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Data Validation Report

Project:	Portland Harbor Pre-Remedial Design Investigation and Baseline Sampling
Laboratory:	SGS AXYS Analytical Services Ltd, Sidney, BC, Canada
Laboratory Group:	WG65310-PCB
Analyses/Method:	Chlorinated Biphenyls by HRGC/HRMS / E1668A
Validation Level:	Stage 2A
AECOM Project Number:	60566335.2.12

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SUMMARY

The samples listed below were collected by AECOM in Portland Harbor in Portland, OR on September 5, 6, 7, 8, and 9, 2018.

Sample ID	Matrix/Sample Type
PDI-TF-SMB012	Fish Tissue
PDI-TF-SMB017	Fish Tissue
PDI-TF-SMB019	Fish Tissue
PDI-TF-SMB026	Fish Tissue
PDI-TF-SMB027	Fish Tissue
PDI-TF-SMB033	Fish Tissue
PDI-TF-SMB037	Fish Tissue
PDI-TF-SMB041	Fish Tissue
PDI-TF-SMB045	Fish Tissue
PDI-TF-SMB047	Fish Tissue
PDI-TF-SMB059	Fish Tissue
PDI-TF-SMB060	Fish Tissue
PDI-TF-SMB071	Fish Tissue
PDI-TF-SMB082	Fish Tissue
PDI-TF-SMB102	Fish Tissue
PDI-TF-SMB113	Fish Tissue
PDI-TF-SMB117	Fish Tissue
PDI-TF-SMB120	Fish Tissue
PDI-TF-SMB132	Fish Tissue

Data validation activities were conducted with reference to:

- *EPA Method 1668A: Chlorinated Biphenyl Congeners in Water, Soil, Sediment, Biosolids, and Tissue by HRGC/HRMS* (USEPA, August 2003),
- *USEPA Contract Laboratory Program National Functional Guidelines for High Resolution Superfund Methods Data Review* (April 2016),
- *Quality Assurance Project Plan, Portland Harbor Pre-Remedial Design Investigation and Baseline Sampling, Portland Harbor Superfund Site (March 2018),* and the
- laboratory quality control (QC) limits.

The National Functional Guidelines were modified to accommodate the non-CLP methodologies. In the absence of method-specific information, laboratory QC limits, project-specific requirements and/or AECOM professional judgment were used as appropriate.

REVIEW ELEMENTS

The data were evaluated based on the following parameters (where applicable to the method):

✓	Data completeness [chain-of-custody (COC)/sample integrity]
✓	Holding times and sample preservation
✗	Laboratory blanks
NA	Matrix spike (MS) and/or matrix spike duplicate (MSD) results
✓	Ongoing precision and recovery results
✓	Matrix duplicate (MD) results
✗	Labeled compounds and labeled clean-up standard recoveries
✗	Sample results/reporting issues

The symbol (✓) indicates that no validation qualifiers were applied based on this parameter. An NA indicates that the parameter was not included as part of this data set or was not applicable to this validation and therefore not reviewed. The symbol (✗) indicates that a QC nonconformance resulted in the qualification of data. Any QC nonconformance that resulted in the qualification of data is discussed below. In addition, nonconformances or other issues that were noted during validation, but did not result in qualification of data, may be discussed for informational purposes only.

The data appear valid as qualified and may be used for decision making purposes. Select data points were qualified as estimated or negated due to nonconformances of certain QC criteria (see discussion below). Qualified sample results are presented in Table 1.

RESULTS

Data Completeness (COC)/Sample Integrity

The data package was reviewed and found to meet acceptance criteria for completeness:

- The COCs were reviewed for completeness of information relevant to the samples and requested analyses, and for signatures indicating transfer of sample custody.
- The laboratory sample login sheet(s) were reviewed for issues potentially affecting sample integrity, including the condition of sample containers upon receipt at the laboratory.

- Completeness of analyses was verified by comparing the reported results to the COC requests.

Holding Times and Sample Preservation

Sample preservation and preparation/analysis holding times were reviewed for conformance with method criteria. All method QC acceptance criteria were met.

