	0.08	0.03	0.01	0	0.1	0.3	0
Long Beach Outer Harbor	Adults	0	0	0.01	0	0.01	0.06	0.03	0.03	0.46	0	0.1	0.3	0
Los Angeles River Estuary	Juveniles	0	0	0	0	0	0	0	0	0	0.2	0.8	0	0
	Adults	0	0	0	0	0	0.02	0	0	0.02	0.2	0.51	0.25	0
Eastern San Pedro Bay	Adults	0	0	0	0	0	0.03	0	0	0.03	0	0.64	0.3	0

Notes:

* Juveniles and adults are age classes 1 to 5 and 6 to 15, respectively. California halibut juveniles are resident except at Dominguez Channel Estuary and Los Angeles River Estuary.

** Exposure proportions are fractions of a year that fish reside in a specific FMZ.

In the model, fish migrate from the starting FMZ to other FMZs in the column order from left to right and reside there for the proportion of time indicated. Exceptions are as follows:

Fish in Seaplane Lagoon migrate to Los Angeles Outer Harbor before migrating in the order above.

Fish in Long Beach Inner Harbor North migrate to Long Beach Inner Harbor South before migrating in the order above.

Fish in Long Beach Outer Harbor migrate to Long Beach Inner Harbor South and Long Beach Inner Harbor North before migrating in the order above.

FMZ = fish movement zone

Table 6-10
Sensitivity Analysis Ranges for WRAP Model Parameters

Chemical	Fish Movement Zone	WRAP Calibration		WRAP Sensitivity: Ocean Boundary				WRAP Sensitivity: Sediment Bed Concentration				WRAP Sensitivity: Watershed Loading			
				Low		High		Low		High		Low		High	
		Water Column Particulate (µg/g OC)	Surface Sediment Bed Concentration (µg/g OC)	Water Column Particulate (µg/g OC)	Surface Sediment Bed Concentration (µg/g OC)	Water Column Particulate (µg/g OC)	Surface Sediment Bed Concentration (µg/g OC)	Water Column Particulate (µg/g OC)	Surface Sediment Bed Concentration (µg/g OC)	Water Column Particulate (µg/g OC)	Surface Sediment Bed Concentration (µg/g OC)	Water Column Particulate (µg/g OC)	Surface Sediment Bed Concentration (µg/g OC)	Water Column Particulate (µg/g OC)	Surface Sediment Bed Concentration (µg/g OC)
Total DDX	Dominguez Channel Estuary	16.81	6.15	16.77	6.15	16.90	6.15	11.27	3.07	27.71	12.29	14.65	6.43	18.48	5.91
	Consolidated Slip	2.06	3.99	1.96	3.99	2.30	3.99	1.40	2.00	3.29	7.99	1.81	4.01	2.26	3.98
	Los Angeles Inner Harbor	0.67	3.93	0.54	3.93	0.96	3.93	0.48	1.97	1.01	7.86	0.62	3.93	0.71	3.93
	Fish Harbor	0.42	5.28	0.30	5.28	0.66	5.28	0.30	2.64	0.62	10.56	0.40	5.28	0.43	5.28
	Seaplane Lagoon	0.47	2.29	0.34	2.29	0.75	2.29	0.36	1.14	0.69	4.58	0.44	2.29	0.50	2.29
	Los Angeles Outer Harbor	0.43	3.59	0.29	3.59	0.73	3.59	0.33	1.79	0.60	7.17	0.41	3.59	0.44	3.58
	Long Beach Inner Harbor North	0.62	1.34	0.50	1.34	0.88	1.34	0.45	0.67	0.93	2.69	0.57	1.34	0.66	1.34
	Long Beach Inner Harbor South	0.44	2.96	0.32	2.96	0.69	2.96	0.34	1.48	0.63	5.93	0.41	2.96	0.46	2.96
	Long Beach Outer Harbor	0.40	2.75	0.27	2.75	0.67	2.75	0.31	1.38	0.56	5.50	0.37	2.75	0.42	2.75
	Los Angeles River Estuary	1.24	0.78	1.16	0.78	1.43	0.78	1.18	0.39	1.35	1.56	0.59	0.81	1.86	0.76
	Eastern San Pedro Bay	0.47	1.37	0.35	1.37	0.73	1.37	0.39	0.68	0.60	2.74	0.37	1.37	0.56	1.37
	Outside Harbor	0.30	8.69	0.16	8.69	0.60	8.69	0.26	4.35	0.39	17.38	0.30	8.69	0.31	8.69
Total PCB	Dominguez Channel Estuary	13.75	12.88	13.72	12.88	13.75	12.88	8.81	6.44	23.69	25.74	12.63	13.17	14.76	12.63
	Consolidated Slip	2.07	15.63	1.99	15.63	2.09	15.63	1.29	7.82	3.71	31.28	2.04	15.76	2.20	15.52
	Los Angeles Inner Harbor	0.59	4.07	0.48	4.07	0.61	4.07	0.41	2.03	0.94	8.13	0.57	4.07	0.62	4.06
	Fish Harbor	0.70	8.87	0.58	8.87	0.72	8.87	0.44	4.43	1.18	17.73	0.69	8.87	0.70	8.87
	Seaplane Lagoon	0.37	2.34	0.28	2.34	0.39	2.34	0.28	1.17	0.56	4.67	0.35	2.34	0.40	2.34
	Los Angeles Outer Harbor	0.29	1.45	0.18	1.45	0.32	1.45	0.25	0.73	0.38	2.90	0.28	1.45	0.31	1.45
	Long Beach Inner Harbor North	0.54	2.87	0.45	2.87	0.56	2.87	0.39	1.43	0.86	5.73	0.52	2.87	0.58	2.86
	Long Beach Inner Harbor South	0.38	5.56	0.29	5.56	0.40	5.56	0.29	2.78	0.56	11.11	0.36	5.56	0.40	5.56
	Long Beach Outer Harbor	0.28	1.20	0.18	1.20	0.30	1.20	0.24	0.60	0.36	2.40	0.26	1.20	0.31	1.20
	Los Angeles River Estuary	1.54	3.32	1.47	3.32	1.56	3.32	1.46	1.66	1.69	6.64	0.68	3.44	2.48	3.22
	Eastern San Pedro Bay	0.40	1.84	0.30	1.84	0.42	1.84	0.36	0.92	0.47	3.68	0.28	1.85	0.52	1.83
	Outside Harbor	0.20	0.38	0.08	0.38	0.23	0.38	0.19	0.19	0.22	0.75	0.20	0.38	0.21	0.38

Notes:
µg = microgram
DDX = dichlorodiphenyltrichloroethane-related compounds (4,4'-DDT, 4,4'-DDE, 4,4'-DDD, 2,4'-DDT, 2,4'-DDE, and 2,4'-DDD)
g = gram
OC = organic carbon
PCB = polychlorinated biphenyl
WRAP = Water Resources Action Plan

Table 6-11
Sensitivity Analysis Parameter Ranges and Descriptions

Sensitivity Parameter	Sensitivity Value			Value Description		
	Base	Low	High	Base	Low	High
Growth Rate - Surfperch	See Figure 4-7	See Figure 6-1		2014 otolith-based age data	Alternate fits to 2014 otolith-based age data based on shiner and white surfperch data separately	
Growth Rate - White Croaker	See Figure 4-6	See Figure 6-2		Moore et al. 1999; MBC 2016	Alternative weight-at-length used to convert length-at-age to weight-at-age (Moore 1999)	NA
Growth Rate - California Halibut	See Figure 4-5	See Figure 6-3		McNair et al. 2001; Hammann and Ramirez-Gonzalez 1990	Distinct female and male length-at-age relationships used to estimate slower and faster growth rates as weight-at-age (MacNair et al. 2001)	
Diet - Surfperch	See Table 5-6	See Table 6-1		Gobas and Arnot 2010	Increased proportion of water-column and decreased proportion of deposit-feeding invertebrates	
Diet - White Croaker	See Table 5-5	See Table 6-2		Malins et al. 1987	Increased proportion of deposit-feeding invertebrates and decreased proportion of water-column invertebrates	
Diet - California Halibut	See Table 5-4	See Table 6-3		Wertz and Domeier 1997	Increased proportion of surfperches and decreased proportion of croaker in fish older than age 5.	
BSAF - Sediment PCB	See Table 4-5	0.12	2.71	Varies by FMZ based on data	Minimum PCB values from 2014 special study	Maximum PCB values from 2014 special study
BSAF - Sediment DDX		0.10	1.47	Varies by FMZ based on data	Minimum Vista reanalysis value	Maximum DDX values from 2014 special study
Water Column Particulate Accumulation Factor - Total PCB	See Table 4-4	4.00	15.64	Best calibration match	Great Lakes study	Maximum values from 2014 special study
Water Column Particulate Accumulation Factor - Total DDX		4.00	15.30			
Migration - FH Alternative, White Croaker	See Table 5-7	See Table 6-4		Best calibration match	Reduced migration to FH and increased migration to PV Shelf	
Migration - FH Alternative, California Halibut	See Table 5-8	See Table 6-7			Reduced migration to FH and increased migration to PV Shelf	
Migration - CS Alternative, White Croaker	See Table 5-7	See Table 6-5			Reduced migration to CS and increased migration to PV Shelf	
Migration - CS Alternative, California Halibut	See Table 5-8	See Table 6-8			Reduced migration to CS and increased migration to PV Shelf	
Migration - No PV Shelf Migration, White Croaker	See Table 5-7	See Table 6-6			Assigned all migration outside of the Harbor to "Outside Harbor"	
Migration - No PV Shelf Migration, California Halibut	See Table 5-8	See Table 6-9				
WRAP Model - Ocean Boundary Total PCB and Total DDX	See Table 4-14*	See Table 6-10**		WRAP model calibration	Range in data from outside harbor (Poon and Ueoka 2016)	
WRAP Model - Sediment Bed Total PCB and Total DDX					Half initial sediment bed organic concentrations	Double initial sediment bed organic concentrations
WRAP Model - Watershed Total PCB and Total DDX					Uncertainty in storm water concentrations (Poon and Ueoka 2016)	

Notes:

* WRAP model inputs for the ocean boundary for the calibration run were 0.25 and 0.24 ng/L for Total PCB and Total DDX, respectively. For the watershed, they were 17.1 and 11.88 kg for Total PCB and Total DDX, respectively (Poon and Ueoka 2016).

** WRAP model inputs for the ocean boundary for the sensitivity low and high runs were 0.0806 and 0.284 ng/L for Total PCB, respectively. For Total DDX low and high, they were 0.0719 and 0.608 ng/L, respectively.
For the watershed, WRAP model inputs for the sensitivity low and high runs were 5.76 and 29.4 kg for Total PCB, respectively. For Total DDX low and high, they were 4.13 and 19.07 kg, respectively (Poon and Ueoka 2016).

BSAF = biota-sediment accumulation factor
CS = Consolidated Slip
DDX = dichlorodiphenyltrichloroethane-related compounds (4,4'-DDT, 4,4'-DDE, 4,4'-DDD, 2,4'-DDT, 2,4'-DDE, and 2,4'-DDD)
FH = Fish Harbor
FMZ = Fish Movement Zone
kg = kilogram
L = liter
NA = not applicable
ng = nanogram
PCB = polychlorinated biphenyl
PV = Palos Verdes
WRAP = Water Resources Action Plan

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Table 6-12
Input Parameters for Alternate Calibration

Fish Movement Zone	Parameter	Upper-bound Sediment Contribution		Lower-bound Sediment Contribution	
		PCB	DDX	PCB	DDX
All Zones	Ocean Boundary (ng/L)	0.08	0.07	0.28	0.61
All Zones	Water Column Accumulation Factor	5.84	1.70	11.63	10.11
Dominguez Channel Estuary	BSAF	3.06	0.87	2.02	0.25
Consolidated Slip	BSAF	1.11	0.87	0.07	0.25
Los Angeles Inner Harbor	BSAF	1.10	0.87	0.05	0.25
Fish Harbor	BSAF	3.23	1.81	2.19	1.20
Seaplane Lagoon	BSAF	3.07	1.78	2.03	1.16
Los Angeles Outer Harbor	BSAF	1.17	1.12	0.13	0.50
Long Beach Inner Harbor North	BSAF	2.13	0.87	1.09	0.25
Long Beach Inner Harbor South	BSAF	2.28	0.87	1.24	0.25
Los Angeles River Estuary	BSAF	3.06	0.87	2.02	0.25
Eastern San Pedro Bay	BSAF	3.06	0.87	2.02	0.25

Notes:
BSAF = biota-sediment accumulation factor
DDX = dichlorodiphenyltrichloroethane-related compounds (4,4'-DDT, 4,4'-DDE, 4,4'-DDD, 2,4'-DDT, 2,4'-DDE, and 2,4'-
ng/L = nanogram per liter
PCB = polychlorinated biphenyl

FIGURES

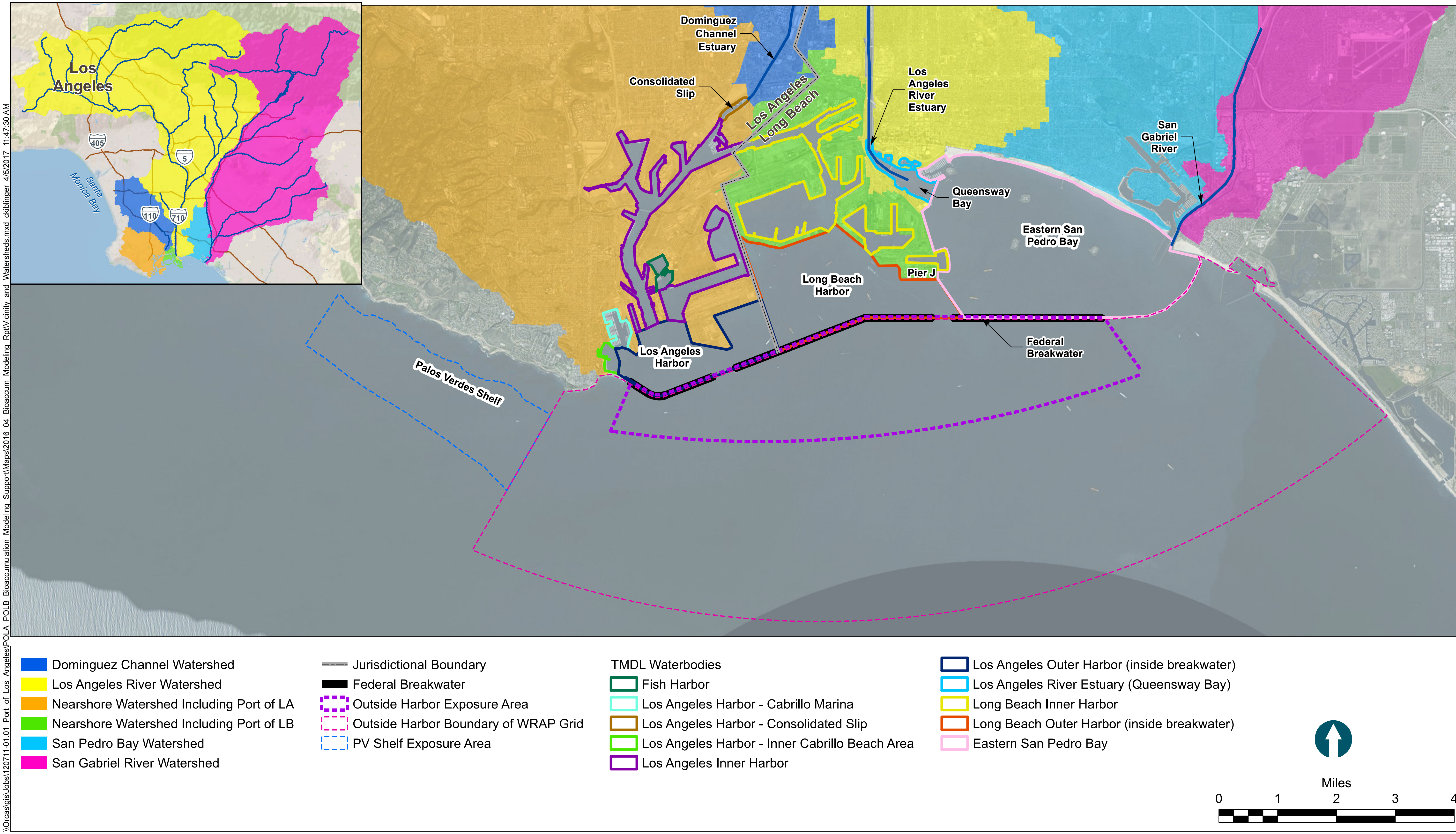

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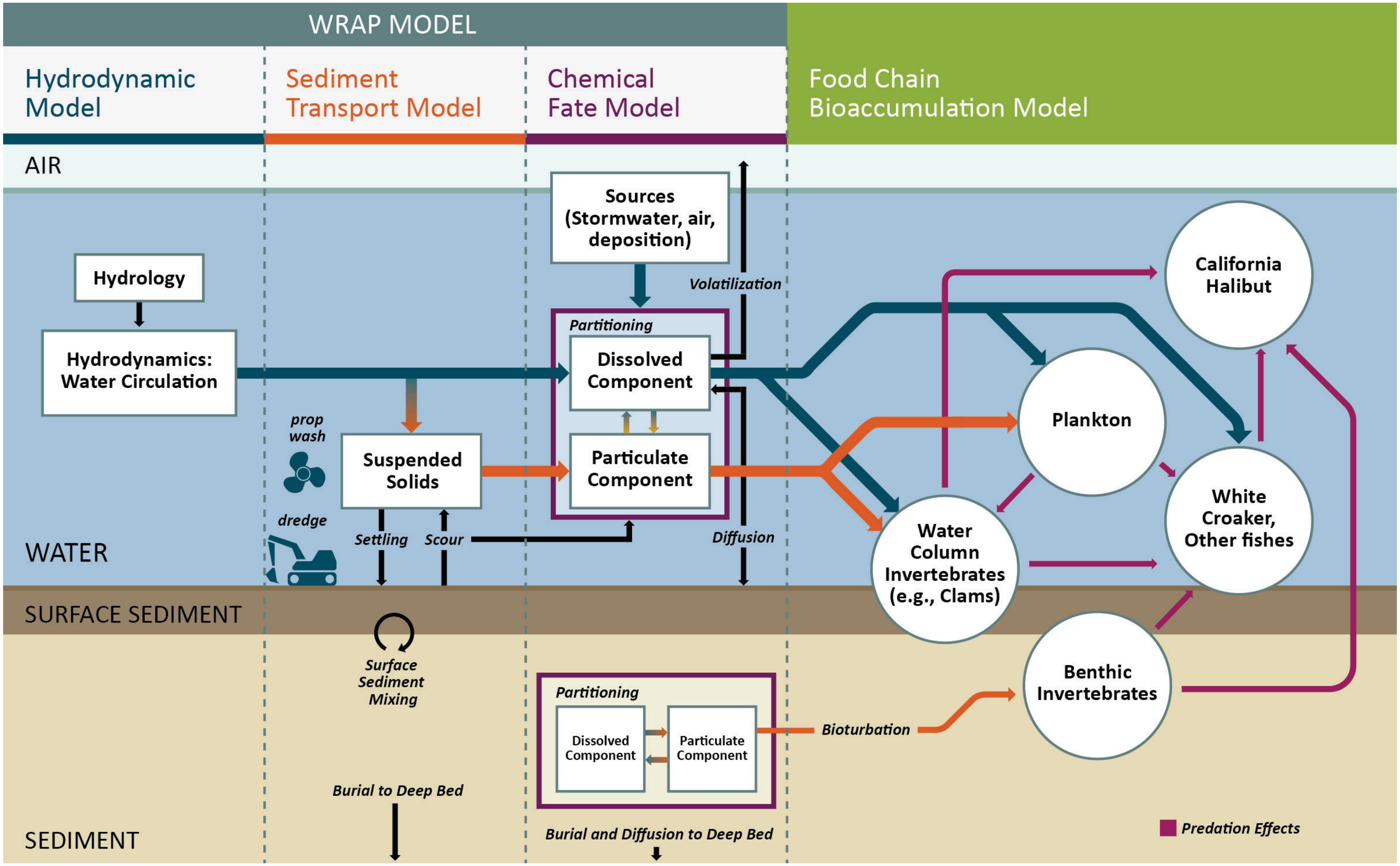
Figure 1-1
Study Area
Bioaccumulation Modeling Report
Greater Los Angeles and Long Beach Harbor Waters

ANCHOR QEA



Note:
The linked model relies on water column particulate concentrations to represent phytoplankton.

S:\PROJECTS\Ports_LA-LB\Harbor_Toxics_TMDL\Bioaccumulation_Model\Deliverables\Bio Model Report\2017\Figures\Section 2\Figure 2-1 Linked Modeling Framework for the Greater Harbor Waters.docx

ANCHOR QEA

Figure 2-1
Linked Modeling Framework for the Greater Harbor Waters
Bioaccumulation Modeling Report
Greater Los Angeles and Long Beach Harbor Waters

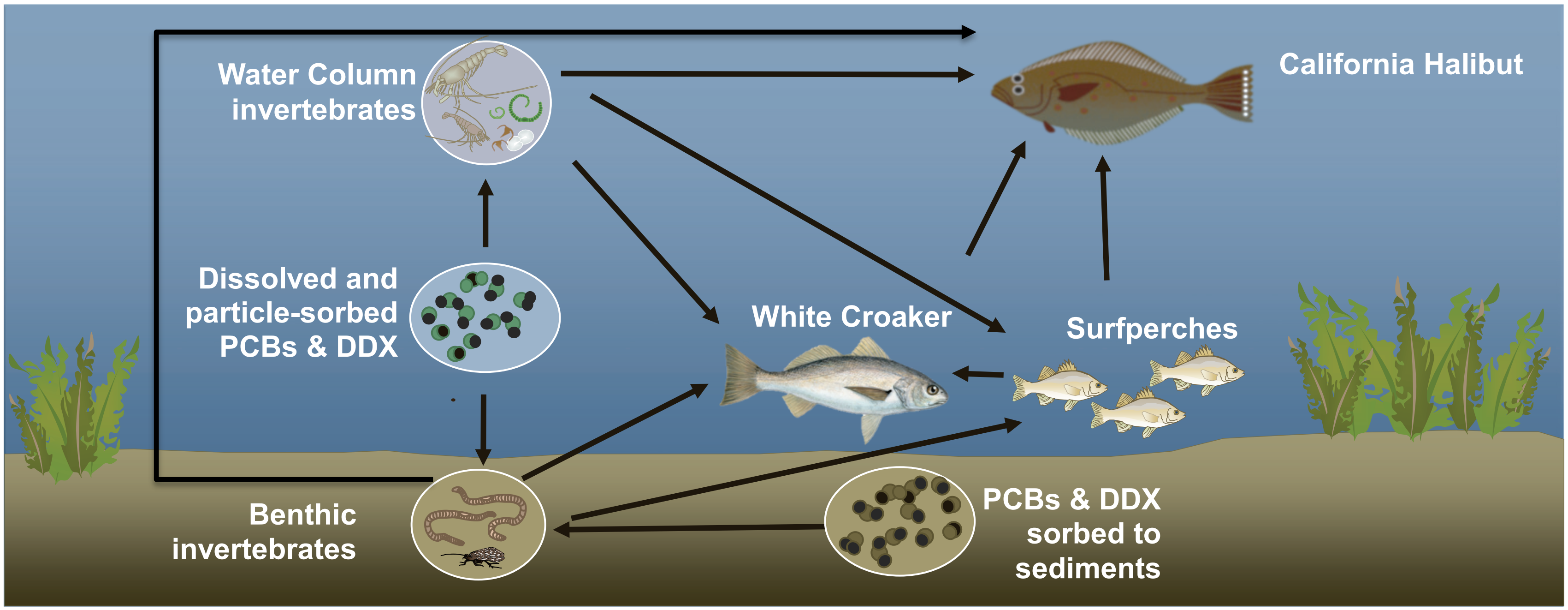
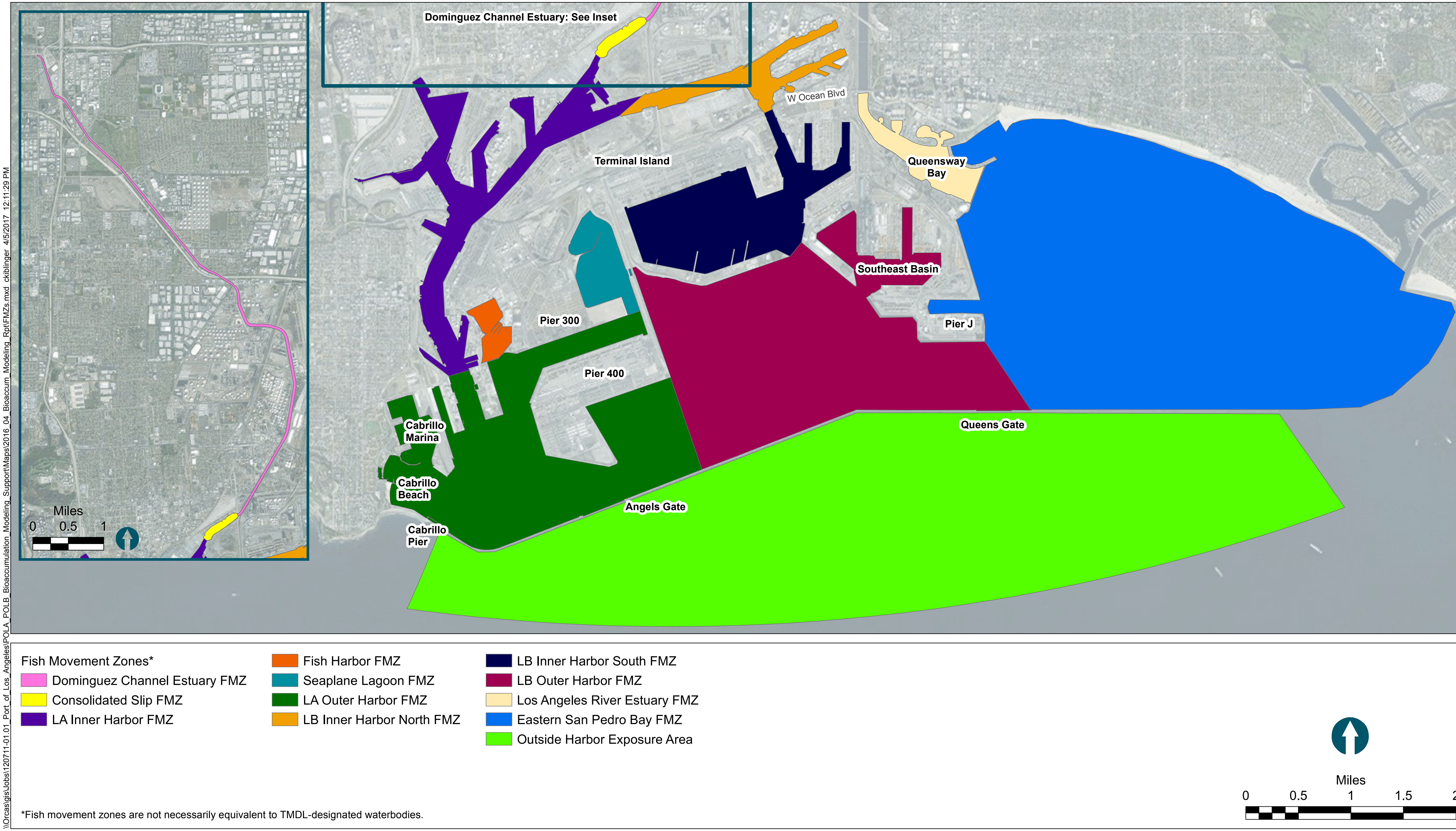


Figure 2-2
PCB and DDX Accumulation in the Food Web
Bioaccumulation Modeling Report
Greater Los Angeles and Long Beach Harbor Waters



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ANCHOR QEA

Figure 2-3
Fish Movement Zones in the Greater Harbor Waters
Bioaccumulation Modeling Report
Greater Los Angeles and Long Beach Harbor Waters

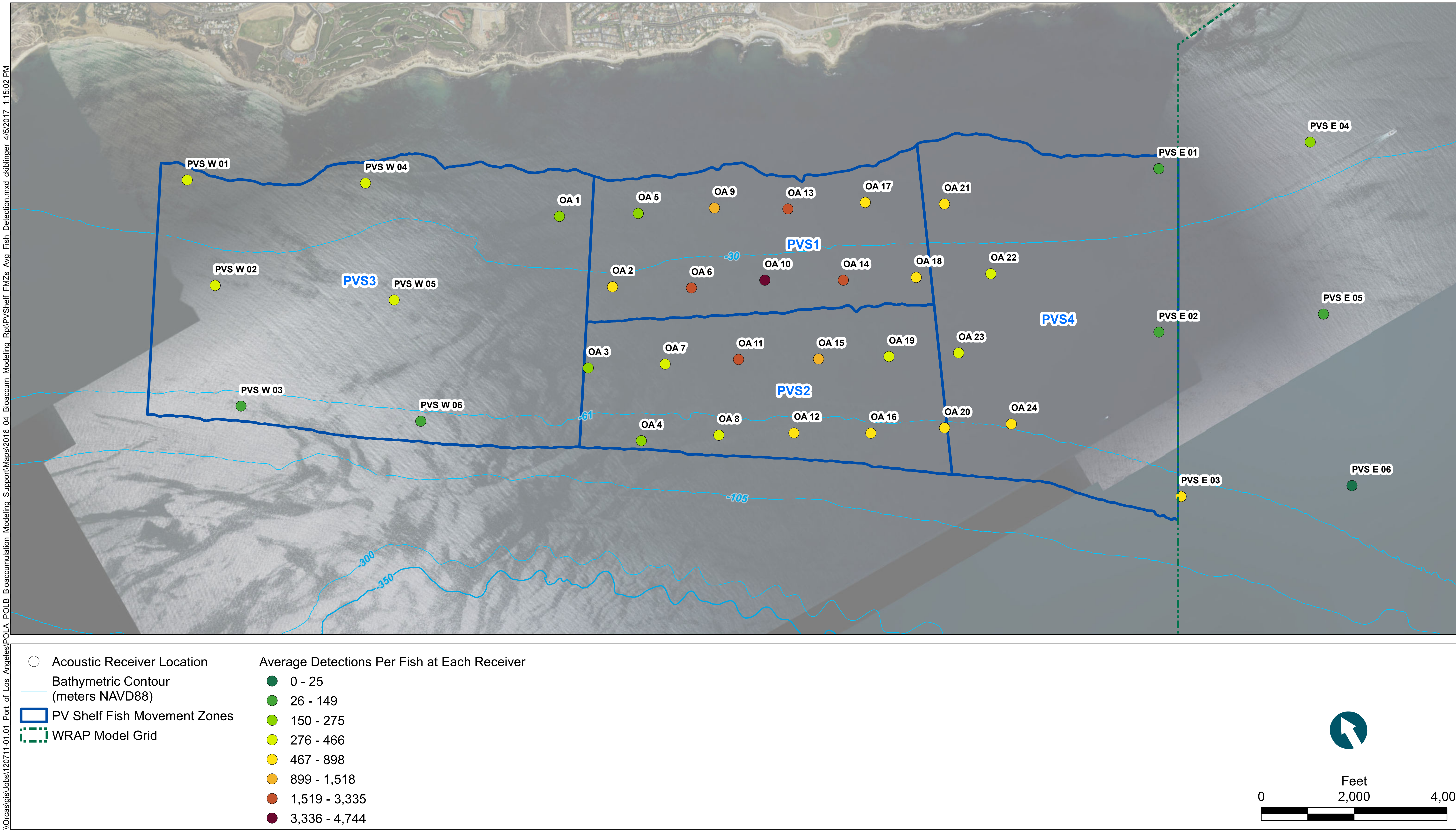
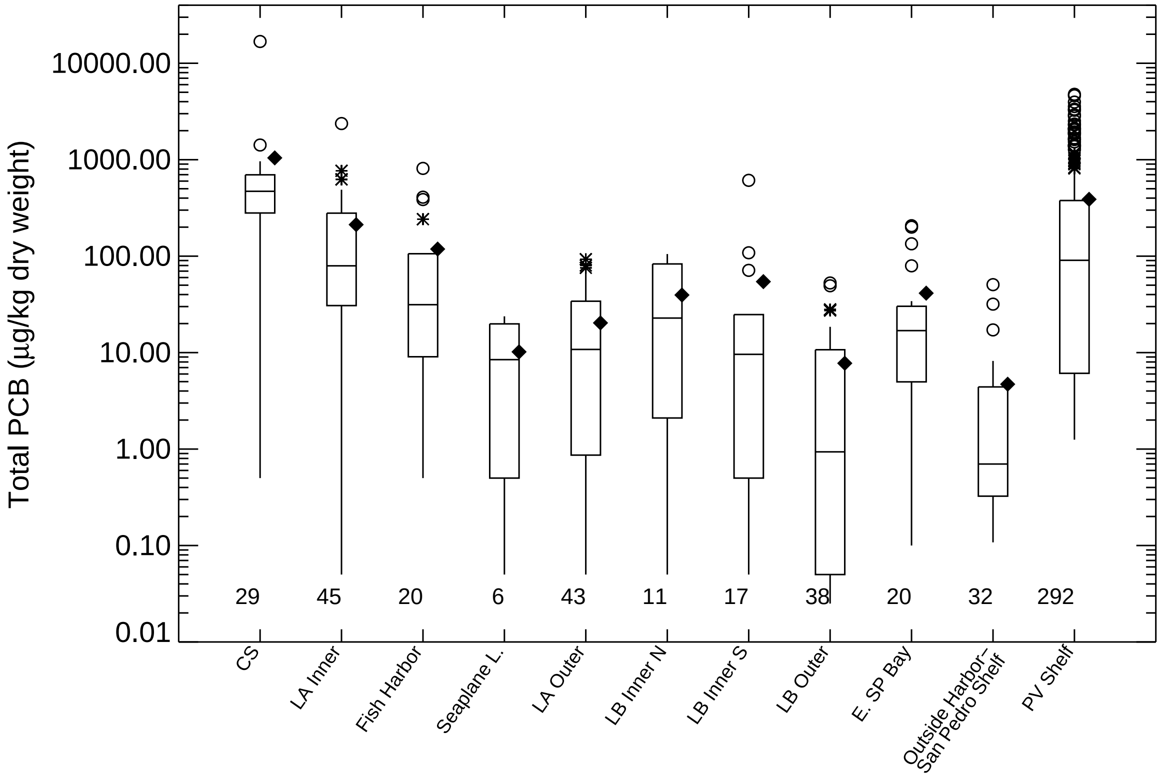


Figure 2-4
Fish Movement Zones on the PV Shelf Relative to Average Detections of Fish at Each Receiver
Bioaccumulation Modeling Report
Greater Los Angeles and Long Beach Harbor Waters

ANCHOR QEA



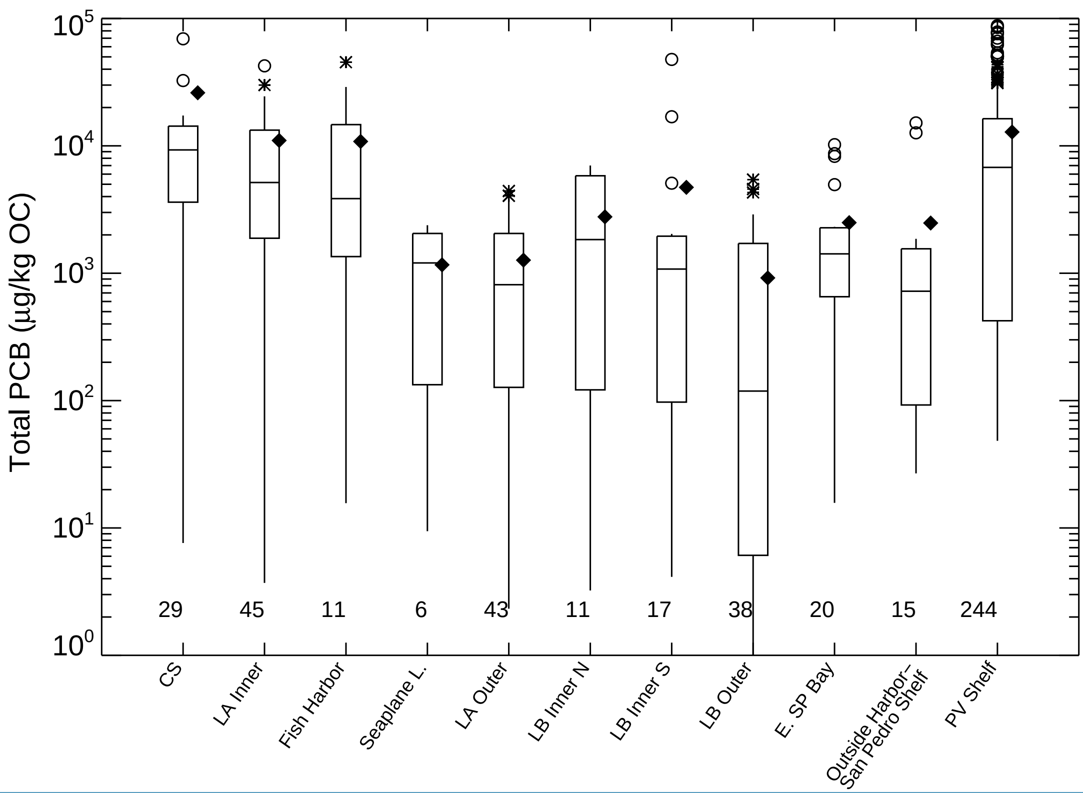


Figure 2−5

Spatial Distribution of PCB Concentrations in Surface Sediment

ANCHOR QEA

Data file used: PortOfLALB_Sediment_20160720.bin. Surface sediment is top 16 cm. Data for 2002−2014 samples. Totals are calculated as sum of detected congeners or Aroclors, or half of highest detection limit if all congeners or Aroclors are non−detects. Weston 2011 dataset excluded from the analysis. Field duplicates are averaged. High−res congener data plotted when paired high−res or low−res congener or Aroclor data exists. Samples with non−detect or without total organic carbon (TOC) data are assigned TOC value of nearest surface sediment sample. Outside Harbor−San Pedro Shelf is a nearby area outside of PoLA/PoLB and south of the breakwater.

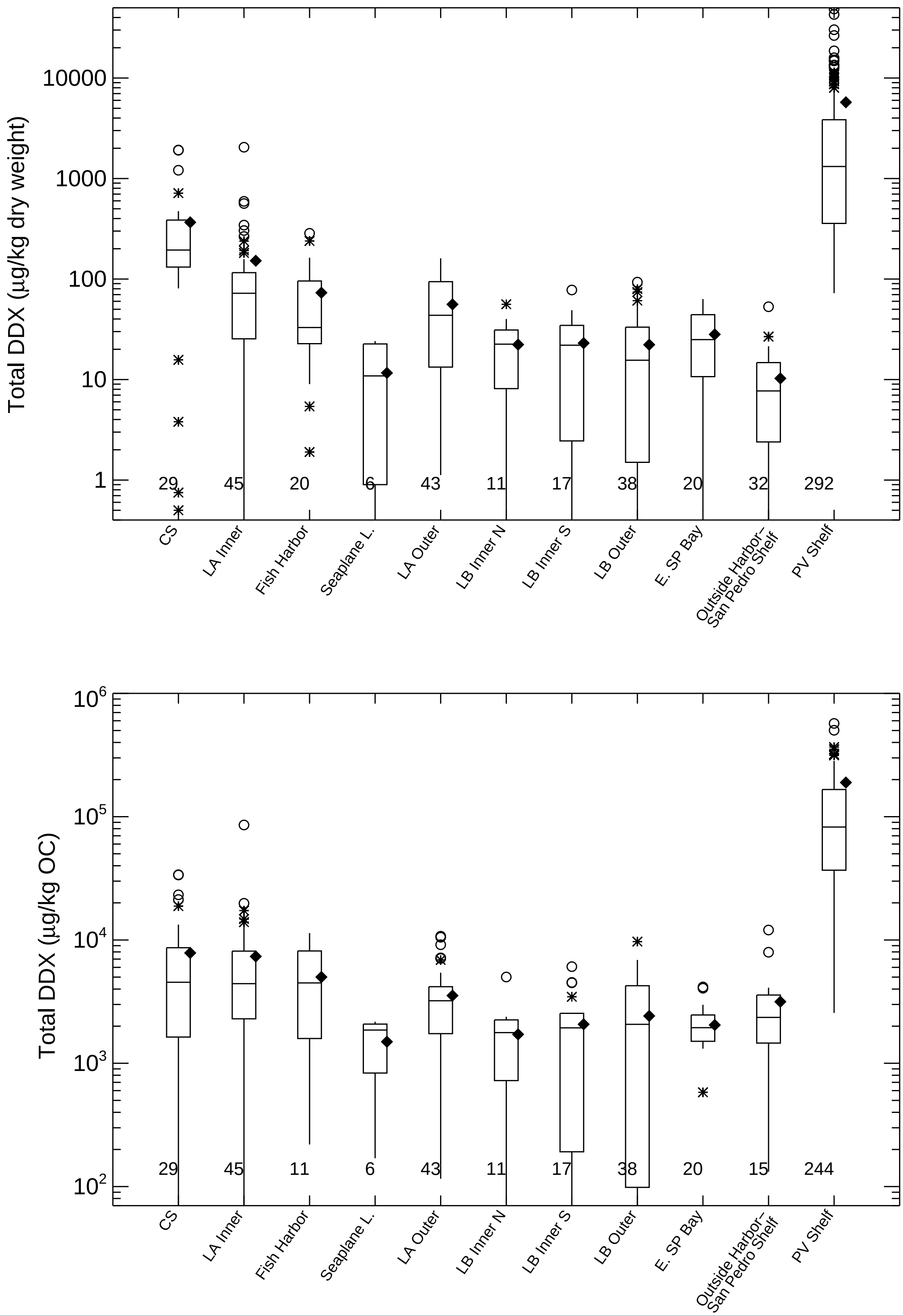
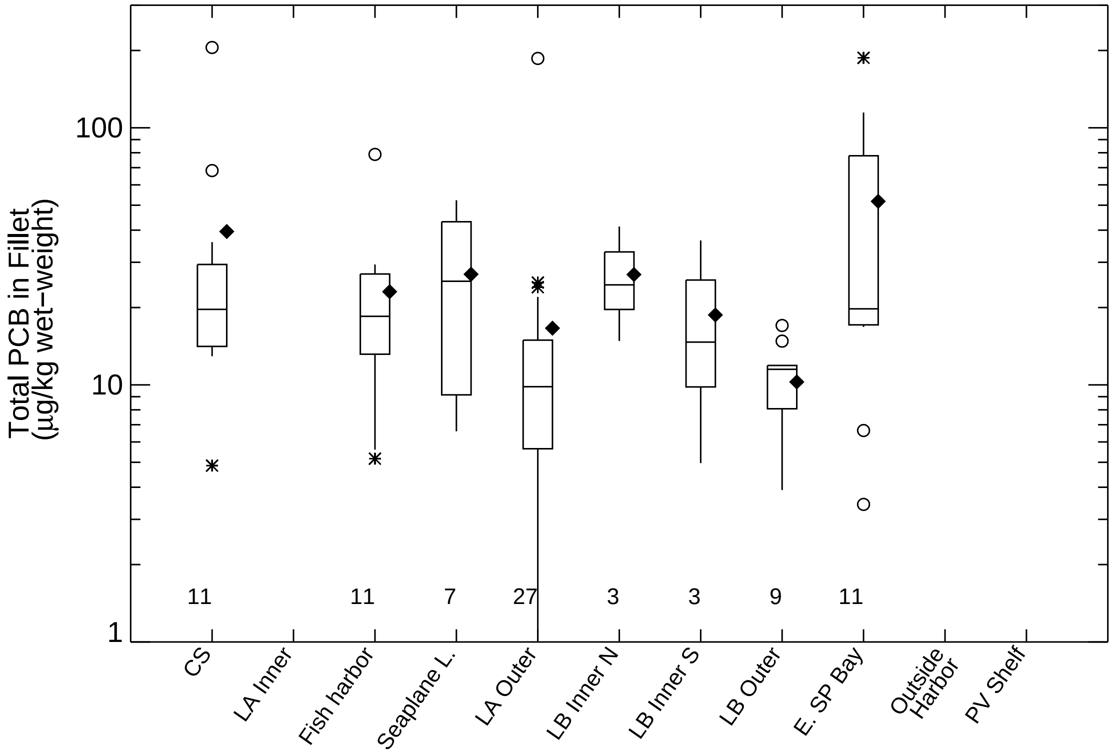


Figure 2−6

Spatial Distribution of DDX Concentrations in Surface Sediment

Data file used: PortOfLALB_Sediment_20160720.bin. Surface sediment is top 16 cm. Data for 2002−2014 samples. Totals are calculated as sum of detected congeners or Aroclors, or half of highest detection limit if all congeners or Aroclors are non−detects. Weston 2011 dataset excluded from the analysis. Field duplicates are averaged. High−res congener data plotted when paired high−res or low−res congener or Aroclor data exists. Samples with non−detect or without total organic carbon (TOC) data are assigned TOC value of nearest surface sediment sample. Outside Harbor−San Pedro Shelf is a nearby area outside of PoLA/PoLB and south of the breakwater.

EC/MM − \\iris\Woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Analysis\Sediment_Plots\lalb_sediment_boxplot_v3.pro Fri Apr 28 02:03:05 2017



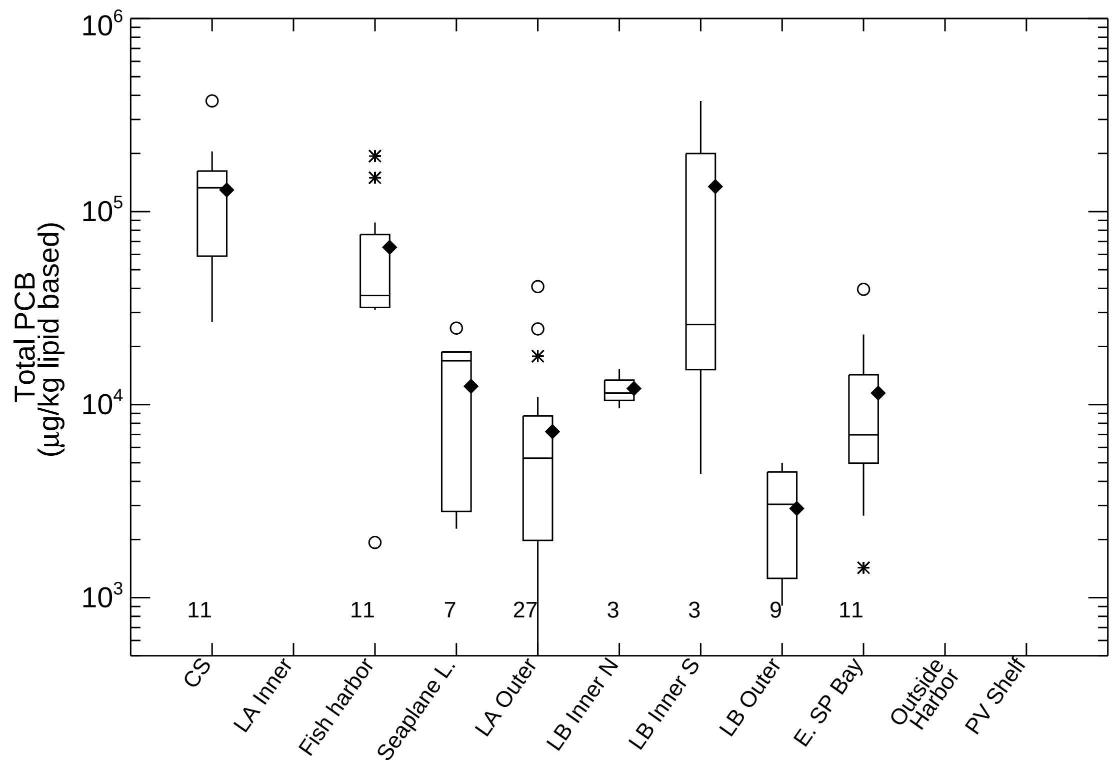


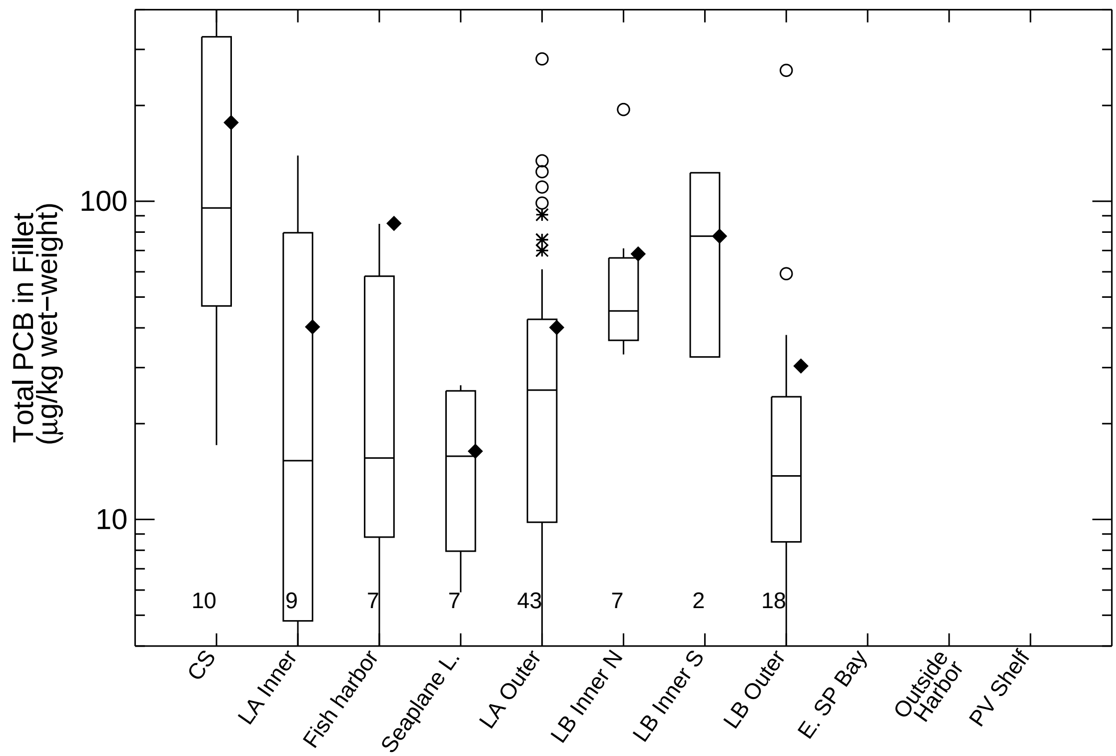
Figure 2−7a

Spatial Distribution of PCB Concentrations in California Halibut

ANCHOR QEA

Data file used: PortOfLALB_Fish_20150902.xlsx. Field duplicates are averaged.
Totals are calculated as sum of detected congeners or aroclors, or half of highest detection limit if all congeners or are non−detects. High−Res Congener data plotted when paired high−res or low−res congener or aroclor data exists.
Fish data shown are for 2002−2014 samples. Fish data excluded: Cabrillo Pier (one station)
Tissue types include: Fillet (all types). Lipid−based plot include fillet (all types) and whole body.
Outside Harbor (local background) is defined as a nearby area outside of PoLA/PoLB and south of the breakwater.

MM − \\iris\Woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Analysis\Fish\lalb_fish_boxplot_v2.pro Fri Apr 28 02:11:25 2017



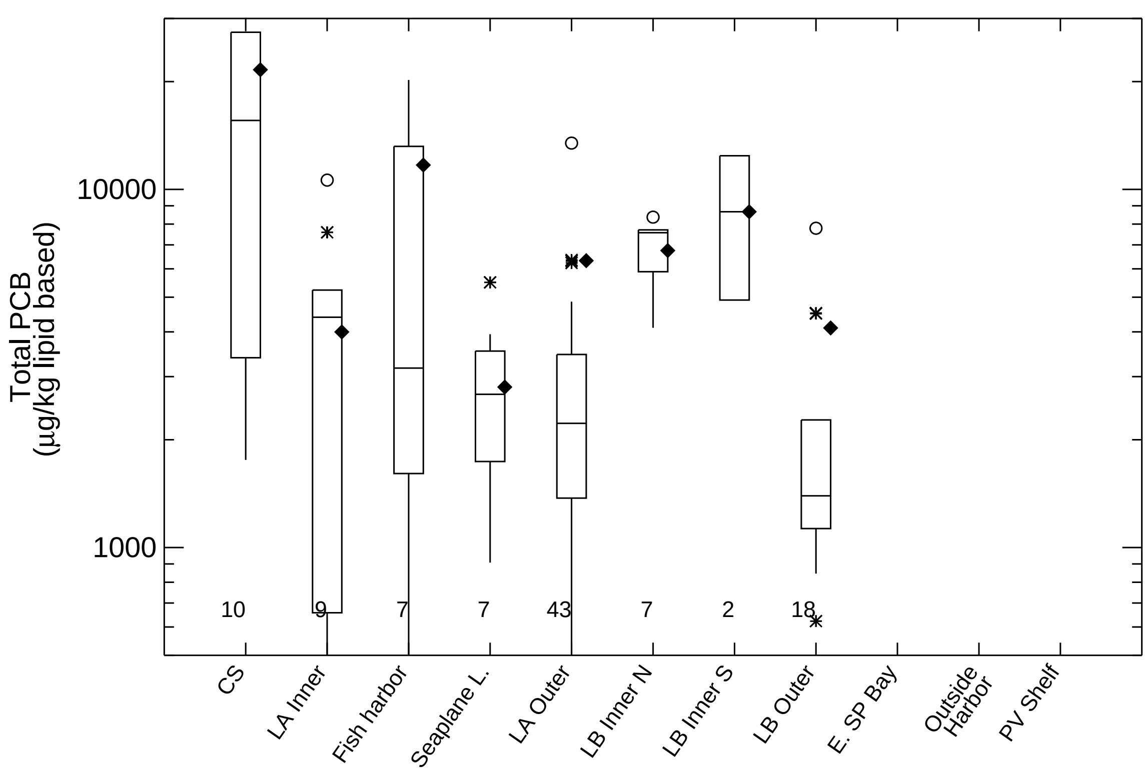


Figure 2−7b

Spatial Distribution of PCB Concentrations in Queenfish

Data file used: PortOfLALB_Fish_20150902.xlsx. Field duplicates are averaged.
Totals are calculated as sum of detected congeners or aroclors, or half of highest detection limit if all congeners or are non−detects. High−Res Congener data plotted when paired high−res or low−res congener or aroclor data exists.
Fish data shown are for 2002−2014 samples. Fish data excluded: Cabrillo Pier (one station)
Tissue types include: Fillet (all types). Lipid−based plot include fillet (all types) and whole body.
Outside Harbor (local background) is defined as a nearby area outside of PoLA/PoLB and south of the breakwater.

MM − \\iris\Woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Analysis\Fish\lalb_fish_boxplot_v2.pro Fri Apr 28 02:11:25 2017

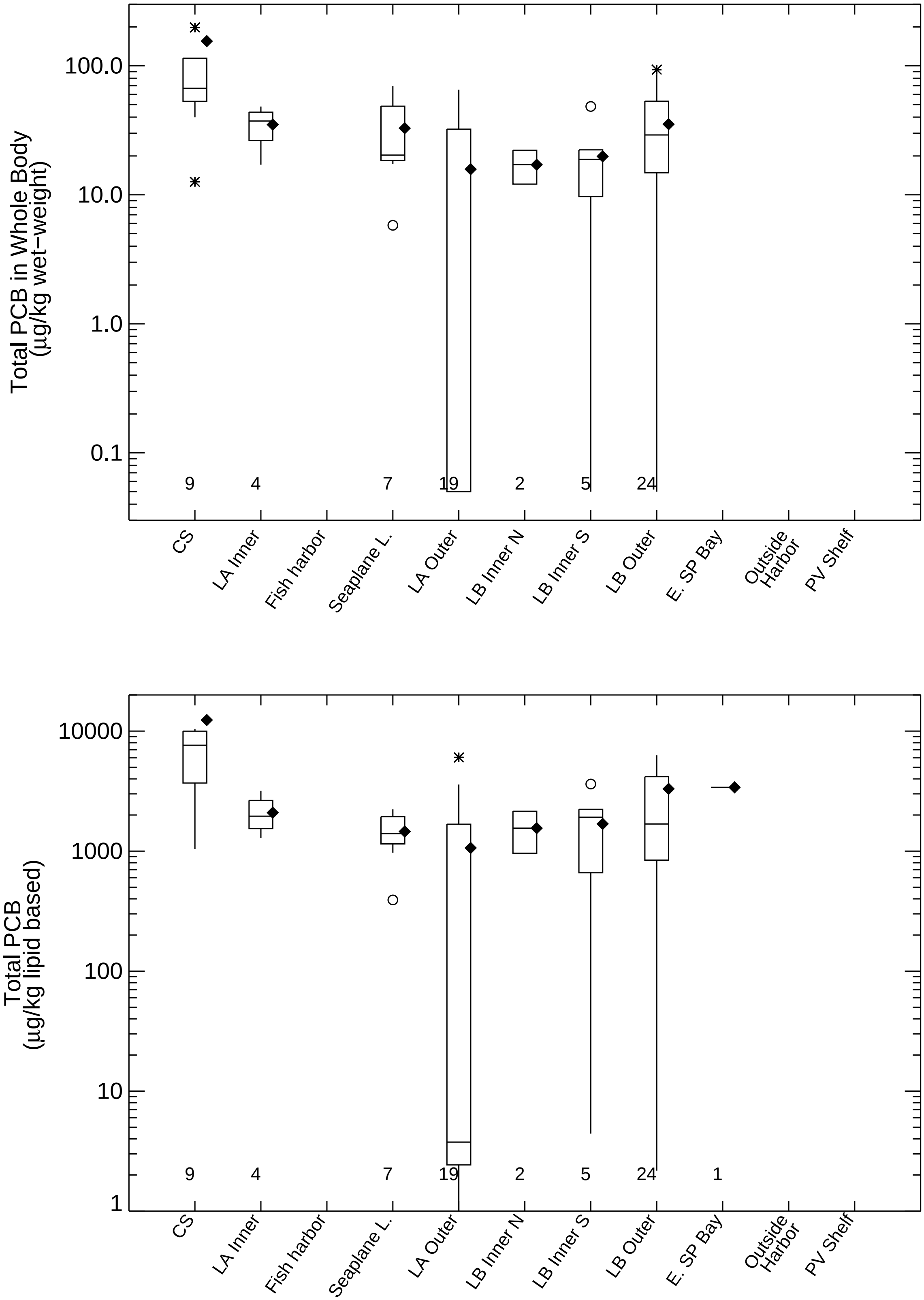


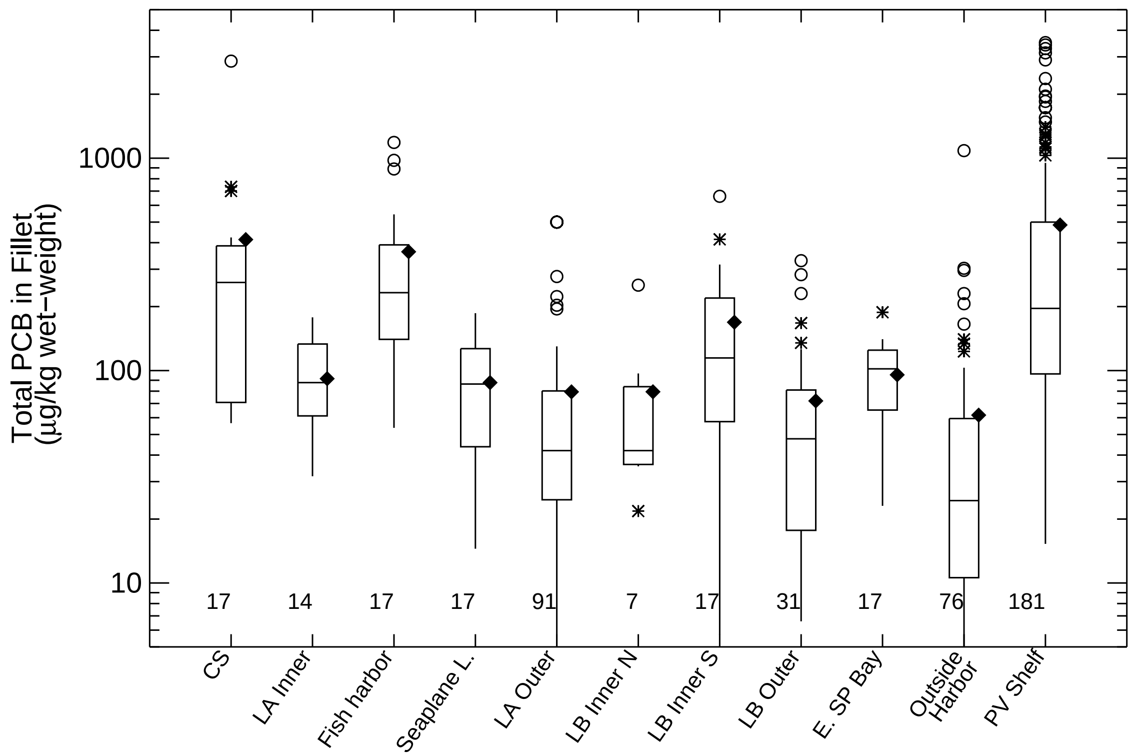
Figure 2−7c

Spatial Distribution of PCB Concentrations in Topsmelt

ANCHOR QEA

Data file used: PortOfLALB_Fish_20150902.xlsx. Field duplicates are averaged.
Totals are calculated as sum of detected congeners or aroclors, or half of highest detection limit if all congeners or are non−detects. High−Res Congener data plotted when paired high−res or low−res congener or aroclor data exists.
Fish data shown are for 2002−2014 samples. Fish data excluded: Cabrillo Pier (one station)
Tissue types include: Whole body. Lipid−based plot include fillet (all types) and whole body.
Outside Harbor (local background) is defined as a nearby area outside of PoLA/PoLB and south of the breakwater.

MM − \\iris\Woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Analysis\Fish\lalb_fish_boxplot_v2.pro Fri Apr 28 02:11:25 2017



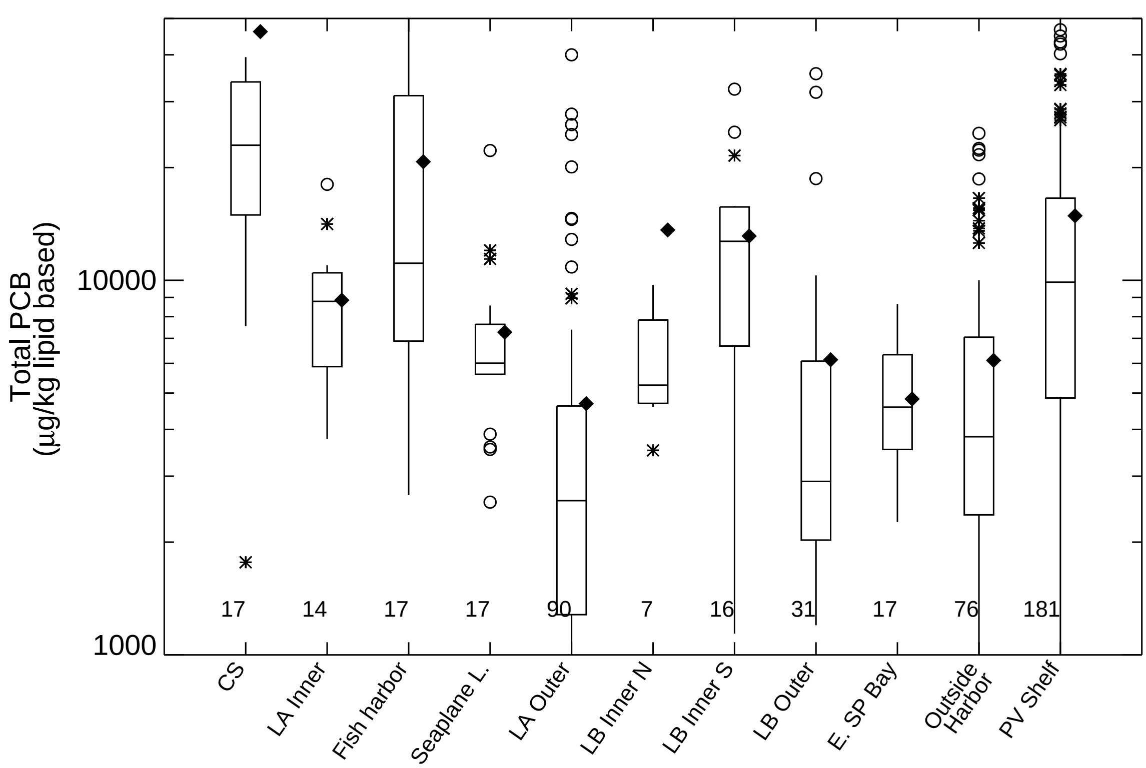


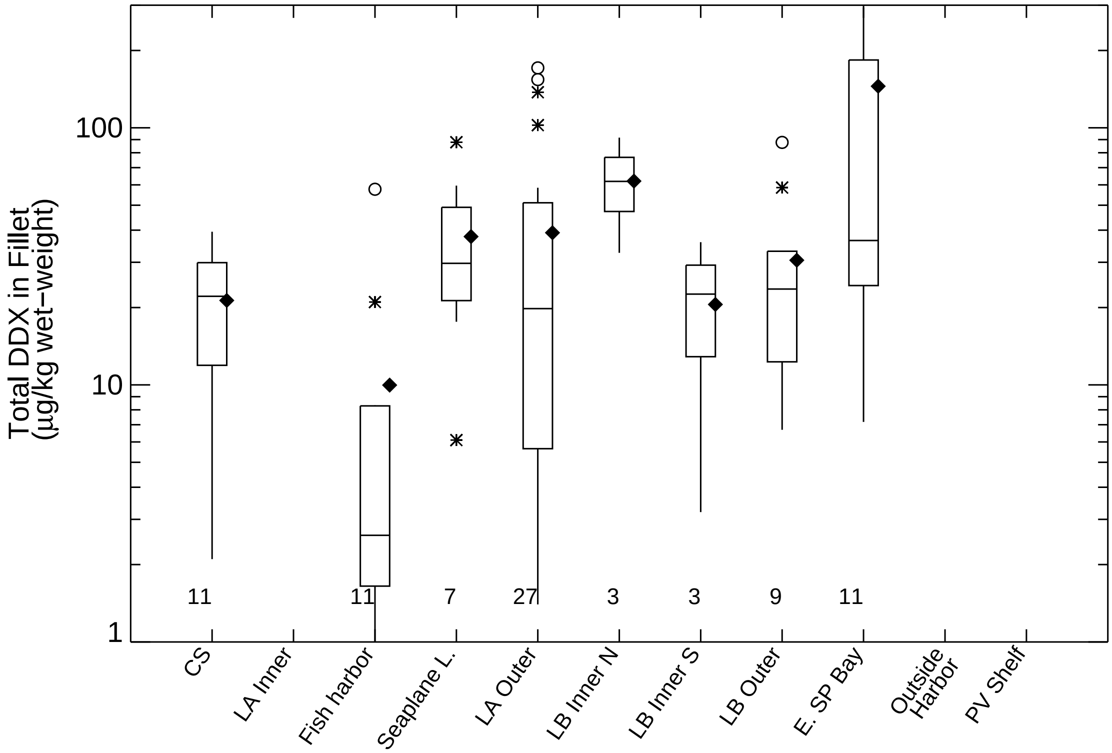
Figure 2−7d

Spatial Distribution of PCB Concentrations in White Croaker

ANCHOR QEA

Data file used: PortOfLALB_Fish_20150902.xlsx. Field duplicates are averaged.
Totals are calculated as sum of detected congeners or aroclors, or half of highest detection limit if all congeners or are non−detects. High−Res Congener data plotted when paired high−res or low−res congener or aroclor data exists.
Fish data shown are for 2002−2014 samples. Fish data excluded: Cabrillo Pier (one station)
Tissue types include: Fillet (all types). Lipid−based plot include fillet (all types) and whole body.
One White Croaker sample (IH5−FFF−7WC) with low lipid (0.05%) excluded.

MM − \\iris\Woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Analysis\Fish\lalb_fish_boxplot_v2.pro Fri Apr 28 02:11:26 2017



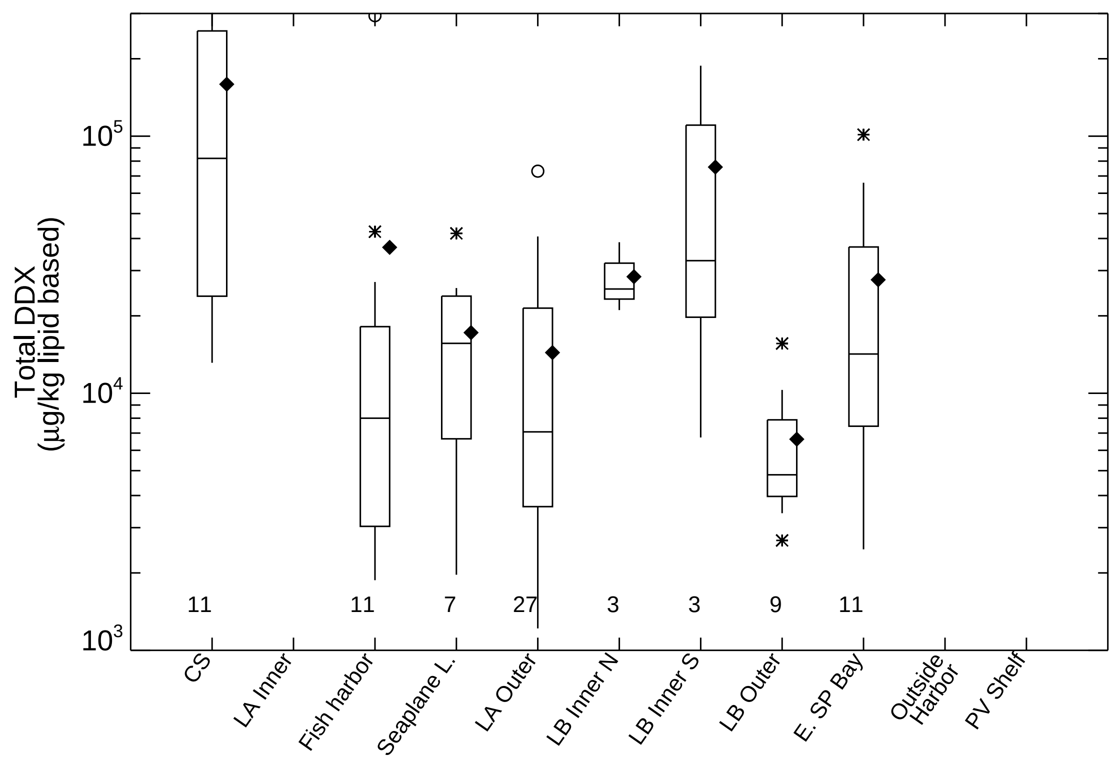


Figure 2−8a

Spatial Distribution of DDX Concentrations in California Halibut

Data file used: PortOfLALB_Fish_20150902.xlsx. Field duplicates are averaged.
Totals are calculated as sum of detected congeners or aroclors, or half of highest detection limit if all congeners or are non−detects. High−Res Congener data plotted when paired high−res or low−res congener or aroclor data exists.
Fish data shown are for 2002−2014 samples. Fish data excluded: Cabrillo Pier (one station)
Tissue types include: Fillet (all types). Lipid−based plot include fillet (all types) and whole body.
Outside Harbor (local background) is defined as a nearby area outside of PoLA/PoLB and south of the breakwater.

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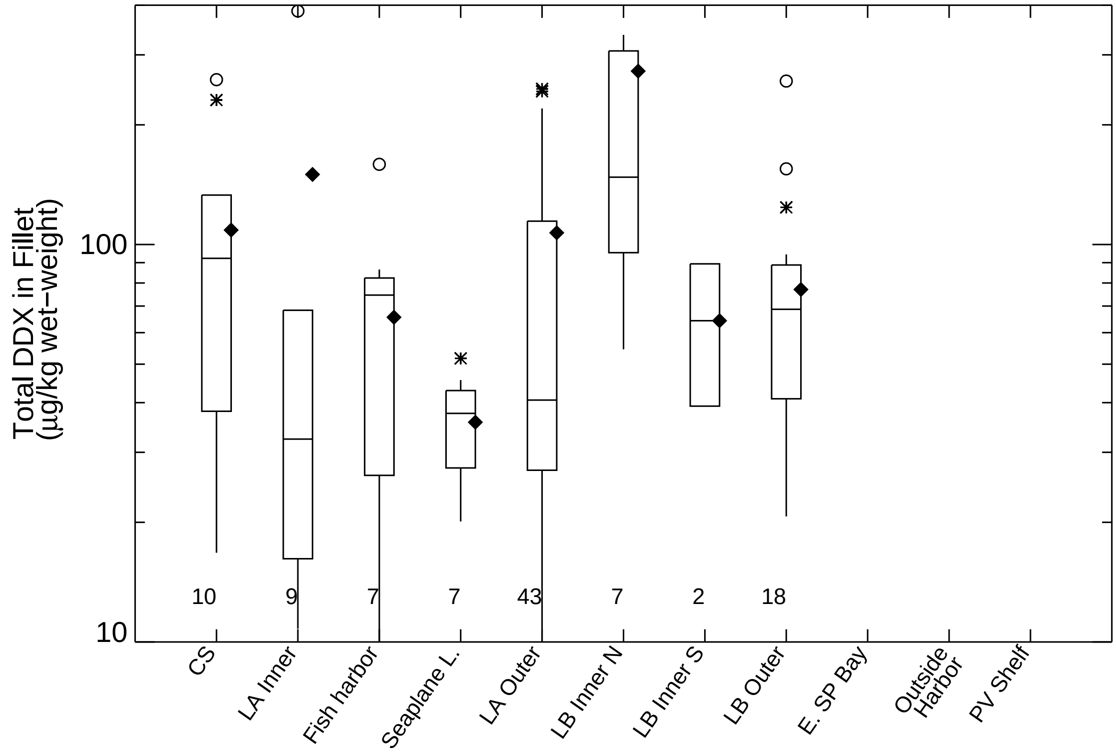


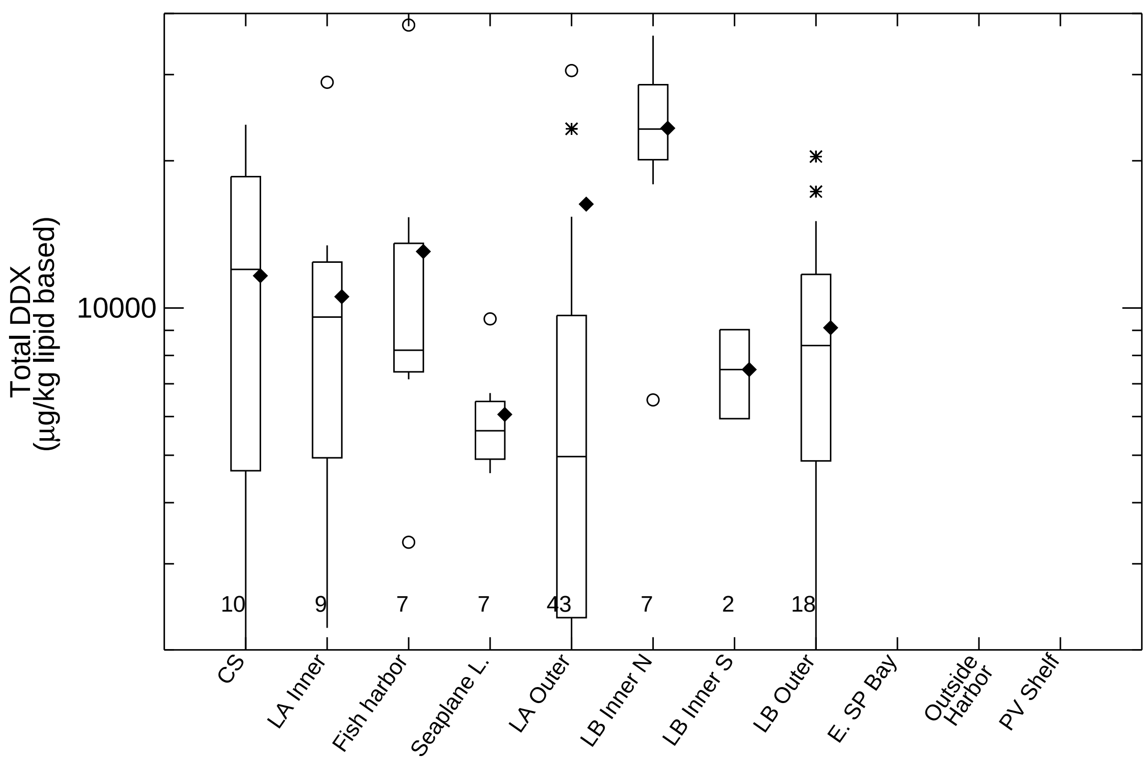


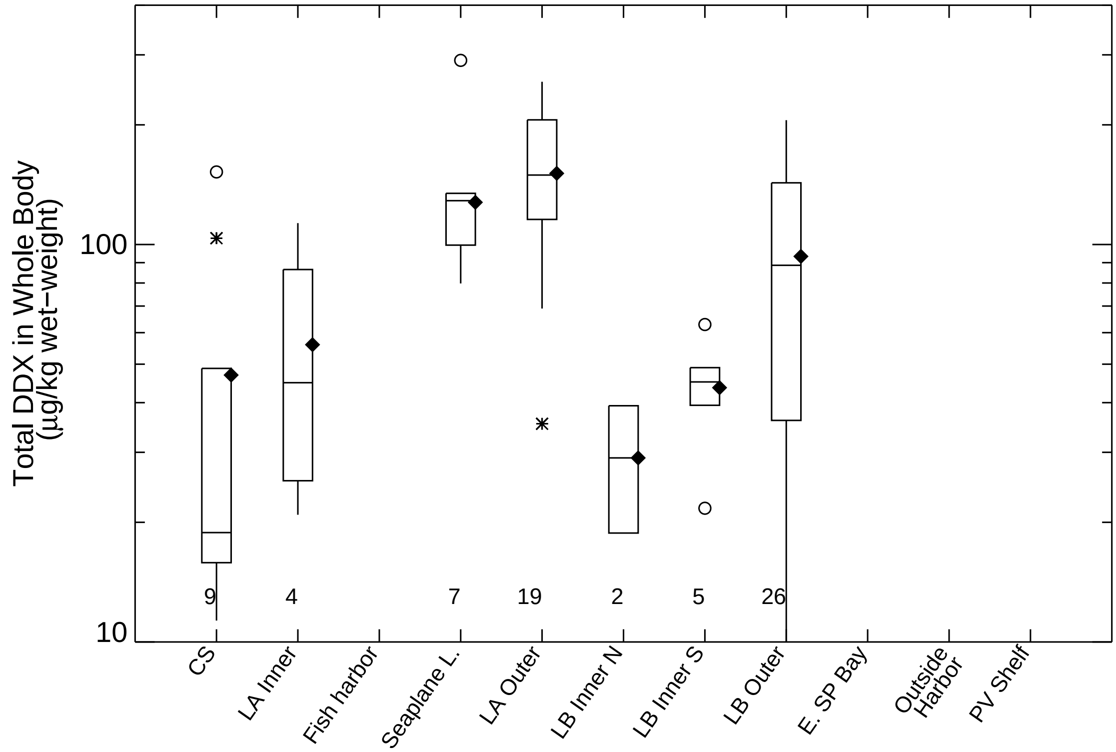
Figure 2−8b

Spatial Distribution of DDX Concentrations in Queenfish

ANCHOR QEA

Data file used: PortOfLALB_Fish_20150902.xlsx. Field duplicates are averaged.
Totals are calculated as sum of detected congeners or aroclors, or half of highest detection limit if all congeners or are non−detects. High−Res Congener data plotted when paired high−res or low−res congener or aroclor data exists.
Fish data shown are for 2002−2014 samples. Fish data excluded: Cabrillo Pier (one station)
Tissue types include: Fillet (all types). Lipid−based plot include fillet (all types) and whole body.
Outside Harbor (local background) is defined as a nearby area outside of PoLA/PoLB and south of the breakwater.

MM − \\iris\Woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Analysis\Fish\lalb_fish_boxplot_v2.pro Fri Apr 28 02:11:25 2017



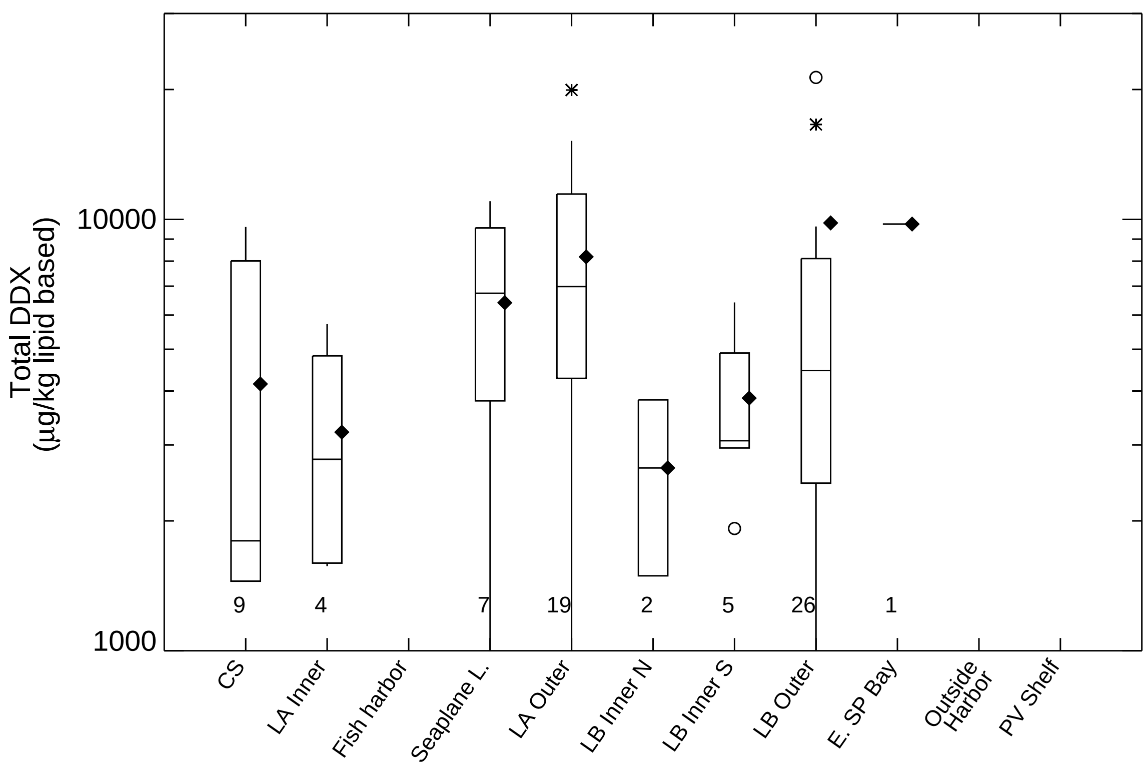


Figure 2−8c

Spatial Distribution of DDX Concentrations in Topsmelt

ANCHOR QEA

Data file used: PortOfLALB_Fish_20150902.xlsx. Field duplicates are averaged.
Totals are calculated as sum of detected congeners or aroclors, or half of highest detection limit if all congeners or are non−detects. High−Res Congener data plotted when paired high−res or low−res congener or aroclor data exists.
Fish data shown are for 2002−2014 samples. Fish data excluded: Cabrillo Pier (one station)
Tissue types include: Whole body. Lipid−based plot include fillet (all types) and whole body.
Outside Harbor (local background) is defined as a nearby area outside of PoLA/PoLB and south of the breakwater.

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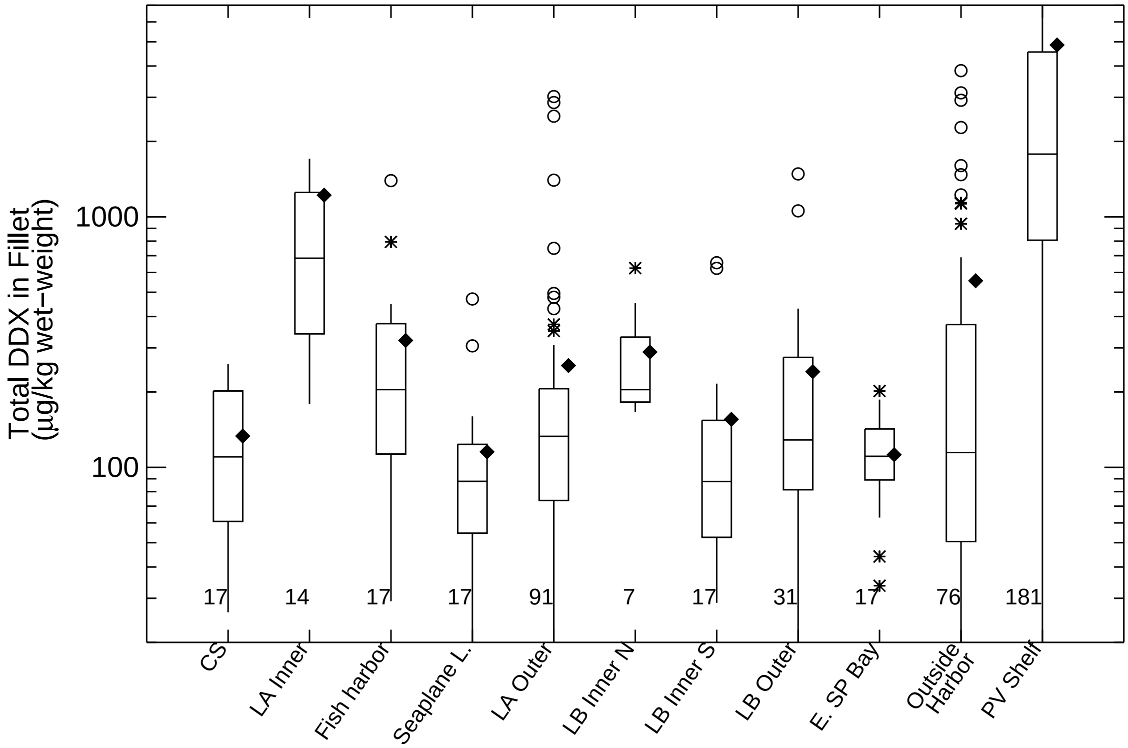

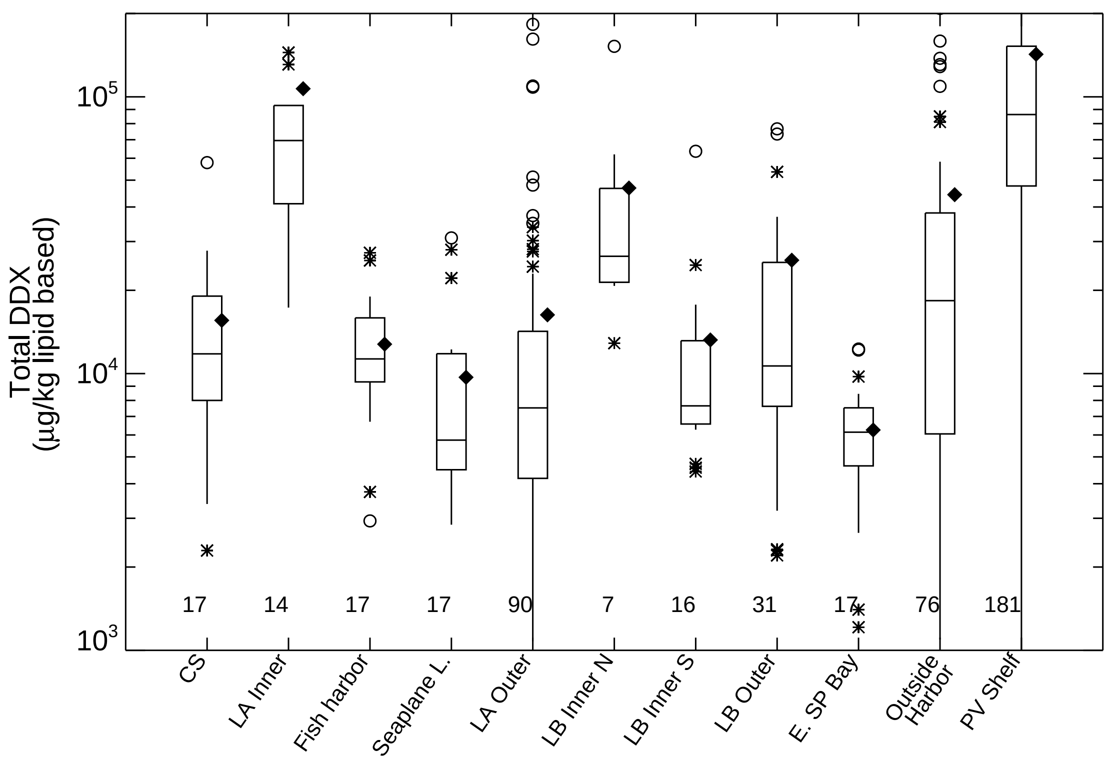

Figure 2−8d

Spatial Distribution of DDX Concentrations in White Croaker

ANCHOR QEA

Data file used: PortOfLALB_Fish_20150902.xlsx. Field duplicates are averaged.
Totals are calculated as sum of detected congeners or aroclors, or half of highest detection limit if all congeners or are non−detects. High−Res Congener data plotted when paired high−res or low−res congener or aroclor data exists.
Fish data shown are for 2002−2014 samples. Fish data excluded: Cabrillo Pier (one station)
Tissue types include: Fillet (all types). Lipid−based plot include fillet (all types) and whole body.
One White Croaker sample (IH5−FFF−7WC) with low lipid (0.05%) excluded.

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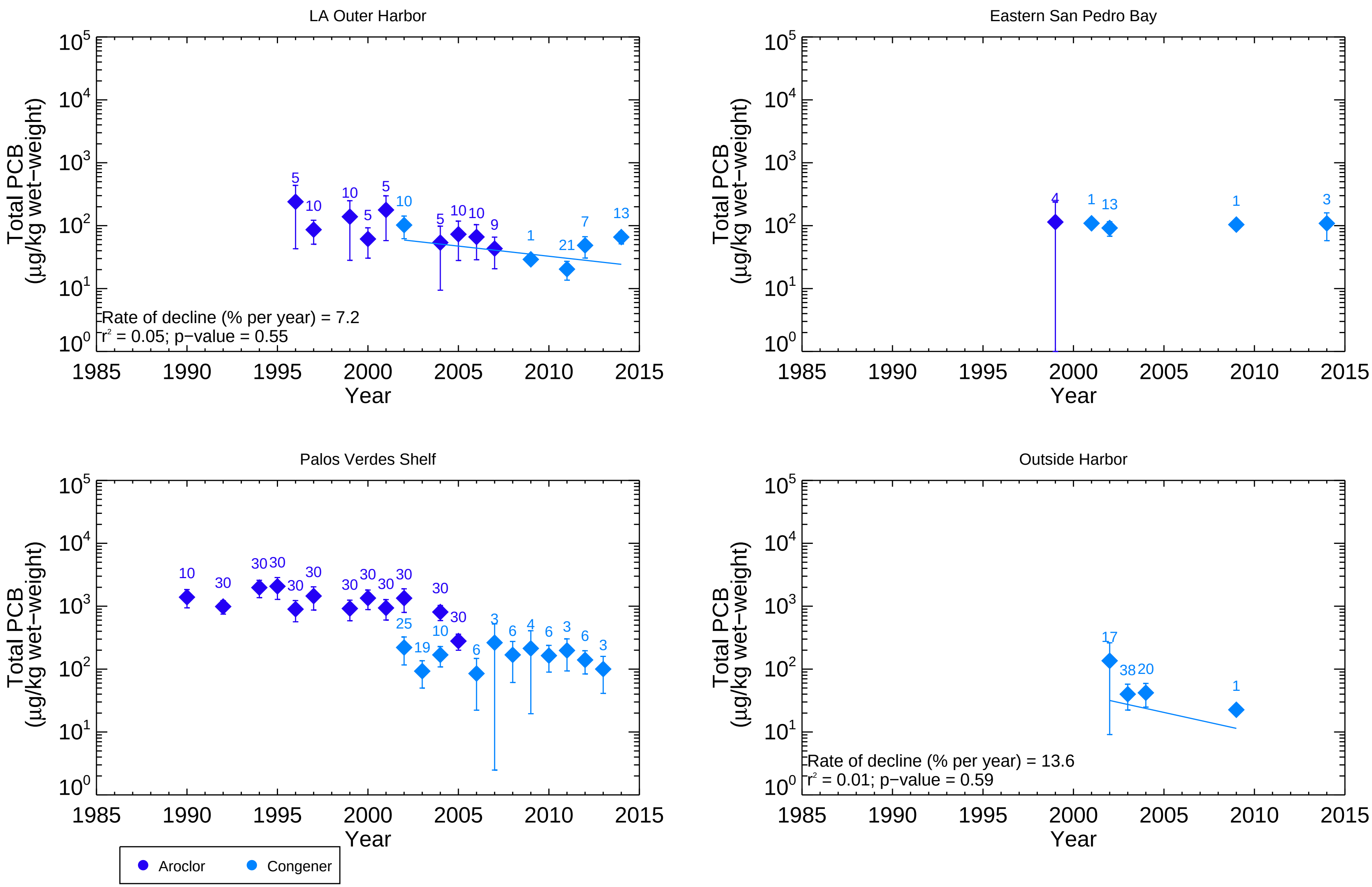

Figure 2−9

Temporal Patterns in Total PCB Concentration in White Croaker on a Wet−weight Basis

Data file used: PortOfLALB_Fish_20160720.xlsx. Field duplicates were averaged. Fillet (all types) preparations are used. Points are means +/− 2 standard errors. Sample counts are posted next to each point. Fish data excluded: Cabrillo Pier (four stations), one white croaker (IH5−FFF−7WC) with low lipid (0.05%), and 6 Aroclor non−detect total PCB results of 500 ppm. The regression and rate of decline were calculated using log−transformed data starting with 2002. Congener data are plotted when paired Aroclors and congener data are available.

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MM − \\iris\Woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Analysis\Fish\lalb_fish_temporal_by_subarea_for_report.pro Fri Apr 28 02:21:04 2017

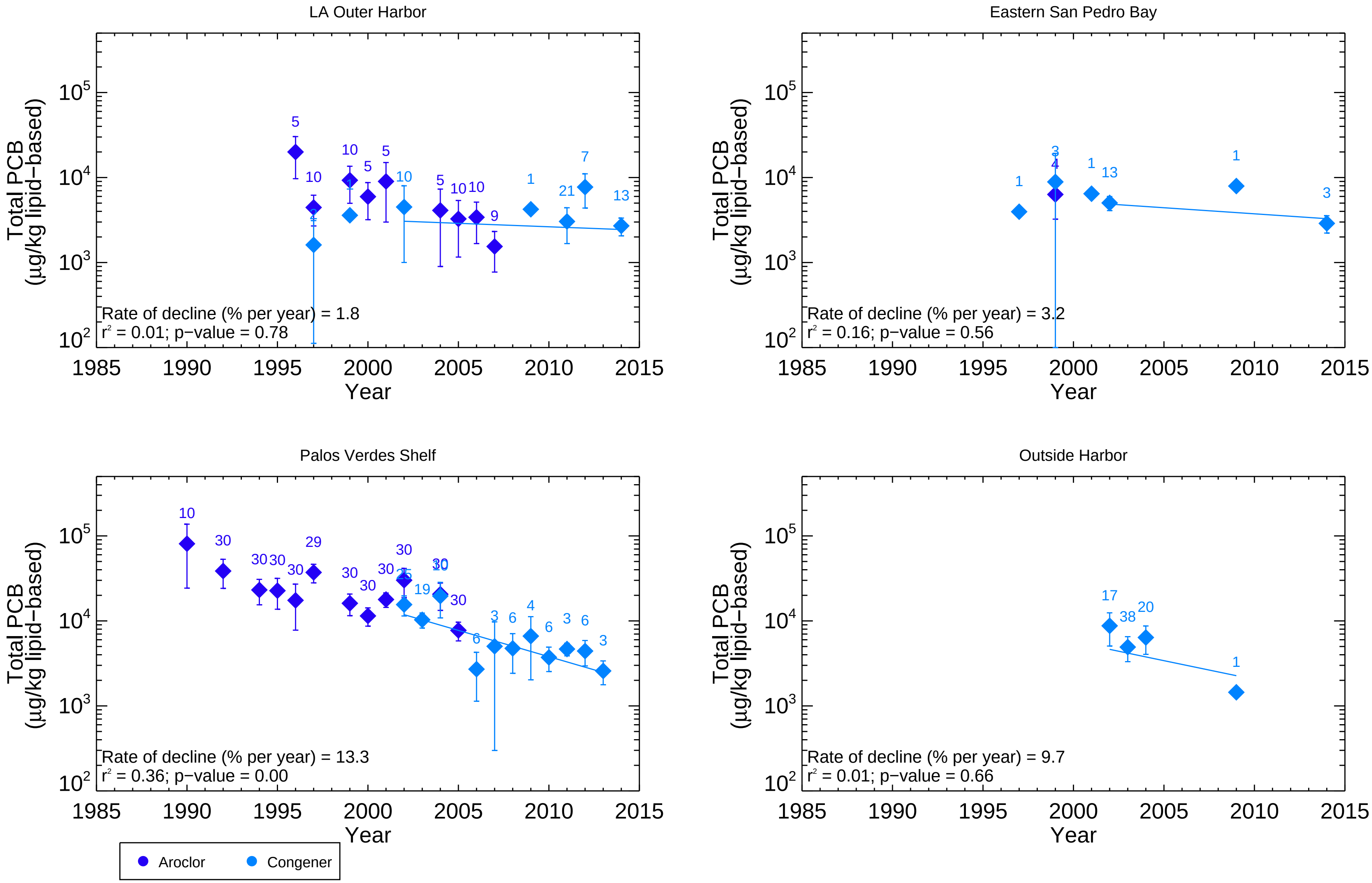

Figure 2−10

Temporal Patterns in Total PCB Concentration in White Croaker on a Lipid−normalized Basis

Data file used: PortOfLALB_Fish_20160720.xlsx. Field duplicates were averaged. Fillet (all types) and whole body preparations are used. Points are means +/− 2 standard errors. Sample counts are posted next to each point. Fish data excluded: Cabrillo Pier (four stations), one white croaker (IH5−FFF−7WC) with low lipid (0.05%), and 6 Aroclor non−detect total PCB results of 500 ppm. The regression and rate of decline were calculated using log−transformed data starting with 2002. Congener data are plotted when paired Aroclors and congener data are available.

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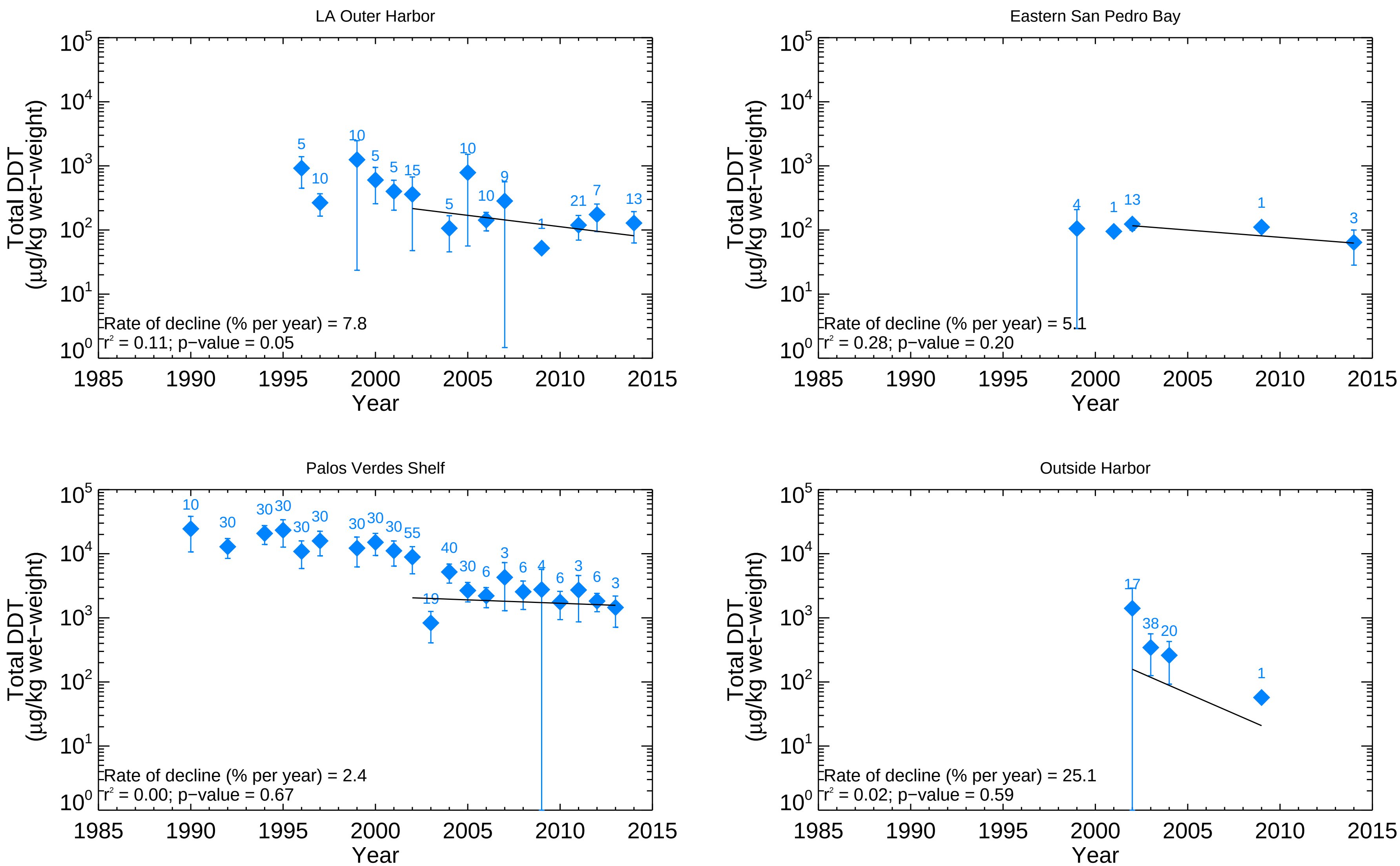

Figure 2−11

Temporal Patterns in Total DDX Concentration in White Croaker on a Wet−weight Basis

Data file used: PortOfLALB_Fish_20160720.xlsx. Field duplicates were averaged. Fillet (all types) preparations are used. Points are means +/− 2 standard errors. Sample counts are posted next to each point. Fish data excluded: Cabrillo Pier (four stations), one white croaker (IH5−FFF−7WC) with low lipid (0.05%), and 6 Aroclor non−detect total PCB results of 500 ppm. The regression and rate of decline were calculated using log−transformed data starting with 2002.

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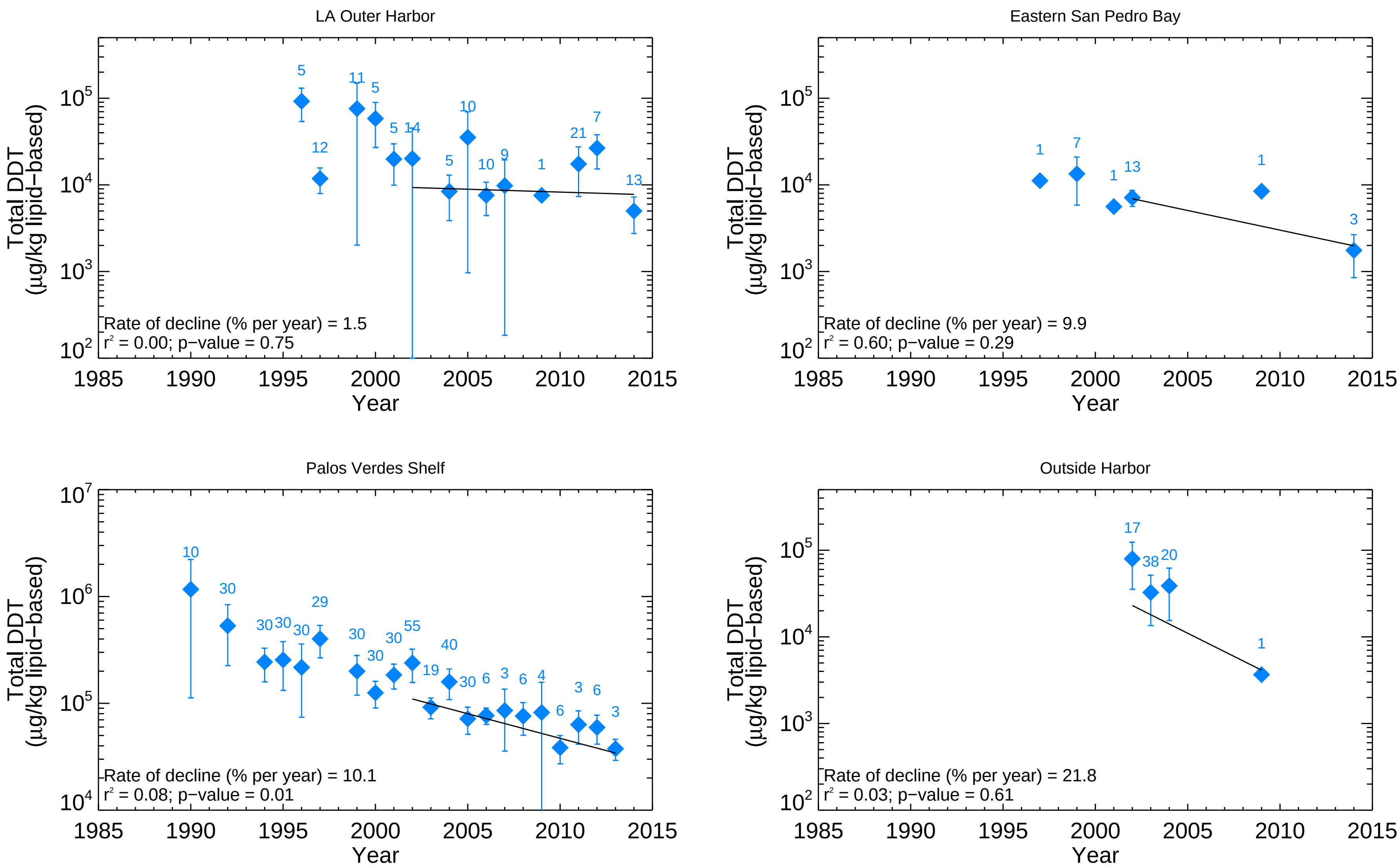

Figure 2−12

Temporal Patterns in Total DDX Concentration in White Croaker on a Lipid−normalized Basis

Data file used: PortOfLALB_Fish_20160720.xlsx. Field duplicates were averaged. Fillet (all types) and whole body preparations are used. Points are means +/− 2 standard errors. Sample counts are posted next to each point. Fish data excluded: Cabrillo Pier (four stations), one white croaker (IH5−FFF−7WC) with low lipid (0.05%), and 6 Aroclor non−detect total PCB results of 500 ppm. The regression and rate of decline were calculated using log−transformed data starting with 2002.

