

## Interlaboratory Comparison on POPs in Food 2014



## Fifteenth Round of an International Study

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Norwegian Institute of Public Health



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# Summary

The fifteenth round of the Interlaboratory Comparison on POPs in Food was conducted in 2014 by the Norwegian Institute of Public Health (NIPH). The study included the determination of the 2,3,7,8-chlorinated dibenzo-*p*-dioxins (PCDDs) and dibenzofurans (PCDFs), as well as dioxin-like non-ortho and mono-ortho chlorinated biphenyls (PCBs) in three different food items. Additionally, the participating laboratories could determine the concentrations of six indicator PCBs, polybrominated diphenyl ethers (PBDEs) and hexabromocyclododecanes (HBCDs) in the same food samples.

The objectives of this interlaboratory comparison study were

- a) To offer a tool for quality assurance to the participating laboratories
- b) To assess the between laboratory reproducibility
- c) To assess the readiness of expert laboratories worldwide to determine levels of chlorinated and brominated persistent organic pollutants in regular foodstuffs.

In 2014 the study was performed on unfortified homogenates of pork meat, herring from the Baltic Sea and bovine whole milk. If desired, the laboratories could also determine the concentrations of PCDDs/PCDFs, non-ortho PCBs, mono-ortho PCBs, indicator PCBs, PBDEs and  $\alpha$ -HBCD in standard solutions from Cambridge Isotope Laboratories, provided by NIPH.

The test materials were sent to 86 laboratories in 40 different countries in January and early February 2014, and results were returned from all 86 of these laboratories by the deadline in April. A draft report was made available on our webpage [www.fhi.no/ILC](http://www.fhi.no/ILC) in July, and the deadline for commenting on the published results was set to the first of October 2014.

This report presents the reported results for all seventeen 2,3,7,8-substituted PCDDs/PCDFs, the four non-ortho substituted PCBs #77, 81, 126 and 169 and the eight mono-ortho substituted PCBs #105, 114, 118, 123, 156, 157, 167, 189 in the three food items on a fresh weight and lipid weight basis. The results of

eight PBDEs #28, 47, 99, 100, 153, 154, 183 and 209, six indicator PCBs #28, 52, 101, 138, 153 and 180, and total HBCDs as well as the  $\alpha$ -,  $\beta$ - and  $\gamma$ -isomers will also be presented.

The consensus concentration (assigned value) for each analyte in the three food samples was determined as follows: For the seventeen 2,3,7,8-substituted PCDDs/PCDFs, the four non-ortho substituted PCBs and the eight mono-ortho substituted PCBs non-detected congeners were assigned a concentration corresponding to the reported detection limits. The median of all reported concentrations for each analyte was then calculated. All values above twice the median were removed from the calculation. The consensus median and consensus mean as well as standard deviation (SD) were calculated from the remaining data.

For the PBDEs, the indicator PCBs and HBCDs the non-detects were removed from the data set. The median of all reported concentrations for each analyte was then calculated. All values above twice the median were removed from the calculation. The consensus median and consensus mean as well as standard deviation (SD) were calculated from the remaining data.

Toxic equivalents (TEQs) were calculated from the consensus values of individual congeners using the toxic equivalency factors derived by WHO in 1998 and 2005.

Z-scores for the PCDD/PCDF TEQs were calculated for each laboratory using  $\pm 20\%$  of the consensus TEQs (from 2012: WHO<sub>2005</sub> TEQs as opposed to WHO<sub>1998</sub> TEQs as in the reports published before 2012) as a value for target standard deviation ( $\sigma$ ). Further, Z-scores were calculated for the non-ortho PCB TEQ, the mono-ortho PCB TEQ, the total TEQ, the sum of six indicator PCBs, the sum of eight PBDEs, total HBCD, and the three isomers of HBCD and for each single congener in all three matrices.

The consensus values of the standard solutions were calculated as mentioned above with the exception of the removal of all values exceeding  $\pm 50\%$  of the median prior to the final calculation of the consensus median and mean.

The consensus values for the lipid contents were calculated by first excluding results deviating more than two SD from the mean of all values, and then re-calculating the median, mean and SD.

For the determination of total TEQs in the three food samples, Z-scores within  $\pm 1$  were obtained by 69-82 % of the laboratories (Corresponding to a trueness of  $\pm 20$  % for all food samples). The majority of all the laboratories (79-92 %) reported results for total TEQ with a trueness of  $\pm 40$  % for all food samples (Z-score  $\pm 2$ ). The relative standard deviation (RSD) calculated for the total TEQ after removal of outliers was 9-14 %. Considering this, it may be concluded that the abilities and performance of laboratories worldwide in determining dioxin-like compounds is generally good for the three food samples included in this study.

For the food samples, 47-59 laboratories reported results for the six indicator PCBs, 29-36 laboratories reported concentrations for all seven of the tetra- to hepta-PBDEs and 19-24 laboratories reported concen-

trations for PBDE-209. The concentrations of the sum of seven PBDEs on fresh weight basis were 93 (21 %), 1054 (20 %) and 11 (25 %) pg/g in pork, herring and milk, respectively, with average RSD given in parentheses. The consensus concentrations for PBDE-209 were 15 (n=19, RSTD=58 %), 81 (n=24, RSTD=37 %) and 15 (n=21, RSTD=56 %) pg/g fresh weight in pork, herring and milk, respectively.

The total concentrations on fresh weight basis for six indicator PCBs were 533 pg/g (16 %) in pork meat, 17569 pg/g (16 %) in herring and 82 pg/g (19 %) in milk, with average RSDs given in parentheses.

The consensus concentrations calculated for HBCDs are just indicative values because only few laboratories reported results (n=8-10).

# Introduction

As many countries request frequent monitoring of the presence of dioxins and dioxin-like PCBs in food and feed both to map and to reduce human and animal exposure to these highly toxic pollutants, there is a large demand for chemical laboratories with the skills and abilities to determine these contaminants at low levels and in complex matrixes. It is usually required by the authorities that laboratories performing such measurements are accredited according to ISO standards and prove their competence by successful participation in interlaboratory studies.

This is the 15<sup>th</sup> round of a world-wide interlaboratory comparison study on dioxin-like compounds in food organized by the Department of Exposure and Risk Assessment, Division of Environmental Medicine, Norwegian Institute of Public Health (NIPH), Oslo, Norway.

The main objective of this exercise is to assess the between laboratory reproducibility of dioxin-like compounds analyses in frequently consumed foods and provide a QA/QC instrument for each participating

laboratory to contribute to its proficiency. Participants were also given the opportunity to voluntarily determine the concentrations of eight PBDEs, six indicator PCBs and HBCD in the food samples in order to assess the readiness of laboratories to analyze these persistent organic pollutants.

The exercise took place from January 2014, when the samples were shipped to the laboratories for analysis, until the reporting deadline in April 2014, when the last reports with results were received. A draft report was made available to the participants on our webpage (<http://www.fhi.no/ILC>) in July.

All participants from previous rounds in this series of "Interlaboratory Comparisons on POPs in Food" were invited to participate. In addition, several other laboratories announced their interest and were invited to participate. There was no limit to the total number of participating laboratories. The 86 laboratories that submitted results, and thereby contributed to the study results, are presented in Table 1.

**Table 1. Participants that reported results in the 15<sup>th</sup> round of Interlaboratory Comparison on POP's in food 2014**

<b>Activaq</b> Santiago de Chile, Chile	<b>China National Center for Food Safety Risk Assessment</b> Beijing, China
<b>Agriparadigma srl</b> Ravenna, Italy	<b>Chinese Academy of Sciences Center for Eco-Environmental Sciences Dioxin Lab</b> Beijing, China
<b>All-Russian State Center for Quality and Standardization of Veterinary Drugs and Feeds Department of safety of feed and food products(VGNKI)</b> Moscow, Russia	<b>Danish Veterinary and Food Administration, Division of Residues</b> Ringsted, Denmark
<b>ALS Czech Republic</b> Pardubice, Czech Republic	<b>Department of the Environment and Primary Prevention, Toxicological Chemistry Unit</b> Rome, Italy
<b>Arkansas Regional Laboratory (ARL), USFDA</b> Jefferson, USA	<b>Dioxin laboratory of Comprehensive test center of Chinese Academy of Inspection and Quarantine</b> Beijing, China
<b>AsureQuality Limited - Wellington Laboratory</b> Wellington, New Zealand	<b>Environmental Laboratory - IQS</b> Barcelona, Spain
<b>BioDetection Systems</b> Amsterdam, The Netherlands	<b>Eurofins GfA Lab Service GmbH</b> Hamburg, Germany
<b>Canadian Food Inspection Agency</b> Calgary, Alberta, Canada	<b>Food GmbH Jena Analytik &amp; Consulting</b> Jena, Germany
<b>CARSO-LSEHL</b> Lyon, France	<b>Food Research Division Health Products and Food Branch</b> Ottawa, CANADA
<b>Central Lab of Residue Analysis of Pesticides and Heavy Metals in Foods</b> Giza, Egypt	<b>GALAB Laboratories GmbH</b> Hamburg, Germany
<b>Centre for Advanced Analytical Toxicology Services (CAATS)</b> Penang, Malaysia	<b>Gesellschaft für Lebensmittel-Forschung mbH</b> Berlin, Germany
<b>Chelab Silliker</b> Resana, Italy	<b>Government Laboratory Additives, Contaminants and Composition Section</b> Hong Kong, P.R. China
<b>Chemical and Veterinary Analytical Institute Münsterland-Emscher-Lippe (CVUA-MEL),</b> Münster, Germany	<b>Guangdong Test Center of Product Quality Supervision(GDQT), Dioxin Analysis Laboratory</b> Shunde, China
<b>Chemisches und mikrobiologisches Institut UEG GmbH</b> Wetzlar, Germany	<b>Helmholtz Zentrum München, Molecular EXposomics</b> Neuherberg, Germany
<b>Chemisches und Veterinäruntersuchungsamt (CVUA) Freiburg</b> Freiburg, Germany	<b>Hessisches Landeslabor</b> Wiesbaden, Germany
<b>Hubei Provincial Centre for Disease Control and Prevention, Hubei Dioxin Lab</b> Hubei Province, China	<b>MicroPollutants Technologie (MPT)</b> Saint Julien Les Metz, France

<b>Institute of Aquaculture</b> <b>Nutritional Analytical Service</b> Stirling, United Kingdom	<b>Ministry of Food &amp; Drug Safety, Food Contaminants Division</b> Chungcheongbuk-do, South of Korea
<b>Istituto Zooprofilattico Sperimentale Abruzzo e Molise "G. Caporale"</b> Teramo, Italy	<b>National Cheng Kung University Research Center for Environmental Trace Toxic Substances</b> Tainan, Taiwan
<b>Istituto Zooprofilattico Sperimentale Lombardia Emilia Romagna</b> Bologna, Italy	<b>National Food Agency Chemistry Division 2</b> Uppsala, Sweden
<b>Japan Food Research Laboratories</b> Japan	<b>National Institute for Health and Welfare Department of Environmental Health</b> Kuopio, Finland
<b>Josera Erbacher GmbH &amp; Co. KG</b> Kleinheubach, Germany	<b>National Measurement Institute - Pymble Dioxin Analysis</b> Sydney, Australia
<b>La Drôme Laboratoire</b> Valence, France	<b>National Laboratory of Health, Environment and Foodstuffs</b> Maribor, Slovenia
<b>LABERCA - ONIRIS</b> Nantes, France	<b>National Institute of Nutrition and Seafood Research (NIFES)</b> Bergen, Norway
<b>Laboratoire De Rouen</b> ROUEN, France	<b>NCSR "Demokritos", Greece</b> <b>Mass Spectrometry and Dioxin Analysis Lab</b> Athens,, Greece
<b>Laboratorio BDS Chile Ltda.</b> Rancagua, Chile	<b>Niedersächsisches Landesamt für Verbraucherschutz und Lebensmittelsicherheit Lebensmittel-und Veterinärinstitut Oldenburg</b> Oldenburg, Germany
<b>Laboratory of SGS Bulgaria Ltd.</b> Varna, Bulgaria	<b>Nofalab BV</b> Schiedam, The Netherlands
<b>Laboratory of Vendee (LEAV)</b> La Roche-sur-Yon, France	<b>Norwegian Institute of Air research (NILU)</b> Kjeller, Norway
<b>Landesamt für Umweltschutz Sachsen-Anhalt</b> Halle, Germany	<b>Oekometric GmbH</b> Bayreuth , Germany
<b>Landesuntersuchungsamt, Institut für Lebensmittelchemie</b> Speyer, Germany	<b>POSTECH</b> Korea
<b>Marchwood Scientific Services</b> Southampton, UK	<b>QLIP N.V.</b> Zutphen, Netherland
<b>mas   münster analytical solutions gmbh</b> Münster , Germany	<b>Research and Productivity Council (RPC)</b> Fredericton, New Brunswick, Canada
<b>RIKILT</b> Wageningen, The Netherlands	<b>Super Micro Mass Research &amp; Technology Center</b> <b>Cheng Shiu University</b> Niaosong District, Kaohsiung City, Taiwan(ROC)
<b>Scientific Analysis Laboratories</b> Manchester, UK	<b>The Food and Environment Research Agency (FERA)</b> York, UK

<b>Servizos de Apoio á Investigación (Scientific Research Support Services)</b> Coruña, Spain	<b>TLR International Laboratories</b> Rotterdam, The Netherlands
<b>SGS Analytical Perspectives</b> Wilmington NC, USA	<b>U.S. Food and Drug Administration</b> Lenexa, Kansas, United States of America
<b>SGS Belgium NV</b> <b>Division IAC</b> Antwerpen, Belgium	<b>Umeå Universitet, Miljökemiska Laboratoriet</b> <b>Trace Analysis Platform</b> Umeå, Sweden
<b>SGS Institut Fresenius GmbH</b> Bayreuth, Germany	<b>Veterinary Public Health Laboratory</b> <b>Chemistry Department</b> Republic of Singapore
<b>SGS Taiwan Environmental Service</b> <b>Dioxin Laboratory</b> New Taipei City, Taiwan (R.O.C.)	<b>Vista Analytical Laboratory</b> El Dorado Hills, USA
<b>Shanghai Municipal Center for Disease Control and Prevention</b> Shanghai, China	<b>Wellington Laboratories Inc.</b> Guelph, Ontario, Canada
<b>Shenzhen Center for Disease Control &amp; Prevention</b> <b>Guangdong POP Lab</b> Shenzhen, Guangdong, China	<b>WESSLING GmbH</b> Altenberge, Germany
<b>SHIMADZU TECHNO-RESEARCH, INC., ENVIRONMENT DIVISION</b> Kyoto, Japan	<b>Western Region Laboratory</b> <b>Health Canada</b> Burnaby, Canada
<b>State Laboratory</b> County Kildare, Ireland	<b>Worthies Engineering Consultants Corp. Environmental Analysis Lab</b> Taichung, Taiwan
<b>Sun Dream Environmental Technology Corporation</b> <b>Food Hygiene Laboratory</b> Taichung City, Taiwan (R.O.C.)	<b>Zhejiang Provincial Centre for Disease Control and Prevention, Dioxin Laboratory</b> Hangzhou, China

# Design and practical implementation

## Study design and reporting of results

As in the previous rounds of this interlaboratory comparison study, the test material chosen represented naturally contaminated food samples. The analytes to be determined were all seventeen 2,3,7,8-substituted PCDDs/PCDFs, the four non-ortho substituted PCBs #77, 81, 126 and 169 and the eight mono-ortho substituted PCBs #105, 114, 118, 123, 156, 157, 167 and 189. If wished for, the laboratories could also determine eight PBDEs #28, 47, 99, 100, 153, 154, 183 and 209, six indicator PCBs #28, 52, 101, 138, 153 and 180, total HBCD and its three isomers ( $\alpha$ -,  $\beta$ -,  $\gamma$ -HBCD). The six PCB congeners belong together with the mono-ortho PCB #118 to the selection of PCBs commonly referred to as ICES-7 (ICES-7: Report of the ICES Advisory Committee, 2010; Book 7).

The analysis should be performed using the laboratories' own methods for sample preparation and instrumental analysis, their own standards and quantification procedures and their own method for lipid determination.

It was recommended that laboratories determined as many as possible of the 2,3,7,8-substituted PCDDs/PCDFs, dioxin-like PCBs, PBDEs, indicator PCBs and HBCD in the samples of pork meat, the herring sample and the sample of milk.

The laboratories were to report the found concentration of each detected congener in the food items on fresh weight basis (e.g. S/N  $\geq 3$ ) as well as the level of determination (LOD, e.g., S/N =3). Non-detected congeners (e.g. S/N <3) were to be marked "ND" in the comments column of the Report forms. As the report was to include the determination of lipid percent in the food samples, the laboratories should also include the determined lipid percent of the samples as well as sample amount used for the analysis.

In addition to the food samples, six standard solutions containing known concentrations of the analytes were to be analyzed using the laboratories' own quantification standards and methods. The standard solutions consisted of the following components:

- 1) Seventeen 2,3,7,8-substituted PCDDs/PCDFs (2:5:10 pg/ml for tetra:penta:hexa:hepta:octa chlorinated dibenzo-p-dioxins/-dibenzo furans respectively)
- 2) Four non-ortho PCBs (10 pg/ml)
- 3) Eight mono-ortho PCBs (100 pg/ml)
- 4) Eight PBDEs (100 pg/ml)
- 5) Six indicator PCBs (100 pg/ml)
- 6)  $\alpha$ -HBCD (500 pg/ml)

The test materials consisted of homogenates of pork meat, herring and milk. The laboratories could choose to analyze one, two or all three food samples.

Each participating laboratory was given an exclusive laboratory code by the co-coordinators. In the present report, the participants are presented in the tables and figures by their unique codes. The participants have access to their own code only and laboratory codes were not revealed to third parties.

When received by the co-coordinators, the raw data from the laboratories were entered into a database. A draft report was generated and made available to all participants on the Internet in July 2014.

## Collection, preparation, and distribution of samples

Samples shipped to the participants comprised one to three of the following:

- Pork meat (~90 g)
- Herring (~100 g)
- Milk (~130 g)

The test materials consisted of natural products unfortified with standards.

The contaminated pork meat and milk sample were generously provided by Dr. Elke Bruns-Weller, LAVES, Oldenburg, Germany and Wim Traag at Rikilt in Wageningen in the Netherlands respectively. Dr. Marie Aune, National Food Agency in Uppsala, Sweden kindly used her time to purchase and ship the herring sample to NIPH.

The pork meat from Germany was ground in a meat grinder at the Norwegian Institute of Public Health and then thoroughly mixed with commercially available Norwegian ground pork meat in a food grinder. The herrings from the Baltic Sea arrived as frozen herring filets. They were ground, pooled and carefully homogenized in a food grinder.

The bovine whole milk sample were homogenized by slowly heating the bulk sample while stirring.

Sub-samples of at least 90 g of pork (Pork-2014), 100 g of herring (Herring-2014) and 130 g of milk (Milk-2014) were placed into screw-cap polystyrene bottles. The bottles were all carefully washed, rinsed with methanol and dried before use. All samples were stored at -20 °C until shipment to the participating laboratories.

## Statistical analysis

Based on experiences from previous rounds, we have chosen the following approach for the calculation of the consensus concentrations for each of the congeners included in the study:

For PCDDs/PCDFs and dioxin-like PCBs: Congener-by-congener medians were calculated from the food sample data of all reporting laboratories. The detection limits were used as concentration for non-detected congeners (upper bound concentration).

For PBDEs, indicator PCBs and HBCD: Non-detected congeners in the food samples were removed from the data set prior to consensus calculation.

Outliers for all congeners were defined as those values exceeding twice the median of all values and thus removed from the data set.

The consensus values were defined as the median of the remaining data for each congener. The consensus mean and SD were calculated from this data set for each congener. The congener data which were removed prior to consensus calculation are marked accordingly in the tables presenting the individual results.

For the standard solutions, outliers were defined as those values outside ±50 % of the median of all reported values and subsequently removed from the data set before the calculation of the median, mean and SD were calculated from the remaining data. The consensus of the lipid content was calculated as the mean after removal of values outside ±2\*SD.

TEQs were calculated from the consensus values for PCDDs/PCDFs, non-ortho PCBs, and mono-ortho PCBs, using the toxic equivalency factors derived by WHO in 1998 and 2005. As the detection limit was used for the concentration of non-detects, these TEQs represent upper bound concentrations.

Z-scores for PCDD/PCDF TEQ as well as for the non-ortho PCB TEQ, the mono-ortho PCB TEQ, the total TEQ (WHO<sub>2005</sub> TEFs), the sum of six indicator PCBs, the sum of eight PBDEs, total HBCD and for each congener were calculated for each laboratory according to the following equation:

$$Z = (x - X)/\sigma$$

Where x = reported value; X = consensus value (assigned value);  $\sigma$  = target value for standard deviation. A s of 0.2 multiplied by the consensus value was used, i.e. Z-scores between +1 and -1 reflect a deviation of ±20 % from the consensus value.

## The final report and certificate

The draft of the final report was prepared by the co-coordinators and published on the web in July 2014.

The final report will be made available to the participants in pdf format at [www.fhi.no/ILC](http://www.fhi.no/ILC)

A certificate, stating the participant's laboratory code, will be sent to each participant who has contributed to the results by the end of 2014.

## Co-ordination

The study was initiated and carried out by the Department of Exposure and Risk Assessment, Division of Environmental Medicine, Norwegian Institute of Public Health, Oslo, Norway. Members of the co-ordination committee were:

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# Results

## Presentation in the report

86 laboratories in 40 different countries submitted their results within the deadline and the results will be presented in the following chapters. Any participating laboratory will be able to compare its performance congener by congener with the other laboratories. Since variations in performances are based on several factors, it is recommended that each laboratory carefully evaluates the factors that, favorably or unfavorably, have contributed to its performance.

Any reader of the report can without access to the laboratory codes get a general overview of the analytical performance of laboratories worldwide on the determination on dioxins, dioxin-like PCBs, indicator PCBs, PBDEs and HBCD in regular food stuffs.

In Appendix E the consensus statistics are given on fresh and lipid weight basis for concentrations of individual congeners and TEQ values, a summary of TEQ values for each food item, and the Z-score plots based on a target deviation of  $\pm 20\%$  from the consensus TEQ2005-values.

Individual results reported by the laboratories for each congener are given for pork meat, herring and milk in Appendix 2, 3 and 4. Results of the lipid determinations are presented in Appendix 5.

## Summarizing comments on results

### *PCDDs/PCDFs*

#### Analyte solution

Concentrations for PCDDs/PCDFs were reported by 72 laboratories, except for 1,2,3,4,6,7,8,9-OCDF which was reported by 71 laboratories. The average RSD for the 17 congeners was 8.9 % ranging from 7.4 % for 1,2,3,6,7,8-HxCDF to 11 % for 2,3,7,8-TCDF. The calculation of Z-scores for the TEQs (target 12.5 pg TEQ/mL based on TEF2005-values) of the PCDD/PCDF standard solution showed that 99 % of the laboratories were within the range of  $\pm 20\%$  of the consensus value. This demonstrates that the calibration solutions used by the laboratories generally are of high quality.

#### Pork meat

For the pork meat sample, PCDD/PCDF results from 63 laboratories were received. The consensus TEQ (PCDD/PCDF TEQ based on WHO<sub>2005</sub>-TEFs) was 0.26 pg TE/g fresh weight and 0.95 pg TE/g lipid weight.

The average RSD was 52 %, ranging from 21-84 % for 1,2,3,4,6,7,8-HxCDD and 1,2,3,7,8,9-HxCDF respectively. Z-scores within  $\pm 1$  were obtained by 73 % of the laboratories and 90 % of the laboratories had Z-scores within  $\pm 2$ .

#### Herring

PCDD/PCDF concentrations in the Baltic herring were reported by 74 laboratories. The consensus TEQ was 2.0 pg TEQ/g fresh weight, and 29 pg TEQ/g lipid weight (PCDD/PCDF TEQ based on WHO<sub>2005</sub>-TEFs). The average RSD was 31 % ranging from 19-57 % (2,3,7,8-TCDF and 1,2,3,4,6,7,8,9-OCDF respectively). Z-scores were within  $\pm 1$  for 82 % of the laboratories and within  $\pm 2$  for 93 % of the laboratories.

#### Milk

PCDD/PCDF concentrations in the milk-sample were determined by 59 laboratories. The consensus TEQ was 0.077 pg TEQ/g on fresh weight basis, and 2.1 pg TEQ/g on lipid weight basis (PCDD/PCDF TEQ based on WHO<sub>2005</sub>-TEFs). The average RSD was 37 % ranging from 21-55 % (2,3,4,7,8-PeCDF and 1,2,3,7,8,9-HxCDF respectively). Z-scores for PCDD/PCDF TEQ within  $\pm 1$  were obtained by 69 % of the laboratories and 82 % had Z-scores within  $\pm 2$ .

### *Dioxin-like PCBs*

#### Analyte solution

The 12 dioxin-like PCBs in the analyte solution were analyzed and reported by 70-71 laboratories. The RSDs for the different congeners were 6.9-9.8 % with an average of 8.2 %.

#### Pork meat

Dioxin-like PCB concentrations in the pork sample were reported from 62 laboratories. The concentrations of the 12 congeners varied between 0.049 pg/g fresh

weight (PCB-169) and 34 pg/g fresh weight (CB-118). The average RSD for concentrations of individual dioxin-like PCB congeners was 35 % ranging from 23 % for PCB-156 to 60 % for PCB-123.

The dioxin-like PCBs contribute 9.5 % to the total TEQ (WHO TEF<sub>2005</sub>) in the sample with PCB-126 as the main contributor (5.5 %).

#### Herring

Of the participating laboratories, 73-74 measured and reported dioxin-like PCB concentrations in the Baltic Herring sample. The concentrations ranged from 0.99 pg/g fresh weight for PCB-81 to 2332 pg/g fresh weight for PCB-118. The average RSD for concentrations of individual dioxin-like PCB congeners on fresh weight basis was 20 % ranging from 13 % for PCB-156 to 46 % for PCB-123.

The dioxin-like PCBs contribute to about 52 % of the total TEQ in the sample with PCB-126 as the main contributor (46 %).

#### Milk

Dioxin-like PCBs in the milk-sample were reported by 59-60 laboratories. Levels were ranging from 0.047 pg/g fresh weigh for PCB-81 to 11 pg/g fresh weight for PCB-118. The average RSD for concentrations of individual dioxin-like PCB congeners on fresh weight basis was 31 % ranging from 22 % for PCB-169 to 48 % for PCB-77. The contribution of the dioxin-like PCBs to the total TEQ was about 29 % with PCB-126 as the main contributor (26 % of total TEQ).

#### Total TEQ

The total TEQ for the pork meat was 0.28 pg TEQ/g fresh weight and 1.0 pg TEQ/g lipid weight (WHO TEF<sub>2005</sub>). The total TEQ of the herring sample was 4.2 pg TEQ/g fresh weight and 62 pg TEQ/g lipid weight, and the milk contained 0.11 pg TEQ/g fresh weight and 3.0 pg TEQ/g lipid weight.

The RSDs for total TEQs on fresh weight basis calculated from the RSD of individual congeners were 14 % for pork meat, 8.7 % for herring and 11 % for milk.

In Figure 1 the contribution on the TEQ-values of the three groups of compounds is depicted based on WHO TEF<sub>2005</sub> and WHO TEF<sub>1998</sub>, respectively. In the selection of food-items included in this study the dioxin-like PCBs contributed from 6.7 % to 52 % to the total TEQ (using WHO TEF<sub>2005</sub>), demonstrating the variation in contribution, and thus the importance of the PCBs for the determination of the total TEQs related to the toxic potency of food samples.

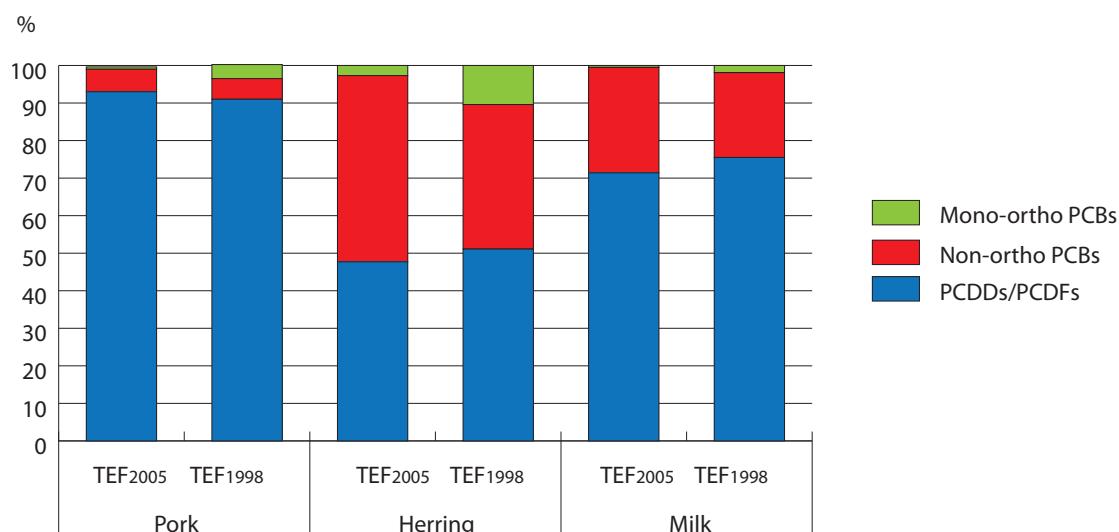
#### Indicator PCBs

##### Analyte solution

58 laboratories reported indicator PCBs in the analyte solution. The average RSD was 9.3 % ranging from 8.0 to 11 %.

##### Pork

For the sample of pork, results for indicator PCBs were received from 53 laboratories. The consensus concentrations varied between 43 pg/g fresh weight (PCB-



**Figure 1.** The contribution of PCDDs/PCDFs, non-ortho PCBs and mono-ortho PCBs to the total TEQ calculated using both the WHO<sub>2005</sub> TEFs and WHO<sub>1998</sub> TEFs, in the three food samples.

28) and 160 pg/g fresh weight (PCB-153). The RSDs were ranging from 33 to 51 % for PCB-180 and PCB-28 respectively, with an average of 37 % for all indicator PCBs. The consensus median for the sum of indicator PCBs was 533 pg/g fresh weight.

#### Herring

Within the deadline, 59 laboratories reported results for indicator PCBs in the herring-sample. The consensus concentrations ranged from 467 pg/g fresh weight (PCB-28) to 6715 pg/g fresh weight (PCB-153) with a consensus median for the sum of indicator PCBs of 17659 pg/g fresh weight. The average RSD was 33 %, ranging from 28 to 42 % for PCB-180 and PCB-28 respectively.

#### Milk

Results were obtained from 47 laboratories. The concentrations of indicator PCBs in the milk-sample ranged from 7.2 pg/g fresh weight (PCB-180) to 21 pg/g (PCB-153) and the consensus median for the sum was 82 pg/g fresh weight. The average RSD was 42 %, ranging from 31 to 54 % for PCB-138 and PCB-28 respectively.

### PBDEs

#### Analyte solution

The tri- to hepta-PBDE standard solution was analyzed by 37 laboratories and 27 laboratories reported values for PBDE-209. The RSDs were between 7.1-12 % for all congeners.

#### Pork

The PBDE concentrations in pork were reported by 29-30 laboratories, except for PBDE-209 for which 19 results were received. The consensus concentrations were in the range from 0.57 pg/g fresh weight for PBDE-28 to 38 pg/g fresh weight for PBDE-99. The consensus concentration for PBDE-209 was 15 pg/g fresh weight. The sum of tri- to hepta-PBDEs was 93 pg/g fresh weight. The range of RSDs on fresh weight basis was 31-58 %, with an average of 41 % including PBDE-209.

#### Herring

Within the deadline, 36-37 laboratories had reported results for tri- to hepta-PBDEs in herring and 24 laboratories had reported results for PBDE-209. The consensus concentrations varied between 2.5 pg/g fresh weight (PBDE-183) and 628 pg/g fresh weight (PBDE-47). The concentration for PBDE-209 was 81 pg/g fresh weight. The sum of tri- to hepta-PBDEs was 1054 pg/g fresh weight. The RSD calculated from the concentrations on fresh weight ranged from 26-42 %, with an average of 34 % for PBDEs including PBDE-209.

#### Milk

29 laboratories reported results for tri- to hepta-PBDEs in milk, and 21 reported results for PBDE-209. The concentrations varied between 0.12 pg/g fresh weight (PBDE-28) and 4.5 pg/g (PBDE-47). The concentration for PBDE-209 was 15 pg/g. The sum of tri- to hepta-PBDEs was 11 pg/g fresh weight. The RSDs for the individual congeners were ranging from 36 to 56 % with an average of 41 % including PBDE-209.

#### HBCD

Also in this round of the study, total HBCD and the isomers α-, β- and γ-HBCD could be determined and reported. A total of 12 laboratories reported α-HBCD in the standard solution and 8-13 laboratories reported one or more of the three isomers in the food samples. The consensus concentrations for the sum of individual HBCD isomers were 116 pg/g fresh weight for the pork sample, 1700 pg/g for the herring and 4.0 pg/g fresh weight for the milk sample. Since only a few laboratories reported HBCD, these results must be regarded as indicative values.

#### Lipid content

The mean and RSDs (in parentheses) for the lipid contents of the food samples were calculated to be 28 % (RSD=6.6 %) for the pork sample, 6.6 % (RSD=13 %) for the herring and 3.6 % (RSD=19 %) for the milk sample.

# Acknowledgements

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Netherlands, for providing the milk sample and Dr. Marie Aune at the Swedish National Food Agency for making the herring sample available. We are also grateful that Mr. Lars Haug provided the Norwegian minced pork meat and to Cambridge Isotope Laboratories, Inc. for providing the standard solutions for this interlaboratory study.



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## **Appendix B:**

Study announcement and  
instructions for participants



## **Announcement for Interlaboratory Comparison on POPs in Food 2014**

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### **Introduction**

We hereby announce the 15<sup>th</sup> round of the Interlaboratory Comparison on the Determination of POPs in Food. The study is open for academic, regulatory as well as commercial laboratories world-wide. The organizer of this study is the Division of Environmental Medicine, Department of Exposure and Risk Assessment at the Norwegian Institute of Public Health, Oslo, Norway. The study is scheduled to take place from January to April 2014. A draft report will be available by mid July 2014, and the final report will be available to the participants by November 2014. All participants who have contributed to the results will receive a certificate of participation in the study.

### **Objectives**

One of the main objectives of this exercise is to assess the interlaboratory consistency in results from analyses of dioxins, PCBs, PBDEs and HBCDs in regular food items known to contribute to the intake in the general population. Further, the world-wide readiness and capacity in analysing halogenated persistent organic pollutants in food will be demonstrated. The study also serves as a tool of quality assurance for the participating laboratories.

### **Participants**

We encourage all laboratories world-wide working in this field to participate and assess their analytical performance. To do this, participants are requested to completely fill out the Registration Form and mark the desired sample types and what analytes they intend to determine.

### **Analytical requirements**

In this interlaboratory comparison, all the seventeen 2, 3, 7, 8-substituted PCDDs and PCDFs, the four non-ortho PCBs, CB-77, 81, 126 and 169 as well as the eight mono-ortho PCBs, CB-105, 114, 118, 123, 156, 157, 167, and 189 will be assessed. In addition, the participants are invited to determine six marker PCBs, eight PBDEs and HBCDs. The concentration of the following congeners can be reported: CB-28, 52, 101, 138, 153 and 180 and BDE-28, 47, 99, 100, 153, 154, 183 and 209. The concentration of α-HBCD, β-HBCD and γ-HBCD as well as the total of these isomers will also be assessed. The test materials consist of three fresh food homogenates. You can choose to analyse one, two or all three of the food items. We encourage you to determine as many analytes as possible. You are further requested to determine and report the lipid content of the foods.

We also include standard solutions of all analytes that should be analysed as solutions of known concentration, which may be used to check your own calibration solutions.

### **Test material**

The test materials consist of three unfortified natural food product homogenates, Pork meat (labelled “Pork-2014”) ~90 g, Milk (labelled “Milk-2014”) ~130 g and Herring (labelled

“Herring-2014”) ~100 g, and will be distributed by an international courier service to the participating laboratories.

**Please note:**

**In order to avoid delay or retention of the samples at customs, please inform us if there are import restrictions in your country for any of the samples.**

**Instructions for analysis and reporting**

Further detailed instructions and reporting forms will be sent by e-mail simultaneously with the dispatch of the samples in January.

In short, the participating laboratories should:

- use their own standard operation procedures for extraction clean-up and instrumental determination
- use their own reference standards for identification and quantification
- report one single concentration for each analyte in each food matrix determined on fresh weight basis
- report limits of detection for all measured analytes in each food item
- report the lipid content

**Time schedule**

Announcement	<b>December 2013</b>
Return of registration form	<b>January 05, 2014</b>
Shipment of test material	<b>Third week, 2014</b>
Confirmation of receipt of test material by participant	<b>Within 7 days</b>
<b>Reporting of test results <sup>a)</sup></b>	<b>April 22, 2014</b>
Publication of draft report on web-site	<b>July 2014</b>
Final report available to all participants	<b>November 2014</b>

- a) Please be sure that your results are reported on time as there will be **no extension of the deadline.**

**Participation fee**

All laboratories that have received the test materials will also receive a corresponding invoice in Norwegian kroner (NOK). The participation fee for any combination of the analytes in one food item is 9 000 NOK, in two food items 11 200 NOK, and for the complete set of all three food items 13 400 NOK.

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## **Interlaboratory Comparison on Dioxins in Food 2014**

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### **Instructions for participants**

**January 2014**

#### **1. Introduction**

This is the 14<sup>th</sup> Round of the Interlaboratory Comparison Study on the Determination of POPs in Food organised by the Department of Exposure and Risk Assessment, Norwegian Institute of Public Health, Oslo, Norway. The objective of this exercise is to assess the interlaboratory comparability of the results from analyses of all dioxins and dioxin-like PCBs included in the WHO-TEF schemes in regular foods. Participants may also determine and report concentrations of six marker PCBs, eight polybrominated diphenylethers (PBDEs) and hexabromocyclododecane (HBCD). The exercise serves as a quality assurance instrument for the participating laboratories. A further objective is to assess the world-wide readiness and capacity for the determination of dioxin-like compounds, marker PCBs, PBDEs and HBCD in food. Instructions for the analysis and submission of results are given below.

**Please read these instructions carefully before starting the experimental work.**

The participating laboratories will collaboratively assess the interlaboratory comparability in the analytical performance for determination of:

- dioxins and furans: all seventeen 2,3,7,8-substituted PCDDs and PCDFs
- non-ortho PCBs: CB-77, 81, 126 and 169
- mono-ortho PCBs: CB-105, 114, 118, 123, 156, 157, 167 and 189.
- marker PCBs: CB-28, 52, 101, 138, 153 and 180
- PBDEs: BDE-28, 47, 99, 100, 153, 154, 183 and 209
- HBCD α-HBCD, β-HBCD, γ-HBCD and total HBCD

in samples of Pork (Pork-2014), Herring (Herring-2014) and Milk (Milk-2014). The mentioned analytes should also be determined in the respective six standard solutions. For HBCD, concentrations of α-HBCD, β-HBCD and γ-HBCD as well as the total of these isomers will be assessed. Both results from GC-MS and LC-MS or LC-MS/MS are welcome.

#### **2. Participants**

A list of participants is attached. 87 laboratories have announced their participation in the study.

### **3. Design of the study**

#### **3.1 Test materials**

##### Samples

One standard solution of each:

- EDF-5008-50 with PCDDs/PCDFs at concentrations 2:5:10 pg/µl for tetra:penta-hexa-hepta:octa chlorinated dibenzo-p-dioxins/-dibenzo furans respectively
- EC-4986/1000 with non-ortho PCBs at concentration 10 pg/µl
- EC-4987/100 with mono-ortho PCBs at concentration 100 pg/µl
- EC-5179/50 with marker PCBs at concentration 100 pg/µl
- EO-5103/100 with PBDEs at concentration 25 pg/µl, except BDE-209 at 100 pg/µl
- ULM-4834-S/100 with α-HBCD at a concentration 500 pg/µl

One sample of each

- ca. 90 g pork
- ca. 130 g milk
- ca. 100 g herring

##### Fortification

The samples are prepared from regular market foods. There is no fortification or spiking of the PCDD, PCDF, PCB, PBDE or HBCD analytes in the food samples.

##### Shipment

The samples are fresh frozen food homogenates. They are distributed by DHL and should reach the receiving laboratory in good condition within a few days. The airwaybill numbers will be made available for the participants to trace the shipment at <http://www.dhl.com>.

#### **3.2 Coding**

##### Coding of laboratories

Upon arrival of the samples in the participant's laboratory, the Microsoft excel file named "Participant confirmation", shall be filled in and **immediately** returned to the co-ordinators by e-mail or telefax. The code of the laboratory will then be given by the co-ordinators. The laboratory codes will not be revealed to the other participants or to third parties.

##### Coding of samples

Pork	Pork-2014
Milk	Milk-2014
Herring	Herring-2014

The above sample coding is marked on the sample bottles.

#### **3.3 Analytical procedure**

##### Methods to be used

Laboratories shall use

- their own methods for sample preparation and instrumental analysis
- their own internal- and quantification standards

- their own lipid determination procedure

#### Standard solutions

The standard solutions should be analysed using the laboratory's own quantification standards and methods and the results shall be reported.

#### General

Beware of the high risk of background contamination and positive blank values when analysing food samples with levels of dioxins, PCBs, PBDEs and HBCD in the low ppt range.

Use sample size according to expected levels of dioxins for the determinations in order to achieve a detection level that leaves as few as possible analytes as non-detected. The sample amount dispatched is not meant for replicate analyses.

The samples might become inhomogeneous during freezing and transport. Re-homogenise all received material of each food item before any portion is taken out for analysis.

### **4. Reporting**

#### 4.1 Results to be reported

Laboratories are recommended to report as many as possible of the congeners mentioned in chapter 1.

The reports must include the determined lipid percent for the samples. Also, the actual sample amount (g) for each determination must be reported.

The analytical report must include concentrations for all the congeners in all the samples on fresh weight basis, see Report forms B, C, D for PCDD/PCDF and dioxin-like PCBs and Report form 2, 3, 4 for marker PCBs, PBDEs and HBCD.

Laboratories must report one concentration on fresh weight basis for each congener which is detected ( $S/N \geq 3$ ), as well as the limit of determination (LOD,  $S/N = 3$ ) for each sample. Non-detected congeners ( $S/N < 3$ ) must be marked ND in the Comments column of the Report form. **Please note that the LOD will be used as concentration of non-detected congeners.**

#### 4.2 Checklist

Please use the attached checklist before returning the Report forms with your results.

#### 4.3 Submitting results

Three Microsoft Excel files are provided to each participant comprising:

#### **Participants confirmation**

- confirmation of receiving test materials

#### **Report form dioxins and dioxinlike PCBs**

- analytical data, Report forms A, B, C and D

## **Report form marker PCBs, PBDEs and HBCD**

- analytical data, Report forms 1, 2, 3 and 4

Participants are requested to submit their reports electronically to avoid possible transcription errors.

### **Please, do not alter rows or columns in the original Report forms!**

The electronic report shall be sent to [dioxin@fhi.no](mailto:dioxin@fhi.no) within the deadline.

If necessary, a hard copy of the Report forms can be provided. Please contact one of the co-ordinators. If a hard copy report is used, it shall either be faxed to: + 47 21 07 66 86 or mailed to:

Norwegian Institute of Public Health  
att. Nanna Bruun Bremnes  
P.O. Box 4403 Nydalen  
N-0403 Oslo, Norway

### **Deadline**

**The reports must be in our hands no later than April 22, 2014** to enable us to prepare the draft report to be published by the end of July 2014. There will be no extension of this deadline. A confirmation for the receipt of your results will be sent to you by e-mail within a week.

### **5. Statistical evaluations**

Prior to the final report, a draft version will be prepared based on the data reported by April 22th. The co-ordinators will calculate mean, median and between-laboratory standard deviations for each congener. Outliers will be removed, and consensus values will be calculated. In case of extreme deviation from normal distribution, appropriate procedures will be used to get a best available estimate of the true value. For the dioxin-like compounds, TEQ values will be calculated for each laboratory and a consensus TEQ value based on the consensus of the congeners. Z-scores will be calculated for laboratories' results for PCDD/PCDF TEQs and PCB TEQs.

### **6. Final report**

The final report will be prepared by the co-ordinators by November 2014 and will then be made available for all interested parties in an electronic version on <http://www.fhi.no>. All participants will be presented by their laboratory code. Prior to this, a draft will be published on the Internet by the end of July.

Certificates of participation in the study will be given to all laboratories submitting results.

## 7. Fee

To all laboratories that have received the materials, an invoice will be sent. The participation fee for any combination of the 29 dioxin-like congeners, six marker PCBs, 8 PBDEs and HBCD is

- NOK 9000 for one food item
- NOK 11200 for two food items
- NOK 13400 for the complete set of all three food items.

Up to six standard solutions will be distributed free of charge to all participants, dependent on which analytes the participating laboratories intend to determine.

Invoices will be sent out after we have received the Participant confirmation from the participants.

## 8. Time schedule

Announcement	<b>December 2013</b>
Return of registration form	<b>January 05, 2014</b>
Shipment of test material	<b>Third week, 2014</b>
Confirmation of receipt of test material by participant	<b>Within 7 days</b>
<b>Reporting of test results <sup>a)</sup></b>	<b>April 22, 2014</b>
Publication of draft report on web-site	<b>July 2014</b>
Final report available to all participants	<b>November 2014</b>

- a) Please be sure that your results are reported in time as there will be no extension of the deadline.

## 9. Co-ordinators of the study

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P.O. Box 4403 Nydalen  
NO-0403 Oslo, Norway

# Interlaboratory Comparison on Dioxins in Food 2014

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## Checklist

In order to avoid possible misunderstandings and errors when reporting your results, we here give a list of possible pitfalls. Please, check this list and your Report forms before reporting your results.

- Are the results for each congener filled out in the correct order? Be especially aware of 2,3,4,6,7,8- and 1,2,3,7,8,9-HxCDF, and PCB 81.
- Are all congener results reported in pg/µl for standards and pg/g for samples?
- Are both concentration and LOD reported for each congener?
- Are sample amount and measured lipid content filled in?
- Are not detected congeners marked with ND in the Comments column?





## **Appendix C:**

WHO TEFs for human risk assessment



**WHO TEFs for human risk assessment based on the conclusions of the World Health Organisation Meeting in Stockholm, Sweden, 15-18 June 1997 and International Programme on Chemical Safety expert meeting in Geneva, June 2005**  
 (M. van den Berg et al., Environ Health Perspect 1998;106:775-792; M. van den Berg et al., Toxicological sciences 93(2), 223-241 (2006))

Congener	TEF values (1998)	TEF values (2005)	Congener	TEF values (1998)	TEF values (2005)
"Dioxins"			"Dioxin-like" PCBs		
<i>Polychlorinated dibenzo-p-dioxins (PCDDs)</i>			<i>Non-ortho PCBs</i>		
2,3,7,8-TCDD	1	1	PCB 77	0.0001	0.0001
1,2,3,7,8-PeCDD	1	1	PCB 81	0.0001	0.0003
1,2,3,4,7,8-HxCDD	0.1	0.1	PCB 126	0.1	0.1
1,2,3,6,7,8-HxCDD	0.1	0.1	PCB 169	0.01	0.03
1,2,3,7,8,9-HxCDD	0.1	0.1			
1,2,3,4,6,7,8-HpCDD	0.01	0.01			
OCDD	0.0001	0.0003			
<i>Polychlorinated dibenzofurans (PCDFs)</i>			<i>Mono-ortho PCBs</i>		
2,3,7,8-TCDF	0.1	0.1	PCB 105	0.0001	0.00003
1,2,3,7,8-PeCDF	0.05	0.03	PCB 114	0.0005	0.00003
2,3,4,7,8-PeCDF	0.5	0.3	PCB 118	0.0001	0.00003
1,2,3,4,7,8-HxCDF	0.1	0.1	PCB 123	0.0001	0.00003
1,2,3,6,7,8-HxCDF	0.1	0.1	PCB 156	0.0005	0.00003
1,2,3,7,8,9-HxCDF	0.1	0.1	PCB 157	0.0005	0.00003
2,3,4,6,7,8-HxCDF	0.1	0.1	PCB 167	0.00001	0.00003
1,2,3,4,6,7,8-HpCDF	0.01	0.01	PCB 189	0.0001	0.00003
1,2,3,4,7,8,9-HpCDF	0.01	0.01			
OCDF	0.0001	0.0003			

Abbreviations used: "T" = tetra; "Pe" = penta; "Hx" = hexa; "Hp" = hepta; "O" = octa; "CDD" = chlorodibenzo-p-dioxin; "CDF" = chlorodibenzofuran; "CB" = chlorobiphenyl.





## **Appendix D:**

Homogeneity testing



# **Homogeneity testing of test materials for “Interlaboratory Comparison on Dioxins in Food” organised by the Norwegian Institute of Public Health**

## **Introduction**

The International Harmonized Protocol for the Proficiency Testing of Analytical Chemistry Laboratories (Pure Appl Chem 2006;78:145-96) states that “The bulk material prepared for the proficiency test must be sufficient homogeneous and stable, in respect of each analyte, to ensure that all laboratories receive distribution units that do not differ to any consequential degree in mean analyte concentration. The scheme provider must clearly state the procedure used to establish the homogeneity of the test material”.

The protocol requires that the variation in composition among the distributed units is negligible in relation to variation introduced by the measurements conducted by the participants of the proficiency test (PT). The estimated variation between the samples ( $s_{sam}$ ) should be less than 30% of the target standard deviation ( $\sigma_p$ ), i.e.,  $s_{sam} < 0.3 \sigma_p$ .

Further the protocol states that homogeneity testing is required to reassure the participants in proficiency testing schemes that the distributed units of the test material are sufficiently similar. The test specified calls for the selection of ten or more units at random after the putative homogenized material has been split and packaged into discrete samples for distribution. The material from each sample is then analyzed in duplicate, under randomized repeatability conditions (that is, all in one run) using a method with sufficient analytical precision. The value of  $\sigma_{sam}$  is then estimated from the mean squares after one-way analysis of variance (ANOVA).

Much depends on the quality of the analytical results of the homogeneity testing. If the analytical precision ( $\sigma_{an}$ ) of the homogeneity test is not small, important sampling variation may be obscured by analytical variation. We may get a non-significant result when testing for heterogeneity, not because it is not present, but the test has no power to detect it. It is recommended that the analytical (repeatability) precision of the method used in the homogeneity test should satisfy  $\sigma_{an} < 0.5 \sigma_p$ .

## **Consequences for the Interlaboratory Comparison on Dioxins in Food**

Below follows the consequences for the Interlaboratory Comparison on Dioxin in Food;

### **1.**

The protocol recommends duplicate analysis of at least 10 distribution units. Due to limited amount of test material in each distribution unit and the requirement for sufficiently low analytical standard deviation, the test analysis has to be restricted to PCB, e.g., 6 indicator PCB or CB-153. It is, however, questionable whether analysis of indicator PCB also reflects the distribution of dioxins and other contaminants in the sample, as the test material is often prepared by mixing specifically contaminated material with background contaminated material in order to achieve a sufficient contamination level. Therefore, the distribution of PCBs in the sample might not be relevant for the distribution of dioxins in the sample. The analytical precision of the method used in the homogeneity test should be less than half of the target standard deviation, i.e.,  $\sigma_{an} < 0.5 \sigma_p$ . For determination of dioxins, the target standard deviation may be approximated by the requirement for trueness (Commission Regulation (EC) No 1883/2006) of  $\pm 20\%$  for total TEQ, i.e., the analytical precision should be less than 10%. This is unrealistic to achieve for the determination of dioxins.

**2.**

The homogeneity testing using, e.g., the determination of indicator PCBs, requires the analysis of at least 60 samples prior to shipment of the distribution units to the participants. This causes problems for the time schedule of the sample preparation and involves high costs.

**3.**

The laboratory conducting the homogeneity test on PT analytes would have access to the test material and knowledge of contamination levels prior to the start of the PT and would therefore not be qualified for participation in the PT.

### **Conclusion**

A valid testing of homogeneity of the test materials of the Interlaboratory Comparison (ILC) on Dioxins in Food with respect to the distribution of dioxins and dioxin-like PCBs is not guaranteed using indicator PCBs. It is doubtful that the analytical precision is small enough to detect a lack in sufficient homogeneity. Given the need for annually testing three different matrices for homogeneity, alternative, rapid and low cost homogeneity tests using surrogate should be applied.

### **Present approach for homogeneity testing for the ILC on Dioxins in Food**

The Harmonized Protocol states under Chapter Testing for sufficient homogeneity: “Tests for sufficient homogeneity are in practice never wholly satisfactory... However, given that sufficient homogeneity is a reasonable prior assumption (because proficiency testing scheme providers do their best to ensure it), and that the cost [and time-consumption] of testing for it is often high, it is sensible to make the main emphasis the avoidance of “Type 1 errors” (that is, false rejection of a satisfactory material).

Having this in mind and the facts that it is impossible to determine all analytes for homogeneity testing of food test material and that a single indicator analyte not necessarily reflects the distribution of the other analytes, we have developed an approach that ensures that the test material is thoroughly blended and evenly distributed among the individual test bottles. The homogeneity testing of solid samples is based on the principle of measuring electrolytic conductivity after addition of sodium chloride to a small portion of the coarsely blended test material. A demonstration of homogeneous distribution of the added salt in the sub samples would indicate our ability to evenly blend the food matrix, i.e., with this approach we ensure the efficiency of our blending procedure. This is especially of importance when blending highly contaminated food matrices with background contaminated food matrices.

When testing homogeneity of the food samples, sodium chloride was added to about 10% of the test material in such an amount that the conductivity was about doubled compared to the natural conductivity. This sub-sample was added to the total sample. For example, to 1 kg of homogenised chicken meat, 150 g NaCl were added resulting in an addition of 1% NaCl to the final test material of 15 kg. Conductivity measurements are performed as follows: boiling water is added to 10.0g of the test material, and the resulting dispersion is ultrasonicated. After centrifugation, the extract is filtered through folded paper filters and allowed to cool to room temperature. The electrolytic conductivity of the water extract is measured using a conductivity meter.

Homogeneity of the test material was demonstrated by comparing the conductivity in water extracts of 10 samples from the same bottle (variation within bottles), and in extracts from 10 different bottles (variation between bottles).

### **Example**

As an example, the relative standard deviation (RSD) of 10 conductivity measurements within a sample bottle containing chicken meat homogenate was 2%. The RSD for the measurement of samples from 10 different, randomly selected bottles was 3%. The contribution of the inhomogeneity to the total variation, calculated from  $RSD_{inhomogeneity}^2 = RSD_{between}^2 - RSD_{within}^2$ <sup>1</sup> was 2.2% and hence small and acceptable. The total uncertainty for the determination of PCDD/Fs is usually considerably larger, so the measured contribution of inhomogeneity to the total uncertainty can be neglected

<sup>1</sup>G. Becher, L.S. Haug, C. Thomsen, World-wide comparison on the quality of analytical determinations of PCDDs/PCDFs and dioxin-like PCBs in food, *Talanta* 63 (2004) 1115-1122.



## Appendix E:

### Summary of results

Consensus of congener concentrations

Consensus of TEQ values

Consensus statistics

Laboratories' reported TEQs

Laboratories' Z-scores

Z-score plots



### Consensus congener concentrations

	<b>Pork</b>		<b>Herring</b>		<b>Milk</b>	
	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.
<b>2,3,7,8-TCDD</b>	0.0030	0.011	0.18	2.6	0.0068	0.19
<b>1,2,3,7,8-PeCDD</b>	0.021	0.074	0.48	7.1	0.019	0.52
<b>1,2,3,4,7,8-HxCDD</b>	0.029	0.10	0.069	1.0	0.0082	0.22
<b>1,2,3,6,7,8-HxCDD</b>	1.8	6.4	0.32	4.7	0.023	0.63
<b>1,2,3,7,8,9-HxCDD</b>	0.24	0.86	0.048	0.71	0.010083	0.28
<b>1,2,3,4,6,7,8-HpCDD</b>	2.9	10	0.076	1.1	0.029	0.79
<b>1,2,3,4,6,7,8,9-OCDD</b>	1.4	4.9	0.071	1.04	0.028	0.77
<b>2,3,7,8-TCDF</b>	0.0070	0.025	2.9	43	0.0055	0.15
<b>1,2,3,7,8-PeCDF</b>	0.0055	0.020	0.78	11	0.0085	0.23
<b>2,3,4,7,8-PeCDF</b>	0.010	0.036	3.0	44	0.099	2.7
<b>1,2,3,4,7,8-HxCDF</b>	0.0090	0.032	0.18	2.7	0.051	1.4
<b>1,2,3,6,7,8-HxCDF</b>	0.0059	0.021	0.26	3.8	0.051	1.4
<b>2,3,4,6,7,8-HxCDF</b>	0.0069	0.025	0.27	3.9	0.058	1.6
<b>1,2,3,7,8,9-HxCDF</b>	0.0033	0.012	0.0088	0.13	0.0021	0.058
<b>1,2,3,4,6,7,8-HpCDF</b>	0.057	0.20	0.041	0.61	0.033	0.90
<b>1,2,3,4,7,8,9-HpCDF</b>	0.0064	0.023	0.0080	0.12	0.0050	0.14
<b>1,2,3,4,6,7,8,9-OCDF</b>	0.026	0.093	0.013	0.19	0.0070	0.19
<b>PCB 77</b>	1.2	4.2	41	605	0.27	7.4
<b>PCB 126</b>	0.16	0.56	19	281	0.28	7.8
<b>PCB 169</b>	0.049	0.18	5.4	79	0.067	1.8
<b>PCB 81</b>	0.051	0.18	0.99	15	0.047	1.3
<b>PCB 105</b>	7.5	27	721	10603	2.9	79
<b>PCB 114</b>	0.71	2.5	42	619	0.26	7.1
<b>PCB 118</b>	34	121	2332	34289	11	292
<b>PCB 123</b>	0.26	0.94	25	369	0.17	4.5
<b>PCB 156</b>	11	39	321	4713	1.4	39
<b>PCB 157</b>	1.6	5.6	77	1133	0.31	8.6
<b>PCB 167</b>	3.1	11	203	2986	0.71	20
<b>PCB 189</b>	1.5	5.5	36	524	0.20	5.5

fw. - fresh weight

lw- - lipid weight

### Consensus congener concentrations

	Pork		Herring		Milk	
	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.
<b>CB 28</b>	43	153	467	6863	15	412
<b>CB 52</b>	59	209	1080	15882	12	321
<b>CB 101</b>	77	276	3285	48302	12	323
<b>CB 138</b>	117	419	4500	66176	16	432
<b>CB 153</b>	160	571	6715	98746	21	572
<b>CB 180</b>	77	273	1613	23721	7.2	196
<b>BDE 28</b>	0.57	2	26	382	0.12	3.4
<b>BDE 47</b>	34	122	628	9232	4.5	124
<b>BDE 99</b>	38	136	141	2077	4.5	123
<b>BDE 100</b>	5.8	21	141	2067	0.79	22
<b>BDE 153</b>	7.7	27	30	441	0.88	24
<b>BDE 154</b>	3.4	12	86	1257	0.42	11
<b>BDE 183</b>	3.4	12	2.5	37	0.22	5.9
<b>BDE 209</b>	15	53	81	1198	15	407
<b><math>\alpha</math>-HBCD</b>	53	189	1583	23272	2.2	60
<b><math>\beta</math>-HBCD</b>	12	43	26	383	0.93	25
<b><math>\gamma</math>-HBCD</b>	95	340	73	1067	1.2	32
<b>Tot HBCD</b>	116	414	1700	25000	4.0	109
<b>Sum PCB</b>	533	1902	17659	259690	82	2256
<b>Sum BDE without 209</b>	93	332	1054	15494	11	314
<b>Sum BDE</b>	108	385	1135	16692	26	721

fw. - fresh weight

lw- - lipid weight

**Consensus of TEQs**

TEF<sub>2005</sub>

	Pork		Herring		Milk	
	pg TE/g fw.	pg TE/g lw.	pg TE/g fw.	pg TE/g lw.	pg TE/g fw.	pg TE/g lw.
<b>2,3,7,8-TCDD</b>	0.0030	0.011	0.18	2.6	0.0068	0.19
<b>1,2,3,7,8-PeCDD</b>	0.021	0.074	0.48	7.1	0.019	0.52
<b>1,2,3,4,7,8-HxCDD</b>	0.0029	0.010	0.0069	0.10	0.00082	0.022
<b>1,2,3,6,7,8-HxCDD</b>	0.18	0.64	0.032	0.47	0.0023	0.063
<b>1,2,3,7,8,9-HxCDD</b>	0.024	0.086	0.0048	0.071	0.0010	0.028
<b>1,2,3,4,6,7,8-HpCDD</b>	0.029	0.10	0.00076	0.011	0.00029	0.0079
<b>1,2,3,4,6,7,8,9-OCDD</b>	0.00041	0.0015	0.000021	0.00031	0.0000084	0.00023
<b>2,3,7,8-TCDF</b>	0.00070	0.0025	0.29	4.3	0.00055	0.015
<b>1,2,3,7,8-PeCDF</b>	0.00017	0.00059	0.023	0.34	0.00026	0.0070
<b>2,3,4,7,8-PeCDF</b>	0.0030	0.011	0.90	13	0.030	0.81
<b>1,2,3,4,7,8-HxCDF</b>	0.00090	0.0032	0.018	0.27	0.0051	0.14
<b>1,2,3,6,7,8-HxCDF</b>	0.00059	0.0021	0.026	0.38	0.0051	0.14
<b>2,3,4,6,7,8-HxCDF</b>	0.00069	0.0025	0.027	0.39	0.0058	0.16
<b>1,2,3,7,8,9-HxCDF</b>	0.00033	0.0012	0.00088	0.013	0.00021	0.0058
<b>1,2,3,4,6,7,8-HpCDF</b>	0.00057	0.0020	0.00041	0.0061	0.00033	0.0090
<b>1,2,3,4,7,8,9-HpCDF</b>	0.000064	0.00023	0.000080	0.0012	0.000050	0.0014
<b>1,2,3,4,6,7,8,9-OCDF</b>	0.0000078	0.000028	0.0000038	0.000056	0.0000021	0.000058
<b>PCB 77</b>	0.00012	0.00042	0.0041	0.060	0.000027	0.00074
<b>PCB 126</b>	0.016	0.056	1.9	28	0.028	0.78
<b>PCB 169</b>	0.0015	0.0053	0.16	2.4	0.0020	0.055
<b>PCB 81</b>	0.000015	0.000055	0.00030	0.0044	0.000014	0.00039
<b>PCB 105</b>	0.00022	0.00080	0.022	0.32	0.000086	0.0024
<b>PCB 114</b>	0.000021	0.000076	0.0013	0.019	0.0000078	0.00021
<b>PCB 118</b>	0.0010	0.0036	0.070	1.0	0.00032	0.0088
<b>PCB 123</b>	0.0000079	0.000028	0.00075	0.011	0.0000050	0.00014
<b>PCB 156</b>	0.00033	0.0012	0.0096	0.14	0.000043	0.0012
<b>PCB 157</b>	0.000047	0.00017	0.0023	0.034	0.0000094	0.00026
<b>PCB 167</b>	0.000094	0.00034	0.0061	0.090	0.000021	0.00059
<b>PCB 189</b>	0.000046	0.00017	0.0011	0.016	0.0000060	0.00016
<b>PCDDs/PCDFs</b>	0.26	0.95	2.0	29	0.077	2.1
<b>Non-ortho PCBs</b>	0.017	0.061	2.1	31	0.030	0.83
<b>Mono-ortho PCBs</b>	0.0018	0.0064	0.11	1.7	0.00050	0.014
<b>Total TEQ</b>	0.28	1.0	4.2	62	0.11	3.0

fw. - fresh weight

lw. - lipid weight

**Consensus of TEQs**

TEF<sub>1998</sub>

	Pork		Herring		Milk	
	pg TE/g fw.	pg TE/g lw.	pg TE/g fw.	pg TE/g lw.	pg TE/g fw.	pg TE/g lw.
<b>2,3,7,8-TCDD</b>	0.0030	0.011	0.18	2.6	0.0068	0.19
<b>1,2,3,7,8-PeCDD</b>	0.021	0.074	0.48	7.1	0.019	0.52
<b>1,2,3,4,7,8-HxCDD</b>	0.0029	0.010	0.0069	0.10	0.00082	0.022
<b>1,2,3,6,7,8-HxCDD</b>	0.18	0.64	0.032	0.47	0.0023	0.063
<b>1,2,3,7,8,9-HxCDD</b>	0.024	0.086	0.0048	0.071	0.0010	0.028
<b>1,2,3,4,6,7,8-HpCDD</b>	0.029	0.10	0.00076	0.011	0.00029	0.0079
<b>1,2,3,4,6,7,8,9-OCDD</b>	0.00014	0.00049	0.0000071	0.00010	0.0000028	0.000077
<b>2,3,7,8-TCDF</b>	0.00070	0.0025	0.29	4.3	0.00055	0.015
<b>1,2,3,7,8-PeCDF</b>	0.00028	0.0010	0.039	0.57	0.00043	0.012
<b>2,3,4,7,8-PeCDF</b>	0.0050	0.018	1.5	22	0.049	1.4
<b>1,2,3,4,7,8-HxCDF</b>	0.00090	0.0032	0.018	0.27	0.0051	0.14
<b>1,2,3,6,7,8-HxCDF</b>	0.00059	0.0021	0.026	0.38	0.0051	0.14
<b>2,3,4,6,7,8-HxCDF</b>	0.00069	0.0025	0.027	0.39	0.0058	0.16
<b>1,2,3,7,8,9-HxCDF</b>	0.00033	0.0012	0.00088	0.013	0.00021	0.0058
<b>1,2,3,4,6,7,8-HpCDF</b>	0.00057	0.0020	0.00041	0.0061	0.00033	0.0090
<b>1,2,3,4,7,8,9-HpCDF</b>	0.000064	0.00023	0.000080	0.0012	0.000050	0.0014
<b>1,2,3,4,6,7,8,9-OCDF</b>	0.0000026	0.0000093	0.0000013	0.000019	0.00000070	0.000019
<b>PCB 77</b>	0.00012	0.00042	0.0041	0.060	0.000027	0.00074
<b>PCB 126</b>	0.016	0.056	1.9	28	0.028	0.78
<b>PCB 169</b>	0.00049	0.0018	0.054	0.79	0.00067	0.018
<b>PCB 81</b>	0.0000051	0.000018	0.00010	0.0015	0.0000047	0.00013
<b>PCB 105</b>	0.00075	0.0027	0.072	1.1	0.00029	0.0079
<b>PCB 114</b>	0.00035	0.0013	0.021	0.31	0.00013	0.0035
<b>PCB 118</b>	0.0034	0.012	0.23	3.4	0.0011	0.029
<b>PCB 123</b>	0.000026	0.000094	0.0025	0.037	0.000017	0.00045
<b>PCB 156</b>	0.0055	0.020	0.16	2.4	0.00072	0.020
<b>PCB 157</b>	0.00078	0.0028	0.039	0.57	0.00016	0.0043
<b>PCB 167</b>	0.000031	0.00011	0.0020	0.030	0.0000071	0.00020
<b>PCB 189</b>	0.00015	0.00055	0.0036	0.052	0.000020	0.00055
<b>PCDDs/PCDFs</b>	0.27	0.95	2.6	38	0.097	2.7
<b>Non-ortho PCBs</b>	0.016	0.058	2.0	29	0.029	0.80
<b>Mono-ortho PCBs</b>	0.011	0.039	0.53	7.8	0.0024	0.066
<b>Total TEQ</b>	0.29	1.0	5.1	75	0.13	3.5

fw. - fresh weight

lw- - lipid weight

## Consensus statistics

### Analyte solution

	Target value pg/µl	Consensus median, pg/µl	Median all values pg/µl	Consensus mean, pg/µl	Standard deviation, pg/µl	Relative standard deviation, %	No. of values reported	No. of values removed
<b>2,3,7,8-TCDD</b>	2.0	2.0	2.0	2.0	0.20	10	72	1
<b>1,2,3,7,8-PeCDD</b>	5.0	4.9	4.9	4.9	0.40	8.3	72	1
<b>1,2,3,4,7,8-HxCDD</b>	5.0	4.9	4.9	4.9	0.42	8.5	72	2
<b>1,2,3,6,7,8-HxCDD</b>	5.0	4.8	4.9	4.8	0.41	8.5	72	1
<b>1,2,3,7,8,9-HxCDD</b>	5.0	5.1	5.1	5.1	0.47	9.2	72	1
<b>1,2,3,4,6,7,8-HpCDD</b>	5.0	4.9	4.9	4.9	0.39	8.0	72	1
<b>1,2,3,4,6,7,8,9-OCDD</b>	10	9.9	9.9	9.8	1.0	11	72	1
<b>2,3,7,8-TCDF</b>	2.0	2.0	2.0	1.9	0.21	11	72	1
<b>1,2,3,7,8-PeCDF</b>	5.0	5.0	5.0	5.0	0.43	8.7	72	1
<b>2,3,4,7,8-PeCDF</b>	5.0	4.9	4.9	4.8	0.42	8.6	72	1
<b>1,2,3,4,7,8-HxCDF</b>	5.0	5.0	5.0	4.9	0.48	10	72	1
<b>1,2,3,6,7,8-HxCDF</b>	5.0	5.0	5.0	4.9	0.36	7.4	72	2
<b>2,3,4,6,7,8-HxCDF</b>	5.0	5.0	5.0	5.0	0.40	8.2	72	2
<b>1,2,3,7,8,9-HxCDF</b>	5.0	4.9	4.9	4.9	0.43	8.8	72	1
<b>1,2,3,4,6,7,8-HpCDF</b>	5.0	4.9	4.9	4.9	0.43	8.6	72	1
<b>1,2,3,4,7,8,9-HpCDF</b>	5.0	5.0	5.0	5.0	0.39	7.9	72	2
<b>1,2,3,4,6,7,8,9-OCDF</b>	10	9.9	9.9	9.9	0.98	10	71	0
<b>PCB 77</b>	10	9.9	9.9	9.8	0.77	7.9	71	2
<b>PCB 126</b>	10	10	10	10	1.0	10	71	2
<b>PCB 169</b>	10	10	10	10	0.88	8.8	71	2
<b>PCB 81</b>	10	10	10	10	0.82	8.0	71	3
<b>PCB 105</b>	100	99	99	99	6.8	6.9	70	3
<b>PCB 114</b>	100	99	99	99	6.9	7.0	70	2
<b>PCB 118</b>	100	100	100	100	8.5	8.5	70	2
<b>PCB 123</b>	100	99	99	99	7.3	7.4	70	2
<b>PCB 156</b>	100	100	100	100	7.5	7.5	70	2
<b>PCB 157</b>	100	99	99	99	9.0	9.1	70	2
<b>PCB 167</b>	100	100	100	100	8.7	8.7	70	2
<b>PCB 189</b>	100	100	100	101	8.7	8.7	70	2

## Consensus statistics

### Analyte solution

	Target value pg/µl	Median, pg/µl all values	Median, pg/µl outliers removed	Mean, pg/µl all values	Mean, pg/µl outliers removed
<b>CB 28</b>	100	101	101	100	101
<b>CB 52</b>	100	100	100	101	101
<b>CB 101</b>	100	100	100	100	100
<b>CB 138</b>	100	98	98	98	98
<b>CB 153</b>	100	99	99	100	100
<b>CB 180</b>	100	99	99	99	99
<b>BDE 28</b>	25	25	25	25	25
<b>BDE 47</b>	25	25	25	25	25
<b>BDE 99</b>	25	25	25	25	25
<b>BDE 100</b>	25	23	23	24	24
<b>BDE 153</b>	25	25	25	25	25
<b>BDE 154</b>	25	24	24	24	24
<b>BDE 183</b>	25	25	25	25	25
<b>BDE 209</b>	100	97	97	103	100
<b><i>a</i>-HBCD *</b>	500	486	486	482	482

	Relative standard deviation, % all values	Relative standard deviation, % outliers removed	Number of reported values	Number of reported outliers
<b>CB 28</b>	14	11	58	1
<b>CB 52</b>	11	11	58	0
<b>CB 101</b>	8.0	8.0	58	0
<b>CB 138</b>	8.5	8.5	58	0
<b>CB 153</b>	8.9	8.9	58	0
<b>CB 180</b>	8.4	8.4	58	0
<b>BDE 28</b>	9.1	9.1	37	0
<b>BDE 47</b>	7.1	7.1	37	0
<b>BDE 99</b>	7.5	7.5	37	0
<b>BDE 100</b>	8.0	8.0	37	0
<b>BDE 153</b>	8.5	8.5	37	0
<b>BDE 154</b>	8.3	8.3	37	0
<b>BDE 183</b>	11	11	37	0
<b>BDE 209</b>	18	12	27	1
<b><i>a</i>-HBCD *</b>	10	10	12	0

NDs: Non-detects

\* : Indicative value due to few reported values

## Consensus statistics

### Pork, fresh weight

	Consensus median, pg/g	Median all values pg/g	Consensus mean, pg/g	Standard deviation, pg/g	Relative standard deviation, %	No. of values reported	No. of values removed	No. of reported non-detects
<b>2,3,7,8-TCDD</b>	0.0030	0.0070	0.0047	0.0039	83	63	20	49
<b>1,2,3,7,8-PeCDD</b>	0.021	0.023	0.022	0.0080	37	63	4	20
<b>1,2,3,4,7,8-HxCDD</b>	0.029	0.029	0.028	0.012	43	63	4	20
<b>1,2,3,6,7,8-HxCDD</b>	1.8	1.8	1.7	0.40	23	63	0	1
<b>1,2,3,7,8,9-HxCDD</b>	0.24	0.24	0.23	0.066	29	63	0	2
<b>1,2,3,4,6,7,8-HpCDD</b>	2.9	2.9	2.8	0.60	21	63	0	1
<b>1,2,3,4,6,7,8,9-OCDD</b>	1.4	1.4	1.3	0.39	29	63	0	3
<b>2,3,7,8-TCDF</b>	0.0070	0.010	0.0083	0.0054	65	63	20	26
<b>1,2,3,7,8-PeCDF</b>	0.0055	0.010	0.0069	0.0053	77	63	14	39
<b>2,3,4,7,8-PeCDF</b>	0.010	0.012	0.011	0.0057	54	63	13	20
<b>1,2,3,4,7,8-HxCDF</b>	0.0090	0.012	0.011	0.0060	56	63	17	24
<b>1,2,3,6,7,8-HxCDF</b>	0.0059	0.010	0.0083	0.0054	66	63	17	29
<b>2,3,4,6,7,8-HxCDF</b>	0.0069	0.010	0.0081	0.0055	68	63	18	35
<b>1,2,3,7,8,9-HxCDF</b>	0.0033	0.010	0.0054	0.0045	84	63	21	49
<b>1,2,3,4,6,7,8-HpCDF</b>	0.057	0.059	0.056	0.020	35	63	12	7
<b>1,2,3,4,7,8,9-HpCDF</b>	0.0064	0.012	0.0080	0.0057	72	63	22	37
<b>1,2,3,4,6,7,8,9-OCDF</b>	0.026	0.031	0.028	0.013	45	63	19	19
<b>PCB 77</b>	1.2	1.2	1.2	0.52	41	62	7	0
<b>PCB 126</b>	0.16	0.17	0.17	0.054	32	62	11	7
<b>PCB 169</b>	0.049	0.057	0.052	0.021	41	62	16	17
<b>PCB 81</b>	0.051	0.060	0.054	0.026	48	62	14	17
<b>PCB 105</b>	7.5	7.9	7.7	2.0	26	62	9	2
<b>PCB 114</b>	0.71	0.77	0.73	0.26	35	62	13	13
<b>PCB 118</b>	34	35	34	11	33	62	7	1
<b>PCB 123</b>	0.26	0.43	0.31	0.19	60	62	20	18
<b>PCB 156</b>	11	11	11	2.6	23	62	2	1
<b>PCB 157</b>	1.6	1.6	1.6	0.45	27	62	5	7
<b>PCB 167</b>	3.1	3.2	3.3	0.92	28	62	5	5
<b>PCB 189</b>	1.5	1.6	1.6	0.43	27	62	5	9

**Consensus statistics**  
**Pork, fresh weight**

	Median, pg/g all values	Median, pg/g outliers removed	Median, pg/g outliers and NDs removed	Mean, pg/g all values	Mean, pg/g outliers removed	Mean, pg/g outliers and NDs removed
<b>CB 28</b>	50	42	43	58	47	48
<b>CB 52</b>	59	58	59	77	58	59
<b>CB 101</b>	77	77	77	83	74	75
<b>CB 138</b>	120	115	117	122	113	116
<b>CB 153</b>	160	160	160	157	150	153
<b>CB 180</b>	77	76	77	73	71	73
<b>BDE 28</b>	0.70	0.55	0.57	1.2	0.58	0.57
<b>BDE 47</b>	35	34	34	42	33	33
<b>BDE 99</b>	39	38	38	42	36	36
<b>BDE 100</b>	6.0	5.9	5.8	7.7	5.6	5.4
<b>BDE 153</b>	7.7	7.7	7.7	7.6	7.2	7.2
<b>BDE 154</b>	3.5	3.4	3.4	3.9	3.3	3.3
<b>BDE 183</b>	3.4	3.4	3.4	3.7	3.3	3.4
<b>BDE 209</b>	24	15	15	33	16	14
<b><math>\alpha</math>-HBCD *</b>	60	53	53	97	54	54
<b><math>\beta</math>-HBCD *</b>	23	17	12	58	20	13
<b><math>\gamma</math>-HBCD *</b>	103	77	95	292	78	84
<b>Tot HBCD *</b>	170	116	116	498	131	131

	Relative standard deviation, % all values	Relative standard deviation, % outliers removed	Relative standard deviation, % outliers and NDs removed	Number of reported values	Number of outliers	Number of reported NDs
<b>CB 28</b>	76	55	51	53	6	3
<b>CB 52</b>	117	40	38	53	5	2
<b>CB 101</b>	65	36	33	53	2	1
<b>CB 138</b>	50	40	37	53	2	1
<b>CB 153</b>	41	36	33	53	2	1
<b>CB 180</b>	38	36	33	53	1	1
<b>BDE 28</b>	95	50	51	29	8	5
<b>BDE 47</b>	98	44	44	30	2	0
<b>BDE 99</b>	64	34	34	30	2	0
<b>BDE 100</b>	91	37	36	30	3	1
<b>BDE 153</b>	47	40	40	30	1	0
<b>BDE 154</b>	60	34	34	30	3	0
<b>BDE 183</b>	53	38	31	30	2	4
<b>BDE 209</b>	75	60	58	19	7	4
<b><math>\alpha</math>-HBCD *</b>	107	31	31	12	3	0
<b><math>\beta</math>-HBCD *</b>	156	58	46	11	2	3
<b><math>\gamma</math>-HBCD *</b>	153	48	40	11	3	1
<b>Tot HBCD *</b>	135	47	47	9	3	0

NDs: Non-detects

\* : Indicative value due to few reported values

## Consensus statistics

### Herring, fresh weight

	Consensus median, pg/g	Median all values pg/g	Consensus mean, pg/g	Standard deviation, pg/g	Relative standard deviation, %	No. of values reported	No. of values removed	No. of reported non-detects
<b>2,3,7,8-TCDD</b>	0.18	0.18	0.18	0.044	24	74	0	3
<b>1,2,3,7,8-PeCDD</b>	0.48	0.48	0.46	0.091	20	74	1	0
<b>1,2,3,4,7,8-HxCDD</b>	0.069	0.069	0.066	0.019	30	74	1	6
<b>1,2,3,6,7,8-HxCDD</b>	0.32	0.32	0.30	0.077	26	74	0	2
<b>1,2,3,7,8,9-HxCDD</b>	0.048	0.048	0.047	0.015	32	74	1	11
<b>1,2,3,4,6,7,8-HpCDD</b>	0.076	0.078	0.076	0.025	32	74	5	6
<b>1,2,3,4,6,7,8,9-OCDD</b>	0.071	0.082	0.078	0.030	39	74	18	14
<b>2,3,7,8-TCDF</b>	2.9	2.9	2.9	0.54	19	74	0	0
<b>1,2,3,7,8-PeCDF</b>	0.78	0.78	0.76	0.16	21	74	1	0
<b>2,3,4,7,8-PeCDF</b>	3.0	3.0	2.9	0.59	20	74	0	0
<b>1,2,3,4,7,8-HxCDF</b>	0.18	0.19	0.18	0.051	28	74	1	2
<b>1,2,3,6,7,8-HxCDF</b>	0.26	0.26	0.26	0.057	22	74	1	0
<b>2,3,4,6,7,8-HxCDF</b>	0.27	0.27	0.25	0.076	30	74	1	2
<b>1,2,3,7,8,9-HxCDF</b>	0.0088	0.010	0.0093	0.0044	48	74	19	30
<b>1,2,3,4,6,7,8-HpCDF</b>	0.041	0.043	0.041	0.014	33	74	11	9
<b>1,2,3,4,7,8,9-HpCDF</b>	0.0080	0.010	0.0089	0.0047	53	74	20	40
<b>1,2,3,4,6,7,8,9-OCDF</b>	0.013	0.020	0.016	0.0088	57	74	22	32
<b>PCB 77</b>	41	42	42	6.7	16	74	2	0
<b>PCB 126</b>	19	19	19	3.1	16	74	3	0
<b>PCB 169</b>	5.4	5.4	5.3	0.89	17	74	1	1
<b>PCB 81</b>	0.99	1.0	0.94	0.32	34	74	5	5
<b>PCB 105</b>	721	730	723	113	16	73	2	0
<b>PCB 114</b>	42	42	43	9.3	22	73	1	0
<b>PCB 118</b>	2332	2340	2292	458	20	73	1	0
<b>PCB 123</b>	25	27	26	12	46	73	15	8
<b>PCB 156</b>	321	321	315	43	13	73	1	0
<b>PCB 157</b>	77	77	76	11	14	73	1	0
<b>PCB 167</b>	203	204	202	28	14	73	3	0
<b>PCB 189</b>	36	36	35	6	18	73	1	0

**Consensus statistics**  
**Herring, fresh weight**

	Median, pg/g all values	Median, pg/g outliers removed	Median, pg/g outliers and NDs removed	Mean, pg/g all values	Mean, pg/g outliers removed	Mean, pg/g outliers and NDs removed
<b>CB 28</b>	470	463	467	488	461	469
<b>CB 52</b>	1080	1080	1080	995	995	1012
<b>CB 101</b>	3280	3280	3285	3003	3003	3055
<b>CB 138</b>	4509	4500	4500	4621	4430	4430
<b>CB 153</b>	6750	6715	6715	6508	6340	6340
<b>CB 180</b>	1613	1613	1613	1560	1521	1547
<b>BDE 28</b>	26	26	26	28	28	28
<b>BDE 47</b>	628	628	628	611	611	611
<b>BDE 99</b>	142	141	141	153	139	139
<b>BDE 100</b>	141	141	141	142	142	142
<b>BDE 153</b>	30	30	30	32	30	30
<b>BDE 154</b>	86	86	86	83	83	83
<b>BDE 183</b>	2.6	2.5	2.5	8.7	2.5	2.6
<b>BDE 209</b>	82	81	81	104	84	84
<b><math>\alpha</math>-HBCD *</b>	1600	1583	1583	1974	1594	1594
<b><math>\beta</math>-HBCD *</b>	27	26	26	70	27	28
<b><math>\gamma</math>-HBCD *</b>	76	73	73	220	73	73
<b>Tot HBCD *</b>	1762	1700	1700	2368	1667	1667

	Relative standard deviation, % all values	Relative standard deviation, % outliers removed	Relative standard deviation, % outliers and NDs removed	Number of reported values	Number of outliers	Number of reported NDs
<b>CB 28</b>	48	45	42	59	3	1
<b>CB 52</b>	35	35	32	59	0	1
<b>CB 101</b>	32	32	29	59	0	1
<b>CB 138</b>	41	37	37	59	2	0
<b>CB 153</b>	37	33	33	59	1	0
<b>CB 180</b>	36	31	28	59	1	1
<b>BDE 28</b>	37	37	37	36	0	0
<b>BDE 47</b>	33	33	33	37	0	0
<b>BDE 99</b>	61	28	28	37	1	0
<b>BDE 100</b>	26	26	26	37	0	0
<b>BDE 153</b>	49	27	27	37	1	0
<b>BDE 154</b>	40	40	40	37	0	0
<b>BDE 183</b>	286	43	42	37	3	3
<b>BDE 209</b>	59	37	37	24	3	0
<b><math>\alpha</math>-HBCD *</b>	72	23	23	13	1	0
<b><math>\beta</math>-HBCD *</b>	160	36	31	12	2	1
<b><math>\gamma</math>-HBCD *</b>	220	18	18	12	2	0
<b>Tot HBCD *</b>	94	15	15	10	1	0

NDs: Non-detects

\* : Indicative value due to few reported values

## Consensus statistics

### Milk, fresh weight

	Consensus median, pg/g	Median all values pg/g	Consensus mean, pg/g	Standard deviation, pg/g	Relative standard deviation, %	No. of values reported	No. of values removed	No. of reported non-detects
<b>2,3,7,8-TCDD</b>	0.0068	0.0071	0.0068	0.0027	40	59	8	16
<b>1,2,3,7,8-PeCDD</b>	0.019	0.019	0.019	0.0057	31	59	2	7
<b>1,2,3,4,7,8-HxCDD</b>	0.0082	0.0085	0.0080	0.0033	41	59	7	13
<b>1,2,3,6,7,8-HxCDD</b>	0.023	0.023	0.023	0.0059	26	59	2	7
<b>1,2,3,7,8,9-HxCDD</b>	0.010	0.011	0.011	0.0036	33	59	6	8
<b>1,2,3,4,6,7,8-HpCDD</b>	0.029	0.029	0.030	0.011	37	59	2	6
<b>1,2,3,4,6,7,8,9-OCDD</b>	0.028	0.036	0.033	0.018	55	59	10	11
<b>2,3,7,8-TCDF</b>	0.0055	0.0070	0.0064	0.0030	47	59	8	14
<b>1,2,3,7,8-PeCDF</b>	0.0085	0.0090	0.0085	0.0027	32	59	8	10
<b>2,3,4,7,8-PeCDF</b>	0.099	0.099	0.095	0.020	21	59	1	1
<b>1,2,3,4,7,8-HxCDF</b>	0.051	0.051	0.051	0.014	28	59	2	3
<b>1,2,3,6,7,8-HxCDF</b>	0.051	0.051	0.051	0.014	27	59	2	3
<b>2,3,4,6,7,8-HxCDF</b>	0.058	0.058	0.056	0.018	33	59	1	4
<b>1,2,3,7,8,9-HxCDF</b>	0.0021	0.0030	0.0024	0.0013	55	59	17	37
<b>1,2,3,4,6,7,8-HpCDF</b>	0.033	0.033	0.033	0.011	33	59	3	4
<b>1,2,3,4,7,8,9-HpCDF</b>	0.0050	0.0060	0.0053	0.0022	42	59	16	26
<b>1,2,3,4,6,7,8,9-OCDF</b>	0.0070	0.0090	0.0071	0.0037	52	59	18	26
<b>PCB 77</b>	0.27	0.31	0.29	0.14	48	59	13	2
<b>PCB 126</b>	0.28	0.29	0.27	0.073	28	59	4	4
<b>PCB 169</b>	0.067	0.069	0.066	0.015	22	59	8	8
<b>PCB 81</b>	0.047	0.049	0.046	0.015	33	59	8	7
<b>PCB 105</b>	2.9	3.0	2.9	0.78	27	60	9	3
<b>PCB 114</b>	0.26	0.27	0.28	0.091	33	60	12	10
<b>PCB 118</b>	11	11	11	3.4	30	60	7	2
<b>PCB 123</b>	0.17	0.19	0.18	0.080	44	59	14	14
<b>PCB 156</b>	1.4	1.5	1.4	0.31	22	60	10	5
<b>PCB 157</b>	0.31	0.33	0.32	0.077	24	60	10	9
<b>PCB 167</b>	0.71	0.75	0.74	0.20	27	60	10	7
<b>PCB 189</b>	0.20	0.21	0.21	0.062	30	59	10	11

## Consensus statistics

### Milk, fresh weight

	Median, pg/g all values	Median, pg/g outliers removed	Median, pg/g outliers and NDs removed	Mean, pg/g all values	Mean, pg/g outliers removed	Mean, pg/g outliers and NDs removed
<b>CB 28</b>	20	15	15	30	15	16
<b>CB 52</b>	15	11	12	22	13	14
<b>CB 101</b>	15	12	12	23	13	14
<b>CB 138</b>	16	16	16	19	16	16
<b>CB 153</b>	21	21	21	25	20	21
<b>CB 180</b>	7.2	7.2	7.2	9	7.3	7.1
<b>BDE 28</b>	0.16	0.11	0.12	0.36	0.12	0.14
<b>BDE 47</b>	5.2	4.9	4.5	6.6	5.0	4.5
<b>BDE 99</b>	4.7	4.5	4.5	5.3	4.3	4.2
<b>BDE 100</b>	0.85	0.82	0.79	1.3	0.85	0.82
<b>BDE 153</b>	0.9	0.88	0.88	1.4	0.92	0.92
<b>BDE 154</b>	0.45	0.41	0.42	0.61	0.43	0.45
<b>BDE 183</b>	0.26	0.22	0.22	1.8	0.24	0.24
<b>BDE 209</b>	15	15	15	17	16	17
<b><math>\alpha</math>-HBCD *</b>	3.6	2.4	2.2	6.6	2.7	2.3
<b><math>\beta</math>-HBCD **</b>	1.5	0.38	1	3.4	0.8	1
<b><math>\gamma</math>-HBCD *</b>	2.0	1.2	1.2	10	1.7	1.2
<b>Tot HBCD *</b>	4.0	3.8	4.0	17	3.4	3.4

	Relative standard deviation, % all values	Relative standard deviation, % outliers removed	Relative standard deviation, % outliers and NDs removed	Number of reported values	Number of outliers	Number of reported NDs
<b>CB 28</b>	88	56	54	47	14	3
<b>CB 52</b>	84	54	50	47	10	4
<b>CB 101</b>	91	53	49	47	11	4
<b>CB 138</b>	65	33	31	47	4	1
<b>CB 153</b>	71	35	32	47	4	1
<b>CB 180</b>	98	35	35	47	3	5
<b>BDE 28</b>	135	56	41	29	9	10
<b>BDE 47</b>	92	45	41	29	3	4
<b>BDE 99</b>	67	38	38	29	3	2
<b>BDE 100</b>	137	42	42	29	3	3
<b>BDE 153</b>	128	39	39	29	3	2
<b>BDE 154</b>	74	43	36	29	5	3
<b>BDE 183</b>	375	46	38	29	7	9
<b>BDE 209</b>	64	60	56	21	1	6
<b><math>\alpha</math>-HBCD *</b>	139	40	40	9	2	4
<b><math>\beta</math>-HBCD **</b>	145	103		8	3	7
<b><math>\gamma</math>-HBCD *</b>	204	69	24	8	2	6
<b>Tot HBCD *</b>	212	45	50	8	2	3

NDs: Non-detects

\* : Indicative value due to few reported values

\*\* : No value calculated due to few reported values

### Laboratories' reported TEQs, sum indicator PCB and sum BDE without BDE 209

TEF <sub>2005</sub>	Median pg/g	Mean pg/g	SD pg/g	RSD %	Min pg/g	Max pg/g	Reporting laboratories
<b>Pork, fresh weight</b>							
PCDD/PCDF TEQ	0,28	0,29	0,068	24	0,039	0,43	67
Non-ortho PCB TEQ	0,020	0,029	0,025	88	0,0039	0,13	62
Mono-ortho PCB TEQ	0,0019	0,0023	0,0018	78	0,00037	0,014	62
Total TEQ	0,30	0,32	0,11	34	0,064	1,0	67
Sum indicator PCB	556	570	293	1	0,46	2028	53
Sum BDE without BDE 209	97	108	74	1	0,14	437	30
<b>Herring, fresh weight</b>							
PCDD/PCDF TEQ	2,0	2,6	0,49	19	0,15	4,8	76
Non-ortho PCB TEQ	2,1	2,3	1,3	57	0,82	12	74
Mono-ortho PCB TEQ	0,11	0,14	0,24	169	0,044	2,2	73
Total TEQ	4,3	4,4	1,5	35	1,1	14	76
Sum indicator PCB	18036	17175	5737	0	8,6	34011	59
Sum BDE without BDE 209	1072	1057	287	0	0,96	1807	37
<b>Milk, fresh weight</b>							
PCDD/PCDF TEQ	0,078	0,10	0,034	33	0,0082	0,29	62
Non-ortho PCB TEQ	0,031	0,039	0,050	128	0,0059	0,39	59
Mono-ortho PCB TEQ	0,00054	0,0011	0,0027	253	0,00022	0,021	60
Total TEQ	0,11	0,12	0,065	54	0,0018	0,45	63
Sum indicator PCB	101	127	83	1	0,081	394	47
Sum BDE without BDE 209	13	17	14	1	0,063	61	29

### Laboratories' reported TEQs, sum indicator PCB and sum BDE without BDE 209

TEF <sub>1998</sub>	Median pg/g	Mean pg/g	SD pg/g	RSD %	Min pg/g	Max pg/g	Reporting laboratories
<b>Pork, fresh weight</b>							
PCDD/PCDF TEQ	0,28	0,29	0,063	22	0,041	0,44	63
Non-ortho PCB TEQ	0,018	0,026	0,021	83	0,0035	0,11	62
Mono-ortho PCB TEQ	0,011	0,013	0,0080	60	0,0022	0,061	62
Total TEQ	0,32	0,32	0,068	21	0,066	0,48	63
Sum indicator PCB	556	570	293	1	0,46	2028	53
Sum BDE without BDE 209	97	108	74	1	0,14	437	30
<b>Herring, fresh weight</b>							
PCDD/PCDF TEQ	2,6	2,6	0,58	22	0,20	5,5	74
Non-ortho PCB TEQ	2,0	2,2	1,3	59	0,71	12	74
Mono-ortho PCB TEQ	0,55	0,63	0,80	127	0,30	7,3	73
Total TEQ	5,2	5,4	1,8	33	1,4	15	74
Sum indicator PCB	18036	17175	5737	0	8,6	34011	59
Sum BDE without BDE 209	1072	1057	287	0	0,96	1807	37
<b>Milk, fresh weight</b>							
PCDD/PCDF TEQ	0,10	0,10	0,040	39	0,0087	0,35	59
Non-ortho PCB TEQ	0,030	0,036	0,043	118	0,0055	0,33	59
Mono-ortho PCB TEQ	0,0026	0,0055	0,012	217	0,0010	0,090	60
Total TEQ	0,13	0,14	0,065	45	0,017	0,46	60
Sum indicator PCB	101	127	83	1	0,081	394	47
Sum BDE without BDE 209	13	17	14	1	0,063	61	29

### Laboratories Z-scores: Analyte solution

LABCODE	Sum TE	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum u/209	Sum m/209
1	-0.055	-0.038	-0.21	-0.29	-0.18	0.61	-1.4
2							
3	-0.091	-0.093	-0.048	-0.16	-0.060	0.19	0.32
4							
5	-0.59	-0.17					
6	0.41	0.49	0.28	-4.4	0.031		
7							
8	0.025	0.0093	0.20	0.15	0.54	-0.24	-0.18
9							
10	-0.28	-0.28	-0.30	0.038	-0.034	-0.28	-2.0
11	0.0045	-0.032	0.42	0.25	0.025	0.0012	-0.032
12							
13							
14	-0.16	-0.23	0.59	0.12	-1.1		
15	0.084	0.093	-0.0044	-0.019	-0.48	-0.033	-0.034
16	-0.39	-0.45	0.24	0.14	0.47		
17							
18							
19	-0.12	-0.11	-0.33	-0.11	-0.12		
20							
21	0.15	0.078	0.91	0.58	0.46		
22	41	42	35				
23							
24	-0.10	-0.18	0.81	0.52	0.16	0.53	0.68
25							
26							
27	-0.10	-0.14	0.32	0.17	0.30	0.19	0.39
28	-0.45	-0.52	0.35	-0.09	0.0073		
29	0.061	0.046	0.32	-0.40	0.26		
30	0.059	-0.0085	0.91	-0.021	-0.037	0.026	-0.071
31							
32	0.0041	-0.045	0.49	0.70	0.72		
33	-0.20	-0.22	0.12	-0.49	-0.14	0.32	0.24
34	-0.087	-0.099	0.050	-0.058			
35	-0.15	-0.21	0.55	-0.19	0.14		
36							
37	0.062	0.045	0.27	0.084	0.14		
38	-0.36	-0.34	-0.57	-0.45		-0.56	-0.50
39							
40	-0.035	0.37		-0.017	0.34		
41	0.021	0.037	-0.18	0.030	0.18	-0.087	-1.9
42	-1.7	-1.8	-0.90				
43	-0.32	-0.33	-0.27	-0.15	0.018	-0.0093	-1.8
44	-0.26	-0.21	-0.82	-0.32	-0.012	0.15	0.25
45	0.019	-0.018	0.45	0.17	-0.34	-0.69	-2.2
46	-0.12	-0.12	-0.21	-0.13	-0.14		
47	-0.019	-0.020	-0.0081	0.014			
48							
49	-0.19	-0.30	1.1	0.38	0.33		
50							
51	-0.12	-0.12	-0.12	-0.20	0.057	-0.27	-0.29
52							
53							
54	-0.33	-0.34	-0.26	-0.29			
55	0.33	0.30	0.71	0.47	0.42	-0.51	-0.50
56							
57							
58	0.17	0.17	0.15	-0.12	-0.049		
59	-0.69	-0.65	-1.0	-1.3			
60	-0.035	-0.034	-0.071	0.088	0.13		
61	-4.6		-0.32	-0.41		-0.12	-0.065
62	-0.25	-0.28	0.080	0.13			
63	0.22	0.28	-0.36	-0.34	-0.20	-0.27	1.3
64	-0.12	-0.12	-0.10	-0.049			
65	-0.0082	0.0035	-0.14	-0.058	-0.062	0.27	-1.6
66							
67							
68							
69							
70							

### Laboratories Z-scores: Analyte solution (continued)

LABCODE	Sum TE	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum u/209	Sum m/209
71	0.080	0.075	0.11	0.30			
72							
73	-0.035	-0.048	0.14	-0.14	-0.087	-0.039	-0.034
74	-0.73	-0.80	0.016	-0.027	0.075		
75	0.060	0.027	0.45	0.19	-0.26	0.0032	-0.09
76	0.10	0.085	0.27	0.19	-0.32	-0.0064	0.11
77	-0.074	-0.14	0.65	0.40	0.21		
78	-0.43	-0.46	-0.050	-0.21	0.18	0.13	0.11
79	-0.16	-0.24	0.68	0.41	-0.31	0.50	-1.5
80	-0.14	-0.17	0.24	-0.36			
81	-0.52	-0.47	-1.0	-0.89	-0.96	-0.14	-0.10
82							
83	0.14	0.14	0.18	-0.036	0.12	-0.26	-2.0
84							
85	-0.20	-0.21	0.041	-0.54	-0.57	-0.37	0.66
86	-0.11	-0.15	0.43	-0.10	-0.25	-0.35	-0.29
87	-0.19	-0.15	-0.71	-0.20	0.030	0.41	0.43
88							
89							
90							
91	0.050	0.075	-0.24	-0.033	0.15	-0.079	-0.028
92	-0.39	-0.43	-0.093	0.28	1.3		
93	0.12	0.090	0.41	0.25	-0.10		
94	0.21	0.26	-0.54	0.38	0.36		
95	0.44	0.47	0.23	-0.39	-0.28	-0.033	-0.090
96							
97							
98					0.29	0.28	-0.026
99							
100							
101							
102	-0.60	-0.64	-0.14	-0.11			
103	1.1	1.2	-0.22	0.035	-0.0018	0.28	-1.6
104							
105							
106	-0.11	-0.073	-0.47	-0.32			
107	0.040	-0.38	4.4	4.8	0.020		
108	-0.024	0.022	-0.60	0.0067	0.28		
109							
110	-0.042	-0.091	0.50	0.26	0.25	0.45	0.48
111							
112	0.46	0.38	1.5	0.69	-0.88		
113	0.22	0.23	0.088	-0.43	-1.1		
114							
115							
116							
117	-0.038	-0.074	0.35	0.35	0.19	0.34	-1.6
118	-0.14	-0.18	0.41	-0.23		0.064	0.16

### Laboratories Z-scores: Pork

LABCODE	Sum TE	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum u/209	Sum m/209
1	-0.048	-0.10	0.84	-0.59	-0.31	-0.030	-0.71
2	-0.52	-0.20			0.15		
3	-0.0034	0.079	-1.0	-2.9	0.22	0.51	-0.25
4							
5	-0.027	0.05	-1.2	-0.32			
6	2.0	0.0081	33	1.3	0.90		
7							
8	0.88	0.91	0.66	-0.21	0.37	1.1	2.8
9							
10	2.2	1.6	11	5.3	1.3	1.6	0.71
11	0.48	0.54	-0.53	0.23	-0.23	3.6	6.4
12							
13	0.36	-0.20	8.9	0.98			
14	2.2	2.3	0.85	5.3	1.6		
15							
16							
17							
18							
19	0.25	0.31	-0.44	-0.91	-5.0		
20	0.21	-0.11					
21	0.48	0.28	3.4	1.4	1.7		
22							
23							
24	0.41	0.46	-0.43	0.80	0.51	0.34	0.24
25							
26							
27	0.021	0.11	-1.3	-0.40	0.16	1.0	3.1
28	1.3	1.0	6.2	0.41	-0.25		
29	0.92	-0.55	24	-0.059	0.64		
30	3.0	3.1	1.8	0.61	0.24	-2.7	-2.2
31							
32							
33	-0.72	-0.89	1.7	1.3	0.52	0.80	1.7
34							
35	0.37	0.37	0.42	0.36	0.62		
36	0.39	0.36	1.3	-3.3	-3.5		
37	0.38	0.38	0.46	0.30	0.90		
38							
39							
40	2.8	2.8	1.3	9.7	2.0		
41							
42	0.12	0.017	1.3	4.7			
43							
44	0.10	0.16	-0.77	-0.22	0.019	-0.033	0.68
45	0.54	0.54	0.62	-0.11	-0.49	-1.1	-1.6
46	0.15	0.18	-0.25	-0.85	-0.82		
47							
48							
49	1.1	0.63	8.1	0.52	0.65		
50							
51	0.25	0.11	2.4	0.20	1.1	7.5	6.5
52							
53							
54	-0.91	-0.87	-1.5	-0.22			
55	-0.27	-0.19	-1.4	-0.025	0.0044	-0.80	-1.1
56							
57	2.7	1.7	18	2.2	1.4		
58	1.3	1.2	3.8	2.0	-0.50		
59							
60	0.29	0.27	0.52	1.1	1.4		
61	-0.18	-0.16	-0.43	0.21		-0.52	-0.96
62							
63							
64	-2.9	-4.3	15	35			
65	0.13	0.21	-1.1	-0.60	-0.64	0.93	0.12
66							
67	0.40	-2.0					
68	-0.42	-0.61	2.6	-0.64			
69	1.4	0.92	7.8	8.7	14		
70							

### Laboratories Z-scores: Pork (continued)

LABCODE	Sum TE	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-ortho PCB	Sum Indicator PCB	Sum u/209	Sum m/209
71							
72							
73	0.56	0.61	0.021	-1.0	-0.64	-0.67	-0.58
74	-1.1	-1.1	-0.72	0.20	0.67		
75	-0.17	-0.20	0.48	-0.88	-0.51	-0.093	1.8
76							
77							
78	-3.9	-3.9	-3.9	-4.0	-3.9	-3.8	-3.8
79	1.7	1.3	8.8	-0.59	2.2	0.14	-0.56
80	0.79	0.81	0.50	-0.15			
81	0.074	0.21	-1.9	-1.8	-0.42	-0.11	-0.036
82							
83	0.10	0.21	-1.5	-1.1	-0.69	19	15
84	13	-2.7					
85	-0.56	-0.83	3.8	-0.77	-0.63	0.25	1.9
86							
87	0.064	0.16	-1.4	-0.10	0.24	0.45	0.84
88	1.2	1.3	0.11	0.086	-0.016		
89							
90							
91	0.10	0.20	-1.5	0.18	0.95	0.13	0.12
92	0.57	0.048	7.8	8.0	7.3	-5.0	-5.0
93	1.5	1.6	0.25	0.44	-0.48		
94	3.4	1.5	33	4.4	-4.7		
95	0.79	0.83	-0.16	5.1	0.26	0.70	-0.081
96							
97							
98							
99							
100							
101							
102							
103							
104							
105							
106	0.54	0.40	2.9	-1.4			
107	0.96	0.93	1.5	-0.067	-0.39		
108	1.2	1.0	4.0	1.6	3.9		
109							
110	-0.82	-0.92	0.71	-0.87	-0.52	0.24	2.7
111							
112	0.27	0.18	1.3	3.5	2.2		
113	1.1	0.42	11	5.9	-5.0		
114							
115	0.64	0.58	1.5	1.0	0.51	-1.6	-2.1
116	-1.7	-3.7					
117	0.27	0.32	-0.61	0.71	-0.26	2.9	1.8
118	0.072	0.074	0.043	0.12		-0.081	2.2

### Laboratories Z-scores: Herring

LABCODE	Sum TE	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum u/209	Sum m/209
1	0.75	0.52	1.0	0.30	-0.16	1.7	1.2
2	-0.082	-0.13	-0.049	0.074	0.66		
3	-0.12	0.024	-0.10	-3.1	0.27	-0.56	-0.87
4							
5	0.21	0.038	0.37	0.27			
6							
7							
8	0.87	0.87	0.92	0.17	1.0	0.24	0.25
9							
10	-0.10	0.34	-0.49	-0.66	-0.93	-0.22	-0.56
11	-0.33	-0.36	-0.28	-0.86	-0.31	0.25	0.23
12							
13	0.21	-0.36	0.71	1.3			
14	0.20	-0.010	0.40	0.16	-0.34		
15	0.22	0.24	0.19	0.45	0.099	0.14	0.086
16	-0.35	-0.044	-0.62	-0.63	0.91		
17							
18							
19	-1.2	-1.1	-1.2	-1.5	-5.0		
20	2.2	2.8					
21	0.057	-0.29	0.38	0.24	0.066		
22	-0.12	0.61	-0.56				
23							
24	0.47	0.32	0.59	1.0	1.0	0.90	0.81
25							
26							
27	0.37	0.50	0.24	0.46	0.92	-0.0072	0.22
28	-0.72	-0.65	-0.79	-0.71	-0.62		
29							
30	0.42	0.39	0.47	0.15	0.28	-2.4	-2.3
31							
32	0.19	0.083	0.30	0.062	0.61		
33	-0.35	-0.50	-0.18	-0.81	-0.55	-0.60	-0.61
34	-0.17	-0.028	-0.30	-0.12			
35	0.46	0.24	0.69	0.070	0.057		
36							
37							
38	-1.2	-1.3	-1.1	-0.80		-1.2	-1.3
39							
40	1.1	1.3	0.86	0.66	0.71		
41	-0.72	-0.64	-0.86	0.21	-5.0	-1.0	-1.3
42	-1.0	-1.6	-0.39	-0.40	-0.45		
43	0.12	0.60	-0.33	-0.044	0.46	1.2	0.76
44	-0.12	-0.17	-0.082	0.044	0.24	0.25	0.30
45	-0.47	-0.32	-0.61	-0.52	-0.91	-0.86	-1.2
46	-1.1	-1.0	-1.1	-1.5	-1.7		
47	-1.9	-2.1	-1.7	-1.1			
48							
49	0.64	0.32	0.96	0.54	0.55		
50							
51	0.87	0.46	1.3	0.57	1.6	0.81	0.72
52							
53							
54	-0.084	-0.45	0.27	-0.12			
55							
56							
57	0.086	0.42	-0.21	-0.42	-0.22		
58	0.37	0.90	-0.16	0.88	-0.10		
59	11	-0.49	23	0.91			
60	1.1	0.82	1.3	0.99	0.90		
61	0.50	0.30	0.67	0.65		0.085	-0.27
62	-0.32	-0.29	-0.38	0.13			
63	-0.50	-0.18	-0.76	-1.4	-1.1	-0.80	0.16
64	-3.7	-4.6	-3.0	0.28			
65	-0.18	-0.13	-0.22	-0.40	0.020	0.38	-0.0094
66							
67	-2.0	0.98					
68	-0.79	-1.7	0.11	-1.1			
69	0.28	0.40	0.16	0.40	0.80		
70							

### Laboratories Z-scores: Herring (continued)

LABCODE	Sum TE	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-ortho PCB	Sum Indicator PCB	Sum u/209	Sum m/209
71							
72							
73	-0.16	0.22	-0.51	-0.71	-0.41	-0.71	-0.70
74	-1.0	-2.4	0.36	-0.31	0.11		
75	-0.043	0.28	-0.30	-0.93	-0.84	-0.20	-0.062
76	0.39	0.93	-0.19	1.4	0.23	0.65	0.72
77	0.38	0.12	0.64	0.14	0.22		
78	4.7	-0.40	9.8	0.15	1.0	-0.24	0.37
79	-0.38	-1.0	0.25	-0.61	0.56	-0.15	-0.50
80	0.36	0.20	0.53	0.11			
81	-1.2	-1.0	-1.4	-0.75	0.34	-0.37	-0.43
82							
83	0.13	0.26	0.036	-0.32	0.44	0.92	0.49
84							
85	-0.22	-0.46	0.023	-0.50	-0.61	-0.70	-0.65
86	0.41	0.42	0.44	-0.23	-0.44	1.0	1.0
87	0.51	0.55	0.47	0.54	0.51	0.44	0.41
88	0.69	-0.24	1.5	1.4	1.2		
89							
90							
91	-0.15	0.18	-0.52	0.67	0.17	0.078	0.039
92	-0.42	-0.39	-0.48	0.032	0.32	-5.00	-5.0
93	0.55	0.74	0.35	0.75	0.67		
94	-0.45	-0.20	-0.72	0.093	-5.0		
95	0.25	0.64	-0.11	-0.088	0.43	0.40	0.48
96							
97							
98							
99							
100							
101							
102							
103	0.23	0.50	-0.0040	-0.14	2.6	3.6	3.0
104							
105							
106	-0.87	-0.56	-1.1	-1.5			
107	0.18	-0.090	0.43	0.31	-0.30		
108	-0.42	0.28	-1.2	1.2	4.6		
109							
110	-0.61	-1.4	0.13	-0.93	-0.39	-0.50	0.12
111							
112	0.88	0.37	1.3	2.0	-1.5		
113	7.6	6.9	8.3	6.4	-5.0		
114							
115	2.5	0.11	-0.0054	91	-0.92	0.086	-0.28
116							
117	0.52	0.31	0.67	1.5	-0.020	2.9	2.3
118	0.70	0.63	0.77	0.56		0.18	0.51

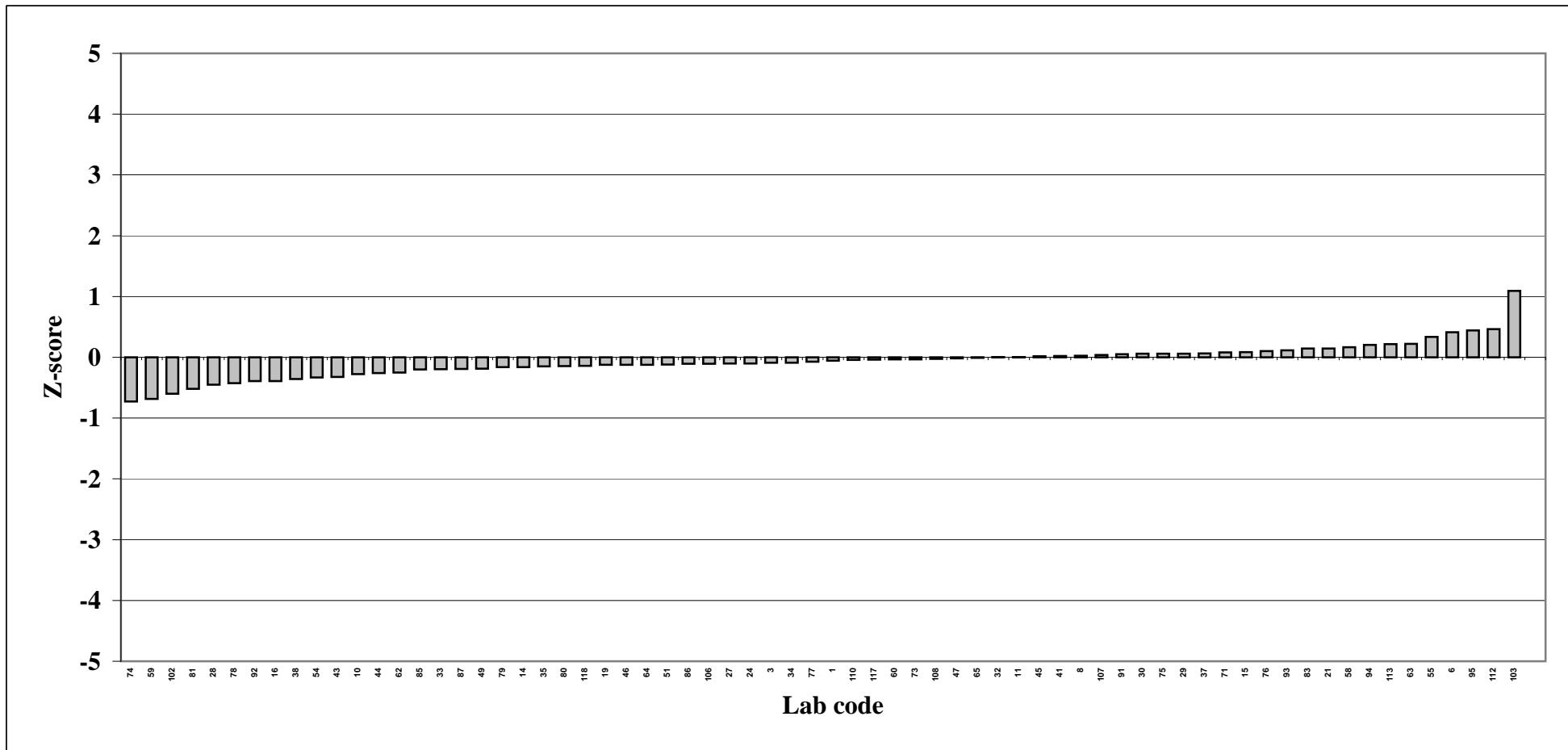
### Laboratories Z-scores: Milk

LABCODE	Sum TE	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum u/209	Sum m/209
1	-0.037	-0.10	0.12	0.79	8.0	0.69	-2.5
2							
3	0.18	0.22	0.10	-1.0	-0.23	13	2.8
4							
5	-0.91	-0.89	-1.0	-1.1			
6							
7							
8	0.67	1.2	-0.73	-0.46	-0.053	5.2	1.6
9							
10	0.86	1.4	-0.59	3.1	9.6	0.37	-2.7
11	-0.039	0.034	-0.23	0.025	-0.73	0.75	0.35
12							
13	-0.10	-0.23	0.22	0.76			
14	-0.026	-0.16	0.31	-0.032	-1.3		
15							
16							
17							
18							
19	0.85	0.87	0.80	0.18	-5.0		
20	-2.4	-3.0					
21	0.096	0.030	0.26	-0.090	1.4		
22							
23							
24	0.077	0.079	0.083	-0.65	-2.1	-0.63	1.6
25							
26							
27	-0.17	0.072	-0.76	-0.89	0.15	1.9	3.0
28							
29							
30	2.3	2.9	1.0	7.4	14	-2.5	1.6
31							
32							
33	-0.0053	-0.47	1.1	4.9	14	22	9.4
34							
35	0.39	0.32	0.58	-0.12	0.058		
36	-0.85	-0.088	-2.8	0.52	9.9		
37	0.47	0.45	0.53	0.019	0.75		
38	-0.36	-0.40	-0.29	0.91		0.25	-2.0
39							
40	-1.6	-1.6	-1.7	-1.3	-1.3		
41							
42							
43							
44	-1.0	-1.1	-0.85	0.37	2.3	0.36	1.8
45	0.26	0.31	0.10	1.5	0.72	1.2	-2.3
46	0.80	0.76	0.92	0.18	1.9		
47	2.1	2.6	1.1	1.6			
48							
49	1.5	1.3	2.0	0.48	-0.18		
50							
51	0.61	0.60	0.62	0.94	6.3	5.7	0.56
52							
53							
54	-0.61	-0.75	-0.23	-0.41			
55	-2.1	-1.4	-4.0	-2.8	-2.6	-2.6	0.82
56							
57	-0.30	-0.61	0.46	2.5	1.3		
58	13	14	11	16	9.0		
59	16	-1.1	59	4.9			
60	3.4	0.54	11	9.1	0.19		
61	-0.60	-0.64	-0.51	-0.44		-0.86	-1.1
62	-0.33	-0.25	-0.59	1.8			
63							
64	-3.1	-4.5	-3.0	209			
65	-0.024	0.022	-0.14	-0.11	2.4		
66							
67	2.5	2.2					
68							
69							
70							

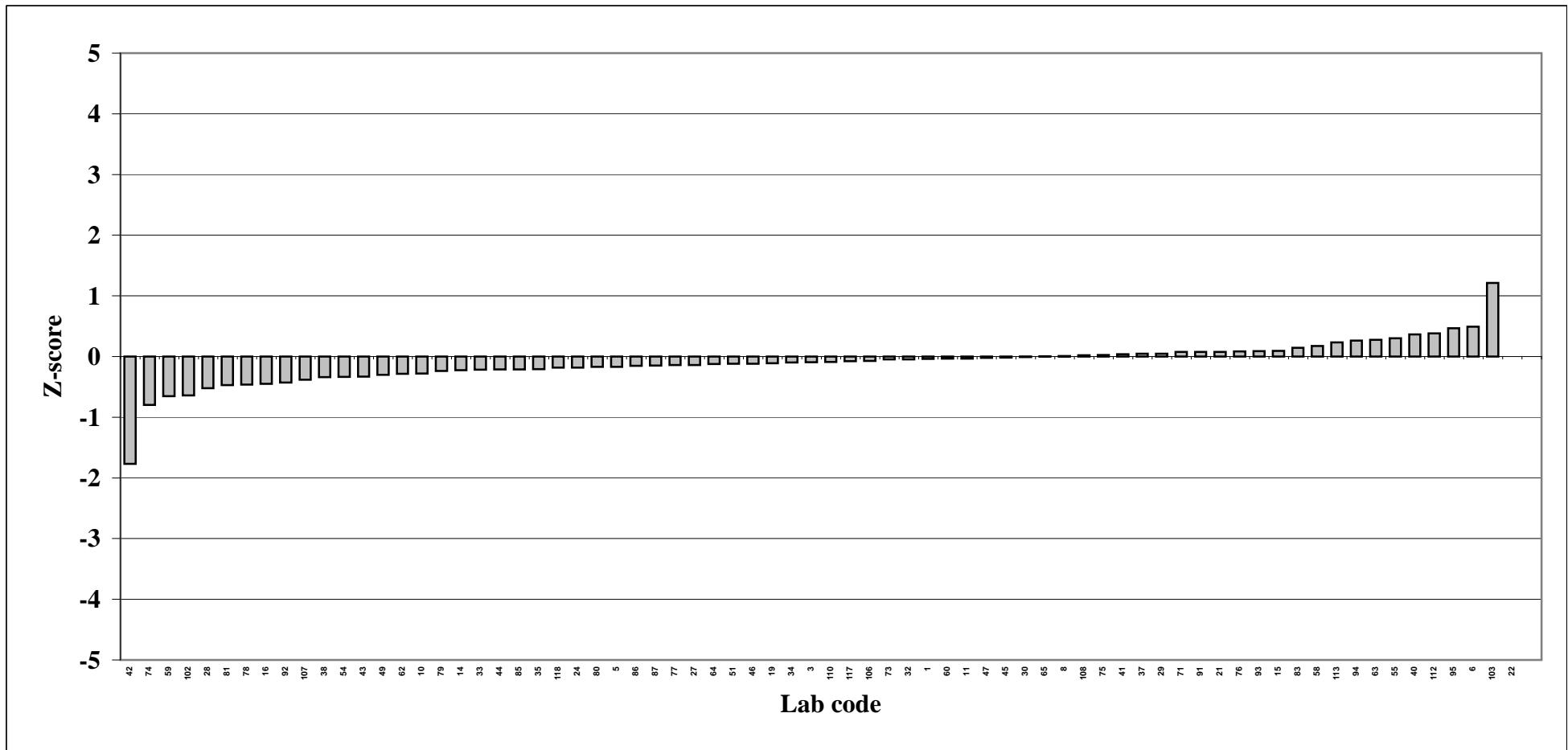
### Laboratories Z-scores: Milk (continued)

LABCODE	Sum TE	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum u/209	Sum m/209
71	0.74	0.39	1.6	4.6			
72							
73	0.28	0.31	0.21	-1.0	-0.68	-0.37	2.7
74	0.15	0.14	0.17	1.5	10		
75	-1.1	-0.71	-2.2	-0.88	4.9	-1.29	2.0
76							
77	-0.61	-0.55	-0.78	1.5	8.9		
78	0.020	-0.22	0.58	3.7	3.0	0.36	-2.2
79							
80	0.51	0.53	0.45	-0.14			
81	0.76	2.0	-2.3	-2.2	-0.34	-0.71	0.73
82							
83	-2.2	-2.2	-2.3	-1.8	-1.9	21	6.3
84	1.4	4.0					
85	-0.014	-0.28	0.68	-0.34	1.1	6.7	3.0
86							
87	0.32	0.36	0.23	0.10	3.7	0.84	-1.13
88	2.2	2.8	0.66	0.45	0.68		
89							
90							
91	0.090	0.51	-0.99	0.22	3.6	1.0	-0.58
92	0.88	1.1	-0.20	28	19	-5.0	-5.0
93							
94	8.4	5.1	16	13	-3.2		
95	0.81	0.97	0.12	19	-0.75		
96							
97							
98	-4.9			13	-0.082	6.4	2.0
99							
100							
101							
102	-0.45	-0.19	-1.1	0.61			
103							
104							
105							
106	-0.56	-0.52	-0.65	-1.3			
107							
108	-0.45	-0.39	-0.63	0.70	4.8		
109					1.2		
110	-0.66	-0.92	-0.00084	-1.1	-0.96	-1.3	-3.0
111							
112	1.1	0.89	1.7	4.4	6.7		
113							
114							
115	-0.13	-0.053	-0.4	4.7	2.0	-0.72	-3.1
116							
117	0.33	0.52	-0.12	0.025	-1.5	2.0	-2.0
118	0.19	0.070	0.50	0.11		1.3	5.7

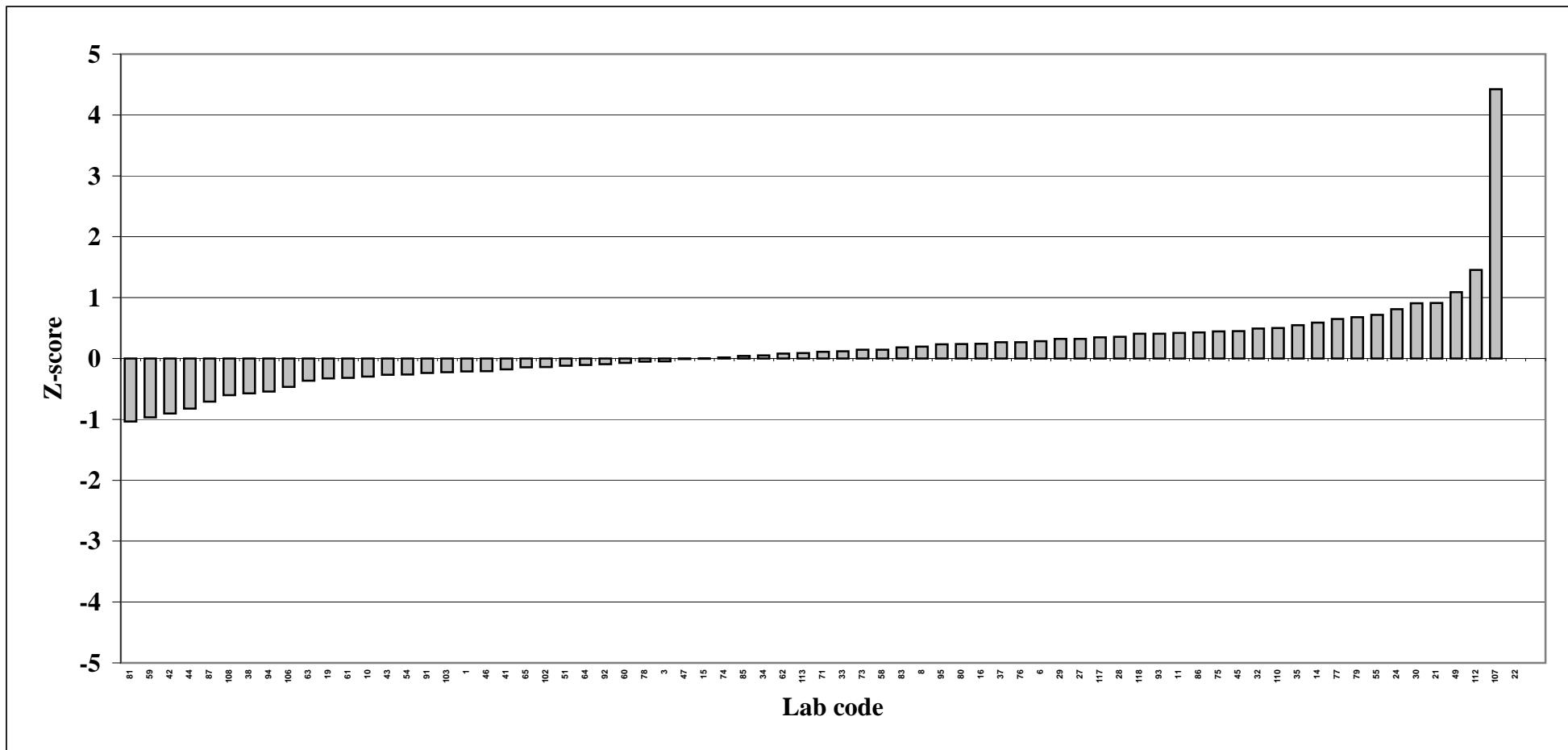
### Z-score analyte solution; total TEQ



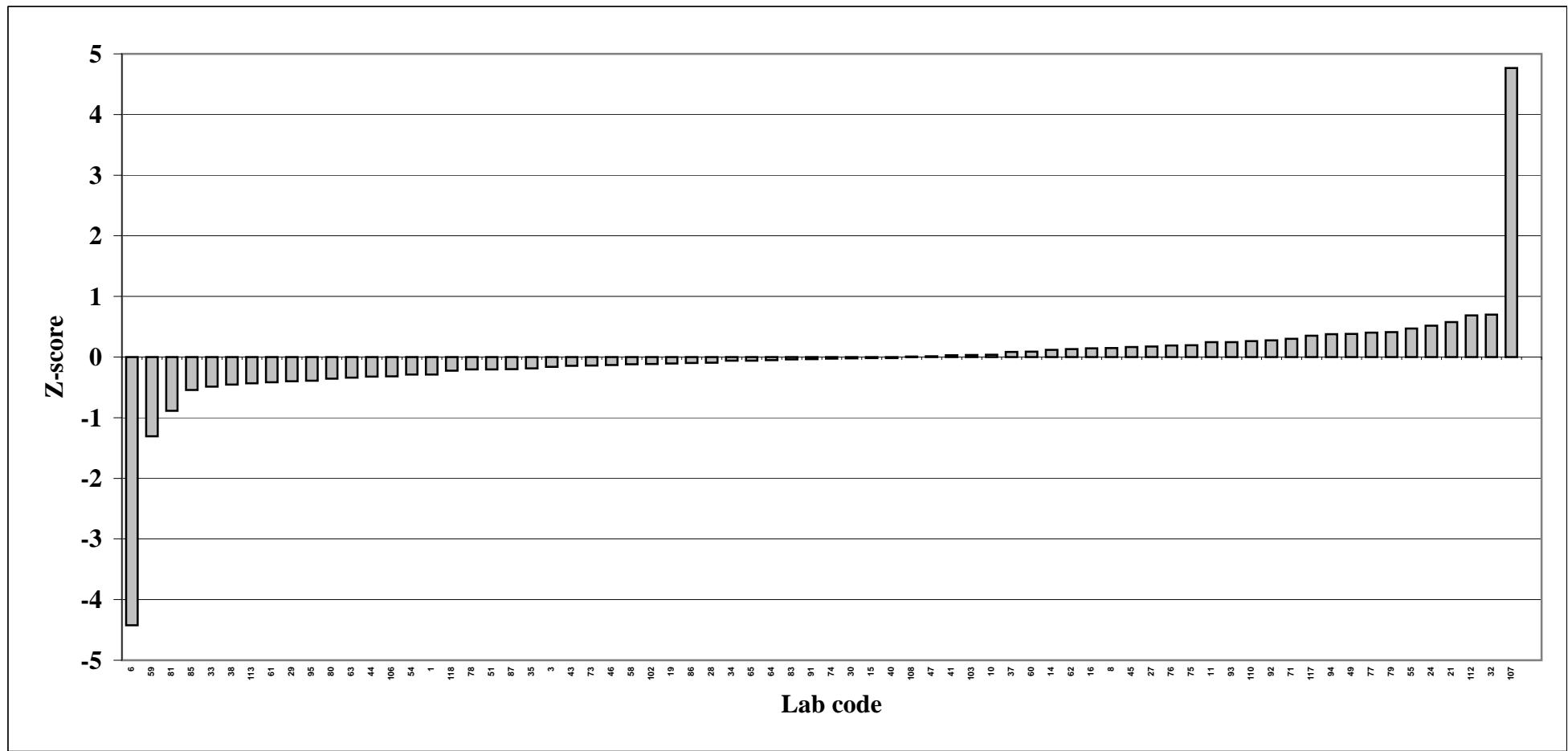
### Z-score analyte solution; PCDD/PCDF TEQ



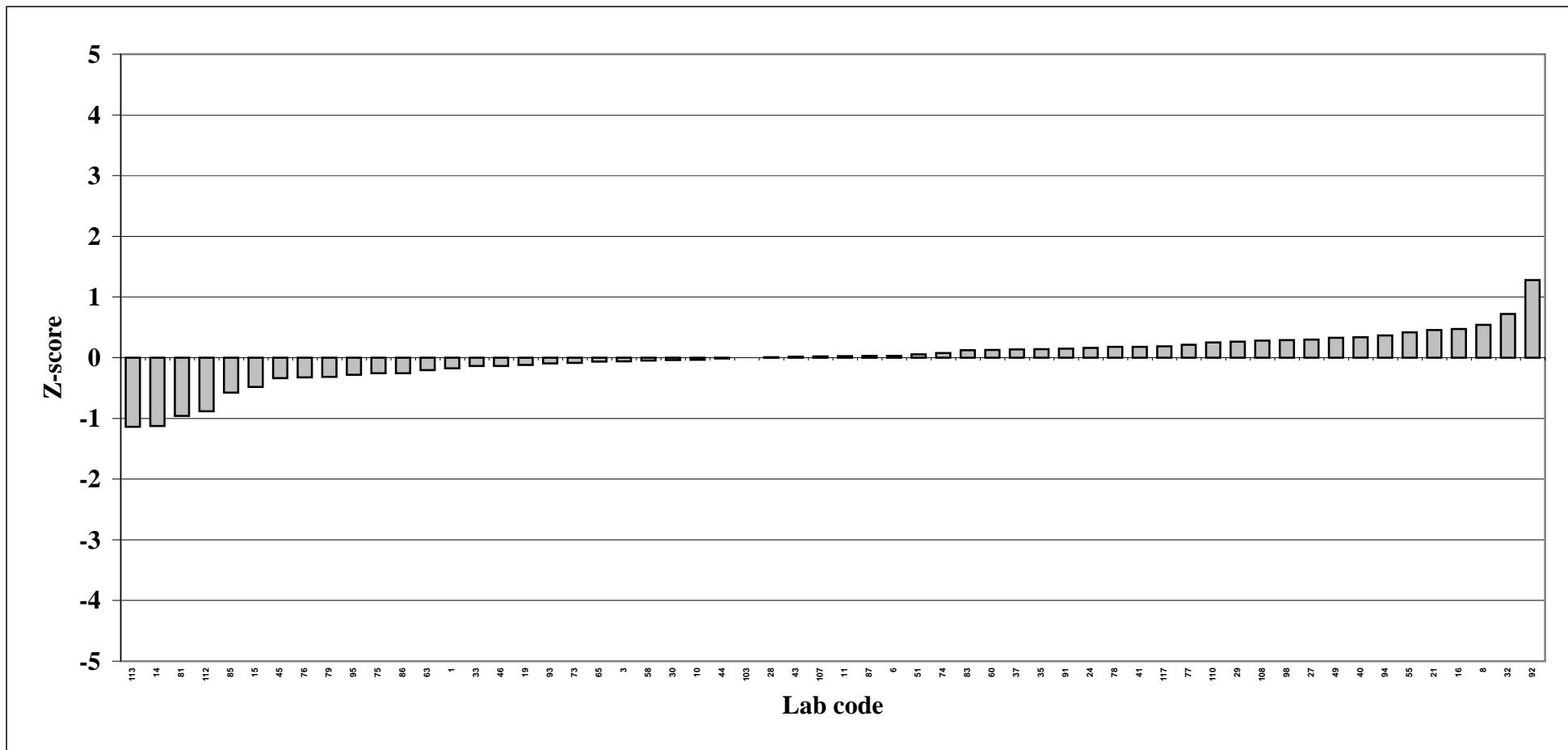
### Z-score analyte solution; non-ortho PCB TEQ



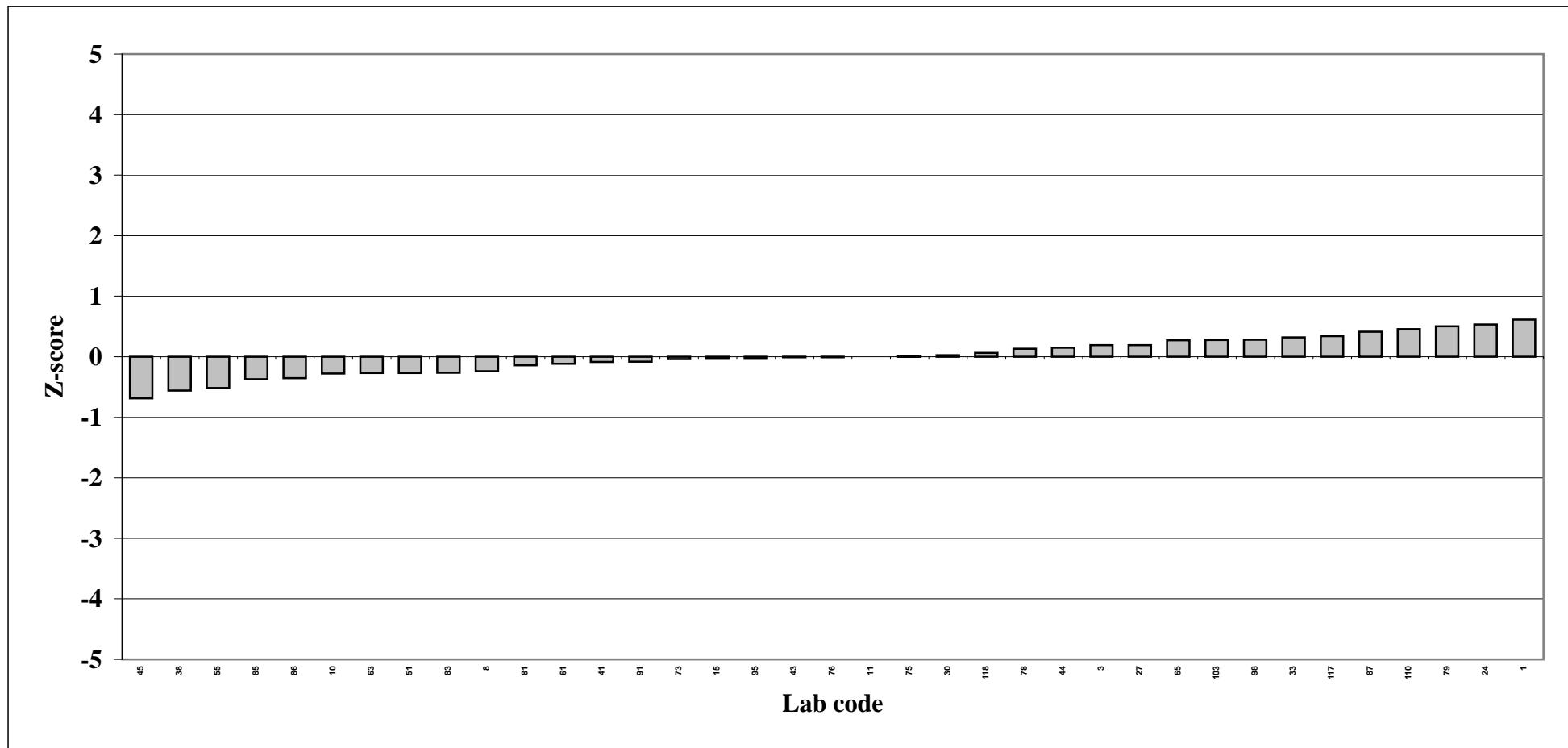
## Z-score analyte solution; mono-ortho PCB TEQ



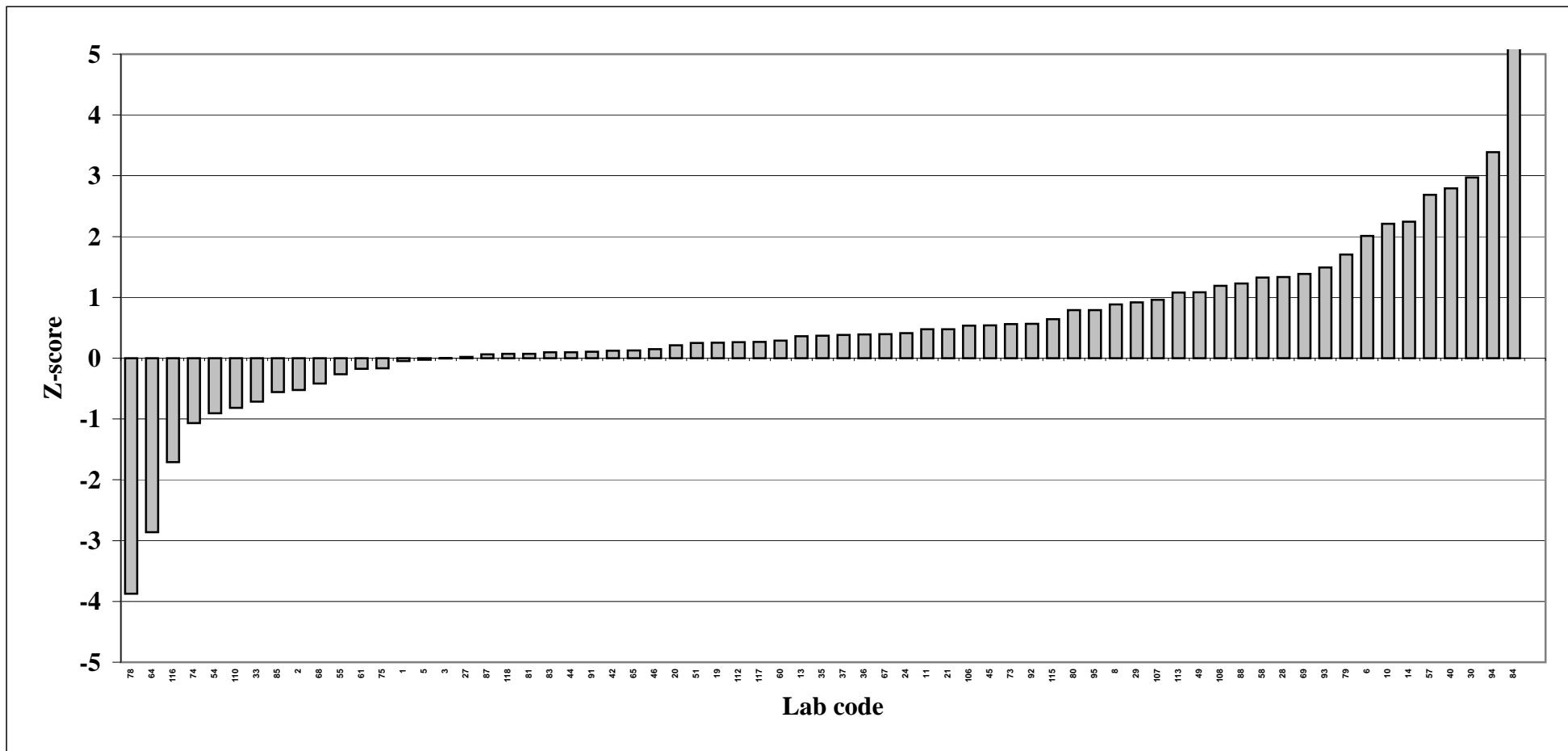
### Z-score analyte solution; sum indicator PCB



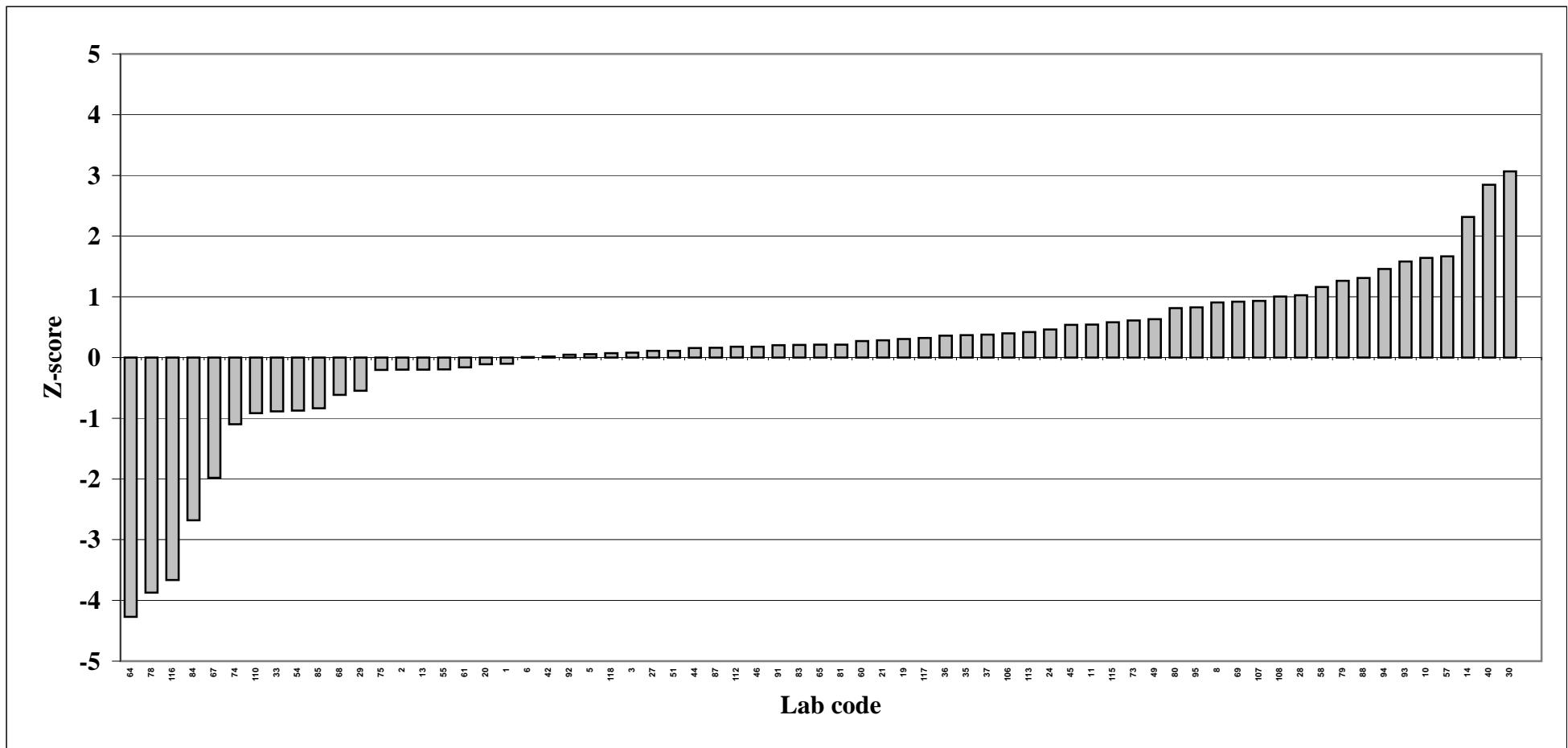
### Z-score analyte solution; sum PBDE without BDE-209



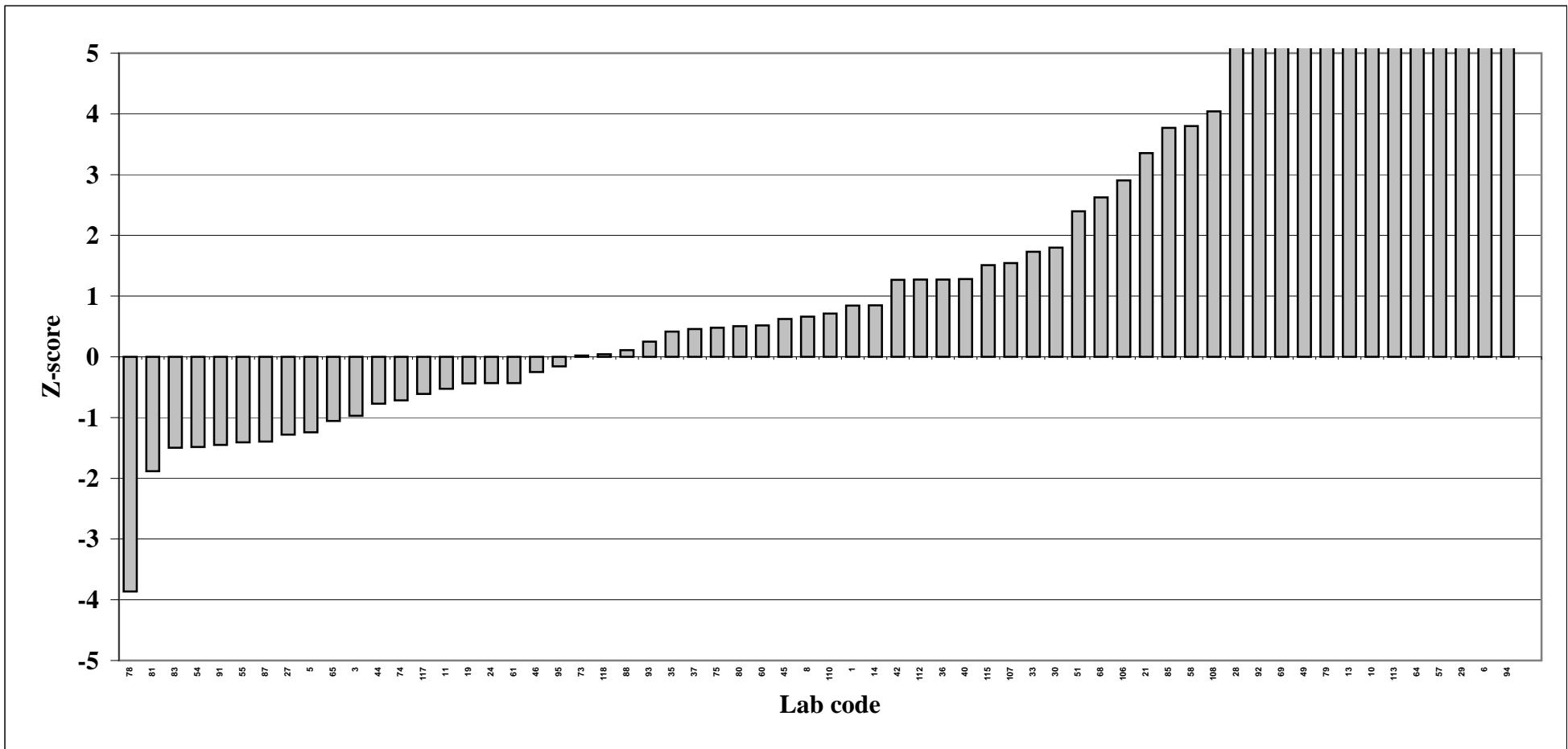
### Z-score Pork; total TEQ



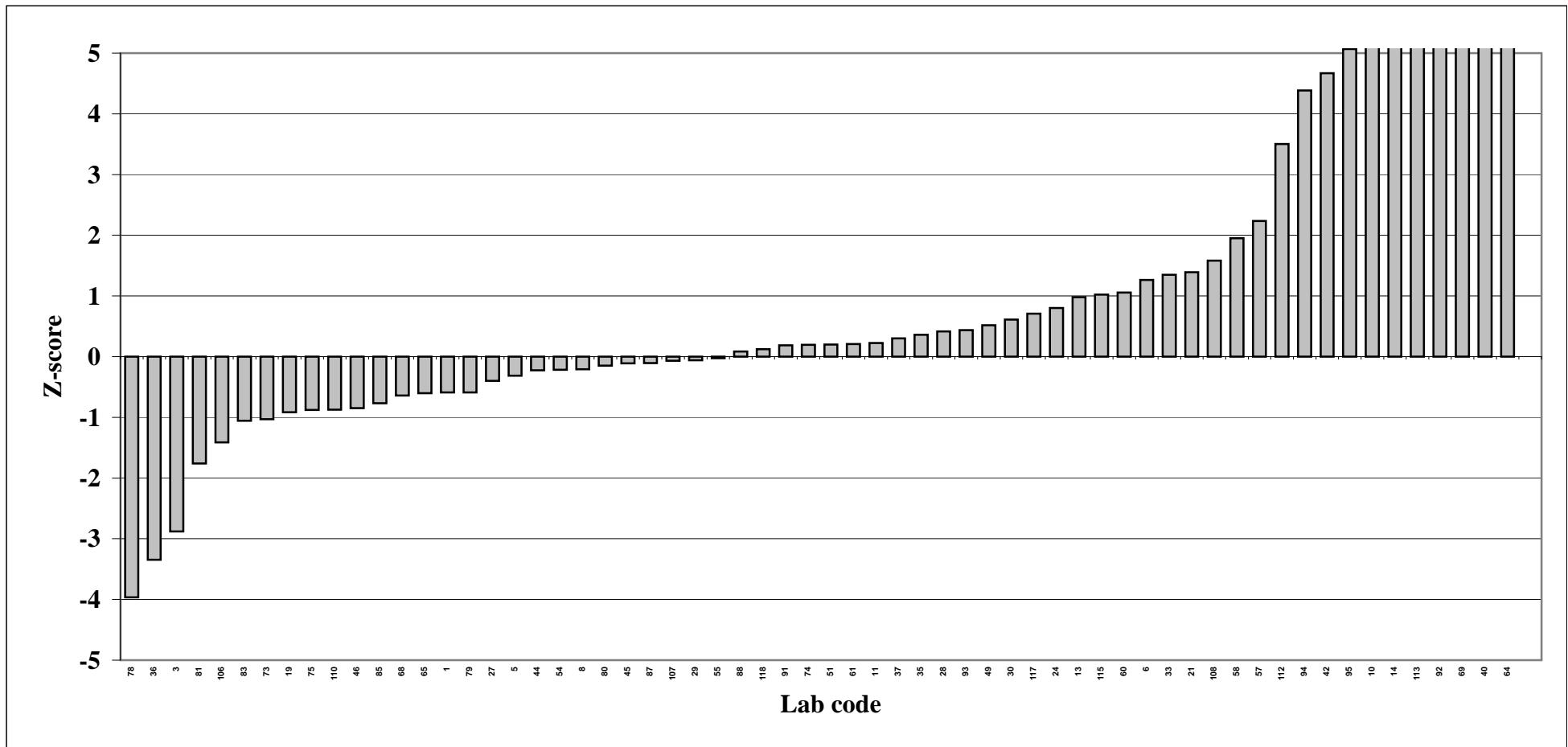
### Z-score Pork; PCDD/PCDF TEQ



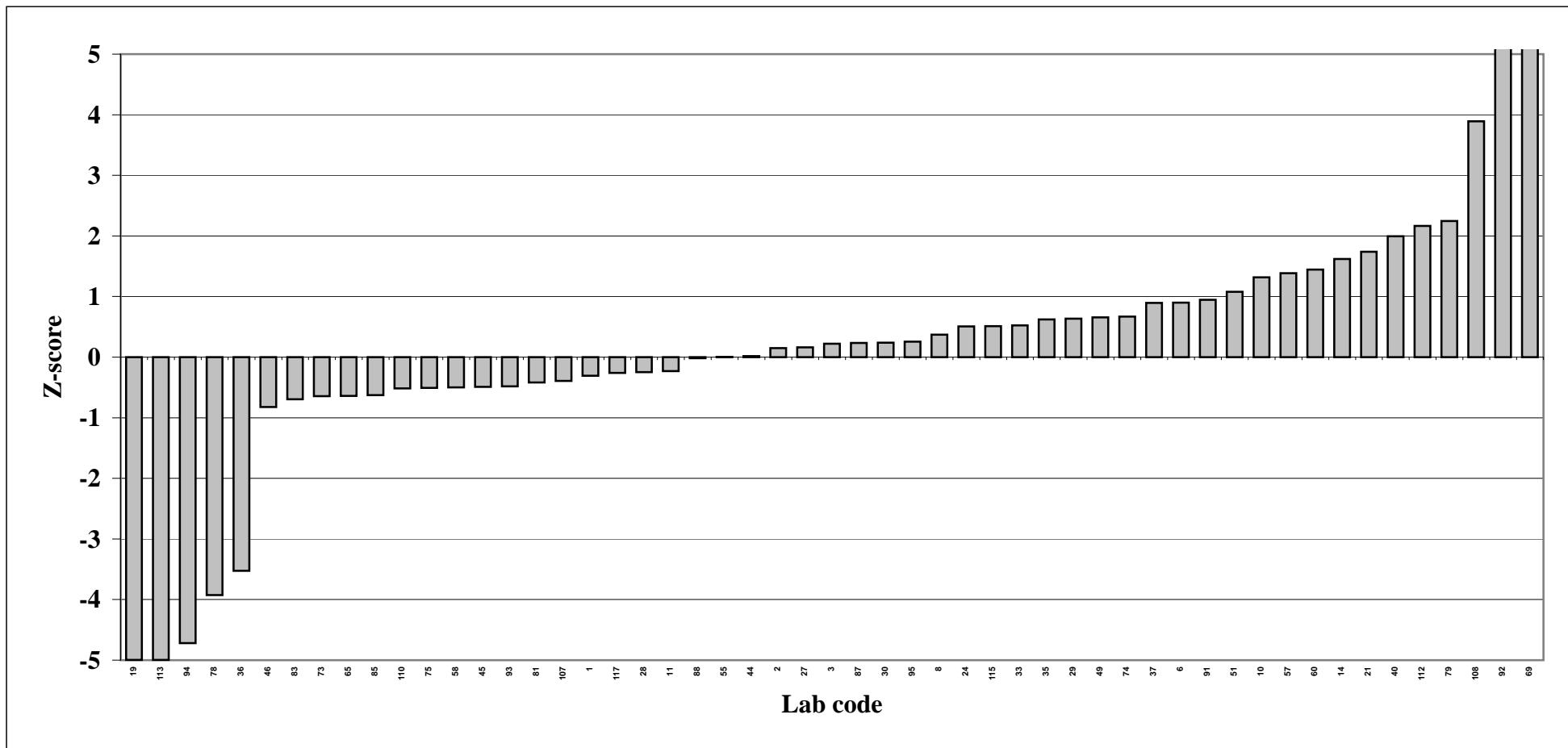
## Z-score Pork; non-ortho PCB TEQ



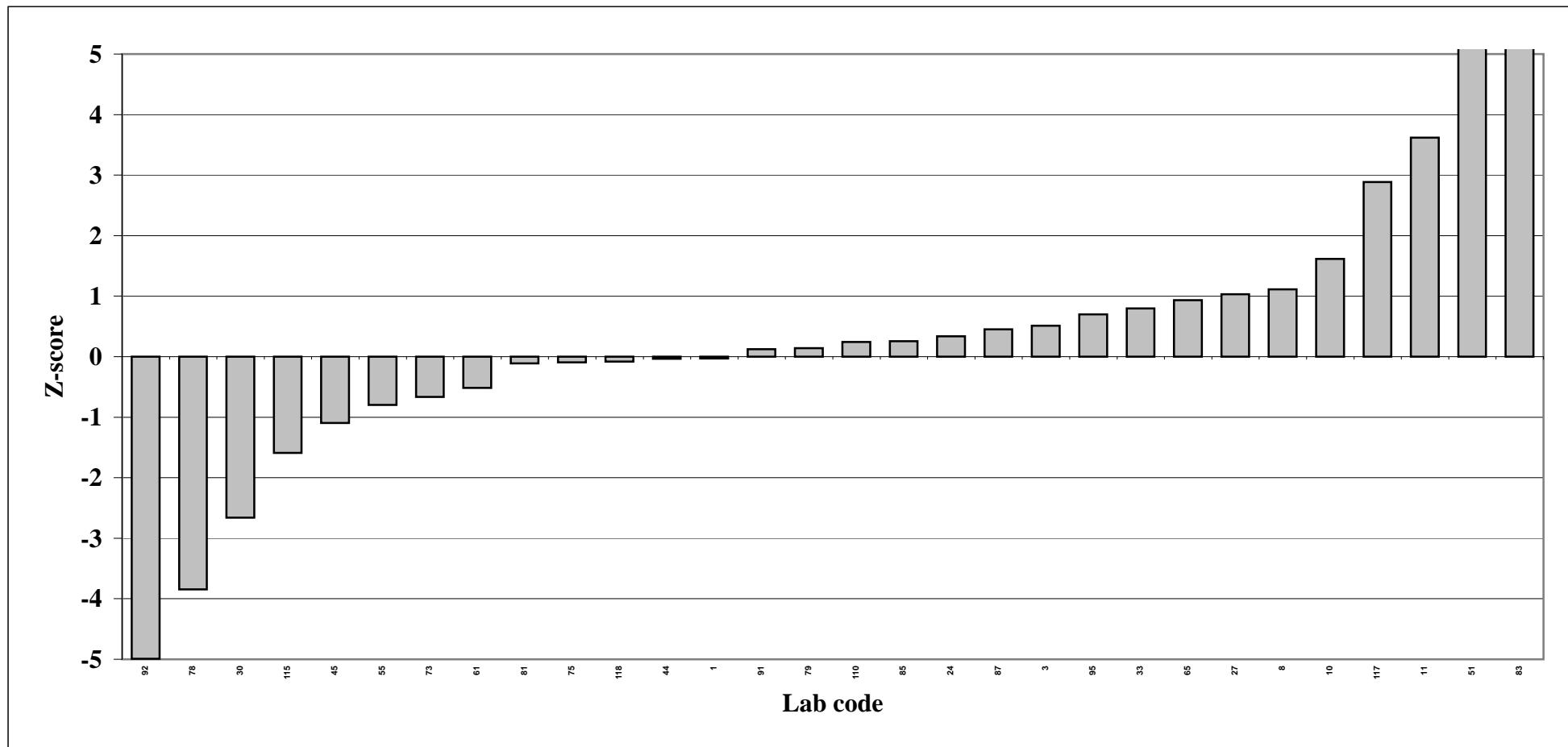
### Z-score Pork; mono-ortho PCB TEQ



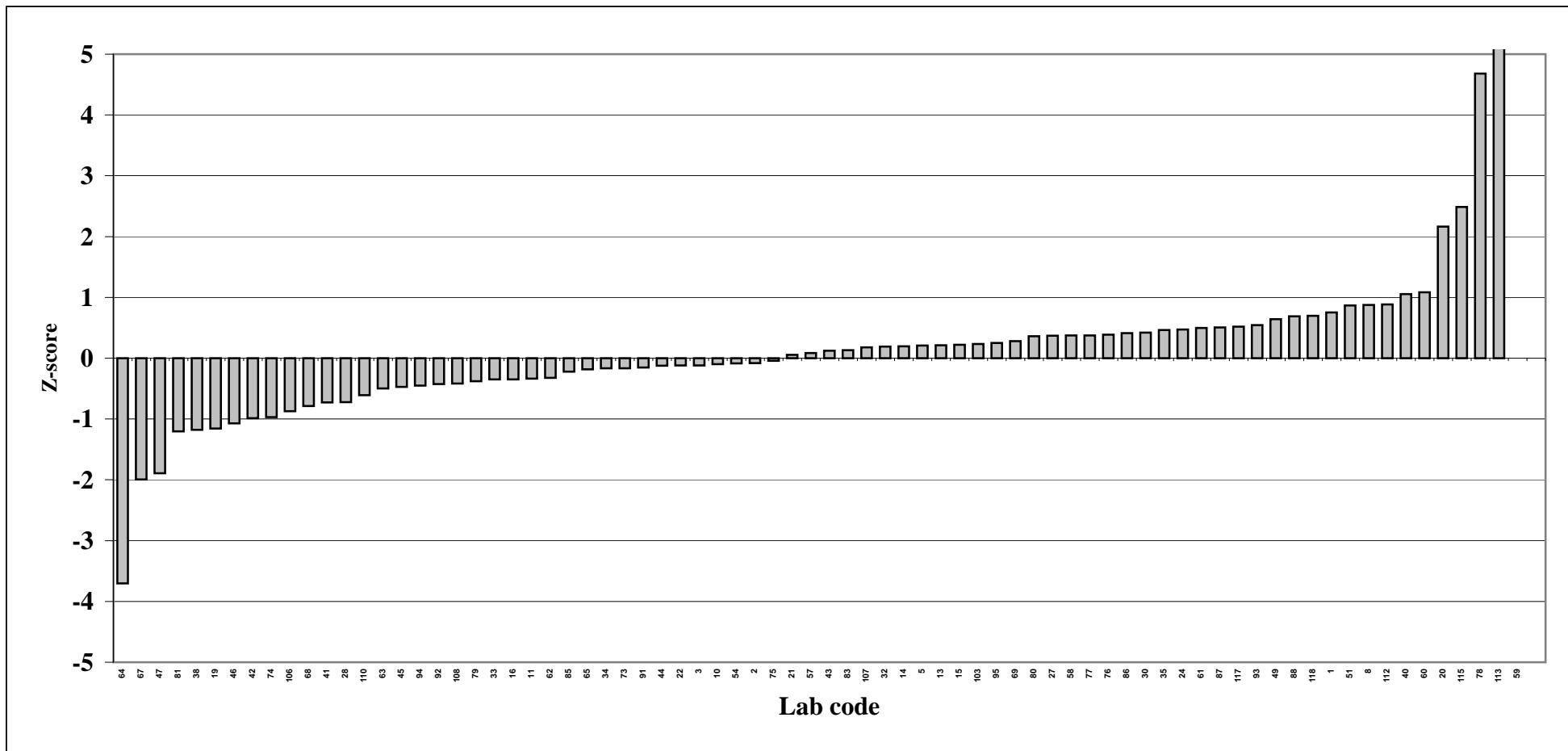
### Z-score Pork; sum indicator PCB



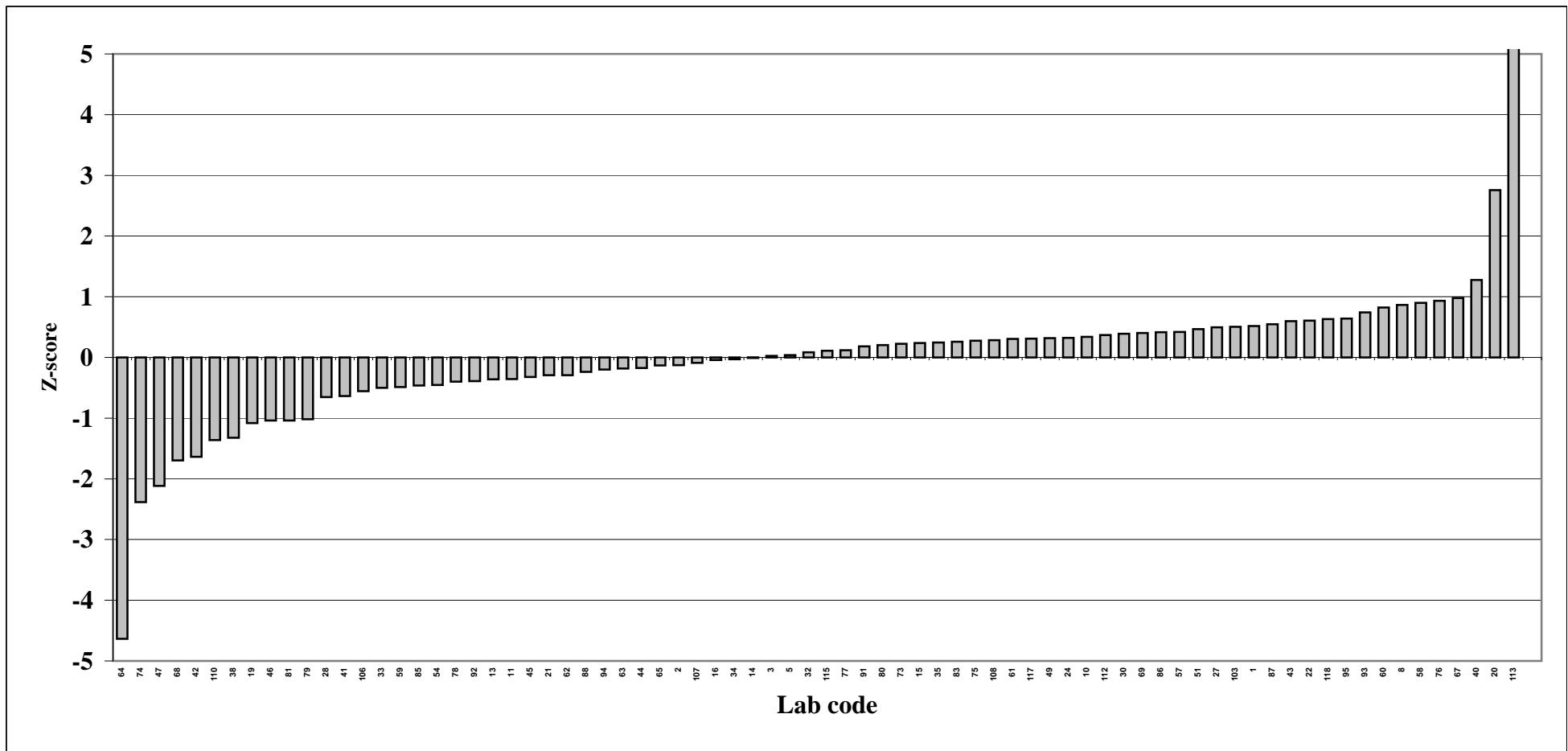
### Z-score Pork; sum PBDE without BDE-209