Laboratory Blanks

Method blank results are evaluated as to whether there are contaminants detected above the estimated detection limit (EDL). Target compounds were detected in the laboratory method blank associated with the samples in this data set. Note, the laboratory does not qualify sample results "B" associated with method blank contamination.

The NFG guidance stipulates that a conservative approach should be taken with regards to qualification of PCB congeners due to the toxicity of these compounds and the reporting of false negative results should be avoided. Therefore, in order to avoid the reporting of false negative results professional judgment was used to qualify the data in the following manner. As allowed in the NFG, a blank action limit (BAL) was determined as 5 times the method blank result:

- When the sample results were < the method blank result, the sample result was qualified as nondetect (U) at the sample result.
- When the sample result was ≥ the method blank result and ≤ the BAL, the sample result was qualified as estimated and potentially biased high (J+).
- When the sample result was > the BAL, sample result was not qualified.

Qualified sample results are summarized in Table 1.

MS/MSD Results

The MS/MSD not performed on a sample in this data set. No data validation actions were taken on this basis.

Ongoing Precision and Recovery

The OPR %Rs and/or RPDs were reviewed for conformance with the method QC acceptance criteria. All method QC acceptance criteria were met.

MD Duplicate Results

MD RPDs were reviewed for conformance with the AECOM QC acceptance criteria of ≤ 40% [if one or both results were greater than five times the practical quantitation limit (PQL)] for solid matrices. All method QC acceptance criteria were met.

Labeled Compounds and Labeled Clean-up Standard Recoveries

The labeled compounds and labeled clean-up standard %Rs were reviewed for conformance with the QC acceptance criteria.

Nonconformances are summarized in Attachment A in Table A-1. Samples were qualified as follows:

Actions: (Based on NFG 2016)

Criteria		Actions	
		Detected	**Nondetected**
%R > Upper Acceptance Limit		J	UJ
%R >10% but < Lower Acceptance Limit		J	UJ
%R <10%		See below	
<10% and S/N >10:1		J	R
<10% and S/N <10:1		R	R
Ion abundance ratio criteria not met	Calibration compliant	J	UJ
	Calibration non-compliant	J	R
Clean-up Standard Recovery < Lower Acceptance Limit		J	UJ
See Table 6 of method for method QC acceptance criteria[1] [2]The PCB congener method is performed using isotope dilution technique; therefore, professional judgment was applied and bias codes were not included in data qualification.			

Qualified sample results are summarized in Table 1.

Sample Results/Reporting Issues

All sample results detected at concentrations less than the lowest calibration standard (or PQL) but greater than the EDL are qualified by the laboratory as estimated (J). This "J" qualifier is retained during data validation.

As stated in the laboratory's case narrative and SOP, the following reporting issue was noted:

Sample specific detection limits (SDLs) were calculated for each target analyte and used as the detection limit qualifier….. To account for lab background levels and variability in instrument response, detection limits are reported no lower than 0.5 pg absolute……The reported detection limit is the greater value of the SDL and the 0.5 pg absolute reporting limit.

Compound Quantitation and Identification

Samples exhibiting lock-mass ion interference are qualified with a "G" by the laboratory. Professional judgement was used to qualify affected results "J" or "UJ".

Sample results which do not meet relative retention time (RRT) method acceptance criteria were qualified as estimated and tentatively identified (JN).

Qualified sample results are summarized in Table 1.

As noted in the laboratory's case narrative, 40% of the extract for sample PDI-TF-SMB037 was lost during sample cleanup. Since the ^{13}C-labelled standards were within QC limits and isotope dilution quantification procedure automatically corrects for such losses, no data validation actions were taken on this basis.

Estimated Maximum Possible Concentrations (EMPCs)

The data were reviewed to identify sample results that were indicated by the laboratory to be EMPCs because of identification criteria not being met.

The laboratory qualified all sample results with a "K" laboratory qualifier to indicate that the ion ratio criterion was not met. All ion ratios were verified and affected sample results which did not meet the ion ratio criteria were qualified as estimated and tentatively identified (JN). Qualified sample results are shown in Table 1.

It should be noted that the "JN" qualifier was retained rather than replacement with the conventional overall "J" and “J+” qualifiers in instances where sample results were qualified for multiple quality control nonconformances.

