Draft Technical Report
for
Tentative Cleanup and Abatement
Order No. ~~R9-2011-0001~~R9-2012-0024

APPENDIX FOR SECTION 15

SUPPLEMENTAL DOCUMENTATION FOR WEIGHT OF EVIDENCE APPROACH

~~September 15, 2010~~March 14, 2012

A15.1. Pore Water Analyses

The San Diego Water Board evaluated the chemistry of pore water (the water occupying the spaces between sediment particles) to evaluate the potential of site chemicals to contribute to ecological risks. This evaluation was carried out by comparing chemical concentrations in pore water to California Toxics Rule (CTR) water quality criteria. Although CTR values are derived based on toxicity to planktonic organisms, and the chemical sensitivities of planktonic and benthic organisms may differ, this comparison provides a screening-level evaluation of which chemicals may deserve further evaluation.

Comparisons were made to the CTR saltwater quality criterion continuous concentration, which is the highest concentration of a pollutant to which marine aquatic life can be exposed for an extended period of time without deleterious effects. Of the 12 site stations sampled for pore water (SW02 was excluded due to the presence of some suspended material remaining after centrifugation), 12 stations exceeded the copper CTR value, 6 stations exceeded the lead CTR value, and 12 stations exceeded the total PCBs CTR value. Although the comparisons to the CTR criteria identified several pollutants for which measured pore water concentrations are above levels of concern, the measured pore water concentrations may be biased high due to the possible presence of very fine suspended or colloidal material in the pore water samples that could not be removed by centrifugation.

A15.1.1. Pore Water

Pore water, the water occupying the spaces between sediment particles, was evaluated to determine compliance with CTR water quality criteria and the potential risks to the benthic community from chemical pollutants present in the sediment at the Shipyard Sediment Site. Pore water is considered one of several key exposure routes for contaminants to benthic organisms associated with sediment (Chapman et al., 2001; U.S. EPA, 1994). Other routes of exposure include sediment ingestion and overlying water. A key advantage of analyzing pore water is that the measured concentrations can be compared to water quality criteria to identify potential risks to the benthic community. A direct comparison can be made between pore water concentrations and water quality criteria because available data suggest that benthic species may exhibit the same sensitivity to chemical pollutants as water column species that were tested to derive water quality criteria (U.S. EPA, 2003b, 2005b).

Pore water was collected at a total of 13 stations at the Shipyard Sediment Site (Exponent 2001a). The measured pore water concentrations at these stations were compared to water quality criteria established in the CTR (U.S. EPA, 2000a) in 40 CFR 131.38. The CTR water quality criteria are applicable as water quality objectives[1] in California's inland surface waters, enclosed bays, and estuaries. Pore water chemical pollutant concentration excursions to levels above the CTR water quality criteria resulting from waste discharges represents a condition of

[1] "Water quality objectives" are defined in Water Code section 13050(h) as "the limits or levels water quality constituents or characteristics which are established for the reasonable protection of beneficial uses of water or the prevention of nuisance within a specific area."

condition of pollution[2] in waters of the state. This pollution condition would provide a basis for issuance of a cleanup and abatement order under CWC section 13304.[3]

Comparisons were made to the saltwater CCC, which is the highest concentration of a chemical pollutant to which marine aquatic life can be exposed for an extended period of time without deleterious effects (Table A15-1) (Exponent, 2003). Of the 12 Shipyard Sediment Site stations sampled for pore water (SW02 was excluded by Exponent due to the presence of some suspended material remaining after centrifugation), 12 stations exceeded the copper CTR value, 6 stations exceeded the lead CTR value, and 12 stations exceeded the total PCBs CTR value (Table A15-2).

Table A15-1 Water Quality Criteria Established in the California Toxics Rule

Compound	Saltwater Criterion Continuous Concentration (µg/L)
Arsenic	36
Cadmium	9.3
Chromium (VI)	50
Copper	3.1
Lead	8.1
Nickel	8.2
Selenium	71
Zinc	81
Total Polychlorinated Biphenyls[1]	0.03

1. Sum of aroclors 1242, 1254, 1221, 1232, 1248, 1260, and 1016.

2 "Pollution" is defined in Water Code section 13050 (1) as "an alteration of the quality of the waters of the state by waste to a degree which unreasonably affects either of the following: (A) The waters for beneficial uses, (B) Facilities which serve these beneficial uses." "Pollution" may include "contamination."

3 Water Code section 13304 contains the cleanup and abatement authority of the Regional Board. Section 13304(a) provides in relevant part that the Regional Board may issue a cleanup and abatement order to any person "who has discharged or discharges waste into the waters of this state in violation of any waste discharge requirements… ...or who has caused or permitted, causes or permits, or threatens to cause or permit any waste to be discharged or deposited where it is, or probably will be, discharged into the waters of the state and creates, or threatens to create, a condition of pollution or nuisance…"

Table A15-2 Comparison of Shipyard Pore Water Concentrations to CTR Water Quality Criteria

	Metals and PCBs (µg/L)								
Station	**As**	**Cd**	**Cr (VI)**	**Cu**	**Pb**	**Ni**	**Se**	**Zn**	**Total PCBs (Sum of Homologs)**
NA01	19	0.05	25	**14**	5.2	2.3	5.2	23	**0.068**
NA06	9.1	0.05	25	**33**	**12**	2.2	2.5	44	**0.20**
NA13	12	0.05	25	**14**	6.5	2.5	2.5	30	**0.056**
NA16	17	0.05	25	**22**	**9**	2.7	2.5	33	**0.094**
NA17	20	0.05	25	**23**	7	2.9	2.5	32	**0.084**
SW01	6.1	0.05	25	**17**	6.6	3	2.5	22	**0.50**
SW02 (outlier)	(11)	(4.2)	(25)	**(390)**	**(120)**	(37)	(6.1)	**(610)**	**(16)**
SW04	15	0.05	25	**55**	**20**	3.3	2.5	60	**0.60**
SW08	9.9	0.05	25	**33**	**12**	2	2.5	34	**0.52**
SW12	19	0.05	25	**17**	7.1	2.8	2.5	32	**0.08**
SW24	10	0.05	25	**25**	**9.8**	2.6	2.5	37	**0.67**
SW25	17	0.05	25	**28**	**13**	2.9	2.5	42	**.018**
SW28	9	0.05	25	**19**	7.5	2.4	2.5	31	**0.29**

Note: Boxed and shaded values for shipyard locations exceed CTR water quality criteria.

