LOCATION_ID	DISPLAY_SAMPLE_DATE	FIELD_PREPARATION_CODE	SAMPLE_PURPOSE	ANALYSIS_TYPE_CODE	ANALYTICAL_METHOD_CATEGORY	PARAMETER_CATEGORY	PARAMETER_NAME	PARAMETER_CODE
Buckman 1	3/22/12	UF	REG	INIT	RAD	RAD	Tritium	H-3
Buckman 6	3/22/12	UF	REG	INIT	RAD	RAD	Tritium	H-3
Buckman 8	3/22/12	UF	REG	INIT	RAD	RAD	Tritium	H-3

DETECT_FLAG	REPORT_RESULT	REPORT_MINIMUM_DETECTABLE_ACTIVITY	REPORT_UNCERTAINTY	REPORT_UNITS	ANALYTICAL_METHOD	DILUTION_FACTOR	SAMPLE_TYPE	LAB_ID
N	1.452	2.18	0.705	pCi/L	Generic:Lo	1	WG	ARSL
N	1.552	2.131	0.698	pCi/L	Generic:Lo	1	WG	ARSL
N	0.784	1.882	0.581	pCi/L	Generic:Lo	1	WG	ARSL

LAB_QUALIFIER	VALIDATION_QUALIFIER	VALIDATION_REASON_CODES
U	U	R5
U	U	R5
U	U	R5

Definitions for Other Codes

SAMPLE_PURPO	
SE	Fld Qc Type Desc
EQB	Equipment Rinsate Blank
FB	Field Blank
FD	Field Duplicate
FR	Field Rinsate
FS	Field Split
FTB	Field Trip Blank
FTR	Field Triplicate
INB	Equipment blank taken during installation and not assoc with a sampling event
ITB	Trip blank taken during installation and not assoc with a sampling event
NA	Not Applicable
PEB	Performance Evaluation Blank
PEK	Performance Evaluation Known
RES	Resample
SS	Special sampling event, data unique
SS-EQB	Equipment Blank of special sampling event, data unique
SS-FB	Field Blank of special sampling event, data unique
SS-FD	Field Duplicate of special sampling event, data unique
SS-FTB	Field Trip Blank of special sampling event, data unique

FIELD_PREPARA TION_CODE	Fld Prep Desc
F	Filtered
UF	Unfiltered

PARAMETER_CA TEGORY	Anyl Suite Desc
ANION	ANION
DIOX/FUR	Dioxin and Furans
DRO	Diesel Range Organics
GAMMA	Gamma Spectroscopy
GAMMA_SPEC	GAMMA_SPEC
GENINORG	General Inorganics
GRO	Gasoline Range Organics
GROSSAB	GROSSAB
HERB	Herbicides
HEXP	High Explosives

INORGANIC	Inorganics
ISOTOPE	Isotopes Ratios
METALS	Metals
PCB	PCB
PCB_CONG	PCB Congeners
PEST	PEST
PEST/PCB	Pesticide and PCBs
PESTPCB	Pesticides/PCBs
RAD	Radiochemistry (Not Gamma)
SVOA	Semivolatiles Organics
SVOC	SVOC
VOA	Volatile Organics
VOC	Volatile Organic Compounds

ANALYSIS_TYPE_	
CODE	Lab Sample Type Desc
REG	Client Sample
DL	Dilution
DUP	Duplicate
RE	Reanalysis
REDL	Reanalysis Dilution
REDP	Reanalysis Duplicate
RI	Reissue
TRP	Triplicate

SAMPLE_TYPE	Fld Matrix Desc
WG	Ground Water
WM	Snowmelt
WP	Persistent Flow
WS	Base Flow
WT	Storm Runoff

LAB_ID	Lab Desc
ALTC	Alta Analytical Lab Incorporated
ARSL	American Radiation Services - Primary
C-INC	Los Alamos National Laboratory-Isotope and Nuclear chemistry divison
COAST	Coastal Science Lab
CST	LANL Chemical Sciences & Technology
EES6	Environmental Sciences Division
ESE	Environmental Sciences & Engineering, Inc., Gainesville, FL
FLD	Measurement taken in Field
GEL	General Engineering Laboratories, Inc.
GELC	General Engineering Laboratories, Inc., Charleston, SC.
GEO	Geochron Lab

HENV	JCNNM
HUFFMAN	Huffman
KA	KEMRON
LVLI	LVLI
PARA	Paragon Analytics, Inc.
PEC	Pacific EcoRisk Laboratories
QESL	Quanterra Environmental Services, St. Louis, MO
QST	QST Environmental, Newberry, FL
RECRAP	RECRA Labnet, Lionville, PA
RFWC	Roy F. Weston, West Chester, PA
SGSW	Paradigm
SILENS	Stable Isotopes Laboratory
STL2	Severn Trent Laboratories - Richland, Historical
STLA	Severn Trent - Los Angeles
STR	Severn Trent Laboratories - Richland
STSL	Severn Trent Laboraties, Inc., St. Louis
SwRI	Southwest Research Institute
UAZ	University of Arizona
UIL	University of Illinios
UMTL	University of Miami Tritium Lab

Analytical Laboratory Qualifier Codes.

Lab Qual Code	Lab Qual Desc
*	(Inorganic) - Duplicate Analysis (relative percent difference) not within control limits.
B	(Organic) - Analyte present in the blank and the sample. (Inorganic) - reported value was obtained from a reading that was less than the Contract Required Detection Limit (CRDL) but greater than or equal to the Instrument Detection Limit (IDL).
BJ	See B code and see J code
BJP	See B code, see J code and see P code
BPX	(B) (Organic) - This analyte was detected in the associated Laboratory Method Blank and the sample. (B) (Inorganic) - The result for this analyte was greater than the Instrument Detection Limit but less than the Contract Required Detection Limit. (P) (Pesticides/PCBs) - The quantitative results for this analyte between the primary and secondary GC columns were greater than 25% difference. (P) (SW-846 EPA Method 8310 High Pressure Liquid Chromotography, HPLC results) - The quantitative results for this analyte between the primary and secondary HPLC columns or primary and secondary HPLC detectors were greater than 40% difference. (X) (Organic/Inorganic) - The result for this analyte should be regarded as not detected.
D	The result for this analyte was reported from a dilution.
DJ	See D code and see J code
DNA	did not analyze due to broken equipment.
E	Analyte exceeded the concentration range (Organics). The serial dilution was exceeded (Inorganics)
E*	See E code and see * code.
EJ	See E code and see J code
EJ*	See E code, See J code and see * code
EJN	(E) (Organic) - The result for this anlayte exceeded the upper range of the instrument initial calibration curve. (E) (Inorganic) (ICP-AES) - The result for this analyte in the serial dilution analysis was outside acceptance criteria. (E) (Inorganic) (GFAA) - The result for this analyte failed one or more CLP acceptance critera as explained in the case narrative. (J) (Organic/General Inorganics) - The result for this analyte was greater than the Method Detection Limit (MDL) but less than the Practical Quantitaion Limit (PQL). (N) (Organic) - The reported analyte is a tentitively idenififed compound (TIC). (N) (Inorganic) - The result for this anlayte in the matrix spike sample was outside acceptance criteria.
EN	See E code and see N code

	(E) (Organic) - The result for this anlayte exceeded the upper range of the instrument initial calibration curve. (E) (Inorganic) (ICP-AES) - The result for this analyte in the serial dilution analysis was outside acceptance criteria. (E) (Inorganic) (GFAA) - The result for this analyte failed one or more CLP acceptance critera as explained in the case narrative. (N) (Organic) - The reported analyte is a tentitively idenififed compound (TIC). (N) (Inorganic) - The result for this anlayte in the matrix spike sample was outside acceptance criteria. * (Inorganic) - The result for this analyte in the Laboratory Replicate analysis was outside acceptance
EN*	criteria.
	(H) (Organic/Inorganic) - The required extraction or analysis holding time for this result was
H	exceeded.
	(H) (Organic/Inorganic) - The required extraction or analysis holding time for this result was exceeded. * (Organic) and (Inorganic) - The result for this analyte in the Laboratory Control
H*	Sample analysis was outside acceptance criteria.
HJ	See H code and see J code
	(H) (Organic/Inorganic) - The required extraction or analysis holding time for this result was exceeded. (J) (Organic/General Inorganics) - The result for this analyte was greater than the Method Detection Limit (MDL) but less than the Practical Quantitaion Limit (PQL). * (Inorganic) - The result for this analyte in the Laboratory Replicate analysis was outside
HJ*	acceptance criteria.
	(d15N) - The d15N of nitrate is a signature of the nitrate present in a sample. Therefore, nitrate has to be present to have a signature. A d15N value can not be given to a blank, since the blank does not have nitrate. This is different than most analytical methods where you would run a blank and use the designator: "non detect" or detected, but below
INS	detection limit.
	(Inorganic) -The associated numerical value is an estimated quantity. (Organic) - The
J	associated numerical value is an estimated quantity.
J*	See J code and see * code.
JB	See J code and see B code
JN	See J code and see N code
JN*	See J code, see N code and see * code
JP	See J code and see P code
N	(Inorganic) - Spiked sample recovery not within control limits.
N*	See N code and see * code.
N*E	See N code, see * code and see E code
NE	See N code and see E code
	Percent difference between the results on the two columns during the analysis differed by
P	more than 40%.
PJ	See P code and see J code
	The material was analyzed for, but was not detected above the level of the associated
U	numeric value.
U*	See U code and see * code
UD	See U code and see D code.
UE	See U code and see E code
UE*	See U code, see E code and see * code
UEN	See U code, see E code and see N code
UH	See U code and see H code.

	(U) (Organic/Inorganic) - The result for this analyte was not detected at the specified reporting limit. (H) (Organic/Inorganic) - The required extraction or analysis holding time for this result was exceeded. * (Inorganic) - The result for this analyte in the Laboratory
UH*	Replicate analysis was outside acceptance criteria.
UI	This code is no longer used.
UN	EPA Flag (Inorganic) Compound was analyzed for,but not detected and spiked sample recovery not within control limits.
UN*	EPA Flag (Inorganic) -see U code, see N code, and see * code.
X	Lab suspects result is a nondetect despite positive quantification results.

Secondary Validation Flag Codes.