Percent Solids Content

Since the sample matrix was fish tissue, all sample results have been reported on a “wet weight” basis.

Verification of calculations was performed on a subset of the data as deemed appropriate. No discrepancies were noted.

QUALIFICATION ACTIONS

Sample results qualified as a result of validation actions are summarized in Table 1. All actions are described above.

ATTACHMENTS

Attachment A: Nonconformance Summary Tables

Attachment B: Qualifier Codes and Explanations

Attachment C: Reason Codes and Explanations

Table 1 - Data Validation Summary of Qualified Data

Sample ID	Matrix	Compound	Result	RDL	EDL	Units	Validation Qualifiers	Validation Reason
PDI-TF-SMB012	TF	PCB-10	11.1	3.25	1.83	pg/g	JN	k
PDI-TF-SMB012	TF	PCB-122	30.3	14.6	1.83	pg/g	JN	k
PDI-TF-SMB012	TF	PCB-126	17.7	13.8	1.83	pg/g	JN	k
PDI-TF-SMB012	TF	PCB-145	2.25	0.556	2.49	pg/g	JN	k
PDI-TF-SMB012	TF	PCB-188	9.67	0.404	1.98	pg/g	JN	k
PDI-TF-SMB012	TF	PCB-204	1.09	0.355	1.83	pg/g	JN	k
PDI-TF-SMB012	TF	PCB-3	3.69	0.333	4.18	pg/g	JN	bl,k
PDI-TF-SMB017	TF	PCB-12/13	4.08	3.39	3.71	pg/g	JN	k
PDI-TF-SMB017	TF	PCB-126	33.1	27.1	1.86	pg/g	JN	k
PDI-TF-SMB017	TF	PCB-145	1.62	0.424	2.53	pg/g	JN	k
PDI-TF-SMB017	TF	PCB-2	1.21	0.404	1.86	pg/g	JN	bl,k
PDI-TF-SMB017	TF	PCB-3	5.38	0.381	4.23	pg/g	J+	bl
PDI-TF-SMB019	TF	PCB-111	13.9	2.51	2.48	pg/g	JN	k
PDI-TF-SMB019	TF	PCB-126	18.9	14.9	1.83	pg/g	JN	k
PDI-TF-SMB019	TF	PCB-145	2.09	0.543	2.48	pg/g	JN	k
PDI-TF-SMB019	TF	PCB-194	800	0.599	1.83	pg/g	J	v
PDI-TF-SMB019	TF	PCB-2	1.41	0.256	1.83	pg/g	J+	bl
PDI-TF-SMB019	TF	PCB-204	0.957	0.242	1.83	pg/g	JN	k
PDI-TF-SMB019	TF	PCB-3	2.31	0.258	4.16	pg/g	J+	bl
PDI-TF-SMB019	TF	PCB-7	4.72	2.72	1.83	pg/g	JN	k
PDI-TF-SMB026	TF	PCB-126	23.4	20.0	1.81	pg/g	JN	k
PDI-TF-SMB026	TF	PCB-145	1.37	0.457	2.47	pg/g	JN	k
PDI-TF-SMB026	TF	PCB-194	935	0.609	1.81	pg/g	J	v
PDI-TF-SMB026	TF	PCB-2	1.68	0.245	1.81	pg/g	J+	bl
PDI-TF-SMB026	TF	PCB-3	3.11	0.232	4.13	pg/g	J+	bl
PDI-TF-SMB026	TF	PCB-58	23.9	13.9	2.47	pg/g	JN	k
PDI-TF-SMB027	TF	PCB-126	25.0	12.2	1.86	pg/g	JN	k
PDI-TF-SMB027	TF	PCB-145	1.57	0.348	2.53	pg/g	JN	k
PDI-TF-SMB027	TF	PCB-2	1.77	0.348	1.86	pg/g	JN	bl,k
PDI-TF-SMB027	TF	PCB-3	3.47	0.336	4.24	pg/g	JN	bl,k
PDI-TF-SMB033	TF	PCB-126	48.5	12.6	1.75	pg/g	JN	k
PDI-TF-SMB033	TF	PCB-145	1.33	0.336	2.38	pg/g	JN	k
PDI-TF-SMB033	TF	PCB-2	1.65	0.244	1.75	pg/g	J+	bl
PDI-TF-SMB033	TF	PCB-204	2.34	0.256	1.75	pg/g	JN	k
PDI-TF-SMB033	TF	PCB-3	3.36	0.234	3.98	pg/g	J+	bl
PDI-TF-SMB033	TF	PCB-57	11.0	7.90	2.10	pg/g	JN	k
PDI-TF-SMB033	TF	PCB-7	4.59	2.13	1.75	pg/g	JN	k
PDI-TF-SMB033	TF	PCB-79	50.7	6.55	1.75	pg/g	JN	rt
PDI-TF-SMB037	TF	PCB-2	1.72	0.500	1.88	pg/g	J+	bl