Although the CTR criteria identified several chemical pollutants for which measured pore water concentrations are above maximum allowable CTR levels, the measured pore water concentrations may be biased high due to the possible presence of very fine suspended or colloidal material in the pore water samples that were not removed by centrifugation (Exponent, 2003). The pore water samples collected at the Shipyard Sediment Site were not filtered, in accordance with U.S. EPA guidance (U.S. EPA, 2001b), and were reported as total concentrations, whereas the CTR values are filtered and are reported as dissolved concentrations. However, the pore water results exceed the CTR criteria by multiples ranging from 1.1 to 20, excluding the results for SW02, as indicated in Table A15-3. Based on the magnitude of these exceedances, it is judged that the accumulation of pollutants in the Shipyard sediment has caused the pore water chemical pollutant concentrations to exceed the CTR water quality criteria. These exceedances represent a condition of pollution in waters of the state.

Table A15-3 Pore Water Concentrations as Multiples of CTR Water Quality Criteria

	Metals and PCBs (µg/L)								
Station	**As**	**Cd**	**Cr (VI)**	**Cu**	**Pb**	**Ni**	**Se**	**Zn**	**Total PCBs (Sum of Homologs)**
NA01	NA	NA	NA	**5**	NA	NA	NA	NA	**2**
NA06	NA	NA	NA	**11**	**15**	NA	NA	NA	**7**
NA13	NA	NA	NA	**5**	NA	NA	NA	NA	**2**
NA16	NA	NA	NA	**7**	**1.1**	NA	NA	NA	**3**
NA17	NA	NA	NA	**7**	NA	NA	NA	NA	**3**
SW01	NA	NA	NA	**5**	NA	NA	NA	NA	**17**
SW02 (outlier)	NA	NA	NA	**(126)**	**(15)**	NA	NA	**(8)**	**(533)**
SW04	NA	NA	NA	**18**	**2**	NA	NA	NA	**20**
SW08	NA	NA	NA	**11**	**1.5**	NA	NA	NA	**17**
SW12	NA	NA	NA	**5**	NA	NA	NA	NA	**3**
SW24	NA	NA	NA	**8**	**12**	NA	NA	NA	**22**
SW25	NA	NA	NA	**9**	**2**	NA	NA	NA	**6**
SW28	NA	NA	NA	**6**	NA	NA	NA	NA	**10**

1. NA = Not applicable because the pore water concentration is below the CTR water quality criteria.

A15.2. Fish Histopathology Analyses

The San Diego Water Board evaluated fish histopathology data to determine the potential exposure and associated adverse effects on fish from chemical pollutants present within and adjacent to the Shipyard Sediment Site. A total of 253 spotted sand bass were examined for various histopathological lesions. These spotted sand bass were collected from four discrete assessment units at the Shipyard Sediment Site and at a reference area located across San Diego Bay near Reference Station 2240. The fish histopathology data indicates a total of 70 types of histopathological lesions were found in the spotted sand bass. Of the 70 types of lesions found, five lesions that exhibited statistically significant elevations relative to reference conditions. The five lesions are abundant lipofuscin in liver, abundant hemosiderin in liver, cholangitis/biliary hyperplasia (CBH) in liver, nephritis in kidney, and shiny gill foci. A sixth lesion (i.e., foci of cellular alteration in livers) was considered important even though no statistical differences were found because the existence of these lesions indicates a harmful effect strongly linked to PAH exposure. Of the six lesions identified as significantly elevated with respect to reference conditions, two lesions, CBH and foci of cellular alteration, have been identified as being associated with contaminant exposure. There were also six lesions types that were significantly elevated in reference area fish, relative to shipyard area fish. Scientific literature describing

lesions that are potential biomarkers of environmental stressors in fish does not attribute causation of lipofuscin, hemosiderin, nephritis, and shiy gill foci to pollution-related factors. It is plausible that the lesions could have been caused by naturally occurring environmental factors such as infectious parasites. Based on these considerations the fish histopathology data does not indicate that the fish lesions observed in the data set can be conclusively attributed to contaminant exposure at the Shipyard Sediment Site.

A15.2.1. Fish Histopathology Analyses

The Phase 1 sediment chemistry and bioaccumulation data indicated the potential for aquatic life impacts from elevated levels of contaminants in the sediment at the Shipyard Sediment Site. The sediment chemistry exceeded published threshold values for PAHs and PCBs therefore it was deemed necessary to assess the impacts on aquatic life from the contaminated sediment at the Shipyard Sediment Site through fish histopathology[4] analyses.

By letter dated July 16, 2002, the San Diego Water Board directed NASSCO and BAE Systems, pursuant to WC 13267, to investigate the potential for contaminant bioaccumulation in fish and the associated risks to fish health from the Shipyard Sediment Site and adjacent areas and to document the results in a technical report. The rationale and general guidelines for the fish histopathology investigation are provided in the July 16, 2002 letter (RWQCB, 2002a). The San Diego Water Board consulted with the Natural Resource Trust Agencies (NRTAs) (U.S. FWS, DFG, NOAA, and OEHHA) to determine the study guidelines. The study was conducted in accordance with their recommendations.

PAHs and PCBs were of concern because the sediment concentrations indicated levels that exceeded published literature values and were potentially harmful to marine/estuarine fish within the Shipyard Investigation Site. PAH concentrations exceed a suggested sediment quality threshold of 1,000 ppb for PAHs at every NASSCO and BAE Systems sample station except for the reference stations (Johnson, 2000). Furthermore, studies on chinook salmon (*Oncorhynchus tshawytscha*) resulted in a PCB threshold value of 300 ppb (for total organic carbon (TOC) at 2 percent dry weight) (Meador, 2000). Of the 43 sample locations analyzed for PCBs at NASSCO and BAE Systems, the average TOC was 2.13 percent and 38 sample locations exceeded the suggested PCB threshold.

PAHs are of particular interest because it is a common sediment contaminant found in coastal urban and industrial waterbodies and are found throughout the Shipyard Sediment Site. PAHs generally do not bioaccumulate in fish tissue like chlorinated hydrocarbons therefore exposure to PAHs cannot be assessed using traditional tissue analysis. PAH compounds are readily metabolized by the liver and secreted in the bile. While metabolism of these compounds serves as a way of breaking down and then excreting the PAH breakdown products, or metabolites, the metabolites have been shown to be carcinogenic, mutagenic, and cytotoxic (Johnson, 2000). Most fish histopathological studies focus on the liver because contaminants tend to concentrate in this organ; however, fish kidneys, gonads, and gills were also examined in the Shipyard Sediment Site.

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[4] Histopathology is the study of microscopic changes in tissue caused by disease.

A15.2.2. Fish Histopathology Results

The findings and conclusions of the fish histopathology investigation are summarized below and are contained in the Shipyard Report (Exponent 2003). Some additional information concerning other lesions is provided in this section of the Technical Report.