Valid Flag Code	Valid Flag Desc
A	The contractually-required supporting documentation for this datum is absent.
I	The calculated sums are considered incomplete due to lack of one or more congener results.
J	The analyte is classified as detected but the reported concentration value is expected to be more uncertain than usual.
J-	The analyte is classified as detected but the reported concentration value is expected to be more uncertain than usual with a potential negative bias.
J+	The analyte is classified as detected but the reported concentration value is expected to be more uncertain than usual with a potential positive bias.
JN-	Presumptive evidence of the presence of the material at an an estimated quantity with a suspected negative bias.
JN+	Presumptive evidence of the presence of the material at an an estimated quantity with a suspected positive bias.
N	Presumptive evidence of the presence of the material.
NJ	(Organic) -Analyte has been tentatively identified and the associated numerical value is estimated based upon 1:1 response factor to the nearest eluting internal standard.
NQ	No validation qualifier flag is associated with this result, and the analyte is classified as detected.
PM	Manual review of raw data is recommended to determine if the observed non-compliances with quality acceptance criteria adversely impacts data use.
R	The reported sample result is classified as rejected due to serious noncompliances regarding quality control acceptance criteria. The presence or absence of the analyte cannot be verified based on routine validation alone
U	The analyte is classified as not detected.
UJ	The analyte is classified as not detected, with an expectation that the reported result is more uncertain than usual.

Secondary Validation Reason Codes.

Valid Reason Code	Valid Reason Description
12a	Metals interference check sample percent recovery value is ≥50% and <80%.
CB0	The absolute RT of CB 209 must be ≥55 minutes if the SPB-octyl column is used. If a GC column or column system alternate to the SPB-octyl column is used, the absolute Retention Time (RT) of CB 209 must be ≥ the laboratory-established minimum RT for CB 209. If the laboratory has not established a minimum RT value for CB 209, the RT for CB 209 must be ≥55 minutes. If an SPB-octyl column was used and the absolute RT of CB 209 is <55 minutes, qualify all associated results as R. If a GC column on column systems alternate to the SPB-octyl column was used and the absolute RT is < the laboratory established minimum RT for CB 209, or <55 minutes if the laboratory has not established a minimum RT, qualify all associated results as R. The absolute retention times of the Labeled Toxics/LOC/window defining standard congeners in the verification test must be within ±15 seconds of the respective retention times in the calibration or, if an alternate column or column system is employed, within ±15 seconds of the respective retention times in the calibration for the alternate column or column system. The relative retention times (RRTs) of native CBs and labeled compounds in the verification test must be within their respective RRT limits or, if an alternate column or column system is employed, with their
CB0b	Required RT documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
CB12	The Ongoing Precision Recovery (OPR) percent recovery was less than 10%.OPR is a method blank spiked with known quantities of analytes. The OPR is analyzed exactly like a sample. Its purpose is to assure that the results produced by the laboratory remain within the limits specified in this EPA Method for precision and recovery. OPR must be established for every batch of samples extracted and analyzed and must meet the recovery and %RSD limits listed in Attachment 5. If the OPR criteria are not met and reanalysis was not performed, the laboratory performance and method accuracy are in question: 1. If the OPR recovery is <10% qualify all detects as J- and all associated non-detects as R. 2. If recoveries of more than half of the compounds in the OPR analysis are below 10%, qualify all associated defects as J- and all associated non-detects as R. [NOTE: If recoveries for more than half of the compounds in the OPR analysis are below the acceptance range, the laboratory has not shown that it can actually meet program required detection limits.]
CB12a	The OPR sample percent recovery was < the Lower Acceptance Limit (LAL) but >10%. If the OPR recovery is < the LAL, qualify all associated detects as J- and all associated non-detects as “UJ” if the recovery is ≥10%.
CB12b	The OPR sample percent recovery was > the Upper Acceptance Limit. If the OPR recover is > the UAL, qualify all associated detects as J+. If recoveries of more than half of the compounds in the OPR analysis are above the acceptance range, qualify all associated detects as J+.
CB12c	The OPR sample documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
CB12d	If recoveries of more than half of the compounds in the OPR analysis exceed the acceptance range, both above and below, qualify all associated detects as J and all associated non-detects as UJ.
CB15	The affected analytes are considered suspect because the sample was diluted without any target analytes identified due to matrix interference. (Qualify as Reject if the analytical laboratory cannot provide proof for matrix interference.)

CB16	Gas chromatograph/mass spectrometer (GC/MS) instrument performance checks are performed to ensure mass resolution, identification, and to some degree, sensitivity. These criteria are not sample specific. Conformance is determined using standard materials; therefore, these criteria should be met in all circumstances. Failure to meet either the resolution or the retention window criteria invalidates all calibration or sample data collected during the 12-hour time window. If mass spectrometer performance was not evaluated at the required frequency or if method criteria were not met, qualify all associated detects and non-detects as R.
CB16c	The required instrument performance sample information is missing. Contact the SMO or external laboratory for information.
CB19	The project chemist identified quality deficiencies in the reported data that require further qualification. This code can only be used under advisement by the project chemist.
CB3	To assess method performance on the sample matrix, the laboratory must spike all samples with the labeled toxics/LOC/window defining standard spiking solution and all sample extracts with the labeled cleanup standard spiking solution. The recovery of each labeled compound must be within the limits listed in Table 6 of the method. If the recovery of any labeled toxics/LOC/window defining standard compound is < 10%, qualify all not detected results as R and all detected results as J-.
CB3a	The labeled compound is < the Lower Acceptance Limit but ≥ 10% R. The recovery of each labeled compound must be within the limits in Table 6 of the method. If the recovery of any labeled toxics/LOC/window defining standard compound is below acceptance limits, qualify all detects for that sample fraction as J and all nondetects for that sample fraction as UJ if the recovery is ≥10%.
CB3b	The labeled compound is > the Upper Acceptance Limit. The recovery of each labeled compound must be within the limits listed in Table 6 of the method. If the recovery of any labeled toxics/LOC/window defining standard compound is above acceptance limits, qualify all detects for that sample fraction as J and all nondetects for that sample fraction as UJ.
CB3d	Required labeled compound information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
CB4	The sample result is ≤5 times the concentration of the related analyte in the method blank, which indicates the reported detection is considered indistinguishable from contamination in the blank.
CB4a	The affected analytes are considered estimated and biased high because this analyte was identified in the method blank but was >5x.
CB4d	The sample result is ≤5x the concentration of the related analyte in the trip blank, rinsate blank, and equipment blank, which indicates the reported detection is considered indistinguishable from contamination in the blank.
CB4e	Required method blank information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
CB7	The affected results were not analyzed with a valid 5-point calibration curve and/or a standard at the reporting limit.

CB7a	Isotope dilution shall be used for calibration of the toxics and beginning and ending level of chlorination (LOC) chlorinated biphenyls (CBs). A 5- or 6-point calibration is prepared for each native congener. The RRF %RSD for all native toxins/LOC CBs must be <20%. If a linear curve is used for initial calibration, the r2 of the curve must be >0.99. 1. If the %RSD for any target compound is >20% but ≤40%, qualify all associated detects as J and, if any other calibration criteria have been exceeded for that compound, qualify all associated non-detects as UJ. 2. If the %RSD for any target compound is >40% but ≤60%, qualify all associated detects as J and all associated non-detects as UJ. 3. If the %RSD for any target compound is >60%, qualify all associated detects as J and all associated non-detects as R. 4. If the r2 for any target compound is <0.99 but ≥0.90, qualify all associated detects as J and , if any other calibration criteria have been exceeded for that compound, qualify all associated non-detects as UJ. 5. If the r2 for any target compound is <0.90 but ≥0.80, qualify all associated detects as J and all associated non-detects as UJ. 6. If the r2 for any target compound is <0.80, qualify all associated detects as J and all associated non-detects as R.
CB7b	The affected analytes did not meet the ion abundance ratios criteria in the initial calibration and/or CCV. Calibration using internal standards is used for determination of native CBs for which a labeled compound is not available. For these CBs, calibration is performed at a single point. Compounds should be quantitated using the appropriate reference internal standard listed in Table 2 of the method. Ion abundance ratios must meet the criteria in Attachment 4, Theoretical Ion Abundance Ratios and QC Limits for EPA Method 1668A, of this procedure, or must be within 15% of the theoretical ratio of the ion monitored. If the ion abundance criteria are not met, qualify all detected results for that analyte as R.
CB7c	The ICV and/or CCV were recovered outside the method limits (see CB7a for ICAL specifications). At the beginning of each 12-hour period during which analysis is performed, calibration is verified for all native CBs and labeled compounds. The ion abundance ratios for all CBs must be within the limits in Attachment 4, and all compounds must meet the calibration verification recovery limits listed in Attachment 5, QA Acceptance Criteria for CBs in Calibration Verification, Initial Precision and Recovery, OPR, and Samples for EPA Method 1668A. RRTs of native CBs and labeled compounds in the calibration verification must be within ±0.5% of the mean RRT determined from the initial calibration or most recent calibration verification standard. The diluted combined 209 congener solution must be analyzed as a final step in the calibration verification and must meet the minimum analysis and resolution specifications of the method. If the ion abundance ratio for any calibration verification compound is outside of the method limits, qualify all associated detects as J and all associated non-detects as UJ. If the verification limits are not met for any calibration verification compound and the recovery is above the verification limits, qualify all associated detects as J+. If the verification limits are not met for any calibration verification compound and the recovery is below the verification limits, qualify all associated detects as J- and all associated non-
CB7d	The ICV and/or CCV were not analyzed at the appropriate method frequency. At the beginning of each 12-hour period during which analysis is performed, calibration is verified for all native CBs and labeled compounds. Use professional judgment based on when ICVs and CCVs were analyzed (also, see CB7f).
CB7f	Required calibration information is missing or samples were analyzed on an expired calibration. Contact the SMO or external laboratory for information.
CB8	The affected analyte is considered rejected because ion abundance ratios did not meet specifications. For identification of any CB or labeled compound, the ion abundance ratios must be within the limits specified in Attachment 4, or ±15% of the calibration verification standard. If ion abundance ratio criteria were not met for any compound, qualify all associated results as R.
CB88	Duplicate, dilution, or reanalysis.
CB8a	The ion ratio documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.