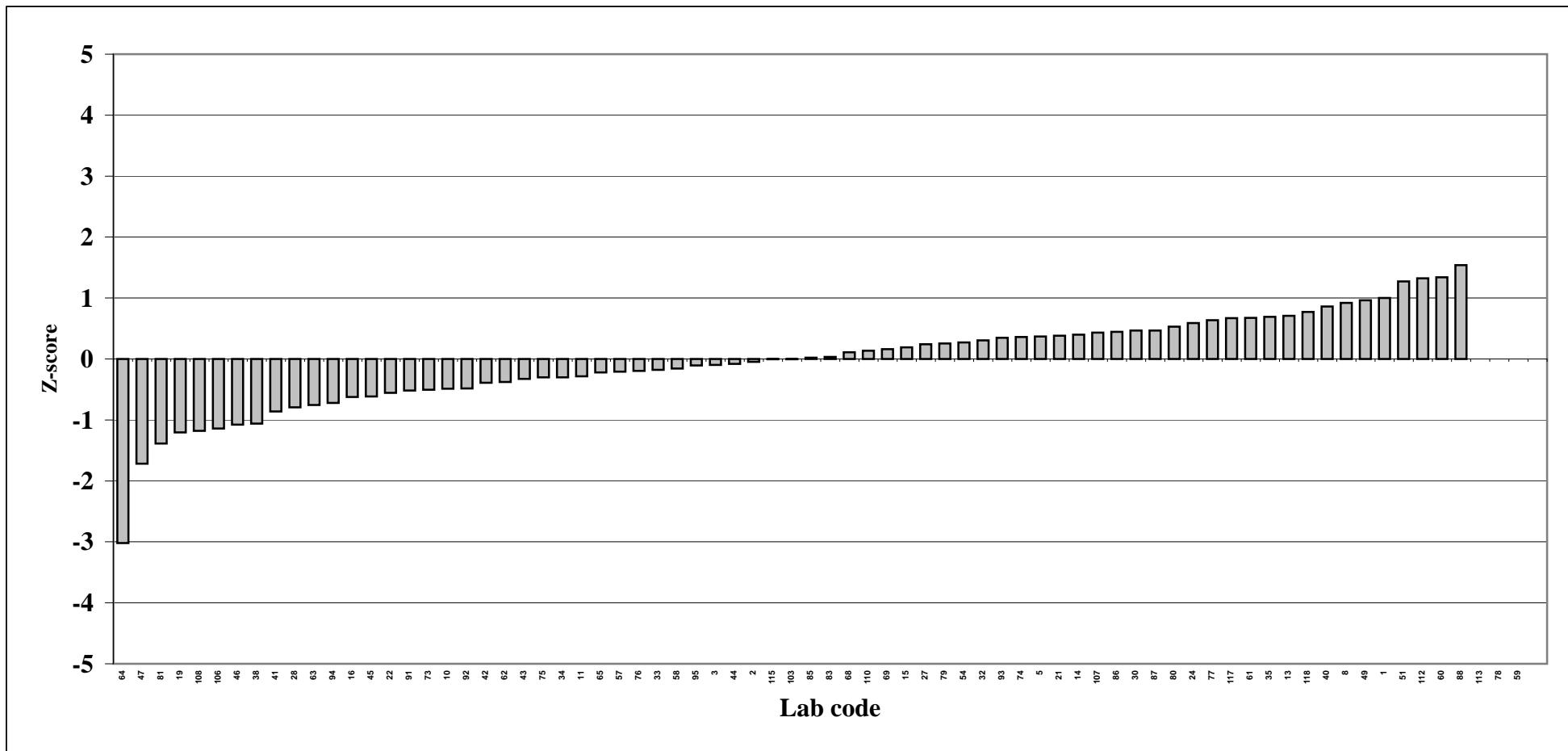
### Z-score Herring; total TEQ



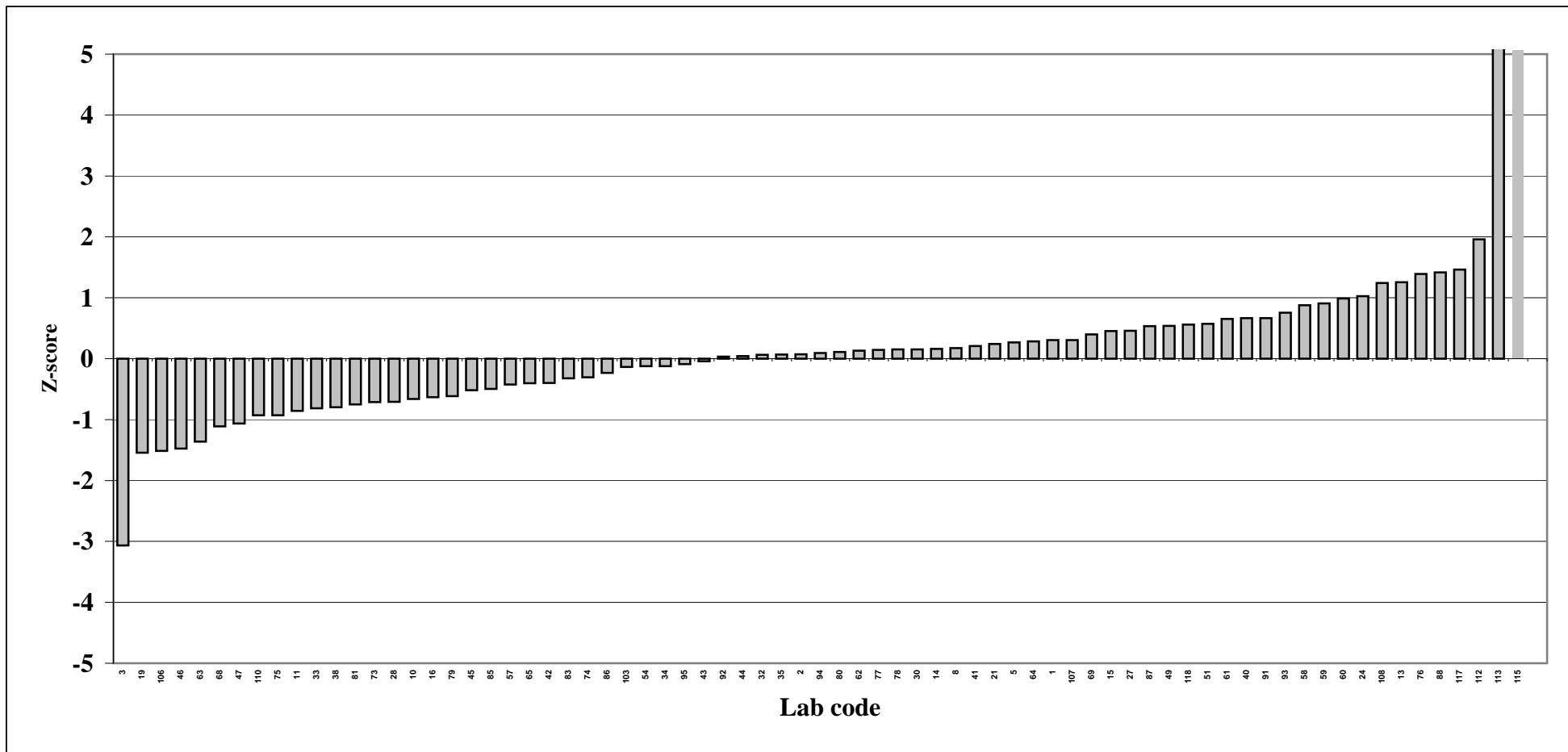
## Z-score Herring; PCDD/PCDF TEQ



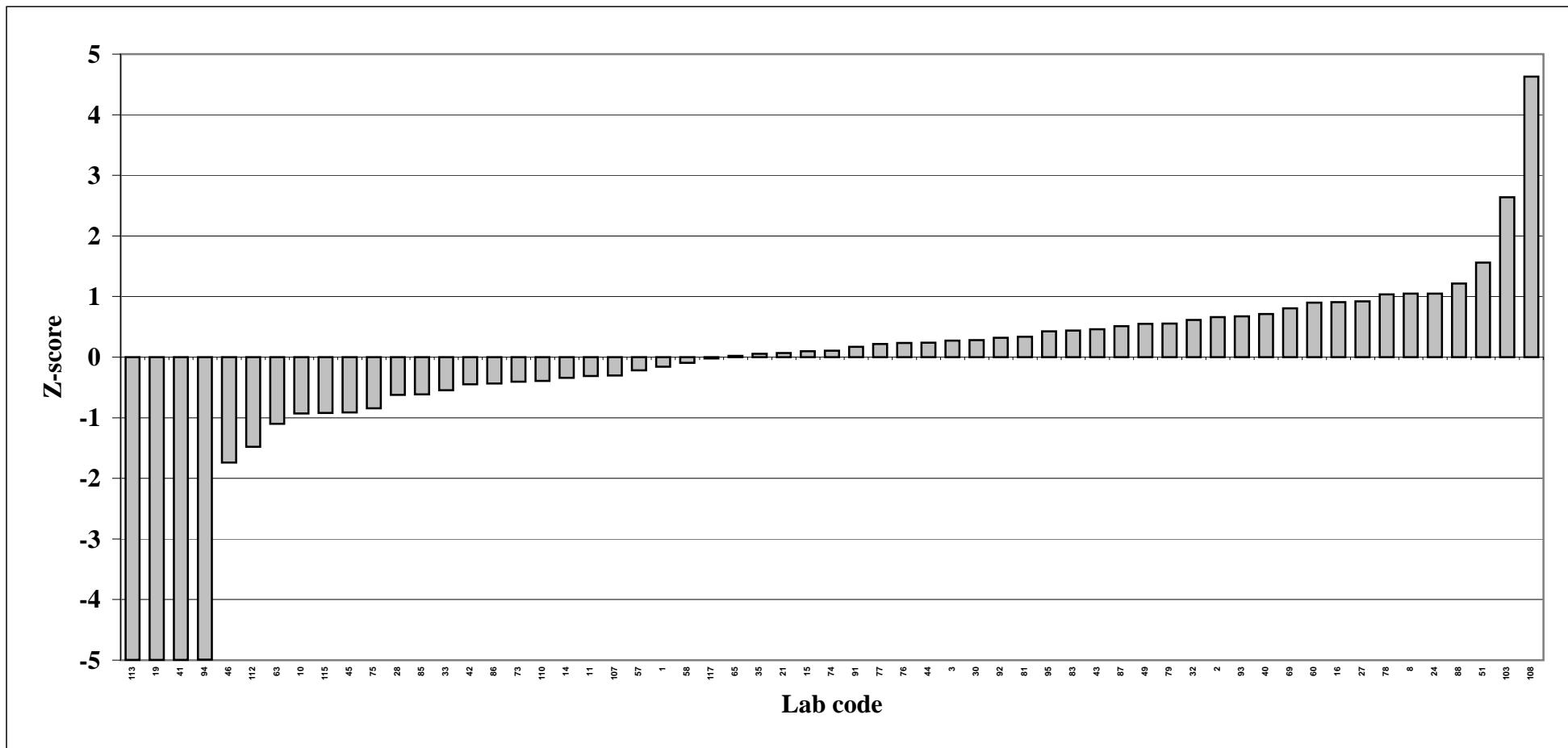
### Z-score Herring; non-ortho PCB TEQ



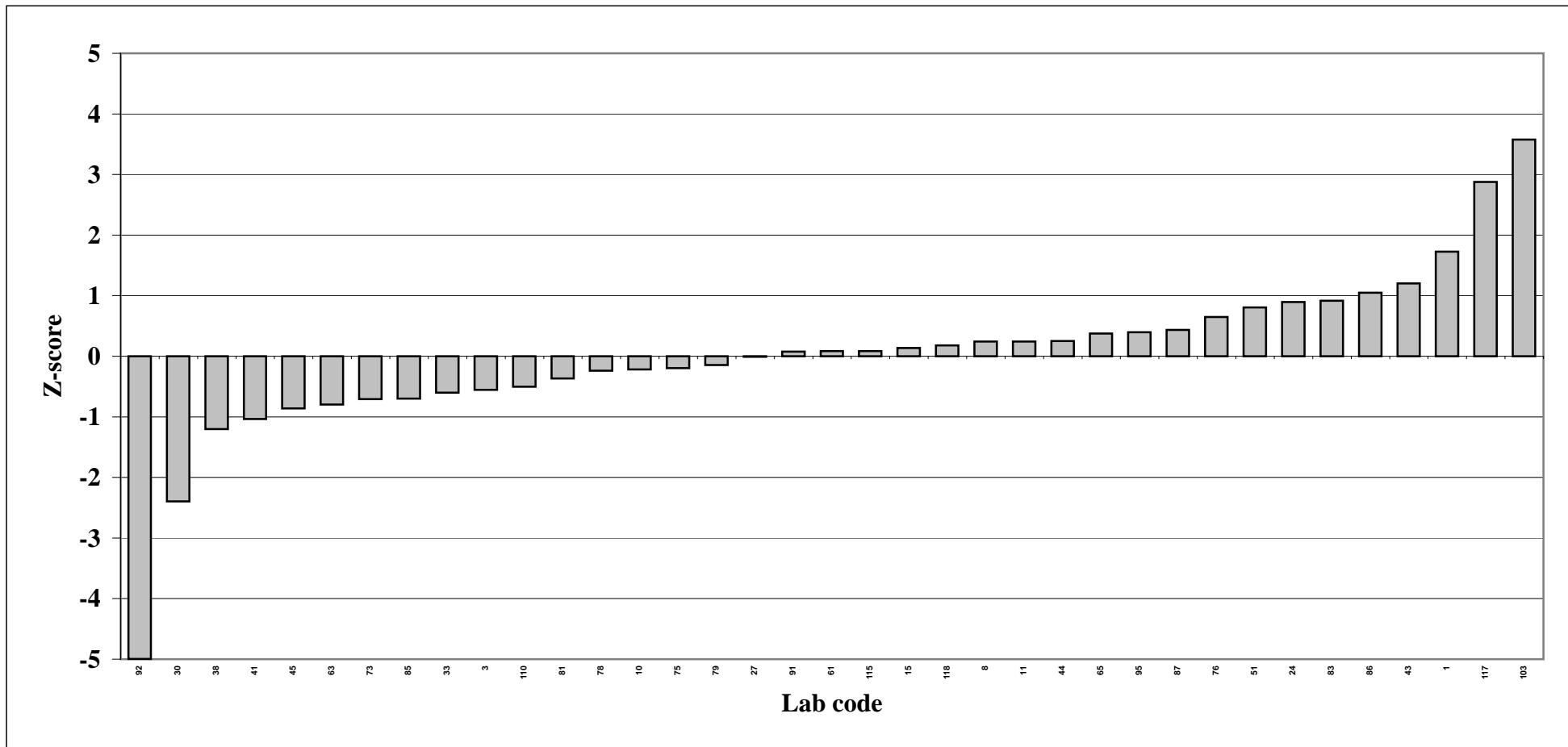
### Z-score Herring; mono-ortho PCB TEQ



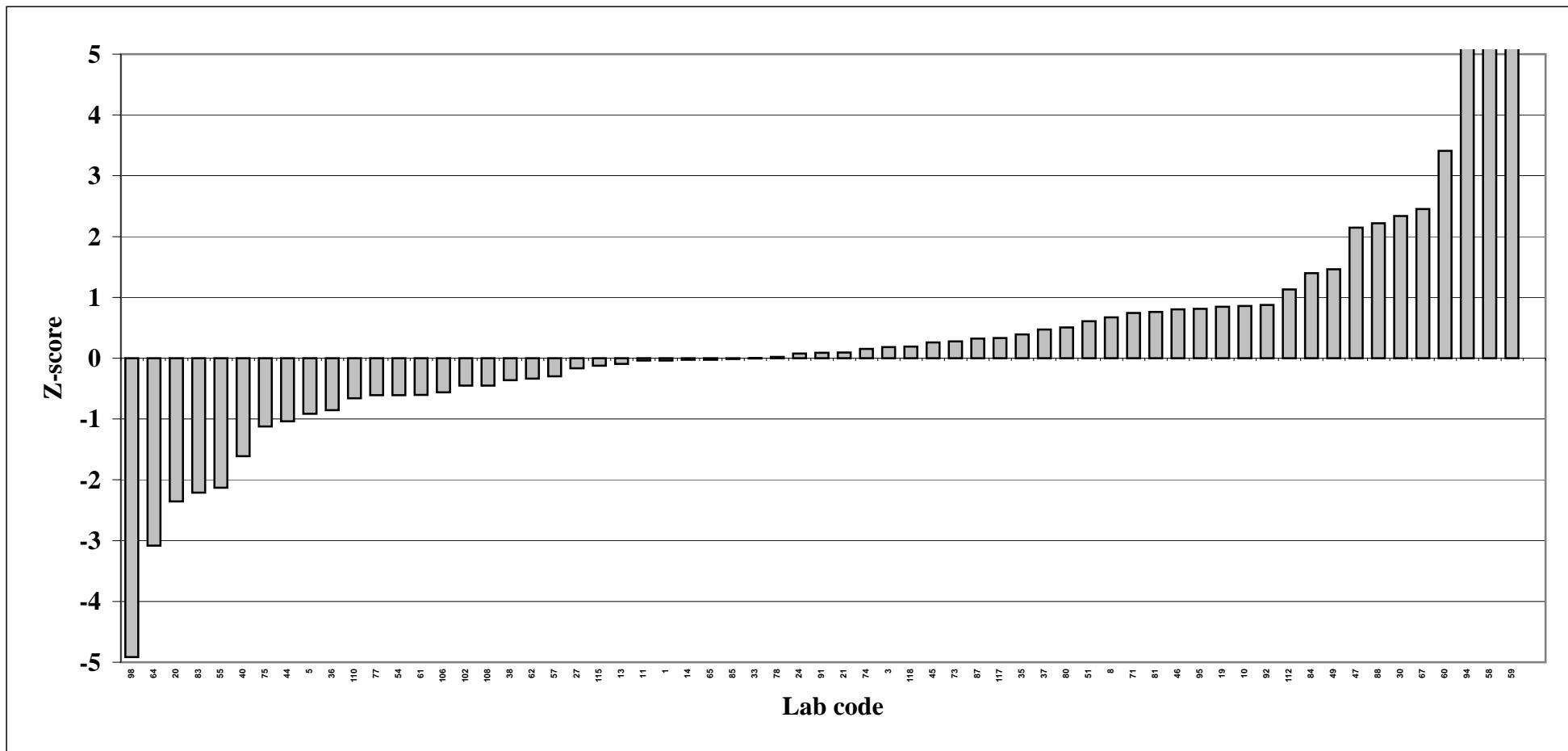
### Z-score Herring; sum indicator PCB



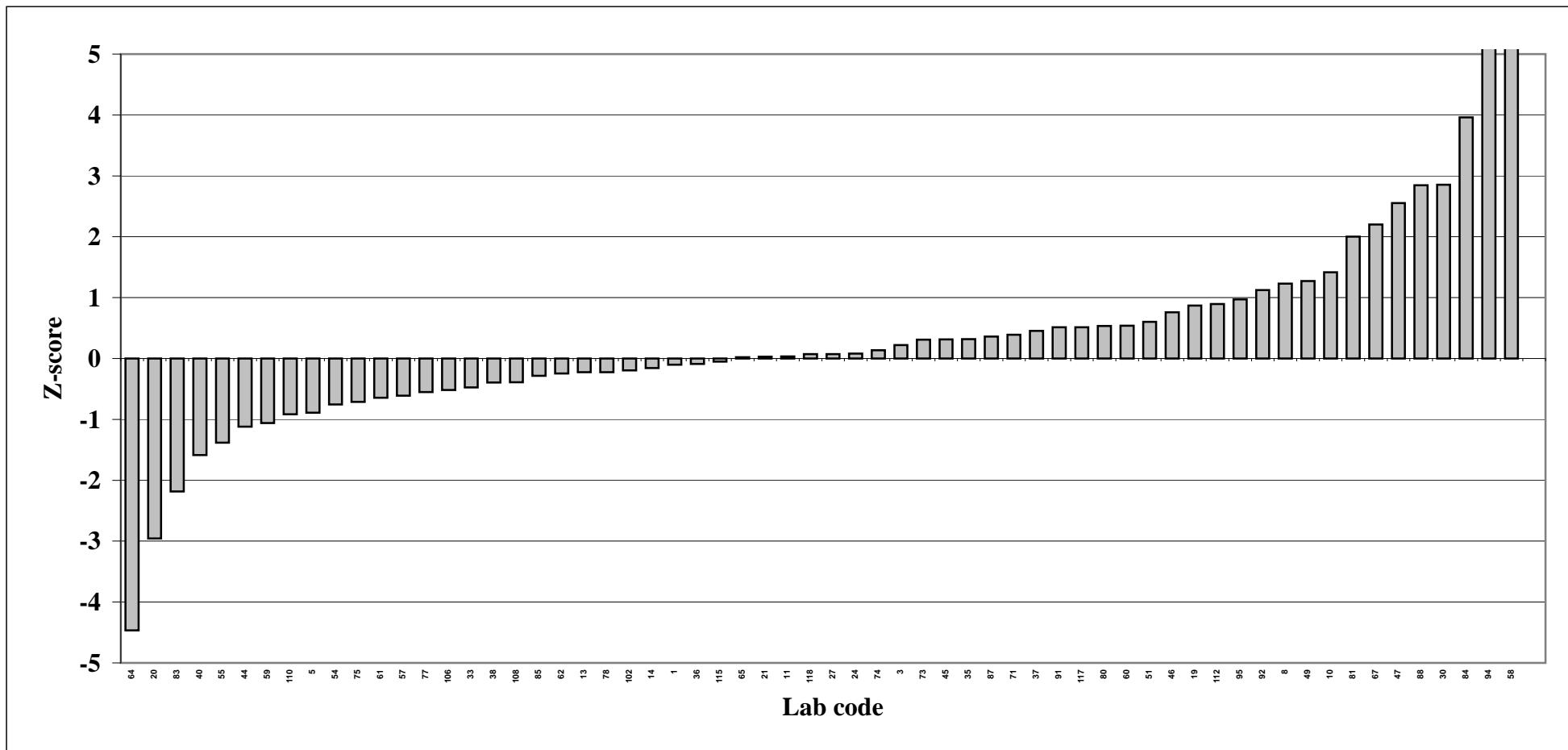
### Z-score Herring; sum PBDE without BDE-209



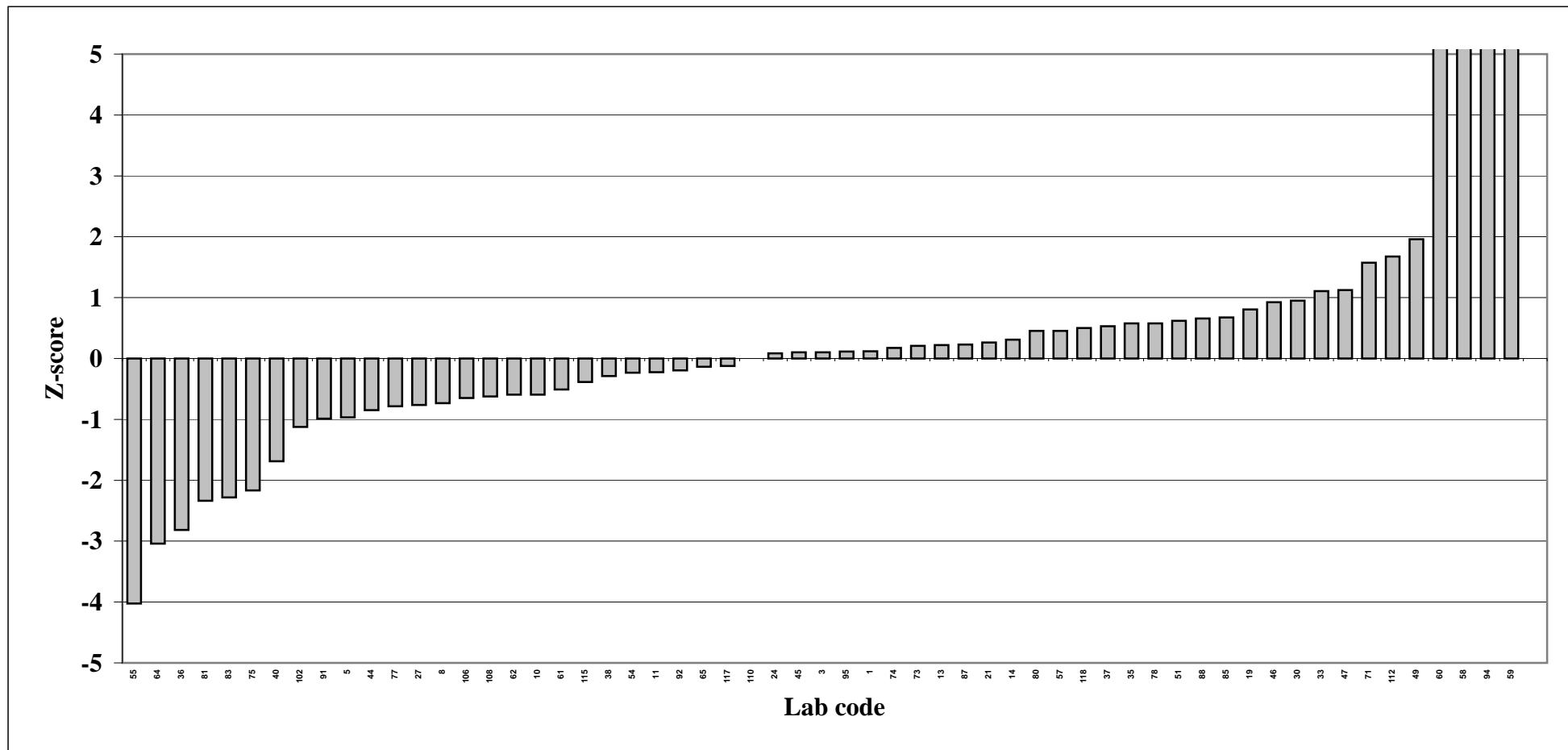
### Z-score Milk; total TEQ



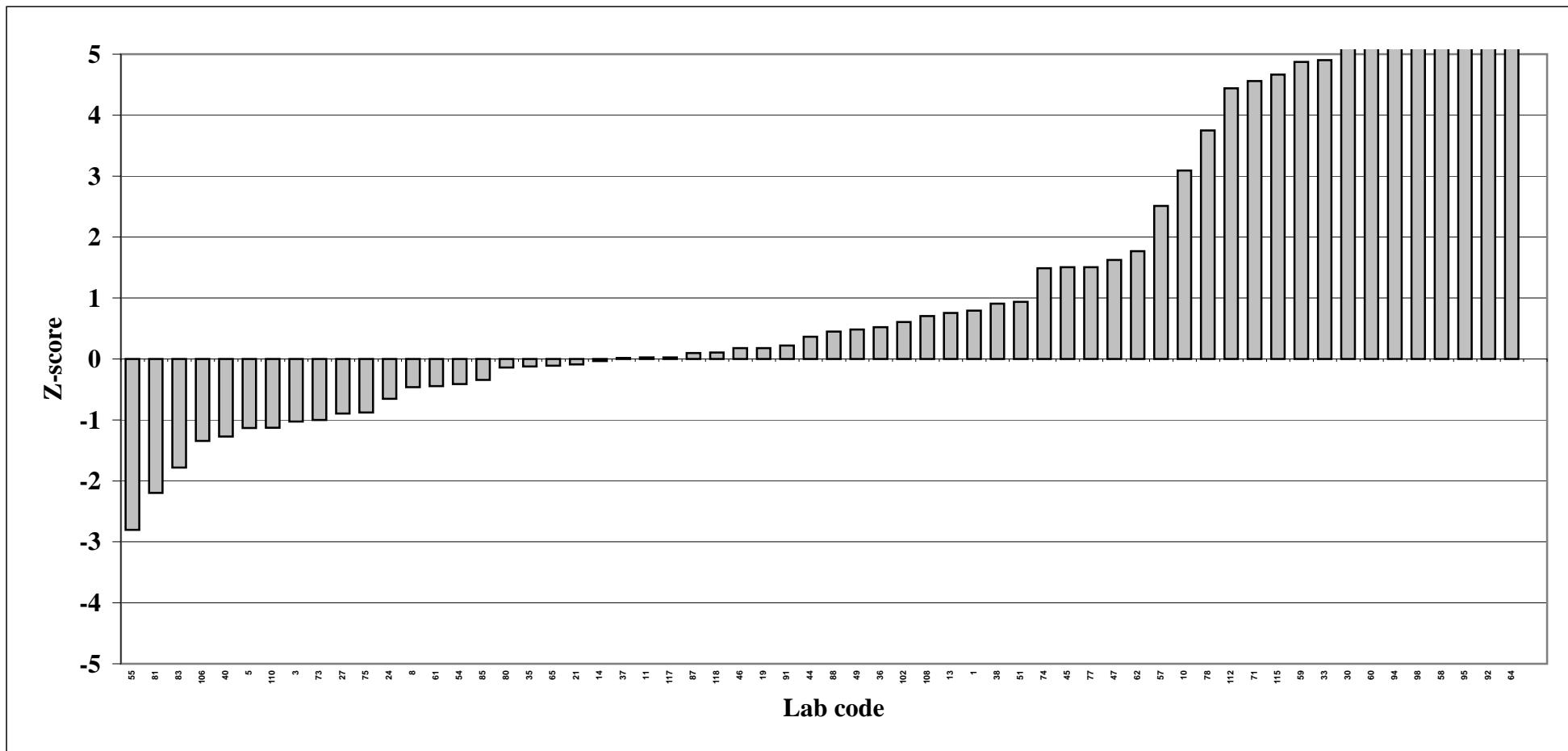
### Z-score Milk; PCDD/PCDF TEQ



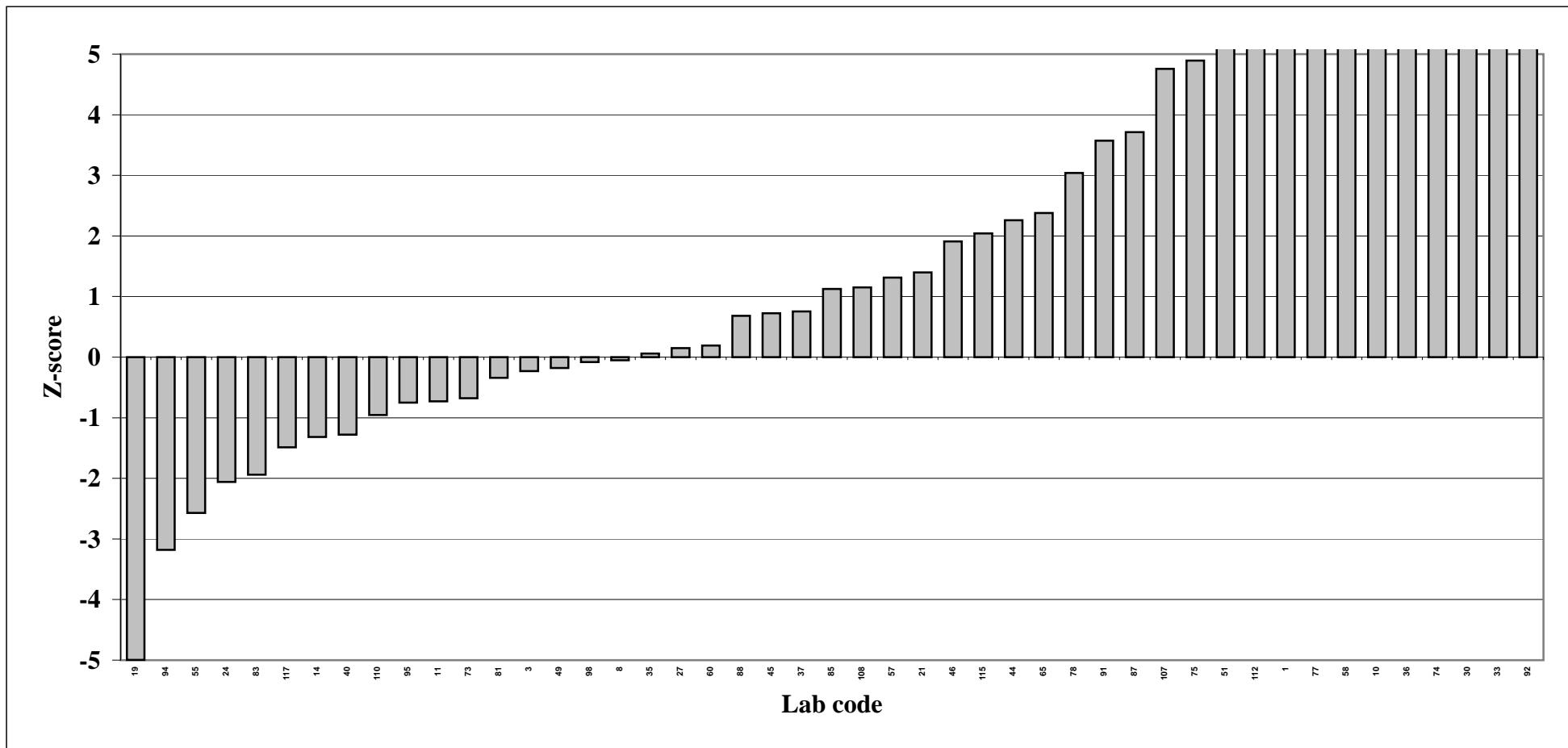
### Z-score Milk; non-ortho PCB TEQ



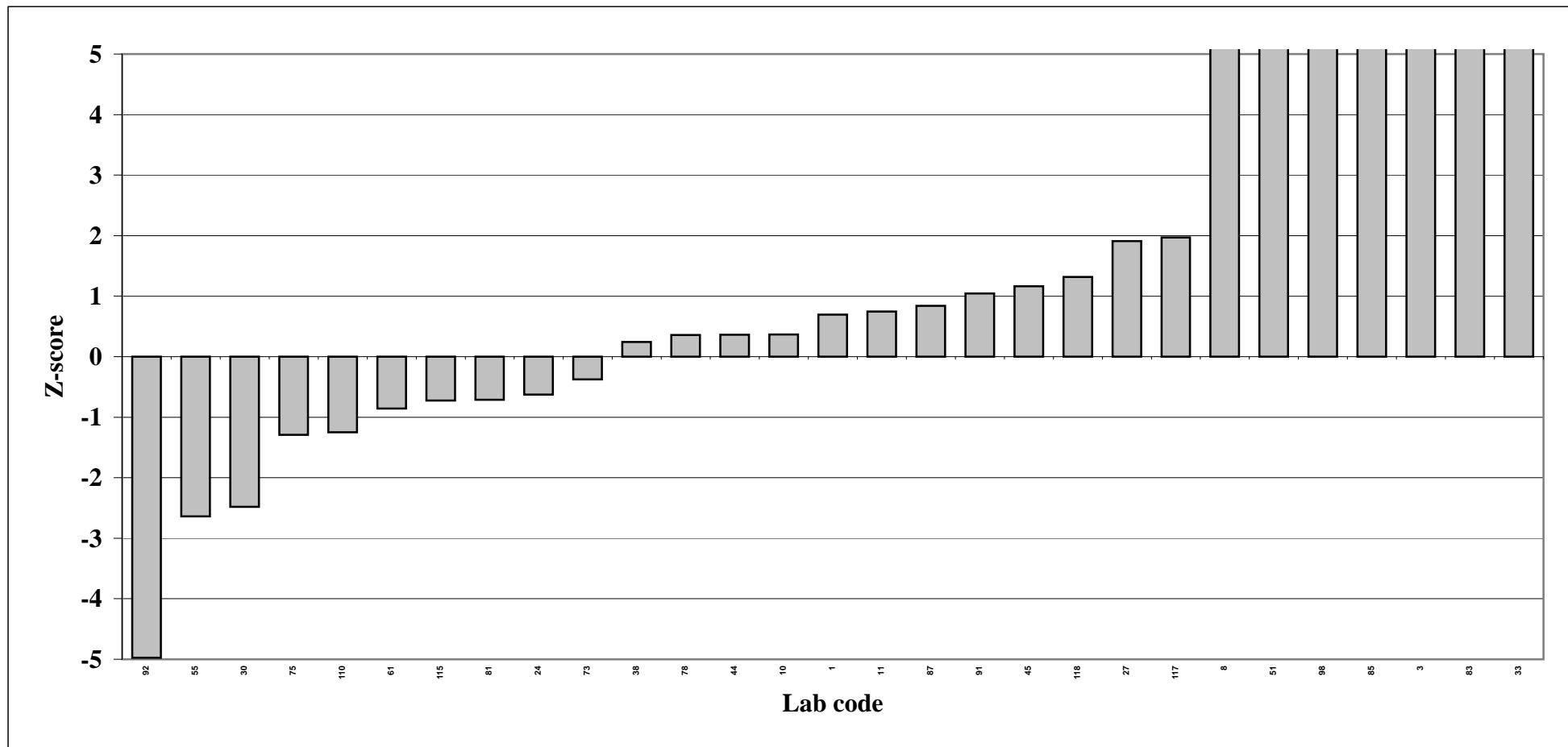
## Z-score Milk; mono-ortho PCB TEQ



### Z-score Milk; sum indicator PCB



### Z-score Milk; sum PBDE without BDE-209







## **Appendix 1:**

Presentation of results  
for analyte solution



## Appendix 1: Presentation of results: Analyte solution

### Statistic calculations for PCDDs, PCDFs, dioxin-like PCBs, indicator PCBs, PBDEs and $\alpha$ -HBCD

The analyte solution contained

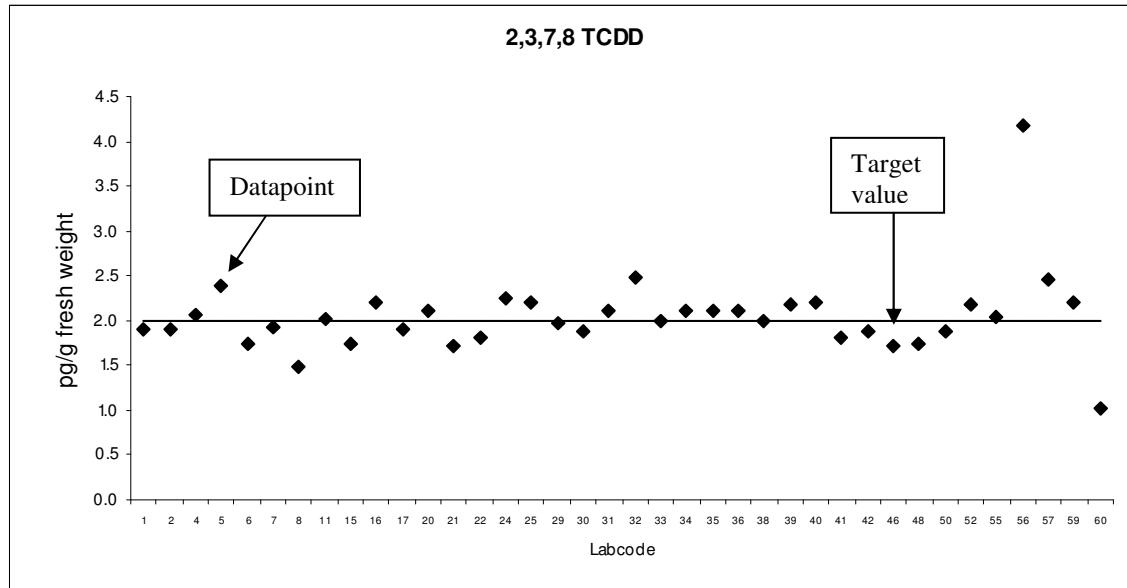
- PCDDs/PCDFs at concentrations of 2:5:10 pg/ $\mu$ l for tetra:penta-hexa-hepta:octa chlorinated dibenzodioxins/furans respectively.
- Non-ortho PCBs at concentration of 10 pg/ $\mu$ l.
- Mono-ortho PCBs and indicator PCBs at concentration of 100 pg/ $\mu$ l.
- PBDE at a concentration of 25 pg/ $\mu$ l, except BDE-209 at 100 pg/ $\mu$ l.
- $\alpha$ -HBCD at a concentration of 500 pg/ $\mu$ l.

These concentrations are called the congeners' target value.

For each congener, the outliers were removed and the consensus calculated according to the following procedure:

1. The median was calculated from all the reported data.
2. Values outside a range of 50 % to 150 % of this median, were defined as outliers and removed from the data set.
3. Median, mean and standard deviation were re-calculated from the remaining data. This median and mean were called consensus median and mean.

The diagram shows the target value and the reported data. Values outside a range of 50 % to 150 % of "median of all values", were defined as outliers and are not shown in the plot.



### Z-Scores of individual congeners

Z-scores of each congener were calculated for each laboratory according to the following equation:

$$z = (x - \bar{X})/\sigma$$

Where  $x$  = reported value;  $\bar{X}$  = assigned value (consensus);  $\sigma$  = target value for standard deviation. A  $\sigma$  of 20% of the consensus was used, i.e. z-scores between +1 and -1 reflect a deviation of  $\pm 20\%$  from the consensus value.

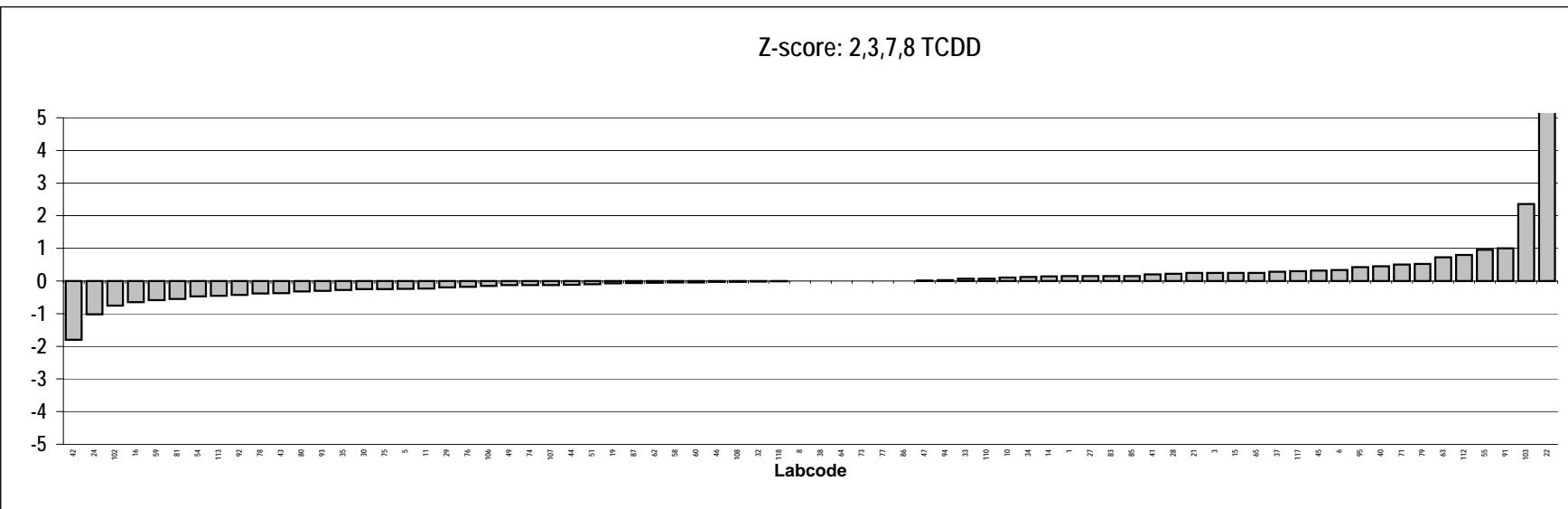
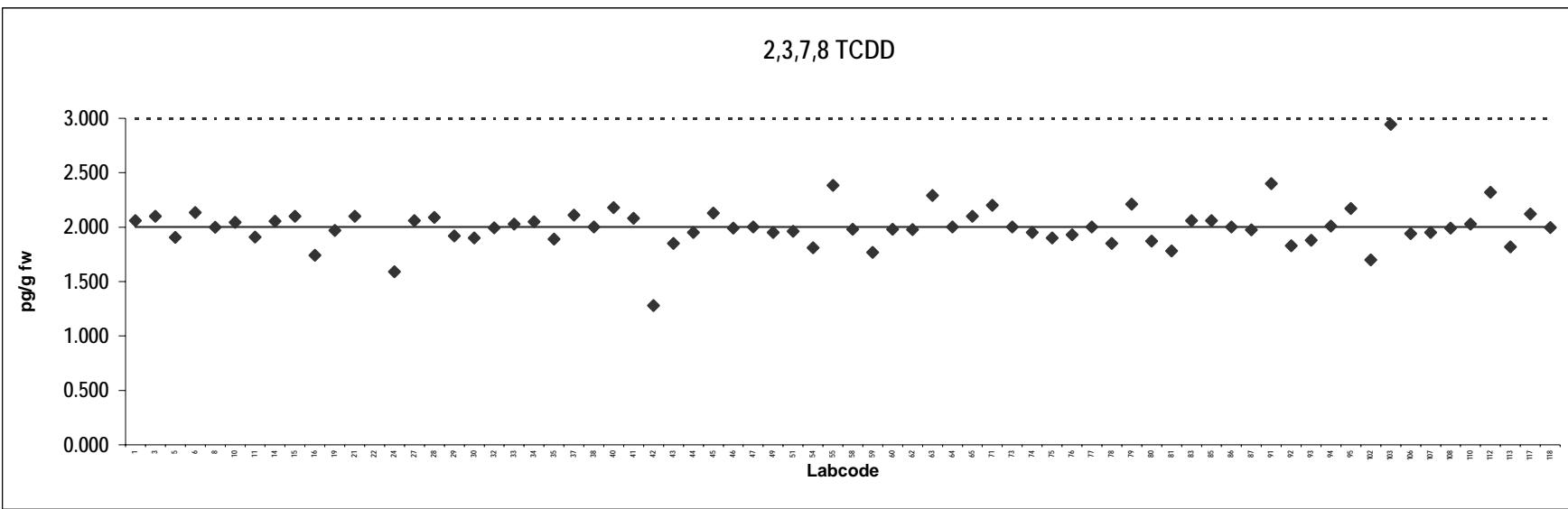


**Analyte solution**  
**Congener: 2,3,7,8 TCDD**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	2.1		74	2.0	
3	2.1		75	1.9	
5	1.9		76	1.9	
6	2.1		77	2.0	
8	2.0		78	1.8	
10	2.0		79	2.2	
11	1.9		80	1.9	
14	2.1		81	1.8	
15	2.1		83	2.1	
16	1.7		85	2.1	
19	2.0		86	2.0	
21	2.1		87	2.0	
22	19	Outlier	91	2.4	
24	1.6		92	1.8	
27	2.1		93	1.9	
28	2.1		94	2.0	
29	1.9		95	2.2	
30	1.9		102	1.7	
32	2.0		103	2.9	
33	2.0		106	1.9	
34	2.1		107	2.0	
35	1.9		108	2.0	
37	2.1		110	2.0	
38	2.0		112	2.3	
40	2.2		113	1.8	
41	2.1		117	2.1	
42	1.3		118	2.0	
43	1.9				
44	2.0				
45	2.1				
46	2.0				
47	2.0				
49	2.0				
51	2.0				
54	1.8				
55	2.4				
58	2.0				
59	1.8				
60	2.0				
62	2.0				
63	2.3				
64	2.0				
65	2.1				
71	2.2				
73	2.0				

**Consensus statistics**

Consensus median, pg/g	2.0
Median all values pg/g	2.0
Consensus mean, pg/g	2.0
Standard deviation, pg/g	0.20
Relative standard deviation, %	10
No. of values reported	72
No. of values removed	1
No. of reported non-detects	0

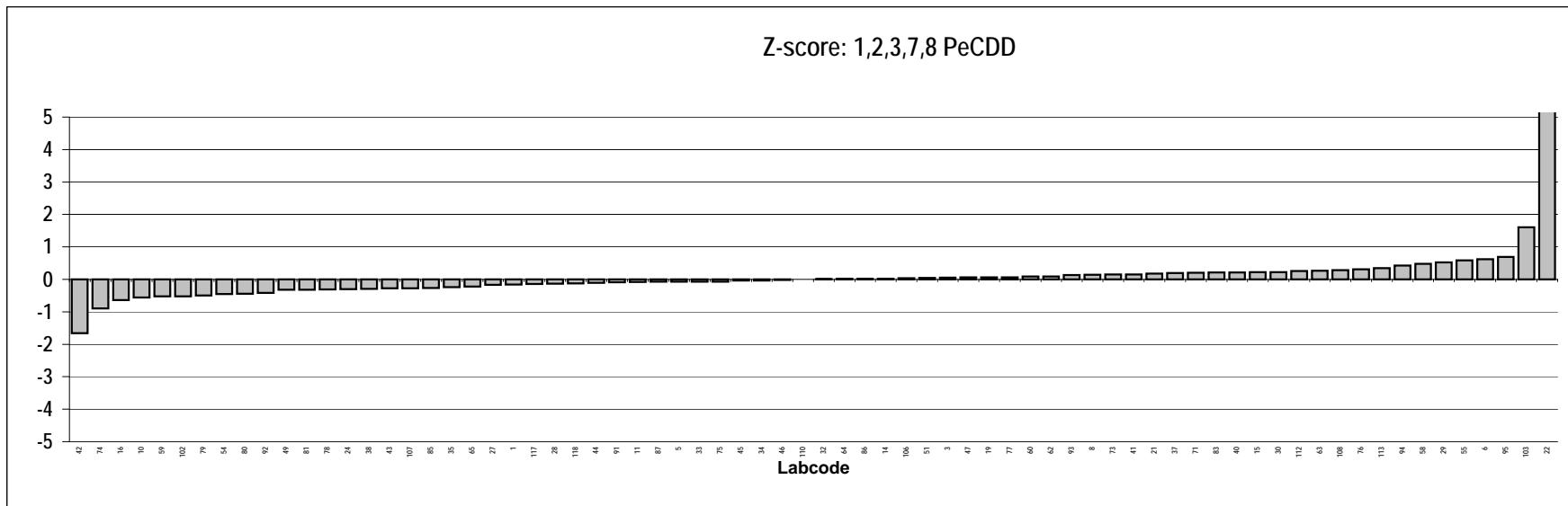
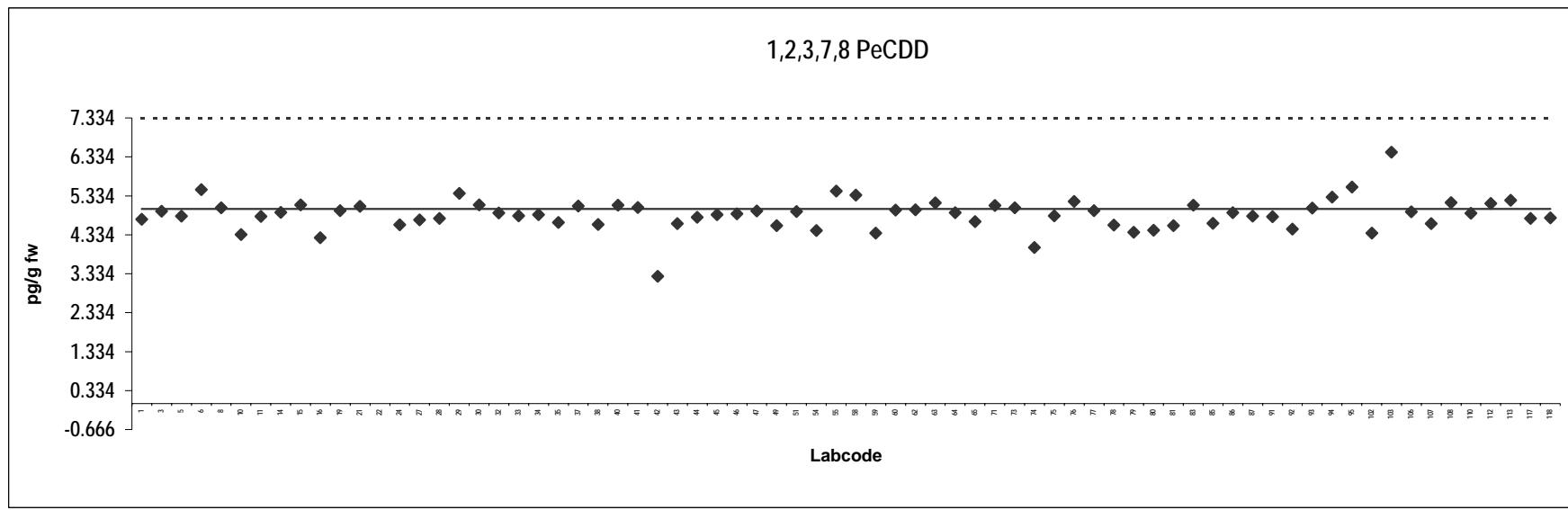


**Analyte solution**  
**Congener: 1,2,3,7,8 PeCDD**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	4.7		74	4.0	
3	4.9		75	4.8	
5	4.8		76	5.2	
6	5.5		77	5.0	
8	5.0		78	4.6	
10	4.3		79	4.4	
11	4.8		80	4.5	
14	4.9		81	4.6	
15	5.1		83	5.1	
16	4.3		85	4.6	
19	5.0		86	4.9	
21	5.1		87	4.8	
22	47	Outlier	91	4.8	
24	4.6		92	4.5	
27	4.7		93	5.0	
28	4.8		94	5.3	
29	5.4		95	5.6	
30	5.1		102	4.4	
32	4.9		103	6.5	
33	4.8		106	4.9	
34	4.9		107	4.6	
35	4.7		108	5.2	
37	5.1		110	4.9	
38	4.6		112	5.1	
40	5.1		113	5.2	
41	5.0		117	4.8	
42	3.3		118	4.8	
43	4.6				
44	4.8				
45	4.8				
46	4.9				
47	4.9				
49	4.6				
51	4.9				
54	4.4				
55	5.5				
58	5.4				
59	4.4				
60	5.0				
62	5.0				
63	5.2				
64	4.9				
65	4.7				
71	5.1				
73	5.0				

**Consensus statistics**

Consensus median, pg/g	4.9
Median all values pg/g	4.9
Consensus mean, pg/g	4.9
Standard deviation, pg/g	0.40
Relative standard deviation, %	8.3
No. of values reported	72
No. of values removed	1
No. of reported non-detects	0

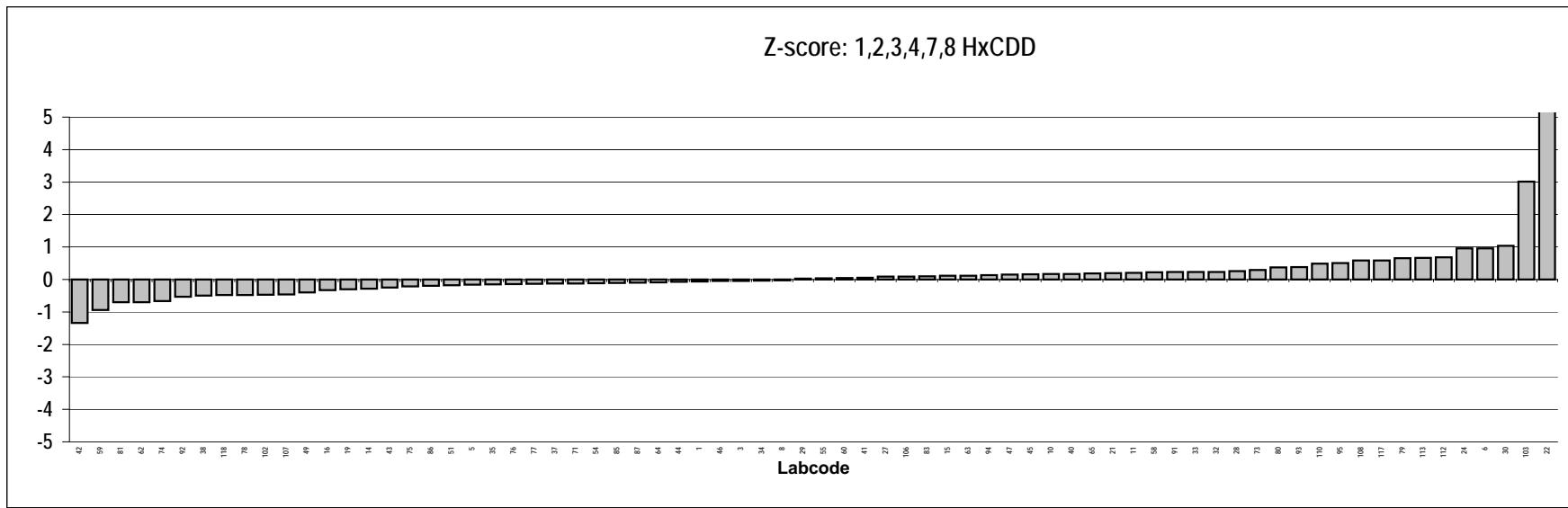
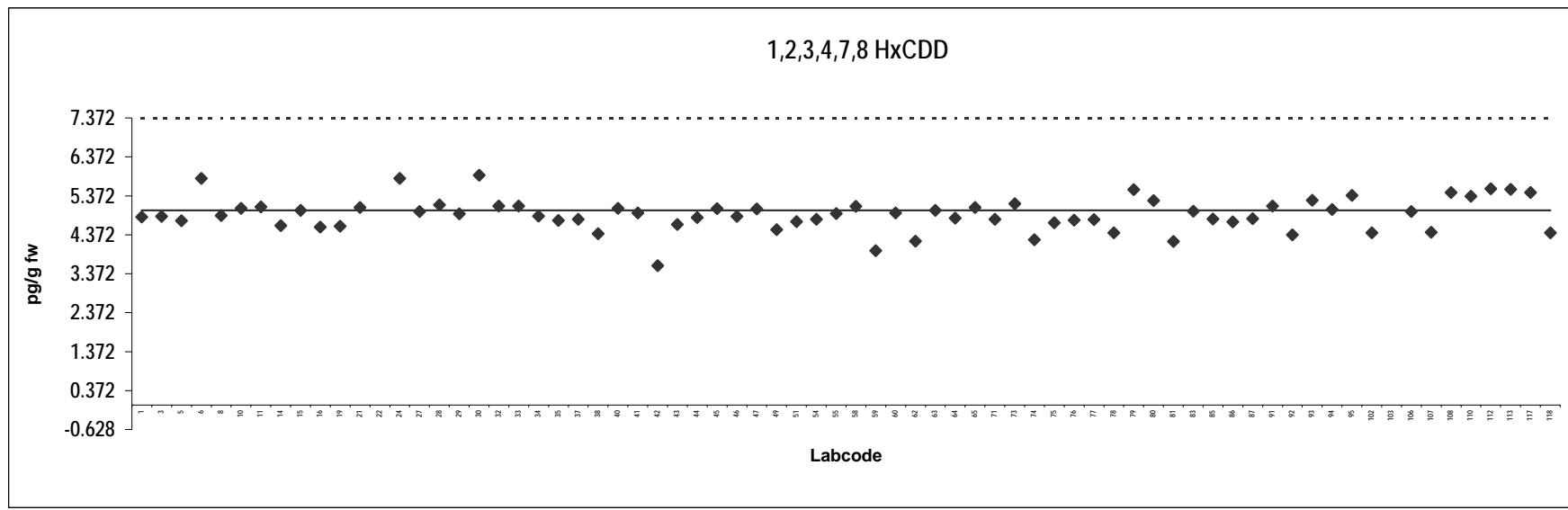


**Analyte solution**  
**Congener: 1,2,3,4,7,8 HxCDD**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	4.8		74	4.2	
3	4.8		75	4.7	
5	4.7		76	4.8	
6	5.8		77	4.8	
8	4.9		78	4.4	
10	5.1		79	5.5	
11	5.1		80	5.3	
14	4.6		81	4.2	
15	5.0		83	5.0	
16	4.6		85	4.8	
19	4.6		86	4.7	
21	5.1		87	4.8	
22	47	Outlier	91	5.1	
24	5.8		92	4.4	
27	5.0		93	5.3	
28	5.1		94	5.0	
29	4.9		95	5.4	
30	5.9		102	4.4	
32	5.1		103	7.8	Outlier
33	5.1		106	5.0	
34	4.9		107	4.4	
35	4.7		108	5.5	
37	4.8		110	5.4	
38	4.4		112	5.6	
40	5.1		113	5.5	
41	4.9		117	5.5	
42	3.6		118	4.4	
43	4.6				
44	4.8				
45	5.0				
46	4.8				
47	5.0				
49	4.5				
51	4.7				
54	4.8				
55	4.9				
58	5.1				
59	4.0				
60	4.9				
62	4.2				
63	5.0				
64	4.8				
65	5.1				
71	4.8				
73	5.2				

**Consensus statistics**

Consensus median, pg/g	4.9
Median all values pg/g	4.9
Consensus mean, pg/g	4.9
Standard deviation, pg/g	0.42
Relative standard deviation, %	8.5
No. of values reported	72
No. of values removed	2
No. of reported non-detects	0

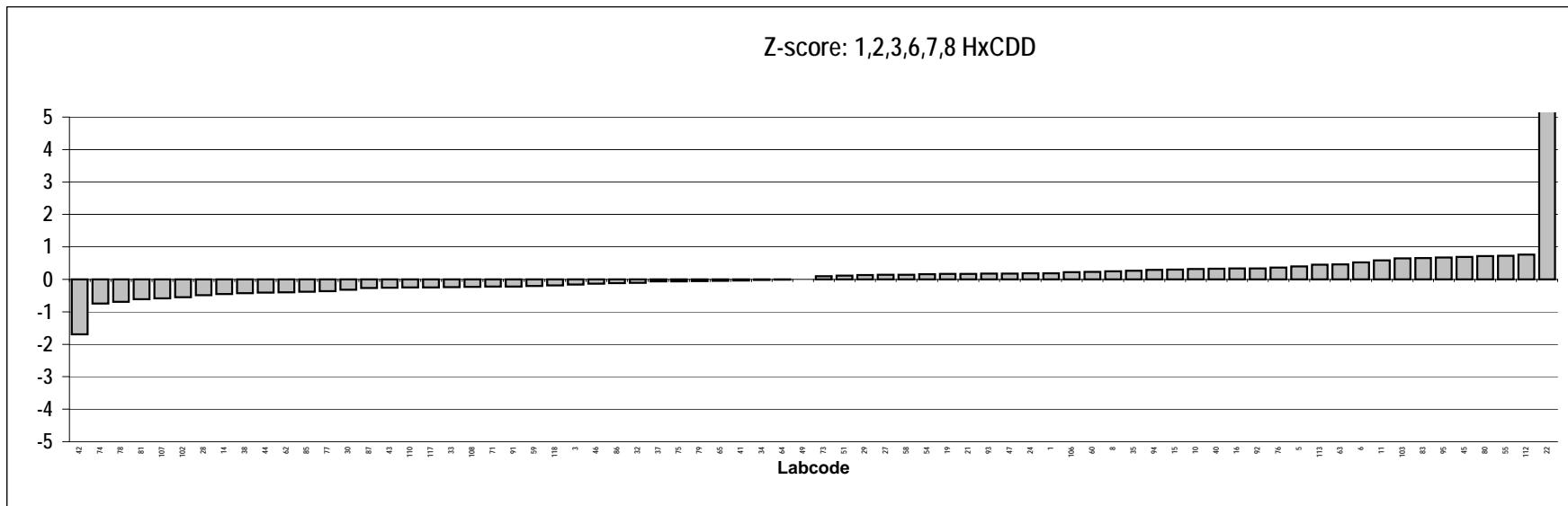
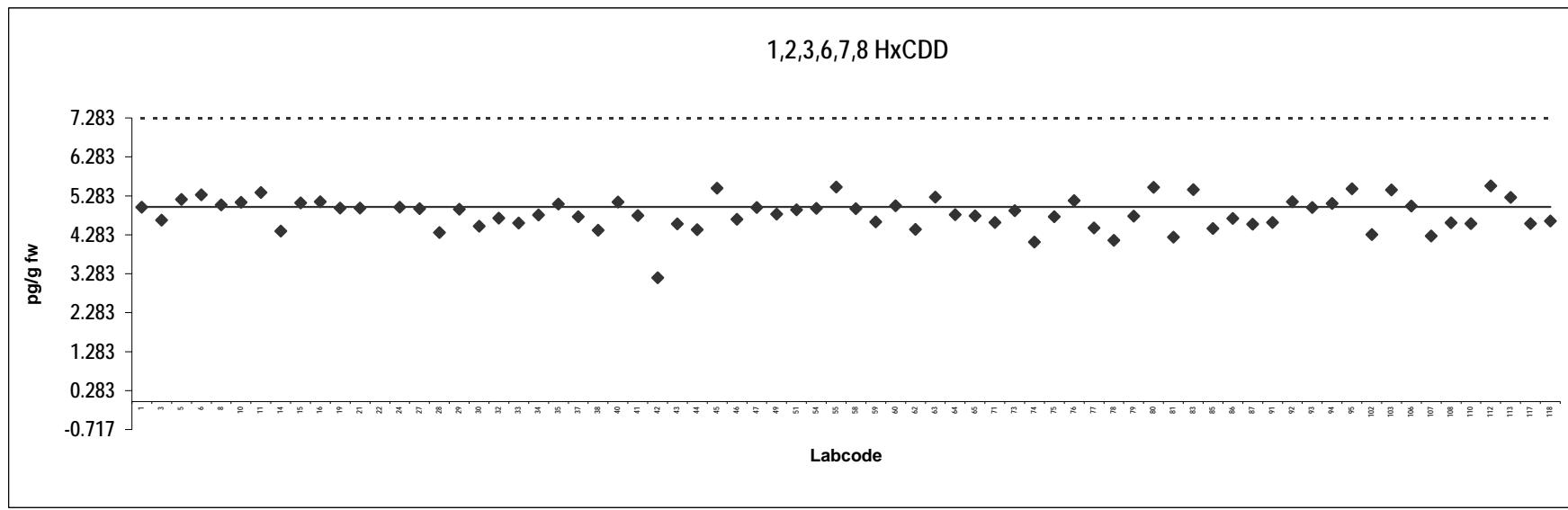


**Analyte solution**  
**Congener: 1,2,3,6,7,8 HxCDD**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.0		74	4.1	
3	4.7		75	4.8	
5	5.2		76	5.2	
6	5.3		77	4.5	
8	5.0		78	4.1	
10	5.1		79	4.8	
11	5.4		80	5.5	
14	4.4		81	4.2	
15	5.1		83	5.4	
16	5.1		85	4.4	
19	5.0		86	4.7	
21	5.0		87	4.6	
22	47	Outlier	91	4.6	
24	5.0		92	5.1	
27	5.0		93	5.0	
28	4.3		94	5.1	
29	4.9		95	5.5	
30	4.5		102	4.3	
32	4.7		103	5.4	
33	4.6		106	5.0	
34	4.8		107	4.3	
35	5.1		108	4.6	
37	4.7		110	4.6	
38	4.4		112	5.5	
40	5.1		113	5.2	
41	4.8		117	4.6	
42	3.2		118	4.6	
43	4.6				
44	4.4				
45	5.5				
46	4.7				
47	5.0				
49	4.8				
51	4.9				
54	5.0				
55	5.5				
58	5.0				
59	4.6				
60	5.0				
62	4.4				
63	5.3				
64	4.8				
65	4.8				
71	4.6				
73	4.9				

**Consensus statistics**

Consensus median, pg/g	4.8
Median all values pg/g	4.9
Consensus mean, pg/g	4.8
Standard deviation, pg/g	0.41
Relative standard deviation, %	8.5
No. of values reported	72
No. of values removed	1
No. of reported non-detects	0

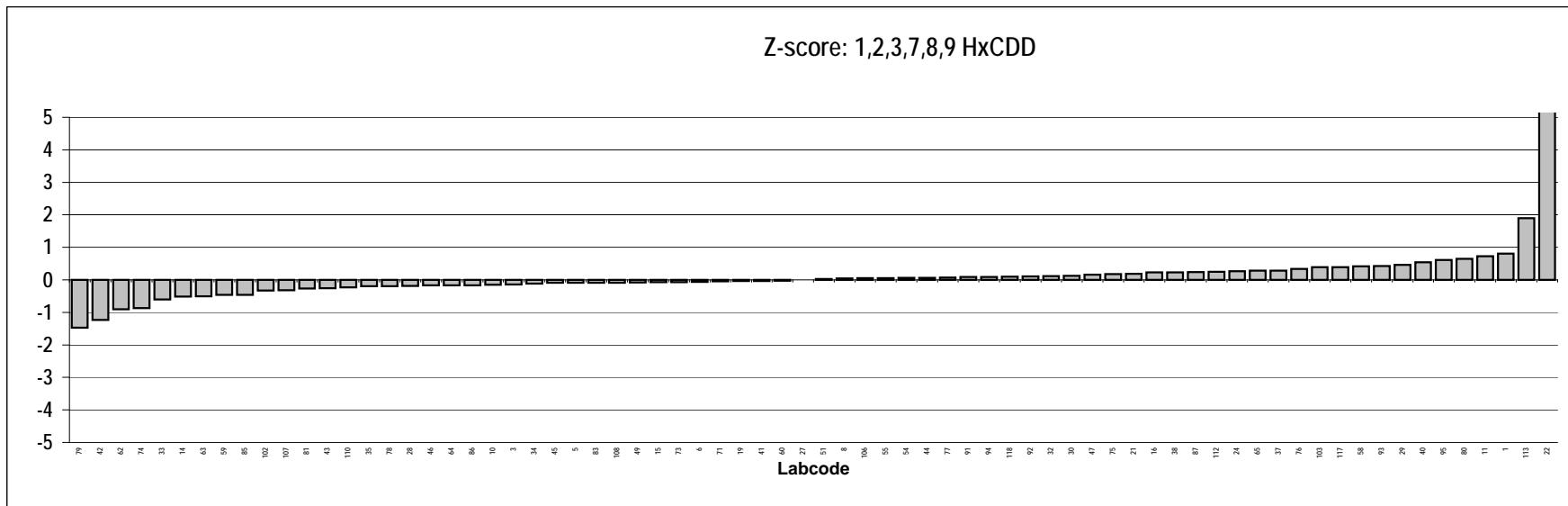
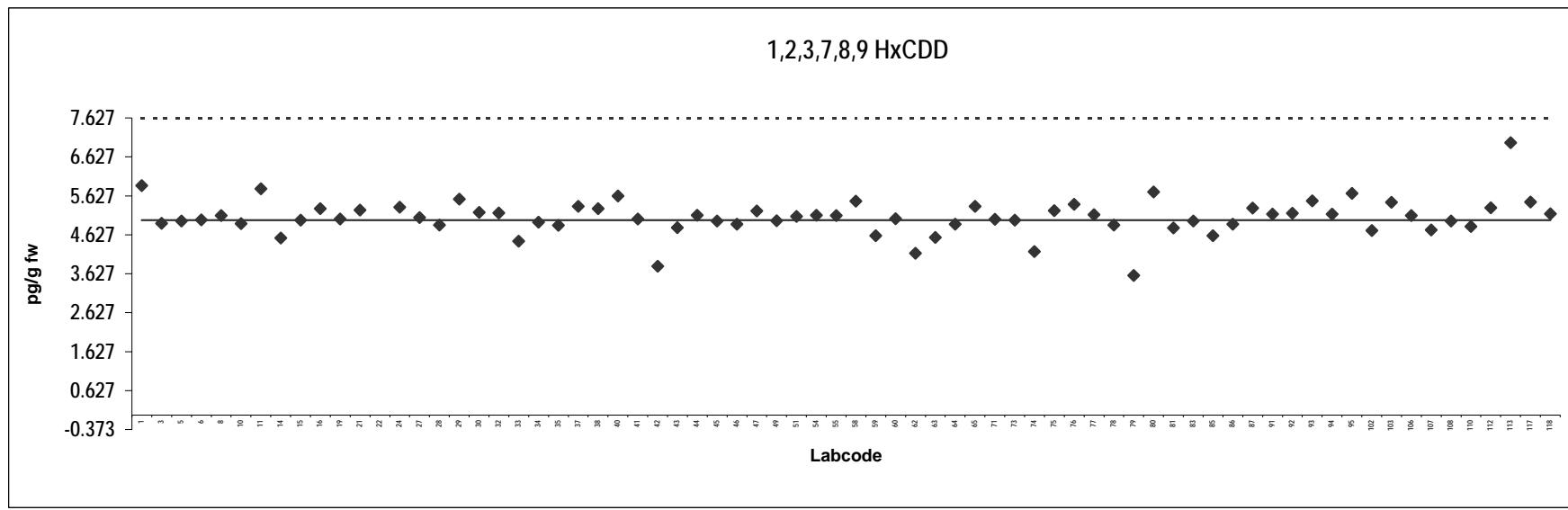


**Analyte solution**  
**Congener: 1,2,3,7,8,9 HxCDD**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.9		74	4.2	
3	4.9		75	5.3	
5	5.0		76	5.4	
6	5.0		77	5.1	
8	5.1		78	4.9	
10	4.9		79	3.6	
11	5.8		80	5.7	
14	4.5		81	4.8	
15	5.0		83	5.0	
16	5.3		85	4.6	
19	5.0		86	4.9	
21	5.3		87	5.3	
22	49	Outlier	91	5.2	
24	5.3		92	5.2	
27	5.1		93	5.5	
28	4.9		94	5.2	
29	5.5		95	5.7	
30	5.2		102	4.7	
32	5.2		103	5.5	
33	4.5		106	5.1	
34	5.0		107	4.8	
35	4.9		108	5.0	
37	5.4		110	4.8	
38	5.3		112	5.3	
40	5.6		113	7.0	
41	5.0		117	5.5	
42	3.8		118	5.2	
43	4.8				
44	5.1				
45	5.0				
46	4.9				
47	5.2				
49	5.0				
51	5.1				
54	5.1				
55	5.1				
58	5.5				
59	4.6				
60	5.0				
62	4.2				
63	4.6				
64	4.9				
65	5.4				
71	5.0				
73	5.0				

**Consensus statistics**

Consensus median, pg/g	5.1
Median all values pg/g	5.1
Consensus mean, pg/g	5.1
Standard deviation, pg/g	0.47
Relative standard deviation, %	9.2
No. of values reported	72
No. of values removed	1
No. of reported non-detects	0

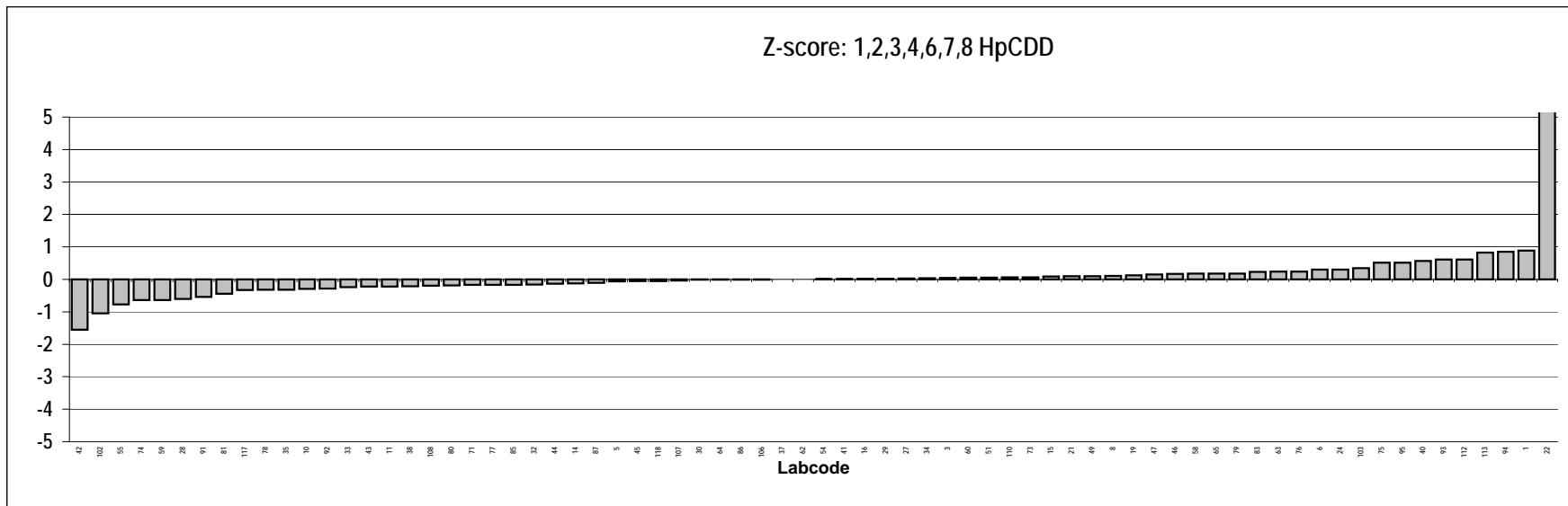
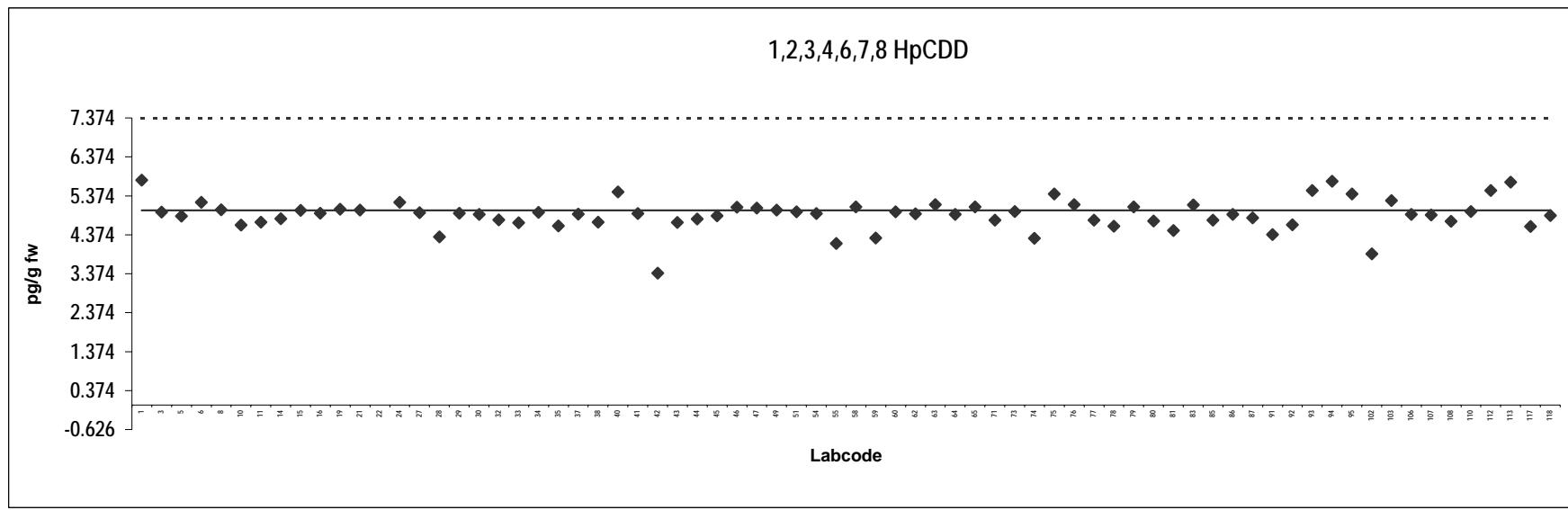


**Analyte solution**  
**Congener: 1,2,3,4,6,7,8 HpCDD**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.8		74	4.3	
3	5.0		75	5.4	
5	4.9		76	5.2	
6	5.2		77	4.8	
8	5.0		78	4.6	
10	4.6		79	5.1	
11	4.7		80	4.7	
14	4.8		81	4.5	
15	5.0		83	5.1	
16	4.9		85	4.8	
19	5.0		86	4.9	
21	5.0		87	4.8	
22	48	Outlier	91	4.4	
24	5.2		92	4.6	
27	4.9		93	5.5	
28	4.3		94	5.8	
29	4.9		95	5.4	
30	4.9		102	3.9	
32	4.8		103	5.3	
33	4.7		106	4.9	
34	5.0		107	4.9	
35	4.6		108	4.7	
37	4.9		110	5.0	
38	4.7		112	5.5	
40	5.5		113	5.7	
41	4.9		117	4.6	
42	3.4		118	4.9	
43	4.7				
44	4.8				
45	4.9				
46	5.1				
47	5.1				
49	5.0				
51	5.0				
54	4.9				
55	4.2				
58	5.1				
59	4.3				
60	5.0				
62	4.9				
63	5.2				
64	4.9				
65	5.1				
71	4.7				
73	5.0				

**Consensus statistics**

Consensus median, pg/g	4.9
Median all values pg/g	4.9
Consensus mean, pg/g	4.9
Standard deviation, pg/g	0.39
Relative standard deviation, %	8.0
No. of values reported	72
No. of values removed	1
No. of reported non-detects	0

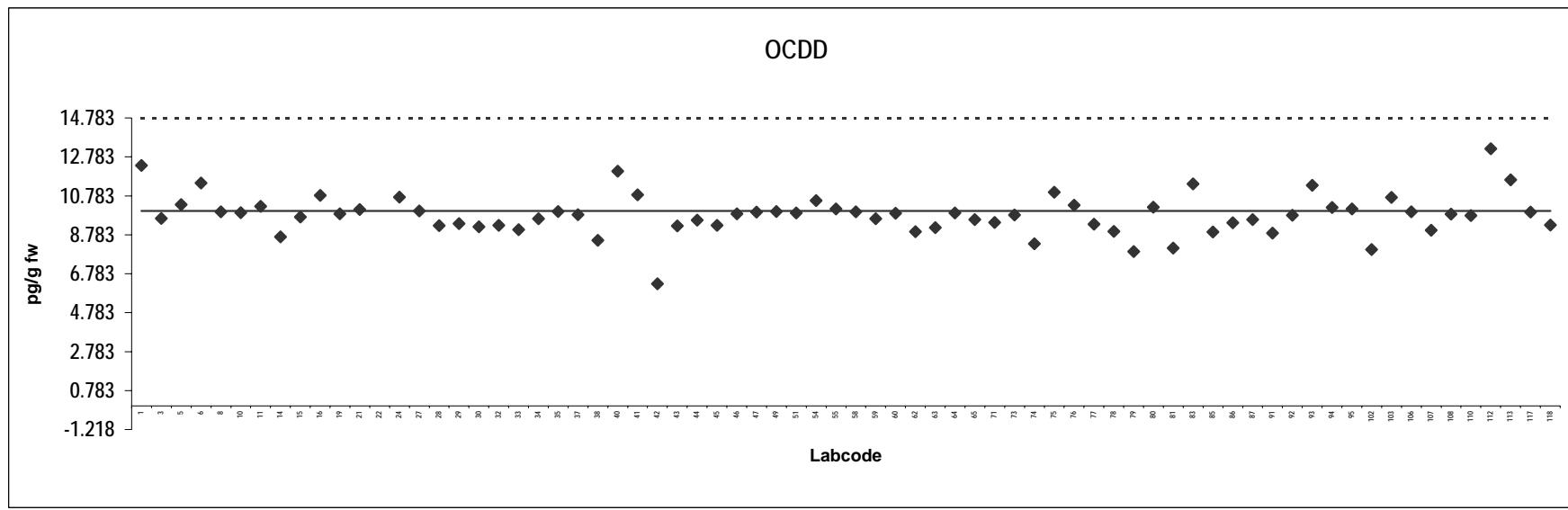


**Analyte solution**  
Congener: OCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	12		74	8.3	
3	9.6		75	11	
5	10		76	10	
6	11		77	9.3	
8	10.0		78	9.0	
10	9.9		79	7.9	
11	10		80	10	
14	8.7		81	8.1	
15	9.7		83	11	
16	11		85	8.9	
19	9.9		86	9.4	
21	10		87	9.6	
22	96	Outlier	91	8.9	
24	11		92	9.8	
27	10		93	11	
28	9.2		94	10	
29	9.4		95	10	
30	9.2		102	8.0	
32	9.3		103	11	
33	9.0		106	10	
34	9.6		107	9.0	
35	10		108	9.9	
37	9.8		110	9.8	
38	8.5		112	13	
40	12		113	12	
41	11		117	10	
42	6.3		118	9.3	
43	9.2				
44	9.5				
45	9.3				
46	9.9				
47	9.9				
49	10				
51	9.9				
54	11				
55	10				
58	10				
59	9.6				
60	9.9				
62	8.9				
63	9.2				
64	9.9				
65	9.6				
71	9.4				
73	9.8				

**Consensus statistics**

Consensus median, pg/g	9.9
Median all values pg/g	9.9
Consensus mean, pg/g	9.8
Standard deviation, pg/g	1.0
Relative standard deviation, %	11
No. of values reported	72
No. of values removed	1
No. of reported non-detects	0

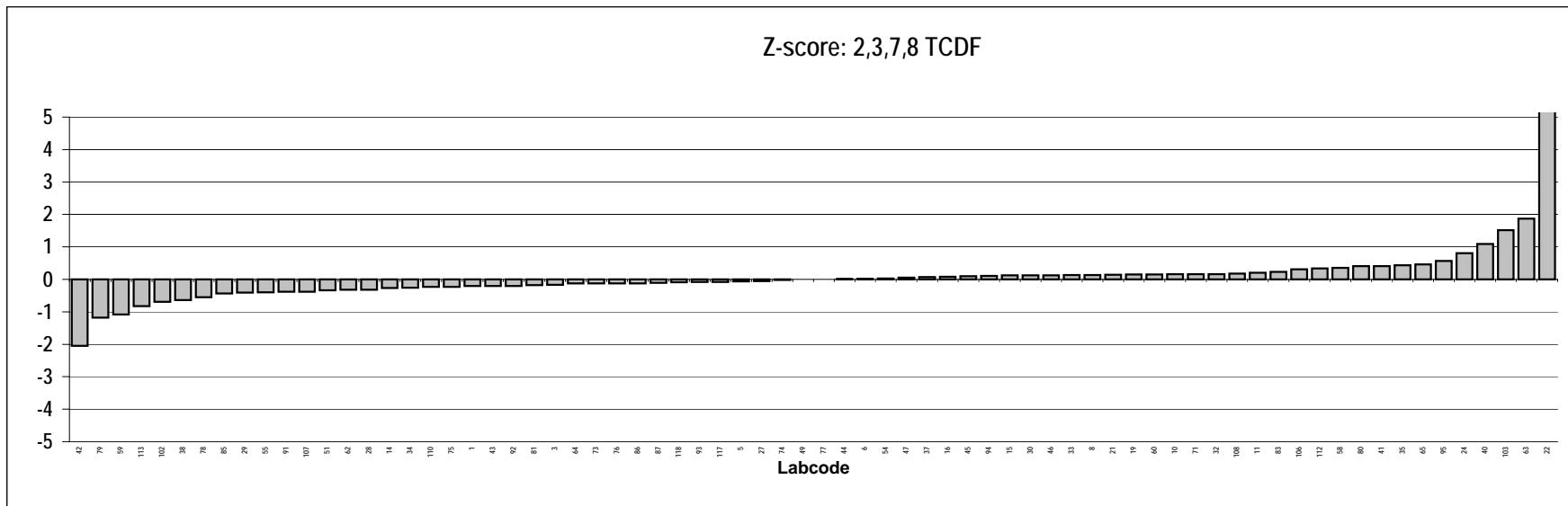
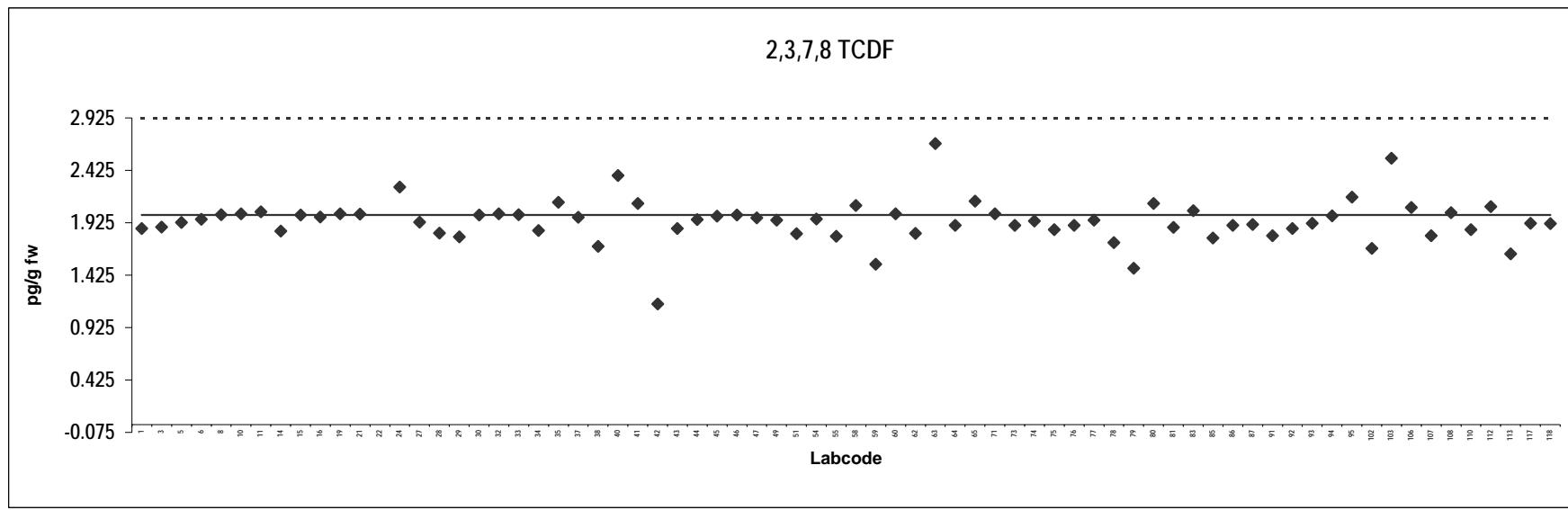


**Analyte solution**  
**Congener: 2,3,7,8 TCDF**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.9		74	1.9	
3	1.9		75	1.9	
5	1.9		76	1.9	
6	2.0		77	2.0	
8	2.0		78	1.7	
10	2.0		79	1.5	
11	2.0		80	2.1	
14	1.8		81	1.9	
15	2.0		83	2.0	
16	2.0		85	1.8	
19	2.0		86	1.9	
21	2.0		87	1.9	
22	2.0	Outlier	91	1.8	
24	2.3		92	1.9	
27	1.9		93	1.9	
28	1.8		94	2.0	
29	1.8		95	2.2	
30	2.0		102	1.7	
32	2.0		103	2.5	
33	2.0		106	2.1	
34	1.9		107	1.8	
35	2.1		108	2.0	
37	2.0		110	1.9	
38	1.7		112	2.1	
40	2.4		113	1.6	
41	2.1		117	1.9	
42	1.2		118	1.9	
43	1.9				
44	2.0				
45	2.0				
46	2.0				
47	2.0				
49	2.0				
51	1.8				
54	2.0				
55	1.8				
58	2.1				
59	1.5				
60	2.0				
62	1.8				
63	2.7				
64	1.9				
65	2.1				
71	2.0				
73	1.9				

**Consensus statistics**

Consensus median, pg/g	2.0
Median all values pg/g	2.0
Consensus mean, pg/g	1.9
Standard deviation, pg/g	0.21
Relative standard deviation, %	11
No. of values reported	72
No. of values removed	1
No. of reported non-detects	0

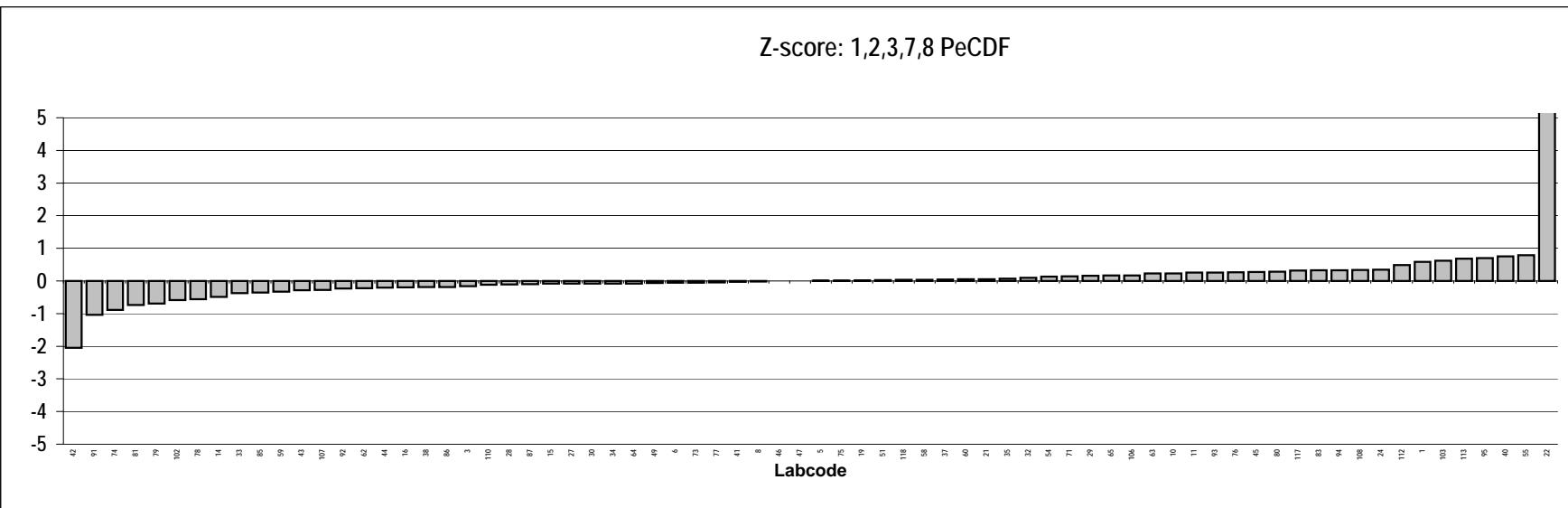
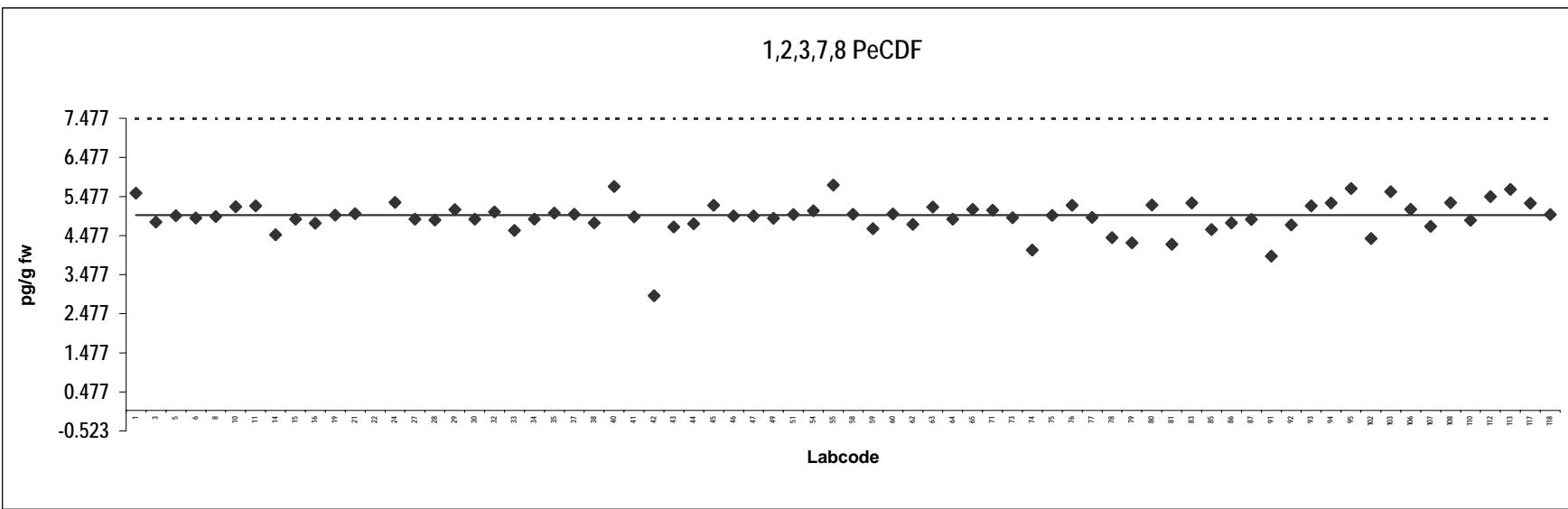


**Analyte solution**  
**Congener: 1,2,3,7,8 PeCDF**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.6		74	4.1	
3	4.8		75	5.0	
5	5.0		76	5.3	
6	4.9		77	4.9	
8	5.0		78	4.4	
10	5.2		79	4.3	
11	5.2		80	5.3	
14	4.5		81	4.3	
15	4.9		83	5.3	
16	4.8		85	4.6	
19	5.0		86	4.8	
21	5.0		87	4.9	
22	48	Outlier	91	4.0	
24	5.3		92	4.8	
27	4.9		93	5.2	
28	4.9		94	5.3	
29	5.1		95	5.7	
30	4.9		102	4.4	
32	5.1		103	5.6	
33	4.6		106	5.2	
34	4.9		107	4.7	
35	5.1		108	5.3	
37	5.0		110	4.9	
38	4.8		112	5.5	
40	5.7		113	5.7	
41	5.0		117	5.3	
42	2.9		118	5.0	
43	4.7				
44	4.8				
45	5.3				
46	5.0				
47	5.0				
49	4.9				
51	5.0				
54	5.1				
55	5.8				
58	5.0				
59	4.7				
60	5.0				
62	4.8				
63	5.2				
64	4.9				
65	5.2				
71	5.1				
73	4.9				

**Consensus statistics**

Consensus median, pg/g	5.0
Median all values pg/g	5.0
Consensus mean, pg/g	5.0
Standard deviation, pg/g	0.43
Relative standard deviation, %	8.7
No. of values reported	72
No. of values removed	1
No. of reported non-detects	0

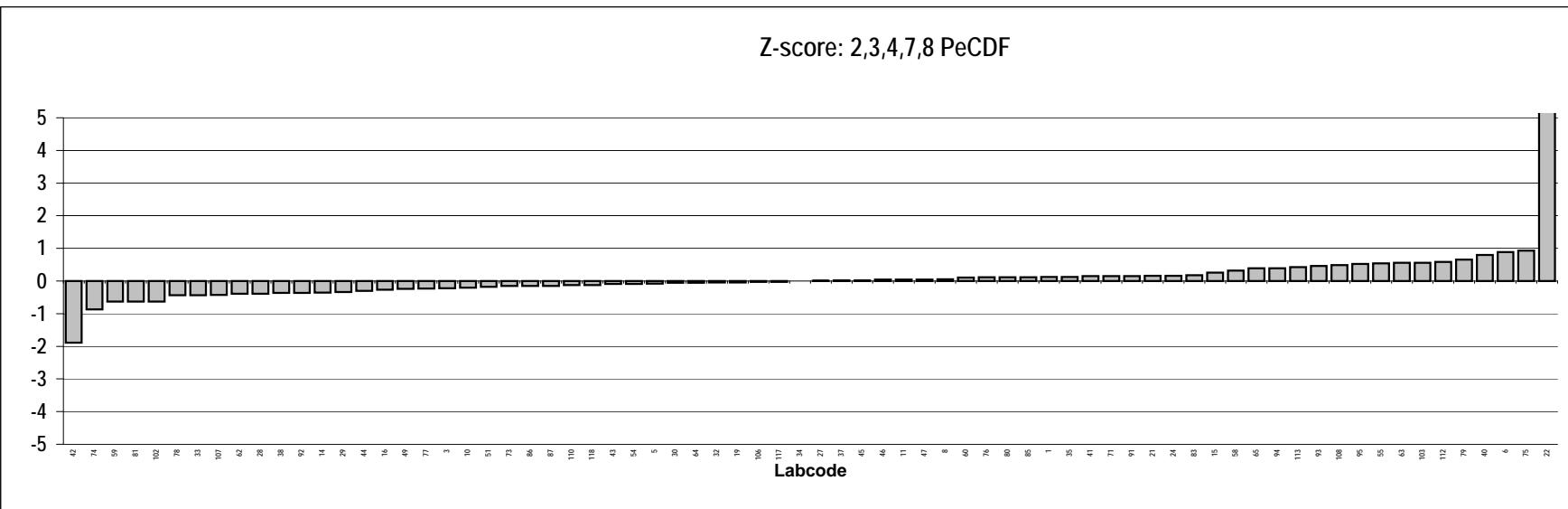
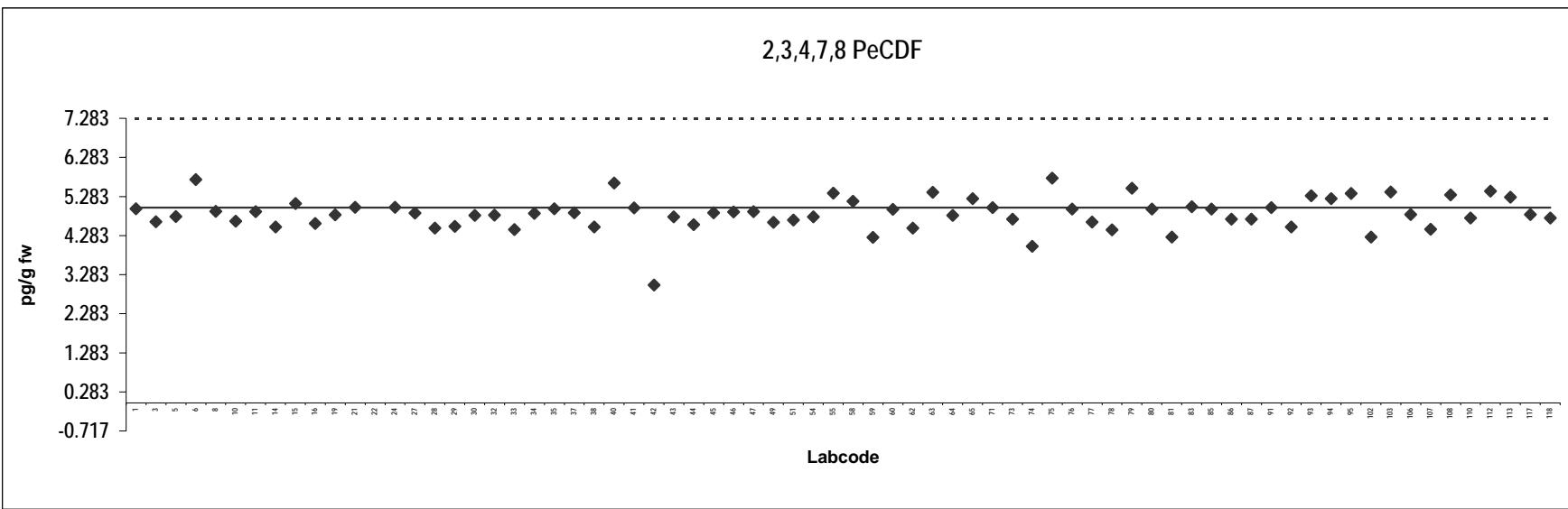


**Analyte solution**  
**Congener: 2,3,4,7,8 PeCDF**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.0		74	4.0	
3	4.6		75	5.8	
5	4.8		76	5.0	
6	5.7		77	4.6	
8	4.9		78	4.4	
10	4.6		79	5.5	
11	4.9		80	5.0	
14	4.5		81	4.2	
15	5.1		83	5.0	
16	4.6		85	5.0	
19	4.8		86	4.7	
21	5.0		87	4.7	
22	48	Outlier	91	5.0	
24	5.0		92	4.5	
27	4.9		93	5.3	
28	4.5		94	5.2	
29	4.5		95	5.4	
30	4.8		102	4.2	
32	4.8		103	5.4	
33	4.4		106	4.8	
34	4.9		107	4.4	
35	5.0		108	5.3	
37	4.9		110	4.7	
38	4.5		112	5.4	
40	5.6		113	5.3	
41	5.0		117	4.8	
42	3.0		118	4.7	
43	4.8				
44	4.6				
45	4.9				
46	4.9				
47	4.9				
49	4.6				
51	4.7				
54	4.8				
55	5.4				
58	5.2				
59	4.2				
60	5.0				
62	4.5				
63	5.4				
64	4.8				
65	5.2				
71	5.0				
73	4.7				

**Consensus statistics**

Consensus median, pg/g	4.9
Median all values pg/g	4.9
Consensus mean, pg/g	4.8
Standard deviation, pg/g	0.42
Relative standard deviation, %	8.6
No. of values reported	72
No. of values removed	1
No. of reported non-detects	0

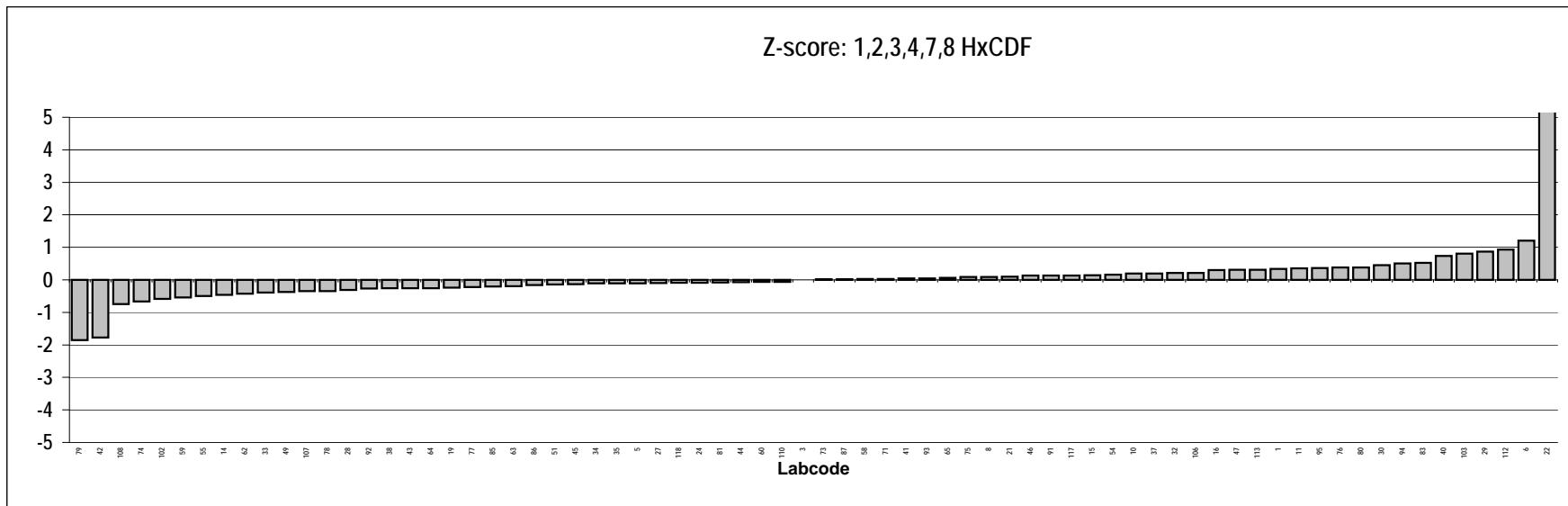
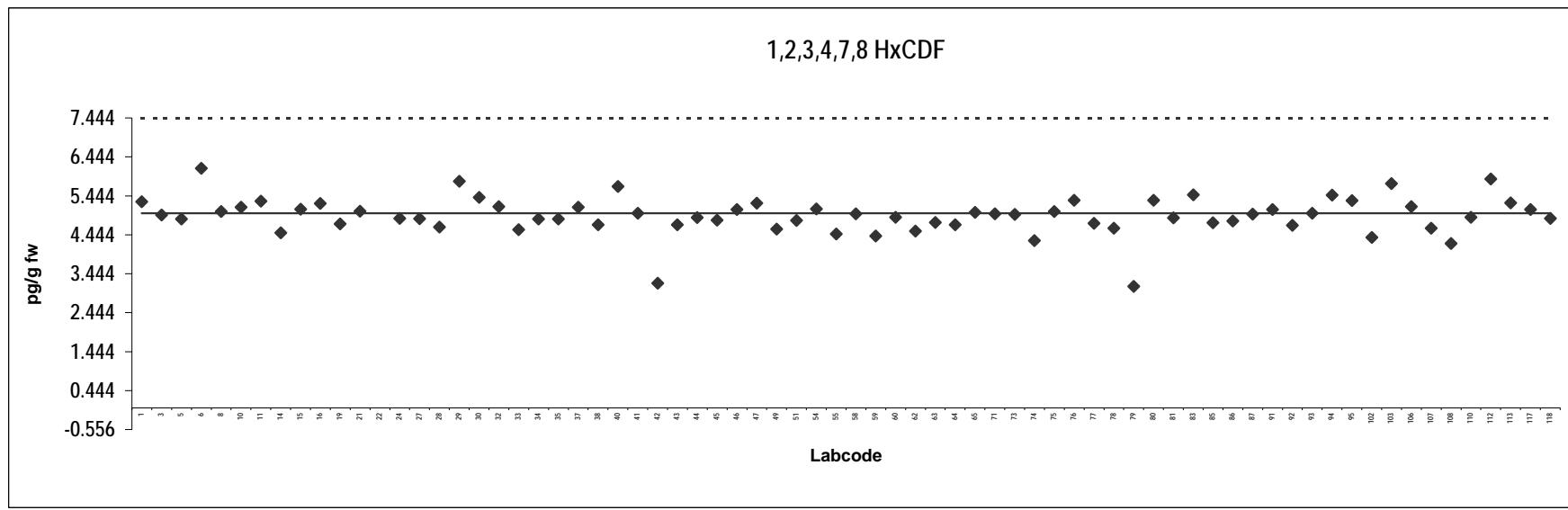


**Analyte solution**  
**Congener: 1,2,3,4,7,8 HxCDF**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.3		74	4.3	
3	5.0		75	5.0	
5	4.9		76	5.3	
6	6.1		77	4.7	
8	5.0		78	4.6	
10	5.1		79	3.1	
11	5.3		80	5.3	
14	4.5		81	4.9	
15	5.1		83	5.5	
16	5.3		85	4.8	
19	4.7		86	4.8	
21	5.0		87	5.0	
22	47	Outlier	91	5.1	
24	4.9		92	4.7	
27	4.9		93	5.0	
28	4.6		94	5.5	
29	5.8		95	5.3	
30	5.4		102	4.4	
32	5.2		103	5.8	
33	4.6		106	5.2	
34	4.9		107	4.6	
35	4.9		108	4.2	
37	5.2		110	4.9	
38	4.7		112	5.9	
40	5.7		113	5.3	
41	5.0		117	5.1	
42	3.2		118	4.9	
43	4.7				
44	4.9				
45	4.8				
46	5.1				
47	5.3				
49	4.6				
51	4.8				
54	5.1				
55	4.5				
58	5.0				
59	4.4				
60	4.9				
62	4.5				
63	4.8				
64	4.7				
65	5.0				
71	5.0				
73	5.0				

**Consensus statistics**

Consensus median, pg/g	5.0
Median all values pg/g	5.0
Consensus mean, pg/g	4.9
Standard deviation, pg/g	0.48
Relative standard deviation, %	10
No. of values reported	72
No. of values removed	1
No. of reported non-detects	0

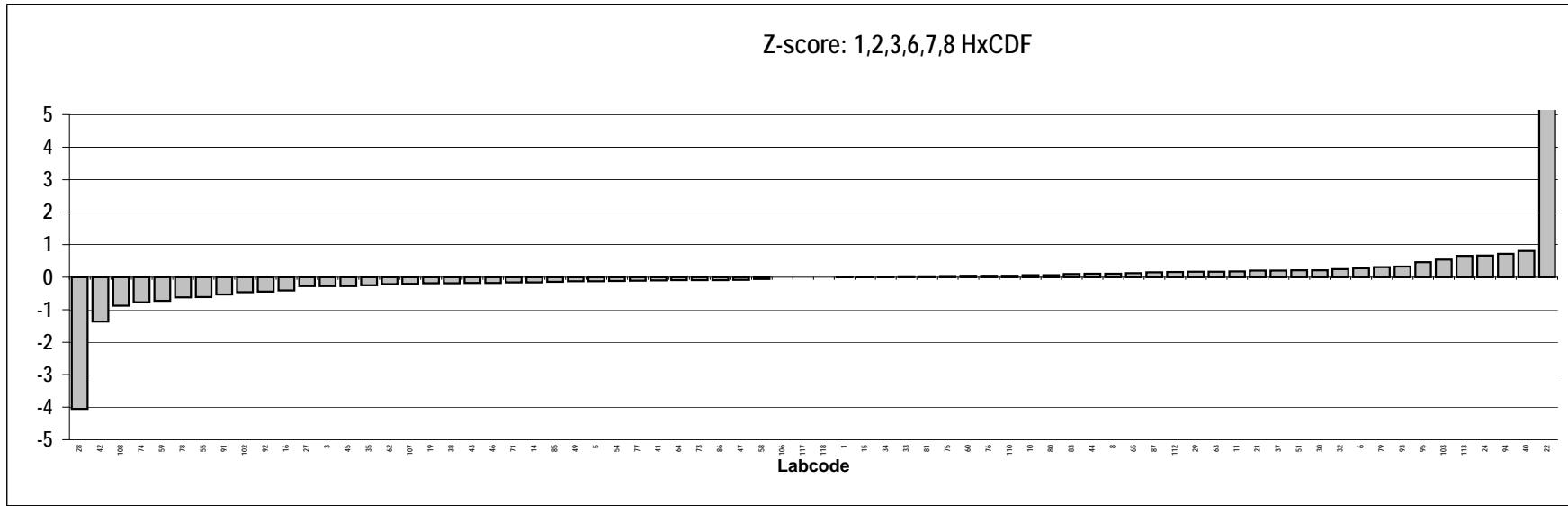
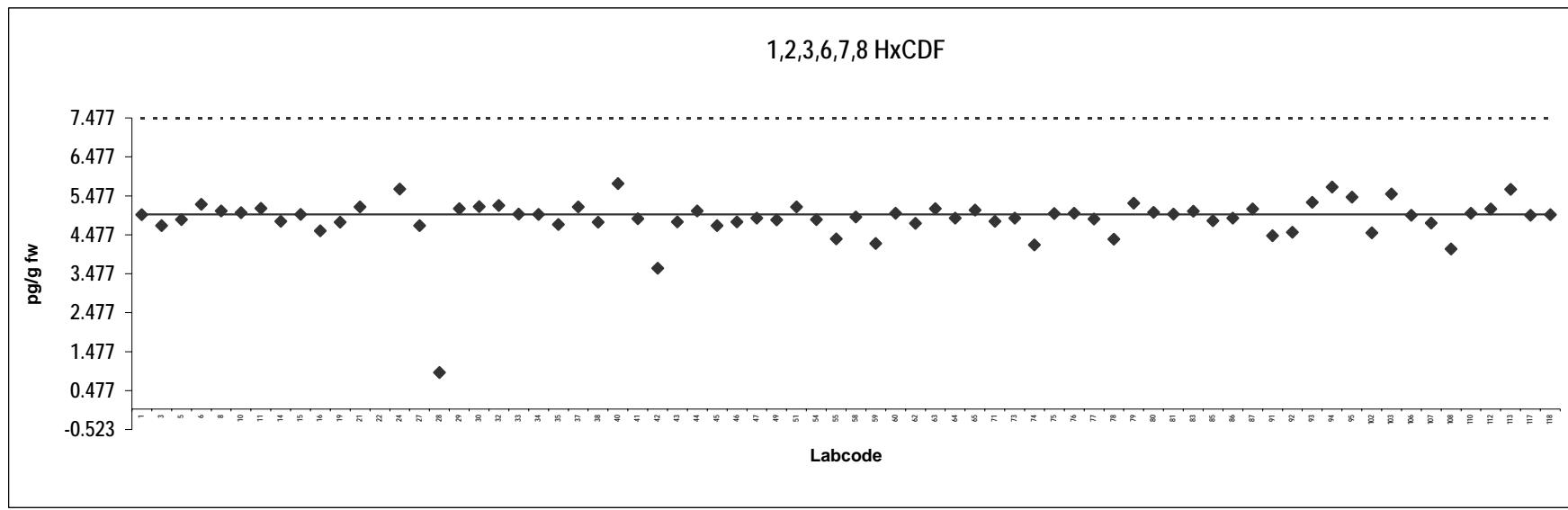


**Analyte solution**  
**Congener: 1,2,3,6,7,8 HxCDF**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.0		74	4.2	
3	4.7		75	5.0	
5	4.9		76	5.0	
6	5.3		77	4.9	
8	5.1		78	4.4	
10	5.0		79	5.3	
11	5.2		80	5.1	
14	4.8		81	5.0	
15	5.0		83	5.1	
16	4.6		85	4.8	
19	4.8		86	4.9	
21	5.2		87	5.1	
22	49	Outlier	91	4.5	
24	5.7		92	4.5	
27	4.7		93	5.3	
28	0.94	Outlier	94	5.7	
29	5.2		95	5.4	
30	5.2		102	4.5	
32	5.2		103	5.5	
33	5.0		106	5.0	
34	5.0		107	4.8	
35	4.7		108	4.1	
37	5.2		110	5.0	
38	4.8		112	5.1	
40	5.8		113	5.6	
41	4.9		117	5.0	
42	3.6		118	5.0	
43	4.8				
44	5.1				
45	4.7				
46	4.8				
47	4.9				
49	4.9				
51	5.2				
54	4.9				
55	4.4				
58	4.9				
59	4.3				
60	5.0				
62	4.8				
63	5.2				
64	4.9				
65	5.1				
71	4.8				
73	4.9				

**Consensus statistics**

Consensus median, pg/g	5.0
Median all values pg/g	5.0
Consensus mean, pg/g	4.9
Standard deviation, pg/g	0.36
Relative standard deviation, %	7.4
No. of values reported	72
No. of values removed	2
No. of reported non-detects	0

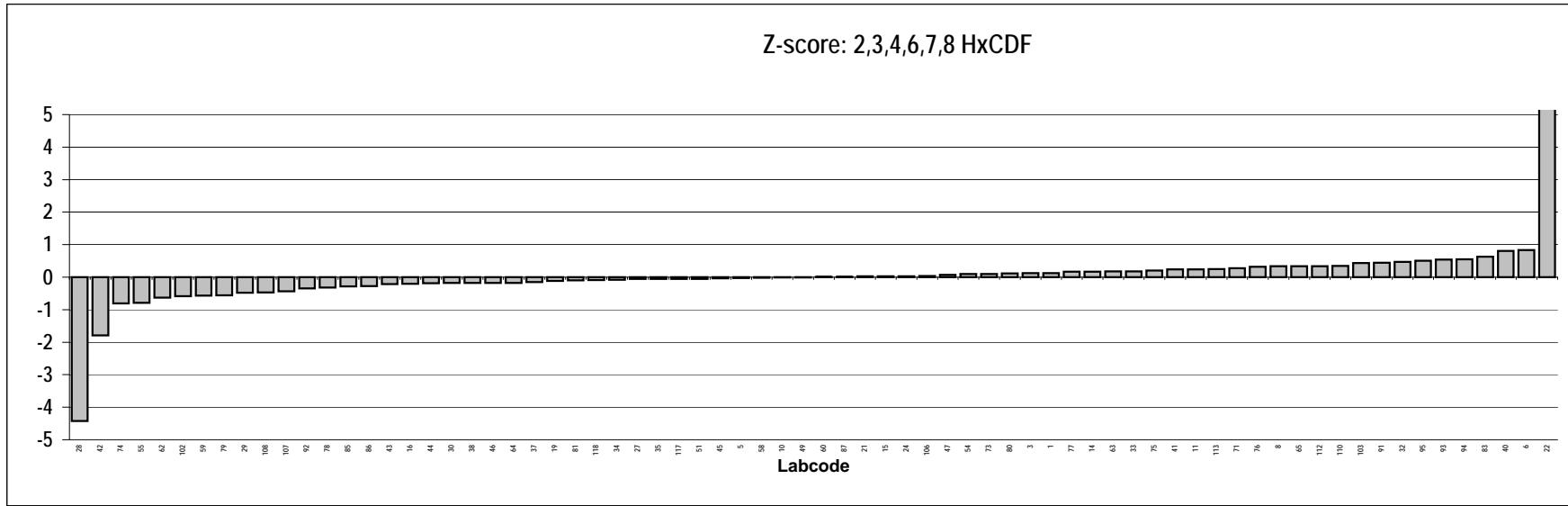
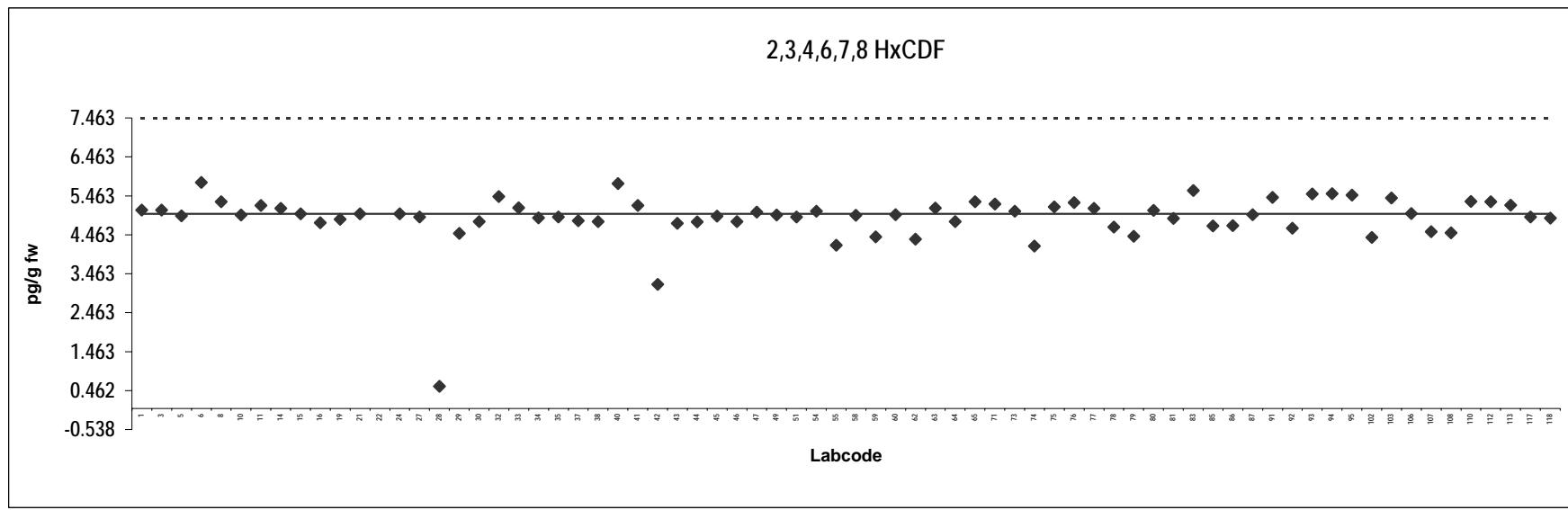


**Analyte solution**  
**Congener: 2,3,4,6,7,8 HxCDF**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.1		74	4.2	
3	5.1		75	5.2	
5	4.9		76	5.3	
6	5.8		77	5.1	
8	5.3		78	4.7	
10	5.0		79	4.4	
11	5.2		80	5.1	
14	5.1		81	4.9	
15	5.0		83	5.6	
16	4.8		85	4.7	
19	4.9		86	4.7	
21	5.0		87	5.0	
22	49	Outlier	91	5.4	
24	5.0		92	4.6	
27	4.9		93	5.5	
28	0.57	Outlier	94	5.5	
29	4.5		95	5.5	
30	4.8		102	4.4	
32	5.4		103	5.4	
33	5.2		106	5.0	
34	4.9		107	4.5	
35	4.9		108	4.5	
37	4.8		110	5.3	
38	4.8		112	5.3	
40	5.8		113	5.2	
41	5.2		117	4.9	
42	3.2		118	4.9	
43	4.8				
44	4.8				
45	4.9				
46	4.8				
47	5.0				
49	5.0				
51	4.9				
54	5.1				
55	4.2				
58	5.0				
59	4.4				
60	5.0				
62	4.4				
63	5.2				
64	4.8				
65	5.3				
71	5.3				
73	5.1				

**Consensus statistics**

Consensus median, pg/g	5.0
Median all values pg/g	5.0
Consensus mean, pg/g	5.0
Standard deviation, pg/g	0.40
Relative standard deviation, %	8.2
No. of values reported	72
No. of values removed	2
No. of reported non-detects	0

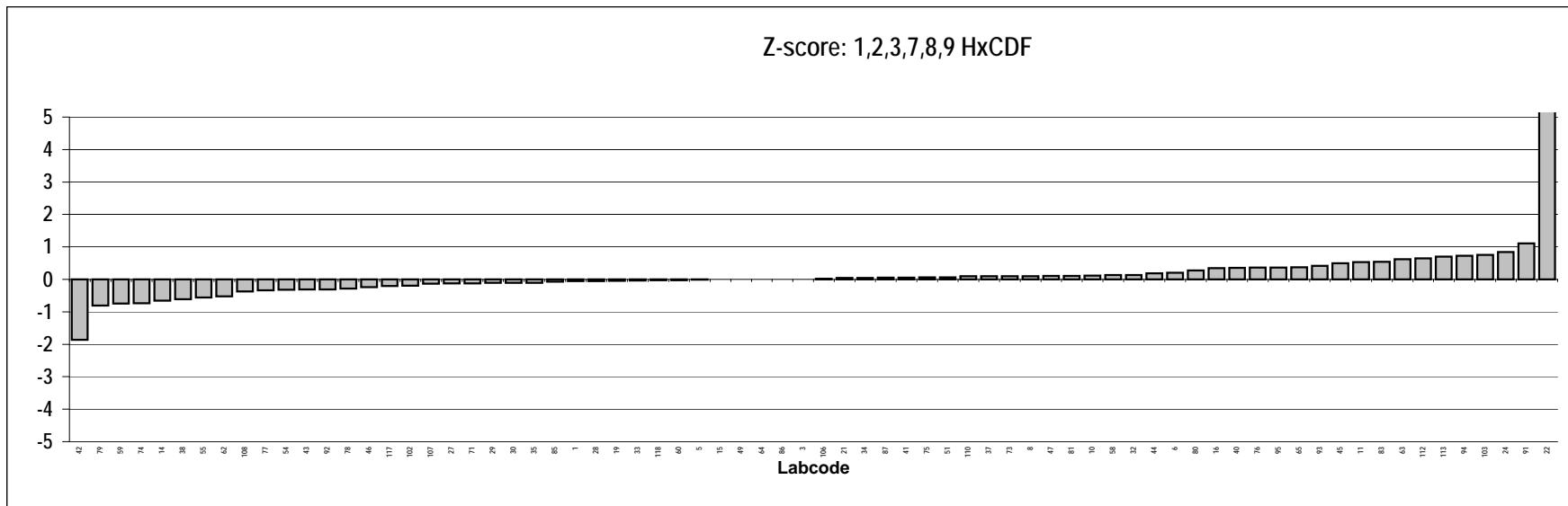
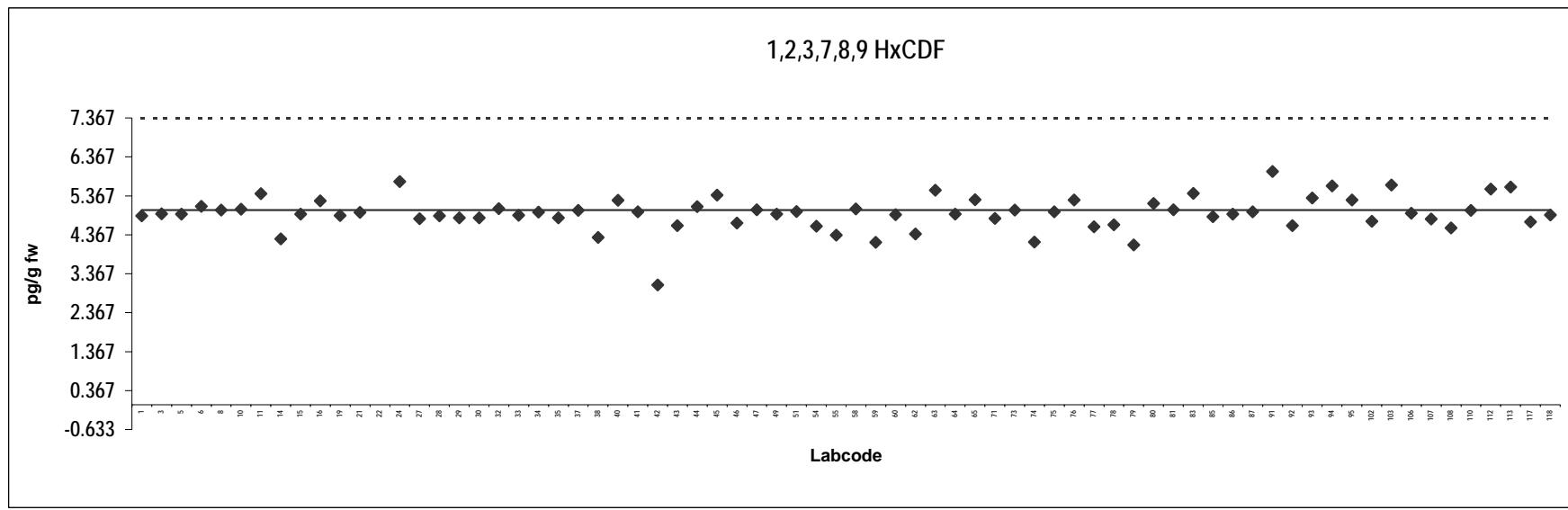


**Analyte solution**  
**Congener: 1,2,3,7,8,9 HxCDF**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	4.9		74	4.2	
3	4.9		75	5.0	
5	4.9		76	5.3	
6	5.1		77	4.6	
8	5.0		78	4.6	
10	5.0		79	4.1	
11	5.4		80	5.2	
14	4.3		81	5.0	
15	4.9		83	5.4	
16	5.2		85	4.8	
19	4.9		86	4.9	
21	4.9		87	5.0	
22	47	Outlier	91	6.0	
24	5.7		92	4.6	
27	4.8		93	5.3	
28	4.9		94	5.6	
29	4.8		95	5.3	
30	4.8		102	4.7	
32	5.0		103	5.6	
33	4.9		106	4.9	
34	5.0		107	4.8	
35	4.8		108	4.5	
37	5.0		110	5.0	
38	4.3		112	5.5	
40	5.3		113	5.6	
41	5.0		117	4.7	
42	3.1		118	4.9	
43	4.6				
44	5.1				
45	5.4				
46	4.7				
47	5.0				
49	4.9				
51	5.0				
54	4.6				
55	4.4				
58	5.0				
59	4.2				
60	4.9				
62	4.4				
63	5.5				
64	4.9				
65	5.3				
71	4.8				
73	5.0				

**Consensus statistics**

Consensus median, pg/g	4.9
Median all values pg/g	4.9
Consensus mean, pg/g	4.9
Standard deviation, pg/g	0.43
Relative standard deviation, %	8.8
No. of values reported	72
No. of values removed	1
No. of reported non-detects	0

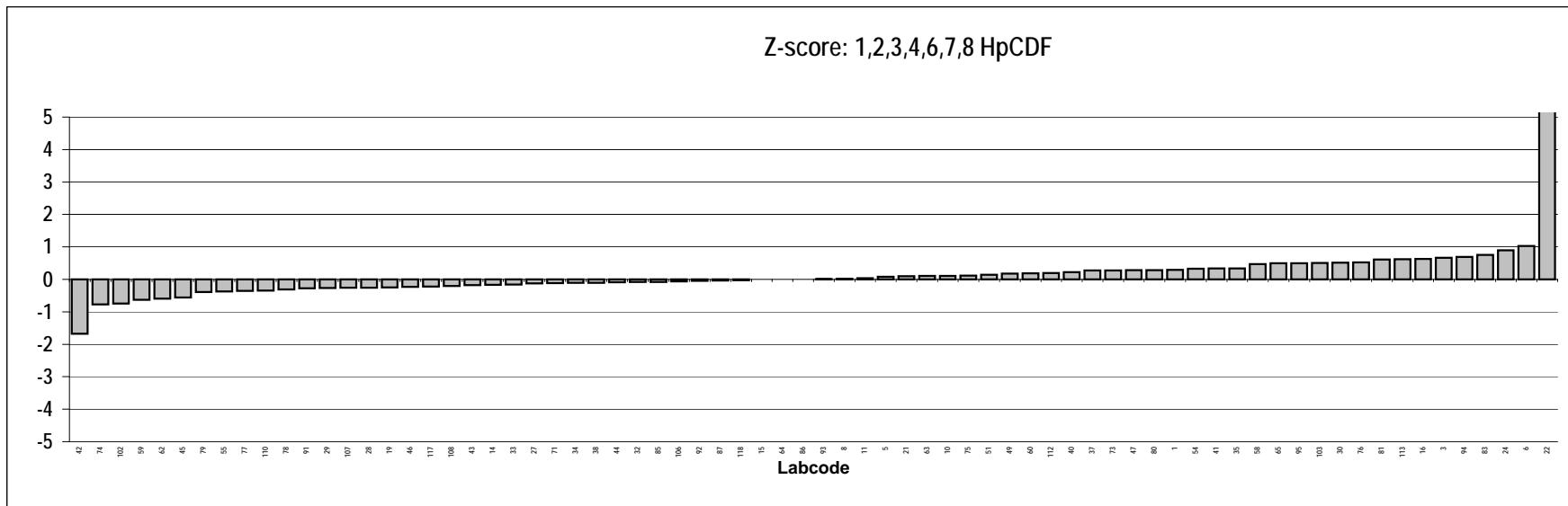
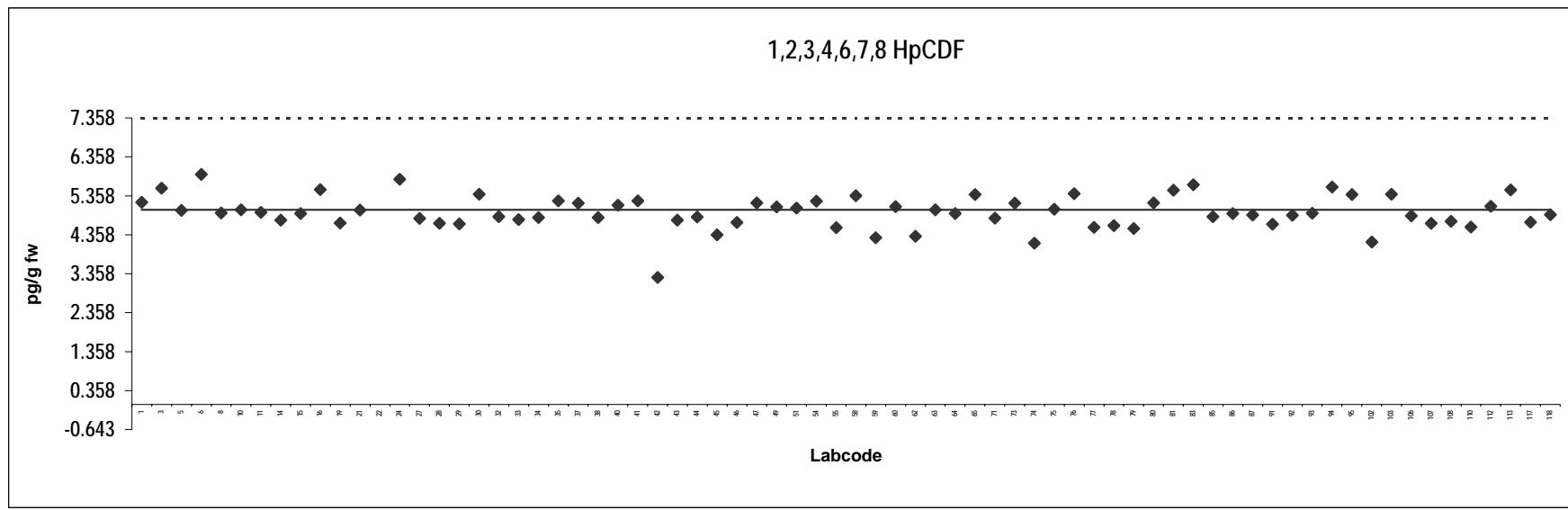


**Analyte solution**  
**Congener: 1,2,3,4,6,7,8 HpCDF**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.2		74	4.1	
3	5.6		75	5.0	
5	5.0		76	5.4	
6	5.9		77	4.6	
8	4.9		78	4.6	
10	5.0		79	4.5	
11	4.9		80	5.2	
14	4.7		81	5.5	
15	4.9		83	5.6	
16	5.5		85	4.8	
19	4.7		86	4.9	
21	5.0		87	4.9	
22	50	Outlier	91	4.6	
24	5.8		92	4.9	
27	4.8		93	4.9	
28	4.7		94	5.6	
29	4.6		95	5.4	
30	5.4		102	4.2	
32	4.8		103	5.4	
33	4.7		106	4.8	
34	4.8		107	4.7	
35	5.2		108	4.7	
37	5.2		110	4.6	
38	4.8		112	5.1	
40	5.1		113	5.5	
41	5.2		117	4.7	
42	3.3		118	4.9	
43	4.7				
44	4.8				
45	4.4				
46	4.7				
47	5.2				
49	5.1				
51	5.0				
54	5.2				
55	4.5				
58	5.4				
59	4.3				
60	5.1				
62	4.3				
63	5.0				
64	4.9				
65	5.4				
71	4.8				
73	5.2				

**Consensus statistics**

Consensus median, pg/g	4.9
Median all values pg/g	4.9
Consensus mean, pg/g	4.9
Standard deviation, pg/g	0.43
Relative standard deviation, %	8.6
No. of values reported	72
No. of values removed	1
No. of reported non-detects	0

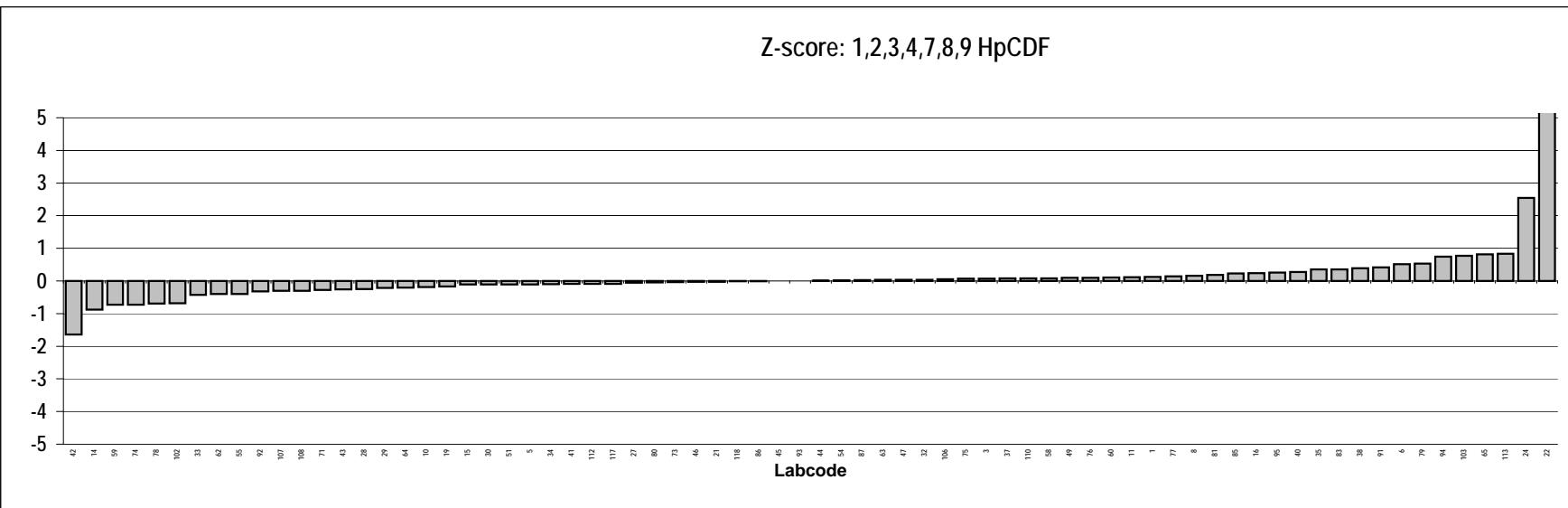
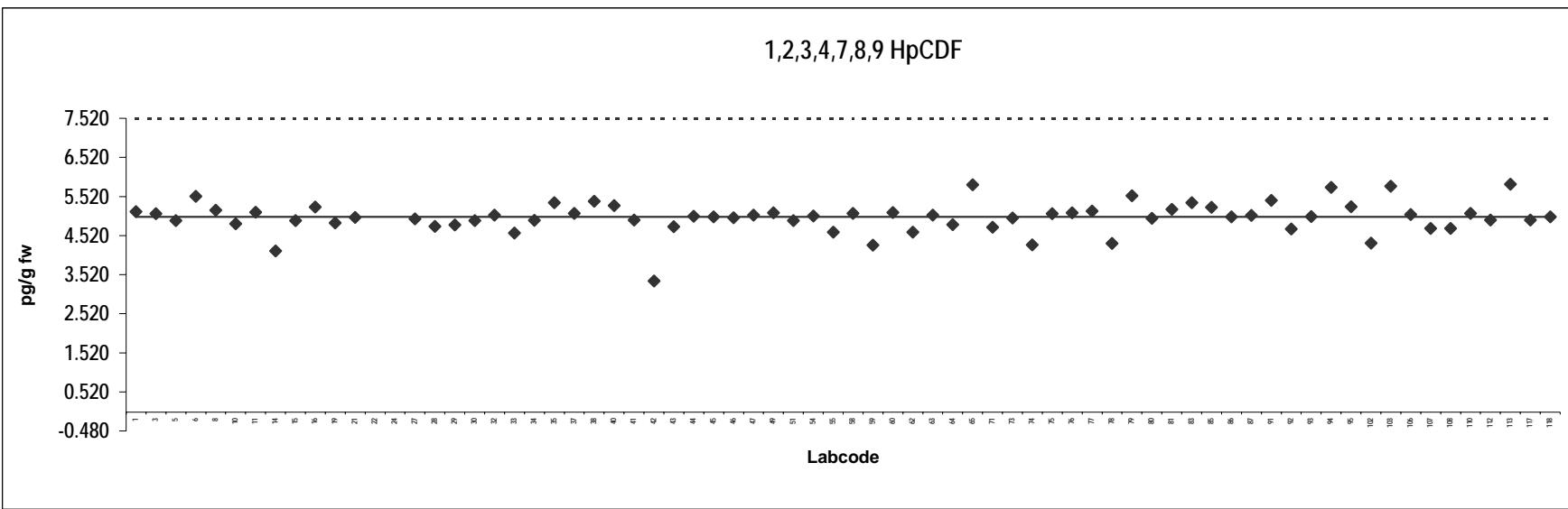


**Analyte solution**  
**Congener: 1,2,3,4,7,8,9 HpCDF**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.1		74	4.3	
3	5.1		75	5.1	
5	4.9		76	5.1	
6	5.5		77	5.2	
8	5.2		78	4.3	
10	4.8		79	5.5	
11	5.1		80	5.0	
14	4.1		81	5.2	
15	4.9		83	5.4	
16	5.3		85	5.2	
19	4.8		86	5.0	
21	5.0		87	5.0	
22	49	Outlier	91	5.4	
24	7.5	Outlier	92	4.7	
27	5.0		93	5.0	
28	4.8		94	5.8	
29	4.8		95	5.3	
30	4.9		102	4.3	
32	5.0		103	5.8	
33	4.6		106	5.1	
34	4.9		107	4.7	
35	5.4		108	4.7	
37	5.1		110	5.1	
38	5.4		112	4.9	
40	5.3		113	5.8	
41	4.9		117	4.9	
42	3.4		118	5.0	
43	4.8				
44	5.0				
45	5.0				
46	5.0				
47	5.0				
49	5.1				
51	4.9				
54	5.0				
55	4.6				
58	5.1				
59	4.3				
60	5.1				
62	4.6				
63	5.0				
64	4.8				
65	5.8				
71	4.7				
73	5.0				

**Consensus statistics**

Consensus median, pg/g	5.0
Median all values pg/g	5.0
Consensus mean, pg/g	5.0
Standard deviation, pg/g	0.39
Relative standard deviation, %	7.9
No. of values reported	72
No. of values removed	2
No. of reported non-detects	0

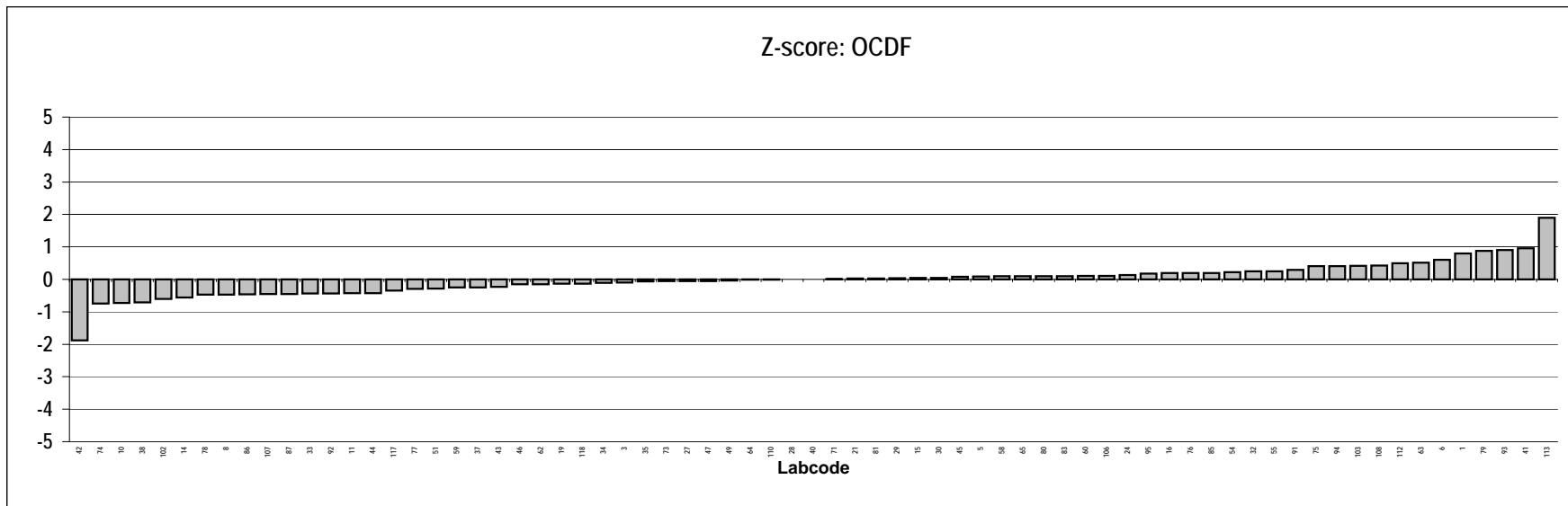
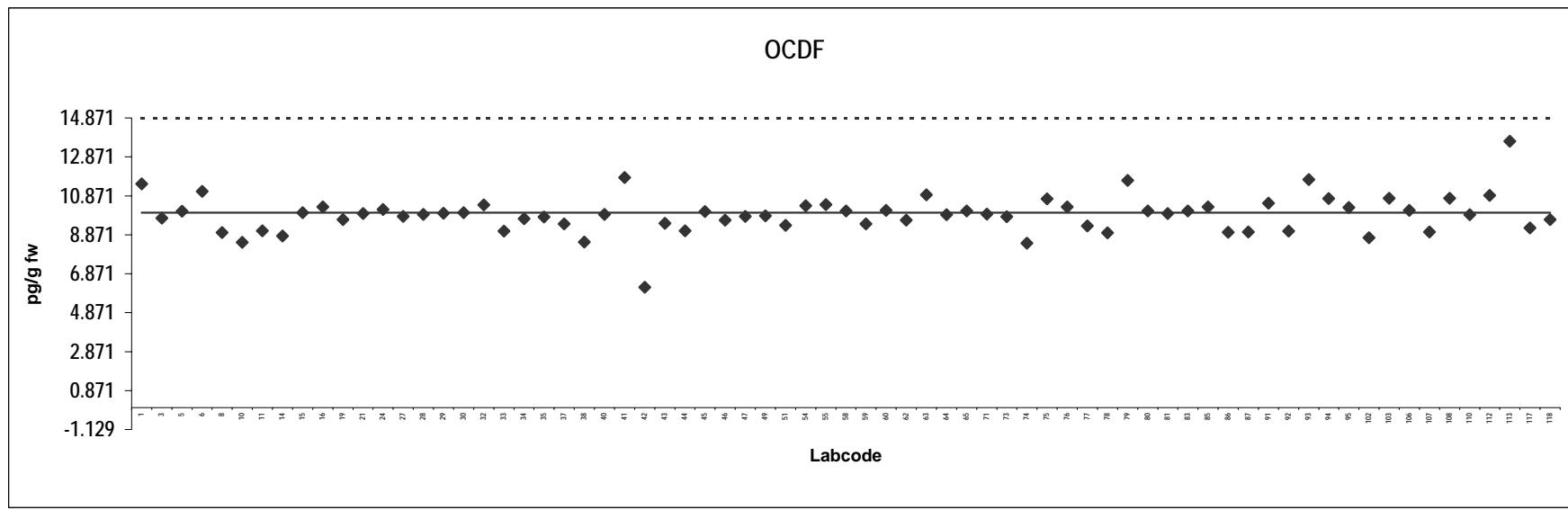


**Analyte solution**  
Congener: OCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	11		75	11	
3	9.7		76	10	
5	10		77	9.3	
6	11		78	9.0	
8	9.0		79	12	
10	8.5		80	10	
11	9.1		81	10	
14	8.8		83	10	
15	10		85	10	
16	10		86	9.0	
19	9.7		87	9.0	
21	10		91	11	
24	10		92	9.1	
27	9.8		93	12	
28	9.9		94	11	
29	10		95	10	
30	10		102	8.7	
32	10		103	11	
33	9.1		106	10	
34	9.7		107	9.0	
35	9.8		108	11	
37	9.4		110	9.9	
38	8.5		112	11	
40	9.9		113	14	
41	12		117	9.2	
42	6.2		118	9.7	
43	9.5				
44	9.1				
45	10				
46	9.6				
47	9.8				
49	9.9				
51	9.3				
54	10				
55	10				
58	10				
59	9.4				
60	10				
62	9.6				
63	11				
64	9.9				
65	10				
71	9.9				
73	9.8				
74	8.4				

**Consensus statistics**

Consensus median, pg/g	9.9
Median all values pg/g	9.9
Consensus mean, pg/g	9.9
Standard deviation, pg/g	0.98
Relative standard deviation, %	10
No. of values reported	71
No. of values removed	0
No. of reported non-detects	0

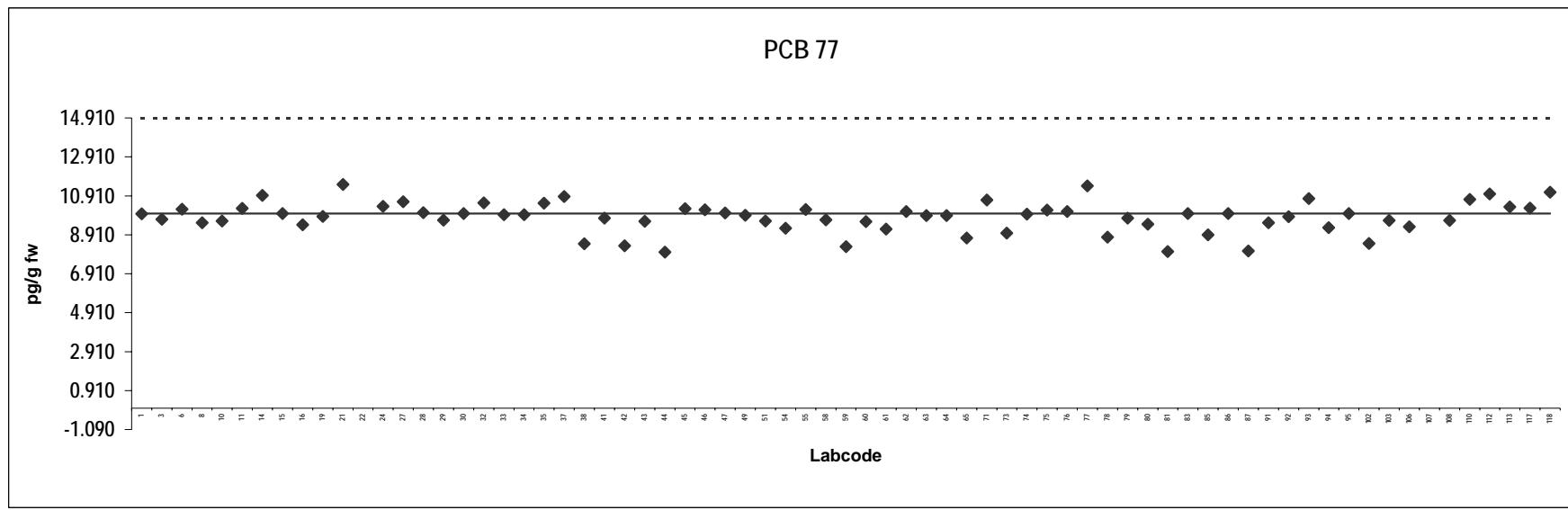


**Analyte solution**  
Congener: PCB 77

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	10		75	10	
3	9.7		76	10	
6	10		77	11	
8	9.5		78	8.8	
10	9.6		79	9.8	
11	10		80	9.5	
14	11		81	8.1	
15	10		83	10	
16	9.4		85	8.9	
19	9.9		86	10	
21	11		87	8.1	
22	76	Outlier	91	9.5	
24	10		92	9.8	
27	11		93	11	
28	10		94	9.3	
29	9.7		95	10	
30	10		102	8.5	
32	11		103	9.6	
33	9.9		106	9.3	
34	9.9		107	20	Outlier
35	11		108	9.7	
37	11		110	11	
38	8.5		112	11	
41	9.8		113	10	
42	8.4		117	10	
43	9.6		118	11	
44	8.0				
45	10				
46	10				
47	10				
49	9.9				
51	9.6				
54	9.3				
55	10				
58	9.7				
59	8.3				
60	9.6				
61	9.2				
62	10				
63	9.9				
64	9.9				
65	8.8				
71	11				
73	9.0				
74	10				

**Consensus statistics**

Consensus median, pg/g	9.9
Median all values pg/g	9.9
Consensus mean, pg/g	9.8
Standard deviation, pg/g	0.77
Relative standard deviation, %	7.9
No. of values reported	71
No. of values removed	2
No. of reported non-detects	0

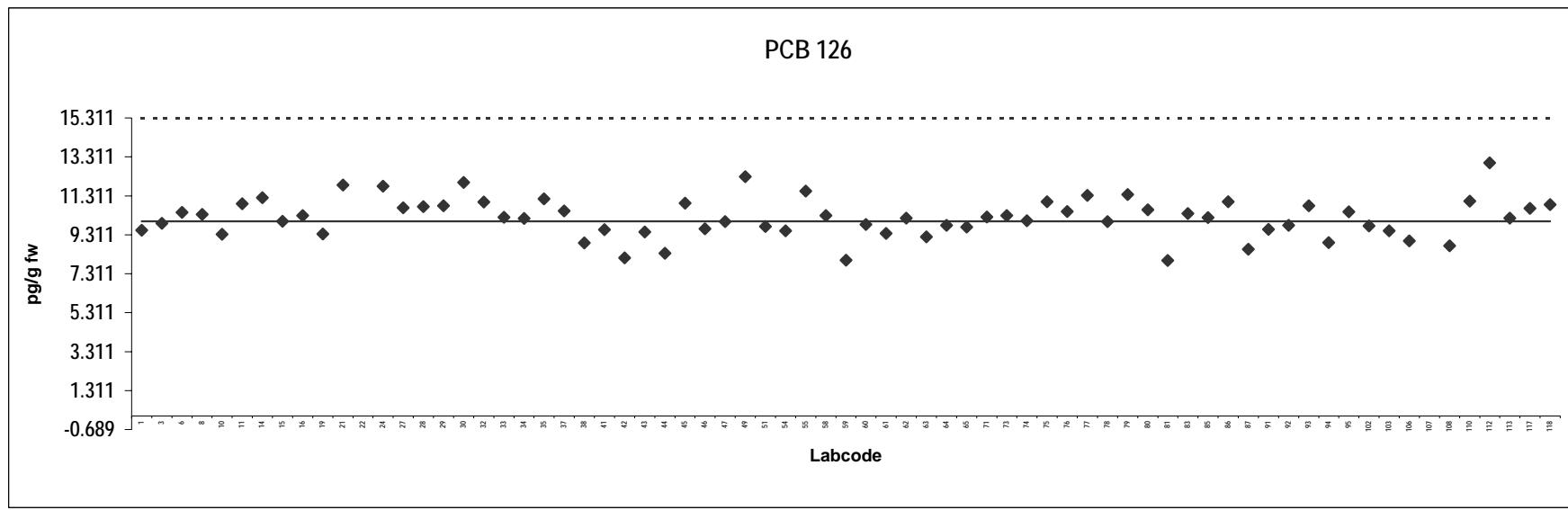


**Analyte solution**  
Congener: PCB 126

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	9.5		75	11	
3	9.9		76	11	
6	10		77	11	
8	10		78	10	
10	9.3		79	11	
11	11		80	11	
14	11		81	8.0	
15	10		83	10	
16	10		85	10	
19	9.4		86	11	
21	12		87	8.6	
22	81	Outlier	91	9.6	
24	12		92	9.8	
27	11		93	11	
28	11		94	8.9	
29	11		95	10	
30	12		102	9.8	
32	11		103	9.5	
33	10		106	9.0	
34	10		107	19	Outlier
35	11		108	8.7	
37	11		110	11	
38	8.9		112	13	
41	9.6		113	10	
42	8.1		117	11	
43	9.5		118	11	
44	8.4				
45	11				
46	9.6				
47	10				
49	12				
51	9.7				
54	9.5				
55	12				
58	10				
59	8.0				
60	9.8				
61	9.4				
62	10				
63	9.2				
64	9.8				
65	9.7				
71	10				
73	10				
74	10				

**Consensus statistics**

Consensus median, pg/g	10
Median all values pg/g	10
Consensus mean, pg/g	10
Standard deviation, pg/g	1.0
Relative standard deviation, %	10
No. of values reported	71
No. of values removed	2
No. of reported non-detects	0

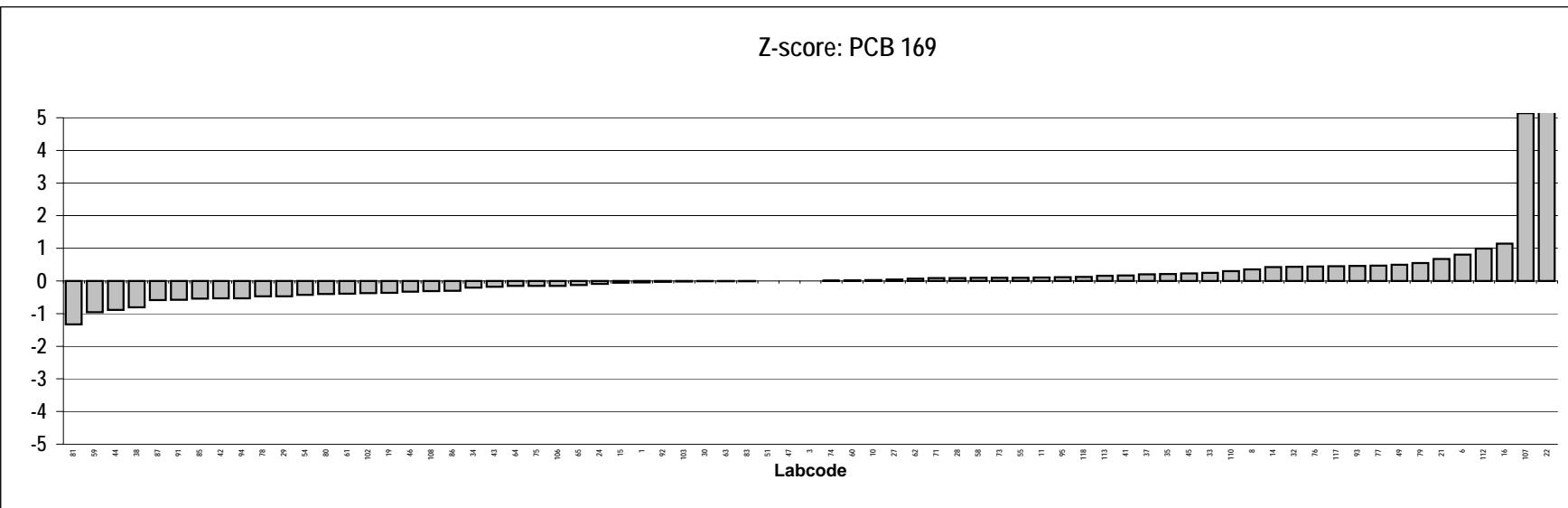
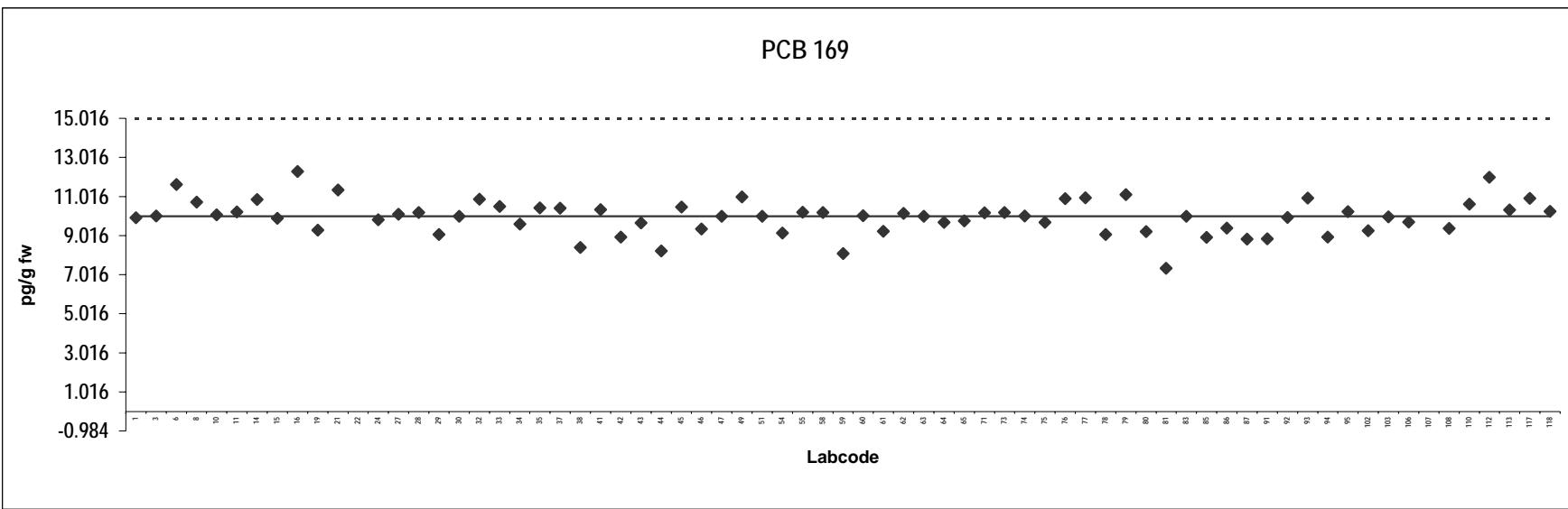


**Analyte solution**  
Congener: PCB 169

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	9.9		75	9.7	
3	10		76	11	
6	12		77	11	
8	11		78	9.1	
10	10		79	11	
11	10		80	9.2	
14	11		81	7.3	
15	9.9		83	10	
16	12		85	8.9	
19	9.3		86	9.4	
21	11		87	8.8	
22	75	Outlier	91	8.9	
24	9.8		92	10	
27	10		93	11	
28	10		94	8.9	
29	9.1		95	10	
30	10		102	9.3	
32	11		103	10	
33	11		106	9.7	
34	9.6		107	20	Outlier
35	10		108	9.4	
37	10		110	11	
38	8.4		112	12	
41	10		113	10	
42	8.9		117	11	
43	9.7		118	10	
44	8.2				
45	10				
46	9.4				
47	10				
49	11				
51	10				
54	9.2				
55	10				
58	10				
59	8.1				
60	10				
61	9.2				
62	10				
63	10				
64	9.7				
65	9.8				
71	10				
73	10				
74	10				

**Consensus statistics**

Consensus median, pg/g	10
Median all values pg/g	10
Consensus mean, pg/g	10
Standard deviation, pg/g	0.88
Relative standard deviation, %	8.8
No. of values reported	71
No. of values removed	2
No. of reported non-detects	0

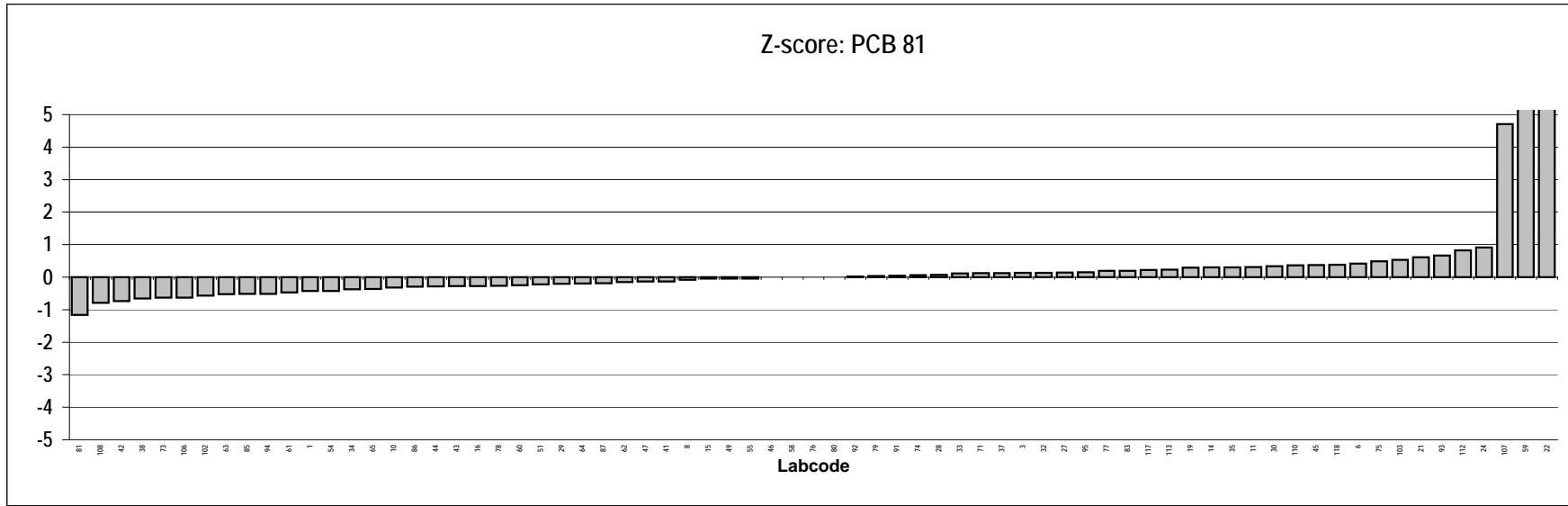
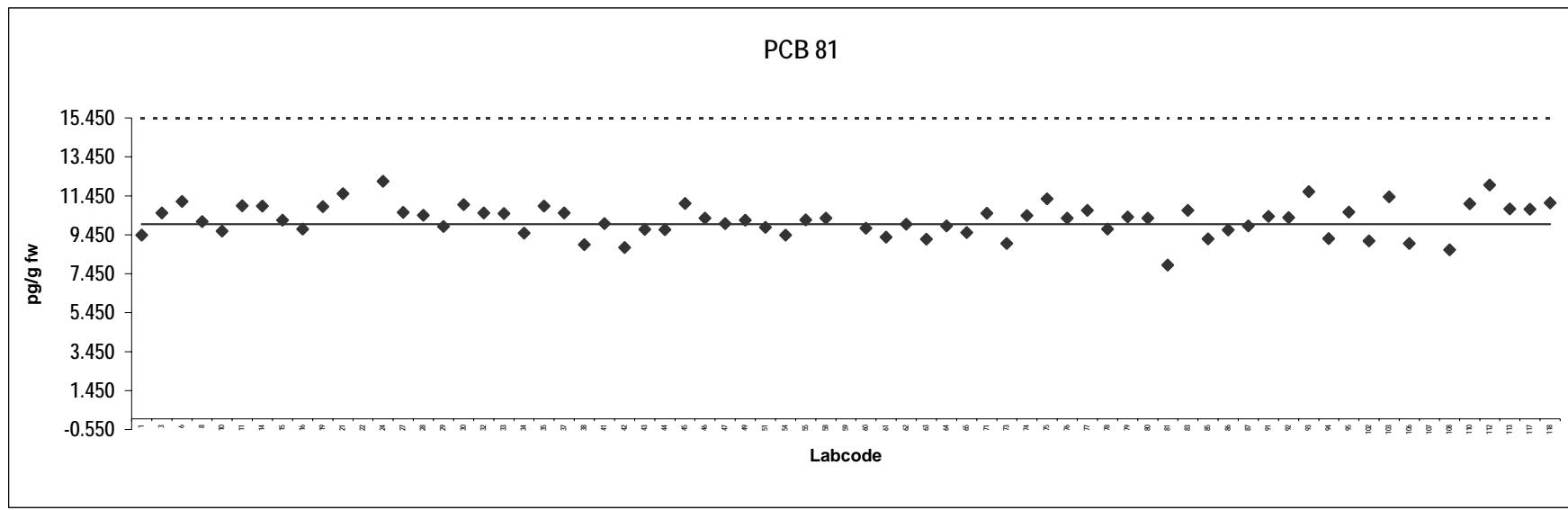


**Analyte solution**  
Congener: PCB 81

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	9.4		75	11	
3	11		76	10	
6	11		77	11	
8	10		78	9.7	
10	9.6		79	10	
11	11		80	10	
14	11		81	7.9	
15	10		83	11	
16	9.7		85	9.2	
19	11		86	9.7	
21	12		87	9.9	
22	76	Outlier	91	10	
24	12		92	10	
27	11		93	12	
28	10		94	9.2	
29	9.9		95	11	
30	11		102	9.1	
32	11		103	11	
33	11		106	9.0	
34	9.5		107	20	Outlier
35	11		108	8.7	
37	11		110	11	
38	9.0		112	12	
41	10		113	11	
42	8.8		117	11	
43	9.7		118	11	
44	9.7				
45	11				
46	10				
47	10				
49	10				
51	9.8				
54	9.4				
55	10				
58	10				
59	75	Outlier			
60	9.8				
61	9.3				
62	10				
63	9.2				
64	9.9				
65	9.6				
71	11				
73	9.0				
74	10				

**Consensus statistics**

Consensus median, pg/g	10
Median all values pg/g	10
Consensus mean, pg/g	10
Standard deviation, pg/g	0.82
Relative standard deviation, %	8.0
No. of values reported	71
No. of values removed	3
No. of reported non-detects	0

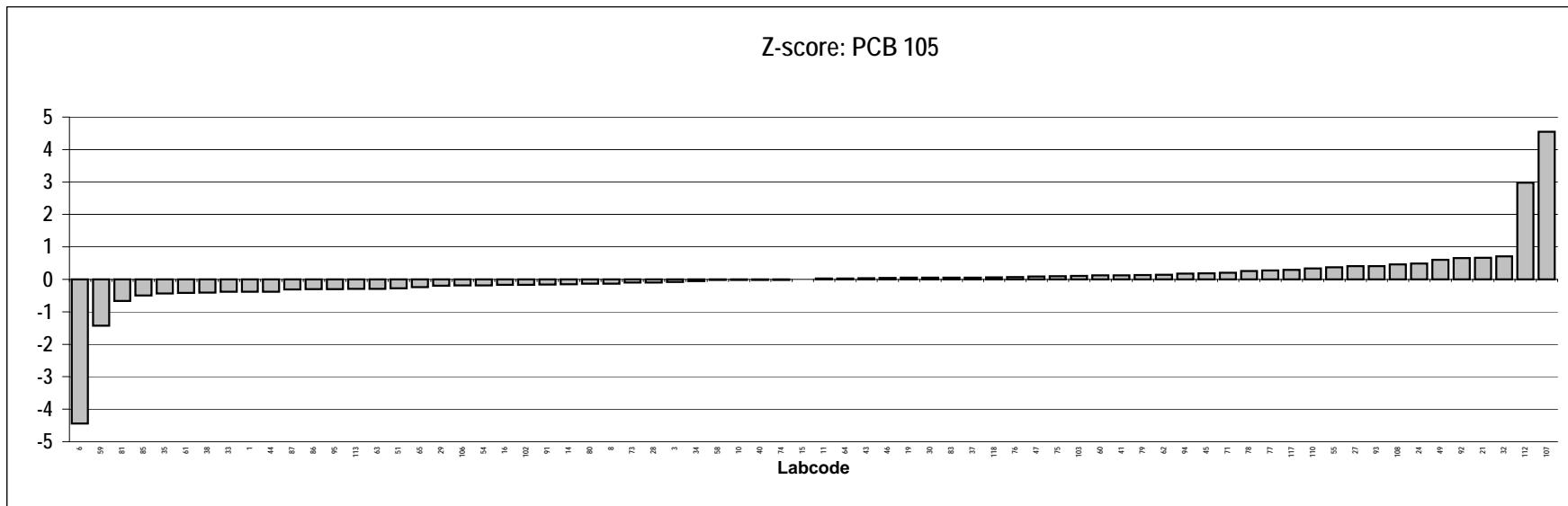
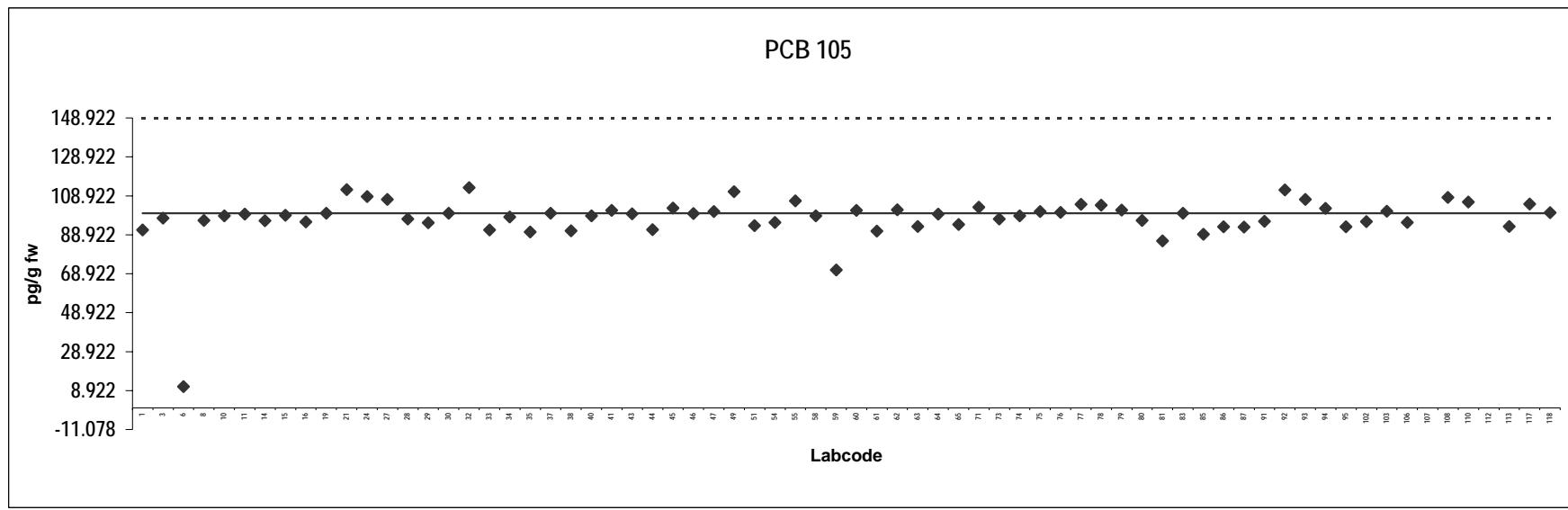