ANCHOR QEA

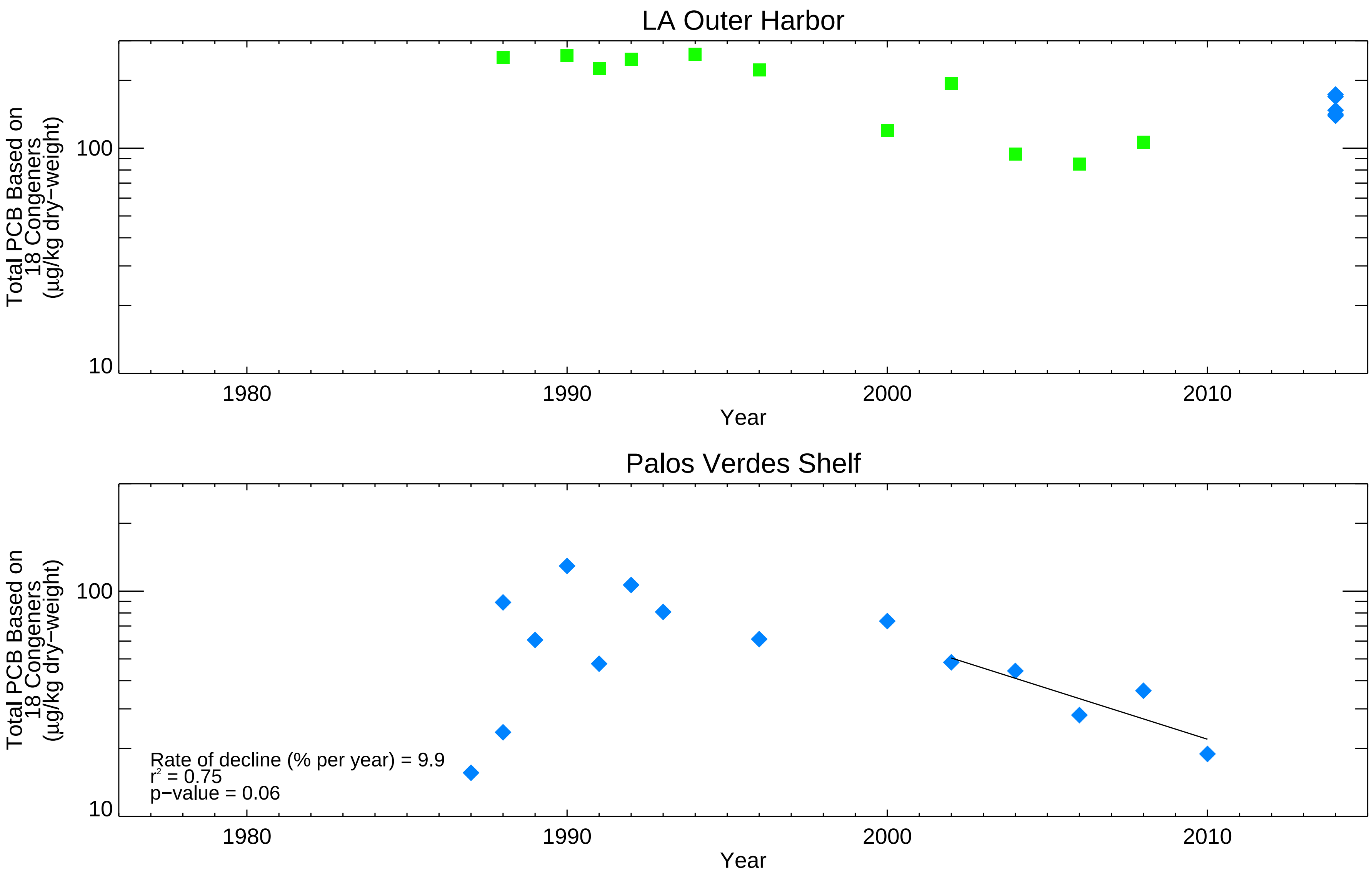

Figure 2−13a

Los Angeles Outer Harbor and Palos Verdes Shelf Mussel and Clam 18−Congener Total PCB over Time

Congeners summed for total PCBs prior to 2006 include 18 analytes;
total PCBs for samples collected in 2006 and later include these 18 analytes plus any coeluting congeners.
LA Outer Harbor data shown are from stations OA−01 and SPFP. Data file: PortOfLALB_Mussel_20160229.
The regression and rate of decline were calculated using log−transformed data starting with 2002.
Data from 2014 were converted from wet weight to dry weight using percent solids.

cf/ec − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Analysis\Mussel\lalb_mussel_tpcb_compare_forPortsPresentation_v2.pro Tue May 02 15:58:18 2017

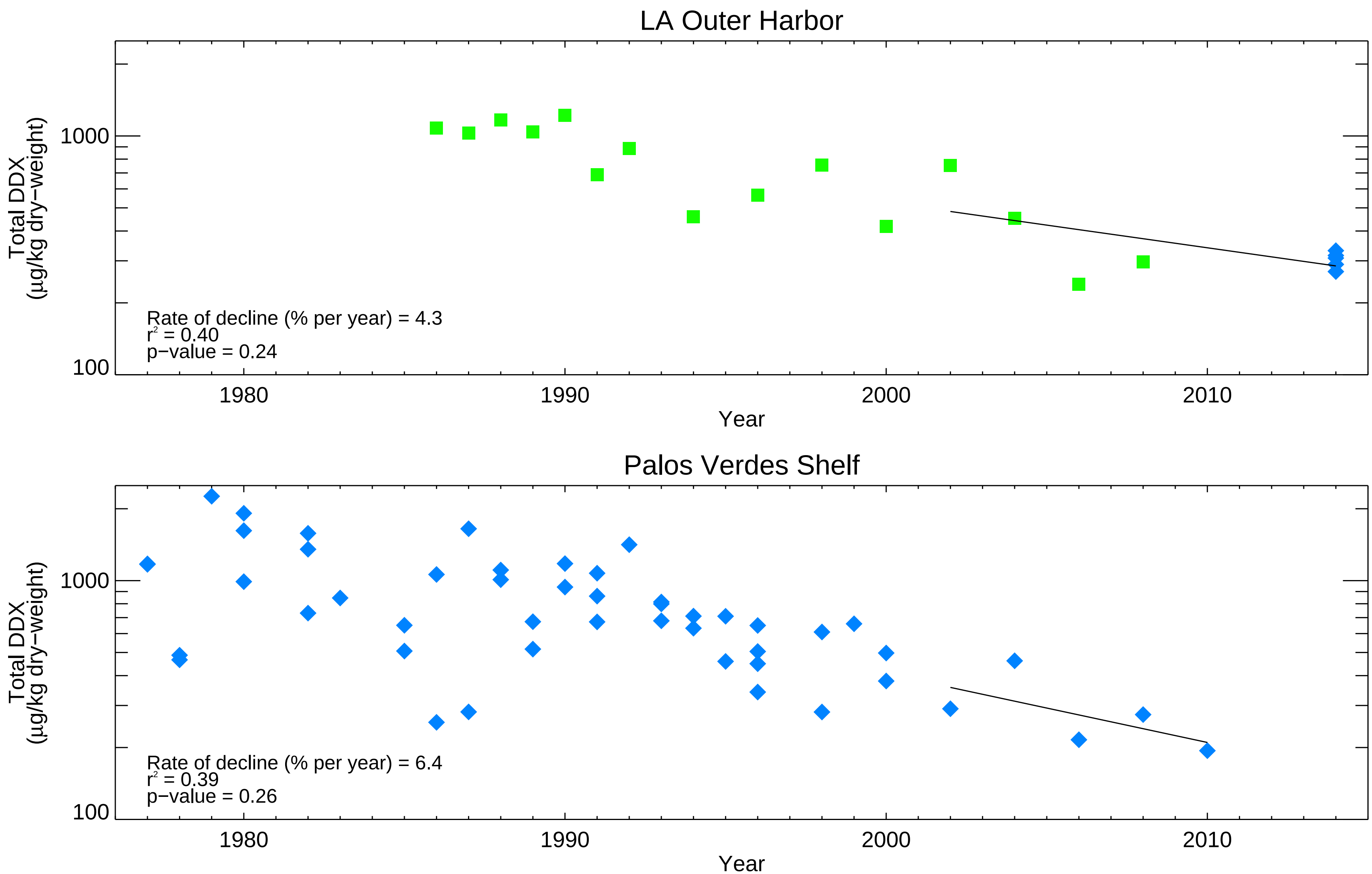

Figure 2−13b

Los Angeles Outer Harbor and Palos Verdes Shelf Mussel and Clam Total DDX over Time

ANCHOR QEA

Clam
Mussel

Species plotted: California mussel (resident), California mussel (transplanted), Mussel, White sand macoma (clam).
LA Outer Harbor data are from stations OA−01 (2014) and SPFP (1986−2008). Data file: PortOfLALB_Mussel_20160229.
Data from 2014 were converted from wet weight to dry weight using percent solids.
The regression and rate of decline were calculated using log−transformed data starting with 2002.

EC − \\iris\Woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Analysis\Mussel\lalb_mussel_tddx_compare_forPortsPresentation_v2.pro Fri Apr 28 02:20:25 2017

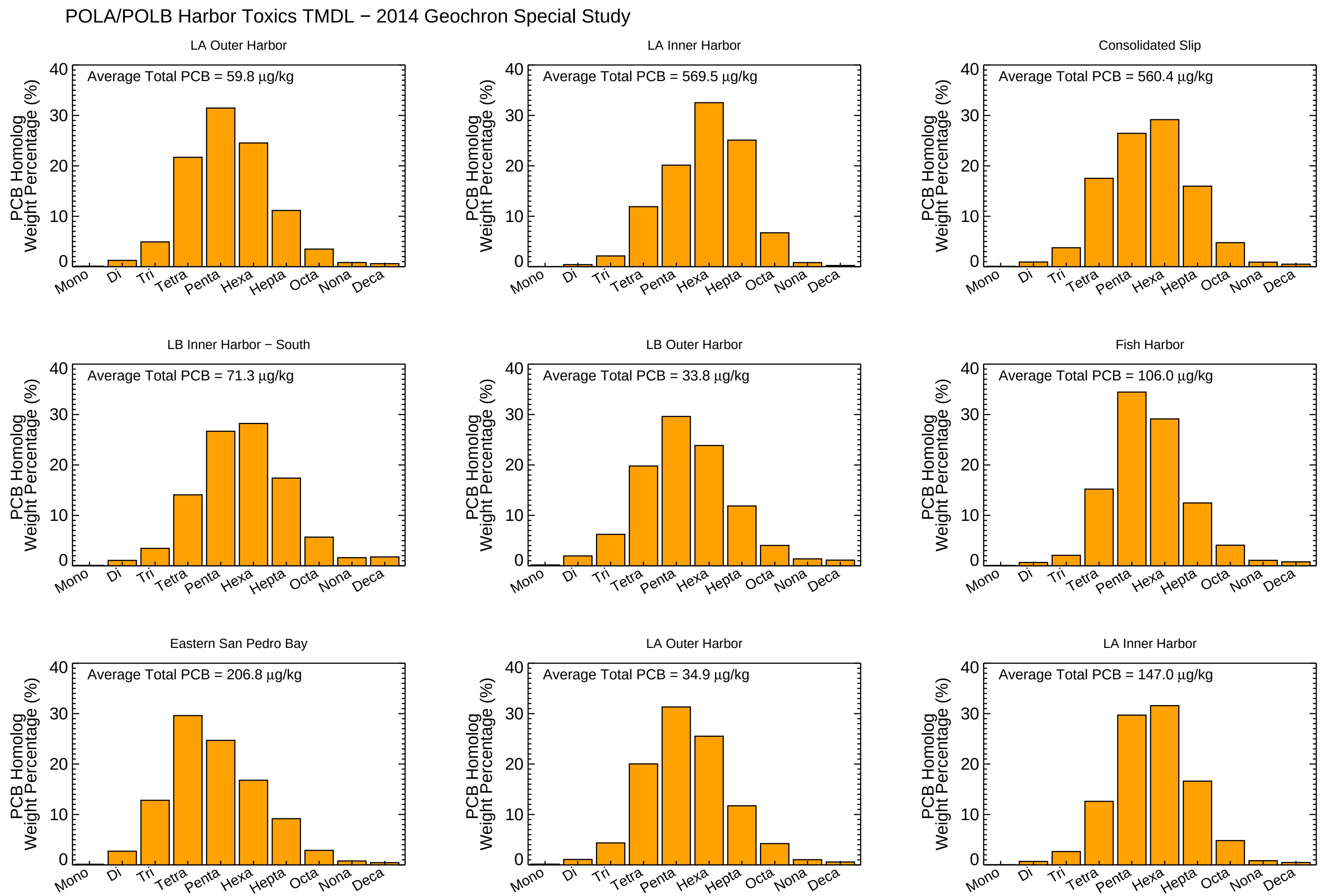

Figure 2−14

Homolog Histogram Plots of Surface Sediment Samples by Zone

Data file used: PortOfLALB_Sediment_20160720.xlsx. Surface sediment is top 16 cm. Data are for 2014 samples. Field duplicates are averaged. Coeluting congeners are included. Non−detect congeners are excluded. FH−SS−05−0−5−20141018 is excluded from the analysis.

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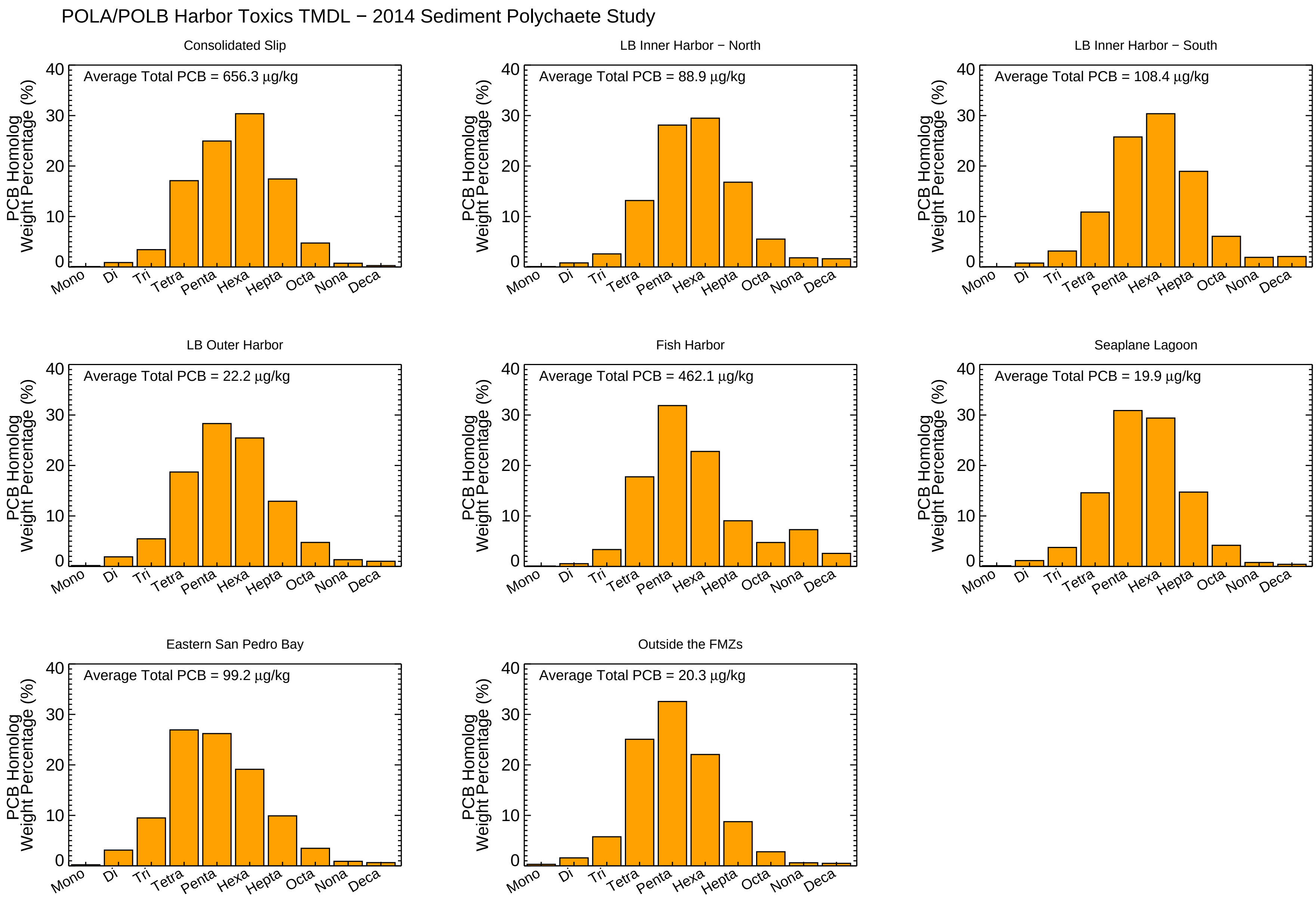


Figure 2−14

Homolog Histogram Plots of Surface Sediment Samples by Zone

Data file used: PortOfLALB_Sediment_20160720.xlsx. Surface sediment is top 16 cm. Data are for 2014 samples. Field duplicates are averaged. Coeluting congeners are included. Non−detect congeners are excluded. FH−SS−05−0−5−20141018 is excluded from the analysis.

ANCHOR QEA

MM − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Analysis\Histograms\lalb_homolog_congener_histograms_by_zones.pro Wed Apr 19 00:17:12 2017

POLA/POLB Harbor Toxics TMDL − 2014 Food Web Special Study, PCB Congeners (µg/kg)

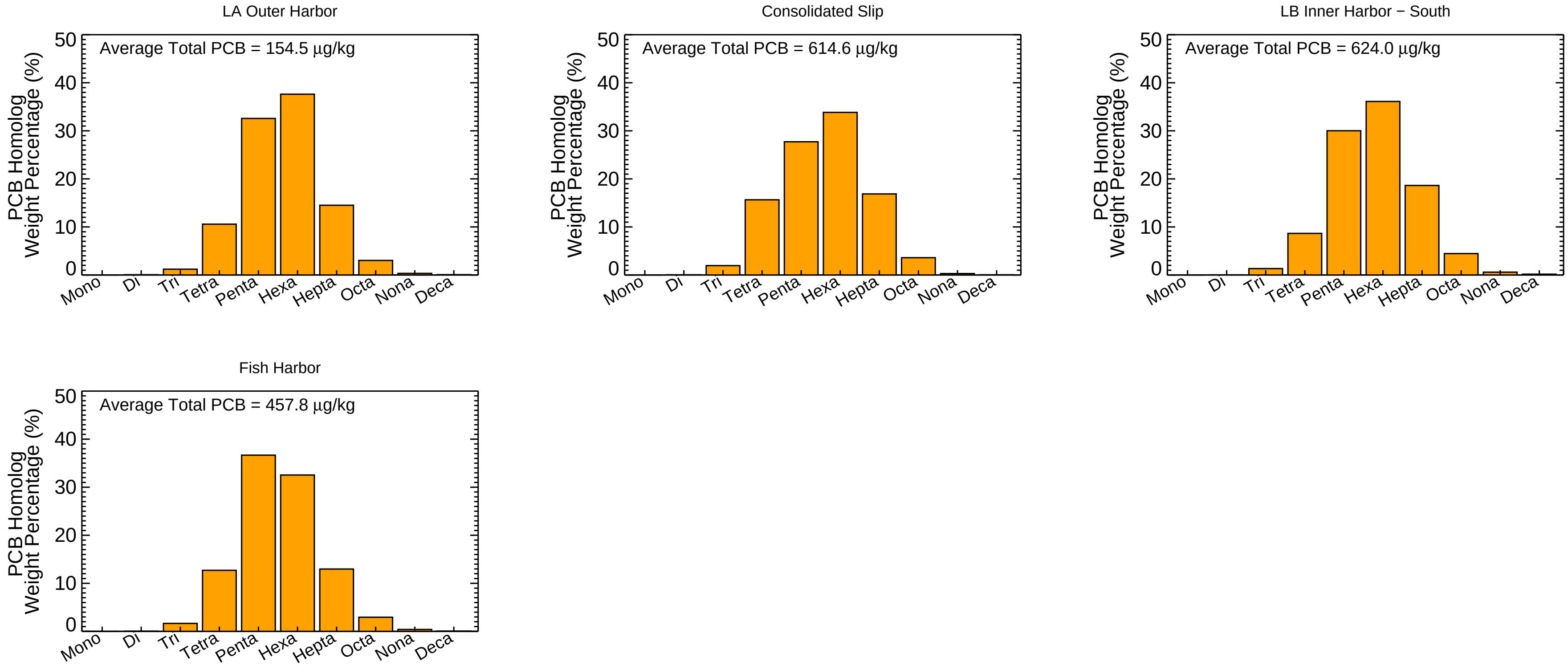


Figure 2−15a

PCB Homolog Histogram Plots of White Surfperch Samples by Zone

Data file used: PortOfLALB_Fish_20160720.xlsx. Field duplicates are averaged.
Totals are calculated as sum of detected congeners or aroclors, or half of highest detection limit if all congeners or aroclors are non−detects.
Coeluting congeners are included. Non−detect congeners are excluded. Tissue types include: Whole body. 2014 samples used.

ANCHOR QEA

MM − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Analysis\Histograms\lalb_fish_ddx_congener_histograms_by_zones.pro Thu Apr 27 17:04:04 2017

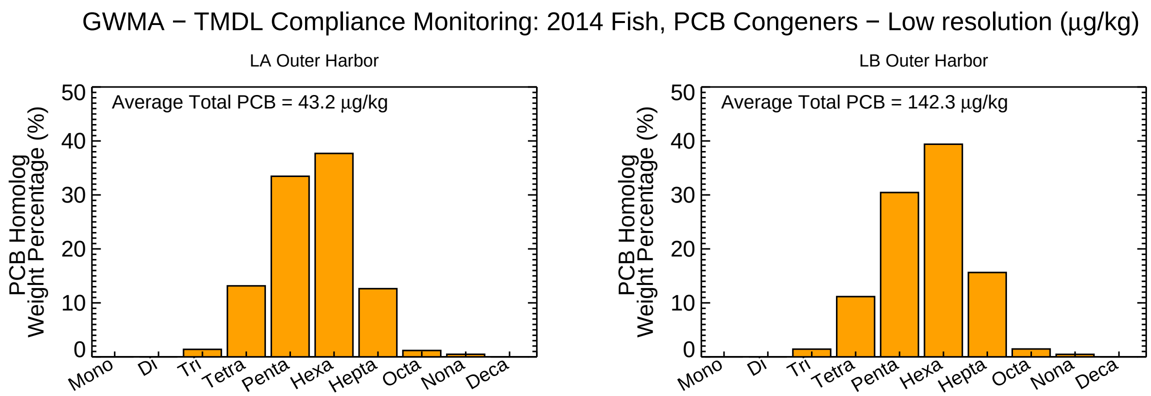


Figure 2−15a

PCB Homolog Histogram Plots of White Surfperch Samples by Zone

Data file used: PortOfLALB_Fish_20160720.xlsx. Field duplicates are averaged.
Totals are calculated as sum of detected congeners or aroclors, or half of highest detection limit if all congeners or aroclors are non−detects.
Coeluting congeners are included. Non−detect congeners are excluded. Tissue types include: Whole body. 2014 samples used.

ANCHOR QEA

MM − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Analysis\Histograms\lalb_fish_ddx_congener_histograms_by_zones.pro Thu Apr 27 17:04:04 2017

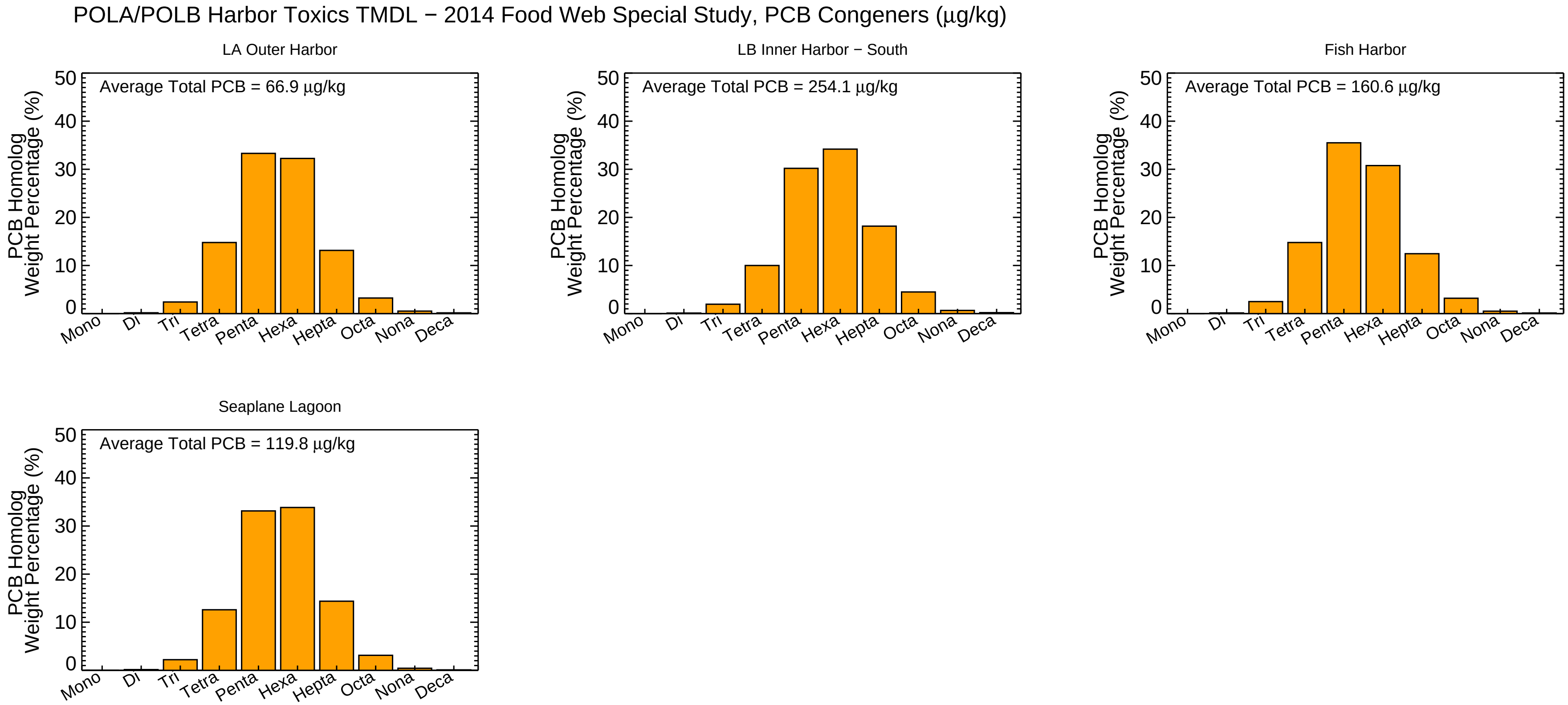


Figure 2−15b

PCB Homolog Histogram Plots of White Croaker Samples by Zone

Data file used: PortOfLALB_Fish_20160720.xlsx. Field duplicates are averaged.
Totals are calculated as sum of detected congeners or aroclors, or half of highest detection limit if all congeners or aroclors are non−detects.
Coeluting congeners are included. Non−detect congeners are excluded. Tissue types include: Fillet (all types). 2014 samples used.

ANCHOR QEA

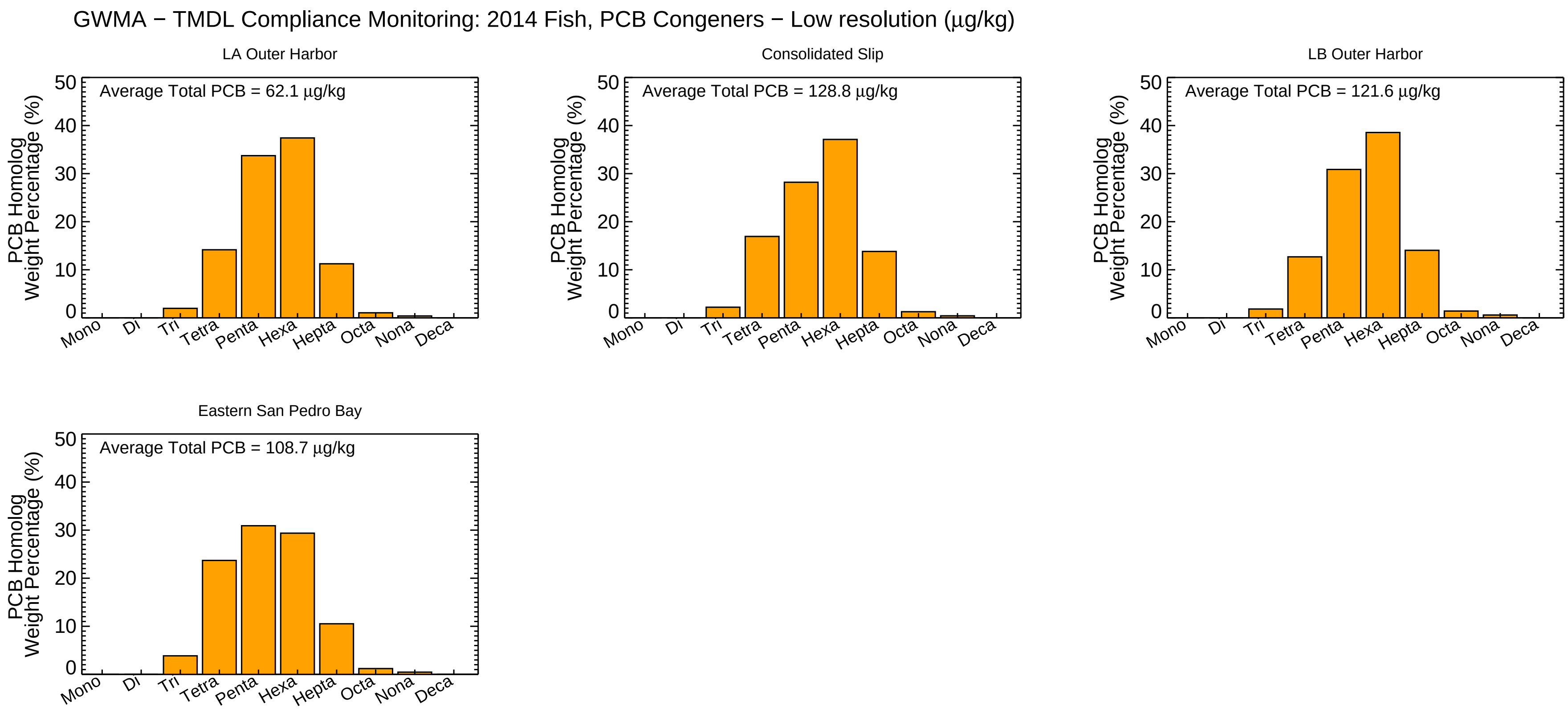


Figure 2−15b

PCB Homolog Histogram Plots of White Croaker Samples by Zone

Data file used: PortOfLALB_Fish_20160720.xlsx. Field duplicates are averaged.
Totals are calculated as sum of detected congeners or aroclors, or half of highest detection limit if all congeners or aroclors are non−detects.
Coeluting congeners are included. Non−detect congeners are excluded. Tissue types include: Fillet (all types). 2014 samples used.

ANCHOR QEA

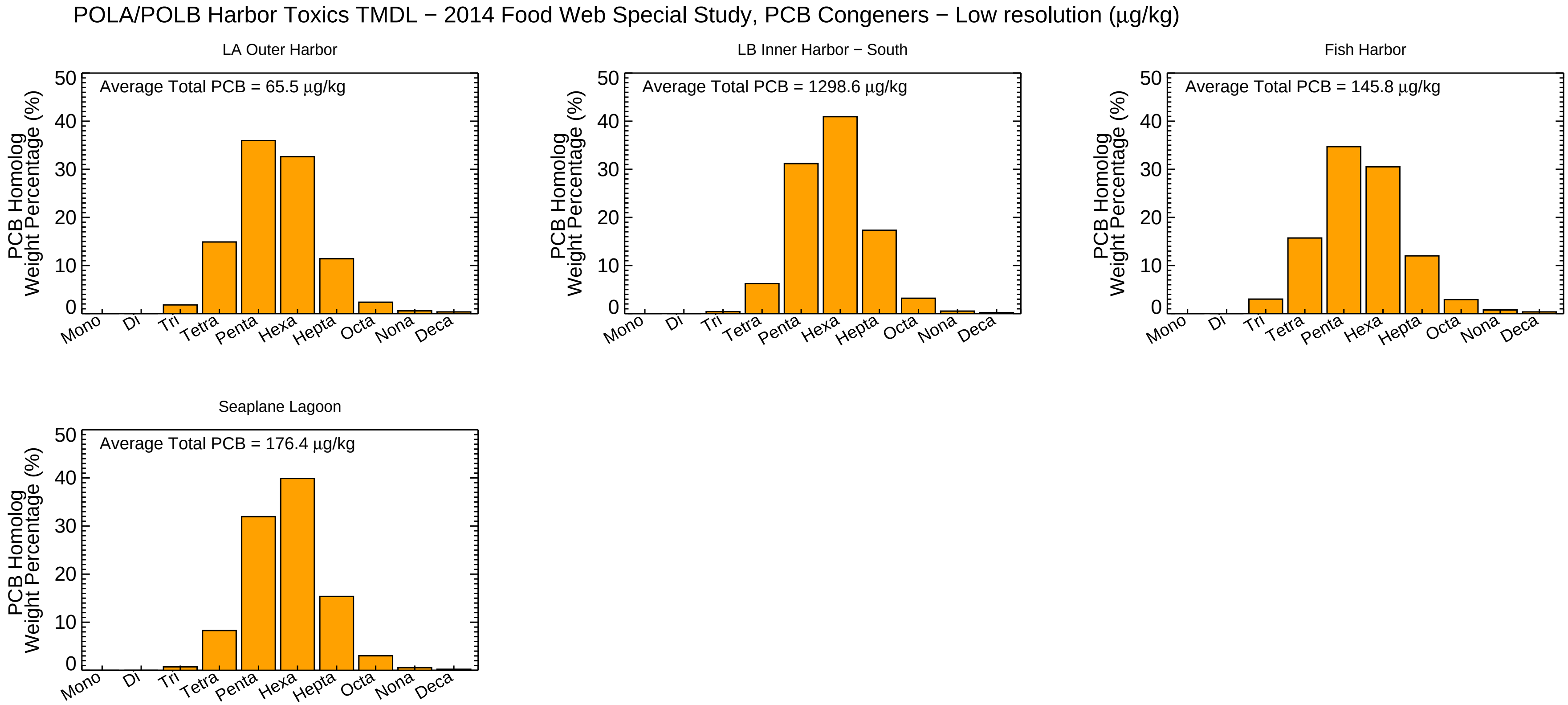


Figure 2−15b

PCB Homolog Histogram Plots of White Croaker Samples by Zone

Data file used: PortOfLALB_Fish_20160720.xlsx. Field duplicates are averaged.
Totals are calculated as sum of detected congeners or aroclors, or half of highest detection limit if all congeners or aroclors are non−detects.
Coeluting congeners are included. Non−detect congeners are excluded. Tissue types include: Fillet (all types). 2014 samples used.

ANCHOR QEA

MM − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Analysis\Histograms\lalb_fish_ddx_congener_histograms_by_zones.pro Thu Apr 27 17:04:03 2017

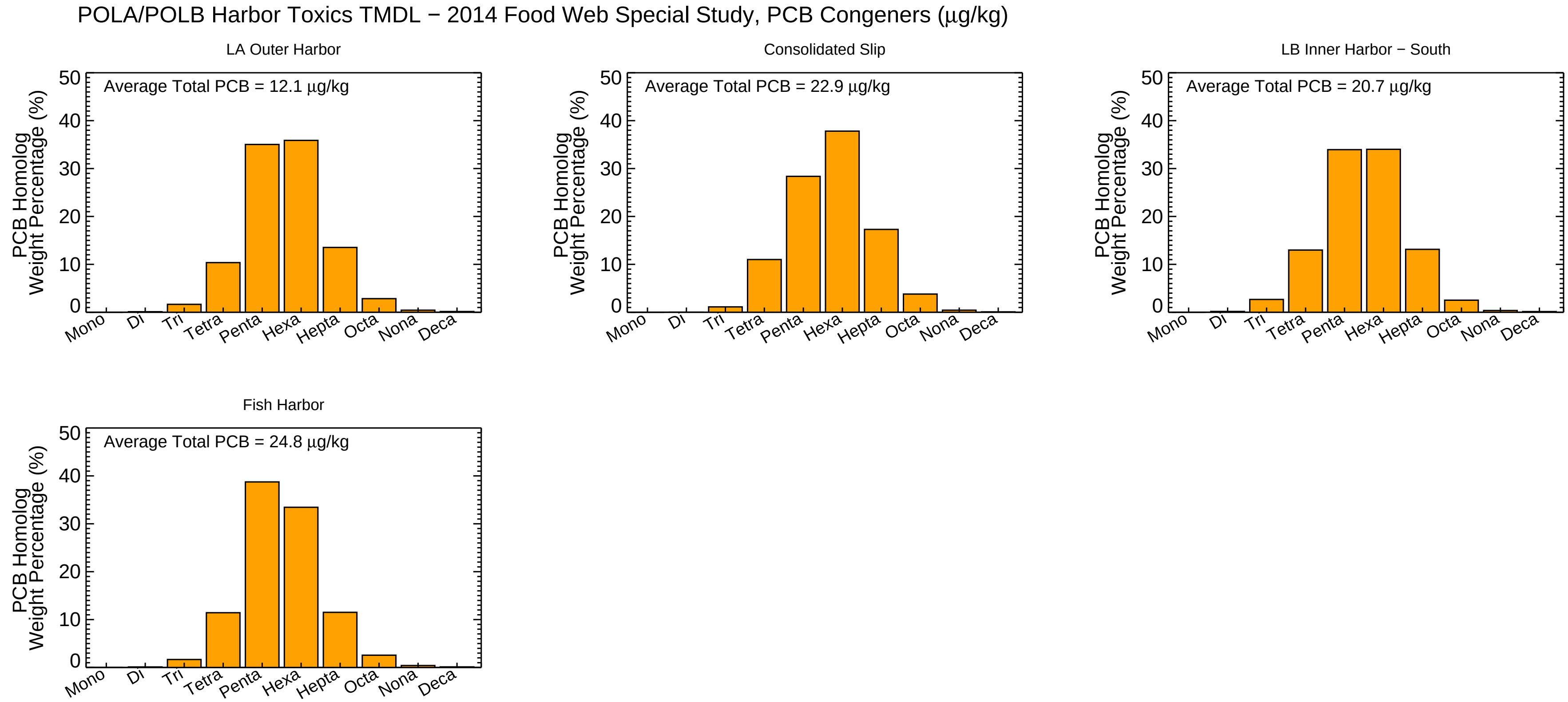


Figure 2−15c

PCB Homolog Histogram Plots of California Halibut Samples by Zone

Data file used: PortOfLALB_Fish_20160720.xlsx. Field duplicates are averaged.
Totals are calculated as sum of detected congeners or aroclors, or half of highest detection limit if all congeners or aroclors are non−detects.
Coeluting congeners are included. Non−detect congeners are excluded. Tissue types include: Fillet (all types). 2014 samples used.

MM − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Analysis\Histograms\lalb_fish_ddx_congener_histograms_by_zones.pro Thu Apr 27 17:04:02 2017

GWMA − TMDL Compliance Monitoring: 2014 Fish, PCB Congeners − Low resolution (µg/kg)

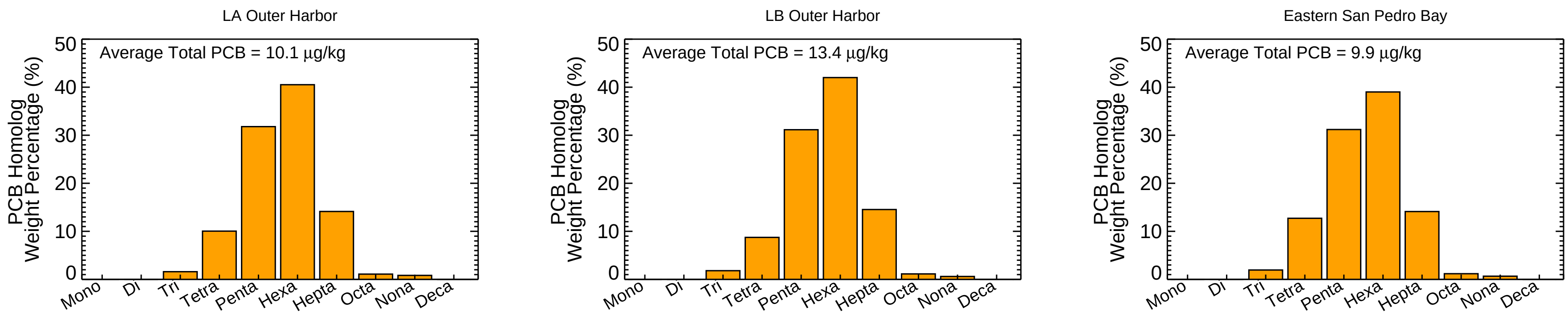


Figure 2−15c

PCB Homolog Histogram Plots of California Halibut Samples by Zone

Data file used: PortOfLALB_Fish_20160720.xlsx. Field duplicates are averaged.
Totals are calculated as sum of detected congeners or aroclors, or half of highest detection limit if all congeners or aroclors are non−detects.
Coeluting congeners are included. Non−detect congeners are excluded. Tissue types include: Fillet (all types). 2014 samples used.

ANCHOR QEA

POLA/POLB Harbor Toxics TMDL − 2014 Food Web Special Study, PCB Congeners − Low resolution (µg/kg)

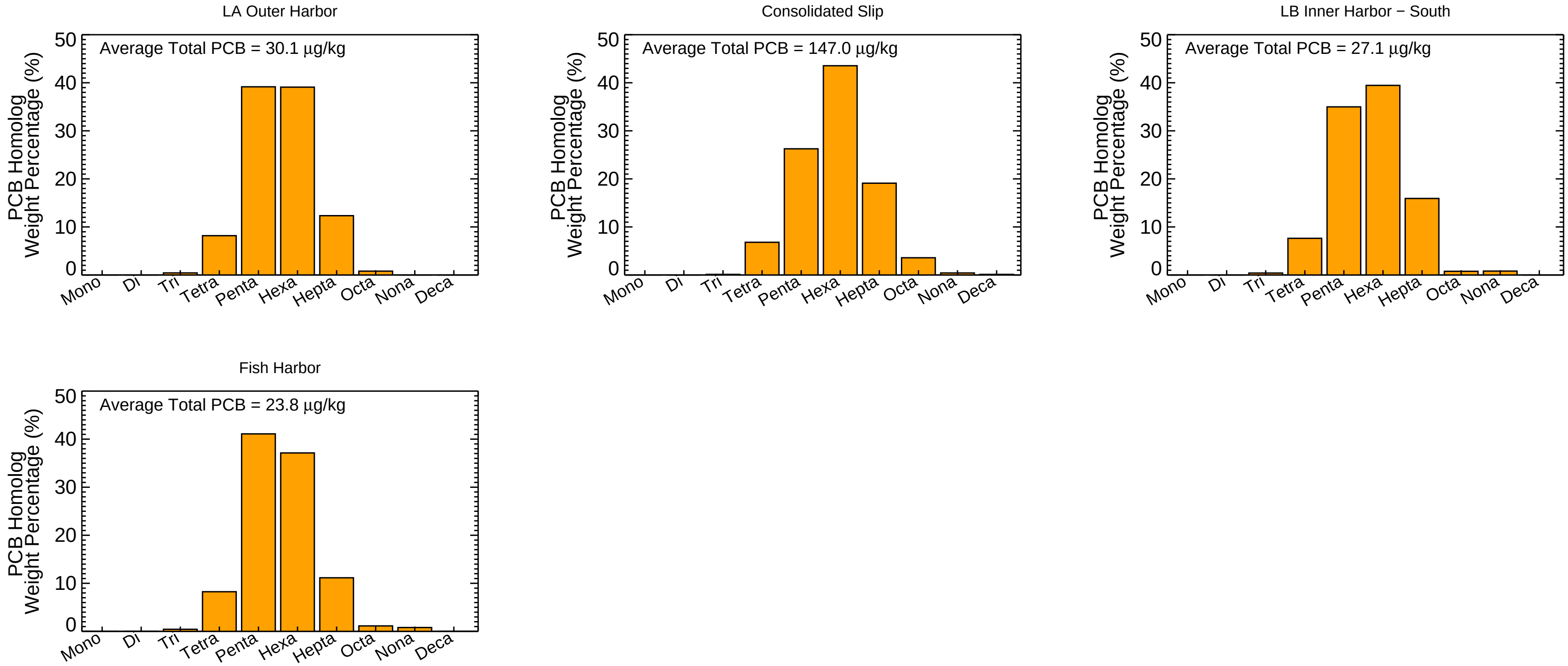


Figure 2−15c

PCB Homolog Histogram Plots of California Halibut Samples by Zone

Data file used: PortOfLALB_Fish_20160720.xlsx. Field duplicates are averaged.
Totals are calculated as sum of detected congeners or aroclors, or half of highest detection limit if all congeners or aroclors are non−detects.
Coeluting congeners are included. Non−detect congeners are excluded. Tissue types include: Fillet (all types). 2014 samples used.

ANCHOR QEA

MM − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Analysis\Histograms\lalb_fish_ddx_congener_histograms_by_zones.pro Thu Apr 27 17:04:02 2017

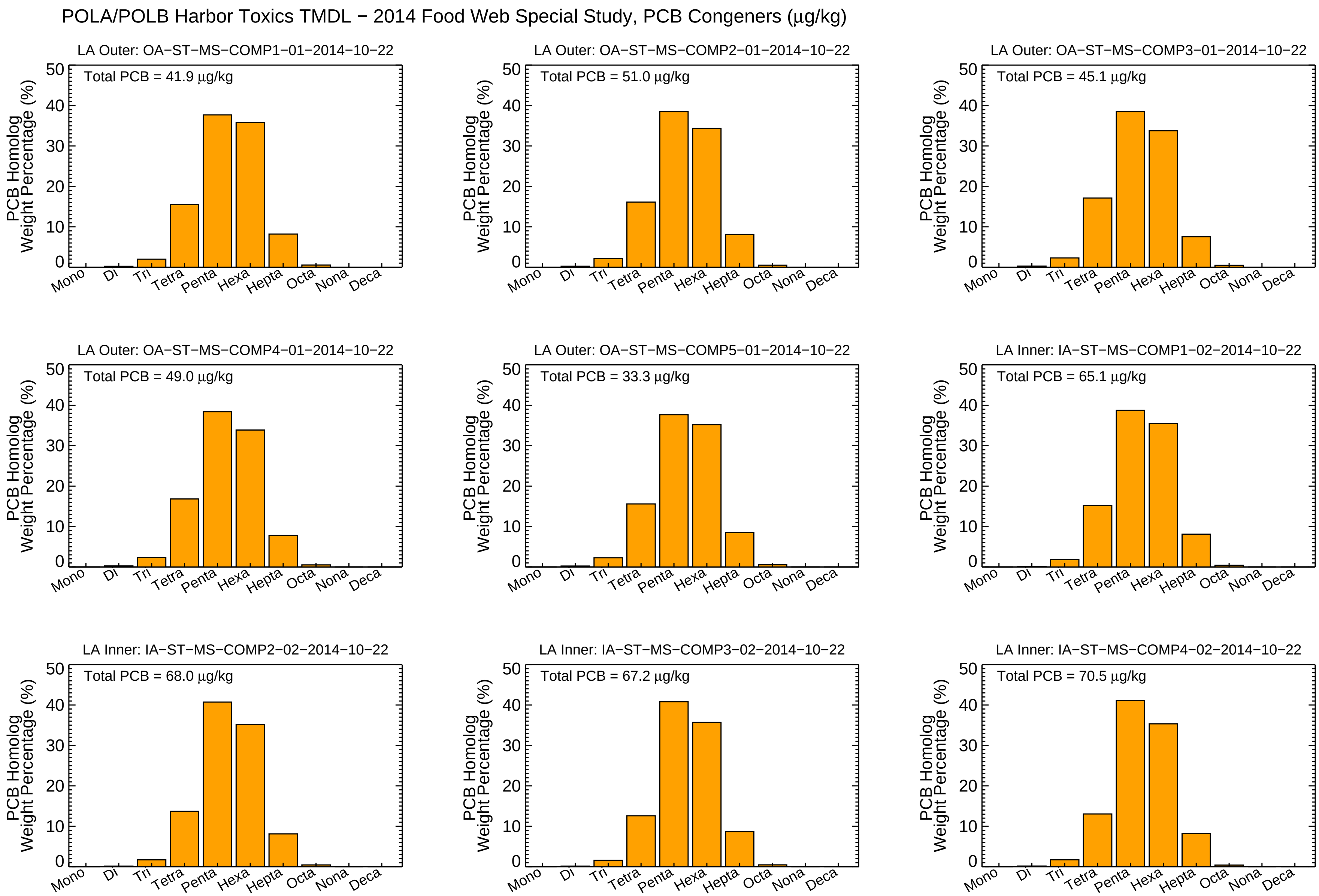


Figure 2−16

PCB Homolog Histogram Plots of 2014 Mussel Samples

ANCHOR QEA

Data file used: PortOfLALB_Mussel_20160720.xlsx. 2014 samples are shown.
Totals are calculated as sum of detected congeners or aroclors, or half of highest detection limit if all congeners or aroclors are non−detects.
Species plotted: Mussel. Coeluting congeners are included. Non−detect congeners are excluded.

MM − \\iris\Woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Analysis\Histograms\lalb_mussel_homolog_congener_histograms.pro Fri Apr 28 01:40:35 2017

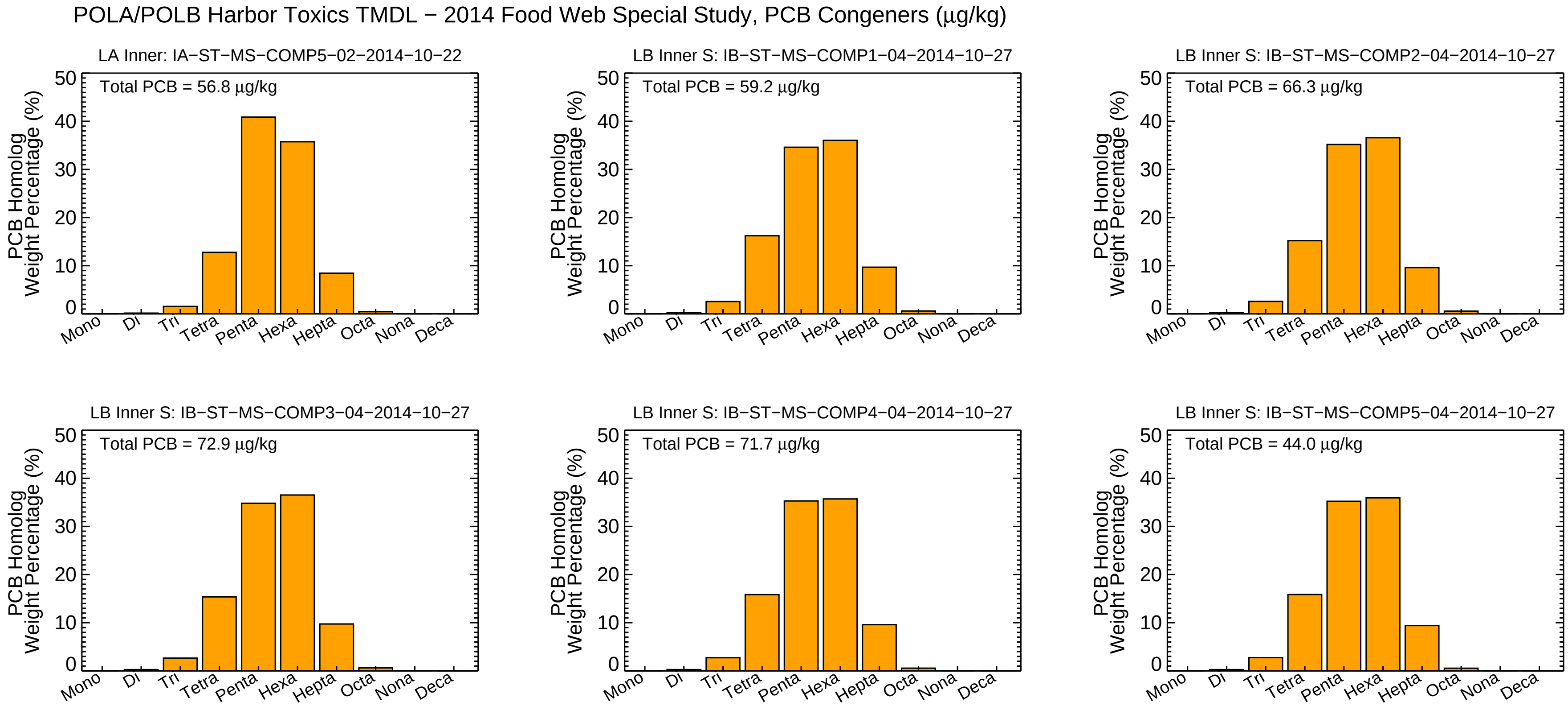


Figure 2−16

PCB Homolog Histogram Plots of 2014 Mussel Samples

Data file used: PortOfLALB_Mussel_20160720.xlsx. 2014 samples are shown.
Totals are calculated as sum of detected congeners or aroclors, or half of highest detection limit if all congeners or aroclors are non−detects.
Species plotted: Mussel. Coeluting congeners are included. Non−detect congeners are excluded.

ANCHOR QEA

MM − \\iris\Woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Analysis\Histograms\lalb_mussel_homolog_congener_histograms.pro Fri Apr 28 01:40:35 2017

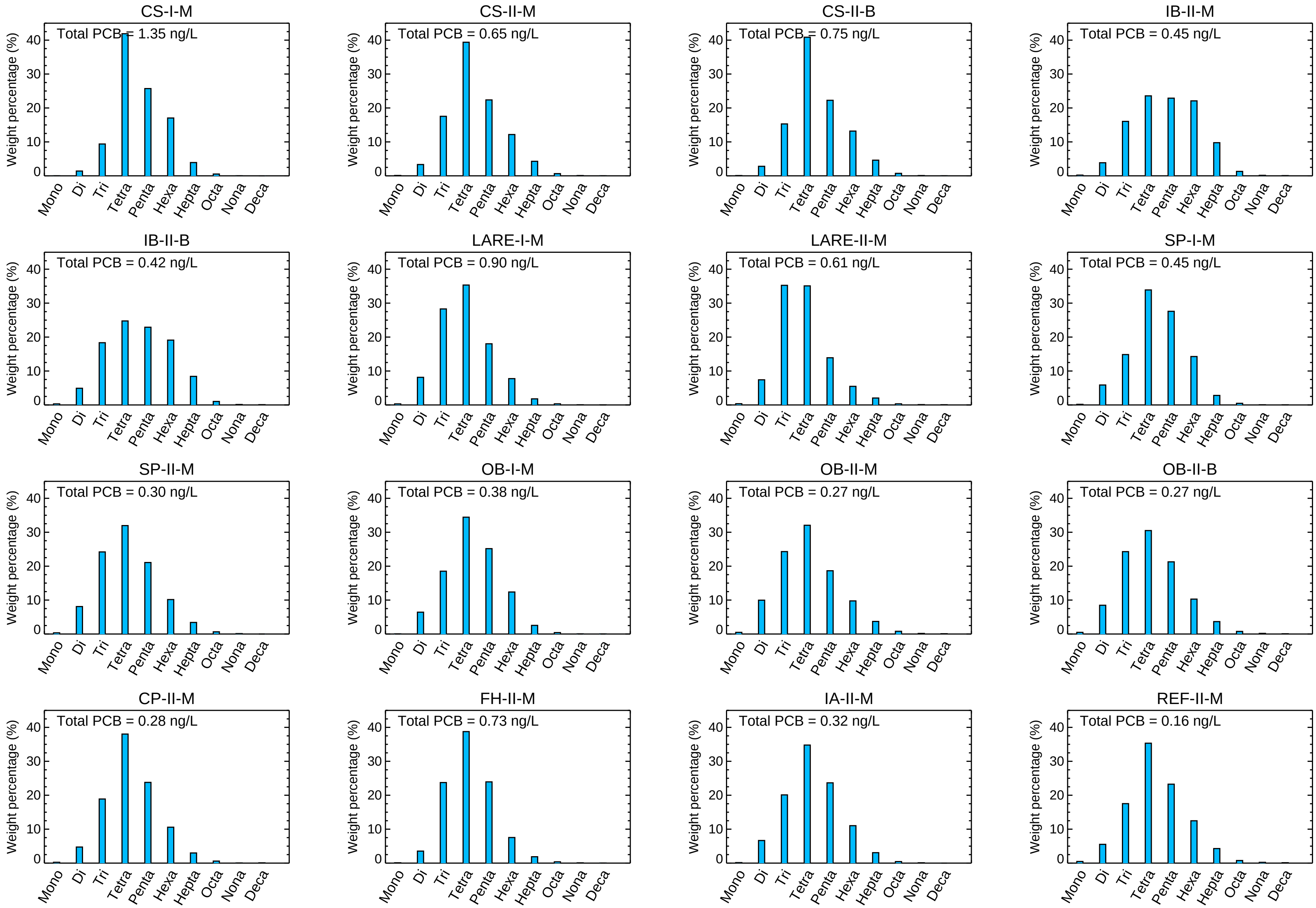


Figure 2-17a

PCB Homolog Distributions for Low Detection Limit Freely Dissolved Column Data from Events 1 and 2

Sampling Events 1 and 2 took place in February 2014 and January 2015, respectively.
Location ID: -I and -II indicate Event 1 and 2, and -M and -B indicate sampling from middle and bottom depths of the water column.
Non-detect concentrations are replaced with zero, or one half of the maximum detection limit if all components are non-detect.
The field duplicate from Event 1 is not included in the figure. The field duplicate was lost in Event 2.
Data file used: PortOfLALB_LDL_Event1_Event2_20150615.xlsx

ANCHOR QEA

XL/EC - \\austin2\Austin\D_drive\Projects\Ports_LA-LB\Harbor_Toxics_TMDL\Special_Studies\Low detection water sampling\Analysis\XLu_LDL Data Analysis\Data analysis\PortLA_LB_LDL_PCBhomolog_weight_fraction_barplot_for_report.pro Mon Apr 24 12:3 9:20 2017

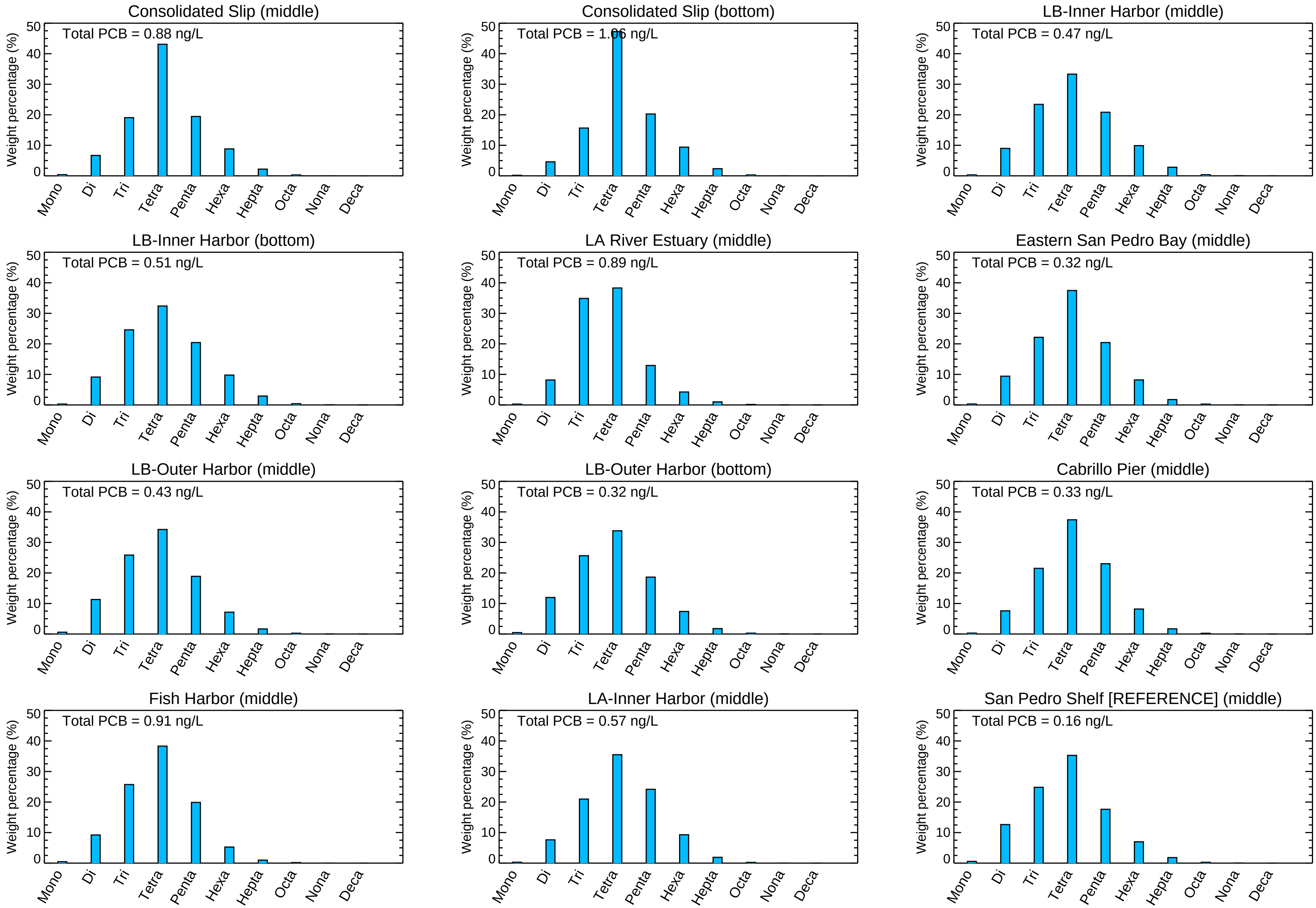


Figure 2-17b

PCB Homolog Distributions for Low Detection Limit Freely Dissolved Water Column Data from Event 3

Sampling Event 3 was conducted in May and June 2015. Water concentrations were calculated from SPME data and corrected for equilibrium.
Non-detect concentrations are replaced with zero. Field duplicate results at LB-Inner Harbor were averaged with parent results.
Samples were collected in the middle and bottom of the water column.
Co-eluting congeners were assigned the homolog group of the first listed congener.
Data file: POLALB_LDL_Event3_SPME_20150818

ANCHOR QEA

EC - \\austin2\Austin\D_drive\Projects\Ports_LA-LB\Harbor_Toxics_TMDL\Special_Studies\Low detection water sampling\Analysis\Event 3\env_samp\PCB_DDX_homolog_barplot\LALB_LDL_Ph3_PCB_DDX_homolog_barplot.pro Mon Apr 24 12:42:49 2017

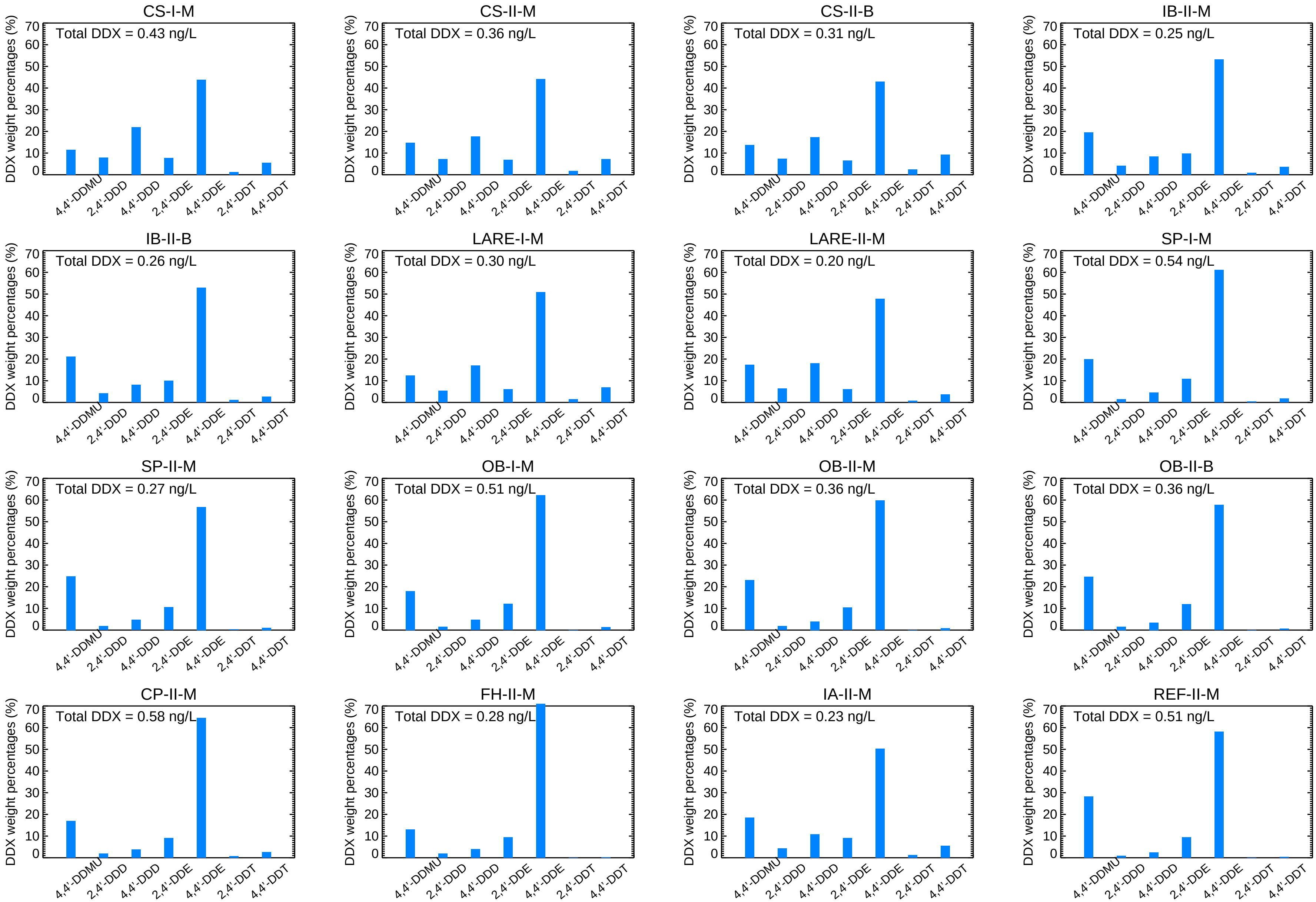


Figure 2-18a

DDX Homolog Distributions for Low Detection Limit Freely Dissolved Water Column Data from Events 1 and 2

Sampling Events 1 and 2 were conducted in February 2014 and January 2015, respectively.
Location ID: -I and -II indicate Event 1 and 2, and -M and -B indicate sampling from middle and bottom depths of the water column.
Non-detect concentrations are replaced with zero.
The field duplicate from Event 1 is not included in the figure. The field duplicate was lost in Event 2.
Data file used: PortOfLALB_LDL_Event1_Event2_20150615.xlsx

ANCHOR QEA

XL/EC - \\austin2\Austin\D_drive\Projects\Ports_LA-LB\Harbor_Toxics_TMDL\Special_Studies\Low detection water sampling\Analysis\XLu_LDL Data Analysis\Data analysis\PortLA_LB_LDL_congeners_barplot_for_report.pro Mon Apr 24 12:39:17 2017

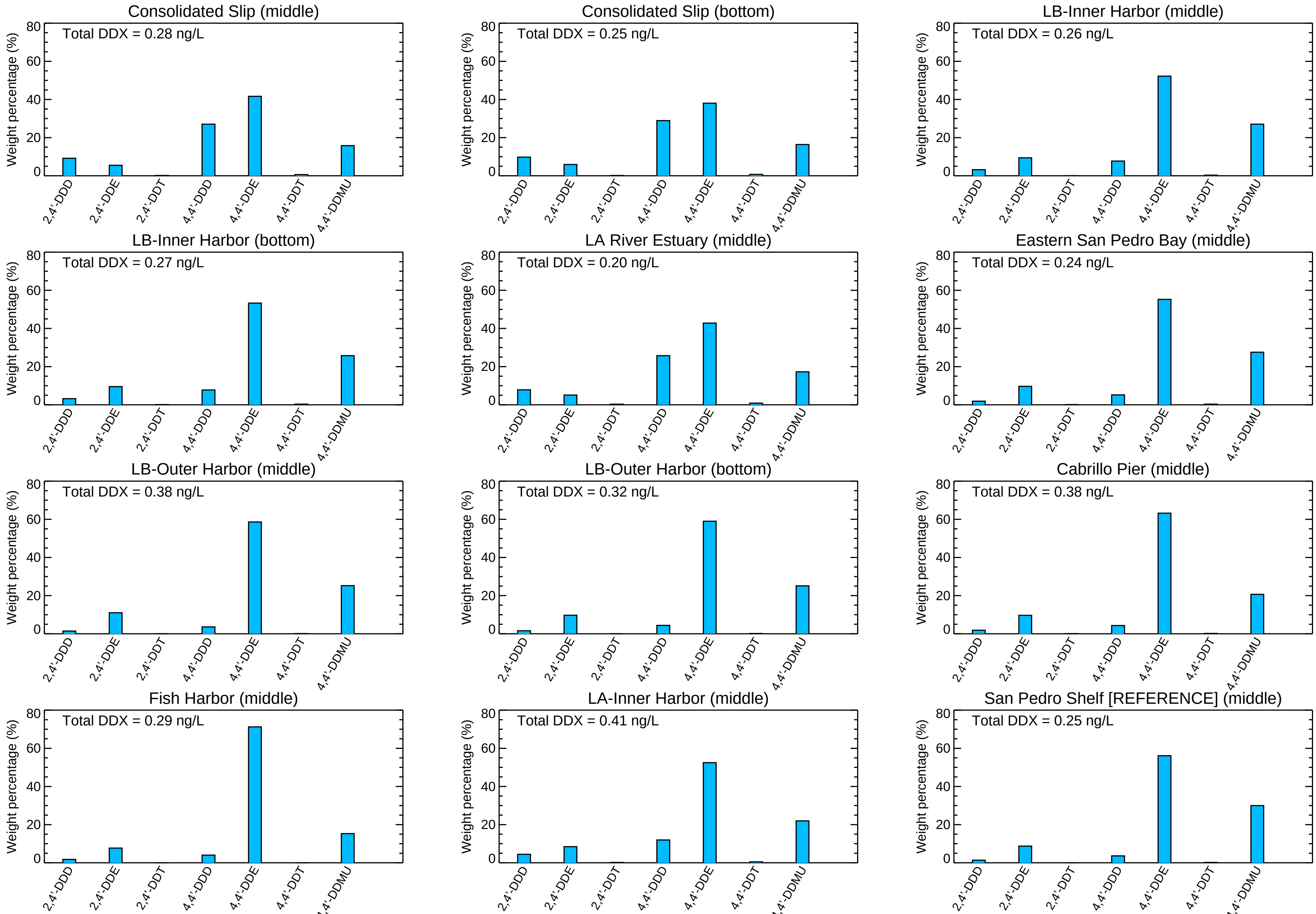


Figure 2-18b

DDX Homolog Distributions for Low Detection Limit Freely Dissolved Water Column Data from Event 3

Sampling Event 3 was conducted in May and June 2015. Water concentrations were calculated from SPME data and corrected for equilibrium. Non-detect concentrations are replaced with zero. Field duplicate results at LB-Inner Harbor were averaged with parent results. Samples were collected in the middle and bottom of the water column. Data file: POLALB_LDL_Event3_SPME_20150818

ANCHOR QEA

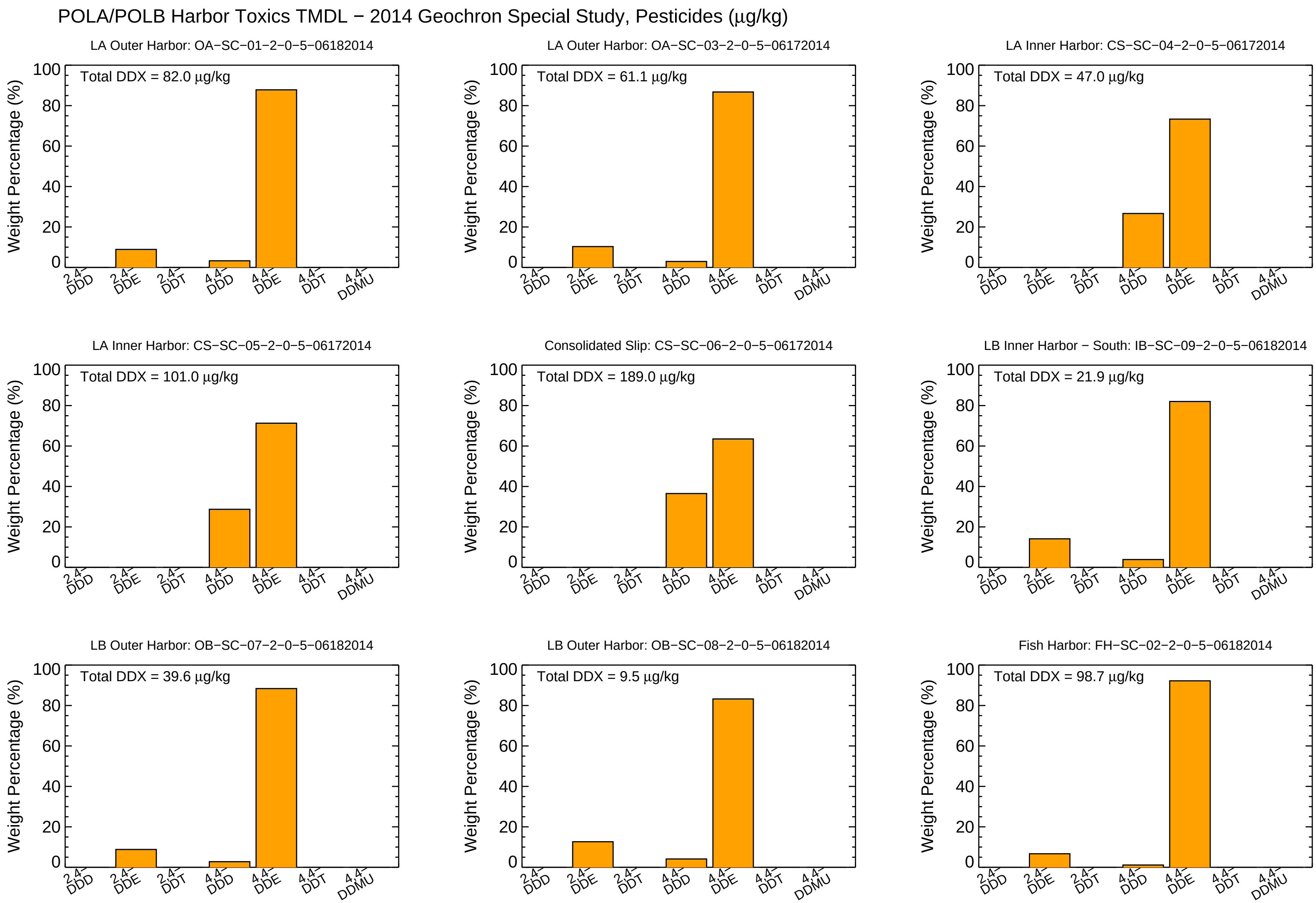


Figure 2−19

DDX Congener Histogram Plots of Surface Sediment Samples

Data file used: PortOfLALB_Sediment_20160720.xlsx. Surface sediment is top 16 cm. Data are for 2014 samples.
Totals are calculated as sum of detected congeners or aroclors, or half of highest detection limit if all congeners or aroclors are non−detects.
Field duplicates are averaged. Non−detect congeners are excluded.

ANCHOR QEA

POLA/POLB Harbor Toxics TMDL − 2014 Geochron Special Study, Pesticides (µg/kg)

Eastern San Pedro Bay: SP−SC−10−2−0−5−06182014

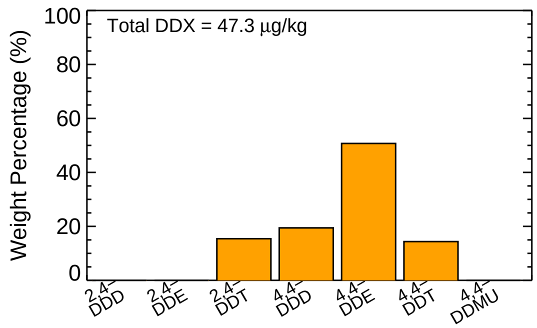


Figure 2−19

DDX Congener Histogram Plots of Surface Sediment Samples

Data file used: PortOfLALB_Sediment_20160720.xlsx. Surface sediment is top 16 cm. Data are for 2014 samples.
Totals are calculated as sum of detected congeners or aroclors, or half of highest detection limit if all congeners or aroclors are non−detects.
Field duplicates are averaged. Non−detect congeners are excluded.

MM − \\iris\Woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Analysis\Histograms\lalb_homolog_congener_histograms.pro Fri Apr 28 01:48:09 2017

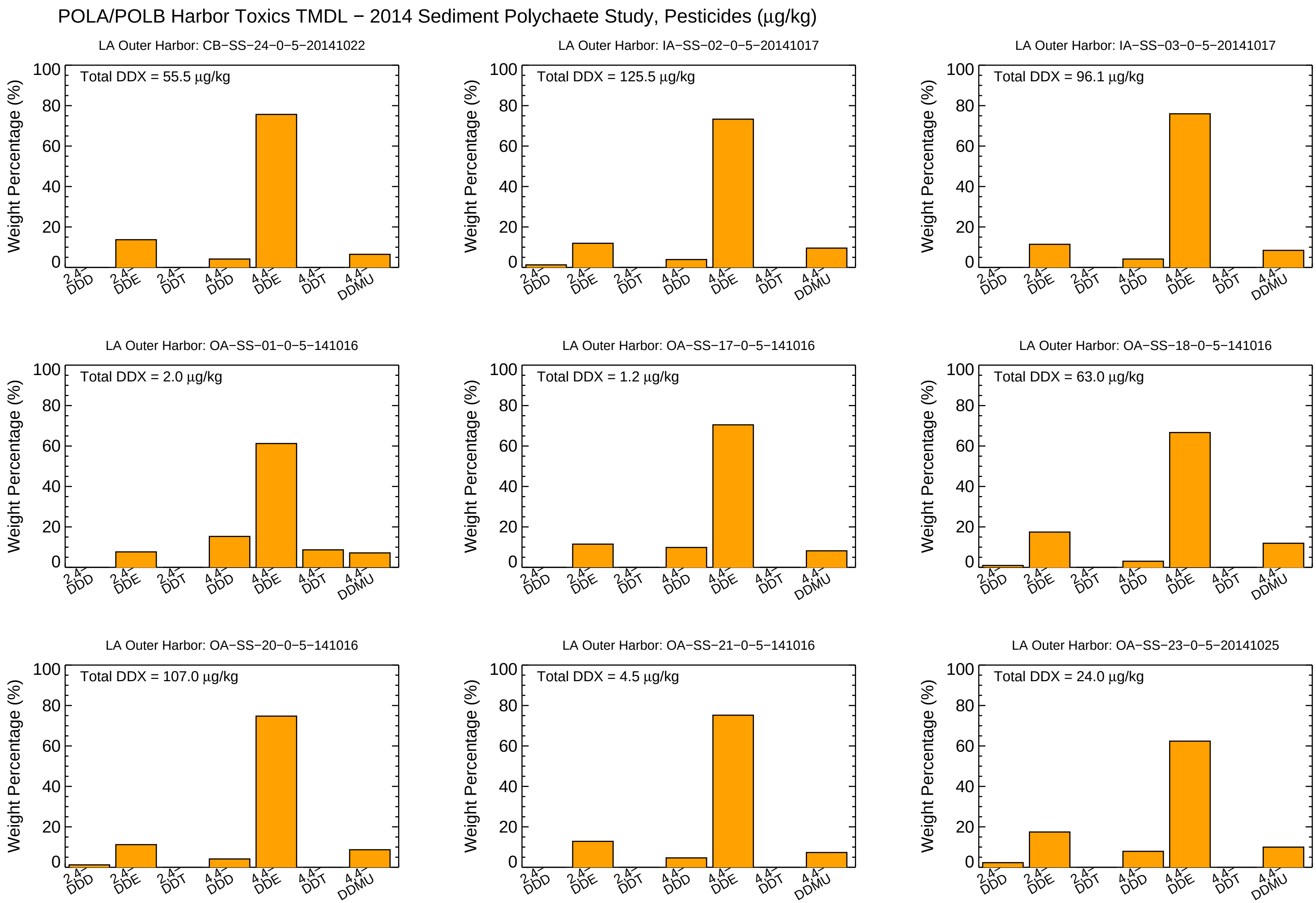


Figure 2−19

DDX Congener Histogram Plots of Surface Sediment Samples

ANCHOR QEA

Data file used: PortOfLALB_Sediment_20160720.xlsx. Surface sediment is top 16 cm. Data are for 2014 samples.
Totals are calculated as sum of detected congeners or aroclors, or half of highest detection limit if all congeners or aroclors are non−detects.
Field duplicates are averaged. Non−detect congeners are excluded.

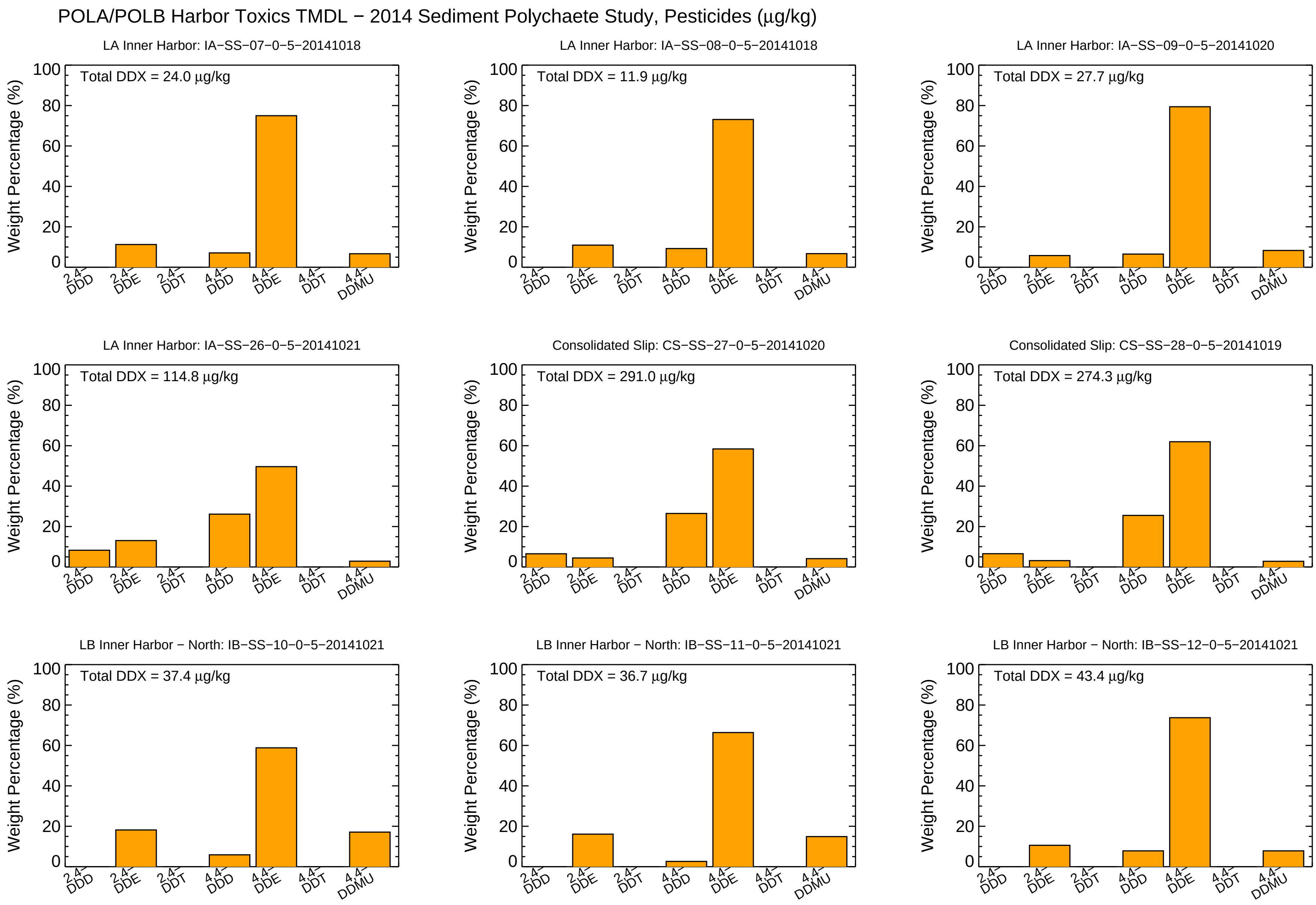


Figure 2−19

DDX Congener Histogram Plots of Surface Sediment Samples

Data file used: PortOfLALB_Sediment_20160720.xlsx. Surface sediment is top 16 cm. Data are for 2014 samples.
Totals are calculated as sum of detected congeners or aroclors, or half of highest detection limit if all congeners or aroclors are non−detects.
Field duplicates are averaged. Non−detect congeners are excluded.

ANCHOR QEA

MM − \\iris\Woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Analysis\Histograms\lalb_homolog_congener_histograms.pro Fri Apr 28 01:48:09 2017

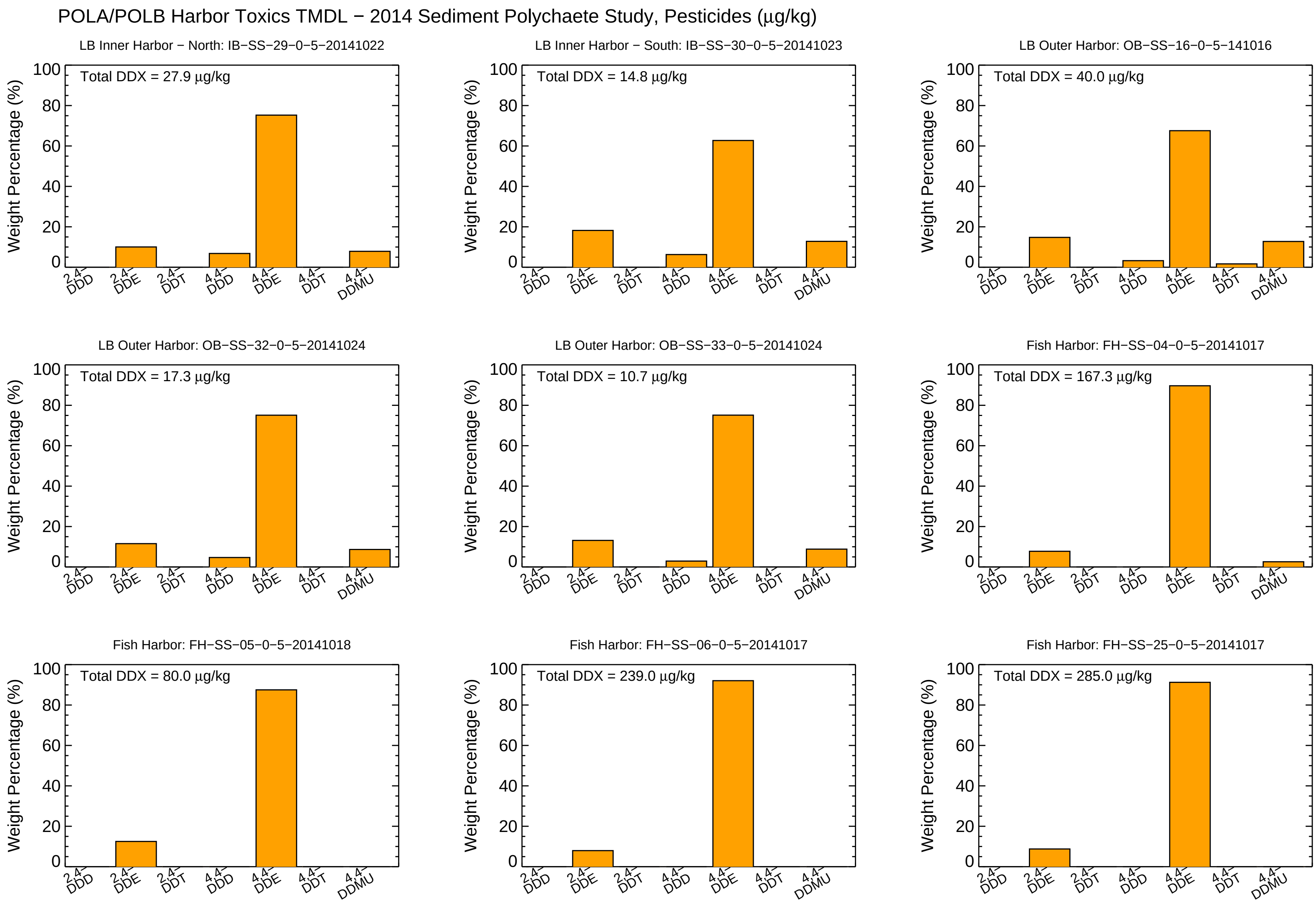


Figure 2−19

DDX Congener Histogram Plots of Surface Sediment Samples

Data file used: PortOfLALB_Sediment_20160720.xlsx. Surface sediment is top 16 cm. Data are for 2014 samples.
Totals are calculated as sum of detected congeners or aroclors, or half of highest detection limit if all congeners or aroclors are non−detects.
Field duplicates are averaged. Non−detect congeners are excluded.

ANCHOR QEA

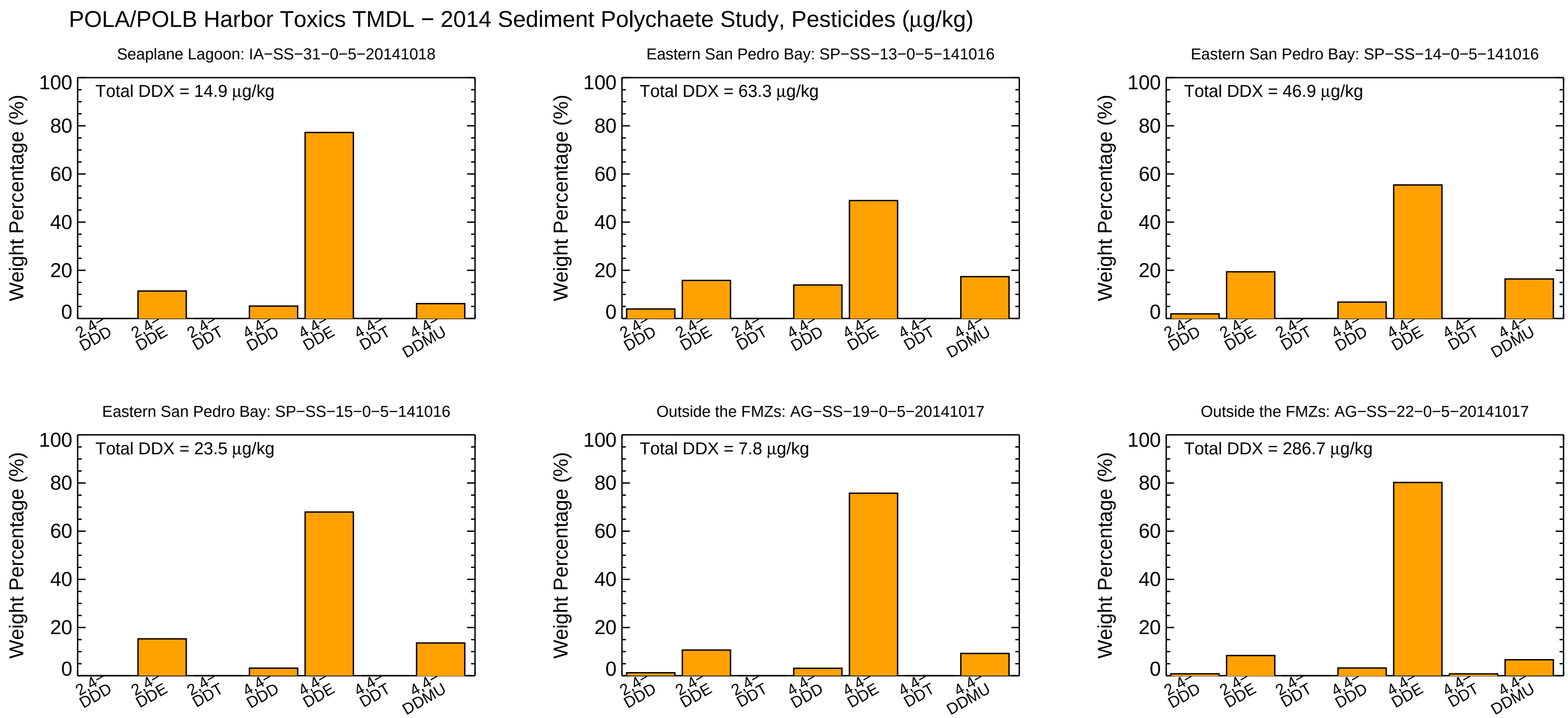


Figure 2−19

DDX Congener Histogram Plots of Surface Sediment Samples

Data file used: PortOfLALB_Sediment_20160720.xlsx. Surface sediment is top 16 cm. Data are for 2014 samples.
Totals are calculated as sum of detected congeners or aroclors, or half of highest detection limit if all congeners or aroclors are non−detects.
Field duplicates are averaged. Non−detect congeners are excluded.

ANCHOR QEA

MM − \\iris\Woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Analysis\Histograms\lalb_homolog_congener_histograms.pro Fri Apr 28 01:48:09 2017

GWMA − TMDL Compliance Monitoring: 2014 Fish, Pesticides (µg/kg)

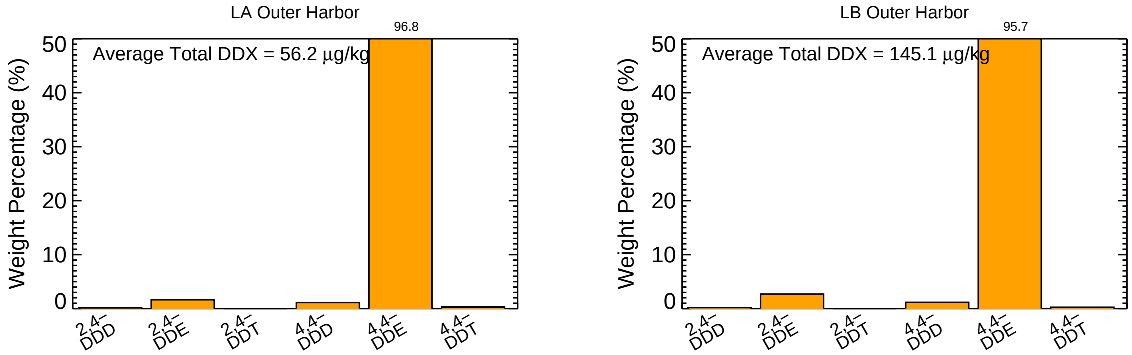


Figure 2−20a

DDX Congener Histogram Plots of White Surfperch Samples by Zone

Data file used: PortOfLALB_Fish_20160720.xlsx. Field duplicates are averaged.
Non−detect congeners are excluded. Tissue types include: Whole body. 2014 samples shown.

ANCHOR QEA

POLA/POLB Harbor Toxics TMDL − 2014 Food Web Special Study, Pesticides (µg/kg)

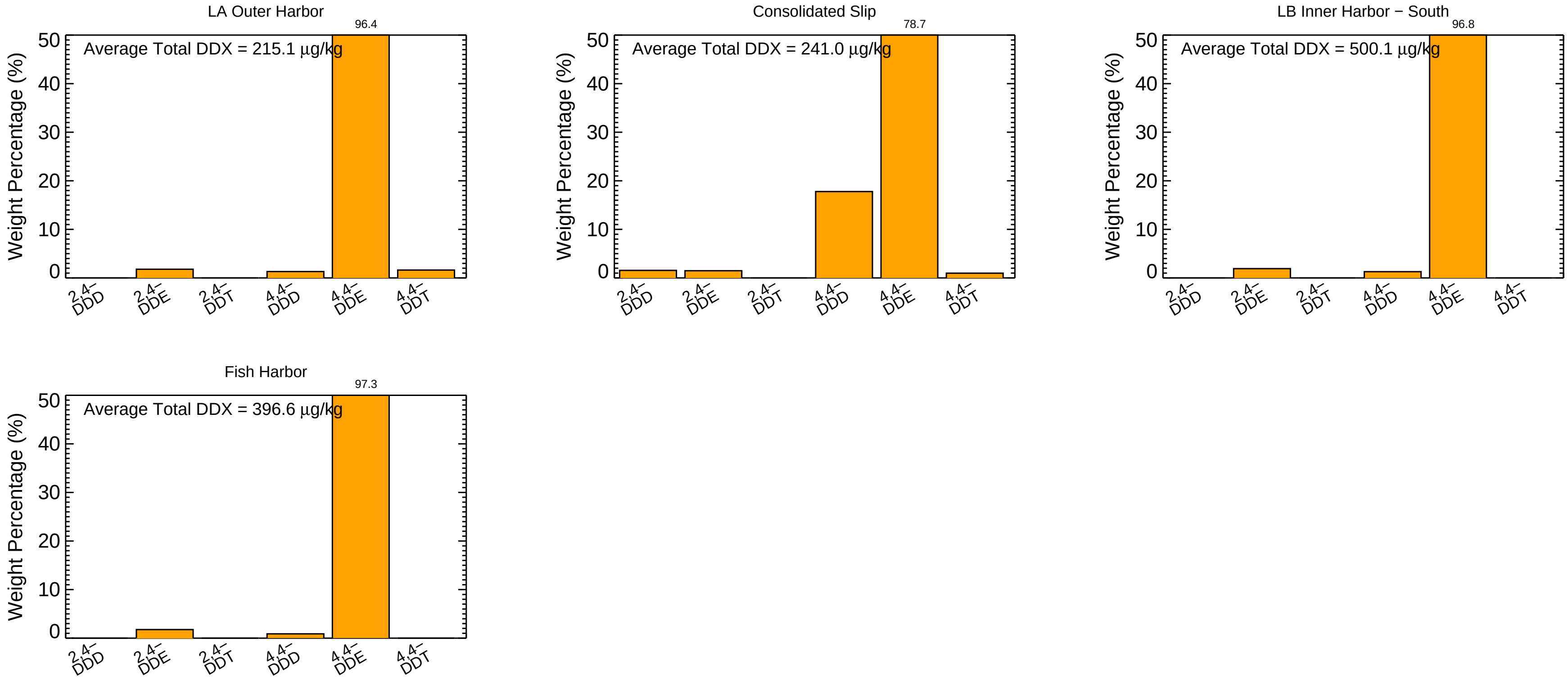


Figure 2−20a

DDX Congener Histogram Plots of White Surfperch Samples by Zone

Data file used: PortOfLALB_Fish_20160720.xlsx. Field duplicates are averaged.
Non−detect congeners are excluded. Tissue types include: Whole body. 2014 samples shown.

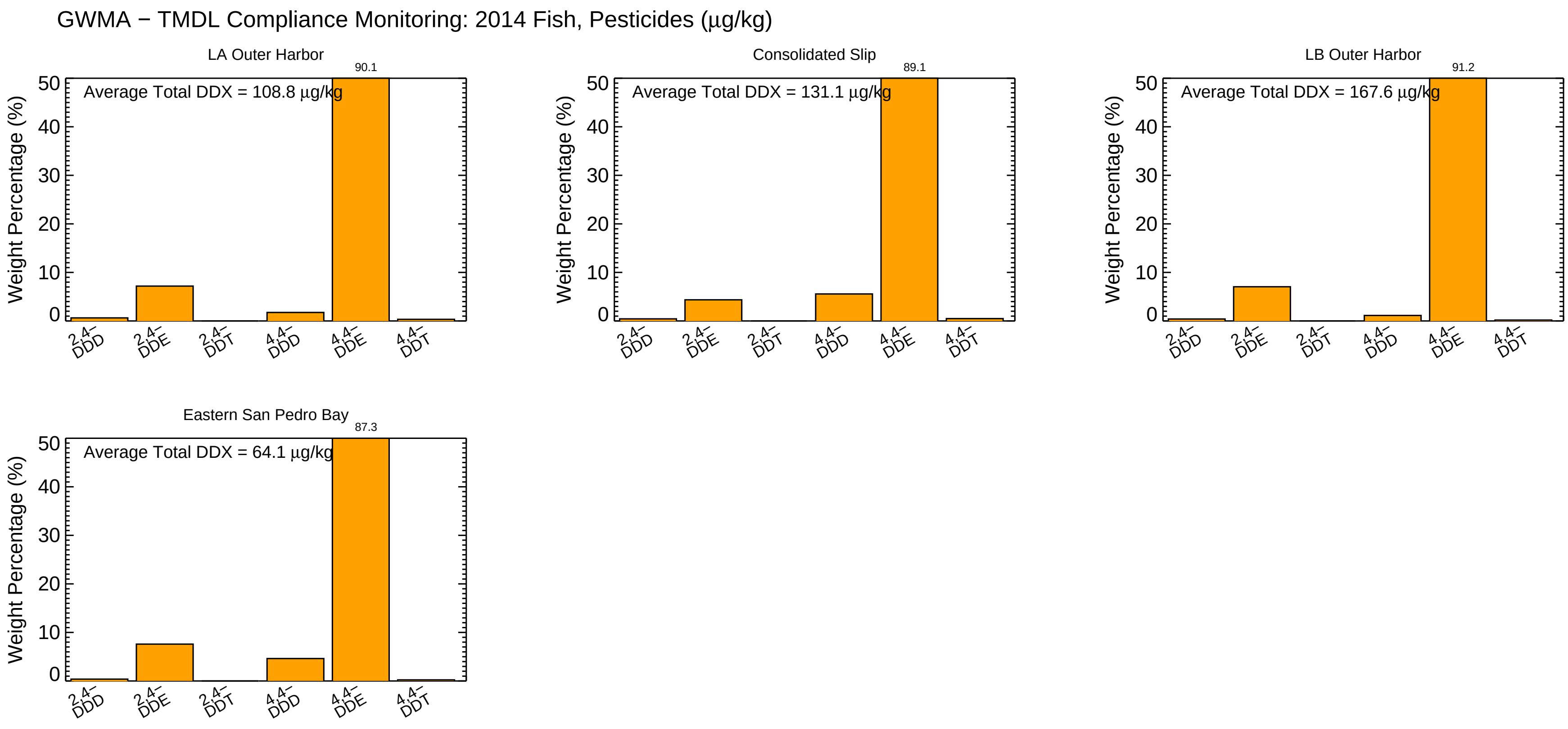


Figure 2−20b

DDX Congener Histogram Plots of White Croaker Samples by Zone

Data file used: PortOfLALB_Fish_20160720.xlsx. Field duplicates are averaged.
Non−detect congeners are excluded. Tissue types include: Fillet (all types). 2014 samples shown.

ANCHOR QEA

MM − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Analysis\Histograms\lalb_fish_ddx_congener_histograms_by_zones.pro Fri Apr 28 01:30:18 2017

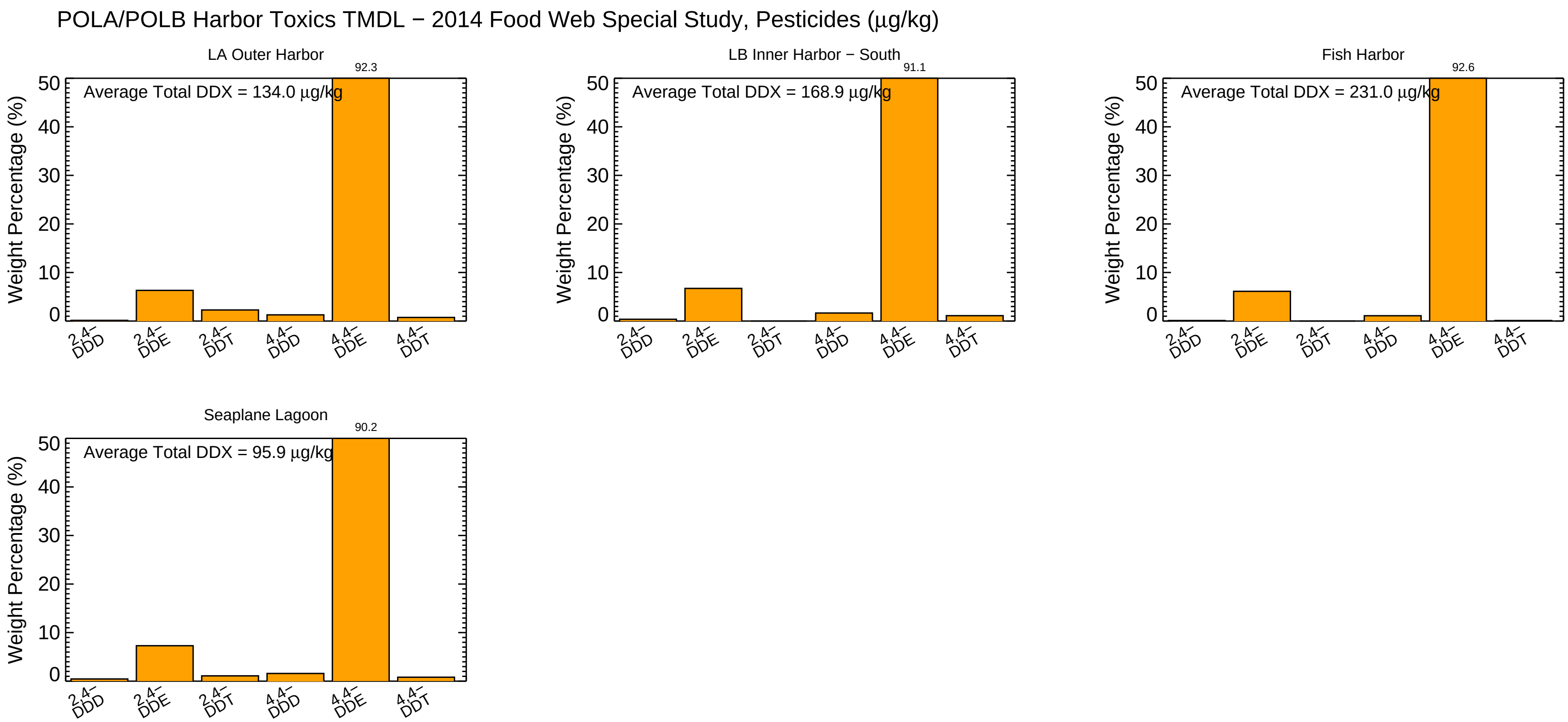


Figure 2−20b

DDX Congener Histogram Plots of White Croaker Samples by Zone

Data file used: PortOfLALB_Fish_20160720.xlsx. Field duplicates are averaged.
Non−detect congeners are excluded. Tissue types include: Fillet (all types). 2014 samples shown.

ANCHOR QEA

GWMA − TMDL Compliance Monitoring: 2014 Fish, Pesticides (µg/kg)

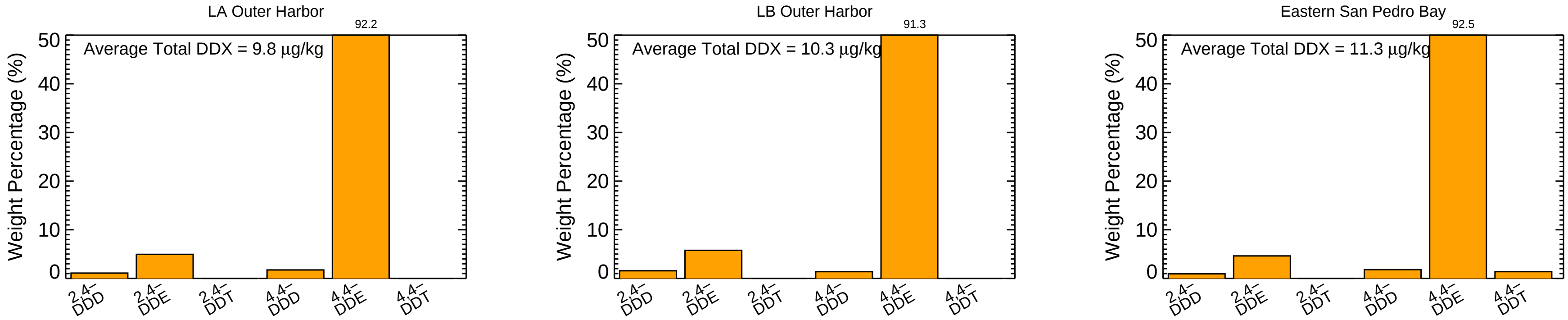


Figure 2−20c

DDX Congener Histogram Plots of California Halibut Samples by Zone

Data file used: PortOfLALB_Fish_20160720.xlsx. Field duplicates are averaged.
Non−detect congeners are excluded. Tissue types include: Fillet (all types). 2014 samples shown.

ANCHOR QEA

MM − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Analysis\Histograms\lalb_fish_ddx_congener_histograms_by_zones.pro Fri Apr 28 01:30:18 2017

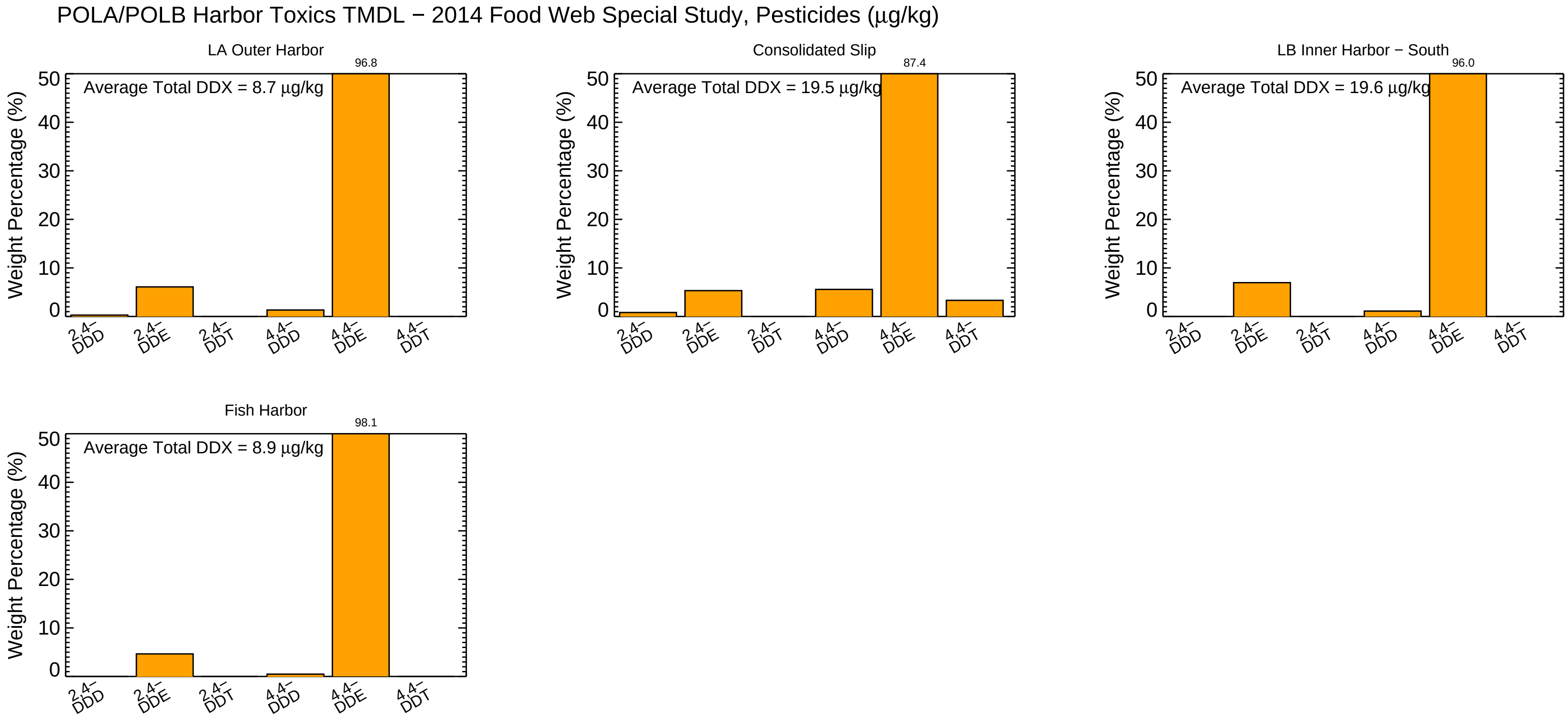


Figure 2−20c

DDX Congener Histogram Plots of California Halibut Samples by Zone

Data file used: PortOfLALB_Fish_20160720.xlsx. Field duplicates are averaged.
Non−detect congeners are excluded. Tissue types include: Fillet (all types). 2014 samples shown.