CB9	The extraction/analytical holding time is exceeded by less than 2x the published method for holding times. There are no demonstrated maximum holding times associated with the CBs in EPA Method 1668, aqueous, solid, semi-solid, tissues, or other sample matrices. If stored in the dark at 0-4ºC and preserved as given above (if required), aqueous samples may be stored for up to one year. Similarly, if stored in the dark at <-10ºC, solid semi-solid, multi-phase, and tissue samples may be stored for up to one year. Store sample extracts in the dark at <-10ºC until analyzed. If stored in the dark at <-10ºC, sample extracts may be stored for up to one year.
CB9a	The extraction/analytical holding time was exceeded by more than 2x the published method for holding times. There are no demonstrated maximum holding times associated with the CBs in EPA Method 1668, aqueous, solid, semi-solid, tissues, or other sample matrices. If stored in the dark at 0-4ºC and preserved as given above (if required), aqueous samples may be stored for up to one year. Similarly, if stored in the dark at <-10ºC, solid, semi-solid, multi-phase, and tissue samples may be stored for up to one year. Store sample extracts in the dark at<-10ºC until analyzed. If stored in the dark at <-10ºC, sample extracts may be stored for up to one year.
DF0	The IS retention time and qualitative criteria for target compound identification were not met. For 2,3,7,8-substituted compounds that have an isotopically-labeled internal standard or recovery standard present in the sample extract, the Retention Time (RT) must be -1 to +3 seconds of the isotopically-labeled standard. For 2,3,7,8-substituted compounds that do not have an isotopically-labeled internal standard or recovery standard present in the sample extract, the RT must fall within 0.005 RRT units of the Required Retention Time (RRT) measured in the continuing calibration. For non-2,3,7,8-substituted compounds, the RT must be within the corresponding homologous RT windows established by analyzing the column performance check solution. If the RT of any compound is outside of the RT window, qualify all associated results as R.
DF0b	RRT documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
DF12	The LCS percent recovery was <10%.
DF12a	The LCS percent recovery was < the Lower Acceptance Limit but >10%. Follow the external laboratory limits.
DF12b	The LCS percent recovery was > the Upper Acceptance Limit. Follow the external laboratory limits.
DF12c	The LCS documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
DF12d	The MS/MSD percent recovery was <10%.
DF12e	The MS/MSD percent recovery was >10% but <70%.
DF12f	The MS/MSD percent recovery was >130%.
DF12g	The MS/MSD relative percent difference was >30%.
DF12h	The laboratory must spike all samples with the sample fortification solution and all sample extracts with recovery standard solution. The recovery acceptance criteria for each compound is 40% to 135%. The fortification sample percent recovery was <10%.
DF12i	The laboratory must spike all samples with the sample fortification solution and all sample extracts with recovery standard solution. The recovery acceptance criteria for each compound is 40% to 135%. The fortification sample percent recovery was <40% but >10%.
DF12j	The laboratory must spike all samples with the sample fortification solution and all sample extracts with recovery standard solution. The recovery acceptance criteria for each compound is 40% to 135%. The fortification sample percent recovery was >135%.
DF12k	The fortification sample documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.

DF15	The affected analytes have elevated detection limits and may not meet project DQOs because the sample was diluted without any target analytes identified due to matrix interference. (Qualify non-detected results as rejected if the analytical laboratory cannot provide proof for matrix interference.)
DF15a	Sample clean-up was not performed. If run log notations, spectral data and/or internal standard or labeled compound recoveries indicate interferences and extract clean-up was not performed, qualify all associated detects as J and all non-detects as UJ.
DF16	The instrument performance sample did not pass method acceptance criteria.
DF16c	The required instrument performance sample information is missing. Contact the SMO or external laboratory for information.
DF19	The project chemist identified quality deficiencies in the reported data that require further qualification. This code can only be used under advisement by the project chemist.
DF1d	Required IS information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
DF4	The sample result is ≤5 times the concentration of the related analyte in the method blank. The criteria for the frequency of extraction and analysis of method blanks as stated in Section 9.5 of Method 1613B shall be followed and demonstrated in the documented data. The maximum amount of PCDD and PCDF isomer contamination in method blanks is stated in Table 2 of Method 1613B. The method blank must be measured on each GC/MS system which is used to measure a group of samples. This requirement includes measuring method blanks on a second GC column if confirmatory analysis of sample extracts on a second column is required by the method or by the laboratory statement of work. Any PCDD or PCDF measurement in a sample that is also measured in any associated blank, is qualified with a U flag if the sample concentration is <5 times the blank concentration.
DF4a	The affected analytes are considered estimated and biased high because this analyte was identified in the method blank but was >5x. The criteria for the frequency of extraction and analysis of method blanks as stated in Section 9.5 of Method 1613B shall be followed and demonstrated in the documented data. The maximum amount of PCDD and PCDF isomer contamination in method blanks is stated in Table 2 of Method 1613B. The method blank must be measured on each GC/MS system which is used to measure a group of samples. This requirement includes measuring method blanks on a second GC column if confirmatory analysis of sample extracts on a second column is required by the method or by the laboratory statement of work. If the maximum contamination requirements of specific TCDD and TCDF isomers stated in Table 2 of Method 1613B are not met, then all isomers in all samples associated with a method blank shall be qualified with a J flag.
DF4d	The sample result is ≤5 times the concentration of the related analyte in the trip blank, rinsate blank, or equipment blank. Any PCDD or PCDF measurement in a sample that is also measured in any associated blank is qualified with a U flag if the sample concentration is less than 5 times the blank concentration.
DF4e	Required method blank information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information. If the frequency of measuring method blanks is not met by the laboratory in the data submitted, then the results of all samples which do not meet the frequency of extraction and measurement of method blanks shall be qualified with an R flag.
DF7	The affected results were not analyzed with a valid 5-point calibration curve and/or a standard at the reporting limit. There shall be an initial calibration curve consisting of five points for each analyte. The initial calibration curve shall be determined < 30 days from the time the first samples of a Sample Delivery Group (SDG) are measured by the laboratory. The laboratory shall use the same calibration standards with the same lot number, for all internal standards, and labeled standards used in measuring the initial calibration curve, verification standards, field samples, and method blanks on both the primary GC column and on the secondary confirmation GC column.

DF7a	The affected analytes were analyzed with an initial calibration curve that exceeded the %RSD criteria. A 5-point calibration is prepared for each labeled and unlabeled compound. The RRF %RSD for the unlabeled standards must be ≤30%. Ion abundance ratios must meet the criteria listed in Attachment 4. If the %RSD is >20% for any unlabeled calibration standard, or >30% for any labeled calibration standard, but ≤40%, qualify all associated detects as J and, if any other calibration criteria have been exceeded for that compound, qualify all associated non-detects as UJ. If the %RSD is >40% but ≤60% for either a labeled or unlabeled calibration standard, qualify all associated detects as J and all associated non-detects as UJ. If the %RSD is >60% for either a labeled or unlabeled calibration standard, qualify all associated detects as J and all associated non-detects as R. If the ion abundance criteria were not met for any calibration compound, qualify all associated detects as J and all associated non-detects as UJ. If the affected results were not analyzed with a valid 5-point calibration curve and/or a standard at the reporting limit qualify the results as not detected. Ion abundance must meet the criteria in Attachment 4.
DF7b	The affected analytes were analyzed with an out-of-range ion abundance in the initial calibration and/or CCV. Ion abundance must meet the criteria in Attachment 4. If the ion abundance criteria are not met, qualify results for that analyte R.
DF7c	The ICV and/or CCV were recovered outside the method specific limits. See DF7a for ICAL specifications. The ion abundance must be within the limits in Attachment 4. For the calibration verification analyzed at the beginning of a 12-hour period, the effect on data quality of a standard that does not meet criteria must be assessed using professional judgment. Guidance is provided in Section 7.7.4.4 of the EPA method 8290. For the calibration verification analyzed at the end of a 12-hour period, a %D of 25% for unlabeled compounds and 35% for labeled compounds is acceptable; however, in this instance, the mean RFs obtained from the beginning and ending daily calibration runs are used to calculate analyte concentrations instead of the RFs obtained from the initial calibration. If the %D of the ending calibration is >25% for any unlabeled compound and/or >35% for any labeled compound, then successful performance of another initial calibration must be analyzed within two hours of sample analysis for the data to be acceptable. In this case, the mean RFs from the beginning and ending daily calibration runs are still used to calculate analyte concentrations. 1. If the ion abundance ratio for any compound is outside of the method limits, qualify all associated detects as J and all associated non-detects as
DF7d	The ICV and/or CCV were not analyzed at the appropriate method frequency. It should be noted that CLP protocol DFLM01.1 requires that the GC/MS system must be calibrated based upon a daily Calibration Check Standard, whereas, EPA Methods 1613B and 8290 require that the GC/MS system criteria of a daily calibration verification standard must be met with each 12-hour batch of samples measured, and that response factors for native target compounds are derived from the 5-point initial calibration.
DF7f	Required calibration information is missing or samples were analyzed on an expired calibration. Contact the SMO or external laboratory for information.
DF8	The affected analyte is considered rejected because the ion abundances did not meet specifications. For identification of any compound, the ion abundance ratios must be within the limits specified in Attachment 4. If ion abundance ratio criteria were not met for any compound, qualify all associated results as R. If the RT of any compound is outside of the RT window, qualify all associated results as R.
DF8	The ion abundance documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
DF88	Duplicate, dilution, or reanalysis.
DF8b	The GC column performance solution is used for defining the homologous GC RT windows and to document the chromatographic resolution. Column performance must be evaluated at the beginning of each analytical period and must meet method acceptance criteria (see Section 8.2 of the 8290) before sample analysis may begin. If GC column performance was not evaluated at the required frequency or if method criteria were not met, qualify all associated detects as J and all associated non-detects as UJ.

DF8c	The DB-5 GC column generally used for PCDD and PCDF analyses does not adequately separate 2,3,7,8-TCDF from its closest eluting isomer. If 2,3,7,8-TCDF is detected in a sample, the result must be confirmed on a second column capable of separating 2,3,7,8-TCDF from all other TCDF homologues (as proven by successful analysis of the GC column performance column mix with <25% valley between 2,3,7,8-TCDF and its closest eluting isomer). If 2,3,7,8-TCDF was detected in a sample and the result was not confirmed on a second column with successful analysis of the GC column performance mix, qualify all associated detects as U.
DF9	The extraction/analytical holding time are exceeded by <2 times the published method for holding times. Regulations require water samples be preserved by neutralizing any chlorine residual with 0.008% sodium thiosulfate, and cooling to 4ºC using a holding time of 7 days from day of collection to day of extraction of the sample. In addition, the maximum holding time of extracts is 40 days from day of extraction to day of injection of the extract. The holdinig time and preservation requirements of 2,3,7,8-TCDD and of other measured PCDD and PCDF isomers in non-water matrixes have not been promulgated by EPA. Therefore, the data validator should use the holding time specified in EPA Method 8290, which specifies that all samples, except fish and adipose tissue samples, must be stored at 4ºC in the dark, extracted within 30 days, and completely analyzed within 45 days of extraction. Fish and adipose samples must be stored at -20ºC in the dark, extracted within 30 days, and completely analyzed within 45 days of collection (see Section 6.4 of EPA Method 8290). EPA Method 1613B does not set holding times for PCDD or PCDF isomers. The EPA method does state that water samples which contain a chlorine residual should be treated with 80-mg of sodium thiosulfate per liter of water, samples should be
DF9a	The extraction/analytical holding time was exceeded by >2 times the published method for holding times.
DR0 or GR0	The retention time criteria were not met.
DR0b or GR0b	Required retention time documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
DR12 or GR12	The LCS percent recovery was less than 10%. Follow the external laboratory limits.
DR12a or GR12a	The LCS percent recovery was less than the Lower Acceptance Limit but greater than or equal to 10%. Follow the external laboratory limits.
DR12b or GR12b	The LCS percent recovery was greater than the Upper Acceptance Limit. Follow the external laboratory limits.
DR12c or GR12c	The LCS documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
DR12d or GR12d	The MS/MSD percent recovery was less than 10%.
DR12e or GR12e	The MS/MSD percent recovery was greater than or equal to 10% but less than 70%.
DR12f or GR12f	The MS/MSD percent recovery was greater than 130%.
DR12g or GR12g	The MS/MSD relative percent difference was greater than 30%.
DR15 or GR15	The affected analytes have elevated detection limits and may not meet project DQOs because the sample was diluted without any target analytes identified due to matrix interference. (Qualify as Reject if the analytical laboratory cannot provide proof for matrix interference.)
DR19 or GR19	The project chemist identified quality deficiencies in the reported data that requires further qualification. This code can only be used under advisement by the project chemist.
DR3 or GR3	The surrogate is less than 10%R, which indicates the potential for a severely low bias in the results. Follow the external laboratory limits.
DR3a or GR3a	The surrogate is less than the Lower Acceptance Limit, but greater than or equal to 10%R, which indicates the potential for a low bias in the results. Follow the external laboratory limits.
DR3b or GR3b	The surrogate %R value is greater than the Upper Acceptance Limit, which indicates a potential for a high bias in the results and a potential for false positive results. Follow the external laboratory limits.
DR3d or GR3d	Required surrogate information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.