**Analyte solution**  
Congener: PCB 105

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	91		76	100	
3	98		77	105	
6	11	Outlier	78	104	
8	96		79	102	
10	99		80	96	
11	100		81	86	
14	96		83	100	
15	99		85	89	
16	96		86	93	
19	100		87	93	
21	112		91	96	
24	109		92	112	
27	107		93	107	
28	97		94	103	
29	95		95	93	
30	100		102	96	
32	113		103	101	
33	91		106	95	
34	98		107	189	Outlier
35	90		108	108	
37	100		110	106	
38	91		112	158	Outlier
40	99		113	93	
41	101		117	105	
43	100		118	100	
44	92				
45	103				
46	100				
47	101				
49	111				
51	94				
54	95				
55	106				
58	99				
59	71				
60	101				
61	91				
62	102				
63	93				
64	100				
65	94				
71	103				
73	97				
74	99				
75	101				

**Consensus statistics**

Consensus median, pg/g	99
Median all values pg/g	99
Consensus mean, pg/g	99
Standard deviation, pg/g	6.8
Relative standard deviation, %	6.9
No. of values reported	70
No. of values removed	3
No. of reported non-detects	0

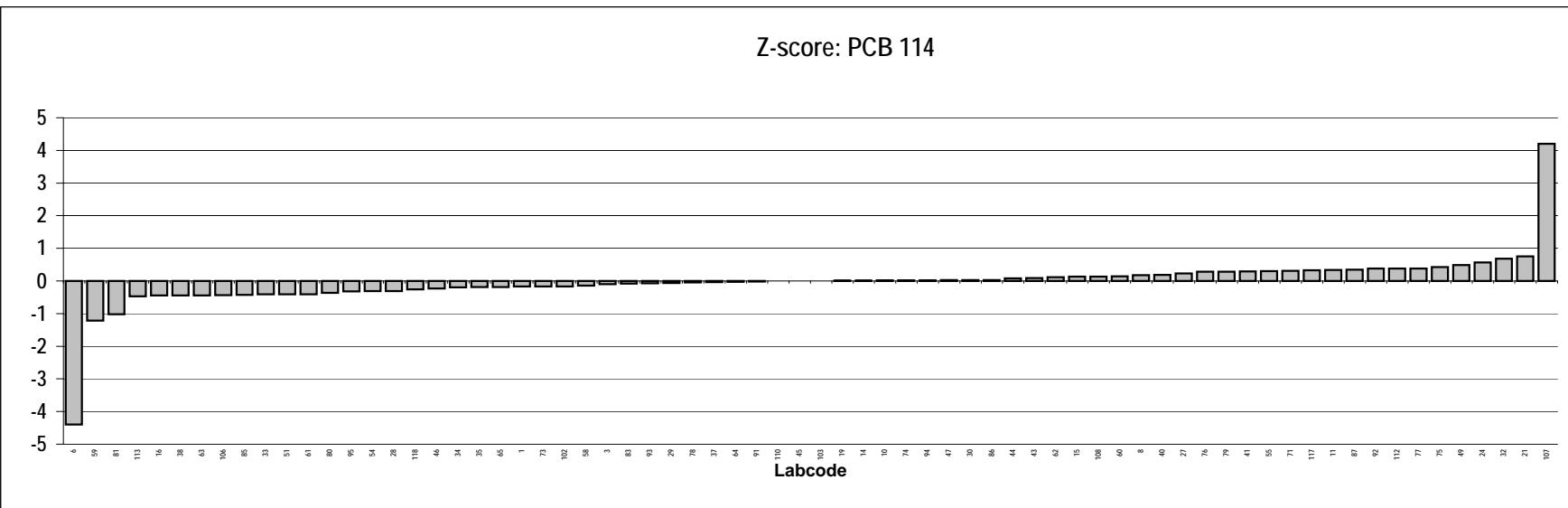
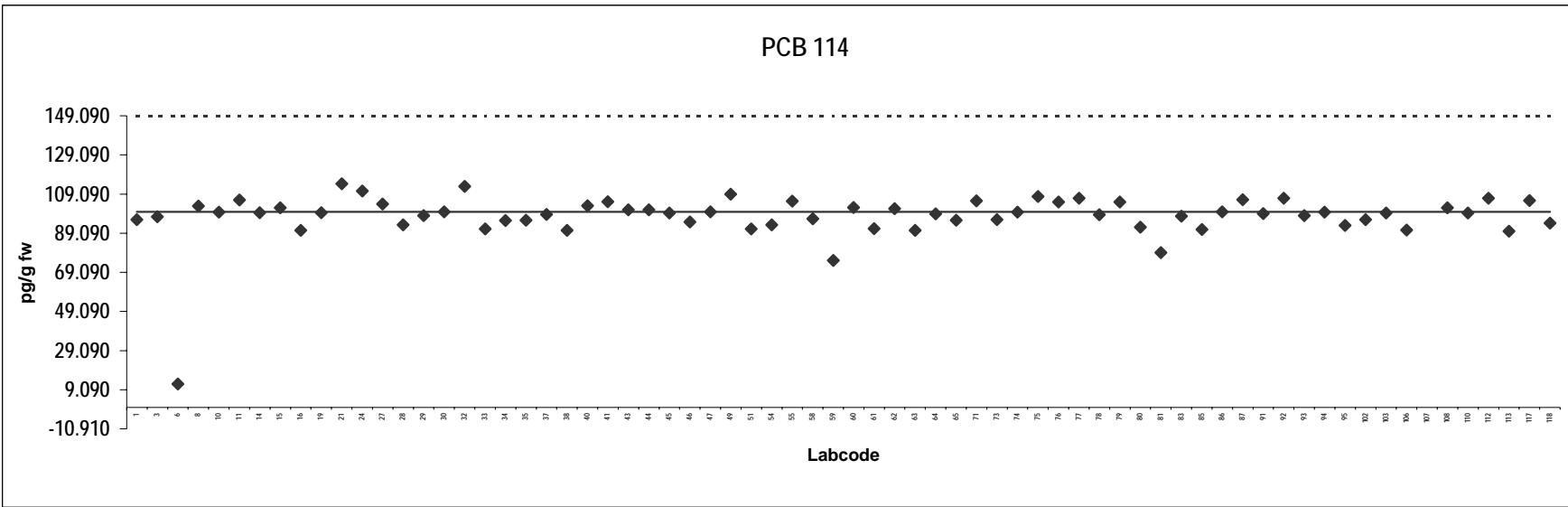


**Analyte solution**  
Congener: PCB 114

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	96		76	105	
3	98		77	107	
6	12	Outlier	78	99	
8	103		79	105	
10	100		80	92	
11	106		81	79	
14	100		83	98	
15	102		85	91	
16	91		86	100	
19	100		87	106	
21	114		91	99	
24	111		92	107	
27	104		93	98	
28	93		94	100	
29	98		95	93	
30	100		102	96	
32	113		103	99	
33	91		106	91	
34	96		107	183	Outlier
35	96		108	102	
37	99		110	99	
38	91		112	107	
40	103		113	90	
41	105		117	106	
43	101		118	94	
44	101				
45	99				
46	95				
47	100				
49	109				
51	91				
54	93				
55	105				
58	97				
59	75				
60	102				
61	91				
62	102				
63	91				
64	99				
65	96				
71	106				
73	96				
74	100				
75	108				

**Consensus statistics**

Consensus median, pg/g	99
Median all values pg/g	99
Consensus mean, pg/g	99
Standard deviation, pg/g	6.9
Relative standard deviation, %	7.0
No. of values reported	70
No. of values removed	2
No. of reported non-detects	0

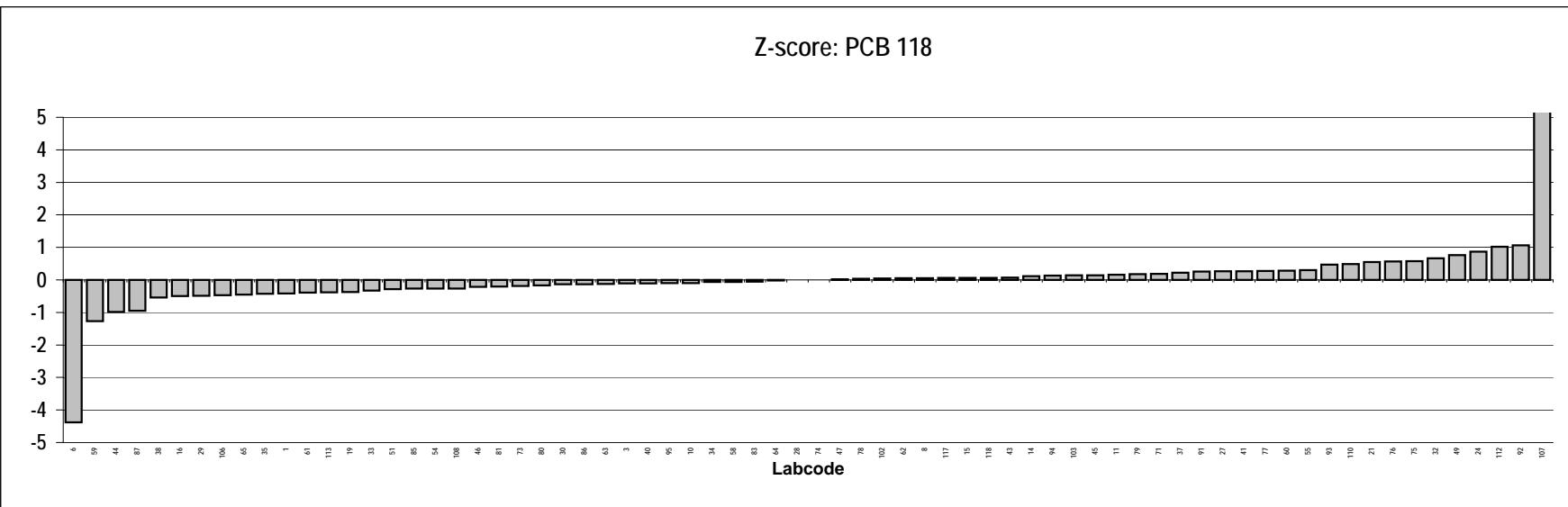
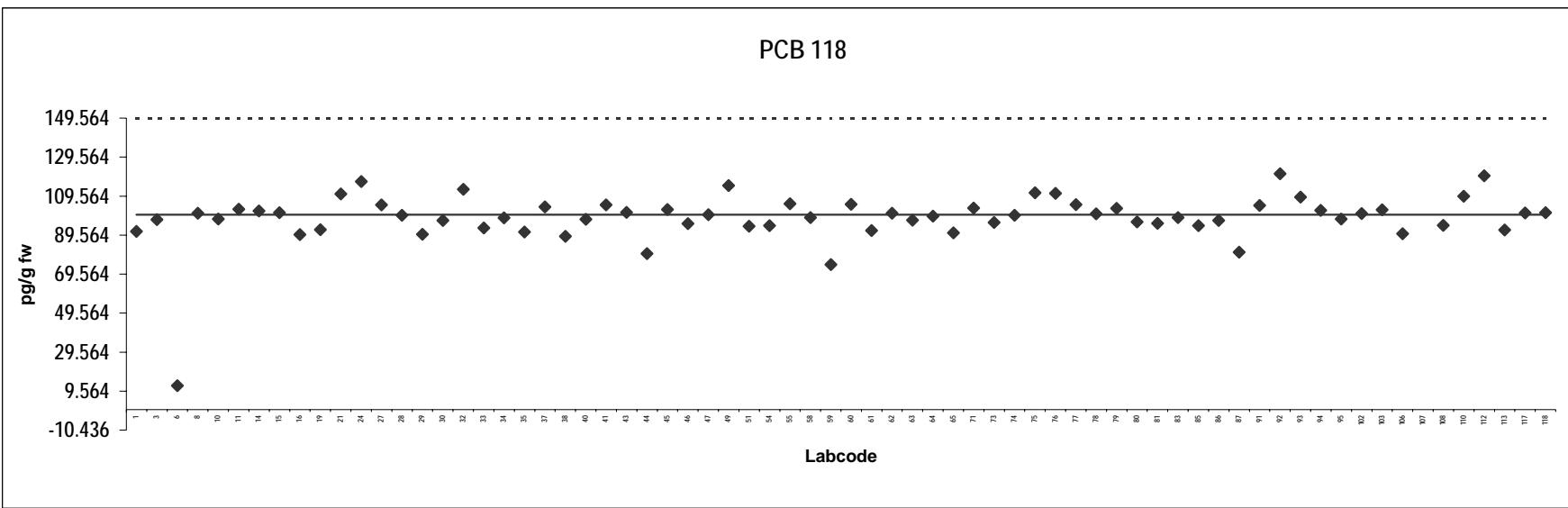


**Analyte solution**  
Congener: PCB 118

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	91		76	111	
3	98		77	105	
6	12	Outlier	78	100	
8	101		79	103	
10	98		80	96	
11	103		81	96	
14	102		83	99	
15	101		85	94	
16	90		86	97	
19	92		87	81	
21	111		91	105	
24	117		92	121	
27	105		93	109	
28	100		94	102	
29	90		95	98	
30	97		102	101	
32	113		103	102	
33	93		106	90	
34	98		107	206	Outlier
35	91		108	94	
37	104		110	109	
38	89		112	120	
40	98		113	92	
41	105		117	101	
43	101		118	101	
44	80				
45	103				
46	95				
47	100				
49	115				
51	94				
54	94				
55	106				
58	99				
59	74				
60	105				
61	92				
62	101				
63	97				
64	99				
65	91				
71	103				
73	96				
74	100				
75	111				

**Consensus statistics**

Consensus median, pg/g	100
Median all values pg/g	100
Consensus mean, pg/g	100
Standard deviation, pg/g	8.5
Relative standard deviation, %	8.5
No. of values reported	70
No. of values removed	2
No. of reported non-detects	0

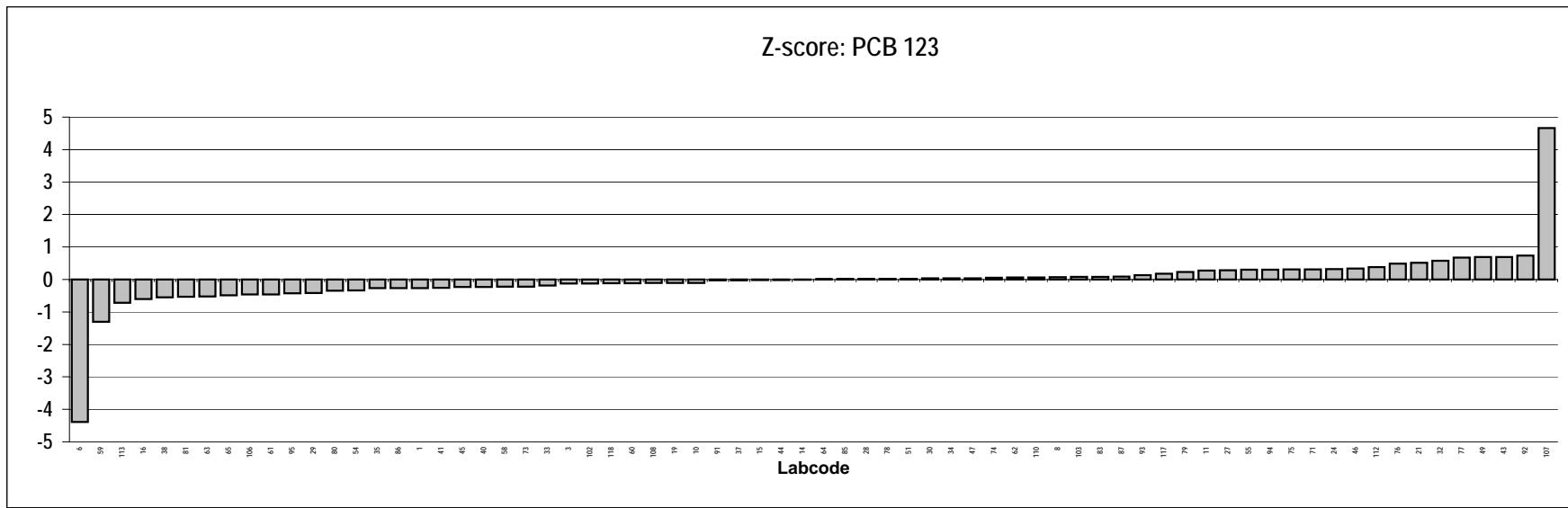
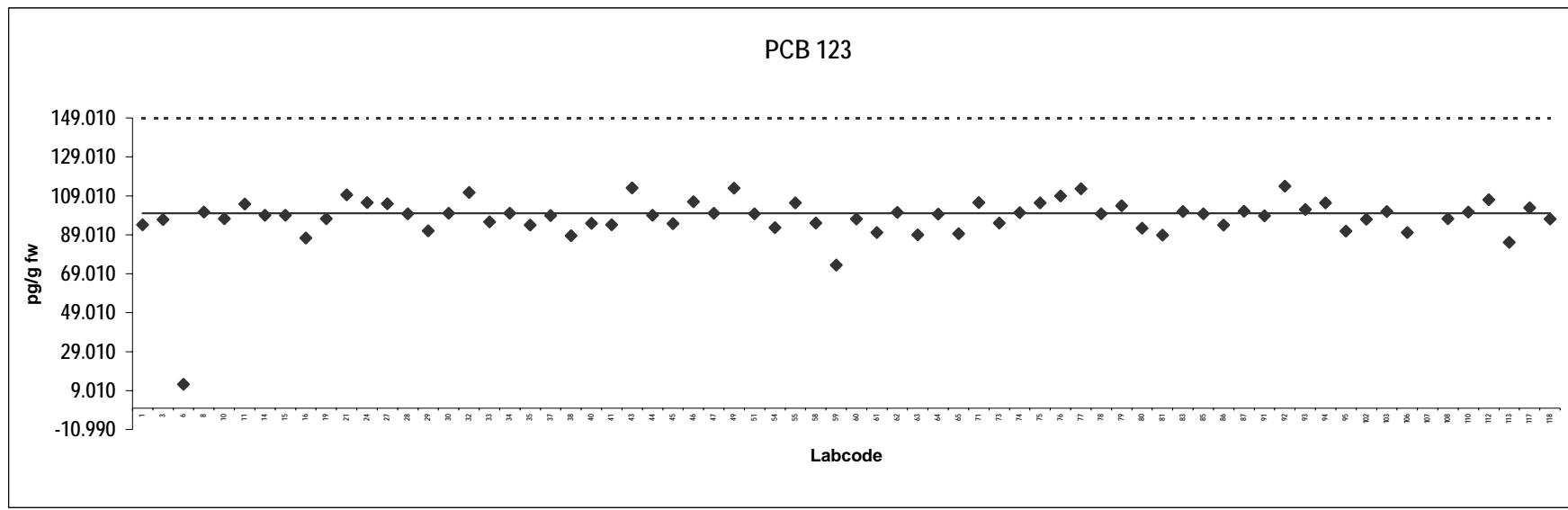


**Analyte solution**  
Congener: PCB 123

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	94		76	109	
3	97		77	113	
6	12	Outlier	78	100	
8	101		79	104	
10	97		80	92	
11	105		81	89	
14	99		83	101	
15	99		85	100	
16	87		86	94	
19	97		87	101	
21	110		91	99	
24	106		92	114	
27	105		93	102	
28	100		94	105	
29	91		95	91	
30	100		102	97	
32	111		103	101	
33	96		106	90	
34	100		107	192	Outlier
35	94		108	97	
37	99		110	101	
38	89		112	107	
40	95		113	85	
41	94		117	103	
43	113		118	97	
44	99				
45	95				
46	106				
47	100				
49	113				
51	100				
54	93				
55	105				
58	95				
59	73				
60	97				
61	90				
62	101				
63	89				
64	100				
65	90				
71	106				
73	95				
74	100				
75	105				

**Consensus statistics**

Consensus median, pg/g	99
Median all values pg/g	99
Consensus mean, pg/g	99
Standard deviation, pg/g	7.3
Relative standard deviation, %	7.4
No. of values reported	70
No. of values removed	2
No. of reported non-detects	0

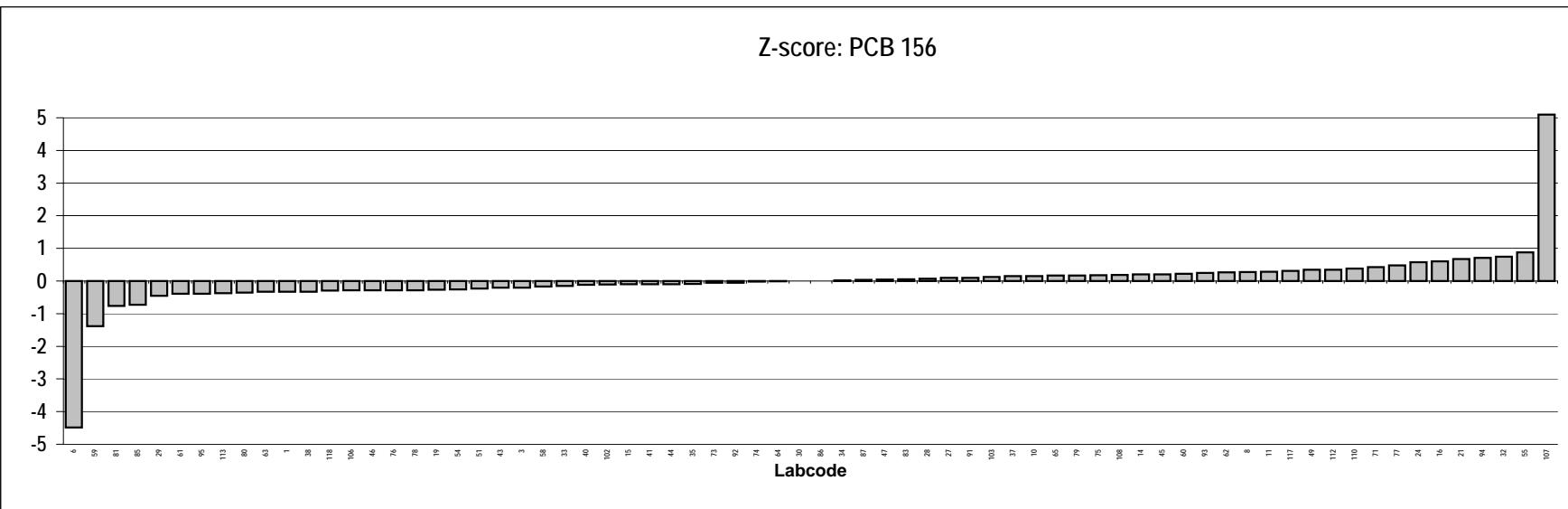
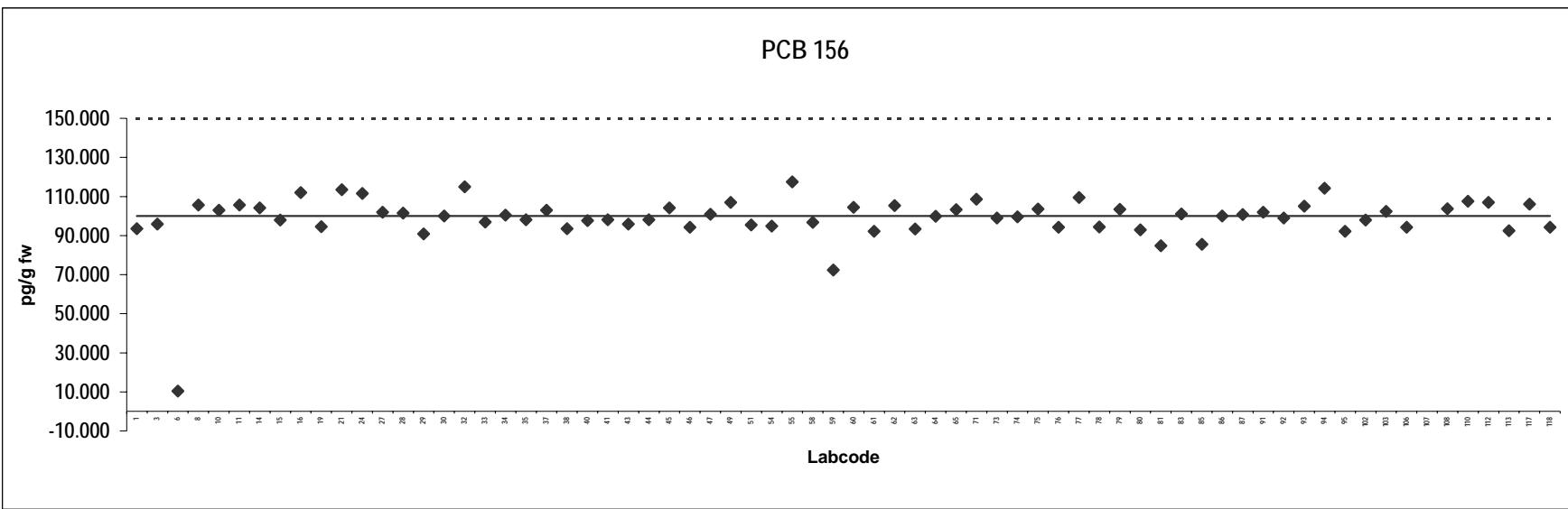


**Analyte solution**  
Congener: PCB 156

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	93		76	94	
3	96		77	110	
6	10	Outlier	78	94	
8	106		79	103	
10	103		80	93	
11	106		81	85	
14	104		83	101	
15	98		85	86	
16	112		86	100	
19	95		87	101	
21	113		91	102	
24	112		92	99	
27	102		93	105	
28	101		94	114	
29	91		95	92	
30	100		102	98	
32	115		103	102	
33	97		106	94	
34	100		107	202	Outlier
35	98		108	104	
37	103		110	108	
38	94		112	107	
40	98		113	92	
41	98		117	106	
43	96		118	94	
44	98				
45	104				
46	94				
47	101				
49	107				
51	95				
54	95				
55	118				
58	97				
59	72				
60	104				
61	92				
62	105				
63	93				
64	100				
65	103				
71	109				
73	99				
74	100				
75	104				

**Consensus statistics**

Consensus median, pg/g	100
Median all values pg/g	100
Consensus mean, pg/g	100
Standard deviation, pg/g	7.5
Relative standard deviation, %	7.5
No. of values reported	70
No. of values removed	2
No. of reported non-detects	0

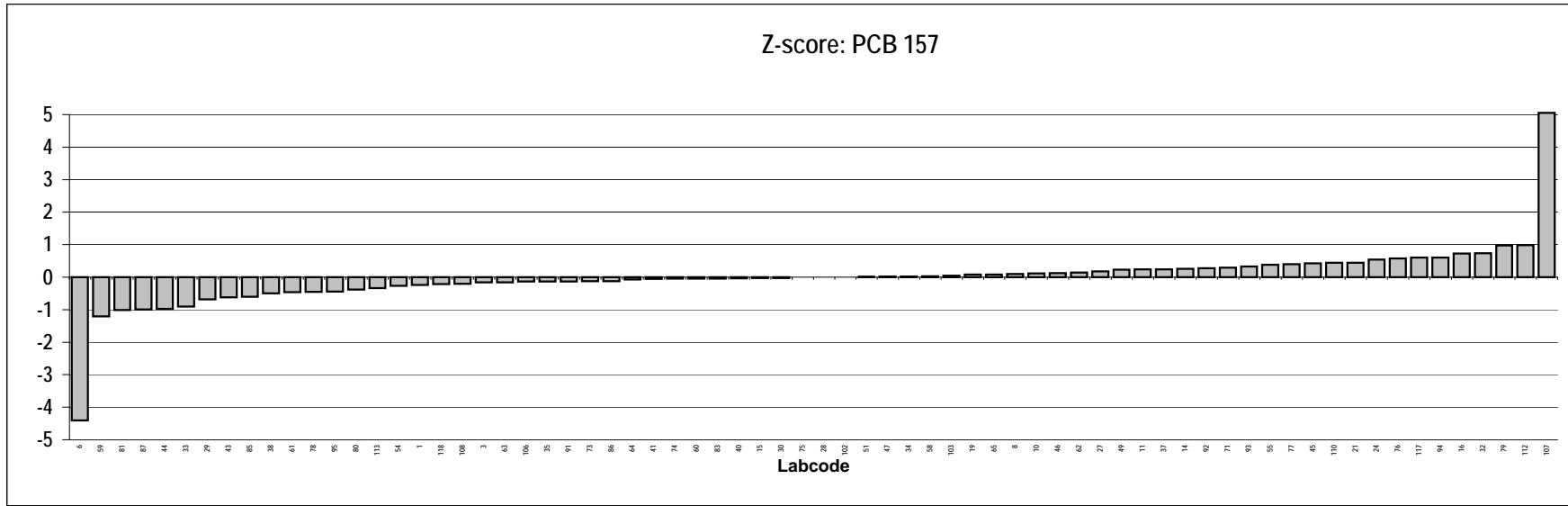
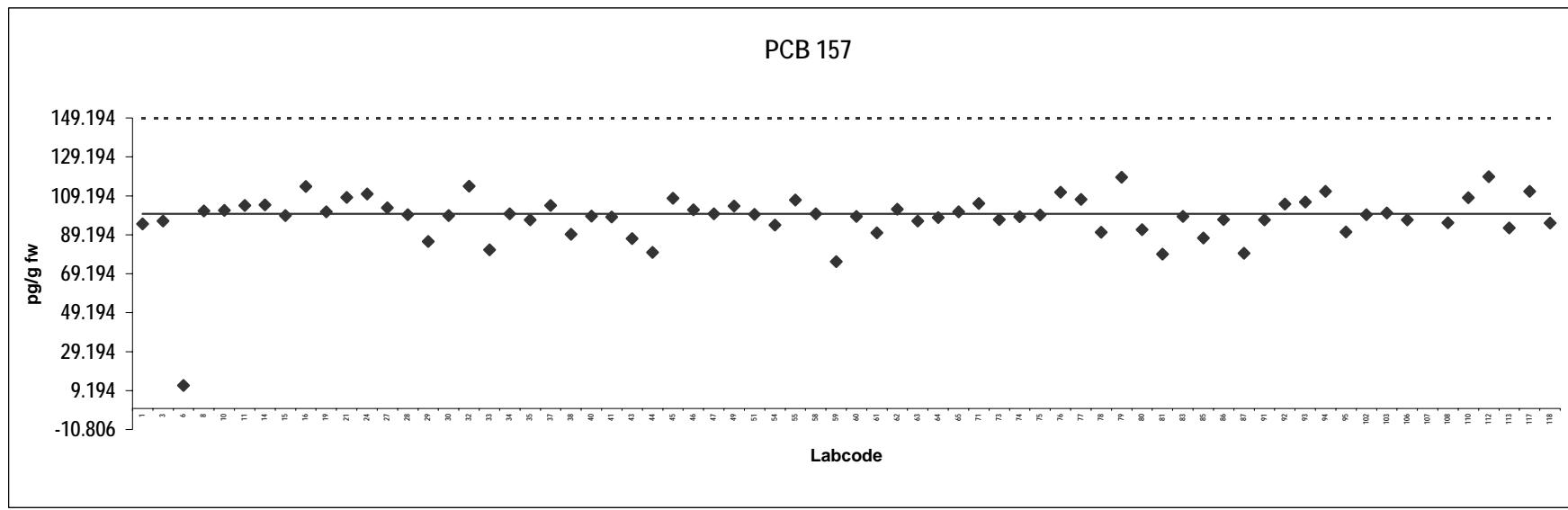


**Analyte solution**  
Congener: PCB 157

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	95		76	111	
3	96		77	107	
6	12	Outlier	78	91	
8	101		79	119	
10	102		80	92	
11	104		81	79	
14	105		83	99	
15	99		85	88	
16	114		86	97	
19	101		87	80	
21	108		91	97	
24	110		92	105	
27	103		93	106	
28	99		94	112	
29	86		95	91	
30	99		102	100	
32	114		103	100	
33	81		106	97	
34	100		107	200	Outlier
35	97		108	95	
37	104		110	108	
38	90		112	119	
40	99		113	93	
41	98		117	112	
43	87		118	95	
44	80				
45	108				
46	102				
47	100				
49	104				
51	100				
54	94				
55	107				
58	100				
59	75				
60	99				
61	90				
62	102				
63	96				
64	98				
65	101				
71	105				
73	97				
74	99				
75	99				

**Consensus statistics**

Consensus median, pg/g	99
Median all values pg/g	99
Consensus mean, pg/g	99
Standard deviation, pg/g	9.0
Relative standard deviation, %	9.1
No. of values reported	70
No. of values removed	2
No. of reported non-detects	0

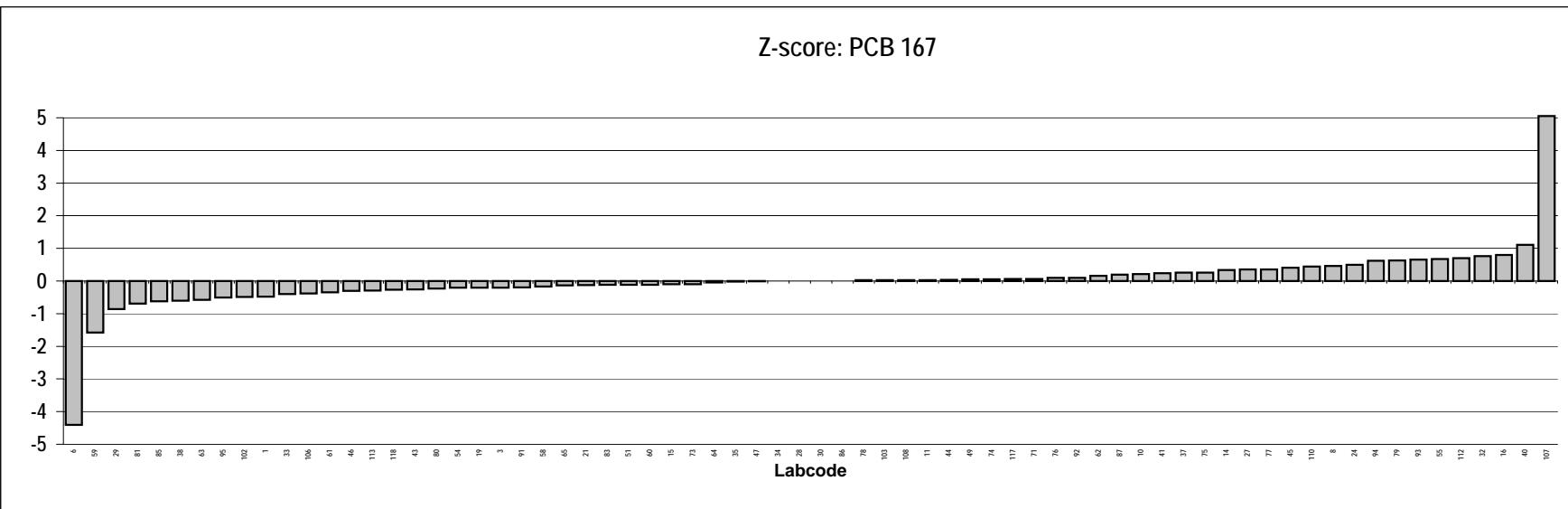
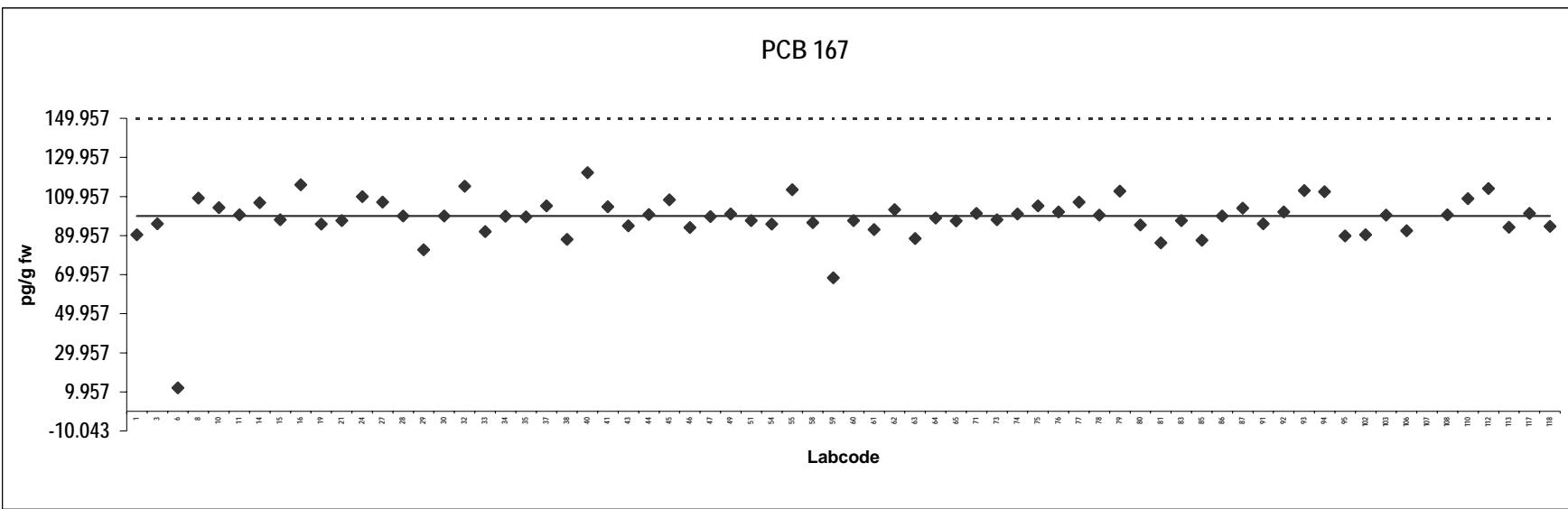


**Analyte solution**  
Congener: PCB 167

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	90		76	102	
3	96		77	107	
6	12	Outlier	78	100	
8	109		79	113	
10	104		80	95	
11	101		81	86	
14	107		83	98	
15	98		85	88	
16	116		86	100	
19	96		87	104	
21	98		91	96	
24	110		92	102	
27	107		93	113	
28	100		94	112	
29	83		95	90	
30	100		102	90	
32	115		103	100	
33	92		106	92	
34	100		107	201	Outlier
35	100		108	101	
37	105		110	109	
38	88		112	114	
40	122		113	94	
41	105		117	101	
43	95		118	95	
44	101				
45	108				
46	94				
47	100				
49	101				
51	98				
54	96				
55	113				
58	97				
59	68				
60	98				
61	93				
62	103				
63	88				
64	99				
65	97				
71	101				
73	98				
74	101				
75	105				

**Consensus statistics**

Consensus median, pg/g	100
Median all values pg/g	100
Consensus mean, pg/g	100
Standard deviation, pg/g	8.7
Relative standard deviation, %	8.7
No. of values reported	70
No. of values removed	2
No. of reported non-detects	0

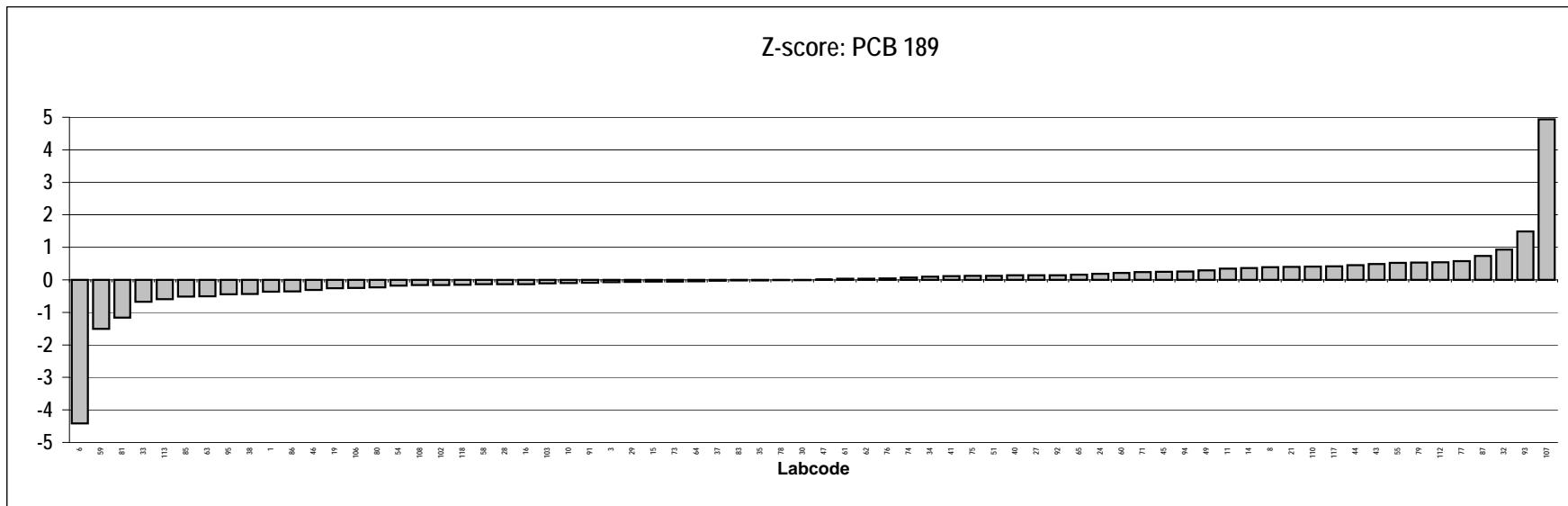
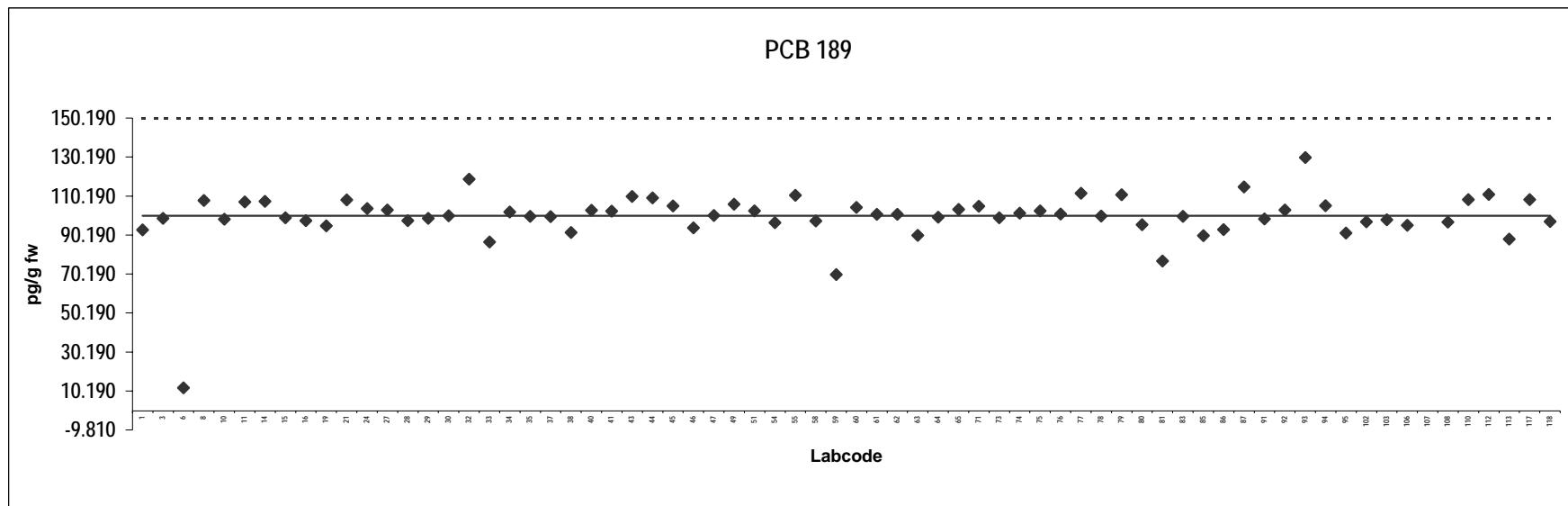


**Analyte solution**  
Congener: PCB 189

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	93		76	101	
3	99		77	112	
6	12	Outlier	78	100	
8	108		79	111	
10	98		80	96	
11	107		81	77	
14	107		83	100	
15	99		85	90	
16	98		86	93	
19	95		87	115	
21	108		91	98	
24	104		92	103	
27	103		93	130	
28	97		94	105	
29	99		95	91	
30	100		102	97	
32	119		103	98	
33	87		106	95	
34	102		107	199	Outlier
35	100		108	97	
37	100		110	108	
38	92		112	111	
40	103		113	88	
41	102		117	108	
43	110		118	97	
44	109				
45	105				
46	94				
47	100				
49	106				
51	103				
54	97				
55	111				
58	97				
59	70				
60	104				
61	101				
62	101				
63	90				
64	99				
65	103				
71	105				
73	99				
74	101				
75	103				

**Consensus statistics**

Consensus median, pg/g	100
Median all values pg/g	100
Consensus mean, pg/g	101
Standard deviation, pg/g	8.7
Relative standard deviation, %	8.7
No. of values reported	70
No. of values removed	2
No. of reported non-detects	0

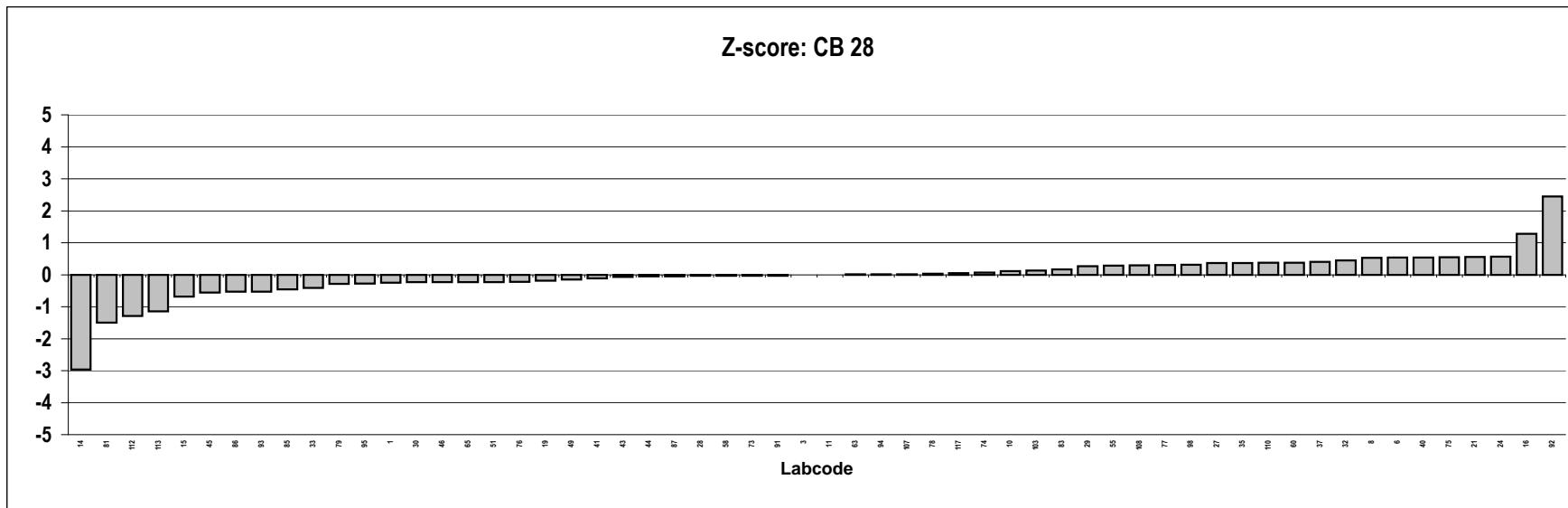
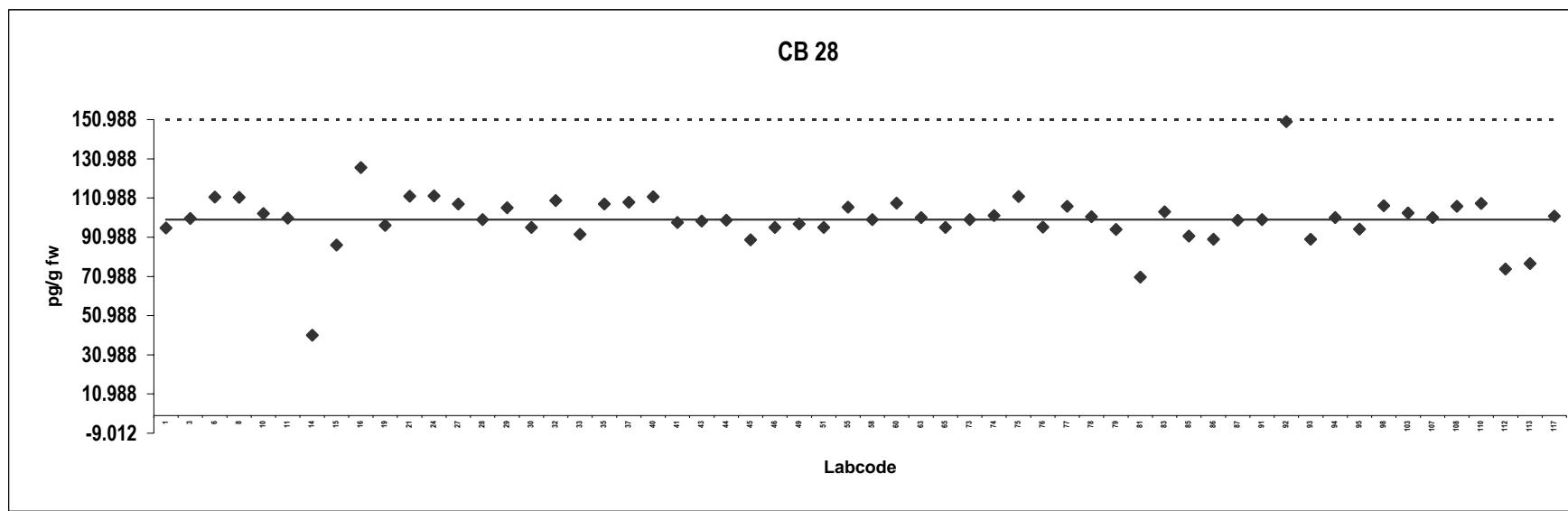


**Analyte solution**  
Congener: CB 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	96		91	100	
3	101		92	150	
6	112		93	90	
8	111		94	101	
10	103		95	95	
11	101		98	107	
14	41	Outlier	103	103	
15	87		107	101	
16	127		108	107	
19	97		110	108	
21	112		112	75	
24	112		113	78	
27	108		117	102	
28	100				
29	106				
30	96				
32	110				
33	92				
35	108				
37	109				
40	112				
41	98				
43	99				
44	100				
45	90				
46	96				
49	98				
51	96				
55	106				
58	100				
60	108				
63	101				
65	96				
73	100				
74	102				
75	112				
76	96				
77	107				
78	101				
79	95				
81	71				
83	104				
85	92				
86	90				
87	100				

**Consensus statistics**

Consensus median, pg/g	101
Median all values pg/g	101
Consensus mean, pg/g	101
Standard deviation, pg/g	12
Relative standard deviation, %	11
No. of values reported	58
No. of values removed	1
No. of reported non-detects	0

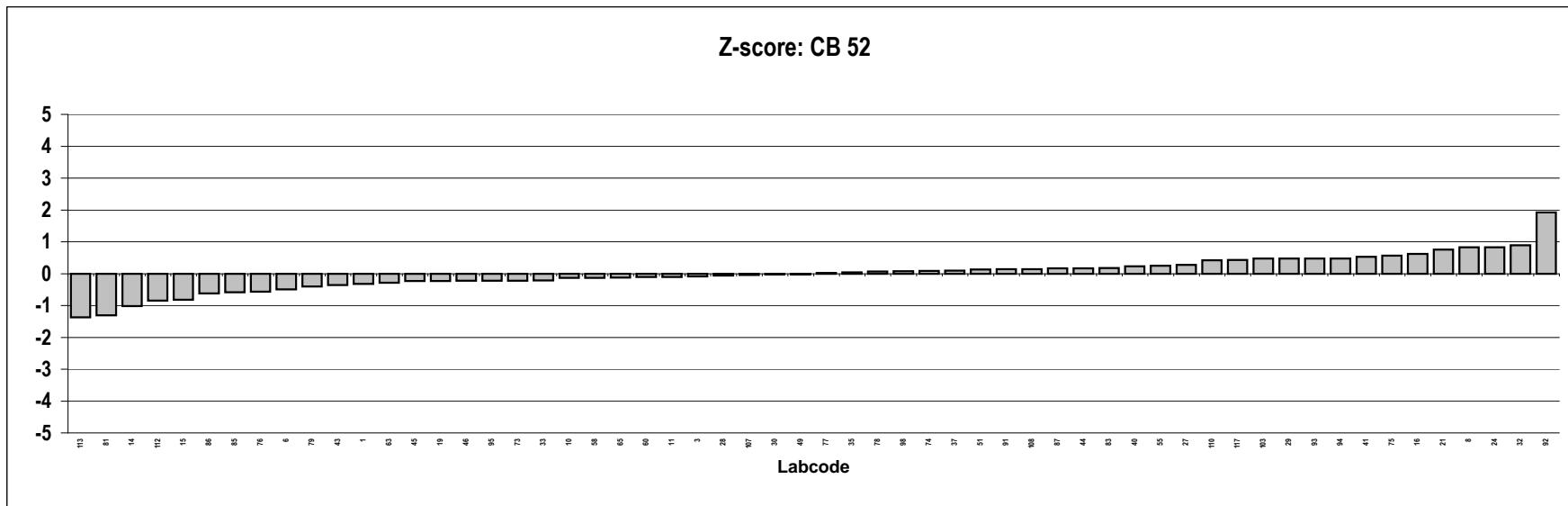
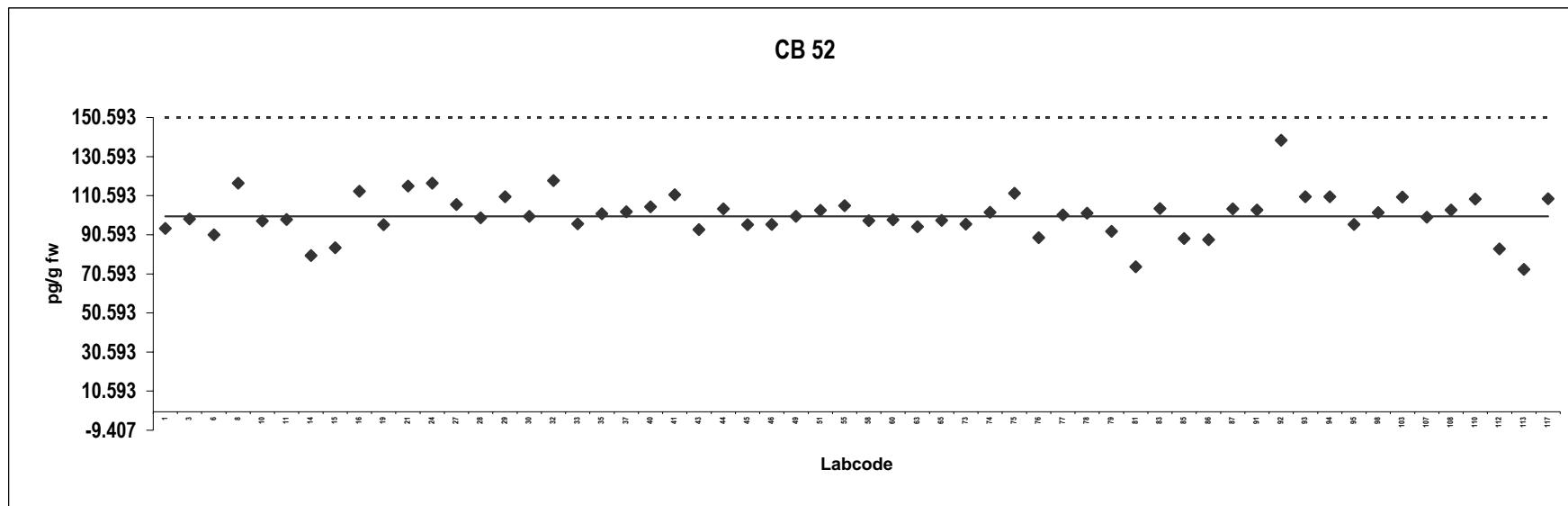


**Analyte solution**  
**Congener: CB 52**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	94		91	103	
3	99		92	139	
6	91		93	110	
8	117		94	110	
10	98		95	96	
11	98		98	102	
14	80		103	110	
15	84		107	100	
16	113		108	103	
19	96		110	109	
21	116		112	83	
24	117		113	73	
27	106		117	109	
28	99				
29	110				
30	100				
32	118				
33	96				
35	101				
37	102				
40	105				
41	111				
43	93				
44	104				
45	96				
46	96				
49	100				
51	103				
55	105				
58	98				
60	98				
63	95				
65	98				
73	96				
74	102				
75	112				
76	89				
77	101				
78	102				
79	92				
81	74				
83	104				
85	89				
86	88				
87	104				

**Consensus statistics**

Consensus median, pg/g	100
Median all values pg/g	100
Consensus mean, pg/g	101
Standard deviation, pg/g	11
Relative standard deviation, %	11
No. of values reported	58
No. of values removed	0
No. of reported non-detects	0

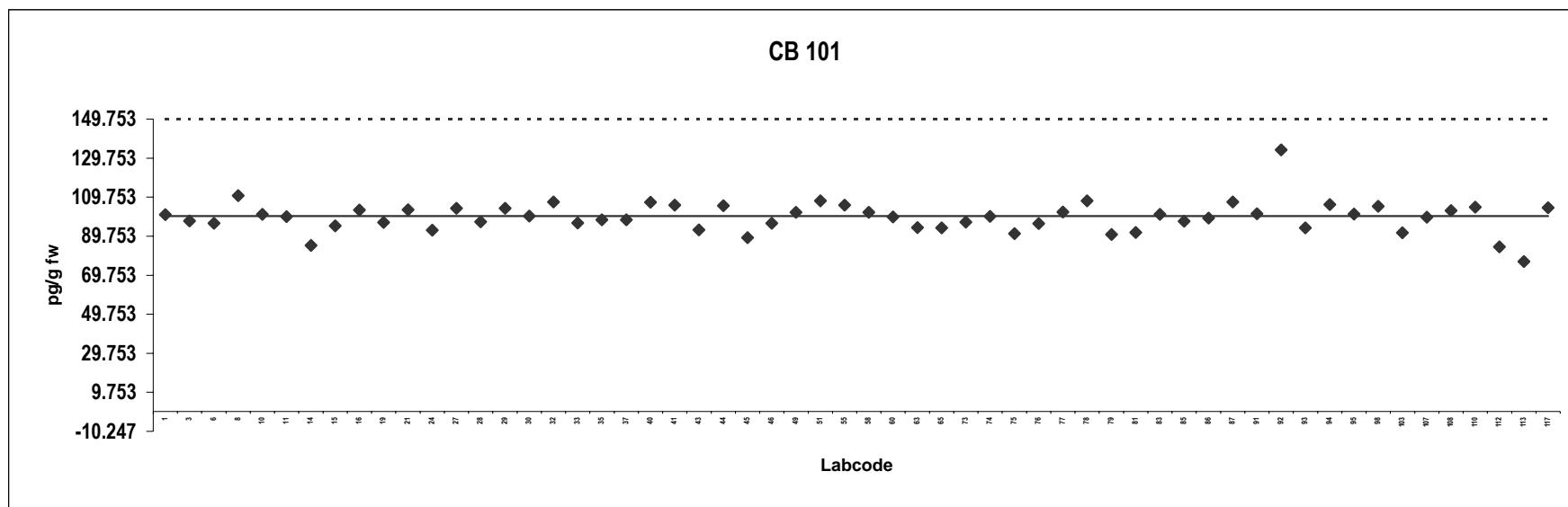


**Analyte solution**  
Congener: CB 101

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	101		91	101	
3	98		92	134	
6	96		93	94	
8	111		94	106	
10	101		95	101	
11	100		98	105	
14	85		103	92	
15	95		107	99	
16	103		108	103	
19	97		110	105	
21	103		112	84	
24	93		113	77	
27	104		117	104	
28	97				
29	104				
30	100				
32	107				
33	97				
35	98				
37	98				
40	107				
41	106				
43	93				
44	105				
45	89				
46	96				
49	102				
51	108				
55	106				
58	102				
60	100				
63	94				
65	94				
73	97				
74	100				
75	91				
76	96				
77	102				
78	108				
79	91				
81	92				
83	101				
85	97				
86	99				
87	107				

**Consensus statistics**

Consensus median, pg/g	100
Median all values pg/g	100
Consensus mean, pg/g	100
Standard deviation, pg/g	7.9
Relative standard deviation, %	8.0
No. of values reported	58
No. of values removed	0
No. of reported non-detects	0

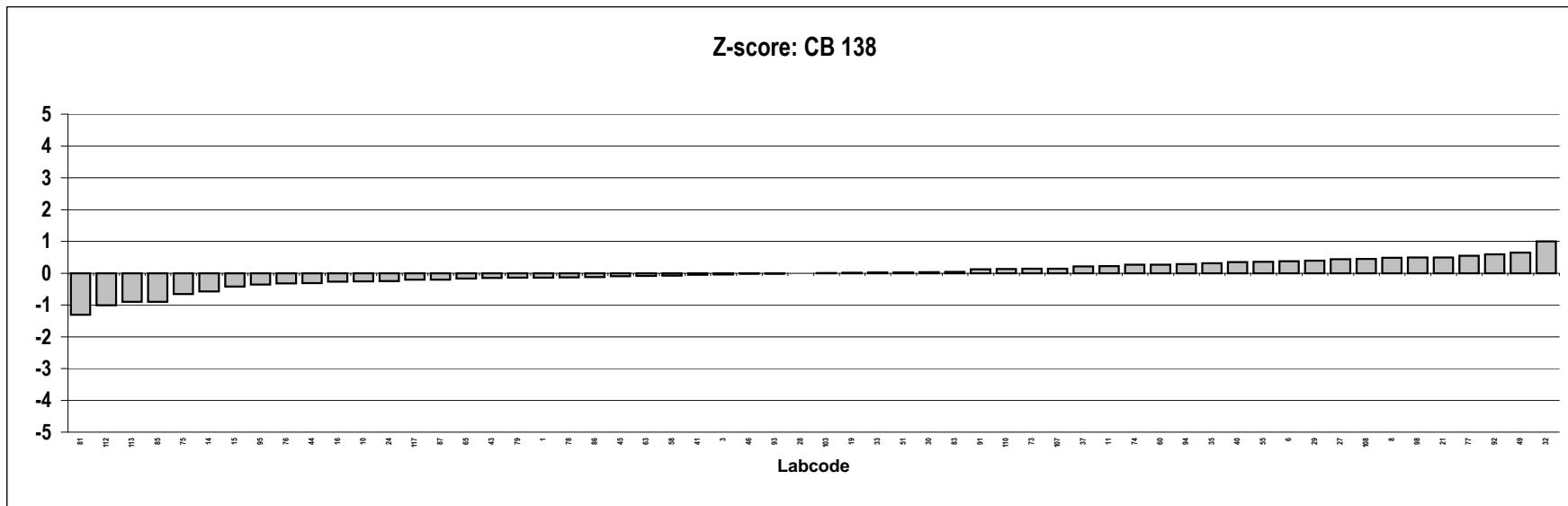
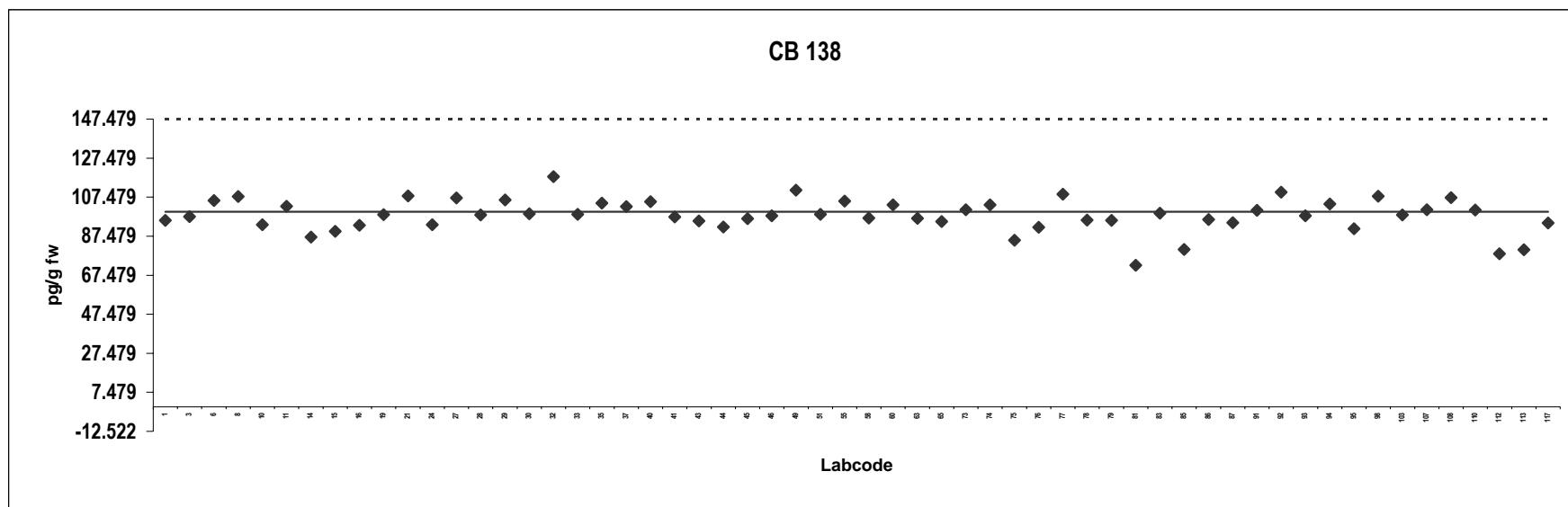


**Analyte solution**  
Congener: CB 138

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	96		91	101	
3	98		92	110	
6	106		93	98	
8	108		94	104	
10	93		95	91	
11	103		98	108	
14	87		103	98	
15	90		107	101	
16	93		108	107	
19	99		110	101	
21	108		112	78	
24	93		113	81	
27	107		117	94	
28	98				
29	106				
30	99				
32	118				
33	99				
35	104				
37	103				
40	105				
41	97				
43	95				
44	92				
45	96				
46	98				
49	111				
51	99				
55	105				
58	97				
60	104				
63	97				
65	95				
73	101				
74	104				
75	85				
76	92				
77	109				
78	96				
79	96				
81	73				
83	99				
85	81				
86	96				
87	94				

**Consensus statistics**

Consensus median, pg/g	98
Median all values pg/g	98
Consensus mean, pg/g	98
Standard deviation, pg/g	8.4
Relative standard deviation, %	8.5
No. of values reported	58
No. of values removed	0
No. of reported non-detects	0

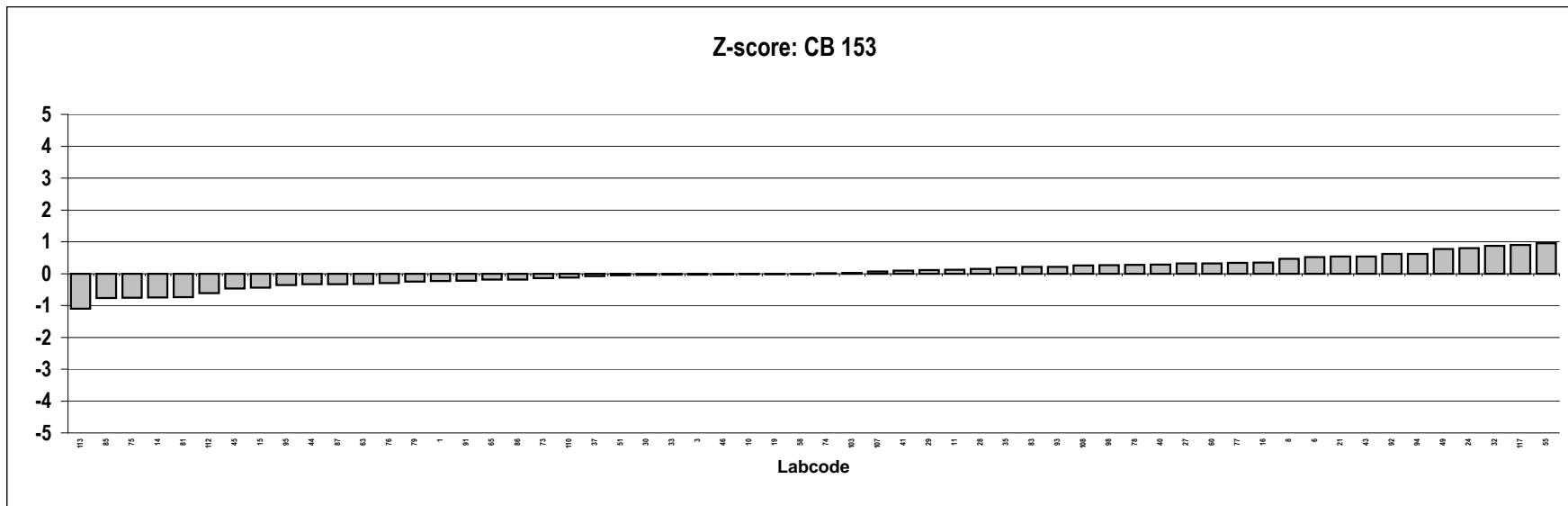
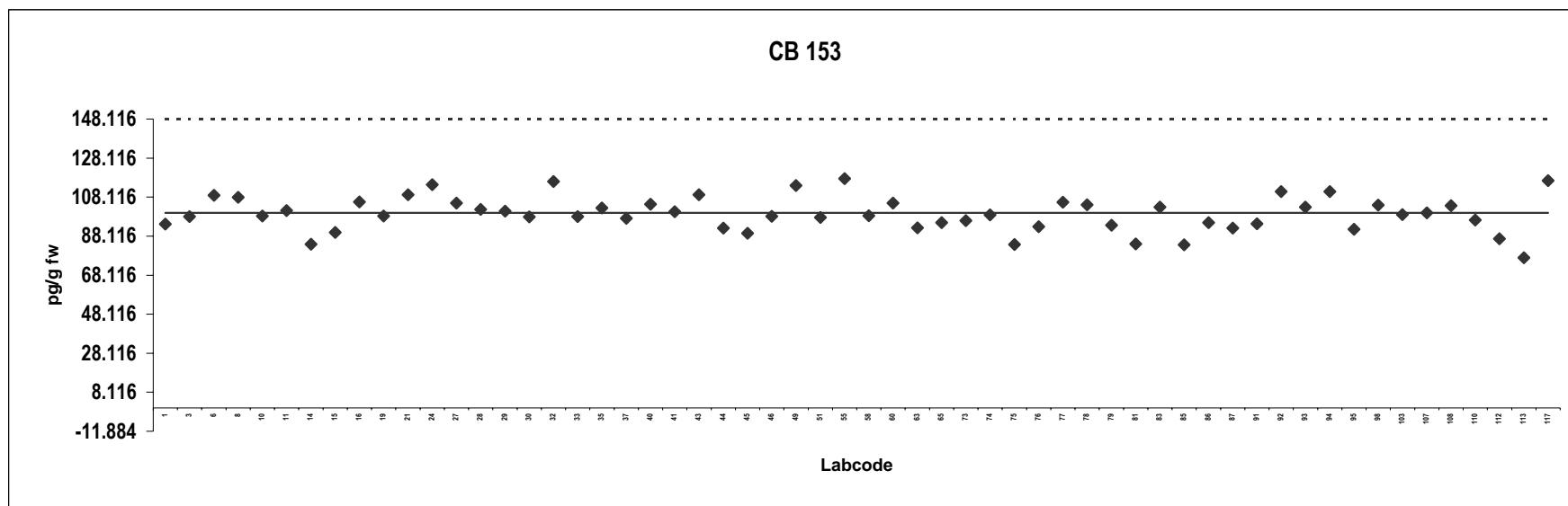


**Analyte solution**  
Congener: CB 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	94		91	94	
3	98		92	111	
6	109		93	103	
8	108		94	111	
10	98		95	92	
11	101		98	104	
14	84		103	99	
15	90		107	100	
16	106		108	104	
19	98		110	96	
21	109		112	87	
24	115		113	77	
27	105		117	117	
28	102				
29	101				
30	98				
32	116				
33	98				
35	103				
37	97				
40	104				
41	101				
43	109				
44	92				
45	90				
46	98				
49	114				
51	98				
55	118				
58	99				
60	105				
63	92				
65	95				
73	96				
74	99				
75	84				
76	93				
77	106				
78	104				
79	94				
81	84				
83	103				
85	84				
86	95				
87	92				

**Consensus statistics**

Consensus median, pg/g	99
Median all values pg/g	99
Consensus mean, pg/g	100
Standard deviation, pg/g	8.9
Relative standard deviation, %	8.9
No. of values reported	58
No. of values removed	0
No. of reported non-detects	0

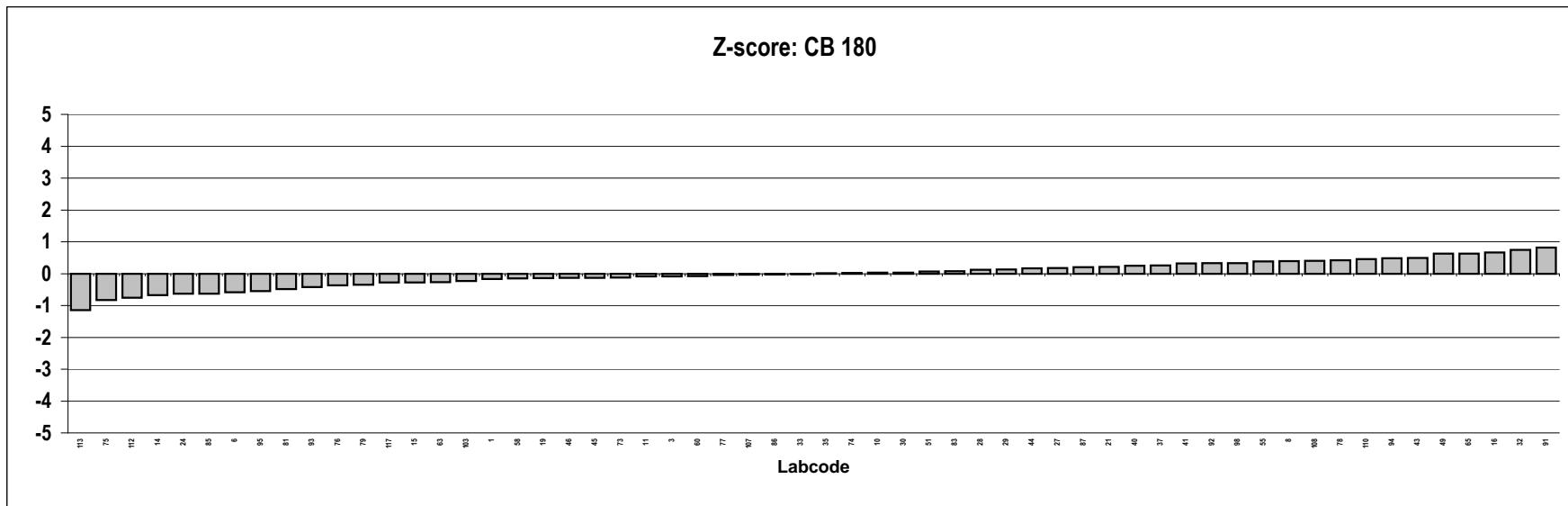
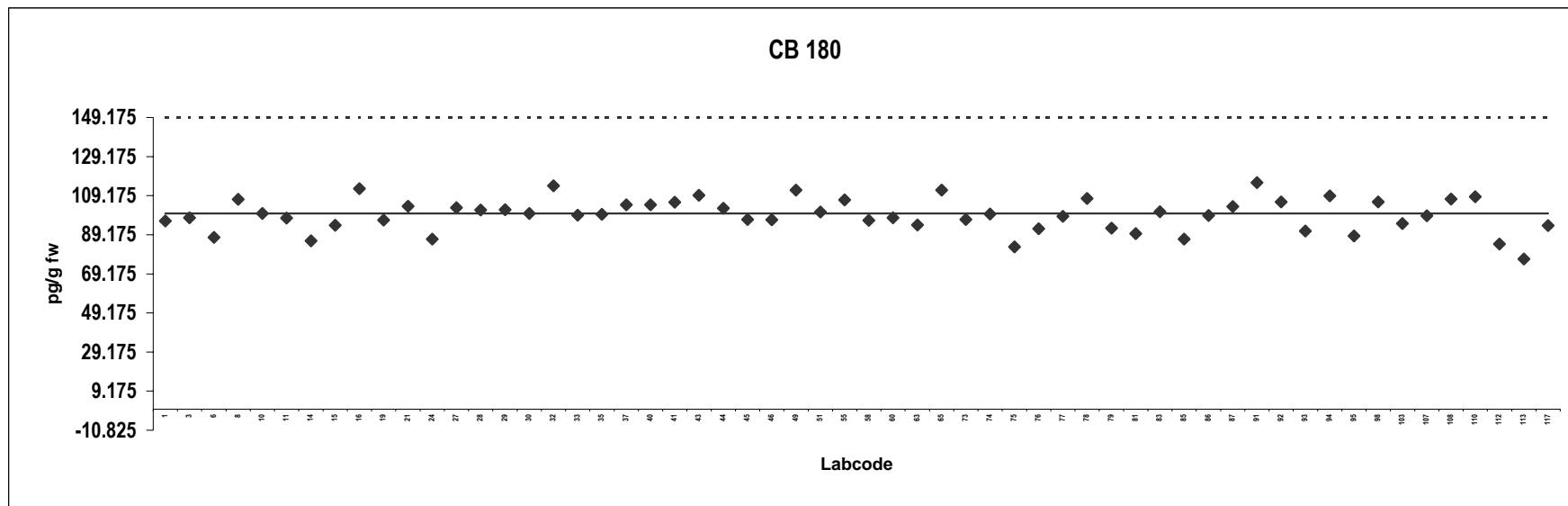


**Analyte solution**  
Congener: CB 180

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	96		91	116	
3	98		92	106	
6	88		93	91	
8	107		94	109	
10	100		95	89	
11	98		98	106	
14	86		103	95	
15	94		107	99	
16	113		108	108	
19	97		110	109	
21	104		112	85	
24	87		113	77	
27	103		117	94	
28	102				
29	102				
30	100				
32	114				
33	99				
35	100				
37	105				
40	104				
41	106				
43	109				
44	103				
45	97				
46	97				
49	112				
51	101				
55	107				
58	97				
60	98				
63	94				
65	112				
73	97				
74	100				
75	83				
76	92				
77	99				
78	108				
79	93				
81	90				
83	101				
85	87				
86	99				
87	104				

**Consensus statistics**

Consensus median, pg/g	99
Median all values pg/g	99
Consensus mean, pg/g	99
Standard deviation, pg/g	8.3
Relative standard deviation, %	8.4
No. of values reported	58
No. of values removed	0
No. of reported non-detects	0

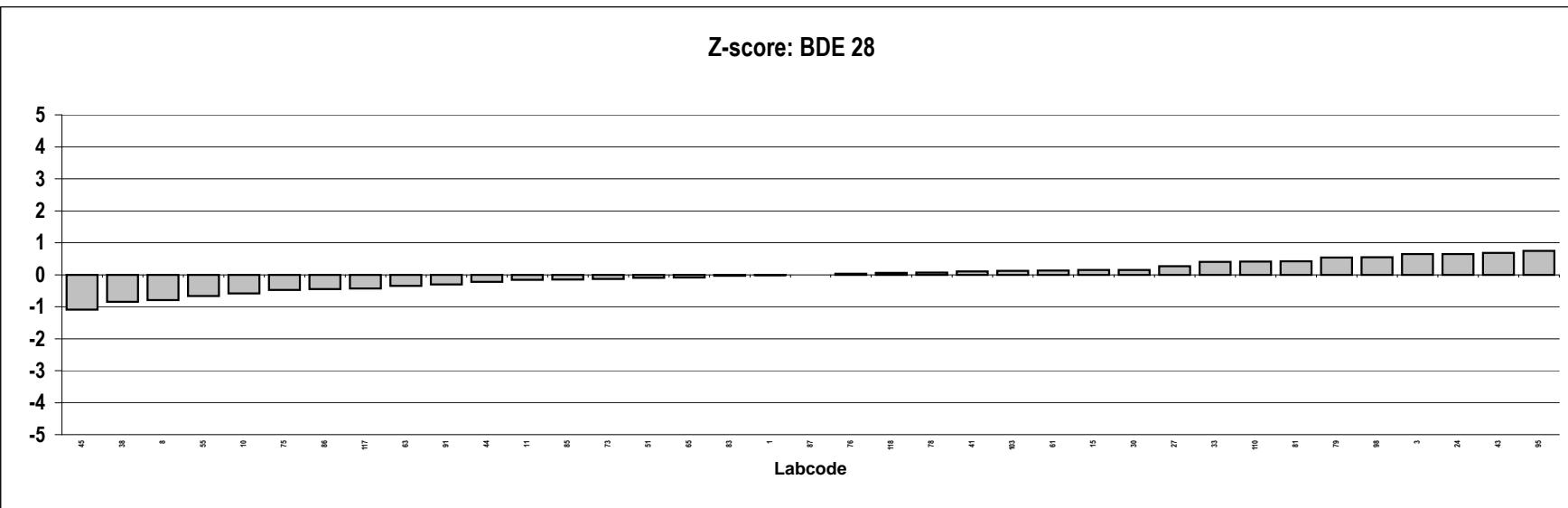
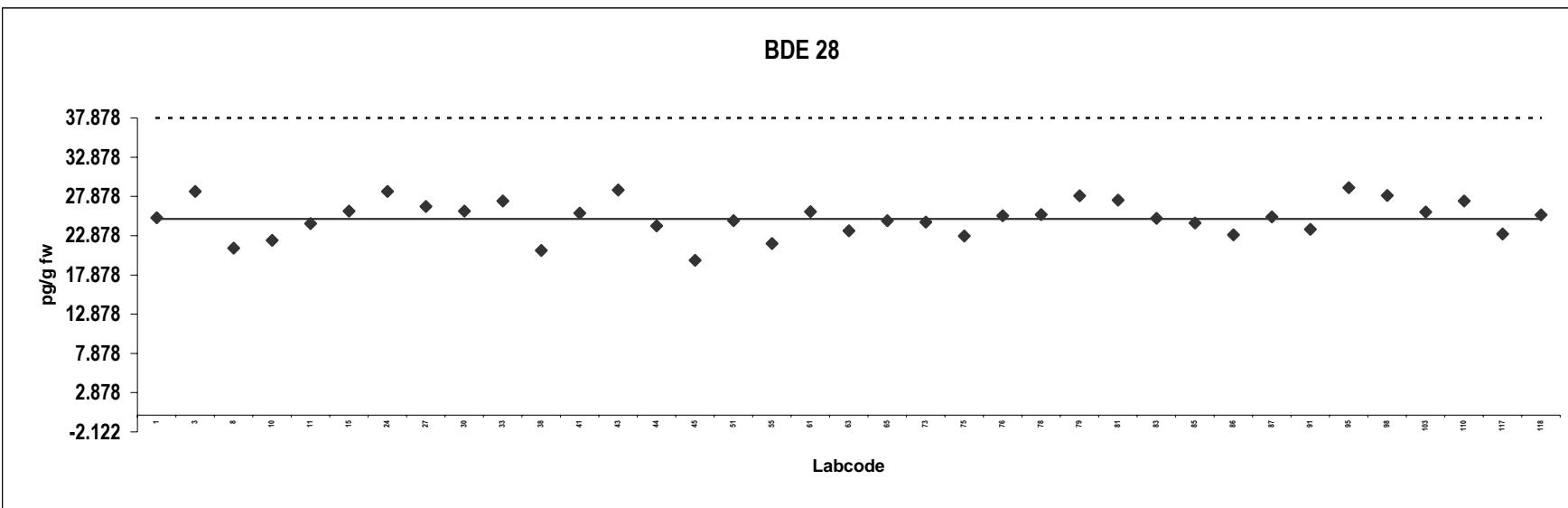


**Analyte solution**  
Congener: BDE 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	25				
3	29				
8	21				
10	22				
11	24				
15	26				
24	29				
27	27				
30	26				
33	27				
38	21				
41	26				
43	29				
44	24				
45	20				
51	25				
55	22				
61	26				
63	24				
65	25				
73	25				
75	23				
76	25				
78	26				
79	28				
81	27				
83	25				
85	25				
86	23				
87	25				
91	24				
95	29				
98	28				
103	26				
110	27				
117	23				
118	26				

**Consensus statistics**

Consensus median, pg/g	25
Median all values pg/g	25
Consensus mean, pg/g	25
Standard deviation, pg/g	2.3
Relative standard deviation, %	9.1
No. of values reported	37
No. of values removed	0
No. of reported non-detects	0

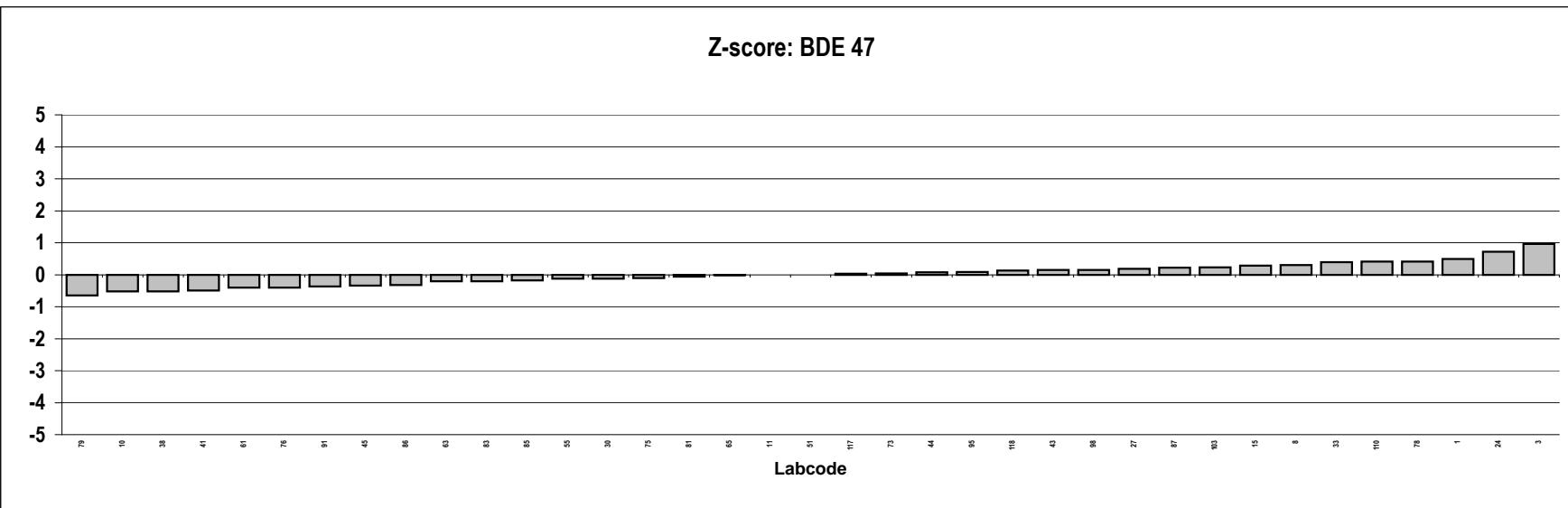
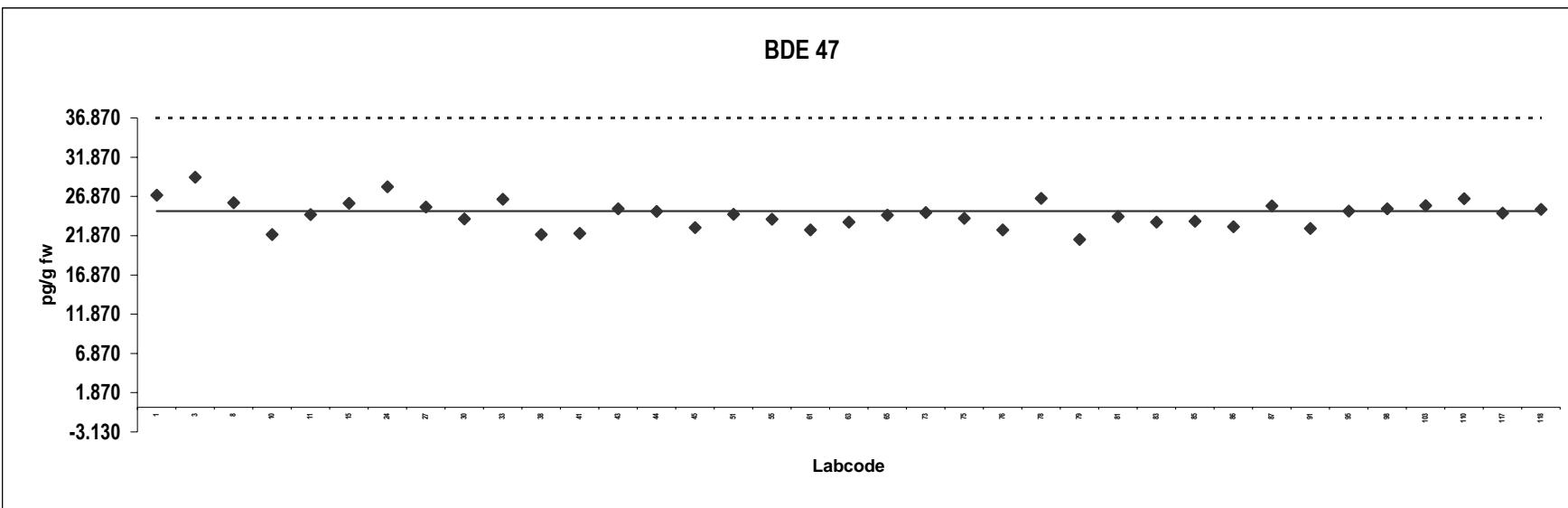


**Analyte solution**  
Congener: BDE 47

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	27				
3	29				
8	26				
10	22				
11	25				
15	26				
24	28				
27	26				
30	24				
33	27				
38	22				
41	22				
43	25				
44	25				
45	23				
51	25				
55	24				
61	23				
63	24				
65	25				
73	25				
75	24				
76	23				
78	27				
79	21				
81	24				
83	24				
85	24				
86	23				
87	26				
91	23				
95	25				
98	25				
103	26				
110	27				
117	25				
118	25				

**Consensus statistics**

Consensus median, pg/g	25
Median all values pg/g	25
Consensus mean, pg/g	25
Standard deviation, pg/g	1.8
Relative standard deviation, %	7.1
No. of values reported	37
No. of values removed	0
No. of reported non-detects	0

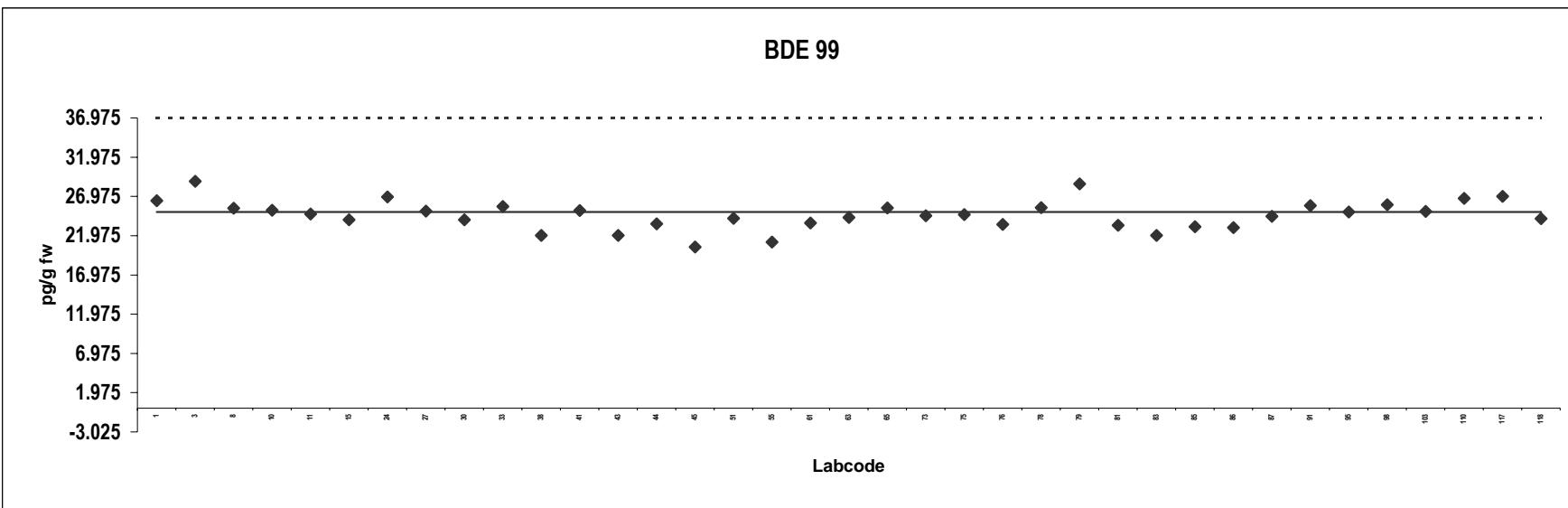


**Analyte solution**  
Congener: BDE 99

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	26				
3	29				
8	25				
10	25				
11	25				
15	24				
24	27				
27	25				
30	24				
33	26				
38	22				
41	25				
43	22				
44	23				
45	21				
51	24				
55	21				
61	24				
63	24				
65	26				
73	25				
75	25				
76	23				
78	26				
79	29				
81	23				
83	22				
85	23				
86	23				
87	24				
91	26				
95	25				
98	26				
103	25				
110	27				
117	27				
118	24				

**Consensus statistics**

Consensus median, pg/g	25
Median all values pg/g	25
Consensus mean, pg/g	25
Standard deviation, pg/g	1.8
Relative standard deviation, %	7.5
No. of values reported	37
No. of values removed	0
No. of reported non-detects	0

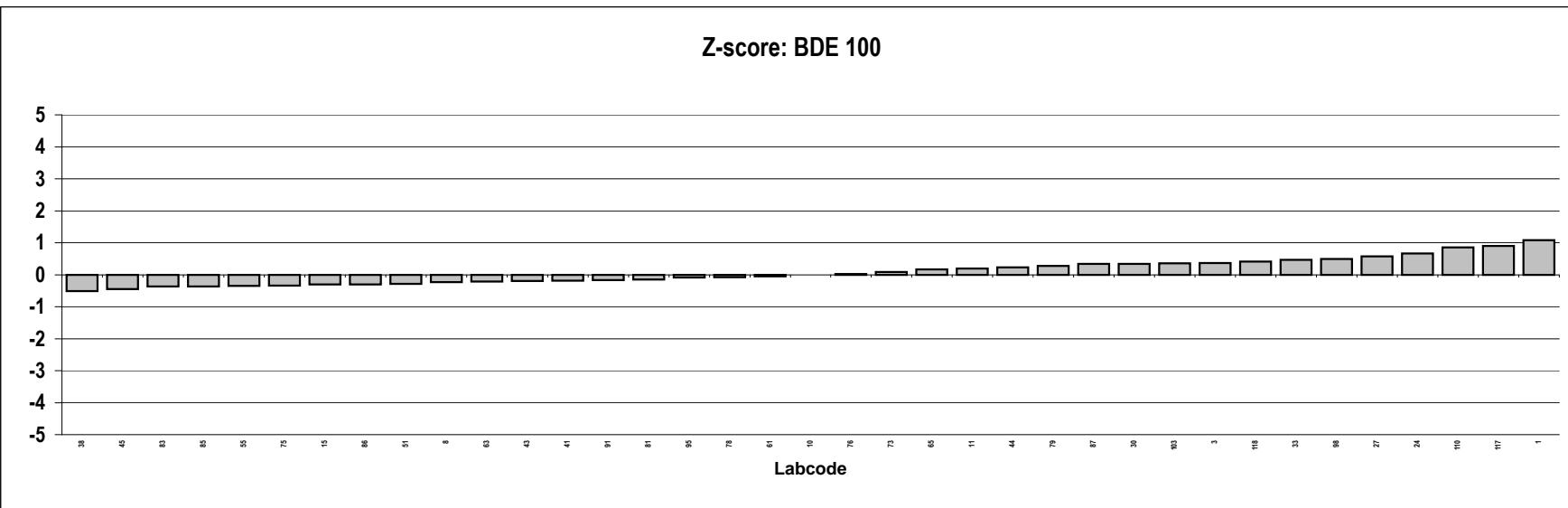
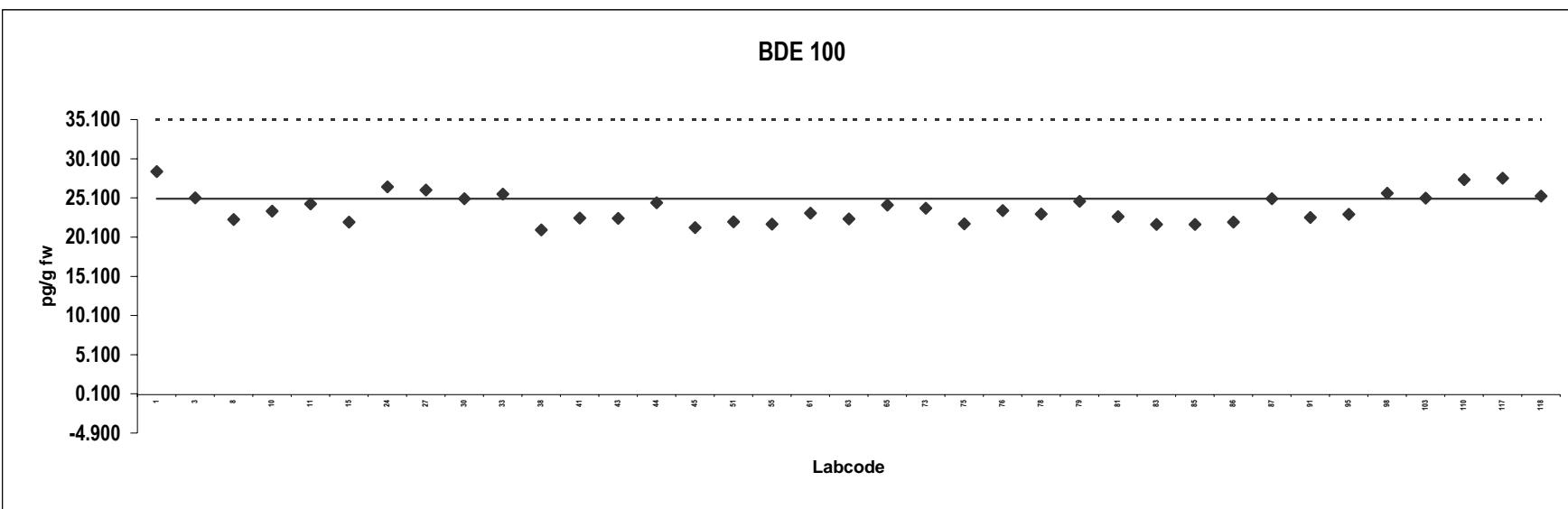


**Analyte solution**  
Congener: BDE 100

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	28				
3	25				
8	22				
10	23				
11	24				
15	22				
24	27				
27	26				
30	25				
33	26				
38	21				
41	23				
43	23				
44	24				
45	21				
51	22				
55	22				
61	23				
63	22				
65	24				
73	24				
75	22				
76	24				
78	23				
79	25				
81	23				
83	22				
85	22				
86	22				
87	25				
91	23				
95	23				
98	26				
103	25				
110	27				
117	28				
118	25				

**Consensus statistics**

Consensus median, pg/g	23
Median all values pg/g	23
Consensus mean, pg/g	24
Standard deviation, pg/g	1.9
Relative standard deviation, %	8.0
No. of values reported	37
No. of values removed	0
No. of reported non-detects	0

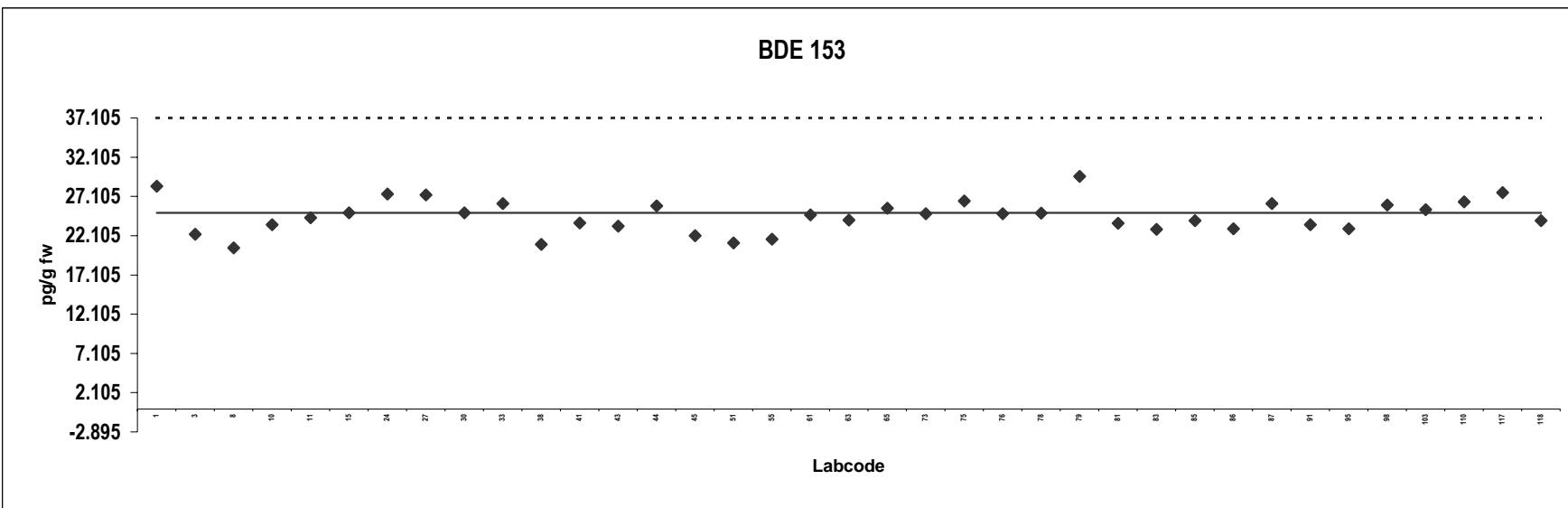


**Analyte solution**  
Congener: BDE 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	28				
3	22				
8	21				
10	24				
11	24				
15	25				
24	27				
27	27				
30	25				
33	26				
38	21				
41	24				
43	23				
44	26				
45	22				
51	21				
55	22				
61	25				
63	24				
65	26				
73	25				
75	27				
76	25				
78	25				
79	30				
81	24				
83	23				
85	24				
86	23				
87	26				
91	24				
95	23				
98	26				
103	25				
110	26				
117	28				
118	24				

**Consensus statistics**

Consensus median, pg/g	25
Median all values pg/g	25
Consensus mean, pg/g	25
Standard deviation, pg/g	2.1
Relative standard deviation, %	8.5
No. of values reported	37
No. of values removed	0
No. of reported non-detects	0

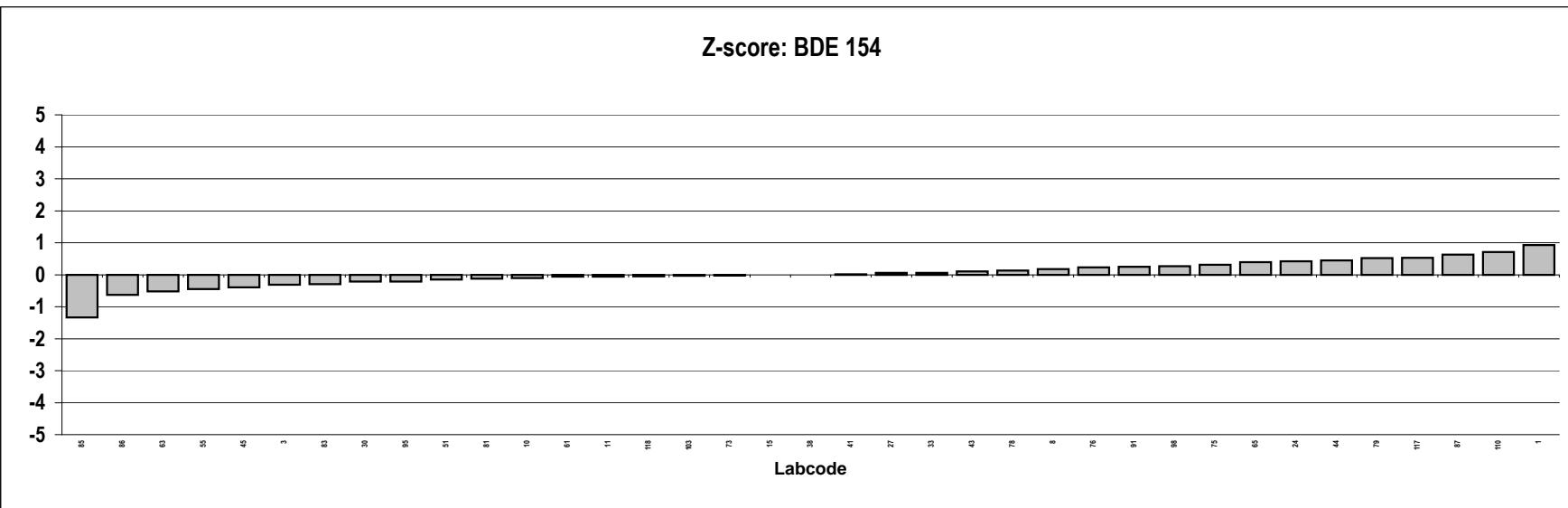
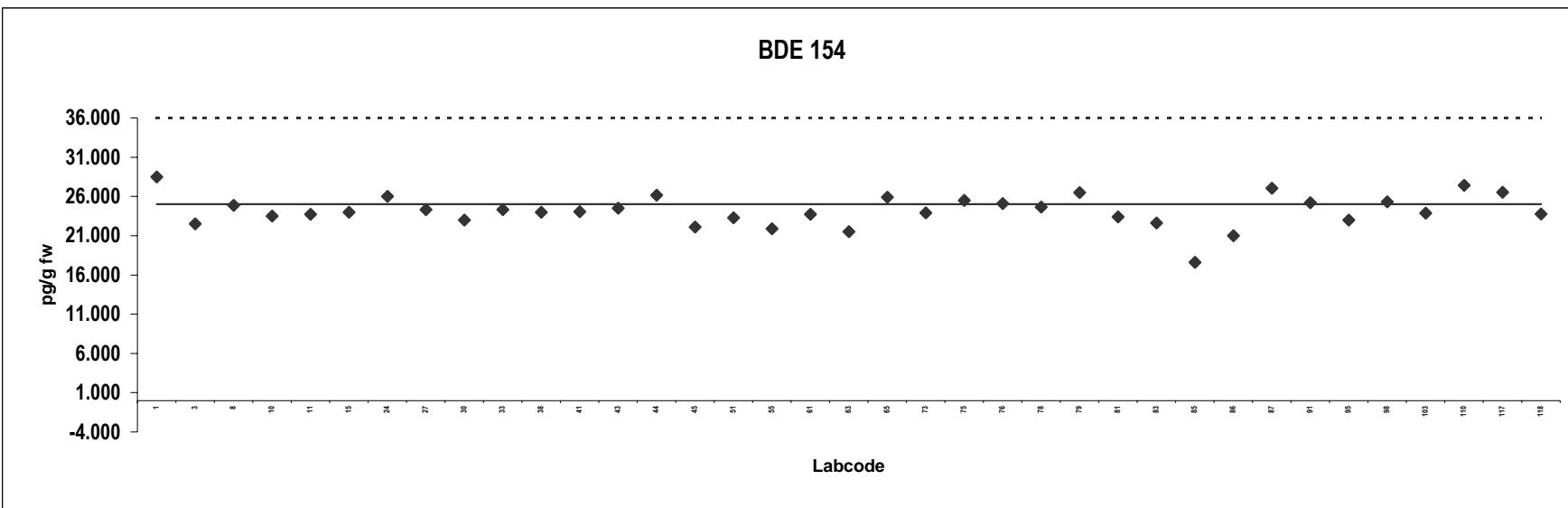


**Analyte solution**  
Congener: BDE 154

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	28				
3	23				
8	25				
10	24				
11	24				
15	24				
24	26				
27	24				
30	23				
33	24				
38	24				
41	24				
43	25				
44	26				
45	22				
51	23				
55	22				
61	24				
63	22				
65	26				
73	24				
75	26				
76	25				
78	25				
79	26				
81	23				
83	23				
85	18				
86	21				
87	27				
91	25				
95	23				
98	25				
103	24				
110	27				
117	27				
118	24				

**Consensus statistics**

Consensus median, pg/g	24
Median all values pg/g	24
Consensus mean, pg/g	24
Standard deviation, pg/g	2.0
Relative standard deviation, %	8.3
No. of values reported	37
No. of values removed	0
No. of reported non-detects	0

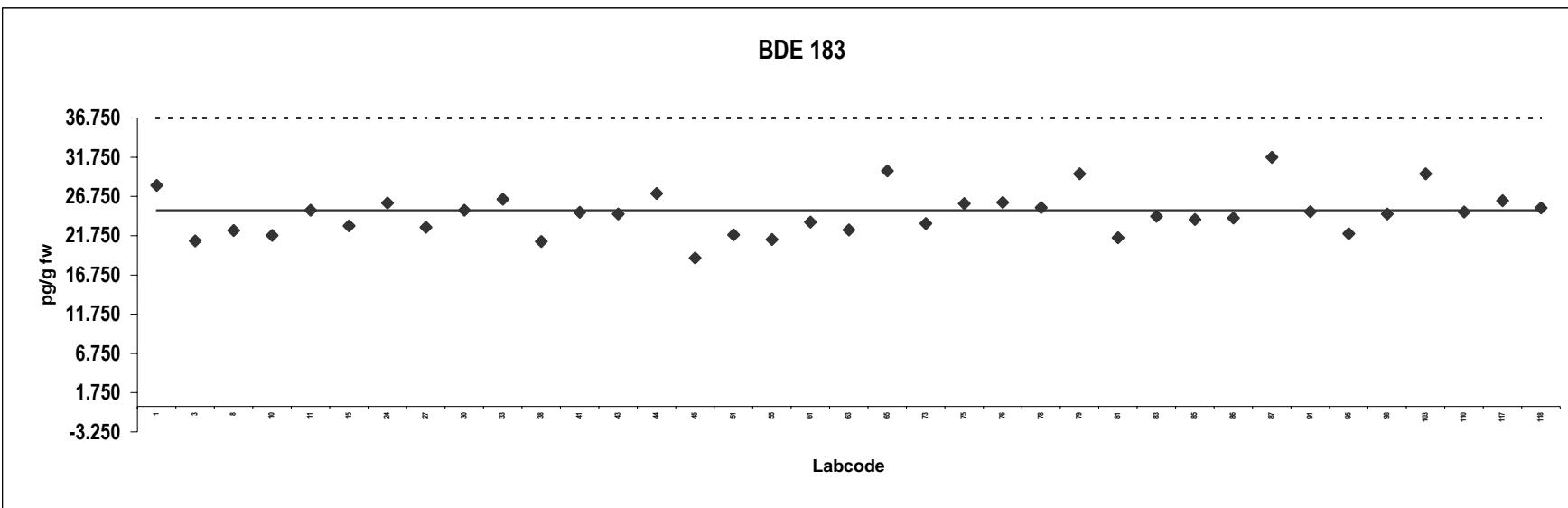


**Analyte solution**  
Congener: BDE 183

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	28				
3	21				
8	22				
10	22				
11	25				
15	23				
24	26				
27	23				
30	25				
33	26				
38	21				
41	25				
43	25				
44	27				
45	19				
51	22				
55	21				
61	23				
63	23				
65	30				
73	23				
75	26				
76	26				
78	25				
79	30				
81	22				
83	24				
85	24				
86	24				
87	32				
91	25				
95	22				
98	25				
103	30				
110	25				
117	26				
118	25				

**Consensus statistics**

Consensus median, pg/g	25
Median all values pg/g	25
Consensus mean, pg/g	25
Standard deviation, pg/g	2.8
Relative standard deviation, %	11
No. of values reported	37
No. of values removed	0
No. of reported non-detects	0

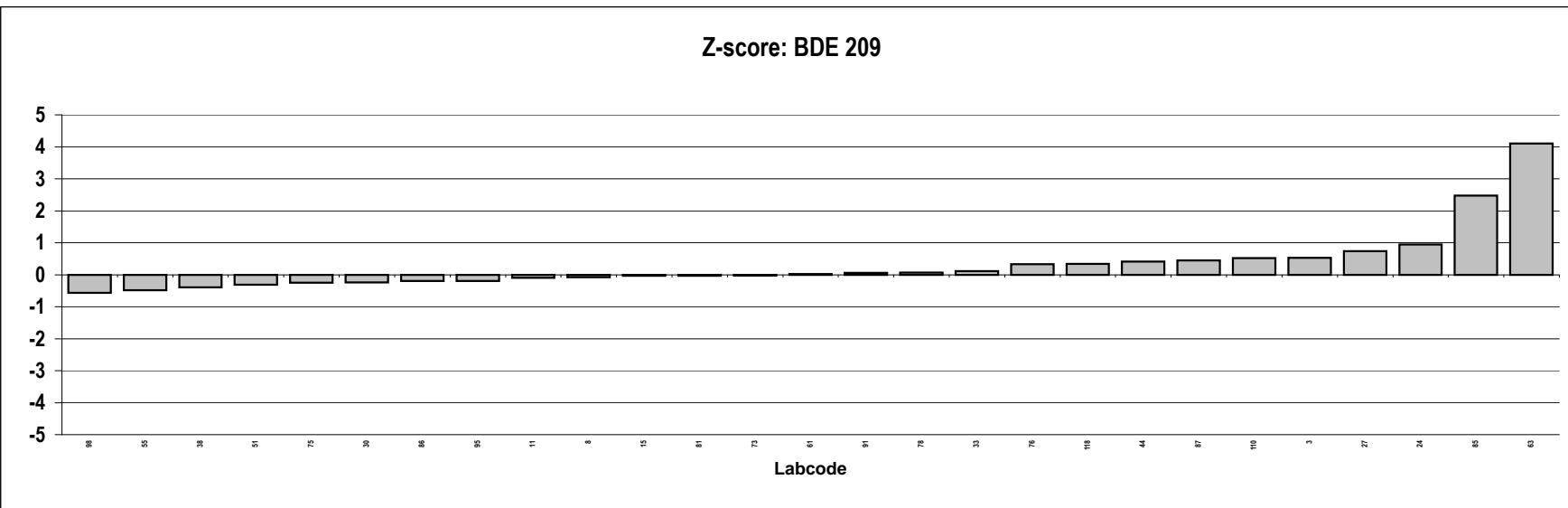
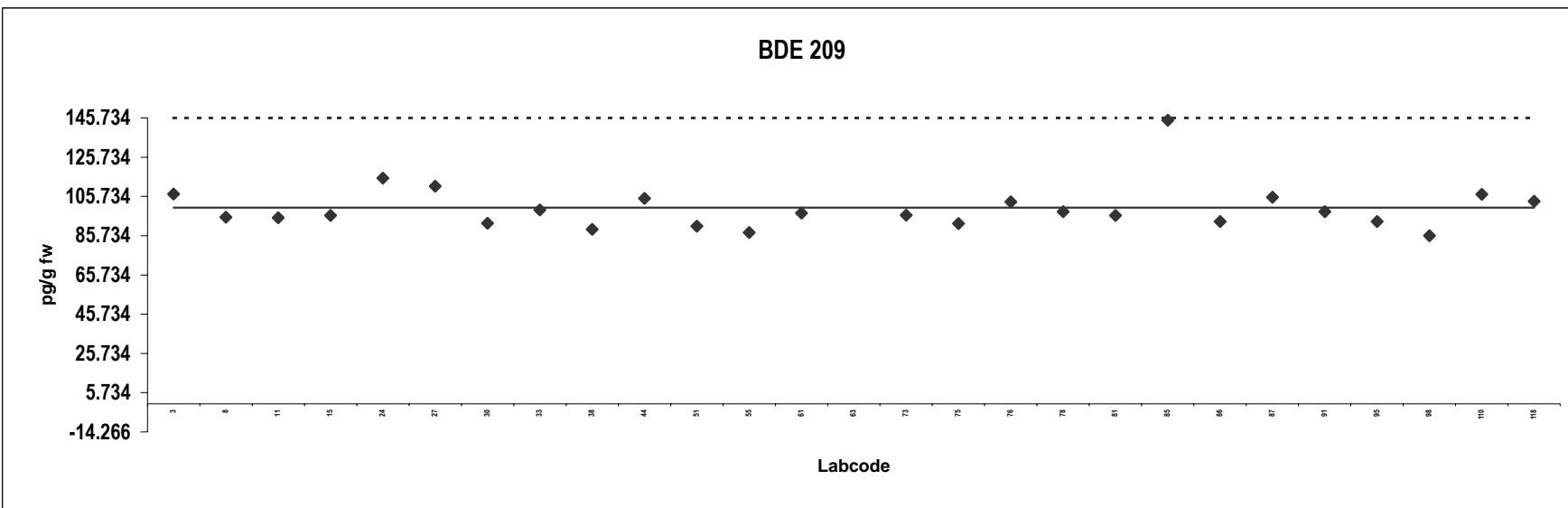


**Analyte solution**  
Congener: BDE 209

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	107				
8	95				
11	95				
15	96				
24	115				
27	111				
30	92				
33	99				
38	89				
44	105				
51	91				
55	87				
61	97				
63	176	Outlier			
73	96				
75	92				
76	103				
78	98				
81	96				
85	145				
86	93				
87	105				
91	98				
95	93				
98	86				
110	107				
118	103				

**Consensus statistics**

Consensus median, pg/g	97
Median all values pg/g	97
Consensus mean, pg/g	100
Standard deviation, pg/g	12
Relative standard deviation, %	12
No. of values reported	27
No. of values removed	1
No. of reported non-detects	0

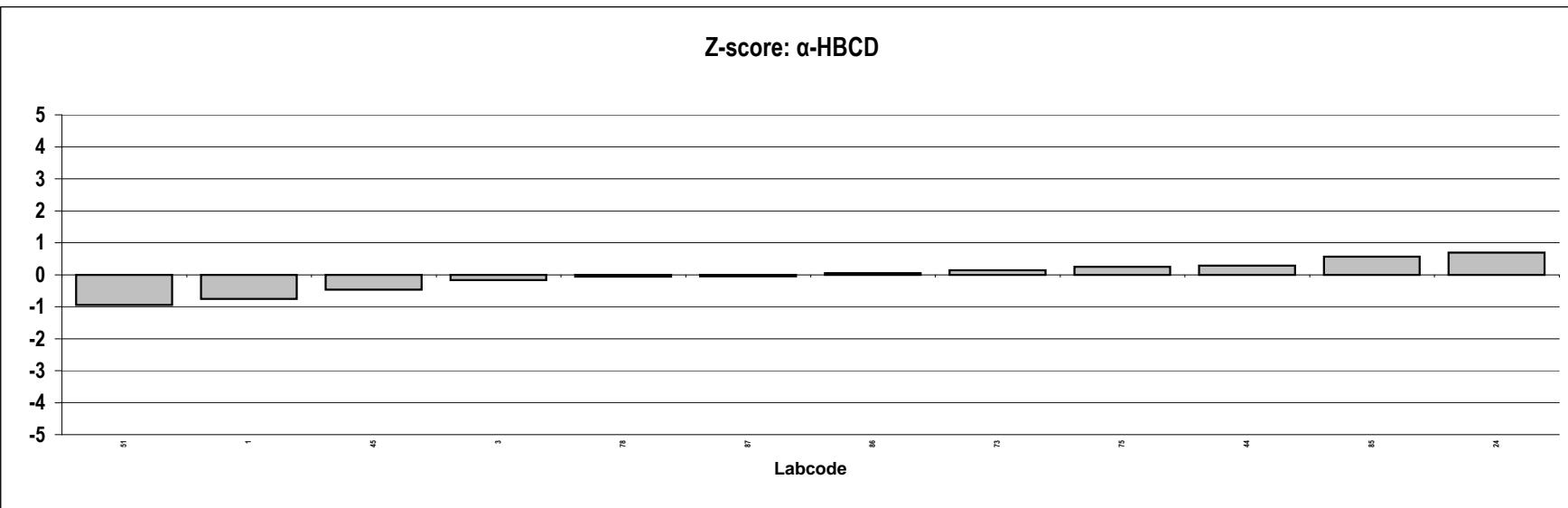
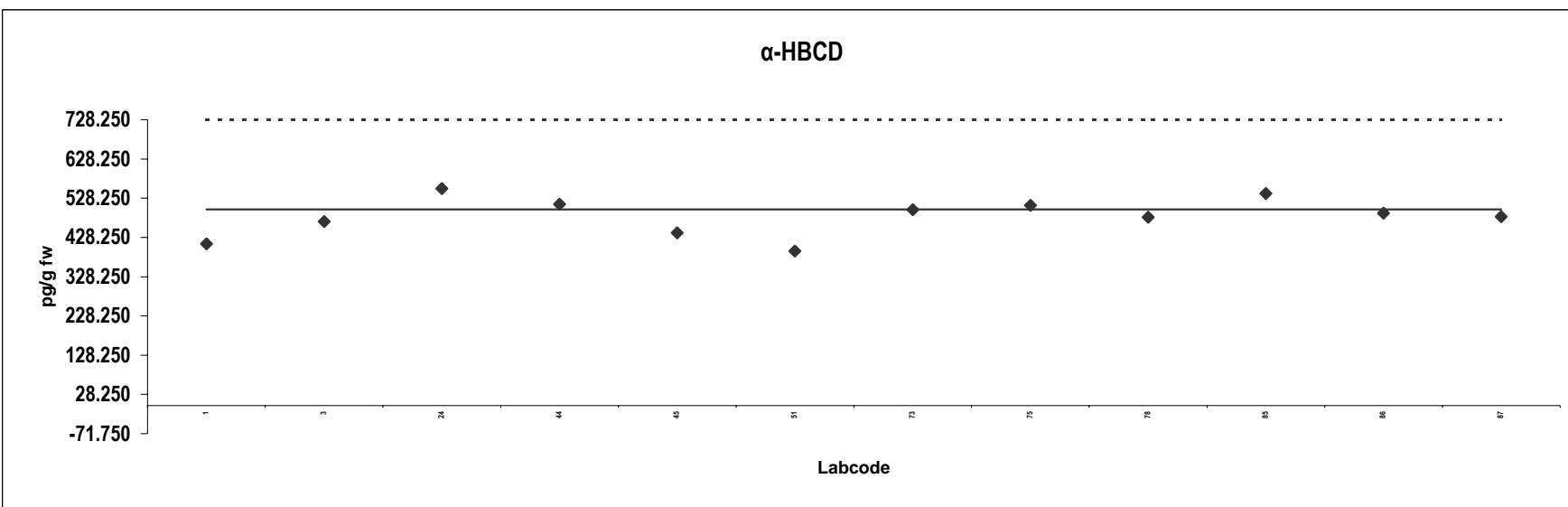


**Analyte solution**  
Congener:  $\alpha$ -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	412				
3	469				
24	553				
44	513				
45	440				
51	394				
73	499				
75	510				
78	480				
85	540				
86	490				
87	481				

**Consensus statistics**

Consensus median, pg/g	486
Median all values pg/g	486
Consensus mean, pg/g	482
Standard deviation, pg/g	48
Relative standard deviation, %	10
No. of values reported	12
No. of values removed	0
No. of reported non-detects	0





## **Appendix 2:**

Presentation of results  
for Pork



## Appendix 2: Presentation of results: Pork

### Statistic calculations for PCDDs, PCDFs and dioxin-like PCBs

For each congener, the outliers were removed and the consensus calculated according to the following procedure:

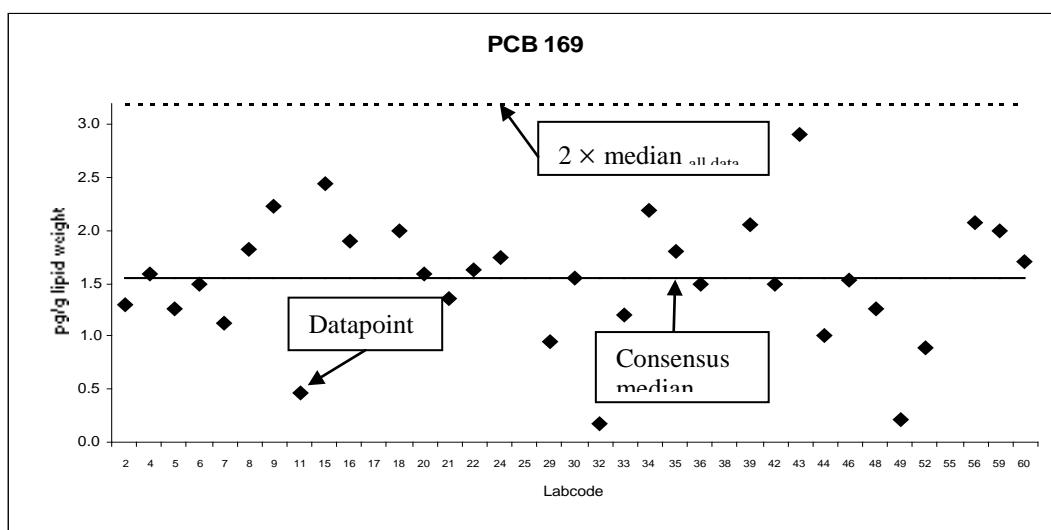
1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners.
2. Values exceeding  $2 \times$  this median were defined as outliers and removed from the data set.
3. Median, mean and standard deviation were re-calculated from the remaining data. This second median was called consensus.

### Statistic calculations for indicator PCBs, PBDEs and HBCD

For each congener, the outliers were removed and the consensus calculated according to the following procedure:

1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners (NDs).
2. Values exceeding  $2 \times$  this median were defined as outliers and removed from the data set. The NDs were also removed.
3. Median, mean and standard deviation were re-calculated from the remaining data. This second median was called consensus.
4. For comparison, median, mean and standard deviation were also calculated without removing NDs.

The diagram shows the reported data up to approximately the limit for outliers ( $2 \times$  the first median).



### Z-Scores of individual congeners

Z-scores of each congener were calculated for each laboratory according to the following equation:

$$z = (x - X)/\sigma$$

where  $x$  = reported value;  $X$  = assigned value (consensus);  $\sigma$  = target value for standard deviation. A  $\sigma$  of 20% of the consensus was used, i.e. z-scores between +1 and -1 reflect a deviation of  $\pm 20\%$  from the consensus value.

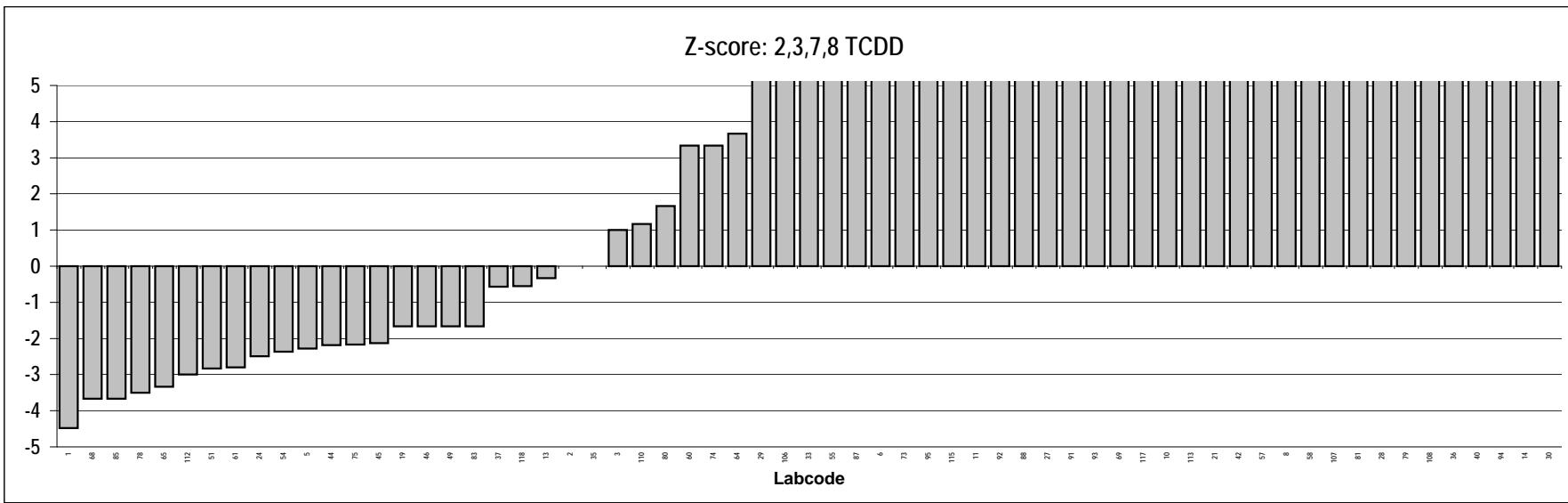
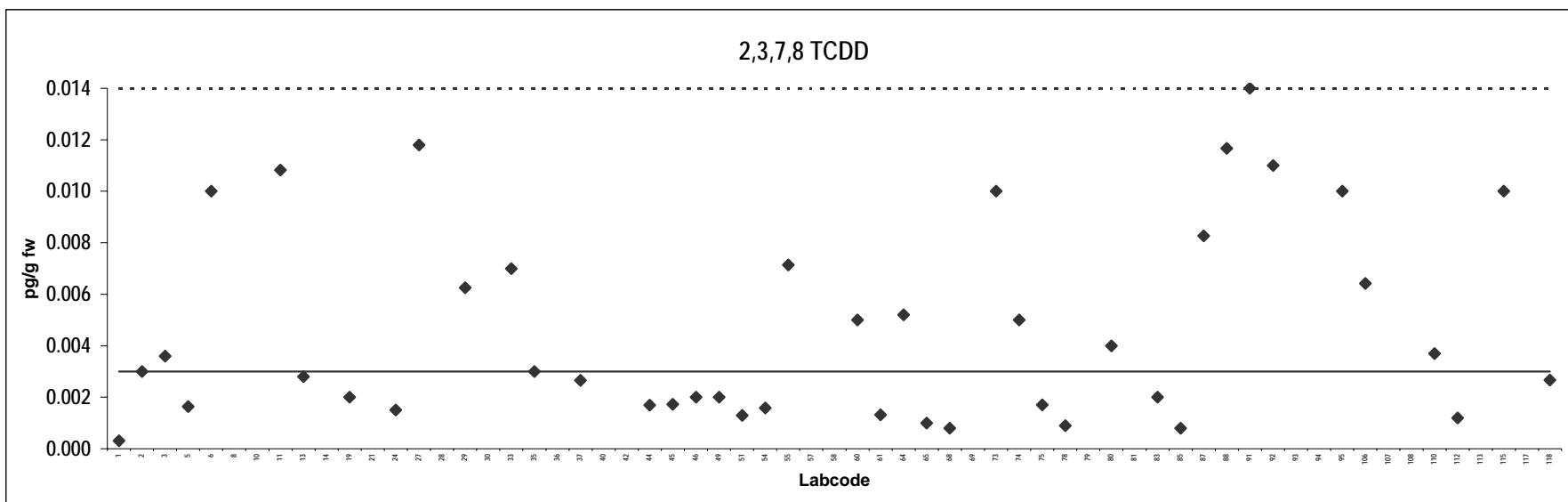


**Pork**  
**Congener: 2,3,7,8 TCDD**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.00031	ND	83	0.0020	
2	0.0030	ND	85	0.00080	ND
3	0.0036	ND	87	0.0083	
5	0.0016		88	0.012	
6	0.010	ND	91	0.014	ND
8	0.021	Outlier	92	0.011	ND
10	0.017	Outlier,ND	93	0.015	Outlier,ND
11	0.011		94	0.040	Outlier,ND
13	0.0028		95	0.010	ND
14	0.051	Outlier,ND	106	0.0064	ND
19	0.0020	ND	107	0.027	Outlier,ND
21	0.019	Outlier,ND	108	0.031	Outlier,ND
24	0.0015		110	0.0037	ND
27	0.012	ND	112	0.0012	ND
28	0.030	Outlier,ND	113	0.018	Outlier,ND
29	0.0063	ND	115	0.010	ND
30	0.052	Outlier,ND	117	0.017	Outlier
33	0.0070	ND	118	0.0027	ND
35	0.0030	ND			
36	0.038	Outlier,ND			
37	0.0027	ND			
40	0.039	Outlier,ND			
42	0.020	Outlier,ND			
44	0.0017				
45	0.0017	ND			
46	0.0020	ND			
49	0.0020	ND			
51	0.0013				
54	0.0016	ND			
55	0.0071	ND			
57	0.020	Outlier,ND			
58	0.025	Outlier,ND			
60	0.0050	ND			
61	0.0013				
64	0.0052	ND			
65	0.0010	ND			
68	0.00080	ND			
69	0.016	Outlier,ND			
73	0.010	ND			
74	0.0050	ND			
75	0.0017				
78	0.00090	ND			
79	0.030	Outlier			
80	0.0040				
81	0.029	Outlier,ND			

**Consensus statistics**

Consensus median, pg/g	0.0030
Median all values pg/g	0.0070
Consensus mean, pg/g	0.0047
Standard deviation, pg/g	0.0039
Relative standard deviation, %	83
No. of values reported	63
No. of values removed	20
No. of reported non-detects	49

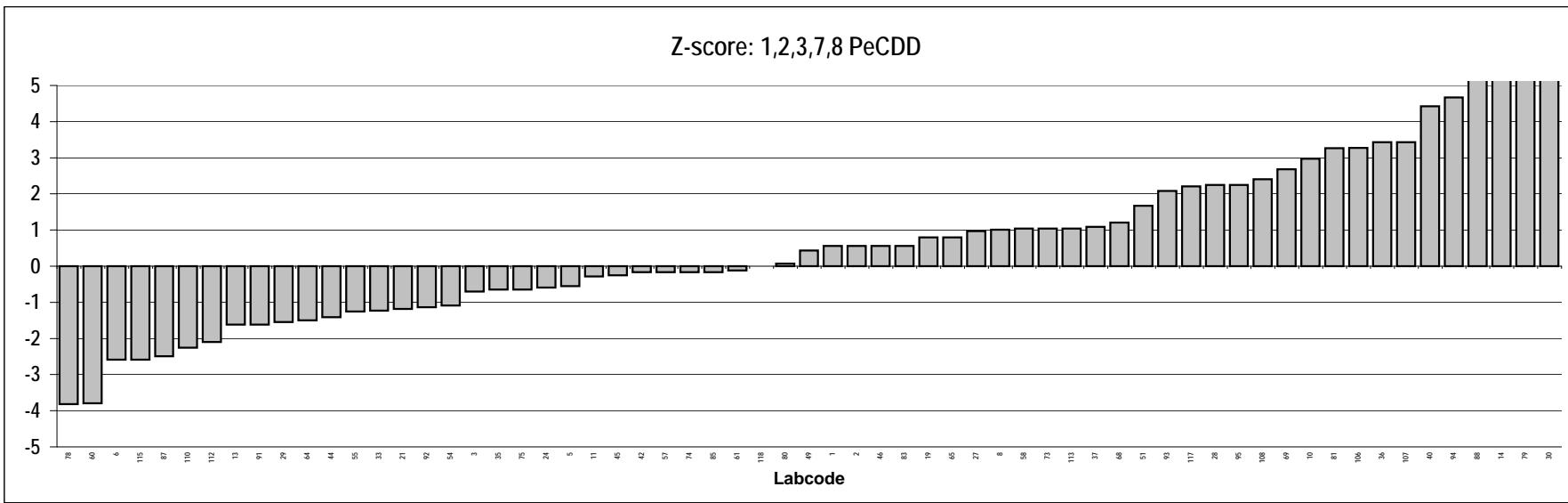
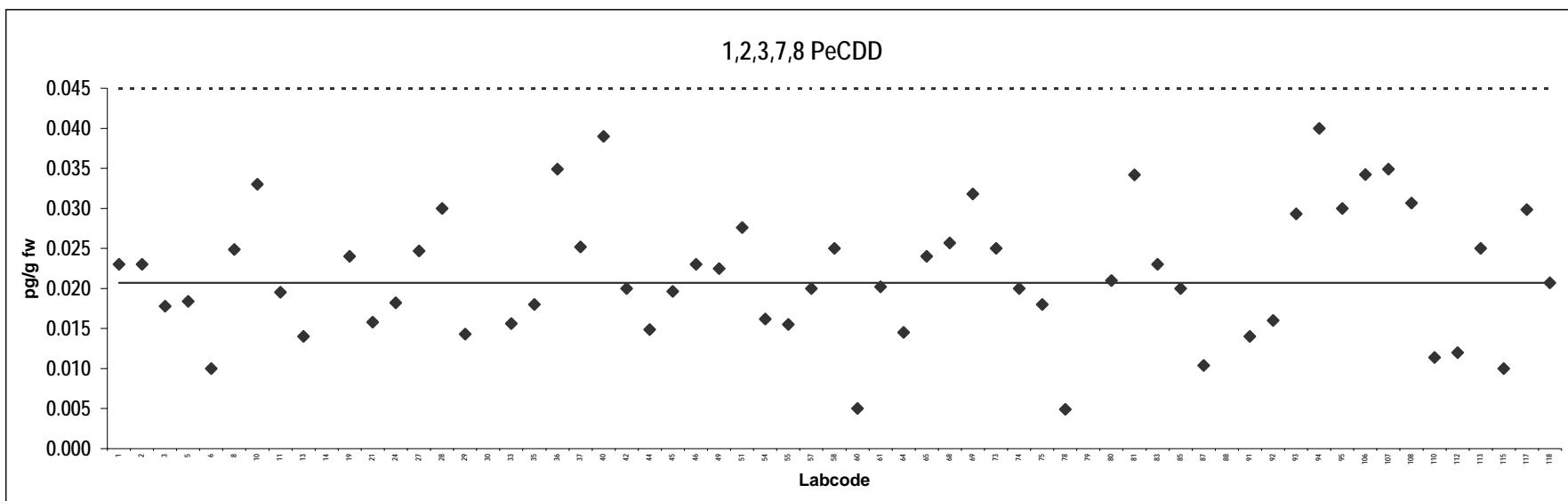


**Pork**  
Congener: 1,2,3,7,8 PeCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.023		83	0.023	
2	0.023		85	0.020	
3	0.018		87	0.010	
5	0.018		88	0.067	Outlier
6	0.010	ND	91	0.014	ND
8	0.025		92	0.016	ND
10	0.033		93	0.029	
11	0.020		94	0.040	ND
13	0.014		95	0.030	
14	0.067	Outlier,ND	106	0.034	
19	0.024	ND	107	0.035	ND
21	0.016	ND	108	0.031	ND
24	0.018		110	0.011	
27	0.025		112	0.012	
28	0.030	ND	113	0.025	ND
29	0.014		115	0.010	ND
30	0.096	Outlier,ND	117	0.030	ND
33	0.016		118	0.021	
35	0.018				
36	0.035	ND			
37	0.025	ND			
40	0.039	ND			
42	0.020				
44	0.015				
45	0.020				
46	0.023				
49	0.023				
51	0.028				
54	0.016				
55	0.015	ND			
57	0.020	ND			
58	0.025	ND			
60	0.0050	ND			
61	0.020				
64	0.015	ND			
65	0.024				
68	0.026				
69	0.032	ND			
73	0.025				
74	0.020				
75	0.018				
78	0.0049				
79	0.070	Outlier			
80	0.021				
81	0.034				

**Consensus statistics**

Consensus median, pg/g	0.021
Median all values pg/g	0.023
Consensus mean, pg/g	0.022
Standard deviation, pg/g	0.0080
Relative standard deviation, %	37
No. of values reported	63
No. of values removed	4
No. of reported non-detects	20

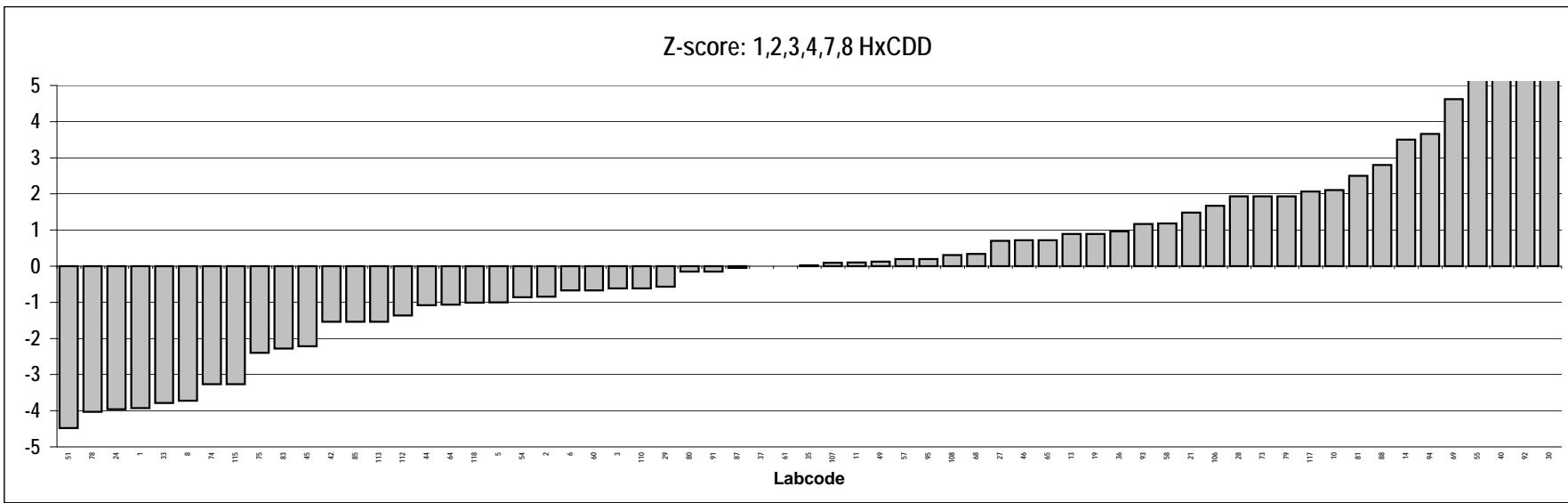
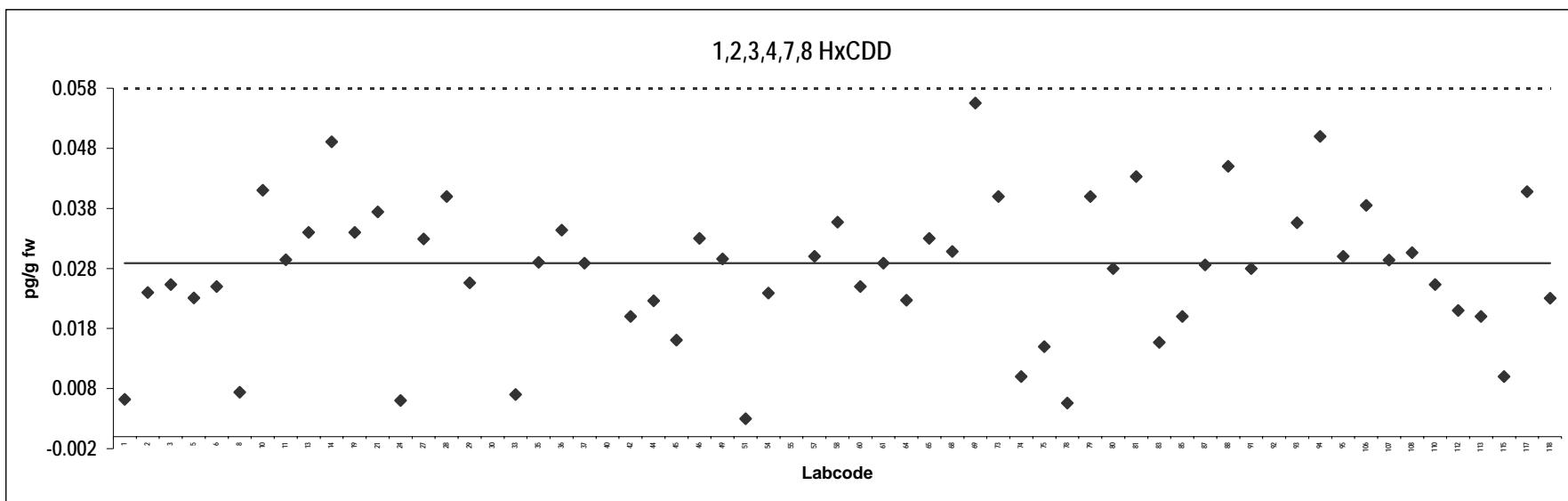


**Pork**  
Congener: 1,2,3,4,7,8 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.0062		83	0.016	
2	0.024		85	0.020	
3	0.025		87	0.029	
5	0.023		88	0.045	
6	0.025	ND	91	0.028	
8	0.0074	ND	92	0.080	Outlier,ND
10	0.041		93	0.036	ND
11	0.029		94	0.050	ND
13	0.034		95	0.030	
14	0.049		106	0.039	
19	0.034		107	0.029	
21	0.037		108	0.031	ND
24	0.0060	ND	110	0.025	
27	0.033		112	0.021	
28	0.040	ND	113	0.020	ND
29	0.026		115	0.010	ND
30	0.10	Outlier,ND	117	0.041	ND
33	0.0070	ND	118	0.023	
35	0.029				
36	0.034	ND			
37	0.029				
40	0.077	Outlier,ND			
42	0.020				
44	0.023				
45	0.016	ND			
46	0.033				
49	0.030				
51	0.0030	ND			
54	0.024				
55	0.064	Outlier,ND			
57	0.030				
58	0.036				
60	0.025				
61	0.029				
64	0.023	ND			
65	0.033				
68	0.031				
69	0.056	ND			
73	0.040				
74	0.010	ND			
75	0.015				
78	0.0056				
79	0.040				
80	0.028				
81	0.043				

**Consensus statistics**

Consensus median, pg/g	0.029
Median all values pg/g	0.029
Consensus mean, pg/g	0.028
Standard deviation, pg/g	0.012
Relative standard deviation, %	43
No. of values reported	63
No. of values removed	4
No. of reported non-detects	20

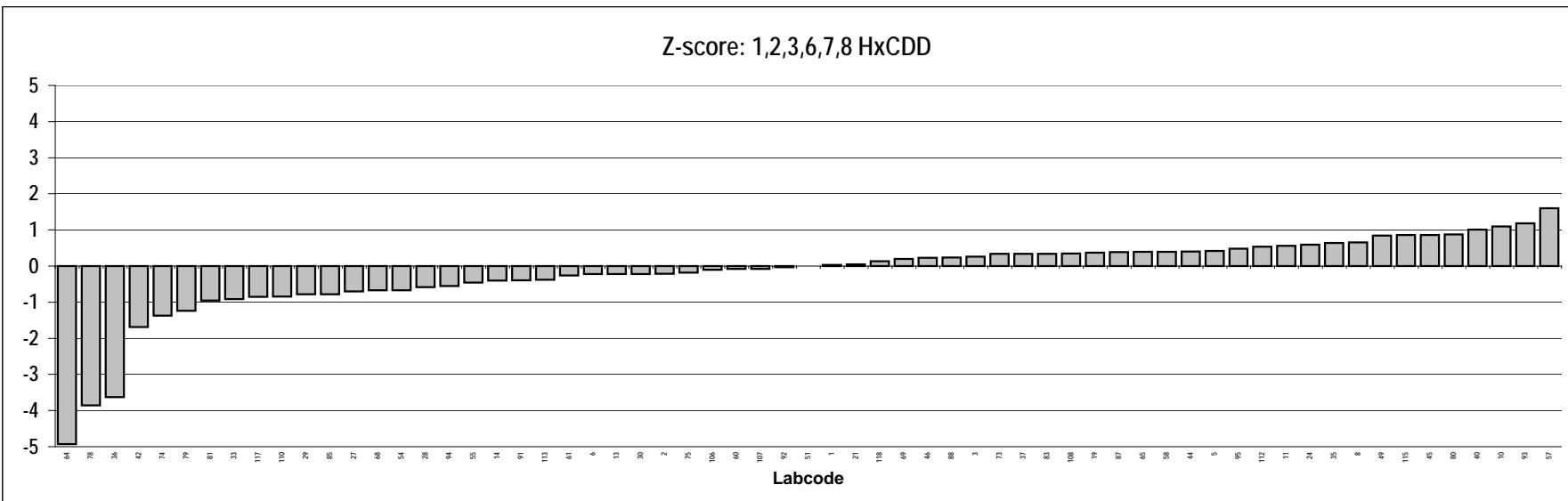
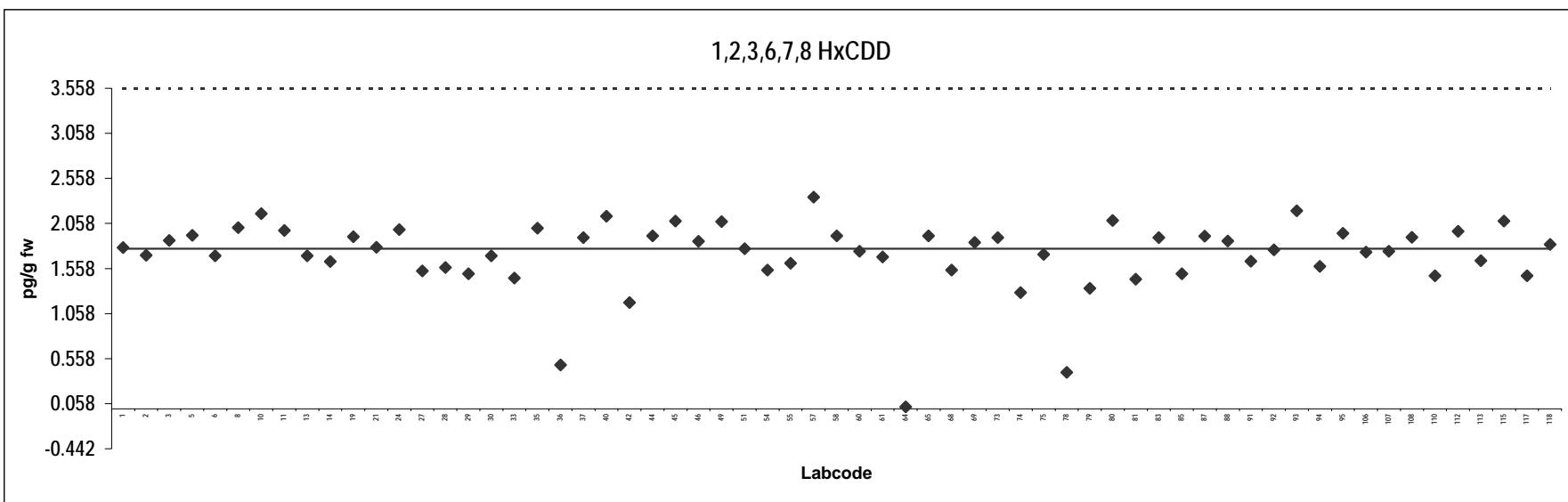


**Pork**  
**Congener: 1,2,3,6,7,8 HxCDD**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.8		83	1.9	
2	1.7		85	1.5	
3	1.9		87	1.9	
5	1.9		88	1.9	
6	1.7		91	1.6	
8	2.0		92	1.8	
10	2.2		93	2.2	
11	2.0		94	1.6	
13	1.7		95	2.0	
14	1.6		106	1.7	
19	1.9		107	1.8	
21	1.8		108	1.9	
24	2.0		110	1.5	
27	1.5		112	2.0	
28	1.6		113	1.6	
29	1.5		115	2.1	
30	1.7		117	1.5	
33	1.5		118	1.8	
35	2.0				
36	0.49				
37	1.9				
40	2.1				
42	1.2				
44	1.9				
45	2.1				
46	1.9				
49	2.1				
51	1.8				
54	1.5				
55	1.6				
57	2.4				
58	1.9				
60	1.8				
61	1.7				
64	0.025	ND			
65	1.9				
68	1.5				
69	1.8				
73	1.9				
74	1.3				
75	1.7				
78	0.41				
79	1.3				
80	2.1				
81	1.4				

**Consensus statistics**

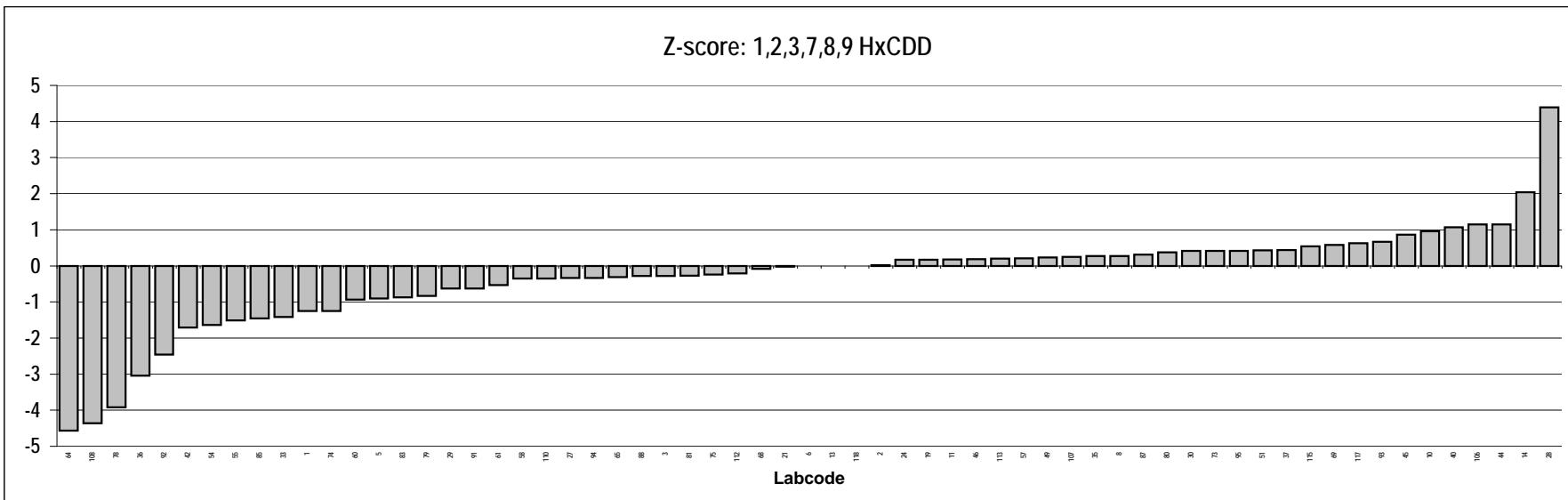
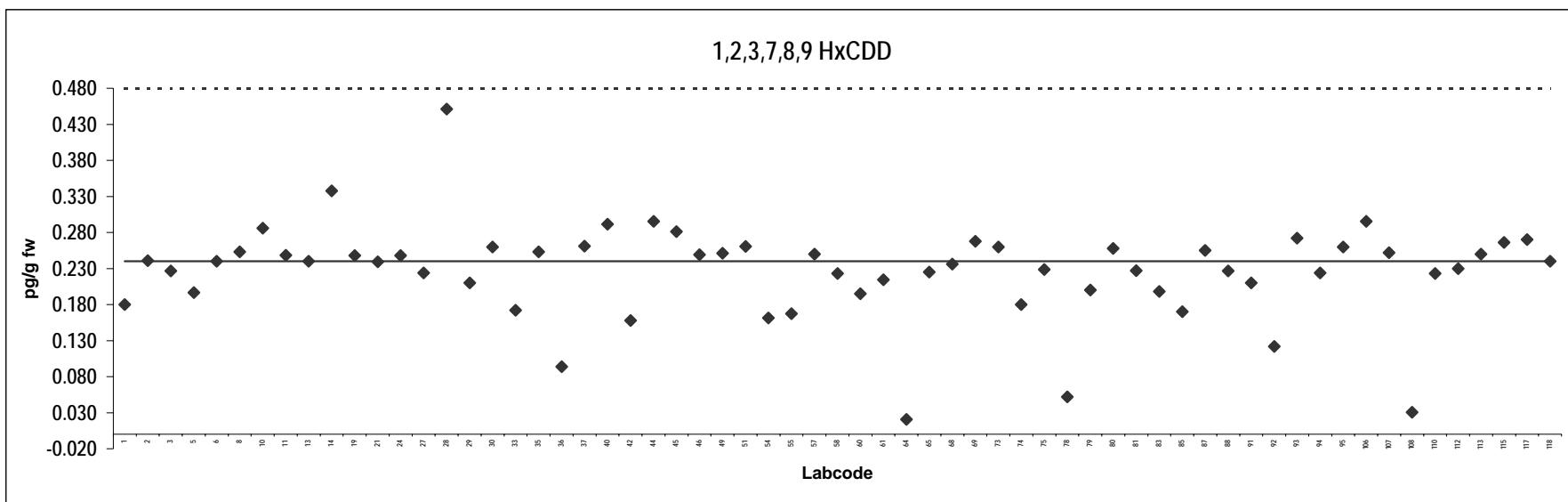
Consensus median, pg/g	1.8
Median all values pg/g	1.8
Consensus mean, pg/g	1.7
Standard deviation, pg/g	0.40
Relative standard deviation, %	23
No. of values reported	63
No. of values removed	0
No. of reported non-detects	1



**Pork**  
**Congener: 1,2,3,7,8,9 HxCDD**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.18		83	0.20	
2	0.24		85	0.17	
3	0.23		87	0.26	
5	0.20		88	0.23	
6	0.24		91	0.21	
8	0.25		92	0.12	
10	0.29		93	0.27	
11	0.25		94	0.22	
13	0.24		95	0.26	
14	0.34		106	0.30	
19	0.25		107	0.25	
21	0.24		108	0.031	ND
24	0.25		110	0.22	
27	0.22		112	0.23	
28	0.45		113	0.25	
29	0.21		115	0.27	
30	0.26		117	0.27	
33	0.17		118	0.24	
35	0.25				
36	0.094				
37	0.26				
40	0.29				
42	0.16				
44	0.30				
45	0.28				
46	0.25				
49	0.25				
51	0.26				
54	0.16				
55	0.17				
57	0.25				
58	0.22				
60	0.20				
61	0.21				
64	0.021	ND			
65	0.23				
68	0.24				
69	0.27				
73	0.26				
74	0.18				
75	0.23				
78	0.052				
79	0.20				
80	0.26				
81	0.23				

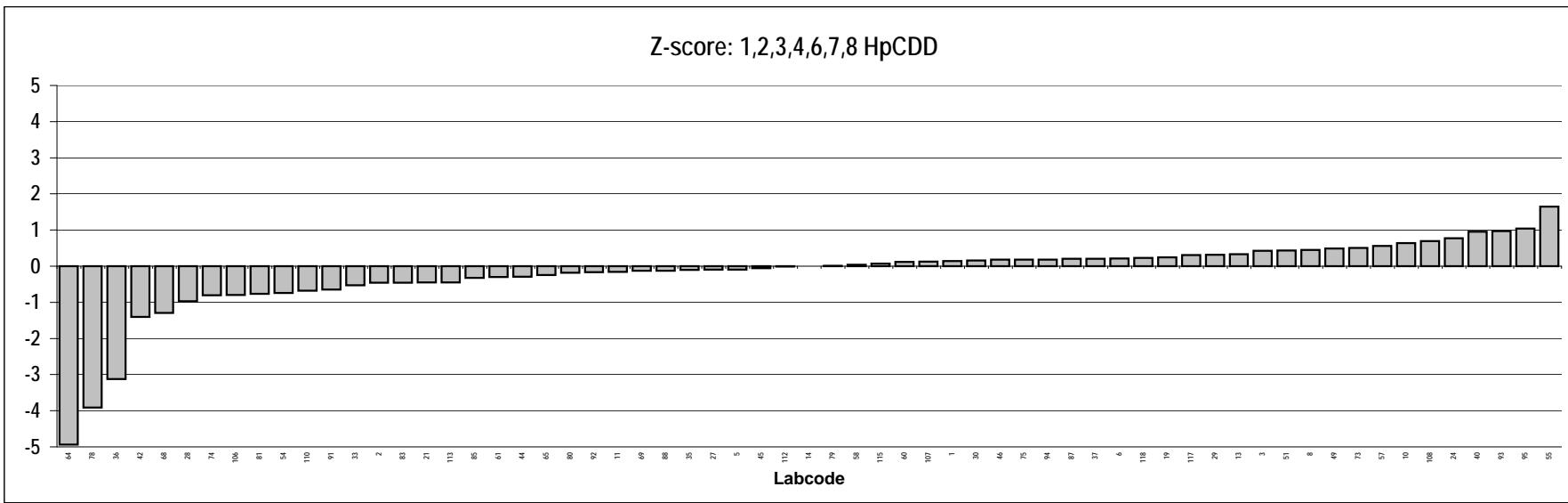
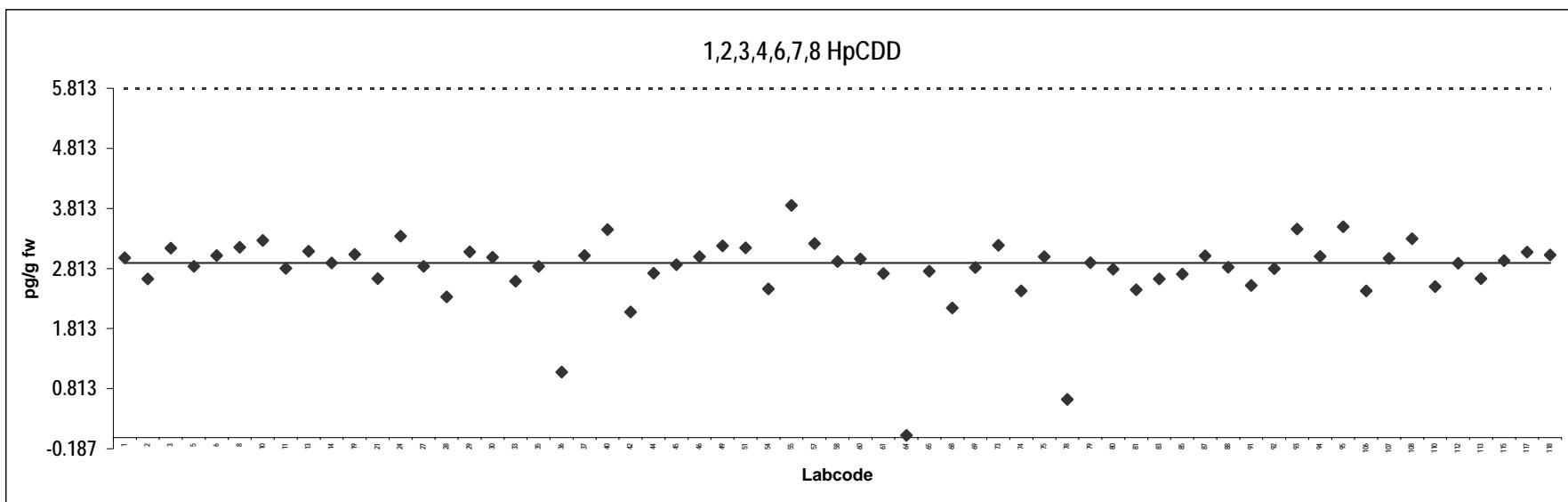
Consensus statistics	
Consensus median, pg/g	0.24
Median all values pg/g	0.24
Consensus mean, pg/g	0.23
Standard deviation, pg/g	0.066
Relative standard deviation, %	29
No. of values reported	63
No. of values removed	0
No. of reported non-detects	2



**Pork**  
**Congener: 1,2,3,4,6,7,8 HpCDD**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	3.0		83	2.6	
2	2.6		85	2.7	
3	3.2		87	3.0	
5	2.9		88	2.8	
6	3.0		91	2.5	
8	3.2		92	2.8	
10	3.3		93	3.5	
11	2.8		94	3.0	
13	3.1		95	3.5	
14	2.9		106	2.4	
19	3.1		107	3.0	
21	2.6		108	3.3	
24	3.4		110	2.5	
27	2.9		112	2.9	
28	2.3		113	2.6	
29	3.1		115	2.9	
30	3.0		117	3.1	
33	2.6		118	3.0	
35	2.8				
36	1.1				
37	3.0				
40	3.5				
42	2.1				
44	2.7				
45	2.9				
46	3.0				
49	3.2				
51	3.2				
54	2.5				
55	3.9				
57	3.2				
58	2.9				
60	3.0				
61	2.7				
64	0.038	ND			
65	2.8				
68	2.2				
69	2.8				
73	3.2				
74	2.4				
75	3.0				
78	0.63				
79	2.9				
80	2.8				
81	2.5				

Consensus statistics	
Consensus median, pg/g	2.9
Median all values pg/g	2.9
Consensus mean, pg/g	2.8
Standard deviation, pg/g	0.60
Relative standard deviation, %	21
No. of values reported	63
No. of values removed	0
No. of reported non-detects	1

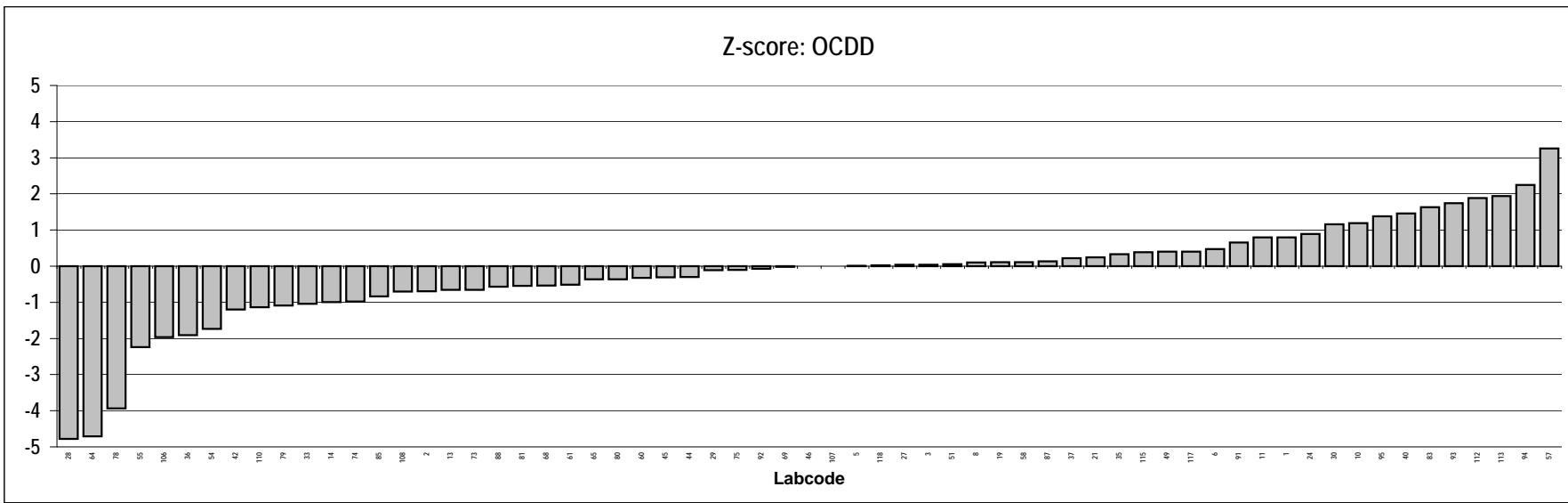
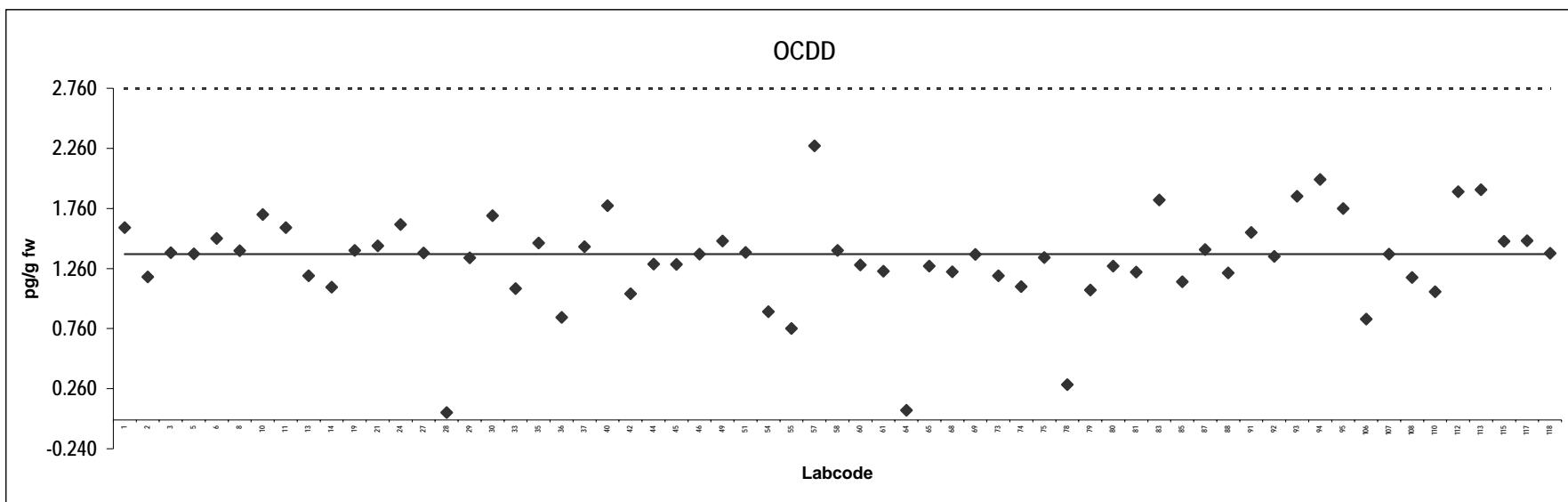


**Pork**  
Congener: OCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.6		83	1.8	
2	1.2		85	1.2	
3	1.4		87	1.4	
5	1.4		88	1.2	
6	1.5		91	1.6	
8	1.4		92	1.4	
10	1.7		93	1.9	
11	1.6		94	2.0	
13	1.2		95	1.8	
14	1.1		106	0.84	
19	1.4		107	1.4	
21	1.4		108	1.2	
24	1.6		110	1.1	
27	1.4		112	1.9	
28	0.060	ND	113	1.9	
29	1.4		115	1.5	
30	1.7		117	1.5	
33	1.1		118	1.4	
35	1.5				
36	0.85				
37	1.4				
40	1.8				
42	1.1				
44	1.3				
45	1.3				
46	1.4				
49	1.5				
51	1.4				
54	0.90				
55	0.76				
57	2.3				
58	1.4				
60	1.3				
61	1.2				
64	0.080	ND			
65	1.3				
68	1.2				
69	1.4				
73	1.2				
74	1.1				
75	1.4				
78	0.29				
79	1.1				
80	1.3				
81	1.2				

**Consensus statistics**

Consensus median, pg/g	1.4
Median all values pg/g	1.4
Consensus mean, pg/g	1.3
Standard deviation, pg/g	0.39
Relative standard deviation, %	29
No. of values reported	63
No. of values removed	0
No. of reported non-detects	3