ANCHOR QEA

MM − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Analysis\Histograms\lalb_fish_ddx_congener_histograms_by_zones.pro Fri Apr 28 01:30:18 2017

POLA/POLB Harbor Toxics TMDL − 2014 Food Web Special Study, Pesticides (µg/kg)

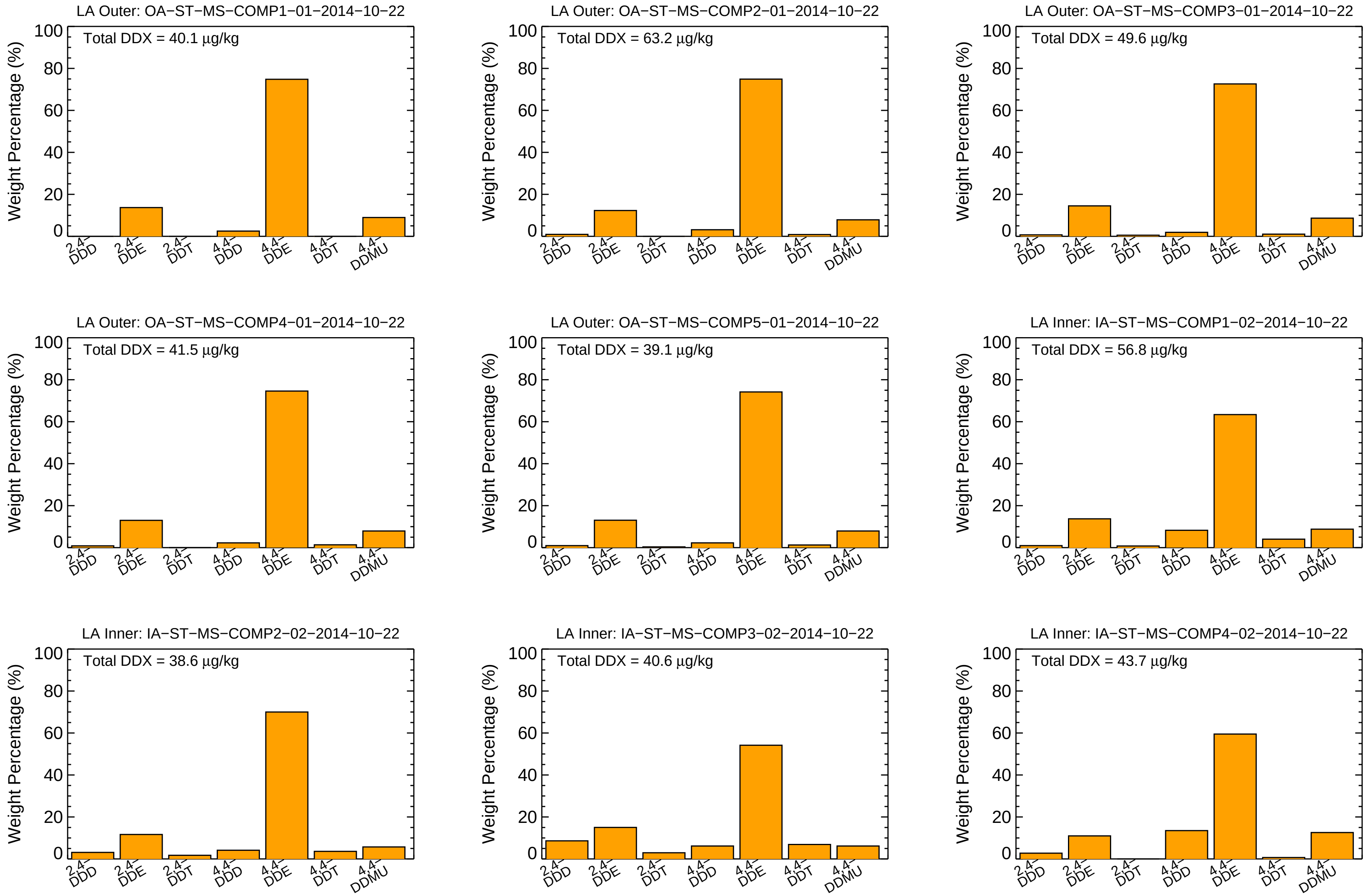


Figure 2−21

DDX Congener Histogram Plots of 2014 Mussel Samples

Data file used: PortOfLALB_Mussel_20160720.xlsx. 2014 samples shown. Species plotted: Mussel.
Totals are calculated as sum of detected congeners or aroclors, or half of highest detection limit if all congeners or aroclors are non−detects.
Non−detect congeners are excluded.

ANCHOR QEA

MM − \\iris\Woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Analysis\Histograms\lalb_mussel_homolog_congener_histograms.pro Fri Apr 28 01:44:00 2017

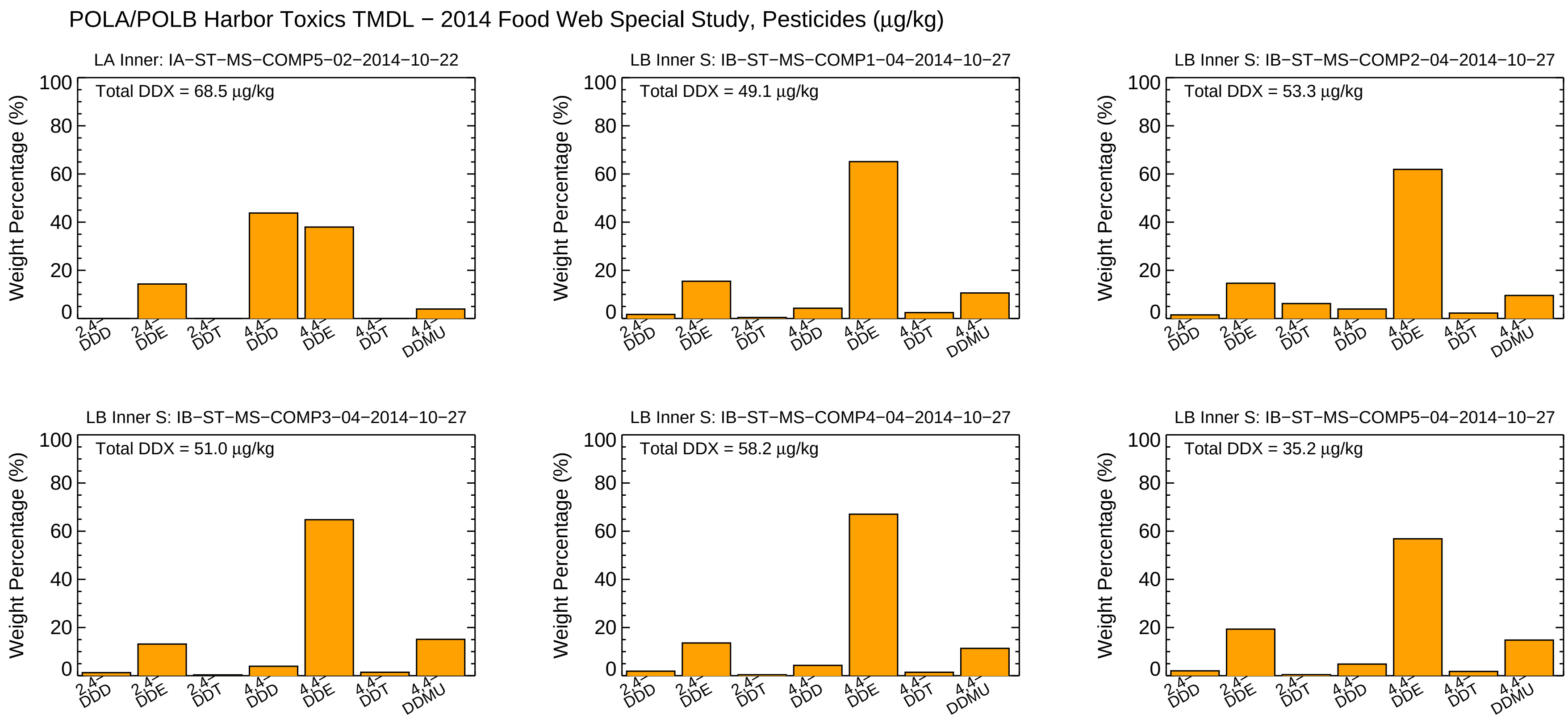
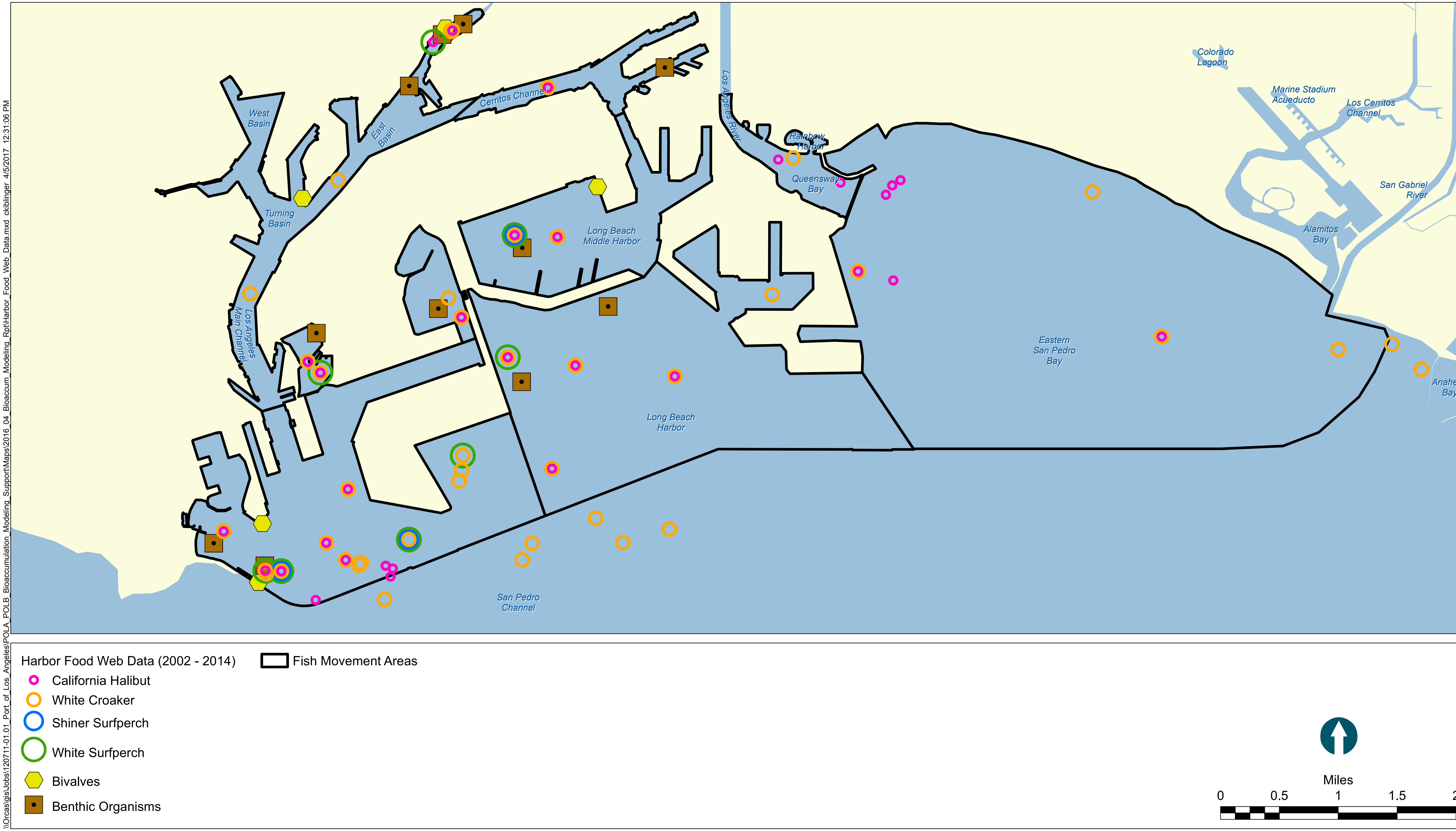


Figure 2−21

DDX Congener Histogram Plots of 2014 Mussel Samples

Data file used: PortOfLALB_Mussel_20160720.xlsx. 2014 samples shown. Species plotted: Mussel.
Totals are calculated as sum of detected congeners or aroclors, or half of highest detection limit if all congeners or aroclors are non−detects.
Non−detect congeners are excluded.

ANCHOR QEA



\\Orcas\gis\Jobs\120711-01.01_Port_of_Los_Angeles\POLA_POLB_Bioaccumulation_Modeling_Support\Maps\2016_04_Bioaccum_Modeling_Rpt\Harbor_Food_Web_Data.mxd ckiblinger 4/5/2017 12:31:06 PM

ANCHOR QEA

Figure 4-1
Harbor Food Web Data
Bioaccumulation Modeling Report
Greater Los Angeles and Long Beach Harbor Waters

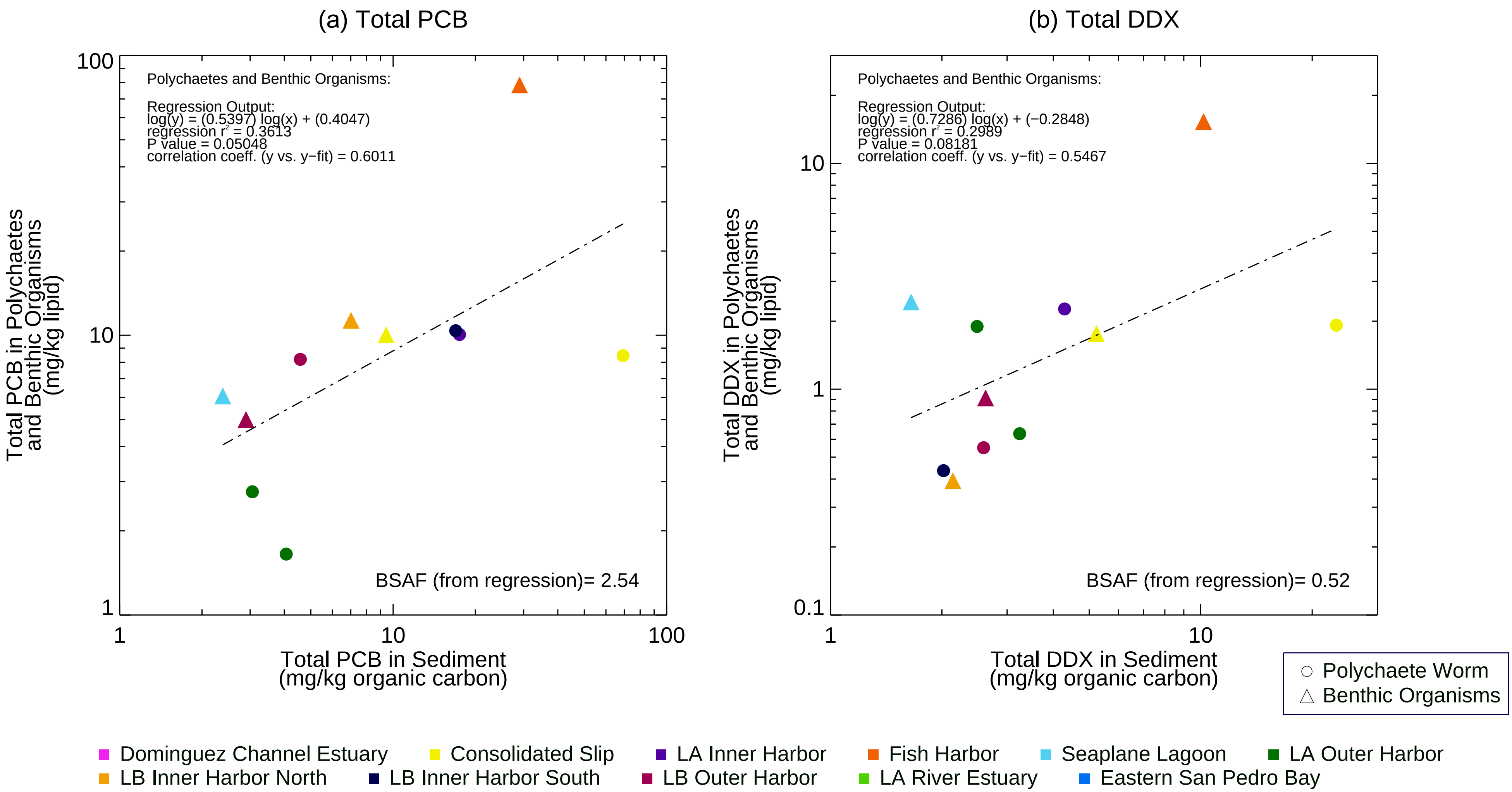


Figure 4−2

Total PCB (a) and Total DDX (b) Concentration in Polychaetes and Benthic Organisms Versus Surface Sediment

Sediment data file used: PortOfLALB_Sediment_20160720.xlsx. Surface sediment is top 16 cm.
Polychaete/benthic organisms data file used: PortOfLALB_Polychaete_20160718.xlsx.
Field duplicates are averaged. Data used: Paired samples from 2014 Sediment Polychaete Study.
Uses reanalysed total DDX concentrations for benthic organisms and polychaete worms, when available. Regression is based on all the samples.

ANCHOR QEA

MM − \\iris\Woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Analysis\Crossplots\Polychaete_Vs_Sediment\LALB_polychaete_vs_sediment_for_report.pro Fri Apr 28 02:26:42 2017

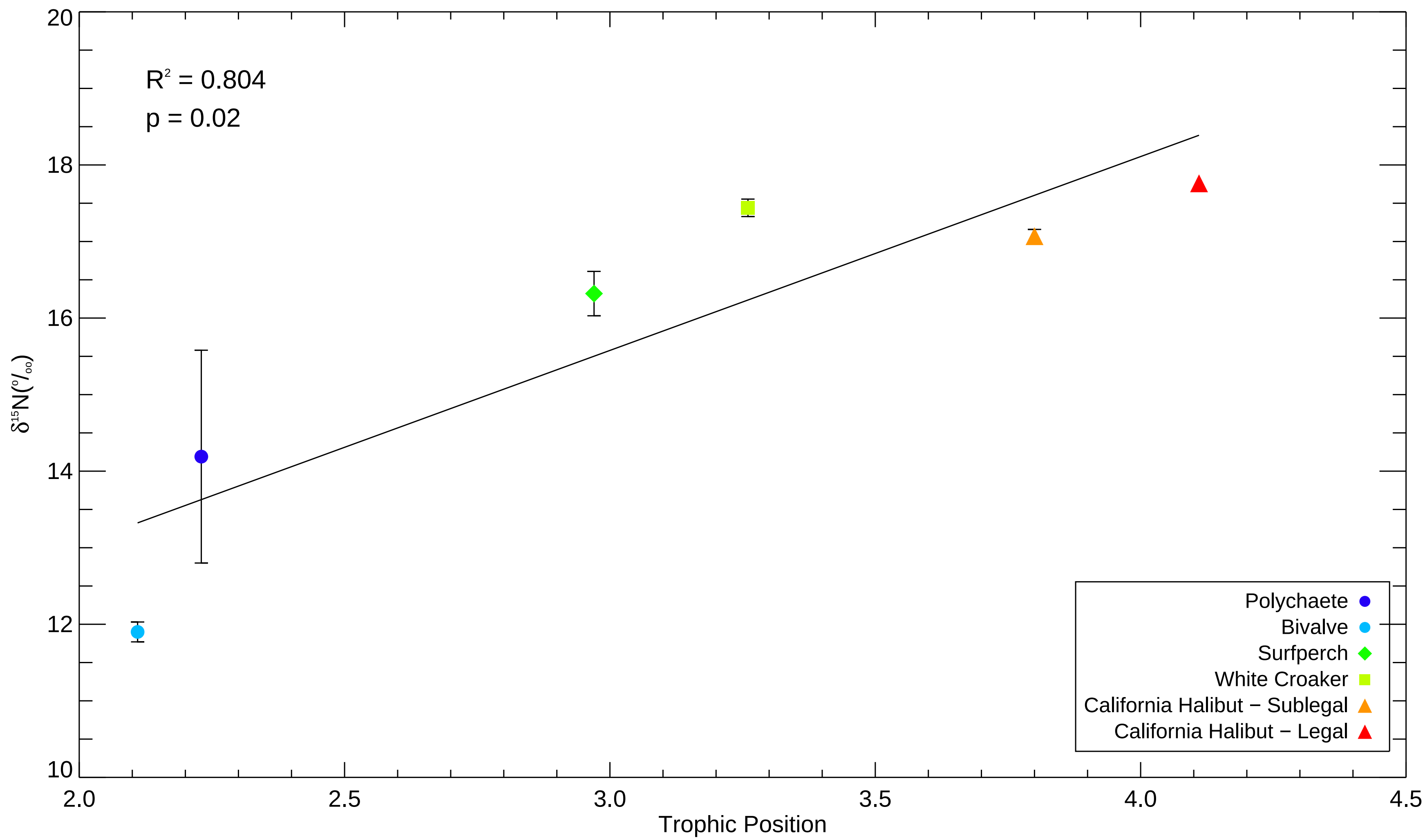


Figure 4−3

Correlation Between Trophic Position and $\delta^{15}N(^{o}/_{oo})$

Mean +/− two standard errors are shown. Trophic position was estimated using the Trophic Position Model based on Adams et al. (1983); values at the base of the food web (sediment and phytoplankton) were assigned according to Vander Zanden and Rasmussen (1996). Bivalve includes mussel and oyster. Surfperch includes white surfperch and shiner surfperch. Legal halibut are assumed to have standard lengths >540 mm. Sublegal halibut size range is 200 to 500 mm. Results for duplicate samples were averaged with parent results. Results for these tissue types were used: surfperch, polychaete − whole body; mussel, oyster − whole body no shell; Calfornia halibut, white croaker − fillet without skin.

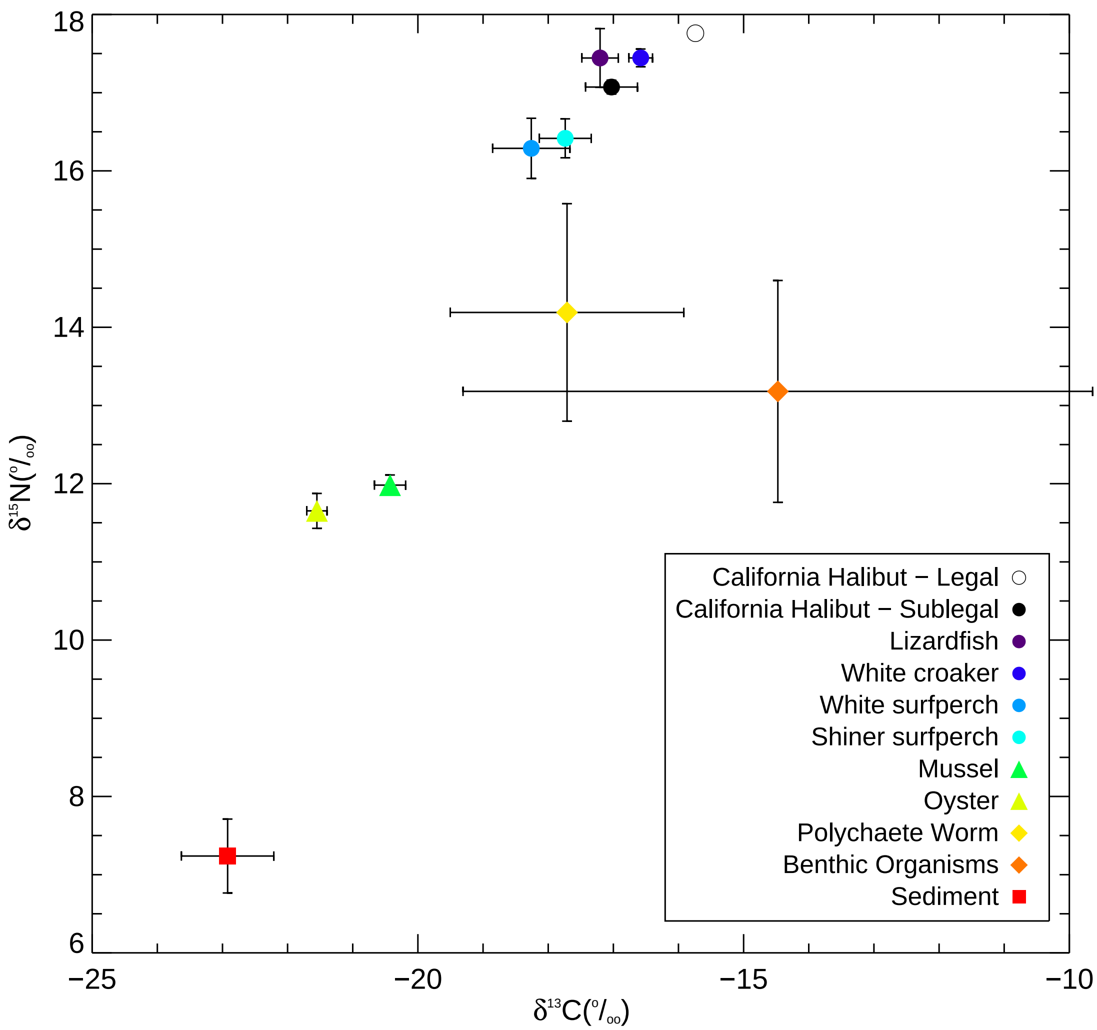


Figure 4−4

Nitrogen Versus Carbon Stable Isotope Data

Mean +/− two standard errors are shown. Data are from the 2014 Food Web Study.
The length for "California Halibut − Legal" is 54 cm. The legal size for halibut is 55.88 cm.
Sublegal halibut size range is 20 to 50 cm. Results for duplicate samples were averaged with parent results.
Results for the following tissue types are shown: surfperches, benthic organisms, polychaete worm − whole body; mussel, oyster − whole body no shell; California halibut, lizardfish, white croaker − fillet without skin

ANCHOR QEA

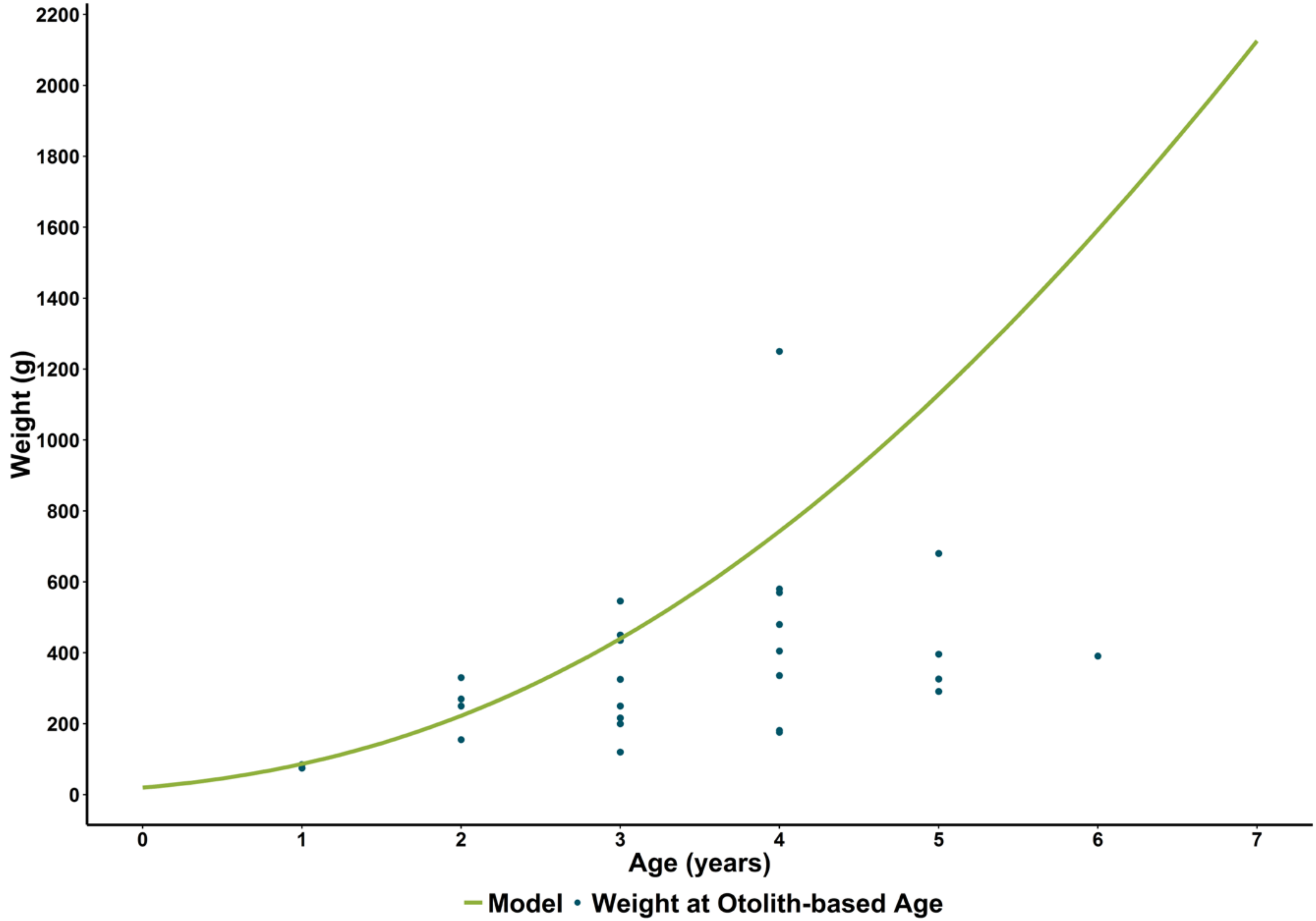


Figure 4-5

California Halibut Weight-at-Age

Note: Model is based on length-at-age data from McNair et al. (2001; TL= $1367.7(1-e^{0.08(t+1.2)})$ *for females and TL* $= 925.3\left(1-e^{0.08(t+2.2)}\right)$ *for males) and weight-at-length data from CDFG (1990;* $W\ = 3.7 * (10-3) * TL^{3.28}$*). The model overlays California halibut data (weight and age based on otolith annuli) collected as part of the Ports' 2014 food web study.*

ANCHOR QEA

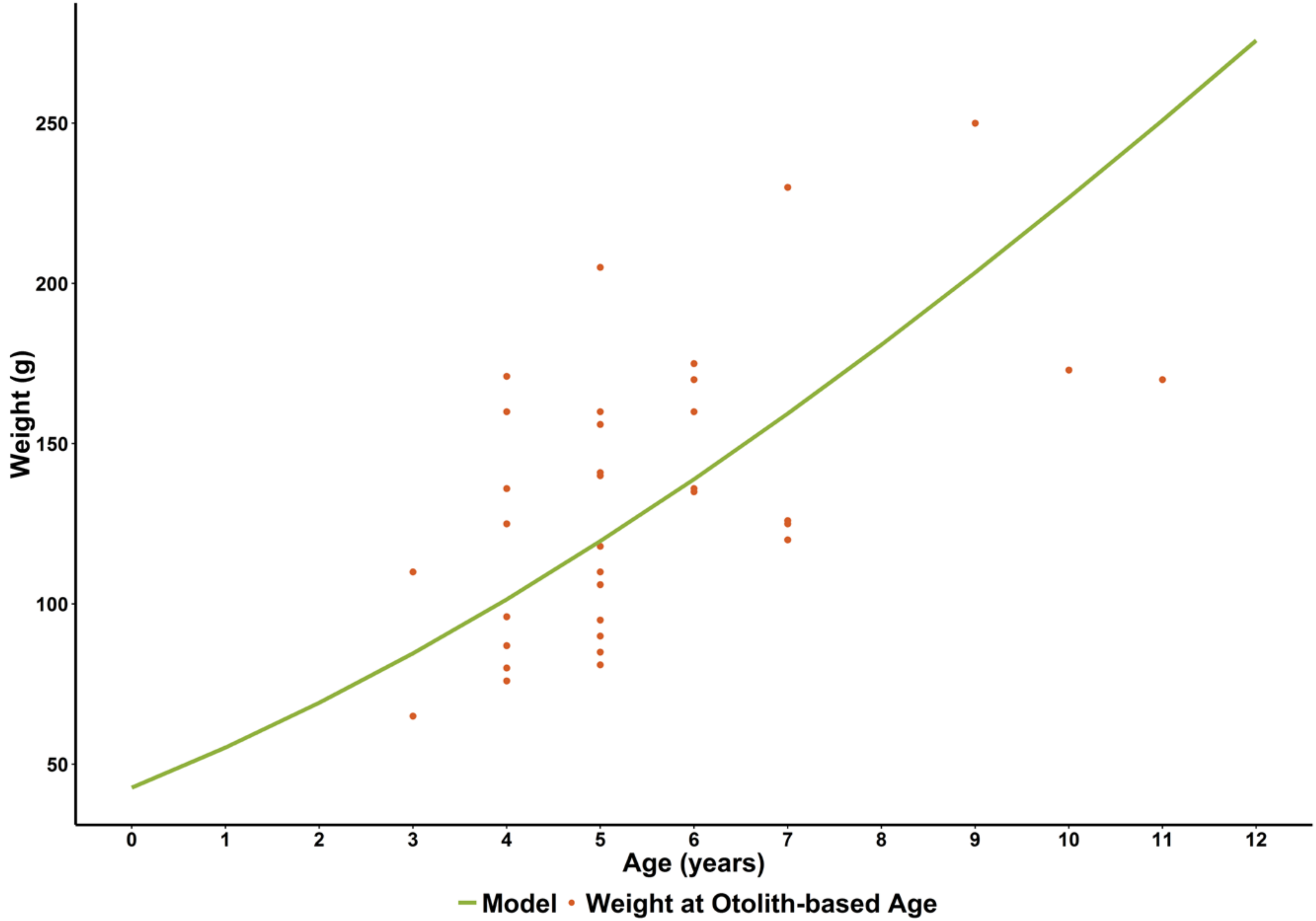
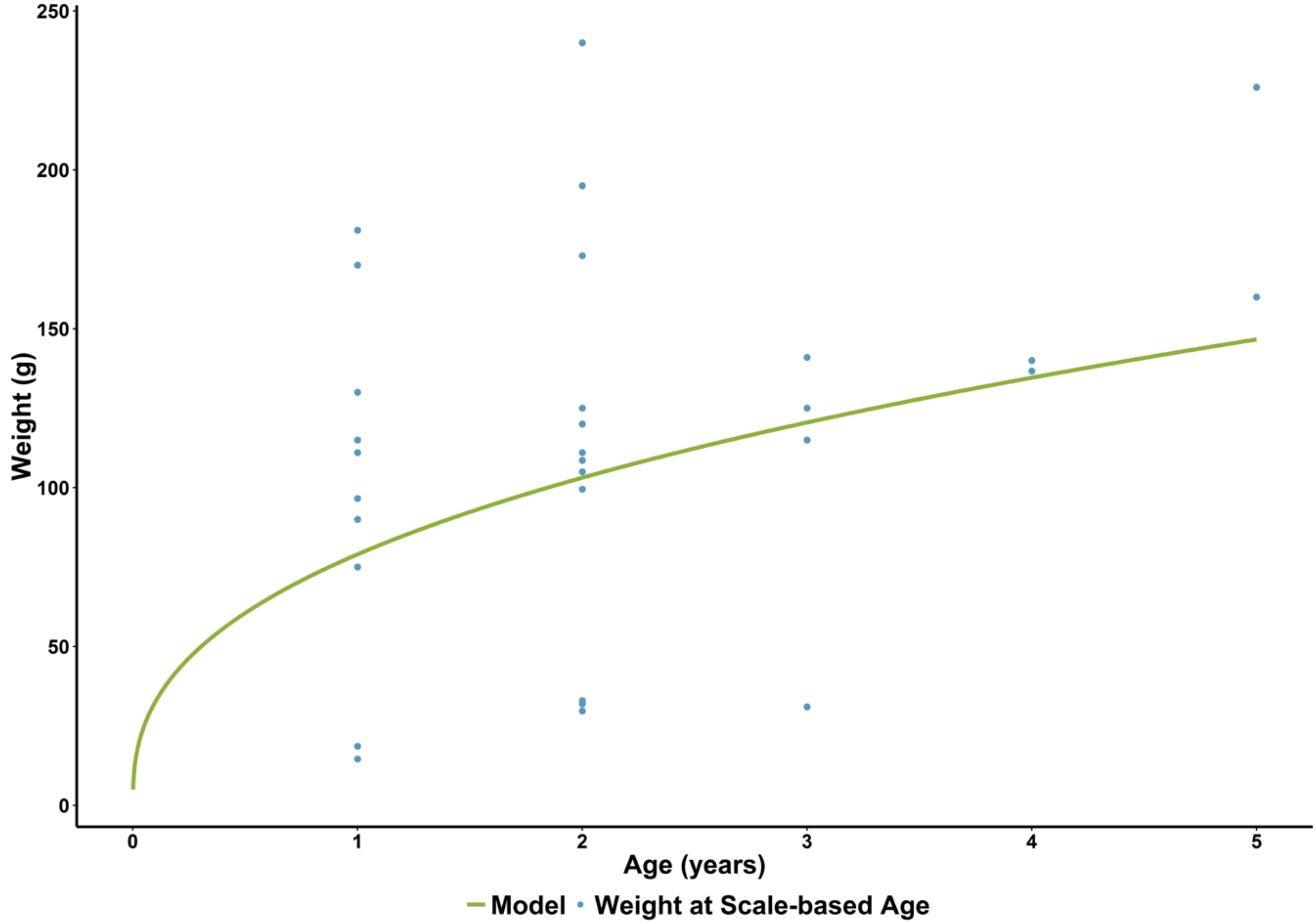


Figure 4-6

White Croaker Weight-at-Age

Note: Model is based on length-at-age data from Moore (1999; $TL = 607.71\left(1 - e^{0.03(t+8.54)}\right)$ for females and $TL = 558.62\left(1 - e^{0.03(t+7.78)}\right)$ for males) and weight-at-length data from Ports Biological Survey Study (2013/14; $W = 2E^{-5} * TL^{2.53}$). The model overlays white croaker data (weight and age based on otolith annuli) collected as part of the Ports' 2014 food web study.

ANCHOR QEA

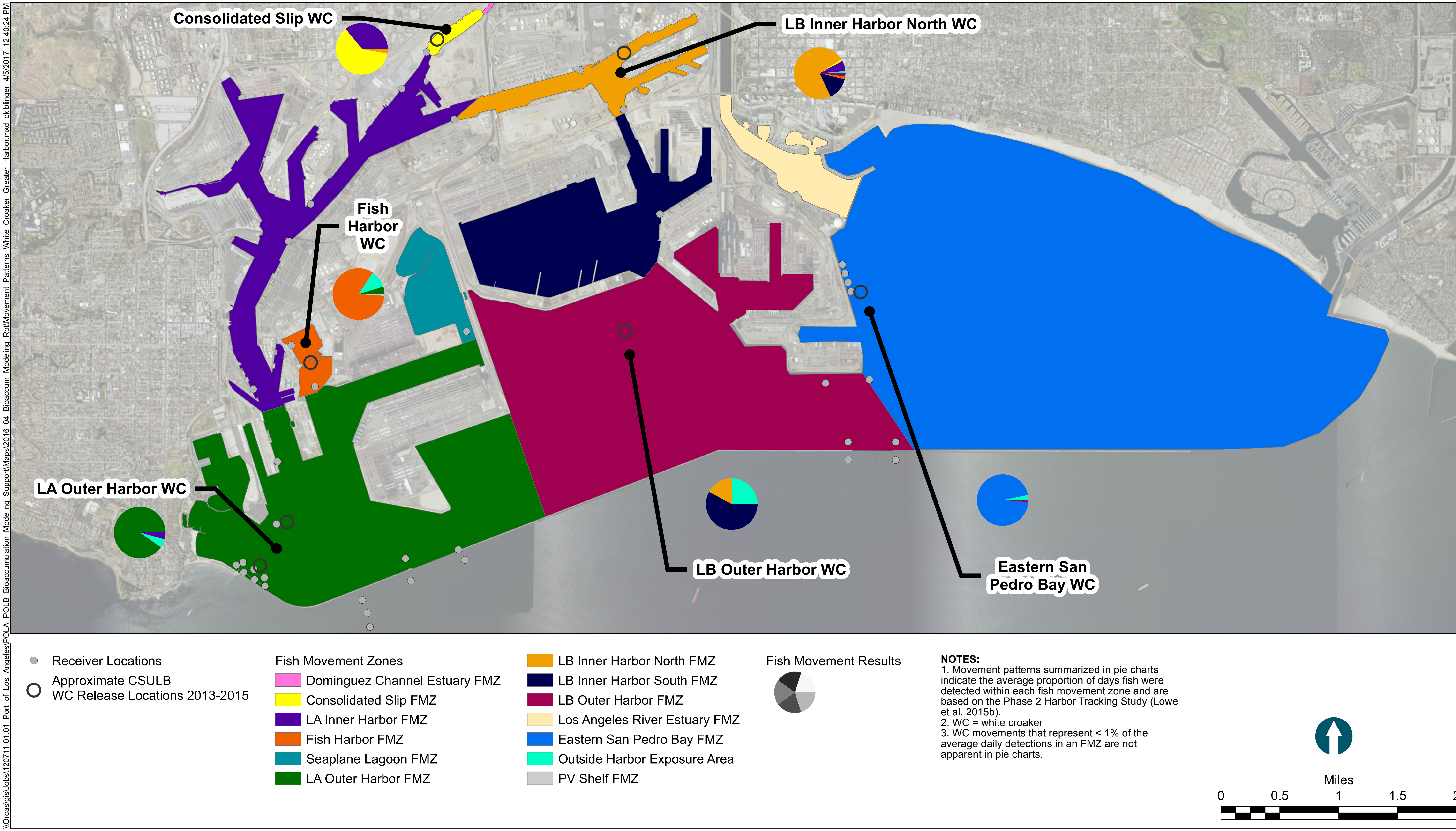


ANCHOR QEA

Figure 4-7

Surfperch Weight-at-Age

Note: Age was determined based on analysis of scales collected from shiner surfperch and white surfperch collected in the Greater Harbor Waters in 2014. The maximum scale-based ages, based on replicate scales analyzed, were used in these plots. Age zero fish were assumed to be approximately 5 grams. Model calculated based on $W = 79.032 * Age^{0.3841}$



ANCHOR QEA

Figure 4-8
Movement Patterns of White Croaker in the Greater Harbor Waters
Bioaccumulation Modeling Report
Greater Los Angeles and Long Beach Harbor Waters

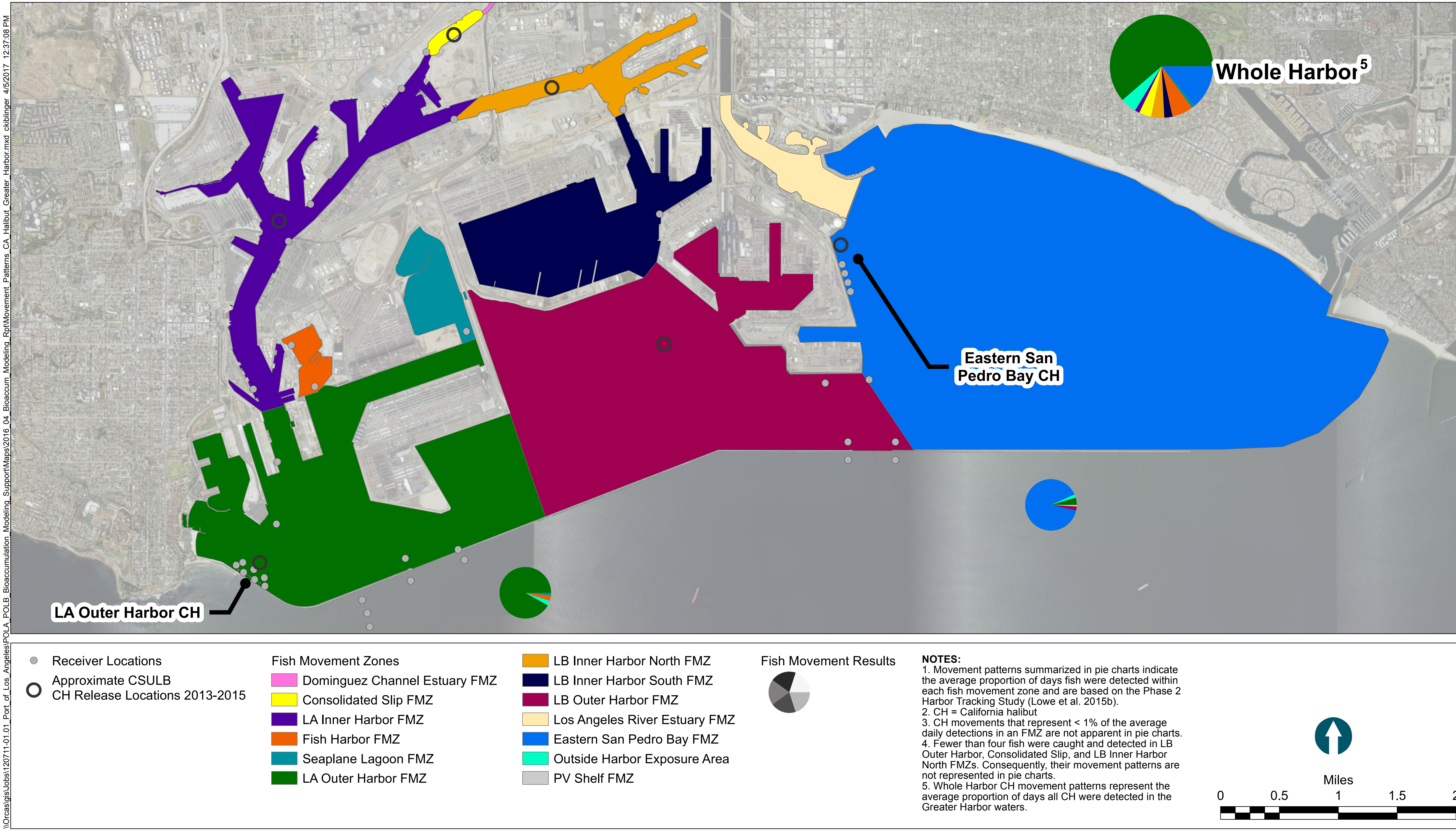
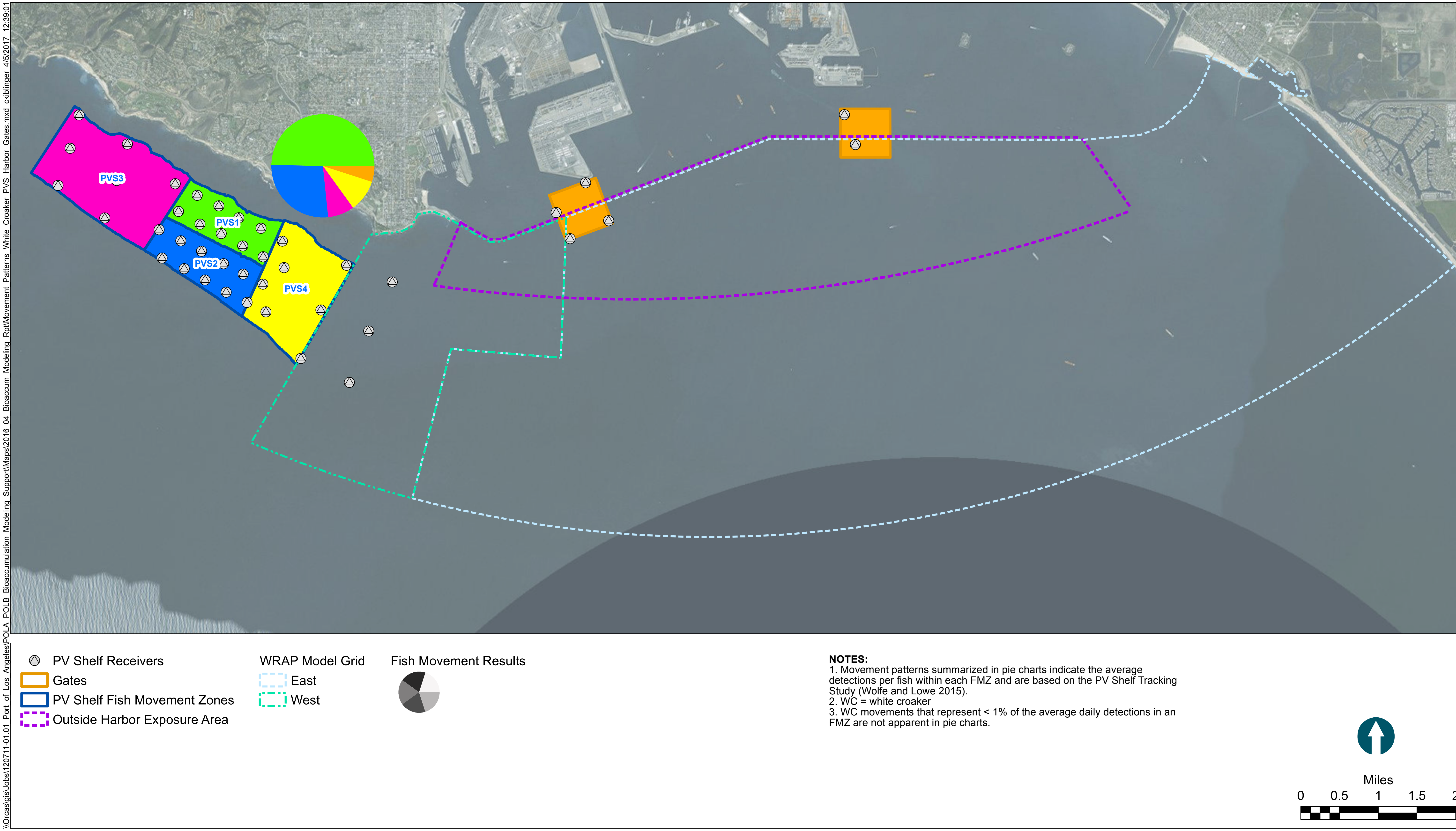


Figure 4-9
Movement Patterns of California Halibut in the Greater Harbor Waters
Bioaccumulation Modeling Report
Greater Los Angeles and Long Beach Harbor Waters

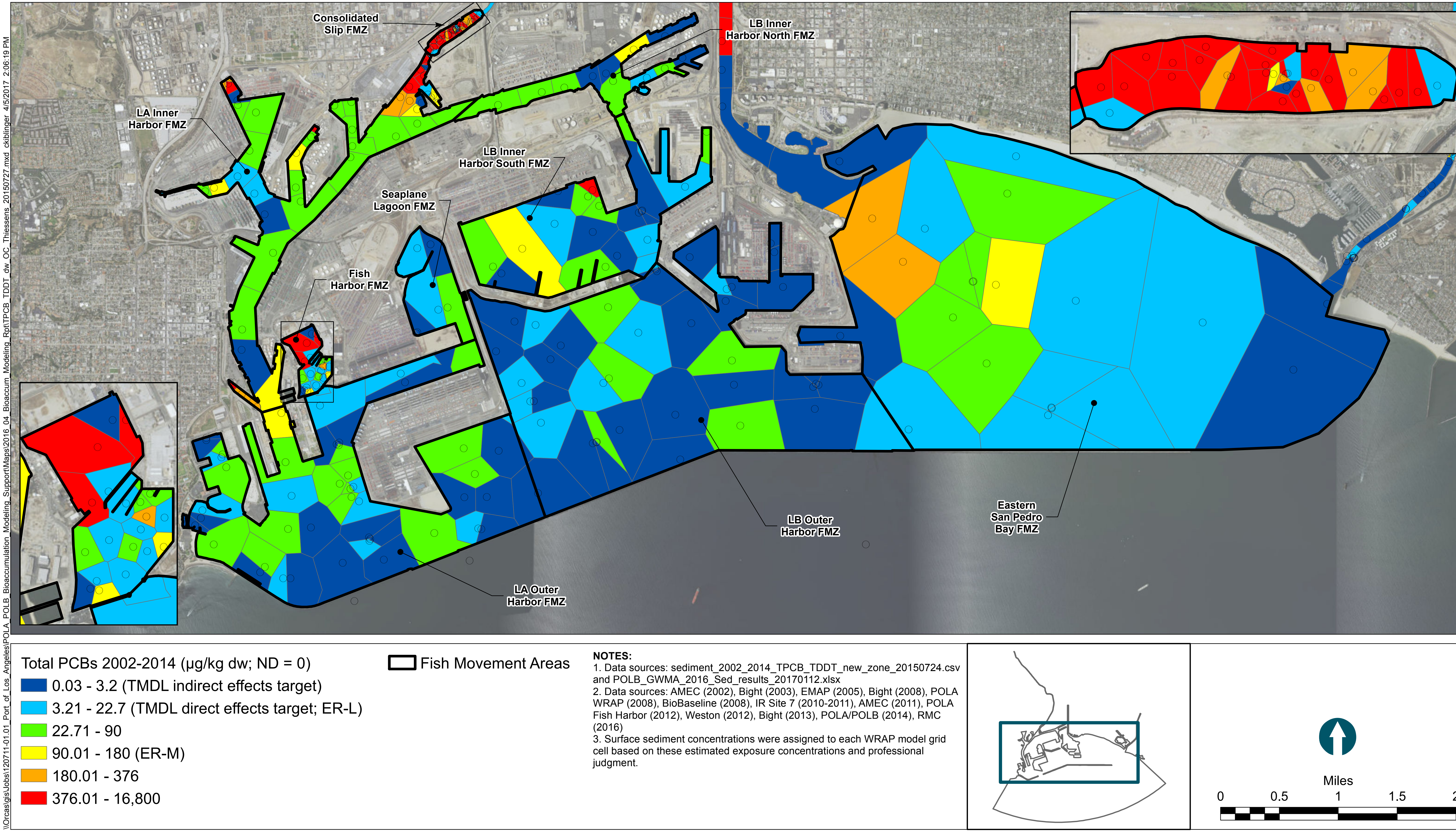


NOTES:
1. Movement patterns summarized in pie charts indicate the average detections per fish within each FMZ and are based on the PV Shelf Tracking Study (Wolfe and Lowe 2015).
2. WC = white croaker
3. WC movements that represent < 1% of the average daily detections in an FMZ are not apparent in pie charts.

\\Orcas\gis\Jobs\120711-01.01_Port_of_Los_Angeles\POLA_POLB_Bioaccumulation_Modeling_Support\Maps\2016_04_Bioaccum_Modeling_Rpt\Movement_Patterns_White_Croaker_PVS_Harbor_Gates.mxd ckiblinger 4/5/2017 12:39:01 PM

ANCHOR QEA

Figure 4-10
Movement Patterns of White Croaker on PV Shelf and to Harbor Gates
Bioaccumulation Modeling Report
Greater Los Angeles and Long Beach Harbor Waters

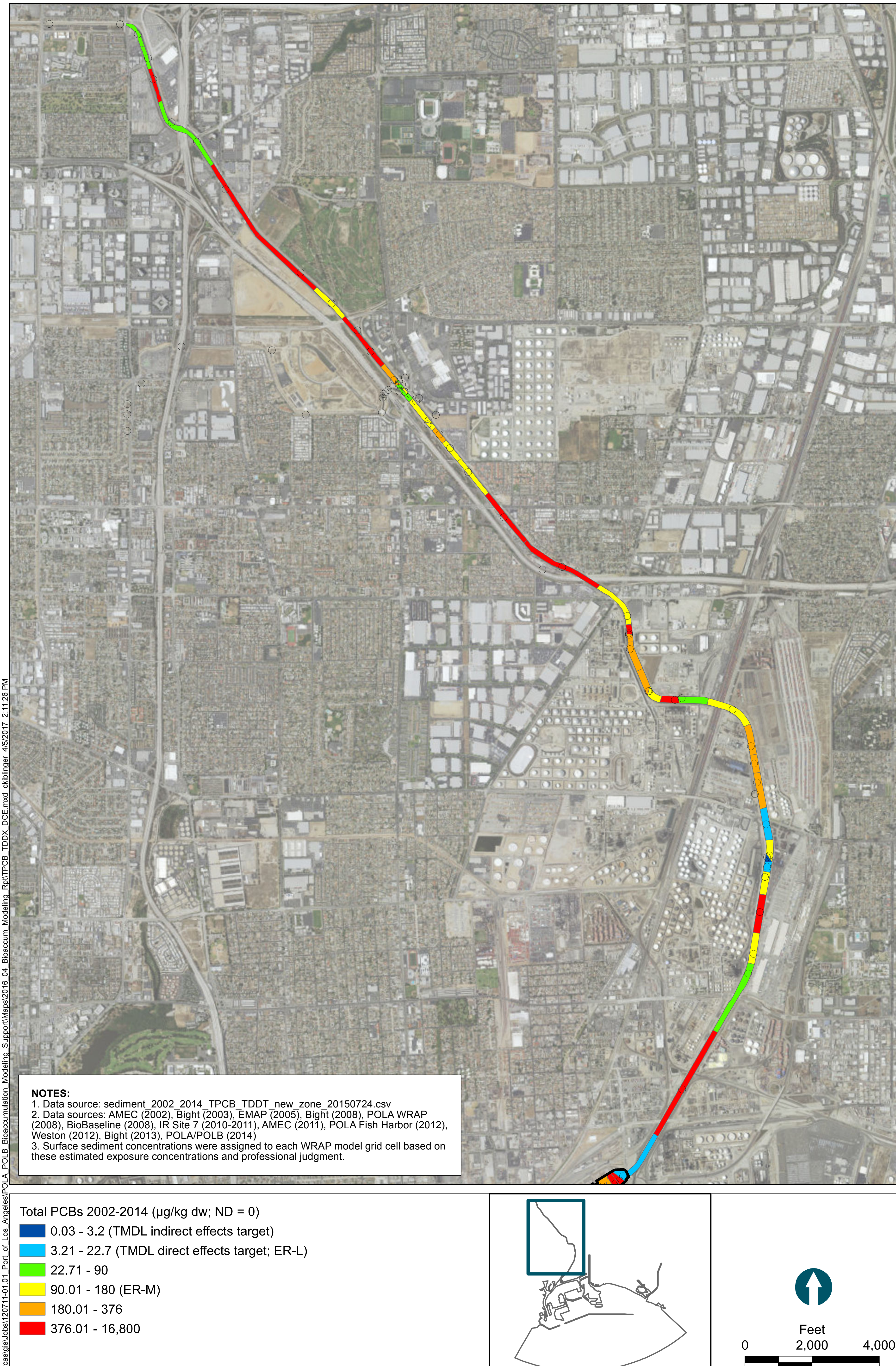


\\Orcas\gis\Jobs\120711-01.01_Port_of_Los_Angeles\POLA_POLB_Bioaccumulation_Modeling_Support\Maps\2016_04_Bioaccum_Modeling_Rpt\TPCB_TDDT_dw_OC_Thiessens_20150727.mxd ckiblinger 4/5/2017 2:06:19 PM

NOTES:

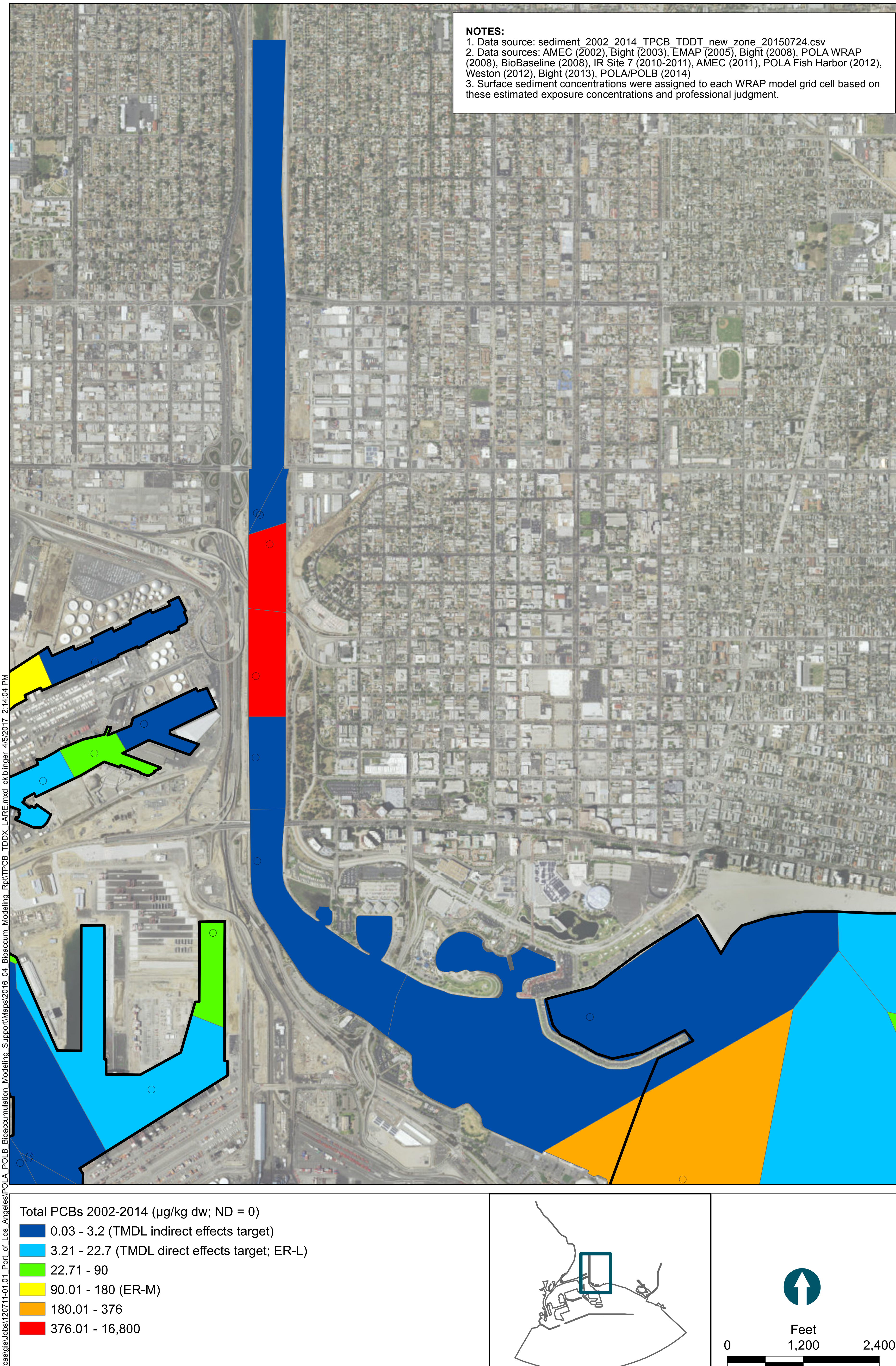
1. Data sources: sediment_2002_2014_TPCB_TDDT_new_zone_20150724.csv and POLB_GWMA_2016_Sed_results_20170112.xlsx
2. Data sources: AMEC (2002), Bight (2003), EMAP (2005), Bight (2008), POLA WRAP (2008), BioBaseline (2008), IR Site 7 (2010-2011), AMEC (2011), POLA Fish Harbor (2012), Weston (2012), Bight (2013), POLA/POLB (2014), RMC (2016)
3. Surface sediment concentrations were assigned to each WRAP model grid cell based on these estimated exposure concentrations and professional judgment.

Figure 4-11a
Thiessen Polygons Showing Total PCB Concentrations in Surface Sediment
Bioaccumulation Modeling Report
Greater Los Angeles and Long Beach Harbor Waters



ANCHOR QEA

Figure 4-11b
Total PCB Concentrations in Surface Sediment in the Dominguez Channel Estuary
Bioaccumulation Modeling Report
Greater Los Angeles and Long Beach Harbor Waters

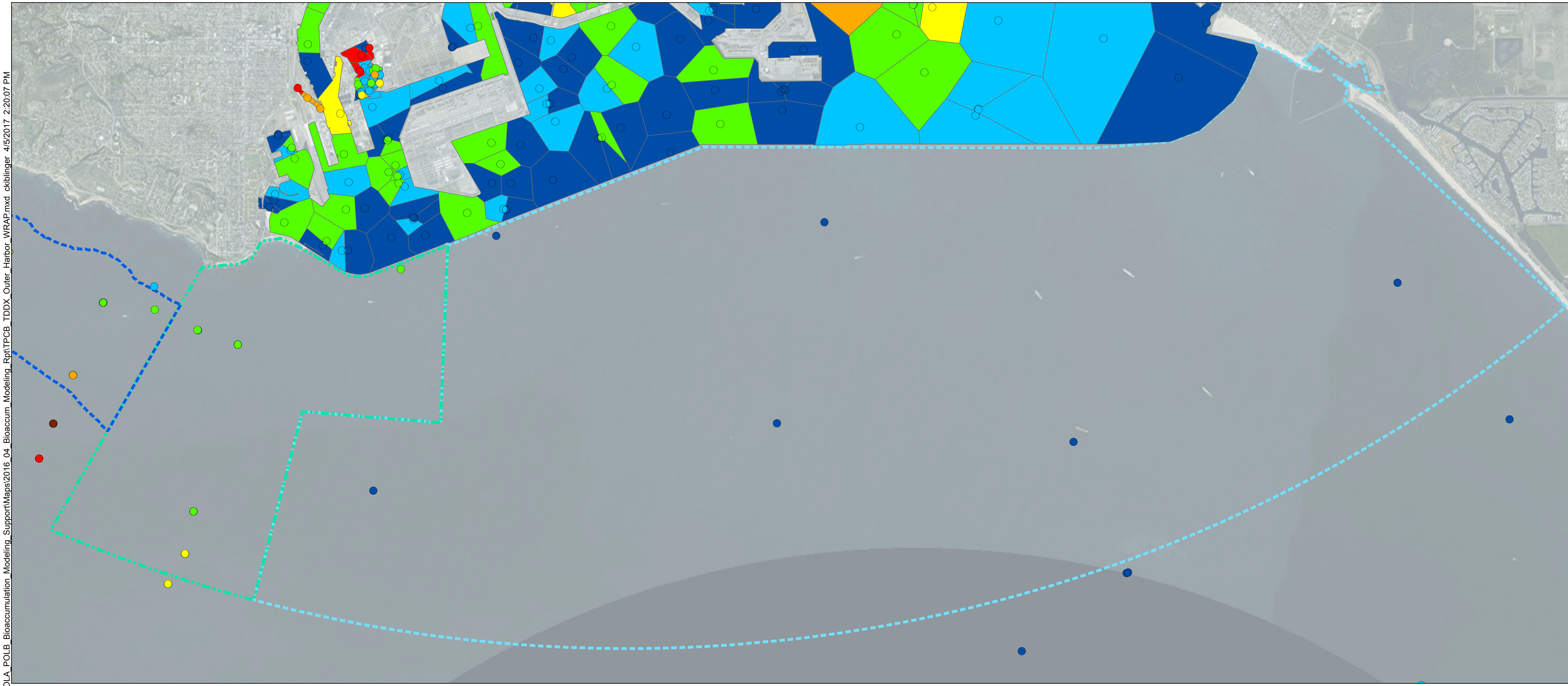


\\Orcas\gis\Jobs\120711-01.01_Port_of_Los_Angeles\POLA_POLB_Bioaccumulation_Modeling_Support\Maps\2016_04_Bioaccum_Modeling_Rpt\TPCB_TDDX_LARE.mxd ckiblinger 4/5/2017 2:14:04 PM

Figure 4-11c
Total PCB Concentrations in Surface Sediment in the Los Angeles River Estuary
Bioaccumulation Modeling Report
Greater Los Angeles and Long Beach Harbor Waters

ANCHOR QEA

\\Orcas\gis\Jobs\120711-01.01_Port_of_Los_Angeles\POLA_POLB_Bioaccumulation_Modeling_Support\Maps\2016_04_Bioaccum_Modeling_Rpt\TPCB_TDDX_Outer_Harbor_WRAP.mxd ckiblinger 4/5/2017 2:20:07 PM

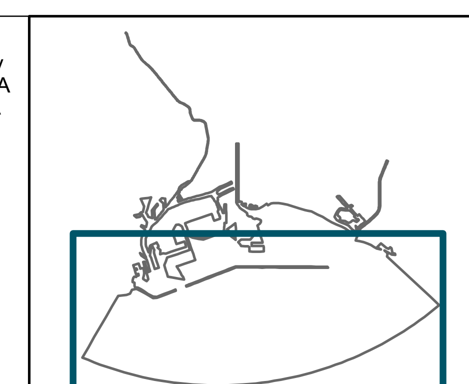


Total PCBs 2002-2014 (µg/kg dw; ND = 0)
- 0.03 - 3.2 (TMDL indirect effects target)
- 3.21 - 22.7 (TMDL direct effects target; ER-L)
- 22.71 - 90
- 90.01 - 180 (ER-M)
- 180.01 - 376
- 376.01 - 16,800

PV Shelf Exposure Area

WRAP Model Grid
- East
- West

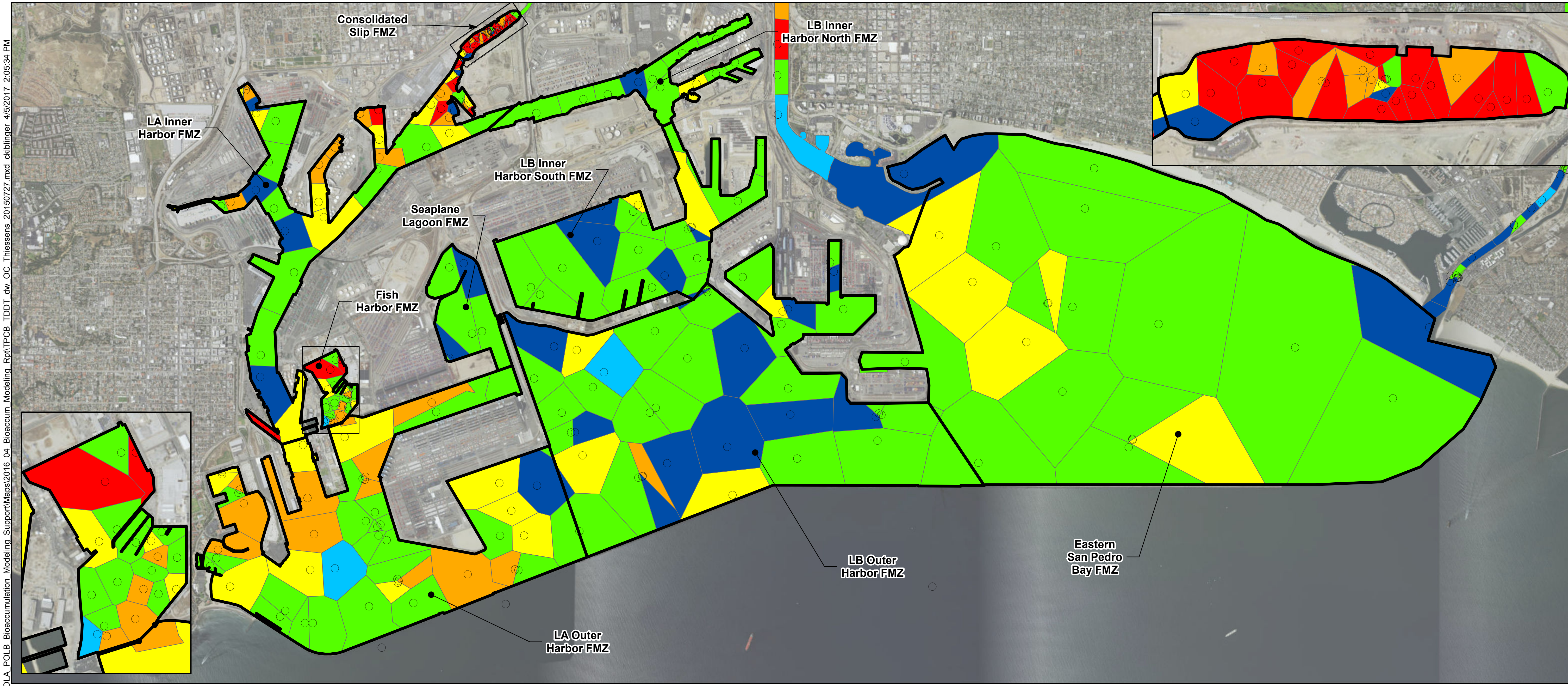
NOTES:
1. Data source: sediment_2002_2014_TPCB_TDDT_new_zone_20150724.csv
2. Data sources: AMEC (2002), Bight (2003), EMAP (2005), Bight (2008), POLA WRAP (2008), BioBaseline (2008), IR Site 7 (2010-2011), AMEC (2011), POLA Fish Harbor (2012), Weston (2012), Bight (2013), POLA/POLB (2014)



Miles
0 1 2

ANCHOR QEA

Figure 4-11d
Total PCB Concentrations in Surface Sediment Outside Harbor
Bioaccumulation Modeling Report
Greater Los Angeles and Long Beach Harbor Waters



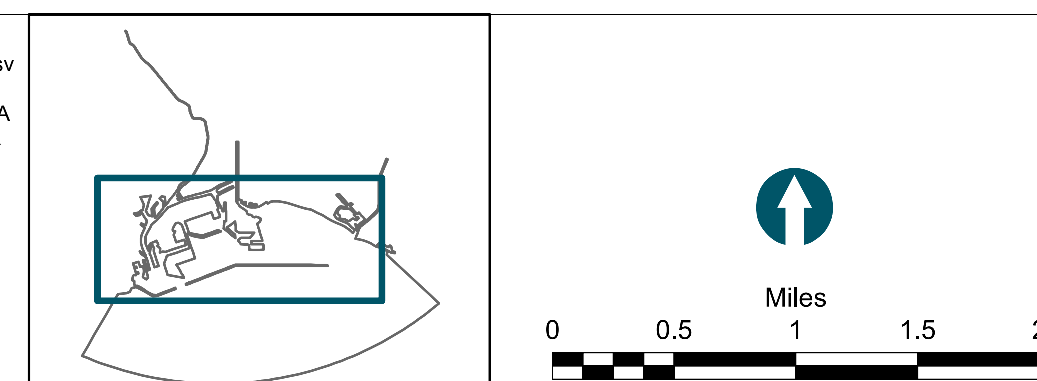
Total DDX 2002-2014 (µg/kg dw; ND = 0)

- 0.03 - 1.58 (TMDL direct effects target; ER-L)
- 1.59 - 1.9 (TMDL indirect effects target)
- 1.91 - 46.1 (ER-M)
- 46.11 - 92.2
- 92.21 - 184
- 184.01 - 2,539

Fish Movement Areas

NOTES:

1. Data sources: sediment_2002_2014_TPCB_TDDT_new_zone_20150724.csv and POLB_GWMA_2016_Sed_results_20170112.xlsx
2. Data sources: AMEC (2002), Bight (2003), EMAP (2005), Bight (2008), POLA WRAP (2008), BioBaseline (2008), IR Site 7 (2010-2011), AMEC (2011), POLA Fish Harbor (2012), Weston (2012), Bight (2013), POLA/POLB (2014), RMC (2016)
3. Surface sediment concentrations were assigned to each WRAP model grid cell based on these estimated exposure concentrations and professional judgment.



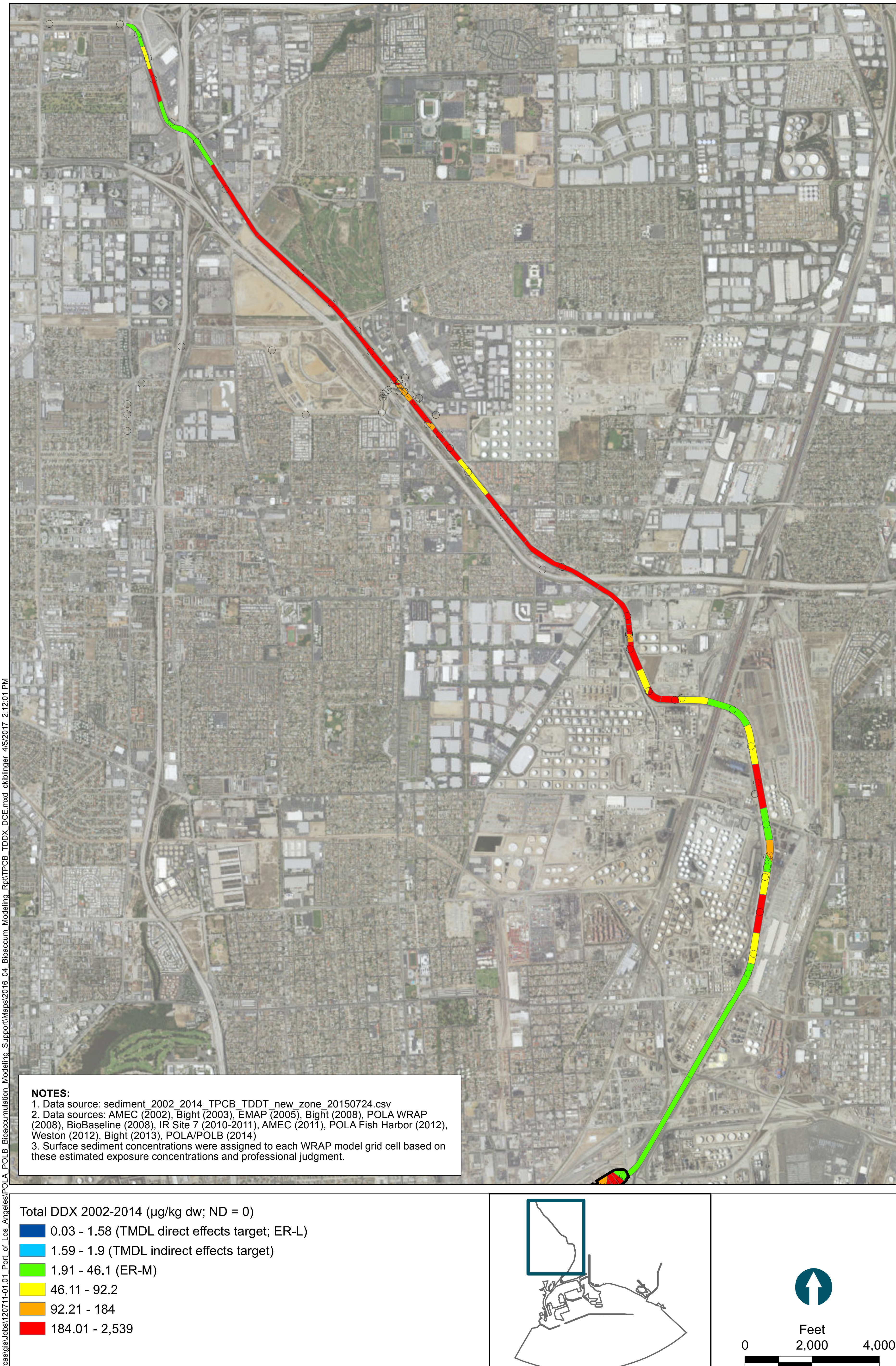
ANCHOR QEA

Figure 4-12a

Thiessen Polygons Showing Total DDX Concentrations in Surface Sediment

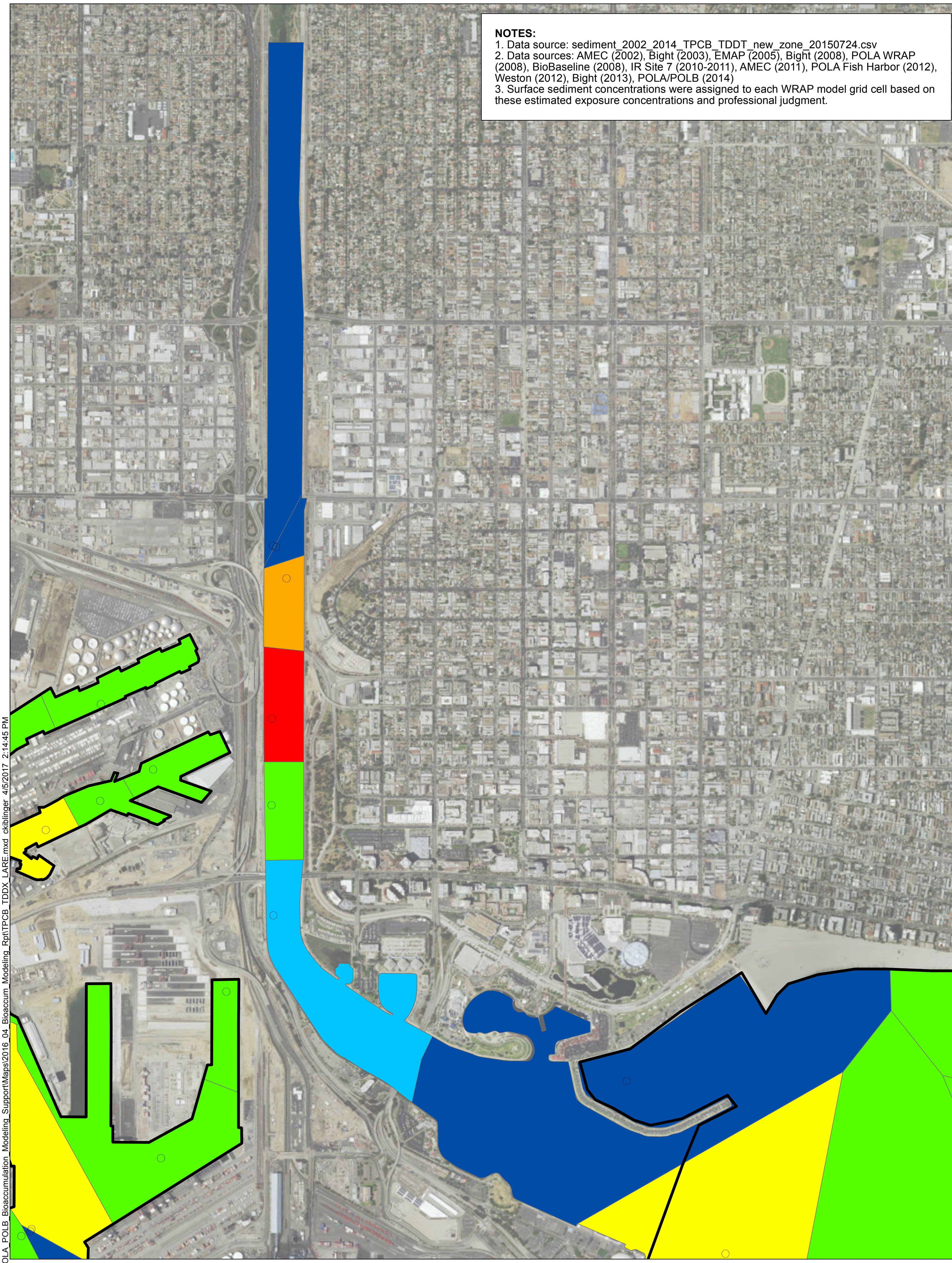
Bioaccumulation Modeling Report

Greater Los Angeles and Long Beach Harbor Waters



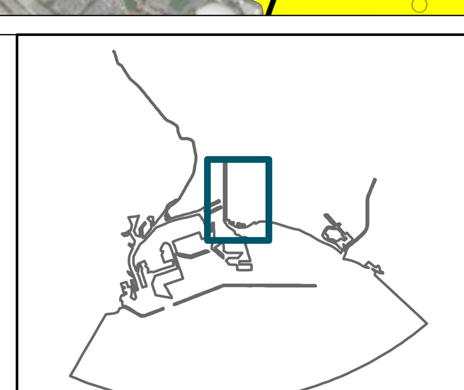
NOTES:
1. Data source: sediment_2002_2014_TPCB_TDDT_new_zone_20150724.csv
2. Data sources: AMEC (2002), Bight (2003), EMAP (2005), Bight (2008), POLA WRAP (2008), BioBaseline (2008), IR Site 7 (2010-2011), AMEC (2011), POLA Fish Harbor (2012), Weston (2012), Bight (2013), POLA/POLB (2014)
3. Surface sediment concentrations were assigned to each WRAP model grid cell based on these estimated exposure concentrations and professional judgment.

Figure 4-12b
Total DDX Concentrations in Surface Sediment in the Dominguez Channel Estuary
Bioaccumulation Modeling Report
Greater Los Angeles and Long Beach Harbor Waters



Total DDX 2002-2014 (µg/kg dw; ND = 0)

- 0.03 - 1.58 (TMDL direct effects target; ER-L)
- 1.59 - 1.9 (TMDL indirect effects target)
- 1.91 - 46.1 (ER-M)
- 46.11 - 92.2
- 92.21 - 184
- 184.01 - 2,539



Feet
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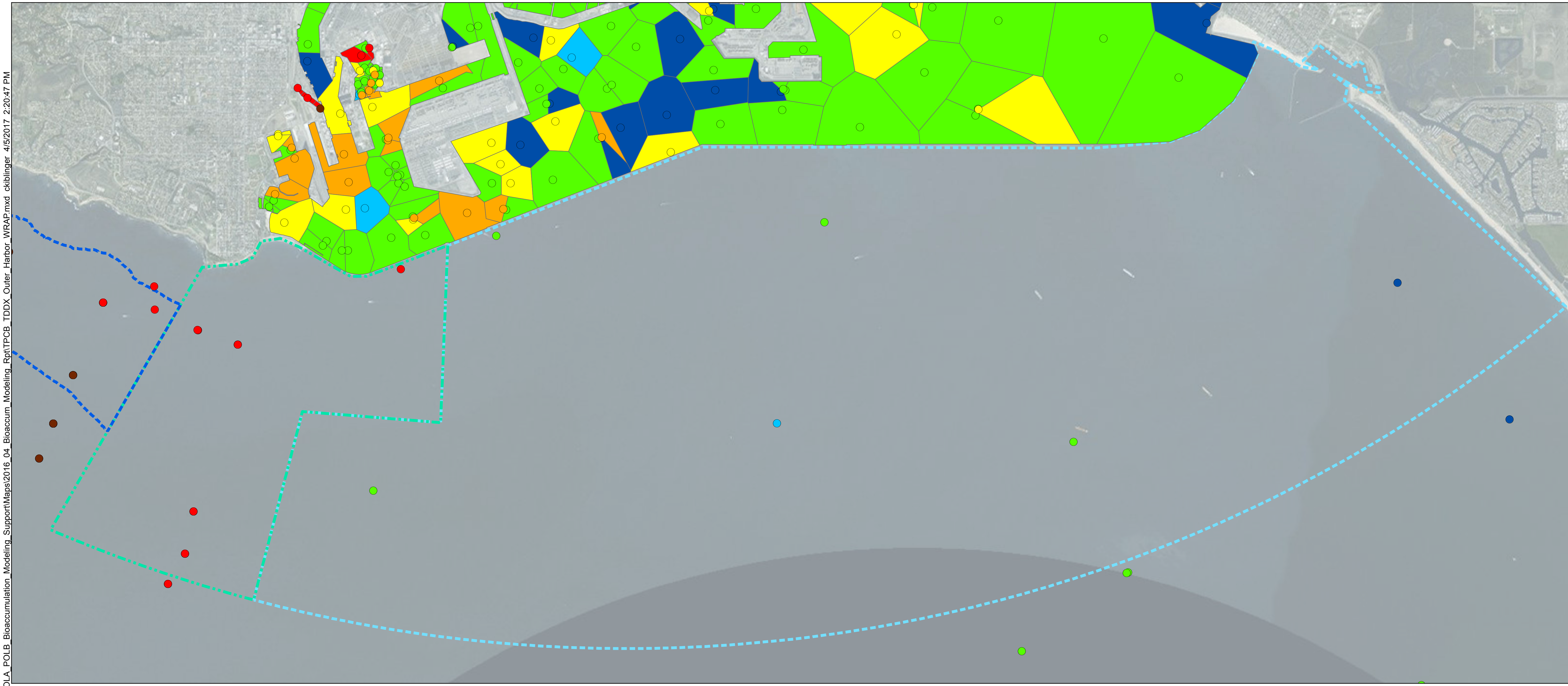
ANCHOR QEA

Figure 4-12c
Total DDX Concentrations in Surface Sediment in the Los Angeles River Estuary
Bioaccumulation Modeling Report
Greater Los Angeles and Long Beach Harbor Waters

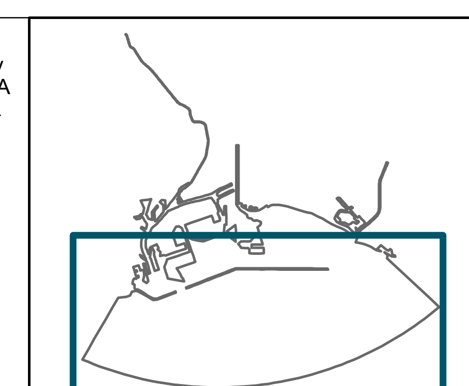


Total DDX 2002-2014 (µg/kg dw; ND = 0)
- 0.03 - 1.58 (TMDL direct effects target; ER-L)
- 1.59 - 1.9 (TMDL indirect effects target)
- 1.91 - 46.1 (ER-M)
- 46.11 - 92.2
- 92.21 - 184
- 184.01 - 2,539

PV Shelf Exposure Area

WRAP Model Grid
- East
- West

NOTES:
1. Data source: sediment_2002_2014_TPCB_TDDT_new_zone_20150724.csv
2. Data sources: AMEC (2002), Bight (2003), EMAP (2005), Bight (2008), POLA WRAP (2008), BioBaseline (2008), IR Site 7 (2010-2011), AMEC (2011), POLA Fish Harbor (2012), Weston (2012), Bight (2013), POLA/POLB (2014)



Miles
0 1 2

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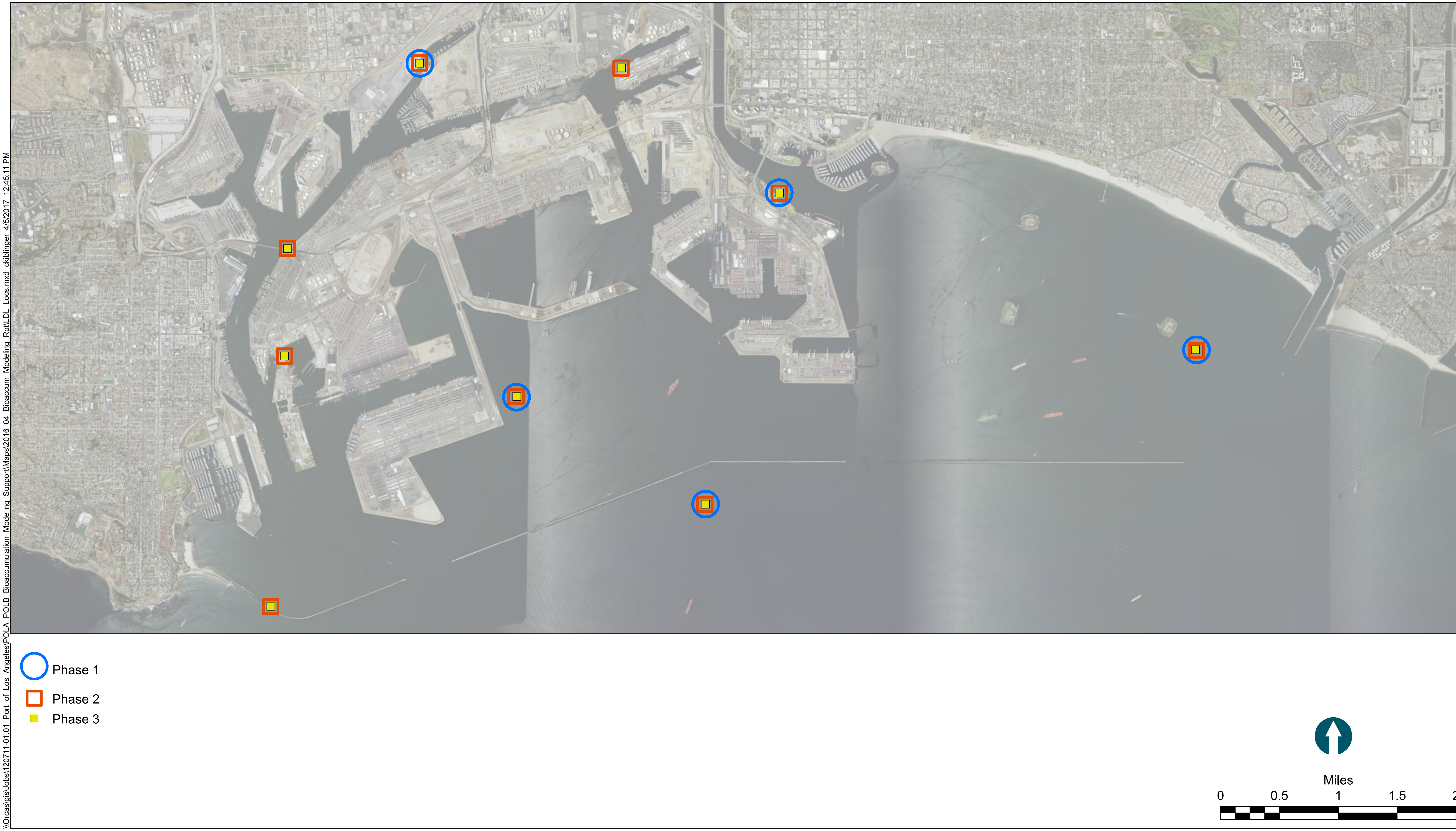
ANCHOR QEA

Figure 4-12d
Total DDX Concentrations in Surface Sediment Outside Harbor
Bioaccumulation Modeling Report
Greater Los Angeles and Long Beach Harbor Waters



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ANCHOR QEA

Figure 4-13
Low-detection Limit Water Column Study Sampling Locations
Bioaccumulation Modeling Report
Greater Los Angeles and Long Beach Harbor Waters

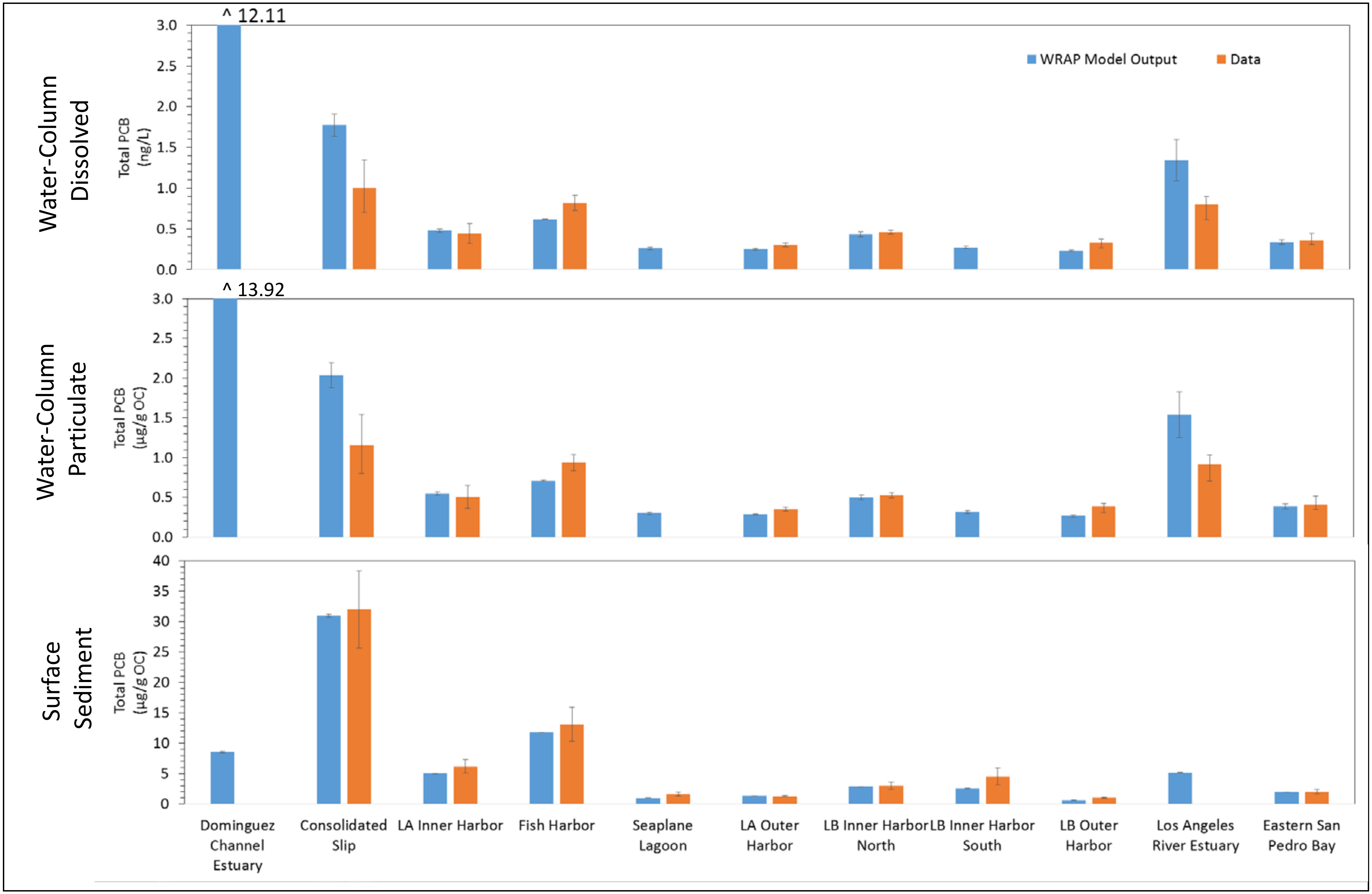


Figure 4-14

Average WRAP Output Compared to Data – Total PCB

Mean +/- two standard errors for WRAP model output and sediment data (surface area weighted).
Mean and range for water column based data (SPME data from LDL Study).

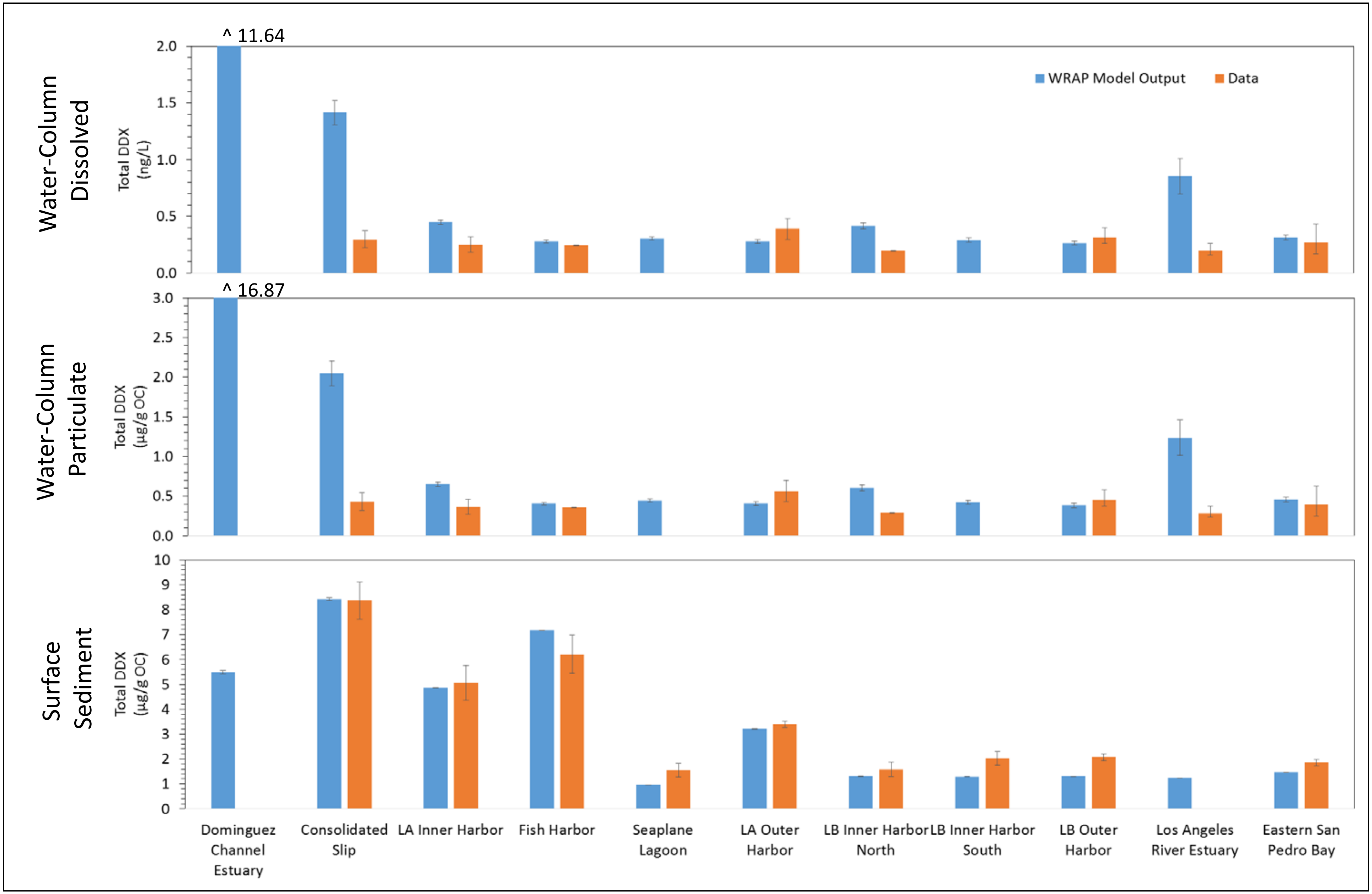
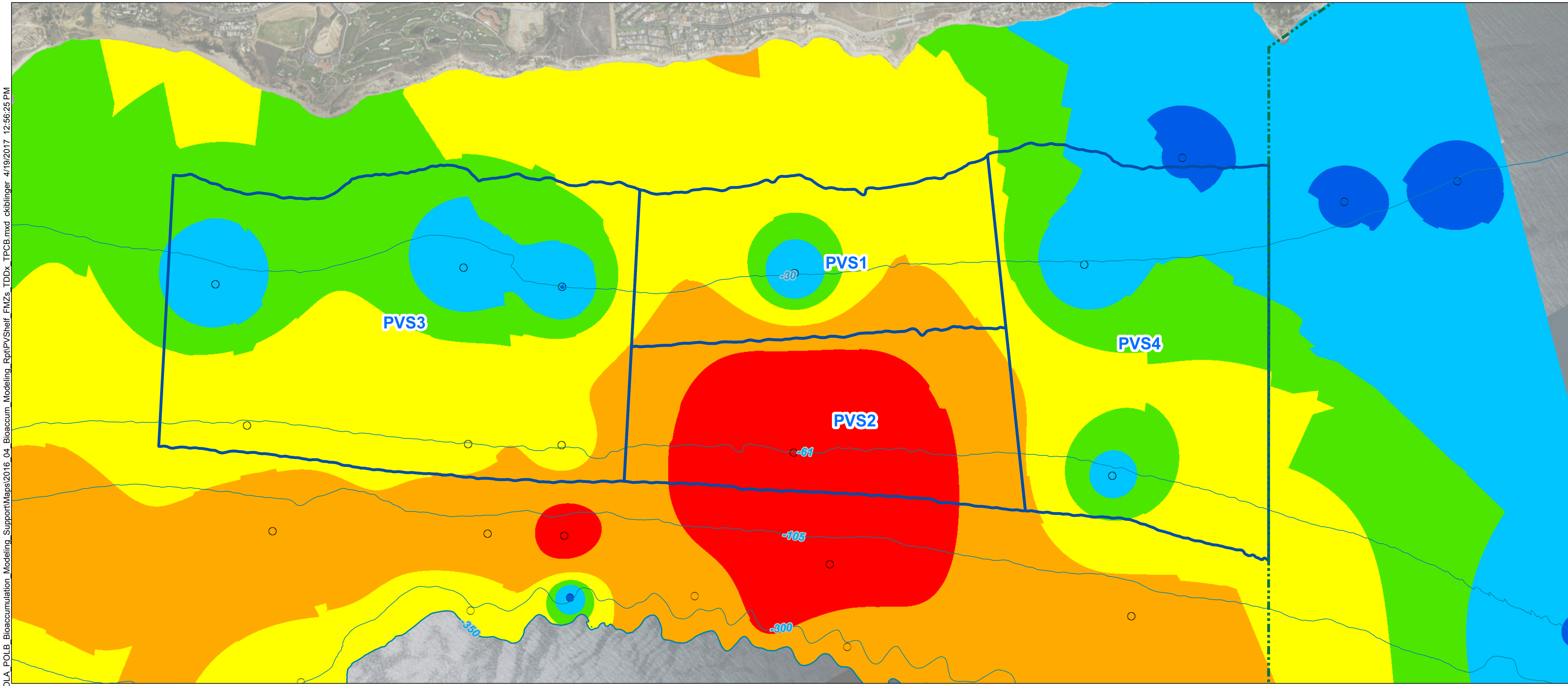


Figure 4-15

Average WRAP Output Compared to Data – Total DDX

Mean +/- two standard errors for WRAP model output and sediment data (surface area weighted).
Mean and range for water column based data (SPME data from LDL Study).