DR4 or GR4	The sample result is less than or equal to 5 times the concentration of the related analyte in the method blank, which indicates the reported detection is considered indistinguishable from contamination in the blank.
DR4a or GR4a	The affected analytes are considered estimated and biased high because this analyte was identified in the method blank but was greater than 5x.
DR4d or GR4d	The sample result is less than or equal to 5 times the concentration of the related analyte in the trip blank, rinsate blank, or equipment blank, which indicates the reported detection is considered indistinguishable from contamination in the blank.
DR4e or GR4e	Required method blank information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
DR7 or GR7	The affected results were not analyzed with a valid 5-point calibration curve and/or a standard at the reporting limit.
DR7a or GR7a	The affected analytes were analyzed with an initial calibration curve that exceeded the %RSD criteria and/or the associated multipoint calibration correlation coefficient is less than 0.995.
DR7c or GR7c	The ICV and/or CCV were recovered outside the method specific limits.
DR7d or GR7d	The ICV and/or CCV were not analyzed at the appropriate method frequency.
DR7f or GR7f	Required calibration information is missing or samples were analyzed on an expired calibration. Contact the SMO or external laboratory for information.
DR88 or GR88	Duplicate, dilution, or reanalysis.
DR9 or GR9	The extraction/analytical holding time is greater than 1x and less than or equal to 2 times the applicable holding time requirement.
DR9a or GR9a	The extraction/analytical holding times were exceeded by more than 2x the published method for holding times.
H0	The analyte RT shifted by more than 0.05 minutes from the mid-level standard of the initial calibration. Reject nondetects for HPLC.
H0a	Analyte is positively confirmed but outside the retention time window; however, spectral matches must be provided (hexp – diode array detector).
H0b	Required retention time documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
H12	The LCS percent recovery was <10%. Follow external laboratory limits located within the associated data package.
H12a	The LCS percent recovery was < the Lower Acceptance Limit (LAL) but >10%. Follow external laboratory limits located within the associated data package.
H12b	The LCS percent recovery was > than the Upper Acceptance Limit (UAL). Follow the external laboratory limits located within the asscociated data package.
H12c	The LCS documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
H15	The affected analytes have elevated detection limits and may not meet project DQOs because the sample was diluted without any target analytes identified due to matrix interference. Qualify as Reject if the analytical laboratory cannot provide proof for cleanup or matrix interference.
H19	The LANL project chemist identified quality deficiencies in the reported data that requires further qualification. This code can ONLY be used and/or under advisement by the project chemist.
H3	The surrogate is <10%R, which indicates the potential for a severely low bias in the results. Follow external laboratory limits located within the associated data package.
H3a	The surrogate is < the LAL but ≥10%R, which indicates the potential for a low bias in the results. Follow the external laboratory limits located within the associated data package.

	The surrogate %R value is > the UAL, which indicates a potential for a high bias in the results and a potential for false positive results.
H3b	Follow the external laboratory limits located within the associated data package.
	At least one surrogate is > the UAL and one surrogate is < the LAL, which indicates a greater than normal degree of uncertainty in the
H3c	result. Follow external laboratory limits located within the associated data package.
	Required surrogate information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for
H3d	information.
	The sample result is ≤5X the concentration of the related analyte in the method blank, which indicates the reported detection is
H4	considered indistinguishable from contamination in the blank.
H4a	The affected analytes are considered estimated and biased high because this analyte was identified in the method blank but was >5X.
	The sample result is ≤5X the concentration of the related analyte in the trip blank, rinsate blank, or equipment blank, which indicates
H4d	the reported detection is considered indistinguishable from contamination in the blank.
	Required method blank information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for
H4e	information.
H7	The affected results were not analyzed with a valid 5-point calibration curve and/or a standard at the reporting limit.
	The affected analytes were analyzed with an initial calibration curve that exceeded the %RSD criteria and/or the associated multipoint
H7a	calibration correlation coefficient is <0.995.
	The Initial Calibration Verification (ICV) and/or Continuing Calibration Verification (CCV) were recovered outside the method-specific
H7c	limits.
H7d	The ICV and/or CCV were not analyzed at the appropriate method frequency.
	Required calibration information is missing or Samples were analyzed on an expired calibration. Contact the SMO or external laboratory
H7f	for information.
H8	The analyte was not confirmed on a second dissimilar column or diode array spectrums do not match library.
H88	Duplicate, dilution, or reanalysis.
	The required second dissimilar column or diode array documentation is missing. Data may not be acceptable for use. Contact the SMO
H8a	or external laboratory for information.
H9	The extraction/analytical holding time was exceeded by <2X the published method for holding times.
H9a	The extraction/analytical holding time was exceeded by >2X the published method for holding times.
H9b	The affected analytes are regarded as rejected because the analytical holding time was exceeded.
HE0	The IS retention time has shifted by >30 seconds.
	Required retention time documentation is missing. Data may not be acceptable for use. Contact the SMO and external laboratory for
HE0b	information.
	An LCS should be analyzed at a frequency of once per data package, once per matrix, An LCS should be analyzed at a frequency of once per data package, once per matrix, or once per 20 analytical samples, whichever is most frequent. The LCS must meet all sample acceptance criteria and all method-specific LCS requirements. The LCS for high explosives must meet laboratory-derived acceptance criteria. If surrogate and IS recovery acceptance criteria are not met for the LCS analysis, the LCS must be reanalyzed. If the recovery acceptance criteria are not reported in the analytical data package recovery limits of 70% to 130% should be used as the criteria. If, based on professional judgment, the laboratory's internal acceptance criteria are excessively wide or acceptable recoveries are significantly biased, notify the program manager. The LCS percent recovery was <10%. Qualify detected results as J- and not detected
HE12	results as R.
	The LCS percent recovery was < the Lower Acceptance Limit but >10%. Follow the external laboratory limits. Qualify detected results as
HE12a	J- and not detected results as UJ.

HE12b	The LCS percent recovery was > the Upper Acceptance Limit. Follow the external laboratory limits. Qualify detected results as J+.
HE12c	The LCS documentation is missing. Data may not be acceptable for use. Contact the SMO or the external laboratory for information.
HE12d	The MS/MSD percent recovery was <10%. The MS/MSD data shall not be used to evaluate associate field sample results unless the MS/MSD sample was from the same client and of similar matrix. If the acceptance criteria are not reported, recovery limits are 70% to 130%. The MS and MSD %R must be within the limits unless the sample concentration is >4X the spike concentration. The MS and MSD results may be used in conjunction with other QC results to determine the need for qualification of the data. An effort to determine to what extent the results of the MS/MSD affect the associated data should determine to what extent the results of the MS/MSD affect the associated data should first be made. This determination should be made considering the MS/MSD sample matrix, the surrogate and internal standard recoveries, and the LCS results. Professional judgment should be used to determine if MS/MSD failure warrants qualification of only the results for the failed compounds or if the compounds associated with the failed MS compound are affected. Generally, unless evidence exists to warrant qualification of other compounds, only the compounds in the MS spiking mixture shall be qualified. If the surrogate, internal standard, and LCS recoveries are within the required acceptance criteria and either the MS or MSD recovery for any target analyte is <10%, qualify results as R.
HE12e	If the MS/MSD percent recovery was >10%, but <70%, qualify all detects as J and all non-detects as UJ.
HE12f	If the MS/MSD percent recovery was >130%, qualify all associated detects as J+.
HE12g	If the MS/MSD relative percent difference was >30%, and the acceptance criteria are not reported, recovery limits of 70% to 130% and an RPD of ≤30% should be used as the criteria. For solid and waste samples, it may be appropriate to accept an RPD of up to 40% based on professional judgment.
HE15	If the affected analytes are considered suspect because the sample was diluted without any target analytes identified due to matrix interference, qualify as Reject if the analytical laboratory cannot provide proof for matrix interference.
HE15a	The Practical Quantitation Limits must be adjusted to reflect all sample dilutions, concentrations, splits, clean-up activities, and dry weight factors that are not accounted for by the method. Samples must be diluted and reanalyzed when any analyte exceeds the calibration range. Data from the original sample analysis should be included when any sample requires dilution due to one or more analytes exceeding the calibration range. The original undiluted results document the actual MDLs for non-detects. If the PQLs have not been properly adjusted, request an amended report from the laboratory. If an initial dilution was required because of expected high concentrations of non-target analytes or because one or more target analytes were expected to greatly exceed the instrument working range and the laboratory was not able to analyze the undiluted sample, note the dilution and elevated MDLs in the data validation report. If any target analyte exceeded the calibration range and the original undiluted sample result was reported, qualify all detects from the undiluted analysis that exceeded the calibration range as J. If any target analyte exceeded the calibration range and the sample was diluted and reanalyzed and the diluted sample data were reported, qualify all non-detects from the diluted analysis as UJ. If
HE16c	The required CRI sample information is missing. Contact the SMO or the external laboratory for information.
HE19	The project chemist identified quality deficiencies in the reported data that require further qualification. This code can ONLY be used and/or under advisement by the project chemist.
HE1a	The quantitating IS area count is <25% of the expected value, which indicates increased potential for false negative results and other possible problems with sample quantitation. Follow the method specific windows. Qualify data as R if the IS area count is <25%.
HE1b	If the internal standard was used for quantification and its area count is <70% but >25% of the average of that obtained from the calibration standards, qualify all associated detects as J+ and all associated non-detects as UJ.