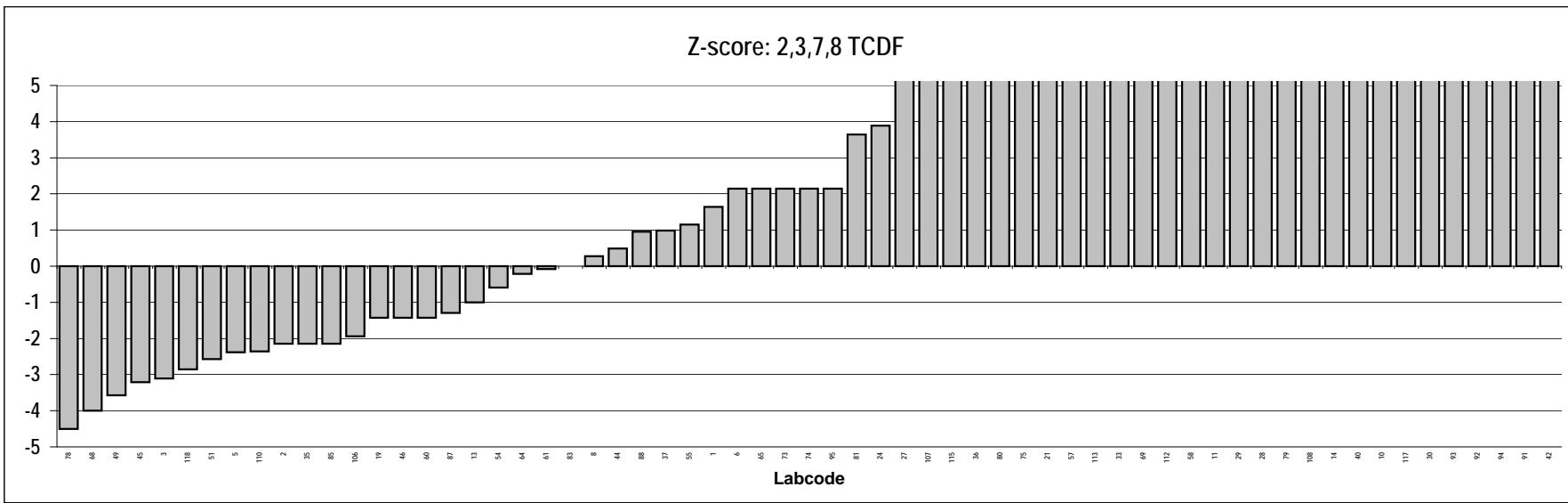
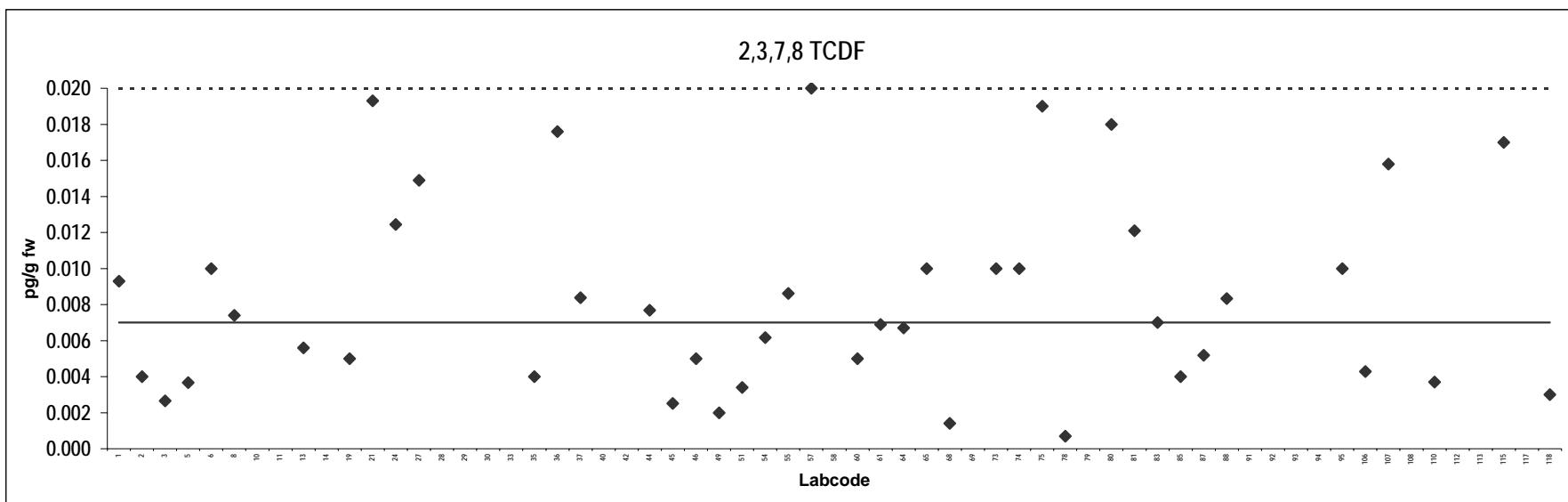


**Pork**  
Congener: 2,3,7,8 TCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.0093		83	0.0070	
2	0.0040		85	0.0040	
3	0.0027	ND	87	0.0052	
5	0.0037		88	0.0083	
6	0.010	ND	91	0.084	Outlier
8	0.0074		92	0.049	Outlier
10	0.040	Outlier	93	0.046	Outlier
11	0.027	Outlier	94	0.051	Outlier
13	0.0056	ND	95	0.010	
14	0.037	Outlier,ND	106	0.0043	
19	0.0050	ND	107	0.016	ND
21	0.019	ND	108	0.031	Outlier,ND
24	0.012		110	0.0037	ND
27	0.015		112	0.026	Outlier
28	0.030	Outlier,ND	113	0.021	Outlier,ND
29	0.028	Outlier	115	0.017	
30	0.043	Outlier,ND	117	0.041	Outlier
33	0.022	Outlier	118	0.0030	ND
35	0.0040				
36	0.018	ND			
37	0.0084				
40	0.039	Outlier,ND			
42	0.10	Outlier			
44	0.0077				
45	0.0025				
46	0.0050	ND			
49	0.0020	ND			
51	0.0034				
54	0.0062				
55	0.0086	ND			
57	0.020	ND			
58	0.026	Outlier			
60	0.0050	ND			
61	0.0069				
64	0.0067	ND			
65	0.010				
68	0.0014	ND			
69	0.024	Outlier			
73	0.010	ND			
74	0.010	ND			
75	0.019				
78	0.00070				
79	0.030	Outlier			
80	0.018				
81	0.012	ND			

**Consensus statistics**

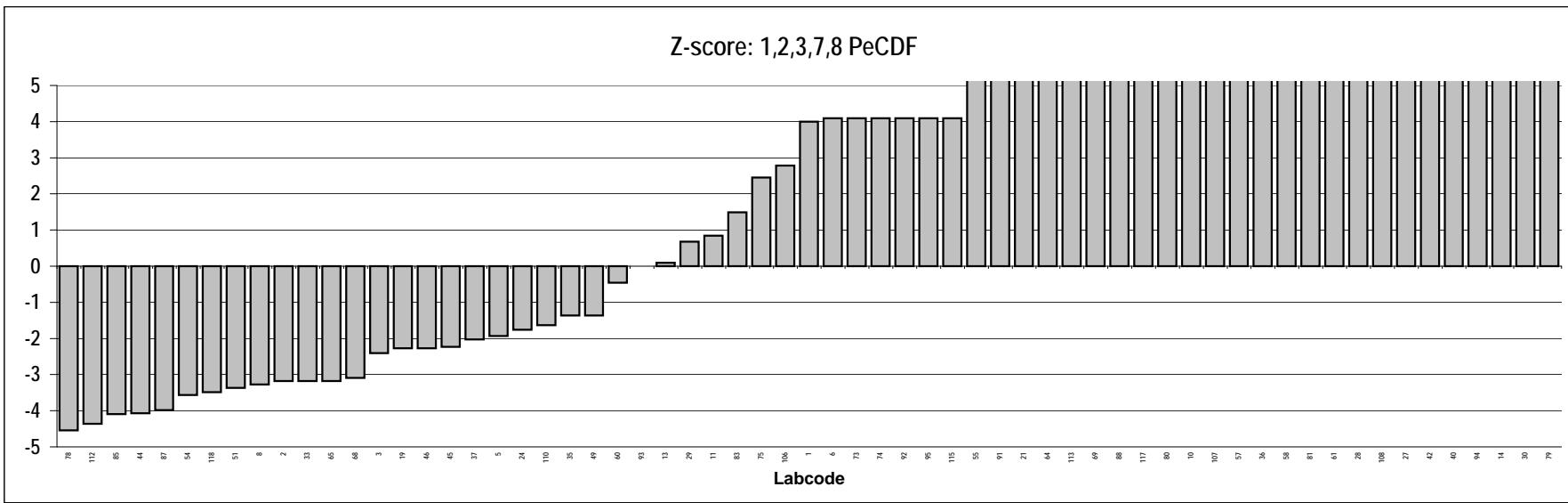
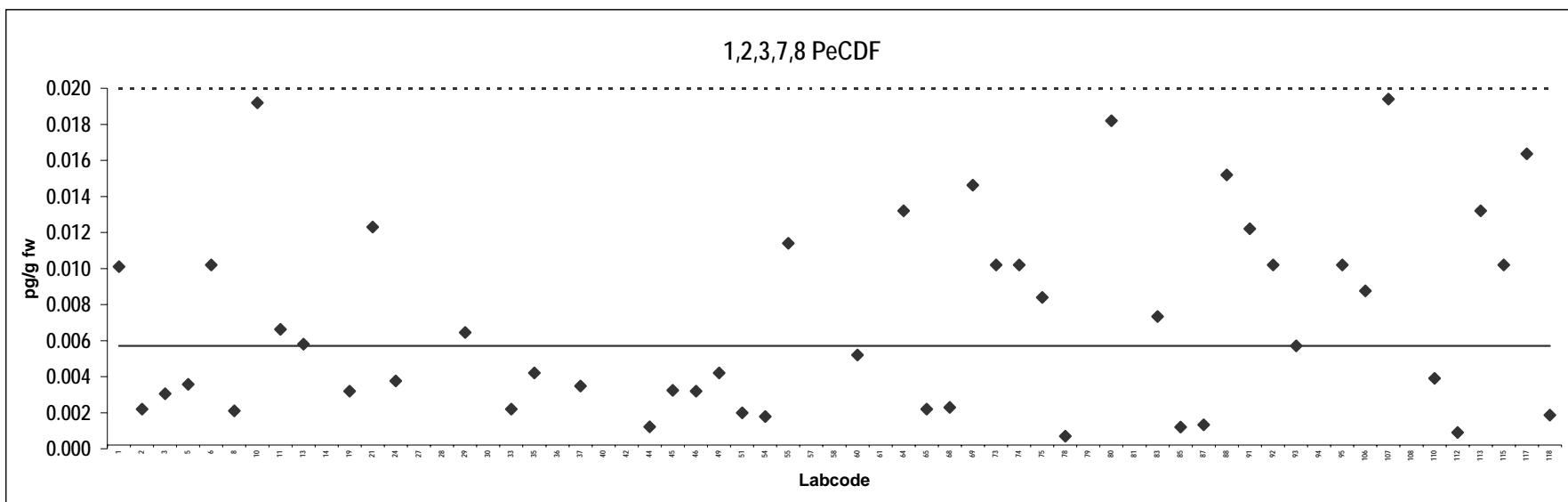
Consensus median, pg/g	0.0070
Median all values pg/g	0.010
Consensus mean, pg/g	0.0083
Standard deviation, pg/g	0.0054
Relative standard deviation, %	65
No. of values reported	63
No. of values removed	20
No. of reported non-detects	26



**Pork**  
**Congener: 1,2,3,7,8 PeCDF**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.0099		83	0.0071	
2	0.0020	ND	85	0.0010	
3	0.0029	ND	87	0.0011	ND
5	0.0034		88	0.015	
6	0.010	ND	91	0.012	
8	0.0019	ND	92	0.010	ND
10	0.019	ND	93	0.0055	ND
11	0.0064		94	0.040	Outlier,ND
13	0.0056	ND	95	0.010	ND
14	0.044	Outlier,ND	106	0.0086	
19	0.0030	ND	107	0.019	ND
21	0.012	ND	108	0.031	Outlier,ND
24	0.0036		110	0.0037	ND
27	0.032	Outlier	112	0.00070	
28	0.030	Outlier,ND	113	0.013	ND
29	0.0063	ND	115	0.010	ND
30	0.053	Outlier,ND	117	0.016	
33	0.0020	ND	118	0.0017	
35	0.0040		ND		
36	0.022	Outlier,ND			
37	0.0033				
40	0.039	Outlier,ND			
42	0.037	Outlier			
44	0.0010				
45	0.0030				
46	0.0030	ND			
49	0.0040	ND			
51	0.0018				
54	0.0016	ND			
55	0.011	ND			
57	0.020	Outlier,ND			
58	0.025	Outlier,ND			
60	0.0050	ND			
61	0.026	Outlier			
64	0.013	ND			
65	0.0020	ND			
68	0.0021	ND			
69	0.014				
73	0.010	ND			
74	0.010	ND			
75	0.0082				
78	0.00050	ND			
79	0.060	Outlier			
80	0.018				
81	0.026	Outlier			

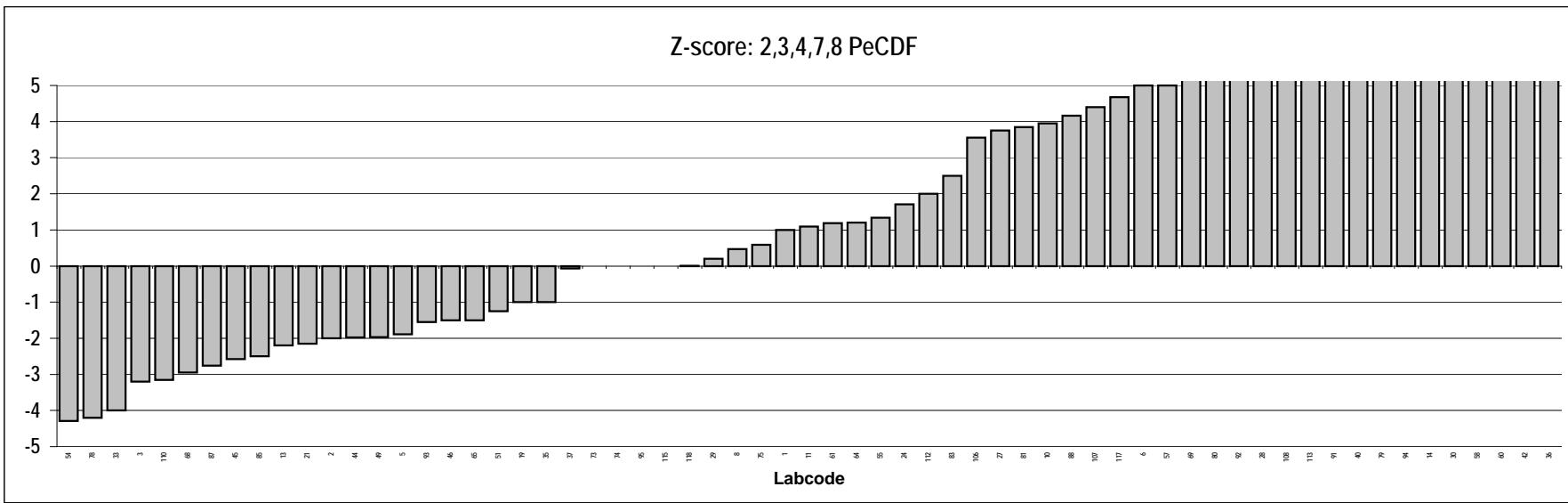
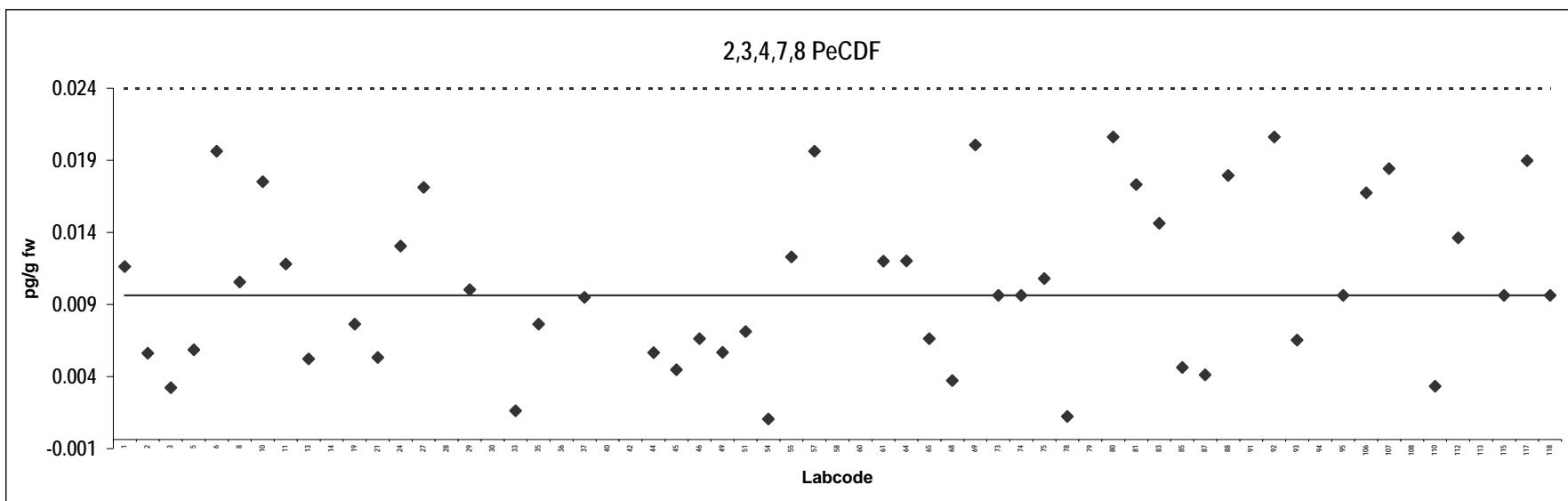
Consensus statistics	
Consensus median, pg/g	0.0055
Median all values pg/g	0.010
Consensus mean, pg/g	0.0069
Standard deviation, pg/g	0.0053
Relative standard deviation, %	77
No. of values reported	63
No. of values removed	14
No. of reported non-detects	39



**Pork**  
**Congener: 2,3,4,7,8 PeCDF**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.012		83	0.015	
2	0.0060		85	0.0050	
3	0.0036		87	0.0045	
5	0.0062		88	0.018	
6	0.020		91	0.037	Outlier,ND
8	0.011		92	0.021	
10	0.018		93	0.0069	ND
11	0.012		94	0.040	Outlier,ND
13	0.0056	ND	95	0.010	
14	0.046	Outlier,ND	106	0.017	
19	0.0080	ND	107	0.019	ND
21	0.0057	ND	108	0.031	Outlier,ND
24	0.013		110	0.0037	ND
27	0.018		112	0.014	
28	0.030	Outlier,ND	113	0.034	Outlier,ND
29	0.010		115	0.010	ND
30	0.049	Outlier,ND	117	0.019	
33	0.0020	ND	118	0.010	
35	0.0080				
36	0.39	Outlier			
37	0.0099				
40	0.039	Outlier,ND			
42	0.16	Outlier			
44	0.0060				
45	0.0048				
46	0.0070				
49	0.0061				
51	0.0075				
54	0.0014	ND			
55	0.013	ND			
57	0.020	ND			
58	0.049	Outlier			
60	0.13	Outlier			
61	0.012				
64	0.012	ND			
65	0.0070				
68	0.0041				
69	0.020				
73	0.010	ND			
74	0.010				
75	0.011				
78	0.0016				
79	0.040	Outlier			
80	0.021				
81	0.018				

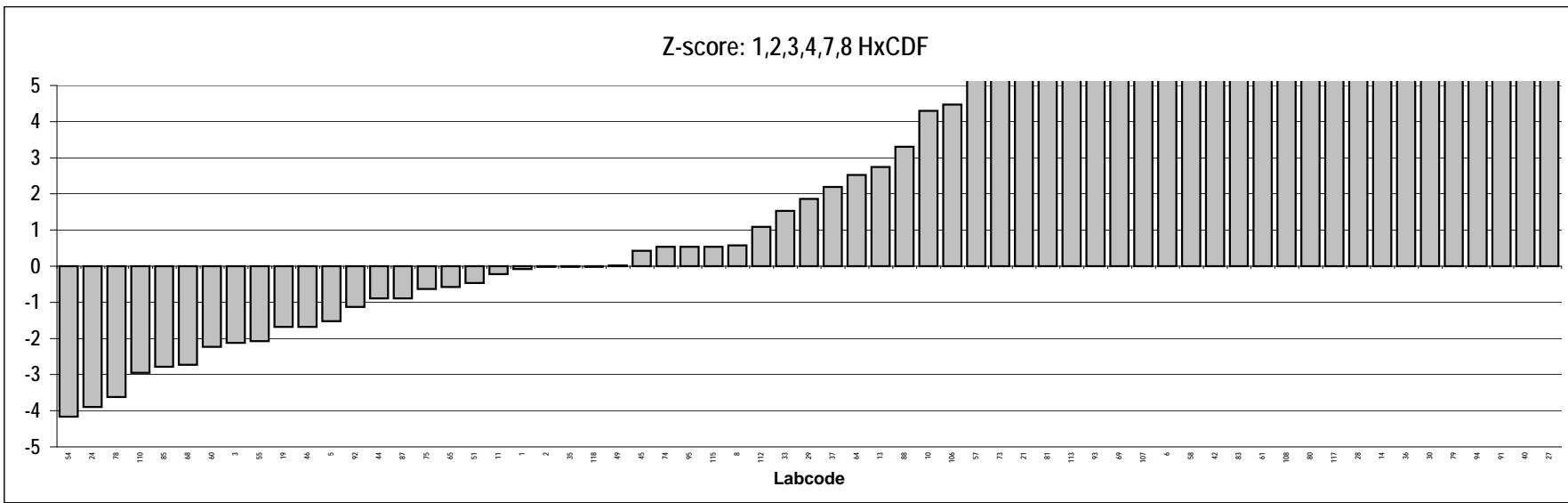
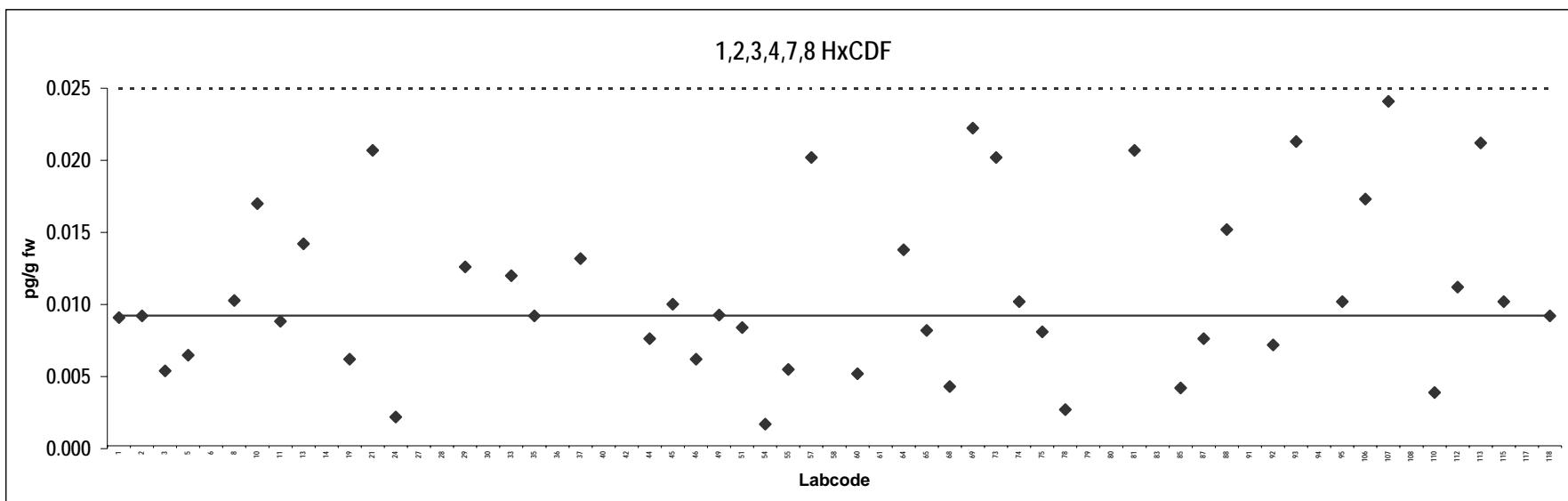
Consensus statistics	
Consensus median, pg/g	0.010
Median all values pg/g	0.012
Consensus mean, pg/g	0.011
Standard deviation, pg/g	0.0057
Relative standard deviation, %	54
No. of values reported	63
No. of values removed	13
No. of reported non-detects	20



**Pork**  
**Congener: 1,2,3,4,7,8 HxCDF**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.0089		83	0.027	Outlier
2	0.0090		85	0.0040	
3	0.0052		87	0.0074	
5	0.0063		88	0.015	
6	0.025	Outlier,ND	91	0.074	Outlier
8	0.010		92	0.0070	ND
10	0.017		93	0.021	ND
11	0.0086		94	0.070	Outlier,ND
13	0.014		95	0.010	ND
14	0.040	Outlier,ND	106	0.017	
19	0.0060		107	0.024	ND
21	0.021		108	0.031	Outlier,ND
24	0.0020	ND	110	0.0037	ND
27	0.090	Outlier	112	0.011	
28	0.040	Outlier,ND	113	0.021	ND
29	0.012		115	0.010	ND
30	0.051	Outlier,ND	117	0.040	Outlier
33	0.012		118	0.0090	
35	0.0090				
36	0.050	Outlier,ND			
37	0.013				
40	0.077	Outlier,ND			
42	0.026	Outlier			
44	0.0074				
45	0.0098				
46	0.0060				
49	0.0091				
51	0.0082				
54	0.0015	ND			
55	0.0053	ND			
57	0.020	ND			
58	0.025	Outlier,ND			
60	0.0050	ND			
61	0.028	Outlier			
64	0.014	ND			
65	0.0080				
68	0.0041				
69	0.022	ND			
73	0.020				
74	0.010				
75	0.0079				
78	0.0025				
79	0.070	Outlier			
80	0.032	Outlier			
81	0.021				

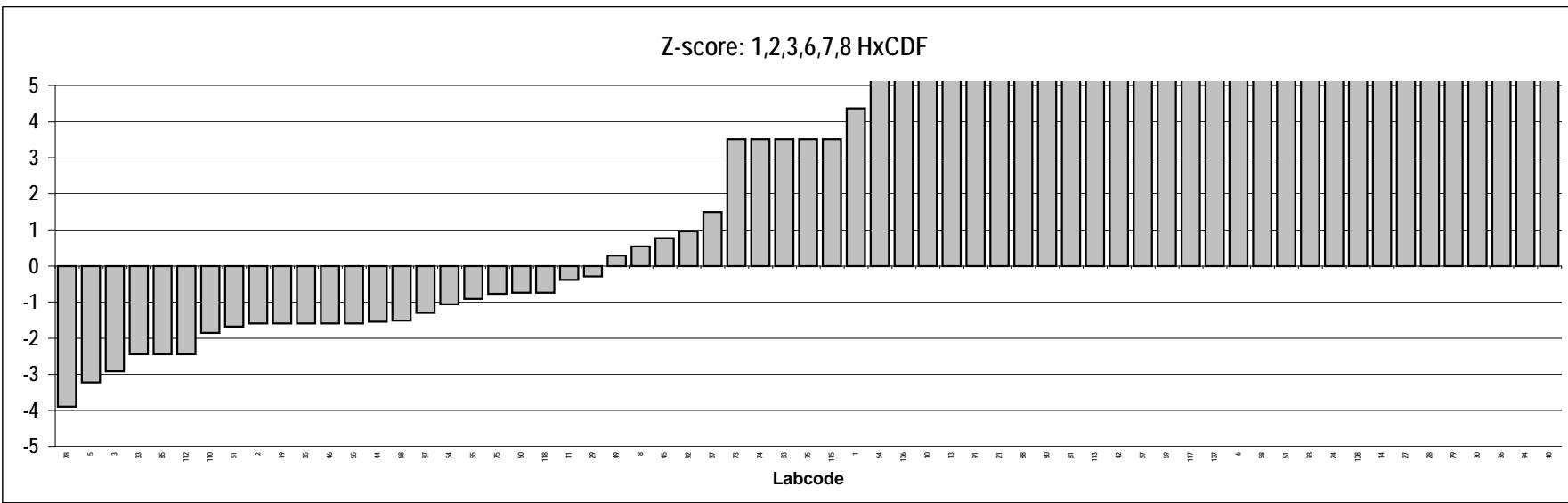
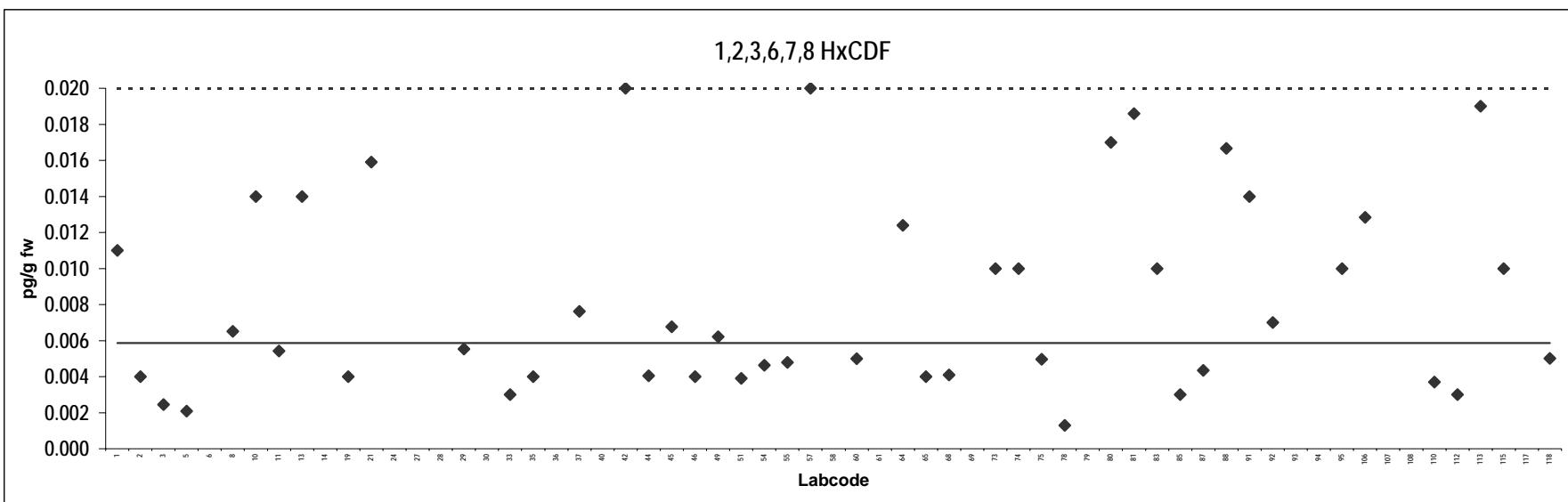
Consensus statistics	
Consensus median, pg/g	0.0090
Median all values pg/g	0.012
Consensus mean, pg/g	0.011
Standard deviation, pg/g	0.0060
Relative standard deviation, %	56
No. of values reported	63
No. of values removed	17
No. of reported non-detects	24



**Pork**  
**Congener: 1,2,3,6,7,8 HxCDF**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.011		83	0.010	
2	0.0040		85	0.0030	
3	0.0025	ND	87	0.0043	
5	0.0021		88	0.017	
6	0.025	Outlier,ND	91	0.014	
8	0.0065		92	0.0070	ND
10	0.014	ND	93	0.027	Outlier,ND
11	0.0054		94	0.070	Outlier,ND
13	0.014	ND	95	0.010	ND
14	0.034	Outlier	106	0.013	
19	0.0040		107	0.023	Outlier,ND
21	0.016		108	0.031	Outlier,ND
24	0.029	Outlier	110	0.0037	ND
27	0.035	Outlier	112	0.0030	ND
28	0.040	Outlier,ND	113	0.019	ND
29	0.0055		115	0.010	ND
30	0.049	Outlier,ND	117	0.022	Outlier
33	0.0030	ND	118	0.0050	
35	0.0040				
36	0.050	Outlier,ND			
37	0.0076				
40	0.077	Outlier,ND			
42	0.020	ND			
44	0.0041				
45	0.0068				
46	0.0040				
49	0.0062				
51	0.0039				
54	0.0046				
55	0.0048	ND			
57	0.020	ND			
58	0.025	Outlier,ND			
60	0.0050	ND			
61	0.025	Outlier			
64	0.012	ND			
65	0.0040				
68	0.0041				
69	0.022	Outlier,ND			
73	0.010	ND			
74	0.010	ND			
75	0.0050				
78	0.0013				
79	0.040	Outlier			
80	0.017				
81	0.019	ND			

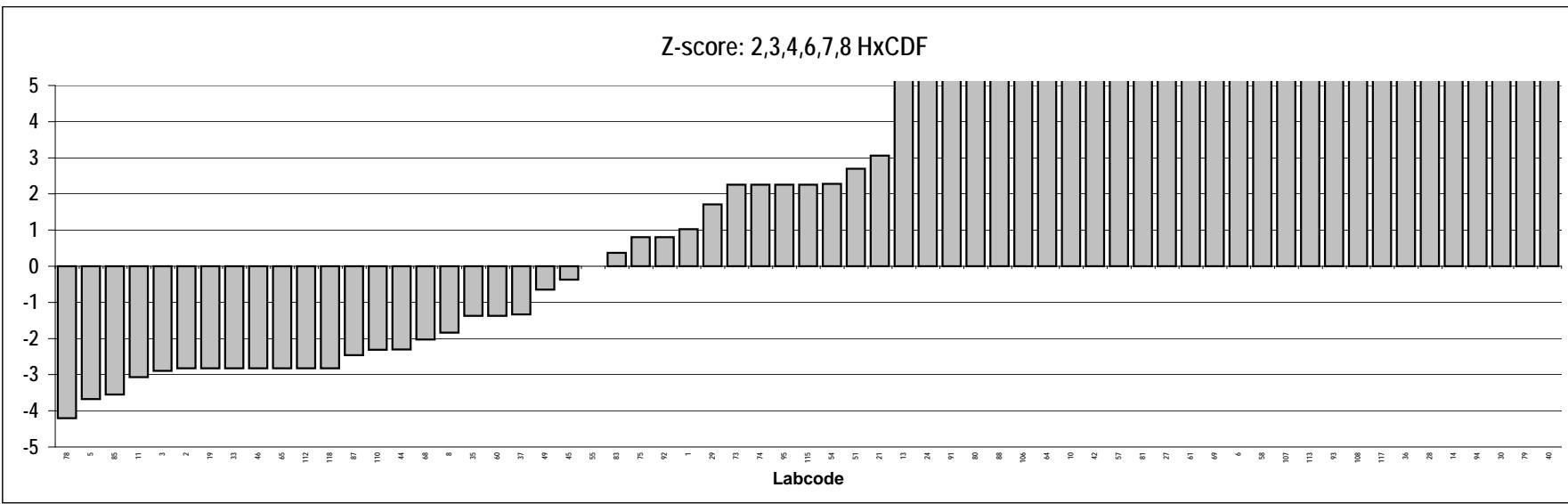
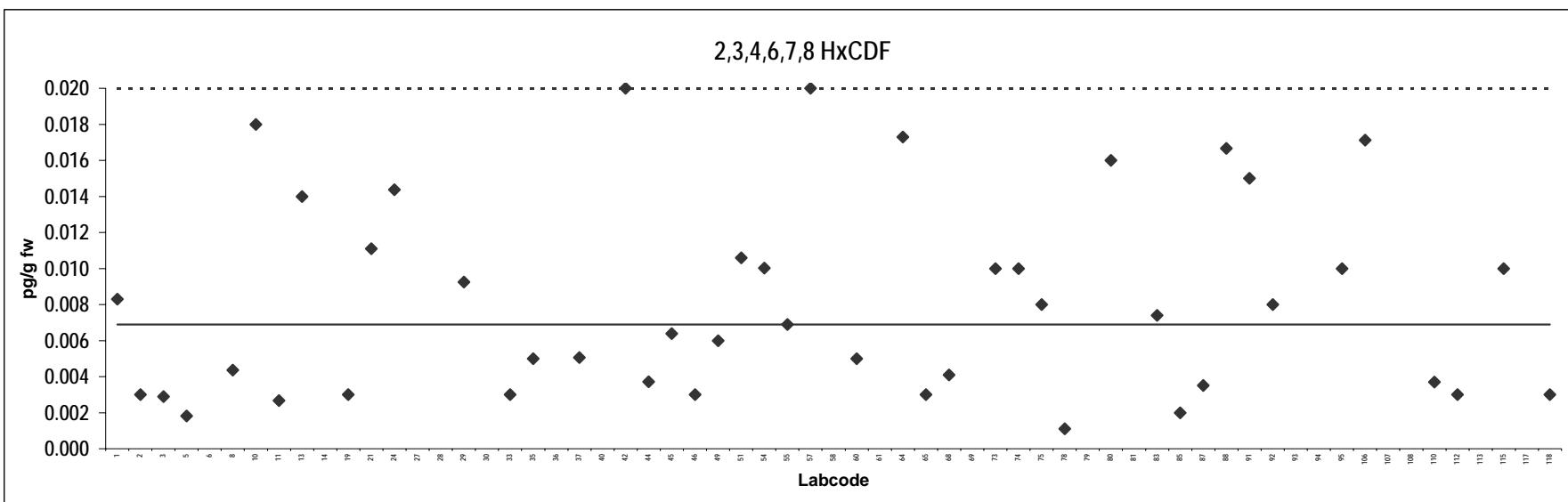
Consensus statistics	
Consensus median, pg/g	0.0059
Median all values pg/g	0.010
Consensus mean, pg/g	0.0083
Standard deviation, pg/g	0.0054
Relative standard deviation, %	66
No. of values reported	63
No. of values removed	17
No. of reported non-detects	29



**Pork**  
**Congener: 2,3,4,6,7,8 HxCDF**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.0083		83	0.0074	
2	0.0030		85	0.0020	
3	0.0029	ND	87	0.0035	
5	0.0018		88	0.017	
6	0.025	Outlier,ND	91	0.015	ND
8	0.0044	ND	92	0.0080	ND
10	0.018		93	0.027	Outlier,ND
11	0.0027	ND	94	0.050	Outlier,ND
13	0.014	ND	95	0.010	ND
14	0.047	Outlier,ND	106	0.017	
19	0.0030		107	0.025	Outlier,ND
21	0.011		108	0.031	Outlier,ND
24	0.014		110	0.0037	ND
27	0.021	Outlier	112	0.0030	ND
28	0.040	Outlier,ND	113	0.026	Outlier,ND
29	0.0093		115	0.010	ND
30	0.051	Outlier,ND	117	0.035	Outlier
33	0.0030	ND	118	0.0030	
35	0.0050				
36	0.037	Outlier,ND			
37	0.0051				
40	0.077	Outlier,ND			
42	0.020	ND			
44	0.0037				
45	0.0064				
46	0.0030				
49	0.0060	ND			
51	0.011				
54	0.010				
55	0.0069	ND			
57	0.020	ND			
58	0.025	Outlier,ND			
60	0.0050	ND			
61	0.023	Outlier			
64	0.017	ND			
65	0.0030	ND			
68	0.0041				
69	0.024	Outlier,ND			
73	0.010	ND			
74	0.010	ND			
75	0.0080				
78	0.0011				
79	0.060	Outlier			
80	0.016				
81	0.020	Outlier,ND			

Consensus statistics	
Consensus median, pg/g	0.0069
Median all values pg/g	0.010
Consensus mean, pg/g	0.0081
Standard deviation, pg/g	0.0055
Relative standard deviation, %	68
No. of values reported	63
No. of values removed	18
No. of reported non-detects	35

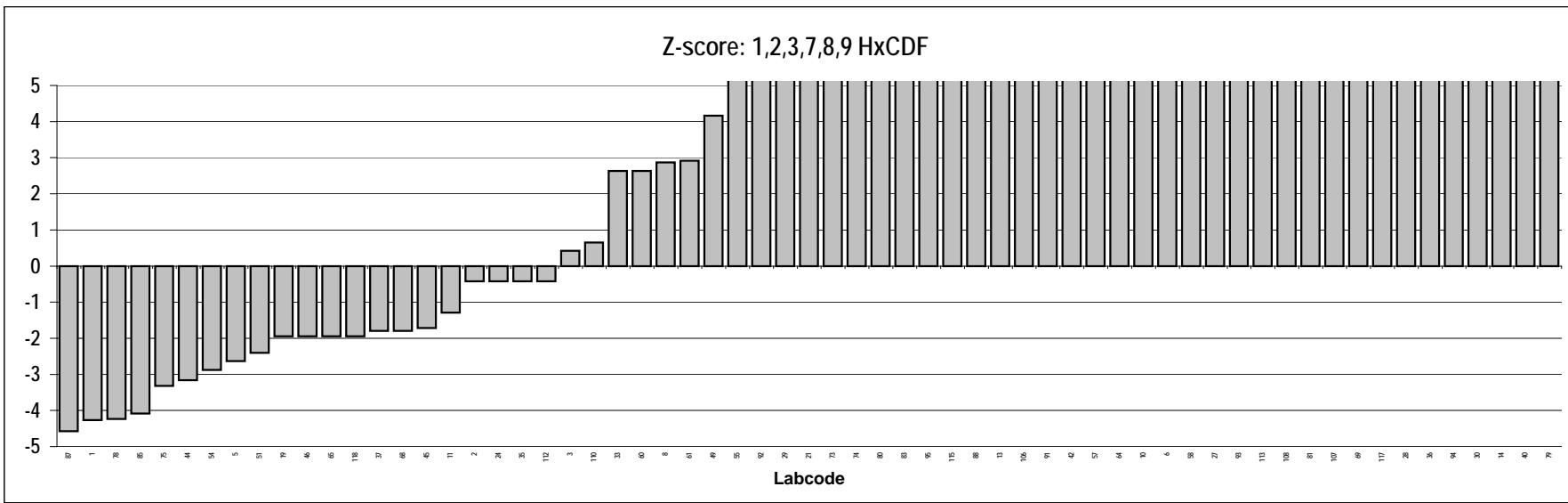
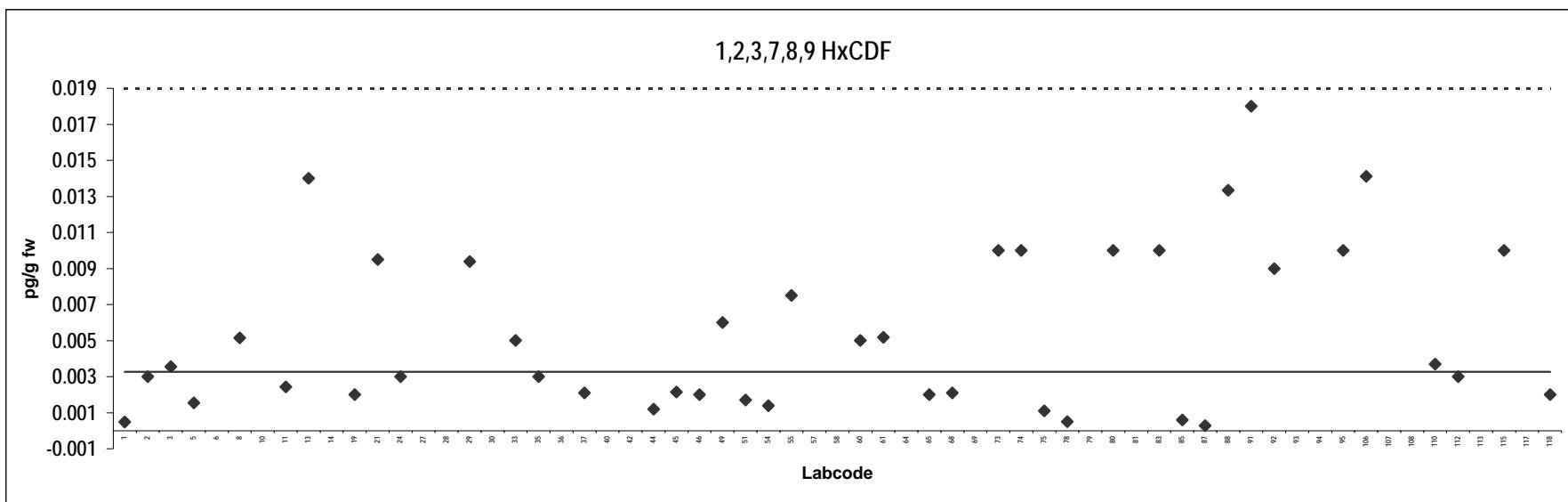


**Pork**  
**Congener: 1,2,3,7,8,9 HxCDF**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.00048		83	0.010	
2	0.0030	ND	85	0.00060	ND
3	0.0036	ND	87	0.00028	ND
5	0.0016		88	0.013	
6	0.025	Outlier,ND	91	0.018	ND
8	0.0052	ND	92	0.0090	ND
10	0.022	Outlier	93	0.029	Outlier,ND
11	0.0024	ND	94	0.050	Outlier,ND
13	0.014	ND	95	0.010	ND
14	0.059	Outlier,ND	106	0.014	ND
19	0.0020	ND	107	0.032	Outlier,ND
21	0.0095	ND	108	0.031	Outlier,ND
24	0.0030	ND	110	0.0037	ND
27	0.028	Outlier	112	0.0030	ND
28	0.040	Outlier,ND	113	0.030	Outlier,ND
29	0.0094	ND	115	0.010	ND
30	0.058	Outlier,ND	117	0.037	Outlier
33	0.0050	ND	118	0.0020	ND
35	0.0030	ND			
36	0.048	Outlier,ND			
37	0.0021	ND			
40	0.077	Outlier,ND			
42	0.020	Outlier,ND			
44	0.0012				
45	0.0022	ND			
46	0.0020	ND			
49	0.0060	ND			
51	0.0017				
54	0.0014	ND			
55	0.0075	ND			
57	0.020	Outlier,ND			
58	0.025	Outlier,ND			
60	0.0050	ND			
61	0.0052				
64	0.021	Outlier,ND			
65	0.0020	ND			
68	0.0021				
69	0.032	Outlier,ND			
73	0.010	ND			
74	0.010	ND			
75	0.0011				
78	0.00050	ND			
79	0.090	Outlier			
80	0.010				
81	0.032	Outlier,ND			

**Consensus statistics**

Consensus median, pg/g	0.0033
Median all values pg/g	0.010
Consensus mean, pg/g	0.0054
Standard deviation, pg/g	0.0045
Relative standard deviation, %	84
No. of values reported	63
No. of values removed	21
No. of reported non-detects	49

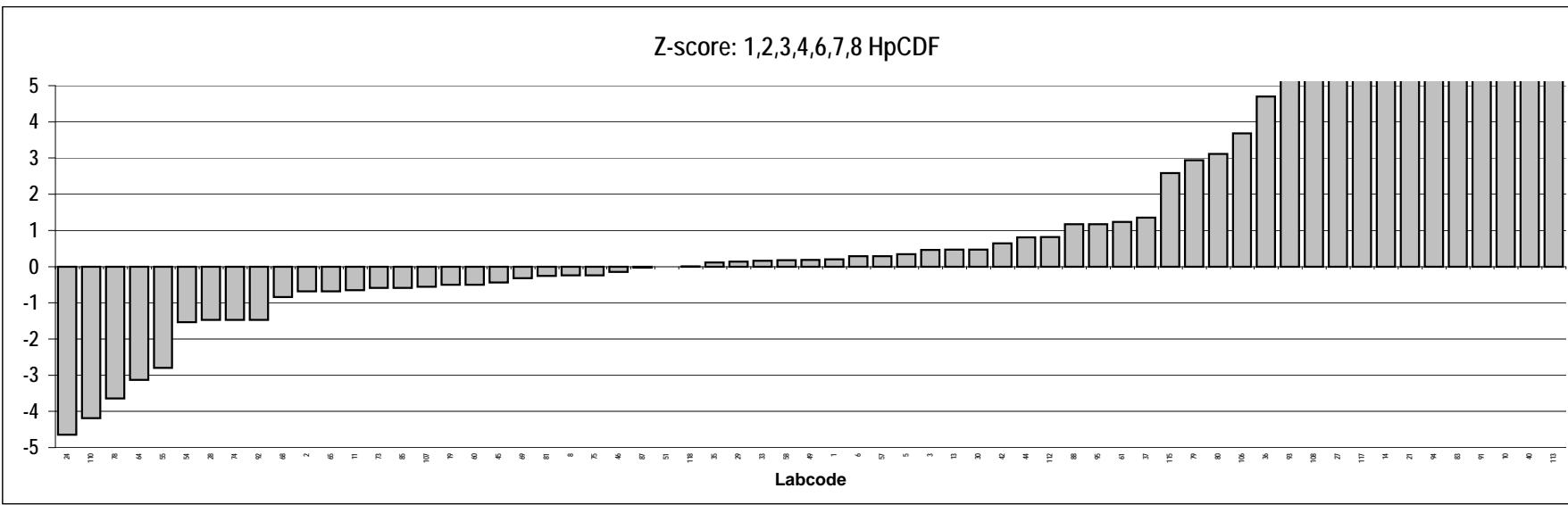
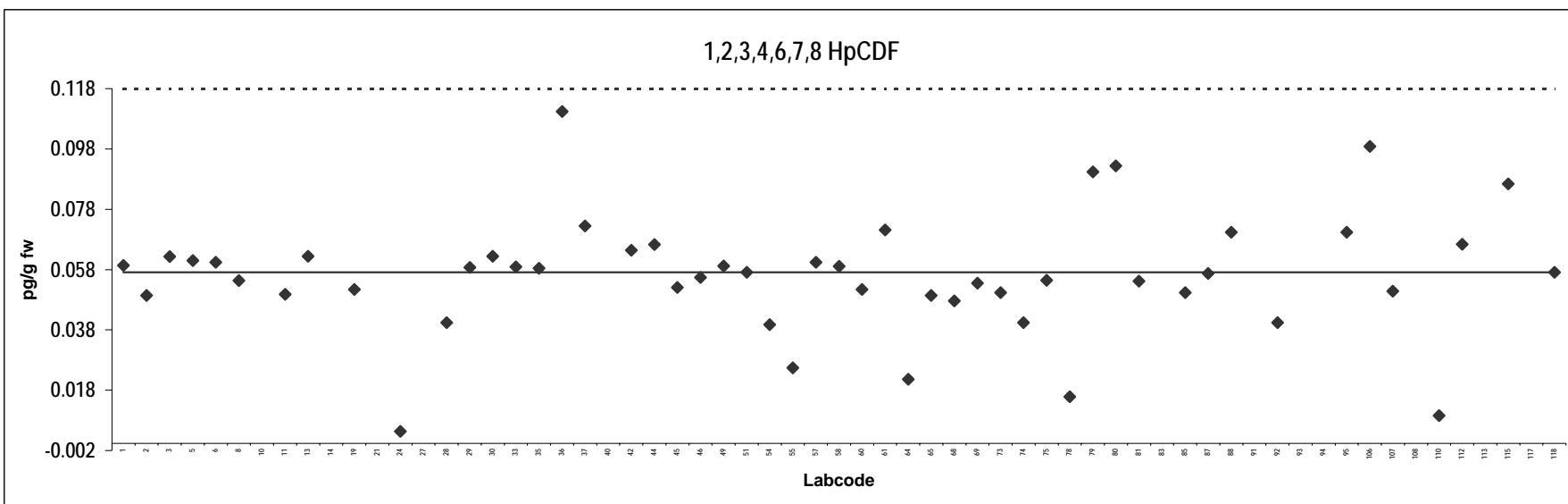


**Pork**  
**Congener: 1,2,3,4,6,7,8 HpCDF**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.059		83	0.15	
2	0.049		85	0.050	
3	0.062		87	0.056	
5	0.061		88	0.070	
6	0.060		91	0.17	Outlier
8	0.054		92	0.040	
10	0.20	Outlier	93	0.12	Outlier
11	0.049		94	0.15	Outlier,ND
13	0.062		95	0.070	
14	0.14	Outlier	106	0.098	
19	0.051		107	0.050	
21	0.14	Outlier	108	0.12	Outlier
24	0.0040	ND	110	0.0092	ND
27	0.12	Outlier	112	0.066	
28	0.040	ND	113	0.32	Outlier
29	0.058		115	0.086	
30	0.062		117	0.13	Outlier
33	0.059		118	0.057	
35	0.058				
36	0.11				
37	0.072				
40	0.21	Outlier,ND			
42	0.064				
44	0.066				
45	0.052				
46	0.055				
49	0.059				
51	0.057				
54	0.039				
55	0.025	ND			
57	0.060				
58	0.059				
60	0.051				
61	0.071				
64	0.021	ND			
65	0.049				
68	0.047				
69	0.053				
73	0.050				
74	0.040				
75	0.054				
78	0.015				
79	0.090				
80	0.092				
81	0.054				

**Consensus statistics**

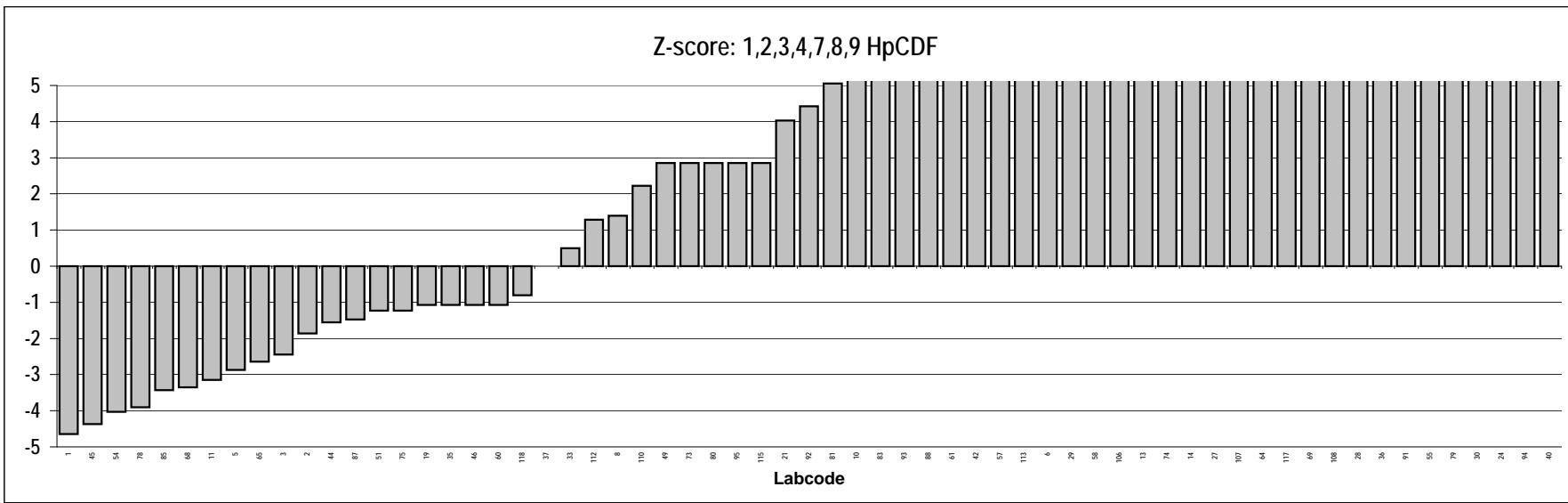
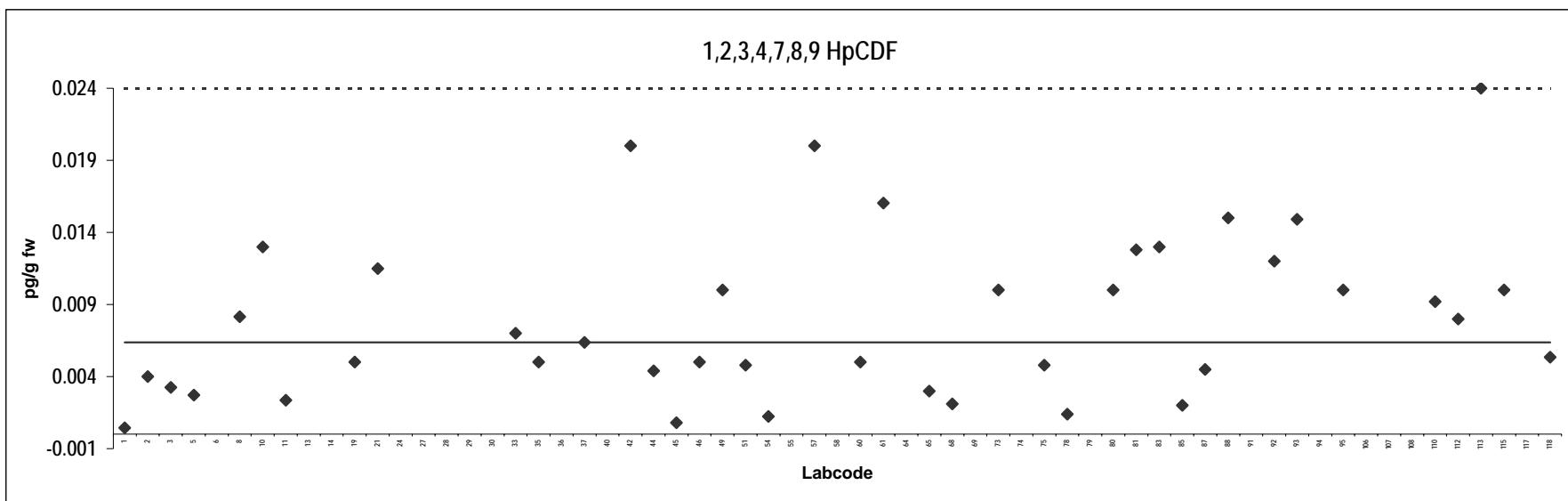
Consensus median, pg/g	0.057
Median all values pg/g	0.059
Consensus mean, pg/g	0.056
Standard deviation, pg/g	0.020
Relative standard deviation, %	35
No. of values reported	63
No. of values removed	12
No. of reported non-detects	7



**Pork**  
**Congener: 1,2,3,4,7,8,9 HpCDF**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.00045		83	0.013	
2	0.0040		85	0.0020	
3	0.0033	ND	87	0.0045	
5	0.0027		88	0.015	
6	0.025	Outlier,ND	91	0.053	Outlier
8	0.0081		92	0.012	ND
10	0.013	ND	93	0.015	ND
11	0.0024		94	0.15	Outlier,ND
13	0.028	Outlier,ND	95	0.010	ND
14	0.031	Outlier,ND	106	0.026	Outlier,ND
19	0.0050	ND	107	0.033	Outlier,ND
21	0.012	ND	108	0.040	Outlier
24	0.11	Outlier	110	0.0092	ND
27	0.032	Outlier	112	0.0080	ND
28	0.040	Outlier,ND	113	0.024	ND
29	0.025	Outlier,ND	115	0.010	ND
30	0.074	Outlier,ND	117	0.036	Outlier,ND
33	0.0070	ND	118	0.0053	
35	0.0050				
36	0.048	Outlier,ND			
37	0.0064				
40	0.21	Outlier,ND			
42	0.020				
44	0.0044				
45	0.00081	ND			
46	0.0050	ND			
49	0.010	ND			
51	0.0048				
54	0.0012	ND			
55	0.054	Outlier,ND			
57	0.020	ND			
58	0.025	Outlier,ND			
60	0.0050	ND			
61	0.016				
64	0.036	Outlier,ND			
65	0.0030				
68	0.0021				
69	0.039	Outlier,ND			
73	0.010	ND			
74	0.030	Outlier,ND			
75	0.0048				
78	0.0014				
79	0.070	Outlier			
80	0.010				
81	0.013	ND			

Consensus statistics	
Consensus median, pg/g	0.0064
Median all values pg/g	0.012
Consensus mean, pg/g	0.0080
Standard deviation, pg/g	0.0057
Relative standard deviation, %	72
No. of values reported	63
No. of values removed	22
No. of reported non-detects	37

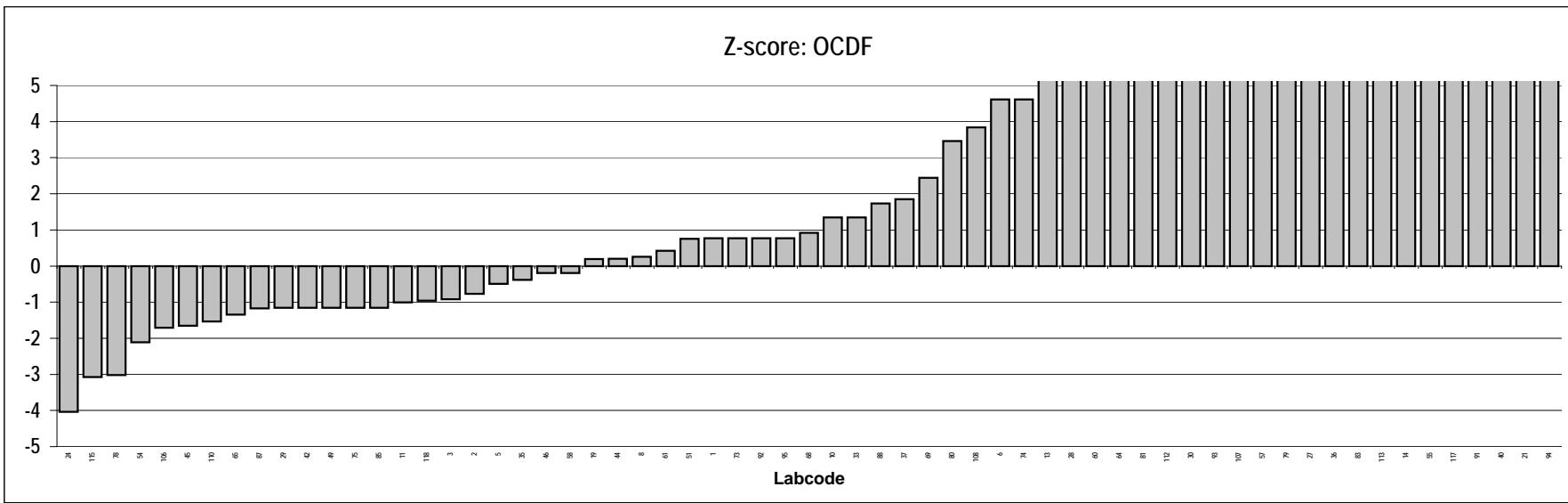
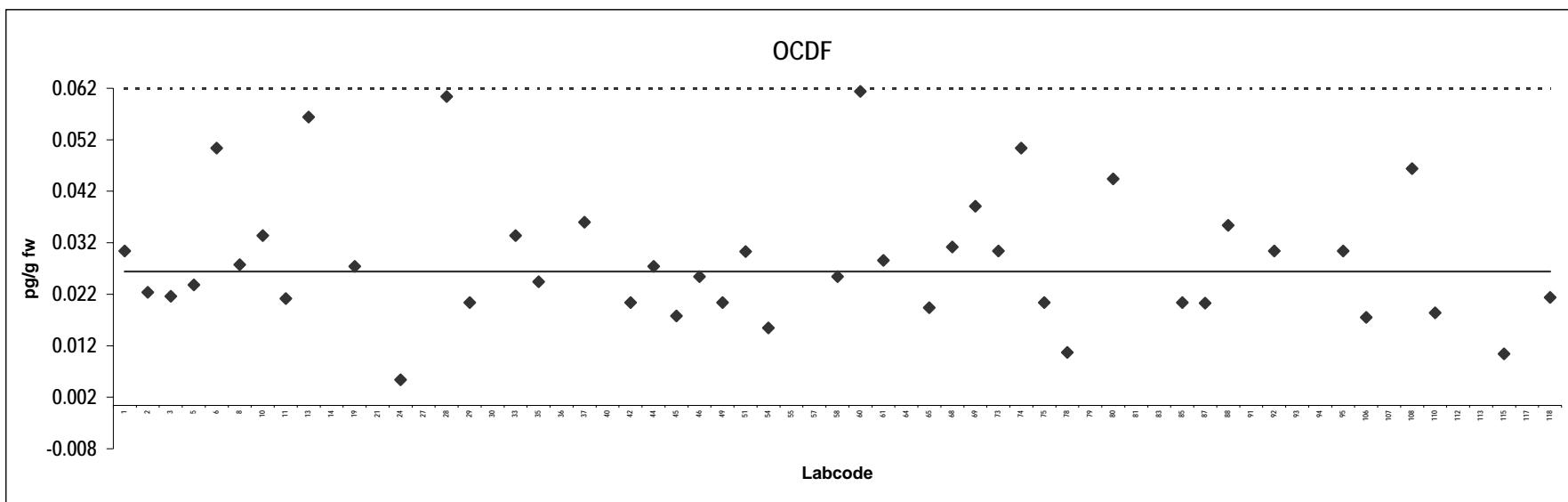


**Pork**  
Congener: OCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.030		83	0.16	
2	0.022		85	0.020	
3	0.021		87	0.020	
5	0.023		88	0.035	
6	0.050	ND	91	0.31	Outlier
8	0.027		92	0.030	
10	0.033		93	0.086	Outlier
11	0.021		94	2.0	Outlier,ND
13	0.056	ND	95	0.030	
14	0.20	Outlier	106	0.017	
19	0.027		107	0.088	Outlier,ND
21	0.57	Outlier	108	0.046	ND
24	0.0050	ND	110	0.018	ND
27	0.12	Outlier	112	0.074	Outlier
28	0.060	ND	113	0.18	Outlier
29	0.020		115	0.010	ND
30	0.079	Outlier	117	0.26	Outlier
33	0.033		118	0.021	
35	0.024				
36	0.14	Outlier			
37	0.036				
40	0.35	Outlier,ND			
42	0.020	ND			
44	0.027				
45	0.017				
46	0.025				
49	0.020	ND			
51	0.030				
54	0.015				
55	0.22	Outlier,ND			
57	0.10	Outlier,ND			
58	0.025	ND			
60	0.061				
61	0.028				
64	0.063	Outlier,ND			
65	0.019				
68	0.031				
69	0.039	ND			
73	0.030	ND			
74	0.050	ND			
75	0.020				
78	0.010				
79	0.10	Outlier			
80	0.044				
81	0.068	Outlier			

**Consensus statistics**

Consensus median, pg/g	0.026
Median all values pg/g	0.031
Consensus mean, pg/g	0.028
Standard deviation, pg/g	0.013
Relative standard deviation, %	45
No. of values reported	63
No. of values removed	19
No. of reported non-detects	19

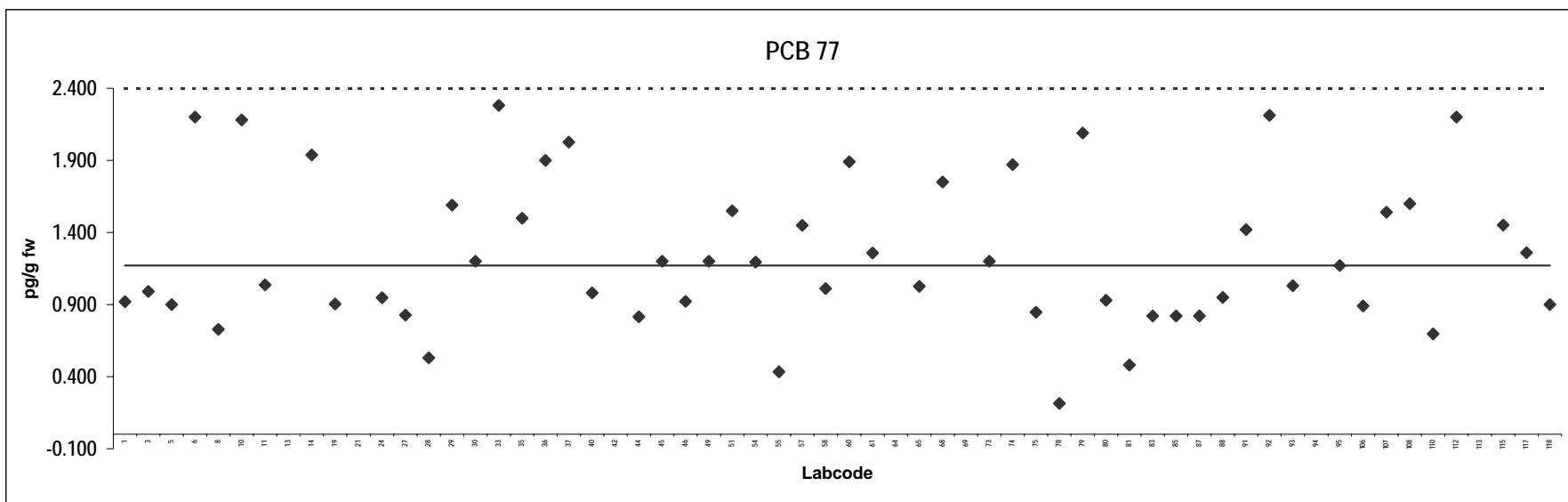


**Pork**  
Congener: PCB 77

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.92		85	0.82	
3	0.99		87	0.82	
5	0.90		88	0.95	
6	2.2		91	1.4	
8	0.73		92	2.2	
10	2.2		93	1.0	
11	1.0		94	3.5	
13	3.0	Outlier	95	1.2	
14	1.9		106	0.89	
19	0.90		107	1.5	
21	2.8	Outlier	108	1.6	
24	0.95		110	0.70	
27	0.83		112	2.2	
28	0.53		113	5.9	
29	1.6		115	1.5	
30	1.2		117	1.3	
33	2.3		118	0.90	
35	1.5				
36	1.9				
37	2.0				
40	0.98				
42	2.9	Outlier			
44	0.82				
45	1.2				
46	0.92				
49	1.2				
51	1.6				
54	1.2				
55	0.43				
57	1.5				
58	1.0				
60	1.9				
61	1.3				
64	13	Outlier			
65	1.0				
68	1.8				
69	6.6	Outlier			
73	1.2				
74	1.9				
75	0.85				
78	0.21				
79	2.1				
80	0.93				
81	0.48				
83	0.82				

**Consensus statistics**

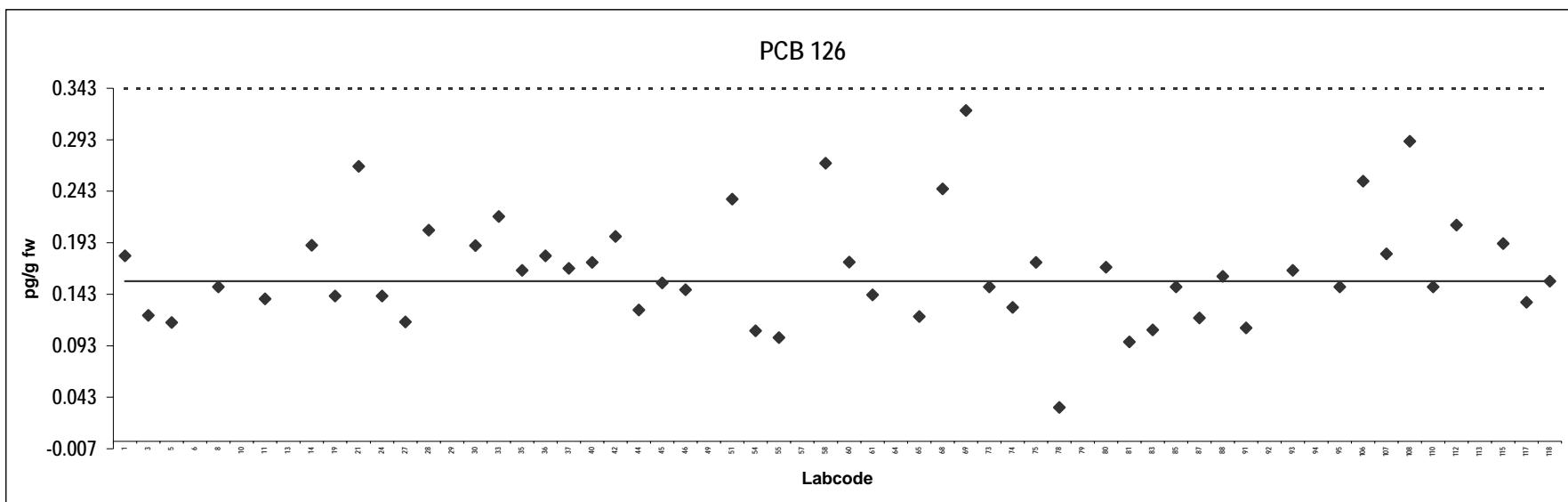
Consensus median, pg/g	1.2
Median all values pg/g	1.2
Consensus mean, pg/g	1.2
Standard deviation, pg/g	0.52
Relative standard deviation, %	41
No. of values reported	62
No. of values removed	7
No. of reported non-detects	0



**Pork**  
**Congener: PCB 126**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.18		85	0.15	
3	0.12		87	0.12	
5	0.12		88	0.16	
6	1.0	Outlier,ND	91	0.11	
8	0.15		92	0.42	Outlier
10	0.50	Outlier	93	0.17	
11	0.14		94	1.0	Outlier,ND
13	0.45	Outlier	95	0.15	
14	0.19		106	0.25	
19	0.14		107	0.18	ND
21	0.27		108	0.29	
24	0.14		110	0.15	ND
27	0.12		112	0.21	
28	0.21		113	0.37	Outlier
29	0.81	Outlier	115	0.19	
30	0.19		117	0.14	
33	0.22		118	0.16	
35	0.17				
36	0.18				
37	0.17				
40	0.17				
42	0.20				
44	0.13				
45	0.15				
46	0.15				
49	0.42	Outlier			
51	0.24				
54	0.11				
55	0.10	ND			
57	0.50	Outlier,ND			
58	0.27				
60	0.17				
61	0.14				
64	0.55	Outlier,ND			
65	0.12				
68	0.25				
69	0.32				
73	0.15				
74	0.13				
75	0.17				
78	0.033				
79	0.46				
80	0.17				
81	0.096				
83	0.11				

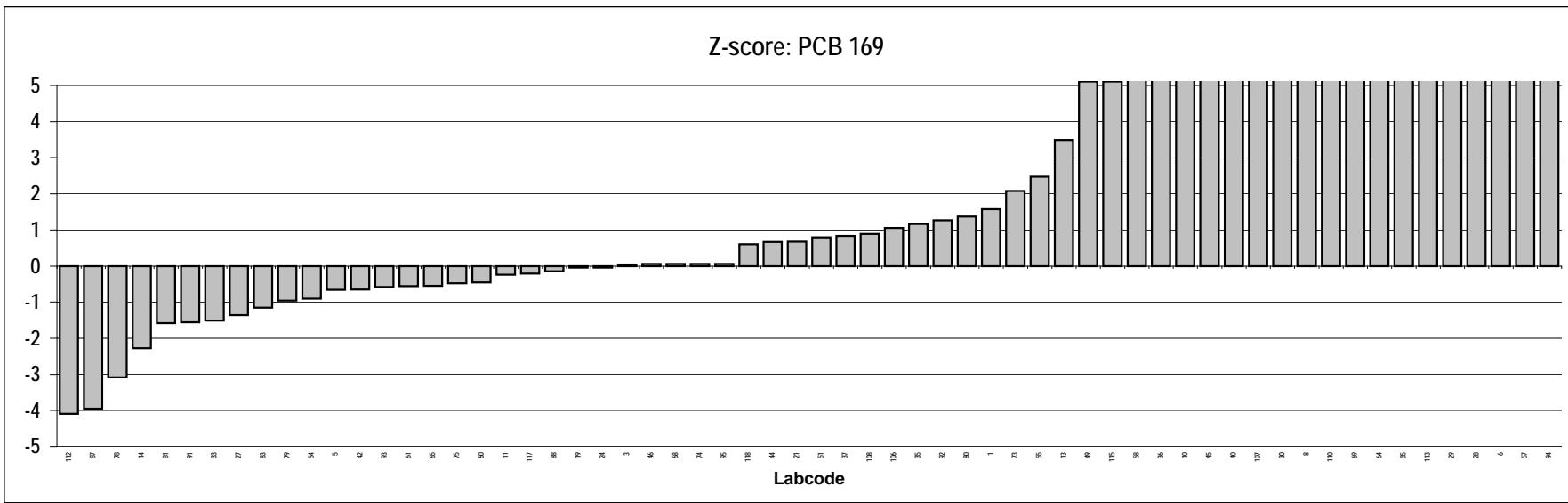
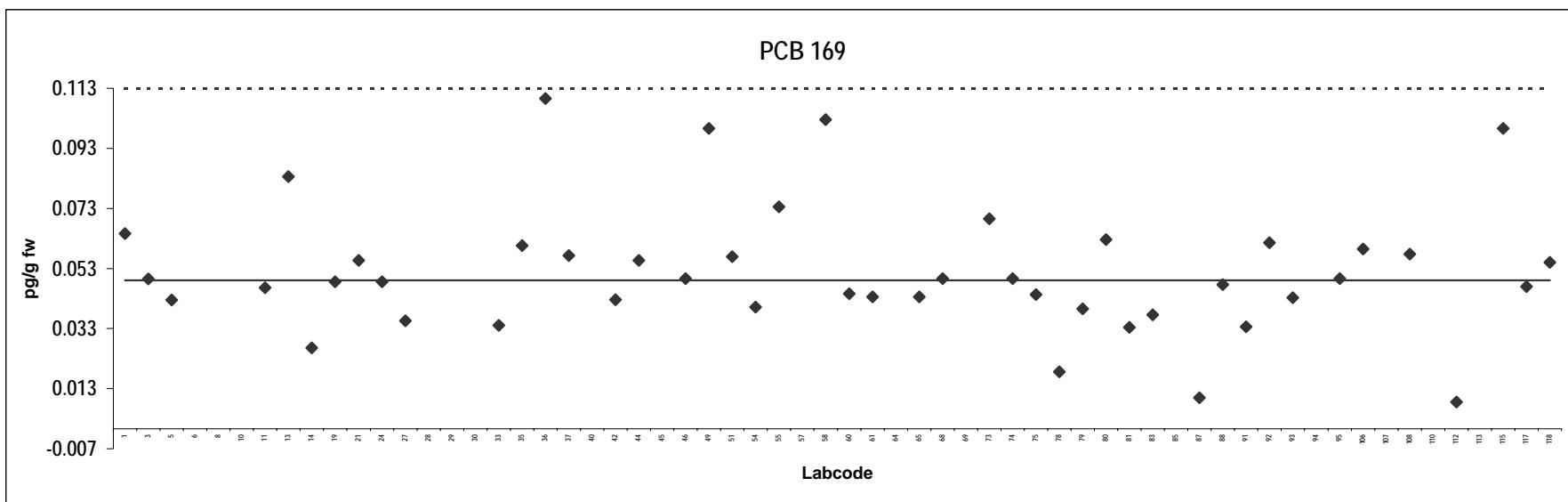
Consensus statistics	
Consensus median, pg/g	0.16
Median all values pg/g	0.17
Consensus mean, pg/g	0.17
Standard deviation, pg/g	0.054
Relative standard deviation, %	32
No. of values reported	62
No. of values removed	11
No. of reported non-detects	7



**Pork**  
**Congener: PCB 169**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.065		85	0.50	Outlier
3	0.050		87	0.010	ND
5	0.043		88	0.048	
6	1.0	Outlier,ND	91	0.034	
8	0.15	Outlier,ND	92	0.062	
10	0.12	Outlier	93	0.044	
11	0.047		94	1.0	Outlier,ND
13	0.084	ND	95	0.050	
14	0.027		106	0.060	
19	0.049		107	0.14	Outlier,ND
21	0.056		108	0.058	
24	0.049		110	0.15	Outlier,ND
27	0.036		112	0.0090	
28	0.60	Outlier,ND	113	0.55	Outlier
29	0.56	Outlier,ND	115	0.10	ND
30	0.14	Outlier,ND	117	0.047	
33	0.035		118	0.055	
35	0.061				
36	0.11				
37	0.058				
40	0.14	Outlier,ND			
42	0.043				
44	0.056				
45	0.13	Outlier			
46	0.050				
49	0.10	ND			
51	0.057				
54	0.041				
55	0.074	ND			
57	1.0	Outlier,ND			
58	0.10				
60	0.045				
61	0.044				
64	0.40	Outlier,ND			
65	0.044				
68	0.050				
69	0.37	Outlier,ND			
73	0.070				
74	0.050				
75	0.045				
78	0.019				
79	0.040				
80	0.063				
81	0.034				
83	0.038				

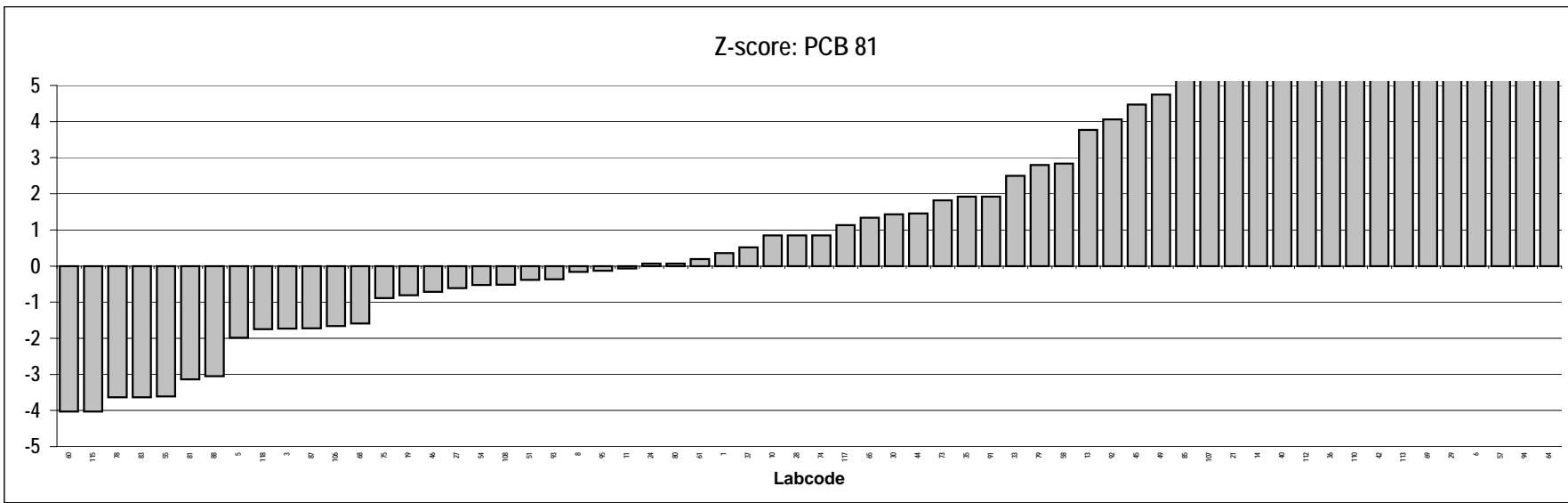
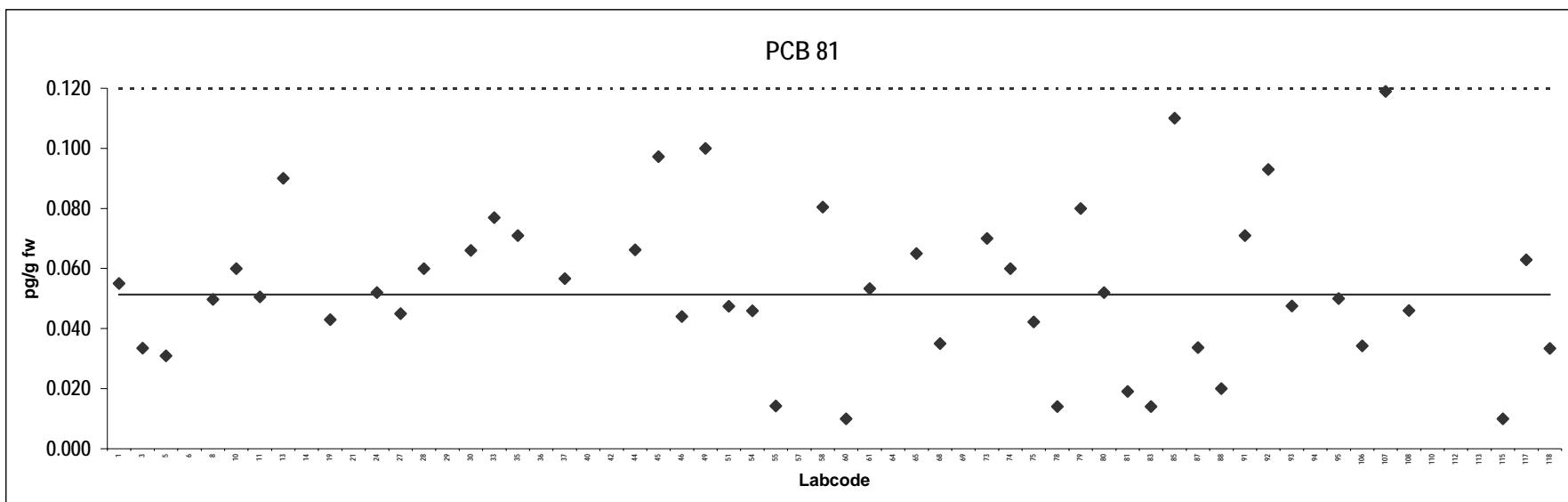
Consensus statistics	
Consensus median, pg/g	0.049
Median all values pg/g	0.057
Consensus mean, pg/g	0.052
Standard deviation, pg/g	0.021
Relative standard deviation, %	41
No. of values reported	62
No. of values removed	16
No. of reported non-detects	17



**Pork**  
Congener: PCB 81

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.055		85	0.11	
3	0.034		87	0.034	
5	0.031		88	0.020	
6	1.0	Outlier,ND	91	0.071	
8	0.050	ND	92	0.093	
10	0.060		93	0.048	
11	0.051		94	1.0	
13	0.090		95	0.050	
14	0.13	Outlier	106	0.034	
19	0.043		107	0.12	
21	0.13	Outlier,ND	108	0.046	
24	0.052		110	0.15	
27	0.045		112	0.14	
28	0.060	ND	113	0.22	
29	0.56	Outlier,ND	115	0.010	ND
30	0.066	ND	117	0.063	
33	0.077		118	0.033	
35	0.071				
36	0.15	Outlier			
37	0.057				
40	0.14	Outlier,ND			
42	0.16	Outlier			
44	0.066				
45	0.097				
46	0.044				
49	0.10	ND			
51	0.047	ND			
54	0.046				
55	0.014	ND			
57	1.0	Outlier,ND			
58	0.080				
60	0.010	ND			
61	0.053				
64	1.2	Outlier,ND			
65	0.065	ND			
68	0.035				
69	0.39	Outlier			
73	0.070				
74	0.060				
75	0.042				
78	0.014				
79	0.080				
80	0.052				
81	0.019				
83	0.014				

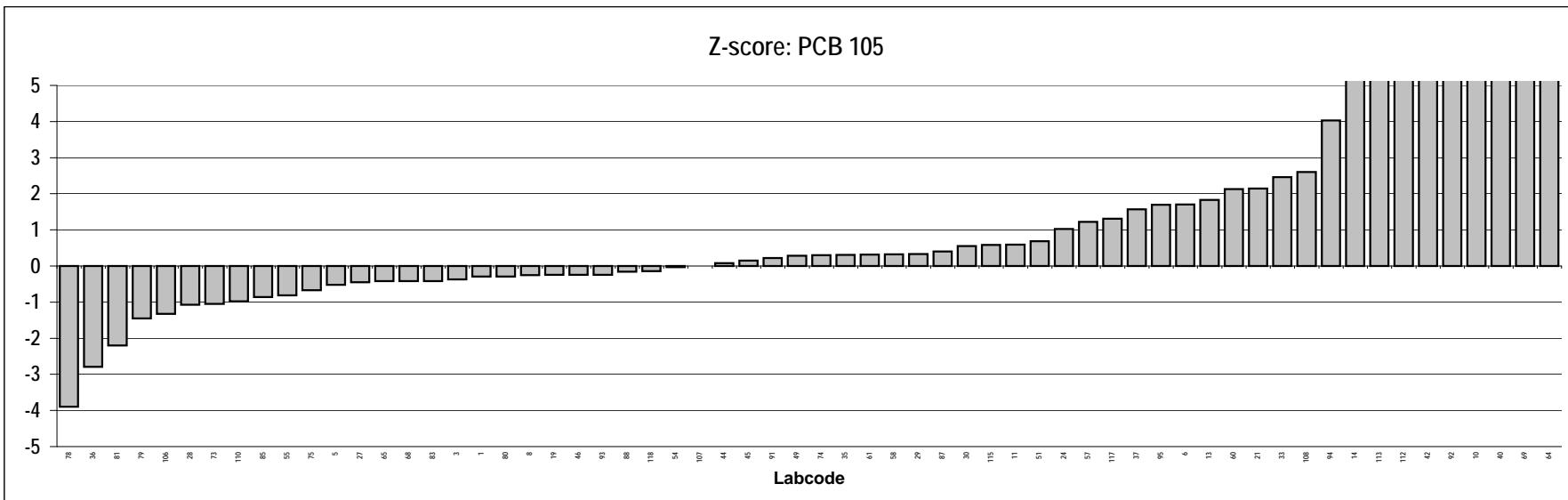
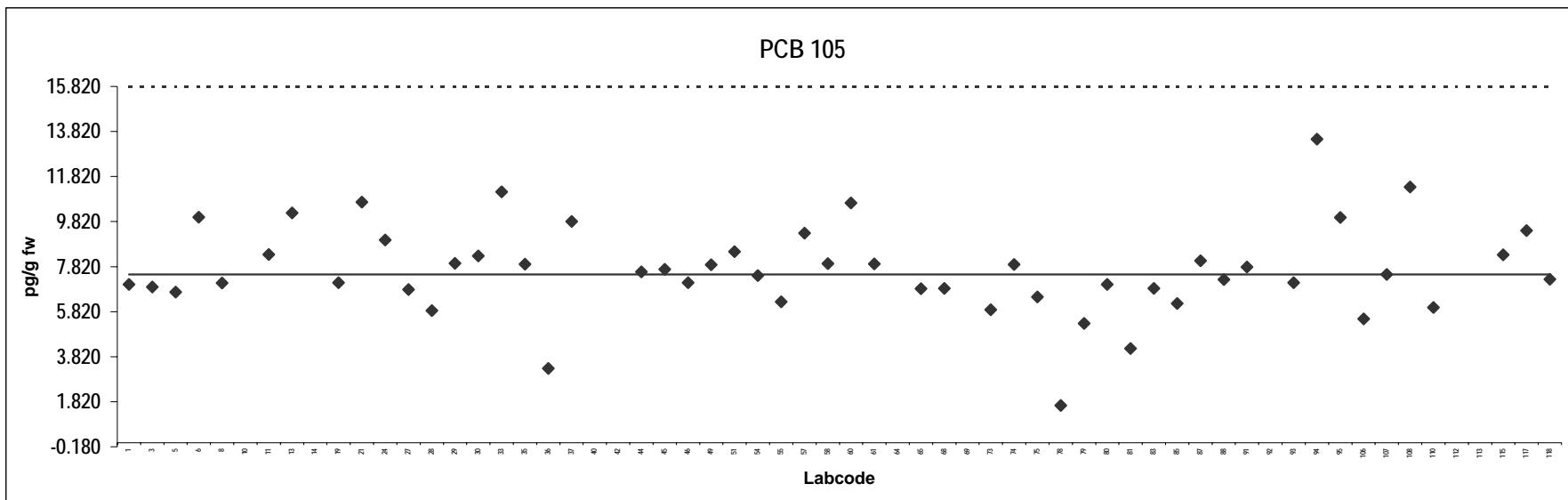
Consensus statistics	
Consensus median, pg/g	0.051
Median all values pg/g	0.060
Consensus mean, pg/g	0.054
Standard deviation, pg/g	0.026
Relative standard deviation, %	48
No. of values reported	62
No. of values removed	14
No. of reported non-detects	17



**Pork**  
**Congener: PCB 105**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	7.0		85	6.2	
3	6.9		87	8.1	
5	6.7		88	7.2	
6	10		91	7.8	
8	7.1		92	25	
10	27	Outlier	93	7.1	
11	8.4		94	13	
13	10		95	10	ND
14	18	Outlier	106	5.5	
19	7.1		107	7.5	
21	11		108	11	
24	9.0		110	6.0	
27	6.8		112	21	
28	5.9		113	20	
29	8.0		115	8.3	
30	8.3		117	9.4	
33	11		118	7.3	
35	7.9				
36	3.3				
37	9.8				
40	27	Outlier,ND			
42	22	Outlier			
44	7.6				
45	7.7				
46	7.1				
49	7.9				
51	8.5				
54	7.4				
55	6.3				
57	9.3				
58	8.0				
60	11				
61	7.9				
64	73	Outlier			
65	6.8				
68	6.9				
69	28	Outlier			
73	5.9				
74	7.9				
75	6.5				
78	1.7				
79	5.3				
80	7.0				
81	4.2				
83	6.9				

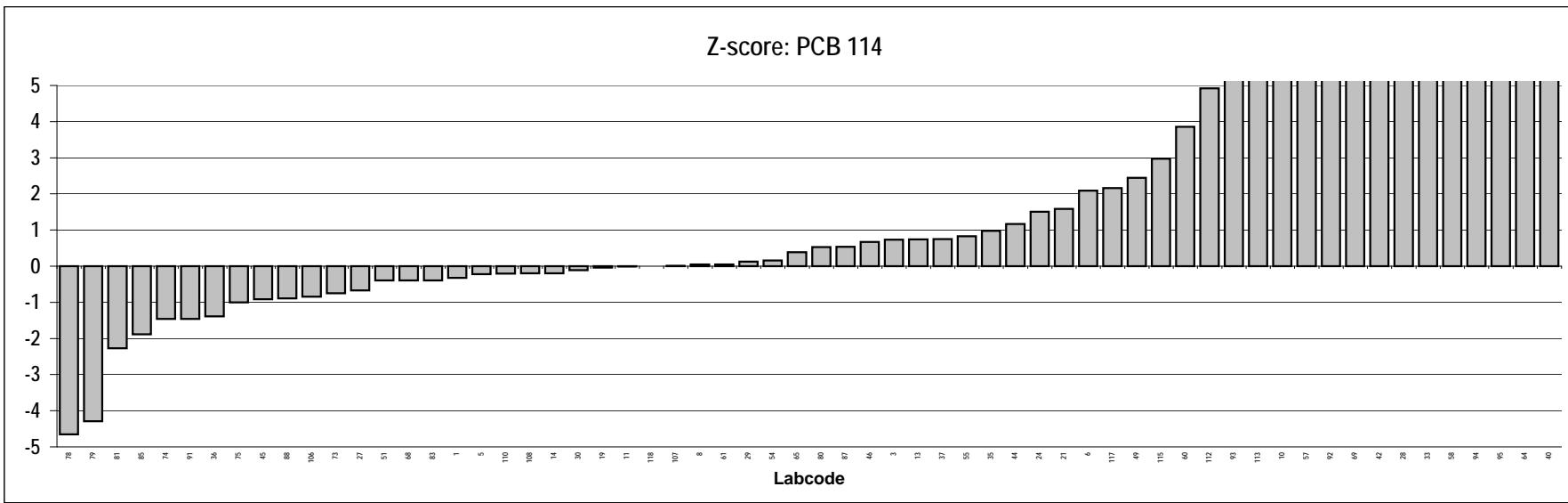
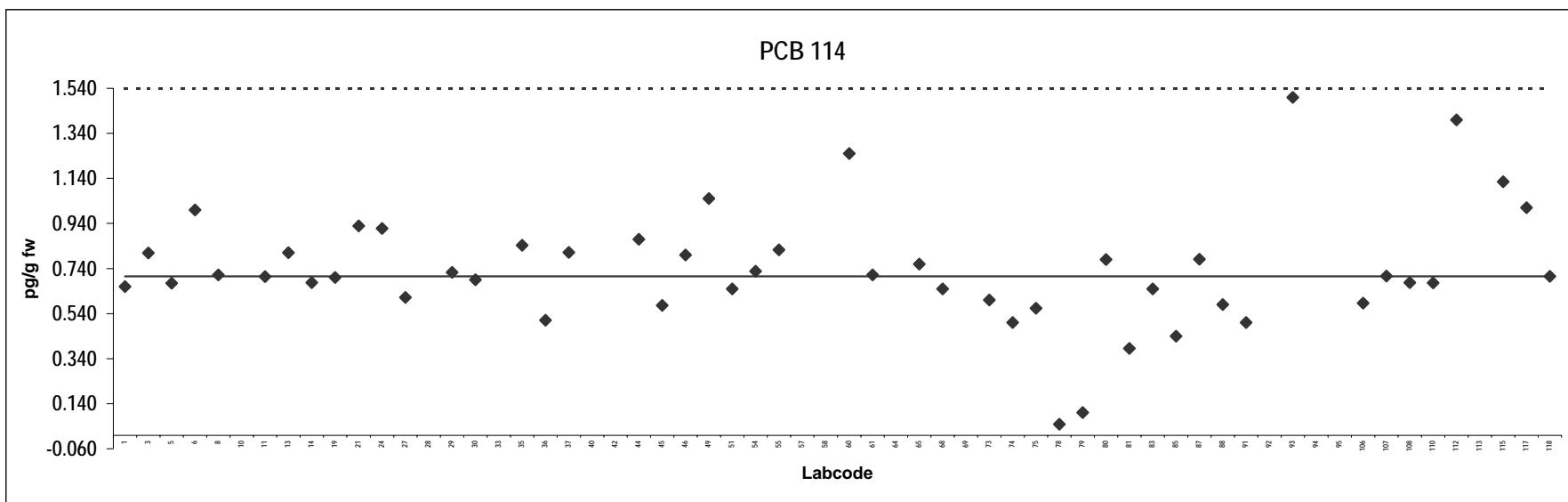
Consensus statistics	
Consensus median, pg/g	7.5
Median all values pg/g	7.9
Consensus mean, pg/g	7.7
Standard deviation, pg/g	2.0
Relative standard deviation, %	26
No. of values reported	62
No. of values removed	9
No. of reported non-detects	2



**Pork**  
**Congener: PCB 114**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.66		85	0.44	
3	0.81		87	0.78	
5	0.67		88	0.58	
6	1.0	ND	91	0.50	ND
8	0.71		92	2.0	Outlier,ND
10	2.0	Outlier	93	1.5	ND
11	0.70		94	10	Outlier,ND
13	0.81		95	10	Outlier,ND
14	0.68		106	0.59	
19	0.70		107	0.71	
21	0.93		108	0.68	
24	0.92		110	0.68	
27	0.61		112	1.4	
28	3.0	Outlier,ND	113	1.9	Outlier
29	0.72		115	1.1	
30	0.69		117	1.0	
33	3.6	Outlier,ND	118	0.71	
35	0.84				
36	0.51				
37	0.81				
40	14	Outlier,ND			
42	2.2	Outlier			
44	0.87				
45	0.58				
46	0.80				
49	1.1				
51	0.65				
54	0.73				
55	0.82				
57	2.0	Outlier,ND			
58	5.0	Outlier,ND			
60	1.3				
61	0.71				
64	12	Outlier			
65	0.76				
68	0.65				
69	2.1	Outlier			
73	0.60				
74	0.50	ND			
75	0.56				
78	0.049	ND			
79	0.10				
80	0.78				
81	0.39				
83	0.65				

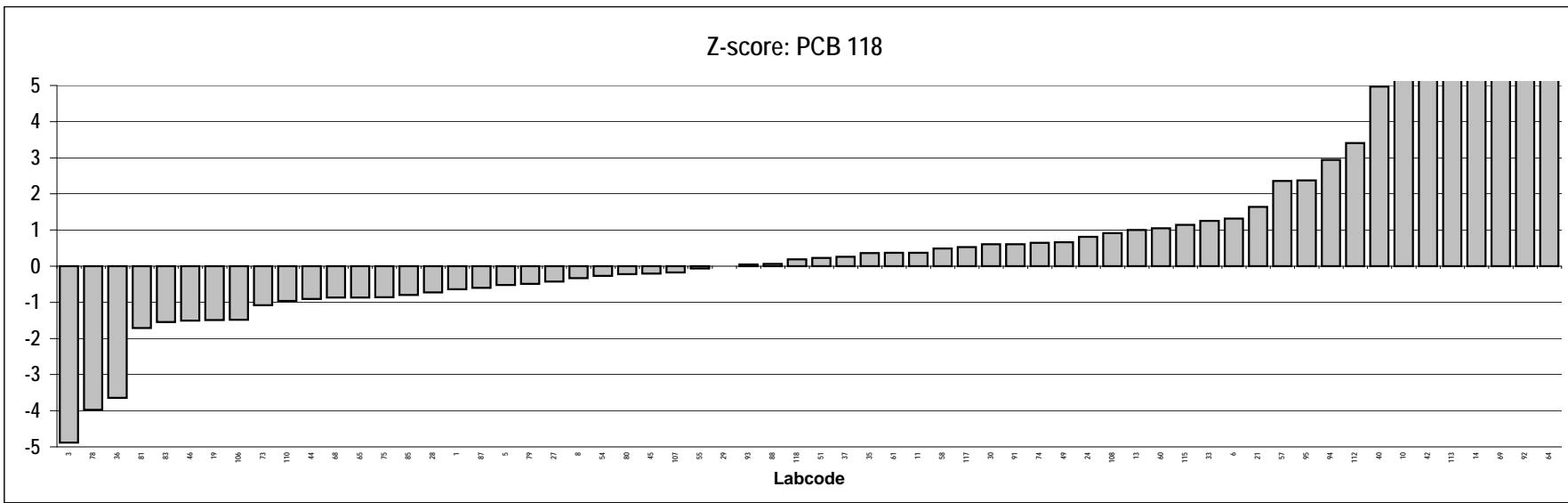
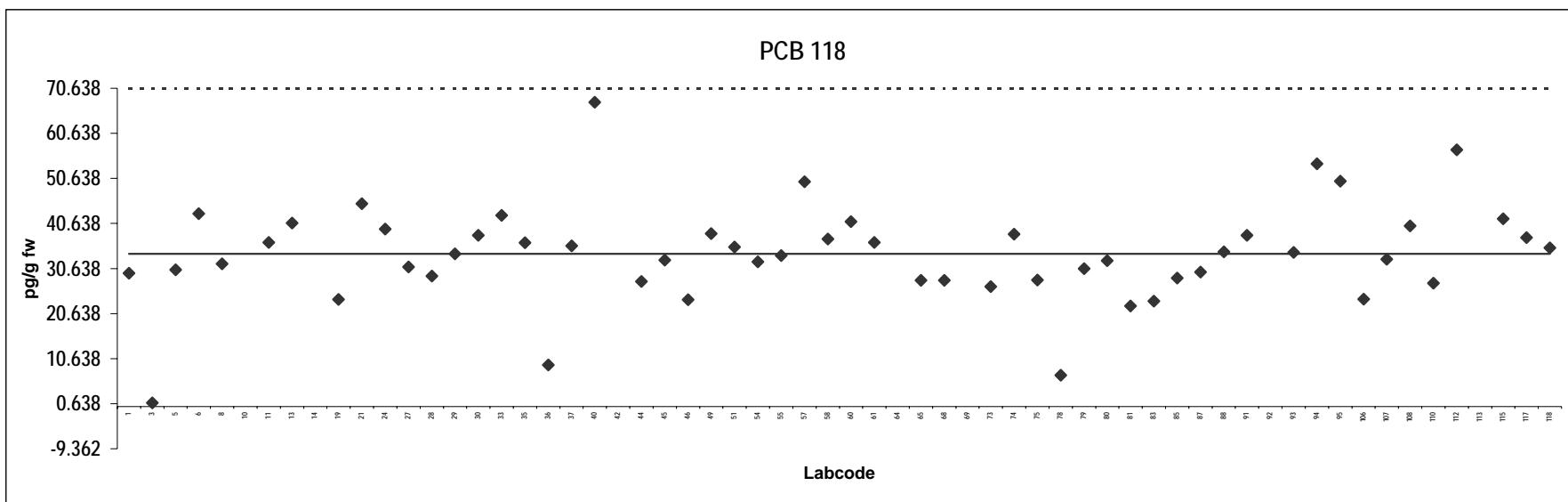
Consensus statistics	
Consensus median, pg/g	0.71
Median all values pg/g	0.77
Consensus mean, pg/g	0.73
Standard deviation, pg/g	0.26
Relative standard deviation, %	35
No. of values reported	62
No. of values removed	13
No. of reported non-detects	13



**Pork**  
**Congener: PCB 118**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	30		85	29	
3	0.81		87	30	
5	30		88	34	
6	43		91	38	
8	32		92	103	
10	71	Outlier	93	34	
11	36		94	54	
13	41		95	50	
14	81	Outlier	106	24	
19	24		107	33	
21	45		108	40	
24	39		110	27	
27	31		112	57	
28	29		113	75	
29	34		115	42	
30	38		117	38	
33	42		118	35	
35	36				
36	9.2				
37	36				
40	68	ND			
42	72	Outlier			
44	28				
45	33				
46	24				
49	38				
51	35				
54	32				
55	33				
57	50				
58	37				
60	41				
61	36				
64	270	Outlier			
65	28				
68	28				
69	94	Outlier			
73	27				
74	38				
75	28				
78	7.0				
79	31				
80	32				
81	22				
83	23				

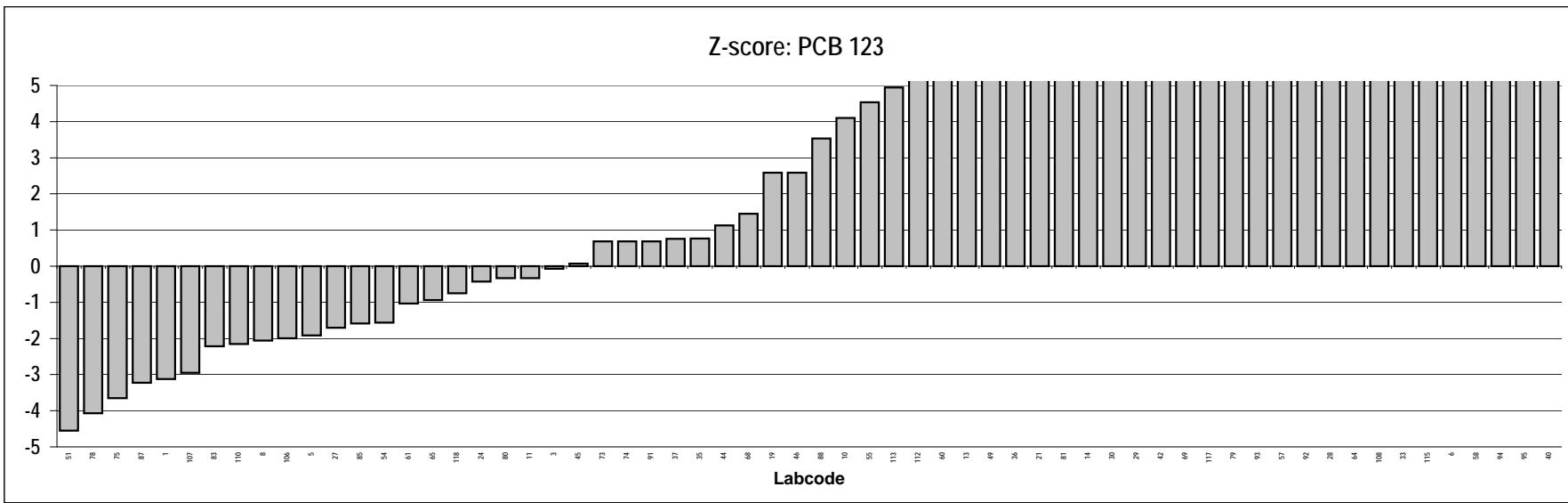
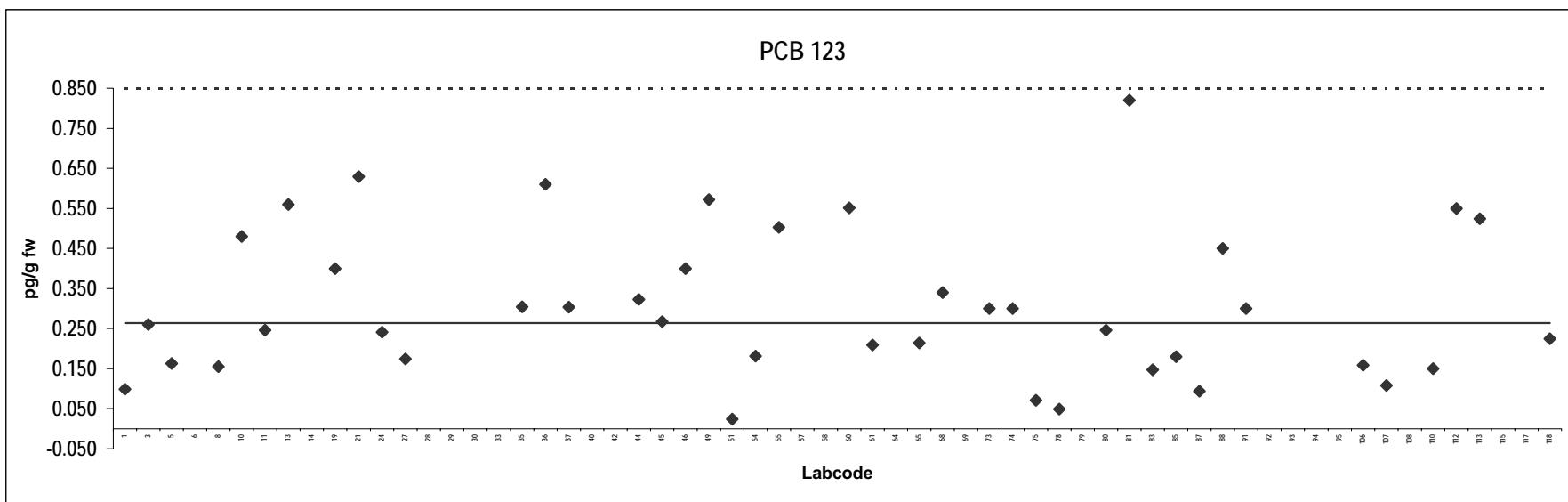
Consensus statistics	
Consensus median, pg/g	34
Median all values pg/g	35
Consensus mean, pg/g	34
Standard deviation, pg/g	11
Relative standard deviation, %	33
No. of values reported	62
No. of values removed	7
No. of reported non-detects	1



**Pork**  
Congener: PCB 123

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.099		85	0.18	
3	0.26	ND	87	0.094	
5	0.16		88	0.45	
6	4.4	Outlier	91	0.30	ND
8	0.16		92	2.5	Outlier
10	0.48		93	1.4	Outlier,ND
11	0.25		94	5.0	Outlier,ND
13	0.56	ND	95	10	Outlier,ND
14	0.92	Outlier	106	0.16	
19	0.40		107	0.11	ND
21	0.63		108	3.5	Outlier
24	0.24	ND	110	0.15	ND
27	0.17		112	0.55	
28	3.0	Outlier,ND	113	0.52	
29	1.0	Outlier	115	4.1	Outlier
30	1.0	Outlier	117	1.4	Outlier
33	3.6	Outlier,ND	118	0.22	
35	0.30				
36	0.61	ND			
37	0.30				
40	14	Outlier,ND			
42	1.1	Outlier			
44	0.32				
45	0.27				
46	0.40				
49	0.57				
51	0.024	ND			
54	0.18				
55	0.50				
57	2.0	Outlier,ND			
58	5.0	Outlier,ND			
60	0.55				
61	0.21				
64	3.2	Outlier			
65	0.21				
68	0.34				
69	1.3	Outlier,ND			
73	0.30				
74	0.30				
75	0.071				
78	0.049	ND			
79	1.4	Outlier			
80	0.25				
81	0.82				
83	0.15				

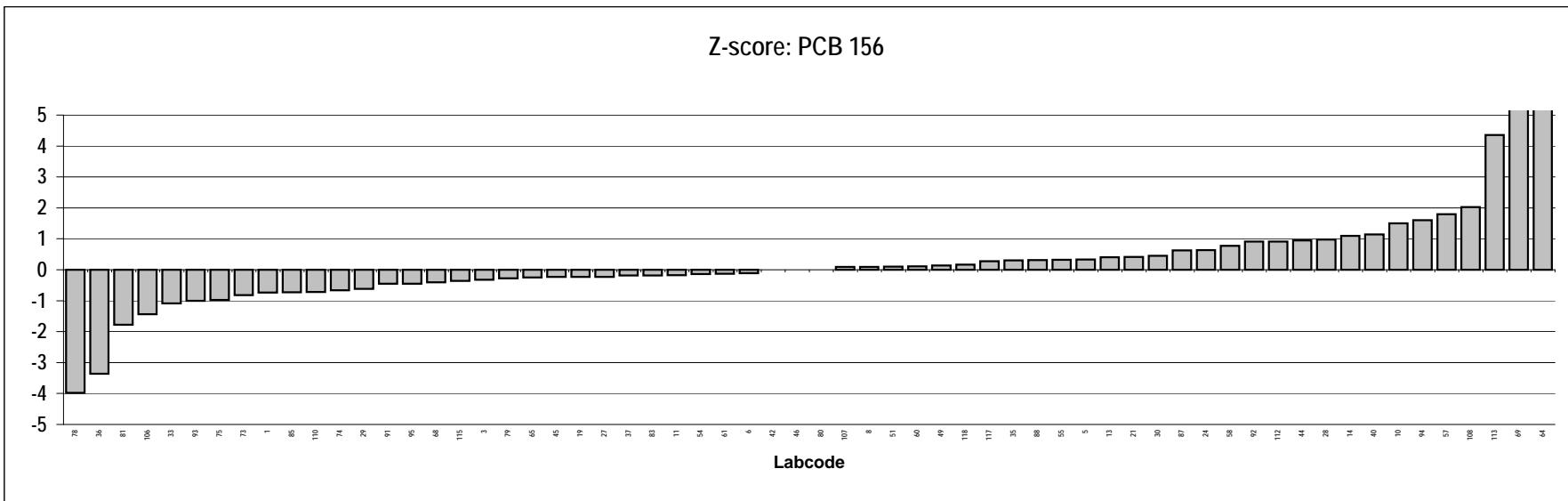
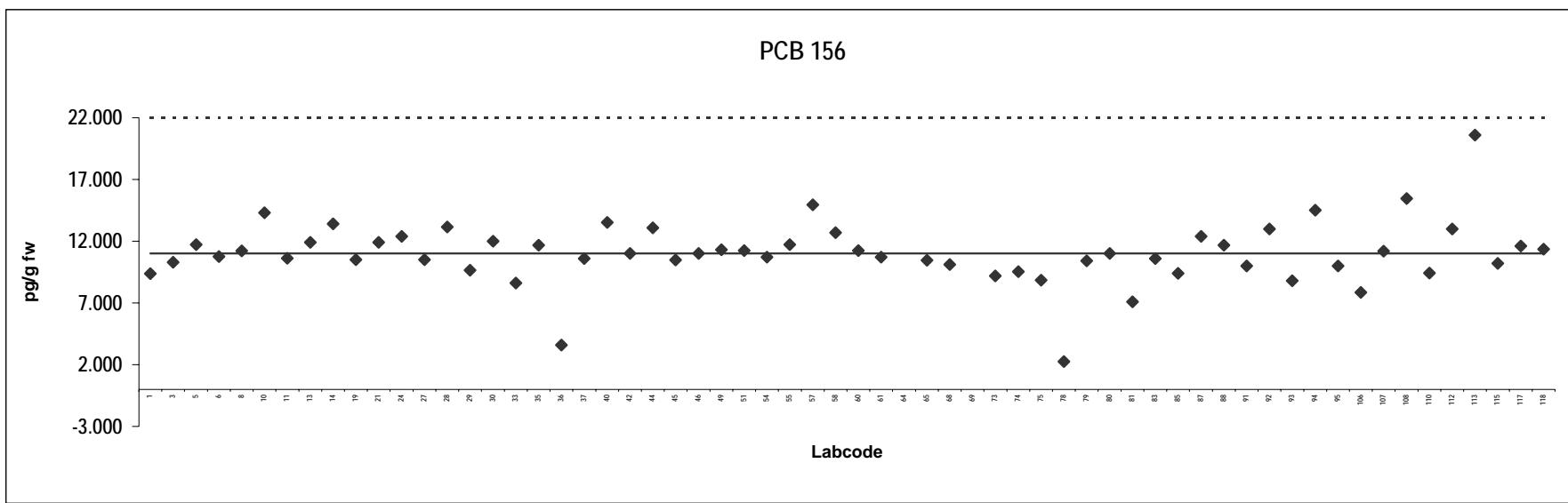
Consensus statistics	
Consensus median, pg/g	0.26
Median all values pg/g	0.43
Consensus mean, pg/g	0.31
Standard deviation, pg/g	0.19
Relative standard deviation, %	60
No. of values reported	62
No. of values removed	20
No. of reported non-detects	18



**Pork**  
**Congener: PCB 156**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	9.4		85	9.4	
3	10		87	12	
5	12		88	12	
6	11		91	10	
8	11		92	13	
10	14		93	8.8	
11	11		94	15	
13	12		95	10	
14	13		106	7.8	
19	11		107	11	
21	12		108	15	
24	12		110	9.4	
27	11		112	13	
28	13		113	21	
29	9.6		115	10	
30	12		117	12	
33	8.6		118	11	
35	12				
36	3.6				
37	11				
40	14	ND			
42	11				
44	13				
45	10				
46	11				
49	11				
51	11				
54	11				
55	12				
57	15				
58	13				
60	11				
61	11				
64	25	Outlier			
65	10				
68	10				
69	22	Outlier			
73	9.2				
74	9.5				
75	8.8				
78	2.2				
79	10				
80	11				
81	7.1				
83	11				

Consensus statistics	
Consensus median, pg/g	11
Median all values pg/g	11
Consensus mean, pg/g	11
Standard deviation, pg/g	2.6
Relative standard deviation, %	23
No. of values reported	62
No. of values removed	2
No. of reported non-detects	1

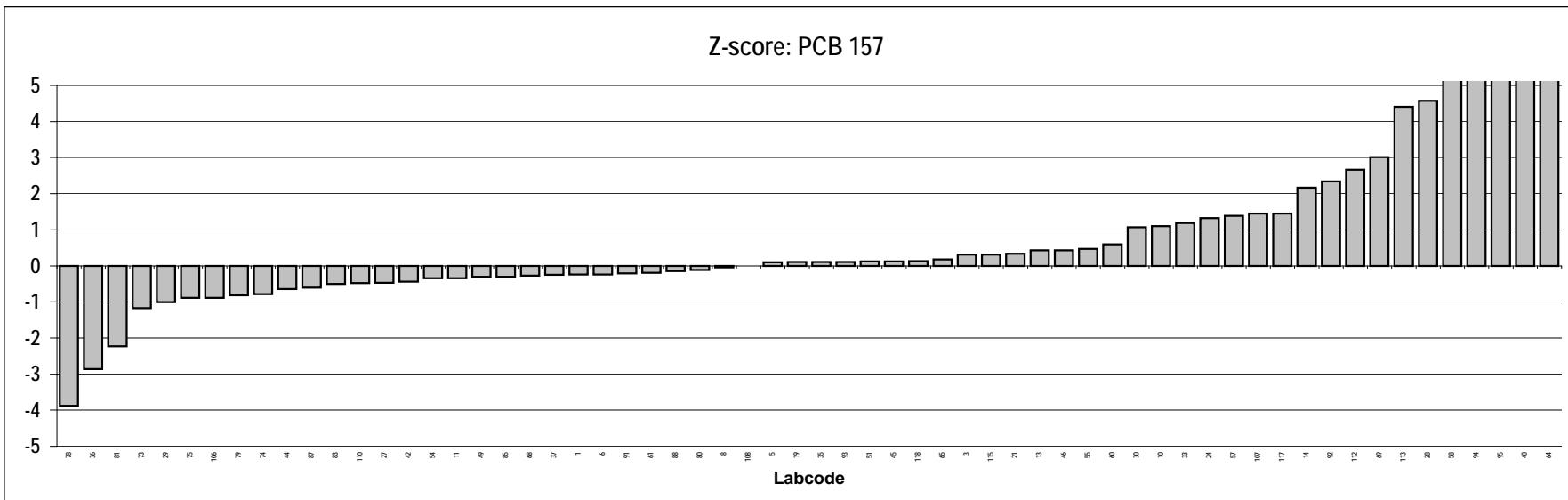
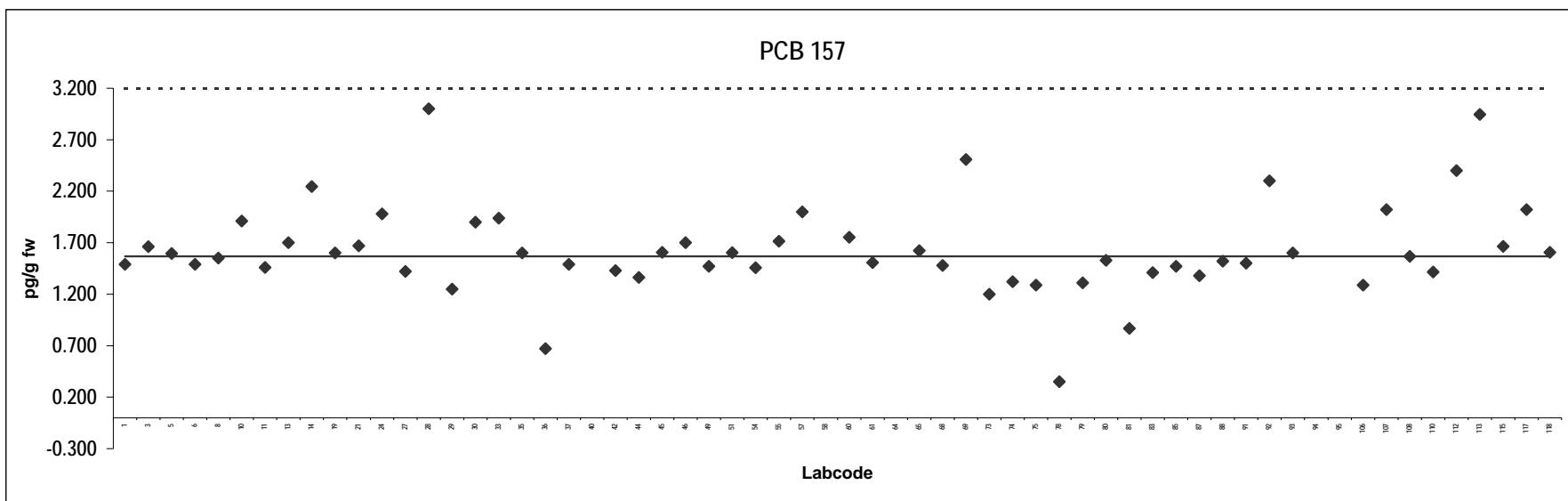


**Pork**  
**Congener: PCB 157**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.5		85	1.5	
3	1.7		87	1.4	
5	1.6		88	1.5	
6	1.5		91	1.5	
8	1.6		92	2.3	
10	1.9		93	1.6	
11	1.5		94	5.0	
13	1.7		95	10	Outlier,ND
14	2.2		106	1.3	Outlier,ND
19	1.6		107	2.0	
21	1.7		108	1.6	
24	2.0		110	1.4	
27	1.4		112	2.4	
28	3.0	ND	113	2.9	
29	1.3		115	1.7	
30	1.9		117	2.0	
33	1.9	ND	118	1.6	
35	1.6				
36	0.67				
37	1.5				
40	14	Outlier,ND			
42	1.4				
44	1.4				
45	1.6				
46	1.7				
49	1.5				
51	1.6				
54	1.5				
55	1.7				
57	2.0	ND			
58	5.0	Outlier,ND			
60	1.8				
61	1.5				
64	14	Outlier			
65	1.6				
68	1.5				
69	2.5				
73	1.2				
74	1.3				
75	1.3				
78	0.35				
79	1.3				
80	1.5				
81	0.87				
83	1.4				

**Consensus statistics**

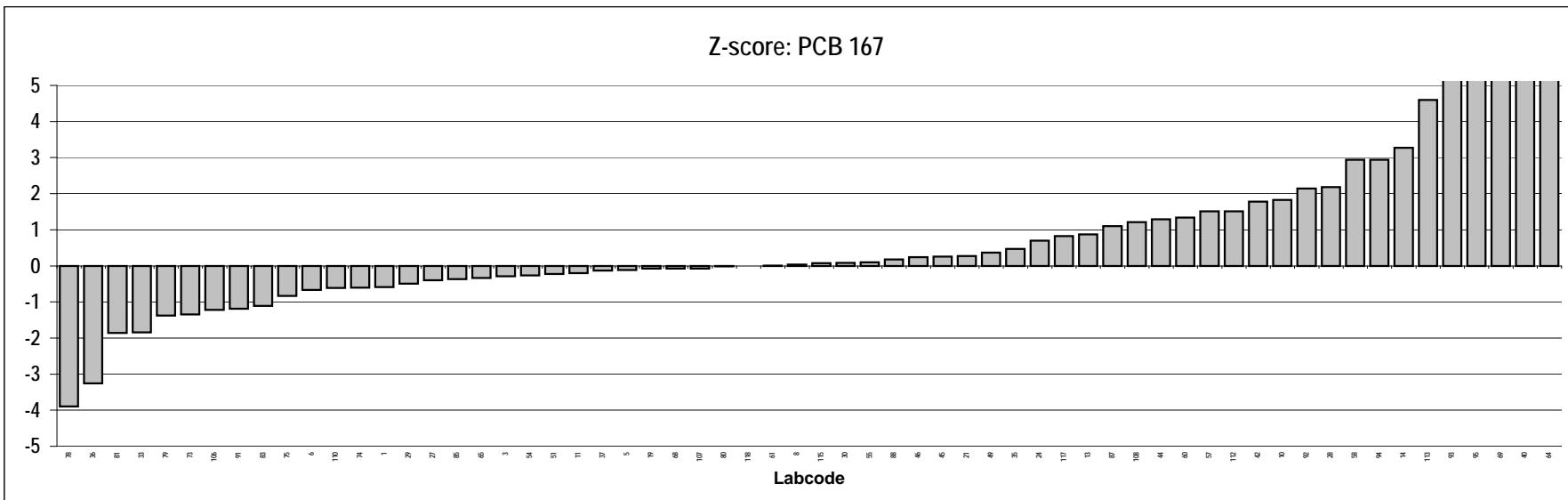
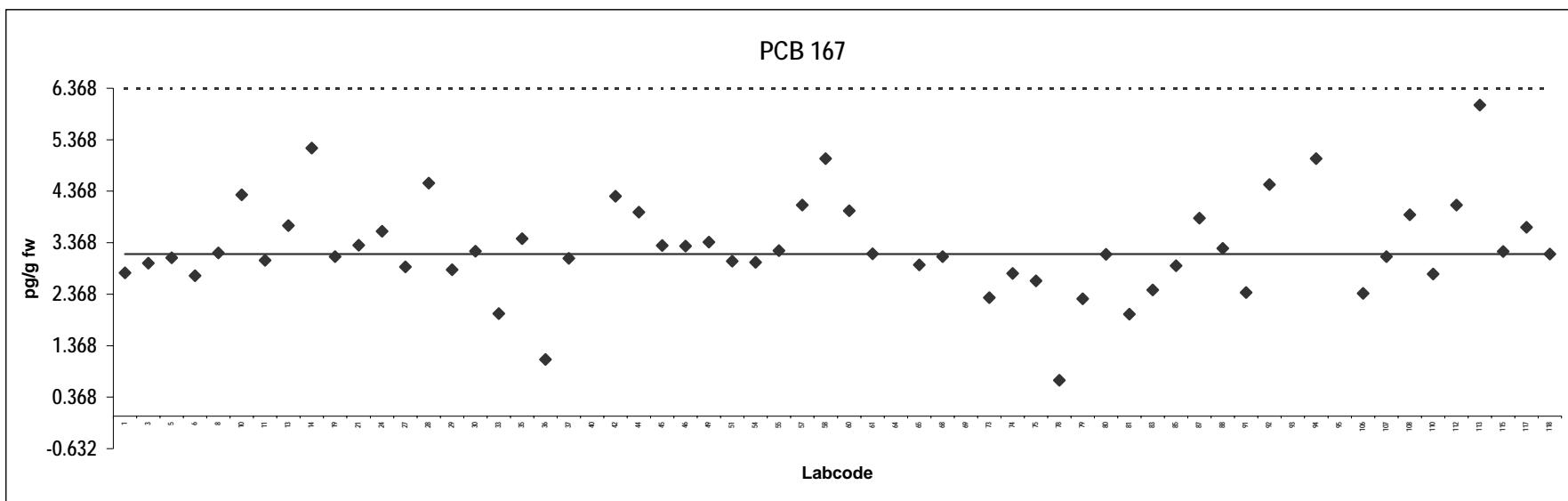
Consensus median, pg/g	1.6
Median all values pg/g	1.6
Consensus mean, pg/g	1.6
Standard deviation, pg/g	0.45
Relative standard deviation, %	27
No. of values reported	62
No. of values removed	5
No. of reported non-detects	7



**Pork**  
**Congener: PCB 167**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	2.8		85	2.9	
3	3.0		87	3.8	
5	3.1		88	3.3	
6	2.7		91	2.4	
8	3.2		92	4.5	
10	4.3		93	9.2	Outlier
11	3.0		94	5.0	ND
13	3.7		95	10	Outlier,ND
14	5.2		106	2.4	
19	3.1		107	3.1	
21	3.3		108	3.9	
24	3.6		110	2.8	
27	2.9		112	4.1	
28	4.5		113	6.0	
29	2.8		115	3.2	
30	3.2		117	3.7	
33	2.0	ND	118	3.1	
35	3.4				
36	1.1				
37	3.1				
40	14	Outlier,ND			
42	4.3				
44	4.0				
45	3.3				
46	3.3				
49	3.4				
51	3.0				
54	3.0				
55	3.2				
57	4.1				
58	5.0	ND			
60	4.0				
61	3.2				
64	70	Outlier			
65	2.9				
68	3.1				
69	10	Outlier			
73	2.3				
74	2.8				
75	2.6				
78	0.70				
79	2.3				
80	3.1				
81	2.0				
83	2.5				

Consensus statistics	
Consensus median, pg/g	3.1
Median all values pg/g	3.2
Consensus mean, pg/g	3.3
Standard deviation, pg/g	0.92
Relative standard deviation, %	28
No. of values reported	62
No. of values removed	5
No. of reported non-detects	5

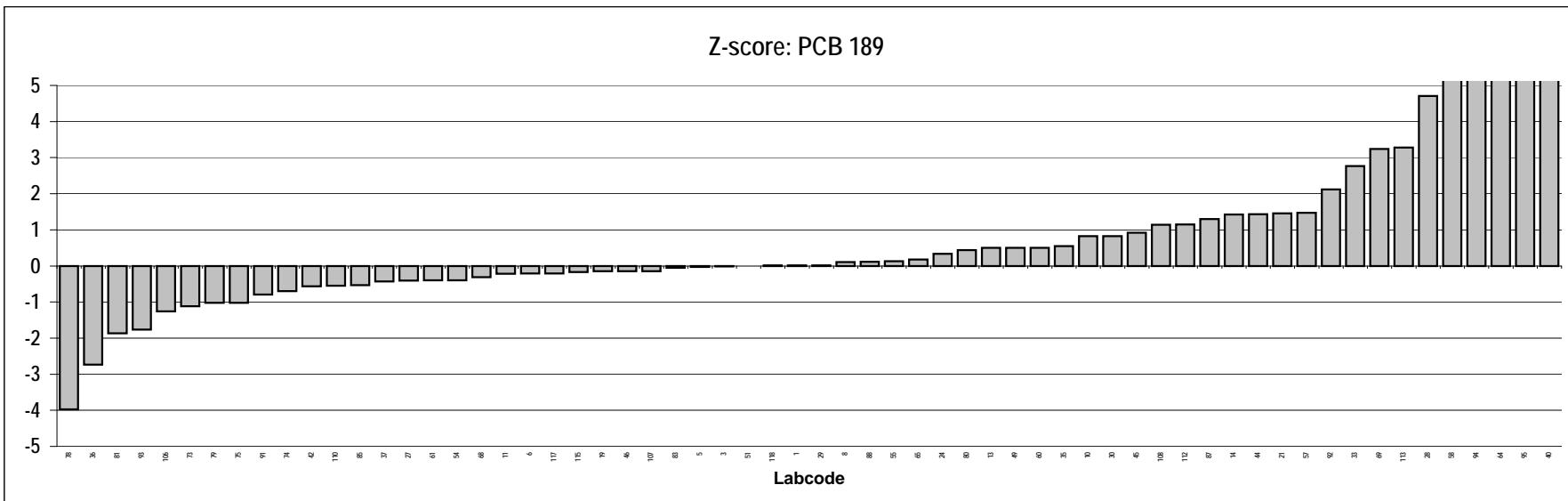
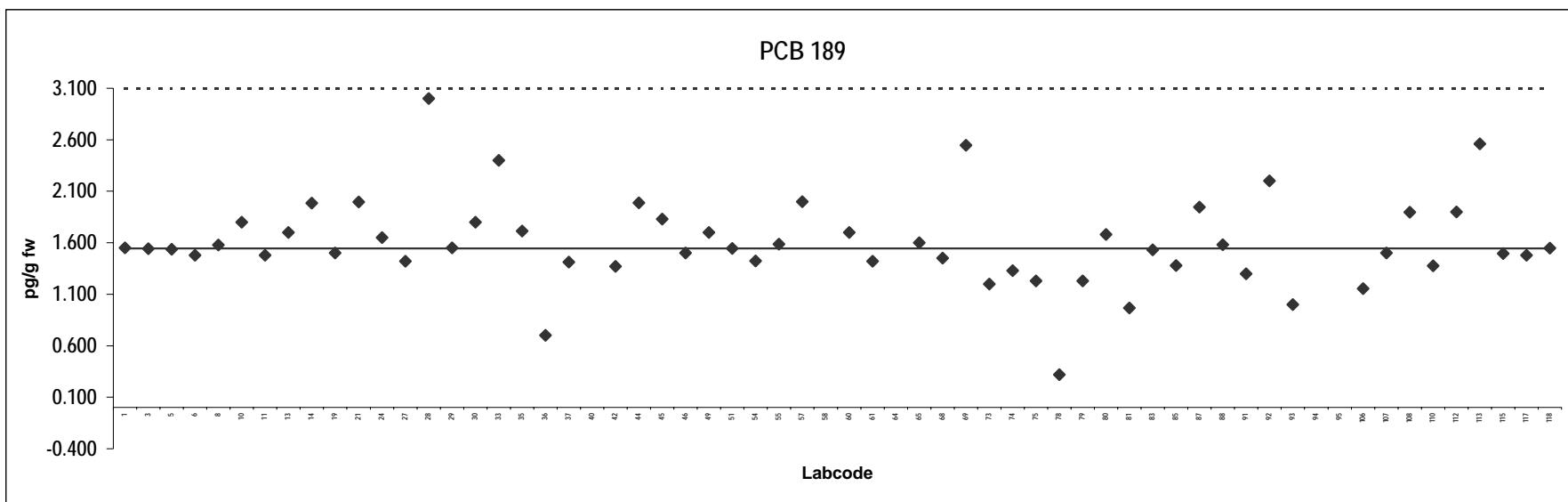


**Pork**  
**Congener: PCB 189**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.6		85	1.4	
3	1.5		87	1.9	
5	1.5		88	1.6	
6	1.5		91	1.3	
8	1.6		92	2.2	
10	1.8		93	1.0	ND
11	1.5		94	5.0	Outlier,ND
13	1.7		95	10	Outlier,ND
14	2.0		106	1.2	
19	1.5		107	1.5	
21	2.0		108	1.9	
24	1.7		110	1.4	
27	1.4		112	1.9	
28	3.0	ND	113	2.6	
29	1.6		115	1.5	
30	1.8		117	1.5	
33	2.4	ND	118	1.5	
35	1.7				
36	0.70	ND			
37	1.4				
40	14	Outlier,ND			
42	1.4				
44	2.0				
45	1.8				
46	1.5				
49	1.7				
51	1.5				
54	1.4				
55	1.6				
57	2.0	ND			
58	5.0	Outlier,ND			
60	1.7				
61	1.4				
64	6.6	Outlier			
65	1.6				
68	1.5				
69	2.5				
73	1.2				
74	1.3				
75	1.2				
78	0.32				
79	1.2				
80	1.7				
81	0.97				
83	1.5				

**Consensus statistics**

Consensus median, pg/g	1.5
Median all values pg/g	1.6
Consensus mean, pg/g	1.6
Standard deviation, pg/g	0.43
Relative standard deviation, %	27
No. of values reported	62
No. of values removed	5
No. of reported non-detects	9

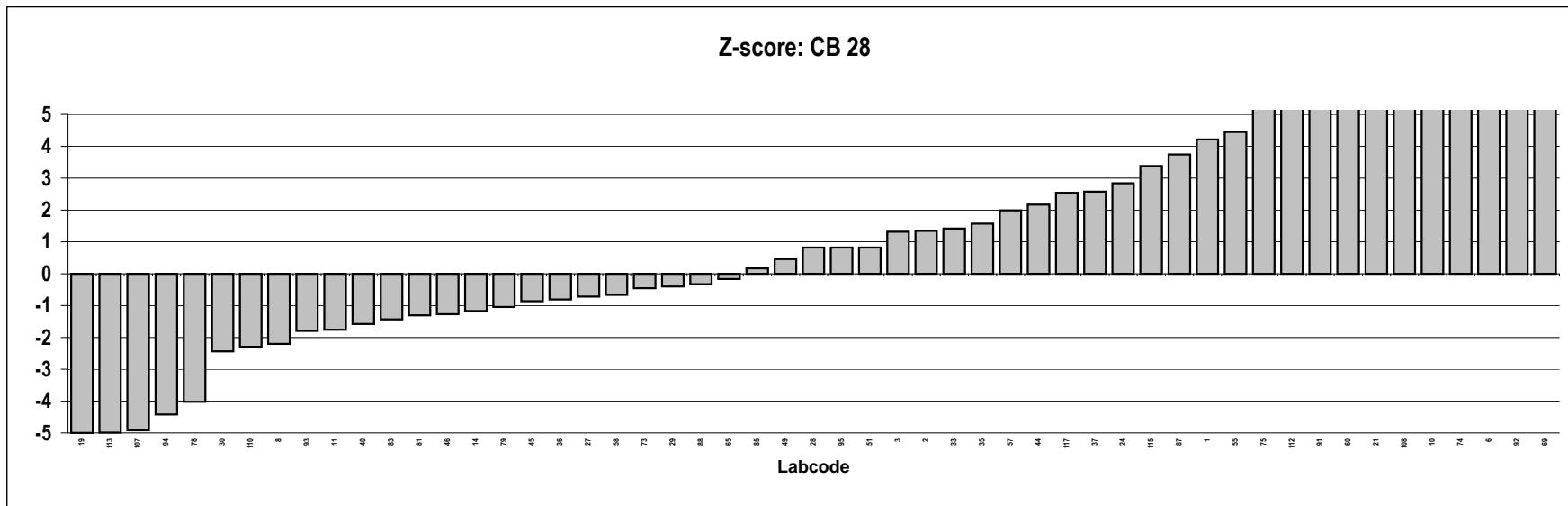
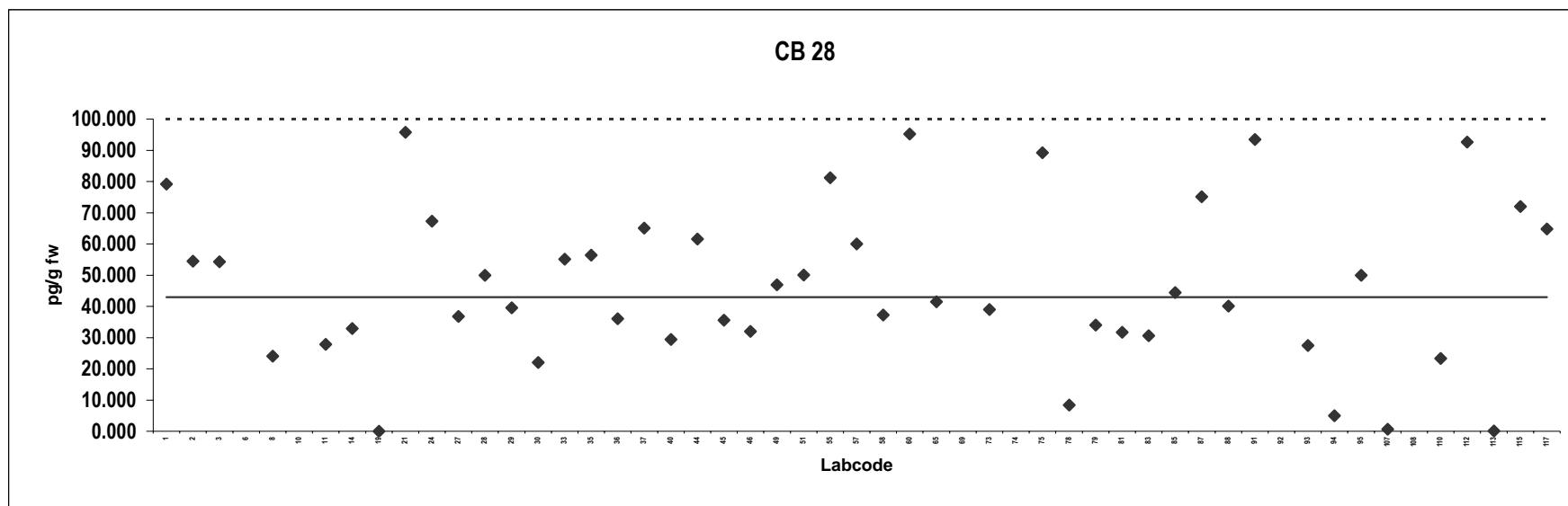


**Pork**  
**Congener: CB 28**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	79		95	50	
2	55		107	0.67	ND
3	54		108	106	Outlier
6	164	Outlier	110	23	
8	24		112	93	
10	106	Outlier	113	0.11	
11	28		115	72	
14	33		117	65	
19	0.035				
21	96				
24	67				
27	37				
28	50	ND			
29	40				
30	22				
33	55				
35	56				
36	36				
37	65				
40	29				
44	62				
45	36				
46	32				
49	47				
51	50				
55	81				
57	60				
58	37				
60	95				
65	42				
69	216	Outlier			
73	39				
74	112	Outlier			
75	89				
78	8.4				
79	34				
81	32				
83	31				
85	44				
87	75				
88	40				
91	94				
92	207	Outlier			
93	28				
94	5.0	ND			

**Consensus statistics**

Consensus median, pg/g	43
Median all values pg/g	50
Consensus mean, pg/g	47
Standard deviation, pg/g	26
Relative standard deviation, %	55
No. of values reported	53
No. of values removed	6
No. of reported non-detects	3

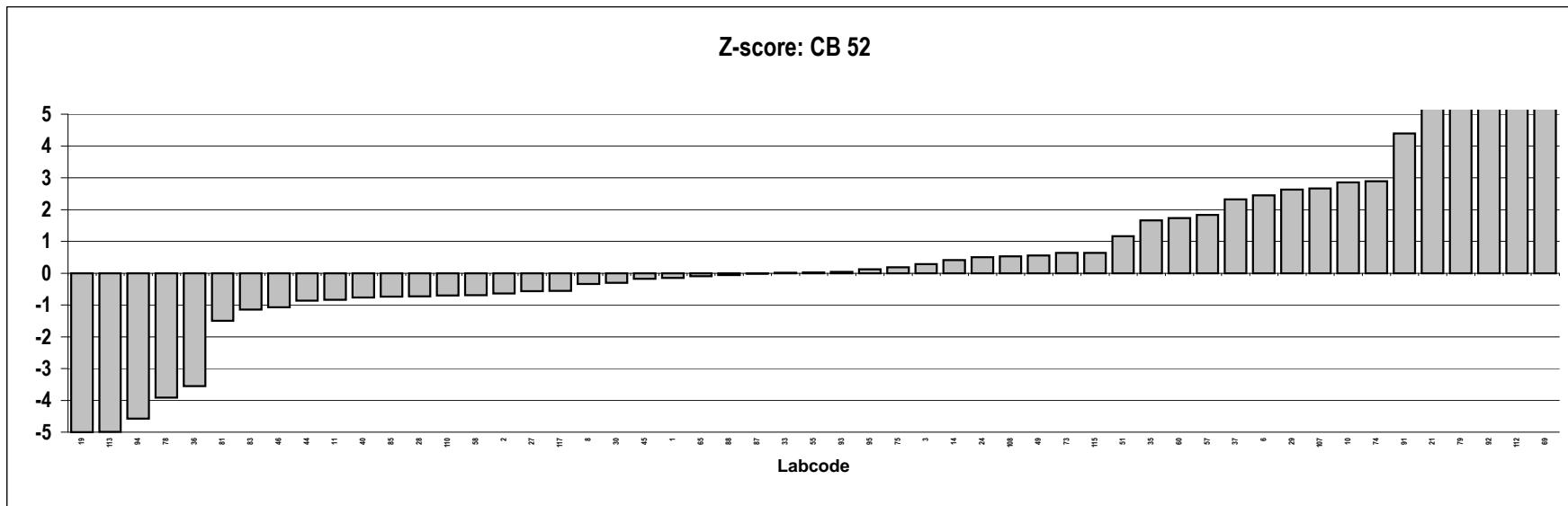
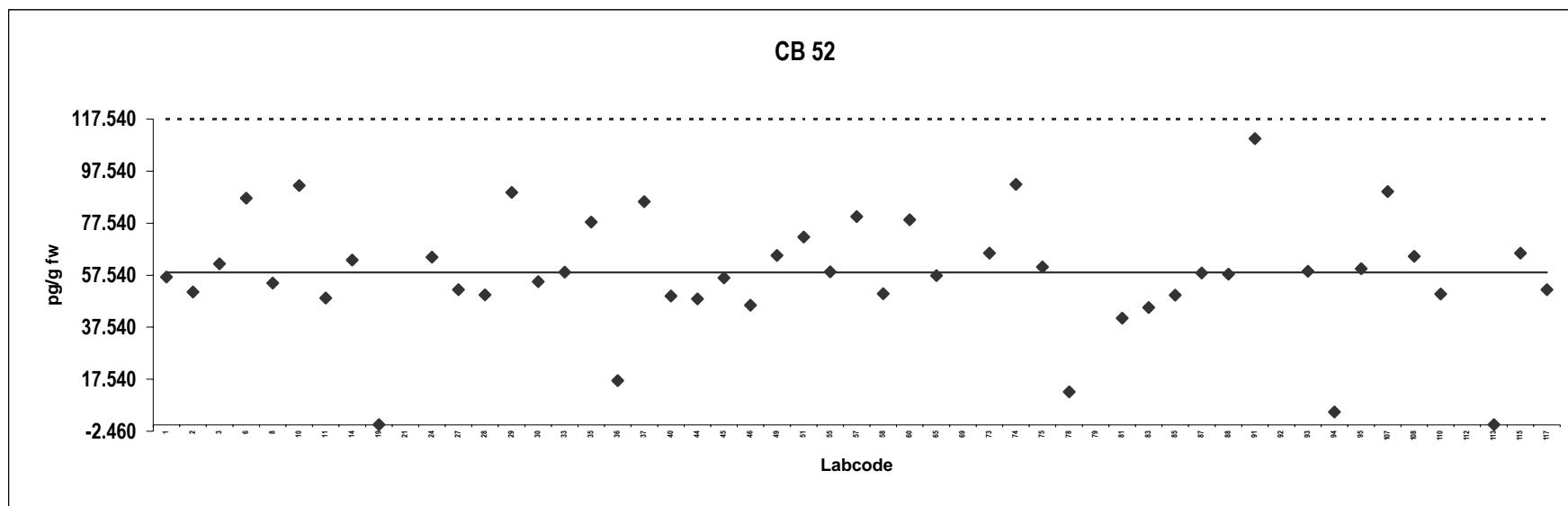


**Pork**  
**Congener: CB 52**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	57		95	60	
2	51		107	90	
3	62		108	65	
6	87		110	50	
8	55		112	176	
10	92		113	0.062	
11	49		115	66	
14	63		117	52	
19	0.048				
21	128	Outlier			
24	64				
27	52				
28	50	ND			
29	89				
30	55				
33	59				
35	78				
36	17				
37	86				
40	50				
44	48				
45	56				
46	46				
49	65				
51	72				
55	59				
57	80				
58	50				
60	79				
65	57				
69	665	Outlier			
73	66				
74	92				
75	61				
78	13				
79	166	Outlier			
81	41				
83	45				
85	50				
87	58				
88	58				
91	110				
92	174	Outlier			
93	59				
94	5.0	ND			

**Consensus statistics**

Consensus median, pg/g	59
Median all values pg/g	59
Consensus mean, pg/g	58
Standard deviation, pg/g	23
Relative standard deviation, %	40
No. of values reported	53
No. of values removed	5
No. of reported non-detects	2

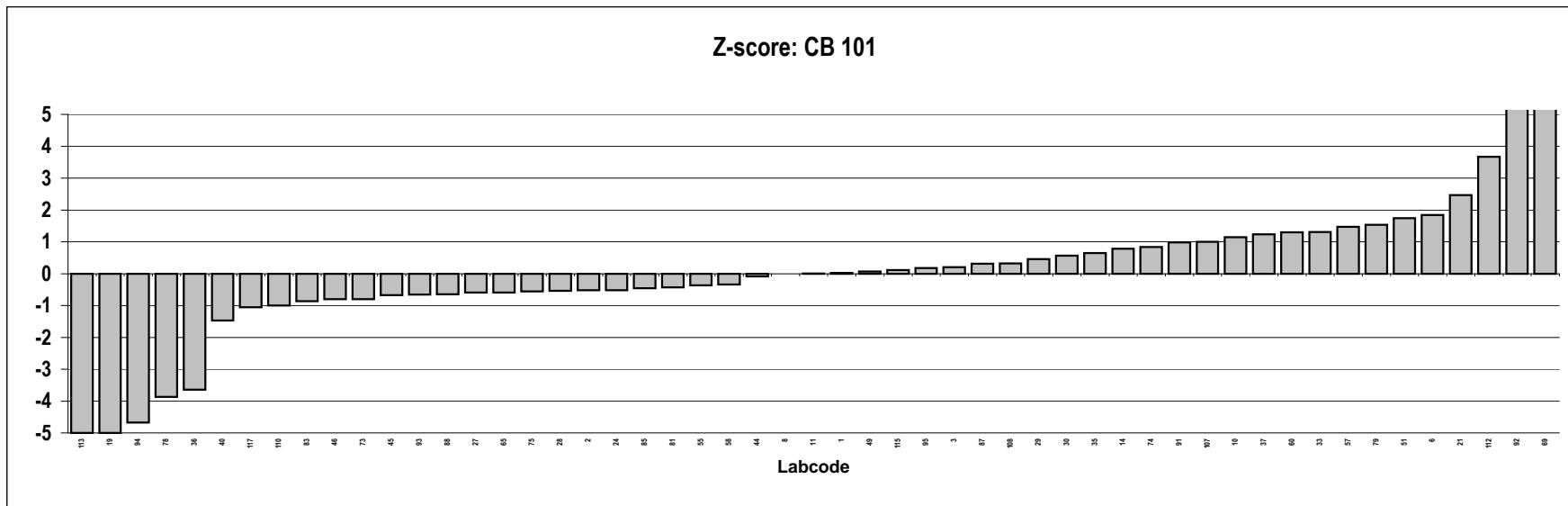
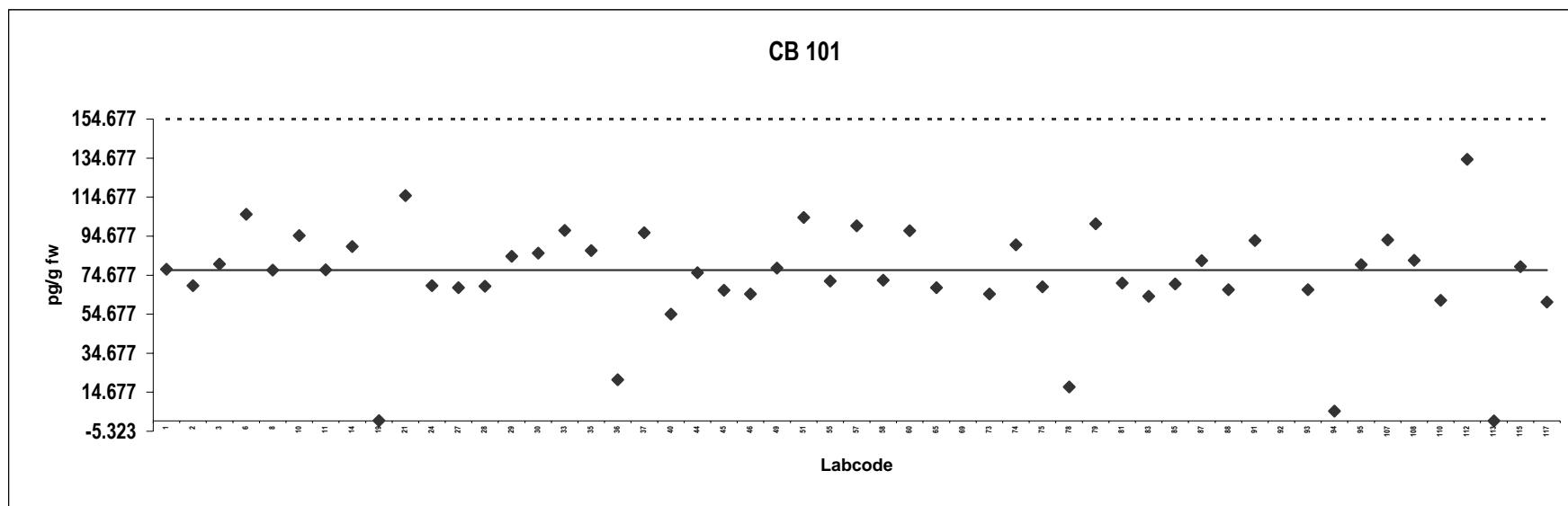


**Pork**  
Congener: CB 101

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	78		95	80	
2	69		107	93	
3	80		108	82	
6	106		110	62	
8	77		112	134	
10	95		113	0.041	
11	77		115	79	
14	89		117	61	
19	0.068				
21	115				
24	69				
27	68				
28	69				
29	84				
30	86				
33	98				
35	87				
36	21				
37	96				
40	55				
44	76				
45	67				
46	65				
49	78				
51	104				
55	72				
57	100				
58	72				
60	97				
65	68				
69	358	Outlier			
73	65				
74	90				
75	69				
78	17				
79	101				
81	71				
83	64				
85	70				
87	82				
88	67				
91	93				
92	278	Outlier			
93	67				
94	5.0	ND			

**Consensus statistics**

Consensus median, pg/g	77
Median all values pg/g	77
Consensus mean, pg/g	74
Standard deviation, pg/g	27
Relative standard deviation, %	36
No. of values reported	53
No. of values removed	2
No. of reported non-detects	1

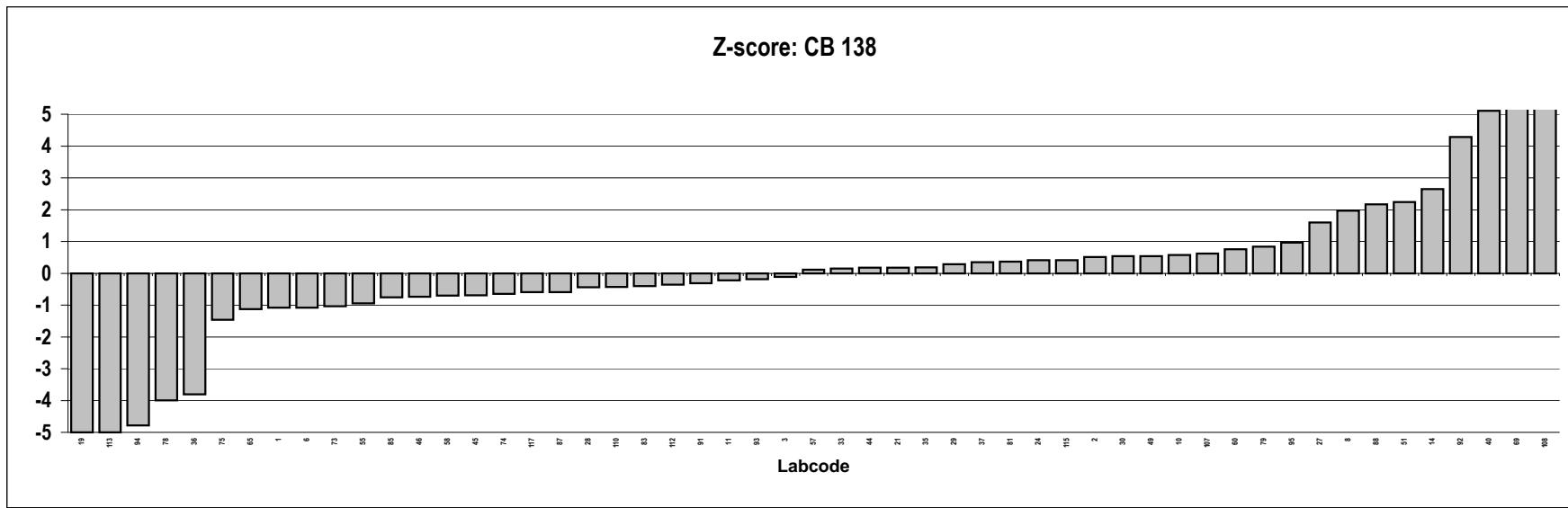
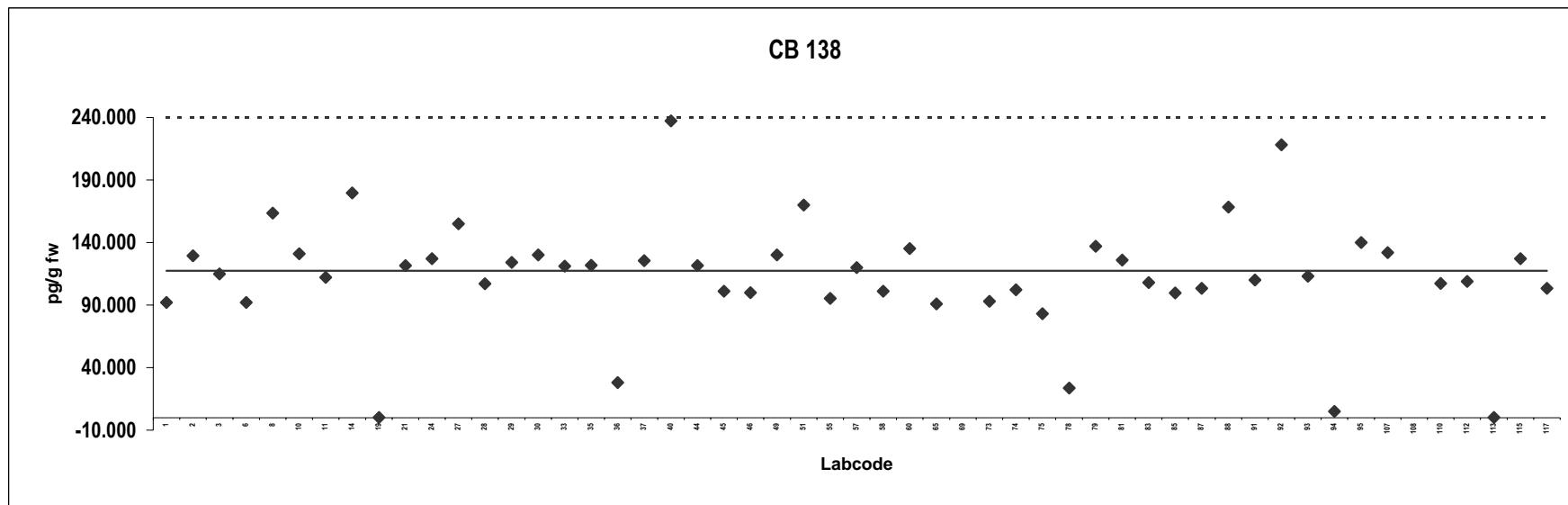


**Pork**  
Congener: CB 138

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	92		95	140	
2	129		107	132	
3	115		108	328	
6	92		110	107	
8	164		112	109	
10	131		113	0.10	
11	112		115	127	
14	180		117	103	
19	0.10				
21	122				
24	127				
27	155				
28	107				
29	124				
30	130				
33	121				
35	122				
36	28				
37	126				
40	237				
44	121				
45	101				
46	100				
49	130				
51	170				
55	95				
57	120				
58	101				
60	135				
65	91				
69	326	Outlier			
73	93				
74	102				
75	83				
78	24				
79	137				
81	126				
83	108				
85	100				
87	103				
88	168				
91	110				
92	218				
93	113				
94	5.0	ND			

**Consensus statistics**

Consensus median, pg/g	117
Median all values pg/g	120
Consensus mean, pg/g	113
Standard deviation, pg/g	45
Relative standard deviation, %	40
No. of values reported	53
No. of values removed	2
No. of reported non-detects	1

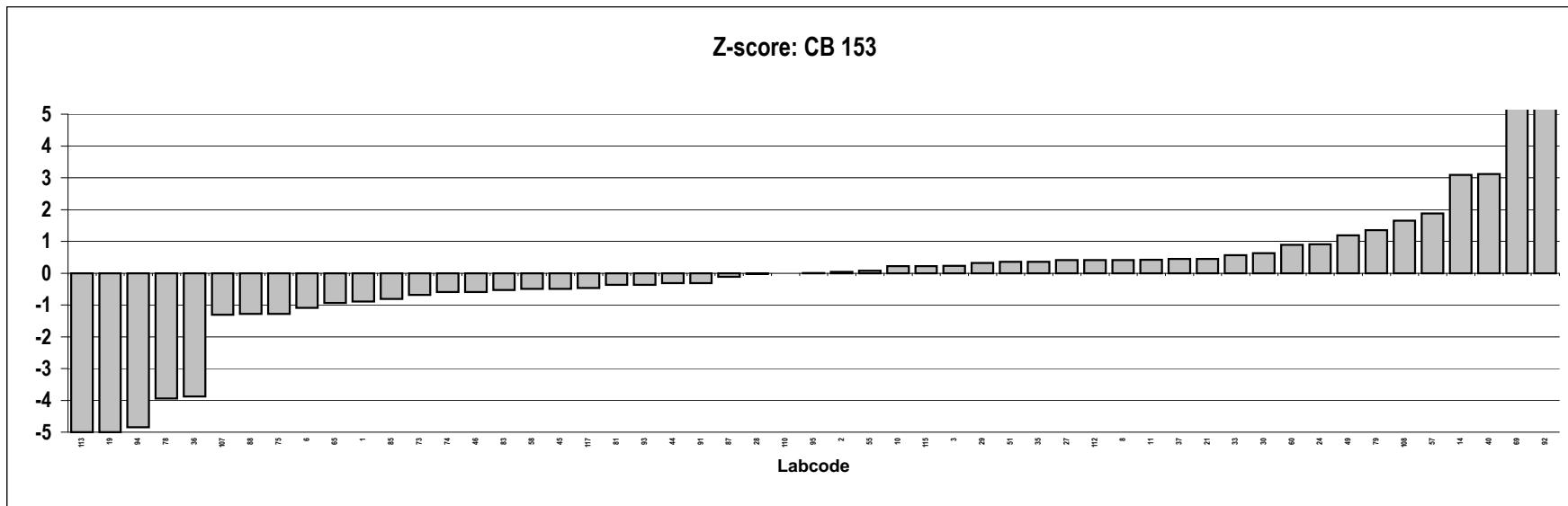
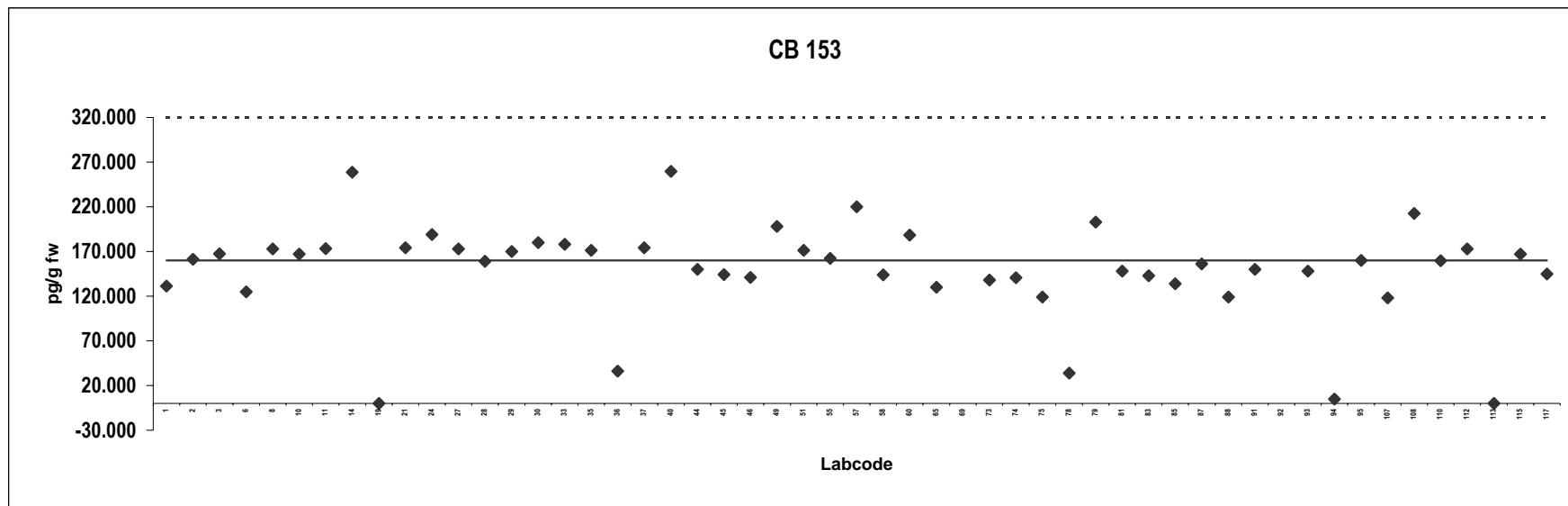


**Pork**  
Congener: CB 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	131		95	160	
2	161		107	118	
3	167		108	213	
6	125		110	160	
8	173		112	173	
10	167		113	0.12	
11	173		115	167	
14	259		117	145	
19	0.14				
21	174				
24	189				
27	173				
28	159				
29	170				
30	180				
33	178				
35	171				
36	36				
37	174				
40	260				
44	150				
45	144				
46	141				
49	198				
51	171				
55	162				
57	220				
58	144				
60	188				
65	130				
69	342	Outlier			
73	138				
74	141				
75	119				
78	34				
79	203				
81	148				
83	143				
85	134				
87	156				
88	119				
91	150				
92	344	Outlier			
93	148				
94	5.0	ND			

**Consensus statistics**

Consensus median, pg/g	160
Median all values pg/g	160
Consensus mean, pg/g	150
Standard deviation, pg/g	54
Relative standard deviation, %	36
No. of values reported	53
No. of values removed	2
No. of reported non-detects	1

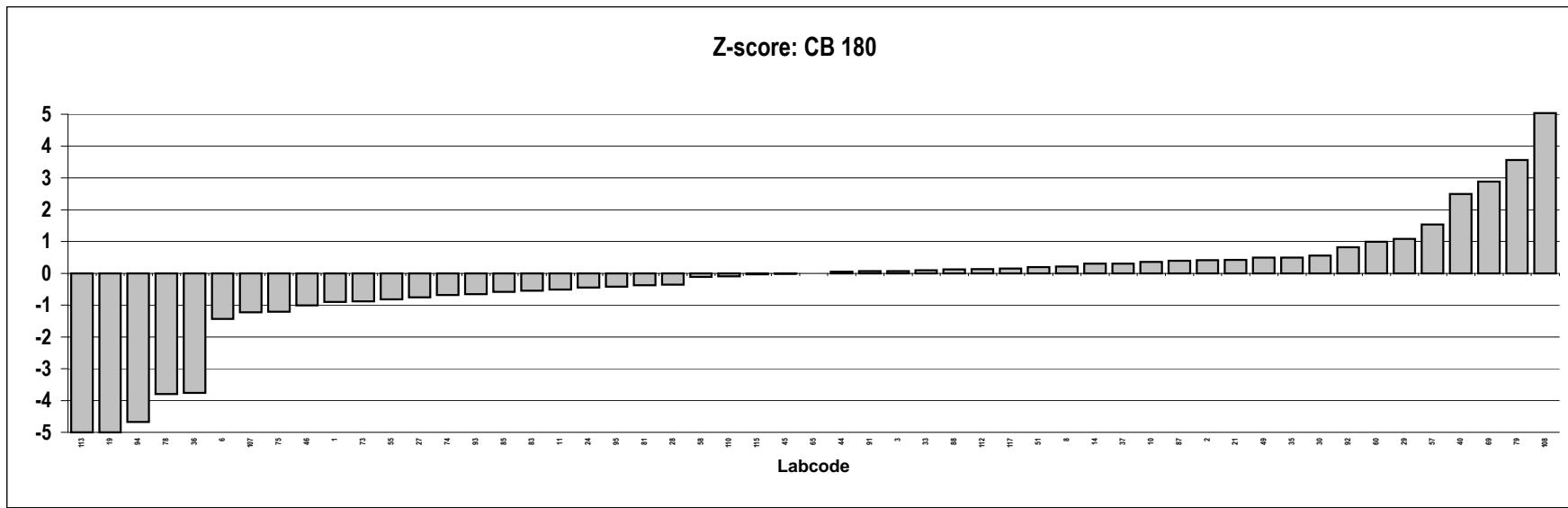
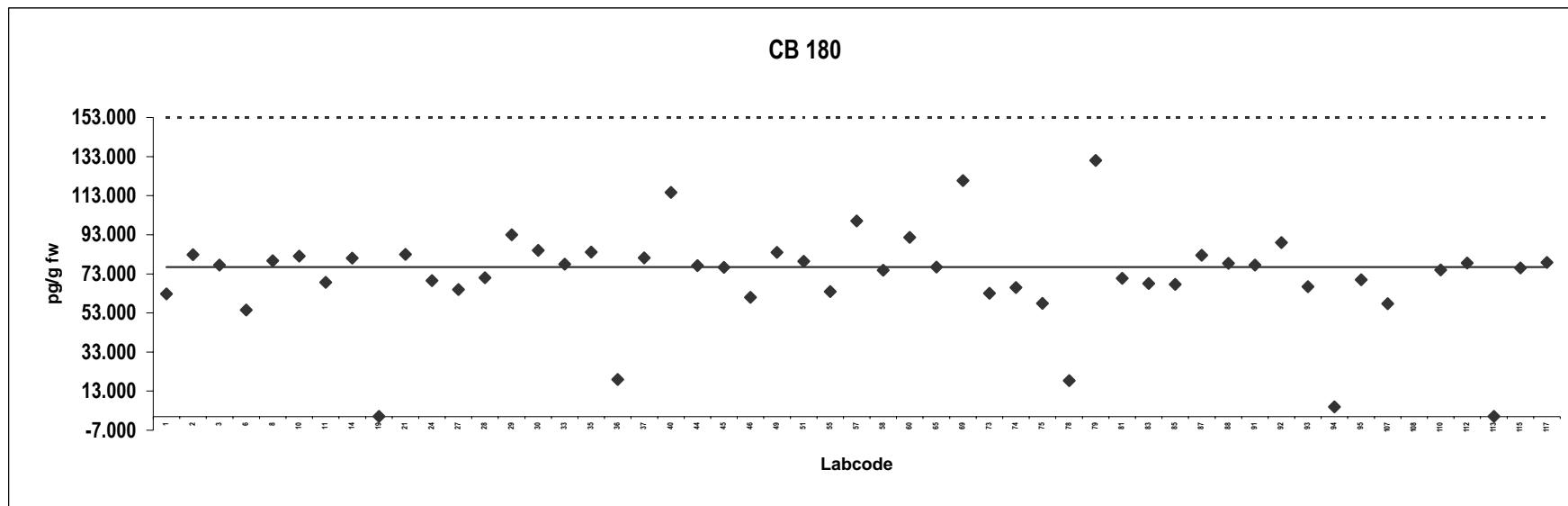


