

Interlaboratory Comparison on POPs in Food 2010



Eleventh Round of an International Study

Veronica Horpestad Liane

Georg Becher

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Summary

In 2010, the eleventh round of the Interlaboratory Comparison on POPs in Food was conducted on 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. In addition laboratories could voluntarily determine and report six Indicator PCBs, polybrominated diphenyl ethers (PBDEs) and hexabromocyclododecane (HBCD). The objectives of this interlaboratory comparison study were a) to offer a quality assurance instrument for the participating laboratories, b) to assess the between laboratory reproducibility and c) to assess the readiness of expert laboratories world-wide to determine levels of chlorinated and brominated persistent organic pollutants in regular foodstuffs.

The 2010 study was performed on sample homogenates of breast milk, pork meat and trout filet. In addition, six standard solutions were provided containing known concentrations of 1) PCDDs/PCDFs, 2) non-ortho PCBs, 3) mono-ortho PCBs, 4) PBDEs, 5) Indicator PCBs and 6) α -HBCD. The testing materials were sent to 94 laboratories in January 2010, and results were returned from 89 laboratories in 31 different countries by the deadline in April. Most laboratories analyzed all the three food items. A draft report was made available on the Internet in August and was discussed among the participants at the Waters New Technology Forum during the DIOXIN 2010 Symposium in San Antonio, Texas, USA.

This report presents the reported results for: all seventeen 2,3,7,8-substituted PCDDs/PCDFs, the 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. In addition, the results for eight PBDEs #28, 47, 99, 100, 153, 154, 183 and 209, six Indicator PCBs #28, 52, 101, 138, 153 and 180, and total HBCD as well as the α -, β - and γ -isomers were reported from those laboratories that voluntarily determined their concentrations. Non-detected congeners were assigned a concentration corresponding to the reported detection limit except for PBDEs, Indicator PCBs and HBCD where non-detects were removed from the data set. The consensus concentration (assigned value) for each analyte in the three food samples was determined as follows: The median of all reported concentrations for each analyte was calculated. All values above two times the median were removed from the calculation. The consensus median and consensus mean plus 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 PCDD/PCDF TEQs were calculated for each laboratory using $\pm 20\%$ of the consensus TEQs (WHO1998TEQs) as a value for target standard deviation (σ). 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 for the standard solutions were calculated as mentioned above except that values outside $\pm 50\%$ of the median of all values were removed prior to the final calculation of the consensus median and mean. The consensus values for the lipid content 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, Z-scores within ± 1 were obtained by 21-76% of the laboratories. The majority of the laboratories (42-86%) reported results for total TEQ with a trueness of $\pm 40\%$ for all food samples (Z-score ± 2). The relative standard deviation (RSD) calculated for the total TEQ after removal of outliers was 10-22%. It is therefore concluded that the performance of laboratories world-wide in determining dioxin-like compounds is generally good for the food samples included in this study. The low levels in the pork sample made the analysis of this sample challenging. Here only 21% and 42% of the laboratories performed within a z-score of 1 and 2 respectively.

For the different food samples, between 52-62 laboratories reported results for the six Indicator PCBs, 32-38 laboratories reported concentrations for the seven tetra- to hepta-BDEs and 22-25 laboratories reported concentrations for BDE-209. The concentrations of the sum of seven PBDEs ranged from 59 pg/g fresh weight in breast milk to 91.8 ng/g fresh weight in trout. The RSD for PBDE concentrations on fresh weight basis was on average 30, 26 and 30% for breast milk, pork and trout, respectively. The consensus concentrations for BDE-209 were 5.4, 23 and 13 pg/g fresh weight in breast milk, pork and trout, respectively. The corresponding RSD on fresh weight basis was 53, 55 and 67%. The consensus concentrations calculated for HBCD are just indicative values as only few laboratories reported results. The sum of concentrations for six Indicator PCBs ranged from 0.12 ng/g fresh weight in pork to 26 ng/g fresh weight in trout. The average RSDs were 34, 35 and 31% for breast milk, pork and trout, respectively.

Introduction

In order to ensure consumer protection and reduce human exposure to dioxins and dioxin-like PCBs through food consumption, many countries request frequent monitoring of the presence of these toxic pollutants in food and feed. Thus, there is a large demand for chemical laboratories that are able to determine these contaminants at low levels in food and feed. 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 study is the eleventh round of a world-wide interlaboratory comparison study on dioxin-like compounds in food organized by the Department of Analytical Chemistry, Division of Environmental Medicine, Norwegian Institute of Public Health, Oslo, Norway.

The exercise took place from January 2010, when the samples were shipped to the laboratories for analysis, to the reporting deadline in April 2010, when the last reports on the results were received. A draft report was

made available to the participants on the new webpage (<http://www.fhi.no/ILC>) in August and was discussed during the Waters New Technology Forum at the DIOXIN 2010 Symposium in San Antonio, Texas, USA.

The main objective of this exercise was 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 asked 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.

All of the participants from previous rounds of this series of "Interlaboratory Comparisons on POPs in Food" were invited to participate. In addition, several other laboratories announced their participation. There was no limit to the total number of participating laboratories. The 89 laboratories that submitted results, and thereby contributed to the study results, are presented in Table 1.

Table 1. Participants that reported results in the eleventh round of Interlaboratory Comparison on POP's in food 2010

AFSSA-LERQAP Maisons Alfort Cedex, France	Danish Veterinary and Food Administration Ringsted, Denmark
Agenzia Regionale Protezione Ambiente Del Piemonte - Polo Microinquinanti Grugliasco, Italy	National Cheng Kung University, College of Medicine Tainan, Taiwan
AGRIPARADIGMA Ravenna, Italia	National Measurement Institute – Pymble Sydney, Australia
ALS Pardubice, Czech Republic	Zhejiang Provincial Center for Disease Control and Prevention Hangzhou, P.R. China
ALS Laboratory Group Edmonton, Canada	Chinese Academy of Inspection and Quarantine Beijing, P.R. China
Analytical Perspectives Wilmington, United States	Eco-research Bolzano, Italy
ASAE Lisboa, Portugal	Institut Quimic de Sarria Barcelona, Spain
AsureQuality Limited Wellington, New Zealand	Eurofins GfA GmbH Hamburg, Germany
Canadian Food Inspection Agency Calgary, Canada	FAVV Tervuren, Belgium
CARSO-LSEHL Lyon, France	FDA Jefferson, USA
CART Liege, Belgium	Federal Environment Agency (UBA) Berlin, Germany
Central Laboratory of Residue Analysis of Pesticides and Heavy Metals in Food Giza, Egypt	Food GmbH Analytik & Consulting Jena, Germany
Chelab Unità Locale di Lusciano Lusciano, Italy	Health Canada Ottawa, Canada
Chemical and Veterinary Analytical Institute Münsterland-Emscher-Lippe (CVUA-MEL) Münster, Germany	Government Laboratory Hong Kong SAR, China
Chemisches und mikrobiologisches Institut UEG GmbH Wetzlar, Germany	Hong Kong Government Laboratory Hong Kong SAR, China
Chemisches und Veterinäruntersuchungsamt (CVUA) Freiburg, Germany	Hubei Provincial Centre for Disease Control and Prevention Wuhan, P.R. China
Consorzio Interuniversitario Nazionale la Chimica per l'Ambiente, Consorzio I.N.C.A. Marghera, Italy	Institute of Aquaculture Stirling, Scotland, UK

Istituto Zooprofilattico Sperimentale Dell'Abruzzo E Del Molise "G. Caporale" Teramo, Italy	National Food And Veterinary Risk Assessment Institute Vilnius, Lithuania
Istituto Zooprofilattico Sperimentale delle Regioni Lazio e Toscana Roma, Italy	National Institute for Health and Welfare Kuopio, Finland
Chinese Center for Disease Control and Prevention Beijing, P.R. China	National Institute of Nutrition and Safety Beijing, P.R. China
LABERCA Nantes, France	National Tsing Hua University Taiwan
LABORATOIRE DE ROUEN Rouen, France	NCSR "Demokritos" Athens, Greece
Institute of Environmental Assessment and Water Research (IDÆA-CSIC) Barcelona, Spain	Niedersächsisches Landesamt für Verbraucherschutz und Lebensmittelsicherheit Oldenburg, Germany
Laboratorio C.S.M.O. , Magistrato Alle Acque Padova, Italy	NIFES Bergen, Norway
Laboratory of SGS Bulgaria Ltd. Varna, Bulgaria	NILU Kjeller, Norway
LEAV La Roche sur Yon, France	Nofer Institute of Occupational Medicine Lodz, Poland
Landeslabor Berlin-Brandenburg Frankfurt, Germany	Norwegian Institute of Public Health Oslo, Norway
Landesuntersuchungsamt, Institut für Lebensmittelchemie Speyer, Germany	Oekometric Bayreuth, Germany
Landwirtschaftliche Untersuchungs- und Forschungsanstalt Speyer Speyer, Germany	Pace Analytical Services, Inc. Minneapolis, USA
LUFA Rostock der LMS Rostock, Germany	Pacific Rim Laboratories Inc. Surrey, Canada
mas münster analytical solutions gmbh Münster, Germany	Shenzhen Center for Disease Control & Prevention Shenzhen, Guangdong, China
Maxxam Analytics Mississauga, Canada	Qlip N.V. Leusden, The Netherlands
MicroPolluants Technologie Thionville, France	R&C LAB SRL Altavilla Vicentina, Italy
National Food Institute Søborg, Denmark	Italian Nationale Institute for Health (Istituto Superiore di Sanità) Rome, Italy

RIKILT Wageningen, The Netherlands	TÜV SÜD Industrie Service GmbH Donzdorf, Germany
Scientific Analysis Laboratories Manchester, UK	U. S. Environmental Protection Agency Stennis Space Center, USA
Scientific Institute of Public Health Brussels, Belgium	Research and Productivity Council (RPC) Fredericton, New Brunswick, Canada
Servizos De Apoyo Á Investigación A Coruña, Spain	Umeå University Umeå, Sweden
SGS Belgium NV Antwerpen, Belgium	Umweltbundesamt GmbH Vienna, Austria
SGS Institut Fresenius GmbH Bayreuth, Germany	USDA, ARS, Biosciences Research Laboratory Fargo, ND, USA
Shanghai Municipal Center for Disease Control and Prevention Shanghai, China	Wellington Laboratories Inc Guelph, Ontario, Canada
State Laboratory County Kildare, Ireland	WESSLING Laboratorien GmbH Altenberge, Germany
Super Micro Mass Research & Technology Center Niaosong Township, Kaohsiung County, Taiwan	Worthies Engineering Consultants Corp. Taichung, Taiwan
The Food And Environment Research Agency (FERA) York, UK	Zavod za zdravstveno varstvo Maribor, Inštitut za varstvo okolja Maribor, Slovenija
TLR Rotterdam, The Netherlands	

Design and practical implementation

Study design and reporting of results

As in the previous rounds of this interlaboratory comparison studies, the test material chosen represented naturally contaminated food samples. The analytes to be determined by each participating laboratory 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. In addition, laboratories were asked to determine on a voluntary basis 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 (α -, β -, γ -HBCD). The six PCB congeners belong together with the mono-ortho PCB #118 to the selection of PCBs commonly referred to as ICES-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 determine as many as possible of the 2,3,7,8-substituted PCDDs/PCDFs, dioxin-like PCBs, PBDEs, Indicator PCBs and HBCD. The report was to include the determined lipid percent for the test samples. Also the actual sample and lipid amount (g) for each determination should be reported. For each sample, laboratories were to report the found concentration on fresh weight basis for each congener which was detected (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 form.

In addition, six standard solutions containing known concentrations of 1) seventeen 2,3,7,8-substituted PCDDs/PCDFs, 2) four non-ortho PCBs, 3) eight mono-ortho PCBs, 4) eight PBDEs, 5) six Indicator PCBs and 6) α -HBCD were to be analyzed using the laboratory's own quantification standards and methods. The results were reported on separate forms.

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

Each participating laboratory was given a specific code by the co-coordinators. In the present report, the participants are presented in the tables and figures by

their laboratory codes. Participants had access to their own code only and laboratory codes were not revealed to third parties.

On receipt by the co-coordinators, the raw data from the laboratories were entered into a database. The draft final report was generated and made available to all participants on the Internet in August 2010. The draft of the final report was discussed at the Waters New Technology Forum at DIOXIN 2010 in September in San Antonio, Texas, USA.

Collection, preparation, and distribution of samples

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

- Breast milk: Obtained from Norway (150mL)
- Pork meat: Obtained from Chile/ Norway (100g)
- Trout filet: Obtained from lake Mjøsa in Norway (100g)

The test materials consisted of three natural products not fortified with standards.

Homogenization of the pork and trout was performed by repeatedly grinding portions of the food item in a grinder and homogenizing these portions in a mixer. The homogeneity of these materials was tested using an approach developed at NIPH. The rationale for and description of the test method is given in Appendix E. Breast milk was heated, thoroughly mixed by stirring and subsequently subdivided. Sub-samples of at least 150mL of breast milk (B), 100g of pork (P) and 100g of trout (T) were placed into carefully cleaned screw-cap glass bottles. All samples were stored at -20°C until shipment. The frozen samples were shipped to the participating laboratories marked as test material B, P and T.

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:

For PCDDs/PCDFs and dioxin-like PCBs congener-by-congener medians were calculated from the food sample data of all reporting laboratories using the detection limit as concentration for non-detected congeners (upperbound concentration). For PBDEs, Indicator PCBs and HBCD, non-detected congeners were removed from the data set prior to consensus calculation. Outliers were defined as those values above two times the median of all values and were removed from the data set. The consensus values were defined as the median of the remaining data for each congener. In addition, the consensus mean and SD were calculated from this data set for each congener. Those congener data which had been removed prior to consensus calculation are marked in the tables presenting the individual results.

For the standard solutions, outliers were defined as those values outside $\pm 50\%$ of the median of all reported values. Consensus 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 $\pm 2SD$.

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 (WHO1998TEQs) 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); σ = target value for standard deviation. A σ 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.

The final report and certificate

The draft of the final report was prepared by the co-coordinators and published on the web in August 2010. The draft was discussed at the Waters New Technology Forum at the DIOXIN2010 Symposium in September in San Antonio, Texas, USA.

A certificate, stating the participant's code, will be sent to each participant contributing to the results at the end of 2010. The final report will be made available to the participants in pdf format at www.fhi.no/ILC.

Co-ordination

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

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Results

The results are presented in the following chapters. A 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. A general reader of the report, who has no access to the laboratory codes, will be able to get a picture of the analytical performance of laboratories world-wide for determining dioxins, dioxin-like PCBs, Indicator PCBs, PBDEs and HBCD in regular foods.

Presentation in the report

Eighty-nine laboratories from 31 different countries have submitted results. In Appendix C the consensus statistics are given on fresh and lipid weight basis for concentrations and TEQ values of individual congeners, a summary of TEQ values for each food item, and the Z-score plots based on a target deviation of $\pm 20\%$. Further, the results of the lipid determinations are presented. Finally, individual results reported by the laboratories for each congener are given for breast milk, pork and trout in Appendix 2, 3 and 4.

Summarising comments on results

PCDDs/PCDFs

Analyte solution

Concentrations for PCDDs/PCDFs were reported by 77 laboratories. The average RSD for the 17 congeners was 9.2% ranging from 7.4% for 1,2,3,7,8-PeCDD to 11% for 1,2,3,4,7,8 HxCDD and 1,2,3,4,7,8,9-HpCDF. The calculation of Z-scores for the TEQs (target 13.6 pg TEQ/ μ l) of the PCDD/PCDF standard solution showed that 95% of the labs were within the range of $\pm 20\%$ of the consensus value. This demonstrates the high quality of the calibration solutions used by the laboratories.

Breast milk

For the breast milk sample, PCDD/PCDF results from 68 laboratories were received. The consensus TEQ was 0.14 pg TE/g fresh weight and 4.2 pg TE/g lipid weight. The average RSD was 36% ranging from 17-70%. Z-scores within ± 1 were obtained by 72% of the laboratories and 84% of the laboratories had Z-scores within ± 2 . About 80% percent of the PCDD/PCDF TEQ is made up by the three congeners 2,3,7,8-TCDD, 1,2,3,7,8-PeCDD and 2,3,4,7,8-PeCDF.

Pork

PCDD/PCDF concentrations in the pork sample were reported by 70 laboratories. The consensus TEQ was 0.02 pg TE/g fresh. The average RSD was 56% ranging from 37-77%. Z-scores were within ± 1 for 17% of the laboratories and within ± 2 for 38% of the laboratories. About 70% percent of the PCDD/PCDF TEQ is made up by the three congeners 2,3,7,8-TCDD, 1,2,3,7,8-PeCDD and 2,3,4,7,8-PeCDF.

Trout

For the trout sample 78 laboratories determined PCDD/PCDF concentrations. The consensus TEQ was 0.78 pg/g fresh weight and 16 pg/g lipid weight. The average RSD was 40% ranging from 25-68%. Z-scores for PCDD/PCDF TEQ within ± 1 were obtained by 73% of the laboratories and 85% had Z-scores within ± 2 . About 97% of the PCDD/PCDF TEQ is made up by the four congeners 2,3,7,8-TCDD, 1,2,3,7,8-PeCDD, 2,3,7,8-TCDF and 2,3,4,7,8-PeCDF.

Dioxin-like PCBs

Analyte solution

The 12 dioxin-like PCBs in the analyte solution were analyzed and reported by 75 to 77 laboratories. The RSDs for the different congeners were 7.7-11% with an average of 9.1%.

Breast milk

Dioxin-like PCB concentrations were reported from 66 to 67 laboratories. The concentrations of the 12 congeners varied between 0.03 pg/g fresh weight (CB-77) and 176 pg/g fresh weight (CB-118). The dioxin-like PCBs contribute 52% to the total TEQ in the sample with CB-126 as the main contributor (22%). The aver-

age RSD for concentrations of individual dioxin-like PCB congeners on fresh weight basis was 32% ranging from 24% to 59% (CB-77).

Pork

The number of laboratories that measured and reported dioxin-like PCB concentrations in pork were between 68 and 70. The concentrations ranged from 0.02 pg/g fresh weight for CB-81 to 14 pg/g fresh weight for CB-118. The dioxin-like PCBs contribute to about 32% of the total TEQ in the sample with CB-126 as the main contributor. The average RSD for concentrations of individual dioxin-like PCB congeners on fresh weight basis was 45% ranging from 31% to 78% for CB-123.

Trout

Dioxin-like PCBs were reported by 78 to 79 laboratories. Levels were ranging from 2.6 pg/g fresh weight

for CB-81 to 3112 pg/g fresh weight for CB-118. The average RSD for concentrations of individual dioxin-like PCB congeners on fresh weight basis was 30% ranging from 27% to 40% for CB-81. The contribution of the dioxin-like PCBs to the total TEQ was about 80% with CB-126 as the main contributor.

Total TEQ

In Figure 1 and 2 the contribution of the three groups of dioxin-like compounds is depicted. For breast milk and trout, dioxin-like PCBs contributed to 50% or more of the total TEQs (using WHO98TEF), demonstrating the importance of PCBs for the determination of the total 2,3,7,8-TCDD related toxic potency of food samples.

The RSD for total TEQ on fresh weight basis calculated from the RSD of individual congeners was 10% for breast milk, 22% for pork and 16% for trout.

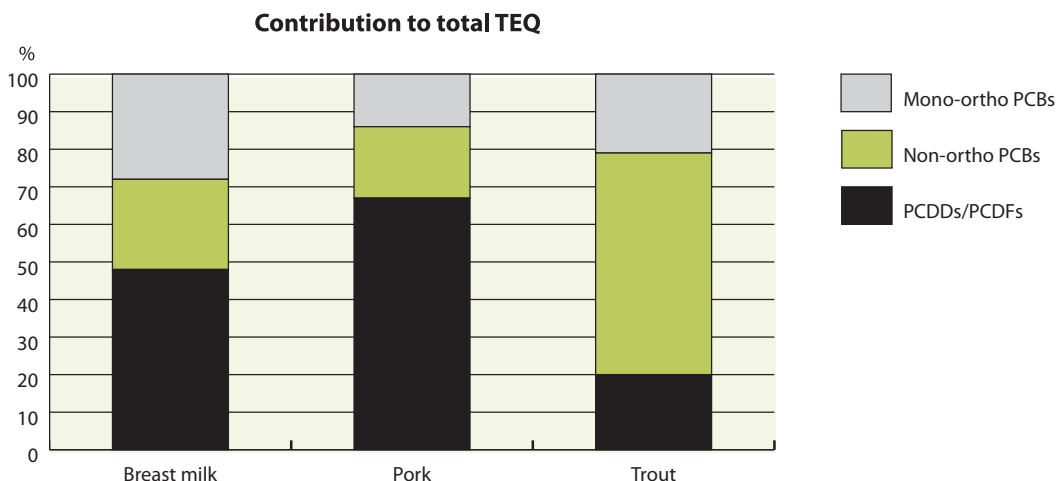


Figure 1. The contribution of PCDDs/PCDFs, non-ortho PCBs and mono-ortho PCBs to the total TEQ calculated using the WHO₁₉₉₈ TEFs, in the three food samples.

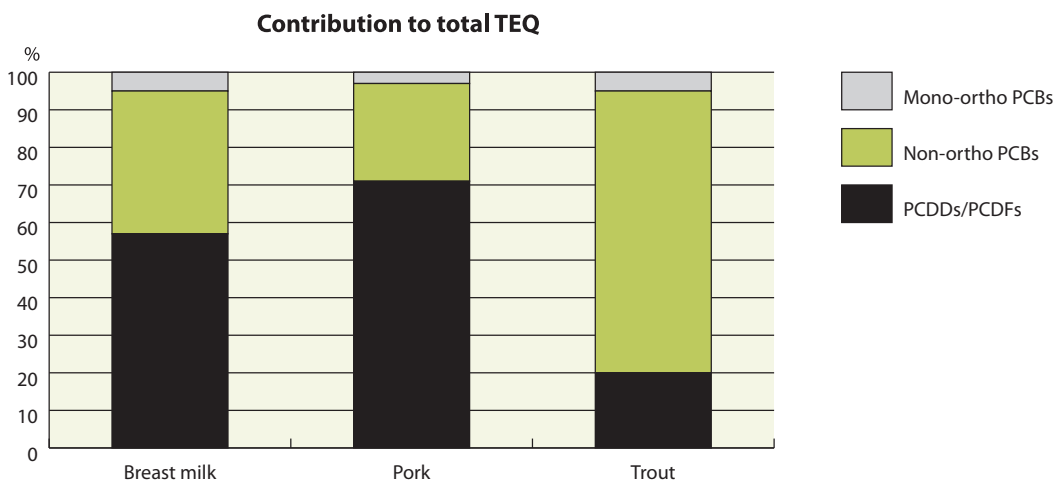


Figure 2. The contribution of PCDDs/PCDFs, non-ortho PCBs and mono-ortho PCBs to the total TEQ calculated using the WHO₂₀₀₆ TEFs, in the three food samples.

Indicator PCBs

Analyte solution

Sixty-three laboratories reported Indicator PCBs in the analyte solution. The average RSD was 10% ranging from 9.5-11%.

Breast milk

For the breast milk sample Indicator PCB results were received from 52 laboratories. The concentrations were varying between 7.7 pg/g fresh weight (CB-52) and 912 pg/g fresh weight (CB-153). The RSDs were ranging from 30-38% with an average of 34%. The consensus median for the sum of Indicator PCBs was 1.9 ng/g fresh weight.

Pork

Within the deadline, 55 laboratories reported results of Indicator PCBs in the pork sample. The concentrations ranged from 19 pg/g fresh weight (CB-28/52) to 71 pg/g fresh weight (CB-153) with a consensus median for the sum of Indicator PCBs of 210 pg/g fresh weight. The average RSD was 35% ranging from 26-56%.

Trout

Results were obtained from 62 laboratories. The concentrations of Indicator PCBs in the trout sample were ranging from 210 pg/g fresh weight (CB-28) to 10 ng/g fresh weight (CB-153) and the consensus median for the sum was 26 ng/g fresh weight. The average RSD was 31% ranging from 26-40%.

PBDEs

Analyte solution

The PBDE standard solution was analyzed by 38 to 39 laboratories and 30 laboratories reported values for BDE-209. The RSDs were between 7.8-13% for all congeners except BDE-209 where the RSD was 10%.

Breast milk

PBDE concentrations were reported by 33 laboratories, except for BDE-209 for which 23 results were received. The consensus concentrations were in the range 0.65 pg/g fresh weight for BDE-154 and 19 pg/g fresh weight for BDE-47. The concentration for BDE-209 was 5.4 pg/g fresh weight. The sum of tri- to heptaBDEs was 53 pg/g fresh weight. The range of RSDs on fresh weight was 22-40% with an average of 30%, excluding BDE-209 for which the RSD was 53%.

Pork

Within the deadline, 32 laboratories had reported results for tri- to hepta BDEs and 22 laboratories reported results for BDE-209. The concentrations varied between 1.6 pg/g fresh weight (BDE-28) and 403 pg/g fresh weight (BDE-99). The concentration for BDE-209 was 23 pg/g fresh weight. The sum of tri- to heptaBDEs was 882 pg/g fresh weight. The RSD calculated from the concentrations on fresh weight ranged from 20-42% with an average of 26% for the tri- to heptaBDEs. The RSD calculated from the concentrations on fresh weight for BDE-209 was 55%.

Trout

Between 36 and 38 laboratories reported results for tri- to heptaBDEs and 25 reported results for BDE-209. The concentrations varied between 8.5 pg/g fresh weight (BDE-183) and 54 ng/g fresh weight (BDE-47). The concentration for BDE-209 was 13 pg/g fresh weight. The sum of tri- to heptaBDEs was 92 ng/g fresh weight. The RSDs for the individual congeners were ranging from 27 to 34% with an average of 30%, excluding BDE-209 for which the RSD was 67%.

HBCD

Also in this round of the study HBCD and the isomers α -, β - and γ -HBCD could be determined and reported. A total of 13 laboratories reported α -HBCD in the standard solution and between 8-14 laboratories reported the other isomers. Since only few laboratories reported HBCD, these values are regarded as indicative.

Lipid content

The mean and RSDs (in parentheses) for the lipid contents of the food samples were calculated to be 3.4% (11%) for breast milk, 17.8% (11%) for pork and 4.8% (23%) for trout.

Acknowledgements

The laboratories are acknowledged for their participation in this interlaboratory comparison and their interest in its overall objectives, thereby making it clear that they value good analytical performance. All the individual analysts are acknowledged for their contributions to the results.

We are grateful to Cambridge Isotope Laboratories, Inc. for providing the standard solutions for this interlaboratory study. We thank Dr. Leondios Leondiadis, Mass Spectrometry and Dioxin Analysis Lab, National Center for Scientific Research 'Demokritos', Athens, Greece for providing pork meat, the Norwegian Institute of Water Research, Oslo for trout filet and Oslo University Hospital for the breast milk samples.

Appendix A:

Participant's affiliations
and addresses

Appendix A: Affiliations and addresses of participants

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Appendix B:

Study announcement and
instructions for participants

Announcement for Interlaboratory Comparison on POPs in Food 2010

Introduction

We hereby announce the 11th round of the interlaboratory comparison on the determination of dioxins, PCBs, PBDEs and HBCD in food. The study is open for academic, regulatory as well as commercial laboratories world-wide. The organizer of this study is the Department of Analytical Chemistry at the Norwegian Institute of Public Health in Oslo, Norway. The study is scheduled to take place from January to April 2010. A draft report will be available prior to the evaluation meeting which will take place at the Dioxin 2010 Symposium in September, San Antonio, Texas, USA. The final report will be available to participants by December 2010 together with a certificate for participation.

Objectives

The objectives of this exercise are to assess the interlaboratory consistency in results from analyses of dioxins, PCBs, PBDEs and HBCD in regular foods known to contribute to the intake in the general population and to assess the world-wide readiness and capacity in analysing dioxins and other halogenated persistent pollutants in food. The study also serves as a quality assurance instrument for the participating laboratories.

Participants

We encourage all laboratories world-wide working in this field to participate and assess their analytical performance. Participants are requested to completely fill out the Registration Form and mark for 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, you are invited to determine six marker PCBs, eight PBDEs and HBCD. 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 P) ~100 g, Trout (labelled T) ~100 g, and Breast milk (labelled B) ~150 g, and will be distributed by an international courier service to the participating laboratories.

Please note:

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

Instructions for analysis and reporting

Further detailed instructions and reporting forms will be sent out simultaneously with the dispatch of the samples in January.

In short, 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 a 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	December 2009
Return of registration form	December 18, 2009
Shipment of test material	January 11, 2010
Confirmation of receipt of test material by participant	Within 7 days
Reporting of test results ^{a)}	April 16, 2010
Publication of draft report on web-site	August 2010
Evaluation meeting at Dioxin 2010 San Antonio, Texas, USA	September 2010
Final report available to all participants	November 2010

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

Participation fee

To all laboratories that have received the test materials, a corresponding invoice will be sent. The participation fee for any combination of the analytes in one food item is 1000 Euro, for two food items 1200 Euro, and for the complete set of all three food items the fee is 1400 Euro.

Co-ordinating group

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Interlaboratory Comparison on Dioxins in Food 2010

Instructions for participants

January 2010

1. Introduction

This is the 11th round of the interlaboratory comparison exercise on the determination of dioxins, PCBs, PBDEs and HBCD in food organised by the Department of Analytical Chemistry, 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 WHO₉₈-TEF scheme 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 pork meat (P), breast milk (B), and trout (T). The mentioned analytes should also be determined in the respective six standard solutions.

In this round of the Interlaboratory comparison study, the concentration 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. 94 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. 100 g pork meat, lipid content about 20%
- ca. 150 mL breast milk, lipid content about 3%
- ca. 100 g trout, lipid content about 5%

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 meat samples	P
Breast milk samples	B
Trout samples	T

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 all three matrixes. 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 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. Veronica Horpestad Liane
P.O. Box 4403 Nydalen
N-0403 Oslo, Norway

Deadline

The reports must be in our hands no later than April 16th, 2010 to enable us to prepare the draft report for the Dioxin 2010 Symposium in San Antonio, Texas, USA. There will be no extension of this deadline. A confirmation for receiving 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 16th. 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.

Statistical results based on the reported data as well as other important information from the evaluation of the data, will be discussed during a consultation meeting in September at the Dioxin 2010 Symposium in San Antonio, Texas, USA.

6. Final report

The final report will be prepared by the co-ordinators. All participants will be presented by their laboratory code. A draft will be published on the internet in July/August. The results will be discussed during the Dioxin 2010 Symposium in San Antonio, Texas, USA. The final report will be available by November 2010. The report will be available in an electronic version on <http://www.fhi.no>. 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

- EURO 1000 for one food item
- EURO 1200 for two food items
- EURO 1400 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	December 2009
Return of registration form	December 18, 2009
Shipment of test material	January 11, 2010
Confirmation of receipt of test material by participant	Within 7 days
Reporting of test results ^{a)}	April 16, 2010
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Evaluation meeting at Dioxin 2010 San Antonio, Texas, USA	September 2010
Final report available to all participants	November 2010

- 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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Interlaboratory Comparison on Dioxins in Food 2010

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/ μ l 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:

Summary results

Consensus of congener concentrations

Consensus of TEQ values

Consensus statistics

Laboratories' reported TEQs

Lipid determination

Laboratories' Z-scores

Z-score plots

Consensus congener concentrations

	Breast milk		Pork meat		Trout	
	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.
2,3,7,8-TCDD	0.018	0.51	0.0040	0.023	0.13	2.5
1,2,3,7,8-PeCDD	0.040	1.2	0.0058	0.033	0.18	3.6
1,2,3,4,7,8-HxCDD	0.014	0.40	0.0050	0.028	0.0081	0.16
1,2,3,6,7,8-HxCDD	0.090	2.6	0.0070	0.040	0.051	1.03
1,2,3,7,8,9-HxCDD	0.022	0.63	0.0050	0.028	0.0092	0.18
1,2,3,4,6,7,8-HpCDD	0.13	3.7	0.026	0.15	0.048	0.96
1,2,3,4,6,7,8,9-OCDD	0.98	28	0.14	0.80	0.21	4.2
2,3,7,8-TCDF	0.015	0.44	0.0090	0.051	2.0	40
1,2,3,7,8-PeCDF	0.0087	0.25	0.0060	0.034	0.18	3.5
2,3,4,7,8-PeCDF	0.12	3.6	0.0084	0.048	0.49	9.8
1,2,3,4,7,8-HxCDF	0.032	0.91	0.0090	0.051	0.023	0.45
1,2,3,6,7,8-HxCDF	0.032	0.94	0.0052	0.030	0.029	0.57
2,3,4,6,7,8-HxCDF	0.016	0.46	0.0057	0.032	0.029	0.57
1,2,3,7,8,9-HxCDF	0.0030	0.086	0.0040	0.023	0.0053	0.11
1,2,3,4,6,7,8-HpCDF	0.033	0.95	0.017	0.097	0.022	0.44
1,2,3,4,7,8,9-HpCDF	0.0048	0.14	0.0056	0.032	0.0064	0.13
1,2,3,4,6,7,8,9-OCDF	0.012	0.35	0.014	0.077	0.031	0.62
PCB 77	0.11	3.1	0.28	1.6	26	512
PCB 126	0.66	19	0.051	0.29	21	428
PCB 169	0.49	14	0.051	0.29	14	285
PCB 81	0.030	0.86	0.021	0.12	2.6	51
PCB 105	40	1157	2.5	14	1180	23599
PCB 114	10	290	0.36	2.0	74	1484
PCB 118	176	5059	14	78	3112	62230
PCB 123	2.1	59	0.12	0.68	62	1242
PCB 156	93	2687	3.6	21	600	11998
PCB 157	19	546	0.80	4.6	125	2498
PCB 167	23	660	0.96	5.5	353	7053
PCB 189	7.3	211	0.36	2.0	60	1204

fw. - fresh weight

lw. - lipid weight

Consensus congener concentrations

	Breast milk		Pork meat		Trout	
	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.
CB 28	40	1149	19	108	210	4204
CB 52	7.7	221	19	107	534	10676
CB 101	11	318	24	136	2765	55306
CB 138	518	14918	54	305	8251	165025
CB 153	912	26290	71	403	10394	207877
CB 180	405	11675	23	132	3856	77110
BDE 28	1.8	51	1.6	8.9	230	4599
BDE 47	19	548	270	1536	53670	1073401
BDE 99	3.9	112	403	2290	10744	214883
BDE 100	6.2	178	74	420	19287	385742
BDE 153	21	604	61	347	2865	57298
BDE 154	0.65	19	48	270	4978	99550
BDE 183	0.73	21	25	142	8.5	171
BDE 209	5.4	157	23	131	13	259
α-HBCD	11	329	8.4	48	19014	380280
β-HBCD	4.3	123	2.1	12	202	4040
γ-HBCD	1.2	34	8.0	45	311	6221
Tot HBCD	21	598	32	184	20291	405820
Sum PCB	1893	54570	210	1192	26010	520198
Sum BDE without 209	53	1533	882	5013	91782	1835644
Sum BDE	59	1689	905	5144	91795	1835903

Consensus of TEQs

TEF1998

	Breast milk		Pork meat		Trout	
	pg TE/g fw.	pg TE/g lw.	pg TE/g fw.	pg TE/g lw.	pg TE/g fw.	pg TE/g lw.
2,3,7,8-TCDD	0.018	0.51	0.0040	0.023	0.13	2.5
1,2,3,7,8-PeCDD	0.040	1.2	0.0058	0.033	0.18	3.6
1,2,3,4,7,8-HxCDD	0.0014	0.040	0.00050	0.0028	0.00081	0.016
1,2,3,6,7,8-HxCDD	0.0090	0.26	0.00070	0.0040	0.0051	0.10
1,2,3,7,8,9-HxCDD	0.0022	0.063	0.00050	0.0028	0.00092	0.018
1,2,3,4,6,7,8-HpCDD	0.0013	0.037	0.00026	0.0015	0.00048	0.010
1,2,3,4,6,7,8,9-OCDD	0.00010	0.0028	0.000014	0.000080	0.000021	0.00042
2,3,7,8-TCDF	0.0015	0.044	0.00090	0.0051	0.20	4.0
1,2,3,7,8-PeCDF	0.00043	0.013	0.00030	0.0017	0.0088	0.18
2,3,4,7,8-PeCDF	0.062	1.8	0.0042	0.024	0.24	4.9
1,2,3,4,7,8-HxCDF	0.0032	0.091	0.00090	0.0051	0.0023	0.045
1,2,3,6,7,8-HxCDF	0.0032	0.094	0.00052	0.0030	0.0029	0.057
2,3,4,6,7,8-HxCDF	0.0016	0.046	0.00057	0.0032	0.0029	0.057
1,2,3,7,8,9-HxCDF	0.00030	0.0086	0.00040	0.0023	0.00053	0.011
1,2,3,4,6,7,8-HpCDF	0.00033	0.0095	0.00017	0.0010	0.00022	0.0044
1,2,3,4,7,8,9-HpCDF	0.000048	0.0014	0.000056	0.00032	0.000064	0.0013
1,2,3,4,6,7,8,9-OCDF	0.0000012	0.000035	0.0000014	0.0000077	0.0000031	0.000062
PCB 77	0.000011	0.00031	0.000028	0.00016	0.0026	0.051
PCB 126	0.066	1.9	0.0051	0.029	2.1	43
PCB 169	0.0049	0.14	0.00051	0.0029	0.14	2.9
PCB 81	0.0000030	0.000086	0.0000021	0.000012	0.00026	0.0051
PCB 105	0.0040	0.12	0.00025	0.0014	0.12	2.4
PCB 114	0.0050	0.15	0.00018	0.0010	0.037	0.74
PCB 118	0.018	0.51	0.0014	0.0078	0.31	6.2
PCB 123	0.00021	0.0059	0.000012	0.000068	0.0062	0.12
PCB 156	0.047	1.3	0.0018	0.010	0.30	6.0
PCB 157	0.0095	0.27	0.00040	0.0023	0.062	1.2
PCB 167	0.00023	0.0066	0.000010	0.000055	0.0035	0.071
PCB 189	0.00073	0.021	0.000036	0.00020	0.0060	0.12
PCDDs/PCDFs	0.14	4.2	0.020	0.11	0.78	16
Non-ortho PCBs	0.071	2.0	0.0056	0.032	2.3	46
Mono-ortho PCBs	0.084	2.4	0.0041	0.023	0.84	17
Total TEQ	0.30	8.6	0.030	0.17	3.9	78

fw. - fresh weight

lw- - lipid weight

Consensus of TEQs

TEF2006

	Breast milk		Pork meat		Trout	
	pg TE/g fw.	pg TE/g lw.	pg TE/g fw.	pg TE/g lw.	pg TE/g fw.	pg TE/g lw.
2,3,7,8-TCDD	0.018	0.51	0.0040	0.023	0.13	2.5
1,2,3,7,8-PeCDD	0.040	1.2	0.0058	0.033	0.18	3.6
1,2,3,4,7,8-HxCDD	0.0014	0.040	0.00050	0.0028	0.00081	0.016
1,2,3,6,7,8-HxCDD	0.0090	0.26	0.00070	0.0040	0.0051	0.10
1,2,3,7,8,9-HxCDD	0.0022	0.063	0.00050	0.0028	0.00092	0.018
1,2,3,4,6,7,8-HpCDD	0.0013	0.037	0.00026	0.0015	0.00048	0.010
1,2,3,4,6,7,8,9-OCDD	0.00029	0.0085	0.000042	0.00024	0.000063	0.0013
2,3,7,8-TCDF	0.0015	0.044	0.00090	0.0051	0.20	4.0
1,2,3,7,8-PeCDF	0.00026	0.0075	0.00018	0.0010	0.0053	0.11
2,3,4,7,8-PeCDF	0.037	1.1	0.0025	0.014	0.15	2.9
1,2,3,4,7,8-HxCDF	0.0032	0.091	0.00090	0.0051	0.0023	0.045
1,2,3,6,7,8-HxCDF	0.0032	0.094	0.00052	0.0030	0.0029	0.057
2,3,4,6,7,8-HxCDF	0.0016	0.046	0.00057	0.0032	0.0029	0.057
1,2,3,7,8,9-HxCDF	0.00030	0.0086	0.00040	0.0023	0.00053	0.011
1,2,3,4,6,7,8-HpCDF	0.00033	0.0095	0.00017	0.0010	0.00022	0.0044
1,2,3,4,7,8,9-HpCDF	0.000048	0.0014	0.000056	0.00032	0.000064	0.0013
1,2,3,4,6,7,8,9-OCDF	0.0000036	0.00010	0.0000041	0.000023	0.0000093	0.00019
PCB 77	0.000011	0.00031	0.000028	0.00016	0.0026	0.051
PCB 126	0.066	1.9	0.0051	0.029	2.1	43
PCB 169	0.015	0.43	0.0015	0.0088	0.43	8.6
PCB 81	0.0000090	0.00026	0.0000063	0.000036	0.00077	0.015
PCB 105	0.0012	0.035	0.000074	0.00042	0.035	0.71
PCB 114	0.00030	0.0087	0.000011	0.000061	0.0022	0.045
PCB 118	0.0053	0.15	0.00041	0.0024	0.093	1.9
PCB 123	0.000062	0.0018	0.0000036	0.000020	0.0019	0.037
PCB 156	0.0028	0.081	0.00011	0.00062	0.018	0.36
PCB 157	0.00057	0.016	0.000024	0.00014	0.0037	0.075
PCB 167	0.00069	0.020	0.000029	0.00016	0.011	0.21
PCB 189	0.00022	0.0063	0.000011	0.000061	0.0018	0.036
PCDDs/PCDFs	0.12	3.4	0.018	0.10	0.67	13
Non-ortho PCBs	0.081	2.3	0.0067	0.038	2.6	51
Mono-ortho PCBs	0.011	0.32	0.00068	0.0038	0.17	3.3
Total TEQ	0.21	6.1	0.025	0.14	3.4	68

fw. - fresh weight

lw- - lipid weight

Consensus statistics

Analyte solution

	Target value pg/ul	Consensus median, pg/ul	Median all values pg/ul	Consensus mean, pg/ul	Standard deviation, pg/ul	Relative standard deviation, %	No. of values reported	No. of values removed
2,3,7,8-TCDD	2.0	2.0	2.0	2.0	0.18	9.1	76	1
1,2,3,7,8-PeCDD	5.0	4.8	4.8	4.8	0.35	7.4	76	1
1,2,3,4,7,8-HxCDD	5.0	4.9	4.9	4.9	0.52	11	77	1
1,2,3,6,7,8-HxCDD	5.0	4.9	4.9	4.8	0.42	8.8	77	1
1,2,3,7,8,9-HxCDD	5.0	5.1	5.1	5.1	0.42	8.2	77	1
1,2,3,4,6,7,8-HpCDD	5.0	5.0	5.0	5.0	0.42	8.4	77	1
1,2,3,4,6,7,8,9-OCDD	10	9.9	9.9	9.9	0.99	10	77	1
2,3,7,8-TCDF	2.0	2.0	2.0	1.9	0.18	9.1	77	3
1,2,3,7,8-PeCDF	5.0	5.0	5.0	5.0	0.47	9.3	77	1
2,3,4,7,8-PeCDF	5.0	4.8	4.8	4.8	0.41	8.5	77	1
1,2,3,4,7,8-HxCDF	5.0	4.9	4.9	4.9	0.43	8.7	77	2
1,2,3,6,7,8-HxCDF	5.0	5.0	5.0	5.0	0.45	9.1	77	1
2,3,4,6,7,8-HxCDF	5.0	5.0	5.0	5.0	0.40	8.0	77	1
1,2,3,7,8,9-HxCDF	5.0	4.9	5.0	5.0	0.50	10	77	1
1,2,3,4,6,7,8-HpCDF	5.0	5.0	5.0	5.0	0.48	9.6	77	1
1,2,3,4,7,8,9-HpCDF	5.0	5.1	5.1	5.1	0.56	11	77	1
1,2,3,4,6,7,8,9-OCDF	10	9.9	9.9	10	1.0	10	77	1
PCB 77	10	10	10	10	0.87	8.5	76	2
PCB 126	10	10	10	10	0.89	8.7	76	1
PCB 169	10	10	10	10	0.85	8.3	76	2
PCB 81	10	10	10	10	0.81	7.7	75	2
PCB 105	100	103	103	104	9.6	9.2	77	1
PCB 114	100	102	102	102	11	11	77	2
PCB 118	100	103	102	101	10	10	77	1
PCB 123	100	103	103	103	11	11	76	1
PCB 156	100	104	104	104	8.5	8.1	77	3
PCB 157	100	105	105	106	10	9.4	76	1
PCB 167	100	105	104	105	9.6	9.1	76	2
PCB 189	100	103	103	103	8.5	8.2	76	1

Consensus statistics

Breast 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
2,3,7,8-TCDD	0.018	0.018	0.017	0.0063	36	68	7	5
1,2,3,7,8-PeCDD	0.040	0.040	0.038	0.012	31	68	3	1
1,2,3,4,7,8-HxCDD	0.014	0.014	0.014	0.0043	31	68	8	9
1,2,3,6,7,8-HxCDD	0.090	0.091	0.087	0.025	28	68	4	2
1,2,3,7,8,9-HxCDD	0.022	0.022	0.022	0.0076	34	68	7	6
1,2,3,4,6,7,8-HpCDD	0.13	0.13	0.13	0.032	24	68	5	1
1,2,3,4,6,7,8,9-OCDD	0.98	1.0	1.0	0.20	20	68	5	0
2,3,7,8-TCDF	0.015	0.016	0.016	0.0048	29	68	9	2
1,2,3,7,8-PeCDF	0.0087	0.0095	0.0090	0.0032	35	68	12	8
2,3,4,7,8-PeCDF	0.12	0.12	0.13	0.022	17	68	3	0
1,2,3,4,7,8-HxCDF	0.032	0.032	0.033	0.0084	25	68	5	1
1,2,3,6,7,8-HxCDF	0.032	0.033	0.033	0.0099	30	68	4	1
2,3,4,6,7,8-HxCDF	0.016	0.016	0.017	0.0064	38	68	8	6
1,2,3,7,8,9-HxCDF	0.0030	0.0050	0.0044	0.0031	70	68	16	38
1,2,3,4,6,7,8-HpCDF	0.033	0.033	0.034	0.011	32	68	6	6
1,2,3,4,7,8,9-HpCDF	0.0048	0.0066	0.0056	0.0036	64	68	16	34
1,2,3,4,6,7,8,9-OCDF	0.012	0.019	0.014	0.0093	66	68	15	26
PCB 77	0.11	0.15	0.13	0.076	59	66	15	7
PCB 126	0.66	0.66	0.65	0.19	29	66	1	1
PCB 169	0.49	0.50	0.47	0.14	30	66	3	2
PCB 81	0.030	0.032	0.032	0.013	42	66	12	11
PCB 105	40	41	38	10	27	67	2	0
PCB 114	10	10	9.8	2.4	24	67	4	0
PCB 118	176	176	168	48	28	67	3	0
PCB 123	2.1	2.1	2.0	0.64	33	67	9	1
PCB 156	93	93	90	25	27	67	2	0
PCB 157	19	19	18	4.7	25	66	4	0
PCB 167	23	23	22	6.2	28	67	1	0
PCB 189	7.3	7.3	7.2	2.1	29	67	1	0

Consensus statistics

Pork meat, 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
2,3,7,8-TCDD	0.0040	0.0060	0.0050	0.0034	68	70	16	47
1,2,3,7,8-PeCDD	0.0058	0.0081	0.0065	0.0040	62	70	18	42
1,2,3,4,7,8-HxCDD	0.0050	0.0073	0.0058	0.0032	56	70	21	40
1,2,3,6,7,8-HxCDD	0.0070	0.010	0.0085	0.0050	58	70	17	31
1,2,3,7,8,9-HxCDD	0.0050	0.0085	0.0057	0.0035	62	70	22	42
1,2,3,4,6,7,8-HpCDD	0.026	0.031	0.029	0.011	37	70	17	11
1,2,3,4,6,7,8,9-OCDD	0.14	0.16	0.15	0.055	37	70	16	6
2,3,7,8-TCDF	0.0090	0.010	0.0090	0.0050	55	70	18	26
1,2,3,7,8-PeCDF	0.0060	0.010	0.0071	0.0045	63	70	15	38
2,3,4,7,8-PeCDF	0.0084	0.010	0.0093	0.0049	53	70	16	21
1,2,3,4,7,8-HxCDF	0.0090	0.010	0.0093	0.0037	40	70	23	21
1,2,3,6,7,8-HxCDF	0.0052	0.0090	0.0071	0.0043	61	70	19	24
2,3,4,6,7,8-HxCDF	0.0057	0.0090	0.0064	0.0035	56	70	21	32
1,2,3,7,8,9-HxCDF	0.0040	0.0060	0.0048	0.0032	66	70	21	49
1,2,3,4,6,7,8-HpCDF	0.017	0.021	0.019	0.0080	42	70	21	14
1,2,3,4,7,8,9-HpCDF	0.0056	0.010	0.0080	0.0061	77	70	21	41
1,2,3,4,6,7,8,9-OCDF	0.014	0.023	0.016	0.0088	54	70	28	22
PCB 77	0.28	0.35	0.32	0.17	54	70	15	3
PCB 126	0.051	0.064	0.057	0.028	50	70	15	20
PCB 169	0.051	0.060	0.055	0.025	46	70	12	16
PCB 81	0.021	0.042	0.029	0.019	65	70	20	26
PCB 105	2.5	3.1	2.9	1.2	42	69	17	6
PCB 114	0.36	0.43	0.39	0.18	47	69	19	16
PCB 118	14	15	16	5.1	32	69	10	1
PCB 123	0.12	0.26	0.16	0.13	78	69	27	24
PCB 156	3.6	3.7	3.8	1.2	31	69	9	5
PCB 157	0.80	0.85	0.86	0.27	31	68	10	7
PCB 167	0.96	1.1	1.1	0.36	34	69	12	10
PCB 189	0.36	0.42	0.37	0.13	35	69	15	13

Consensus statistics

Trout, 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
2,3,7,8-TCDD	0.13	0.13	0.12	0.041	34	78	2	5
1,2,3,7,8-PeCDD	0.18	0.18	0.17	0.057	33	78	2	5
1,2,3,4,7,8-HxCDD	0.0081	0.010	0.010	0.0045	47	78	20	27
1,2,3,6,7,8-HxCDD	0.051	0.053	0.051	0.014	27	78	7	8
1,2,3,7,8,9-HxCDD	0.0092	0.010	0.010	0.0040	41	78	20	27
1,2,3,4,6,7,8-HpCDD	0.048	0.050	0.048	0.019	40	78	15	12
1,2,3,4,6,7,8,9-OCDD	0.21	0.27	0.24	0.12	52	78	16	5
2,3,7,8-TCDF	2.0	2.0	1.9	0.47	25	78	1	1
1,2,3,7,8-PeCDF	0.18	0.18	0.17	0.050	29	78	5	3
2,3,4,7,8-PeCDF	0.49	0.49	0.46	0.13	28	78	1	4
1,2,3,4,7,8-HxCDF	0.023	0.024	0.023	0.0078	34	78	16	11
1,2,3,6,7,8-HxCDF	0.029	0.030	0.029	0.010	35	78	12	10
2,3,4,6,7,8-HxCDF	0.029	0.030	0.029	0.011	39	78	15	11
1,2,3,7,8,9-HxCDF	0.0053	0.0082	0.0062	0.0038	61	78	23	49
1,2,3,4,6,7,8-HpCDF	0.022	0.026	0.024	0.011	47	78	18	22
1,2,3,4,7,8,9-HpCDF	0.0064	0.010	0.0080	0.0054	68	78	26	44
1,2,3,4,6,7,8,9-OCDF	0.031	0.040	0.033	0.016	49	78	25	24
PCB 77	26	26	26	7.3	28	79	2	1
PCB 126	21	21	21	5.9	28	79	1	0
PCB 169	14	14	14	4.2	31	79	2	2
PCB 81	2.6	2.6	2.4	0.94	40	78	4	5
PCB 105	1180	1190	1102	310	28	79	1	0
PCB 114	74	75	72	20	28	79	3	0
PCB 118	3112	3117	2923	912	31	79	1	0
PCB 123	62	68	62	21	35	78	14	0
PCB 156	600	601	571	152	27	79	1	0
PCB 157	125	125	121	33	27	78	3	0
PCB 167	353	355	335	104	31	78	1	1
PCB 189	60	60	56	16	29	78	1	1

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
CB 28	100	103	103	103	104
CB 52	100	104	104	103	104
CB 101	100	98	98	98	98
CB 138	100	104	104	106	105
CB 153	100	104	104	103	103
CB 180	100	106	106	107	107
BDE 28	25	25	25	25	25
BDE 47	25	24	24	25	25
BDE 99	25	25	25	25	25
BDE 100	25	25	25	25	25
BDE 153	25	25	25	25	25
BDE 154	25	25	25	25	25
BDE 183	25	26	26	25	25
BDE 209	100	100	100	99	25
α -HBCD *	500	500	500	511	511

	Relative standard deviation, % all values	Relative standard deviation, % outliers removed	Number of reported values	Number of reported outliers
CB 28	18	11	63	2
CB 52	18	9.5	63	2
CB 101	18	10	63	2
CB 138	13	11	63	1
CB 153	15	11	63	2
CB 180	12	9.5	63	1
BDE 28	10	9.9	39	0
BDE 47	8.4	8.4	39	0
BDE 99	7.8	7.8	39	0
BDE 100	8.1	8.1	39	0
BDE 153	10	10	39	0
BDE 154	9.9	9.9	39	0
BDE 183	13	13	38	0
BDE 209	15	10	30	1
α -HBCD *	6.0	6.0	13	0

NDs: Non-detects

* : Indicative value due to few reported values

Consensus statistics

Breast 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
CB 28	41	40	40	72	40	40
CB 52	8.0	7.7	7.7	40	8.0	8.0
CB 101	12	11	11	31	12	12
CB 138	534	518	518	576	524	524
CB 153	913	912	912	912	864	864
CB 180	414	405	405	429	410	410
BDE 28	1.9	1.8	1.8	4.6	2.0	2.0
BDE 47	20	19	19	22	20	20
BDE 99	4.2	3.9	3.9	5.8	4.0	4.1
BDE 100	6.2	6.2	6.2	7.0	6.4	6.4
BDE 153	21	21	21	710	22	22
BDE 154	0.73	0.66	0.65	2.2	0.70	0.69
BDE 183	0.90	0.79	0.73	2.8	0.81	0.76
BDE 209	6.7	5.0	5.4	27	5.6	6.4
α -HBCD *	30	27	11	103	25	20
β -HBCD *	6.0	0.88	4.3	8.0	2.8	4.3
γ -HBCD *	10	3.1	1.2	323	4.9	1.2
Tot HBCD *	105	69	21	437	74	62

	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
CB 28	181	35	33	52	7	1
CB 52	355	41	37	52	9	4
CB 101	310	37	38	52	9	4
CB 138	60	36	36	52	2	0
CB 153	47	30	30	52	1	0
CB 180	44	31	31	52	1	0
BDE 28	179	38	38	33	5	2
BDE 47	41	25	25	33	2	0
BDE 99	103	41	40	33	4	1
BDE 100	55	26	26	33	1	0
BDE 153	557	22	22	33	1	0
BDE 154	240	31	31	33	4	5
BDE 183	209	31	29	33	8	5
BDE 209	233	71	53	23	6	9
α -HBCD *	188	61	88	10	2	3
β -HBCD *	97	118	124	8	3	6
γ -HBCD *	278	95	NA	9	4	7
Tot HBCD *	250	93	149	9	1	4

NDs: Non-detects

* : Indicative value due to few reported values

Consensus statistics Pork meat, 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
CB 28	25	19	19	60	23	21
CB 52	22	19	19	61	20	20
CB 101	25	24	24	63	26	25
CB 138	57	54	54	81	55	54
CB 153	71	71	71	97	74	74
CB 180	24	23	23	47	24	24
BDE 28	1.7	1.6	1.6	2.6	1.6	1.6
BDE 47	270	270	270	274	274	274
BDE 99	403	403	403	400	400	400
BDE 100	74	74	74	75	75	75
BDE 153	61	61	61	61	61	61
BDE 154	48	48	48	47	47	47
BDE 183	25	25	25	26	24	24
BDE 209	30	22	23	78	22	25
α -HBCD *	20	17	8.4	70	17	10
β -HBCD *	10	8.5	2.1	31	8.1	3.2
γ -HBCD *	40	22	8.0	49	30	7.2
Tot HBCD *	79	67	32	124	63	36

	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
CB 28	236	57	56	55	12	5
CB 52	236	36	36	55	14	4
CB 101	224	33	31	55	10	4
CB 138	162	32	31	55	5	3
CB 153	134	31	31	55	3	2
CB 180	282	26	26	55	7	5
BDE 28	109	42	42	32	5	3
BDE 47	23	23	23	32	0	0
BDE 99	22	22	22	32	0	0
BDE 100	21	21	21	32	0	0
BDE 153	22	22	22	32	0	0
BDE 154	20	20	20	32	0	0
BDE 183	55	33	33	32	1	0
BDE 209	168	59	55	22	9	5
α -HBCD *	167	48	54	11	4	6
β -HBCD *	223	87	103	9.0	1	6
γ -HBCD *	98	86	90	10	2	6
Tot HBCD *	142	56	85	8.0	1	4

NDs: Non-detects

* : Indicative value due to few reported values

Consensus statistics

Trout, 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
CB 28	211	210	210	264	226	226
CB 52	542	536	534	650	542	534
CB 101	2773	2765	2765	2801	2636	2636
CB 138	8374	8251	8251	8703	8227	8227
CB 153	10446	10394	10394	10691	9949	9949
CB 180	3874	3856	3856	3948	3772	3772
BDE 28	230	230	230	236	236	236
BDE 47	53670	53670	53670	51266	51266	51266
BDE 99	10744	10744	10744	10114	10114	10114
BDE 100	19287	19287	19287	17850	17850	17850
BDE 153	2865	2865	2865	2681	2681	2681
BDE 154	4978	4978	4978	4597	4597	4597
BDE 183	8.8	8.6	8.5	10	8.6	8.6
BDE 209	32	12	13	67	18	19
α -HBCD *	19014	19014	19014	16686	16686	16686
β -HBCD *	192	192	202	168	168	196
γ -HBCD *	440	311	311	672	370	370
Tot HBCD *	20291	20291	20291	20233	20233	20233

	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
CB 28	65	40	40	62	5	1
CB 52	96	32	30	62	3	1
CB 101	43	26	26	62	2	0
CB 138	43	33	33	62	2	0
CB 153	41	27	27	62	3	0
CB 180	38	30	30	62	2	0
BDE 28	31	31	31	38	0	0
BDE 47	34	34	34	37	0	0
BDE 99	27	27	27	37	0	0
BDE 100	28	28	28	37	0	0
BDE 153	28	28	28	38	0	0
BDE 154	30	30	30	38	0	0
BDE 183	66	39	34	36	3	3
BDE 209	121	68	67	25	9	6
α -HBCD *	58	58	58	14	0	0
β -HBCD *	61	61	44	12	0	2
γ -HBCD *	90	53	53	13	4	0
Tot HBCD *	45	45	45	10	0	0

NDs: Non-detects

* : Indicative value due to few reported values

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

	Median pg/g	Mean pg/g	SD pg/g	RSD %	Min pg/g	Max pg/g	Reporting laboratories
Breastmilk fresh weight							
PCDD/PCDF TEQ	0.15	0.25	0.57	232	0.072	4.5	68
Non-ortho PCB TEQ	0.071	0.11	0.31	287	0.00076	2.6	66
Mono-ortho PCB TEQ	0.086	0.15	0.53	350	0.00049	4.4	67
Total TEQ	0.31	0.50	1.4	274	0.12	11	68
Sum indicator PCB	1992	2060	991	48	9.7	7659	52
Sum BDE without BDE 209	57	755	3952	524	34	22769	33
Pork fresh weight							
PCDD/PCDF TEQ	0.030	0.073	0.11	151	0.0060	0.59	71
Non-ortho PCB TEQ	0.0074	0.020	0.043	216	0.00080	0.22	70
Mono-ortho PCB TEQ	0.0048	0.0091	0.014	153	0.00092	0.10	69
Total TEQ	0.047	0.10	0.15	145	0.011	0.84	72
Sum indicator PCB	225	410	806	197	61	6000	55
Sum BDE without BDE 209	897	885	192	22	346	1365	32
Trout fresh weight							
PCDD/PCDF TEQ	0.78	1.1	2.5	236	0.052	23	79
Non-ortho PCB TEQ	2.3	2.3	0.73	32	0.034	5.8	79
Mono-ortho PCB TEQ	0.85	0.87	0.36	42	0.012	2.9	79
Total TEQ	3.9	4.2	2.7	66	0.41	26	80
Sum indicator PCB	26570	27057	10595	39	405	81240	62
Sum BDE without BDE 209	88956	84668	27034	32	8468	121187	38

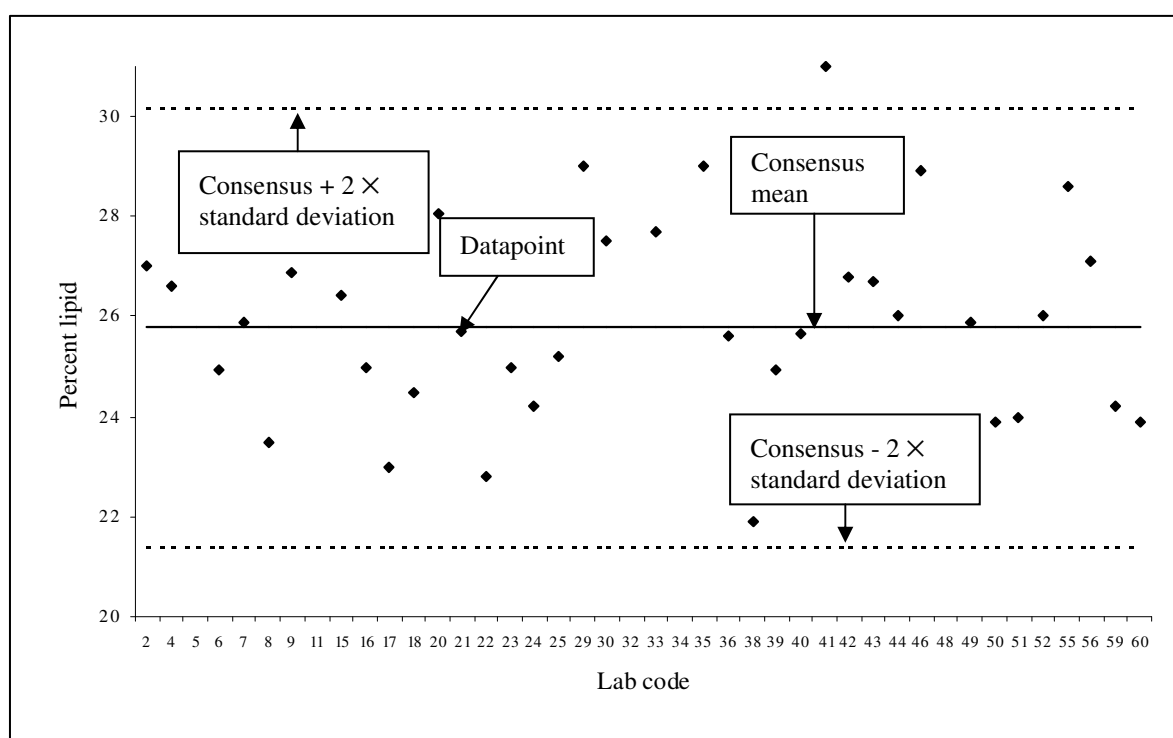
TEF1998

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); σ = target value for standard deviation. A σ 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 meat

Lab code	% lipid	Notes	Lab code	% lipid	Notes	Lab code	% lipid	Notes
1	20.2		70	18.5				
3	17.7		71	17.4				
6	17.5		73	17.4				
7	16.8		78	17.1				
8	17.5		79	53.7	outlier			
9	18.0		80	14.3				
11	18.4		81	24.0				
14	18.0		82	15.7				
15	17.0		84	5.3	outlier			
16	17.2		87	17.9				
18	17.4		88	18.6				
19	16.2		89	17.5				
20	17.5		90	17.6				
23	20.0		92	17.6				
24	18.8		94	17.1				
25	16.5		95	19.7				
27	17.1		96	17.9				
29	17.5		98	20.0				
30	18.9		102	14.0				
31	21.6		105	26.0				
32	20.2		107	17.6				
33	17.5		108	17.0				
34	17.6		109	15.6				
36	11.6		110	15.1				
37	4.0	outlier	111	16.7				
38	18.3		113	16.7				
39	16.0		114	18.0				
40	22.2		117	17.6				
43	18.2		118	18.0				
44	17.4		119	16.7				
46	18.8							
48	16.8							
49	17.4							
53	18.2							
54	18.0							
55	17.5							
56	18.0							
57	19.6							
59	17.7							
60	18.6							
63	16.5							
64	18.9							
65	16.5							
66	18.1							
68	18.3							
69	16.8							

Mean	Standard deviation	Relative standard deviation	Median
17.8	1.97	11.1	17.6

Lipid determination for Breast milk

Lab code	% lipid	Notes	Lab code	% lipid	Notes	Lab code	% lipid	Notes
3	3.5		80	3.4				
4	3.5		81	5.0	outlier			
6	3.5		82	3.3				
7	3.8		84	3.2				
8	3.7		85	3.9				
9	3.0		87	3.2				
10	2.3		88	4.4				
11	3.6		89	3.3				
15	3.8		92	3.3				
16	2.9		93	4.1				
18	3.4		94	3.5				
19	3.9		95	3.0				
20	3.5		96	3.5				
24	3.7		98	3.9				
25	2.7		102	2.5				
27	3.3		107	2.9				
28	3.5		108	3.0				
29	3.1		109	3.7				
30	3.5		110	2.8				
32	3.1		111	3.5				
33	3.5		113	0.9	outlier			
34	3.2		114	3.7				
36	3.4		116	2.8				
37	1.6	outlier	117	3.9				
38	3.5		118	3.8				
39	2.8							
43	3.3							
44	3.6							
46	3.8							
49	3.4							
53	3.1							
55	3.2							
56	3.6							
57	3.6							
59	1.5	outlier						
60	3.8							
63	3.5							
64	3.7							
65	2.7							
66	3.4							
68	4.1							
69	3.5							
70	3.6							
73	3.2							
76	3.3							
79	3.4							

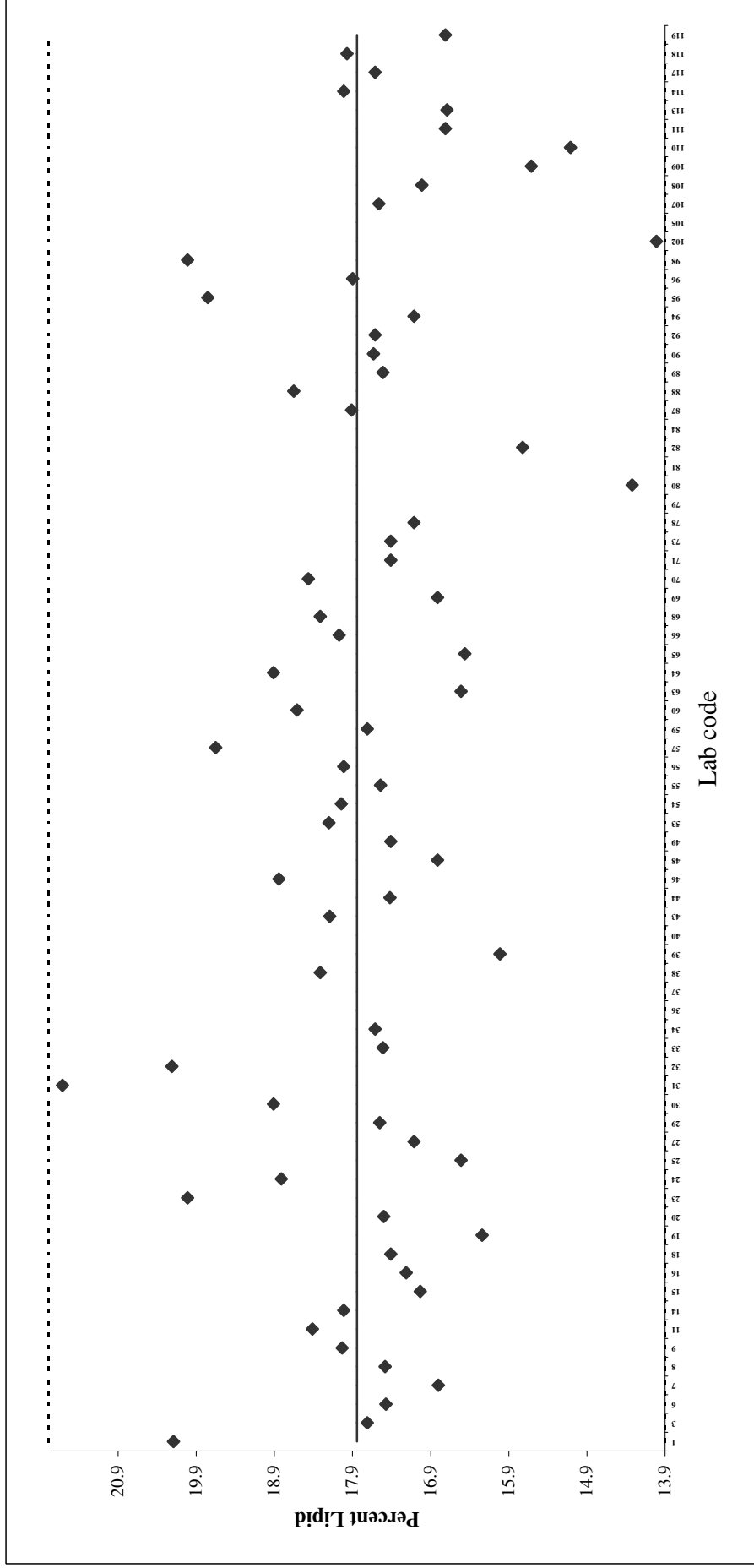
Mean	Standard deviation	Relative standard deviation	Median
3.4	0.39	11.4	3.5

Lipid determination for Trout

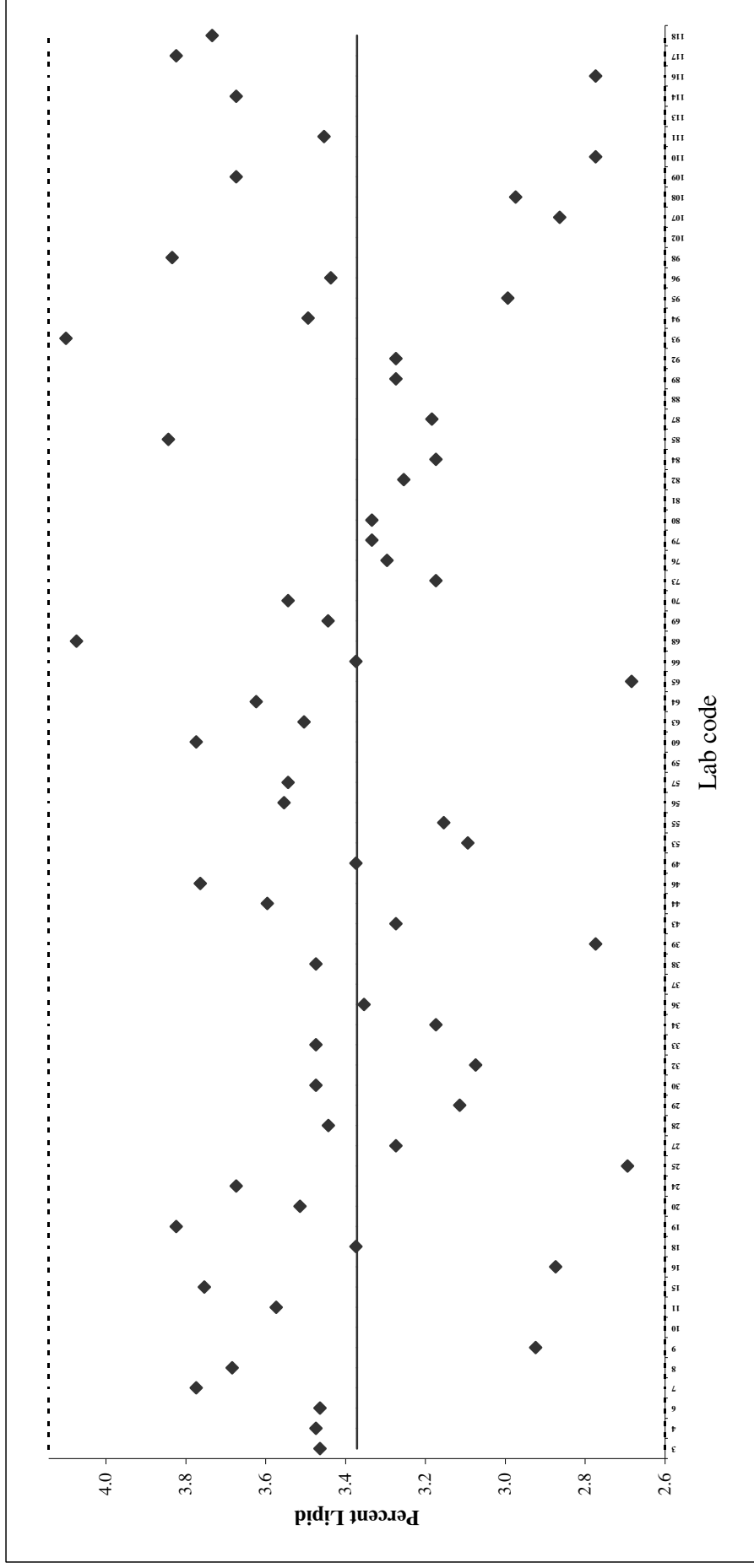
Lab code	% lipid	Notes	Lab code	% lipid	Notes	Lab code	% lipid	Notes
1	3.9		64	5.4				
2	17.6	outlier	65	4.7				
3	5.2		66	5.6				
4	5.1		68	5.6				
6	2.4		69	10.9	outlier			
7	5.3		70	4.9				
8	4.1		71	2.7				
9	5.6		73	5.8				
10	5.0		78	5.3				
11	4.6		79	19.6	outlier			
12	5.2		80	4.4				
15	4.2		81	3.9				
16	5.1		82	2.9				
18	5.6		84	5.3				
19	5.5		85	4.2				
20	5.3		86	2.6				
23	3.5		87	5.2				
24	5.5		88	3.6				
25	5.0		89	4.8				
27	5.5		90	5.3				
29	4.5		92	4.9				
30	5.6		94	4.3				
31	5.0		95	5.5				
32	5.5		96	5.2				
33	5.3		97	3.8				
34	4.3		98	6.5				
36	0.6		99	4.9				
37	2.1		102	2.5				
38	4.1		105	3.0				
39	4.6		107	4.3				
40	5.9		108	4.5				
43	5.6		109	5.7				
44	4.9		110	4.5				
46	5.6		111	4.5				
48	5.1		113	4.4				
49	5.0		114	6.0				
51	8.5		117	5.4				
52	4.6		118	5.8				
53	4.7		119	4.0				
54	5.3							
55	5.6							
56	5.2							
57	4.8							
59	4.7							
60	5.4							
63	5.0							

Mean	Standard deviation	Relative standard deviation	Median
4.8	1.08	22.8	5.0

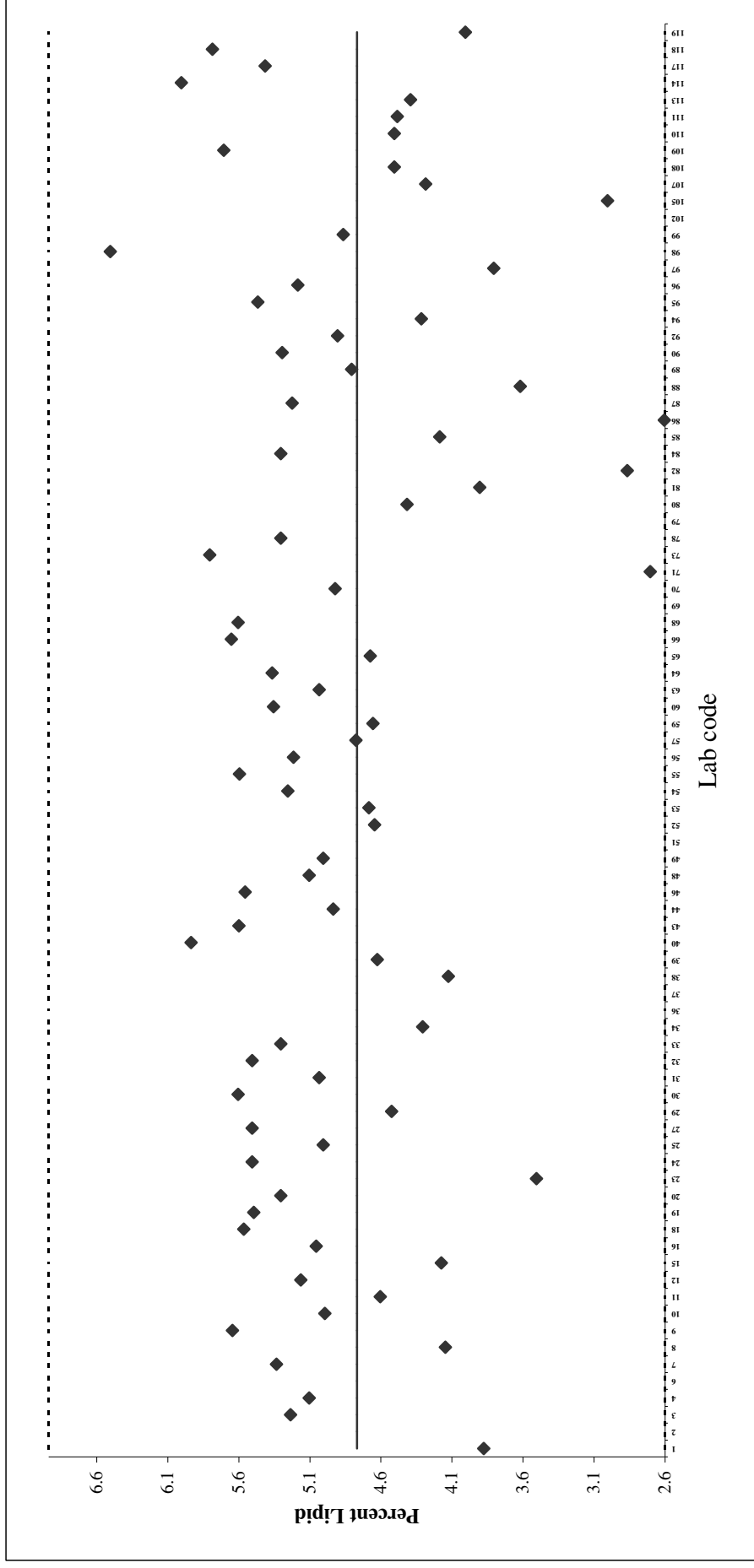
Lipid determination; Pork meat



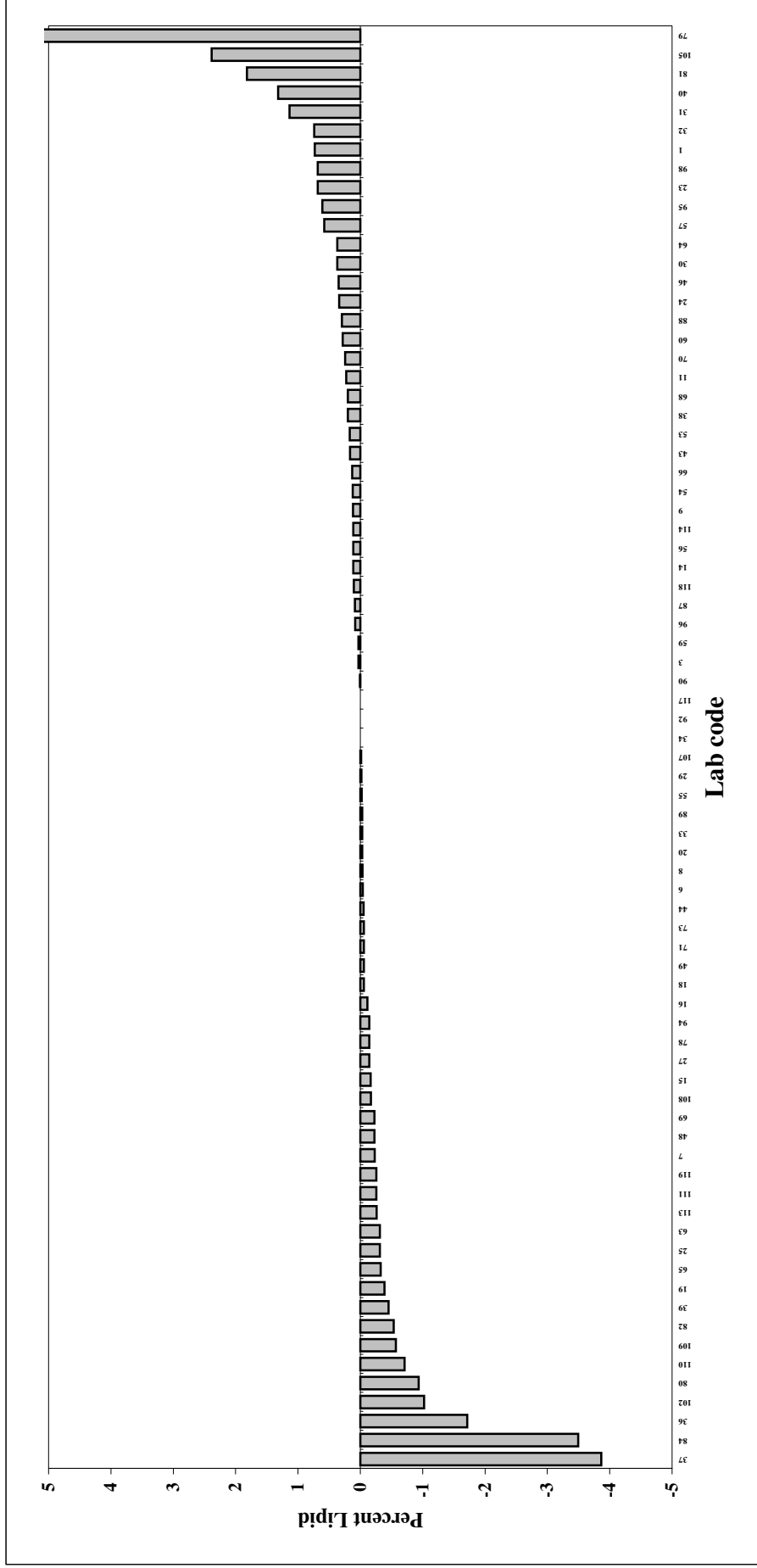
Lipid determination; Breast milk



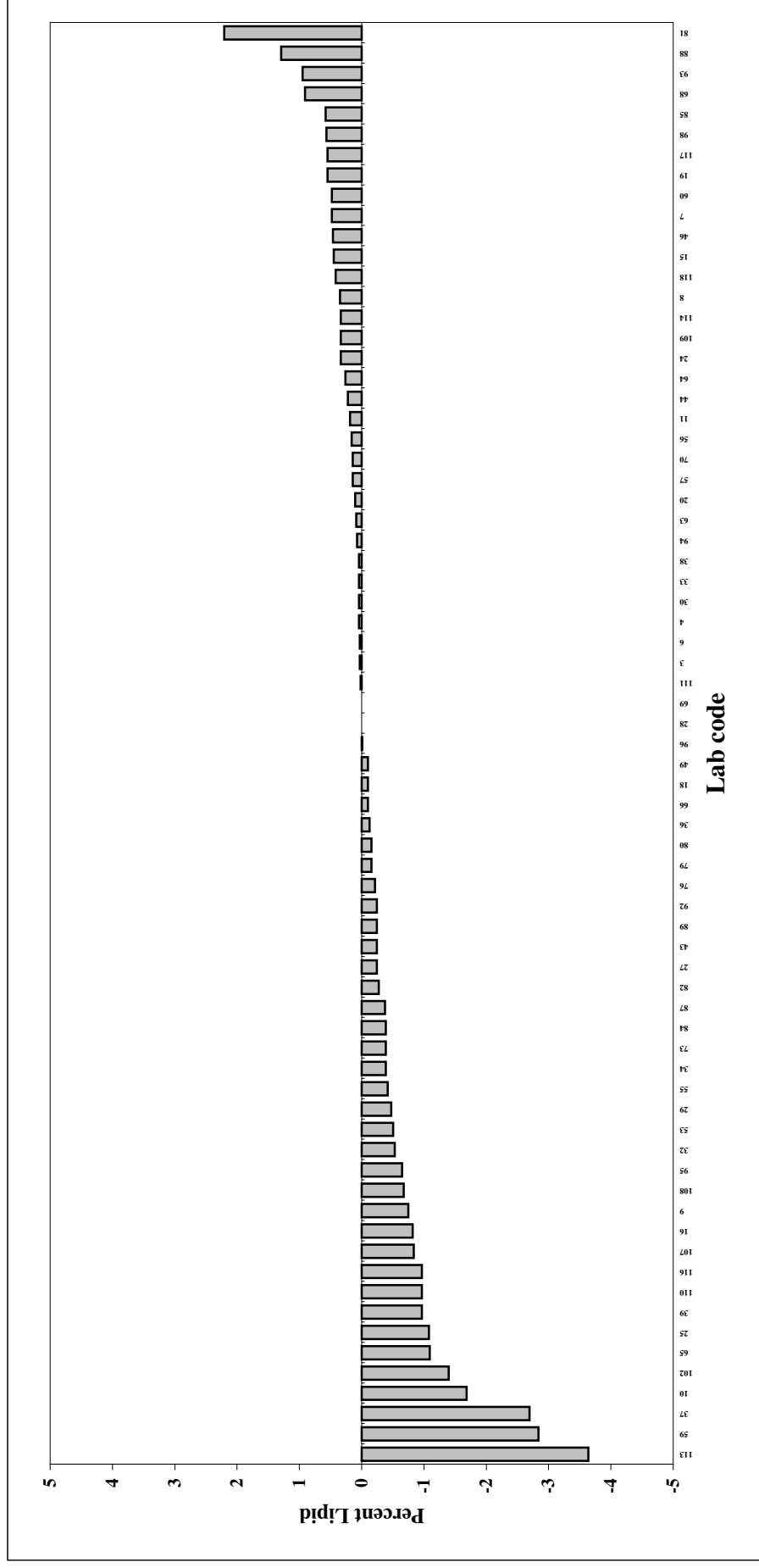
Lipid determination; Trout



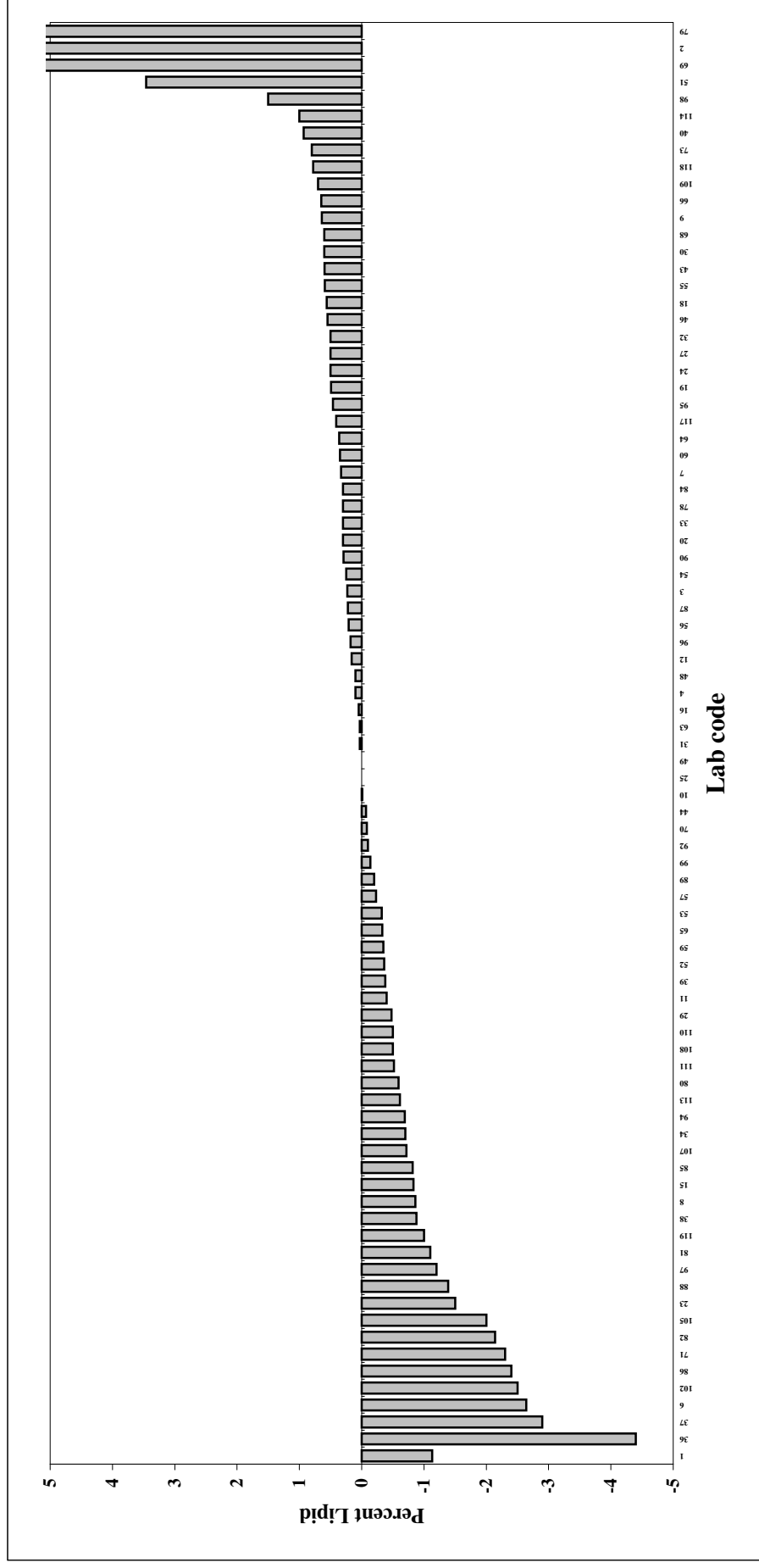
Z-score lipid determination; Pork meat



Z-score lipid determination; Breast milk



Z-score lipid determination; Trout



Laboratories Z-scores: Analyte solution

LABCODE:	Sum TE PCDD/PCDF	Sum TE non- ortho PCB	Sum TE mono-orto PCB	Sum TE totalt	Sum Indicator PCB	Sum u/209	Sum m/209
1	-0.070	0.030	0.37	-0.057	-0.34		
2	-0.34	-0.33	0.41	-0.33	0.31		
3	-0.29	-0.25	0.15	-0.29	-0.27	-0.23	
4	-0.33	-0.17	0.073	-0.31	-0.13	-0.37	-0.25
6	-0.16	-0.25	-0.24	-0.17	-0.26	0.41	0.59
7	-0.31	-0.71	-0.83	-0.35	-3.2		
8	-0.17	-0.15	1.3	-0.15	3.1	1.3	-0.26
9	-0.24	-0.13	-1.1	-0.25	-0.10		
10	0.19	-0.68	-0.68	0.11			
11					-0.43		
14	1.4	0.069	0.55	1.3	-0.084		
15	-0.020	0.19	0.043	-0.0031	-0.22	0.10	0.091
16	-0.32	0.39	0.20	-0.26			
18	-0.079			-0.51*		0.11	0.063
19	-0.031	-0.37	0.19	-0.053			
20	-0.27	0.85	0.18	-0.18	0.079		
24	-0.30	1.4	0.55	-0.16	0.51		
25	-0.24	0.28	0.45	-0.19	-0.22		
27	-0.075	0.25	0.13	-0.048			
28	-0.36	0.038	-0.44	-0.33	-0.27		
29	0.11	0.091	0.25	0.11	0.12	-0.049	
30	-0.32	-0.39	-0.53	-0.33	-0.18	0.066	-0.064
31	-0.13	0.14	0.16	-0.11			
32	-0.032	0.44	0.13	0.0048	0.20	-0.058	0.037
33	0.19	1.6	1.4	0.32			
34	41	0.83	0.29*	37*			
36	-0.10	0.032	0.11	-0.086			
37	-0.43	0.50	0.50	-0.35	-0.24		
38	-0.15	0.045	-0.21	-0.14	0.071	-0.39	-0.39
39	-0.030	-0.14	-0.0090	-0.038	-0.12		
40	0.030	-3.7	-3.7	-0.29			
43	-0.0090	-0.22	1.0	-0.011	-0.17	-0.072	-0.046
44	0.065	-0.085	0.49	0.059	0.49	-0.21	-0.34
46	-0.40	-0.34	0.048	-0.39		0.12	0.13
48		-0.10	0.32	-4.6*	-0.39		
51	0.65	0.18	0.069	0.61		0.86	
52					0.13	-0.34	
53	-0.023	-0.24	-0.20	-0.041	-0.35	0.042	
55	0.20	-0.10	0.56	0.18			
56	0.10	0.72	0.79	0.16	0.25	0.092	0.24

* These values are based on determination of a limited number of congeners

Laboratories Z-scores: Analyte solution

LABCODE:	Sum TE PCDD/PCDF	Sum TE non- ortho PCB	Sum TE mono-orto PCB	Sum TE totalt	Sum Indicator PCB	Sum u/209	Sum m/209
57	-0.25	0.10	0.46	-0.22	0.60	-0.20	-0.15
59	-0.055	-0.18	0.57	-0.056	-0.072		
60	0.011	-0.012	0.021	0.0091			
64	-0.011	-0.0062	0.0083	-0.011			
65	-0.43	-0.25	0.37	-0.41	-0.75		
66	-0.20	-0.11	0.14	-0.19	-0.27	-0.043	0.043
68	-0.093	-0.49	-0.032	-0.12	0.10	0.29	
69	0.018	0.53	-0.45	0.050	0.57		
70	0.24	0.89	0.48	0.29	0.38	-0.34	-0.28
71	-3.3		-0.72	-3.4*	-0.95		
73	0.37	-0.021	-0.63	0.33	-0.034		
76	0.30	-0.28	0.25	0.26	-0.37	-0.23	-0.064
78					0.36	-0.11	-0.068
79	-0.78	-0.37	0.77	-0.73	-0.69		
80	-0.19	0.18	0.62	-0.15	0.18	-0.078	-0.050
82	0.14	0.26	-0.14	0.15			
84	-0.21	0.068	0.17	-0.19	-0.27	0.38	0.50
85	-0.63	0.24	0.10	-0.55		0.21	0.0036
87	0.14	0.091	0.17	0.14	-0.080		
88	-0.14	0.042	0.10	-0.13	0.39		
89	-0.040	0.46	0.51	0.0036	0.18	1.1	
90	-0.32	0.51	0.59	-0.25	-0.082		
92	0.14	0.19	0.56	0.15	0.00	-0.50	
94					-0.030	0.064	0.18
95	-0.23	0.36	0.70	-0.18	0.45	-0.27	-0.32
96	-0.16	0.060	0.26	-0.14	-0.32	-0.22	-0.27
97	-0.29	-0.057	0.0034	-0.27	0.42	-0.44	
98	-0.27	-0.071	0.10	-0.25	0.23		
99	-0.32	0.15*	-0.64*	-0.29*	-0.13	-0.50*	
102	-0.44	-0.37	0.10	-0.43	-0.37	0.41	0.36
105	-0.26	-0.16	-0.28	-0.26	0.73		
107	-0.31	-0.47	0.38	-0.31	0.13	-0.34	0.52
108	0.040	-0.23	0.26	0.022	0.31		
109	-1.0	-0.19	-0.84	-0.97	-0.090	-0.11	-0.23
110	-0.11	0.23	-0.079	-0.088	-0.048		
111	0.18	-0.033	0.39	0.17	0.79	0.11	0.10
113	-0.20	0.36	0.43	-0.15			
114	0.20	0.67	0.37	0.24	0.10	0.32	0.23
116	-0.46	-0.090	0.80	-0.41			
117	0.016	0.059	0.44	0.025	0.48	0.13	-0.24
118	0.31	1.1	0.71	0.37	1.3		
119	0.078	0.21	0.079	0.087	-0.48		

* These values are based on determination of a limited number of congeners

Laboratories Z-scores: Pork

LABCODE:	Sum TE PCDD/PCDF	Sum TE non- ortho PCB	Sum TE mono-orto PCB	Sum TE totalt	Sum Indicator PCB	Sum u/209	Sum m/209
1	55	182	3.4	72	1.4		
3	20	14	2.8	17	1.1	0.13	
6	1.2	-0.65	-2.0	0.42	0.029	0.68	
7	12	0.58	12	10	0.12		
8	21	-0.81	0.040	14	2.5	2.7	2.6
9	2.7	5.3	0.48	2.9	0.79		
11					28		
14	4.6	10	2.9	5.4	2.6		
15	1.1	2.5	2.8	1.6	3.8	1.6	1.8
16	-0.45	4.6	13	2.4			
18	-2.0	-1.4	-0.58	-1.7		-0.25	-0.30
19	32	0.39	8.6	22			
20	-2.2	-1.2	-0.21	-1.7	-0.54		
23	144			137*			
24	-0.40	0.36	-0.25	-0.24	0.36		
25	17	1.5	1.8	12	-1.3		
27	-1.7	-1.8	-0.42	-1.6			
29	-3.5	-4.0	-0.13	-3.1	-0.88	-0.13	
30	-1.9	-2.1	-0.33	-1.7	-0.96	-0.10	-0.084
31	-0.16	19	22	6.5			
32	0.22	4.9	-0.032	1.1	-0.42	-0.85	-0.82
33	0.31	1.9	1.3	0.74			
34	104	169	2.7*	102*			
36	42	25	46	40			
37	12	3.2	-0.15	8.9	-0.56		
38	8.5	1.2	3.3	6.4	6.7	-3.0	-2.9
39	-1.8	2.7	-0.11	-0.74	0.92		
40	1.5	-1.8	2.3	1.0			
43	4.4	-1.9	-0.28	2.5	-0.47	-0.16	-0.22
44	-1.4	0.19	2.3	-0.61	3.4	-0.013	0.31
46	-1.5	-2.2	-1.1	-1.6		0.23	0.45
48		25	21	4.4*	1.5		
49	6.5	-1.0	-0.12	4.1	0.026		
53	2.2	2.5	0.11	2.0	1.4	0.15	
54	18	2.4	-0.20	13			
55	2.4	9.8	1.1	3.6			
56	-1.8	2.3	0.83	-0.64	0.59	0.28	0.77
57	10	-2.0	-0.70	6.3	-0.35	-0.066	
59	12	6.2	1.0	9.1	2.1		
60	4.4	6.7	19	6.8			

* These values are based on determination of a limited number of congeners

Laboratories Z-scores: Pork

LABCODE:	Sum TE PCDD/PCDF	Sum TE non- ortho PCB	Sum TE mono-orto PCB	Sum TE totalt	Sum Indicator PCB	Sum u/209	Sum m/209
63	14	14	5.4	13			
64	16	2.7	4.3	12			
65	3.6	14	0.43	5.1	9.7		
66	-0.036	1.2	-0.28	0.18	-0.59	0.037	0.47
68	16	-0.017	-0.41	11	-0.30	-0.57	
69	1.6	-1.5	2.7	1.1	-0.51		
70	0.21	2.5	0.21	0.65	0.084	-2.2	-2.1
71	39	190	71	72	138		
73	-1.3	5.8	5.4	0.98	20		
78					1.7	0.47	3.8
79	26	51	15	29	22		
80	4.8	-1.2	0.41	3.1	0.62	0.27	0.19
82	6.1	-0.32	-0.045	4.0			
84	-2.4	-1.3	-0.38	-1.9	-1.6	0.32	0.26
87	0.29	-0.10	-0.18	0.15	-0.40		
88	-0.46	-4.3	-3.9	-1.7	-3.5		
89	-2.2	1.9	1.1	-0.94	3.2	0.58	
90	-1.0			-2.3*			
92	-2.5	0.63	1.1	-1.4	0.21	-0.89	
94					0.36	0.20	0.48
95	0.82	4.4	-0.46	1.3	-0.14	-0.56	
96	-0.082	-1.8	-0.60	-0.48	-1.1	0.17	
98	5.4	84	7.8	21	-1.1		
102	50	-2.3	0.32	33	0.31	-0.48	-0.45
105	67	32	1.5	51	9.3		
107	124	-2.6		82*		-1.1	-0.50
108	-1.9	-3.8	0.92	-1.9	0.12		
109	7.0	17	13	9.7	9.8	2.6	3.4
110	3.7	1.9	0.96	3.0	1.1		
111	-0.82	1.6	2.7	0.12	0.88	0.21	0.44
113	1.3	-1.5	0.16	0.59			
114	3.6	-0.20	111	18	0.0056	0.50	0.46
117	2.1	-1.8	-0.34	1.0	-0.86	-0.33	-0.31
118	10	0.047	0.20	6.7	0.048		
119	32	1.9	19	24	2.2		

* These values are based on determination of a limited number of congeners

Laboratories Z-scores: Breastmilk

LABCODE:	Sum TE PCDD/PCDF	Sum TE non- ortho PCB	Sum TE mono-orto PCB	Sum TE totalt	Sum Indicator PCB	Sum u/209	Sum m/209
3	1.6	-0.055	-0.11	0.74	0.23	2.0	
4	-0.40	0.32	0.40	-0.0086	-0.048	-1.0	-1.0
6	0.34	0.51	-0.31	0.20	-0.35	2.3	
7	-0.075	0.18	0.48	0.14	1.1		
8	0.70	-1.1	1.2	0.42	4.4	2.2	1.9
9	-0.35	-0.11	-0.093	-0.22	0.12		
10	4.1	1.3	0.66	2.5			
11					15		
15	1.1	0.17	0.41	0.69	-0.0063	0.40	0.043
16	-0.30	-0.019	0.17	-0.10	0.50		
18	-0.38	0.17	0.068	-0.13		-0.51	-0.59
19	1.6	1.3	4.9	2.5			
20	-0.12	0.82	0.17	0.18	0.64		
24	0.28	1.5	0.17	0.53	0.13		
25	-2.2	-0.68	-1.5	-1.6	-2.7		
27	0.59	1.5	0.91	0.89			
28	0.45	-3.8	6.5	1.1	2.1		
29	-0.013	0.51	0.11	0.14	-0.18	1.2	
30	-0.0076	-0.079	-0.67	-0.21	-0.61	-0.34	0.076
32	-0.82	-0.59	-0.68	-0.73	-1.0	-1.0	-0.50
33	0.61	1.1	-0.0038	0.55			
34	-0.065	1.6	0.35*	0.44*			
36	2.2	-1.3	-0.51	0.59			
37	4.1	0.57	1.0	2.4	0.80		
38	-1.5	-0.65	-1.2	-1.2	-0.91	-1.8	-1.0
39	-1.0	1.1	-0.21	-0.31	-0.0065		
43	-1.0	-0.38	1.0	-0.29	0.30	-0.45	-0.30
44	0.21	-0.075	0.63	0.26	0.18	0.29	1.7
46	-0.50	-0.38	-0.25	-0.40		-0.21	1.4
49	-0.77	0.11	0.32	-0.26	0.21		
53	-0.55	-0.35	-0.77	-0.56	1.4	1.7	
55	-0.24	0.60	-0.75	-0.18			
56	0.62	0.52	1.1	0.73	0.61	0.21	-0.27
57	0.13	-1.1	-0.029	-0.20	0.57	0.67	
59	-2.5	-2.6	-2.6	-2.6	-2.8		
60	0.68	0.75	0.87	0.75			
63	-0.44	-0.19	-0.24	-0.32			
64	66	-0.24	-1.1	32			
65	0.94	-0.45	-0.20	0.29	-1.2		
66	0.12	-0.0013	-0.067	0.041	-0.59	14	35

* These values are based on determination of a limited number of congeners

Laboratories Z-scores: Breastmilk

LABCODE:	Sum TE PCDD/PCDF	Sum TE non- ortho PCB	Sum TE mono-orto PCB	Sum TE totalt	Sum Indicator PCB	Sum u/209	Sum m/209
68	-0.10	0.041	-0.58	-0.20	2.0	0.78	
69	0.36	0.12	-0.093	0.18	0.71		
70	3.0	-0.68	0.020	1.3	1.0	0.68	0.61
73	0.40	-0.027	-0.22	0.12	0.36		
76	0.40	1.3	1.7	1.0	1.6	0.17	1.7
79	0.86	7.7	4.2	3.4	3.8		
80	2.0	0.38	0.65	1.3	1.0	2136	1938
82	0.24	-2.3	-2.6	-1.1			
84	-1.0	-0.86	-0.55	-0.85	-0.87	-0.42	-0.42
85	-0.95	-0.36	0.45	-0.42		2.0	1.8
87	-0.10	-0.53	-0.26	-0.25	-0.21		
88	0.91	-4.8	-4.8	-2.0	-4.8		
89	-0.91	0.11	-0.49	-0.55	-0.52	13	
92	-0.12	-0.025	-0.26	-0.14	-0.59	-0.20	
93	12		1.2	5.2*			
94					0.51	0.35	-0.15
95	-0.31	-0.36	0.48	-0.10	0.20	-1.0	
96	-0.12	-0.0082	0.12	-0.025	-0.25	1.1	
98	-2.5	-1.3	3.1	-0.62	1.0		
102	0.22	-4.9	-5.0	-2.5	-5.0	0.58	1.0
107	1.0	-0.49	0.56	0.51	1.2	-1.1	13
108	0.88	1.6	1.2	1.1	1.1		
109	-0.90			-3.0*			
110	-1.0	0.92	-0.24	-0.35	-0.0070		
111	0.38	0.47	1.4	0.70	0.59	1.1	0.55
113	-0.095	0.28	0.035	0.030			
114	0.034	0.43	0.44	0.24	0.55	4.4	4.8
116	149	179	259	187			
117	0.66	0.68	0.60	0.65	0.44	0.16	0.19
118	0.31	1.1	0.45	0.53	1.1		

* These values are based on determination of a limited number of congeners

Laboratories Z-scores: Trout

LABCODE:	Sum TE PCDD/PCDF	Sum TE non- ortho PCB	Sum TE mono-orto PCB	Sum TE totalt	Sum Indicator PCB	Sum u/209	Sum m/209
1	-0.21	-3.6	-1.8	-2.6	-2.3		
2	7.7	7.6	12	8.6	11		
3	0.94	-0.041	-0.89	-0.028	0.094	-0.12	
4	-0.21	0.32	0.69	0.30	-0.17	0.33	0.33
6	-2.1	-2.4	-2.6	-2.4	-2.8	-1.9	
7	0.37	0.029	0.84	0.27	1.3		
8	1.5	-0.53	1.1	0.23	5.8	0.30	0.30
9	-0.074	-0.18	-0.036	-0.13	-0.15		
10	2.0	-1.8	0.0059	-0.68			
11					-0.17		
12	0.61	0.80	0.82	0.77			
15	0.57	0.11	0.31	0.24	0.12	-0.69	-0.68
16	-0.018	-0.10	-0.54	-0.18			
18	0.24	0.58	0.63	0.52		-0.19	-0.19
19	1.5	0.46	9.4	2.6			
20	0.21	0.63	0.11	0.43	1.2		
23	3.4			-0.65*			
24	0.51	0.83	-0.091	0.56	0.69		
25	0.15	1.2	0.42	0.83	0.22		
27	0.99	0.97	0.56	0.89			
29	0.71	1.1	0.29	0.85	0.28	-4.5*	
30	0.30	-0.28	-0.23	-0.16	-0.34	1.2	1.2
31	-0.43	-0.37	-0.23	-0.35			
32	0.024	-0.017	0.11	0.019	-0.22	-0.26	-0.26
33	0.36	0.97	0.65	0.78			
34	143	-0.70	0.23*	28*			
36	-2.1	-4.8	-4.6	-4.2			
37	0.55	1.0	1.2	0.97	0.94		
38	-2.4	-2.1	-2.3	-2.2	-1.9	-3.6	-3.6
39	-1.6	-1.5	-1.6	-1.5	-1.5		
40	0.58	0.36	4.1	1.2			
43	-0.066	-0.64	1.2	-0.12	1.4	-1.9	-1.9
44	-0.14	0.0089	-0.74	-0.18	-1.2	-1.8	-1.8
46	-0.20	-0.42	-0.39	-0.37		0.83	0.83
48		0.063	0.14	-0.93*	-0.22		
49	-0.55	0.46	0.74	0.32	1.6		
51	0.40	-0.30	-0.39	-0.18		-3.1*	
52					0.038	0.99*	
53	1.4	1.0	-0.17	0.84	-0.50	-0.36	
54	-1.1	0.49	-0.90	-0.13			
55	-0.40	0.69	0.72	0.48			
56	-0.11	1.4	0.76	0.97	0.53	1.4	1.4
57	1.4	-0.63	-0.28	-0.15	0.023	-1.3	-1.3
59	-0.78	-0.40	-0.26	-0.45	-2.1		
60	-0.10	0.15	0.10	0.093			
63	-0.84	-0.018	-0.58	-0.30			
64	-4.4	-2.7	-2.3	-3.0			
65	0.79	-1.5	-1.1	-0.96	-0.78		
66	0.28	-0.059	-0.065	0.0074	0.84	0.85	0.87
68	0.0057	-0.92	0.14	-0.51	0.72	-0.23	

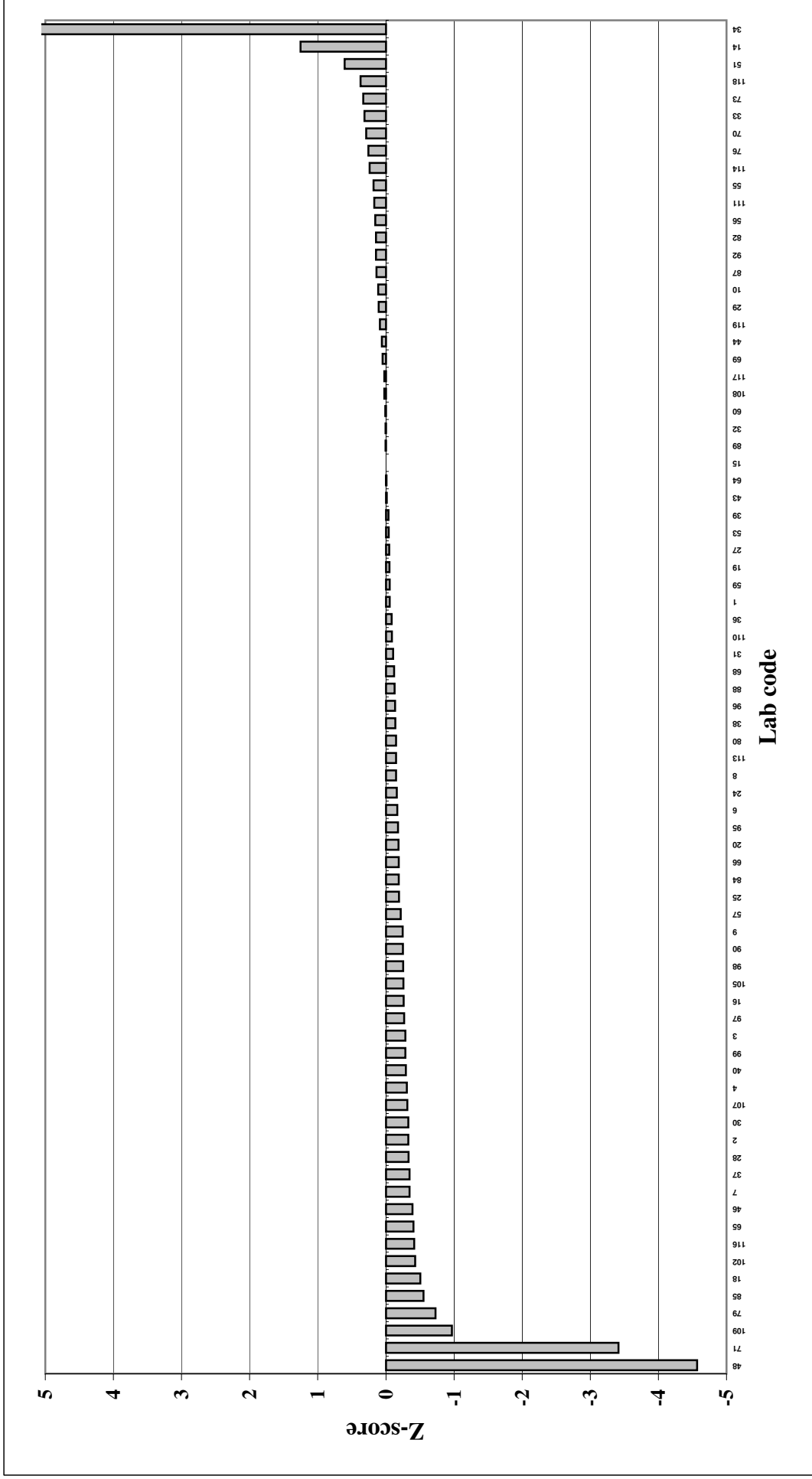
* These values are based on determination of a limited number of congeners

Laboratories Z-scores: Trout

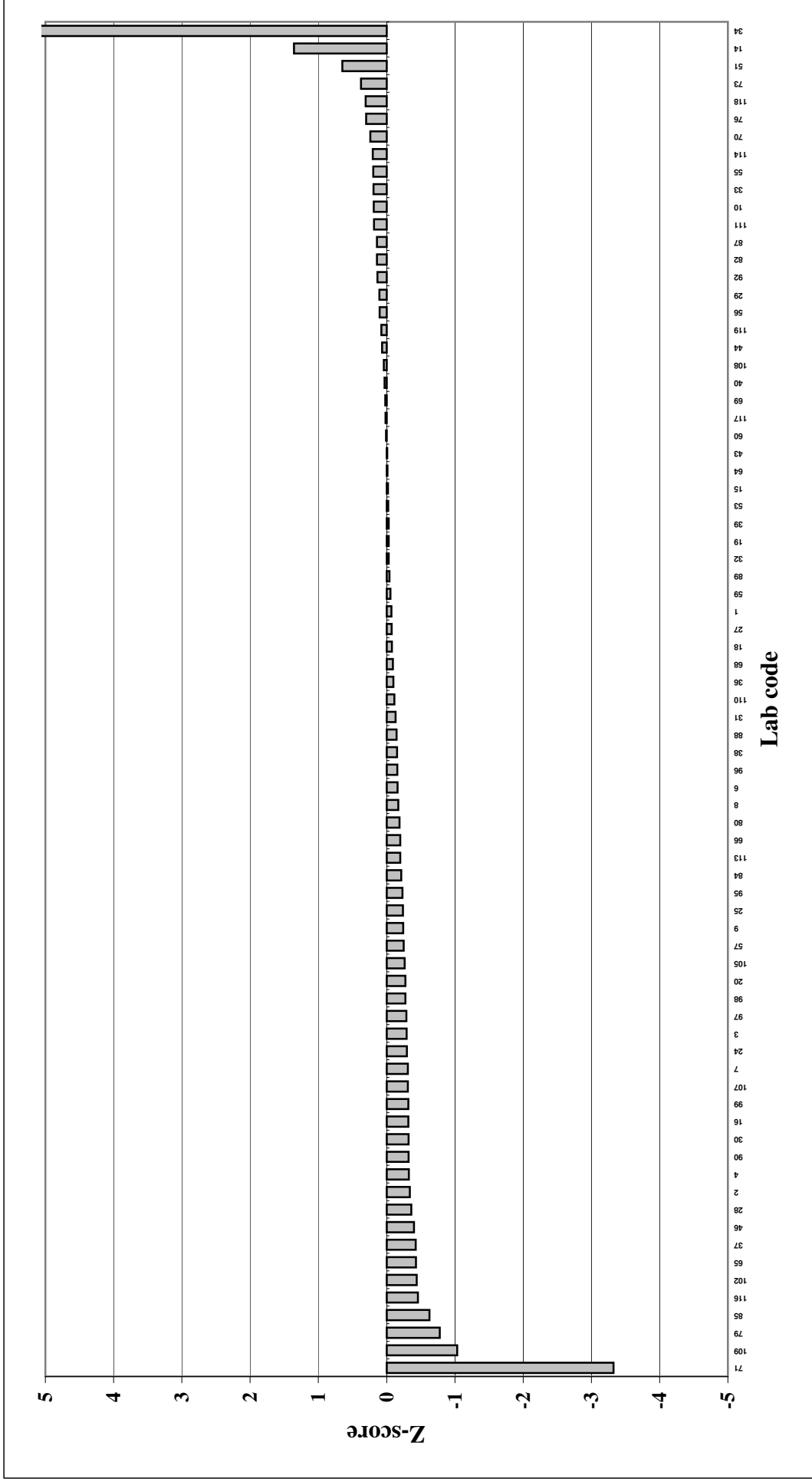
LABCODE:	Sum TE PCDD/PCDF	Sum TE non- ortho PCB	Sum TE mono-orto PCB	Sum TE totalt	Sum Indicator PCB	Sum u/209	Sum m/209
69	-0.14	-0.36	-0.22	-0.29	0.33		
70	0.060	1.9	1.0	1.4	1.9	-1.6	-1.6
71	-2.5	-2.5	-2.3	-2.4	-1.9		
73	0.29	-0.33	-0.51	-0.25	0.76		
78					0.61	1.0	1.0
79	-4.7	-0.44	1.4	-0.89	0.055		
80	0.83	0.55	1.2	0.75	1.3	0.39	0.39
82	0.35	0.18	0.075	0.19			
84	-0.065	0.82	0.50	0.57	0.019	1.6	1.6
85	-1.5	-1.6	-1.4	-1.6		-1.0	-1.0
86	9.5	1.5	1.2	3.0	0.70	-2.4	-2.4
87	-0.23	-0.20	0.33	-0.089	0.53		
88	-2.7	-4.9	-4.9	-4.5	-4.9		
89	-0.81	0.054	-0.20	-0.17	-0.92	-0.33	
90	-0.14	-0.17	0.0091	-0.13	0.68		
92	0.11	0.13	-0.059	0.084	-0.29	0.38	
94					0.50	1.5	1.5
95	0.33	-0.068	-0.32	-0.042	-0.86	0.36	
96	-0.056	-0.042	0.24	0.016	-0.14	-0.11	
97	-0.62	-0.89	-0.25	-0.70	0.91	-1.5	
98	-0.79	-1.3	0.30	-0.83	0.27		
99	0.46	0.32*	-0.88*	0.088*	-0.21	-0.33*	
102	-0.60	0.95	1.5	0.76	4.2	1.2	1.2
105	-1.6	1.3	-2.2	-0.026	-2.9		
107	-0.60	-1.2	0.16	-0.79	-0.0090	-1.2	-1.2
108	0.63	2.0	0.93	1.5	0.65		
109	0.26	2.1	0.071	1.3	0.49		
110	-1.5	-1.6	-1.7	-1.6	-2.2		
111	0.44	2.4	0.96	1.7	0.53	1.5	1.5
113	-0.34	0.06	-0.13	-0.063			
114	-0.25	-0.30	-0.16	-0.26	0.13	-0.089	
117	-0.27	0.26	0.012	0.10	0.0019	0.24	0.24
118	0.57	1.0	0.57	0.84	1.2		
119	0.34	-0.058	-0.61	-0.10	-1.1		

* These values are based on determination of a limited number of congeners

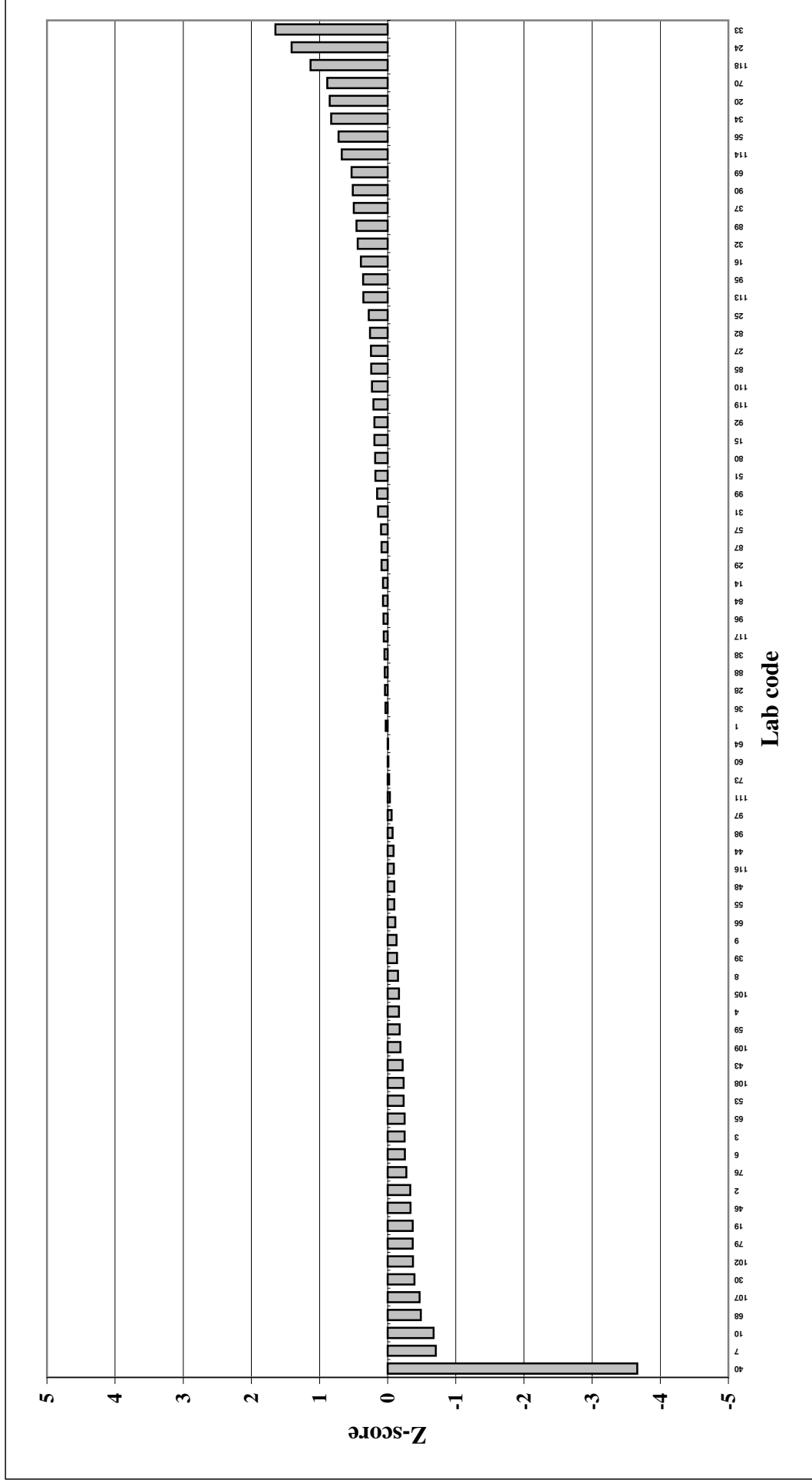
Z-score analyte solution; total TEQ



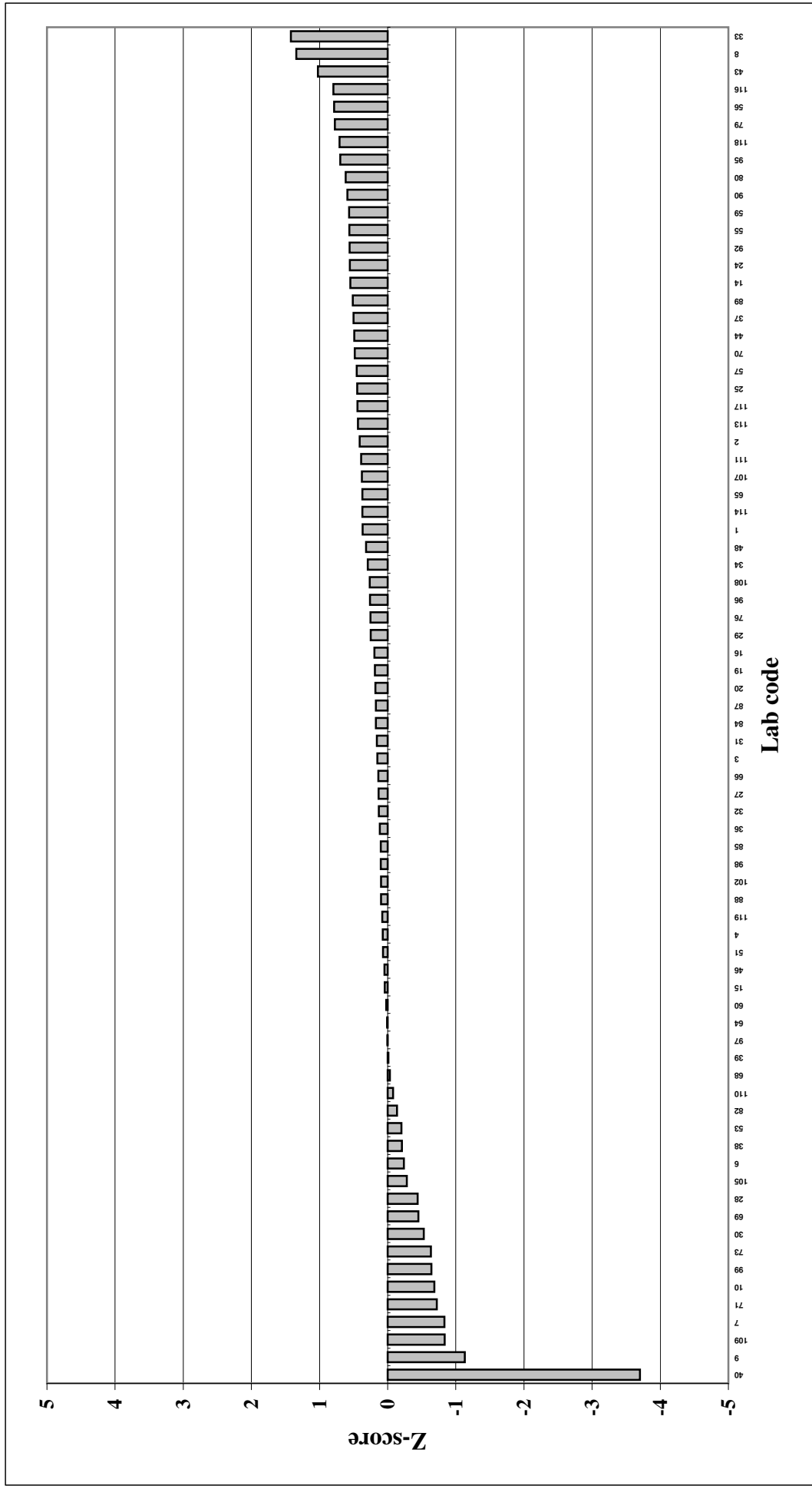
Z-score analyte solution; PCDD/PCDF TEQ



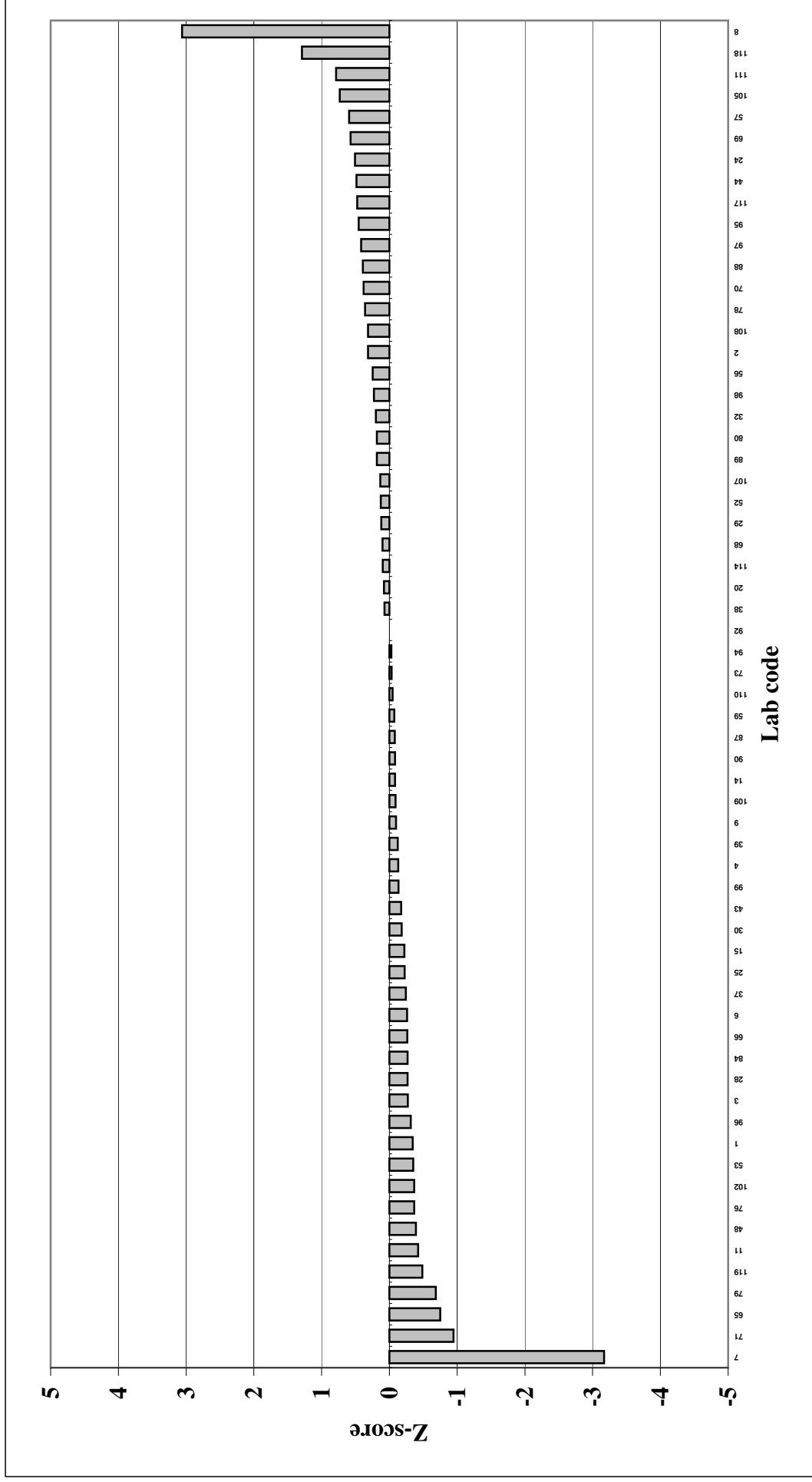
Z-score analyte solution; non-ortho PCB TEQ