Sample ID	Matrix	Compound	Result	RDL	EDL	Units	Validation Qualifiers	Validation Reason
PDI-TF-SMB037	TF	PCB-204	1.98	0.503	1.88	pg/g	JN	k
PDI-TF-SMB037	TF	PCB-3	3.06	0.480	4.28	pg/g	JN	bl,k
PDI-TF-SMB037	TF	PCB-7	4.51	4.05	1.88	pg/g	JN	k
PDI-TF-SMB037	TF	PCB-79	44.6	11.4	1.88	pg/g	JN	k
PDI-TF-SMB037	TF	PCB-9	6.80	3.90	1.88	pg/g	JN	k
PDI-TF-SMB041	TF	PCB-111	13.4	3.03	2.49	pg/g	JN	k
PDI-TF-SMB041	TF	PCB-126	36.5	26.0	1.83	pg/g	JN	k
PDI-TF-SMB041	TF	PCB-145	1.78	0.427	2.49	pg/g	JN	k
PDI-TF-SMB041	TF	PCB-162	40.8	16.5	1.83	pg/g	JN	k
PDI-TF-SMB041	TF	PCB-2	1.79	0.356	1.83	pg/g	J+	bl
PDI-TF-SMB041	TF	PCB-3	3.91	0.336	4.17	pg/g	J+	bl
PDI-TF-SMB045	TF	PCB-12/13	3.84	2.45	3.68	pg/g	JN	k
PDI-TF-SMB045	TF	PCB-126	27.7	27.2	1.84	pg/g	JN	k
PDI-TF-SMB045	TF	PCB-155	16.4	0.314	3.17	pg/g	JN	k
PDI-TF-SMB045	TF	PCB-194	1260	0.828	1.84	pg/g	J	v
PDI-TF-SMB045	TF	PCB-2	1.54	0.384	1.84	pg/g	J+	bl
PDI-TF-SMB045	TF	PCB-204	4.16	0.349	1.84	pg/g	JN	k
PDI-TF-SMB045	TF	PCB-3	3.67	0.371	4.20	pg/g	J+	bl
PDI-TF-SMB045	TF	PCB-38	5.80	2.10	1.92	pg/g	JN	k
PDI-TF-SMB047	TF	PCB-11	10.3	4.85	2.86	pg/g	J+	bl
PDI-TF-SMB047	TF	PCB-126	38.8	5.10	1.79	pg/g	JN	k
PDI-TF-SMB047	TF	PCB-192	1.91	0.760	2.29	pg/g	JN	k
PDI-TF-SMB047	TF	PCB-24	40.6	0.267	3.15	pg/g	JN	k
PDI-TF-SMB047	TF	PCB-86/87/97/108/119/125	15500	8.08	17.2	pg/g	J	v
PDI-TF-SMB059	TF	PCB-2	2.52	0.318	1.79	pg/g	JN	k
PDI-TF-SMB059	TF	PCB-204	2.86	0.317	1.79	pg/g	JN	k
PDI-TF-SMB059	TF	PCB-5	4.76	2.35	1.79	pg/g	JN	k
PDI-TF-SMB059	TF	PCB-81	26.6	14.6	1.79	pg/g	JN	k
PDI-TF-SMB060	TF	PCB-126	55.2	14.2	1.74	pg/g	JN	k
PDI-TF-SMB060	TF	PCB-204	2.10	0.245	1.74	pg/g	JN	k
PDI-TF-SMB060	TF	PCB-38	3.82	2.07	1.81	pg/g	JN	k
PDI-TF-SMB060	TF	PCB-81	6.06	3.35	1.74	pg/g	JN	k
PDI-TF-SMB071	TF	PCB-126	185	71.3	1.76	pg/g	JN	k
PDI-TF-SMB071	TF	PCB-145	9.00	0.593	2.40	pg/g	JN	k
PDI-TF-SMB082	TF	PCB-12/13	1.84	1.68	3.69	pg/g	JN	k
PDI-TF-SMB082	TF	PCB-126	23.8	9.57	1.84	pg/g	JN	k
PDI-TF-SMB082	TF	PCB-15	10.8	1.65	4.80	pg/g	JN	k
PDI-TF-SMB082	TF	PCB-162	23.2	3.55	1.84	pg/g	JN	k
PDI-TF-SMB082	TF	PCB-2	0.903	0.428	1.84	pg/g	JN	bl,k
PDI-TF-SMB082	TF	PCB-204	1.39	0.478	1.84	pg/g	JN	k

