Appendix G
Statistical Analyses

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ABBREVIATIONS

95CI	95% confidence interval
95UCL	95% upper confidence limit (on the mean)
ANOVA	analysis of variance
CV	coefficient of variation
DQO	data quality objective
GOF	goodness-of-fit
LDW	Lower Duwamish Waterway
PCB	polychlorinated biphenyl
PPCC	probability plot correlation coefficient
RM	river mile
ROS	regression on order statistics
RPD	relative percent difference
SD	standard deviation
SE	standard error (of the mean)
TEQ	toxic equivalent
ww	wet weight

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1   Introduction and Methods

This appendix to the *Data Report: 2023 Periodic Monitoring of Fish, Crab, Clam, and Surface Water in the Lower Duwamish Waterway* (LDW) presents the analytical methods and detailed results of the statistical evaluations used to interpret the periodic monitoring datasets in light of the data quality objectives (DQOs).

The remainder of this appendix is organized into sections that parallel the structure of the data report, as follows:

- Section 2 – Fish and Crab Tissue
- Section 3 – Clam Tissue
- Section 4 – Surface Water Passive Samplers
- Section 5 – References

The statistical methods applied to one or more datasets in later sections are described in the remainder of this section.

1.1   Choosing the Distributional Form for Calculating 95UCLs

The 95% upper confidence limit (on the mean) (95UCL) is a summary statistic required for many of the LDW baseline datasets. Following identification of the most appropriate distributional form (i.e., normal, log-normal, or gamma), the 95UCL was calculated for each dataset using appropriate parametric equations. If none of the parametric distributions were appropriate for a dataset, then a non-parametric approach was used. This process also allowed for identification of any possible outliers in a dataset so that such elevated values could be further examined.

Each dataset was evaluated using tools in ProUCL 5.1 (EPA 2016) and select packages (e.g., EnvStats (Millard 2013) and ggplot2 (Wickham 2009)) in R (v4.4.0, R Core Team 2024). The statistical tools used during this assessment included probability plots, distributional goodness-of-fit (GOF) tests, and graphical and formal outlier tests.

1.1.1   Goodness-of-Fit Test

A formal GOF test was conducted for each individual chemical dataset, and each test was confirmed by patterns observed in the probability plots (Section 1.1.2). The best-fitting distribution was identified as the one that passed the GOF test and had the highest probability plot correlation coefficient (PPCC). If no distributions provided a reasonable fit to the data, then non-parametric estimates for the 95UCL were required.

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For this evaluation, GOF testing relied on the significance of the PPCC[1] for normal, lognormal, and gamma distributions; the hypothesized distribution was rejected when p < 0.05. Once the best distributional fit for a dataset had been identified, the 95UCL was calculated in R (v4.4.0, R Core Team 2024) using the methods described in Section 1.2.

1.1.2   Probability Plots

Probability plots[2] show the observed quantiles for the dataset on the y-axis vs. the expected quantiles under the theorized distribution on the x-axis.[3] If the theoretical distribution is a reasonable description for the dataset, then the probability plot should follow an approximately straight line. The best-fit regression line is added to a plot to facilitate interpretation of the GOF indicated by the plot. The presence of potential outliers and systematic deviations from the theorized distribution can also be observed on these plots; if present, such outliers and deviations may lead to a formal outlier test, as described in Section 1.1.3. Figure 1-1 shows example probability plots for a skewed dataset that is poorly described by a normal distribution (i.e., the observed quantiles do not fit a straight line when plotted against the normal quantiles) but adequately described by a lognormal distribution (i.e., the probability plot follows an approximately straight line).

Normal QQPlot   **LogNormal QQPlot**
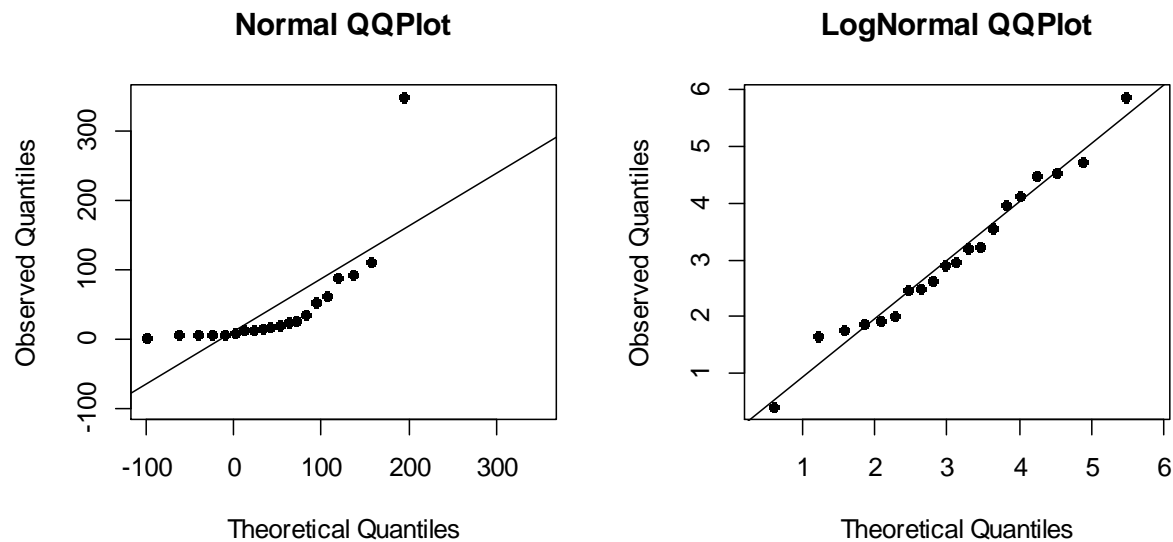
Figure 1-1   Example Probability Plots for a Skewed Dataset that does not Follow a Normal Distribution (Left) but does Follow a Lognormal Distribution (Right)

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[1] The PPCCs were generated using *EnvStats::gofTest(x, test="ppcc", estimate.params=TRUE)* in R.
[2] These plots are generated in R using the function *EnvStats::qqPlot(x, estimate.params=TRUE)*.
[3] A probability plot is also called a "QQ Plot," which stands for quantile-quantile plot.

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1.1.3   Outlier Tests

The presence of potential outliers was identified initially through visual inspection of the probability plots. When data points appeared to be extreme (at either the high or low end), a formal outlier test was used. Outlier tests require the assumption of parametric distribution for the underlying data; there is no such thing as an outlier for a non-parametric distribution. The two outlier tests used are based on an underlying normal distribution. Usually, the skewness introduced by extreme values can be adequately described by a log-normal or gamma distribution. Alternatively, once extreme values have been removed, the data may be adequately described by a normal distribution, which is the basis for the two outlier tests: Dixon's (n < 25, single outliers only) and Rosner's (n ≥ 25, multiple outliers). Both tests were applied using tools in ProUCL 5.1 (EPA 2016).