A total of 70 types of histopathological lesions were found in the spotted sand bass collected from four discrete assessment units at the Shipyard Sediment Site and within a reference area located across the bay from the shipyard sites. The four assessment units are as follows:

- Inside NASSCO – the area inside the NASSCO leasehold;
- Outside NASSCO – the area between the NASSCO leasehold and the shipping channel;
- Inside BAE Systems – the area inside the BAE Systems leasehold; and
- Outside BAE Systems – the area between the BAE Systems leasehold and the shipping channel.

Of the 70 types of lesions, five exhibited significant ($p \leq 0.05$) elevations at one or more shipyard locations relative to reference conditions. A sixth lesion (i.e., foci of cellular alteration in liver) was considered important even though no statistical differences were found because the existence of these lesions at any location indicates a harmful effect strongly linked to PAH. The six significant lesions included the following:

- Liver – Abundant lipofuscin – greater inside NASSCO and BAE Systems shipyards than in the reference area;
- Liver – Abundant hemosiderin – greater outside the NASSCO shipyard than in the reference area;
- Liver – Foci of cellular alteration – No significant differences from reference;
- Liver – Cholangitis/biliary hyperplasia (CBH) – greater inside the NASSCO shipyard than in the reference area;
- Kidney – Nephritis – greater outside the NASSCO shipyard than in the reference area; and
- Gill – Shiny gill foci – greater inside the BAE Systems shipyard than in the reference area.

The documented contaminate-related lesions are shown in Table A15-4. The severity of CBH lesions elevated above reference conditions were considered none to mild in most individual fish, with a few individual fish that had a lesion score of moderate. The presence foci of cellular alteration (eosinophilic foci, basophilic foci, and clear cell foci) were found not to be statistically elevated above reference but the presence of these lesions indicate exposure effects are occurring from PAHs.

Six different lesion types were found to be significantly elevated in reference area fish, relative to fish caught at the Shipyard Site. These included:

- **Kidney**: Renal tubular regeneration—greater in the reference area than outside the NASSCO shipyard
- **Gonads**: Atresia of yolked follicles—greater in the reference area than inside the Southwest Marine shipyard
- **Fins**: Caudal fin reddening—greater in the reference area than outside the Southwest Marine shipyard
- **Fins**: Caudal fin fraying—greater in the reference area than inside or outside the NASSCO shipyard
- **Body cavity**: Diffuse opaque epicardium—greater in the reference area than inside the two shipyards
- **Body cavity**: Mean number of Anisakis parasites—greater in the reference area than inside the two shipyards.

Table A15-4 Summary of Prevalence of Contaminant-Related Lesions

		Prevalence of Lesions (Percent)				
		Nassco		BAE Systems		Reference Area
Lesion	Severity Scores	Inside	Outside	Inside	Outside	
Microscopic						
Liver						
Cholangitis/ Biliary Hyperplasia	0 – None	**66**	76	80	80	88
	1 – Mild	**28**	24	14	20	12
	2 – Moderate	**6**	0	6	0	0
	3 – Severe	**0**	0	0	0	0
Foci of Cellular Alteration						
Eosinophilic Foci	NA	8	4	0	6	4
Basophilic Foci	NA	10	10	4	8	13
Clear Cell Foci	NA	10	2	6	4	2

Note: Boxed and shaded values for shipyard locations are significantly greater relative to reference values.

As shown in Table A15-5, the severity of the four other lesions elevated above reference conditions were considered none to mild in most individual fish, while relatively few individual fish had lesions that were considered moderate (with the exception of shiny gill foci inside BAE Systems and severe. Moderate levels were observed in three of the lesions exceeding reference conditions with the most notable being shiny gill foci. Inside BAE Systems, all 51 fish had shiny gill foci lesion scores of 2 (moderate). Severe levels were observed in only one lesion elevated above reference conditions. Inside NASSCO and BAE Systems, 12 of the 101 fish collected had a lipofuscin lesion score of 3 (severe).

Table A15-5 Summary of Other Microscopic and Macroscopic Lesions Significantly Elevated Relative to Reference Conditions

		Prevalence of Lesions (Percent)				
		Nassco		BAE Systems		Reference Area
Lesion	Severity Scores	Inside	Outside	Inside	Outside	
Microscopic						
Liver						
Abundant Lipofuscin	0 – None	**74**	92	**75**	88	96
	1 – Mild	**12**	6	**6**	12	4
	2 – Moderate	**2**	2	**8**	0	0
	3 – Severe	**12**	0	**12**	0	0
Abundant Hemosiderin	0 – None	98	**78**	98	80	94
	1 – Mild	12	**6**	6	12	4
	2 – Moderate	2	**2**	8	0	0
	3 – Severe	12	**0**	12	0	0
Kidney						
Nephritis	0 – None	**48**	66	76	66	75
	1 – Mild	**48**	32	22	32	25
	2 – Moderate	**4**	2	0	2	0
	3 – Severe	**0**	0	2	0	0
Macroscopic						
Gill						
Shiny Gill Foci	0 – None	12	10	**0**	0	10
	1 – Mild	62	81	**0**	70	69
	2 – Moderate	24	8	**100**	28	20
	3 – Severe	2	0	**0**	2	2

Note: Boxed and shaded values for shipyard locations are significantly greater relative to reference values.

A15.2.3. Fish Histopathology Evaluation

A total of 253 spotted sand bass were collected using nets and by hook and line in five locations within San Diego Bay:

- Inside the NASSCO leasehold (50 fish);
- Immediately outside of the NASSCO leasehold (50 fish);
- Inside the BAE Systems leasehold (51 fish);
- Immediately outside of the BAE Systems leasehold (50 fish); and
- Within a reference area near Station 2240 located across the bay from NASSCO and BAE Systems (52 fish).

Field and laboratory methods used in the fish health assessment are presented in the Shipyard Report (Exponent, 2003) and Dr. Gary Marty's fish histopathology report (Marty, 2003).

Similar to the other lines of evidence, a key step in the fish histopathology evaluation is to determine whether the site conditions pose a greater risk than reference conditions. For the fish histopathology line of evidence, the lesions found in the spotted sand bass at the Shipyard Sediment Site were statistically compared to the presence (or absence) of lesions identified in spotted sand bass at the reference area. As specified by the San Diego Water Board (RWQCB, 2002a), the reference area used for the fish histopathology evaluation is located near Station 2240 located across the bay from the shipyards. This reference area was selected because of its similar physical characteristics to the shipyard sites (grain size and water depth) and because of its relatively low PCB and PAH sediment concentrations. The statistical procedure used to compare site lesions to reference conditions consisted of nonparametric ANOVA, based upon the severity score for each lesion in each fish (i.e., scores of 0, 1, 2, and 3) (Exponent, 2003). When the ANOVA results were significant, two-tailed *a posteriori* comparisons were made between the results for each shipyard location and the results for the reference area.