Sample ID	Matrix	Compound	Result	RDL	EDL	Units	Validation Qualifiers	Validation Reason
PDI-TF-SMB082	TF	PCB-24	1.75	0.270	3.25	pg/g	JN	k
PDI-TF-SMB082	TF	PCB-3	2.30	0.421	4.21	pg/g	JN	bl,k
PDI-TF-SMB082	TF	PCB-57	3.52	2.14	2.21	pg/g	JN	k
PDI-TF-SMB082	TF	PCB-86/87/97/108/119/125	996	2.16	17.7	pg/g	J	v
PDI-TF-SMB082	TF	PCB-89	4.65	2.71	4.35	pg/g	JN	k
PDI-TF-SMB082	TF	PCB-9	2.56	1.56	1.84	pg/g	JN	k
PDI-TF-SMB102	TF	PCB-111	5.57	0.980	2.39	pg/g	JN	k
PDI-TF-SMB102	TF	PCB-121	7.60	1.04	4.08	pg/g	JN	k
PDI-TF-SMB102	TF	PCB-126	10.4	9.77	1.76	pg/g	JN	k
PDI-TF-SMB102	TF	PCB-152	4.36	0.415	1.90	pg/g	JN	k
PDI-TF-SMB102	TF	PCB-165	9.67	5.20	1.76	pg/g	JN	k
PDI-TF-SMB102	TF	PCB-170	2090	0.656	1.97	pg/g	J	i
PDI-TF-SMB102	TF	PCB-182	16.7	0.635	1.76	pg/g	JN	k
PDI-TF-SMB102	TF	PCB-2	0.828	0.388	1.76	pg/g	JN	bl,k
PDI-TF-SMB102	TF	PCB-204	0.967	0.392	1.76	pg/g	JN	k
PDI-TF-SMB102	TF	PCB-23	0.403	0.307	4.43	pg/g	JN	k
PDI-TF-SMB102	TF	PCB-24	1.74	0.196	3.09	pg/g	JN	k
PDI-TF-SMB102	TF	PCB-3	1.34	0.401	4.01	pg/g	J+	bl
PDI-TF-SMB102	TF	PCB-38	0.939	0.305	1.83	pg/g	JN	k
PDI-TF-SMB102	TF	PCB-57	4.23	2.69	2.11	pg/g	JN	k
PDI-TF-SMB102	TF	PCB-58	8.57	2.82	2.39	pg/g	JN	k
PDI-TF-SMB102	TF	PCB-6	11.1	1.36	1.76	pg/g	JN	k
PDI-TF-SMB102	TF	PCB-7	2.45	1.40	1.76	pg/g	JN	k
PDI-TF-SMB102	TF	PCB-73	15.6	0.290	1.76	pg/g	JN	k
PDI-TF-SMB102	TF	PCB-81	3.95	2.64	1.76	pg/g	JN	k
PDI-TF-SMB102	TF	PCB-86/87/97/108/119/125	2060	1.15	16.9	pg/g	J	v
PDI-TF-SMB102	TF	PCB-89	11.3	1.44	4.15	pg/g	JN	k
PDI-TF-SMB102	TF	PCB-9	3.50	1.31	1.76	pg/g	JN	k
PDI-TF-SMB113	TF	PCB-104	2.03	0.212	3.14	pg/g	JN	k
PDI-TF-SMB113	TF	PCB-126	14.9	8.13	1.83	pg/g	JN	k
PDI-TF-SMB113	TF	PCB-145	0.937	0.258	2.48	pg/g	JN	k
PDI-TF-SMB113	TF	PCB-2	1.23	0.248	1.83	pg/g	J+	bl
PDI-TF-SMB113	TF	PCB-3	1.40	0.251	4.16	pg/g	JN	bl,k
PDI-TF-SMB113	TF	PCB-34	2.50	0.632	4.31	pg/g	JN	k
PDI-TF-SMB113	TF	PCB-81	2.71	2.40	1.83	pg/g	JN	k
PDI-TF-SMB113	TF	PCB-89	6.34	1.76	4.31	pg/g	JN	k
PDI-TF-SMB113	TF	PCB-9	5.09	2.78	1.83	pg/g	JN	k
PDI-TF-SMB117	TF	PCB-1	1.44	0.358	1.74	pg/g	JN	bl,k
PDI-TF-SMB117	TF	PCB-11	7.41	2.79	2.79	pg/g	J+	bl
PDI-TF-SMB117	TF	PCB-122	16.9	6.37	1.74	pg/g	JN	k