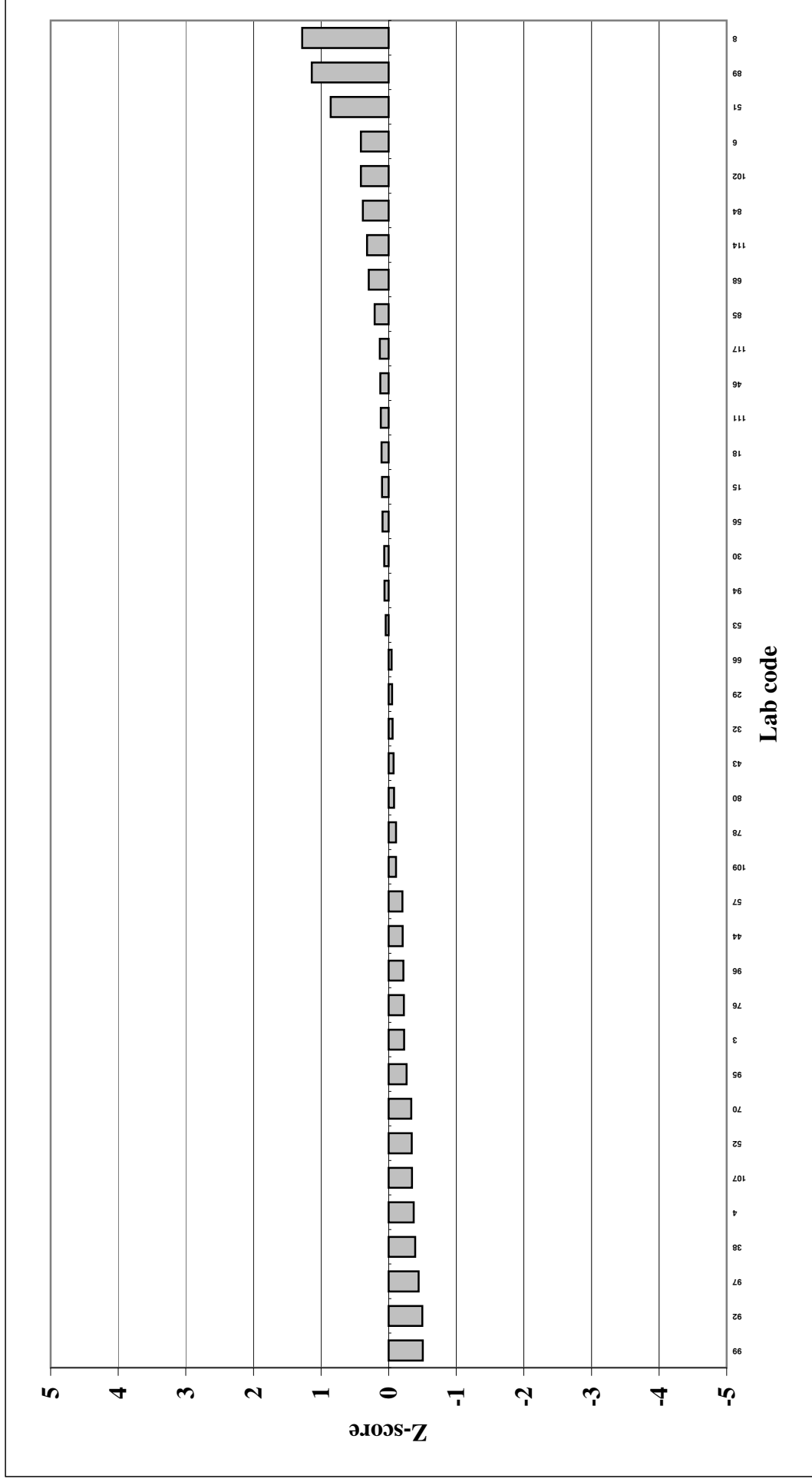
Z-score analyte solution; mono-ortho PCB TEQ



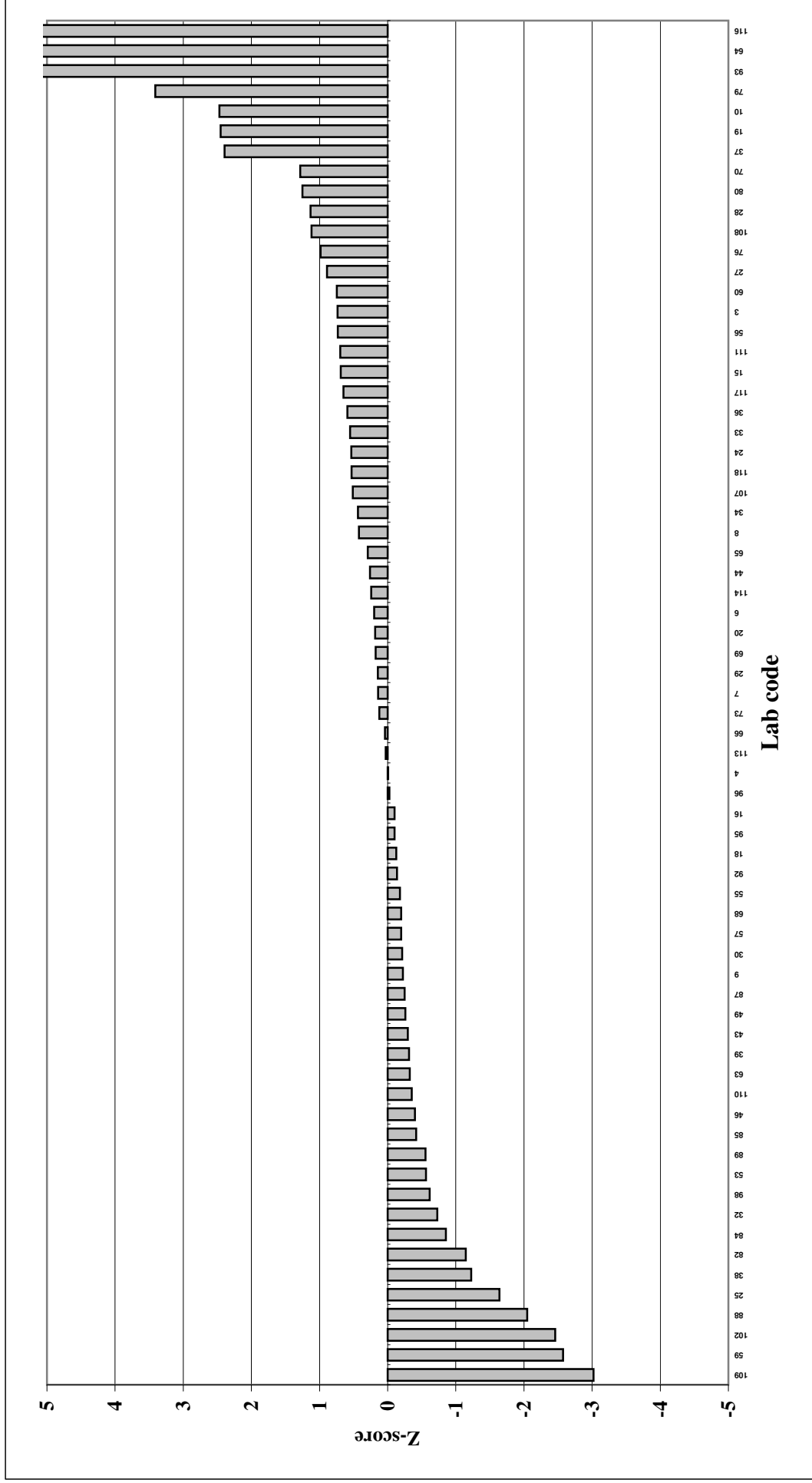
Z-score analyte solution; sum indicator PCB



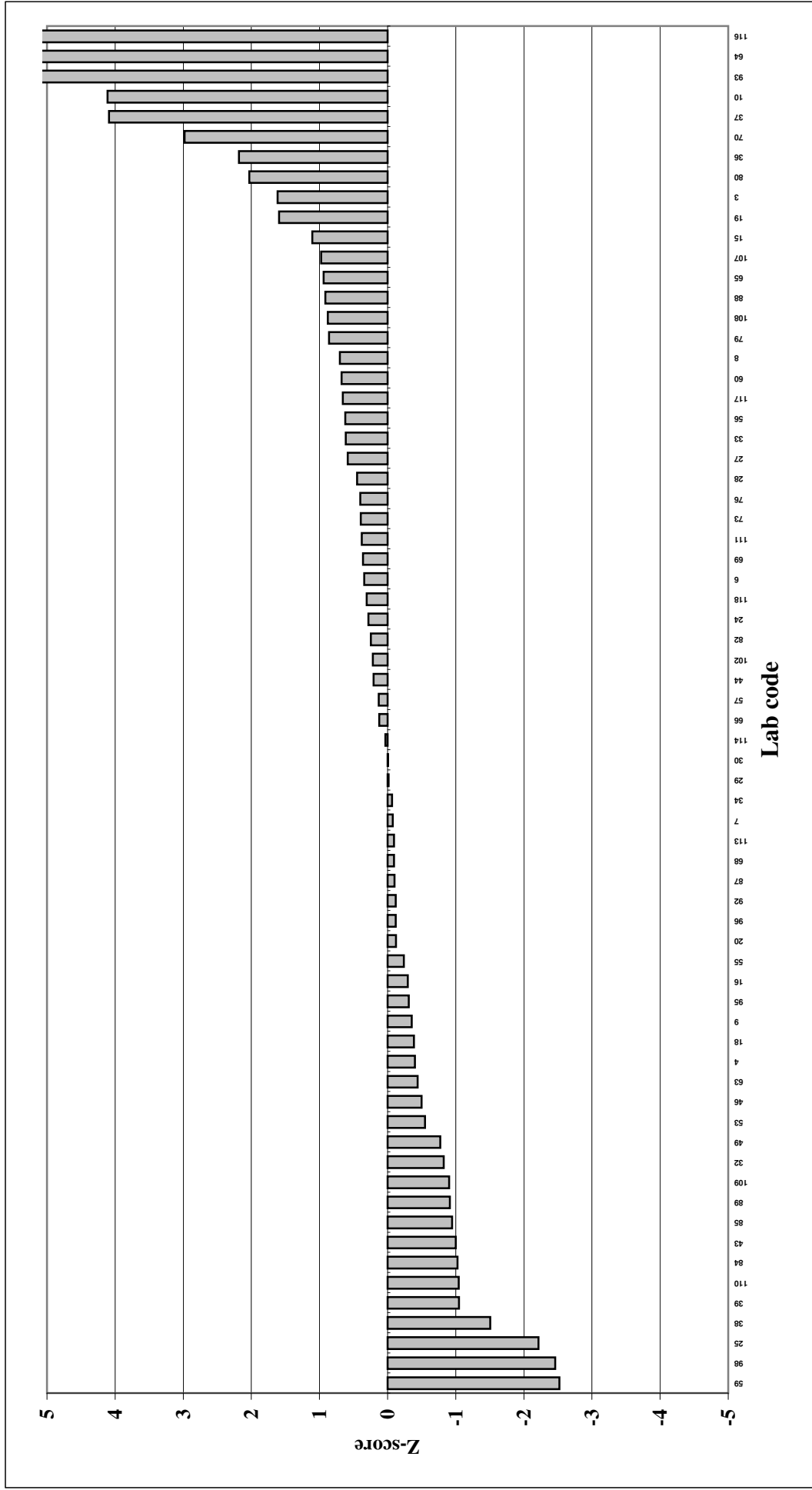
Z-score analyte solution; sum PBDE without BDE-209



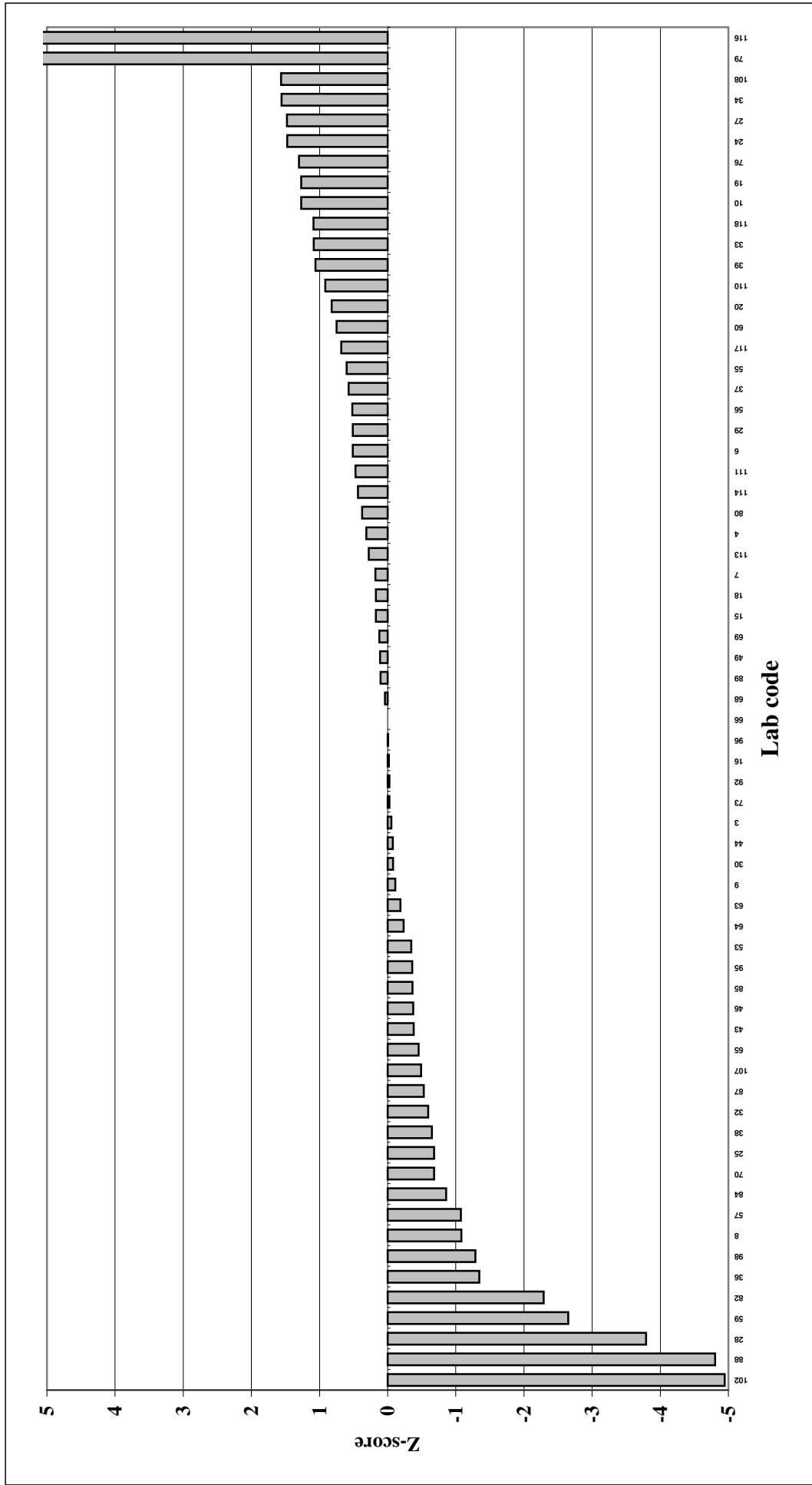
Z-score Breast milk; total TEQ



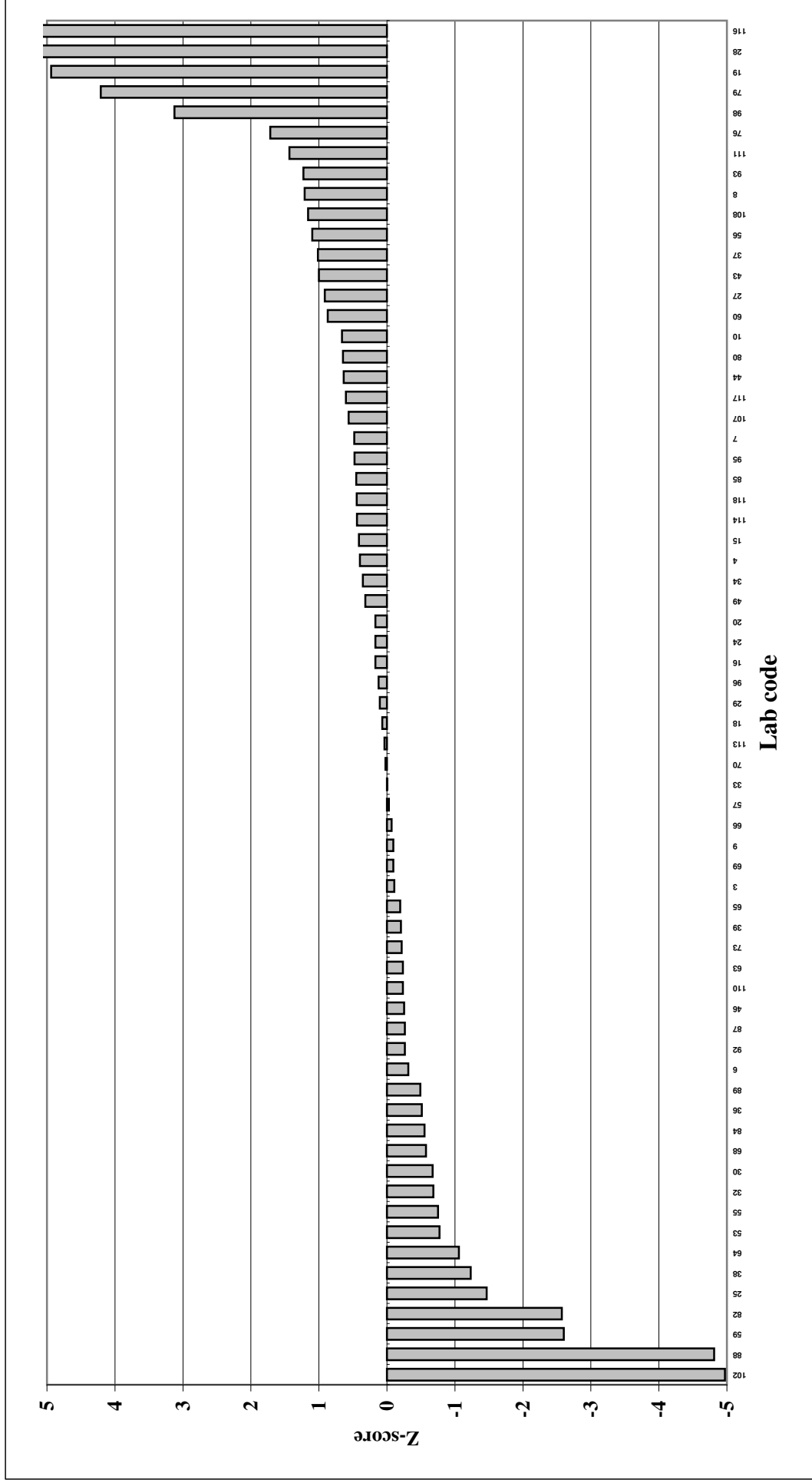
Z-score Breast milk; PCDD/PCDF TEQ



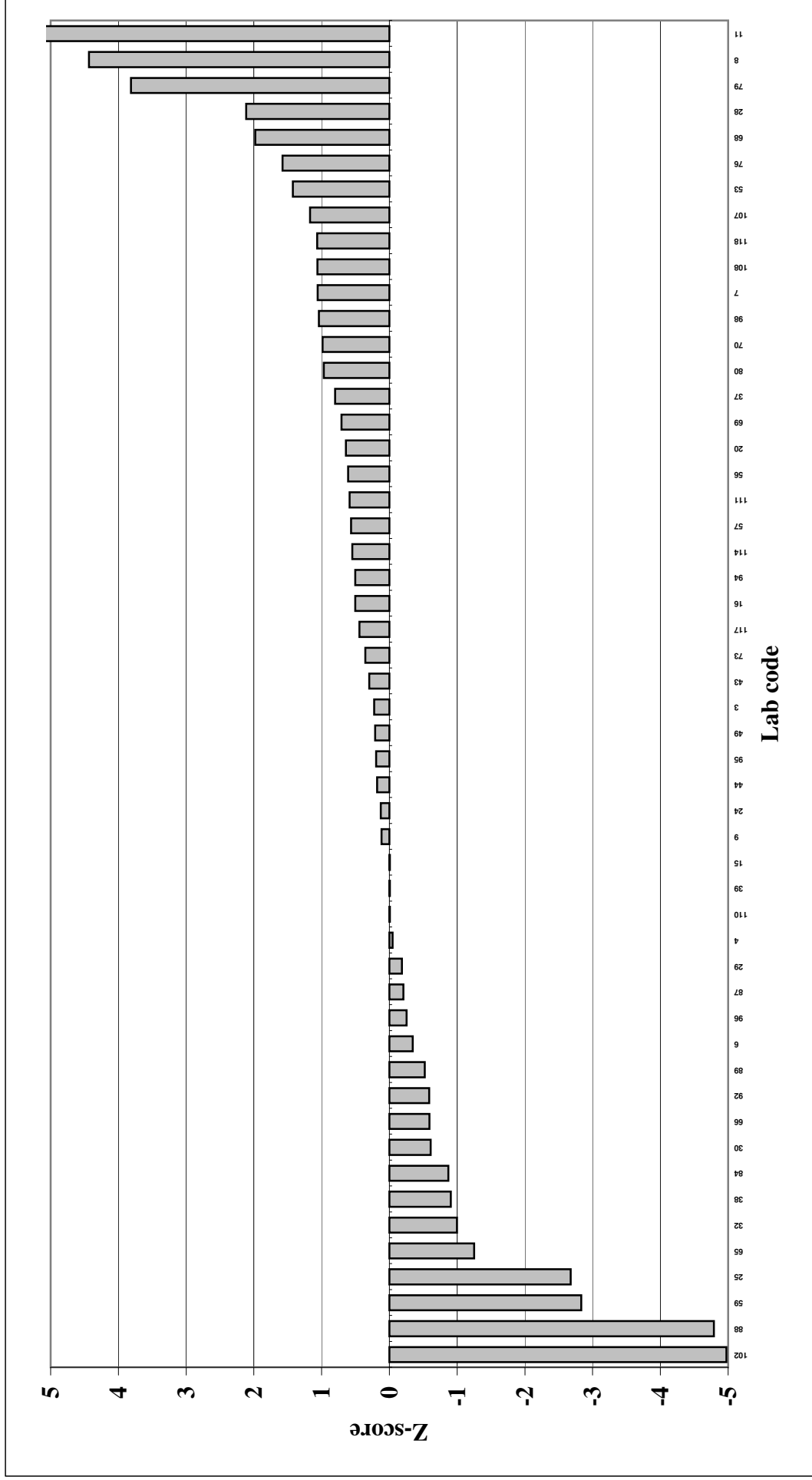
Z-score Breast milk; non-ortho PCB TEQ



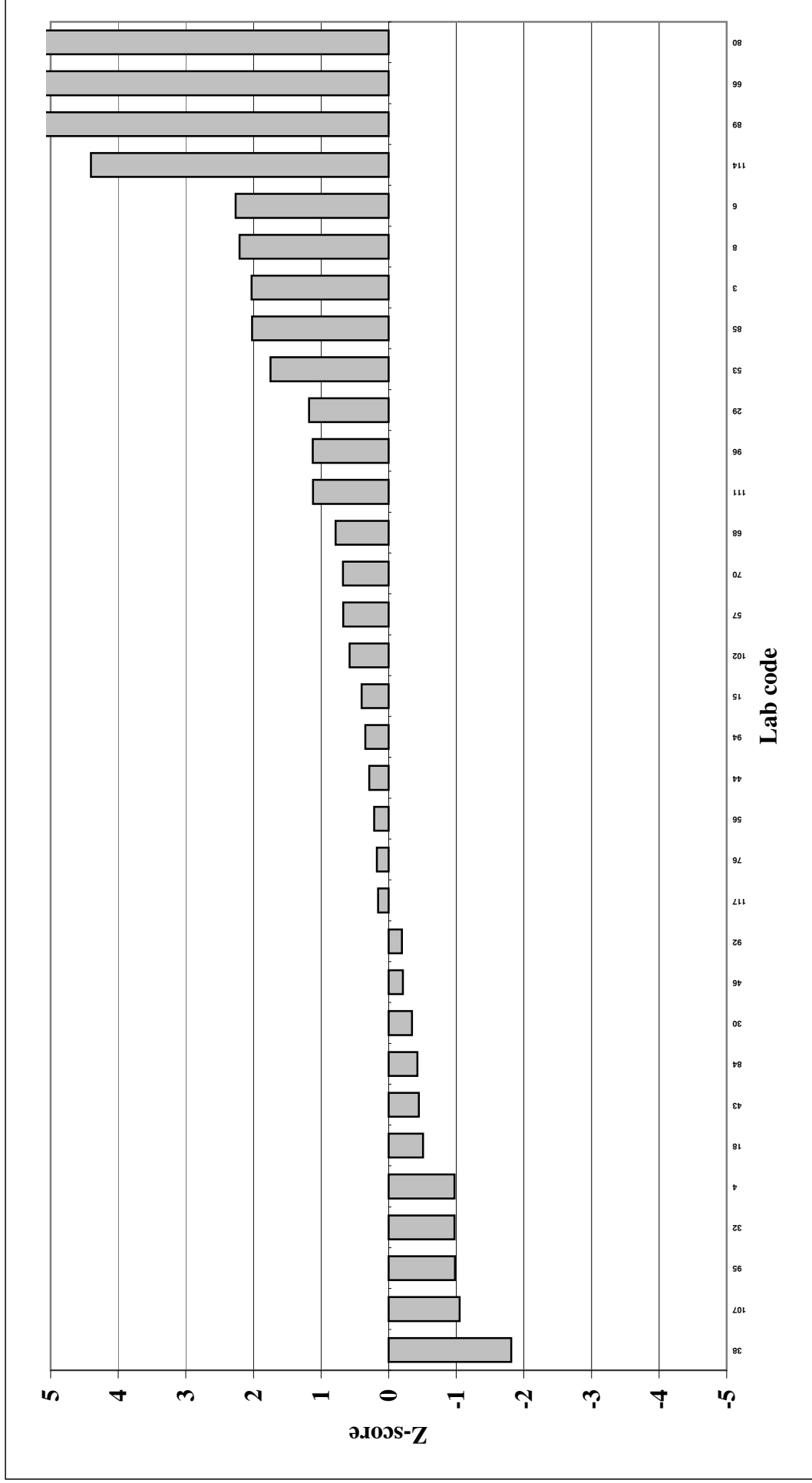
Z-score Breast milk; mono-ortho PCB TEQ



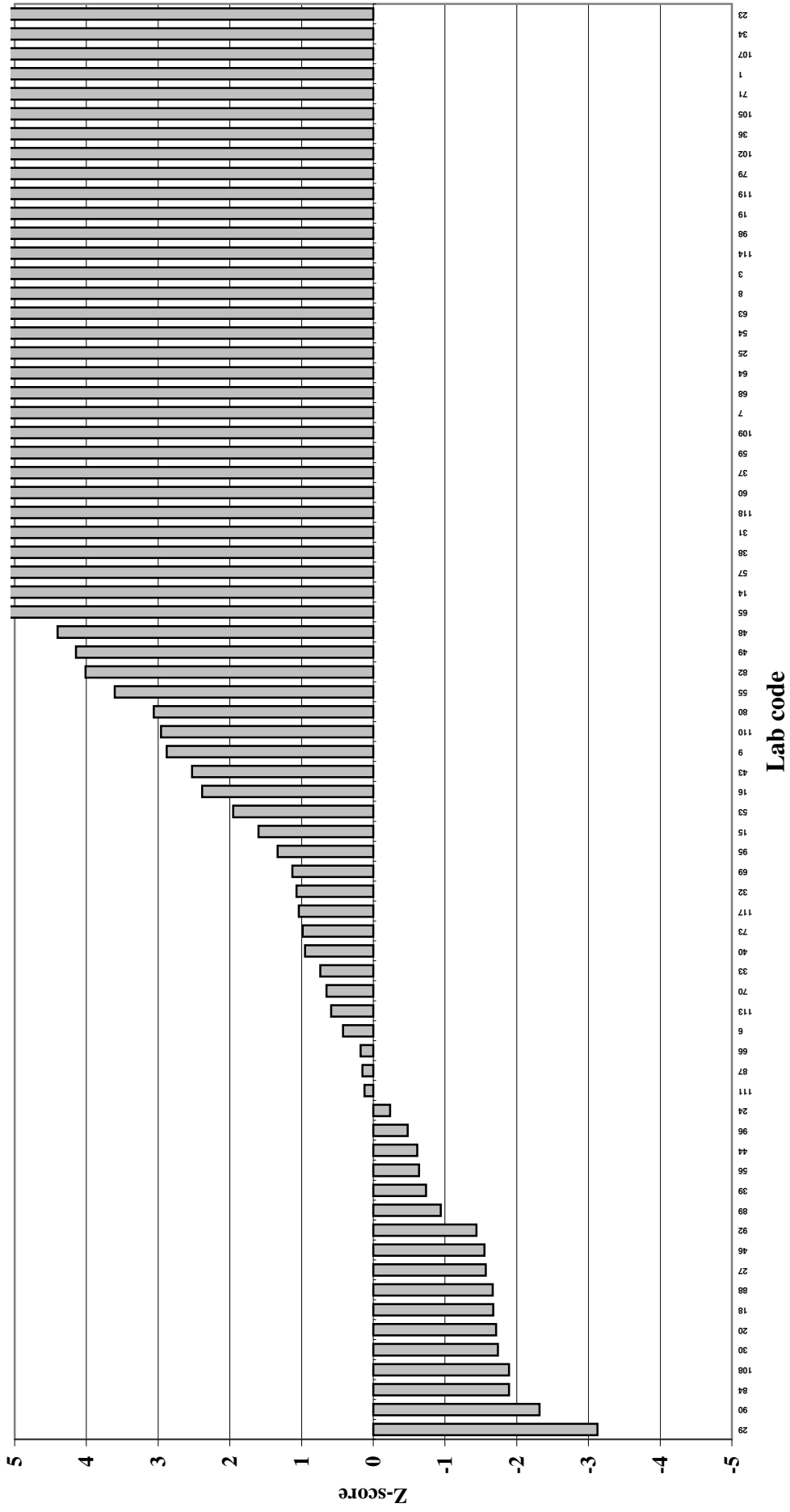
Z-score Breast milk; sum indicator PCB



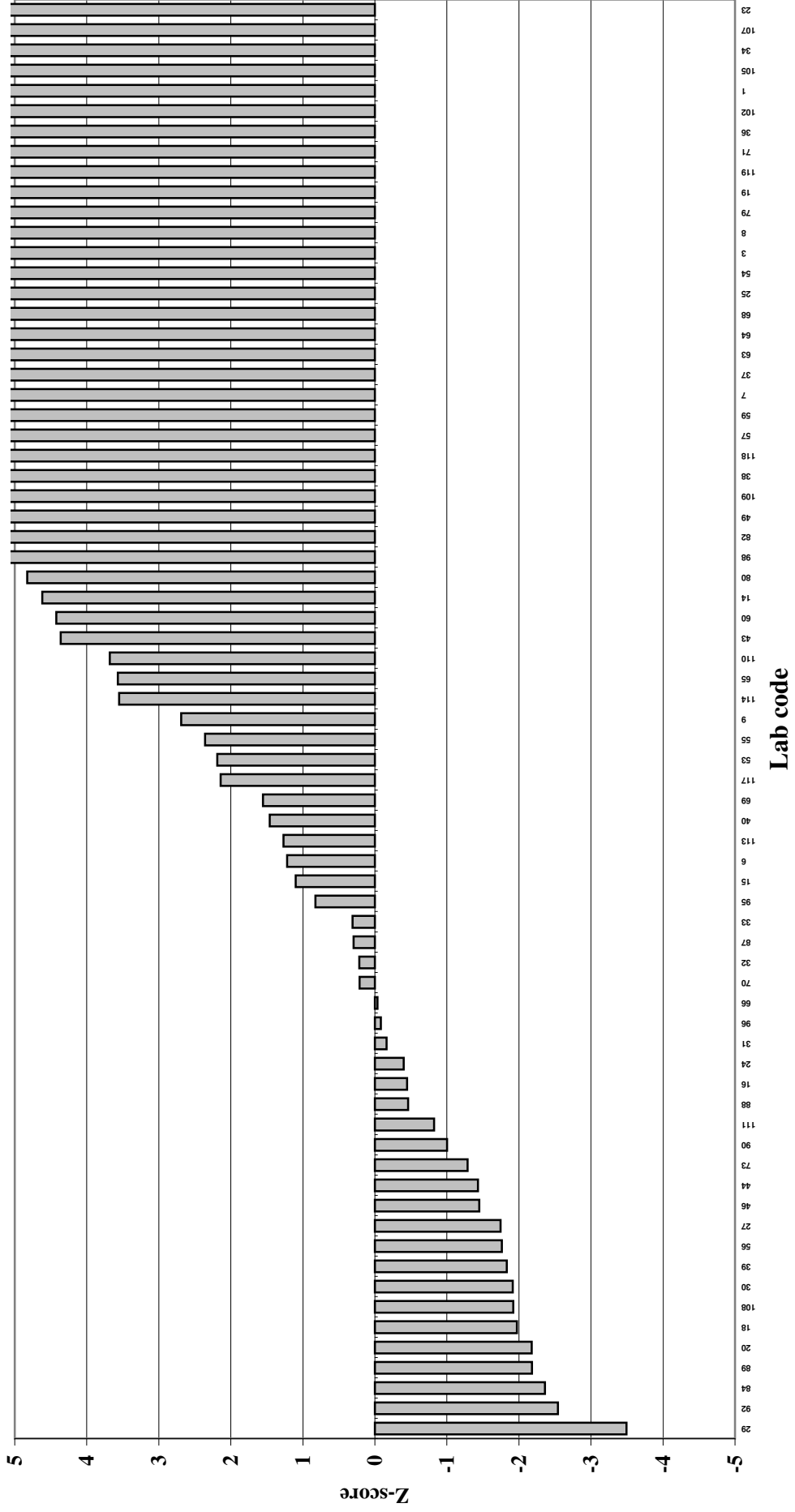
Z-score Breast milk; sum PBDE without BDE-209



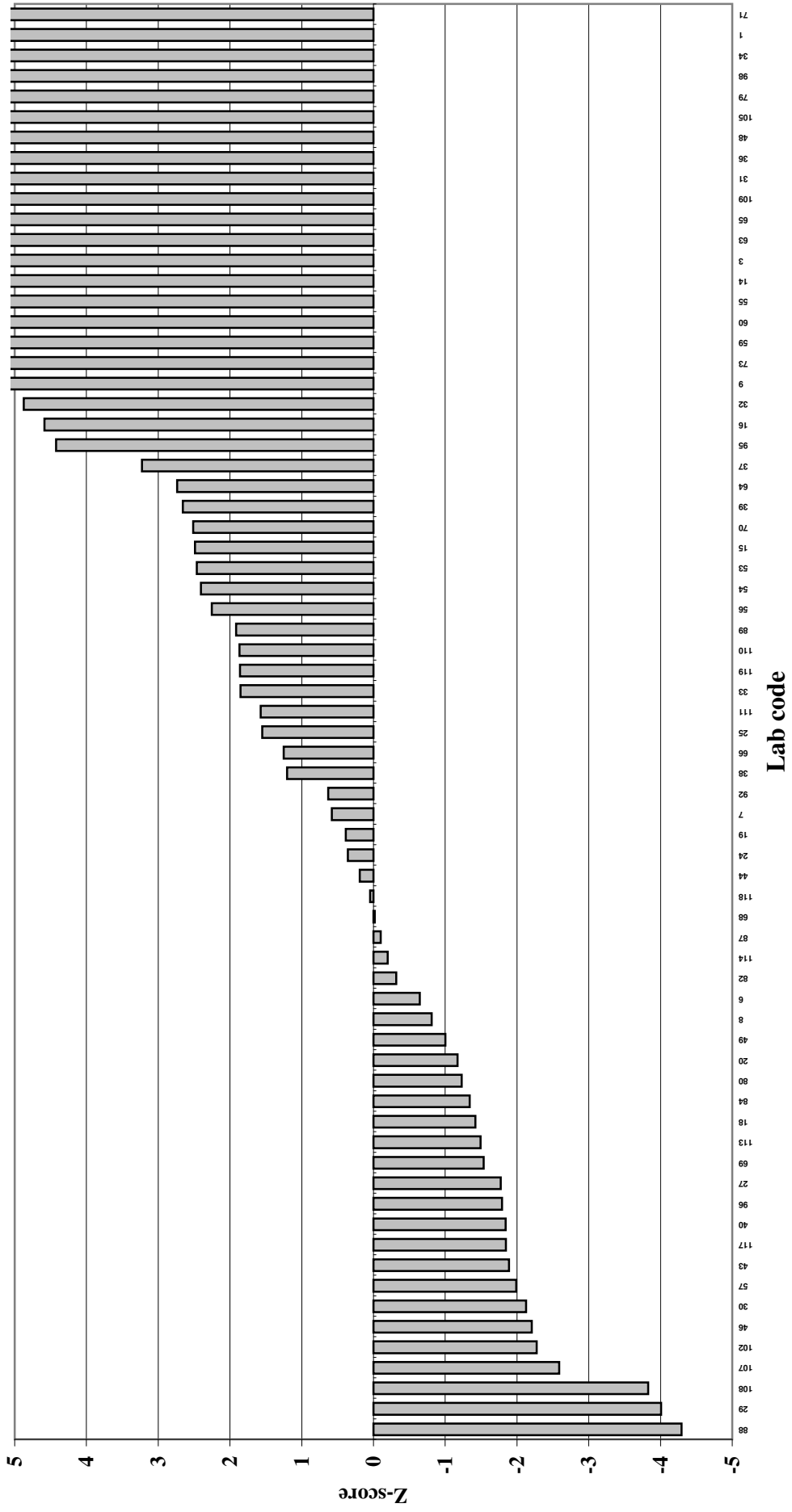
Z-score Pork meat; total TEQ



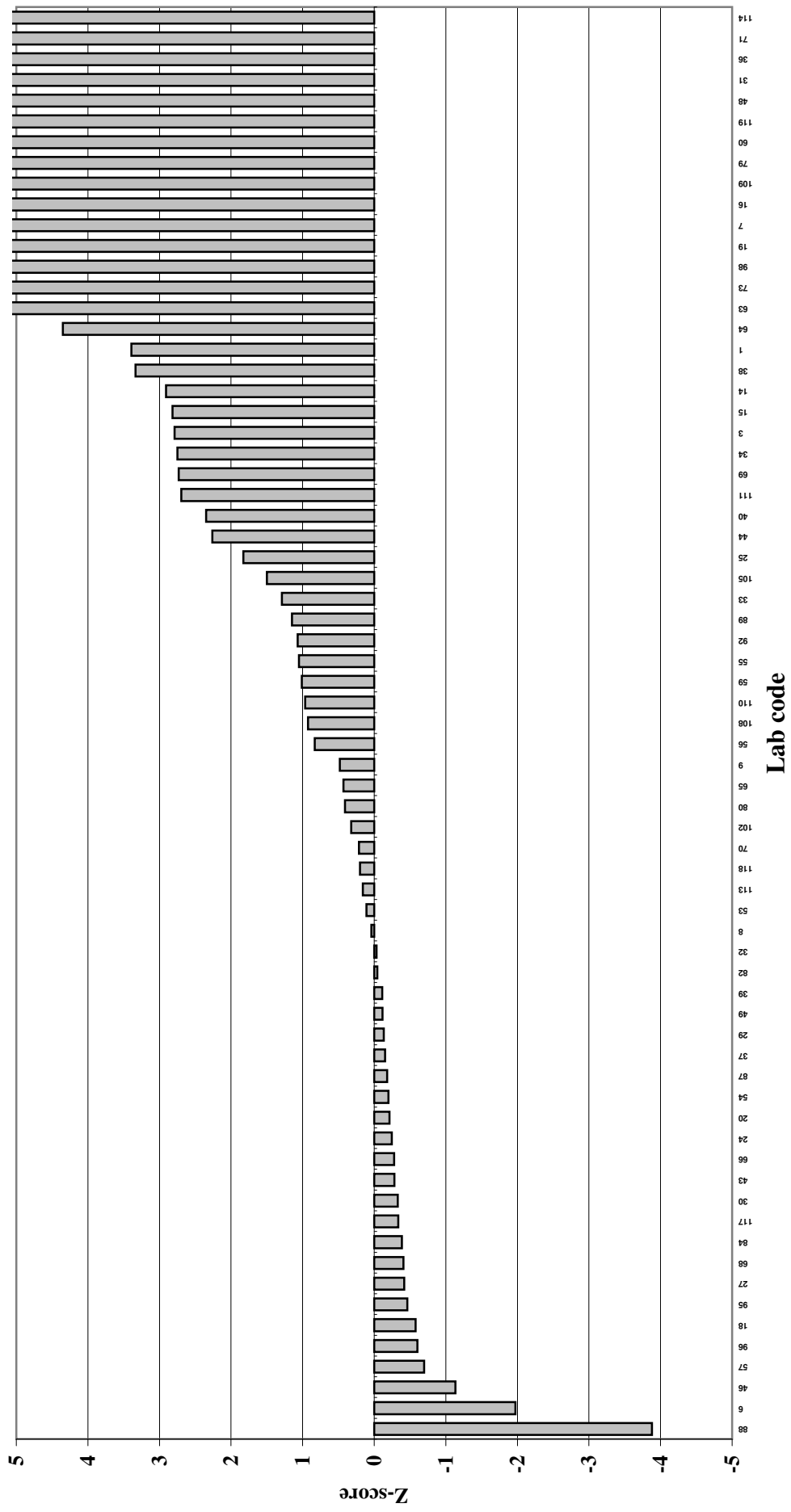
Z-score Pork meat; PCDD/PCDF TEQ



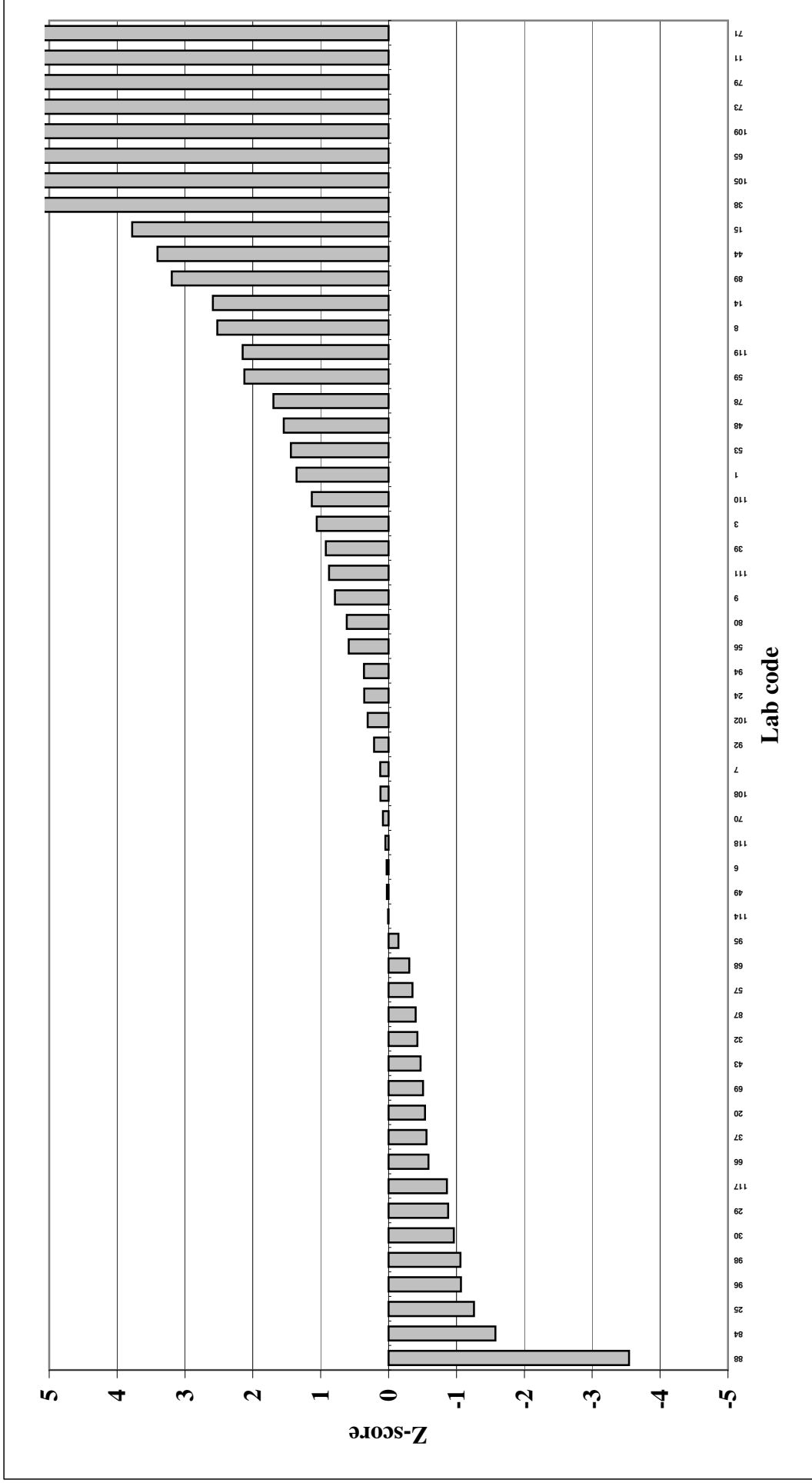
Z-score Pork meat; non-ortho PCB TEQ



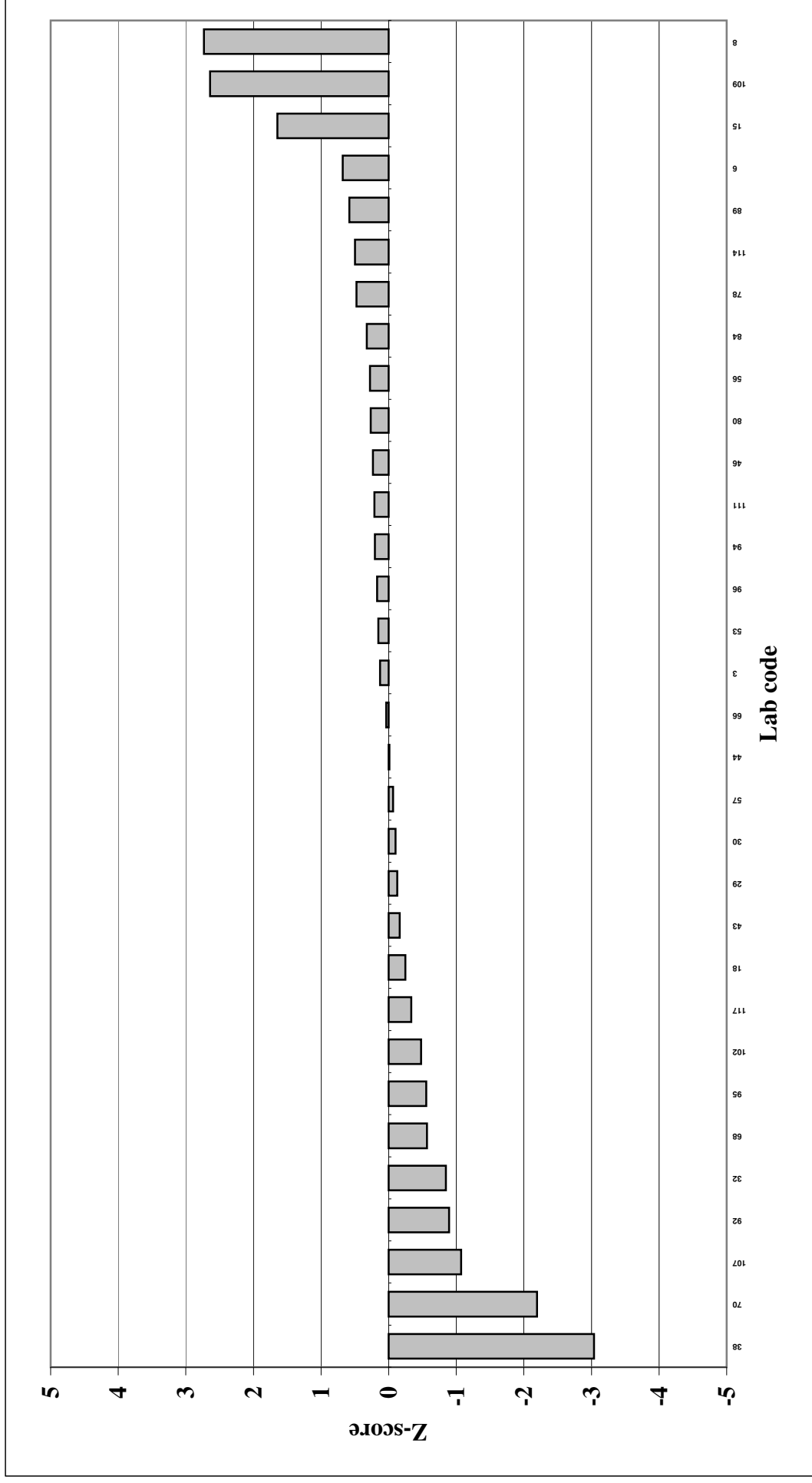
Z-score Pork meat; mono-ortho PCB TEQ



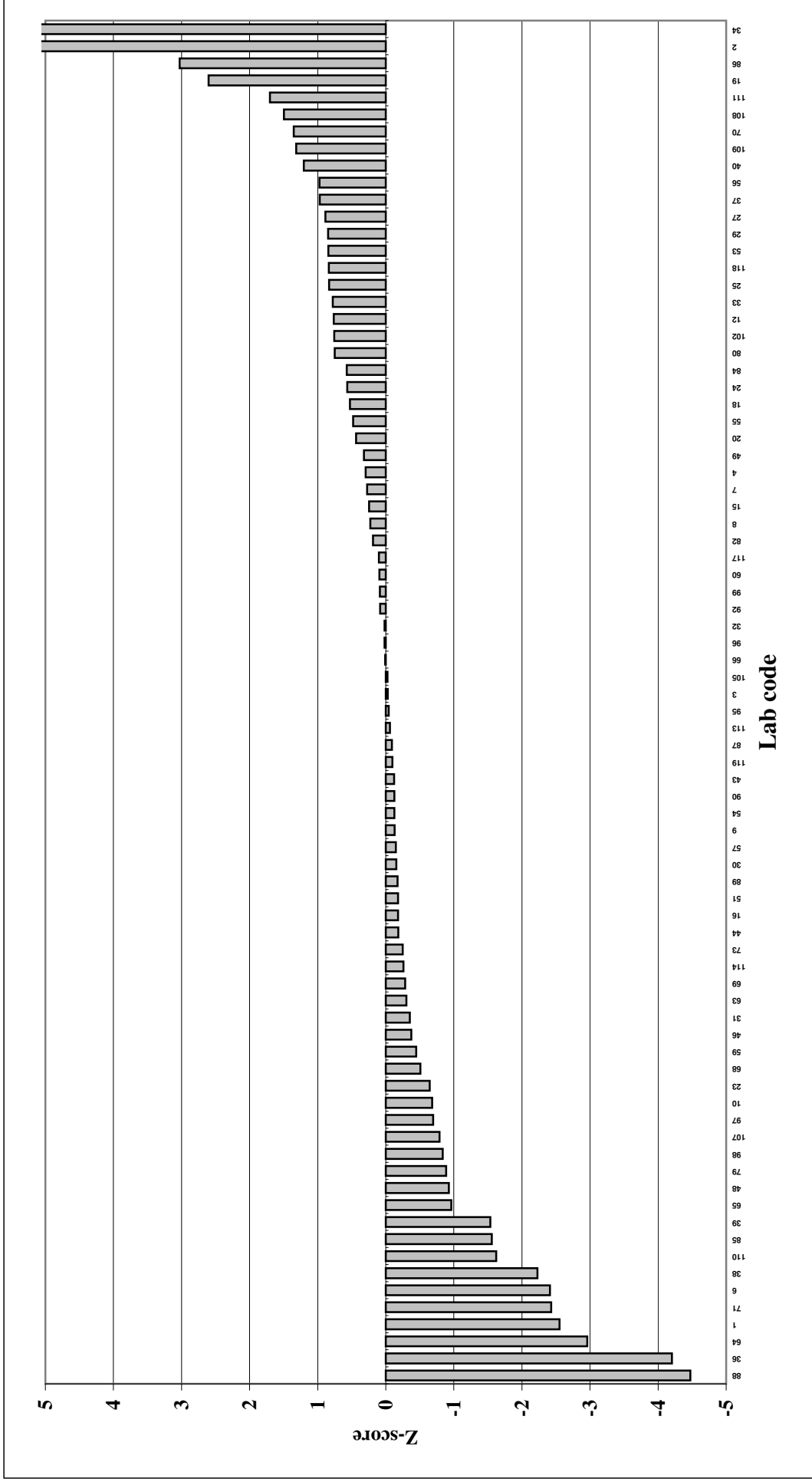
Z-score Pork meat; sum indicator PCB



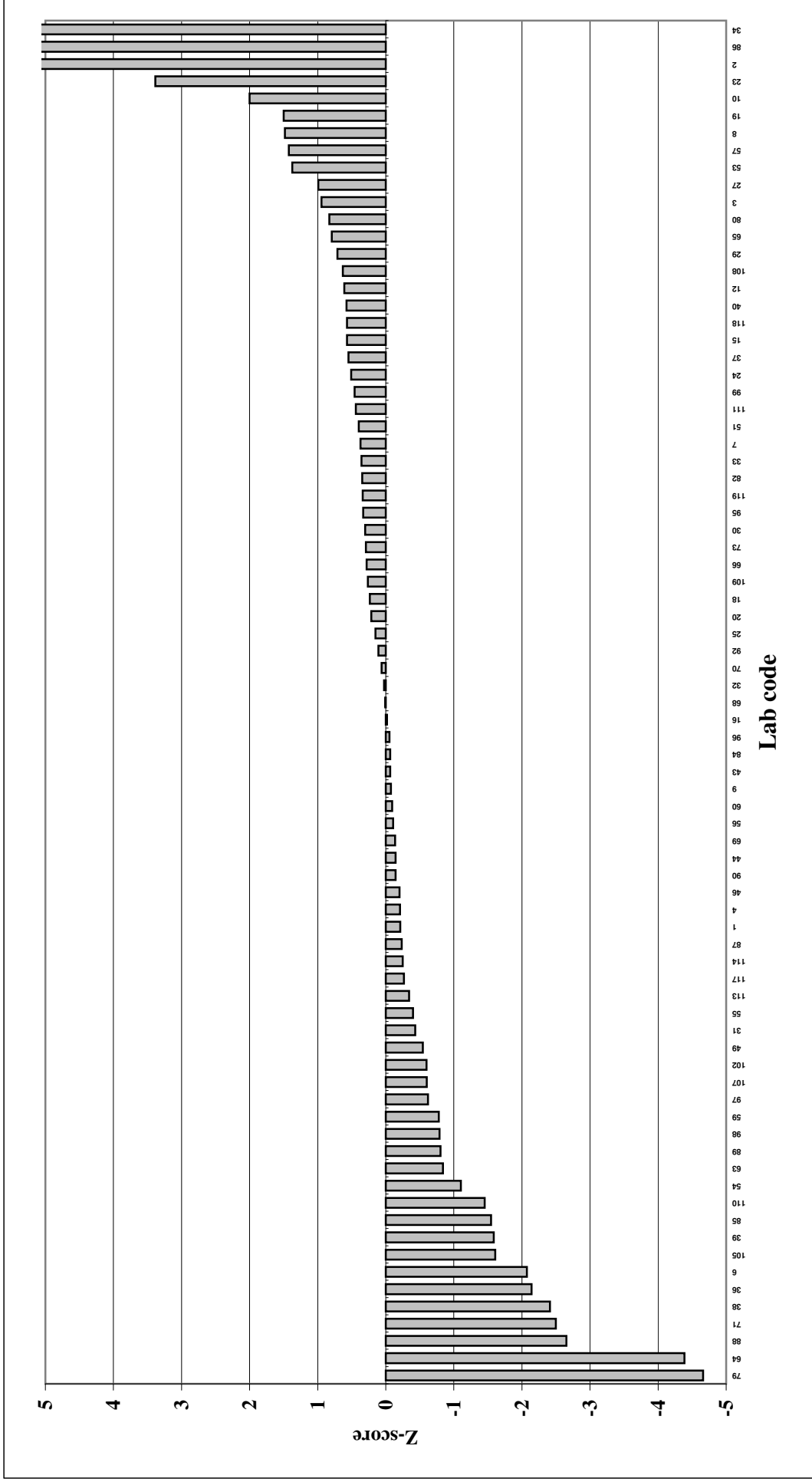
Z-score Pork meat; sum PBDE without BDE-209



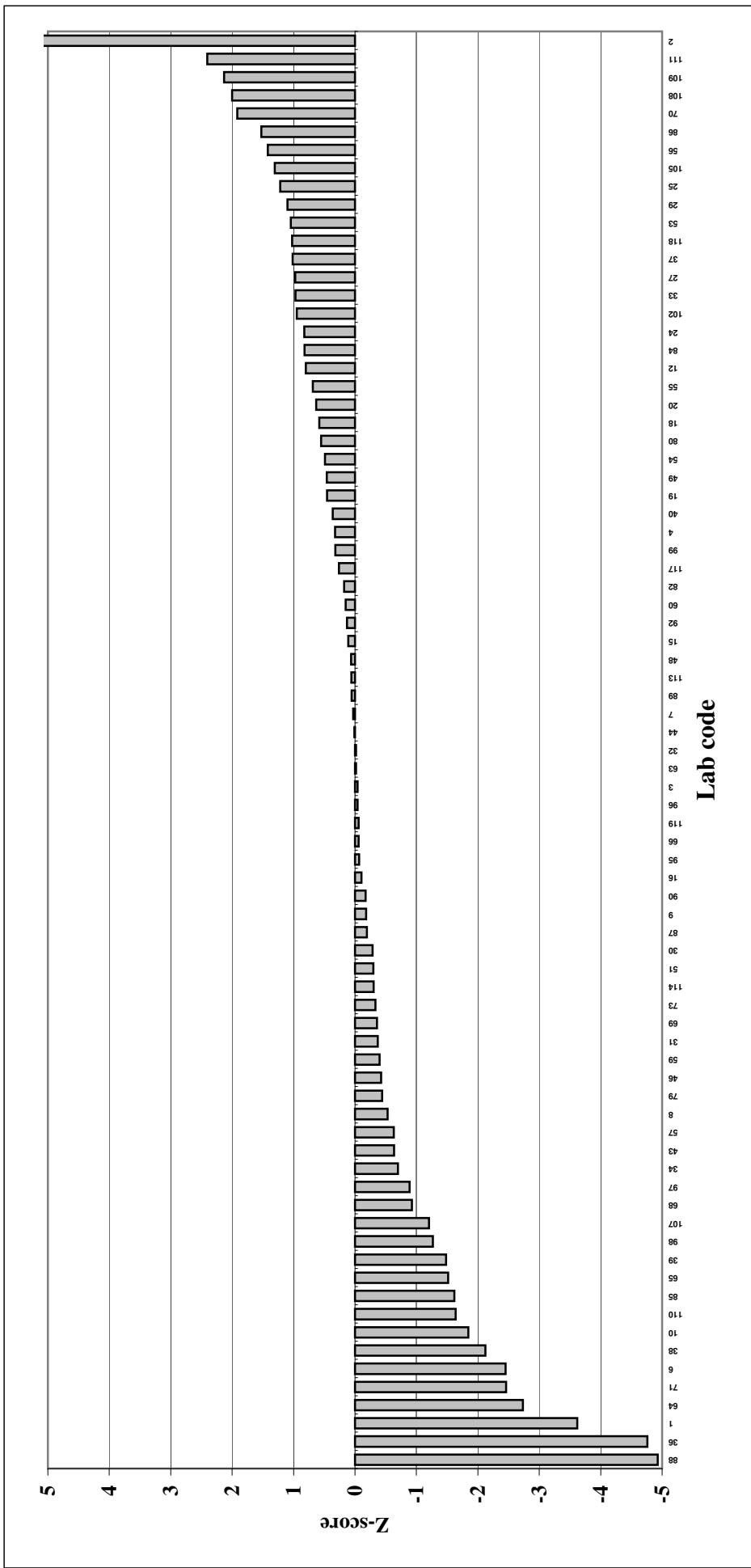
Z-score Trout; total TEQ



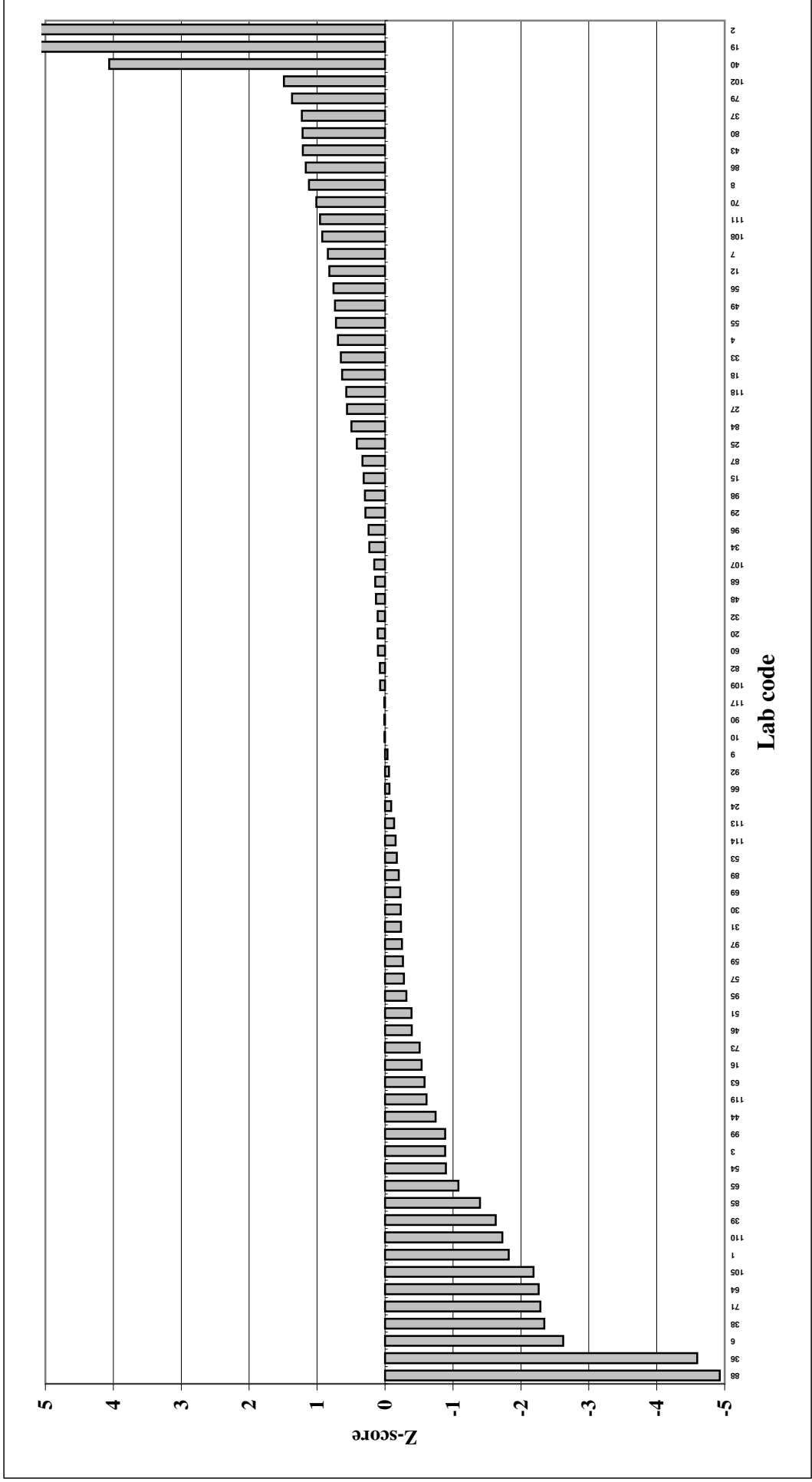
Z-score Trout; PCDD/PCDF TEQ



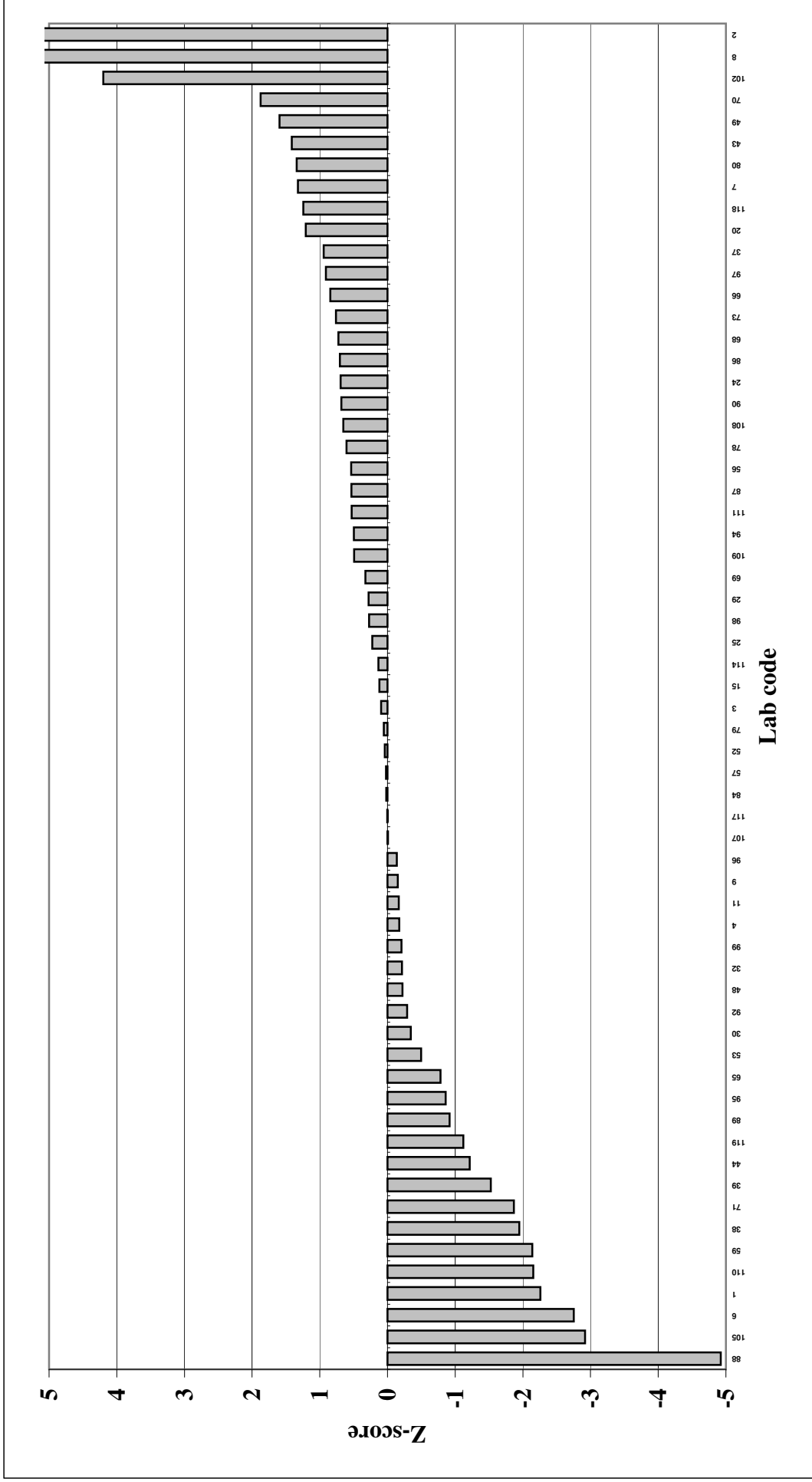
Z-score Trout; non-ortho PCB TEQ



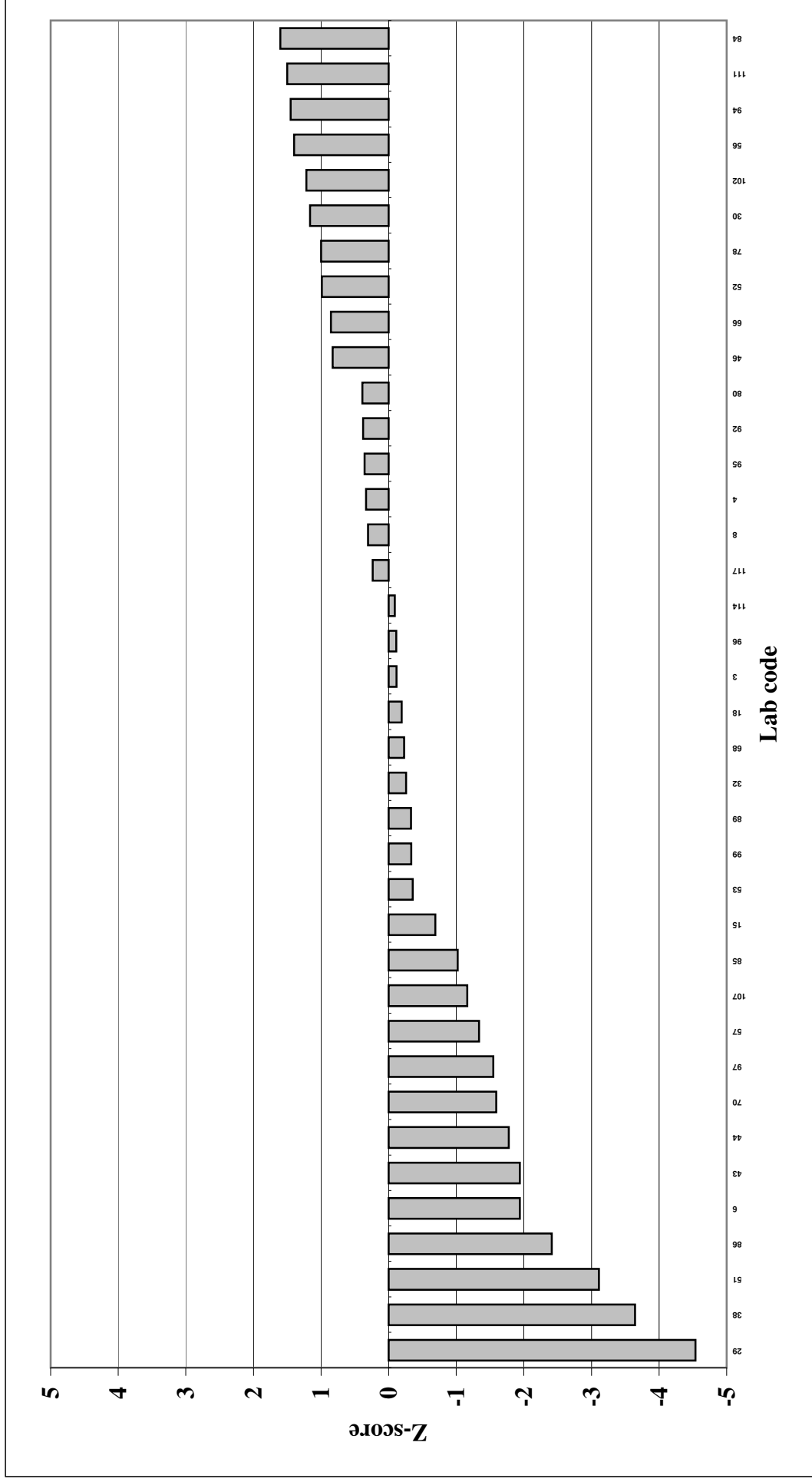
Z-score Trout; mono-ortho PCB TEQ



Z-score Trout; sum indicator PCB



Z-score Trout; sum PBDE without BDE-209



Appendix D:

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 (2006)	Congener	TEF values (1998)	TEF values (2006)
"Dioxins"			"Dioxin-like" PCBs		
Polychlorinated dibenzo-p-dioxins (PCDDs)			Non-ortho PCBs		
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			
Polychlorinated dibenzofurans (PCDFs)			Mono-ortho PCBs		
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 E:

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 (σ_p), i.e., $s_{\text{sam}} < 0.3 \sigma_p$.

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 σ_{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 (σ_{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 $\sigma_{\text{an}} < 0.5 \sigma_p$

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., $\sigma_{\text{an}} < 0.5 \sigma_p$. 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 $RSD^2_{\text{inhomogeneity}} = RSD^2_{\text{between}} - RSD^2_{\text{within}}$ ¹ 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

¹G. 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 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 α -HBCD

The analyte solution contained

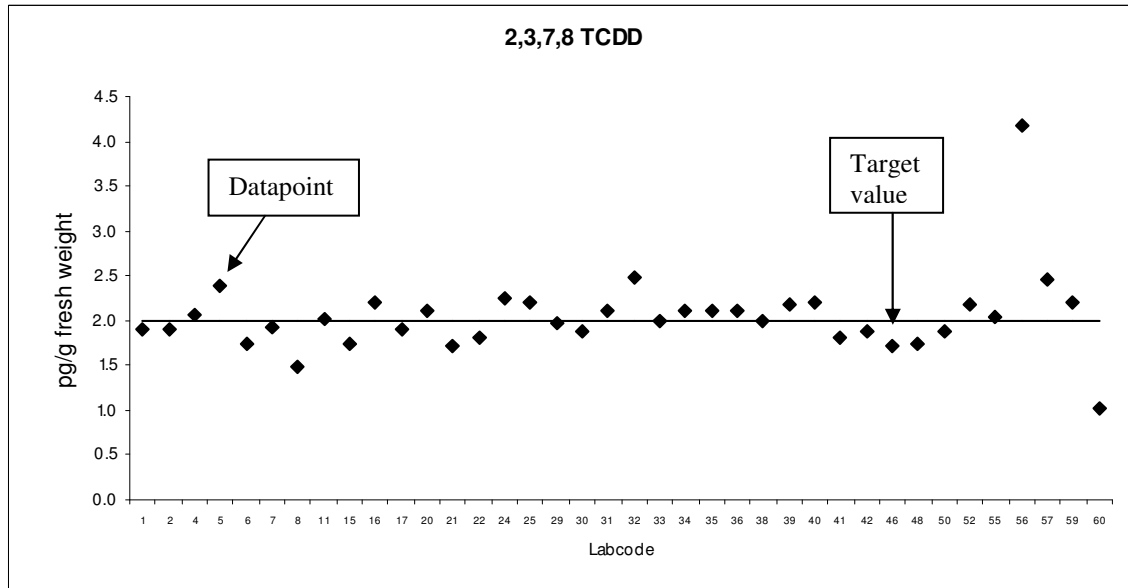
- PCDDs/PCDFs at concentrations of 2:5:10 pg/ μ l for tetra:penta-hexa-hepta:octa chlorinated dibenzodioxins/furans respectively.
- Non-ortho PCBs at concentration of 10 pg/ μ l.
- Mono-ortho PCBs and indicator PCBs at concentration of 100 pg/ μ l.
- PBDE at a concentration of 25 pg/ μ l, except BDE-209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

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

Where x = reported value; X = assigned value (consensus); σ = target value for standard deviation. A σ 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.

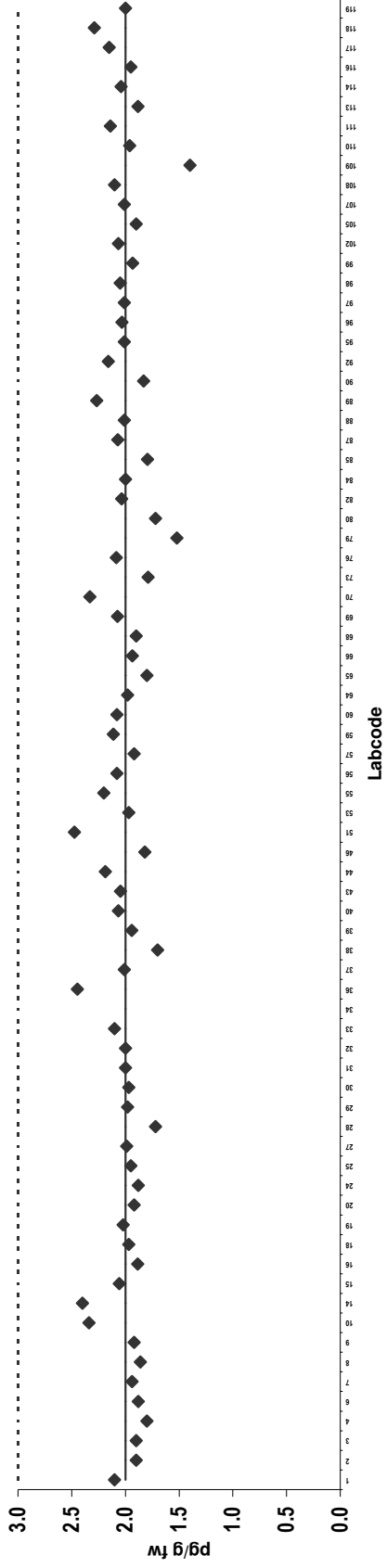
Analyte solution

Congener: 2,3,7,8 TCDD

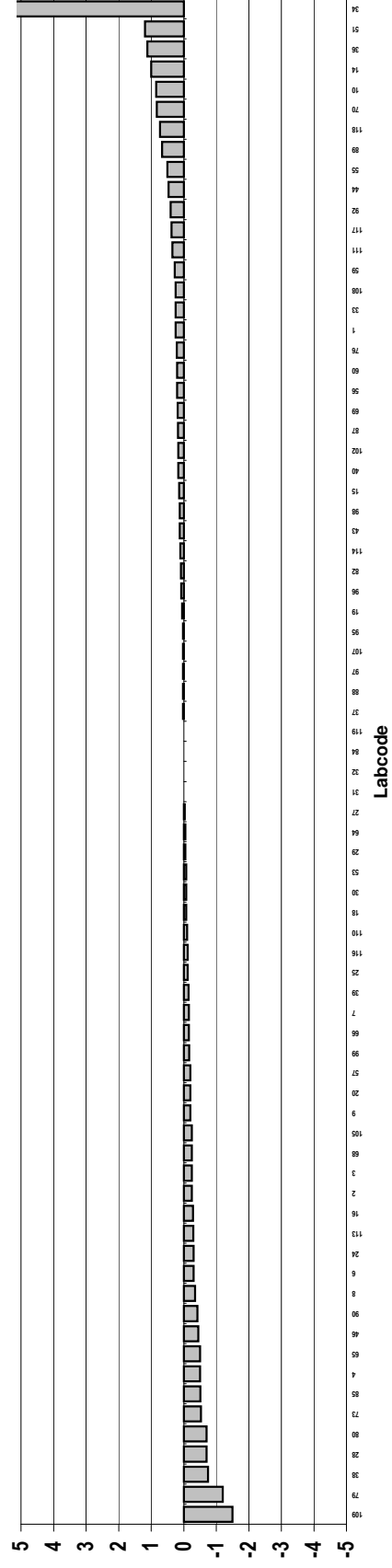
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	2.1		70	2.3	
2	1.9		73	1.8	
3	1.9		76	2.1	
4	1.8		79	1.5	
6	1.9		80	1.7	
7	1.9		82	2.0	
8	1.9		84	2.0	
9	1.9		85	1.8	
10	2.3		87	2.1	
14	2.4		88	2.0	
15	2.1		89	2.3	
16	1.9		90	1.8	
18	2.0		92	2.2	
19	2.0		95	2.0	
20	1.9		96	2.0	
24	1.9		97	2.0	
25	2.0		98	2.1	
27	2.0		99	1.9	
28	1.7		102	2.1	
29	2.0		105	1.9	
30	2.0		107	2.0	
31	2.0		108	2.1	
32	2.0		109	1.4	
33	2.1		110	2.0	
34	1.0	Outlier	111	2.1	
36	2.4		113	1.9	
37	2.0		114	2.0	
38	1.7		116	2.0	
39	1.9		117	2.2	
40	2.1		118	2.3	
43	2.0		119	2.0	
44	2.2				
46	1.8				
51	2.5				
53	2.0				
55	2.2				
56	2.1				
57	1.9				
59	2.1				
60	2.1				
64	2.0				
65	1.8				
66	1.9				
68	1.9				
69	2.1				

Consensus statistics	
Consensus median, pg/μL	2.0
Median all values pg/μL	2.0
Consensus mean, pg/μL	2.0
Standard deviation, pg/μL	0.2
Relative standard deviation, %	9.1
No. of values reported	76
No. of values removed	1
No. of reported non-detects	0

2,3,7,8 TCDD



Z-score: 2,3,7,8 TCDD



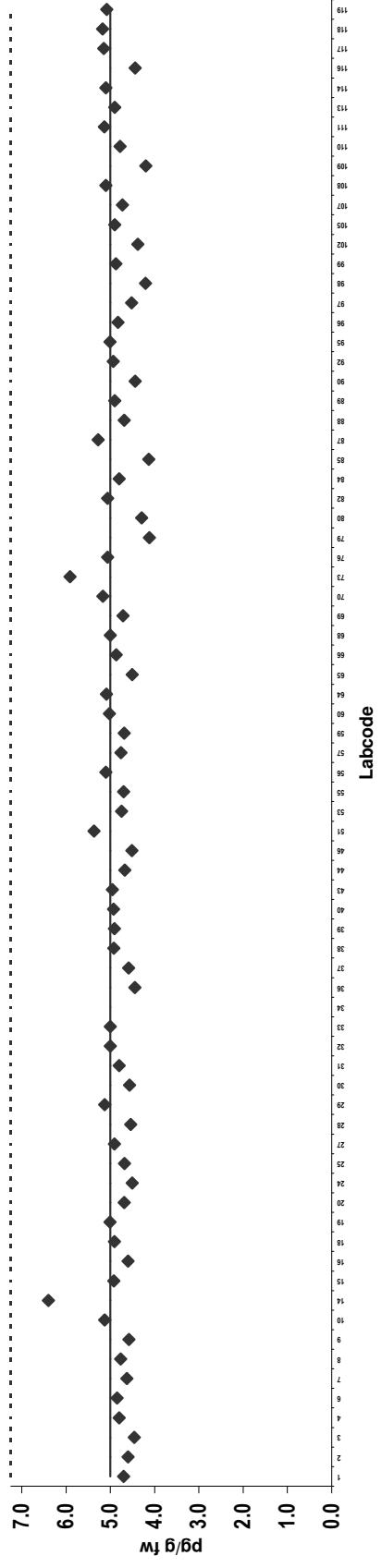
Analyte solution

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

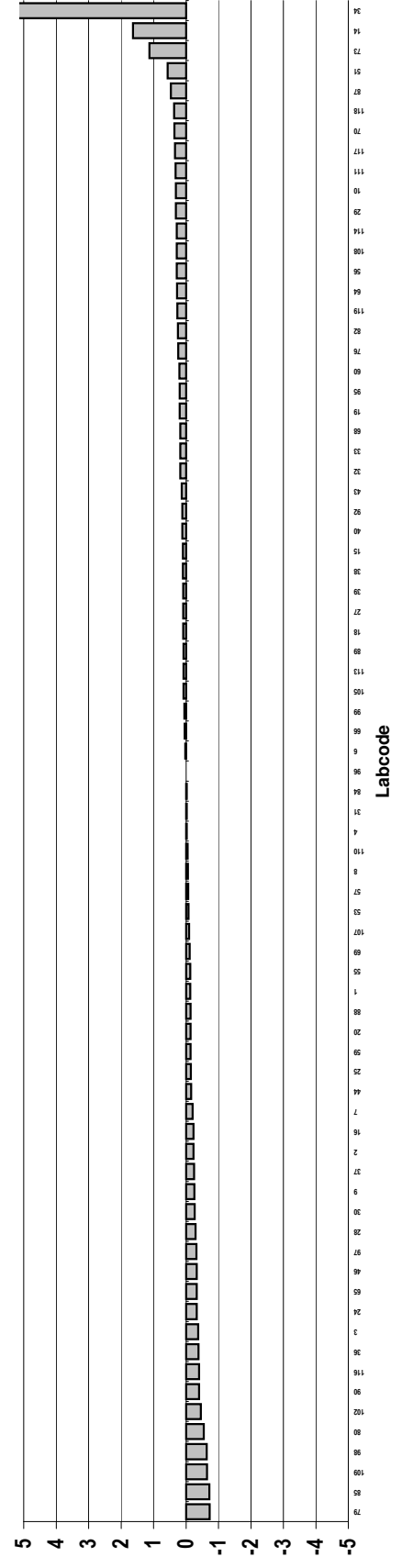
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	4.7		70	5.2	
2	4.6		73	5.9	
3	4.5		76	5.1	
4	4.8		79	4.1	
6	4.9		80	4.3	
7	4.6		82	5.1	
8	4.8		84	4.8	
9	4.6		85	4.1	
10	5.1		87	5.3	
14	6.4		88	4.7	
15	4.9		89	4.9	
16	4.6		90	4.4	
18	4.9		92	4.9	
19	5.0		95	5.0	
20	4.7		96	4.8	
24	4.5		97	4.5	
25	4.7		98	4.2	
27	4.9		99	4.9	
28	4.5		102	4.4	
29	5.1		105	4.9	
30	4.6		107	4.7	
31	4.8		108	5.1	
32	5.0		109	4.2	
33	5.0		110	4.8	
34	5.0		111	5.1	
36	4.5	Outlier	113	4.9	
37	4.6		114	5.1	
38	4.9		116	4.4	
39	4.9		117	5.2	
40	4.9		118	5.2	
43	5.0		119	5.1	
44	4.7				
46	4.5				
51	5.4				
53	4.8				
55	4.7				
56	5.1				
57	4.8				
59	4.7				
60	5.0				
64	5.1				
65	4.5				
66	4.9				
68	5.0				
69	4.7				

Consensus statistics	
Consensus median, pg/μL	4.8
Median all values pg/μL	4.8
Consensus mean, pg/μL	4.8
Standard deviation, pg/μL	0.35
Relative standard deviation, %	7.4
No. of values reported	76
No. of values removed	1
No. of reported non-detects	0

1,2,3,7,8 PeCDD



Z-score: 1,2,3,7,8 PeCDD

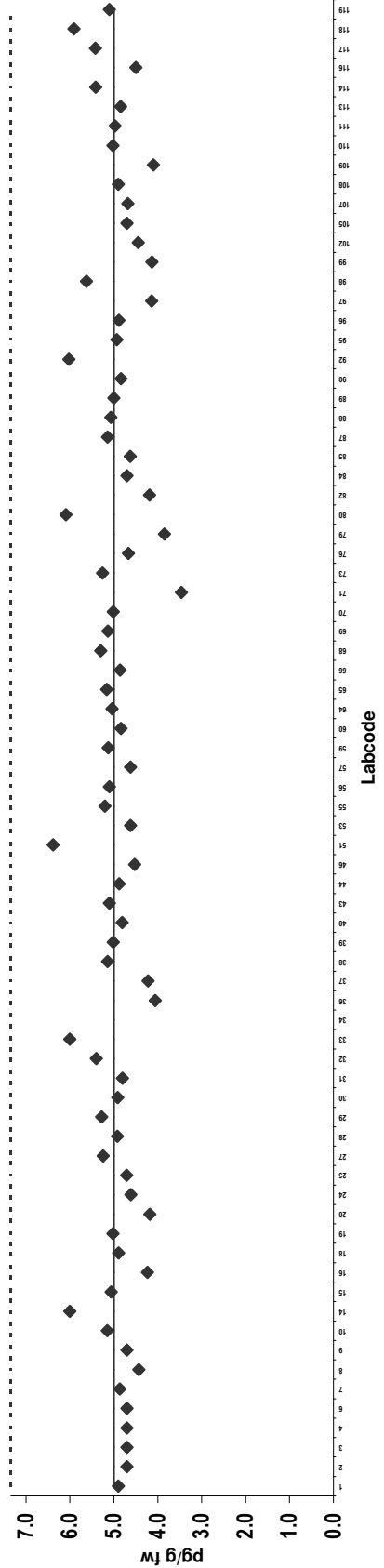


Analyte solution
Congener: 1,2,3,4,7,8 HxCDD

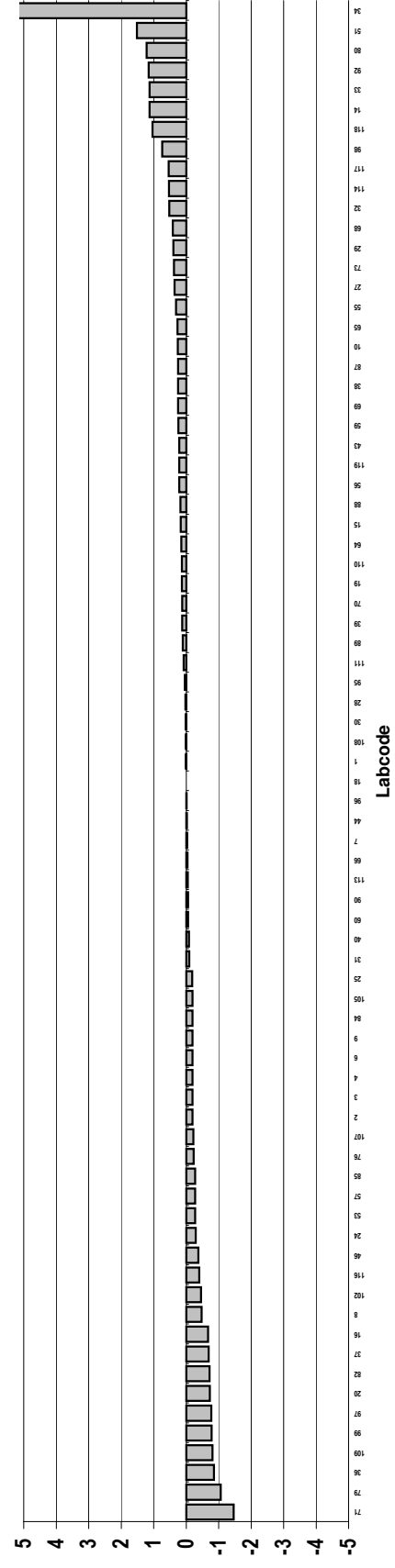
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	4.9		70	5.0	
2	4.7		71	3.5	
3	4.7		73	5.3	
4	4.7		76	4.7	
6	4.7		79	3.9	
7	4.9		80	6.1	
8	4.4		82	4.2	
9	4.7		84	4.7	
10	5.2		85	4.6	
14	6.0		87	5.1	
15	5.1		88	5.1	
16	4.2		89	5.0	
18	4.9		90	4.8	
19	5.0		92	6.0	
20	4.2		95	4.9	
24	4.6		96	4.9	
25	4.7		97	4.1	
27	5.2		98	5.6	
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30	4.9		105	4.7	
31	4.8		107	4.7	
32	5.4		108	4.9	
33	6.0		109	4.1	
34	5.0		110	5.0	
36	4.1		111	5.0	
37	4.2		113	4.8	
38	5.1		114	5.4	
39	5.0		116	4.5	
40	4.8		117	5.4	
43	5.1		118	5.9	
44	4.9		119	5.1	
46	4.5				
51	6.4				
53	4.6				
55	5.2				
56	5.1				
57	4.6				
59	5.1				
60	4.8				
64	5.0				
65	5.2				
66	4.9				
68	5.3				
69	5.1				
		Outlier			

Consensus statistics	
Consensus median, pg/μL	4.9
Median all values pg/μL	4.9
Consensus mean, pg/μL	4.9
Standard deviation, pg/μL	0.52
Relative standard deviation, %	11
No. of values reported	77
No. of values removed	1
No. of reported non-detects	0

1,2,3,4,7,8 HxCDD



Z-score: 1,2,3,4,7,8 HxCDD

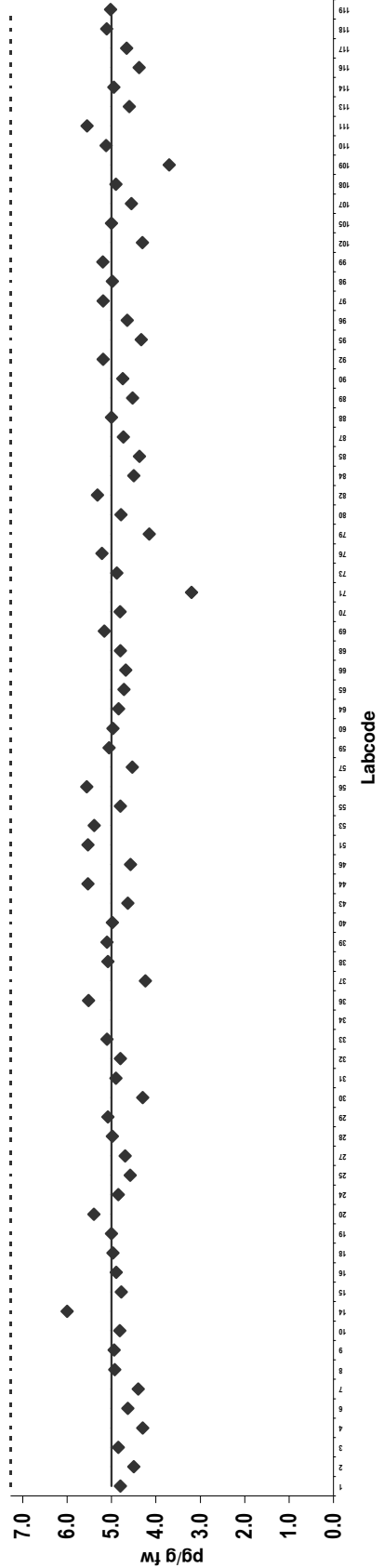


Analyte solution
Congener: 1,2,3,6,7,8 HxCDD

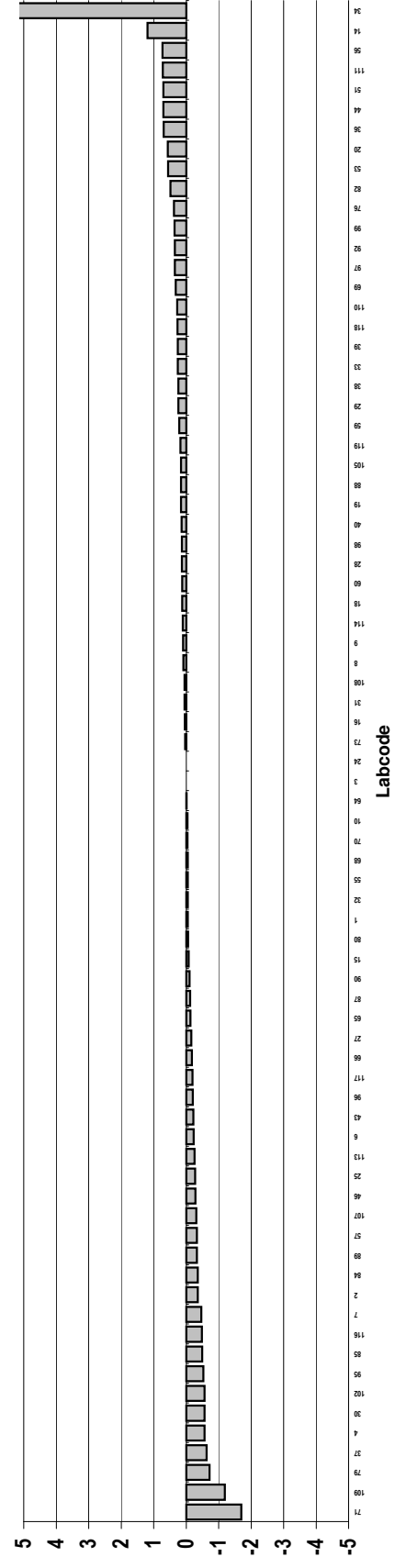
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	4.8		70	4.8	
2	4.5		71	3.2	
3	4.9		73	4.9	
4	4.3		76	5.2	
6	4.6		79	4.2	
7	4.4		80	4.8	
8	4.9		82	5.3	
9	4.9		84	4.5	
10	4.8		85	4.4	
14	6.0		87	4.7	
15	4.8		88	5.0	
16	4.9		89	4.5	
18	5.0		90	4.8	
19	5.0		92	5.2	
20	5.4		95	4.3	
24	4.9		96	4.6	
25	4.6		97	5.2	
27	4.7		98	5.0	
28	5.0		99	5.2	
29	5.1		102	4.3	
30	4.3		105	5.0	
31	4.9		107	4.6	
32	4.8		108	4.9	
33	5.1		109	3.7	
34	5.0		110	5.1	
36	5.5		111	5.6	
37	4.2		113	4.6	
38	5.1		114	5.0	
39	5.1		116	4.4	
40	5.0		117	4.7	
43	4.6		118	5.1	
44	5.5		119	5.0	
46	4.6				
51	5.5				
53	5.4				
55	4.8				
56	5.6				
57	4.5				
59	5.1				
60	5.0				
64	4.8				
65	4.7				
66	4.7				
68	4.8				
69	5.2				
		Outlier			

Consensus statistics	
Consensus median, pg/ μ L	4.9
Median all values pg/ μ L	4.9
Consensus mean, pg/ μ L	4.8
Standard deviation, pg/ μ L	0.42
Relative standard deviation, %	8.8
No. of values reported	77
No. of values removed	1
No. of reported non-detects	0

1,2,3,6,7,8 HxCDD



Z-score: 1,2,3,6,7,8 HxCDD



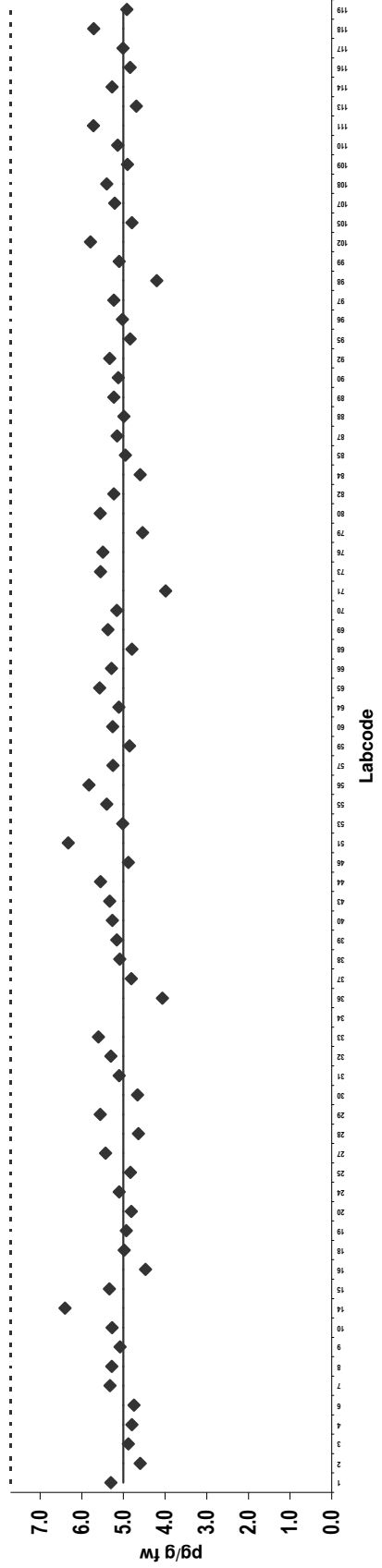
Analyte solution
Congener: 1,2,3,7,8,9 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.3		70	5.2	
2	4.6		71	4.0	
3	4.9		73	5.6	
4	4.8		76	5.5	
6	4.8		79	4.5	
7	5.3		80	5.6	
8	5.3		82	5.2	
9	5.1		84	4.6	
10	5.3		85	5.0	
14	6.4		87	5.1	
15	5.3		88	5.0	
16	4.5		89	5.2	
18	5.0		90	5.1	
19	4.9		92	5.3	
20	4.8		95	4.8	
24	5.1		96	5.0	
25	4.8		97	5.2	
27	5.4		98	4.2	
28	4.6		99	5.1	
29	5.6		102	5.8	
30	4.7		105	4.8	
31	5.1		107	5.2	
32	5.3		108	5.4	
33	5.6		109	4.9	
34	5.0		110	5.1	
36	4.1		111	5.7	
37	4.8		113	4.7	
38	5.1		114	5.3	
39	5.2		116	4.8	
40	5.3		117	5.0	
43	5.3		118	5.7	
44	5.5		119	4.9	
46	4.9				
51	6.3				
53	5.0				
55	5.4				
56	5.8				
57	5.3				
59	4.9				
60	5.3				
64	5.1				
65	5.6				
66	5.3				
68	4.8				
69	5.4				

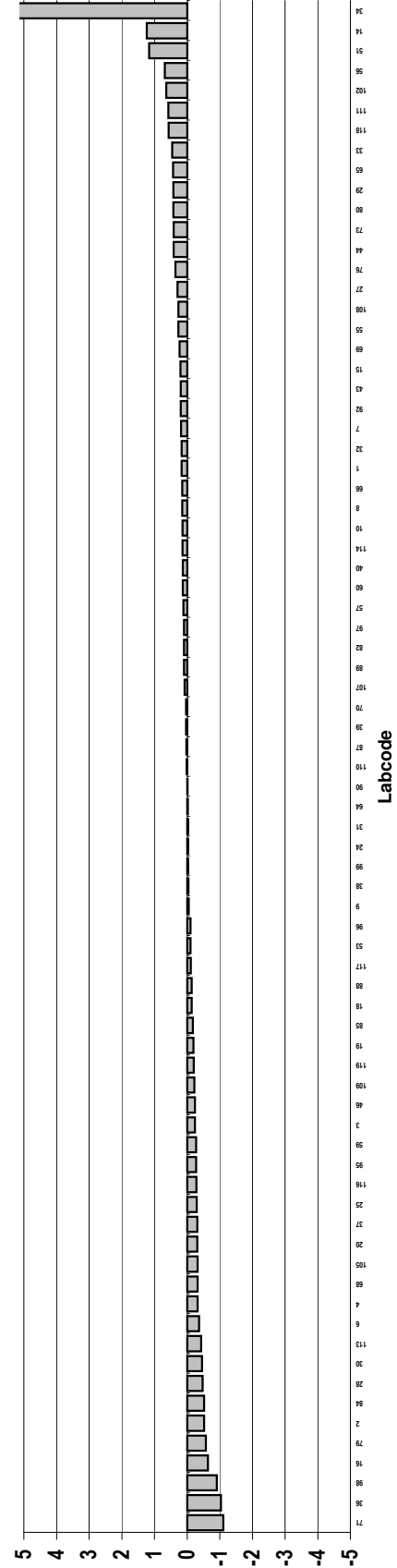
Outlier

Consensus statistics	
Consensus median, pg/μL	5.1
Median all values pg/μL	5.1
Consensus mean, pg/μL	5.1
Standard deviation, pg/μL	0.42
Relative standard deviation, %	8.2
No. of values reported	77
No. of values removed	1
No. of reported non-detects	0

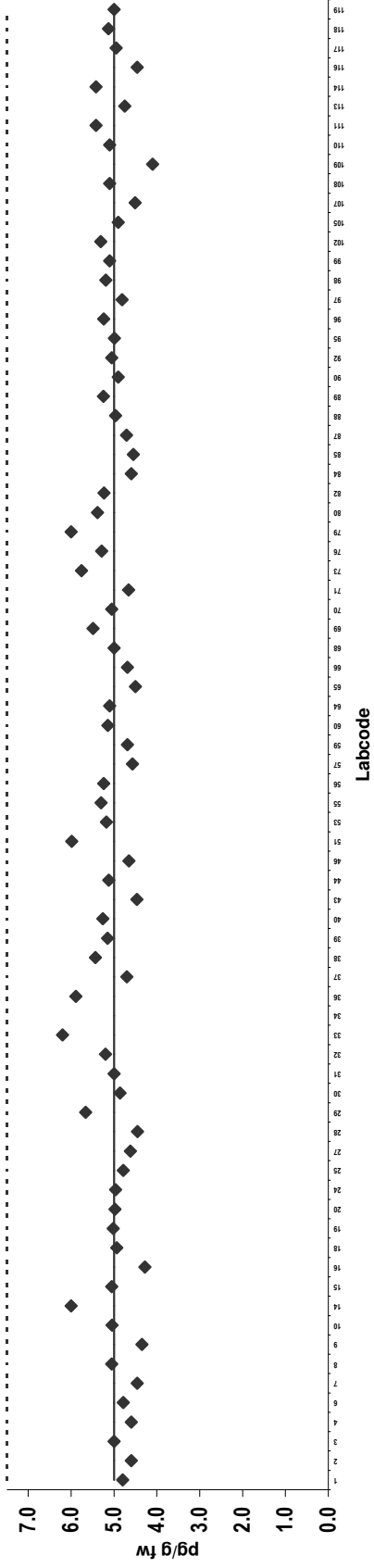
1,2,3,7,8,9 HxCDD



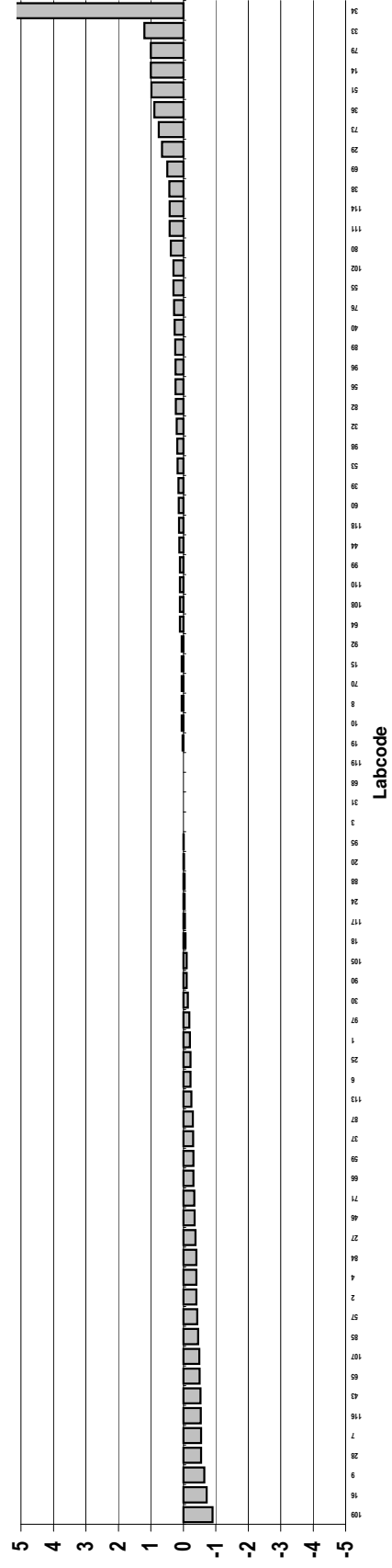
Z-score: 1,2,3,7,8,9 HxCDD



1,2,3,4,6,7,8 HpCDD



Z-score: 1,2,3,4,6,7,8 HpCDD



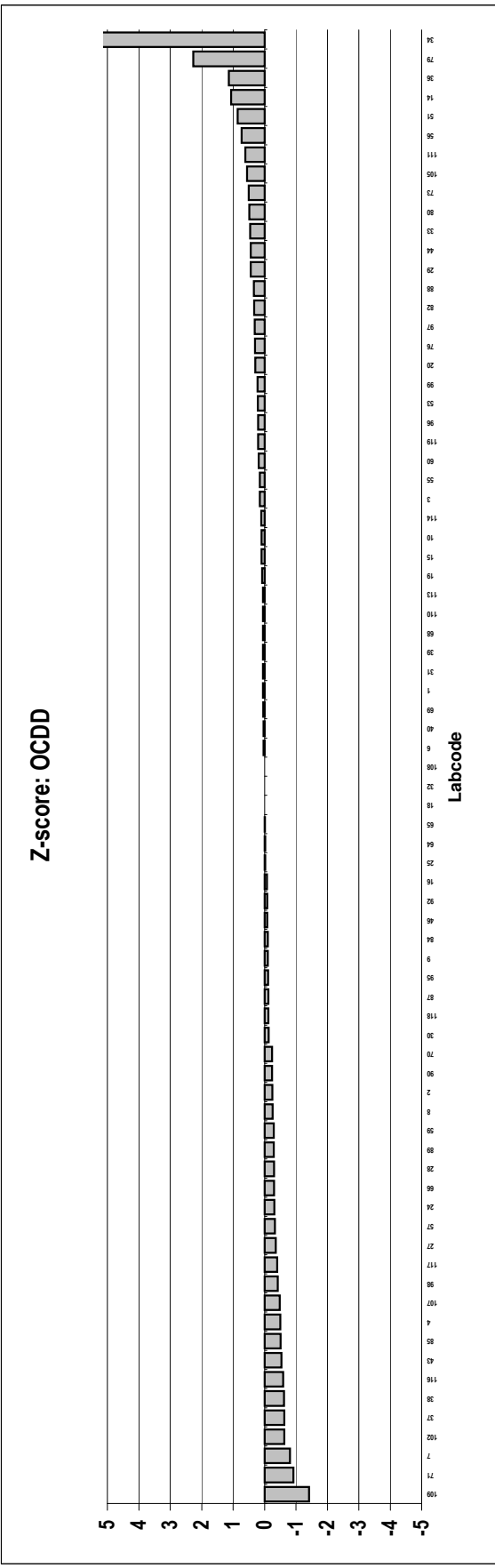
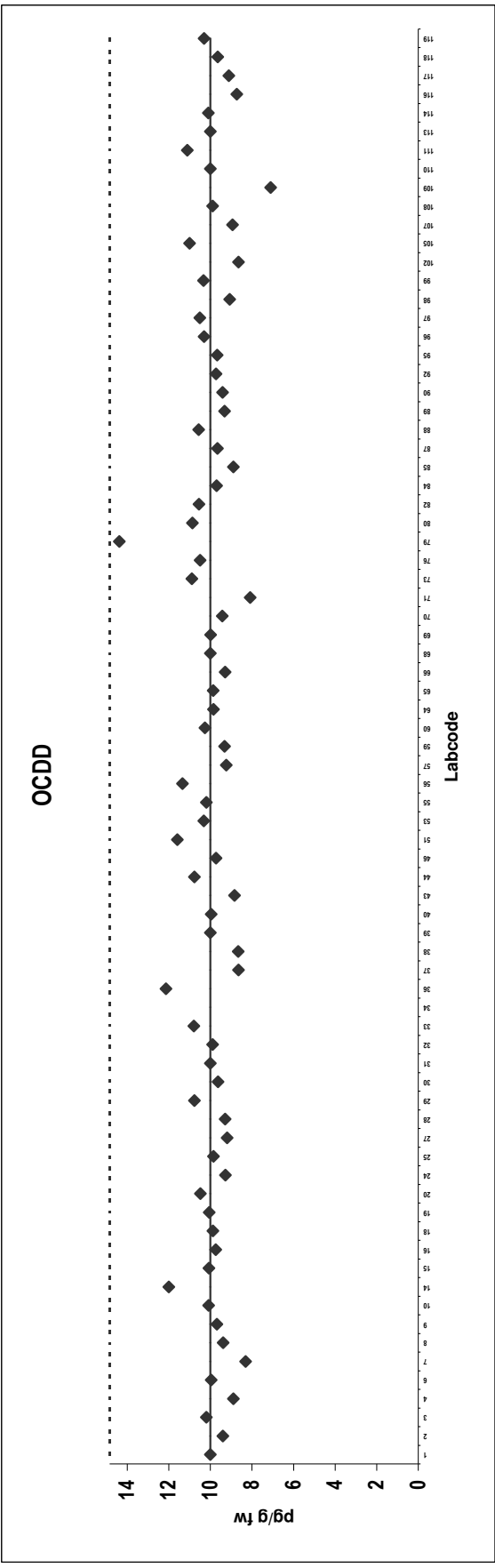
Analyte solution

Congener: OCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	10		70	9.4	
2	9.4		71	8.1	
3	10		73	11	
4	8.9		76	10	
6	10		79	14	
7	8.3		80	11	
8	9.4		82	11	
9	9.7		84	9.7	
10	10		85	8.9	
14	12		87	9.7	
15	10		88	11	
16	9.8		89	9.3	
18	9.9		90	9.4	
19	10		92	9.7	
20	10		95	9.7	
24	9.3		96	10	
25	9.9		97	11	
27	9.2		98	9.1	
28	9.3		99	10	
29	11		102	8.6	
30	9.6		105	11	
31	10		107	8.9	
32	9.9		108	9.9	
33	11		109	7.1	
34	100	Outlier	110	10	
36	12		111	11	
37	8.7		113	10	
38	8.7		114	10	
39	10		116	8.7	
40	10		117	9.1	
43	8.8		118	9.7	
44	11		119	10	
46	9.7				
51	12				
53	10				
55	10				
56	11				
57	9.2				
59	9.3				
60	10				
64	9.9				
65	9.9				
66	9.3				
68	10				
69	10				

Consensus statistics

Consensus median, pg/ μ L	9.9
Median all values pg/ μ L	9.9
Consensus mean, pg/ μ L	9.9
Standard deviation, pg/ μ L	0.99
Relative standard deviation, %	10
No. of values reported	77
No. of values removed	1
No. of reported non-detects	0



Analyte solution

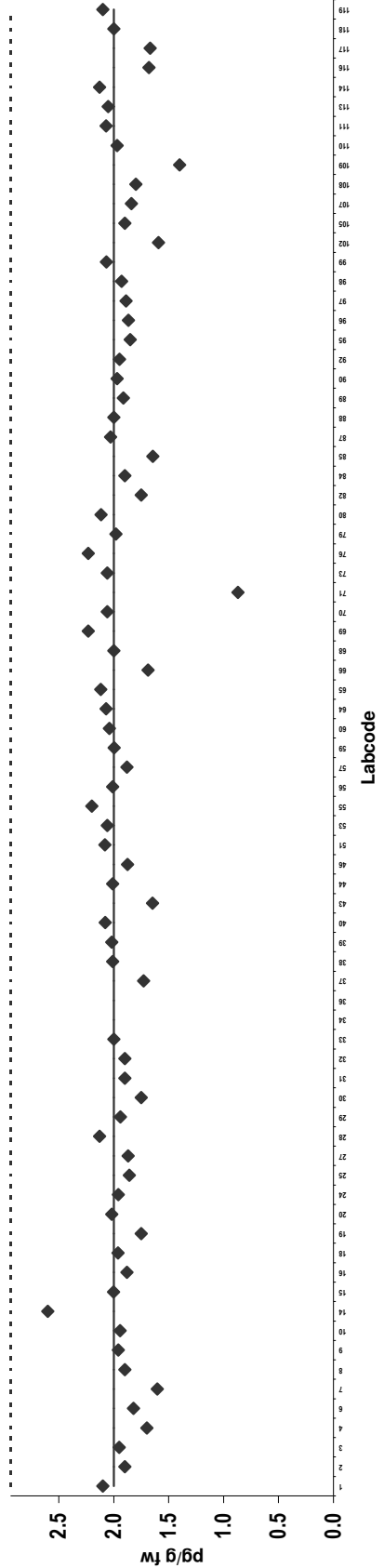
Congener: 2,3,7,8 TCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	2.1		70	2.1	
2	1.9		71	0.87	Outlier
3	2.0		73	2.1	
4	1.7		76	2.2	
6	1.8		79	2.0	
7	1.6		80	2.1	
8	1.9		82	1.8	
9	2.0		84	1.9	
10	1.9		85	1.6	
14	2.6		87	2.0	
15	2.0		88	2.0	
16	1.9		89	1.9	
18	2.0		90	2.0	
19	1.8		92	1.9	
20	2.0		95	1.8	
24	2.0		96	1.9	
25	1.9		97	1.9	
27	1.9		98	1.9	
28	2.1		99	2.1	
29	1.9		102	1.6	
30	1.8		105	1.9	
31	1.9		107	1.8	
32	1.9		108	1.8	
33	2.0		109	1.4	
34	1.0		110	2.0	
36	3.1	Outlier	111	2.1	
37	1.7	Outlier	113	2.1	
38	2.0		114	2.1	
39	2.0		116	1.7	
40	2.1		117	1.7	
43	1.6		118	2.0	
44	2.0		119	2.1	
46	1.9				
51	2.1				
53	2.1				
55	2.2				
56	2.0				
57	1.9				
59	2.0				
60	2.0				
64	2.1				
65	2.1				
66	1.7				
68	2.0				
69	2.2				

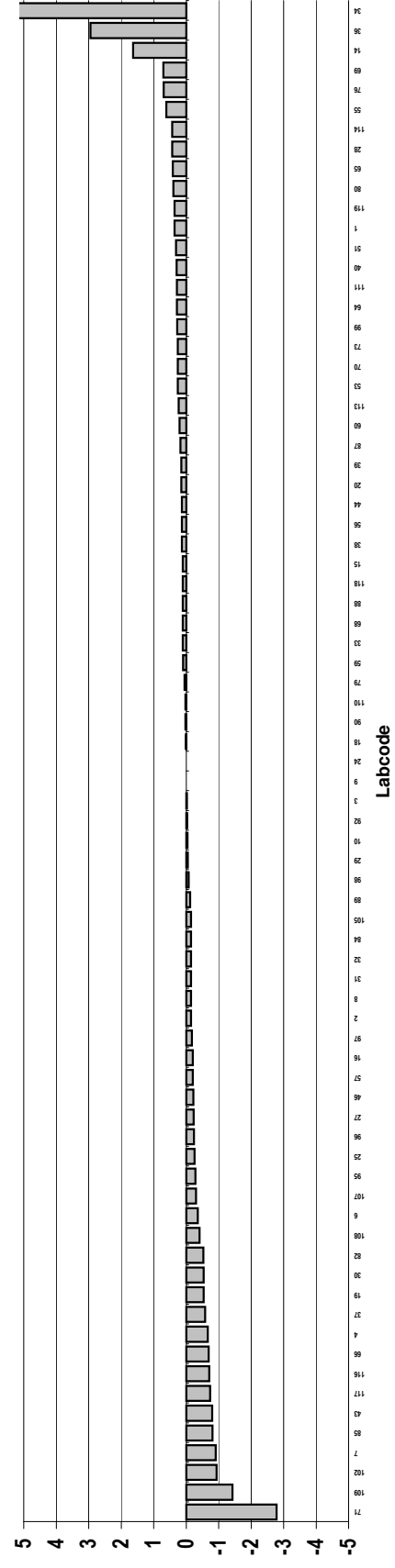
Consensus statistics

Consensus median, pg/μL	2.0
Median all values pg/μL	2.0
Consensus mean, pg/μL	1.9
Standard deviation, pg/μL	0.18
Relative standard deviation, %	9.1
No. of values reported	77
No. of values removed	3
No. of reported non-detects	0

2,3,7,8 TCDF



Z-score: 2,3,7,8 TCDF



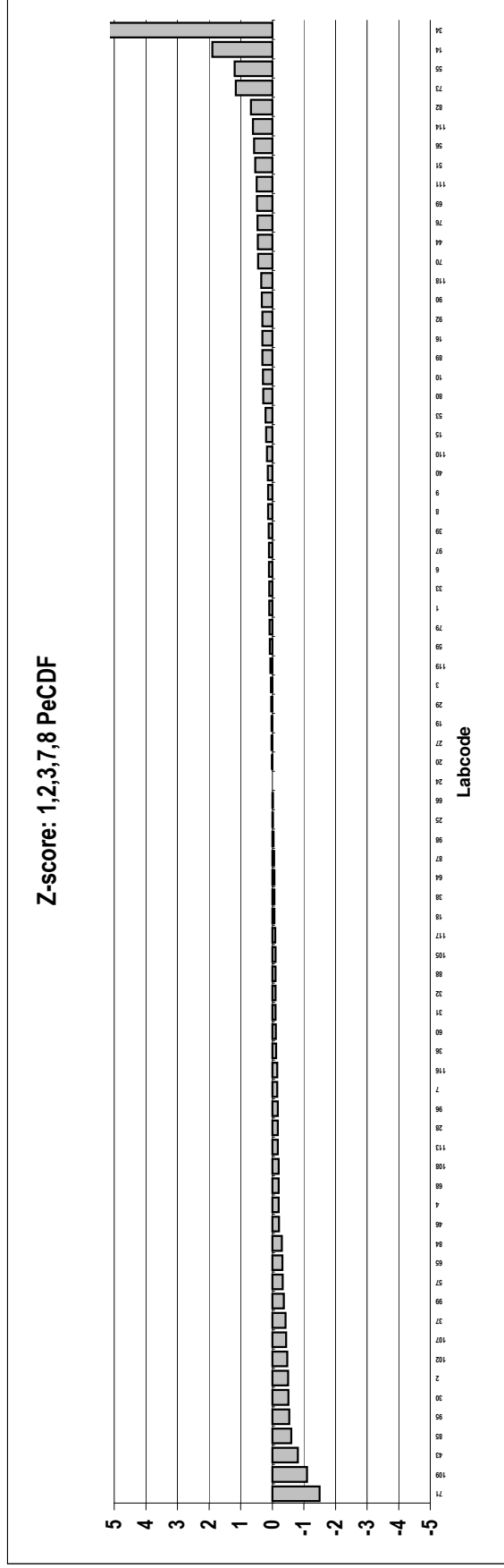
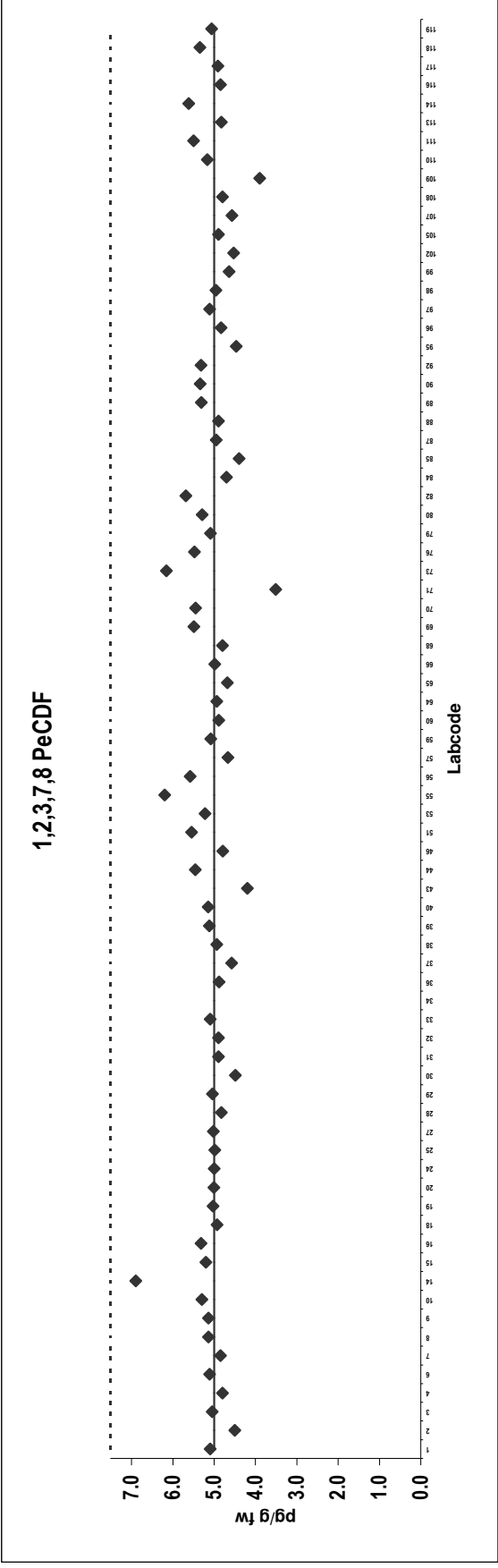
Analyte solution

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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.1		70	5.5	
2	4.5		71	3.5	
3	5.1		73	6.2	
4	4.8		76	5.5	
6	5.1		79	5.1	
7	4.8		80	5.3	
8	5.1		82	5.7	
9	5.1		84	4.7	
10	5.3		85	4.4	
14	6.9		87	5.0	
15	5.2		88	4.9	
16	5.3		89	5.3	
18	4.9		90	5.3	
19	5.0		92	5.3	
20	5.0		95	4.5	
24	5.0		96	4.8	
25	5.0		97	5.1	
27	5.0		98	5.0	
28	4.8		99	4.6	
29	5.0		102	4.5	
30	4.5		105	4.9	
31	4.9		107	4.6	
32	4.9		108	4.8	
33	5.1		109	3.9	
34	5.0		110	5.2	
36	4.9		111	5.5	
37	4.6		113	4.8	
38	4.9		114	5.6	
39	5.1		116	4.9	
40	5.1		117	4.9	
43	4.2		118	5.4	
44	5.5		119	5.1	
46	4.8				
51	5.5				
53	5.2				
55	6.2				
56	5.6				
57	4.7				
59	5.1				
60	4.9				
64	4.9				
65	4.7				
66	5.0				
68	4.8				
69	5.5				

Outlier

Consensus statistics	
Consensus median, pg/μL	5.0
Median all values pg/μL	5.0
Consensus mean, pg/μL	5.0
Standard deviation, pg/μL	0.47
Relative standard deviation, %	9.3
No. of values reported	77
No. of values removed	1
No. of reported non-detects	0



Analyte solution

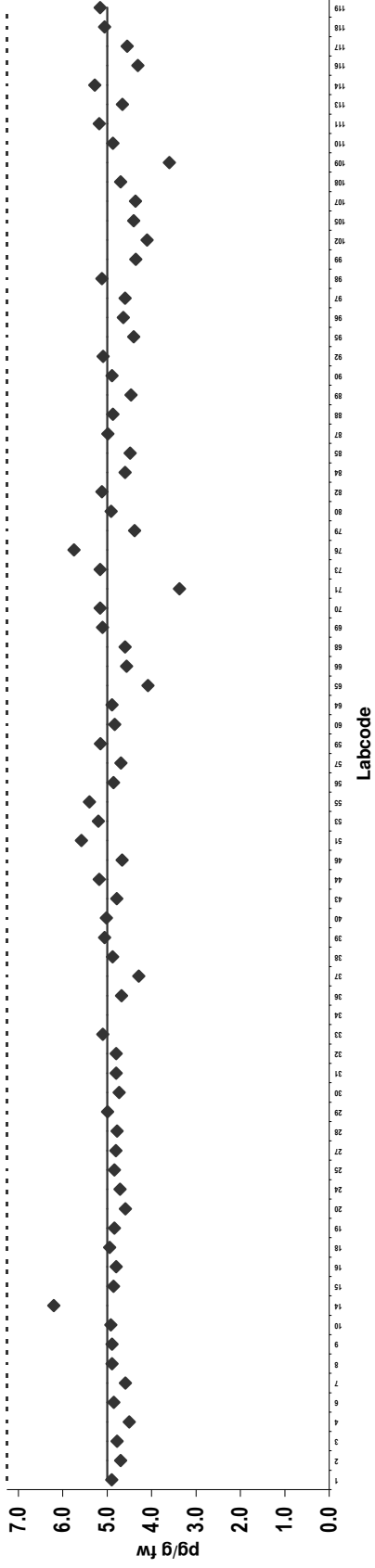
Congener: 2,3,4,7,8 PeCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	4.9		70	5.2	
2	4.7		71	3.4	
3	4.8		73	5.2	
4	4.5		76	5.7	
6	4.9		79	4.4	
7	4.6		80	4.9	
8	4.9		82	5.1	
9	4.9		84	4.6	
10	4.9		85	4.5	
14	6.2		87	5.0	
15	4.9		88	4.9	
16	4.8		89	4.5	
18	4.9		90	4.9	
19	4.8		92	5.1	
20	4.6		95	4.4	
24	4.7		96	4.6	
25	4.8		97	4.6	
27	4.8		98	5.1	
28	4.8		99	4.4	
29	5.0		102	4.1	
30	4.7		105	4.4	
31	4.8		107	4.4	
32	4.8		108	4.7	
33	5.1		109	3.6	
34	5.0		110	4.9	
36	4.7		111	5.2	
37	4.3		113	4.7	
38	4.9		114	5.3	
39	5.1		116	4.3	
40	5.0		117	4.6	
43	4.8		118	5.1	
44	5.2		119	5.2	
46	4.7				
51	5.6				
53	5.2				
55	5.4				
56	4.9				
57	4.7				
59	5.2				
60	4.8				
64	4.9				
65	4.1				
66	4.6				
68	4.6				
69	5.1				

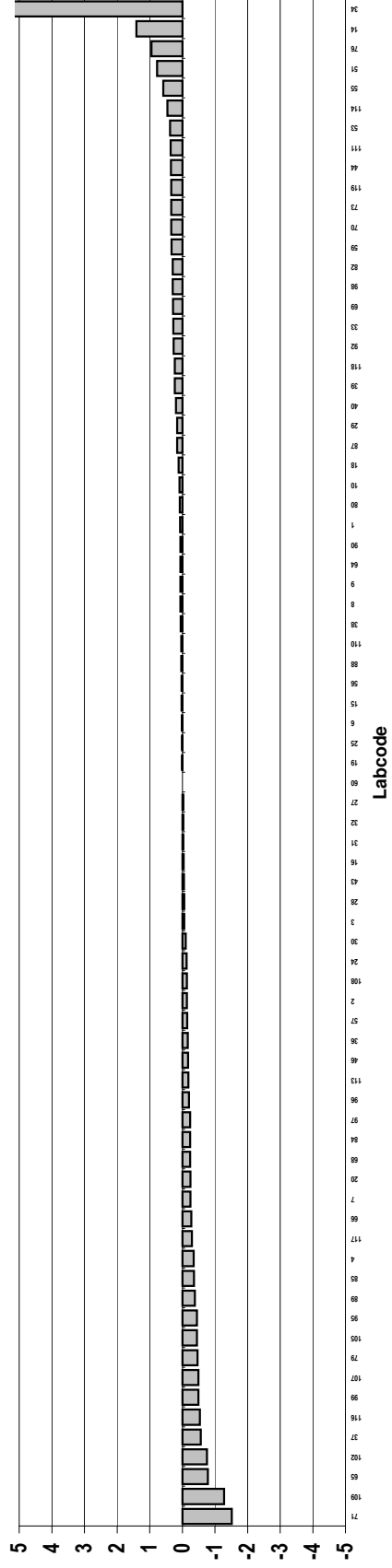
Outlier

Consensus statistics	
Consensus median, pg/μL	4.8
Median all values pg/μL	4.8
Consensus mean, pg/μL	4.8
Standard deviation, pg/μL	0.41
Relative standard deviation, %	8.5
No. of values reported	77
No. of values removed	1
No. of reported non-detects	0