1.2   Calculations for a Stratified Mean

Given that the fish and crab tissue sampling approach used a stratified design to account for possible differences of mean and variability in composite tissue concentrations across reaches (English sole and crab) or subreaches (shiner surfperch), the calculation of a stratified mean was necessary. Because mean concentrations may differ among reaches or subreaches, stratified estimators are used to reduce the variance of the site-wide mean.

Using equal weights for each area (reach or subreach), the site-wide mean can be estimated as the grand mean of the mean concentrations within each reach as follows:

Equation 1

$$\overline{\overline{X}} = w \sum_{i=1}^{k} \overline{X_i}$$

Where:

$\overline{X_i}$ is the average concentration in area i (i = 1 to k, where k = 2 for English sole and crab and k= 4 for shiner surfperch).

$w = 1/k$ (i.e., 0.50 for sole and crab, and 0.25 for perch).

The sampling variance of the stratified mean when each of the *k* reaches is weighted equally is:

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Equation 2

$$Var\widehat{(\overline{\overline{X}})} = \frac{1}{k^2} \sum_{i=1}^{k} s_{\overline{X}_i}^2$$

Where:

$$s_{\overline{X}_i}^2 = s_i^2 / n_i$$

s_i^2 is the usual sample variance estimate of the n_i observations in area i (i = 1 to k, k = 2 for English sole and crab, and k = 4 for shiner surfperch)

n_i is the sample size in area i

For a stratified mean, the Central Limit Theorem—which holds that the sampling distribution of means is approximately normally distributed—is invoked for the 95UCL estimate (Levy and Lemeshow 1999), although a more conservative Student's *t*-interval is used instead of a Z-interval due to the uncertainty inherent in small samples with unknown population variance. When sample size and/or variance differ among strata, degrees of freedom are estimated using the Welch-Satterthwaite equation; this confidence interval is referred to as Welch's approximate *t*-interval.

$$95UCL = \overline{\overline{X}} + t_{(0.05,df)} \times SE(\overline{\overline{X}}) \qquad \text{Equation 3}$$

Where:

$\overline{\overline{X}}$ is the site-wide mean, as calculated in Equation 1

$SE(\overline{\overline{X}})$ is the standard error of the stratified mean, equal to the square root of the variance estimator in Equation 2

df = degrees of freedom estimated using the Welch-Satterthwaite equation, which is a function of the sample size and the variance within each stratum

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2   Fish and Crab Tissue

This section provides statistical details regarding the interpretation of the fish and crab tissue data, as presented in Section 5.1 of the data report.

2.1   95UCL Calculations

To evaluate DQO 1 for fish and crab tissue, a 95UCL for the site-wide mean was calculated for each risk driver and tissue type. The sampling approach used a stratified design to account for possible differences of mean and variability in composite tissue concentrations across reaches and subreaches. As appropriate for the stratified sampling design, the site-wide mean was calculated as a stratified mean (i.e., a grand mean across strata with equal weights per stratum).

Due to the relatively small sample sizes within each reach or subreach, standardized residuals[4] within each reach or subreach were combined 1to give the distributional tests greater power. The methods described in Section 1.1 were then used to identify the best distributional form for each risk driver and tissue type. In most cases, the normal distribution provided a reasonable fit to the data, and no outliers were present (Table 2-1 and Figures 2-1 and 2-2). The exceptions were dioxin/furan toxic equivalents (TEQs) in graceful crab edible meat and whole-body (calculated) samples, which included one and two outliers, respectively. The edible meat data from Reach 2 had a single outlier (Dixon's test, $p<0.01$). For the whole-body (calculated) data from Reach 2, the highest value was not an outlier because it was masked by the second-highest value. Removing the highest value, the second-highest was found to be an outlier (Dixon's test $p<0.01$). For both datasets, no parametric distributions were deemed a good fit using all the data, but they satisfied the normal distribution when the outliers were excluded. In this situation for a single random sample, ProUCL guidance (EPA 2016) would recommend bootstrapping or Chebyshev's inequality to estimate the 95UCL, with a preference for Chebyshev due to the small number of samples available for bootstrapping. However, there is no precedent for using Chebyshev's inequality on a stratified sample. Therefore, a bootstrap-t estimate was used to determine an approximate 95UCL for the stratified mean (Section 1.2).

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[4] GOF was applied to the standardized residuals from a stratified model (i.e., the differences between each composite value and the mean for all samples from the same LDW river reach, divided by the standard deviation (SD) from the same river reach).

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Table 2-1
GOF and CV Summary for Risk Drivers in 2023 Fish and Crab Tissues

Species and Tissue Type	Count	Best Fit Distribution	PPCC[1]	p-Value[2]	CV[3]
Total PCB Congeners (µg/kg ww)					
Benthic fish – English sole – fillet	12	Normal	0.98	0.80	0.44
Benthic fish – English sole – whole body	12	Normal	0.99	0.96	0.30
Pelagic fish – shiner surfperch – whole body	12	Normal	0.96	0.31	0.28
Crab – graceful crab – edible meat	12	Normal	0.97	0.34	0.40
Crab – graceful crab – whole body	12	Normal	0.98	0.67	0.26
Dioxin/furan TEQ (ng/kg ww)					
Benthic fish – English sole – fillet	12	Normal[4]	0.95	0.12	0.38
Benthic fish – English sole – whole body	12	Normal	0.97	0.43	0.20
Pelagic fish – shiner surfperch – whole body	12	Normal	0.96	0.26	0.25
Crab – graceful crab – edible meat	12	None	0.89	0.01	0.96
Crab – graceful crab – edible meat (excluding outlier value from Reach 2)	11	Normal	0.94	0.12	0.17
Crab – graceful crab – whole body	12	None	0.92	0.03	1.06
Crab – graceful crab – whole body (excluding two outlier values from Reach 2)	10	Normal	0.98	0.87	0.27