Sample ID	Matrix	Compound	Result	RDL	EDL	Units	Validation Qualifiers	Validation Reason
PDI-TF-SMB117	TF	PCB-126	10.9	5.93	1.74	pg/g	JN	k
PDI-TF-SMB117	TF	PCB-148	14.4	0.635	1.95	pg/g	JN	k
PDI-TF-SMB117	TF	PCB-150	5.52	0.488	1.74	pg/g	JN	k
PDI-TF-SMB117	TF	PCB-16	15.8	0.634	1.74	pg/g	JN	k
PDI-TF-SMB117	TF	PCB-162	19.0	4.70	1.74	pg/g	JN	k
PDI-TF-SMB117	TF	PCB-188	5.46	0.567	1.88	pg/g	JN	k
PDI-TF-SMB117	TF	PCB-19	9.83	0.562	3.00	pg/g	JN	k
PDI-TF-SMB117	TF	PCB-2	0.570	0.522	1.74	pg/g	JN	bl,k
PDI-TF-SMB117	TF	PCB-201	69.4	0.546	1.81	pg/g	JN	k
PDI-TF-SMB117	TF	PCB-24	0.683	0.379	3.07	pg/g	JN	k
PDI-TF-SMB117	TF	PCB-3	1.16	0.544	3.97	pg/g	J+	bl
PDI-TF-SMB117	TF	PCB-86/87/97/108/119/125	1260	1.82	16.7	pg/g	J	v
PDI-TF-SMB117	TF	PCB-9	2.58	2.54	1.74	pg/g	JN	k
PDI-TF-SMB117	TF	PCB-94	2.82	2.33	3.14	pg/g	JN	k
PDI-TF-SMB120	TF	PCB-1	0.966	0.593	1.82	pg/g	J+	bl
PDI-TF-SMB120	TF	PCB-111	1.81	1.11	2.48	pg/g	JN	k
PDI-TF-SMB120	TF	PCB-126	6.68	6.31	1.82	pg/g	JN	k
PDI-TF-SMB120	TF	PCB-127	11.7	5.78	1.97	pg/g	JN	k
PDI-TF-SMB120	TF	PCB-15	1.51	0.936	4.73	pg/g	JN	k
PDI-TF-SMB120	TF	PCB-182	5.84	0.426	1.82	pg/g	JN	k
PDI-TF-SMB120	TF	PCB-188	2.72	0.308	1.97	pg/g	JN	k
PDI-TF-SMB120	TF	PCB-19	4.38	0.347	3.13	pg/g	JN	k
PDI-TF-SMB120	TF	PCB-2	1.04	0.927	1.82	pg/g	JN	bl,k
PDI-TF-SMB120	TF	PCB-204	0.663	0.340	1.82	pg/g	JN	k
PDI-TF-SMB120	TF	PCB-24	0.686	0.296	3.20	pg/g	JN	k
PDI-TF-SMB120	TF	PCB-27	6.60	0.289	1.89	pg/g	JN	k
PDI-TF-SMB120	TF	PCB-3	1.29	1.08	4.15	pg/g	JN	bl,k
PDI-TF-SMB120	TF	PCB-39	1.92	0.850	1.89	pg/g	JN	k
PDI-TF-SMB120	TF	PCB-7	0.749	0.748	1.82	pg/g	JN	k
PDI-TF-SMB120	TF	PCB-81	3.01	2.11	1.82	pg/g	JN	k
PDI-TF-SMB132	TF	PCB-126	9.29	7.42	1.75	pg/g	JN	k
PDI-TF-SMB132	TF	PCB-165	3.97	2.70	1.75	pg/g	JN	k
PDI-TF-SMB132	TF	PCB-188	4.11	0.582	1.89	pg/g	JN	k
PDI-TF-SMB132	TF	PCB-194	433	0.439	1.75	pg/g	J	v
PDI-TF-SMB132	TF	PCB-2	1.33	0.342	1.75	pg/g	J+	bl
PDI-TF-SMB132	TF	PCB-3	1.68	0.338	3.98	pg/g	JN	bl,k
PDI-TF-SMB132	TF	PCB-34	1.69	0.970	4.12	pg/g	JN	k
PDI-TF-SMB132	TF	PCB-57	2.20	0.913	2.09	pg/g	JN	k
PDI-TF-SMB132	TF	PCB-81	1.10	0.898	1.75	pg/g	JN	k
PDI-TF-SMB132	TF	PCB-94	1.81	1.18	3.14	pg/g	JN	k