2,3,4,7,8 PeCDF



Z-score: 2,3,4,7,8 PeCDF



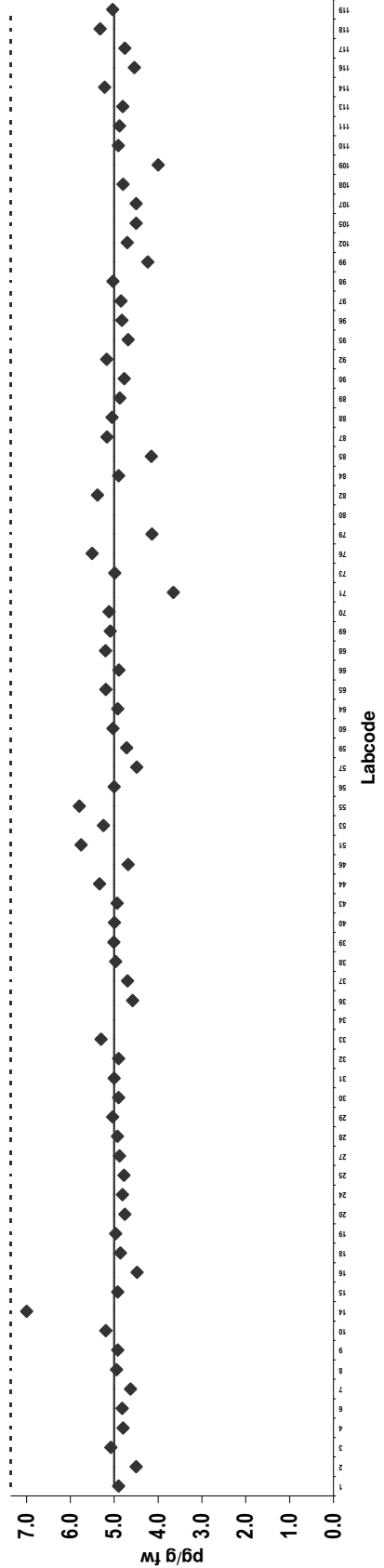
Analyte solution
Congener: 1,2,3,4,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	4.9		70	5.1	
2	4.5		71	3.7	
3	5.1		73	5.0	
4	4.8		76	5.5	
6	4.8		79	4.1	
7	4.6		80	7.6	Outlier
8	5.0		82	5.4	
9	4.9		84	4.9	
10	5.2		85	4.2	
14	7.0		87	5.2	
15	4.9		88	5.1	
16	4.5		89	4.9	
18	4.9		90	4.8	
19	5.0		92	5.2	
20	4.8		95	4.7	
24	4.8		96	4.8	
25	4.8		97	4.9	
27	4.9		98	5.0	
28	4.9		99	4.2	
29	5.0		102	4.7	
30	4.9		105	4.5	
31	5.0		107	4.5	
32	4.9		108	4.8	
33	5.3		109	4.0	
34	5.0		110	4.9	
36	4.6		111	4.9	
37	4.7		113	4.8	
38	5.0		114	5.2	
39	5.0		116	4.5	
40	5.0		117	4.8	
43	4.9		118	5.3	
44	5.3		119	5.0	
46	4.7				
51	5.8				
53	5.3				
55	5.8				
56	5.0				
57	4.5				
59	4.7				
60	5.0				
64	4.9				
65	5.2				
66	4.9				
68	5.2				
69	5.1				

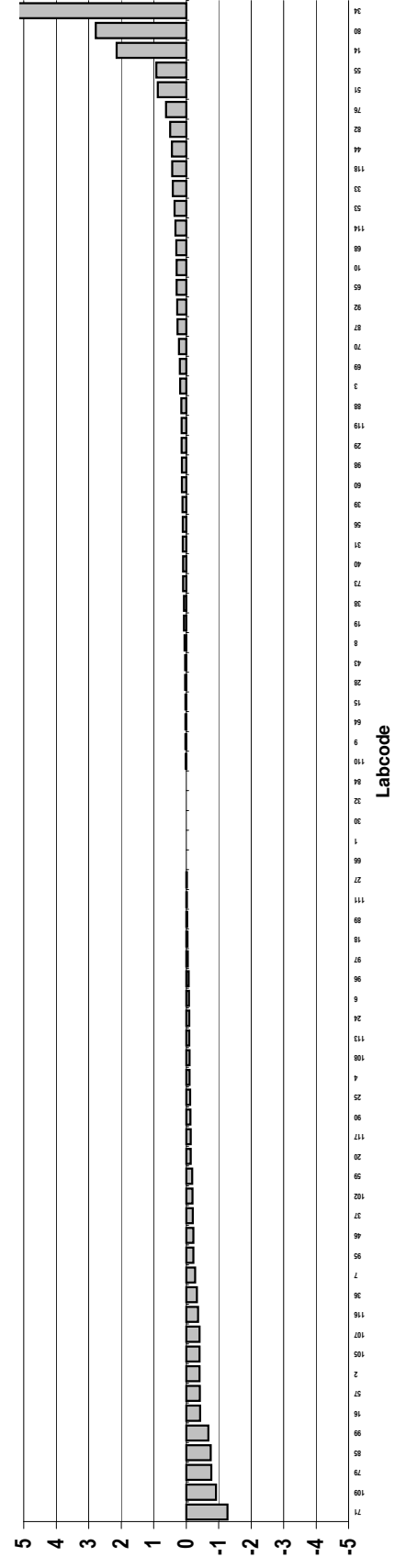
Consensus statistics

Consensus median, pg/μL	4.9
Median all values pg/μL	4.9
Consensus mean, pg/μL	4.9
Standard deviation, pg/μL	0.43
Relative standard deviation, %	8.7
No. of values reported	77
No. of values removed	2
No. of reported non-detects	0

1,2,3,4,7,8 HxCDF



Z-score: 1,2,3,4,7,8 HxCDF



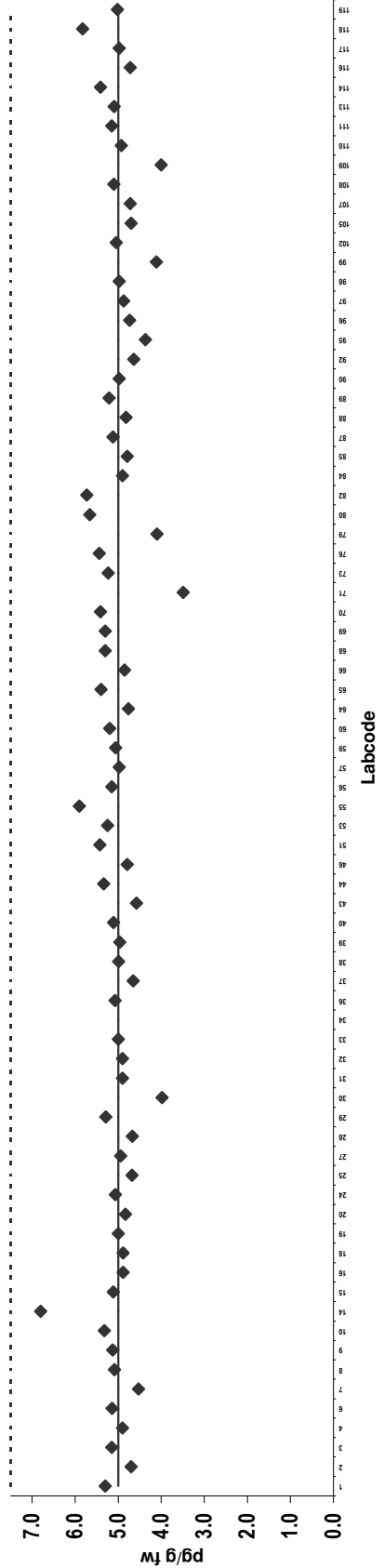
Analyte solution
Congener: 1,2,3,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.3		70	5.4	
2	4.7		71	3.5	
3	5.2		73	5.2	
4	4.9		76	5.4	
6	5.1		79	4.1	
7	4.5		80	5.7	
8	5.1		82	5.7	
9	5.1		84	4.9	
10	5.3		85	4.8	
14	6.8		87	5.1	
15	5.1		88	4.8	
16	4.9		89	5.2	
18	4.9		90	5.0	
19	5.0		92	4.6	
20	4.8		95	4.4	
24	5.1		96	4.7	
25	4.7		97	4.9	
27	4.9		98	5.0	
28	4.7		99	4.1	
29	5.3		102	5.0	
30	4.0		105	4.7	
31	4.9		107	4.7	
32	4.9		108	5.1	
33	5.0		109	4.0	
34	5.0		110	4.9	
36	5.1		111	5.2	
37	4.7		113	5.1	
38	5.0		114	5.4	
39	5.0		116	4.7	
40	5.1		117	5.0	
43	4.6		118	5.8	
44	5.3		119	5.0	
46	4.8				
51	5.4				
53	5.3				
55	5.9				
56	5.2				
57	5.0				
59	5.1				
60	5.2				
64	4.8				
65	5.4				
66	4.9				
68	5.3				
69	5.3				

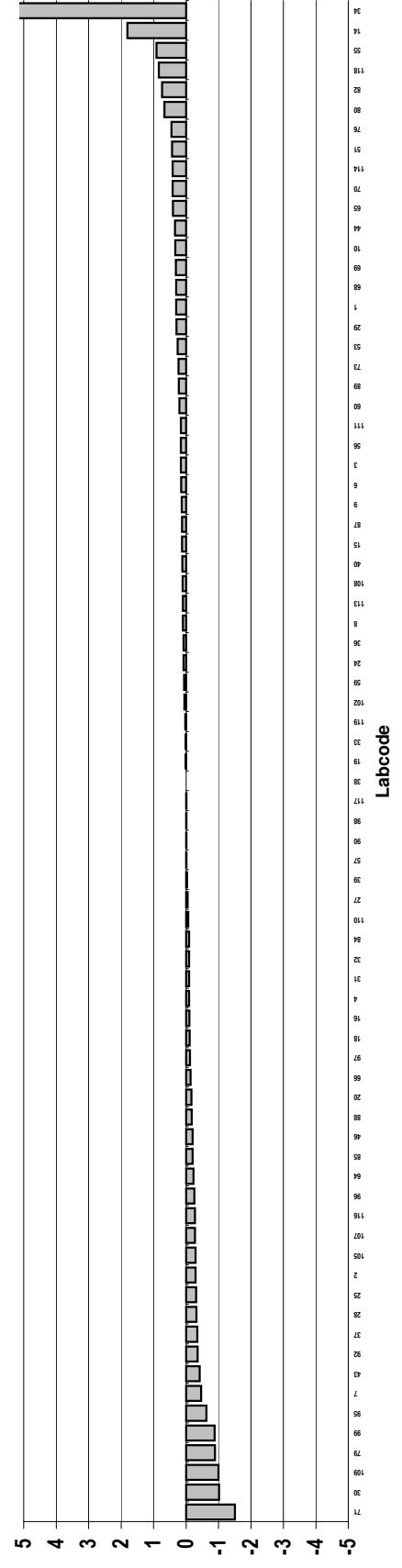
Outlier

Consensus statistics	
Consensus median, pg/μL	5.0
Median all values pg/μL	5.0
Consensus mean, pg/μL	5.0
Standard deviation, pg/μL	0.45
Relative standard deviation, %	9.1
No. of values reported	77
No. of values removed	1
No. of reported non-detects	0

1,2,3,6,7,8 HxCDF



Z-score: 1,2,3,6,7,8 HxCDF



Analyte solution

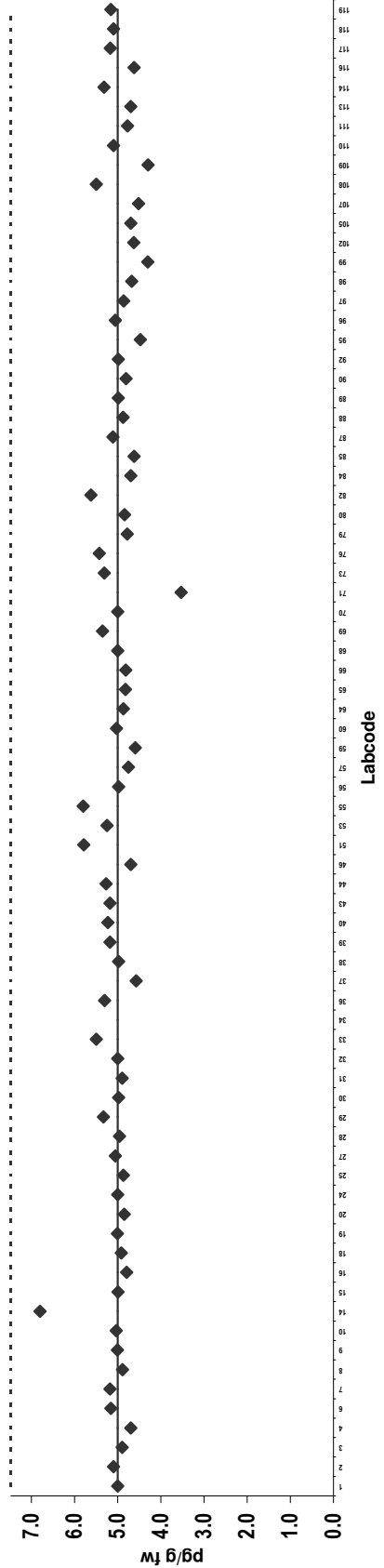
Congener: 2,3,4,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.0		70	5.0	
2	5.1		71	3.5	
3	4.9		73	5.3	
4	4.7		76	5.4	
6	5.2		79	4.8	
7	5.2		80	4.8	
8	4.9		82	5.6	
9	5.0		84	4.7	
10	5.0		85	4.6	
14	6.8		87	5.1	
15	5.0		88	4.9	
16	4.8		89	5.0	
18	4.9		90	4.8	
19	5.0		92	5.0	
20	4.9		95	4.5	
24	5.0		96	5.1	
25	4.9		97	4.9	
27	5.1		98	4.7	
28	5.0		99	4.3	
29	5.3		102	4.6	
30	5.0		105	4.7	
31	4.9		107	4.5	
32	5.0		108	5.5	
33	5.5		109	4.3	
34	5.0		110	5.1	
36	5.3		111	4.8	
37	4.6		113	4.7	
38	5.0		114	5.3	
39	5.2		116	4.6	
40	5.2		117	5.2	
43	5.2		118	5.1	
44	5.3		119	5.2	
46	4.7				
51	5.8				
53	5.3				
55	5.8				
56	5.0				
57	4.8				
59	4.6				
60	5.0				
64	4.9				
65	4.8				
66	4.8				
68	5.0				
69	5.4				
		Outlier			

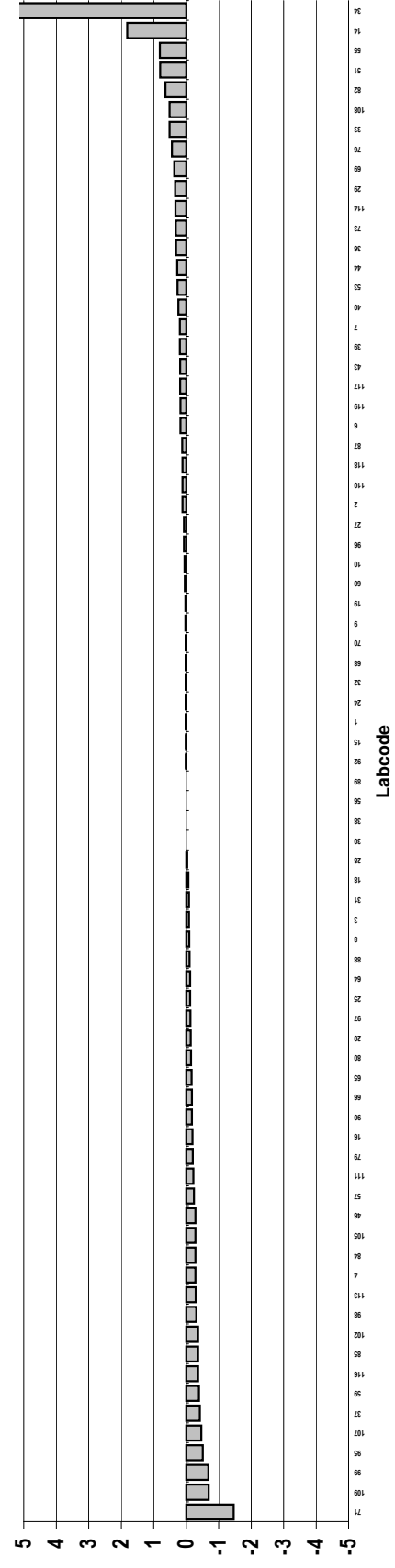
Consensus statistics

Consensus median, pg/μL	5.0
Median all values pg/μL	5.0
Consensus mean, pg/μL	5.0
Standard deviation, pg/μL	0.40
Relative standard deviation, %	8.0
No. of values reported	77
No. of values removed	1
No. of reported non-detects	0

2,3,4,6,7,8 HxCDF



Z-score: 2,3,4,6,7,8 HxCDF



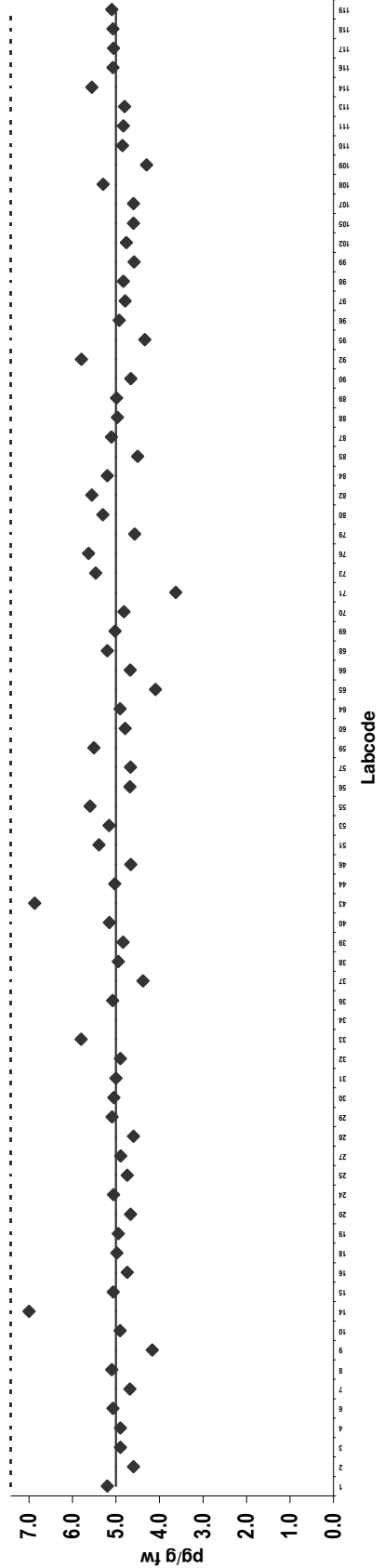
Analyte solution

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

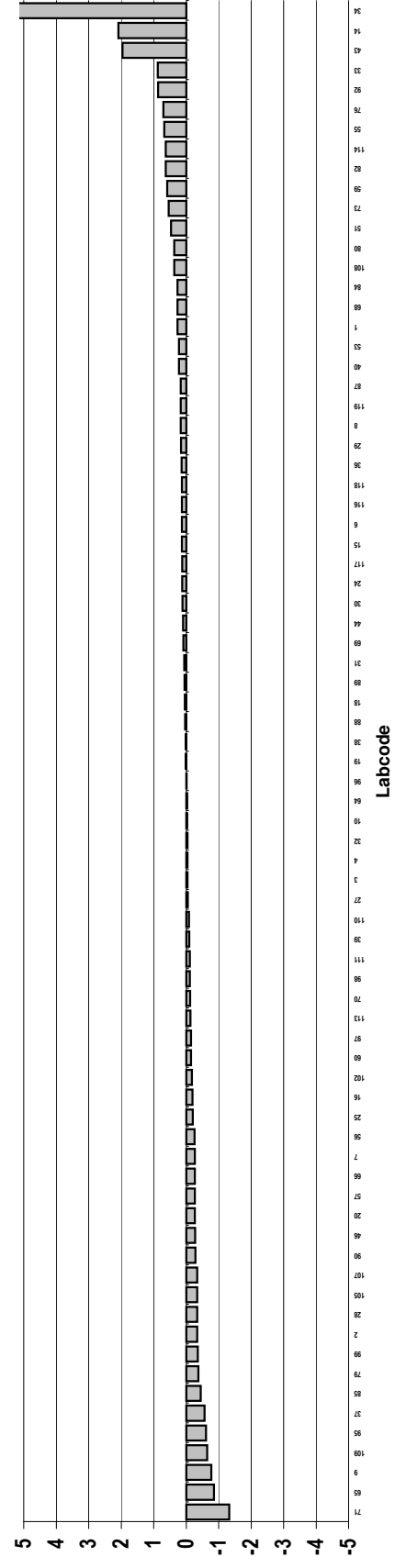
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.2		70	4.8	
2	4.6		71	3.6	
3	4.9		73	5.5	
4	4.9		76	5.6	
6	5.1		79	4.6	
7	4.7		80	5.3	
8	5.1		82	5.6	
9	4.2		84	5.2	
10	4.9		85	4.5	
14	7.0		87	5.1	
15	5.1		88	5.0	
16	4.7		89	5.0	
18	5.0		90	4.7	
19	5.0		92	5.8	
20	4.7		95	4.3	
24	5.1		96	4.9	
25	4.7		97	4.8	
27	4.9		98	4.8	
28	4.6		99	4.6	
29	5.1		102	4.8	
30	5.1		105	4.6	
31	5.0		107	4.6	
32	4.9		108	5.3	
33	5.8		109	4.3	
34	5.0		110	4.9	
36	5.1		111	4.8	
37	4.4		113	4.8	
38	5.0		114	5.6	
39	4.8		116	5.1	
40	5.2		117	5.1	
43	6.9		118	5.1	
44	5.0		119	5.1	
46	4.7				
51	5.4				
53	5.2				
55	5.6				
56	4.7				
57	4.7				
59	5.5				
60	4.8				
64	4.9				
65	4.1				
66	4.7				
68	5.2				
69	5.0				
		Outlier			

Consensus statistics	
Consensus median, pg/μL	4.9
Median all values pg/μL	5.0
Consensus mean, pg/μL	5.0
Standard deviation, pg/μL	0.50
Relative standard deviation, %	10
No. of values reported	77
No. of values removed	1
No. of reported non-detects	0

1,2,3,7,8,9 HxCDF



Z-score: 1,2,3,7,8,9 HxCDF



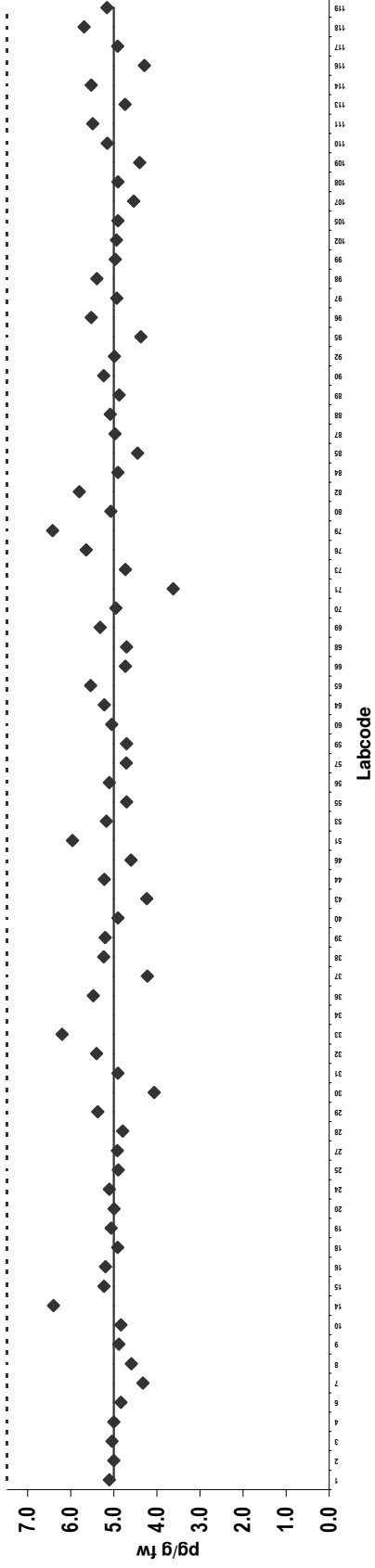
Analyte solution

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

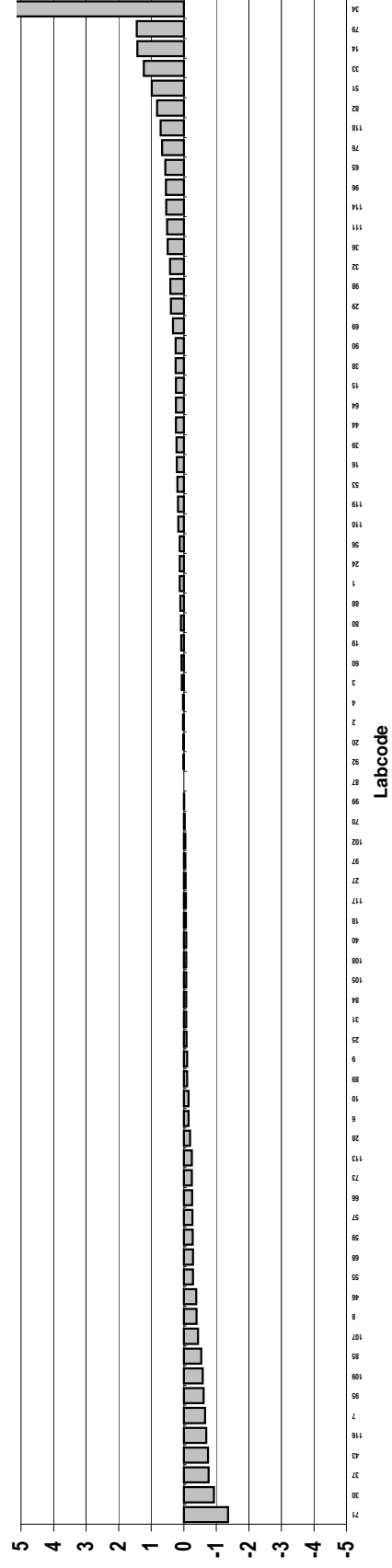
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.1		70	5.0	
2	5.0		71	3.6	
3	5.0		73	4.7	
4	5.0		76	5.6	
6	4.8		79	6.4	
7	4.3		80	5.1	
8	4.6		82	5.8	
9	4.9		84	4.9	
10	4.8		85	4.4	
14	6.4		87	5.0	
15	5.2		88	5.1	
16	5.2		89	4.9	
18	4.9		90	5.2	
19	5.1		92	5.0	
20	5.0		95	4.4	
24	5.1		96	5.5	
25	4.9		97	4.9	
27	4.9		98	5.4	
28	4.8		99	5.0	
29	5.4		102	4.9	
30	4.1		105	4.9	
31	4.9		107	4.5	
32	5.4		108	4.9	
33	6.2		109	4.4	
34	5.0		110	5.2	
36	5.5		111	5.5	
37	4.2		113	4.7	
38	5.2		114	5.5	
39	5.2		116	4.3	
40	4.9		117	4.9	
43	4.2		118	5.7	
44	5.2		119	5.2	
46	4.6				
51	6.0				
53	5.2				
55	4.7				
56	5.1				
57	4.7				
59	4.7				
60	5.1				
64	5.2				
65	5.5				
66	4.7				
68	4.7				
69	5.3				
		Outlier			

Consensus statistics	
Consensus median, pg/μL	5.0
Median all values pg/μL	5.0
Consensus mean, pg/μL	5.0
Standard deviation, pg/μL	0.48
Relative standard deviation, %	9.6
No. of values reported	77
No. of values removed	1
No. of reported non-detects	0

1,2,3,4,6,7,8 HpCDF



Z-score: 1,2,3,4,6,7,8 HpCDF



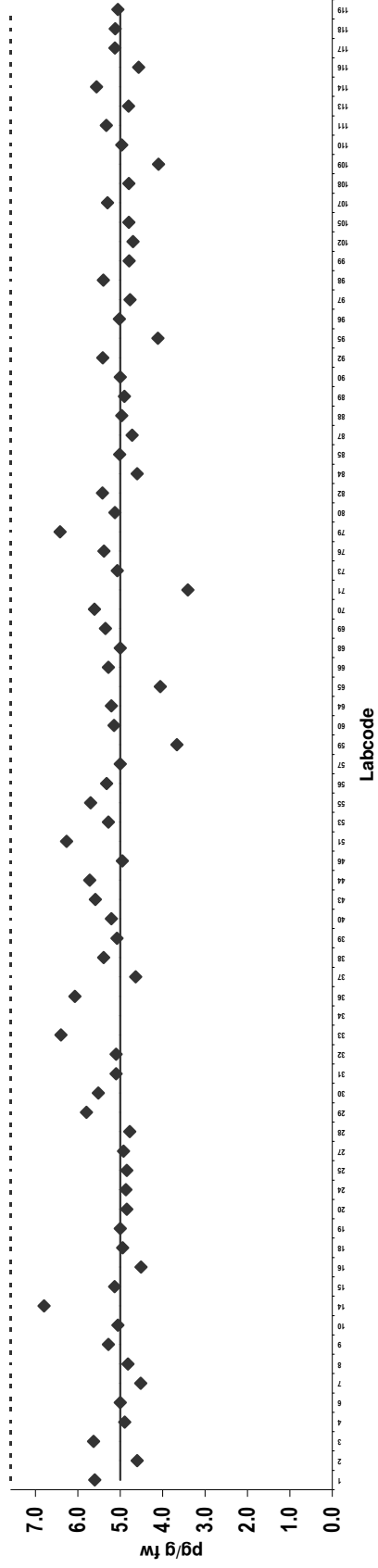
Analyte solution

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

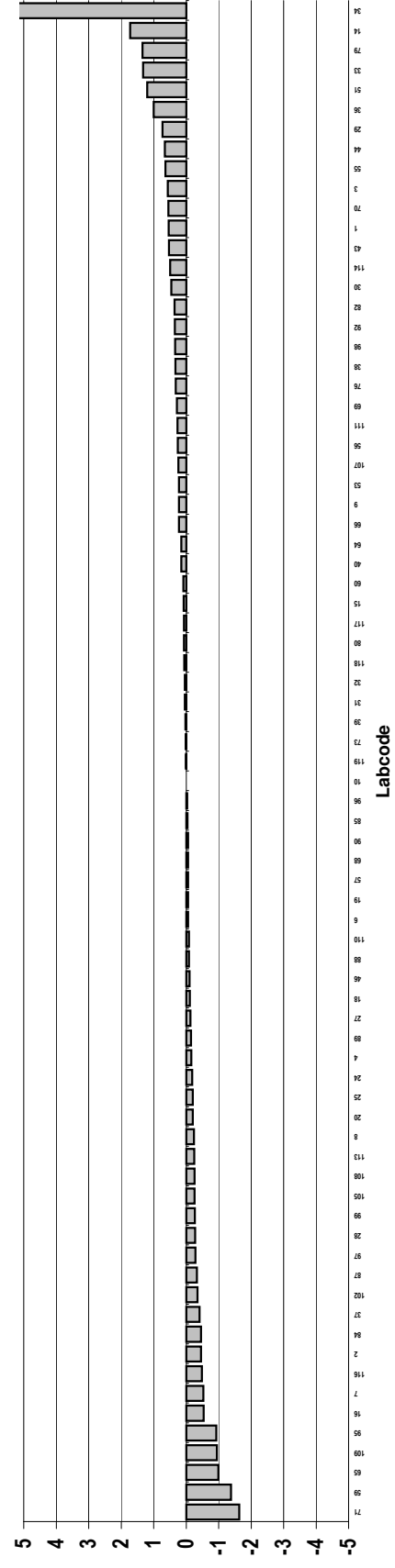
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.6		70	5.6	
2	4.6		71	3.4	
3	5.6		73	5.1	
4	4.9		76	5.4	
6	5.0		79	6.4	
7	4.5		80	5.1	
8	4.8		82	5.4	
9	5.3		84	4.6	
10	5.1		85	5.0	
14	6.8		87	4.7	
15	5.1		88	5.0	
16	4.5		89	4.9	
18	4.9		90	5.0	
19	5.0		92	5.4	
20	4.9		95	4.1	
24	4.9		96	5.0	
25	4.9		97	4.8	
27	4.9		98	5.4	
28	4.8		99	4.8	
29	5.8		102	4.7	
30	5.5		105	4.8	
31	5.1		107	5.3	
32	5.1		108	4.8	
33	6.4		109	4.1	
34	5.0		110	5.0	
36	6.1		111	5.3	
37	4.6		113	4.8	
38	5.4		114	5.6	
39	5.1		116	4.6	
40	5.2		117	5.1	
43	5.6		118	5.1	
44	5.7		119	5.1	
46	5.0				
51	6.3				
53	5.3				
55	5.7				
56	5.3				
57	5.0				
59	3.7				
60	5.2				
64	5.2				
65	4.1				
66	5.3				
68	5.0				
69	5.4				
		Outlier			

Consensus statistics	
Consensus median, pg/ μ L	5.1
Median all values pg/ μ L	5.1
Consensus mean, pg/ μ L	5.1
Standard deviation, pg/ μ L	0.56
Relative standard deviation, %	11
No. of values reported	77
No. of values removed	1
No. of reported non-detects	0

1,2,3,4,7,8,9 HpCDF



Z-score: 1,2,3,4,7,8,9 HpCDF



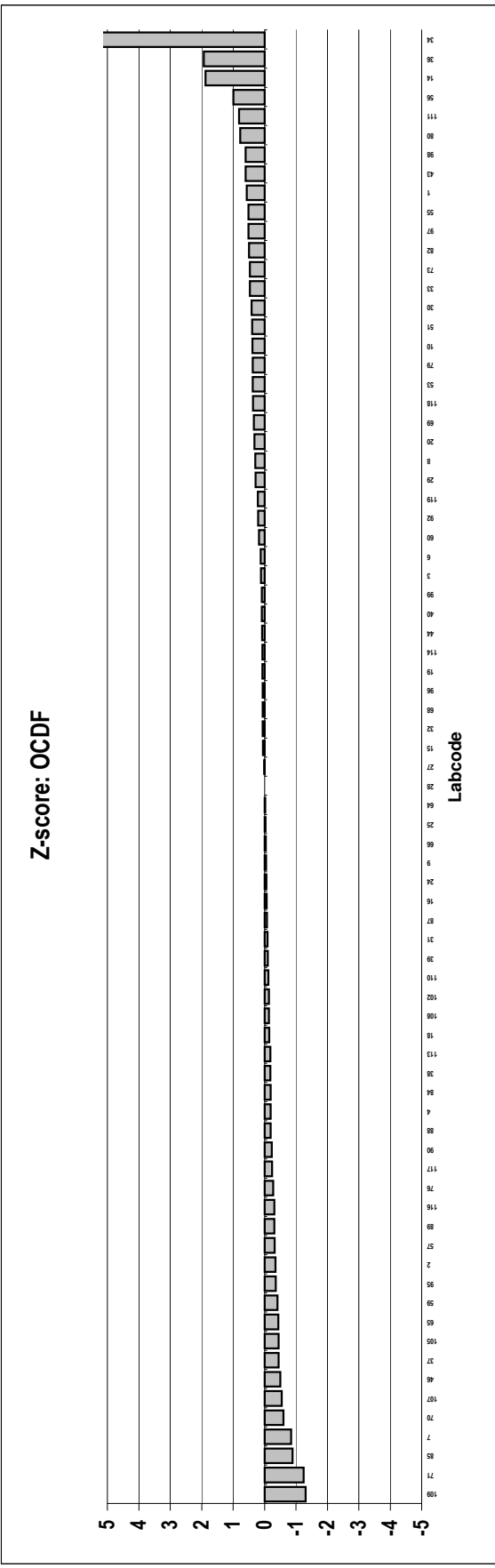
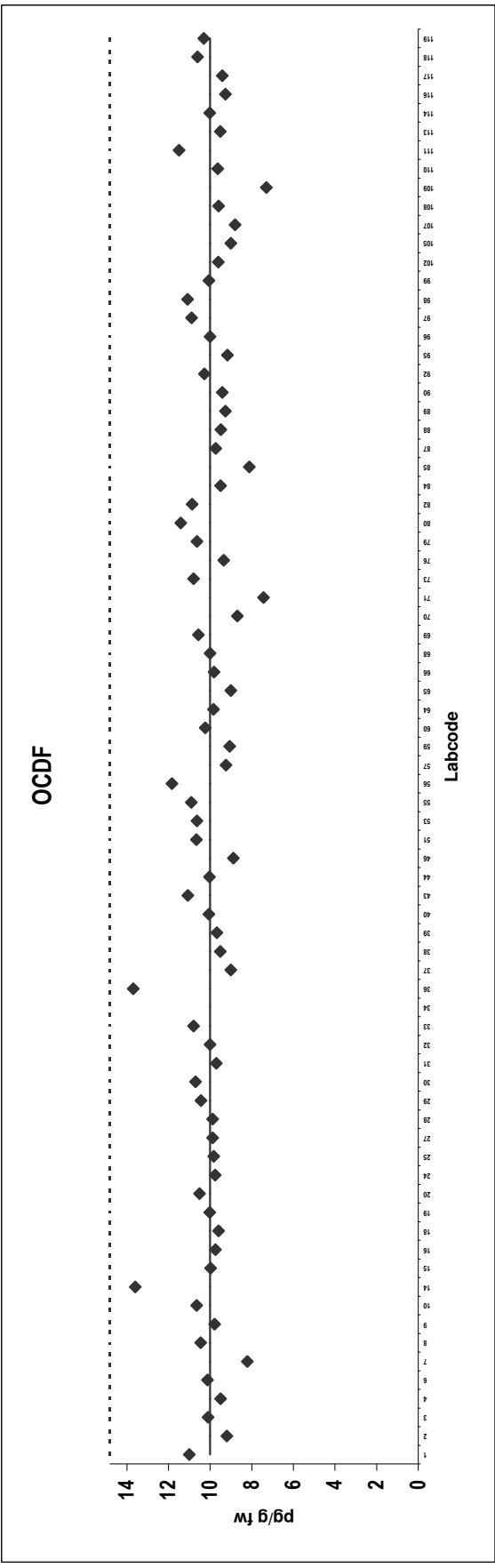
Analyte solution

Congener: OCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	11		70	8.7	
2	9.2		71	7.4	
3	10		73	11	
4	9.5		76	9.3	
6	10		79	11	
7	8.2		80	11	
8	10		82	11	
9	9.8		84	9.5	
10	11		85	8.1	
14	14		87	9.7	
15	10		88	9.5	
16	9.7		89	9.3	
18	9.6		90	9.4	
19	10		92	10	
20	11		95	9.2	
24	9.8		96	10	
25	9.8		97	11	
27	9.9		98	11	
28	9.9		99	10	
29	10		102	9.6	
30	11		105	9.0	
31	9.7		107	8.8	
32	10		108	9.6	
33	11		109	7.3	
34	100	Outlier	110	9.6	
36	14		111	11	
37	9.0		113	9.5	
38	9.5		114	10	
39	9.7		116	9.3	
40	10		117	9.4	
43	11		118	11	
44	10		119	10	
46	8.9				
51	11				
53	11				
55	11				
56	12				
57	9.2				
59	9.1				
60	10				
64	9.8				
65	9.0				
66	9.8				
68	10				
69	11				

Consensus statistics

Consensus median, pg/μL	9.9
Median all values pg/μL	9.9
Consensus mean, pg/μL	10
Standard deviation, pg/μL	1.0
Relative standard deviation, %	10
No. of values reported	77
No. of values removed	1
No. of reported non-detects	0



Analyte solution

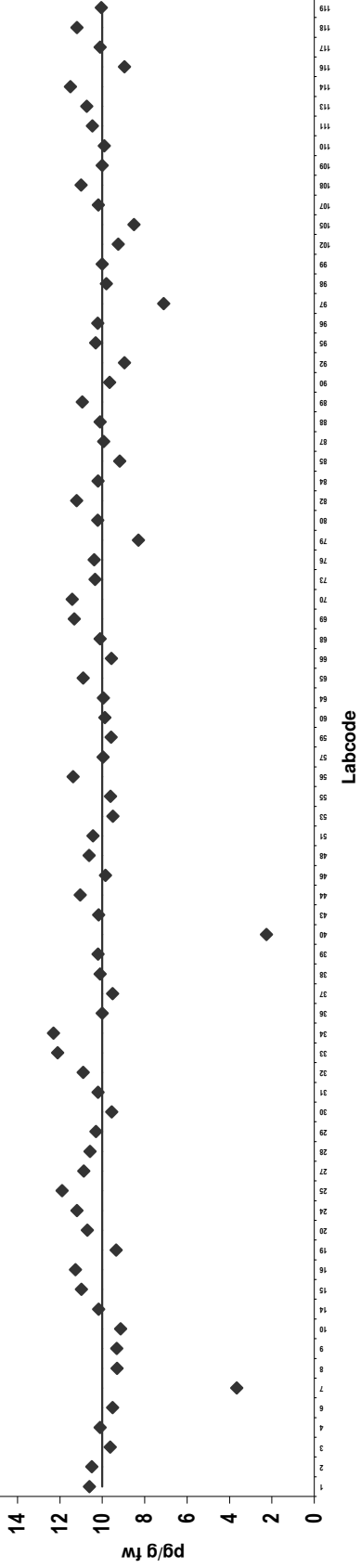
Congener: PCB 77

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	11		70	11	
2	11		73	10	
3	9.6		76	10	
4	10		79	8.3	
6	9.5		80	10	
7	3.7		82	11	
8	9.3		84	10	
9	9.3		85	9.2	
10	9.1		87	9.9	
14	10		88	10	
15	11		89	11	
16	11		90	9.7	
19	9.3		92	9.0	
20	11		95	10	
24	11		96	10	
25	12		97	7.1	
27	11		98	9.8	
28	11		99	10	
29	10		102	9.3	
30	9.6		105	8.5	
31	10		107	10	
32	11		108	11	
33	12		109	10	
34	12		110	9.9	
36	10		111	10	
37	9.5		113	11	
38	10		114	12	
39	10		116	9.0	
40	2.3		117	10	
43	10		118	11	
44	11		119	10	
46	9.8				
48	11				
51	10				
53	9.5				
55	9.6				
56	11				
57	10				
59	9.6				
60	9.9				
64	10				
65	11				
66	9.6				
68	10				
69	11				

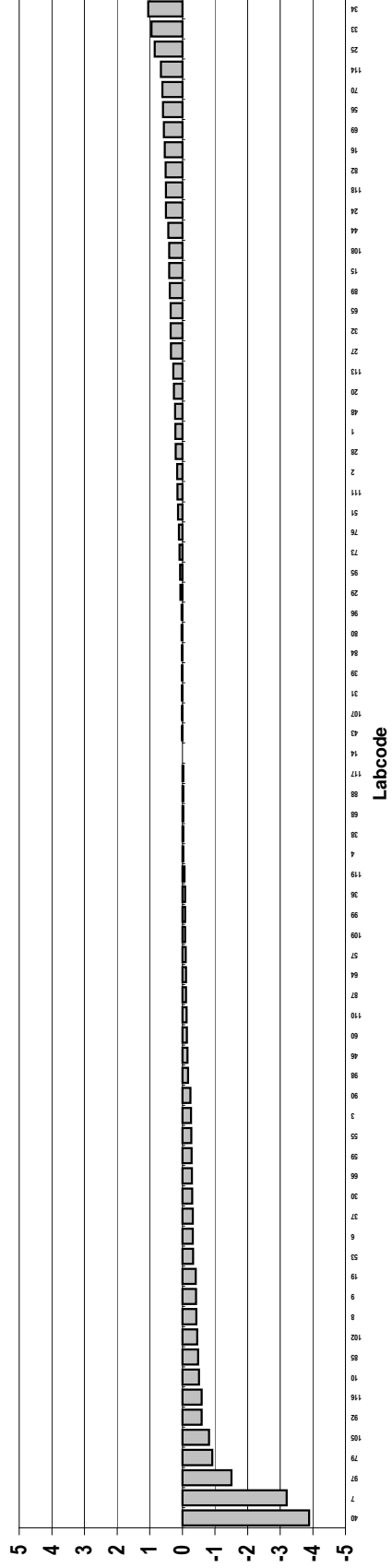
Consensus statistics

Consensus median, pg/μL	10
Median all values pg/μL	10
Consensus mean, pg/μL	10
Standard deviation, pg/μL	0.87
Relative standard deviation, %	8.5
No. of values reported	76
No. of values removed	2
No. of reported non-detects	0

PCB 77



Z-score: PCB 77



Analyte solution

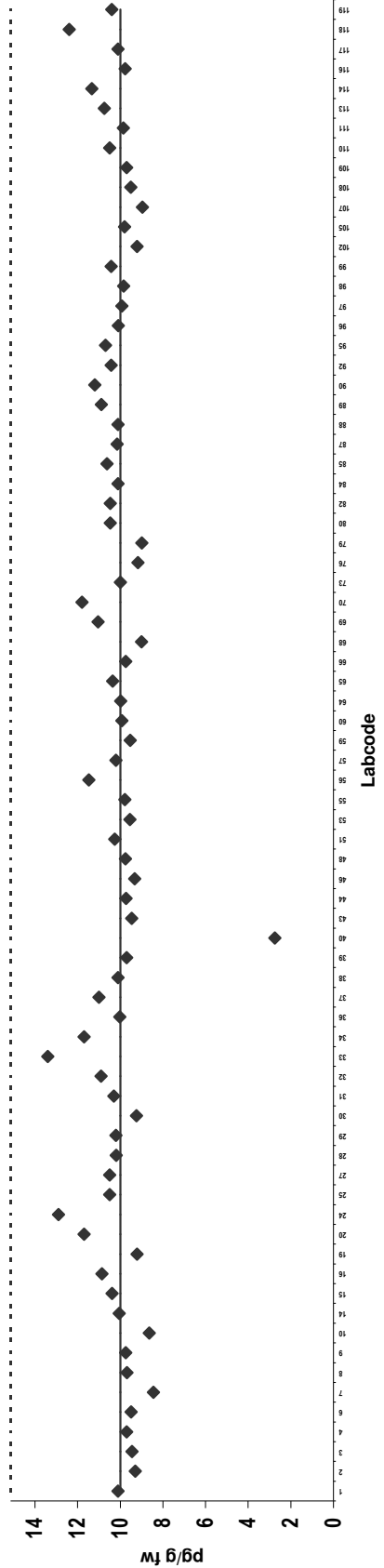
Congener: PCB 126

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	10		70	12	
2	9.3		73	10	
3	9.5		76	9.2	
4	9.7		79	9.0	
6	9.5		80	10	
7	8.4		82	10	
8	9.7		84	10	
9	9.7		85	11	
10	8.6		87	10	
14	10		88	10	
15	10		89	11	
16	11		90	11	
19	9.2		92	10	
20	12		95	11	
24	13		96	10	
25	11		97	9.9	
27	11		98	9.8	
28	10		99	10	
29	10		102	9.2	
30	9.2		105	9.8	
31	10		107	9.0	
32	11		108	9.5	
33	13		109	9.7	
34	12		110	11	
36	10		111	9.9	
37	11		113	11	
38	10		114	11	
39	9.7		116	9.8	
40	2.7	Outlier	117	10	
43	9.5		118	12	
44	9.7		119	10	
46	9.3				
48	9.8				
51	10				
53	9.5				
55	9.8				
56	11				
57	10				
59	9.5				
60	9.9				
64	10				
65	10				
66	9.7				
68	9.0				
69	11				

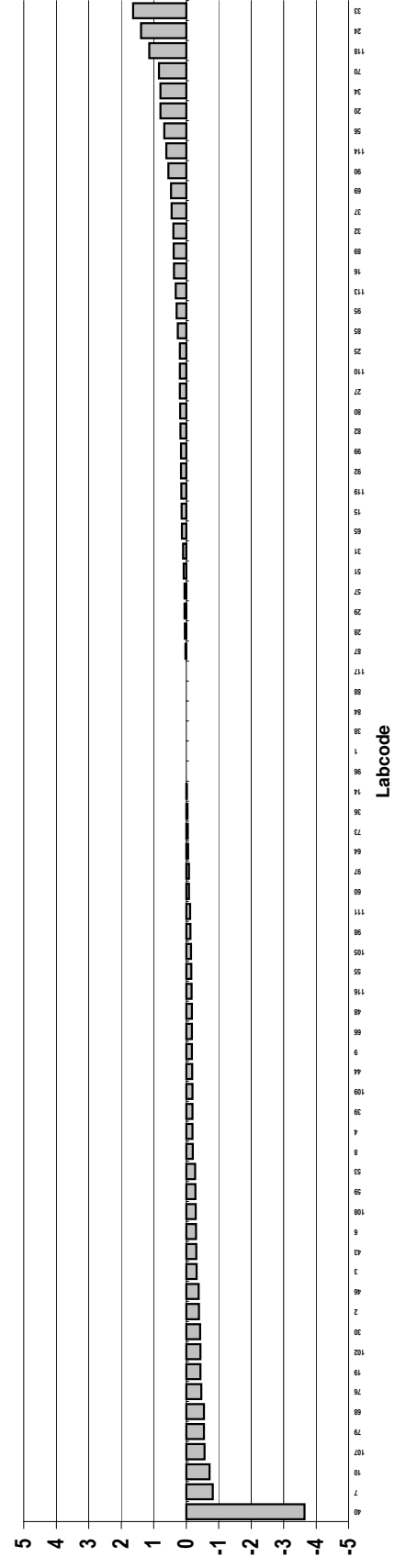
Consensus statistics

Consensus median, pg/μL	10
Median all values pg/μL	10
Consensus mean, pg/μL	10
Standard deviation, pg/μL	0.89
Relative standard deviation, %	8.7
No. of values reported	76
No. of values removed	1
No. of reported non-detects	0

PCB 126



Z-score: PCB 126



Analyte solution

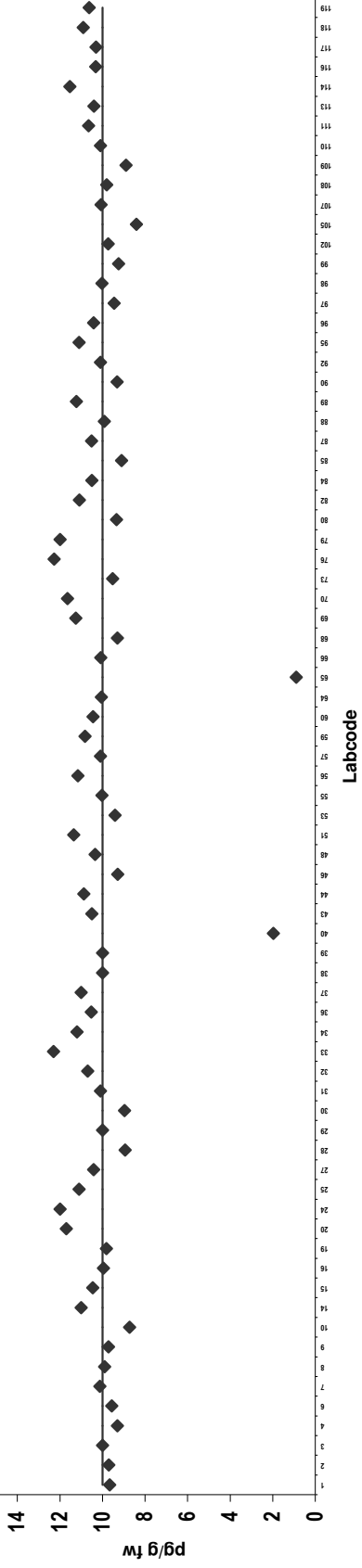
Congener: PCB 169

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	9.7		70	12	
2	9.7		73	9.5	
3	10		76	12	
4	9.3		79	12	
6	9.6		80	9.3	
7	10		82	11	
8	9.9		84	11	
9	9.7		85	9.1	
10	8.7		87	11	
14	11		88	9.9	
15	10		89	11	
16	10		90	9.3	
19	9.8		92	10	
20	12		95	11	
24	12		96	10	
25	11		97	9.5	
27	10		98	10	
28	8.9		99	9.2	
29	10		102	9.7	
30	9.0		105	8.4	
31	10		107	10	
32	11		108	9.8	
33	12		109	8.9	
34	11		110	10	
36	11		111	11	
37	11		113	10	
38	10		114	12	
39	10		116	10	
40	2.0	Outlier	117	10	
43	10		118	11	
44	11		119	11	
46	9.3				
48	10				
51	11				
53	9.4				
55	10				
56	11				
57	10				
59	11				
60	10				
64	10				
65	0.90				
66	10				
68	9.3				
69	11				

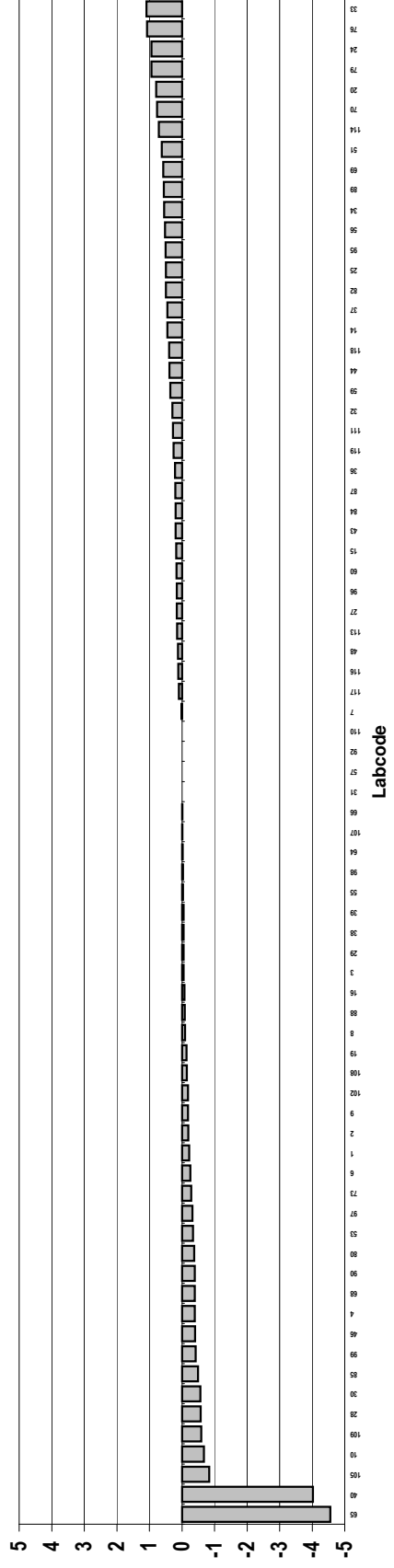
Consensus statistics

Consensus median, pg/μL	10
Median all values pg/μL	10
Consensus mean, pg/μL	10
Standard deviation, pg/μL	0.85
Relative standard deviation, %	8.3
No. of values reported	76
No. of values removed	2
No. of reported non-detects	0

PCB 169



Z-score: PCB 169



Analyte solution

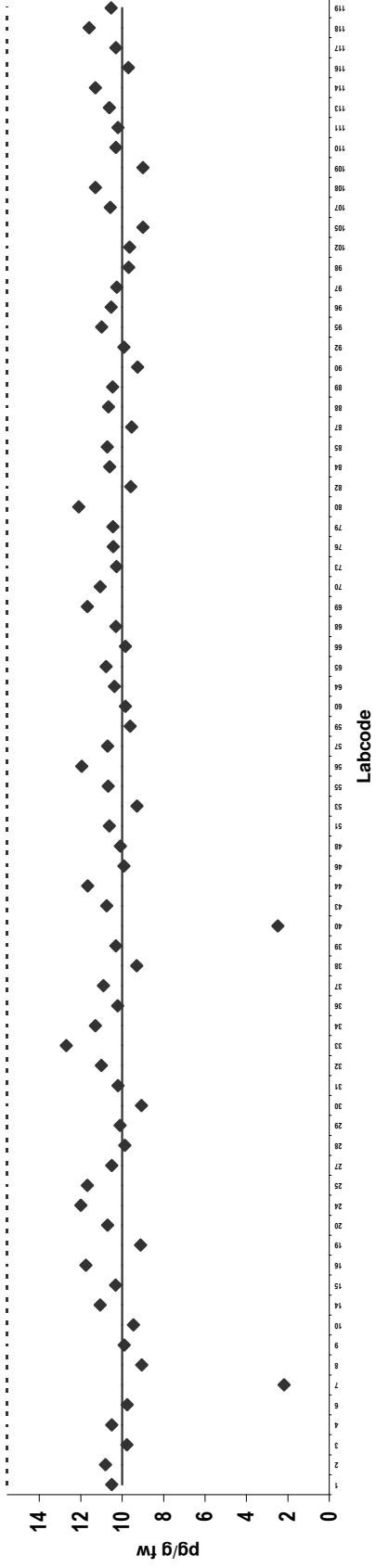
Congener: PCB 81

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	11		70	11	
2	11		73	10	
3	9.8		76	10	
4	11		79	10	
6	9.8		80	12	
7	2.2		82	9.6	
8	9.1		84	11	
9	9.9		85	11	
10	9.5		87	9.5	
14	11		88	11	
15	10		89	10	
16	12		90	9.3	
19	9.1		92	9.9	
20	11		95	11	
24	12		96	11	
25	12		97	10	
27	11		98	9.7	
28	9.9		102	9.7	
29	10		105	9.0	
30	9.1		107	11	
31	10		108	11	
32	11		109	9.0	
33	13		110	10	
34	11		111	10	
36	10		113	11	
37	11		114	11	
38	9.3		116	9.7	
39	10		117	10	
40	2.5		118	12	
43	11		119	11	
44	12				
46	9.9				
48	10				
51	11				
53	9.3				
55	11				
56	12				
57	11				
59	9.6				
60	9.9				
64	10				
65	11				
66	9.8				
68	10				
69	12				

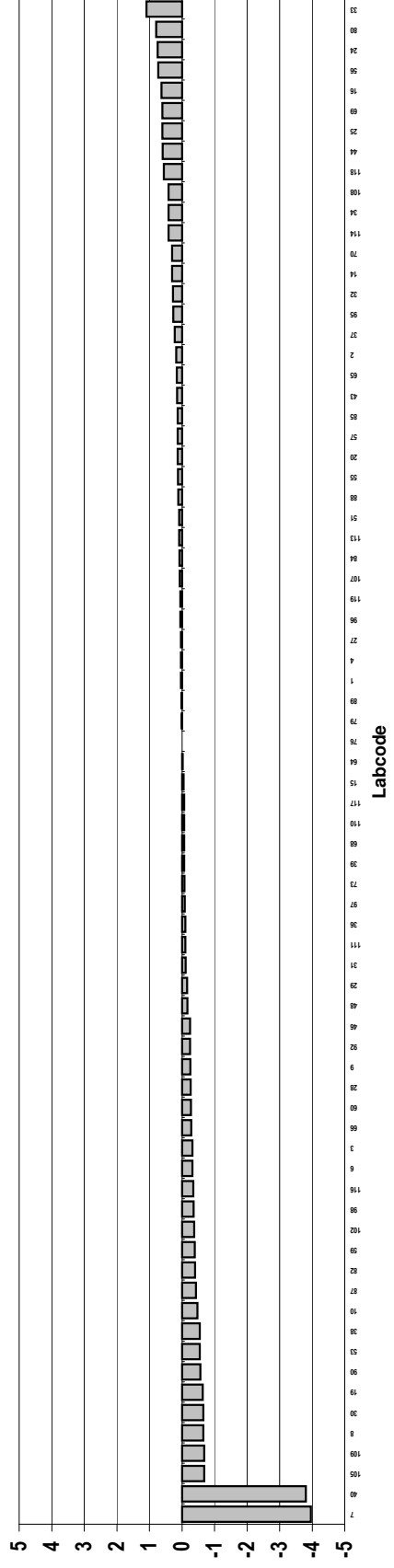
Consensus statistics

Consensus median, pg/μL	10
Median all values pg/μL	10
Consensus mean, pg/μL	10
Standard deviation, pg/μL	0.81
Relative standard deviation, %	7.7
No. of values reported	75
No. of values removed	2
No. of reported non-detects	0

PCB 81



Z-score: PCB 81



Analyte solution

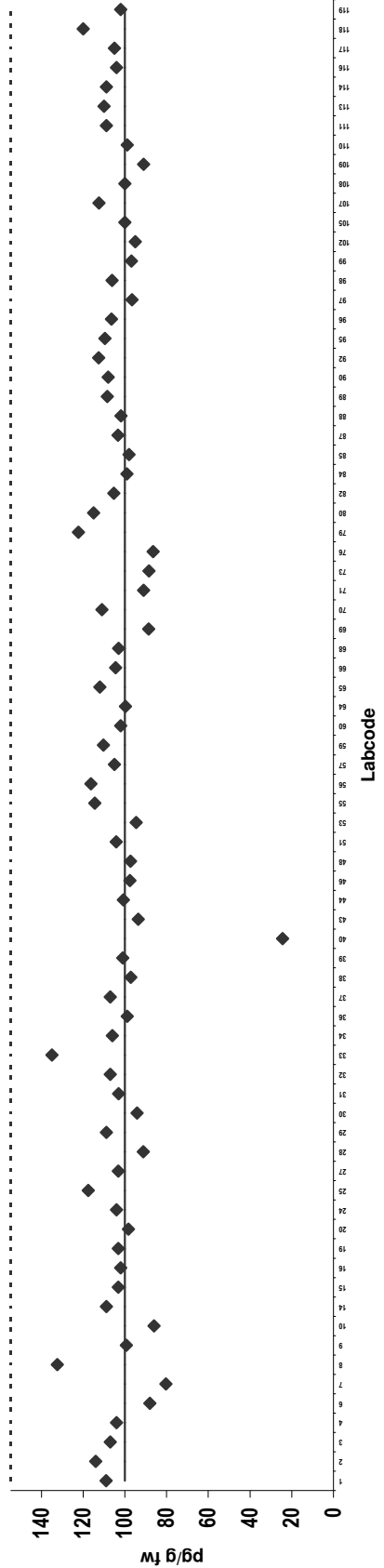
Congener: PCB 105

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	109		70	111	
2	114		71	91	
3	107		73	89	
4	104		76	87	
6	88		79	122	
7	80		80	115	
8	132		82	105	
9	99		84	99	
10	86		85	98	
14	109		87	103	
15	103		88	102	
16	102		89	108	
19	103		90	108	
20	98		92	113	
24	104		95	110	
25	118		96	106	
27	103		97	97	
28	91		98	106	
29	109		99	97	
30	94		102	95	
31	103		105	100	
32	107		107	113	
33	135		108	100	
34	106		109	91	
36	99		110	99	
37	107		111	109	
38	97		113	110	
39	101		114	109	
40	24		116	104	
43	94		117	105	
44	101		118	120	
46	98		119	102	
48	97				
51	104				
53	95				
55	114				
56	116				
57	105				
59	110				
60	102				
64	100				
65	112				
66	104				
68	103				
69	89				
		Outlier			

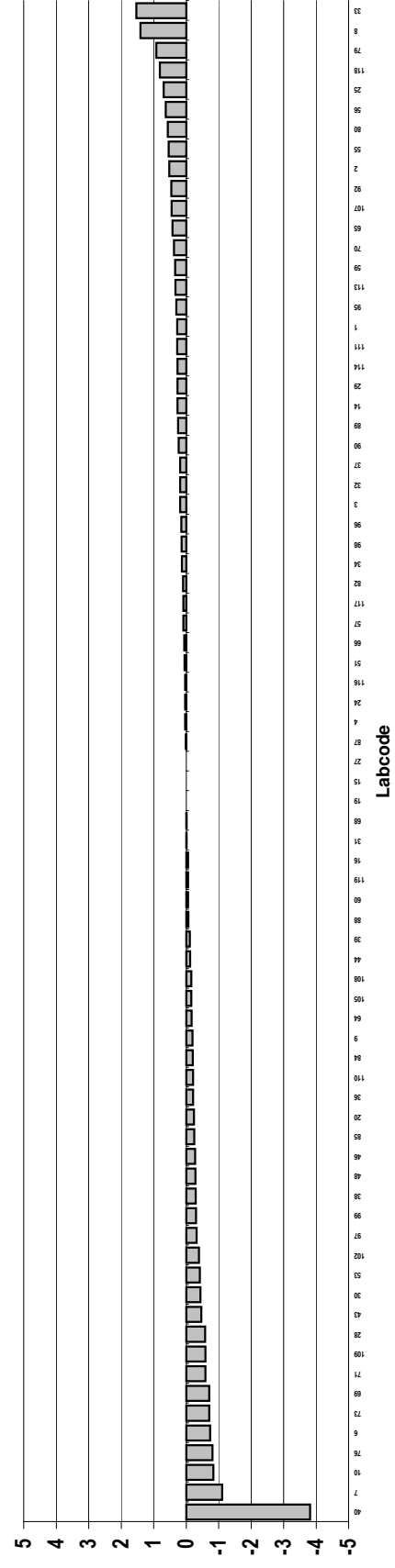
Consensus statistics

Consensus median, pg/µL	103
Median all values pg/µL	103
Consensus mean, pg/µL	104
Standard deviation, pg/µL	9.6
Relative standard deviation, %	9.2
No. of values reported	77
No. of values removed	1
No. of reported non-detects	0

PCB 105



Z-score: PCB 105



Analyte solution

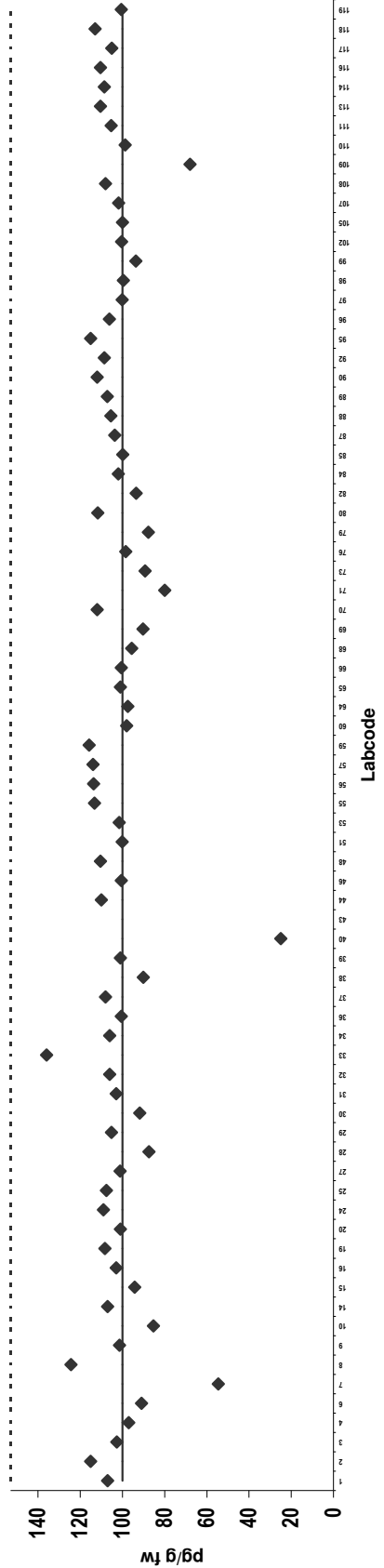
Congener: PCB 114

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	107		70	112	
2	115		71	80	
3	103		73	89	
4	97		76	98	
6	91		79	88	
7	55		80	112	
8	124		82	93	
9	101		84	102	
10	85		85	100	
14	107		87	104	
15	94		88	106	
16	103		89	107	
19	108		90	112	
20	101		92	109	
24	109		95	115	
25	108		96	106	
27	101		97	100	
28	87		98	100	
29	105		99	94	
30	92		102	100	
31	103		105	100	
32	106		107	102	
33	136		108	108	
34	106		109	68	
36	101		110	99	
37	108		111	105	
38	90		113	110	
39	101		114	109	
40	25		116	110	
43	158	Outlier	117	105	
44	110	Outlier	118	113	
46	101		119	101	
48	110				
51	100				
53	102				
55	113				
56	114				
57	114				
59	116				
60	98				
64	98				
65	101				
66	101				
68	96				
69	90				

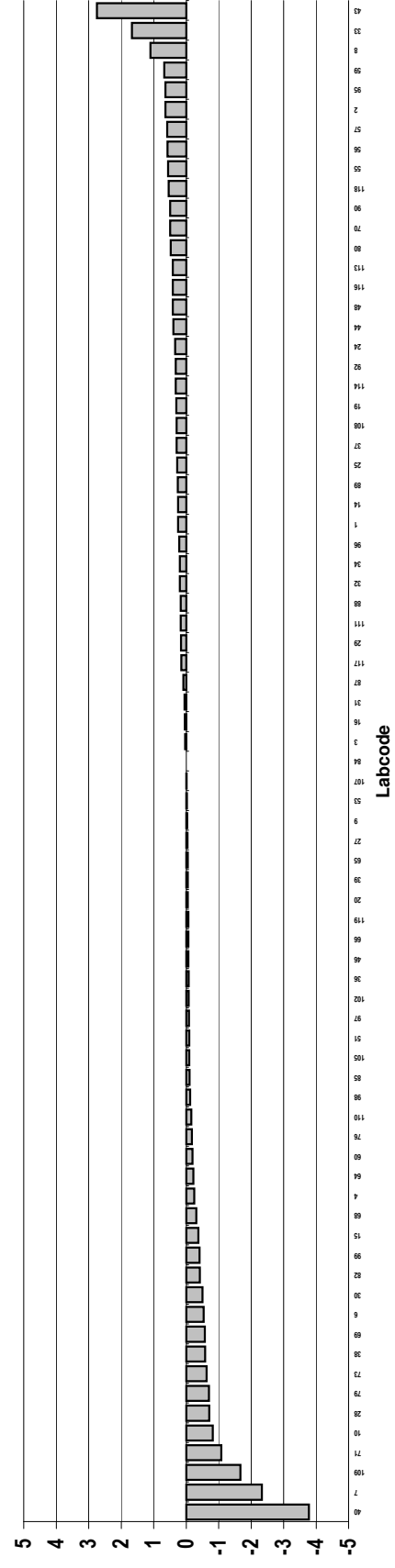
Consensus statistics

Consensus median, pg/μL	102
Median all values pg/μL	102
Consensus mean, pg/μL	102
Standard deviation, pg/μL	11
Relative standard deviation, %	11
No. of values reported	77
No. of values removed	2
No. of reported non-detects	0

PCB 114



Z-score: PCB 114



Analyte solution

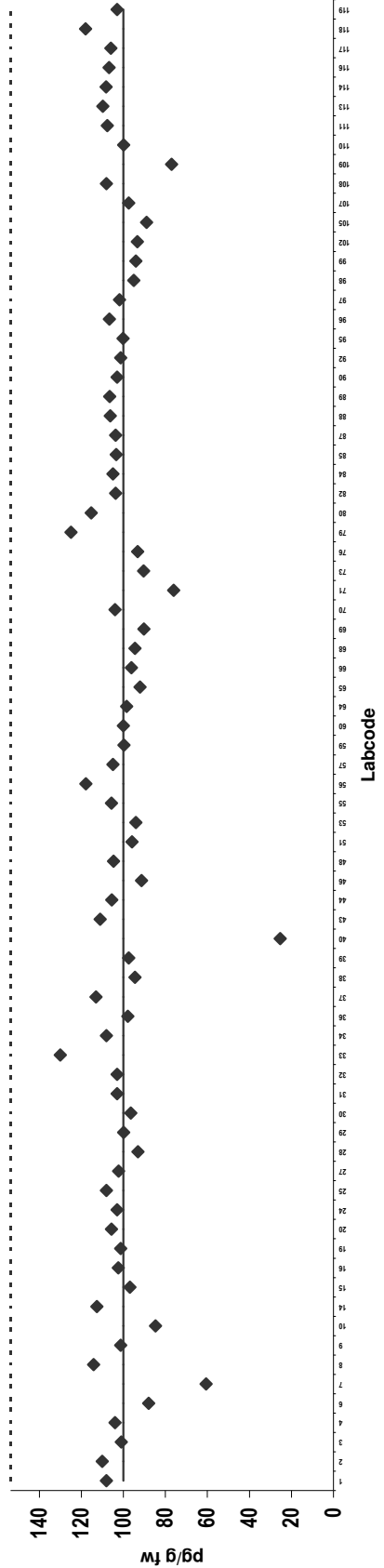
Congener: PCB 118

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	108		70	104	
2	110		71	76	
3	101		73	90	
4	104		76	93	
6	88		79	125	
7	61		80	115	
8	114		82	104	
9	101		84	105	
10	85		85	103	
14	113		87	104	
15	97		88	106	
16	102		89	107	
19	101		90	103	
20	106		92	101	
24	103		95	100	
25	108		96	107	
27	102		97	102	
28	93		98	95	
29	100		99	94	
30	96		102	93	
31	103		105	89	
32	103		107	98	
33	130		108	108	
34	108		109	77	
36	98		110	100	
37	113		111	108	
38	95		113	110	
39	97		114	108	
40	25		116	107	
43	111		117	106	
44	106		118	118	
46	91		119	103	
48	105				
51	96				
53	94				
55	106				
56	118				
57	105				
59	100				
60	100				
64	98				
65	92				
66	96				
68	94				
69	90				
		Outlier			

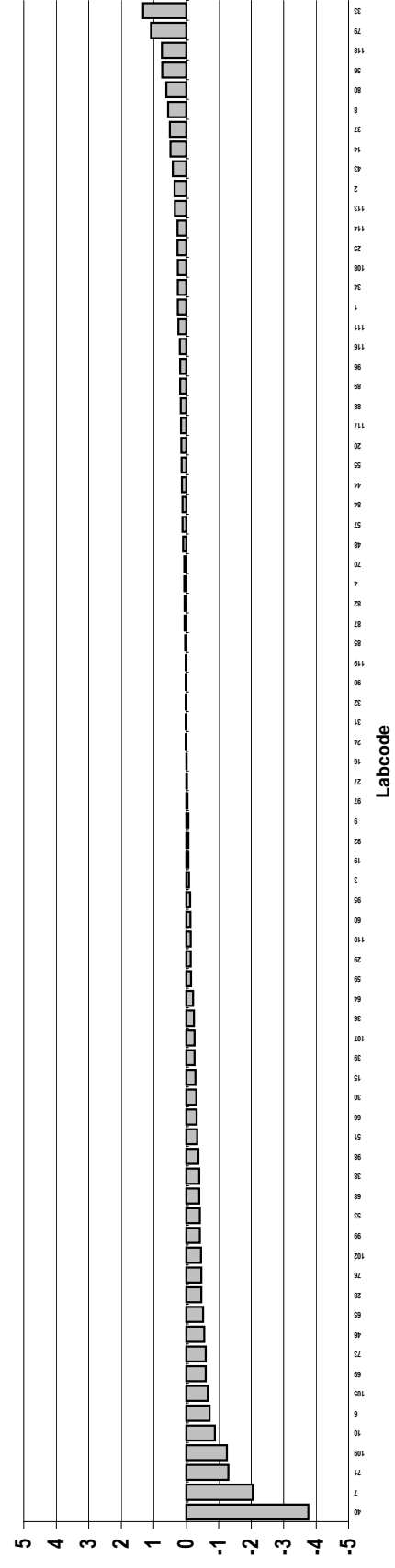
Consensus statistics

Consensus median, pg/μL	103
Median all values pg/μL	102
Consensus mean, pg/μL	101
Standard deviation, pg/μL	10
Relative standard deviation, %	10
No. of values reported	77
No. of values removed	1
No. of reported non-detects	0

PCB 118



Z-score: PCB 118



Analyte solution

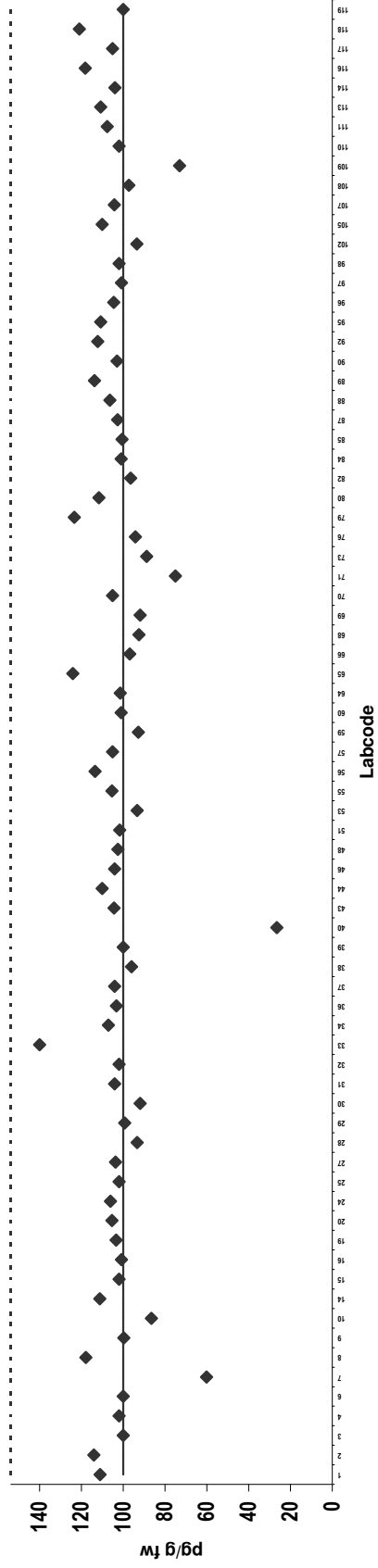
Congener: PCB 123

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	111		70	105	
2	114		71	75	
3	100		73	89	
4	102		76	94	
6	100		79	123	
7	60		80	112	
8	118		82	96	
9	100		84	101	
10	86		85	100	
14	111		87	103	
15	102		88	106	
16	101		89	114	
19	103		90	103	
20	105		92	112	
24	106		95	111	
25	102		96	105	
27	104		97	101	
28	93		98	102	
29	99		102	93	
30	92		105	110	
31	104		107	104	
32	102		108	97	
33	140		109	73	
34	107		110	102	
36	103		111	108	
37	104		113	111	
38	96		114	104	
39	100		116	118	
40	27		117	105	
43	104		118	121	
44	110		119	100	
46	104				
48	103				
51	102				
53	93				
55	105				
56	113				
57	105				
59	93				
60	101				
64	101				
65	124				
66	97				
68	92				
69	92				

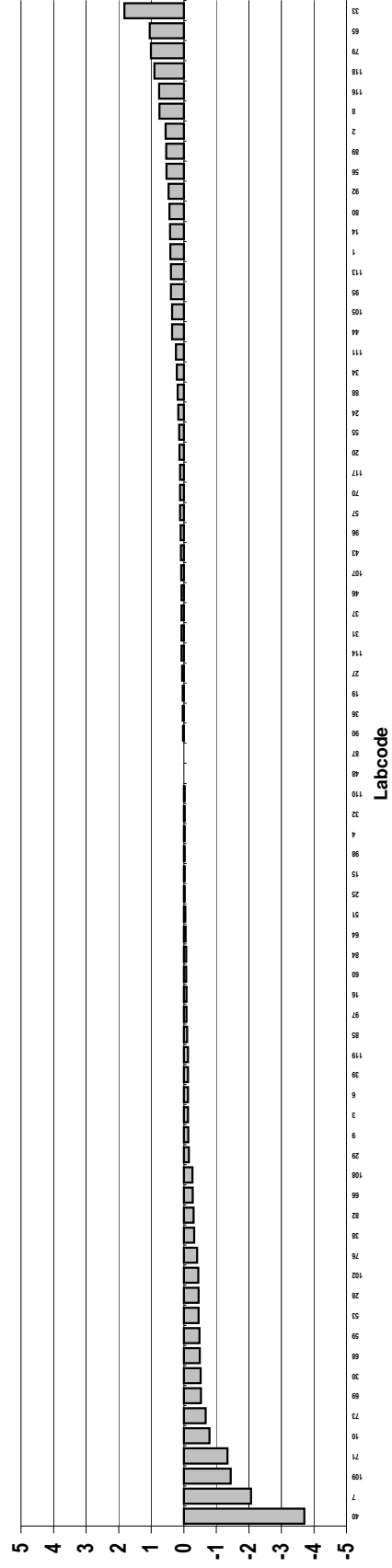
Outlier

Consensus statistics	
Consensus median, pg/μL	103
Median all values pg/μL	103
Consensus mean, pg/μL	103
Standard deviation, pg/μL	11
Relative standard deviation, %	11
No. of values reported	76
No. of values removed	1
No. of reported non-detects	0

PCB 123



Z-score: PCB 123



Analyte solution

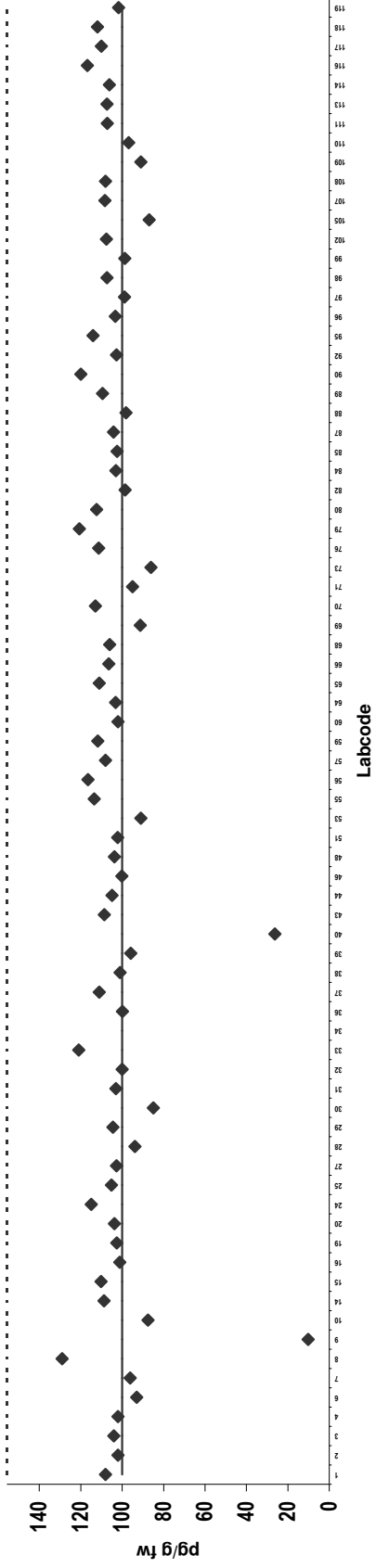
Congener: PCB 156

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	108		70	113	
2	102		71	95	
3	104		73	86	
4	102		76	111	
6	93		79	121	
7	96		80	112	
8	129		82	99	
9	10		84	103	
10	88		85	102	
14	109		87	104	
15	110		88	98	
16	101		89	110	
19	103		90	120	
20	104		92	103	
24	115		95	114	
25	105		96	103	
27	103		97	99	
28	94		98	107	
29	104		99	99	
30	85		102	108	
31	103		105	87	
32	100		107	108	
33	121		108	108	
34	212		109	91	
36	100		110	97	
37	111		111	107	
38	101		113	107	
39	96		114	106	
40	26		116	117	
43	109		117	110	
44	105		118	112	
46	100		119	102	
48	104				
51	102				
53	91				
55	114				
56	117				
57	108				
59	112				
60	102				
64	103				
65	111				
66	107				
68	106				
69	91				

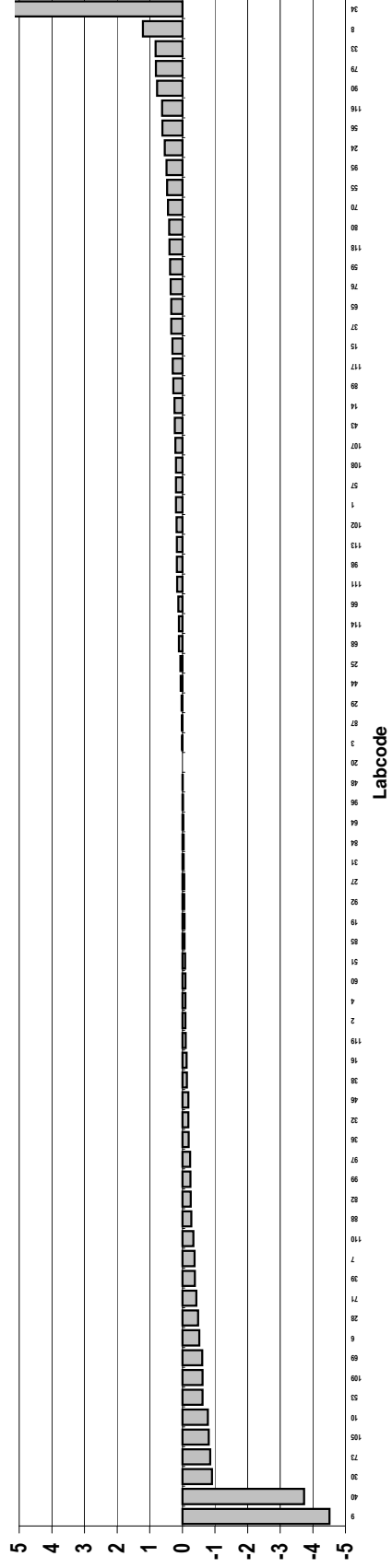
Consensus statistics

Consensus median, pg/μL	104
Median all values pg/μL	104
Consensus mean, pg/μL	104
Standard deviation, pg/μL	8
Relative standard deviation, %	8
No. of values reported	77
No. of values removed	3
No. of reported non-detects	0

PCB 156



Z-score: PCB 156



Analyte solution

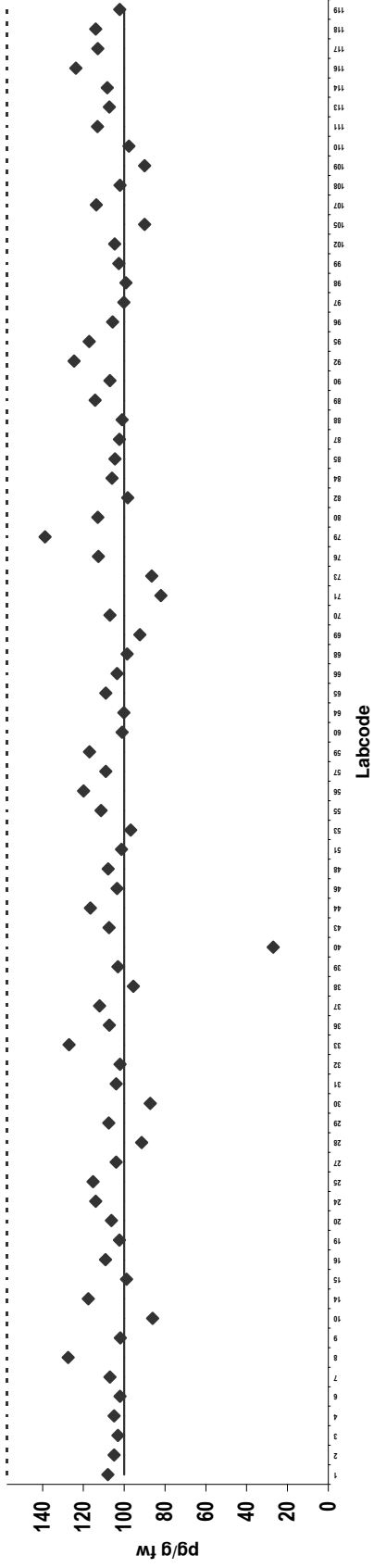
Congener: PCB 157

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	108		71	82	
2	105		73	86	
3	103		76	113	
4	105		79	139	
6	102		80	113	
7	107		82	98	
8	128		84	106	
9	102		85	104	
10	86		87	102	
14	118		88	101	
15	99		89	114	
16	109		90	107	
19	102		92	124	
20	106		95	117	
24	114		96	106	
25	115		97	100	
27	104		98	99	
28	91		99	103	
29	108		102	105	
30	87		105	90	
31	104		107	114	
32	102		108	102	
33	127		109	90	
36	107		110	98	
37	112		111	113	
38	96		113	107	
39	103		114	108	
40	27		116	124	
43	107		117	113	
44	117		118	114	
46	103		119	102	
48	108				
51	101				
53	97				
55	111				
56	120				
57	109				
59	117				
60	101				
64	100				
65	109				
66	104				
68	99				
69	92				
70	107				

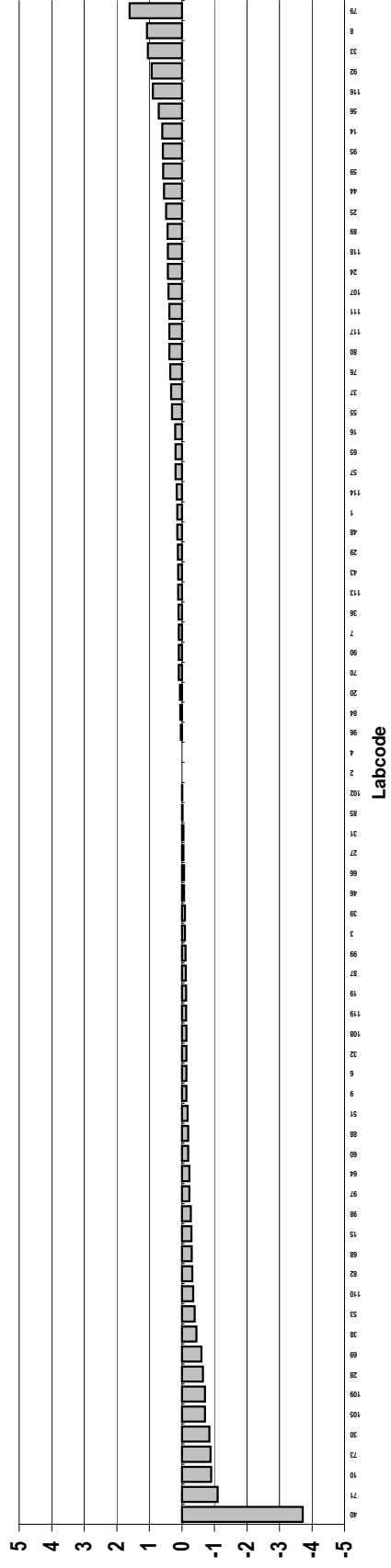
Consensus statistics

Consensus median, pg/μL	105
Median all values pg/μL	105
Consensus mean, pg/μL	106
Standard deviation, pg/μL	10
Relative standard deviation, %	9.4
No. of values reported	76
No. of values removed	1
No. of reported non-detects	0

PCB 157



Z-score: PCB 157



Analyte solution

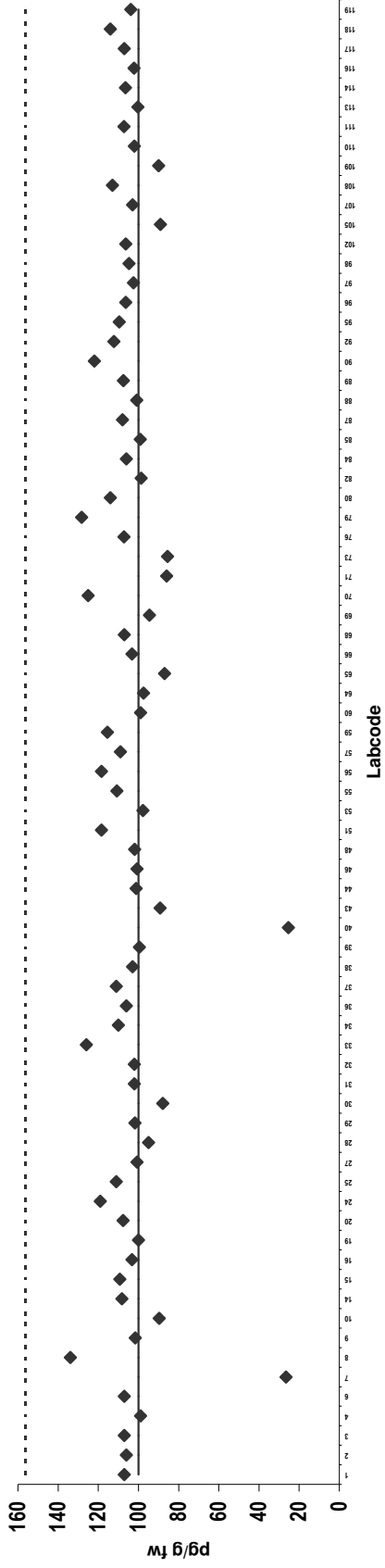
Congener: PCB 167

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	107		70	125	
2	106		71	86	
3	107		73	86	
4	99		76	107	
6	107		79	128	
7	26		80	114	
8	134		82	99	
9	102		84	106	
10	90		85	99	
14	108		87	108	
15	109		88	101	
16	103		89	107	
19	100		90	122	
20	108		92	112	
24	119		95	110	
25	111		96	106	
27	101		97	102	
28	95		98	105	
29	102		102	106	
30	88		105	89	
31	102		107	103	
32	102		108	113	
33	126		109	90	
34	110		110	102	
36	106		111	107	
37	111		113	100	
38	103		114	107	
39	100		116	102	
40	25		117	107	
43	89		118	114	
44	101		119	104	
46	101				
48	102				
51	118				
53	98				
55	111				
56	118				
57	109				
59	115				
60	99				
64	97				
65	87				
66	103				
68	107				
69	95				
		Outlier			
		Outlier			

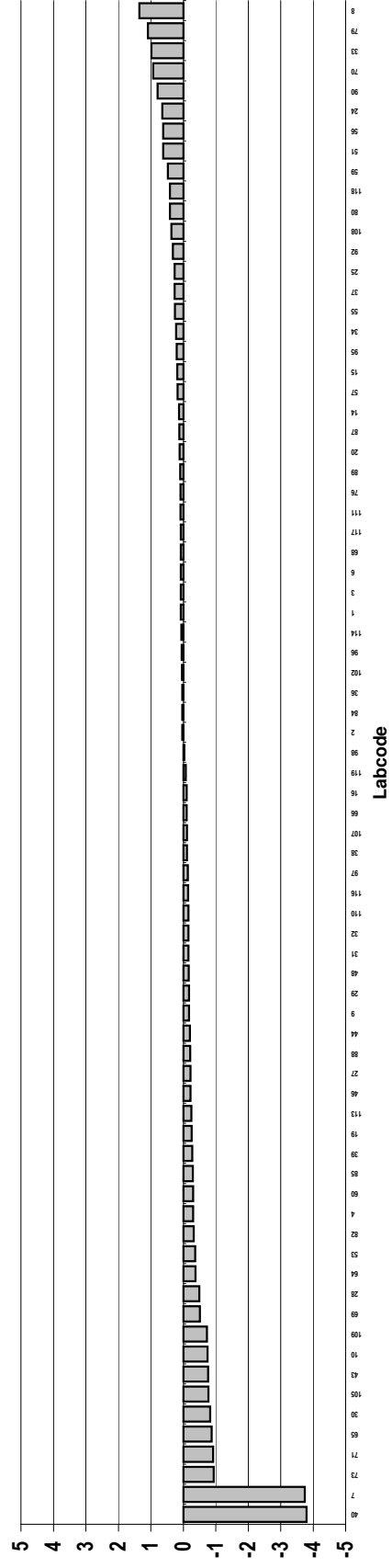
Consensus statistics

Consensus median, pg/μL	105
Median all values pg/μL	104
Consensus mean, pg/μL	105
Standard deviation, pg/μL	9.6
Relative standard deviation, %	9.1
No. of values reported	76
No. of values removed	2
No. of reported non-detects	0

PCB 167



Z-score: PCB 167



Analyte solution

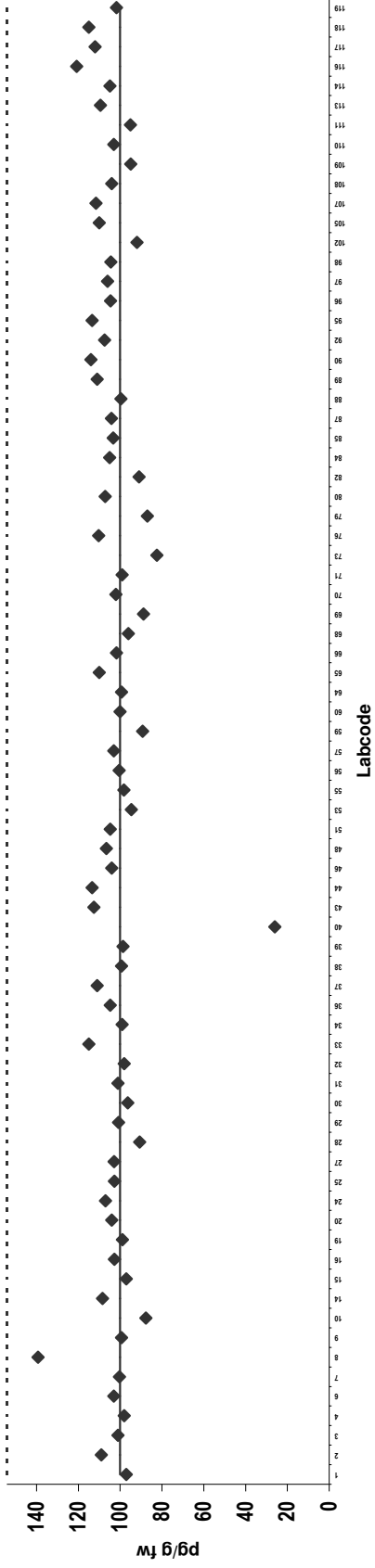
Congener: PCB 189

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	97		70	102	
2	109		71	99	
3	101		73	82	
4	98		76	110	
6	103		79	87	
7	100		80	107	
8	139		82	91	
9	99		84	105	
10	88		85	103	
14	108		87	104	
15	97		88	100	
16	103		89	111	
19	99		90	114	
20	104		92	107	
24	107		95	113	
25	103		96	105	
27	103		97	106	
28	91		98	104	
29	101		102	92	
30	96		105	110	
31	101		107	112	
32	98		108	104	
33	115		109	95	
34	99		110	103	
36	105		111	95	
37	111		113	109	
38	99		114	105	
39	99		116	121	
40	26		117	112	
43	113		118	115	
44	113		119	102	
46	104				
48	107				
51	105				
53	95				
55	98				
56	100				
57	103				
59	89				
60	100				
64	99				
65	110				
66	102				
68	96				
69	89				
		Outlier			

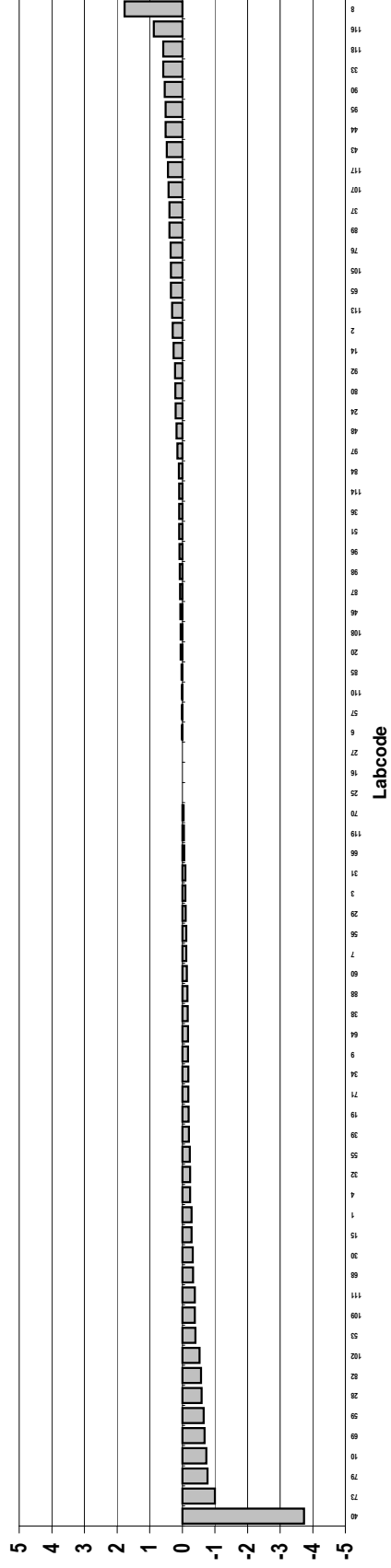
Consensus statistics

Consensus median, pg/μL	103
Median all values pg/μL	103
Consensus mean, pg/μL	103
Standard deviation, pg/μL	8.5
Relative standard deviation, %	8.2
No. of values reported	76
No. of values removed	1
No. of reported non-detects	0

PCB 189



Z-score: PCB 189



Analyte solution

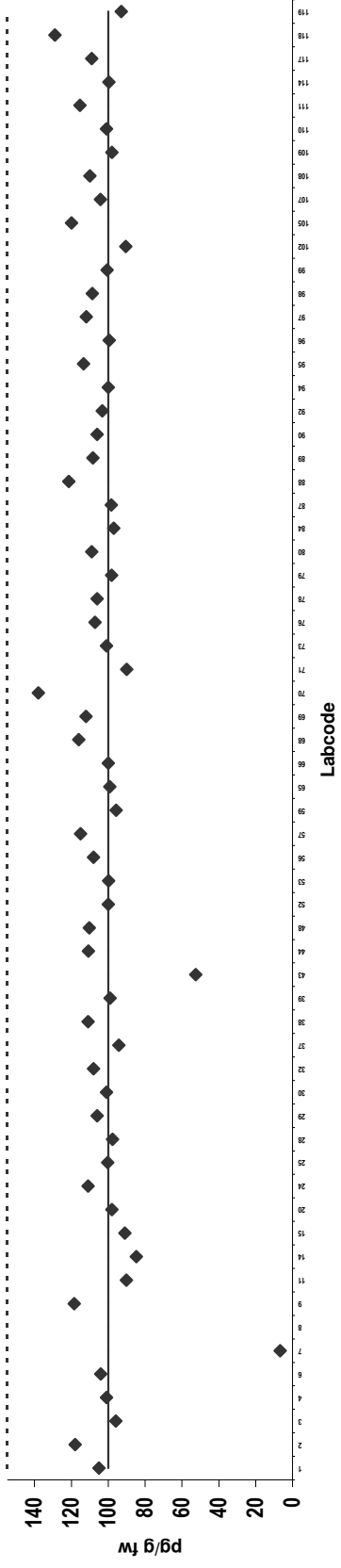
Congener: CB 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	105		92	103	
2	118		94	100	
3	96		95	113	
4	101		96	100	
6	104		97	112	
7	6.8		98	109	
8	163		99	101	
9	118		102	91	
11	90		105	120	
14	85		107	104	
15	91		108	110	
20	98		109	98	
24	111		110	101	
25	100		111	115	
28	98		114	100	
29	106		117	109	
30	101		118	129	
32	108		119	93	
37	94				
38	111				
39	99				
43	53				
44	111				
48	110				
52	100				
53	100				
56	108				
57	115				
59	96				
65	99				
66	100				
68	116				
69	112				
70	138				
71	90				
73	101				
76	107				
78	106				
79	98				
80	109				
84	97				
87	98				
88	122				
89	108				
90	106				

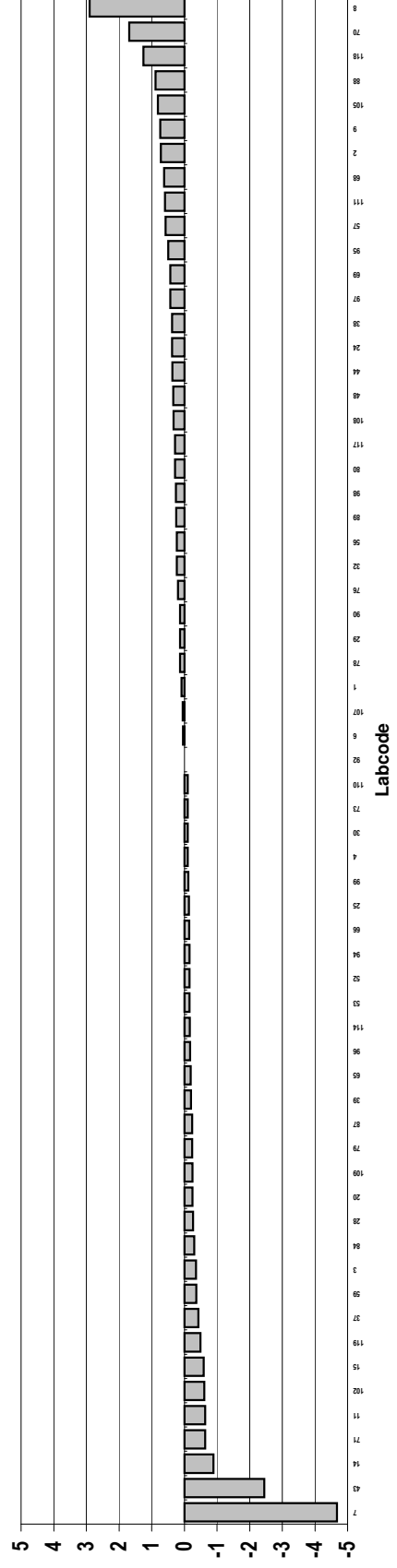
Consensus statistics

Consensus median, pg/μL	103
Median all values pg/μL	103
Consensus mean, pg/μL	104
Standard deviation, pg/μL	12
Relative standard deviation, %	11
No. of values reported	63
No. of values removed	2
No. of reported non-detects	0

CB 28



Z-score: CB 28



Analyte solution

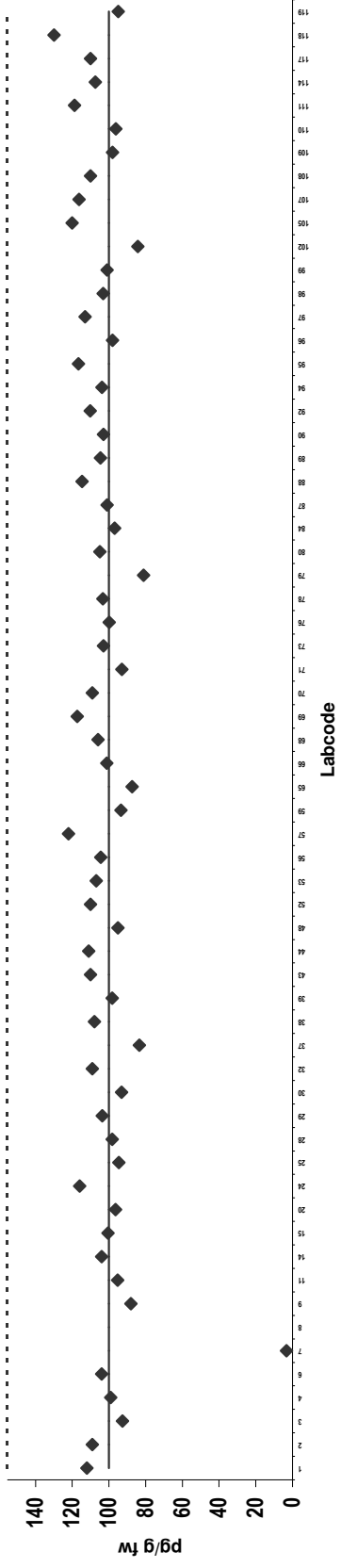
Congener: CB 52

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	112		92	110	
2	109		94	104	
3	93		95	117	
4	99		96	98	
6	104		97	113	
7	3.3	Outlier	98	103	
8	179	Outlier	99	101	
9	88		102	84	
11	95		105	120	
14	104		107	116	
15	100		108	110	
20	97		109	98	
24	116		110	96	
25	95		111	119	
28	98		114	108	
29	104		117	110	
30	93		118	130	
32	109		119	95	
37	84				
38	108				
39	98				
43	110				
44	111				
48	95				
52	110				
53	107				
56	104				
57	122				
59	93				
65	87				
66	101				
68	106				
69	117				
70	109				
71	93				
73	103				
76	100				
78	103				
79	81				
80	105				
84	97				
87	101				
88	115				
89	105				
90	103				

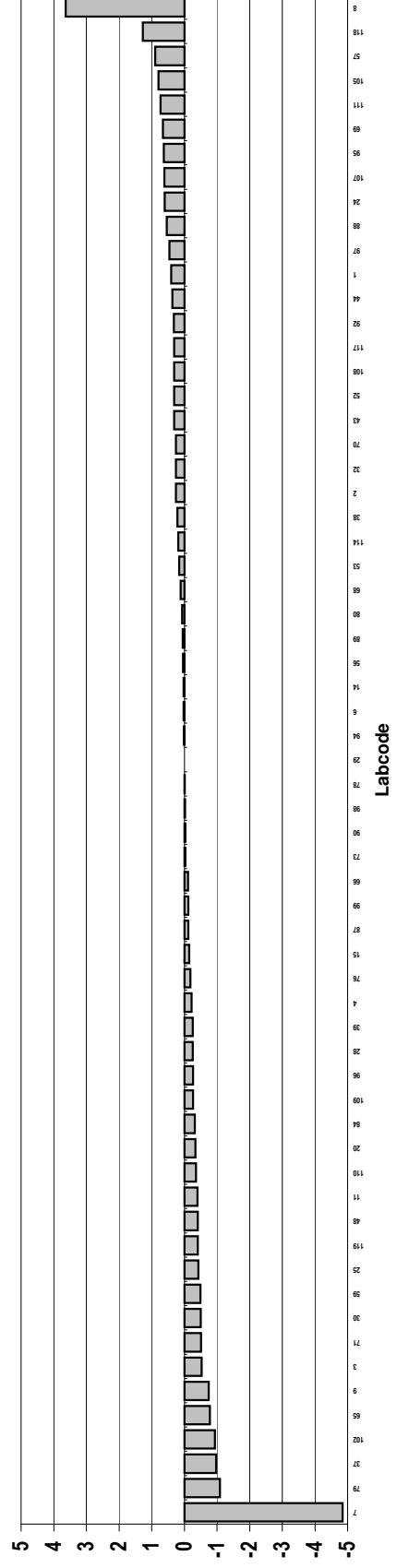
Consensus statistics

Consensus median, pg/μL	104
Median all values pg/μL	104
Consensus mean, pg/μL	104
Standard deviation, pg/μL	9.8
Relative standard deviation, %	9.5
No. of values reported	63
No. of values removed	2
No. of reported non-detects	0

CB 52



Z-score: CB 52



Analyte solution

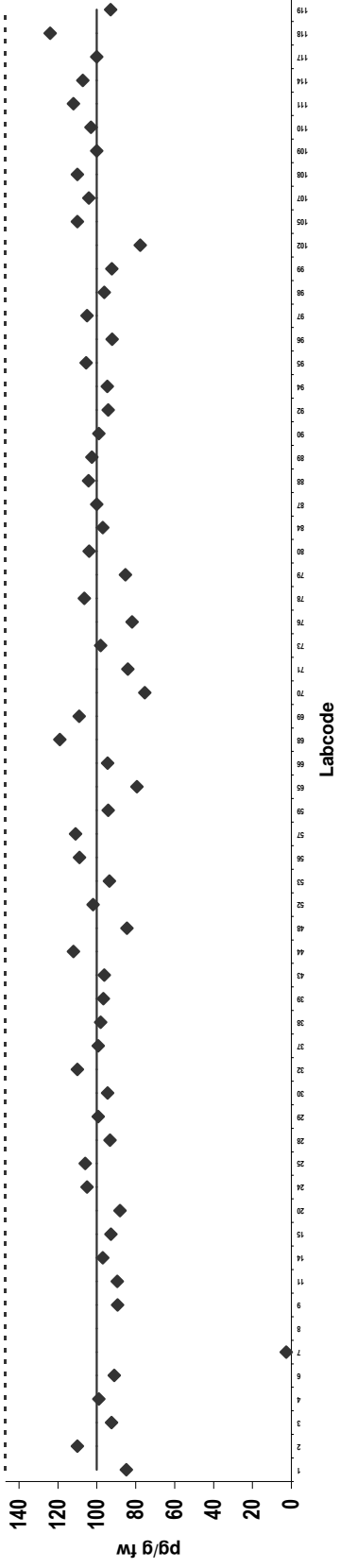
Congener: CB 101

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	85		92	94	
2	110		94	95	
3	92		95	106	
4	99		96	92	
6	91		97	105	
7	2.7		98	96	
8	156		99	92	
9	89		102	78	
11	90		105	110	
14	97		107	104	
15	93		108	110	
20	88		109	100	
24	105		110	103	
25	106		111	112	
28	93		114	107	
29	99		117	100	
30	95		118	124	
32	110		119	93	
37	99				
38	98				
39	97				
43	96				
44	112				
48	85				
52	102				
53	94				
56	109				
57	111				
59	94				
65	79				
66	94				
68	119				
69	109				
70	75				
71	84				
73	98				
76	82				
78	106				
79	85				
80	104				
84	97				
87	100				
88	104				
89	103				
90	99				

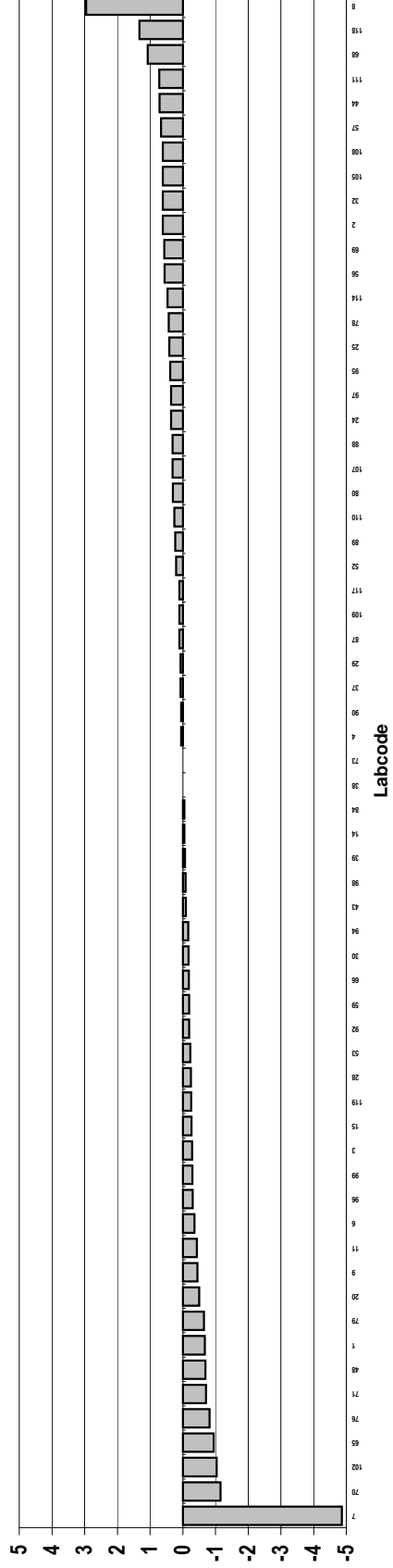
Consensus statistics

Consensus median, pg/μL	98
Median all values pg/μL	98
Consensus mean, pg/μL	98
Standard deviation, pg/μL	9.9
Relative standard deviation, %	10
No. of values reported	63
No. of values removed	2
No. of reported non-detects	0

CB 101



Z-score: CB 101



Analyte solution

Congener: CB 138

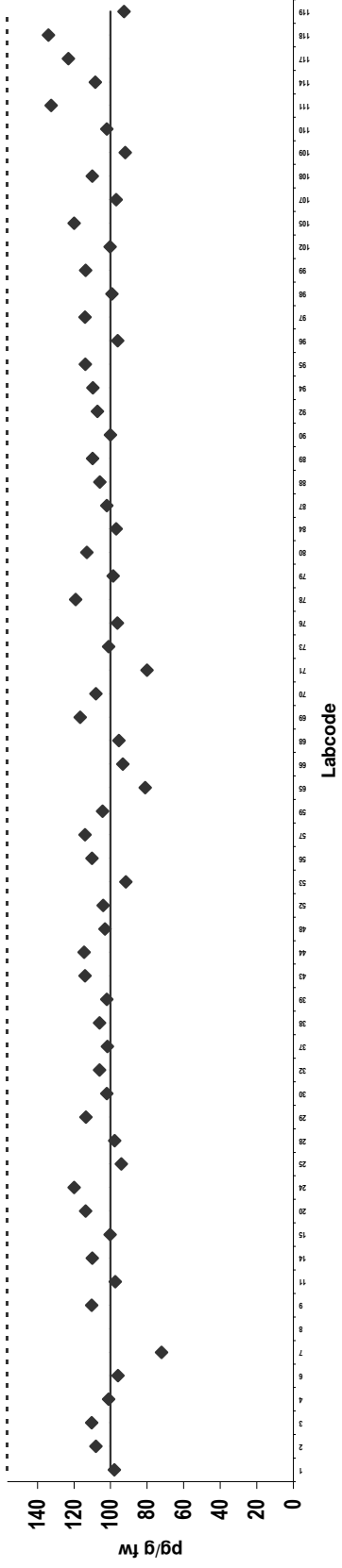
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	98		92	107	
2	108		94	110	
3	110		95	114	
4	101		96	96	
6	96		97	114	
7	72		98	99	
8	171		99	114	
9	110		102	100	
11	98		105	120	
14	110		107	97	
15	100		108	110	
20	114		109	92	
24	120		110	102	
25	94		111	133	
28	98		114	108	
29	114		117	123	
30	102		118	134	
32	106		119	93	
37	102				
38	106				
39	102				
43	114				
44	114				
48	103				
52	104				
53	92				
56	110				
57	114				
59	104				
65	81				
66	93				
68	95				
69	117				
70	108				
71	80				
73	101				
76	96				
78	119				
79	99				
80	113				
84	97				
87	102				
88	106				
89	110				
90	100				

Outlier

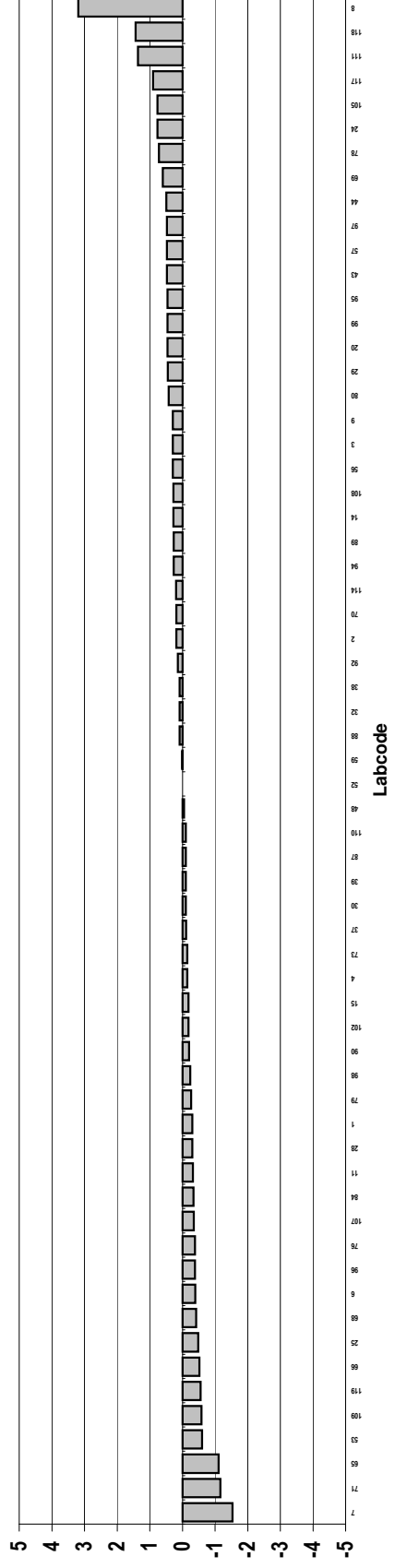
Consensus statistics

Consensus median, pg/μL	104
Median all values pg/μL	104
Consensus mean, pg/μL	105
Standard deviation, pg/μL	11
Relative standard deviation, %	11
No. of values reported	63
No. of values removed	1
No. of reported non-detects	0

CB 138



Z-score: CB 138



Analyte solution

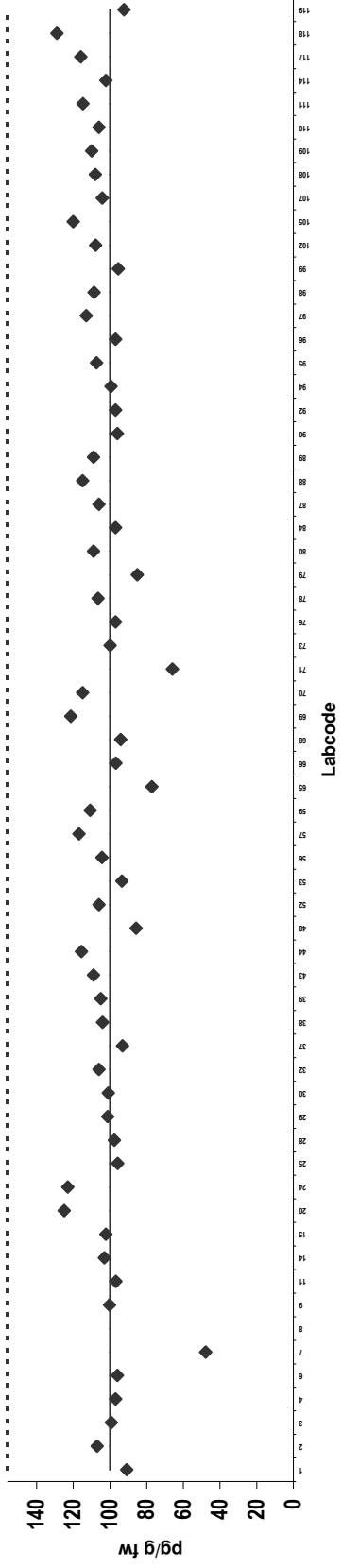
Congener: CB 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	91		92	97	
2	107		94	99	
3	99		95	107	
4	97		96	97	
6	96		97	113	
7	48		98	109	
8	163		99	96	
9	100		102	108	
11	97		105	120	
14	103		107	104	
15	102		108	108	
20	125		109	110	
24	123		110	106	
25	96		111	115	
28	98		114	102	
29	101		117	116	
30	101		118	129	
32	106		119	92	
37	93				
38	104				
39	105				
43	109				
44	116				
48	86				
52	106				
53	93				
56	104				
57	117				
59	111				
65	77				
66	97				
68	94				
69	121				
70	115				
71	66				
73	100				
76	97				
78	107				
79	85				
80	109				
84	97				
87	106				
88	115				
89	109				
90	96				

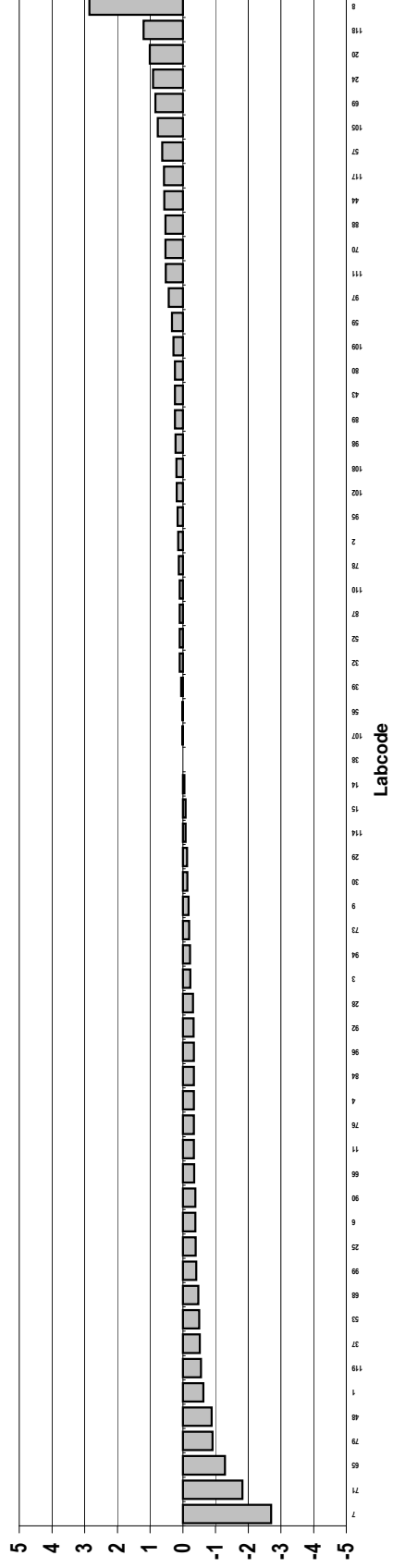
Consensus statistics

Consensus median, pg/μL	104
Median all values pg/μL	104
Consensus mean, pg/μL	103
Standard deviation, pg/μL	11
Relative standard deviation, %	11
No. of values reported	63
No. of values removed	2
No. of reported non-detects	0

CB 153



Z-score: CB 153



Analyte solution

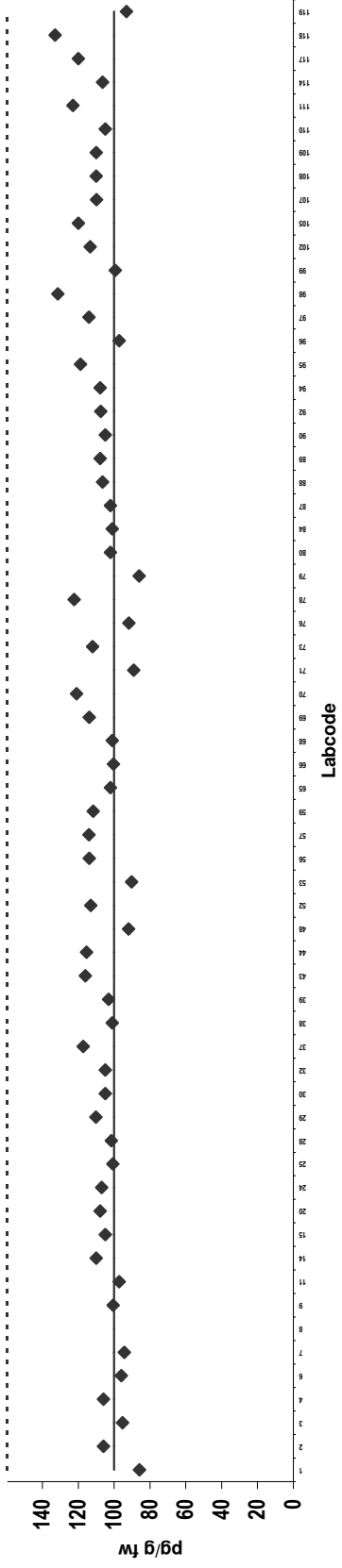
Congener: CB 180

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	86		92	107	
2	106		94	108	
3	95		95	119	
4	106		96	97	
6	96		97	114	
7	94		98	131	
8	166		99	99	
9	101		102	113	
11	97		105	120	
14	110		107	110	
15	105		108	110	
20	108		109	110	
24	107		110	105	
25	101		111	123	
28	102		114	106	
29	110		117	120	
30	105		118	133	
32	105		119	93	
37	117				
38	101				
39	103				
43	116				
44	115				
48	92				
52	113				
53	90				
56	114				
57	114				
59	112				
65	102				
66	100				
68	101				
69	114				
70	121				
71	89				
73	112				
76	92				
78	122				
79	86				
80	102				
84	101				
87	102				
88	106				
89	108				
90	105				

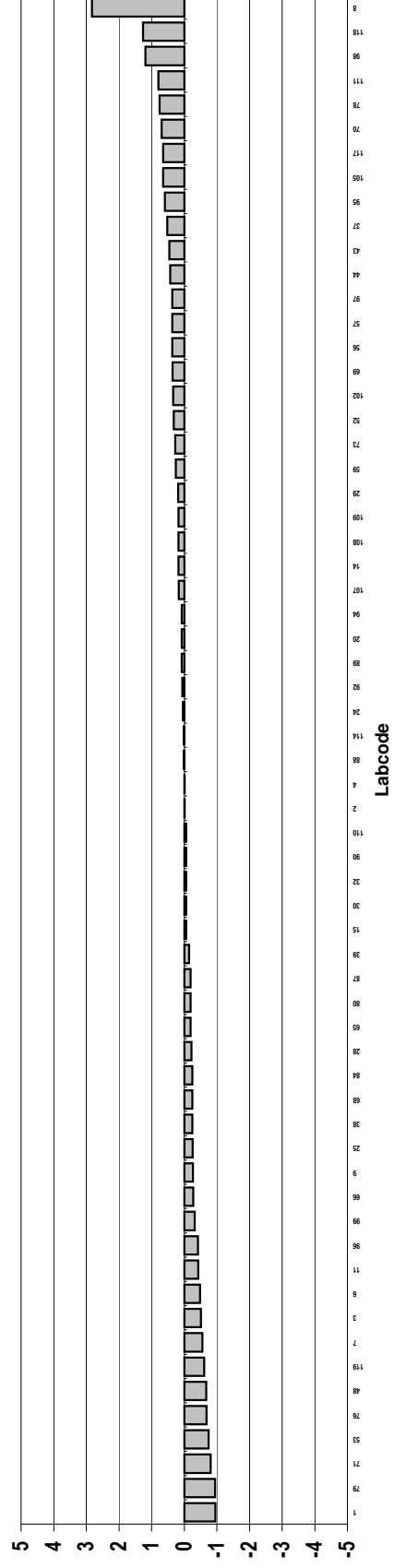
Consensus statistics

Consensus median, pg/μL	106
Median all values pg/μL	106
Consensus mean, pg/μL	107
Standard deviation, pg/μL	10
Relative standard deviation, %	9.5
No. of values reported	63
No. of values removed	1
No. of reported non-detects	0

CB 180



Z-score: CB 180



Analyte solution

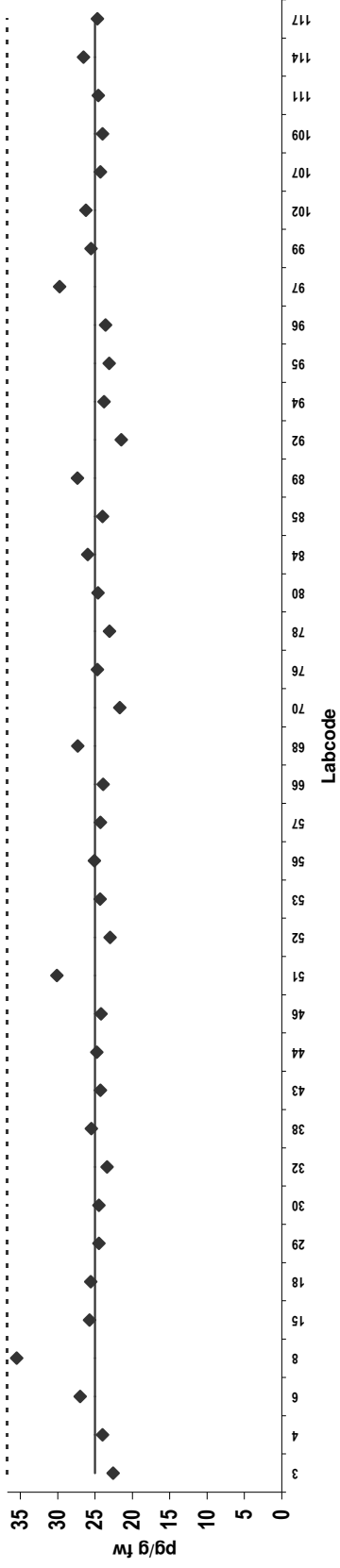
Congener: BDE 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	23				
4	24				
6	27				
8	35				
15	26				
18	26				
29	25				
30	25				
32	23				
38	26				
43	24				
44	25				
46	24				
51	30				
52	23				
53	24				
56	25				
57	24				
66	24				
68	27				
70	22				
76	25				
78	23				
80	25				
84	26				
85	24				
89	27				
92	21				
94	24				
95	23				
96	24				
97	30				
99	26				
102	26				
107	24				
109	24				
111	25				
114	27				
117	25				