Notes:
1. PPCC for the normal distribution.
2. p-value for the PPCC GOF test on the standardized residuals.
3. CV is based on the observed values in the full dataset.
4. Goodness of fit test run using ROS method for non-detects (ProUCL5.1).
CV: coefficient of variation
GOF: goodness-of-fit
PCB: polychlorinated biphenyl
PPCC: probability plot correlation coefficient
ROS: regression on order statistics
TEQ: toxic equivalent
ww: wet weight
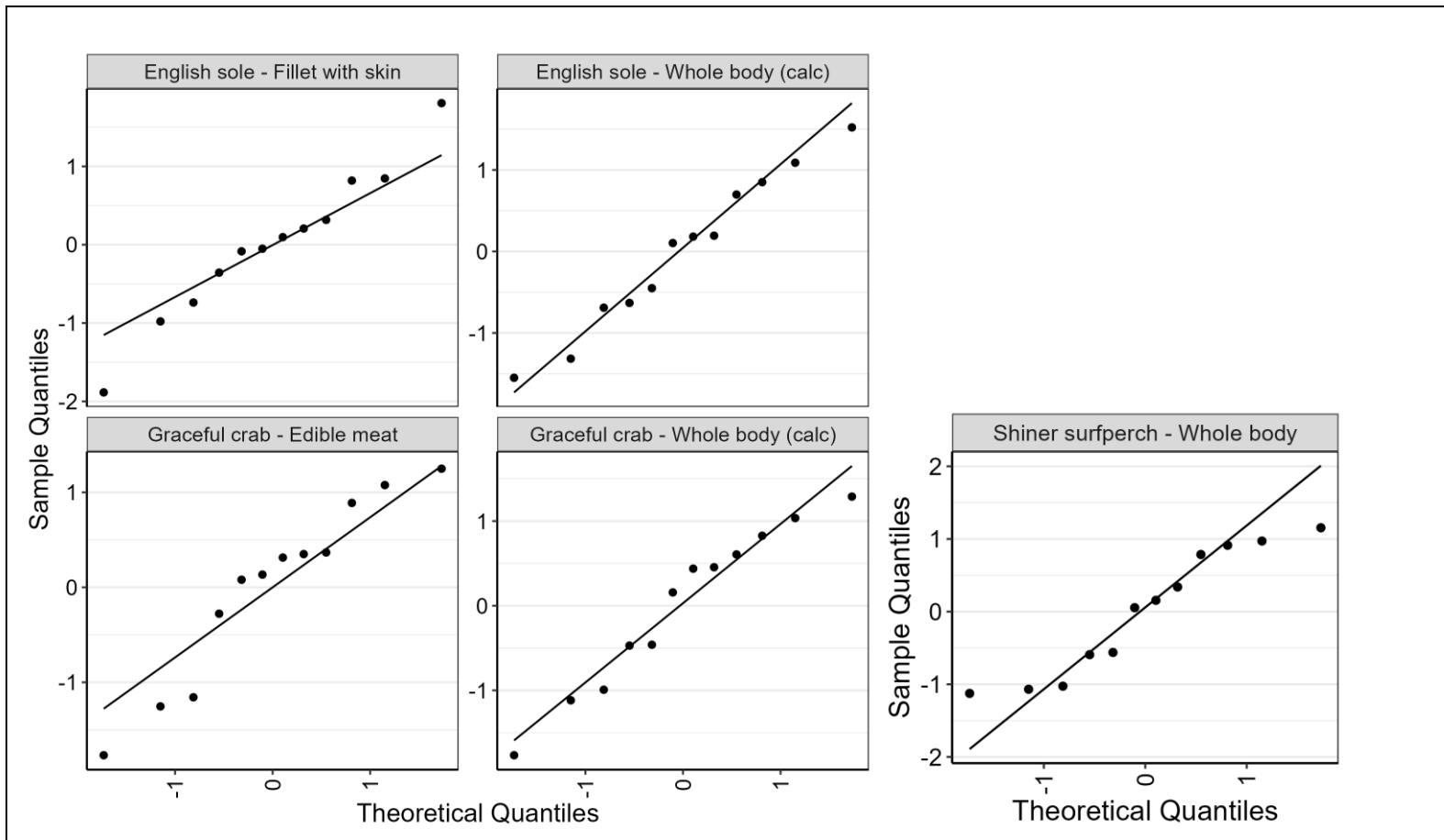
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Results are shown for combined residuals from each LDW river reach/subreach, as appropriate for the stratified model.

Figure 2-1   Normal Probability Plots of Standardized Residuals by Reach/Subreach for 2023 Total PCB Congeners (µg/kg ww) Composite Tissue Samples

Note: Results are shown for combined residuals from each LDW river reach/subreach, as appropriate for the stratified model.
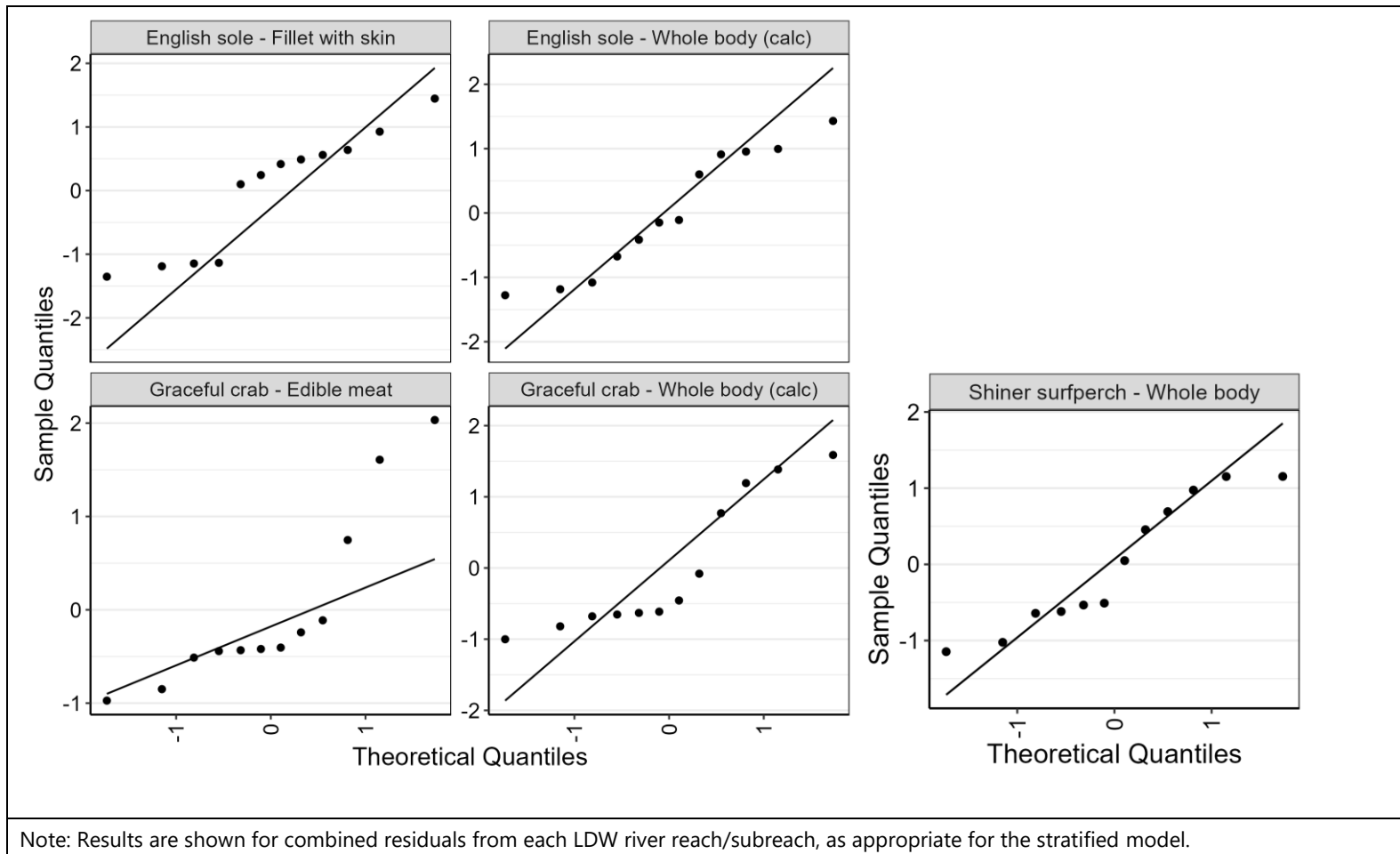
Figure 2-2   Normal Probability Plots of Standardized Residuals by Reach/Subreach for 2023 Dioxin/Furan TEQ (ng/kg ww) in Composite Tissue Samples