ANCHOR QEA



Sample Location
Bathymetric Contour (meters NAVD88)
PV Shelf Fish Movement Zones
WRAP Model Grid

Total PCB 2005-2014 (mg/kg-OC, ND=1/2)

- 0.0773 - 0.25
- 0.251 - 2.5
- 2.51 - 5
- 5.01 - 10
- 10.1 - 20
- 20.1 - 64.1

NOTES:
1. IDW interpolation was based on the mean value of co-located samples.
2. Data source: sediment_2002_2014_TPCB_TDDT_OCNormalized_new_zone_20150724.csv

Feet
0 2,000 4,000

Figure 4-16
Fish Movement Zones on the PV Shelf Relative to Total PCB Concentrations
Bioaccumulation Modeling Report
Greater Los Angeles and Long Beach Harbor Waters

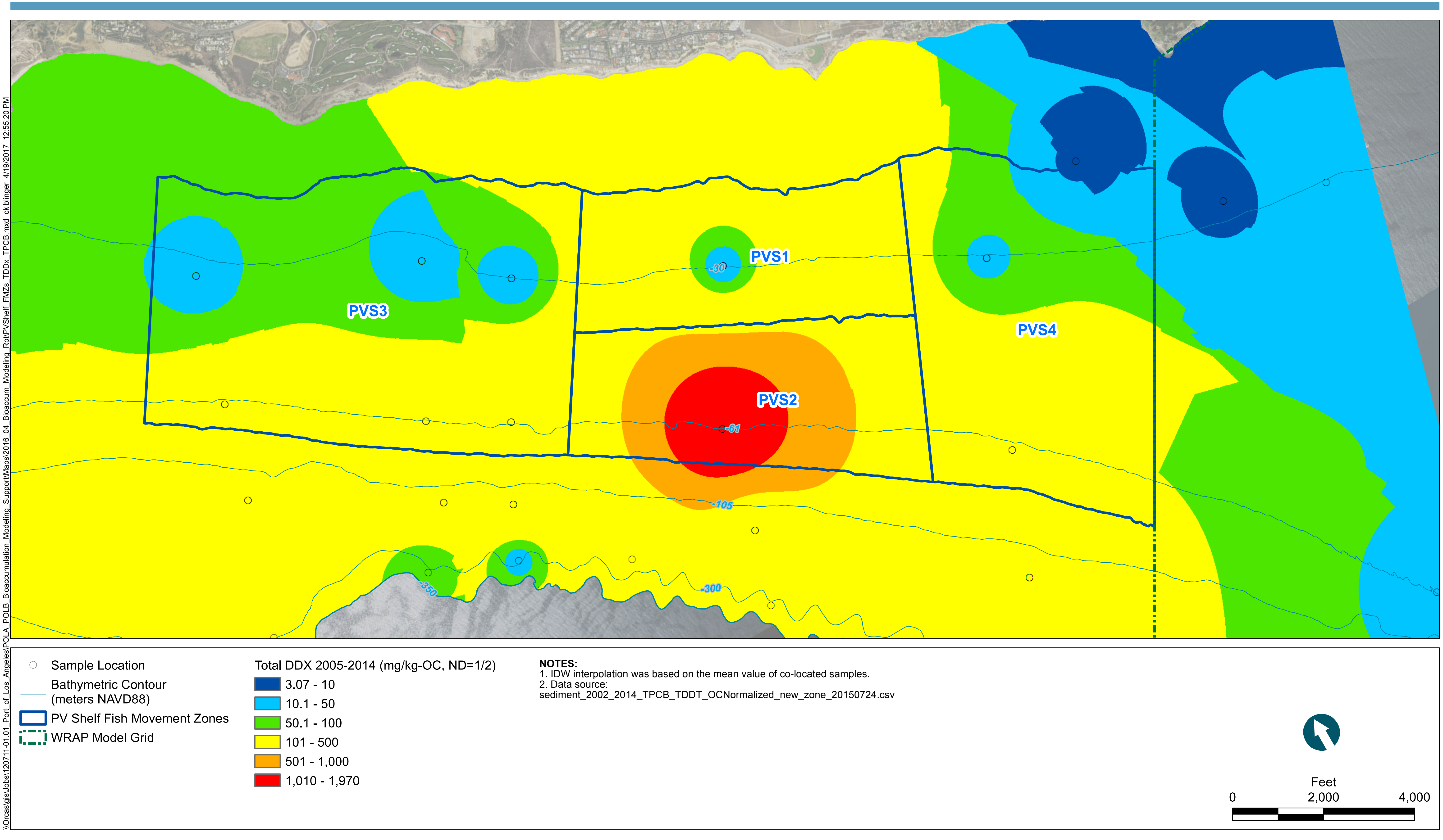


Figure 4-17
Fish Movement Zones on the PV Shelf Relative to Total DDX Concentrations
Bioaccumulation Modeling Report
Greater Los Angeles and Long Beach Harbor Waters

ANCHOR QEA

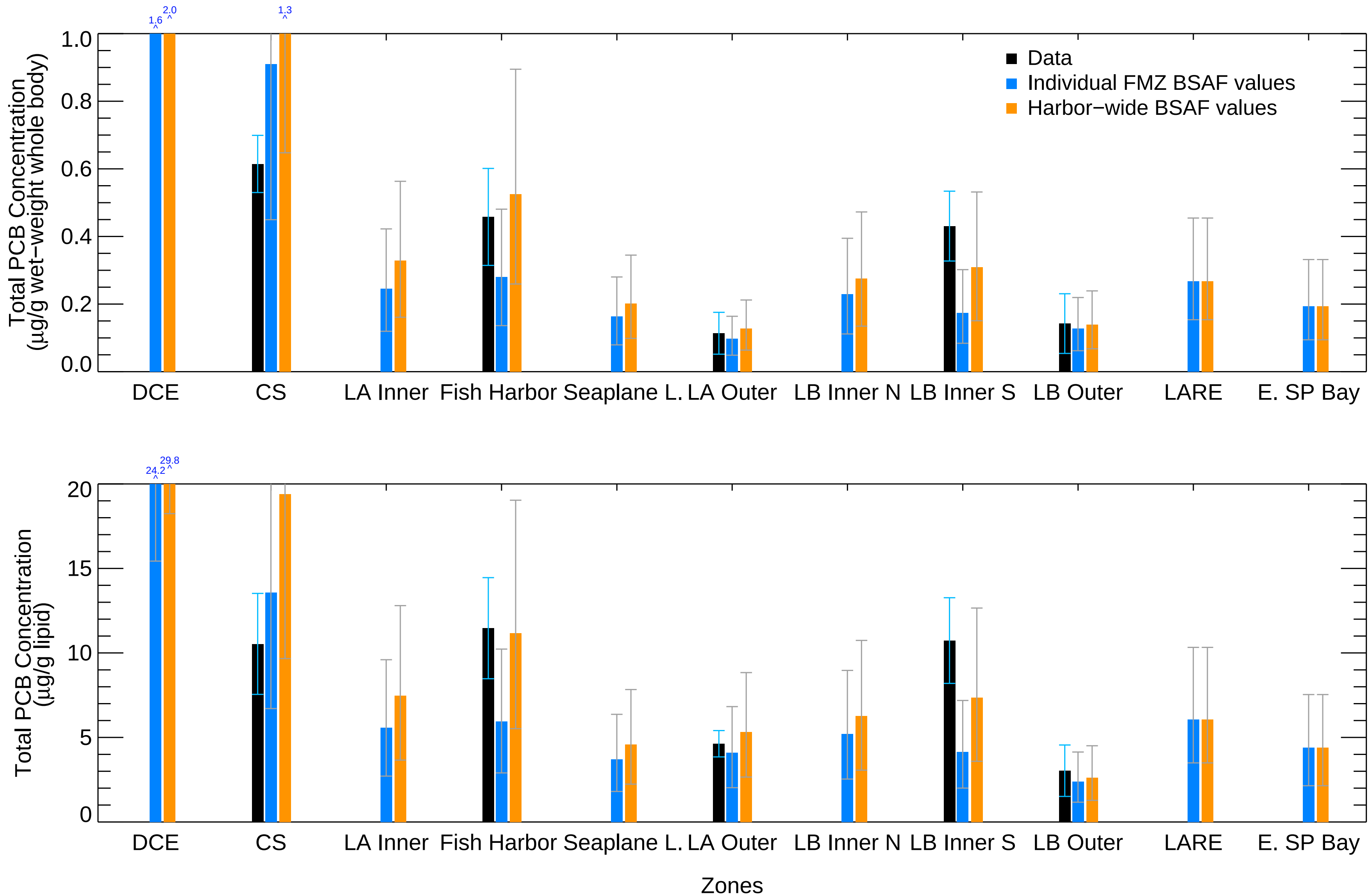


Figure 5−1a

Effects of Biota Sediment Accumulation Factor on Total PCB Concentration in Surfperch

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ files v.1677, 1677 and biota files v.1727, 16151 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Tue Apr 25 12:43:58 2017

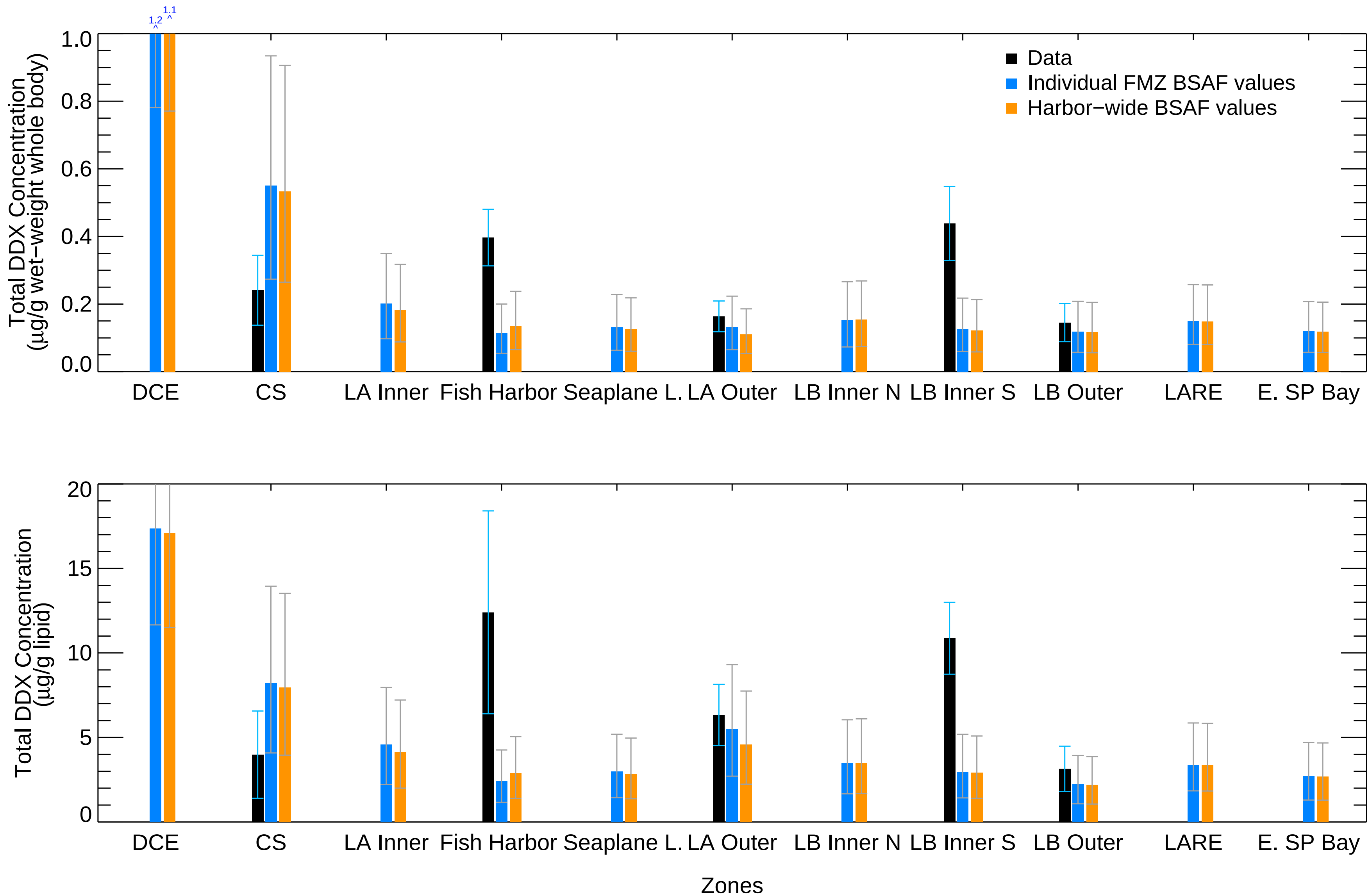


Figure 5−1b

Effects of Biota Sediment Accumulation Factor on Total DDX Concentration in Surfperch

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ files v.1677, 1677 and biota files v.1727, 16151 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Tue Apr 25 12:43:59 2017

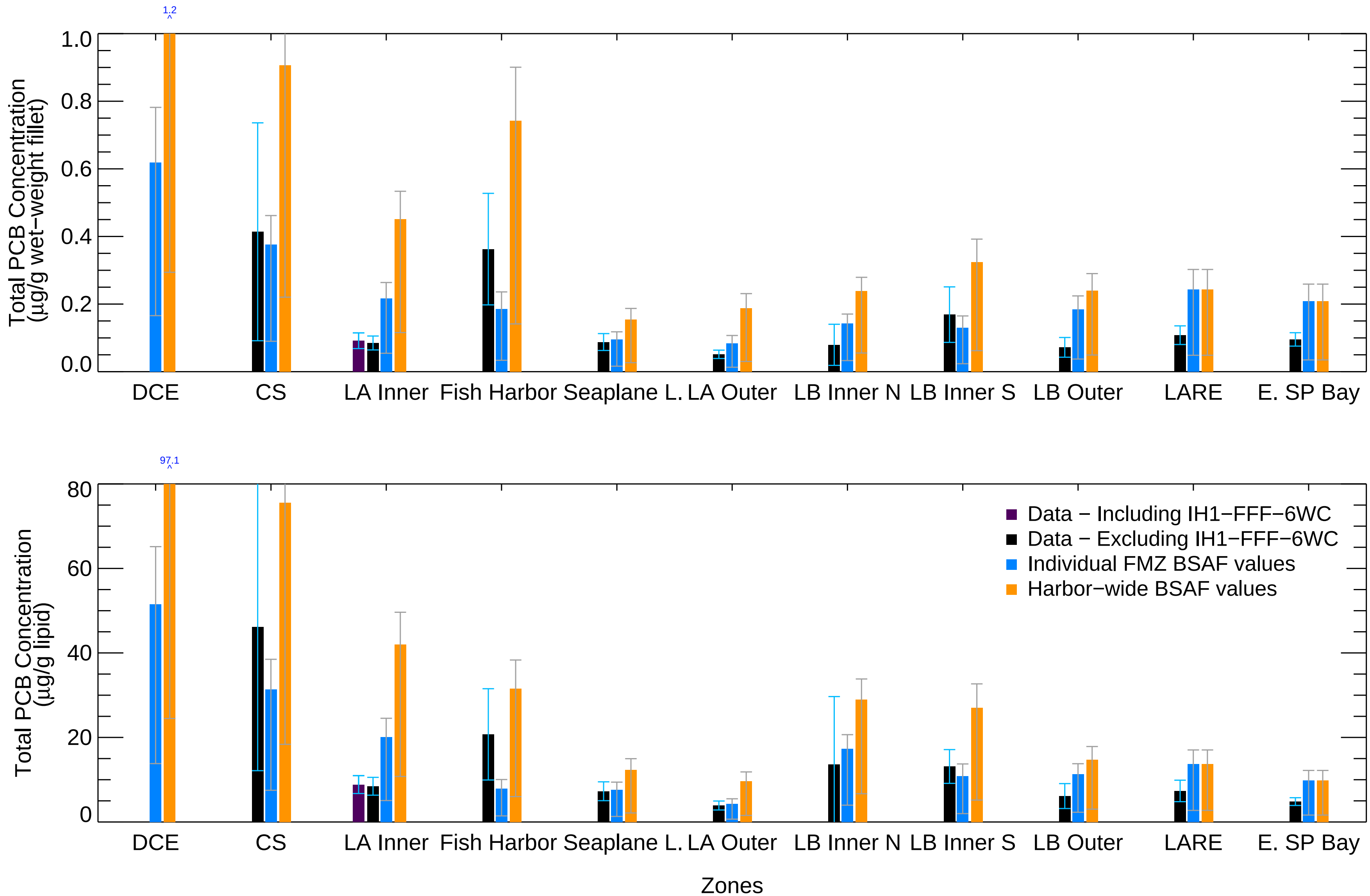


Figure 5−1c

Effects of Biota Sediment Accumulation Factor on Total PCB Concentration in White Croaker

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx. Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value), IH1−FFF−6WC (high value). Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1677 and biota files v.1727, 16151 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Tue Apr 25 12:43:59 2017

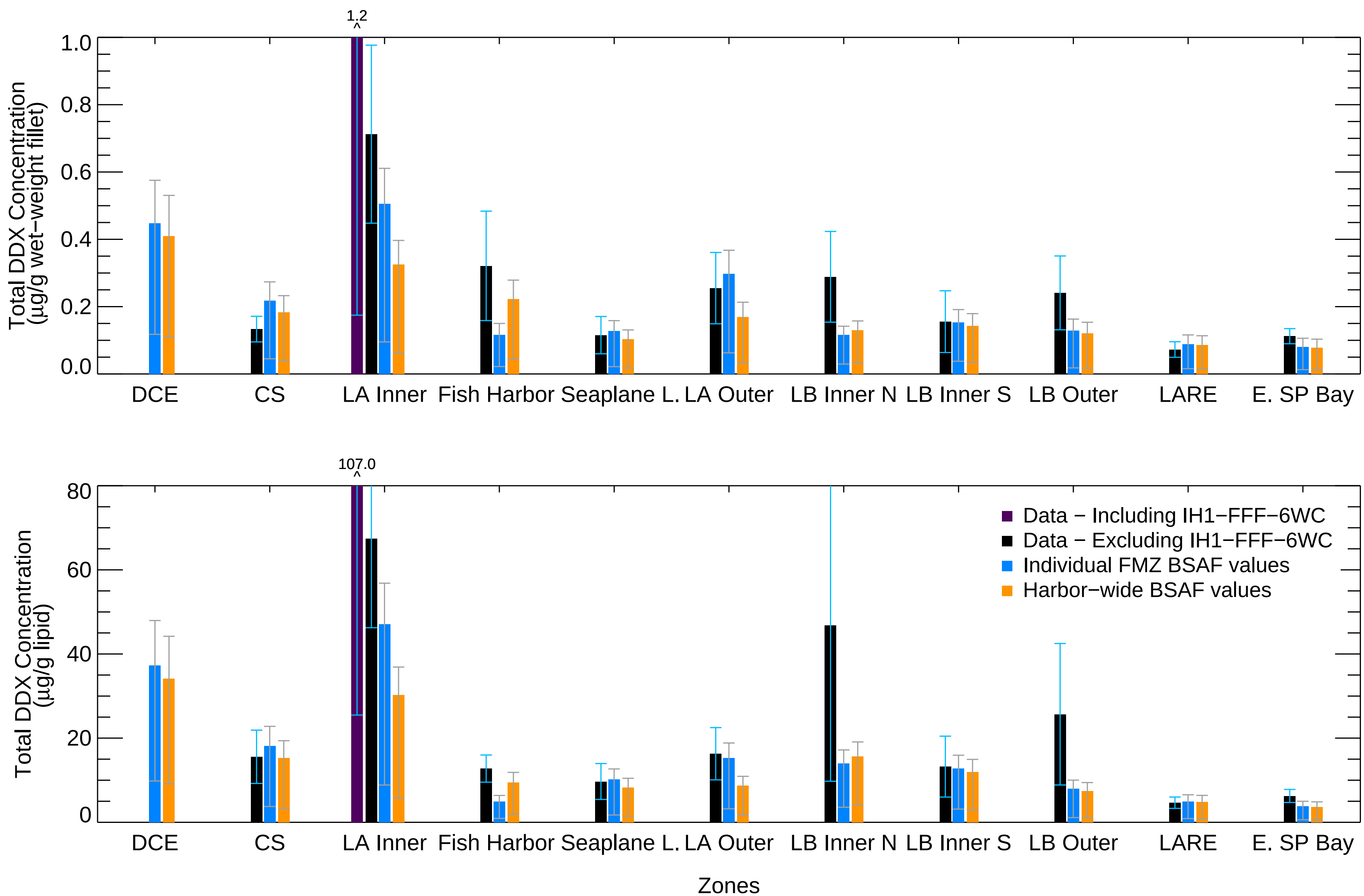


Figure 5−1d

Effects of Biota Sediment Accumulation Factor on Total DDX Concentration in White Croaker

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx. Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value), IH1−FFF−6WC (high value). Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1677 and biota files v.1727, 16151 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Tue Apr 25 12:43:59 2017

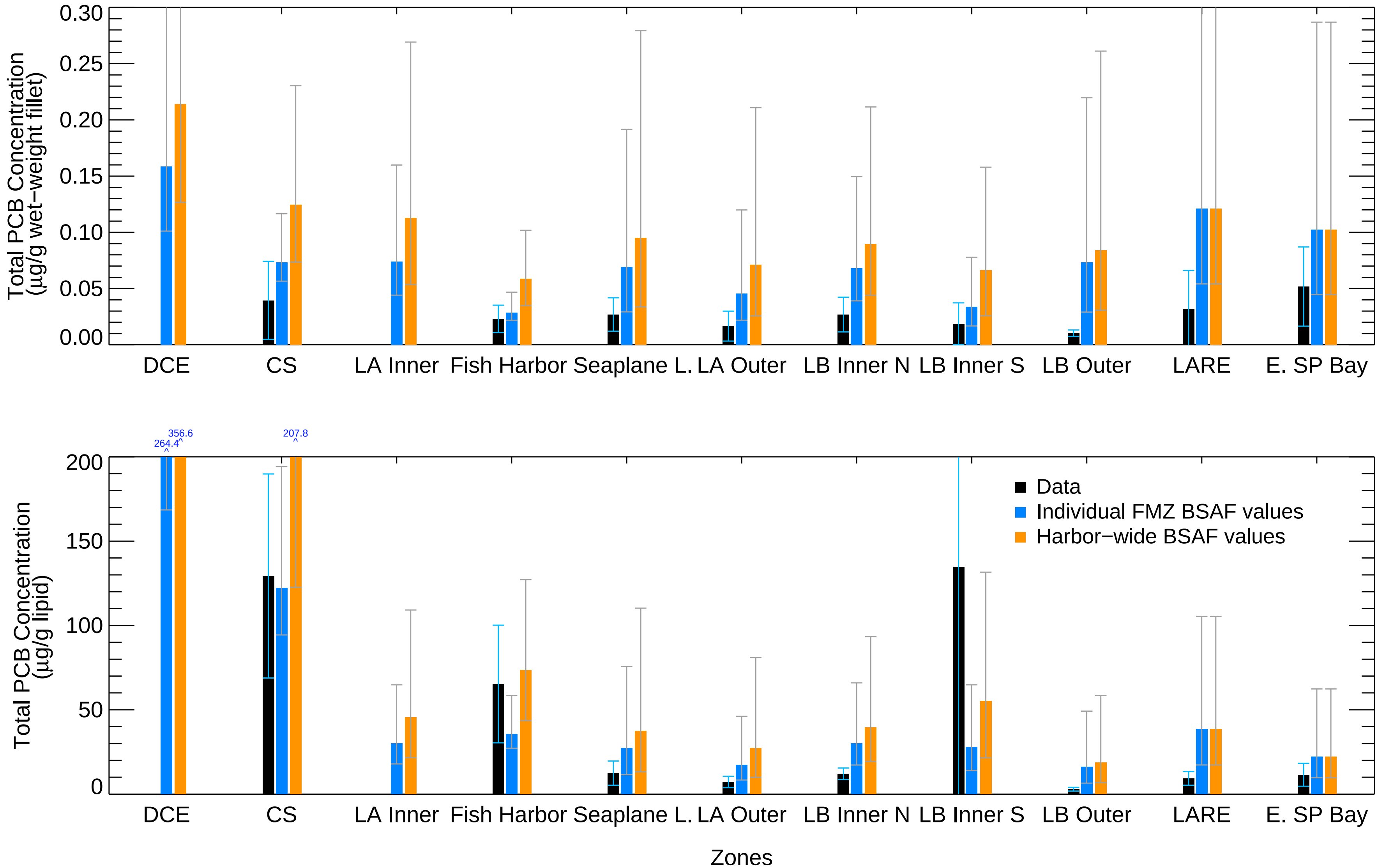


Figure 5−1e

Effects of Biota Sediment Accumulation Factor on Total PCB Concentration in California Halibut

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx. Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1677 and biota files v.1727, 16151 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Tue Apr 25 12:43:59 2017

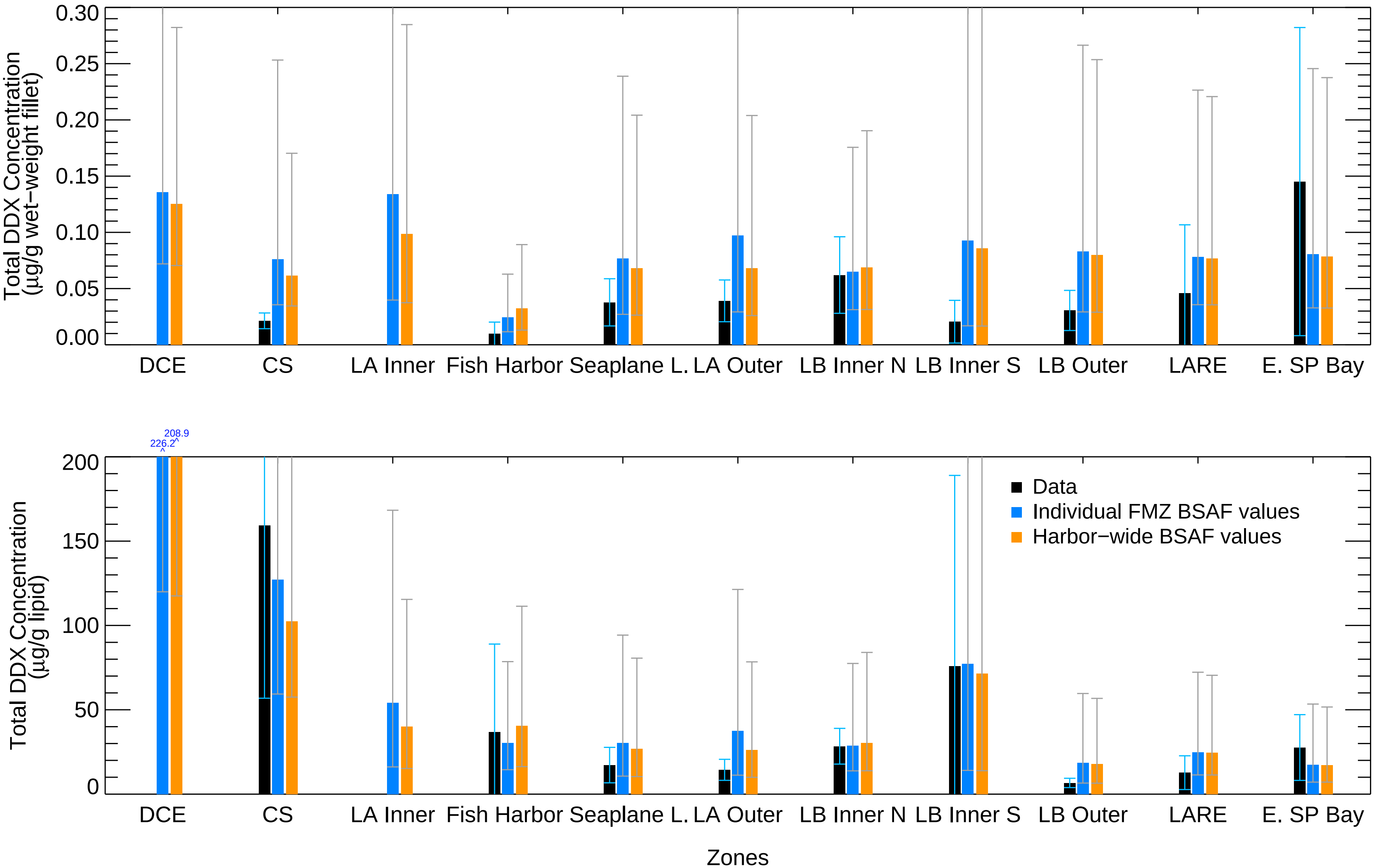


Figure 5−1f

Effects of Biota Sediment Accumulation Factor on Total DDX Concentration in California Halibut

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1677 and biota files v.1727, 16151 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Tue Apr 25 12:43:59 2017

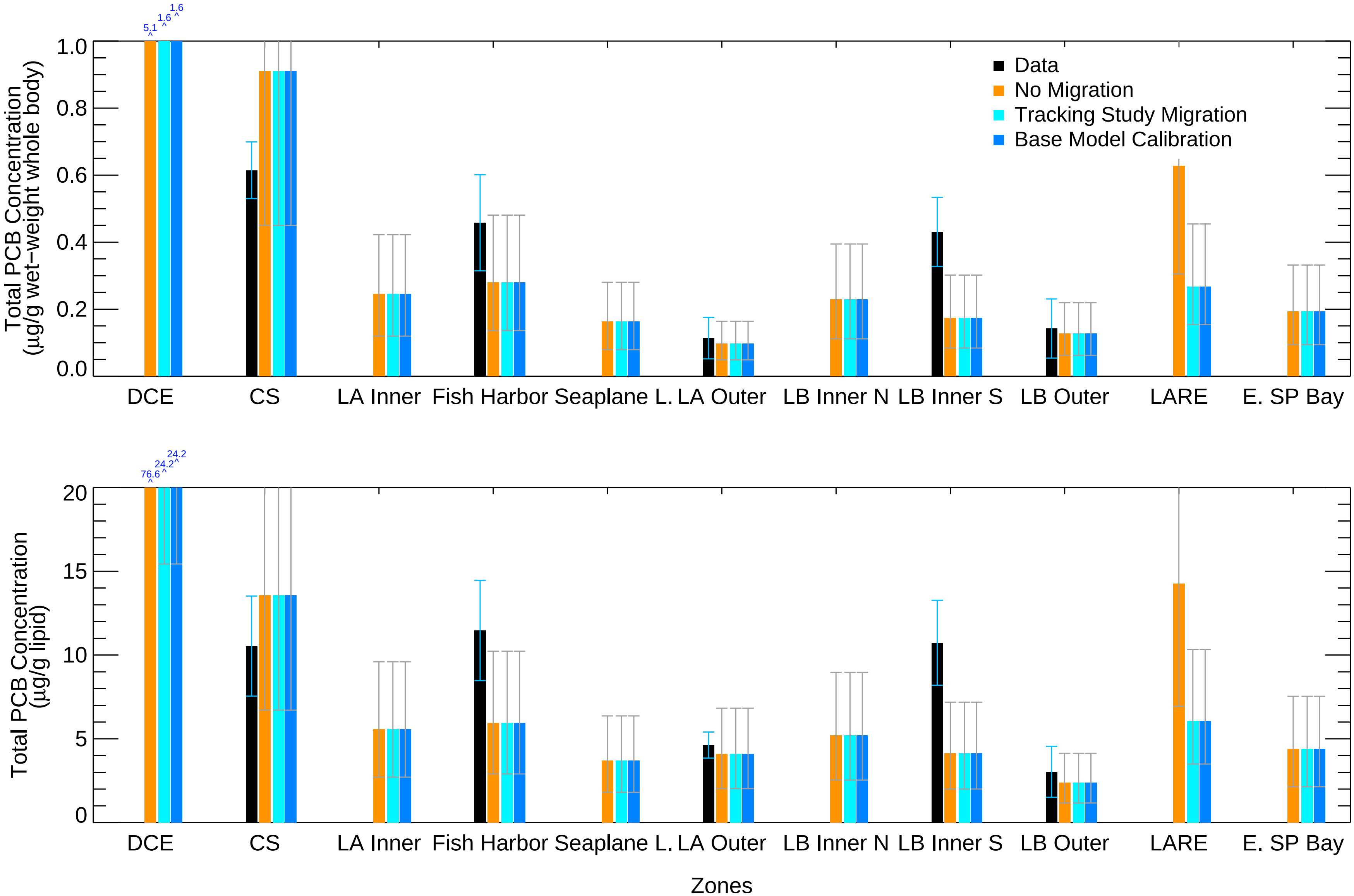


Figure 5−2a

Effects of Fish Migration on Total PCB Concentration in Surfperch

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ files v.16109, 16111, 1677 and biota files v.1730, 1731, 1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Mon Feb 27 15:13:14 2017

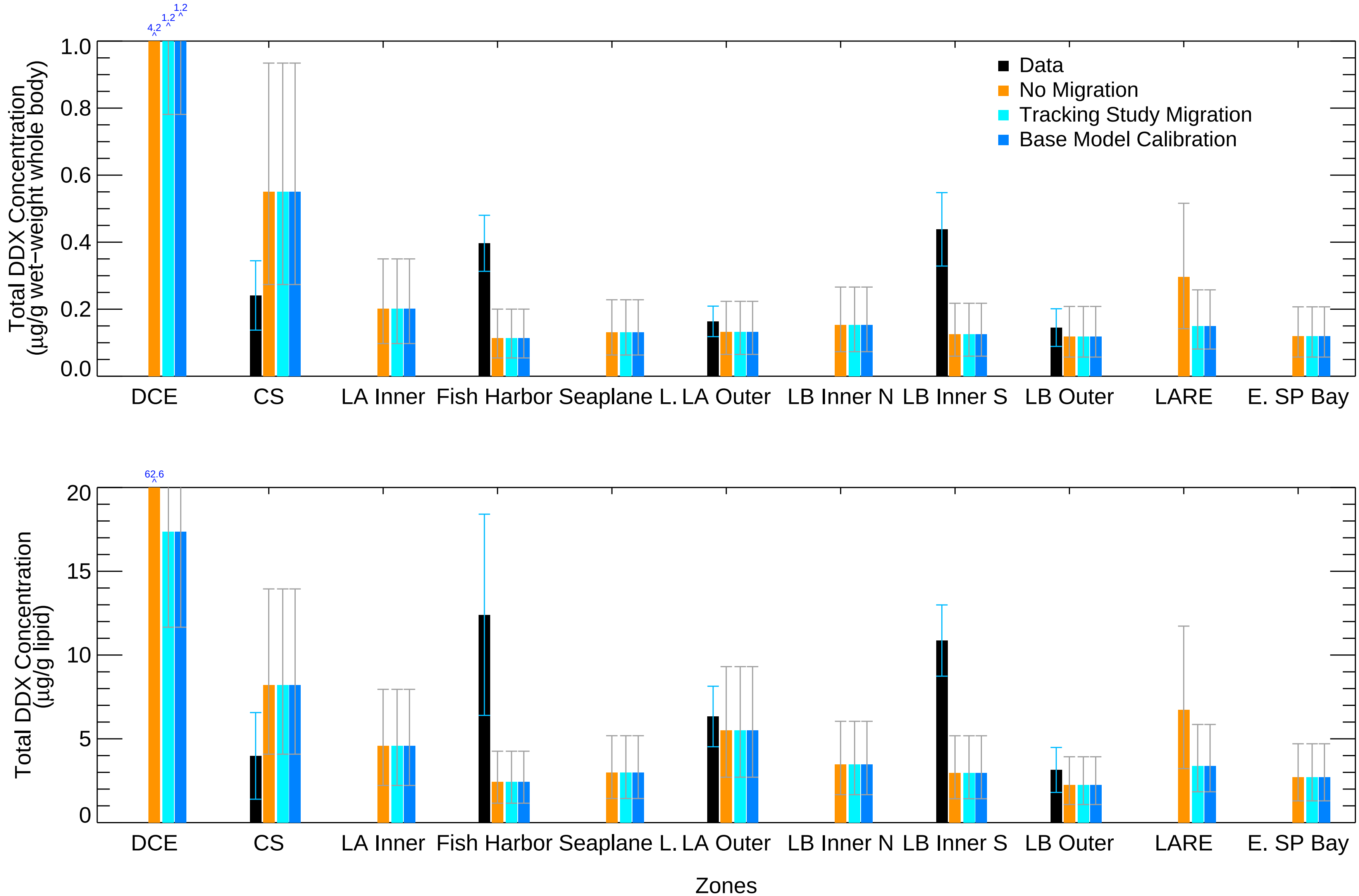


Figure 5−2b

Effects of Fish Migration on Total DDX Concentration in Surfperch

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ files v.16109, 16111, 1677 and biota files v.1730, 1731, 1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Mon Feb 27 15:13:14 2017

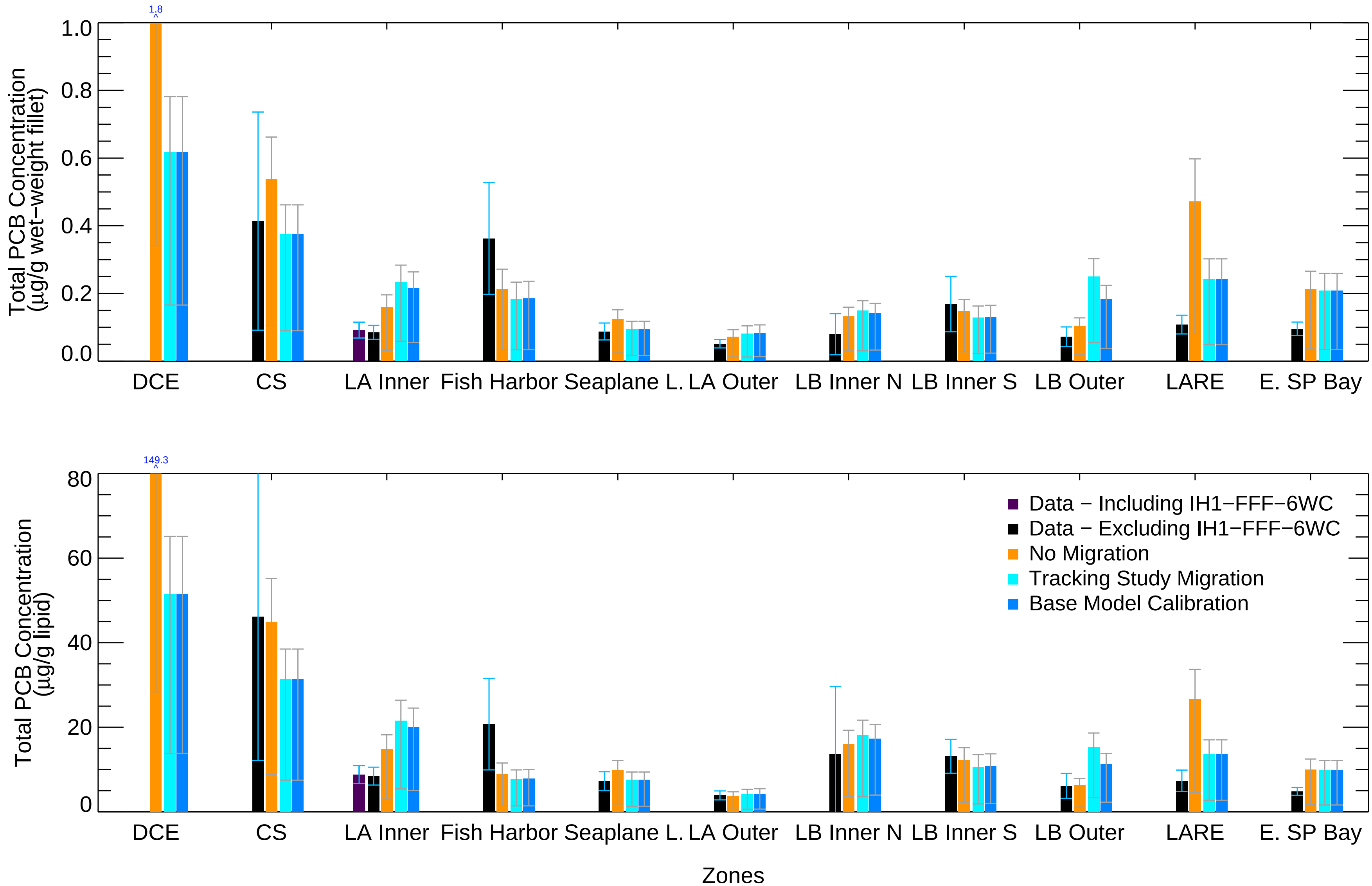


Figure 5−2c

Effects of Fish Migration on Total PCB Concentration in White Croaker

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx. Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value), IH1−FFF−6WC (high value). Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.16109, 16111, 1677 and biota files v.1730, 1731, 1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Mon Feb 27 15:13:14 2017

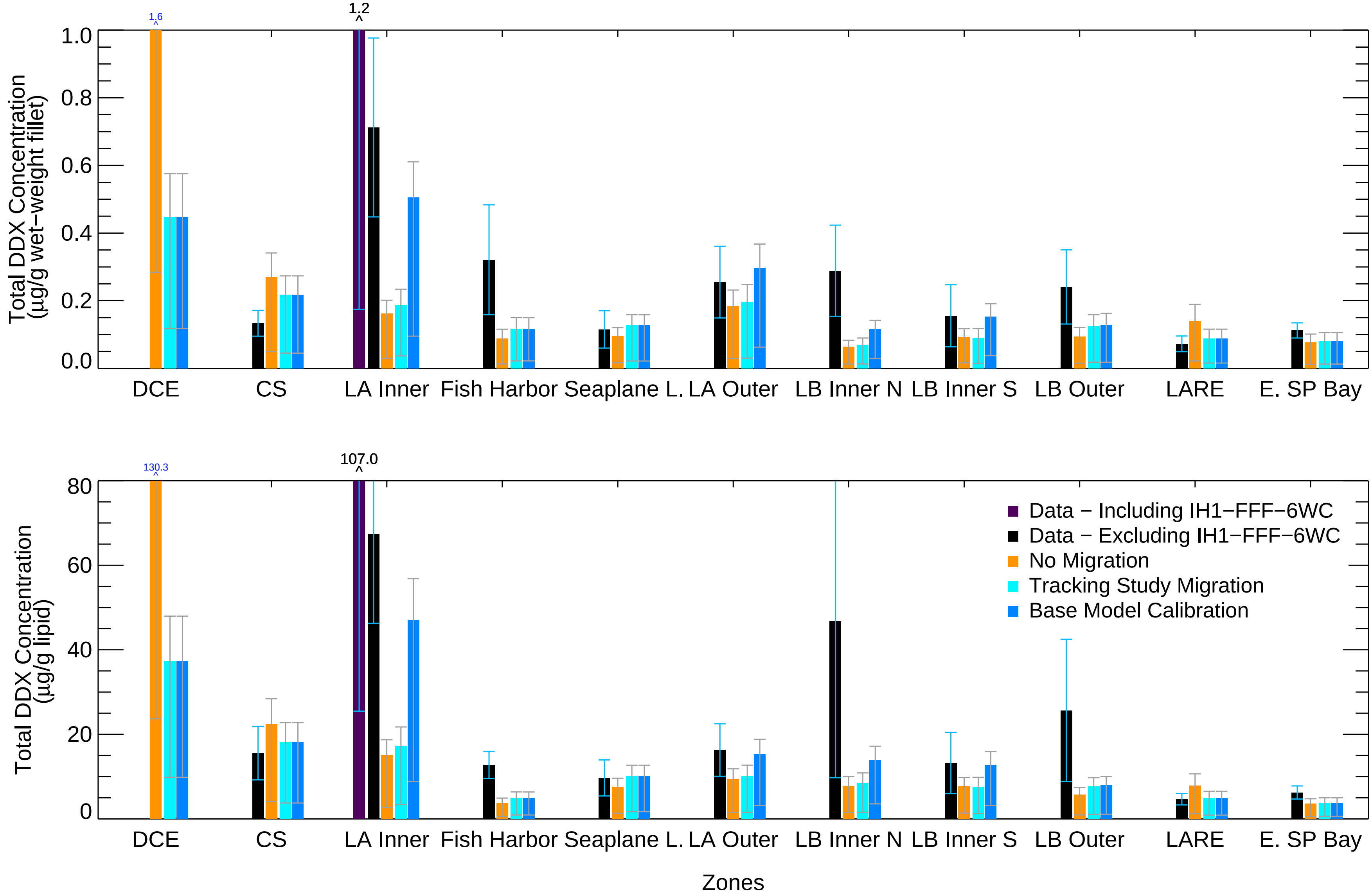


Figure 5−2d

Effects of Fish Migration on Total DDX Concentration in White Croaker

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value), IH1−FFF−6WC (high value). Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.16109, 16111, 1677 and biota files v.1730, 1731, 1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Mon Feb 27 15:13:14 2017

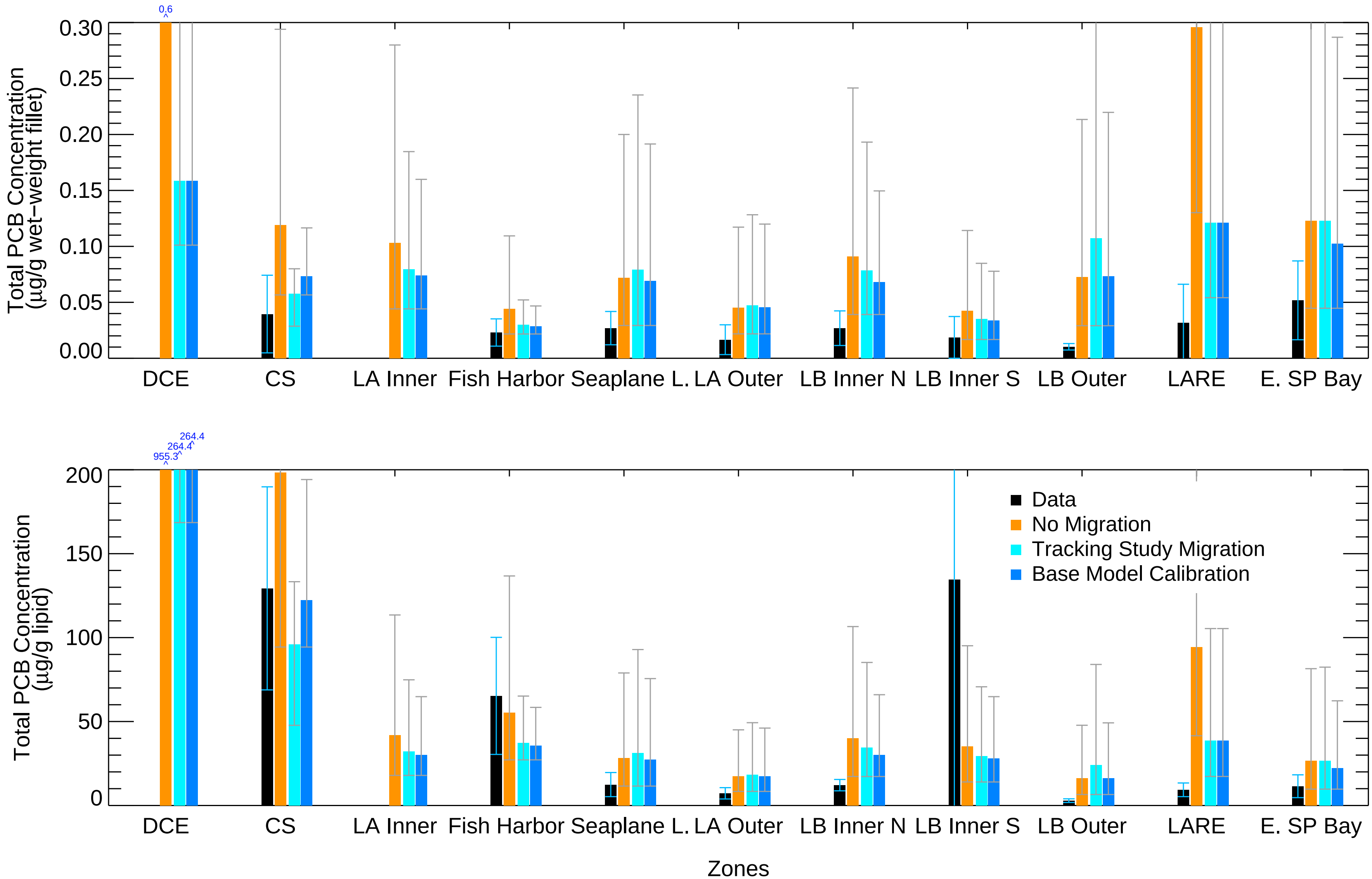


Figure 5−2e

Effects of Fish Migration on Total PCB Concentration in California Halibut

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.16109, 16111, 1677 and biota files v.1730, 1731, 1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Mon Feb 27 15:13:14 2017

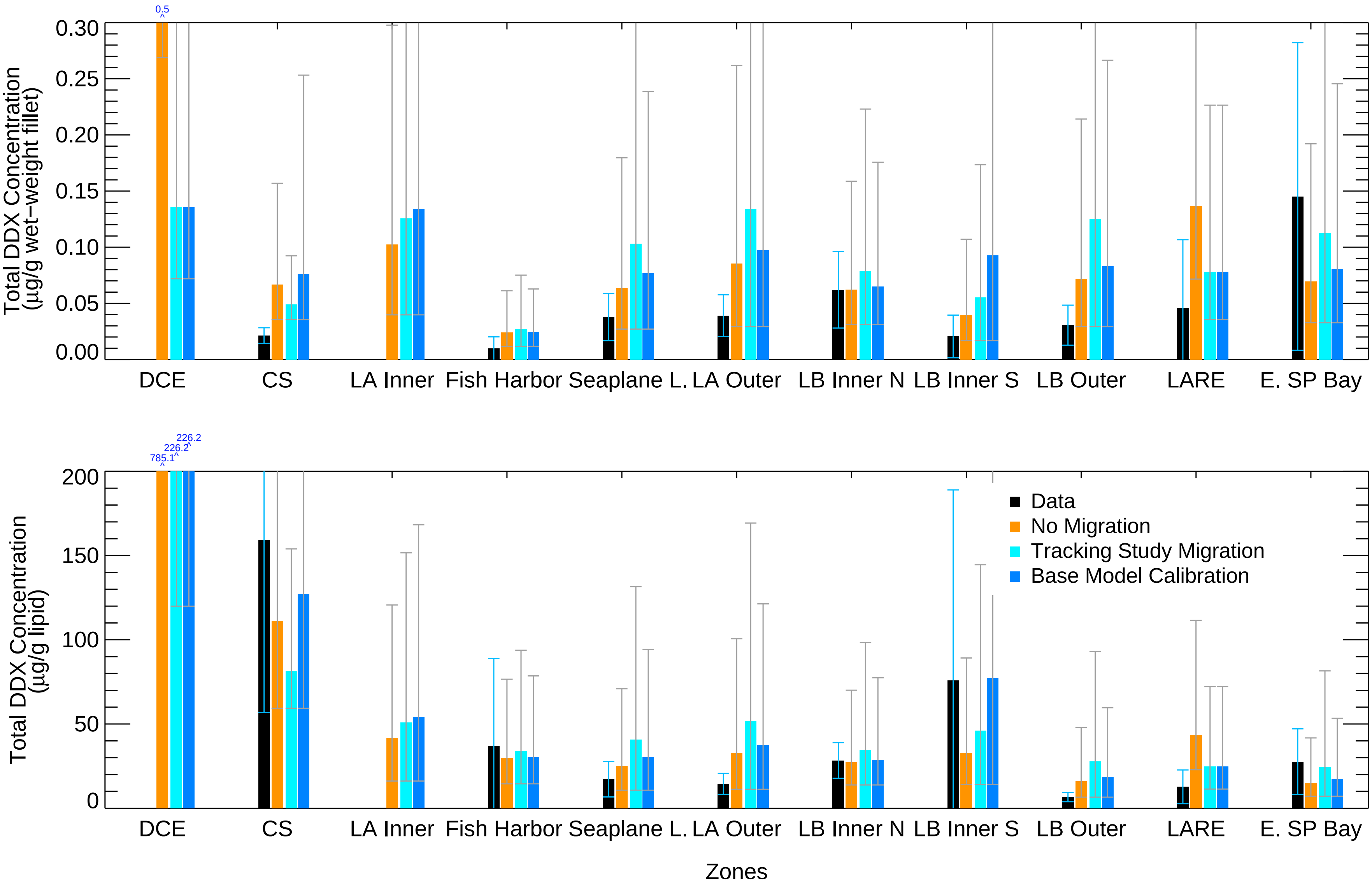


Figure 5−2f

Effects of Fish Migration on Total DDX Concentration in California Halibut

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.16109, 16111, 1677 and biota files v.1730, 1731, 1727 used for model.

ANCHOR QEA

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Mon Feb 27 15:13:14 2017

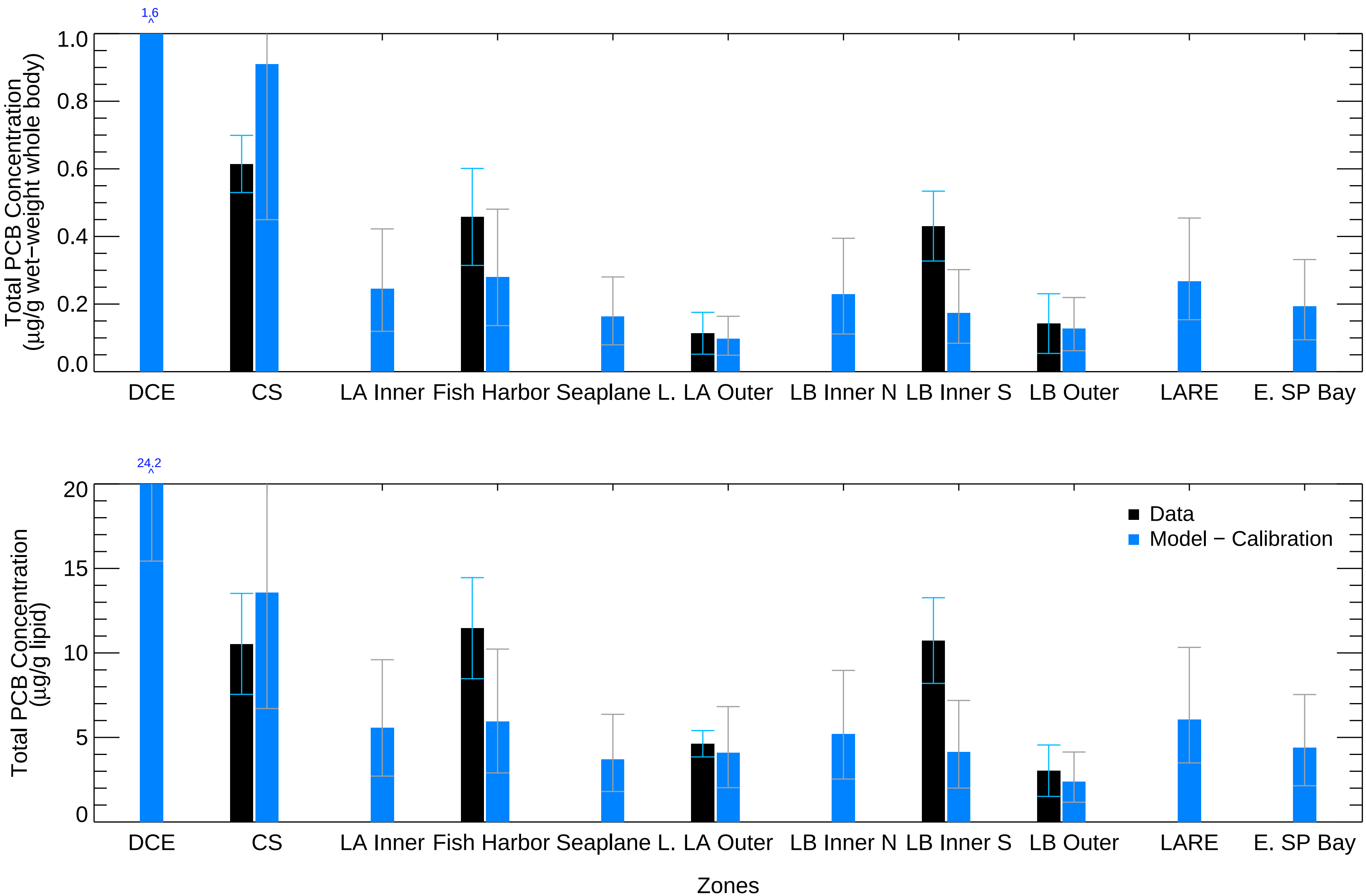


Figure 5−3

Model to Data Comparison of Total PCB Concentrations in Surfperch

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ file v.1677 and biota file v.1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_fish_model_data_comparison_wMigration_calib.pro Mon Feb 27 16:07:40 2017

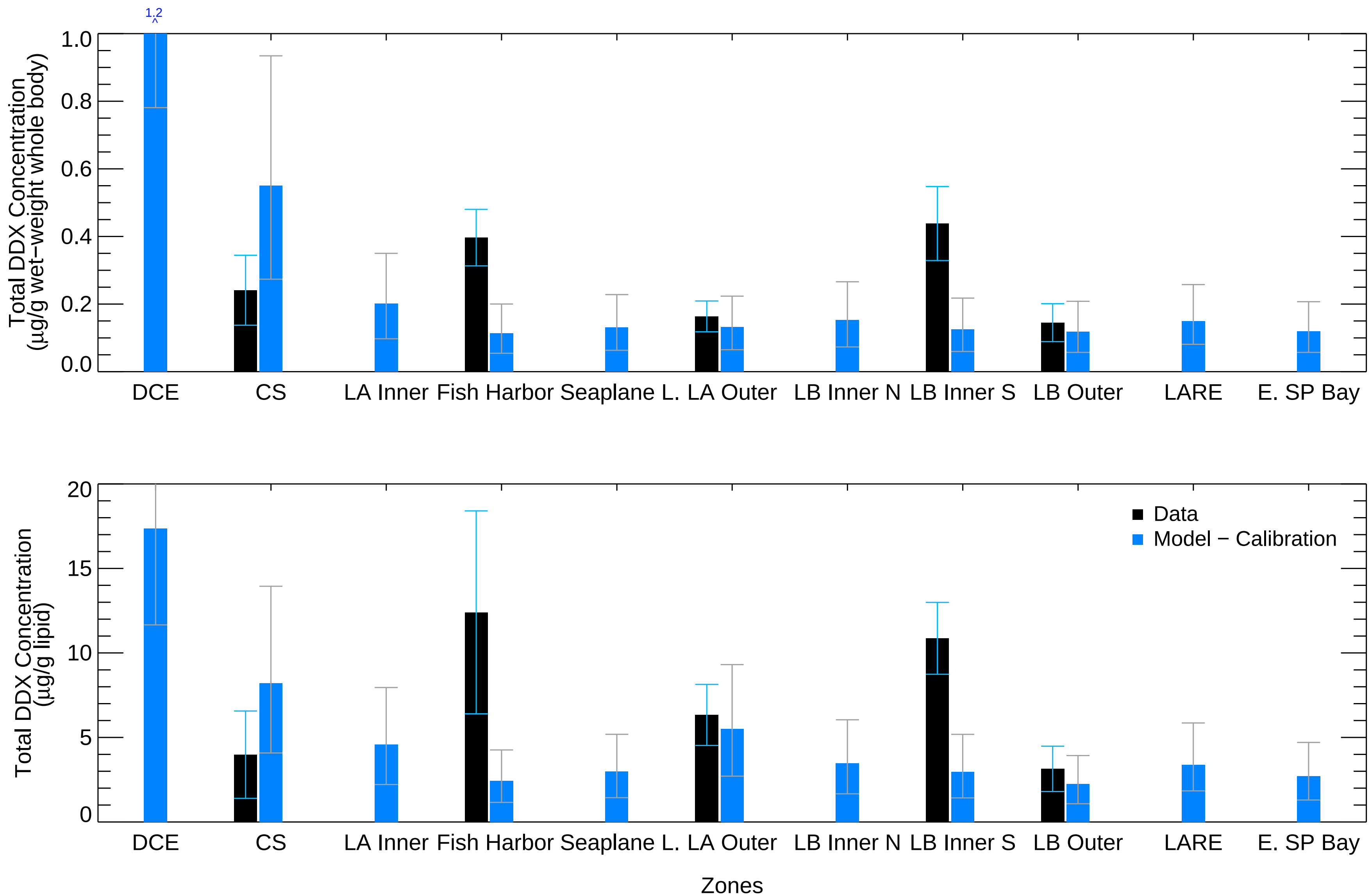


Figure 5−4

Model to Data Comparison of Total DDX Concentrations in Surfperch

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ file v.1677 and biota file v.1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_fish_model_data_comparison_wMigration_calib.pro Mon Feb 27 16:07:40 2017

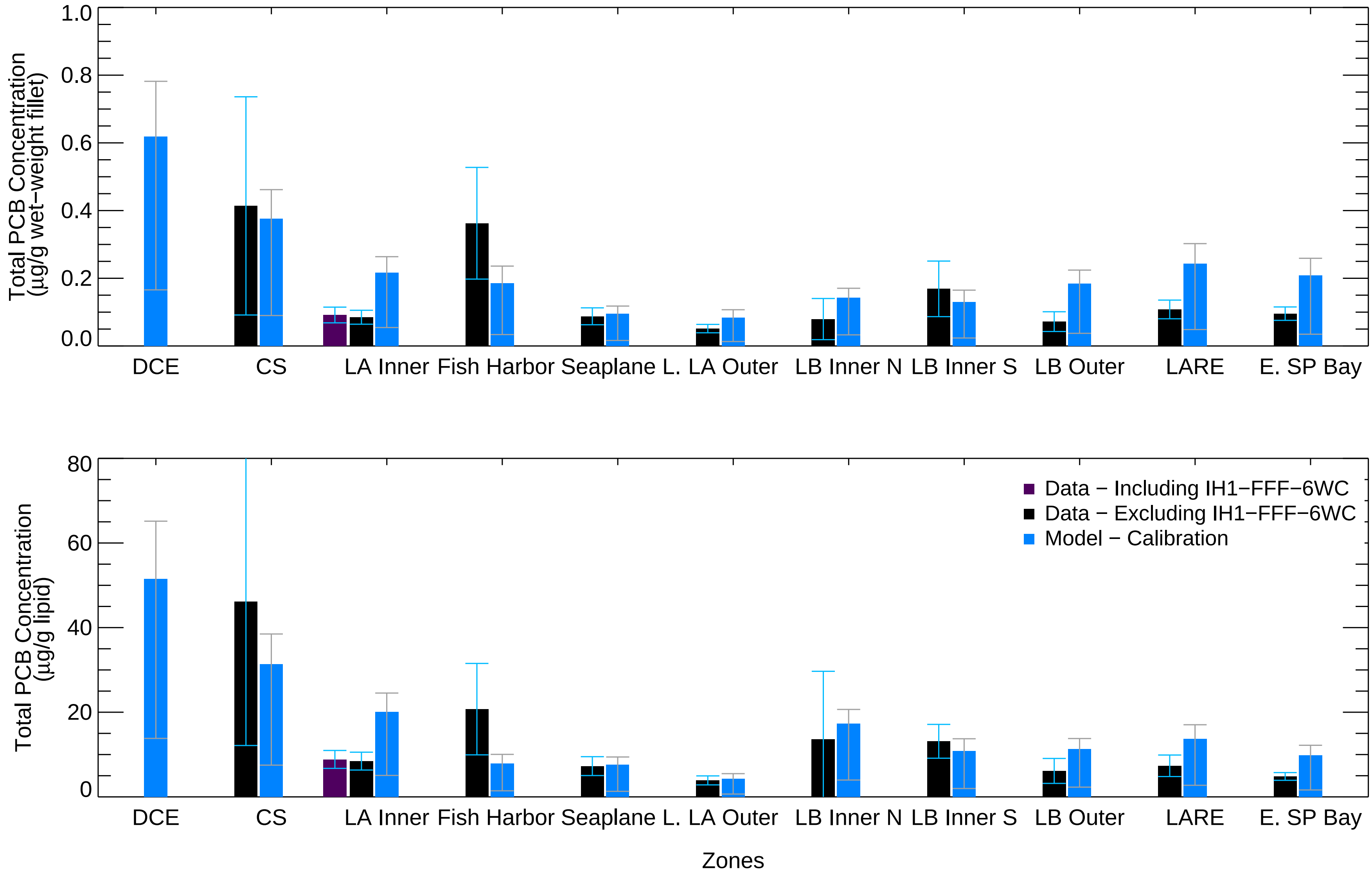


Figure 5−5

Model to Data Comparison of Total PCB Concentrations in White Croaker

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx. Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value). Model results are averaged over all days within the last year and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ file v.1677 and biota file v.1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_fish_model_data_comparison_wMigration_calib.pro Mon Feb 27 16:07:40 2017

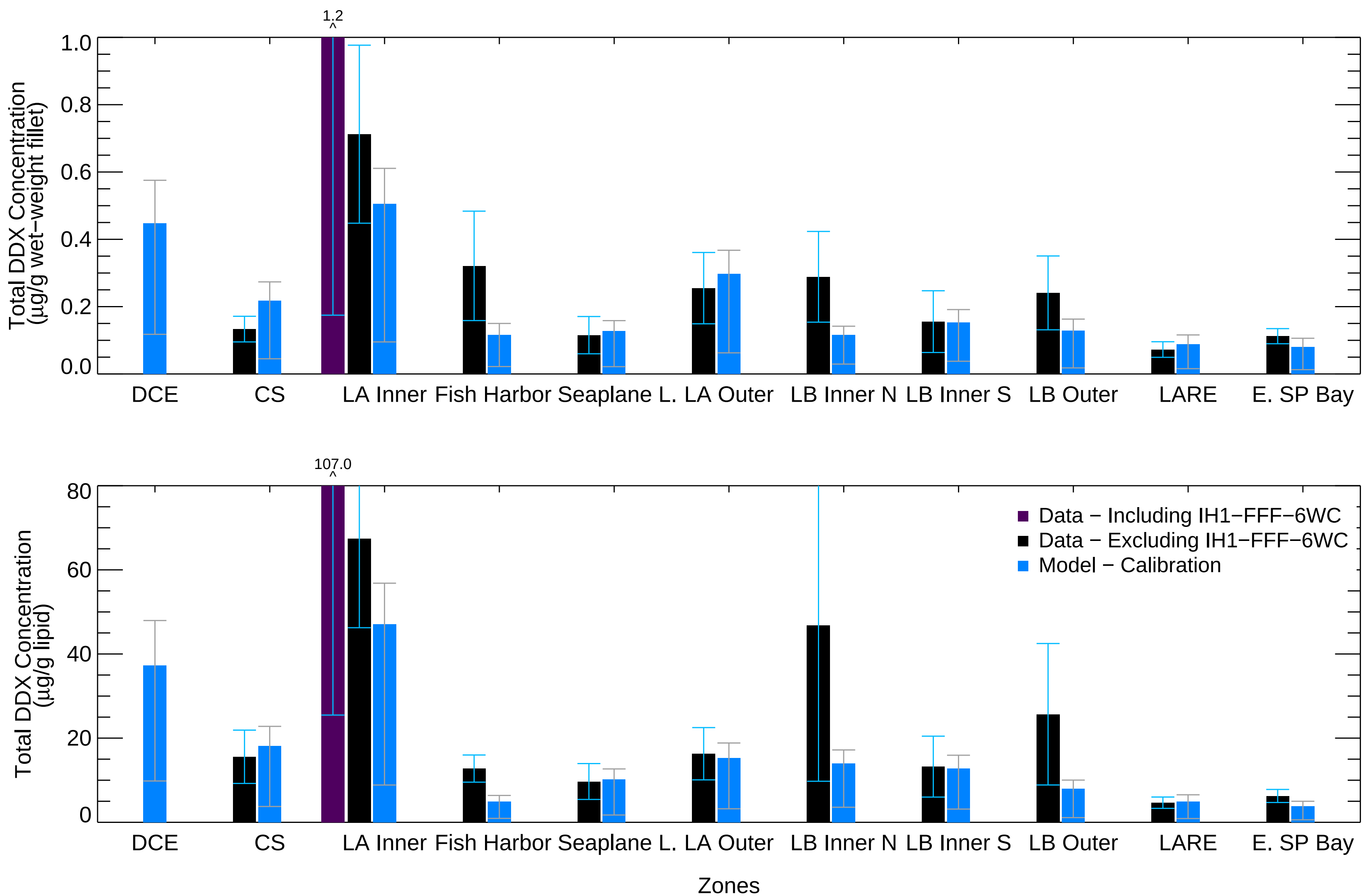


Figure 5−6

Model to Data Comparison of Total DDX Concentrations in White Croaker

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx. Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value). Model results are averaged over all days within the last year and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ file v.1677 and biota file v.1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_fish_model_data_comparison_wMigration_calib.pro Mon Feb 27 16:07:40 2017

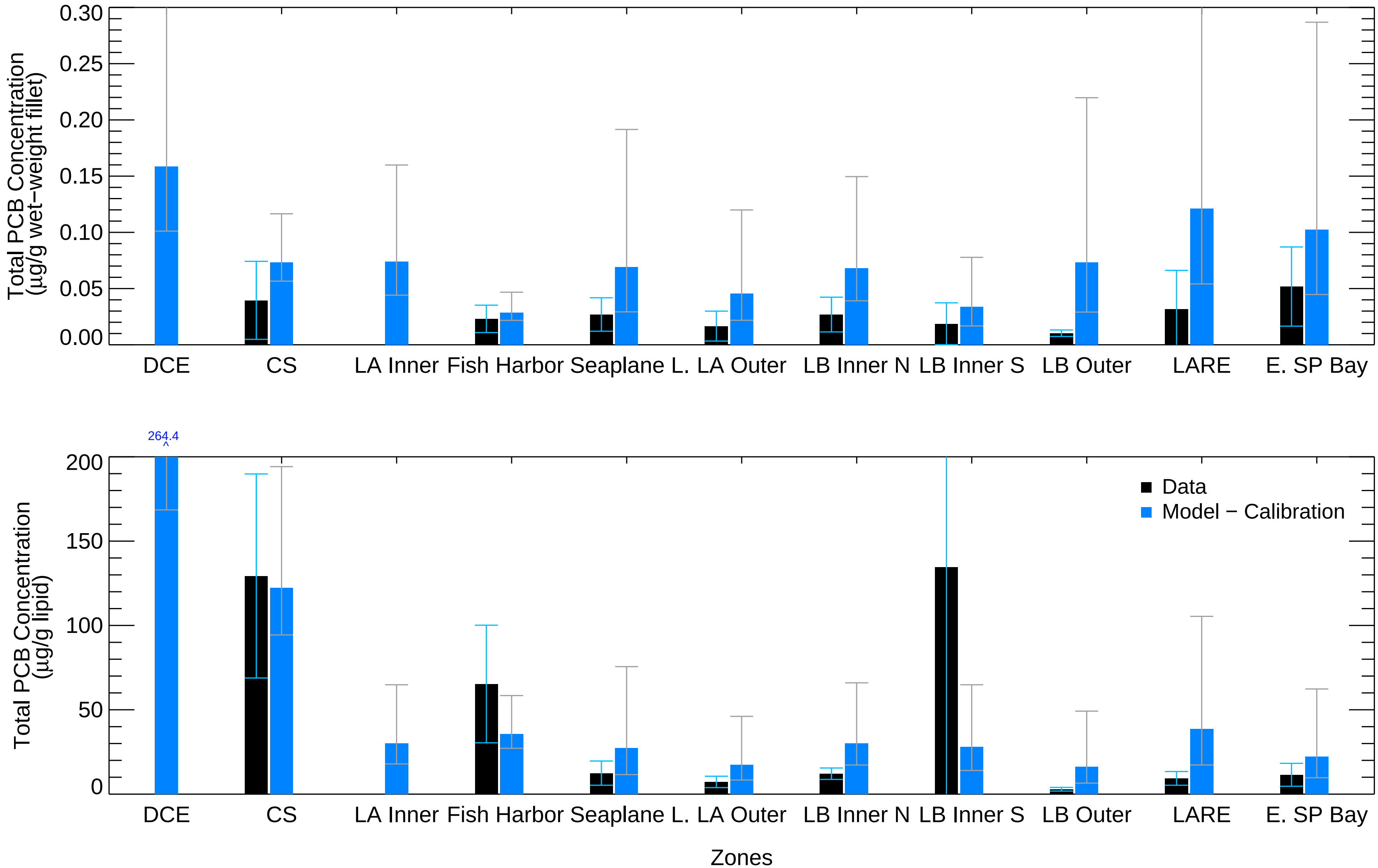


Figure 5−7

Model to Data Comparison of Total PCB Concentrations in California Halibut

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx. Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ file v.1677 and biota file v.1727 used for model.

ANCHOR QEA

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_fish_model_data_comparison_wMigration_calib.pro Mon Feb 27 16:07:40 2017

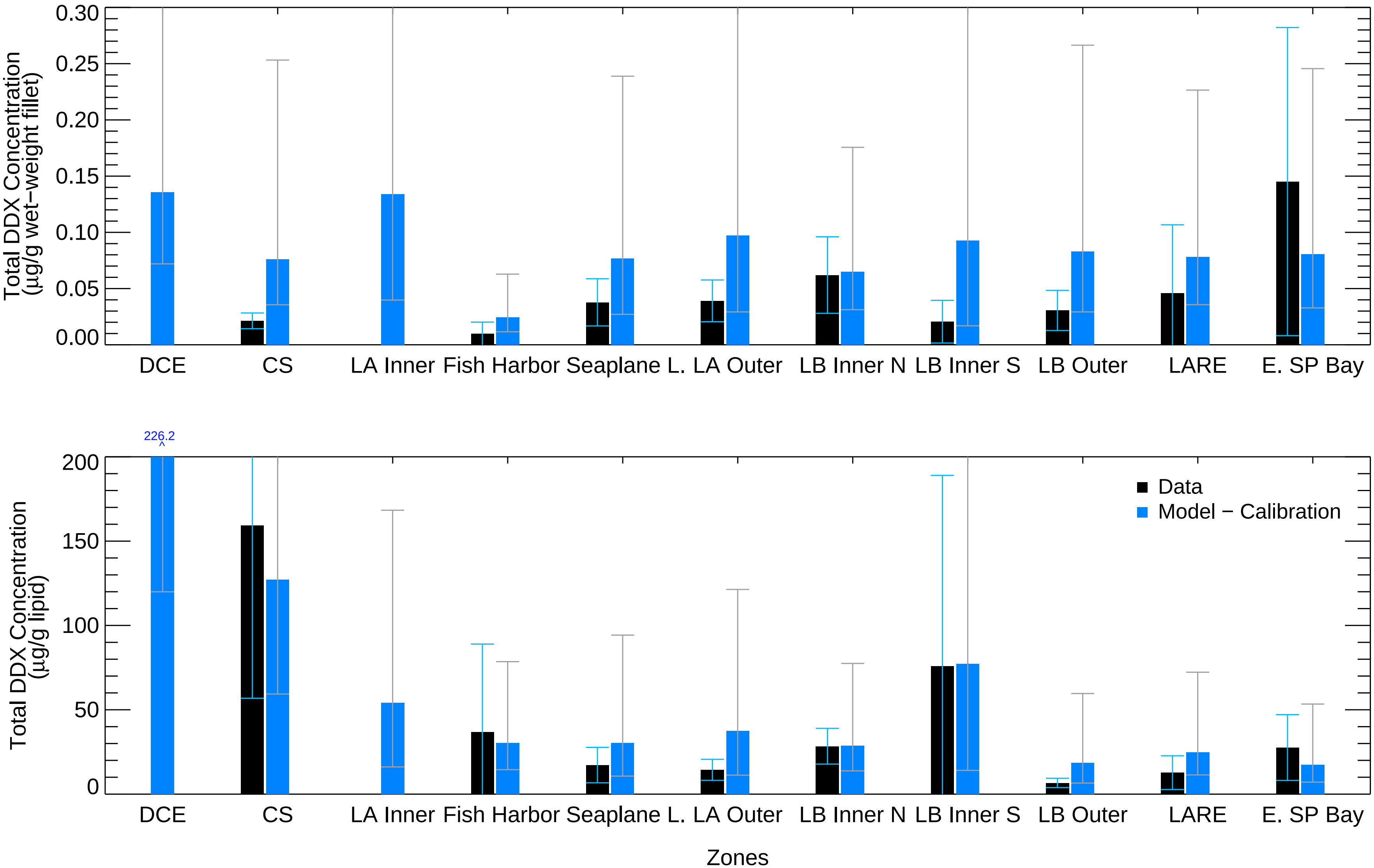


Figure 5−8

Model to Data Comparison of Total DDX Concentrations in California Halibut

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ file v.1677 and biota file v.1727 used for model.

ANCHOR QEA

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_fish_model_data_comparison_wMigration_calib.pro Mon Feb 27 16:07:40 2017

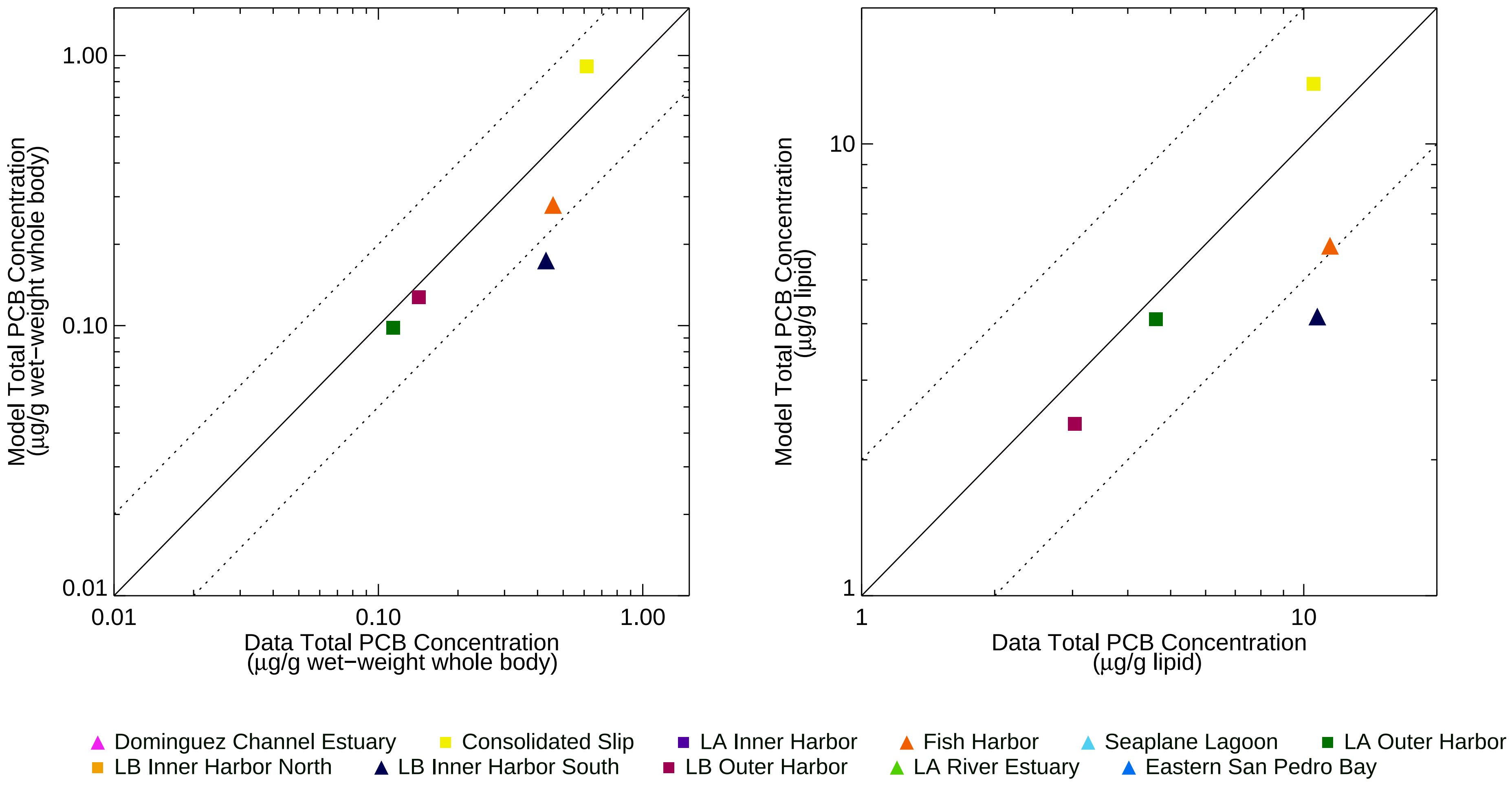


Figure 5−9a

Model to Data Cross Plots of Total PCB in Surfperch

ANCHOR QEA

File used: PortOfLALB_Fish_20160720.xlsx. Spatial average concentrations for 2002 to 2014 samples are shown. Congener data are shown. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages over various age classes. WQ file v.1677 and biota file v.1727 used for model.

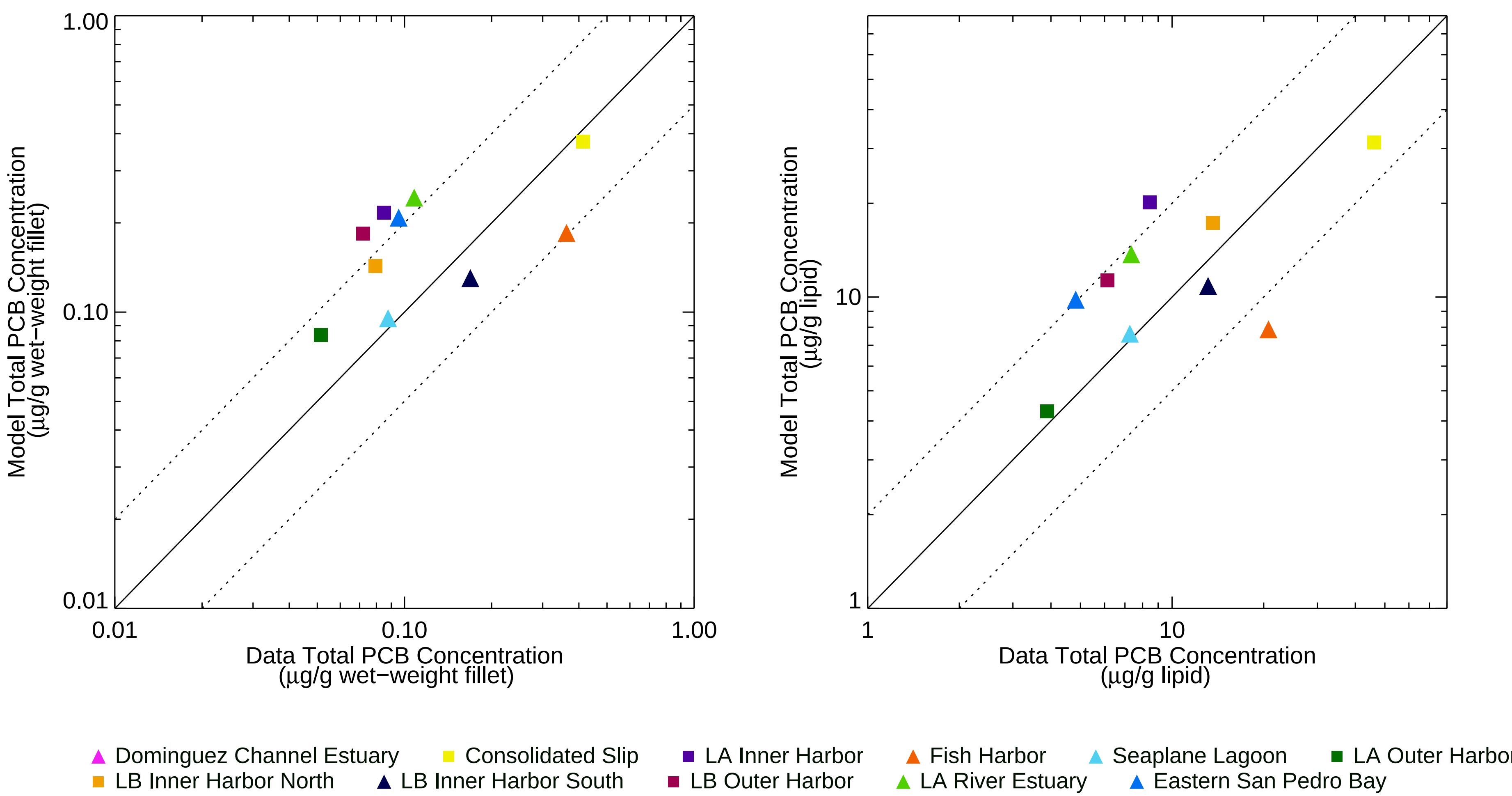


Figure 5−9b

Model to Data Cross Plots of Total PCB in White Croaker

ANCHOR QEA

File used: PortOfLALB_Fish_20160720.xlsx. Spatial average concentrations for 2002 to 2014 samples are shown. Congener data are shown. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value), IH1−FFF−6WC (high value). Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages over various age classes. WQ file v.1677 and biota file v.1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\Cross_Plots\LALB_model_data_wMigration_cross_plots_for_report.pro Tue Apr 25 11:49:28 2017

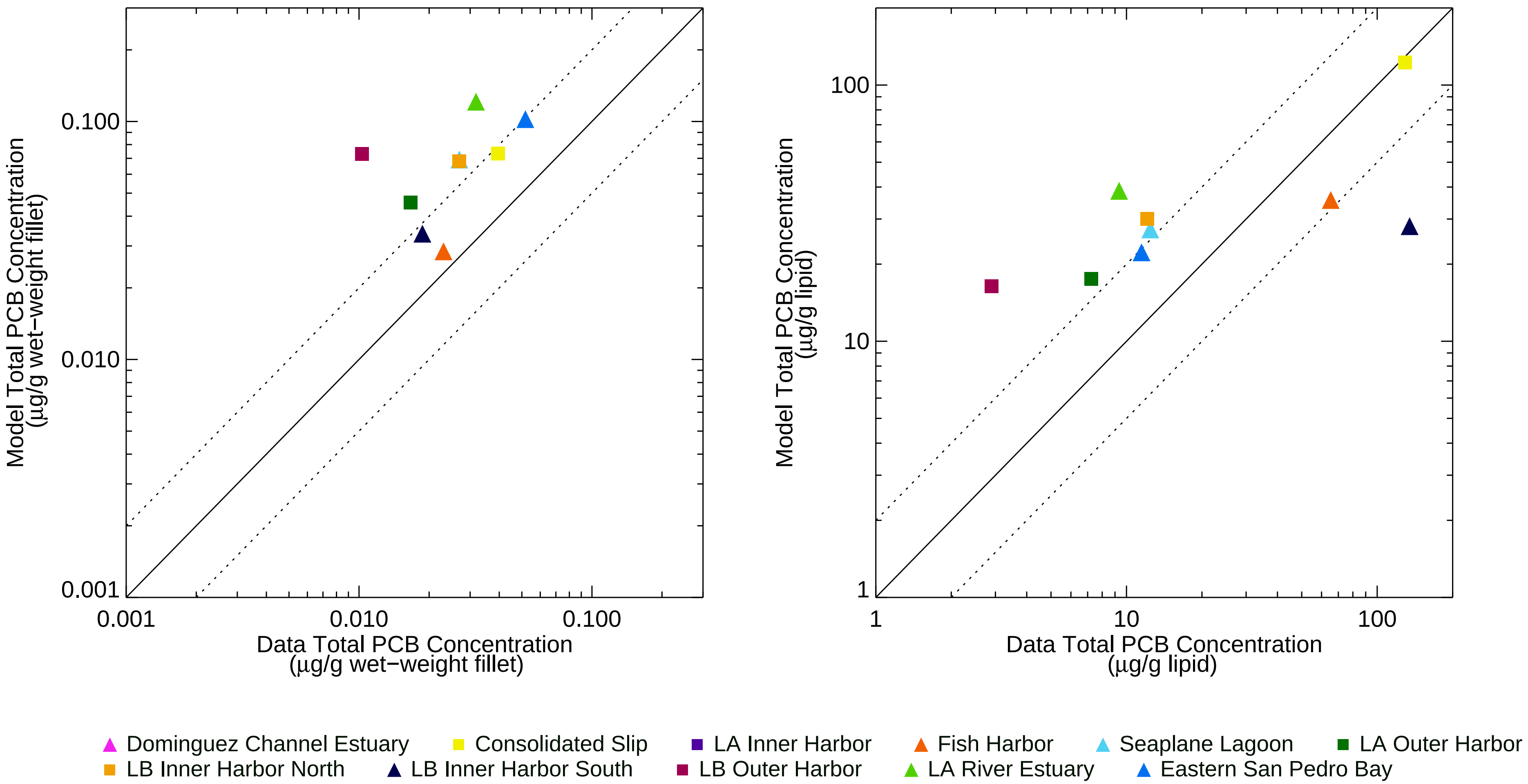


Figure 5−9c

Model to Data Cross Plots of Total PCB in California Halibut

ANCHOR QEA

File used: PortOfLALB_Fish_20160720.xlsx. Spatial average concentrations for 2002 to 2014 samples are shown. Congener data are shown. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipids are included in the lipid−based average. Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages over various age classes. WQ file v.1677 and biota file v.1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\Cross_Plots\LALB_model_data_wMigration_cross_plots_for_report.pro Tue Apr 25 11:49:28 2017

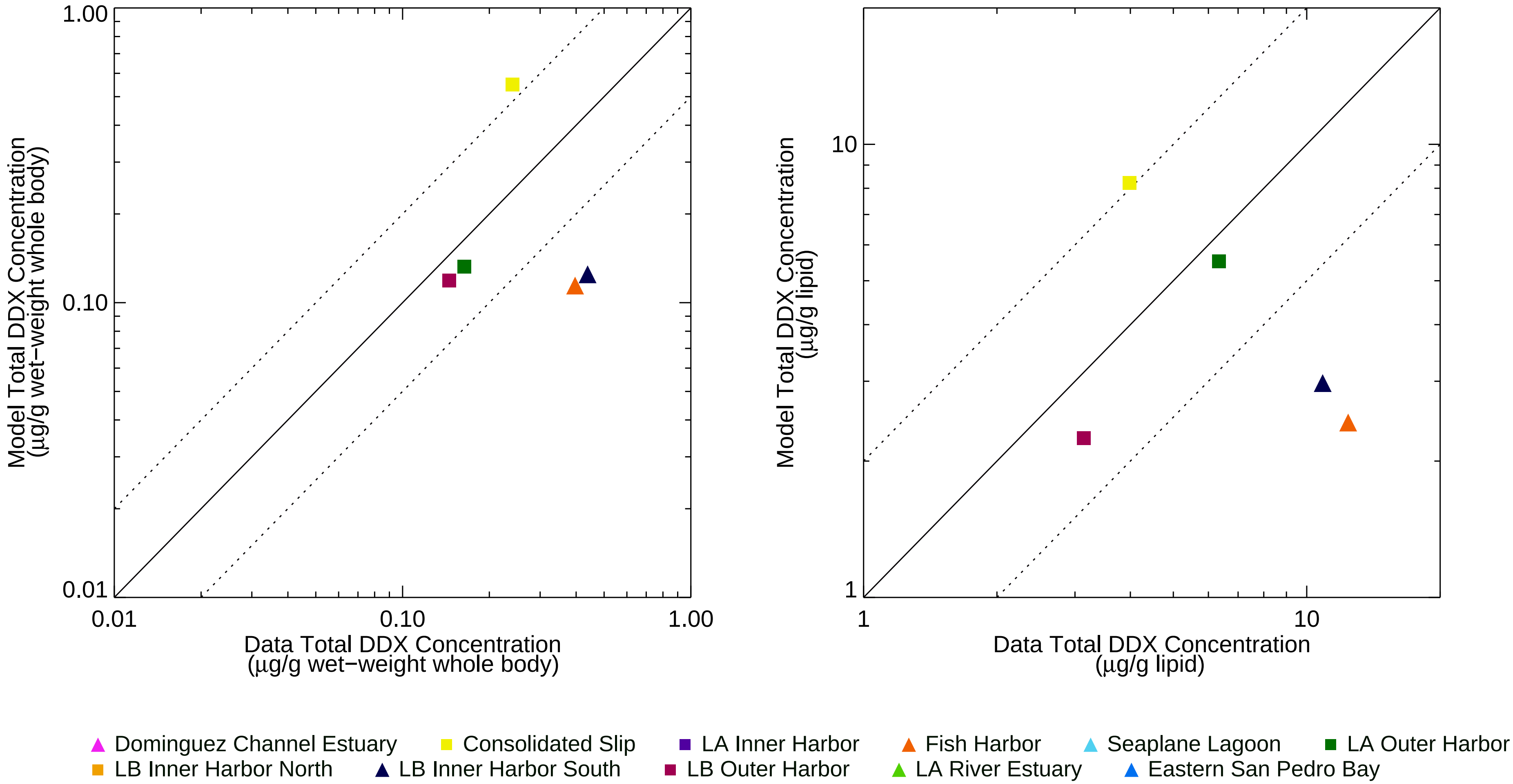


Figure 5−10a

Model to Data Cross Plots of Total DDX in Surfperch

ANCHOR QEA

File used: PortOfLALB_Fish_20160720.xlsx. Spatial average concentrations for 2002 to 2014 samples are shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages over various age classes.
WQ file v.1677 and biota file v.1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\Cross_Plots\LALB_model_data_wMigration_cross_plots_for_report.pro Tue Apr 25 11:49:28 2017

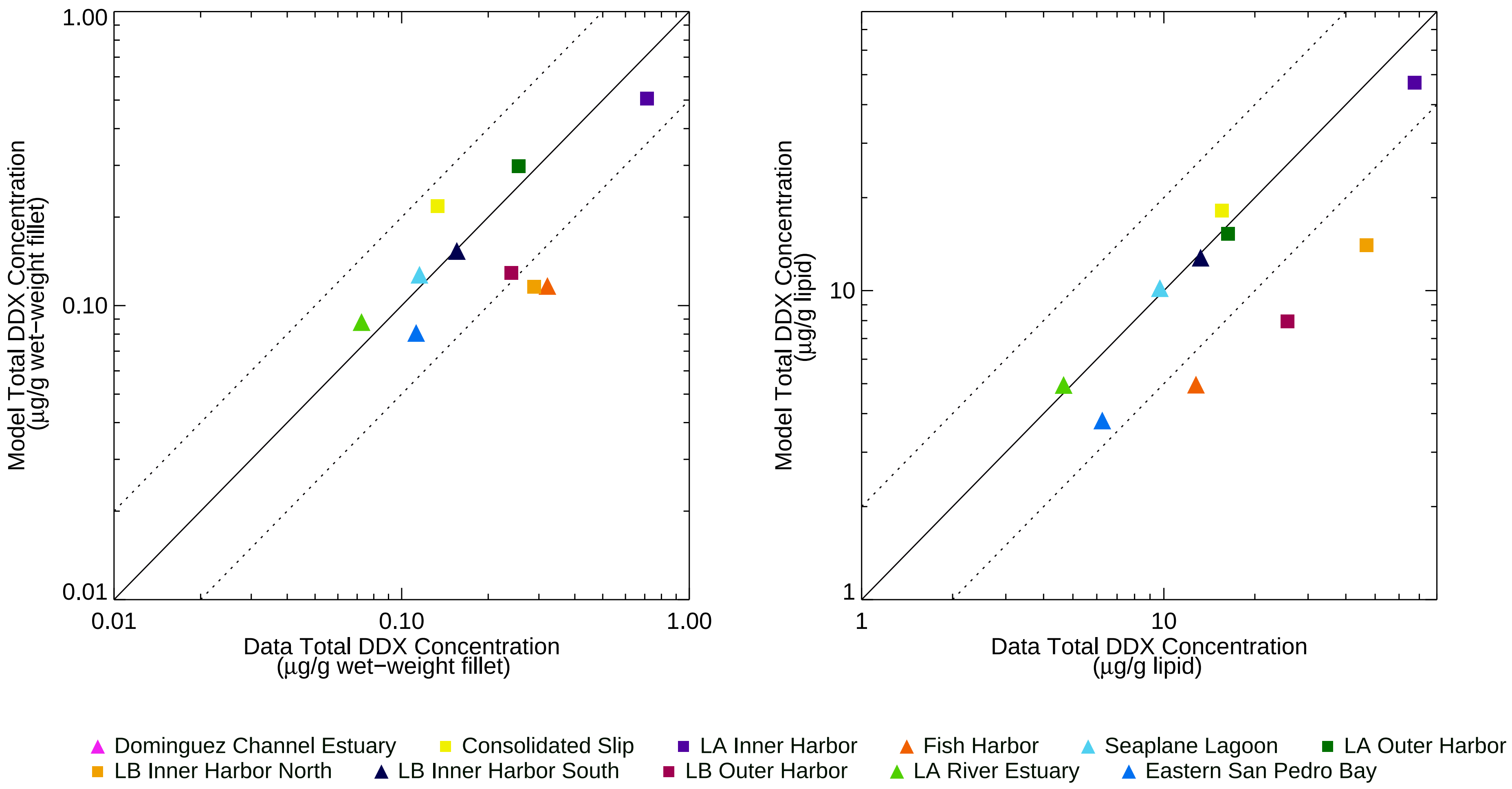


Figure 5−10b

Model to Data Cross Plots of Total DDX in White Croaker

ANCHOR QEA

File used: PortOfLALB_Fish_20160720.xlsx. Spatial average concentrations for 2002 to 2014 samples are shown. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value), IH1−FFF−6WC (high value). Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages over various age classes. WQ file v.1677 and biota file v.1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\Cross_Plots\LALB_model_data_wMigration_cross_plots_for_report.pro Tue Apr 25 11:49:28 2017

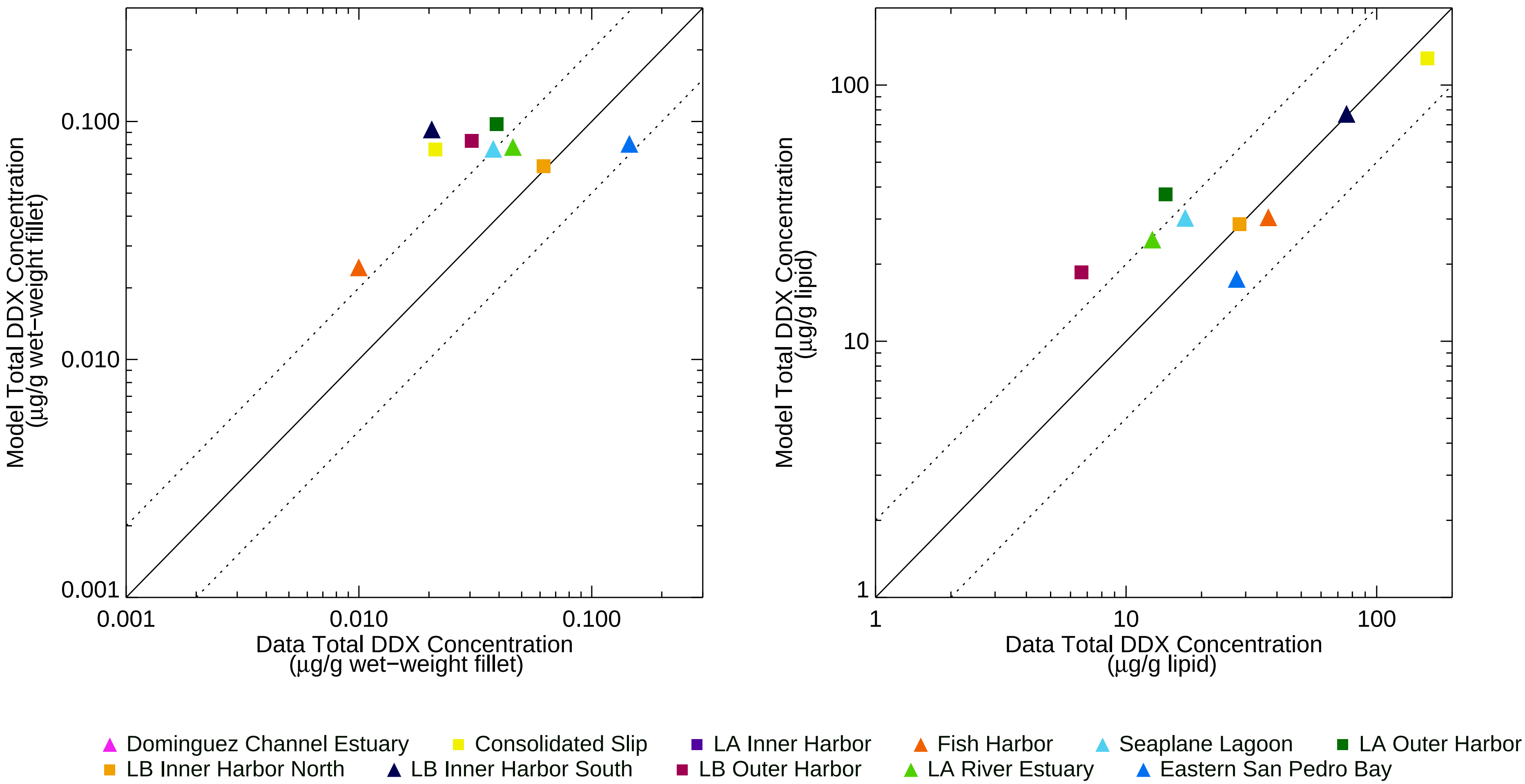


Figure 5−10c

Model to Data Cross Plots of Total DDX in California Halibut

ANCHOR QEA

File used: PortOfLALB_Fish_20160720.xlsx. Spatial average concentrations for 2002 to 2014 samples are shown. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipids are included in the lipid−based average. Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages over various age classes. WQ file v.1677 and biota file v.1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\Cross_Plots\LALB_model_data_wMigration_cross_plots_for_report.pro Tue Apr 25 11:49:29 2017

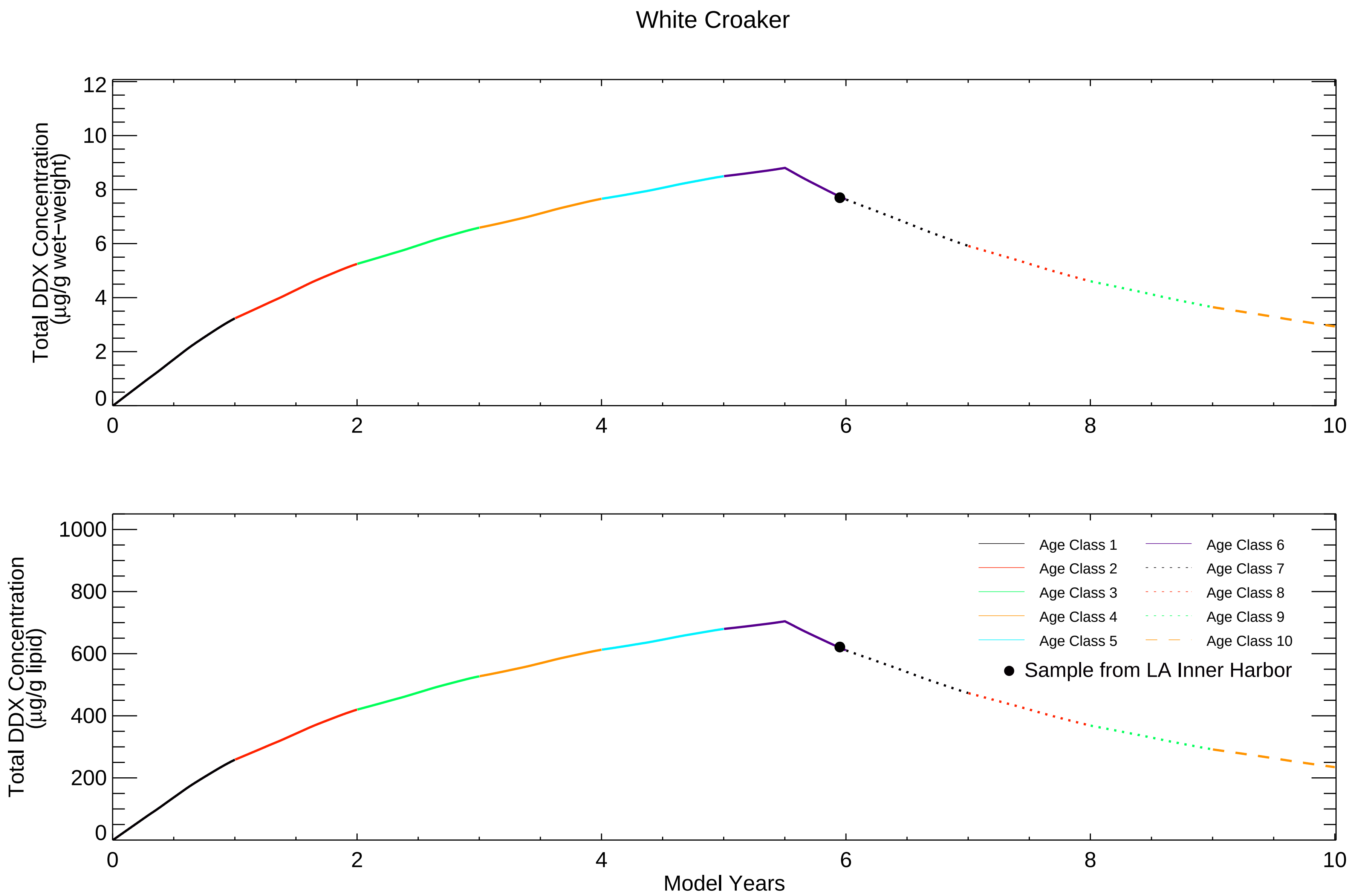


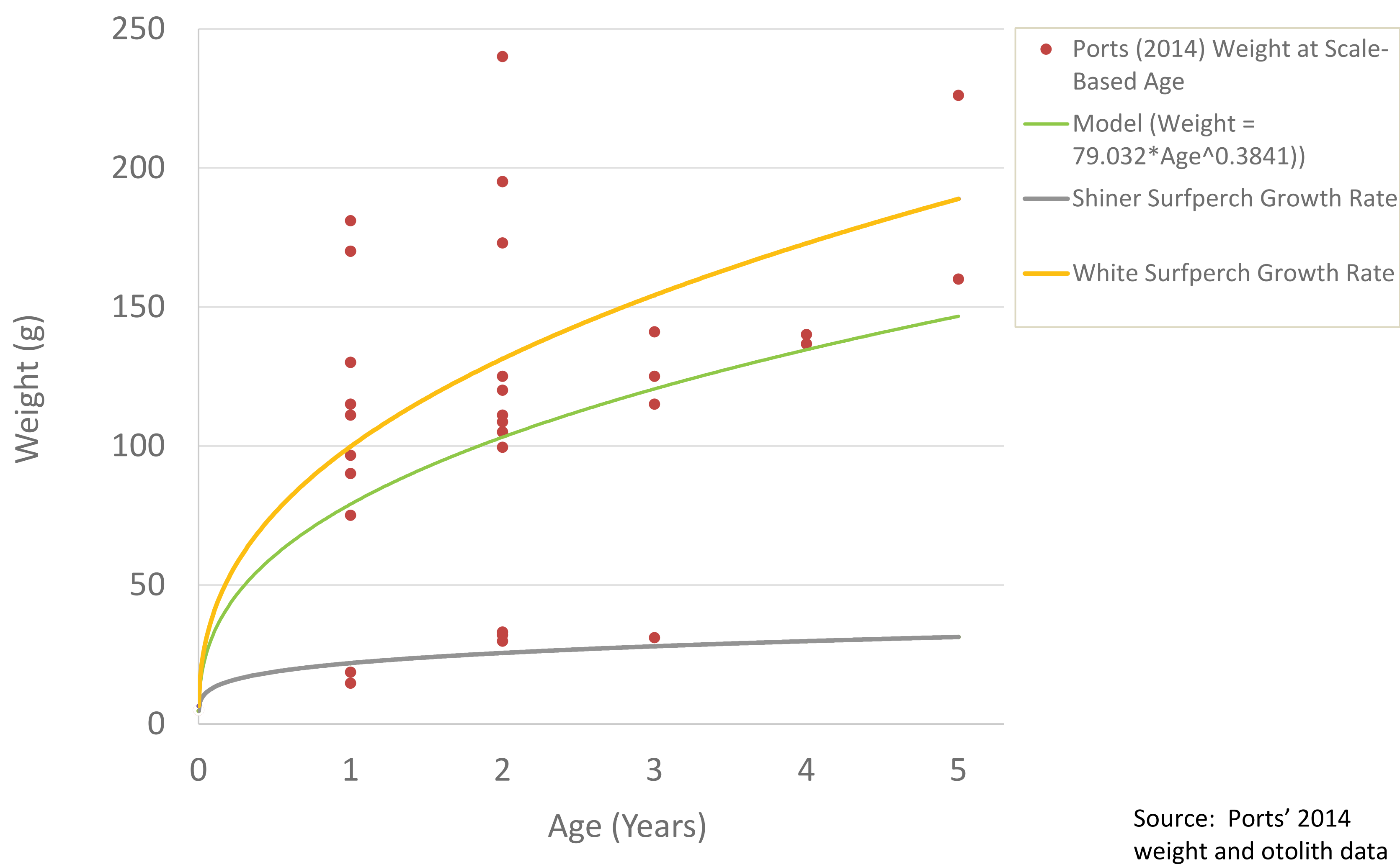
Figure 5−11

Simulation of LA Inner Harbor White Croaker with Elevated Total DDX Concentration

A simulation was conducted where a white croaker spent the first 5.5 years of its life on the Palos Verdes Shelf and then moved into the Harbor for the next 4.5 years. Results are shown by age class to track the same fish as it ages within the model. This hypothetical exposure pattern may explain the elevated Total DDX concentration measured in a fish about 6 years of age.
Fish Model Output file: fdchaina_Zone02DDT_1678_B_16118.OUT

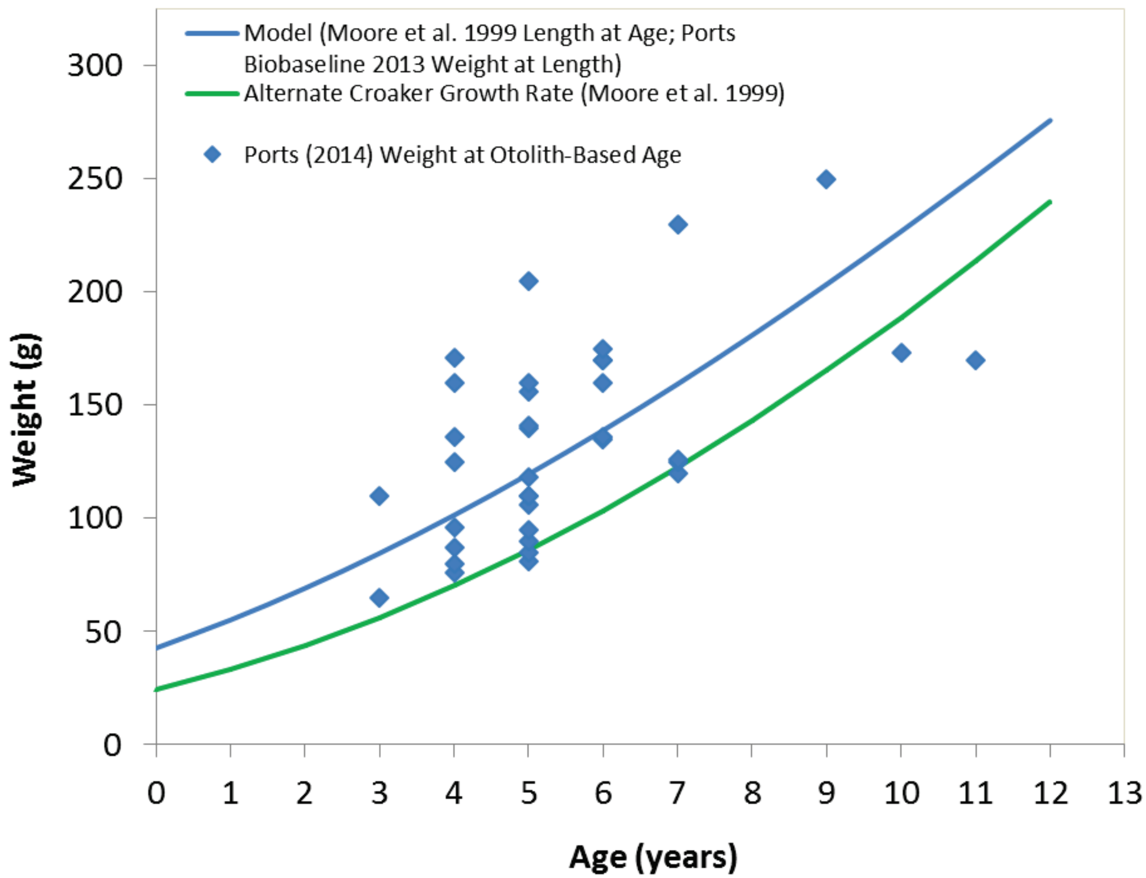
ANCHOR QEA

MM − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\LALB_fish_model_ageclass_cascade_plot_LA_Inner.pro Wed Apr 19 15:29:12 2017



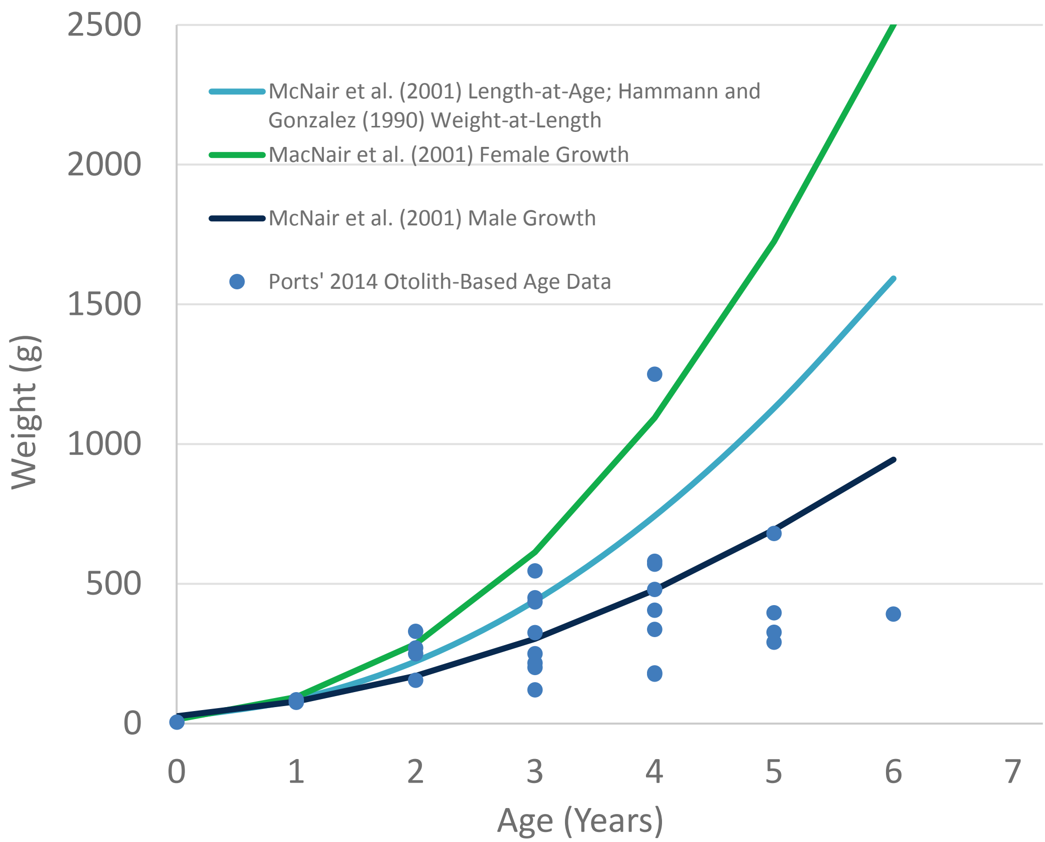
ANCHOR QEA

Figure 6-1
Alternative Surfperch Growth Rates
Bioaccumulation Modeling Report
Greater Los Angeles and Long Beach Harbor Waters



Notes: The model is based on length-at-age data from Moore (1999; Lt=607.71[1-e-0.03(t+8.54)] for females and Lt=558.62[1-e-0.03(t+7.78)] for males) and weight at length data from Ports Biological Survey Study (2013/14; W = 2E-05*total length^2.53). The model overlays white croaker data (weight and age based on otolith annular rings) collected as part of the Ports' food web study.