HE1c	The internal standard area counts must not vary by >70% to 130% from the average of those obtained from the calibration standards or from the mid-level calibration standard. If the internal standard was used for quantification and its area count is >130% of the average of that obtained from the calibration standards, qualify all associated detects as J- and all associated non-detects as UJ.
HE1d	Required IS information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
HE3	The surrogate is <10% recovery, which indicates the potential for a severely low bias in the results. Follow the external laboratory limits. Qualify non-detected results as R and detected results as J-. Also, if an initial dilution was performed on any sample and surrogate recovery is <10% recovery and all results are non-detect, qualify all sample results as R.
HE3a	The surrogate is < the Lower Acceptance Limit but ≥10% recovery, which indicates the potential for a low bias in the results. Follow the external laboratory limits. Qualify non-detected results as UJ and detected results as J-. Also, if an initial dilution was performed on any sample and at least one surrogate recover is < the Lower Acceptance Limit, but ≥10%, or all surrogate recoveries are <10% and the results for one or more compounds are > the PQL, qualify non-detected results as UJ and detected results as J-.
HE3b	The surrogate % recovery value is > the Upper Acceptance Limit, which indicates the potential for a high bias in the results and a potential for false positive results. Follow the external laboratory limits.
HE3c	At least one surrogate is > the Upper Acceptance Limit and one surrogate is < the Lower Acceptance Limit, which indicates a > normal degree of uncertainty in the result. Follow the external laboratory limits.
He3d	Required surrogate information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information. Sample and blank surrogate recoveries must be within limits specified by the laboratory. Surrogate compound recoveries shall be calculated using the procedure described in SW-846 EPA Method 8000B. Reported recoveries shall be accompanied by the applicable acceptance limits. Results from spiked or replicate QC samples that have surrogate recoveries <10% cannot be used to evaluate associated sample results.
HE4	The sample result is ≤5 times the concentration of the related analyte in the method blank, which indicates the reported detection is considered indistinguishable from contamination in the blank.
HE4a	The affected analytes are considered estimates and biased high because this analyte was identified in the method blank but was >5x.
HE4d	The sample result is ≤5 times the concentration of the related analyte in the trip blank, rinsate blank, and equipment blank, which indicates the reported detection is considered indistinguishable from contamination in the blank.
HE4e	Required method blank information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
HE4f	The absence of sample carry-over must be determined and verified. If examination of the run logs indicates that any samples in the analytical run of interest required dilution and there is no documentation of a rinse or blank analysis immediately following the original undiluted analysis, then sample carry-over may be suspected in the subsequent sample. If any target analyte found in the sample requiring dilution exceeded the high calibration standard and was also found in the following sample at a concentration <5x the PQL, qualify the result for that analyte in the second sample as R. If no data are available for the sample that required dilution, the laboratory has not documented that carry-over was evaluated, and any analyte was also found in the following sample as a concentration <5x the PQL, qualify the result for that analyte in the second sample as N.

HE7	The affected results were not analyzed with a valid 5-point calibration curve and/or a standard at the reporting limit. LC/MS/MS instrument calibration shall be performed using a minimum of five (5) calibration standards. The lowest point of the curve must be at or below the reporting limit. If calibration curves are used, five (5) standards are required for a linear (first order) calibration model, six (6) standards are required for a quadratic (second order) model, and seven (7) standards are required for a third order polynomial. Higher order curves should not normally be used. If the laboratory uses a higher order equation to and all associated non-detects as UJ. establish a calibration curve, it should be evaluated for the appropriate application. If an insufficient number of calibration standards was used, the PQLs were incorrect, or all points were not analyzed within a 24-hour period, qualify all associated detects as J.
HE7a	The affected analytes were analyzed with an initial calibration curve that exceeded the %RSD or r2. If the %RSD for any target analyte is >20% but ≤40%, qualify all associated detects as J and, if any other calibration criteria have been exceeded for that compound, qualify all associated non-detects as UJ. If the %RSD for any target analyte is >40% but ≤60%, qualify all associated detects as J and all associated non-detects as UJ. If the %RSD for any target analyte is >60%, qualify all associated detects as J and all associated non-detects as R. If the r2 for any target analyte is <0.99 but ≥0.90, qualify all associated detects as J and, if any other calibration criteria have been exceeded for that compound, qualify all associated non-detects as UJ. If the r2 for any target analyte is >0.90 but ≤0.80, qualify all associated detects as J and all associated non-detects as UJ. If the r2 for any target analyte is <0.80, qualify all associated detects as J and all associated non-detects if the intercept for any target analyte is positive and >3x the intercept J+ as R.
HE7b	The affected analytes were analyzed with a RRF of <0.05 in the initial calibration and/or CCV. If the average RF for any target analyte is < the specified minimum RF, or <0.05 if no minimum is specified, qualify all associated detects as J and all associated nondetects as UJ if the RF is ≥0.01 and as R if the RF is <0.01.
HE7c	The ICV and/or CCV were recovered outside the method limits. The %D between the ICV and CCV standard concentrations and their true values shall be calculated according to the formula in Attachment 4, and must be ≤20%. The evaluation of CCV data applies to all CCVs that bracket samples of interest. If the %D was reported with the wrong sign (e.g., +%D for negative bias), document the occurrence in the data validation report and assess any infractions using the correct sign. 1. If the %D between a measured ICV and/or CCV concentration and its true value for any analyte is >20%, qualify all associated detects as J+. 2. If the %D between a measured ICV and/or CCV concentration and is true value for any analyte is >20% but ≤40% and negative (low bias), qualify all associated detects as J- and, if any other calibration criteria have been exceeded for that compound, qualify all associated non-detects as UJ. 3. If the %D between a measured ICV and/or CCV concentration and its true value for any analyte is >40% but ≤60% and negative, qualify all associated detects as J and all associated non-detects as UJ. 4. If the %D between a measured ICV and/or CCV concentration and its true value for any analyte is >60% and is negative, qualify all associated detects as J- and all associated non-detects as R.
HE7d	The ICV and/or CCV were not analyzed at the appropriate method frequency. An ICV standard is analyzed immediately following an initial calibration. For high explosive analysis, the ICV standard analysis results are not required to be reported in the data package unless the samples in the SDG were analyzed after the initial calibration but before a CCV standard analysis was performed. In this case, the ICV %D is assessed according to the calibration verification criteria described below for the associated samples. If a CCV is analyzed prior to samples and ICV data are also reported in the package, both the ICV %D and the appropriate CCV %D are to be assessed as described below. If both ICV %D and CCV %D infractions occur, the worst infraction should be evaluated for result qualification. A CCV must be analyzed in the following instances: • at the beginning of each analytical run; • at least once every 10 samples; and • at the end of each analytical run. If multiple CCVs were analyzed to obtain a passing CCV, the calibration is not verified and the calibration frequency is not met. If the ICV and CCV standards were not analyzed at the proper frequency, or if either a required ICV or CCV was not analyzed, or if all target compounds were not present in any ICV or CCV standard, qualify all associated detects as J and all
HE7f	Required calibration information is missing or samples were analyzed on an expired calibration. Contact the SMO or external laboratory for information.

HE8a	The mass spectral documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
HE9	The extraction/analytical holding time is exceeded by <2x the published method for holding times.
HE99	Duplicate, dilution, or reanalysis.
HE9a	The extraction/analytical holding time was exceeded by more than 2x the published method for holding times.
I1	The sample result was reported as detected between the IDL and the EDL.
I10a	The sample and the duplicate sample results were ≥5X the RL and the duplicate RPD was >20% for water samples and >35% for soil samples.
I10a	The sample and the duplicate sample results were ≥5X the RL and the duplicate RPD was >20% for water samples and >35% for soil samples.
I10d	The duplicate sample was not prepared and/or analyzed with the samples for unspecified reasons. The duplicate information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
I10d	The duplicate sample was not prepared and/or analyzed with the samples for unspecified reasons. The duplicate information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
I12	The LCS percent recovery was <10%. Follow the external laboratory limits located within the associated data package.
I12	The LCS percent recovery was <10%. Follow external laboratory limits located within the associated data package.
I12a	The LCS percent recovery was < the Lower Acceptance Limit (LAL) but >10%. Follow the external laboratory limits located within the associated data package.
I12a	The LCS percent recovery was < the Lower Acceptance Limit (LAL) but >10%. Follow the external laboratory limits located within the associated data package.
I12b	The LCS percent recovery was > Upper Acceptance Limit (UAL). Follow the external laboratory limits located within the associated data package.
I12b	The LCS percent recovery was > Upper Acceptance Limit (UAL). Follow the external laboratory limits located within the associated data package.
I12c	The LCS documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information. Do not Reject if MS/MSD information is present. Qualify according to MS/MSD criteria.
I12c	The LCS documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information. Do not Reject if MS/MSD information is present. Qualify according to MS/MSD criteria.
I16	The instrument performance sample did not pass the method acceptance criteria.
I16a	The mass calibration is not within 0.1 amu or %RSD exceeds 5% for any isotope (Be, Mg, Co, In, Pb).
I16b	Samples were analyzed outside specific method tune time criteria.
I16c	The required instrument performance sample information is missing. Contact the SMO or external laboratory for information.
I18	Serial dilution sample RPD was >10% and the sample results was >50X the MDL (>100X the MDL for ICPMS). Qualify ONLY the sample used for the serial dilution.
I18a	Serial dilution sample was not analyzed with the samples.
I19	The project chemist identified quality deficiencies in the reported data that requires further qualification. This code can ONLY be used and/or under the advisement by the project chemist.
I19	The project chemist identified quality deficiencies in the reported data that require further qualification. This code can ONLY be used and/or under advisement by the project chemist.
I1a	The quantitating IS area could is <10% for metals window in relation to the initial calibration blank. Follow method-specific windows.