The sitewide mean and 95UCL for the 2023 fish and crab tissue results were calculated for the complete dataset for each risk driver (i.e., extreme values were not excluded) using *t*-intervals for the stratified mean (Section 1.2). The two datasets that did not pass normality were dioxin/furan TEQ in graceful crab edible meat and whole-body samples. Due to outliers, no parametric distribution was deemed a good fit (Table 2-1); hence, the 95UCLs for the two datasets not found to have normal distributions were calculated with a bootstrap-t method and are presented in Table 2-2.

Table 2-2
Summary Statistics for 2023 Fish and Crab Tissue

| Risk Driver, Species, and Tissue Type	Detection Frequency	Mean	Minimum	Maximum	95UCL[1]
Total PCB Congeners (µg/kg ww)					
Benthic fish – English sole – fillet	12/12	395	159 J	814 J	463
Benthic fish – English sole – whole body	12/12	758	292 J	1050 J	848
Pelagic fish – shiner surfperch – whole body	12/12	370	235 J	561 J	420
Crab – graceful crab – edible meat	12/12	71.4	34.8 J	121 J	81.0
Crab – graceful crab – whole body	12/12	212	140 J	312 J	231
Dioxin/furan TEQ (ng/kg ww)					
Benthic fish – English sole – fillet	8/12	0.215	0.0975 U	0.360 J	0.255
Benthic fish – English sole – whole body	12/12	0.518	0.362 J	0.710 J	0.560
Pelagic fish – shiner surfperch – whole body	12/12	0.656	0.484 J	1.08 J	0.759
Crab – graceful crab – edible meat	12/12	0.313	0.169 J	1.26 J	0.53[2]
Crab – graceful crab – edible meat (excluding outlier value from Reach 2)	11/11	0.226	0.169 J	0.290 J	0.248
Crab – graceful crab – whole body	12/12	1.35	0.487 J	4.57 J	2.27[2]
Crab – graceful crab – whole body (excluding two outlier values from Reach 2)	10/10	0.715	0.487 J	1.12 J	0.781

Notes:
1. The 95UCL was calculated using the equations for a stratified population. See Section 1.2 for details.
2. These distributions included one or more extreme value and did not fit at normal distribution, so these 95UCLs were estimated using a bootstrap-t method.
95UCL: 95% upper confidence limit (on the mean)
J: estimated concentration
PCB: polychlorinated biphenyl
TEQ: toxic equivalent
U: not detected (above the reporting limit)
ww: wet weight

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2.2 Statistical Comparisons Between 2017 Samples (Pre-Design Studies Dataset) and 2023 Samples

As part of evaluating DQO 2 for fish and crab tissue, a comparison of the 2017 baseline results to the 2023 results was conducted using a confidence interval on the mean of 2023 data minus the mean of baseline data and Welch's approximate *t*-interval (Table 2-3). A positive value for the difference indicated an increase in concentration over time, whereas a negative value for the difference indicated a decrease in concentration over time. Furthermore, when the 95% confidence interval (95CI) excluded zero, the difference was statistically significant (two-tailed alpha = 0.05). In Table 2-3, statistically significant decreases are shaded in blue. Comparisons were performed both by reach and site wide using all available data from each year (i.e., any extreme values were included in the comparison).

Table 2-3
Comparison between 2017 and 2023 Fish and Crab Tissue Results (revised)

Species and Tissue Type	Area[1]	2017 Results			2023 Results			Comparison of 2017 and 2023	
		n	Mean	SE	n	Mean	SE	Difference of Means	95CI for the Difference
Total PCB Congeners (µg/kg ww)									
Benthic fish – English sole – fillet	Sitewide	6	319	35.7	12	395	35.2	75.4	[-38.0, 189]
	R1	3	381	28.9	6	521	66.2	140	[-34, 313]
	R2	3	258	65.4	6	269	23.9	11.1	[-234, 256]
Benthic fish – English sole – whole body	Sitewide	6	808	53.7	12	758	48.9	-50.4	[-210, 109]
	R1	3	1010	101	6	911	52.9	-99.6	[-451, 252]
	R2	3	606	37.7	6	605	82.4	-1.17	[-218, 216]
Pelagic fish – shiner surfperch – whole body	Sitewide	8	446	16.2	12	370	24.5	-76.0	[-145, -6.71]
	R1	4	450	19	6	303	16.6	-147	[-211, -83.1]
	R2	4	442	26.3	6	437	46.1	-5.0	[-140, 130]
Crab – graceful crab – edible meat	Sitewide	8	113	6.91	12	71.4	5.08	-41.6	[-60.1, -23.2]
	R1	4	143	11	6	93.2	8.94	-49.8	[-83.8, -15.7]
	R2	4	83.1	8.32	6	49.6	4.82	-33.5	[-58.2, -8.84]
Crab – graceful crab – whole body	Sitewide	6	257	14.0	12	212	9.42	-44.7	[-82.3, -7.09]
	R1	3	302	26.7	6	256	17.7	-45.6	[-126, 34.3]
	R2	3	212	8.12	6	169	6.56	-43.7	[-68.8, -18.7]