Figure 6-2
Alternative White Croaker Growth Rates



Notes: The model is based on length-at-age data from McNair et al. (2001; Lt=1367.7(1-e-0.08(t+1.2)) for females and Lt=925.3(1-e-0.08(t+2.2)) for males) and weight-at-length data from Hammann and Gonzalez (1990; W = 3.7*(10-3)*total length^3.28). The model overlays California halibut data (weight and age based on otolith annular rings) collected as part of the Ports' food web study (AMEC Foster Wheeler 2015).

Figure 6-3
Alternative California Halibut Growth Rates
Bioaccumulation Modeling Report
Greater Los Angeles and Long Beach Harbor Waters

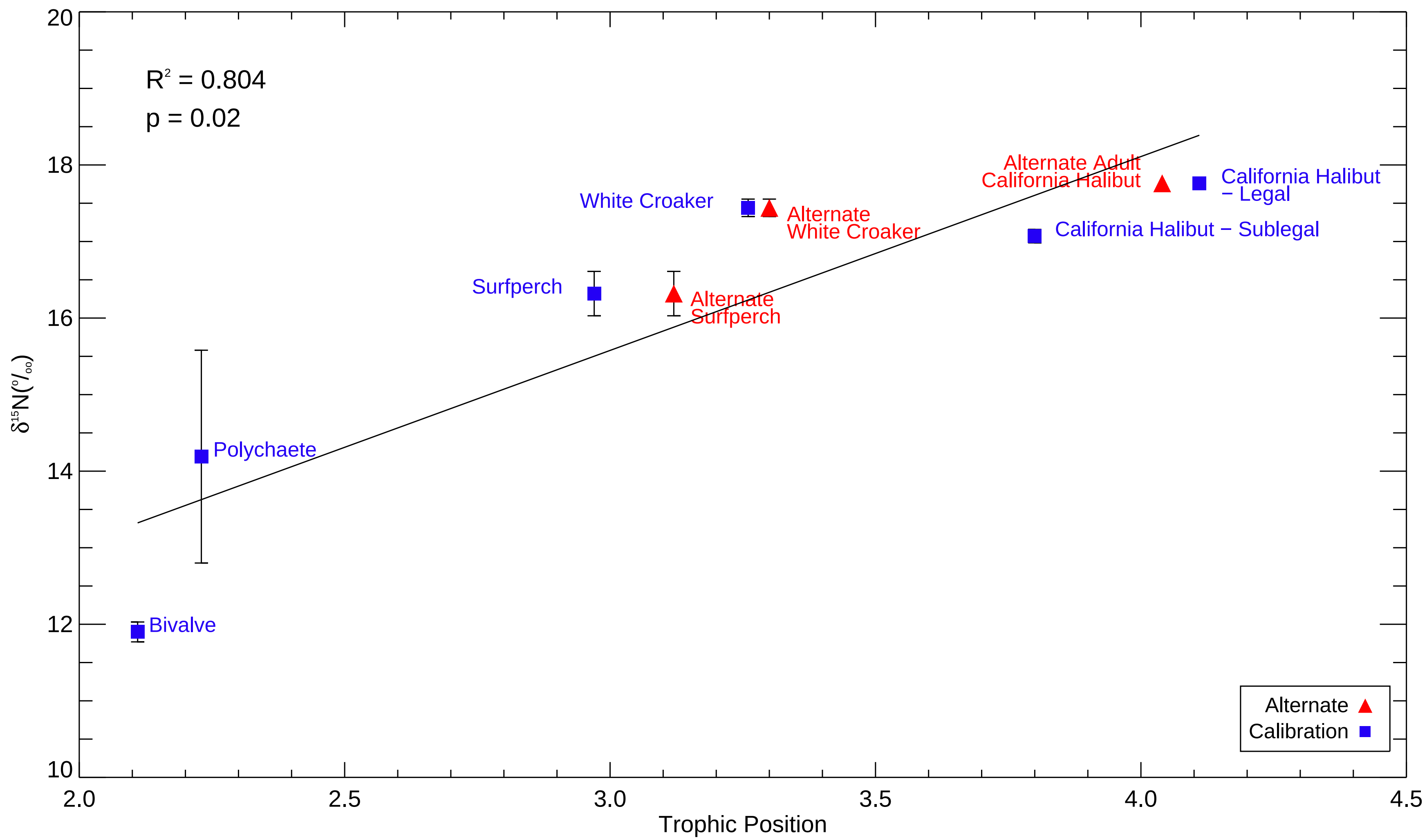


Figure 6−4

Alternate Diet Based on Site−specific Data

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Mean +/− two standard errors are shown. Trophic position was estimated using the Trophic Position Model based on Adams et al. (1983); values at the base of the food web (sediment and phytoplankton) were assigned according to Vander Zanden and Rasmussen (1996). Bivalve includes mussel and oyster. Surfperch includes white surfperch and shiner surfperch. Legal halibut are assumed to have standard lengths >540 mm. Sublegal halibut size range is 200 to 500 mm. Results for duplicate samples were averaged with parent results. Results for these tissue types were used: surfperch, polychaete − whole body; mussel, oyster − whole body no shell; California halibut, white croaker − fillet without skin.

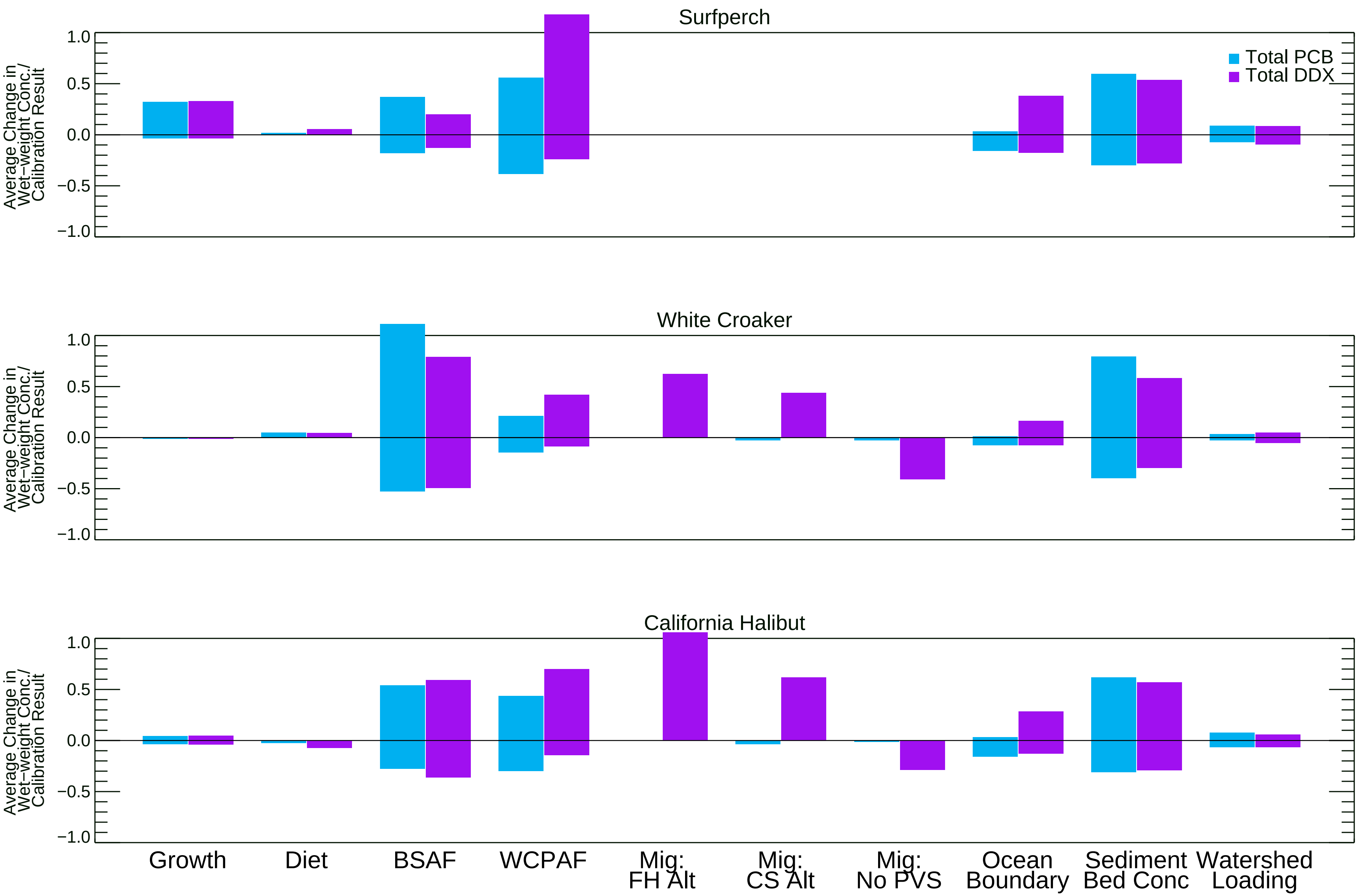

Figure 6−5

Sensitivity Analysis Results: Average Change in Contaminant Results to the Calibration Results in Modeled Fish Tissue

Bars represent the average of the ratios of the difference between the model results for sensitivity and calibration, divided by the calibration result, for all the fish movement zones. Minimum and maximum model parameter values result in sensitivity model results that are above or below the line, respectively.
Input file used: LALB_bio_sensitivity_result_input_08222016.csv
BSAF = Biota Sediment Accumulation Factor; WCPAF = Water Column Particulate Accumulation Factor; Mig:FH Alt = Migration: Fish Harbor Alternative
Mig:CS Alt = Migration: Consolidated Slip Alternative; Mig:No PVS = Migration: No Palos Verdes Shelf Alternative

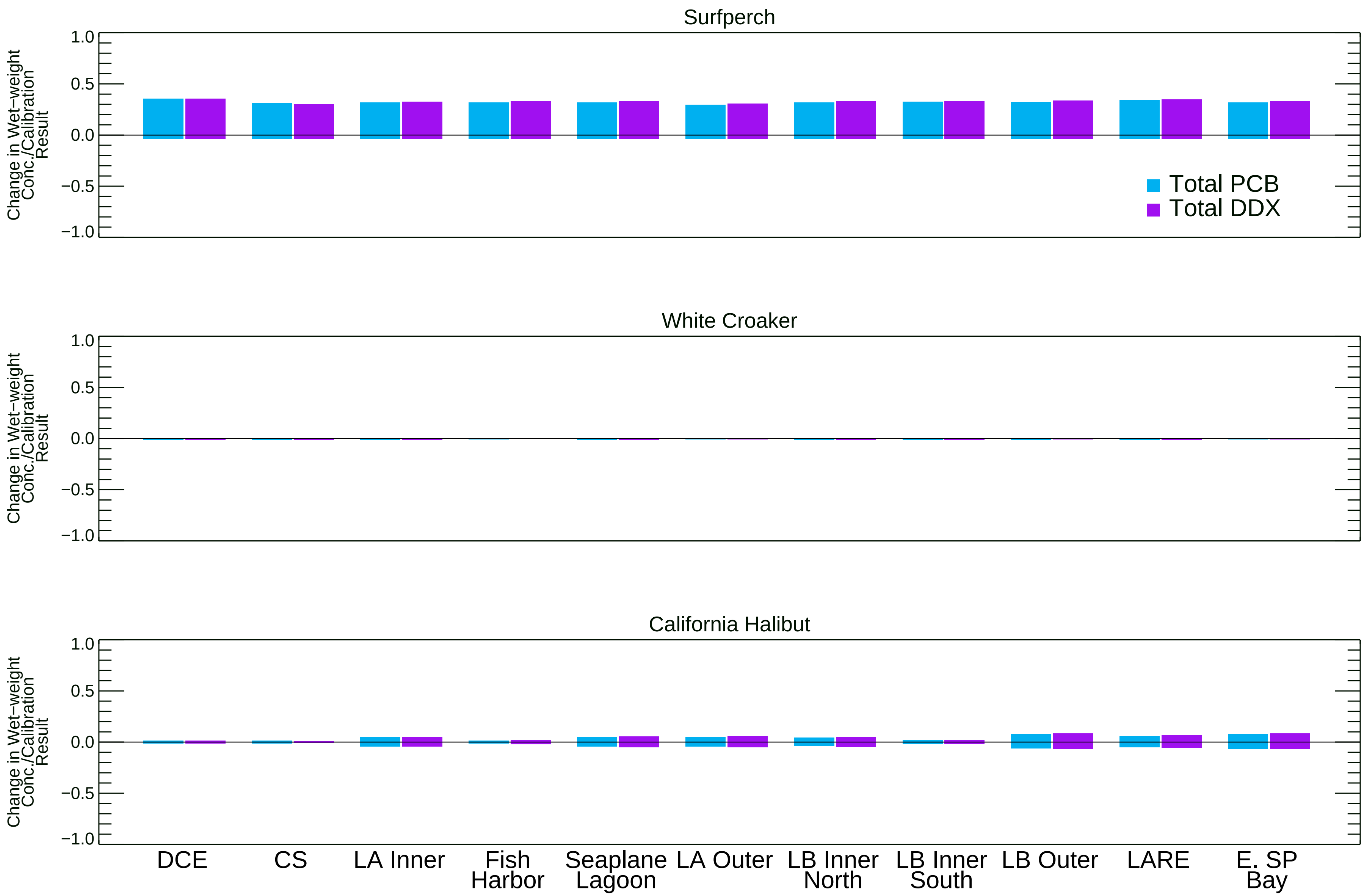

Figure 6−6

Sensitivity Analysis Results by Fish Movement Zone − Growth

Bars represent the ratios of the difference between the model results for sensitivity and calibration, divided by the calibration result.
Minimum and maximum model parameter values result in sensitivity model results that are above or below the line, respectively.
Input file used: LALB_bio_sensitivity_result_input_08222016.csv

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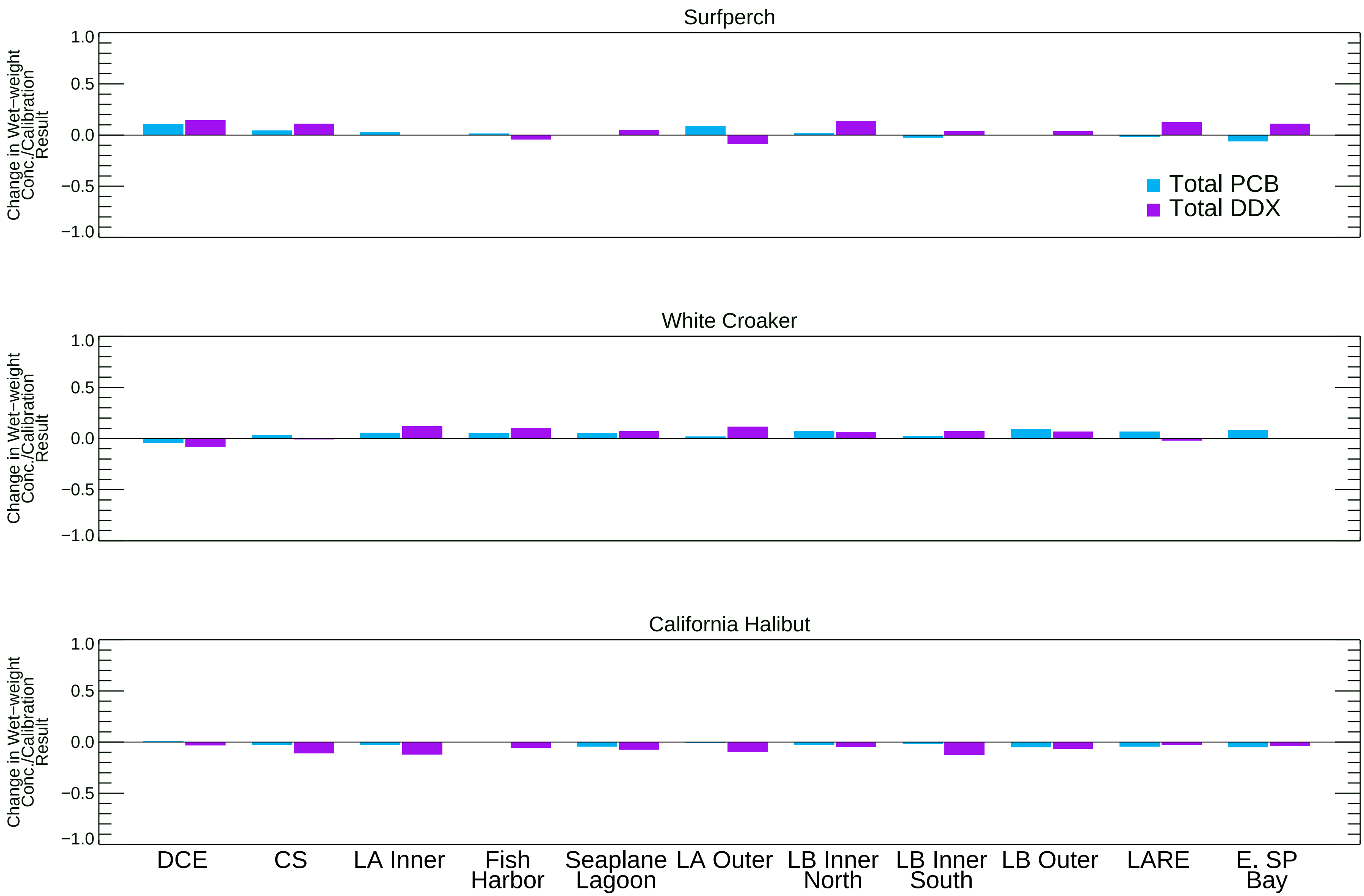

Figure 6−7

Sensitivity Analysis Results by Fish Movement Zone − Diet

Bars represent the ratios of the difference between the model results for sensitivity and calibration, divided by the calibration result. Minimum and maximum model parameter values result in sensitivity model results that are above or below the line, respectively. Input file used: LALB_bio_sensitivity_result_input_08222016.csv

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MM − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\Sensitivity\percent_change_TPCB_TDDX_in_fish_landscape.pro Wed Apr 19 15:58:34 2017

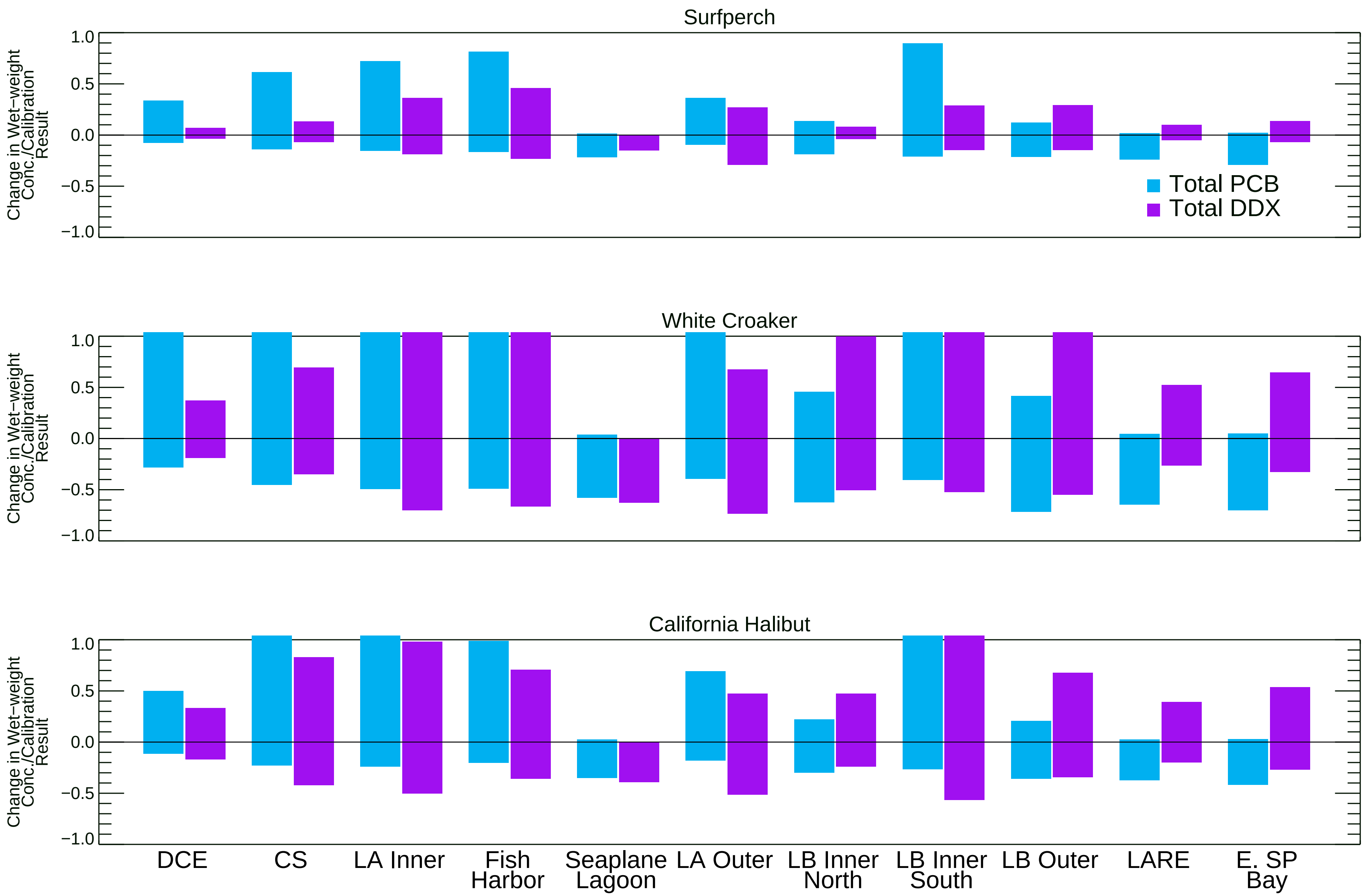


Figure 6−8

Sensitivity Analysis Results by Fish Movement Zone − Biota Sediment Accumulation Factor

Bars represent the ratios of the difference between the model results for sensitivity and calibration, divided by the calibration result.
Minimum and maximum model parameter values result in sensitivity model results that are above or below the line, respectively.
Input file used: LALB_bio_sensitivity_result_input_08222016.csv

ANCHOR QEA

MM − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\Sensitivity\percent_change_TPCB_TDDX_in_fish_landscape.pro Wed Apr 19 15:58:34 2017

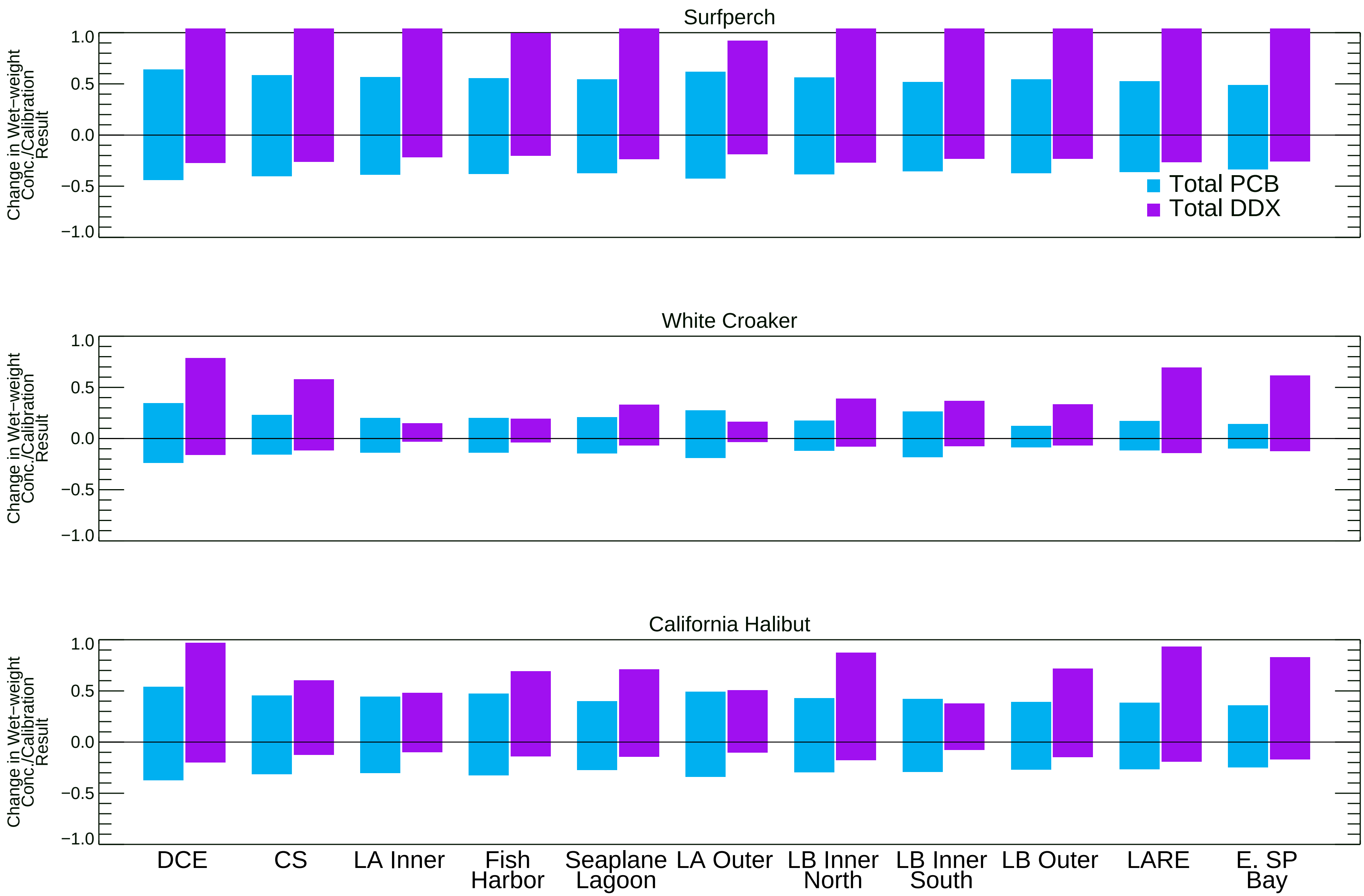


Figure 6−9

Sensitivity Analysis Results by Fish Movement Zone − Water Column Particulate Accumulation Factor

Bars represent the ratios of the difference between the model results for sensitivity and calibration, divided by the calibration result.
Minimum and maximum model parameter values result in sensitivity model results that are above or below the line, respectively.
Input file used: LALB_bio_sensitivity_result_input_08222016.csv

ANCHOR QEA

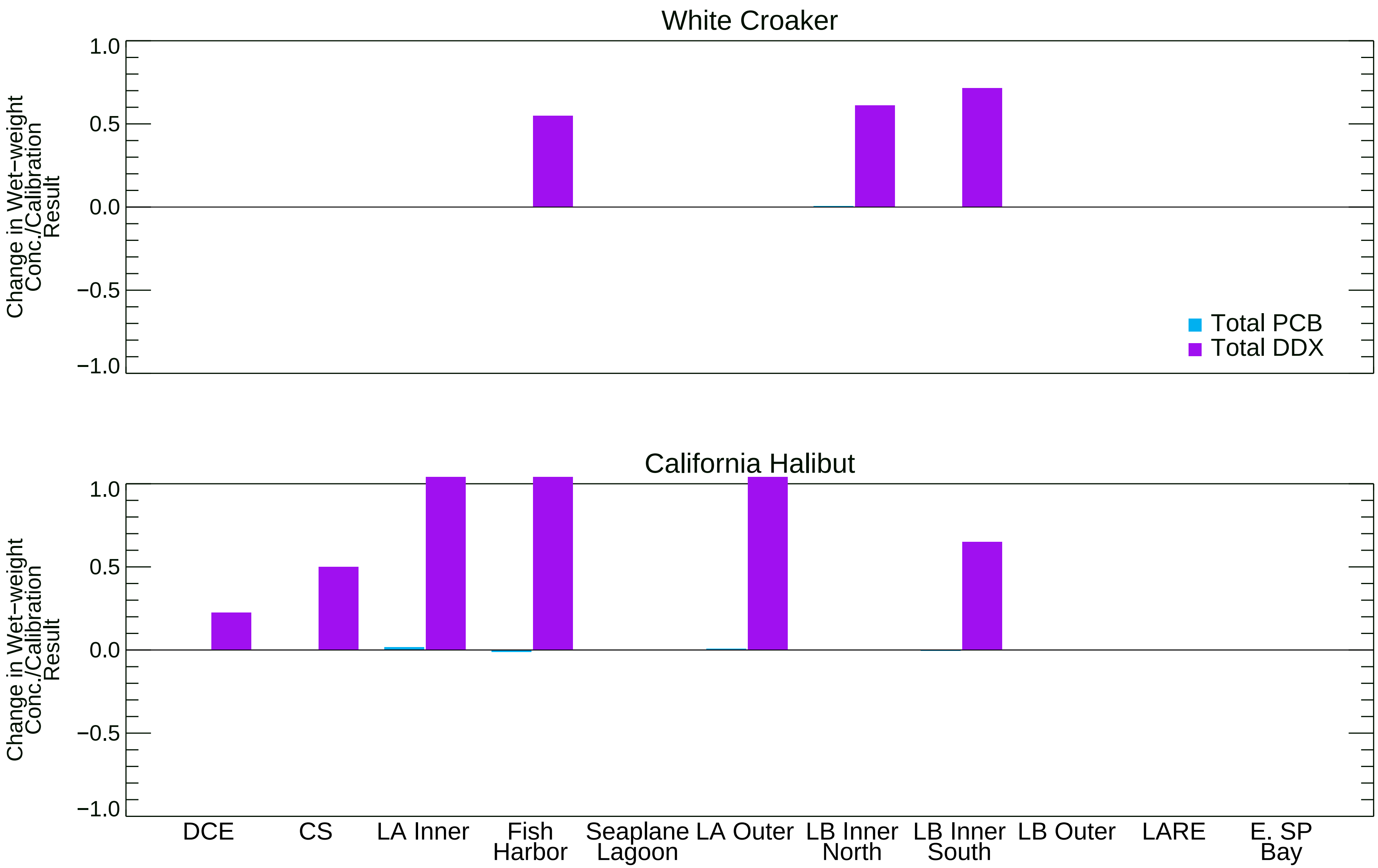


Figure 6−10

Sensitivity Analysis Results by Fish Movement Zone − Migration: Fish Harbor Alternative

Bars represent the ratios of the difference between the model results for sensitivity and calibration, divided by the calibration result.
Minimum and maximum model parameter values result in sensitivity model results that are above or below the line, respectively.
Input file used: LALB_bio_sensitivity_result_input_08222016.csv

ANCHOR QEA

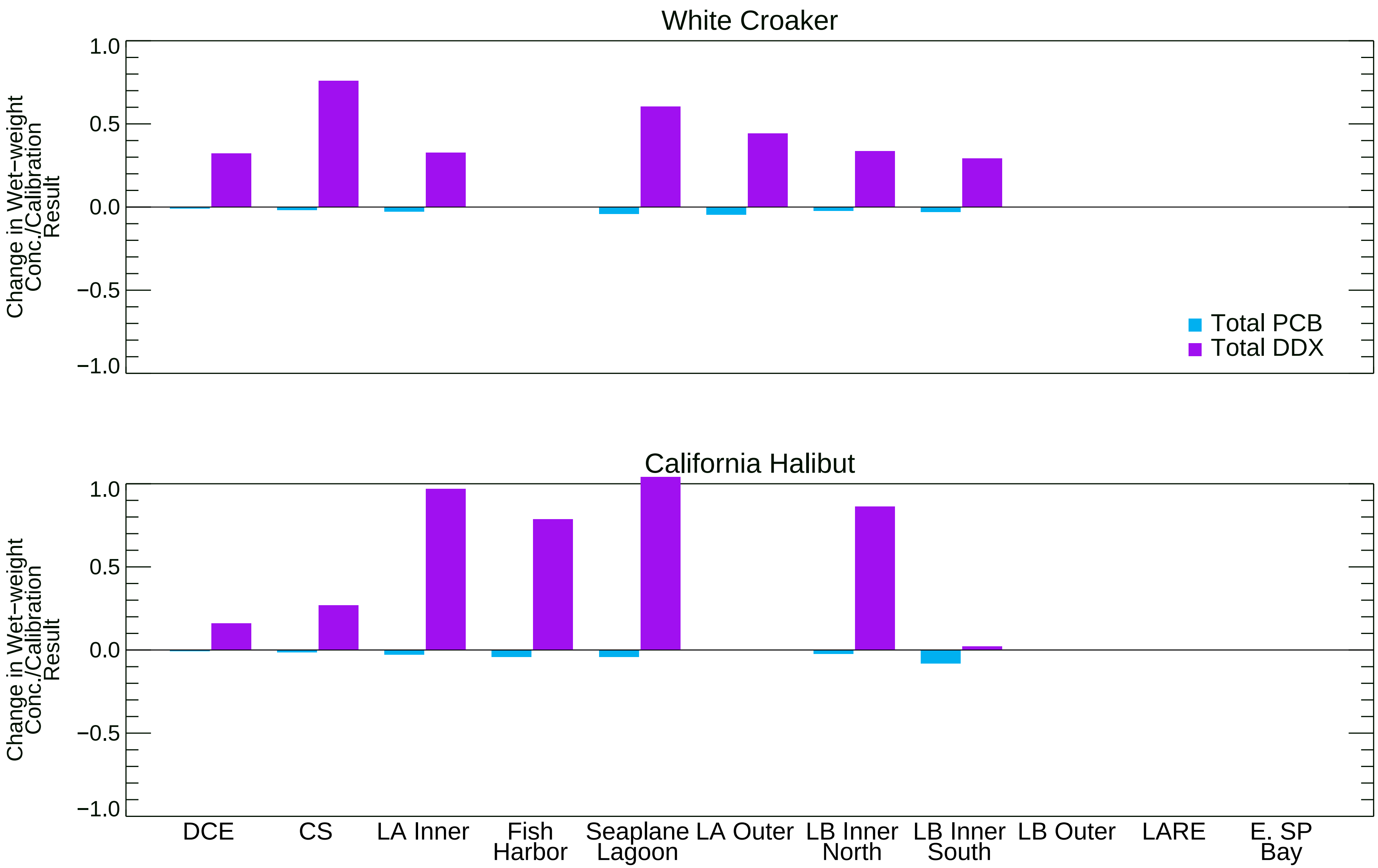


Figure 6−11

Sensitivity Analysis Results by Fish Movement Zone − Migration: Consolidated Slip Alternative

Bars represent the ratios of the difference between the model results for sensitivity and calibration, divided by the calibration result.
Minimum and maximum model parameter values result in sensitivity model results that are above or below the line, respectively.
Input file used: LALB_bio_sensitivity_result_input_08222016.csv

ANCHOR QEA

MM − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\Sensitivity\percent_change_TPCB_TDDX_in_fish_landscape.pro Wed Apr 19 15:58:34 2017

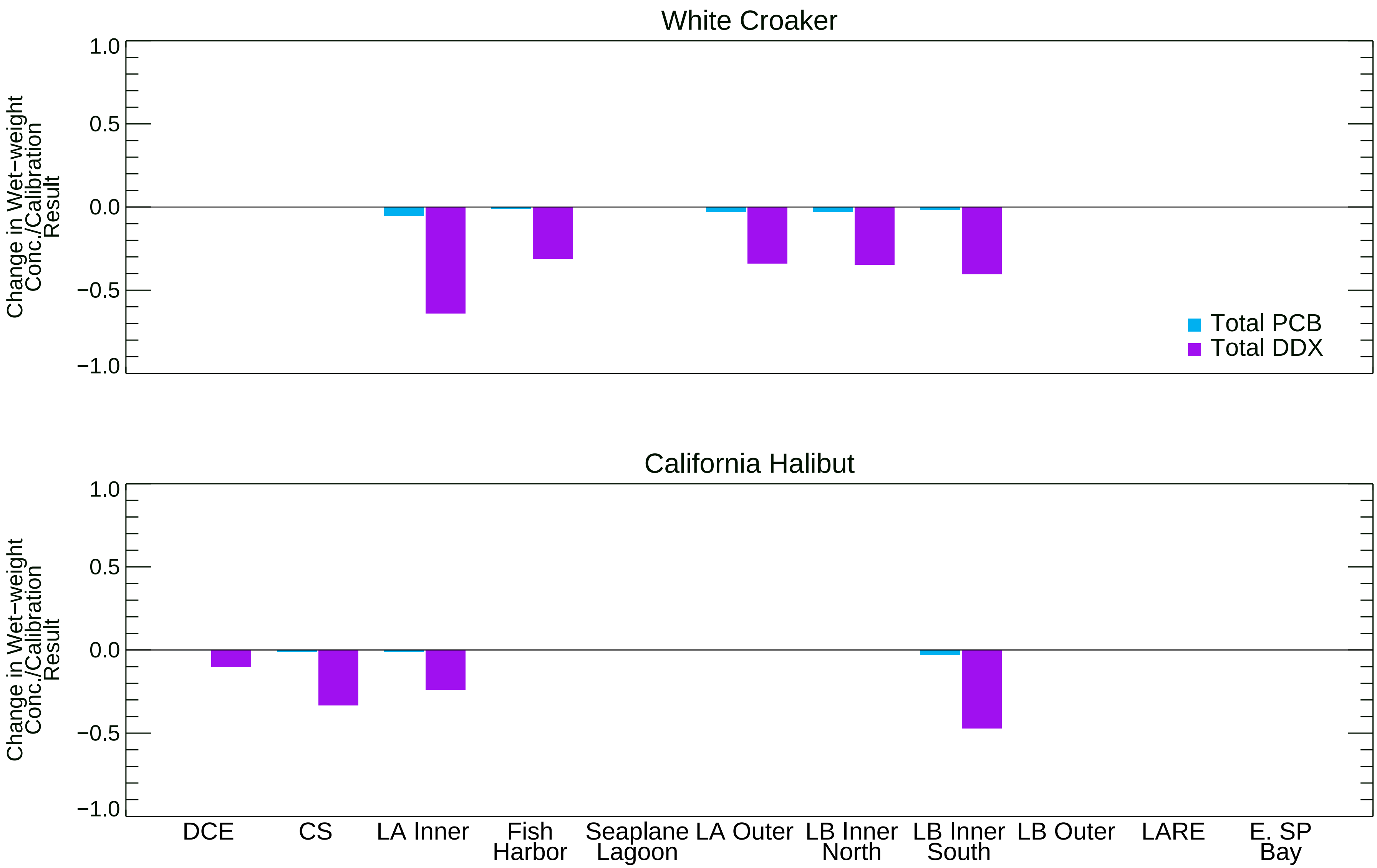


Figure 6−12

Sensitivity Analysis Results by Fish Movement Zone − Migration: No Palos Verdes Shelf Migration

Bars represent the ratios of the difference between the model results for sensitivity and calibration, divided by the calibration result.
Minimum and maximum model parameter values result in sensitivity model results that are above or below the line, respectively.
Input file used: LALB_bio_sensitivity_result_input_08222016.csv

ANCHOR QEA

MM − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\Sensitivity\percent_change_TPCB_TDDX_in_fish_landscape.pro Wed Apr 19 15:58:35 2017

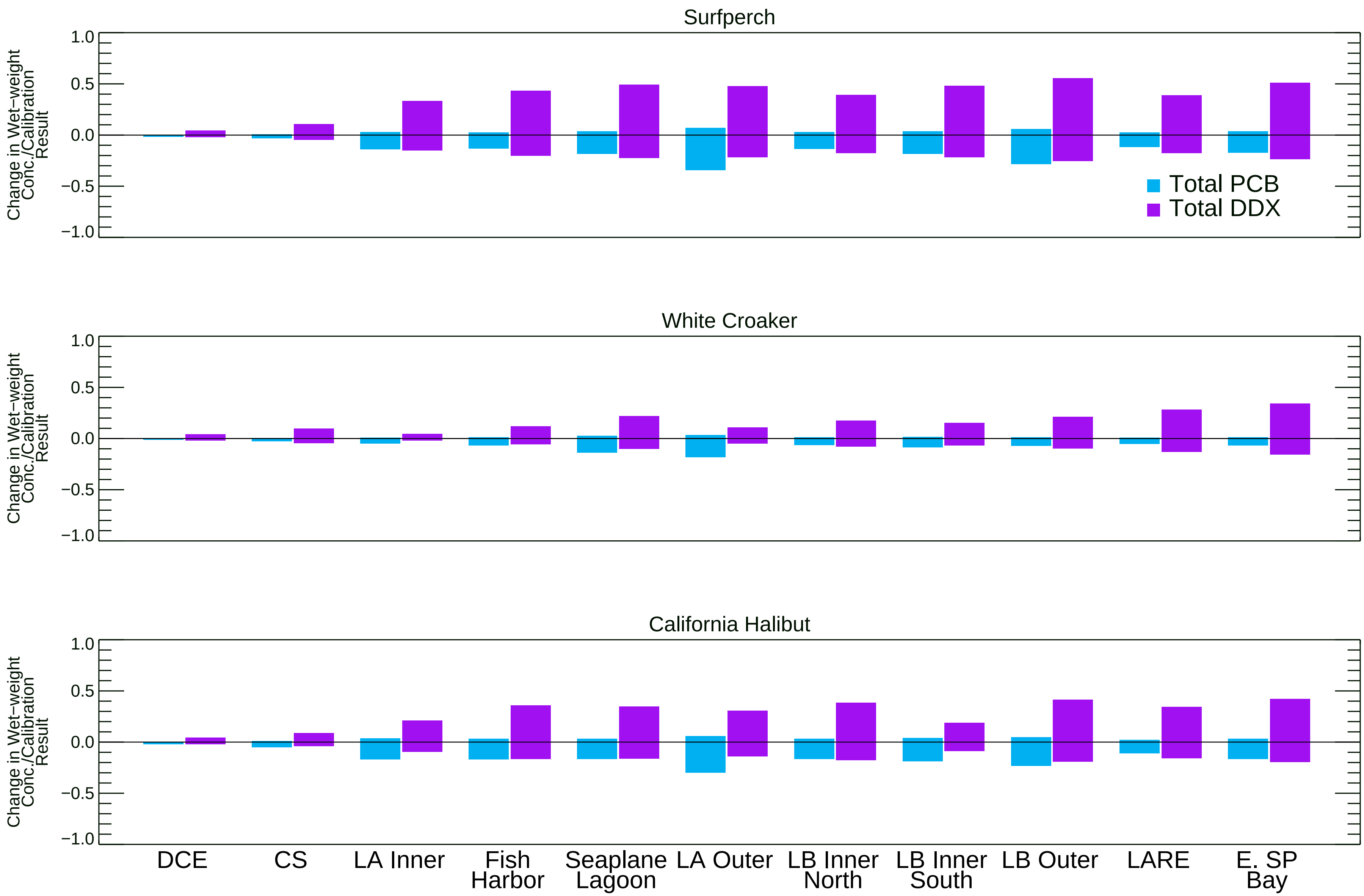


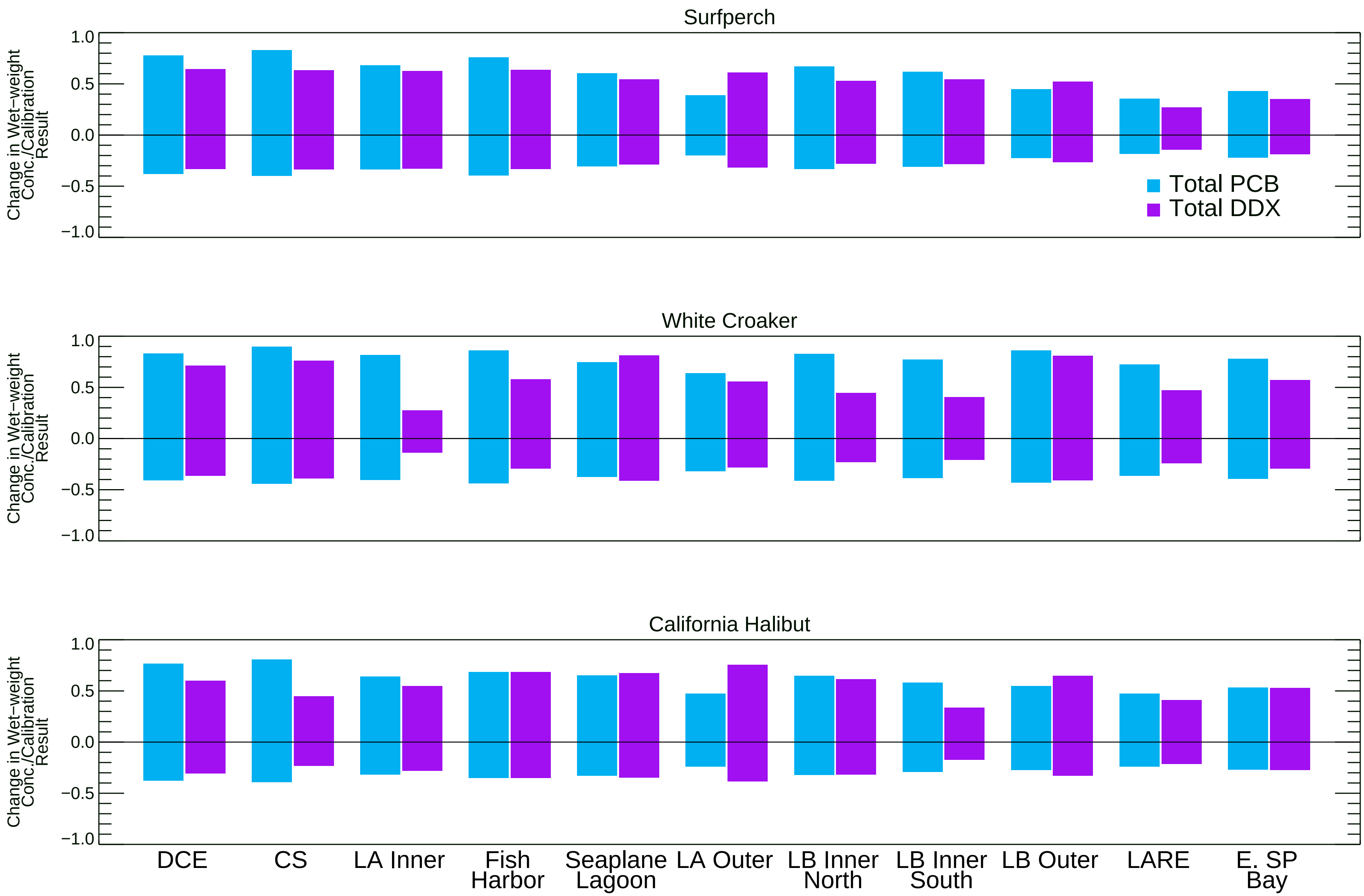
Figure 6−13

Sensitivity Analysis Results by Fish Movement Zone − WRAP Sensitivity: Ocean Boundary

Bars represent the ratios of the difference between the model results for sensitivity and calibration, divided by the calibration result.
Minimum and maximum model parameter values result in sensitivity model results that are above or below the line, respectively.
Input file used: LALB_bio_sensitivity_result_input_08222016.csv

ANCHOR QEA

MM − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\Sensitivity\percent_change_TPCB_TDDX_in_fish_landscape.pro Wed Apr 19 15:58:35 2017



ANCHOR QEA

Figure 6−14

Sensitivity Analysis Results by Fish Movement Zone − WRAP Sensitivity: Sediment Bed Concentration

Bars represent the ratios of the difference between the model results for sensitivity and calibration, divided by the calibration result.
Minimum and maximum model parameter values result in sensitivity model results that are above or below the line, respectively.
Input file used: LALB_bio_sensitivity_result_input_08222016.csv

MM − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\Sensitivity\percent_change_TPCB_TDDX_in_fish_landscape.pro Wed Apr 19 15:58:35 2017

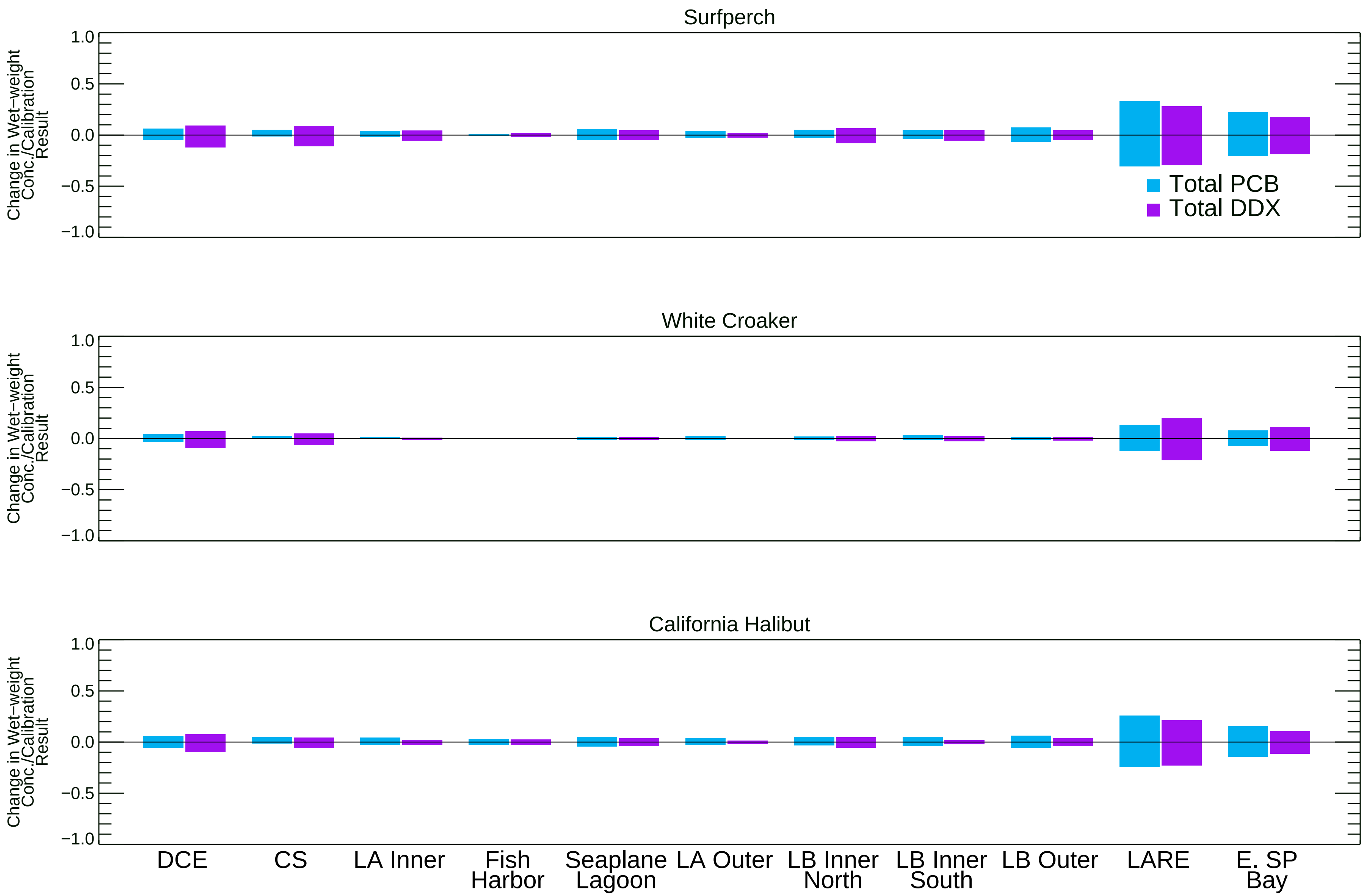


Figure 6−15

Sensitivity Analysis Results by Fish Movement Zone − WRAP Sensitivity: Watershed Loading

Bars represent the ratios of the difference between the model results for sensitivity and calibration, divided by the calibration result.
Minimum and maximum model parameter values result in sensitivity model results that are above or below the line, respectively.
Input file used: LALB_bio_sensitivity_result_input_08222016.csv

ANCHOR QEA

MM − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\Sensitivity\percent_change_TPCB_TDDX_in_fish_landscape.pro Wed Apr 19 15:58:35 2017

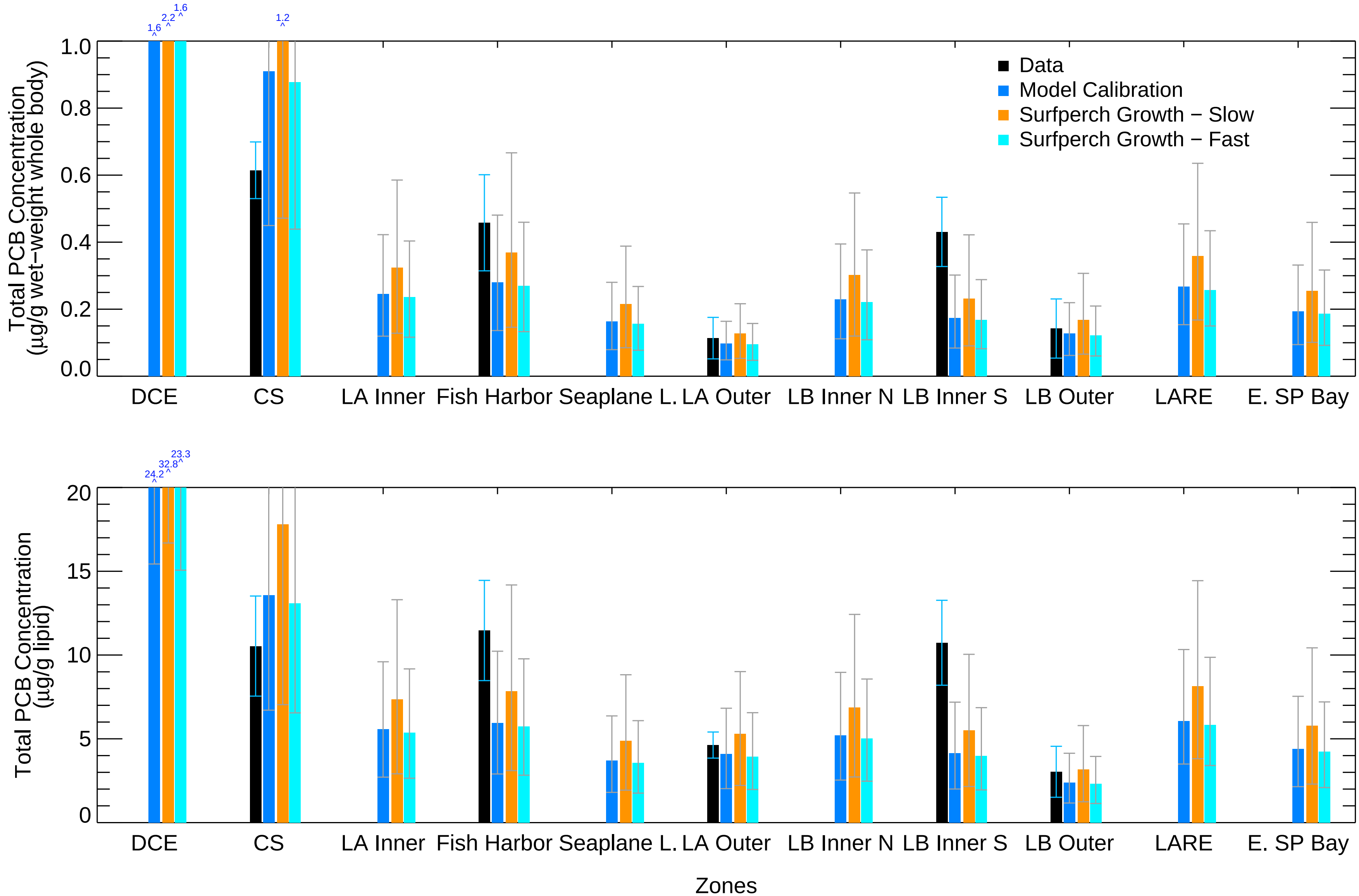


Figure 6−16a

Effects of Alternate Growth on Total PCB Concentration in Surfperch

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ files v.1677, 1677, 1677 and biota files v.1727, 1734, 1735 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Tue Apr 25 16:21:11 2017

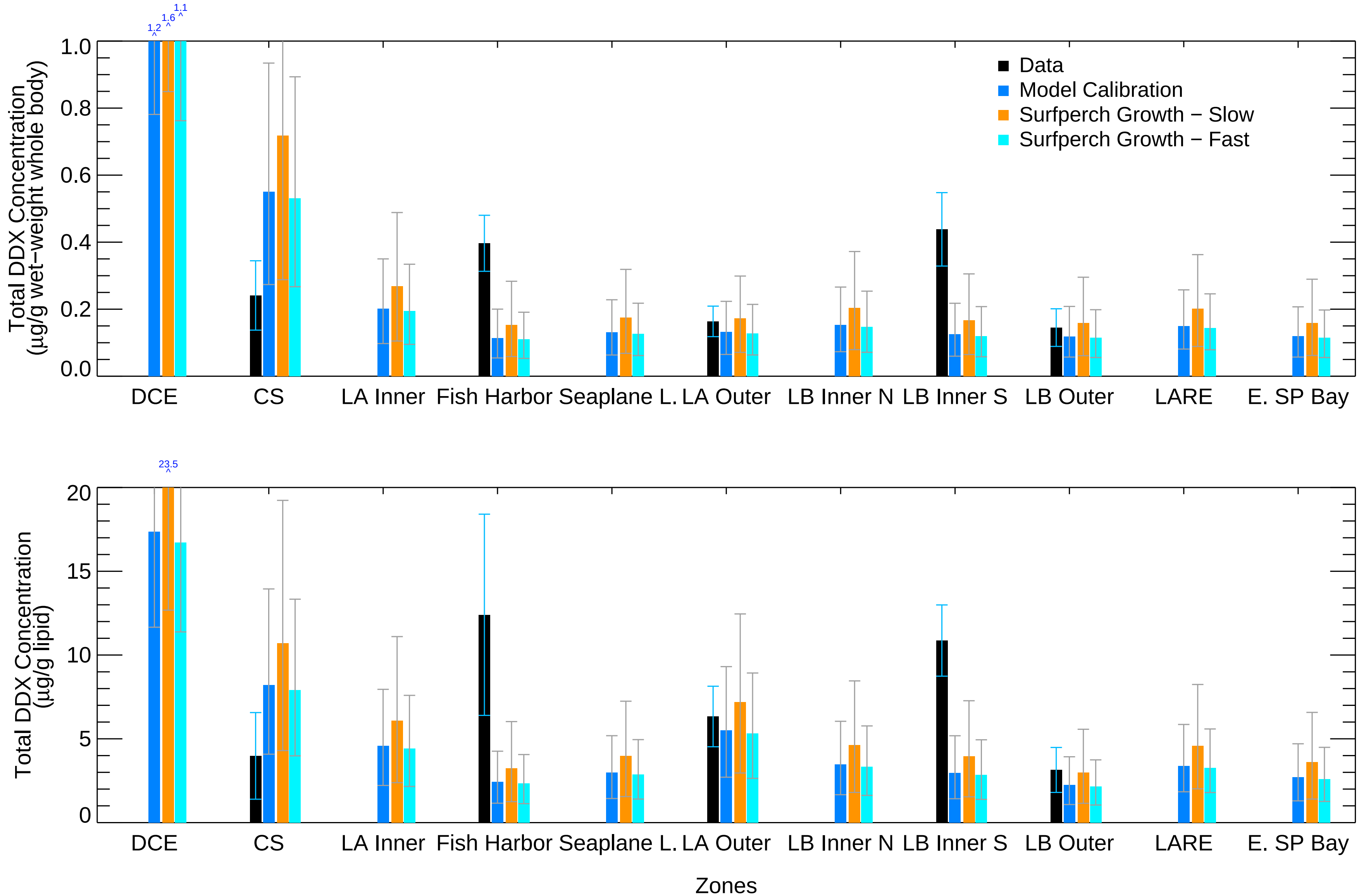


Figure 6−16b

Effects of Alternate Growth on Total DDX Concentration in Surfperch

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ files v.1677, 1677, 1677 and biota files v.1727, 1734, 1735 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Tue Apr 25 16:21:11 2017

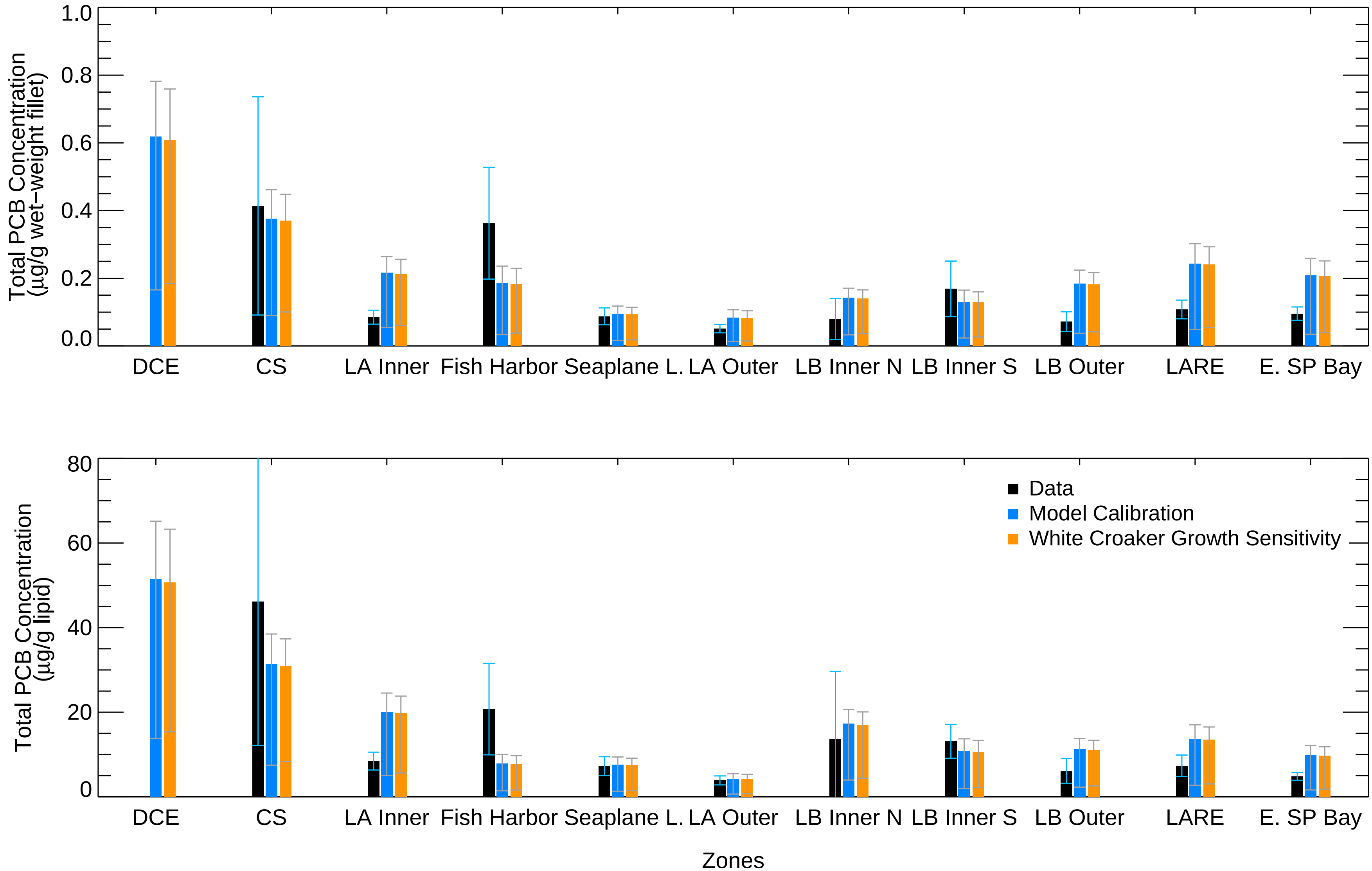


Figure 6−16c

Effects of Alternate Growth on Total PCB Concentration in White Croaker

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx. Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value), IH1−FFF−6WC (high value). Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1677 and biota files v.1727, 1736 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Tue Apr 25 17:15:49 2017

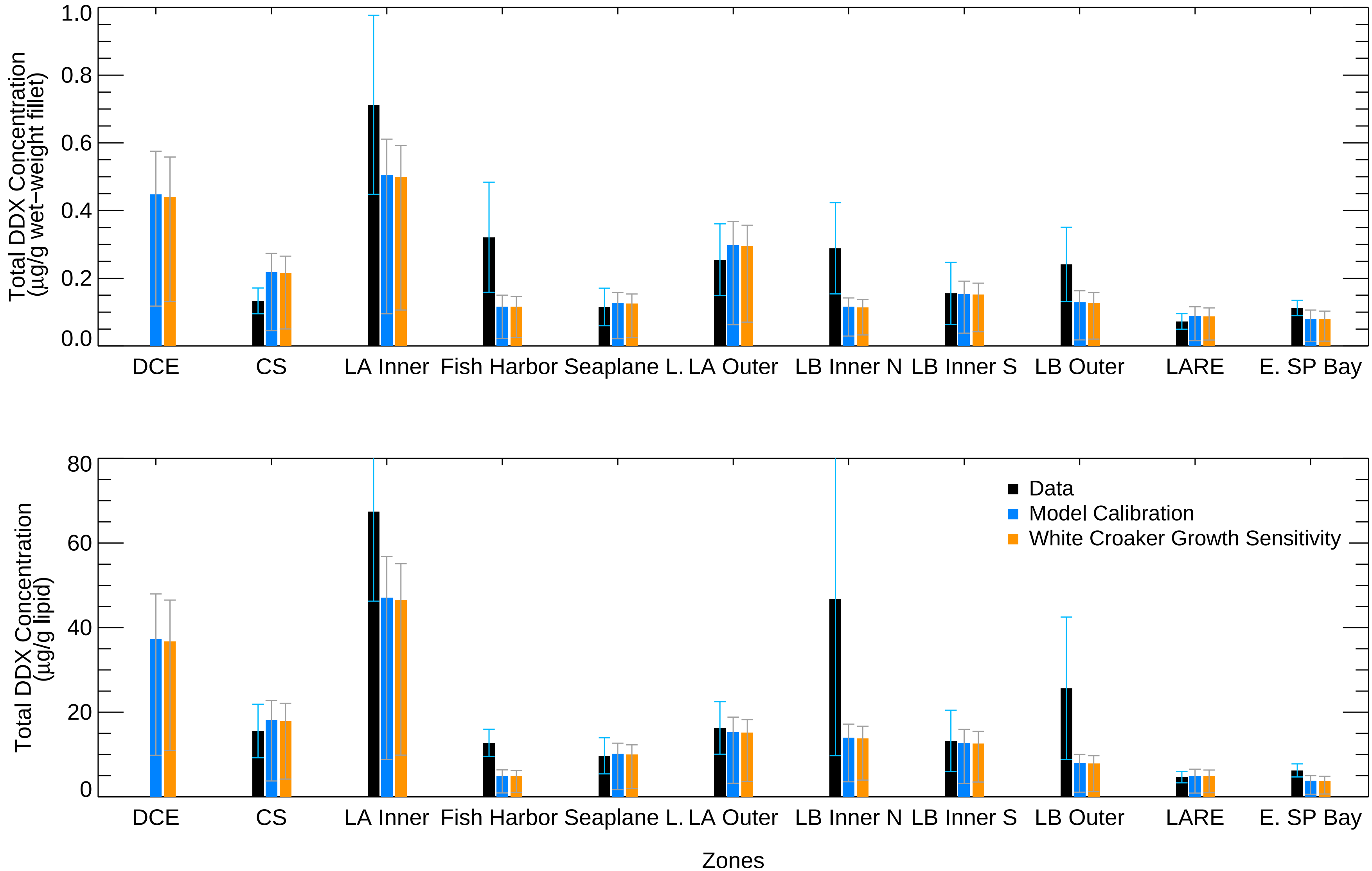


Figure 6−16d

Effects of Alternate Growth on Total DDX Concentration in White Croaker

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value), IH1−FFF−6WC (high value). Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1677 and biota files v.1727, 1736 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Tue Apr 25 17:15:49 2017

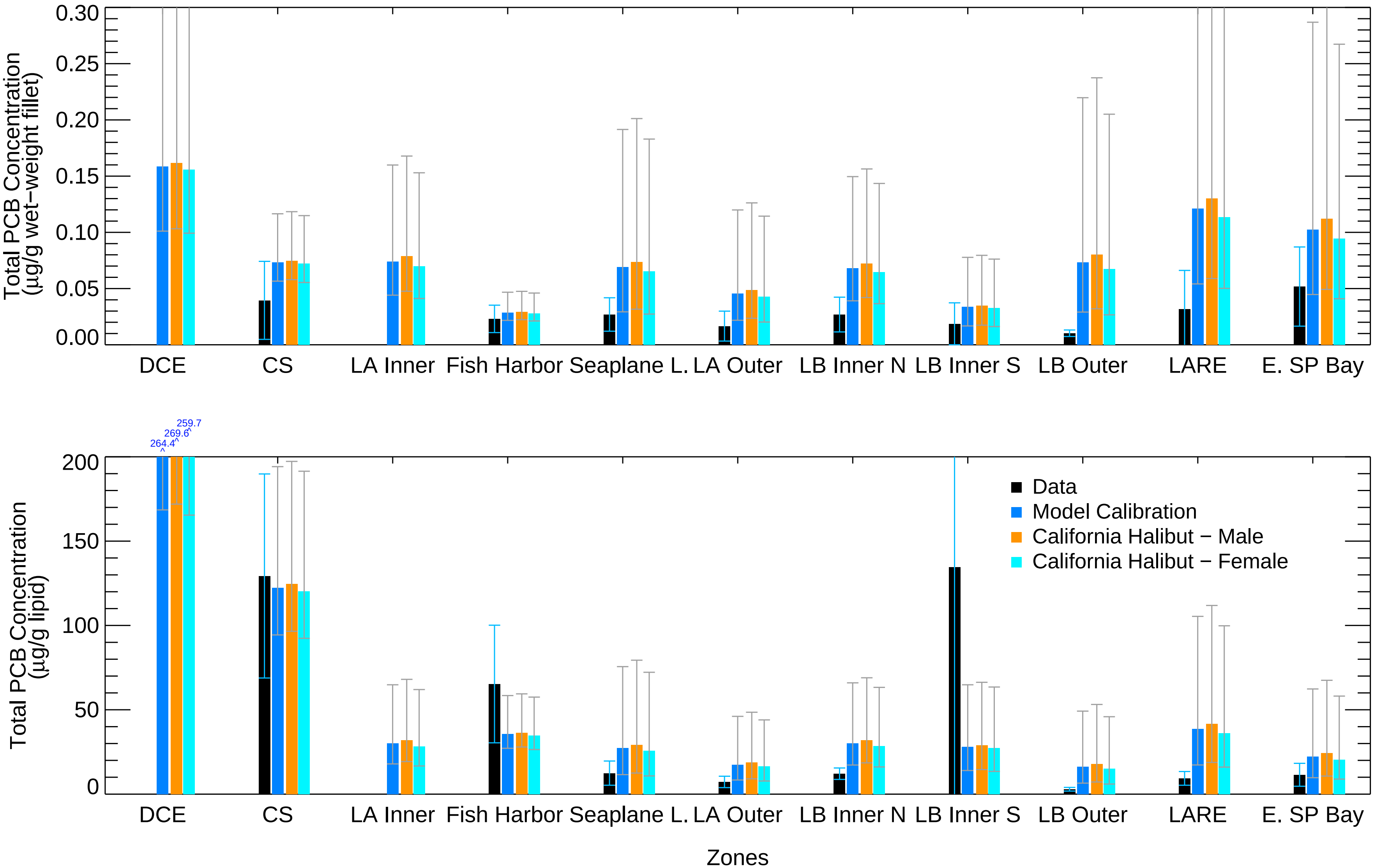


Figure 6−16e

Effects of Alternate Growth on Total PCB Concentration in California Halibut

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1677, 1677 and biota files v.1727, 1737, 1738 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Tue Apr 25 17:49:54 2017

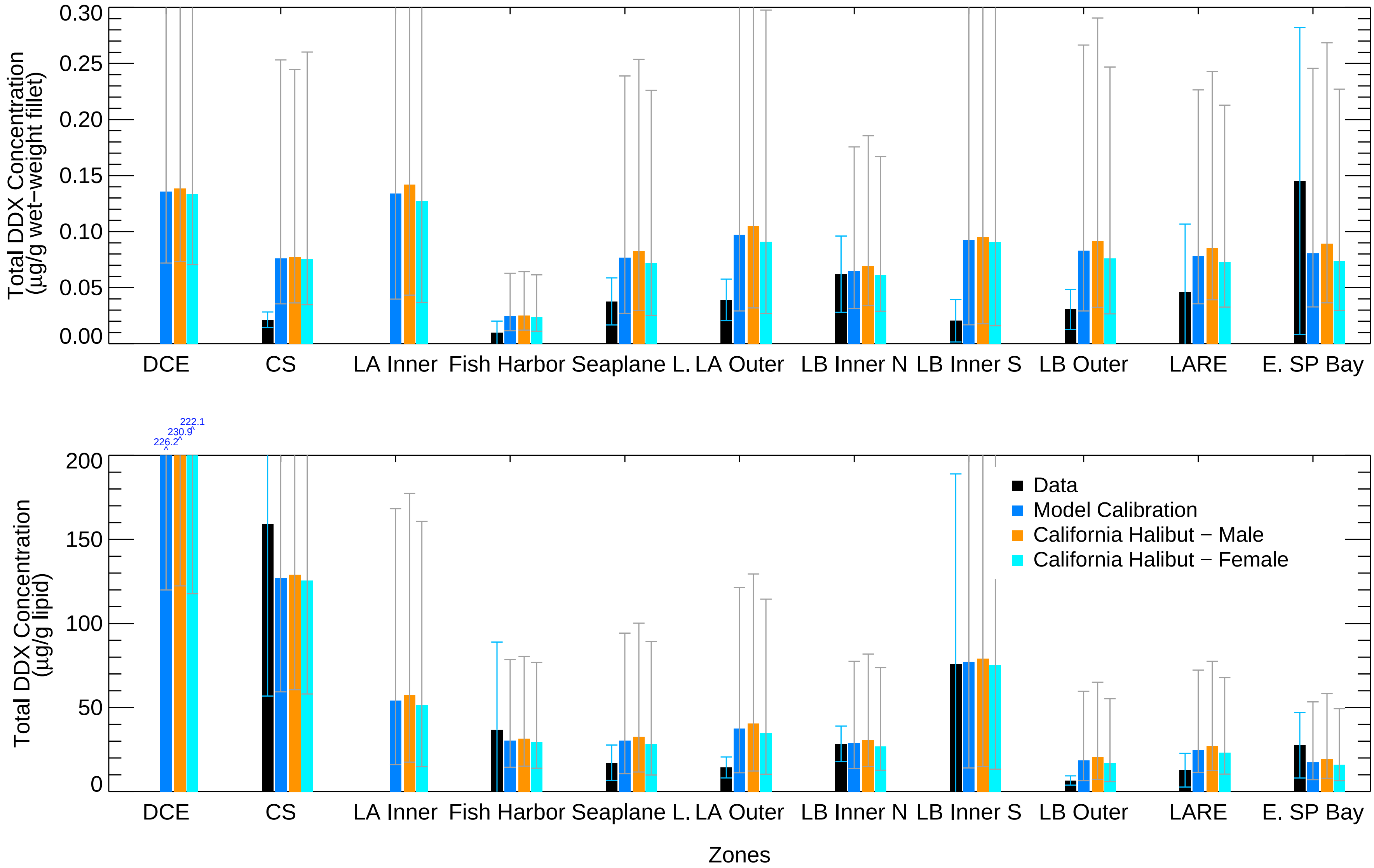


Figure 6−16f

Effects of Alternate Growth on Total DDX Concentration in California Halibut

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1677, 1677 and biota files v.1727, 1737, 1738 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Tue Apr 25 17:49:54 2017

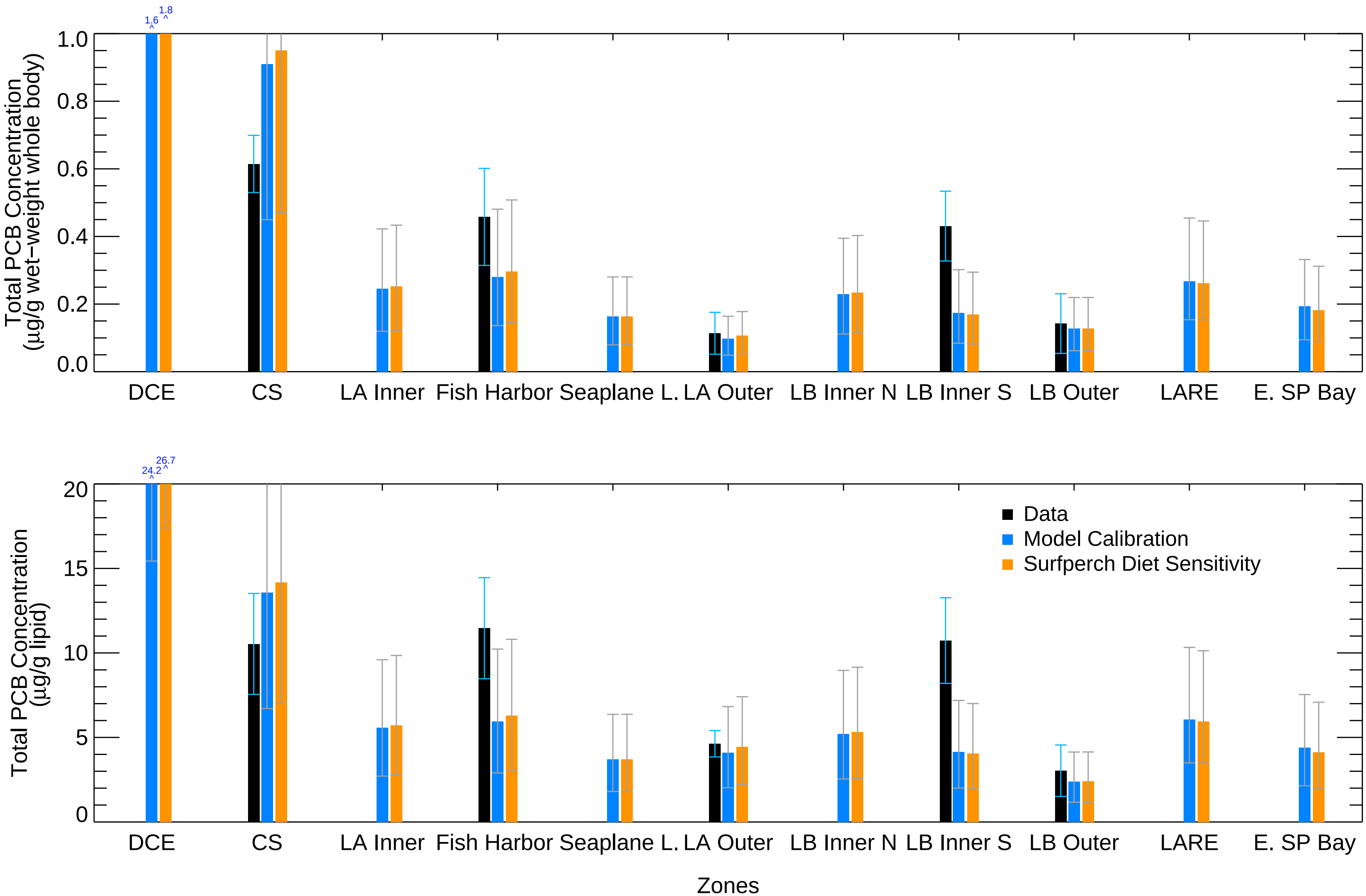


Figure 6−17a

Effects of Alternate Diet on Total PCB Concentration in Surfperch

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ files v.1677, 1677 and biota files v.1727, 1739 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 10:36:16 2017

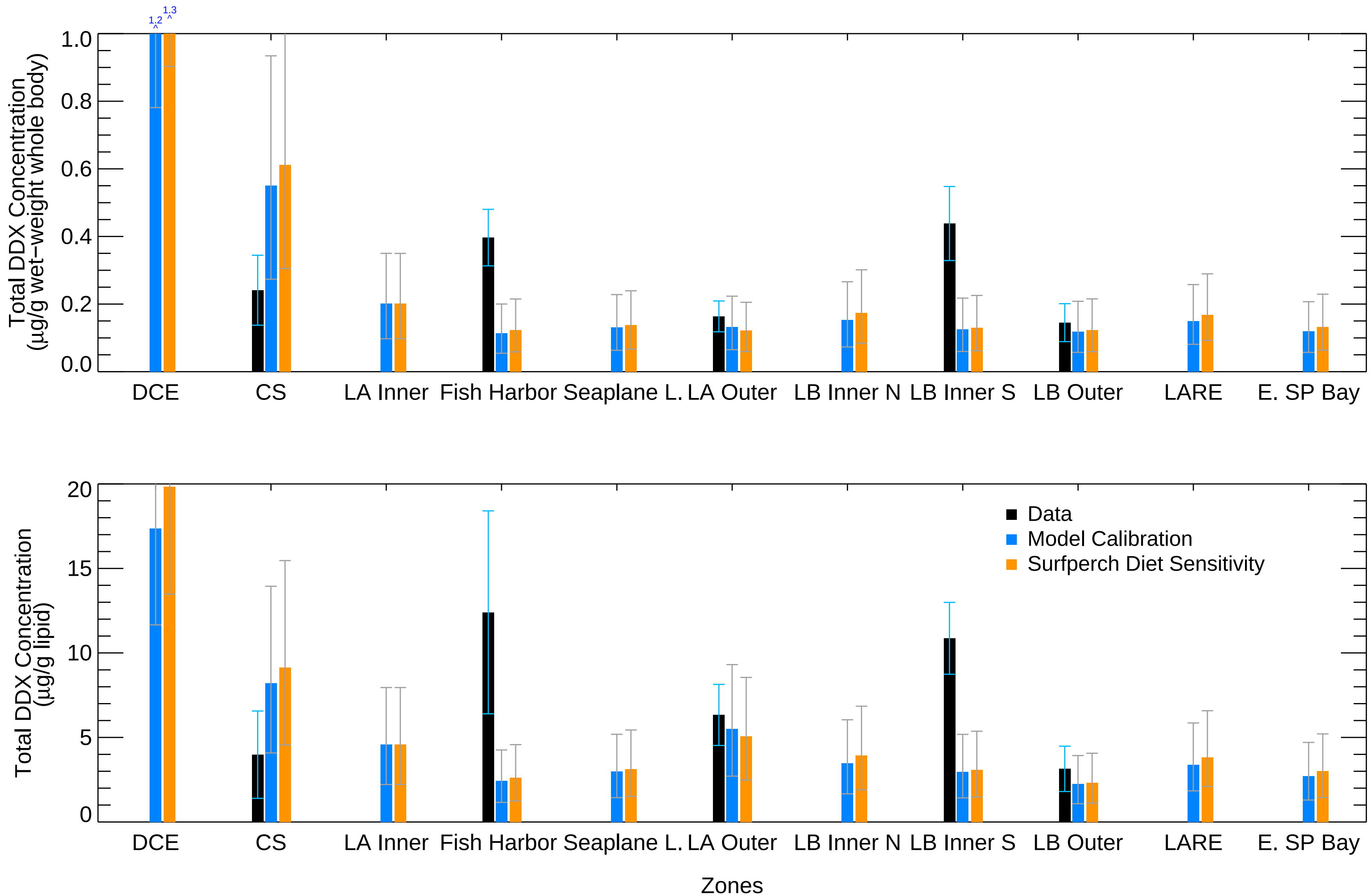


Figure 6−17b

Effects of Alternate Diet on Total DDX Concentration in Surfperch

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ files v.1677, 1677 and biota files v.1727, 1739 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 10:36:16 2017

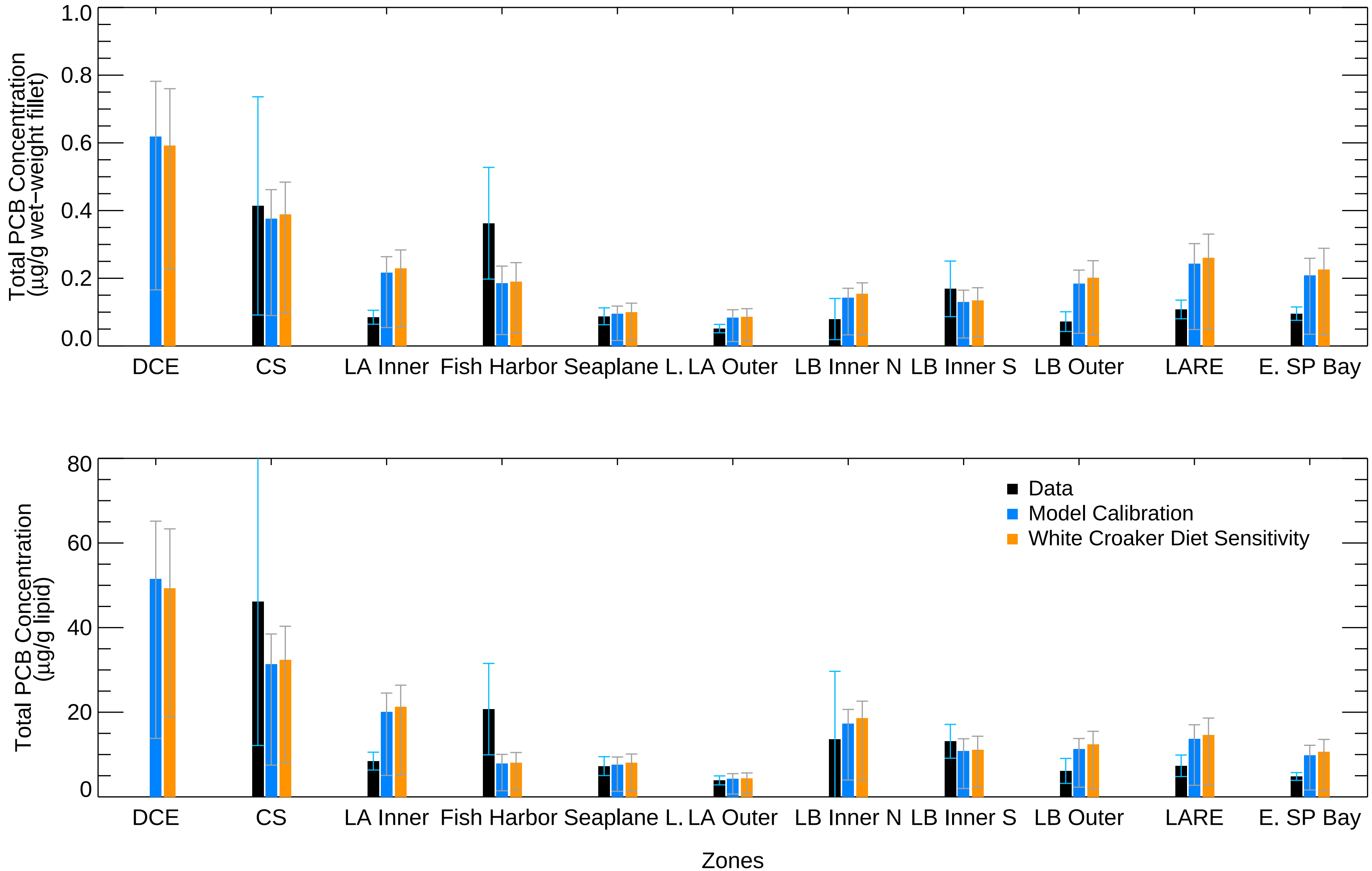


Figure 6−17c

Effects of Alternate Diet on Total PCB Concentration in White Croaker

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx. Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value), IH1−FFF−6WC (high value). Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1677 and biota files v.1727, 1740 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 10:56:33 2017

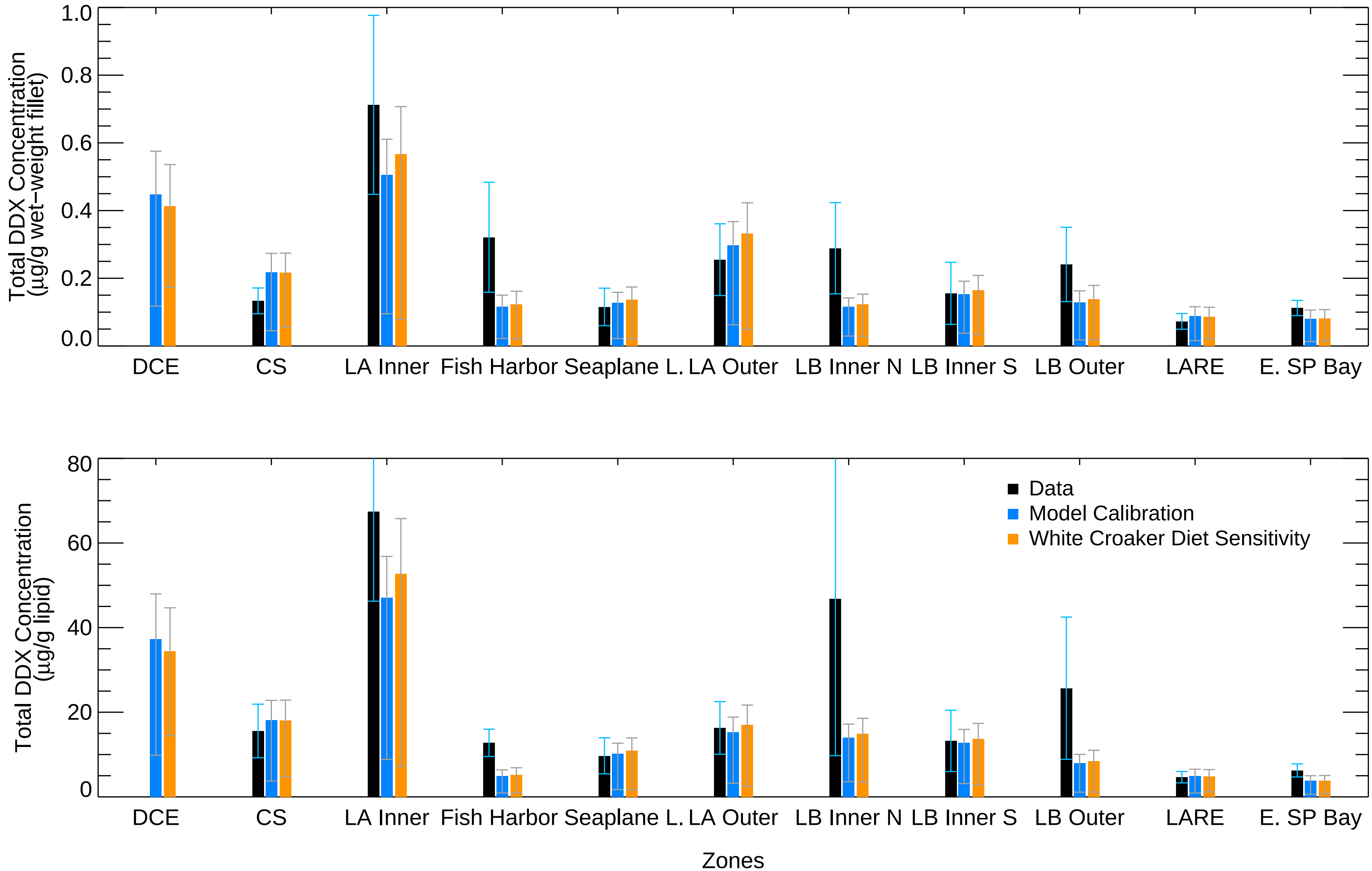


Figure 6−17d

Effects of Alternate Diet on Total DDX Concentration in White Croaker

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx. Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value), IH1−FFF−6WC (high value). Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1677 and biota files v.1727, 1740 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 10:56:33 2017

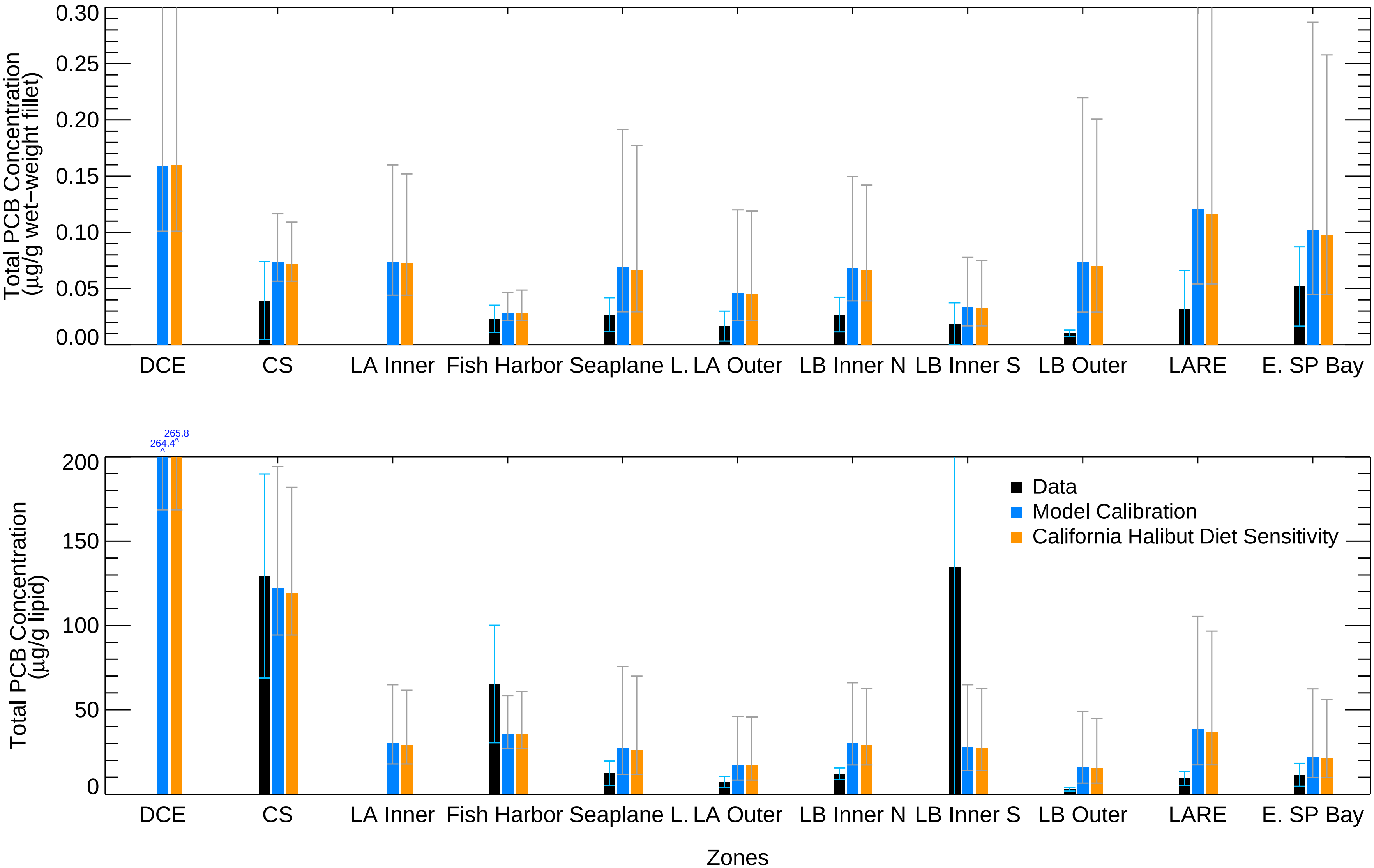


Figure 6−17e

Effects of Alternate Diet on Total PCB Concentration in California Halibut

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx. Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1677 and biota files v.1727, 1741 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 11:09:18 2017

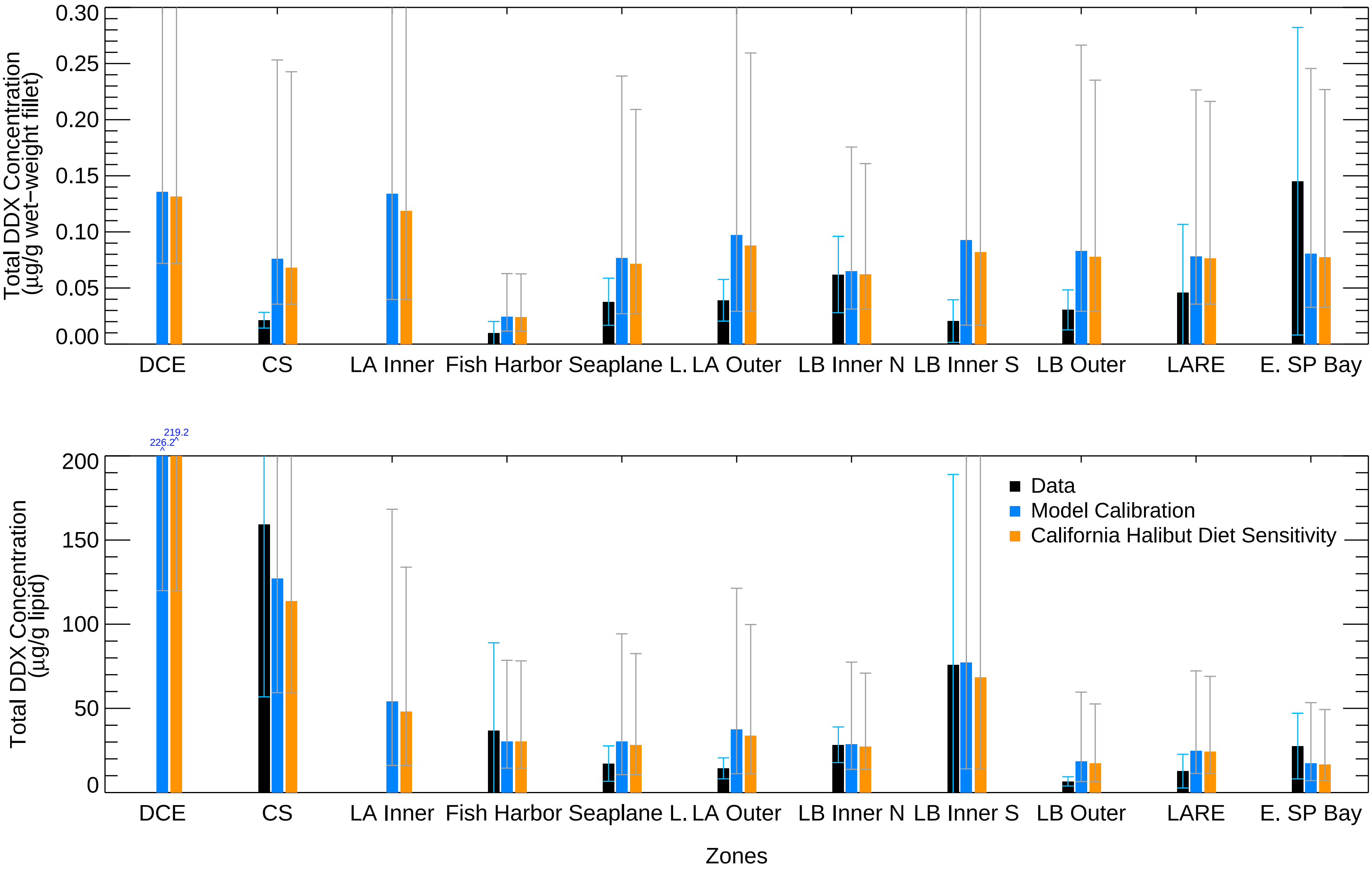


Figure 6−17f

Effects of Alternate Diet on Total DDX Concentration in California Halibut

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1677 and biota files v.1727, 1741 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 11:09:18 2017

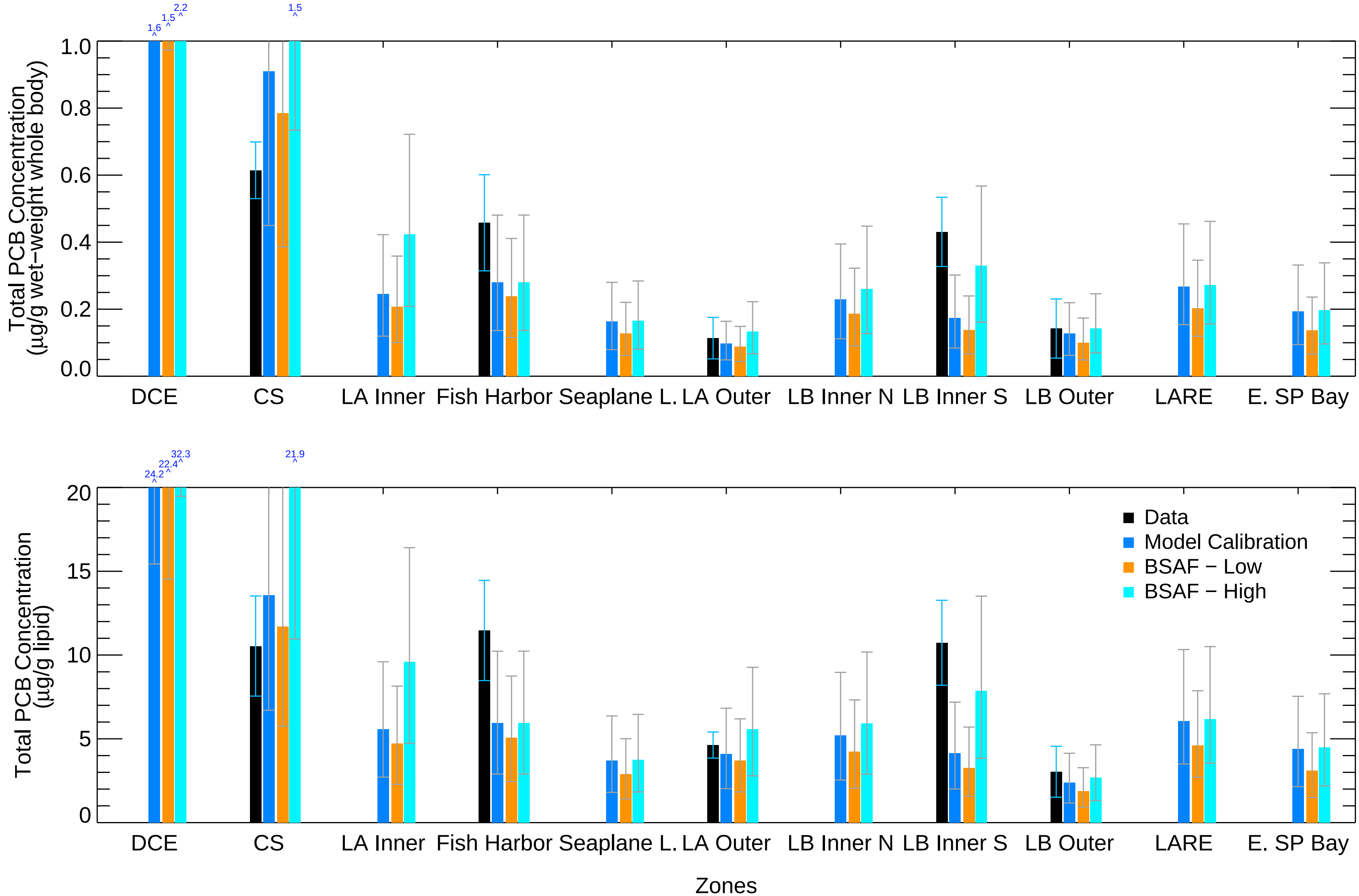


Figure 6−18a

Effects of Alternate Biota Sediment Accumulation Factor on Total PCB Concentration in Surfperch

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ files v.1677, 1677, 1677 and biota files v.1727, 1742, 1743 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 11:43:47 2017

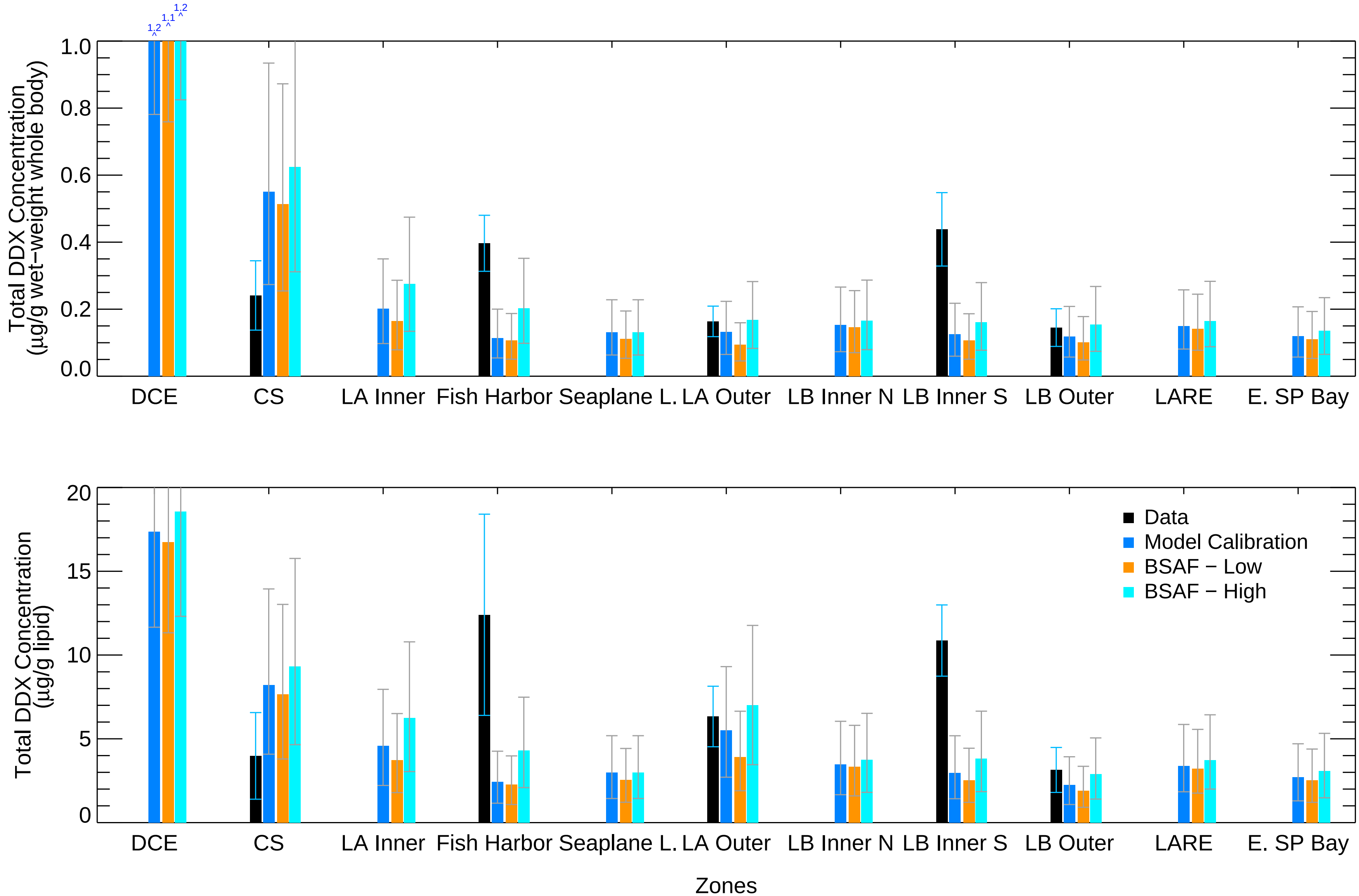


Figure 6−18b

Effects of Alternate Biota Sediment Accumulation Factor on Total DDX Concentration in Surfperch

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ files v.1677, 1677, 1677 and biota files v.1727, 1742, 1743 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 11:43:47 2017

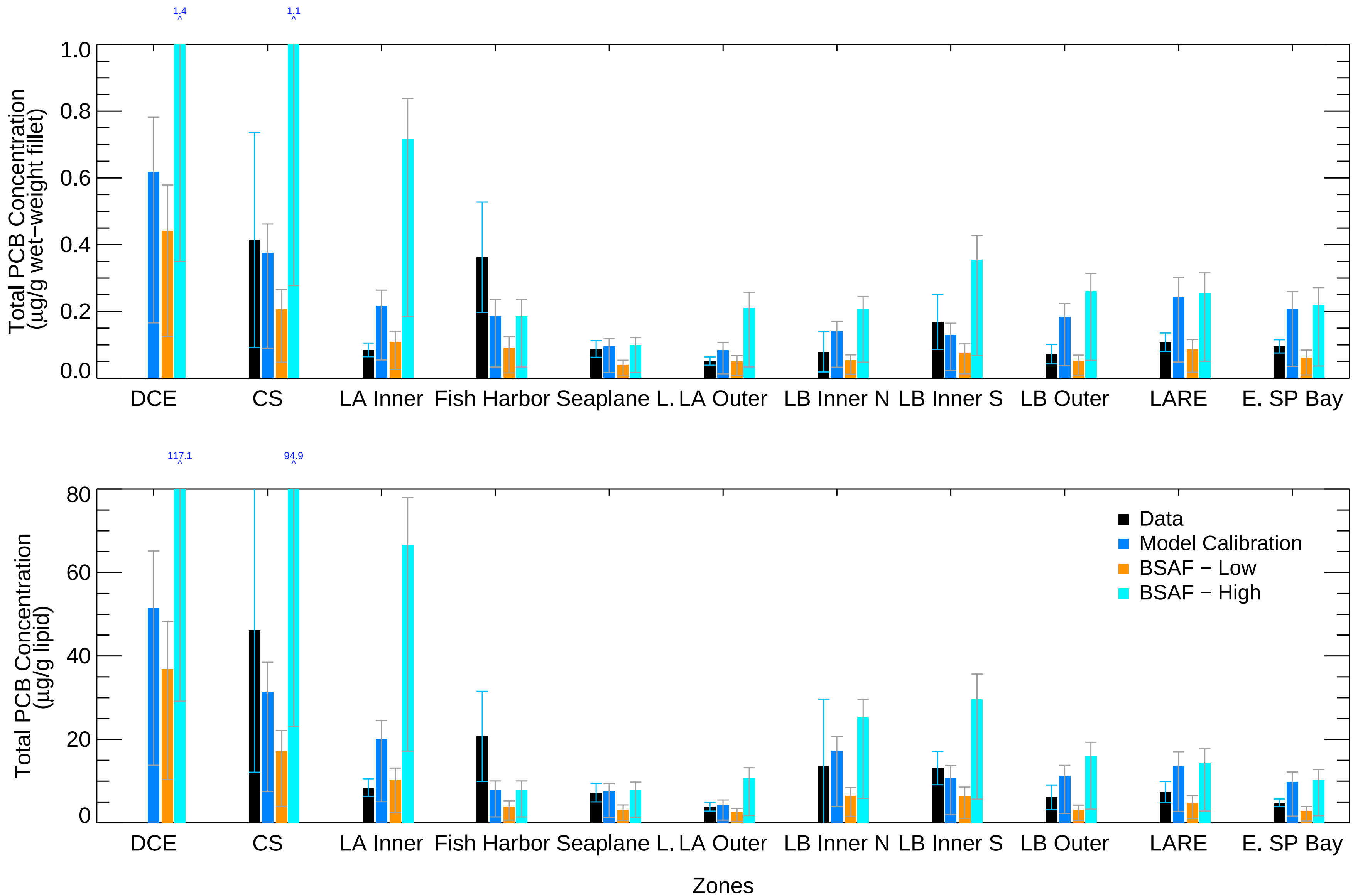


Figure 6−18c

Effects of Alternate Biota Sediment Accumulation Factor on Total PCB Concentration in White Croaker

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx. Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value), IH1−FFF−6WC (high value). Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1677, 1677 and biota files v.1727, 1742, 1743 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 11:43:47 2017

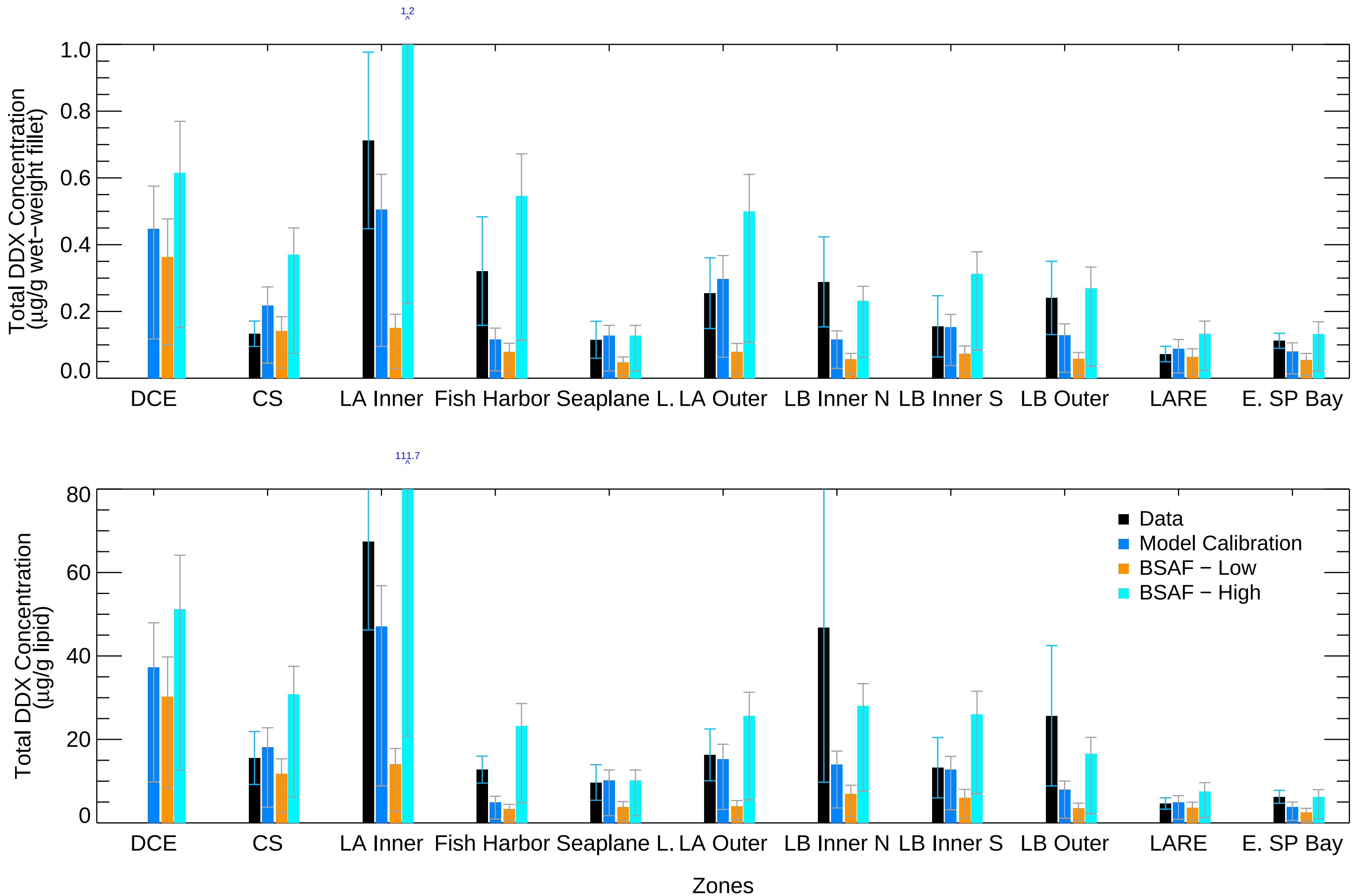


Figure 6−18d

Effects of Alternate Biota Sediment Accumulation Factor on Total DDX Concentration in White Croaker

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx. Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value), IH1−FFF−6WC (high value). Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1677, 1677 and biota files v.1727, 1742, 1743 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 11:43:47 2017

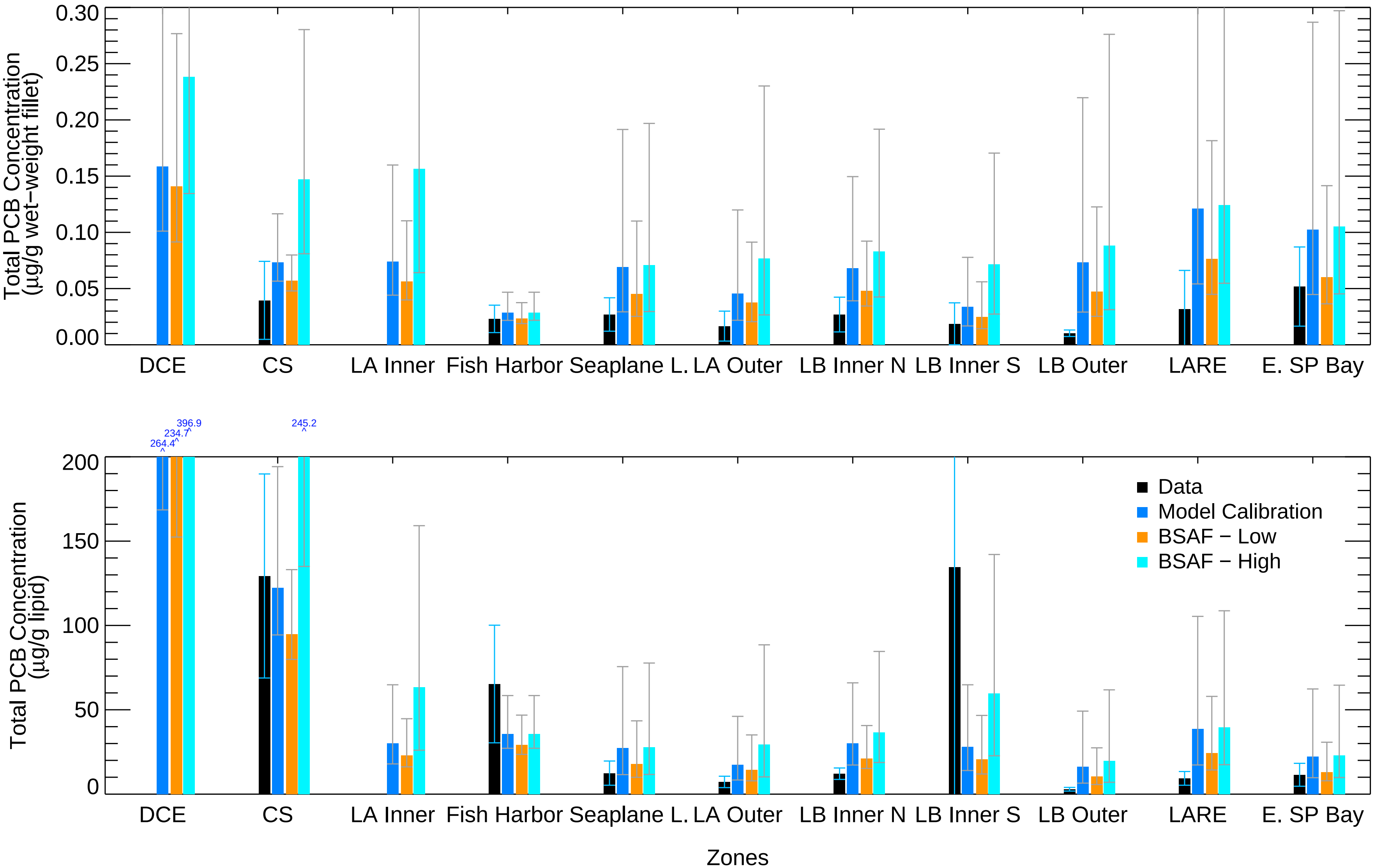


Figure 6−18e

Effects of Alternate Biota Sediment Accumulation Factor on Total PCB Concentration in California Halibut

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1677, 1677 and biota files v.1727, 1742, 1743 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 11:43:48 2017

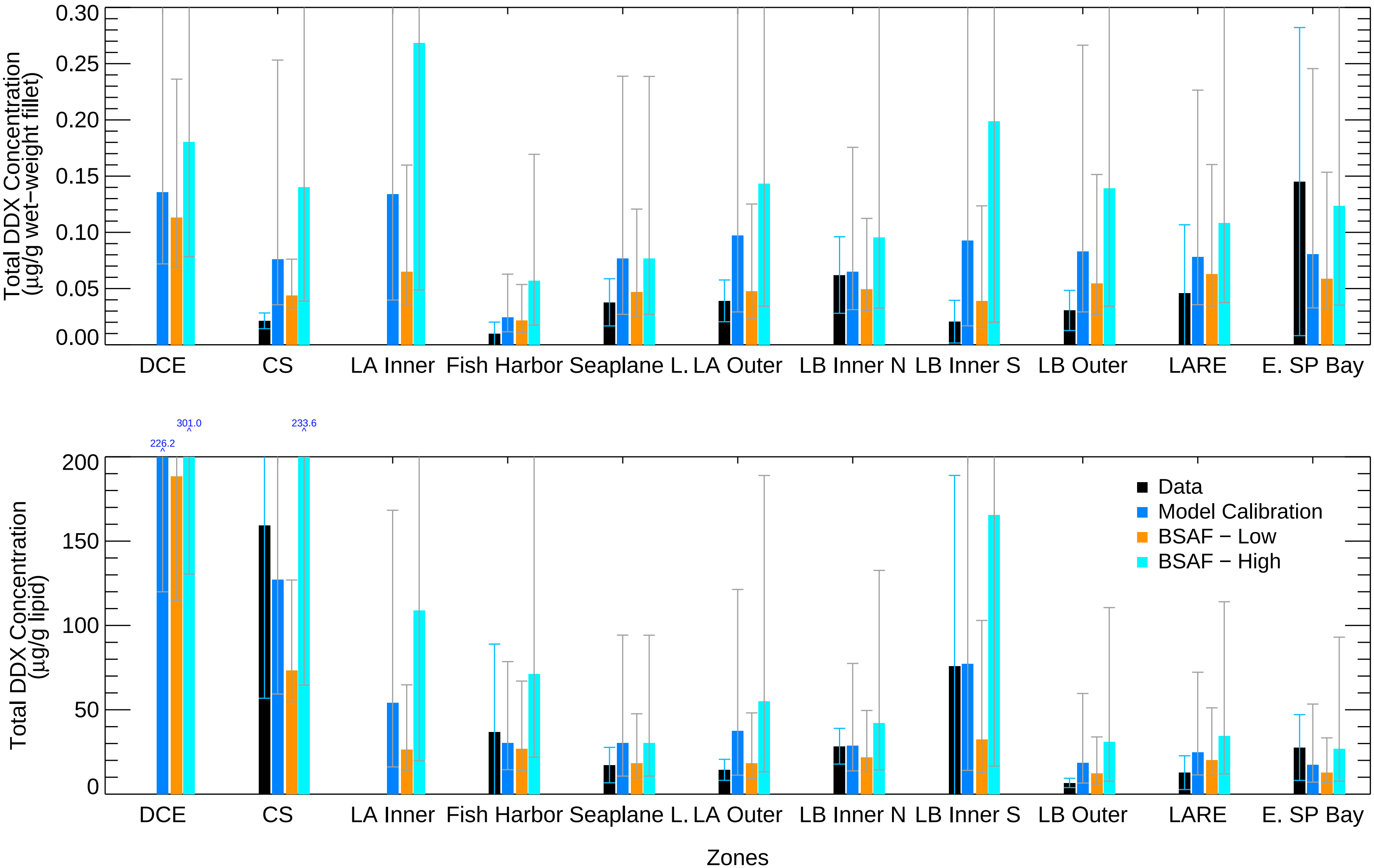


Figure 6−18f

Effects of Alternate Biota Sediment Accumulation Factor on Total DDX Concentration in California Halibut

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1677, 1677 and biota files v.1727, 1742, 1743 used for model.