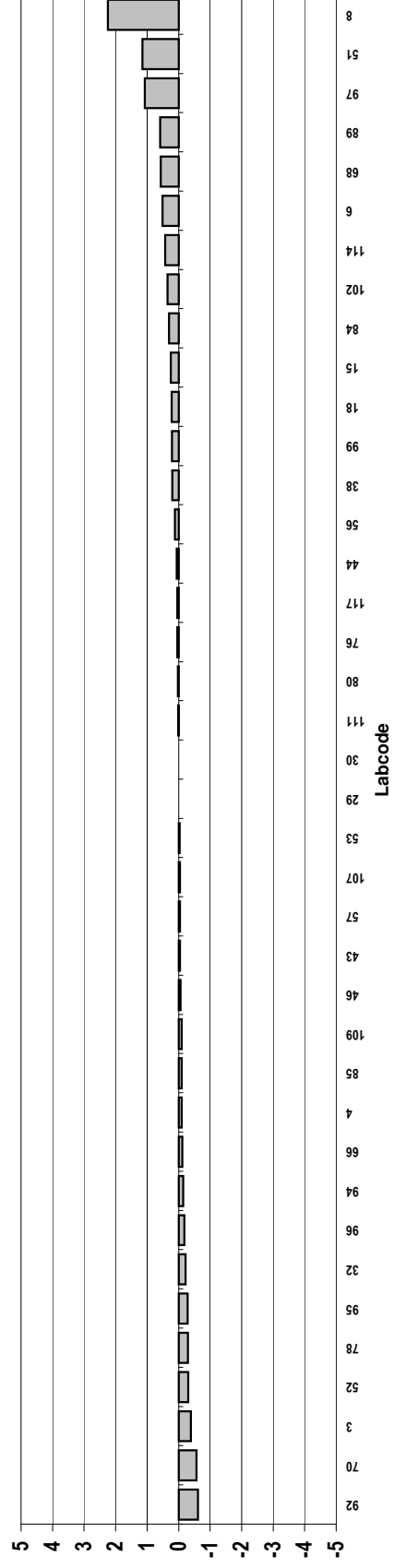
Consensus statistics

Consensus median, pg/μL	25
Median all values pg/μL	25
Consensus mean, pg/μL	25
Standard deviation, pg/μL	2.5
Relative standard deviation, %	9.9
No. of values reported	39
No. of values removed	0
No. of reported non-detects	0

BDE 28



Z-score: BDE 28



Analyte solution

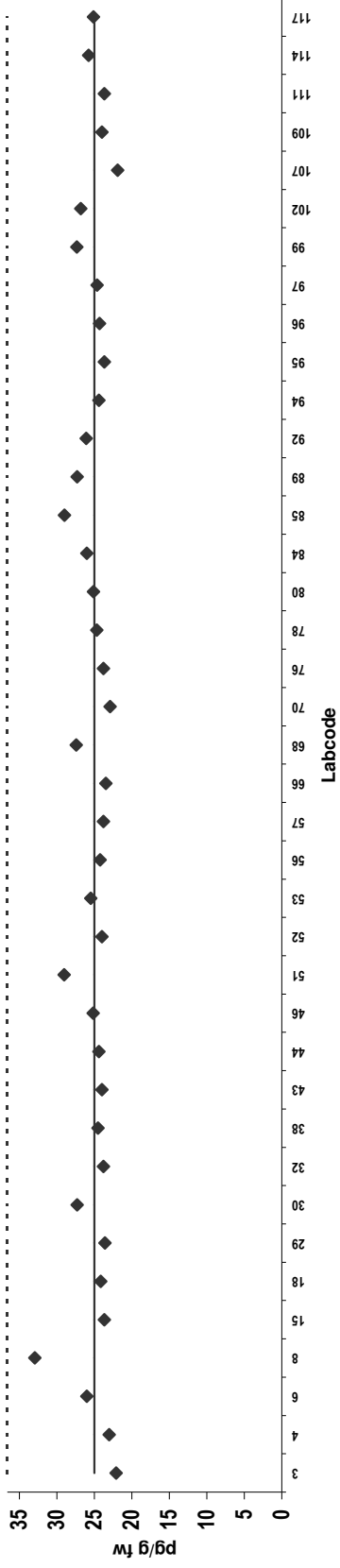
Congener: BDE 47

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	22				
4	23				
6	26				
8	33				
15	24				
18	24				
29	24				
30	27				
32	24				
38	25				
43	24				
44	24				
46	25				
51	29				
52	24				
53	25				
56	24				
57	24				
66	23				
68	27				
70	23				
76	24				
78	25				
80	25				
84	26				
85	29				
89	27				
92	26				
94	24				
95	24				
96	24				
97	25				
99	27				
102	27				
107	22				
109	24				
111	24				
114	26				
117	25				

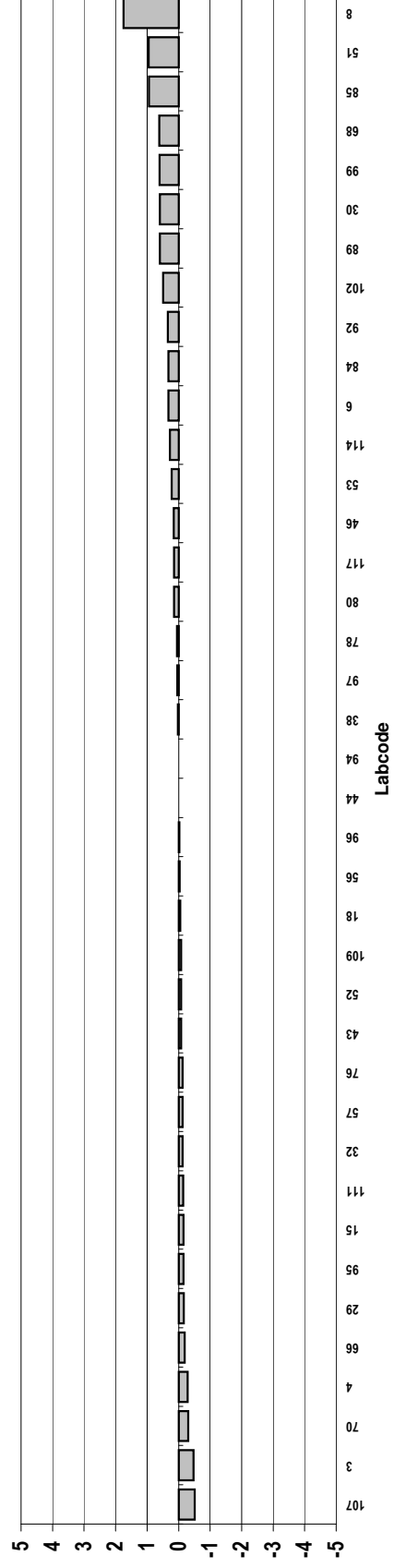
Consensus statistics

Consensus median, pg/μL	24
Median all values pg/μL	24
Consensus mean, pg/μL	25
Standard deviation, pg/μL	2.1
Relative standard deviation, %	8.4
No. of values reported	39
No. of values removed	0
No. of reported non-detects	0

BDE 47



Z-score: BDE 47



Analyte solution

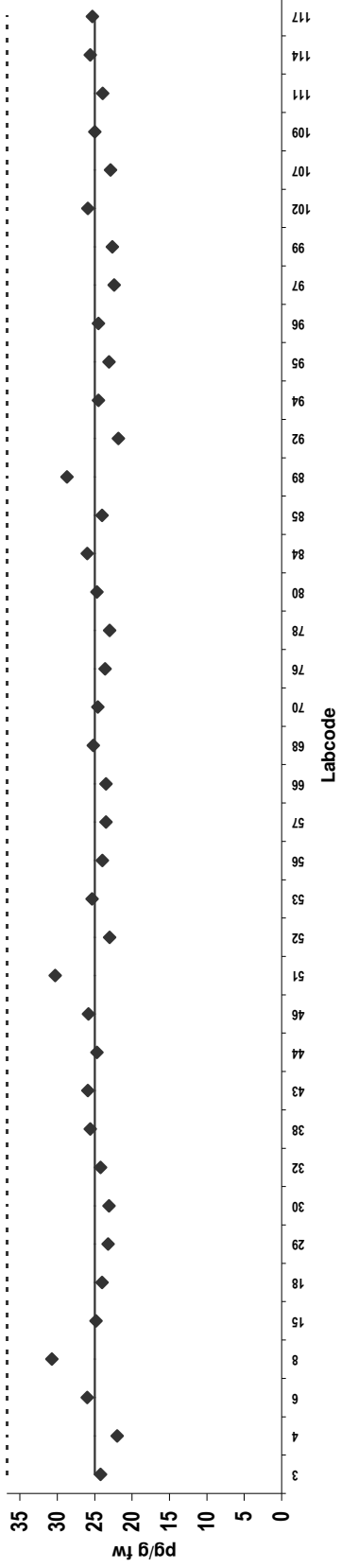
Congener: BDE 99

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	24				
4	22				
6	26				
8	31				
15	25				
18	24				
29	23				
30	23				
32	24				
38	26				
43	26				
44	25				
46	26				
51	30				
52	23				
53	25				
56	24				
57	24				
66	23				
68	25				
70	25				
76	24				
78	23				
80	25				
84	26				
85	24				
89	29				
92	22				
94	25				
95	23				
96	25				
97	22				
99	23				
102	26				
107	23				
109	25				
111	24				
114	26				
117	25				

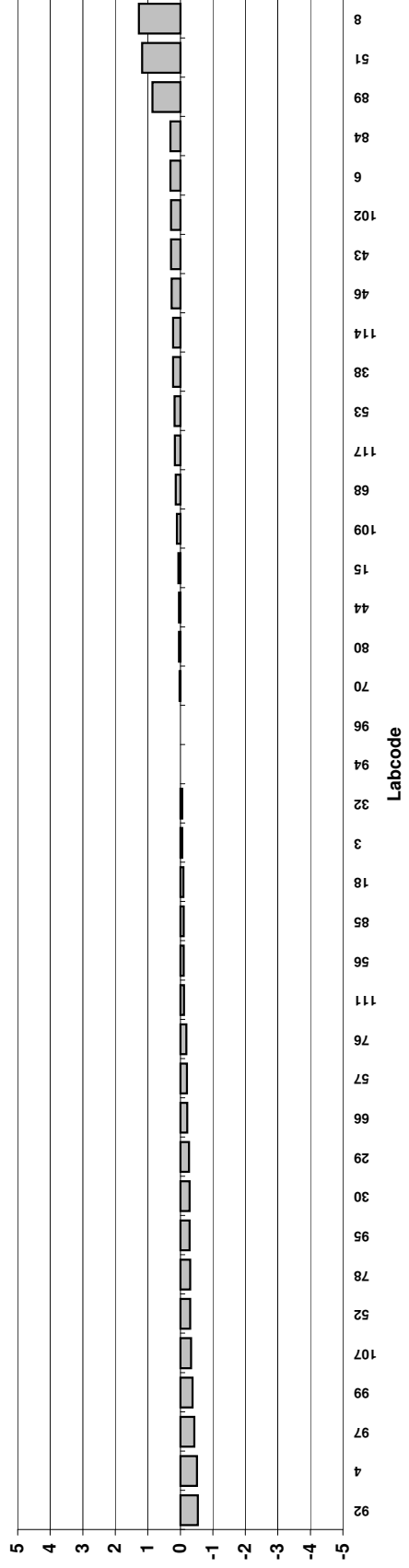
Consensus statistics

Consensus median, pg/μL	25
Median all values pg/μL	25
Consensus mean, pg/μL	25
Standard deviation, pg/μL	1.9
Relative standard deviation, %	7.8
No. of values reported	39
No. of values removed	0
No. of reported non-detects	0

BDE 99



Z-score: BDE 99



Analyte solution

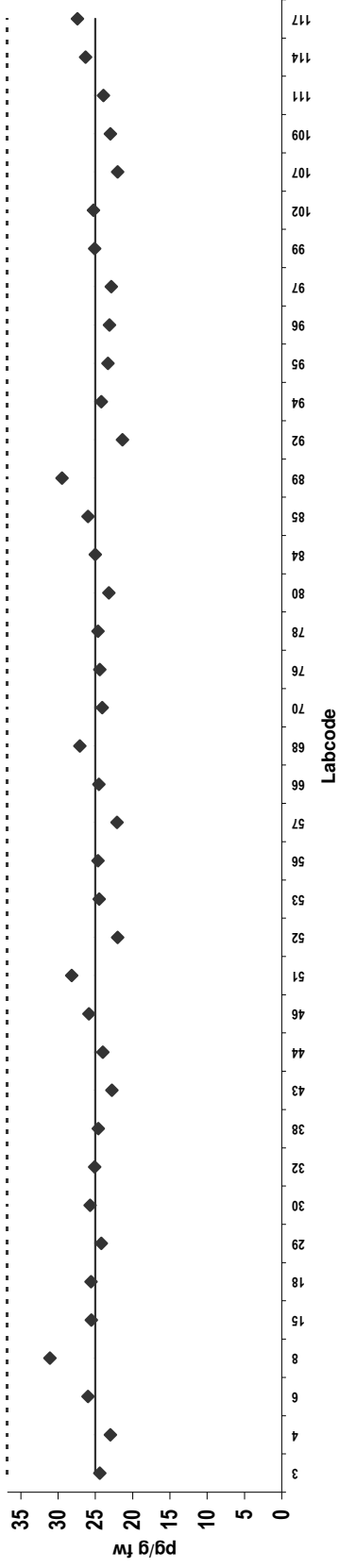
Congener: BDE 100

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	24				
4	23				
6	26				
8	31				
15	26				
18	26				
29	24				
30	26				
32	25				
38	25				
43	23				
44	24				
46	26				
51	28				
52	22				
53	24				
56	25				
57	22				
66	25				
68	27				
70	24				
76	24				
78	25				
80	23				
84	25				
85	26				
89	29				
92	21				
94	24				
95	23				
96	23				
97	23				
99	25				
102	25				
107	22				
109	23				
111	24				
114	26				
117	27				

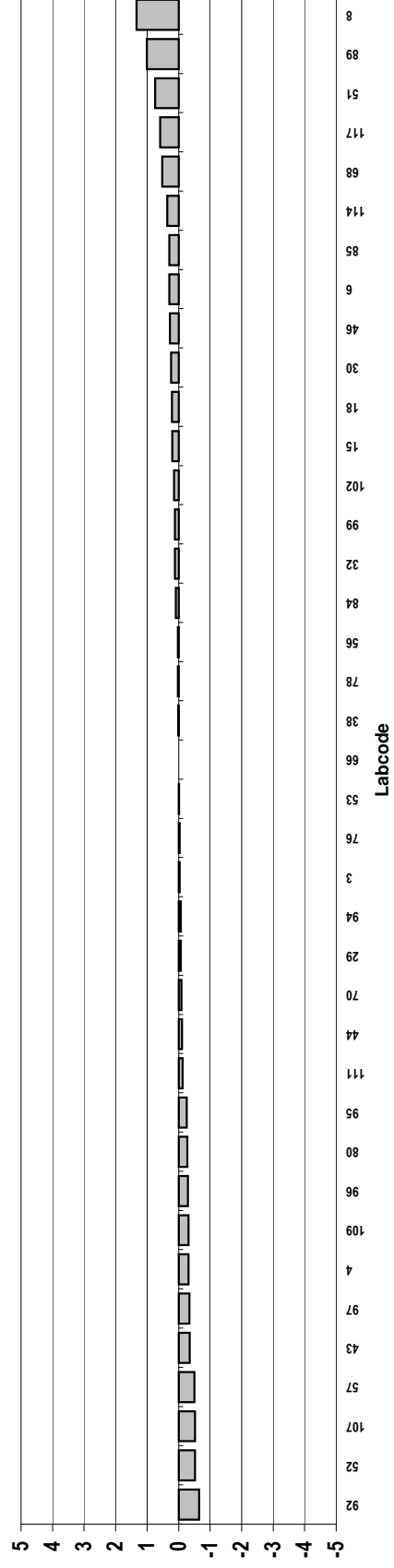
Consensus statistics

Consensus median, pg/μL	25
Median all values pg/μL	25
Consensus mean, pg/μL	25
Standard deviation, pg/μL	2.0
Relative standard deviation, %	8.1
No. of values reported	39
No. of values removed	0
No. of reported non-detects	0

BDE 100



Z-score: BDE 100



Analyte solution

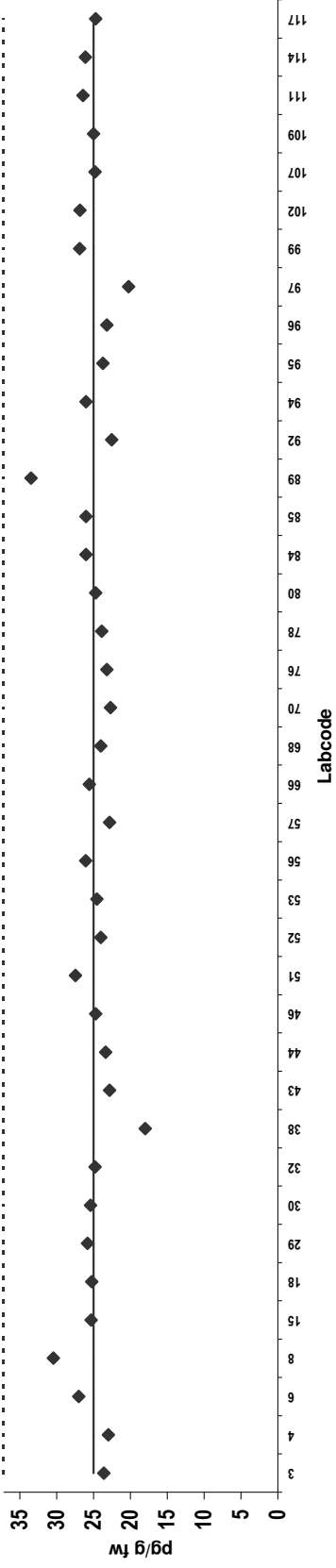
Congener: BDE 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	24				
4	23				
6	27				
8	30				
15	25				
18	25				
29	26				
30	25				
32	25				
38	18				
43	23				
44	23				
46	25				
51	27				
52	24				
53	25				
56	26				
57	23				
66	26				
68	24				
70	23				
76	23				
78	24				
80	25				
84	26				
85	26				
89	33				
92	23				
94	26				
95	24				
96	23				
97	20				
99	27				
102	27				
107	25				
109	25				
111	26				
114	26				
117	25				

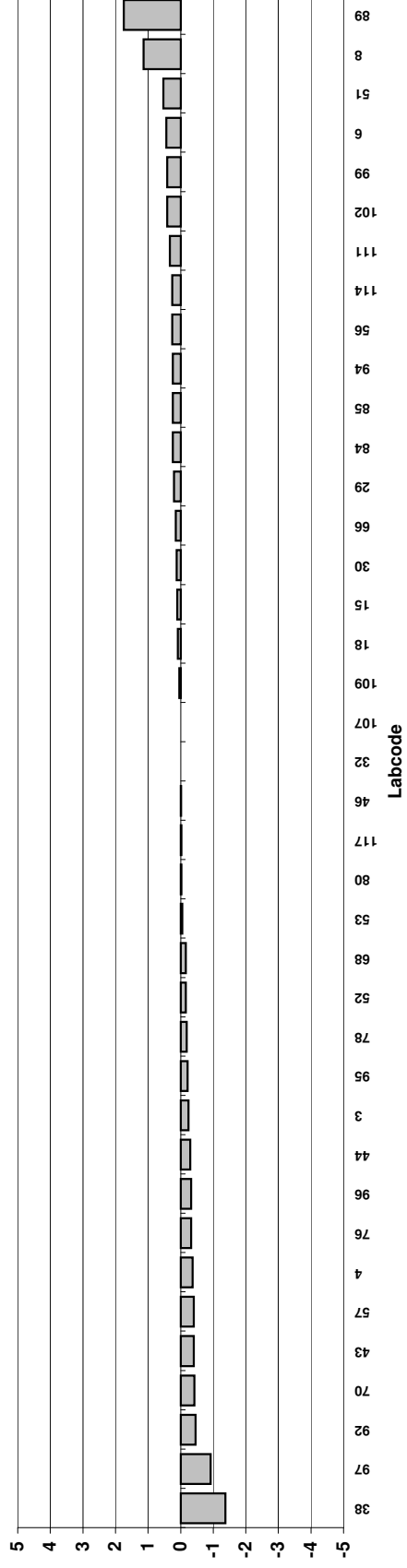
Consensus statistics

Consensus median, pg/ μ L	25
Median all values pg/ μ L	25
Consensus mean, pg/ μ L	25
Standard deviation, pg/ μ L	2.5
Relative standard deviation, %	10
No. of values reported	39
No. of values removed	0
No. of reported non-detects	0

BDE 153



Z-score: BDE 153



Analyte solution

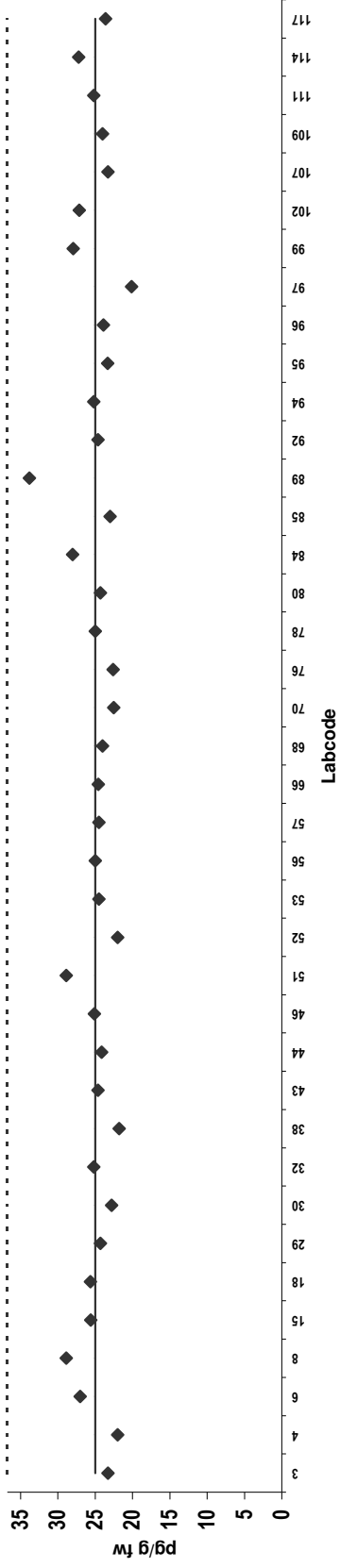
Congener: BDE 154

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	23				
4	22				
6	27				
8	29				
15	26				
18	26				
29	24				
30	23				
32	25				
38	22				
43	25				
44	24				
46	25				
51	29				
52	22				
53	25				
56	25				
57	25				
66	25				
68	24				
70	23				
76	23				
78	25				
80	24				
84	28				
85	23				
89	34				
92	25				
94	25				
95	23				
96	24				
97	20				
99	28				
102	27				
107	23				
109	24				
111	25				
114	27				
117	24				

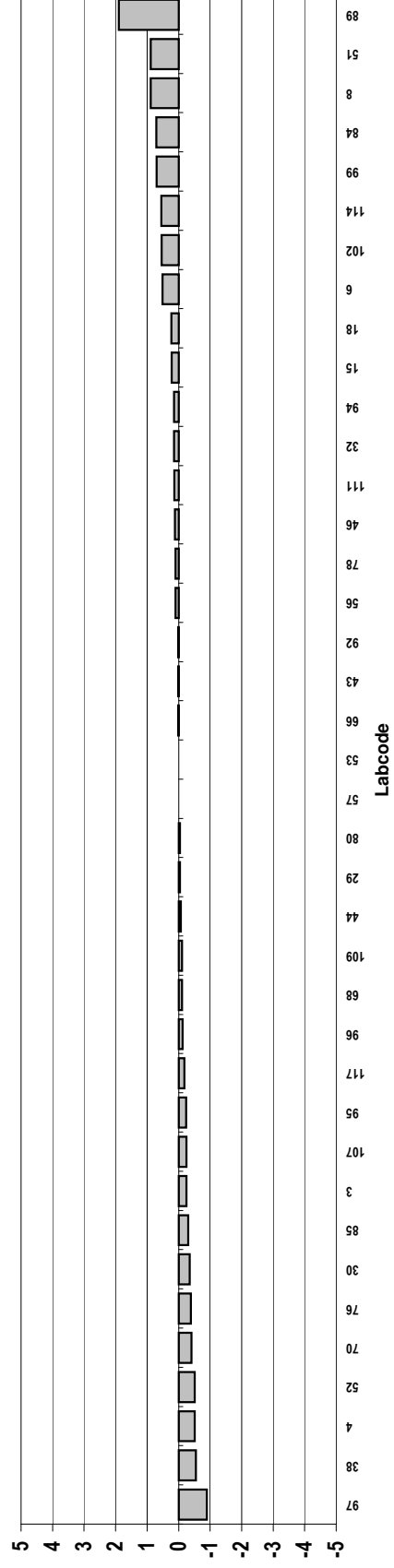
Consensus statistics

Consensus median, pg/μL	25
Median all values pg/μL	25
Consensus mean, pg/μL	25
Standard deviation, pg/μL	2.4
Relative standard deviation, %	9.9
No. of values reported	39
No. of values removed	0
No. of reported non-detects	0

BDE 154



Z-score: BDE 154



Analyte solution

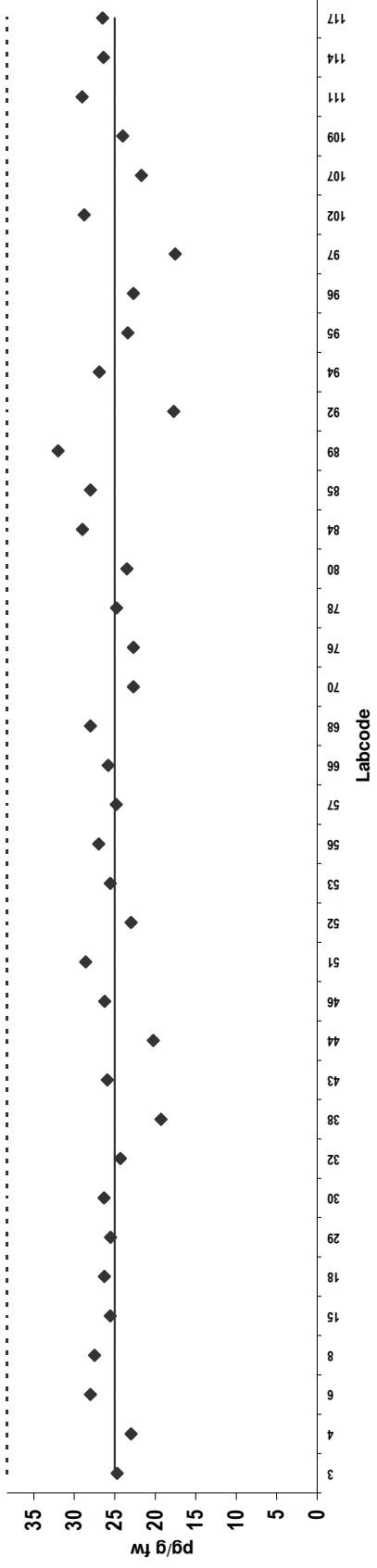
Congener: BDE 183

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	25				
4	23				
6	28				
8	27				
15	26				
18	26				
29	26				
30	26				
32	24				
38	19				
43	26				
44	20				
46	26				
51	29				
52	23				
53	26				
56	27				
57	25				
66	26				
68	28				
70	23				
76	23				
78	25				
80	24				
84	29				
85	28				
89	32				
92	18				
94	27				
95	23				
96	23				
97	18				
102	29				
107	22				
109	24				
111	29				
114	26				
117	27				

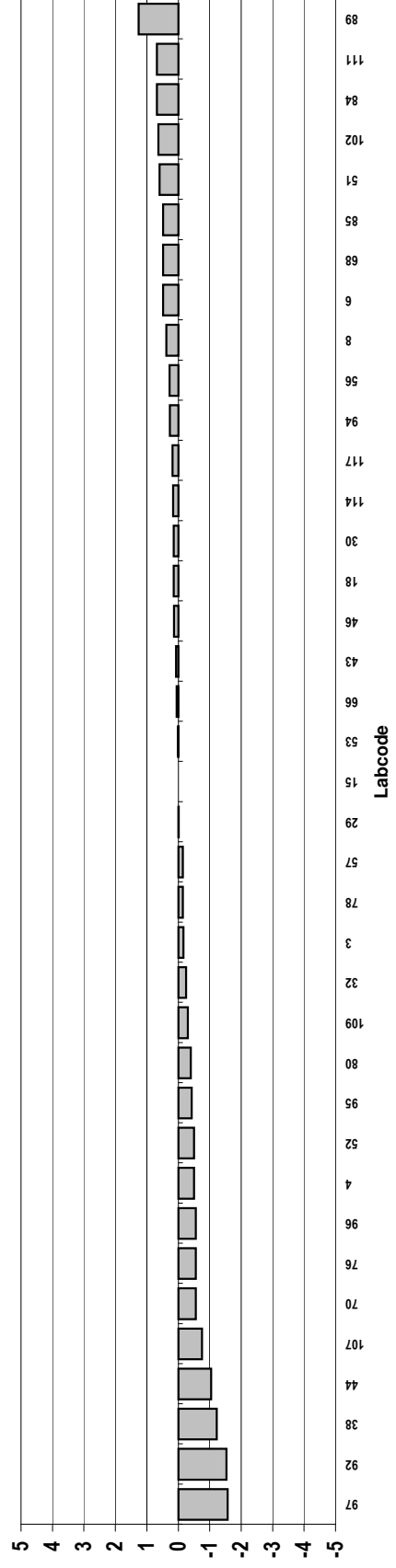
Consensus statistics

Consensus median, pg/μL	26
Median all values pg/μL	26
Consensus mean, pg/μL	25
Standard deviation, pg/μL	3.1
Relative standard deviation, %	13
No. of values reported	38
No. of values removed	0
No. of reported non-detects	0

BDE 183



Z-score: BDE 183



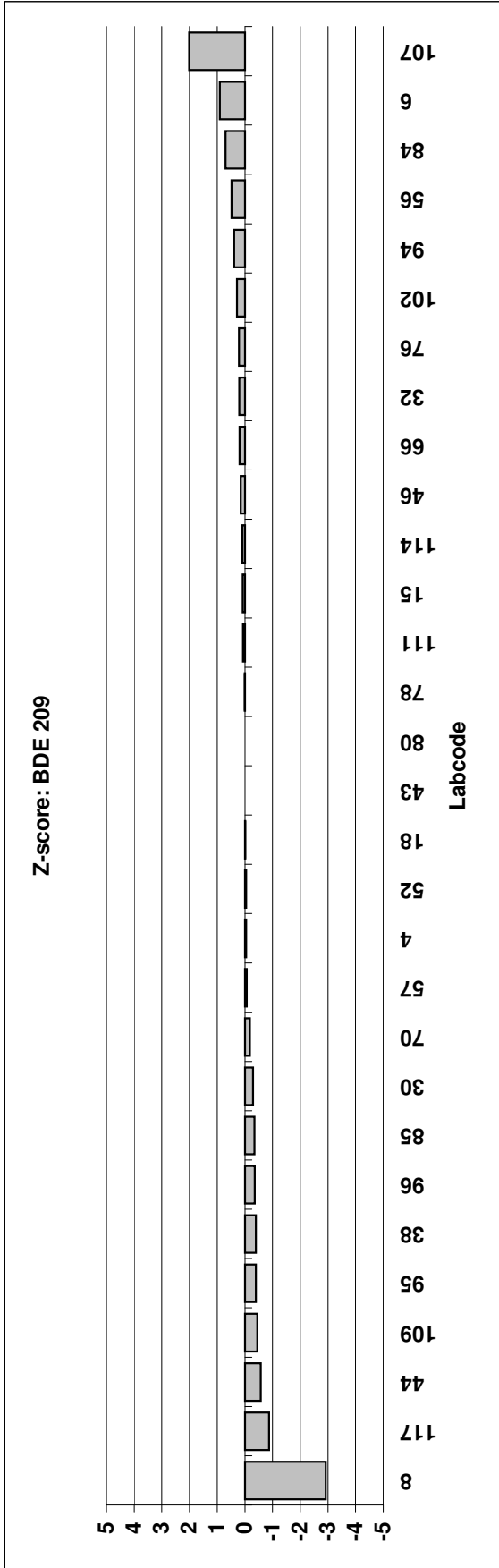
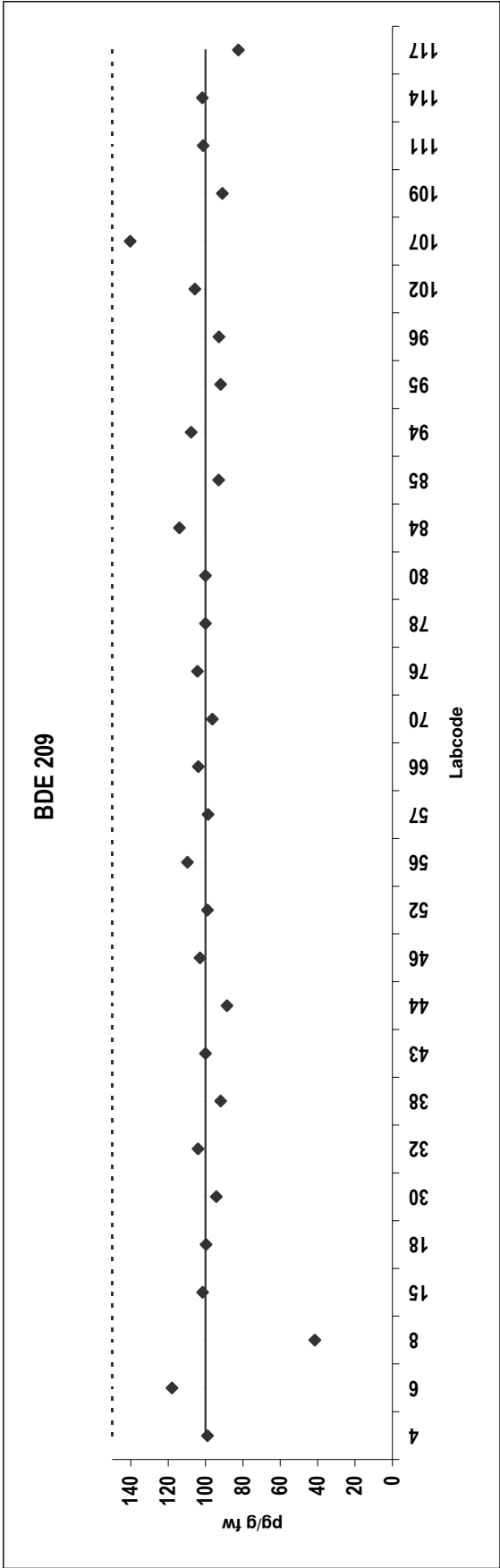
Analyte solution

Congener: BDE 209

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	99				
6	118				
8	42				
15	102				
18	100				
30	94				
32	104				
38	92				
43	100				
44	89				
46	103				
52	99				
56	110				
57	99				
66	104				
70	96				
76	104				
78	100				
80	100				
84	114				
85	93				
94	108				
95	92				
96	93				
102	106				
107	140				
109	91				
111	101				
114	102				
117	83				
		Outlier			

Consensus statistics

Consensus median, pg/μL	100
Median all values pg/μL	100
Consensus mean, pg/μL	101
Standard deviation, pg/μL	11
Relative standard deviation, %	10
No. of values reported	30
No. of values removed	1
No. of reported non-detects	0



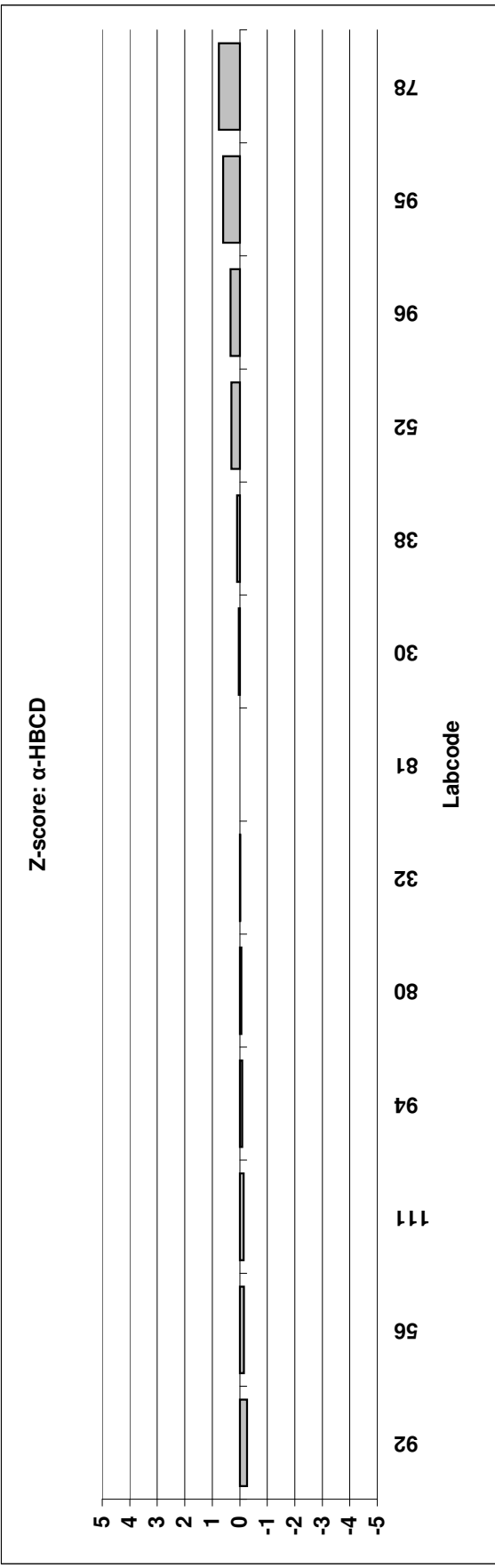
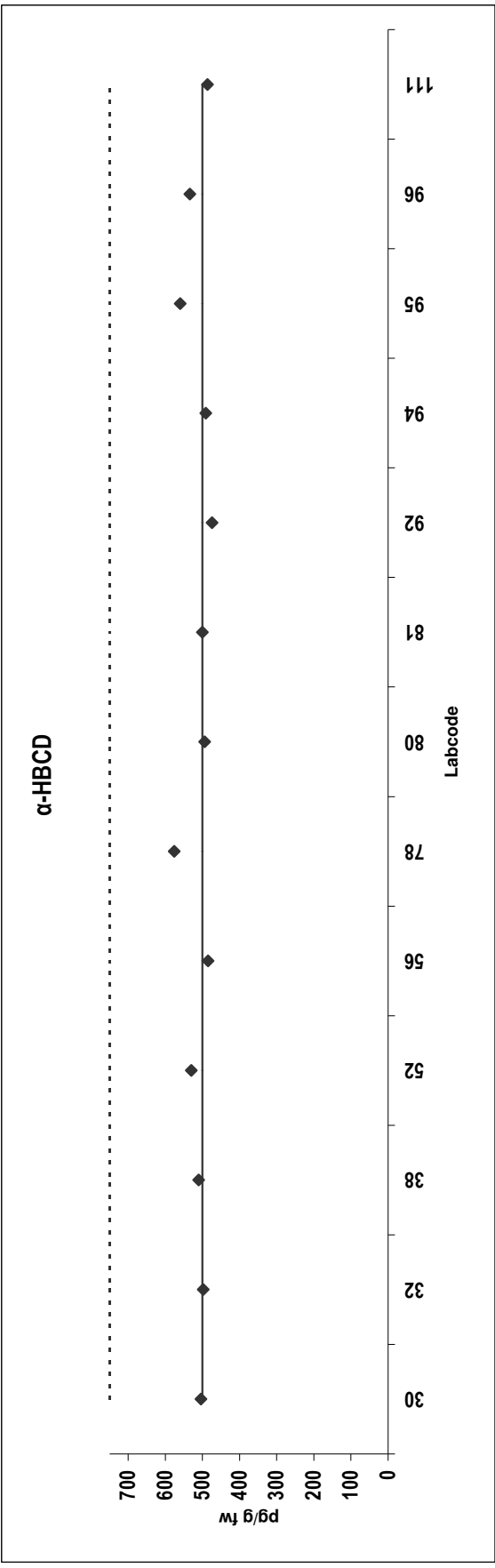
Analyte solution

Congener: α -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
30	504				
32	498				
38	510				
52	530				
56	485				
78	576				
80	494				
81	500				
92	474				
94	491				
95	560				
96	534				
111	486				

Consensus statistics

Consensus median, pg/ μ L	500
Median all values pg/ μ L	500
Consensus mean, pg/ μ L	511
Standard deviation, pg/ μ L	31
Relative standard deviation, %	6.0
No. of values reported	13
No. of values removed	0
No. of reported non-detects	0



Appendix 2:

Presentation of results
for breast milk

Appendix 2: Presentation of results: Breast 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:

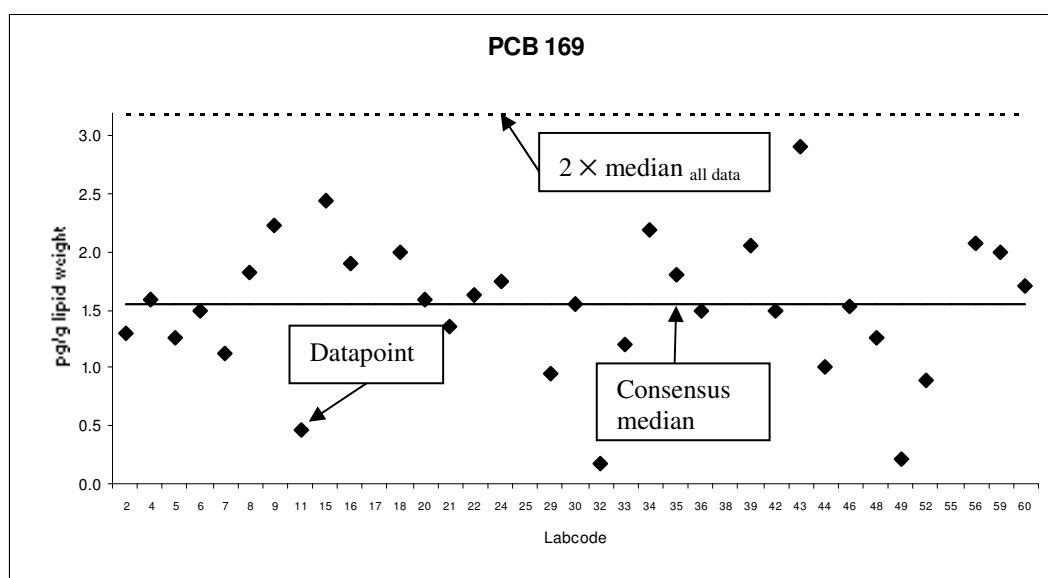
1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners.
2. Values exceeding $2 \times$ this median, were defined as outliers and removed from the data set.
3. Median, mean and standard deviation were re-calculated from the remaining 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); σ = target value for standard deviation. A σ 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.

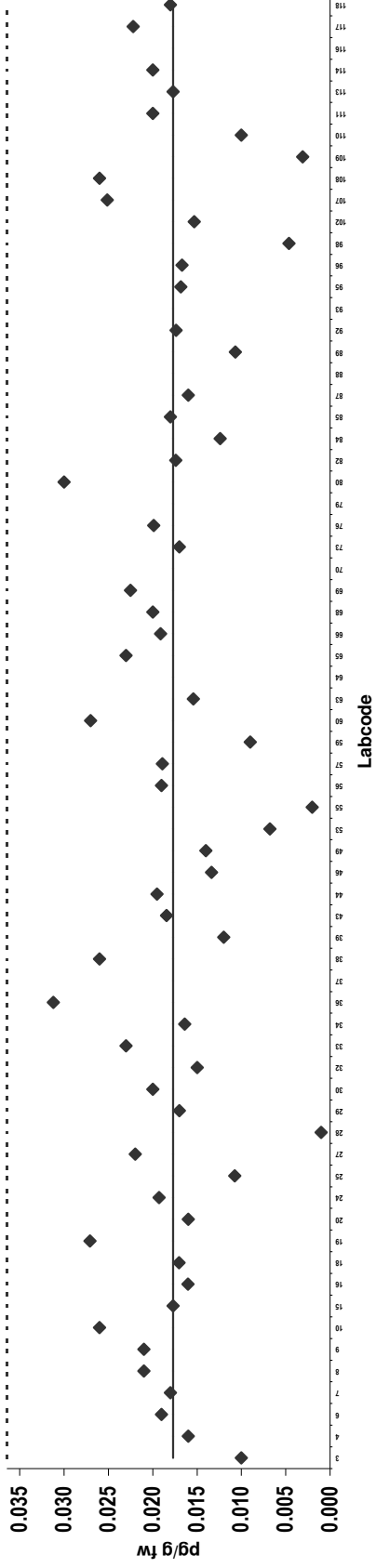
Breast milk
Congener: 2,3,7,8 TCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.010	ND	80	0.030	
4	0.016		82	0.017	
6	0.019		84	0.012	
7	0.018		85	0.018	
8	0.021		87	0.016	
9	0.021		88	0.041	Outlier
10	0.026		89	0.011	
15	0.018		92	0.017	Outlier
16	0.016		93	0.092	
18	0.017		95	0.017	
19	0.027		96	0.017	
20	0.016		98	0.0046	
24	0.019		102	0.015	
25	0.011		107	0.025	
27	0.022		108	0.026	
28	0.0010		109	0.0031	ND
29	0.017		110	0.010	
30	0.020		111	0.020	
32	0.015		113	0.018	
33	0.023		114	0.020	
34	0.016		116	0.57	Outlier
36	0.031		117	0.022	
37	0.058	Outlier,ND	118	0.018	
38	0.026				
39	0.012				
43	0.018				
44	0.020				
46	0.013				
49	0.014				
53	0.0068				
55	0.0020				
56	0.019				
57	0.019				
59	0.0090				
60	0.027				
63	0.015				
64	0.43	Outlier			
65	0.023				
66	0.019				
68	0.020				
69	0.023				
70	0.038	Outlier			
73	0.017				
76	0.020				
79	0.044	Outlier			

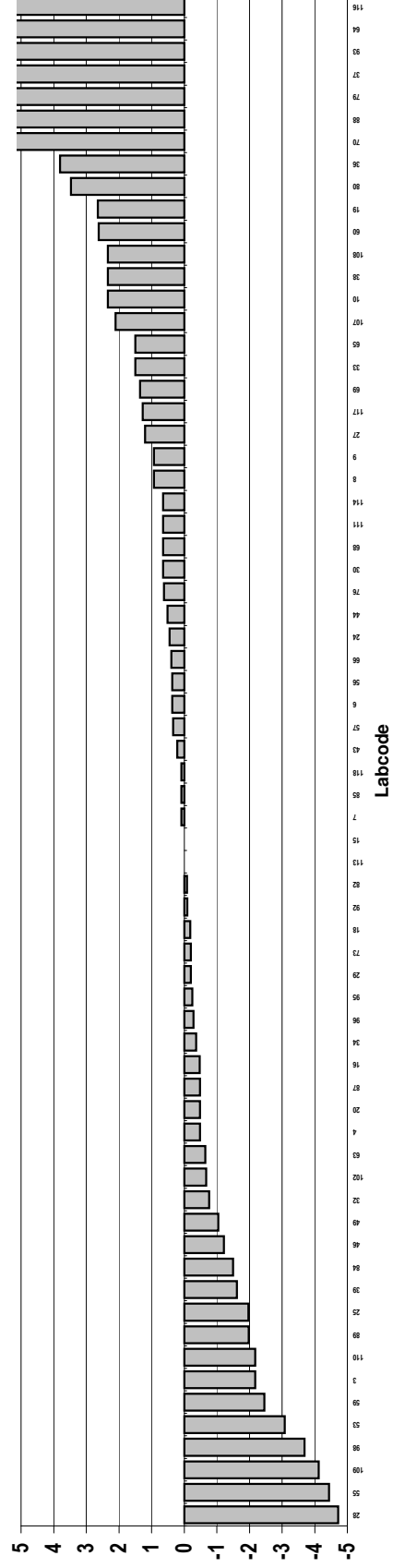
Consensus statistics

Consensus median, pg/g	0.018
Median all values pg/g	0.018
Consensus mean, pg/g	0.017
Standard deviation, pg/g	0.0063
Relative standard deviation, %	36
No. of values reported	68
No. of values removed	7
No. of reported non-detects	5

2,3,7,8 TCDD



Z-score: 2,3,7,8 TCDD

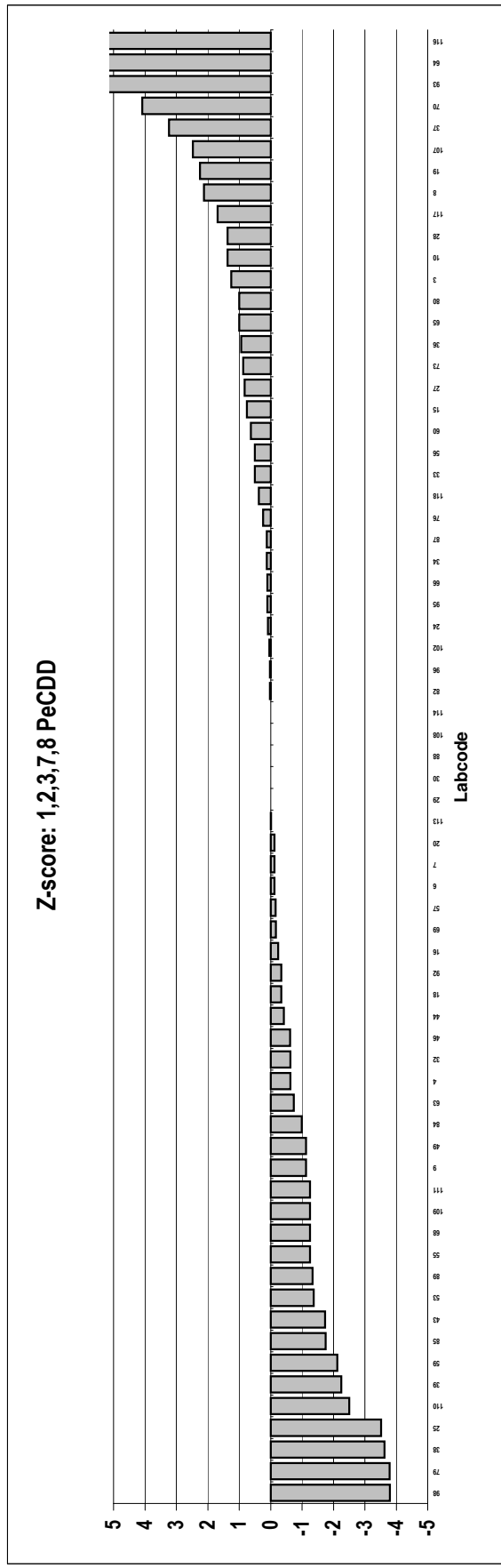
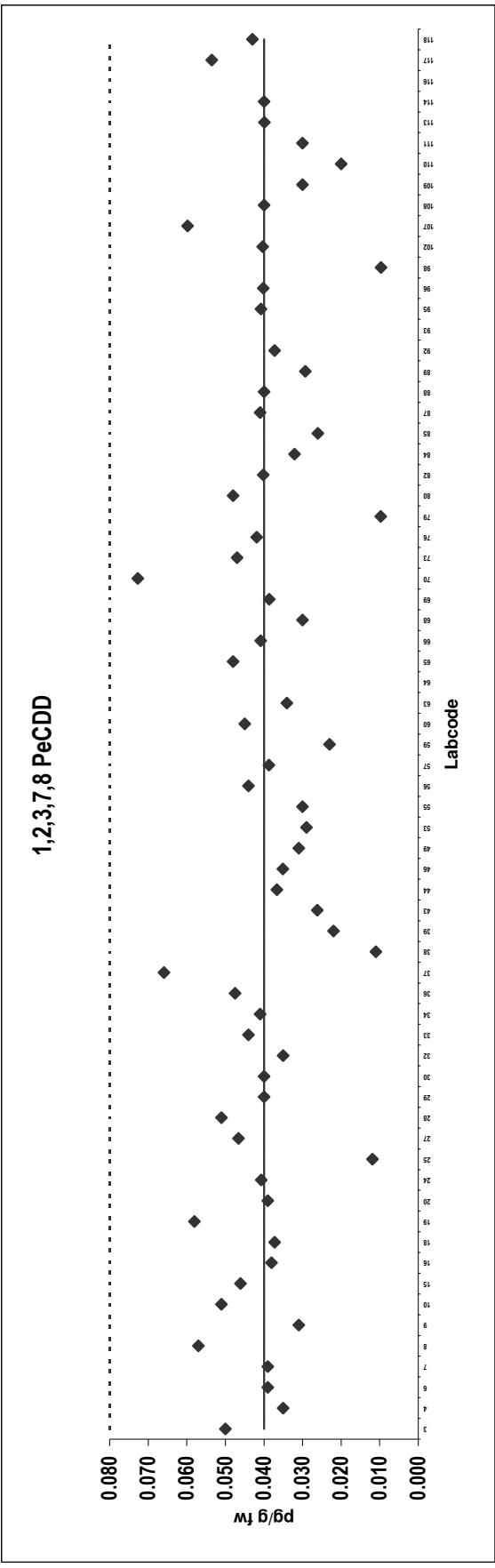


Breast milk
Congener: 1,2,3,7,8 PeCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.050		80	0.048	
4	0.035		82	0.040	
6	0.039		84	0.032	
7	0.039		85	0.026	
8	0.057		87	0.041	
9	0.031		88	0.040	
10	0.051		89	0.029	
15	0.046		92	0.037	
16	0.038		93	0.15	Outlier
18	0.037		95	0.041	
19	0.058		96	0.040	
20	0.039		98	0.0097	
24	0.041		102	0.040	
25	0.012		107	0.060	
27	0.047		108	0.040	
28	0.051		109	0.030	
29	0.040		110	0.020	
30	0.040		111	0.030	
32	0.035		113	0.040	
33	0.044		114	0.040	
34	0.041		116	1.2	Outlier
36	0.048		117	0.054	
37	0.066		118	0.043	
38	0.011				
39	0.022				
43	0.026				
44	0.037				
46	0.035				
49	0.031				
53	0.029				
55	0.030				
56	0.044				
57	0.039				
59	0.023				
60	0.045				
63	0.034				
64	0.63				
65	0.048				
66	0.041				
68	0.030				
69	0.039				
70	0.073				
73	0.047				
76	0.042				
79	0.0097				

Consensus statistics

Consensus median, pg/g	0.040
Median all values pg/g	0.040
Consensus mean, pg/g	0.038
Standard deviation, pg/g	0.012
Relative standard deviation, %	31
No. of values reported	68
No. of values removed	3
No. of reported non-detects	1



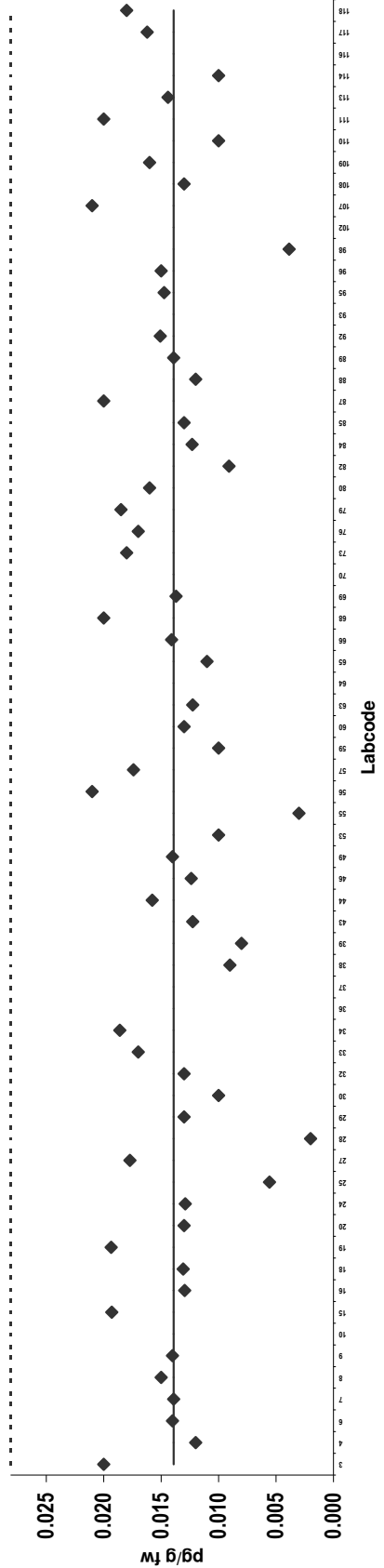
Breast milk
Congener: 1,2,3,4,7,8 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.020		80	0.016	ND
4	0.012		82	0.0091	
6	0.014		84	0.012	
7	0.014		85	0.013	
8	0.015	ND	87	0.020	
9	0.014		88	0.012	
10	0.029	Outlier	89	0.014	
15	0.019		92	0.015	
16	0.013		93	0.14	Outlier
18	0.013		95	0.015	
19	0.019		96	0.015	
20	0.013		98	0.0039	ND
24	0.013		102	0.039	Outlier
25	0.0056		107	0.021	ND
27	0.018		108	0.013	
28	0.0020		109	0.016	
29	0.013	ND	110	0.010	
30	0.010		111	0.020	
32	0.013		113	0.014	
33	0.017		114	0.010	
34	0.019		116	0.43	Outlier
36	0.044		117	0.016	
37	0.098	Outlier,ND	118	0.018	
38	0.0090				
39	0.0080				
43	0.012				
44	0.016				
46	0.012				
49	0.014				
53	0.010				
55	0.0030				
56	0.021				
57	0.017				
59	0.010	ND			
60	0.013				
63	0.012				
64	0.64	Outlier			
65	0.011				
66	0.014				
68	0.020	ND			
69	0.014				
70	0.029	Outlier			
73	0.018				
76	0.017	ND			
79	0.019				

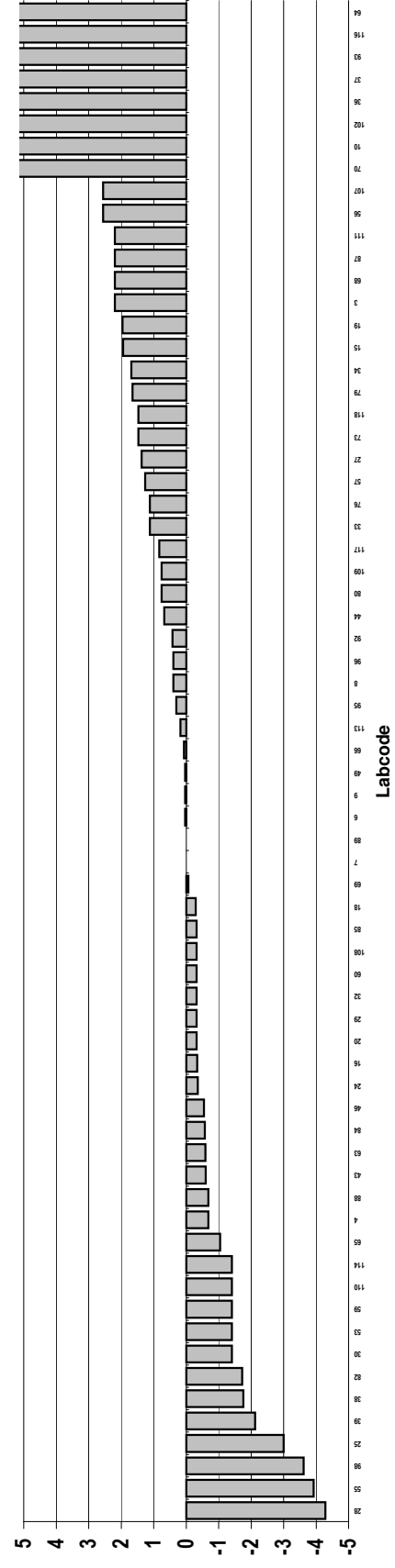
Consensus statistics

Consensus median, pg/g	0.014
Median all values pg/g	0.014
Consensus mean, pg/g	0.014
Standard deviation, pg/g	0.0043
Relative standard deviation, %	31
No. of values reported	68
No. of values removed	8
No. of reported non-detects	9

1,2,3,4,7,8 HxCDD



Z-score: 1,2,3,4,7,8 HxCDD



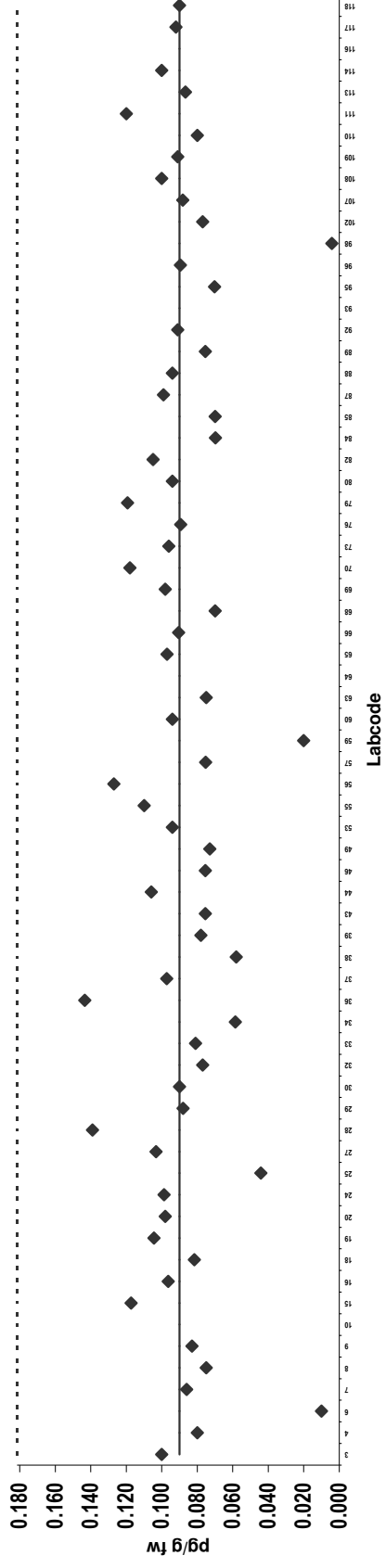
Breast milk
Congener: 1,2,3,6,7,8 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.10		80	0.094	
4	0.080		82	0.10	
6	0.010		84	0.070	
7	0.086		85	0.070	
8	0.075		87	0.099	
9	0.083		88	0.094	
10	0.19		89	0.075	
15	0.12		92	0.091	
16	0.096		93	0.23	Outlier
18	0.082		95	0.070	
19	0.10		96	0.090	
20	0.098		98	0.0042	
24	0.099		102	0.077	
25	0.044		107	0.088	
27	0.10		108	0.10	
28	0.14		109	0.091	
29	0.088		110	0.080	
30	0.090		111	0.12	
32	0.077		113	0.087	
33	0.081		114	0.10	
34	0.059		116	2.7	Outlier
36	0.14		117	0.092	
37	0.097	ND	118	0.090	
38	0.058				
39	0.078				
43	0.076				
44	0.11				
46	0.075				
49	0.073				
53	0.094				
55	0.11				
56	0.13				
57	0.075				
59	0.020				
60	0.094				
63	0.075				
64	0.41				
65	0.097	Outlier			
66	0.091				
68	0.070				
69	0.098				
70	0.12				
73	0.096				
76	0.089				
79	0.12				

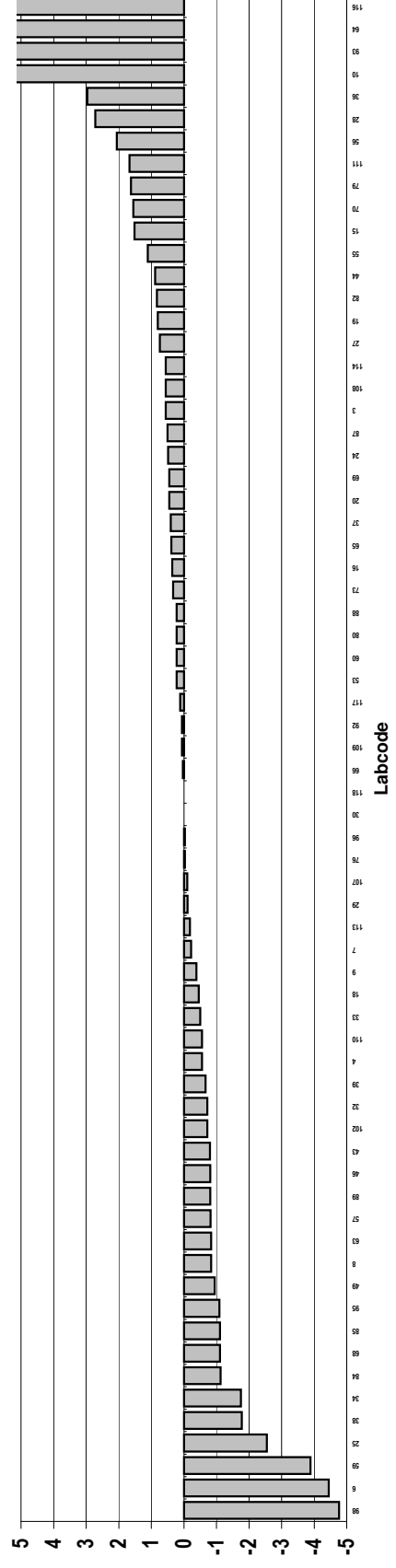
Consensus statistics

Consensus median, pg/g	0.090
Median all values pg/g	0.091
Consensus mean, pg/g	0.087
Standard deviation, pg/g	0.025
Relative standard deviation, %	28
No. of values reported	68
No. of values removed	4
No. of reported non-detects	2

1,2,3,6,7,8 HxCDD



Z-score: 1,2,3,6,7,8 HxCDD

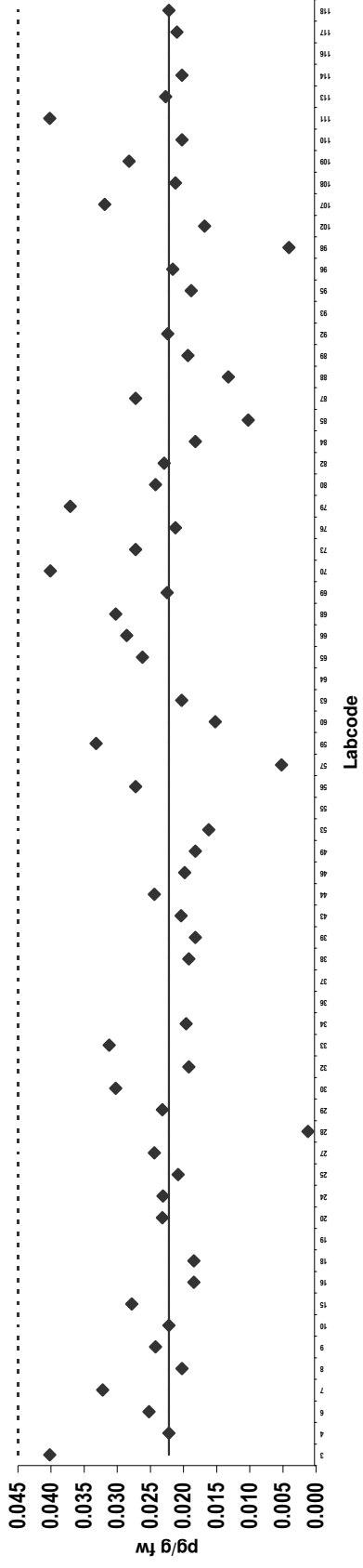


Breast milk
Congener: 1,2,3,7,8,9 HxCDD

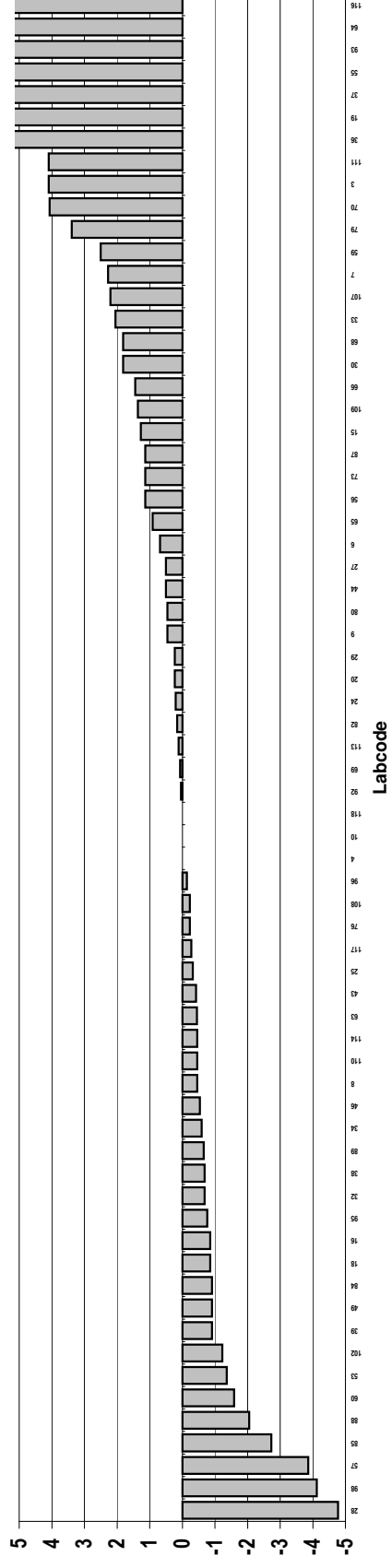
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.040		80	0.024	
4	0.022		82	0.023	
6	0.025		84	0.018	
7	0.032		85	0.010	ND
8	0.020		87	0.027	
9	0.024		88	0.013	
10	0.022		89	0.019	
15	0.028		92	0.022	
16	0.018		93	0.19	Outlier
18	0.018		95	0.019	
19	0.10		96	0.021	
20	0.023	Outlier	98	0.0039	
24	0.023		102	0.017	ND
25	0.021		107	0.032	
27	0.024		108	0.021	
28	0.0010		109	0.028	
29	0.023	ND	110	0.020	
30	0.030		111	0.040	
32	0.019		113	0.023	
33	0.031		114	0.020	
34	0.019		116	0.72	Outlier
36	0.074	Outlier	117	0.021	
37	0.10	Outlier,ND	118	0.022	
38	0.019				
39	0.018				
43	0.020				
44	0.024				
46	0.020				
49	0.018				
53	0.016				
55	0.12				
56	0.027	Outlier			
57	0.0050	ND			
59	0.033				
60	0.015				
63	0.020				
64	0.49	Outlier			
65	0.026				
66	0.028				
68	0.030				
69	0.022				
70	0.040				
73	0.027				
76	0.021	ND			
79	0.037				

Consensus statistics	
Consensus median, pg/g	0.022
Median all values pg/g	0.022
Consensus mean, pg/g	0.022
Standard deviation, pg/g	0.0076
Relative standard deviation, %	34
No. of values reported	68
No. of values removed	7
No. of reported non-detects	6

1,2,3,7,8,9 HxCDD



Z-score: 1,2,3,7,8,9 HxCDD

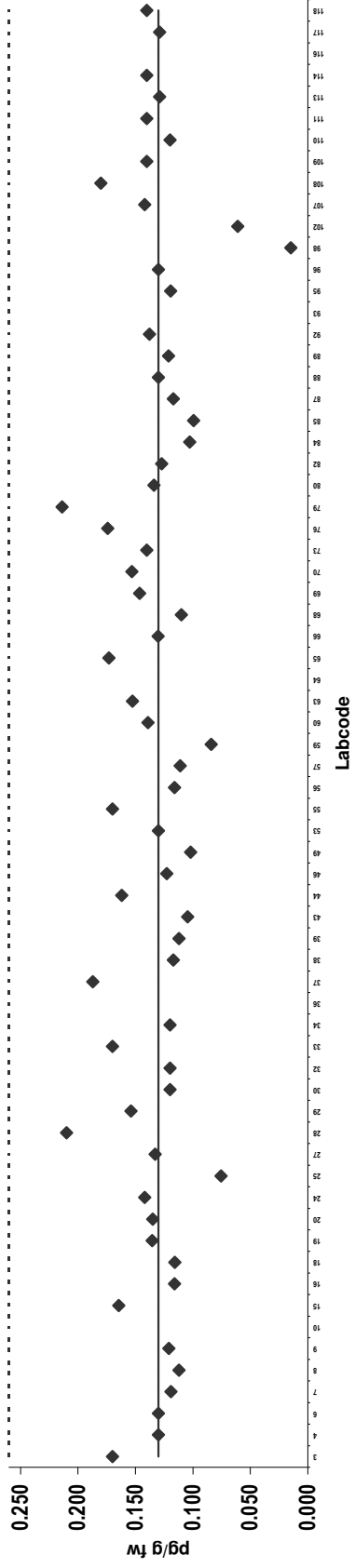


Breast milk
Congener: 1,2,3,4,6,7,8 HpCDD

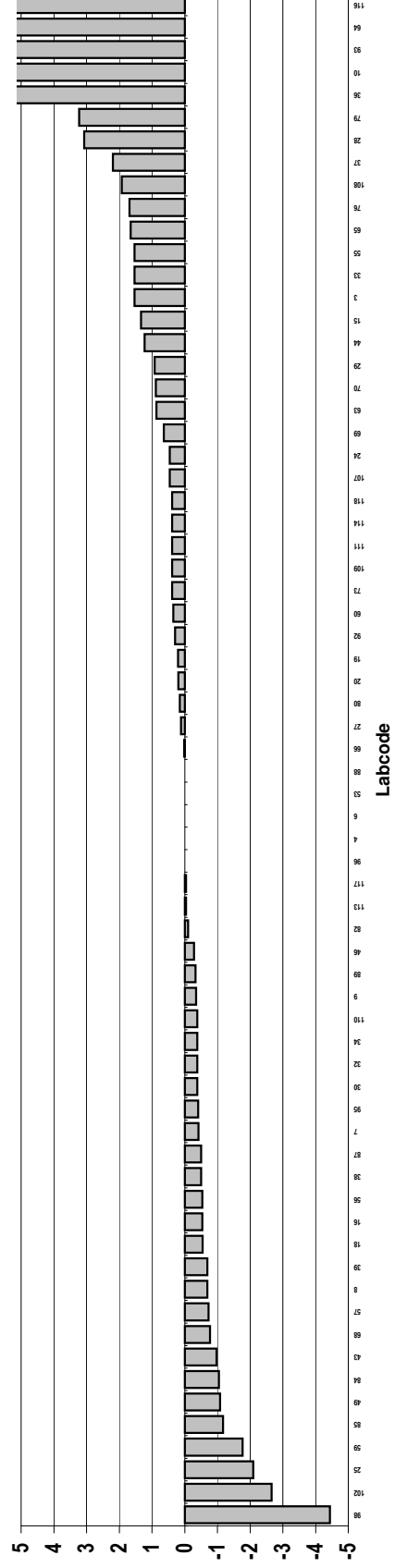
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.17		80	0.13	
4	0.13		82	0.13	
6	0.13		84	0.10	
7	0.12		85	0.10	
8	0.11		87	0.12	
9	0.12		88	0.13	
10	0.31		89	0.12	
15	0.16		92	0.14	
16	0.12		93	0.58	Outlier
18	0.12		95	0.12	
19	0.14		96	0.13	
20	0.14		98	0.015	
24	0.14		102	0.061	ND
25	0.075		107	0.14	
27	0.13		108	0.18	
28	0.21		109	0.14	
29	0.15		110	0.12	
30	0.12		111	0.14	
32	0.12		113	0.13	
33	0.17		114	0.14	
34	0.12		116	4.3	Outlier
36	0.29		117	0.13	
37	0.19		118	0.14	
38	0.12				
39	0.11				
43	0.10				
44	0.16				
46	0.12				
49	0.10				
53	0.13				
55	0.17				
56	0.12				
57	0.11				
59	0.084				
60	0.14				
63	0.15				
64	0.61				
65	0.17				
66	0.13				
68	0.11				
69	0.15				
70	0.15				
73	0.14				
76	0.17				
79	0.21				

Consensus statistics	
Consensus median, pg/g	0.13
Median all values pg/g	0.13
Consensus mean, pg/g	0.13
Standard deviation, pg/g	0.032
Relative standard deviation, %	24
No. of values reported	68
No. of values removed	5
No. of reported non-detects	1

1,2,3,4,6,7,8 HpCDD



Z-score: 1,2,3,4,6,7,8 HpCDD

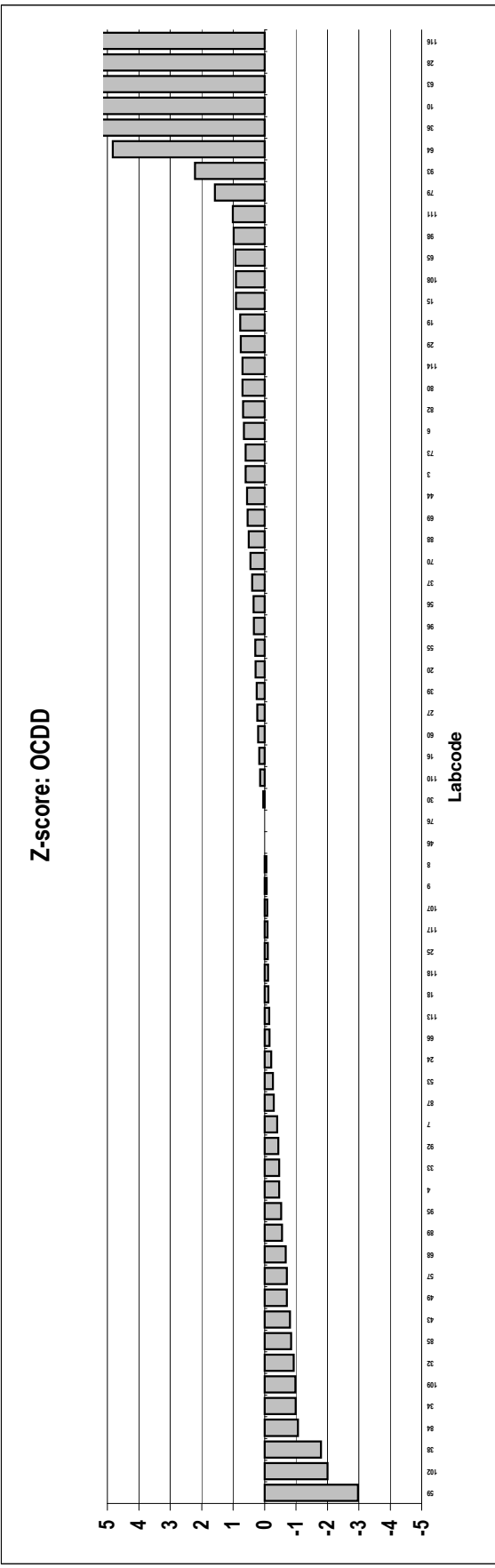
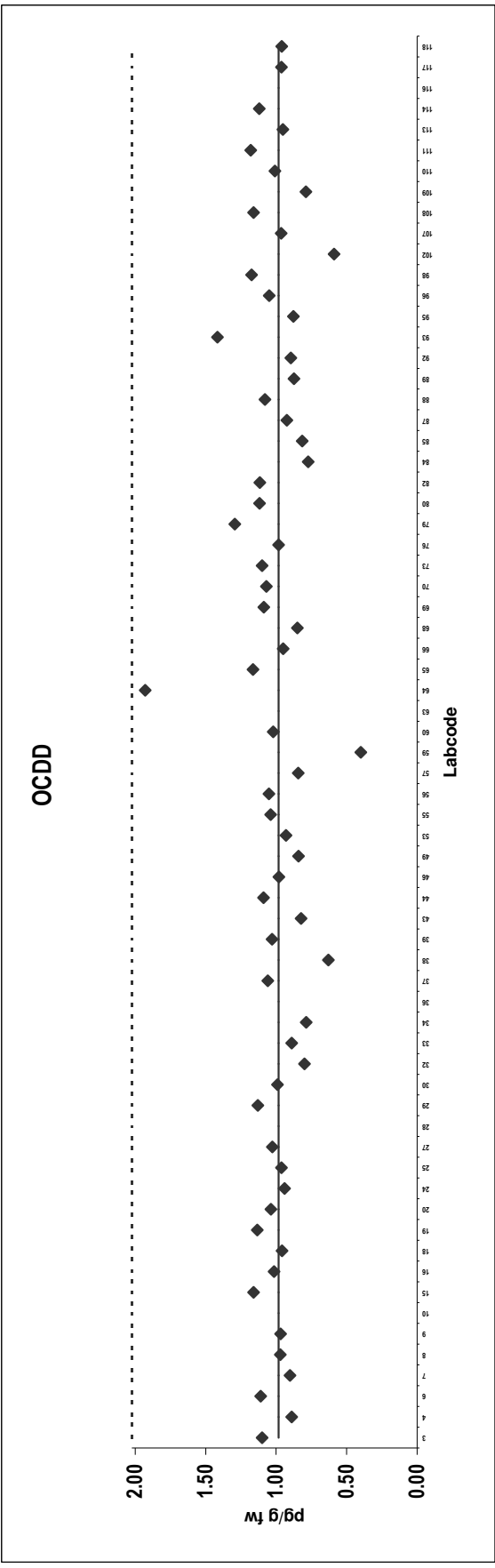


Breast milk Congener: OCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	1.1		80	1.1	
4	0.89		82	1.1	
6	1.1		84	0.77	
7	0.90		85	0.82	
8	0.97		87	0.93	
9	0.97		88	1.1	
10	2.1		89	0.87	
15	1.2		92	0.90	
16	1.0		93	1.4	
18	0.96		95	0.88	
19	1.1		96	1.0	
20	1.0		98	1.2	
24	0.94		102	0.59	
25	0.96		107	0.97	
27	1.0		108	1.2	
28	2.2		109	0.79	
29	1.1		110	1.0	
30	0.99		111	1.2	
32	0.80		113	0.95	
33	0.89		114	1.1	
34	0.79		116	32	Outlier
36	2.0		117	0.96	
37	1.1		118	0.96	
38	0.63				
39	1.0				
43	0.82				
44	1.1				
46	0.98				
49	0.84				
53	0.93				
55	1.0				
56	1.1				
57	0.84				
59	0.40				
60	1.0				
63	2.2				
64	1.9				
65	1.2				
66	0.95				
68	0.85				
69	1.1				
70	1.1				
73	1.1				
76	0.98				
79	1.3				

Consensus statistics

Consensus median, pg/g	0.98
Median all values pg/g	1.0
Consensus mean, pg/g	1.0
Standard deviation, pg/g	0.20
Relative standard deviation, %	20
No. of values reported	68
No. of values removed	5
No. of reported non-detects	0

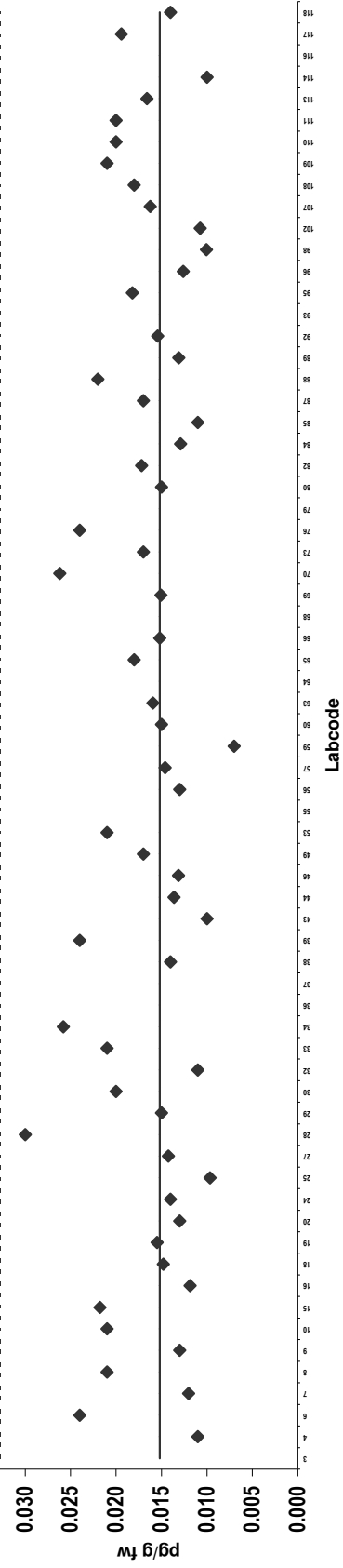


Breast milk
Congener: 2,3,7,8 TCDF

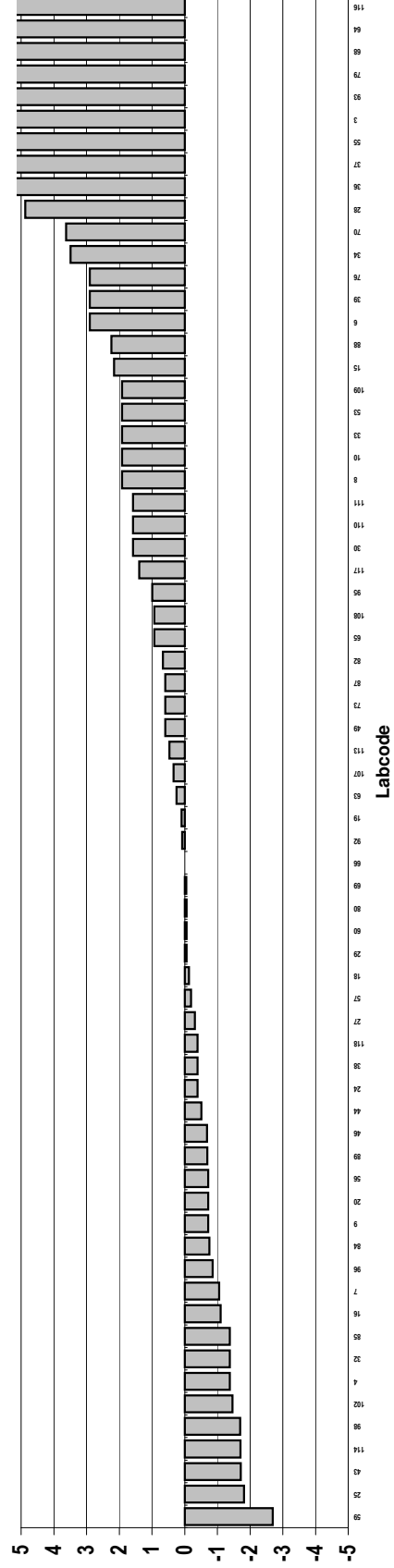
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.050		80	0.015	
4	0.011	Outlier	82	0.017	
6	0.024		84	0.013	
7	0.012		85	0.011	
8	0.021		87	0.017	
9	0.013		88	0.022	
10	0.021		89	0.013	
15	0.022		92	0.015	
16	0.012		93	0.057	Outlier
18	0.015		95	0.018	
19	0.015		96	0.013	
20	0.013		98	0.010	
24	0.014		102	0.011	
25	0.0097		107	0.016	
27	0.014		108	0.018	
28	0.030		109	0.021	
29	0.015		110	0.020	
30	0.020		111	0.020	
32	0.011		113	0.017	
33	0.021		114	0.010	
34	0.026		116	0.42	Outlier
36	0.037		117	0.019	
37	0.038	Outlier,ND	118	0.014	
38	0.014				
39	0.024				
43	0.010				
44	0.014				
46	0.013				
49	0.017				
53	0.021				
55	0.040				
56	0.013				
57	0.015				
59	0.0070				
60	0.015				
63	0.016				
64	0.34	Outlier			
65	0.018				
66	0.015				
68	0.060	Outlier			
69	0.015				
70	0.026				
73	0.017				
76	0.024	ND			
79	0.059	Outlier			

Consensus statistics	
Consensus median, pg/g	0.015
Median all values pg/g	0.016
Consensus mean, pg/g	0.016
Standard deviation, pg/g	0.0048
Relative standard deviation, %	29
No. of values reported	68
No. of values removed	9
No. of reported non-detects	2

2,3,7,8 TCDF



Z-score: 2,3,7,8 TCDF



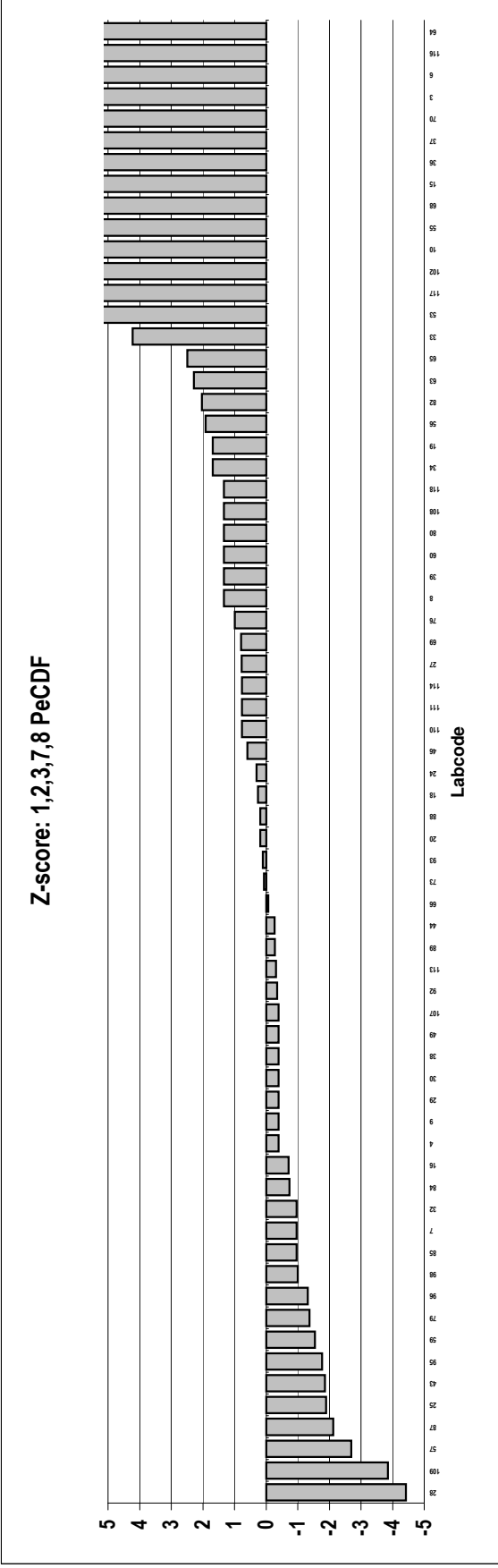
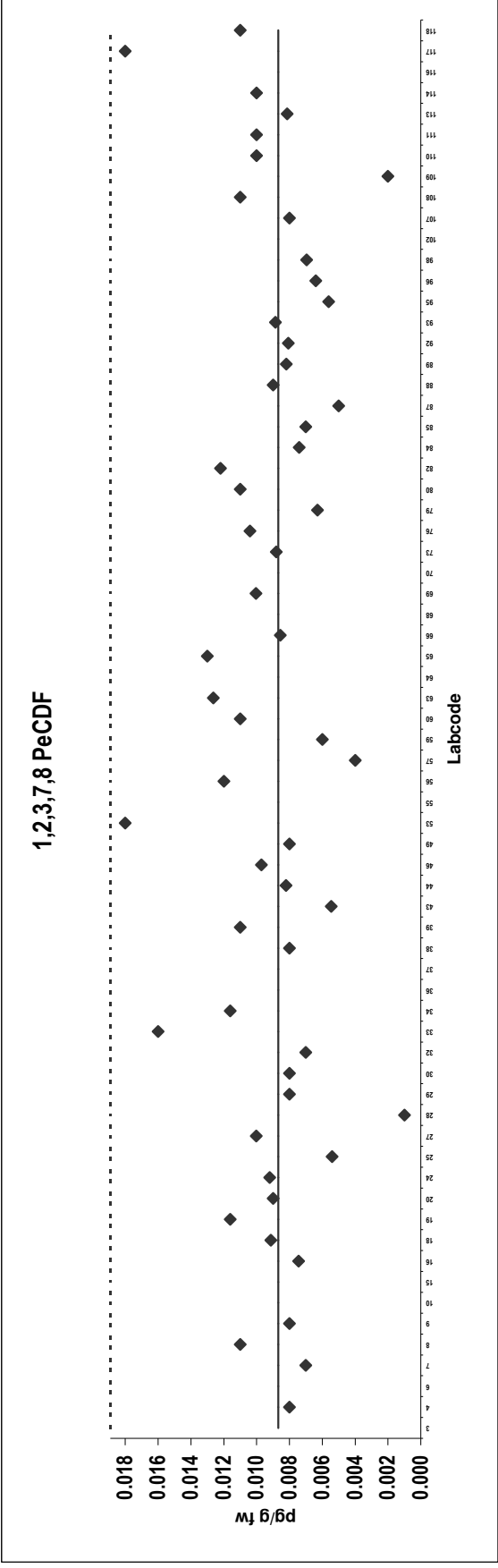
Breast milk

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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.050	Outlier	80	0.011	
4	0.0080		82	0.012	
6	0.14	Outlier	84	0.0074	
7	0.0070		85	0.0070	
8	0.011		87	0.0050	ND
9	0.0080		88	0.0090	
10	0.020	Outlier	89	0.0082	
15	0.022	Outlier	92	0.0081	
16	0.0074		93	0.0089	
18	0.0091		95	0.0056	
19	0.012		96	0.0064	
20	0.0090		98	0.0069	
24	0.0092		102	0.020	Outlier
25	0.0054		107	0.0080	ND
27	0.010		108	0.011	
28	0.0010	ND	109	0.0020	ND
29	0.0080		110	0.010	
30	0.0080		111	0.010	
32	0.0070		113	0.0081	
33	0.016		114	0.010	
34	0.012	ND	116	0.23	Outlier
36	0.026	Outlier	117	0.018	
37	0.041	Outlier,ND	118	0.011	
38	0.0080				
39	0.011				
43	0.0055				
44	0.0082				
46	0.0097				
49	0.0080				
53	0.018	Outlier			
55	0.020				
56	0.012				
57	0.0040	ND			
59	0.0060				
60	0.011				
63	0.013				
64	0.29	Outlier			
65	0.013				
66	0.0086				
68	0.020	Outlier			
69	0.010				
70	0.044	Outlier			
73	0.0088				
76	0.010	ND			
79	0.0063				

Consensus statistics

Consensus median, pg/g	0.0087
Median all values pg/g	0.0095
Consensus mean, pg/g	0.0090
Standard deviation, pg/g	0.0032
Relative standard deviation, %	35
No. of values reported	68
No. of values removed	12
No. of reported non-detects	8

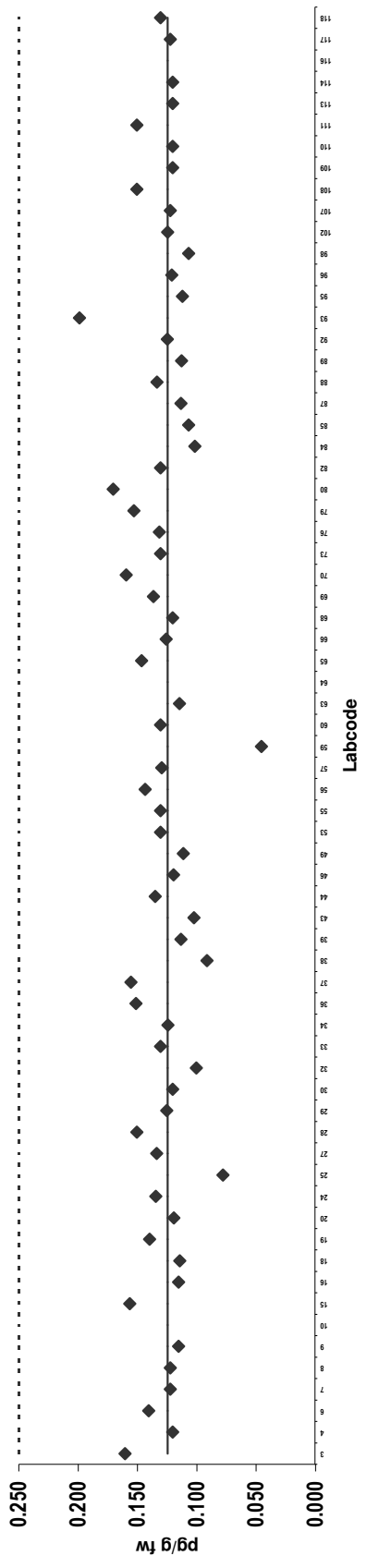


Breast milk
Congener: 2,3,4,7,8 PeCDF

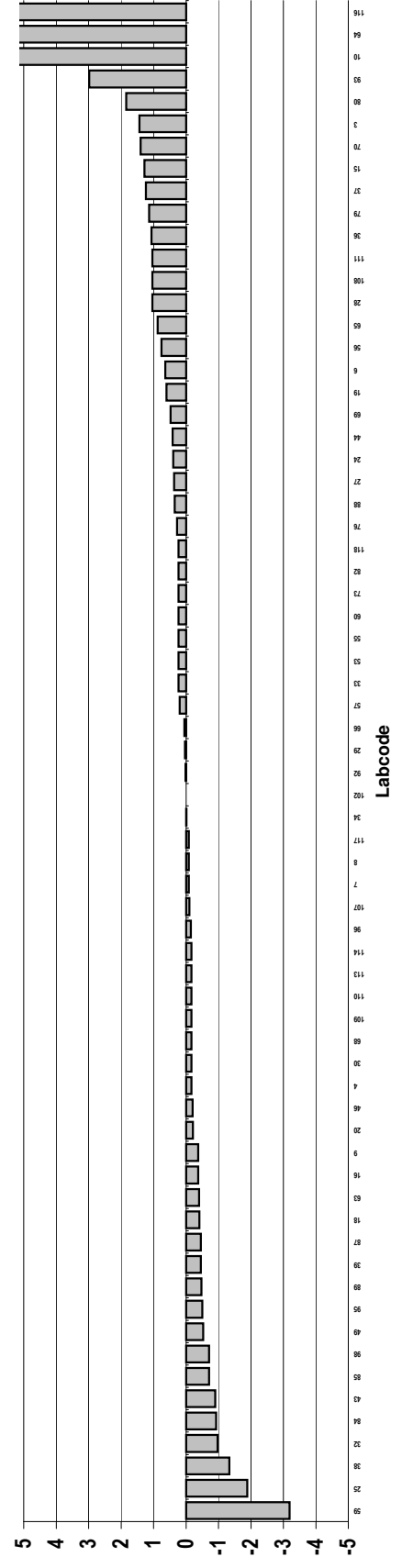
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.16		80	0.17	
4	0.12		82	0.13	
6	0.14		84	0.10	
7	0.12		85	0.11	
8	0.12		87	0.11	
9	0.12		88	0.13	
10	0.29		89	0.11	
15	0.16		92	0.12	
16	0.11		93	0.20	
18	0.11		95	0.11	
19	0.14		96	0.12	
20	0.12		98	0.11	
24	0.13		102	0.12	
25	0.077		107	0.12	
27	0.13		108	0.15	
28	0.15		109	0.12	
29	0.13		110	0.12	
30	0.12		111	0.15	
32	0.10		113	0.12	
33	0.13		114	0.12	
34	0.12		116	3.8	Outlier
36	0.15		117	0.12	
37	0.16		118	0.13	
38	0.091				
39	0.11				
43	0.10				
44	0.13				
46	0.12				
49	0.11				
53	0.13				
55	0.13				
56	0.14				
57	0.13				
59	0.045				
60	0.13				
63	0.11				
64	0.94				
65	0.15				
66	0.13				
68	0.12				
69	0.14				
70	0.16				
73	0.13				
76	0.13				
79	0.15				

Consensus statistics	
Consensus median, pg/g	0.12
Median all values pg/g	0.12
Consensus mean, pg/g	0.13
Standard deviation, pg/g	0.022
Relative standard deviation, %	17
No. of values reported	68
No. of values removed	3
No. of reported non-detects	0

2,3,4,7,8 PeCDF



Z-score: 2,3,4,7,8 PeCDF



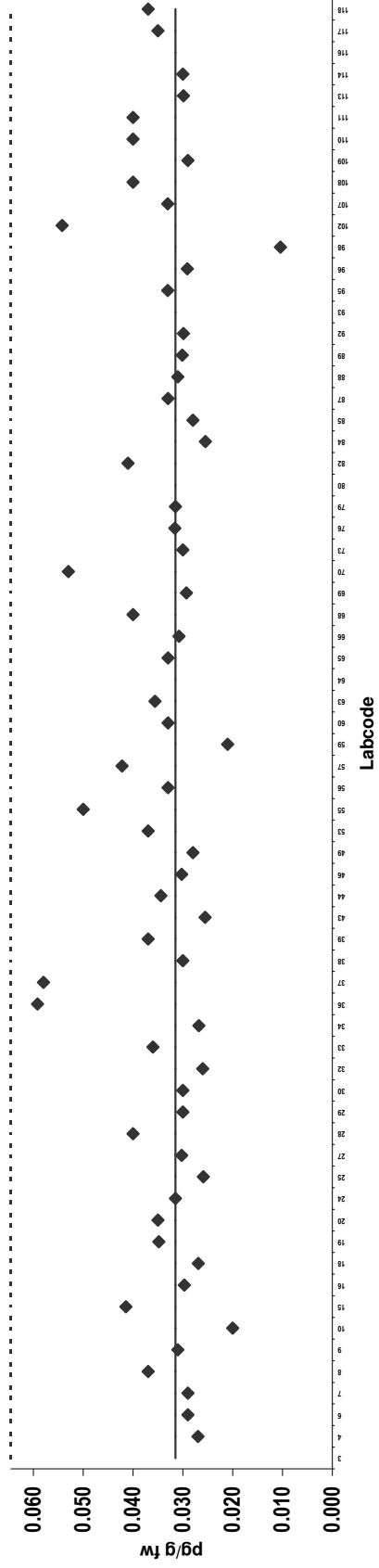
Breast milk
Congener: 1,2,3,4,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.090	Outlier	80	0.18	Outlier
4	0.027		82	0.041	
6	0.029		84	0.026	
7	0.029		85	0.028	
8	0.037		87	0.033	
9	0.031		88	0.031	
10	0.020		89	0.030	
15	0.041		92	0.030	
16	0.030		93	0.13	Outlier
18	0.027		95	0.033	
19	0.035		96	0.029	
20	0.035		98	0.010	
24	0.032		102	0.054	
25	0.026		107	0.033	
27	0.030		108	0.040	
28	0.040		109	0.029	
29	0.030		110	0.040	
30	0.030		111	0.040	
32	0.026		113	0.030	
33	0.036		114	0.030	
34	0.027		116	0.94	Outlier
36	0.059		117	0.035	
37	0.058		118	0.037	
38	0.030				
39	0.037				
43	0.026				
44	0.034				
46	0.030				
49	0.028				
53	0.037				
55	0.050				
56	0.033				
57	0.042				
59	0.021				
60	0.033				
63	0.036				
64	0.80	Outlier			
65	0.033				
66	0.031				
68	0.040				
69	0.029				
70	0.053				
73	0.030				
76	0.032				
79	0.032				

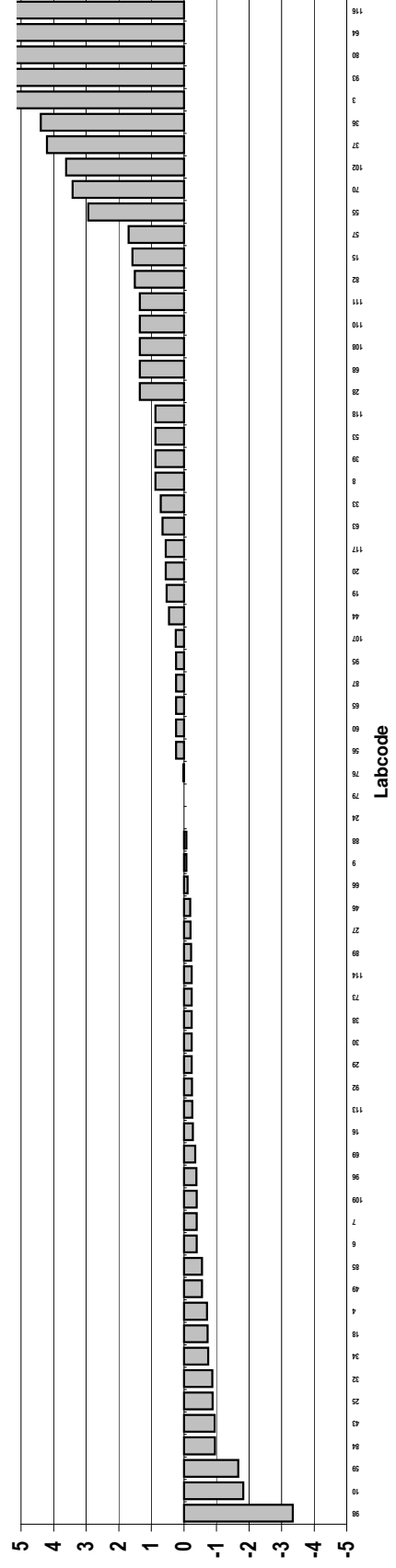
Consensus statistics

Consensus median, pg/g	0.032
Median all values pg/g	0.032
Consensus mean, pg/g	0.033
Standard deviation, pg/g	0.0084
Relative standard deviation, %	25
No. of values reported	68
No. of values removed	5
No. of reported non-detects	1

1,2,3,4,7,8 HxCDF



Z-score: 1,2,3,4,7,8 HxCDF



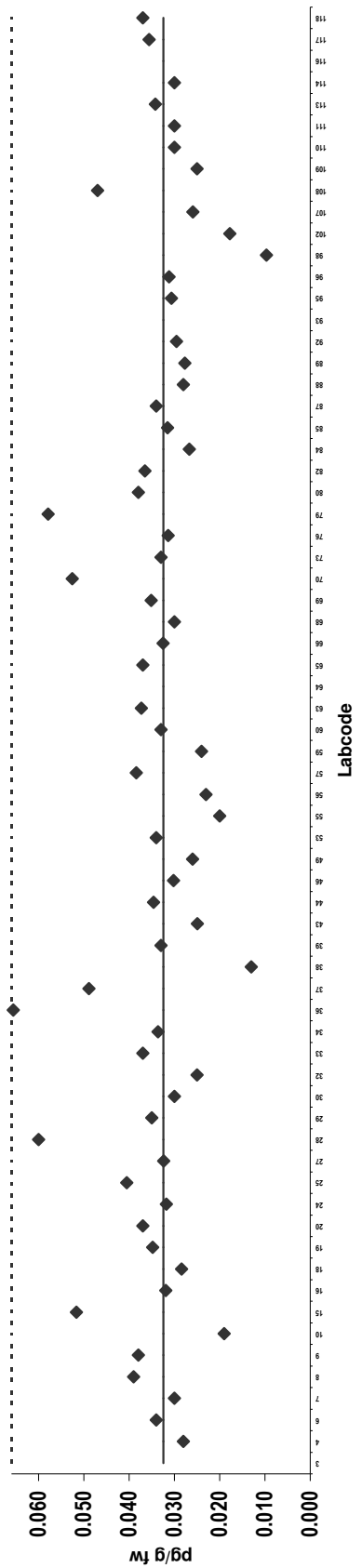
Breast milk
Congener: 1,2,3,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.080		80	0.038	
4	0.028	Outlier	82	0.037	
6	0.034		84	0.027	
7	0.030		85	0.032	
8	0.039		87	0.034	
9	0.038		88	0.028	
10	0.019		89	0.028	
15	0.052		92	0.030	
16	0.032		93	0.17	Outlier
18	0.028		95	0.031	
19	0.035		96	0.031	
20	0.037		98	0.0097	
24	0.032		102	0.018	
25	0.041		107	0.026	
27	0.032		108	0.047	
28	0.060		109	0.025	
29	0.035		110	0.030	
30	0.030		111	0.030	
32	0.025		113	0.034	
33	0.037		114	0.030	
34	0.034		116	0.96	Outlier
36	0.066		117	0.036	
37	0.049		118	0.037	
38	0.013				
39	0.033				
43	0.025				
44	0.035				
46	0.030				
49	0.026				
53	0.034				
55	0.020				
56	0.023				
57	0.038				
59	0.024				
60	0.033				
63	0.037				
64	0.93				
65	0.037				
66	0.033				
68	0.030				
69	0.035				
70	0.053				
73	0.033				
76	0.031				
79	0.058				

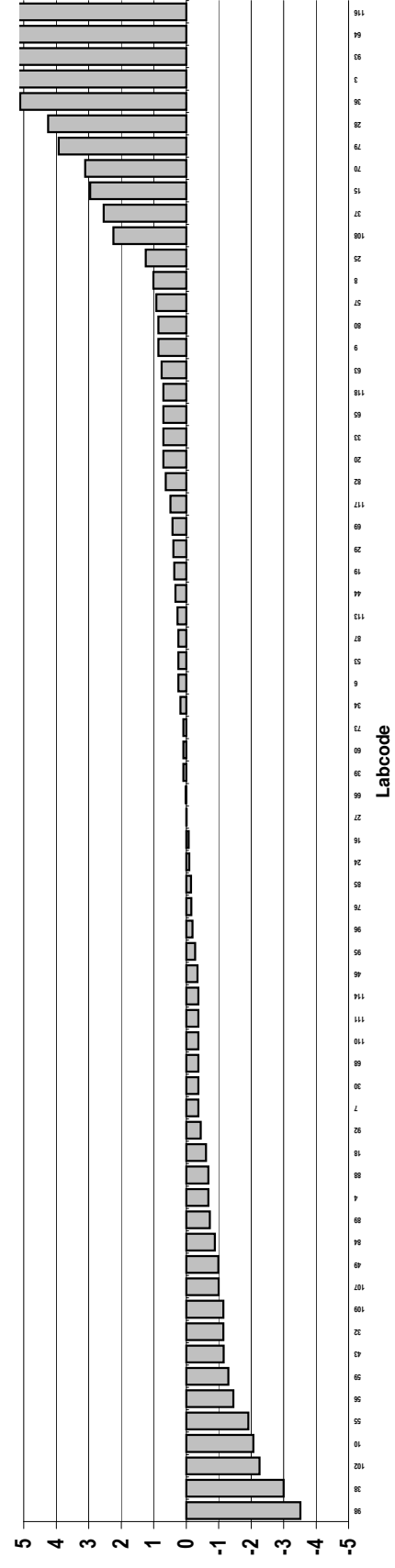
Consensus statistics

Consensus median, pg/g	0.032
Median all values pg/g	0.033
Consensus mean, pg/g	0.033
Standard deviation, pg/g	0.0099
Relative standard deviation, %	30
No. of values reported	68
No. of values removed	4
No. of reported non-detects	1

1,2,3,6,7,8 HxCDF



Z-score: 1,2,3,6,7,8 HxCDF



Breast milk

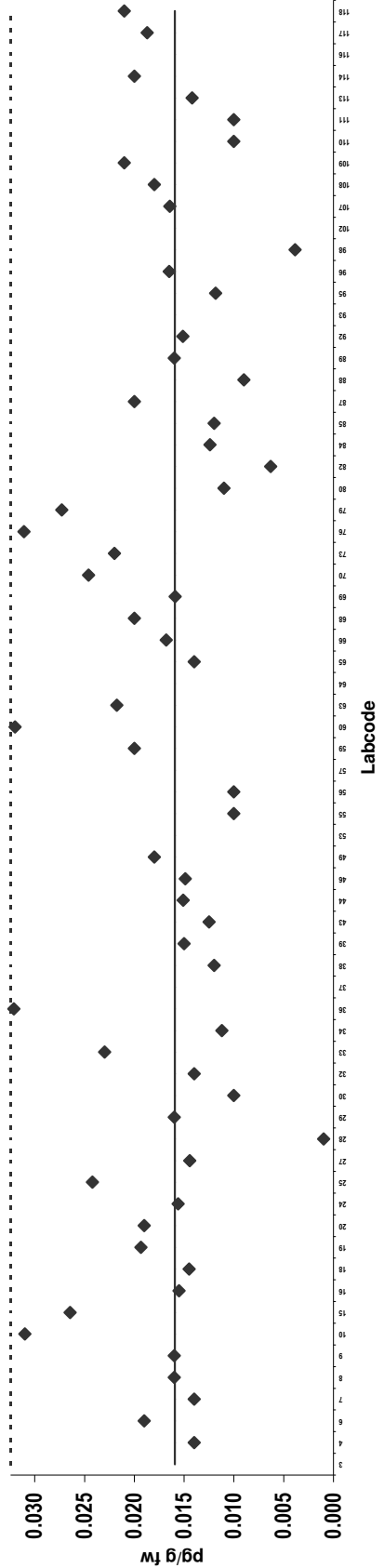
Congener: 2,3,4,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.060		80	0.011	
4	0.014	Outlier	82	0.0063	
6	0.019		84	0.012	
7	0.014		85	0.012	
8	0.016		87	0.020	
9	0.016		88	0.0090	
10	0.031		89	0.016	
15	0.026		92	0.015	
16	0.016		93	0.20	Outlier
18	0.014		95	0.012	
19	0.019		96	0.017	
20	0.019		98	0.0039	
24	0.016		102	0.043	ND
25	0.024		107	0.016	Outlier
27	0.014		108	0.018	
28	0.0010		109	0.021	
29	0.016		110	0.010	
30	0.010		111	0.010	
32	0.014		113	0.014	
33	0.023		114	0.020	
34	0.011		116	0.45	Outlier
36	0.032		117	0.019	
37	0.054	Outlier,ND	118	0.021	
38	0.012				
39	0.015				
43	0.013				
44	0.015				
46	0.015				
49	0.018				
53	0.035	Outlier			
55	0.010				
56	0.010				
57	0.048	Outlier			
59	0.020	ND			
60	0.032				
63	0.022				
64	0.44	Outlier			
65	0.014				
66	0.017				
68	0.020	ND			
69	0.016				
70	0.025				
73	0.022				
76	0.031				
79	0.027				

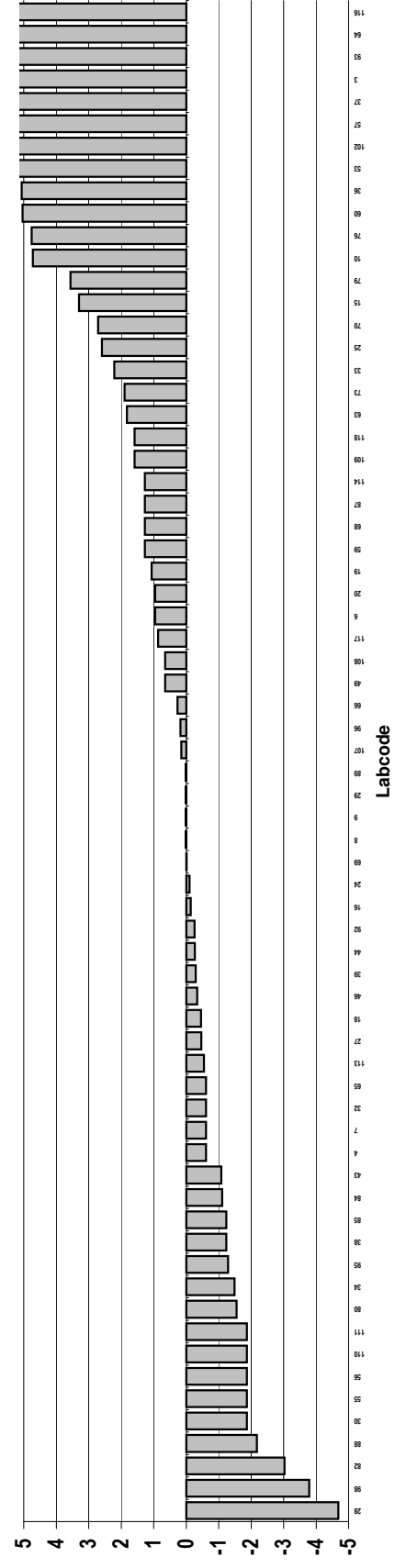
Consensus statistics

Consensus median, pg/g	0.016
Median all values pg/g	0.016
Consensus mean, pg/g	0.017
Standard deviation, pg/g	0.0064
Relative standard deviation, %	38
No. of values reported	68
No. of values removed	8
No. of reported non-detects	6

2,3,4,6,7,8 HxCDF



Z-score: 2,3,4,6,7,8 HxCDF

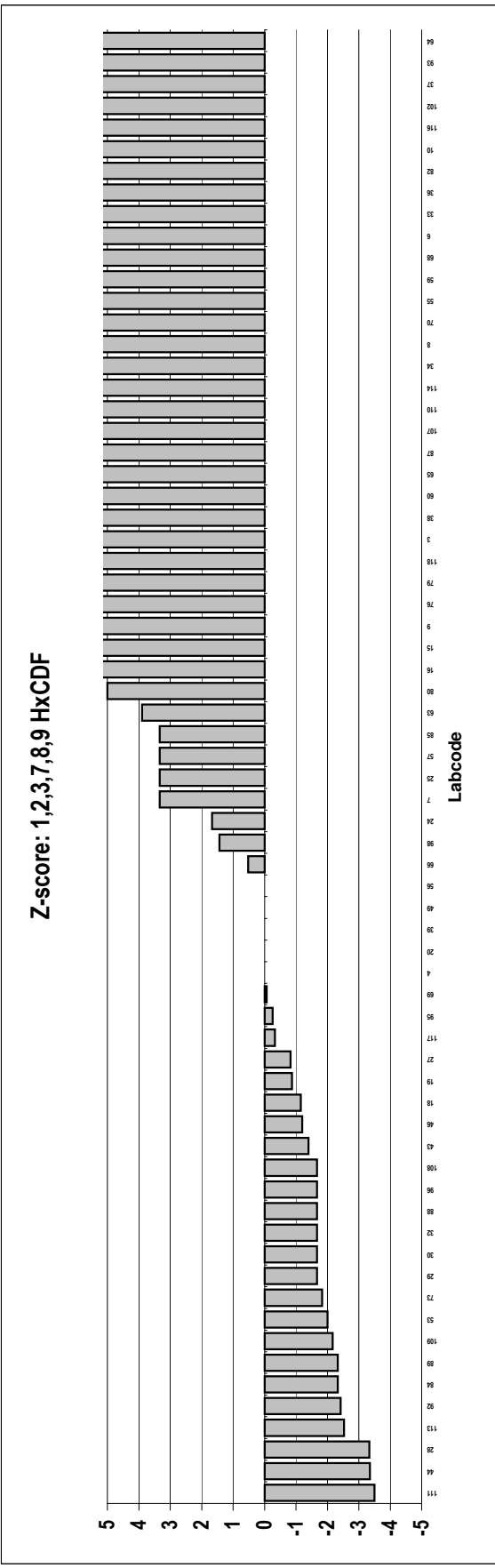
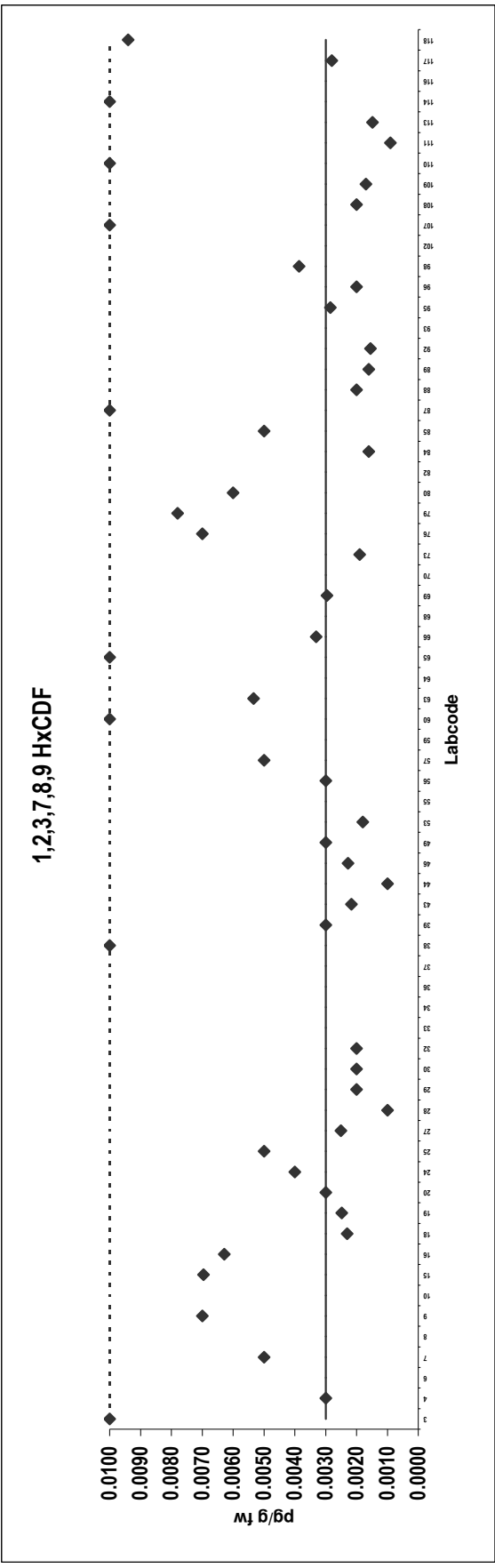


Breast milk

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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.010		80	0.0060	ND
4	0.0030	ND	82	0.026	Outlier
6	0.021	Outlier	84	0.0016	
7	0.0050	ND	85	0.0050	ND
8	0.014	Outlier,ND	87	0.010	ND
9	0.0070	ND	88	0.0020	ND
10	0.030	Outlier,ND	89	0.0016	ND
15	0.0070	ND	92	0.0015	
16	0.0063		93	0.41	Outlier
18	0.0023		95	0.0028	ND
19	0.0025	ND	96	0.0020	
20	0.0030		98	0.0039	ND
24	0.0040	ND	102	0.046	Outlier
25	0.0050	ND	107	0.010	ND
27	0.0025		108	0.0020	ND
28	0.0010	ND	109	0.0017	ND
29	0.0020	ND	110	0.010	ND
30	0.0020	ND	111	0.010	ND
32	0.0020	ND	113	0.00090	ND
33	0.021	Outlier	114	0.0015	
34	0.011	Outlier,ND	116	0.010	
36	0.023	Outlier	117	0.032	Outlier,ND
37	0.067	Outlier,ND	118	0.0028	
38	0.010	ND		0.0094	
39	0.0030	ND			
43	0.0022	ND			
44	0.00099				
46	0.0023				
49	0.0030				
53	0.0018	ND			
55	0.020	Outlier			
56	0.0030				
57	0.0050				
59	0.020	Outlier,ND			
60	0.010	ND			
63	0.0053				
64	0.82	Outlier			
65	0.010	ND			
66	0.0033	ND			
68	0.020	Outlier,ND			
69	0.0030				
70	0.014				
73	0.0019	Outlier			
76	0.0070	ND			
79	0.0078				

Consensus statistics	
Consensus median, pg/g	0.0030
Median all values pg/g	0.0050
Consensus mean, pg/g	0.0044
Standard deviation, pg/g	0.0031
Relative standard deviation, %	70
No. of values reported	68
No. of values removed	16
No. of reported non-detects	38



Breast milk

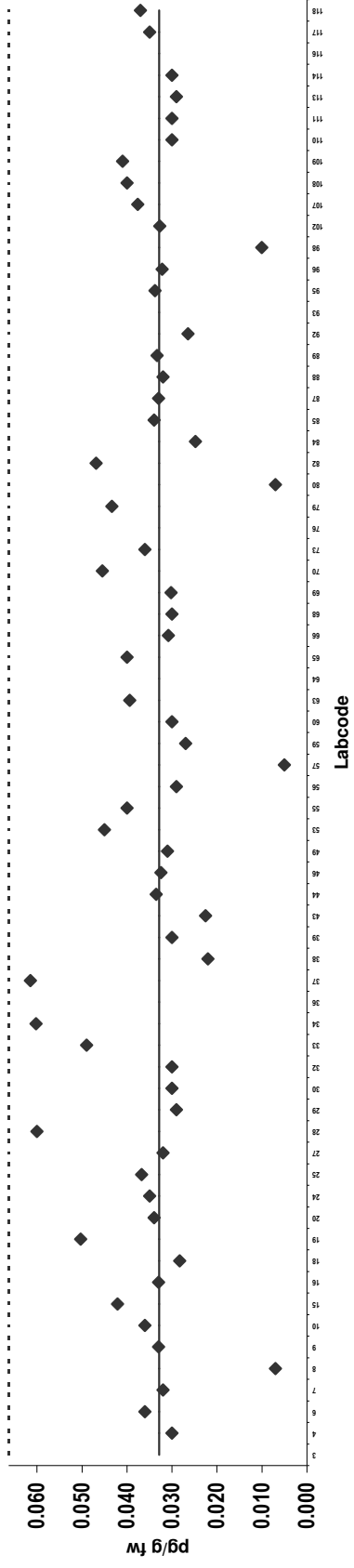
Congener: 1,2,3,4,6,7,8 HpCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.15		80	0.0070	ND
4	0.030	Outlier	82	0.047	
6	0.036		84	0.025	
7	0.032		85	0.034	
8	0.0070	ND	87	0.033	
9	0.033		88	0.032	
10	0.036		89	0.033	
15	0.042		92	0.026	
16	0.033		93	0.14	Outlier
18	0.028		95	0.034	
19	0.050		96	0.032	
20	0.034		98	0.010	
24	0.035		102	0.033	
25	0.037		107	0.038	
27	0.032		108	0.040	
28	0.060		109	0.041	
29	0.029		110	0.030	
30	0.030		111	0.030	
32	0.030		113	0.029	
33	0.049		114	0.030	
34	0.060	ND	116	0.91	Outlier
36	0.089	Outlier	117	0.035	
37	0.062	ND	118	0.037	
38	0.022				
39	0.030				
43	0.023				
44	0.033				
46	0.032				
49	0.031				
53	0.045				
55	0.040				
56	0.029				
57	0.0050				
59	0.027	ND			
60	0.030				
63	0.039				
64	1.8	Outlier			
65	0.040				
66	0.031				
68	0.030				
69	0.030				
70	0.046				
73	0.036				
76	0.080	Outlier,ND			
79	0.043				

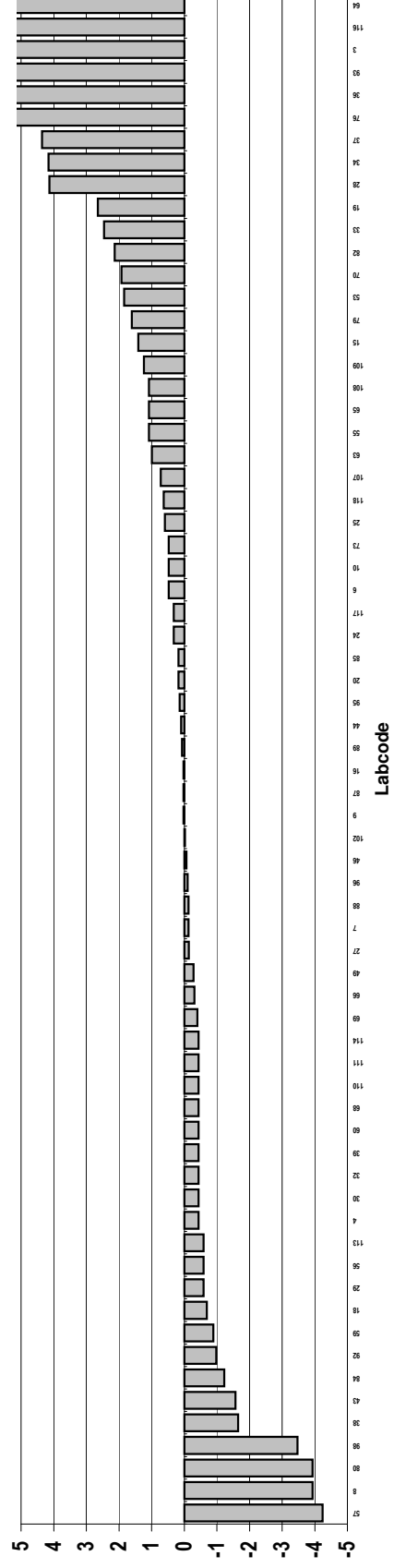
Consensus statistics

Consensus median, pg/g	0.033
Median all values pg/g	0.033
Consensus mean, pg/g	0.034
Standard deviation, pg/g	0.011
Relative standard deviation, %	32
No. of values reported	68
No. of values removed	6
No. of reported non-detects	6

1,2,3,4,6,7,8 HpCDF



Z-score: 1,2,3,4,6,7,8 HpCDF



Breast milk

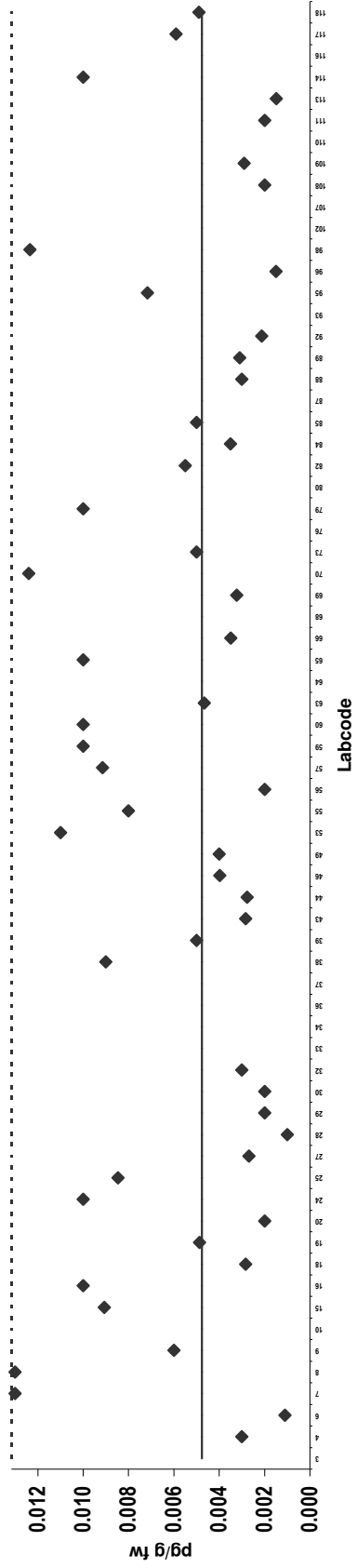
Congener: 1,2,3,4,7,8,9 HpCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.030	Outlier	80	0.016	Outlier
4	0.0030	ND	82	0.0055	
6	0.0011	ND	84	0.0035	
7	0.013	ND	85	0.0050	ND
8	0.013	ND	87	0.020	Outlier,ND
9	0.0060	ND	88	0.0030	ND
10	0.030	Outlier	89	0.0031	
15	0.0091		92	0.0021	
16	0.010	ND	93	0.29	Outlier
18	0.0028		95	0.0072	
19	0.0049	ND	96	0.0015	
20	0.0020		98	0.012	
24	0.010	ND	102	0.042	Outlier,ND
25	0.0085		107	0.018	Outlier,ND
27	0.0027		108	0.0020	ND
28	0.0010	ND	109	0.0029	ND
29	0.0020	ND	110	0.020	Outlier,ND
30	0.0020	ND	111	0.0020	
32	0.0030	ND	113	0.0015	ND
33	0.039	Outlier	114	0.010	
34	0.016	Outlier,ND	116	0.050	Outlier
36	0.024	Outlier	117	0.0059	
37	0.093	Outlier,ND	118	0.0049	
38	0.0090				
39	0.0050	ND			
43	0.0028	ND			
44	0.0028				
46	0.0040				
49	0.0040				
53	0.011				
55	0.0080	ND			
56	0.0020				
57	0.0092				
59	0.010	ND			
60	0.010	ND			
63	0.0047				
64	0.73	Outlier			
65	0.010	ND			
66	0.0035	ND			
68	0.020	Outlier,ND			
69	0.0032	ND			
70	0.012				
73	0.0050				
76	0.031	Outlier,ND			
79	0.010	ND			