**Pork**  
**Congener: CB 180**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	63		95	70	
2	83		107	58	
3	78		108	153	
6	55		110	75	
8	80		112	79	
10	82		113	0.021	
11	69		115	76	
14	81		117	79	
19	0.062				
21	83				
24	70				
27	65				
28	71				
29	93				
30	85				
33	78				
35	84				
36	19				
37	81				
40	115				
44	77				
45	76				
46	61				
49	84				
51	79				
55	64				
57	100				
58	75				
60	92				
65	77				
69	121				
73	63				
74	66				
75	58				
78	18				
79	131				
81	71				
83	68				
85	68				
87	83				
88	78				
91	78				
92	89				
93	67				
94	5.0	ND			

**Consensus statistics**

Consensus median, pg/g	77
Median all values pg/g	77
Consensus mean, pg/g	71
Standard deviation, pg/g	25
Relative standard deviation, %	36
No. of values reported	53
No. of values removed	1
No. of reported non-detects	1

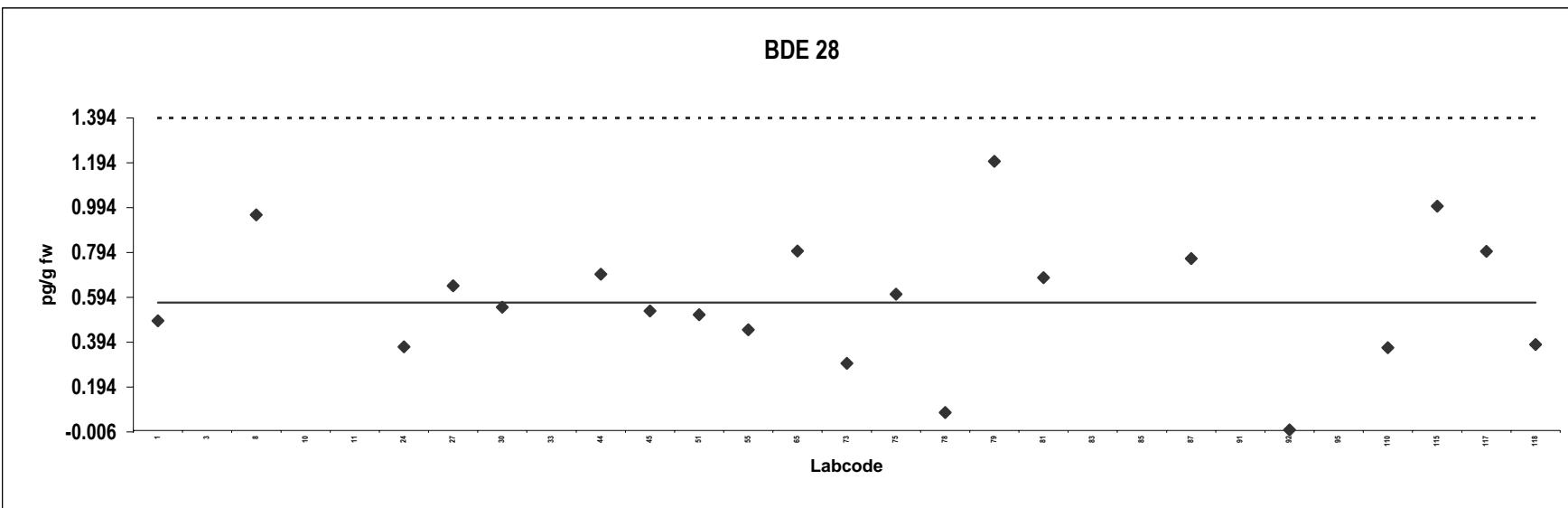


**Pork**  
Congener: BDE 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.49				
3	2.0	Outlier,ND			
8	0.96				
10	2.4	Outlier			
11	3.1	Outlier			
24	0.37				
27	0.65				
30	0.55	ND			
33	2.2	Outlier			
44	0.70				
45	0.53				
51	0.52				
55	0.45				
65	0.80				
73	0.30				
75	0.61				
78	0.080				
79	1.2				
81	0.68				
83	4.0	Outlier			
85	4.2	Outlier			
87	0.77				
91	1.9	Outlier			
92	0.0030				
95	2.0	Outlier,ND			
110	0.37	ND			
115	1.0	ND			
117	0.80				
118	0.38				

**Consensus statistics**

Consensus median, pg/g	0.57
Median all values pg/g	0.70
Consensus mean, pg/g	0.58
Standard deviation, pg/g	0.29
Relative standard deviation, %	50
No. of values reported	29
No. of values removed	8
No. of reported non-detects	5

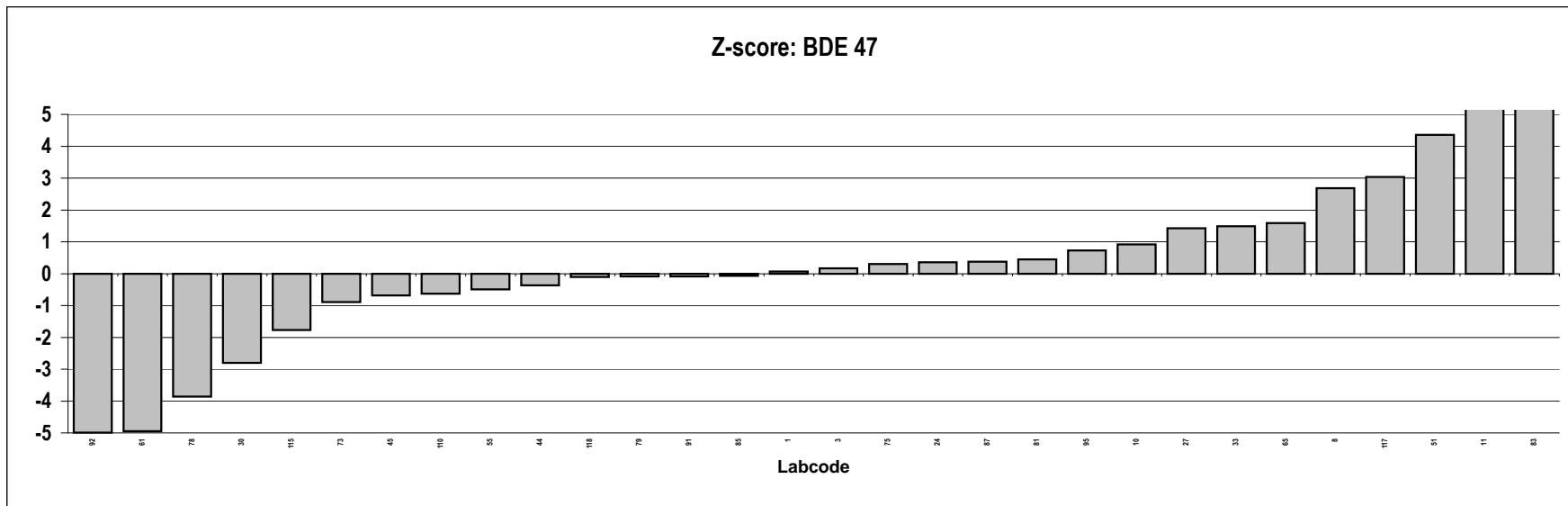
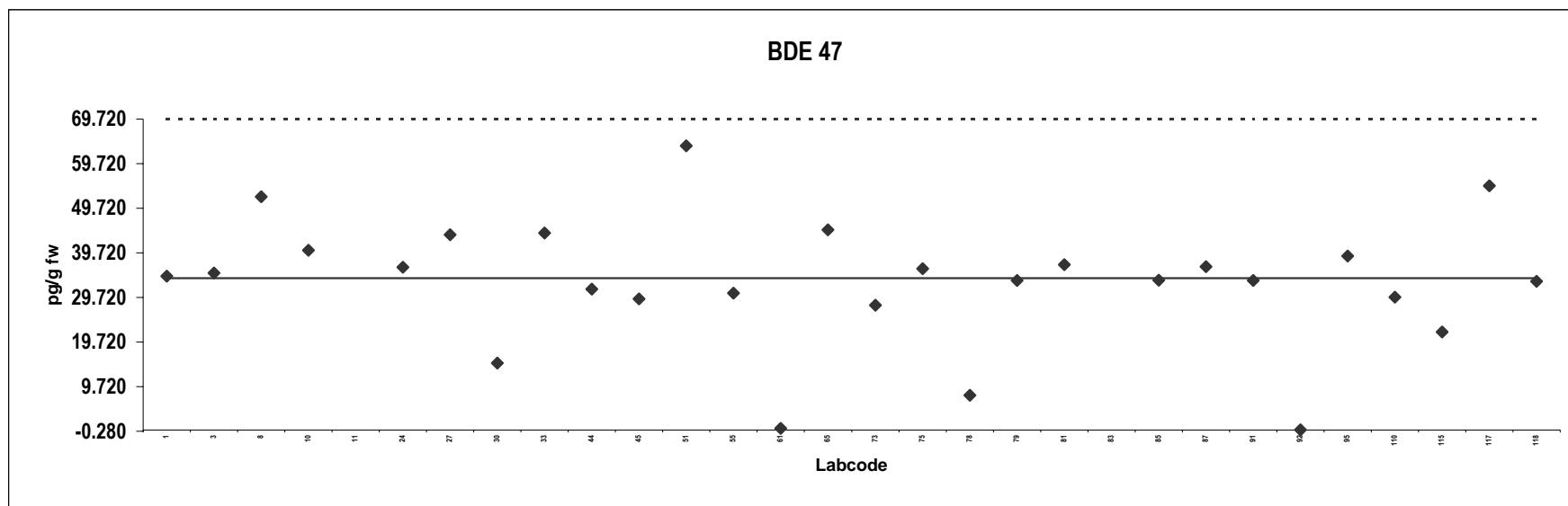


**Pork**  
Congener: BDE 47

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	35				
3	35				
8	52				
10	40				
11	92				
24	37				
27	44				
30	15				
33	44				
44	32				
45	29				
51	64				
55	31				
61	0.36				
65	45				
73	28				
75	36				
78	7.8				
79	34				
81	37				
83	239	Outlier			
85	34				
87	37				
91	34				
92	0.060				
95	39				
110	30				
115	22				
117	55				
118	33				

**Consensus statistics**

Consensus median, pg/g	34
Median all values pg/g	35
Consensus mean, pg/g	33
Standard deviation, pg/g	14
Relative standard deviation, %	44
No. of values reported	30
No. of values removed	2
No. of reported non-detects	0

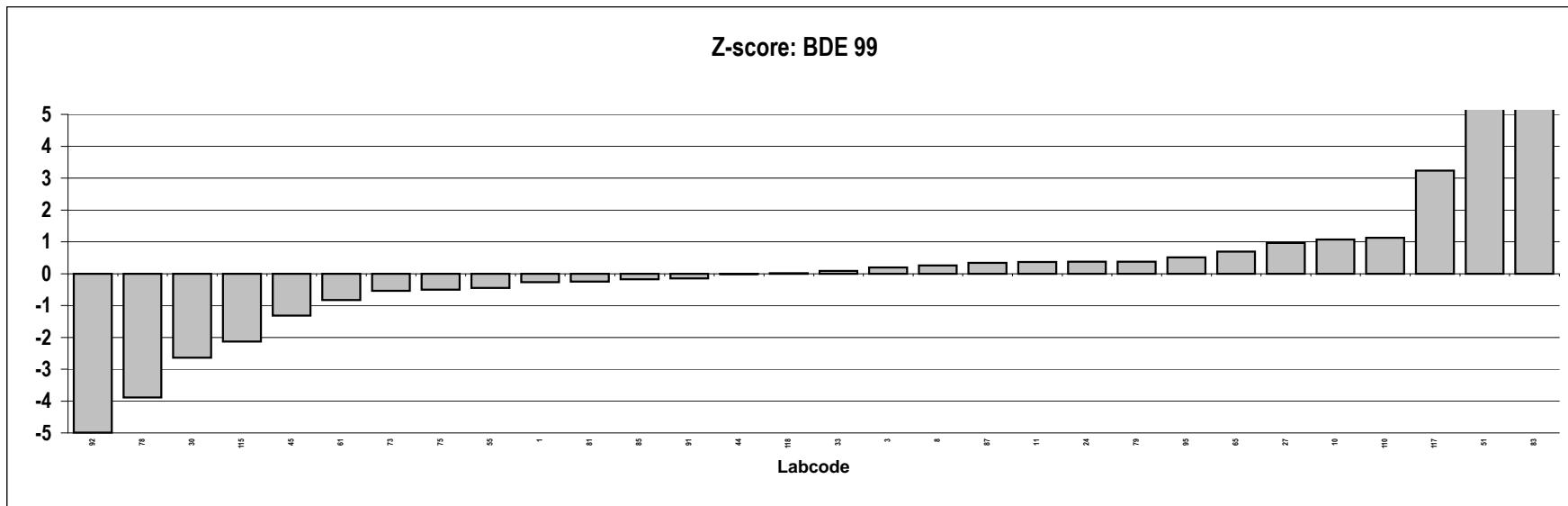
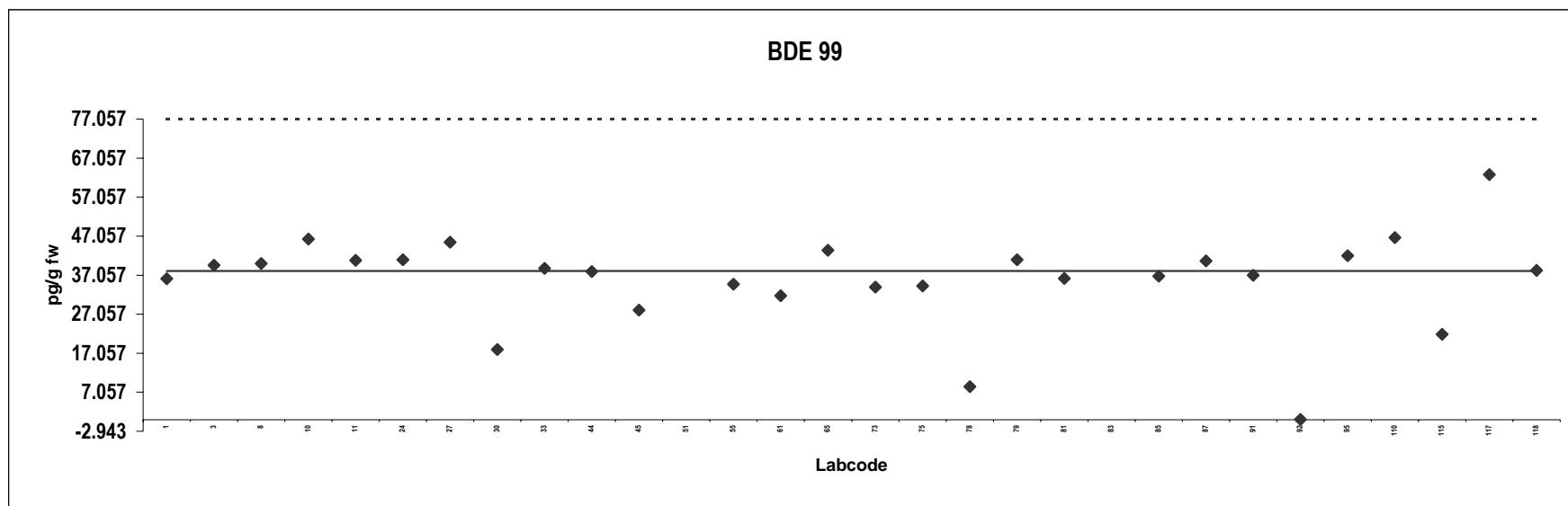


**Pork**  
**Congener: BDE 99**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	36				
3	40				
8	40				
10	46				
11	41				
24	41				
27	46				
30	18				
33	39				
44	38				
45	28				
51	112	Outlier			
55	35				
61	32				
65	43				
73	34				
75	34				
78	8.5				
79	41				
81	36				
83	146	Outlier			
85	37				
87	41				
91	37				
92	0.050				
95	42				
110	47				
115	22				
117	63				
118	38				

**Consensus statistics**

Consensus median, pg/g	38
Median all values pg/g	39
Consensus mean, pg/g	36
Standard deviation, pg/g	12
Relative standard deviation, %	34
No. of values reported	30
No. of values removed	2
No. of reported non-detects	0

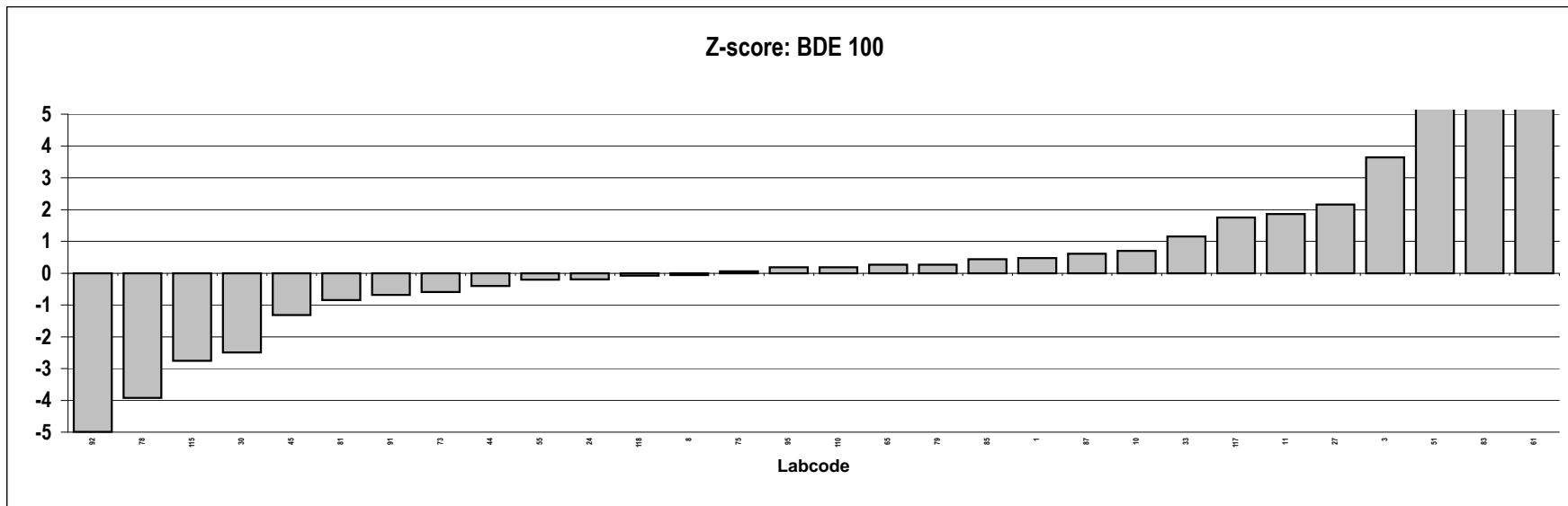
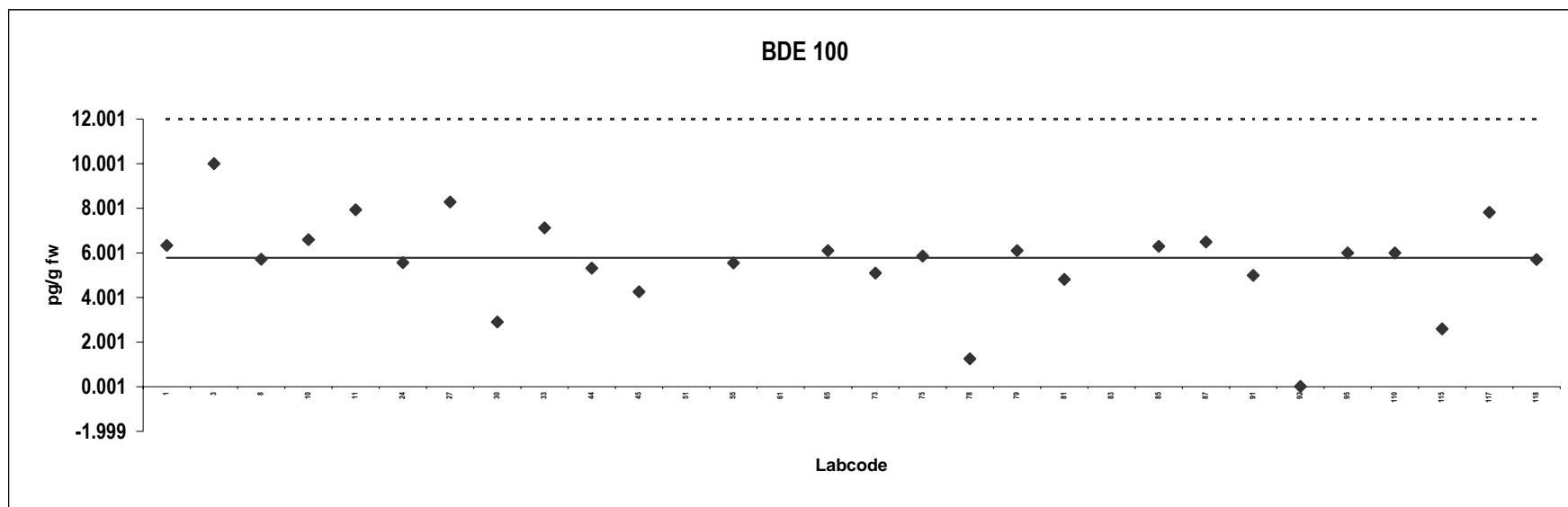


**Pork**  
Congener: BDE 100

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	6.3				
3	10	ND			
8	5.7				
10	6.6				
11	7.9				
24	5.6				
27	8.3				
30	2.9				
33	7.1				
44	5.3				
45	4.3				
51	21	Outlier			
55	5.6				
61	35	Outlier			
65	6.1				
73	5.1				
75	5.9				
78	1.2				
79	6.1				
81	4.8				
83	25	Outlier			
85	6.3				
87	6.5				
91	5.0				
92	0.0090				
95	6.0				
110	6.0				
115	2.6				
117	7.8				
118	5.7				

**Consensus statistics**

Consensus median, pg/g	5.8
Median all values pg/g	6.0
Consensus mean, pg/g	5.6
Standard deviation, pg/g	2.1
Relative standard deviation, %	37
No. of values reported	30
No. of values removed	3
No. of reported non-detects	1

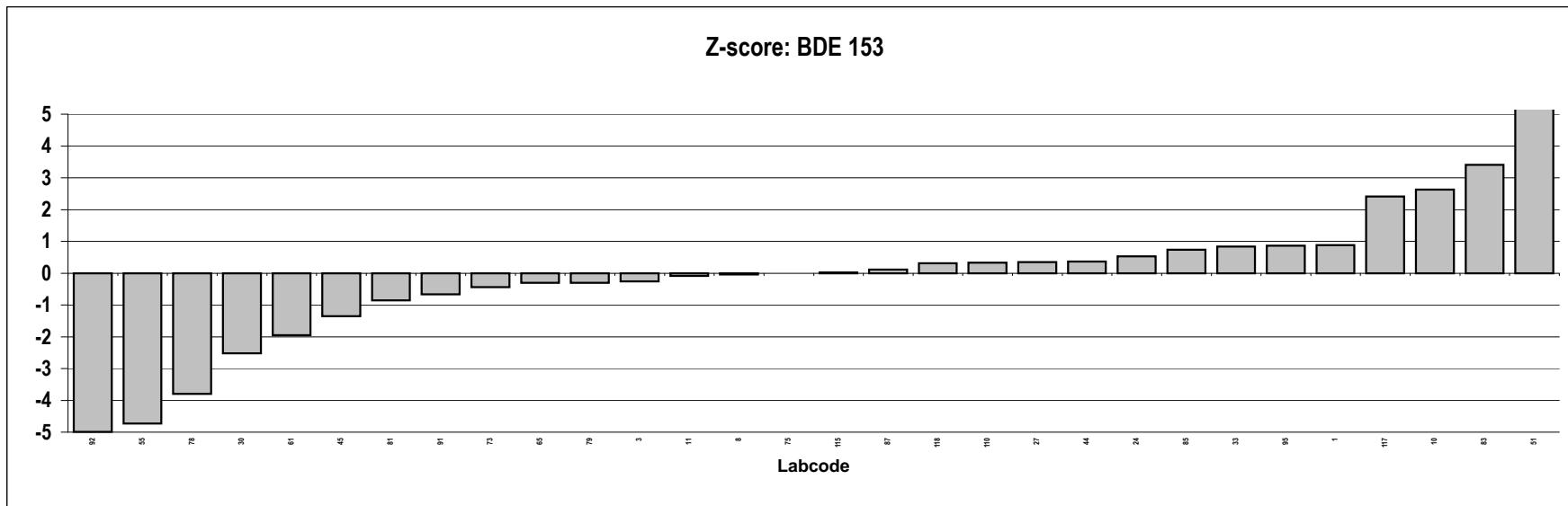
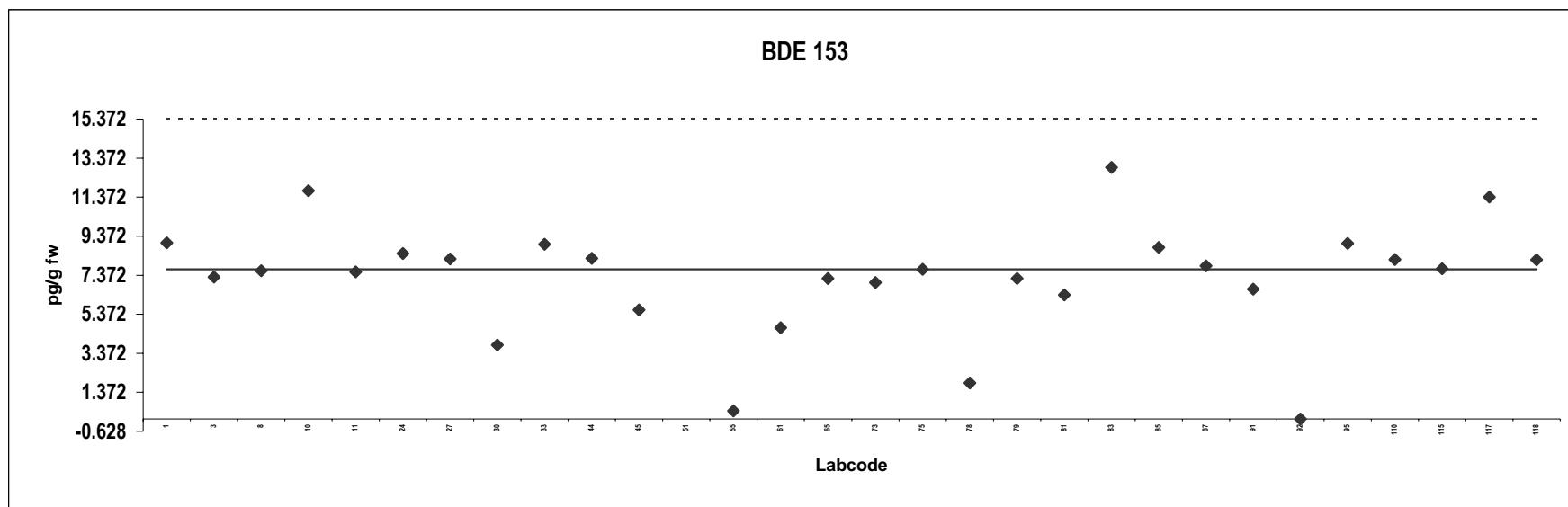


**Pork**  
Congener: BDE 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	9.0				
3	7.3				
8	7.6				
10	12				
11	7.5				
24	8.5				
27	8.2				
30	3.8				
33	9.0				
44	8.2				
45	5.6				
51	19				
55	0.42				
61	4.7				
65	7.2				
73	7.0				
75	7.7				
78	1.8				
79	7.2				
81	6.4				
83	13				
85	8.8				
87	7.9				
91	6.7				
92	0.010				
95	9.0				
110	8.2				
115	7.7				
117	11				
118	8.2				

**Consensus statistics**

Consensus median, pg/g	7.7
Median all values pg/g	7.7
Consensus mean, pg/g	7.2
Standard deviation, pg/g	2.9
Relative standard deviation, %	40
No. of values reported	30
No. of values removed	1
No. of reported non-detects	0

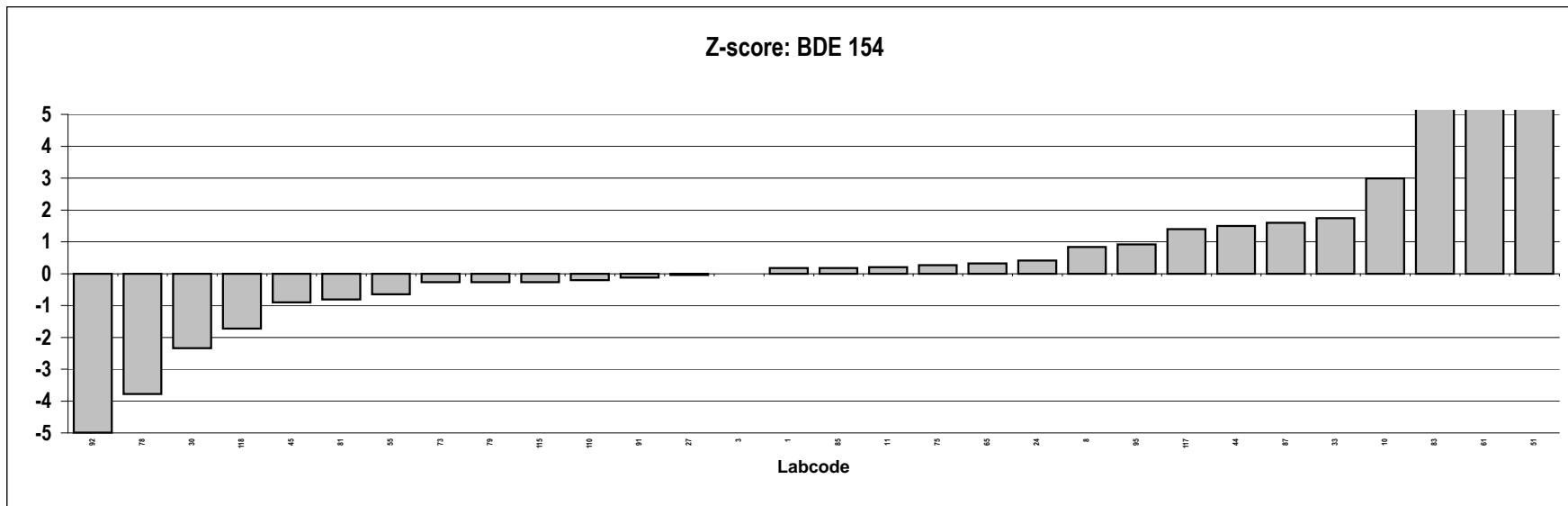
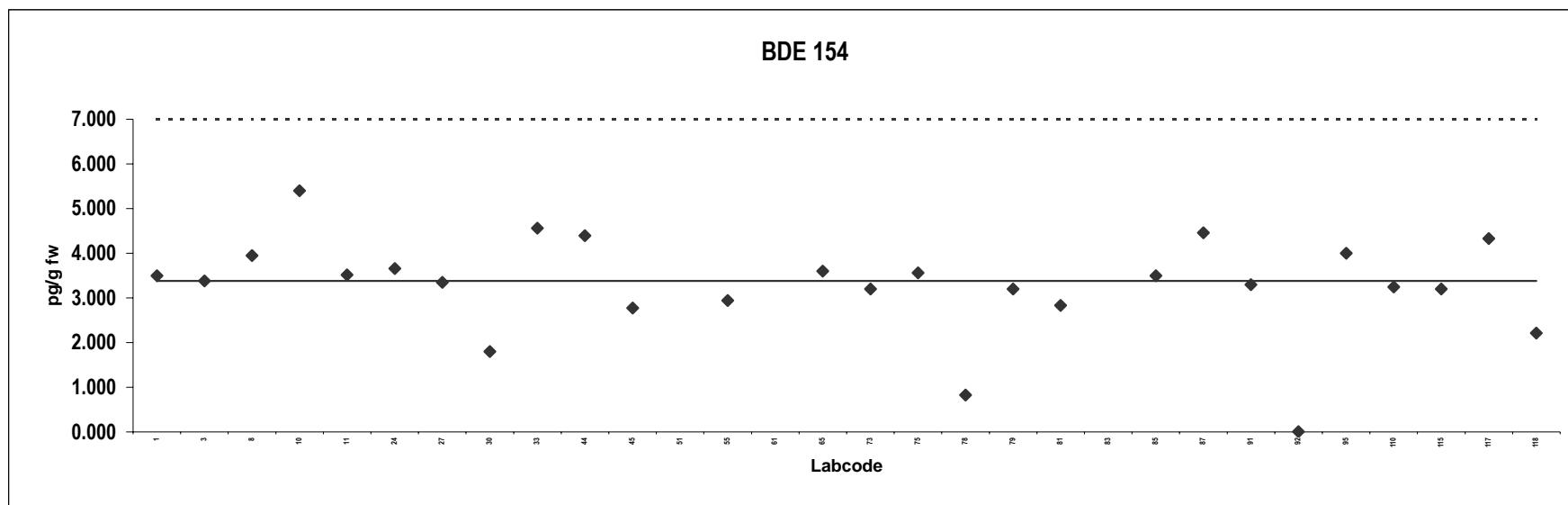


**Pork**  
Congener: BDE 154

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	3.5				
3	3.4				
8	3.9				
10	5.4				
11	3.5				
24	3.7				
27	3.4				
30	1.8				
33	4.6				
44	4.4				
45	2.8				
51	13	Outlier			
55	2.9				
61	8.3	Outlier			
65	3.6				
73	3.2				
75	3.6				
78	0.82				
79	3.2				
81	2.8				
83	8.1	Outlier			
85	3.5				
87	4.5				
91	3.3				
92	0.0040				
95	4.0				
110	3.2				
115	3.2				
117	4.3				
118	2.2				

**Consensus statistics**

Consensus median, pg/g	3.4
Median all values pg/g	3.5
Consensus mean, pg/g	3.3
Standard deviation, pg/g	1.1
Relative standard deviation, %	34
No. of values reported	30
No. of values removed	3
No. of reported non-detects	0

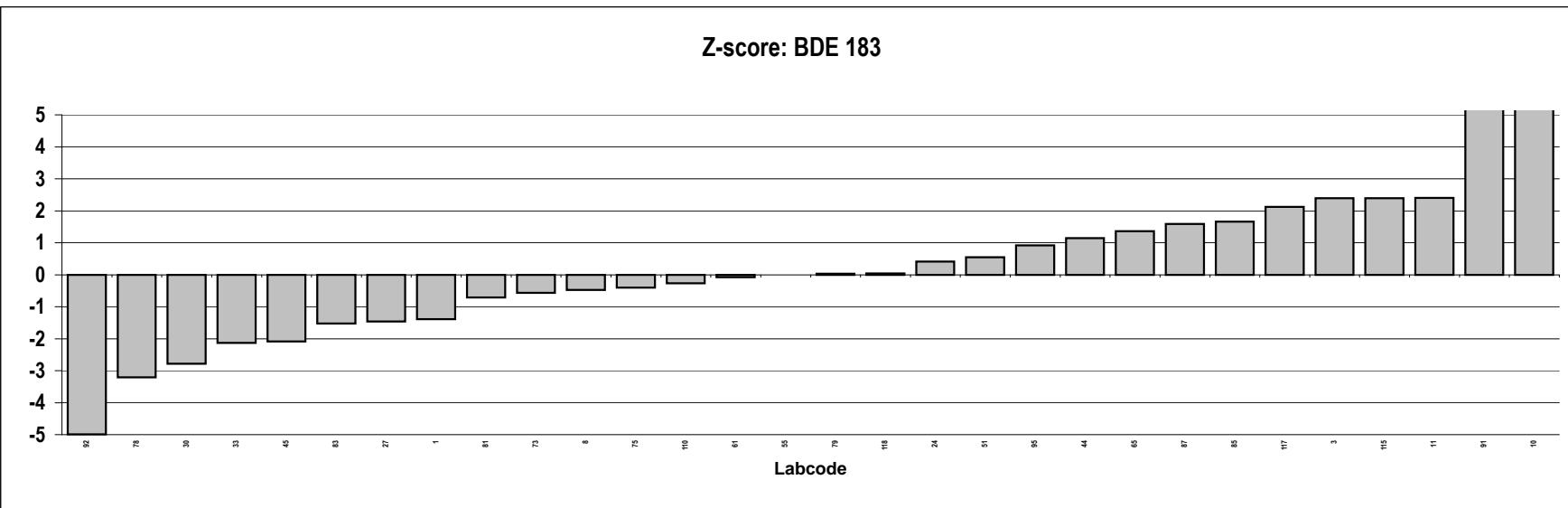
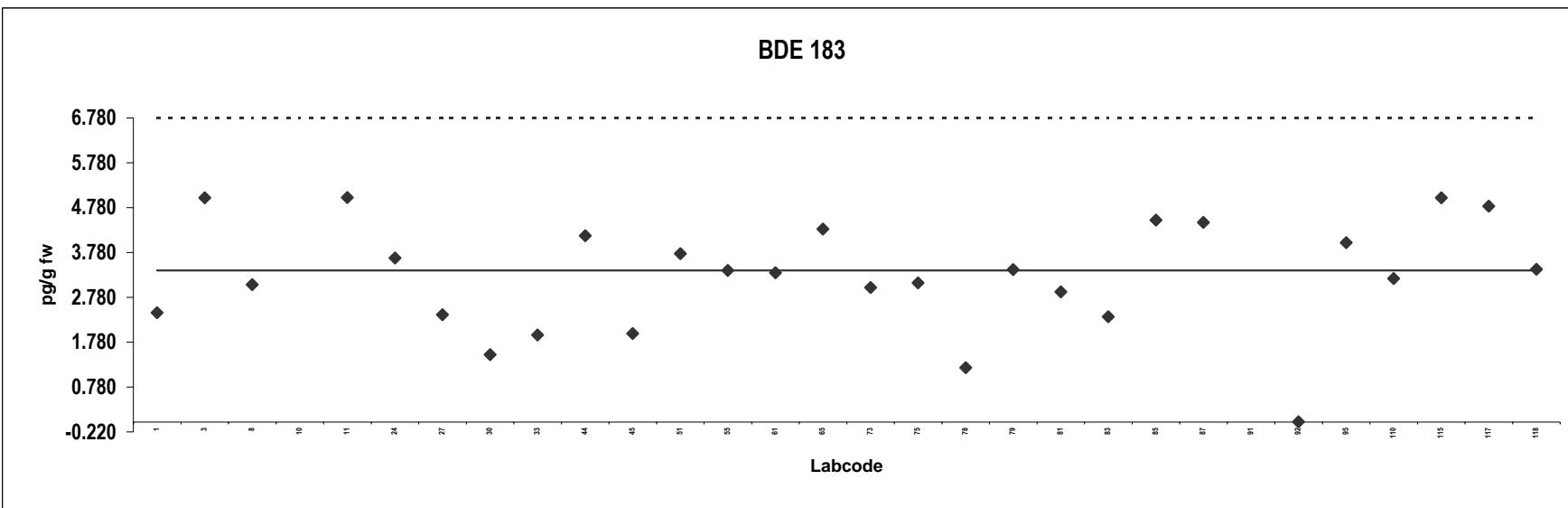


**Pork**  
Congener: BDE 183

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	2.4				
3	5.0	ND			
8	3.1				
10	10	Outlier			
11	5.0				
24	3.7				
27	2.4				
30	1.5				
33	1.9	ND			
44	4.2				
45	2.0				
51	3.8				
55	3.4				
61	3.3				
65	4.3				
73	3.0				
75	3.1				
78	1.2				
79	3.4				
81	2.9				
83	2.4				
85	4.5				
87	4.5				
91	8.0	Outlier,ND			
92	0.0039	ND			
95	4.0				
110	3.2				
115	5.0				
117	4.8				
118	3.4				

**Consensus statistics**

Consensus median, pg/g	3.4
Median all values pg/g	3.4
Consensus mean, pg/g	3.3
Standard deviation, pg/g	1.2
Relative standard deviation, %	38
No. of values reported	30
No. of values removed	2
No. of reported non-detects	4

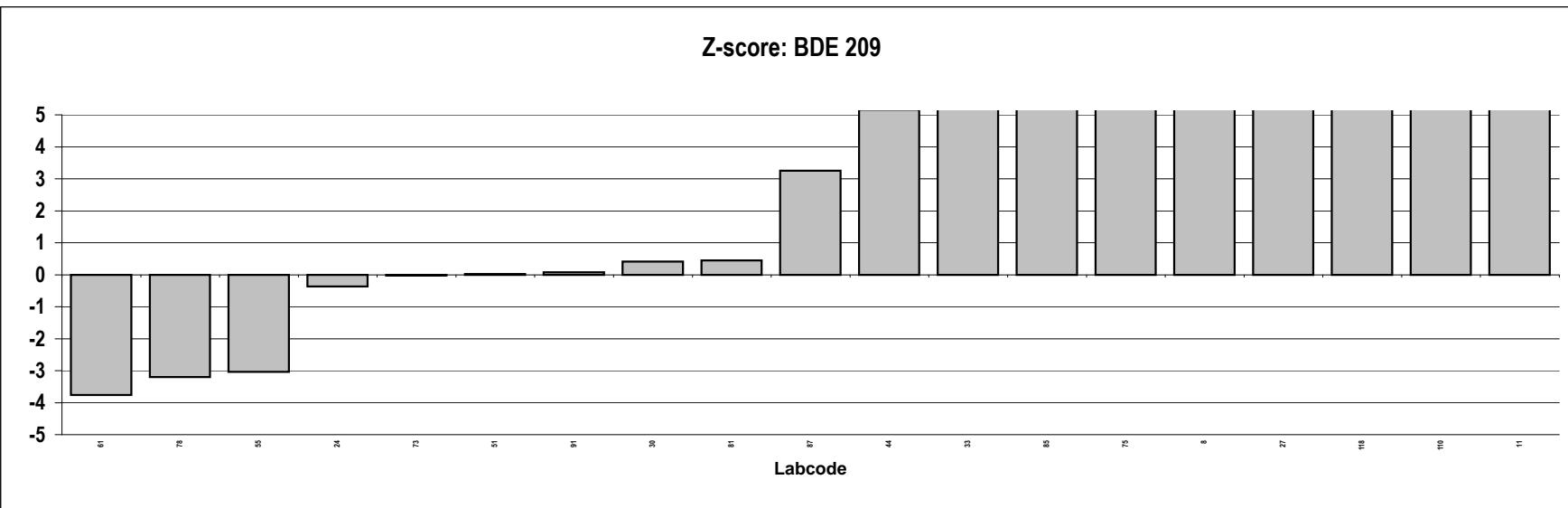
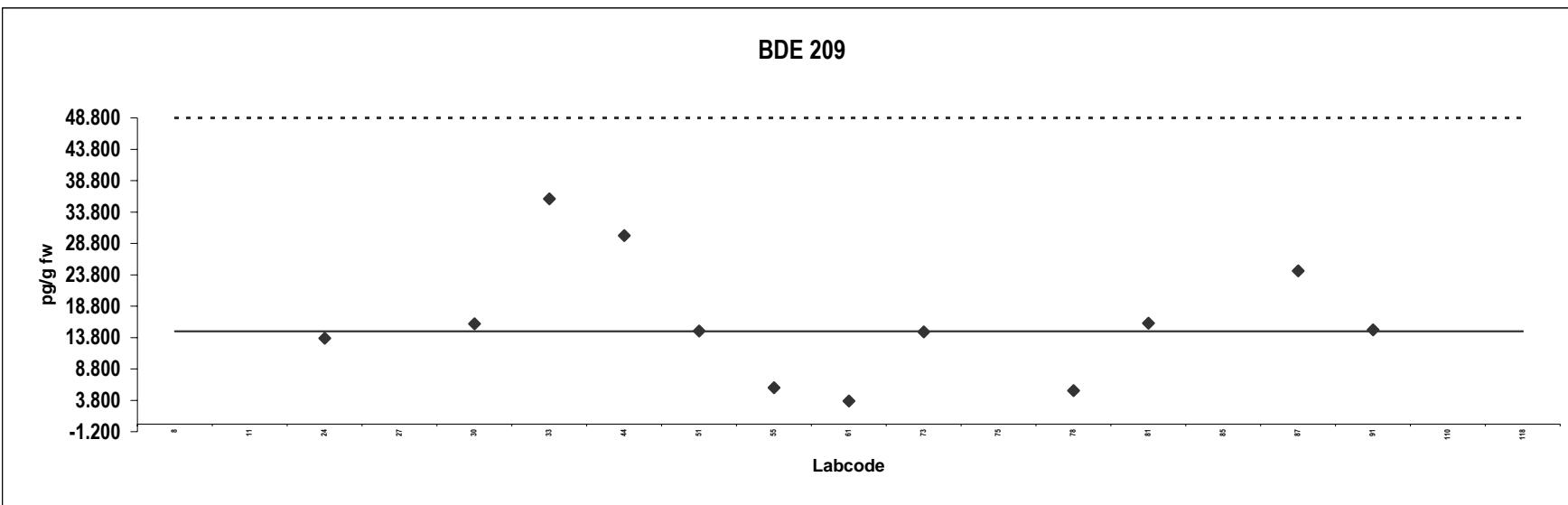


**Pork**  
Congener: BDE 209

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
8	55	Outlier			
11	85	Outlier,ND			
24	14				
27	62	Outlier,ND			
30	16				
33	36	ND			
44	30				
51	15				
55	5.8				
61	3.7				
73	15				
75	55	Outlier			
78	5.3				
81	16				
85	51	Outlier			
87	24				
91	15	ND			
110	68	Outlier			
118	63	Outlier			

**Consensus statistics**

Consensus median, pg/g	15
Median all values pg/g	24
Consensus mean, pg/g	16
Standard deviation, pg/g	9.7
Relative standard deviation, %	60
No. of values reported	19
No. of values removed	7
No. of reported non-detects	4

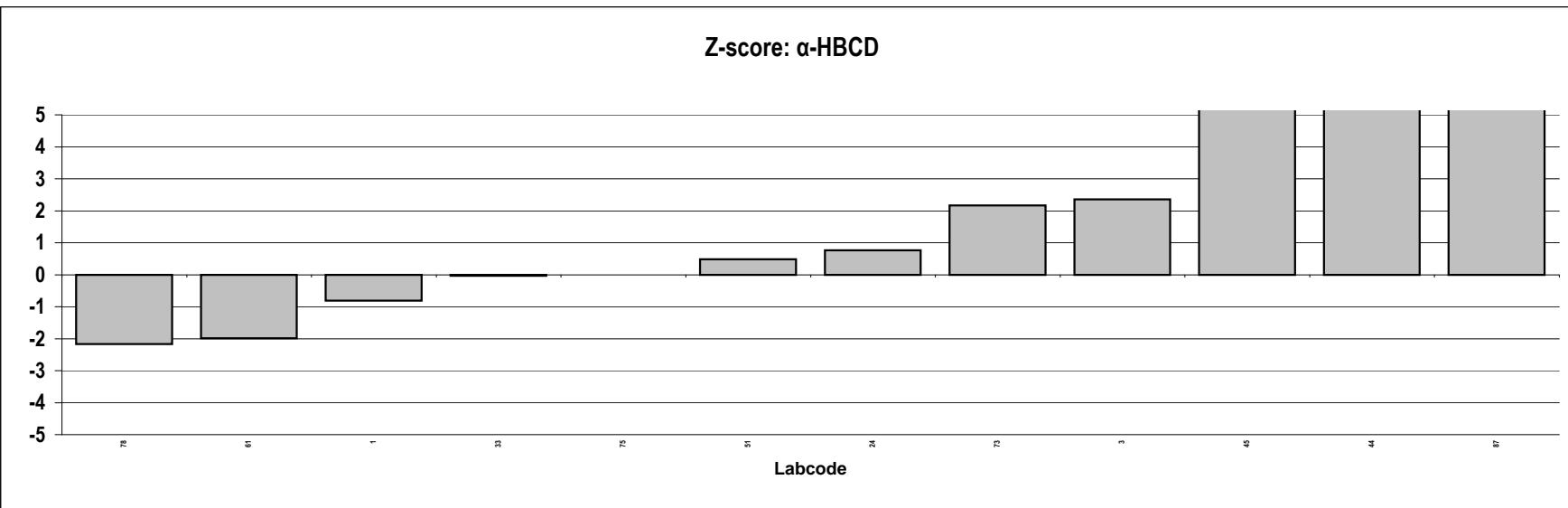
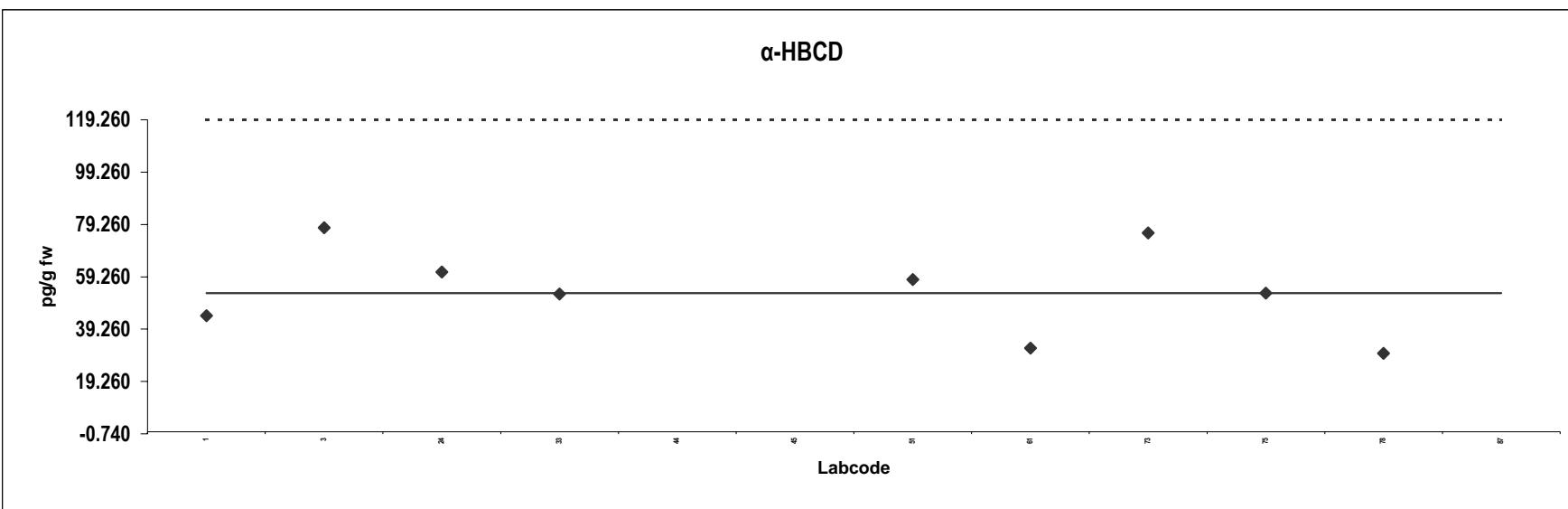


**Pork**  
Congener:  $\alpha$ -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	44				
3	78				
24	61				
33	53				
44	140	Outlier			
45	130	Outlier			
51	58				
61	32				
73	76				
75	53				
78	30				
87	405	Outlier			

**Consensus statistics**

Consensus median, pg/g	53
Median all values pg/g	60
Consensus mean, pg/g	54
Standard deviation, pg/g	17
Relative standard deviation, %	31
No. of values reported	12
No. of values removed	3
No. of reported non-detects	0

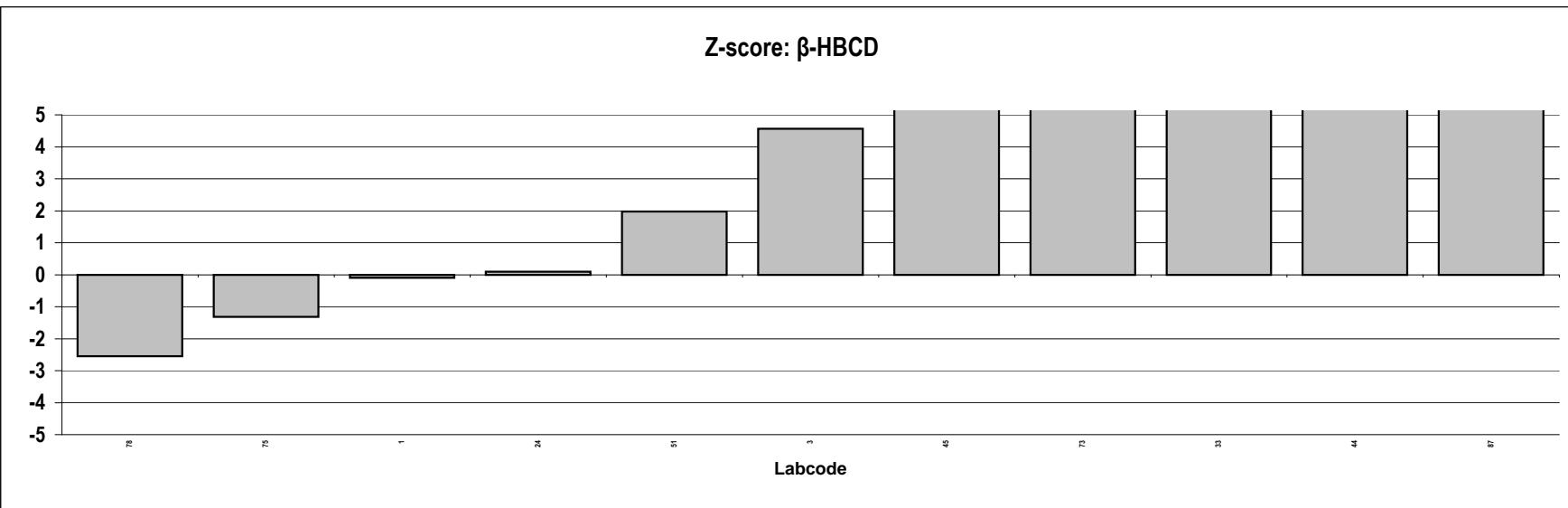
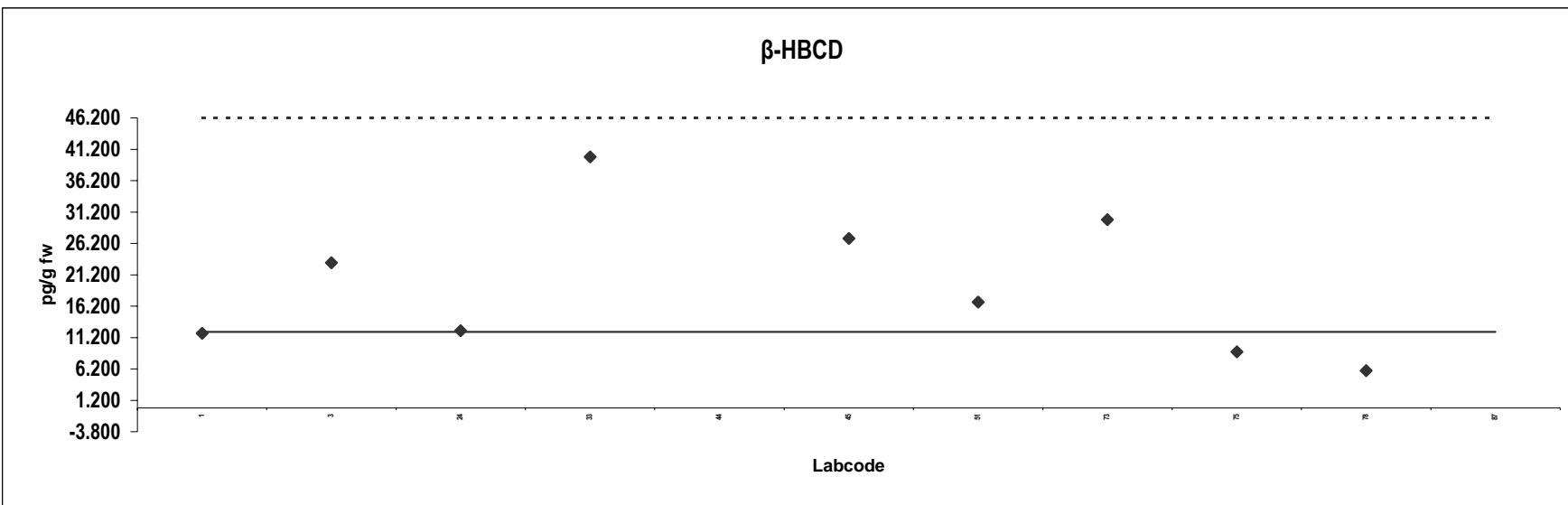


**Pork**  
**Congener:  $\beta$ -HBCD**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	12				
3	23				
24	12				
33	40	ND			
44	170	Outlier			
45	27	ND			
51	17				
73	30	ND			
75	8.9				
78	5.9				
87	296	Outlier			

**Consensus statistics**

Consensus median, pg/g	12
Median all values pg/g	23
Consensus mean, pg/g	20
Standard deviation, pg/g	11
Relative standard deviation, %	58
No. of values reported	11
No. of values removed	2
No. of reported non-detects	3

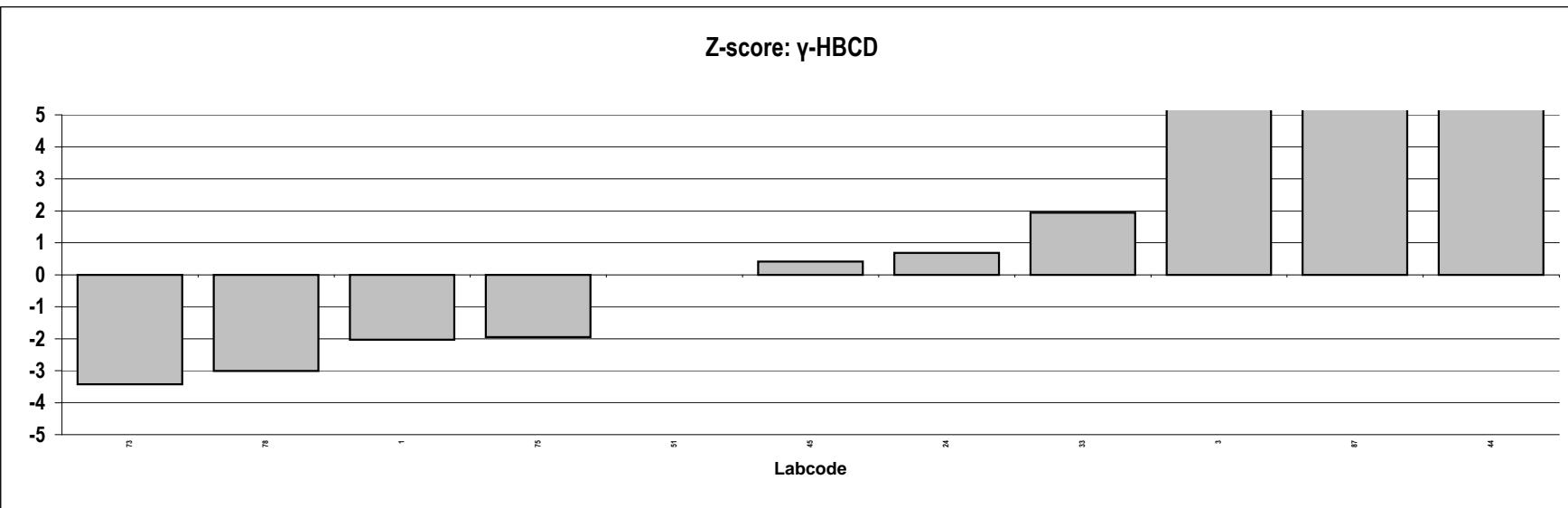
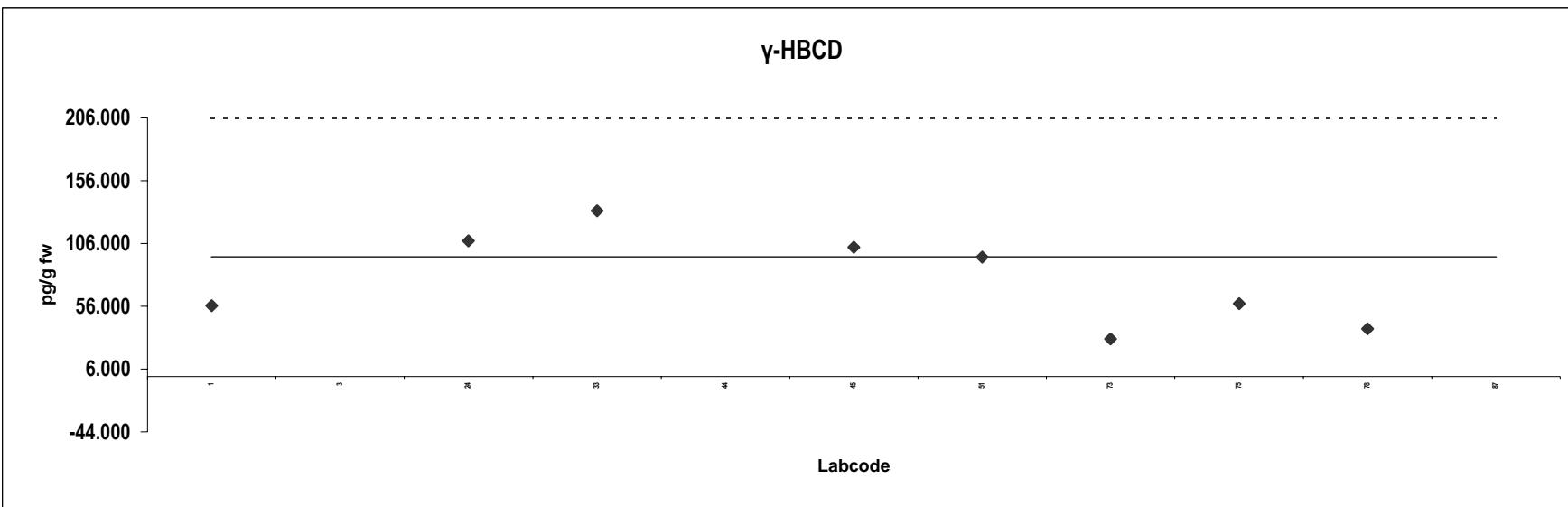


**Pork**  
Congener:  $\gamma$ -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	56				
3	242	Outlier			
24	108				
33	132				
44	1337	Outlier			
45	103				
51	95				
73	30	ND			
75	58				
78	38				
87	1010	Outlier			

**Consensus statistics**

Consensus median, pg/g	95
Median all values pg/g	103
Consensus mean, pg/g	78
Standard deviation, pg/g	37
Relative standard deviation, %	48
No. of values reported	11
No. of values removed	3
No. of reported non-detects	1

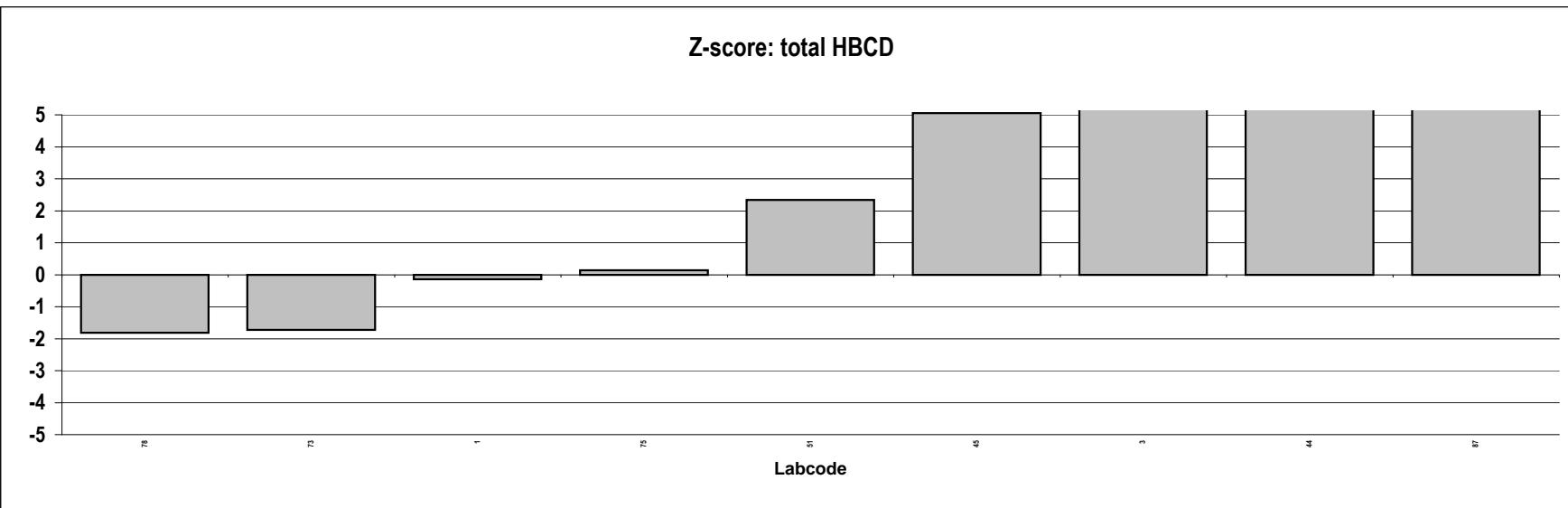
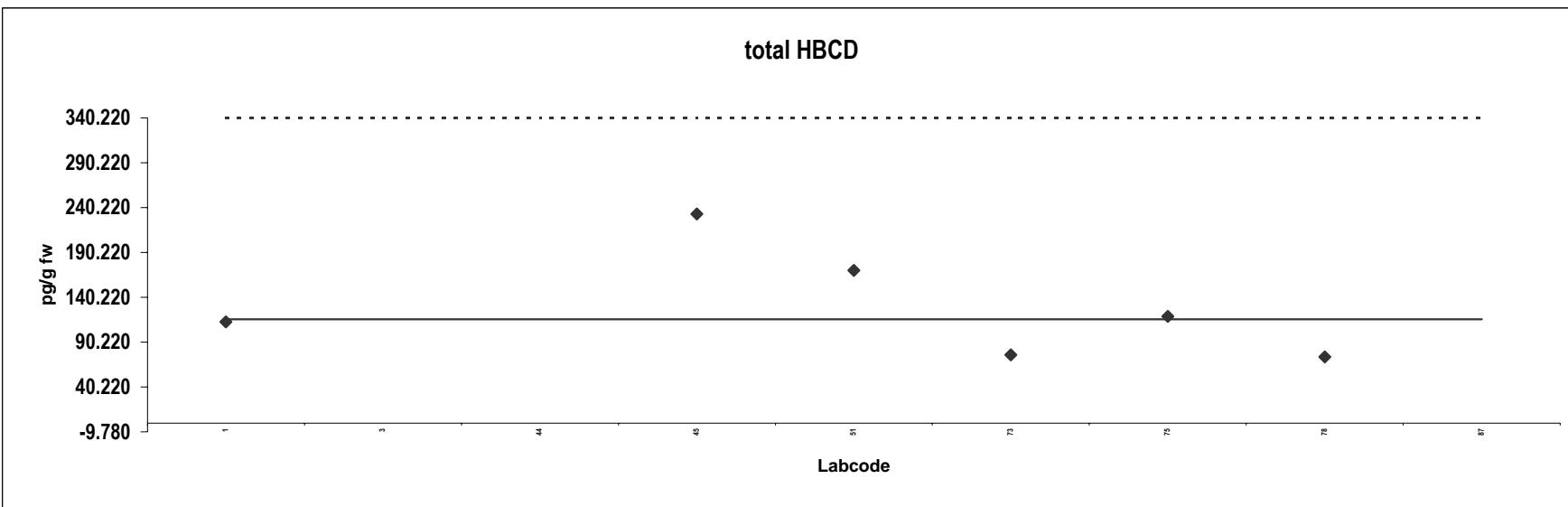


**Pork**  
**Congener: total HBCD**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	113				
3	343				
44	1647	Outlier			
45	233	Outlier			
51	170				
73	76				
75	119				
78	74				
87	1711	Outlier			

**Consensus statistics**

Consensus median, pg/g	116
Median all values pg/g	170
Consensus mean, pg/g	131
Standard deviation, pg/g	61
Relative standard deviation, %	47
No. of values reported	9
No. of values removed	3
No. of reported non-detects	0





## **Appendix 3:**

Presentation of results  
for Herring



## Appendix 3: Presentation of results: Herring

### Statistic calculations for PCDDs, PCDFs and dioxin-like PCBs

For each congener, the outliers were removed and the consensus calculated according to the following procedure:

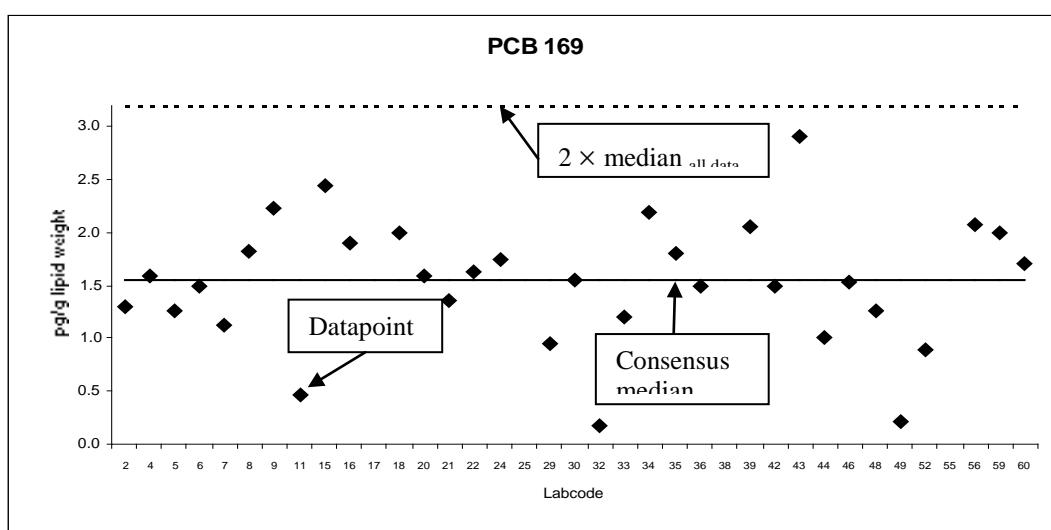
1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners.
2. Values exceeding  $2 \times$  this median were defined as outliers and removed from the data set.
3. Median, mean and standard deviation were re-calculated from the remaining data. This second median was called consensus.

### Statistic calculations for indicator PCBs, PBDEs and HBCD

For each congener, the outliers were removed and the consensus calculated according to the following procedure:

1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners (NDs).
2. Values exceeding  $2 \times$  this median were defined as outliers and removed from the data set. The NDs were also removed.
3. Median, mean and standard deviation were re-calculated from the remaining data. This second median was called consensus.
4. For comparison, median, mean and standard deviation were also calculated without removing NDs.

The diagram shows the reported data up to approximately the limit for outliers ( $2 \times$  the first median).



### Z-Scores of individual congeners

Z-scores of each congener were calculated for each laboratory according to the following equation:

$$z = (x - X)/\sigma$$

where  $x$  = reported value;  $X$  = assigned value (consensus);  $\sigma$  = target value for standard deviation. A  $\sigma$  of 20% of the consensus was used, i.e. z-scores between +1 and -1 reflect a deviation of  $\pm 20\%$  from the consensus value.

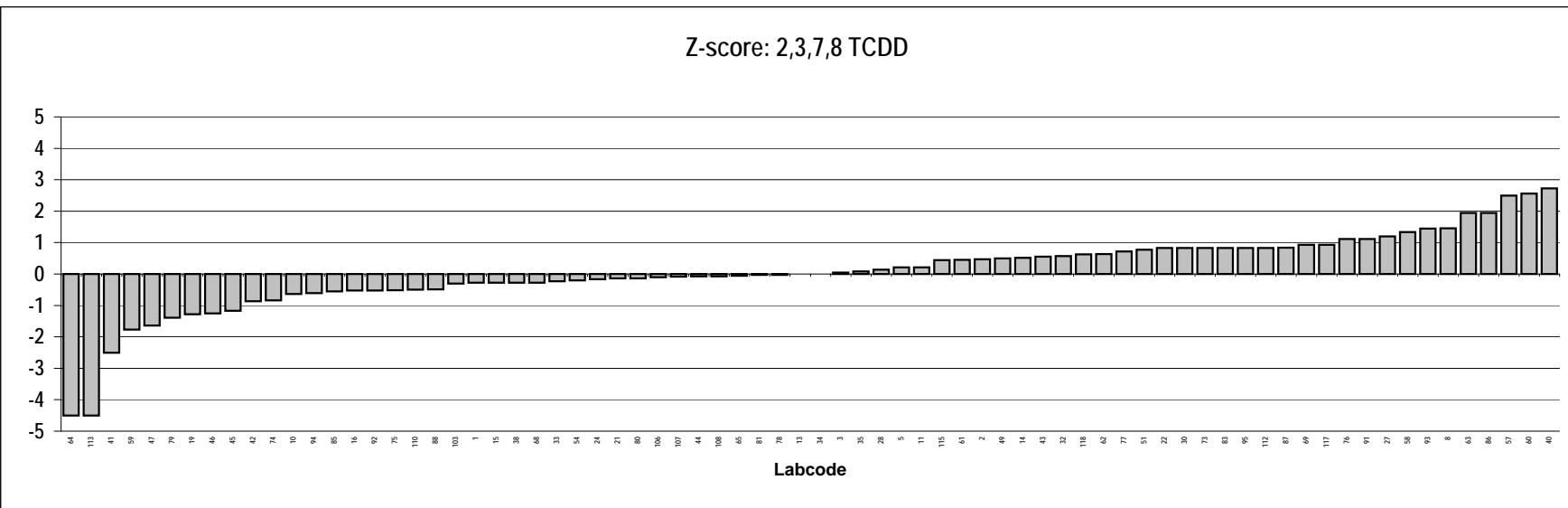
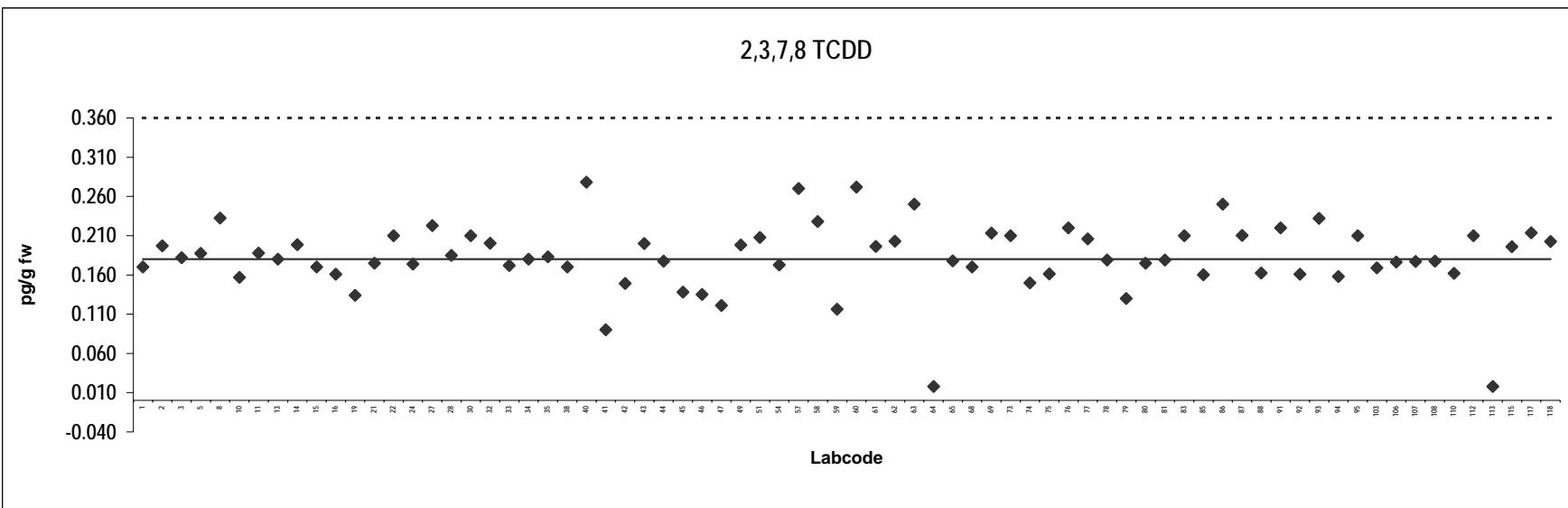


**Herring**  
Congener: 2,3,7,8 TCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.17		73	0.21	
2	0.20		74	0.15	
3	0.18		75	0.16	
5	0.19		76	0.22	
8	0.23		77	0.21	
10	0.16		78	0.18	
11	0.19		79	0.13	
13	0.18		80	0.18	
14	0.20		81	0.18	
15	0.17		83	0.21	
16	0.16		85	0.16	
19	0.13		86	0.25	
21	0.17		87	0.21	
22	0.21		88	0.16	
24	0.17		91	0.22	
27	0.22		92	0.16	
28	0.19		93	0.23	
30	0.21		94	0.16	
32	0.20		95	0.21	
33	0.17		103	0.17	
34	0.18		106	0.18	
35	0.18		107	0.18	
38	0.17		108	0.18	
40	0.28		110	0.16	
41	0.090		112	0.21	
42	0.15		113	0.018	
43	0.20		115	0.20	
44	0.18		117	0.21	
45	0.14		118	0.20	
46	0.14				
47	0.12				
49	0.20				
51	0.21				
54	0.17				
57	0.27				
58	0.23				
59	0.12				
60	0.27				
61	0.20				
62	0.20				
63	0.25				
64	0.018				
65	0.18				
68	0.17				
69	0.21				

**Consensus statistics**

Consensus median, pg/g	0.18
Median all values pg/g	0.18
Consensus mean, pg/g	0.18
Standard deviation, pg/g	0.044
Relative standard deviation, %	24
No. of values reported	74
No. of values removed	0
No. of reported non-detects	3

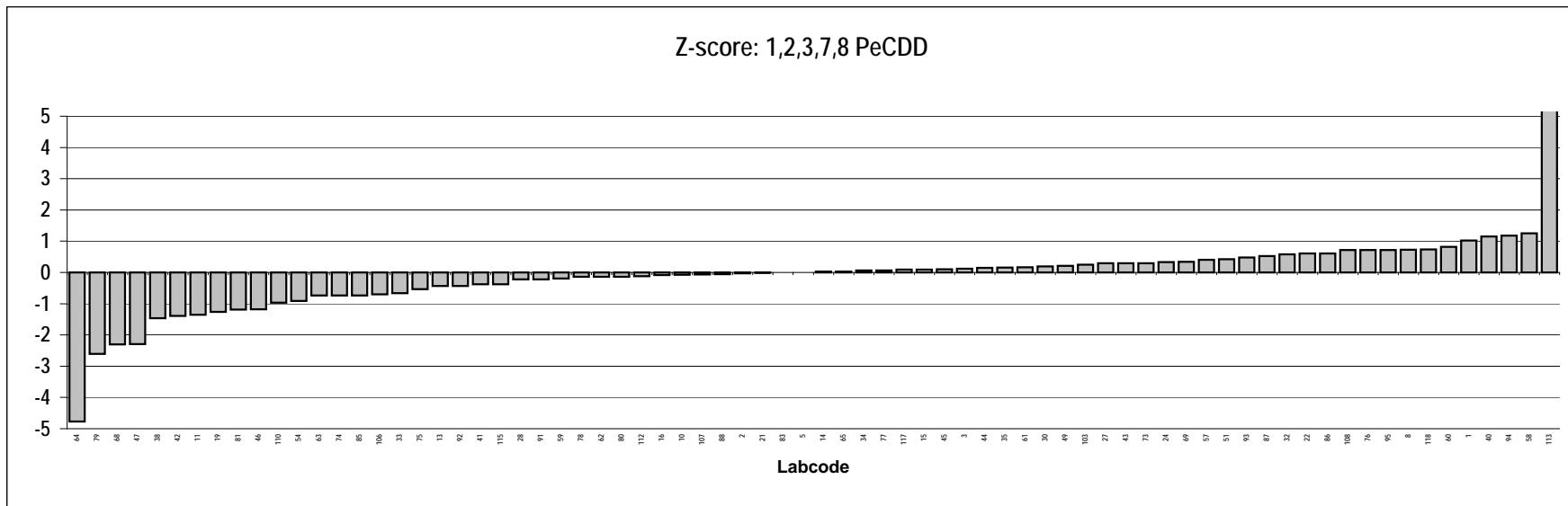
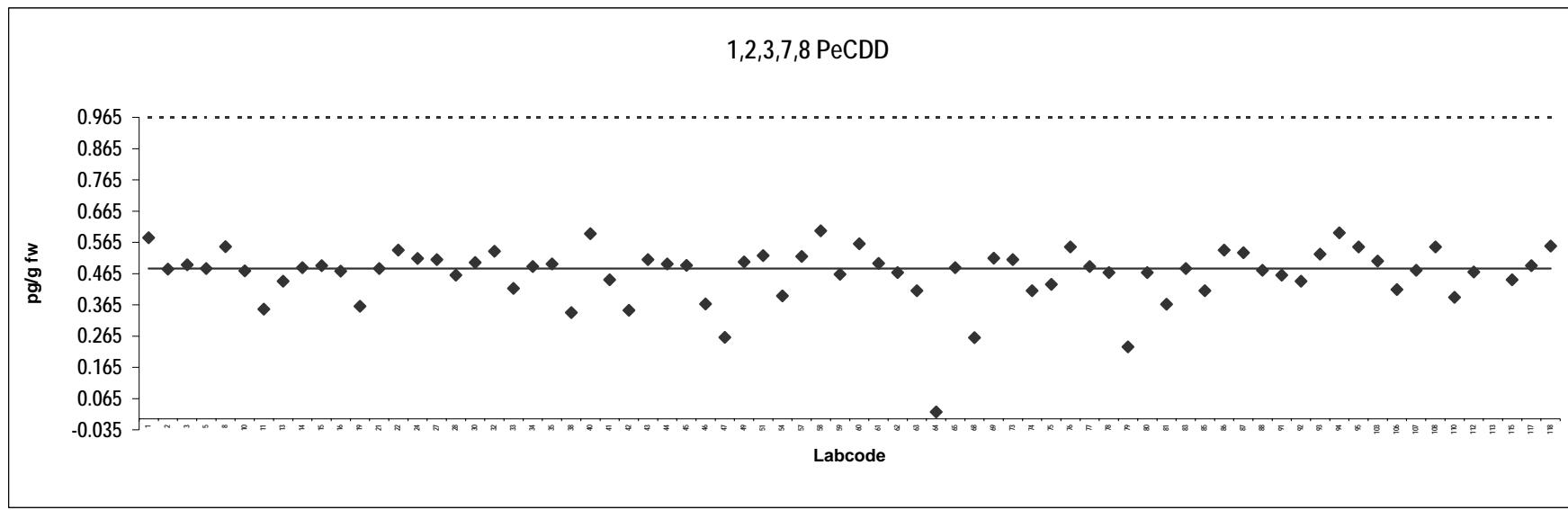


**Herring**  
Congener: 1,2,3,7,8 PeCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.58		73	0.51	
2	0.48		74	0.41	
3	0.49		75	0.43	
5	0.48		76	0.55	
8	0.55		77	0.49	
10	0.47		78	0.47	
11	0.35		79	0.23	
13	0.44		80	0.47	
14	0.48		81	0.37	
15	0.49		83	0.48	
16	0.47		85	0.41	
19	0.36		86	0.54	
21	0.48		87	0.53	
22	0.54		88	0.48	
24	0.51		91	0.46	
27	0.51		92	0.44	
28	0.46		93	0.53	
30	0.50		94	0.60	
32	0.54		95	0.55	
33	0.42		103	0.51	
34	0.49		106	0.41	
35	0.50		107	0.48	
38	0.34		108	0.55	
40	0.59		110	0.39	
41	0.45		112	0.47	
42	0.35		113	3.0	Outlier
43	0.51		115	0.45	
44	0.50		117	0.49	
45	0.49		118	0.55	
46	0.37				
47	0.26				
49	0.50				
51	0.52				
54	0.39				
57	0.52				
58	0.60				
59	0.46				
60	0.56				
61	0.50				
62	0.47				
63	0.41				
64	0.022				
65	0.48				
68	0.26				
69	0.51				

**Consensus statistics**

Consensus median, pg/g	0.48
Median all values pg/g	0.48
Consensus mean, pg/g	0.46
Standard deviation, pg/g	0.091
Relative standard deviation, %	20
No. of values reported	74
No. of values removed	1
No. of reported non-detects	0

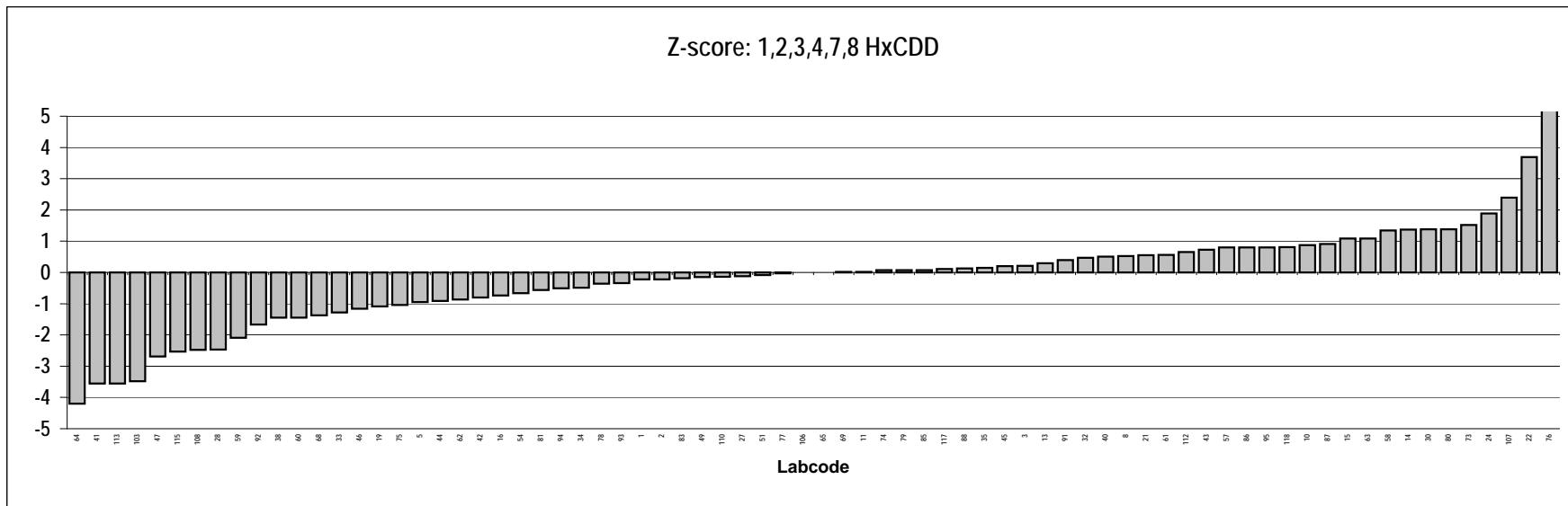
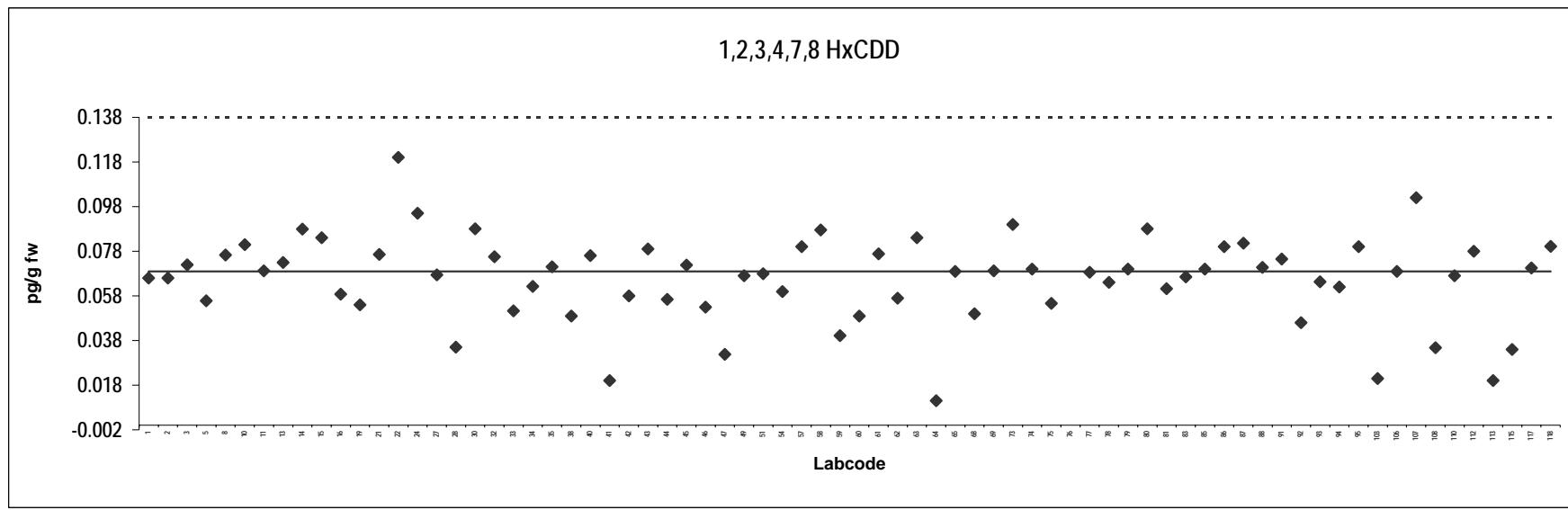


**Herring**  
**Congener: 1,2,3,4,7,8 HxCDD**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.066		73	0.090	
2	0.066		74	0.070	
3	0.072		75	0.055	
5	0.056		76	0.30	
8	0.076		77	0.069	
10	0.081		78	0.064	
11	0.069		79	0.070	
13	0.073		80	0.088	
14	0.088		81	0.061	
15	0.084		83	0.067	
16	0.059		85	0.070	
19	0.054		86	0.080	
21	0.077		87	0.082	
22	0.12	ND	88	0.071	
24	0.095		91	0.075	
27	0.067		92	0.046	
28	0.035	ND	93	0.064	
30	0.088		94	0.062	
32	0.075		95	0.080	
33	0.051		103	0.021	
34	0.062		106	0.069	
35	0.071		107	0.10	
38	0.049		108	0.035	
40	0.076	ND	110	0.067	
41	0.020		112	0.078	
42	0.058		113	0.020	
43	0.079		115	0.034	
44	0.056		117	0.071	
45	0.072		118	0.080	
46	0.053				
47	0.032				
49	0.067				
51	0.068				
54	0.060				
57	0.080				
58	0.088				
59	0.040				
60	0.049				
61	0.077				
62	0.057				
63	0.084				
64	0.011	ND			
65	0.069				
68	0.050				
69	0.069				

**Consensus statistics**

Consensus median, pg/g	0.069
Median all values pg/g	0.069
Consensus mean, pg/g	0.066
Standard deviation, pg/g	0.019
Relative standard deviation, %	30
No. of values reported	74
No. of values removed	1
No. of reported non-detects	6

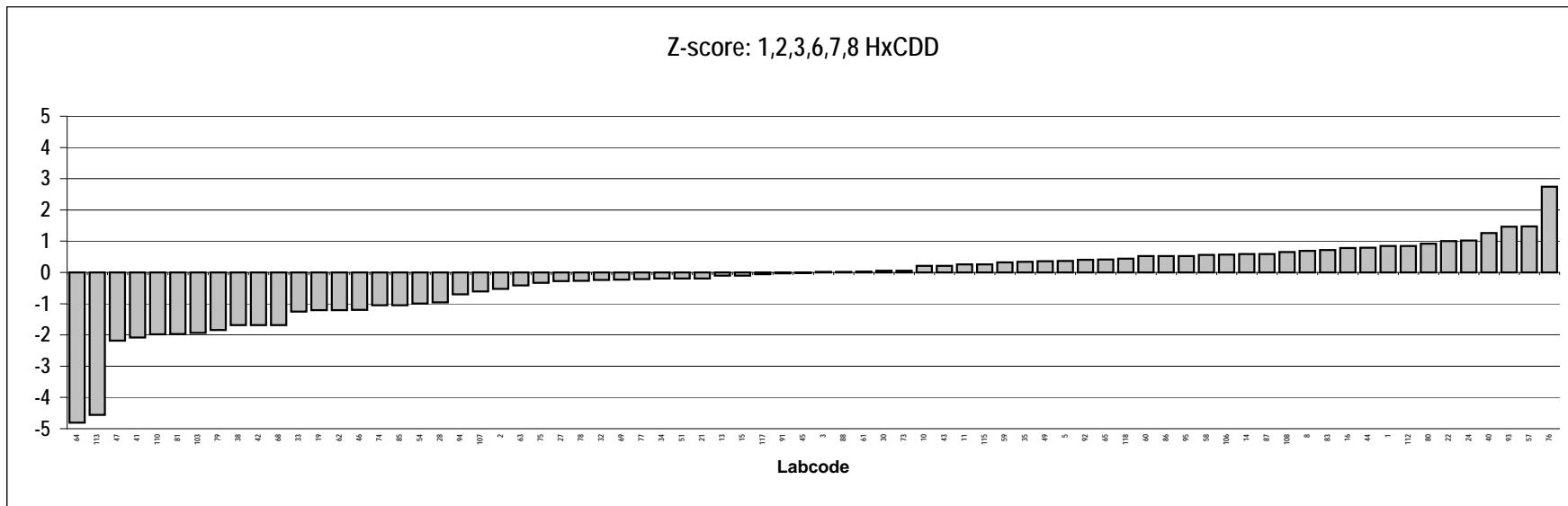
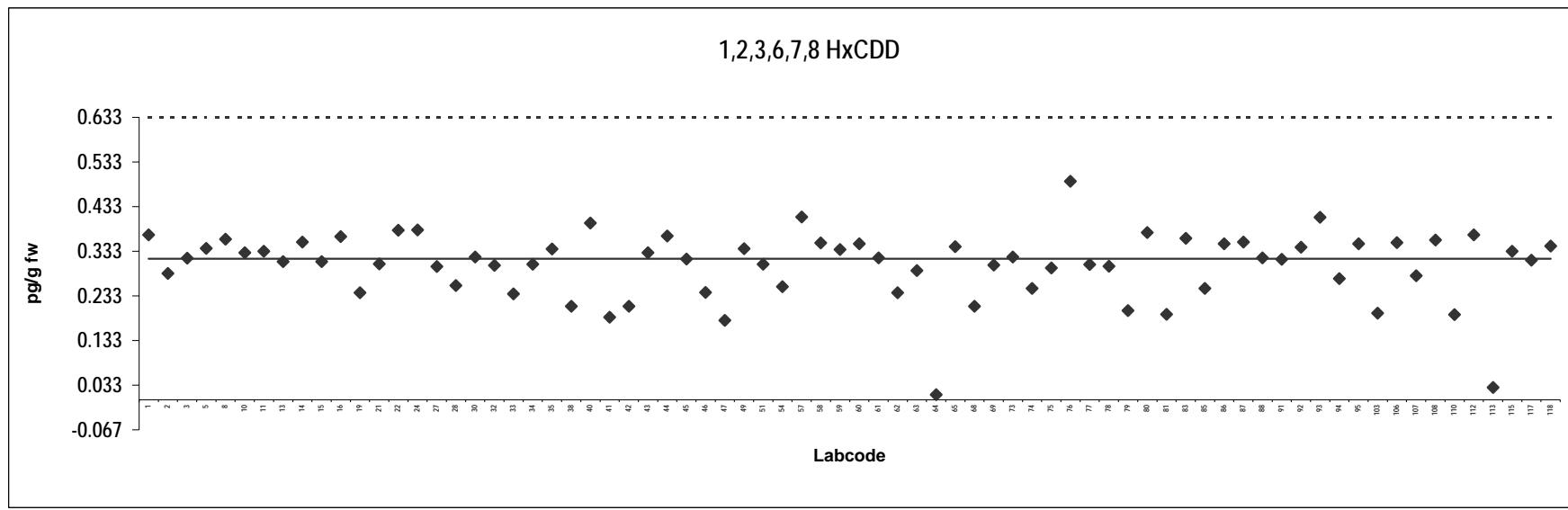


**Herring**  
Congener: 1,2,3,6,7,8 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.37		73	0.32	
2	0.28		74	0.25	
3	0.32		75	0.30	
5	0.34		76	0.49	
8	0.36		77	0.30	
10	0.33		78	0.30	
11	0.33		79	0.20	
13	0.31		80	0.38	
14	0.35		81	0.19	
15	0.31		83	0.36	
16	0.37		85	0.25	
19	0.24		86	0.35	
21	0.30		87	0.35	
22	0.38		88	0.32	
24	0.38		91	0.32	
27	0.30		92	0.34	
28	0.26		93	0.41	
30	0.32		94	0.27	
32	0.30		95	0.35	
33	0.24		103	0.19	
34	0.30		106	0.35	
35	0.34		107	0.28	
38	0.21		108	0.36	
40	0.40		110	0.19	
41	0.19		112	0.37	
42	0.21		113	0.028	ND
43	0.33		115	0.33	
44	0.37		117	0.31	
45	0.32		118	0.34	
46	0.24				
47	0.18				
49	0.34				
51	0.30				
54	0.25				
57	0.41				
58	0.35				
59	0.34				
60	0.35				
61	0.32				
62	0.24				
63	0.29				
64	0.012	ND			
65	0.34				
68	0.21				
69	0.30				

**Consensus statistics**

Consensus median, pg/g	0.32
Median all values pg/g	0.32
Consensus mean, pg/g	0.30
Standard deviation, pg/g	0.077
Relative standard deviation, %	26
No. of values reported	74
No. of values removed	0
No. of reported non-detects	2

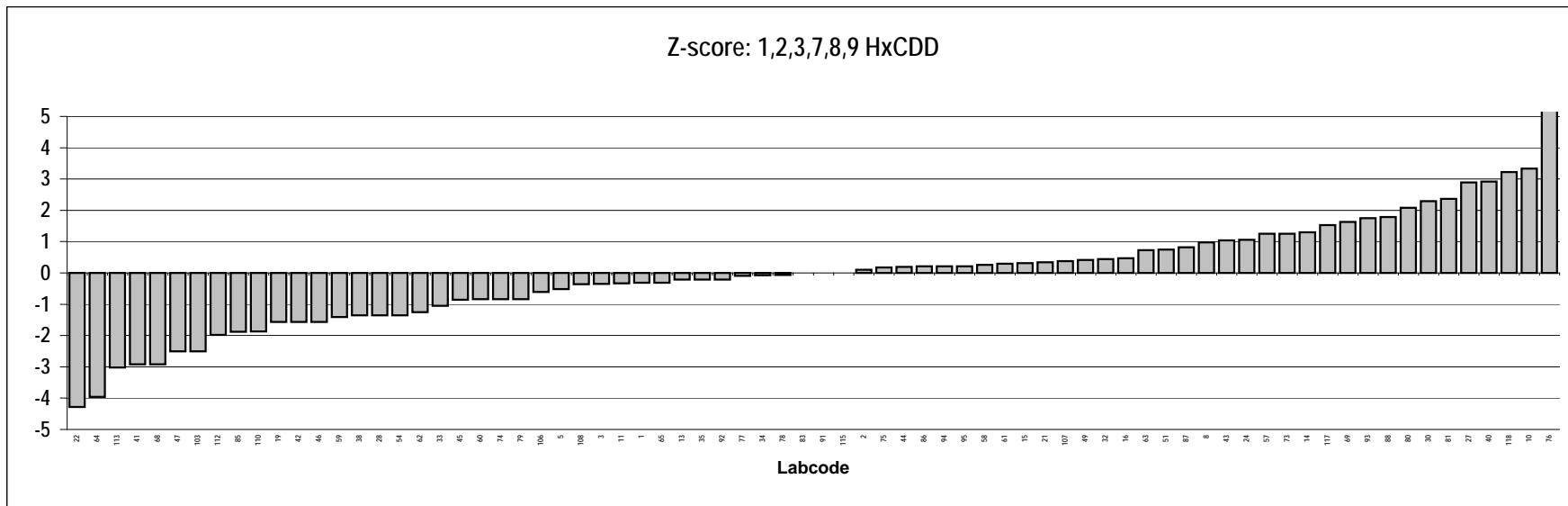
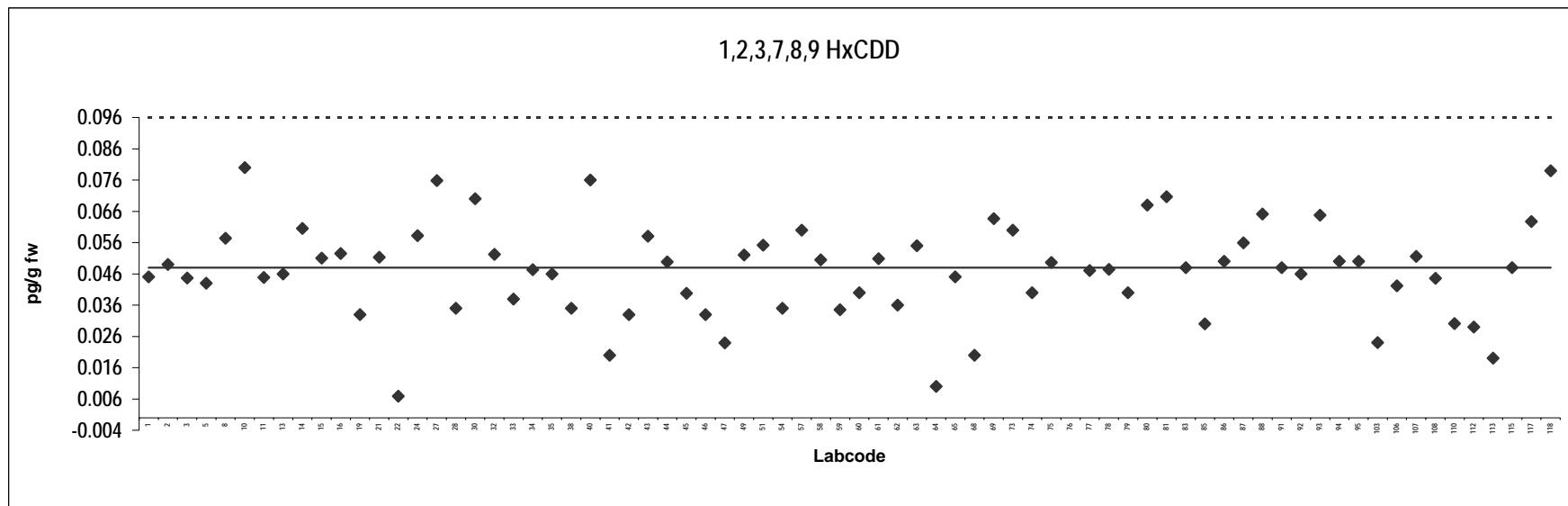


**Herring**  
Congener: 1,2,3,7,8,9 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.045		73	0.060	
2	0.049		74	0.040	
3	0.045		75	0.050	
5	0.043		76	0.30	Outlier,ND
8	0.057		77	0.047	
10	0.080		78	0.047	
11	0.045		79	0.040	
13	0.046		80	0.068	
14	0.060		81	0.071	
15	0.051		83	0.048	
16	0.053		85	0.030	
19	0.033		86	0.050	
21	0.051		87	0.056	
22	0.0069	ND	88	0.065	
24	0.058		91	0.048	
27	0.076		92	0.046	
28	0.035	ND	93	0.065	
30	0.070	ND	94	0.050	ND
32	0.052		95	0.050	
33	0.038		103	0.024	
34	0.047		106	0.042	
35	0.046		107	0.052	ND
38	0.035		108	0.045	
40	0.076	ND	110	0.030	
41	0.020	ND	112	0.029	
42	0.033		113	0.019	ND
43	0.058		115	0.048	
44	0.050		117	0.063	
45	0.040		118	0.079	
46	0.033				
47	0.024				
49	0.052				
51	0.055				
54	0.035				
57	0.060				
58	0.051				
59	0.035				
60	0.040				
61	0.051				
62	0.036				
63	0.055				
64	0.010	ND			
65	0.045				
68	0.020				
69	0.064	ND			

**Consensus statistics**

Consensus median, pg/g	0.048
Median all values pg/g	0.048
Consensus mean, pg/g	0.047
Standard deviation, pg/g	0.015
Relative standard deviation, %	32
No. of values reported	74
No. of values removed	1
No. of reported non-detects	11

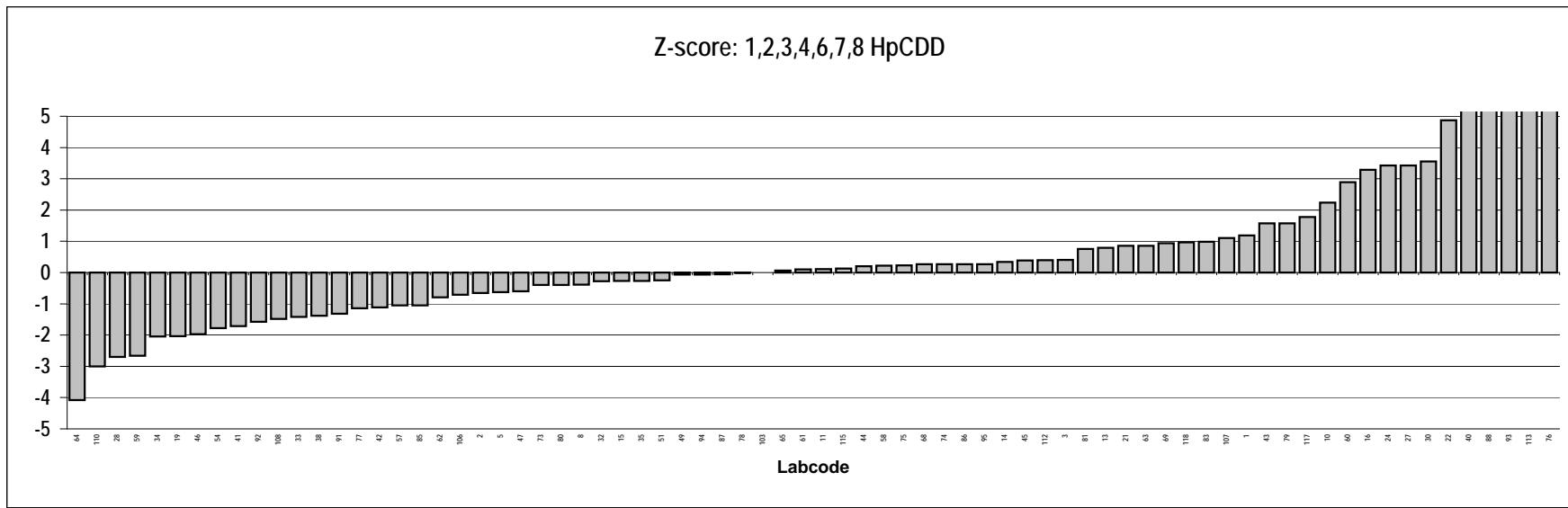
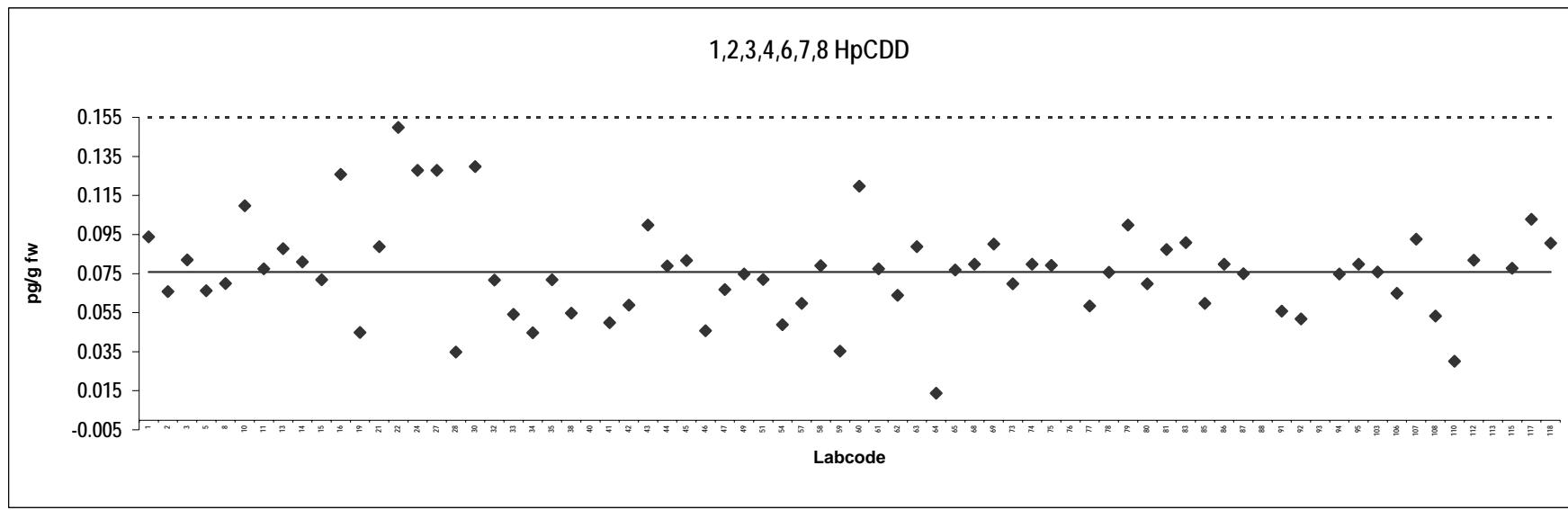


**Herring**  
Congener: 1,2,3,4,6,7,8 HpCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.094		73	0.070	
2	0.066		74	0.080	
3	0.082		75	0.079	
5	0.066		76	0.50	Outlier,ND
8	0.070		77	0.059	
10	0.11		78	0.076	
11	0.078		79	0.10	
13	0.088		80	0.070	
14	0.081		81	0.088	
15	0.072		83	0.091	
16	0.13		85	0.060	
19	0.045		86	0.080	
21	0.089		87	0.075	
22	0.15	ND	88	0.23	Outlier
24	0.13		91	0.056	
27	0.13		92	0.052	
28	0.035	ND	93	0.24	Outlier
30	0.13		94	0.075	
32	0.072		95	0.080	
33	0.054		103	0.076	
34	0.045		106	0.065	
35	0.072		107	0.093	
38	0.055		108	0.053	
40	0.21	Outlier,ND	110	0.030	
41	0.050		112	0.082	
42	0.059		113	0.26	Outlier
43	0.10		115	0.078	
44	0.079		117	0.10	
45	0.082		118	0.091	
46	0.046				
47	0.067				
49	0.075				
51	0.072				
54	0.049				
57	0.060				
58	0.079				
59	0.036				
60	0.12				
61	0.078				
62	0.064				
63	0.089				
64	0.014	ND			
65	0.077				
68	0.080				
69	0.090	ND			

**Consensus statistics**

Consensus median, pg/g	0.076
Median all values pg/g	0.078
Consensus mean, pg/g	0.076
Standard deviation, pg/g	0.025
Relative standard deviation, %	32
No. of values reported	74
No. of values removed	5
No. of reported non-detects	6

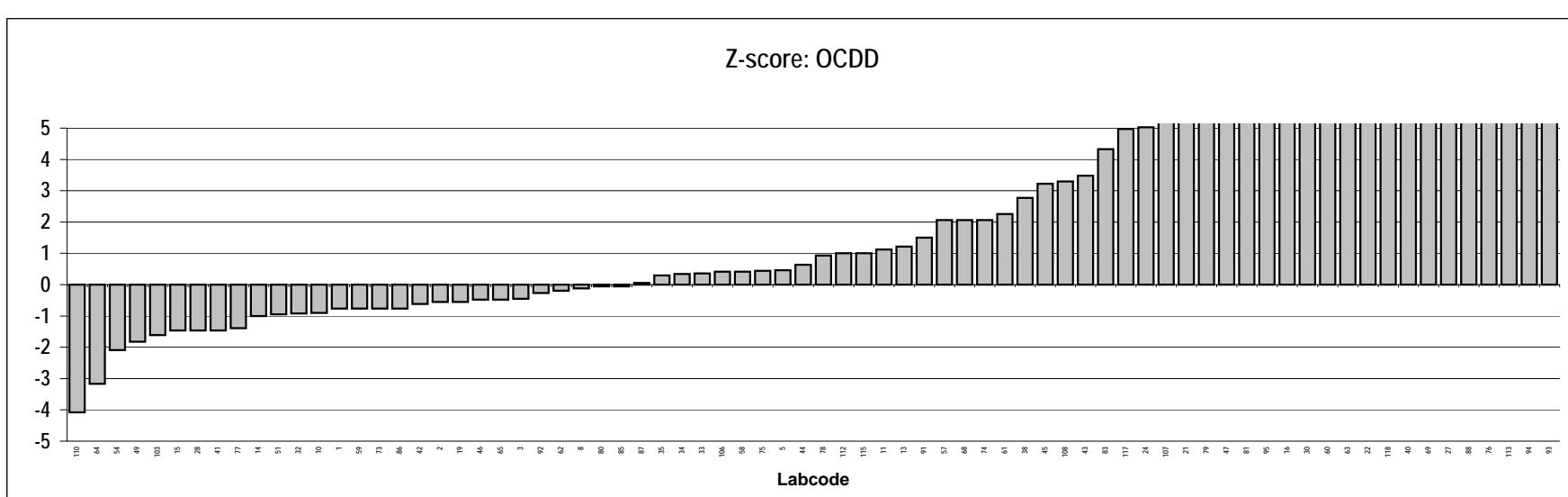
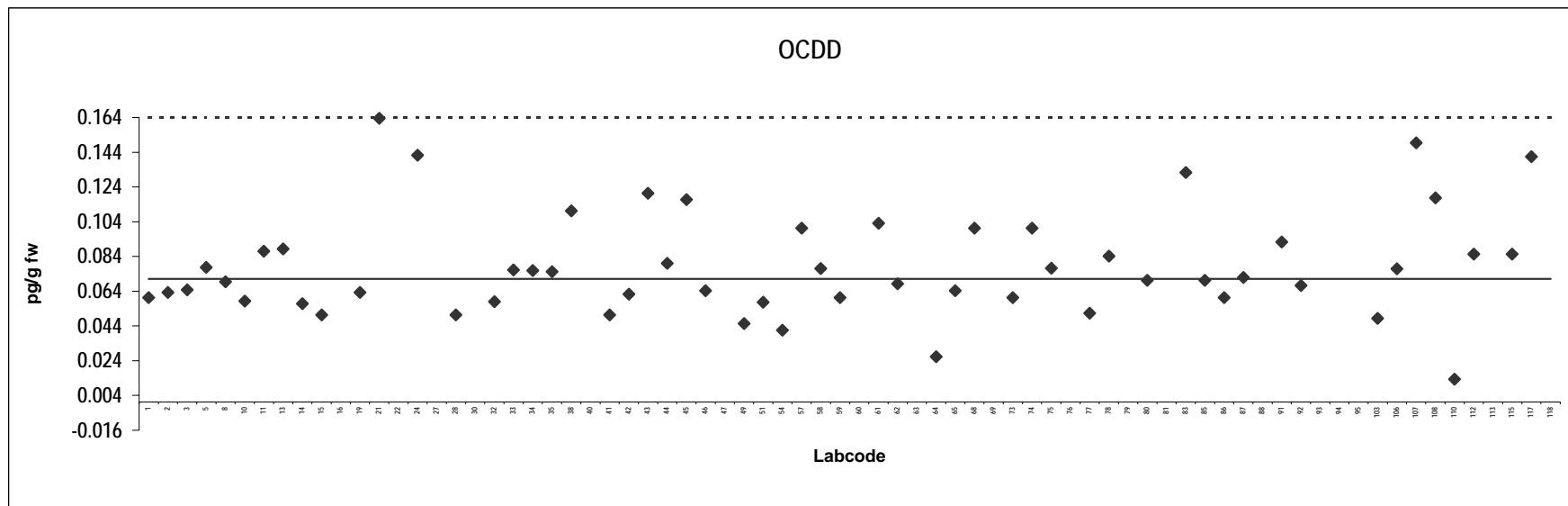


**Herring**  
Congener: OCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.060		73	0.060	
2	0.063		74	0.10	
3	0.064		75	0.077	
5	0.077		76	1.0	Outlier,ND
8	0.069		77	0.051	
10	0.058	ND	78	0.084	
11	0.087		79	0.17	Outlier
13	0.088		80	0.070	
14	0.057		81	0.17	Outlier
15	0.050		83	0.13	
16	0.21	Outlier	85	0.070	
19	0.063		86	0.060	
21	0.16		87	0.072	
22	0.26	Outlier,ND	88	0.64	Outlier
24	0.14		91	0.092	
27	0.41	Outlier	92	0.067	
28	0.050	ND	93	2.4	Outlier
30	0.21	Outlier	94	2.0	Outlier,ND
32	0.058		95	0.20	Outlier,ND
33	0.076		103	0.048	
34	0.076		106	0.077	
35	0.075		107	0.15	ND
38	0.11		108	0.12	
40	0.34	Outlier,ND	110	0.013	ND
41	0.050	ND	112	0.085	
42	0.062	ND	113	1.6	Outlier
43	0.12		115	0.085	
44	0.080		117	0.14	
45	0.12		118	0.32	Outlier
46	0.064				
47	0.17	Outlier			
49	0.045	ND			
51	0.057				
54	0.041				
57	0.10				
58	0.077				
59	0.060				
60	0.22	Outlier			
61	0.10				
62	0.068				
63	0.23	Outlier			
64	0.026	ND			
65	0.064				
68	0.10				
69	0.35	Outlier,ND			

**Consensus statistics**

Consensus median, pg/g	0.071
Median all values pg/g	0.082
Consensus mean, pg/g	0.078
Standard deviation, pg/g	0.030
Relative standard deviation, %	39
No. of values reported	74
No. of values removed	18
No. of reported non-detects	14

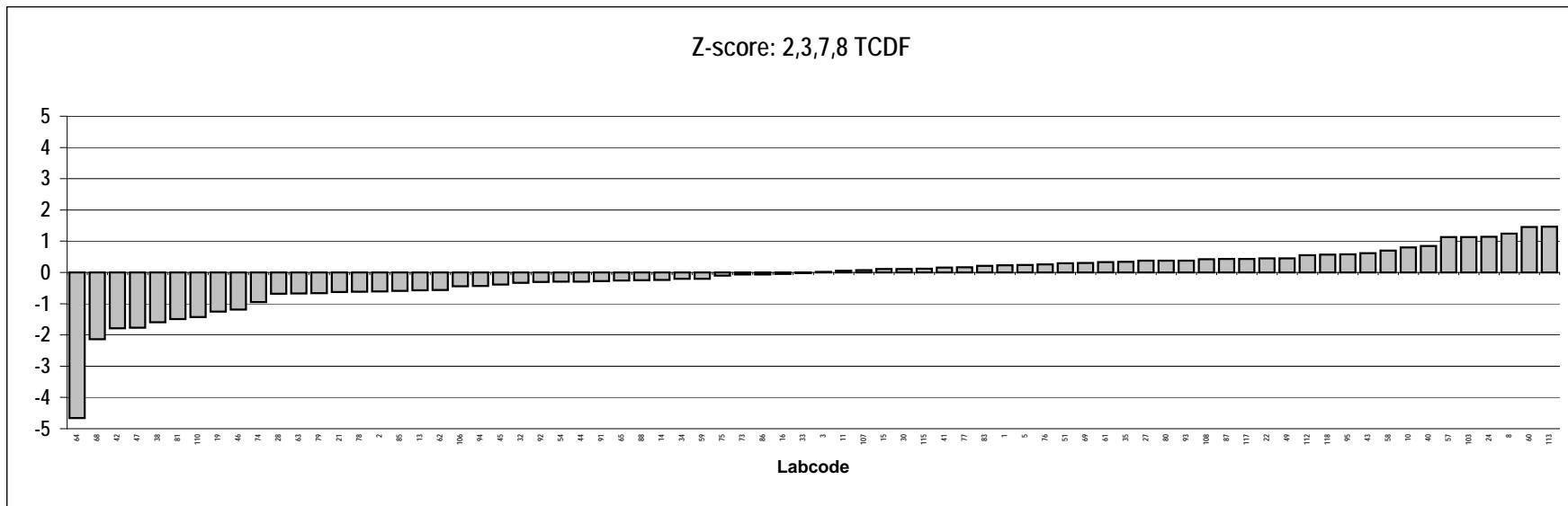
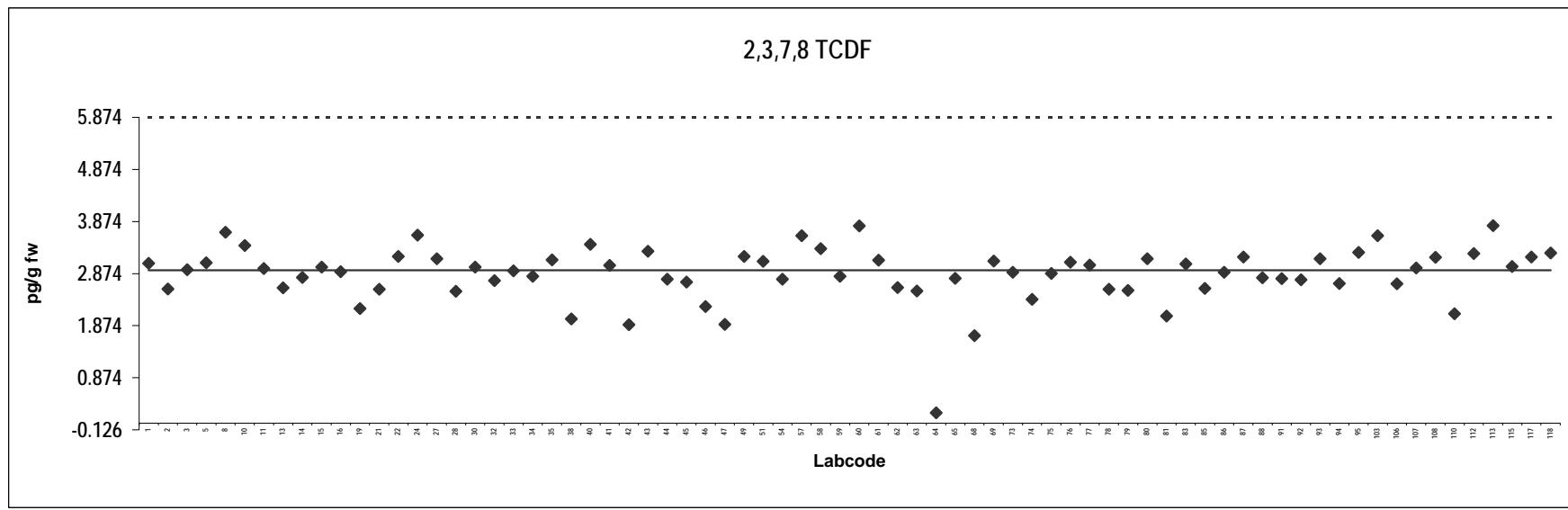


**Herring**  
Congener: 2,3,7,8 TCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	3.1		73	2.9	
2	2.6		74	2.4	
3	2.9		75	2.9	
5	3.1		76	3.1	
8	3.7		77	3.0	
10	3.4		78	2.6	
11	3.0		79	2.6	
13	2.6		80	3.2	
14	2.8		81	2.1	
15	3.0		83	3.1	
16	2.9		85	2.6	
19	2.2		86	2.9	
21	2.6		87	3.2	
22	3.2		88	2.8	
24	3.6		91	2.8	
27	3.2		92	2.8	
28	2.5		93	3.2	
30	3.0		94	2.7	
32	2.7		95	3.3	
33	2.9		103	3.6	
34	2.8		106	2.7	
35	3.1		107	3.0	
38	2.0		108	3.2	
40	3.4		110	2.1	
41	3.0		112	3.3	
42	1.9		113	3.8	
43	3.3		115	3.0	
44	2.8		117	3.2	
45	2.7		118	3.3	
46	2.2				
47	1.9				
49	3.2				
51	3.1				
54	2.8				
57	3.6				
58	3.4				
59	2.8				
60	3.8				
61	3.1				
62	2.6				
63	2.5				
64	0.20				
65	2.8				
68	1.7				
69	3.1				

**Consensus statistics**

Consensus median, pg/g	2.9
Median all values pg/g	2.9
Consensus mean, pg/g	2.9
Standard deviation, pg/g	0.54
Relative standard deviation, %	19
No. of values reported	74
No. of values removed	0
No. of reported non-detects	0



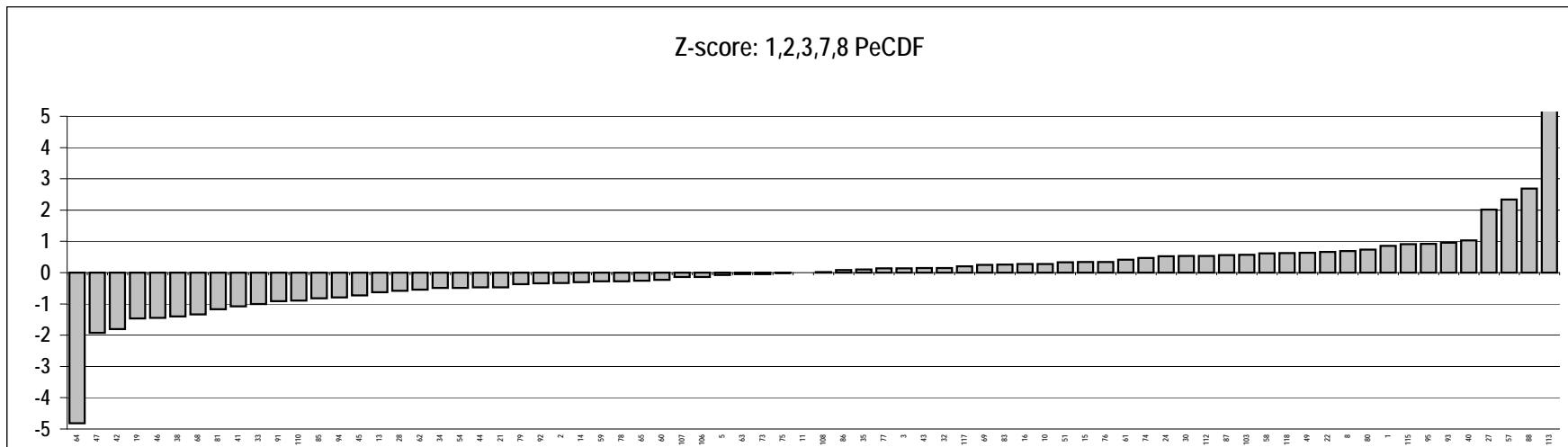
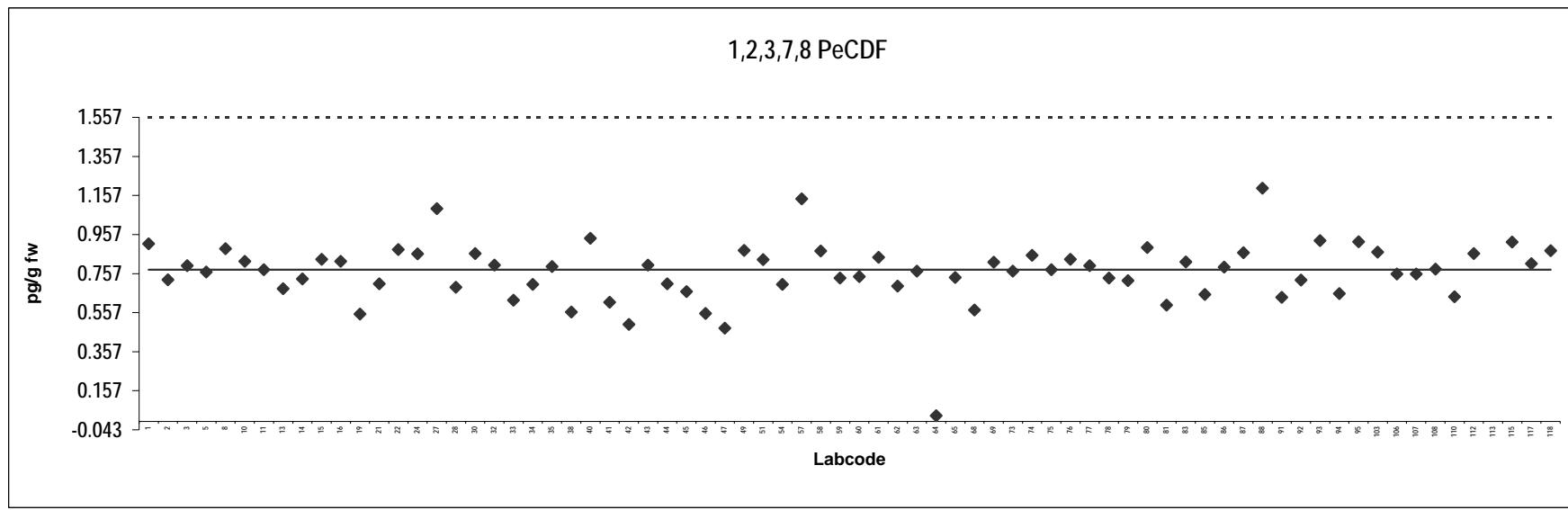
**Herring**  
Congener: 1,2,3,7,8 PeCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.91		73	0.77	
2	0.73		74	0.85	
3	0.80		75	0.78	
5	0.76		76	0.83	
8	0.88		77	0.80	
10	0.82		78	0.73	
11	0.78		79	0.72	
13	0.68		80	0.89	
14	0.73		81	0.60	
15	0.83		83	0.82	
16	0.82		85	0.65	
19	0.55		86	0.79	
21	0.70		87	0.86	
22	0.88		88	1.2	
24	0.86		91	0.64	
27	1.1		92	0.72	
28	0.69		93	0.93	
30	0.86		94	0.65	
32	0.80		95	0.92	
33	0.62		103	0.87	
34	0.70		106	0.76	
35	0.79		107	0.76	
38	0.56		108	0.78	
40	0.94		110	0.64	
41	0.61		112	0.86	
42	0.50		113	2.3	
43	0.80		115	0.92	
44	0.70		117	0.81	
45	0.66		118	0.87	
46	0.55				
47	0.48				
49	0.88				
51	0.83				
54	0.70				
57	1.1				
58	0.87				
59	0.73				
60	0.74				
61	0.84				
62	0.69				
63	0.77				
64	0.029				
65	0.74				
68	0.57				
69	0.82				

Outlier

**Consensus statistics**

Consensus median, pg/g	0.78
Median all values pg/g	0.78
Consensus mean, pg/g	0.76
Standard deviation, pg/g	0.16
Relative standard deviation, %	21
No. of values reported	74
No. of values removed	1
No. of reported non-detects	0

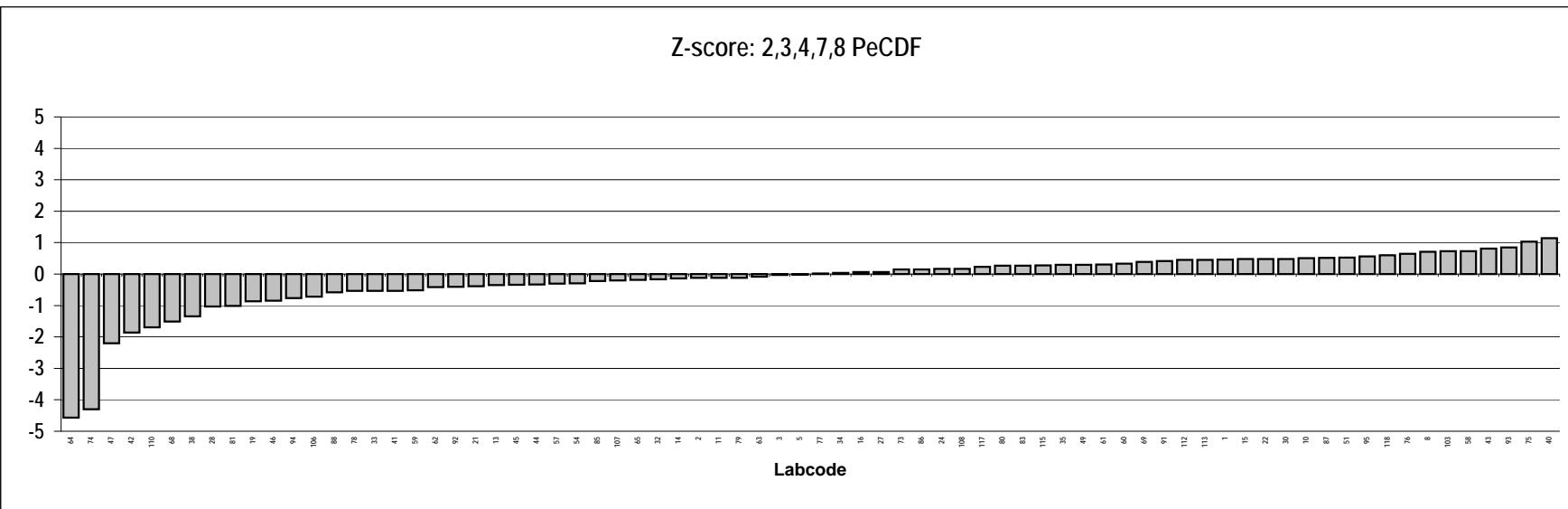
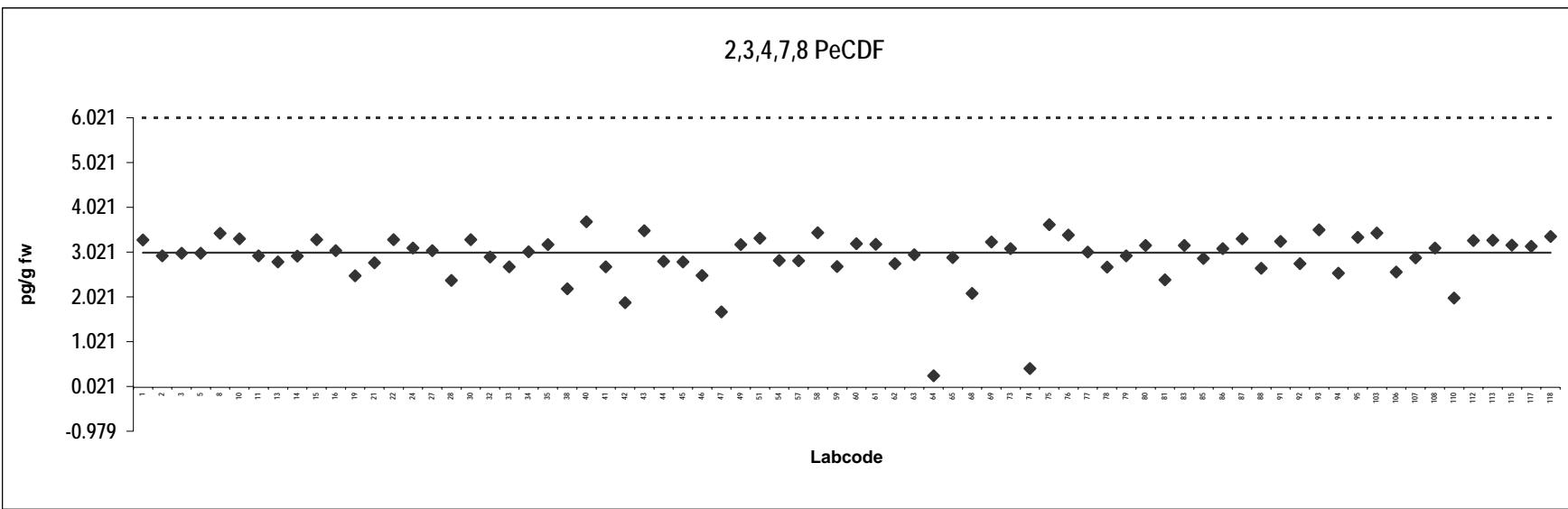


**Herring**  
Congener: 2,3,4,7,8 PeCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	3.3		73	3.1	
2	2.9		74	0.42	
3	3.0		75	3.6	
5	3.0		76	3.4	
8	3.4		77	3.0	
10	3.3		78	2.7	
11	2.9		79	2.9	
13	2.8		80	3.2	
14	2.9		81	2.4	
15	3.3		83	3.2	
16	3.1		85	2.9	
19	2.5		86	3.1	
21	2.8		87	3.3	
22	3.3		88	2.7	
24	3.1		91	3.3	
27	3.1		92	2.8	
28	2.4		93	3.5	
30	3.3		94	2.6	
32	2.9		95	3.4	
33	2.7		103	3.4	
34	3.0		106	2.6	
35	3.2		107	2.9	
38	2.2		108	3.1	
40	3.7		110	2.0	
41	2.7		112	3.3	
42	1.9		113	3.3	
43	3.5		115	3.2	
44	2.8		117	3.2	
45	2.8		118	3.4	
46	2.5				
47	1.7				
49	3.2				
51	3.3				
54	2.8				
57	2.8				
58	3.5				
59	2.7				
60	3.2				
61	3.2				
62	2.8				
63	3.0				
64	0.26				
65	2.9				
68	2.1				
69	3.2				

**Consensus statistics**

Consensus median, pg/g	3.0
Median all values pg/g	3.0
Consensus mean, pg/g	2.9
Standard deviation, pg/g	0.59
Relative standard deviation, %	20
No. of values reported	74
No. of values removed	0
No. of reported non-detects	0



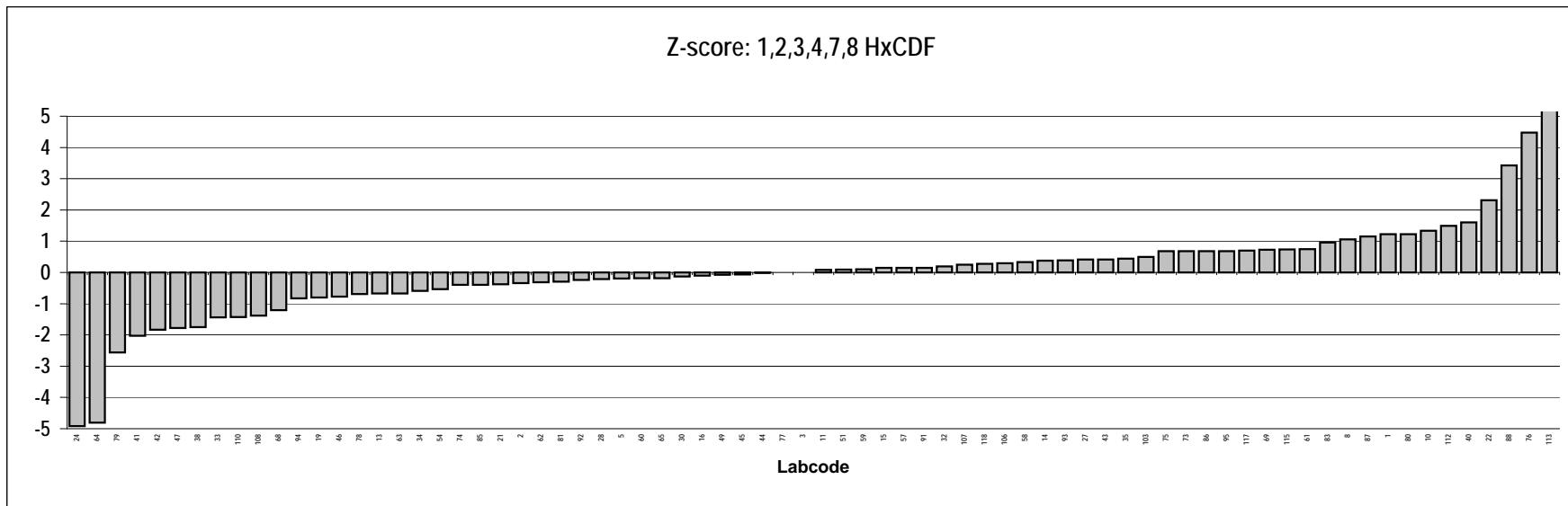
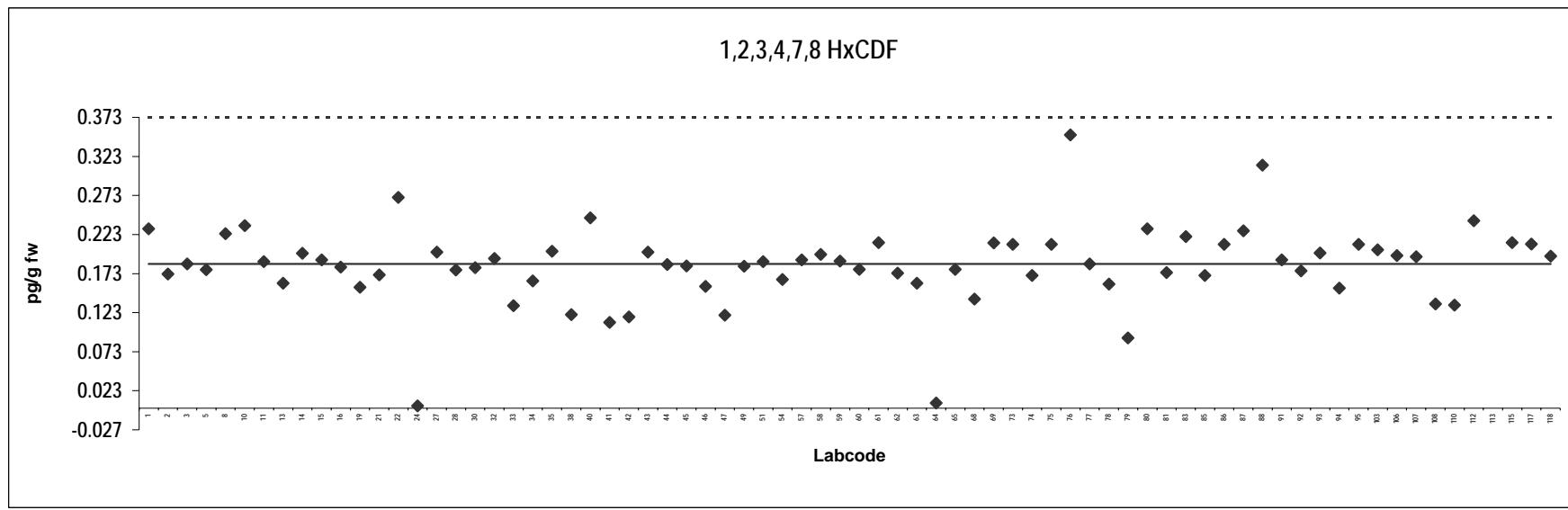
**Herring**  
Congener: 1,2,3,4,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.23		73	0.21	
2	0.17		74	0.17	
3	0.18		75	0.21	
5	0.18		76	0.35	
8	0.22		77	0.18	
10	0.23		78	0.16	
11	0.19		79	0.090	
13	0.16		80	0.23	
14	0.20		81	0.17	
15	0.19		83	0.22	
16	0.18		85	0.17	
19	0.16		86	0.21	
21	0.17		87	0.23	
22	0.27	ND	88	0.31	
24	0.0030	ND	91	0.19	
27	0.20		92	0.18	
28	0.18		93	0.20	
30	0.18		94	0.15	
32	0.19		95	0.21	
33	0.13		103	0.20	
34	0.16		106	0.20	
35	0.20		107	0.19	
38	0.12		108	0.13	
40	0.24		110	0.13	
41	0.11		112	0.24	
42	0.12		113	0.41	
43	0.20		115	0.21	
44	0.18		117	0.21	
45	0.18		118	0.19	
46	0.16				
47	0.12				
49	0.18				
51	0.19				
54	0.16				
57	0.19				
58	0.20				
59	0.19				
60	0.18				
61	0.21				
62	0.17				
63	0.16				
64	0.0070				
65	0.18				
68	0.14				
69	0.21				

Outlier

**Consensus statistics**

Consensus median, pg/g	0.18
Median all values pg/g	0.19
Consensus mean, pg/g	0.18
Standard deviation, pg/g	0.051
Relative standard deviation, %	28
No. of values reported	74
No. of values removed	1
No. of reported non-detects	2

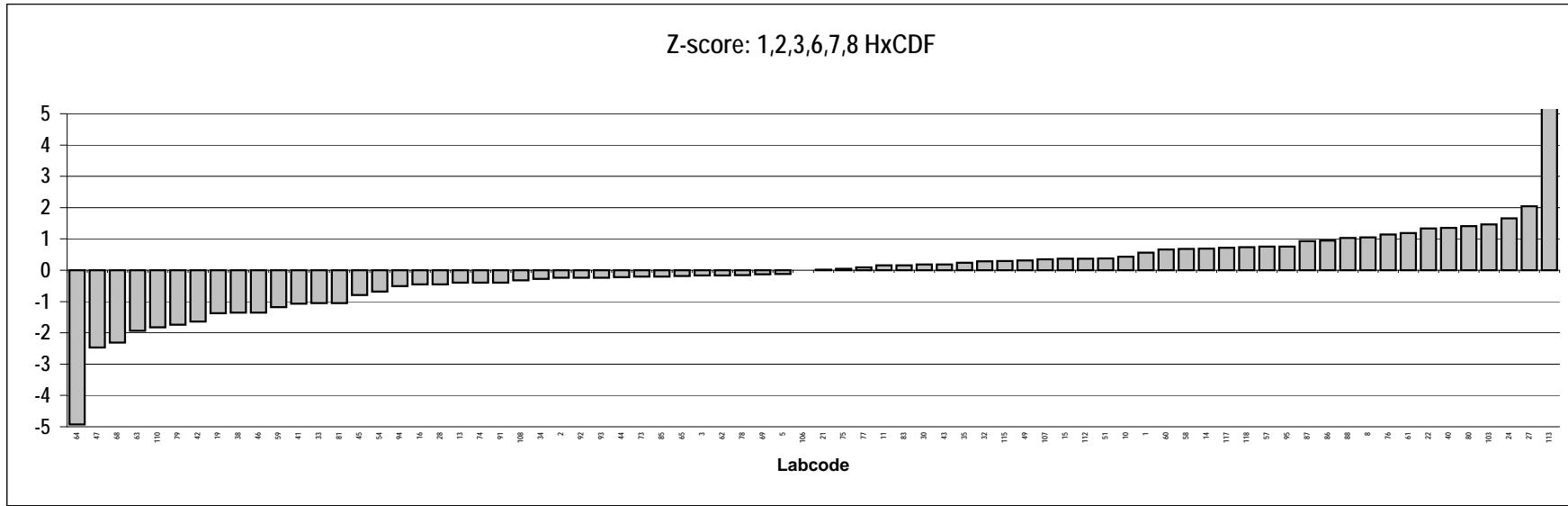
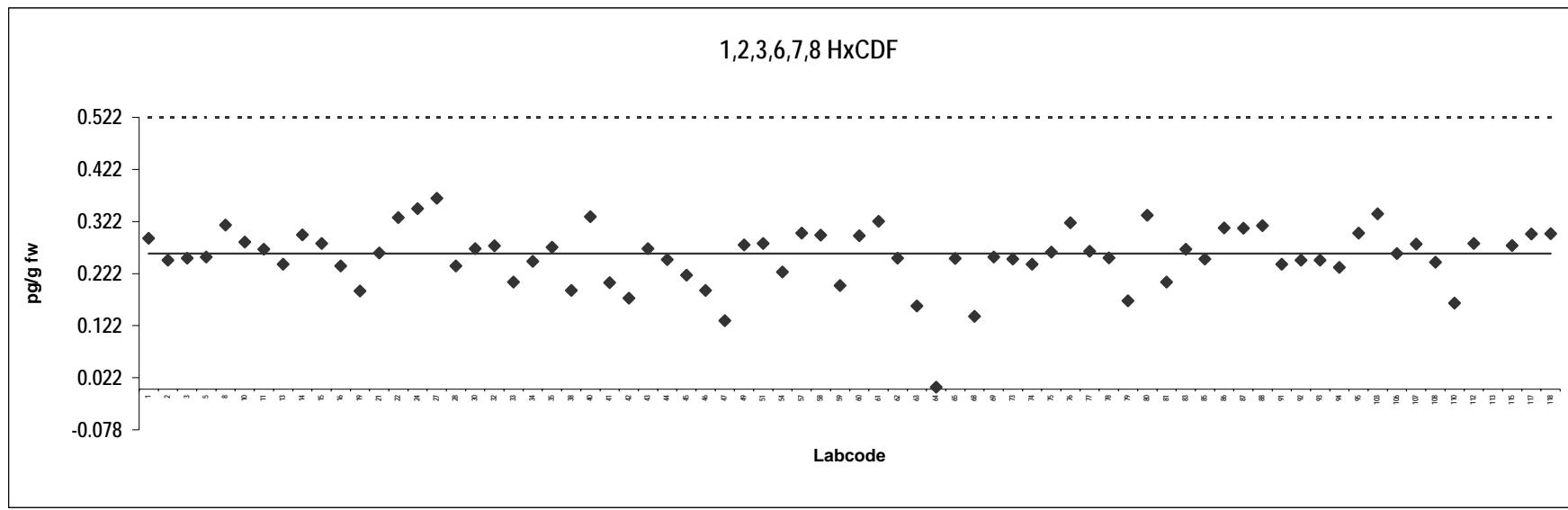


**Herring**  
Congener: 1,2,3,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.29		73	0.25	
2	0.25		74	0.24	
3	0.25		75	0.26	
5	0.25		76	0.32	
8	0.32		77	0.27	
10	0.28		78	0.25	
11	0.27		79	0.17	
13	0.24		80	0.33	
14	0.30		81	0.21	
15	0.28		83	0.27	
16	0.24		85	0.25	
19	0.19		86	0.31	
21	0.26		87	0.31	
22	0.33		88	0.31	
24	0.35		91	0.24	
27	0.37		92	0.25	
28	0.24		93	0.25	
30	0.27		94	0.23	
32	0.28		95	0.30	
33	0.21		103	0.34	
34	0.25		106	0.26	
35	0.27		107	0.28	
38	0.19		108	0.24	
40	0.33		110	0.17	
41	0.21		112	0.28	
42	0.18		113	1.6	Outlier
43	0.27		115	0.28	
44	0.25		117	0.30	
45	0.22		118	0.30	
46	0.19				
47	0.13				
49	0.28				
51	0.28				
54	0.23				
57	0.30				
58	0.30				
59	0.20				
60	0.30				
61	0.32				
62	0.25				
63	0.16				
64	0.0040				
65	0.25				
68	0.14				
69	0.25				

**Consensus statistics**

Consensus median, pg/g	0.26
Median all values pg/g	0.26
Consensus mean, pg/g	0.26
Standard deviation, pg/g	0.057
Relative standard deviation, %	22
No. of values reported	74
No. of values removed	1
No. of reported non-detects	0

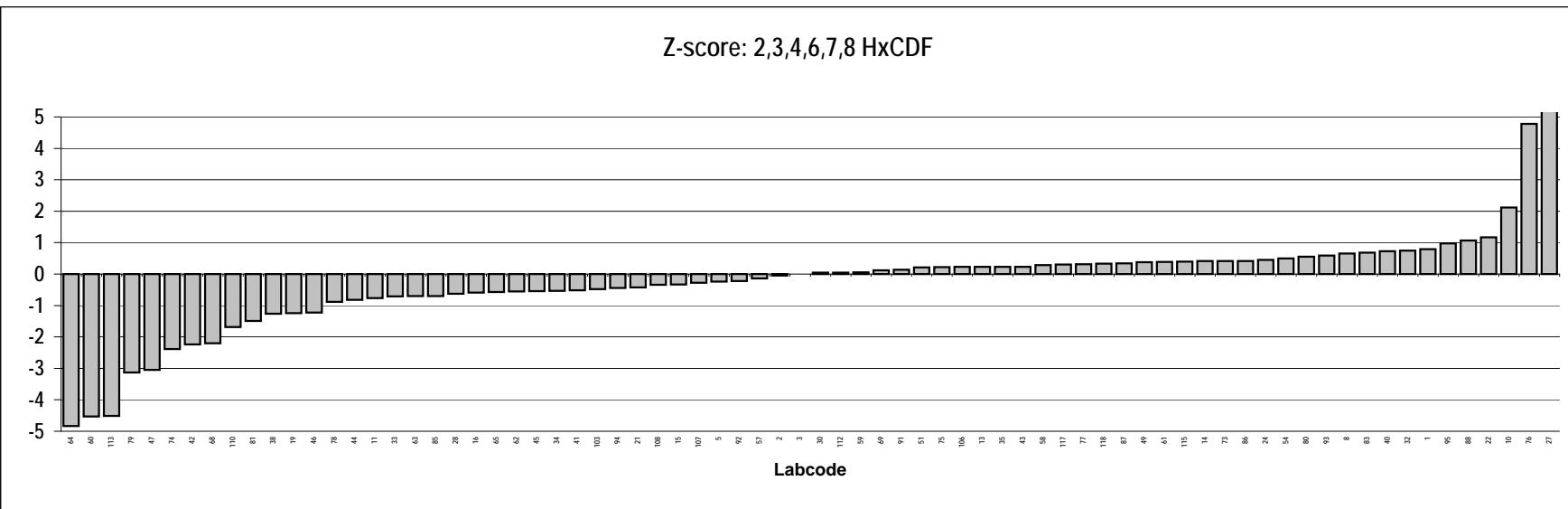
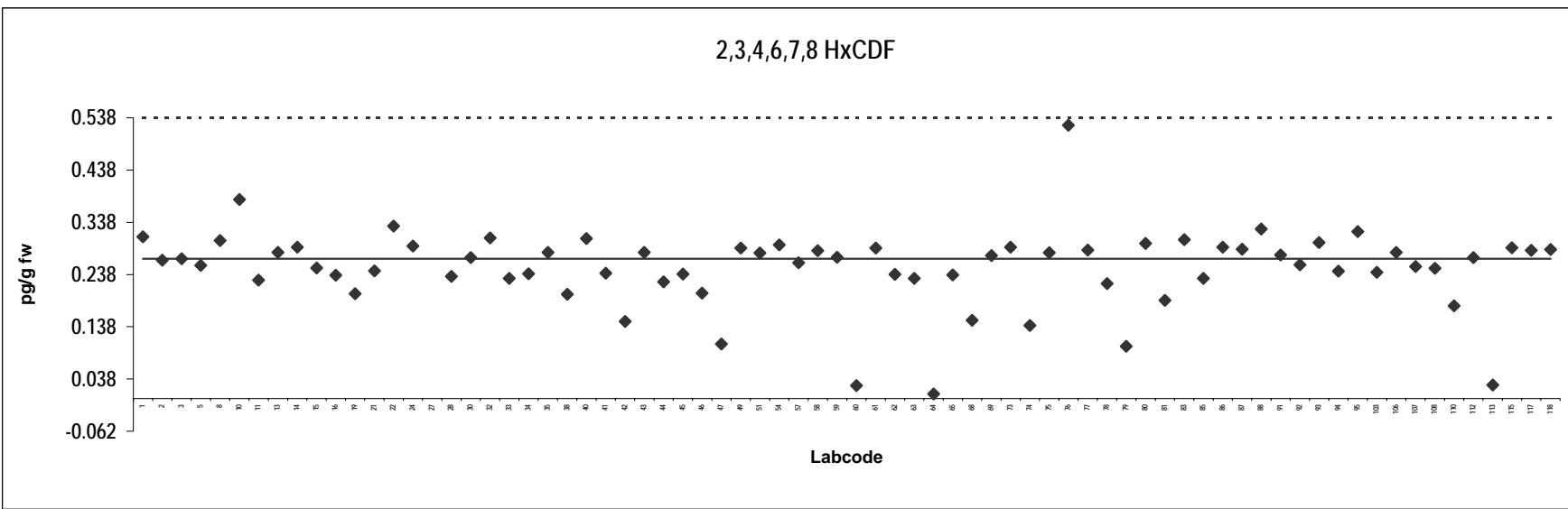


**Herring**  
Congener: 2,3,4,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.31		73	0.29	
2	0.27		74	0.14	
3	0.27		75	0.28	
5	0.25		76	0.52	
8	0.30		77	0.28	
10	0.38		78	0.22	
11	0.23		79	0.10	
13	0.28		80	0.30	
14	0.29		81	0.19	
15	0.25		83	0.30	
16	0.24		85	0.23	
19	0.20		86	0.29	
21	0.24		87	0.29	
22	0.33		88	0.32	
24	0.29		91	0.28	
27	0.92	Outlier	92	0.26	
28	0.23		93	0.30	
30	0.27		94	0.24	
32	0.31		95	0.32	
33	0.23		103	0.24	
34	0.24		106	0.28	
35	0.28		107	0.25	
38	0.20		108	0.25	
40	0.31		110	0.18	
41	0.24		112	0.27	
42	0.15		113	0.026	ND
43	0.28		115	0.29	
44	0.22		117	0.28	
45	0.24		118	0.29	
46	0.20				
47	0.10				
49	0.29				
51	0.28				
54	0.29				
57	0.26				
58	0.28				
59	0.27				
60	0.025	ND			
61	0.29				
62	0.24				
63	0.23				
64	0.0090				
65	0.24				
68	0.15				
69	0.27				

**Consensus statistics**

Consensus median, pg/g	0.27
Median all values pg/g	0.27
Consensus mean, pg/g	0.25
Standard deviation, pg/g	0.076
Relative standard deviation, %	30
No. of values reported	74
No. of values removed	1
No. of reported non-detects	2

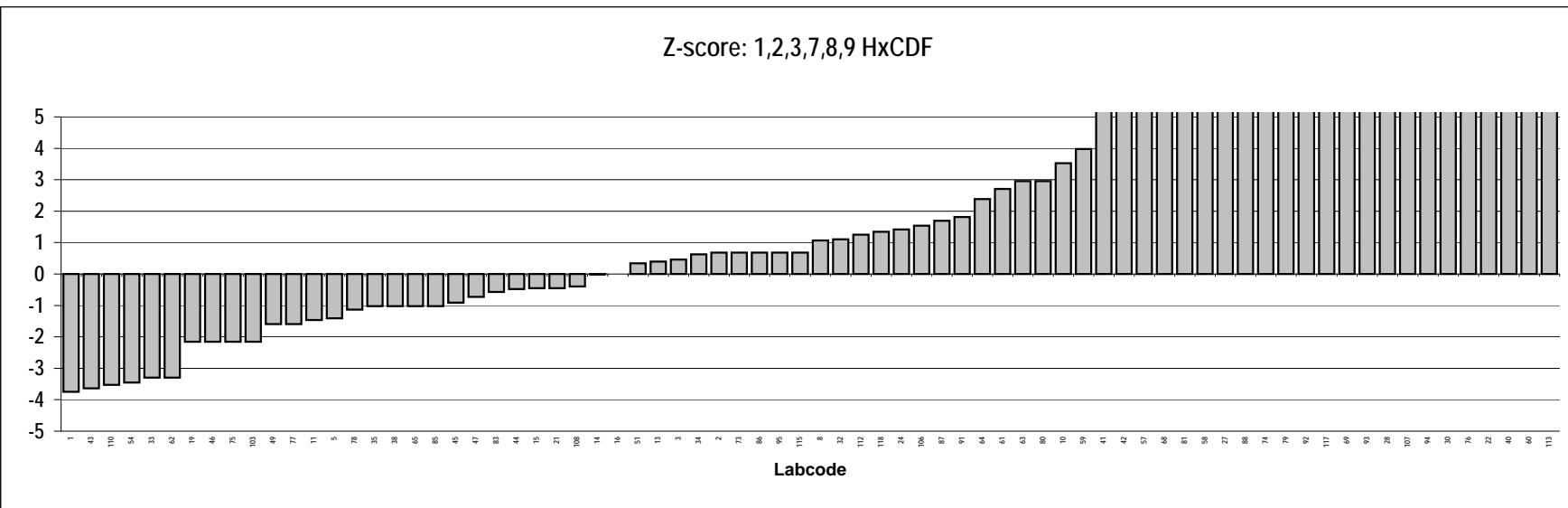
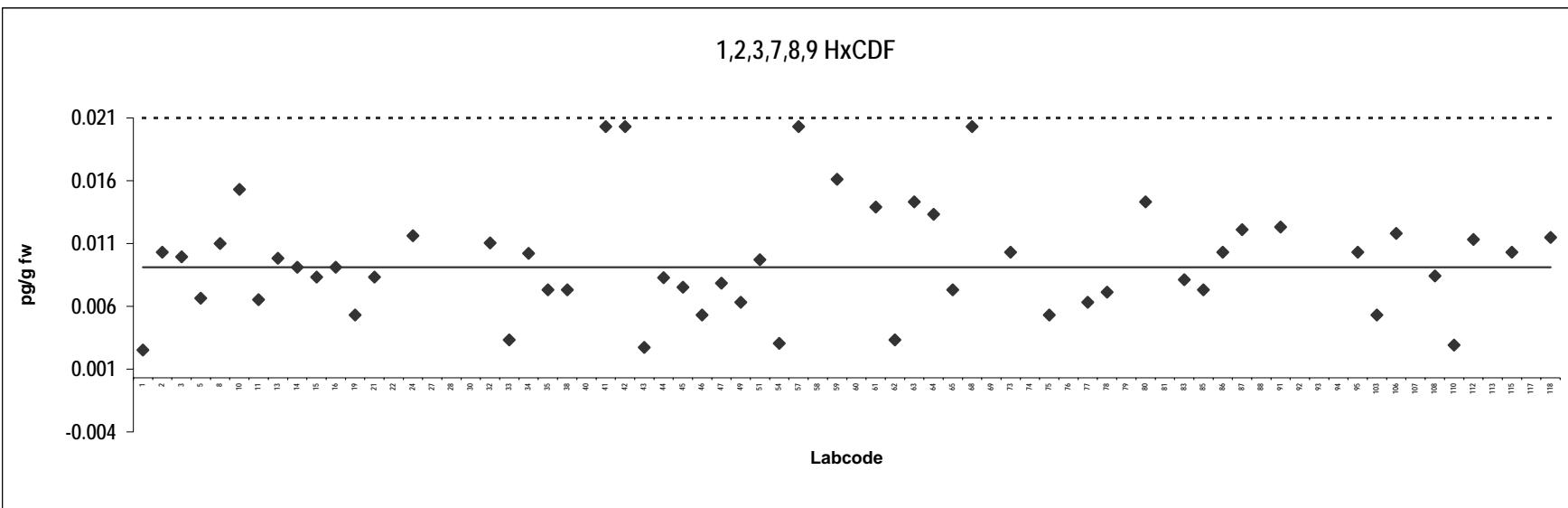


**Herring**  
Congener: 1,2,3,7,8,9 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.0022		73	0.010	ND
2	0.010		74	0.030	Outlier
3	0.0096		75	0.0050	
5	0.0063		76	0.061	Outlier,ND
8	0.011		77	0.0060	
10	0.015		78	0.0068	
11	0.0062		79	0.030	Outlier
13	0.0095		80	0.014	
14	0.0088		81	0.024	Outlier
15	0.0080		83	0.0078	
16	0.0088		85	0.0070	
19	0.0050	ND	86	0.010	ND
21	0.0080	ND	87	0.012	
22	0.070	Outlier,ND	88	0.030	Outlier
24	0.011		91	0.012	
27	0.028	Outlier	92	0.030	Outlier,ND
28	0.035	Outlier,ND	93	0.033	Outlier,ND
30	0.053	Outlier,ND	94	0.050	Outlier,ND
32	0.011	ND	95	0.010	ND
33	0.0030	ND	103	0.0050	
34	0.0099		106	0.011	
35	0.0070		107	0.048	Outlier,ND
38	0.0070	ND	108	0.0081	ND
40	0.076	Outlier,ND	110	0.0026	ND
41	0.020	ND	112	0.011	
42	0.020	ND	113	0.37	Outlier
43	0.0024	ND	115	0.010	
44	0.0080		117	0.031	Outlier
45	0.0072	ND	118	0.011	
46	0.0050	ND			
47	0.0075				
49	0.0060				
51	0.0094				
54	0.0027				
57	0.020	ND			
58	0.025	Outlier,ND			
59	0.016				
60	0.35	Outlier			
61	0.014				
62	0.0030				
63	0.014	ND			
64	0.013	ND			
65	0.0070				
68	0.020	ND			
69	0.032	Outlier,ND			

**Consensus statistics**

Consensus median, pg/g	0.0088
Median all values pg/g	0.010
Consensus mean, pg/g	0.009
Standard deviation, pg/g	0.0044
Relative standard deviation, %	48
No. of values reported	74
No. of values removed	19
No. of reported non-detects	30

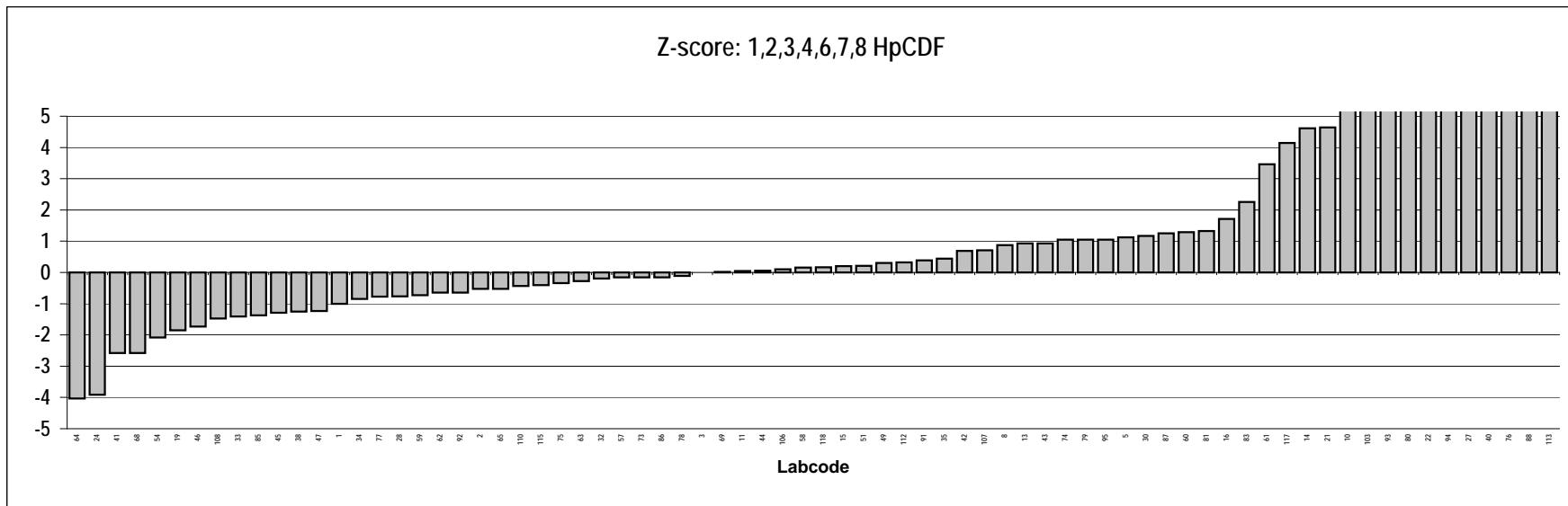
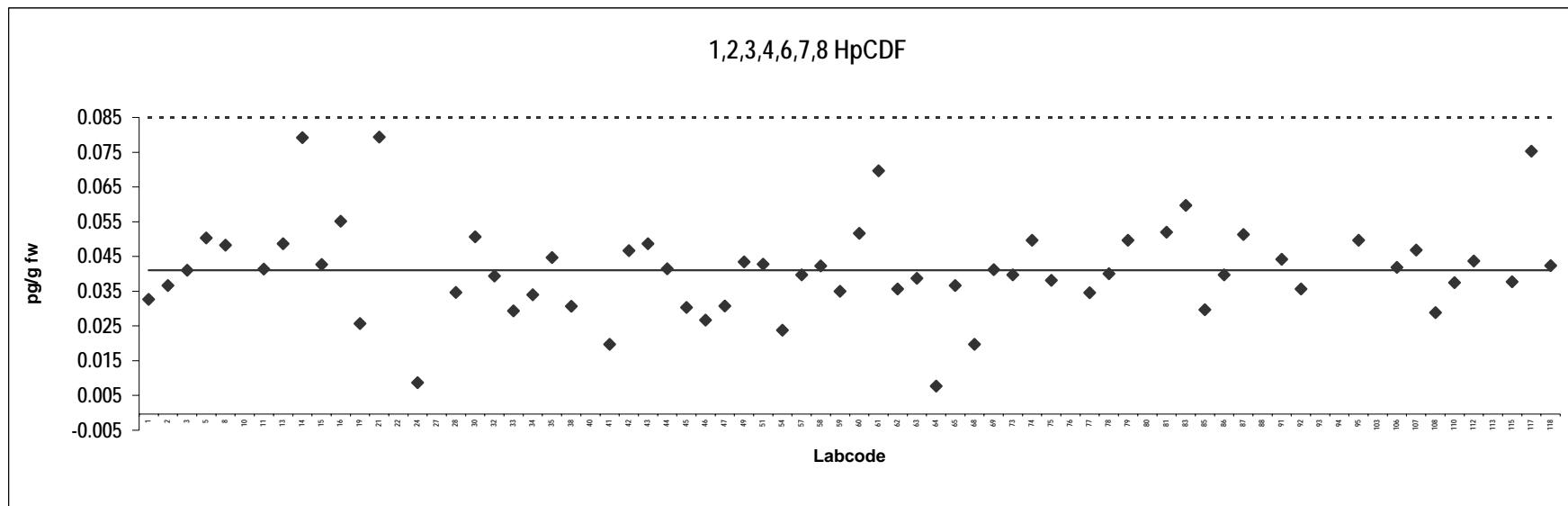


**Herring**  
Congener: 1,2,3,4,6,7,8 HpCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.033		73	0.040	
2	0.037		74	0.050	
3	0.041		75	0.038	
5	0.051		76	0.50	
8	0.049		77	0.035	
10	0.10	Outlier	78	0.040	
11	0.042		79	0.050	
13	0.049		80	0.12	Outlier
14	0.079		81	0.052	
15	0.043		83	0.060	
16	0.056		85	0.030	
19	0.026		86	0.040	
21	0.080		87	0.052	
22	0.15	Outlier,ND	88	0.64	Outlier
24	0.0090	ND	91	0.045	
27	0.16	Outlier	92	0.036	
28	0.035	ND	93	0.10	Outlier
30	0.051		94	0.15	Outlier,ND
32	0.040		95	0.050	
33	0.030		103	0.10	Outlier
34	0.034		106	0.042	
35	0.045		107	0.047	
38	0.031		108	0.029	
40	0.21	Outlier,ND	110	0.038	
41	0.020	ND	112	0.044	
42	0.047		113	2.4	Outlier
43	0.049	ND	115	0.038	
44	0.042		117	0.076	
45	0.031		118	0.043	
46	0.027				
47	0.031				
49	0.044				
51	0.043				
54	0.024				
57	0.040				
58	0.043				
59	0.035				
60	0.052				
61	0.070				
62	0.036				
63	0.039				
64	0.0080	ND			
65	0.037				
68	0.020				
69	0.042				

**Consensus statistics**

Consensus median, pg/g	0.041
Median all values pg/g	0.043
Consensus mean, pg/g	0.041
Standard deviation, pg/g	0.014
Relative standard deviation, %	33
No. of values reported	74
No. of values removed	11
No. of reported non-detects	9