ANCHOR QEA

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 11:43:48 2017

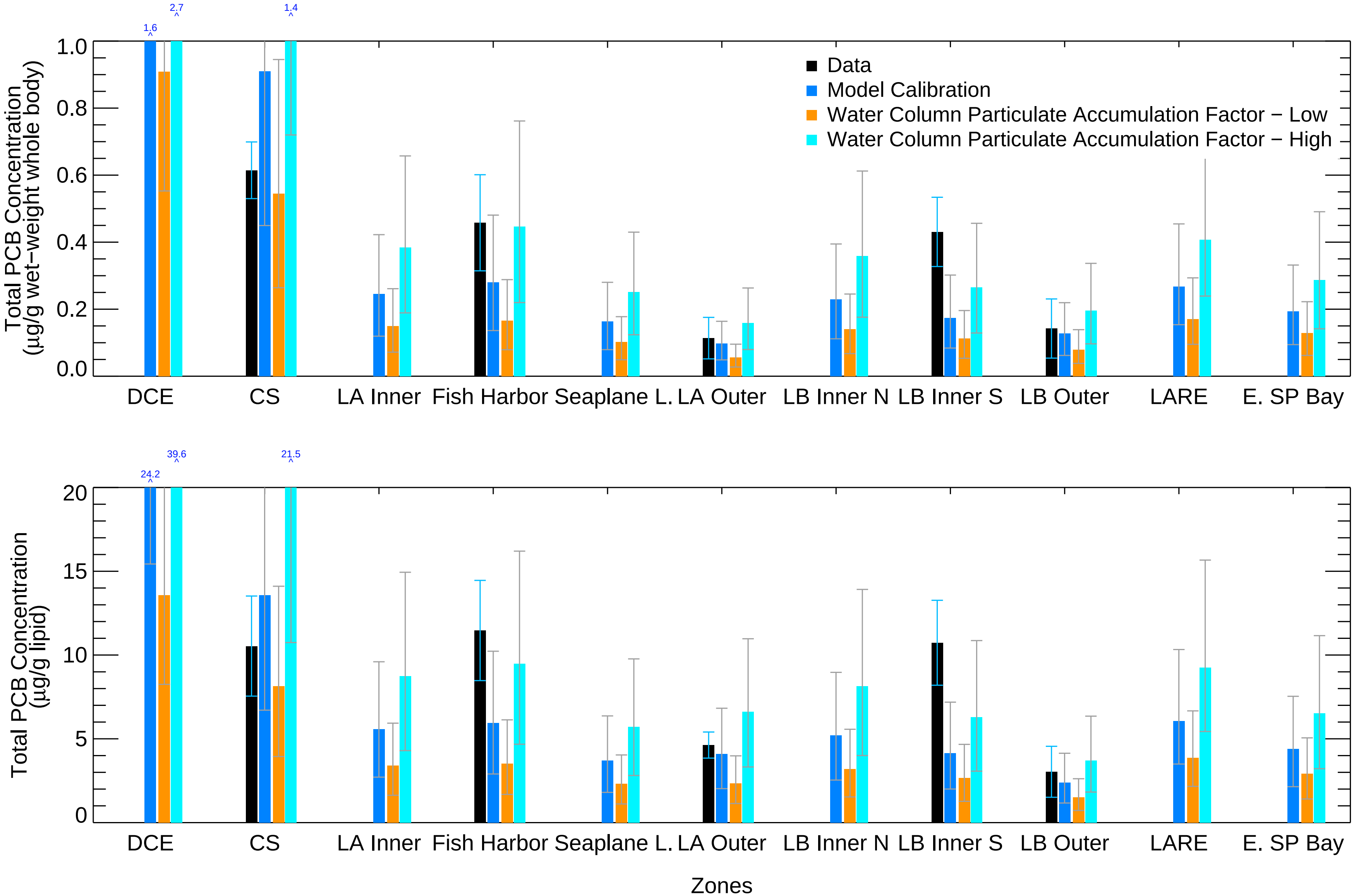


Figure 6−19a

Effects of Alternate Water Column Particulate Accumulation Factor on Total PCB Concentration in Surfperch

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ files v.1677, 1677, 1677 and biota files v.1727, 1744, 1745 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 12:24:26 2017

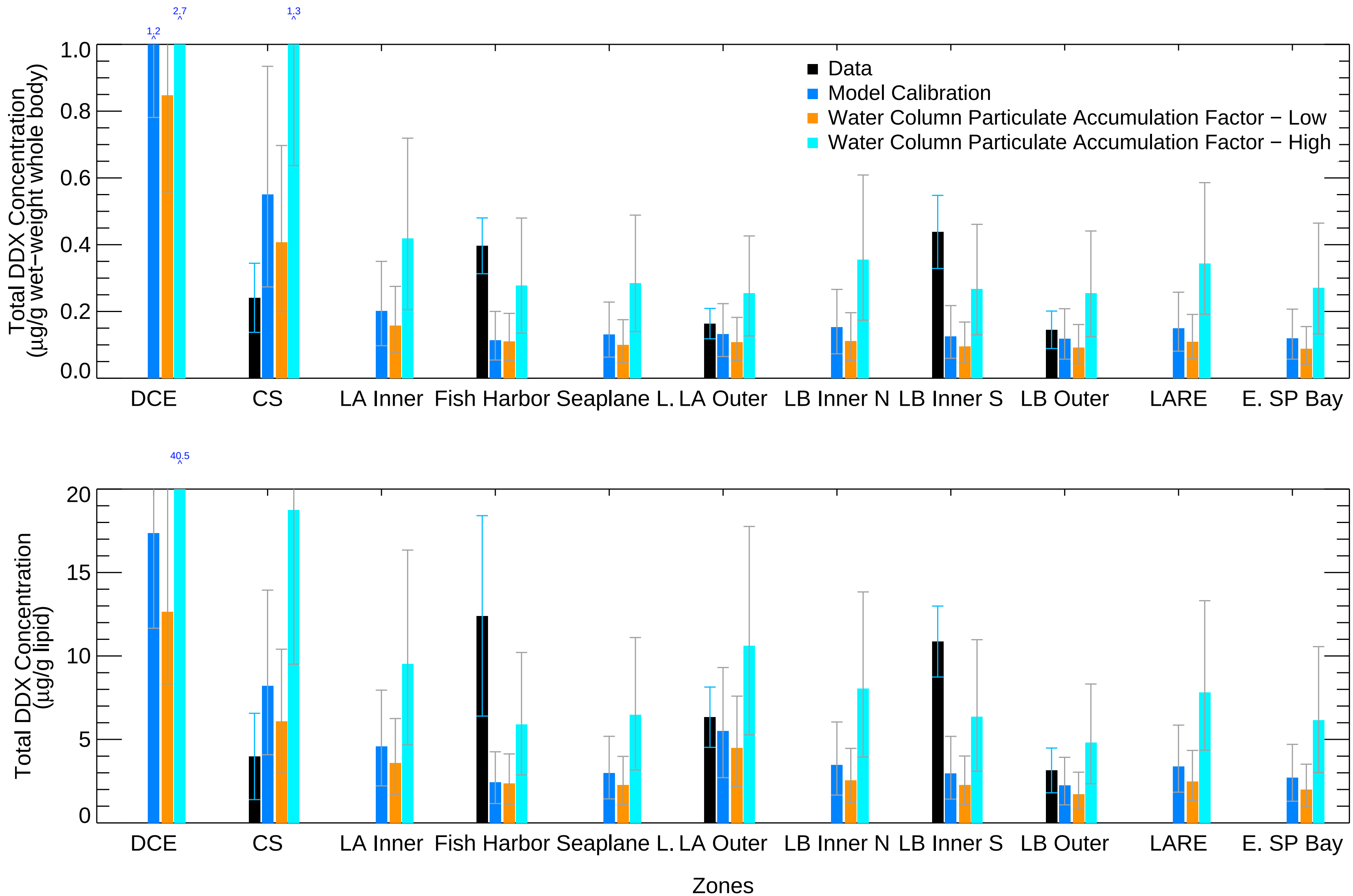


Figure 6−19b

Effects of Alternate Water Column Particulate Accumulation Factor on Total DDX Concentration in Surfperch

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ files v.1677, 1677, 1677 and biota files v.1727, 1744, 1745 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 12:24:26 2017

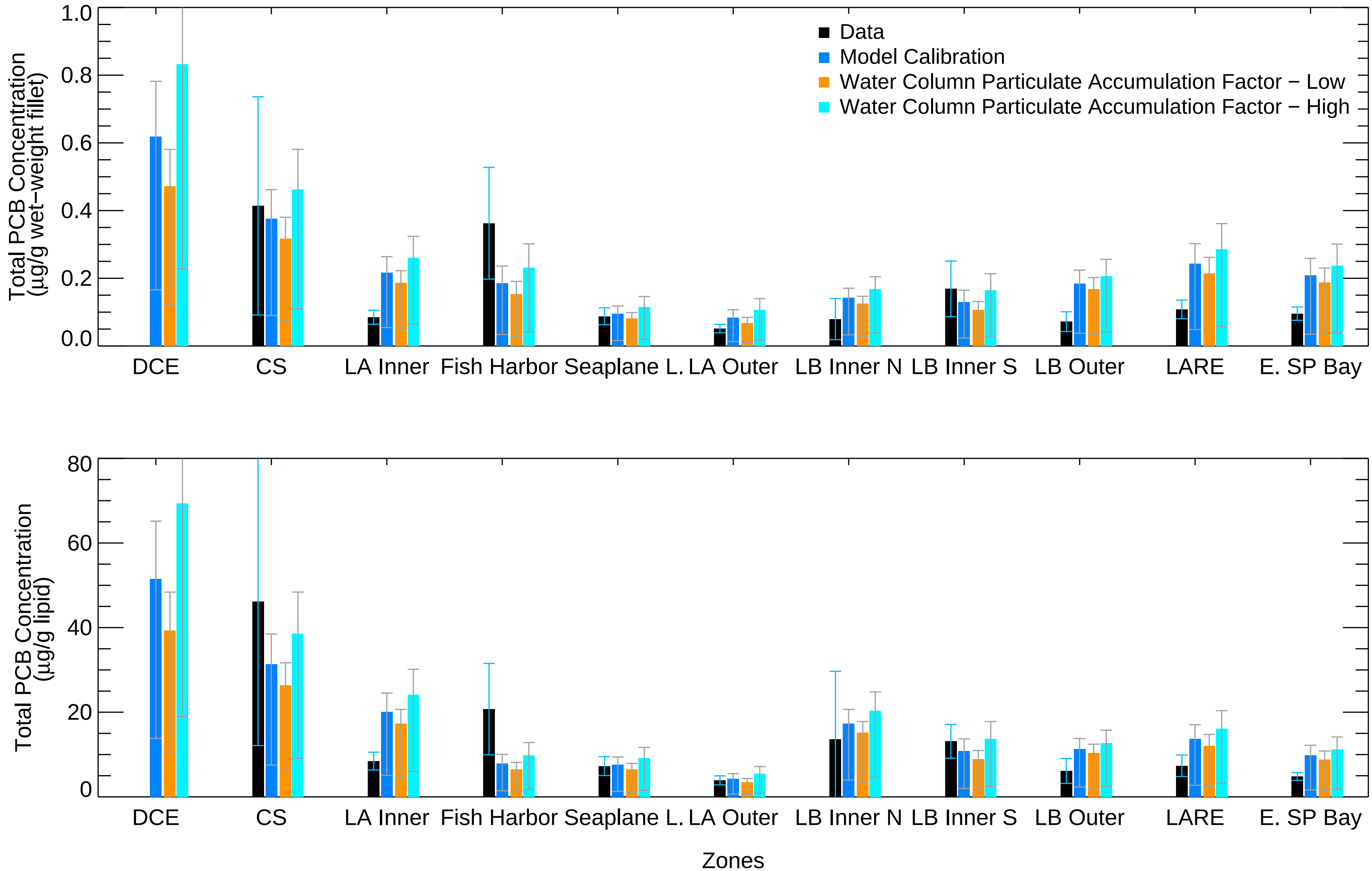


Figure 6−19c

Effects of Alternate Water Column Particulate Accumulation Factor on Total PCB Concentration in White Croaker

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx. Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value), IH1−FFF−6WC (high value). Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1677, 1677 and biota files v.1727, 1744, 1745 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 12:24:26 2017

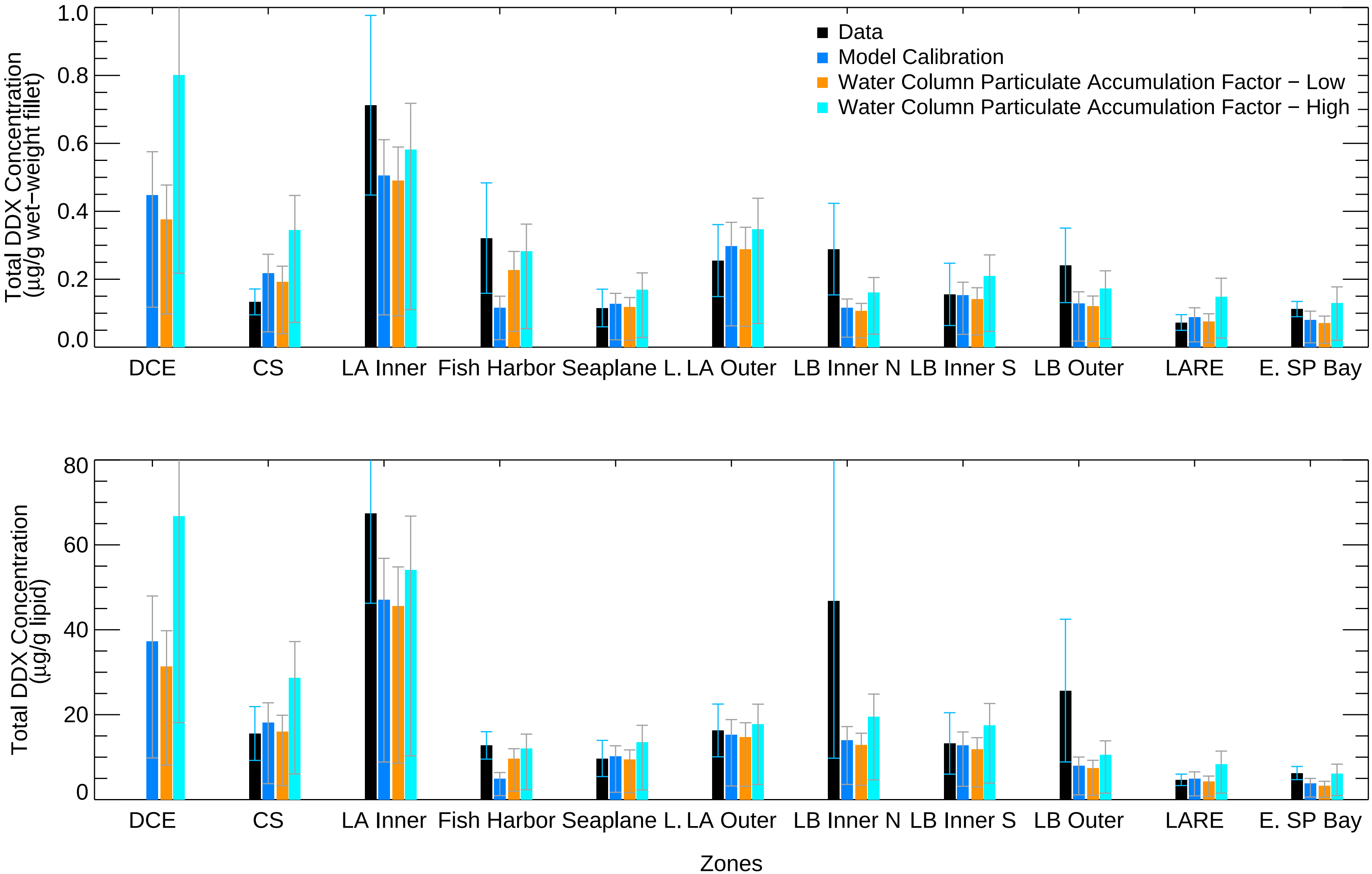


Figure 6−19d

Effects of Alternate Water Column Particulate Accumulation Factor on Total DDX Concentration in White Croaker

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value), IH1−FFF−6WC (high value). Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1677, 1677 and biota files v.1727, 1744, 1745 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 12:24:26 2017

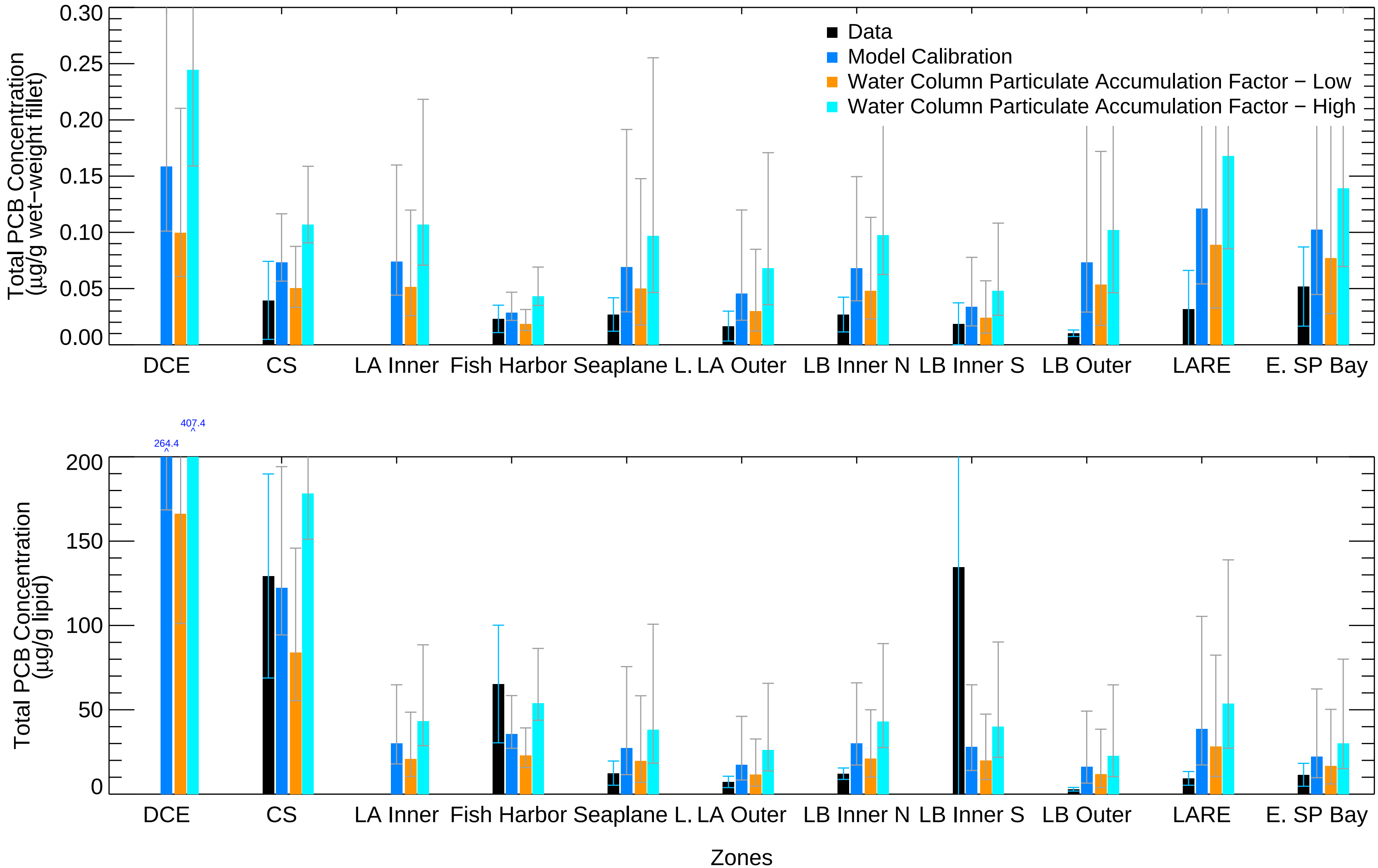


Figure 6−19e

Effects of Alternate Water Column Particulate Accumulation Factor on Total PCB Concentration in California Halibut

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx. Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1677, 1677 and biota files v.1727, 1744, 1745 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 12:24:26 2017

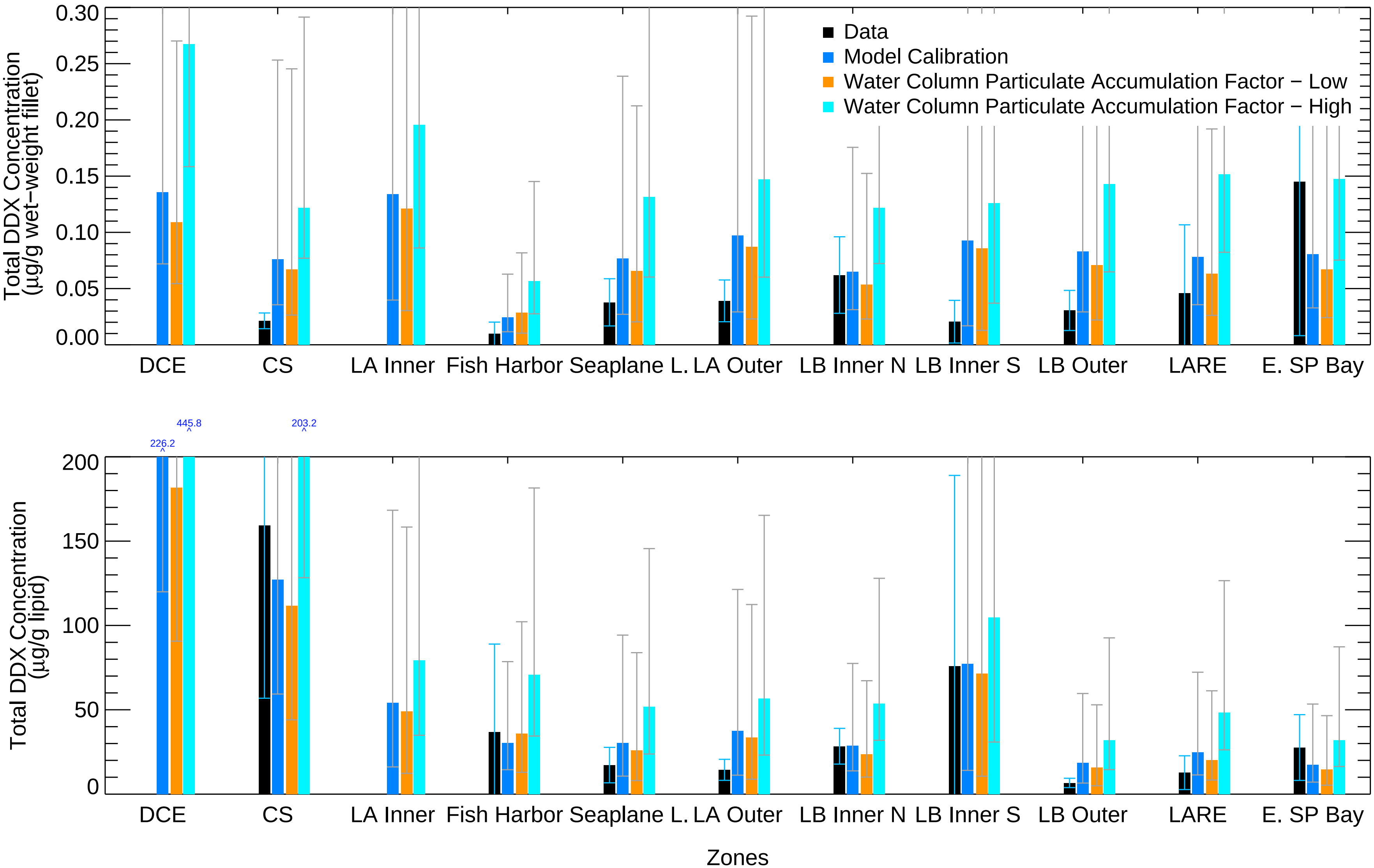


Figure 6−19f

Effects of Alternate Water Column Particulate Accumulation Factor on Total DDX Concentration in California Halibut

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx. Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1677, 1677 and biota files v.1727, 1744, 1745 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 12:24:27 2017

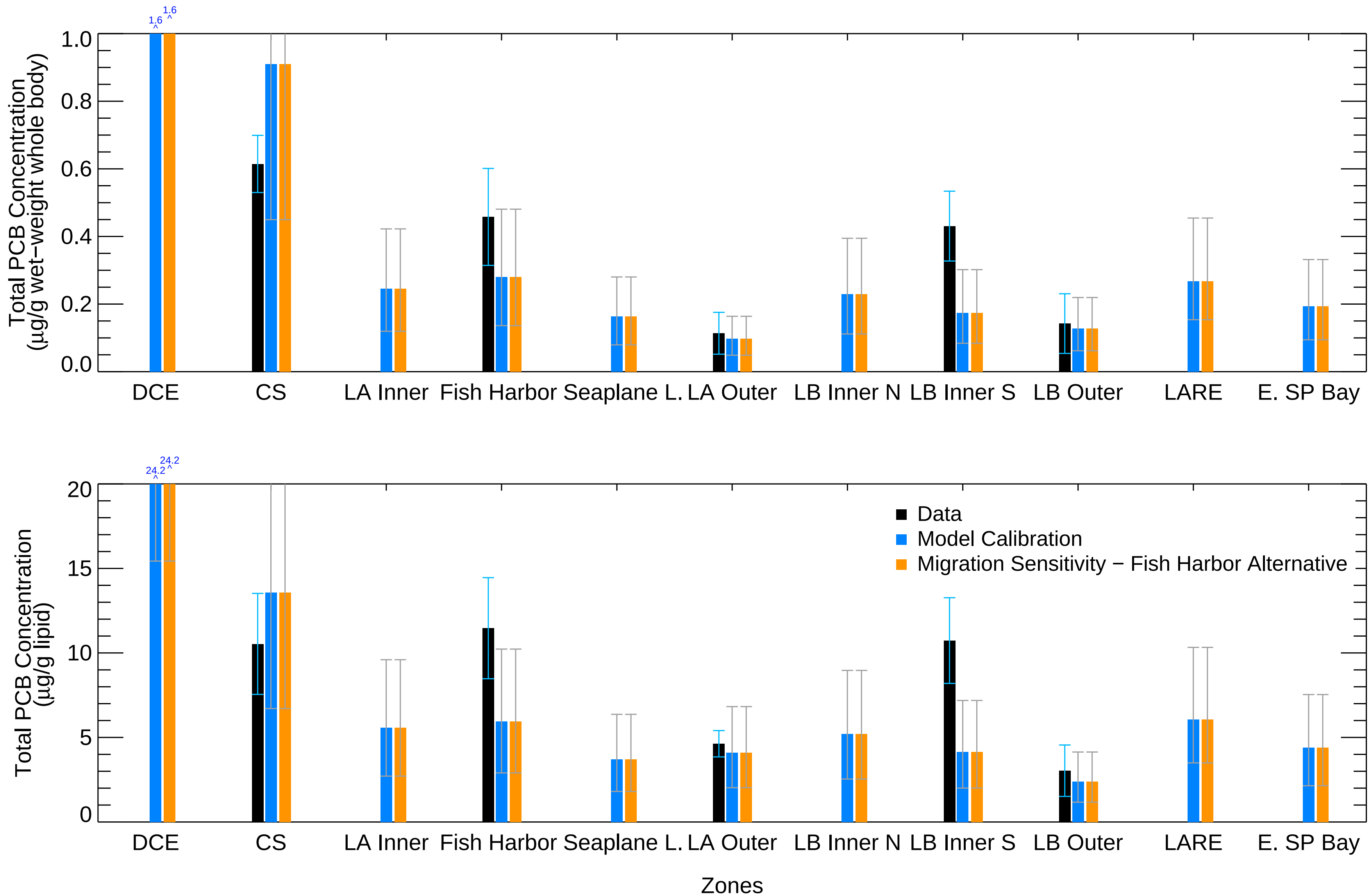


Figure 6−20a

Effects of Decrease in Exposure at Fish Harbor (Increase at PV Shelf) on Total PCB Concentration in Surfperch

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ files v.1677, 1702 and biota files v.1727, 1746 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 14:34:45 2017

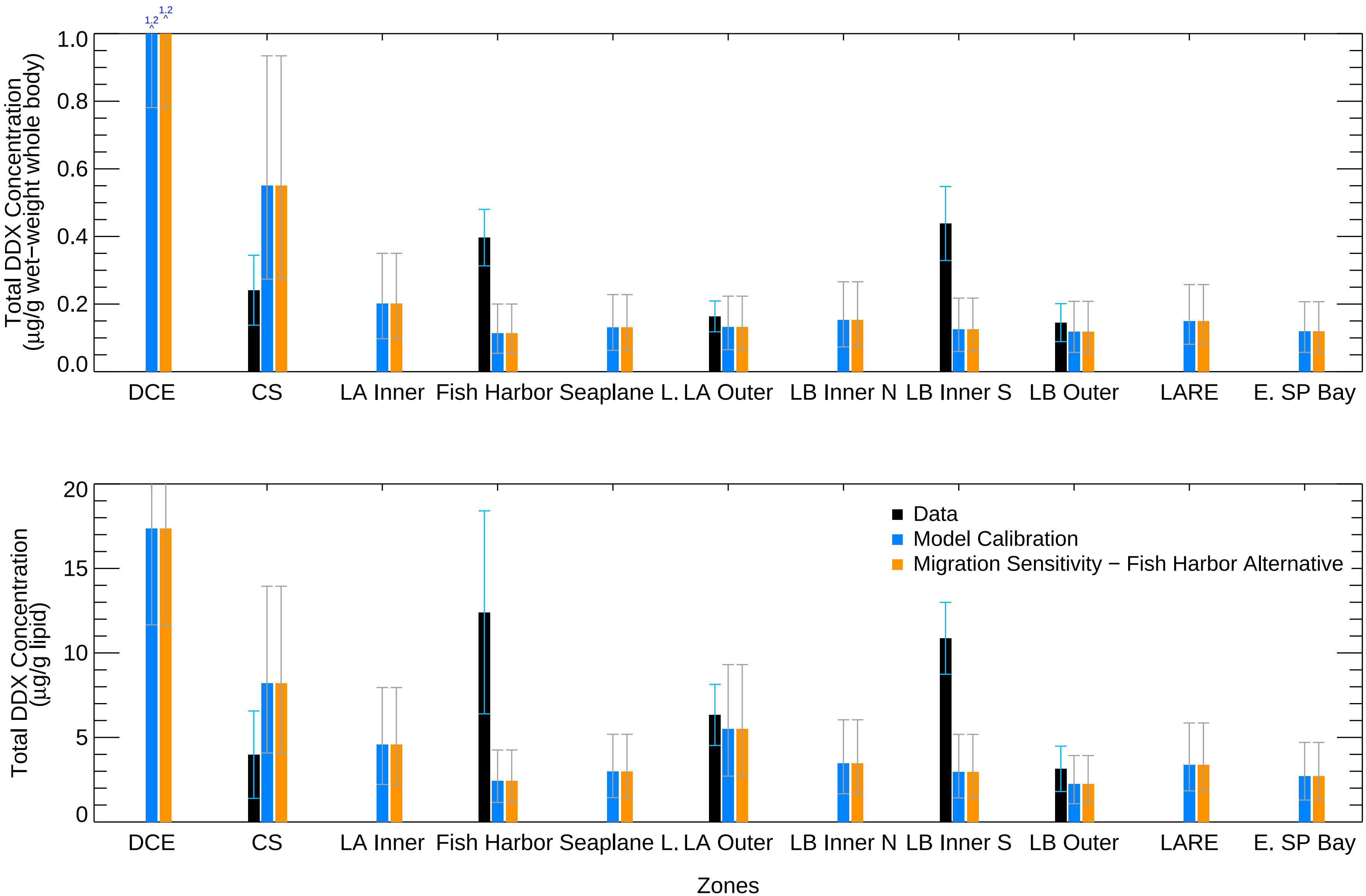


Figure 6−20b

Effects of Decrease in Exposure at Fish Harbor (Increase at PV Shelf) on Total DDX Concentration in Surfperch

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ files v.1677, 1702 and biota files v.1727, 1746 used for model.

ANCHOR QEA

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 14:34:45 2017

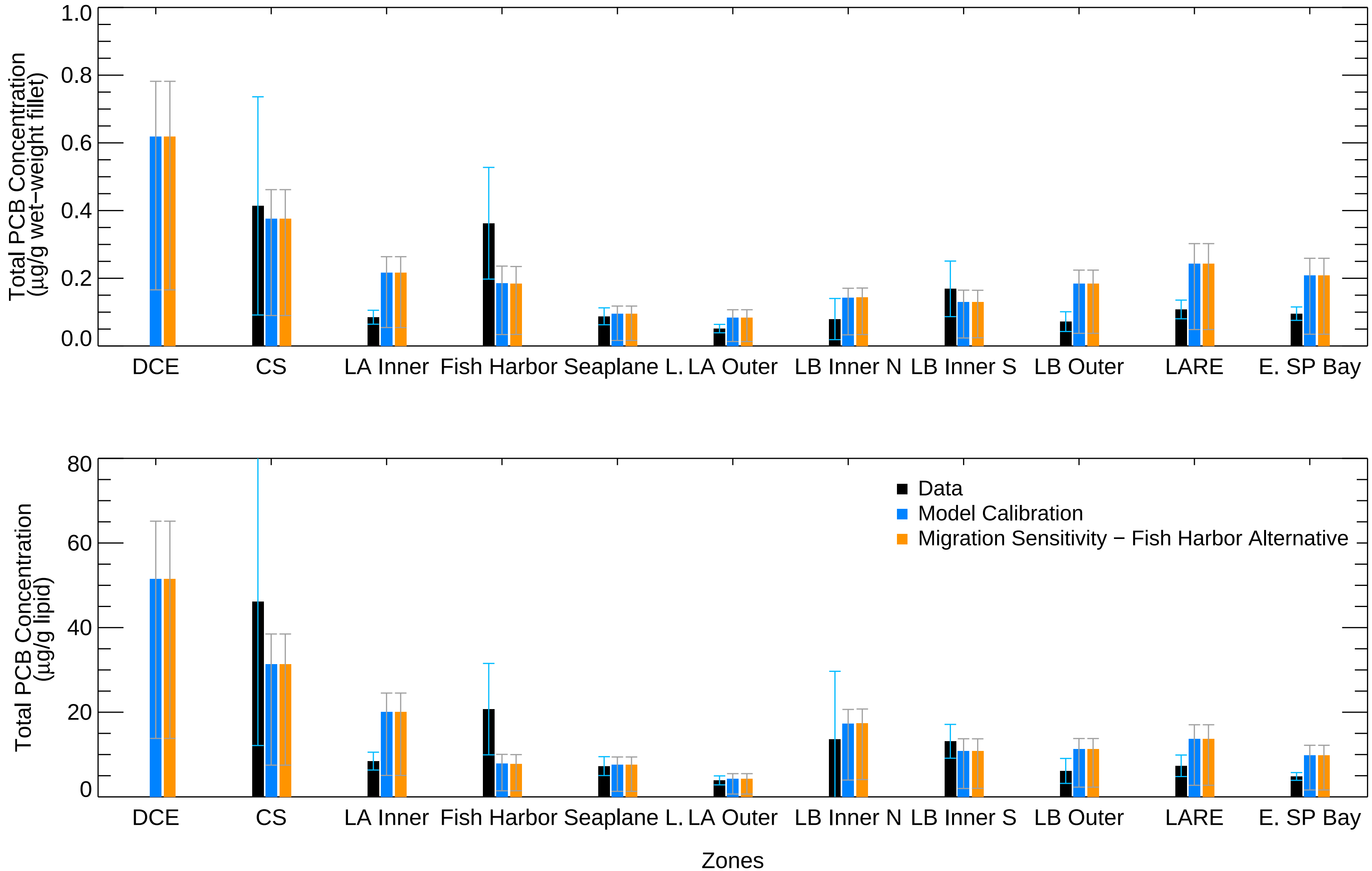


Figure 6−20c

Effects of Decrease in Exposure at Fish Harbor (Increase at PV Shelf) on Total PCB Concentration in White Croaker

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx. Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value), IH1−FFF−6WC (high value). Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1702 and biota files v.1727, 1746 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 14:34:45 2017

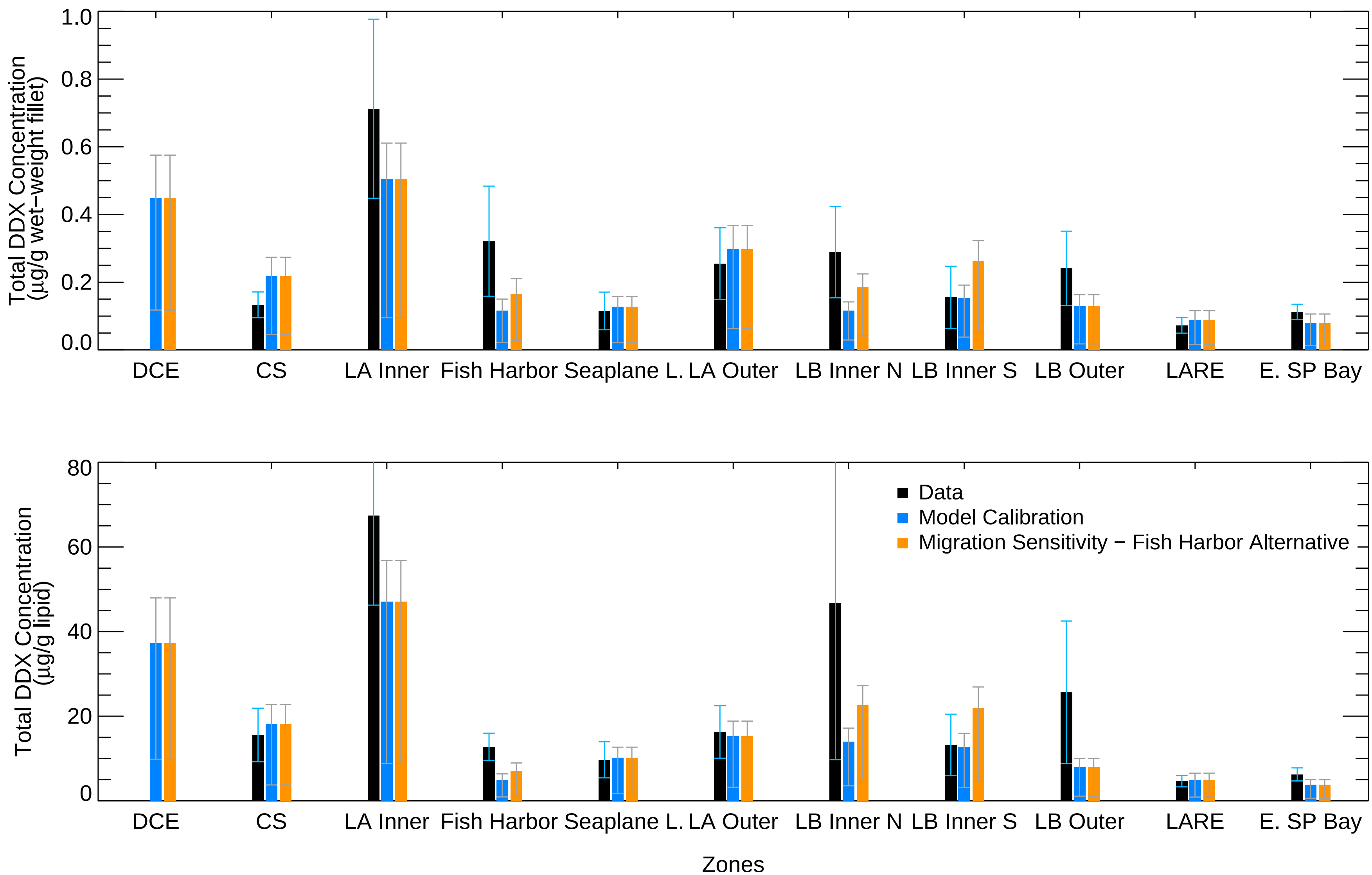


Figure 6−20d

Effects of Decrease in Exposure at Fish Harbor (Increase at PV Shelf) on Total DDX Concentration in White Croaker

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value), IH1−FFF−6WC (high value). Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1702 and biota files v.1727, 1746 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 14:34:46 2017

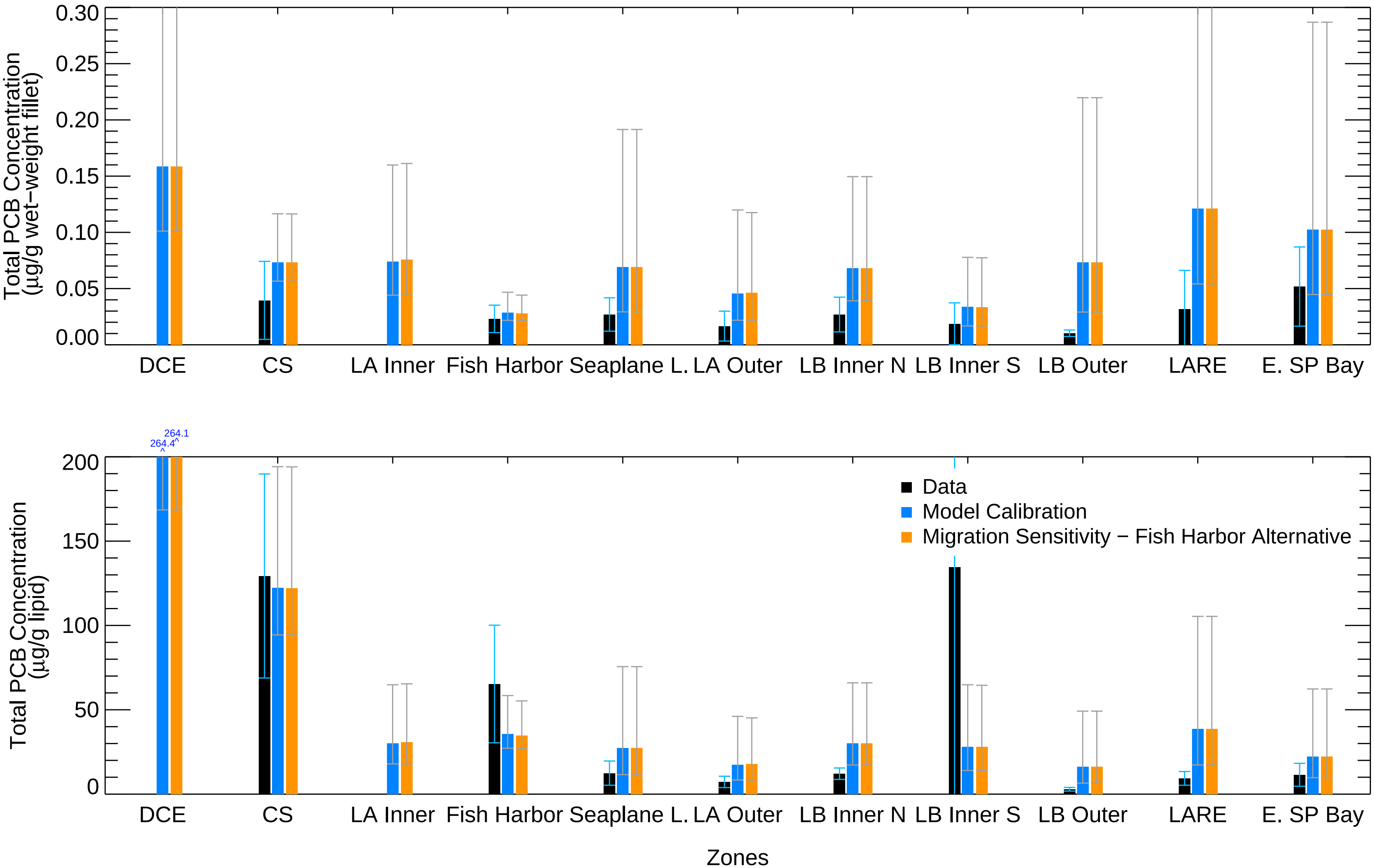


Figure 6−20e

Effects of Decrease in Exposure at Fish Harbor (Increase at PV Shelf) on Total PCB Concentration in California Halibut

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1702 and biota files v.1727, 1746 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 14:34:46 2017

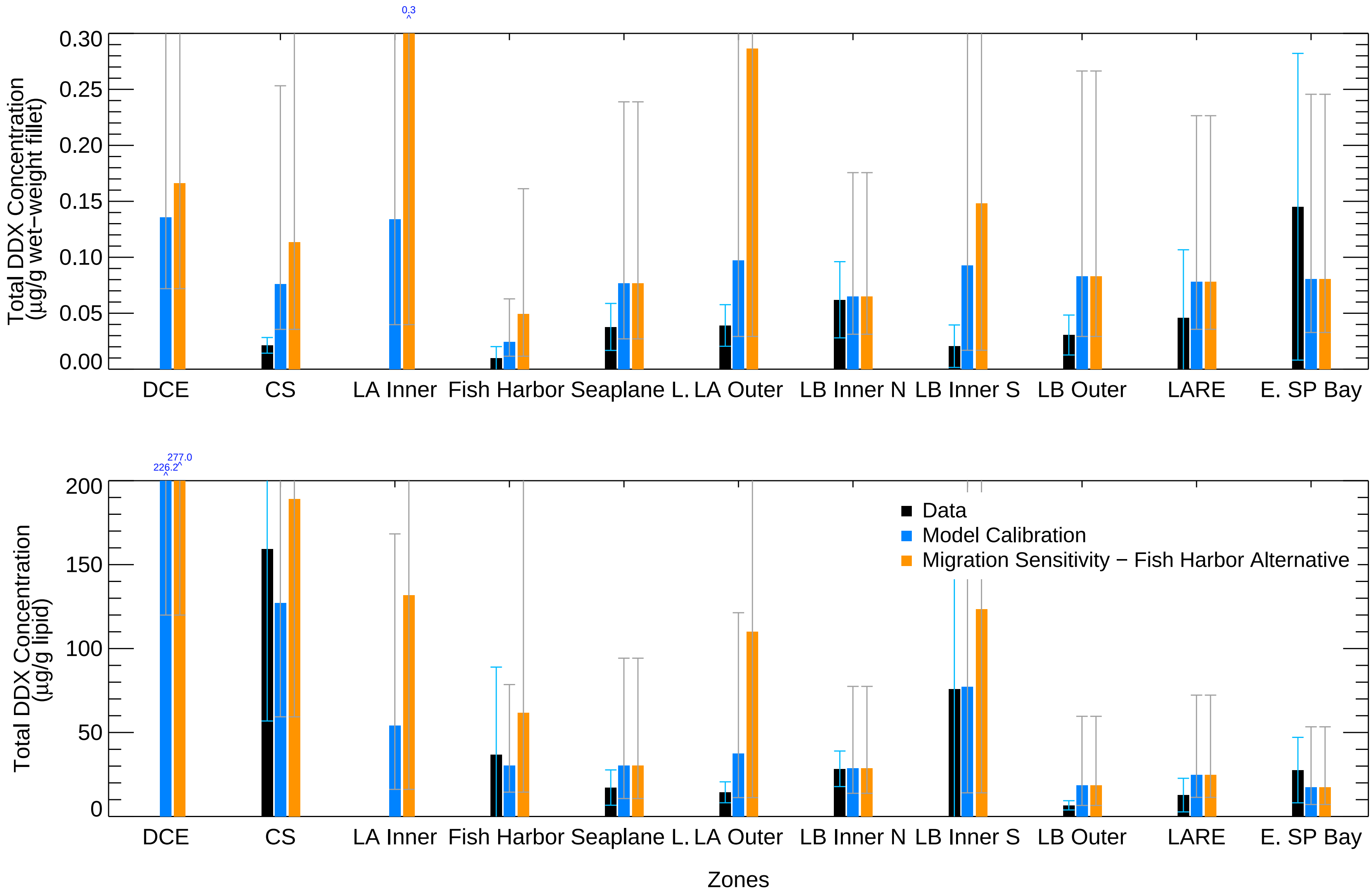


Figure 6−20f

Effects of Decrease in Exposure at Fish Harbor (Increase at PV Shelf) on Total DDX Concentration in California Halibut

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1702 and biota files v.1727, 1746 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 14:34:46 2017

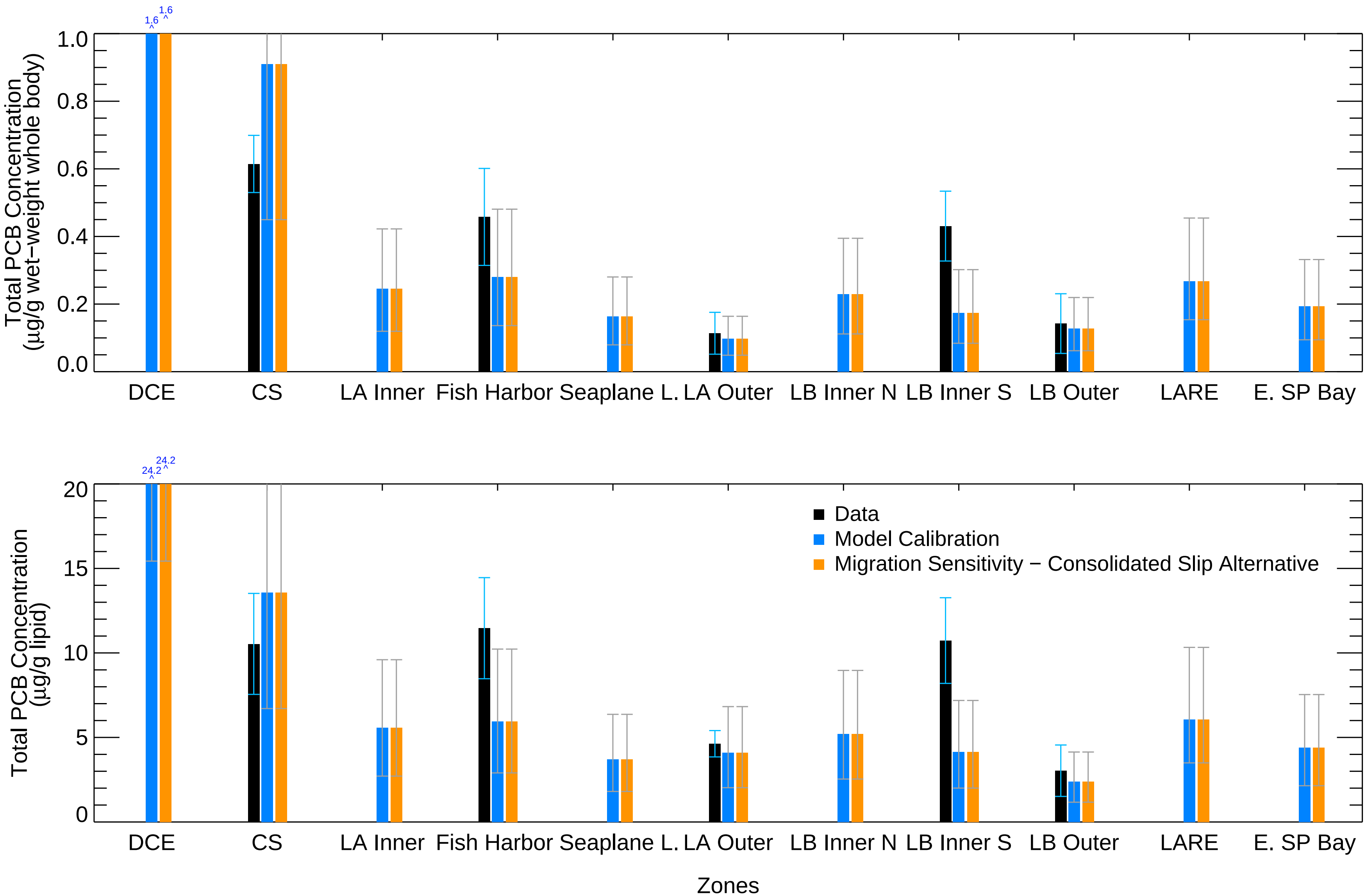


Figure 6−21a

Effects of Decrease in Exposure at Consolidated Slip (Increase at PV Shelf) on Total PCB Concentration in Surfperch

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ files v.1677, 1703 and biota files v.1727, 1747 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 13:51:48 2017

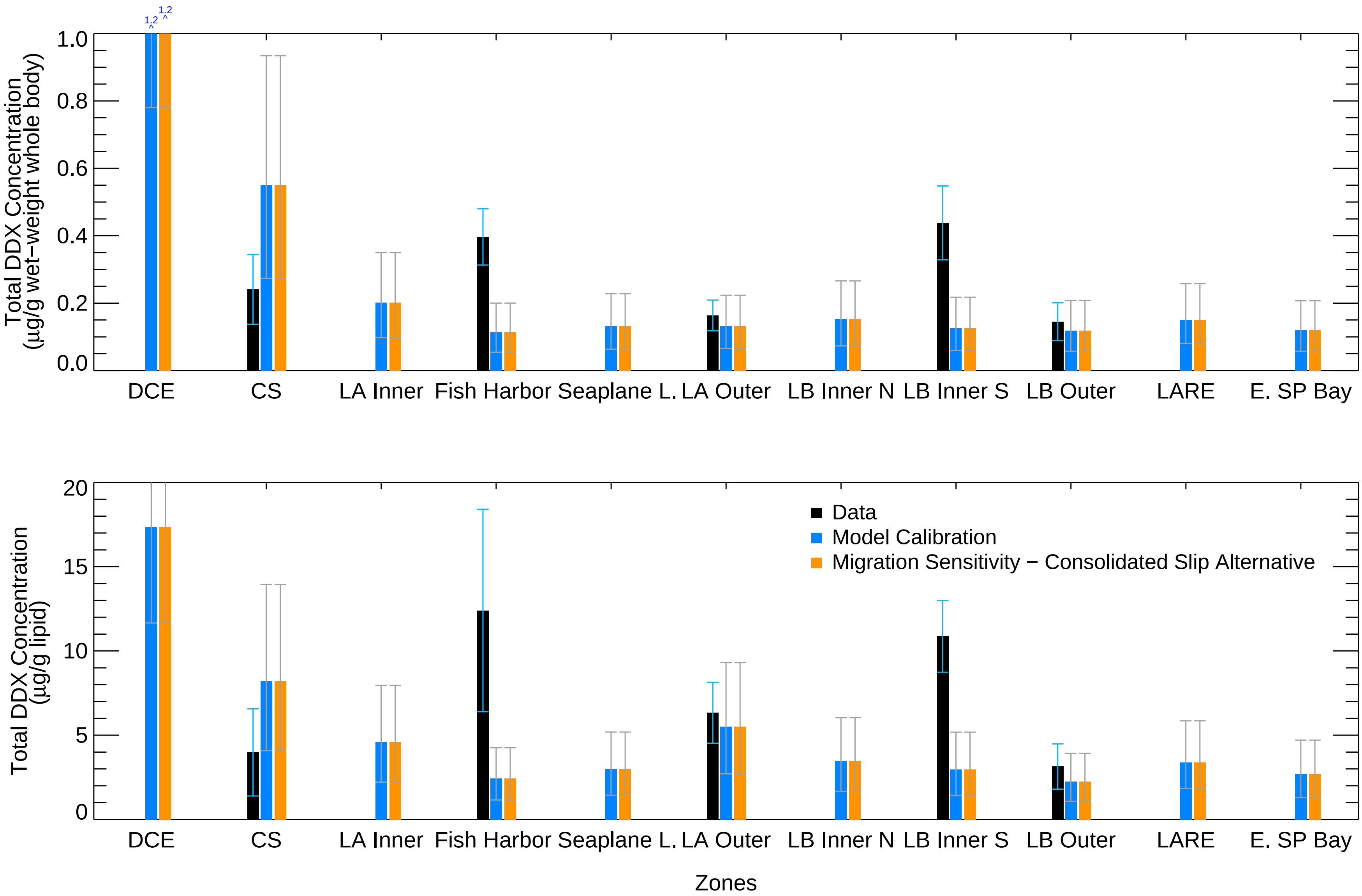


Figure 6−21b

Effects of Decrease in Exposure at Consolidated Slip (Increase at PV Shelf) on Total DDX Concentration in Surfperch

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ files v.1677, 1703 and biota files v.1727, 1747 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 13:51:48 2017

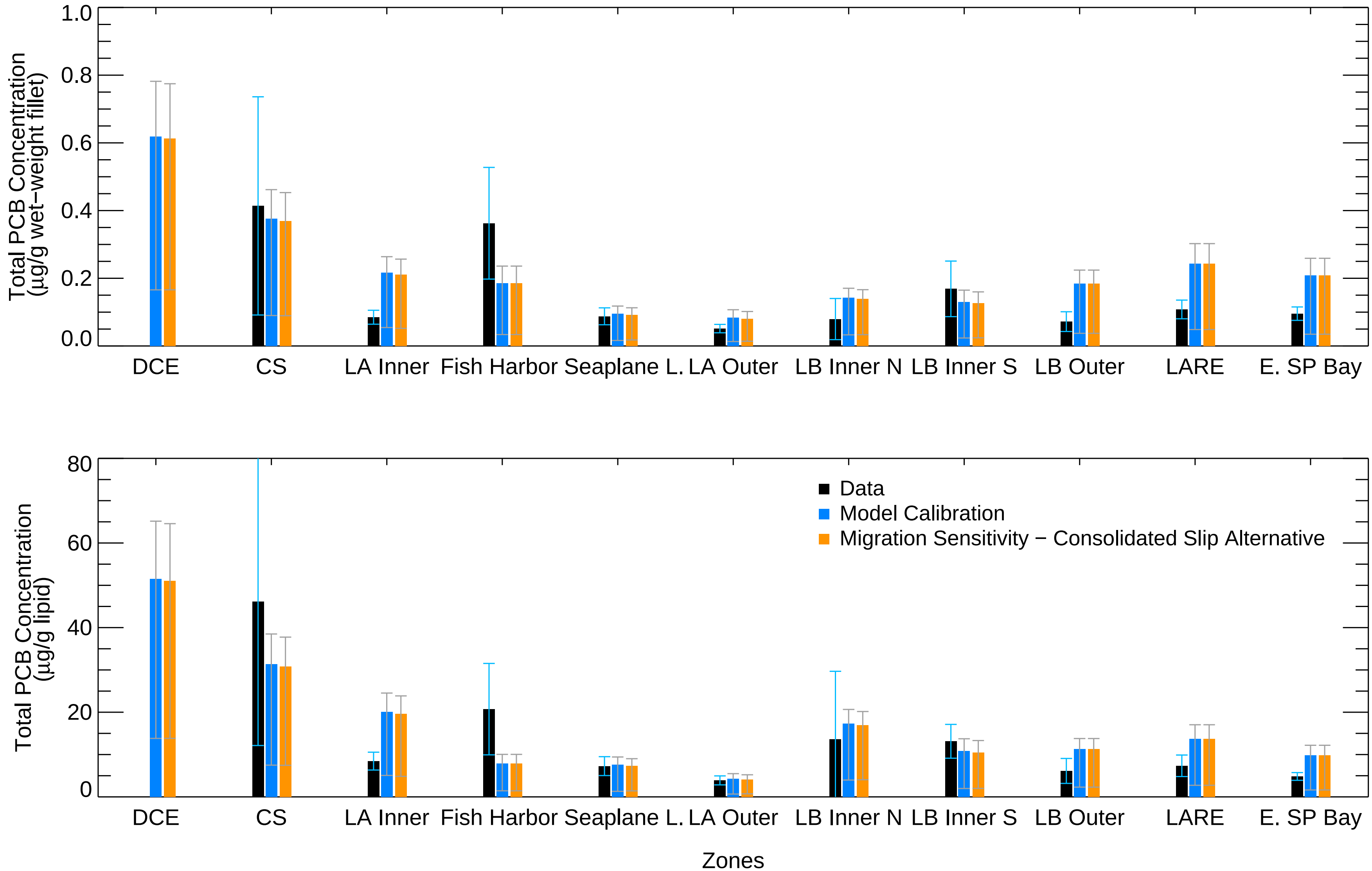


Figure 6−21c

Effects of Decrease in Exposure at Consolidated Slip (Increase at PV Shelf) on Total PCB Concentration in White Croaker

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx. Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value), IH1−FFF−6WC (high value). Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1703 and biota files v.1727, 1747 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 13:51:48 2017

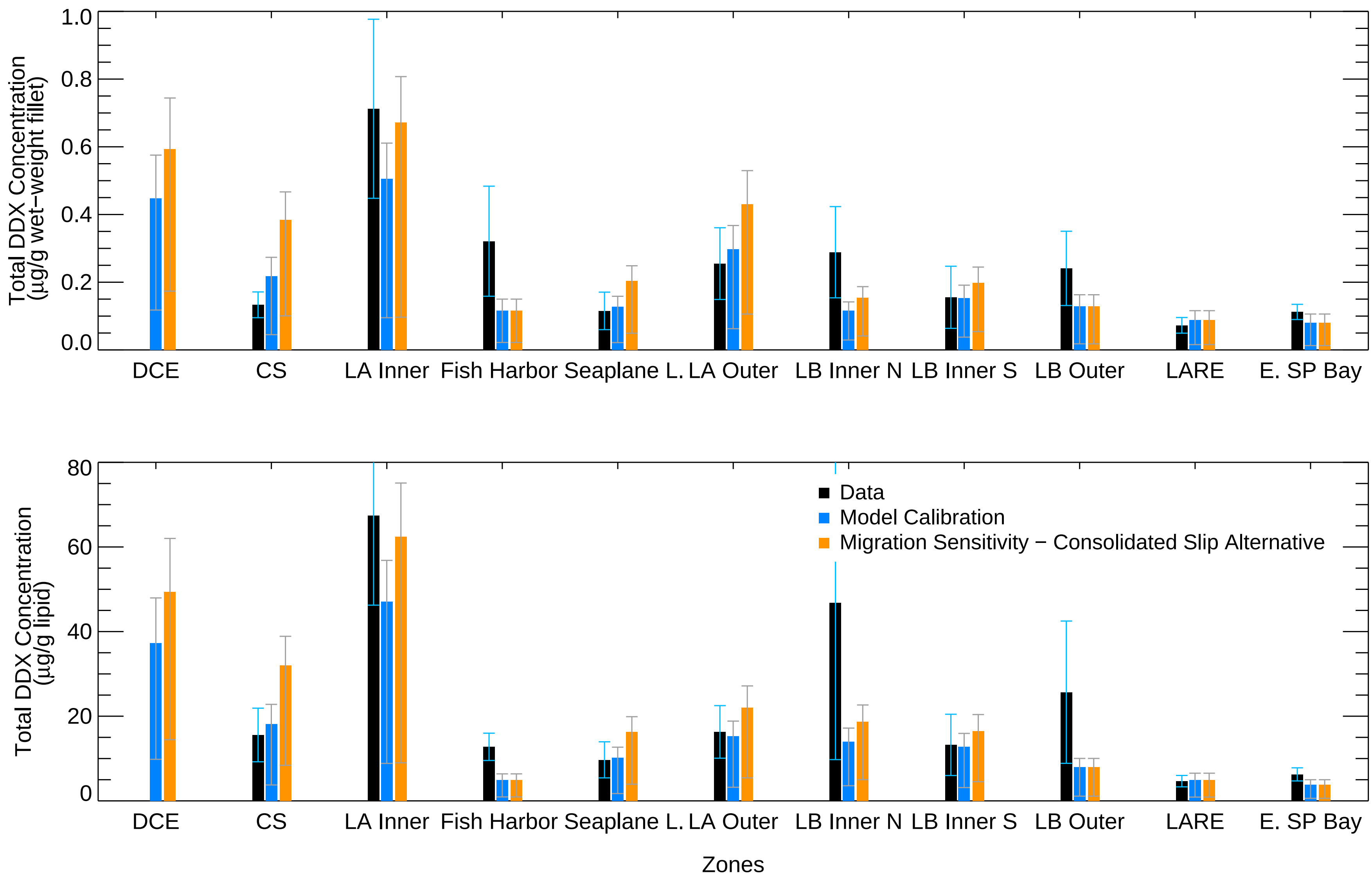


Figure 6−21d

Effects of Decrease in Exposure at Consolidated Slip (Increase at PV Shelf) on Total DDX Concentration in White Croaker

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value), IH1−FFF−6WC (high value). Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1703 and biota files v.1727, 1747 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 13:51:48 2017

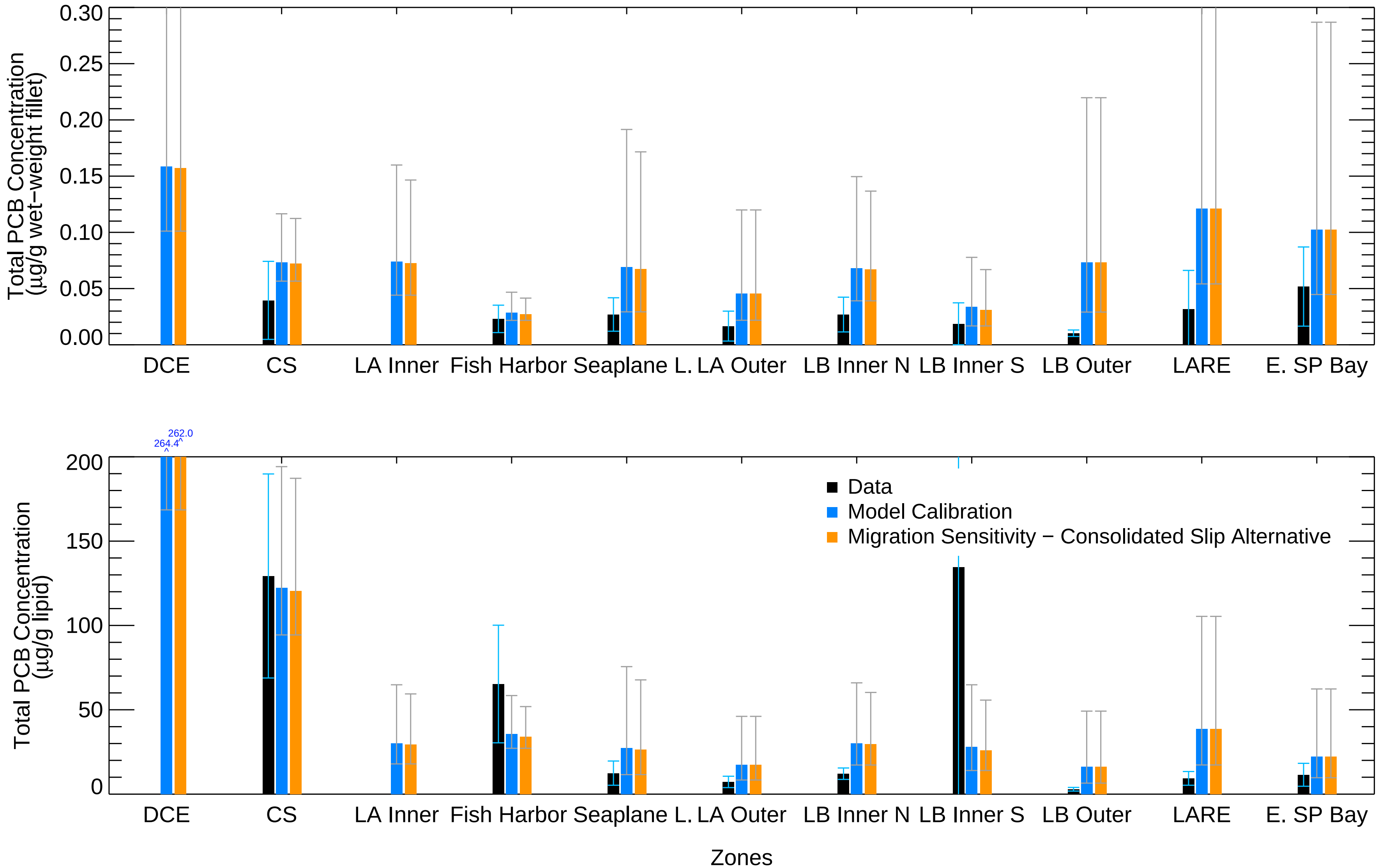


Figure 6−21e

Effects of Decrease in Exposure at Consolidated Slip (Increase at PV Shelf) on Total PCB Concentration in California Halibut

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1703 and biota files v.1727, 1747 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 13:51:48 2017

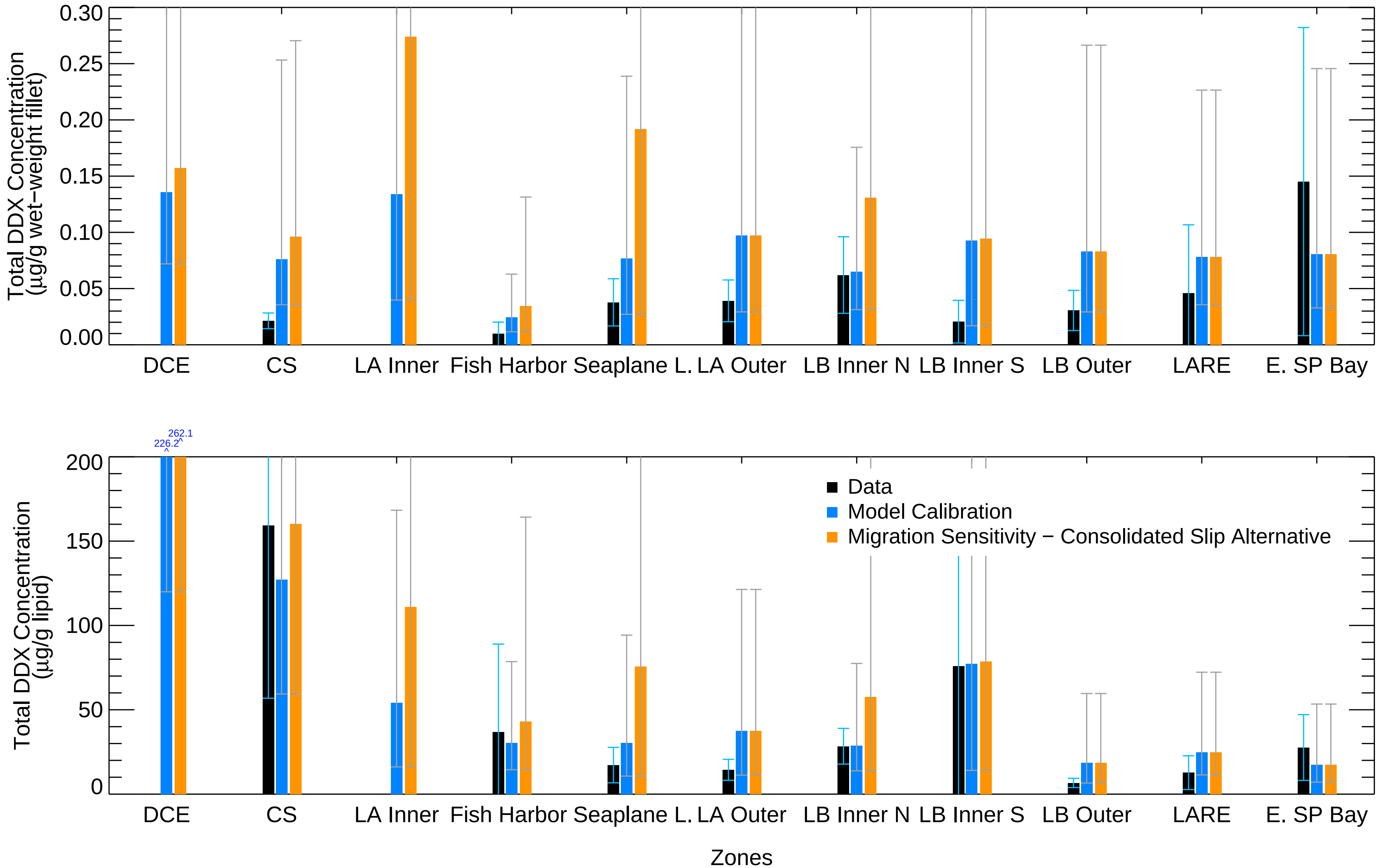


Figure 6−21f

Effects of Decrease in Exposure at Consolidated Slip (Increase at PV Shelf) on Total DDX Concentration in California Halibut

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1703 and biota files v.1727, 1747 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 13:51:48 2017

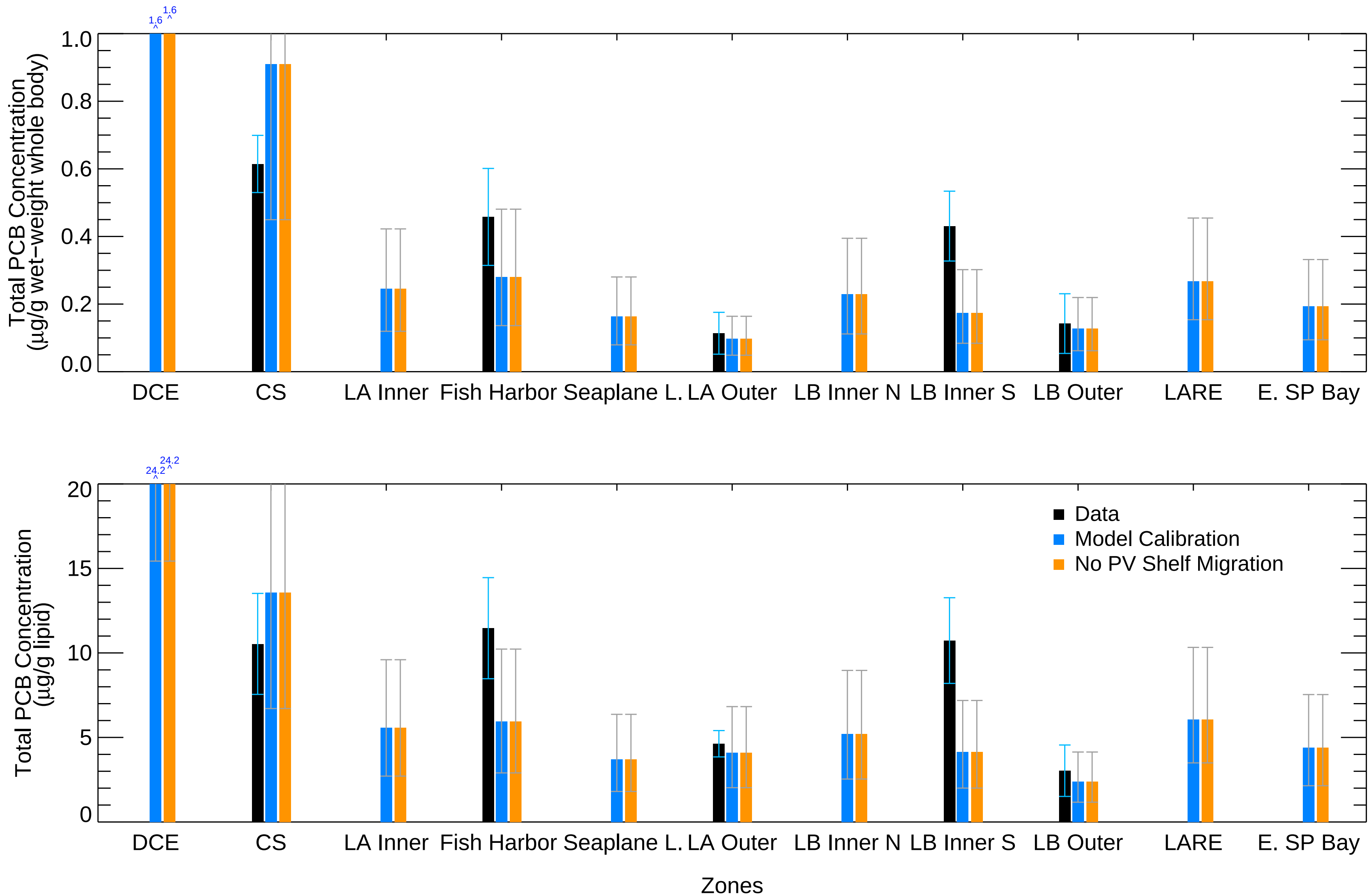


Figure 6−22a

Effects of Decrease in Exposure at PV Shelf (Increase at Outside Harbor) on Total PCB Concentration in Surfperch

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ files v.1677, 1704 and biota files v.1727, 1748 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 15:00:36 2017

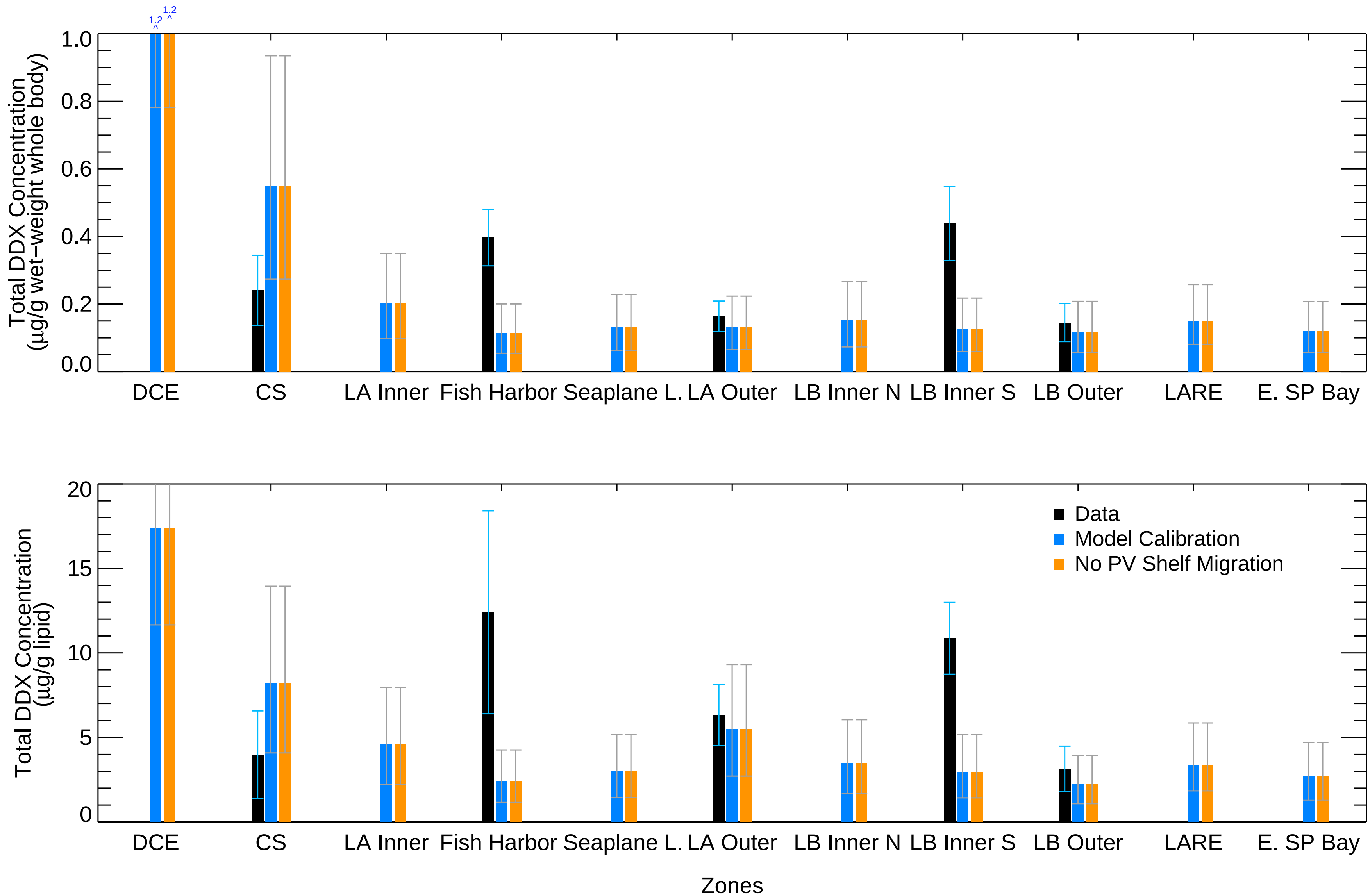


Figure 6−22b

Effects of Decrease in Exposure at PV Shelf (Increase at Outside Harbor) on Total DDX Concentration in Surfperch

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ files v.1677, 1704 and biota files v.1727, 1748 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 15:00:36 2017

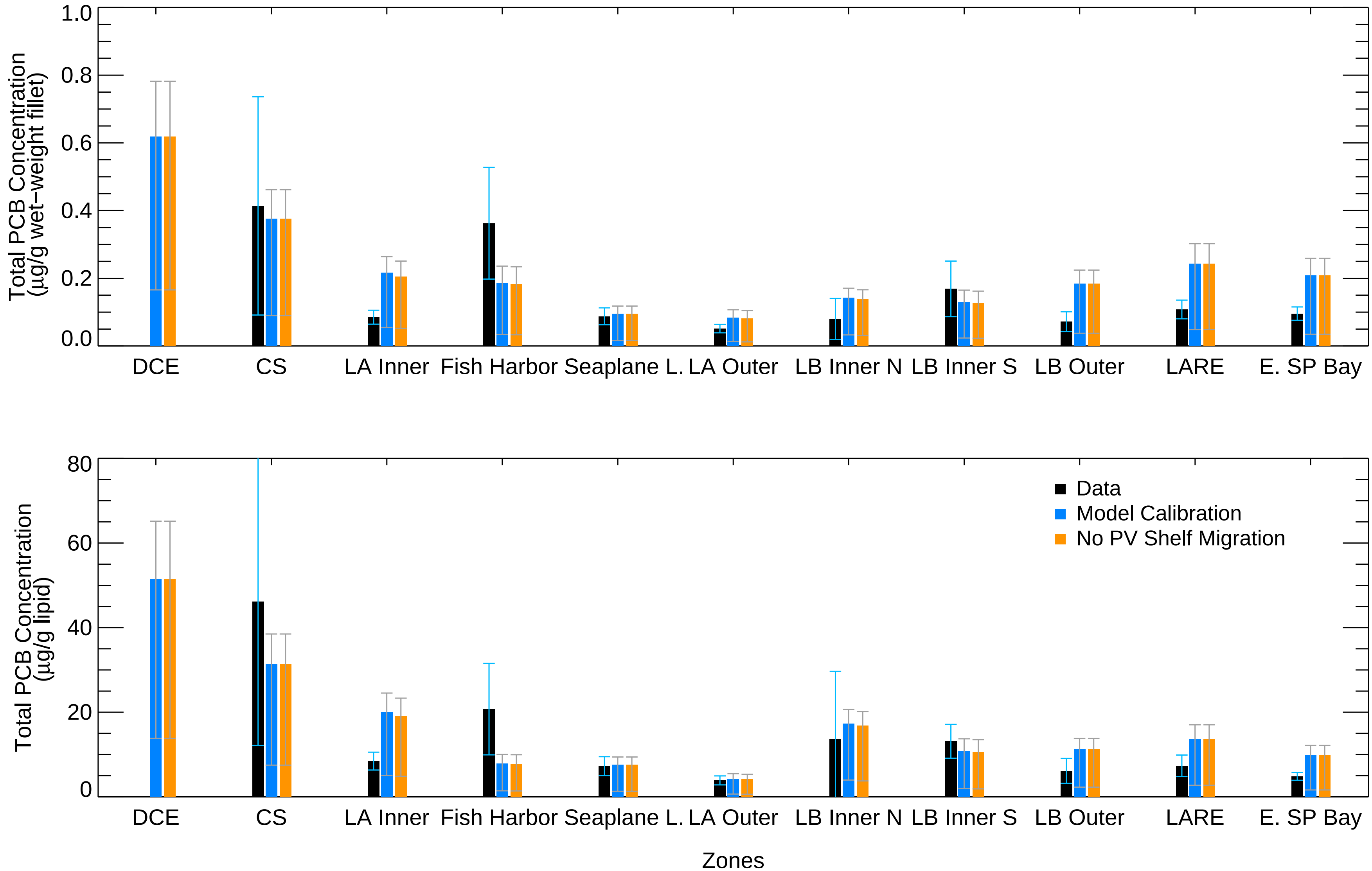


Figure 6−22c

Effects of Decrease in Exposure at PV Shelf (Increase at Outside Harbor) on Total PCB Concentration in White Croaker

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx. Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value), IH1−FFF−6WC (high value). Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1704 and biota files v.1727, 1748 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 15:00:36 2017

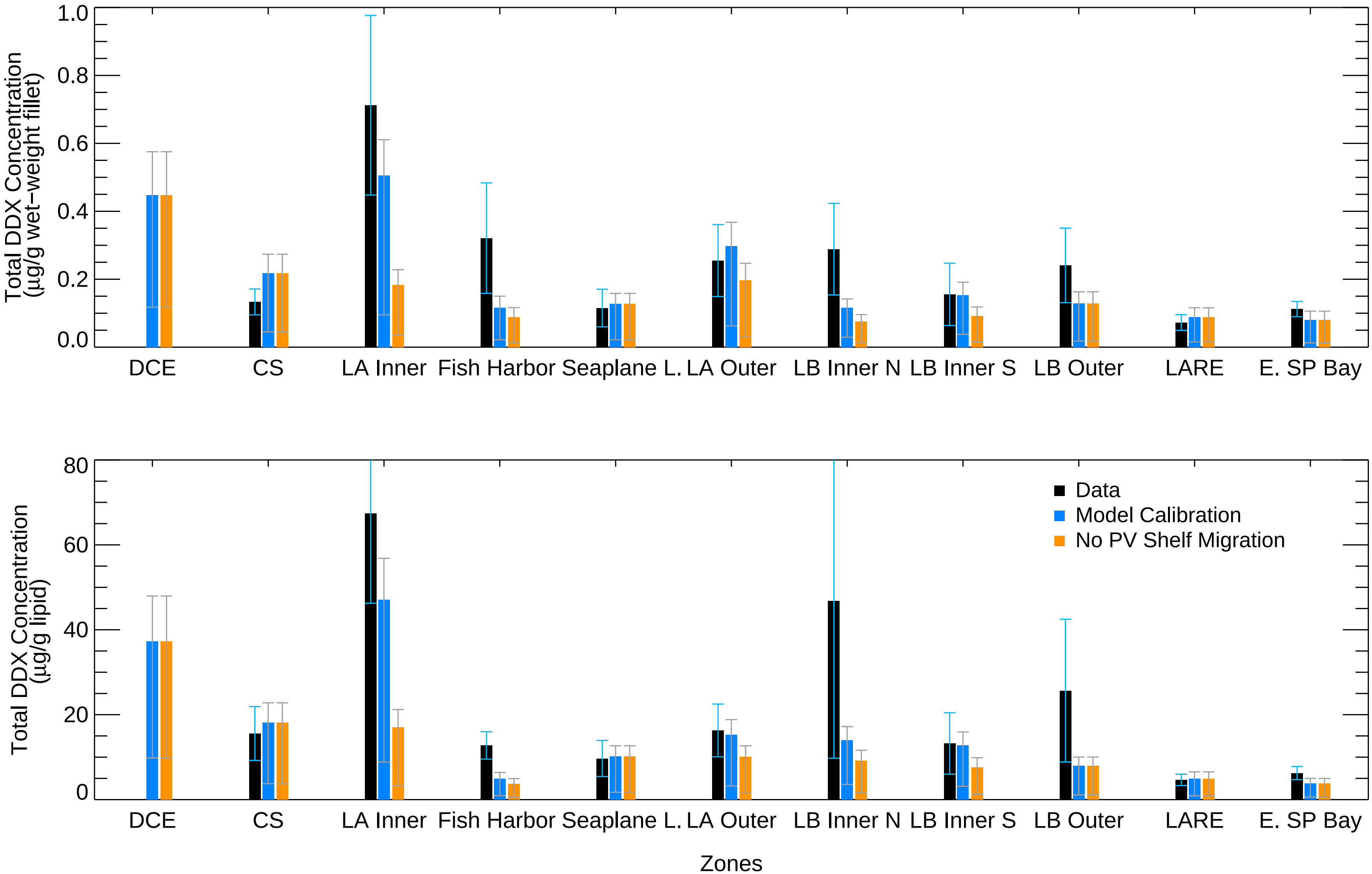


Figure 6−22d

Effects of Decrease in Exposure at PV Shelf (Increase at Outside Harbor) on Total DDX Concentration in White Croaker

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value), IH1−FFF−6WC (high value). Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1704 and biota files v.1727, 1748 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 15:00:36 2017

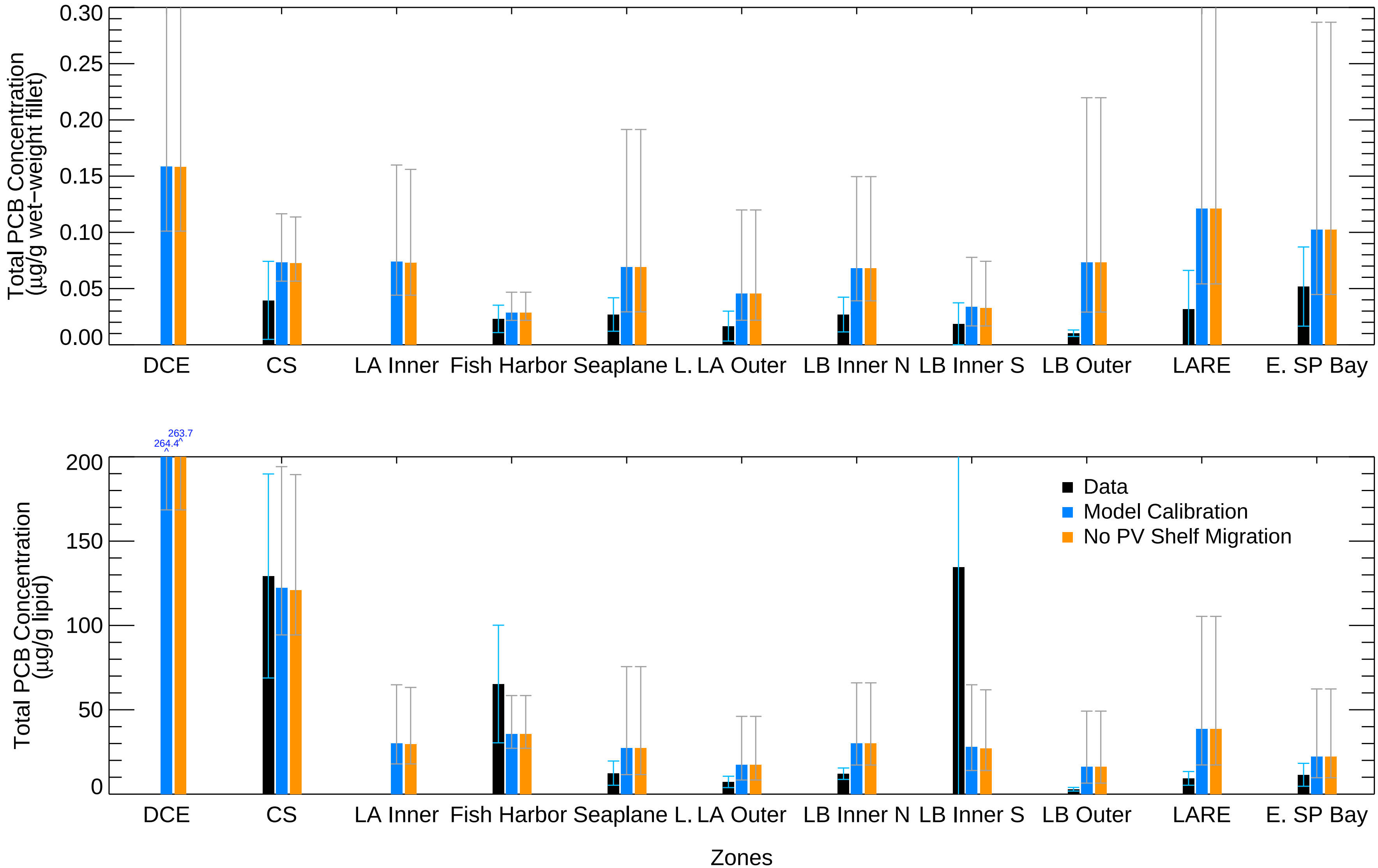


Figure 6−22e

Effects of Decrease in Exposure at PV Shelf (Increase at Outside Harbor) on Total PCB Concentration in California Halibut

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1704 and biota files v.1727, 1748 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 15:00:36 2017

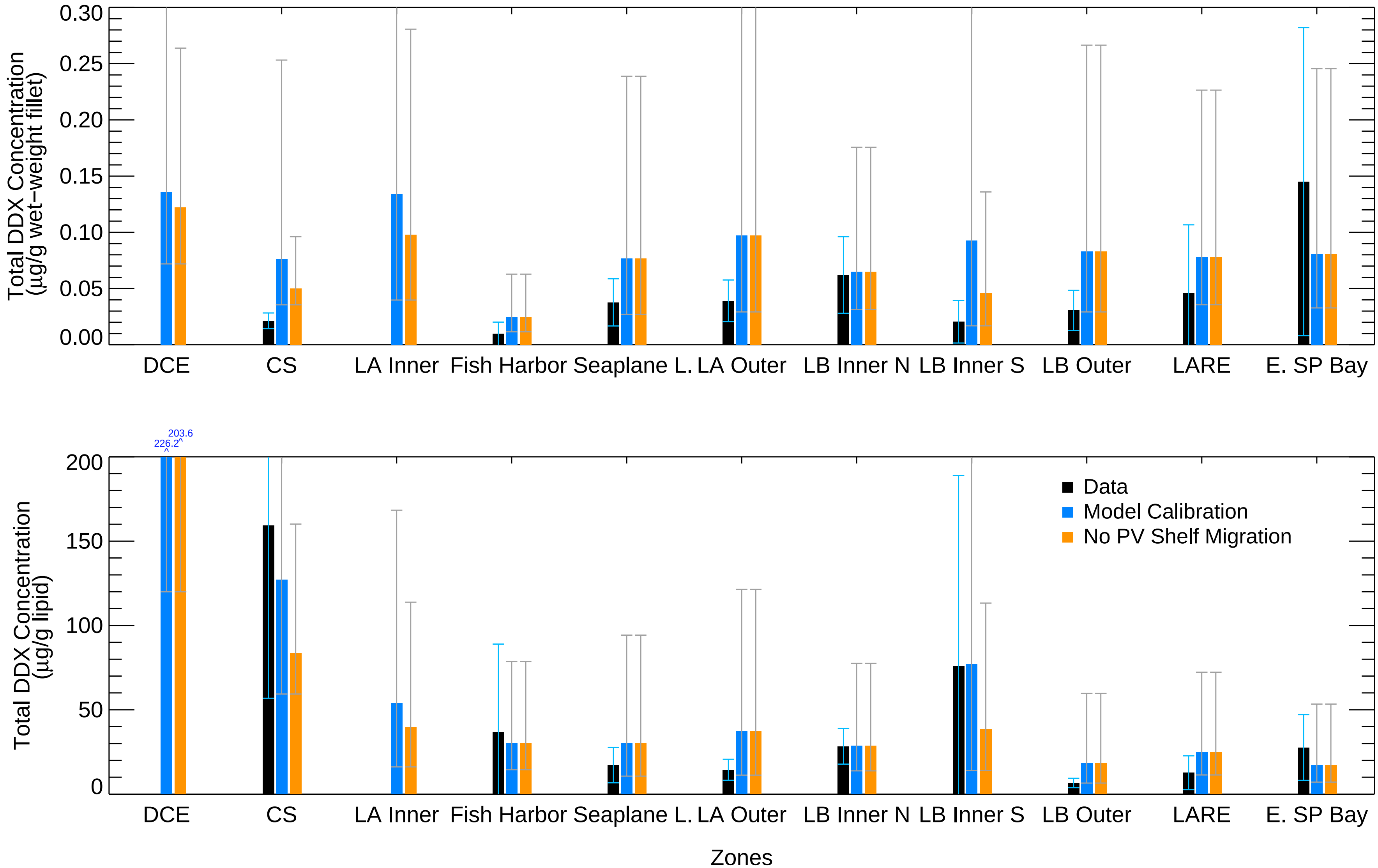


Figure 6−22f

Effects of Decrease in Exposure at PV Shelf (Increase at Outside Harbor) on Total DDX Concentration in California Halibut

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1704 and biota files v.1727, 1748 used for model.