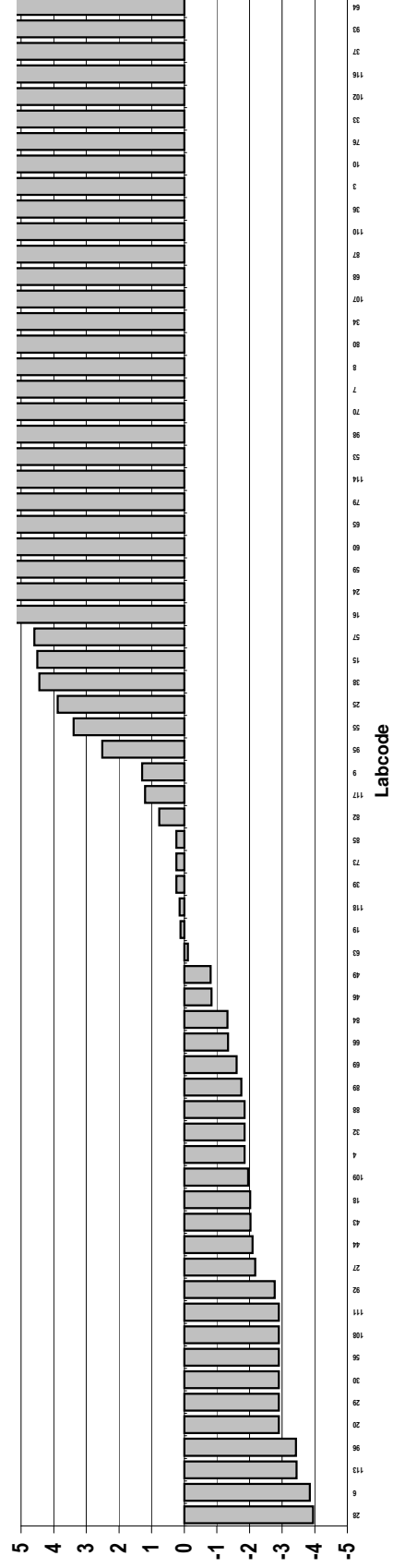
Consensus statistics

Consensus median, pg/g	0.0048
Median all values pg/g	0.0066
Consensus mean, pg/g	0.0056
Standard deviation, pg/g	0.0036
Relative standard deviation, %	64
No. of values reported	68
No. of values removed	16
No. of reported non-detects	34

1,2,3,4,7,8,9 HpCDF



Z-score: 1,2,3,4,7,8,9 HpCDF

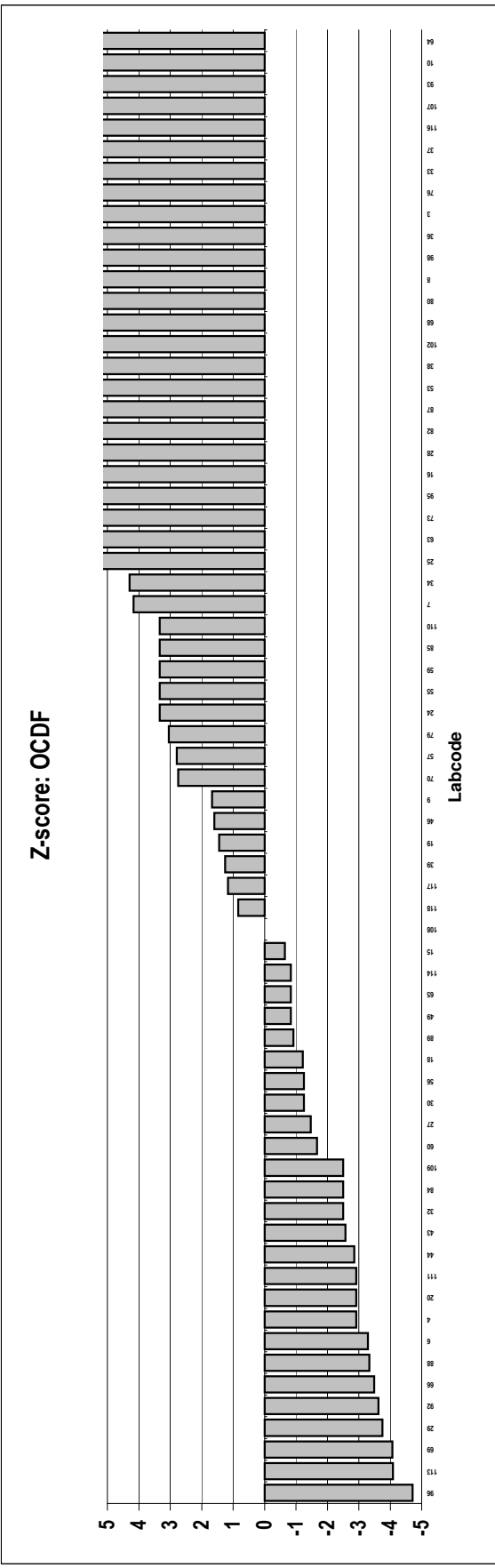
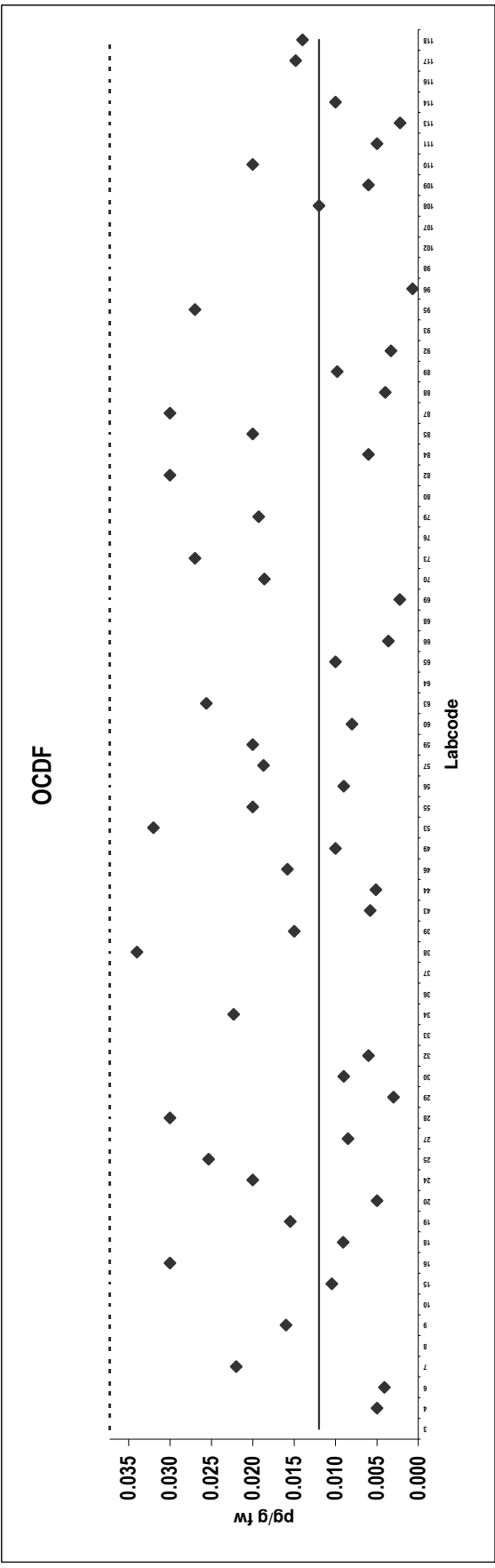


Breast milk
Congener: OCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.090	Outlier	80	0.050	Outlier,ND
4	0.0050	ND	82	0.030	
6	0.0041		84	0.0060	
7	0.022	ND	85	0.020	ND
8	0.057	Outlier,ND	87	0.030	ND
9	0.016	ND	88	0.0040	
10	0.43	Outlier	89	0.0098	
15	0.010	ND	92	0.0033	
16	0.030	ND	93	0.31	Outlier
18	0.0091		95	0.027	
19	0.015		96	0.00070	ND
20	0.0050		98	0.076	Outlier
24	0.020	ND	102	0.049	Outlier
25	0.025		107	0.25	Outlier,ND
27	0.0085		108	0.012	
28	0.030		109	0.0060	
29	0.0030		110	0.020	ND
30	0.0090		111	0.0050	
32	0.0060	ND	113	0.0022	ND
33	0.14	Outlier	114	0.010	ND
34	0.022	ND	116	0.25	Outlier
36	0.088	Outlier	117	0.015	
37	0.24	Outlier,ND	118	0.014	
38	0.034				
39	0.015	ND			
43	0.0058	ND			
44	0.0051				
46	0.016				
49	0.010				
53	0.032				
55	0.020				
56	0.0090				
57	0.019				
59	0.020	ND			
60	0.0080				
63	0.026				
64	1.2	Outlier			
65	0.010	ND			
66	0.0036	ND			
68	0.050	Outlier,ND			
69	0.0022	ND			
70	0.019				
73	0.027				
76	0.11	Outlier,ND			
79	0.019				

Consensus statistics

Consensus median, pg/g	0.012
Median all values pg/g	0.019
Consensus mean, pg/g	0.014
Standard deviation, pg/g	0.0093
Relative standard deviation, %	66
No. of values reported	68
No. of values removed	15
No. of reported non-detects	26



Breast milk

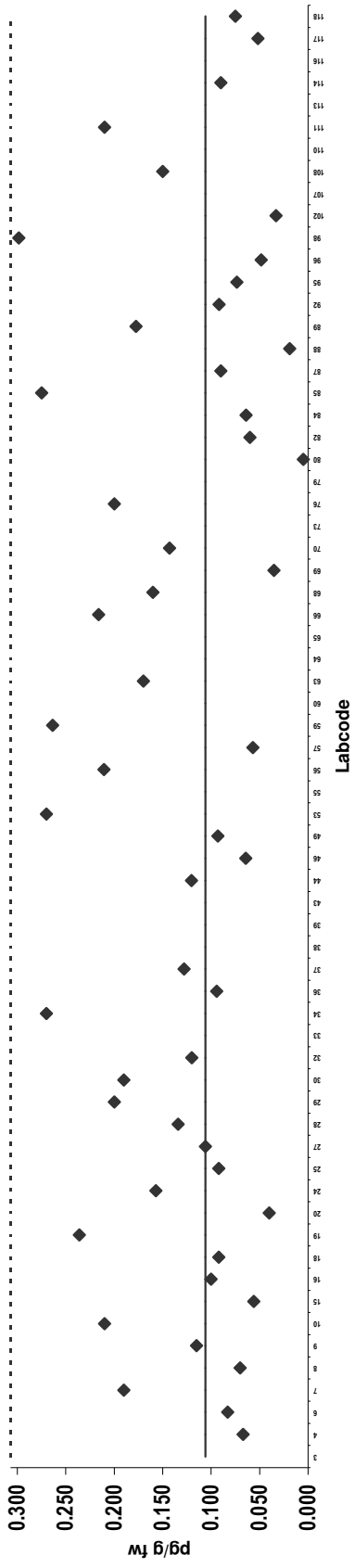
Congener: PCB 77

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.47	Outlier	80	0.0050	ND
4	0.067		82	0.060	
6	0.083		84	0.064	
7	0.19		85	0.28	
8	0.070		87	0.090	
9	0.12		88	0.019	
10	0.21		89	0.18	
15	0.056		92	0.092	
16	0.10	ND	95	0.073	
18	0.092		96	0.048	
19	0.24		98	0.30	
20	0.040		102	0.033	
24	0.16		107	3.9	Outlier,ND
25	0.092		108	0.15	
27	0.11		110	0.52	Outlier
28	0.13		111	0.21	
29	0.20		113	1.1	Outlier
30	0.19	ND	114	0.090	ND
32	0.12		116	2.3	Outlier
33	0.47	Outlier	117	0.052	
34	0.27	ND	118	0.075	
36	0.094				
37	0.13				
38	0.39	Outlier			
39	0.52	Outlier			
43	0.47	Outlier			
44	0.12				
46	0.064				
49	0.093				
53	0.27				
55	0.65	Outlier			
56	0.21				
57	0.057				
59	0.26				
60	0.31	Outlier			
63	0.17				
64	0.86	Outlier			
65	0.46	Outlier			
66	0.22				
68	0.16				
69	0.035				
70	0.14				
73	0.51	Outlier			
76	0.20	ND			
79	58	Outlier			

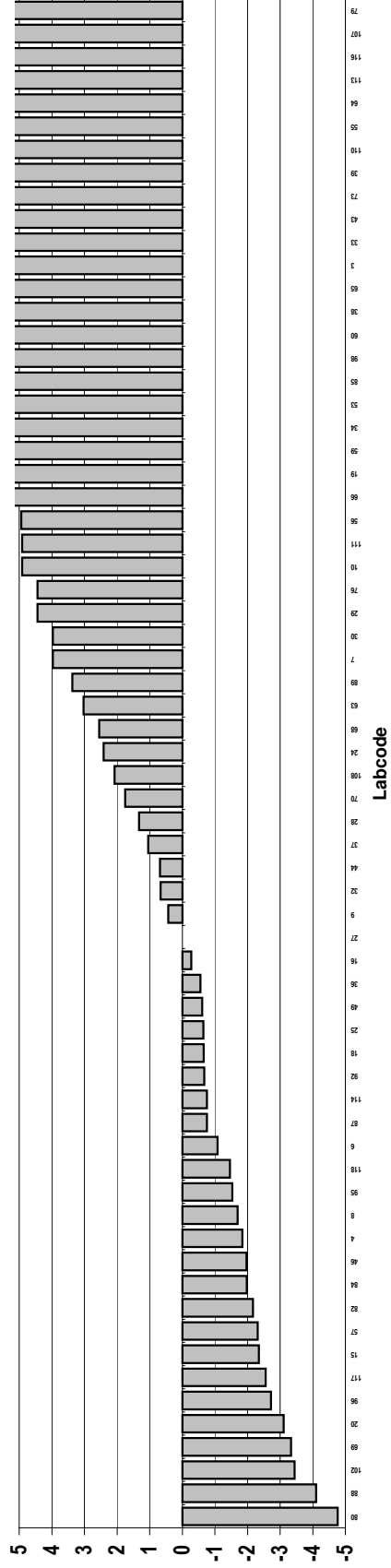
Consensus statistics

Consensus median, pg/g	0.11
Median all values pg/g	0.15
Consensus mean, pg/g	0.13
Standard deviation, pg/g	0.076
Relative standard deviation, %	59
No. of values reported	66
No. of values removed	15
No. of reported non-detects	7

PCB 77



Z-score: PCB 77



Breast milk

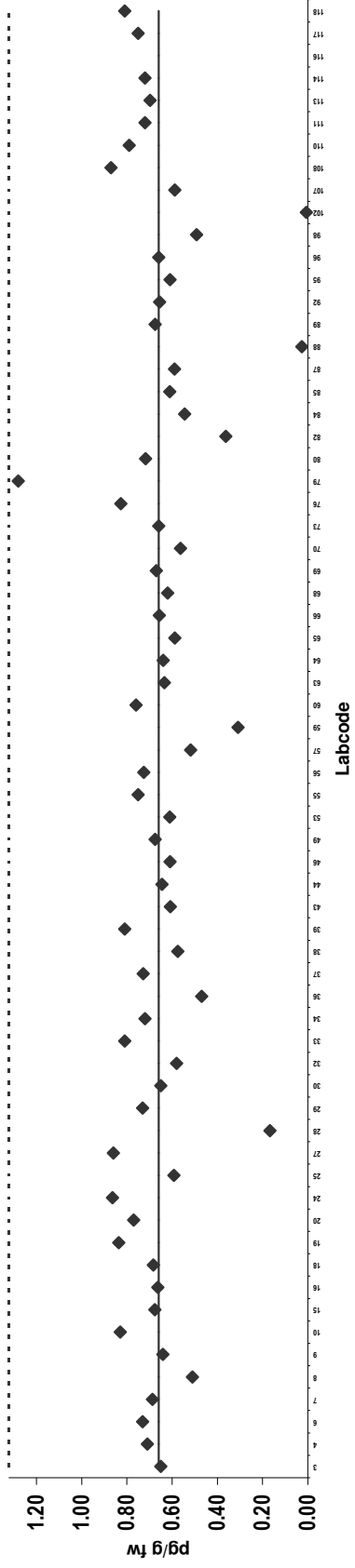
Congener: PCB 126

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.65		80	0.72	
4	0.71		82	0.36	
6	0.73		84	0.54	
7	0.69		85	0.61	
8	0.51		87	0.59	
9	0.64		88	0.026	
10	0.83		89	0.68	
15	0.68		92	0.66	
16	0.66		95	0.61	
18	0.68		96	0.66	
19	0.84		98	0.49	
20	0.77		102	0.0060	
24	0.86		107	0.59	
25	0.59		108	0.87	
27	0.86		110	0.79	
28	0.17		111	0.72	
29	0.73	ND	113	0.70	
30	0.65		114	0.72	
32	0.58		116	24	Outlier
33	0.81		117	0.75	
34	0.72		118	0.81	
36	0.47				
37	0.73				
38	0.58				
39	0.81				
43	0.61				
44	0.64				
46	0.61				
49	0.68				
53	0.61				
55	0.75				
56	0.73				
57	0.52				
59	0.31				
60	0.76				
63	0.63				
64	0.64				
65	0.59				
66	0.66				
68	0.62				
69	0.67				
70	0.56				
73	0.66				
76	0.83				
79	1.3				

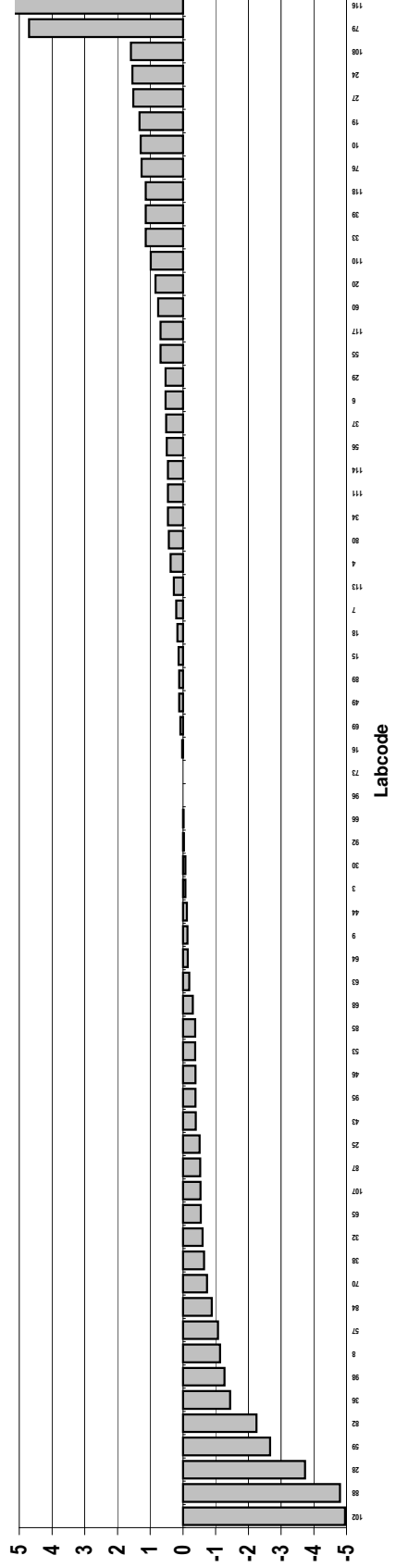
Consensus statistics

Consensus median, pg/g	0.66
Median all values pg/g	0.66
Consensus mean, pg/g	0.65
Standard deviation, pg/g	0.19
Relative standard deviation, %	29
No. of values reported	66
No. of values removed	1
No. of reported non-detects	1

PCB 126



Z-score: PCB 126



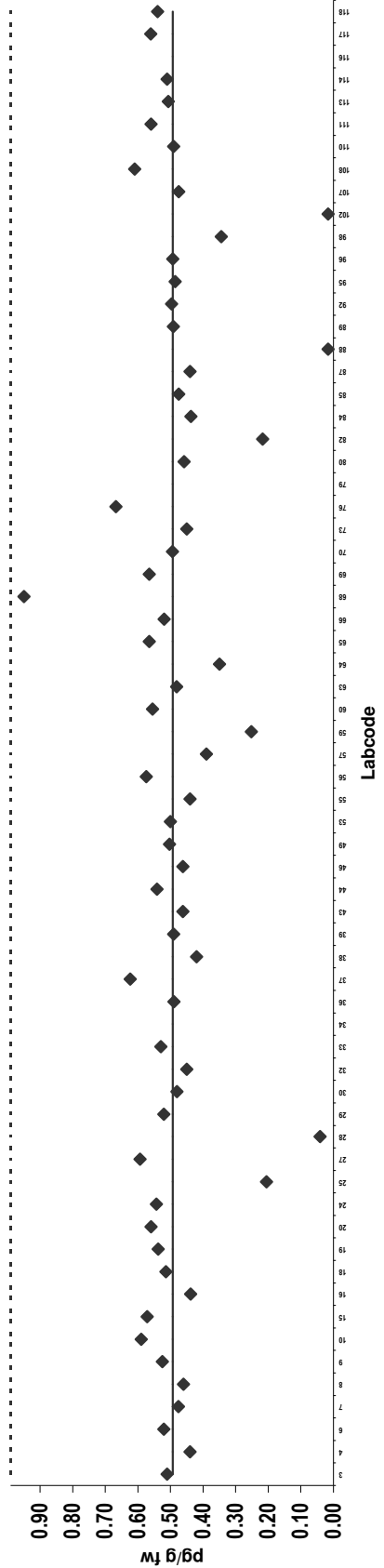
Breast milk
Congener: PCB 169

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.51		80	0.46	
4	0.44		82	0.22	
6	0.52		84	0.44	
7	0.48		85	0.48	
8	0.46		87	0.44	
9	0.53		88	0.016	
10	0.59		89	0.49	
15	0.57		92	0.50	
16	0.44		95	0.49	
18	0.51		96	0.49	
19	0.54		98	0.34	
20	0.56		102	0.016	
24	0.54		107	0.47	
25	0.21		108	0.61	
27	0.59		110	0.49	
28	0.041		111	0.56	
29	0.52	ND	113	0.51	
30	0.48		114	0.51	
32	0.45		116	17	Outlier
33	0.53		117	0.56	
34	2.1	Outlier,ND	118	0.54	
36	0.49				
37	0.62				
38	0.42				
39	0.49				
43	0.46				
44	0.54				
46	0.46				
49	0.50				
53	0.50				
55	0.44				
56	0.57				
57	0.39				
59	0.25				
60	0.56				
63	0.48				
64	0.35				
65	0.57				
66	0.52				
68	0.95				
69	0.56				
70	0.49				
73	0.45				
76	0.67				
79	4.5	Outlier			

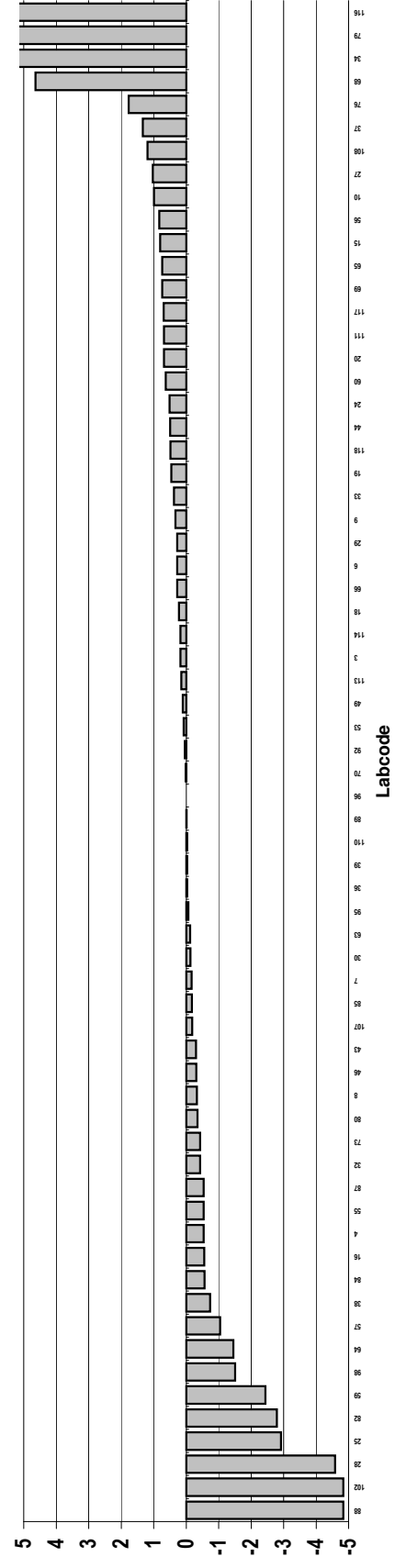
Consensus statistics

Consensus median, pg/g	0.49
Median all values pg/g	0.50
Consensus mean, pg/g	0.47
Standard deviation, pg/g	0.14
Relative standard deviation, %	30
No. of values reported	66
No. of values removed	3
No. of reported non-detects	2

PCB 169



Z-score: PCB 169



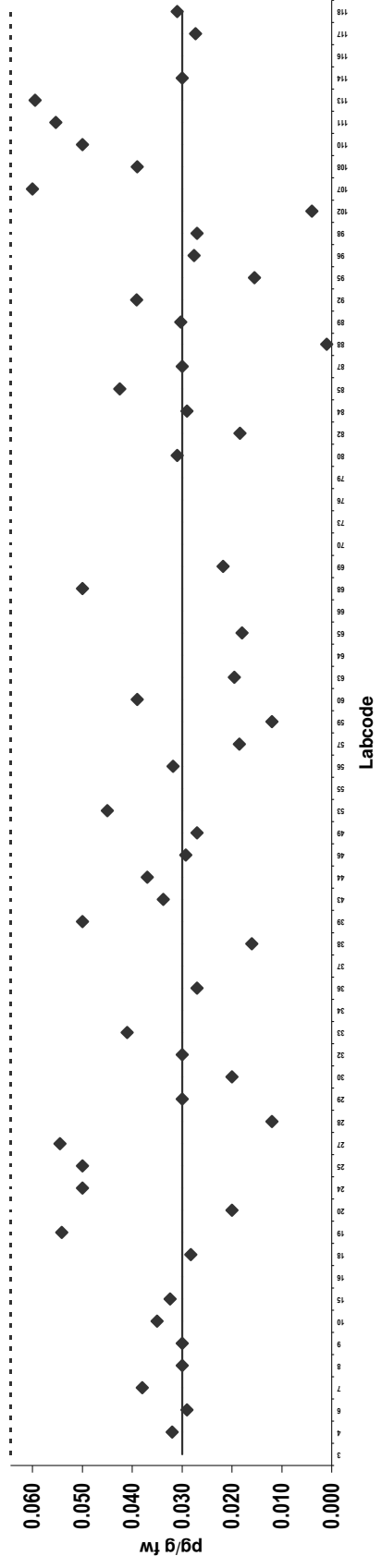
Breast milk
Congener: PCB 81

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.13		80	0.031	
4	0.032	Outlier	82	0.018	
6	0.029		84	0.029	
7	0.038		85	0.043	
8	0.030		87	0.030	
9	0.030		88	0.0010	
10	0.035		89	0.030	
15	0.032		92	0.039	
16	0.10	Outlier,ND	95	0.015	
18	0.028		96	0.028	
19	0.054		98	0.027	
20	0.020		102	0.0040	
24	0.050	ND	107	0.060	
25	0.050	ND	108	0.039	
27	0.055		110	0.050	
28	0.012	ND	111	0.055	
29	0.030		113	0.059	
30	0.020	ND	114	0.030	
32	0.030		116	0.72	Outlier
33	0.041		117	0.027	
34	0.27	Outlier,ND	118	0.031	
36	0.027				
37	0.076	Outlier,ND			
38	0.016				
39	0.050				
43	0.034				
44	0.037				
46	0.029				
49	0.027				
53	0.045				
55	0.10	Outlier			
56	0.032				
57	0.019				
59	0.012				
60	0.039				
63	0.020	ND			
64	0.070	Outlier			
65	0.018				
66	0.074	Outlier,ND			
68	0.050	ND			
69	0.022				
70	0.11	Outlier			
73	0.12	Outlier			
76	0.080	Outlier,ND			
79	2.9	Outlier			

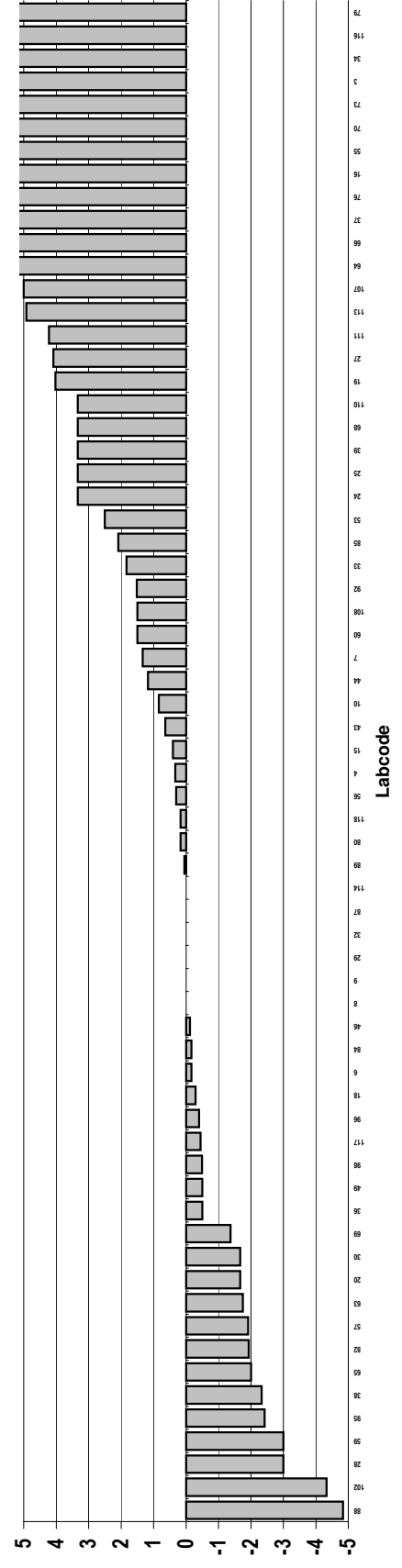
Consensus statistics

Consensus median, pg/g	0.030
Median all values pg/g	0.032
Consensus mean, pg/g	0.032
Standard deviation, pg/g	0.013
Relative standard deviation, %	42
No. of values reported	66
No. of values removed	12
No. of reported non-detects	11

PCB 81



Z-score: PCB 81



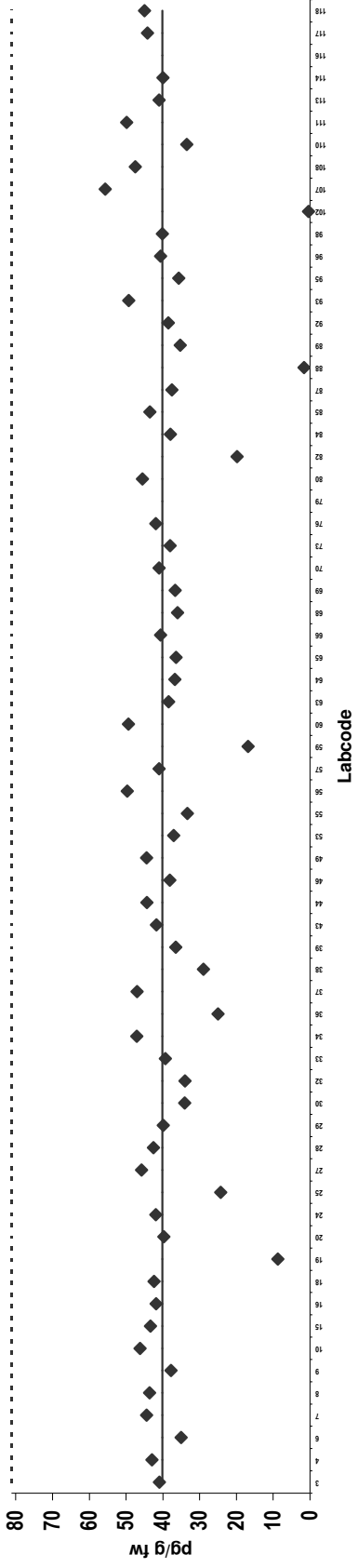
Breast milk

Congener: PCB 105

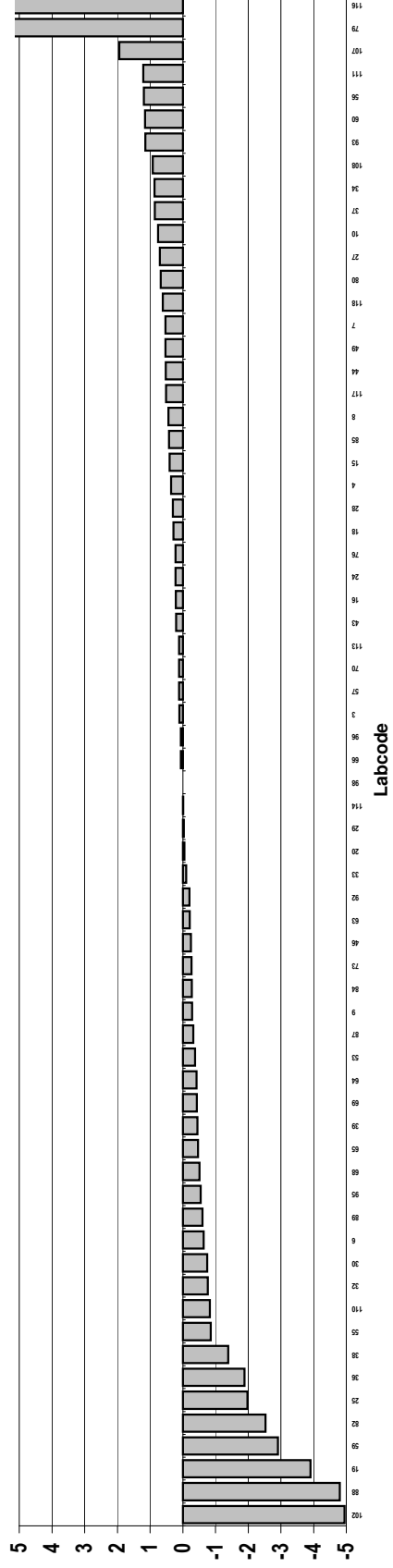
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	41		80	46	
4	43		82	20	
6	35		84	38	
7	44		85	44	
8	44		87	38	
9	38		88	1.6	
10	46		89	35	
15	43		92	39	
16	42		93	49	
18	42		95	36	
19	8.8		96	41	
20	40		98	40	
24	42		102	0.42	
25	24		107	56	
27	46		108	48	
28	43		110	34	
29	40		111	50	
30	34		113	41	
32	34		114	40	
33	39		116	2713	Outlier
34	47		117	44	
36	25		118	45	
37	47				
38	29				
39	37				
43	42				
44	44				
46	38				
49	44				
53	37				
55	33				
56	50				
57	41				
59	17				
60	49				
63	38				
64	37				
65	36				
66	41				
68	36				
69	37				
70	41				
73	38				
76	42				
79	227	Outlier			

Consensus statistics	
Consensus median, pg/g	40
Median all values pg/g	41
Consensus mean, pg/g	38
Standard deviation, pg/g	10
Relative standard deviation, %	27
No. of values reported	67
No. of values removed	2
No. of reported non-detects	0

PCB 105



Z-score: PCB 105



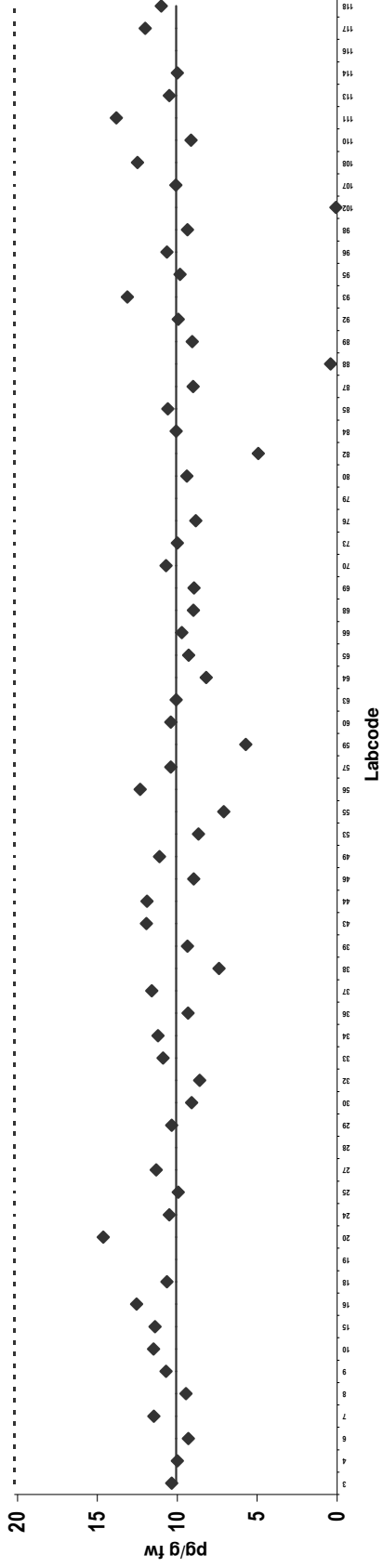
Breast milk
Congener: PCB 114

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	10		80	9.4	
4	10		82	4.9	
6	9.3		84	10	
7	11		85	11	
8	9.5		87	9.0	
9	11		88	0.42	
10	11		89	9.1	
15	11		92	9.9	
16	13		93	13	
18	11		95	9.8	
19	193		96	11	
20	15		98	9.4	
24	11		102	0.072	
25	9.9		107	10	
27	11		108	13	
28	23		110	9.2	
29	10	Outlier	111	14	
30	9.1		113	11	
32	8.6		114	10	
33	11		116	797	Outlier
34	11		117	12	
36	9.3		118	11	
37	12				
38	7.4				
39	9.4				
43	12				
44	12				
46	9.0				
49	11				
53	8.7				
55	7.1				
56	12				
57	10				
59	5.7				
60	10				
63	10				
64	8.2				
65	9.3				
66	9.7				
68	9.0				
69	9.0				
70	11				
73	10				
76	8.8				
79	26	Outlier			

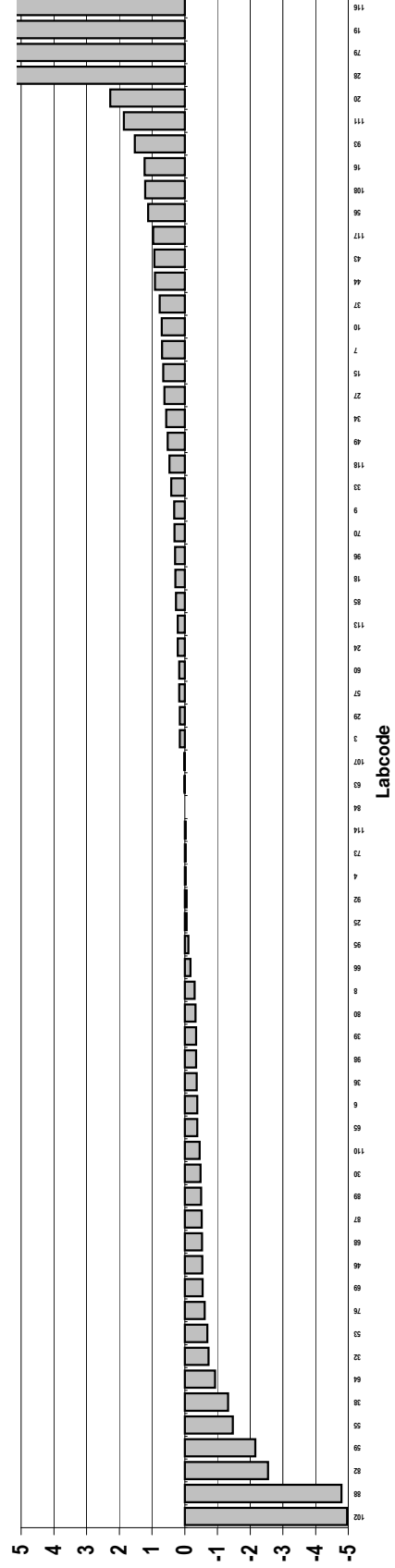
Consensus statistics

Consensus median, pg/g	10
Median all values pg/g	10
Consensus mean, pg/g	10
Standard deviation, pg/g	2.4
Relative standard deviation, %	24
No. of values reported	67
No. of values removed	4
No. of reported non-detects	0

PCB 114



Z-score: PCB 114



Breast milk

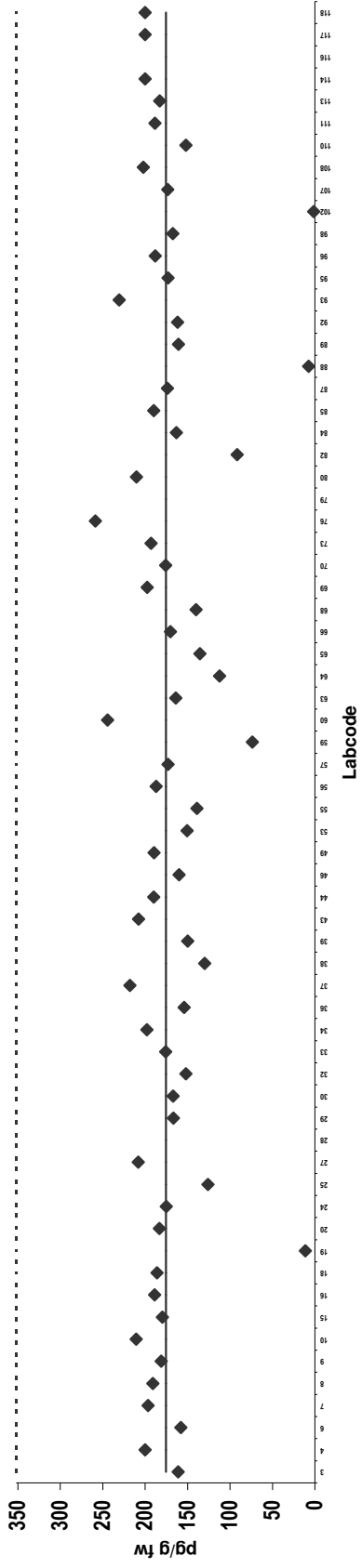
Congener: PCB 118

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	161		80	210	
4	200		82	92	
6	158		84	163	
7	197		85	190	
8	191		87	174	
9	181		88	7.3	
10	211		89	161	
15	180		92	162	
16	189		93	231	
18	186		95	173	
19	11		96	188	
20	183		98	167	
24	175		102	1.3	
25	126		107	173	
27	208		108	202	
28	435		110	152	
29	167		111	189	
30	167		113	183	
32	152		114	200	
33	176		116	8829	
34	198		117	200	
36	154		118	200	
37	218				
38	130				
39	150				
43	208				
44	190				
46	160				
49	189				
53	151				
55	139				
56	187				
57	173				
59	74				
60	244				
63	164				
64	112				
65	135				
66	170				
68	140				
69	197				
70	176				
73	193				
76	259				
79	858	Outlier			Outlier

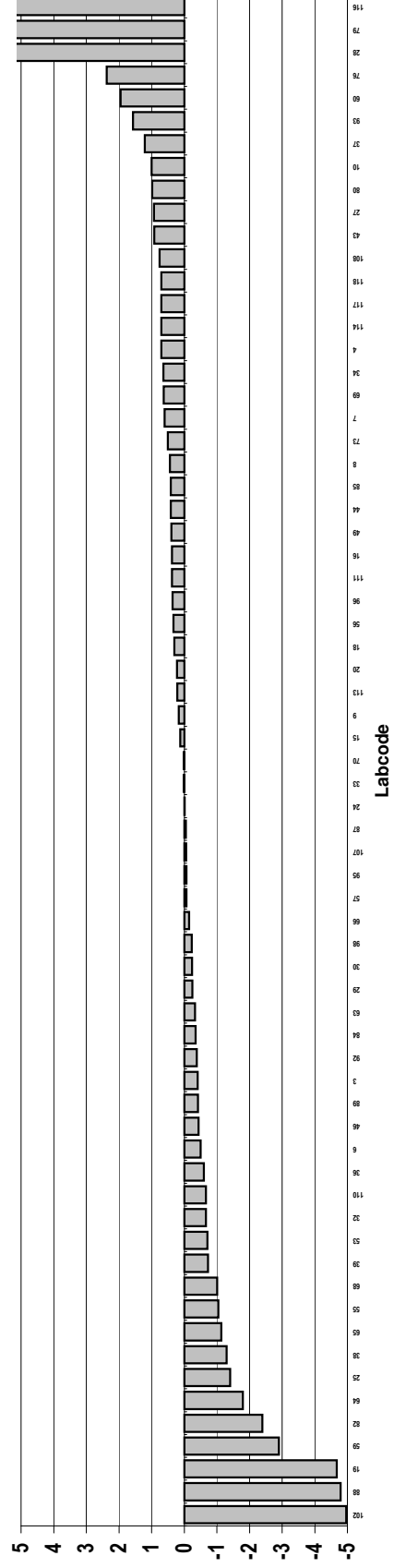
Consensus statistics

Consensus median, pg/g	176
Median all values pg/g	176
Consensus mean, pg/g	168
Standard deviation, pg/g	48
Relative standard deviation, %	28
No. of values reported	67
No. of values removed	3
No. of reported non-detects	0

PCB 118



Z-score: PCB 118



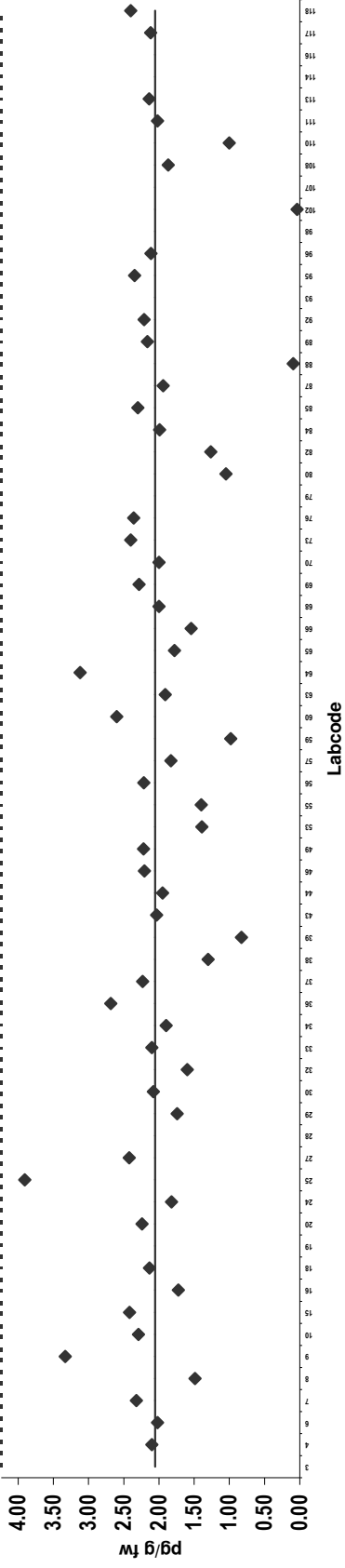
Breast milk
Congener: PCB 123

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	6.3		80	1.1	
4	2.1	Outlier	82	1.3	
6	2.0		84	2.0	
7	2.3		85	2.3	
8	1.5		87	1.9	
9	3.3		88	0.094	
10	2.3		89	2.2	
15	2.4		92	2.2	
16	1.7		93	10	Outlier
18	2.1		95	2.3	
19	4.4		96	2.1	
20	2.2		98	185	Outlier
24	1.8		102	0.037	
25	3.9		107	5.1	Outlier
27	2.4		108	1.9	
28	4.3		110	1.0	
29	1.7		111	2.0	
30	2.1		113	2.1	
32	1.6		114	10	Outlier
33	2.1		116	268	Outlier
34	1.9		117	2.1	
36	2.7		118	2.4	
37	2.2				
38	1.3				
39	0.83				
43	2.0				
44	2.0				
46	2.2				
49	2.2				
53	1.4				
55	1.4				
56	2.2				
57	1.8				
59	0.98				
60	2.6				
63	1.9				
64	3.1				
65	1.8				
66	1.5				
68	2.0				
69	2.3				
70	2.0				
73	2.4				
76	2.4				
79	7.0	Outlier			

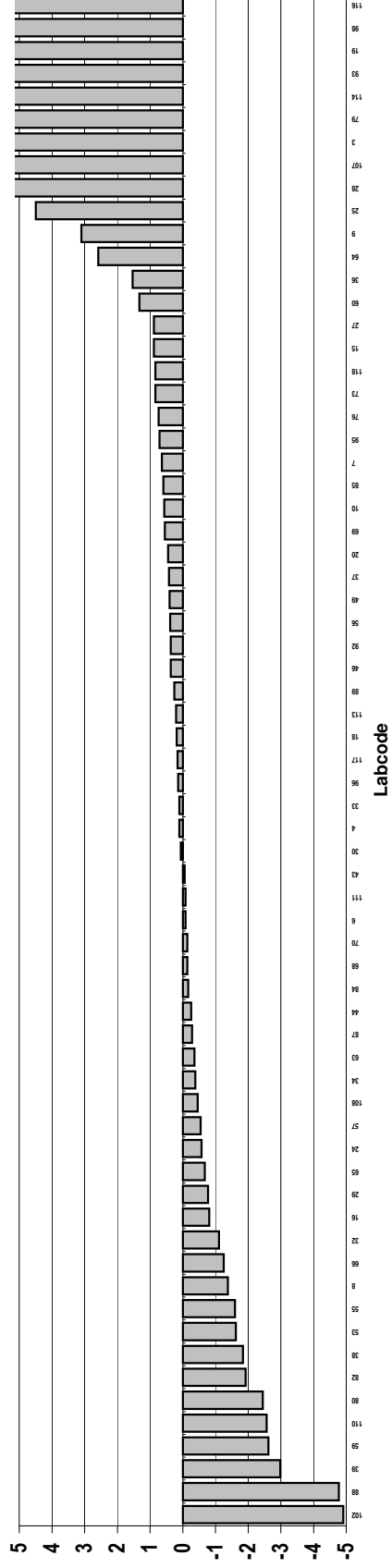
Consensus statistics

Consensus median, pg/g	2.1
Median all values pg/g	2.1
Consensus mean, pg/g	2.0
Standard deviation, pg/g	0.64
Relative standard deviation, %	33
No. of values reported	67
No. of values removed	9
No. of reported non-detects	1

PCB 123



Z-score: PCB 123



Breast milk

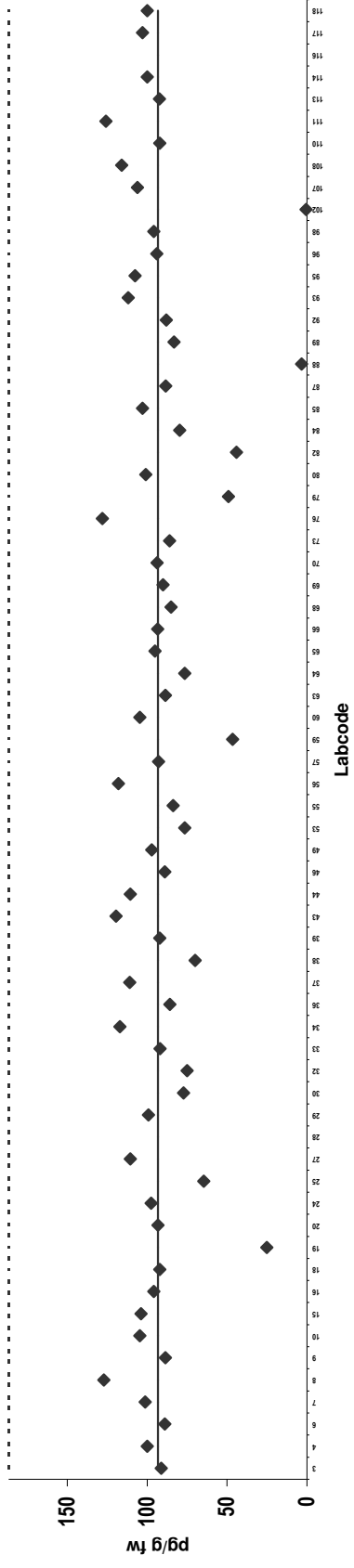
Congener: PCB 156

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	91		80	101	
4	100		82	44	
6	89		84	80	
7	101		85	103	
8	127		87	88	
9	89		88	3.3	
10	105		89	83	
15	104		92	88	
16	96		93	112	
18	92		95	108	
19	25		96	94	
20	93		98	96	
24	98		102	0.47	
25	65		107	106	
27	111		108	116	
28	223		110	92	
29	99	Outlier	111	126	
30	77		113	92	
32	75		114	100	
33	92		116	4713	
34	117		117	103	Outlier
36	86		118	100	
37	111				
38	70				
39	92				
43	119				
44	111				
46	89				
49	97				
53	77				
55	84				
56	118				
57	93				
59	47				
60	105				
63	89				
64	76				
65	95				
66	93				
68	85				
69	90				
70	94				
73	86				
76	128				
79	49				

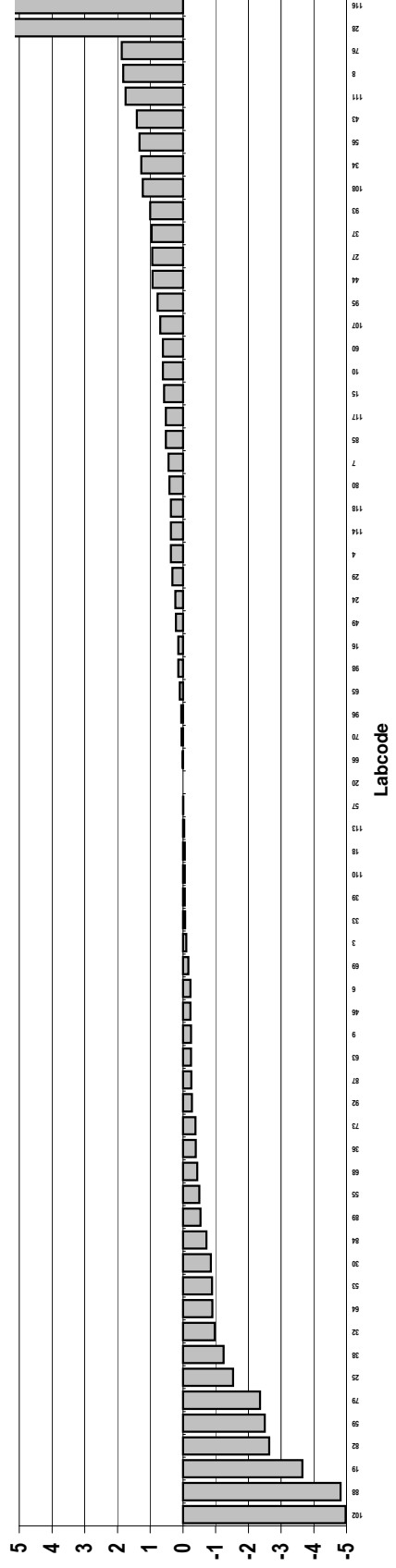
Consensus statistics

Consensus median, pg/g	93
Median all values pg/g	93
Consensus mean, pg/g	90
Standard deviation, pg/g	25
Relative standard deviation, %	27
No. of values reported	67
No. of values removed	2
No. of reported non-detects	0

PCB 156



Z-score: PCB 156



Breast milk

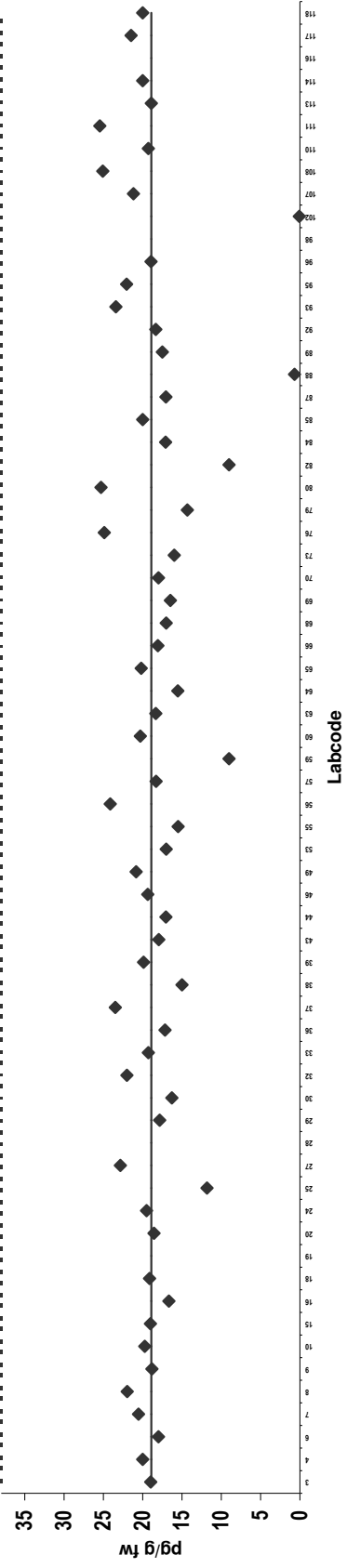
Congener: PCB 157

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	19		82	9.0	
4	20		84	17	
6	18		85	20	
7	21		87	17	
8	22		88	0.70	
9	19		89	17	
10	20		92	18	
15	19		93	23	
16	17		95	22	
18	19		96	19	
19	100		98	87	Outlier
20	19	Outlier	102	0.083	
24	20		107	21	
25	12		108	25	
27	23		110	19	
28	39		111	25	
29	18	Outlier	113	19	
30	16		114	20	
32	22		116	890	Outlier
33	19		117	22	
36	17		118	20	
37	24				
38	15				
39	20				
43	18				
44	17				
46	19				
49	21				
53	17				
55	16				
56	24				
57	18				
59	9.0				
60	20				
63	18				
64	16				
65	20				
66	18				
68	17				
69	16				
70	18				
73	16				
76	25				
79	14				
80	25				

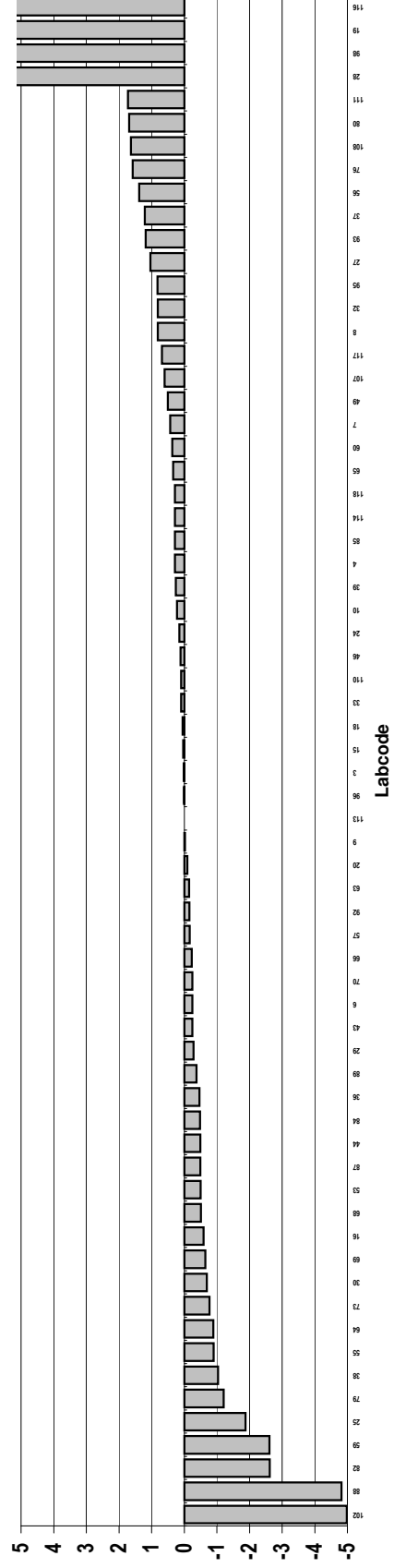
Consensus statistics

Consensus median, pg/g	19
Median all values pg/g	19
Consensus mean, pg/g	18
Standard deviation, pg/g	4.7
Relative standard deviation, %	25
No. of values reported	66
No. of values removed	4
No. of reported non-detects	0

PCB 157



Z-score: PCB 157



Breast milk

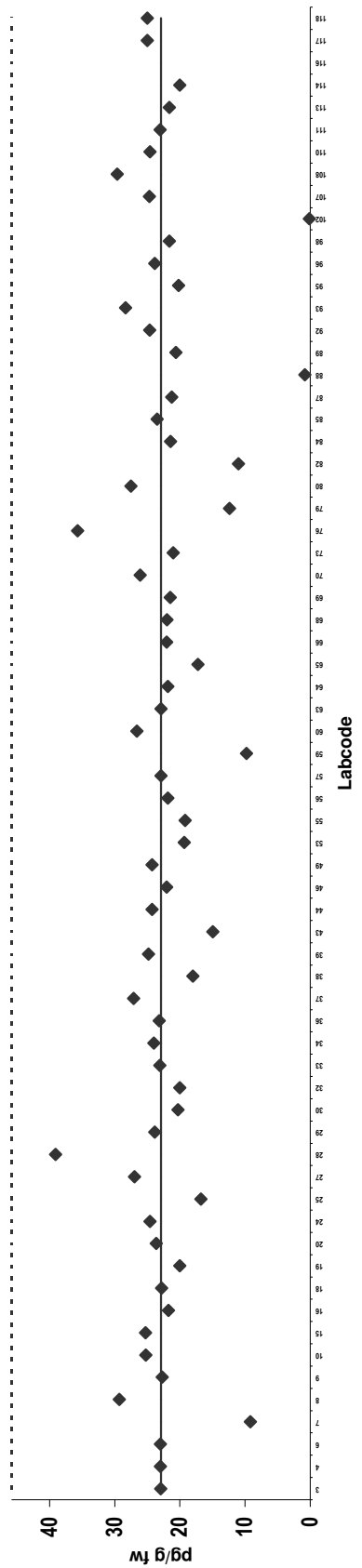
Congener: PCB 167

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	23		80	28	
4	23		82	11	
6	23		84	21	
7	9.2		85	24	
8	29		87	21	
9	23		88	0.84	
10	25		89	21	
15	25		92	25	
16	22		93	28	
18	23		95	20	
19	20		96	24	
20	24		98	22	
24	25		102	0.14	
25	17		107	25	
27	27		108	30	
28	39		110	25	
29	24		111	23	
30	20		113	22	
32	20		114	20	
33	23		116	1006	Outlier
34	24		117	25	
36	23		118	25	
37	27				
38	18				
39	25				
43	15				
44	24				
46	22				
49	24				
53	19				
55	19				
56	22				
57	23				
59	9.8				
60	27				
63	23				
64	22				
65	17				
66	22				
68	22				
69	21				
70	26				
73	21				
76	36				
79	12				

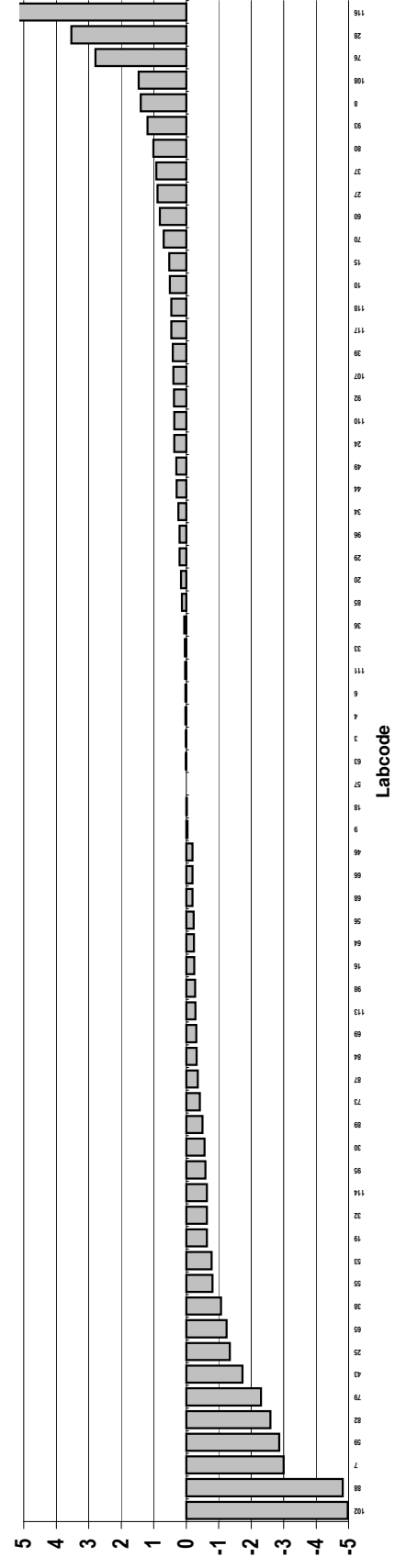
Consensus statistics

Consensus median, pg/g	23
Median all values pg/g	23
Consensus mean, pg/g	22
Standard deviation, pg/g	6.2
Relative standard deviation, %	28
No. of values reported	67
No. of values removed	1
No. of reported non-detects	0

PCB 167



Z-score: PCB 167



Breast milk

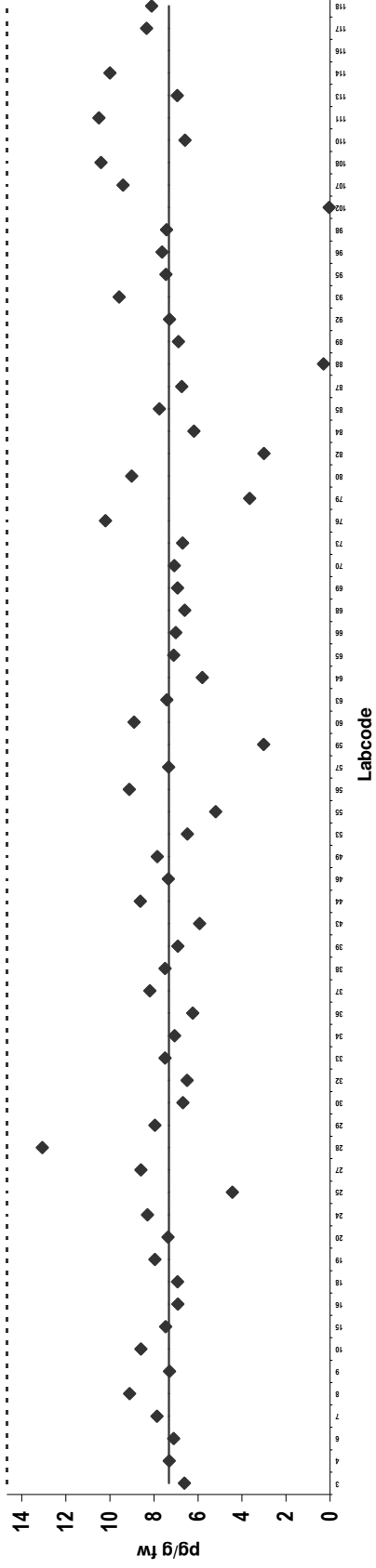
Congener: PCB 189

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	6.6		80	9.0	
4	7.3		82	3.0	
6	7.1		84	6.2	
7	7.9		85	7.8	
8	9.1		87	6.7	
9	7.3		88	0.29	
10	8.6		89	6.9	
15	7.5		92	7.3	
16	6.9		93	9.6	
18	6.9		95	7.5	
19	8.0		96	7.6	
20	7.4		98	7.4	
24	8.3		102	0.041	
25	4.4		107	9.4	
27	8.6		108	10	
28	13		110	6.6	
29	8.0		111	10	
30	6.7		113	6.9	
32	6.5		114	10	
33	7.5		116	301	Outlier
34	7.1		117	8.3	
36	6.2		118	8.1	
37	8.2				
38	7.5				
39	6.9				
43	5.9				
44	8.6				
46	7.3				
49	7.8				
53	6.5				
55	5.2				
56	9.1				
57	7.3				
59	3.0				
60	8.9				
63	7.4				
64	5.8				
65	7.1				
66	7.0				
68	6.6				
69	6.9				
70	7.1				
73	6.7				
76	10				
79	3.7				

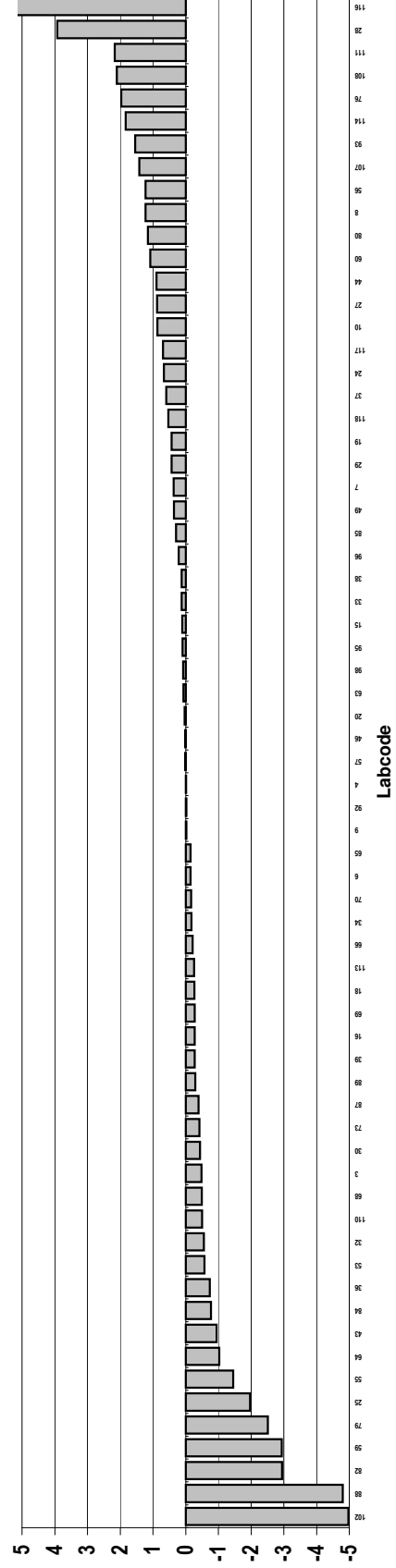
Consensus statistics

Consensus median, pg/g	7.3
Median all values pg/g	7.3
Consensus mean, pg/g	7.2
Standard deviation, pg/g	2.1
Relative standard deviation, %	29
No. of values reported	67
No. of values removed	1
No. of reported non-detects	0

PCB 189



Z-score: PCB 189



Breast milk

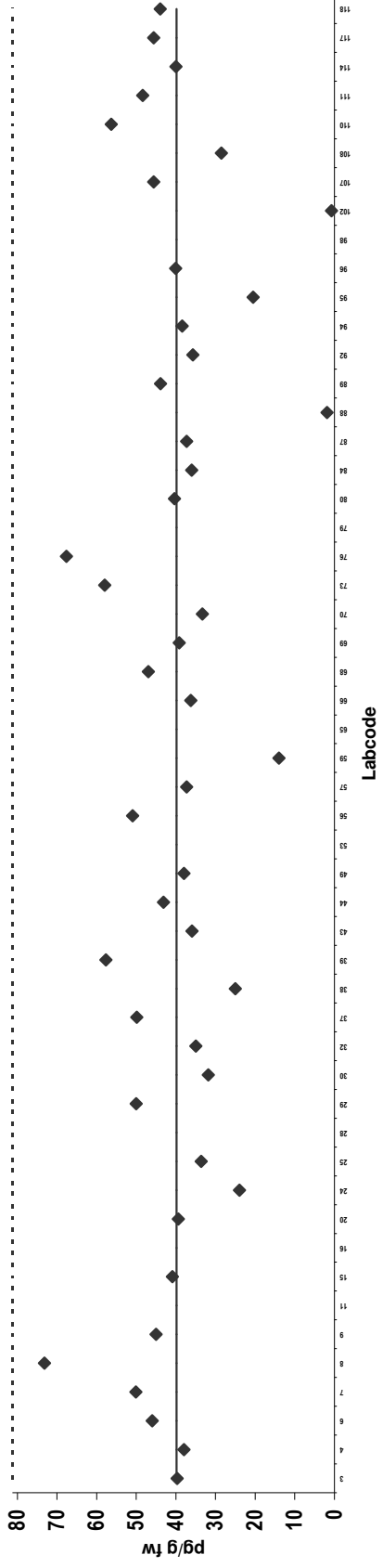
Congener: CB 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	40		107	46	
4	38		108	29	
6	46		110	56	
7	50		111	48	
8	73		114	40	
9	45		117	46	
11	179	Outlier	118	44	
15	41				
16	91	Outlier			
20	39				
24	24				
25	34				
28	108	Outlier			
29	50				
30	32				
32	35				
37	50				
38	25				
39	58				
43	36				
44	43				
49	38				
53	736	Outlier			
56	51				
57	37				
59	14	ND			
65	97	Outlier			
66	36				
68	47				
69	39				
70	33				
73	58				
76	68				
79	673	Outlier			
80	40				
84	36				
87	37				
88	1.8				
89	44				
92	36				
94	38				
95	21				
96	40	Outlier			
98	95				
102	0.71				

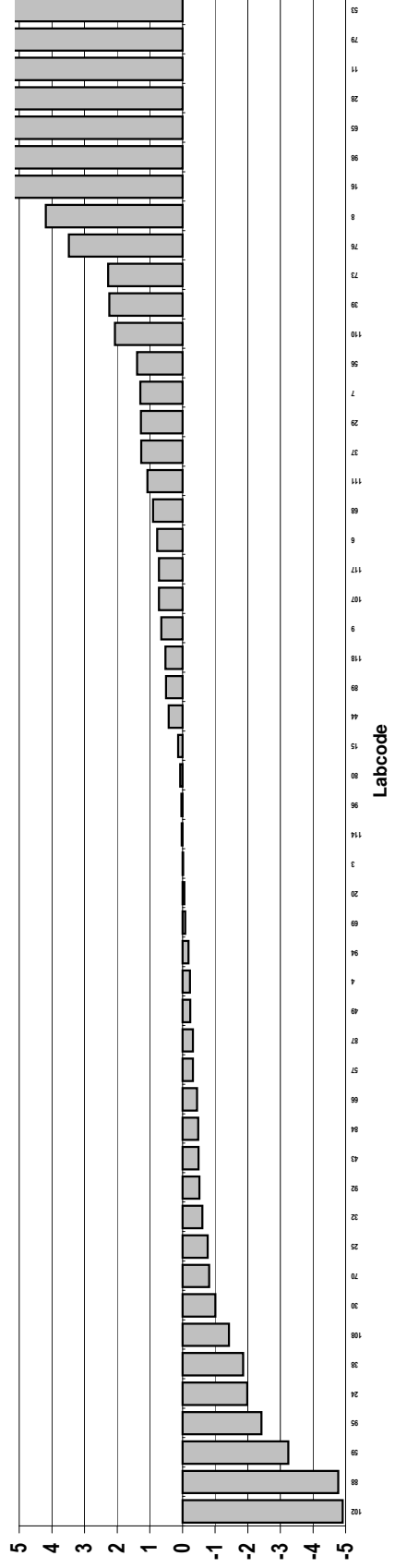
Consensus statistics

Consensus median, pg/g	40
Median all values pg/g	41
Consensus mean, pg/g	40
Standard deviation, pg/g	14
Relative standard deviation, %	35
No. of values reported	52
No. of values removed	7
No. of reported non-detects	1

CB 28



Z-score: CB 28



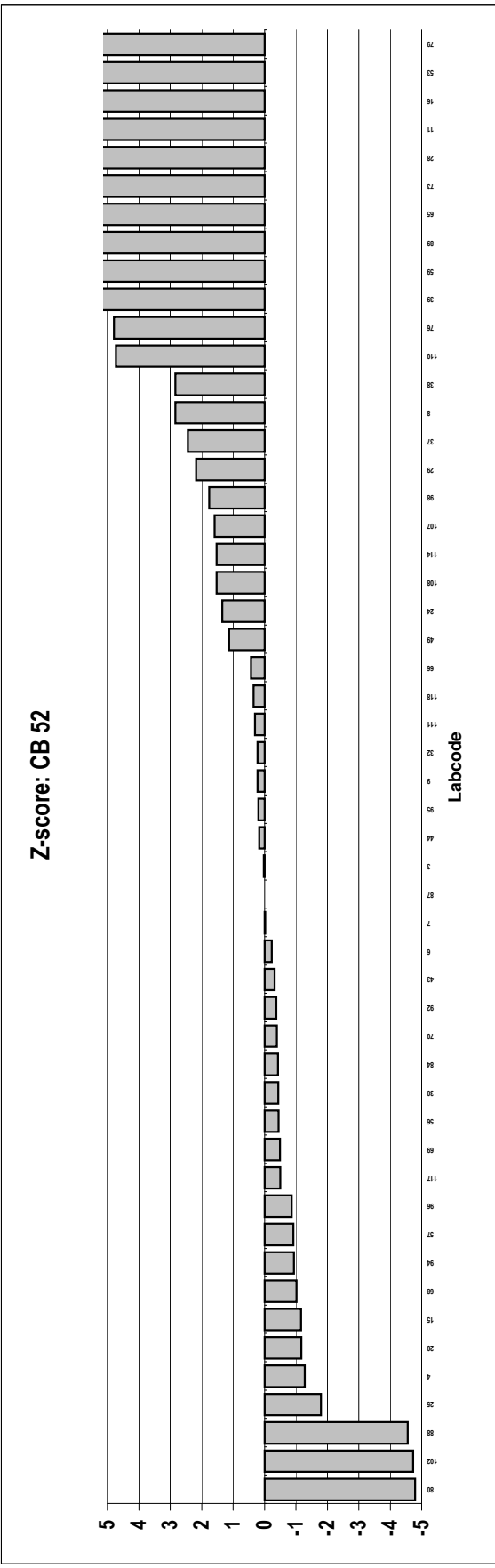
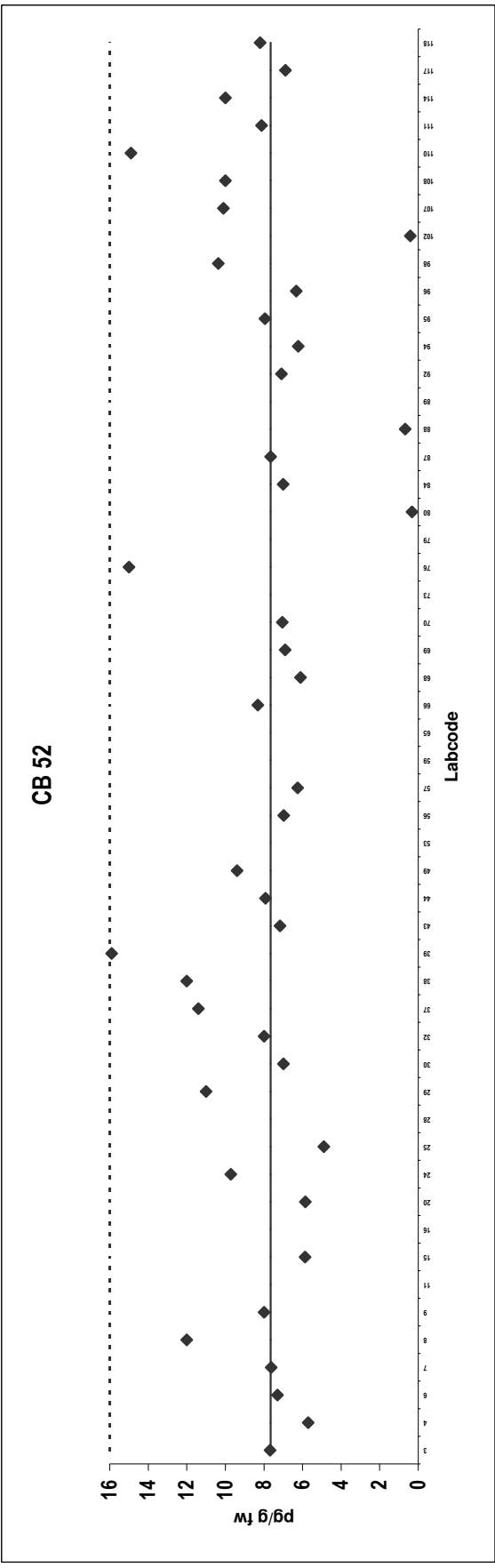
Breast milk

Congener: CB 52

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	7.7		107	10	
4	5.7		108	10	
6	7.3		110	15	
7	7.6		111	8.1	
8	12		114	10	
9	8.0		117	6.9	
11	7.3	Outlier,ND	118	8.2	
15	5.9				
16	210	Outlier			
20	5.9				
24	9.7				
25	4.9				
28	70	Outlier,ND			
29	11				
30	7.0				
32	8.0				
37	11				
38	12				
39	16				
43	7.2				
44	7.9				
49	9.4				
53	235	Outlier			
56	7.0				
57	6.3				
59	18	Outlier			
65	47	Outlier			
66	8.3				
68	6.1				
69	6.9				
70	7.1				
73	50	Outlier			
76	15	ND			
79	1000	Outlier			
80	0.32	ND			
84	7.0				
87	7.7				
88	0.68				
89	41	Outlier			
92	7.1				
94	6.2				
95	8.0				
96	6.3				
98	10				
102	0.41				

Consensus statistics

Consensus median, pg/g	7.7
Median all values pg/g	8.0
Consensus mean, pg/g	8.0
Standard deviation, pg/g	3.3
Relative standard deviation, %	41
No. of values reported	52
No. of values removed	9
No. of reported non-detects	4



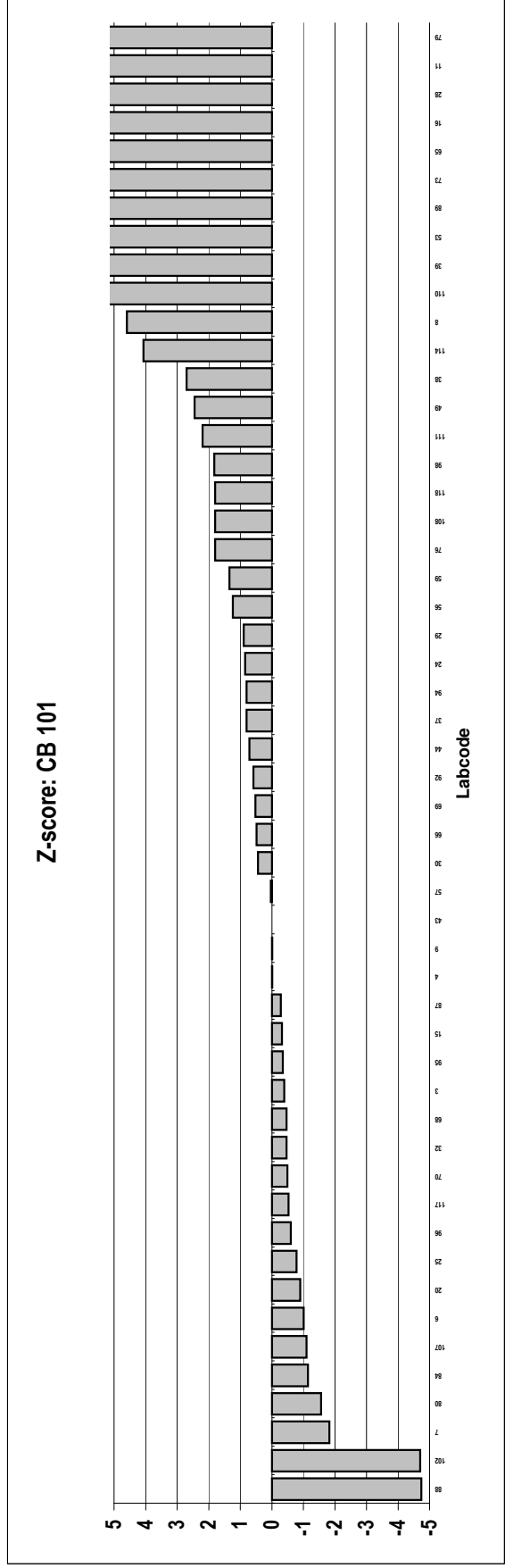
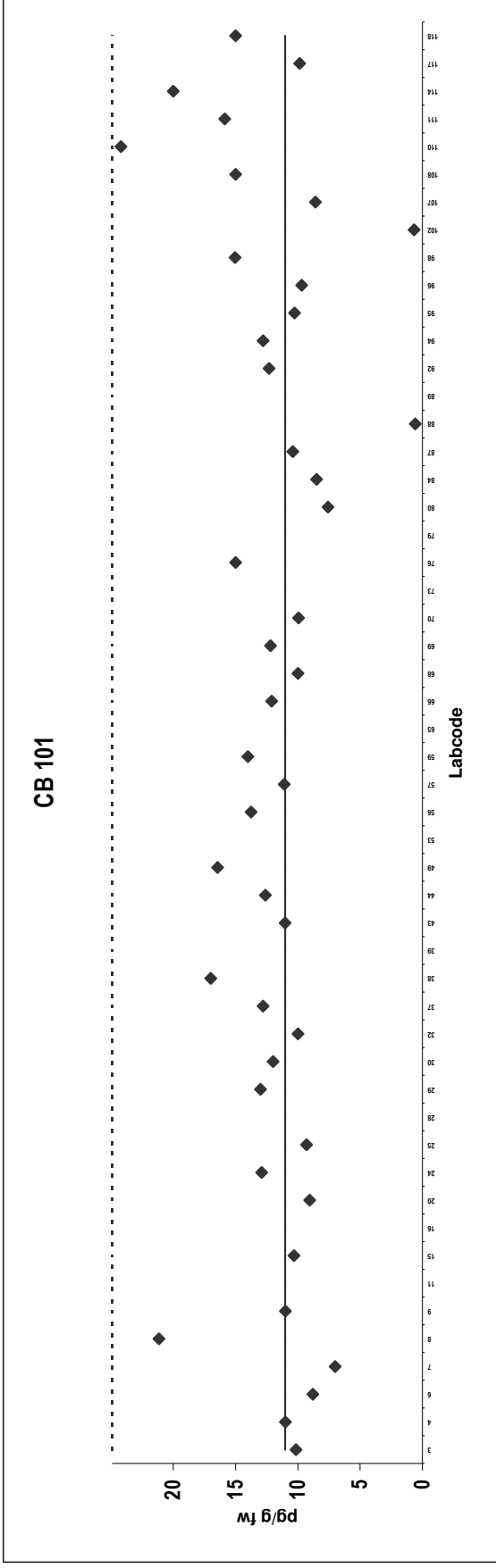
Breast milk

Congener: CB 101

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	10		107	8,6	
4	11		108	15	
6	8,8		110	24	
7	7,0		111	16	
8	21		114	20	
9	11		117	9,9	
11	73	Outlier,ND	118	15	
15	10				
16	58	Outlier			
20	9,0				
24	13				
25	9,3				
28	66	Outlier,ND			
29	13				
30	12				
32	10				
37	13				
38	17				
39	25	Outlier			
43	11				
44	13				
49	16				
53	28	Outlier			
56	14				
57	11				
59	14	ND			
65	54	Outlier			
66	12				
68	10				
69	12				
70	10				
73	52	Outlier			
76	15	ND			
79	693	Outlier			
80	7,6				
84	8,5				
87	10				
88	0,58				
89	36	Outlier			
92	12				
94	13				
95	10				
96	9,7				
98	15				
102	0,66				

Consensus statistics

Consensus median, pg/g	11
Median all values pg/g	12
Consensus mean, pg/g	12
Standard deviation, pg/g	4,3
Relative standard deviation, %	37
No. of values reported	52
No. of values removed	9
No. of reported non-detects	4



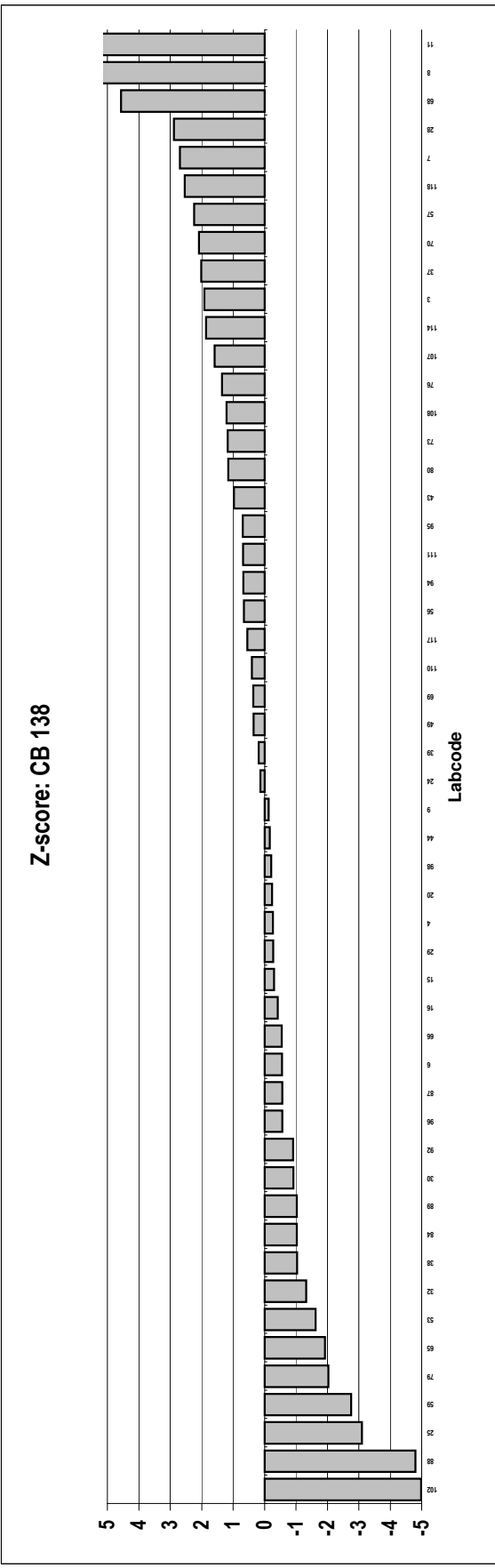
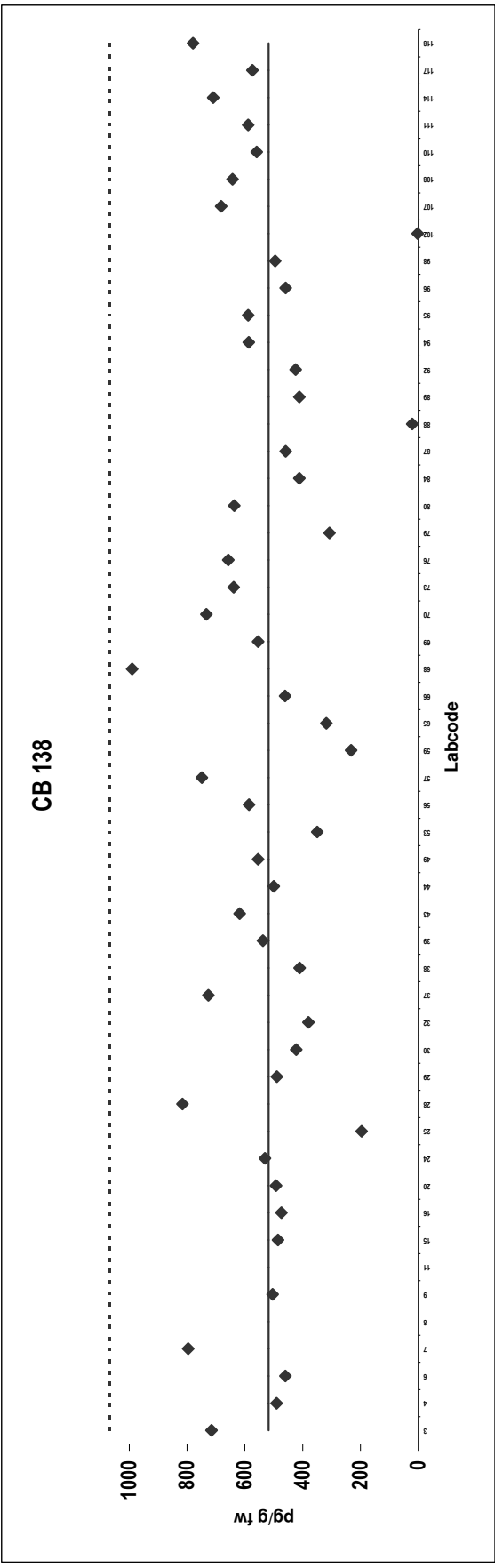
Breast milk

Congener: CB 138

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	716		107	682	
4	490		108	643	
6	460		110	559	
7	796		111	588	
8	1195	Outlier	114	710	
9	504		117	574	
11	2529	Outlier	118	780	
15	486				
16	474				
20	492				
24	531				
25	196				
28	816				
29	489				
30	422				
32	380				
37	726				
38	410				
39	537				
43	618				
44	500				
49	554				
53	350				
56	586				
57	749				
59	232				
65	318				
66	461				
68	990				
69	554				
70	733				
73	639				
76	657				
79	307				
80	637				
84	411				
87	459				
88	21				
89	411				
92	424				
94	587				
95	589				
96	459				
98	495				
102	2.2				

Consensus statistics

Consensus median, pg/g	518
Median all values pg/g	534
Consensus mean, pg/g	524
Standard deviation, pg/g	187
Relative standard deviation, %	36
No. of values reported	52
No. of values removed	2
No. of reported non-detects	0



Breast milk

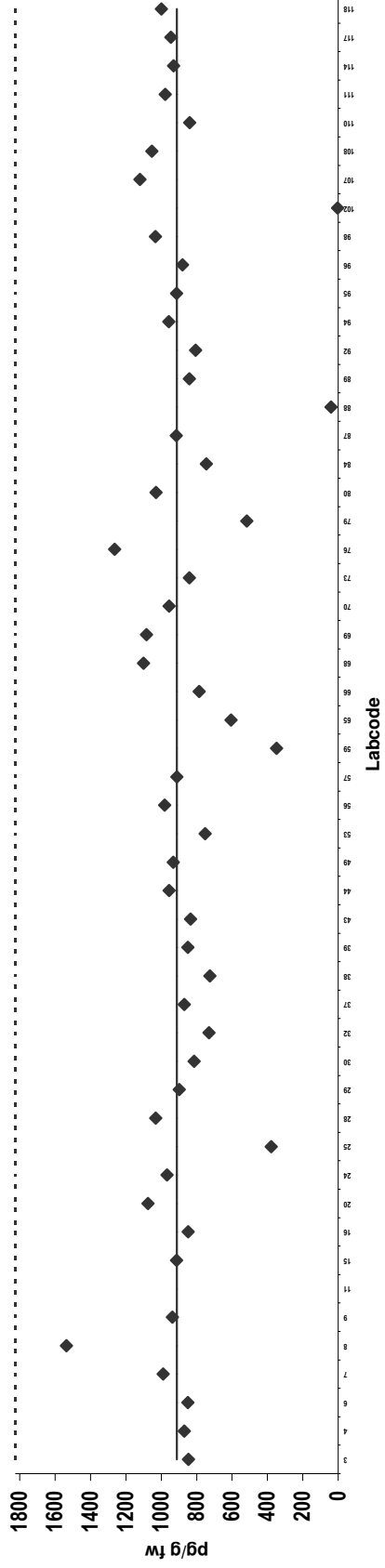
Congener: CB 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	847		107	1121	
4	870		108	1054	
6	850		110	840	
7	989		111	978	
8	1537		114	930	
9	937		117	946	
11	3384		118	1000	
15	914				
16	848				
20	1075				
24	968				
25	379				
28	1032				
29	898				
30	815				
32	730				
37	870				
38	725				
39	850				
43	835				
44	956				
49	933				
53	753				
56	982				
57	912				
59	349				
65	606				
66	785				
68	1100				
69	1084				
70	956				
73	842				
76	1264				
79	517				
80	1030				
84	745				
87	916				
88	40				
89	841				
92	806				
94	958				
95	914				
96	880				
98	1033				
102	3.8				

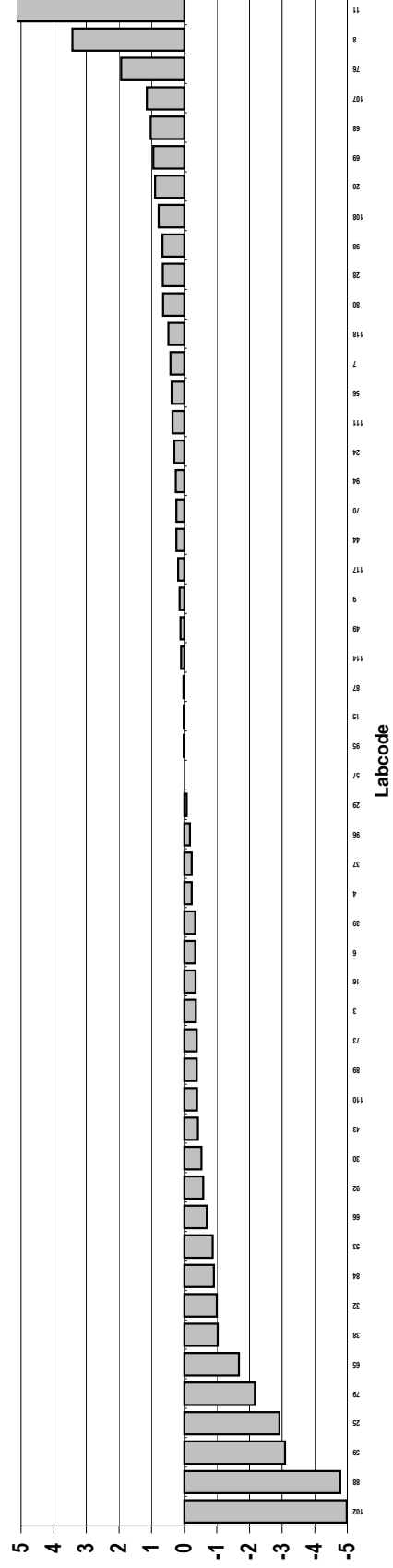
Consensus statistics

Consensus median, pg/g	912
Median all values pg/g	913
Consensus mean, pg/g	864
Standard deviation, pg/g	255
Relative standard deviation, %	30
No. of values reported	52
No. of values removed	1
No. of reported non-detects	0

CB 153



Z-score: CB 153



Breast milk

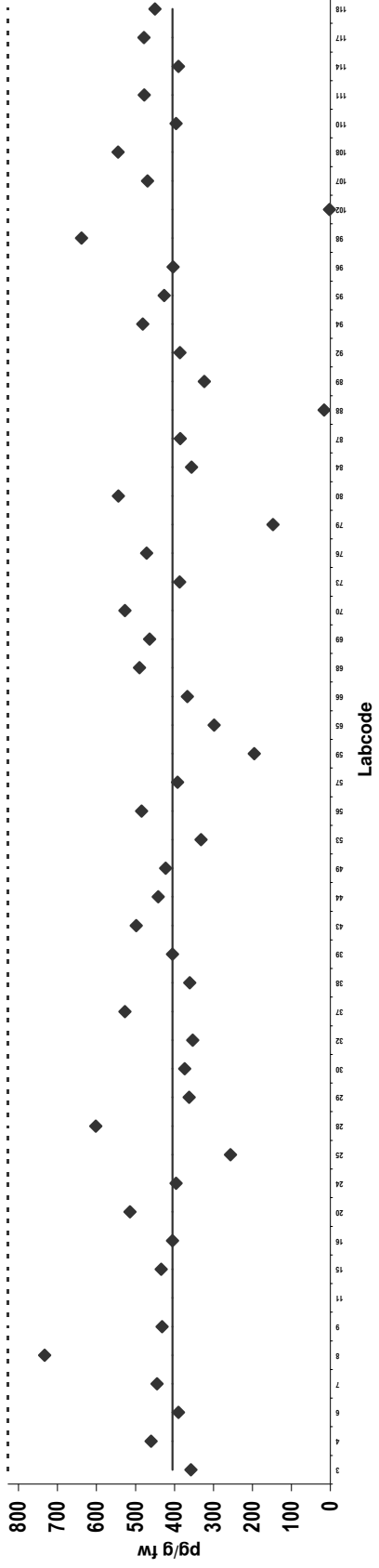
Congener: CB 180

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	358		107	470	
4	460		108	545	
6	390		110	396	
7	444		111	477	
8	733		114	390	
9	432		117	478	
11	1421		118	450	
15	434				
16	405				
20	514				
24	396				
25	256				
28	602				
29	362				
30	374				
32	353				
37	527				
38	361				
39	405				
43	498				
44	442				
49	423				
53	332				
56	484				
57	392				
59	195				
65	298				
66	367				
68	490				
69	464				
70	527				
73	387				
76	471				
79	147				
80	544				
84	356				
87	385				
88	16				
89	323				
92	386				
94	482				
95	426				
96	404				
98	638				
102	1.9				

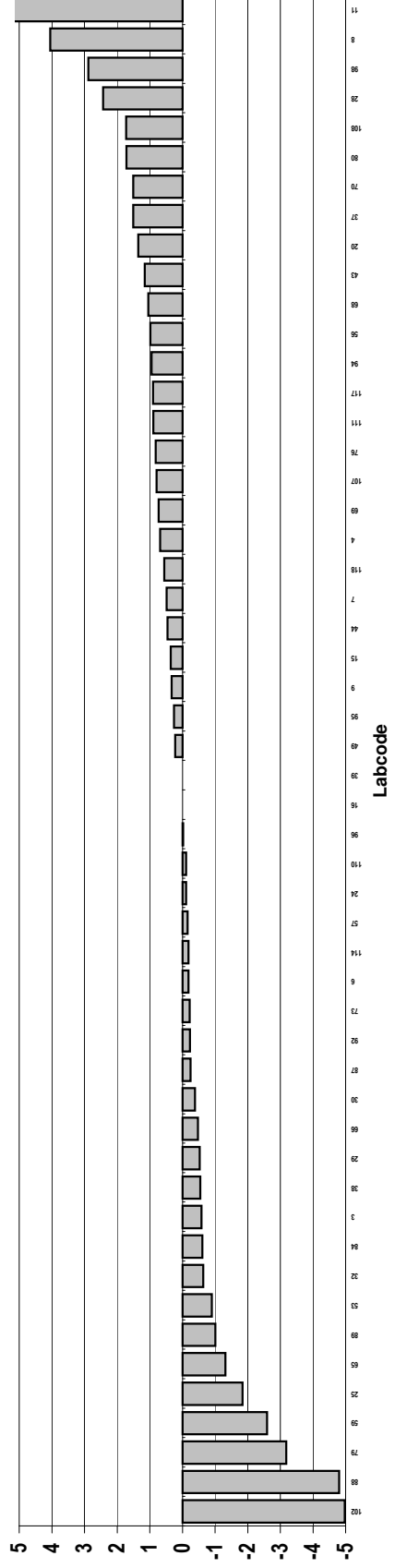
Consensus statistics

Consensus median, pg/g	405
Median all values pg/g	414
Consensus mean, pg/g	410
Standard deviation, pg/g	129
Relative standard deviation, %	31
No. of values reported	52
No. of values removed	1
No. of reported non-detects	0

CB 180



Z-score: CB 180

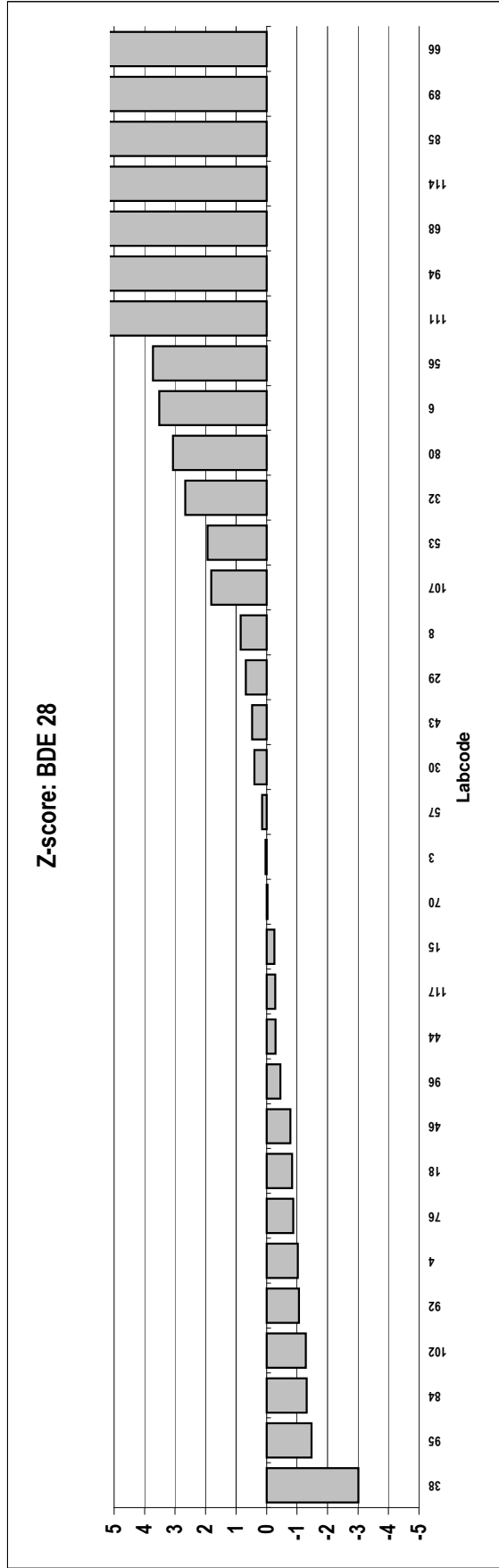
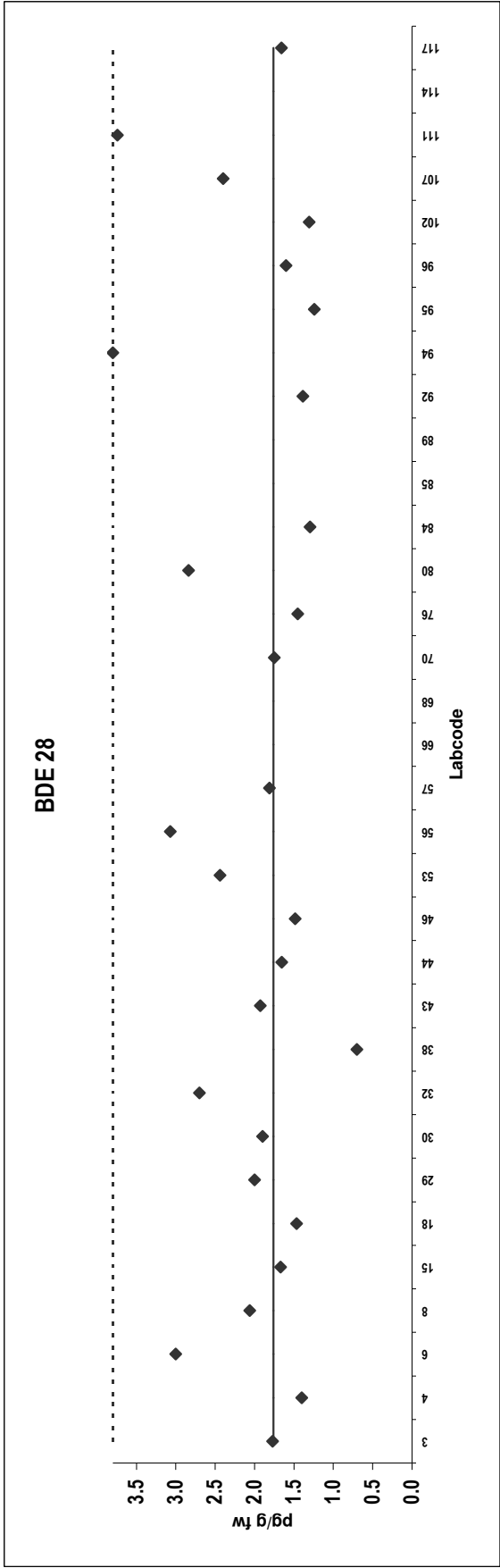


Breast milk
Congener: BDE 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	1.8				
4	1.4				
6	3.0				
8	2.1				
15	1.7				
18	1.5				
29	2.0				
30	1.9				
32	2.7				
38	0.70				
43	1.9				
44	1.7				
46	1.5				
53	2.4				
56	3.1				
57	1.8				
66	42	Outlier,ND			
68	5.3	Outlier			
70	1.8				
76	1.5				
80	2.8				
84	1.3				
85	13	Outlier			
89	25	Outlier			
92	1.4				
94	3.8				
95	1.2				
96	1.6				
102	1.3				
107	2.4				
111	3.7				
114	10	Outlier,ND			
117	1.7				

Consensus statistics

Consensus median, pg/g	1.8
Median all values pg/g	1.9
Consensus mean, pg/g	2.0
Standard deviation, pg/g	0.76
Relative standard deviation, %	38
No. of values reported	33
No. of values removed	5
No. of reported non-detects	2



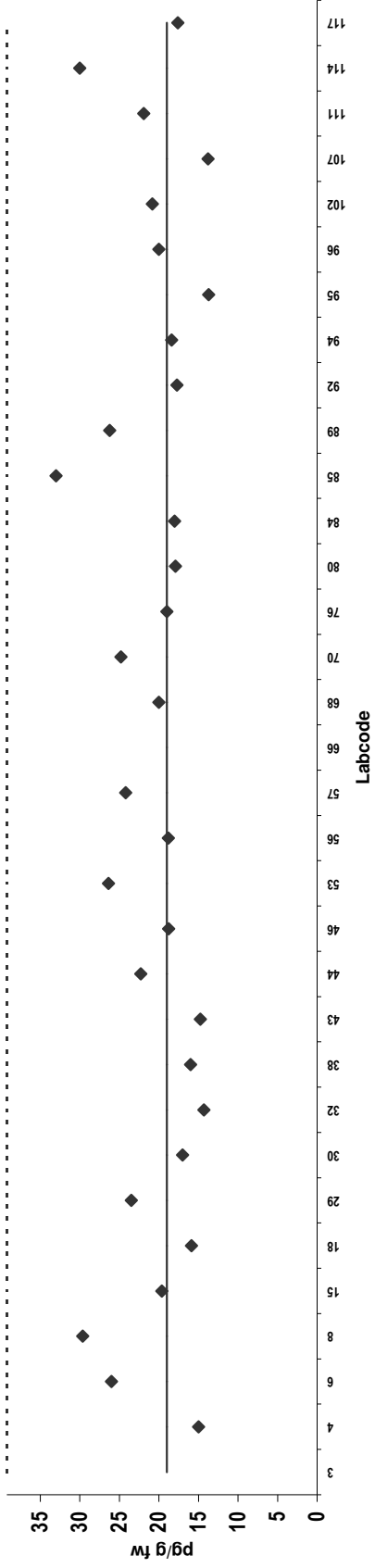
Breast milk
Congener: BDE 47

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	43	Outlier			
4	15				
6	26	Outlier			
8	30				
15	20				
18	16				
29	24				
30	17				
32	14				
38	16				
43	15				
44	22				
46	19				
53	26				
56	19				
57	24				
66	59				
68	20				
70	25				
76	19				
80	18				
84	18				
85	33				
89	26				
92	18				
94	18				
95	14				
96	20				
102	21				
107	14				
111	22				
114	30				
117	18				

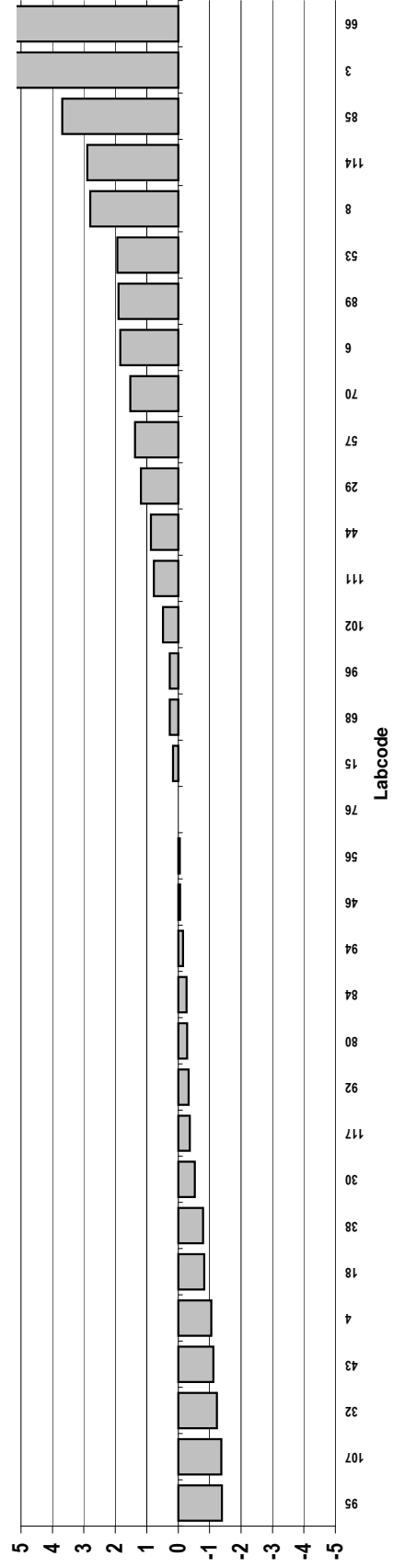
Consensus statistics

Consensus median, pg/g	19
Median all values pg/g	20
Consensus mean, pg/g	20
Standard deviation, pg/g	5.0
Relative standard deviation, %	25
No. of values reported	33
No. of values removed	2
No. of reported non-detects	0

BDE 47



Z-score: BDE 47

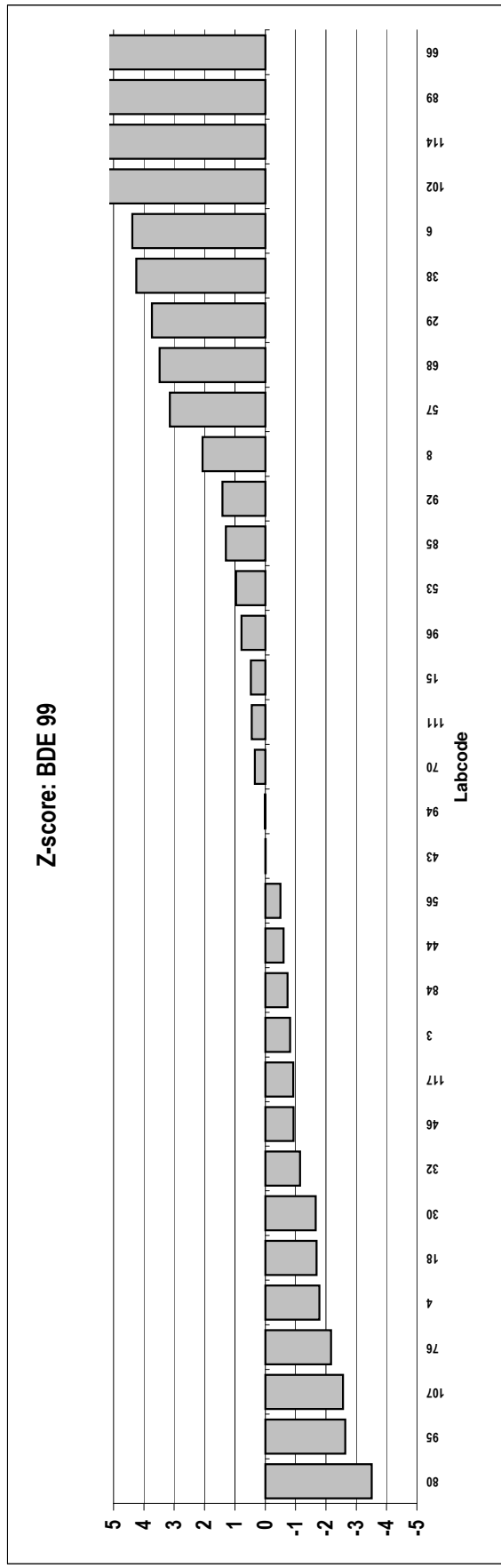
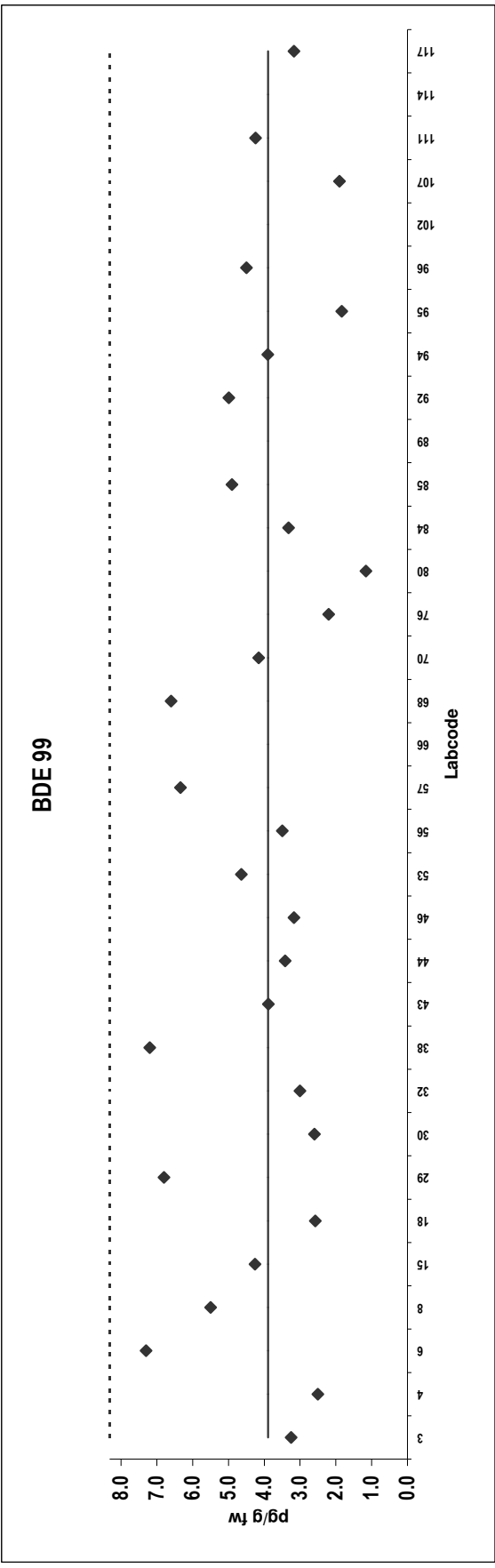


Breast milk
Congener: BDE 99

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	3.3				
4	2.5				
6	7.3				
8	5.5				
15	4.3				
18	2.6				
29	6.8				
30	2.6				
32	3.0				
38	7.2				
43	3.9				
44	3.4				
46	3.2				
53	4.6				
56	3.5				
57	6.3				
66	29	Outlier			
68	6.6				
70	4.2				
76	2.2	ND			
80	1.2				
84	3.3				
85	4.9				
89	26	Outlier			
92	5.0				
94	3.9				
95	1.8				
96	4.5				
102	9.0	Outlier			
107	1.9				
111	4.2				
114	10	Outlier			
117	3.2				

Consensus statistics

Consensus median, pg/g	3.9
Median all values pg/g	4.2
Consensus mean, pg/g	4.0
Standard deviation, pg/g	1.7
Relative standard deviation, %	41
No. of values reported	33
No. of values removed	4
No. of reported non-detects	1

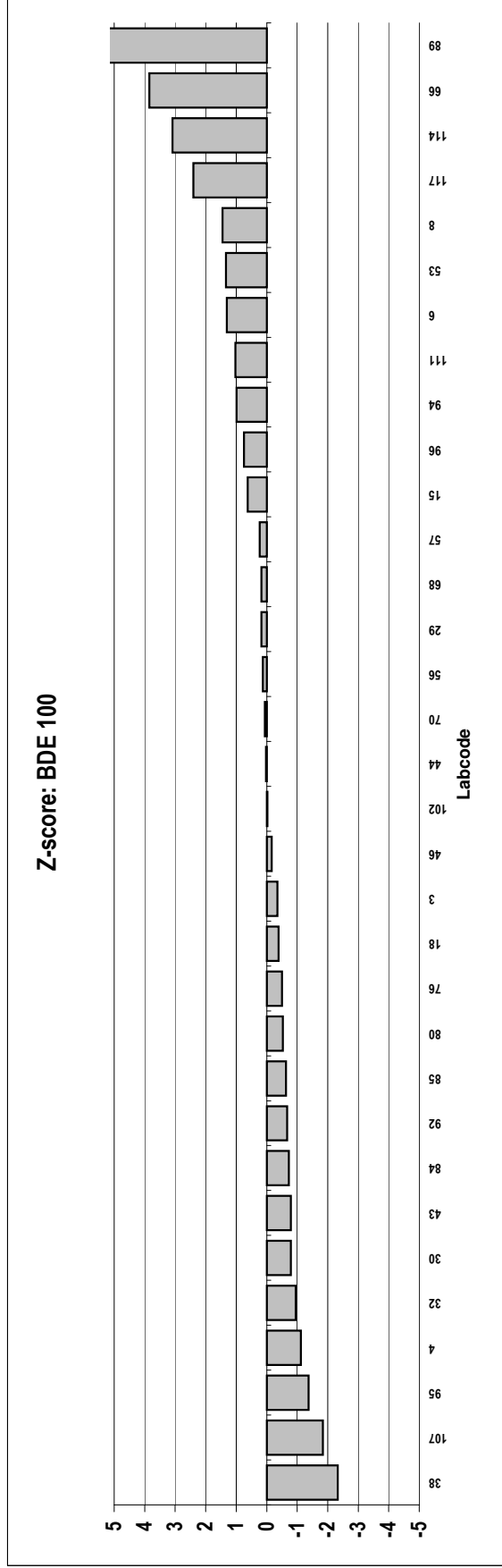
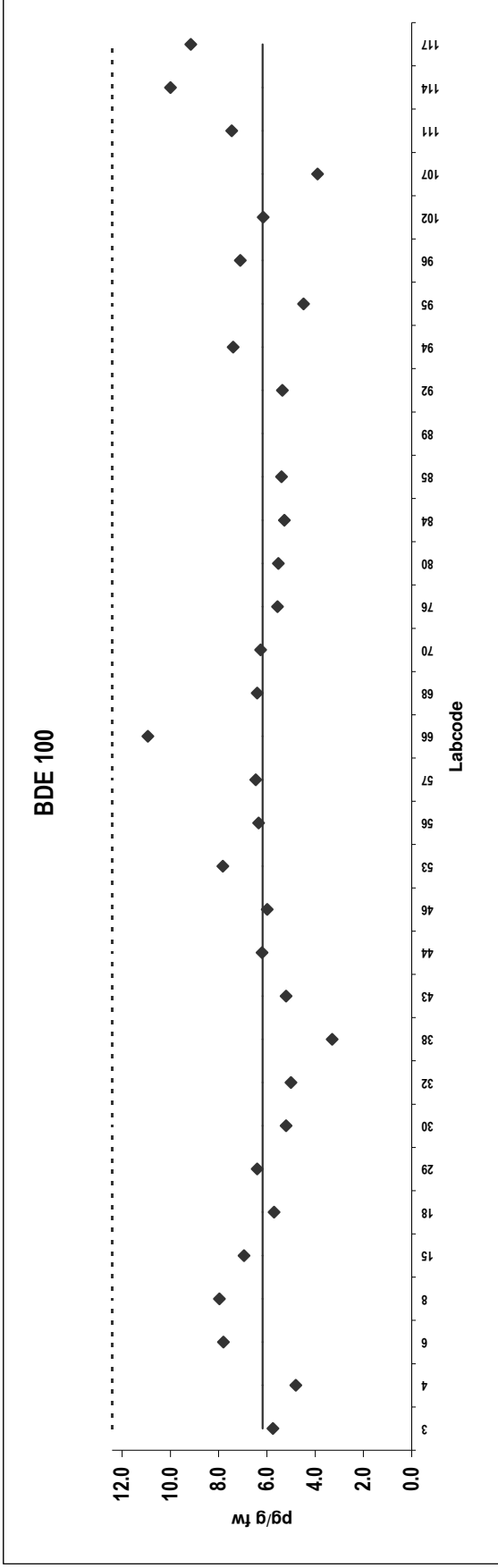


Breast milk
Congener: BDE 100

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	5.8				
4	4.8				
6	7.8				
8	8.0				
15	6.9				
18	5.7				
29	6.4				
30	5.2				
32	5.0				
38	3.3				
43	5.2				
44	6.2				
46	6.0				
53	7.8				
56	6.3				
57	6.5				
66	11				
68	6.4				
70	6.3				
76	5.6				
80	5.5				
84	5.3				
85	5.4				
89	26				
92	5.4	Outlier			
94	7.4				
95	4.5				
96	7.1				
102	6.2				
107	3.9				
111	7.5				
114	10				
117	9.2				

Consensus statistics

Consensus median, pg/g	6.2
Median all values pg/g	6.2
Consensus mean, pg/g	6.4
Standard deviation, pg/g	1.6
Relative standard deviation, %	26
No. of values reported	33
No. of values removed	1
No. of reported non-detects	0



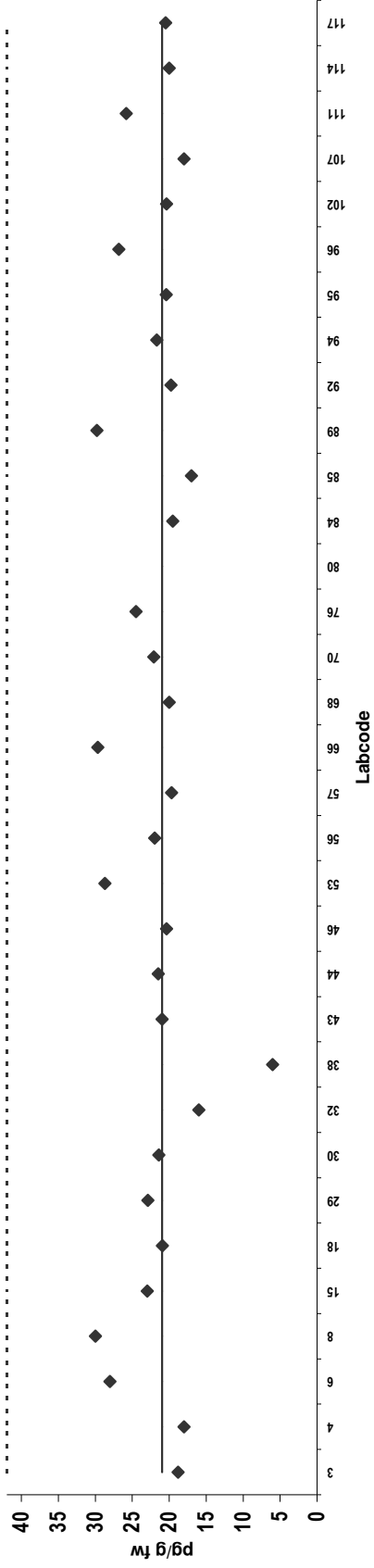
Breast milk
Congener: BDE 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	19				
4	18				
6	28				
8	30				
15	23				
18	21				
29	23				
30	21				
32	16				
38	6.0				
43	21				
44	22				
46	20				
53	29				
56	22				
57	20				
66	30				
68	20				
70	22				
76	25				
80	22740	Outlier			
84	20				
85	17				
89	30				
92	20				
94	22				
95	20				
96	27				
102	20				
107	18				
111	26				
114	20				
117	21				

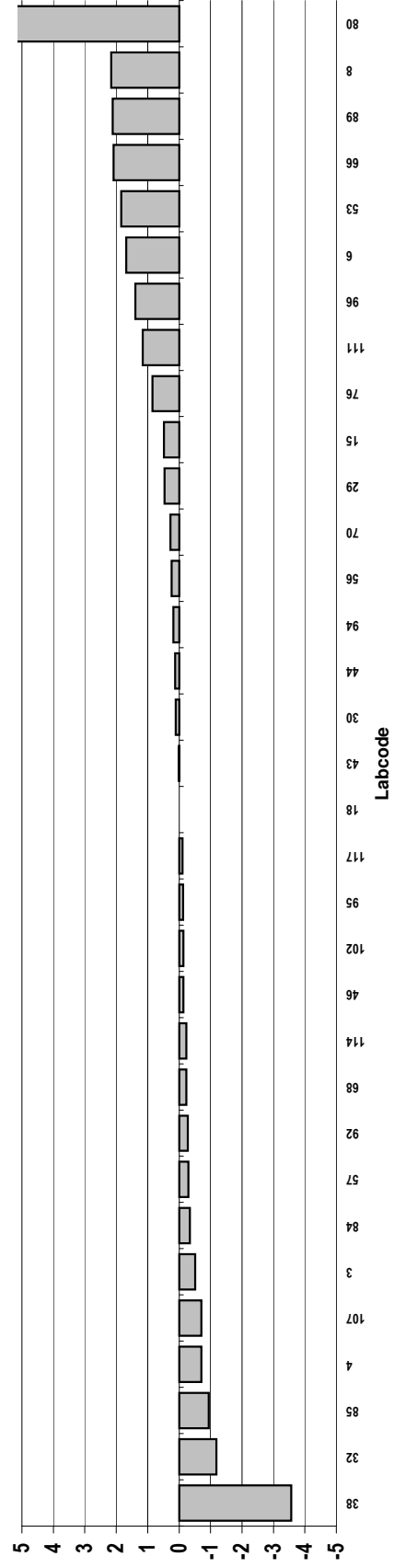
Consensus statistics

Consensus median, pg/g	21
Median all values pg/g	21
Consensus mean, pg/g	22
Standard deviation, pg/g	4.8
Relative standard deviation, %	22
No. of values reported	33
No. of values removed	1
No. of reported non-detects	0