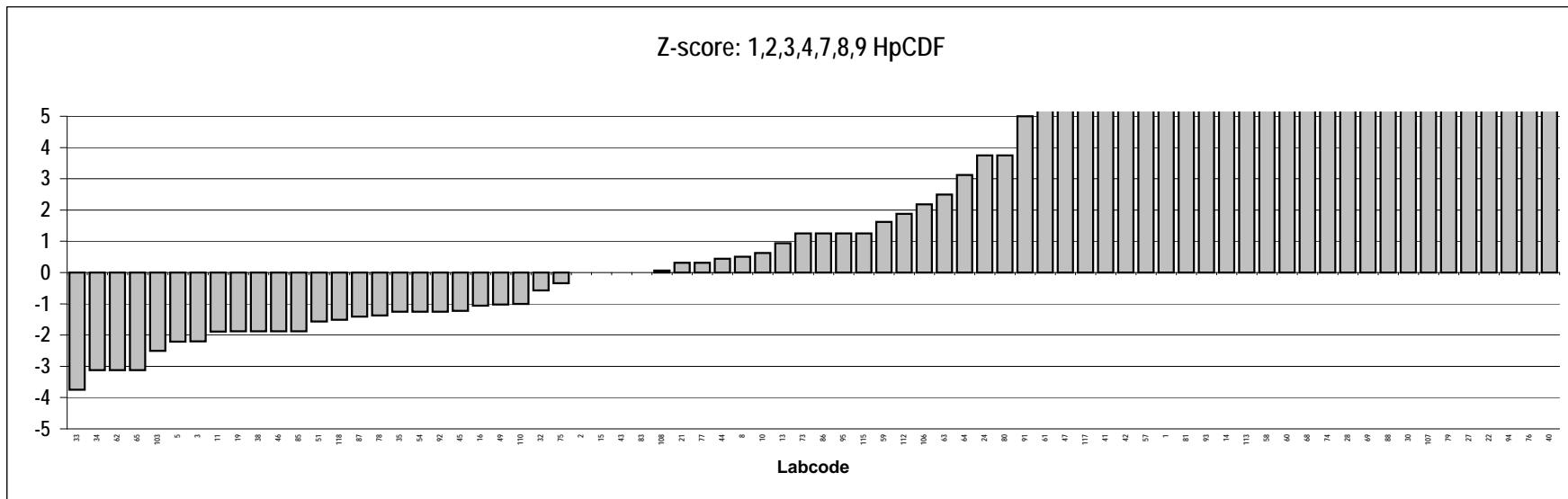
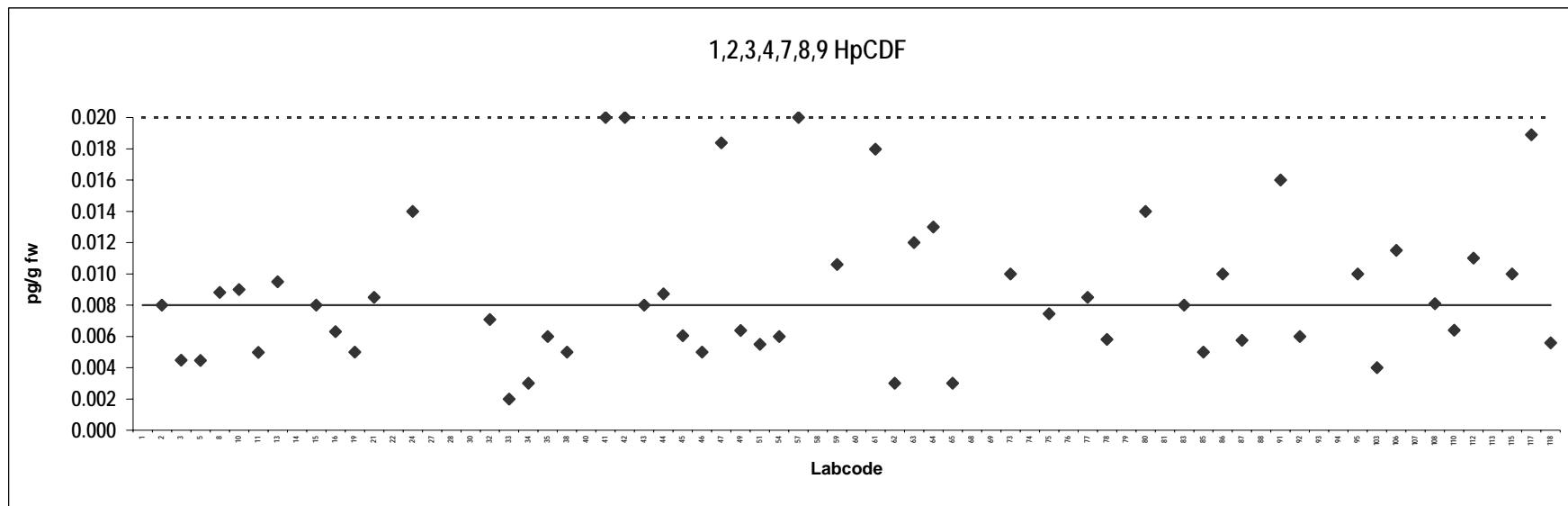


**Herring**  
**Congener: 1,2,3,4,7,8,9 HpCDF**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.021	Outlier	73	0.010	ND
2	0.0080		74	0.030	Outlier
3	0.0045		75	0.0074	
5	0.0045		76	0.20	Outlier,ND
8	0.0088	ND	77	0.0085	
10	0.0090	ND	78	0.0058	
11	0.0050		79	0.050	Outlier
13	0.0095		80	0.014	
14	0.023	Outlier,ND	81	0.022	Outlier
15	0.0080	ND	83	0.0080	
16	0.0063	ND	85	0.0050	
19	0.0050	ND	86	0.010	ND
21	0.0085	ND	87	0.0058	
22	0.078	Outlier,ND	88	0.045	Outlier
24	0.014	ND	91	0.016	ND
27	0.056	Outlier	92	0.0060	ND
28	0.035	Outlier,ND	93	0.023	Outlier,ND
30	0.048	Outlier,ND	94	0.15	Outlier,ND
32	0.0071		95	0.010	ND
33	0.0020	ND	103	0.0040	
34	0.0030	ND	106	0.011	
35	0.0060		107	0.049	Outlier,ND
38	0.0050	ND	108	0.0081	ND
40	0.21	Outlier,ND	110	0.0064	ND
41	0.020	ND	112	0.011	
42	0.020	ND	113	0.024	Outlier,ND
43	0.0080	ND	115	0.010	ND
44	0.0087		117	0.019	ND
45	0.0060		118	0.0056	
46	0.0050	ND			
47	0.018				
49	0.0064				
51	0.0055				
54	0.0060	ND			
57	0.020	ND			
58	0.025	Outlier,ND			
59	0.011				
60	0.025	Outlier,ND			
61	0.018				
62	0.0030				
63	0.012	ND			
64	0.013	ND			
65	0.0030				
68	0.030	Outlier			
69	0.039	Outlier,ND			

**Consensus statistics**

Consensus median, pg/g	0.0080
Median all values pg/g	0.010
Consensus mean, pg/g	0.0089
Standard deviation, pg/g	0.0047
Relative standard deviation, %	53
No. of values reported	74
No. of values removed	20
No. of reported non-detects	40

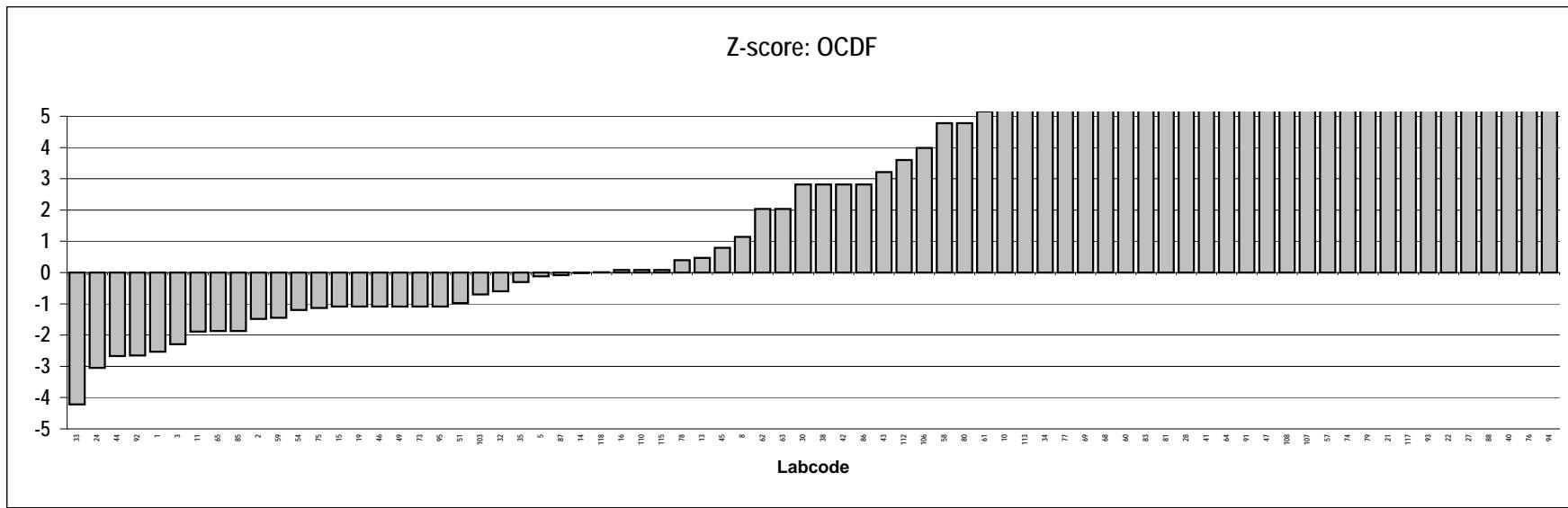
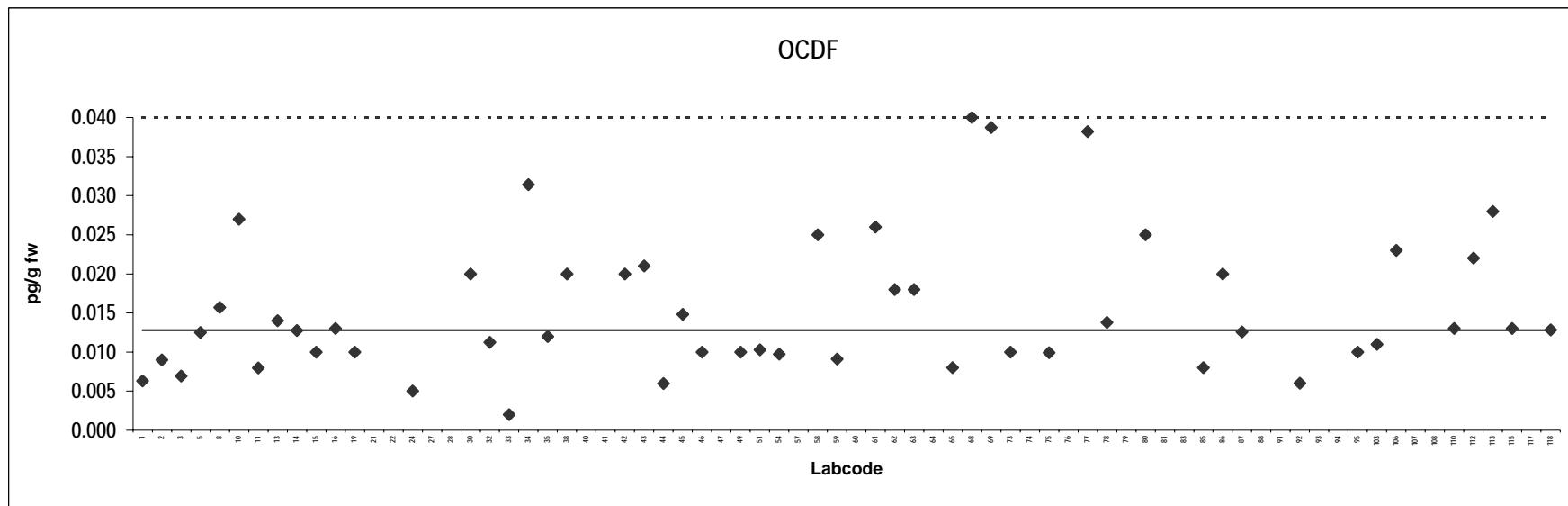


**Herring**  
Congener: OCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.0063		73	0.010	ND
2	0.0090		74	0.10	Outlier
3	0.0069		75	0.0099	
5	0.012		76	0.50	Outlier,ND
8	0.016	ND	77	0.038	
10	0.027	ND	78	0.014	
11	0.0080		79	0.10	Outlier
13	0.014	ND	80	0.025	
14	0.013		81	0.048	Outlier
15	0.010	ND	83	0.042	Outlier
16	0.013	ND	85	0.0080	
19	0.010	ND	86	0.020	ND
21	0.11	Outlier	87	0.013	
22	0.16	Outlier,ND	88	0.21	Outlier
24	0.0050	ND	91	0.058	Outlier,ND
27	0.20	Outlier	92	0.0060	
28	0.050	Outlier,ND	93	0.15	Outlier
30	0.020	ND	94	2.0	Outlier,ND
32	0.011	ND	95	0.010	
33	0.0020	ND	103	0.011	
34	0.031		106	0.023	
35	0.012	ND	107	0.080	Outlier,ND
38	0.020	ND	108	0.066	Outlier
40	0.34	Outlier,ND	110	0.013	ND
41	0.050	Outlier,ND	112	0.022	
42	0.020	ND	113	0.028	ND
43	0.021	ND	115	0.013	
44	0.0060		117	0.11	Outlier
45	0.015		118	0.013	
46	0.010	ND			
47	0.062	Outlier			
49	0.010	ND			
51	0.010				
54	0.0097				
57	0.10	Outlier,ND			
58	0.025	ND			
59	0.0091				
60	0.041	Outlier			
61	0.026				
62	0.018				
63	0.018	ND			
64	0.057	Outlier			
65	0.0080				
68	0.040				
69	0.039	ND			

**Consensus statistics**

Consensus median, pg/g	0.013
Median all values pg/g	0.020
Consensus mean, pg/g	0.016
Standard deviation, pg/g	0.0088
Relative standard deviation, %	57
No. of values reported	74
No. of values removed	22
No. of reported non-detects	32

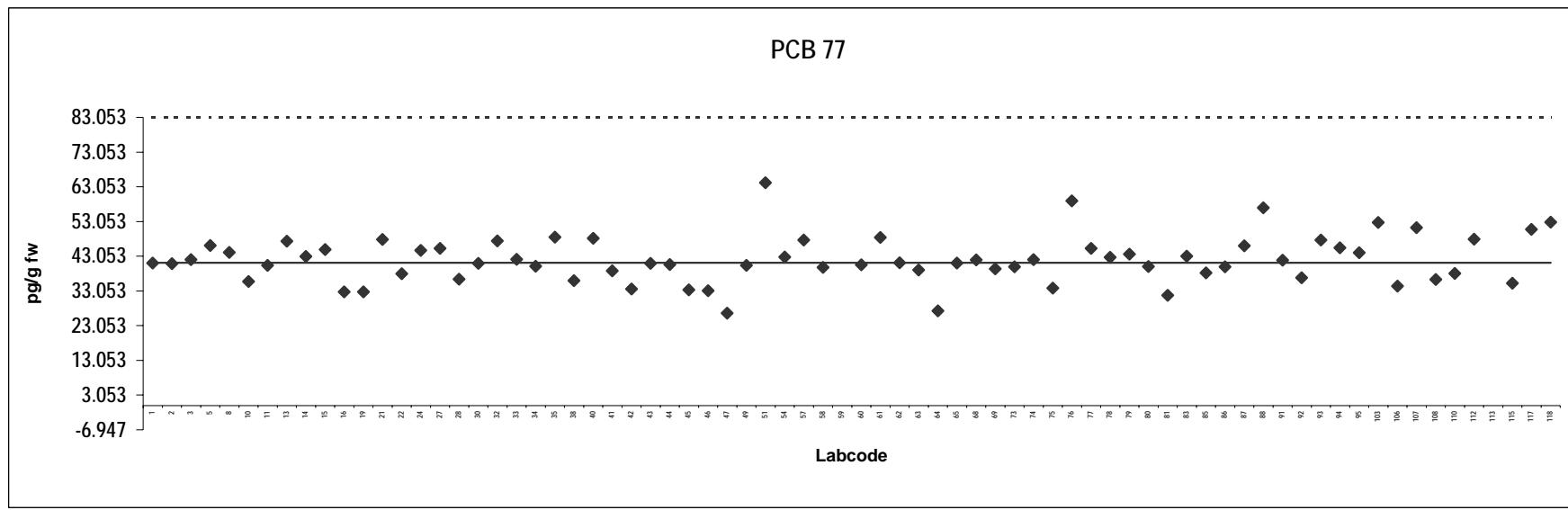


**Herring**  
Congener: PCB 77

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	41		73	40	
2	41		74	42	
3	42		75	34	
5	46		76	59	
8	44		77	45	
10	36		78	43	
11	40		79	44	
13	47		80	40	
14	43		81	32	
15	45		83	43	
16	33		85	38	
19	33		86	40	
21	48		87	46	
22	38		88	57	
24	45		91	42	
27	45		92	37	
28	36		93	48	
30	41		94	45	
32	47		95	44	
33	42		103	53	
34	40		106	34	
35	49		107	51	
38	36		108	36	
40	48		110	38	
41	39		112	48	
42	34		113	94	Outlier
43	41		115	35	
44	41		117	51	
45	33		118	53	
46	33				
47	27				
49	40				
51	64				
54	43				
57	48				
58	40				
59	405	Outlier			
60	41				
61	48				
62	41				
63	39				
64	27				
65	41				
68	42				
69	39				

**Consensus statistics**

Consensus median, pg/g	41
Median all values pg/g	42
Consensus mean, pg/g	42
Standard deviation, pg/g	6.7
Relative standard deviation, %	16
No. of values reported	74
No. of values removed	2
No. of reported non-detects	0

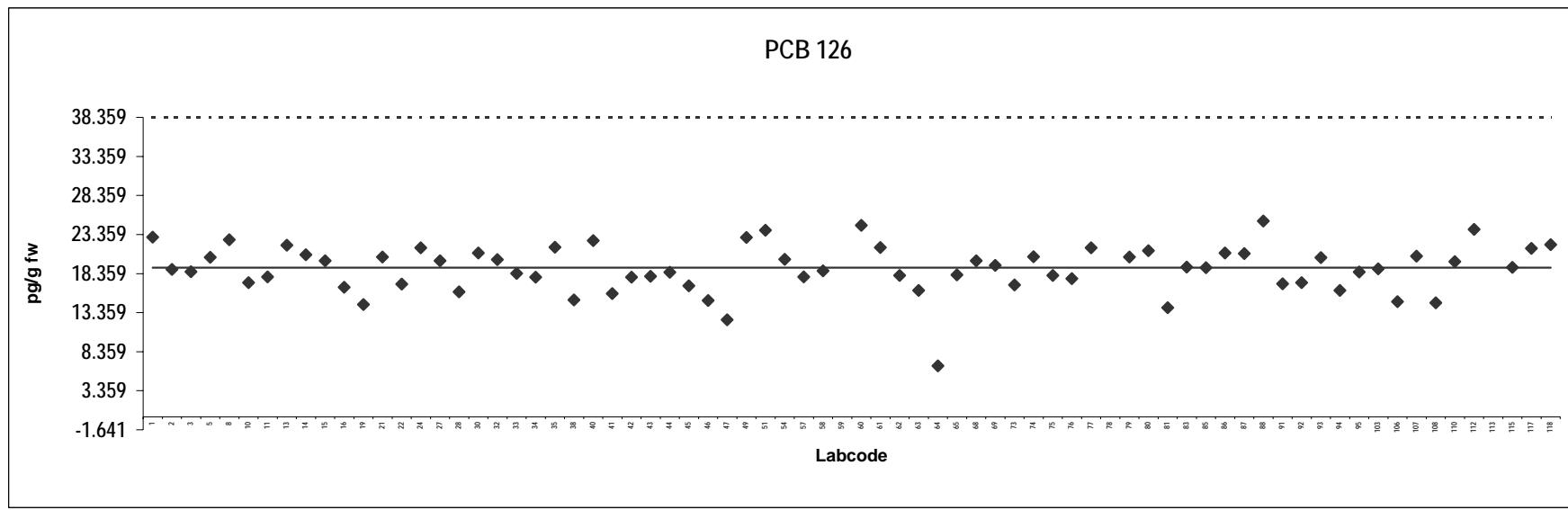


**Herring**  
Congener: PCB 126

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	23		73	17	
2	19		74	21	
3	19		75	18	
5	20		76	18	
8	23		77	22	
10	17		78	60	
11	18		79	20	
13	22		80	21	
14	21		81	14	
15	20		83	19	
16	17		85	19	
19	14		86	21	
21	20		87	21	
22	17		88	25	
24	22		91	17	
27	20		92	17	
28	16		93	20	
30	21		94	16	
32	20		95	19	
33	18		103	19	
34	18		106	15	
35	22		107	21	
38	15		108	15	
40	23		110	20	
41	16		112	24	
42	18		113	50	
43	18		115	19	
44	19		117	22	
45	17		118	22	
46	15				
47	12				
49	23				
51	24				
54	20				
57	18				
58	19				
59	115	Outlier			
60	25				
61	22				
62	18				
63	16				
64	6.6				
65	18				
68	20				
69	19				

**Consensus statistics**

Consensus median, pg/g	19
Median all values pg/g	19
Consensus mean, pg/g	19
Standard deviation, pg/g	3.1
Relative standard deviation, %	16
No. of values reported	74
No. of values removed	3
No. of reported non-detects	0

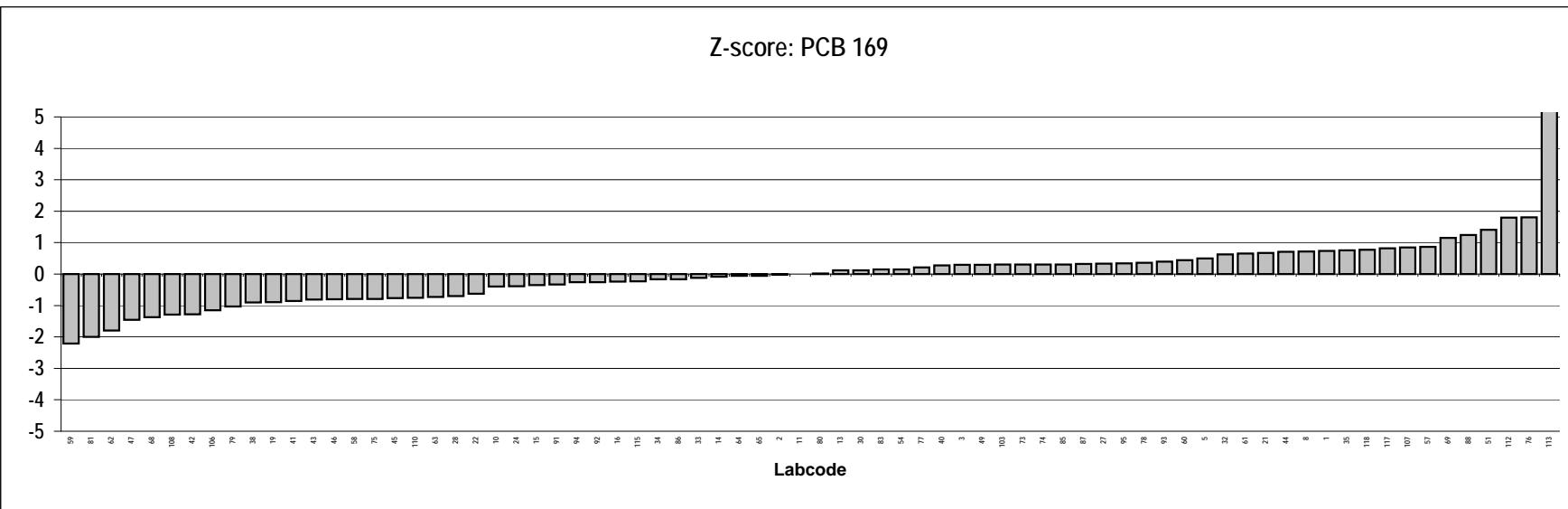
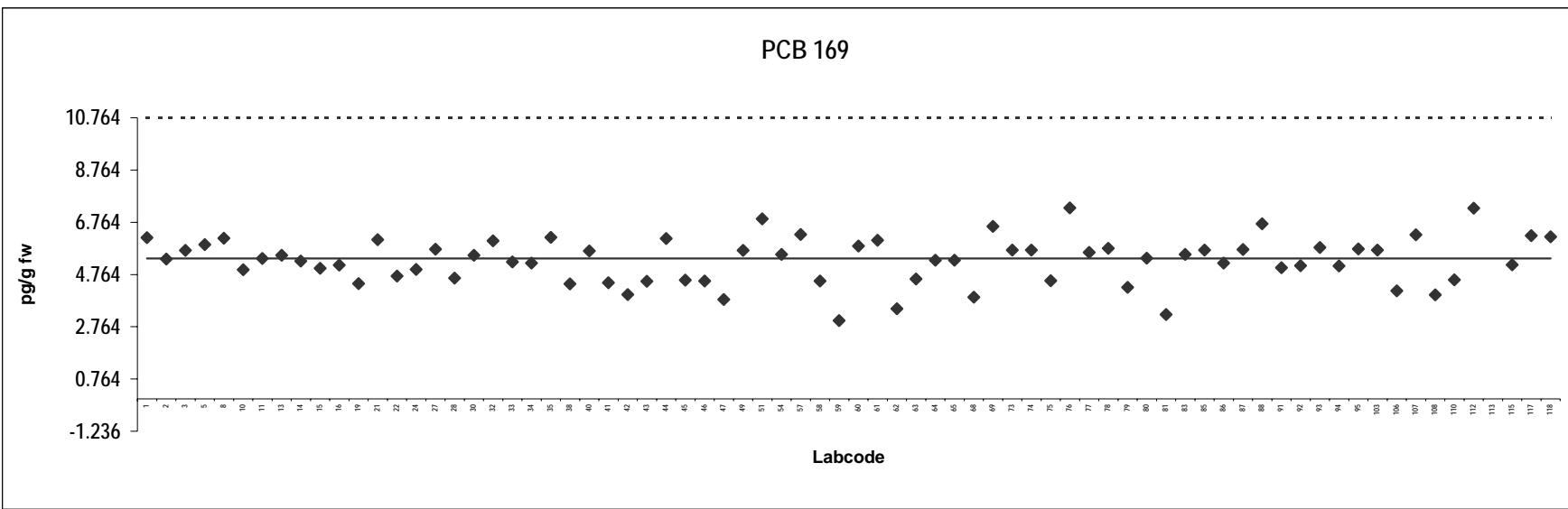


**Herring**  
Congener: PCB 169

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	6.2		73	5.7	
2	5.4		74	5.7	
3	5.7		75	4.5	
5	5.9		76	7.3	
8	6.2		77	5.6	
10	5.0		78	5.8	
11	5.4		79	4.3	
13	5.5		80	5.4	
14	5.3		81	3.2	
15	5.0		83	5.5	
16	5.1		85	5.7	
19	4.4		86	5.2	
21	6.1		87	5.7	
22	4.7		88	6.7	
24	5.0		91	5.0	
27	5.7		92	5.1	
28	4.6		93	5.8	
30	5.5		94	5.1	
32	6.0		95	5.7	
33	5.2		103	5.7	
34	5.2		106	4.1	
35	6.2		107	6.3	
38	4.4		108	4.0	
40	5.7		110	4.6	
41	4.5		112	7.3	
42	4.0		113	17	Outlier
43	4.5		115	5.1	
44	6.1		117	6.3	
45	4.6		118	6.2	
46	4.5				
47	3.8				
49	5.7				
51	6.9				
54	5.5				
57	6.3				
58	4.5				
59	3.0	ND			
60	5.9				
61	6.1				
62	3.4				
63	4.6				
64	5.3				
65	5.3				
68	3.9				
69	6.6				

**Consensus statistics**

Consensus median, pg/g	5.4
Median all values pg/g	5.4
Consensus mean, pg/g	5.3
Standard deviation, pg/g	0.89
Relative standard deviation, %	17
No. of values reported	74
No. of values removed	1
No. of reported non-detects	1

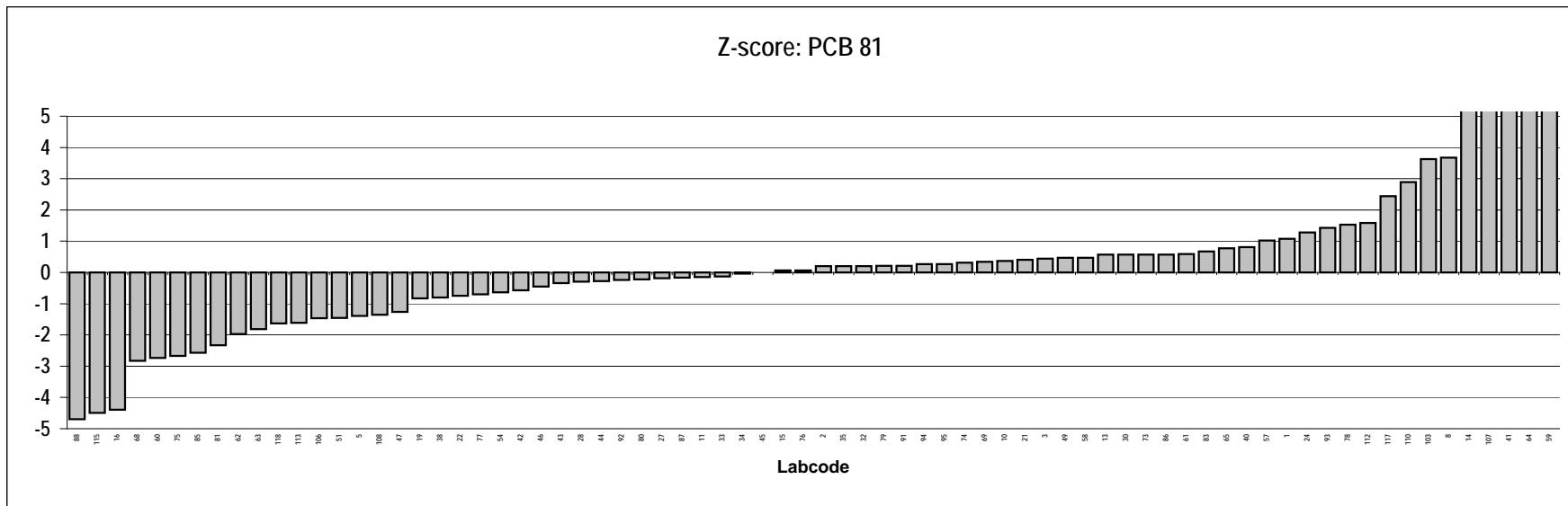
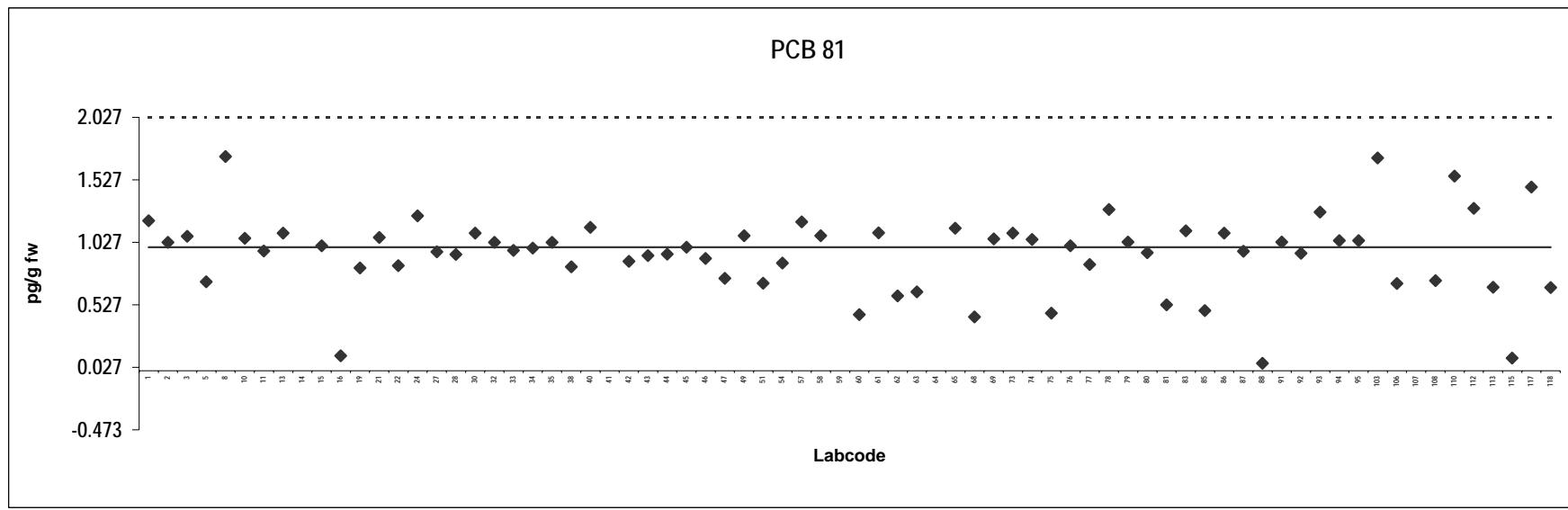


**Herring**  
Congener: PCB 81

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.2		73	1.1	
2	1.0		74	1.1	
3	1.1		75	0.46	
5	0.71		76	1.0	
8	1.7	ND	77	0.85	
10	1.1		78	1.3	
11	0.96		79	1.0	
13	1.1		80	0.94	
14	2.3	Outlier	81	0.53	
15	1.0		83	1.1	
16	0.12	ND	85	0.48	
19	0.82		86	1.1	
21	1.1		87	0.96	
22	0.84		88	0.060	
24	1.2		91	1.0	
27	0.95		92	0.94	
28	0.93		93	1.3	
30	1.1		94	1.0	
32	1.0		95	1.0	
33	0.96		103	1.7	
34	0.98		106	0.70	
35	1.0		107	3.6	Outlier
38	0.83		108	0.72	
40	1.1		110	1.6	
41	4.8	Outlier	112	1.3	
42	0.87		113	0.67	
43	0.92		115	0.10	
44	0.93		117	1.5	
45	0.99		118	0.67	
46	0.90				
47	0.74				
49	1.1				
51	0.70	ND			
54	0.86				
57	1.2				
58	1.1				
59	96	Outlier			
60	0.45				
61	1.1				
62	0.60				
63	0.63				
64	17	Outlier			
65	1.1				
68	0.43				
69	1.1				

**Consensus statistics**

Consensus median, pg/g	0.99
Median all values pg/g	1.0
Consensus mean, pg/g	0.94
Standard deviation, pg/g	0.32
Relative standard deviation, %	34
No. of values reported	74
No. of values removed	5
No. of reported non-detects	5

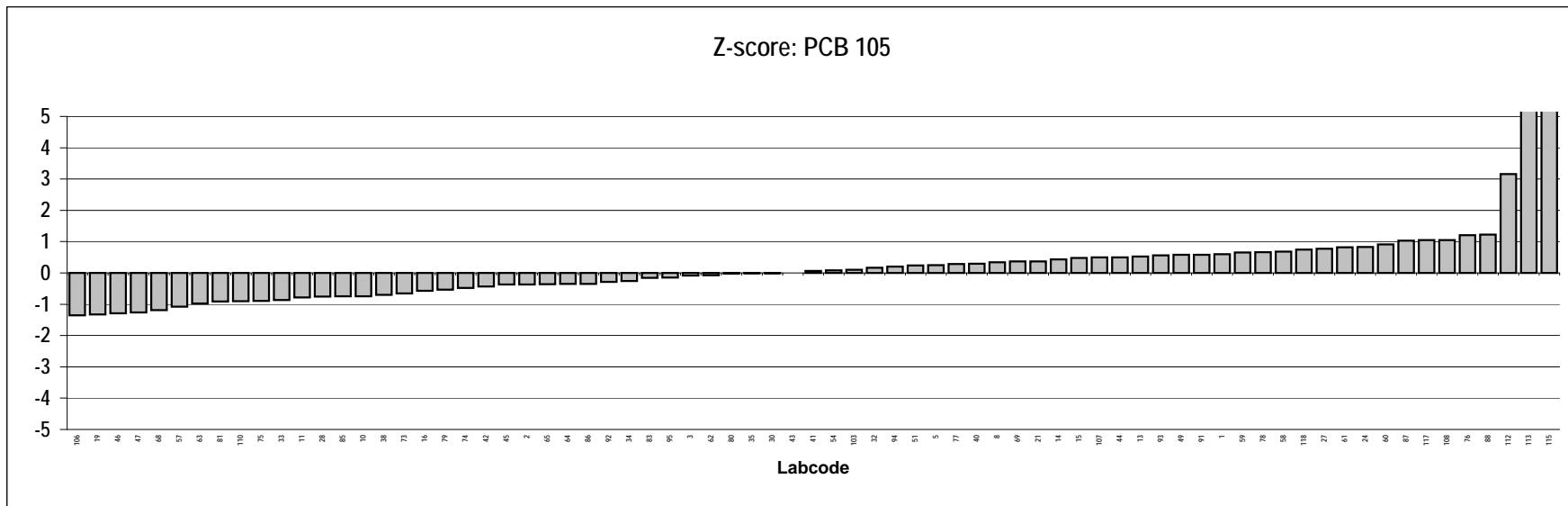
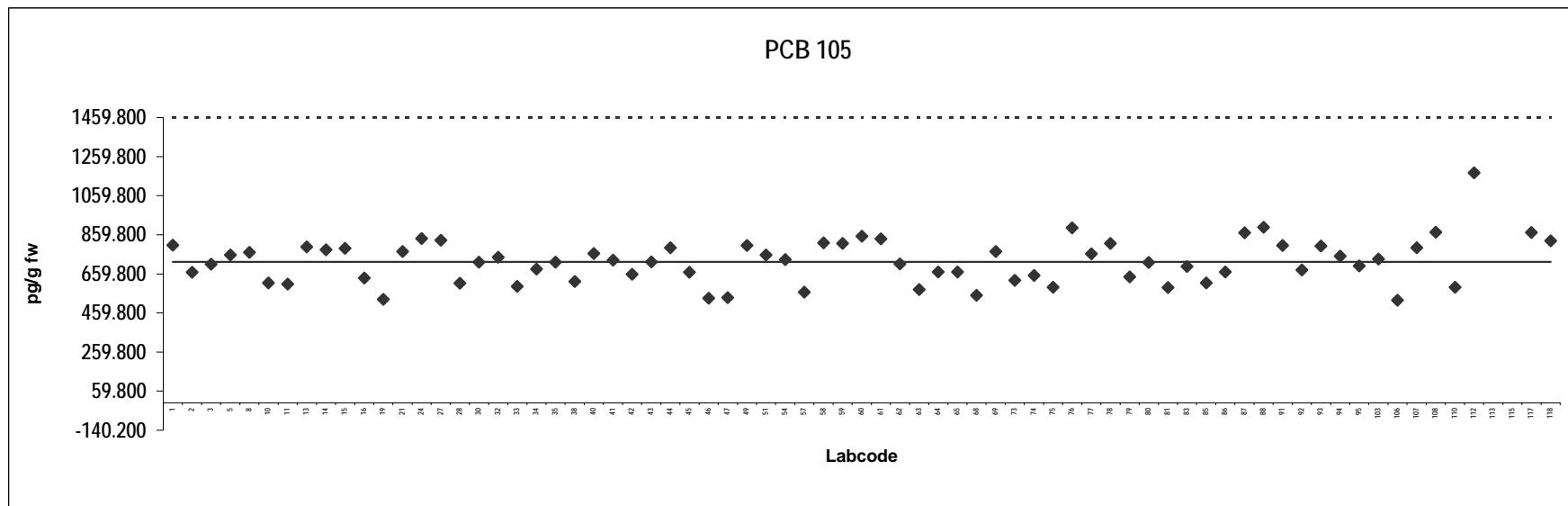


**Herring**  
Congener: PCB 105

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	807		74	652	
2	668		75	592	
3	709		76	895	
5	757		77	763	
8	770		78	816	
10	614		79	644	
11	608		80	718	
13	797		81	590	
14	783		83	698	
15	790		85	613	
16	639		86	670	
19	530		87	870	
21	775		88	898	
24	840		91	805	
27	832		92	680	
28	612		93	802	
30	720		94	750	
32	745		95	700	
33	596		103	736	
34	684		106	525	
35	719		107	793	
38	620		108	872	
40	764		110	591	
41	730		112	1177	
42	658		113	1646	
43	721		115	68820	Outlier
44	793		117	872	
45	668		118	828	
46	535				
47	539				
49	805				
51	756				
54	733				
57	566				
58	819				
59	815				
60	853				
61	840				
62	711				
63	580				
64	670				
65	670				
68	550				
69	774				
73	627				

**Consensus statistics**

Consensus median, pg/g	721
Median all values pg/g	730
Consensus mean, pg/g	723
Standard deviation, pg/g	113
Relative standard deviation, %	16
No. of values reported	73
No. of values removed	2
No. of reported non-detects	0

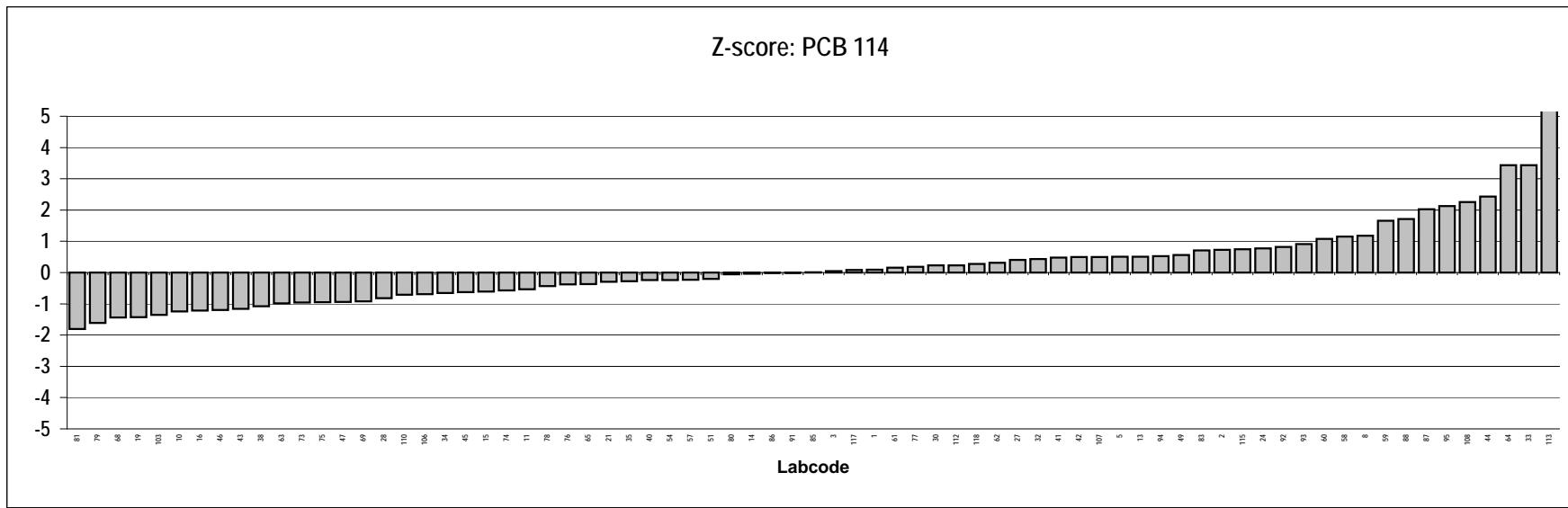
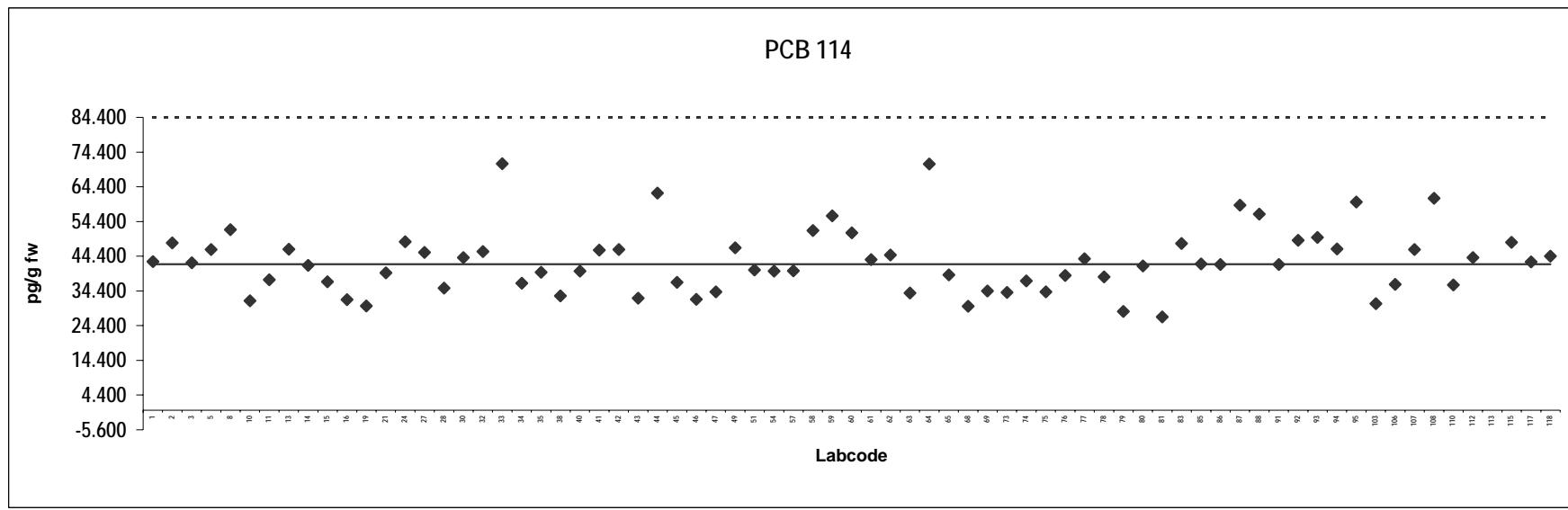


**Herring**  
Congener: PCB 114

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	43		74	37	
2	48		75	34	
3	43		76	39	
5	46		77	44	
8	52		78	38	
10	32		79	29	
11	38		80	42	
13	46		81	27	
14	42		83	48	
15	37		85	42	
16	32		86	42	
19	30		87	59	
21	40		88	57	
24	49		91	42	
27	46		92	49	
28	35		93	50	
30	44		94	47	
32	46		95	60	
33	71		103	31	
34	37		106	36	
35	40		107	46	
38	33		108	61	
40	40		110	36	
41	46		112	44	
42	46		113	97	Outlier
43	32		115	48	
44	63		117	43	
45	37		118	44	
46	32				
47	34				
49	47				
51	40				
54	40				
57	40				
58	52				
59	56				
60	51				
61	43				
62	45				
63	34				
64	71				
65	39				
68	30				
69	34				
73	34				

**Consensus statistics**

Consensus median, pg/g	42
Median all values pg/g	42
Consensus mean, pg/g	43
Standard deviation, pg/g	9.3
Relative standard deviation, %	22
No. of values reported	73
No. of values removed	1
No. of reported non-detects	0



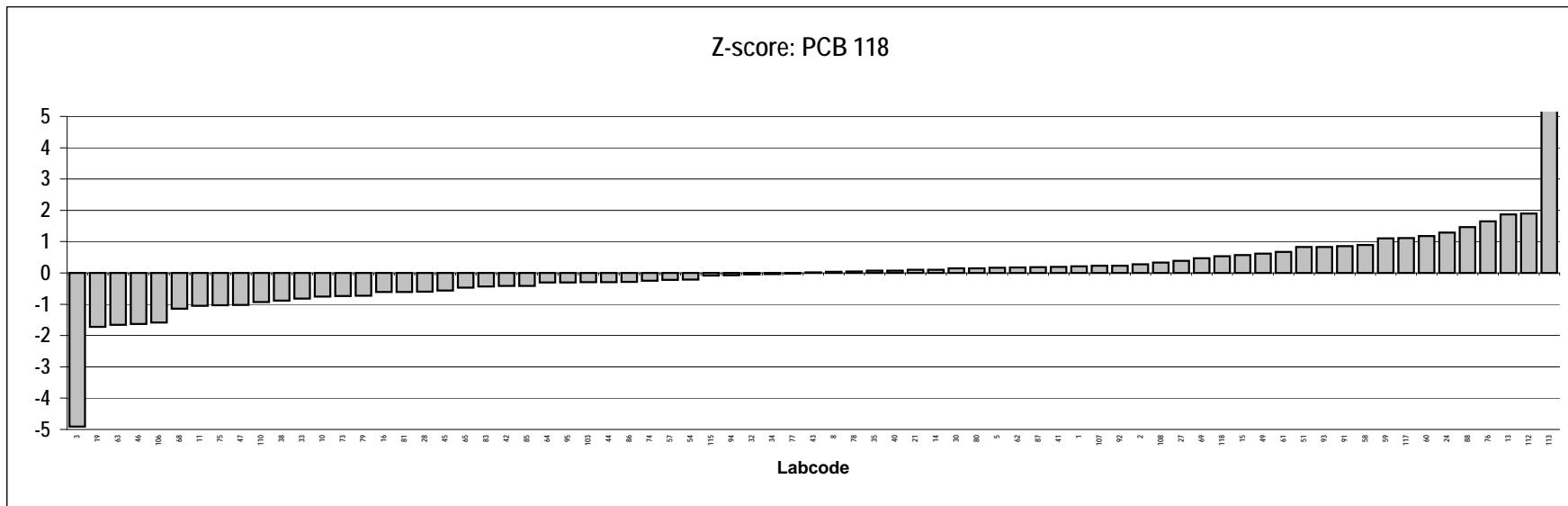
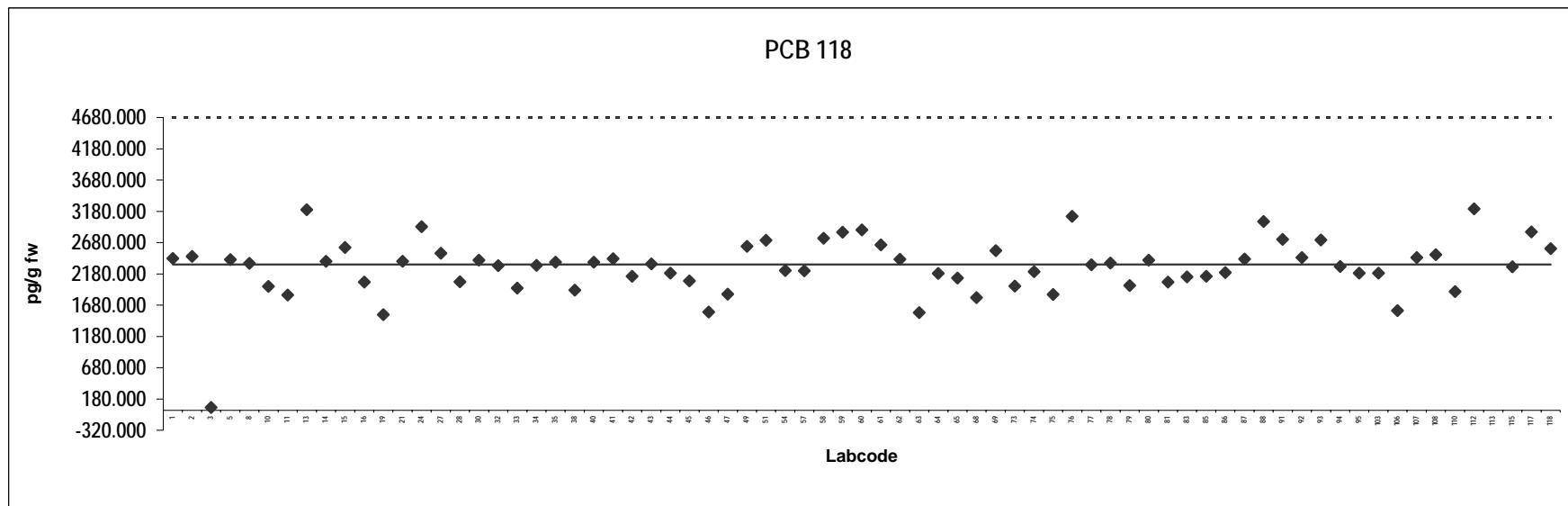
**Herring**  
Congener: PCB 118

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	2428		74	2215	
2	2461		75	1849	
3	43		76	3100	
5	2409		77	2323	
8	2349		78	2353	
10	1981		79	1993	
11	1842		80	2400	
13	3204		81	2050	
14	2381		83	2130	
15	2600		85	2140	
16	2050		86	2200	
19	1530		87	2419	
21	2381		88	3015	
24	2932		91	2730	
27	2510		92	2441	
28	2054		93	2720	
30	2400		94	2296	
32	2312		95	2190	
33	1951		103	2192	
34	2315		106	1593	
35	2365		107	2440	
38	1920		108	2487	
40	2366		110	1898	
41	2421		112	3218	
42	2140		113	5381	
43	2340		115	2295	
44	2193		117	2850	
45	2068		118	2581	
46	1570				
47	1856				
49	2620				
51	2719				
54	2232				
57	2229				
58	2750				
59	2847				
60	2882				
61	2645				
62	2415				
63	1559				
64	2188				
65	2112				
68	1800				
69	2552				
73	1986				

Outlier

**Consensus statistics**

Consensus median, pg/g	2332
Median all values pg/g	2340
Consensus mean, pg/g	2292
Standard deviation, pg/g	458
Relative standard deviation, %	20
No. of values reported	73
No. of values removed	1
No. of reported non-detects	0

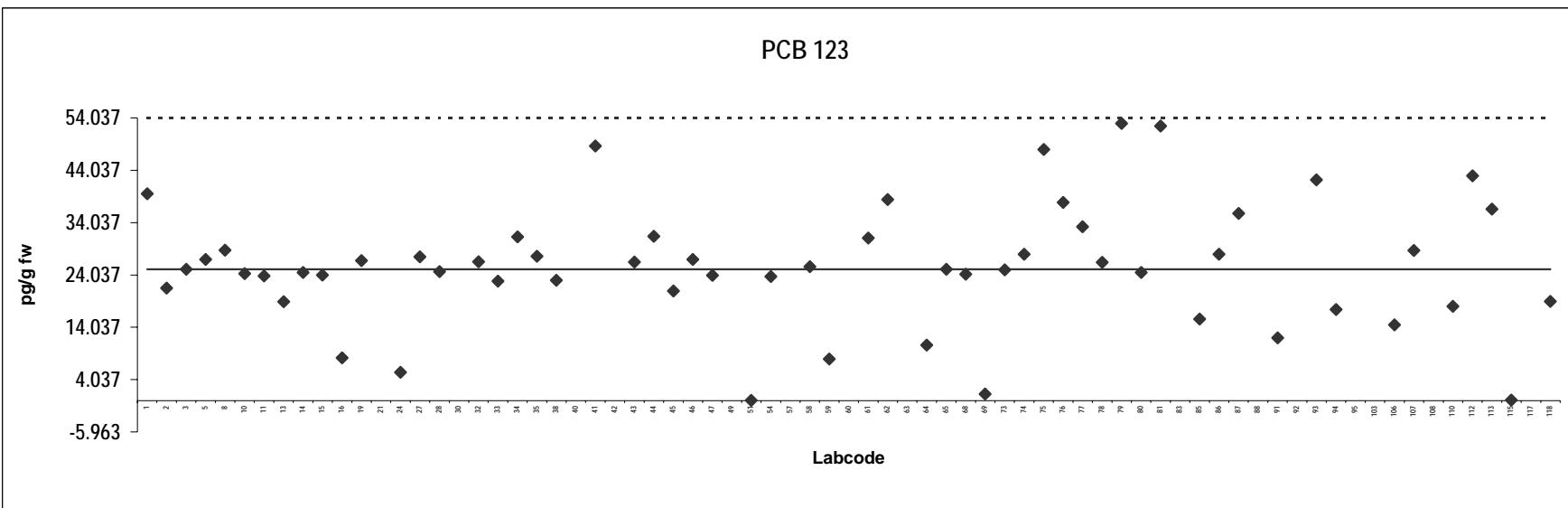


**Herring**  
Congener: PCB 123

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	40		74	28	
2	22		75	48	
3	25	ND	76	38	
5	27		77	33	
8	29		78	26	
10	24		79	53	
11	24		80	25	
13	19		81	53	
14	24		83	59	Outlier
15	24		85	16	
16	8.2	ND	86	28	
19	27		87	36	
21	88	Outlier	88	59	Outlier
24	5.4	ND	91	12	ND
27	28		92	61	Outlier
28	25		93	42	
30	78	Outlier	94	17	
32	27		95	60	Outlier
33	23		103	57	Outlier
34	31		106	15	
35	28		107	29	
38	23		108	507	Outlier
40	83	Outlier	110	18	
41	49		112	43	
42	114	Outlier	113	37	
43	27		115	0.10	ND
44	31		117	345	Outlier
45	21		118	19	
46	27				
47	24				
49	59	Outlier			
51	0.064	ND			
54	24				
57	62	Outlier			
58	26				
59	8.0	ND			
60	62	Outlier			
61	31				
62	38				
63	55	Outlier			
64	11				
65	25				
68	24				
69	1.3	ND			
73	25				

**Consensus statistics**

Consensus median, pg/g	25
Median all values pg/g	27
Consensus mean, pg/g	26
Standard deviation, pg/g	12
Relative standard deviation, %	46
No. of values reported	73
No. of values removed	15
No. of reported non-detects	8



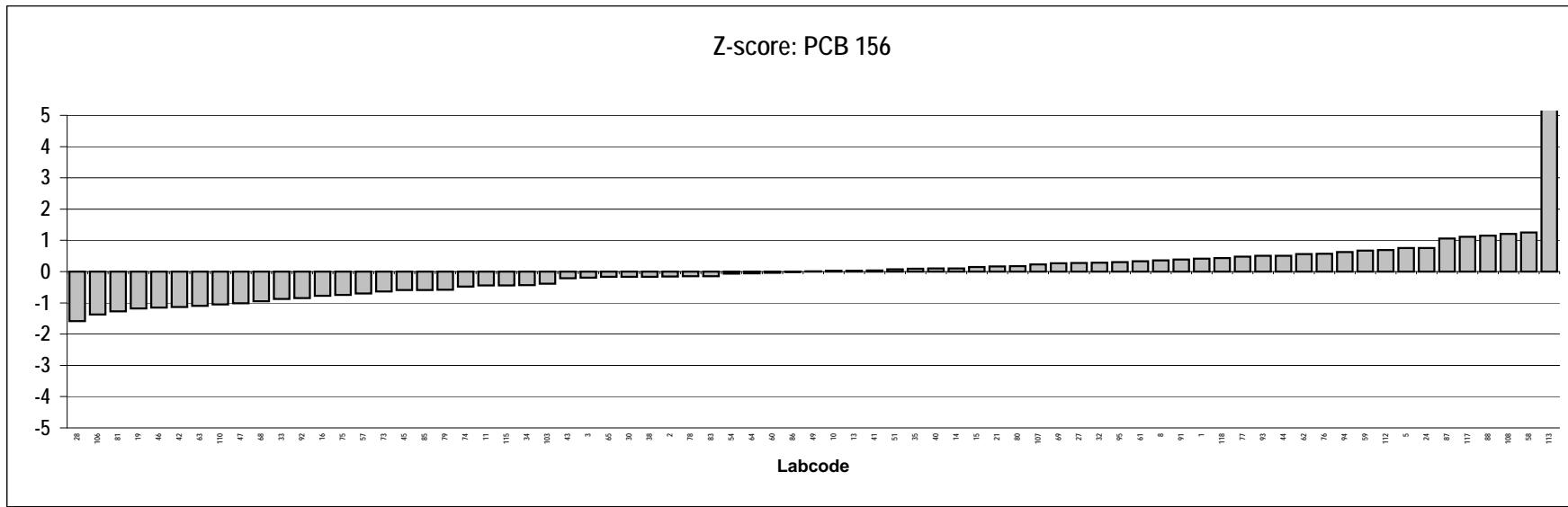
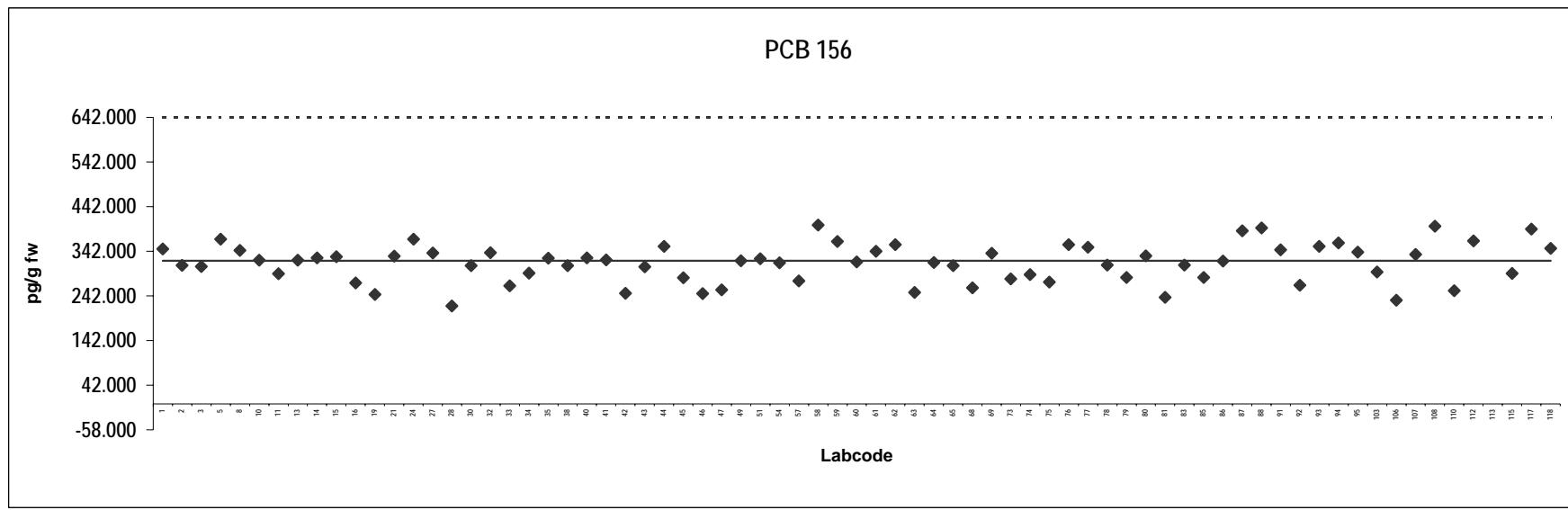
**Herring**  
Congener: PCB 156

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	347		74	290	
2	310		75	273	
3	308		76	357	
5	369		77	351	
8	344		78	311	
10	322		79	283	
11	292		80	332	
13	322		81	239	
14	327		83	311	
15	330		85	283	
16	271		86	320	
19	245		87	388	
21	331		88	394	
24	369		91	345	
27	338		92	266	
28	219		93	353	
30	310		94	361	
32	339		95	340	
33	264		103	296	
34	293		106	232	
35	326		107	335	
38	310		108	398	
40	327		110	253	
41	323		112	365	
42	248		113	769	
43	307		115	292	
44	353		117	392	
45	283		118	348	
46	247				
47	255				
49	321				
51	325				
54	316				
57	276				
58	401				
59	364				
60	318				
61	342				
62	357				
63	250				
64	317				
65	310				
68	260				
69	337				
73	280				

Outlier

**Consensus statistics**

Consensus median, pg/g	321
Median all values pg/g	321
Consensus mean, pg/g	315
Standard deviation, pg/g	43
Relative standard deviation, %	13
No. of values reported	73
No. of values removed	1
No. of reported non-detects	0

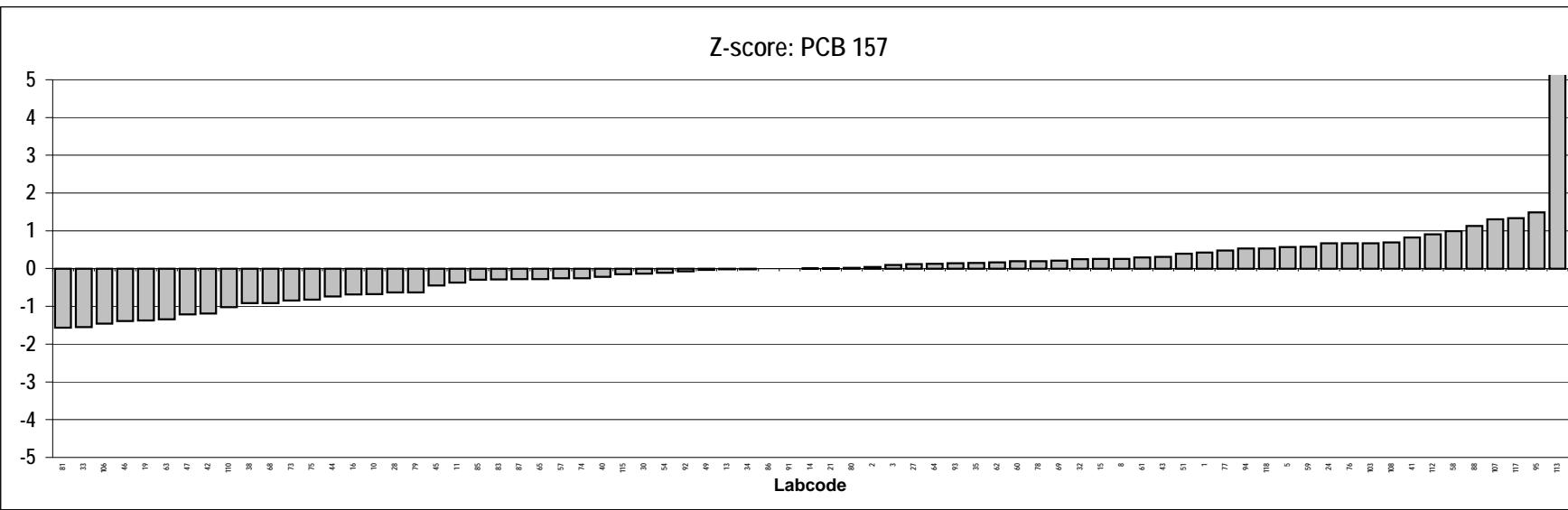
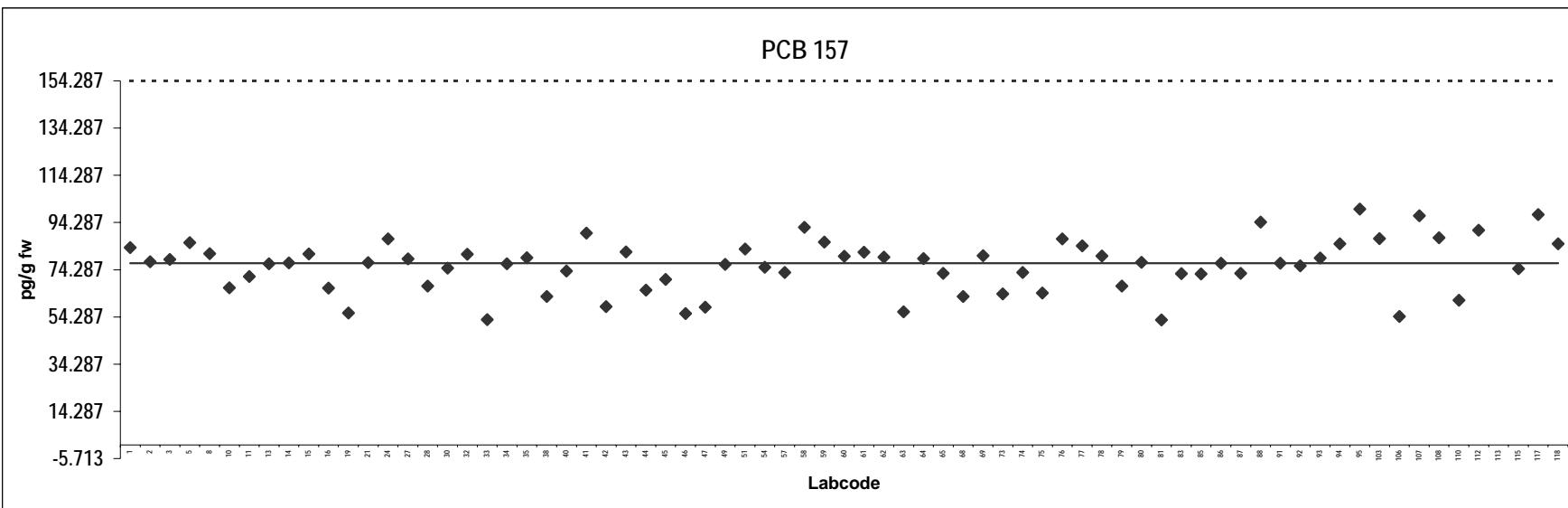


**Herring**  
Congener: PCB 157

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	84		74	73	
2	78		75	64	
3	79		76	87	
5	86		77	84	
8	81		78	80	
10	67		79	67	
11	71		80	77	
13	77		81	53	
14	77		83	73	
15	81		85	73	
16	67		86	77	
19	56		87	73	
21	77		88	95	
24	87		91	77	
27	79		92	76	
28	67		93	79	
30	75		94	85	
32	81		95	100	
33	53		103	87	
34	77		106	55	
35	79		107	97	
38	63		108	88	
40	74		110	61	
41	90		112	91	
42	59		113	175	Outlier
43	82		115	75	
44	66		117	98	
45	70		118	85	
46	56				
47	58				
49	77				
51	83				
54	75				
57	73				
58	92				
59	86				
60	80				
61	82				
62	80				
63	56				
64	79				
65	73				
68	63				
69	80				
73	64				

**Consensus statistics**

Consensus median, pg/g	77
Median all values pg/g	77
Consensus mean, pg/g	76
Standard deviation, pg/g	11
Relative standard deviation, %	14
No. of values reported	73
No. of values removed	1
No. of reported non-detects	0

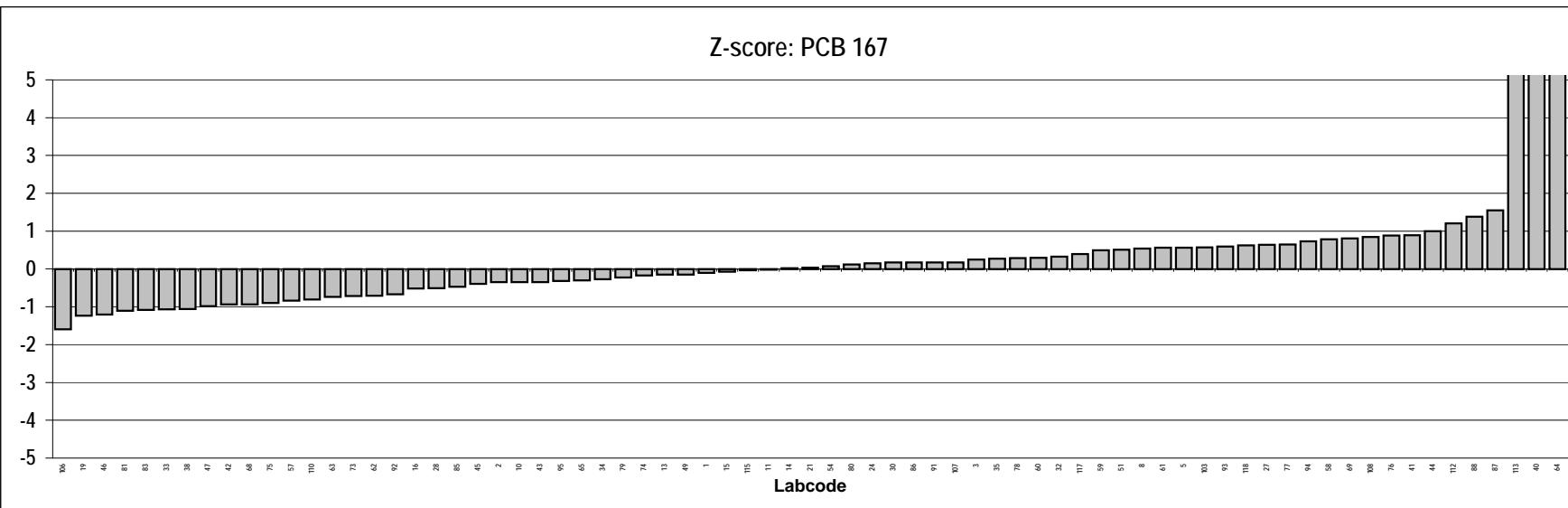
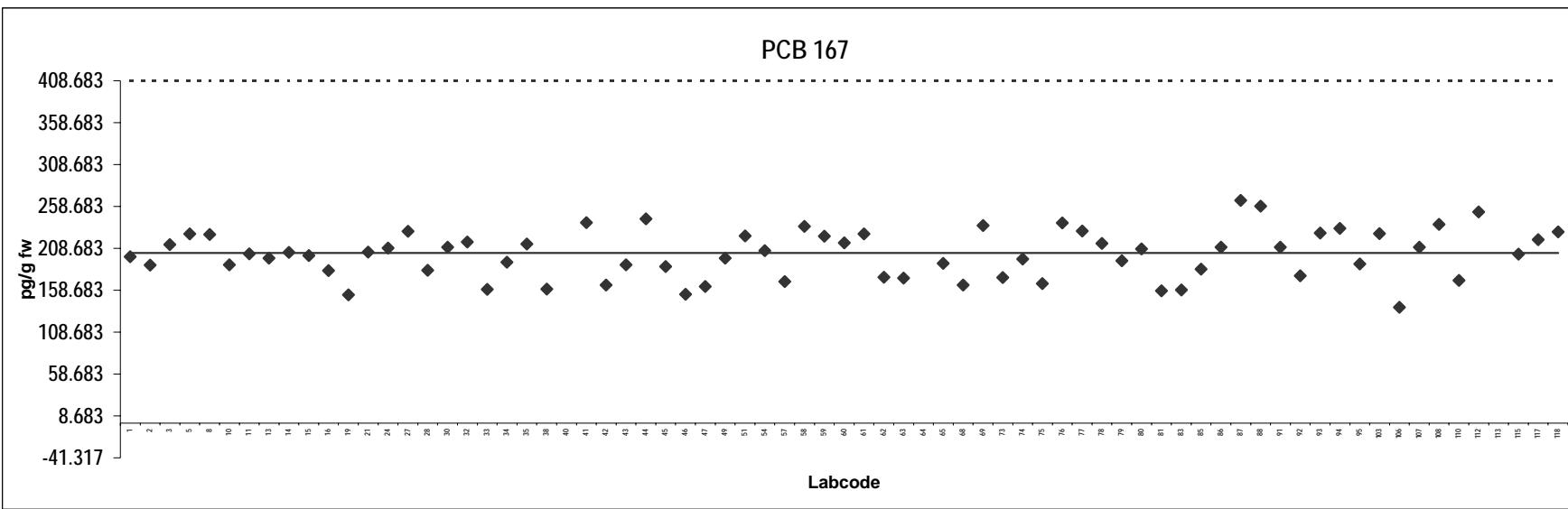


**Herring**  
Congener: PCB 167

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	199		74	196	
2	189		75	166	
3	213		76	239	
5	226		77	229	
8	225		78	215	
10	189		79	194	
11	202		80	208	
13	197		81	158	
14	204		83	159	
15	200		85	184	
16	182		86	210	
19	153		87	266	
21	204		88	259	
24	209		91	210	
27	229		92	176	
28	182		93	227	
30	210		94	233	
32	216		95	190	
33	160		103	226	
34	192		106	138	
35	214		107	210	
38	160		108	237	
40	564	Outlier	110	170	
41	239		112	252	
42	165		113	416	
43	189		115	202	
44	244		117	219	
45	187		118	228	
46	154				
47	163				
49	197				
51	224				
54	206				
57	169				
58	235				
59	223				
60	215				
61	226				
62	174				
63	173				
64	599	Outlier			
65	191				
68	165				
69	236				
73	174				

**Consensus statistics**

Consensus median, pg/g	203
Median all values pg/g	204
Consensus mean, pg/g	202
Standard deviation, pg/g	28
Relative standard deviation, %	14
No. of values reported	73
No. of values removed	3
No. of reported non-detects	0

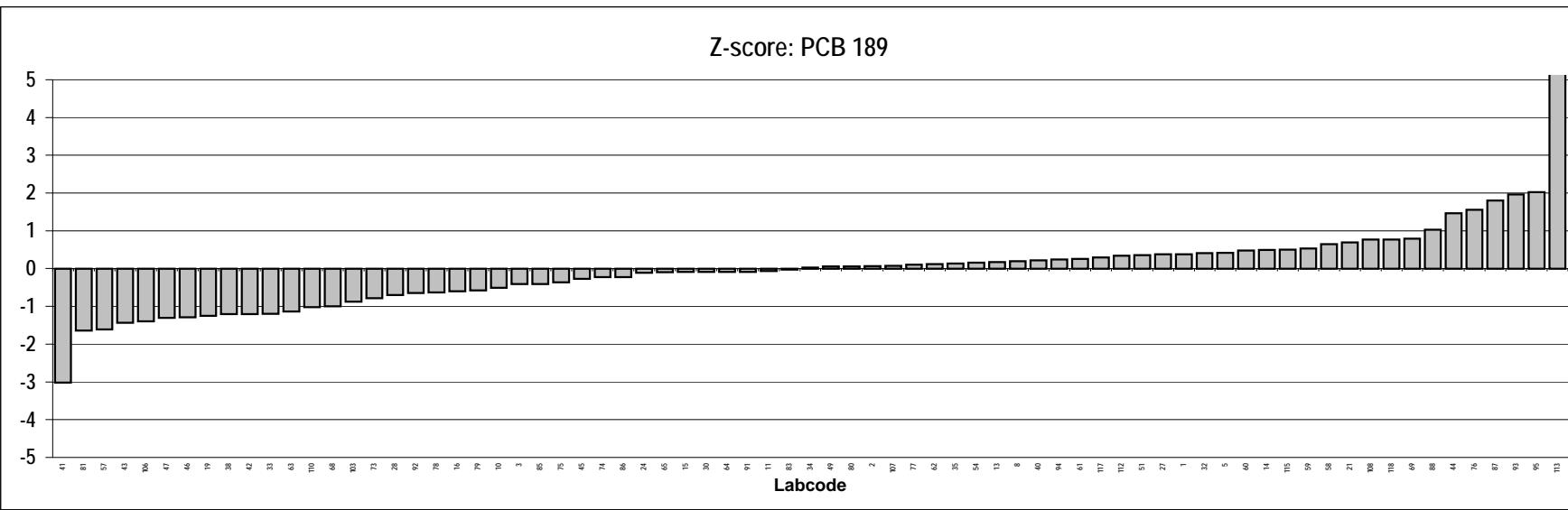
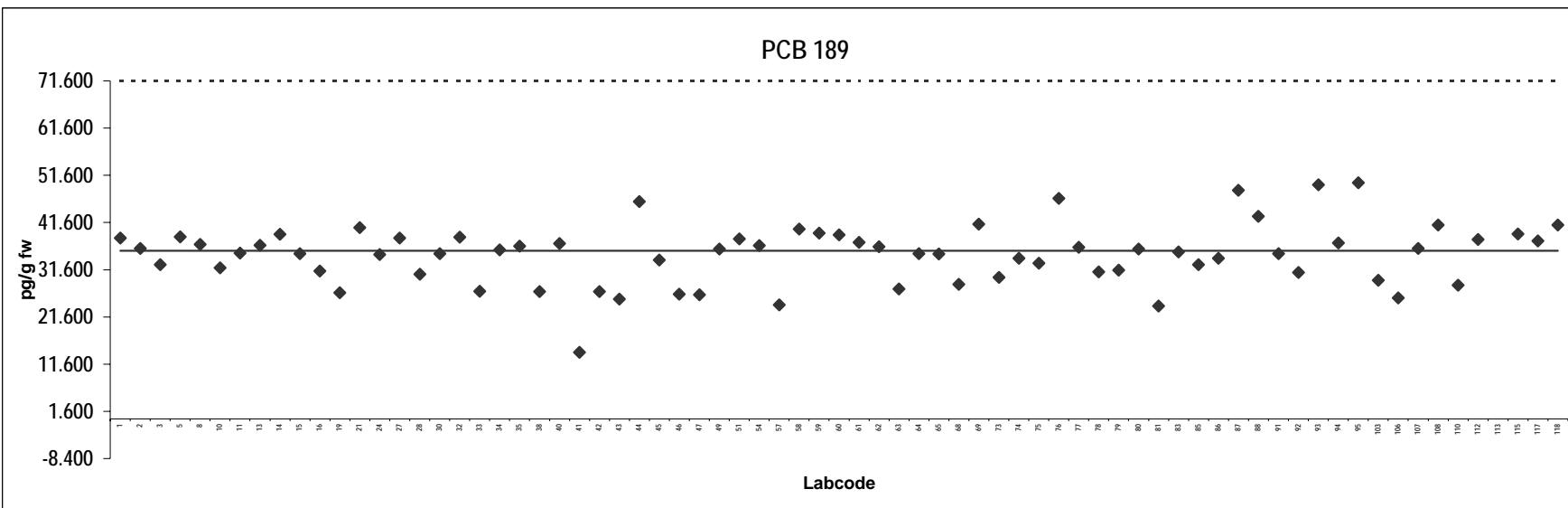


**Herring**  
Congener: PCB 189

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	38		74	34	
2	36		75	33	
3	33		76	47	
5	39		77	36	
8	37		78	31	
10	32		79	32	
11	35		80	36	
13	37		81	24	
14	39		83	35	
15	35		85	33	
16	31		86	34	
19	27		87	48	
21	41		88	43	
24	35		91	35	
27	38		92	31	
28	31		93	50	
30	35		94	37	
32	39		95	50	
33	27		103	29	
34	36		106	26	
35	37		107	36	
38	27		108	41	
40	37		110	28	
41	14		112	38	
42	27		113	81	Outlier
43	25		115	39	
44	46		117	38	
45	34		118	41	
46	26				
47	26				
49	36				
51	38				
54	37				
57	24				
58	40				
59	39				
60	39				
61	37				
62	36				
63	28				
64	35				
65	35				
68	29				
69	41				
73	30				

**Consensus statistics**

Consensus median, pg/g	36
Median all values pg/g	36
Consensus mean, pg/g	35
Standard deviation, pg/g	6
Relative standard deviation, %	18
No. of values reported	73
No. of values removed	1
No. of reported non-detects	0

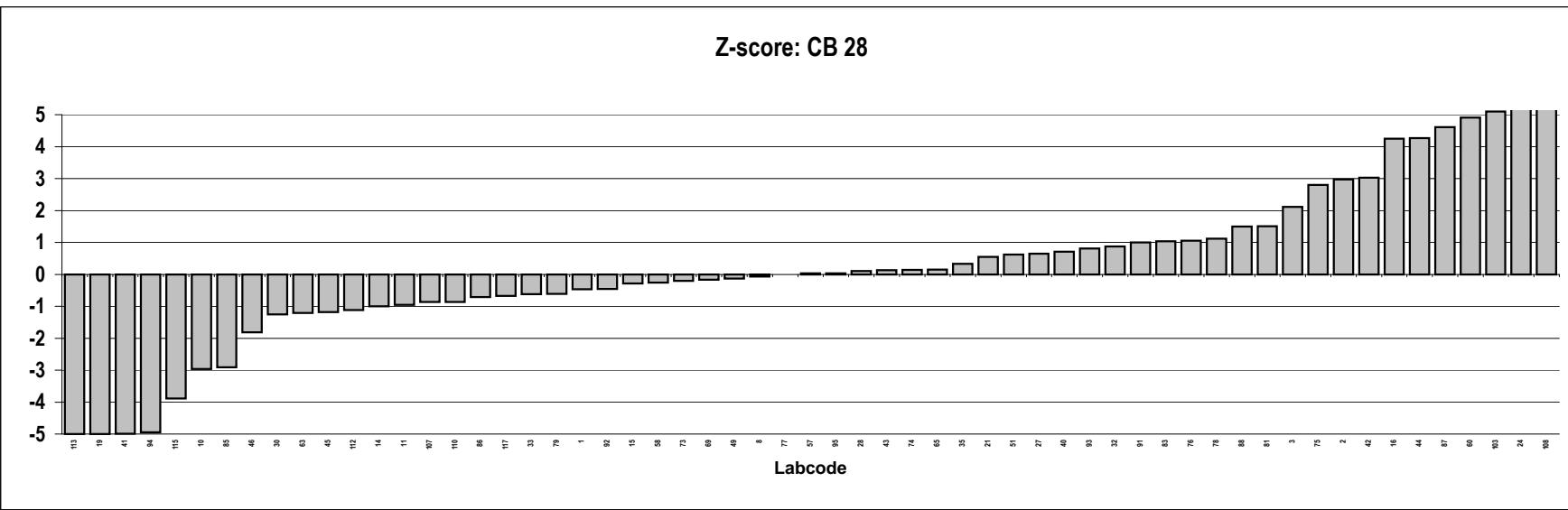
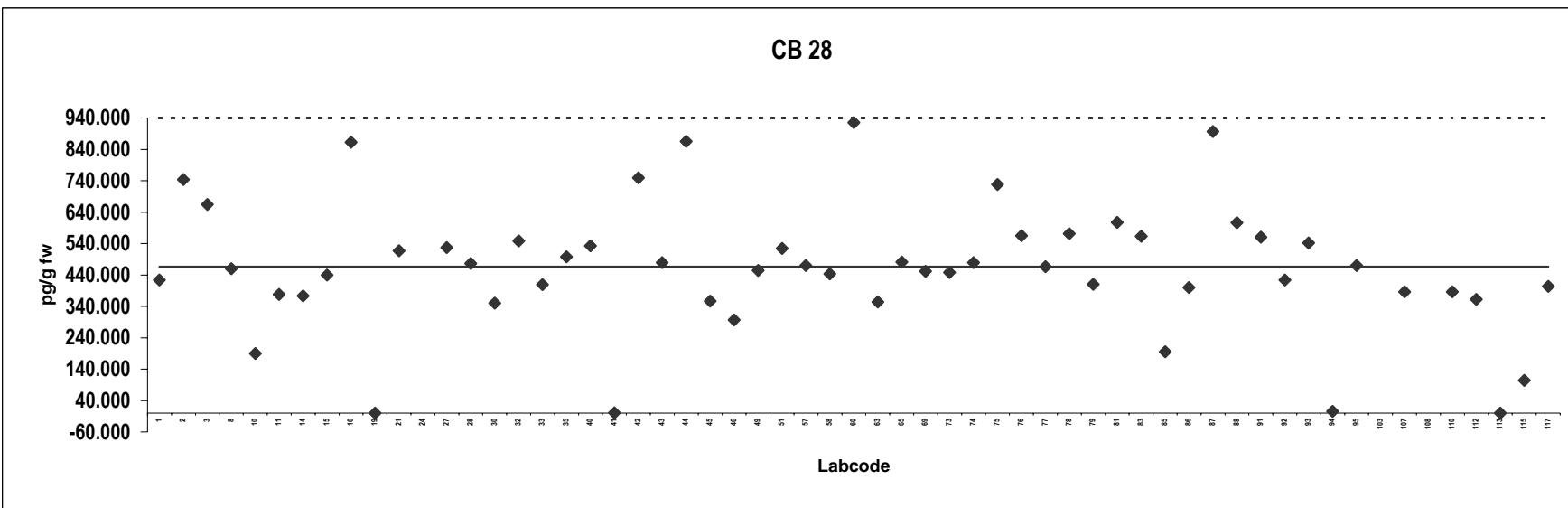


**Herring**  
Congener: CB 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	424		88	607	
2	744		91	560	
3	664		92	424	
8	460		93	542	
10	190		94	5.0	ND
11	378		95	470	
14	373		103	943	Outlier
15	440		107	386	
16	863		108	1009	Outlier
19	0.29		110	386	
21	517		112	362	
24	988	Outlier	113	0.0070	
27	527		115	104	
28	476		117	404	
30	350				
32	548				
33	409				
35	498				
40	533				
41	0.57				
42	749				
43	479				
44	865				
45	357				
46	297				
49	454				
51	524				
57	470				
58	443				
60	925				
63	354				
65	481				
69	451				
73	448				
74	480				
75	728				
76	565				
77	467				
78	571				
79	410				
81	607				
83	563				
85	195				
86	400				
87	897				

**Consensus statistics**

Consensus median, pg/g	467
Median all values pg/g	470
Consensus mean, pg/g	461
Standard deviation, pg/g	207
Relative standard deviation, %	45
No. of values reported	59
No. of values removed	3
No. of reported non-detects	1

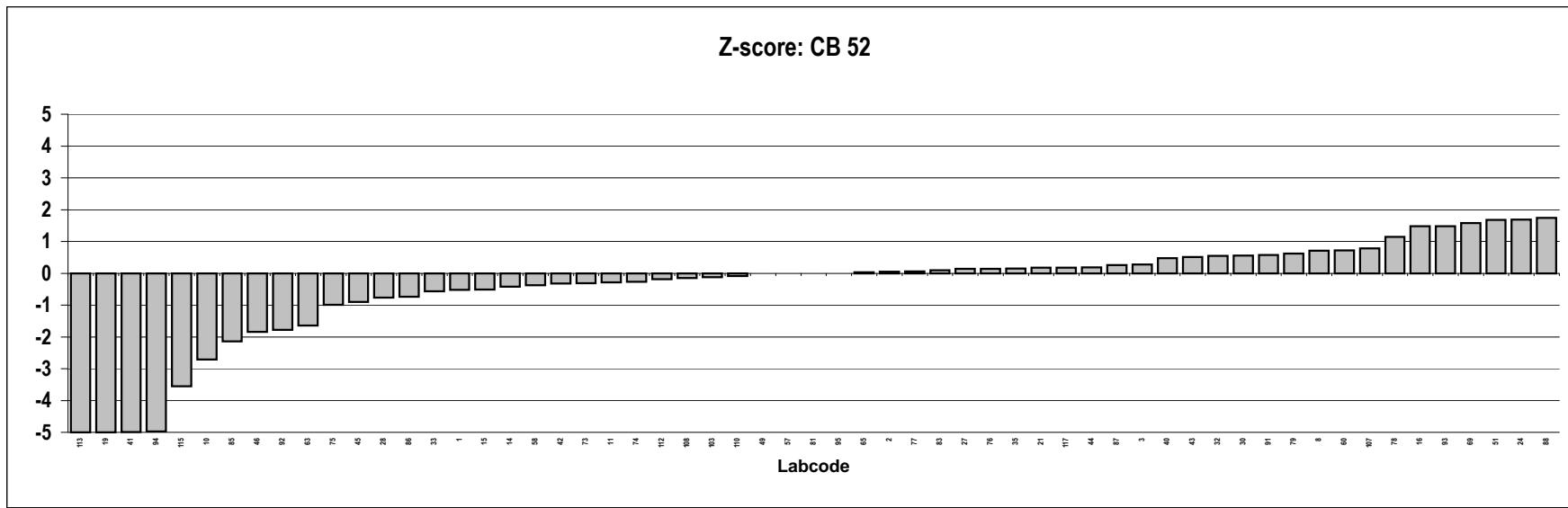
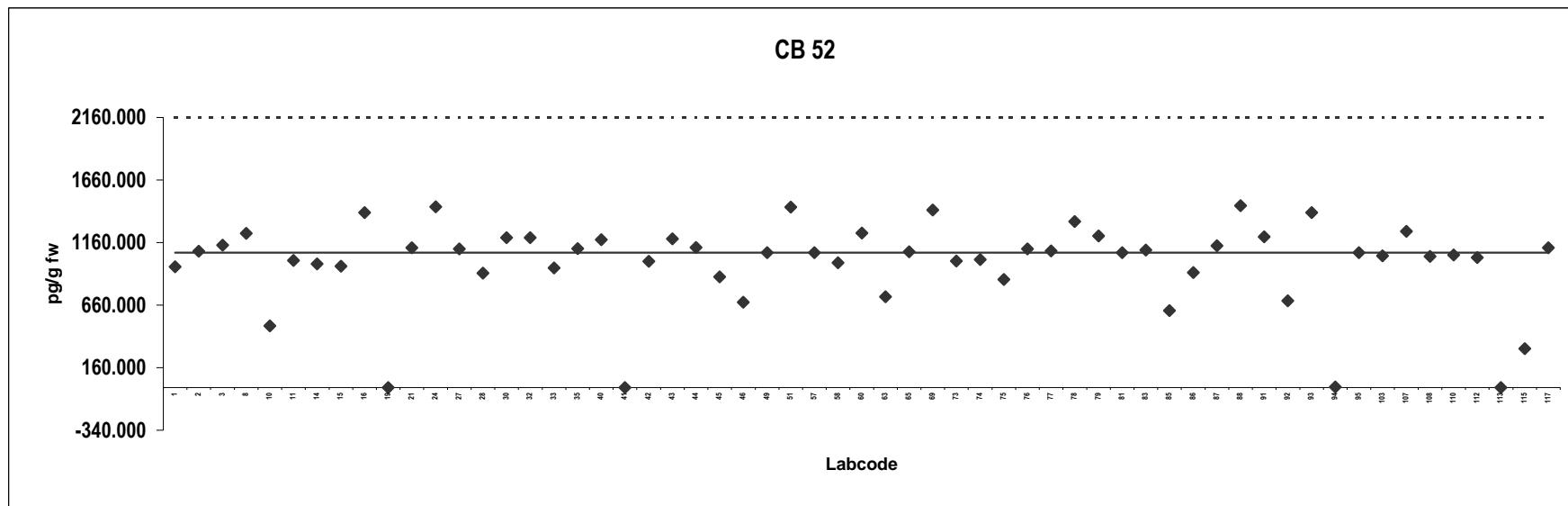


**Herring**  
Congener: CB 52

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	967		88	1455	
2	1090		91	1205	
3	1140		92	695	
8	1233		93	1400	
10	494		94	5.0	
11	1018		95	1080	
14	990		103	1053	
15	970		107	1250	
16	1400		108	1049	
19	0.69		110	1062	
21	1118		112	1040	
24	1445		113	0.34	
27	1110		115	313	
28	915		117	1119	
30	1200				
32	1199				
33	957				
35	1112				
40	1183				
41	1.1				
42	1010				
43	1190				
44	1120				
45	886				
46	683				
49	1080				
51	1443				
57	1080				
58	999				
60	1235				
63	726				
65	1086				
69	1421				
73	1012				
74	1023				
75	866				
76	1110				
77	1094				
78	1328				
79	1213				
81	1080				
83	1100				
85	617				
86	920				
87	1135				

**Consensus statistics**

Consensus median, pg/g	1080
Median all values pg/g	1080
Consensus mean, pg/g	995
Standard deviation, pg/g	347
Relative standard deviation, %	35
No. of values reported	59
No. of values removed	0
No. of reported non-detects	1

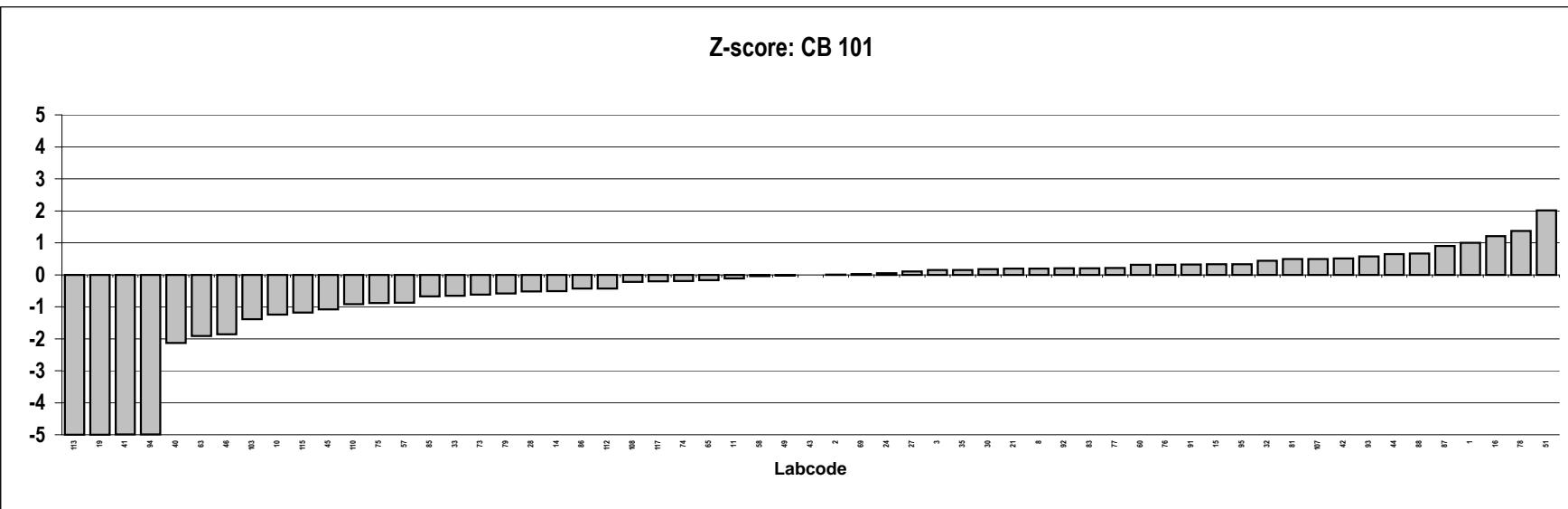
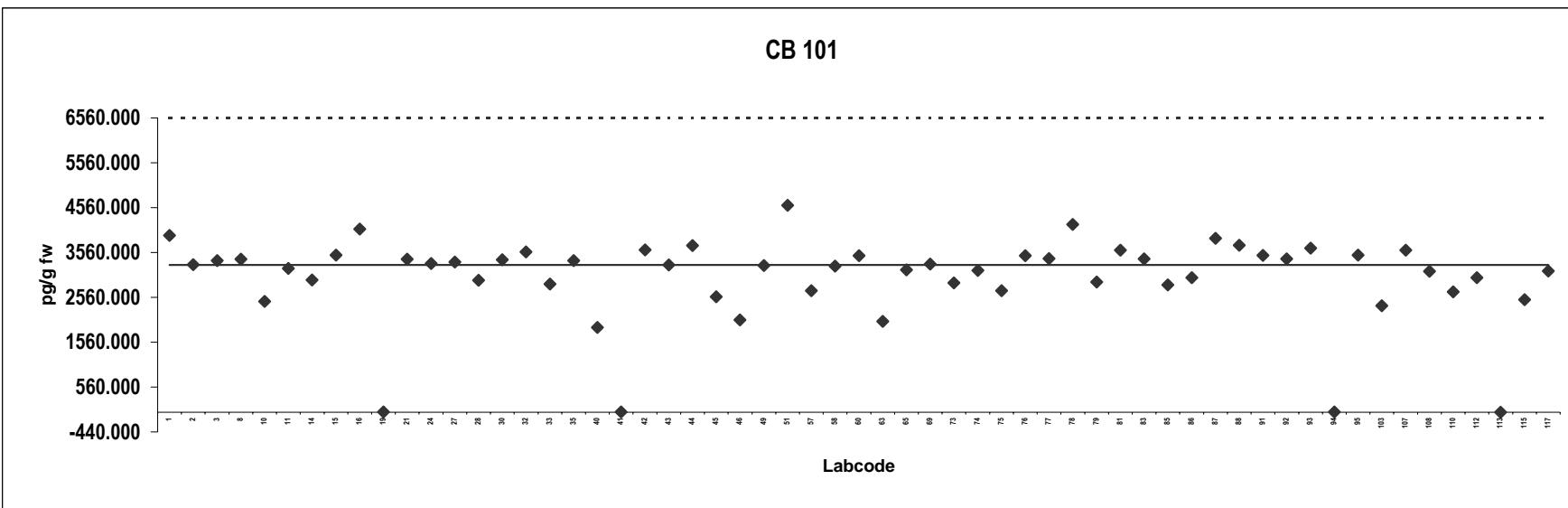


**Herring**  
Congener: CB 101

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	3940		88	3723	
2	3289		91	3495	
3	3380		92	3416	
8	3412		93	3660	
10	2469		94	5.0	
11	3207		95	3500	
14	2949		103	2372	
15	3500		107	3610	
16	4080		108	3140	
19	2.1		110	2681	
21	3412		112	3000	
24	3318		113	1.3	
27	3350		115	2511	
28	2942		117	3148	
30	3400				
32	3573				
33	2856				
35	3381				
40	1886				
41	3.1				
42	3620				
43	3280				
44	3712				
45	2576				
46	2060				
49	3270				
51	4609				
57	2710				
58	3260				
60	3489				
63	2026				
65	3174				
69	3301				
73	2880				
74	3157				
75	2708				
76	3490				
77	3423				
78	4184				
79	2903				
81	3610				
83	3420				
85	2840				
86	3000				
87	3878				

**Consensus statistics**

Consensus median, pg/g	3285
Median all values pg/g	3280
Consensus mean, pg/g	3003
Standard deviation, pg/g	960
Relative standard deviation, %	32
No. of values reported	59
No. of values removed	0
No. of reported non-detects	1



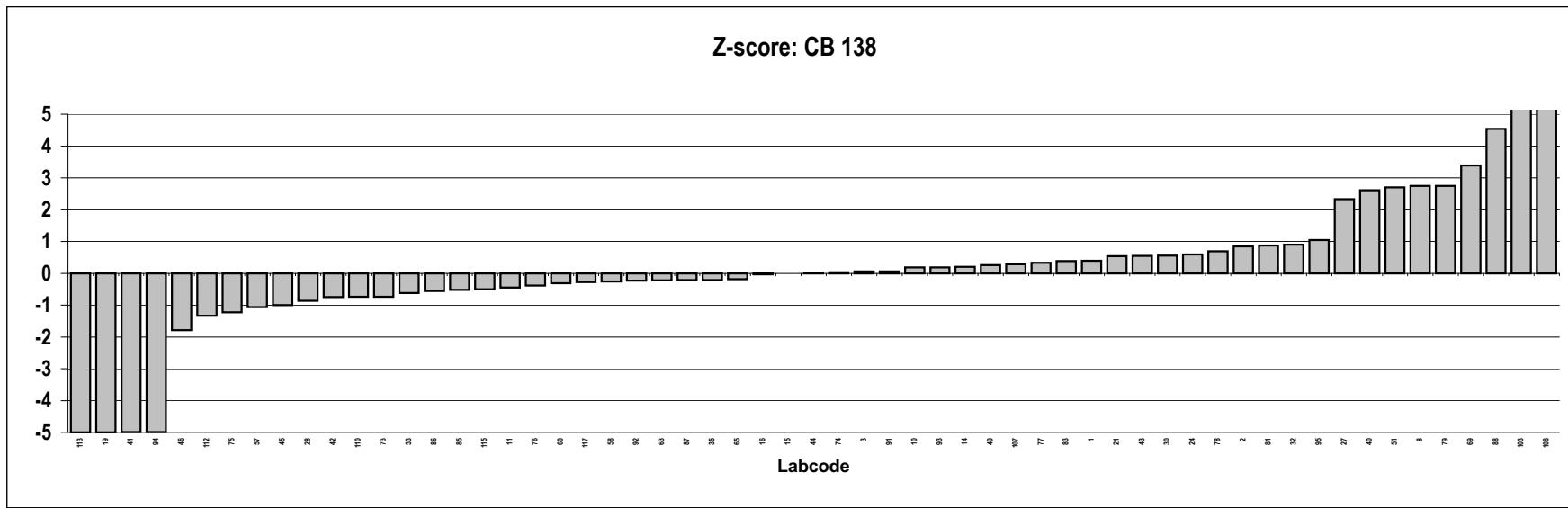
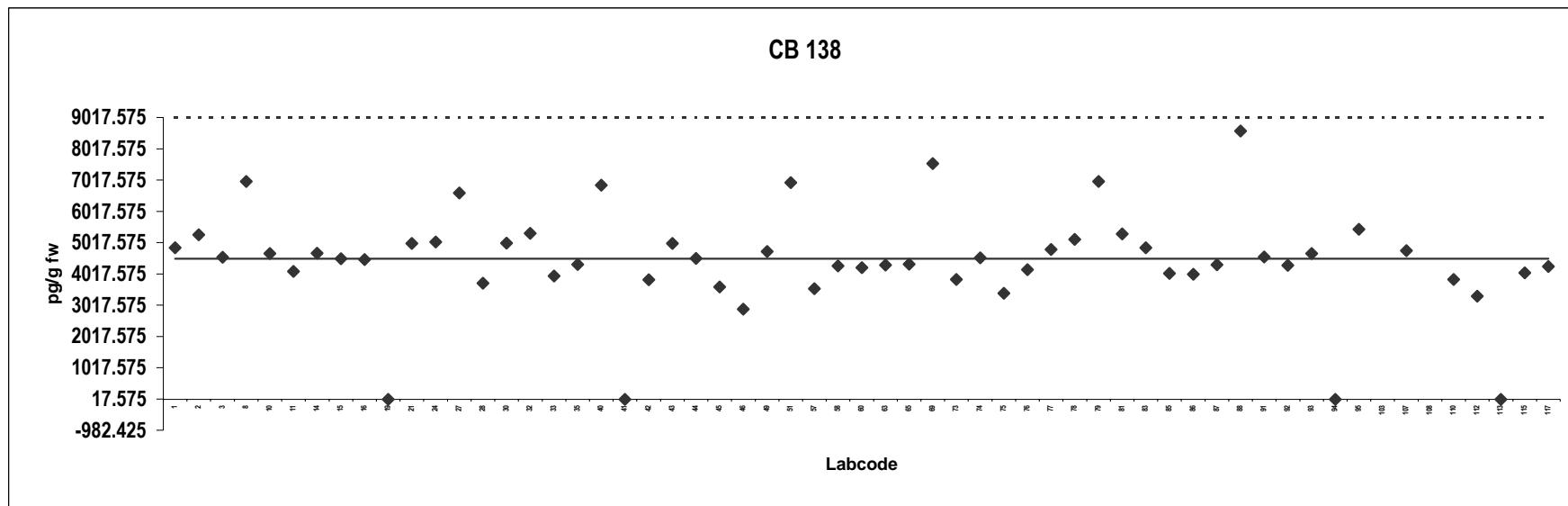
# Herring

Congener: CB 138

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	4855		88	8585	
2	5263		91	4555	
3	4550		92	4294	
8	6969		93	4670	
10	4663		94	6.0	
11	4095		95	5440	
14	4680		103	9469	Outlier
15	4500		107	4760	
16	4470		108	10637	Outlier
19	2.8		110	3837	
21	4986		112	3300	
24	5037		113	2.8	
27	6600		115	4047	
28	3721		117	4250	
30	5000				
32	5308				
33	3944				
35	4313				
40	6849				
41	5.3				
42	3830				
43	4990				
44	4509				
45	3601				
46	2890				
49	4730				
51	6931				
57	3540				
58	4270				
60	4215				
63	4299				
65	4330				
69	7547				
73	3840				
74	4532				
75	3399				
76	4150				
77	4795				
78	5120				
79	6975				
81	5290				
83	4850				
85	4030				
86	4000				
87	4308				

#### Consensus statistics

Consensus median, pg/g	4500
Median all values pg/g	4509
Consensus mean, pg/g	4430
Standard deviation, pg/g	1636
Relative standard deviation, %	37
No. of values reported	59
No. of values removed	2
No. of reported non-detects	0



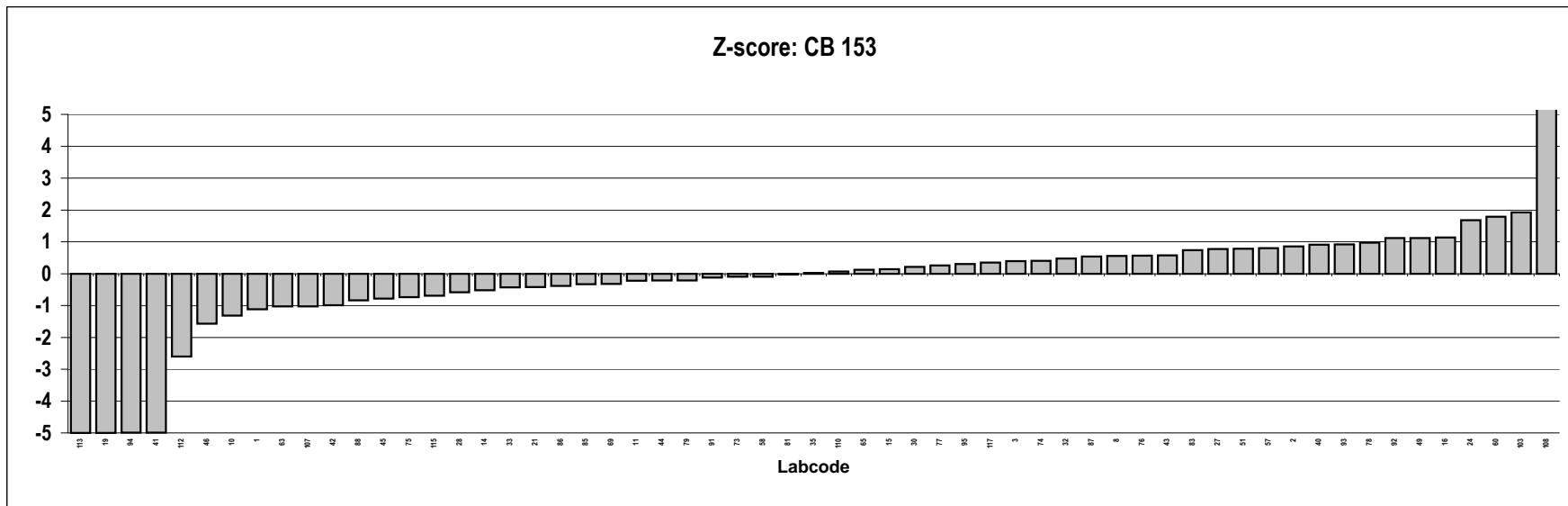
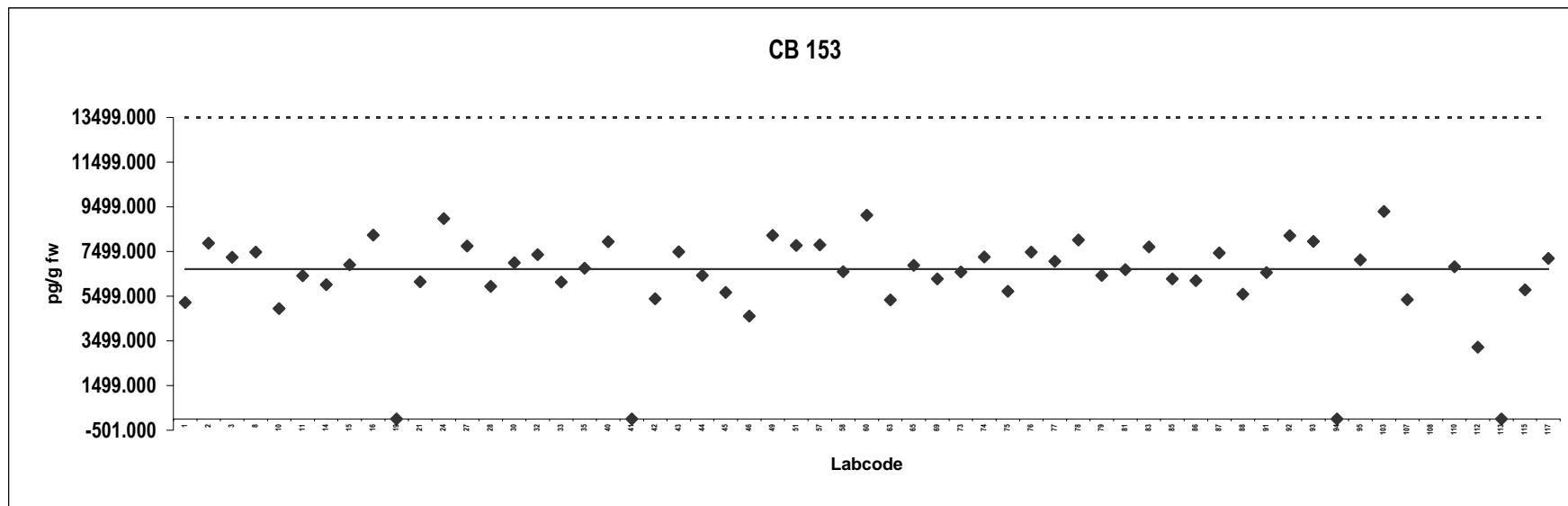
# Herring

Congener: CB 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5212		88	5585	
2	7869		91	6555	
3	7240		92	8213	
8	7467		93	7950	
10	4942		94	7.6	
11	6413		95	7120	
14	6014		103	9291	
15	6900		107	5340	
16	8240		108	16254	Outlier
19	4.6		110	6810	
21	6150		112	3220	
24	8965		113	3.7	
27	7750		115	5783	
28	5933		117	7187	
30	7000				
32	7353				
33	6135				
35	6750				
40	7939				
41	7.9				
42	5380				
43	7490				
44	6425				
45	5661				
46	4610				
49	8220				
51	7767				
57	7790				
58	6590				
60	9121				
63	5331				
65	6874				
69	6278				
73	6588				
74	7260				
75	5720				
76	7470				
77	7060				
78	8016				
79	6430				
81	6680				
83	7700				
85	6270				
86	6200				
87	7437				

#### Consensus statistics

Consensus median, pg/g	6715
Median all values pg/g	6750
Consensus mean, pg/g	6340
Standard deviation, pg/g	2074
Relative standard deviation, %	33
No. of values reported	59
No. of values removed	1
No. of reported non-detects	0

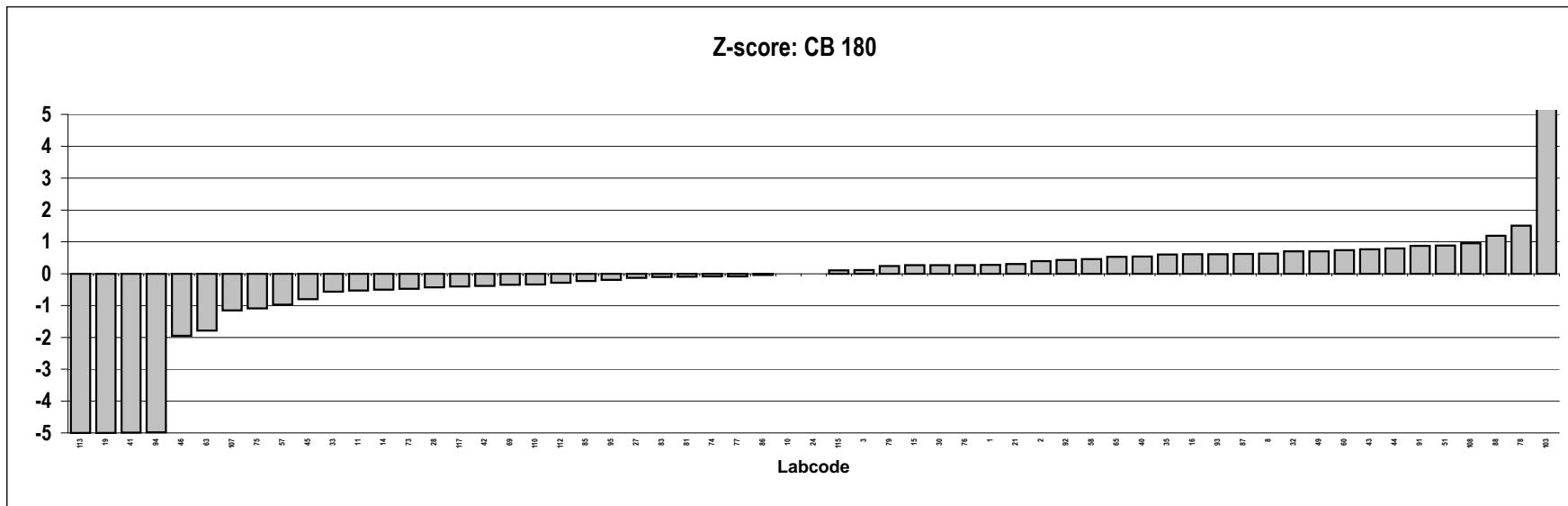
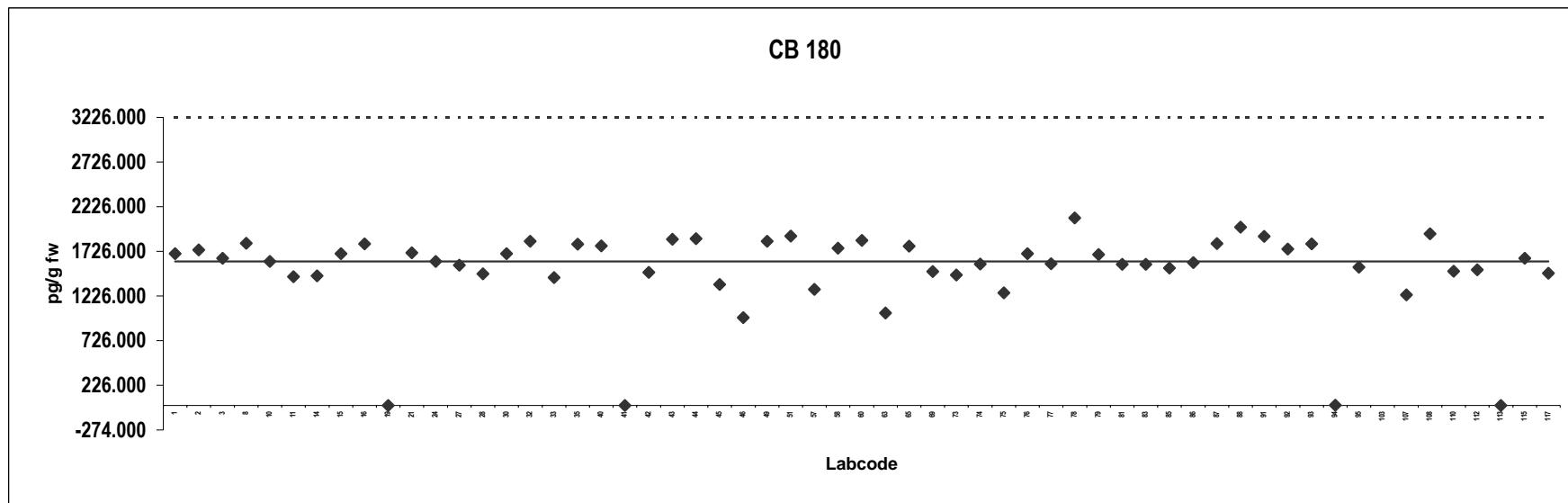


**Herring**  
Congener: CB 180

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1701		88	1996	
2	1741		91	1895	
3	1650		92	1751	
8	1816		93	1810	
10	1613		94	5.0	ND
11	1442		95	1550	
14	1451		103	3847	Outlier
15	1700		107	1240	
16	1810		108	1922	
19	0.98		110	1504	
21	1709		112	1520	
24	1613		113	0.48	
27	1570		115	1648	
28	1475		117	1482	
30	1700				
32	1840				
33	1431				
35	1807				
40	1787				
41	1.7				
42	1490				
43	1860				
44	1867				
45	1354				
46	984				
49	1840				
51	1897				
57	1300				
58	1760				
60	1850				
63	1037				
65	1784				
69	1501				
73	1460				
74	1584				
75	1261				
76	1700				
77	1586				
78	2100				
79	1689				
81	1582				
83	1580				
85	1540				
86	1600				
87	1812				

**Consensus statistics**

Consensus median, pg/g	1613
Median all values pg/g	1613
Consensus mean, pg/g	1521
Standard deviation, pg/g	469
Relative standard deviation, %	31
No. of values reported	59
No. of values removed	1
No. of reported non-detects	1

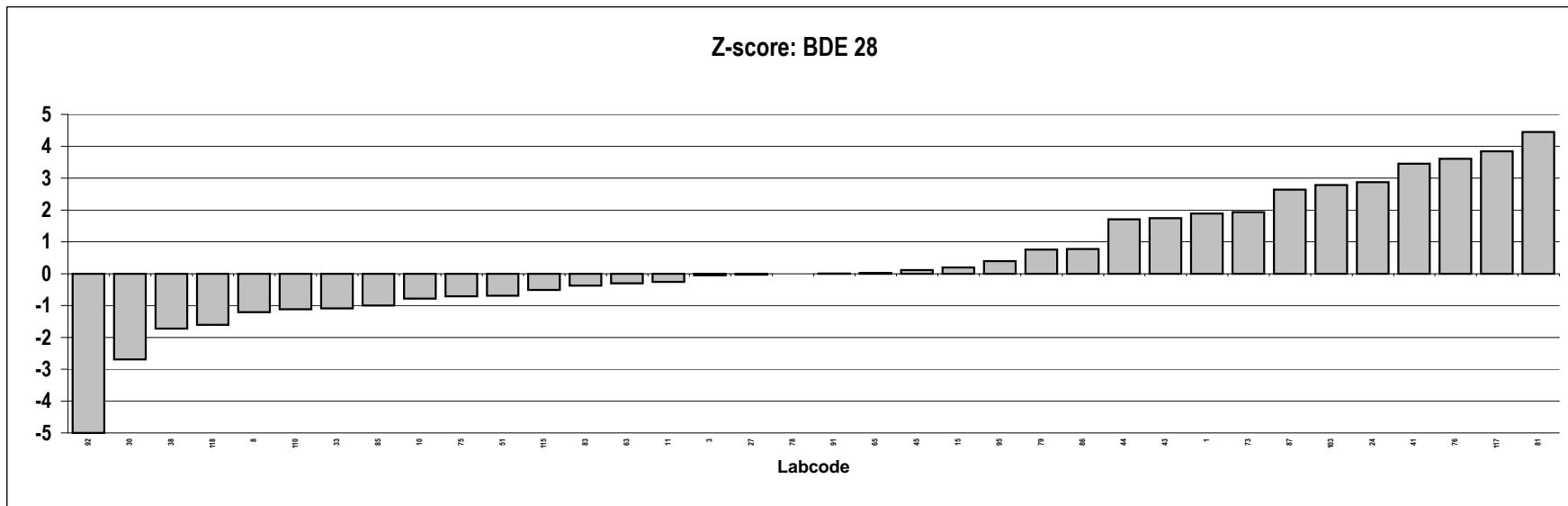
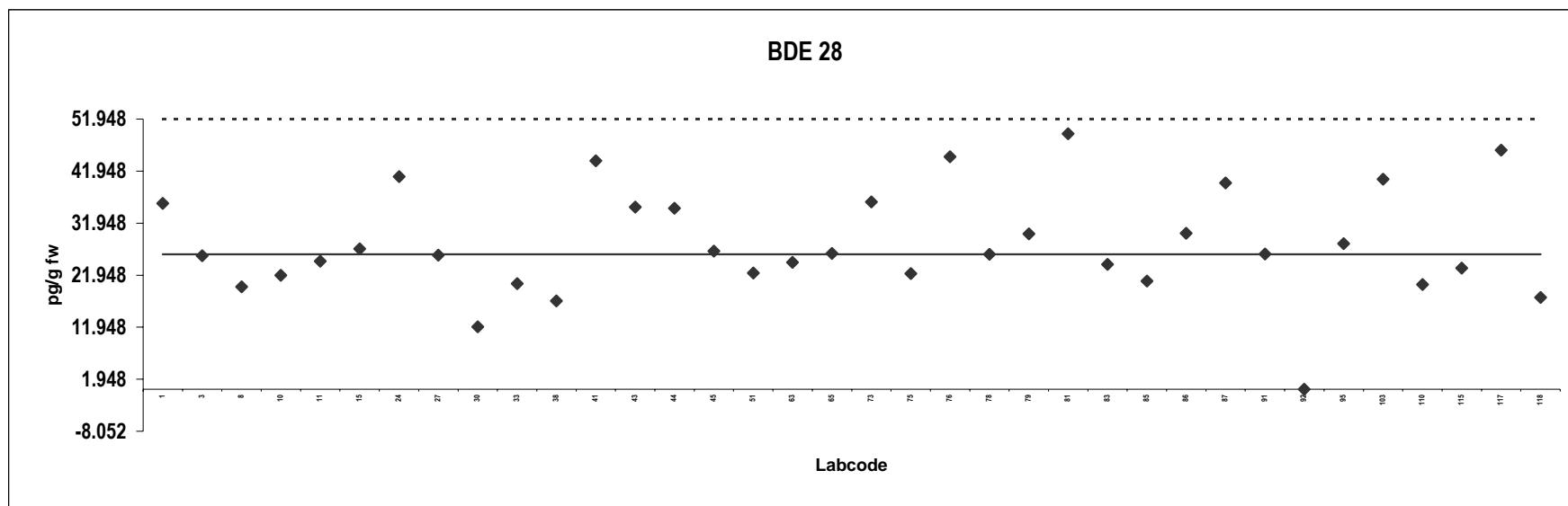


**Herring**  
Congener: BDE 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	36				
3	26				
8	20				
10	22				
11	25				
15	27				
24	41				
27	26				
30	12				
33	20				
38	17				
41	44				
43	35				
44	35				
45	27				
51	22				
63	24				
65	26				
73	36				
75	22				
76	45				
78	26				
79	30				
81	49				
83	24				
85	21				
86	30				
87	40				
91	26				
92	0.021				
95	28				
103	40				
110	20				
115	23				
117	46				
118	18				

**Consensus statistics**

Consensus median, pg/g	26
Median all values pg/g	26
Consensus mean, pg/g	28
Standard deviation, pg/g	10
Relative standard deviation, %	37
No. of values reported	36
No. of values removed	0
No. of reported non-detects	0

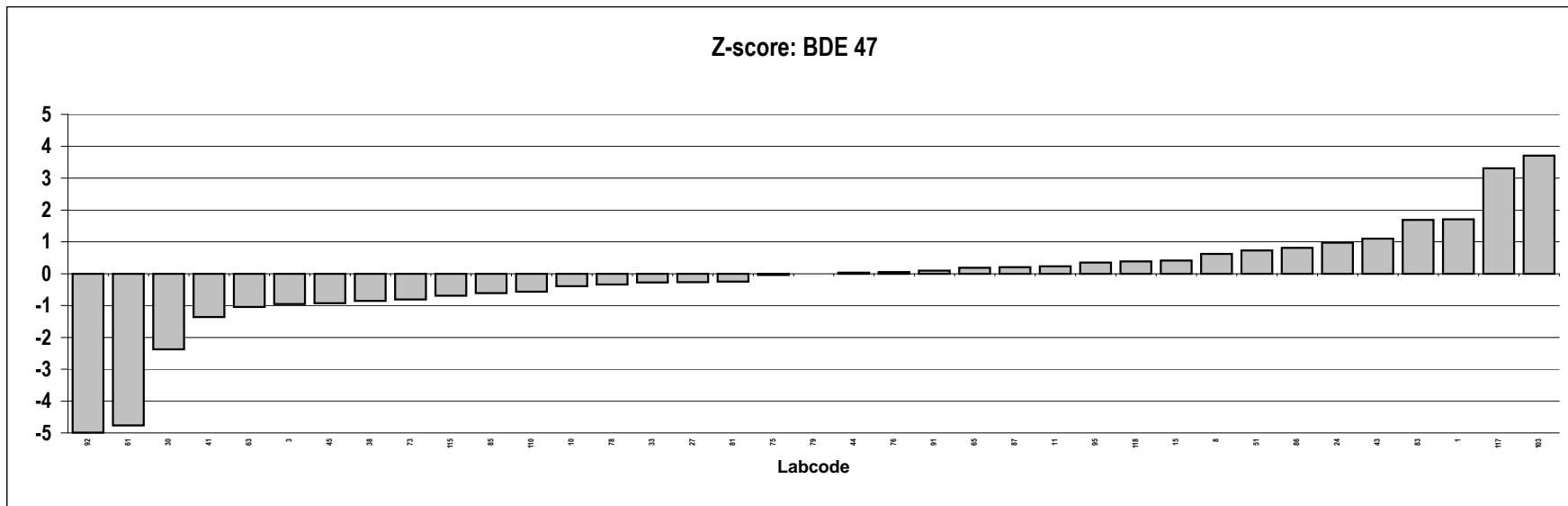
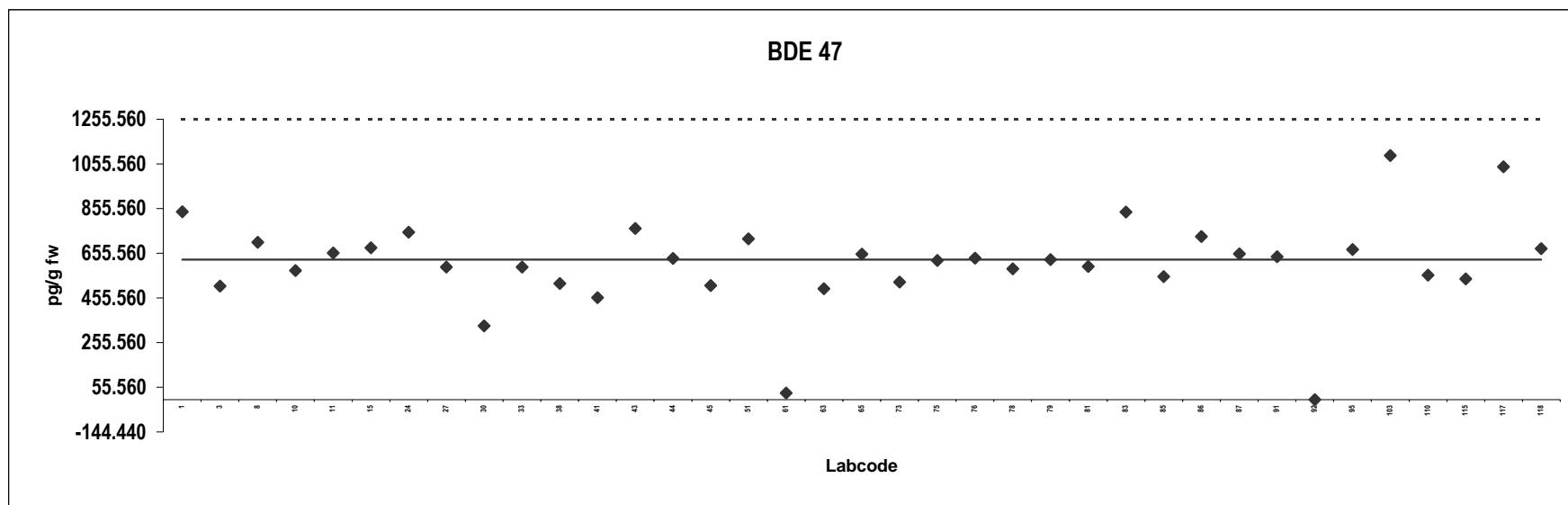


**Herring**  
Congener: BDE 47

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	842				
3	508				
8	705				
10	578				
11	657				
15	680				
24	750				
27	594				
30	330				
33	593				
38	520				
41	457				
43	766				
44	632				
45	511				
51	720				
61	29				
63	497				
65	651				
73	526				
75	623				
76	634				
78	586				
79	628				
81	596				
83	840				
85	551				
86	730				
87	653				
91	640				
92	0.60				
95	672				
103	1094				
110	557				
115	541				
117	1043				
118	676				

**Consensus statistics**

Consensus median, pg/g	628
Median all values pg/g	628
Consensus mean, pg/g	611
Standard deviation, pg/g	204
Relative standard deviation, %	33
No. of values reported	37
No. of values removed	0
No. of reported non-detects	0

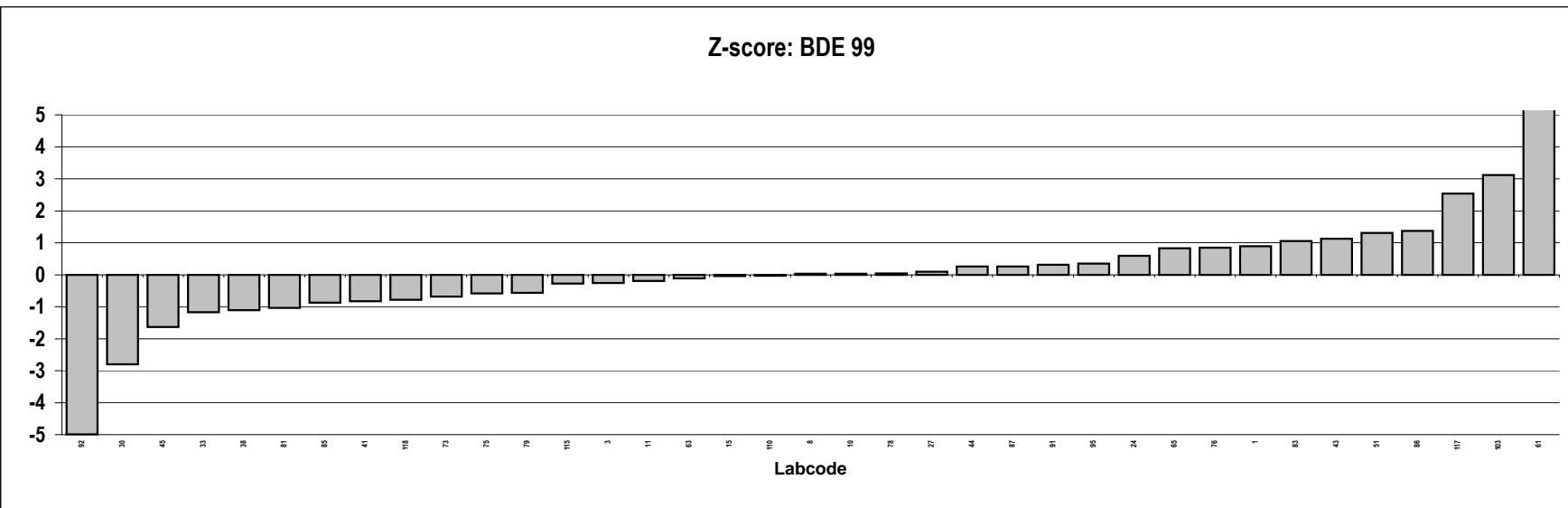
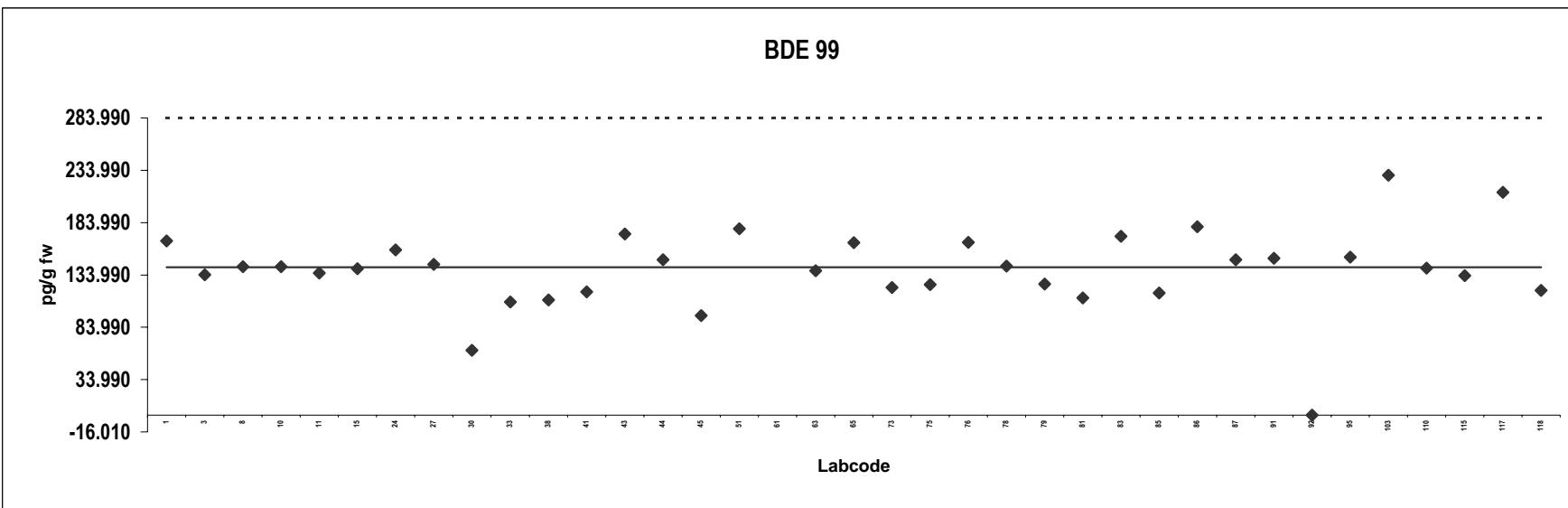


**Herring**  
Congener: BDE 99

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	166				
3	134				
8	142				
10	142				
11	136				
15	140				
24	158				
27	144				
30	62				
33	108				
38	110				
41	118				
43	173				
44	149				
45	95				
51	178				
61	659	Outlier			
63	138				
65	165				
73	122				
75	125				
76	165				
78	142				
79	125				
81	112				
83	171				
85	117				
86	180				
87	149				
91	150				
92	0.13				
95	151				
103	229				
110	140				
115	133				
117	213				
118	119				

**Consensus statistics**

Consensus median, pg/g	141
Median all values pg/g	142
Consensus mean, pg/g	139
Standard deviation, pg/g	39
Relative standard deviation, %	28
No. of values reported	37
No. of values removed	1
No. of reported non-detects	0

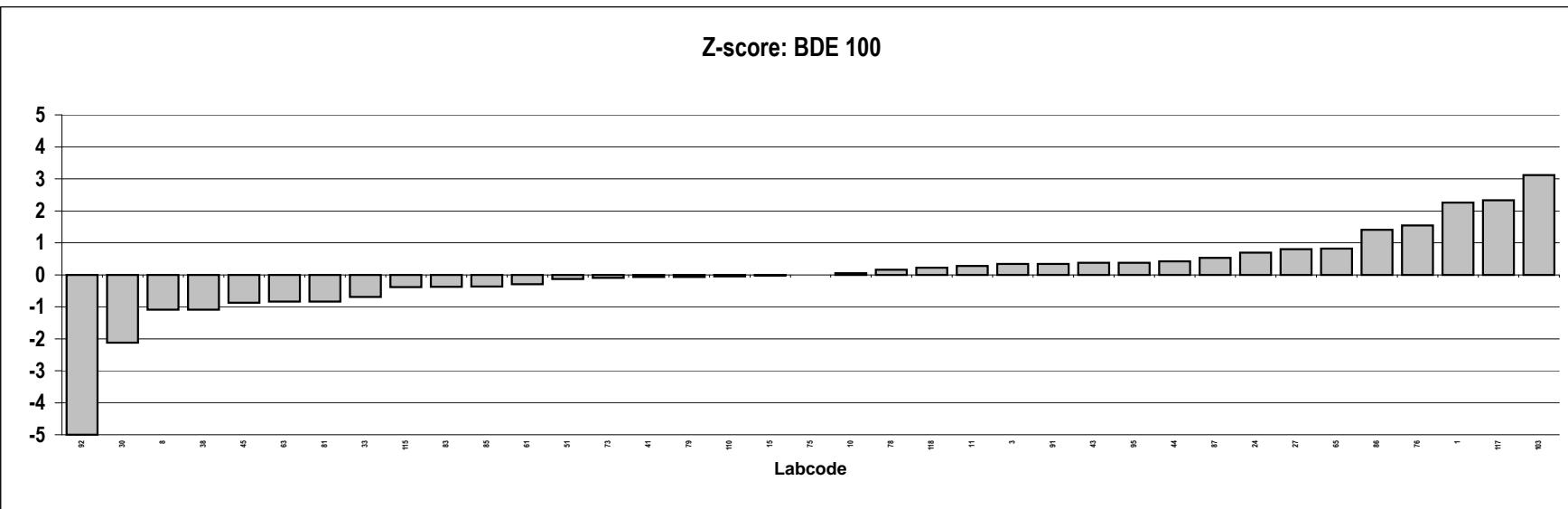
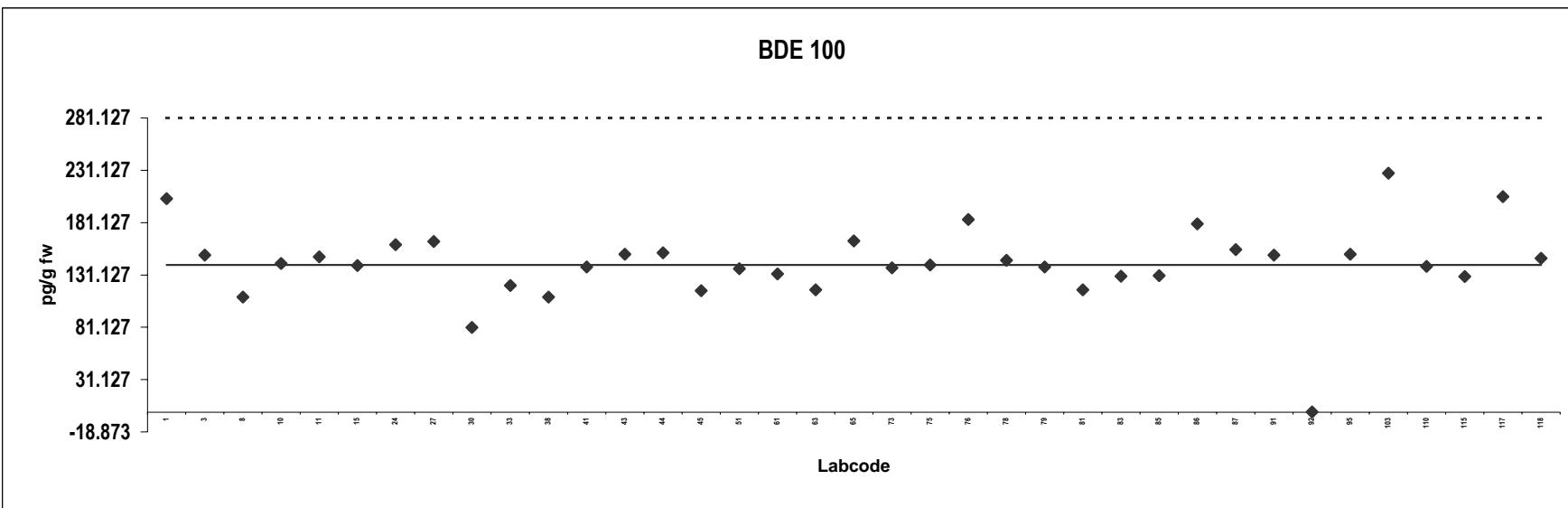


**Herring**  
Congener: BDE 100

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	204				
3	150				
8	110				
10	142				
11	148				
15	140				
24	160				
27	163				
30	81				
33	121				
38	110				
41	139				
43	151				
44	152				
45	116				
51	137				
61	132				
63	117				
65	164				
73	138				
75	141				
76	184				
78	145				
79	139				
81	117				
83	130				
85	130				
86	180				
87	155				
91	150				
92	0.10				
95	151				
103	228				
110	139				
115	130				
117	206				
118	147				

**Consensus statistics**

Consensus median, pg/g	141
Median all values pg/g	141
Consensus mean, pg/g	142
Standard deviation, pg/g	37
Relative standard deviation, %	26
No. of values reported	37
No. of values removed	0
No. of reported non-detects	0

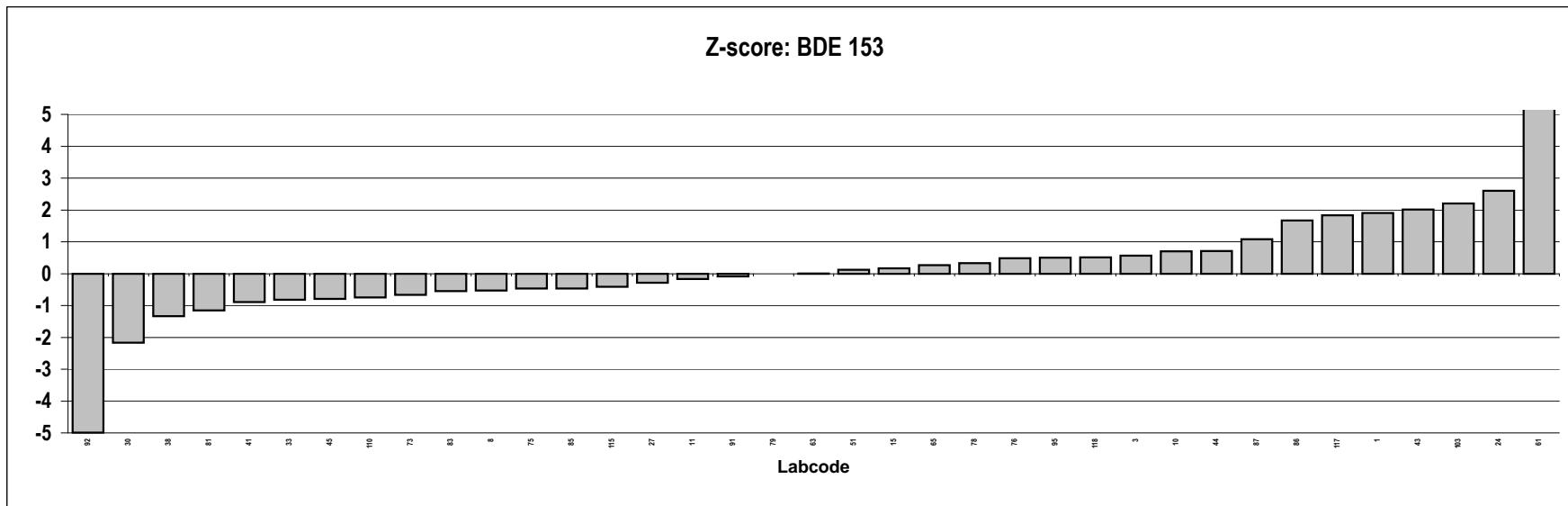
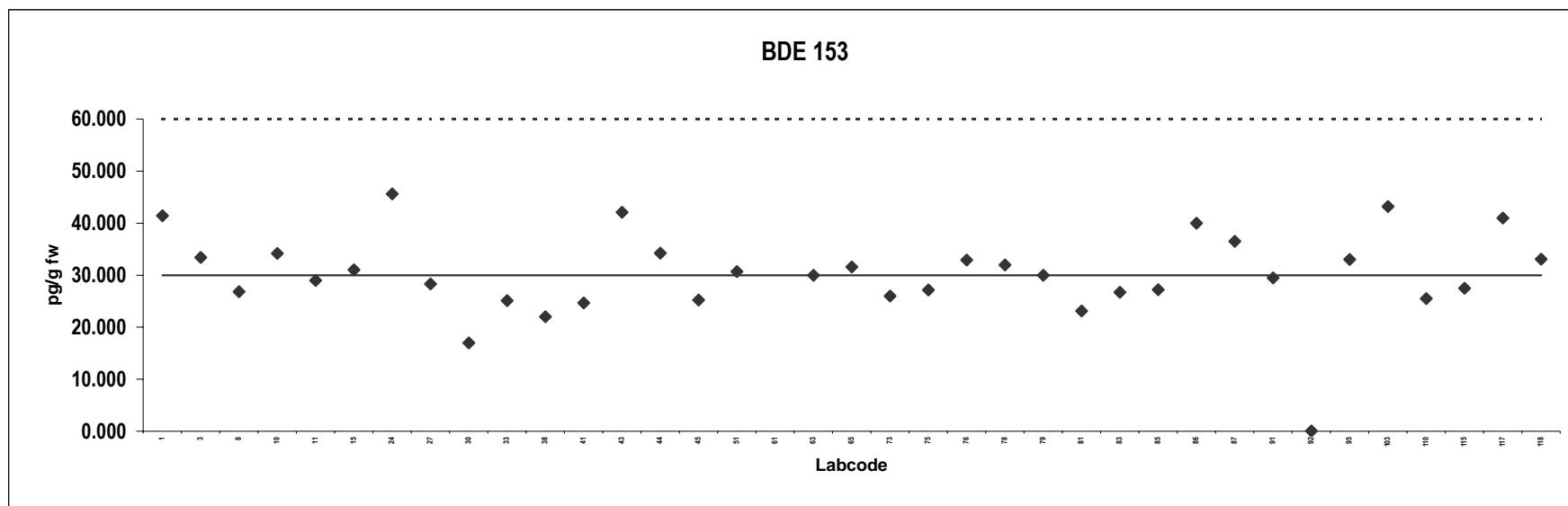


**Herring**  
Congener: BDE 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	41				
3	33				
8	27				
10	34				
11	29				
15	31				
24	46				
27	28				
30	17				
33	25				
38	22				
41	25				
43	42				
44	34				
45	25				
51	31				
61	113	Outlier			
63	30				
65	32				
73	26				
75	27				
76	33				
78	32				
79	30				
81	23				
83	27				
85	27				
86	40				
87	36				
91	30				
92	0.030				
95	33				
103	43				
110	26				
115	28				
117	41				
118	33				

**Consensus statistics**

Consensus median, pg/g	30
Median all values pg/g	30
Consensus mean, pg/g	30
Standard deviation, pg/g	8.2
Relative standard deviation, %	27
No. of values reported	37
No. of values removed	1
No. of reported non-detects	0

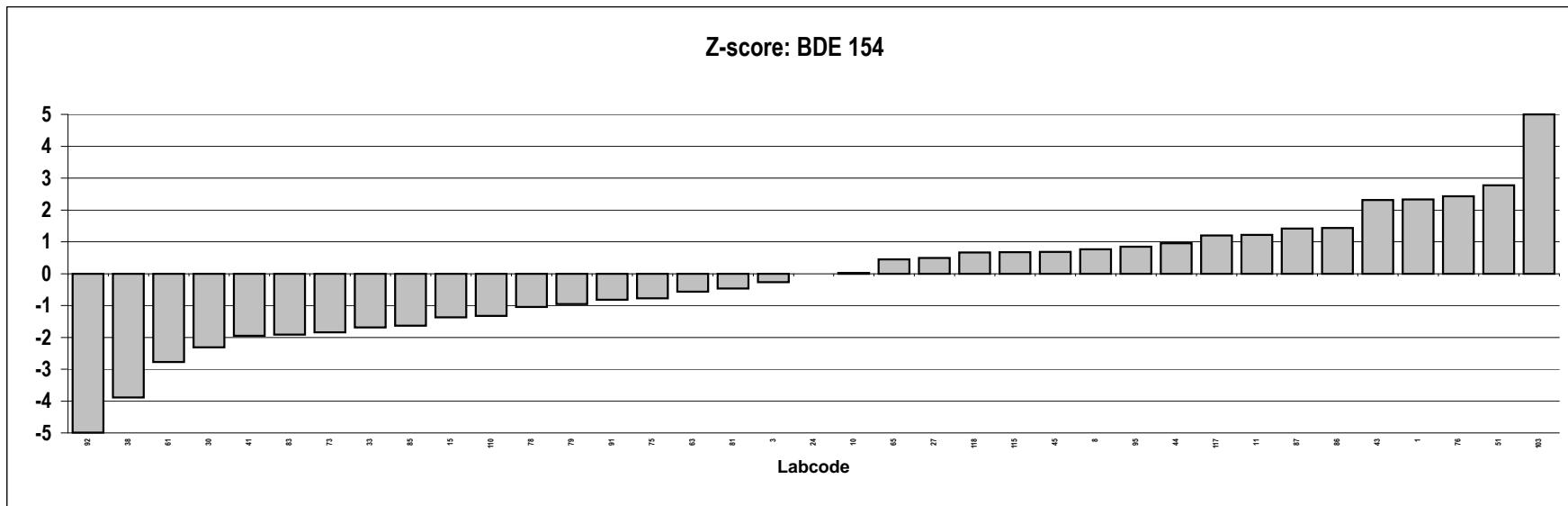
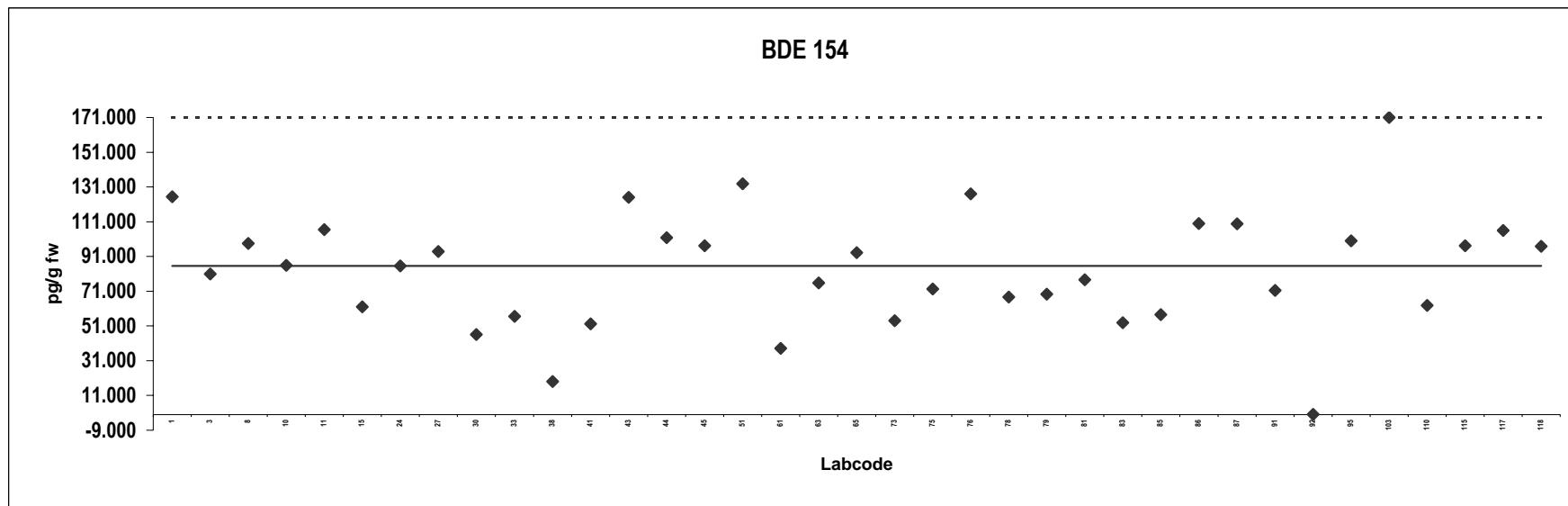


**Herring**  
Congener: BDE 154

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	125				
3	81				
8	99				
10	86				
11	106				
15	62				
24	86				
27	94				
30	46				
33	57				
38	19				
41	52				
43	125				
44	102				
45	97				
51	133				
61	38				
63	76				
65	93				
73	54				
75	72				
76	127				
78	68				
79	69				
81	78				
83	53				
85	58				
86	110				
87	110				
91	72				
92	0.080				
95	100				
103	171				
110	63				
115	97				
117	106				
118	97				

**Consensus statistics**

Consensus median, pg/g	86
Median all values pg/g	86
Consensus mean, pg/g	83
Standard deviation, pg/g	33
Relative standard deviation, %	40
No. of values reported	37
No. of values removed	0
No. of reported non-detects	0

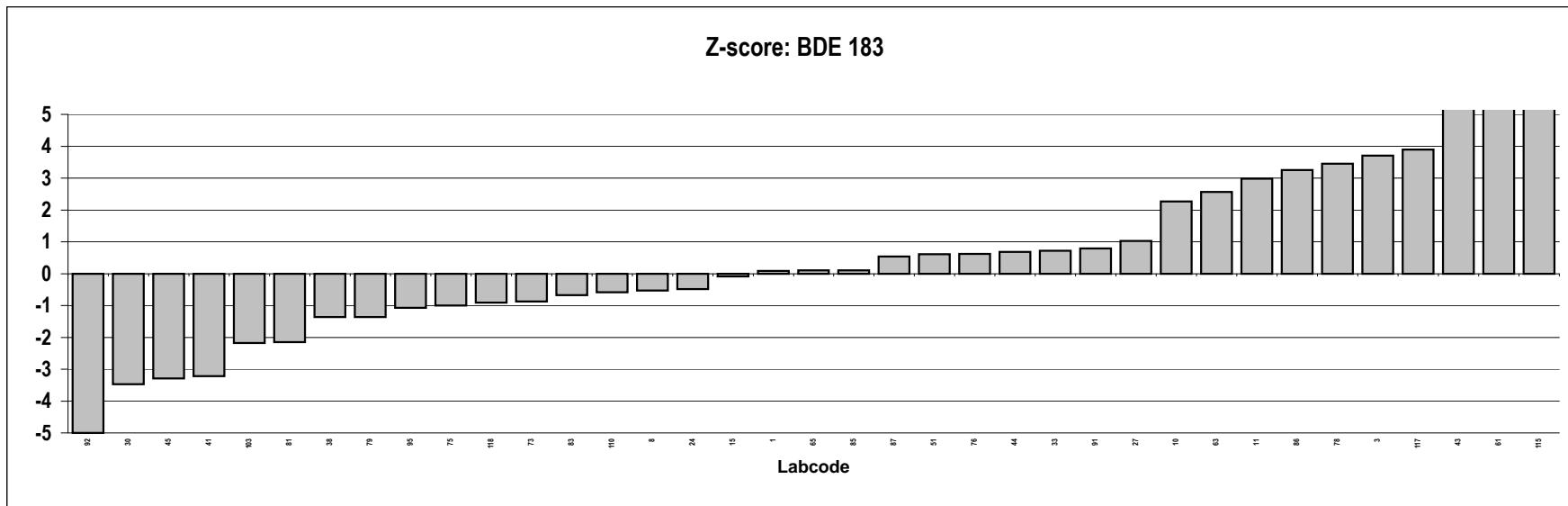
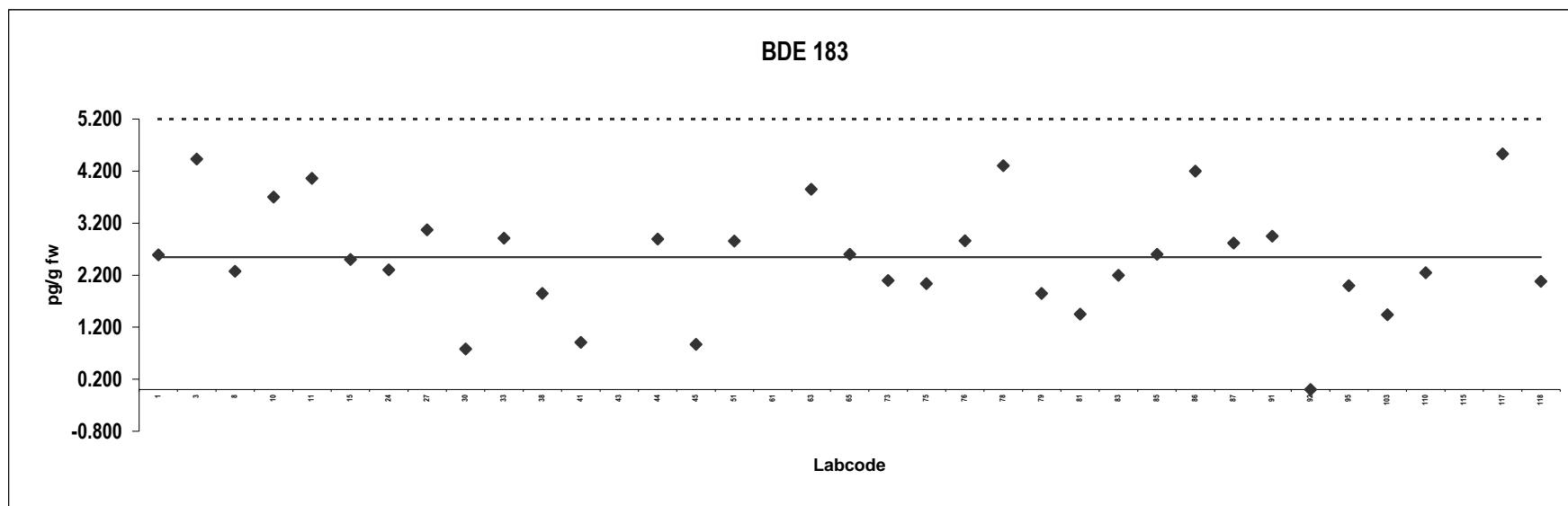


**Herring**  
Congener: BDE 183

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	2.6				
3	4.4				
8	2.3				
10	3.7				
11	4.1				
15	2.5				
24	2.3				
27	3.1				
30	0.78				
33	2.9				
38	1.9				
41	0.91				
43	15	Outlier,ND			
44	2.9				
45	0.87	ND			
51	2.9				
61	100	Outlier			
63	3.9				
65	2.6				
73	2.1				
75	2.0				
76	2.9				
78	4.3				
79	1.9				
81	1.5				
83	2.2				
85	2.6				
86	4.2				
87	2.8				
91	3.0				
92	0.0020	ND			
95	2.0				
103	1.4				
110	2.2				
115	120	Outlier			
117	4.5				
118	2.1				

**Consensus statistics**

Consensus median, pg/g	2.5
Median all values pg/g	2.6
Consensus mean, pg/g	2.5
Standard deviation, pg/g	1.1
Relative standard deviation, %	43
No. of values reported	37
No. of values removed	3
No. of reported non-detects	3

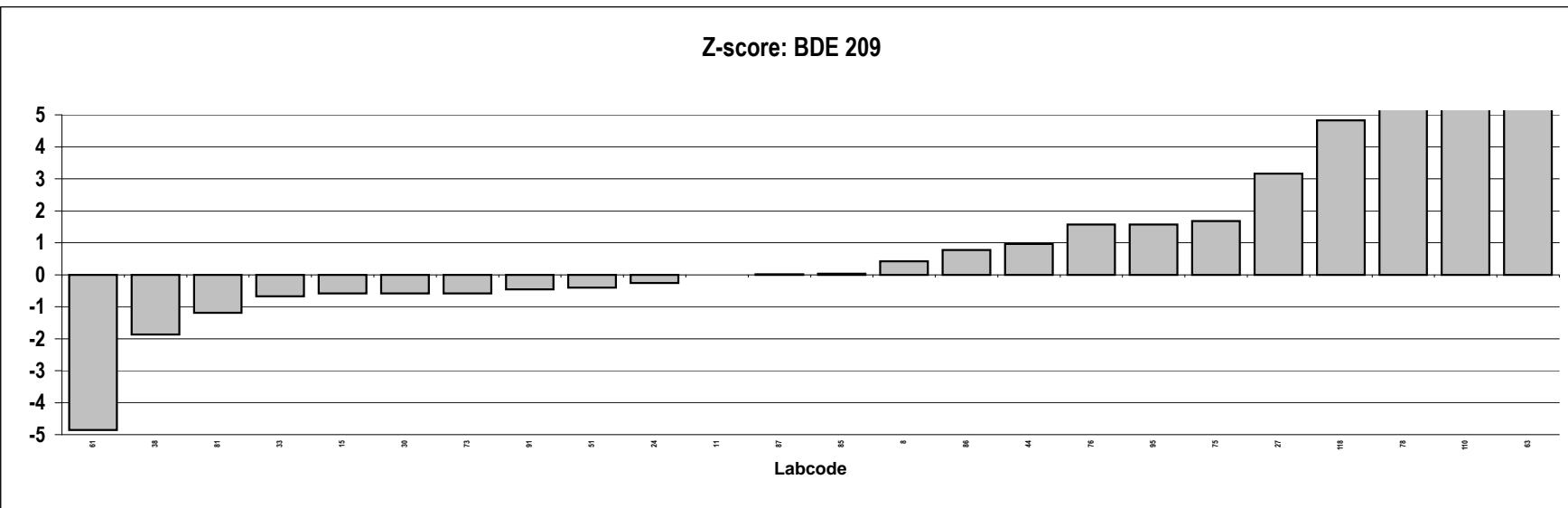
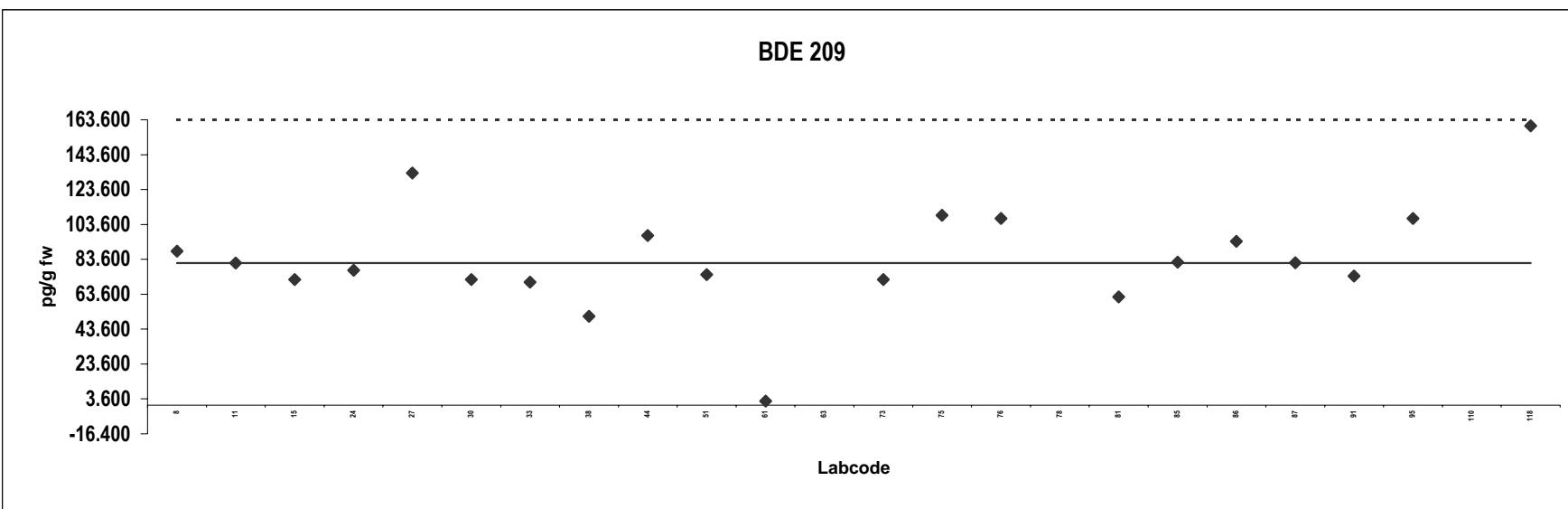


**Herring**  
Congener: BDE 209

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
8	88				
11	81				
15	72				
24	77				
27	133				
30	72				
33	71				
38	51				
44	97				
51	75				
61	2.3				
63	285	Outlier			
73	72				
75	109				
76	107				
78	215	Outlier			
81	62				
85	82				
86	94				
87	82				
91	74				
95	107				
110	216	Outlier			
118	160				

**Consensus statistics**

Consensus median, pg/g	81
Median all values pg/g	82
Consensus mean, pg/g	84
Standard deviation, pg/g	31
Relative standard deviation, %	37
No. of values reported	24
No. of values removed	3
No. of reported non-detects	0

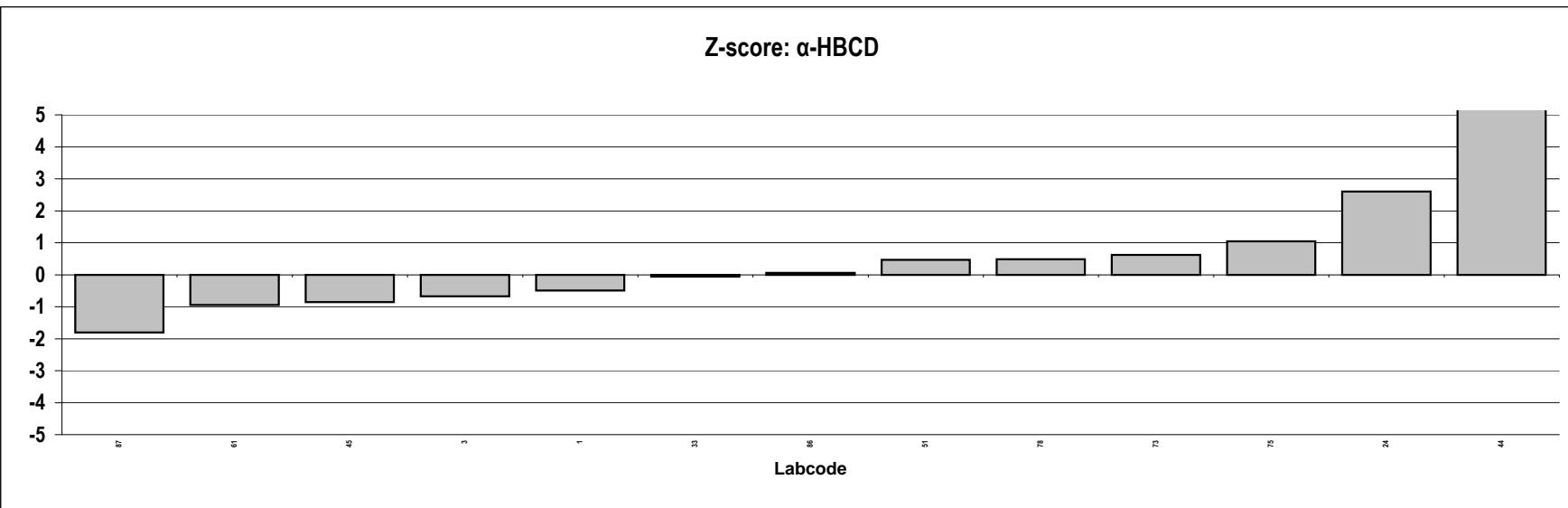
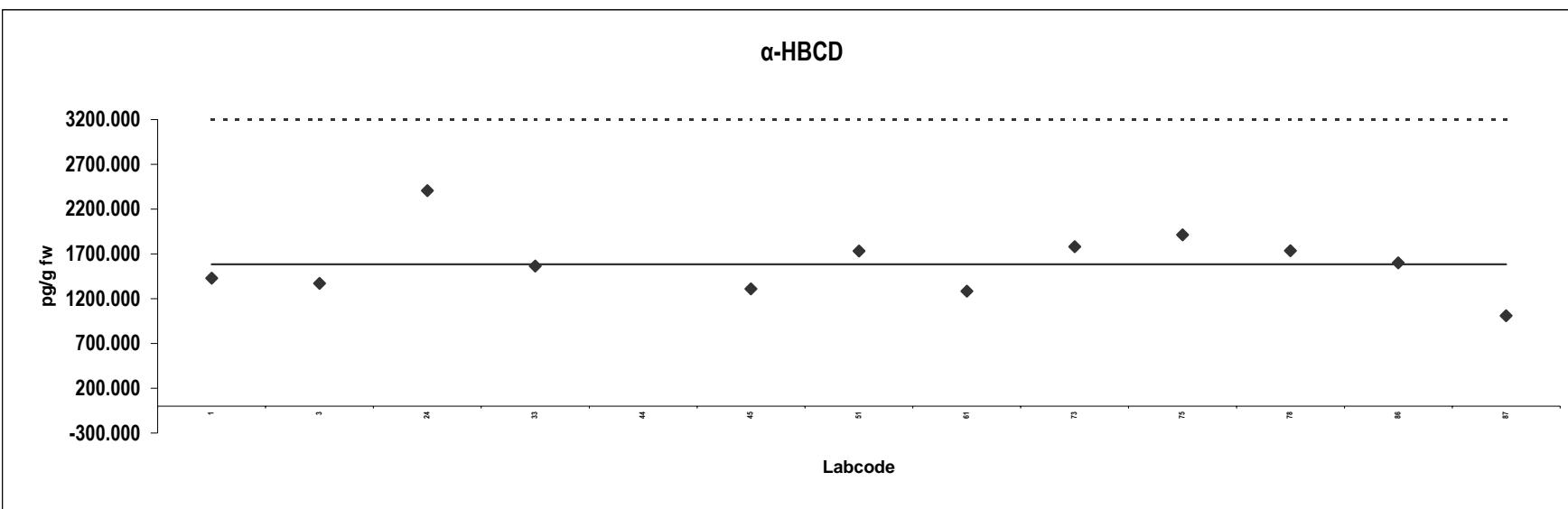


**Herring**  
Congener:  $\alpha$ -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1428				
3	1370				
24	2407				
33	1565				
44	6534				
45	1310				
51	1731				
61	1283				
73	1780				
75	1912				
78	1736				
86	1600				
87	1011				
		Outlier			

**Consensus statistics**

Consensus median, pg/g	1583
Median all values pg/g	1600
Consensus mean, pg/g	1594
Standard deviation, pg/g	361
Relative standard deviation, %	23
No. of values reported	13
No. of values removed	1
No. of reported non-detects	0

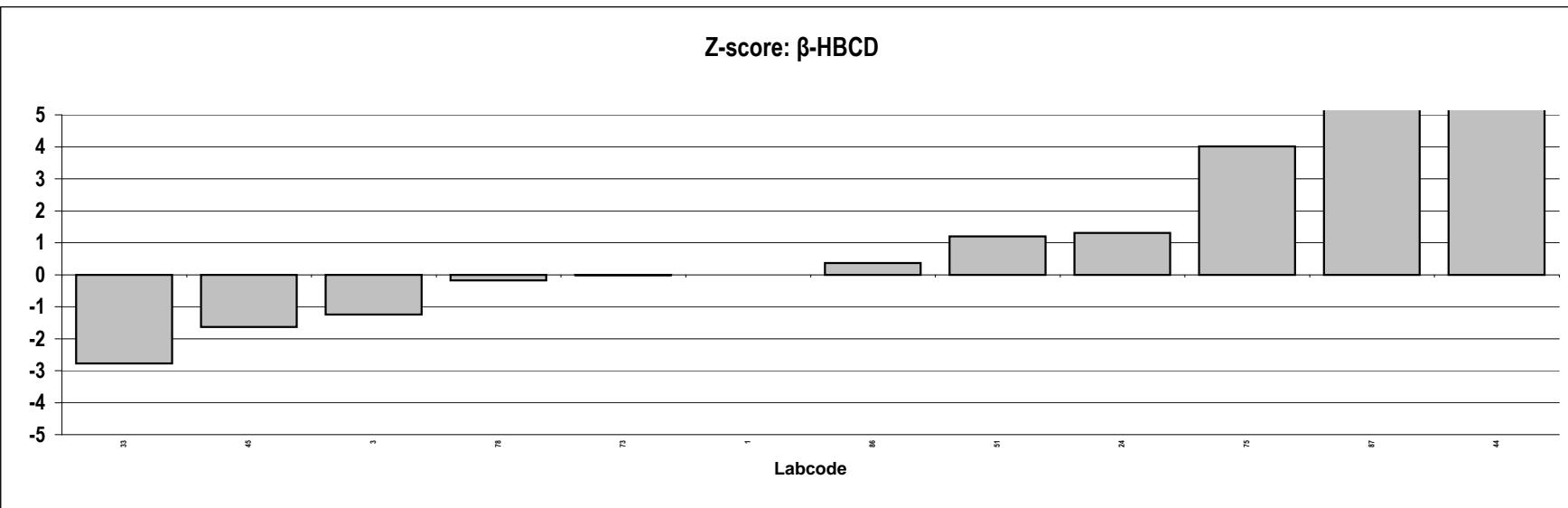
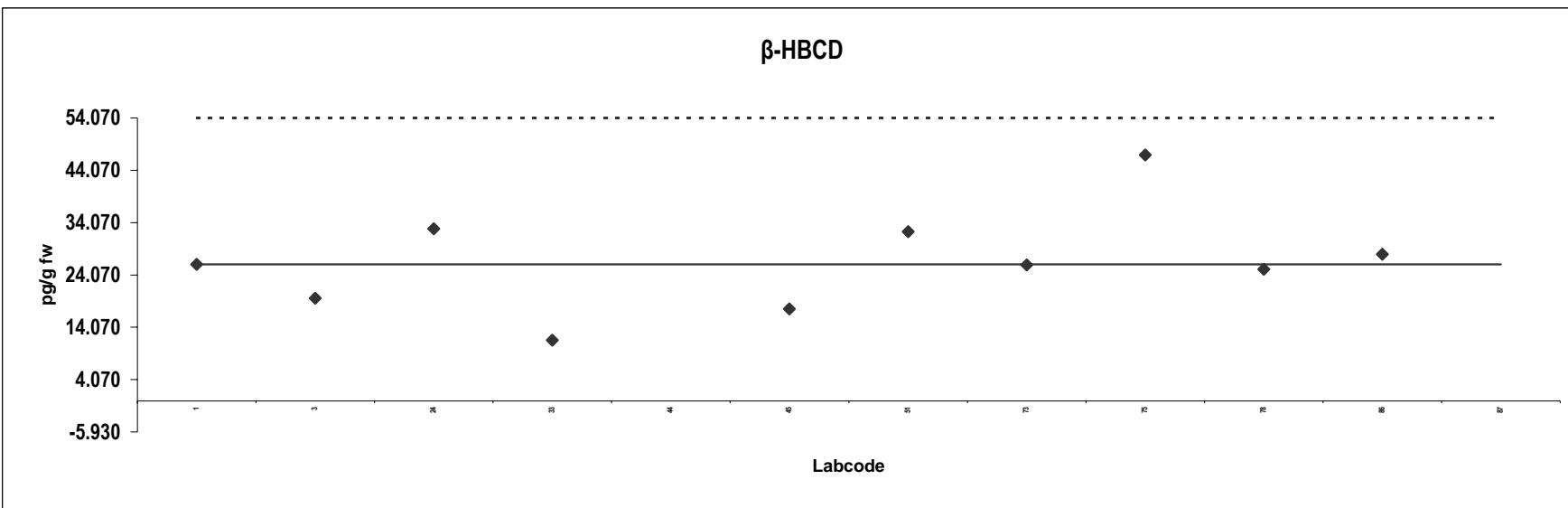


**Herring**  
Congener:  $\beta$ -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	26				
3	20				
24	33				
33	12				
44	394	ND Outlier			
45	18				
51	32				
73	26				
75	47				
78	25				
86	28				
87	175	Outlier			

**Consensus statistics**

Consensus median, pg/g	26
Median all values pg/g	27
Consensus mean, pg/g	27
Standard deviation, pg/g	9.7
Relative standard deviation, %	36
No. of values reported	12
No. of values removed	2
No. of reported non-detects	1

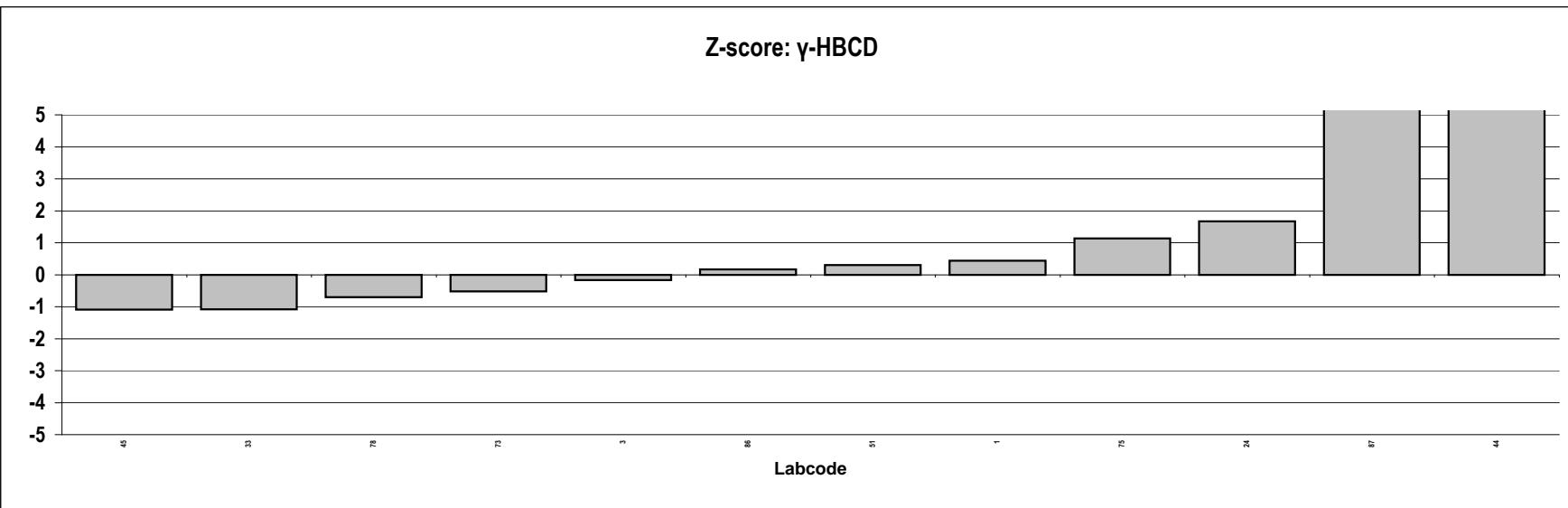
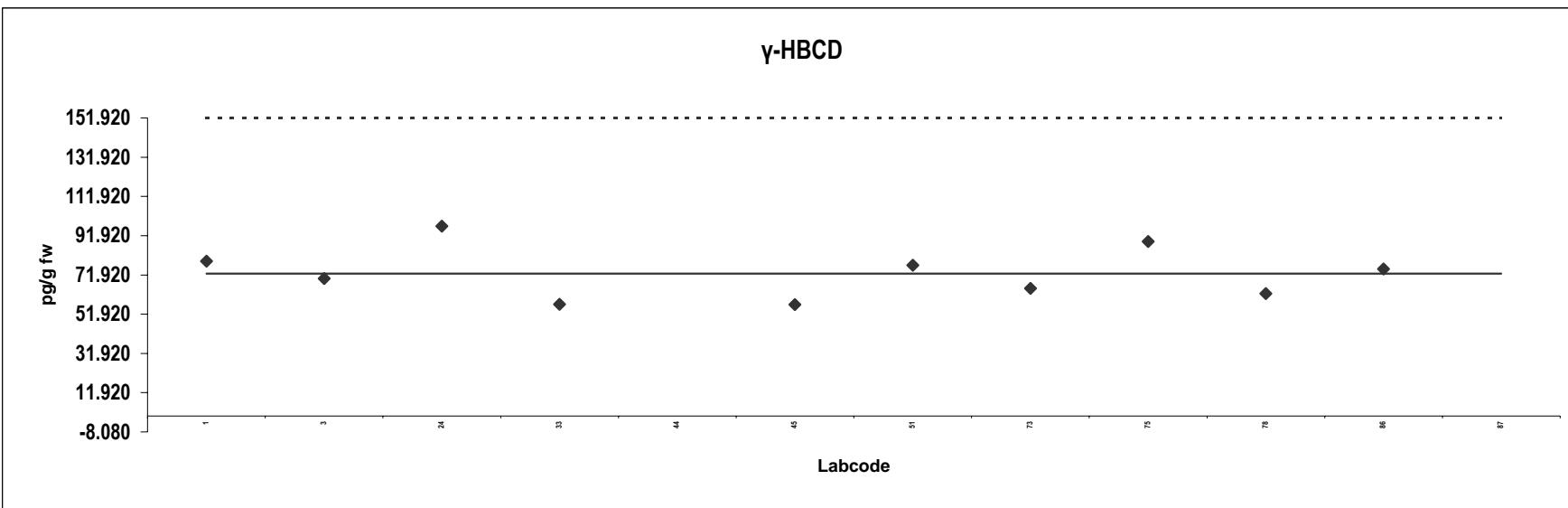


**Herring**  
Congener:  $\gamma$ -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	79				
3	70				
24	97				
33	57				
44	1750	Outlier			
45	57				
51	77				
73	65				
75	89				
78	62				
86	75				
87	160	Outlier			

**Consensus statistics**

Consensus median, pg/g	73
Median all values pg/g	76
Consensus mean, pg/g	73
Standard deviation, pg/g	13
Relative standard deviation, %	18
No. of values reported	12
No. of values removed	2
No. of reported non-detects	0

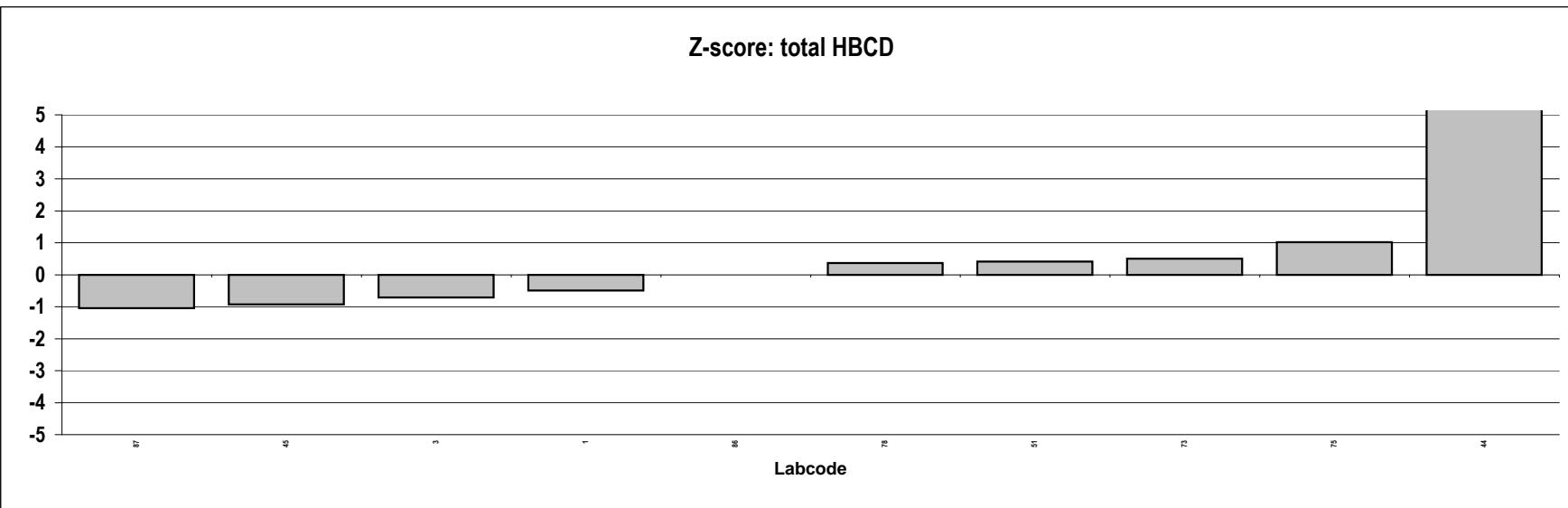
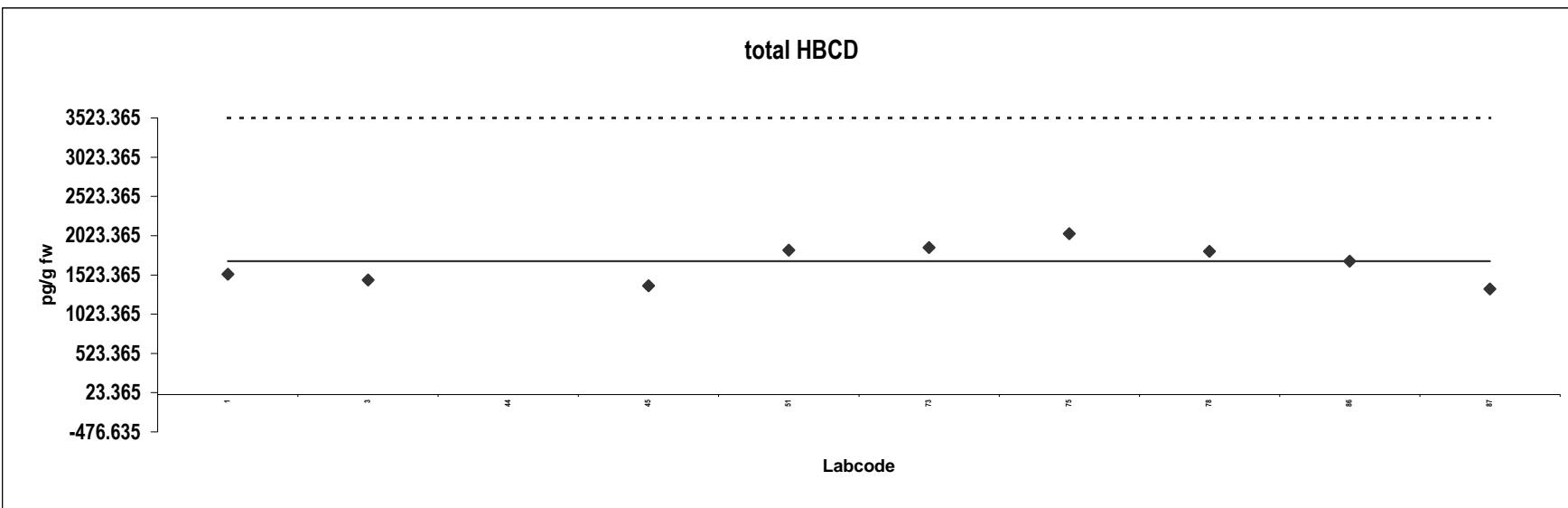


**Herring**  
Congener: total HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1533				
3	1460				
44	8678	Outlier			
45	1385				
51	1840				
73	1871				
75	2047				
78	1823				
86	1700				
87	1346				

**Consensus statistics**

Consensus median, pg/g	1700
Median all values pg/g	1762
Consensus mean, pg/g	1667
Standard deviation, pg/g	246
Relative standard deviation, %	15
No. of values reported	10
No. of values removed	1
No. of reported non-detects	0





## **Appendix 4:**

Presentation of results  
for Milk



## Appendix 34: Presentation of results: Milk

### Statistic calculations for PCDDs, PCDFs and dioxin-like PCBs

For each congener, the outliers were removed and the consensus calculated according to the following procedure:

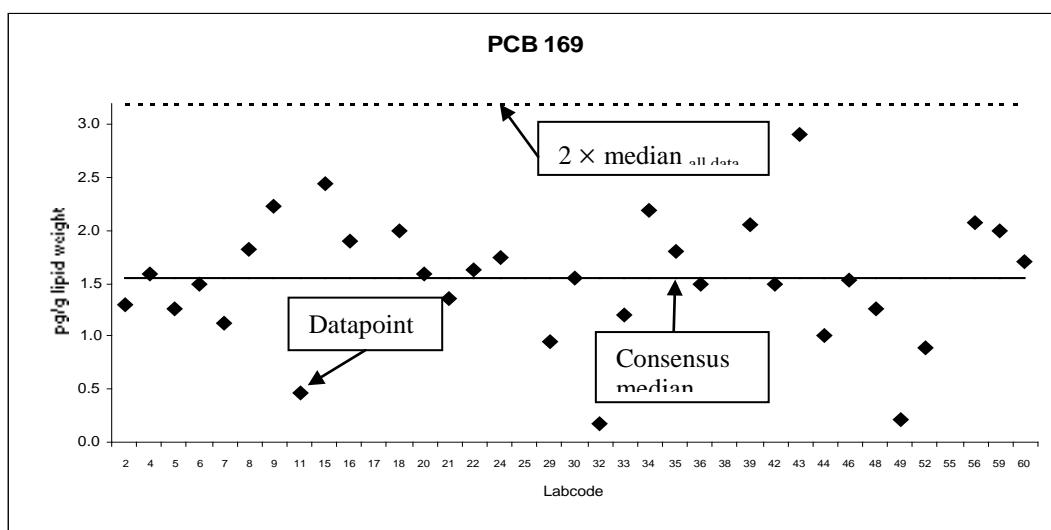
1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners.
2. Values exceeding  $2 \times$  this median were defined as outliers and removed from the data set.
3. Median, mean and standard deviation were re-calculated from the remaining data. This second median was called consensus.