The fish histopathology line of evidence was assessed by identifying lesions in each fish and then comparing the lesions to reference conditions in San Diego Bay. Identification of lesions and comparisons to reference conditions address absolute risk and site-specific relative risk, respectively. To determine whether lesion prevalence and severity were greater than the reference population and were potentially related to chemical exposure, the lesions were crosschecked against a list of toxicopathic lesions likely associated with contaminant exposure (Exponent, 2004; Klimas, 2004).

While it is difficult to establish a clear linkage between lesions in field-collected fish and contaminant exposure, studies have established lesions associated with contaminated sediment exposure (Johnson, 2000; Myers et al., 1994; Myers et al., 1998). Specifically, Exponent (2004) and NOAA (Klimas, 2004) identified lesions in field-collected fish that were contaminant-related. The lesions identified by Exponent are listed in the Table A15-6. Of the six types of lesions specifically mentioned in this section two are listed in Table A15-6: CBH (referred to in Table A15-6 as hepatocellular/biliary epithelial cell regeneration and hyperplasia) and FCA.

Table A15-6 Lesions Associated with Sediment Contaminant Exposure

Organ	Lesion
Liver	Loss of glycogen/increased basophilia
Liver	Hepatocellular coagulative necrosis, hypertrophy, hydropic degeneration, hepatocellular hyalinization
Liver	**Hepatocellular/biliary epithelial cell regeneration and hyperplasia; oval cell proliferation and cholangio-fibrosis**
Liver	Hepatocellular nuclear pleomorphism, megalocytosis
Liver	Hydropic vacuolation of biliary epithelial cells/hepatocytes
Liver	**Foci of cellular alteration (FCA) or altered hepatocellular foci (AHF), includes clear cell, vacuolated, eosinophilic, and basophilic foci**
Liver	Enzyme-altered foci
Liver	Hepatocellular adenoma and carcinoma; cholangioma, cholangiocarcinoma; mixed hepatobiliary carcinoma
Kidney	Tubular epithelial degeneration, necrosis, vacuolation, hyalinization, and exfoliation
Kidney	Glomerular lesions such as mesangiolysis and mesangiosclerosis
Ovary	Atresia of oocytes
Ovary	Intersex condition
Ovary	Atrophy, inhibited development
Ovary	Alteration in maturation
Testis	Germinal epithelial degeneration, necrosis, atrophy
Testis	Intersex condition

(Exponent, 2004)

Based on these considerations the fish histopathology data does not conclusively indicate that the fish lesions observed in the data set can be attributed to contaminant exposure at the Shipyard Sediment Site.

A15.3. Fish Bile Analyses

The San Diego Water Board evaluated fish bile sampling results to determine the potential exposure of fish to PAH compounds within and adjacent to the Shipyard Sediment Site. The bile samples were analyzed for fluorescent aromatic compounds (FACs) and total proteins. Three groups of FACs were measured that correspond to metabolites (PAH breakdown products) from naphthalene, phenanthrene, and benzo[a]pyrene (BAP). Metabolites were detected in bile of spotted sand bass captured inside and outside of the Shipyard Sediment Site and within a reference area located across the bay from the shipyard sites near Reference Station 2240. Metabolites of two contaminants exhibited elevated levels relative to reference conditions in spotted sand bass collected immediately outside of the Shipyard Sediment Site when their mean concentrations were compared against reference data. No metabolites were significantly

elevated relative to reference conditions in spotted sand bass collected inside of the Shipyard Sediment Sites.

The upper prediction limit (UPL) at the 95 percent confidence interval was also calculated for the metabolites of the reference area fish and compared to replicate fish bile samples from the four areas of the Shipyard Sediment Site (i.e., inside and outside of both NASSCO and BAE Systems leaseholds). The inside and outside areas of NASSCO had samples that exceeded the UPL. Inside NASSCO accounted for six of the 19 UPL exceedances. Two fish bile samples from inside NASSCO exceeded the UPL for naphthalene, phenanthrene, and BAP metabolites. From Outside NASSCO, 12 of the 13 UPL exceedances came from phenanthrene and BAP metabolite samples.

For BAE Systems, all exceedances came from outside BAE Systems of which nine of 11 exceedances were for the BAP metabolite samples. The remaining two exceedances were for the phenanthrene metabolite samples. No exceedances were found from inside BAE Systems; however, the PAH sediment chemistry data from inside BAE Systems showed the highest levels of sediment contamination.

The inconsistent relationship between the levels of FACs in fish and PAH contaminated sediment indicates that this data is inconclusive and the FAC concentrations observed in the fish cannot be exclusively attributed to contaminant exposure at the Shipyard Sediment Site. The variable nature of the sediment contamination found in bays and the mobility of the fish are confounding factors when attempting to correlate fish sampling results with sediment contamination.

A15.3.1. Fish Bile

To evaluate the potential aquatic life impacts from PAHs in the sediment at the Shipyard Investigation Site, fish bile from fish collected within and adjacent to the NASSCO and BAE Systems leaseholds was evaluated as one indicator of exposure of fish to PAHs. Unlike some metals and chlorinated hydrocarbons, PAHs are readily metabolized by fish and do not bioaccumulate in their tissue. Metabolism of PAHs occurs in the livers of fish and the process produces polar organic compounds that can be found and measured in the bile. These breakdown products or metabolites can be analyzed and can serve as an indication of the fish's recent exposure to PAHs.

A15.3.2. Fish Bile Sampling and Analysis

A total of 253 spotted sand bass were collected using nets and by hook and line in five locations within San Diego Bay. The same fish were used in Finding 20: Fish Histopathology. These five areas are as follows:

- Inside the NASSCO leasehold (50 fish);
- Immediately outside of the NASSCO leasehold (50 fish);
- Inside the BAE Systems leasehold (51 fish);
- Immediately outside of the BAE Systems leasehold (50 fish); and

- A reference area near Station 2240 located across the bay from NASSCO and BAE Systems (52 fish).

As specified by the San Diego Water Board (RWQCB, 2002a), the reference area used for the fish bile evaluation is located near Station 2240 located across the bay from the Shipyard Sediment Site. This reference area was selected because of its similar physical characteristics to the Shipyard Sediment Site (grain size and water depth) and because of its relatively low polychlorinated biphenyl (PCB) and PAH sediment concentrations.