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Species and Tissue Type	Area[1]	2017 Results			2023 Results			Comparison of 2017 and 2023	
		n	Mean	SE	n	Mean	SE	Difference of Means	95CI for the Difference
Dioxin/Furan TEQ (ng/kg ww)									
Benthic fish – English sole – fillet[2]	Sitewide	12	0.428	0.0250	12	0.216	0.0241	-0.214	[-0.284, -0.144]
	R1	6	0.507	0.0783	6	0.230	0.0823	-0.277	[-0.381, -0.174]
	R2	6	0.350	0.0942	6	0.199	0.0727	-0.150	[-0.260, -0.041]
Benthic fish – English sole – whole body	Sitewide	12	1.18	0.0383	12	0.518	0.0231	-0.658	[-0.752, -0.564]
	R2	6	1.41	0.0375	6	0.584	0.0361	-0.825	[-0.941, -0.709]
	R2	6	0.943	0.0667	6	0.452	0.0289	-0.491	[-0.664, -0.318]
Pelagic fish – shiner surfperch – whole body	Sitewide	12	0.952	0.0759	12	0.656	0.0471	-0.295	[-0.500, -0.0905]
	R1	6	1.02	0.129	6	0.732	0.0785	-0.291	[-0.688, 0.105]
	R2	6	0.880	0.0804	6	0.581	0.0522	-0.299	[-0.530, -0.0687]
Crab – graceful crab – edible meat	Sitewide	12	0.406	0.0219	12	0.313	0.0878	-0.0932	[-0.287, 0.100]
	R1	6	0.458	0.0262	6	0.238	0.0133	-0.220	[-0.289, -0.151]
	R2	6	0.355	0.0351	6	0.388	0.175	0.033	[-0.415, 0.482]
Crab – graceful crab – whole body	Sitewide	12	1.21	0.0571	12	1.35	0.405	0.141	[-0.739, 1.02]
	R1	6	1.44	0.0957	6	0.875	0.0629	-0.561	[-0.822, -0.301]
	R2	6	0.987	0.0622	6	1.83	0.808	0.843	[-1.23, 2.92]

Notes:

1. Sampling areas include Reach 1 (RM 0 to RM 2.9) and Reach 2 (RM 2.9 to RM 4.8).

2. The 2023 results for dioxin/furan TEQ in English sole fillets included values below detection limits in both reaches; hence, the mean and SE were calculated using Kaplan-Meier.

95CI: 95% confidence interval

PCB: polychlorinated biphenyl

SE: standard error

TEQ: toxic equivalent

ww: wet weight

3   Clam Tissue

This section provides statistical details regarding the interpretation of the clam tissue data presented in Section 5.2 of the data report.

3.1   95UCL Calculations

To evaluate DQO 1 for clam tissue, a 95UCL for the site-wide mean was calculated from this dataset for the four risk drivers. Following the methods described in Section 1.1, the best distributional form for each risk driver was identified, so that the most appropriate result generated using ProUCL5.1 could be used as the basis for the 95UCL. The best-fitting probability plots are shown in Figures 3-2 through 3-4, and results are summarized in Table 3-1.

Note: Total PCB congeners in whole-body tissues.
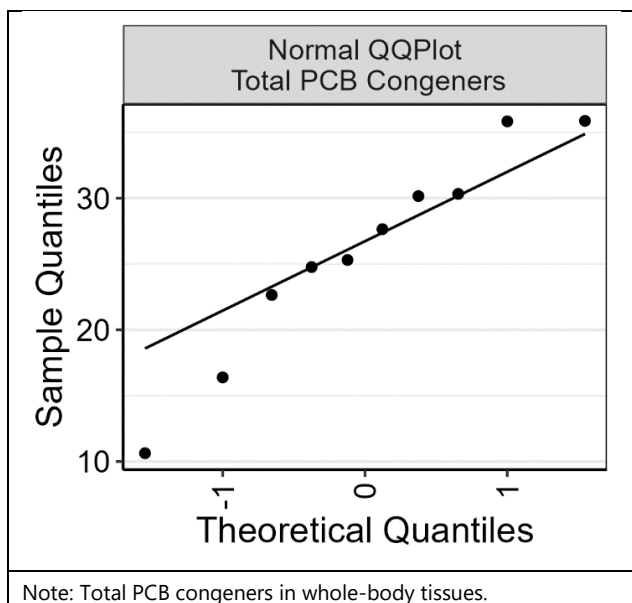
Figure 3-2   Probability Plot of Total PCB Congeners (µg/kg ww) Results in Clam Tissue Composite Samples

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Plots Including All Data

Plots Excluding Extreme Values

Note: cPAH TEQs and dioxin/furan TEQs in whole-body tissues are for all data using one-half method detection limit for non-detects (top row). Results exclude the extreme value in area C05 (Slip 2) for cPAH TEQ, or area C04 for dioxin/furan TEQ (bottom row).
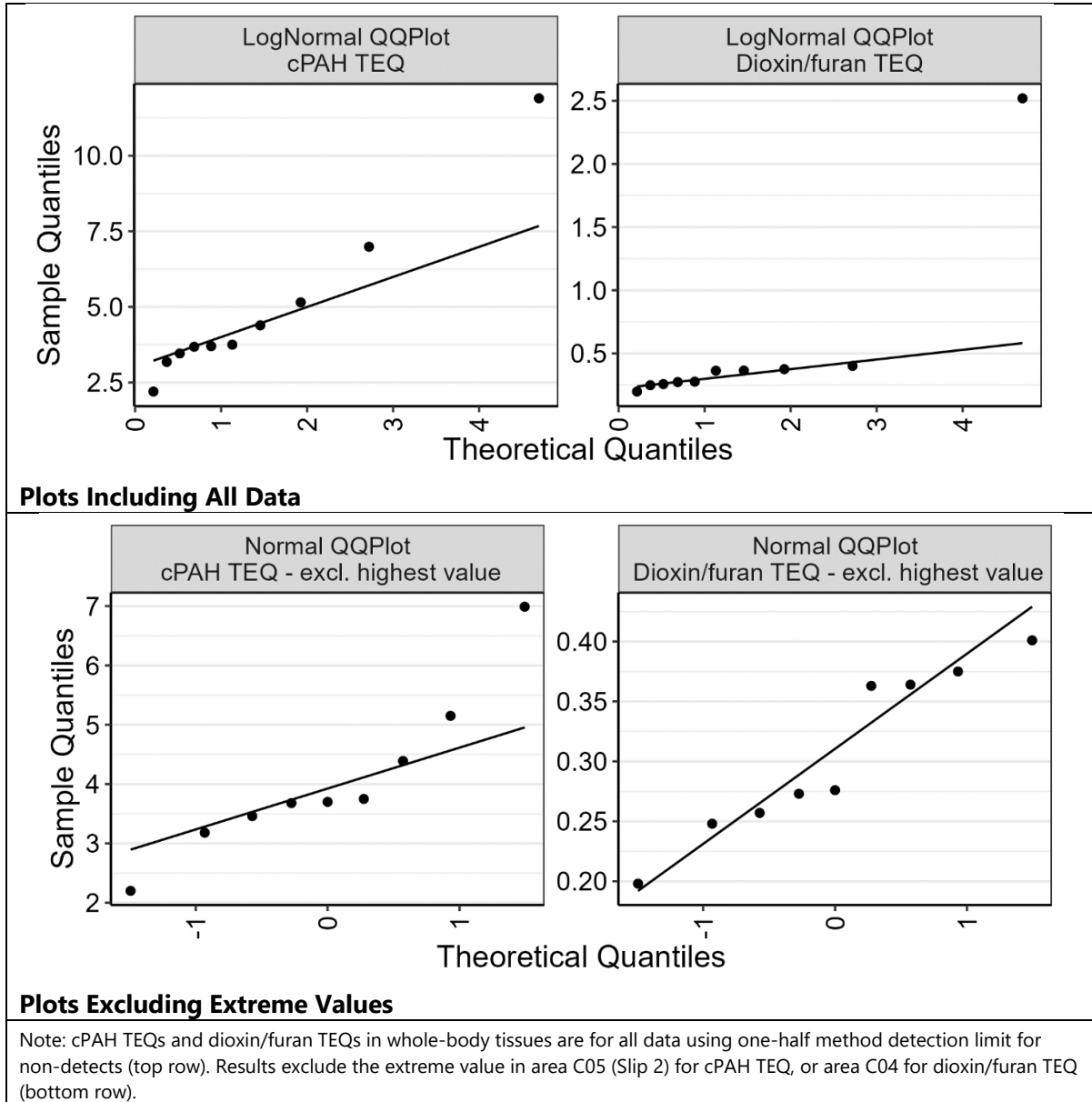
Figure 3-3   Probability Plots of cPAH TEQ (µg/kg ww) and Dioxin/Furan TEQ Results in Clam Tissue Composite Samples