ANCHOR QEA

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 15:00:37 2017

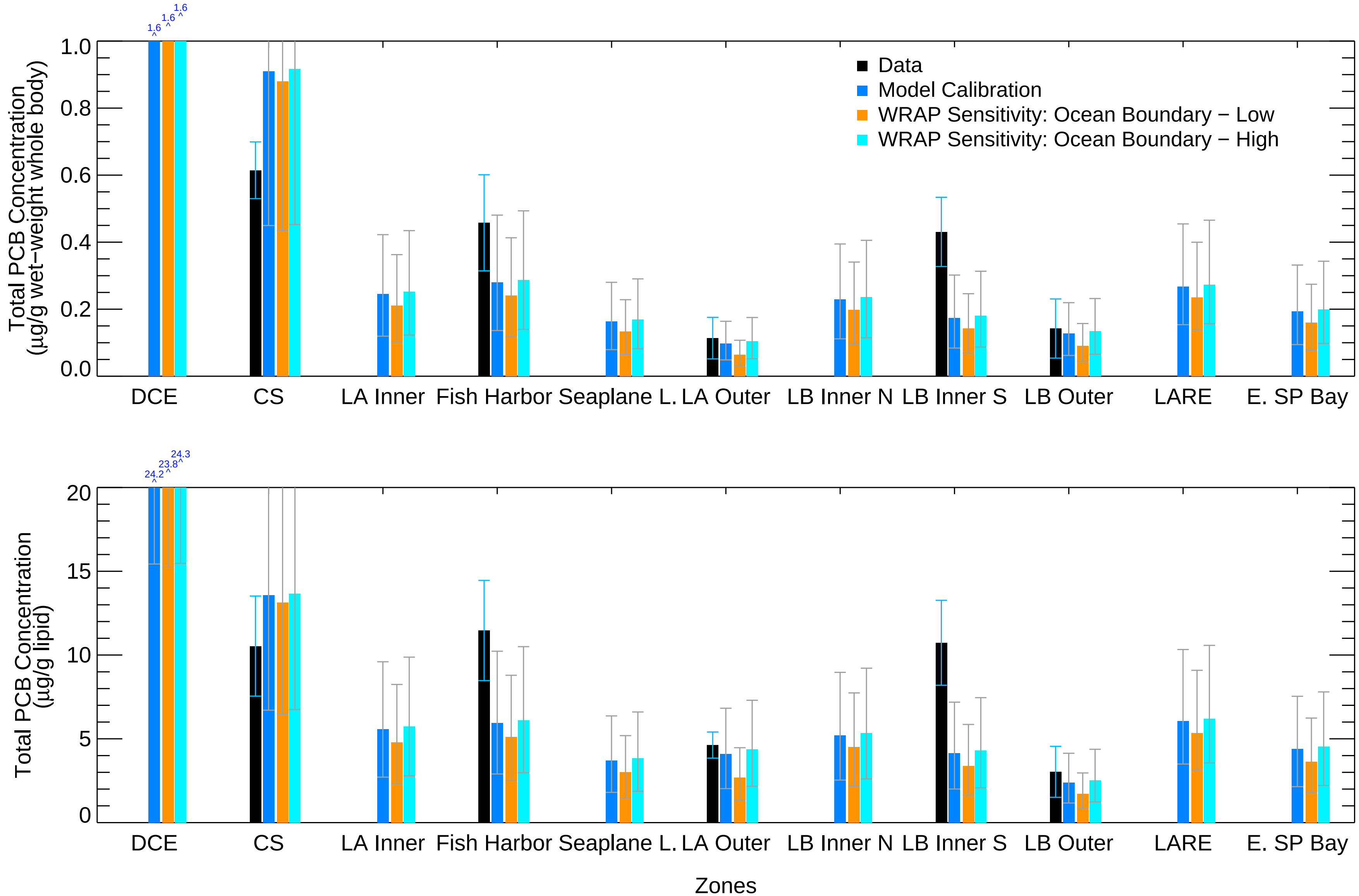


Figure 6−23a

Effects of Alternate Ocean Boundary on Total PCB Concentration in Surfperch

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ files v.1677, 1685, 1686 and biota files v.1727, 1727, 1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 15:22:25 2017

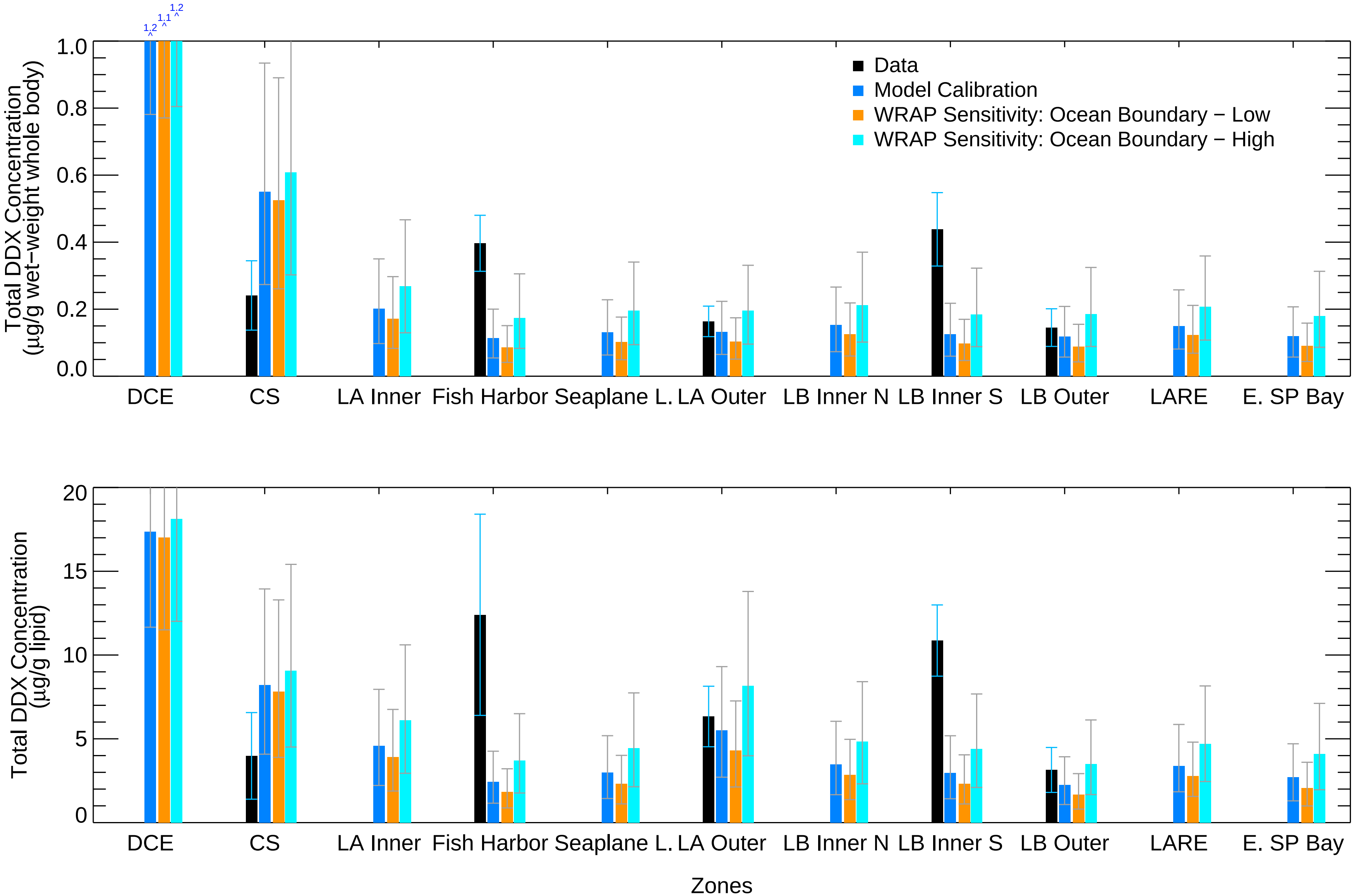


Figure 6−23b

Effects of Alternate Ocean Boundary on Total DDX Concentration in Surfperch

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ files v.1677, 1685, 1686 and biota files v.1727, 1727, 1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 15:22:26 2017

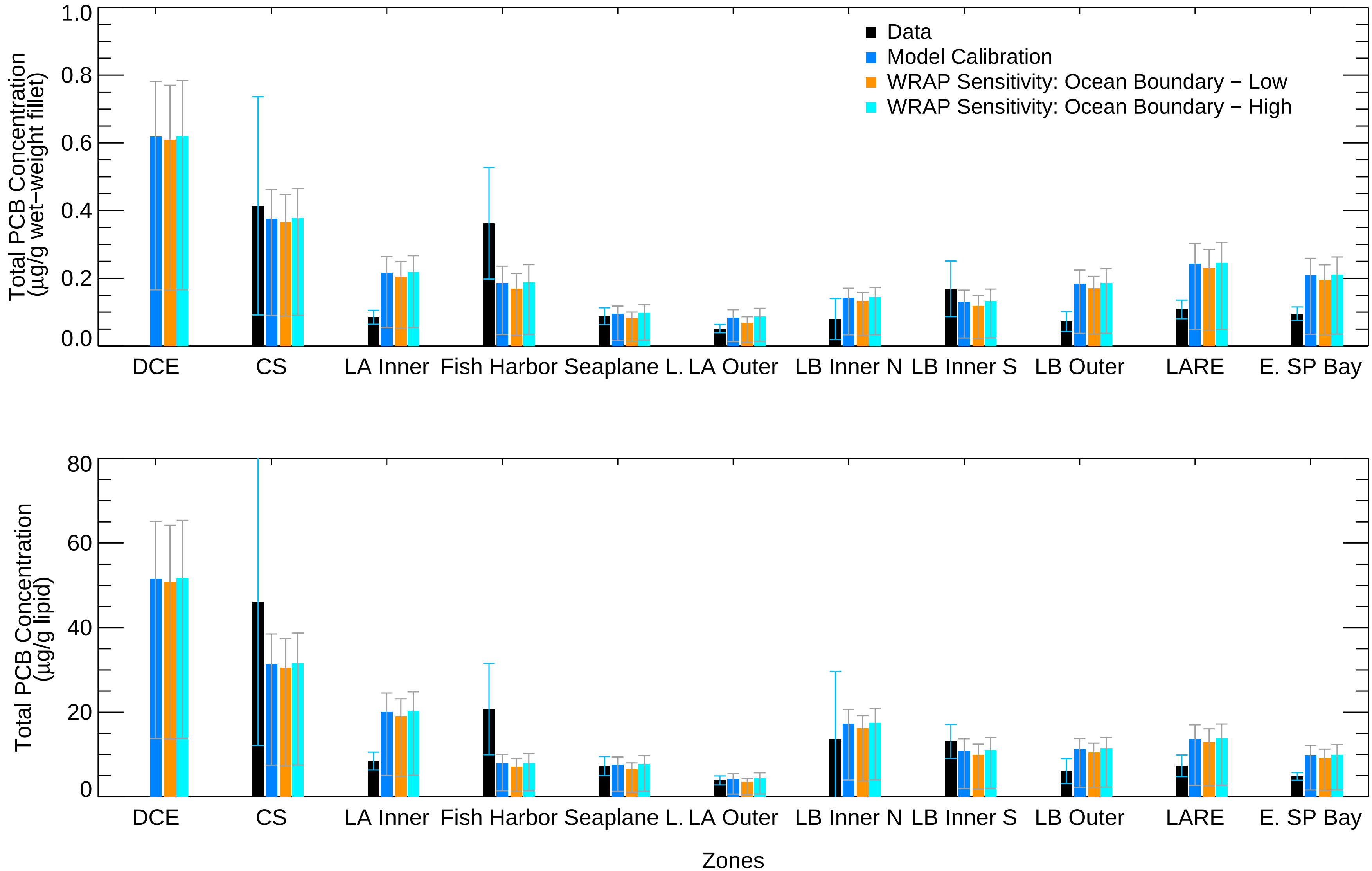


Figure 6−23c

Effects of Alternate Ocean Boundary on Total PCB Concentration in White Croaker

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx. Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value), IH1−FFF−6WC (high value). Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1685, 1686 and biota files v.1727, 1727, 1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 15:22:26 2017

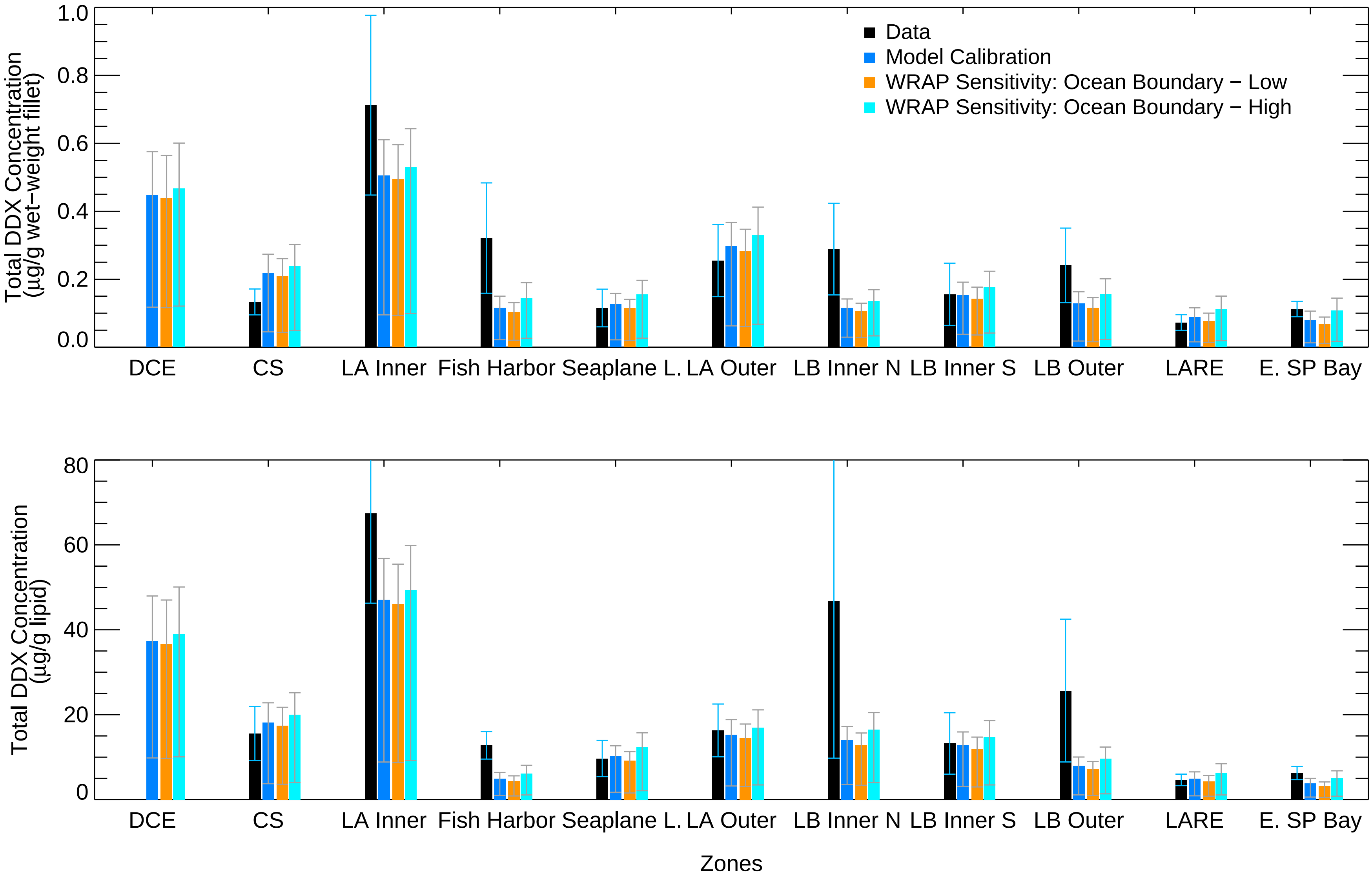


Figure 6−23d

Effects of Alternate Ocean Boundary on Total DDX Concentration in White Croaker

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx. Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value), IH1−FFF−6WC (high value). Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1685, 1686 and biota files v.1727, 1727, 1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 15:22:26 2017

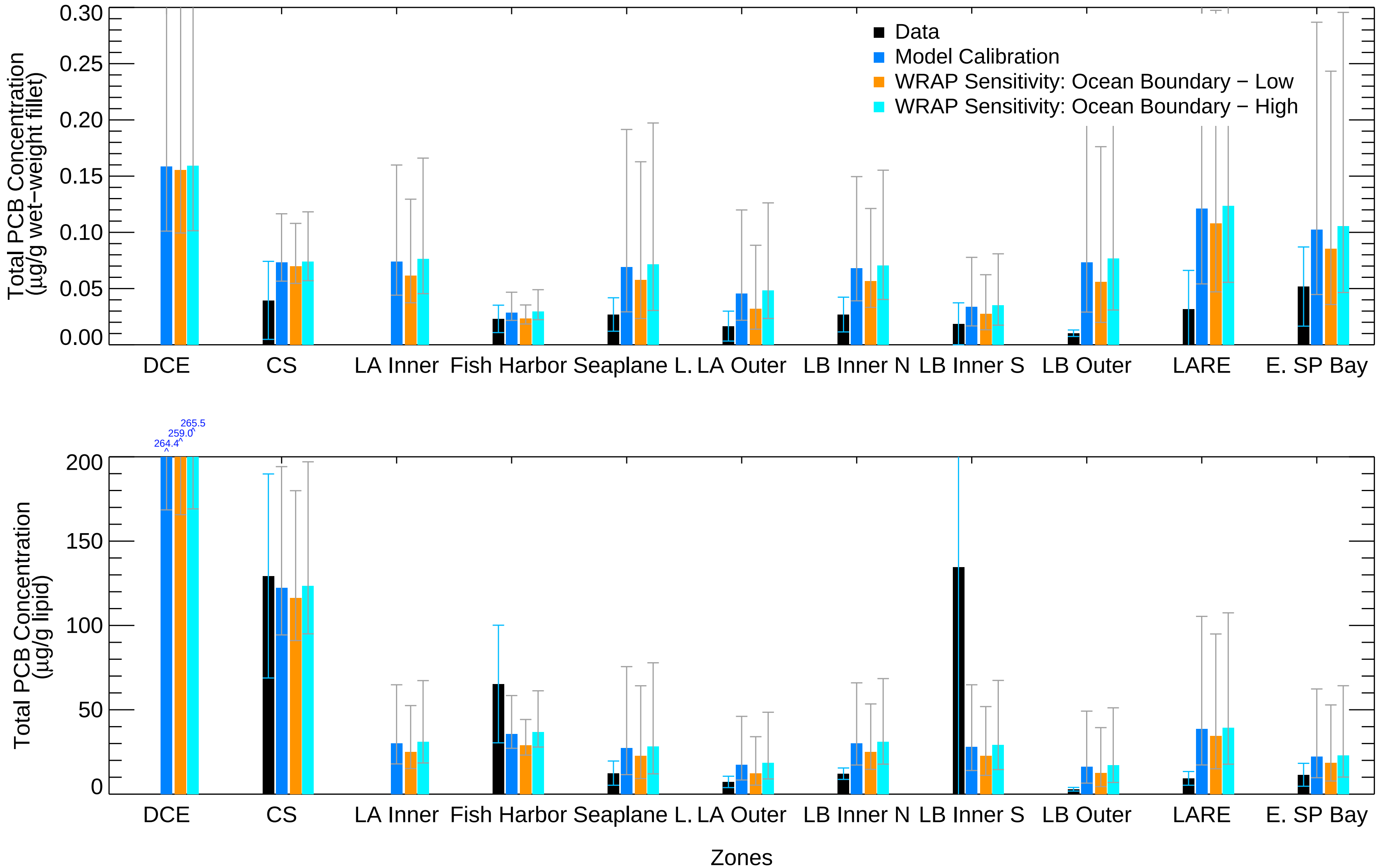


Figure 6−23e

Effects of Alternate Ocean Boundary on Total PCB Concentration in California Halibut

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1685, 1686 and biota files v.1727, 1727, 1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 15:22:26 2017

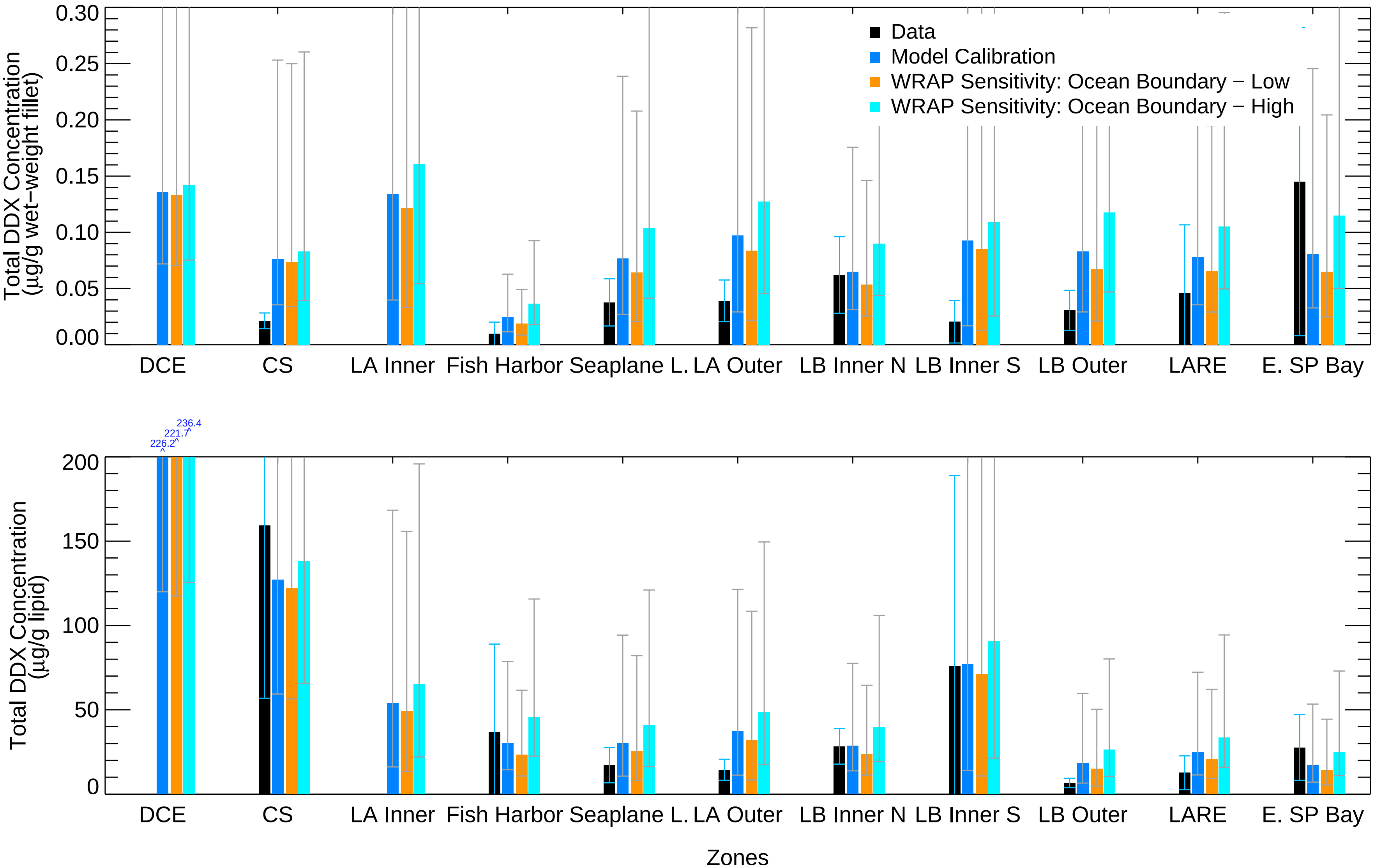


Figure 6−23f

Effects of Alternate Ocean Boundary on Total DDX Concentration in California Halibut

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1685, 1686 and biota files v.1727, 1727, 1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 15:22:26 2017

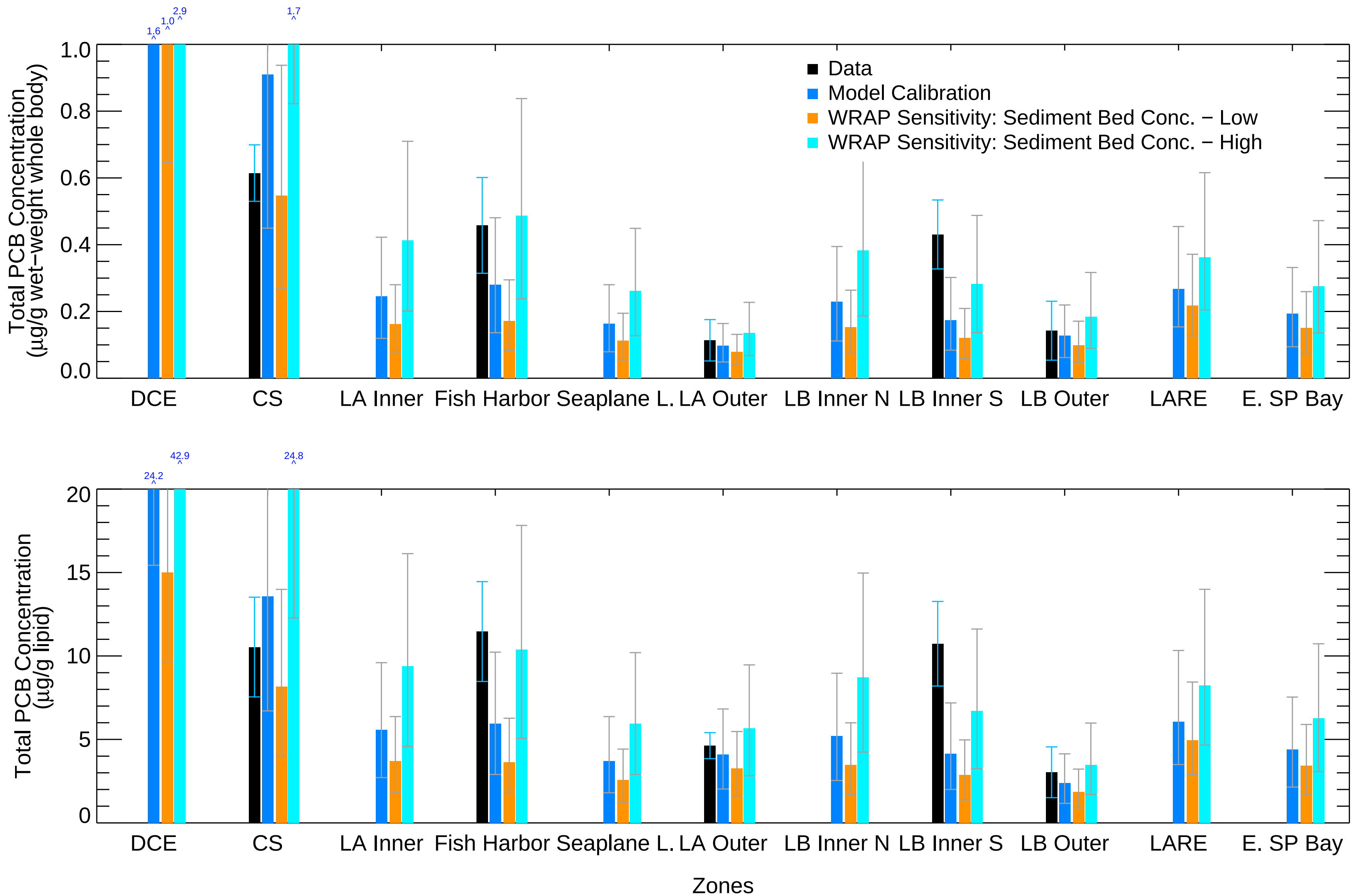


Figure 6−24a

Effects of Alternate Sediment Bed Concentration on Total PCB Concentration in Surfperch

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ files v.1677, 1687, 1688 and biota files v.1727, 1727, 1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 16:02:44 2017

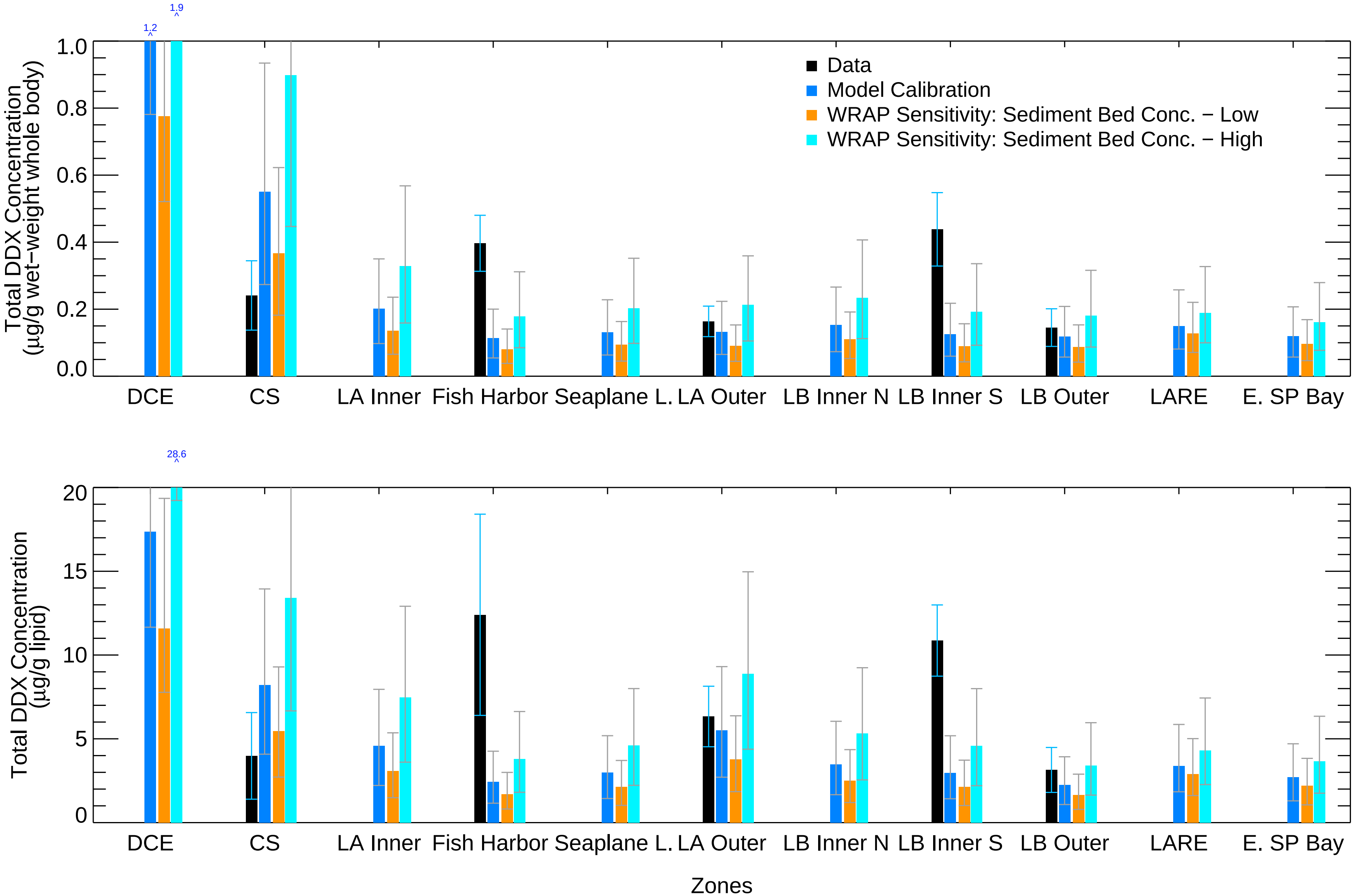


Figure 6−24b

Effects of Alternate Sediment Bed Concentration on Total DDX Concentration in Surfperch

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ files v.1677, 1687, 1688 and biota files v.1727, 1727, 1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 16:02:44 2017

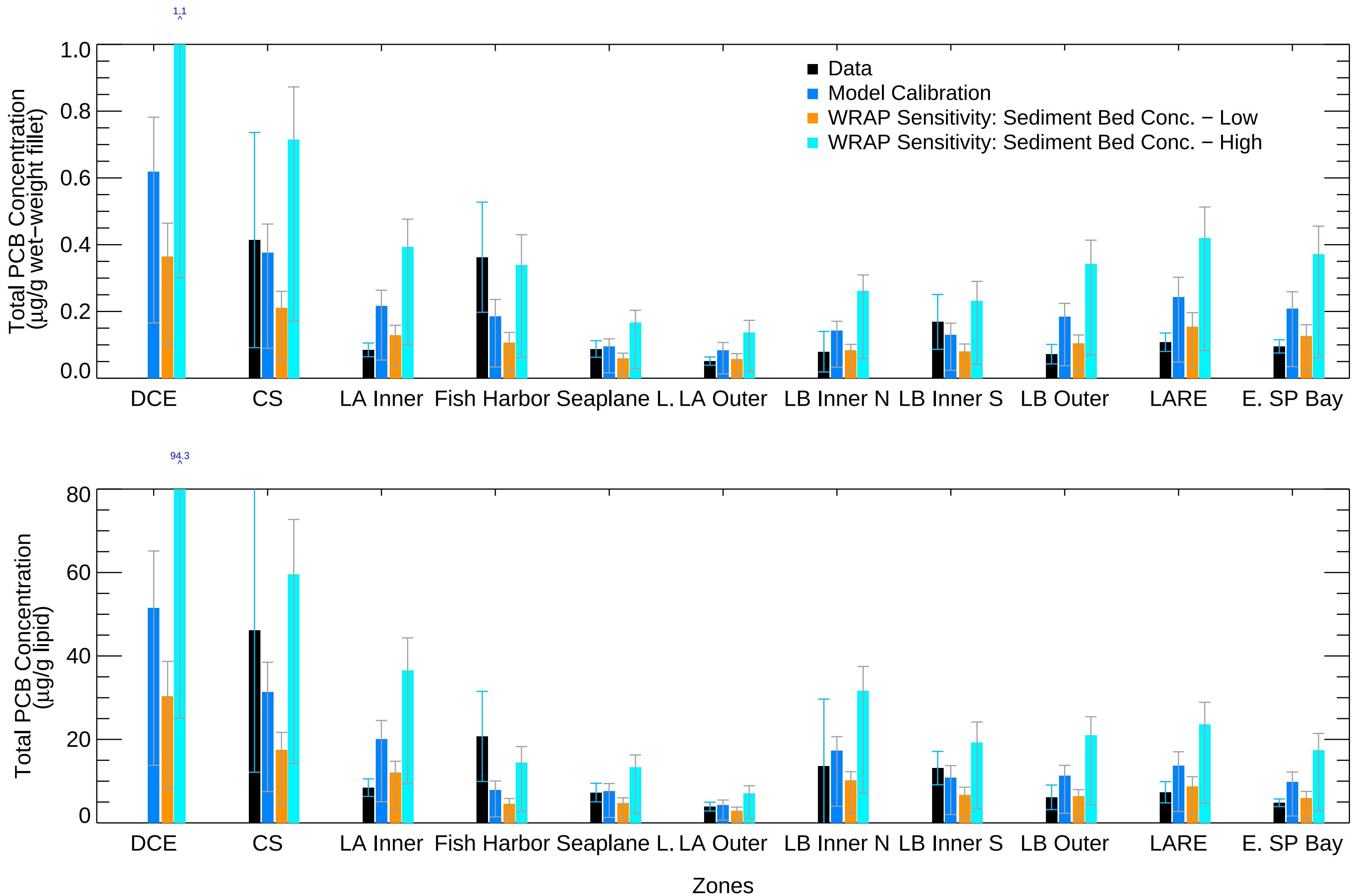


Figure 6−24c

Effects of Alternate Sediment Bed Concentration on Total PCB Concentration in White Croaker

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx. Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value), IH1−FFF−6WC (high value). Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1687, 1688 and biota files v.1727, 1727, 1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 16:02:44 2017

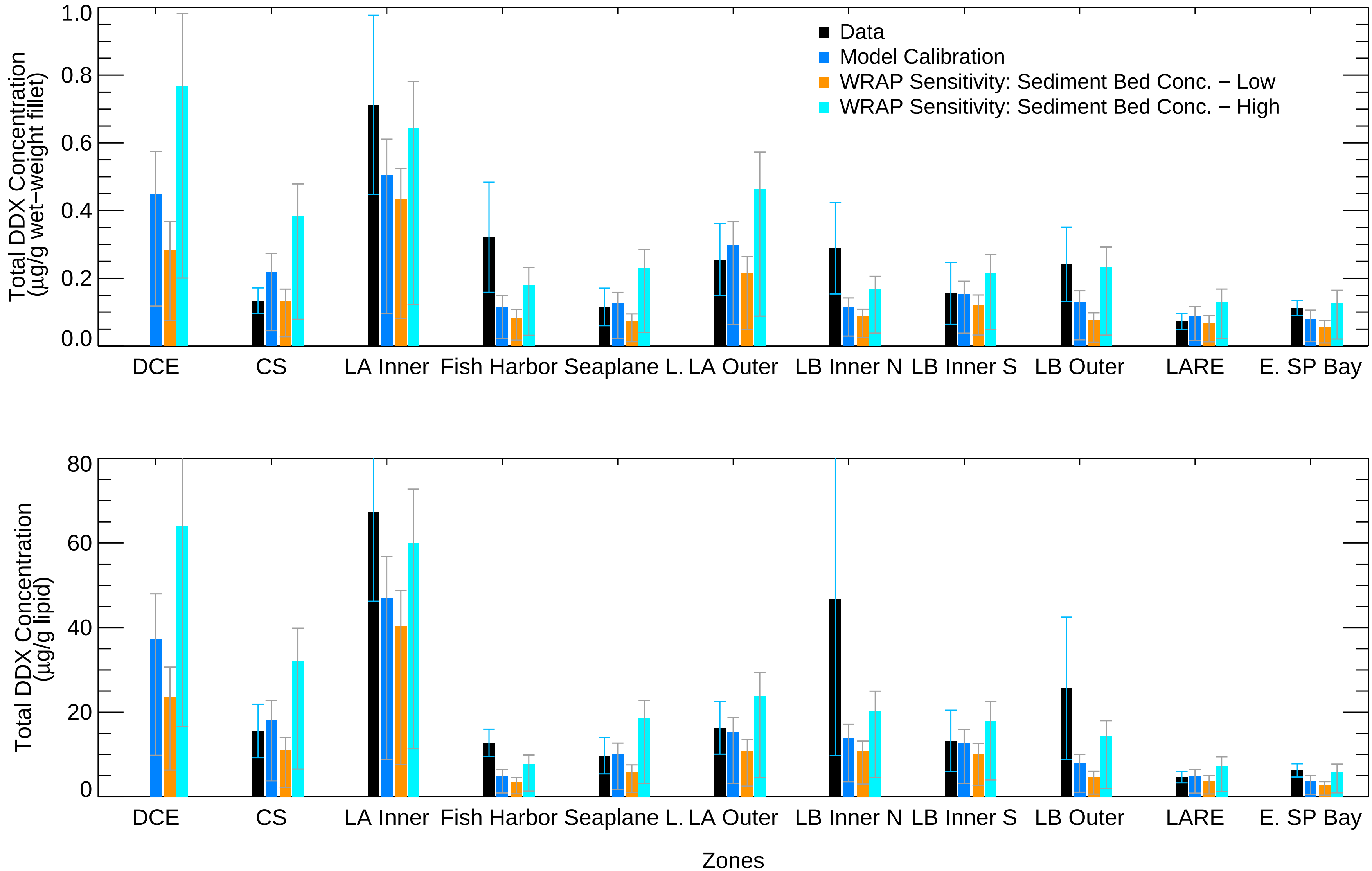


Figure 6−24d

Effects of Alternate Sediment Bed Concentration on Total DDX Concentration in White Croaker

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value), IH1−FFF−6WC (high value). Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1687, 1688 and biota files v.1727, 1727, 1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 16:02:44 2017

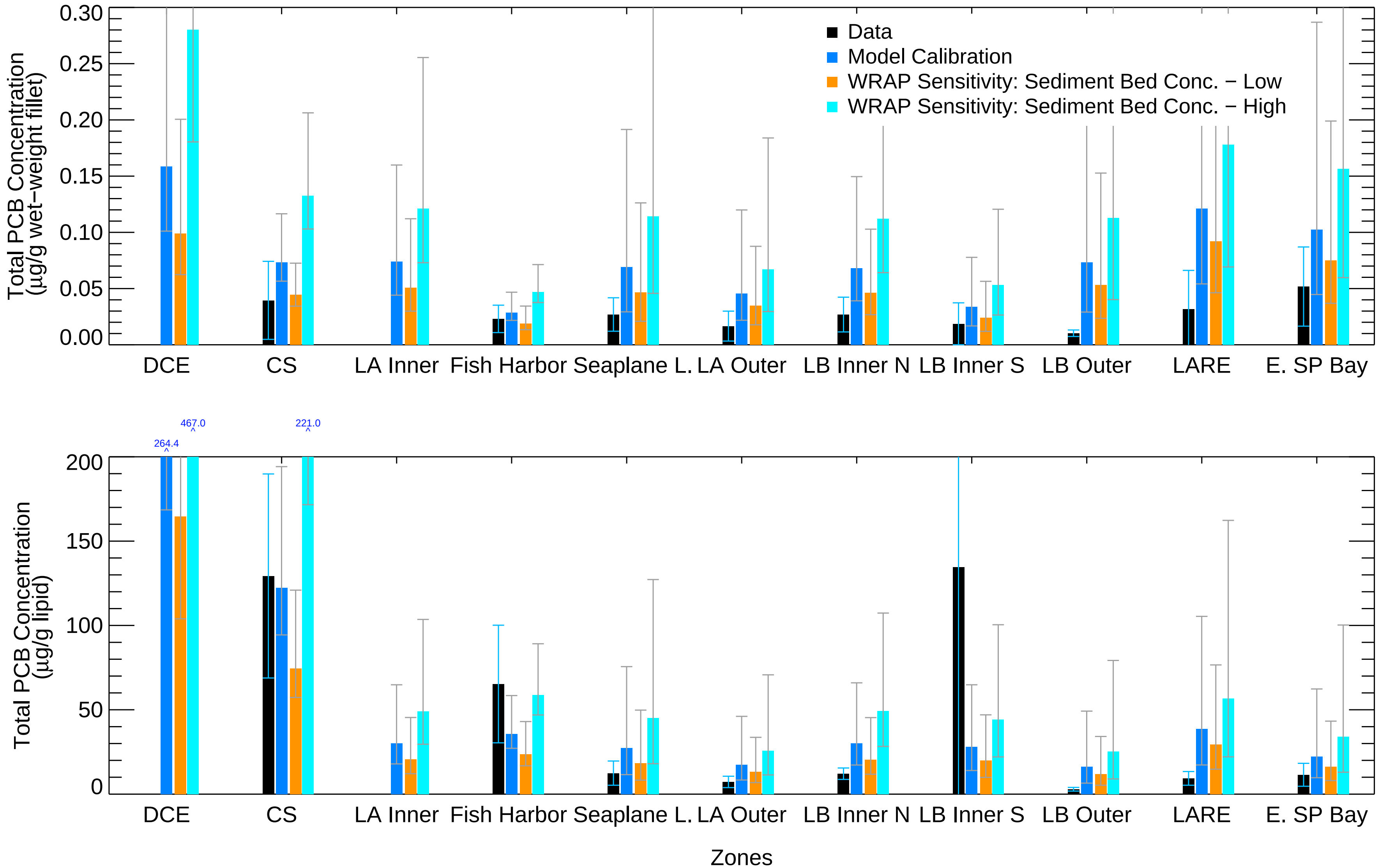


Figure 6−24e

Effects of Alternate Sediment Bed Concentration on Total PCB Concentration in California Halibut

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx. Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1687, 1688 and biota files v.1727, 1727, 1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 16:02:44 2017

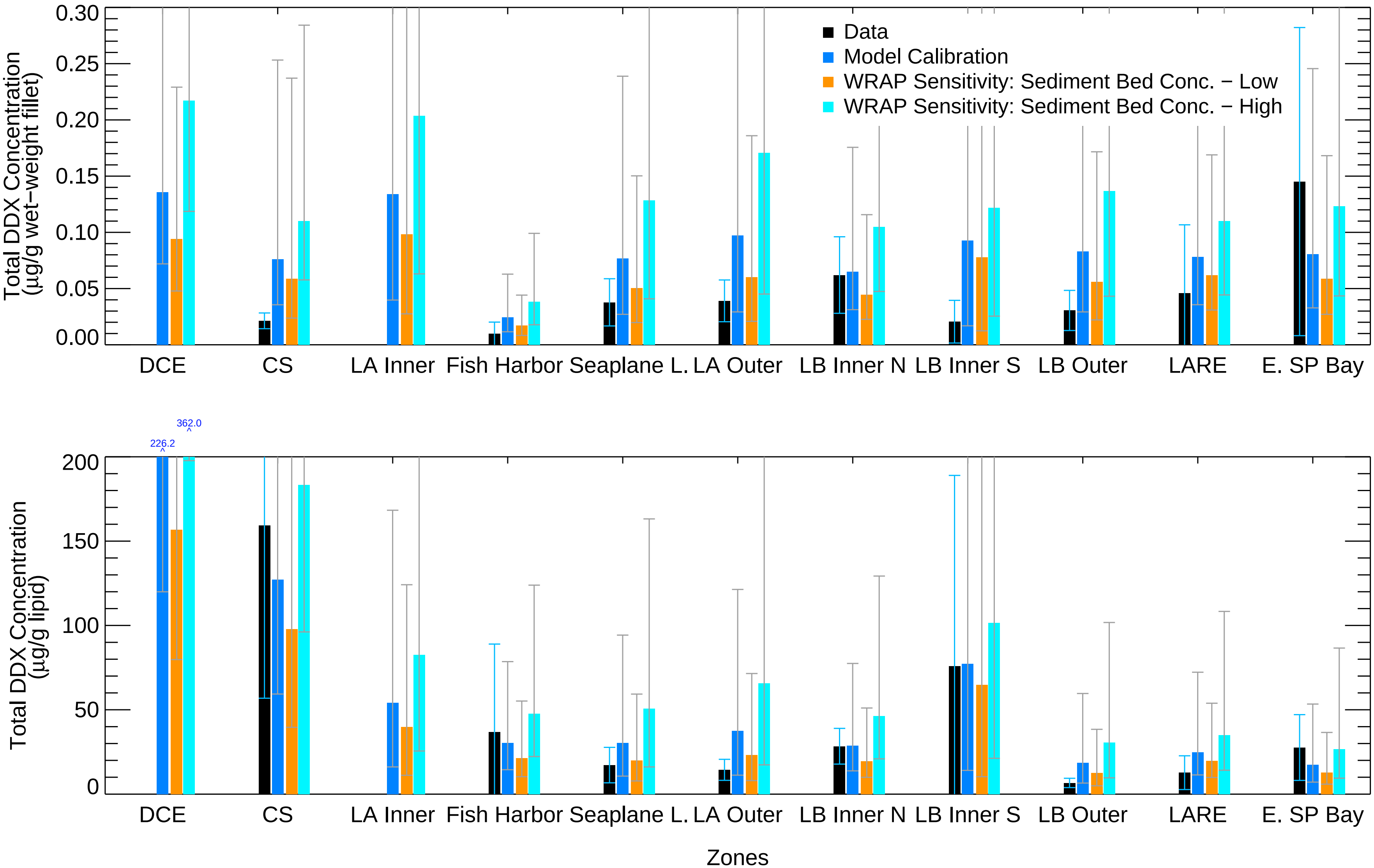


Figure 6−24f

Effects of Alternate Sediment Bed Concentration on Total DDX Concentration in California Halibut

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1687, 1688 and biota files v.1727, 1727, 1727 used for model.

ANCHOR QEA

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 16:02:44 2017

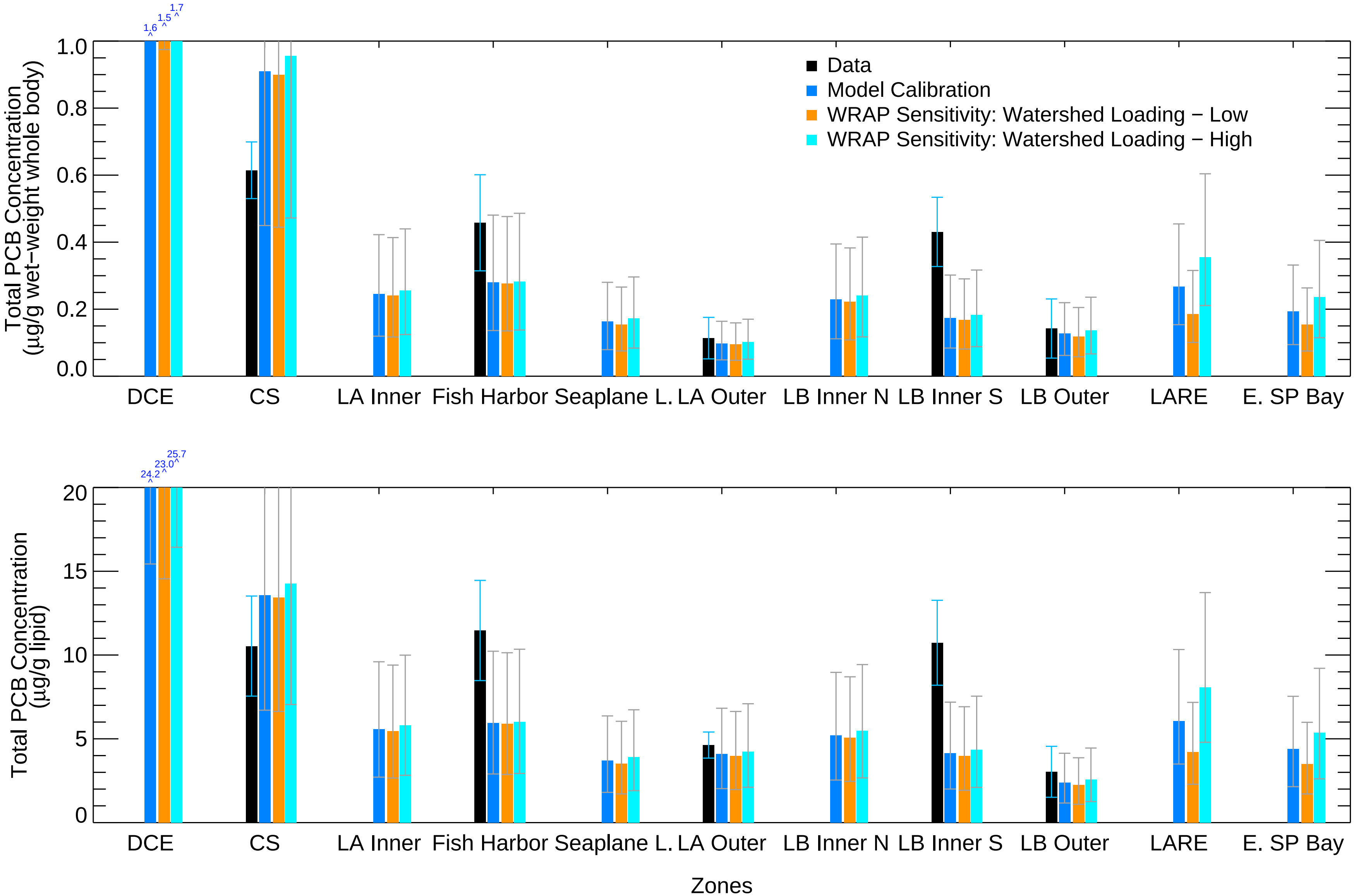


Figure 6−25a

Effects of Alternate Watershed Loading on Total PCB Concentration in Surfperch

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ files v.1677, 1689, 1690 and biota files v.1727, 1727, 1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 16:29:05 2017

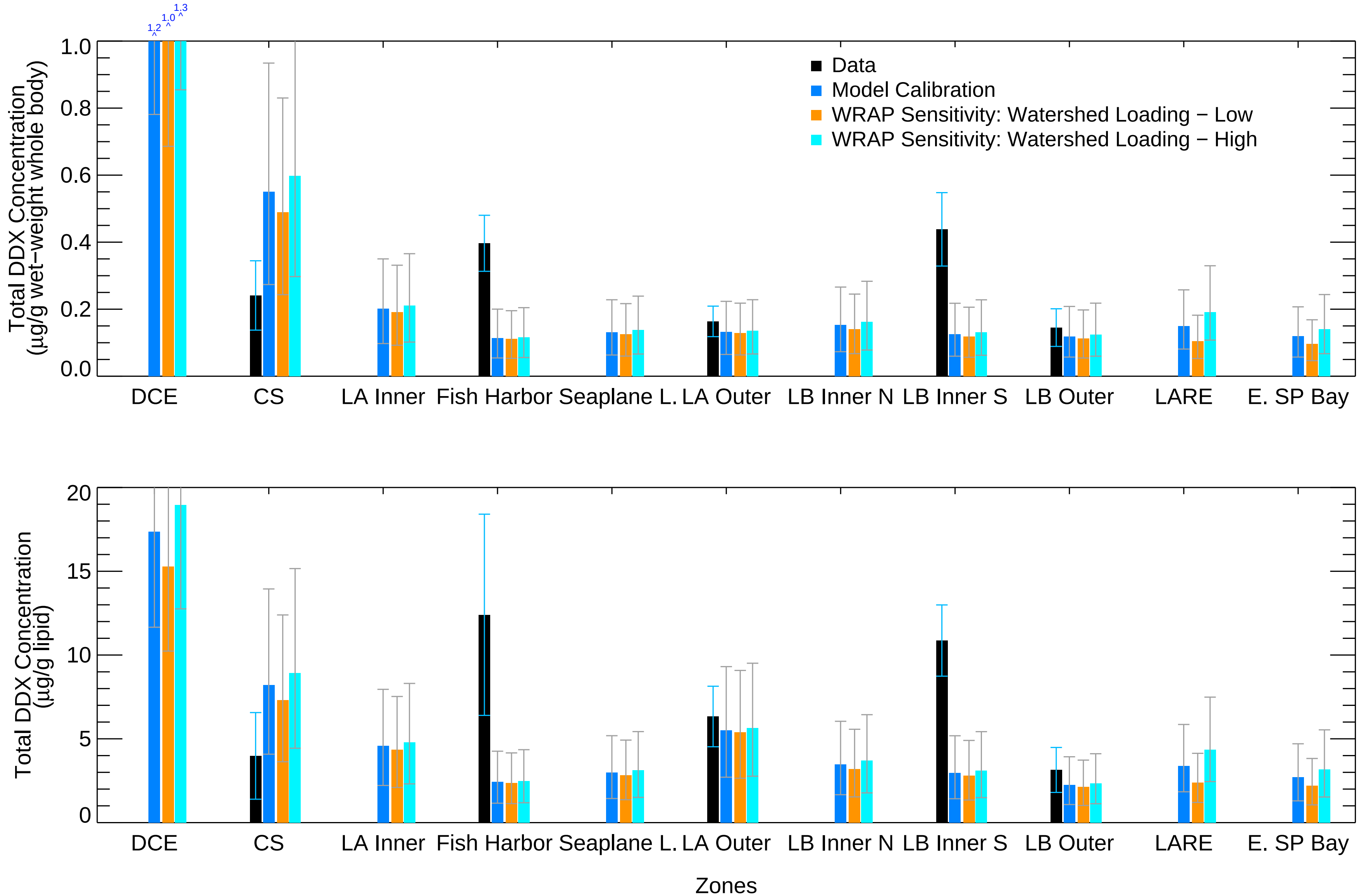


Figure 6−25b

Effects of Alternate Watershed Loading on Total DDX Concentration in Surfperch

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ files v.1677, 1689, 1690 and biota files v.1727, 1727, 1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 16:29:05 2017

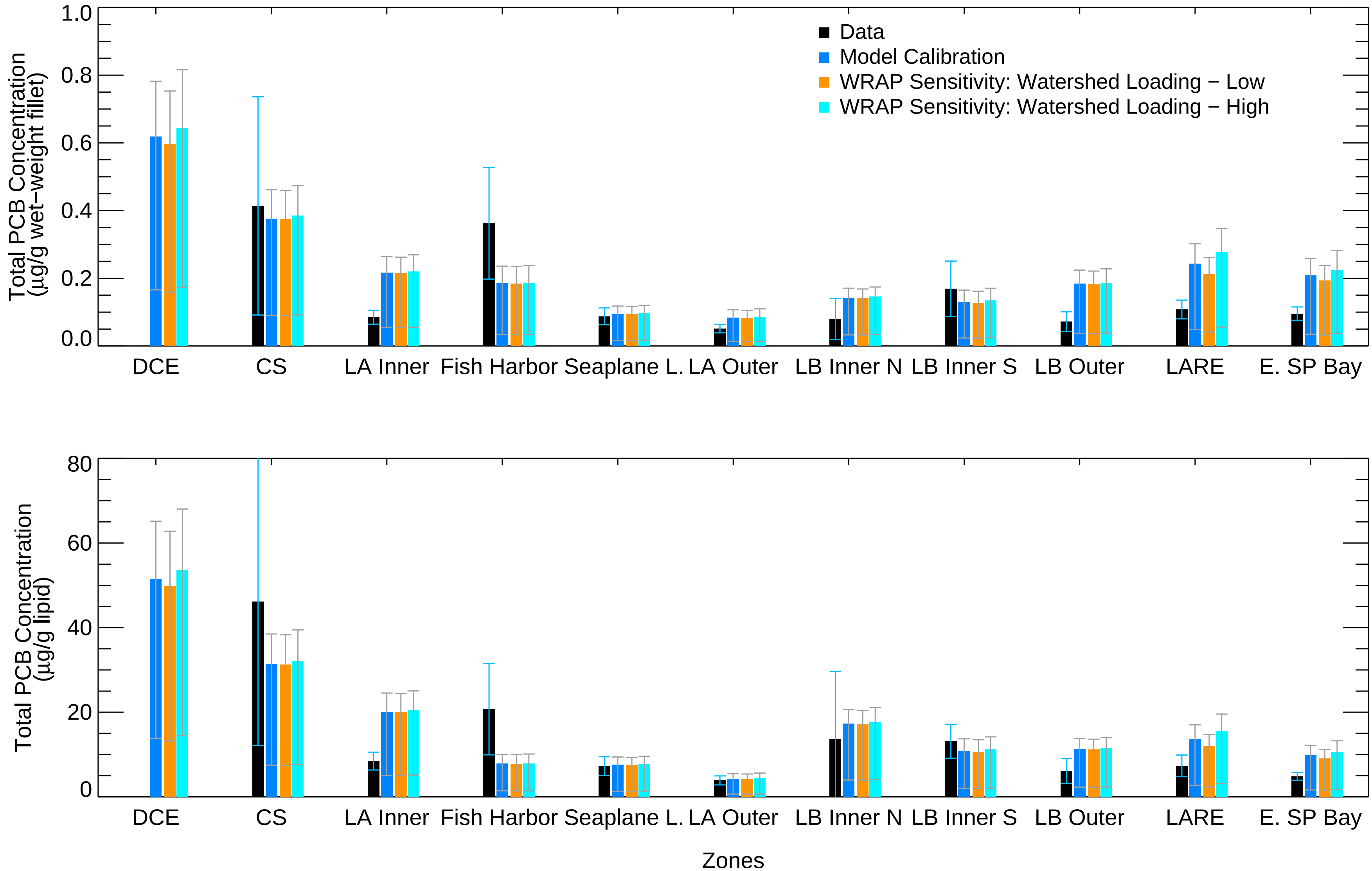


Figure 6−25c

Effects of Alternate Watershed Loading on Total PCB Concentration in White Croaker

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx. Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value), IH1−FFF−6WC (high value). Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1689, 1690 and biota files v.1727, 1727, 1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 16:29:05 2017

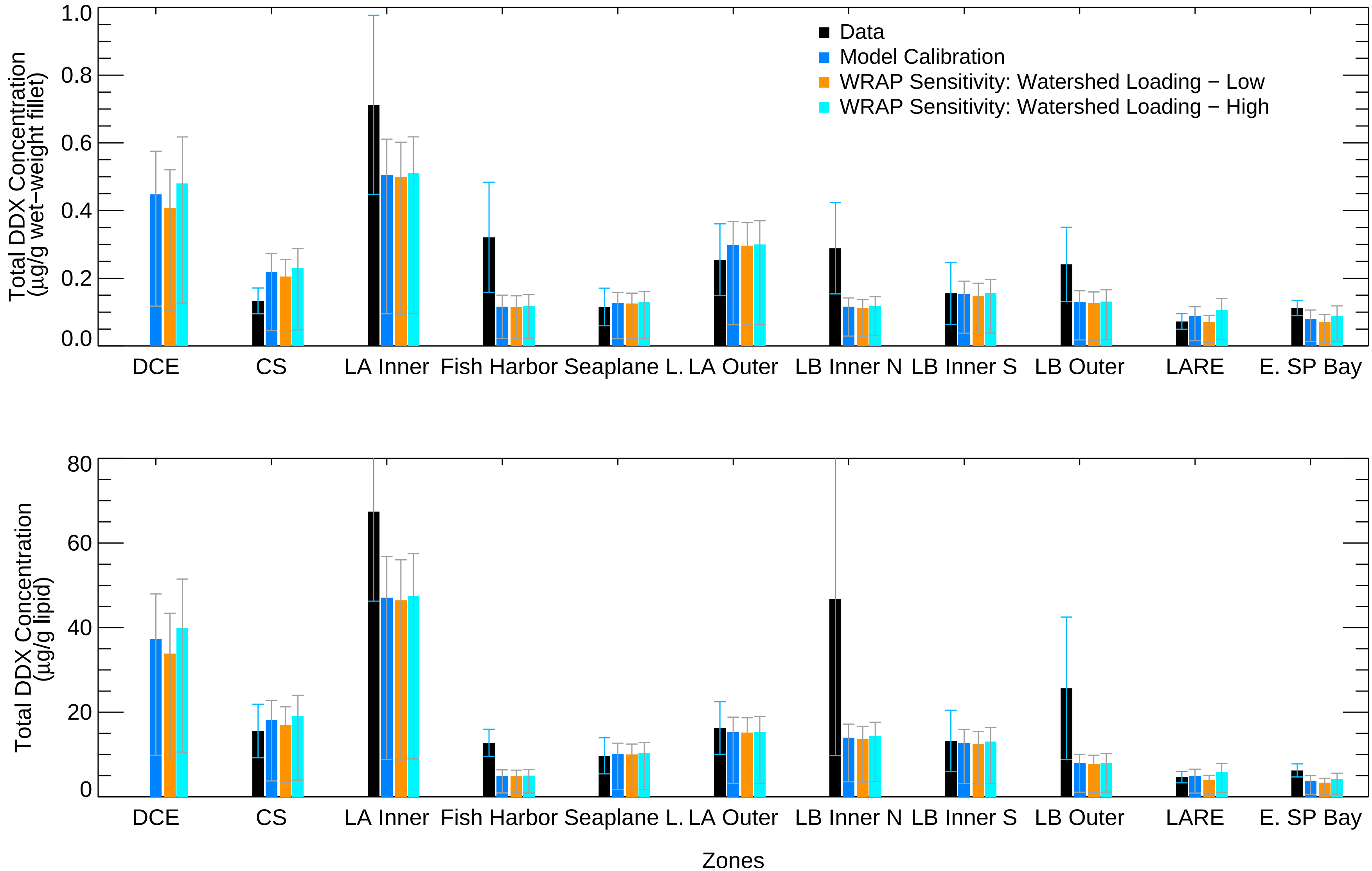


Figure 6−25d

Effects of Alternate Watershed Loading on Total DDX Concentration in White Croaker

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value), IH1−FFF−6WC (high value). Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1689, 1690 and biota files v.1727, 1727, 1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 16:29:05 2017

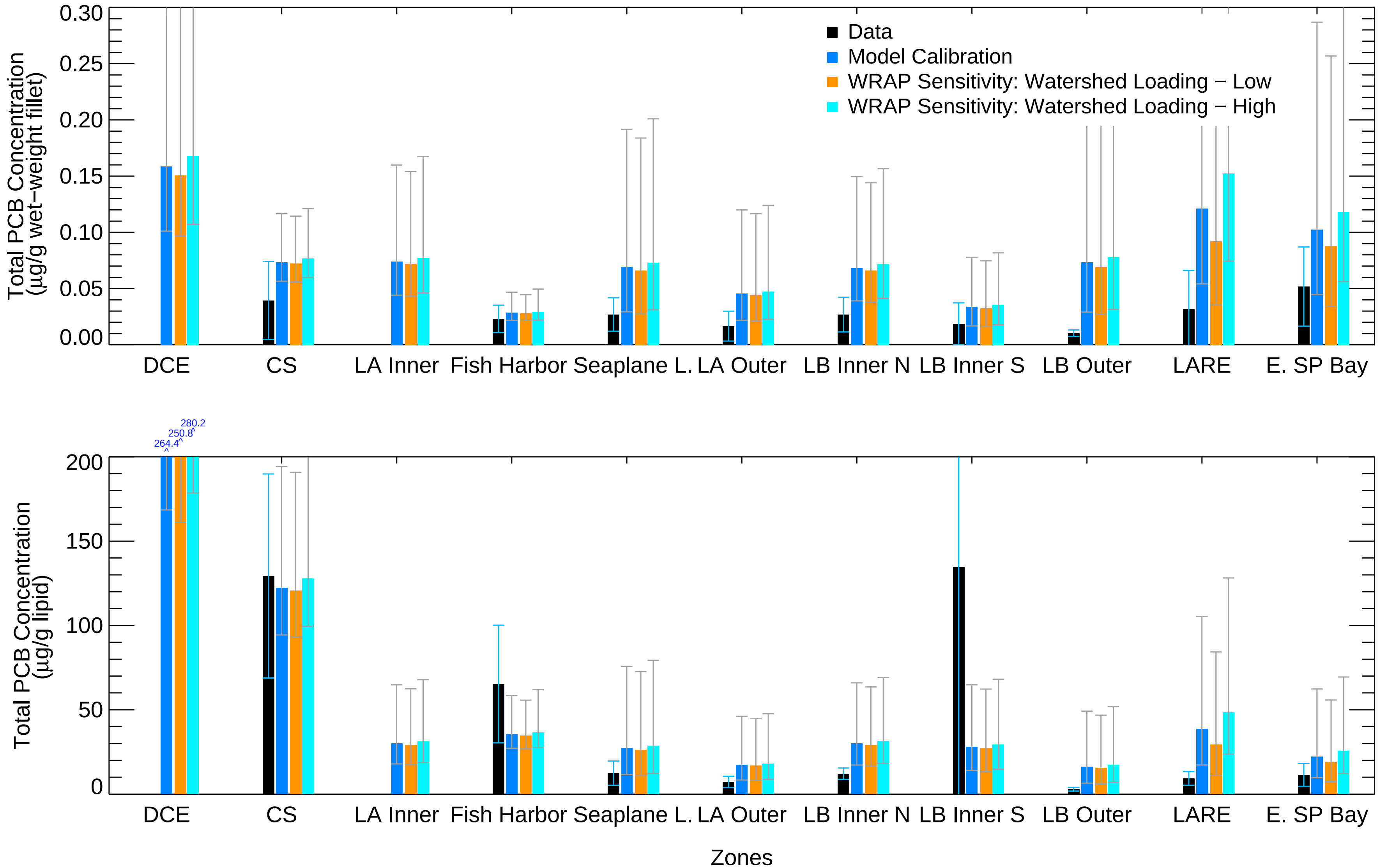


Figure 6−25e

Effects of Alternate Watershed Loading on Total PCB Concentration in California Halibut

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1689, 1690 and biota files v.1727, 1727, 1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 16:29:06 2017

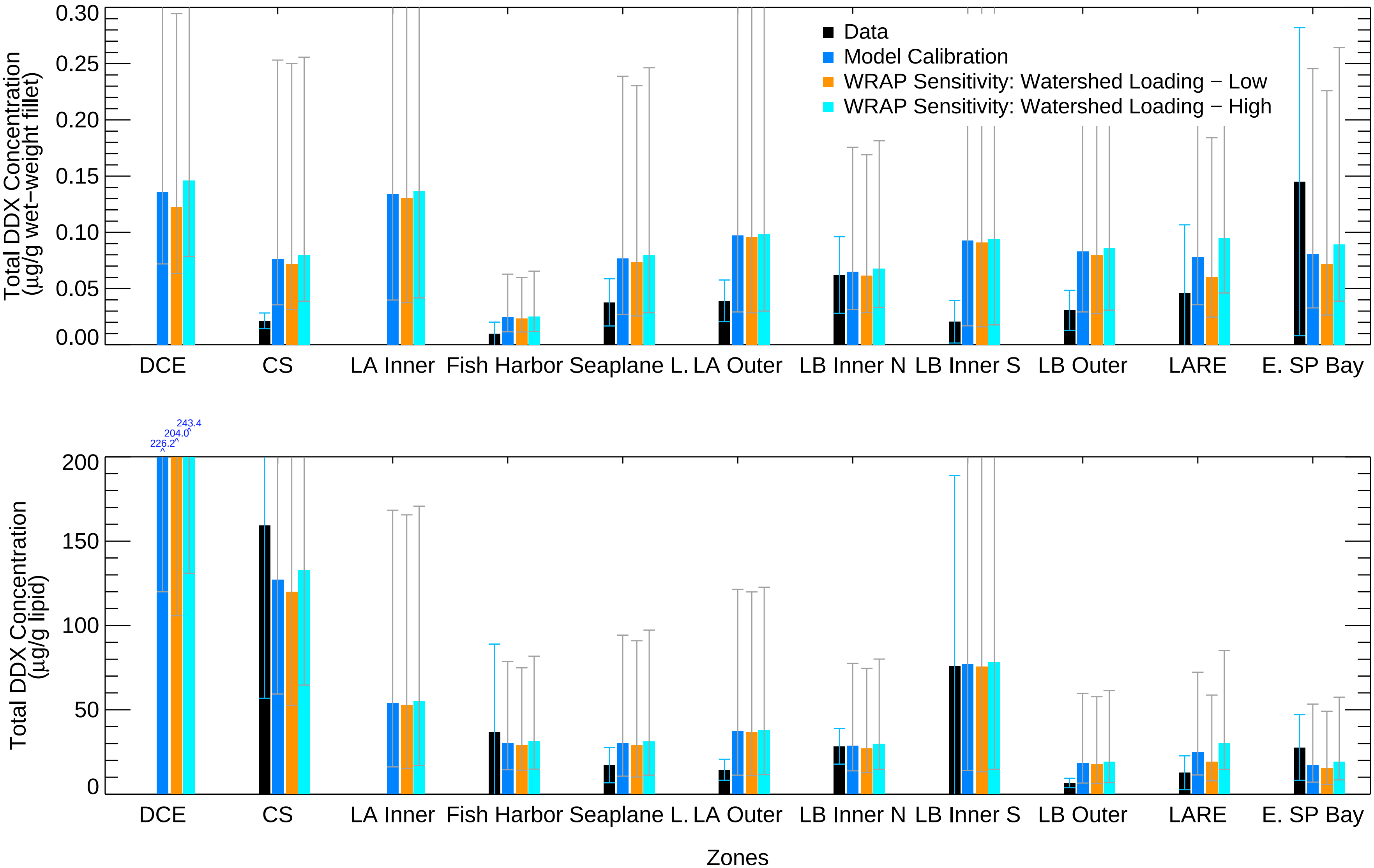


Figure 6−25f

Effects of Alternate Watershed Loading on Total DDX Concentration in California Halibut

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year of simulation and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ files v.1677, 1689, 1690 and biota files v.1727, 1727, 1727 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_CH_model_data_comparison_wMigration_v3.pro Wed Apr 26 16:29:06 2017

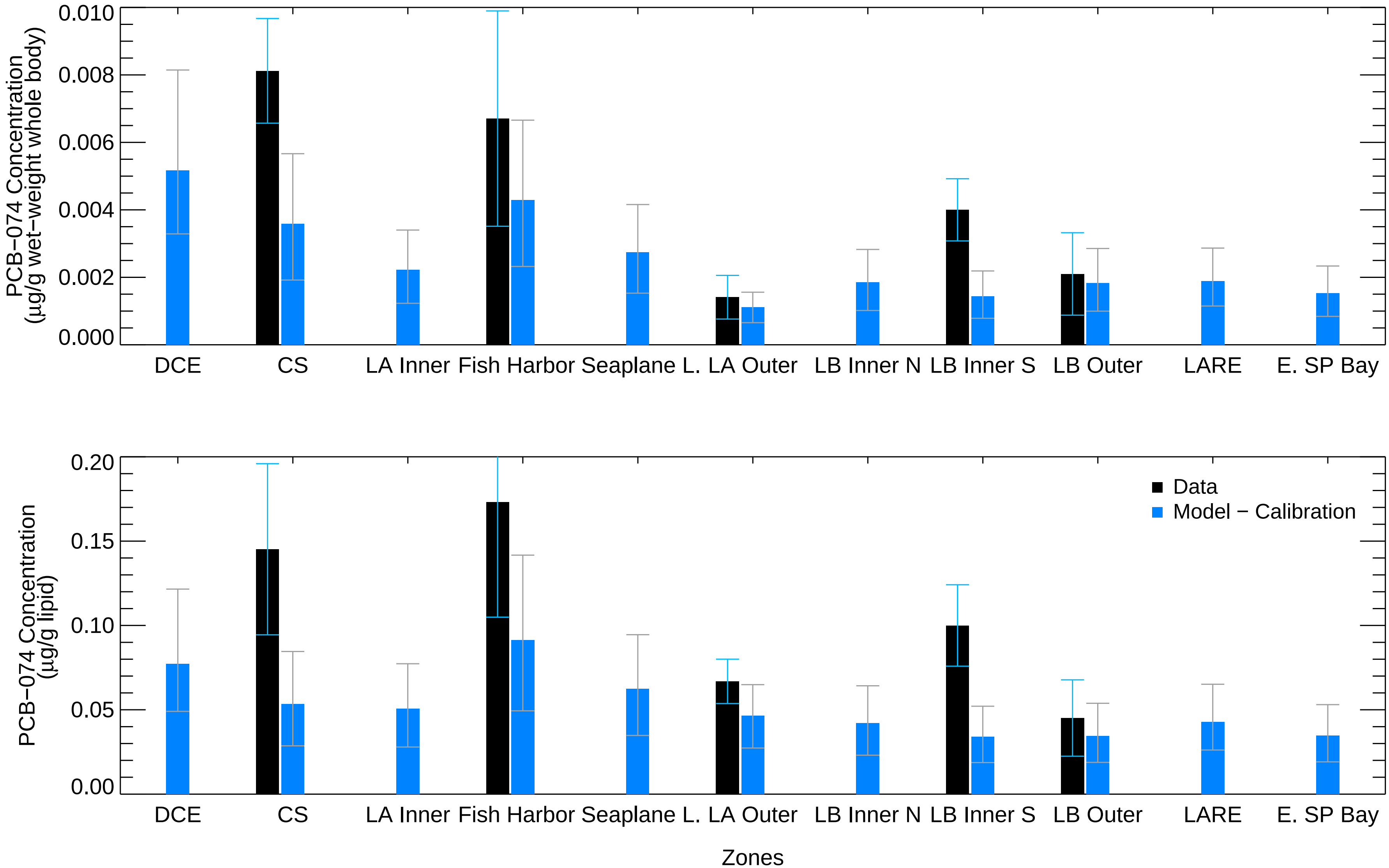


Figure 6−26a

Model to Data Comparison of PCB−074 Concentrations in Surfperch

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ file v.1707 and biota file v.1749 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_fish_model_data_comparison_wMigration_congener.pro Fri Apr 28 11:22:10 2017

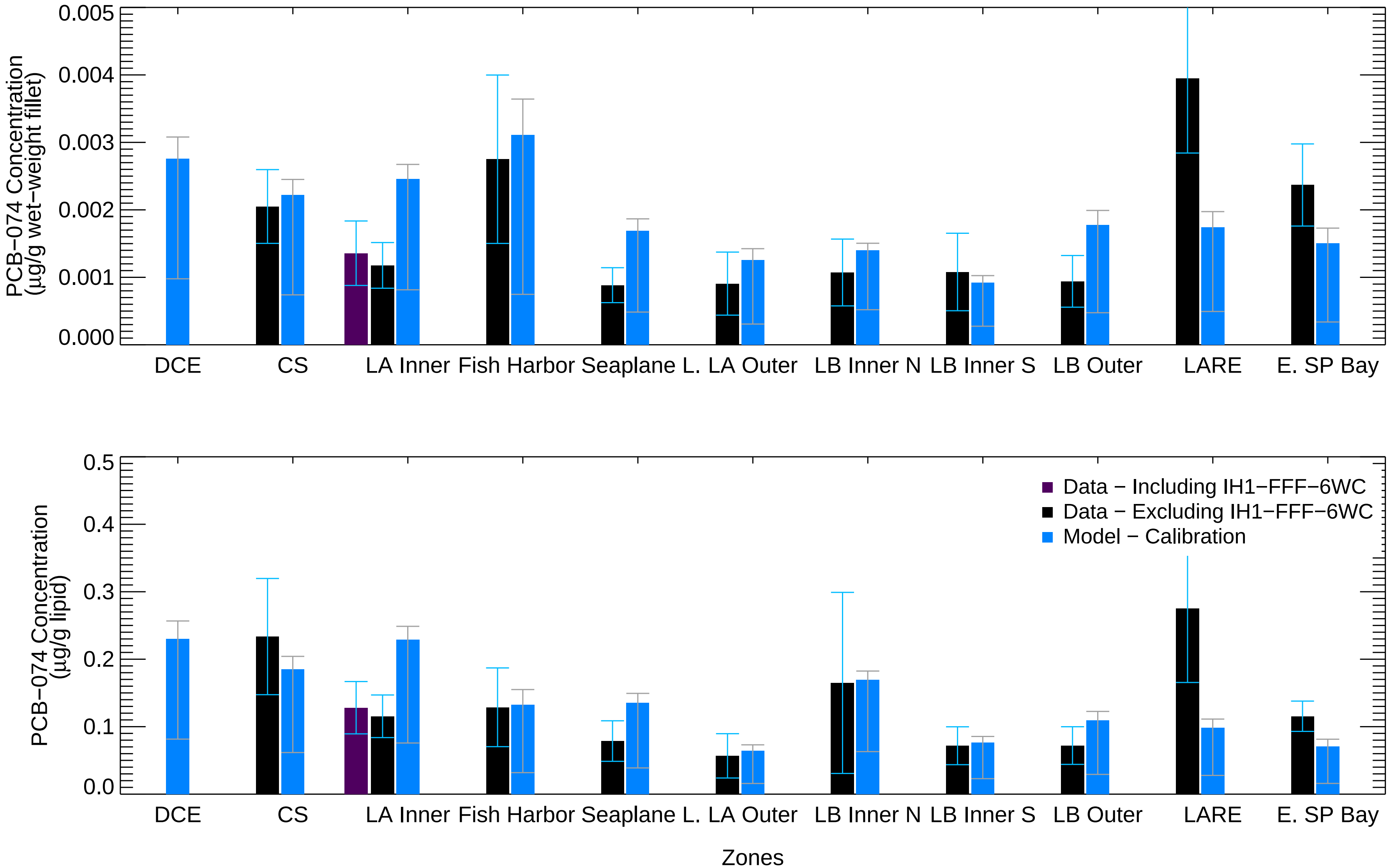


Figure 6−26b

Model to Data Comparison of PCB−074 Concentrations in White Croaker

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx. Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value). Model results are averaged over all days within the last year and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ file v.1707 and biota file v.1749 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_fish_model_data_comparison_wMigration_congener.pro Fri Apr 28 11:22:10 2017

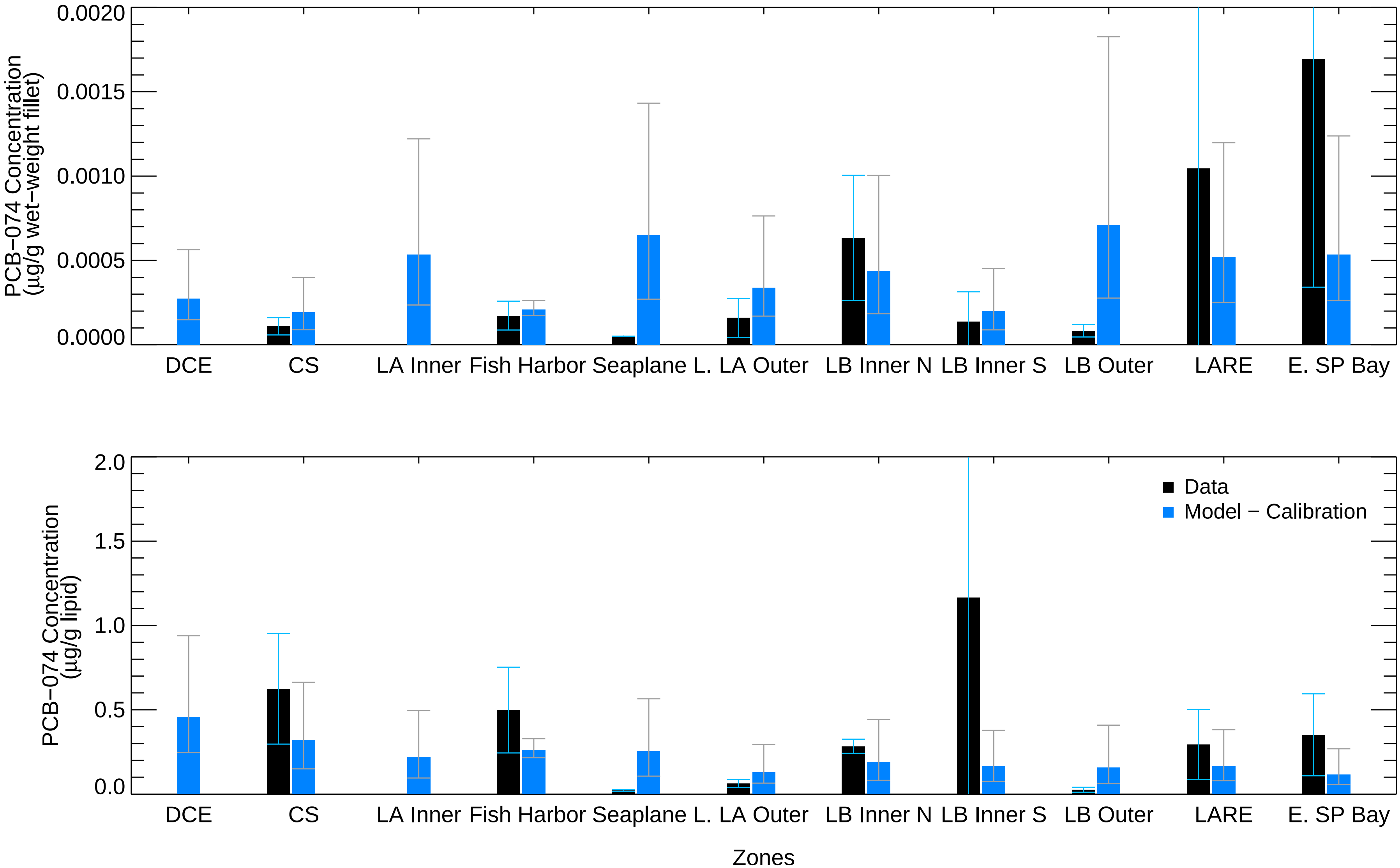


Figure 6−26c

Model to Data Comparison of PCB−074 Concentrations in California Halibut

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ file v.1707 and biota file v.1749 used for model.

ANCHOR QEA

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_fish_model_data_comparison_wMigration_congener.pro Fri Apr 28 11:22:10 2017

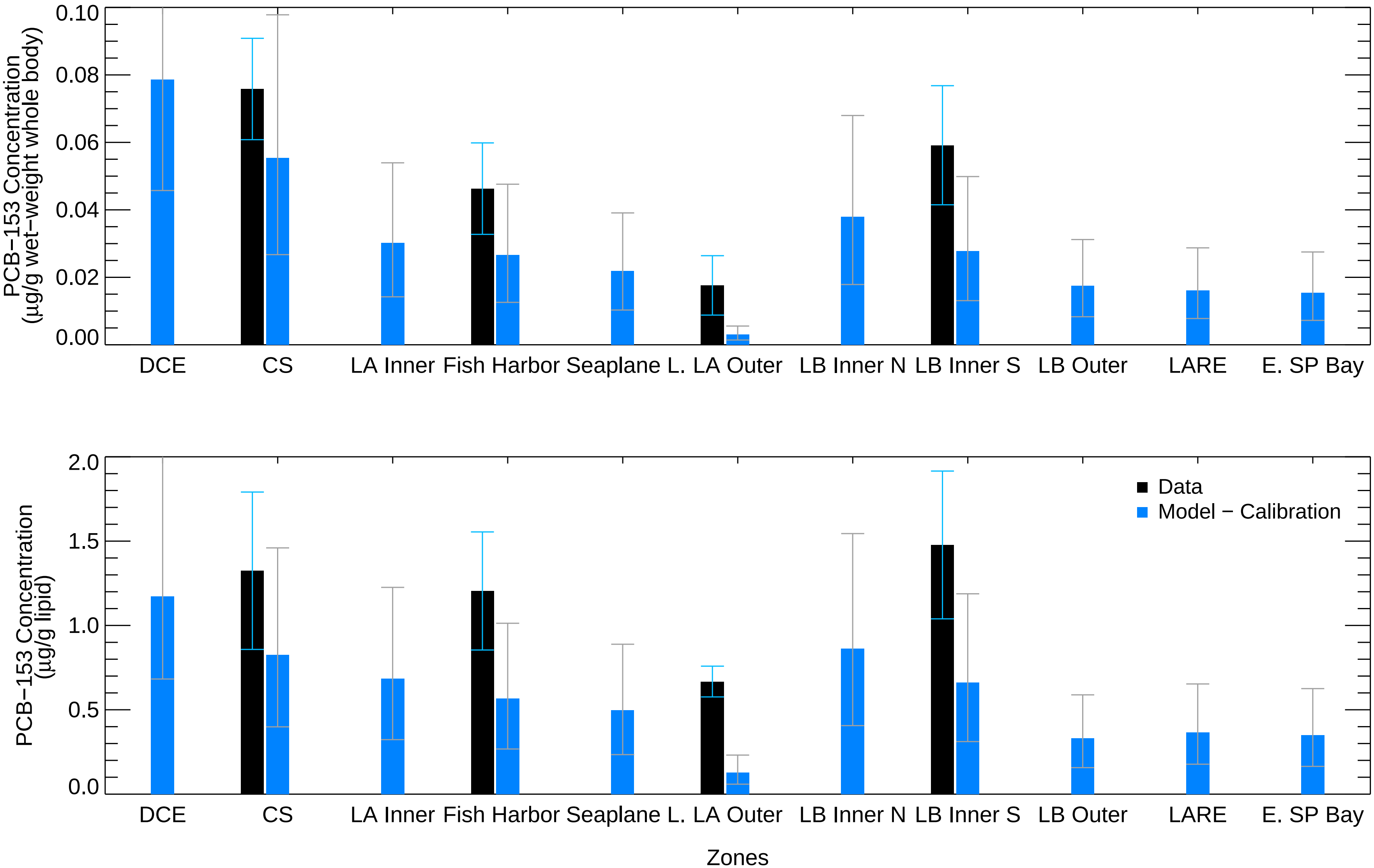


Figure 6−27a

Model to Data Comparison of PCB−153 Concentrations in Surfperch

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ file v.1708 and biota file v.1750 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_fish_model_data_comparison_wMigration_congener.pro Fri Apr 28 11:00:06 2017

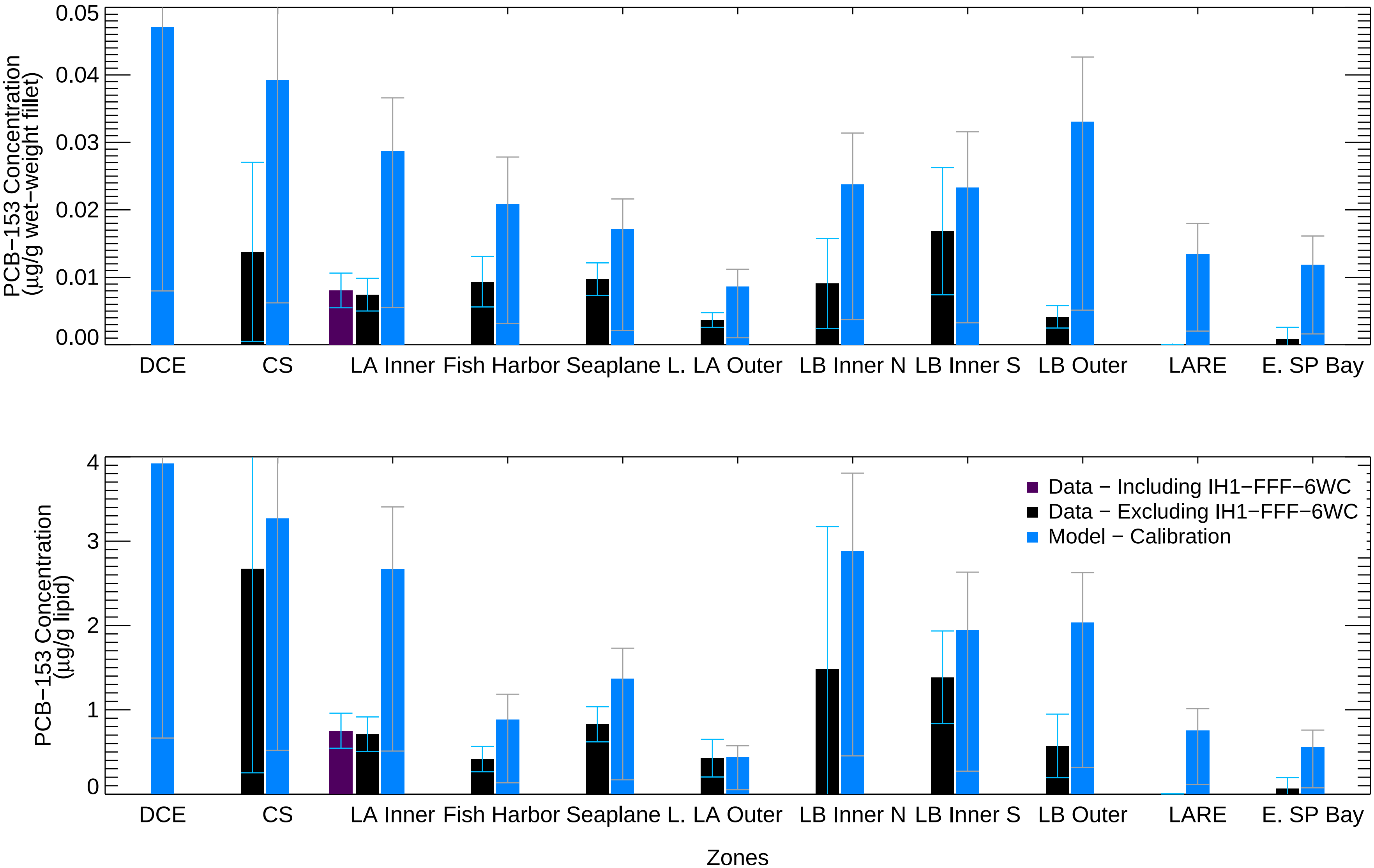


Figure 6−27b

Model to Data Comparison of PCB−153 Concentrations in White Croaker

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx. Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean. Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value). Model results are averaged over all days within the last year and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ file v.1708 and biota file v.1750 used for model.

ANCHOR QEA

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_fish_model_data_comparison_wMigration_congener.pro Fri Apr 28 11:00:06 2017

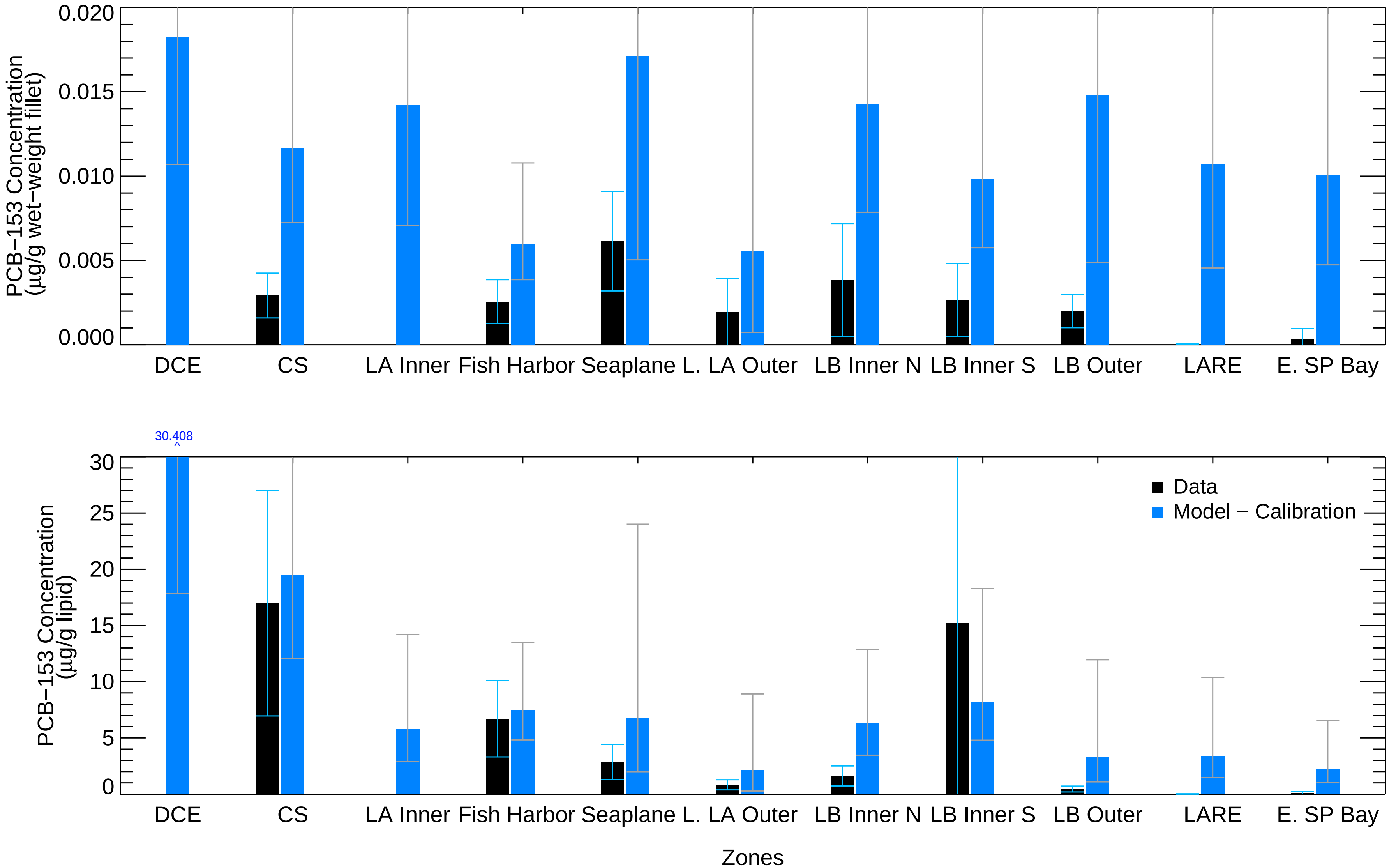


Figure 6−27c

Model to Data Comparison of PCB−153 Concentrations in California Halibut

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ file v.1708 and biota file v.1750 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_fish_model_data_comparison_wMigration_congener.pro Fri Apr 28 11:00:06 2017

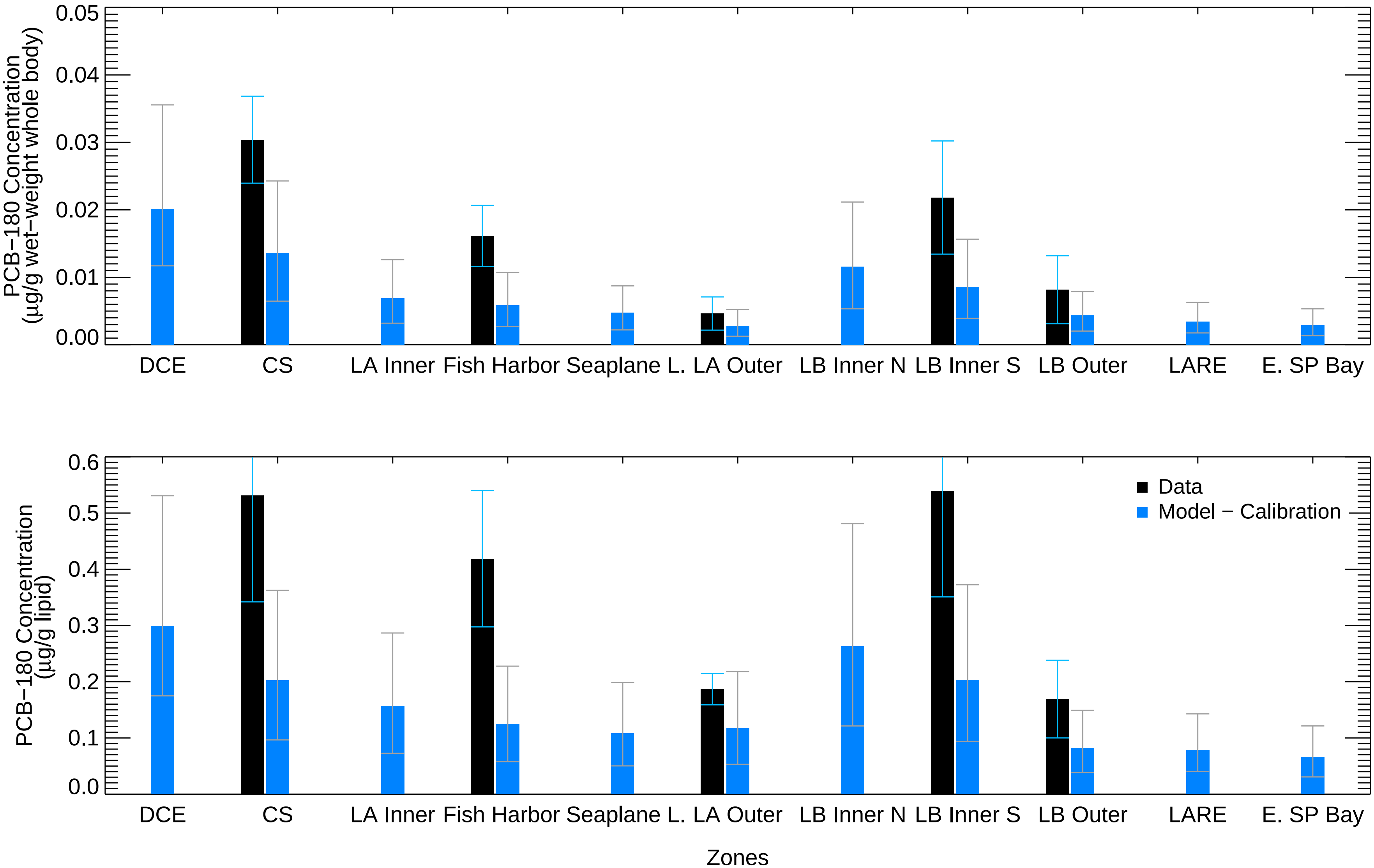


Figure 6−28a

Model to Data Comparison of PCB−180 Concentrations in Surfperch

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within the last year and then shown as age−weighted averages (bars) and range (error bars) over various age classes.
WQ file v.1709 and biota file v.1751 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_fish_model_data_comparison_wMigration_congener.pro Fri Apr 28 10:41:05 2017

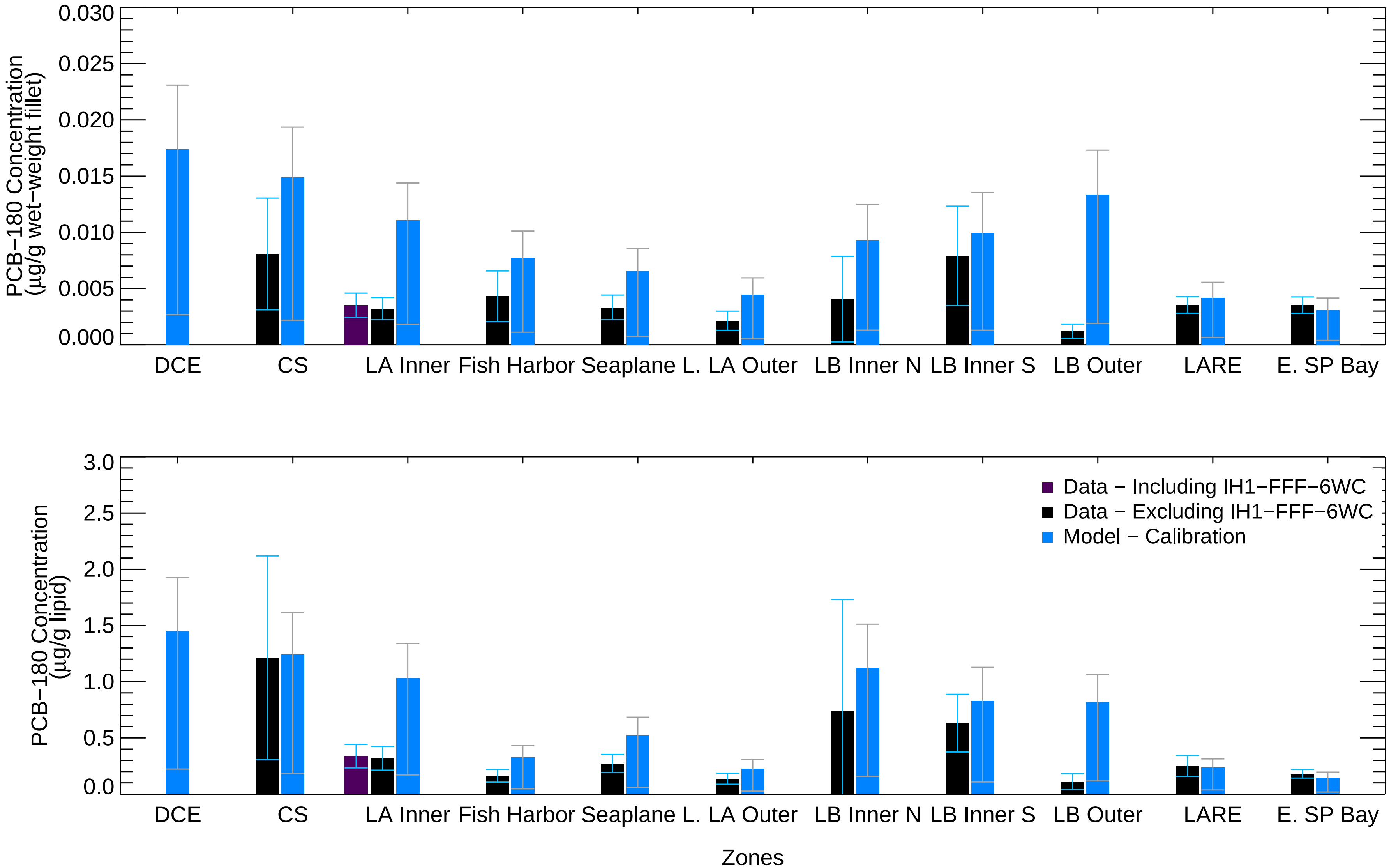


Figure 6−28b

Model to Data Comparison of PCB−180 Concentrations in White Croaker

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. The following white croaker samples were excluded: IH5−FFF−7WC (lipid normalized results − due to low lipid value). Model results are averaged over all days within the last year and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ file v.1709 and biota file v.1751 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_fish_model_data_comparison_wMigration_congener.pro Fri Apr 28 10:41:05 2017

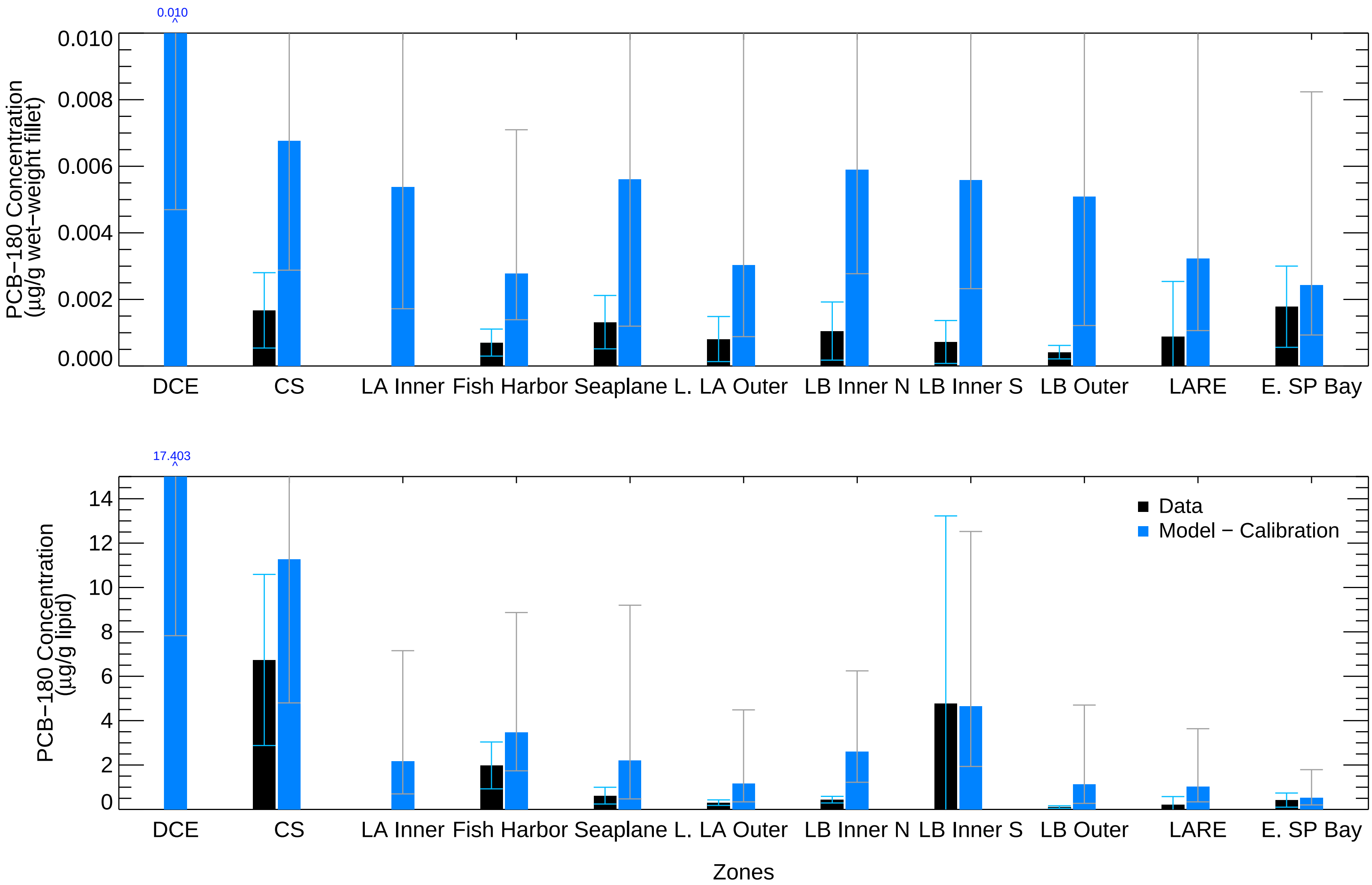


Figure 6−28c

Model to Data Comparison of PCB−180 Concentrations in California Halibut

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data bars represent spatial average concentrations for 2002 to 2014 samples and error bars show +/− 2 standard errors of the mean.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects. California halibut samples with non−detect lipid results are set to their detection limits. Model results are averaged over all days within the last year and then shown as age−weighted averages (bars) and range (error bars) over various age classes. WQ file v.1709 and biota file v.1751 used for model.

MM/BG − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\spatial_fish_model_data_comparison_wMigration_congener.pro Fri Apr 28 10:41:05 2017

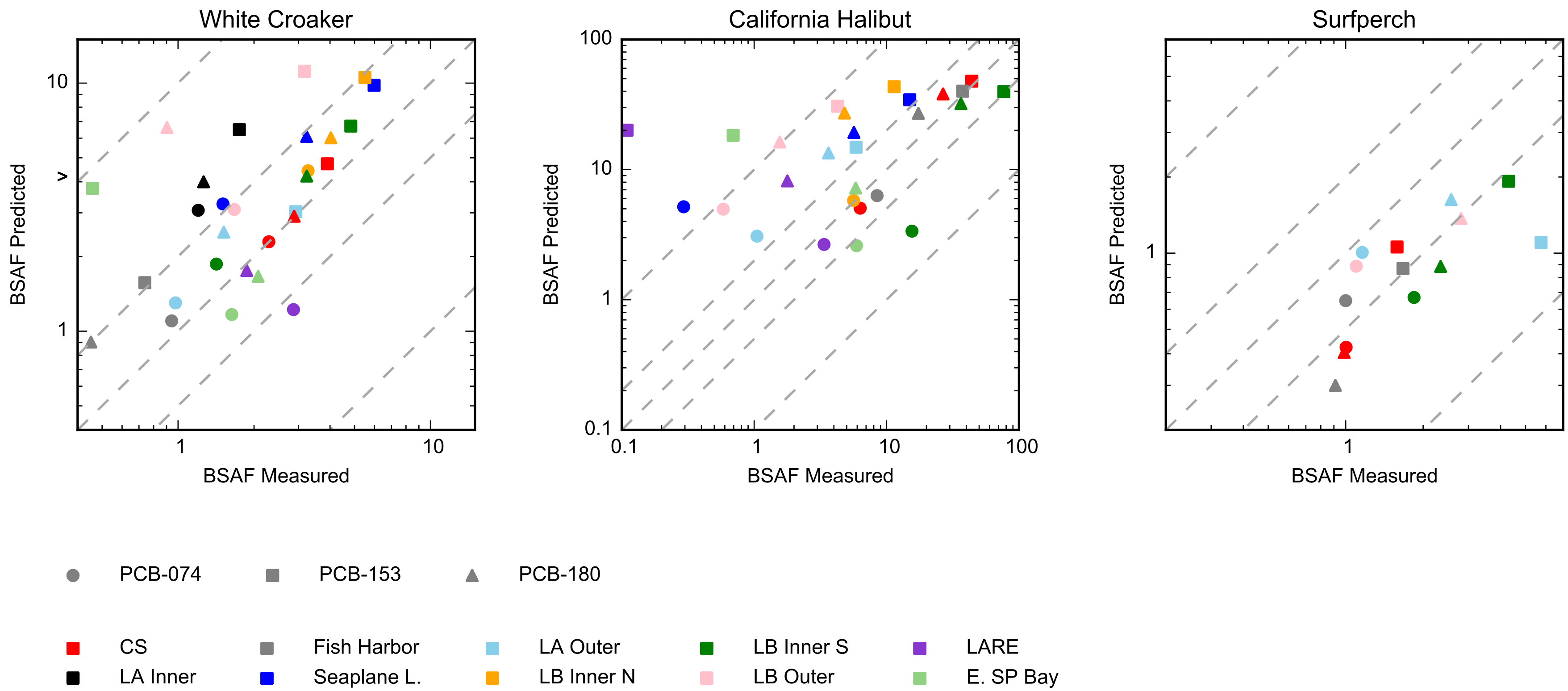


Figure 6-29a
BSAF Comparison

Note: A data point for PCB-153 is outside the plot range; the measured BSAF is 0.02 and the predicted is 3.94.