Bile samples were composited to produce up to 10 samples from each of the five sampling locations. The bile samples were analyzed for fluorescent aromatic compounds (FACs) and total proteins. Three groups of FACs were measured, corresponding to the products from the metabolization of naphthalene, phenanthrene, and BAP. Total protein was measured to allow the concentrations of PAH metabolites to be adjusted for differences in the nutritional state of the fish.

PAH metabolites were detected in bile of spotted sand bass captured inside and outside of the NASSCO and BAE Systems leaseholds, and within a reference area located across the bay from the Shipyard Sediment Site (Table A15-7).

A15.3.3. Comparison of the Mean Concentrations in Fish Bile at the Shipyard Sediment Site with Reference Conditions

The mean metabolite concentrations from the reference area and the four areas of the Shipyard Sediment Site were calculated and compared to identify statistical differences. Table A15-7 presents the summary statistics of Shipyard Sediment Site and Reference area samples. Two of the three contaminant-related metabolite products exhibited statistically significant differences in the sand bass collected in the areas immediately outside of the NASSCO and BAE Systems leaseholds when their mean concentrations were compared against reference fish. No bile metabolites were significantly elevated relative to reference conditions for the spotted sand bass collected inside of either shipyard leasehold. The contaminants with significantly elevated metabolite levels include the following:

- Naphthalene – Concentrations in fish bile were greater outside NASSCO leasehold than in the reference area; and

- BAP – Concentrations in fish bile were greater outside NASSCO and BAE Systems leaseholds than in the reference area.

Table A15-7 Summary of PAH Metabolites Measured in Fish Bile

		NASSCO		BAE Systems	
	Reference Area	**Inside**	**Outside**	**Inside**	**Outside**
Naphthalene Metabolites (µg/mg protein)					
Mean	79	74.5	84.2	68.9	74
Standard Deviation	27.4	45.7	24.8	11.2	25.5
Minimum	58	26	64	55	49
Maximum	150	160	150	96	130
95% Upper Confidence Limit	131.7				
Naphthalene Metabolites (µg/mg protein)					
Mean[1]	12.8	13.6	**26.7**	13.9	18.9
Standard Deviation	4.7	7.4	7.8	1.9	3.1
Minimum	7.1	5.7	20	11	14
Maximum	25	28	46	18	25
95% Upper Confidence Limit	21.9				
Benzo[a]pyrene Matabolites (µg/mg protein)					
Mean[1]	2.1	2.9	**5.3**	1.7	**6.0**
Standard Deviation	1.2	1.6	2.1	0.9	1.6
Minimum	0.7	0.5	2.7	0.7	2.8
Maximum	4.6	6	9.8	3.7	8.5
95% Upper Confidence Limit	4.5				

1. Some or all of the data was qualified as estimates. See Table E-4 from the Shipyard Report (Exponent, 2003).
Note: Boxed and shaded values for shipyard locations are significantly greater relative to reference values.

A15.3.4. Comparison of the Upper Prediction Limit to Replicate Data

The upper prediction limit (UPL) at the 95 percent confidence interval was also calculated for the reference area fish. The field replicate data from the four Shipyard Sediment Site areas was compared against the 95 percent UPL for the reference fish bile samples. Table A15-8, below, provides a summary of the fish bile samples from the Shipyard Sediment Site that exceeded the 95 percent UPL. A summary of the descriptive statistics and ANOVA results is provided in Attachment A. The replicate data can be found in Appendix E of the Shipyard Report (Exponent, 2003).

Table A15-8 Summary of Fish Bile Samples that Exceeded the 95% UPL

	NASSCO		BAE Systems	
	Inside	**Outside**	**Inside**	**Outside**
Naphthalene Metabolites	2	1	0	0
Phenanthrene Metabolites[1]	2	7	0	2
Benzo [a] pyrene Metabolites[1]	2	5	0	9
Sample Size	**10**	**10**	**10**	**10**

1. Some or all of the data was qualified as estimates. See Table E-4 from the Shipyard Report (Exponent, 2003).

Both the inside and outside areas of the NASSCO leasehold had samples that exceeded the 95 percent UPL. The outside area of NASSCO accounted for 13 of the 19 UPL exceedances, which were almost exclusively from phenanthrene and benzo [a] pyrene metabolite samples. The outside area of BAE Systems accounted for all of their UPL exceedances with 9 of the 11 exceedances from benzo [a] pyrene. No exceedances were found from the inside area of BAE Systems for any of the three PAH metabolites.

A15.3.5. Discussion

The fish bile line of evidence was assessed by determining the presence of PAH metabolites and then comparing the PAH bile concentrations to reference conditions in San Diego Bay. The objective was to determine if the fish from the Shipyard Sediment Site were exposed to PAHs and, if so, was this exposure greater than those indicated in the fish from the reference area. Identification of PAH metabolites and comparisons to reference conditions address absolute risk and site-specific relative risk, respectively.

The PAH sediment chemistry data from inside BAE Systems showed the highest levels of sediment contamination but the metabolite levels from fish collected from inside BAE showed no significant differences from reference. Therefore, the FAC concentrations observed in the fish collected cannot be exclusively attributed to contaminant exposure at the Shipyard Sediment Site.

These results are similar to other studies conducted in Southern California, which have found an inconsistent relationship between FACs in fish and sediment contaminated with PAHs (Brown and Steinert, 2004). The variable nature of the sediment contamination found in bays along with mobility of the fish species selected are confounding factors when attempting to correlate fish sampling results with sediment contamination.

Attachment A

Summary of Descriptive Statistics

Naphthalene Meta (ref)	
Mean	79.00
Standard Error	8.67
Median	72.00
Mode	72.00
Standard Deviation	27.41
Sample Variance	751.11
Kurtosis	5.71
Skewness	2.24
Range	92.00
Minimum	58.00
Maximum	150.00
Sum	790.00
Count	10.00
Confidence Level (95.0%)	19.61

Naphthalene Meta (In NAS)	
Mean	74.50
Standard Error	14.46
Median	70.50
Mode	#N/A
Standard Deviation	45.74
Sample Variance	2092.28
Kurtosis	-0.01
Skewness	0.85
Range	134.00
Minimum	26.00
Maximum	160.00
Sum	745.00
Count	10.00
Confidence Level (95.0%)	32.72

Naphthalene Meta (Out NAS)	
Mean	84.20
Standard Error	7.84
Median	81.00
Mode	64.00
Standard Deviation	24.80
Sample Variance	614.84
Kurtosis	6.73
Skewness	2.39
Range	86.00
Minimum	64.00
Maximum	150.00
Sum	842.00
Count	10.00
Confidence Level (95.0%)	17.74