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Plots Showing Data for Whole-body Clams

Plots Showing Data for Whole-body Clams Excluding Siphon Skin

Note: Inorganic arsenic in whole-body (calculated) tissues for all data (top left) and excluding the outlier in area C11 (RM 3.8E) (top right). Inorganic arsenic in whole-body tissues without siphon skin for all data (bottom left) and excluding influential values from areas C04 and C11 (RM 1.5W and RM 3.8E) (bottom left). The means of the two composites from each clamming area are used in this analysis.

Figure 3-4   Probability Plots for Inorganic Arsenic (mg/kg ww) in Clam Tissue Composite Samples

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Table 3-1
GOF and Variance Statistics for Risk Drivers in Clam Tissue Composite Samples

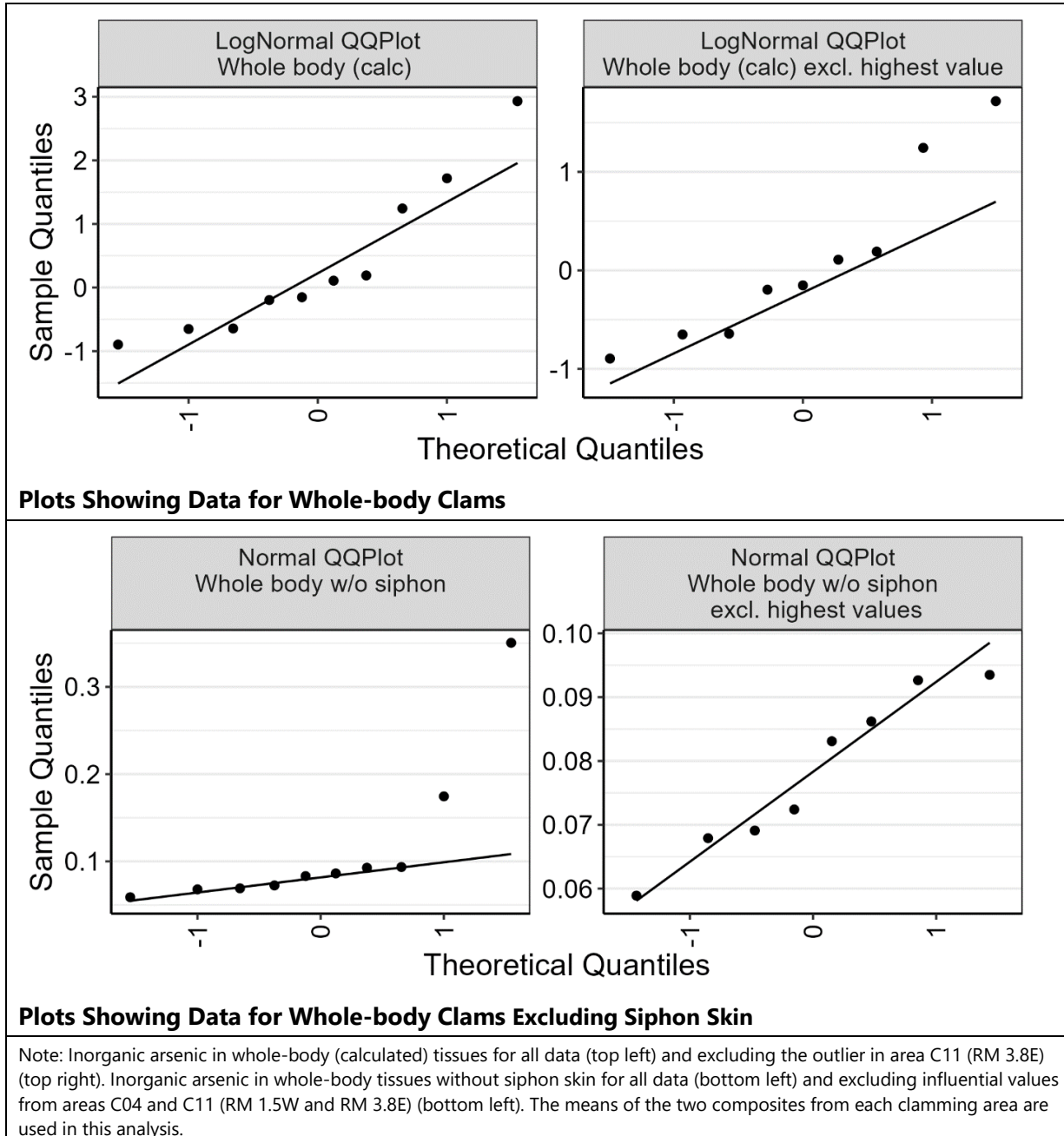| Dataset	n	Best Fit Distribution	PPCC	p-Value	CV
Total PCBs (µg/kg ww)					
Whole body, all data	10	Normal	0.97	0.59	0.31
cPAH TEQ (µg/kg ww)					
Whole body, all data	10	Lognormal	0.94	0.15	0.58
Dioxin/Furan TEQ (ng/kg ww)					
Whole body, all data	10	None	0.65	< 0.001	1.3
Inorganic Arsenic (mg/kg ww)[1]					
Whole body (calculated), all data	10	Lognormal	0.94	0.11	1.7
Whole body without siphon skin, all data	10	None	0.77	< 0.001	0.77