I1b	The IS area count for the quantitating IS is <60% but >10% for metals window in relation to the initial calibration blank. Follow method-specific windows.
I1c	The IS area count for the quantitiating IS is >125% in relation to the metals initial calibration blank. Follow method-specific windows.
I1d	Required IS information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
I2	Metals interference check sample percent recovery value is <50%.
I2	Metals interference check sample percent recovery value is <50%.
I2a	Metals interference check sample percent recovery value is ≥50% and <80%.
I2b	Metals interference check sample percent recovery value is >120%.
I2b	Metals interference check sample percent recovery value is >120%.
I2c	Metals interference check sample was not analyzed with the samples.
I2c	Metals interference check sample was not analyzed with the samples.
I4	The sample result is ≤5X the concentration of the related analyte in the method blank, which indicates the reported detection is considered indistinguishable from contamination in the blank.
I4	The sample result is ≤5X the concentration of the related analyte in the method blank, which indicates the reported detection is considered indistinguishable from contamination in the blank.
I4a	The affected analytes are considered estimated and biased high because this analyte was identified in the method blank but was >5X.
I4a	The affected analytes are considered estimated and biased high because this analyte was identified in the method blank but was >5X.
I4b	The sample result is ≤5X the concentration of the related analyte in the ICB/CCB, which indicates the reported detection is considered indistinguishable from contamination in the blank.
I4b	The sample result is ≤5X the concentration of the related analyte in the instrument blank and continuing calibration blank, which indicates the reported detection is considered indistinguishable from contamination in the blank.
I4c	Continuing calibration blanks were not analyzed at the appropriate method frequency.
I4c	Continuing calibration blanks were not analyzed at the appropriate method frequency.
I4d	The sample result is ≤5X the concentration of the related analyte in the trip blank, equipment blank, or rinsate, which indicates the reported detection is considered indistinguishable from contamination in the blank.
I4d	The sample result is ≤5X the concentration of the related analyte in the trip blank, rinsate blank, or equipment blank, which indicates the reported detection is considered indistinguishable from contamination in the blank.
I4e	Required method blank information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
I4e	Required method blank information is missing. Data may not be acceptable for use.
I6	The associated matrix spike recovery was <10%. Follow the external laboratory limits located within the associated data package.
I6	The associated matrix spike recovery was <10%. Follow the external laboratory limits located within the associated data package.
I6a	The associated matrix spike recovery was < the LAL but >10%. Follow the external laboratory limits located within the associated data package.
I6a	The associated matrix spike recovery was < the LAL but > 10%. Follow the external laboratory limits located within the associated data package.

I6b	The associated matrix spike recovery was > the UAL. Follow the external laboratory limits located within the associated data package.
I6b	The associated matrix spike recovery was > the UAL. Follow the external laboratory limits located within the associated data package.
I6c	Required matrix spike information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
I6c	Required matrix spike information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information. If LCS information is present, do not Reject. Qualify data based on LCS information.
I7	The affected results were not analyzed with a valid 5-point calibration curve and/or a standard at the reporting limit.
I7	The affected results were not analyzed with a valid 5-point calibration curve and/or a standard at the reporting limit.
I7a	The affected analytes were analyzed with a initial calibration curve that exceeded the %RSD criteria and/or the associated multipoint calibration correlation coefficient is <0.995.
I7a	The affected analytes were analyzed with an initial calibration curve that exceeded the %RSD criteria and/or the associated multipoint calibration correlation coefficient is <0.995.
I7c	The ICV and/or CCV were recovered outside the method-specific limits.
I7c	The Initial Calibration Verification (ICV) and/or Continuing Calibration Verification (CCV) were recovered outside the method specific limits.
I7d	The ICV and/or CCV were not analyzed at the appropriate method frequency.
I7d	The ICV and/or CCV were not analyzed at the appropriate method frequency.
I7f	Required calibration information is missing or samples were analyzed on an expired calibration. Contact the SMO or external laboratory for information.
I7f	Required calibration information is missing or samples were analyzed on an expired calibration. Contact the SMO or external laboratory for information.
I88	Duplicate, dilution, or reanalysis.
I88	Duplicate, dilution, or reanalysis.
I9	The extraction/analytical holding time are exceeded by <2X the published method for holding times.
I9	The extraction holding time was exceeded by <2X the published method for holding times.
I9a	The extraction/analytical holding time are exceeded by >2X the published method for holding times.
I9a	The extraction holding time was exceeded by >2X the published method for holding times.
I9b	The affected analytes are regarded as rejected because the analytical holding time was exceeded.
P0	The analyte RT shifted by >0.05 minutes from the mid-level standard of the initial calibration.
P0b	Required retention time documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
P12	The LCS percent recovery was <10%. Follow the external laboratory limits located within the associated data package.
P12a	The LCS percent recovery was < the Lower Acceptance Limit (LAL) but >10%. Follow the external laboratory limits located within the associated data package.
P12b	The LCS percent recovery was > the Upper Acceptance Limit (UAL). Follow the external laboratory limits located within the associated data package.
P12c	The LCS documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information located within the associated data package.
P13	The breakdown criteria have been exceeded. This can cause low bias in reported results. If compound is detected, qualify J-. If compounds not present, but breakdown products are present, qualify R. If compounds and no breakdown products are present, qualify UJ (4,4' DDT and Endrin).

P13a	The breakdown criteria have been exceeded. This can cause high bias in the reported results and potential false positive results for the breakdown products Endrin ketone, Endrin aldehyde, DDD, and DDE.
P13b	The breakdown documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
P15	The affected analytes have elevated detection limits and may not meet project DQOs because the sample was diluted without any target analytes identified due to matrix interference. Qualify as Reject if the analytical laboratory cannot provide proof for cleanup or matrix interference.
P19	The project chemist identified quality deficiencies in the reported data that requires further qualification. This code can ONLY be used and/or under advisement by the project chemist.
P3	The surrogate is <10%R, which indicates the potential for a severely low bias in the results. Follow the external laboratory limits located within the associated data package.
P3a	The surrogate is < the LAL but ≥10%R, which indicates the potential for a low bias in the results. Follow the external laboratory limits.
P3b	The surrogate %R value is > the UAL, which indicates a potential for a high bias in the results and a potential for false positive results. Follow the external laboratory limits located within the associated data package.
P3c	At least one surrogate is > the UAL and one surrogate is < the LAL, which indicates a > normal degree of uncertainty in the result. Follow the external laboratory limits located within the associated data package.
P3d	Required surrogate information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
P4	The sample result is ≤5X the concentration of the related analyte in the method blank, which indicates the reported detection is considered indistinguishable from contamination in the blank.
P4a	The affected analytes are considered estimated and biased high because this analyte was identified in the method blank but was >5X.
P4b	The sample result is ≤5X the concentration of the related analyte in the instrument and CCB, which indicates the reported detection is considered indistinguishable from contamination in the blank.
P4d	The sample result is ≤5X the concentration of the related analyte in the trip blank, rinsate blank, or equipment blank, which indicates the reported detection is considered indistinguishable from contamination in the blank.
P4e	Required blank information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
P7	The affected results were not analyzed with a valid 5-point calibration curve and/or a standard at the reporting limit.
P7a	The affected analytes were analyzed with an initial calibration curve that exceeded the %RSD criteria and/or the associated multipoint calibration correlation coefficient is <0.995.
P7c	The ICV and/or CCV were recovered outside the method-specific limits.
P7d	The ICV and/or CCV were not analyzed at the appropriate method frequency.
P7e	The multicomponent standard was not analyzed within 72 hours of the initial analysis.
P7f	Required calibration information is missing or samples were analyzed on an expired calibration. Contact the SMO or external laboratory for information.
P8	The analyte was not confirmed on a second dissimilar column.
P88	Duplicate, dilution, or reanalysis.
P8a	The required dissimilar column documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
P9	The extraction/analytical holding time is exceeded by <2X the published method for holding times.
P9a	The extraction/analytical holding time was exceeded by >2X the published method for holding times.

P9b	The affected analytes are regarded as Rejected because the analytical holding time was exceeded.
PE0	The perchlorate RRT is outside the acceptance range of 0.98 to 1.02 seconds.
PE0b	Required retention time documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
PE12	An LCS should be analyzed at a frequency of once per data package, once per matrix, or once per 20 analytical samples, whichever is most frequent. The LCS must meet all sample acceptance criteria and all method-specific LCS requirements. The LCS for perchlorate must meet laboratory-derived acceptance criteria. If IS recovery acceptance criteria are not met for the LCS analysis, the LCS must be reanalyzed. If the recovery acceptance criteria are not reported in the analytical data package recovery limits of 85% to 115% (perchlorate limits) should be used as the criteria. The LCS percent recovery was <10%. Qualify detected results as J- and not detected results as R.
PE12a	The LCS percent recovery was < the Lower Acceptance Limit but >10%. Follow the external laboratory limits. Qualify detected results as J- and not detected results as UJ.
PE12b	The LCS percent recovery was > the Upper Acceptance Limit. Follow the external laboratory limits. Qualify detected results as J+.
PE12c	The LCS documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
PE12d	The MS/MSD percent recovery was <10%. The MS/MSD data shall not be used to evaluate associate field sample results unless the MS/MSD sample was from the same client and of similar matrix. For perchlorate, the MS/MSD recovery acceptance criteria are 75% to 125% with an RPD of ≤20%. For solid and waste samples, it may be appropriate to accept an RPD of up to 30% based on professional judgment. The MS and MSD %R must be within the limits unless the sample concentration is >4X the spike concentration. The MS and MSD results may be used in conjunction with othe QC results to determine the need for qualification of the data. An effort to determine to what extent the results of the MS/MSD affect the associated data should first be made. This determination should be made considering the MS/MSD sample matrix, the surrogate and internal standard recoveries, and the LCS results. Professional judgment should be used to determine if MS/MSD failure warrants qualification of only the results for the failed compounds or if results for all compounds associated with the failed MS compound are affected. Generally, unless evidence exists to warrant qualification of other compounds, only the compounds in the MS spiking mixture shall be qualified. If the surrogate, internal standard, and LCS recoveries are within the required acceptance criteria and either the MS or MSD recovery for any target analyte is <10% qualify
PE12e	The MS/MSD percent recovery was >10% but <75%. Qualify all detects as J and all non-detects as UJ.
PE12f	The MS/MSD percent recovery was >125%. Qualify all associated detects as J+.
PE12g	The MS/MSD relative percent difference was >20%. If the acceptance criteria are not reported, recovery limits of 75% to 125% and an RPD of 20% should be used as the criteria. For solid and waste samples, it may be appropriate to accept an RPD of up to 30% based on professional judgment.
PE15	The affected analytes are considered suspect because the sample was diluted without any target analytes identified due to matrix interference. Qualify as Reject if the analytical laboratory cannot provide proof for matrix interference.