Naphthalene Meta (In SWM)	
Mean	68.9
Standard Error	3.54
Median	65.50
Mode	#N/A
Standard Deviation	11.18
Sample Variance	124.99
Kurtosis	3.82
Skewness	1.64
Range	41.00
Minimum	55.00
Maximum	96.00
Sum	689.00
Count	10.00
Confidence Level (95.0%)	8.00

Naphthalene Meta (Out SWM)	
Mean	74.00
Standard Error	8.06
Median	65.00
Mode	#N/A
Standard Deviation	25.50
Sample Variance	650.22
Kurtosis	1.32
Skewness	1.27
Range	81.00
Minimum	49.00
Maximum	130.00
Sum	740.00
Count	10.00
Confidence Level (95.0%)	18.24

Benzo[a]pyrene Meta (ug/mg protein)	
Mean	2.07
Standard Error	0.39
Median	1.85
Mode	#N/A
Standard Deviation	1.25
Sample Variance	1.56
Kurtosis	0.28
Skewness	0.88
Range	3.90
Minimum	0.70
Maximum	4.60
Sum	20.70
Count	10.00
Confidence Level (95.0%)	0.89

Benzo[a]pyrene Meta In NAS	
Mean	2.92
Standard Error	0.51
Median	2.55
Mode	2.30
Standard Deviation	1.63
Sample Variance	2.65
Kurtosis	0.34
Skewness	0.63
Range	5.50
Minimum	0.50
Maximum	6.00
Sum	29.20
Count	10.00
Confidence Level (95.0%)	1.16

Benzo[a]pyrene Meta Out NAS	
Mean	5.32
Standard Error	0.65
Median	4.85
Mode	#N/A
Standard Deviation	2.06
Sample Variance	4.25
Kurtosis	1.46
Skewness	1.03
Range	7.10
Minimum	2.70
Maximum	9.80
Sum	53.20
Count	10.00
Confidence Level (95.0%)	1.47

Benzo[a]pyrene Meta In SWM	
Mean	1.67
Standard Error	0.27
Median	1.60
Mode	1.90
Standard Deviation	0.87
Sample Variance	0.75
Kurtosis	2.78
Skewness	1.44
Range	3.00
Minimum	0.70

Benzo[a]pyrene Meta Out SWM	
Mean	5.95
Standard Error	0.49
Median	6.15
Mode	#N/A
Standard Deviation	1.55
Sample Variance	2.42
Kurtosis	1.16
Skewness	-0.50
Range	5.70
Minimum	2.80

Phenanthrene Meta ref	
Mean	12.75
Standard Error	1.50
Median	12.00
Mode	11.00
Standard Deviation	4.74
Sample Variance	22.46
Kurtosis	5.91
Skewness	2.10
Range	17.90
Minimum	7.10

Phenanthrene Meta In NAS	
Mean	13.55
Standard Error	2.35
Median	13.00
Mode	#N/A
Standard Deviation	7.44
Sample Variance	55.40
Kurtosis	0.08
Skewness	0.83
Range	22.30
Minimum	5.70

Benzo[a]pyrene Meta In SWM	
Maximum	3.70
Sum	16.70
Count	10.00
Confidence Level (95.0%)	0.62

Benzo[a]pyrene Meta Out SWM	
Maximum	8.50
Sum	59.50
Count	10.00
Confidence Level (95.0%)	1.11

Phenanthrene Meta ref	
Maximum	25.00
Sum	127.50
Count	10.00
Confidence Level (95.0%)	3.39

Phenanthrene Meta In NAS	
Maximum	28.00
Sum	135.50
Count	10.00
Confidence Level (95.0%)	5.32

Phenanthrene Meta Out NAS	
Mean	26.70
Standard Error	2.46
Median	25.50
Mode	20.00
Standard Deviation	7.79
Sample Variance	60.68
Kurtosis	4.29
Skewness	1.88
Range	26.00
Minimum	20.00
Maximum	46.00
Sum	267.00
Count	10.00
Confidence Level (95.0%)	5.57

Phenanthrene Meta In SWM	
Mean	13.90
Standard Error	0.59
Median	14.00
Mode	14.00
Standard Deviation	1.85
Sample Variance	3.43
Kurtosis	2.48
Skewness	0.84
Range	7.00
Minimum	11.00
Maximum	18.00
Sum	139.00
Count	10.00
Confidence Level (95.0%)	1.33

Phenanthrene Meta Out SWM	
Mean	18.90
Standard Error	0.98
Median	18.50
Mode	17.00
Standard Deviation	3.11
Sample Variance	9.66
Kurtosis	0.61
Skewness	0.59
Range	11.00
Minimum	14.00
Maximum	25.00
Sum	189.00
Count	10.00
Confidence Level (95.0%)	2.22

Data Used to Calculate Analysis of Variance

	Reference			Inside NASSCO			Outside NASSCO			Inside SWM			Outside SWM		
	Naphthalene Meta (ug/mg protein)	Benzo[a]pyrene Meta (ug/mg protein)	Phenanthrene Meta (ug/mg protein)	Naphthalene Meta (ug/mg protein)	Benzo[a]pyrene Meta (ug/mg protein)	Phenanthrene Meta (ug/mg protein)	Naphthalene Meta (ug/mg protein)	Benzo[a]pyrene Meta (ug/mg protein)	Phenanthrene Meta (ug/mg protein)	Naphthalene Meta (ug/mg protein)	Benzo[a]pyrene Meta (ug/mg protein)	Phenanthrene Meta (ug/mg protein)	Naphthalene Meta (ug/mg protein)	Benzo[a]pyrene Meta (ug/mg protein)	Phenanthrene Meta (ug/mg protein)
	72	1	9.4	140	6	23	77	4.7	20	72	2.2	15	130	6.2	25
	62	1.9	11	27	3.6	6.2	79	3.2	20	66	1.9	13	57	5.4	17
	58	0.7	7.1	57	2.5	9.8	87	2.7	27	96	1.4	18	95	6.1	19
	150	1.3	25	65	2.3	12	64	5	25	65	1.8	14	54	8.5	18
	86	1.8	13	26	2.3	5.8	86	6.7	27	74	3.7	14	72	5	17
	78	3.3	14	160	1.3	28	150	9.8	46	64	0.9	14	92	6.9	22
	58	4.6	11	79	3.1	14	67	4.3	26	73	1.1	14	49	2.8	14
	91	2.9	13	86	2.6	16	64	4.2	20	61	0.7	12	55	6.4	19
	72	0.8	12	29	0.5	5.7	85	6	24	63	1.1	14	58	7.3	17
	63	2.4	12	76	5	15	83	6.6	32	55	1.9	11	78	4.9	21
Mean	**79**	**2.07**	**12.75**	**74.5**	**2.92**	**13.55**	**84.2**	**5.32**	**26.7**	**68.9**	**1.67**	**13.9**	**74**	**5.95**	**18.9**
SD	**27.4**	**1.2**	**4.7**	**45.7**	**1.6**	**7.4**	**24.8**	**2.1**	**7.8**	**11.2**	**0.9**	**1.9**	**25.5**	**1.6**	**3.1**
SE	**8.7**	**0.4**	**1.5**	**14.5**	**0.5**	**2.4**	**7.8**	**0.7**	**2.5**	**3.5**	**0.3**	**0.6**	**8.1**	**0.5**	**1.0**
Min	**58**	**0.7**	**7.1**	**26**	**0.5**	**5.7**	**64**	**2.7**	**20**	**55**	**0.7**	**11**	**49**	**2.8**	**14**
Max	**150**	**4.6**	**25**	**160**	**6**	**28**	**150**	**9.8**	**46**	**96**	**3.7**	**18**	**130**	**8.5**	**25**