Notes:
1. Summary statistics for inorganic arsenic (including the 95UCL) were calculated by first averaging the concentrations for the two composite samples collected from each clam collection area. Calculating site-wide summary statistics based on each individual value (i.e., without initial averaging) would have suggested that each area had the same mean and variance. Since the data show that this is not a reasonable assumption (Section 3.3), the initial averaging step was necessary to more accurately reflect variance across the site.
95UCL: 95% upper confidence limit (on the mean)
cPAH: carcinogenic polycyclic aromatic hydrocarbon
CV: coefficient of variation
GOF: goodness-of-fit
PCB: polychlorinated biphenyl
PPCC: probability plot correlation coefficient
RM: river mile
TEQ: toxic equivalent
ww: wet weight

The sitewide mean and 95UCL for the 2023 clam tissue results were estimated for the complete dataset for each risk driver using the best-fit distribution from Table 3-1. When individual elevated sample(s) were responsible for the skewness in a distribution, that dataset was also evaluated without the elevated sample(s). Results shown in Table 3-2.

Table 3-2
Summary Statistics for 2023 Clam Tissue

Dataset	Detection Frequency	Mean Value	Min. Detect	Max. Detect	Estimation Method for 95UCL	95UCL[1]
Total PCBs (µg/kg ww)						
Whole body, all data	10/10	26.0	10.6	35.9	Normal	30.6
cPAH TEQ (µg/kg ww)						
Whole body, all data	10/10	4.84	2.20	11.9	Lognormal	6.71

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Dataset	Detection Frequency	Mean Value	Min. Detect	Max. Detect	Estimation Method for 95UCL	95UCL[1]
Dioxin/Furan TEQ (ng/kg ww)						
Whole body, all data	10/10	0.528	0.198 J	2.52 J	Nonparametric (Chebyshev)	1.50
Inorganic Arsenic (mg/kg ww)						
Whole body (calculated), all data	20/20[2]	3.33	0.409	18.8 J	Lognormal	13.2
Whole body without siphon skin, all data	20/20[2]	0.115	0.0589	0.351	Nonparametric (Chebyshev)	0.237

Notes:

Tissue type is whole body unless otherwise specified.

1. The 95UCL was calculated using the equation for normal, lognormal, or gamma distribution, or Chebyshev's inequality for a non-parametric estimate, as determined by the data.

2. Detection frequencies shown are for individual samples across all clamming areas; summary statistics shown are calculated from the average of the two composites from each clamming area (see Section 3.3).

95UCL: 95% upper confidence limit (on the mean)

cPAH: carcinogenic polycyclic aromatic hydrocarbon

PCB: polychlorinated biphenyl

RM: river mile

TEQ: toxic equivalent

ww: wet weight

3.2 Statistical Comparisons Between 2018 Samples and 2023 Samples

As part of evaluating DQO 2 for clam tissue, a comparison of the 2018 baseline results to the 2023 results was conducted using a confidence interval on the mean of 2023 data minus the mean of baseline data and Welch's approximate *t*-interval (Table 3-3). A positive value for the difference indicated an increase in concentration over time, and when the 95CI excluded zero, the difference was statistically significant (two-tailed alpha = 0.05). In Table 3-3, none of the changes are statistically significant. Comparisons were performed twice: once using all available data from each year, and once using only data from the clamming areas sampled in both years.

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Table 3-3
Comparison of 2018 and 2023 Clam Tissue Results

Dataset	2018 Results			2023 Results			Comparison of 2018 and 2023	
	n	Mean	SE	n	Mean	SE	Difference of Means	95CI for the Difference
Total PCB Congeners (µg/kg ww)								
Whole body, all data	6	22.3	1.68	10	26.0	2.53	3.65	[-2.87, 10.2]
Whole body, same locations both years	6	22.3	1.68	6	23.4	3.72	1.09	[-8.57, 10.8]
cPAH TEQ (µg/kg ww)								
Whole body, all data	9	4.29	0.734	10	4.84	0.883	0.554	[-1.87, 2.98]
Whole body, same locations both years	9	4.29	0.734	9	5.02	0.966	0.739	[-1.85, 3.33]
Dioxin/Furan TEQ (ng/kg ww)								
Whole body, all data	9	0.869	0.586	10	0.528	0.222	-0.342	[-1.73, 1.05]
Whole body, same locations both years	9	0.869	0.586	9	0.556	0.247	-0.313	[-1.72, 1.09]
Inorganic Arsenic (mg/kg ww)								
Whole body (calculated), all data[1]	10	5.53	3.56	10	3.33	1.79	-2.20	[-10.8, 6.38]
Whole body without siphon skin, all data[1]	10	0.0872	0.0159	10	0.115	0.0281	0.0277	[-0.042, 0.097]

Notes:
1. The 2023 results were calculated from the average of the two composites from each clamming area (see Section 3.3).
95CI: 95% confidence interval
cPAH: carcinogenic polycyclic aromatic hydrocarbon
PCB: polychlorinated biphenyl
SE: standard error (on the mean)
TEQ: toxic equivalent
ww: wet weight

3.3 Relative Percent Differences Among Composites for Inorganic Arsenic in a Given Area

Inorganic arsenic results were measured in two composites from each of the clamming areas, with each composite sample comprising three individuals. The variability among these composites, expressed as the relative percent difference (RPD), may be used to assess sampling variability (i.e., variability of concentrations within the clam population for each area), homogenization, and analytical variability. The RPDs among composite samples from the 10 clamming areas ranged from 3% to 35% in remainder tissues (i.e., whole-body without the siphon skin), and from 0% to 111% in calculated whole-body tissues. Results are shown graphically in Figure 3-1. These results help