BDE 153



Z-score: BDE 153



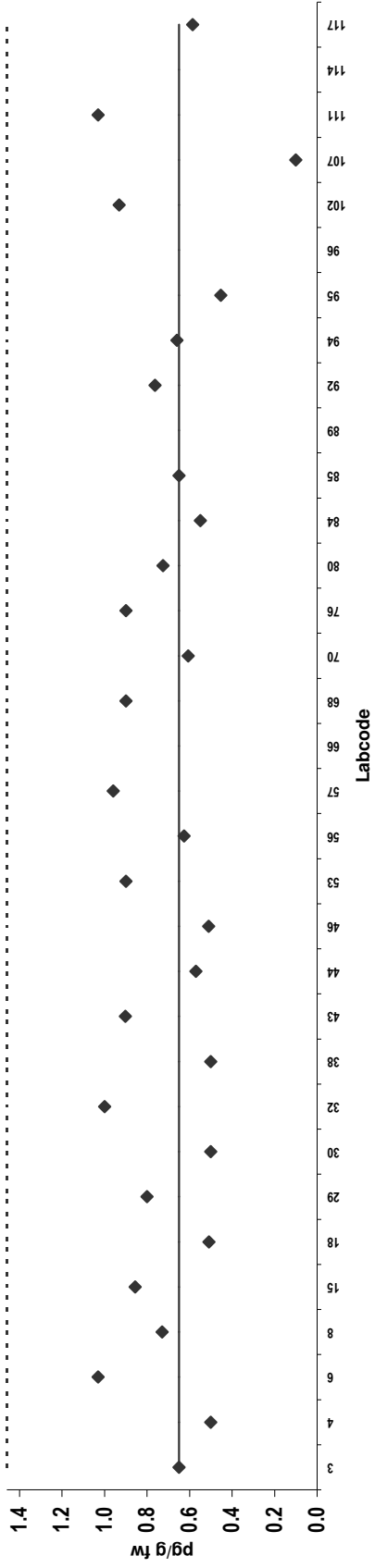
Breast milk
Congener: BDE 154

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.65				
4	0.50				
6	1.0				
8	0.73				
15	0.86	ND			
18	0.51				
29	0.80				
30	0.50	ND			
32	1.0	ND			
38	0.50				
43	0.90				
44	0.57				
46	0.51				
53	0.90				
56	0.63				
57	0.96				
66	8.5	Outlier,ND			
68	0.90				
70	0.61				
76	0.90	ND			
80	0.73				
84	0.55				
85	0.65				
89	29	Outlier			
92	0.76				
94	0.66				
95	0.45				
96	4.1	Outlier			
102	0.93				
107	0.10				
111	1.0				
114	10	Outlier			
117	0.59				

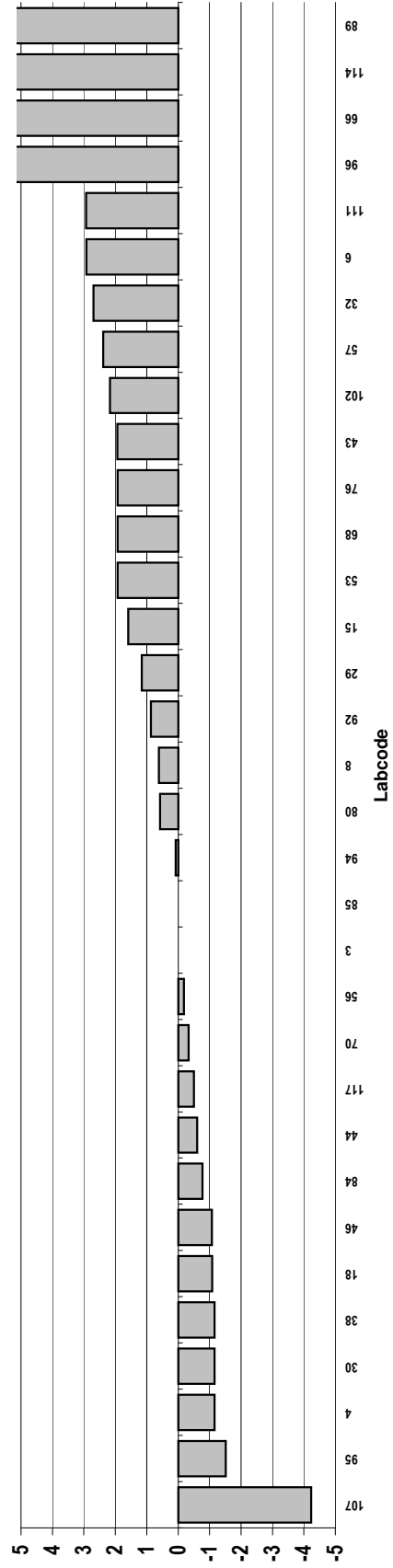
Consensus statistics

Consensus median, pg/g	0.65
Median all values pg/g	0.73
Consensus mean, pg/g	0.70
Standard deviation, pg/g	0.22
Relative standard deviation, %	31
No. of values reported	33
No. of values removed	4
No. of reported non-detects	5

BDE 154



Z-score: BDE 154

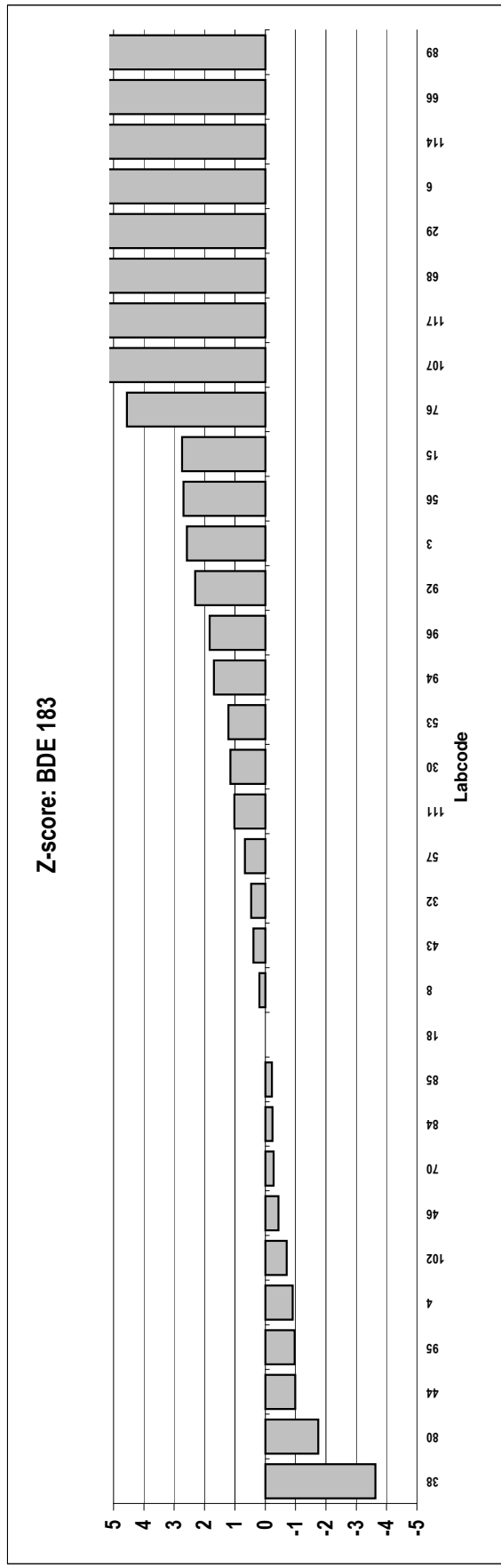
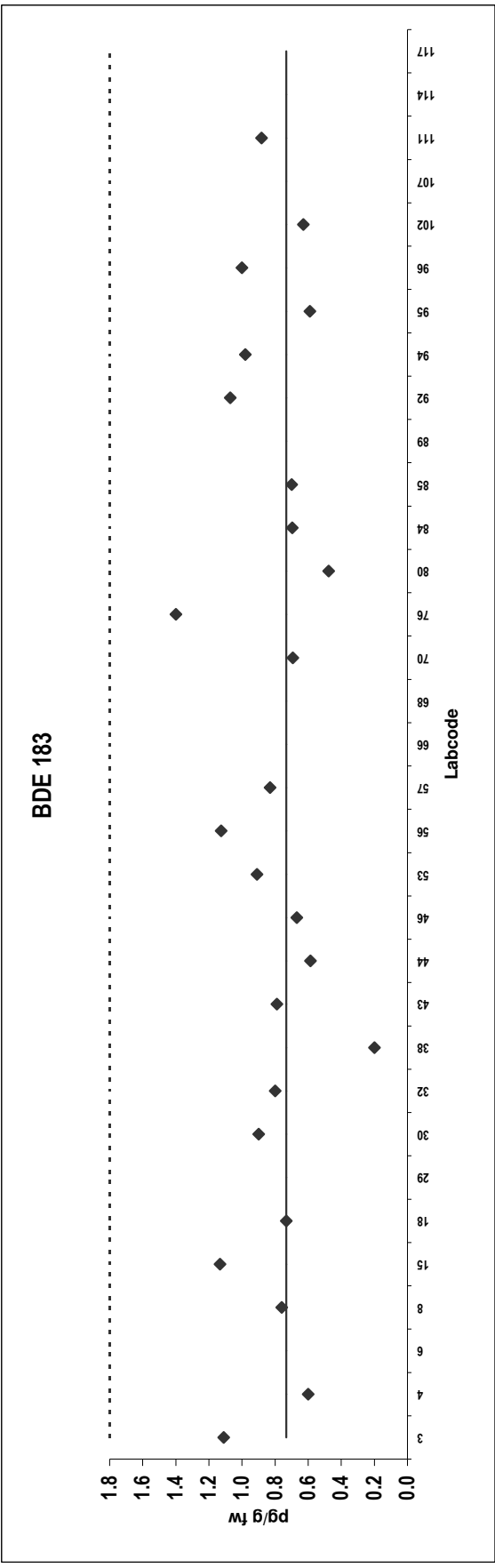


Breast milk
Congener: BDE 183

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	1.1				
4	0.60				
6	4.1	Outlier			
8	0.76				
15	1.1	ND			
18	0.73				
29	3.3	Outlier			
30	0.90				
32	0.80				
38	0.20				
43	0.79	ND			
44	0.59				
46	0.67				
53	0.91				
56	1.1				
57	0.83				
66	20	Outlier,ND			
68	2.3	Outlier			
70	0.69				
76	1.4	ND			
80	0.48				
84	0.70				
85	0.70				
89	28	Outlier			
92	1.1				
94	0.98				
95	0.59				
96	1.0	ND			
102	0.63				
107	1.9	Outlier			
111	0.88				
114	10	Outlier			
117	2.2	Outlier			

Consensus statistics

Consensus median, pg/g	0.73
Median all values pg/g	0.90
Consensus mean, pg/g	0.81
Standard deviation, pg/g	0.25
Relative standard deviation, %	31
No. of values reported	33
No. of values removed	8
No. of reported non-detects	5

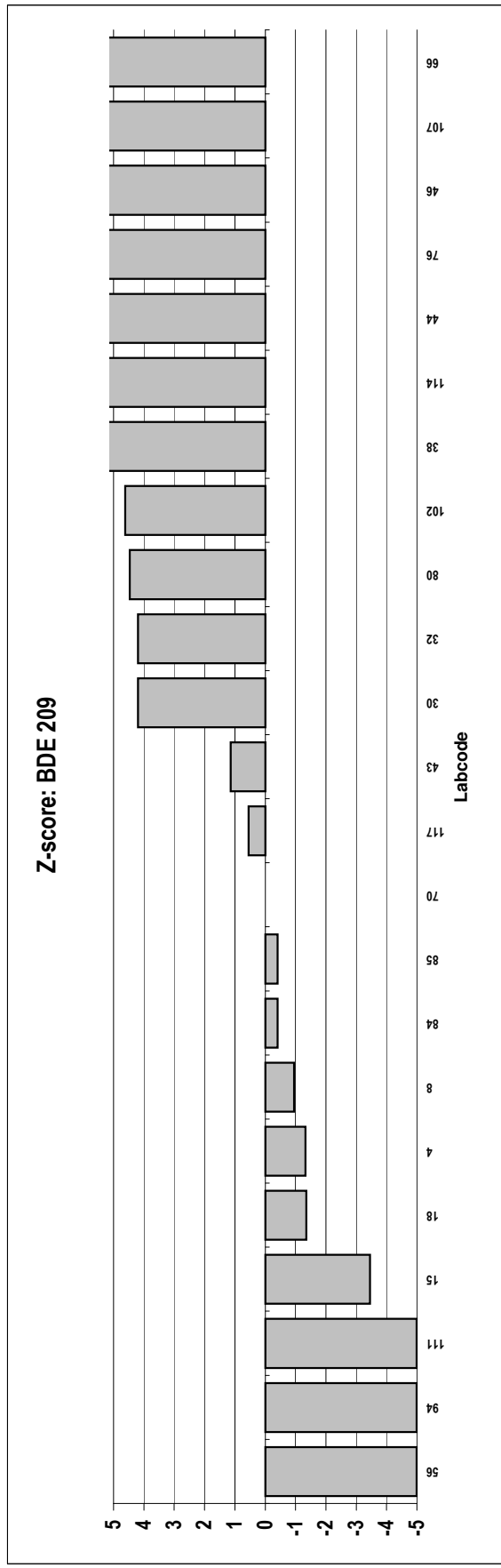
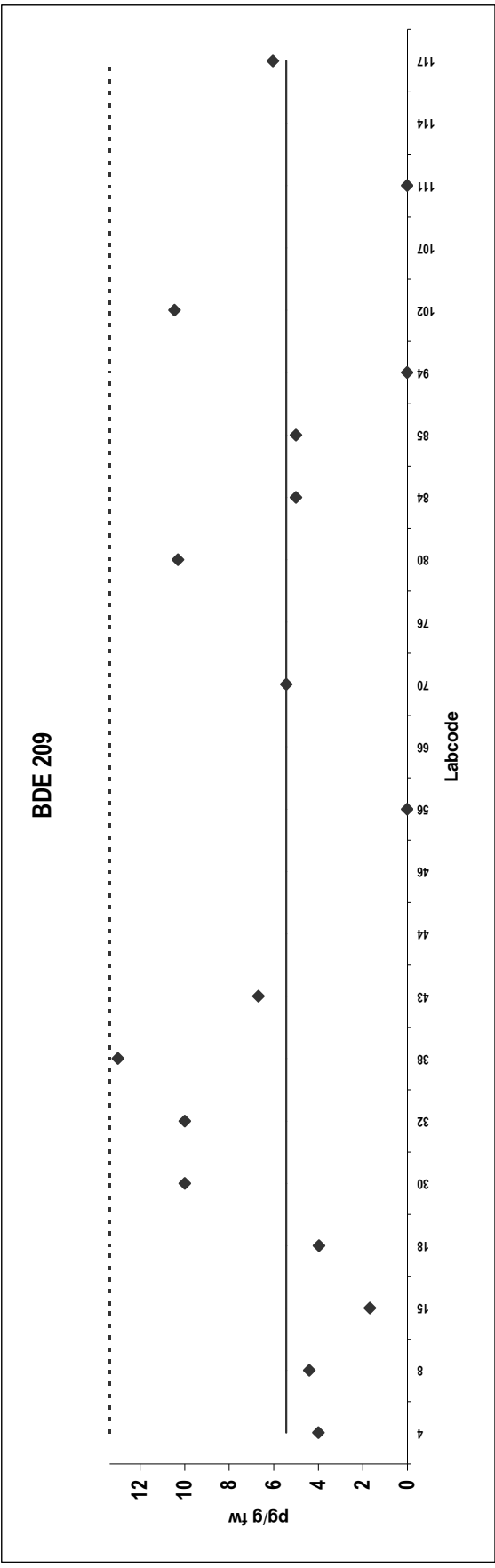


Breast milk
Congener: BDE 209

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	4.0				
8	4.4				
15	1.7				
18	4.0				
30	10	ND			
32	10				
38	13				
43	6.7				
44	22	Outlier			
46	24	Outlier			
56	0.010	ND			
66	268	Outlier			
70	5.4				
76	24	Outlier,ND			
80	10	ND			
84	5.0				
85	5.0	ND			
94	0.010	ND			
102	10				
107	174	Outlier,ND			
111	0.010	ND			
114	15	Outlier			
117	6.0				

Consensus statistics

Consensus median, pg/g	5.4
Median all values pg/g	6.7
Consensus mean, pg/g	5.6
Standard deviation, pg/g	4.0
Relative standard deviation, %	71
No. of values reported	23
No. of values removed	6
No. of reported non-detects	9

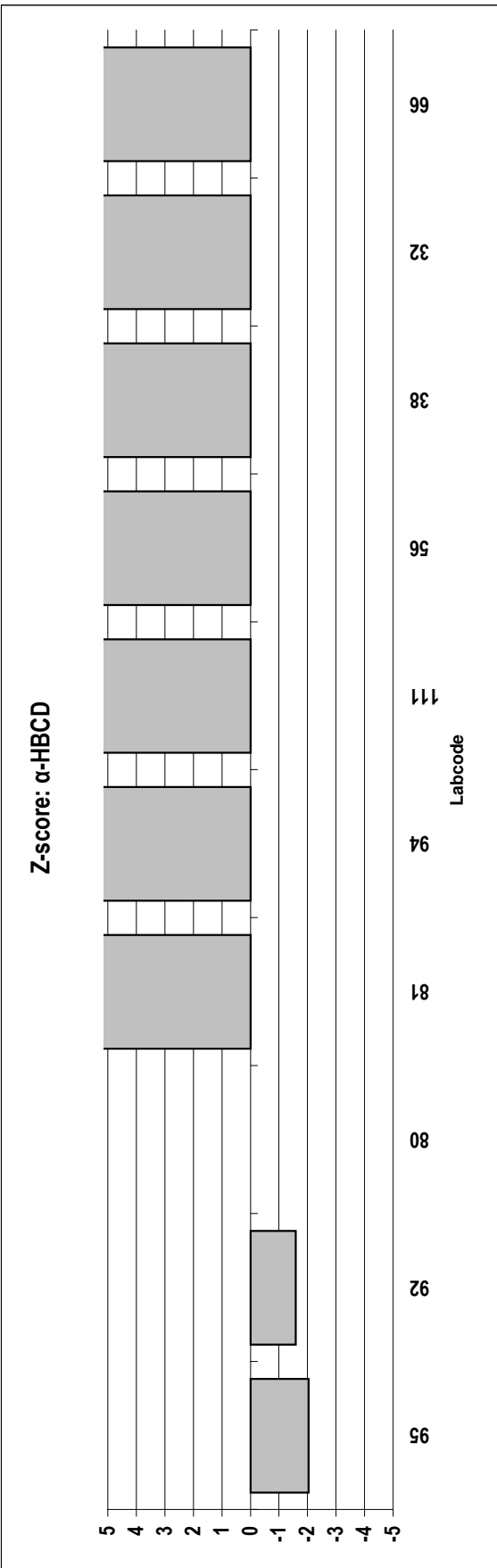
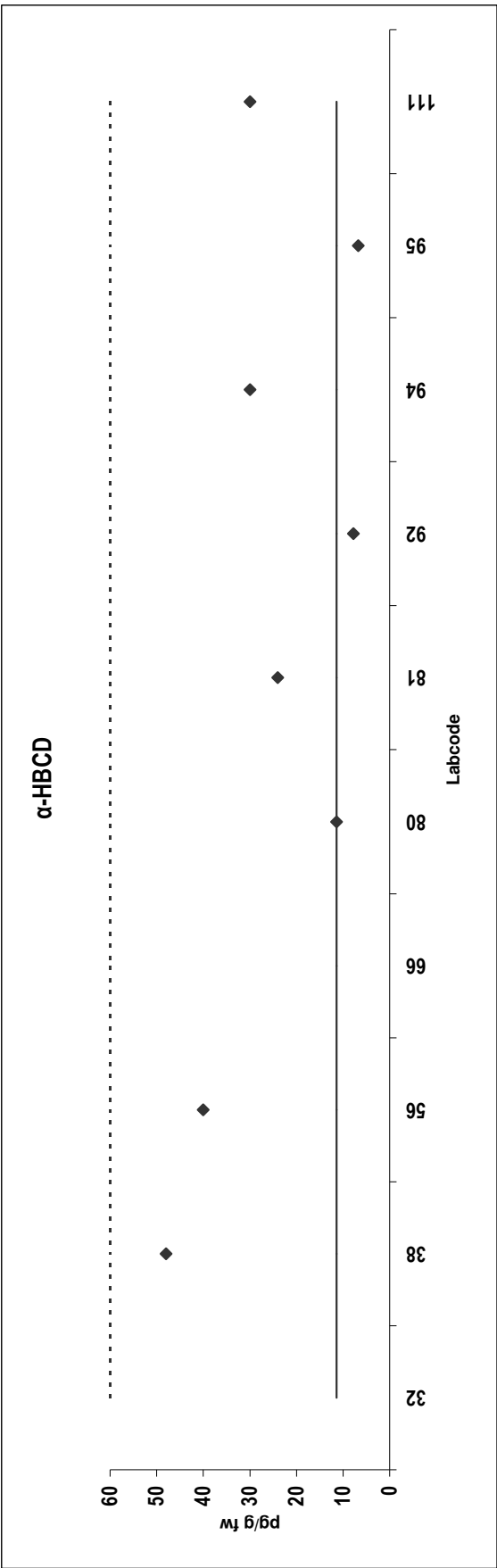


Breast milk
Congener: α -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
32	200	Outlier			
38	48				
56	40	ND			
66	630	Outlier			
80	11				
81	24				
92	7.8				
94	30	ND			
95	6.8				
111	30	ND			

Consensus statistics

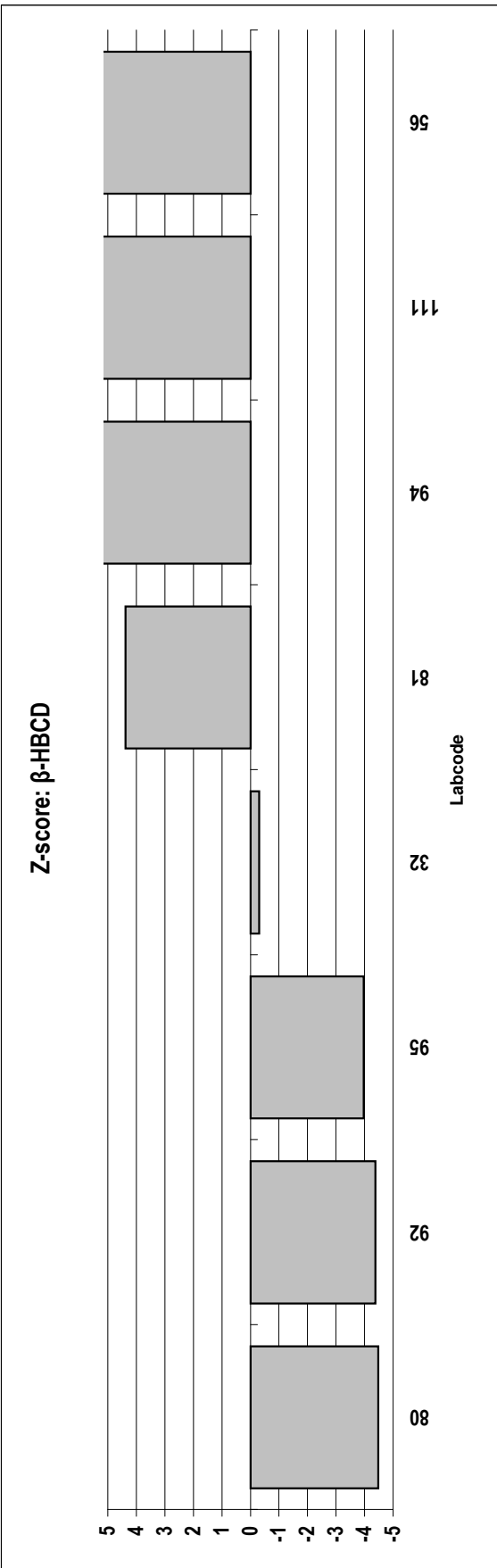
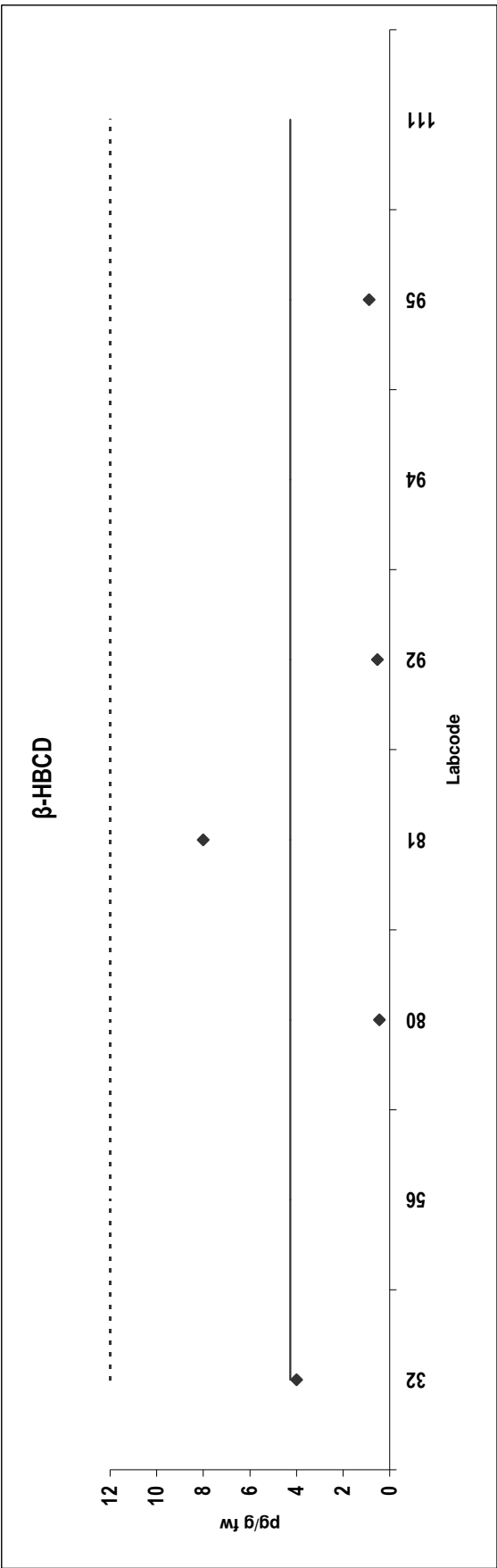
Consensus median, pg/g	11
Median all values pg/g	30
Consensus mean, pg/g	25
Standard deviation, pg/g	15
Relative standard deviation, %	61
No. of values reported	10
No. of values removed	2
No. of reported non-detects	3



Breast milk
Congener: β -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
32	4.0	ND			
56	20	Outlier,ND			
80	0.44	ND			
81	8.0				
92	0.53				
94	15	Outlier,ND			
95	0.88	ND			
111	15	Outlier,ND			

Consensus statistics	
Consensus median, pg/g	4.3
Median all values pg/g	6.0
Consensus mean, pg/g	2.8
Standard deviation, pg/g	3.3
Relative standard deviation, %	118
No. of values reported	8
No. of values removed	3
No. of reported non-detects	6



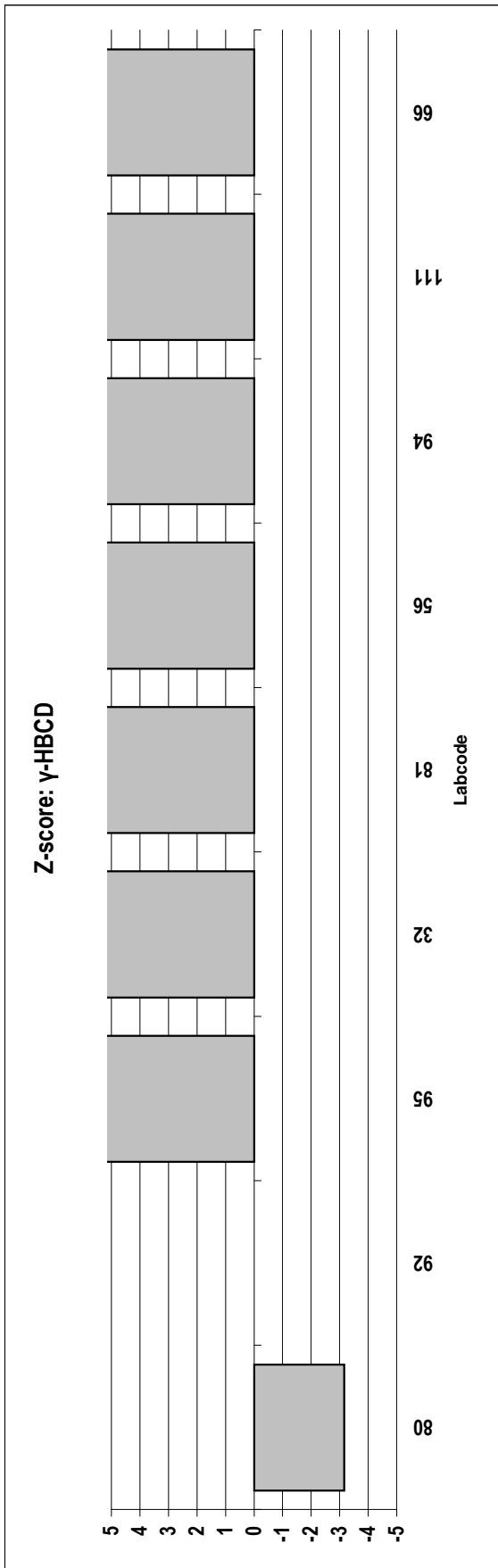
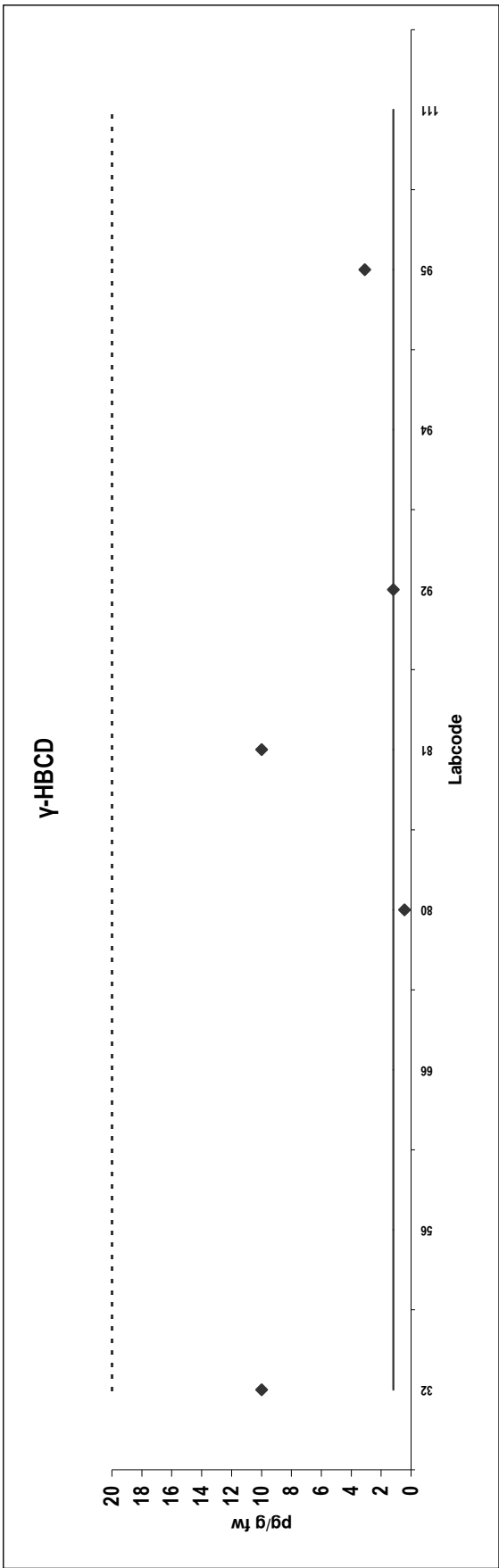
Breast milk

Congener: γ -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
32	10	ND			
56	50	Outlier,ND			
66	2715	Outlier			
80	0.44	ND			
81	10	ND			
92	1.2				
94	60	Outlier,ND			
95	3.1	ND			
111	60	Outlier,ND			

Consensus statistics

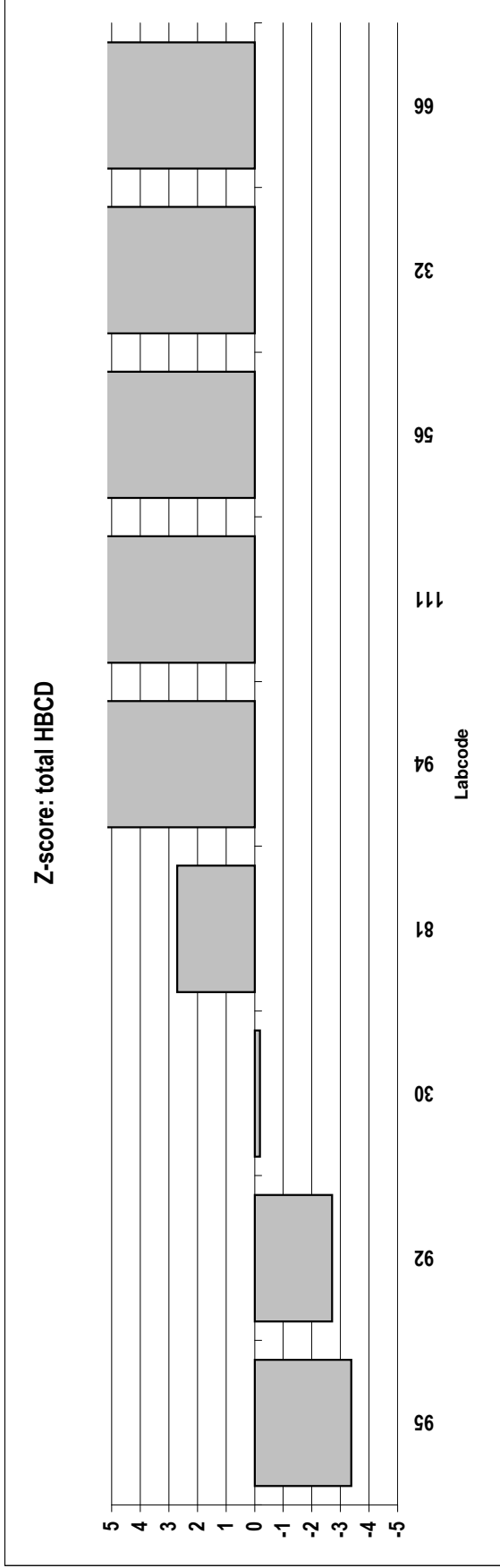
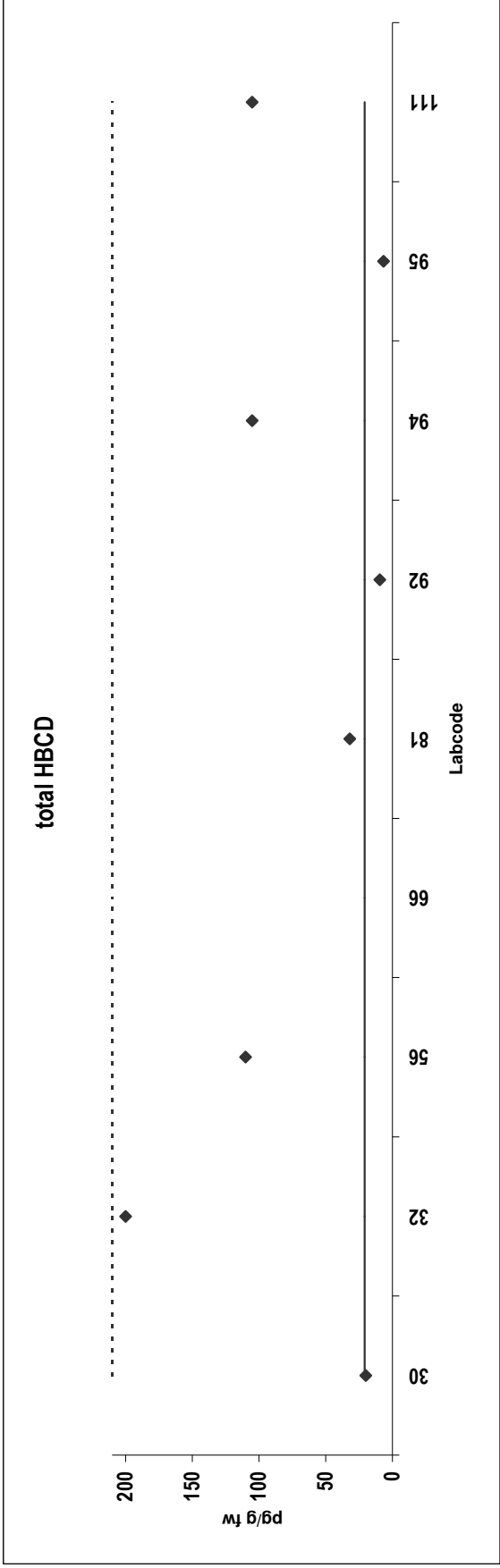
Consensus median, pg/g	1.2
Median all values pg/g	10
Consensus mean, pg/g	4.9
Standard deviation, pg/g	4.7
Relative standard deviation, %	95
No. of values reported	9
No. of values removed	4
No. of reported non-detects	7



Breast milk
Congener: total HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
30	20	ND			
32	200	ND			
56	110	ND			
66	3344	Outlier			
81	32				
92	9.5				
94	105	ND			
95	6.8				
111	105	ND			

Consensus statistics	
Consensus median, pg/g	21
Median all values pg/g	105
Consensus mean, pg/g	74
Standard deviation, pg/g	68
Relative standard deviation, %	93
No. of values reported	9
No. of values removed	1
No. of reported non-detects	4



Appendix 3:

Presentation of results
for pork meat

Appendix 3: Presentation of results: Pork meat

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:

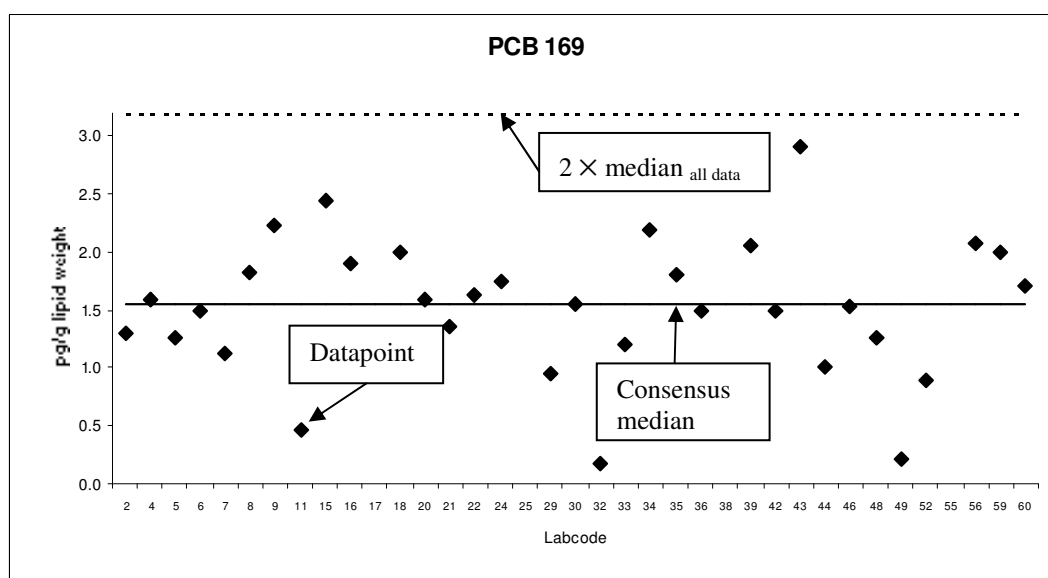
1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners.
2. Values exceeding $2 \times$ this median, were defined as outliers and removed from the data set.
3. Median, mean and standard deviation were re-calculated from the remaining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

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

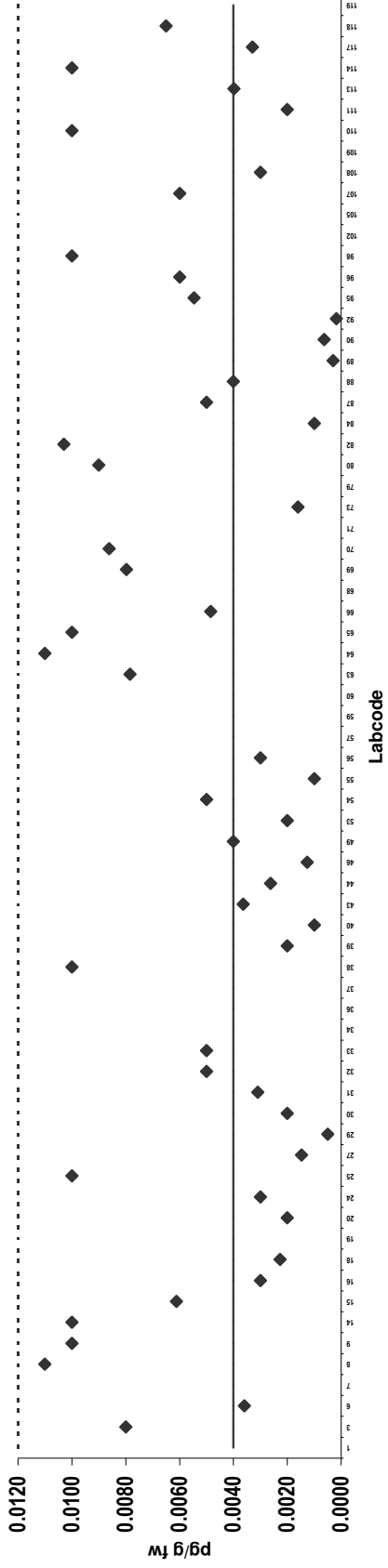
where x = reported value; X = assigned value (consensus); σ = target value for standard deviation. A σ of 20% of the consensus was used, i.e. z-scores between +1 and -1 reflect a deviation of $\pm 20\%$ from the consensus value.

Pork
Congener: 2,3,7,8 TCDD

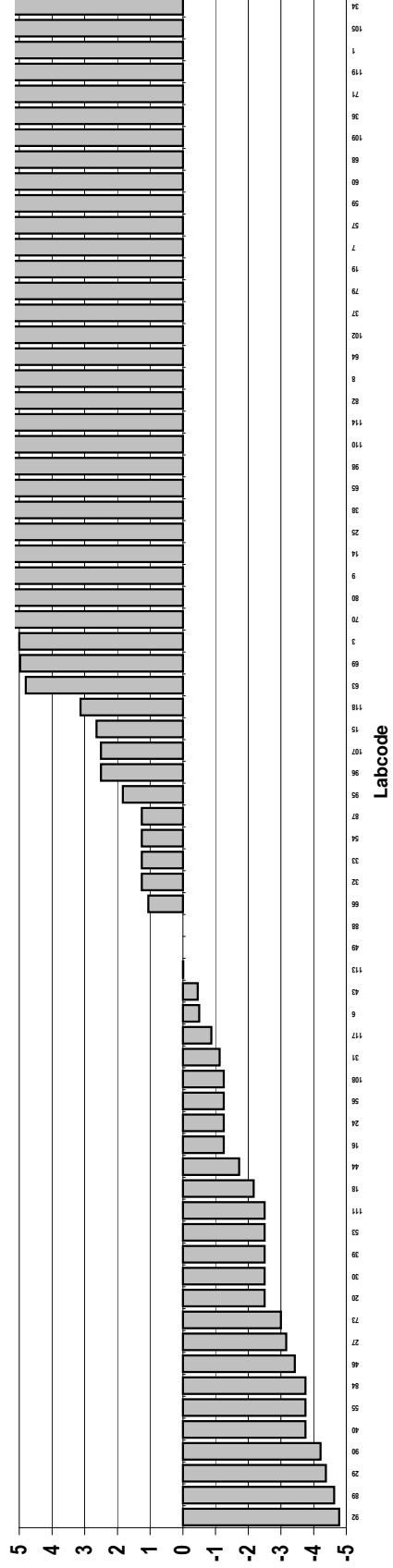
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.055	Outlier,ND	73	0.0016	ND
3	0.0080	ND	79	0.015	Outlier
6	0.0036	ND	80	0.0090	
7	0.016	Outlier,ND	82	0.010	
8	0.011	ND	84	0.0010	
9	0.010	ND	87	0.0050	ND
14	0.010	ND	88	0.0040	ND
15	0.0061	ND	89	0.00030	ND
16	0.0030	ND	90	0.00063	ND
18	0.0023	ND	92	0.00018	ND
19	0.016	Outlier	95	0.0055	ND
20	0.0020	ND	96	0.0060	ND
24	0.0030	ND	98	0.010	ND
25	0.010	ND	102	0.013	Outlier
27	0.0015	ND	105	0.079	Outlier,ND
29	0.00050	ND	107	0.0060	ND
30	0.0020	ND	108	0.0030	ND
31	0.0031	ND	109	0.021	Outlier,ND
32	0.0050	ND	110	0.010	ND
33	0.0050	ND	111	0.0020	ND
34	0.12	Outlier,ND	113	0.0040	ND
36	0.029	Outlier	114	0.010	ND
37	0.015	Outlier,ND	117	0.0033	ND
38	0.010	ND	118	0.0065	ND
39	0.0020	ND	119	0.050	Outlier,ND
40	0.0010	ND			
43	0.0036	ND			
44	0.0026				
46	0.0013				
49	0.0040				
53	0.0020				
54	0.0050				
55	0.0010				
56	0.0030				
57	0.020	Outlier,ND			
59	0.020	Outlier,ND			
60	0.020	Outlier			
63	0.0078	ND			
64	0.011	ND			
65	0.010	ND			
66	0.0048	ND			
68	0.020	Outlier,ND			
69	0.0080	ND			
70	0.0086	ND			
71	0.050	Outlier,ND			

Consensus statistics	
Consensus median, pg/g	0.0040
Median all values pg/g	0.0060
Consensus mean, pg/g	0.0050
Standard deviation, pg/g	0.0034
Relative standard deviation, %	68
No. of values reported	70
No. of values removed	16
No. of reported non-detects	47

2,3,7,8 TCDD



Z-score: 2,3,7,8 TCDD



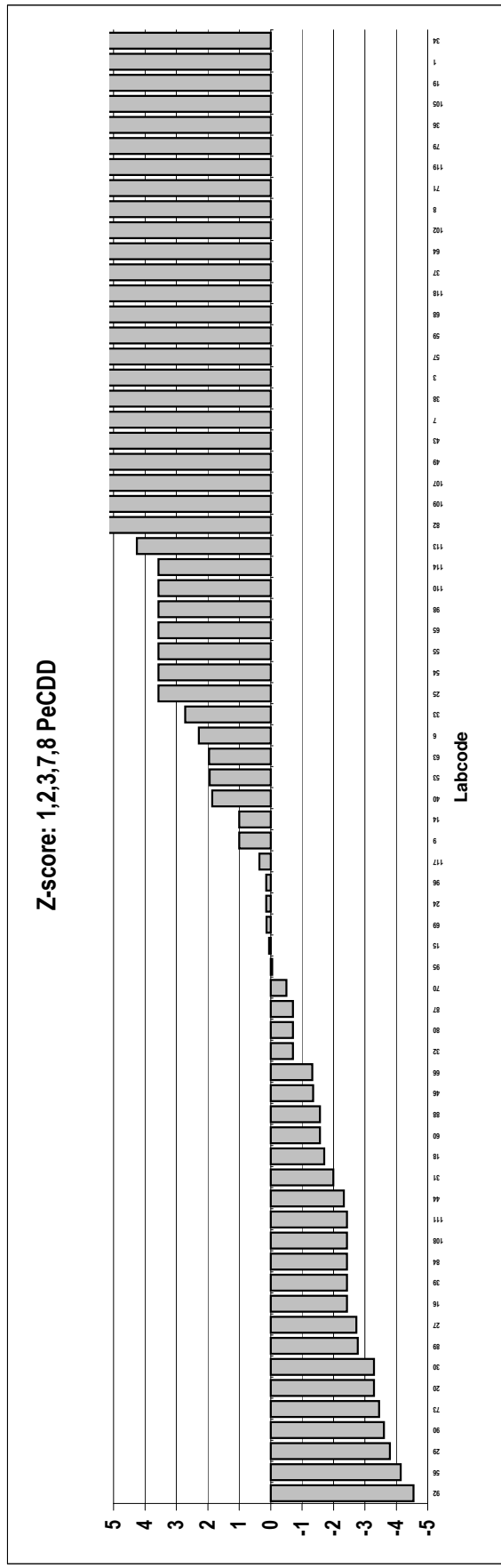
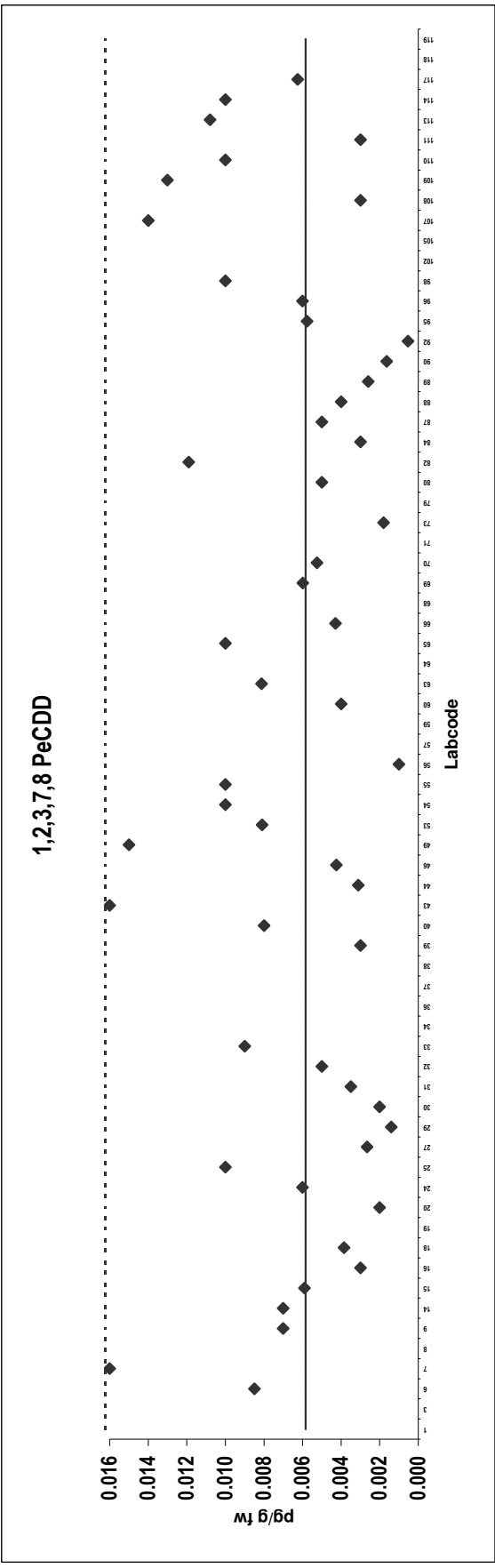
Pork

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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.094	Outlier,ND	73	0.0018	ND
3	0.020	Outlier	79	0.051	Outlier
6	0.0085	ND	80	0.0050	ND
7	0.016	ND	82	0.012	
8	0.050	Outlier,ND	84	0.0030	
9	0.0070		87	0.0050	ND
14	0.0070		88	0.0040	ND
15	0.0059	ND	89	0.0026	ND
16	0.0030	ND	90	0.0016	ND
18	0.0038		92	0.00053	ND
19	0.086	Outlier	95	0.0058	
20	0.0020	ND	96	0.0060	ND
24	0.0060	ND	98	0.010	ND
25	0.010	ND	102	0.037	Outlier
27	0.0026		105	0.086	Outlier,ND
29	0.0014		107	0.014	ND
30	0.0020	ND	108	0.0030	ND
31	0.0035		109	0.013	ND
32	0.0050	ND	110	0.010	ND
33	0.0090	ND	111	0.0030	
34	0.13	Outlier,ND	113	0.011	ND
36	0.063	Outlier	114	0.010	ND
37	0.027	Outlier,ND	117	0.0063	
38	0.018	Outlier	118	0.022	Outlier
39	0.0030	ND	119	0.050	Outlier,ND
40	0.0080				
43	0.016	ND			
44	0.0031				
46	0.0042				
49	0.015				
53	0.0081				
54	0.010				
55	0.010				
56	0.0010	ND			
57	0.020	Outlier,ND			
59	0.020	Outlier,ND			
60	0.0040				
63	0.0081	ND			
64	0.030	Outlier			
65	0.010	ND			
66	0.0043	ND			
68	0.020	Outlier,ND			
69	0.0060	ND			
70	0.0052				
71	0.050	Outlier,ND			

Consensus statistics

Consensus median, pg/g	0.0058
Median all values pg/g	0.0081
Consensus mean, pg/g	0.0065
Standard deviation, pg/g	0.0040
Relative standard deviation, %	62
No. of values reported	70
No. of values removed	18
No. of reported non-detects	42



Pork

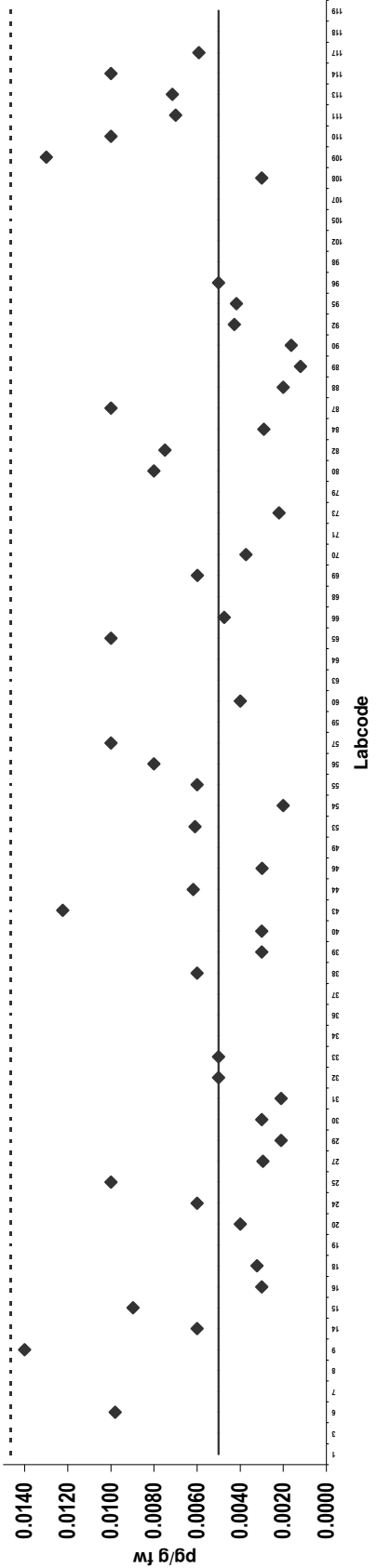
Congener: 1,2,3,4,7,8 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.053	Outlier,ND	73	0.0022	ND
3	0.020	Outlier	79	0.054	Outlier
6	0.0098	ND	80	0.0080	ND
7	0.032	Outlier,ND	82	0.0075	
8	0.022	Outlier,ND	84	0.0029	
9	0.014	ND	87	0.010	ND
14	0.0060		88	0.0020	ND
15	0.0090	ND	89	0.0012	
16	0.0030	ND	90	0.0016	ND
18	0.0032		92	0.0043	
19	0.063	Outlier	95	0.0042	
20	0.0040	ND	96	0.0050	ND
24	0.0060	ND	98	0.020	Outlier,ND
25	0.010	ND	102	0.042	Outlier
27	0.0029		105	0.061	Outlier,ND
29	0.0021		107	0.052	Outlier
30	0.0030	ND	108	0.0030	ND
31	0.0021	ND	109	0.013	ND
32	0.0050	ND	110	0.010	ND
33	0.0050	ND	111	0.0070	
34	0.12	Outlier,ND	113	0.0071	ND
36	0.026	Outlier	114	0.010	
37	0.028	Outlier,ND	117	0.0059	
38	0.0060		118	0.017	Outlier
39	0.0030	ND	119	0.050	Outlier,ND
40	0.0030	ND			
43	0.012	ND			
44	0.0062	ND			
46	0.0030				
49	0.021	Outlier			
53	0.0061				
54	0.0020				
55	0.0060				
56	0.0080				
57	0.010	ND			
59	0.020	Outlier,ND			
60	0.0040				
63	0.042	Outlier			
64	0.026	Outlier			
65	0.010	ND			
66	0.0047	ND			
68	0.020	Outlier,ND			
69	0.0060	ND			
70	0.0037	ND			
71	0.050	Outlier,ND			

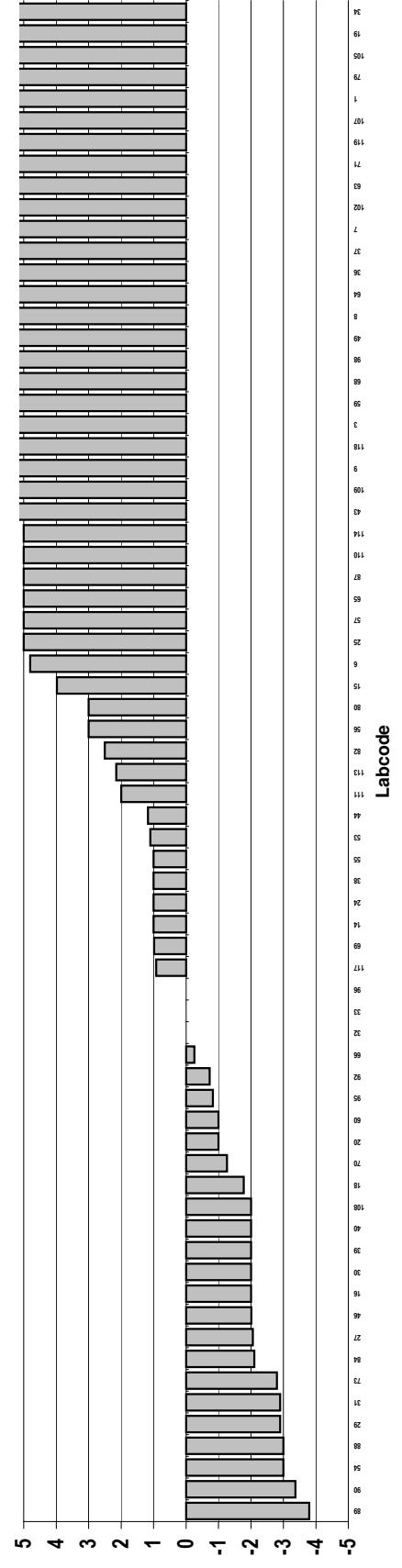
Consensus statistics

Consensus median, pg/g	0.0050
Median all values pg/g	0.0073
Consensus mean, pg/g	0.0058
Standard deviation, pg/g	0.0032
Relative standard deviation, %	56
No. of values reported	70
No. of values removed	21
No. of reported non-detects	40

1,2,3,4,7,8 HxCDD



Z-score: 1,2,3,4,7,8 HxCDD



Pork

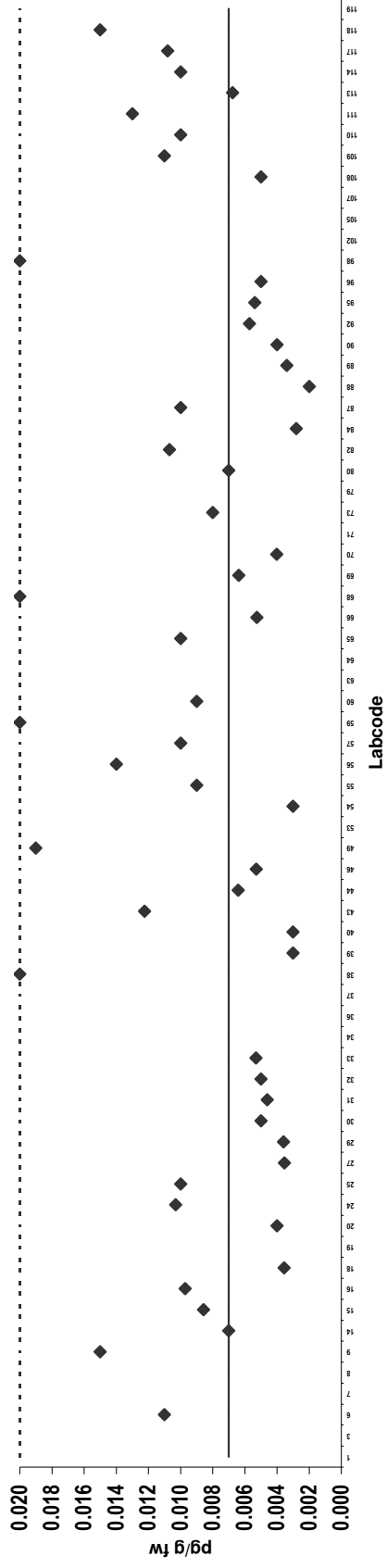
Congener: 1,2,3,6,7,8 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.057	Outlier	73	0.0080	
3	0.040	Outlier	79	0.032	Outlier
6	0.011	ND	80	0.0070	ND
7	0.032	Outlier,ND	82	0.011	
8	0.026	Outlier,ND	84	0.0028	
9	0.015	ND	87	0.010	ND
14	0.0070	ND	88	0.0020	ND
15	0.0086	ND	89	0.0034	
16	0.0097		90	0.0040	
18	0.0036		92	0.0057	
19	0.14	Outlier	95	0.0054	
20	0.0040	ND	96	0.0050	ND
24	0.010	ND	98	0.020	ND
25	0.010	ND	102	0.088	Outlier
27	0.0035		105	0.073	Outlier,ND
29	0.0036		107	0.27	Outlier
30	0.0050	ND	108	0.0050	
31	0.0046	ND	109	0.011	ND
32	0.0050	ND	110	0.010	ND
33	0.0053		111	0.013	
34	0.13	Outlier,ND	113	0.0068	ND
36	0.065	Outlier	114	0.010	
37	0.028	Outlier,ND	117	0.011	
38	0.020		118	0.015	
39	0.0030	ND	119	0.050	Outlier,ND
40	0.0030	ND			
43	0.012	ND			
44	0.0064				
46	0.0053				
49	0.019				
53	0.022	Outlier			
54	0.0030				
55	0.0090				
56	0.014				
57	0.010	ND			
59	0.020	ND			
60	0.0090				
63	0.023	Outlier			
64	0.032	Outlier			
65	0.010	ND			
66	0.0053	ND			
68	0.020	ND			
69	0.0064				
70	0.0040	ND			
71	0.050	Outlier,ND			

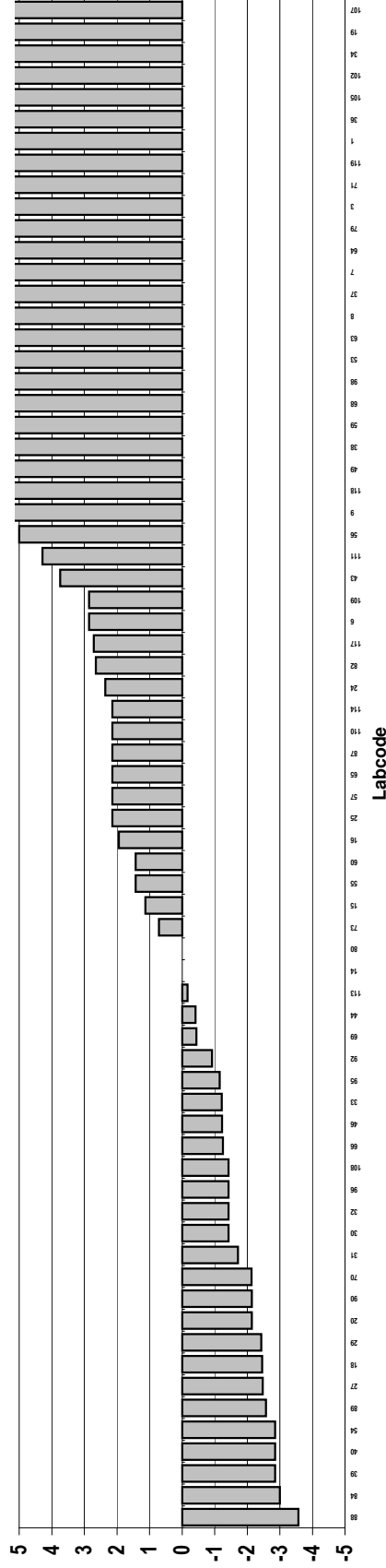
Consensus statistics

Consensus median, pg/g	0.0070
Median all values pg/g	0.010
Consensus mean, pg/g	0.0085
Standard deviation, pg/g	0.0050
Relative standard deviation, %	58
No. of values reported	70
No. of values removed	17
No. of reported non-detects	31

1,2,3,6,7,8 HxCDD



Z-score: 1,2,3,6,7,8 HxCDD



Pork

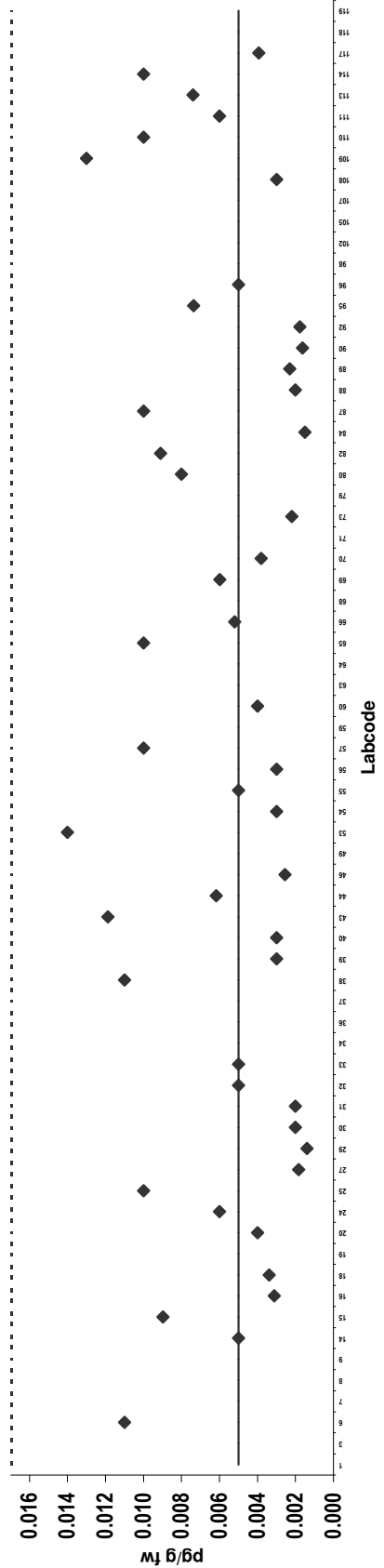
Congener: 1,2,3,7,8,9 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.052	Outlier,ND	73	0.0022	ND
3	0.030	Outlier	79	0.065	Outlier
6	0.011	ND	80	0.0080	ND
7	0.032	Outlier,ND	82	0.0091	
8	0.025	Outlier,ND	84	0.0015	
9	0.023	Outlier,ND	87	0.010	ND
14	0.0050		88	0.0020	ND
15	0.0090	ND	89	0.0023	ND
16	0.0031		90	0.0016	ND
18	0.0034		92	0.0018	
19	0.13	Outlier	95	0.0074	ND
20	0.0040	ND	96	0.0050	ND
24	0.0060	ND	98	0.020	Outlier,ND
25	0.010	ND	102	0.13	Outlier
27	0.0018		105	0.073	Outlier,ND
29	0.0014	ND	107	4.5	Outlier
30	0.0020	ND	108	0.0030	ND
31	0.0020		109	0.013	ND
32	0.0050	ND	110	0.010	ND
33	0.0050	ND	111	0.0060	
34	0.13	Outlier,ND	113	0.0074	ND
36	0.066	Outlier	114	0.010	ND
37	0.030	Outlier,ND	117	0.0039	
38	0.011		118	0.019	Outlier
39	0.0030	ND	119	0.050	Outlier,ND
40	0.0030	ND			
43	0.012	ND			
44	0.0062	ND			
46	0.0026				
49	0.028	Outlier			
53	0.014				
54	0.0030				
55	0.0050				
56	0.0030				
57	0.010	ND			
59	0.020	Outlier,ND			
60	0.0040				
63	0.025	Outlier			
64	0.051	Outlier			
65	0.010	ND			
66	0.0052	ND			
68	0.020	Outlier,ND			
69	0.0060	ND			
70	0.0038	ND			
71	0.050	Outlier,ND			

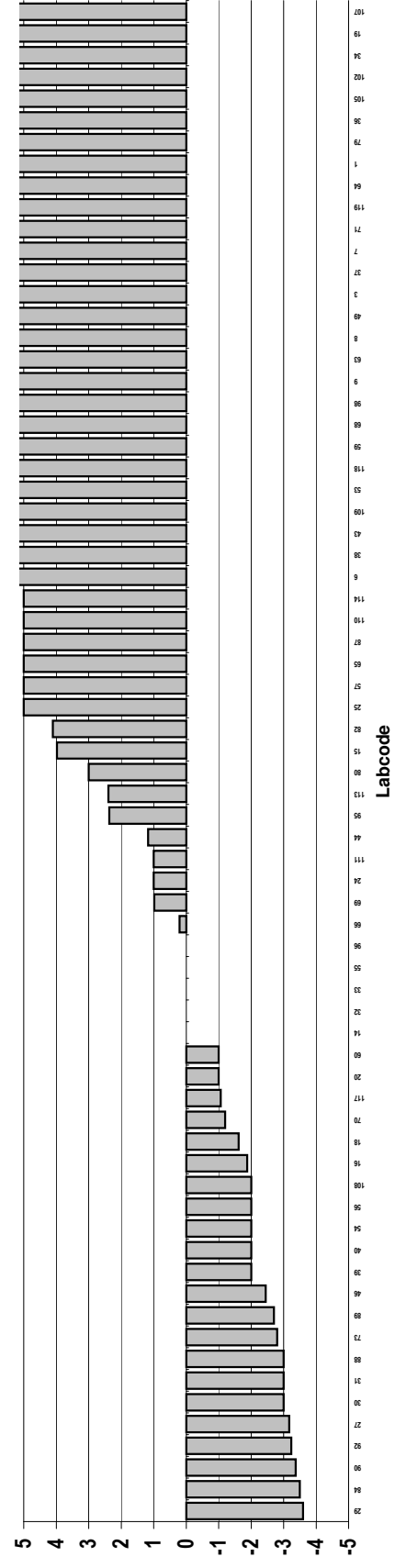
Consensus statistics

Consensus median, pg/g	0.0050
Median all values pg/g	0.0085
Consensus mean, pg/g	0.0057
Standard deviation, pg/g	0.0035
Relative standard deviation, %	62
No. of values reported	70
No. of values removed	22
No. of reported non-detects	42

1,2,3,7,8,9 HxCDD



Z-score: 1,2,3,7,8,9 HxCDD



Pork

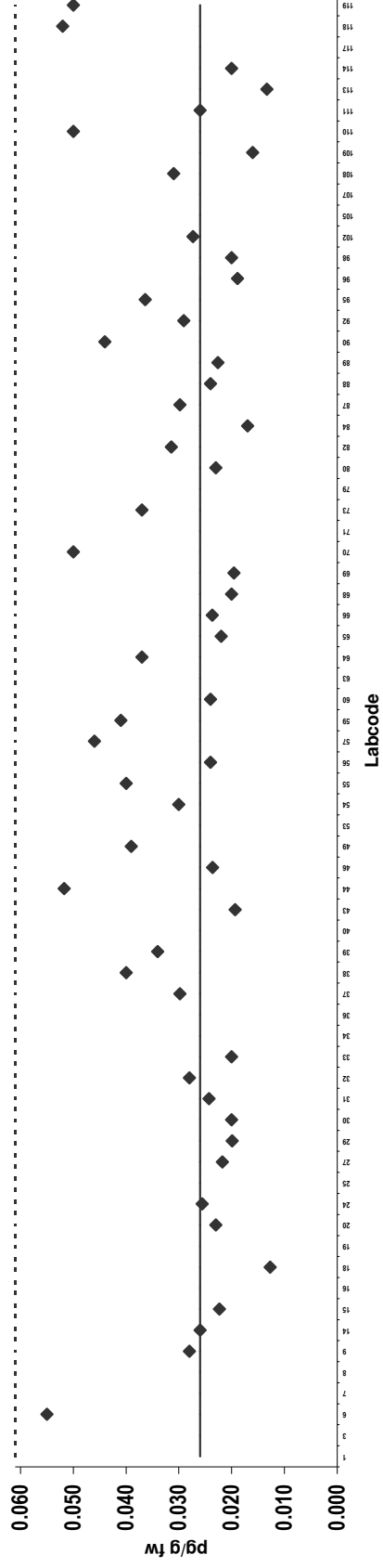
Congener: 1,2,3,4,6,7,8 HpCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.29	Outlier,ND	73	0.037	
3	0.080	Outlier	79	0.095	Outlier
6	0.055		80	0.023	
7	0.089	Outlier,ND	82	0.031	
8	0.097	Outlier	84	0.017	
9	0.028		87	0.030	
14	0.026		88	0.024	
15	0.022		89	0.023	
16	0.087	Outlier	90	0.044	
18	0.013		92	0.029	
19	0.49	Outlier	95	0.036	
20	0.023		96	0.019	
24	0.026		98	0.020	ND
25	0.096		102	0.027	
27	0.022	Outlier	105	0.10	Outlier,ND
29	0.020		107	0.079	Outlier
30	0.020	ND	108	0.031	
31	0.024		109	0.016	ND
32	0.028		110	0.050	ND
33	0.020		111	0.026	
34	0.22	ND	113	0.013	
36	0.20	Outlier	114	0.020	
37	0.030	Outlier	117	0.063	Outlier
38	0.040	ND	118	0.052	
39	0.034		119	0.050	ND
40	0.23	Outlier			
43	0.019				
44	0.052				
46	0.024				
49	0.039				
53	0.21	Outlier			
54	0.030				
55	0.040				
56	0.024				
57	0.046				
59	0.041				
60	0.024				
63	0.25	Outlier			
64	0.037				
65	0.022				
66	0.024				
68	0.020				
69	0.020				
70	0.050	Outlier,ND			
71	0.10				

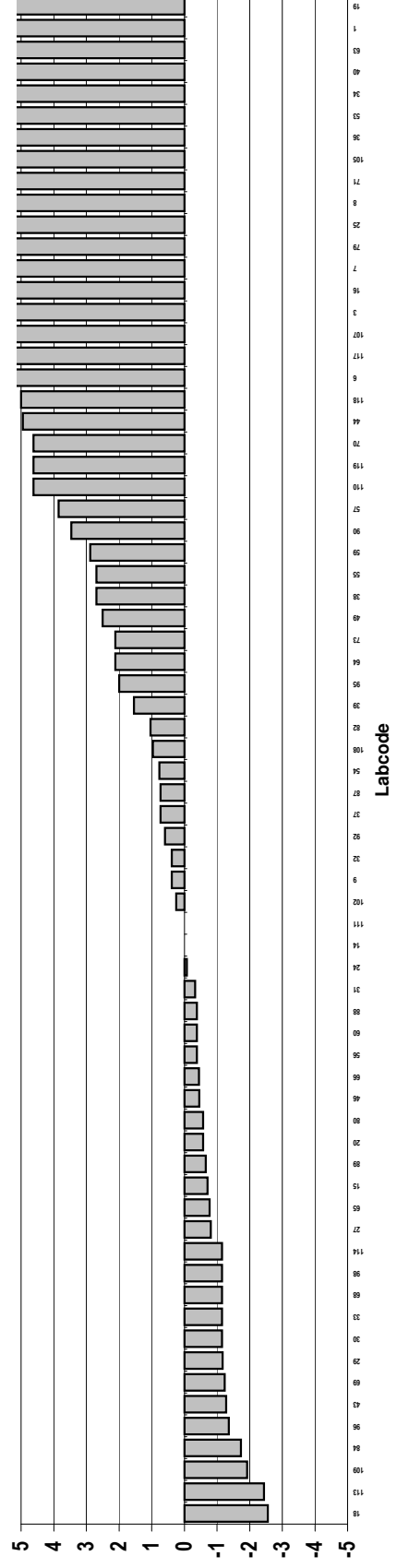
Consensus statistics

Consensus median, pg/g	0.026
Median all values pg/g	0.031
Consensus mean, pg/g	0.029
Standard deviation, pg/g	0.011
Relative standard deviation, %	37
No. of values reported	70
No. of values removed	17
No. of reported non-detects	11

1,2,3,4,6,7,8 HpCDD



Z-score: 1,2,3,4,6,7,8 HpCDD



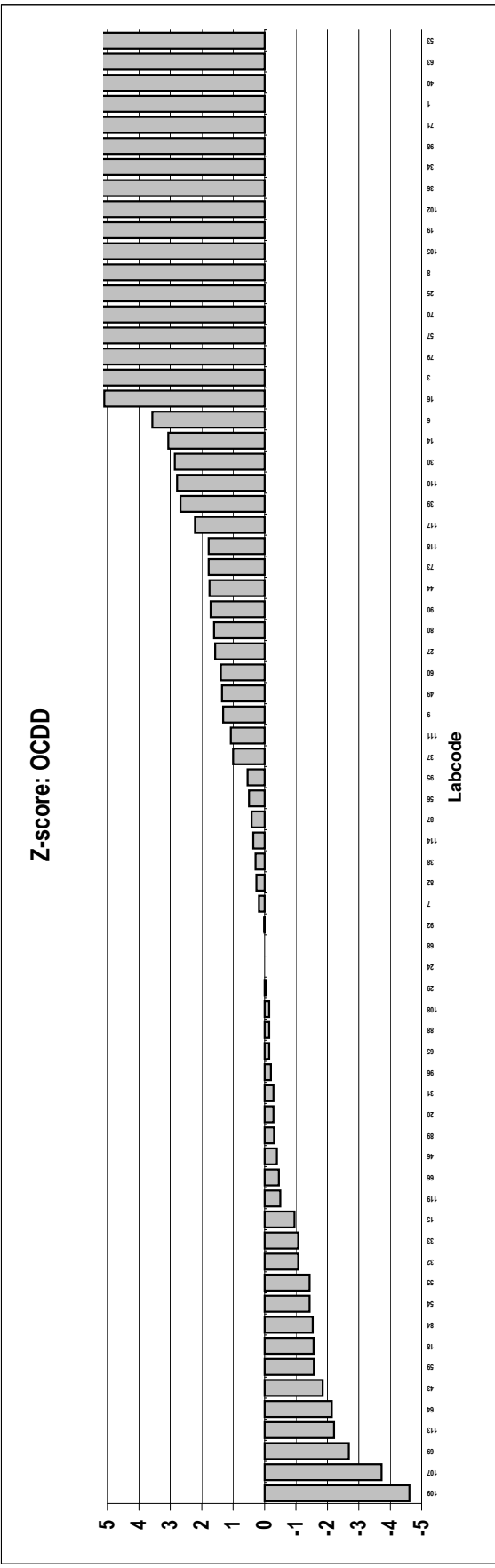
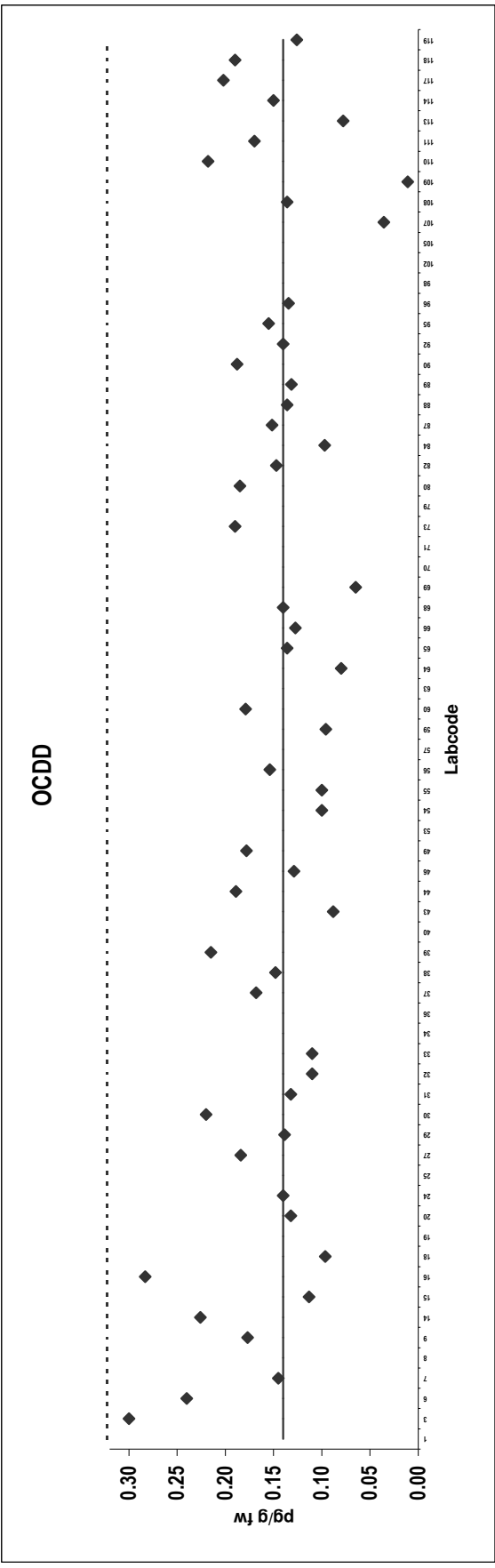
Pork

Congener: OCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	2.3	Outlier	73	0.19	
3	0.30		79	0.33	Outlier
6	0.24		80	0.19	
7	0.15	ND	82	0.15	
8	0.49	Outlier	84	0.097	
9	0.18		87	0.15	
14	0.23		88	0.14	
15	0.11		89	0.13	
16	0.28		90	0.19	
18	0.096		92	0.14	
19	0.61		95	0.16	
20	0.13	Outlier	96	0.13	
24	0.14		98	0.78	
25	0.41		102	0.64	Outlier
27	0.18	Outlier	105	0.50	Outlier
29	0.14		107	0.036	Outlier,ND
30	0.22		108	0.14	
31	0.13	ND	109	0.011	
32	0.11		110	0.22	
33	0.11		111	0.17	
34	0.71		113	0.078	
36	0.65	Outlier	114	0.15	
37	0.17	ND	117	0.20	
38	0.15		118	0.19	
39	0.22		119	0.13	
40	2.4	Outlier			
43	0.088				
44	0.19				
46	0.13				
49	0.18				
53	16				
54	0.10	Outlier			
55	0.10				
56	0.15				
57	0.33				
59	0.096	Outlier			
60	0.18				
63	6.6				
64	0.080	Outlier			
65	0.14				
66	0.13				
68	0.14				
69	0.065				
70	0.40	Outlier			
71	1.0	Outlier,ND			

Consensus statistics

Consensus median, pg/g	0.14
Median all values pg/g	0.16
Consensus mean, pg/g	0.15
Standard deviation, pg/g	0.055
Relative standard deviation, %	37
No. of values reported	70
No. of values removed	16
No. of reported non-detects	6

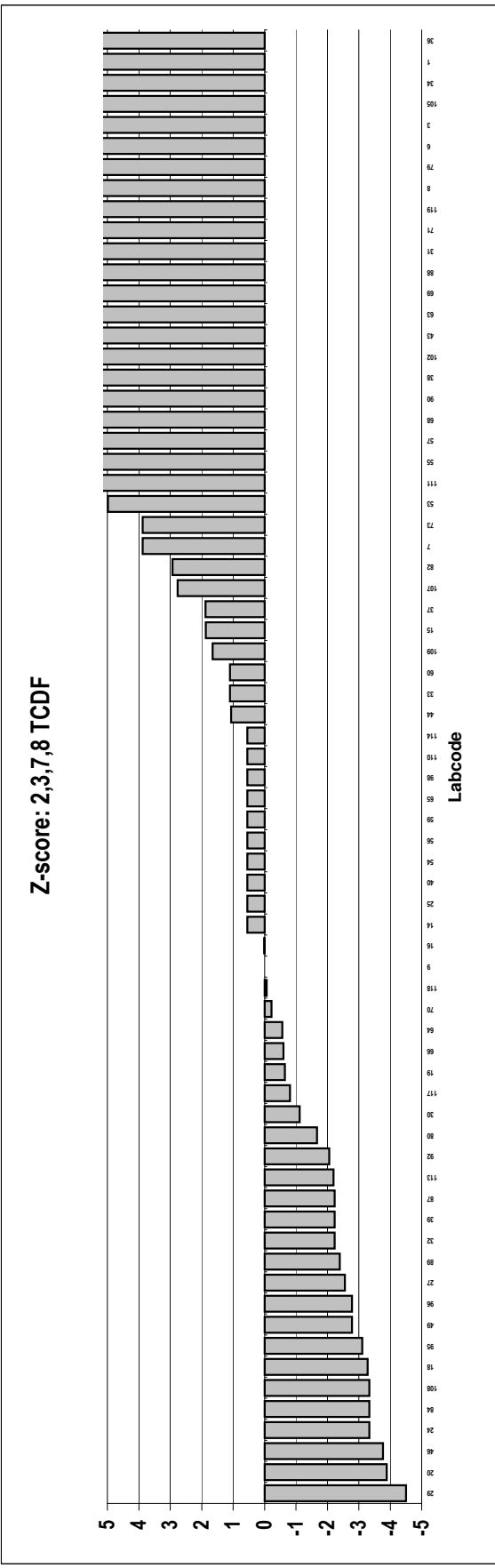
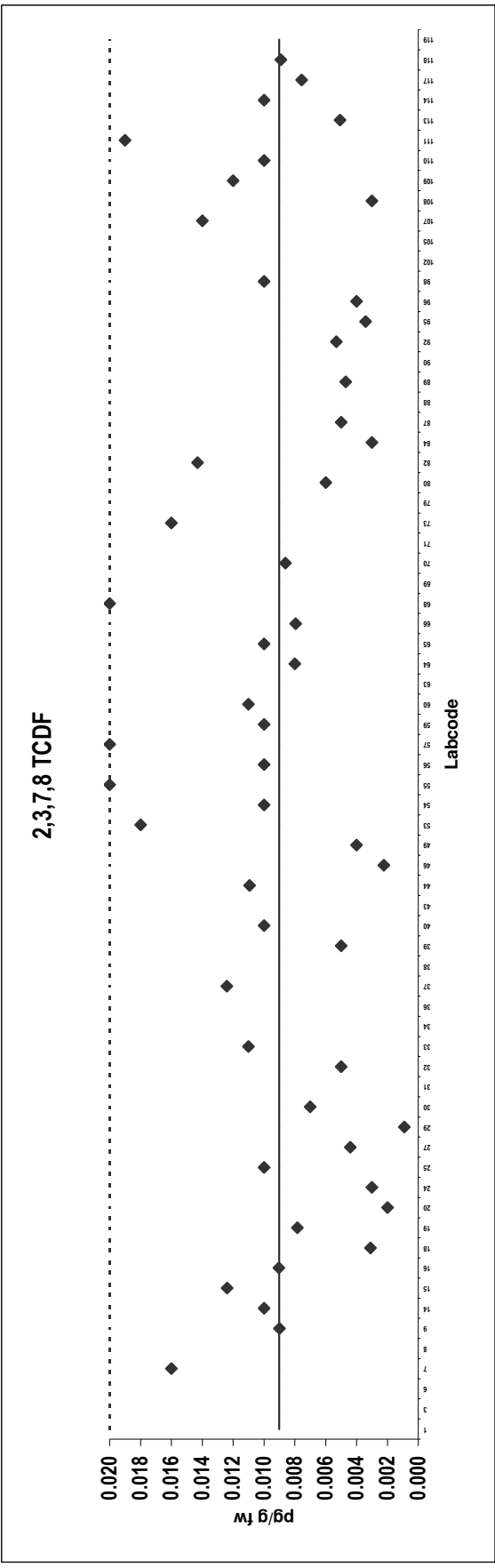


Pork
Congener: 2,3,7,8 TCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.18	Outlier	73	0.016	
3	0.070	Outlier	79	0.055	Outlier
6	0.057	Outlier	80	0.0060	ND
7	0.016	ND	82	0.014	
8	0.051	Outlier	84	0.0030	
9	0.0090		87	0.0050	ND
14	0.010		88	0.037	Outlier
15	0.012		89	0.0047	
16	0.0090		90	0.022	Outlier
18	0.0031		92	0.0053	
19	0.0078		95	0.0034	
20	0.0020	ND	96	0.0040	ND
24	0.0030	ND	98	0.010	ND
25	0.010	ND	102	0.025	Outlier
27	0.0044		105	0.074	Outlier,ND
29	0.00090		107	0.014	ND
30	0.0070	ND	108	0.0030	ND
31	0.048	Outlier	109	0.012	ND
32	0.0050	ND	110	0.010	ND
33	0.011		111	0.019	
34	0.13	Outlier,ND	113	0.0051	ND
36	0.21	Outlier	114	0.010	ND
37	0.012	ND	117	0.0076	
38	0.024	Outlier	118	0.0089	
39	0.0050	ND	119	0.050	Outlier,ND
40	0.010				
43	0.031				
44	0.011	Outlier			
46	0.0022				
49	0.0040				
53	0.018				
54	0.010				
55	0.020				
56	0.010				
57	0.020	ND			
59	0.010	ND			
60	0.011				
63	0.031	Outlier			
64	0.0080				
65	0.010	ND			
66	0.0079				
68	0.020	ND			
69	0.032	Outlier			
70	0.0086				
71	0.050	Outlier,ND			

Consensus statistics

Consensus median, pg/g	0.0090
Median all values pg/g	0.010
Consensus mean, pg/g	0.0090
Standard deviation, pg/g	0.0050
Relative standard deviation, %	55
No. of values reported	70
No. of values removed	18
No. of reported non-detects	26



Pork

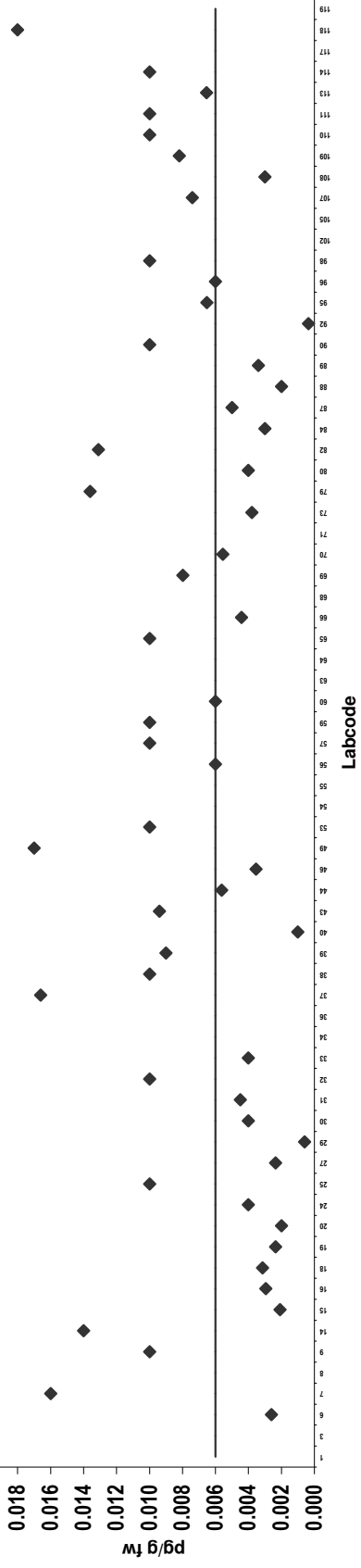
Congener: 1,2,3,7,8 PeCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.053	Outlier,ND	73	0.0038	
3	0.040	Outlier	79	0.014	
6	0.0026	ND	80	0.0040	ND
7	0.016	ND	82	0.013	
8	0.025	Outlier,ND	84	0.0030	
9	0.010	ND	87	0.0050	ND
14	0.014		88	0.0020	
15	0.0021		89	0.0034	
16	0.0029		90	0.010	
18	0.0031		92	0.00035	ND
19	0.0024	ND	95	0.0065	ND
20	0.0020	ND	96	0.0060	ND
24	0.0040	ND	98	0.010	ND
25	0.010	ND	102	0.084	Outlier
27	0.0024		105	0.074	Outlier,ND
29	0.00060	ND	107	0.0074	
30	0.0040	ND	108	0.0030	ND
31	0.0045		109	0.0082	ND
32	0.010	ND	110	0.010	ND
33	0.0040	ND	111	0.010	
34	0.13	Outlier,ND	113	0.0065	ND
36	0.045	Outlier	114	0.010	ND
37	0.017	ND	117	0.022	Outlier
38	0.010		118	0.018	
39	0.0090	ND	119	0.050	Outlier,ND
40	0.0010	ND			
43	0.0094	ND			
44	0.0056				
46	0.0035				
49	0.017				
53	0.010				
54	0.080	Outlier			
55	0.020	Outlier			
56	0.0060				
57	0.010	ND			
59	0.010	ND			
60	0.0060				
63	0.038	Outlier			
64	0.026	Outlier			
65	0.010	ND			
66	0.0044	ND			
68	0.020	Outlier,ND			
69	0.0080	ND			
70	0.0055				
71	0.050	Outlier,ND			

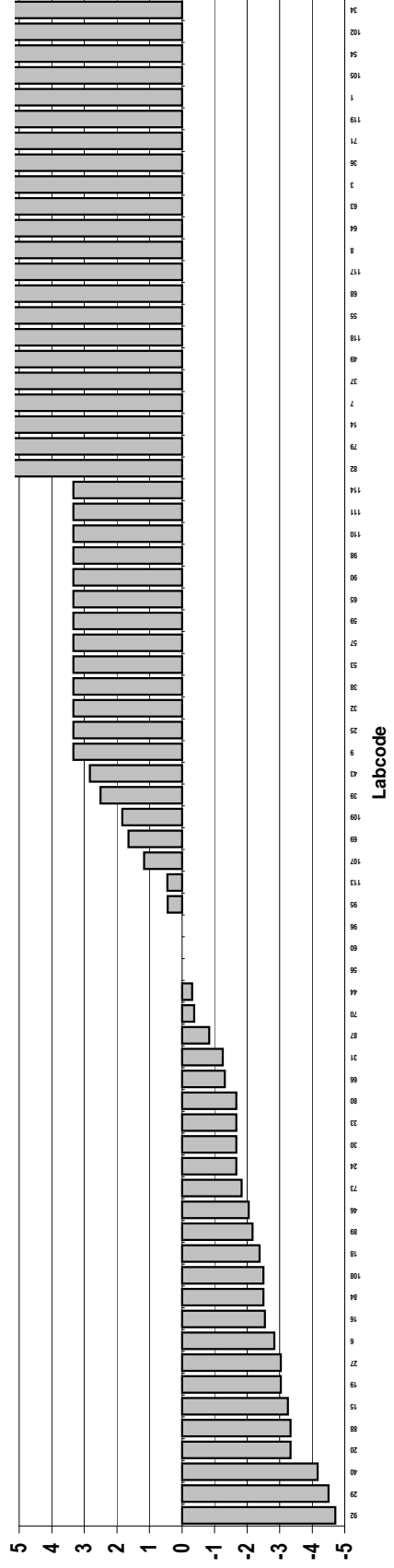
Consensus statistics

Consensus median, pg/g	0.0060
Median all values pg/g	0.010
Consensus mean, pg/g	0.0071
Standard deviation, pg/g	0.0045
Relative standard deviation, %	63
No. of values reported	70
No. of values removed	15
No. of reported non-detects	38

1,2,3,7,8 PeCDF



Z-score: 1,2,3,7,8 PeCDF



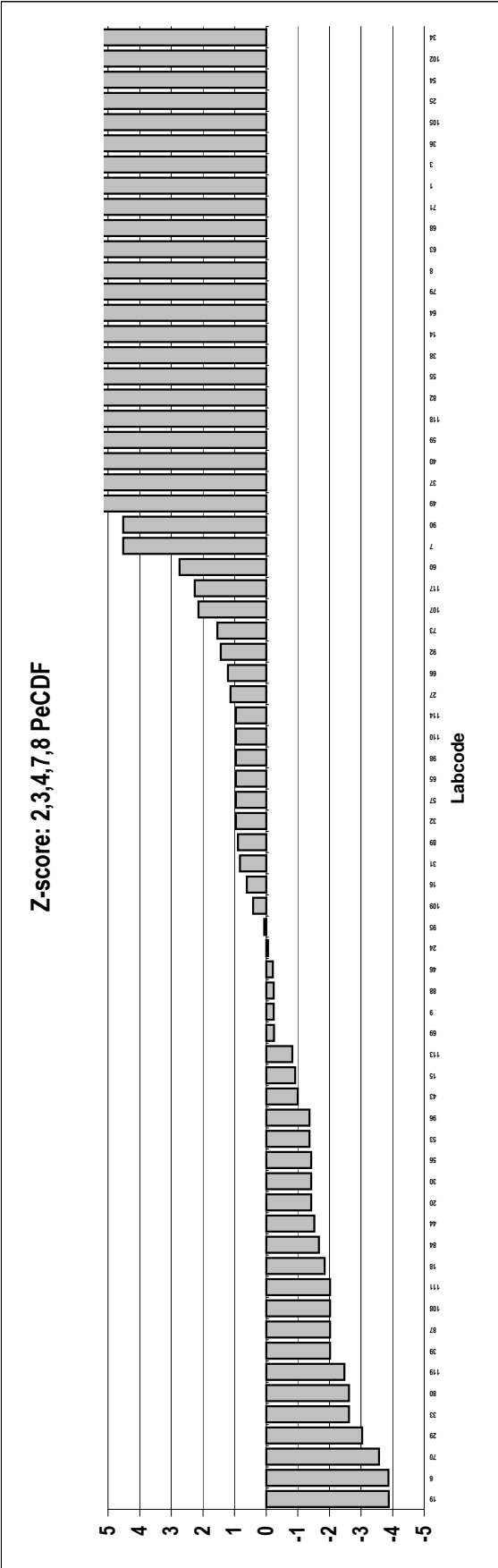
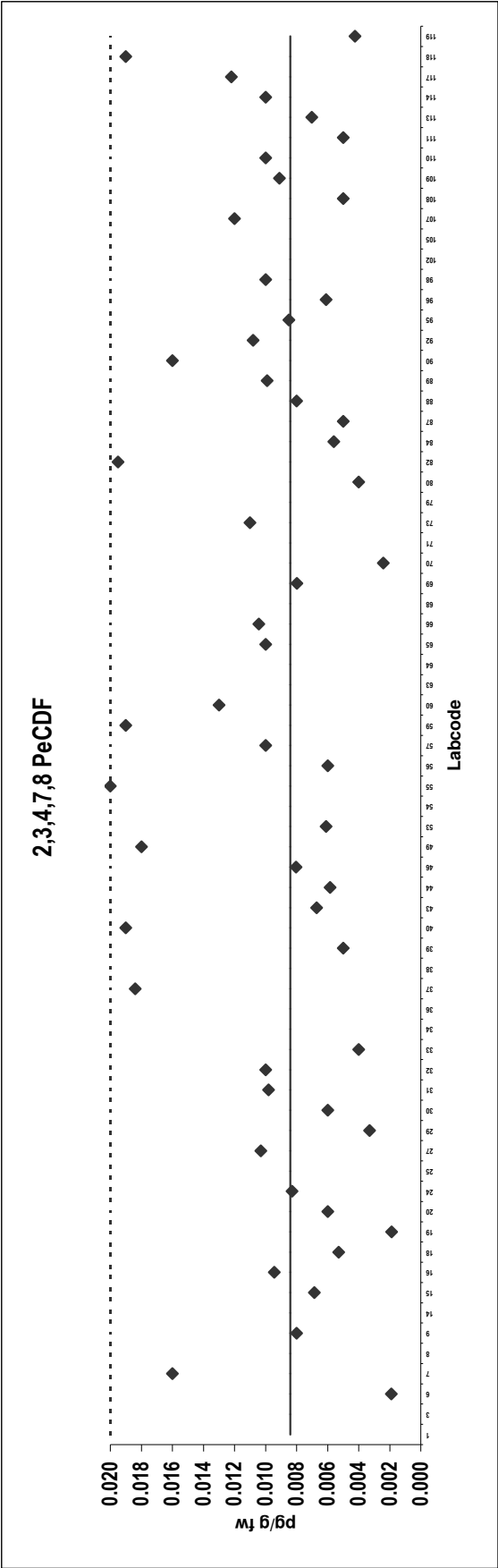
Pork

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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.054	Outlier	73	0.011	
3	0.060	Outlier	79	0.028	Outlier
6	0.0019	ND	80	0.0040	ND
7	0.016	ND	82	0.020	
8	0.039	Outlier	84	0.0056	
9	0.0080		87	0.0050	ND
14	0.025	Outlier	88	0.0080	
15	0.0069		89	0.0099	
16	0.0094		90	0.016	
18	0.0053		92	0.011	
19	0.0019	ND	95	0.0085	
20	0.0060		96	0.0061	
24	0.0083		98	0.010	ND
25	0.077	Outlier	102	0.13	Outlier
27	0.010		105	0.072	Outlier,ND
29	0.0033		107	0.012	ND
30	0.0060	ND	108	0.0050	
31	0.0098		109	0.0091	ND
32	0.010	ND	110	0.010	ND
33	0.0040	ND	111	0.0050	
34	0.14	Outlier	113	0.0070	ND
36	0.070	Outlier	114	0.010	
37	0.018	ND	117	0.012	
38	0.024	Outlier	118	0.019	
39	0.0050	ND	119	0.0042	
40	0.019				
43	0.0067	Outlier			
44	0.0058				
46	0.0080				
49	0.018				
53	0.0061				
54	0.11				
55	0.020	Outlier			
56	0.0060				
57	0.010	ND			
59	0.019				
60	0.013				
63	0.044	Outlier			
64	0.027	Outlier			
65	0.010	ND			
66	0.010				
68	0.050	Outlier			
69	0.0080	ND			
70	0.0024	ND			
71	0.050	Outlier,ND			

Consensus statistics

Consensus median, pg/g	0.0084
Median all values pg/g	0.010
Consensus mean, pg/g	0.0093
Standard deviation, pg/g	0.0049
Relative standard deviation, %	53
No. of values reported	70
No. of values removed	16
No. of reported non-detects	21



Pork

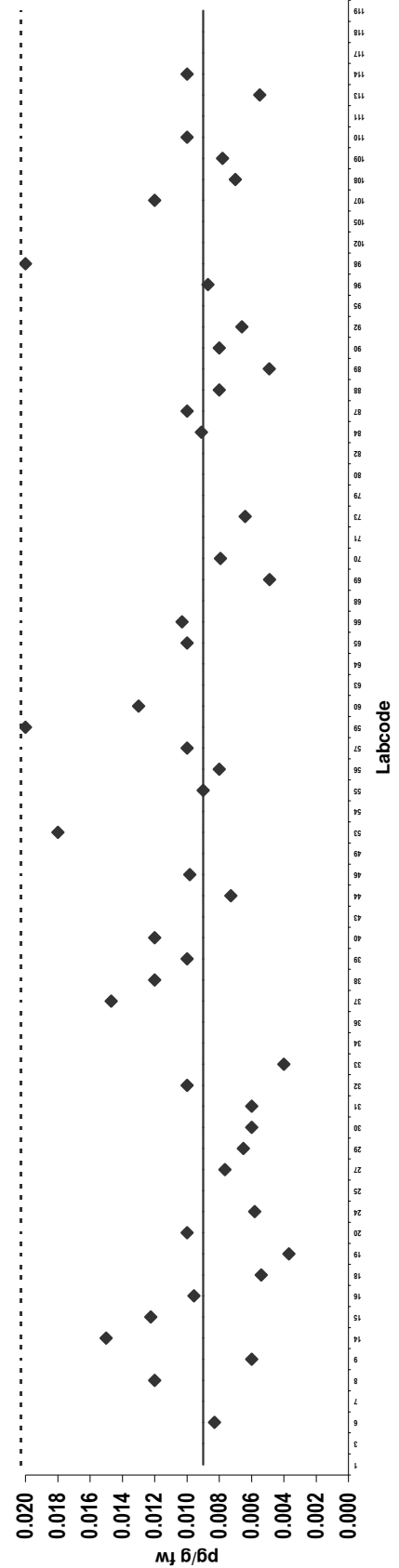
Congener: 1,2,3,4,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.042	Outlier,ND	73	0.0064	
3	0.060	Outlier	79	0.055	Outlier
6	0.0083		80	0.18	Outlier
7	0.032	Outlier,ND	82	0.027	Outlier
8	0.012	ND	84	0.0091	
9	0.0060		87	0.010	ND
14	0.015		88	0.0080	
15	0.012		89	0.0049	
16	0.0096		90	0.0080	
18	0.0054		92	0.0066	
19	0.0037	ND	95	0.024	Outlier
20	0.010		96	0.0087	
24	0.0058		98	0.020	ND
25	0.12	Outlier	102	0.045	Outlier
27	0.0076		105	0.20	Outlier,ND
29	0.0065		107	0.012	ND
30	0.0060	ND	108	0.0070	
31	0.0060		109	0.0078	ND
32	0.010		110	0.010	ND
33	0.0040	ND	111	0.021	Outlier
34	0.12	Outlier,ND	113	0.0055	ND
36	0.058	Outlier	114	0.010	
37	0.015	ND	117	0.029	Outlier
38	0.012		118	0.024	Outlier
39	0.010	ND	119	0.050	Outlier,ND
40	0.012				
43	0.034	Outlier			
44	0.0073				
46	0.0098				
49	0.022	Outlier			
53	0.018				
54	0.060	Outlier			
55	0.0090				
56	0.0080				
57	0.010	ND			
59	0.020	ND			
60	0.013				
63	0.061	Outlier			
64	0.028	Outlier			
65	0.010	ND			
66	0.010				
68	0.040	Outlier			
69	0.0049				
70	0.0079				
71	0.050	Outlier,ND			

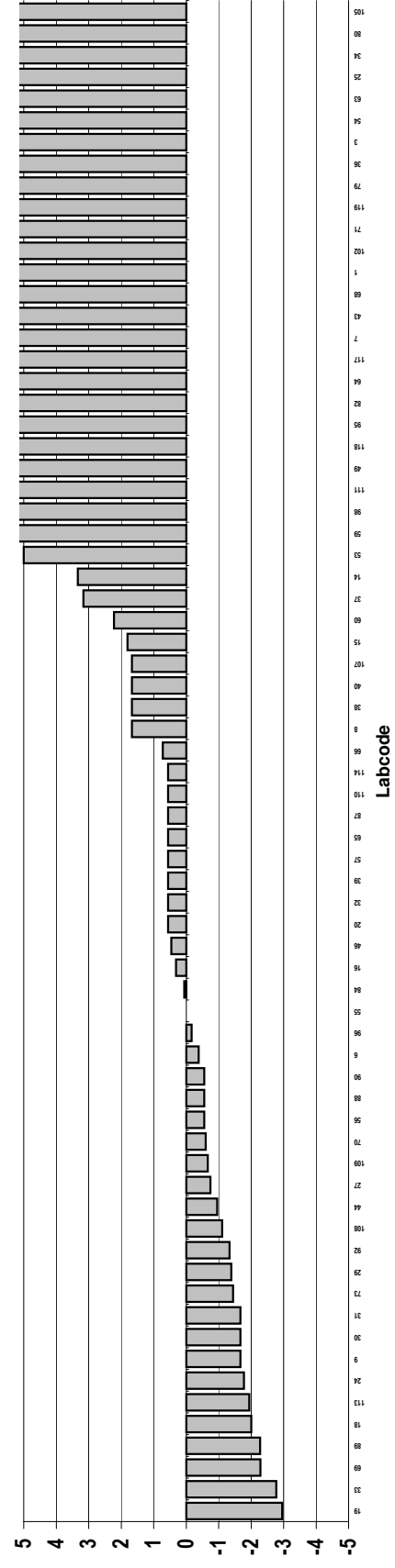
Consensus statistics

Consensus median, pg/g	0.0090
Median all values pg/g	0.010
Consensus mean, pg/g	0.0093
Standard deviation, pg/g	0.0037
Relative standard deviation, %	40
No. of values reported	70
No. of values removed	23
No. of reported non-detects	21

1,2,3,4,7,8 HxCDF



Z-score: 1,2,3,4,7,8 HxCDF



Pork

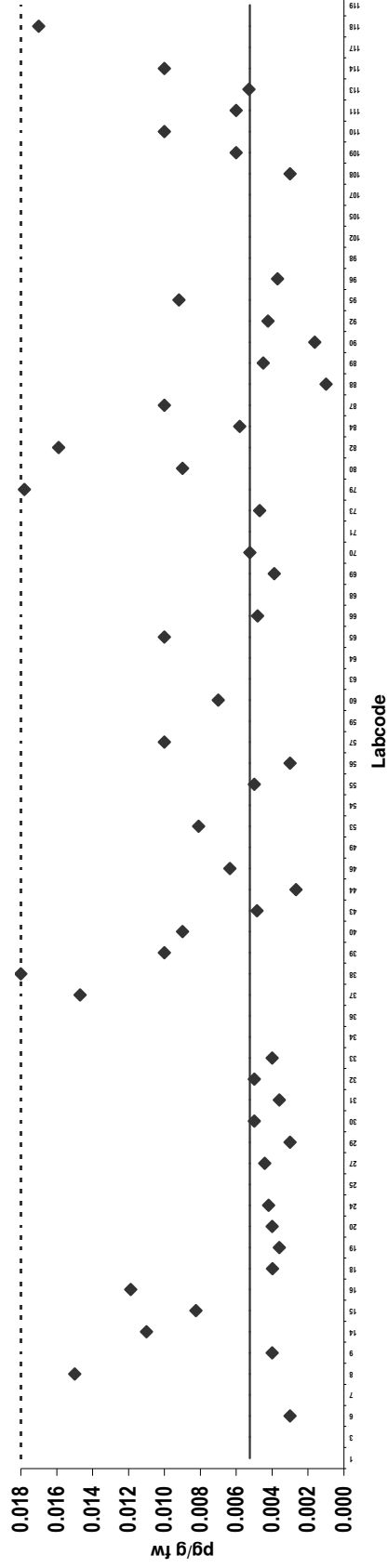
Congener: 1,2,3,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.051		73	0.0047	
3	0.080	Outlier	79	0.018	
6	0.0030	Outlier	80	0.0090	
7	0.032	ND	82	0.016	
8	0.015	Outlier,ND	84	0.0058	
9	0.0040		87	0.010	ND
14	0.011		88	0.0010	ND
15	0.0082		89	0.0045	
16	0.012		90	0.0016	ND
18	0.0040		92	0.0042	
19	0.0036	ND	95	0.0092	
20	0.0040	ND	96	0.0037	
24	0.0042		98	0.020	Outlier,ND
25	0.029	Outlier	102	0.056	Outlier
27	0.0044		105	0.058	Outlier,ND
29	0.0030		107	0.026	Outlier
30	0.0050	ND	108	0.0030	ND
31	0.0036		109	0.0060	ND
32	0.0050	ND	110	0.010	ND
33	0.0040	ND	111	0.0060	ND
34	0.13	Outlier,ND	113	0.0053	ND
36	0.067	Outlier	114	0.010	
37	0.015	ND	117	0.027	Outlier
38	0.018		118	0.017	
39	0.010	ND	119	0.050	Outlier,ND
40	0.0090				
43	0.0048				
44	0.0027				
46	0.0063				
49	0.020	Outlier			
53	0.0081				
54	0.060	Outlier			
55	0.0050				
56	0.0030				
57	0.010	ND			
59	0.020	Outlier,ND			
60	0.0070				
63	0.042	Outlier			
64	0.029	Outlier			
65	0.010	ND			
66	0.0048				
68	0.020	Outlier			
69	0.0039				
70	0.0052				
71	0.050	Outlier,ND			

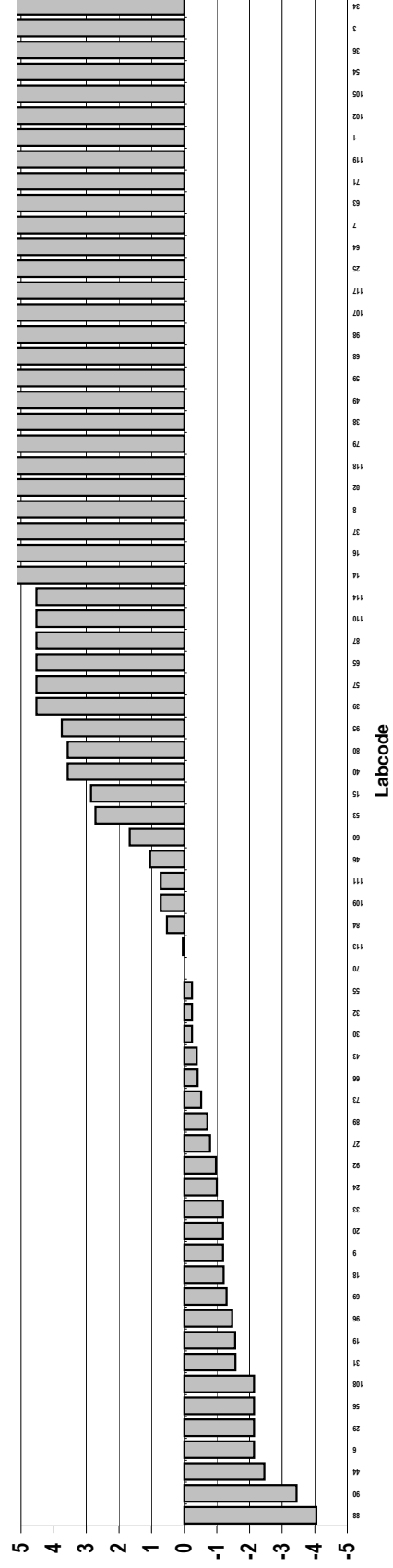
Consensus statistics

Consensus median, pg/g	0.0052
Median all values pg/g	0.0090
Consensus mean, pg/g	0.0071
Standard deviation, pg/g	0.0043
Relative standard deviation, %	61
No. of values reported	70
No. of values removed	19
No. of reported non-detects	24

1,2,3,6,7,8 HxCDF



Z-score: 1,2,3,6,7,8 HxCDF



Pork

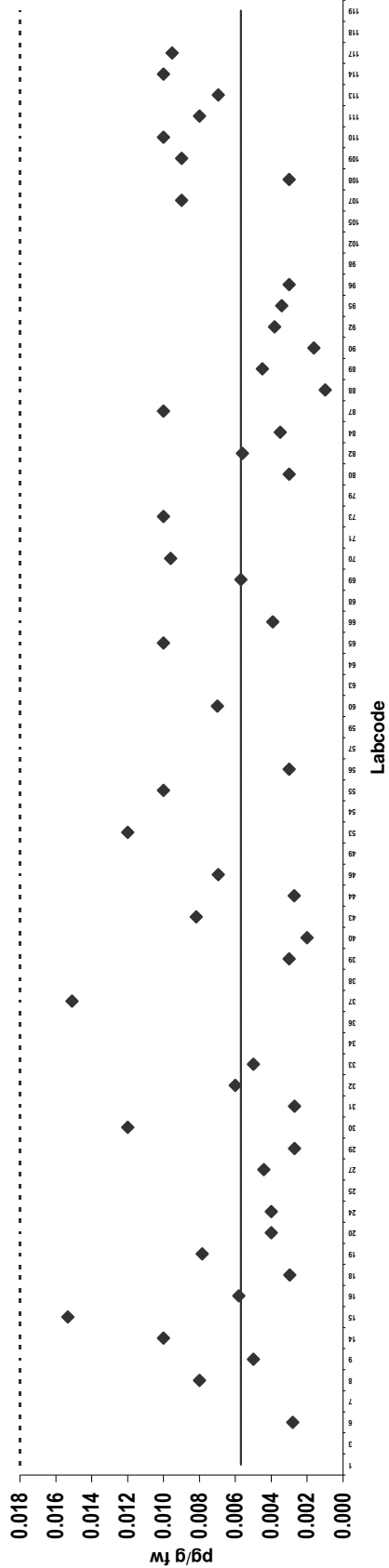
Congener: 2,3,4,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.045	Outlier,ND	73	0.010	
3	0.080	Outlier	79	0.053	Outlier
6	0.0028	ND	80	0.0030	
7	0.032	Outlier,ND	82	0.0056	
8	0.0080	ND	84	0.0035	
9	0.0050	ND	87	0.010	ND
14	0.010		88	0.0010	ND
15	0.015		89	0.0045	
16	0.0058		90	0.0016	ND
18	0.0030		92	0.0038	
19	0.0078		95	0.0034	
20	0.0040	ND	96	0.0030	ND
24	0.0040	ND	98	0.020	Outlier,ND
25	0.068	Outlier	102	0.11	Outlier
27	0.0044		105	0.10	Outlier,ND
29	0.0027		107	0.0090	ND
30	0.012	ND	108	0.0030	ND
31	0.0027		109	0.0090	ND
32	0.0060	ND	110	0.010	ND
33	0.0050	ND	111	0.0080	
34	0.12	Outlier,ND	113	0.0070	ND
36	0.047	Outlier	114	0.010	ND
37	0.015	ND	117	0.0095	
38	0.020	Outlier	118	0.031	Outlier
39	0.0030	ND	119	0.050	Outlier,ND
40	0.0020	ND			
43	0.0082	ND			
44	0.0027				
46	0.0069				
49	0.019	Outlier			
53	0.012				
54	0.030	Outlier			
55	0.010				
56	0.0030				
57	0.049	Outlier			
59	0.020	Outlier,ND			
60	0.0070				
63	0.052	Outlier			
64	0.026	Outlier			
65	0.010	ND			
66	0.0039				
68	0.020	Outlier,ND			
69	0.0057				
70	0.0096				
71	0.050	Outlier,ND			

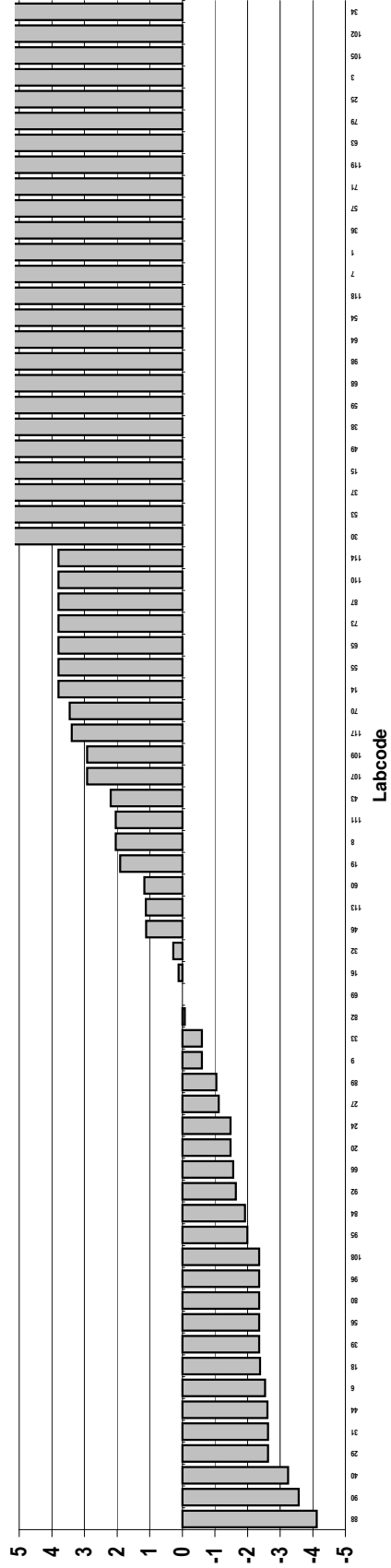
Consensus statistics

Consensus median, pg/g	0.0057
Median all values pg/g	0.0090
Consensus mean, pg/g	0.0064
Standard deviation, pg/g	0.0035
Relative standard deviation, %	56
No. of values reported	70
No. of values removed	21
No. of reported non-detects	32

2,3,4,6,7,8 HxCDF



Z-score: 2,3,4,6,7,8 HxCDF



Pork

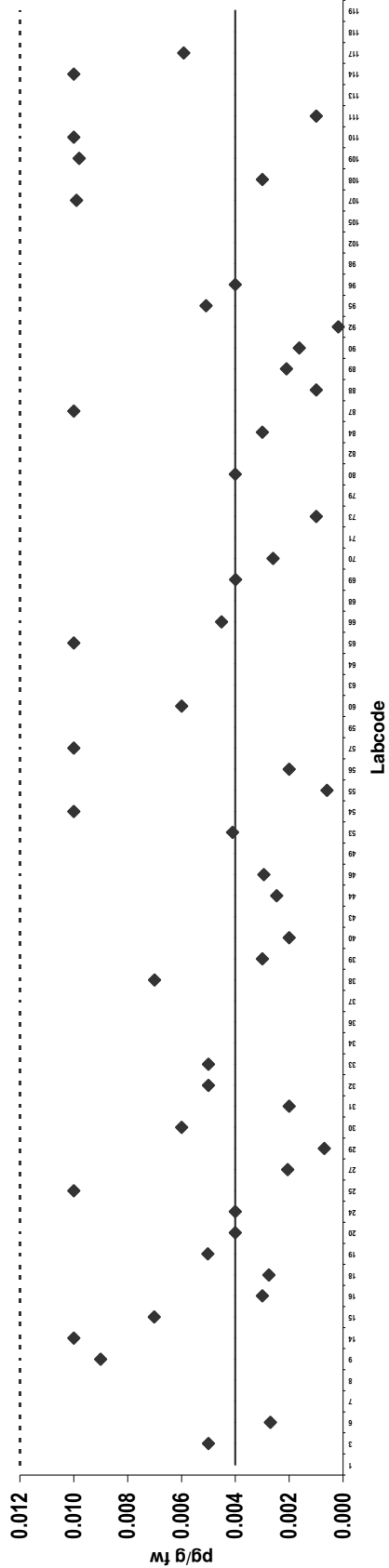
Congener: 1,2,3,7,8,9 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.061	Outlier,ND	73	0.0010	ND
3	0.0050	ND	79	0.054	Outlier
6	0.0027	ND	80	0.0040	ND
7	0.032	Outlier,ND	82	0.016	Outlier
8	0.022	Outlier,ND	84	0.0030	
9	0.0090	ND	87	0.010	ND
14	0.010	ND	88	0.0010	ND
15	0.0070	ND	89	0.0021	
16	0.0030	ND	90	0.0016	ND
18	0.0028	ND	92	0.00018	ND
19	0.0050	ND	95	0.0051	ND
20	0.0040	ND	96	0.0040	ND
24	0.0040	ND	98	0.020	Outlier,ND
25	0.010	ND	102	0.46	Outlier
27	0.0021	ND	105	0.10	Outlier,ND
29	0.00070	ND	107	0.0099	
30	0.0060	ND	108	0.0030	ND
31	0.0020	ND	109	0.0098	ND
32	0.0050	ND	110	0.010	ND
33	0.0050	ND	111	0.0010	
34	0.13	Outlier,ND	113	0.015	Outlier,ND
36	0.023	Outlier	114	0.010	ND
37	0.019	Outlier,ND	117	0.0059	
38	0.0070		118	0.061	Outlier
39	0.0030	ND	119	0.050	Outlier,ND
40	0.0020	ND			
43	0.014	Outlier,ND			
44	0.0025	ND			
46	0.0029				
49	0.024	Outlier			
53	0.0041				
54	0.010				
55	0.00060	ND			
56	0.0020	ND			
57	0.010	ND			
59	0.020	Outlier,ND			
60	0.0060	ND			
63	0.039	Outlier			
64	0.044	Outlier			
65	0.010	ND			
66	0.0045	ND			
68	0.020	Outlier,ND			
69	0.0040	ND			
70	0.0026	ND			
71	0.050	Outlier,ND			

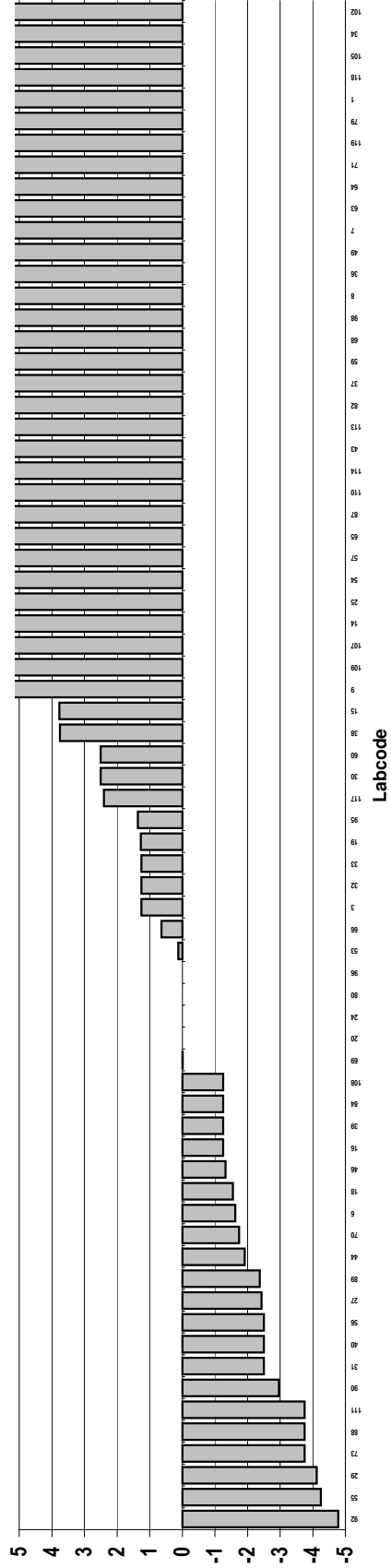
Consensus statistics

Consensus median, pg/g	0.0040
Median all values pg/g	0.0060
Consensus mean, pg/g	0.0048
Standard deviation, pg/g	0.0032
Relative standard deviation, %	66
No. of values reported	70
No. of values removed	21
No. of reported non-detects	49

1,2,3,7,8,9 HxCDF



Z-score: 1,2,3,7,8,9 HxCDF



Pork

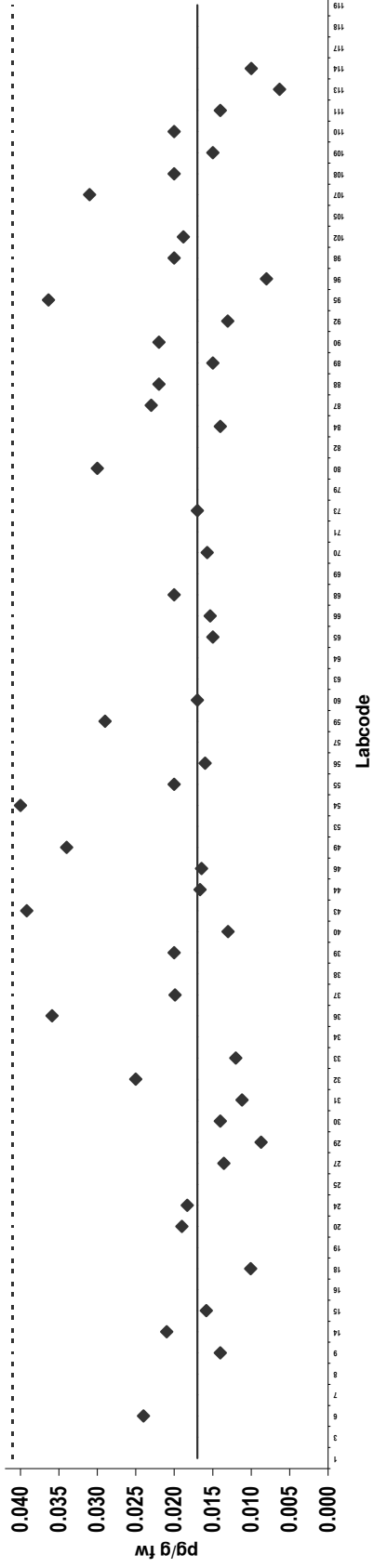
Congener: 1,2,3,4,6,7,8 HpCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.16		73	0.017	
3	0.080	Outlier	79	0.086	Outlier
6	0.024	Outlier	80	0.030	ND
7	0.089	Outlier,ND	82	0.043	Outlier
8	0.051	Outlier	84	0.014	
9	0.014		87	0.023	
14	0.021		88	0.022	
15	0.016		89	0.015	
16	0.074		90	0.022	
18	0.010	Outlier	92	0.013	
19	0.078	Outlier	95	0.036	
20	0.019		96	0.0080	
24	0.018		98	0.020	ND
25	0.17	Outlier	102	0.019	ND
27	0.014		105	0.50	Outlier,ND
29	0.0087		107	0.031	ND
30	0.014	ND	108	0.020	
31	0.011		109	0.015	ND
32	0.025		110	0.020	ND
33	0.012		111	0.014	
34	0.16	Outlier,ND	113	0.0063	
36	0.036		114	0.010	
37	0.020	ND	117	0.083	Outlier
38	0.062	Outlier	118	0.044	Outlier
39	0.020	ND	119	0.050	Outlier,ND
40	0.013				
43	0.039				
44	0.017				
46	0.016				
49	0.034				
53	0.045	Outlier			
54	0.040				
55	0.020				
56	0.016				
57	0.092	Outlier			
59	0.029				
60	0.017				
63	0.079	Outlier			
64	0.29	Outlier			
65	0.015				
66	0.015				
68	0.020				
69	0.047	Outlier			
70	0.016				
71	0.20	Outlier,ND			

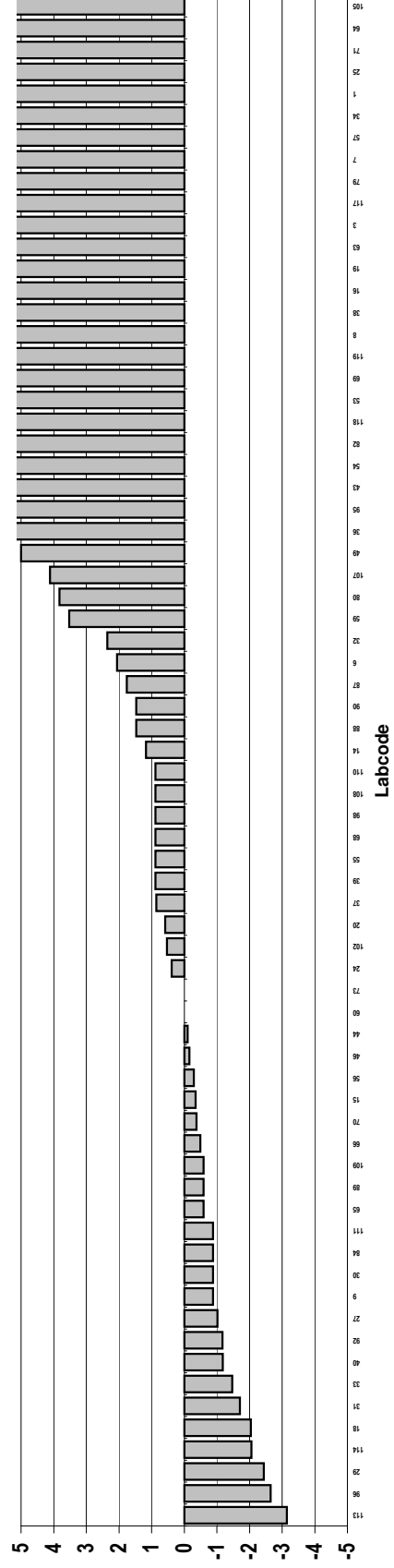
Consensus statistics

Consensus median, pg/g	0.017
Median all values pg/g	0.021
Consensus mean, pg/g	0.019
Standard deviation, pg/g	0.0080
Relative standard deviation, %	42
No. of values reported	70
No. of values removed	21
No. of reported non-detects	14