### Statistic calculations for indicator PCBs, PBDEs and HBCD

For each congener, the outliers were removed and the consensus calculated according to the following procedure:

1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners (NDs).
2. Values exceeding  $2 \times$  this median were defined as outliers and removed from the data set. The NDs were also removed.
3. Median, mean and standard deviation were re-calculated from the remaining data. This second median was called consensus.
4. For comparison, median, mean and standard deviation were also calculated without removing NDs.

The diagram shows the reported data up to approximately the limit for outliers ( $2 \times$  the first median).



### Z-Scores of individual congeners

Z-scores of each congener were calculated for each laboratory according to the following equation:

$$z = (x - X)/\sigma$$

where  $x$  = reported value;  $X$  = assigned value (consensus);  $\sigma$  = target value for standard deviation. A  $\sigma$  of 20% of the consensus was used, i.e. z-scores between +1 and -1 reflect a deviation of  $\pm 20\%$  from the consensus value.

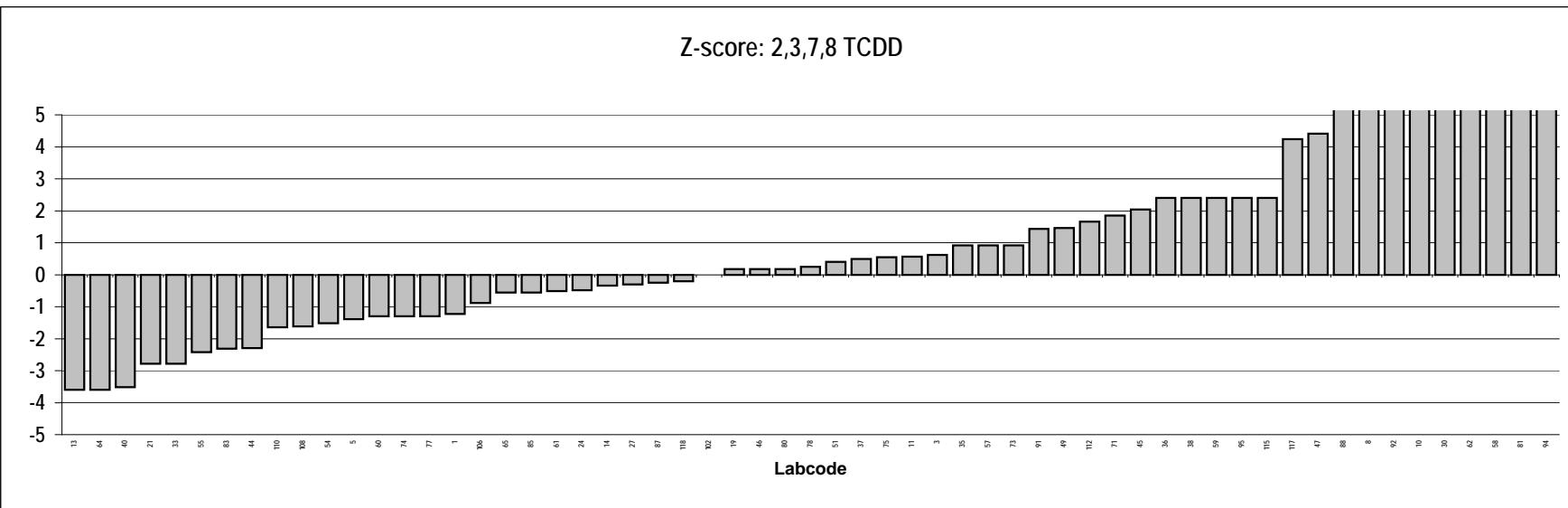
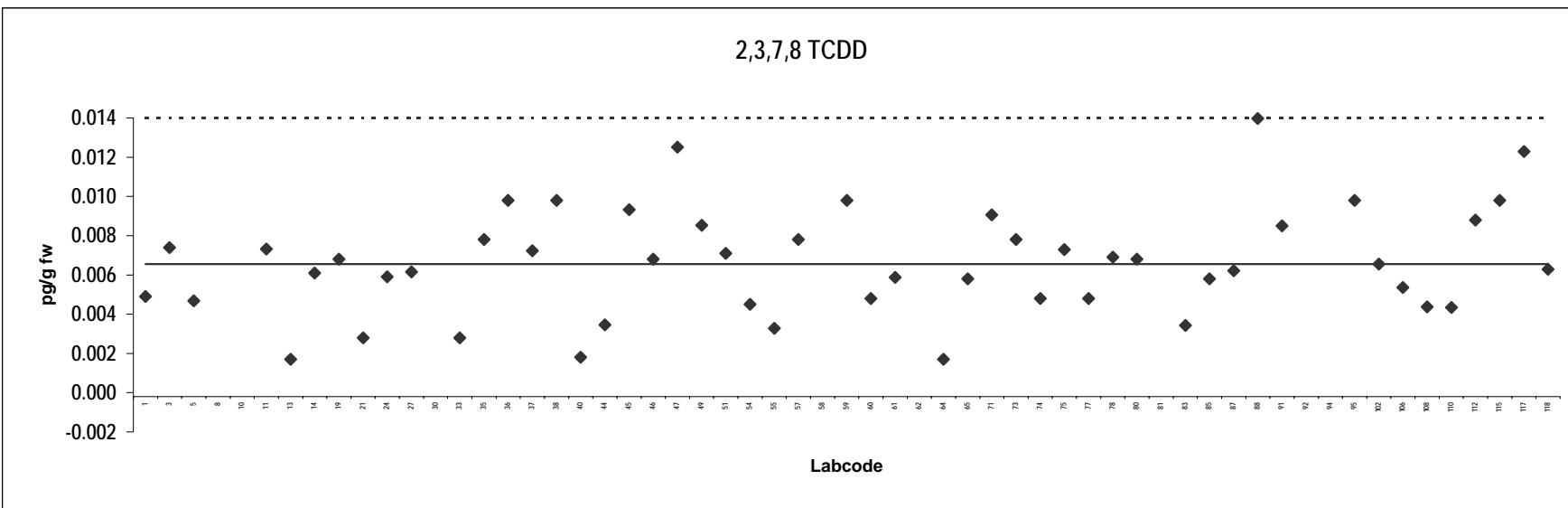


**Milk**  
Congener: 2,3,7,8 TCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.0051		87	0.0064	
3	0.0076		88	0.014	
5	0.0049		91	0.0087	
8	0.017	Outlier	92	0.018	Outlier
10	0.019	Outlier,ND	94	0.040	Outlier,ND
11	0.0075		95	0.010	ND
13	0.0019	ND	102	0.0068	
14	0.0063		106	0.0056	
19	0.0070		108	0.0046	ND
21	0.0030		110	0.0045	
24	0.0061		112	0.0090	
27	0.0064		115	0.010	
30	0.022	Outlier,ND	117	0.012	ND
33	0.0030	ND	118	0.0065	
35	0.0080				
36	0.010	ND			
37	0.0074				
38	0.010	ND			
40	0.0020	ND			
44	0.0037				
45	0.0095				
46	0.0070				
47	0.013				
49	0.0087				
51	0.0073				
54	0.0047				
55	0.0035	ND			
57	0.0080				
58	0.030	Outlier			
59	0.010				
60	0.0050	ND			
61	0.0061				
62	0.024	Outlier			
64	0.0019	ND			
65	0.0060				
71	0.0093				
73	0.0080				
74	0.0050	ND			
75	0.0075				
77	0.0050				
78	0.0071				
80	0.0070				
81	0.035	Outlier,ND			
83	0.0036				
85	0.0060				

**Consensus statistics**

Consensus median, pg/g	0.0068
Median all values pg/g	0.0071
Consensus mean, pg/g	0.0068
Standard deviation, pg/g	0.0027
Relative standard deviation, %	40
No. of values reported	59
No. of values removed	8
No. of reported non-detects	16

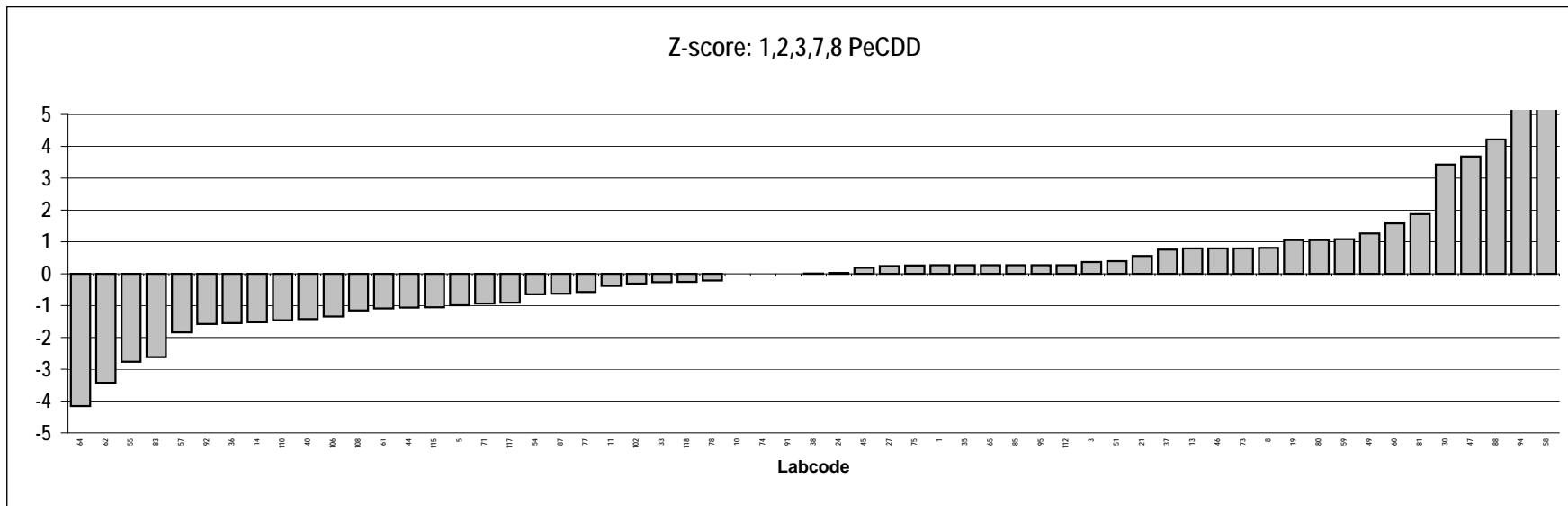
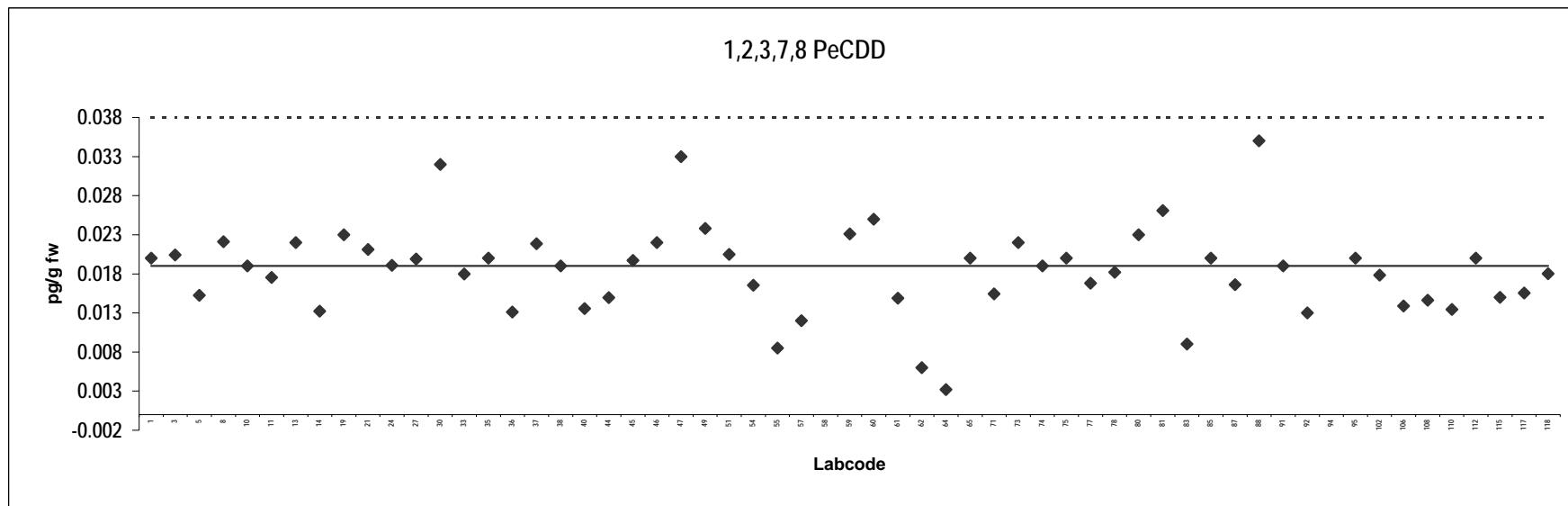


**Milk**  
Congener: 1,2,3,7,8 PeCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.020		87	0.017	
3	0.020		88	0.035	
5	0.015		91	0.019	
8	0.022		92	0.013	
10	0.019	ND	94	0.040	
11	0.018		95	0.020	
13	0.022		102	0.018	
14	0.013		106	0.014	
19	0.023		108	0.015	
21	0.021		110	0.013	
24	0.019		112	0.020	
27	0.020		115	0.015	
30	0.032	ND	117	0.016	
33	0.018		118	0.018	
35	0.020				
36	0.013				
37	0.022				
38	0.019				
40	0.014				
44	0.015				
45	0.020				
46	0.022				
47	0.033				
49	0.024				
51	0.021				
54	0.017				
55	0.0085	ND			
57	0.012				
58	0.080	Outlier			
59	0.023				
60	0.025				
61	0.015				
62	0.0060				
64	0.0032	ND			
65	0.020				
71	0.015				
73	0.022				
74	0.019				
75	0.020				
77	0.017				
78	0.018				
80	0.023				
81	0.026	ND			
83	0.0090				
85	0.020				

**Consensus statistics**

Consensus median, pg/g	0.019
Median all values pg/g	0.019
Consensus mean, pg/g	0.019
Standard deviation, pg/g	0.0057
Relative standard deviation, %	31
No. of values reported	59
No. of values removed	2
No. of reported non-detects	7

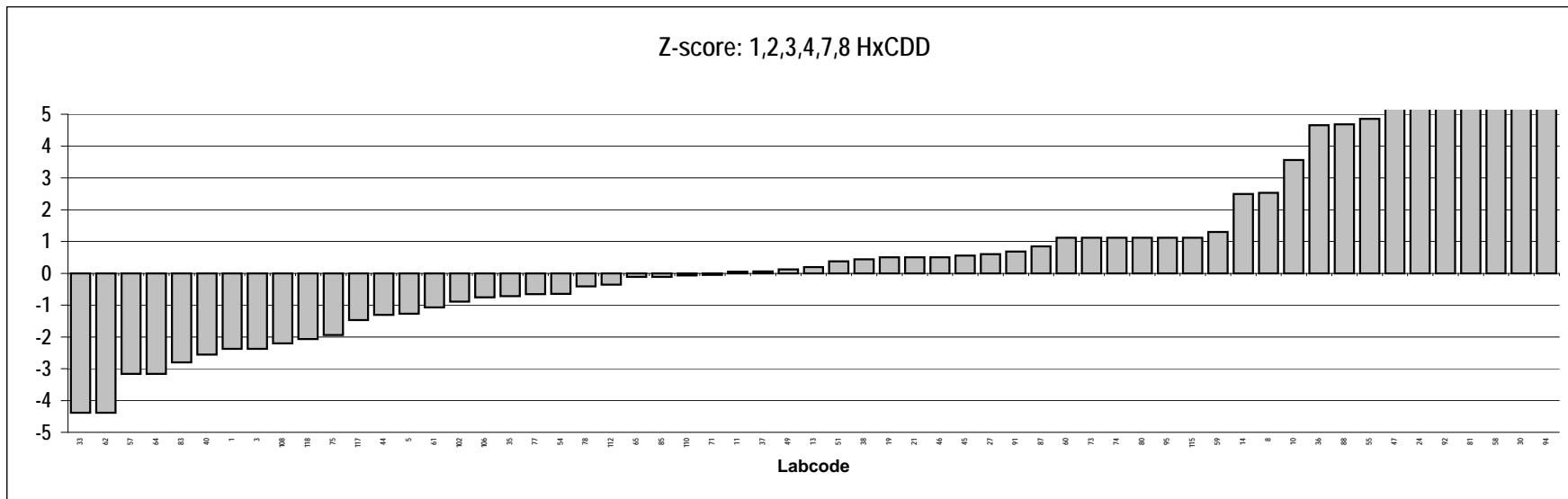
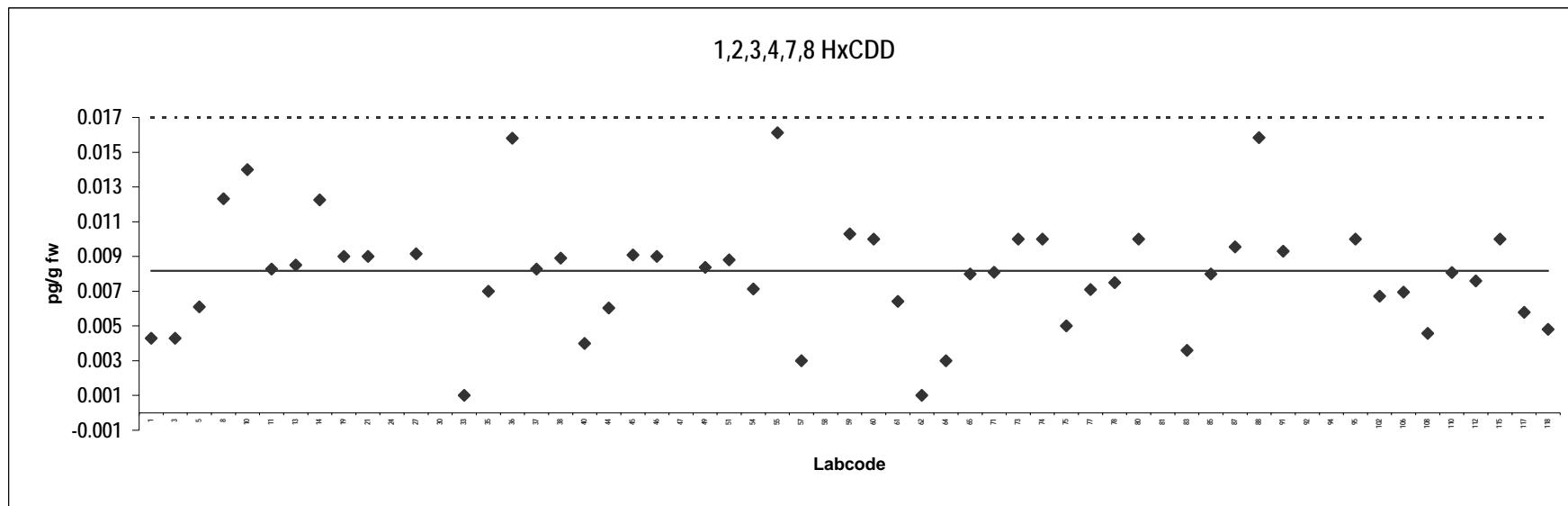


**Milk**  
**Congener: 1,2,3,4,7,8 HxCDD**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.0043		87	0.0096	
3	0.0043		88	0.016	
5	0.0061		91	0.0093	
8	0.012		92	0.022	Outlier,ND
10	0.014	ND	94	0.050	Outlier,ND
11	0.0083		95	0.010	ND
13	0.0085		102	0.0067	
14	0.012		106	0.0069	
19	0.0090		108	0.0046	ND
21	0.0090		110	0.0081	
24	0.021	Outlier	112	0.0076	
27	0.0092		115	0.010	
30	0.029	Outlier,ND	117	0.0058	ND
33	0.0010	ND	118	0.0048	
35	0.0070				
36	0.016				
37	0.0083				
38	0.0089				
40	0.0040	ND			
44	0.0060				
45	0.0091				
46	0.0090				
47	0.020	Outlier			
49	0.0084				
51	0.0088				
54	0.0071				
55	0.016	ND			
57	0.0030				
58	0.027	Outlier			
59	0.010				
60	0.010				
61	0.0064				
62	0.0010				
64	0.0030	ND			
65	0.0080				
71	0.0081				
73	0.010				
74	0.010	ND			
75	0.0050				
77	0.0071				
78	0.0075				
80	0.010				
81	0.027	Outlier,ND			
83	0.0036				
85	0.0080				

**Consensus statistics**

Consensus median, pg/g	0.0082
Median all values pg/g	0.0085
Consensus mean, pg/g	0.0080
Standard deviation, pg/g	0.0033
Relative standard deviation, %	41
No. of values reported	59
No. of values removed	7
No. of reported non-detects	13

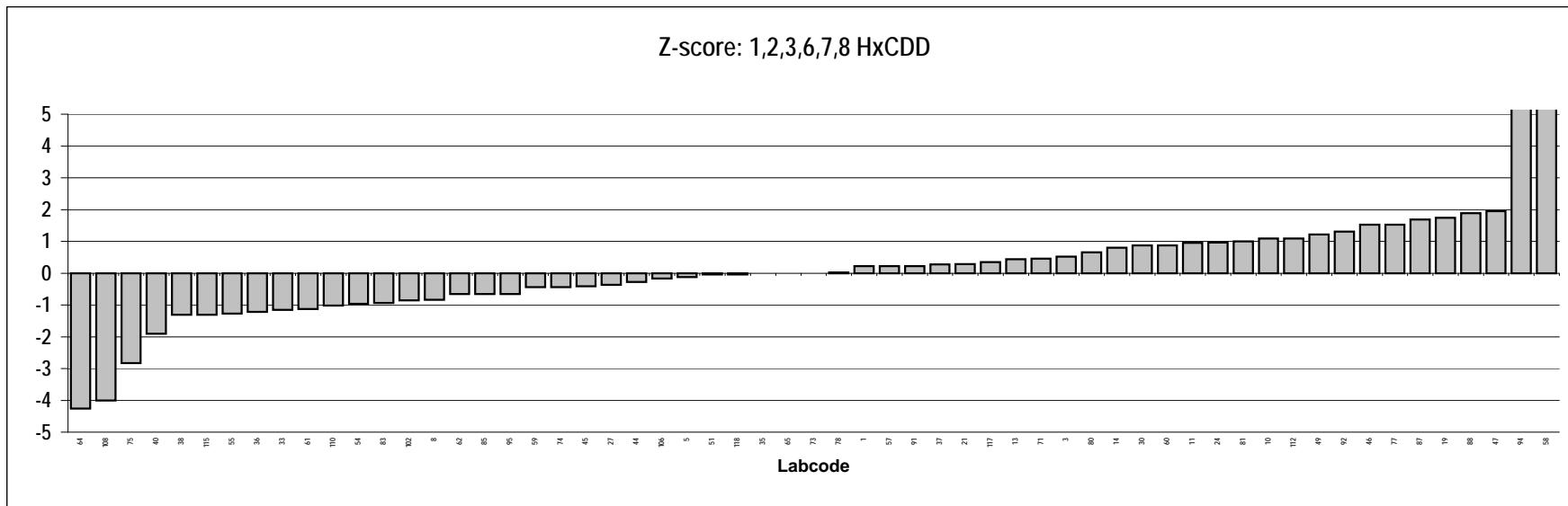
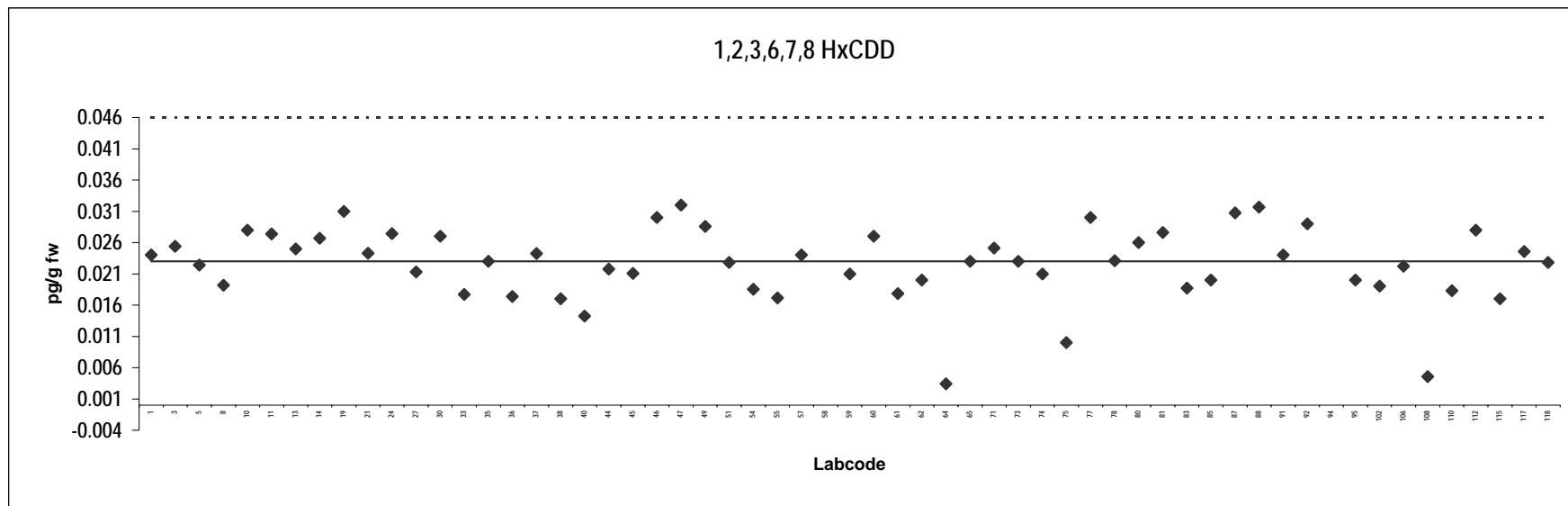


**Milk**  
**Congener: 1,2,3,6,7,8 HxCDD**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.024		87	0.031	
3	0.025		88	0.032	
5	0.022		91	0.024	
8	0.019		92	0.029	
10	0.028		94	0.050	
11	0.027		95	0.020	
13	0.025		102	0.019	
14	0.027		106	0.022	
19	0.031		108	0.0046	ND
21	0.024		110	0.018	
24	0.027		112	0.028	
27	0.021		115	0.017	
30	0.027	ND	117	0.025	
33	0.018		118	0.023	
35	0.023				
36	0.017				
37	0.024				
38	0.017				
40	0.014				
44	0.022				
45	0.021				
46	0.030				
47	0.032				
49	0.029				
51	0.023				
54	0.019				
55	0.017	ND			
57	0.024				
58	0.078	Outlier			
59	0.021				
60	0.027				
61	0.018				
62	0.020				
64	0.0034	ND			
65	0.023				
71	0.025				
73	0.023				
74	0.021				
75	0.010				
77	0.030				
78	0.023				
80	0.026				
81	0.028	ND			
83	0.019				
85	0.020				

**Consensus statistics**

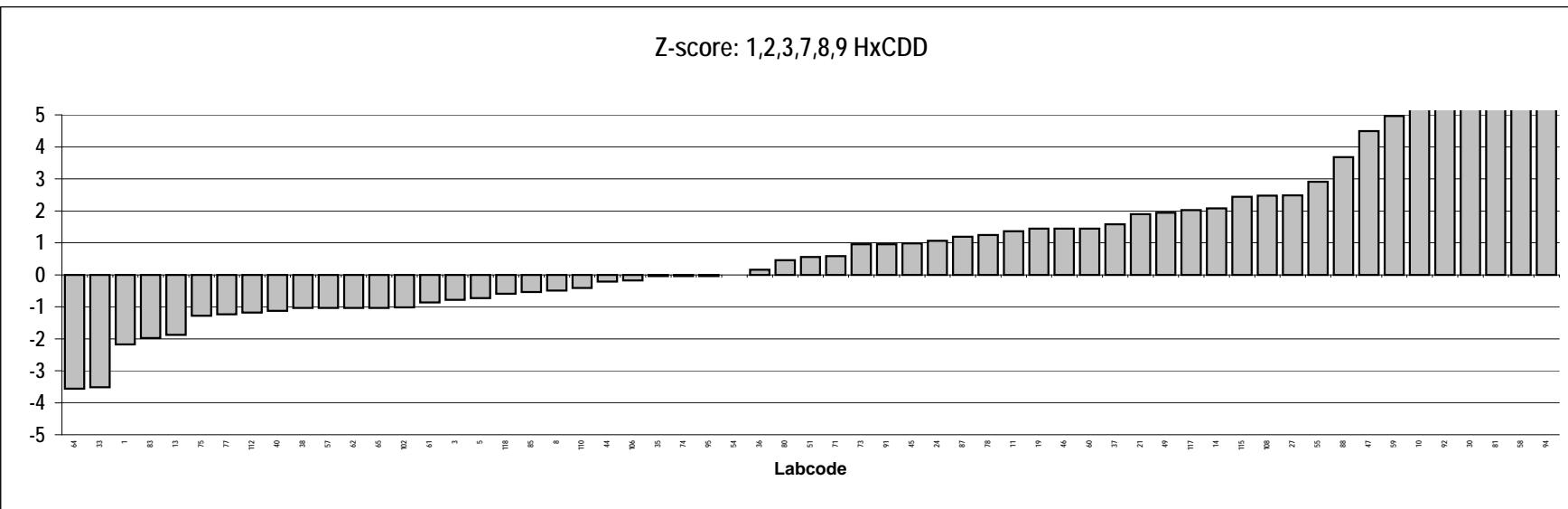
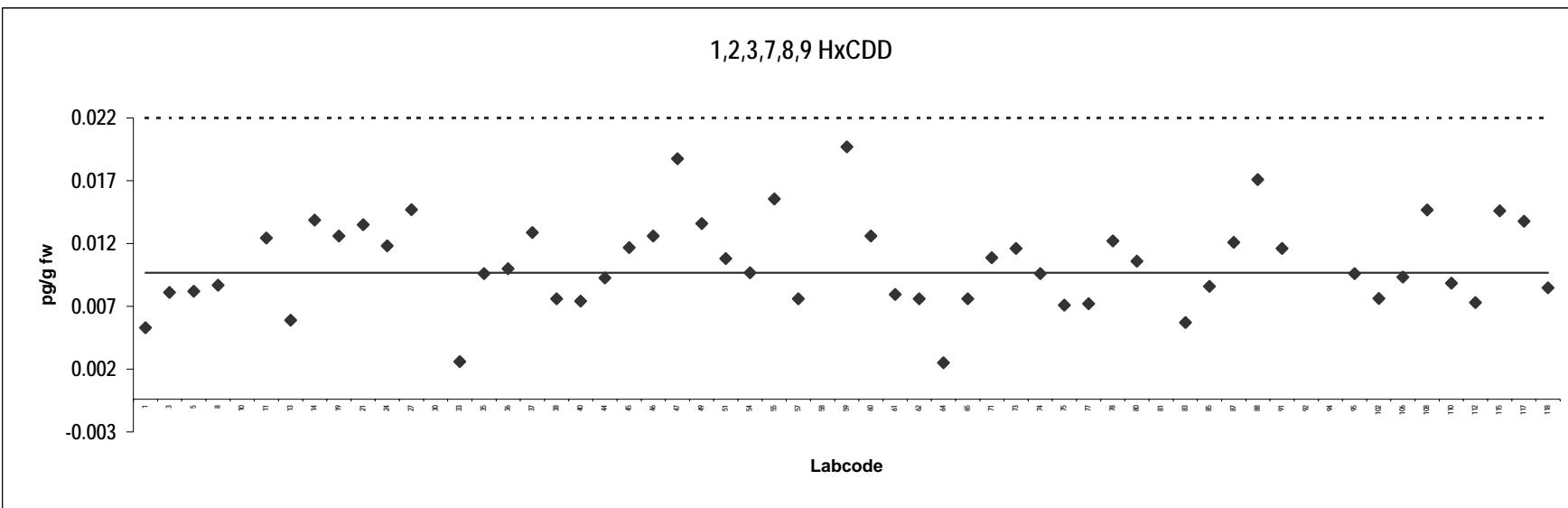
Consensus median, pg/g	0.023
Median all values pg/g	0.023
Consensus mean, pg/g	0.023
Standard deviation, pg/g	0.0059
Relative standard deviation, %	26
No. of values reported	59
No. of values removed	2
No. of reported non-detects	7



**Milk**  
**Congener: 1,2,3,7,8,9 HxCDD**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.0057		87	0.012	
3	0.0085		88	0.018	
5	0.0086		91	0.012	
8	0.0091		92	0.025	
10	0.023	Outlier	94	0.050	Outlier,ND
11	0.013		95	0.010	Outlier,ND
13	0.0063		102	0.0080	
14	0.014		106	0.0097	
19	0.013		108	0.015	
21	0.014		110	0.0092	
24	0.012		112	0.0077	
27	0.015		115	0.015	
30	0.027	Outlier,ND	117	0.014	
33	0.0030	ND	118	0.0089	
35	0.010				
36	0.010				
37	0.013				
38	0.0080	ND			
40	0.0078				
44	0.0097				
45	0.012				
46	0.013				
47	0.019				
49	0.014				
51	0.011				
54	0.010				
55	0.016	ND			
57	0.0080				
58	0.045	Outlier			
59	0.020				
60	0.013				
61	0.0083				
62	0.0080				
64	0.0029	ND			
65	0.0080				
71	0.011				
73	0.012				
74	0.010				
75	0.0075				
77	0.0076				
78	0.013				
80	0.011				
81	0.031	Outlier,ND			
83	0.0061				
85	0.0090				

Consensus statistics	
Consensus median, pg/g	0.010
Median all values pg/g	0.011
Consensus mean, pg/g	0.011
Standard deviation, pg/g	0.0036
Relative standard deviation, %	33
No. of values reported	59
No. of values removed	6
No. of reported non-detects	8

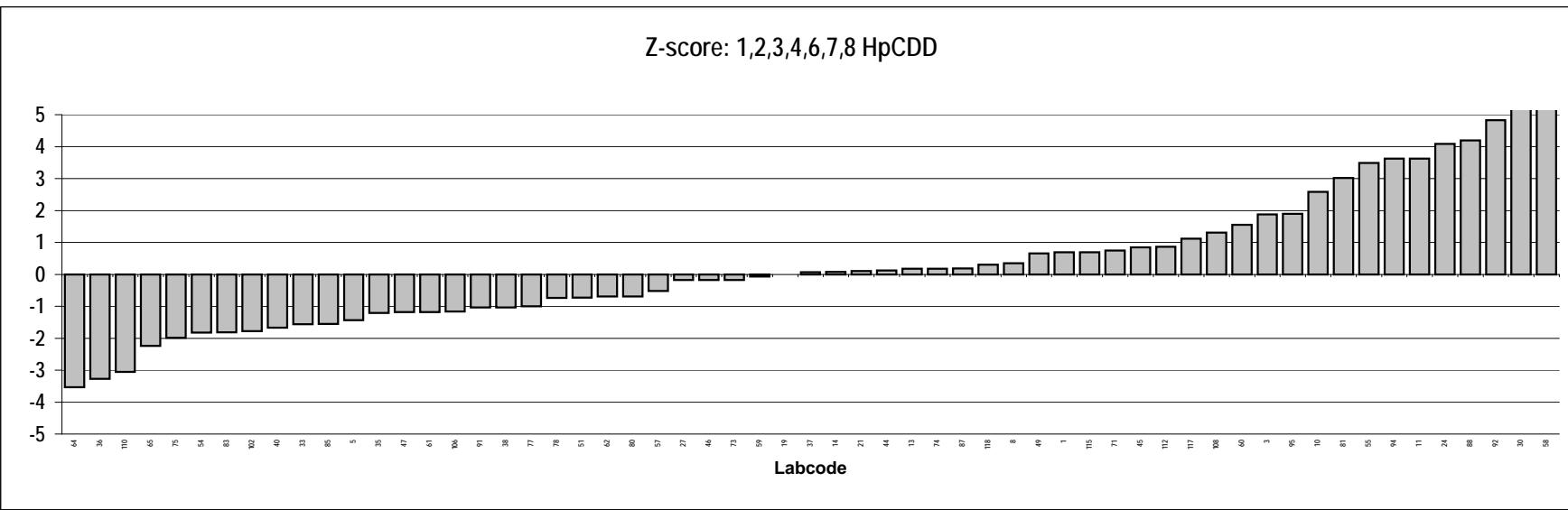
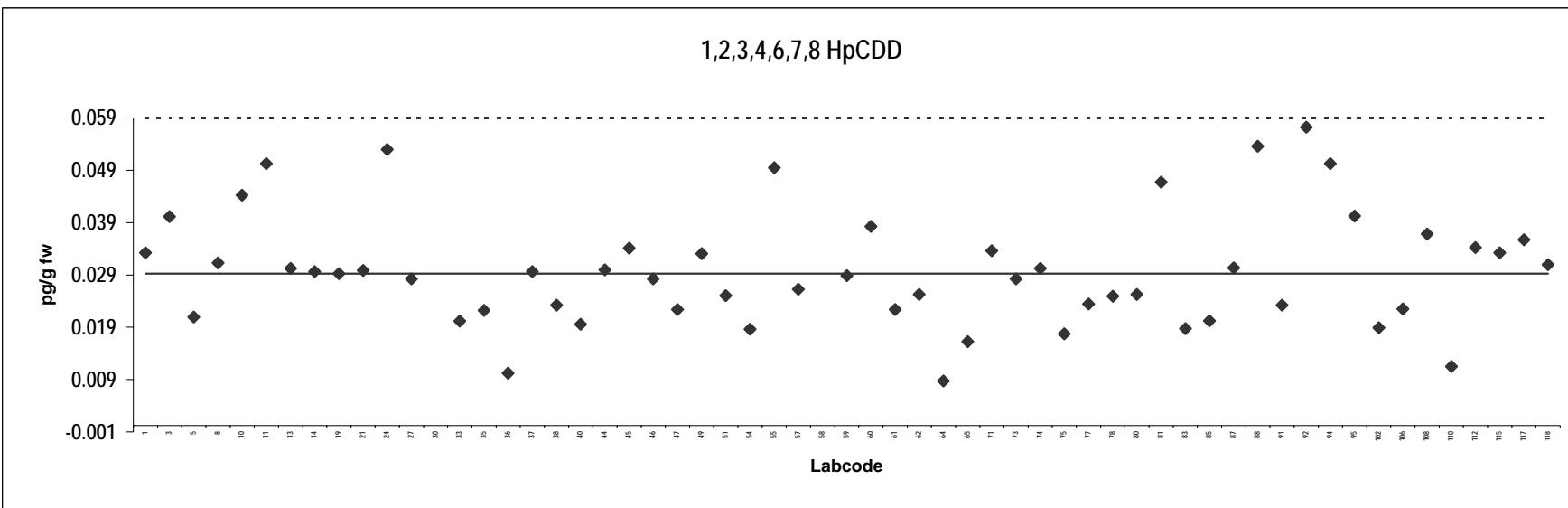


**Milk**  
**Congener: 1,2,3,4,6,7,8 HpCDD**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.033		87	0.030	
3	0.040		88	0.053	
5	0.021		91	0.023	
8	0.031		92	0.057	
10	0.044		94	0.050	ND
11	0.050		95	0.040	ND
13	0.030		102	0.019	
14	0.029		106	0.022	
19	0.029		108	0.037	
21	0.030		110	0.011	
24	0.053		112	0.034	
27	0.028		115	0.033	
30	0.062	Outlier	117	0.035	
33	0.020		118	0.031	
35	0.022				
36	0.010	ND			
37	0.029				
38	0.023				
40	0.019				
44	0.030				
45	0.034				
46	0.028				
47	0.022				
49	0.033				
51	0.025				
54	0.018				
55	0.049	ND			
57	0.026				
58	0.082	Outlier			
59	0.029				
60	0.038				
61	0.022				
62	0.025				
64	0.0085	ND			
65	0.016				
71	0.033				
73	0.028				
74	0.030				
75	0.017				
77	0.023				
78	0.025				
80	0.025				
81	0.047	ND			
83	0.019				
85	0.020				

**Consensus statistics**

Consensus median, pg/g	0.029
Median all values pg/g	0.029
Consensus mean, pg/g	0.030
Standard deviation, pg/g	0.011
Relative standard deviation, %	37
No. of values reported	59
No. of values removed	2
No. of reported non-detects	6

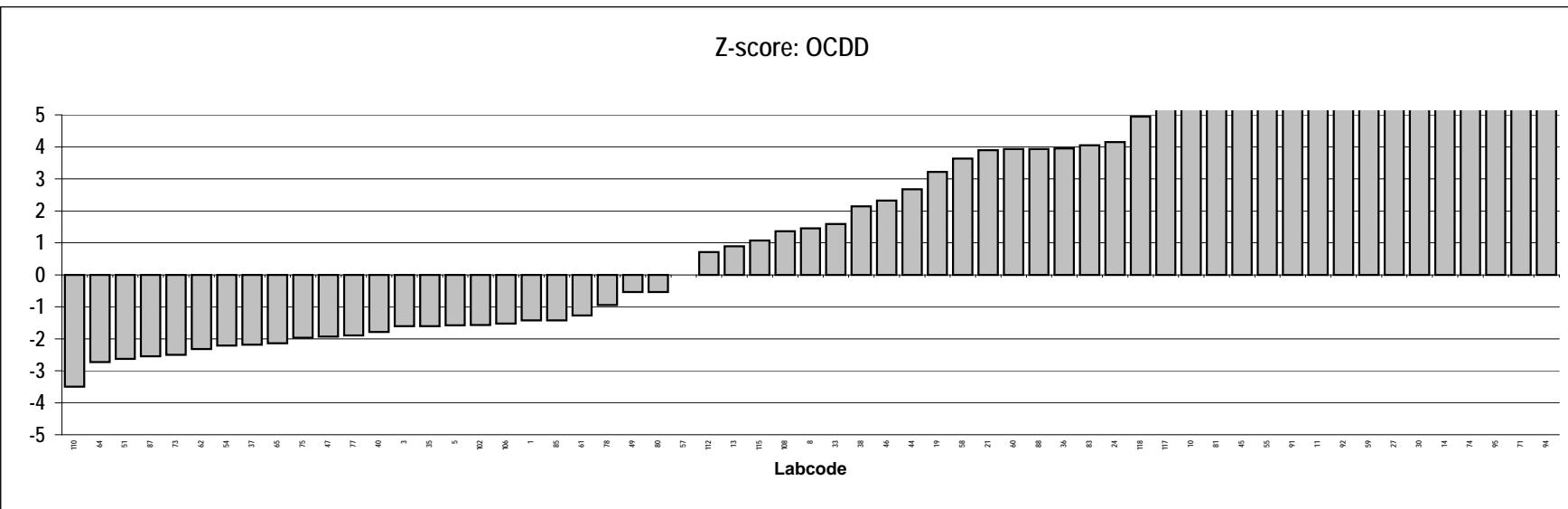
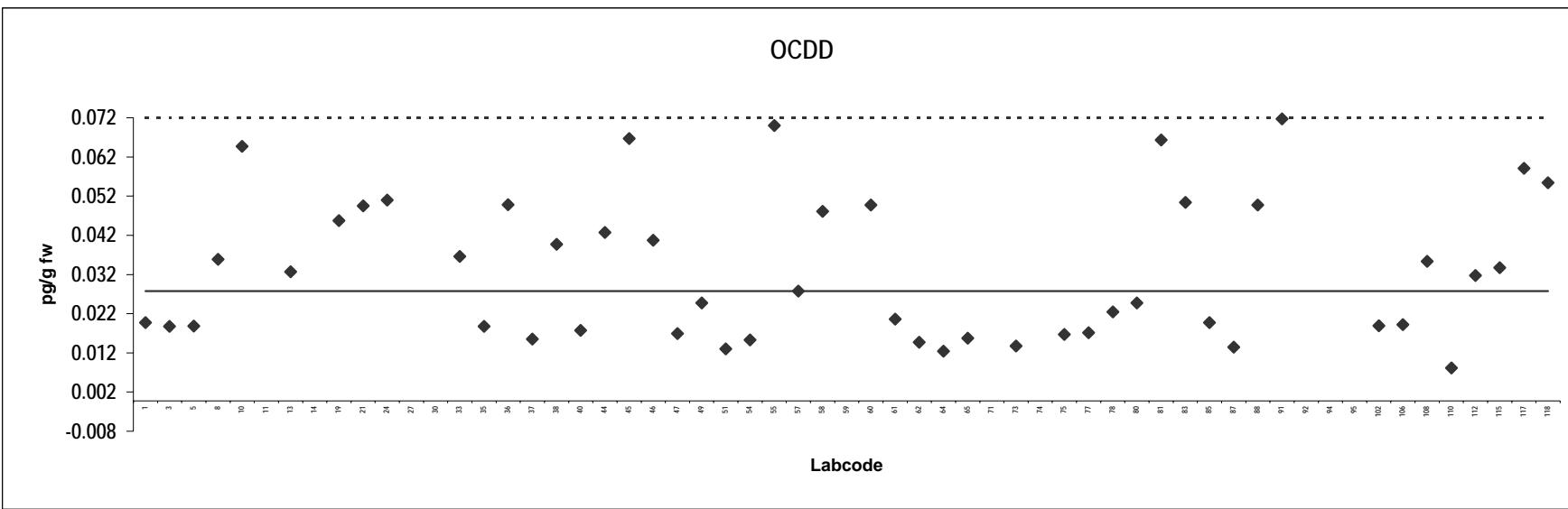


**Milk**  
Congener: OCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.020		87	0.014	
3	0.019		88	0.050	
5	0.019		91	0.072	ND
8	0.036		92	0.073	Outlier
10	0.065		94	2.0	Outlier,ND
11	0.073	Outlier	95	0.10	Outlier,ND
13	0.033		102	0.019	ND
14	0.098	Outlier	106	0.019	
19	0.046		108	0.036	
21	0.050		110	0.0084	ND
24	0.051		112	0.032	
27	0.090	Outlier	115	0.034	
30	0.090	Outlier	117	0.059	
33	0.037		118	0.056	
35	0.019				
36	0.050				
37	0.016				
38	0.040	ND			
40	0.018	ND			
44	0.043				
45	0.067				
46	0.041				
47	0.017				
49	0.025	ND			
51	0.013				
54	0.016				
55	0.070	ND			
57	0.028				
58	0.048				
59	0.088	Outlier			
60	0.050				
61	0.021				
62	0.015				
64	0.013	ND			
65	0.016				
71	0.11	Outlier			
73	0.014				
74	0.10	Outlier			
75	0.017				
77	0.017				
78	0.023				
80	0.025				
81	0.067	ND			
83	0.051				
85	0.020				

**Consensus statistics**

Consensus median, pg/g	0.028
Median all values pg/g	0.036
Consensus mean, pg/g	0.033
Standard deviation, pg/g	0.018
Relative standard deviation, %	55
No. of values reported	59
No. of values removed	10
No. of reported non-detects	11

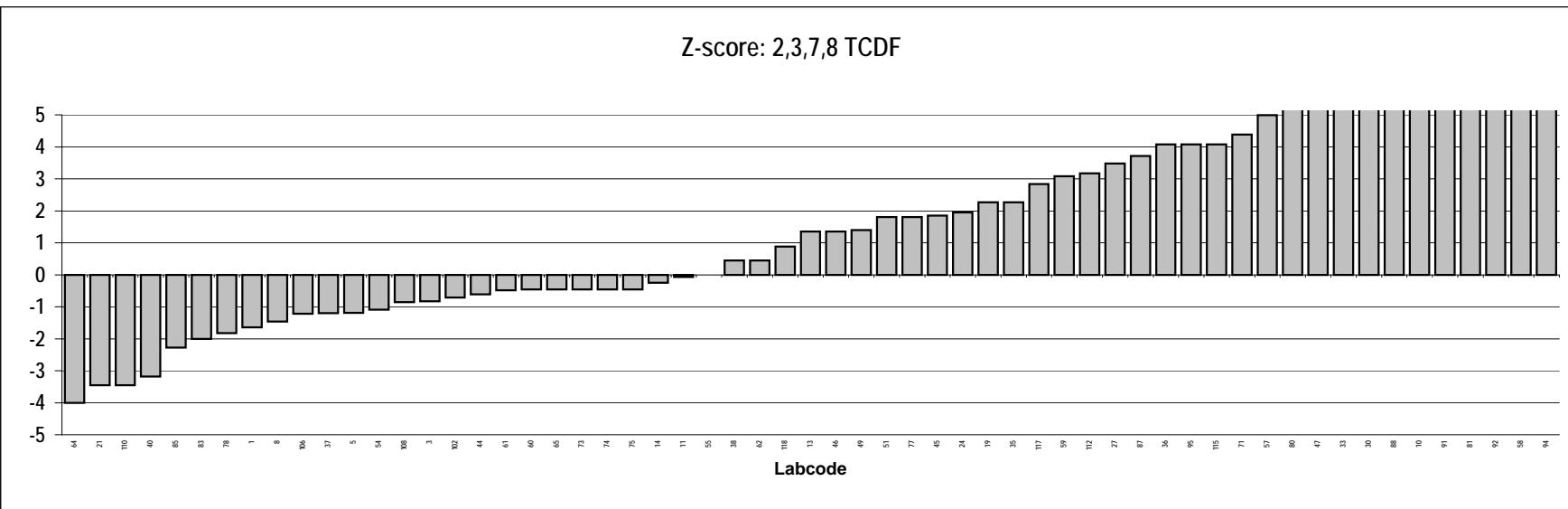
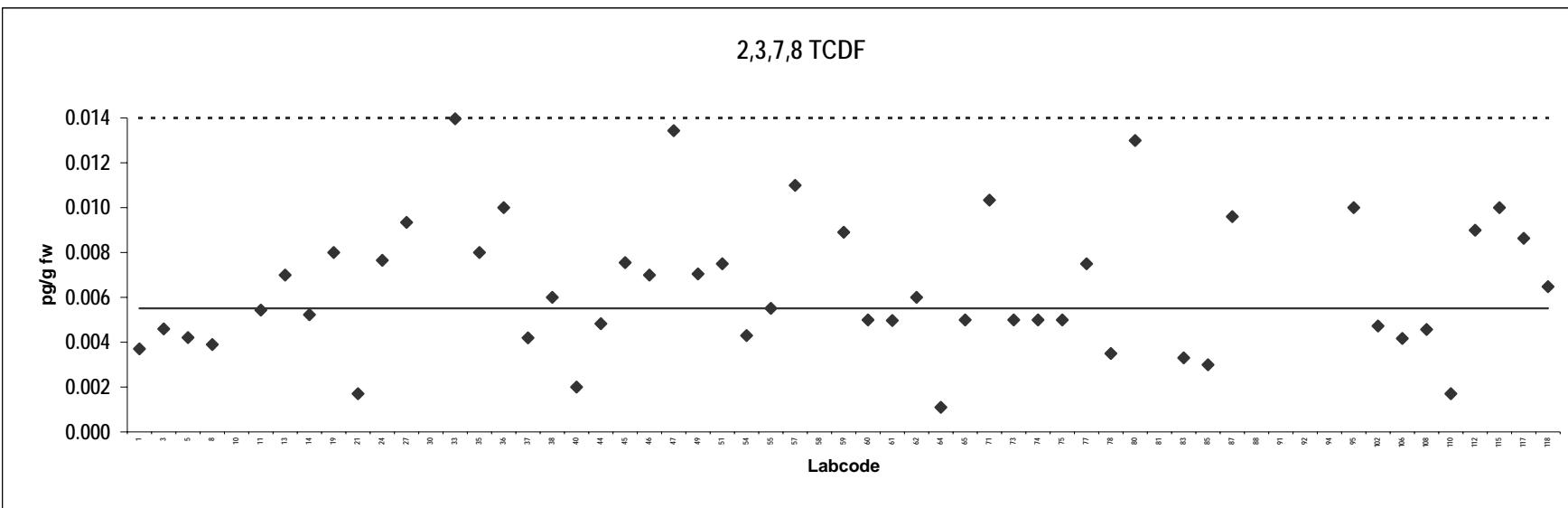


**Milk**  
Congener: 2,3,7,8 TCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.0037		87	0.0096	
3	0.0046		88	0.015	Outlier
5	0.0042		91	0.025	Outlier,ND
8	0.0039		92	0.034	Outlier
10	0.020	Outlier	94	0.067	Outlier
11	0.0054		95	0.010	ND
13	0.0070		102	0.0047	
14	0.0052		106	0.0042	
19	0.0080		108	0.0046	ND
21	0.0017	ND	110	0.0017	ND
24	0.0077		112	0.0090	
27	0.0093		115	0.010	ND
30	0.015	Outlier,ND	117	0.0086	
33	0.014		118	0.0065	
35	0.0080				
36	0.010	ND			
37	0.0042				
38	0.0060	ND			
40	0.0020	ND			
44	0.0048				
45	0.0075				
46	0.0070				
47	0.013				
49	0.0071				
51	0.0075				
54	0.0043				
55	0.0055				
57	0.011				
58	0.036	Outlier			
59	0.0089				
60	0.0050	ND			
61	0.0050				
62	0.0060				
64	0.0011	ND			
65	0.0050				
71	0.010				
73	0.0050				
74	0.0050	ND			
75	0.0050				
77	0.0075				
78	0.0035				
80	0.013				
81	0.026	Outlier,ND			
83	0.0033				
85	0.0030				

**Consensus statistics**

Consensus median, pg/g	0.0055
Median all values pg/g	0.0070
Consensus mean, pg/g	0.0064
Standard deviation, pg/g	0.0030
Relative standard deviation, %	47
No. of values reported	59
No. of values removed	8
No. of reported non-detects	14

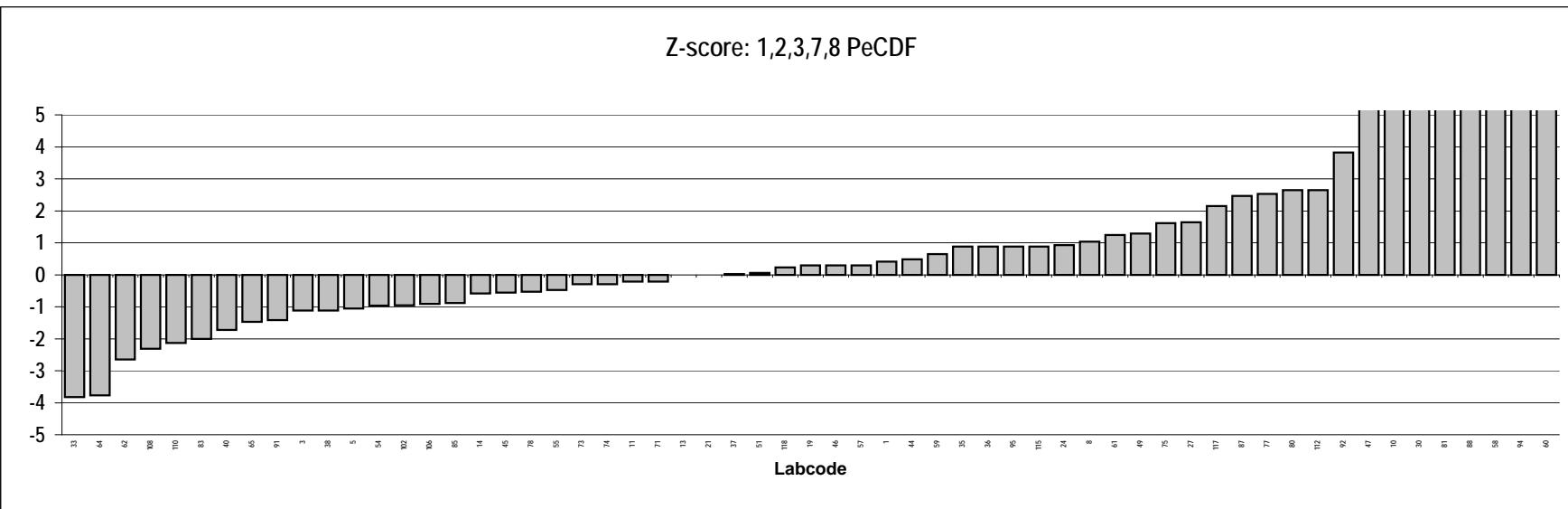
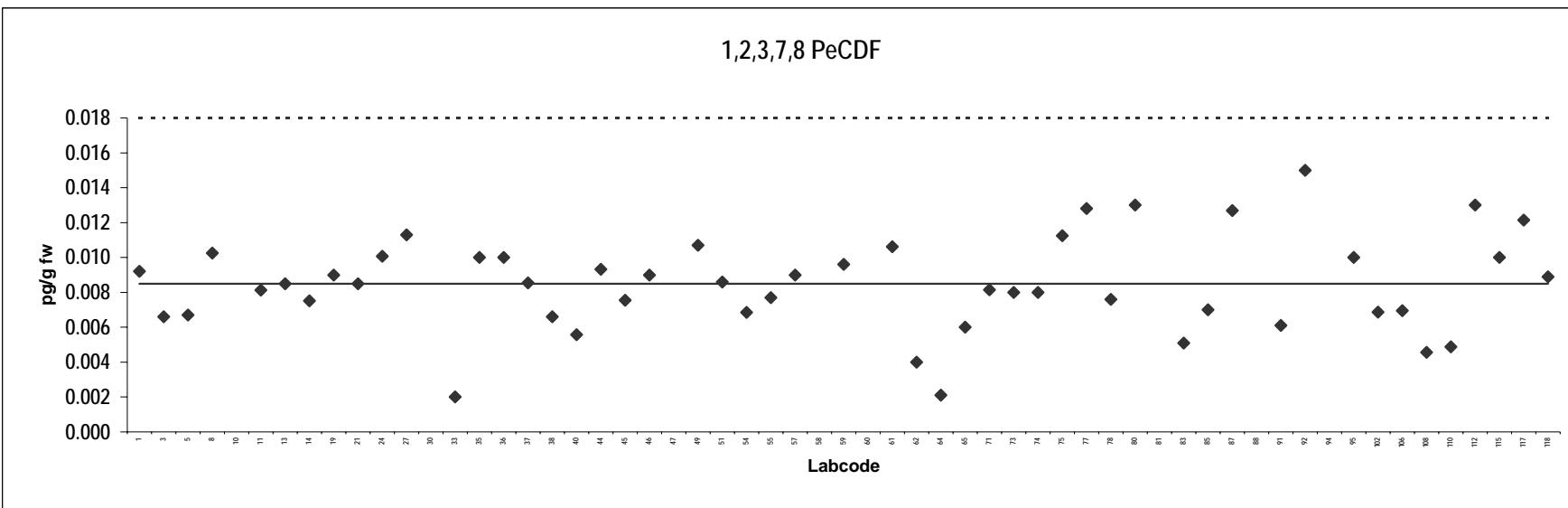


**Milk**  
Congener: 1,2,3,7,8 PeCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.0092		87	0.013	
3	0.0066		88	0.027	
5	0.0067		91	0.0061	Outlier
8	0.010		92	0.015	ND
10	0.020	Outlier	94	0.040	Outlier,ND
11	0.0081		95	0.010	ND
13	0.0085		102	0.0069	
14	0.0075		106	0.0069	
19	0.0090		108	0.0046	ND
21	0.0085		110	0.0049	
24	0.010		112	0.013	
27	0.011		115	0.010	
30	0.020	Outlier,ND	117	0.012	
33	0.0020	ND	118	0.0089	
35	0.010				
36	0.010	ND			
37	0.0085				
38	0.0066				
40	0.0056				
44	0.0093				
45	0.0076				
46	0.0090				
47	0.019	Outlier			
49	0.011				
51	0.0086				
54	0.0069				
55	0.0077	ND			
57	0.0090				
58	0.031	Outlier			
59	0.0096				
60	0.095	Outlier			
61	0.011				
62	0.0040				
64	0.0021	ND			
65	0.0060				
71	0.0081				
73	0.0080				
74	0.0080				
75	0.011				
77	0.013				
78	0.0076				
80	0.013				
81	0.023	Outlier,ND			
83	0.0051				
85	0.0070				

**Consensus statistics**

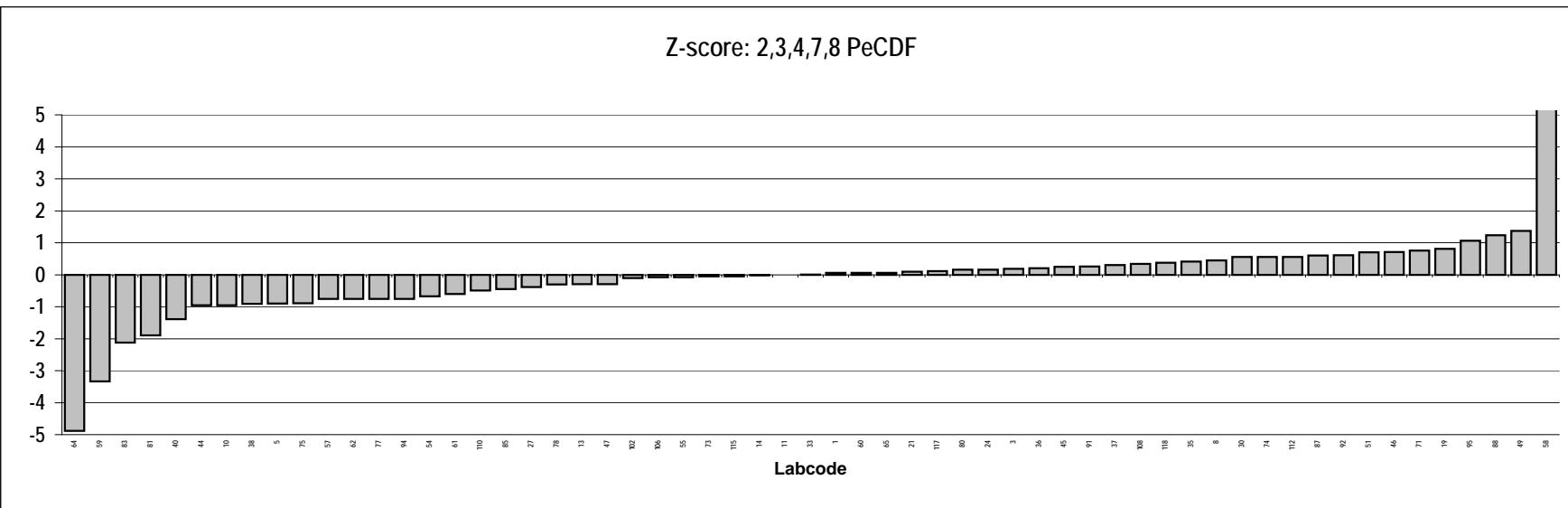
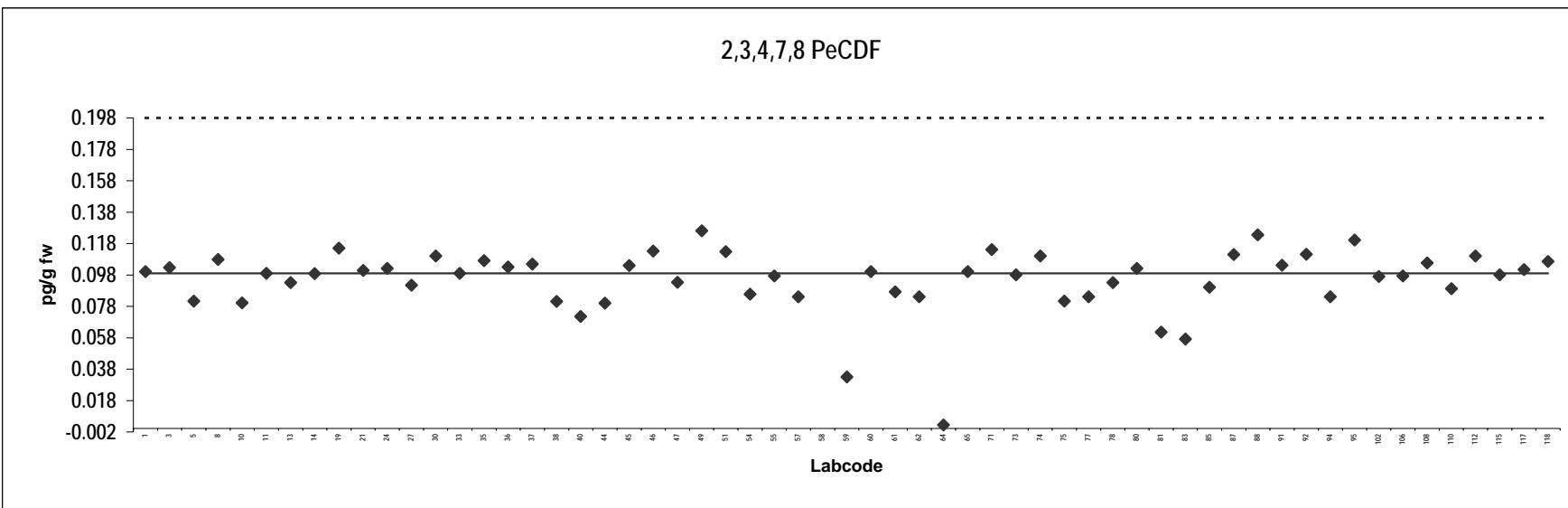
Consensus median, pg/g	0.0085
Median all values pg/g	0.0090
Consensus mean, pg/g	0.0085
Standard deviation, pg/g	0.0027
Relative standard deviation, %	32
No. of values reported	59
No. of values removed	8
No. of reported non-detects	10



**Milk**  
Congener: 2,3,4,7,8 PeCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.10		87	0.11	
3	0.10		88	0.12	
5	0.081		91	0.10	
8	0.11		92	0.11	
10	0.080		94	0.084	
11	0.099		95	0.12	
13	0.093		102	0.097	
14	0.099		106	0.097	
19	0.12		108	0.11	
21	0.10		110	0.089	
24	0.10		112	0.11	
27	0.091		115	0.098	
30	0.11		117	0.10	
33	0.099		118	0.11	
35	0.11				
36	0.10				
37	0.10				
38	0.081				
40	0.071				
44	0.080				
45	0.10				
46	0.11				
47	0.093				
49	0.13				
51	0.11				
54	0.086				
55	0.097				
57	0.084				
58	0.32				
59	0.033				
60	0.10				
61	0.087				
62	0.084				
64	0.0023	ND			
65	0.10				
71	0.11				
73	0.098				
74	0.11				
75	0.081				
77	0.084				
78	0.093				
80	0.10				
81	0.061				
83	0.057				
85	0.090				

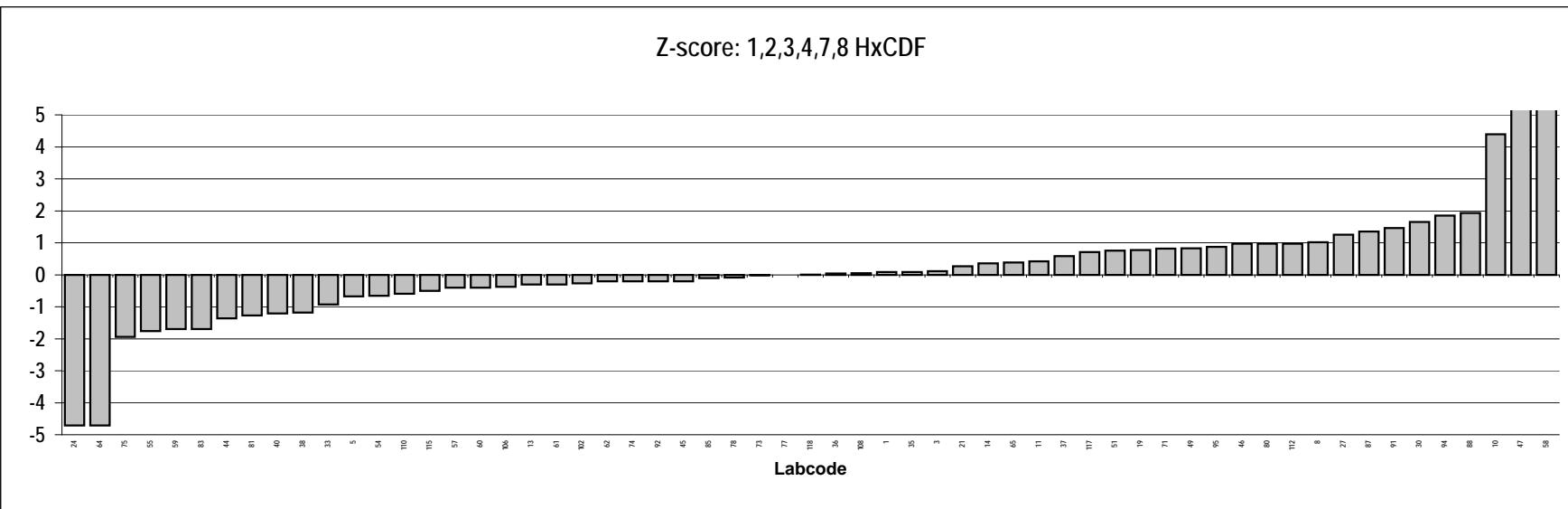
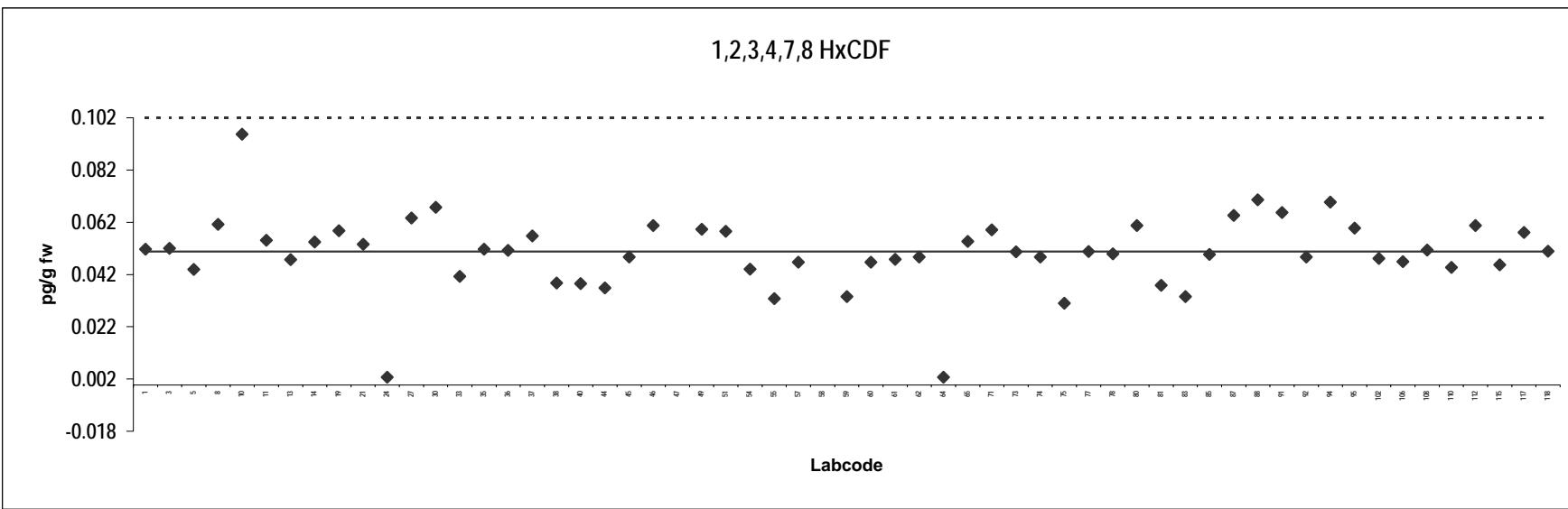
Consensus statistics	
Consensus median, pg/g	0.099
Median all values pg/g	0.099
Consensus mean, pg/g	0.095
Standard deviation, pg/g	0.020
Relative standard deviation, %	21
No. of values reported	59
No. of values removed	1
No. of reported non-detects	1



**Milk**  
Congener: 1,2,3,4,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.052		87	0.065	
3	0.052		88	0.071	
5	0.044		91	0.066	
8	0.062		92	0.049	
10	0.096		94	0.070	
11	0.055		95	0.060	ND
13	0.048		102	0.048	
14	0.055		106	0.047	
19	0.059		108	0.052	
21	0.054		110	0.045	
24	0.0030	ND	112	0.061	
27	0.064		115	0.046	
30	0.068		117	0.058	
33	0.042		118	0.051	
35	0.052				
36	0.052				
37	0.057				
38	0.039				
40	0.039				
44	0.037				
45	0.049				
46	0.061				
47	0.13	Outlier			
49	0.060				
51	0.059				
54	0.044				
55	0.033				
57	0.047				
58	0.18	Outlier			
59	0.034				
60	0.047				
61	0.048				
62	0.049				
64	0.0030	ND			
65	0.055				
71	0.059				
73	0.051				
74	0.049				
75	0.031				
77	0.051				
78	0.050				
80	0.061				
81	0.038				
83	0.034				
85	0.050				

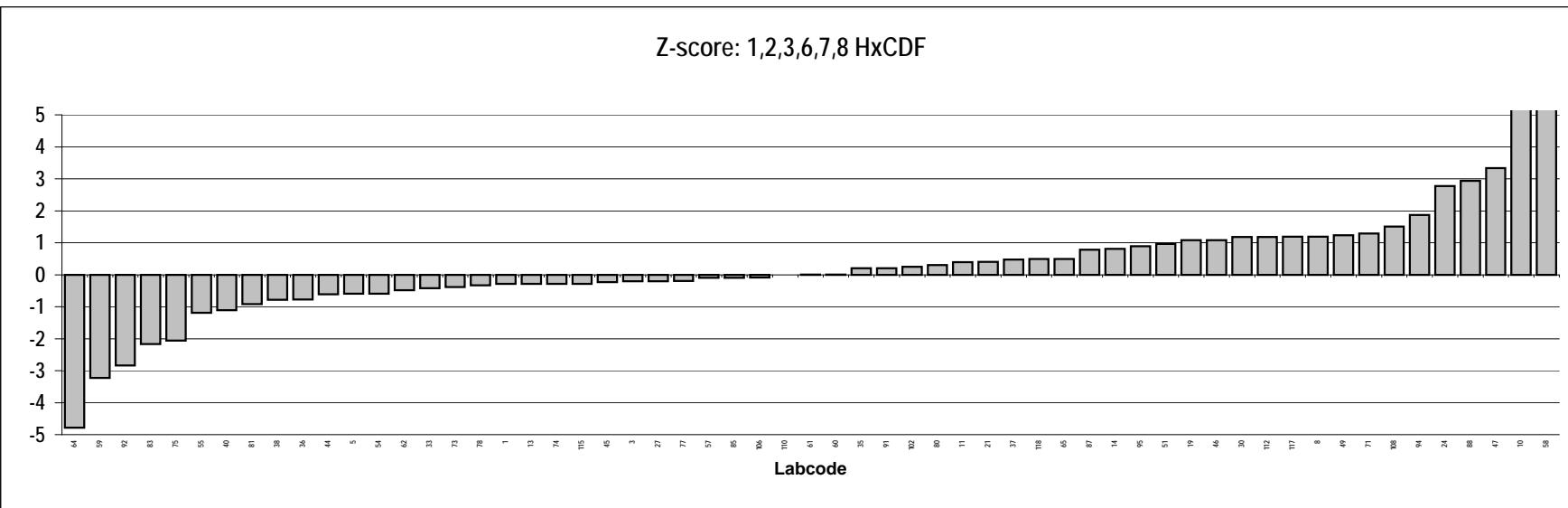
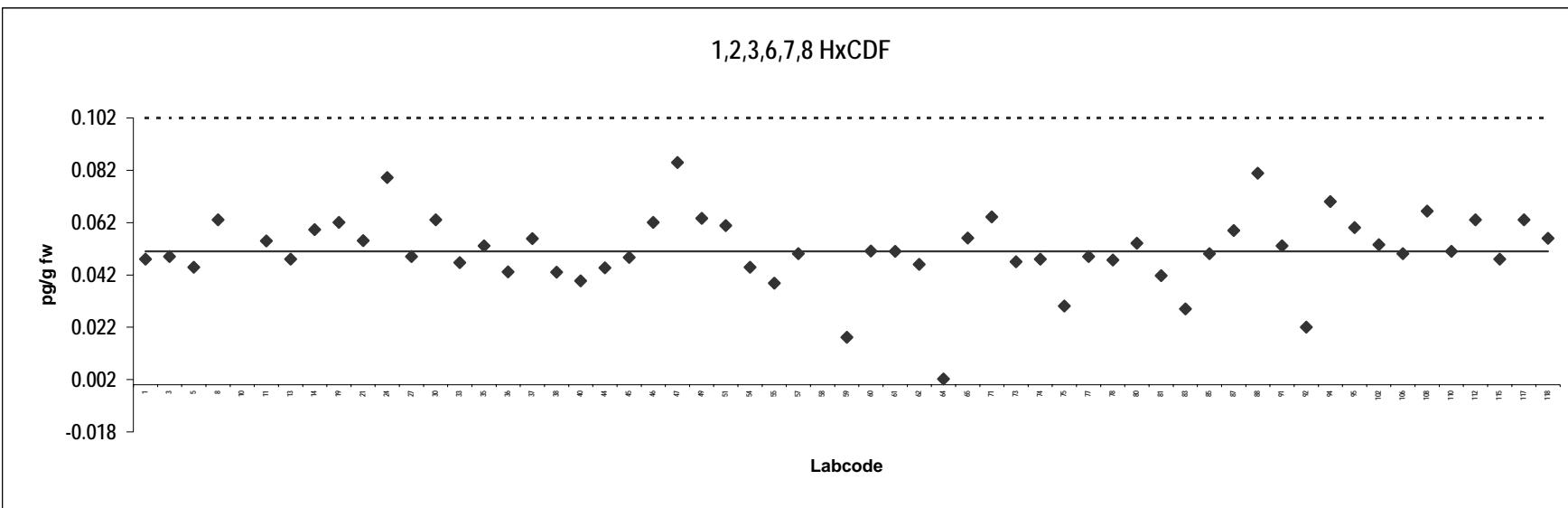
Consensus statistics	
Consensus median, pg/g	0.051
Median all values pg/g	0.051
Consensus mean, pg/g	0.051
Standard deviation, pg/g	0.014
Relative standard deviation, %	28
No. of values reported	59
No. of values removed	2
No. of reported non-detects	3



**Milk**  
**Congener: 1,2,3,6,7,8 HxCDF**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.048		87	0.059	
3	0.049		88	0.081	
5	0.045		91	0.053	
8	0.063		92	0.022	
10	0.10	Outlier	94	0.070	ND
11	0.055		95	0.060	
13	0.048		102	0.053	
14	0.059		106	0.050	
19	0.062		108	0.066	
21	0.055		110	0.051	
24	0.079		112	0.063	
27	0.049		115	0.048	
30	0.063		117	0.063	
33	0.047		118	0.056	
35	0.053				
36	0.043				
37	0.056				
38	0.043				
40	0.040				
44	0.045				
45	0.049				
46	0.062				
47	0.085				
49	0.064				
51	0.061				
54	0.045				
55	0.039				
57	0.050				
58	0.18	Outlier			
59	0.018				
60	0.051				
61	0.051				
62	0.046				
64	0.0022	ND			
65	0.056				
71	0.064				
73	0.047				
74	0.048				
75	0.030				
77	0.049				
78	0.048				
80	0.054				
81	0.042				
83	0.029				
85	0.050				

Consensus statistics	
Consensus median, pg/g	0.051
Median all values pg/g	0.051
Consensus mean, pg/g	0.051
Standard deviation, pg/g	0.014
Relative standard deviation, %	27
No. of values reported	59
No. of values removed	2
No. of reported non-detects	3

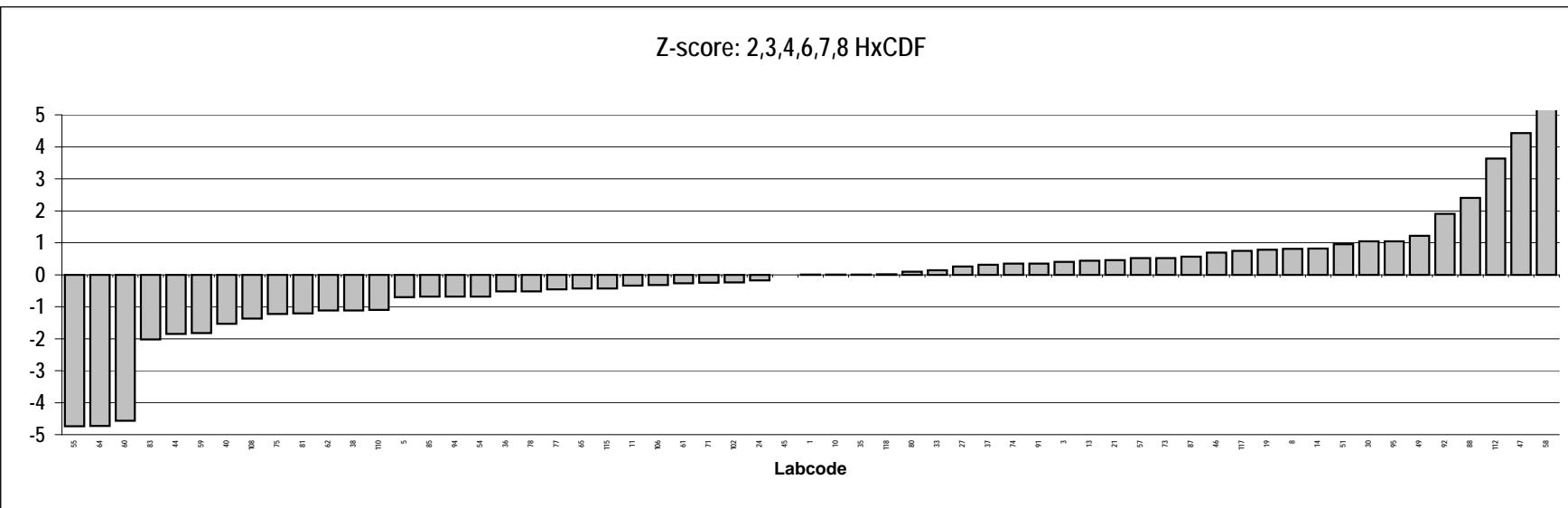
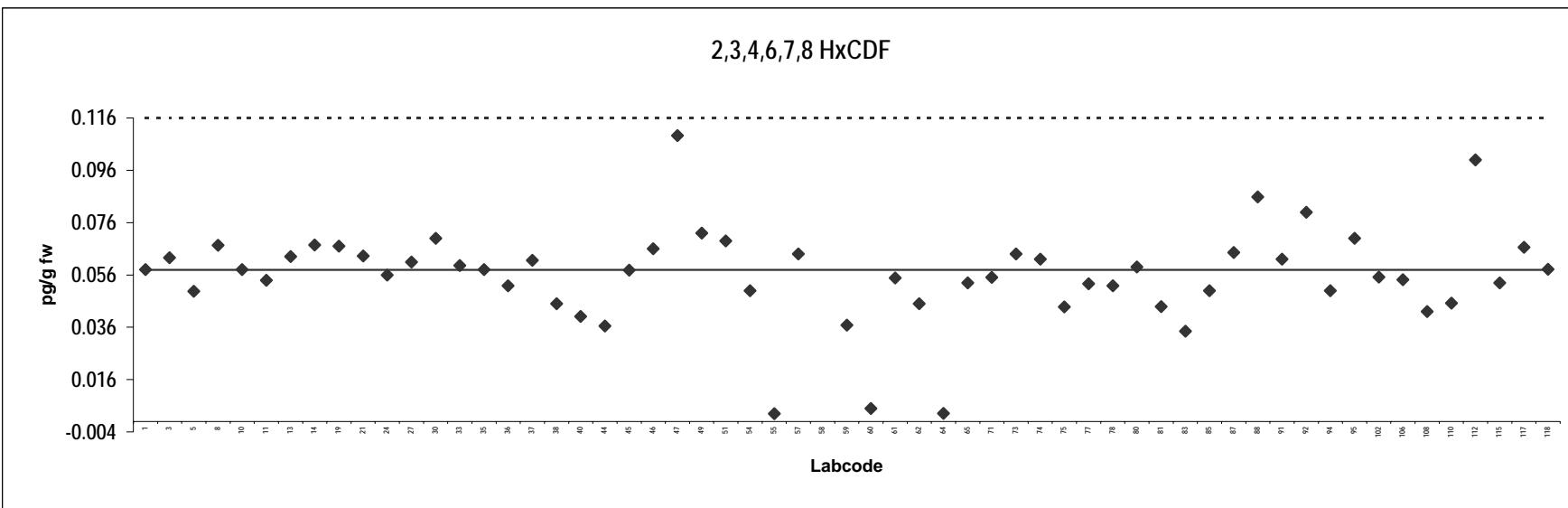


**Milk**  
Congener: 2,3,4,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.058		87	0.065	
3	0.063		88	0.086	
5	0.050		91	0.062	
8	0.067		92	0.080	
10	0.058		94	0.050	
11	0.054		95	0.070	
13	0.063		102	0.055	
14	0.067		106	0.054	
19	0.067		108	0.042	
21	0.063		110	0.045	
24	0.056		112	0.10	
27	0.061		115	0.053	
30	0.070		117	0.067	
33	0.060		118	0.058	
35	0.058				
36	0.052				
37	0.062				
38	0.045				
40	0.040				
44	0.036				
45	0.058				
46	0.066				
47	0.11				
49	0.072				
51	0.069				
54	0.050	ND			
55	0.0030				
57	0.064				
58	0.19	Outlier			
59	0.037				
60	0.0050	ND			
61	0.055				
62	0.045				
64	0.0031	ND			
65	0.053				
71	0.055				
73	0.064				
74	0.062				
75	0.044				
77	0.053				
78	0.052				
80	0.059				
81	0.044				
83	0.035				
85	0.050				

**Consensus statistics**

Consensus median, pg/g	0.058
Median all values pg/g	0.058
Consensus mean, pg/g	0.056
Standard deviation, pg/g	0.018
Relative standard deviation, %	33
No. of values reported	59
No. of values removed	1
No. of reported non-detects	4

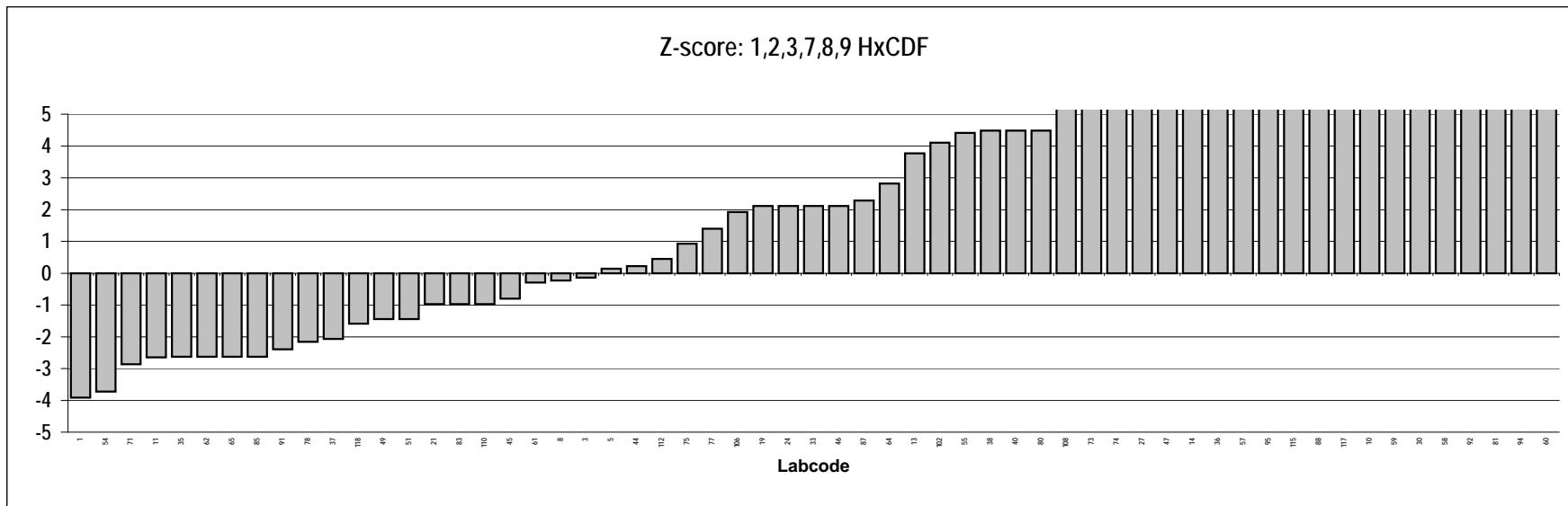
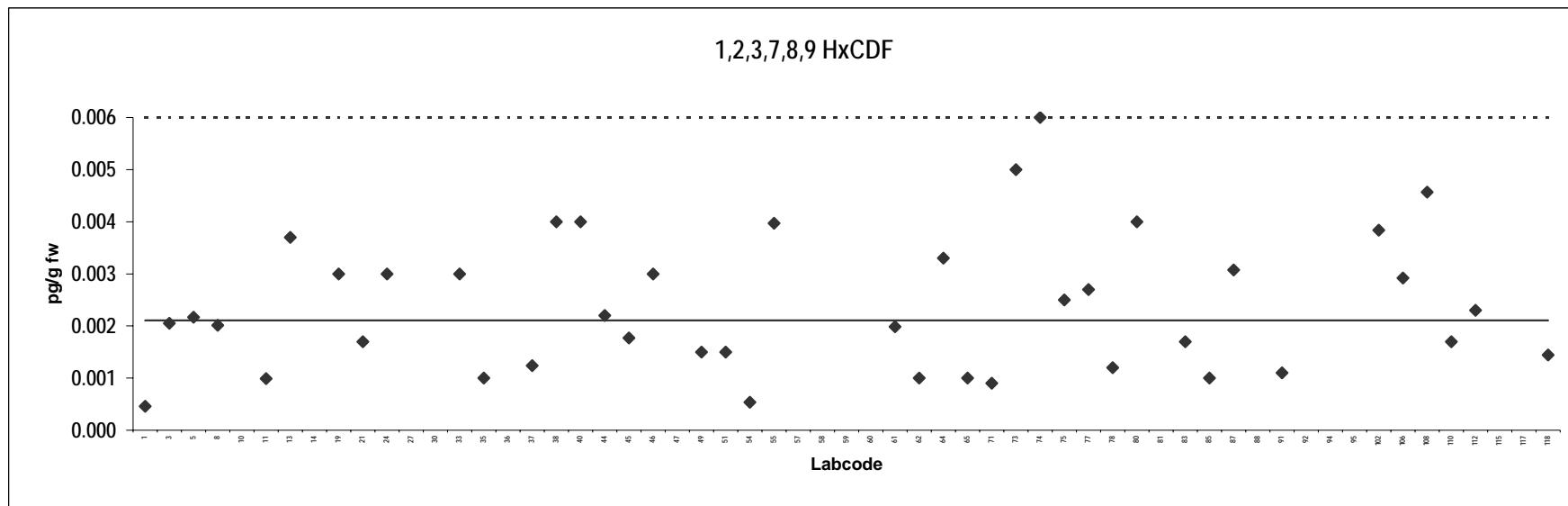


**Milk**  
**Congener: 1,2,3,7,8,9 HxCDF**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.00046		87	0.0031	
3	0.0021	ND	88	0.011	Outlier
5	0.0022		91	0.0011	ND
8	0.0020	ND	92	0.027	Outlier,ND
10	0.013	Outlier,ND	94	0.050	Outlier,ND
11	0.00099		95	0.010	Outlier,ND
13	0.0037	ND	102	0.0038	ND
14	0.0077	Outlier,ND	106	0.0029	ND
19	0.0030	ND	108	0.0046	ND
21	0.0017	ND	110	0.0017	ND
24	0.0030	ND	112	0.0023	ND
27	0.0067	Outlier	115	0.010	Outlier,ND
30	0.022	Outlier,ND	117	0.012	Outlier,ND
33	0.0030	ND	118	0.0014	
35	0.0010	ND			
36	0.010	Outlier,ND			
37	0.0012				
38	0.0040	ND			
40	0.0040	ND			
44	0.0022				
45	0.0018	ND			
46	0.0030	ND			
47	0.0067	Outlier			
49	0.0015	ND			
51	0.0015				
54	0.00054				
55	0.0040	ND			
57	0.010	Outlier,ND			
58	0.022	Outlier,ND			
59	0.019	Outlier			
60	0.062	Outlier			
61	0.0020				
62	0.0010				
64	0.0033	ND			
65	0.0010	ND			
71	0.00090	ND			
73	0.0050	ND			
74	0.0060	ND			
75	0.0025				
77	0.0027				
78	0.0012				
80	0.0040				
81	0.036	Outlier,ND			
83	0.0017				
85	0.0010				

**Consensus statistics**

Consensus median, pg/g	0.0021
Median all values pg/g	0.0030
Consensus mean, pg/g	0.0024
Standard deviation, pg/g	0.0013
Relative standard deviation, %	55
No. of values reported	59
No. of values removed	17
No. of reported non-detects	37

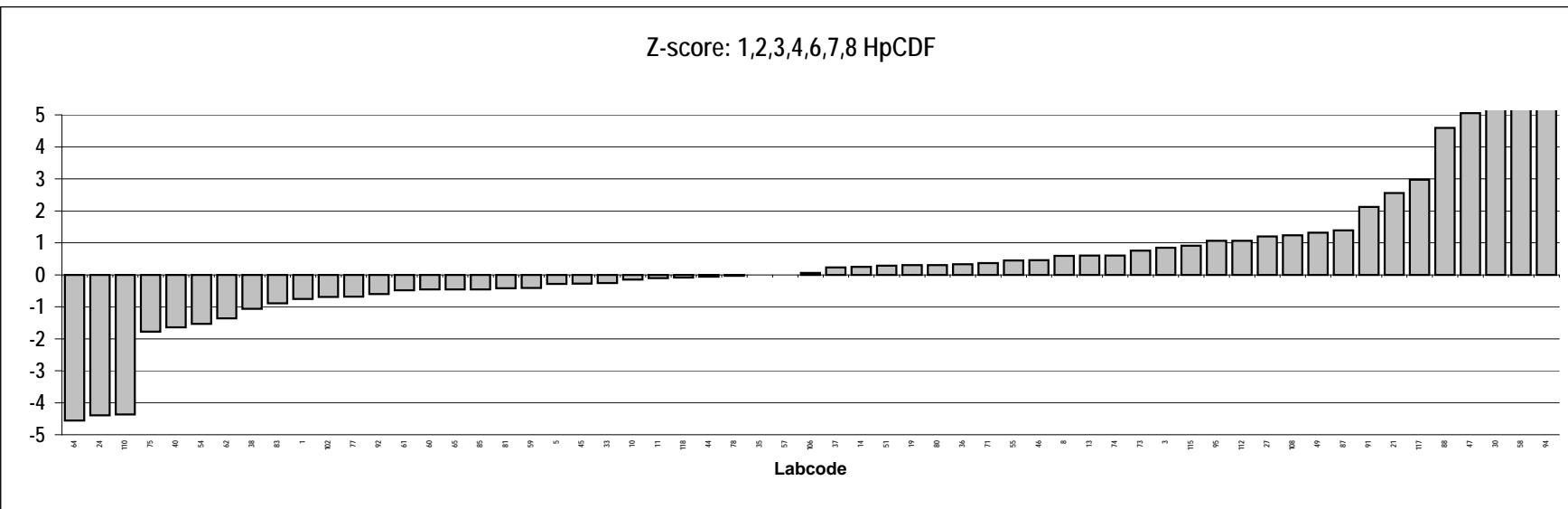
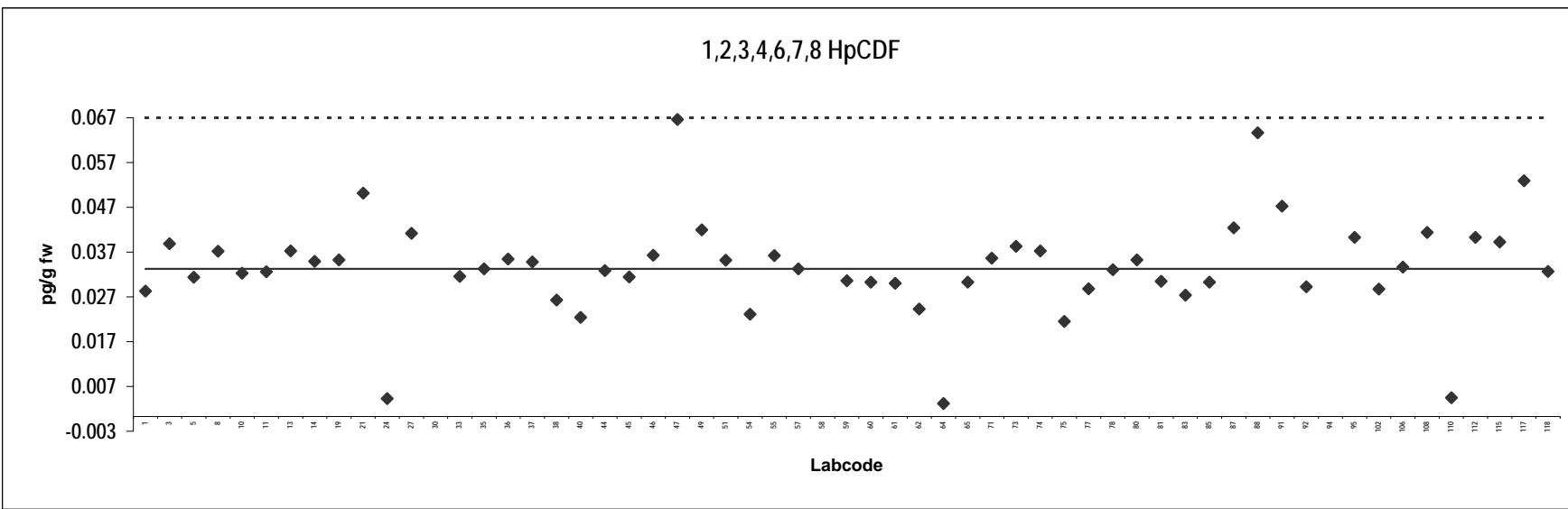


**Milk**  
**Congener: 1,2,3,4,6,7,8 HpCDF**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.028		87	0.042	
3	0.039		88	0.063	
5	0.031		91	0.047	
8	0.037		92	0.029	
10	0.032		94	0.15	
11	0.032		95	0.040	Outlier,ND
13	0.037		102	0.028	
14	0.035		106	0.033	
19	0.035		108	0.041	
21	0.050		110	0.0042	
24	0.0040	ND	112	0.040	
27	0.041		115	0.039	
30	0.069	Outlier	117	0.053	
33	0.031		118	0.032	
35	0.033				
36	0.035				
37	0.035				
38	0.026				
40	0.022				
44	0.033				
45	0.031				
46	0.036				
47	0.066				
49	0.042				
51	0.035				
54	0.023				
55	0.036				
57	0.033				
58	0.12				
59	0.030				
60	0.030				
61	0.030				
62	0.024				
64	0.0029	ND			
65	0.030				
71	0.035				
73	0.038				
74	0.037				
75	0.021				
77	0.029				
78	0.033				
80	0.035				
81	0.030				
83	0.027				
85	0.030				

**Consensus statistics**

Consensus median, pg/g	0.033
Median all values pg/g	0.033
Consensus mean, pg/g	0.033
Standard deviation, pg/g	0.011
Relative standard deviation, %	33
No. of values reported	59
No. of values removed	3
No. of reported non-detects	4

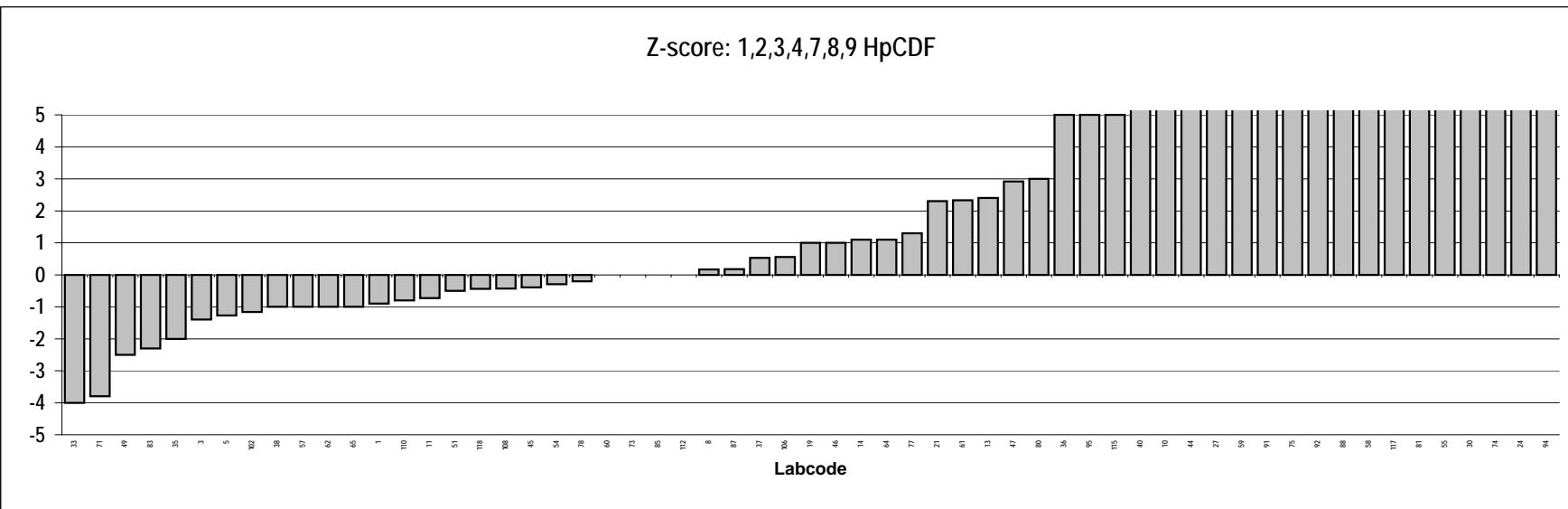
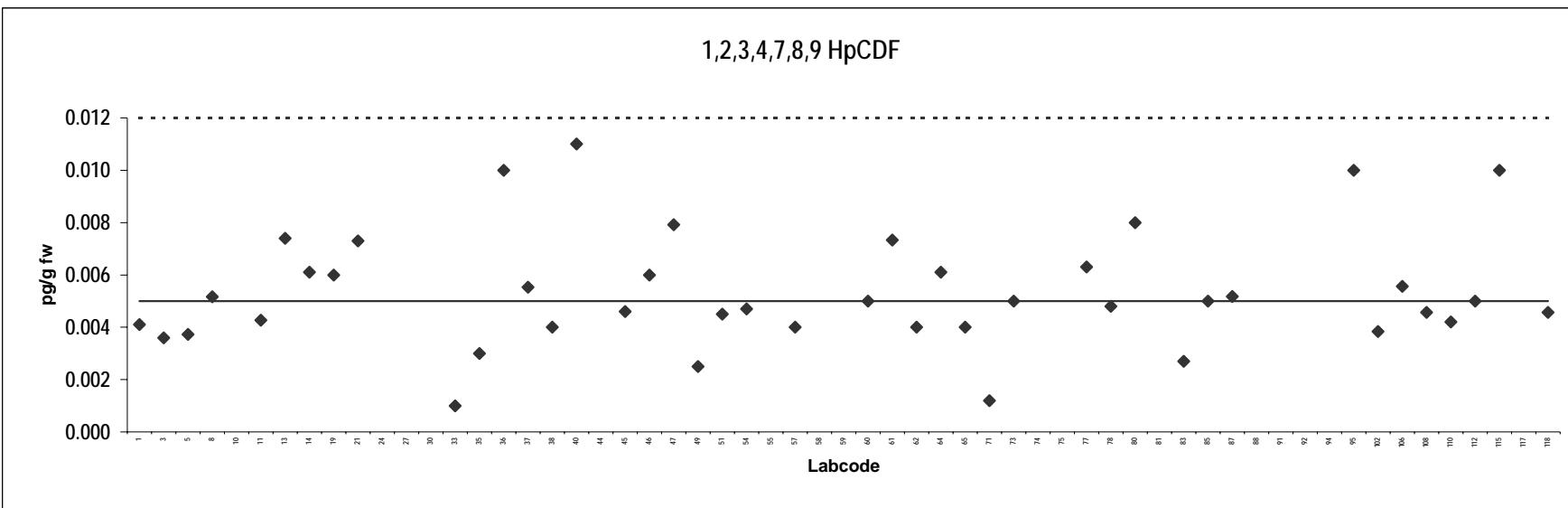


**Milk**  
**Congener: 1,2,3,4,7,8,9 HpCDF**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.0041		87	0.0052	
3	0.0036		88	0.021	Outlier
5	0.0037		91	0.014	Outlier
8	0.0052		92	0.017	Outlier,ND
10	0.013	Outlier,ND	94	0.15	Outlier,ND
11	0.0043		95	0.010	ND
13	0.0074	ND	102	0.0038	ND
14	0.0061	ND	106	0.0056	
19	0.0060	ND	108	0.0046	ND
21	0.0073		110	0.0042	ND
24	0.081	Outlier	112	0.0050	
27	0.013	Outlier	115	0.010	ND
30	0.029	Outlier,ND	117	0.022	Outlier
33	0.0010	ND	118	0.0046	
35	0.0030				
36	0.010	ND			
37	0.0055				
38	0.0040	ND			
40	0.011	ND			
44	0.013	Outlier			
45	0.0046				
46	0.0060	ND			
47	0.0079				
49	0.0025	ND			
51	0.0045				
54	0.0047				
55	0.025	Outlier,ND			
57	0.0040				
58	0.022	Outlier,ND			
59	0.014	Outlier			
60	0.0050	ND			
61	0.0073				
62	0.0040				
64	0.0061	ND			
65	0.0040				
71	0.0012	ND			
73	0.0050	ND			
74	0.030	Outlier,ND			
75	0.015	Outlier			
77	0.0063				
78	0.0048				
80	0.0080				
81	0.024	Outlier,ND			
83	0.0027				
85	0.0050				

**Consensus statistics**

Consensus median, pg/g	0.0050
Median all values pg/g	0.0060
Consensus mean, pg/g	0.0053
Standard deviation, pg/g	0.0022
Relative standard deviation, %	42
No. of values reported	59
No. of values removed	16
No. of reported non-detects	26

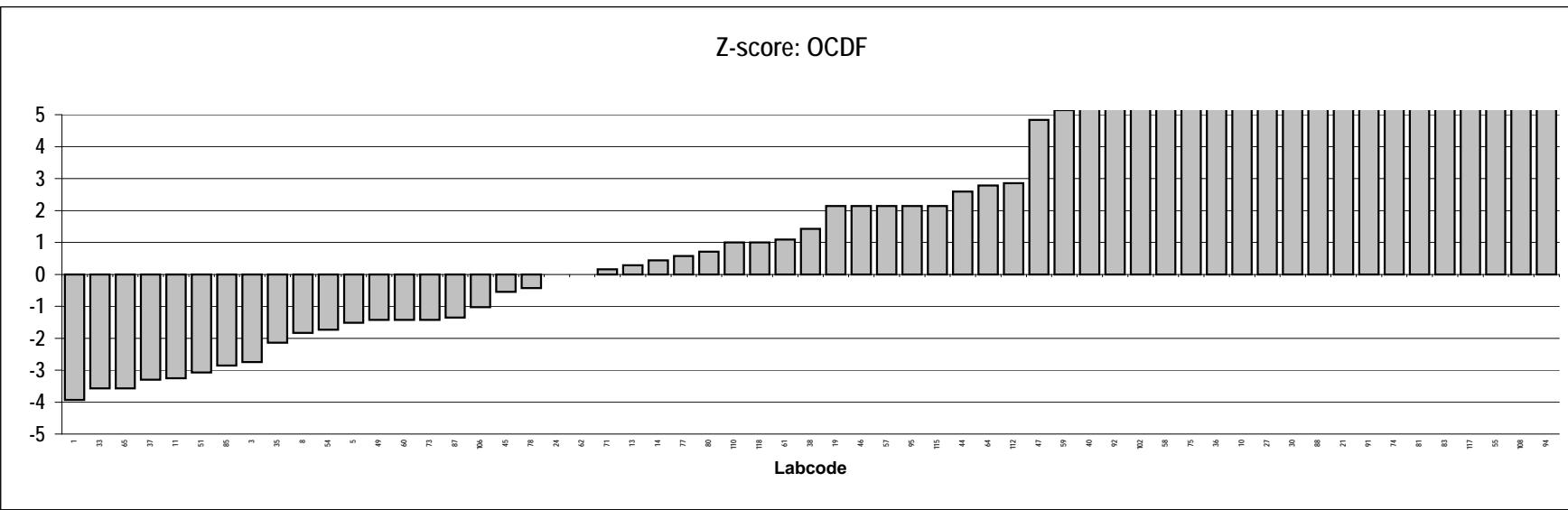
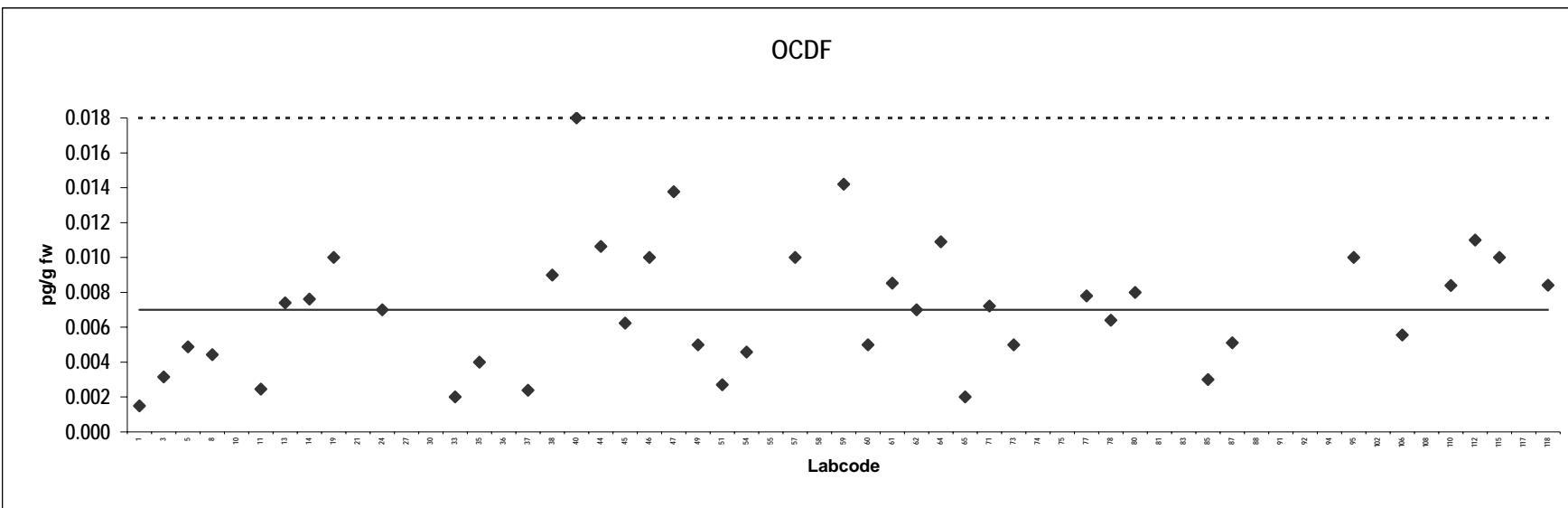


**Milk**  
Congener: OCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.0015		87	0.0051	
3	0.0032	ND	88	0.031	Outlier
5	0.0049		91	0.039	Outlier
8	0.0044	ND	92	0.019	Outlier,ND
10	0.024	Outlier,ND	94	2.0	Outlier,ND
11	0.0024		95	0.010	ND
13	0.0074	ND	102	0.019	Outlier,ND
14	0.0076		106	0.0056	
19	0.010	ND	108	0.20	Outlier
21	0.039	Outlier	110	0.0084	ND
24	0.0070	ND	112	0.011	
27	0.027	Outlier	115	0.010	ND
30	0.028	Outlier	117	0.078	Outlier
33	0.0020	ND	118	0.0084	
35	0.0040	ND			
36	0.023	Outlier			
37	0.0024				
38	0.0090	ND			
40	0.018	ND			
44	0.011				
45	0.0062				
46	0.010	ND			
47	0.014				
49	0.0050	ND			
51	0.0027				
54	0.0046				
55	0.087	Outlier,ND			
57	0.010	ND			
58	0.022	Outlier,ND			
59	0.014				
60	0.0050	ND			
61	0.0085				
62	0.0070				
64	0.011	ND			
65	0.0020				
71	0.0072				
73	0.0050	ND			
74	0.050	Outlier,ND			
75	0.022	Outlier			
77	0.0078				
78	0.0064				
80	0.0080				
81	0.054	Outlier,ND			
83	0.069	Outlier			
85	0.0030				

**Consensus statistics**

Consensus median, pg/g	0.0070
Median all values pg/g	0.0090
Consensus mean, pg/g	0.0071
Standard deviation, pg/g	0.0037
Relative standard deviation, %	52
No. of values reported	59
No. of values removed	18
No. of reported non-detects	26

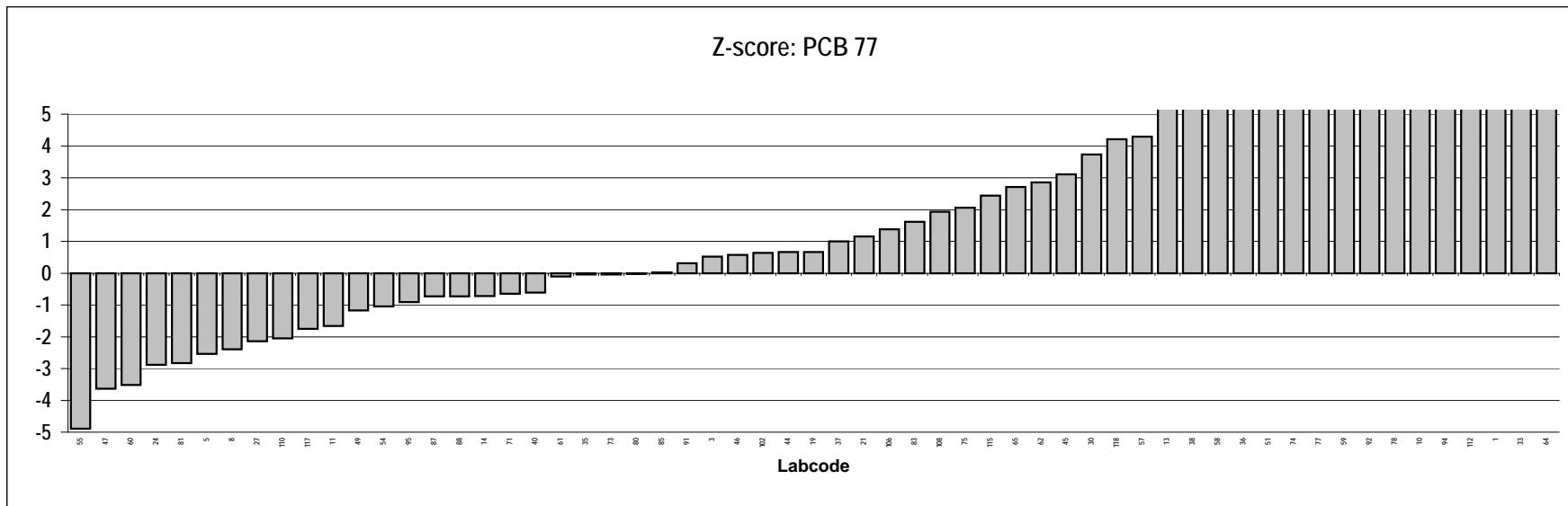
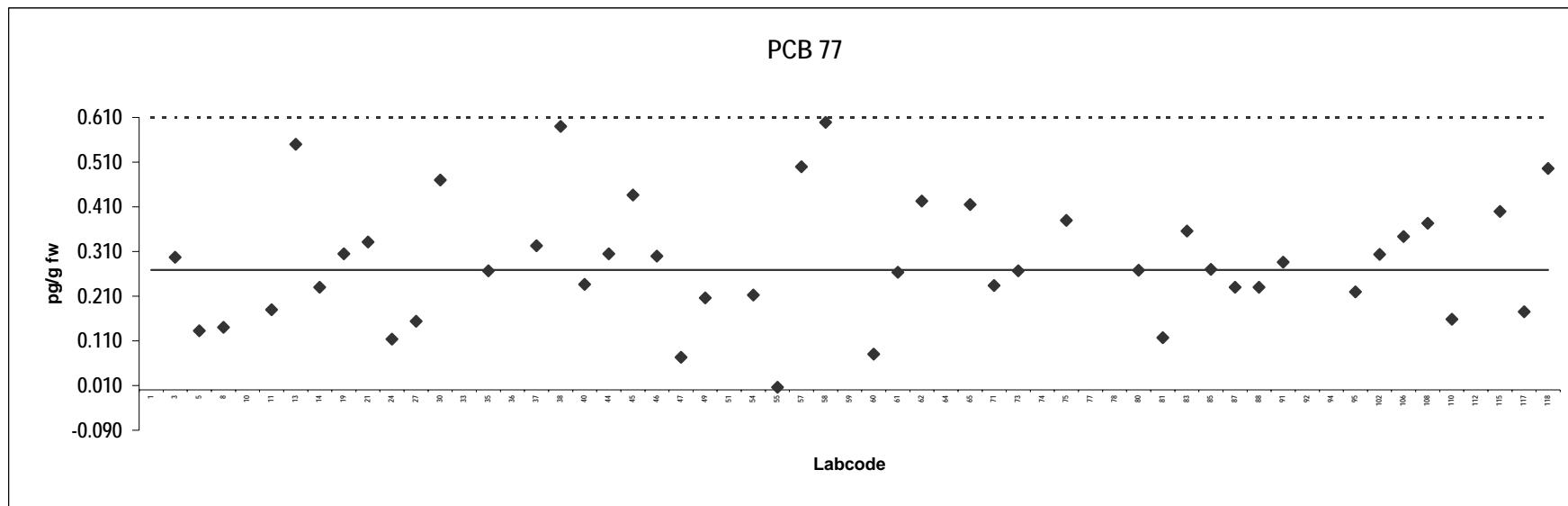


**Milk**  
Congener: PCB 77

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.9		87	0.23	
3	0.30		88	0.23	
5	0.13		91	0.29	
8	0.14		92	1.1	
10	1.4	Outlier	94	1.5	Outlier
11	0.18		95	0.22	
13	0.55		102	0.30	
14	0.23		106	0.34	
19	0.31		108	0.37	
21	0.33		110	0.16	
24	0.11		112	1.9	Outlier
27	0.15		115	0.40	
30	0.47		117	0.18	
33	2.4	Outlier	118	0.50	
35	0.27				
36	0.69	Outlier			
37	0.32				
38	0.59				
40	0.24				
44	0.30				
45	0.44				
46	0.30				
47	0.073				
49	0.21				
51	0.70	Outlier			
54	0.21				
55	0.0058		ND		
57	0.50		ND		
58	0.60				
59	0.98	Outlier			
60	0.080				
61	0.26				
62	0.42				
64	20	Outlier			
65	0.42				
71	0.23				
73	0.27				
74	0.75	Outlier			
75	0.38				
77	0.76	Outlier			
78	1.3	Outlier			
80	0.27				
81	0.12				
83	0.36				
85	0.27				

**Consensus statistics**

Consensus median, pg/g	0.27
Median all values pg/g	0.31
Consensus mean, pg/g	0.29
Standard deviation, pg/g	0.14
Relative standard deviation, %	48
No. of values reported	59
No. of values removed	13
No. of reported non-detects	2

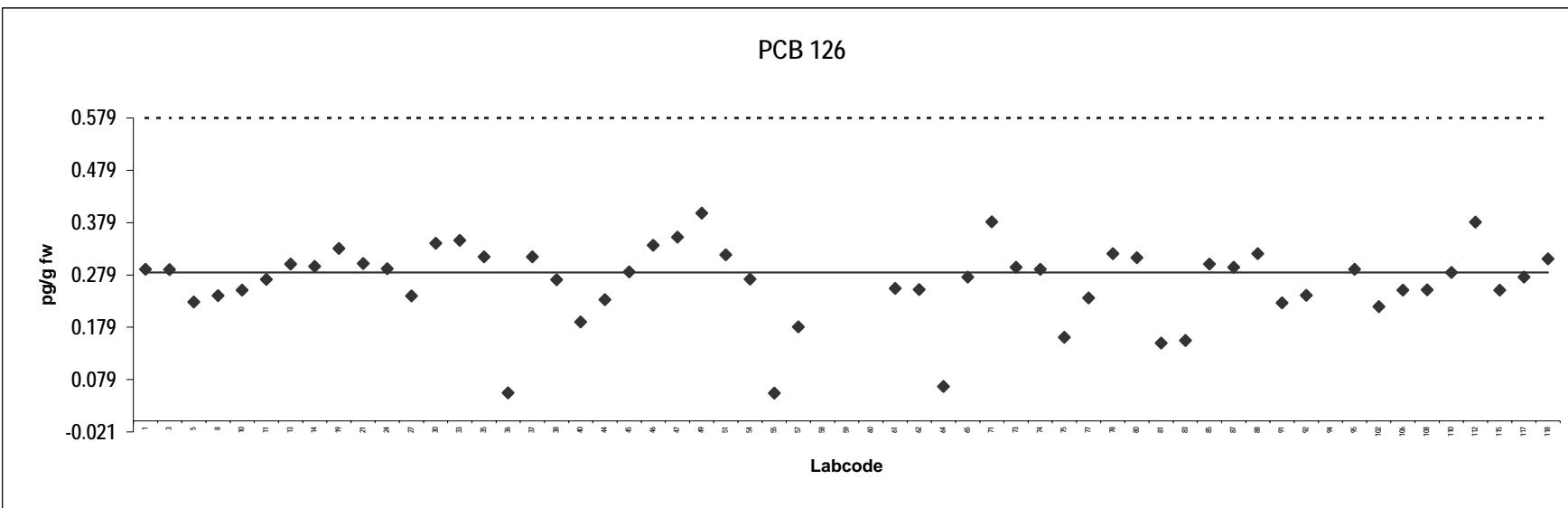


**Milk**  
Congener: PCB 126

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.29		87	0.29	
3	0.29		88	0.32	
5	0.23		91	0.23	
8	0.24		92	0.24	
10	0.25		94	1.0	
11	0.27		95	0.29	
13	0.30		102	0.22	
14	0.30		106	0.25	
19	0.33		108	0.25	
21	0.30		110	0.28	
24	0.29		112	0.38	
27	0.24		115	0.25	
30	0.34		117	0.28	
33	0.35		118	0.31	
35	0.31				
36	0.054				
37	0.31				
38	0.27				
40	0.19				
44	0.23				
45	0.29				
46	0.34				
47	0.35				
49	0.40				
51	0.32				
54	0.27				
55	0.053	ND			
57	0.18				
58	0.91	Outlier			
59	3.0	Outlier,ND			
60	0.88	Outlier			
61	0.25				
62	0.25				
64	0.066	ND			
65	0.28				
71	0.38				
73	0.29				
74	0.29				
75	0.16				
77	0.24				
78	0.32				
80	0.31				
81	0.15				
83	0.15				
85	0.30				

**Consensus statistics**

Consensus median, pg/g	0.28
Median all values pg/g	0.29
Consensus mean, pg/g	0.27
Standard deviation, pg/g	0.073
Relative standard deviation, %	28
No. of values reported	59
No. of values removed	4
No. of reported non-detects	4

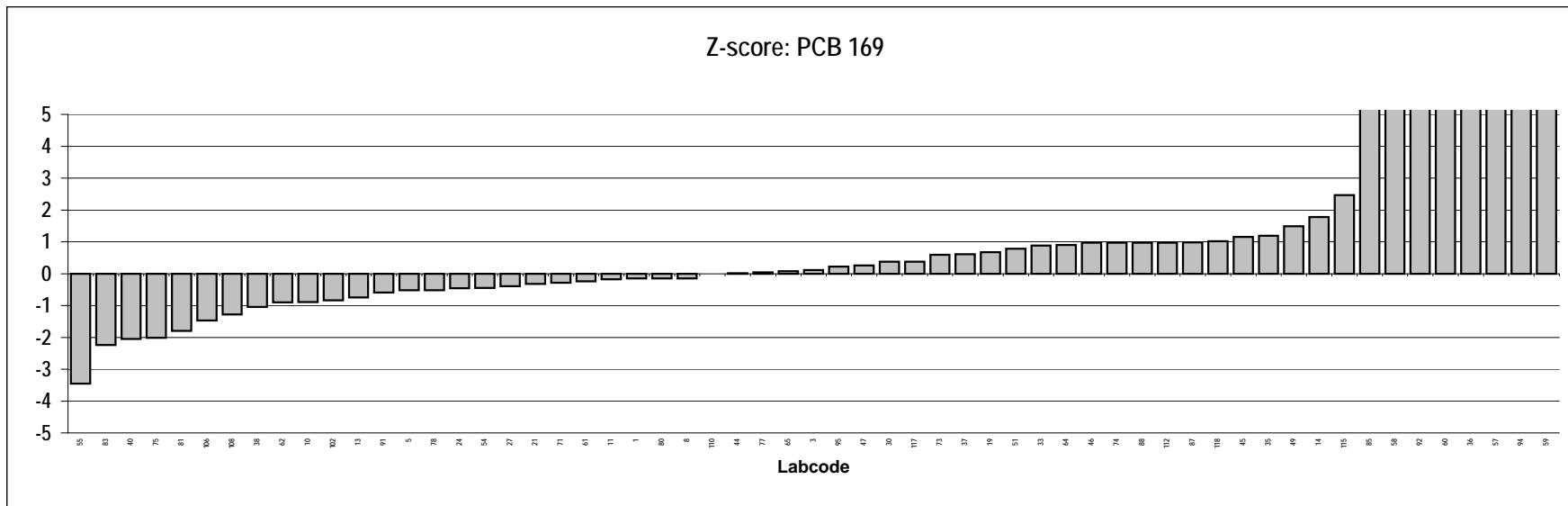
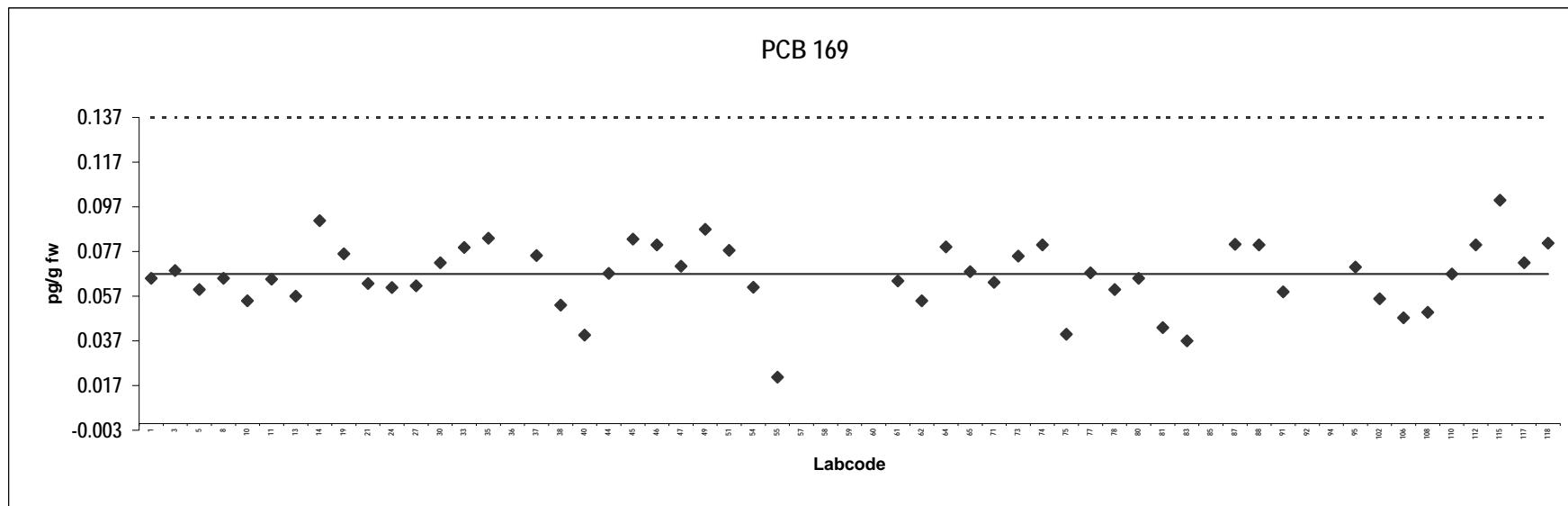


**Milk**  
Congener: PCB 169

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.065		87	0.080	
3	0.069		88	0.080	
5	0.060		91	0.059	
8	0.065	ND	92	0.17	Outlier
10	0.055		94	1.0	Outlier,ND
11	0.065		95	0.070	
13	0.057		102	0.056	
14	0.091		106	0.047	
19	0.076		108	0.050	
21	0.063		110	0.067	ND
24	0.061		112	0.080	
27	0.062		115	0.10	ND
30	0.072		117	0.072	
33	0.079		118	0.081	
35	0.083				
36	0.26	Outlier			
37	0.075				
38	0.053				
40	0.040				
44	0.067				
45	0.082				
46	0.080				
47	0.070				
49	0.087				
51	0.078				
54	0.061				
55	0.021	ND			
57	0.50	Outlier,ND			
58	0.16	Outlier			
59	3.0	Outlier,ND			
60	0.23	Outlier			
61	0.064				
62	0.055				
64	0.079	ND			
65	0.068				
71	0.063				
73	0.075				
74	0.080				
75	0.040				
77	0.068				
78	0.060				
80	0.065				
81	0.043				
83	0.037				
85	0.15	Outlier			

**Consensus statistics**

Consensus median, pg/g	0.067
Median all values pg/g	0.069
Consensus mean, pg/g	0.066
Standard deviation, pg/g	0.015
Relative standard deviation, %	22
No. of values reported	59
No. of values removed	8
No. of reported non-detects	8

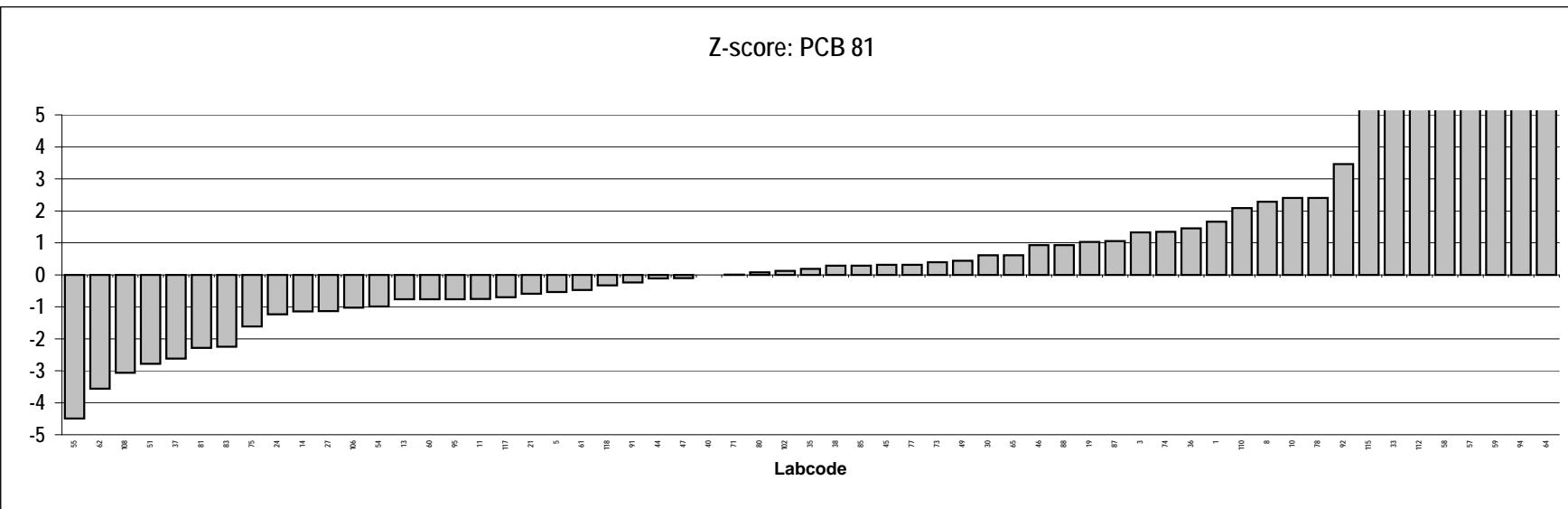
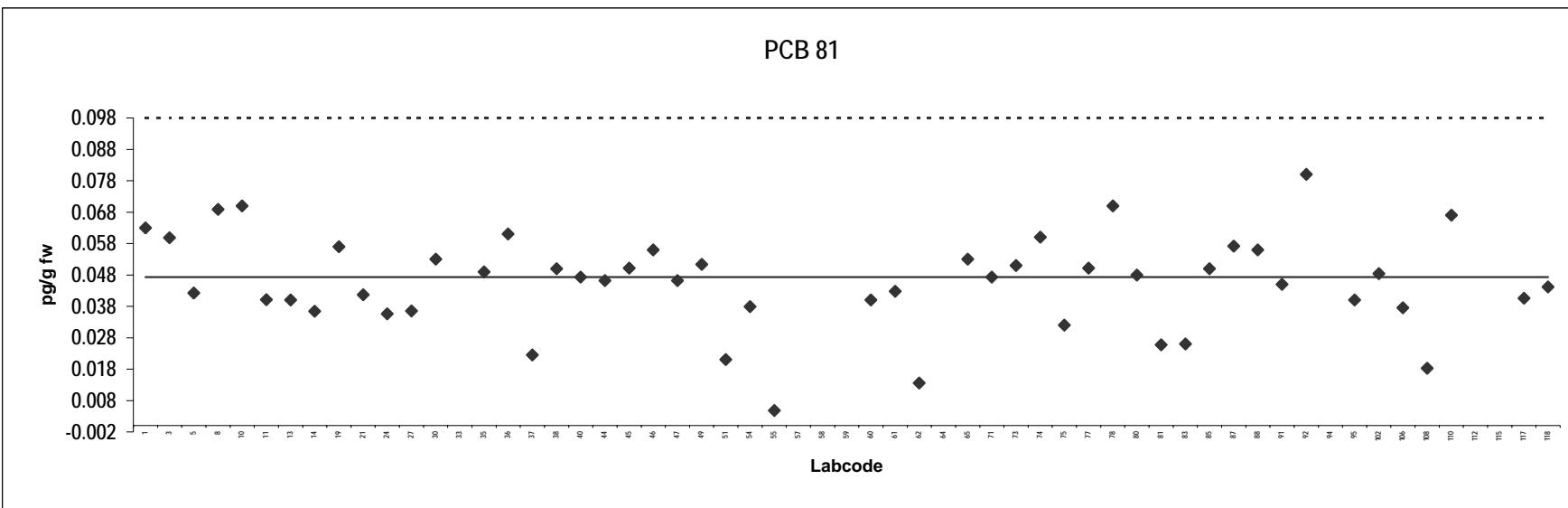


**Milk**  
Congener: PCB 81

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.063		87	0.057	
3	0.060		88	0.056	
5	0.042		91	0.045	
8	0.069		92	0.080	
10	0.070	ND	94	1.0	
11	0.040		95	0.040	
13	0.040		102	0.048	
14	0.036		106	0.038	
19	0.057		108	0.018	
21	0.042		110	0.067	
24	0.036		112	0.11	
27	0.037		115	0.10	
30	0.053		117	0.041	
33	0.10	Outlier	118	0.044	
35	0.049				
36	0.061				
37	0.023				
38	0.050				
40	0.047				
44	0.046				
45	0.050				
46	0.056				
47	0.046				
49	0.051				
51	0.021	ND			
54	0.038				
55	0.0048				
57	0.50	ND			
58	0.14	Outlier,ND			
59	0.51	Outlier			
60	0.040				
61	0.043				
62	0.014				
64	3.3	Outlier			
65	0.053				
71	0.047				
73	0.051				
74	0.060				
75	0.032				
77	0.050				
78	0.070				
80	0.048				
81	0.026				
83	0.026				
85	0.050				

**Consensus statistics**

Consensus median, pg/g	0.047
Median all values pg/g	0.049
Consensus mean, pg/g	0.046
Standard deviation, pg/g	0.015
Relative standard deviation, %	33
No. of values reported	59
No. of values removed	8
No. of reported non-detects	7

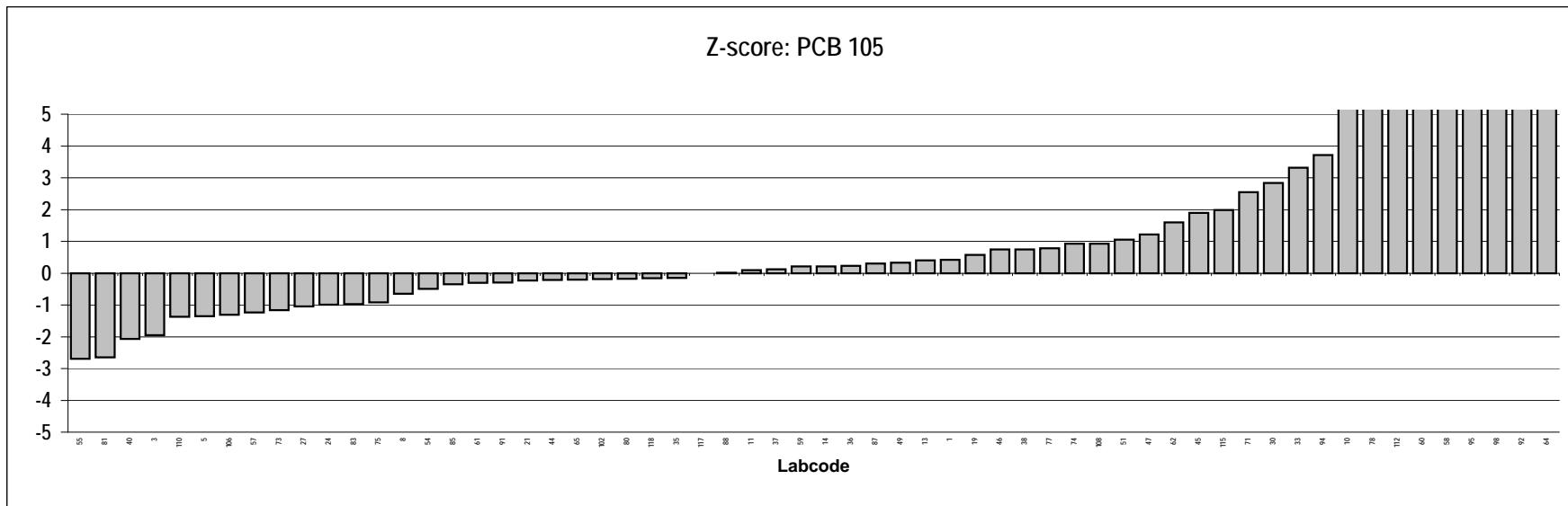
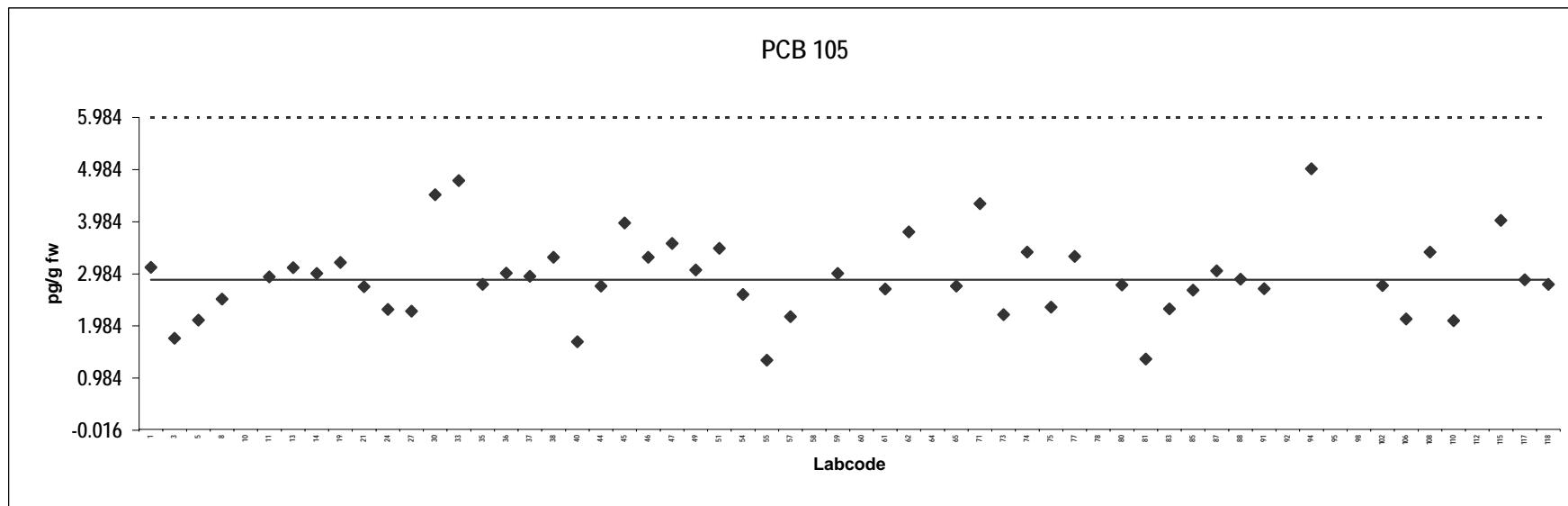


**Milk**  
Congener: PCB 105

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	3.1		87	3.0	
3	1.7		88	2.9	
5	2.1		91	2.7	
8	2.5		92	13	Outlier
10	6.3	Outlier	94	5.0	ND
11	2.9		95	10	Outlier,ND
13	3.1		98	10	Outlier,ND
14	3.0		102	2.8	
19	3.2		106	2.1	
21	2.7		108	3.4	
24	2.3		110	2.1	
27	2.3		112	6.9	Outlier
30	4.5		115	4.0	
33	4.8		117	2.9	
35	2.8		118	2.8	
36	3.0				
37	2.9				
38	3.3				
40	1.7				
44	2.7				
45	4.0				
46	3.3				
47	3.6				
49	3.1				
51	3.5				
54	2.6				
55	1.3				
57	2.2				
58	9.4	Outlier			
59	3.0	Outlier			
60	8.0	Outlier			
61	2.7				
62	3.8				
64	125	Outlier			
65	2.8				
71	4.3				
73	2.2				
74	3.4				
75	2.3				
77	3.3				
78	6.7	Outlier			
80	2.8				
81	1.4				
83	2.3				
85	2.7				

**Consensus statistics**

Consensus median, pg/g	2.9
Median all values pg/g	3.0
Consensus mean, pg/g	2.9
Standard deviation, pg/g	0.78
Relative standard deviation, %	27
No. of values reported	60
No. of values removed	9
No. of reported non-detects	3

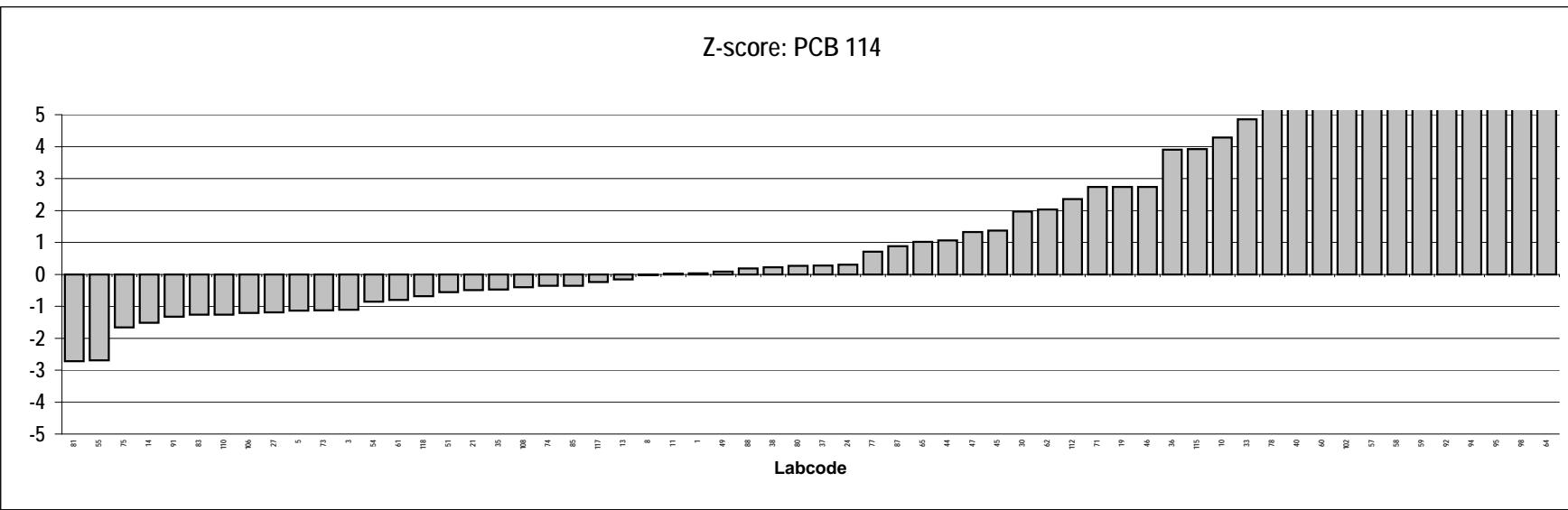
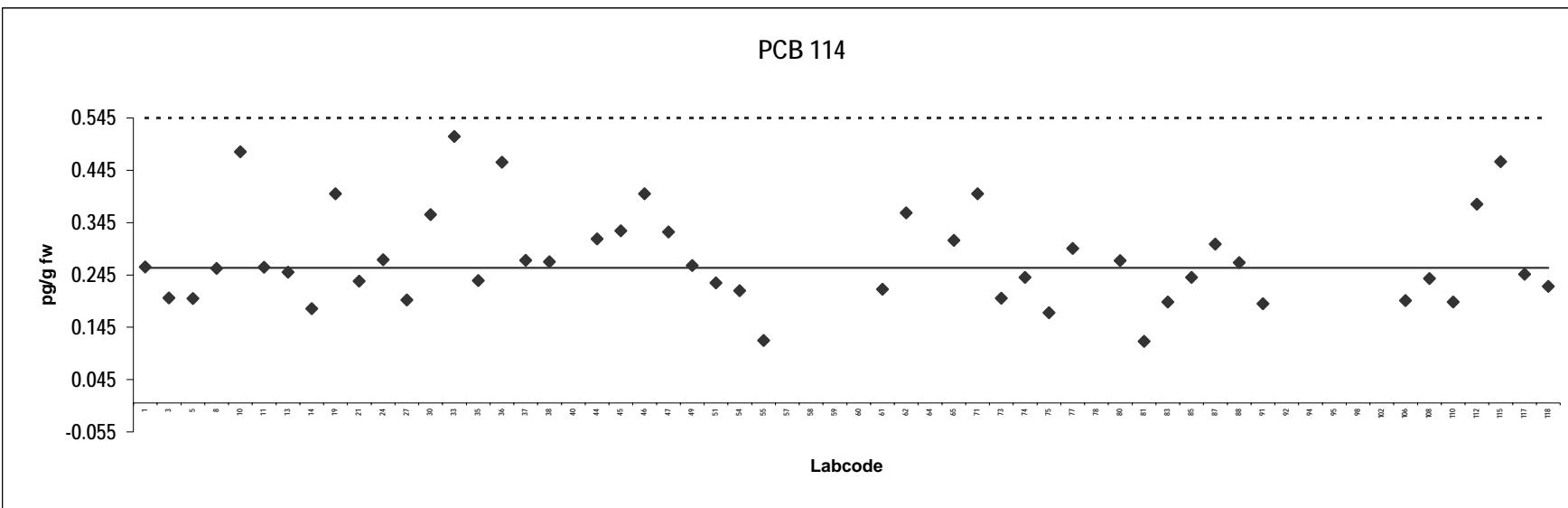


**Milk**  
Congener: PCB 114

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.26		87	0.30	
3	0.20		88	0.27	
5	0.20		91	0.19	
8	0.26		92	8.0	Outlier,ND
10	0.48		94	10	Outlier,ND
11	0.26		95	10	Outlier,ND
13	0.25		98	10	Outlier,ND
14	0.18		102	0.77	Outlier,ND
19	0.40		106	0.20	
21	0.23		108	0.24	
24	0.27		110	0.19	
27	0.20		112	0.38	
30	0.36		115	0.46	
33	0.51		117	0.25	
35	0.23		118	0.22	
36	0.46	ND			
37	0.27				
38	0.27				
40	0.68	Outlier,ND			
44	0.31				
45	0.33				
46	0.40				
47	0.33				
49	0.26				
51	0.23				
54	0.21				
55	0.12				
57	2.0	Outlier,ND			
58	4.4	Outlier,ND			
59	8.0	Outlier,ND			
60	0.75	Outlier			
61	0.22				
62	0.36				
64	13	Outlier			
65	0.31				
71	0.40				
73	0.20				
74	0.24				
75	0.17				
77	0.30				
78	0.56	Outlier			
80	0.27				
81	0.12				
83	0.19				
85	0.24				

**Consensus statistics**

Consensus median, pg/g	0.26
Median all values pg/g	0.27
Consensus mean, pg/g	0.28
Standard deviation, pg/g	0.091
Relative standard deviation, %	33
No. of values reported	60
No. of values removed	12
No. of reported non-detects	10