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quantify the level of natural variability in these tissue concentrations. For the sitewide estimates calculated in Section 3.1 and 3.2, the means of the two field replicates from each clamming area are used for a sample size of 10. Calculating site-wide summary statistics based on each individual value (i.e., without initial averaging) would have suggested that each area had the same mean and variance. Since the data show that this is not a reasonable assumption, the initial averaging step was necessary to more accurately reflect variance across the site.
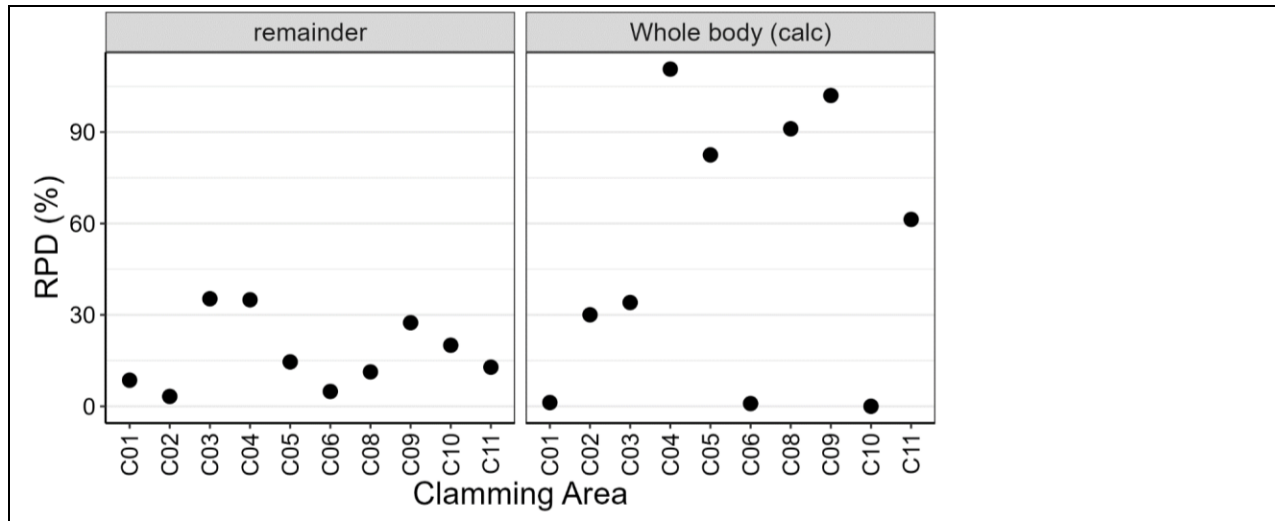

Figure 3-1 **RPD for Inorganic Arsenic in Composite Tissue Samples by Clamming Area and Tissue Type**

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4   Surface Water Passive Samplers

This section provides statistical details regarding the interpretation of passive sampler data relative to DQO 3, as presented in Section 5.3 of the data report.

4.1   Distributional Form

The 2023 dataset was sufficient (n = 10) to investigate the distributional form, so it was evaluated graphically using normal probability plots and formally using GOF tests that applied the methods described in Section 1.1. The normal probability plot for the station residuals[5] (Figure 4-1) indicates that PCB C_{free} data were normally distributed; the PPCC GOF test did not reject normality (p = 0.97). Consequently, a parametric analysis of variance (ANOVA) model may be used to compare results among stations for the 2023 dataset and results between the 2023 and baseline datasets. Summary statistics for the 2023 passive sampler polychlorinated biphenyl (PCB) results are shown in Table 4-1 by location.
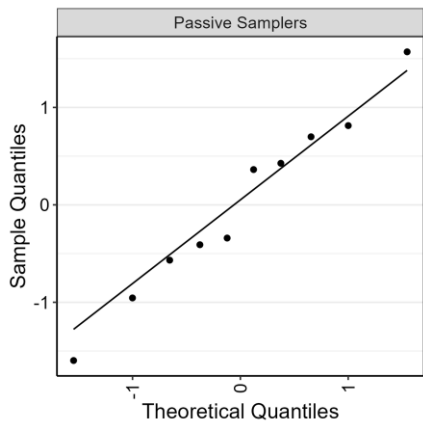

Figure 4-1   Normal Probability Plot of Station Year Standardized Residuals for the 2023 Passive Sampler Dataset (n=10)

Table 4-1
Summary Statistics by Station for 2023 Freely Dissolved Total PCBs Data Calculated from Passive Samplers

Location Name	Count	Best Fit Distribution	PCB C_{free} Concentration (pg/L)	
			Mean	SD
PS1 (South Park Bridge), RM 3.3E	5	Normal	2.07	0.284
PS2 (Lineage Logistics), RM 1.9W	5	Normal	2.17	0.165

Notes:

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[5] Standardized residuals are the individual observations minus the station mean and divided by the SD. The station residuals have a common mean (zero) and SD (one), which allows results from the two stations to be pooled to evaluate the shape and variance of these data, without the result being influenced by differences in the means and variances from locations.

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PCB: polychlorinated biphenyl
RM: river mile
SD: standard deviation

4.2   Statistical Comparisons Between Stations for 2023 Data

An ANOVA comparing the two locations sampled in 2023 indicated that the observed difference between the means of the PCB C_{free} concentration (0.10 ng/L) was not statistically significant ($p = 0.49$). The 95% confidence interval for the difference between station means in 2023 was [-0.44 ng/L, +0.23 ng/L].

4.3   Statistical Comparisons Between 2023 and Baseline Data

A comparison of the baseline results to the 2023 results was conducted using a confidence interval on the mean of 2023 data minus the mean of baseline data (average of 2017 and 2018). The 95CI was calculated using Welch's approximate *t*-interval, which assumes normality but allows for unequal population variances. The temporal differences at both stations indicated an increase in concentration that was statistically significant (2-tailed alpha = 0.05). Results are shown in Table 4-2.

Table 4-2
Comparison Between Baseline and 2023 Datasets for Freely Dissolved Total PCB Data Calculated from Passive Samplers

| | | | PCB C_{free} Concentration (pg/L) | | |
Station	Year	Count	Mean	SE	Temporal Difference (2023 vs. Baseline) and 95CI[1]
PS1 (South Park Bridge), RM 3.3E	Baseline (2017 & 2018)	17	1.14	0.053	0.928 [0.603, 1.25]
	2023	5	2.07	0.127	
PS2 (Lineage Logistics), RM 1.9W	Baseline (2017 & 2018)	18	1.11	0.052	1.06 [0.883, 1.24]
	2023	5	2.17	0.074	

Notes:
1. A comparison of baseline and 2023 results was conducted using a confidence interval on the mean of the 2023 data minus the mean of the baseline data and Welch's approximate t-interval. A positive value for the difference indicates an increase in concentration over time, whereas a negative value indicates a decrease in concentration over time. When the 95CI excludes zero, the difference is statistically significant (two-tailed alpha = 0.05).
95CI: 95% confidence interval
PCB: polychlorinated biphenyl
RM: river mile
SE: standard error (on the mean)

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