1,2,3,4,6,7,8 HpCDF



Z-score: 1,2,3,4,6,7,8 HpCDF



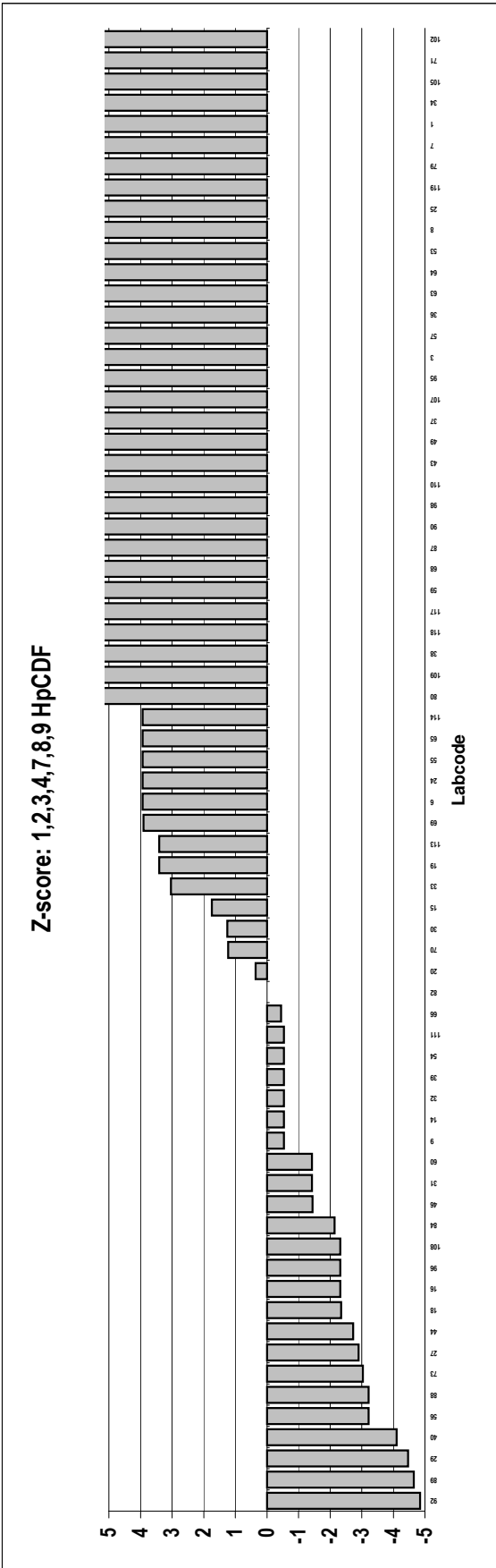
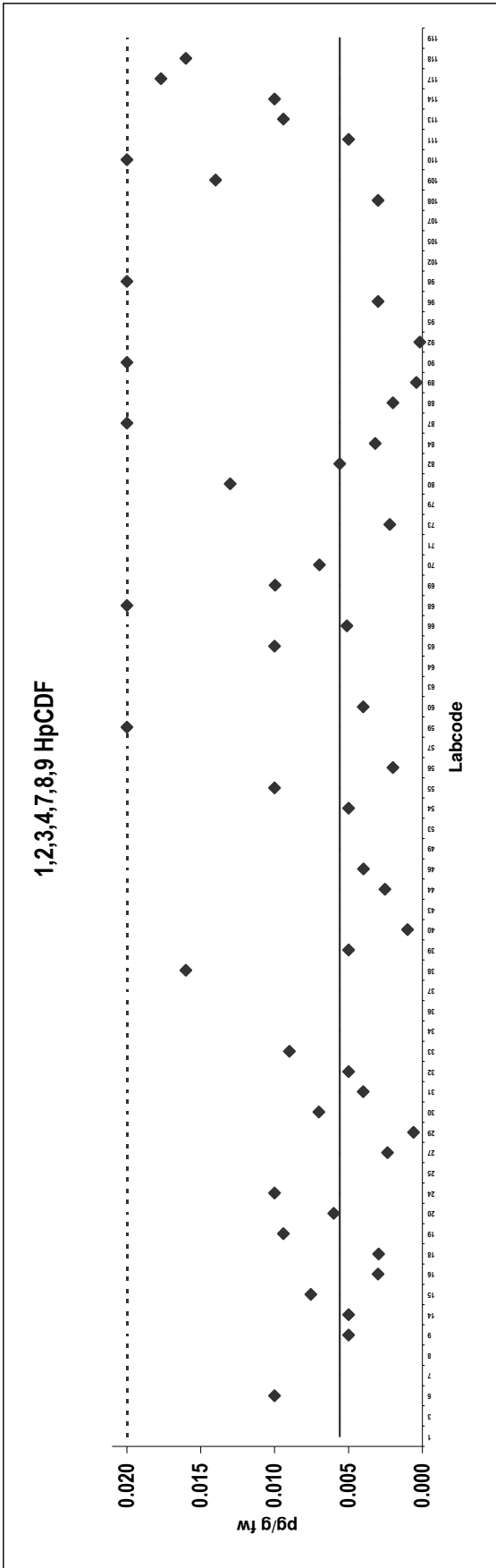
Pork

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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.094	Outlier,ND	73	0.0022	
3	0.030	Outlier	79	0.065	Outlier
6	0.010	ND	80	0.013	ND
7	0.089	Outlier,ND	82	0.0056	
8	0.048	Outlier,ND	84	0.0032	
9	0.0050	ND	87	0.020	ND
14	0.0050	ND	88	0.0020	ND
15	0.0076	ND	89	0.00040	ND
16	0.0030	ND	90	0.020	
18	0.0030	ND	92	0.00018	ND
19	0.0094	ND	95	0.030	Outlier
20	0.0060	ND	96	0.0030	ND
24	0.010	ND	98	0.020	ND
25	0.050	Outlier,ND	102	0.43	Outlier
27	0.0024		105	0.15	Outlier,ND
29	0.00060		107	0.029	Outlier,ND
30	0.0070	ND	108	0.0030	ND
31	0.0040	ND	109	0.014	ND
32	0.0050	ND	110	0.020	ND
33	0.0090	ND	111	0.0050	
34	0.13	Outlier,ND	113	0.0094	ND
36	0.037	Outlier	114	0.010	ND
37	0.028	Outlier,ND	117	0.018	
38	0.016		118	0.016	
39	0.0050	ND	119	0.050	Outlier,ND
40	0.0010	ND			
43	0.025	Outlier			
44	0.0025				
46	0.0040				
49	0.027	Outlier			
53	0.047	Outlier			
54	0.0050				
55	0.010				
56	0.0020				
57	0.035	Outlier			
59	0.020	ND			
60	0.0040	ND			
63	0.043	Outlier			
64	0.045	Outlier			
65	0.010	ND			
66	0.0051	ND			
68	0.020	ND			
69	0.010	ND			
70	0.0070	ND			
71	0.20	Outlier,ND			

Consensus statistics

Consensus median, pg/g	0.0056
Median all values pg/g	0.010
Consensus mean, pg/g	0.0080
Standard deviation, pg/g	0.0061
Relative standard deviation, %	77
No. of values reported	70
No. of values removed	21
No. of reported non-detects	41

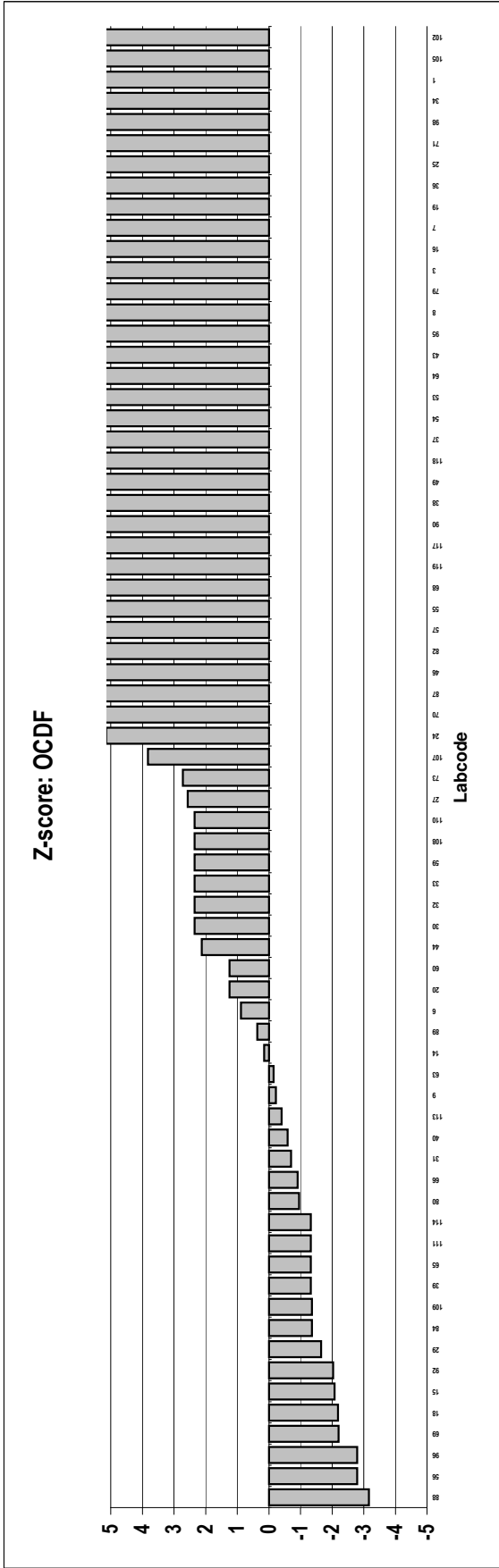
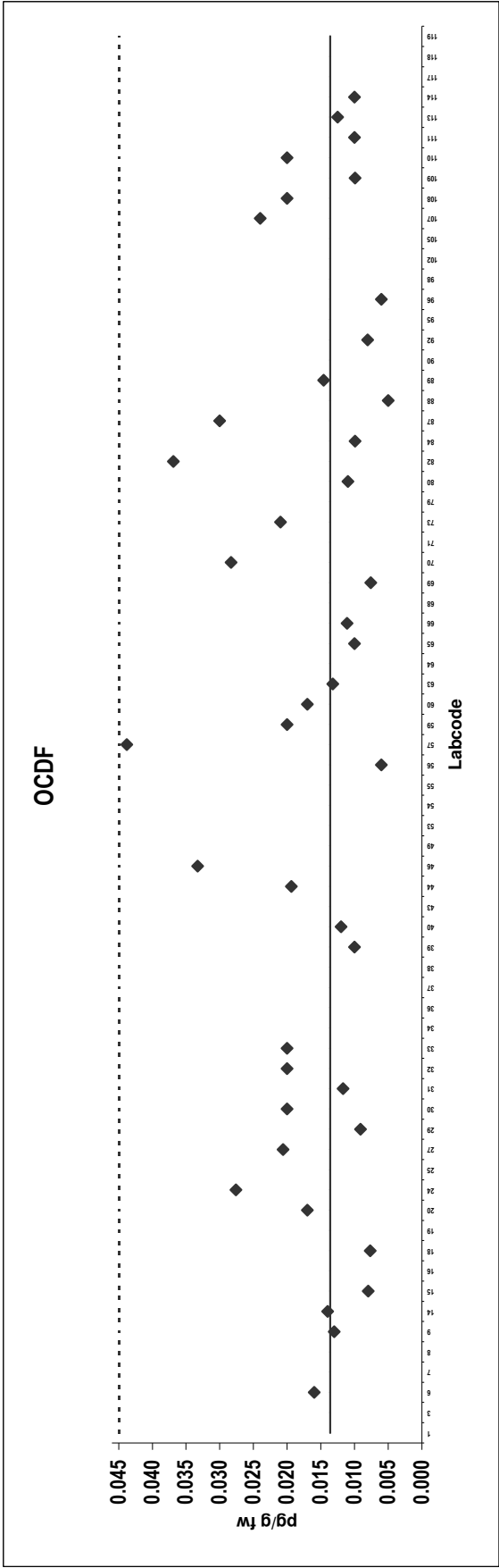


Pork
Congener: OCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.37	Outlier	73	0.021	
3	0.12	Outlier	79	0.12	Outlier
6	0.016		80	0.011	ND
7	0.15	Outlier,ND	82	0.037	
8	0.12	Outlier,ND	84	0.0099	
9	0.013	ND	87	0.030	ND
14	0.014		88	0.0050	
15	0.0080		89	0.015	
16	0.14	Outlier	90	0.060	Outlier
18	0.0077		92	0.0081	
19	0.16	Outlier	95	0.11	Outlier
20	0.017		96	0.0060	ND
24	0.028		98	0.22	Outlier
25	0.20	Outlier	102	0.78	Outlier
27	0.021		105	0.50	Outlier,ND
29	0.0091		107	0.024	ND
30	0.020	ND	108	0.020	ND
31	0.012		109	0.0099	ND
32	0.020	ND	110	0.020	ND
33	0.020	ND	111	0.010	
34	0.28	Outlier	113	0.013	ND
36	0.19	Outlier	114	0.010	
37	0.080	Outlier,ND	117	0.053	Outlier
38	0.071	Outlier	118	0.076	Outlier
39	0.010	ND	119	0.050	Outlier,ND
40	0.012				
43	0.10	Outlier			
44	0.019				
46	0.033				
49	0.074	Outlier			
53	0.085	Outlier			
54	0.080	Outlier			
55	0.050	Outlier			
56	0.0060				
57	0.044				
59	0.020	ND			
60	0.017				
63	0.013	ND			
64	0.085	Outlier			
65	0.010	ND			
66	0.011				
68	0.050	Outlier,ND			
69	0.0076				
70	0.028				
71	0.20	Outlier,ND			

Consensus statistics

Consensus median, pg/g	0.014
Median all values pg/g	0.023
Consensus mean, pg/g	0.016
Standard deviation, pg/g	0.0088
Relative standard deviation, %	54
No. of values reported	70
No. of values removed	28
No. of reported non-detects	22



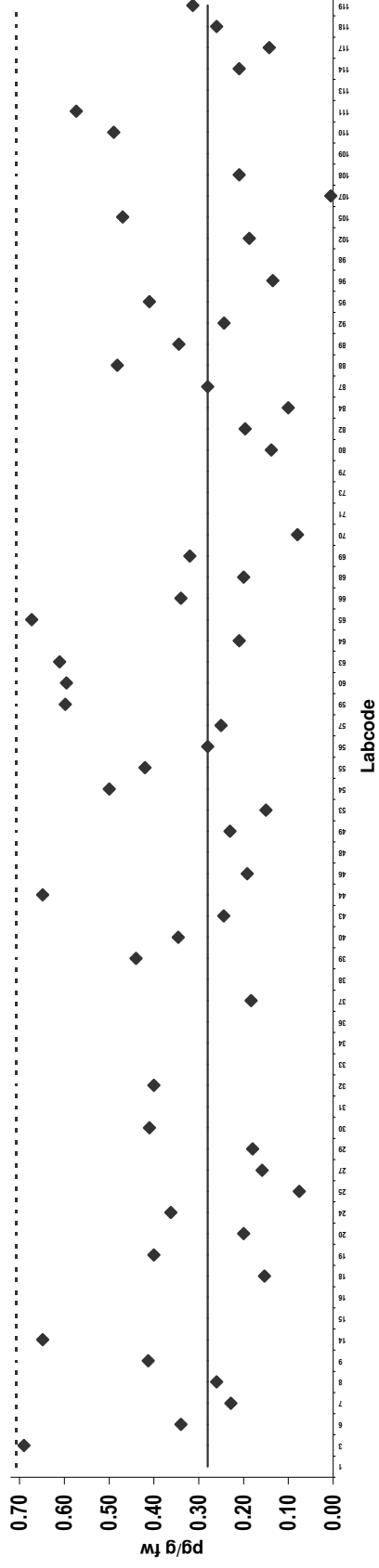
Pork
Congener: PCB 77

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	2.6	Outlier	71	2.0	Outlier,ND
3	0.69		73	1.1	Outlier
6	0.34		79	1.8	Outlier
7	0.23		80	0.14	
8	0.26		82	0.20	
9	0.41		84	0.10	
14	0.65		87	0.28	
15	1.8	Outlier	88	0.48	
16	2.4	Outlier	89	0.34	
18	0.15		92	0.24	
19	0.40		95	0.41	
20	0.20		96	0.13	
24	0.36		98	1.9	Outlier
25	0.076		102	0.19	
27	0.16		105	0.47	
29	0.18		107	0.0050	
30	0.41		108	0.21	
31	1.7	Outlier	109	3.9	Outlier
32	0.40		110	0.49	
33	0.73	Outlier	111	0.57	
34	1.0	Outlier,ND	113	1.5	Outlier,ND
36	3.9	Outlier	114	0.21	
37	0.18		117	0.14	
38	1.0	Outlier	118	0.26	
39	0.44		119	0.31	
40	0.35				
43	0.24				
44	0.65				
46	0.19				
48	0.82	Outlier			
49	0.23				
53	0.15				
54	0.50				
55	0.42				
56	0.28				
57	0.25				
59	0.60				
60	0.60				
63	0.61				
64	0.21				
65	0.67				
66	0.34				
68	0.20				
69	0.32				
70	0.080				

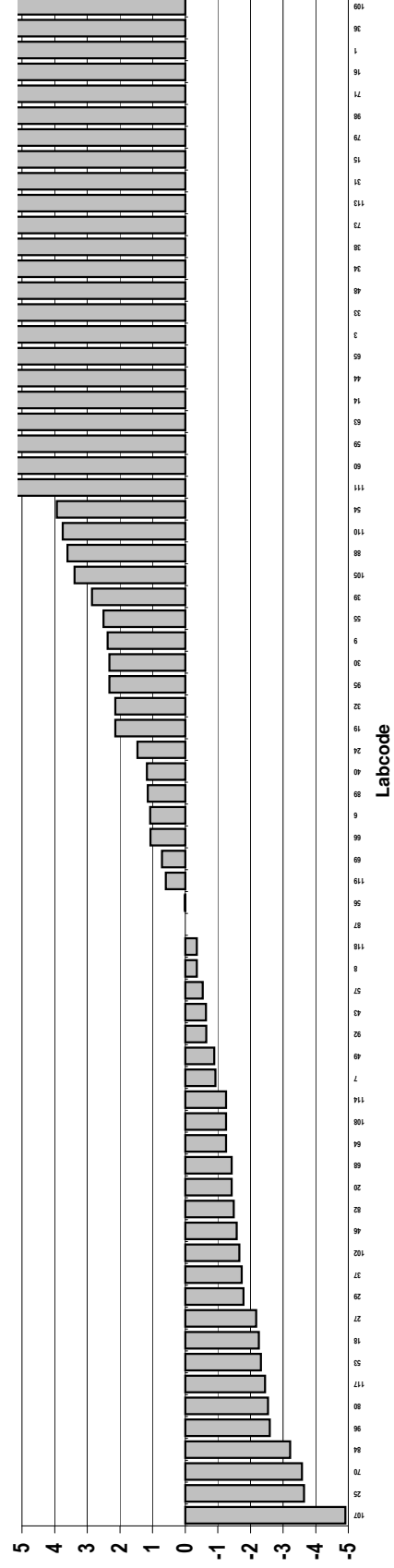
Consensus statistics

Consensus median, pg/g	0.28
Median all values pg/g	0.35
Consensus mean, pg/g	0.32
Standard deviation, pg/g	0.17
Relative standard deviation, %	54
No. of values reported	70
No. of values removed	15
No. of reported non-detects	3

PCB 77



Z-score: PCB 77



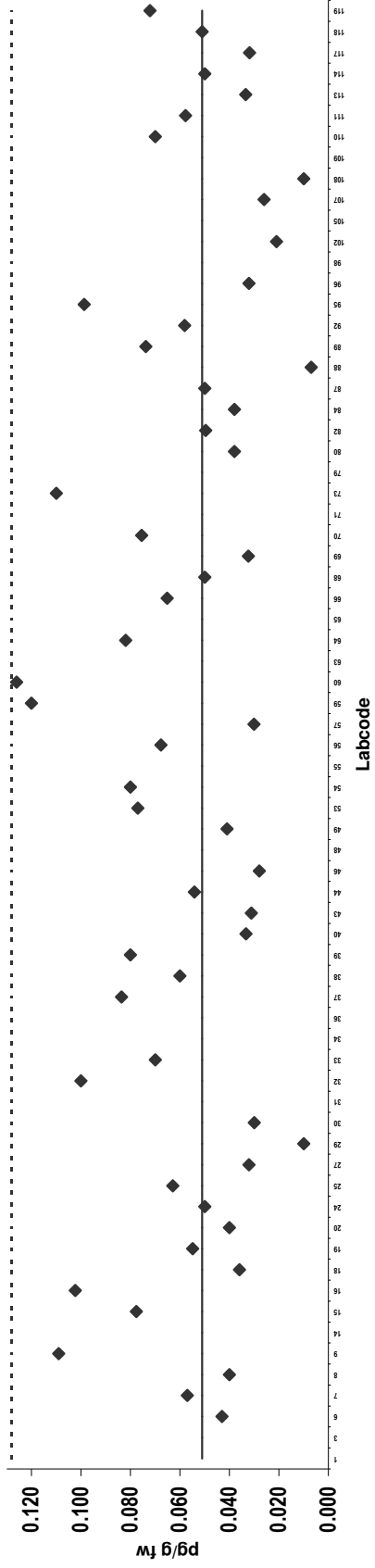
Pork
Congener: PCB 126

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.9	Outlier,ND	71	2.0	Outlier,ND
3	0.19	Outlier	73	0.11	
6	0.043		79	0.59	Outlier
7	0.057	ND	80	0.038	
8	0.040		82	0.050	
9	0.11		84	0.038	
14	0.16	Outlier	87	0.050	ND
15	0.078		88	0.0070	
16	0.10		89	0.074	
18	0.036		92	0.058	
19	0.055		95	0.099	ND
20	0.040		96	0.032	
24	0.050	ND	98	0.94	Outlier
25	0.063		102	0.021	
27	0.032		105	0.37	Outlier,ND
29	0.010	ND	107	0.026	ND
30	0.030	ND	108	0.010	ND
31	0.26	Outlier	109	0.20	Outlier,ND
32	0.10		110	0.070	
33	0.070	ND	111	0.058	
34	1.8	Outlier,ND	113	0.033	
36	0.33	Outlier	114	0.050	
37	0.084	ND	117	0.032	
38	0.060		118	0.051	
39	0.080		119	0.072	
40	0.033				
43	0.031				
44	0.054				
46	0.028				
48	0.30	Outlier,ND			
49	0.041				
53	0.077				
54	0.080				
55	0.16				
56	0.068	Outlier			
57	0.030				
59	0.12				
60	0.13				
63	0.19	Outlier,ND			
64	0.082				
65	0.21	Outlier			
66	0.065	ND			
68	0.050	ND			
69	0.032				
70	0.075	ND			

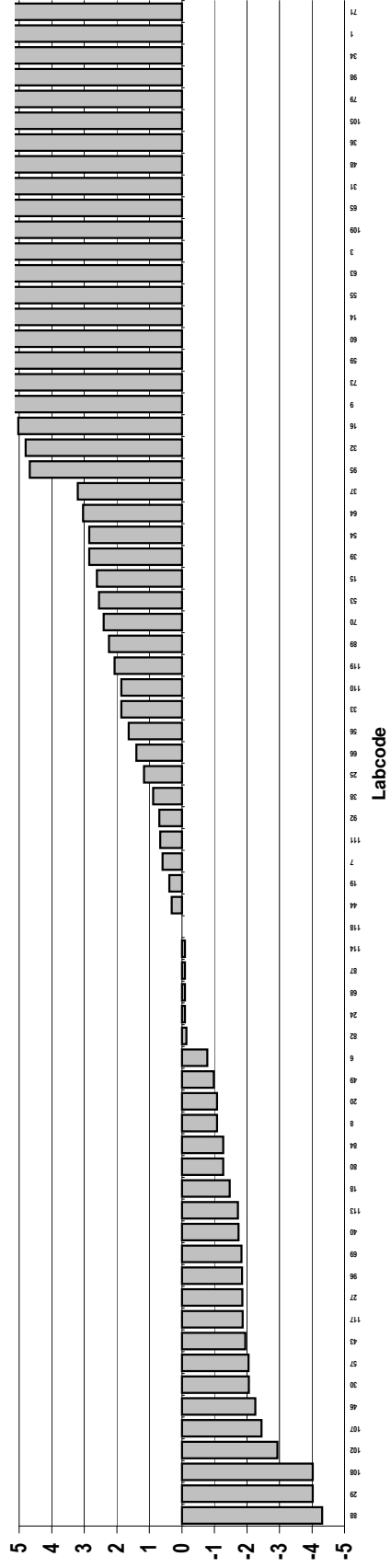
Consensus statistics

Consensus median, pg/g	0.051
Median all values pg/g	0.064
Consensus mean, pg/g	0.057
Standard deviation, pg/g	0.028
Relative standard deviation, %	50
No. of values reported	70
No. of values removed	15
No. of reported non-detects	20

PCB 126



Z-score: PCB 126



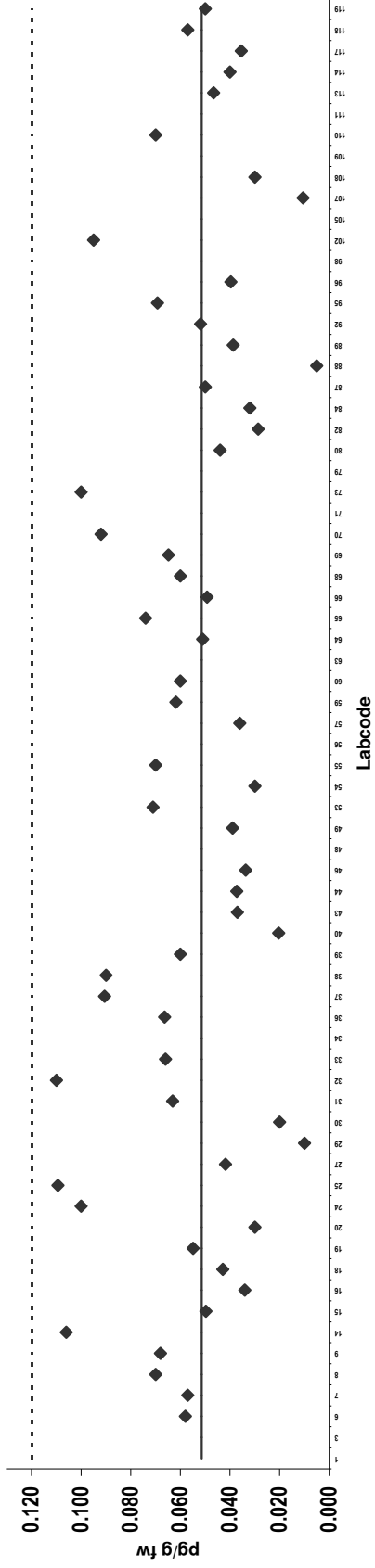
Pork
Congener: PCB 169

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.9	Outlier,ND	71	2.0	Outlier,ND
3	0.19	Outlier	73	0.10	
6	0.058		79	0.36	Outlier
7	0.057	ND	80	0.044	
8	0.070		82	0.029	
9	0.068		84	0.032	
14	0.11		87	0.050	ND
15	0.050		88	0.0050	
16	0.034		89	0.039	
18	0.043		92	0.052	
19	0.055		95	0.069	ND
20	0.030		96	0.040	
24	0.10	ND	98	0.57	Outlier
25	0.11		102	0.095	
27	0.042		105	0.44	Outlier,ND
29	0.010		107	0.011	
30	0.020	ND	108	0.030	
31	0.063		109	0.38	Outlier
32	0.11		110	0.070	
33	0.066		111	0.16	Outlier
34	1.6	Outlier,ND	113	0.047	
36	0.066		114	0.040	
37	0.091	ND	117	0.036	
38	0.090		118	0.057	
39	0.060	ND	119	0.050	ND
40	0.020				
43	0.037				
44	0.037				
46	0.034				
48	0.40	Outlier,ND			
49	0.039				
53	0.071				
54	0.030				
55	0.070				
56	0.14	Outlier			
57	0.036				
59	0.062				
60	0.060	Outlier,ND			
63	0.26				
64	0.051				
65	0.074	ND			
66	0.049				
68	0.060				
69	0.065				
70	0.092	ND			

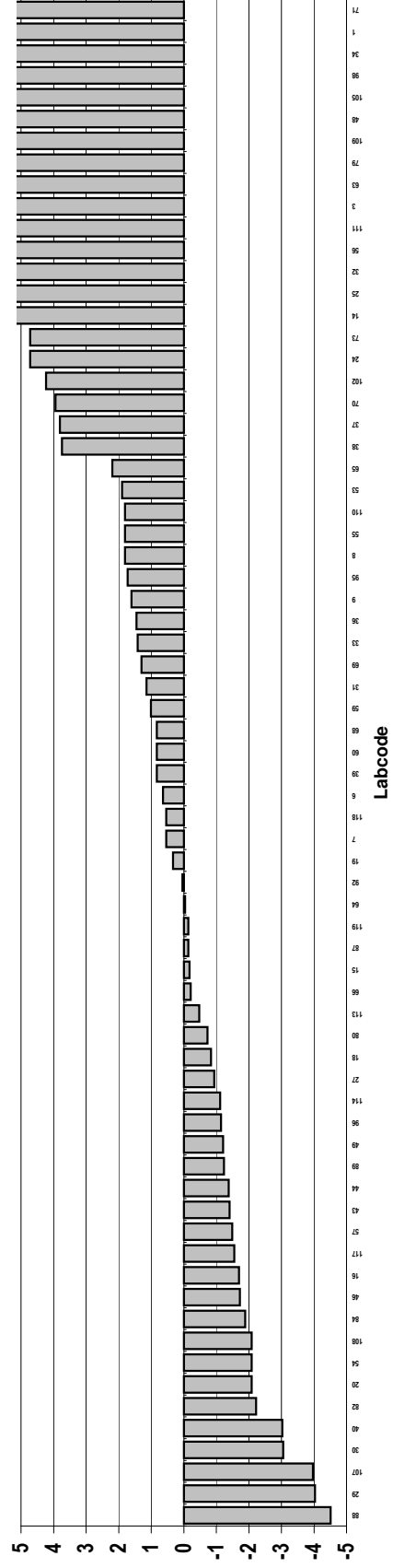
Consensus statistics

Consensus median, pg/g	0.051
Median all values pg/g	0.060
Consensus mean, pg/g	0.055
Standard deviation, pg/g	0.025
Relative standard deviation, %	46
No. of values reported	70
No. of values removed	12
No. of reported non-detects	16

PCB 169



Z-score: PCB 169



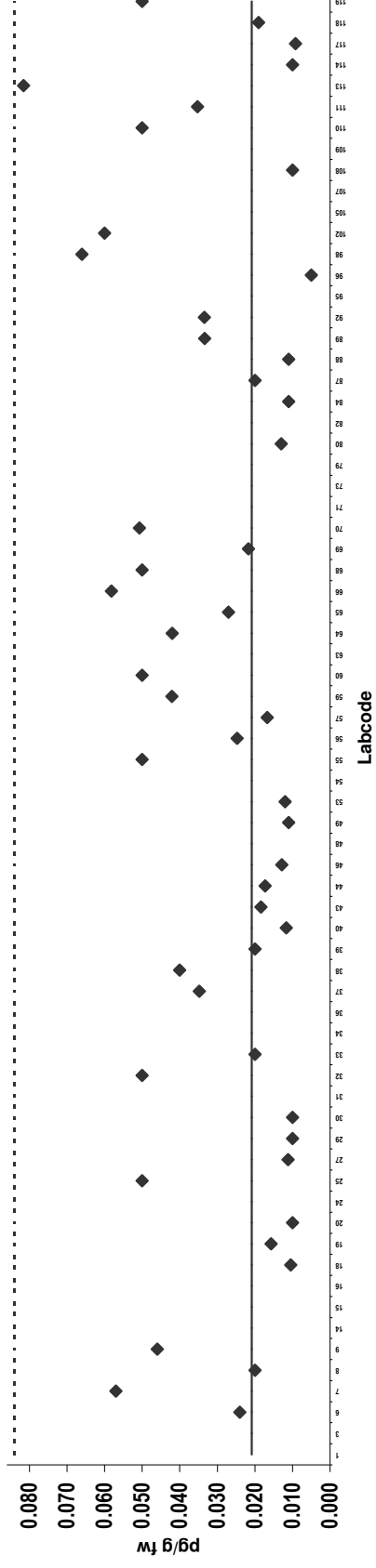
Pork
Congener: PCB 81

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.9	Outlier,ND	71	2.0	Outlier,ND
3	0.33	Outlier	73	0.28	Outlier
6	0.024		79	0.14	Outlier
7	0.057	ND	80	0.013	
8	0.020	ND	82	0.22	Outlier
9	0.046		84	0.011	
14	0.088	Outlier	87	0.020	
15	0.11	Outlier	88	0.011	
16	0.14	Outlier	89	0.033	ND
18	0.010		92	0.033	
19	0.016		95	0.35	Outlier,ND
20	0.010		96	0.0050	ND
24	0.10	Outlier,ND	98	0.066	
25	0.050	ND	102	0.060	
27	0.011		105	0.39	
29	0.010	ND	107	0.17	Outlier,ND
30	0.010	ND	108	0.010	Outlier
31	0.19	Outlier	109	0.89	ND
32	0.050	ND	110	0.050	Outlier
33	0.020	ND	111	0.035	ND
34	1.0	Outlier,ND	113	0.082	ND
36	1.2	Outlier	114	0.010	
37	0.035	ND	117	0.0092	
38	0.040		118	0.019	
39	0.020		119	0.050	ND
40	0.012	ND			
43	0.018				
44	0.017				
46	0.013				
48	0.30	Outlier,ND			
49	0.011				
53	0.012				
54	0.090				
55	0.050	Outlier			
56	0.025				
57	0.017				
59	0.042				
60	0.050				
63	0.11	Outlier,ND			
64	0.042				
65	0.027				
66	0.058	ND			
68	0.050	ND			
69	0.022				
70	0.051	ND			

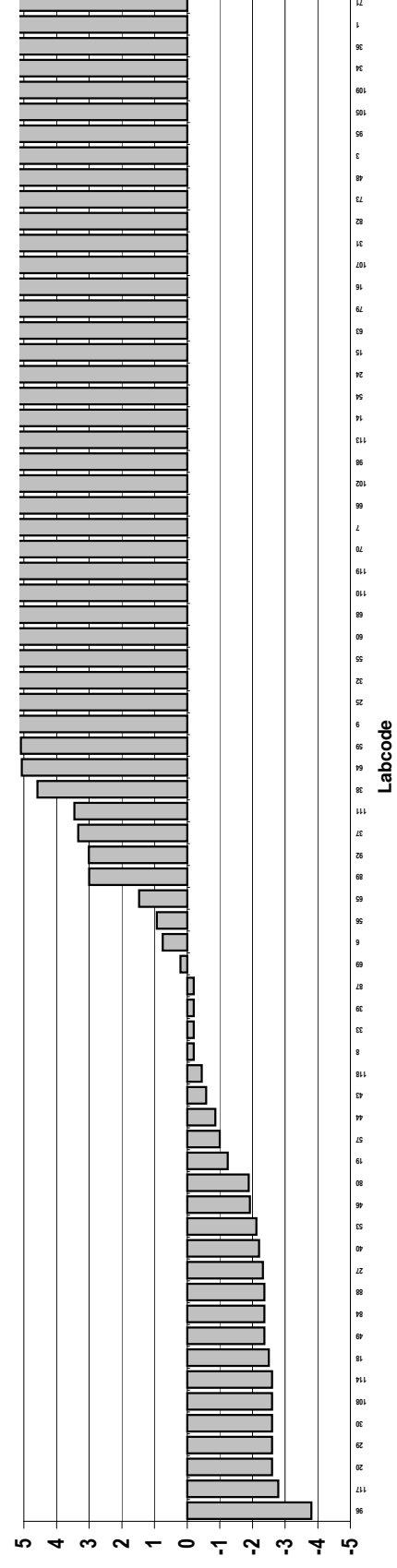
Consensus statistics

Consensus median, pg/g	0.021
Median all values pg/g	0.042
Consensus mean, pg/g	0.029
Standard deviation, pg/g	0.019
Relative standard deviation, %	65
No. of values reported	70
No. of values removed	20
No. of reported non-detects	26

PCB 81



Z-score: PCB 81



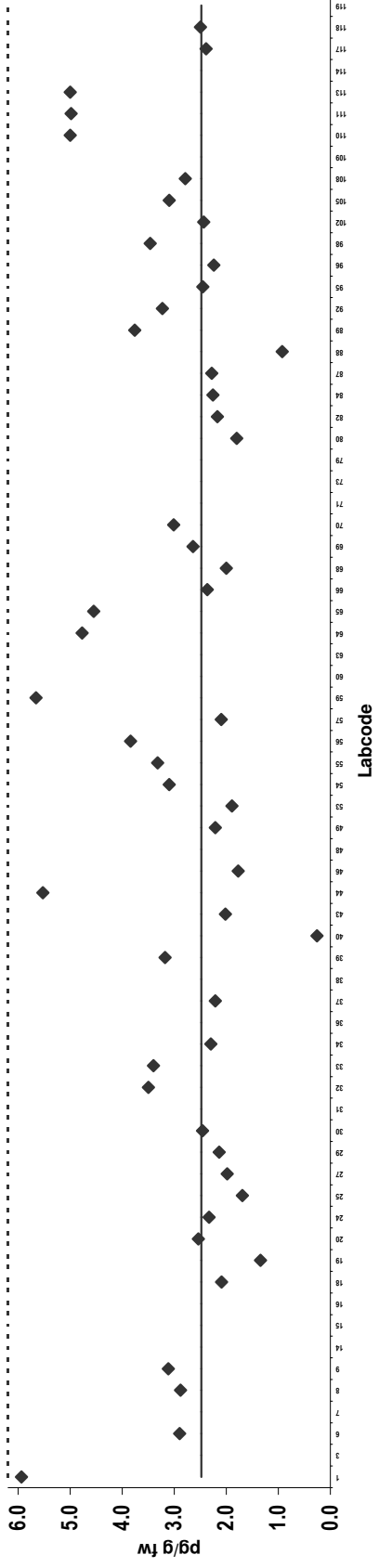
Pork
Congener: PCB 105

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.9		71	32	Outlier
3	6.7	Outlier	73	7.0	Outlier
6	2.9		79	16	Outlier
7	11	Outlier,ND	80	1.8	
8	2.9		82	2.2	
9	3.1		84	2.3	
14	6.3	Outlier	87	2.3	
15	7.7	Outlier	88	0.93	
16	24	Outlier	89	3.8	
18	2.1		92	3.2	
19	1.3		95	2.5	
20	2.5		96	2.2	
24	2.3		98	3.5	
25	1.7		102	2.4	
27	2.0		105	3.1	
29	2.1		108	2.8	
30	2.5		109	13	Outlier
31	33	Outlier	110	5.0	ND
32	3.5		111	5.0	
33	3.4		113	5.0	ND
34	2.3	ND	114	10	Outlier
36	79	Outlier	117	2.4	
37	2.2		118	2.5	
38	8.9	Outlier	119	10	Outlier,ND
39	3.2				
40	0.25				
43	2.0				
44	5.5				
46	1.8				
48	40	Outlier			
49	2.2				
53	1.9				
54	3.1				
55	3.3				
56	3.8				
57	2.1				
59	5.7				
60	9.9	Outlier			
63	6.8	Outlier			
64	4.8				
65	4.6				
66	2.4				
68	2.0	ND			
69	2.6				
70	3.0				

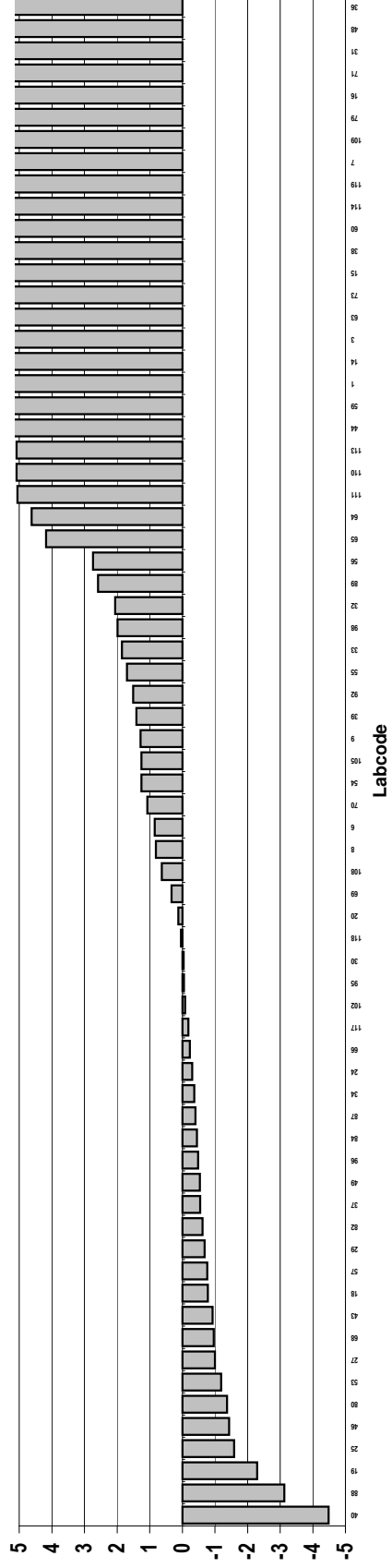
Consensus statistics

Consensus median, pg/g	2.5
Median all values pg/g	3.1
Consensus mean, pg/g	2.9
Standard deviation, pg/g	1.2
Relative standard deviation, %	42
No. of values reported	69
No. of values removed	17
No. of reported non-detects	6

PCB 105



Z-score: PCB 105



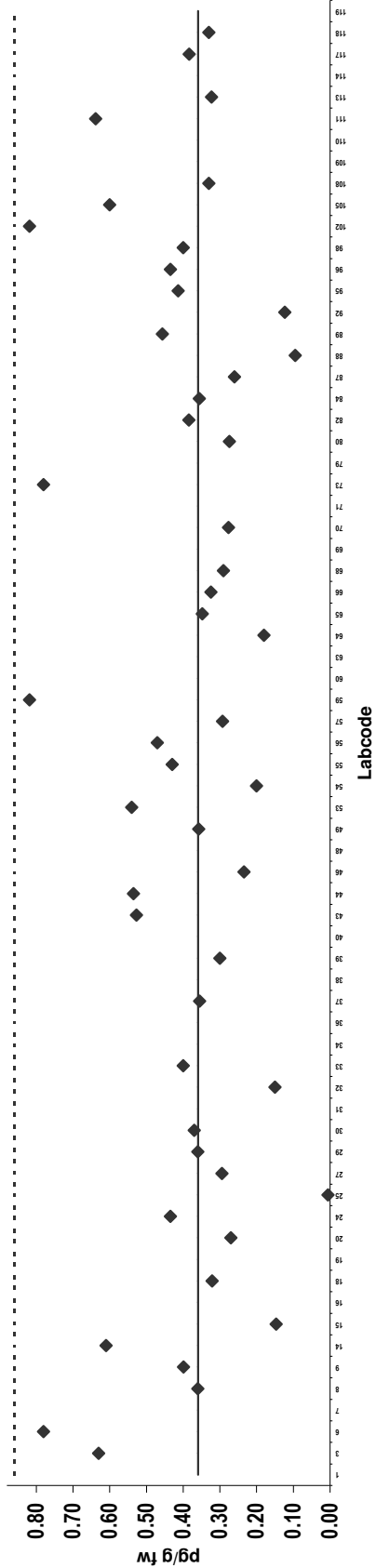
Pork
Congener: PCB 114

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.9	Outlier,ND	71	10	Outlier,ND
3	0.63		73	0.78	ND
6	0.78	ND	79	2.9	Outlier
7	5.7	Outlier,ND	80	0.27	ND
8	0.36		82	0.38	
9	0.40		84	0.36	
14	0.61		87	0.26	
15	0.15	ND	88	0.095	
16	2.4	Outlier	89	0.46	
18	0.32		92	0.12	ND
19	17	Outlier	95	0.41	
20	0.27		96	0.43	
24	0.44		98	0.40	ND
25	0.0058		102	0.82	
27	0.29		105	0.60	ND
29	0.36		108	0.33	
30	0.37		109	1.2	Outlier
31	3.7	Outlier	110	1.0	Outlier,ND
32	0.15	ND	111	0.64	
33	0.40		113	0.32	
34	1.9	Outlier,ND	114	10	Outlier
36	8.9	Outlier	117	0.38	
37	0.36		118	0.33	
38	1.1	Outlier	119	10	Outlier,ND
39	0.30	ND			
40	2.6	Outlier			
43	0.53				
44	0.54				
46	0.23				
48	3.1	Outlier			
49	0.36				
53	0.54				
54	0.20				
55	0.43				
56	0.47				
57	0.29				
59	0.82				
60	1.1				
63	0.89	Outlier			
64	0.18	Outlier			
65	0.35				
66	0.32				
68	0.29				
69	2.3	Outlier,ND			
70	0.28				

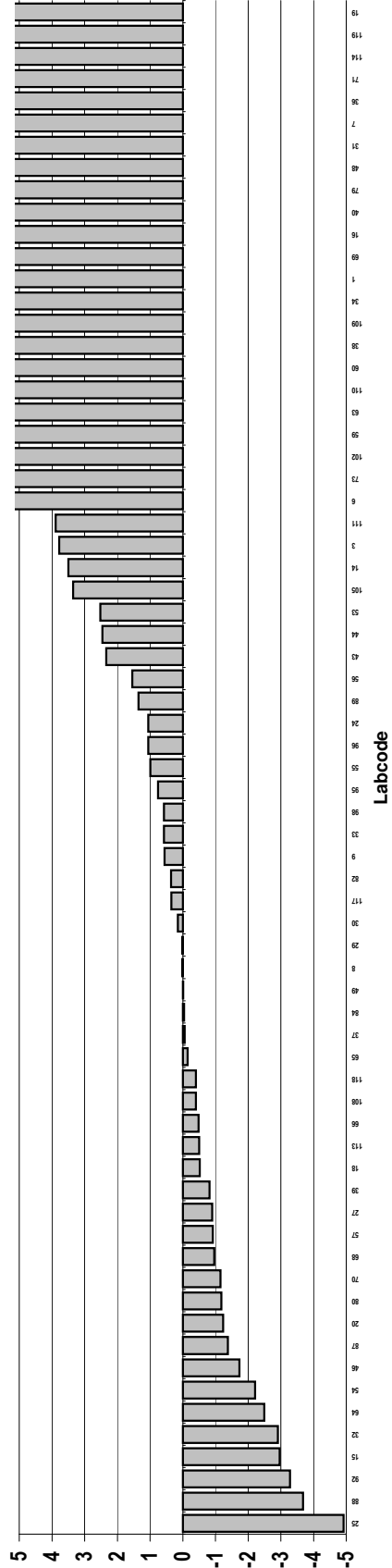
Consensus statistics

Consensus median, pg/g	0.36
Median all values pg/g	0.43
Consensus mean, pg/g	0.39
Standard deviation, pg/g	0.18
Relative standard deviation, %	47
No. of values reported	69
No. of values removed	19
No. of reported non-detects	16

PCB 114



Z-score: PCB 114



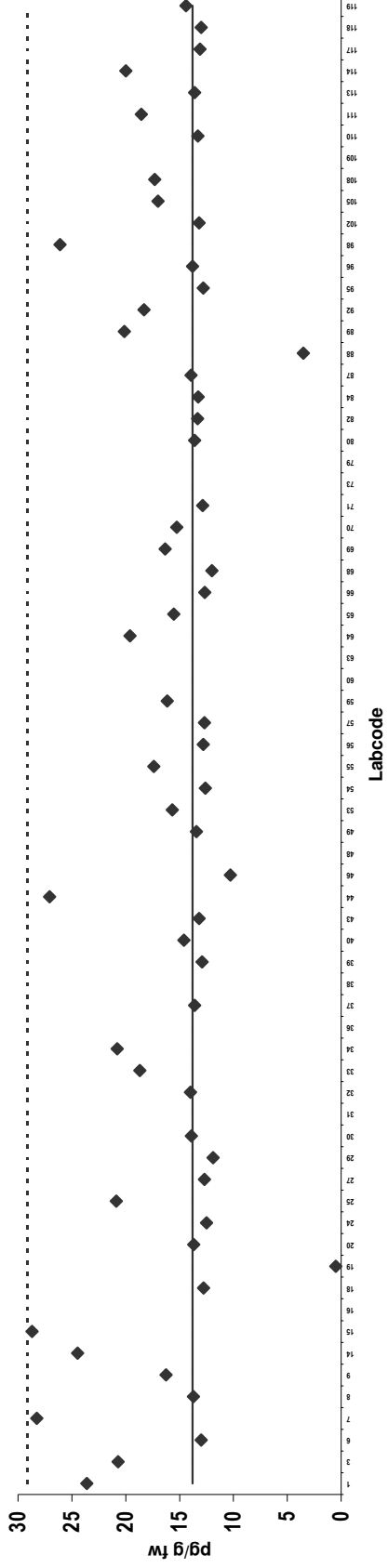
Pork
Congener: PCB 118

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	24		71	13	
3	21		73	41	Outlier
6	13		79	83	Outlier
7	28	ND	80	14	
8	14		82	13	
9	16		84	13	
14	24		87	14	
15	29		88	3.5	
16	80	Outlier	89	20	
18	13		92	18	
19	0.49		95	13	
20	14		96	14	
24	13		98	26	
25	21		102	13	
27	13		105	17	
29	12		108	17	
30	14		109	37	
31	124	Outlier	110	13	Outlier
32	14		111	19	
33	19		113	14	
34	21		114	20	
36	235	Outlier	117	13	
37	14		118	13	
38	33	Outlier	119	14	
39	13				
40	15				
43	13				
44	27				
46	10				
48	90	Outlier			
49	13				
53	16				
54	13				
55	17				
56	13				
57	13				
59	16				
60	72	Outlier			
63	31	Outlier			
64	20				
65	16				
66	13				
68	12				
69	16				
70	15				

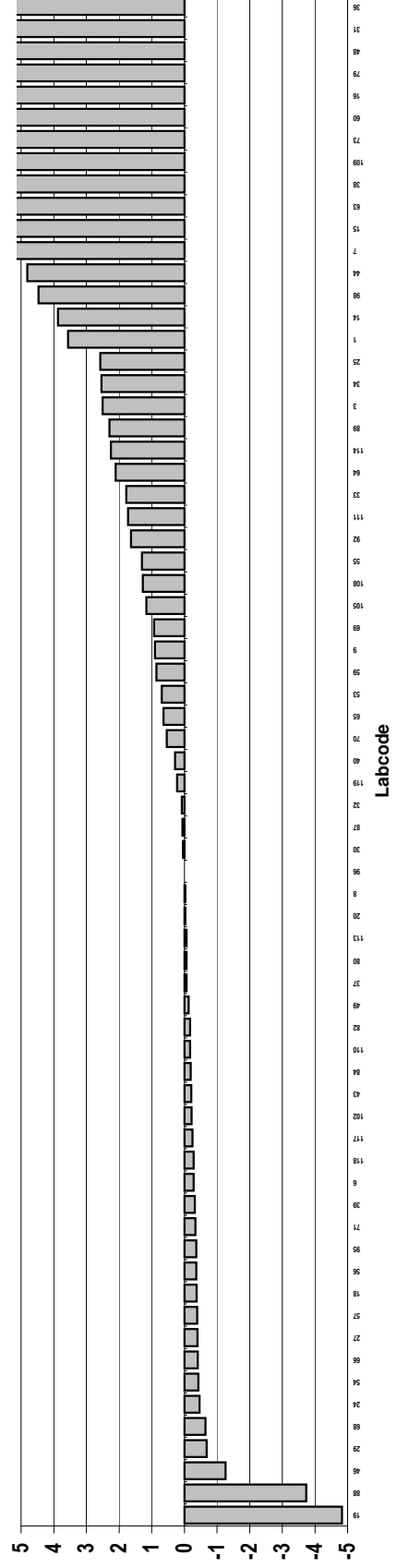
Consensus statistics

Consensus median, pg/g	14
Median all values pg/g	15
Consensus mean, pg/g	16
Standard deviation, pg/g	5.1
Relative standard deviation, %	32
No. of values reported	69
No. of values removed	10
No. of reported non-detects	1

PCB 118



Z-score: PCB 118



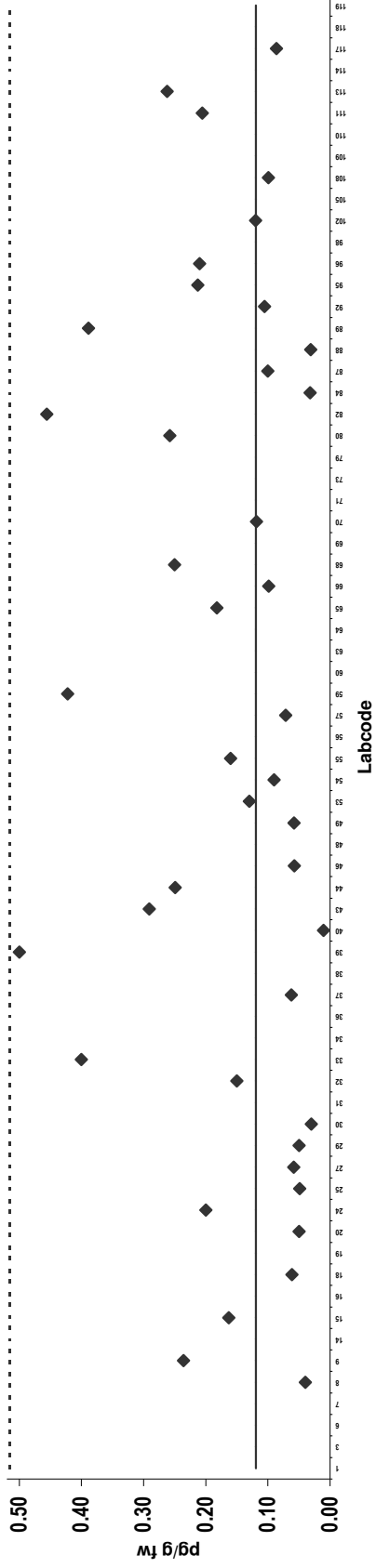
Pork
Congener: PCB 123

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.9	Outlier,ND	71	10	Outlier,ND
3	1.6	Outlier	73	5.7	Outlier
6	0.87	Outlier,ND	79	3.2	Outlier
7	5.7	Outlier,ND	80	0.26	ND
8	0.040		82	0.46	
9	0.24		84	0.032	
14	2.2	Outlier	87	0.10	ND
15	0.16	ND	88	0.031	
16	1.5	Outlier	89	0.39	
18	0.061		92	0.11	ND
19	3.1	Outlier	95	0.21	
20	0.050		96	0.21	ND
24	0.20	ND	98	22	Outlier
25	0.049		102	0.12	
27	0.058		105	0.70	Outlier,ND
29	0.050		108	0.099	
30	0.030	ND	109	36	Outlier
31	1.7	Outlier	110	1.0	Outlier,ND
32	0.15	ND	111	0.21	
33	0.40	ND	113	0.26	ND
34	1.9	Outlier,ND	114	10	Outlier,ND
36	8.0	Outlier	117	0.086	
37	0.062	ND	118	0.73	Outlier
38	0.58	Outlier	119	10	Outlier,ND
39	0.50	ND			
40	0.011	ND			
43	0.29	ND			
44	0.25				
46	0.057				
48	5.3	Outlier			
49	0.058				
53	0.13				
54	0.090				
55	0.16				
56	0.68				
57	0.071	Outlier			
59	0.42				
60	0.65				
63	1.6	Outlier			
64	0.66	Outlier			
65	0.18				
66	0.099				
68	0.25				
69	2.2	Outlier,ND			
70	0.12				

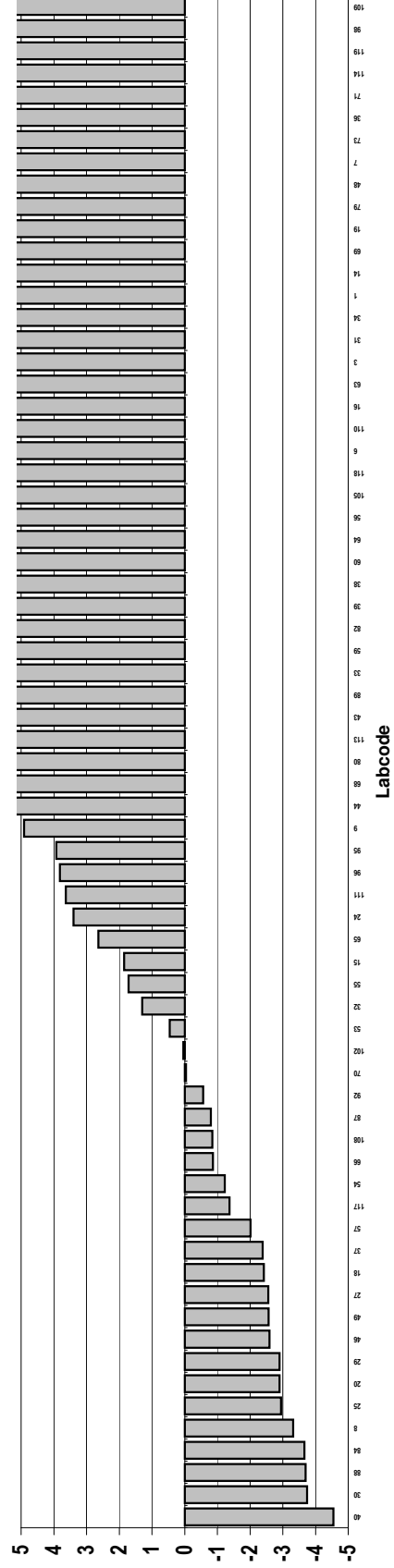
Consensus statistics

Consensus median, pg/g	0.12
Median all values pg/g	0.26
Consensus mean, pg/g	0.16
Standard deviation, pg/g	0.13
Relative standard deviation, %	78
No. of values reported	69
No. of values removed	27
No. of reported non-detects	24

PCB 123



Z-score: PCB 123



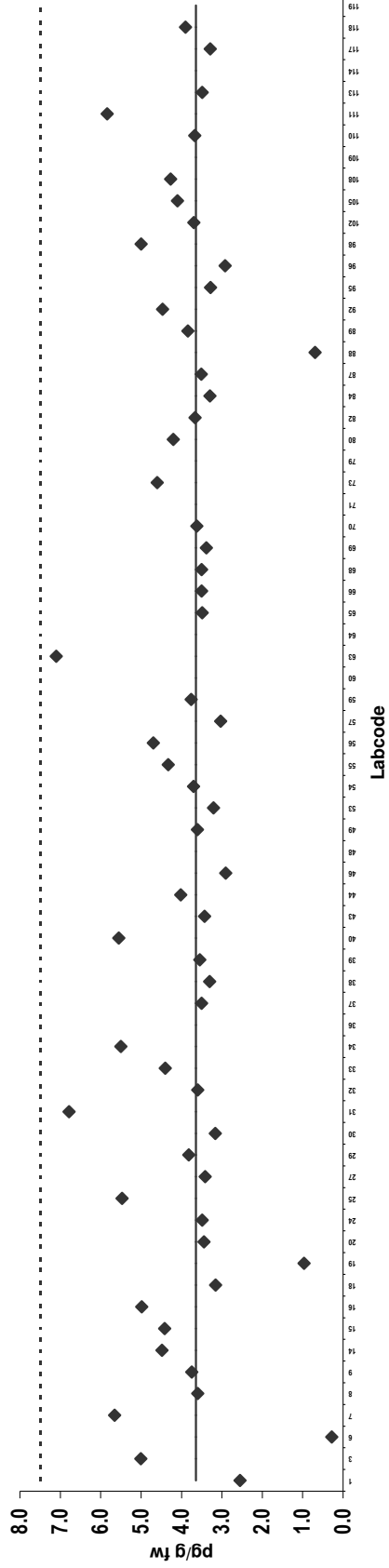
Pork
Congener: PCB 156

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	2.6	ND	71	50	Outlier,ND
3	5.0		73	4.6	
6	0.28	ND	79	8.3	Outlier
7	5.7	ND	80	4.2	
8	3.6		82	3.7	
9	3.7		84	3.3	
14	4.5		87	3.5	
15	4.4		88	0.69	
16	5.0		89	3.8	
18	3.2		92	4.5	
19	0.96		95	3.3	
20	3.4		96	2.9	
24	3.5		98	5.0	
25	5.5		102	3.7	
27	3.4		105	4.1	
29	3.8		108	4.3	
30	3.2		109	9.4	Outlier
31	6.8		110	3.7	
32	3.6		111	5.8	
33	4.4		113	3.5	
34	5.5		114	100	Outlier
36	8.8	Outlier	117	3.3	
37	3.5		118	3.9	
38	3.3		119	10	Outlier,ND
39	3.6				
40	5.6				
43	3.4				
44	4.0				
46	2.9				
48	9.8	Outlier			
49	3.6				
53	3.2				
54	3.7				
55	4.3				
56	4.7				
57	3.0				
59	3.8				
60	18	Outlier			
63	7.1				
64	8.1	Outlier			
65	3.5				
66	3.5				
68	3.5				
69	3.4				
70	3.6				

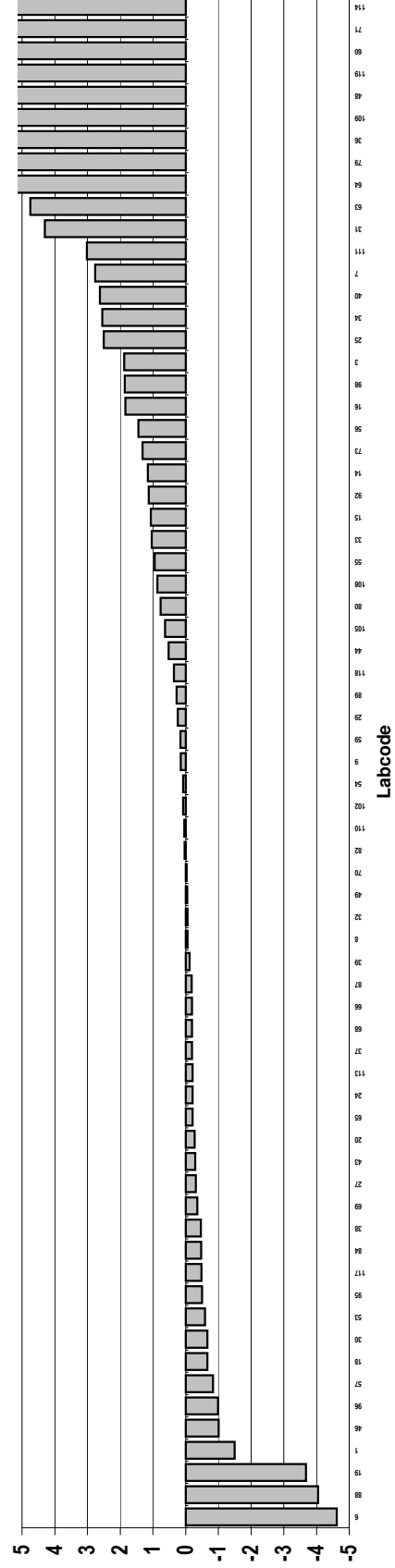
Consensus statistics

Consensus median, pg/g	3.6
Median all values pg/g	3.7
Consensus mean, pg/g	3.8
Standard deviation, pg/g	1.2
Relative standard deviation, %	31
No. of values reported	69
No. of values removed	9
No. of reported non-detects	5

PCB 156



Z-score: PCB 156



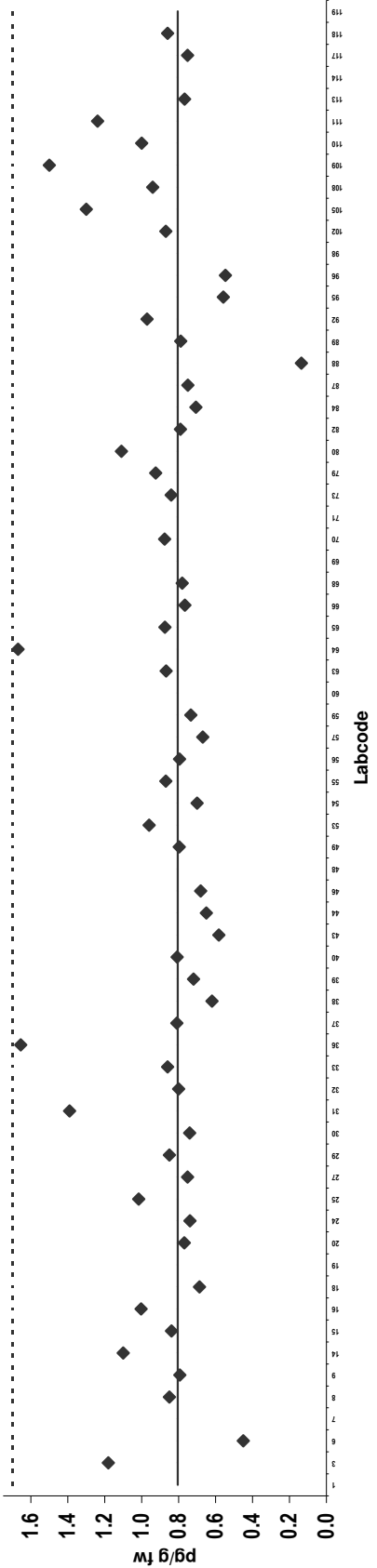
Pork
Congener: PCB 157

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	2.6	Outlier,ND	73	0.84	
3	1.2		79	0.92	
6	0.45	ND	80	1.1	
7	5.7	Outlier,ND	82	0.79	
8	0.85		84	0.71	
9	0.79		87	0.75	
14	1.1		88	0.14	
15	0.84		89	0.79	
16	1.0		92	0.97	
18	0.69		95	0.56	
19	3.7		96	0.55	
20	0.77	Outlier	98	4.5	Outlier
24	0.74		102	0.87	
25	1.0		105	1.3	ND
27	0.75		108	0.94	
29	0.85		109	1.5	
30	0.74		110	1.0	ND
31	1.4		111	1.2	
32	0.80		113	0.77	
33	0.86		114	70	Outlier
36	1.7		117	0.75	
37	0.81		118	0.86	
38	0.62		119	10	Outlier,ND
39	0.72				
40	0.81				
43	0.58				
44	0.65				
46	0.68				
48	2.8	Outlier			
49	0.80				
53	0.96				
54	0.70				
55	0.87				
56	0.80				
57	0.67				
59	0.73				
60	2.2	Outlier			
63	0.87				
64	1.7				
65	0.87				
66	0.77				
68	0.78				
69	2.2	Outlier			
70	0.88	Outlier,ND			
71	50				

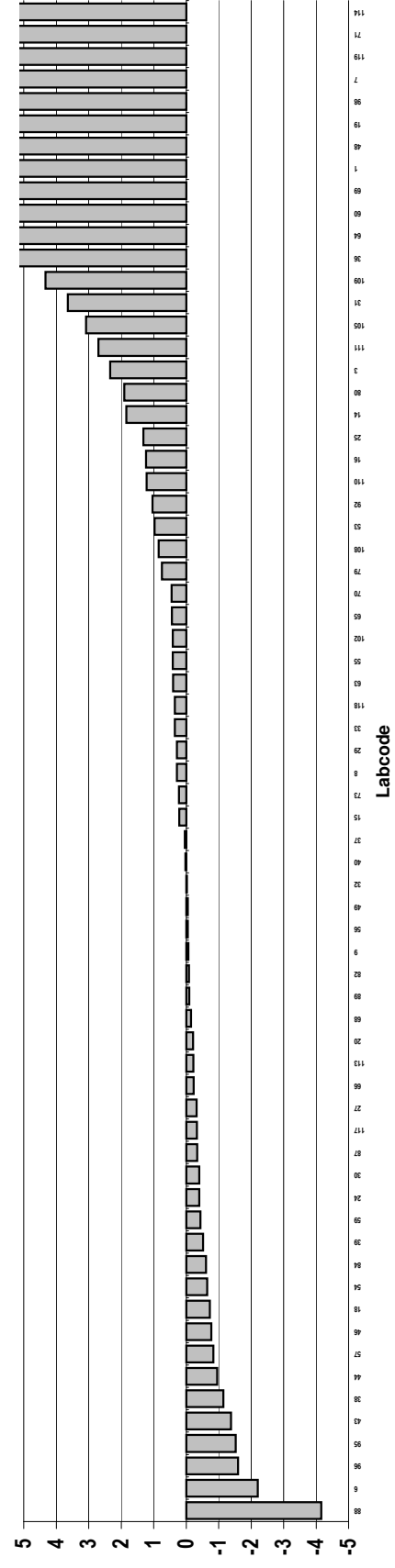
Consensus statistics

Consensus median, pg/g	0.80
Median all values pg/g	0.85
Consensus mean, pg/g	0.86
Standard deviation, pg/g	0.27
Relative standard deviation, %	31
No. of values reported	68
No. of values removed	10
No. of reported non-detects	7

PCB 157



Z-score: PCB 157



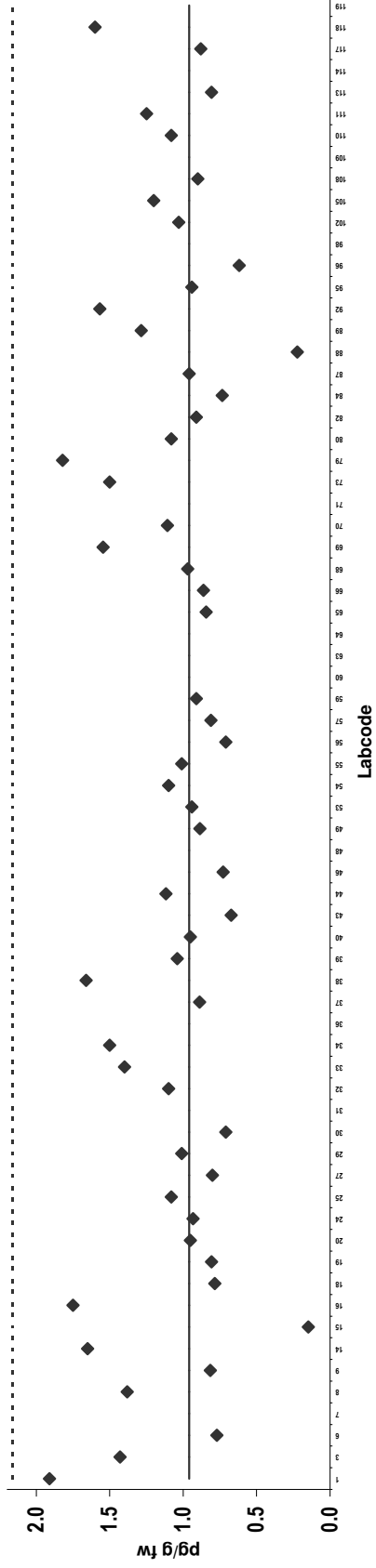
Pork
Congener: PCB 167

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.9	ND	71	50	Outlier,ND
3	1.4		73	1.5	
6	0.77	ND	79	1.8	
7	5.7	Outlier,ND	80	1.1	
8	1.4		82	0.91	
9	0.82		84	0.74	
14	1.7		87	0.96	
15	0.15	ND	88	0.22	
16	1.7		89	1.3	
18	0.79		92	1.6	
19	0.81		95	0.94	
20	0.95		96	0.62	
24	0.93		98	27	Outlier
25	1.1		102	1.0	
27	0.80		105	1.2	ND
29	1.0		108	0.90	
30	0.71		109	3.9	Outlier
31	3.4		110	1.1	
32	1.1	Outlier	111	1.2	
33	1.4		113	0.81	
34	1.5	ND	114	10	Outlier,ND
36	4.0	Outlier	117	0.88	
37	0.89		118	1.6	
38	1.7		119	10	Outlier,ND
39	1.0				
40	0.95				
43	0.67				
44	1.1				
46	0.73				
48	4.1	Outlier			
49	0.89				
53	0.94				
54	1.1				
55	1.0				
56	0.71				
57	0.81				
59	0.91				
60	7.6				
63	2.4	Outlier			
64	2.3	Outlier			
65	0.84	Outlier			
66	0.86				
68	0.97				
69	1.5	ND			
70	1.1				

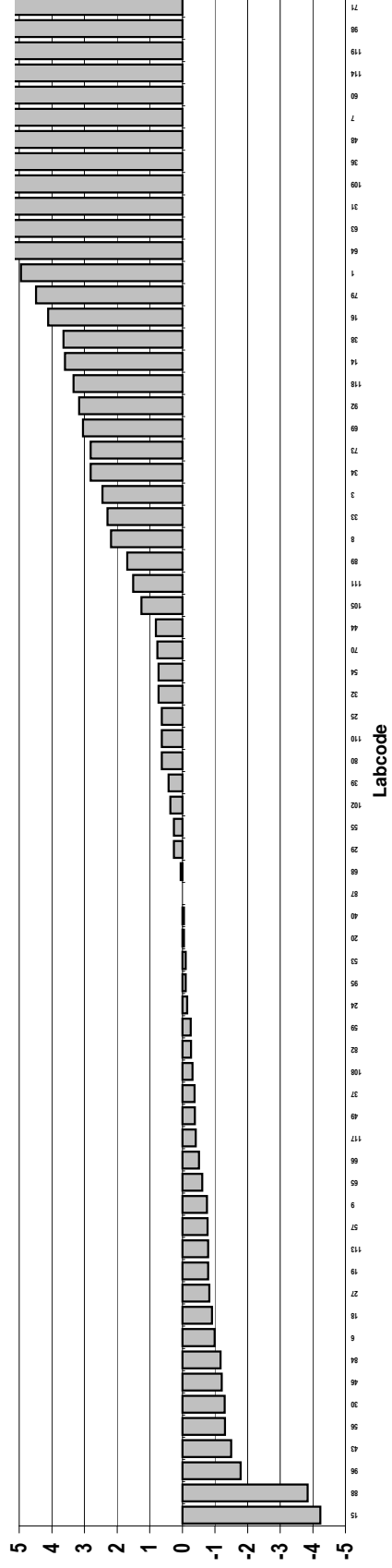
Consensus statistics

Consensus median, pg/g	0.96
Median all values pg/g	1.1
Consensus mean, pg/g	1.1
Standard deviation, pg/g	0.36
Relative standard deviation, %	34
No. of values reported	69
No. of values removed	12
No. of reported non-detects	10

PCB 167



Z-score: PCB 167



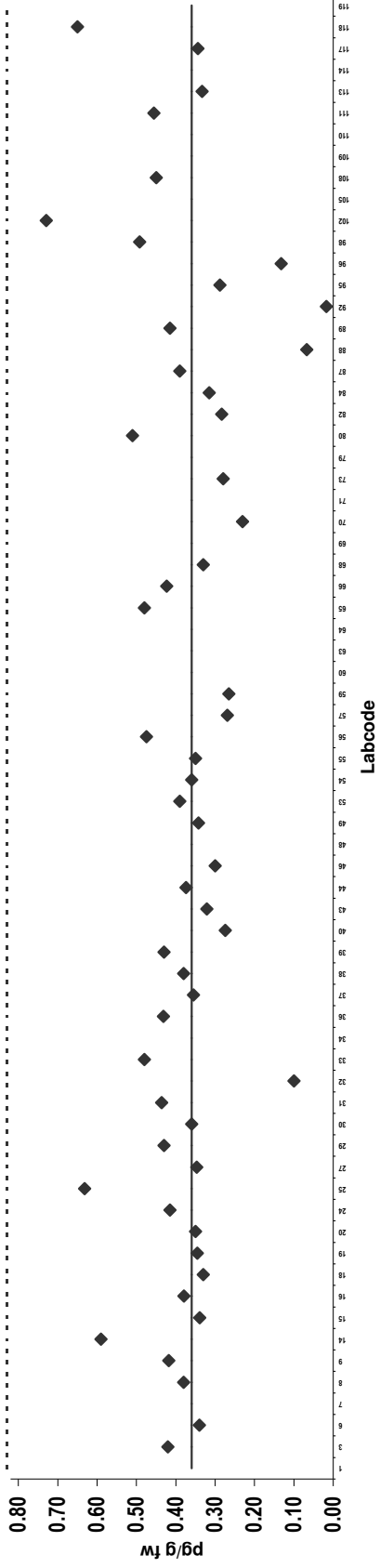
Pork
Congener: PCB 189

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.9	Outlier,ND	71	10	Outlier,ND
3	0.42		73	0.28	
6	0.34	ND	79	1.2	Outlier
7	5.7	Outlier,ND	80	0.51	
8	0.38		82	0.28	
9	0.42		84	0.32	
14	0.59		87	0.39	
15	0.34		88	0.067	
16	0.38		89	0.42	
18	0.33		92	0.018	ND
19	0.35		95	0.29	
20	0.35		96	0.13	ND
24	0.42		98	0.49	
25	0.63		102	0.73	
27	0.35		105	2.2	Outlier,ND
29	0.43		108	0.45	
30	0.36		109	1.5	Outlier
31	0.44		110	1.0	Outlier,ND
32	0.10		111	0.46	
33	0.48		113	0.33	
34	1.2	Outlier,ND	114	10	Outlier,ND
36	0.43		117	0.34	
37	0.36		118	0.65	
38	0.38		119	10	Outlier,ND
39	0.43				
40	0.27				
43	0.32	ND			
44	0.37				
46	0.30				
48	0.99	Outlier			
49	0.34				
53	0.39				
54	0.36				
55	0.35				
56	0.47				
57	0.27				
59	0.26				
60	2.2				
63	0.96	Outlier			
64	1.3	Outlier			
65	0.48				
66	0.42				
68	0.33				
69	2.2	Outlier,ND			
70	0.23				

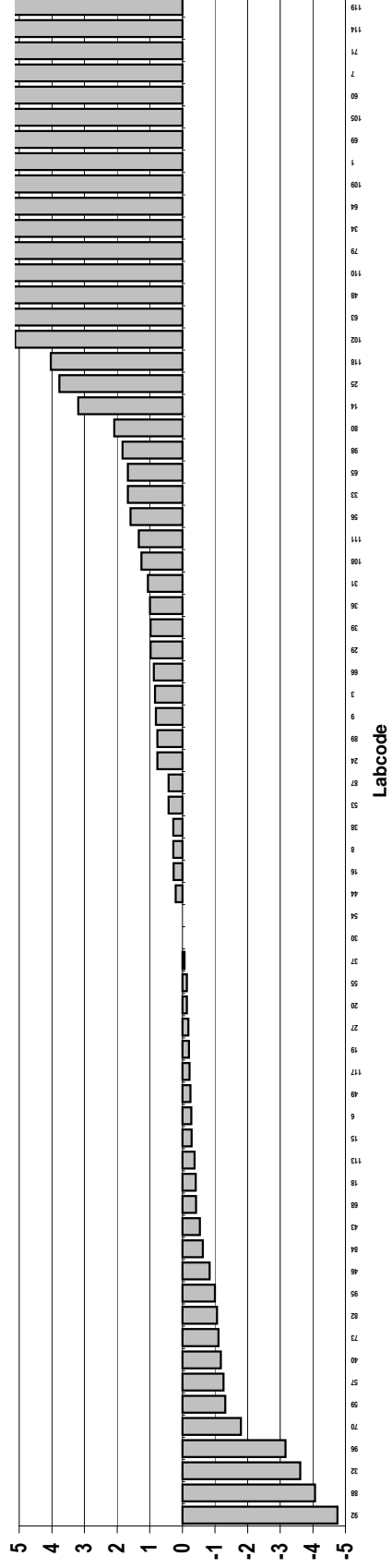
Consensus statistics

Consensus median, pg/g	0.36
Median all values pg/g	0.42
Consensus mean, pg/g	0.37
Standard deviation, pg/g	0.13
Relative standard deviation, %	35
No. of values reported	69
No. of values removed	15
No. of reported non-detects	13

PCB 189



Z-score: PCB 189



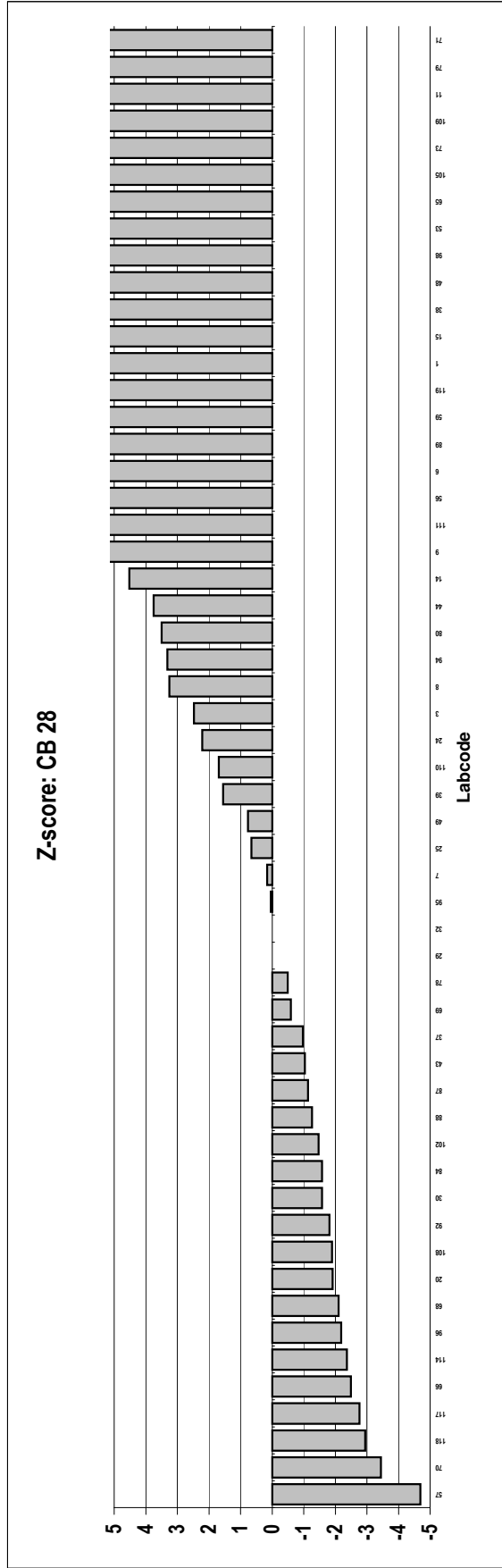
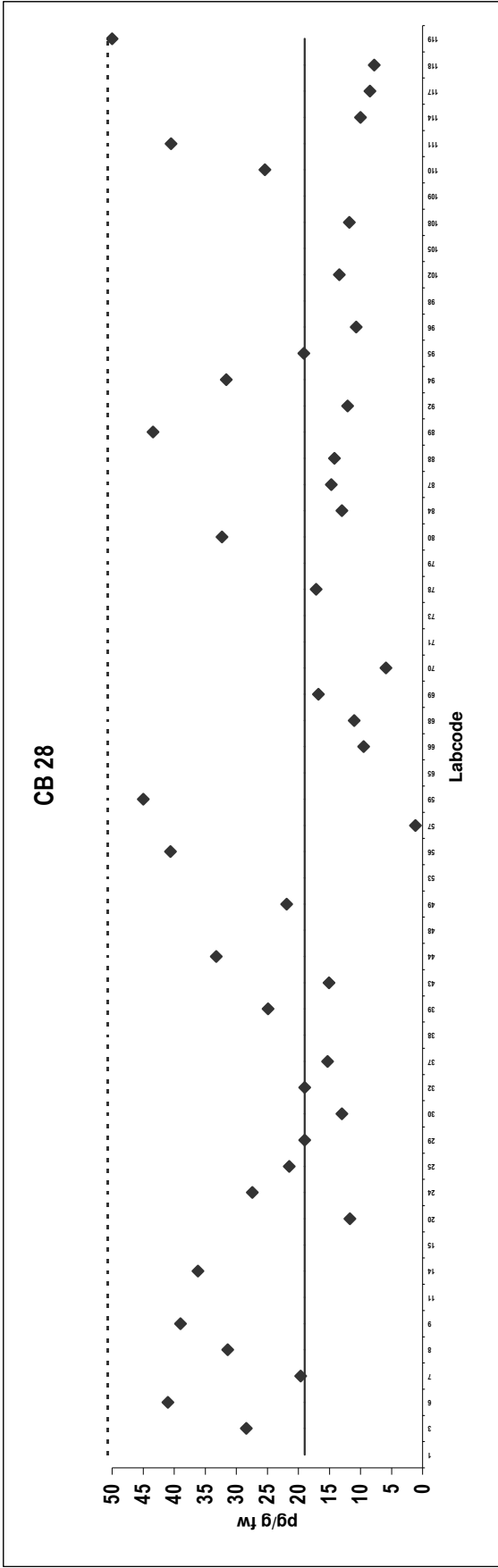
Pork meat

Congener: CB 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	50		102	13	Outlier,ND
3	28		105	100	
6	41		108	12	
7	20		109	130	Outlier
8	31		110	25	
9	39		111	41	
11	208	Outlier	114	10	
14	36		117	8.5	
15	55	Outlier	118	7.8	
20	12		119	50	ND
24	27				
25	21				
29	19				
30	13				
32	19				
37	15				
38	56	Outlier			
39	25				
43	15				
44	33				
48	56	Outlier			
49	22				
53	78	Outlier			
56	41				
57	1.2				
59	45	ND			
65	80	Outlier,ND			
66	9.5				
68	11				
69	17				
70	5.9				
71	1000	Outlier,ND			
73	110	Outlier			
78	17				
79	384	Outlier			
80	32				
84	13				
87	15				
88	14				
89	43				
92	12				
94	32				
95	19				
96	11				
98	71	Outlier			

Consensus statistics

Consensus median, pg/g	19
Median all values pg/g	25
Consensus mean, pg/g	23
Standard deviation, pg/g	13
Relative standard deviation, %	57
No. of values reported	55
No. of values removed	12
No. of reported non-detects	5



Pork meat

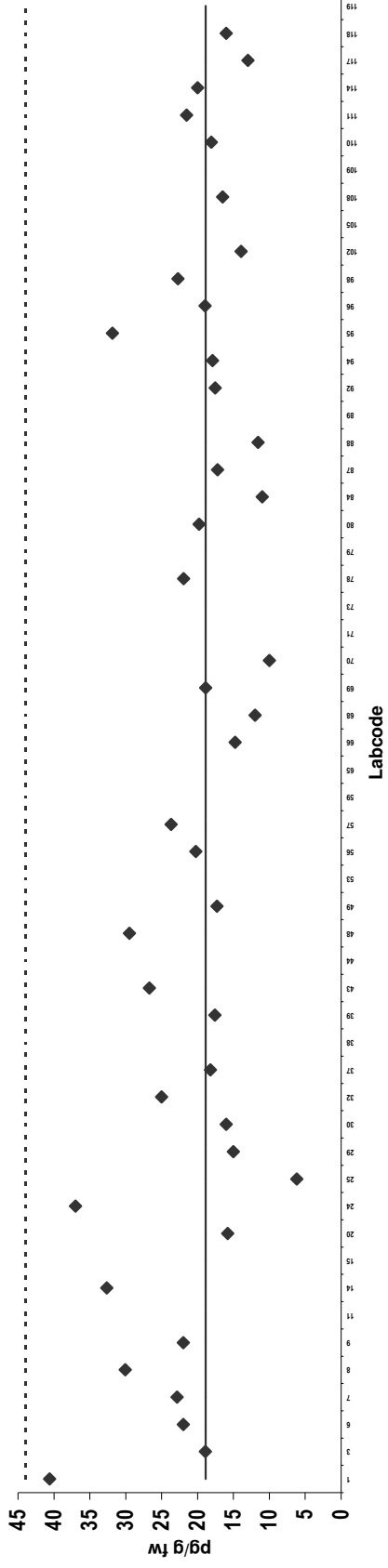
Congener: CB 52

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	41		102	14	
3	19		105	100	Outlier,ND
6	22		108	17	
7	23		109	71	Outlier
8	30		110	18	
9	22		111	22	
11	247		114	20	
14	33	Outlier	117	13	
15	71	Outlier	118	16	
20	16		119	50	Outlier,ND
24	37				
25	6.2				
29	15				
30	16				
32	25				
37	18				
38	92	Outlier			
39	18				
43	27				
44	52	Outlier			
48	29				
49	17				
53	51	Outlier			
56	20				
57	24				
59	60	Outlier			
65	80	Outlier,ND			
66	15				
68	12				
69	19				
70	10				
71	1000	Outlier,ND			
73	243	Outlier			
78	22				
79	393	Outlier			
80	20				
84	11				
87	17				
88	12				
89	45	Outlier			
92	18				
94	18				
95	32				
96	19				
98	23				

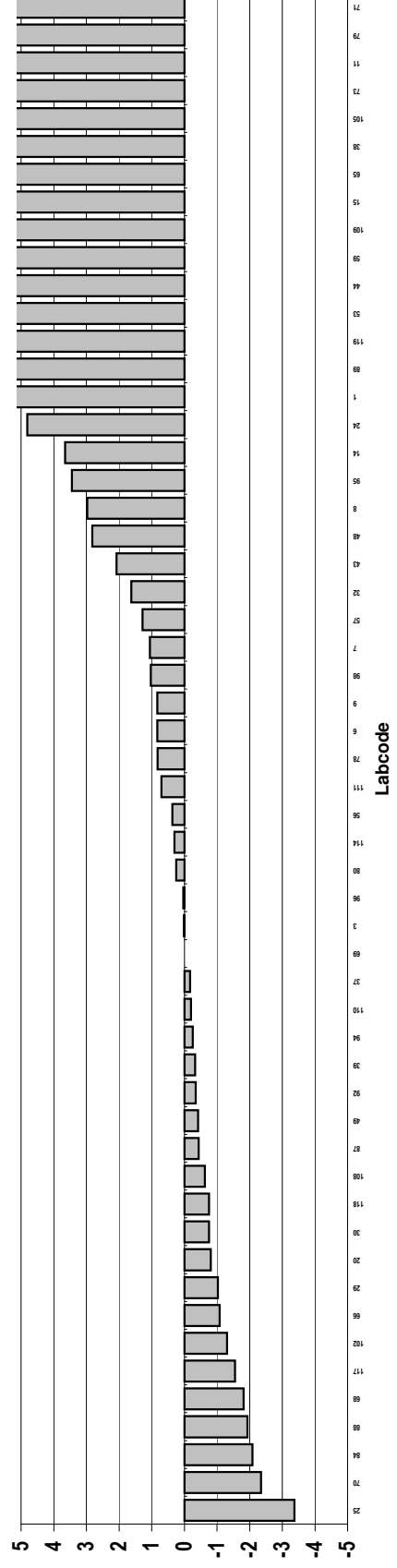
Consensus statistics

Consensus median, pg/g	19
Median all values pg/g	22
Consensus mean, pg/g	20
Standard deviation, pg/g	7.2
Relative standard deviation, %	36
No. of values reported	55
No. of values removed	14
No. of reported non-detects	4

CB 52



Z-score: CB 52



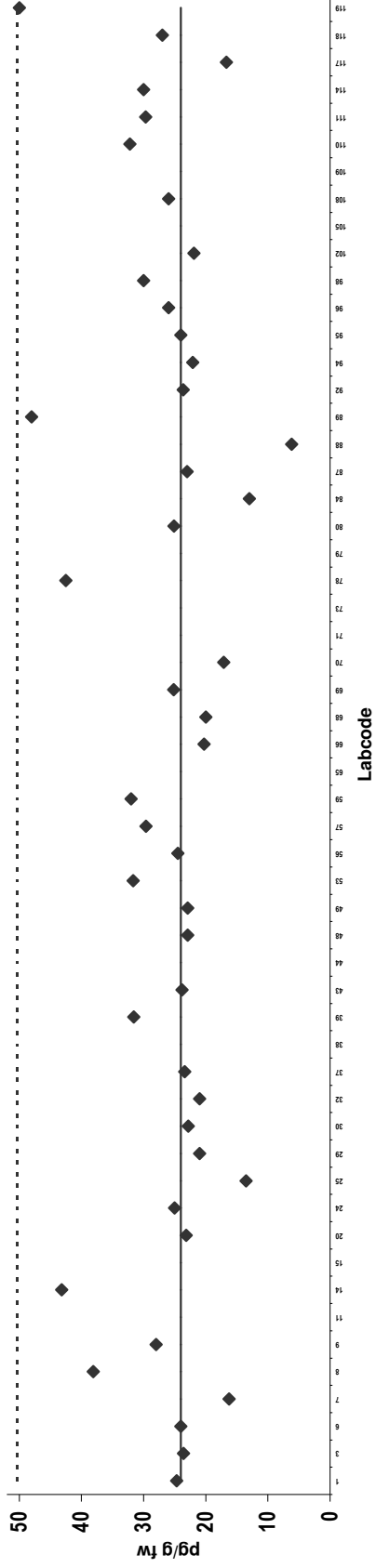
Pork meat
Congener: CB 101

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	25		102	22	
3	24		105	100	Outlier,ND
6	24		108	26	
7	16		109	92	Outlier
8	38		110	32	
9	28		111	30	
11	288	Outlier	114	30	
14	43		117	17	
15	73	Outlier	118	27	ND
20	23		119	50	
24	25				
25	14				
29	21				
30	23				
32	21				
37	23				
38	109	Outlier			
39	32				
43	24				
44	63	Outlier			
48	23				
49	23				
53	32				
56	24				
57	30				
59	32				
65	80	Outlier,ND			
66	20				
68	20				
69	25				
70	17				
71	1000	Outlier,ND			
73	303	Outlier			
78	43				
79	172	Outlier			
80	25				
84	13				
87	23				
88	6.2				
89	48				
92	24				
94	22				
95	24				
96	26				
98	30				

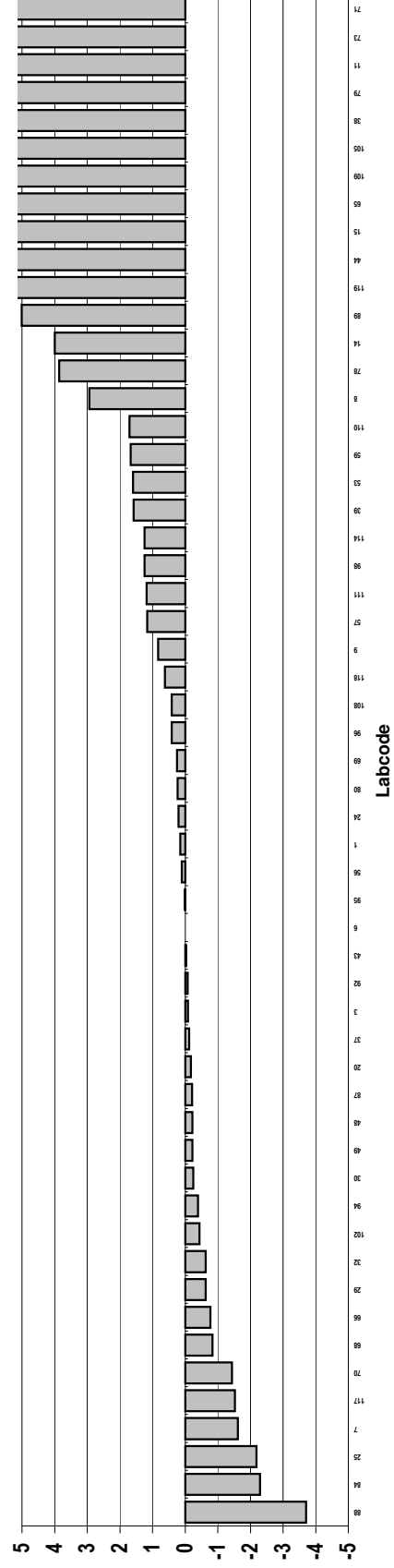
Consensus statistics

Consensus median, pg/g	24
Median all values pg/g	25
Consensus mean, pg/g	26
Standard deviation, pg/g	8.5
Relative standard deviation, %	33
No. of values reported	55
No. of values removed	10
No. of reported non-detects	4

CB 101



Z-score: CB 101



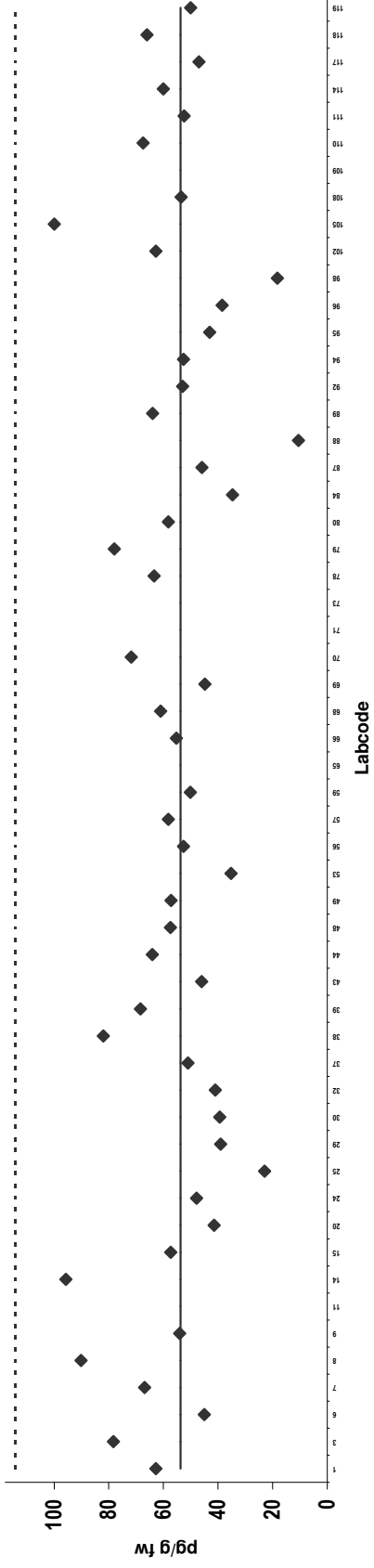
Pork meat
Congener: CB 138

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	63		102	63	
3	78		105	100	ND
6	45		108	54	
7	67		109	130	Outlier
8	90		110	67	
9	54		111	52	
11	237	Outlier	114	60	
14	96		117	47	
15	57		118	66	
20	41		119	50	ND
24	48				
25	23				
29	39				
30	39				
32	41				
37	51				
38	82				
39	68				
43	46				
44	64				
48	57				
49	57				
53	35				
56	53				
57	58				
59	50				
65	181				
66	55				
68	61				
69	45				
70	72				
71	1000	Outlier,ND			
73	172	Outlier			
78	63				
79	78				
80	58				
84	35				
87	46				
88	11				
89	64				
92	53				
94	53				
95	43				
96	39				
98	18				

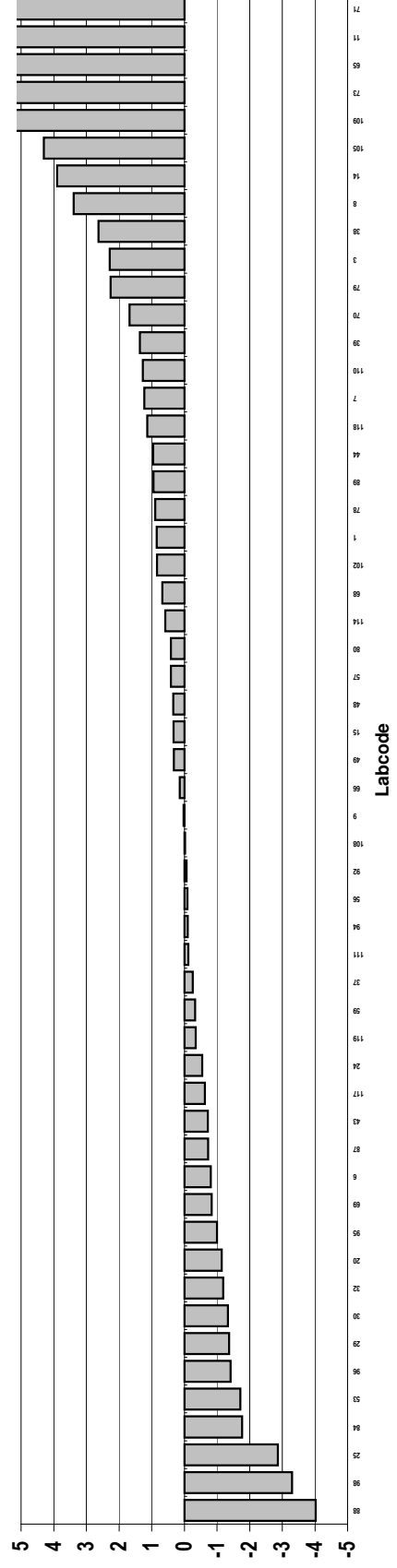
Consensus statistics

Consensus median, pg/g	54
Median all values pg/g	57
Consensus mean, pg/g	55
Standard deviation, pg/g	18
Relative standard deviation, %	32
No. of values reported	55
No. of values removed	5
No. of reported non-detects	3

CB 138



Z-score: CB 138



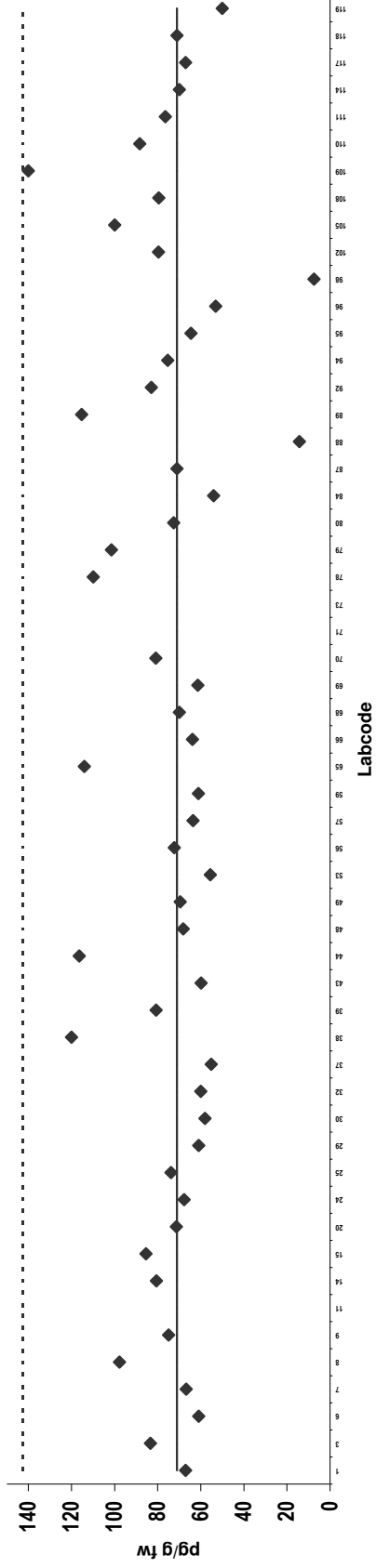
Pork meat
Congener: CB 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	67		102	80	
3	83		105	100	ND
6	61		108	80	
7	67		109	140	
8	98		110	88	
9	75		111	76	
11	311	Outlier	114	70	
14	81		117	67	
15	85		118	71	
20	71		119	50	
24	68				
25	74				
29	61				
30	58				
32	60				
37	55				
38	120				
39	81				
43	60				
44	116				
48	68				
49	70				
53	56				
56	72				
57	64				
59	61				
65	114				
66	64				
68	70				
69	61				
70	81				
71	1000	Outlier,ND			
73	178	Outlier			
78	110				
79	101				
80	73				
84	54				
87	71				
88	14				
89	115				
92	83				
94	75				
95	65				
96	53				
98	7.4				

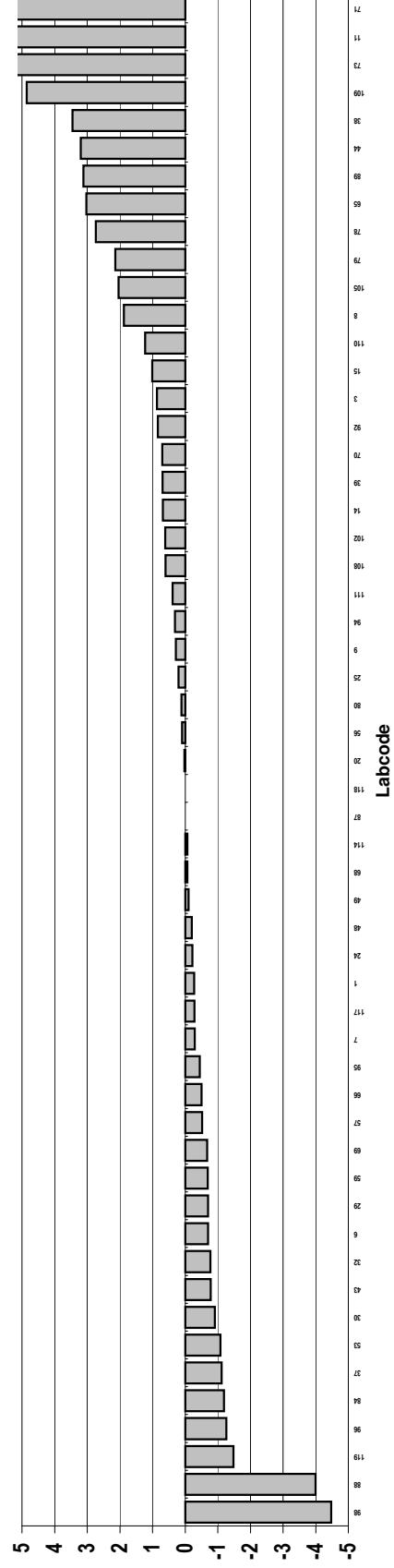
Consensus statistics

Consensus median, pg/g	71
Median all values pg/g	71
Consensus mean, pg/g	74
Standard deviation, pg/g	23
Relative standard deviation, %	31
No. of values reported	55
No. of values removed	3
No. of reported non-detects	2

CB 153



Z-score: CB 153



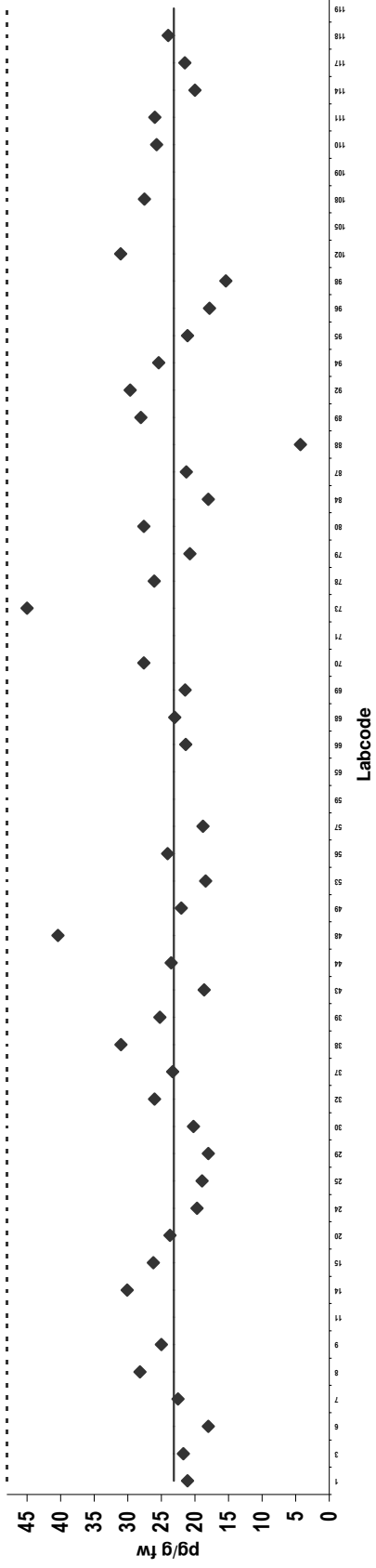
Pork meat
Congener: CB 180

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	21		102	31	Outlier,ND
3	22		105	100	
6	18		108	28	
7	23		109	60	Outlier
8	28		110	26	
9	25		111	26	
11	100	Outlier,ND	114	20	
14	30		117	22	
15	26		118	24	Outlier,ND
20	24		119	50	
24	20				
25	19				
29	18				
30	20				
32	26				
37	23				
38	31				
39	25				
43	19				
44	24				
48	40				
49	22				
53	18				
56	24				
57	19				
59	51	Outlier			
65	80	Outlier,ND			
66	21				
68	23				
69	21				
70	28				
71	1000	Outlier,ND			
73	45				
78	26				
79	21				
80	28				
84	18				
87	21				
88	4.3				
89	28				
92	30				
94	25				
95	21				
96	18				
98	15				

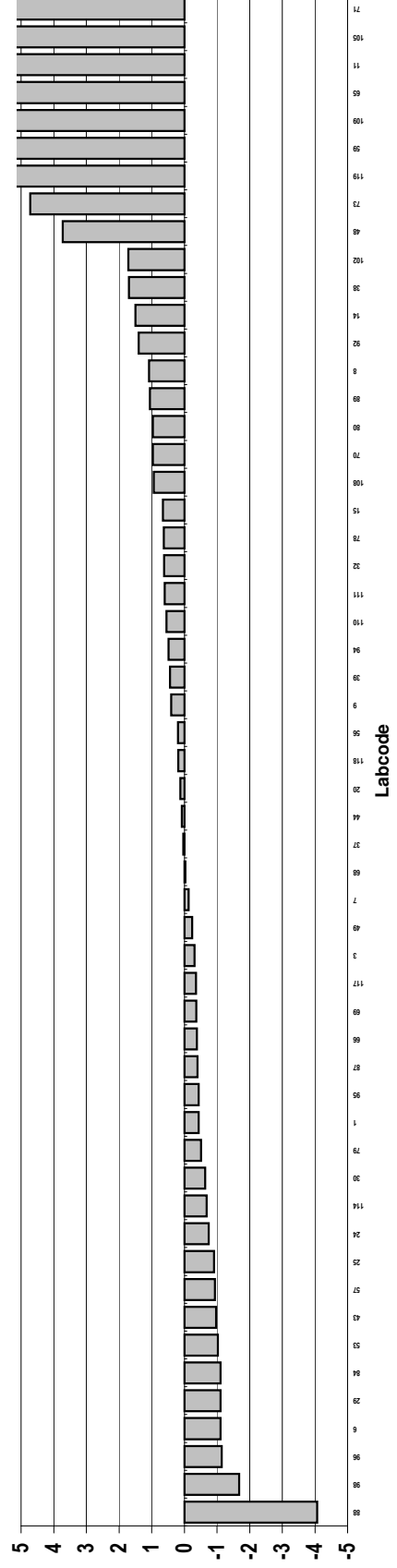
Consensus statistics

Consensus median, pg/g	23
Median all values pg/g	24
Consensus mean, pg/g	24
Standard deviation, pg/g	6.2
Relative standard deviation, %	26
No. of values reported	55
No. of values removed	7
No. of reported non-detects	5

CB 180



Z-score: CB 180

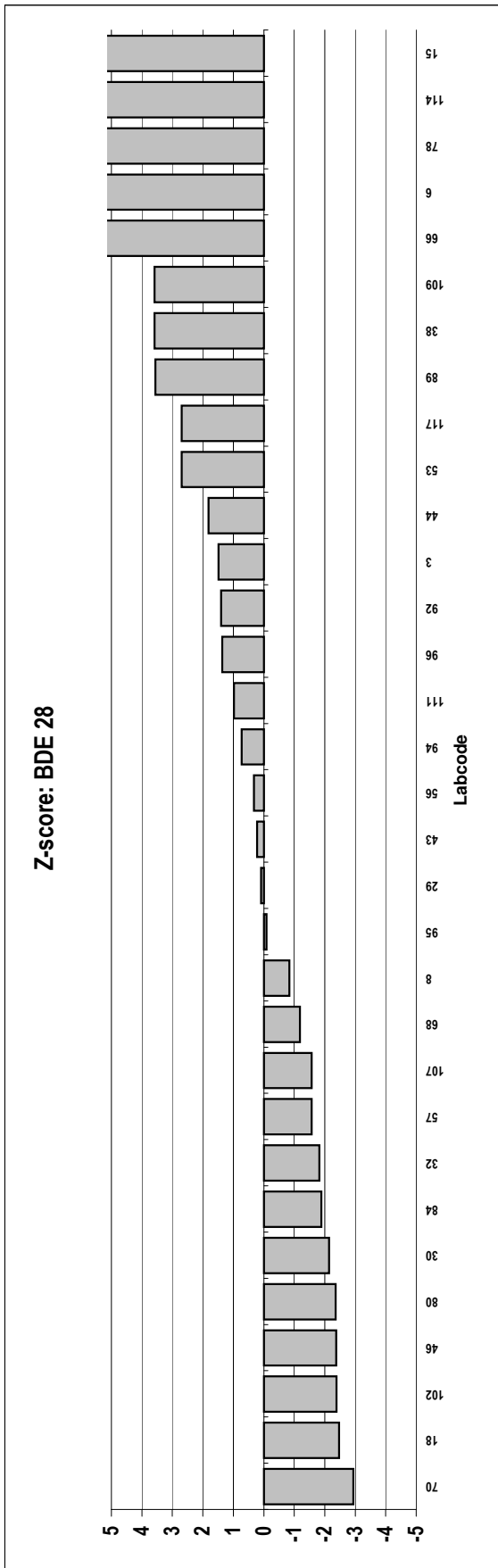
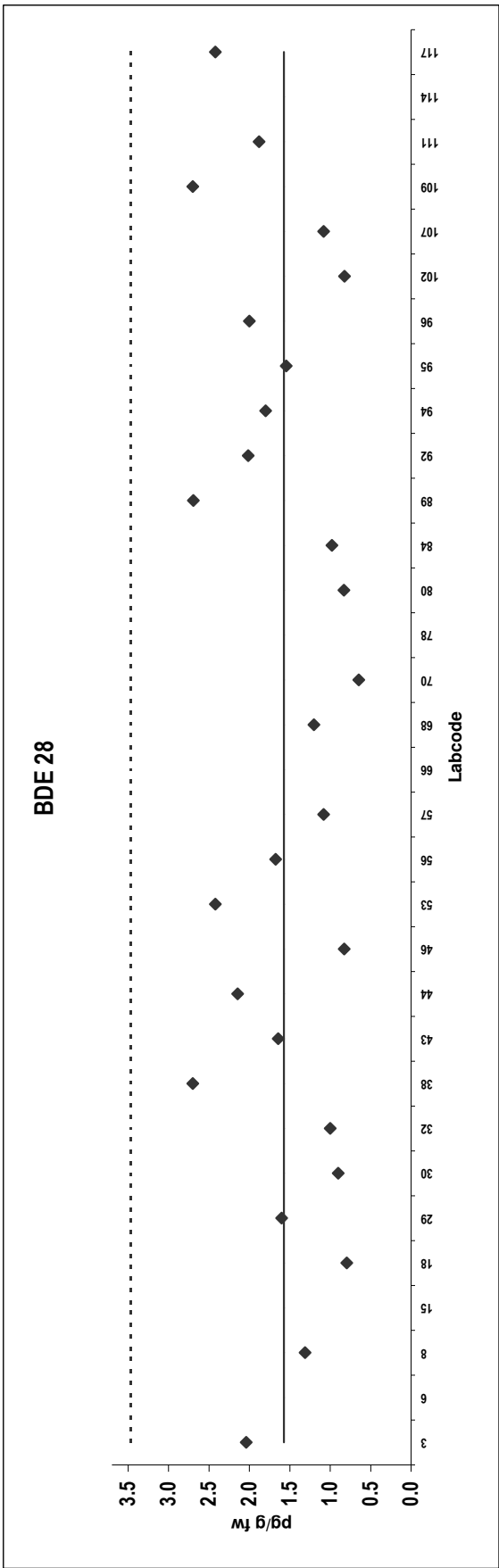


Pork meat
Congener: BDE 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	2.0				
6	6.0	Outlier			
8	1.3				
15	14	Outlier			
18	0.79				
29	1.6				
30	0.90				
32	1.0				
38	2.7				
43	1.6				
44	2.1				
46	0.83				
53	2.4				
56	1.7				
57	1.1				
66	4.3	Outlier,ND			
68	1.2				
70	0.65				
78	6.7	Outlier			
80	0.83				
84	0.98				
89	2.7				
92	2.0				
94	1.8				
95	1.5				
96	2.0	ND			
102	0.82				
107	1.1				
109	2.7				
111	1.9				
114	10	Outlier,ND			
117	2.4				

Consensus statistics

Consensus median, pg/g	1.6
Median all values pg/g	1.7
Consensus mean, pg/g	1.6
Standard deviation, pg/g	0.66
Relative standard deviation, %	42
No. of values reported	32
No. of values removed	5
No. of reported non-detects	3



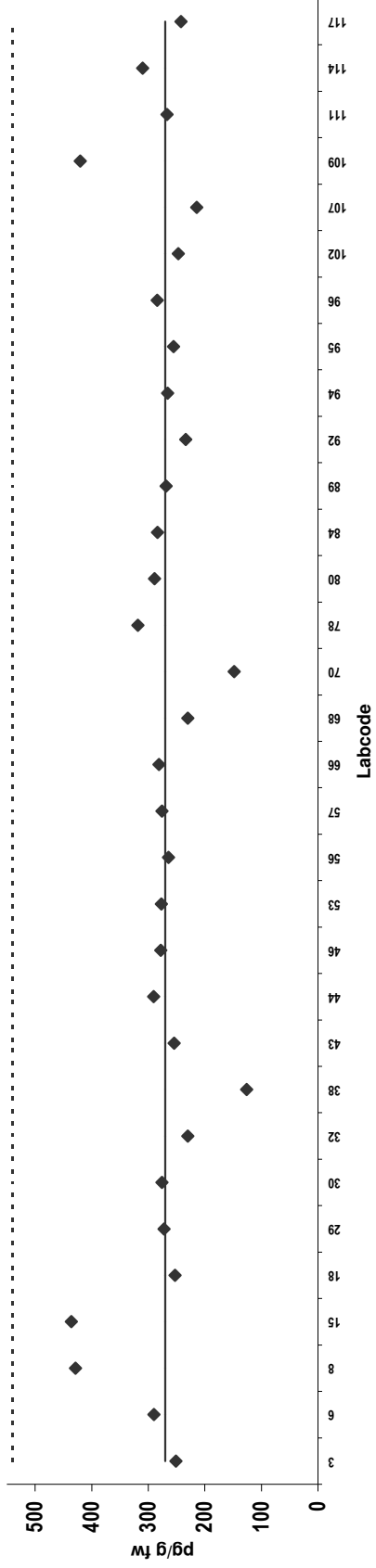
Pork meat
Congener: BDE 47

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	251				
6	290				
8	428				
15	436				
18	253				
29	272				
30	276				
32	230				
38	126				
43	254				
44	290				
46	278				
53	277				
56	264				
57	276				
66	281				
68	230				
70	148				
78	318				
80	289				
84	284				
89	268				
92	234				
94	266				
95	255				
96	284				
102	247				
107	214				
109	420				
111	267				
114	310				
117	242				

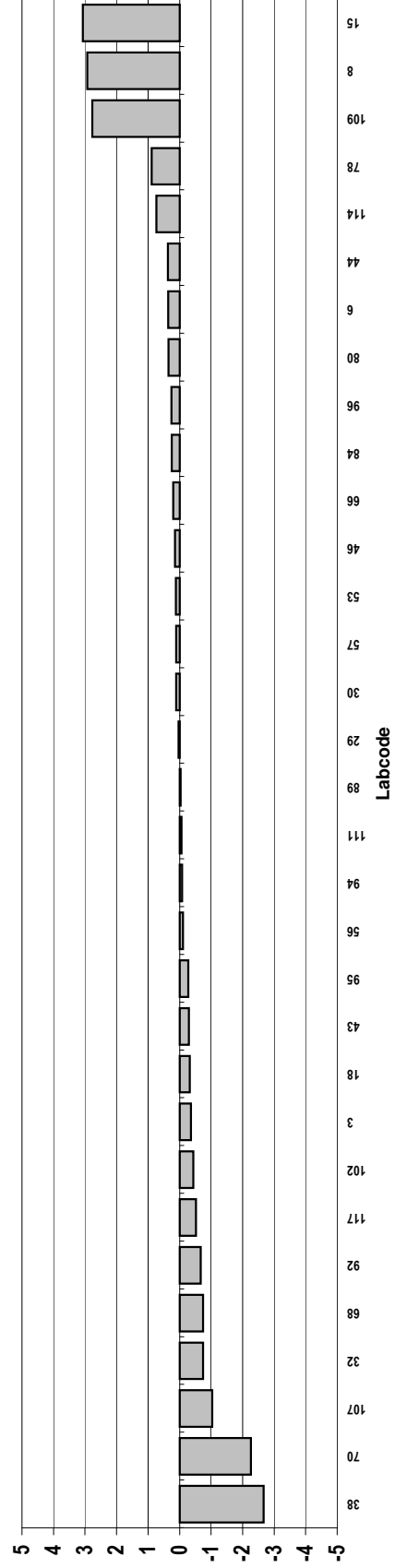
Consensus statistics

Consensus median, pg/g	270
Median all values pg/g	270
Consensus mean, pg/g	274
Standard deviation, pg/g	64
Relative standard deviation, %	23
No. of values reported	32
No. of values removed	0
No. of reported non-detects	0

BDE 47



Z-score: BDE 47

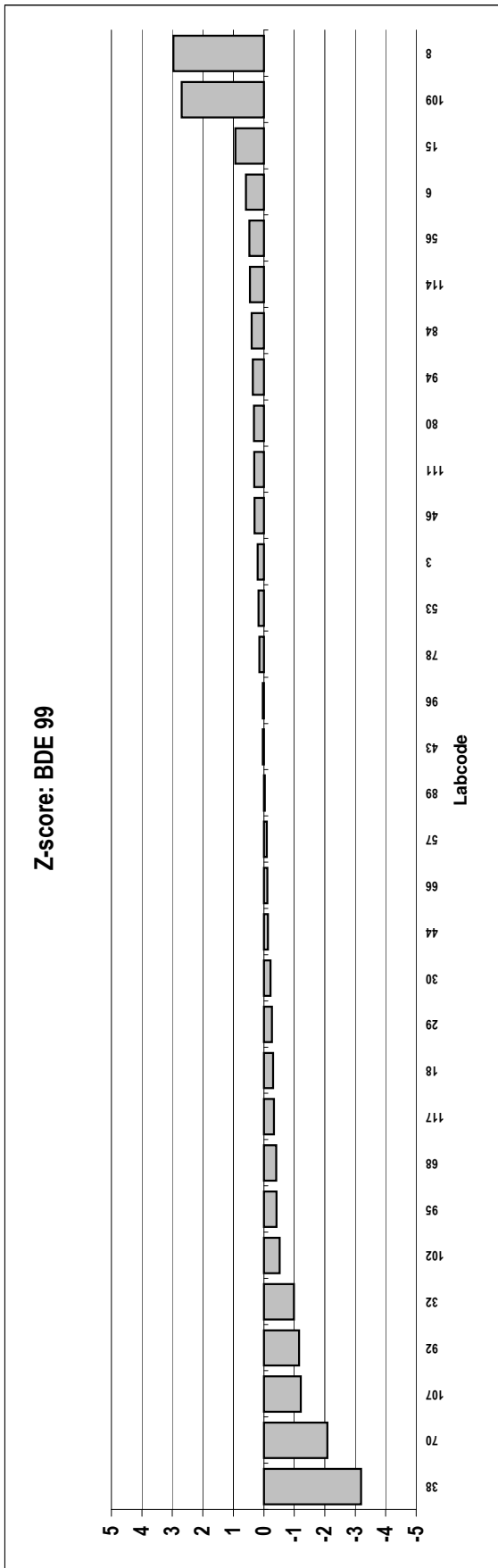
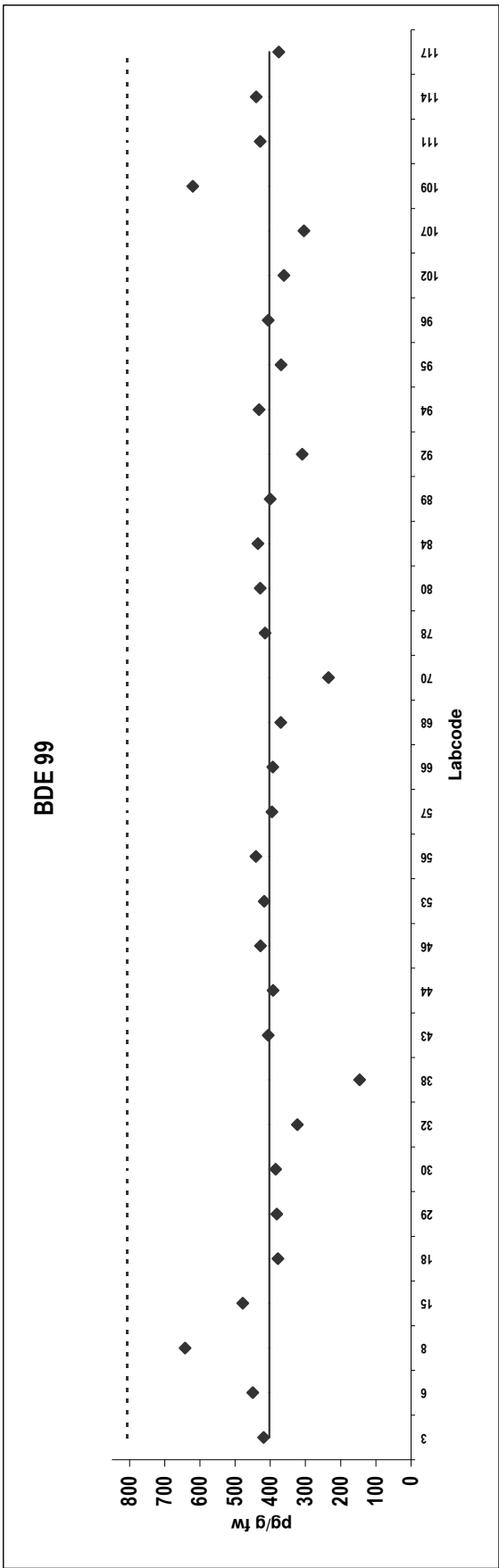


Pork meat
Congener: BDE 99

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	419				
6	450				
8	642				
15	478				
18	378				
29	382				
30	385				
32	323				
38	146				
43	406				
44	392				
46	428				
53	417				
56	441				
57	395				
66	393				
68	370				
70	235				
78	415				
80	429				
84	435				
89	400				
92	310				
94	432				
95	369				
96	406				
102	361				
107	305				
109	620				
111	429				
114	440				
117	376				

Consensus statistics

Consensus median, pg/g	403
Median all values pg/g	403
Consensus mean, pg/g	400
Standard deviation, pg/g	89
Relative standard deviation, %	22
No. of values reported	32
No. of values removed	0
No. of reported non-detects	0

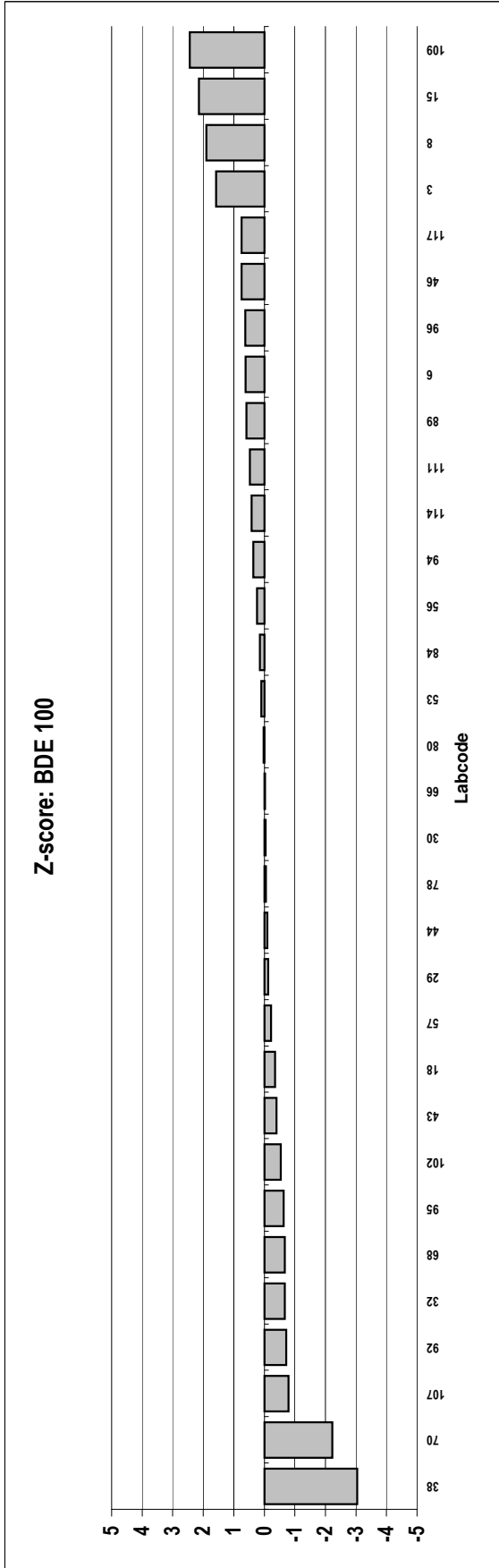
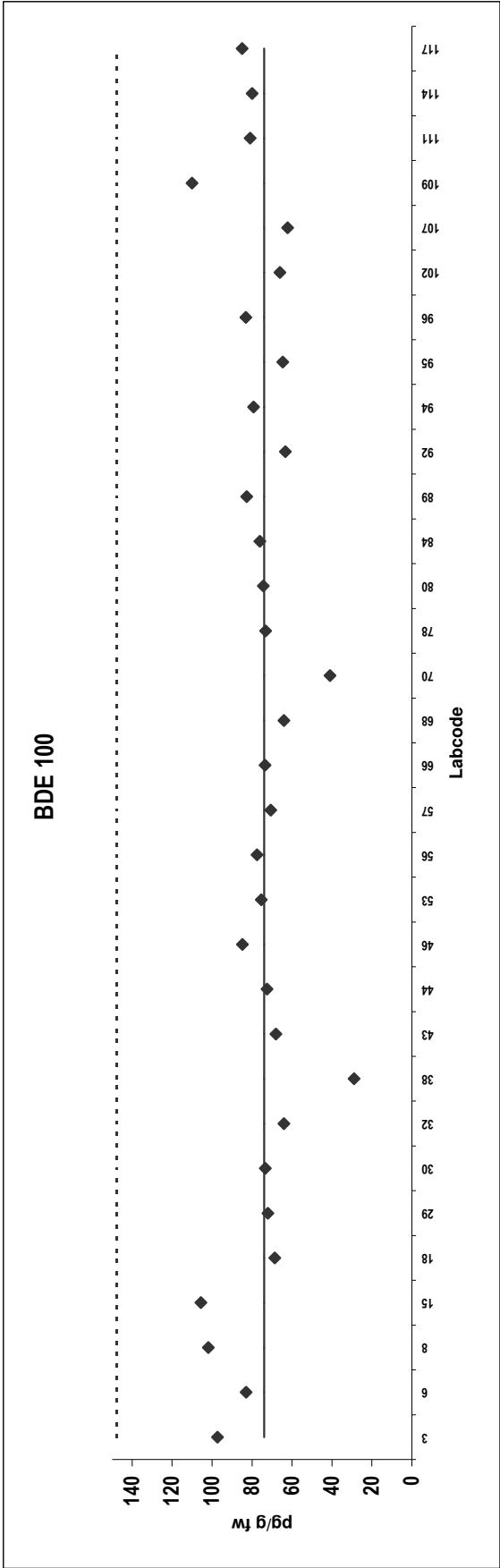