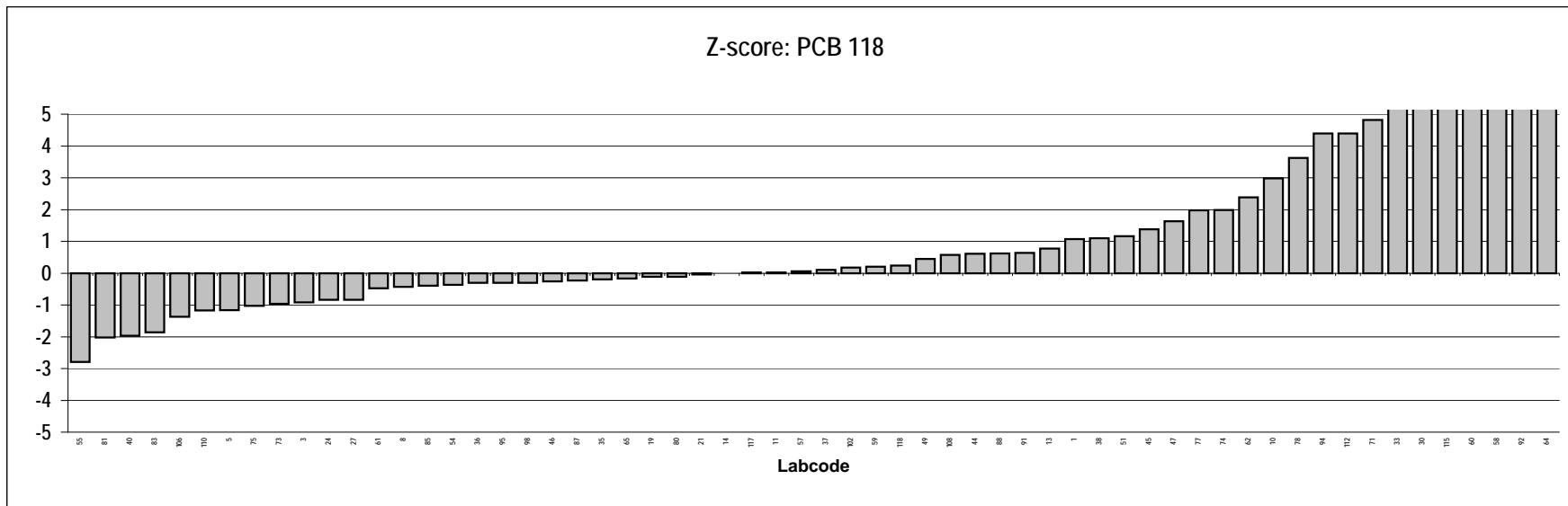
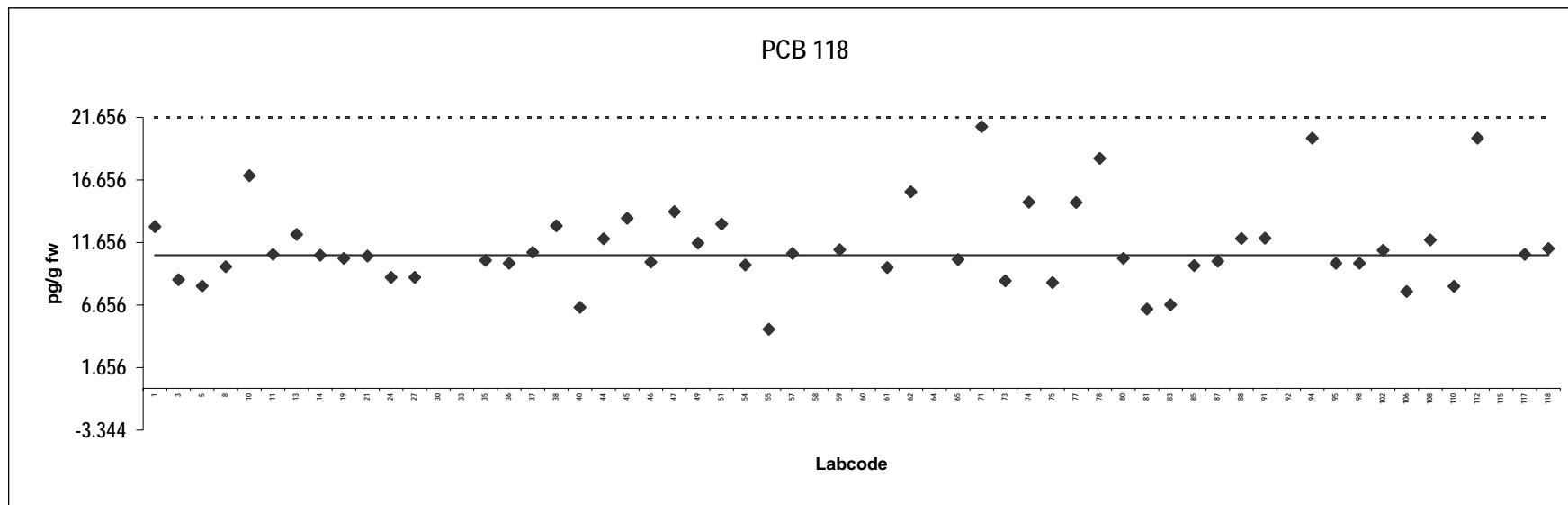


**Milk**  
Congener: PCB 118

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	13		87	10	
3	8.7		88	12	
5	8.2		91	12	
8	9.7		92	48	Outlier
10	17		94	20	ND
11	11		95	10	
13	12		98	10	ND
14	11		102	11	
19	10		106	7.7	
21	11		108	12	
24	8.9		110	8.2	
27	8.9		112	20	
30	24	Outlier	115	25	Outlier
33	22	Outlier	117	11	
35	10		118	11	
36	10				
37	11				
38	13				
40	6.5				
44	12				
45	14				
46	10				
47	14				
49	12				
51	13				
54	9.9				
55	4.7				
57	11				
58	33	Outlier			
59	11	Outlier			
60	29				
61	9.6				
62	16				
64	421	Outlier			
65	10				
71	21				
73	8.6				
74	15				
75	8.5				
77	15				
78	18				
80	10				
81	6.3				
83	6.7				
85	9.8				

**Consensus statistics**

Consensus median, pg/g	11
Median all values pg/g	11
Consensus mean, pg/g	11
Standard deviation, pg/g	3.4
Relative standard deviation, %	30
No. of values reported	60
No. of values removed	7
No. of reported non-detects	2

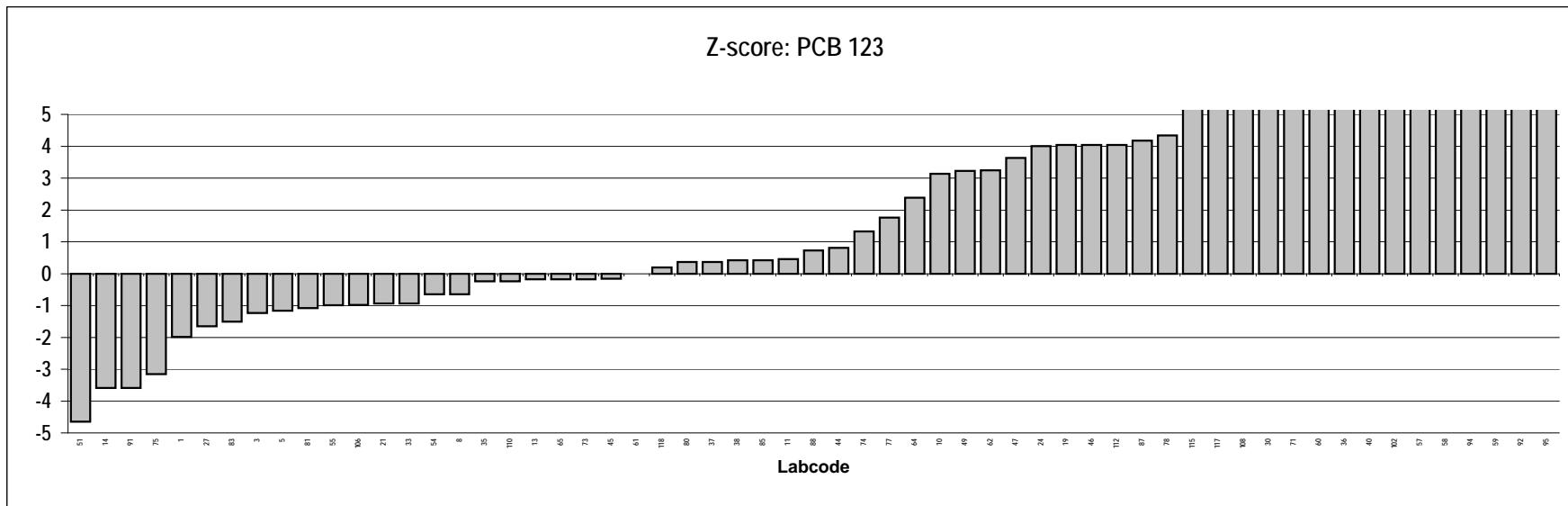
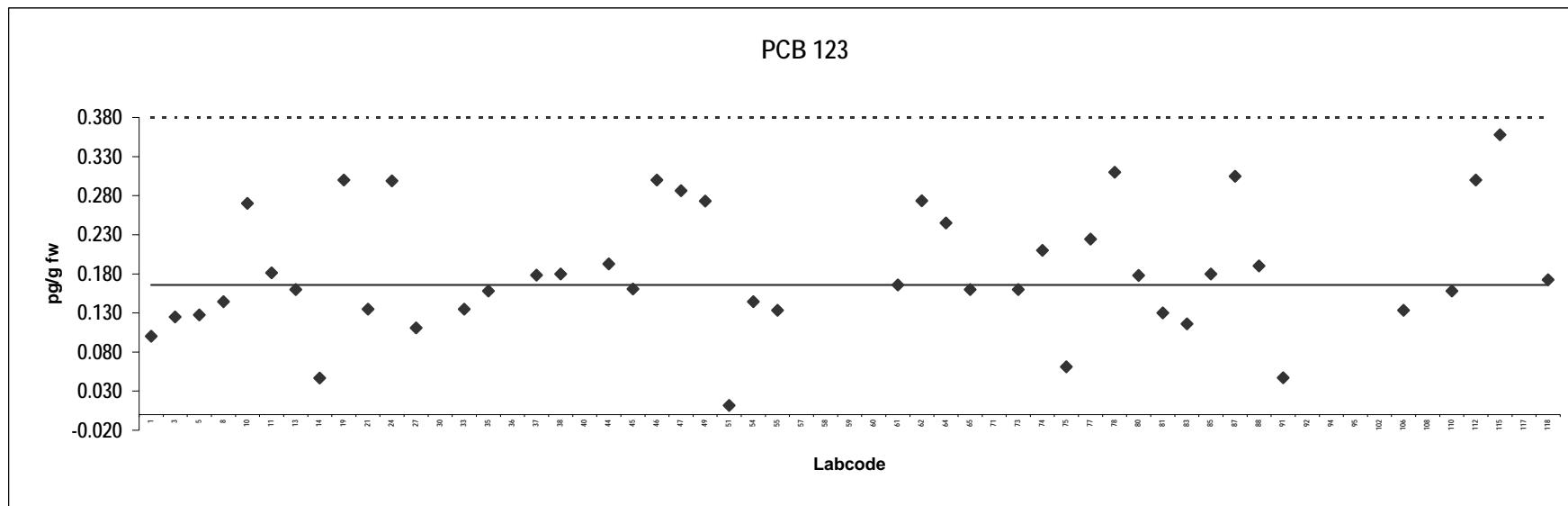


**Milk**  
Congener: PCB 123

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.10		87	0.30	
3	0.13	ND	88	0.19	
5	0.13		91	0.047	ND
8	0.14		92	8.0	Outlier,ND
10	0.27		94	5.0	Outlier,ND
11	0.18		95	10	Outlier,ND
13	0.16		102	0.77	Outlier,ND
14	0.047		106	0.13	
19	0.30		108	0.39	Outlier
21	0.13		110	0.16	
24	0.30	ND	112	0.30	
27	0.11		115	0.36	
30	0.44	Outlier	117	0.39	
33	0.14	ND	118	0.17	Outlier
35	0.16				
36	0.58	Outlier			
37	0.18				
38	0.18				
40	0.68	Outlier,ND			
44	0.19				
45	0.16				
46	0.30				
47	0.29				
49	0.27				
51	0.012	ND			
54	0.14				
55	0.13				
57	2.0	Outlier,ND			
58	4.4	Outlier,ND			
59	8.0	Outlier,ND			
60	0.48	Outlier			
61	0.17				
62	0.27				
64	0.25	ND			
65	0.16				
71	0.47	Outlier			
73	0.16				
74	0.21				
75	0.061				
77	0.22				
78	0.31				
80	0.18				
81	0.13				
83	0.12				
85	0.18				

**Consensus statistics**

Consensus median, pg/g	0.17
Median all values pg/g	0.19
Consensus mean, pg/g	0.18
Standard deviation, pg/g	0.080
Relative standard deviation, %	44
No. of values reported	59
No. of values removed	14
No. of reported non-detects	14

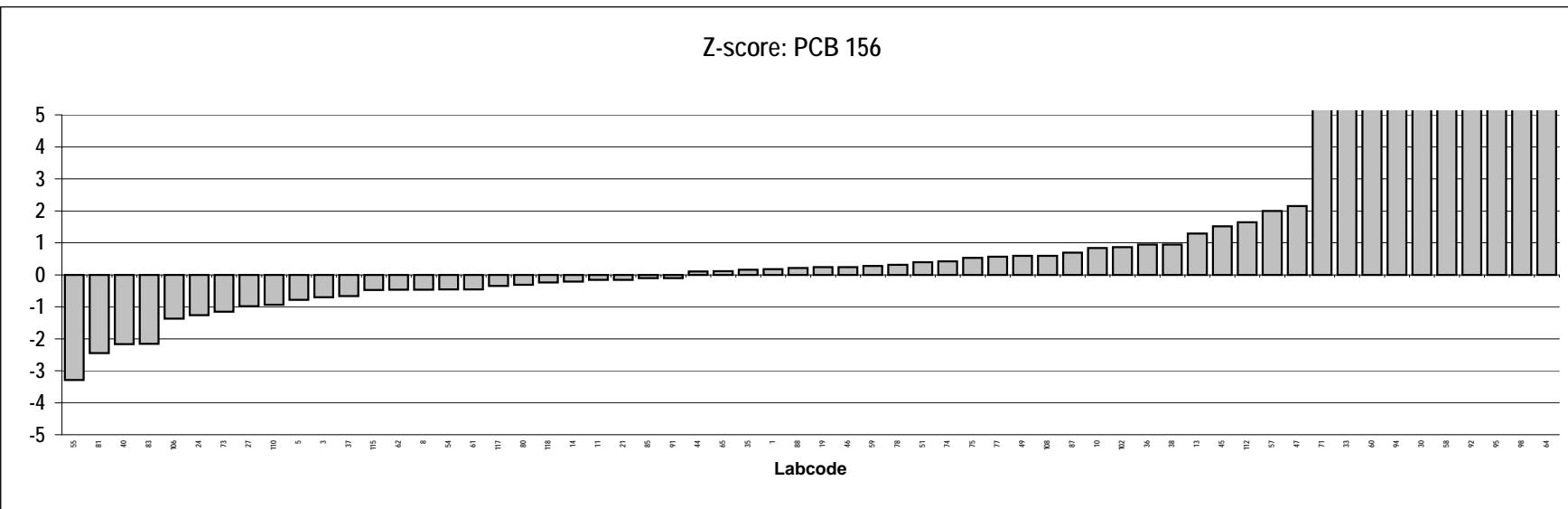
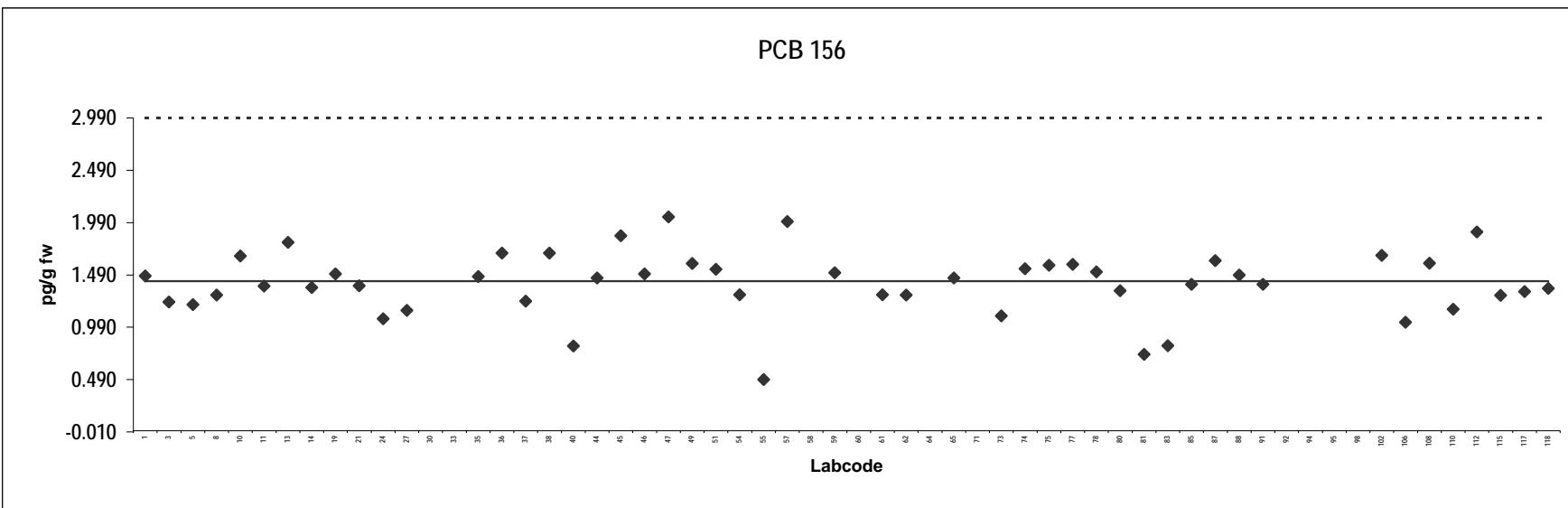


**Milk**  
Congener: PCB 156

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.5		87	1.6	
3	1.2		88	1.5	
5	1.2		91	1.4	
8	1.3		92	8.0	Outlier,ND
10	1.7		94	5.0	Outlier,ND
11	1.4		95	10	Outlier,ND
13	1.8		98	10	Outlier,ND
14	1.4		102	1.7	
19	1.5		106	1.0	
21	1.4		108	1.6	
24	1.1		110	1.2	
27	1.2		112	1.9	
30	7.0	Outlier	115	1.3	
33	3.6	Outlier	117	1.3	
35	1.5		118	1.4	
36	1.7				
37	1.2				
38	1.7				
40	0.81				
44	1.5				
45	1.9				
46	1.5				
47	2.0				
49	1.6				
51	1.5				
54	1.3				
55	0.49				
57	2.0	ND			
58	7.6	Outlier			
59	1.5				
60	4.1	Outlier			
61	1.3				
62	1.3				
64	47	Outlier			
65	1.5				
71	3.2	Outlier			
73	1.1				
74	1.6				
75	1.6				
77	1.6				
78	1.5				
80	1.3				
81	0.73				
83	0.81				
85	1.4				

**Consensus statistics**

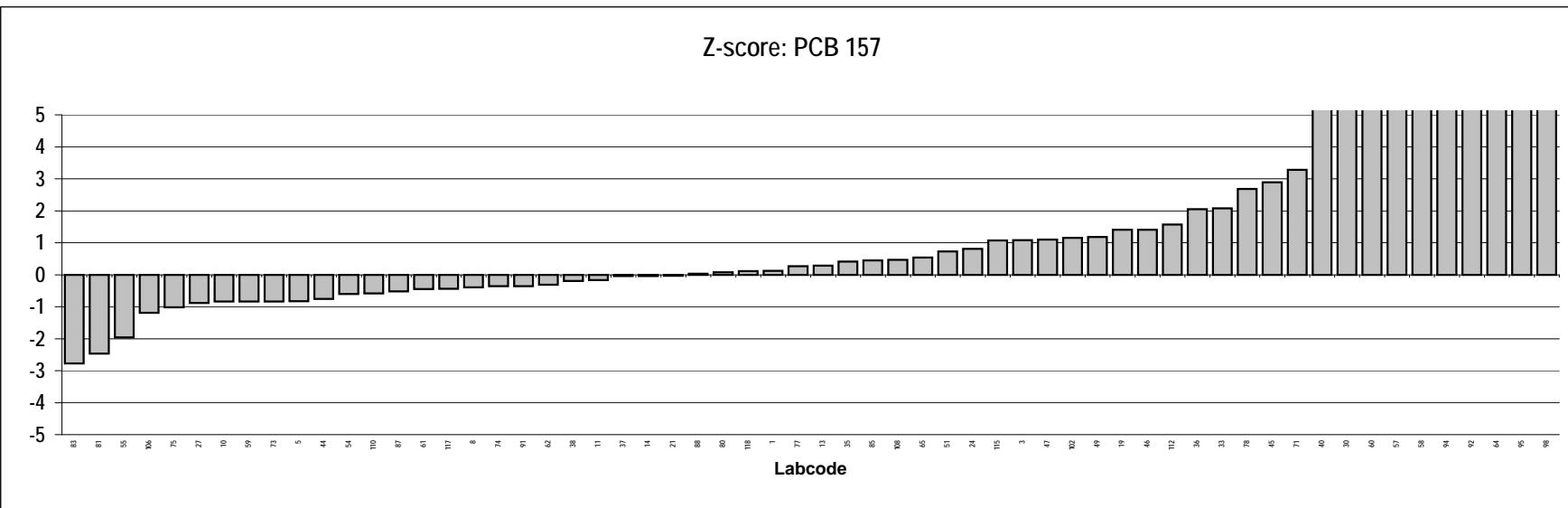
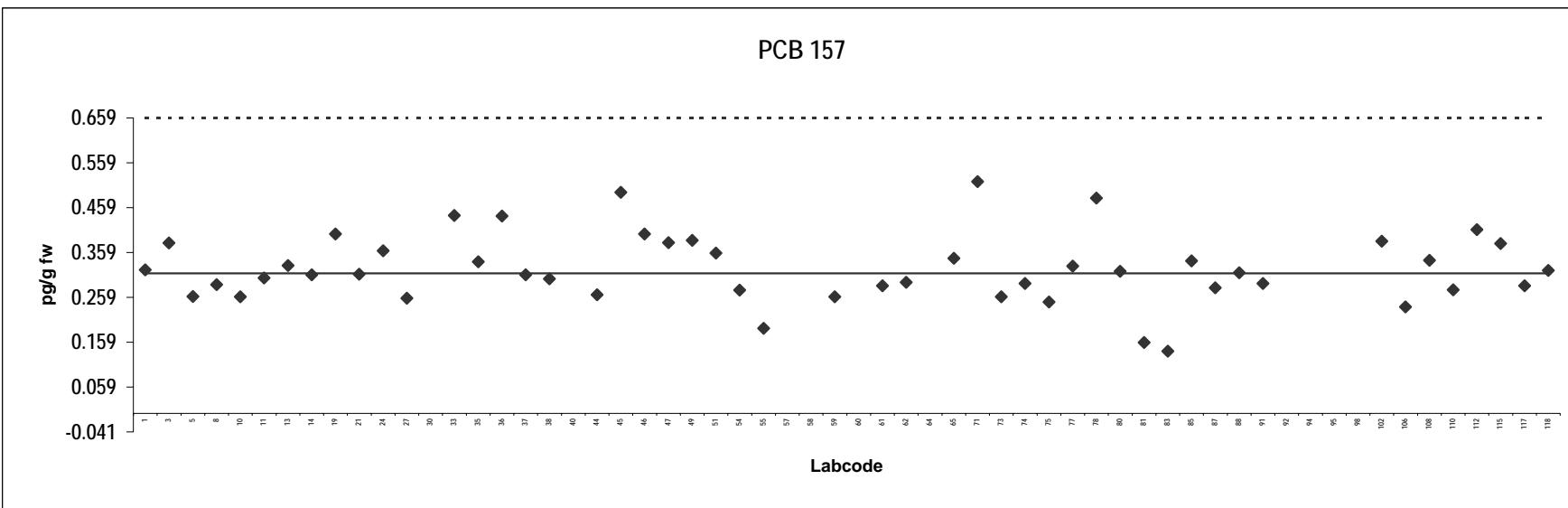
Consensus median, pg/g	1.4
Median all values pg/g	1.5
Consensus mean, pg/g	1.4
Standard deviation, pg/g	0.31
Relative standard deviation, %	22
No. of values reported	60
No. of values removed	10
No. of reported non-detects	5



**Milk**  
Congener: PCB 157

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.32		87	0.28	
3	0.38		88	0.31	
5	0.26		91	0.29	
8	0.29		92	8.0	Outlier,ND
10	0.26		94	5.0	Outlier,ND
11	0.30		95	10	Outlier,ND
13	0.33		98	10	Outlier,ND
14	0.31		102	0.38	ND
19	0.40		106	0.24	
21	0.31		108	0.34	
24	0.36		110	0.28	
27	0.26		112	0.41	
30	0.82	Outlier	115	0.38	
33	0.44		117	0.29	
35	0.34		118	0.32	
36	0.44	ND			
37	0.31				
38	0.30				
40	0.68	Outlier,ND			
44	0.26				
45	0.49				
46	0.40				
47	0.38				
49	0.39				
51	0.36				
54	0.27				
55	0.19				
57	2.0	Outlier,ND			
58	4.4	Outlier,ND			
59	0.26				
60	1.0	Outlier			
61	0.28				
62	0.29				
64	9.2	Outlier			
65	0.35				
71	0.52				
73	0.26				
74	0.29				
75	0.25				
77	0.33				
78	0.48				
80	0.32				
81	0.16				
83	0.14				
85	0.34				

Consensus statistics	
Consensus median, pg/g	0.31
Median all values pg/g	0.33
Consensus mean, pg/g	0.32
Standard deviation, pg/g	0.077
Relative standard deviation, %	24
No. of values reported	60
No. of values removed	10
No. of reported non-detects	9

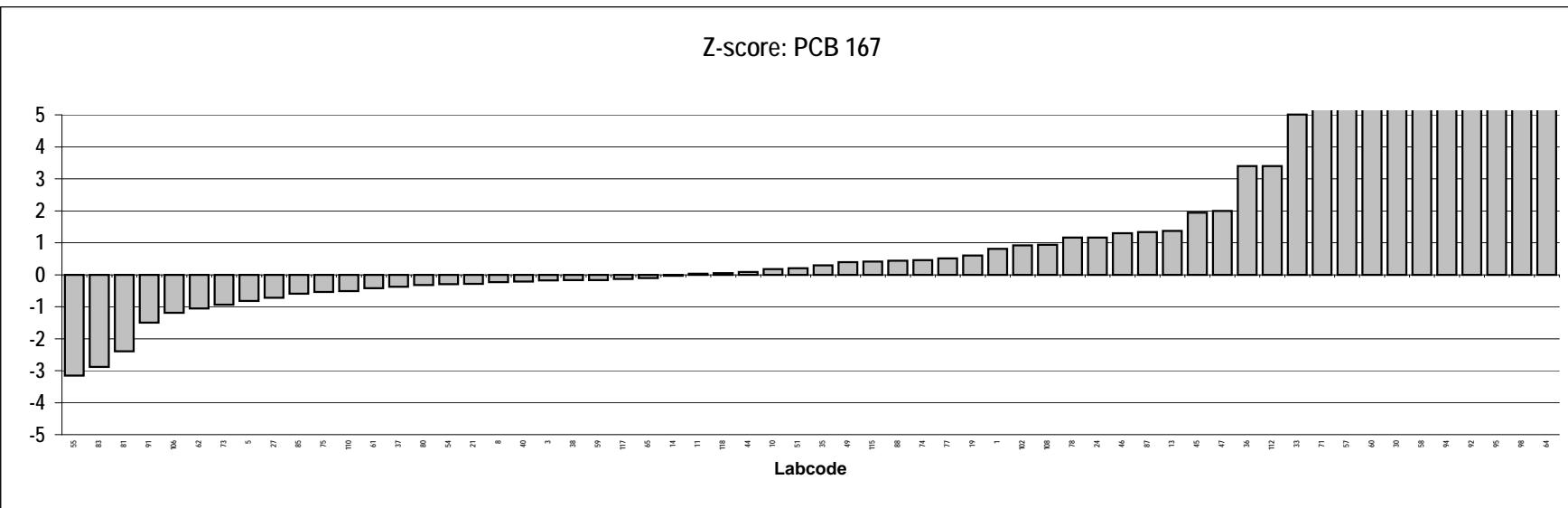
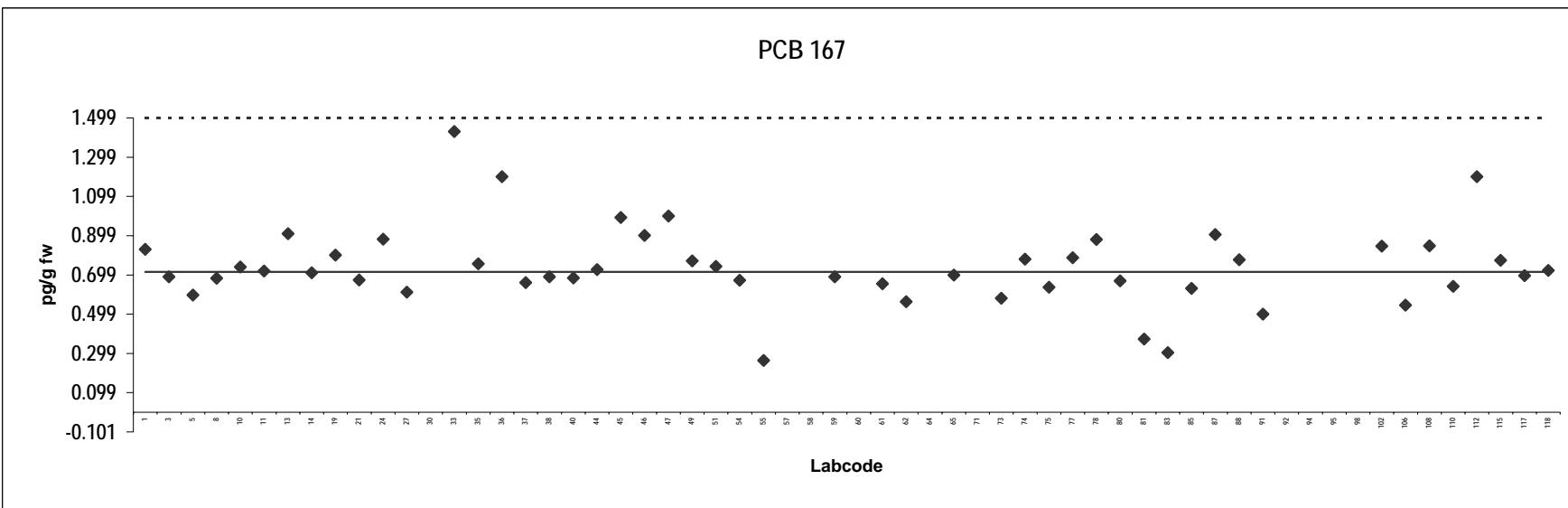


**Milk**  
Congener: PCB 167

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.83		87	0.91	
3	0.69		88	0.78	
5	0.60		91	0.50	
8	0.68		92	8.0	Outlier,ND
10	0.74		94	5.0	Outlier,ND
11	0.72		95	10	Outlier,ND
13	0.91		98	10	Outlier,ND
14	0.71		102	0.85	
19	0.80		106	0.54	
21	0.67		108	0.85	
24	0.88		110	0.64	
27	0.61		112	1.2	
30	3.3	Outlier	115	0.77	
33	1.4		117	0.70	
35	0.76		118	0.72	
36	1.2				
37	0.66				
38	0.69				
40	0.68	ND			
44	0.73				
45	0.99				
46	0.90				
47	1.00				
49	0.77				
51	0.74				
54	0.67				
55	0.26				
57	2.0	Outlier,ND			
58	4.4	Outlier,ND			
59	0.69				
60	2.3	Outlier			
61	0.65				
62	0.56				
64	.87	Outlier			
65	0.70				
71	1.6	Outlier			
73	0.58				
74	0.78				
75	0.64				
77	0.79				
78	0.88				
80	0.67				
81	0.37				
83	0.30				
85	0.63				

**Consensus statistics**

Consensus median, pg/g	0.71
Median all values pg/g	0.75
Consensus mean, pg/g	0.74
Standard deviation, pg/g	0.20
Relative standard deviation, %	27
No. of values reported	60
No. of values removed	10
No. of reported non-detects	7

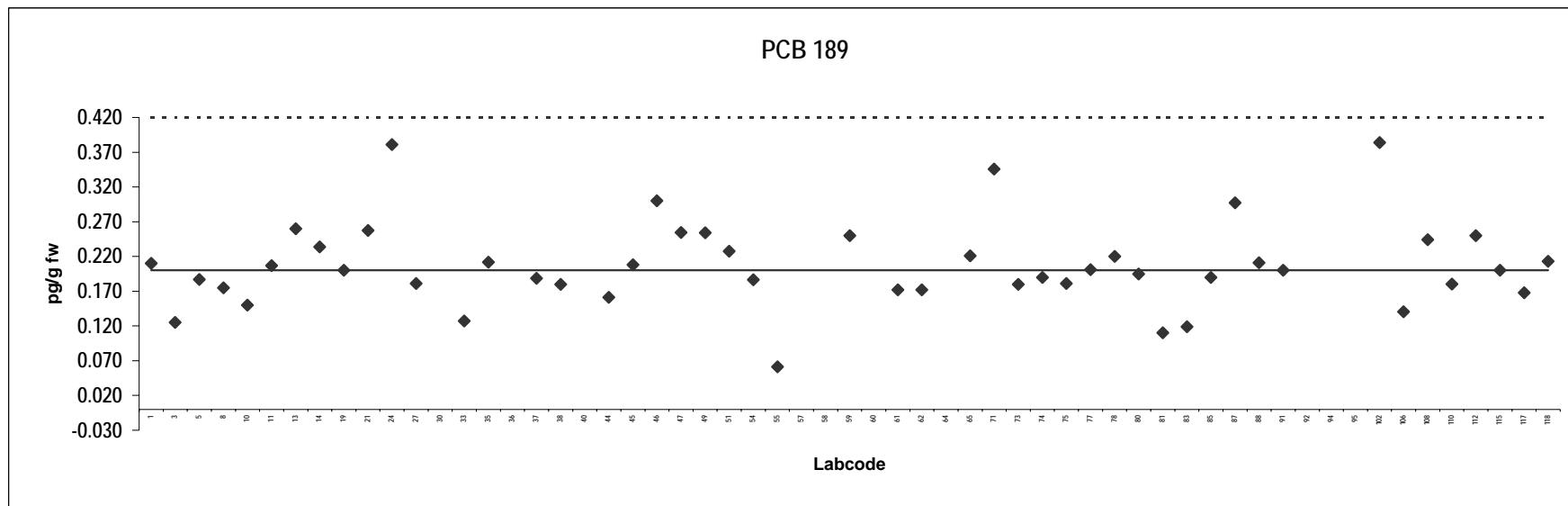


**Milk**  
Congener: PCB 189

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.21		87	0.30	
3	0.13	ND	88	0.21	
5	0.19		91	0.20	
8	0.17		92	8.0	Outlier,ND
10	0.15		94	5.0	Outlier,ND
11	0.21		95	10	Outlier,ND
13	0.26		102	0.38	ND
14	0.23		106	0.14	
19	0.20		108	0.24	
21	0.26		110	0.18	
24	0.38		112	0.25	
27	0.18		115	0.20	
30	0.67	Outlier	117	0.17	
33	0.13	ND	118	0.21	
35	0.21				
36	0.95	Outlier,ND			
37	0.19				
38	0.18				
40	0.68	Outlier,ND			
44	0.16				
45	0.21				
46	0.30				
47	0.25				
49	0.25				
51	0.23				
54	0.19				
55	0.061	ND			
57	2.0	Outlier,ND			
58	4.4	Outlier,ND			
59	0.25				
60	0.74	Outlier			
61	0.17				
62	0.17				
64	7.1	Outlier			
65	0.22				
71	0.35				
73	0.18				
74	0.19				
75	0.18				
77	0.20				
78	0.22				
80	0.20				
81	0.11				
83	0.12				
85	0.19				

**Consensus statistics**

Consensus median, pg/g	0.20
Median all values pg/g	0.21
Consensus mean, pg/g	0.21
Standard deviation, pg/g	0.062
Relative standard deviation, %	30
No. of values reported	59
No. of values removed	10
No. of reported non-detects	11

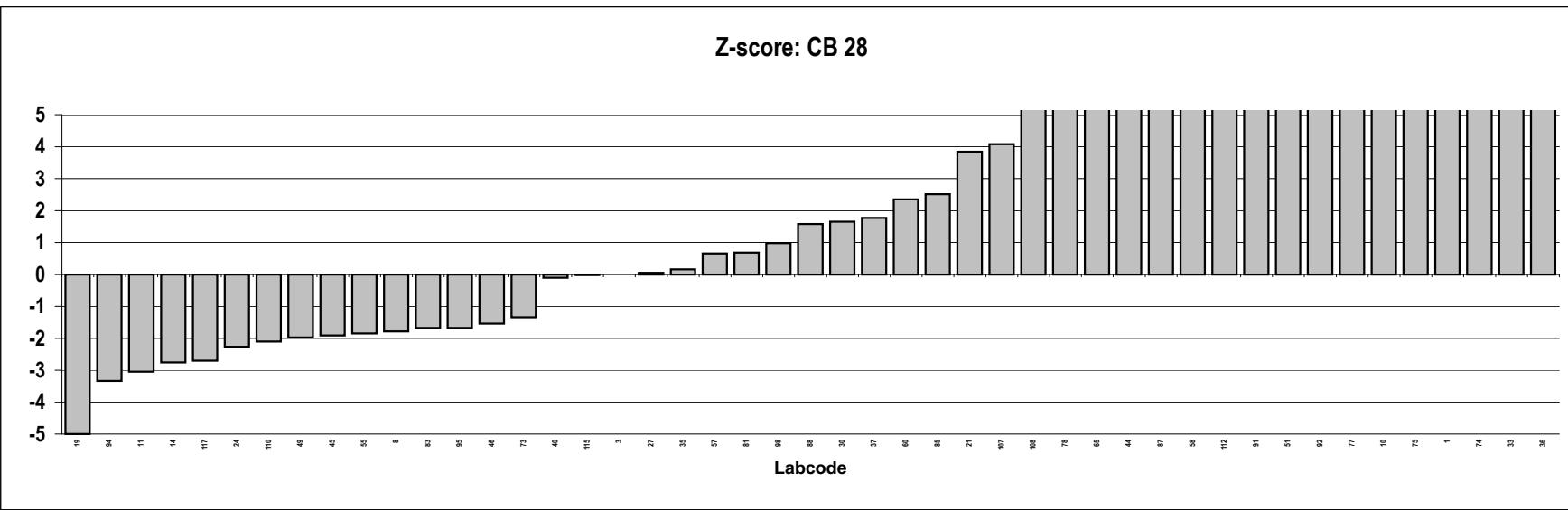
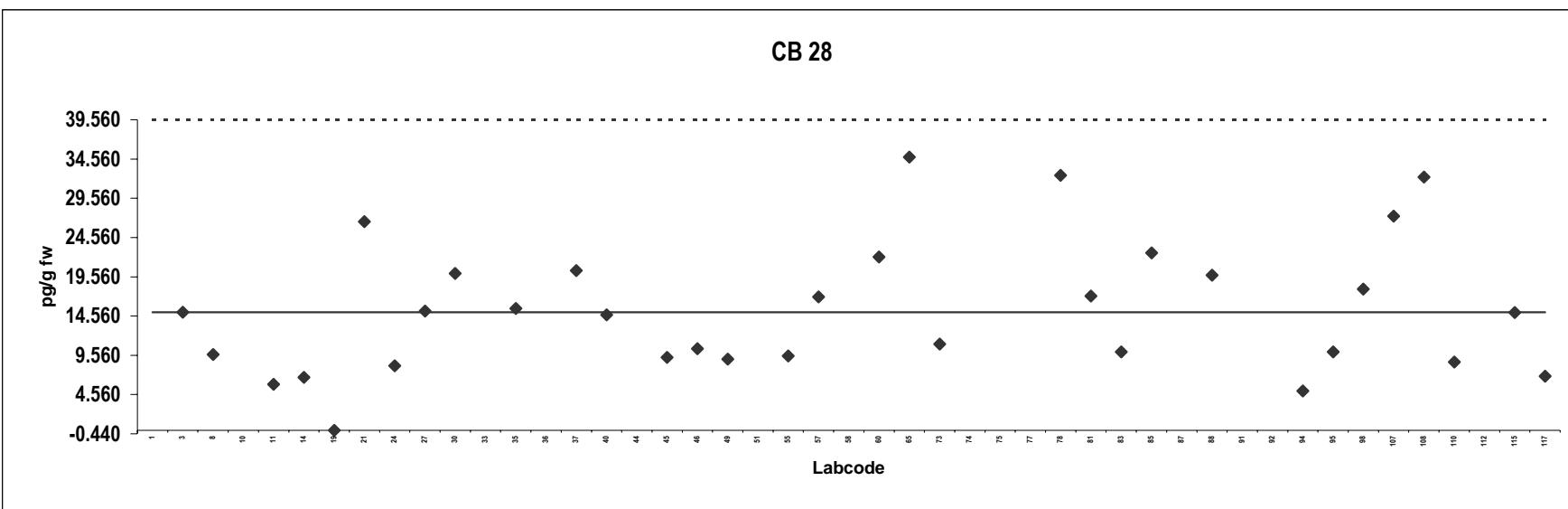


**Milk**  
Congener: CB 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	75	Outlier	115	15	
3	15		117	6.9	
8	9.7				
10	71	Outlier			
11	5.9				
14	6.7				
19	0.011				
21	27				
24	8.2				
27	15				
30	20				
33	81	Outlier			
35	16				
36	120	Outlier			
37	20				
40	15				
44	43	Outlier			
45	9.3				
46	10				
49	9.1				
51	51	Outlier			
55	9.5				
57	17				
58	48	Outlier			
60	22				
65	35				
73	11				
74	81	Outlier			
75	73	Outlier			
77	68	Outlier			
78	32				
81	17				
83	10				
85	23				
87	43	Outlier			
88	20				
91	49	Outlier			
92	51	Outlier,ND			
94	5.0	ND			
95	10	ND			
98	18				
107	27				
108	32				
110	8.7				
112	48	Outlier			

**Consensus statistics**

Consensus median, pg/g	15
Median all values pg/g	20
Consensus mean, pg/g	15
Standard deviation, pg/g	8.5
Relative standard deviation, %	56
No. of values reported	47
No. of values removed	14
No. of reported non-detects	3

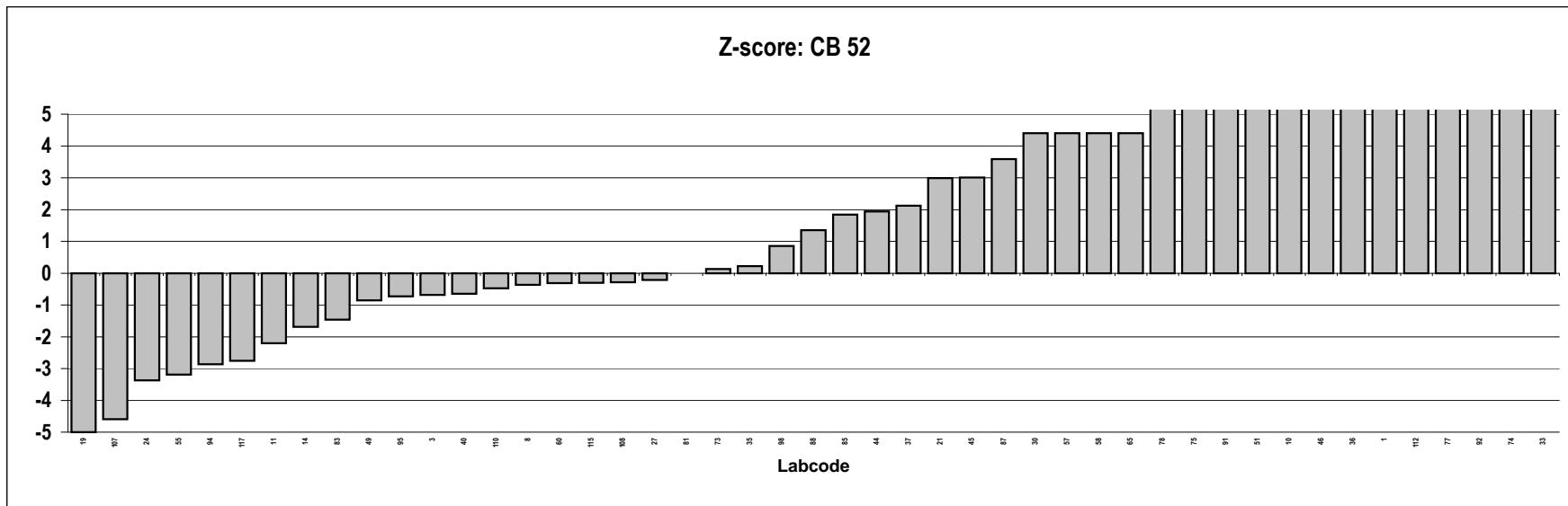
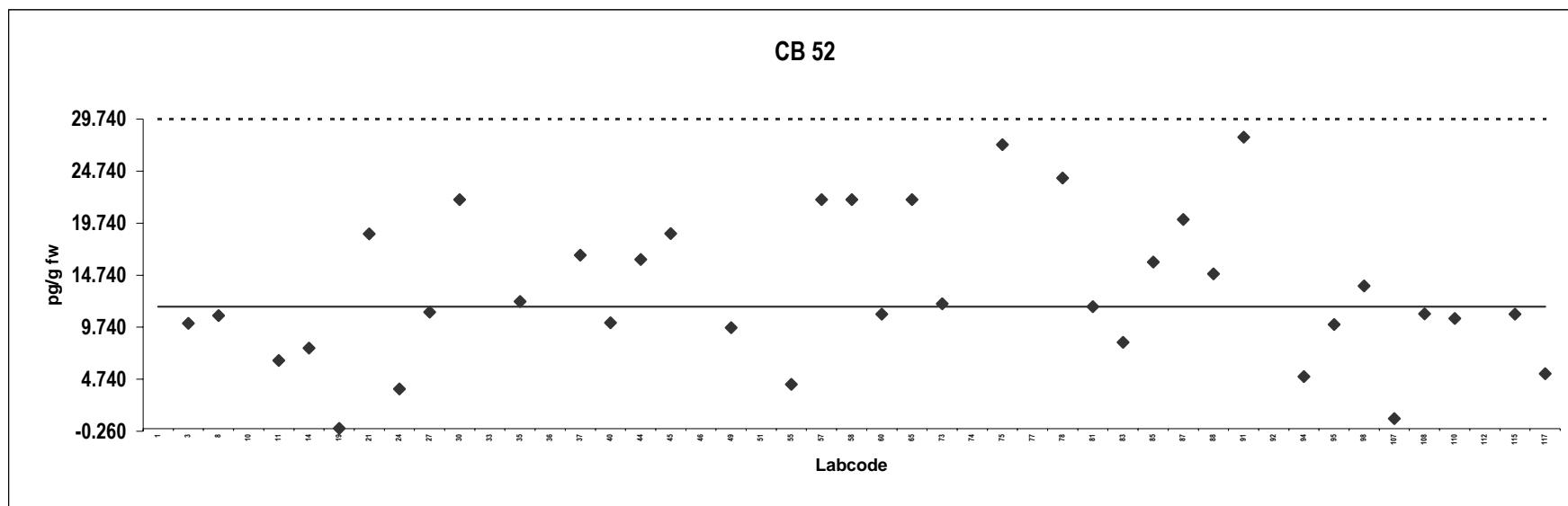


**Milk**  
**Congener: CB 52**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	48	Outlier	115	11	
3	10		117	5.3	
8	11				
10	41	Outlier			
11	6.6				
14	7.7				
19	0.0080				
21	19				
24	3.8				
27	11				
30	22				
33	75	Outlier			
35	12				
36	48	Outlier			
37	17				
40	10				
44	16				
45	19				
46	46	Outlier			
49	9.7				
51	38	Outlier			
55	4.2				
57	22				
58	22	ND			
60	11				
65	22				
73	12				
74	60	Outlier			
75	27				
77	56	Outlier			
78	24				
81	12				
83	8.3				
85	16				
87	20				
88	15				
91	28				
92	57	Outlier			
94	5.0	ND			
95	10	ND			
98	14				
107	0.96	ND			
108	11				
110	11				
112	55	Outlier			

**Consensus statistics**

Consensus median, pg/g	12
Median all values pg/g	15
Consensus mean, pg/g	13
Standard deviation, pg/g	7.0
Relative standard deviation, %	54
No. of values reported	47
No. of values removed	10
No. of reported non-detects	4

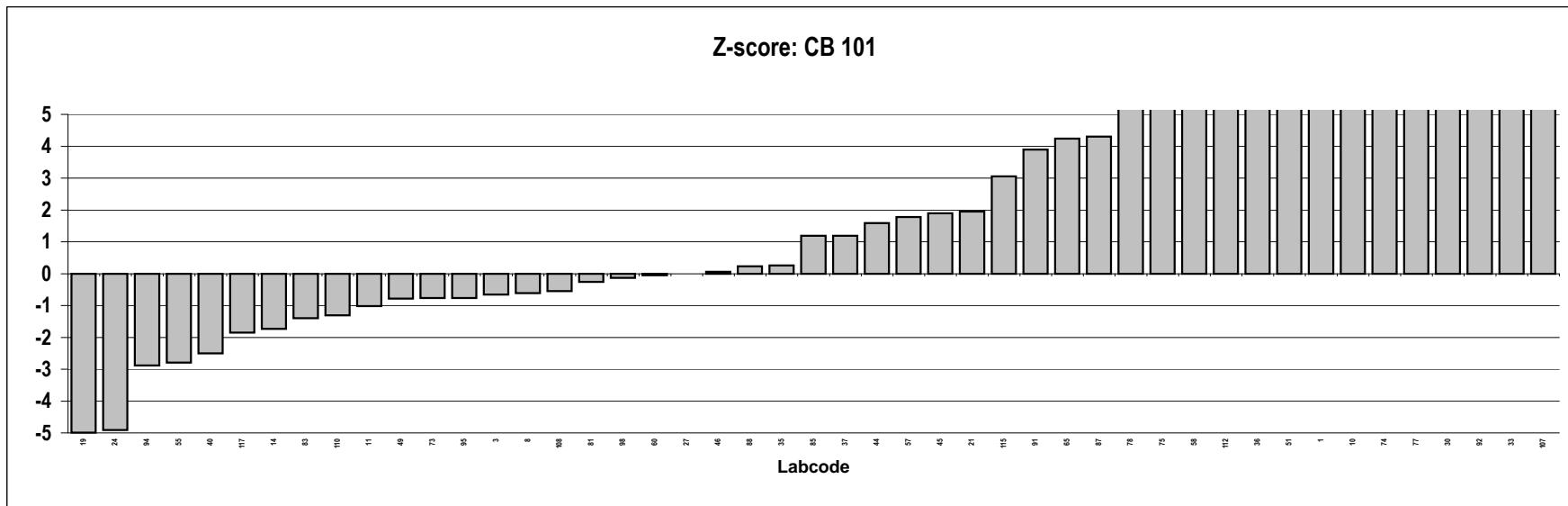
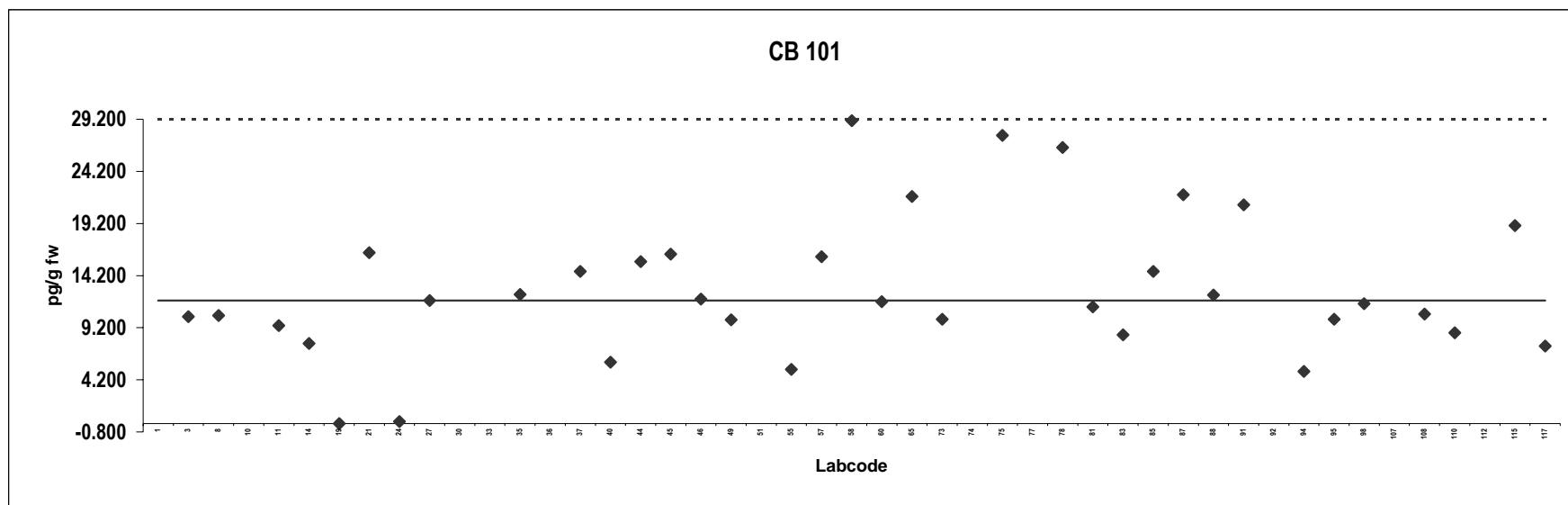


**Milk**  
Congener: CB 101

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	41	Outlier	115	19	
3	10		117	7.4	
8	10				
10	45	Outlier			
11	9.4				
14	7.7				
19	0.013				
21	16				
24	0.21	ND			
27	12				
30	64	Outlier			
33	69	Outlier			
35	12				
36	38	Outlier			
37	15				
40	5.9				
44	16				
45	16				
46	12				
49	10				
51	39	Outlier			
55	5.2				
57	16				
58	29				
60	12				
65	22				
73	10				
74	55	Outlier			
75	28				
77	56	Outlier			
78	26				
81	11				
83	8.5				
85	15				
87	22				
88	12				
91	21				
92	69	Outlier			
94	5.0	ND			
95	10	ND			
98	12				
107	92	Outlier,ND			
108	11				
110	8.7				
112	38	Outlier			

**Consensus statistics**

Consensus median, pg/g	12
Median all values pg/g	15
Consensus mean, pg/g	13
Standard deviation, pg/g	6.8
Relative standard deviation, %	53
No. of values reported	47
No. of values removed	11
No. of reported non-detects	4

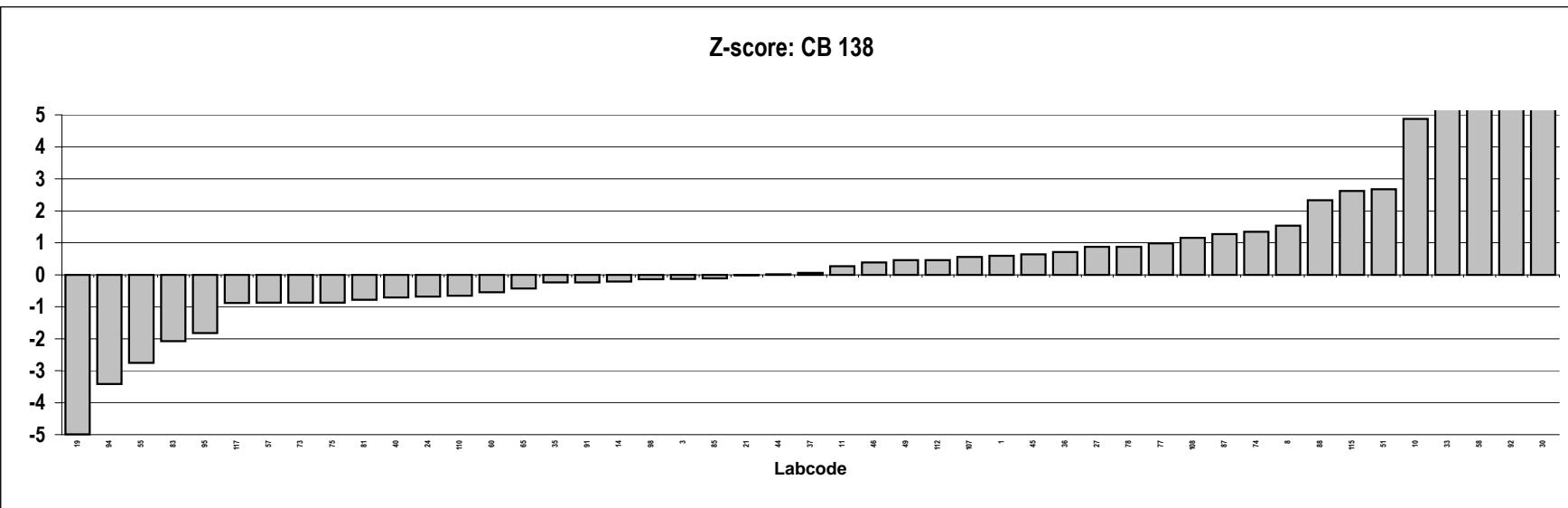
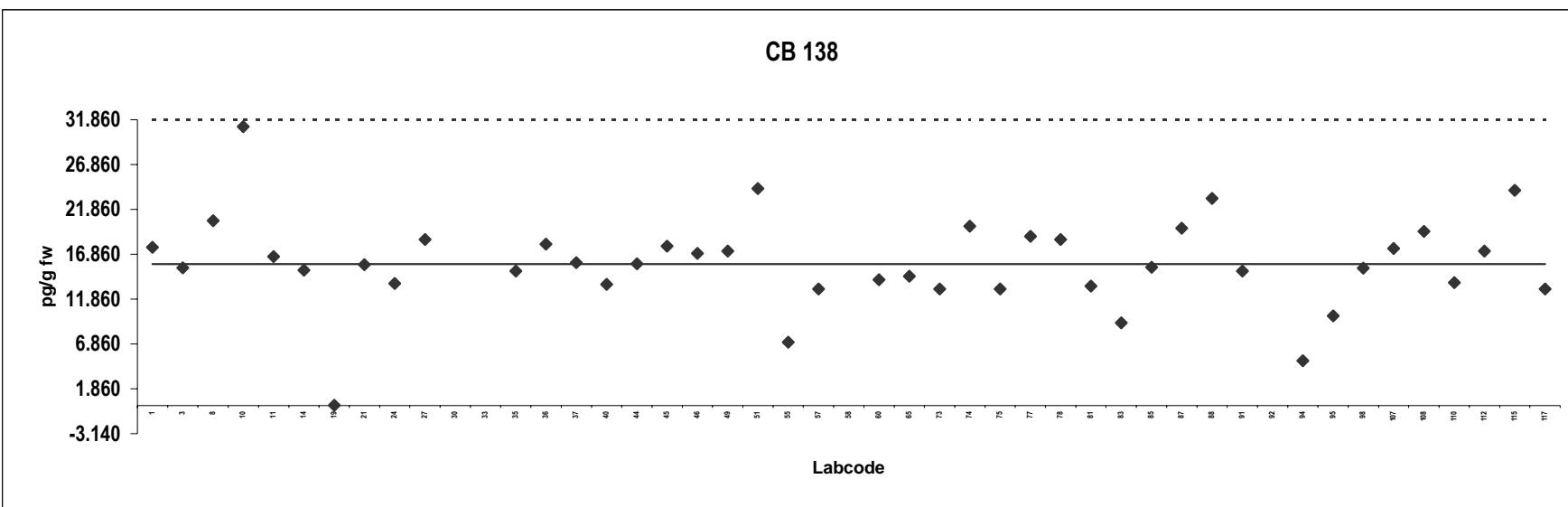


**Milk**  
Congener: CB 138

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	18		115	24	
3	15		117	13	
8	21				
10	31				
11	17				
14	15				
19	0.019				
21	16				
24	14				
27	19				
30	68				
33	34	Outlier			
35	15	Outlier			
36	18				
37	16				
40	14				
44	16				
45	18				
46	17				
49	17				
51	24				
55	7.1				
57	13				
58	46	Outlier			
60	14				
65	14				
73	13				
74	20				
75	13				
77	19				
78	19				
81	13				
83	9.2				
85	15				
87	20				
88	23				
91	15				
92	65	Outlier			
94	5.0	ND			
95	10				
98	15				
107	18				
108	19				
110	14				
112	17				

**Consensus statistics**

Consensus median, pg/g	16
Median all values pg/g	16
Consensus mean, pg/g	16
Standard deviation, pg/g	5.2
Relative standard deviation, %	33
No. of values reported	47
No. of values removed	4
No. of reported non-detects	1

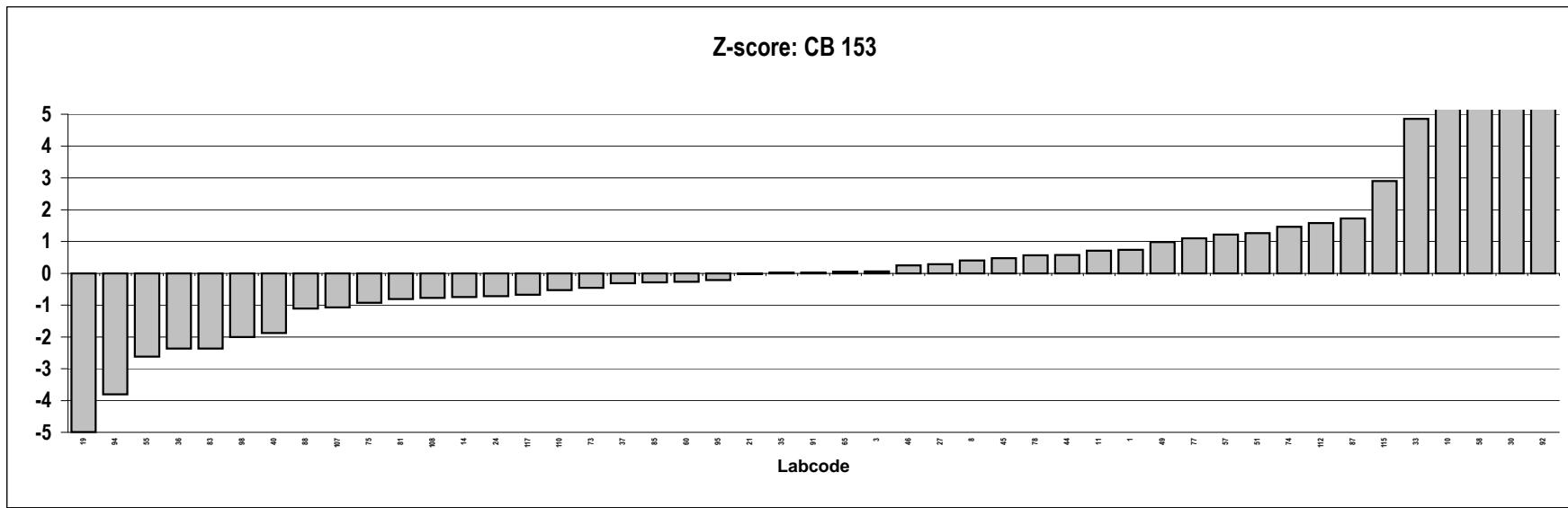
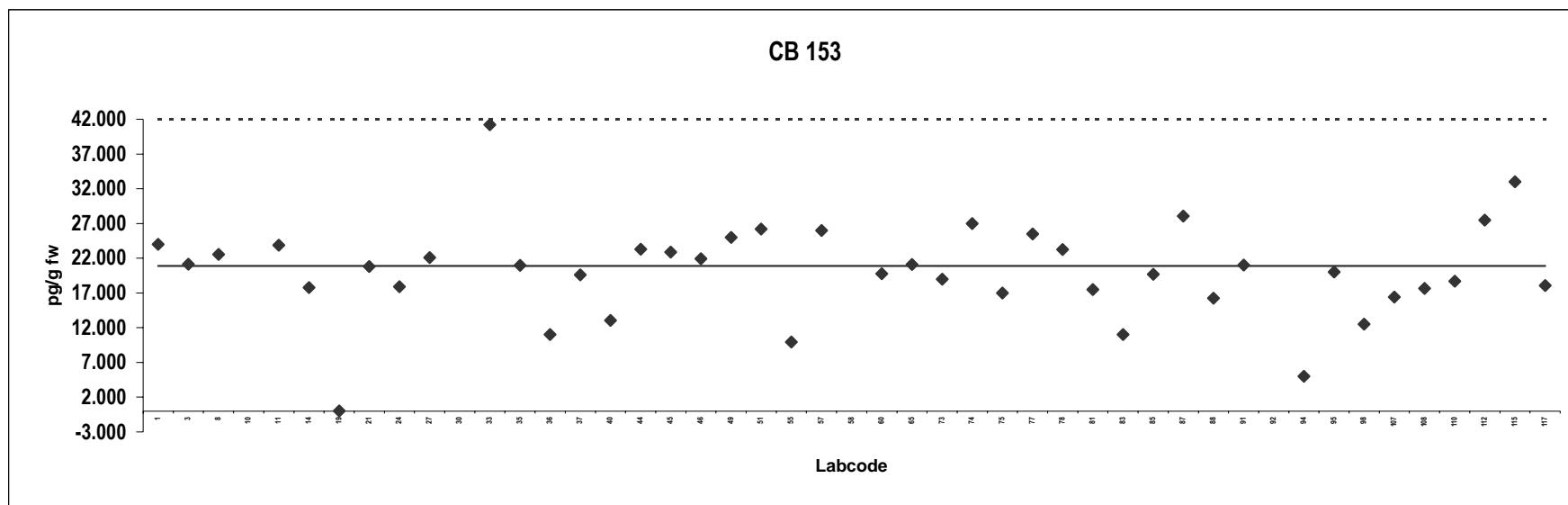


**Milk**  
Congener: CB 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	24		115	33	
3	21		117	18	
8	23				
10	45	Outlier			
11	24				
14	18				
19	0.023				
21	21				
24	18				
27	22				
30	85	Outlier			
33	41				
35	21				
36	11				
37	20				
40	13				
44	23				
45	23				
46	22				
49	25				
51	26				
55	10				
57	26				
58	63	Outlier			
60	20				
65	21				
73	19				
74	27				
75	17				
77	26				
78	23				
81	18				
83	11				
85	20				
87	28				
88	16				
91	21				
92	101	Outlier			
94	5.0	ND			
95	20				
98	13				
107	16				
108	18				
110	19				
112	28				

**Consensus statistics**

Consensus median, pg/g	21
Median all values pg/g	21
Consensus mean, pg/g	20
Standard deviation, pg/g	7.0
Relative standard deviation, %	35
No. of values reported	47
No. of values removed	4
No. of reported non-detects	1

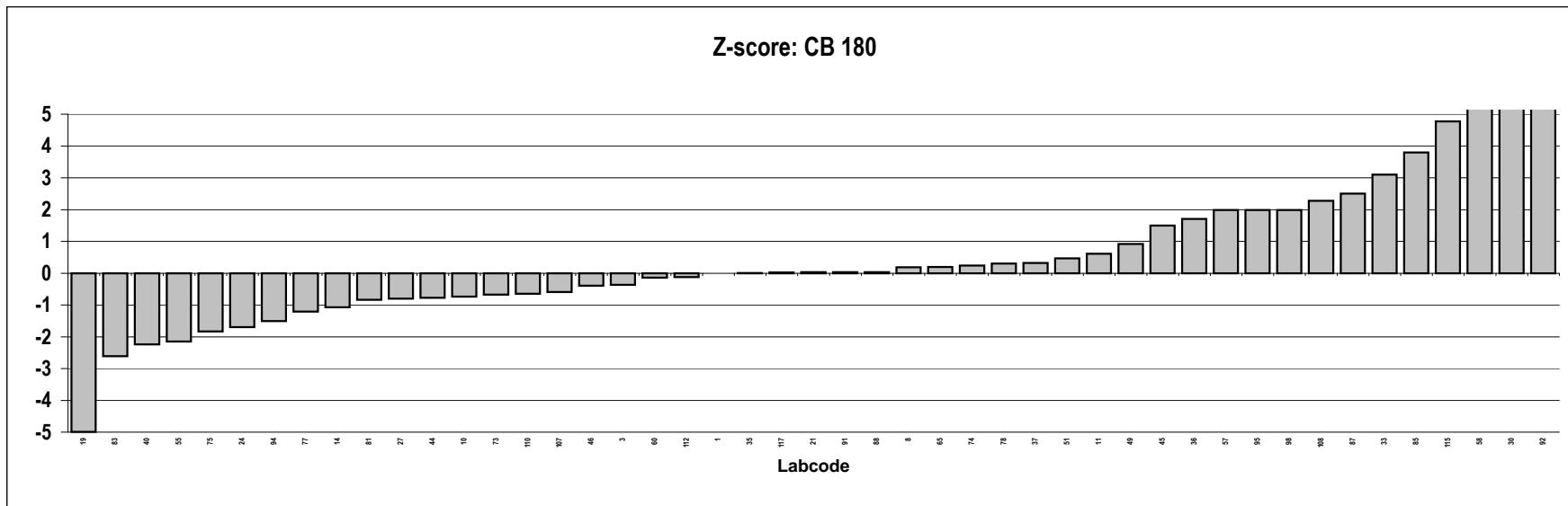
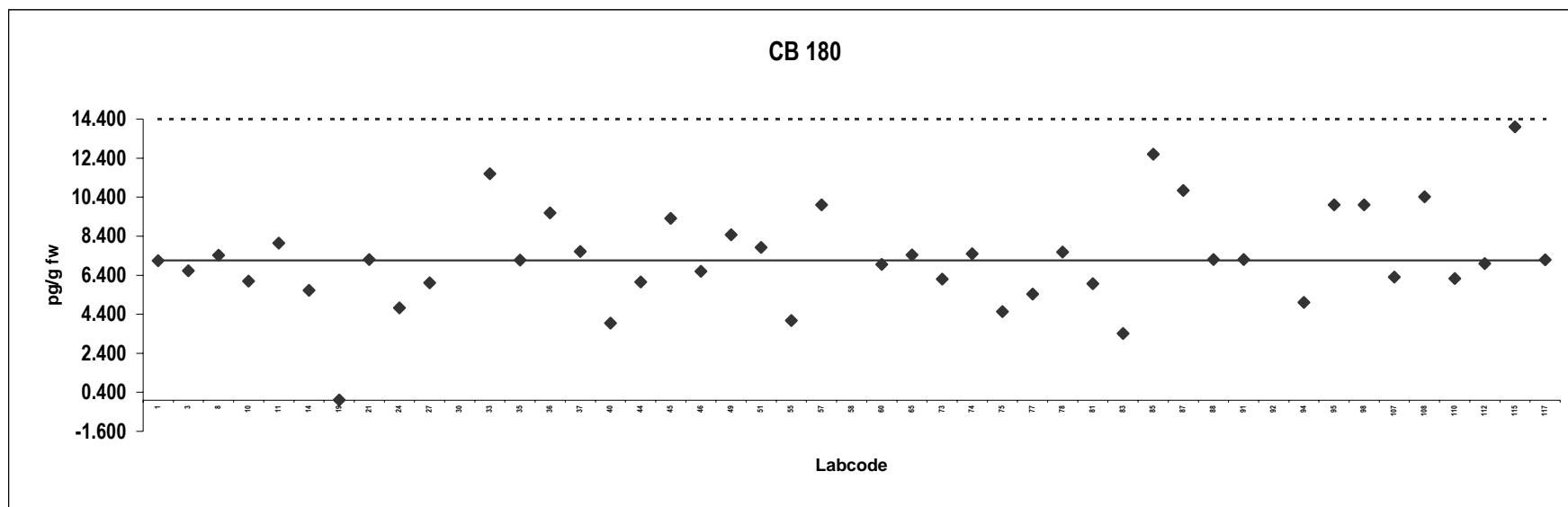


**Milk**  
Congener: CB 180

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	7.2		115	14	
3	6.6		117	7.2	
8	7.4				
10	6.1				
11	8.0				
14	5.6				
19	0.0070				
21	7.2				
24	4.7				
27	6.0				
30	48				
33	12				
35	7.2				
36	9.6				
37	7.6				
40	3.9				
44	6.1				
45	9.3				
46	6.6				
49	8.5				
51	7.8				
55	4.1				
57	10	ND			
58	23	Outlier			
60	7.0				
65	7.4				
73	6.2				
74	7.5				
75	4.5				
77	5.4				
78	7.6				
81	6.0				
83	3.4				
85	13				
87	11				
88	7.2				
91	7.2				
92	51	Outlier,ND			
94	5.0	ND			
95	10	ND			
98	10	ND			
107	6.3				
108	10				
110	6.2				
112	7.0				

**Consensus statistics**

Consensus median, pg/g	7.2
Median all values pg/g	7.2
Consensus mean, pg/g	7.3
Standard deviation, pg/g	2.5
Relative standard deviation, %	35
No. of values reported	47
No. of values removed	3
No. of reported non-detects	5

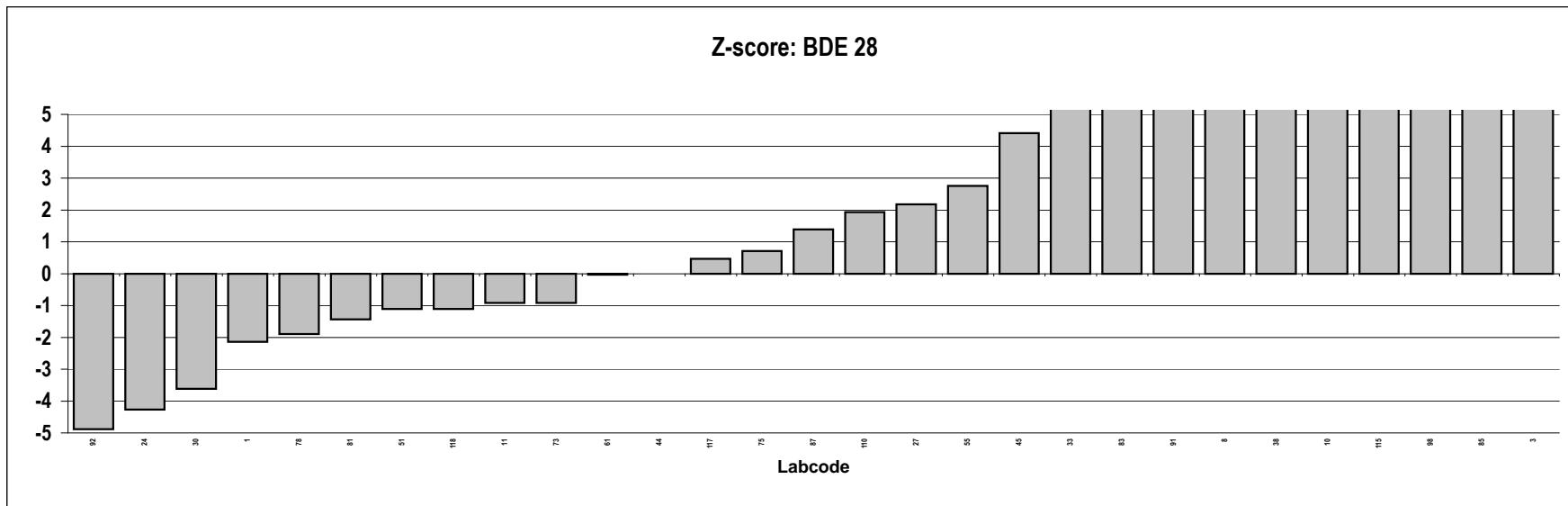
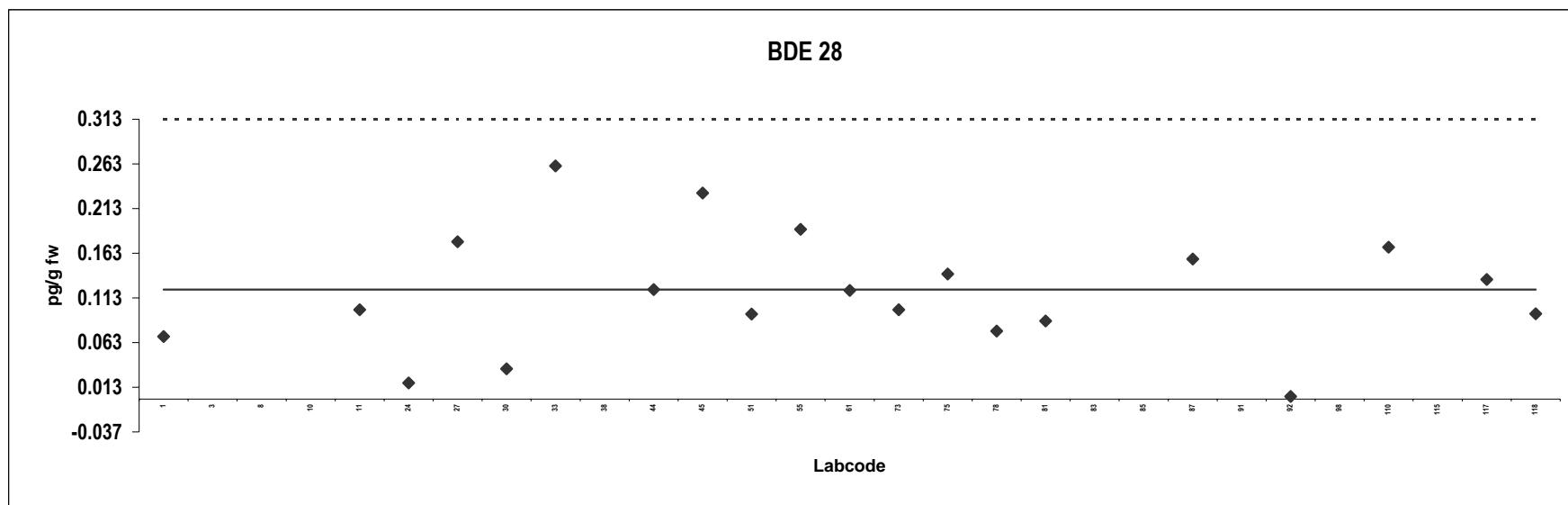


**Milk**  
**Congener: BDE 28**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.070				
3	2.0	Outlier,ND			
8	0.41	Outlier			
10	0.60	Outlier			
11	0.10	ND			
24	0.018	ND			
27	0.18				
30	0.034	ND			
33	0.26				
38	0.50	Outlier,ND			
44	0.12				
45	0.23				
51	0.095				
55	0.19				
61	0.12				
73	0.10				
75	0.14				
78	0.076				
81	0.088				
83	0.35	Outlier			
85	1.5	Outlier			
87	0.16				
91	0.39	Outlier,ND			
92	0.0028	ND			
98	1.3	Outlier,ND			
110	0.17	ND			
115	1.0	Outlier,ND			
117	0.13				
118	0.095				

**Consensus statistics**

Consensus median, pg/g	0.12
Median all values pg/g	0.16
Consensus mean, pg/g	0.12
Standard deviation, pg/g	0.066
Relative standard deviation, %	56
No. of values reported	29
No. of values removed	9
No. of reported non-detects	10

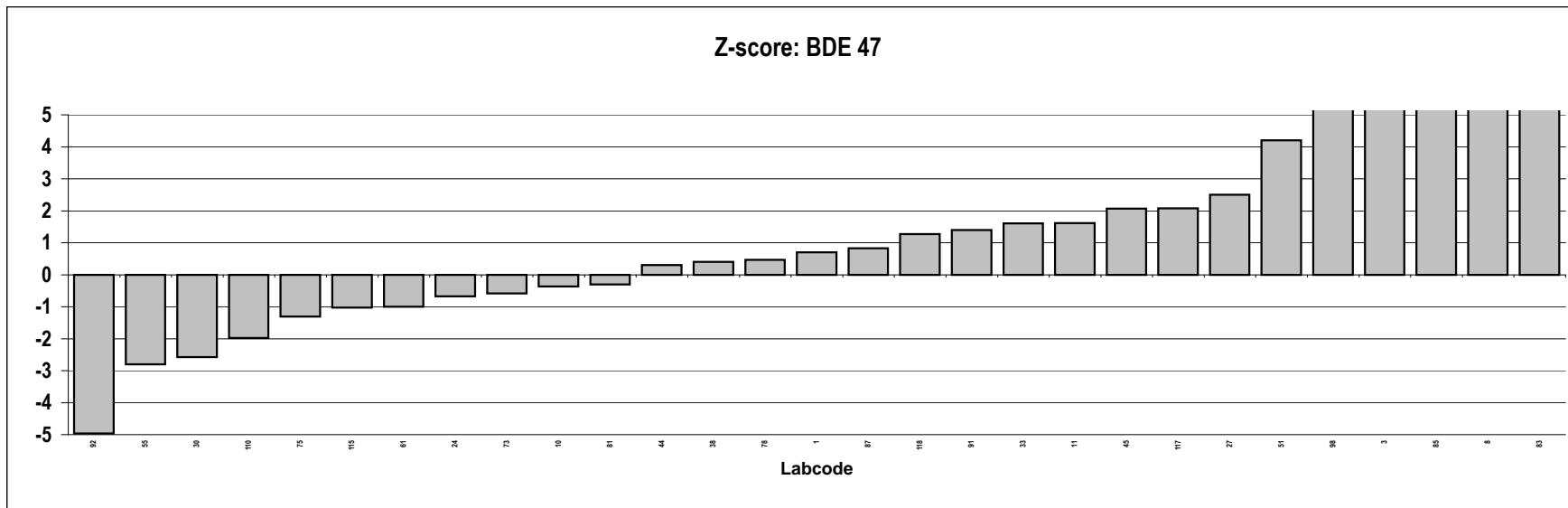
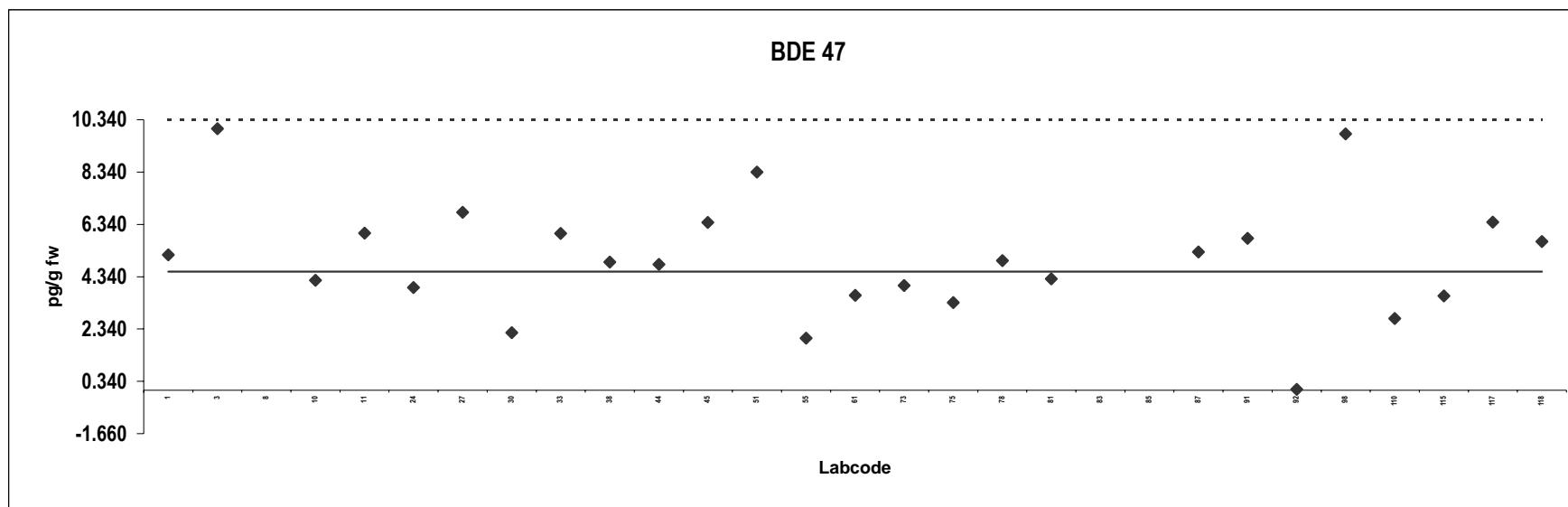


**Milk**  
**Congener: BDE 47**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.2				
3	10				
8	14	Outlier			
10	4.2				
11	6.0	ND			
24	3.9				
27	6.8				
30	2.2				
33	6.0				
38	4.9				
44	4.8				
45	6.4				
51	8.3				
55	2.0				
61	3.6				
73	4.0				
75	3.3				
78	5.0				
81	4.3				
83	34	Outlier			
85	13	Outlier			
87	5.3				
91	5.8	ND			
92	0.030				
98	9.8	ND			
110	2.7				
115	3.6				
117	6.4				
118	5.7				

**Consensus statistics**

Consensus median, pg/g	4.5
Median all values pg/g	5.2
Consensus mean, pg/g	5.0
Standard deviation, pg/g	2.2
Relative standard deviation, %	45
No. of values reported	29
No. of values removed	3
No. of reported non-detects	4

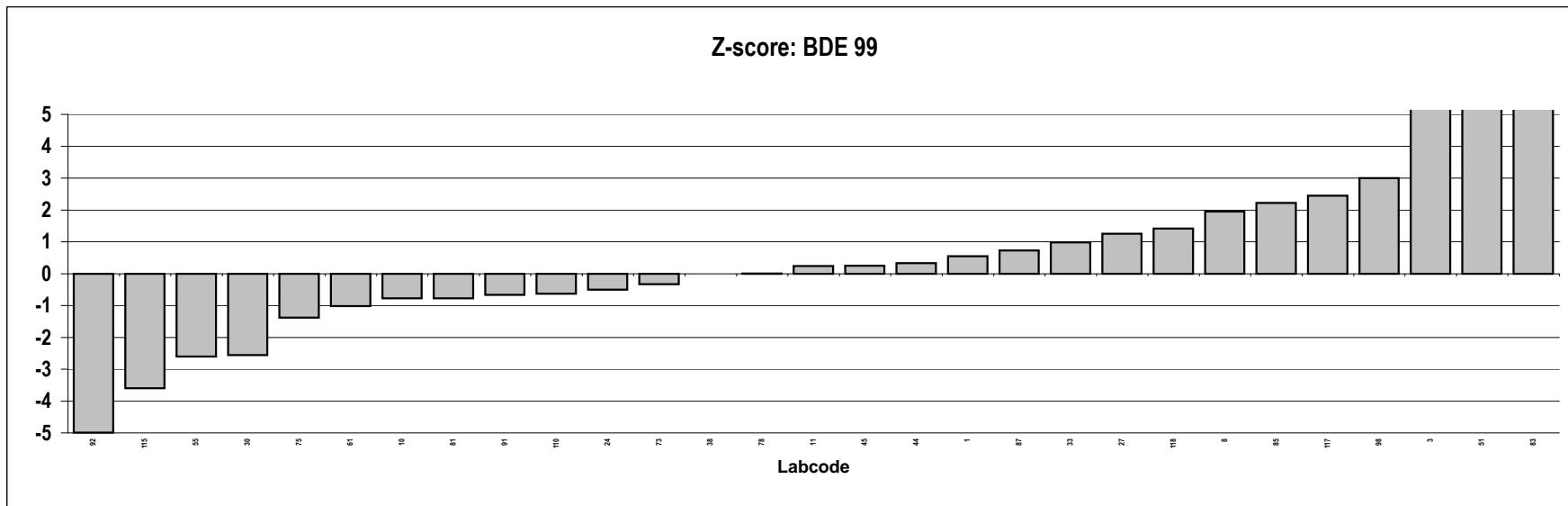
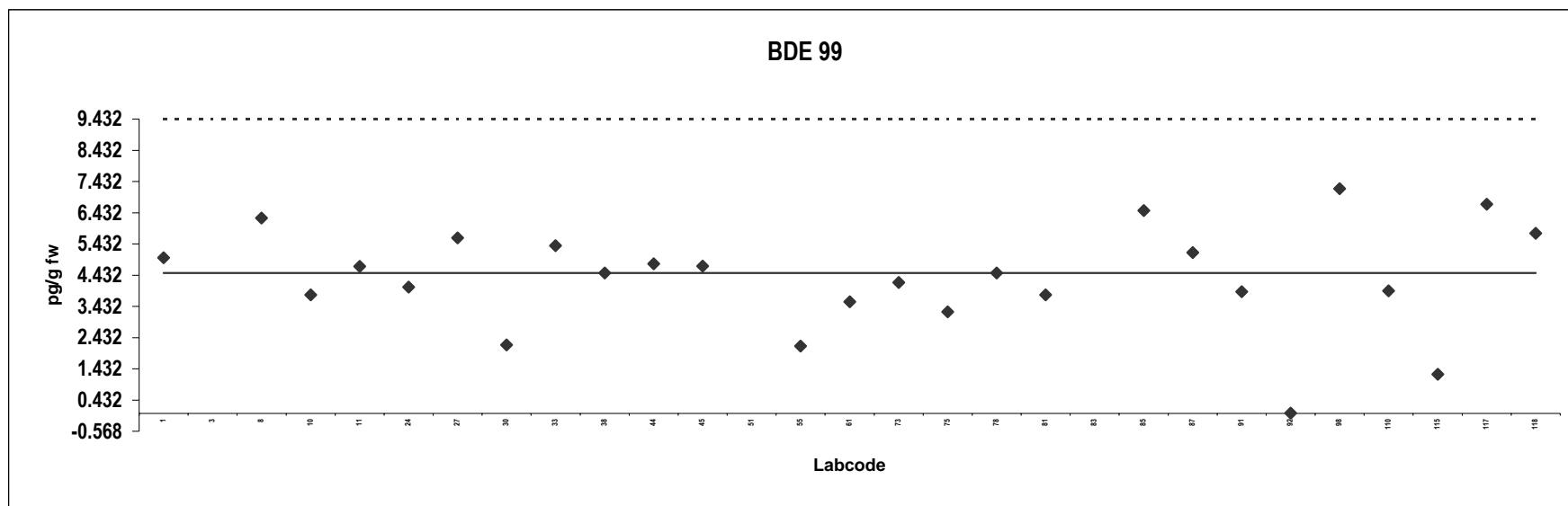


**Milk**  
**Congener: BDE 99**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.0				
3	10	Outlier,ND			
8	6.3				
10	3.8				
11	4.7				
24	4.1				
27	5.6				
30	2.2				
33	5.4				
38	4.5				
44	4.8				
45	4.7				
51	11	Outlier			
55	2.2				
61	3.6				
73	4.2				
75	3.3				
78	4.5				
81	3.8				
83	19	Outlier			
85	6.5				
87	5.2				
91	3.9				
92	0.010				
98	7.2	ND			
110	3.9				
115	1.3				
117	6.7				
118	5.8				

**Consensus statistics**

Consensus median, pg/g	4.5
Median all values pg/g	4.7
Consensus mean, pg/g	4.3
Standard deviation, pg/g	1.7
Relative standard deviation, %	38
No. of values reported	29
No. of values removed	3
No. of reported non-detects	2

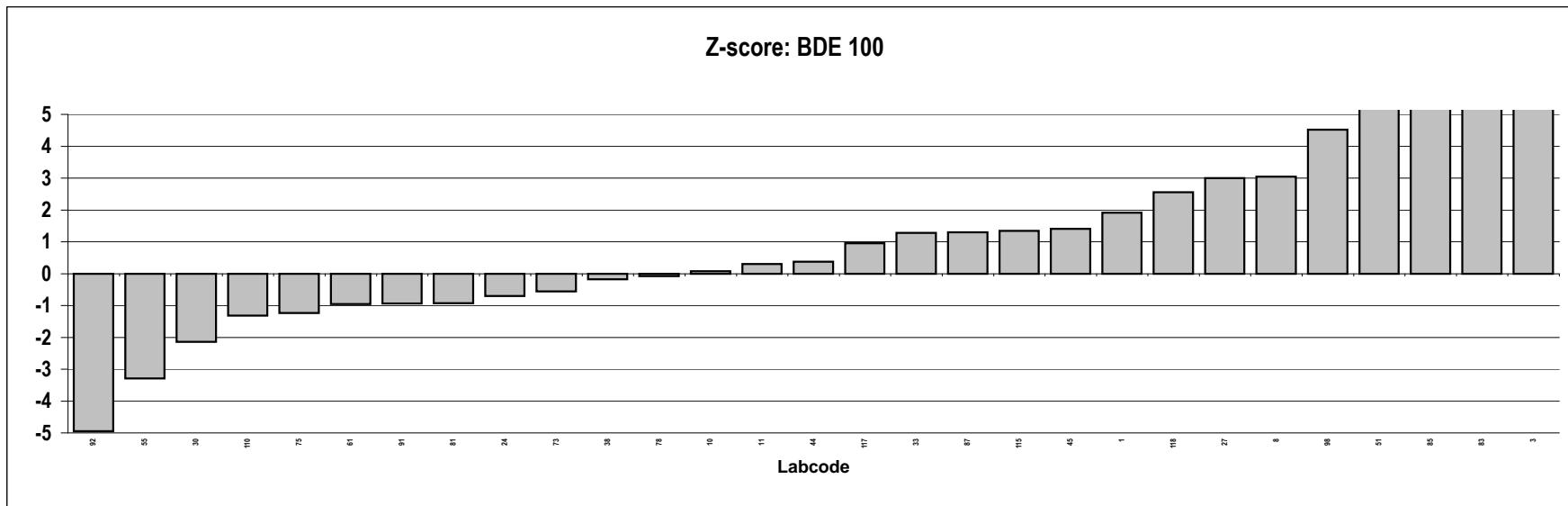
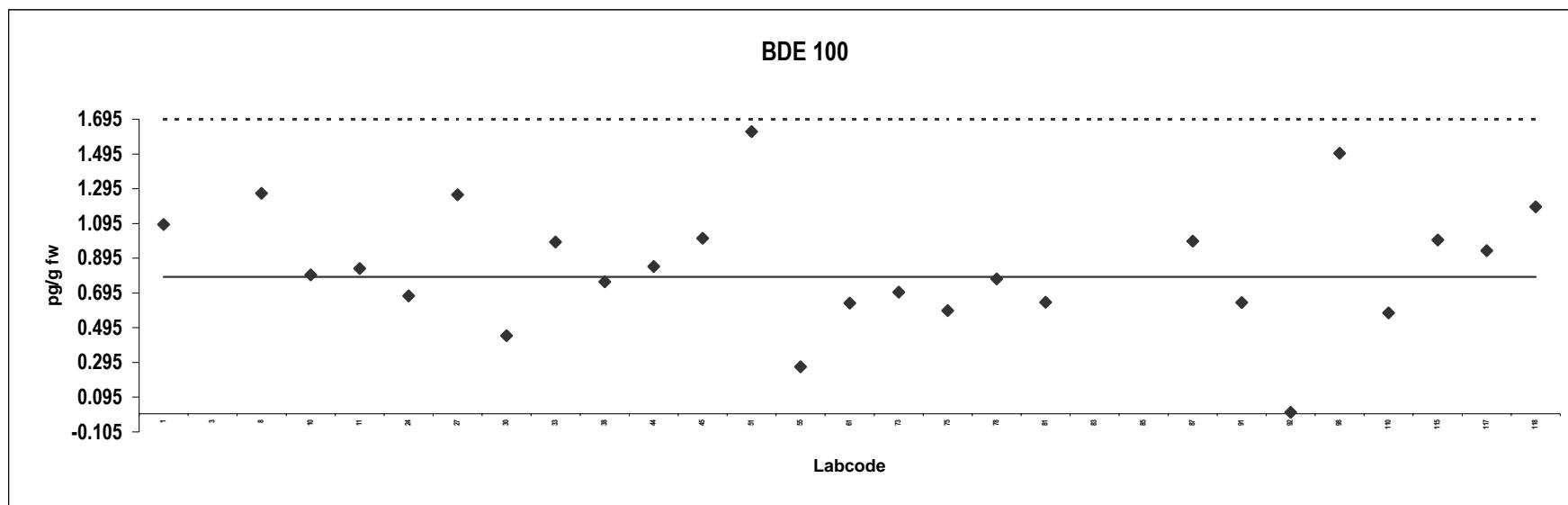


**Milk**  
Congener: BDE 100

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.1				
3	10	Outlier,ND			
8	1.3				
10	0.80				
11	0.84				
24	0.68				
27	1.3				
30	0.45				
33	0.99				
38	0.76				
44	0.85				
45	1.0				
51	1.6				
55	0.27				
61	0.64				
73	0.70				
75	0.59				
78	0.78				
81	0.64				
83	2.9	Outlier			
85	2.8	Outlier			
87	0.99				
91	0.64				
92	0.0080				
98	1.5	ND			
110	0.58	ND			
115	1.0				
117	0.94				
118	1.2				

**Consensus statistics**

Consensus median, pg/g	0.79
Median all values pg/g	0.85
Consensus mean, pg/g	0.85
Standard deviation, pg/g	0.36
Relative standard deviation, %	42
No. of values reported	29
No. of values removed	3
No. of reported non-detects	3

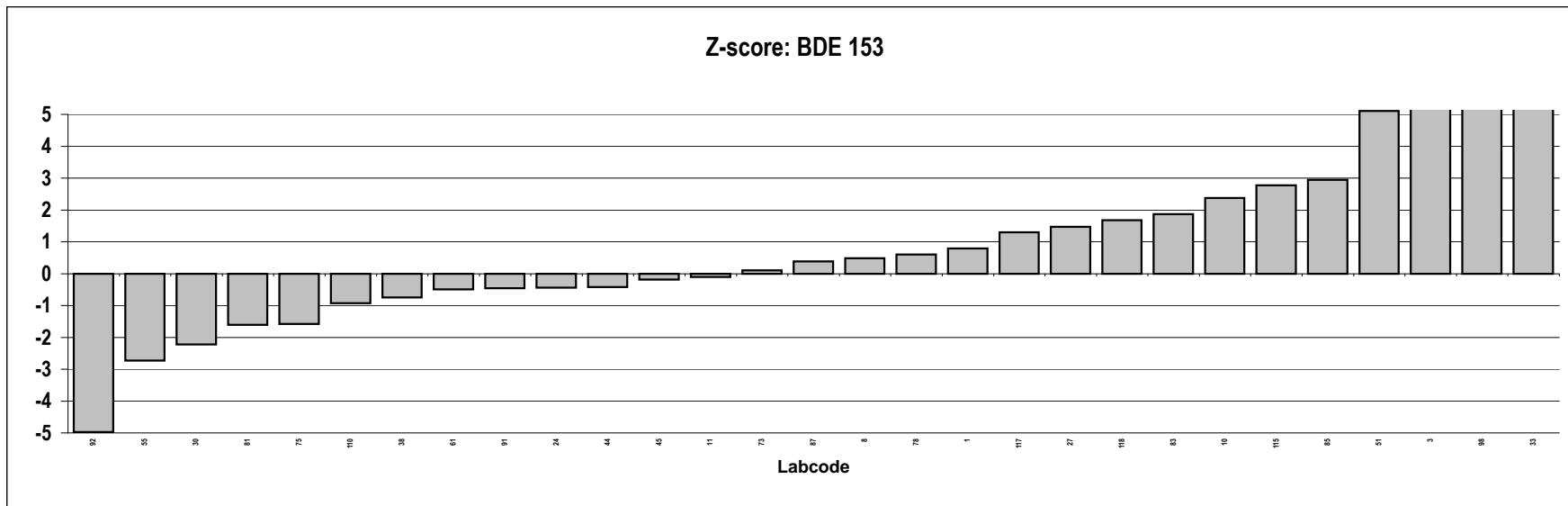
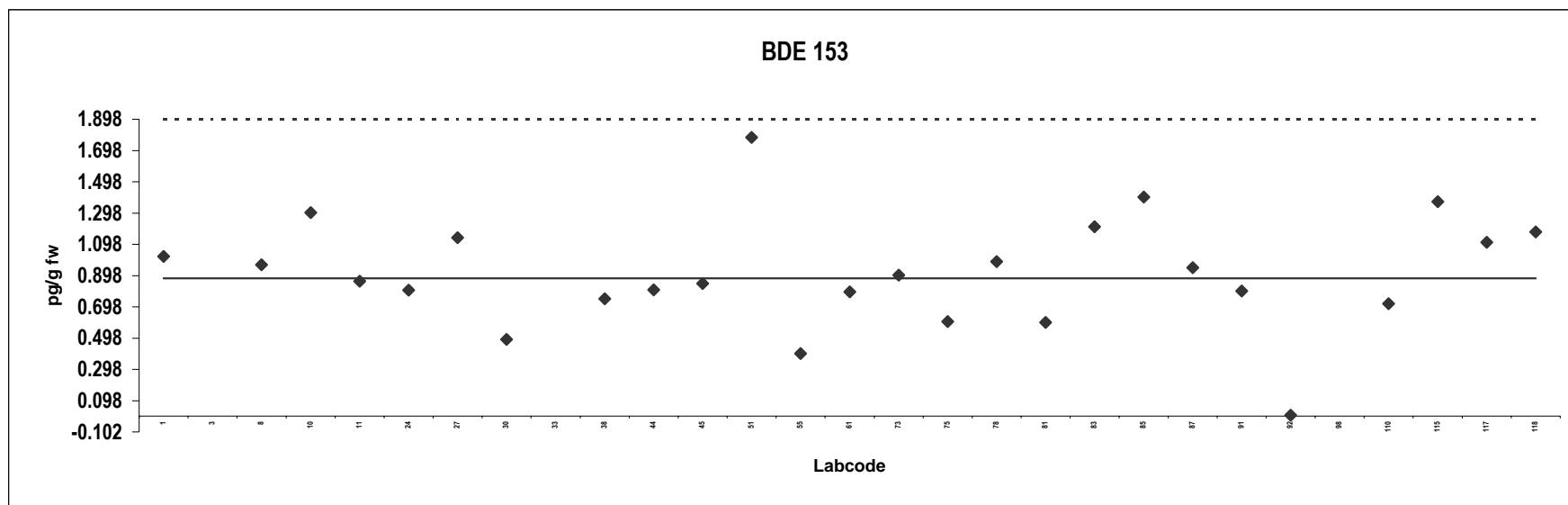


**Milk**  
Congener: BDE 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.0				
3	2.0	Outlier,ND			
8	0.97				
10	1.3				
11	0.86				
24	0.80				
27	1.1				
30	0.49				
33	9.7	Outlier			
38	0.75				
44	0.81				
45	0.85				
51	1.8				
55	0.40				
61	0.79				
73	0.90				
75	0.60				
78	0.99				
81	0.60				
83	1.2				
85	1.4				
87	0.95				
91	0.80				
92	0.0040				
98	3.8	Outlier,ND			
110	0.72				
115	1.4				
117	1.1				
118	1.2				

**Consensus statistics**

Consensus median, pg/g	0.88
Median all values pg/g	0.95
Consensus mean, pg/g	0.92
Standard deviation, pg/g	0.36
Relative standard deviation, %	39
No. of values reported	29
No. of values removed	3
No. of reported non-detects	2

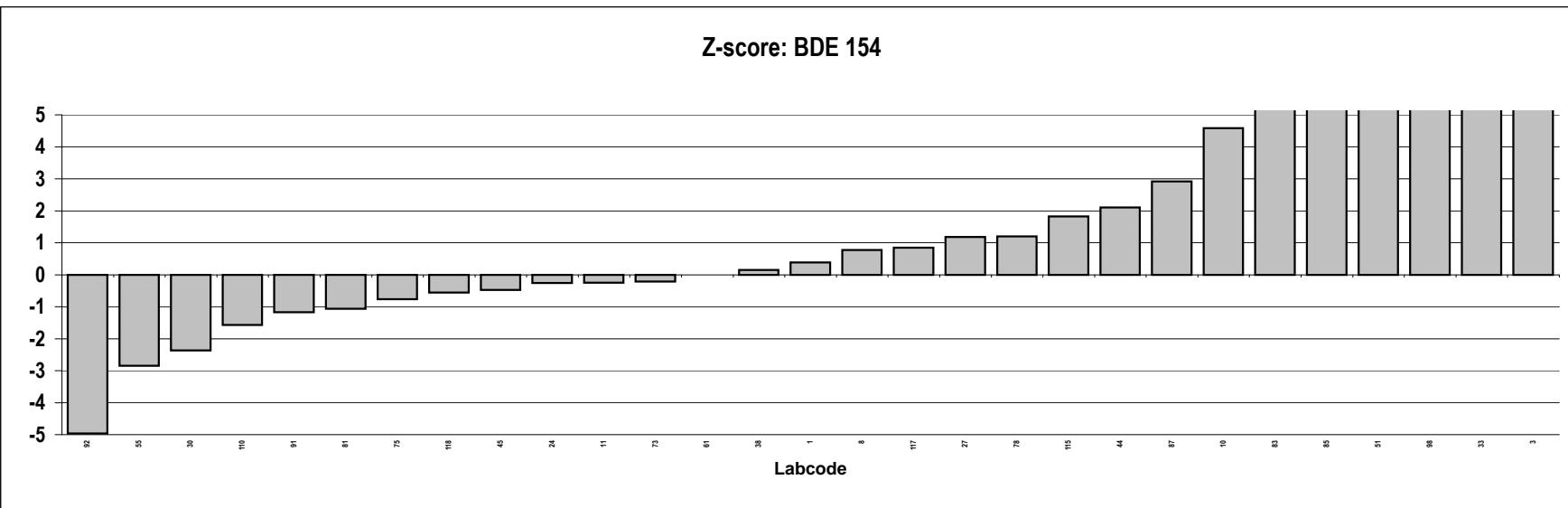
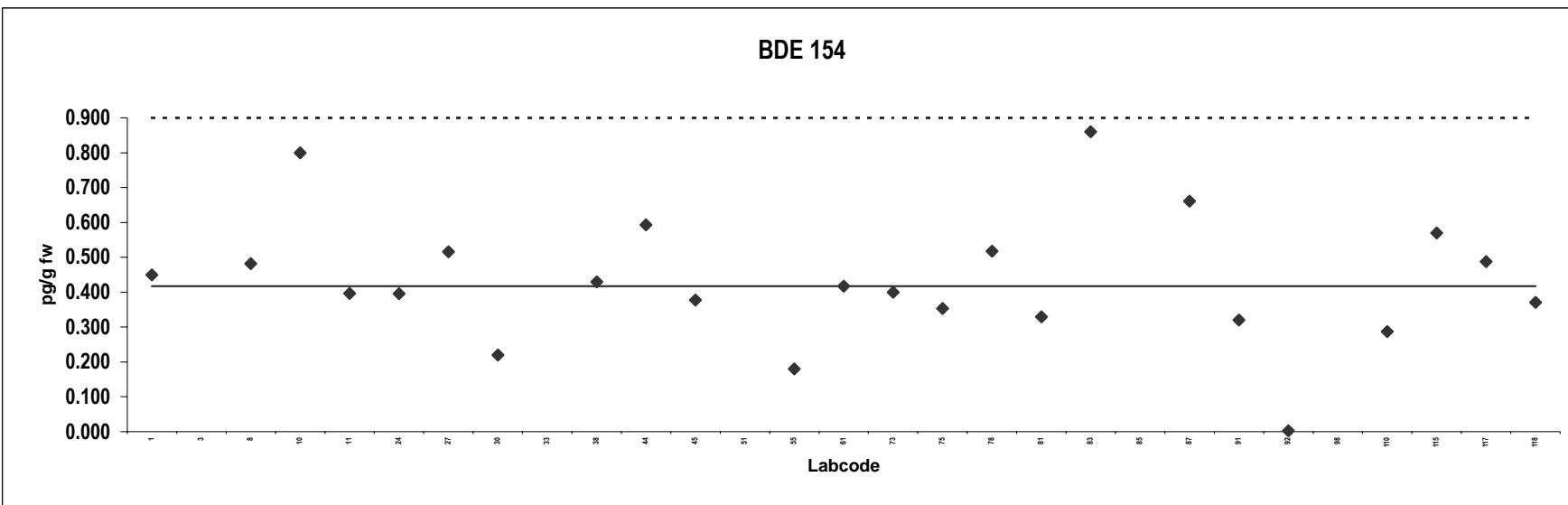


**Milk**  
Congener: BDE 154

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.45				
3	2.0	Outlier,ND			
8	0.48				
10	0.80				
11	0.40				
24	0.40				
27	0.52				
30	0.22				
33	1.7	Outlier			
38	0.43				
44	0.59				
45	0.38				
51	1.2	Outlier			
55	0.18				
61	0.42				
73	0.40				
75	0.35				
78	0.52				
81	0.33				
83	0.86				
85	1.1	Outlier			
87	0.66				
91	0.32				
92	0.0028	ND			
98	1.3	Outlier,ND			
110	0.29				
115	0.57				
117	0.49				
118	0.37				

**Consensus statistics**

Consensus median, pg/g	0.42
Median all values pg/g	0.45
Consensus mean, pg/g	0.43
Standard deviation, pg/g	0.19
Relative standard deviation, %	43
No. of values reported	29
No. of values removed	5
No. of reported non-detects	3

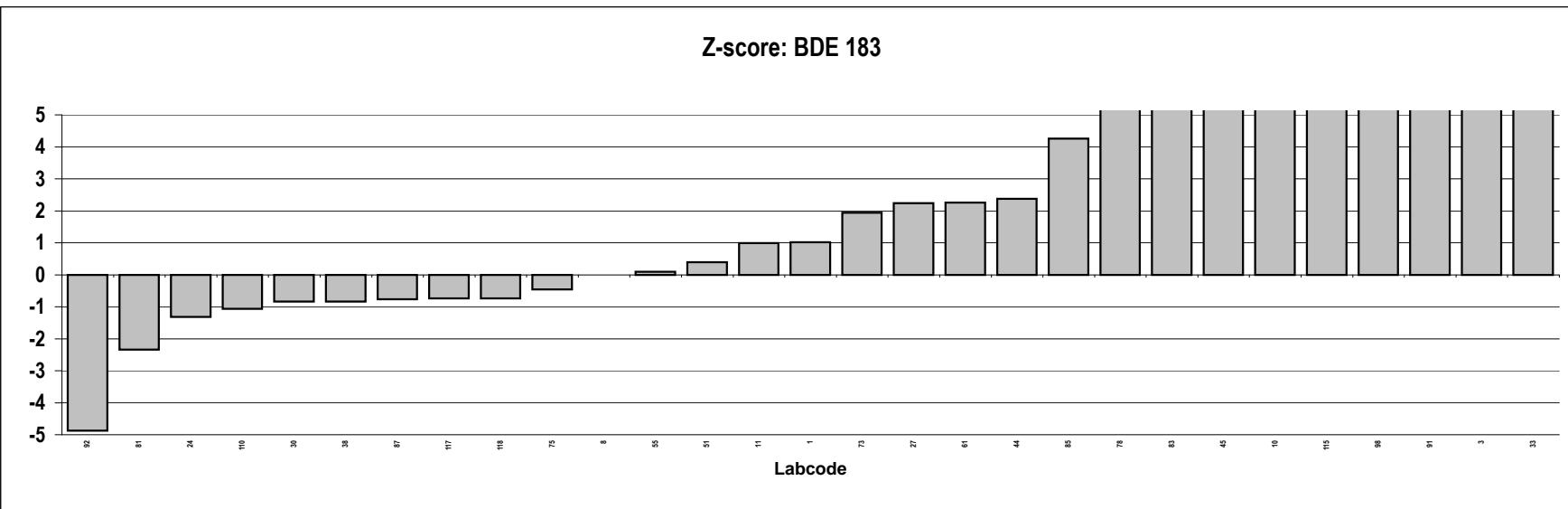
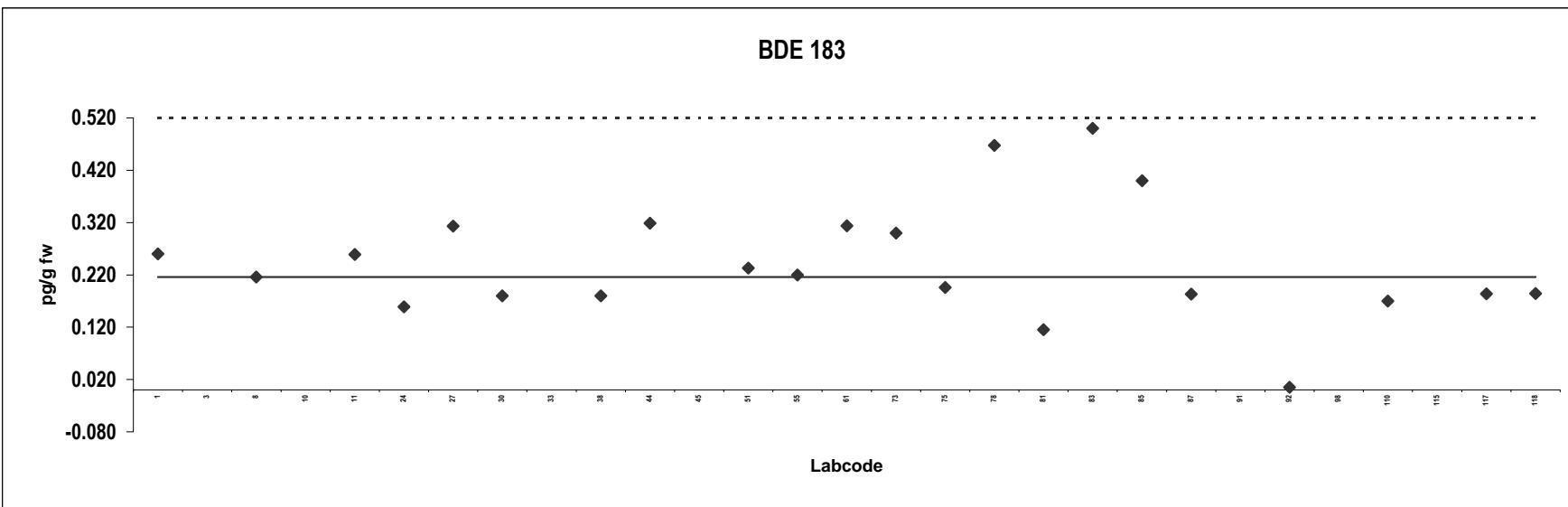


**Milk**  
Congener: BDE 183

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.26				
3	5.0	Outlier,ND			
8	0.22				
10	0.80	Outlier			
11	0.26				
24	0.16				
27	0.31	ND			
30	0.18				
33	37	Outlier			
38	0.18				
44	0.32				
45	0.53				
51	0.23	Outlier			
55	0.22	ND			
61	0.31				
73	0.30				
75	0.20				
78	0.47				
81	0.12				
83	0.50	ND			
85	0.40				
87	0.18				
91	2.0	Outlier,ND			
92	0.0054	ND			
98	1.3	Outlier,ND			
110	0.17	ND			
115	1.0	Outlier,ND			
117	0.18				
118	0.18				

**Consensus statistics**

Consensus median, pg/g	0.22
Median all values pg/g	0.26
Consensus mean, pg/g	0.24
Standard deviation, pg/g	0.11
Relative standard deviation, %	46
No. of values reported	29
No. of values removed	7
No. of reported non-detects	9

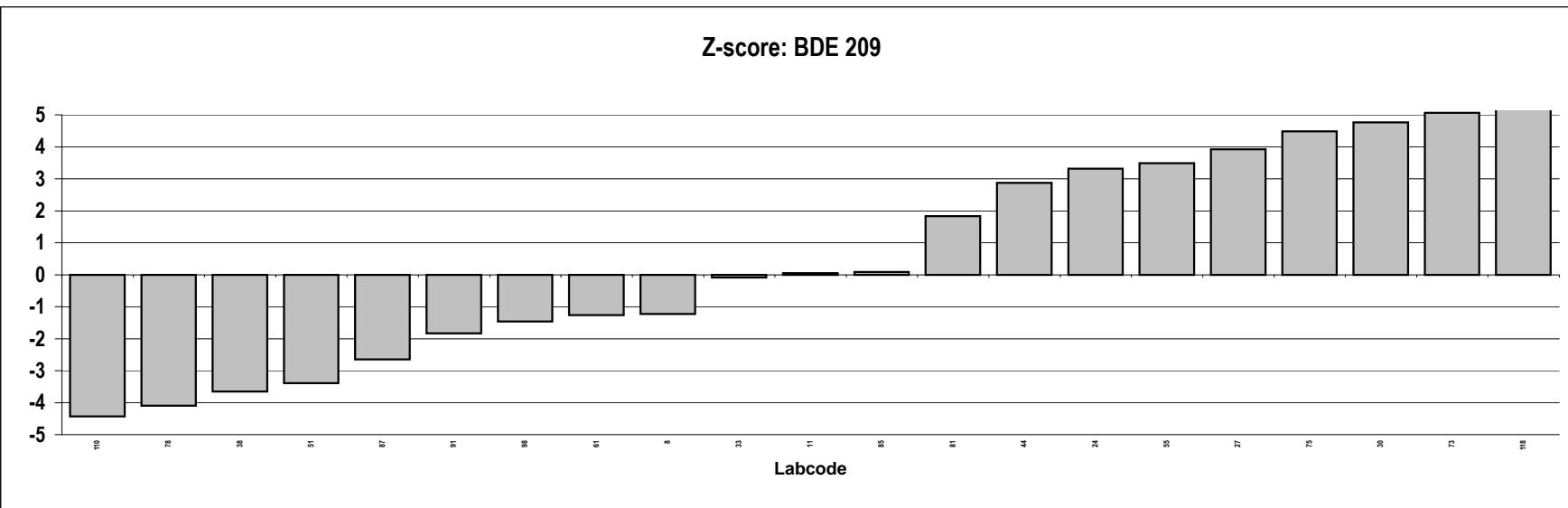
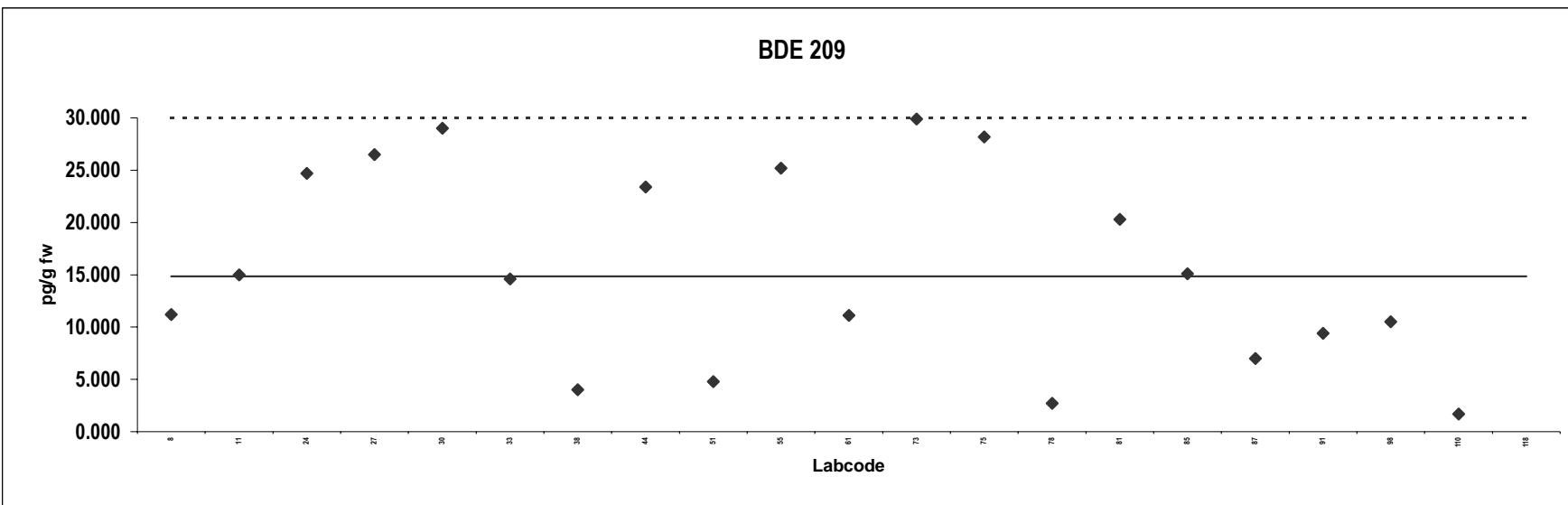


**Milk**  
Congener: BDE 209

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
8	11				
11	15	ND			
24	25				
27	27	ND			
30	29				
33	15				
38	4.0	ND			
44	23				
51	4.8				
55	25				
61	11				
73	30				
75	28				
78	2.7				
81	20	ND			
85	15				
87	7.0				
91	9.4	ND			
98	11				
110	1.7	ND			
118	42	Outlier			

**Consensus statistics**

Consensus median, pg/g	15
Median all values pg/g	15
Consensus mean, pg/g	16
Standard deviation, pg/g	9.5
Relative standard deviation, %	60
No. of values reported	21
No. of values removed	1
No. of reported non-detects	6

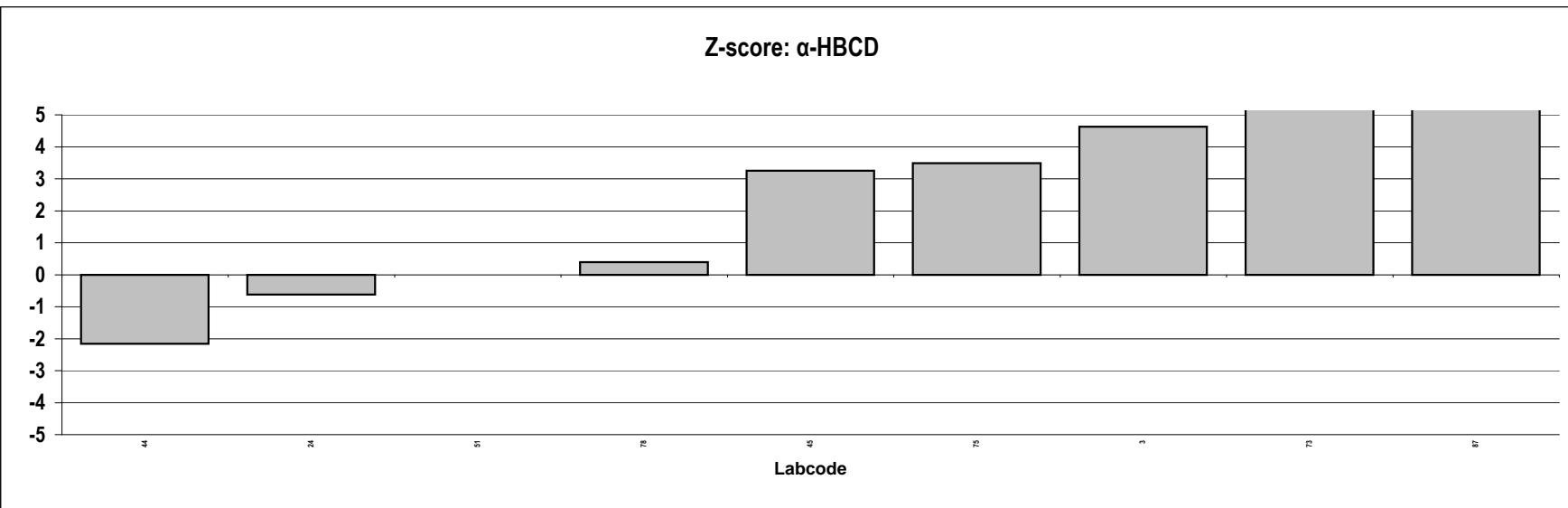
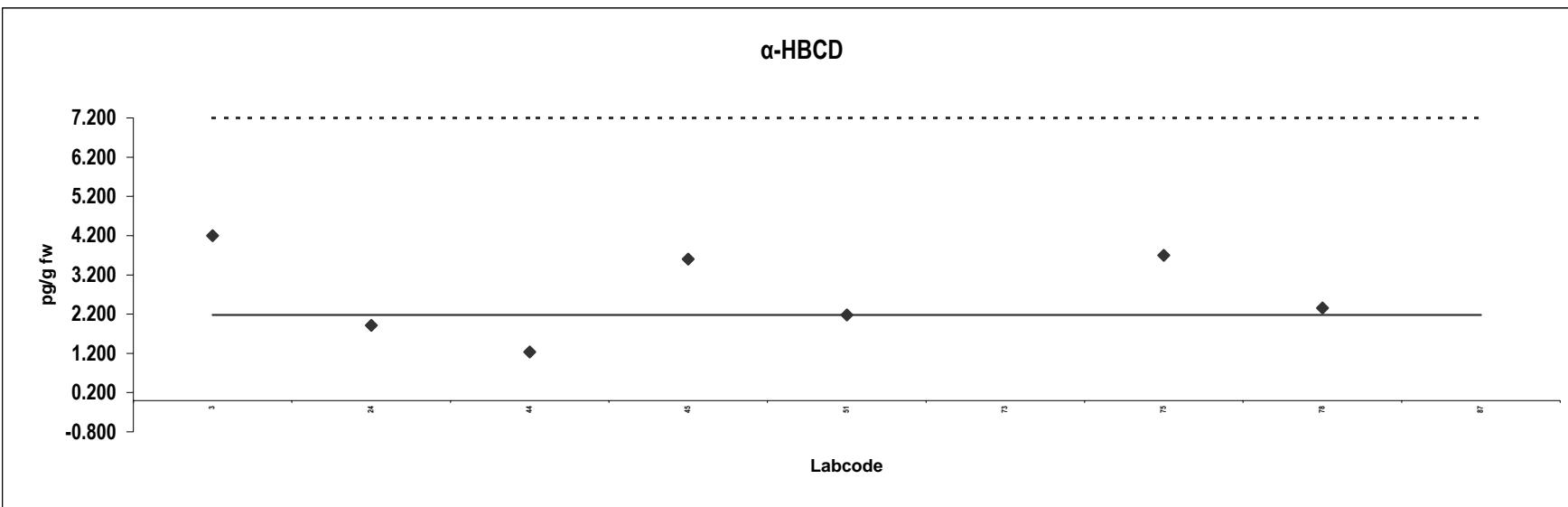


**Milk**  
**Congener:  $\alpha$ -HBCD**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	4.2	ND			
24	1.9				
44	1.2				
45	3.6	ND			
51	2.2				
73	10	Outlier,ND			
75	3.7				
78	2.4				
87	30	Outlier,ND			

**Consensus statistics**

Consensus median, pg/g	2.2
Median all values pg/g	3.6
Consensus mean, pg/g	2.7
Standard deviation, pg/g	1.1
Relative standard deviation, %	40
No. of values reported	9
No. of values removed	2
No. of reported non-detects	4

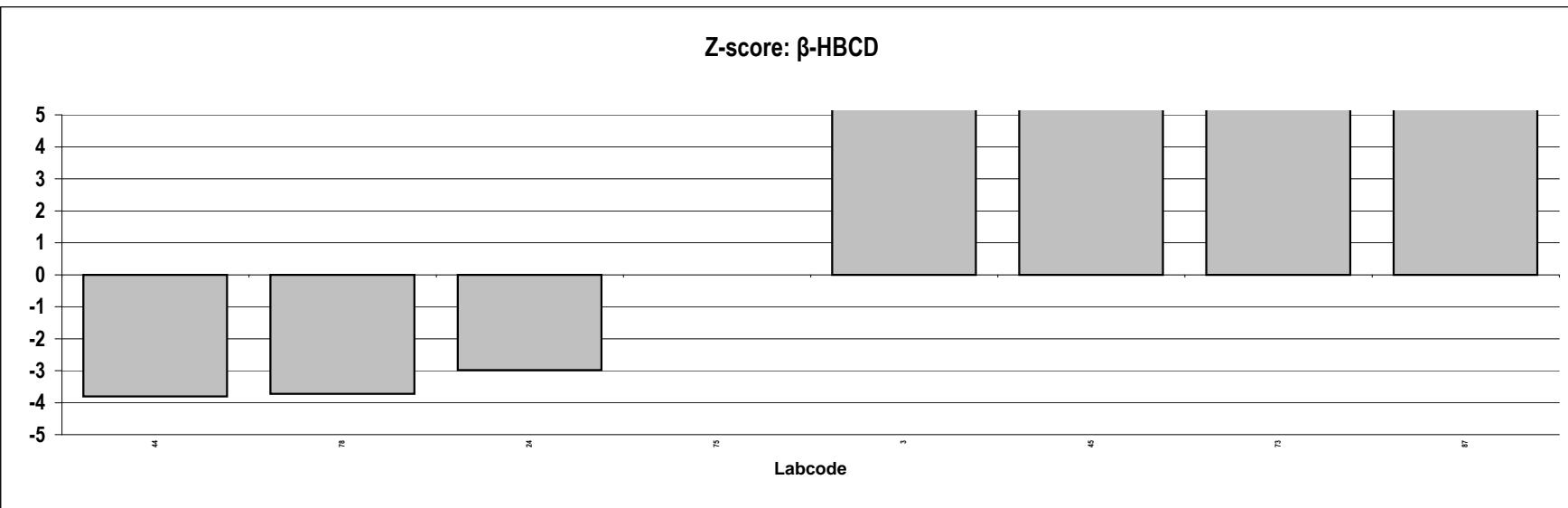
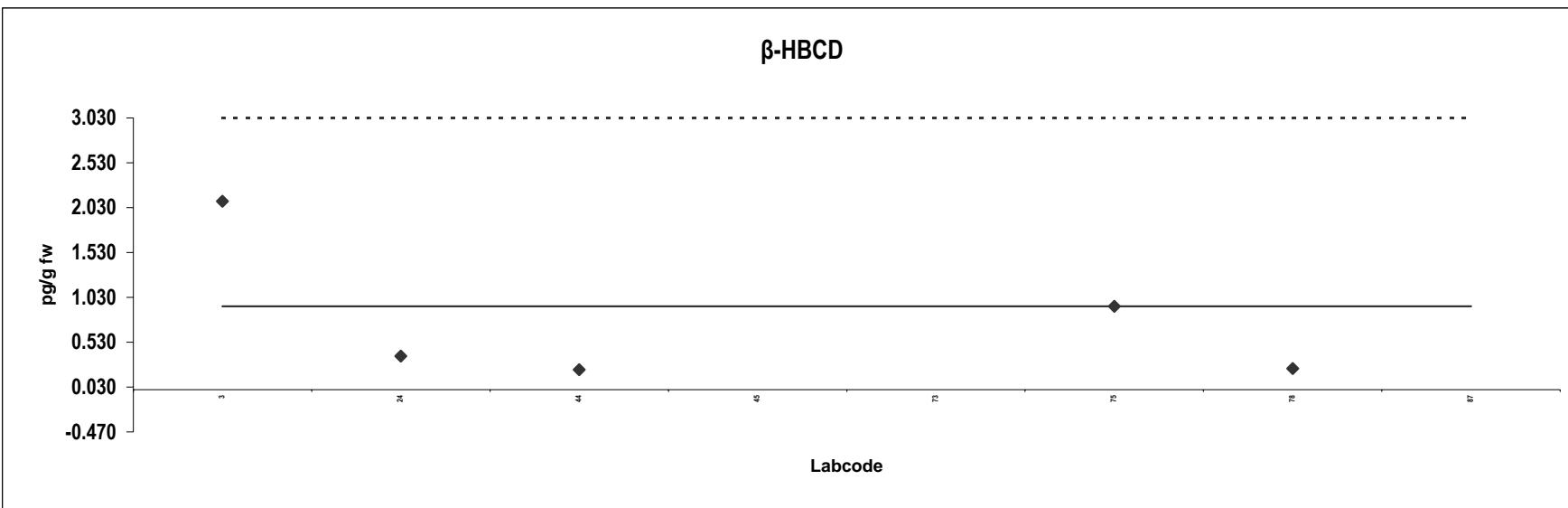


**Milk**  
**Congener:  $\beta$ -HBCD**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	2.1	ND			
24	0.38	ND			
44	0.22	ND			
45	3.6	Outlier,ND			
73	5.0	Outlier,ND			
75	0.93				
78	0.24	ND			
87	15	Outlier,ND			

**Consensus statistics**

Consensus median, pg/g	0.93
Median all values pg/g	1.5
Consensus mean, pg/g	0.77
Standard deviation, pg/g	0.80
Relative standard deviation, %	103
No. of values reported	8
No. of values removed	3
No. of reported non-detects	7

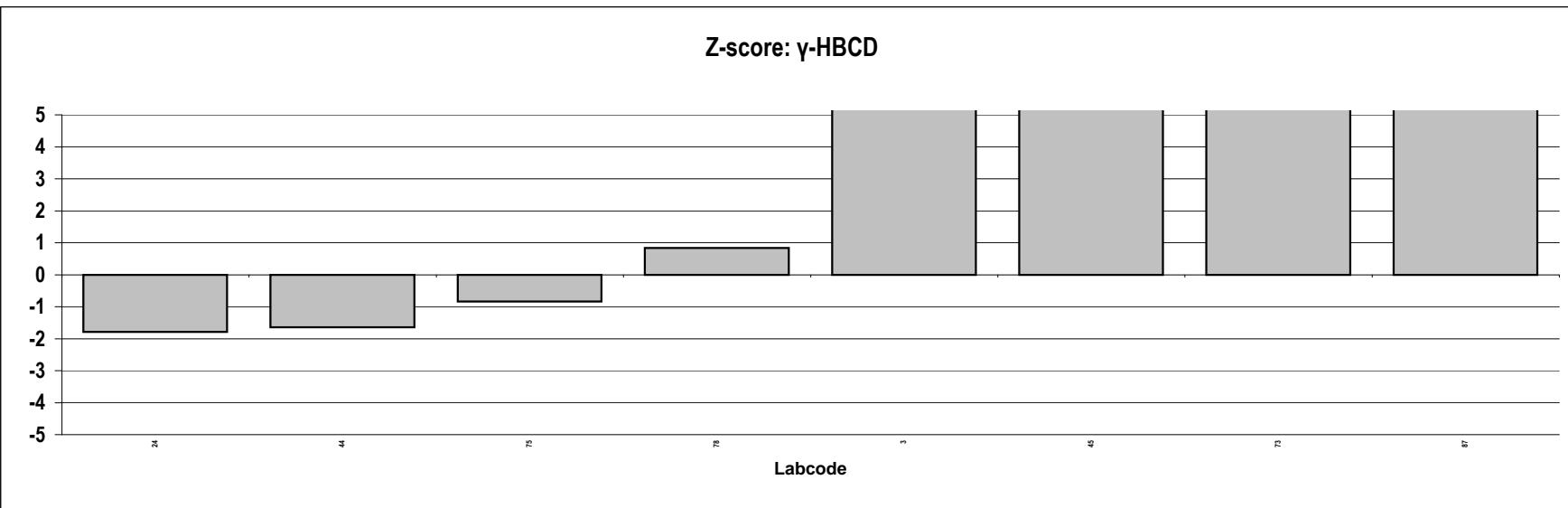
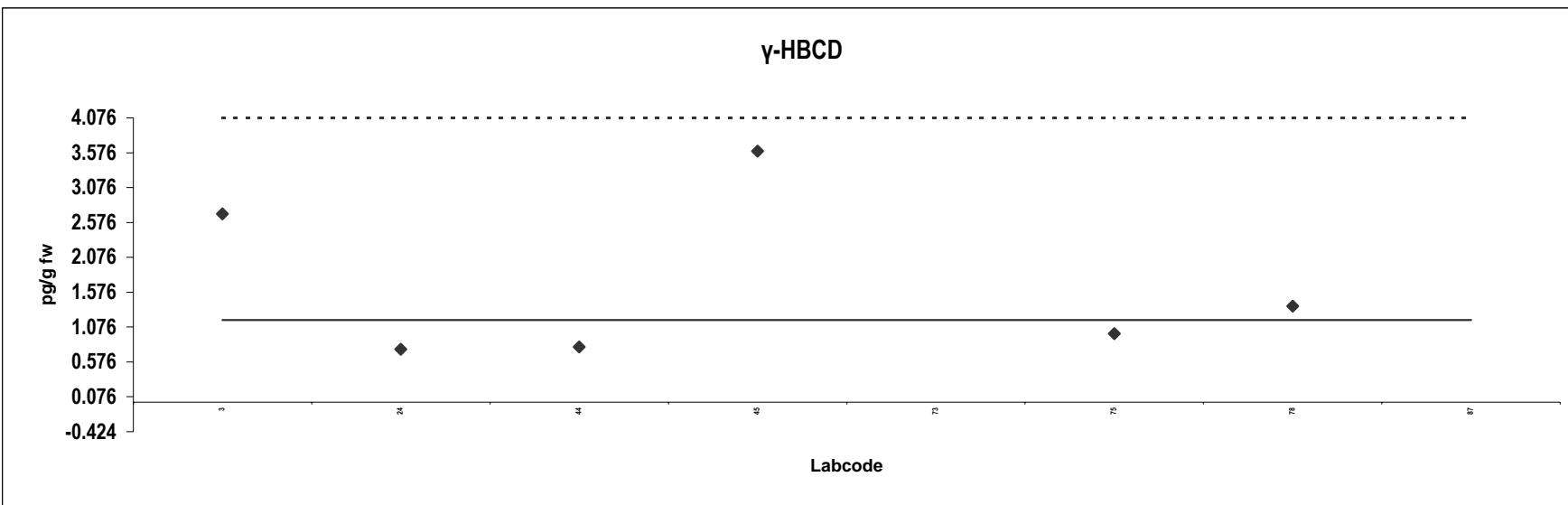


**Milk**  
**Congener:  $\gamma$ -HBCD**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	2.7	ND			
24	0.76	ND			
44	0.79	ND			
45	3.6	ND			
73	10	Outlier,ND			
75	0.98				
78	1.4	Outlier,ND			
87	60				

**Consensus statistics**

Consensus median, pg/g	1.2
Median all values pg/g	2.0
Consensus mean, pg/g	1.7
Standard deviation, pg/g	1.2
Relative standard deviation, %	69
No. of values reported	8
No. of values removed	2
No. of reported non-detects	6

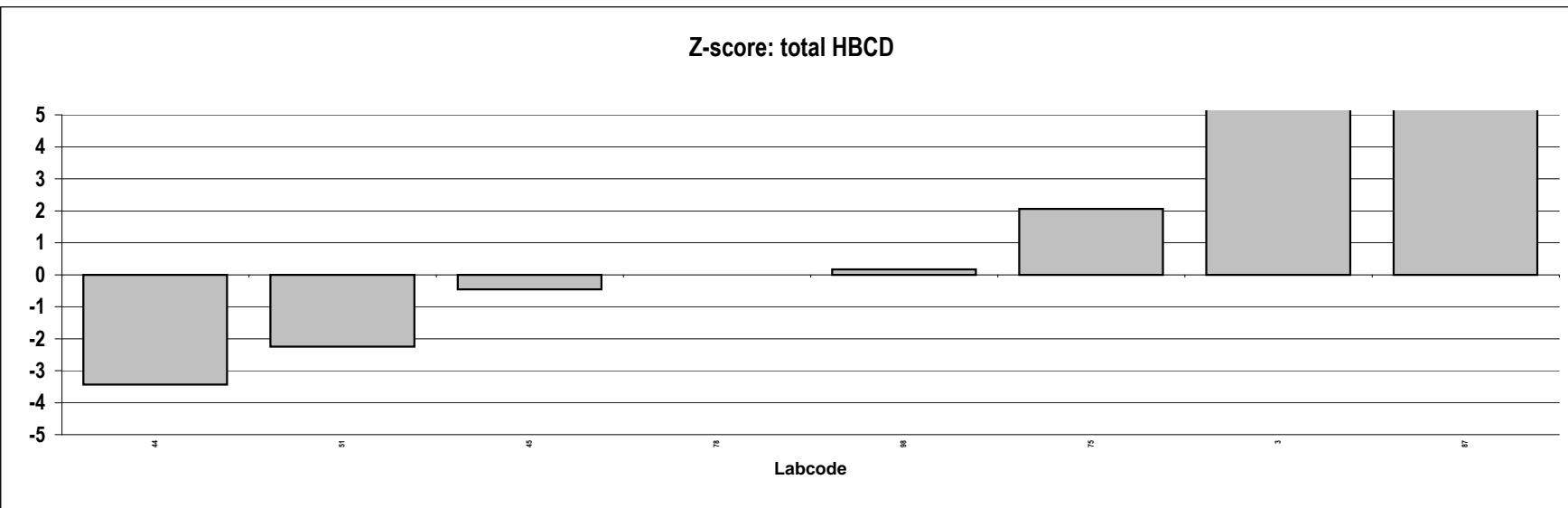
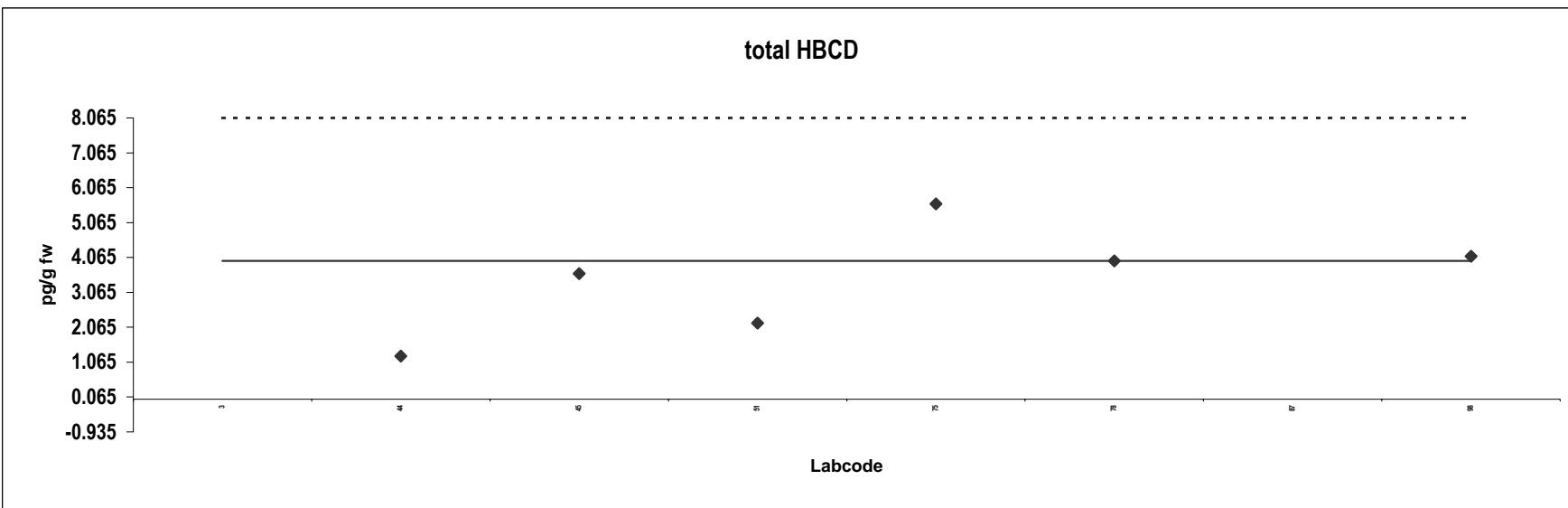


**Milk**  
**Congener: total HBCD**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	9.0	Outlier,ND			
44	1.2				
45	3.6	ND			
51	2.2				
75	5.6				
78	4.0				
87	105	Outlier,ND			
98	4.1				

**Consensus statistics**

Consensus median, pg/g	4.0
Median all values pg/g	4.0
Consensus mean, pg/g	3.4
Standard deviation, pg/g	1.5
Relative standard deviation, %	45
No. of values reported	8
No. of values removed	2
No. of reported non-detects	3





## **Appendix 5:**

Presentation of results  
for lipid determination

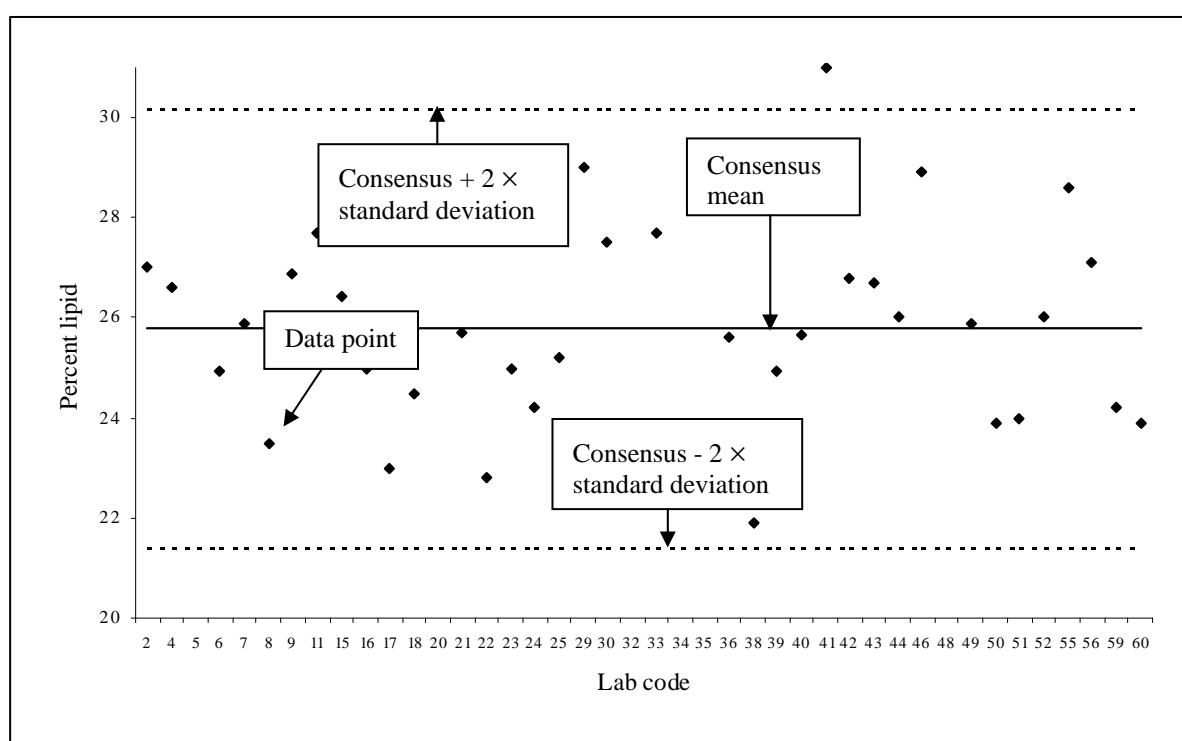


## Presentation of results for lipid determination

Removal of outliers and calculation of consensus were done by the following procedure:

1. The mean was calculated from all the reported data.
2. Values outside a range of  $\pm 2 \times$  the standard deviation of this mean were defined as outliers and removed from the data set.
3. Mean, standard deviation and median were re-calculated from the remaining data. This mean was called consensus.

The diagram shows the reported data with consensus and consensus  $\pm$  the new standard deviation  $\times 2$ .



### Z-Scores of lipid content

Z-scores of lipid content were calculated for each laboratory according to the following equation:

$$z = (x - X)/\sigma$$

where  $x$  = reported value;  $X$  = assigned value (consensus);  $\sigma$  = target value for standard deviation. A  $\sigma$  of 20% of the consensus was used, i.e. z-scores between +1 and -1 reflect a deviation of  $\pm 20\%$  from the consensus value.



## Lipid determination for Pork

Lab code	% lipid	Notes	Lab code	% lipid	Notes	Lab code	% lipid	Notes
1	28		83	29				
2	28		84	27				
3	29		85	29				
5	29		87	28				
6	24		88	28				
8	28		91	27				
10	26		92	29				
11	27		93	29				
13	28		94	29				
14	28		95	28				
19	27		106	32				
20	22		107	28				
21	28		108	31				
24	28		110	29				
27	29		112	31				
28	26		113	32				
29	30		115	23				
30	27		116	28				
33	28		117	28				
35	28		118	27				
36	4.5							
37	27							
42	29							
44	27							
45	27							
46	27							
49	29							
51	27							
54	27							
55	27							
57	30							
58	28							
60	25							
61	27							
64	30							
65	29							
67	26							
68	29							
69	30							
73	29							
74	28							
75	27							
78	15							
79	24							
80	26							
81	28							

Mean	Standard deviation	Relative standard deviation	Median
28	1.8	6.6	28

### Lipid determination for Herring

Lab code	% lipid	Notes	Lab code	% lipid	Notes	Lab code	% lipid	Notes
1	7.9		74	7.3				
2	6.8		75	6.9				
3	8.6		76	6.2				
5	7.5		77	7.6				
8	7.1		78	7.1				
10	7.1		79	6.1				
11	6.7		80	6.6				
13	6.8		81	6.0				
14	6.8		83	7.2				
15	6.4		85	7.5				
16	29		86	3.6				
19	4.7		87	6.8				
20	6.5		88	6.0				
21	7.1		91	7.4				
24	6.6		92	7.3				
27	7.4		93	7.4				
28	6.0		94	6.2				
30	6.9		95	7.0				
32	7.2		103	6.9				
33	6.4		106	7.7				
34	5.7		107	5.7				
35	7.2		108	8.1				
38	5.3		110	8.2				
41	7.2		112	7.4				
42	4.8		113	5.8				
43	6.0		115	4.3				
44	6.6		117	6.6				
45	5.9		118	7.1				
46	4.8							
47	6.6							
49	7.0							
51	6.7							
54	7.0							
57	6.3							
58	7.1							
59	7.4							
60	5.3							
61	7.1							
62	6.0							
63	6.2							
64	7.2							
65	6.6							
67	5.5							
68	6.8							
69	6.7							
73	7.1							

Mean	Standard deviation	Relative standard deviation	Median
6.6	0.89	13	6.8

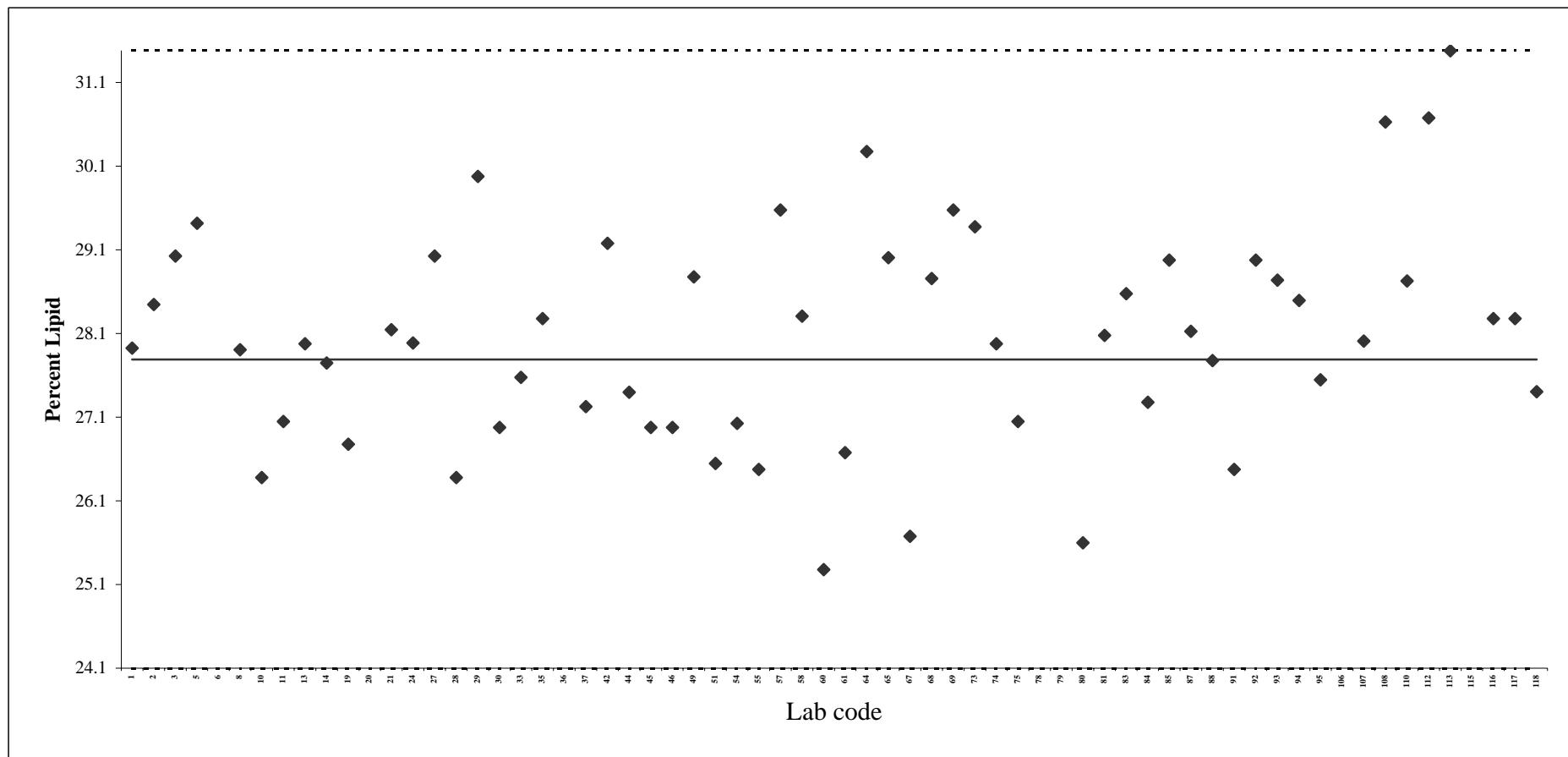
### Lipid determination for Milk

Lab code	% lipid	Notes	Lab code	% lipid	Notes	Lab code	% lipid	Notes
1	3.8		84	4.6				
3	3.6		85	4.4				
5	2.4		87	4.0				
8	3.9		88	3.9				
10	3.6		91	3.9				
11	3.9		92	4.0				
13	3.7		94	2.6				
14	4.1		95	3.5				
19	4.2		98	3.4				
20	3.5		102	3.8				
21	3.3		106	2.4				
24	3.6		107	1.5				
27	3.6		108	4.6				
30	3.9		110	4.4				
33	3.7		112	4.5				
35	3.5		115	3.3				
36	3.0		117	2.9				
37	3.7		118	3.8				
38	3.6							
40	2.2							
44	2.4							
45	3.7							
46	4.2							
47	3.3							
49	4.4							
51	4.0							
54	4.2							
55	2.6							
57	4.2							
58	13							
59	4.9							
60	3.5							
61	3.2							
62	3.7							
64	3.3							
65	3.5							
67	2.5							
71	3.9							
73	4.0							
74	4.0							
75	3.2							
77	3.6							
78	4.6							
80	3.6							
81	3.3							
83	2.2							

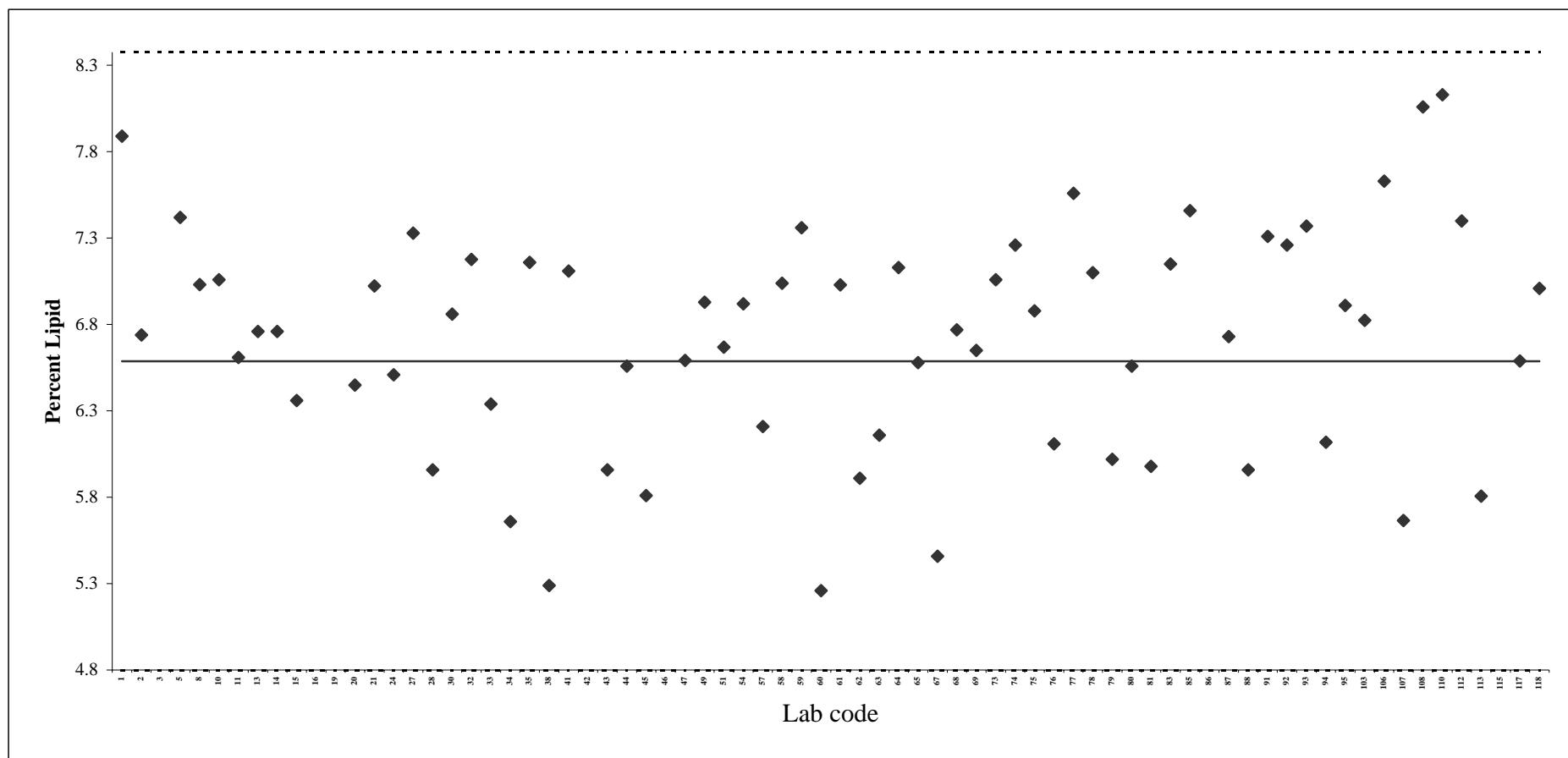
outlier

Mean	Standard deviation	Relative standard deviation	Median
3.6	0.68	19	3.7

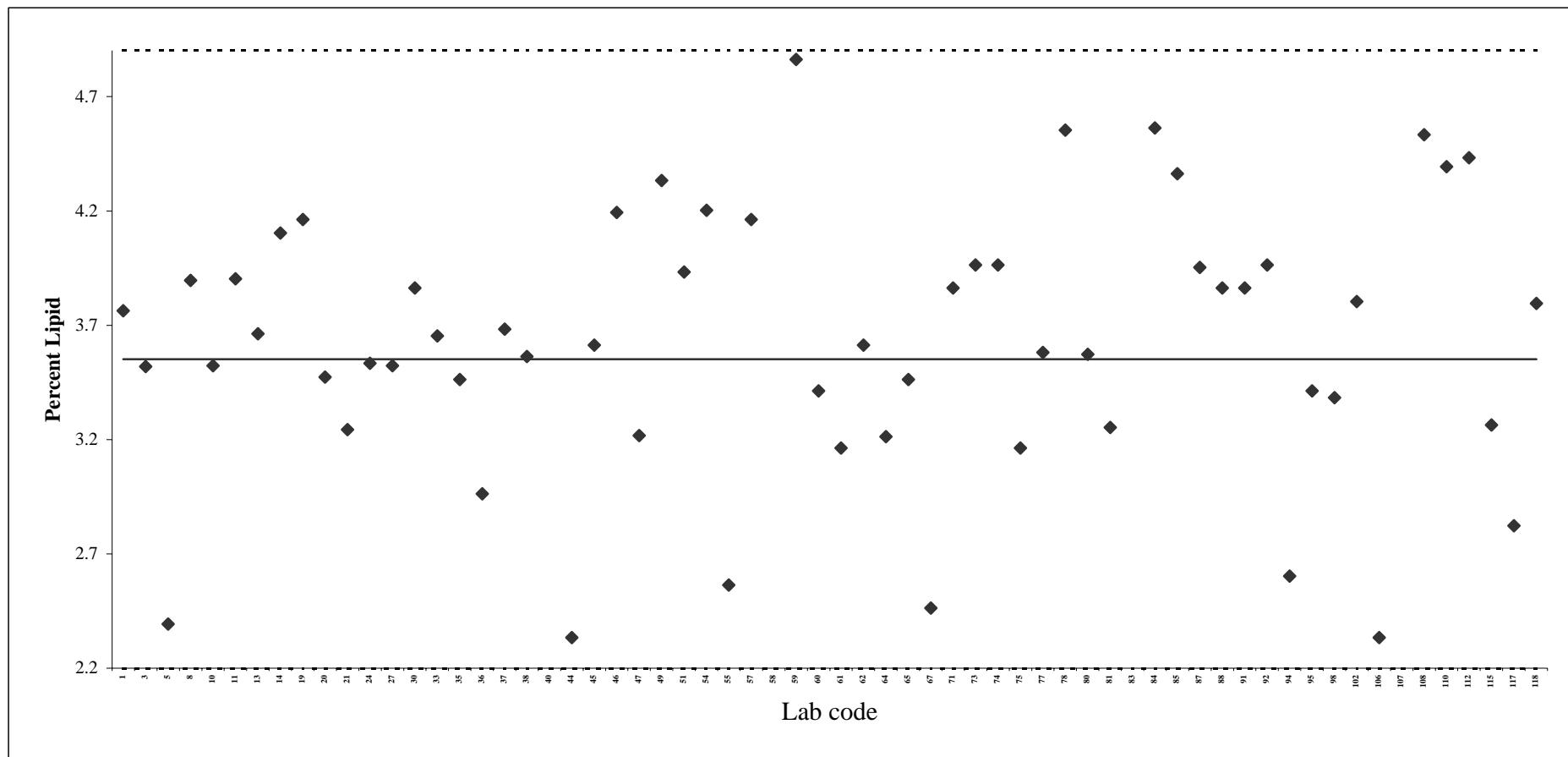
## Lipid determination; Pork



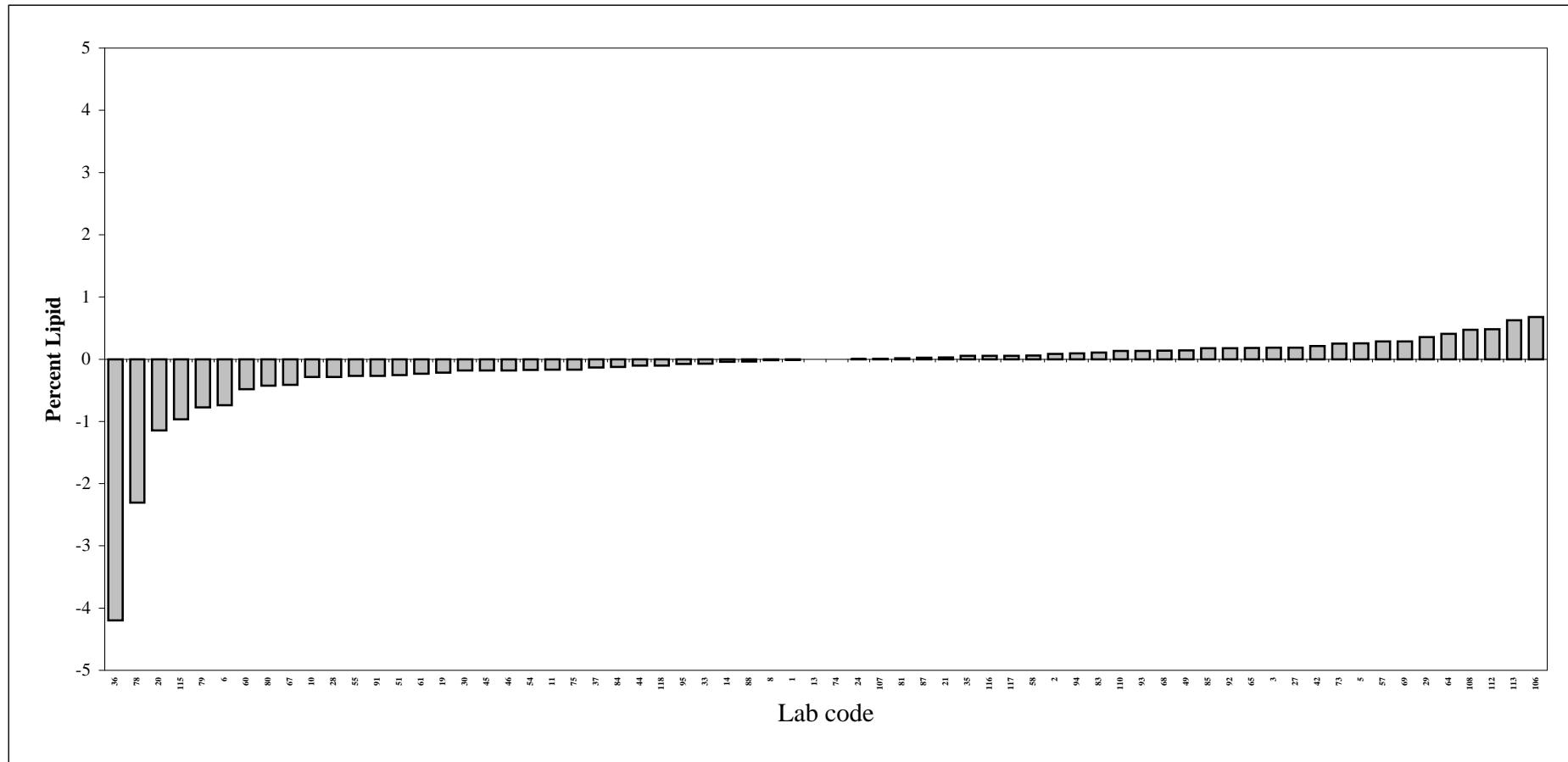
## Lipid determination; Herring



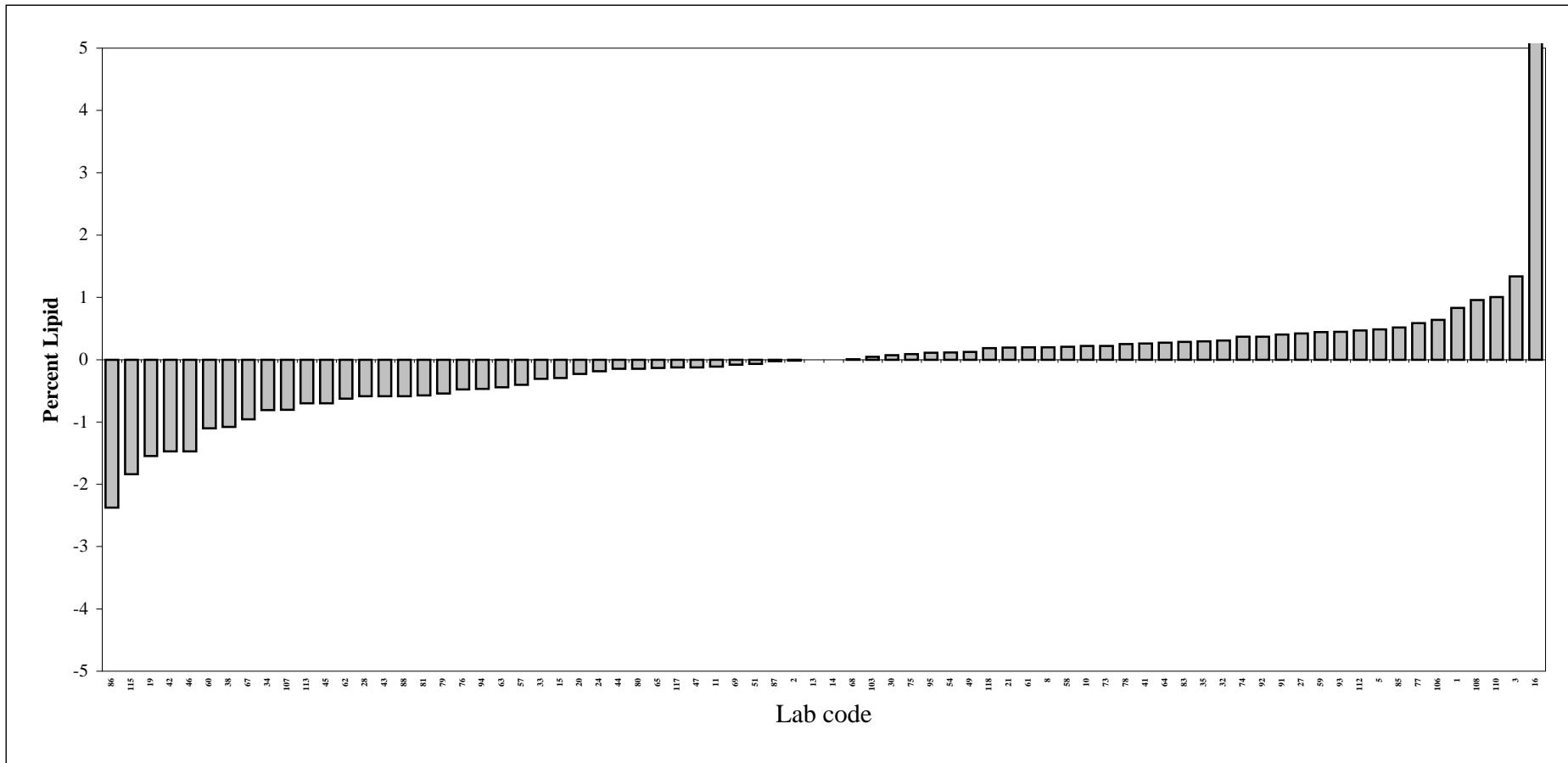
## Lipid determination; Milk



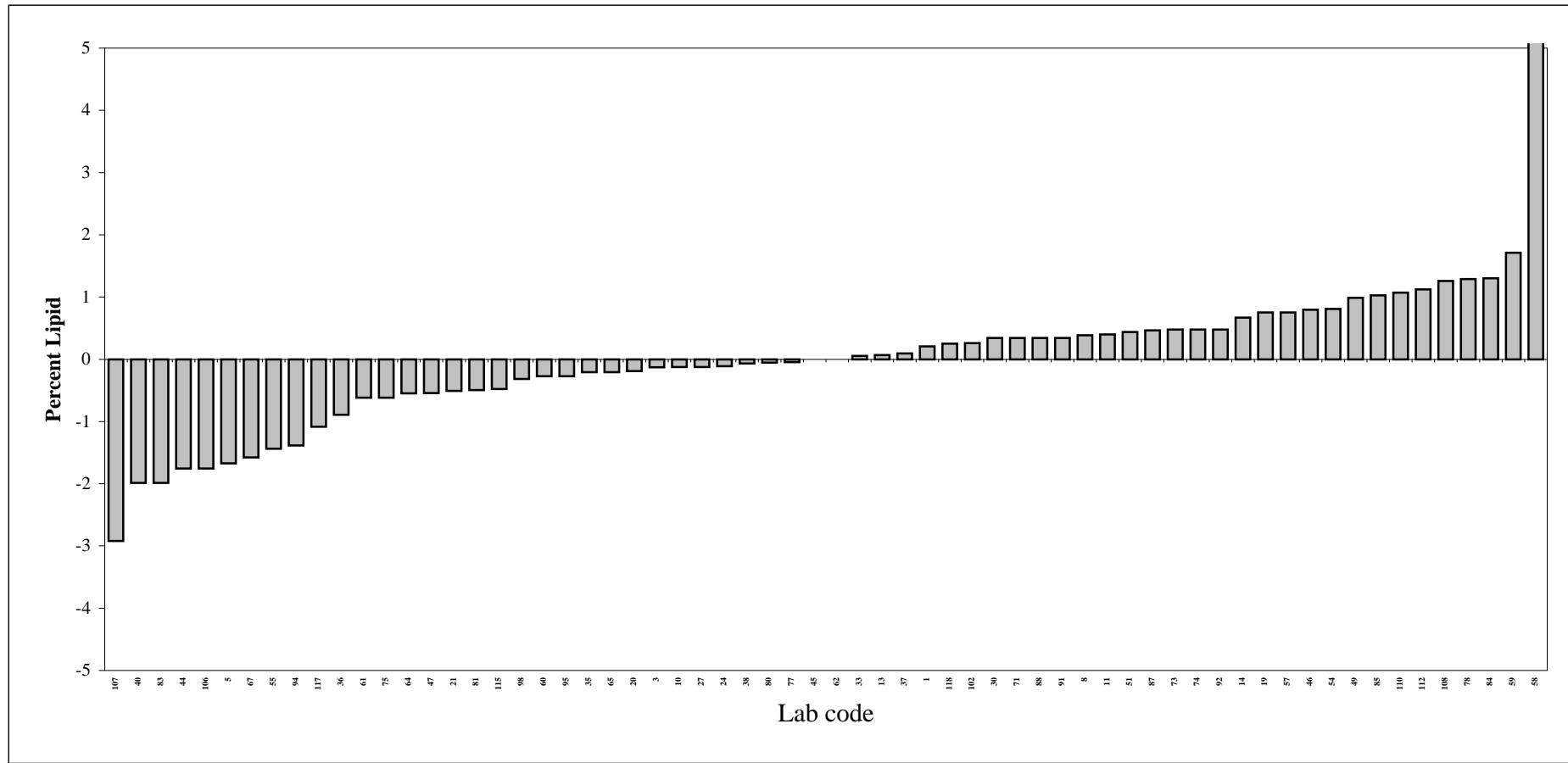
## Z-score lipid determination; Pork



## Z-score lipid determination; Herring



## Z-score lipid determination; Milk





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