PE15a	The sample was diluted because target analytes were > the initial verification calibration. The Practical Quantitation Limits must be adjusted to reflect all sample dilutions, concentrations, splits, clean-up activities, and dry weight factors that are not accounted for by the method. Samples must be diluted and reanalyzed when any analyte exceeds the calibration range. Data from the original sample analysis should be included when any sample requires dilution due to one or more analytes exceeding the calibration range. The original undiluted results document the actual MDLs for non-detects. If the PQLs have not been properly adjusted, request an amended report from the laboratory. If an initial dilution was required because of expected high concentrations of non-target analytes or because one or more target analytes were expected to greatly exceed the instrument working range and the laboratory was not able to analyze the undiluted sample, note the dilution and elevated MDLs in the data validation report. If any target analyte exceeded the calibration range and the original undiluted sample result was reported, qualify all detects from the undiluted analysis that exceeded the calibration range as J. If any target analyte exceeded the calibration range and the sample was diluted and reanalyzed and the
PE16	The Contract Required Detection Limit check standard (CRI) sample did not pass method-acceptance criteria. CRI analysis recoveries for perchlorate analysis must be within limits specified by the Laboratory. If acceptance criteria are not reported, the recovery acceptance range shall be 70% to 130%. 1. If frequency criteria were not met, qualify all detects <5X the PQL as J and all non-detects as UJ. 2. If the recovery is > the upper acceptance limit, qualify all associated detects <5X the PQL as J+. 3. If the recovery is < the lower acceptance limit but ≥30%, qualify all associated detects <5X the PQL as J- and all associated non-detects as UJ. If the recovery is <30%, qualify all associated detects <5X the PQL as J- and all associated non-detects as R.
PE16a	The Interference Check Sample recovery was not within ±20% of the known value. The laboratory shall analyze an Interference Check Sample from a matrix containing 500 ppm each of chloride, sulfate, carbonate, and bicarbonate in every batch. The concentration of this standard will be at the PQL. To determine that perchlorate is adequately isolated and recovered under the specific conditions used, this standard should recover within ±20% of the known value. If frequency criteria were not met, note the deficiency in the data validation report. If the recovery is not within ±20% of the known value, note the deficiency in the data validation report. Qualify not detected results as UJ and detected results as J.
PE16c	The required CRI sample information is missing. Contact the SMO or external laboratory for information.
PE19	The project chemist identified quality deficiencies in the reported data that require further qualification. This code can ONLY be used and/or under advisement by the project chemist.
PE1a	This IS area count is <25% of the expected value. If the internal standard is used only as a Retention Time (RT) check (perchlorate analysis), the Relative Retention Time (RRT) of the internal standard must fall within the acceptance range of 0.98 to 1.02, and the internal standard recovery should be evaluated using the surrogate criteria. If recovery acceptance limits are not reported in the data package, recovery should be evaluated based on reported Matrix Spike acceptance limits.
PE1b	The internal standard area could is <70% but >25% of the average of that obtained from the calibration standards, qualify all associated detects as J and all associated non-detects as UJ. If the internal standard is used only as a RT check (perchlorate analysis), the RRT of the internal standard must fall within the acceptance range of 0.98 to 1.02, and the internal standard recovery should be evaluated using the surrogate criteria. If recovery acceptance limits are not reported in the data package, recovery should be evaluated based on reported Matrix Spike acceptance limits.
PE1c	If the internal standard is >130% of the average of that obtained from the calibration standards, qualify all associated detects as J and all associated non-detects as UJ. If the internal standard is used only as a RT check (perchlorate analysis), the RRT of the internal standard must fall within the acceptance range of 0.98 to 1.02, and the internal standard recovery should be evaluated using the surrogate criteria. If recovery acceptance limits are not reported in the data package, recovery should be evaluated based on reported Matrix Spike acceptance limits.

PE1d	Required Internal Standard information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
PE4	The sample result is ≤5X the concentration of the related analyte in the method blank, which indicates the reported detection is considered indistinguishable from contamination in the blank.
PE4a	The affected analytes are considered estimated and biased high because this analyte was identified in the method blank but was >5X.
PE4d	The sample result is ≤5X the concentration of the related analyte in the trip blank, rinsate blank, and equipment blank, which indicates the reported detection is considered indistinguishable from contamination in the blank.
PE4e	Required method blank information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
PE7	The affected results were not analyzed with a valid 5-point calibration curve and/or a standard at the reporting limit. LC/MS/MS instrument calibration shall be performed using a minimum of five (5) calibration standards. The lowest point of the curve must be at or below the reporting limit. If calibration curves are used, five (5) standards are required for a linear (first-order) calibration model, six (6) standards are required for a quadratic (secondorder) model, and seven (7) standards are required for a third-order polynomial. Higher-order curve should not normally be used. If the laboratory uses a higher-order equation to establish a calibration curve, it should be evaluated for the appropriate application. If an insufficient number of calibration standards was used, the PQLs were incorrect, or all points were not analyzed within a 24-hour period, qualify all associated detects as J and all associated non-detects as UJ.
PE7a	The affected analytes were analyzed with an initial calibration curve that exceeded the %RSD or r2. If the %RSD for any target analyte is >15% but ≤40%, qualify all associated detects as J and, if any other calibration criteria have been exceeded for that compound, qualify all associated non-detects as UJ. If the %RSD for any target analyte is >40% but ≤60%, qualify all associated detects as J and all associated nondetects as UJ. If the %RSD for any target analyte is >60%, qualify all associated detects as J and all associated non-detects as R. If the r2 for any target analyte is <0.99 but ≥0.90, qualify all associated detects as J and, if any other calibration criteria have been exceeded for that compound, qualify all associated non-detects as UJ. If the r2 for any target analyte is <0.90 but ≥0.80, qualify all associated detects as J and all associated non-detects as UJ. If the r2 for any target analyte is <0.80, qualify all associated detects as J and all associated non-detects, if the intercept for any target analyte is positive and >3X the MDL, qualify all associated detects <3X the intercept as J+ as R.
PE7c	The ICV and/or CCV were recovered outside the method limits. The %D between the ICV and CCV standard concentrations and their true values must be ≤15%. The evaluation of CCV data applies to all CCVs that bracket samples of interest. If the %D was reported with the wrong sign (e.g., +%D for negative bias), document the occurrence in the data validation report and assess any infractions using the correct sign. 1. If the %D between a measured ICV and/or CCV concentration and its true value for any analyte is >15%, qualify all associated detects as J+. 2. If the %D between a measured ICV and/or CCV concentration and is true value for any analyte is >15% but ≤40% and negative (low bias), qualify all associated detects as J- and, if any other calibration criteria have been exceeded for that compound, qualify all associated non-detects as UJ. 3. If the %D between a measured ICV and/or CCV concentration and its true value for any analyte is >40% but ≤60% and negative, qualify all associated detects as J- and all associated non-detects as UJ. 4. If the %D between a measured ICV and/or CCV concentration and its true value for any analyte is >60% and is negative, qualify all associated detects as J- and all associated non-detects as R.

PE7d	The ICV and/or CCV were not analyzed at the appropriate method frequency. An ICV standard is analyzed immediately following an initial calibration. The ICV standard analysis results are not required to be reported in the data package unless the samples in the SDG were analyzed after the initial calibration but before a CCV standard analysis was performed. In this case, the ICV %D is assessed according to the calibration verification criteria described below for the associated samples. If a CCV is analyzed prior to samples and ICV data are also reported in the package, both the ICV %D and the appropriate CCV %D are to be assessed as described below. If both %D and CCV %D infractions occur, the worst infraction should be evaluated for result qualification. A CCV must be analyzed in the following instances: • at the beginning of each analytical run; • at least once every 10 samples; and • at the end of each analytical run. If multiple CCVs were analyzed to obtain a passing CCV, the calibration is not verified and the calibration frequency is not met. If the ICV and CCV standards were not analyzed at the proper frequency, or if either a required ICV or CCV was not analyzed, or if all target compounds were not present in any ICV or CCV standard, qualify all associated detects as J and all associated non-detects as UJ. If all
PE7f	Required calibration information is missing or samples were analyzed on an expired calibration. Contact the SMO or external laboratory for information.
PE8	The affected analyte is considered not detected because ion abundance ratios did not meet specifications. The natural isotopic abundances for the chlorine isotopes give a 35Cl/37Cl ratio of approximately 3.08. Laboratories must statistically derive isotope ratio acceptance criteria to be used as an additional confirmation of analyte identity. When the laboratory does not specify acceptance criteria, the mean of the ration population shall not deviate by more than 10% from the 3.08 theoretical value and the standard deviation shall not significantly exceed 0.2. Between the MDL and the PQL, the individual sample isotope acceptance limits shall be near the population mean ±20% (approximately 3 sigma). Above the PQL, the individual sample isotope ratio acceptance limits shall be near the population mean ±15% (approximately 2 sigma). When isotope ratio acceptance criteria are not met, the laboratory must provide supporting data and explanatory case narrative comments in the data package. If the isotope ratios were not reported, calculate the ratio if the raw data were supplied or request an amended report from the laboratory if the raw data were not supplied. If an isotope ratio is outside the acceptance limits, qualify the detect results as J or R based on professional judgment.
PE88	Duplicate, dilution, or reanalysis.
PE8a	The ion ratio documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
PE9	The extraction/analytical holding time is exceeded by less than 2X the published method for holding times.
PE9a	The extraction/analytical holding time is exceeded by less than 2X the published method for holding times.
R10	Associated duplicate sample has DER or RER > the analytical laboratory's acceptance limits.
R10d	The duplicate sample was not prepared and/or analyzed with the samples for unspecified reasons. The duplicate information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
R11	The results for the affected analytes should be regarded as not detected (U) because the associated sample concentration was less than 3X the 1 sigma TPU.
R12	The LCS percent recovery was <10%. Follow the external laboratory limits located within the associated data package.
R12a	The LCS percent recovery was < the LAL but >10%. Follow the external laboratory limits located within the associated data package.
R12b	The LCS percent recovery was > the UAL. Follow the external laboratory limits located within the associated data package.
R12c	The LCS documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
R19	The LANL project chemist identified quality deficiencies in the reported data that require further qualification. This code can ONLY be used and/or under advisement by the LANL project chemist.
R3	The tracer is <10%R. Follow the external laboratory limits located within the associated data package. Tracer%R is not applicable for Gamma Spectroscopy.