Naphthalene Meta (ref)	Naphthalene Meta (In NAS)	Naphthalene Meta (Out NAS)	Naphthalene Meta (In SWM)	Naphthalene Meta (Out SWM)	Benzo[a]pyrene Meta (ug/mg protein)	Benzo[a]pyrene Meta In NAS	Benzo[a]pyrene Meta Out NAS	Benzo[a]pyrene Meta In SWM	Benzo[a]pyrene Meta Out SWM	Phenanthrene Meta ref	Phenanthrene Meta In NAS	Phenanthrene Meta Out NAS	Phenanthrene Meta In SWM	Phenanthrene Meta Out SWM
72	140	77	72	130	1	6	4.7	2.2	6.2	9.4	23	20	15	25
62	27	79	66	57	1.9	3.6	3.2	1.9	5.4	11	6.2	20	13	17
58	57	87	96	95	0.7	2.5	2.7	1.4	6.1	7.1	9.8	27	18	19
150	65	64	65	54	1.3	2.3	5	1.8	8.5	25	12	25	14	18
86	26	86	74	72	1.8	2.3	6.7	3.7	5	13	5.8	27	14	17
78	160	150	64	92	3.3	1.3	9.8	0.9	6.9	14	28	46	14	22
58	79	67	73	49	4.6	3.1	4.3	1.1	2.8	11	14	26	14	14
91	86	64	61	55	2.9	2.6	4.2	0.7	6.4	13	16	20	12	19
72	29	85	63	58	0.8	0.5	6	1.1	7.3	12	5.7	24	14	17
63	76	83	55	78	2.4	5	6.6	1.9	4.9	12	15	32	11	21

Analysis of Variance Calculations for Naphthalene

Anova: Single Factor

SUMMARY						
Groups	**Count**	**Sum**	**Average**	**Variance**		
Naphthalene Meta (ref)	10	790	79	751.1111		
Naphthalene Meta In NAS)	10	745	74.5	2092.278		
Naphthalene Meta (Out NAS)	10	842	84.2	614.8444		
Naphthalene Meta In SWM)	10	689	68.9	124.9889		
Naphthalene Meta (Out SWM)	10	740	74	650.2222		
ANOVA						
Source of Variation	**SS**	**df**	**MS**	**F**	**P-value**	**F crit**
Between Groups	1328.28	4	332.07	0.392198	0.813123	2.578737
Within Groups	38101	45	846.6889			
Total	39429.28	49				

Analysis of Variance Calculations for Benzo[a]pyrene

Anova: Single Factor

SUMMARY						
Groups	**Count**	**Sum**	**Average**	**Variance**		
Benzo[a]pyrene Meta (ug/mg protein)	10	20.7	2.07	1.560111		
Benzo[a]pyrene Meta In NAS	10	29.2	2.92	2.648444		
Benzo[a]pyrene Meta Out NAS	10	53.2	5.32	4.246222		
Benzo[a]pyrene Meta In SWM	10	16.7	1.67	0.753444		
Benzo[a]pyrene Meta Out SWM	10	59.5	5.95	2.416111		
ANOVA						
Source of Variation	**SS**	**df**	**MS**	**F**	**P-value**	**F crit**
Between Groups	150.0812	4	37.5203	16.13869	2.88163E-08	2.578737
Within Groups	104.619	45	2.324867			
Total	254.7002	49				

Analysis of Variance Calculations for Phenanthrene

Anova: Single Factor

SUMMARY						
Groups	**Count**	**Sum**	**Average**	**Variance**		
Phenanthrene Meta ref	10	127.5	12.75	22.46055556		
Phenanthrene Meta In NAS	10	135.5	13.55	55.39833333		
Phenanthrene Meta Out NAS	10	267	26.7	60.67777778		
Phenanthrene Meta In SWM	10	139	13.9	3.433333333		
Phenanthrene Meta Out SWM	10	189	18.9	9.655555556		
ANOVA						
Source of Variation	**SS**	**df**	**MS**	**F**	**P-value**	**F crit**
Between Groups	1371.47	4	342.8675	11.30638891	1.95658E-06	2.578737224
Within Groups	1364.63	45	30.32511111			
Total	2736.1	49				

Additional Analysis of Variance for Naphthalene With Bonferroni Correction

Pairwise Mean Diff. (row - column)

	Naphthalene Meta (ref)	**Naphthalene Meta (In NAS)**	**Naphthalene Meta (Out NAS)**	**Naphthalene Meta (In SWM)**	**Naphthalene Meta (Out SWM)**
Naphthalene Meta (ref)	0	4.5	-5.2	10.1	5
Naphthalene Meta (In NAS)		0	-9.7	5.6	0.5
Naphthalene Meta (Out NAS)			0	15.3	10.2
Naphthalene Meta (In SWM)				0	-5.1
Naphthalene Meta (Out SWM)					0
MSE = 846.688888888889					
Pairwise Comparison Probabilities (Bonferroni Correction)					
	Naphthalene Meta (ref)	**Naphthalene Meta (In NAS)**	**Naphthalene Meta (Out NAS)**	**Naphthalene Meta (In SWM)**	**Naphthalene Meta (Out SWM)**
Naphthalene Meta (ref)	1.000	1.000	1.000	1.000	1.000
Naphthalene Meta (In NAS)		1.000	1.000	1.000	1.000
Naphthalene Meta (Out NAS)			1.000	1.000	1.000
Naphthalene Meta (In SWM)				1.000	1.000
Naphthalene Meta (Out SWM)					1.000

Additional Analysis of Variance for Benzo[a]pyrene With Bonferroni Correction

Pairwise Mean Diff. (row - column)