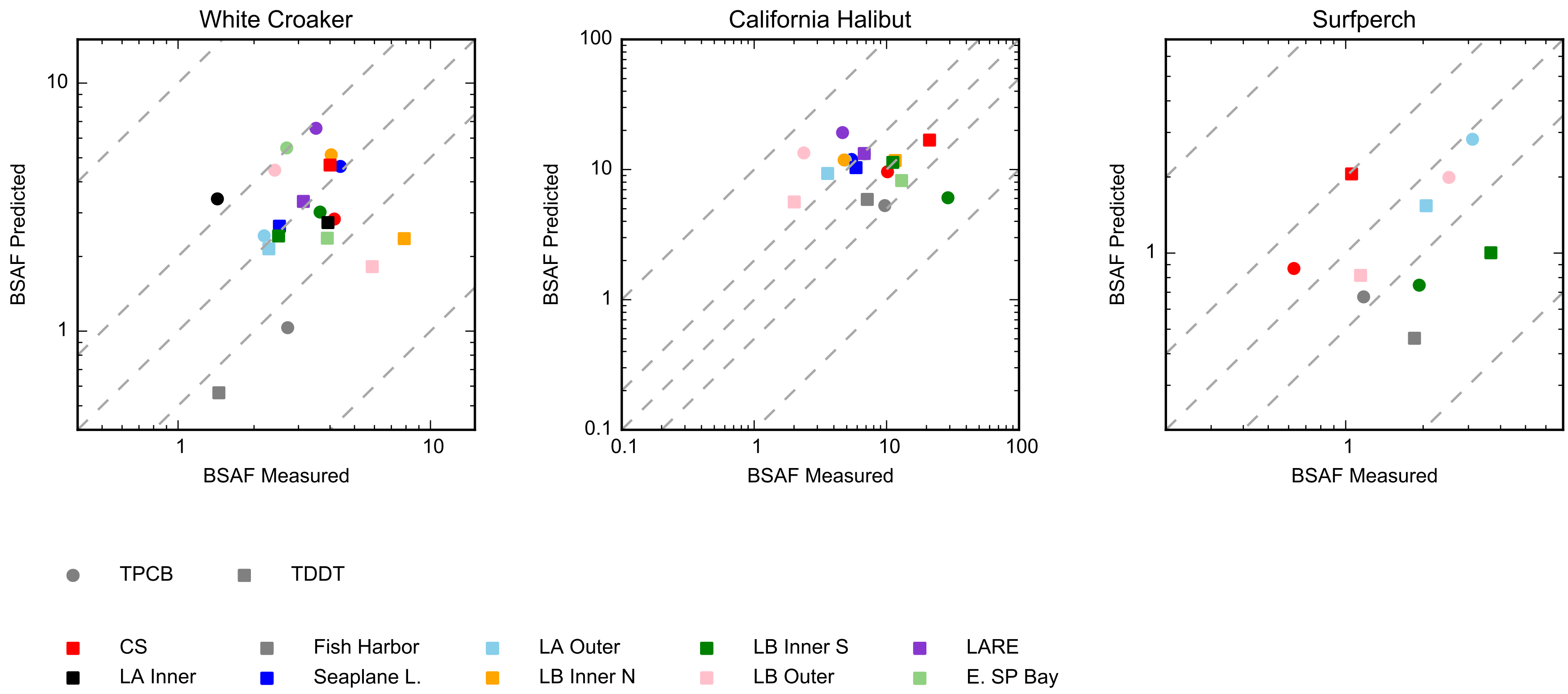


Figure 6-29b
BSAF Comparison

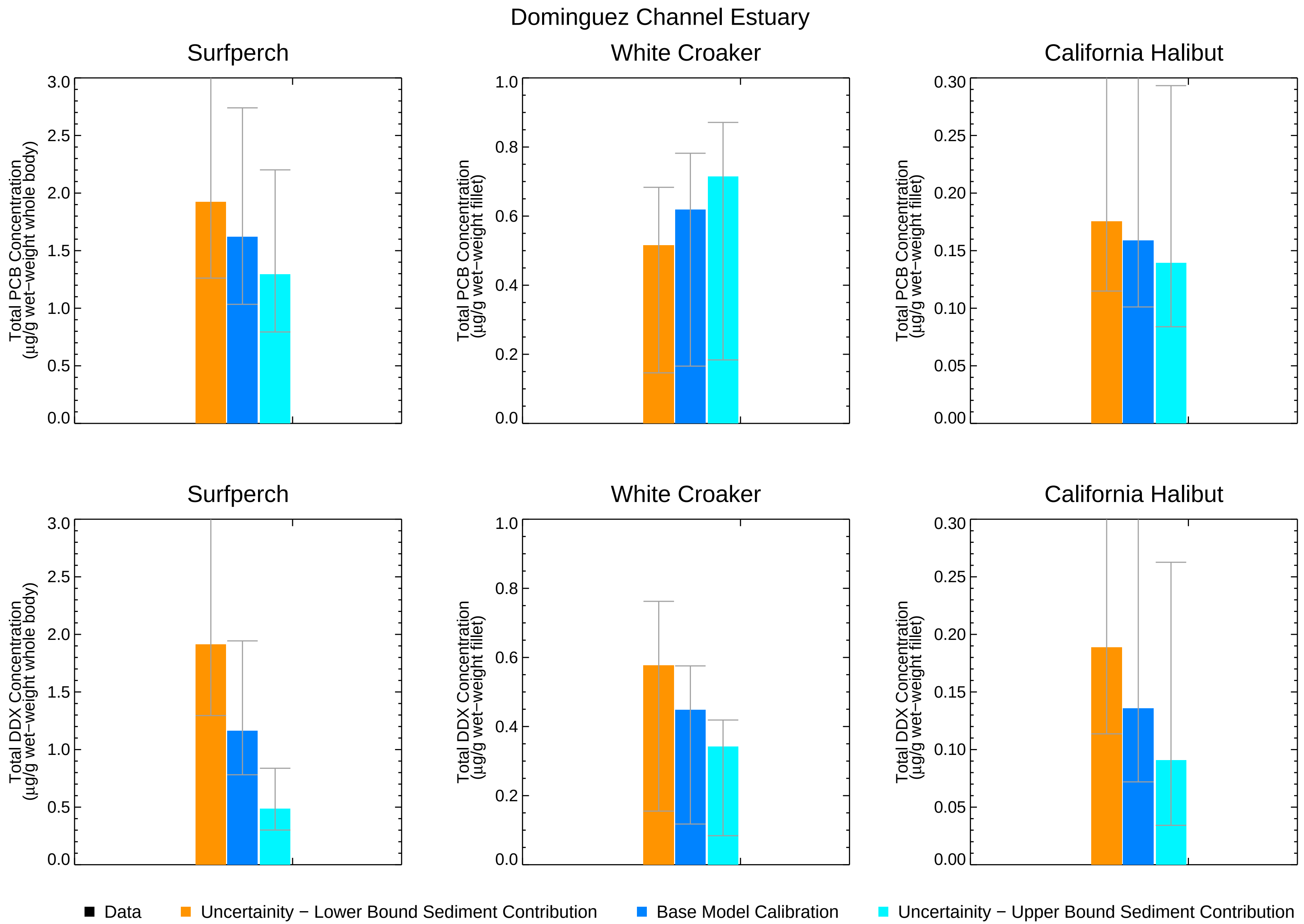


Figure 6−30a

Effects of Uncertainty Bounds (BSAF, WCPAF, Ocean Boundary) on Contaminant Concentration at Dominguez Channel Estuary

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data represent the average and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within each year of simulation and then shown as age−weighted averages over various age classes.
WQ files v.1686, 1677, 1685 and biota files v.1728, 1727, 1729 used for model.

MM − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\fish_model_data_comparison_wMigration_byzone.pro Fri Apr 07 16:30:44 2017

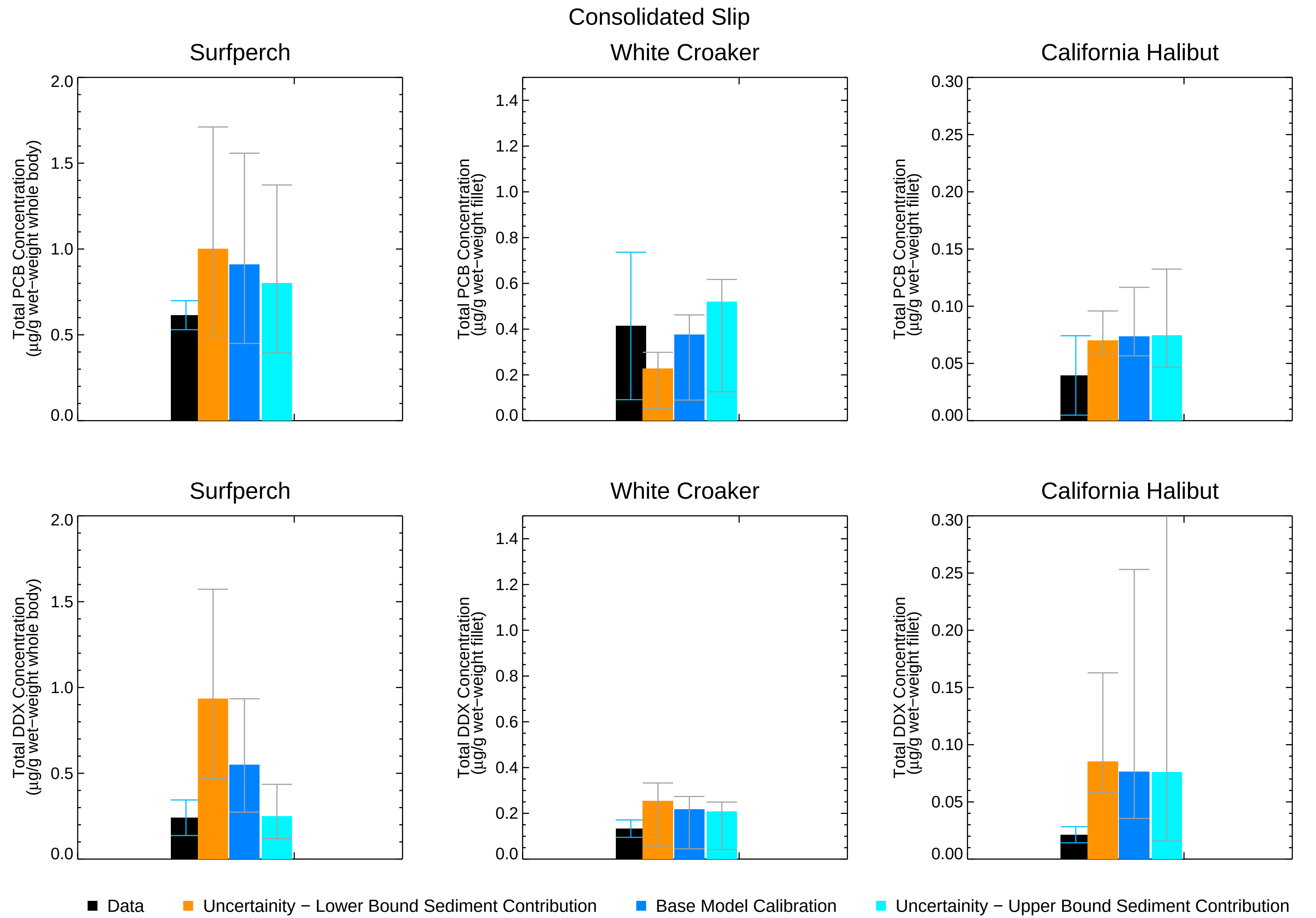


Figure 6−30b

Effects of Uncertainty Bounds (BSAF, WCPAF, Ocean Boundary) on Contaminant Concentration at Consolidated Slip

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data represent the average and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within each year of simulation and then shown as age−weighted averages over various age classes.
WQ files v.1686, 1677, 1685 and biota files v.1728, 1727, 1729 used for model.

MM − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\fish_model_data_comparison_wMigration_byzone.pro Fri Apr 07 16:30:44 2017

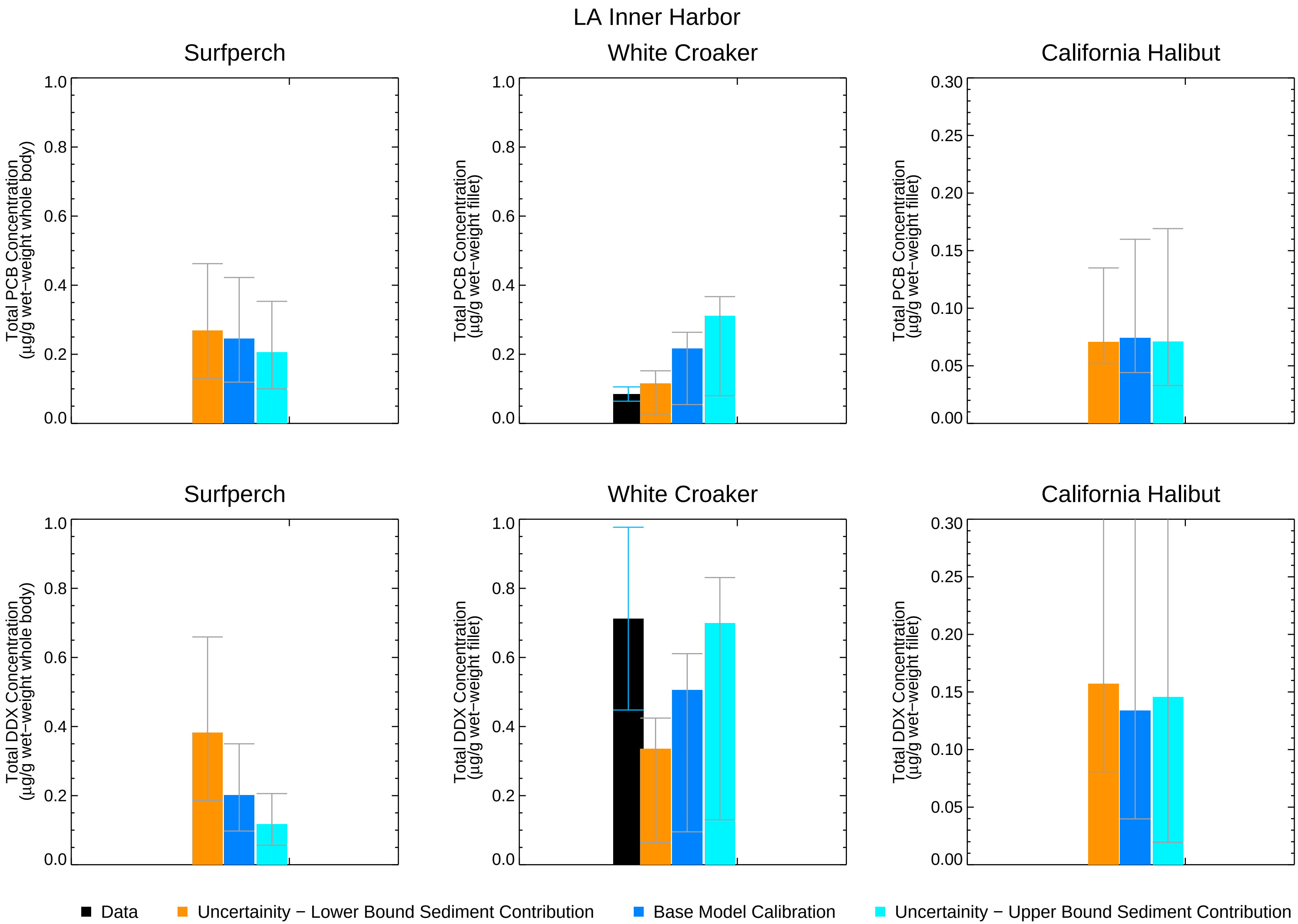


Figure 6−30c

Effects of Uncertainty Bounds (BSAF, WCPAF, Ocean Boundary) on Contaminant Concentration at LA Inner Harbor

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data represent the average and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within each year of simulation and then shown as age−weighted averages over various age classes.
WQ files v.1686, 1677, 1685 and biota files v.1728, 1727, 1729 used for model.

MM − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\fish_model_data_comparison_wMigration_byzone.pro Fri Apr 07 16:30:44 2017

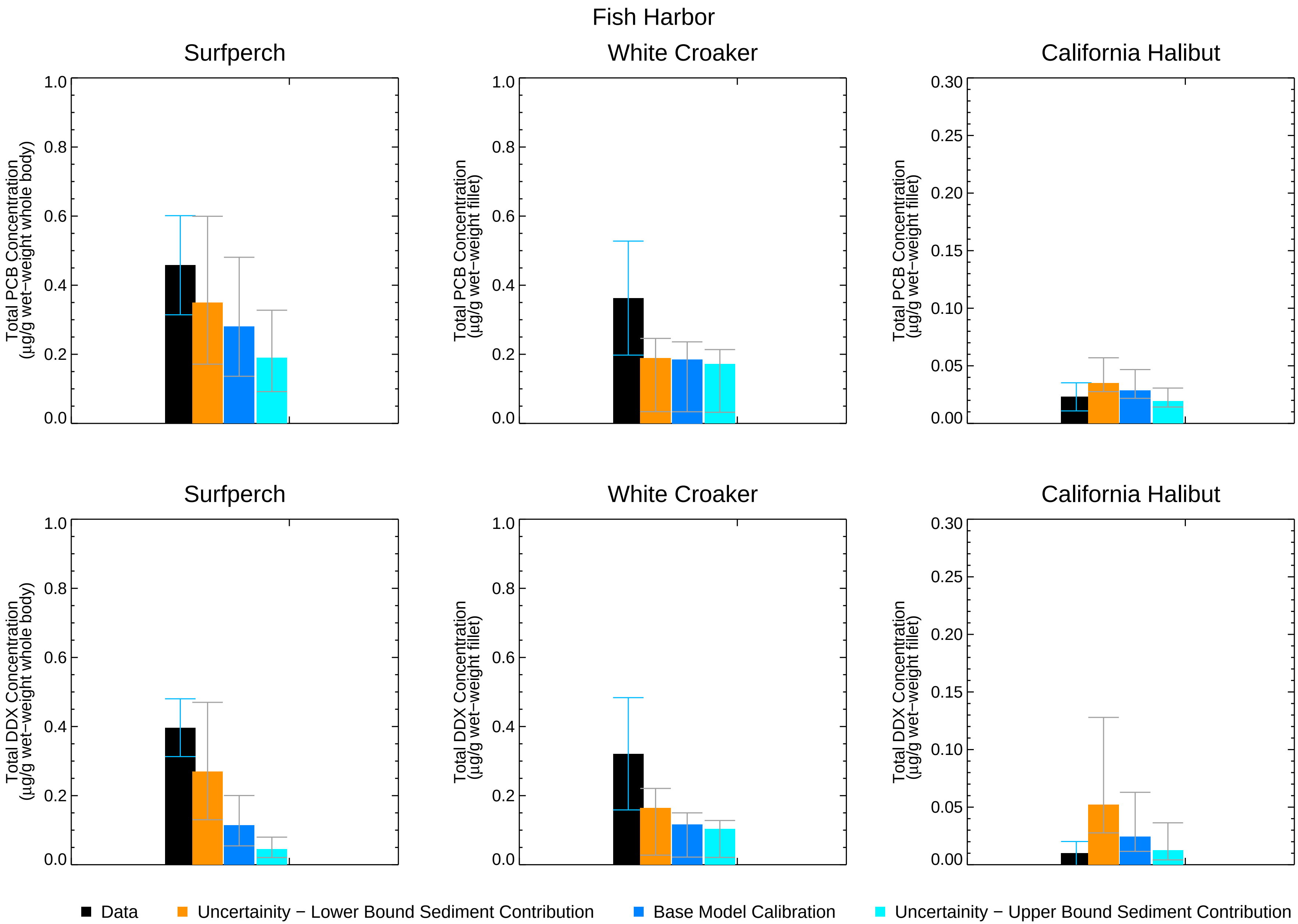


Figure 6−30d

Effects of Uncertainty Bounds (BSAF, WCPAF, Ocean Boundary) on Contaminant Concentration at Fish Harbor

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data represent the average and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within each year of simulation and then shown as age−weighted averages over various age classes.
WQ files v.1686, 1677, 1685 and biota files v.1728, 1727, 1729 used for model.

MM − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\fish_model_data_comparison_wMigration_byzone.pro Fri Apr 07 16:30:44 2017

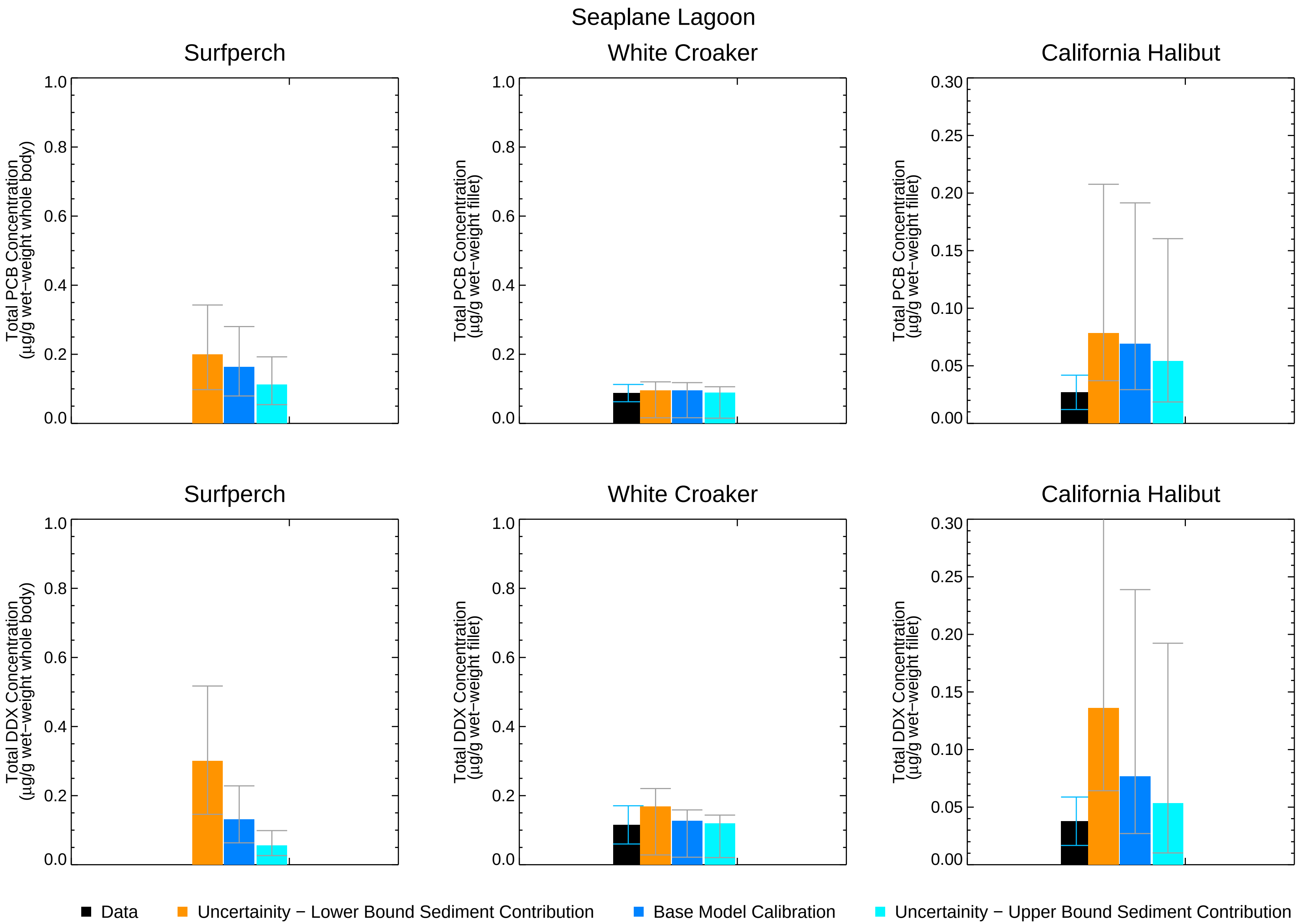


Figure 6−30e

Effects of Uncertainty Bounds (BSAF, WCPAF, Ocean Boundary) on Contaminant Concentration at Seaplane Lagoon

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data represent the average and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within each year of simulation and then shown as age−weighted averages over various age classes.
WQ files v.1686, 1677, 1685 and biota files v.1728, 1727, 1729 used for model.

MM − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\fish_model_data_comparison_wMigration_byzone.pro Fri Apr 07 16:30:44 2017

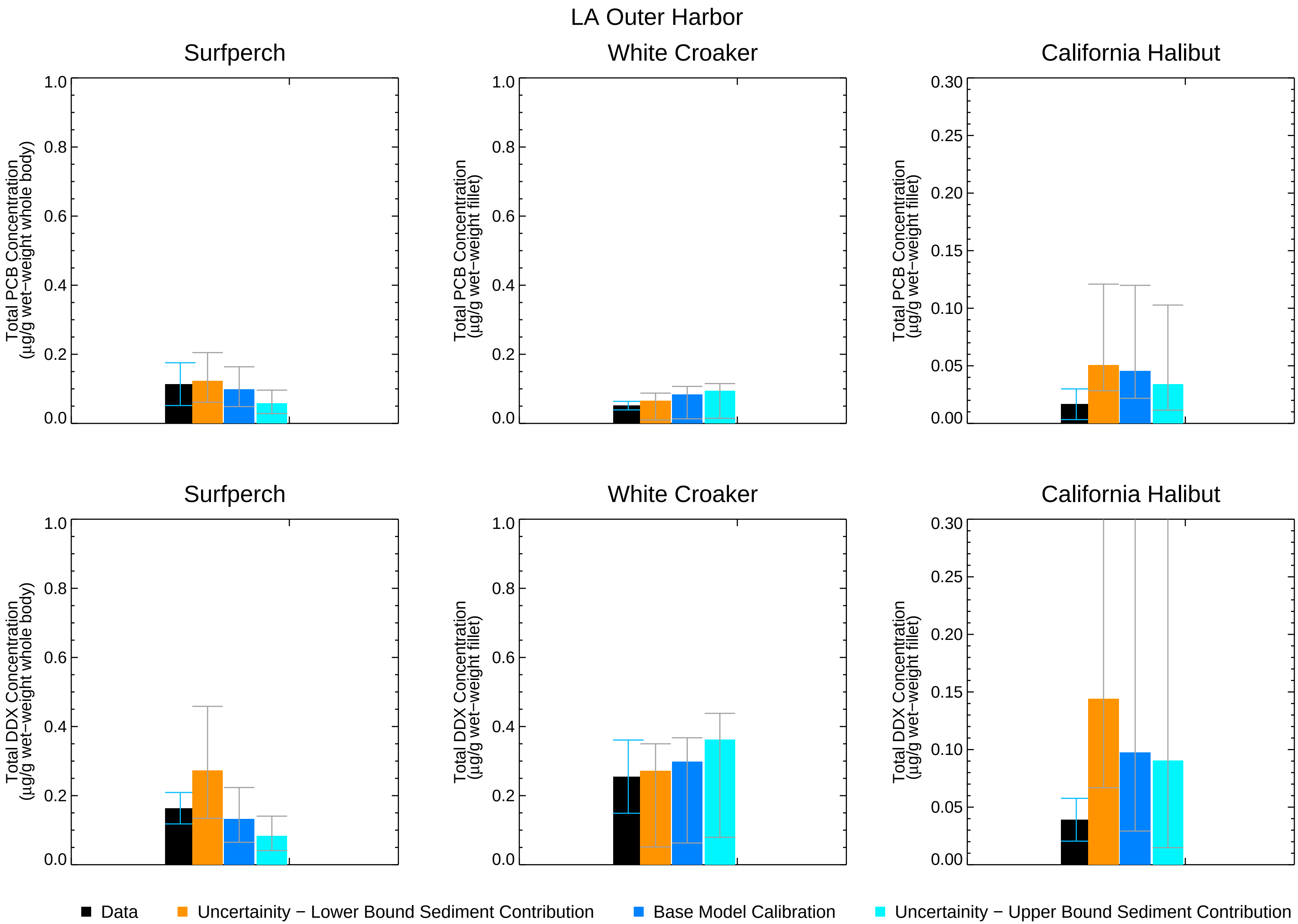


Figure 6−30f

Effects of Uncertainty Bounds (BSAF, WCPAF, Ocean Boundary) on Contaminant Concentration at LA Outer Harbor

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data represent the average and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within each year of simulation and then shown as age−weighted averages over various age classes.
WQ files v.1686, 1677, 1685 and biota files v.1728, 1727, 1729 used for model.

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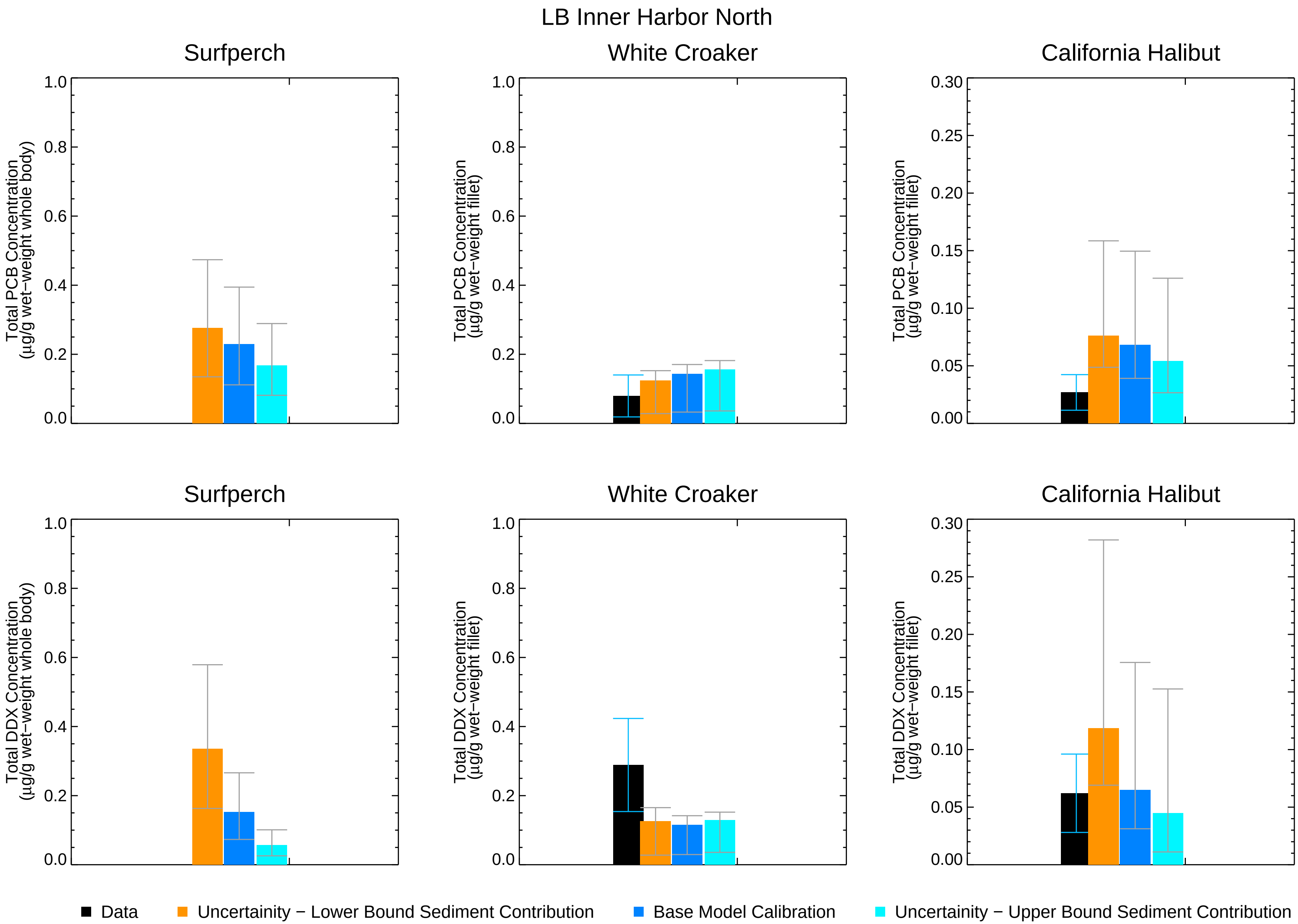

Figure 6−30g

Effects of Uncertainty Bounds (BSAF, WCPAF, Ocean Boundary) on Contaminant Concentration at LB Inner Harbor North

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data represent the average and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within each year of simulation and then shown as age−weighted averages over various age classes.
WQ files v.1686, 1677, 1685 and biota files v.1728, 1727, 1729 used for model.

MM − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\fish_model_data_comparison_wMigration_byzone.pro Fri Apr 07 16:30:44 2017

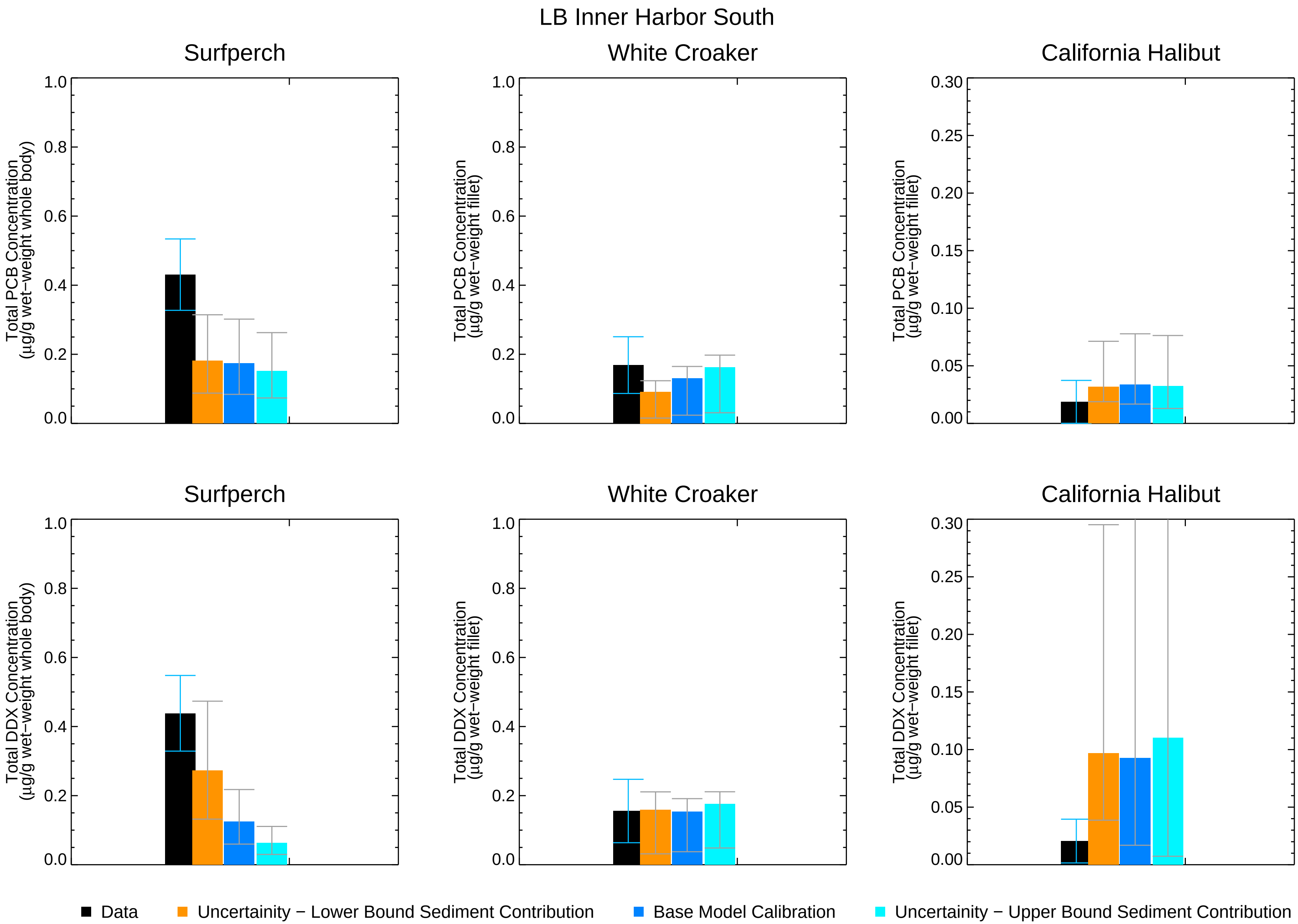

Figure 6−30h

Effects of Uncertainty Bounds (BSAF, WCPAF, Ocean Boundary) on Contaminant Concentration at LB Inner Harbor South

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data represent the average and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within each year of simulation and then shown as age−weighted averages over various age classes.
WQ files v.1686, 1677, 1685 and biota files v.1728, 1727, 1729 used for model.

MM − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\fish_model_data_comparison_wMigration_byzone.pro Fri Apr 07 16:30:44 2017

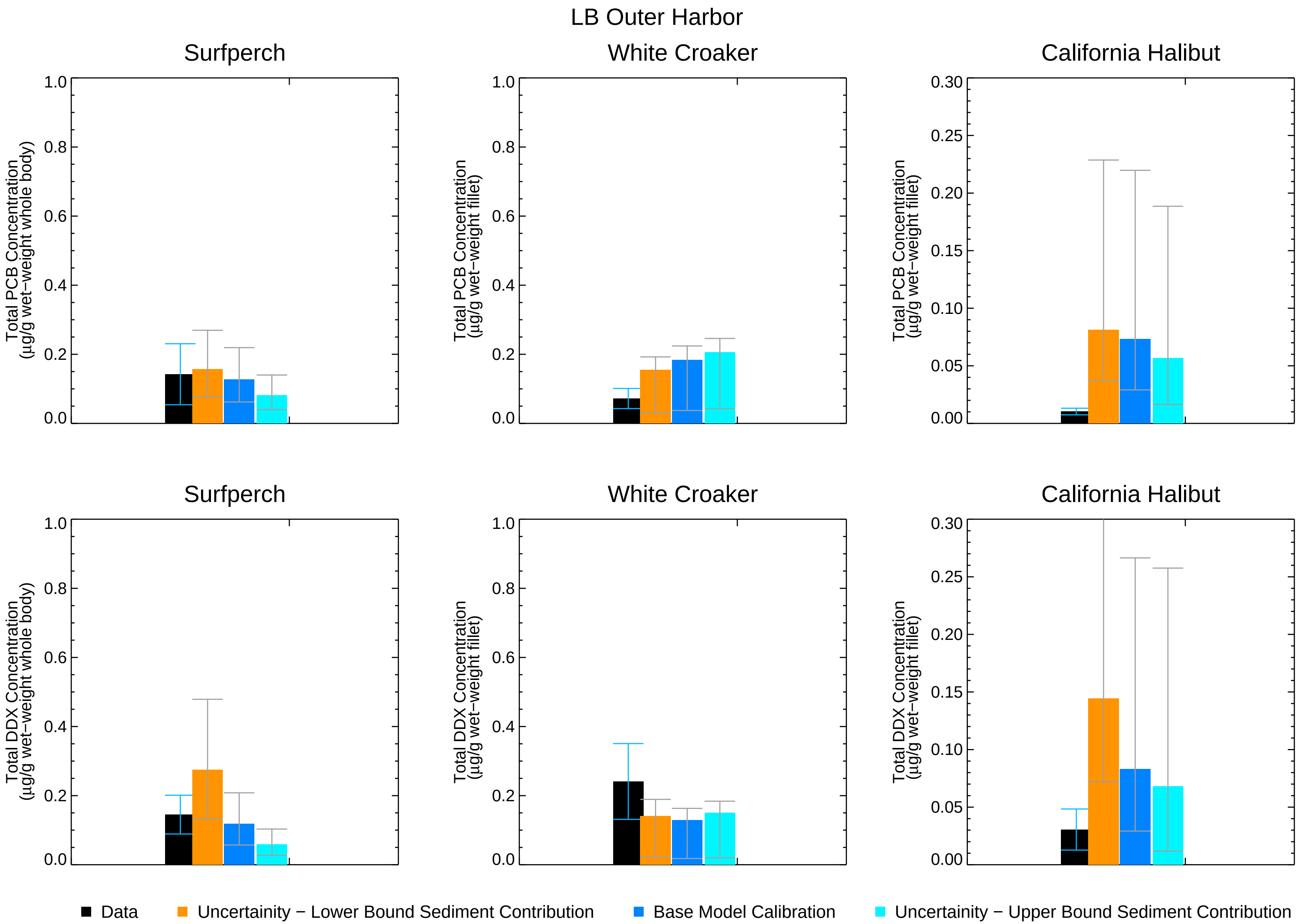

Figure 6−30i

Effects of Uncertainty Bounds (BSAF, WCPAF, Ocean Boundary) on Contaminant Concentration at LB Outer Harbor

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data represent the average and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within each year of simulation and then shown as age−weighted averages over various age classes.
WQ files v.1686, 1677, 1685 and biota files v.1728, 1727, 1729 used for model.

MM − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\fish_model_data_comparison_wMigration_byzone.pro Fri Apr 07 16:30:44 2017

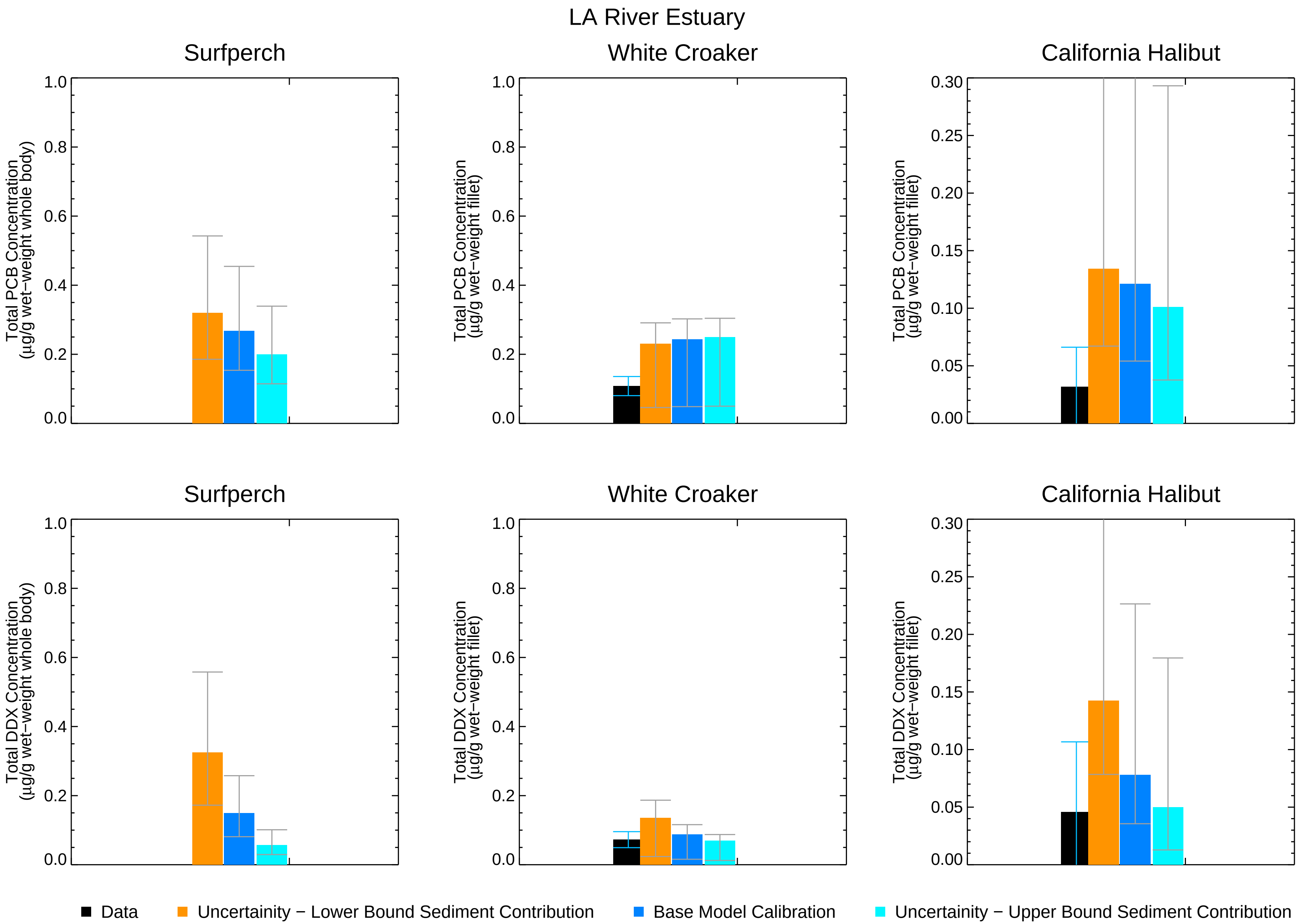

Figure 6−30j

Effects of Uncertainty Bounds (BSAF, WCPAF, Ocean Boundary) on Contaminant Concentration at LA River Estuary

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data represent the average and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within each year of simulation and then shown as age−weighted averages over various age classes.
WQ files v.1686, 1677, 1685 and biota files v.1728, 1727, 1729 used for model.

MM − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\fish_model_data_comparison_wMigration_byzone.pro Fri Apr 07 16:30:45 2017

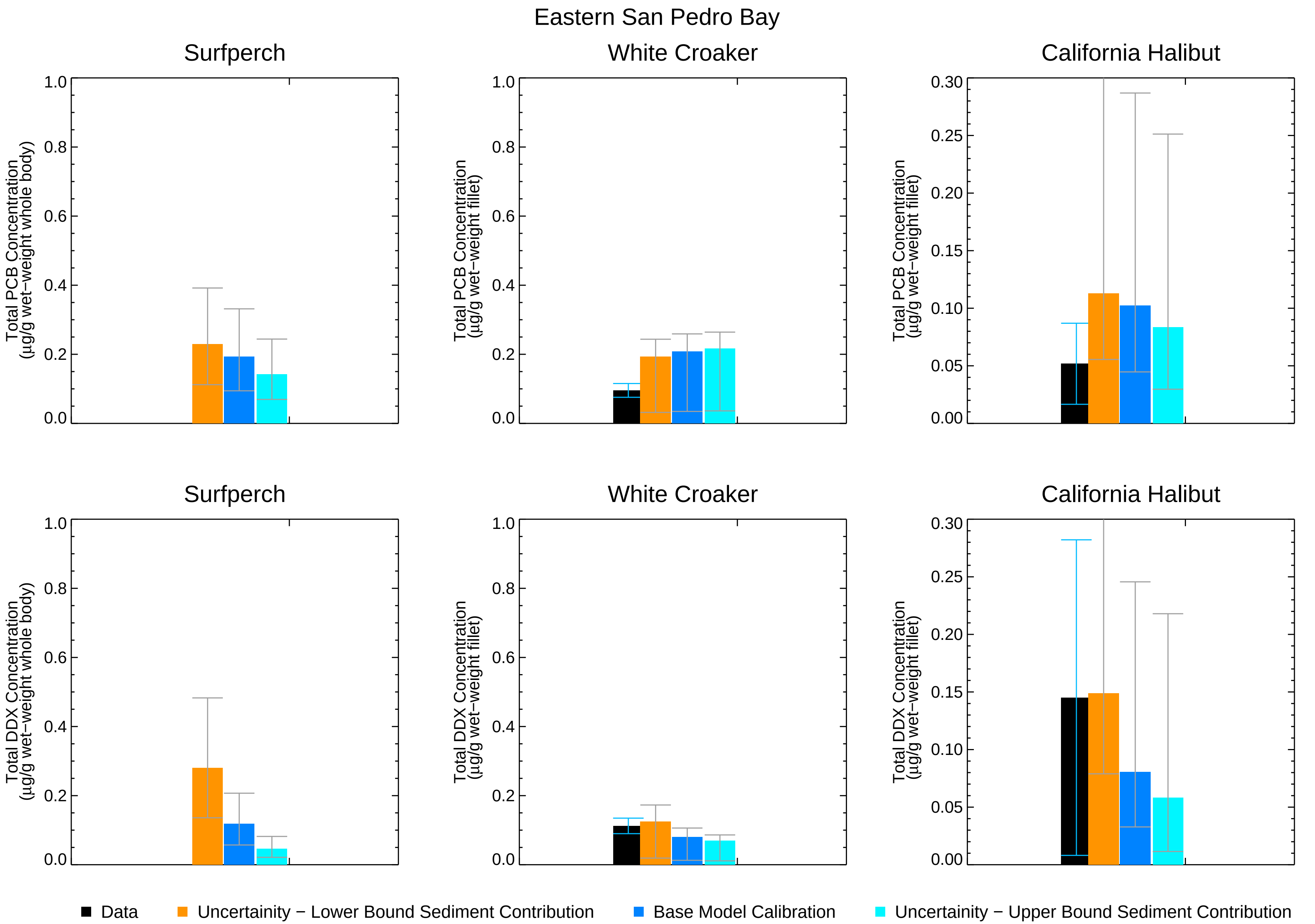

Figure 6−30k

Effects of Uncertainty Bounds (BSAF, WCPAF, Ocean Boundary) on Contaminant Concentration at Eastern San Pedro Bay

ANCHOR QEA

Subareas delineated based on white croaker movements. Data file used: PortOfLALB_Fish_20160720.xlsx.
Data represent the average and error bars show +/− 2 standard errors of the mean. Congener data shown.
Totals are calculated as sum of detected components, or half of highest detection limit if all components are non−detects.
Model results are averaged over all days within each year of simulation and then shown as age−weighted averages over various age classes.
WQ files v.1686, 1677, 1685 and biota files v.1728, 1727, 1729 used for model.

MM − \\iris\woodcliff\Projects\PoLAPoLB_TMDL_2012\2012−2015_TMDL_Contract_(120343−01)\Model\LALB\Plots\fish\fish_model_data_comparison_wMigration_byzone.pro Fri Apr 07 16:30:45 2017

APPENDIX A
SUMMARY OF HARBOR AND PALOS VERDES SHELF FISH MOVEMENT STUDIES AND ANALYSES SUPPORTING MIGRATION USED IN THE MODEL

SUMMARY OF HARBOR AND PV SHELF FISH MOVEMENT STUDIES AND ANALYSES SUPPORTING MIGRATION USED IN THE MODEL

This appendix[10] includes a complete summary of the fish tracking studies recently conducted in the Harbor and adjacent areas, a description of how movement data were used to establish FMZs for purposes of sediment contaminant exposure in the model, and a description of how fish movement patterns were quantified for different fish subpopulations.

1 Summary of Fish Tracking Studies

A CSULB team of scientists led by Dr. Chris Lowe recently completed passive fish tracking studies in the Harbor (Lowe et al. 2015a, 2015b) and on PV Shelf (Wolfe and Lowe 2015). The goals of these studies were to understand the movements of white croaker (Lowe et al. 2015a; Wolfe et al. 2015) and California halibut (Lowe et al. 2015b), as well as other fishes, and their potential exposure to sediment contaminants in San Pedro Bay, PV Shelf, and adjacent coastal areas. A brief discussion of these studies is provided below and is focused on the passive tracking studies conducted using acoustic telemetry; however, active tracking studies were also conducted as part of the CSULB investigations, and results were used qualitatively to support the understanding of fish movement patterns.

From June 2010 through December 2012, CSULB conducted a fish tracking study on behalf of USEPA in which 97 white croaker on PV Shelf were tagged and tracked using 42 receivers (Wolfe and Lowe 2015). In August 2011, CSULB initiated the first phase of a separate fish tracking study in the Harbor on behalf of the Ports. This study was conducted until August 2012 and involved tagging and tracking 99 white croaker, using 12 receivers that were placed throughout the Harbor. Due to the overlap in the timing of the Harbor study and the PV Shelf study, it was possible to track fish movement between these two areas (to a limited extent) during the duration of the study overlap period. The second phase of the Harbor tracking study was initiated in July 2013 and conducted through May 2014 and involved tagging and tracking 198 white croaker and 42 California halibut, using 38 receivers that were strategically placed for purposes of evaluating fish movement near piers, throughout the Harbor, out of the Harbor, and toward PV Shelf. The second fish tracking study was initiated after the PV Shelf tracking study had been completed; consequently, the

[10] This appendix is part of the Bioaccumulation Model Report and is not considered a standalone document.

understanding of movements of fish between San Pedro Bay and PV Shelf was limited to the receivers placed at Angels Gate, Queens Gate, and just outside the Harbor in the direction of PV Shelf. In general, for each of the passive tracking studies, stationary underwater acoustic receivers were deployed prior to tagging fish (with a few exceptions), and upon their release, the tagged fish were detected by any deployed receivers when they were within the range of the receiver (i.e., 150-meter [m] radius). On PV Shelf, a Vemco Positioning System (VPS) acoustic telemetry array was used to collect fine-scale fish movement data to better understand area use and preferences on PV Shelf in relationship to existing contamination levels. The approximate locations of fish caught and tagged in the Harbor (and PV Shelf), and the locations of underwater receivers to detect the tagged fish as part of the three CSULB tracking studies, are shown in Figure A-1.

Passive tracking data from the Harbor were compiled and processed by CSULB and were provided to the Ports in units of the number of detections per fish per day at each receiver. Similarly compiled and processed data collected as part of the USEPA PV Shelf tracking study were provided in units of total detections of tagged fish at each PV Shelf receiver.

Additional details about the methods and findings from these passive tracking studies are provided in Lowe et al. 2015a and 2015b, Ahr et al. 2015, and Wolfe and Lowe 2015.

2 Analysis of Fish Movement Data and Determination of Fish Movement Zones

Passive tracking data collected as part of the Harbor and PV Shelf tracking studies were evaluated to determine if there were apparent subpopulations of white croaker in the Harbor that had different movement patterns and site fidelities that would consequently affect their exposures to PCBs and DDX. The Harbor fish were split into subpopulations defined by their movement patterns; to support this division, the Harbor was divided into fish subpopulation areas, or FMZs. Due to differences in study design and location between fish tracking studies conducted on PV Shelf (Wolfe and Lowe 2015) relative to those conducted in the Harbor (Lowe et al. 2015a, 2015b), data analyses conducted were specific for each data type collected as part of the two programs, as described below.

3 Fish Movement Zone Determination

The extensive white croaker tracking data were used to establish FMZs. However, after establishment, the FMZs were further evaluated to determine if they were appropriate for movement of halibut and surfperches in the Harbor. The final determination of FMZs in the Harbor was based on the following steps:

1. Fish movements (measured as the number of detects per fish per day at each receiver) were evaluated by the FMZ, in which groups of fish were originally tagged to determine if there were any consistent movement patterns. Daily presence was assumed if a tagged fish was detected at least two times by a receiver on a given day.
2. For each subarea, patterns in fish movement were established for each separate phase of the Harbor fish tracking study.
3. Results of Phases 1 and 2 of the fish tracking study indicated that there were patterns in movement that were specific to different groups or subpopulations of white croaker in the Harbor. Consequently, FMZs were initially designated based on movement patterns found for different white croaker subpopulations in the first phase of the study and were then refined based on movement patterns found as part of the Phase 2 of the study.
4. To confirm the appropriateness of the designated FMZs, Harbor characteristics potentially affecting fish movement and exposure (i.e., habitat, benthic infauna abundance, fish abundance, bathymetry, grain size, total OC content, and spatial distribution of sediment PCBs and DDX) were evaluated, as described in the Data Gaps Analysis Report (Anchor QEA 2014a), and adjustments were made as appropriate. In some cases, FMZs indicated Harbor subareas identified in the Harbor Toxics TMDL as priority sites for potential management actions (i.e., Consolidated Slip and Fish Harbor), areas where few fish were detected (i.e., Seaplane Lagoon), or areas where fish were not caught and tagged (i.e., LA Inner Harbor, DCE, and LARE).

Specific changes to the original FMZs documented in the Data Gaps Analysis (Anchor QEA 2014) included the following:

- LA Outer Harbor FMZ was expanded to include an adjacent area between Piers 300 and 400 with similar chemical concentrations and water depths.

- LA Inner Harbor FMZs (formerly zones 2 and 3) were merged to create one LA Inner Harbor FMZ based on fish movement and sediment chemical concentration similarities.
- LB Outer Harbor was expanded to include the Southeast Basin (an area of similar water depth and chemical concentrations).
- LB Inner Harbor FMZ was split into two areas (which reflect different fish migration to these areas by different subpopulations of fish).
- Two FMZs (i.e., DCE FMZ and LARE FMZ) were added for purposes of evaluating estuarine and marine areas described within the Harbor Toxics TMDL.

The final FMZs used to evaluate fishes exposure to sediment and the water column as part of the bioaccumulation model are shown in Figure 2-3 and briefly described below.

DCE FMZ: The DCE FMZ is the 8.2-mile, unlined, estuarine portion of the Dominguez Channel that receives freshwater inflows from the Dominguez Channel watershed mixed with inputs of saline, tidally-influenced Harbor waters. The Harbor tracking study did not attempt to tag white croaker in this FMZ and evaluate movements; however, croaker have been caught previously in DCE (CH2M Hill 2001) and were assumed to forage there. Based on the site fidelity of other subpopulations of croaker, it is likely that fish from this FMZ spend some of their time in DCE. However, due to the connectivity with Consolidated Slip, and ephemeral wet weather conditions of DCE (during which conditions become unsuitable for white croaker due to low salinity and high turbidity [Everest 2017), it is also possible that fish move out of DCE into Consolidated Slip and at which time it is assumed their movements are similar to those of the Consolidated Slip subpopulation. The Harbor Toxics TMDL identifies DCE as a priority site for implementation of potential management actions.

Consolidated Slip FMZ: The Consolidated Slip FMZ represents the most upstream portion of LA/LB Harbor and is the area that first receives pollutant loads from the Dominguez Channel watershed. Based on an analysis of recent bathymetry data, higher sedimentation rates have been estimated in this FMZ as compared to other FMZs, suggesting that Consolidated Slip has been trapping sediments coming from DCE over time (Everest 2017). Levels of PCBs, DDTs, and other contaminants are known to be elevated in this FMZ relative to other FMZs, likely in part due to deposition of upstream sediments. Because of contaminant concentrations, the Harbor Toxics TMDL identifies Consolidated Slip as a priority site for implementation of potential management actions. White croaker tagged in Consolidated Slip demonstrated site fidelity to this subarea, with some movements to adjacent areas including LA Inner Harbor and LB Inner Harbor.

LA Inner Harbor FMZ: The LA Inner Harbor FMZ includes the main channel of LA Harbor and the area that connects Consolidated Slip with LB Inner Harbor and LA Outer Harbor. The Harbor tracking study did not attempt to tag white croaker in this FMZ and evaluate movements; however, fish movement data collected as part of both passive and active tracking studies have shown that fish may be primarily using this area as a corridor between Consolidated Slip and Inner LB Harbor or Outer LA Harbor (Lowe et al. 2015b).

Fish Harbor FMZ: The Fish Harbor FMZ is an inlet on the southwest portion of Terminal Island that was historically a hub for commercial fishing vessels and canneries. Legacy contaminants have been identified in sediments in Fish Harbor in association with historical landside and waterside activities. Consequently, the Harbor Toxics TMDL identifies Fish Harbor as a priority site for implementation of potential management actions. Fish tagged in Fish Harbor demonstrated site fidelity to this FMZ with some movements to Outer LA Harbor and outside Harbor areas.

Seaplane Lagoon FMZ: The Seaplane Lagoon FMZ includes the inlet in the middle of Terminal Island, which connects to LA Harbor via the channel that runs between Piers 300 and 400. The Seaplane Lagoon FMZ is a shallow water area with some eelgrass and poor water circulation, which differs from the adjacent LA Outer Harbor FMZ in which there are deep, well-mixed areas that are accessible by large cargo and container ships. The Harbor tracking study did not attempt to tag white croaker in this FMZ and evaluate movements. In addition, movement of croaker tagged in other FMZs indicated limited use of this FMZ. Due to the limited use of this FMZ and the connectivity with LA Outer Harbor, it is likely that Seaplane Lagoon croaker movements are similar to those of fish from LA Outer Harbor.

LA Outer Harbor FMZ: The LA Outer Harbor FMZ includes the following TMDL-designated areas (Figure 3-2): Outer Harbor (Port of Los Angeles side), Inner Cabrillo Beach, Cabrillo Marina, and the deep channel between Piers 300 and 400. Fish tagged in this FMZ demonstrated site fidelity to this subarea, with some movements to adjacent FMZs including the outside Harbor area, PV Shelf, and the LA Inner Harbor FMZ.

LB Inner Harbor North and South FMZ: Together, the LB Inner Harbor North and South FMZs include the TMDL-designated area identified as Inner Harbor that is within the jurisdiction of Port of Long Beach (Figure 2-3). Fish tagged in these FMZs demonstrated site fidelity to LB Inner Harbor North and South FMZs, with some movements to adjacent areas including LA Inner Harbor. The LB Inner Harbor was divided into two FMZs due to the different movement patterns of fish tagged in either the North or South portions of the LB Inner Harbor FMZ in the first phase of the Harbor tracking study, and their preferences for North or South portions of the LB Inner Harbor, respectively (Lowe et al. 2015a), and based on the preference for the LB Inner Harbor South FMZ by LB Outer Harbor fish in the Phase 2 of the Harbor tracking study (Lowe et al. 2015b).

LB Outer Harbor FMZ: The LB Outer Harbor FMZ includes the Southeast Basin (Figure 2-3) and the TMDL-designated area identified as Outer Harbor (Port of Long Beach side; Figure 1-1). Data are inconclusive regarding whether or not fish tagged in this FMZ demonstrate site fidelity. Receiver data suggest that these fish instead showed preference for LB Inner Harbor North and South FMZs and outside Harbor areas. However, only 4 of 25 fish tagged in this area were detected after being tagged and released, and there were limited receivers placed in LB Outer Harbor as a consequence of the shipping channel and anchorages dispersed throughout the area. Based on the site fidelity of other subpopulations of croaker, it is possible that fish from this subarea spend more time in the LB Outer Harbor than the limited data indicate.

LARE FMZ: The LARE FMZ is equivalent to the TMDL-designated area identified as LARE, including the waterside area just south of West Ocean Boulevard to the convergence of Queensway Bay and Eastern San Pedro Bay (Figure 2-3). The Harbor tracking study did not attempt to tag white croaker in this FMZ and evaluate movements; however, croaker have been caught in LARE (SCCWRP 2010) and likely forage there. Based on the site fidelity of other subpopulations of croaker, it is likely that fish from this FMZ not only spend time in LARE but also spend time in Eastern San Pedro Bay, due to the connectivity with Eastern

San Pedro Bay. Consequently, it is also possible that the LARE white croaker subpopulation movements are similar to those of fish from Eastern San Pedro Bay.

Eastern San Pedro Bay FMZ: The Eastern San Pedro Bay FMZ includes the entrance channel to Pier J and the TMDL-designated area identified as San Pedro Bay that is inside the breakwater (Figure 2-3). Fish tagged in this FMZ demonstrated site fidelity to this subarea, with some movements to adjacent areas including outside Harbor areas. However, due to limited receivers in Eastern San Pedro Bay, it is unknown whether there are preferences of fish for specific subareas of Eastern San Pedro Bay.

Outside Harbor Exposure Area: In addition to the Harbor and PV Shelf FMZs, fish movement data from the Phase 2 Harbor tracking study showed numerous detections of fish at Angels Gate and Queens Gate. Lowe et al. (2015b) found that white croaker detected at either gate demonstrated very few subsequent detections, indicating that the fish likely had left the Harbor. Consequently, outside Harbor exposure was assumed for fish with detections at Angels Gate or Queens Gate receivers. The area that represents the outside Harbor exposure area covers a portion of the area outside the Harbor that is part of the WRAP model grid.

Palos Verdes Shelf FMZs: While the PV Shelf white croaker population is not directly evaluated in the Harbor bioaccumulation model, exposure to PV Shelf sediments occurs through migration of Harbor croaker and halibut to PV Shelf; therefore, there was a need to characterize the PV Shelf exposure area. White croaker movement data from the USEPA-funded PV Shelf tracking study (Wolfe and Lowe 2015) were used to establish the PCB/DDX exposure area for Harbor subpopulations migrating to PV Shelf. PV Shelf white croaker patterns were quantified by evaluating all PV Shelf fish movement data (i.e., including measured movements to the Harbor gates) and by evaluating white croaker movements solely on PV Shelf (i.e., excluding measured movements to the Harbor gates). The former was used to understand the proportion of detections of tagged fish in the vicinity of the Harbor, while the latter was used to allocate exposures of Harbor fish among PV Shelf FMZs for fish that migrate to PV Shelf.

The relative use of habitat near each receiver (within different PV Shelf areas or at Harbor gates) was calculated as the average detections per fish per receiver. These data were evaluated in conjunction with spatial sediment contaminant concentrations and bathymetry to establish PV Shelf movement zones. Fine-scale movement patterns (provided by CSULB) based on VPS-rendered locations were also qualitatively considered in this evaluation and are described by Wolfe and Lowe (2015).

Four PV Shelf FMZs were designated based on fish movement patterns and the spatial distribution of DDX and PCB concentrations on PV Shelf; water depth was also evaluated as part of FMZ determination. Figure 4-12 shows the final PV Shelf FMZs compared with the average detects per fish per receiver within each PV Shelf FMZ. PVS1 includes the area that is used to the greatest extent by white croaker on PV Shelf (i.e., with the highest average detections per fish per day per receiver) and with water depths ranging from 20 to 45 m. PVS2 is an area also used by white croaker (with the second highest average detections per fish per receiver) but to a lesser extent than PVS1; water depths in PVS2 range from 45 to 80 m. PVS3 and PVS4 are the areas that border PVS1 and PVS2 to the northwest and southeast, respectively, with lower detections of tagged fish. The PVS4 boundary ends at the western boundary of the WRAP model grid because sediment data to the east of the boundary were already included in the WRAP model initial conditions of sediment concentrations (Section 4.3.3).

Figure 4-10 shows the average proportion of detections of white croaker in each PV Shelf FMZ (including the Harbor gates as an FMZ). Table 4-13 presents the average proportion of detections of white croaker in each PV Shelf FMZ, both including and excluding the Harbor gates. White croaker caught and tagged on PV Shelf were detected most often in PVS1 and PVS2 FMZs (Figure 4-10 and Table 4-13; based on Wolfe and Lowe 2015); the average proportions of detections per fish per day were 0.50 and 0.27, respectively, when the Harbor gates were included as an FMZ and 0.52 and 0.28, respectively, when the Harbor gates were excluded. White croaker used PVS3 and PVS4 FMZs less frequently; the average proportions of detections per fish per day were 0.08 and 0.10, respectively, when the Harbor gates were included as an FMZ, and 0.09 and 0.11, respectively, when the Harbor gates were excluded. When the Harbor gates were included as an FMZ, PV Shelf white croaker also were detected at Angels and Queens Gates with an average proportion of detections per fish per day of 0.05.

4 Quantification of Harbor Fish Movement Patterns

After FMZs were finalized, fish movement patterns of white croaker were quantified by calculating the average proportion of days fish were detected at receivers in each FMZ for each separate subpopulation of white croaker. The proportions were based on the tracking study data from Phase 2, which provided more coverage of fish movements throughout the Harbor than Phase 1 (Appendix B). Nonetheless, movement patterns were compared between Phases 1 and 2 and were determined to be similar, thereby supporting the use of the more comprehensive Phase 2 results in the quantification of movement patterns. For FMZs in which no fish were caught and tagged, fish movement was estimated based on overall movement patterns observed for white croaker in the Harbor, movement patterns observed for white croaker tagged in adjacent areas, and characteristics of the FMZ that could affect fish movement (e.g., water depths and seasonal changes in salinity).

Additional assumptions were made pertaining to exposure of fish in the estuaries. As described above, no fish were caught and tagged in DCE or LARE. Additionally, PCB and DDX tissue data in these areas are limited to a few measurements for white croaker in LARE. Given that total PCB and total DDX water column concentrations in DCE and LARE are high relative to other concentrations in the Harbor, and sediment concentrations of total PCB are relatively high in LARE, fish tissue concentrations estimated by the model for fish residing in the estuaries and exposed to these concentrations all year are unreasonably high. Thus, based on the information presented in Sections 4.3.2.1 and 4.3.2.2, fish are estimated to be resident in the estuaries for only 20% of the year (Tables 4-11 and 4-12).

California halibut movement data were similarly evaluated within and among the FMZs. The appropriateness of migrating halibut within the FMZs based on croaker data was qualitatively assessed. Based on the limited halibut tracking data available (i.e., most data were collected from movement of fish caught and tagged in Outer LA Harbor) and movement information from the literature (Section 4.3.2.2), the FMZs were determined to be appropriate because juvenile halibut showed limited migration among FMZs. In addition, based on the literature, migration distance increases with age such that by age 5 or more, adult halibut may be moving both within and outside of embayments. Based on this information, halibut data were not used to refine FMZ boundaries but were used, together with movement information from the literature (Section 4.3.2.2), to establish migration (of adult halibut) and exposure of halibut in the bioaccumulation model.

4.1 White Croaker

The movement patterns of white croaker subpopulations are summarized in Figure 4-8 and Table 4-11 and are described below by subpopulation.

DCE: Fish were not tagged in this FMZ as part of the Harbor tracking study. Based on the site fidelity of other Harbor subpopulations of croaker, it was assumed that the DCE white croaker subpopulation spends some time in DCE (0.2 proportion of time). In addition, due to the connectivity with Consolidated Slip and ephemeral wet weather conditions of DCE (in which salinity drops to zero and the water becomes turbid for short periods of time [Everest 2017]), it was also assumed that during the wet season, fish move out of DCE for 80% of the year. DCE white croaker movement patterns were assumed to be similar to those from Consolidated Slip.

Consolidated Slip: White croaker caught and tagged in Consolidated Slip were detected most frequently in the Consolidated Slip and LA Inner Harbor FMZs, with average proportions of days detected at 0.61 and 0.36, respectively (Figure 4-8 and Table 4-11). Consolidated Slip croaker were also detected less frequently in LB Inner Harbor North (proportion of days fish were detected was 0.03), and very rarely (proportion of days detected was less than 0.002) in Outer LA Harbor, outside Harbor areas[11], PV Shelf[12], and LB Inner Harbor South FMZs.

LA Inner Harbor: Fish were not caught and tagged in this FMZ as part of the Harbor tracking study. However, fish movement data collected as part of both passive and active tracking studies have shown that fish may be primarily using this area as a corridor between Consolidated Slip and LA Outer Harbor (Lowe et al. 2015b). The proportion of time that LA Inner Harbor fish were estimated to spend in different fish movement areas was based on averaged fish movement results for the Consolidated Slip and LA Outer Harbor white croaker (Table 4-11).

[11] Detections at the Angels Gate and/or Queens Gate were assumed to indicate fish that left the Harbor via the gates and were exposed to outside Harbor areas.

[12] Detections at the receivers placed outside of the Angels Gate on route to PV Shelf were assumed to indicate exposure of fish in PV Shelf FMZs.

Fish Harbor: On average, white croaker initially caught and tagged in Fish Harbor were detected most frequently in the Fish Harbor FMZ and the outside Harbor area, with the proportions of days detected of 0.82 and 0.11, respectively (Figure 4-8 and Table 4-11). Fish Harbor croaker were also detected less frequently in LA Outer Harbor and PV Shelf (proportion of days detected was 0.05 and 0.01, respectively), and very rarely (proportion of days detected was less than 0.004) in LA Inner Harbor, LB Inner Harbor North and South, Seaplane Lagoon, and Eastern San Pedro Bay FMZs.

Seaplane Lagoon: Fish were not tagged in this FMZ as part of the Harbor tracking study. White croaker tagged in other FMZs showed limited detections (i.e., movement into Seaplane Lagoon) possibly due to the poor water circulation and low oxygen levels in portions of this FMZ. Due to the limited movement of croaker into this FMZ and the connectivity with LA Outer Harbor, it was assumed that fish movements are equivalent to those of fish from LA Outer Harbor (Table 4-11).

LA Outer Harbor: On average, white croaker initially caught and tagged in LA Outer Harbor FMZ were detected most frequently in LA Outer Harbor FMZ, LA Inner Harbor FMZ, and outside Harbor area, with the average proportions of days fish were detected at 0.90, 0.04, and 0.05, respectively (Figure 4-8 and Table 4-11). LA Outer Harbor croaker were also detected less frequently in Consolidated Slip (proportion of days fish were detected was 0.01) and very rarely (proportion of days fish were detected was less than 0.003) in Fish Harbor and PV Shelf FMZs.

LB Inner Harbor North: On average, white croaker initially caught and tagged in LB Inner Harbor North were detected most frequently in the LB Inner Harbor North and LB Inner Harbor South FMZs, with the proportions of days detected of 0.72 and 0.14, respectively (Figure 4-10 and Table 4-13). LB Inner Harbor croaker were also detected less frequently in LA Inner Harbor, LA Outer Harbor, Consolidated Slip, LB Outer Harbor, Fish Harbor, and outside Harbor areas (proportions of days detected were 0.06, 0.01, 0.01, 0.02, 0.02, and 0.01, respectively) and very rarely (proportion of days detected was less than 0.005) in PV Shelf FMZ.

LB Inner Harbor South: Fish were not tagged in this FMZ as part of the Phase 2 Harbor tracking study. Based on the site fidelity of other Harbor subpopulations of croaker, movement patterns of white croaker during Phase 1 of the Harbor tracking study (which showed similar movements of fish caught in LB Inner Harbor North relative to LB Inner Harbor South; Appendix B), and the proximity and connectivity with the LB Inner Harbor North FMZ, it was assumed that movement of fish in LB Inner Harbor South was equivalent to those caught and tagged in LB Inner Harbor North (Table 4-11).

LB Outer Harbor: On average, white croaker initially caught and tagged in LB Outer Harbor were detected most frequently in the LB Inner Harbor South FMZ, LB Inner Harbor North FMZ, and outside Harbor areas, with the proportions of days detected of 0.58, 0.17, and 0.25, respectively (Figure 4-8 and Table 4-11). LB Outer Harbor croaker were also detected less frequently in Seaplane Lagoon (proportions of days fish were detected was 0.01).

LARE: Fish were not tagged in this FMZ as part of the Harbor tracking study. However, based on the site fidelity of other Harbor subpopulations of croaker, it was assumed that fish from this area spend a portion of time in LARE (assumed to be 0.20). In addition, due to the connectivity with Eastern San Pedro Bay, it was also assumed that for the remainder of time, fish movements are similar to those of fish from Eastern San Pedro Bay (Table 4-11).

Eastern San Pedro Bay: On average, white croaker initially caught and tagged in Eastern San Pedro Bay were detected most frequently in the Eastern San Pedro Bay FMZ, with the proportion of days detected of 0.96 (Figure 4-8 and Table 4-11). Eastern San Pedro Bay croaker were also detected less frequently in outside Harbor areas and LB Outer Harbor (proportions of days fish were detected were 0.03 and 0.01, respectively).

Movements of Croaker Between Harbor and PV Shelf: Both the Harbor tracking study and PV Shelf tracking study measured some movement of croaker between the Harbor and PV Shelf (Figures 4-8 and 4-10). As part of the Phase 2 Harbor tracking study, the average proportion of days fish were detected at PV Shelf (Figure A-1) was 0.003 for all fish tagged in the study; one subpopulation of croaker (Fish Harbor) was detected at a higher frequency at PV Shelf (0.01). These results suggest that there is some movement to PV Shelf, but due to the limited number of receivers along the corridor to PV Shelf and the lack of receivers on PV Shelf at the time the Harbor Phase 2 tracking study was conducted, there is some uncertainty regarding the proportion of fish movement to PV Shelf from the Harbor.

Additional support for movement of fish between the Harbor and PV Shelf was provided as part of the PV Shelf tracking study. During the period of overlap between the PV Shelf and Phase 1 Harbor tracking studies, 47% of the fish tagged on PV Shelf were observed at Angel's Gate or Queen's Gate (Wolfe and Lowe 2015). Taking into account the number of fish and the frequency of detection, as indicated above, the overall average proportion of fish detected per day at the Harbor gates by fish tagged on PV Shelf was 0.05. Wolfe and Lowe (2015) also found that 4% of the fish tagged (which equates to four fish) were detected at one or more receivers in the LA main channel during the period in which the PV Shelf tracking study was conducted. Together, these findings suggest that a small proportion of fish caught in the Harbor have been exposed to sediment on PV Shelf; however, due to the lack of complete overlap between the tracking studies, the proportion of PV Shelf exposure for Harbor fish is uncertain. This was considered further during model calibration (see Section 5.1.3).

4.2 California Halibut

A summary of halibut movement results is provided in Table 4-12 and Figure 4-9. The evaluation of halibut movement within the Harbor and outside was limited by the number of halibut that were caught and tagged in this study and the locations in which fish were caught. Of the 42 halibut tagged in the Harbor, 28 were caught and tagged in LA Outer Harbor and 6 were tagged near Pier J (in Eastern San Pedro Bay). Fewer than 3 fish were caught, tagged, and subsequently detected by any receiver in Consolidated Slip (4 fish tagged and 3 detected), LA Outer Harbor (2 fish tagged and detected), LB Inner Harbor North (2 fish tagged and detected), and LB Outer Harbor (2 fish tagged and detected) FMZs. Despite much effort, no halibut were caught and tagged in any other FMZ (i.e., LB Inner Harbor South, Seaplane Lagoon, LA Inner Harbor, Fish Harbor, DCE, LARE, or PV Shelf FMZs). Movement patterns were determined for two specific FMZs, LA Outer Harbor and Eastern San Pedro Bay, in which there were sufficient data to quantify movements. Due to the limited information available in the remaining FMZs, estimates of movement patterns for fish in these areas were not determined. However, a whole Harbor exposure estimate was calculated using all halibut passive tracking data to provide an estimate for adult halibut that migrate into the Harbor seasonally, as described below, and potentially use the whole Harbor as habitat during this time.

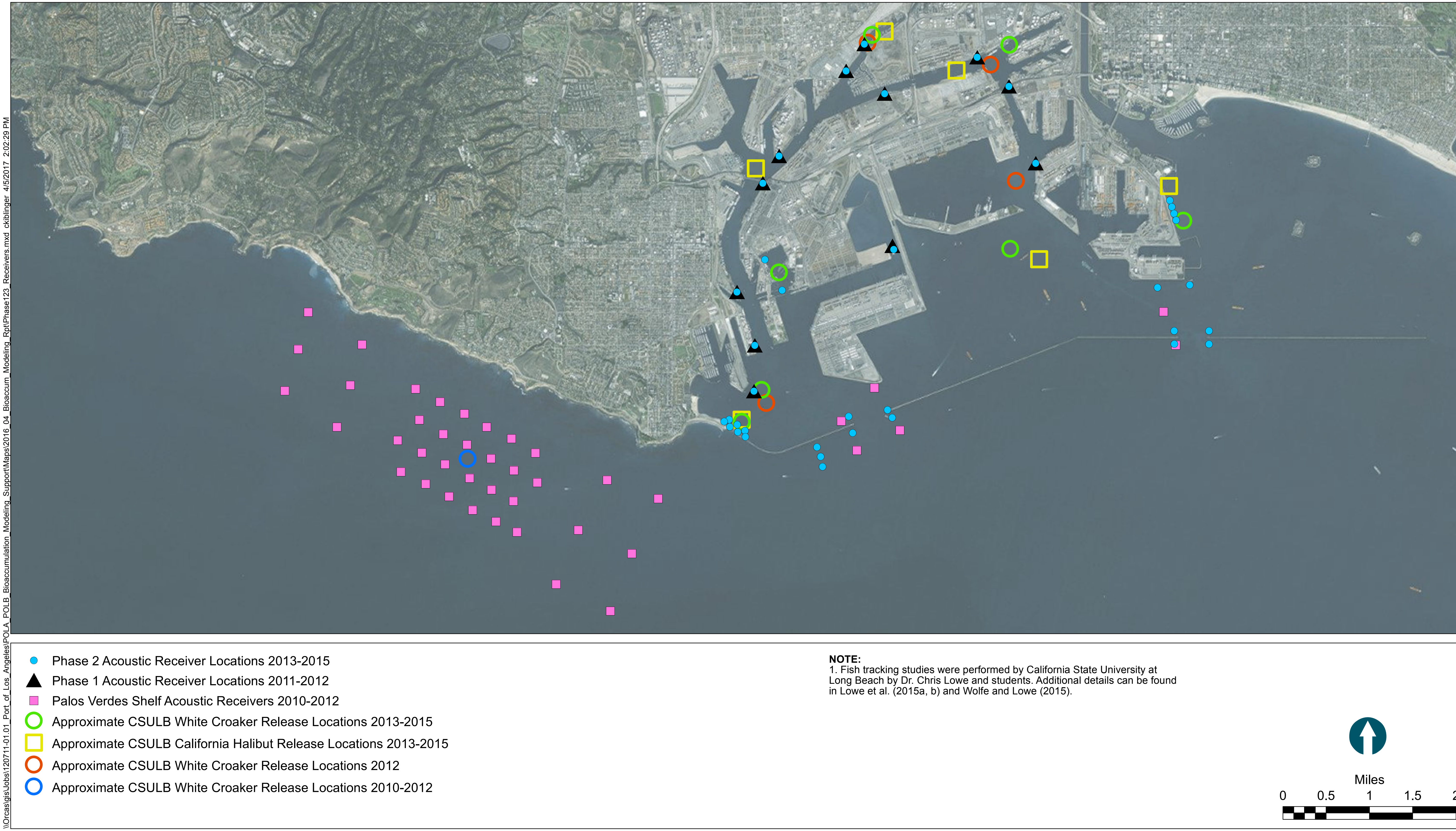

Figure A-1
Acoustic Receiver Locations and Approximate Tag and Release Locations of Fish from CSULB Fish Tracking Studies
Bioaccumulation Modeling Report
Greater Los Angeles and Long Beach Harbor Waters

APPENDIX B
SUMMARY OF WHITE CROAKER MOVEMENT RESULTS, PHASE 1 OF THE HARBOR TRACKING STUDY

Table B-1
Proportion of Days Detected for Each White Croaker Subpopulation by Zone (Phase 1)

White Croaker Subpopulation	Fish Movement Zone Where Fish Were Detected					
	Consolidated Slip	LA Inner Harbor	LA Outer Harbor	LB Inner Harbor North	LB Inner Harbor South	Eastern San Pedro Bay
Consolidated Slip	0.42	0.51	0.004	0.07	0.003	0.0003
LA Outer Harbor	0.001	0.33	0.67	0.00	--	0.004
LB Inner Harbor North	0.06	0.22	0.0002	0.48	0.23	--
LB Inner Harbor South	0.02	0.05	0.001	0.12	0.81	0.004

Notes:

-- = not detected

LA = Los Angeles

LB = Long Beach

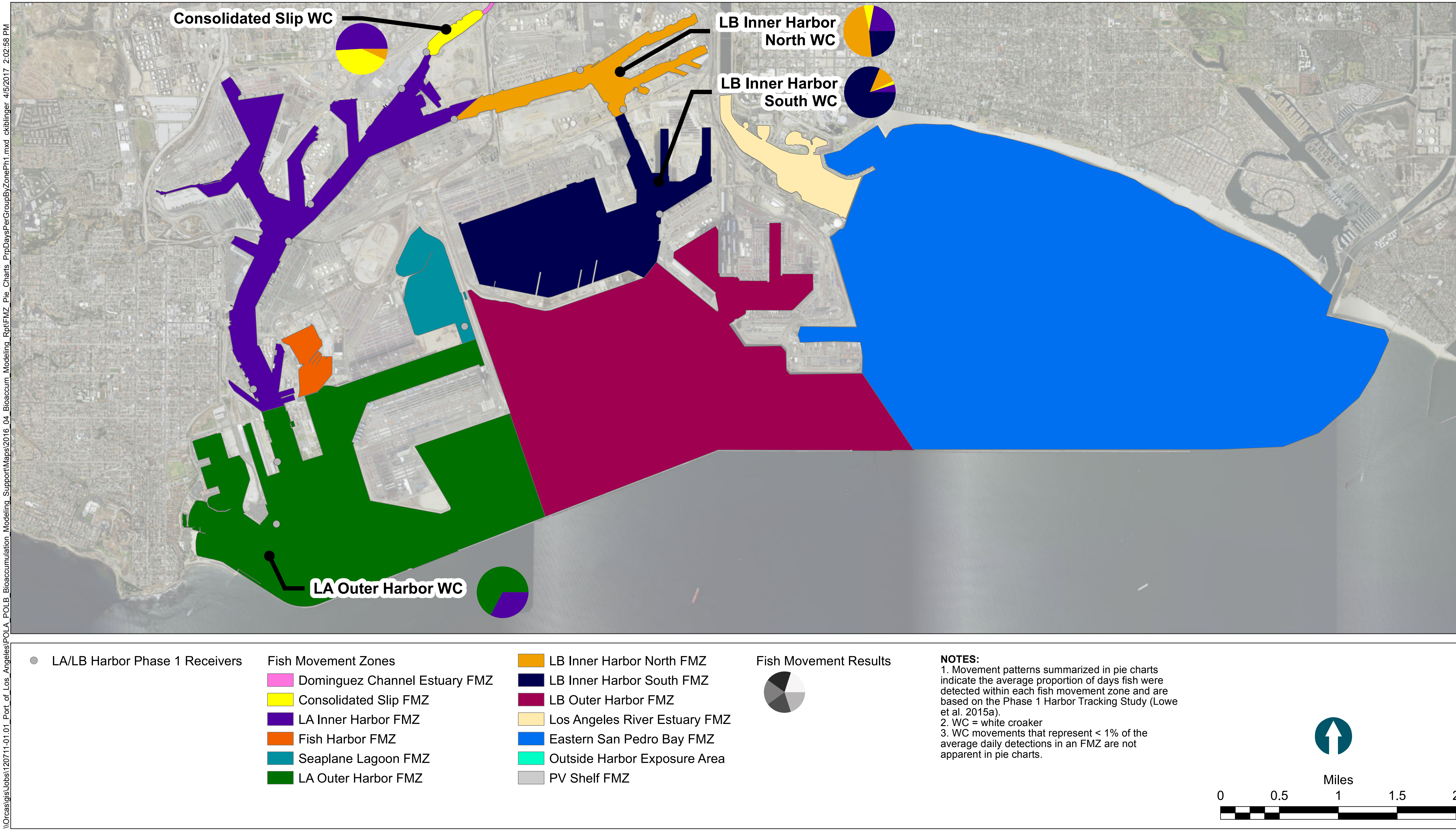

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Figure B-1
Phase 1 Harbor Tracking Study Fish Movement Results
Bioaccumulation Modeling Report
Greater Los Angeles and Long Beach Harbor Waters

APPENDIX C
CALCULATION OF PARTICULATE WATER COLUMN PCB AND DDX CONCENTRATIONS

CALCULATION OF PARTICULATE WATER COLUMN PCBS AND DDX

In spring 2014, the Ports performed Event 1 of a low detection limit water column study in which three sampling methods (i.e., SPME, high volume [HV] sampling, and grab sampling) were used along with high-resolution gas chromatography/mass spectrometry (i.e., USEPA Methods 1668 and 1699 for PCBs and DDX, respectively) to measure ultra low concentrations of PCBs and DDX in the water column[13]. SPMEs were deployed for 32 to 34 days at five locations, and both high volume and grab samples were collected at the end of the deployment period. Collected grab samples were analyzed for PCBs, DDX, and particulate organic carbon (POC).

For each location, partition coefficients were calculated from paired particulate, high volume ($C_{part,HV}$) and freely dissolved SPME ($C_{diss,SPME}$) samples as follows:

$$K_{POC} = \frac{C_{part,HV} / C_{diss,SPME}}{POC} \qquad (1)$$

where:

K_{POC} = partition coefficient between particulate (POC-bound) and freely dissolved phases (L/kg)

$C_{part,HV}$ = water column particulate (i.e., POC-bound) concentrations of PCBs or DDX (nanograms per liter [ng/L])

$C_{diss,SPME}$ = freely dissolved water column concentrations of PCBs or DDX (ng/L)

POC = particulate organic carbon concentration (kg/L)

These site-specific partition coefficients were used to estimate water column particulate concentrations (C_{part}) based on SPME freely dissolved (C_{diss}) PCB and DDX concentration, POC, and total suspended solids data collected as part of three separate SPME sampling events (in which five to nine stations were sampled across the Harbor) as follows:

[13] Presentation to the Harbor Technical Working Group. Low Detection Limit Water Column Method Development Study. Presented by Anchor QEA (Wendy Hovel, Xiaoxia Lu, Joy Dunay, David Glaser, Elaine Darby, and Dan Opdyke). July 24, 2014.

$$C_{part} = \frac{C_{diss,SPME} \times K_{POC} \times POC}{TSS} \qquad (2)$$

where:

C_{part} = water column particulate (i.e., POC-bound) concentrations of PCBs or DDX (mass chemical/mass dry weight)

$C_{diss,SPME}$ = freely dissolved water column concentrations of PCBs or DDX (ng/L)

K_{POC} = partition coefficient between particulate (POC-bound) and freely dissolved phases (L/kg)

POC = particulate organic carbon concentration (Kg/L)

TSS = total suspended solids (mg/L)

APPENDIX D
DESCRIPTION OF CALIBRATION MIGRATION ADJUSTMENTS

DESCRIPTION OF CALIBRATION MIGRATION ADJUSTMENTS

Initial exposure patterns for the migrating species, California halibut and white croaker, were determined by fish tracking data (Section 4.3.1), literature (Section 4.3.1), and the fit between fish and sediment PCB and DDX concentrations. These initial exposure patterns were subsequently adjusted during calibration. Then, prior to calibration, the average concentrations of total PCB and total DDX in the fish were compared with average WRAP model sediment concentrations for each of the FMZs. Next, the average fish concentrations were compared with average WRAP model sediment concentrations that represent weighted-averages of the concentrations in each of the FMZs that the subpopulation migrates to, in proportions determined from the tracking study. The expectation is that fish and sediment concentrations should have a positive, linear relationship, given that sediment is an important exposure source. Finally, the relationship between average fish concentrations and weighted-average WRAP model sediment concentrations was improved through slight adjustments to exposure proportions of the FMZs for each fish subpopulation, resulting in improvements to the model calibration. Migration pattern adjustments affect both total PCB and total DDX; if the total PCB calibration was reasonable, then the migration adjustment focused on improving the total DDX calibration, while honoring the fish tracking data and without degrading that for total PCB.

The relationship between average total DDX concentrations in white croaker to the average WRAP model surface sediment concentrations across FMZs is not strong (Figure D-1a; note that this plot assumes no migration), suggesting that exposure is not limited to the FMZ the fish were caught in. The croaker:sediment DDX relationship improves after weighting the sediment concentrations by the exposure proportions determined by the fish tracking data (Table 4-13; Figure D-1b) and improves further after adjusting the exposure area proportions (Table 5-7; Figure D-1c). The croaker:sediment total PCB relationship also improves after weighting the exposure concentrations by the proportions from the fish tracking study (Figures D-2a and D-2b); further improvements after adjusting the fish tracking study proportions (Table 5-7) are minor (Figure D-2c). As shown in Figure D-1c, average total DDX concentrations in white croaker are still high compared with the weighted average sediment concentrations for LB Outer and LB Inner Harbor North. Further adjustments were not made to the migration pattern for the fish from these areas, either because they would degrade the croaker:sediment total PCB relationship or they would not be supported by the fish tracking studies.

A similar approach to obtaining the exposure proportions was taken for California halibut (Figures D-3 and D-4). However, as discussed in Section 2.2 of Appendix A, tracking information that was sufficient for analysis was limited to LA Outer Harbor and Eastern San Pedro Bay; thus, the data analyzed for the whole Harbor were used as a starting point for the rest of the FMZs (Table 4-12). Additionally, the supplemental information discussed in Section 4.3.1 was incorporated into the California halibut migration scheme; juvenile halibut under age 5 are residential to each FMZ, and migration is limited to adults ages 5 and older, with halibut from all FMZs migrating outside the Harbor from November to February. The proportional exposure that occurs outside Harbor versus on PV Shelf was adjusted to improve the model-data comparison; final calibration exposure proportions for California halibut are shown in Table 5-8.

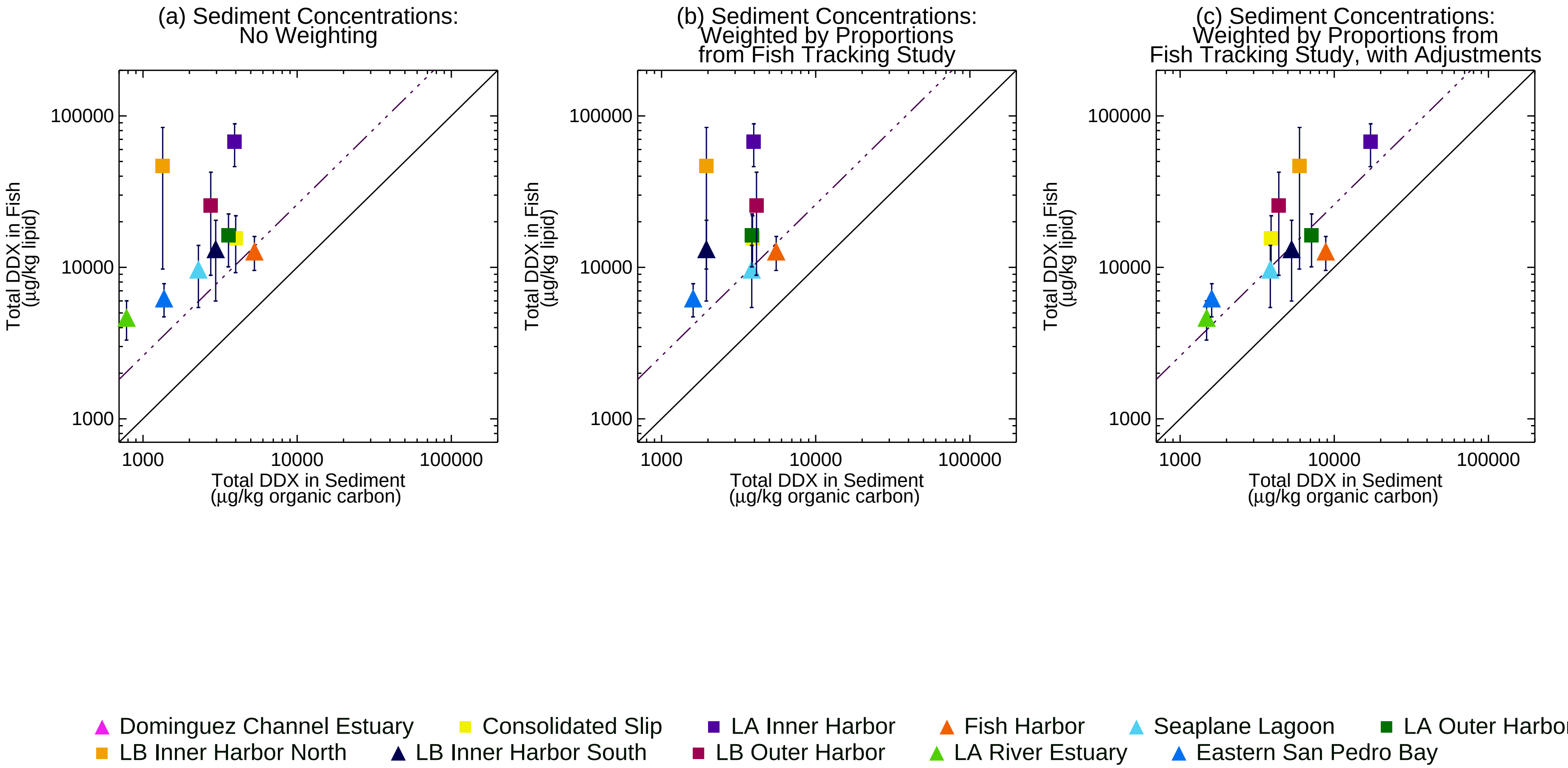

Figure D-1

Total DDX in White Croaker Versus WRAP Model Surface Sediment

Fish concentrations shown are the arithmetric averages for fish collected between 2002 and 2014.
Error bars show +/− 2 standard errors of the mean. Non−detects set to half detection limit. Tissue types include fillet (all types) and whole fish.
Surface sediment concentrations are WRAP Model averages for 2014 and 2015.
The line represent the fish:sediment (2.6:1) relationship from the Palos Verdes model.'
Fish data excluded: Cabrillo Pier (one station), IH5−FFF−7WC with low lipid (0.05%), IH1−FFF−6WC (high value).
Database exports: WRAP Model Calibration Version − 07/27/2016, PortOfLALB_Fish_20160229.xlsx

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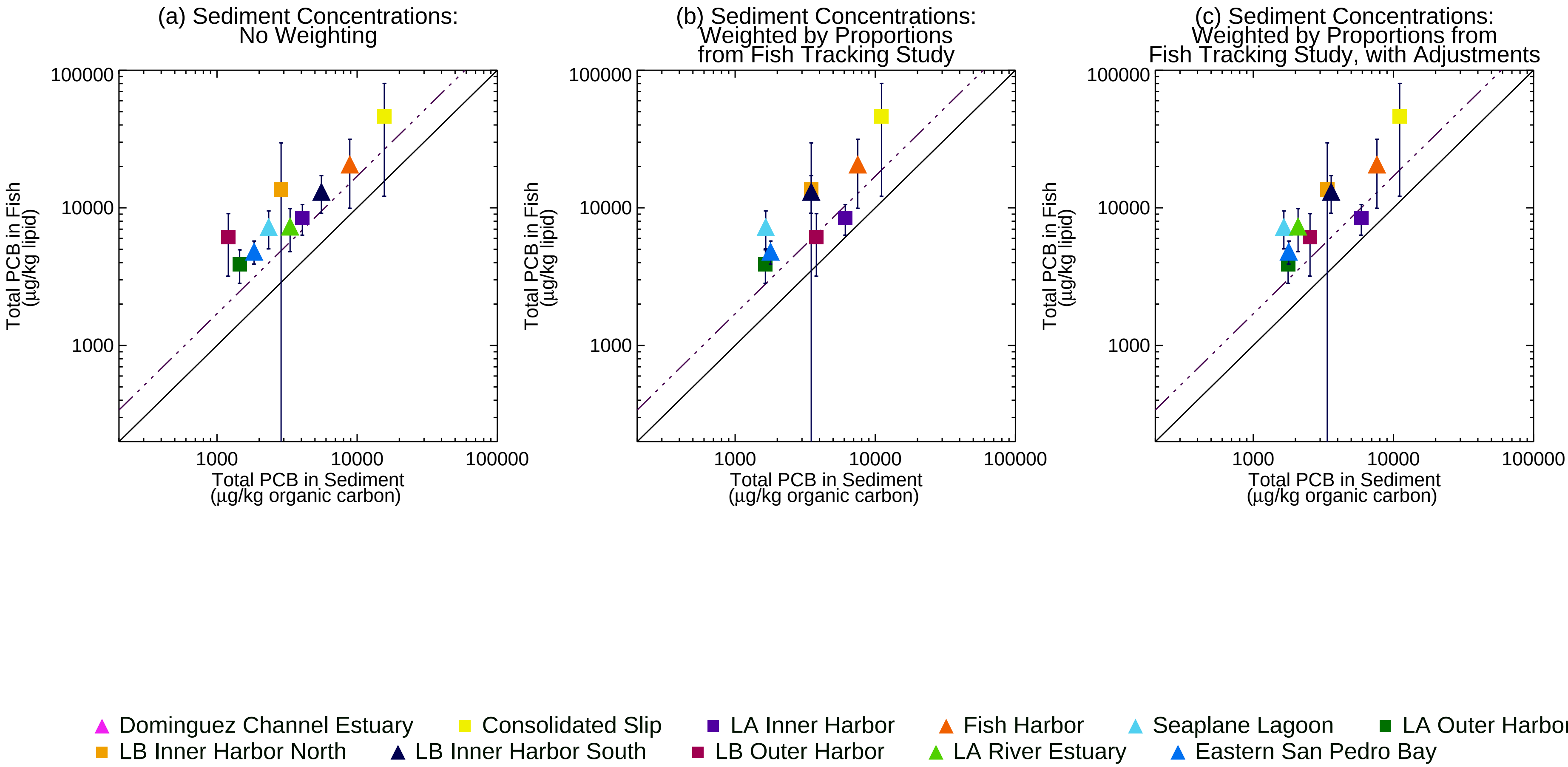

Figure D-2

Total PCB in White Croaker Versus WRAP Model Surface Sediment

Fish concentrations shown are the arithmetic averages for fish collected between 2002 and 2014.
Error bars show +/− 2 standard errors of the mean. Non−detects set to half detection limit. Tissue types include fillet (all types) and whole fish.
Surface sediment concentrations are WRAP Model averages for 2014 and 2015. High−resolution data used where paired low−resolution data exist.
The line represent the fish:sediment (1.7:1) relationship from the Palos Verdes model.
Fish data excluded: Cabrillo Pier (one station), IH5−FFF−7WC with low lipid (0.05%), IH1−FFF−6WC (high value).
Database exports: WRAP Model Calibration Version − 07/27/2016, PortOfLALB_Fish_20160229.xlsx

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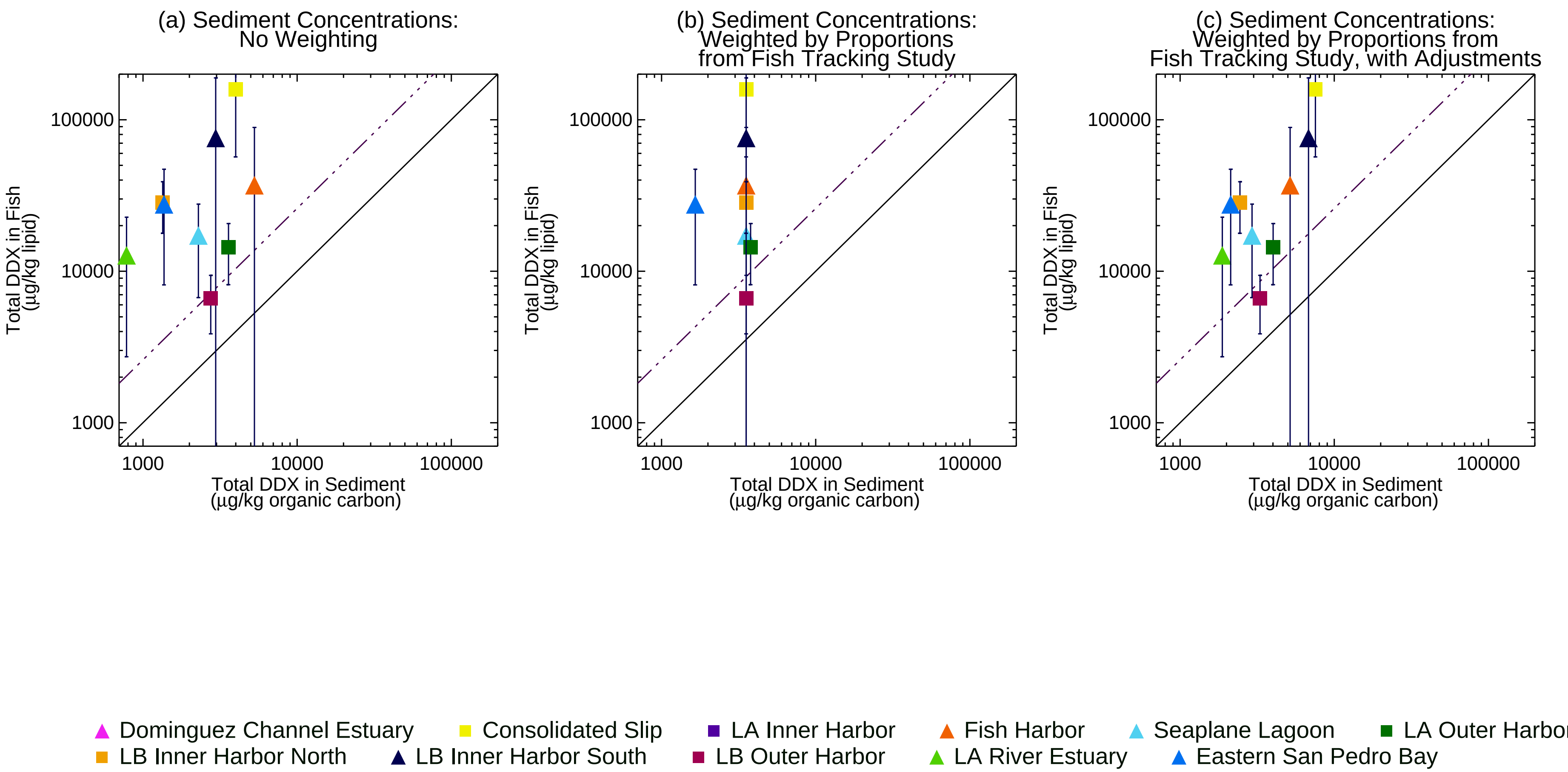

Figure D-3

Total DDX in California Halibut Versus WRAP Model Surface Sediment

Fish concentrations shown are the arithmetic averages for fish collected between 2002 and 2014.
Error bars show +/− 2 standard errors of the mean. Non−detects set to half detection limit. Tissue types include fillet (all types) and whole fish.
Surface sediment concentrations are WRAP Model averages for 2014 and 2015.
The line represent the fish:sediment (2.6:1) relationship from the Palos Verdes model.'
Fish data excluded: Cabrillo Pier (one station). California Halibut samples with non−detect lipid results are included.
Database exports: WRAP Model Calibration Version − 07/27/2016, PortOfLALB_Fish_20160229.xlsx

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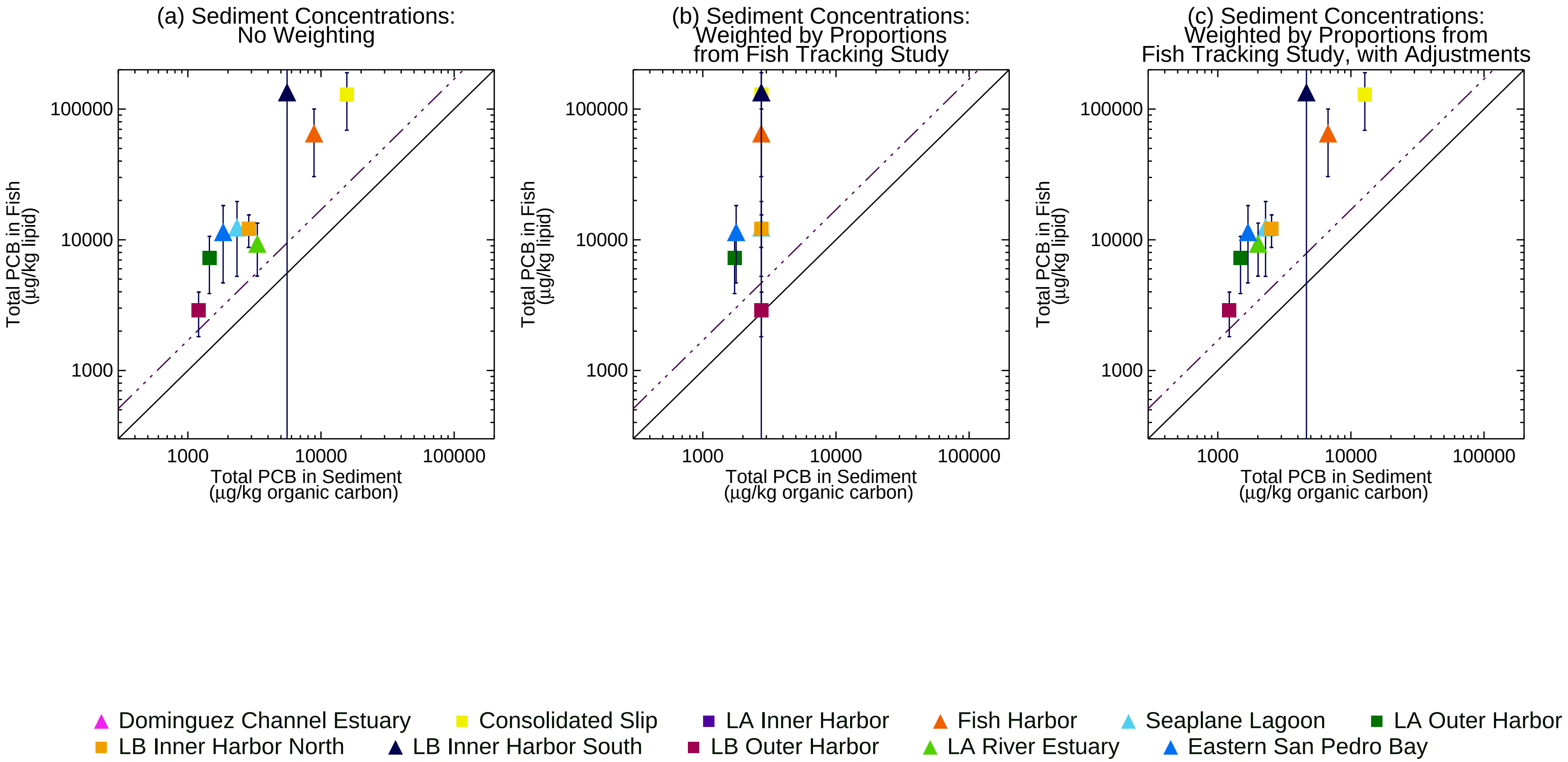

Figure D-4

Total PCB in California Halibut Versus WRAP Model Surface Sediment

Fish concentrations shown are the arithmetic averages for fish collected between 2002 and 2014.
Error bars show +/− 2 standard errors of the mean. Non−detects set to half detection limit. Tissue types include fillet (all types) and whole fish.
Surface sediment concentrations are WRAP Model averages for 2014 and 2015. High−resolution data used where paired low−resolution data exist.
The line represent the fish:sediment (1.7:1) relationship from the Palos Verdes model.
Fish data excluded: Cabrillo Pier (one station). California Halibut samples with non−detect lipid results are included.
Database exports: WRAP Model Calibration Version − 07/27/2016, PortOfLALB_Fish_20160229.xlsx

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