Attachment A

Nonconformance Summary Tables

T

Table A-1 - Labeled Compound Ion Abundance Ratios

Sample ID	Labeled Compound	Ion Abundance Ratio	Lower Limit	Upper Limit
PDI-TF-SMB102	13C-PCB-170	1.24	0.89	1.21

Attachment B

Qualifier Codes and Explanations

Qualifier	Explanation
J	The analyte was positively identified; the associated numerical value is the approximate concentration of the analyte in the sample.
J-	The analyte was positively identified; the associated numerical value is the approximate concentration of the analyte in the sample with a potential low bias.
J+	The analyte was positively identified; the associated numerical value is the approximate concentration of the analyte in the sample with a potential high bias.
JN	The analyte was tentatively identified; the associated numerical value is the approximate concentration of the analyte in the sample.
UJ	The analyte was not detected above the reported sample quantitation limit. However, the reported quantitation limit is approximate and may or may not represent the actual limit of quantitation necessary to accurately and precisely measure the analyte in the sample.
U	The analyte was analyzed for, but was not detected above the reported sample quantitation limit.
R	The sample results are rejected due to serious deficiencies in the ability to analyze the sample and meet quality control criteria. The presence or absence of the analyte cannot be verified.

Attachment C

Reason Codes and Explanations

Reason Code	Explanation
be	Equipment blank contamination
bf	Field blank contamination
bl	Laboratory blank contamination
c	Calibration issue
cl	Clean-up standard recovery
cr	Chromatographic resolution
d	Reporting limit raised due to chromatographic interference
fd	Field duplicate RPDs
h	Holding times
i	Internal standard areas
k	Estimated Maximum Possible Concentration (EMPC)
l	LCS or OPR recoveries
lc	Labeled compound recovery
ld	Laboratory duplicate RPDs
lp	Laboratory control sample/laboratory control sample duplicate RPDs
m	Matrix spike recovery
ma	Multiple analyses. Sample analyzed more than once, a value from another analysis should be used.
md	Matrix spike/matrix spike duplicate RPDs
nb	Negative laboratory blank contamination
p	Chemical preservation issue
q	Quantitation issue
r	Dual column RPD
rt	SIM ions not within + 2 seconds, or not within relative retention time (RRT) windowQuantitation issue
s	Surrogate recovery
su	Ion suppression
t	Temperature preservation issue
v	Compound identification issue
x	Percent solids
y	Serial dilution results
z	ICS results