	Benzo[a]pyrene Meta (ug/mg protein)	Benzo[a]pyrene Meta In NAS	Benzo[a]pyrene Meta Out NAS	Benzo[a]pyrene Meta In SWM	Benzo[a]pyrene Meta Out SWM
Benzo[a]pyrene Meta (ug/mg protein)	0	-0.85	-3.25	0.4	-3.88
Benzo[a]pyrene Meta In NAS		0	-2.4	1.25	-3.03
Benzo[a]pyrene Meta Out NAS			0	3.65	-0.63
Benzo[a]pyrene Meta In SWM				0	-4.28
Benzo[a]pyrene Meta Out SWM					0
MSE = 2.32486666666667					
Pairwise Comparison Probabilities (Bonferroni Correction)					
	Benzo[a]pyrene Meta (ug/mg protein)	**Benzo[a]pyrene Meta In NAS**	**Benzo[a]pyrene Meta Out NAS**	**Benzo[a]pyrene Meta In SWM**	**Benzo[a]pyrene Meta Out SWM**
Benzo[a]pyrene Meta (ug/mg protein)	1.000	1.000	0.000	1.000	0.000
Benzo[a]pyrene Meta In NAS		1.000	0.010	0.734	0.001
Benzo[a]pyrene Meta Out NAS			1.000	0.000	1.000
Benzo[a]pyrene Meta In SWM				1.000	0.000
Benzo[a]pyrene Meta Out SWM					1.000

Additional Analysis of Variance for Phenanthrene With Bonferroni Correction

Pairwise Mean Diff. (row - column)

	Phenanthrene Meta ref	Phenanthrene Meta In NAS	Phenanthrene Meta Out NAS	Phenanthrene Meta In SWM	Phenanthrene Meta Out SWM
Phenanthrene Meta ref	0	-0.8	-13.95	-1.15	-6.15
Phenanthrene Meta In NAS		0	-13.15	-0.35	-5.35
Phenanthrene Meta Out NAS			0	12.8	7.8
Phenanthrene Meta In SWM				0	-5
Phenanthrene Meta Out SWM					0
MSE = 30.3251111111111					
Pairwise Comparison Probabilities (Bonferroni Correction)					
	Phenanthrene Meta ref	**Phenanthrene Meta In NAS**	**Phenanthrene Meta Out NAS**	**Phenanthrene Meta In SWM**	**Phenanthrene Meta Out SWM**
Phenanthrene Meta ref	1.000	1.000	0.000	1.000	0.162
Phenanthrene Meta In NAS		1.000	0.000	1.000	0.351
Phenanthrene Meta Out NAS			1.000	0.000	0.028
Phenanthrene Meta In SWM				1.000	0.483
Phenanthrene Meta Out SWM					1.000

Additional Analysis of Variance for Naphthalene Without Bonferroni Correction

Pairwise Mean Diff. (row - column)

	Naphthalene Meta (ref)	Naphthalene Meta (In NAS)	Naphthalene Meta (Out NAS)	Naphthalene Meta (In SWM)	Naphthalene Meta (Out SWM)
Naphthalene Meta (ref)	0	4.5	-5.2	10.1	5
Naphthalene Meta In NAS)		0	-9.7	5.6	0.5
Naphthalene Meta (Out NAS)			0	15.3	10.2
Naphthalene Meta In SWM)				0	-5.1
Naphthalene Meta (Out SWM)					0
MSE = 846.688888888889					
Pairwise Comparison Probabilities					
	Naphthalene Meta (ref)	**Naphthalene Meta (In NAS)**	**Naphthalene Meta (Out NAS)**	**Naphthalene Meta (In SWM)**	**Naphthalene Meta (Out SWM)**
Naphthalene Meta (ref)	1.000	0.731	0.691	0.442	0.703
Naphthalene Meta In NAS)		1.000	0.460	0.669	0.970
Naphthalene Meta (Out NAS)			1.000	0.246	0.437
Naphthalene Meta In SWM)				1.000	0.697
Naphthalene Meta (Out SWM)					1.000

Additional Analysis of Variance for Benzo[a]pyrene Without Bonferroni Correction

Pairwise Mean Diff. (row - column)

	Benzo[a]pyrene Meta (ug/mg protein)	Benzo[a]pyrene Meta In NAS	Benzo[a]pyrene Meta Out NAS	Benzo[a]pyrene Meta In SWM	Benzo[a]pyrene Meta Out SWM
Benzo[a]pyrene Meta (ug/mg protein)	0	-0.85	-3.25	0.4	-3.88
Benzo[a]pyrene Meta In NAS		0	-2.4	1.25	-3.03
Benzo[a]pyrene Meta Out NAS			0	3.65	-0.63
Benzo[a]pyrene Meta In SWM				0	-4.28
Benzo[a]pyrene Meta Out SWM					0
MSE = 2.32486666666667					
Pairwise Comparison Probabilities					
	Benzo[a]pyrene Meta (ug/mg protein)	**Benzo[a]pyrene Meta In NAS**	**Benzo[a]pyrene Meta Out NAS**	**Benzo[a]pyrene Meta In SWM**	**Benzo[a]pyrene Meta Out SWM**
Benzo[a]pyrene Meta (ug/mg protein)	1.000	0.219	0.000	0.560	0.000
Benzo[a]pyrene Meta In NAS		1.000	0.001	0.073	0.000
Benzo[a]pyrene Meta Out NAS			1.000	0.000	0.360
Benzo[a]pyrene Meta In SWM				1.000	0.000
Benzo[a]pyrene Meta Out SWM					1.000

Additional Analysis of Variance for Phenanthrene Without Bonferroni Correction

Pairwise Mean Diff. (row - column)

	Phenanthrene Meta ref	Phenanthrene Meta In NAS	Phenanthrene Meta Out NAS	Phenanthrene Meta In SWM	Phenanthrene Meta Out SWM
Phenanthrene Meta ref	0	-0.8	-13.95	-1.15	-6.15
Phenanthrene Meta In NAS		0	-13.15	-0.35	-5.35
Phenanthrene Meta Out NAS			0	12.8	7.8
Phenanthrene Meta In SWM				0	-5
Phenanthrene Meta Out SWM					0
MSE = 30.3251111111111					
Pairwise Comparison Probabilities					
	Phenanthrene Meta ref	**Phenanthrene Meta In NAS**	**Phenanthrene Meta Out NAS**	**Phenanthrene Meta In SWM**	**Phenanthrene Meta Out SWM**
Phenanthrene Meta ref	1.000	0.747	0.000	0.643	0.016
Phenanthrene Meta In NAS		1.000	0.000	0.888	0.035
Phenanthrene Meta Out NAS			1.000	0.000	0.003
Phenanthrene Meta In SWM				1.000	0.048
Phenanthrene Meta Out SWM					1.000