R3a	The tracer is < the Lower Acceptance Level (LAL) but ≥10%R. Follow the external laboratory limits located within the associated data package. Tracer%R is not applicable for Gamma Spectroscopy.
R3b	The Tracer%R value is > the Upper Acceptance Limit (UAL). Follow the external laboratory limits located within the associated data package. Tracer%R is not applicable for Gamma Spectroscopy.
R3d	Required tracer information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information. Tracer%R is not applicable for Gamma Spectroscopy.
R4	The sample result is ≤5X the concentration of the related analyte in the method blank.
R4a	The affected analytes are considered estimated and biased high because this analyte was identified in the method blank but was >5X.
R4d	The sample result is ≤5X the concentration of the related analyte in the trip blank, rinsate blank, or equipment blank.
R4e	Required method blank information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
R5	The results for the affected analytes are considered not detected (U) because the associated sample concentration was less than or equal to the MDC.
R5a	The analyte should be regarded as rejected because spectral interferences prevent positive identification of the analytes.
R5b	The MDC and/or TPU documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
R6	The associated matrix spike recovery was <10%. Follow the external laboratory limits. MS/MSD is not applicable to Gamma Spectroscopy.
R6a	The associated matrix spike recovery was <10%. Follow the external laboratory limits. MS/MSD is not applicable to Gamma Spectroscopy.
R6b	The associated matrix spike recovery was above the UAL. Follow the external laboratory limits. MS/MSD is not applicable to Gamma Spectroscopy.
R6c	Required matrix spike information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information. If LCS information is present, do not Reject. Qualify data based on LCS information. MS/MSD is not applicable to Gamma Spectroscopy.
R88	Duplicate, dilution, or reanalysis.
R9	The holding time was >1 and ≤2 times the applicable holding time requirement.
R9a	The holding time was >2 times the applicable holding time requirement.
SV0	The IS retention time has shifted by >30 seconds.
SV0a	Analyte is positively confirmed but outside the IS retention window; however, spectral matches must be provided.
SV0b	Required retention time documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
SV12	The LCS percent recovery was <10%. Follow the external laboratory limits located within the associated data package.
SV12a	The LCS percent recovery was < the Lower Acceptance Limit (LAL) but >10%. Follow the external laboratory limits located within the associated data package.
SV12b	The LCS percent recovery was > the Upper Acceptance Limit (UAL). Follow the external laboratory limits located within the associated data package.
SV12c	The LCS documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information located within the associated data package.

SV15	The affected analytes have elevated detection limits and may not meet project DQOs because the sample was diluted without any target analytes identified due to matrix interference. Qualify as Reject if the analytical laboratory cannot provide proof for matrix interference.
SV16	The instrument performance sample did not pass the method acceptance criteria.
SV16b	Samples were analyzed outside specific method tune time criteria.
SV16c	The required instrument performance sample information is missing. Contact the SMO or external laboratory for information.
SV19	The project chemist identified quality deficiencies in the reported data that requires further qualification. This code can ONLY be used and/or under advisement by the project chemist.
SV1a	The quantitating IS area count is <10% of the expected value. Follow the method-specific windows.
SV1b	The IS area count for the quantitating IS is <50% but >10% for organics window relation to the previous continuing calibration. Follow the method-specific windows.
SV1c	The IS area count for the quantitating IS is >200% of the area count for the previous organic continuing calibration. Follow the method-specific windows.
SV1d	Required IS information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
SV3	The surrogate is <10%R, which indicates the potential for a severely low bias in the results. Follow the external laboratory limits located within the associated data package.
SV3a	The surrogate is < the LAL but ≥10%R, which indicates the potential for a low bias in the results. Follow the external laboratory limits.
SV3b	The surrogate %R value is > the UAL, which indicates a potential for a high bias in the results and a potential for false positive results. Follow the external laboratory limits located within the associated data package.
SV3c	At least one surrogate is > the UAL and one surrogate is < the LAL, which indicates a > normal degree of uncertainty in the result. Follow the external laboratory limits located within the associated data package.
SV3d	Required surrogate/tracer information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
SV4	The sample result is ≤5X (10X for common organic laboratory contaminants) the concentration of the related analyte in the method blank, which indicates the reported detection is considered indistinguishable from contamination in the blank.
SV4a	The affected analytes are considered estimated and biased high because this analyte was identified in the method blank but was >5X (10X for common laboratory contaminants).
SV4d	The sample result is ≤5X the concentration of the related analyte in the trip blank, rinsate blank, or equipment blank, which indicates the reported detection is considered indistinguishable from contamination in the blank.
SV4e	Required method blank information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
SV7	The affected results were not analyzed with a valid 5-point calibration curve and/or a standard at the reporting limit.
SV7a	The affected analytes were analyzed with an initial calibration curve that exceeded the %RSD criteria and/or the associated multipoint calibration correlation coefficient is <0.995.
SV7b	The affected analytes were analyzed with an RRF of <0.05 in the initial calibration and/or CCV.
SV7c	The ICV and/or CCV were recovered outside the method-specific limits.
SV7d	The ICV and/or CCV were not analyzed at the appropriate method frequency.
SV7f	Required calibration information is missing or samples were analyzed on an expired calibration. Contact the SMO or external laboratory for information.

SV8	The affected analyte is considered not detected because mass spectrum did not meet specifications.
SV88	Duplicate, dilution, or reanalysis.
SV8a	The mass spectrum column documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
SV9	The extraction holding time is exceeded by <2X the published method for holding times.
SV9a	The extraction holding time was exceeded by >2X the published method for holding times.
SV9b	The affected analytes are regarded as rejected because the analytical holding time was exceeded.
U_LAB, J_LAB, NQ	Qualification of data via data validation did not occur based on Quality Control requirements in this procedure. Adhere to the external laboratory qualifiers found within the Form I analytical data summary sheets generated by the external laboratory.
U_LAB, J_LAB, NQ	Qualification of data via data validation did not occur based on Quality Control requirements in this procedure. Adhere to the external laboratory qualifiers found within the Form I analytical data summary sheets generated by the external laboratory.
U_LAB, J_LAB, NQ	Qualification of data via data validation did not occur based on Quality Control requirements in this procedure. Adhere to the external laboratory qualifiers found within the Form I analytical data summary sheets generated by the external laboratory.
U_LAB, J_LAB, NQ	Qualification of data via data validation did not occur based on Quality Control requirements in this procedure. Adhere to the external laboratory qualifiers found with the Form 1 analytical data summary sheets generated by the external laboratory.
U_LAB, J_LAB, NQ	Qualification of the data via data validation did not occur because of Quality Control requirements in this procedure. Adhere to external laboratory qualifiers found within the Form I analytical data summary sheets generated by the external laboratory.
U_LAB, J_LAB, NQ	Quantification of data via data validation did not occur based on Quality Control requirements in this procedure. Adhere to the external laboratory qualifiers found within the Form I analytical data summary sheets generated by the external laboratory.
U_LAB, J_LAB, NQ	Quantification of data via data validation did not occur based on Quality Control requirements in this procedure. Adhere to the external laboratory qualifiers found within the Form I analytical data summary sheets generated by the external laboratory.
V0	The IS retention time has shifted by >30 seconds.
V0a	Analyte is positively confirmed but outside the IS retention window; however, spectral matches must be provided.
V0b	Required retention time documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
V12	The LCS percent recovery was <10%. Follow the external laboratory limits located within the associated data package.
V12a	The LCS percent recovery was < the Lower Acceptance Limit (LAL) but >10%. Follow the external laboratory limits located within the associated data package.
V12b	The LCS percent recovery was > the Upper Acceptance Limit (UAL). Follow the external laboratory limits located within the associated data package.
V12c	The LCS documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information located within the associated data package.
V15	The affected analytes have elevated detection limits and may not meet project DQOs because the sample was diluted without any target analytes identified due to matrix interference. Qualify as Reject if the analytical laboratory cannot provide proof for matrix interference.
V16	The instrument performance sample did not pass the method acceptance criteria.

V16b	Samples were analyzed outside specific method tune time criteria.
V16c	The required instrument performance sample information is missing. Contact the SMO or external laboratory for information.
V19	The project chemist identified quality deficiencies in the reported data that requires further qualification. This code can ONLY be used under advisement by the project chemist.
V1a	The quantitating IS area count is <10% of the expected value. Follow the method-specific windows.
V1b	The IS area count for the quantitating IS is <50% but >10% for organics window relation to the previous continuing calibration. Follow the method-specific windows.
V1c	The IS area count for the quantitating IS is >200% of the area count for the previous organic continuing calibration. Follow the method-specific windows.
V1d	Required IS information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
V3	The surrogate is <10%R, which indicates the potential for a severely low bias in the results. Follow the external laboratory limits located within the associated data package.
V3a	The surrogate is < the LAL but ≥10%R, which indicates the potential for a low bias in the results. Follow the external laboratory limits.
V3b	The surrogate %R value is > the UAL, which indicates a potential for a high bias in the results and a potential for false positive results. Follow the external laboratory limits located within the associated data package.
V3c	At least one surrogate is > the UAL and one surrogate is < the LAL, which indicates a > normal degree of uncertainty in the result. Follow the external laboratory limits located within the associated data package.
V3d	Required surrogate/tracer information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
V4	The sample result is ≤5X (10X for common organic laboratory contaminants) the concentration of the related analyte in the method blank, which indicates the reported detection is considered indistinguishable from contamination in the blank.
V4a	The affected analytes are considered estimated and biased high because this analyte was identified in the method blank but was >5X (10X for common laboratory contaminants).
V4d	The sample result is ≤5X the concentration of the related analyte in the trip blank, rinsate blank, or equipment blank, which indicates the reported detection is considered indistinguishable from contamination in the blank.
V4e	Required method blank information is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.
V7	The affected results were not analyzed with a valid 5-point calibration curve and/or a standard at the reporting limit.
V7a	The affected analytes were analyzed with an initial calibration curve that exceeded the %RSD criteria and/or the associated multipoint calibration correlation coefficient is <0.995.
V7b	The affected analytes were analyzed with an RRF of <0.05 in the initial calibration and/or CCV.
V7c	The ICV and/or CCV were recovered outside the method-specific limits.
V7d	The ICV and/or CCV were not analyzed at the appropriate method frequency.
V7f	Required calibration information is missing or samples were analyzed on an expired calibration. Contact the SMO or external laboratory for information.
V8	The affected analyte is considered not detected because mass spectrum did not meet specifications.
V88	Duplicate, dilution, or reanalysis.
V8a	The mass spectrum column documentation is missing. Data may not be acceptable for use. Contact the SMO or external laboratory for information.

V9	The extraction/analytical holding time is exceeded by <2X the published method for holding times.
V9a	The extraction/analytical holding time was exceeded by >2X the published method for holding times.

The Contract Required Detection Limit check standard (CRI) sample did not pass method-acceptance criteria. CRI analysis recoveries for high explosives analysis must be within limits specified by the Laboratory. If acceptance criteria are not reported, the recovery acceptance range shall be 70% to 130%. 1. If frequency criteria were not met, qualify all detects <5X the PQL as J and all nondetects as UJ. 2. If the recovery is > the upper acceptance limit, qualify all associated detects <5X the PQL as J+. 3. If the recovery is < the lower acceptance limit but ≥30%, qualify all associated detects <5X the PQL as J- and all associated non-detects as UJ. 4. If the recovery is <30%, qualify all associated detects <5X the PQL as J- and all associated non-detects as R.