Pork meat
Congener: BDE 100

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	97				
6	83				
8	102				
15	106				
18	69				
29	72				
30	73				
32	64				
38	29				
43	68				
44	73				
46	85				
53	75				
56	77				
57	71				
66	74				
68	64				
70	41				
78	73				
80	74				
84	76				
89	83				
92	63				
94	79				
95	65				
96	83				
102	66				
107	62				
109	110				
111	81				
114	80				
117	85				

Consensus statistics

Consensus median, pg/g	74
Median all values pg/g	74
Consensus mean, pg/g	75
Standard deviation, pg/g	16
Relative standard deviation, %	21
No. of values reported	32
No. of values removed	0
No. of reported non-detects	0



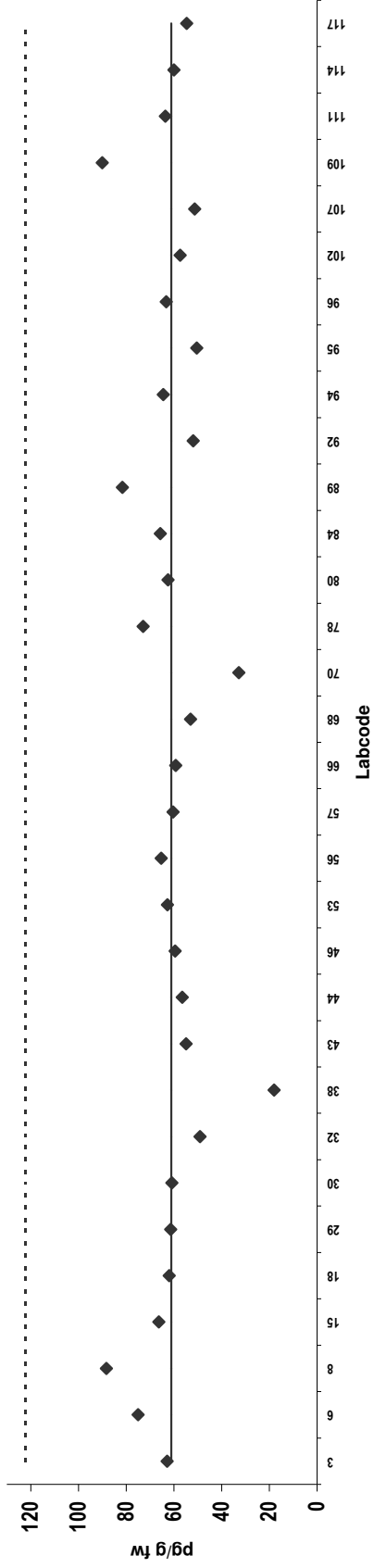
Pork meat
Congener: BDE 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	63				
6	75				
8	88				
15	66				
18	62				
29	61				
30	61				
32	49				
38	18				
43	55				
44	56				
46	59				
53	63				
56	65				
57	60				
66	59				
68	53				
70	33				
78	73				
80	62				
84	66				
89	82				
92	52				
94	64				
95	50				
96	63				
102	57				
107	51				
109	90				
111	64				
114	60				
117	55				

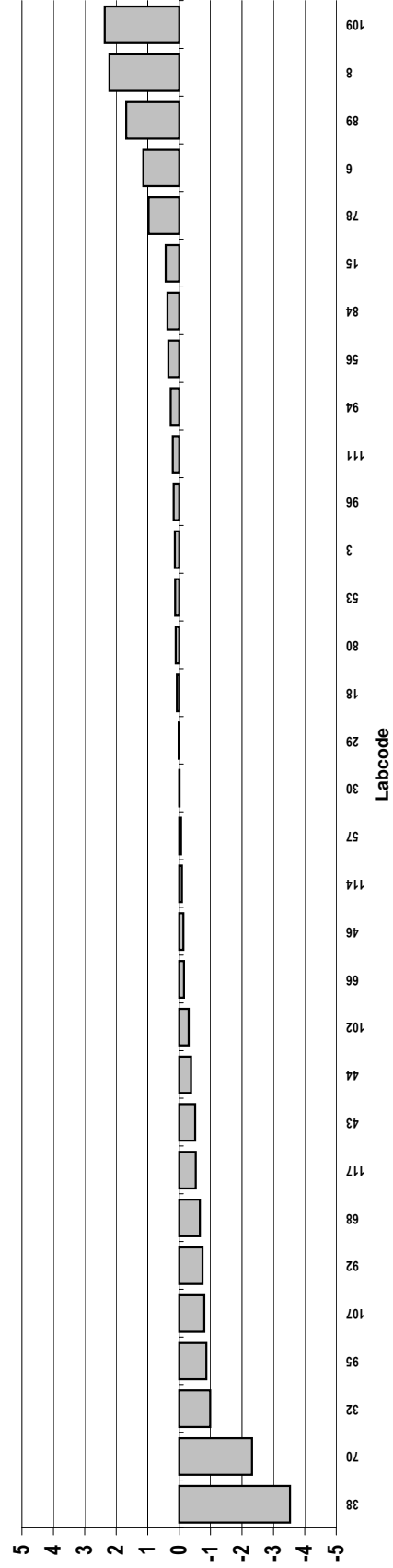
Consensus statistics

Consensus median, pg/g	61
Median all values pg/g	61
Consensus mean, pg/g	61
Standard deviation, pg/g	14
Relative standard deviation, %	22
No. of values reported	32
No. of values removed	0
No. of reported non-detects	0

BDE 153



Z-score: BDE 153



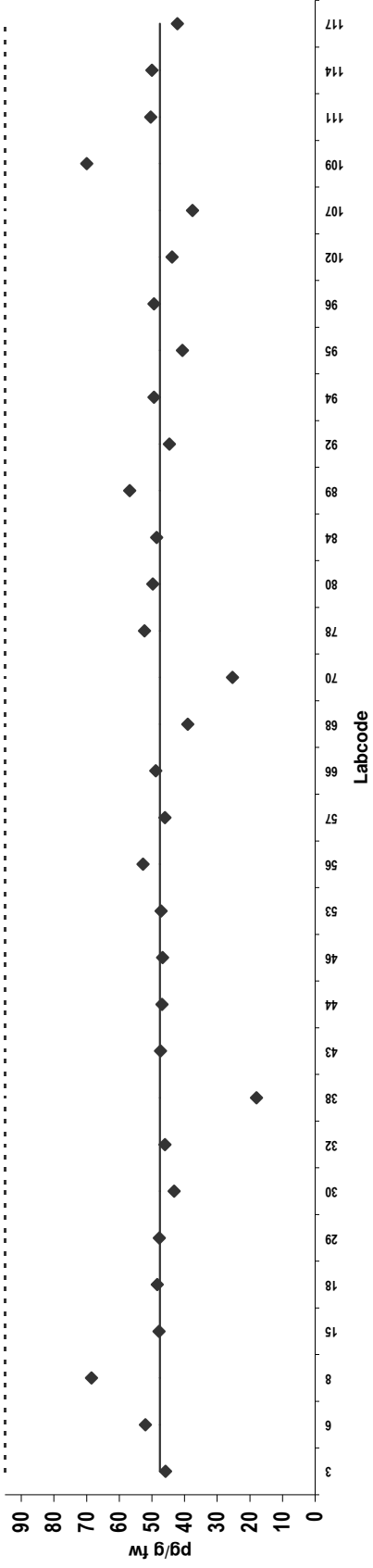
Pork meat
Congener: BDE 154

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	46				
6	52				
8	69				
15	48				
18	48				
29	48				
30	43				
32	46				
38	18				
43	47				
44	47				
46	47				
53	47				
56	53				
57	46				
66	49				
68	39				
70	25				
78	52				
80	50				
84	49				
89	57				
92	45				
94	49				
95	41				
96	49				
102	44				
107	38				
109	70				
111	50				
114	50				
117	42				

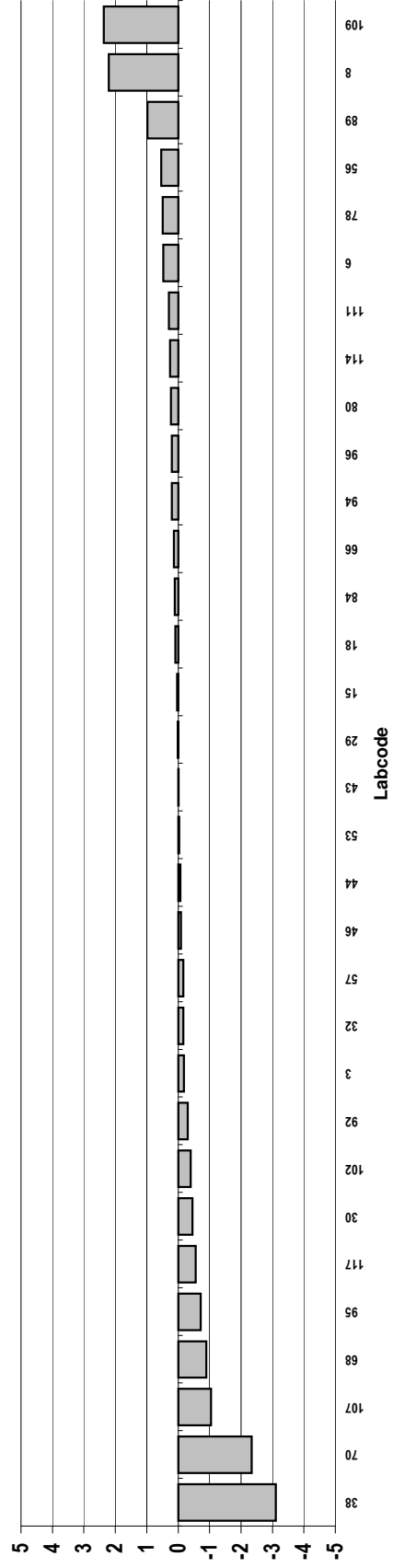
Consensus statistics

Consensus median, pg/g	48
Median all values pg/g	48
Consensus mean, pg/g	47
Standard deviation, pg/g	9.5
Relative standard deviation, %	20
No. of values reported	32
No. of values removed	0
No. of reported non-detects	0

BDE 154



Z-score: BDE 154



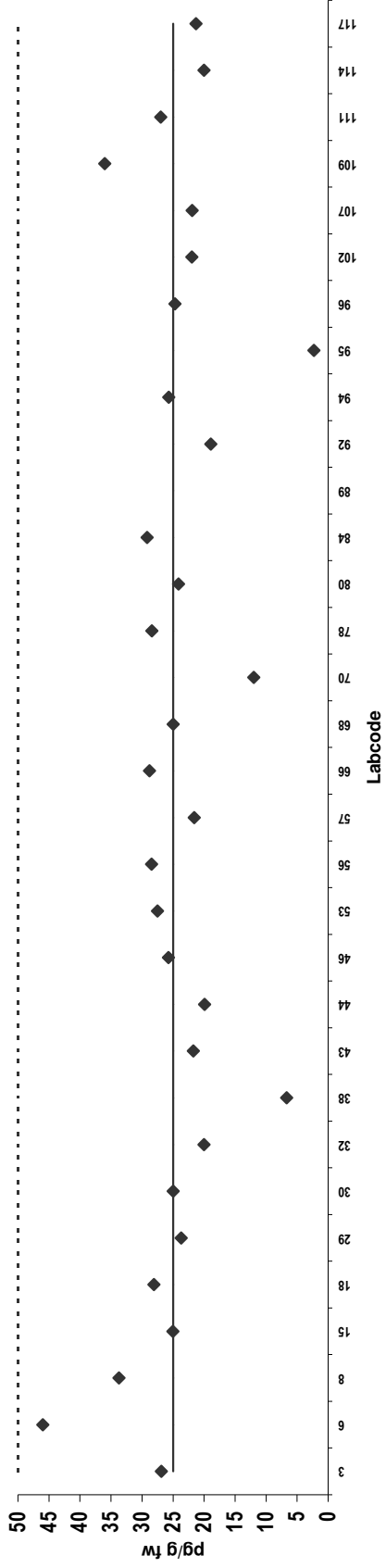
Pork meat
Congener: BDE 183

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	27				
6	46				
8	34				
15	25				
18	28				
29	24				
30	25				
32	20				
38	6.7				
43	22				
44	20				
46	26				
53	28				
56	28				
57	22				
66	29				
68	25				
70	12				
78	28				
80	24				
84	29				
89	92	Outlier			
92	19				
94	26				
95	2.3				
96	25				
102	22				
107	22				
109	36				
111	27				
114	20				
117	21				

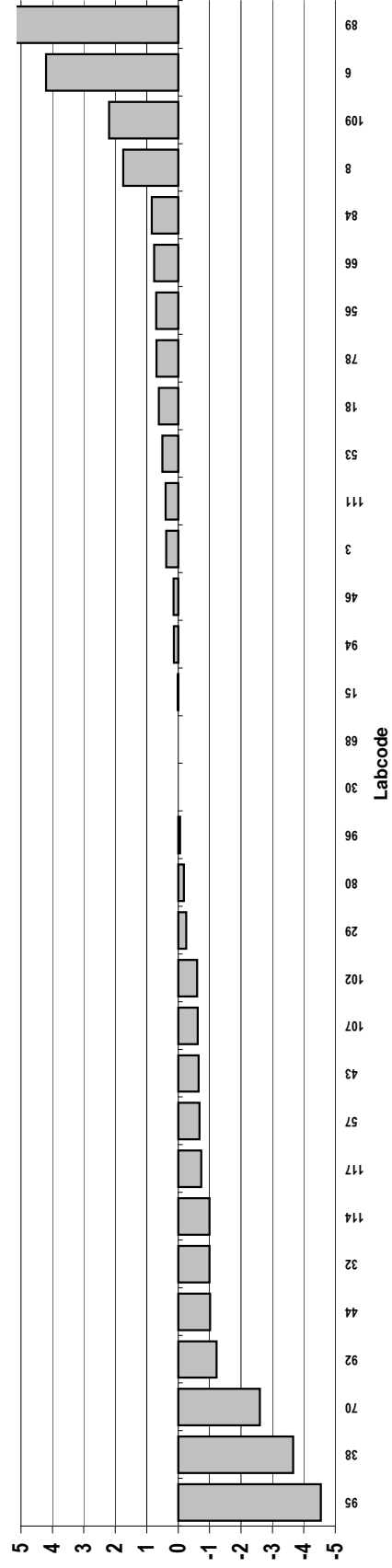
Consensus statistics

Consensus median, pg/g	25
Median all values pg/g	25
Consensus mean, pg/g	24
Standard deviation, pg/g	7.9
Relative standard deviation, %	33
No. of values reported	32
No. of values removed	1
No. of reported non-detects	0

BDE 183



Z-score: BDE 183

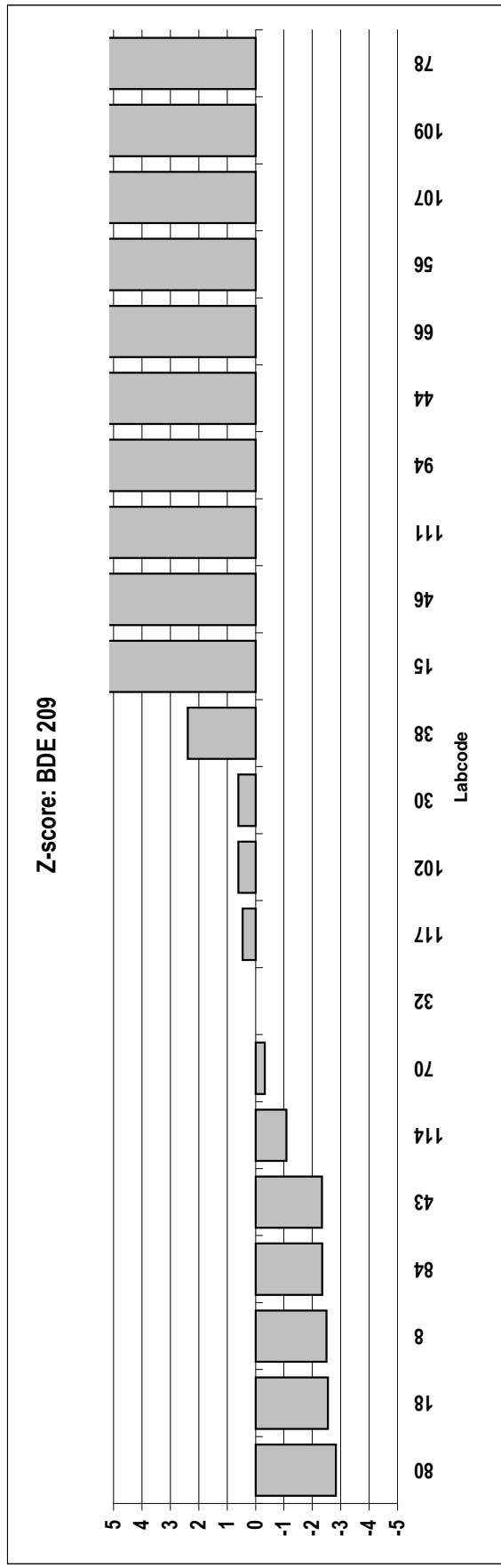
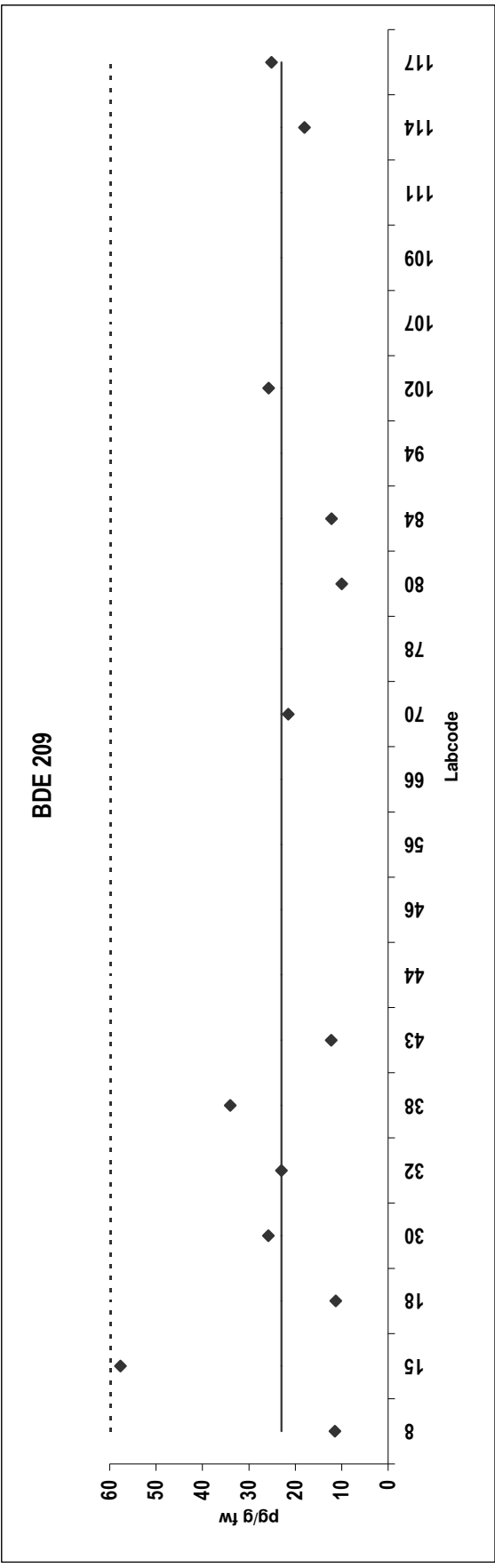


Pork meat
Congener: BDE 209

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
8	11	ND			
15	58				
18	11				
30	26	ND			
32	23				
38	34				
43	12	ND			
44	81	Outlier			
46	63	Outlier			
56	113	Outlier			
66	102	Outlier			
70	22				
78	626	Outlier,ND			
80	10	ND			
84	12				
94	75	Outlier			
102	26				
107	123	Outlier			
109	170	Outlier			
111	65	Outlier			
114	18				
117	25				

Consensus statistics

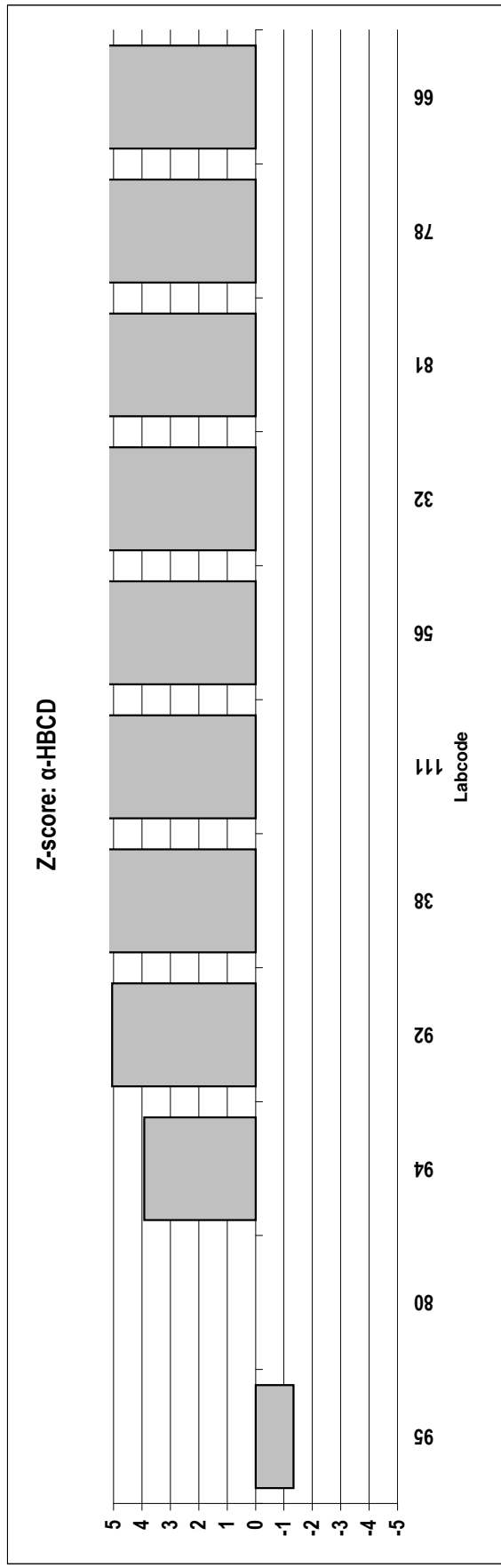
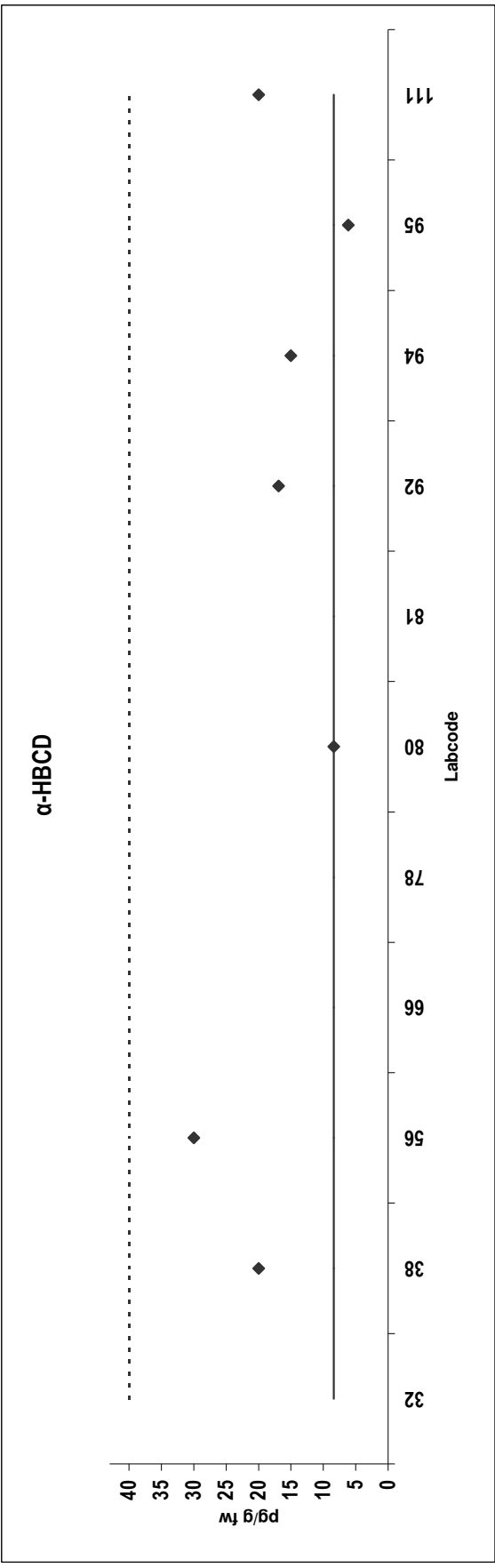
Consensus median, pg/g	23
Median all values pg/g	30
Consensus mean, pg/g	22
Standard deviation, pg/g	13
Relative standard deviation, %	59
No. of values reported	22
No. of values removed	9
No. of reported non-detects	5



Pork meat
Congener: α -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
32	50	Outlier,ND			
38	20	ND			
56	30	ND			
66	403	Outlier			
78	1.42	Outlier,ND			
80	8.4				
81	60	Outlier			
92	17				
94	15	ND			
95	6.2				
111	20	ND			

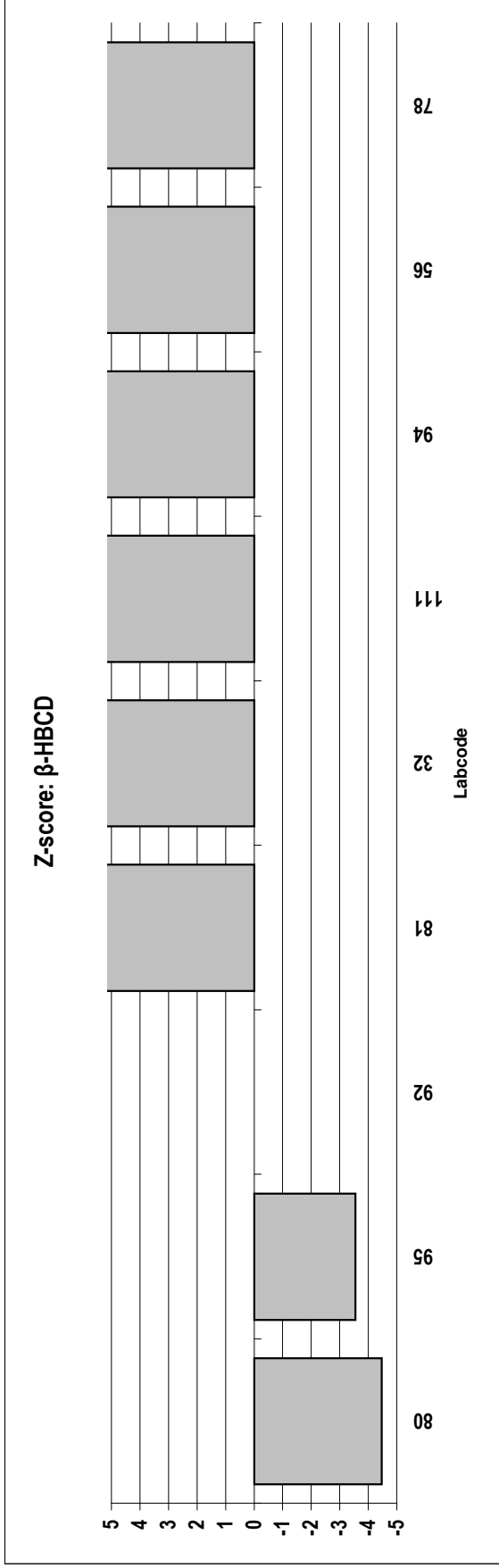
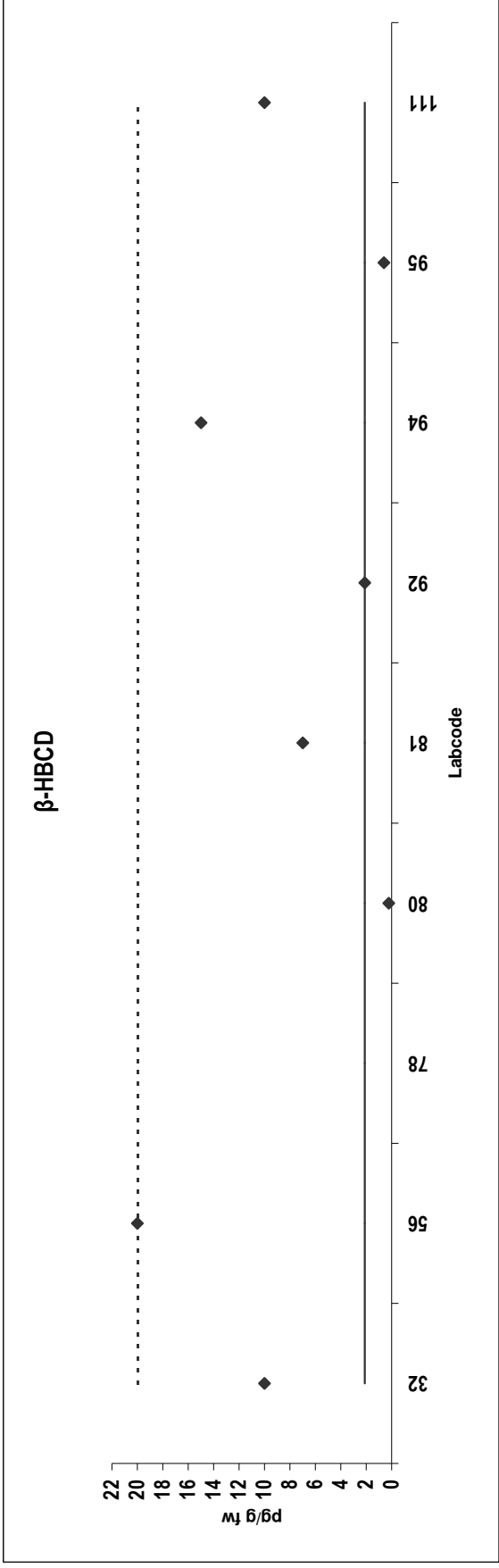
Consensus statistics	
Consensus median, pg/g	8.4
Median all values pg/g	20
Consensus mean, pg/g	17
Standard deviation, pg/g	8.0
Relative standard deviation, %	48
No. of values reported	11
No. of values removed	4
No. of reported non-detects	6



Pork meat
Congener: β -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
32	10	ND			
56	20	ND			
78	216	Outlier,ND			
80	0.22	ND			
81	7.0				
92	2.1				
94	15	ND			
95	0.61				
111	10	ND			

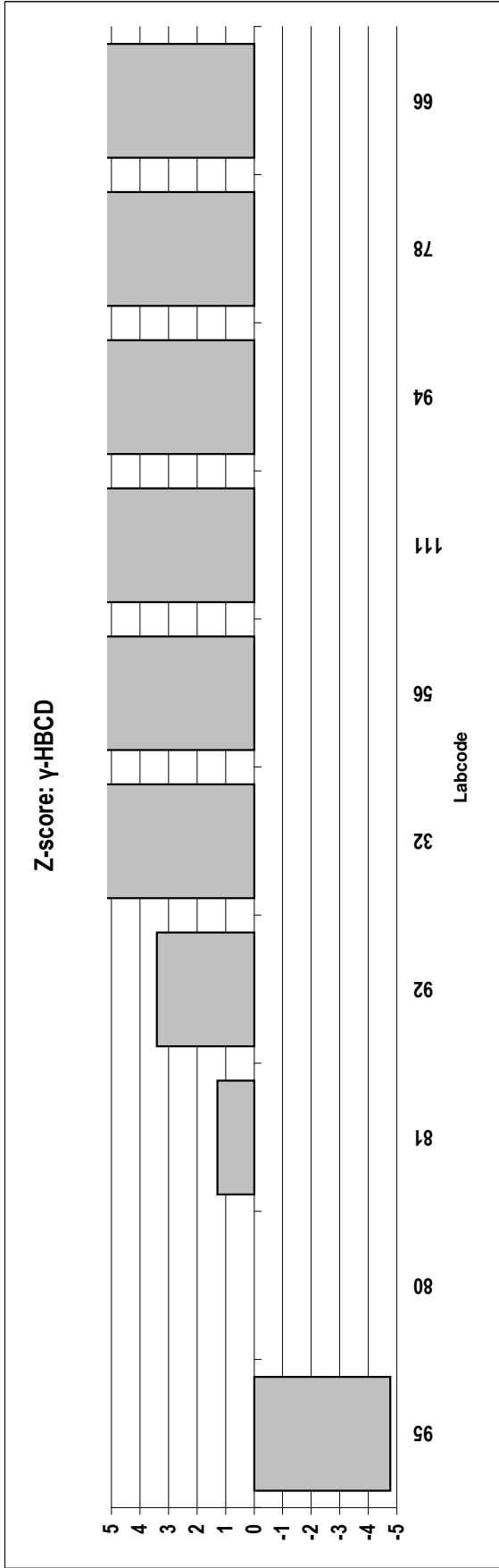
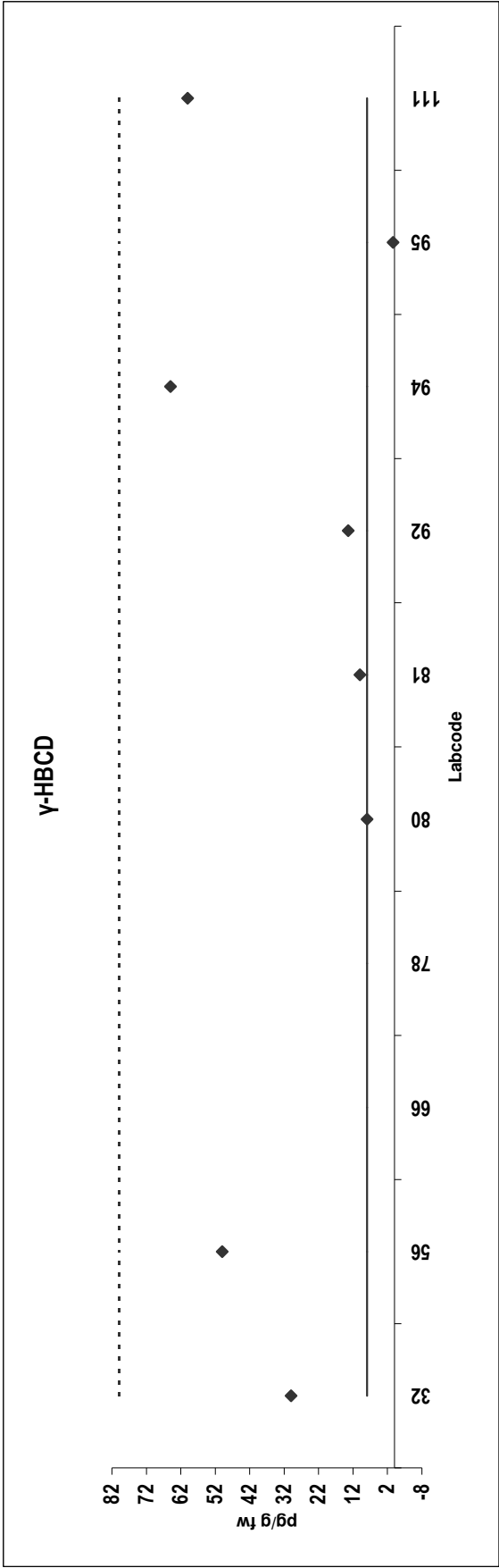
Consensus statistics	
Consensus median, pg/g	2.1
Median all values pg/g	10
Consensus mean, pg/g	8.1
Standard deviation, pg/g	7.1
Relative standard deviation, %	87
No. of values reported	9
No. of values removed	1
No. of reported non-detects	6



Pork meat
Congener: γ -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
32	30	ND			
56	50	ND			
66	150	Outlier			
78	107	Outlier,ND			
80	8.0				
81	10	ND			
92	13				
94	65	ND			
95	0.37				
111	60	ND			

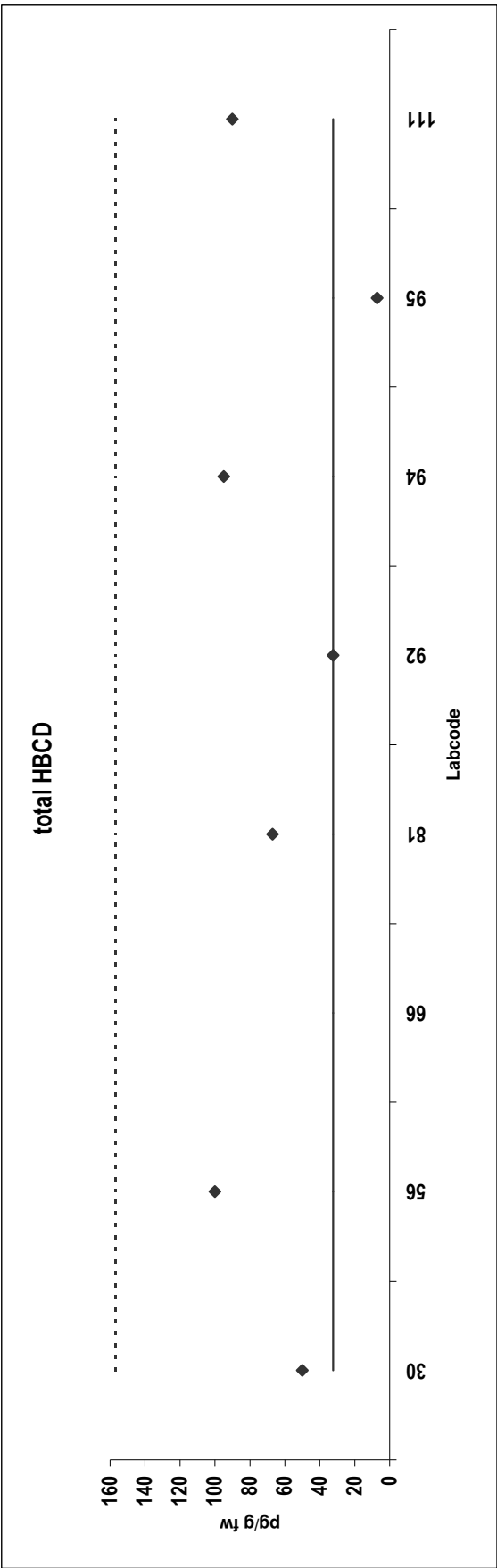
Consensus statistics	
Consensus median, pg/g	8.0
Median all values pg/g	40
Consensus mean, pg/g	30
Standard deviation, pg/g	26
Relative standard deviation, %	86
No. of values reported	10
No. of values removed	2
No. of reported non-detects	6



Pork meat
Congener: total HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
30	50	ND			
56	100	ND			
66	553	Outlier			
81	67				
92	32				
94	95	ND			
95	7.1				
111	90	ND			

Consensus statistics	
Consensus median, pg/g	32
Median all values pg/g	79
Consensus mean, pg/g	63
Standard deviation, pg/g	35
Relative standard deviation, %	56
No. of values reported	8
No. of values removed	1
No. of reported non-detects	4



Appendix 4:

Presentation of results
for trout

Appendix 4: Presentation of results: Trout

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:

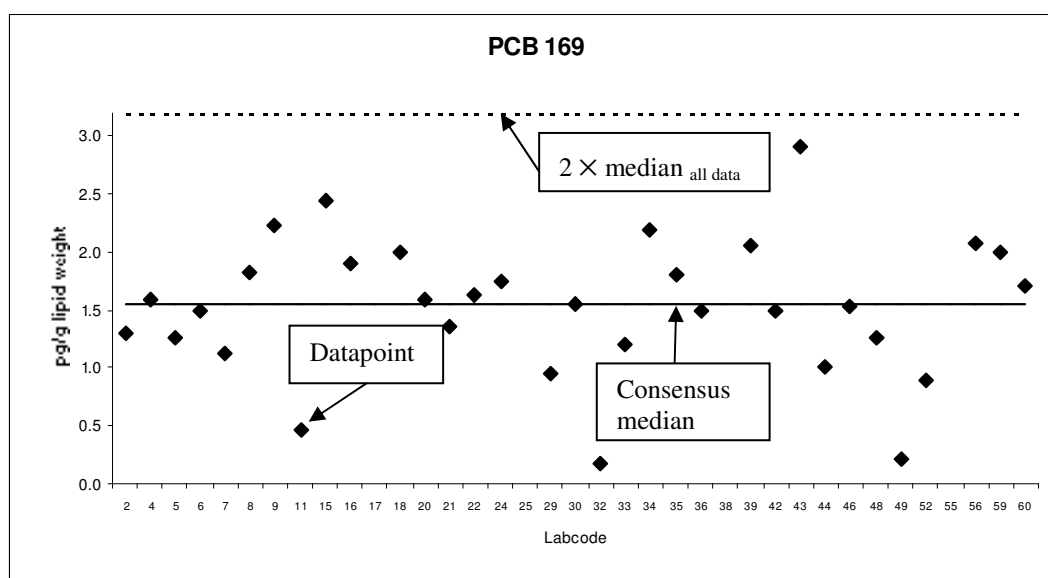
1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners.
2. Values exceeding $2 \times$ this median, were defined as outliers and removed from the data set.
3. Median, mean and standard deviation were re-calculated from the remaining 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); σ = target value for standard deviation. A σ 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.

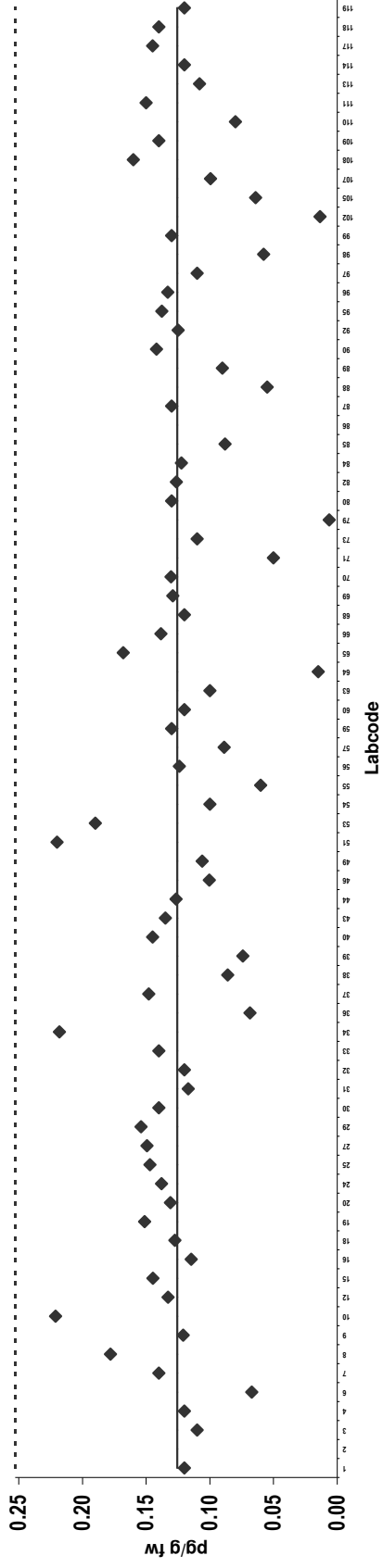
Trout
Congener: 2,3,7,8 TCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.12		68	0.12	
2	0.30		69	0.13	
3	0.11	Outlier	70	0.13	
4	0.12		71	0.050	ND
6	0.067		73	0.11	
7	0.14		79	0.0063	ND
8	0.18		80	0.13	
9	0.12		82	0.13	
10	0.22		84	0.12	
12	0.13		85	0.088	
15	0.14		86	0.50	Outlier,ND
16	0.11		87	0.13	
18	0.13		88	0.055	
19	0.15		89	0.090	
20	0.13		90	0.14	
24	0.14		92	0.12	
25	0.15		95	0.14	
27	0.15		96	0.13	
29	0.15		97	0.11	
30	0.14		98	0.058	
31	0.12		99	0.13	
32	0.12		102	0.013	ND
33	0.14		105	0.064	
34	0.22		107	0.10	
36	0.068		108	0.16	
37	0.15		109	0.14	
38	0.086		110	0.080	
39	0.074		111	0.15	
40	0.15		113	0.11	
43	0.13		114	0.12	
44	0.13		117	0.15	
46	0.10		118	0.14	
49	0.11		119	0.12	
51	0.22				
53	0.19				
54	0.10				
55	0.060				
56	0.12				
57	0.089				
59	0.13				
60	0.12				
63	0.10				
64	0.015	ND			
65	0.17				
66	0.14				

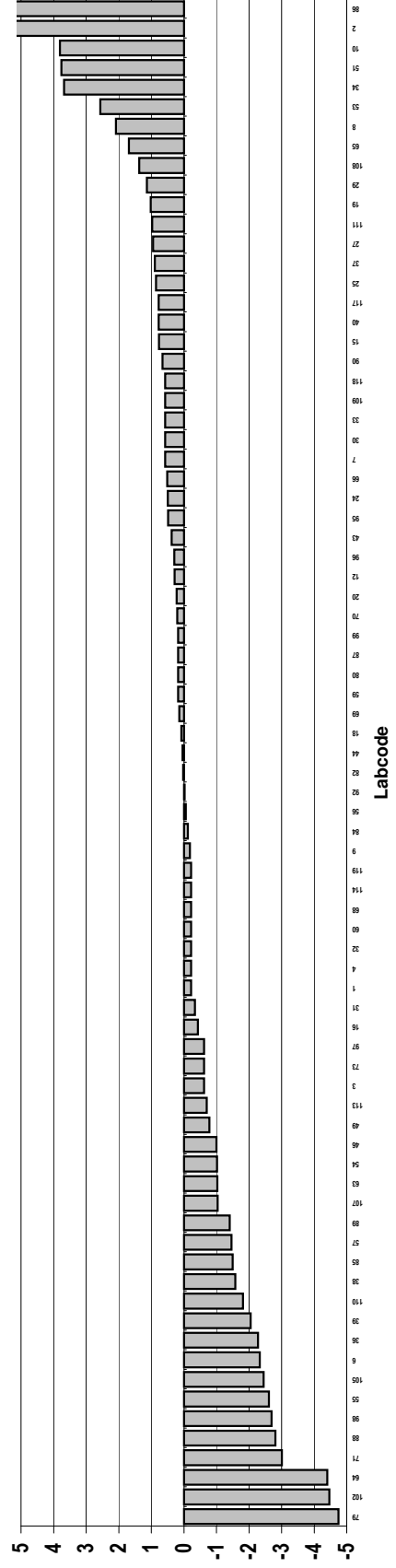
Consensus statistics

Consensus median, pg/g	0.13
Median all values pg/g	0.13
Consensus mean, pg/g	0.12
Standard deviation, pg/g	0.041
Relative standard deviation, %	34
No. of values reported	78
No. of values removed	2
No. of reported non-detects	5

2,3,7,8 TCDD



Z-score: 2,3,7,8 TCDD



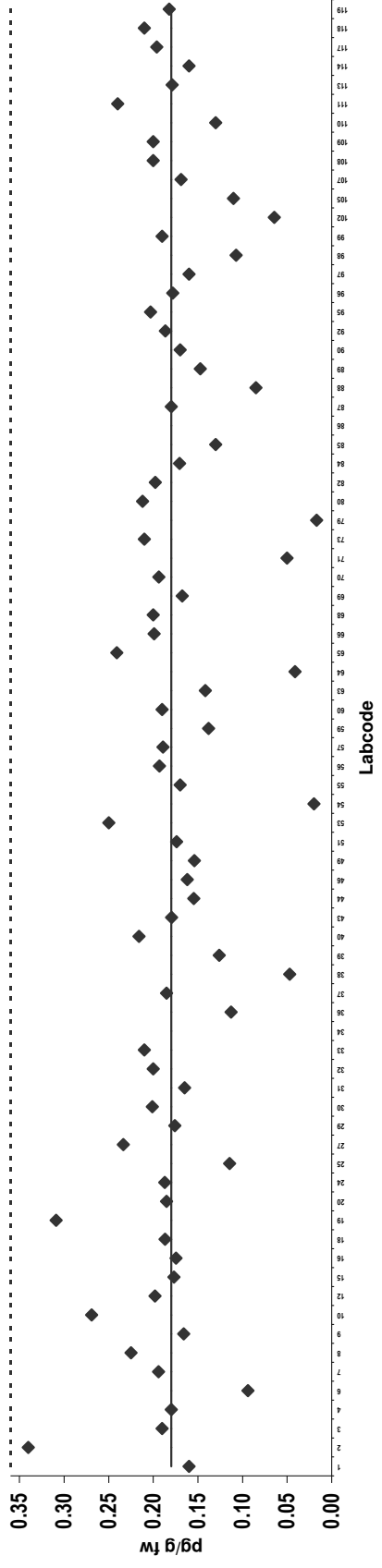
Trout
Congener: 1,2,3,7,8 PeCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.16	ND	68	0.20	
2	0.34		69	0.17	
3	0.19		70	0.19	
4	0.18		71	0.050	ND
6	0.094		73	0.21	
7	0.19		79	0.017	ND
8	0.23		80	0.21	
9	0.17		82	0.20	
10	0.27		84	0.17	
12	0.20		85	0.13	
15	0.18		86	0.50	
16	0.17		87	0.18	Outlier,ND
18	0.19		88	0.085	
19	0.31		89	0.15	
20	0.19		90	0.17	
24	0.19		92	0.19	
25	0.11		95	0.20	
27	0.23		96	0.18	
29	0.18		97	0.16	
30	0.20		98	0.11	
31	0.17		99	0.19	
32	0.20		102	0.064	ND
33	0.21		105	0.11	
34	22	Outlier	107	0.17	
36	0.11		108	0.20	
37	0.19		109	0.20	
38	0.047		110	0.13	
39	0.13		111	0.24	
40	0.22		113	0.18	
43	0.18		114	0.16	
44	0.15		117	0.20	
46	0.16		118	0.21	
49	0.15		119	0.18	
51	0.17				
53	0.25				
54	0.020				
55	0.17				
56	0.19				
57	0.19				
59	0.14				
60	0.19				
63	0.14				
64	0.041				
65	0.24				
66	0.20				

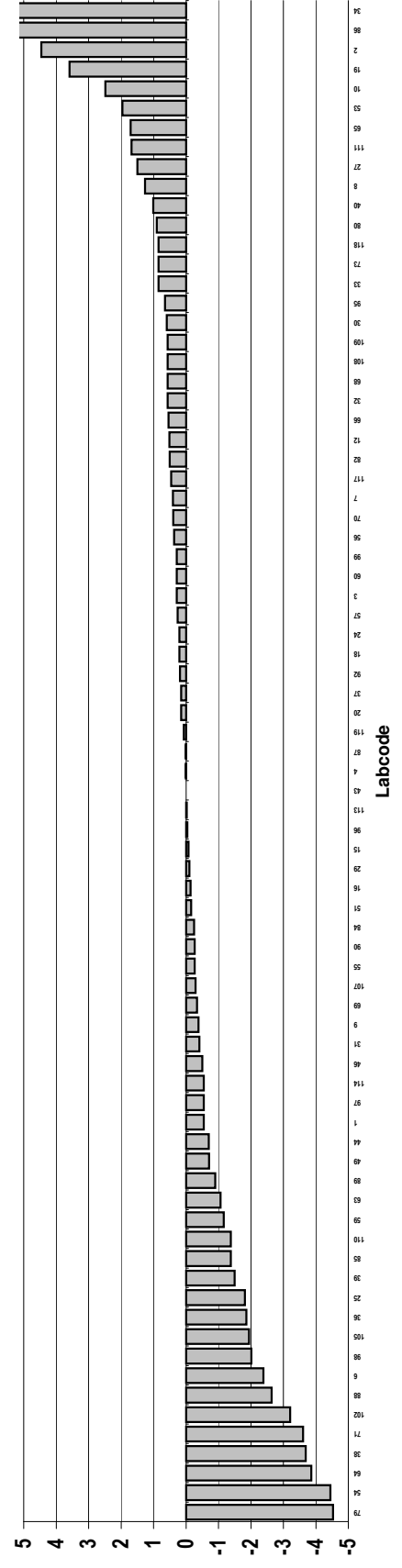
Consensus statistics

Consensus median, pg/g	0.18
Median all values pg/g	0.18
Consensus mean, pg/g	0.17
Standard deviation, pg/g	0.057
Relative standard deviation, %	33
No. of values reported	78
No. of values removed	2
No. of reported non-detects	5

1,2,3,7,8 PeCDD



Z-score: 1,2,3,7,8 PeCDD

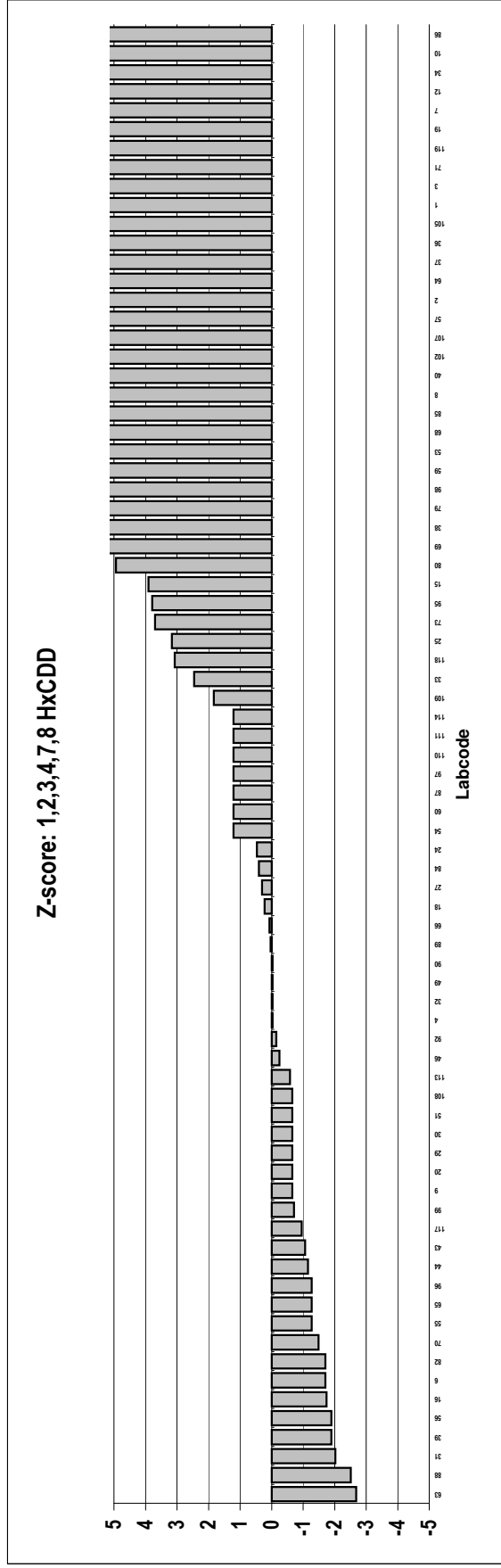
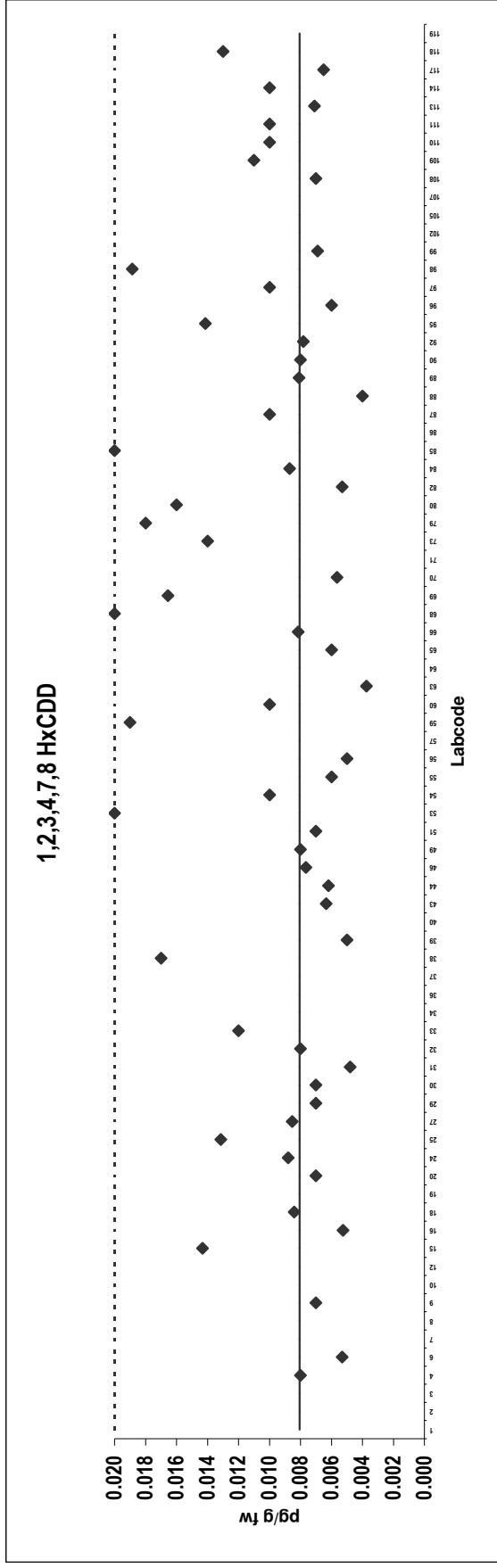


Trout
Congener: 1,2,3,4,7,8 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.047		68	0.020	ND
2	0.030	Outlier,ND	69	0.017	ND
3	0.050	Outlier,ND	70	0.0056	ND
4	0.0080	Outlier	71	0.050	Outlier,ND
5	0.0053		73	0.014	
6	0.062	ND	79	0.018	ND
7	0.021	Outlier	80	0.016	ND
8	0.0070	Outlier,ND	82	0.0053	
9	0.15	Outlier	84	0.0087	
10	0.063	Outlier,ND	85	0.020	ND
12	0.014		86	1.0	Outlier,ND
15	0.0053		87	0.010	ND
16	0.0084		88	0.0040	
18	0.0053		89	0.0081	
19	0.0070	Outlier	90	0.0080	
20	0.0088		92	0.0078	
24	0.013		95	0.014	ND
25	0.085		96	0.0060	ND
27	0.0070		97	0.010	ND
29	0.0070		98	0.019	
30	0.0048		99	0.0069	
31	0.0080		102	0.025	Outlier,ND
32	0.012		105	0.040	Outlier,ND
33	0.11	Outlier,ND	107	0.026	Outlier,ND
34	0.038	Outlier	108	0.0070	
36	0.036	Outlier,ND	109	0.011	
37	0.017		110	0.010	ND
38	0.0050	ND	111	0.010	
39	0.023	Outlier	113	0.0071	
40	0.0063		114	0.010	
43	0.0062		117	0.0065	
44	0.0077		118	0.013	
46	0.0080		119	0.050	Outlier,ND
49	0.0070				
51	0.020				
53	0.010				
54	0.060				
55	0.0050				
56	0.026	Outlier			
57	0.019				
59	0.010				
60	0.0037				
63	0.031	ND			
64	0.060	Outlier			
65	0.0082	ND			
66					

Consensus statistics

Consensus median, pg/g	0.0081
Median all values pg/g	0.010
Consensus mean, pg/g	0.010
Standard deviation, pg/g	0.0045
Relative standard deviation, %	47
No. of values reported	78
No. of values removed	20
No. of reported non-detects	27



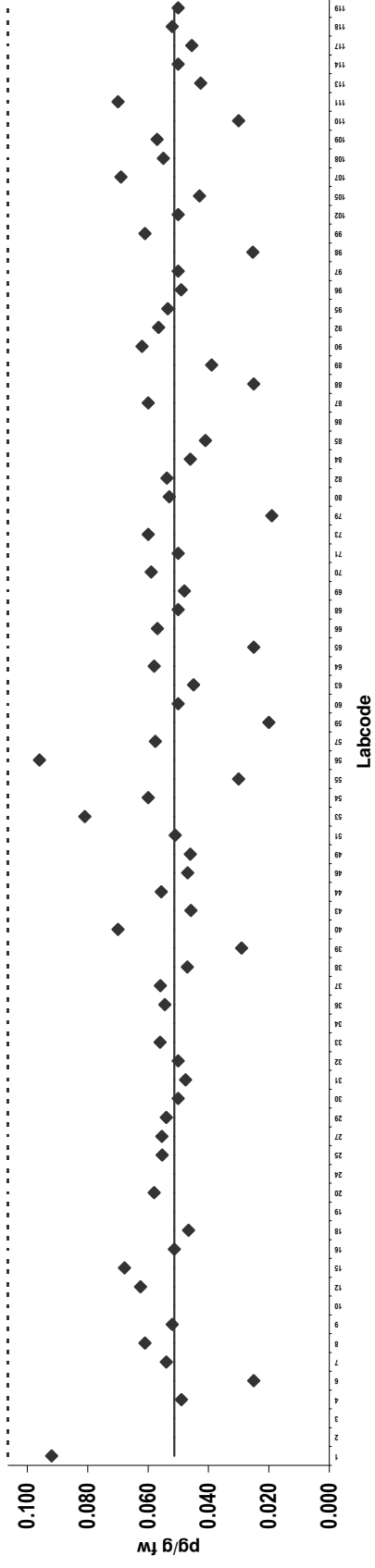
Trout
Congener: 1,2,3,6,7,8 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.092	ND	68	0.050	
2	0.12	Outlier	69	0.048	
3	0.11	Outlier	70	0.059	
4	0.049		71	0.050	ND
6	0.025		73	0.060	
7	0.054		79	0.019	ND
8	0.061		80	0.053	
9	0.052		82	0.054	
10	0.20	Outlier	84	0.046	
12	0.063	ND	85	0.041	Outlier,ND
15	0.068		86	1.0	
16	0.051		87	0.060	
18	0.047		88	0.025	
19	0.16	Outlier	89	0.039	
20	0.058		90	0.062	
24	0.60	Outlier	92	0.057	
25	0.055		95	0.053	
27	0.055		96	0.049	
29	0.054		97	0.050	
30	0.050		98	0.025	
31	0.048		99	0.061	
32	0.050		102	0.050	
33	0.056		105	0.043	
34	0.12	Outlier,ND	107	0.069	ND
36	0.055		108	0.055	
37	0.056		109	0.057	
38	0.047		110	0.030	
39	0.029		111	0.070	
40	0.070		113	0.043	
43	0.046		114	0.050	
44	0.056		117	0.046	
46	0.047		118	0.052	
49	0.046		119	0.050	ND
51	0.051				
53	0.081				
54	0.060				
55	0.030				
56	0.096				
57	0.058				
59	0.020				
60	0.050				
63	0.045				
64	0.058				
65	0.025				
66	0.057				

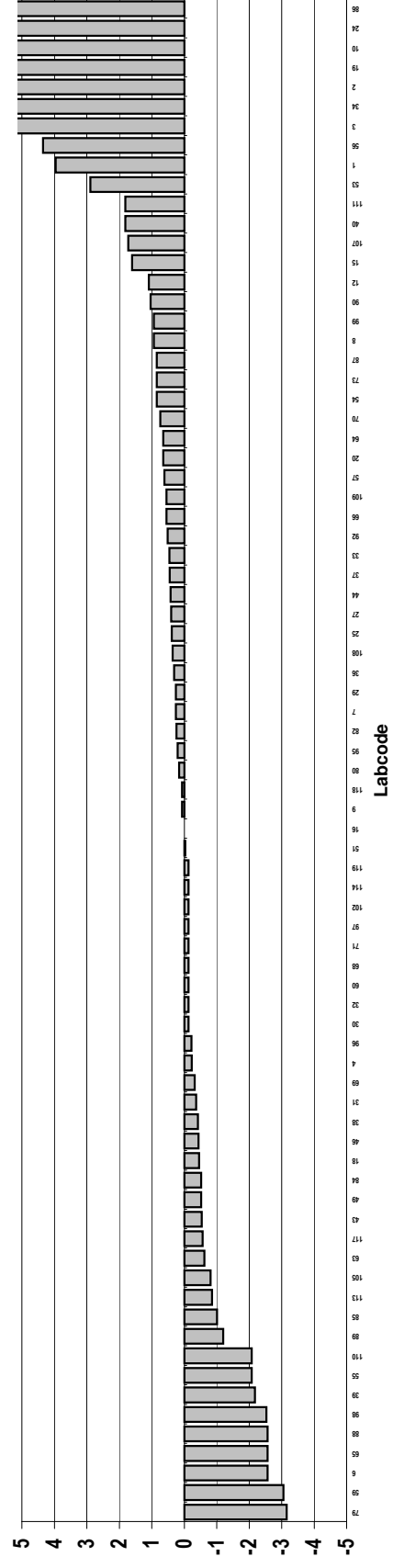
Consensus statistics

Consensus median, pg/g	0.051
Median all values pg/g	0.053
Consensus mean, pg/g	0.051
Standard deviation, pg/g	0.014
Relative standard deviation, %	27
No. of values reported	78
No. of values removed	7
No. of reported non-detects	8

1,2,3,6,7,8 HxCDD



Z-score: 1,2,3,6,7,8 HxCDD



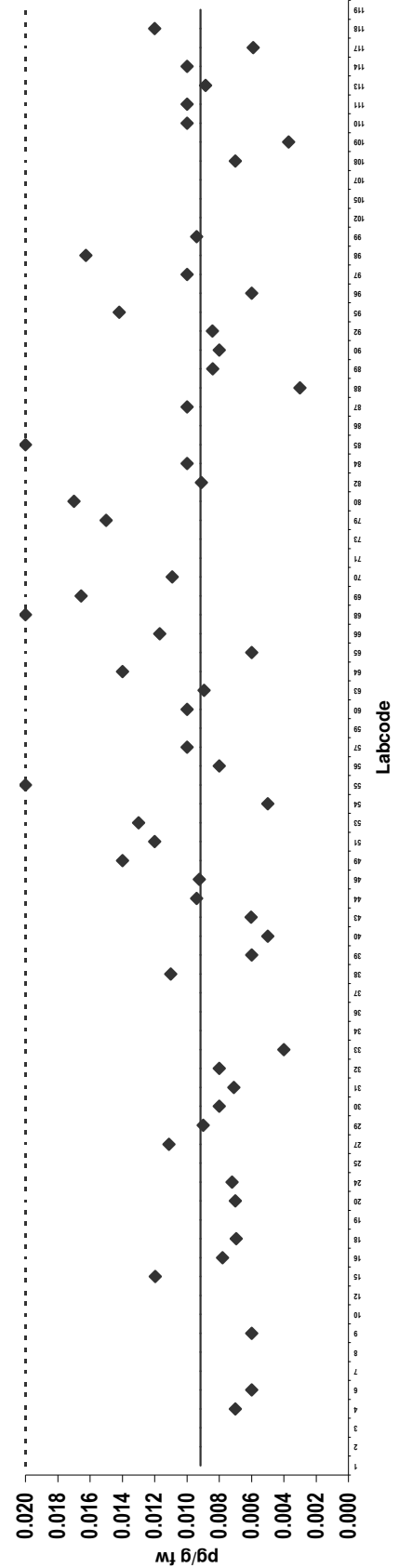
Trout
Congener: 1,2,3,7,8,9 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.043	Outlier,ND	68	0.020	ND
2	0.070	Outlier	69	0.017	ND
3	0.070	Outlier	70	0.011	
4	0.0070		71	0.050	Outlier,ND
6	0.0060	ND	73	0.021	Outlier
7	0.032	Outlier,ND	79	0.015	ND
8	0.050	Outlier,ND	80	0.017	ND
9	0.0060		82	0.0091	
10	0.18	Outlier	84	0.010	
12	0.063	Outlier,ND	85	0.020	ND
15	0.012	ND	86	1.0	Outlier,ND
16	0.0078		87	0.010	ND
18	0.0069		88	0.0030	
19	0.16	Outlier	89	0.0084	
20	0.0070		90	0.0080	
24	0.0072		92	0.0084	
25	0.023	Outlier	95	0.014	
27	0.011		96	0.0060	ND
29	0.0090		97	0.010	
30	0.0080		98	0.016	
31	0.0071		99	0.0094	
32	0.0080		102	0.064	Outlier
33	0.0040	ND	105	0.041	Outlier,ND
34	0.12	Outlier,ND	107	0.053	Outlier,ND
36	0.10	Outlier	108	0.0070	
37	0.040	Outlier,ND	109	0.0037	ND
38	0.011		110	0.010	ND
39	0.0060	ND	111	0.010	
40	0.0050	ND	113	0.0088	
43	0.0060		114	0.010	
44	0.0094		117	0.0059	
46	0.0092		118	0.012	
49	0.014		119	0.050	Outlier,ND
51	0.012				
53	0.013				
54	0.0050				
55	0.020				
56	0.0080				
57	0.010	ND			
59	0.046	Outlier			
60	0.010				
63	0.0089				
64	0.014				
65	0.0060	ND			
66	0.012				

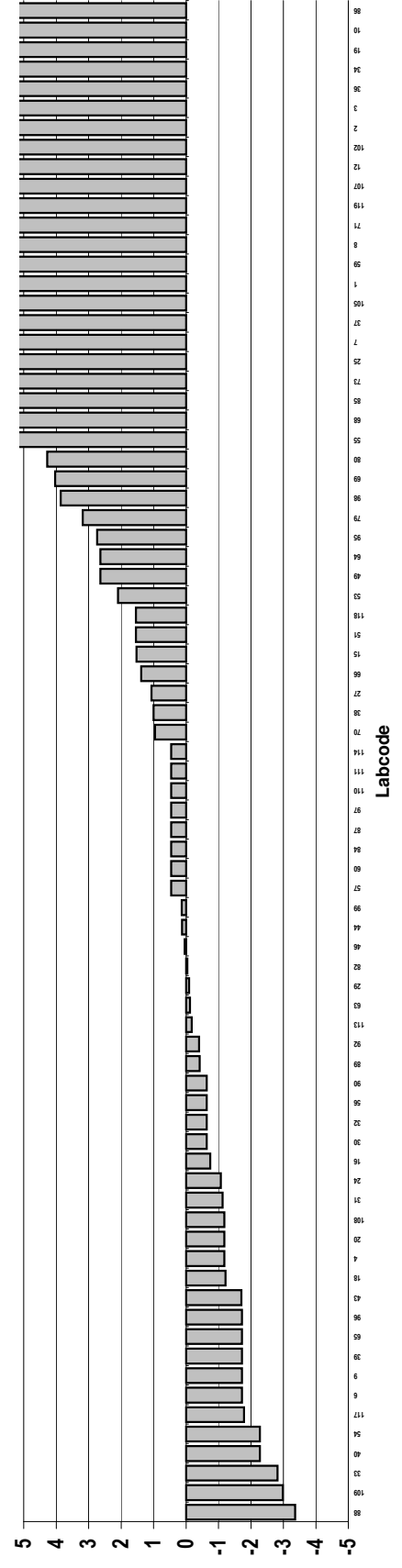
Consensus statistics

Consensus median, pg/g	0.0092
Median all values pg/g	0.010
Consensus mean, pg/g	0.010
Standard deviation, pg/g	0.0040
Relative standard deviation, %	41
No. of values reported	78
No. of values removed	20
No. of reported non-detects	27

1,2,3,7,8,9 HxCDD



Z-score: 1,2,3,7,8,9 HxCDD



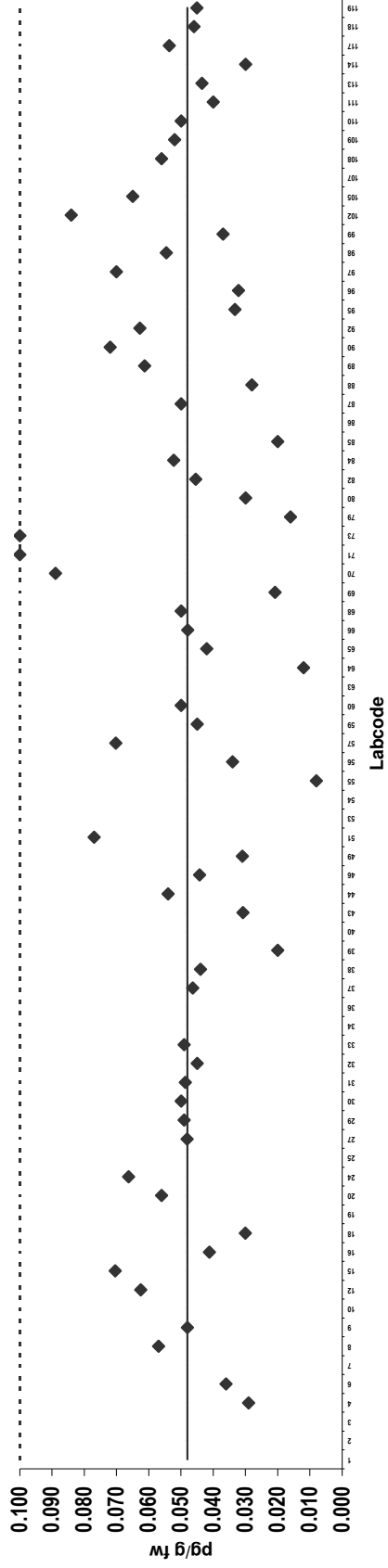
Trout
Congener: 1,2,3,4,6,7,8 HpCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.32		68	0.050	
2	0.15	Outlier	69	0.021	
3	0.20	Outlier	70	0.089	
4	0.029	Outlier	71	0.10	ND
6	0.036		73	0.10	
7	0.30	Outlier	79	0.016	ND
8	0.057	ND	80	0.030	
9	0.048		82	0.045	
10	0.44	Outlier	84	0.052	
12	0.063	ND	85	0.020	ND
15	0.070		86	1.0	Outlier,ND
16	0.041		87	0.050	
18	0.030		88	0.028	
19	0.30	Outlier	89	0.061	
20	0.056		90	0.072	
24	0.066		92	0.063	
25	0.11	Outlier	95	0.033	
27	0.048		96	0.032	
29	0.049		97	0.070	
30	0.050		98	0.055	
31	0.049		99	0.037	ND
32	0.045		102	0.084	ND
33	0.049		105	0.065	ND
34	0.26	Outlier	107	0.12	Outlier
36	0.41	Outlier	108	0.056	
37	0.046	ND	109	0.052	
38	0.044		110	0.050	
39	0.020	ND	111	0.040	ND
40	0.26	Outlier	113	0.044	
43	0.031		114	0.030	
44	0.054		117	0.054	
46	0.044		118	0.046	
49	0.031		119	0.045	
51	0.077				
53	0.13	Outlier			
54	0.13	Outlier			
55	0.0080				
56	0.034				
57	0.070				
59	0.045				
60	0.050				
63	0.19				
64	0.012	Outlier			
65	0.042				
66	0.048				

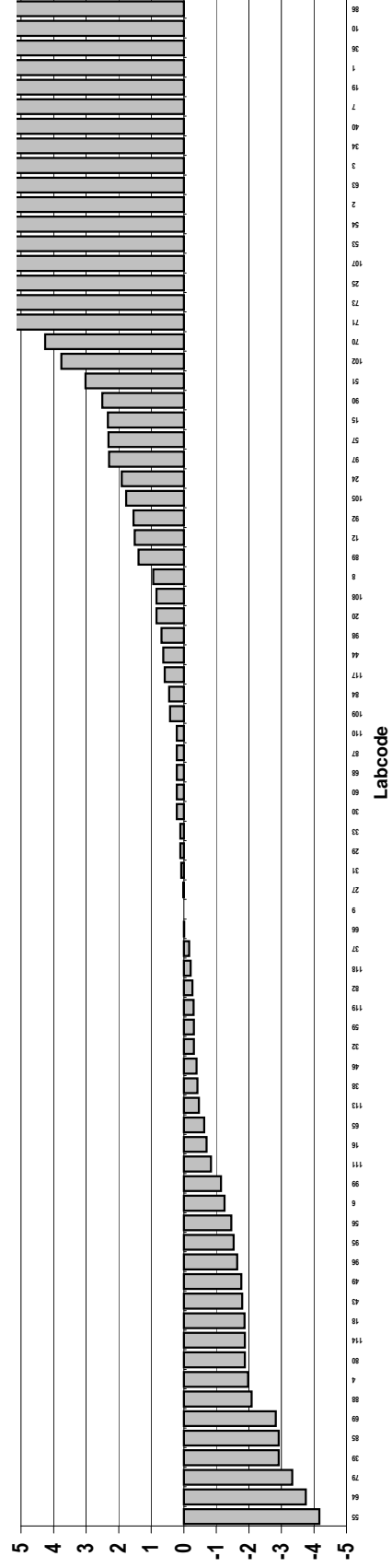
Consensus statistics

Consensus median, pg/g	0.048
Median all values pg/g	0.050
Consensus mean, pg/g	0.048
Standard deviation, pg/g	0.019
Relative standard deviation, %	40
No. of values reported	78
No. of values removed	15
No. of reported non-detects	12

1,2,3,4,6,7,8 HpCDD



Z-score: 1,2,3,4,6,7,8 HpCDD



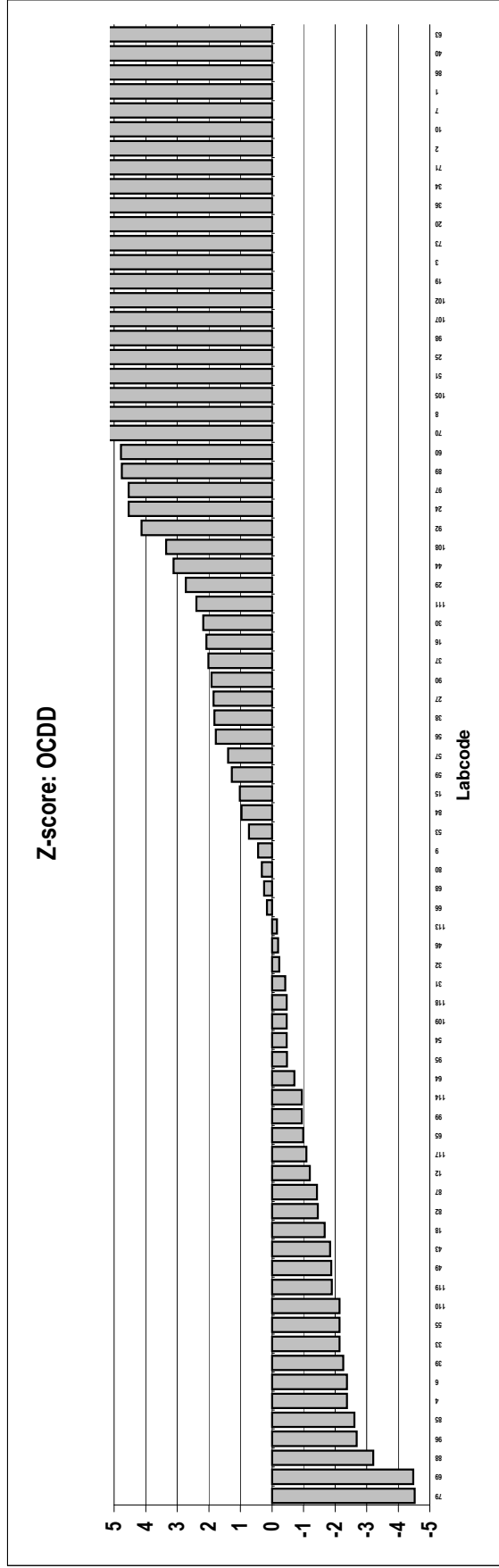
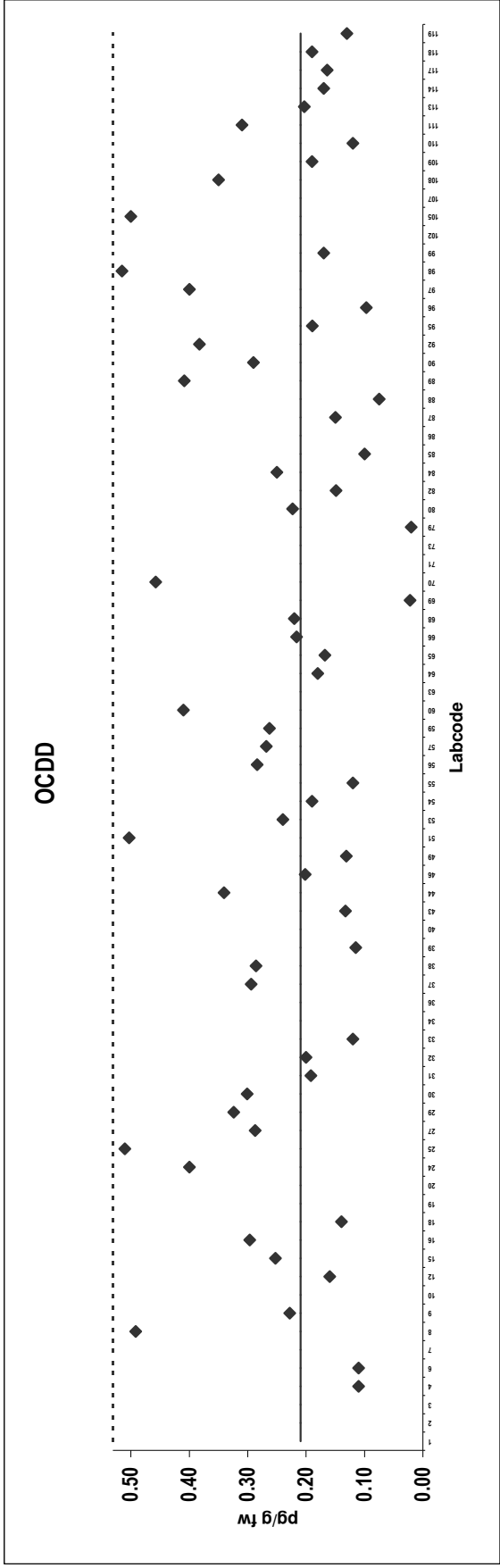
Trout

Congener: OCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.9	Outlier	68	0.22	
2	1.1	Outlier	69	0.022	
3	0.66	Outlier	70	0.46	
4	0.11		71	1.0	Outlier,ND
6	0.11		73	0.68	Outlier
7	1.3	Outlier	79	0.020	
8	0.49		80	0.22	
9	0.23		82	0.15	
10	1.2	Outlier	84	0.25	
12	0.16		85	0.10	ND
15	0.25		86	2.0	Outlier,ND
16	0.30		87	0.15	
18	0.14		88	0.075	
19	0.60	Outlier	89	0.41	
20	0.69	Outlier	90	0.29	
24	0.40		92	0.38	
25	0.51		95	0.19	
27	0.29		96	0.097	
29	0.32		97	0.40	
30	0.30		98	0.52	
31	0.19		99	0.17	
32	0.20		102	0.58	ND
33	0.12		105	0.50	Outlier
34	0.93	Outlier	107	0.55	ND
36	0.82	Outlier	108	0.35	Outlier
37	0.29		109	0.19	
38	0.29		110	0.12	
39	0.12		111	0.31	
40	2.3	Outlier	113	0.20	
43	0.13		114	0.17	
44	0.34		117	0.16	
46	0.20		118	0.19	
49	0.13		119	0.13	
51	0.50				
53	0.24				
54	0.19				
55	0.12				
56	0.28				
57	0.27				
59	0.26				
60	0.41				
63	3.4	Outlier			
64	0.18				
65	0.17				
66	0.22				

Consensus statistics

Consensus median, pg/g	0.21
Median all values pg/g	0.27
Consensus mean, pg/g	0.24
Standard deviation, pg/g	0.12
Relative standard deviation, %	52
No. of values reported	78
No. of values removed	16
No. of reported non-detects	5



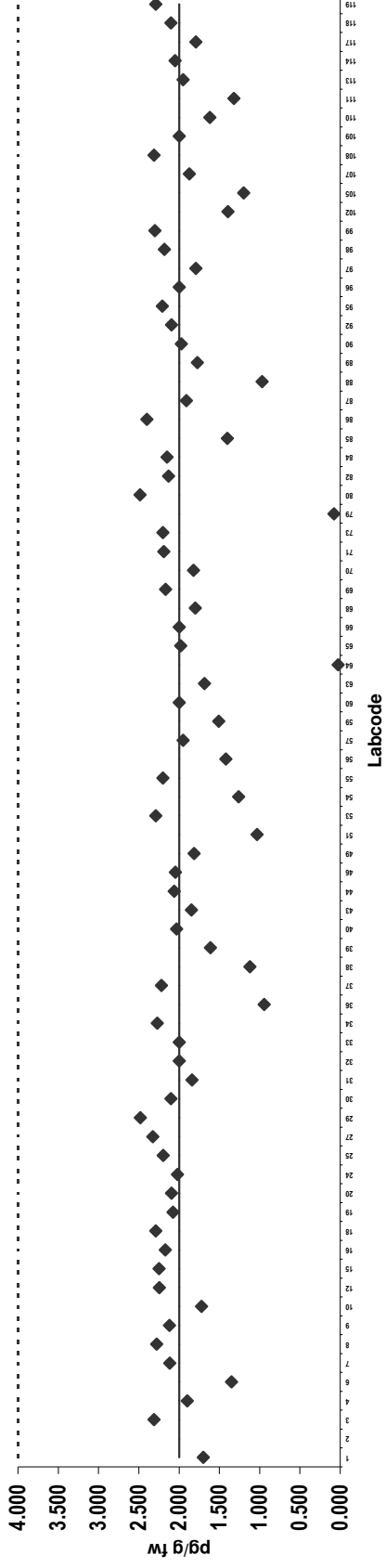
Trout
Congener: 2,3,7,8 TCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.7		68	1.8	
2	6.0		69	2.2	
3	2.3	Outlier	70	1.8	
4	1.9		71	2.2	
6	1.4		73	2.2	
7	2.1		79	0.077	
8	2.3		80	2.5	
9	2.1		82	2.1	
10	1.7		84	2.1	
12	2.2		85	1.4	
15	2.3		86	2.4	
16	2.2		87	1.9	
18	2.3		88	0.97	
19	2.1		89	1.8	
20	2.1		90	2.0	
24	2.0		92	2.1	
25	2.2		95	2.2	
27	2.3		96	2.0	
29	2.5		97	1.8	
30	2.1		98	2.2	
31	1.8		99	2.3	
32	2.0		102	1.4	
33	2.0		105	1.2	
34	2.3		107	1.9	
36	0.94		108	2.3	
37	2.2		109	2.0	
38	1.1		110	1.6	
39	1.6		111	1.3	
40	2.0		113	2.0	
43	1.8		114	2.1	
44	2.1		117	1.8	
46	2.0		118	2.1	
49	1.8		119	2.3	
51	1.0				
53	2.3				
54	1.3				
55	2.2				
56	1.4				
57	2.0				
59	1.5				
60	2.0				
63	1.7				
64	0.026				
65	2.0				
66	2.0				

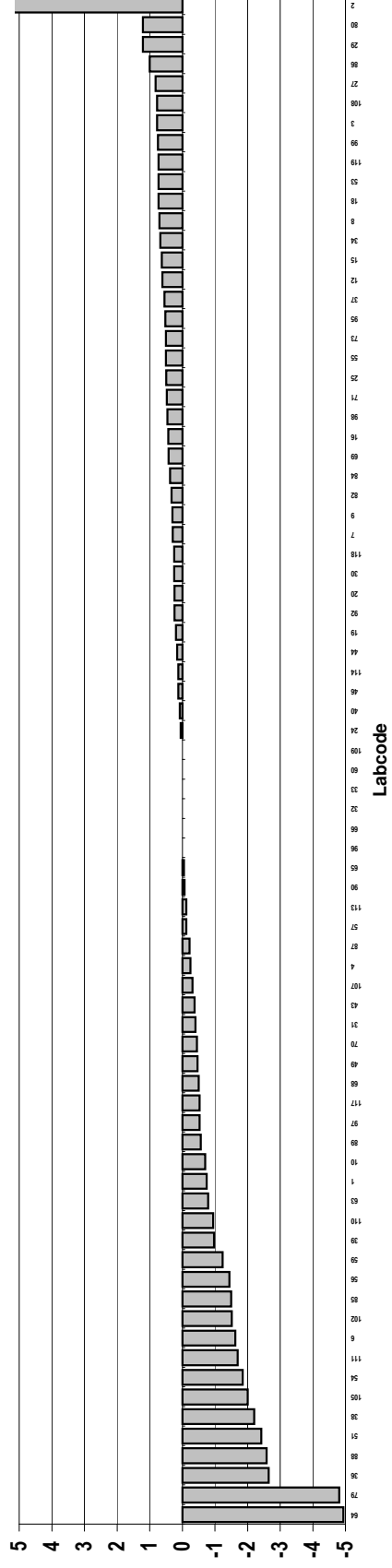
Consensus statistics

Consensus median, pg/g	2.0
Median all values pg/g	2.0
Consensus mean, pg/g	1.9
Standard deviation, pg/g	0.47
Relative standard deviation, %	25
No. of values reported	78
No. of values removed	1
No. of reported non-detects	1

2,3,7,8 TCDF



Z-score: 2,3,7,8 TCDF

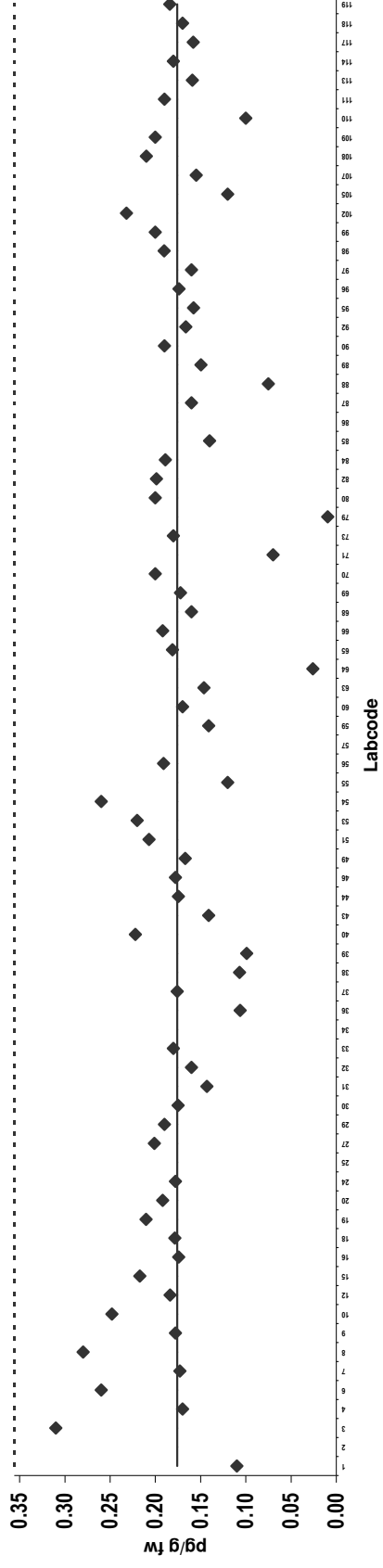


Trout
Congener: 1,2,3,7,8 PeCDF

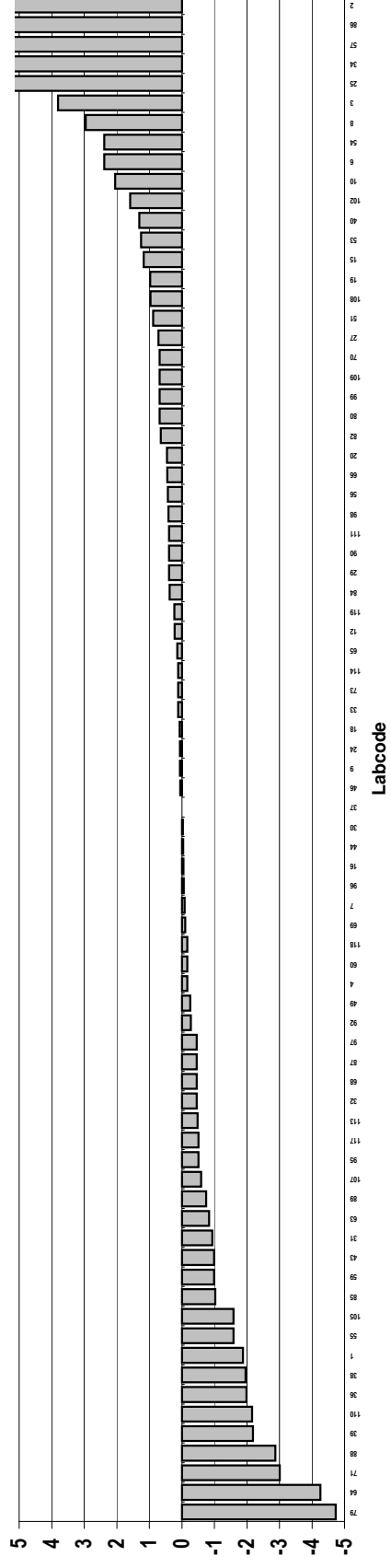
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.11		68	0.16	
2	1.7	Outlier	69	0.17	
3	0.31		70	0.20	
4	0.17		71	0.070	
6	0.26		73	0.18	
7	0.17		79	0.0095	ND
8	0.28		80	0.20	
9	0.18		82	0.20	
10	0.25		84	0.19	
12	0.18		85	0.14	
15	0.22		86	0.50	
16	0.17		87	0.16	
18	0.18		88	0.075	Outlier,ND
19	0.21		89	0.15	
20	0.19		90	0.19	
24	0.18		92	0.17	
25	0.40		95	0.16	
27	0.20		96	0.17	
29	0.19		97	0.16	
30	0.18		98	0.19	
31	0.14		99	0.20	
32	0.16		102	0.23	
33	0.18		105	0.12	
34	0.41	Outlier	107	0.16	
36	0.11		108	0.21	
37	0.18		109	0.20	
38	0.11		110	0.10	
39	0.099		111	0.19	
40	0.22		113	0.16	
43	0.14		114	0.18	
44	0.17		117	0.16	
46	0.18		118	0.17	
49	0.17		119	0.18	
51	0.21				
53	0.22				
54	0.26				
55	0.12				
56	0.19				
57	0.45	Outlier			
59	0.14				
60	0.17				
63	0.15				
64	0.026	ND			
65	0.18				
66	0.19				

Consensus statistics	
Consensus median, pg/g	0.18
Median all values pg/g	0.18
Consensus mean, pg/g	0.17
Standard deviation, pg/g	0.050
Relative standard deviation, %	29
No. of values reported	78
No. of values removed	5
No. of reported non-detects	3

1,2,3,7,8 PeCDF



Z-score: 1,2,3,7,8 PeCDF

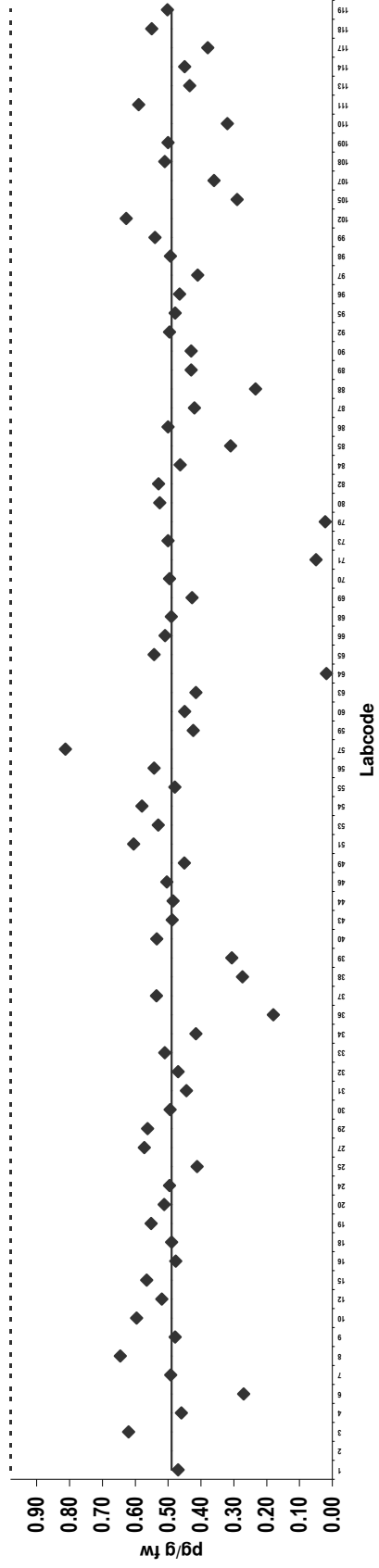


Trout
Congener: 2,3,4,7,8 PeCDF

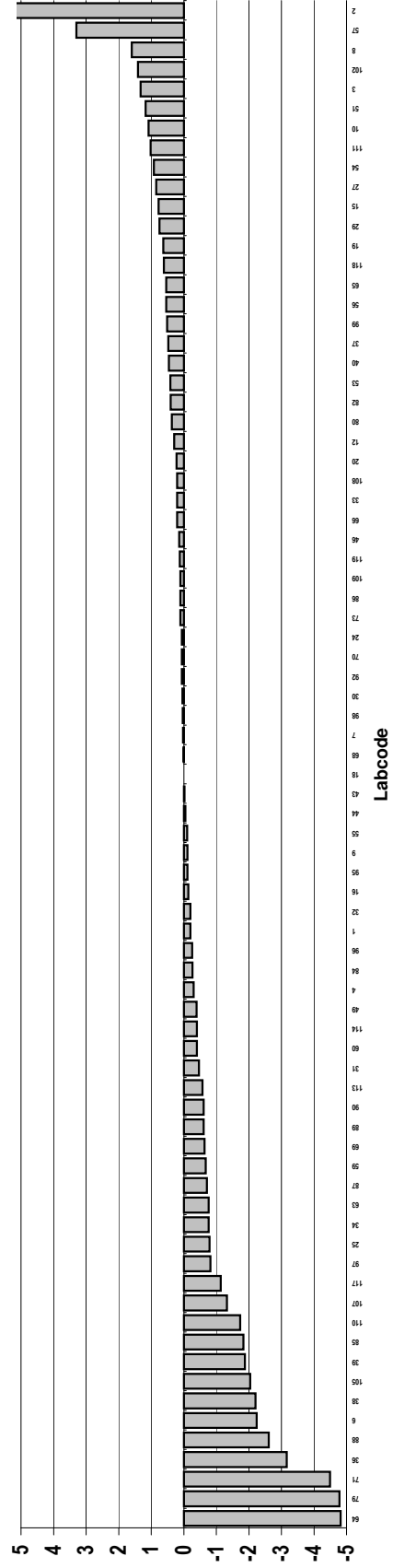
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.47		68	0.49	
2	1.2		69	0.43	
3	0.62	Outlier	70	0.50	
4	0.46		71	0.050	ND
6	0.27		73	0.50	
7	0.49		79	0.021	
8	0.65		80	0.53	
9	0.48		82	0.53	
10	0.60		84	0.46	
12	0.52		85	0.31	
15	0.57		86	0.50	ND
16	0.48		87	0.42	
18	0.49		88	0.23	
19	0.55		89	0.43	
20	0.51		90	0.43	
24	0.50		92	0.50	
25	0.41		95	0.48	
27	0.57		96	0.46	
29	0.56		97	0.41	
30	0.49		98	0.49	
31	0.44		99	0.54	
32	0.47		102	0.63	
33	0.51		105	0.29	
34	0.42	ND	107	0.36	
36	0.18		108	0.51	
37	0.54		109	0.50	
38	0.27		110	0.32	
39	0.31		111	0.59	
40	0.54		113	0.43	
43	0.49		114	0.45	
44	0.48		117	0.38	
46	0.50		118	0.55	
49	0.45		119	0.50	
51	0.61				
53	0.53				
54	0.58				
55	0.48				
56	0.54				
57	0.81				
59	0.42				
60	0.45				
63	0.42				
64	0.018	ND			
65	0.54				
66	0.51				

Consensus statistics	
Consensus median, pg/g	0.49
Median all values pg/g	0.49
Consensus mean, pg/g	0.46
Standard deviation, pg/g	0.13
Relative standard deviation, %	28
No. of values reported	78
No. of values removed	1
No. of reported non-detects	4

2,3,4,7,8 PeCDF



Z-score: 2,3,4,7,8 PeCDF



Trout

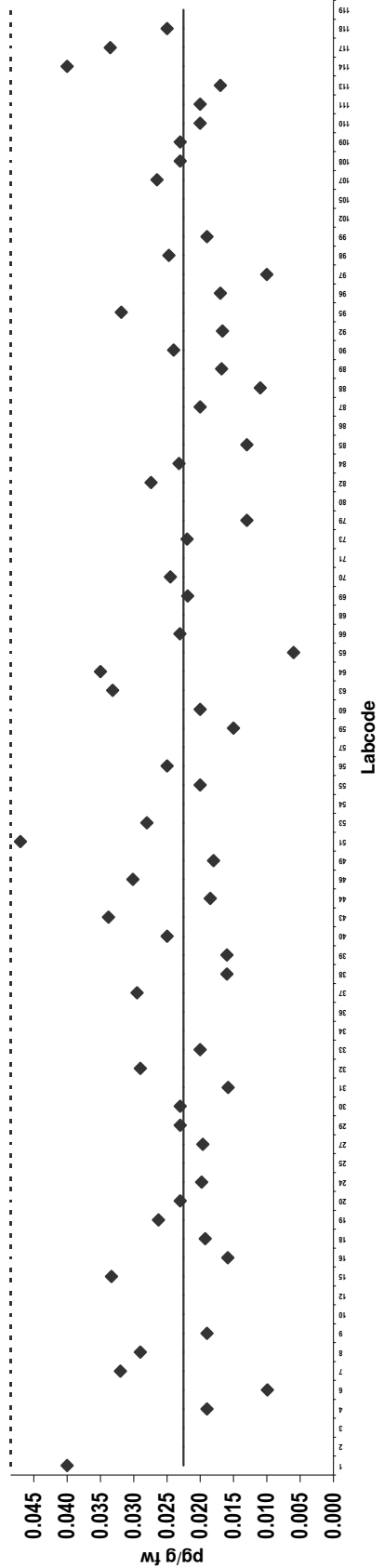
Congener: 1,2,3,4,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.040	ND	68	0.050	Outlier
2	0.070	Outlier	69	0.022	
3	0.13	Outlier	70	0.024	
4	0.019		71	0.050	Outlier,ND
6	0.0099		73	0.022	
7	0.032	ND	79	0.013	ND
8	0.029	ND	80	0.22	Outlier
9	0.019		82	0.027	
10	0.13	Outlier	84	0.023	
12	0.063	Outlier,ND	85	0.013	Outlier,ND
15	0.033		86	1.0	
16	0.016		87	0.020	
18	0.019		88	0.011	
19	0.026		89	0.017	
20	0.023		90	0.024	
24	0.020		92	0.017	
25	0.65	Outlier	95	0.032	
27	0.020		96	0.017	
29	0.023		97	0.010	
30	0.023		98	0.025	
31	0.016		99	0.019	
32	0.029		102	0.10	Outlier
33	0.020	Outlier,ND	105	0.36	Outlier
34	0.12	Outlier	107	0.027	
36	0.10	Outlier,ND	108	0.023	
37	0.030	Outlier	109	0.023	
38	0.016	ND	110	0.020	
39	0.016		111	0.020	
40	0.025		113	0.017	
43	0.034		114	0.040	
44	0.019		117	0.034	
46	0.030		118	0.025	
49	0.018		119	0.050	Outlier,ND
51	0.047				
53	0.028				
54	0.17	Outlier			
55	0.020				
56	0.025				
57	0.049	Outlier			
59	0.015				
60	0.020				
63	0.033				
64	0.035				
65	0.0060	ND			
66	0.023				

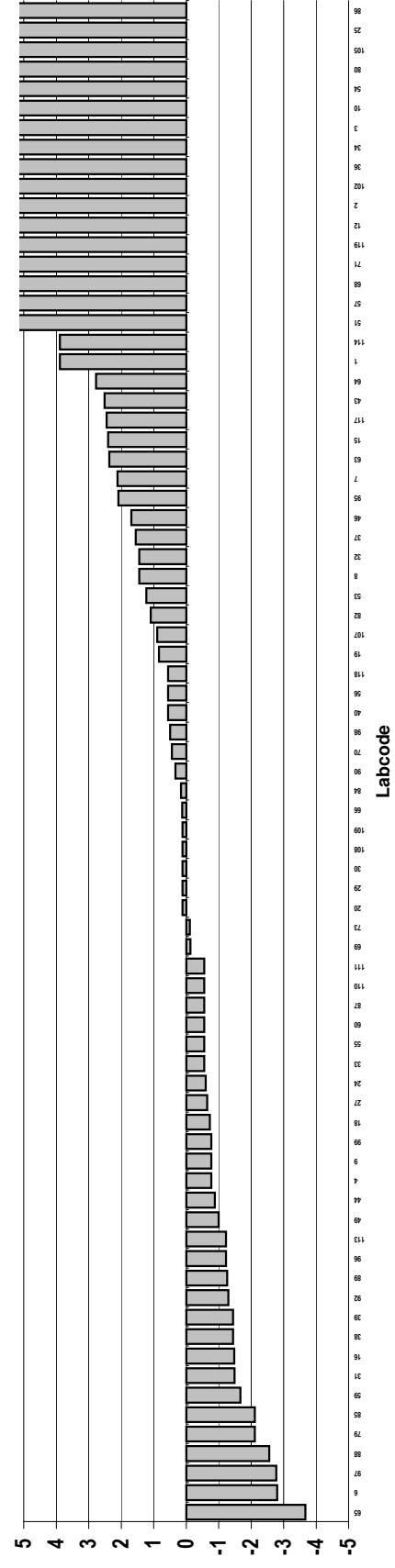
Consensus statistics

Consensus median, pg/g	0.023
Median all values pg/g	0.024
Consensus mean, pg/g	0.023
Standard deviation, pg/g	0.0078
Relative standard deviation, %	34
No. of values reported	78
No. of values removed	16
No. of reported non-detects	11

1,2,3,4,7,8 HxCDF



Z-score: 1,2,3,4,7,8 HxCDF

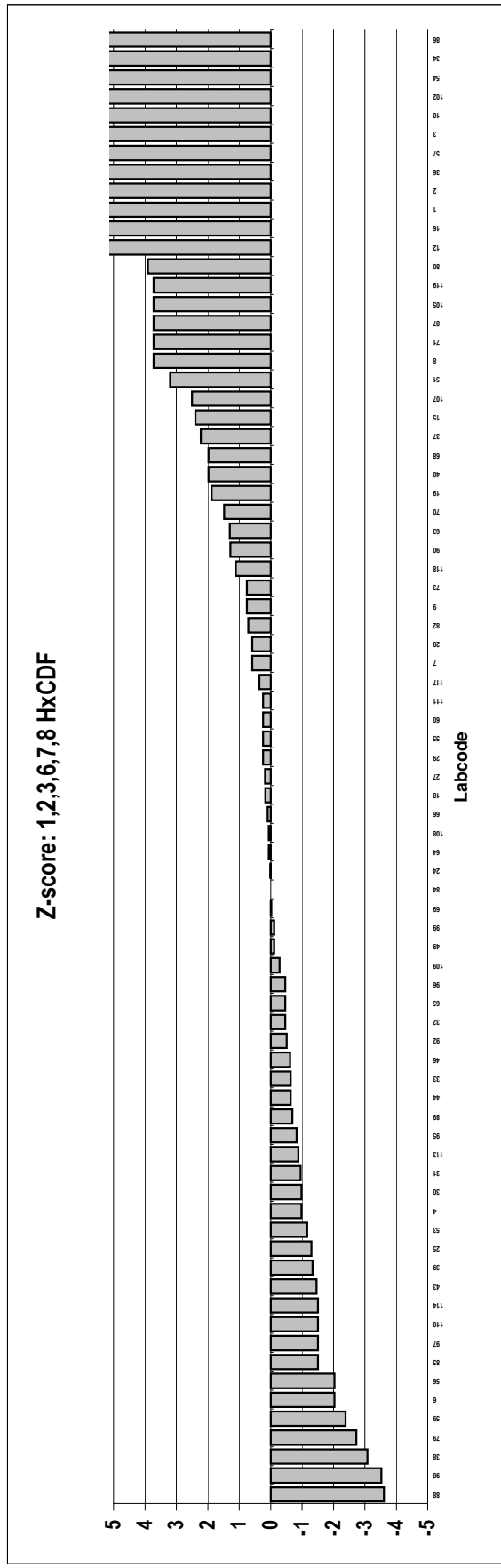
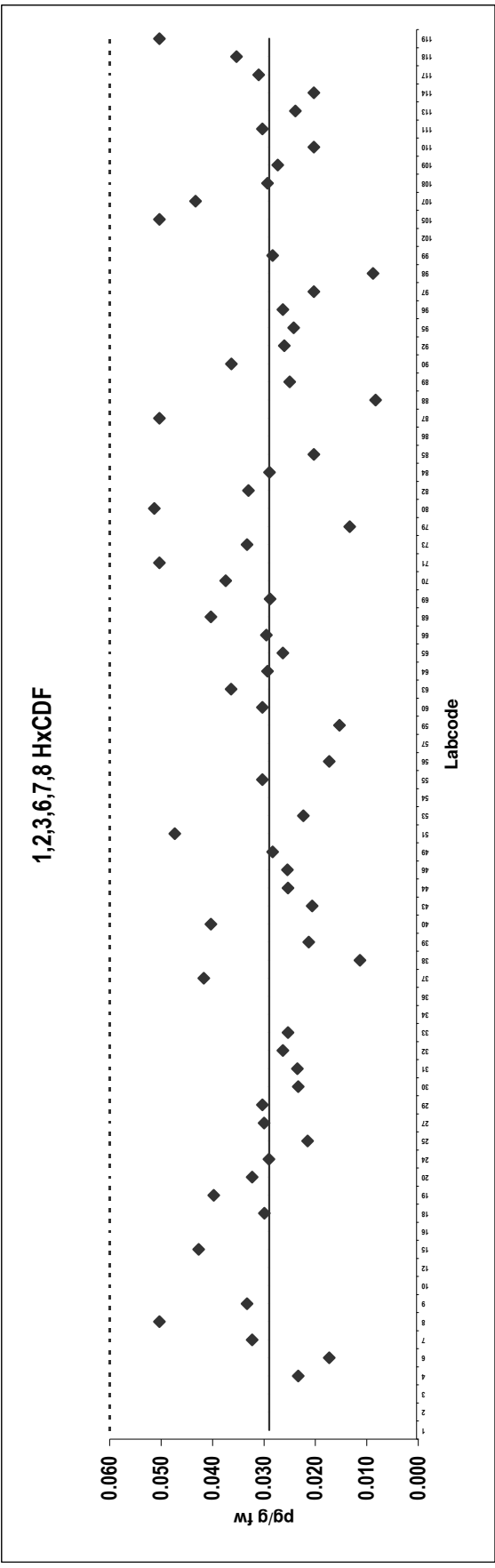


Trout
Congener: 1,2,3,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.069	Outlier,ND	68	0.040	
2	0.070	Outlier	69	0.029	
3	0.12	Outlier	70	0.037	
4	0.023		71	0.050	ND
6	0.017		73	0.033	
7	0.032	ND	79	0.013	ND
8	0.050		80	0.051	
9	0.033		82	0.033	
10	0.14	Outlier	84	0.029	
12	0.063	Outlier,ND	85	0.020	ND
15	0.042		86	1.0	Outlier,ND
16	0.063	Outlier	87	0.050	
18	0.030		88	0.0080	
19	0.039		89	0.025	
20	0.032		90	0.036	
24	0.029		92	0.026	
25	0.021		95	0.024	
27	0.030		96	0.026	
29	0.030		97	0.020	
30	0.023		98	0.0085	
31	0.023		99	0.028	
32	0.026		102	0.14	Outlier
33	0.025		105	0.050	
34	0.47	Outlier,ND	107	0.043	ND
36	0.11	Outlier	108	0.029	
37	0.041		109	0.027	
38	0.011		110	0.020	
39	0.021		111	0.030	
40	0.040		113	0.024	
43	0.020		114	0.020	
44	0.025		117	0.031	
46	0.025		118	0.035	
49	0.028		119	0.050	ND
51	0.047				
53	0.022				
54	0.22	Outlier			
55	0.030				
56	0.017	Outlier			
57	0.12				
59	0.015				
60	0.030				
63	0.036				
64	0.029				
65	0.026				
66	0.029				

Consensus statistics

Consensus median, pg/g	0.029
Median all values pg/g	0.030
Consensus mean, pg/g	0.029
Standard deviation, pg/g	0.010
Relative standard deviation, %	35
No. of values reported	78
No. of values removed	12
No. of reported non-detects	10



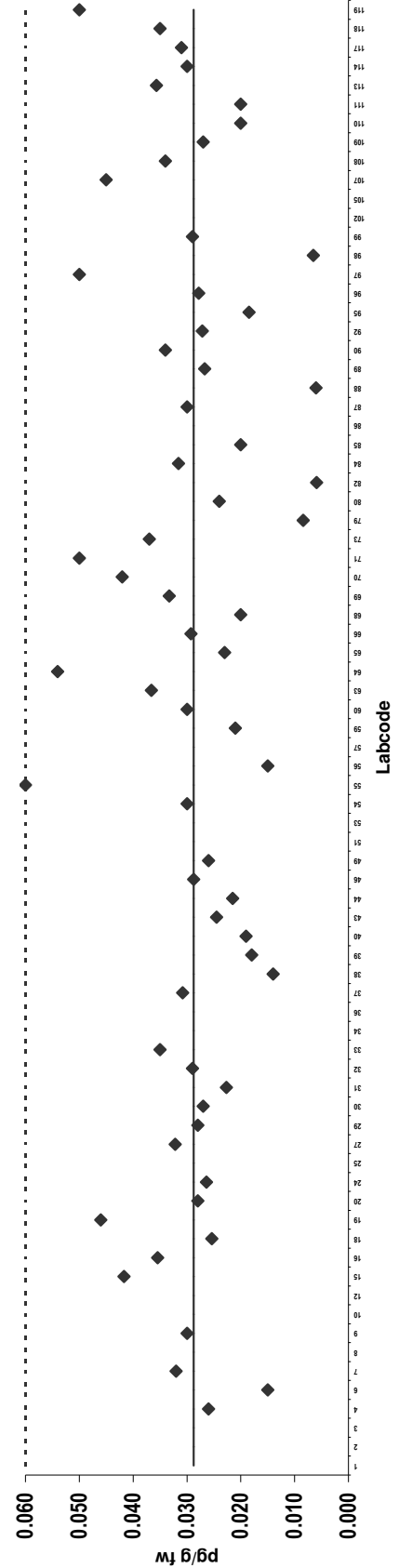
Trout
Congener: 2,3,4,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.080	Outlier,ND	68	0.020	
2	0.070	Outlier	69	0.033	
3	0.11	Outlier	70	0.042	
4	0.026		71	0.050	ND
6	0.015		73	0.037	
7	0.032	ND	79	0.0084	ND
8	0.064	Outlier	80	0.024	
9	0.030		82	0.0059	
10	0.13	Outlier	84	0.032	
12	0.063	Outlier,ND	85	0.020	Outlier,ND
15	0.042		86	1.0	
16	0.035		87	0.030	
18	0.025		88	0.0060	
19	0.046		89	0.027	
20	0.028		90	0.034	
24	0.026		92	0.027	
25	0.079	Outlier	95	0.018	
27	0.032		96	0.028	
29	0.028		97	0.050	
30	0.027		98	0.0065	ND
31	0.023		99	0.029	
32	0.029		102	0.67	Outlier
33	0.035		105	0.13	Outlier
34	0.12	Outlier,ND	107	0.045	ND
36	0.13	Outlier	108	0.034	
37	0.031	ND	109	0.027	
38	0.014		110	0.020	
39	0.018		111	0.020	
40	0.019		113	0.036	
43	0.024		114	0.030	
44	0.021		117	0.031	
46	0.029		118	0.035	
49	0.026		119	0.050	ND
51	0.073	Outlier			
53	0.24	Outlier			
54	0.030				
55	0.060				
56	0.015				
57	0.64	Outlier			
59	0.021				
60	0.030				
63	0.037				
64	0.054				
65	0.023				
66	0.029				

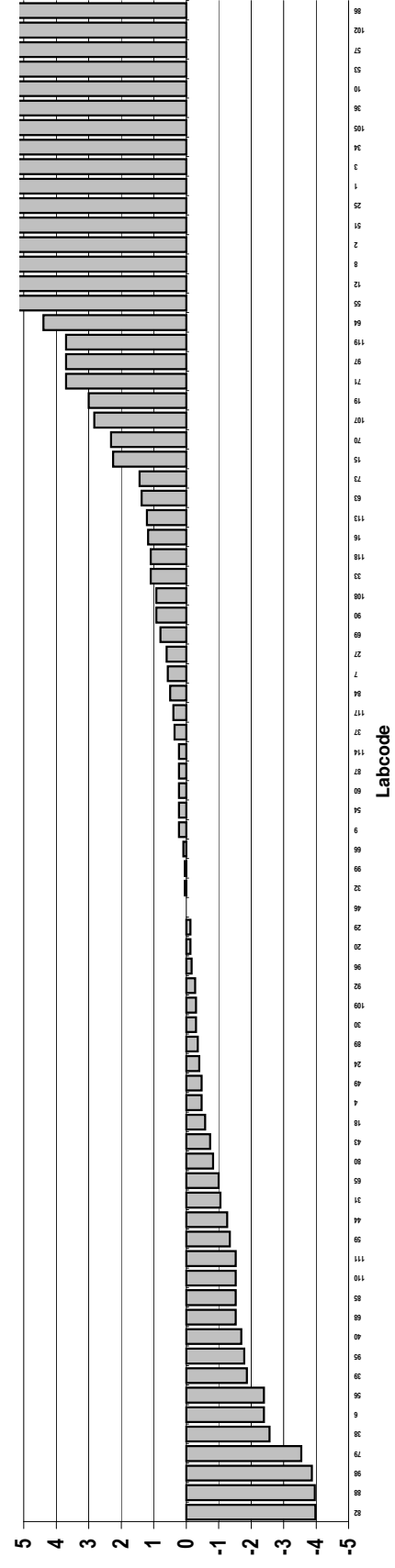
Consensus statistics

Consensus median, pg/g	0.029
Median all values pg/g	0.030
Consensus mean, pg/g	0.029
Standard deviation, pg/g	0.011
Relative standard deviation, %	39
No. of values reported	78
No. of values removed	15
No. of reported non-detects	11

2,3,4,6,7,8 HxCDF



Z-score: 2,3,4,6,7,8 HxCDF



Trout

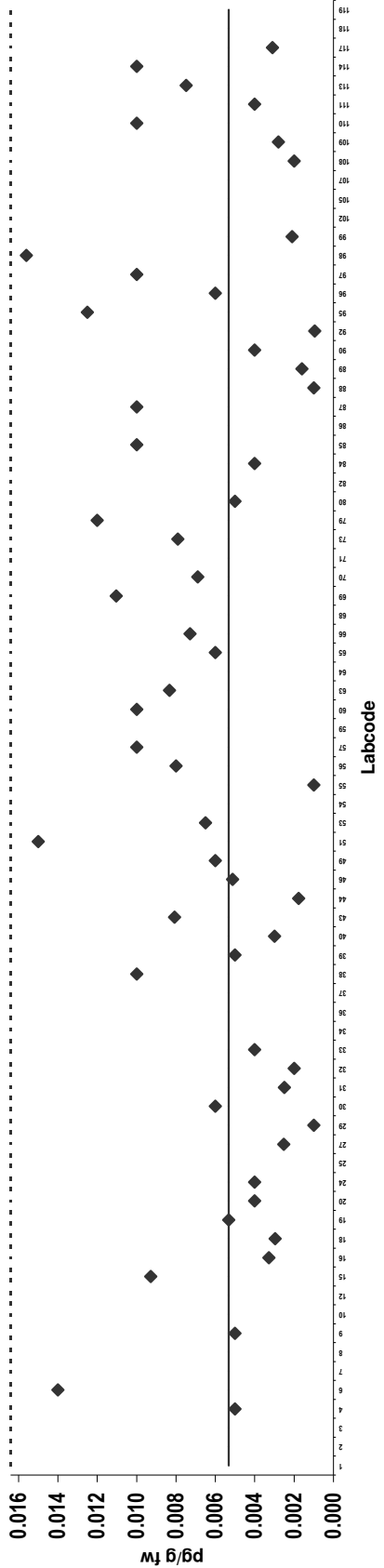
Congener: 1,2,3,7,8,9 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.083	Outlier,ND	68	0.020	Outlier
2	0.020	Outlier,ND	69	0.011	ND
3	0.020	Outlier	70	0.0069	ND
4	0.0050	ND	71	0.050	Outlier,ND
6	0.014		73	0.0079	
7	0.032	Outlier,ND	79	0.012	ND
8	0.063	Outlier,ND	80	0.0050	ND
9	0.0050	ND	82	0.030	Outlier
10	0.13	Outlier	84	0.0040	
12	0.063	Outlier,ND	85	0.010	ND
15	0.0093	ND	86	1.0	Outlier,ND
16	0.0033		87	0.010	ND
18	0.0030		88	0.0010	ND
19	0.0053	ND	89	0.0016	ND
20	0.0040	ND	90	0.0040	
24	0.0040	ND	92	0.00096	
25	0.043	Outlier	95	0.013	ND
27	0.0025		96	0.0060	ND
29	0.0010	ND	97	0.010	ND
30	0.0060	ND	98	0.016	
31	0.0025	ND	99	0.0021	ND
32	0.0020	ND	102	0.30	Outlier
33	0.0040	ND	105	0.10	Outlier,ND
34	0.13	Outlier,ND	107	0.078	Outlier,ND
36	0.12	Outlier	108	0.0020	
37	0.034	Outlier,ND	109	0.0028	
38	0.010	ND	110	0.010	ND
39	0.0050	ND	111	0.0040	
40	0.0030	ND	113	0.0075	ND
43	0.0081	ND	114	0.010	ND
44	0.0018		117	0.0031	ND
46	0.0051		118	0.021	Outlier
49	0.0060		119	0.050	Outlier,ND
51	0.015				
53	0.0065				
54	0.030	Outlier			
55	0.0010	ND			
56	0.0080				
57	0.010	ND			
59	0.020	Outlier,ND			
60	0.010				
63	0.0083				
64	0.024	Outlier			
65	0.0060	ND			
66	0.0073	ND			

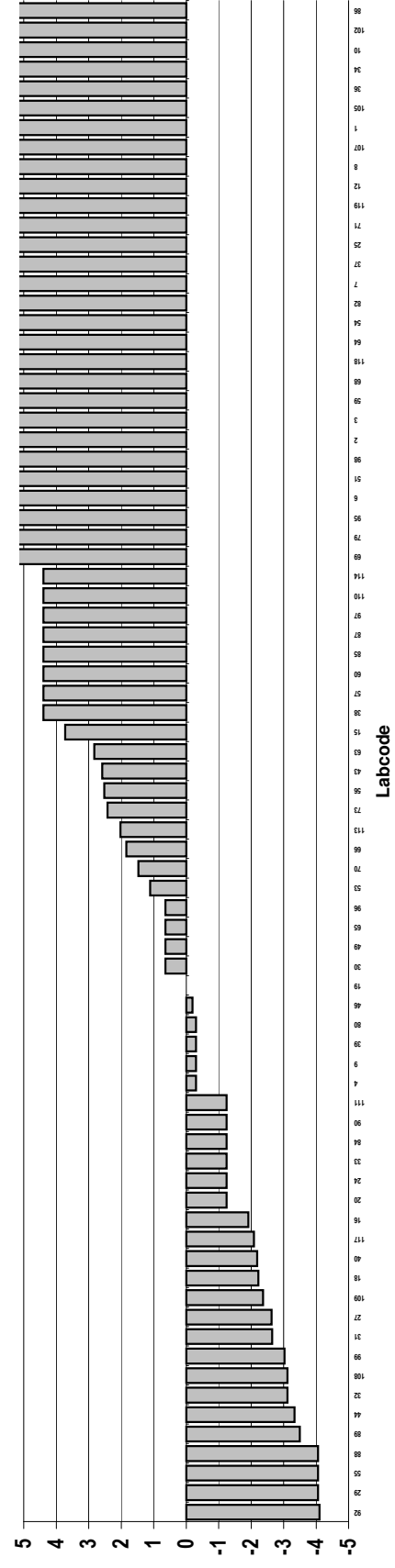
Consensus statistics

Consensus median, pg/g	0.0053
Median all values pg/g	0.0082
Consensus mean, pg/g	0.0062
Standard deviation, pg/g	0.0038
Relative standard deviation, %	61
No. of values reported	78
No. of values removed	23
No. of reported non-detects	49

1,2,3,7,8,9 HxCDF



Z-score: 1,2,3,7,8,9 HxCDF



Trout

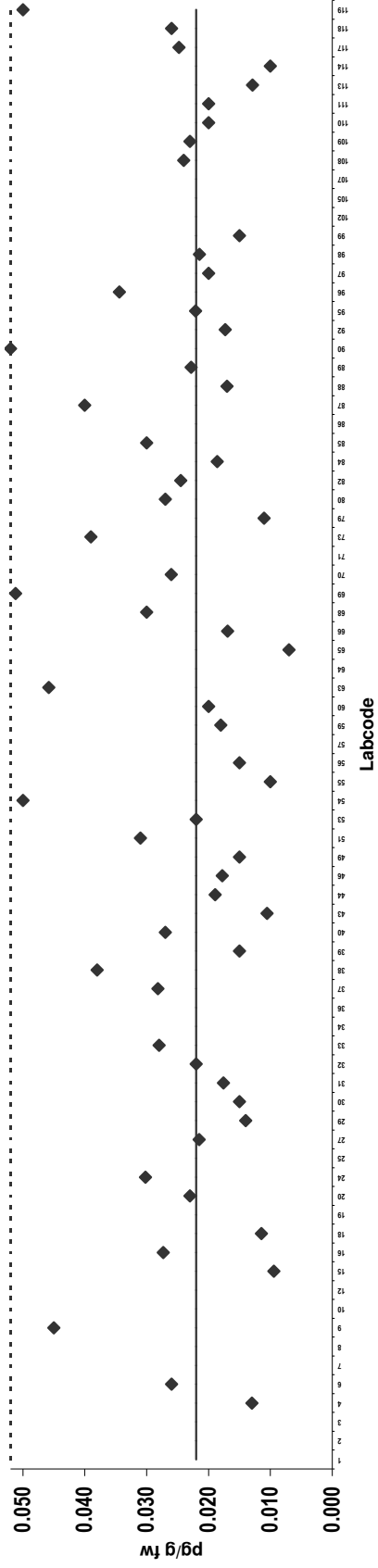
Congener: 1,2,3,4,6,7,8 HpCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.14	Outlier,ND	68	0.030	
2	0.070	Outlier	69	0.051	
3	0.16	Outlier	70	0.026	
4	0.013		71	0.20	Outlier,ND
6	0.026		73	0.039	
7	0.088	Outlier,ND	79	0.011	ND
8	0.065	Outlier,ND	80	0.027	ND
9	0.045		82	0.025	
10	0.16	Outlier	84	0.019	
12	0.063	Outlier,ND	85	0.030	ND
15	0.0094	ND	86	1.0	Outlier,ND
16	0.027		87	0.040	
18	0.011		88	0.017	
19	0.066		89	0.023	
20	0.023	Outlier	90	0.052	
24	0.030		92	0.017	
25	0.14	Outlier	95	0.022	
27	0.022		96	0.034	
29	0.014		97	0.020	
30	0.015		98	0.021	
31	0.018	ND	99	0.015	ND
32	0.022		102	0.074	Outlier,ND
33	0.028		105	0.30	Outlier,ND
34	0.20	Outlier,ND	107	0.15	Outlier,ND
36	0.12	Outlier	108	0.024	
37	0.028	ND	109	0.023	
38	0.038		110	0.020	ND
39	0.015		111	0.020	
40	0.027	ND	113	0.013	
43	0.011		114	0.010	ND
44	0.019		117	0.025	
46	0.018		118	0.026	
49	0.015		119	0.050	ND
51	0.031				
53	0.022				
54	0.050				
55	0.010				
56	0.015				
57	0.071	Outlier			
59	0.018				
60	0.020				
63	0.046				
64	0.11	Outlier			
65	0.0070	ND			
66	0.017				

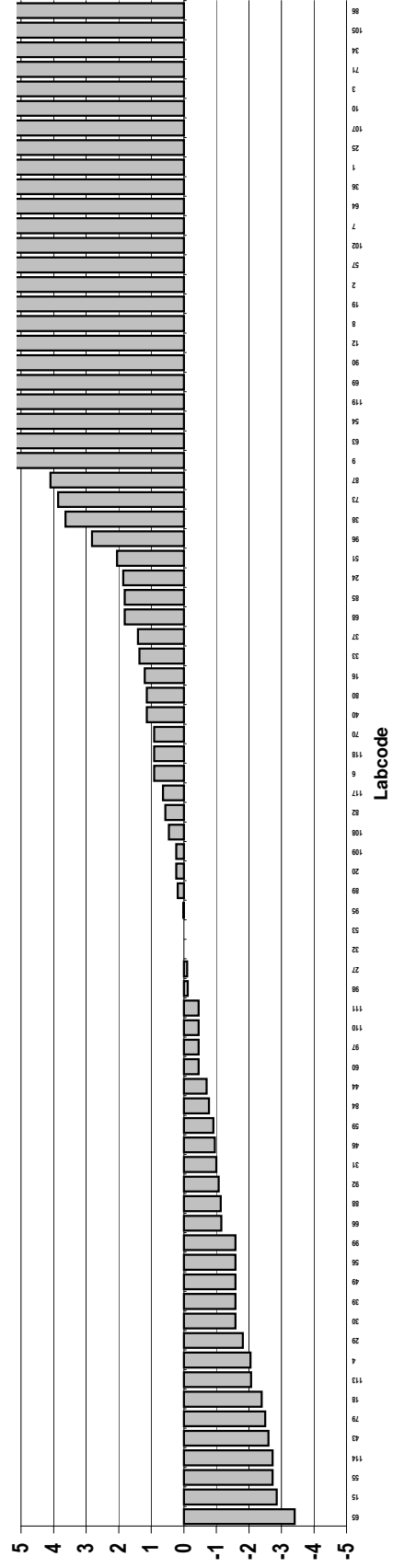
Consensus statistics

Consensus median, pg/g	0.022
Median all values pg/g	0.026
Consensus mean, pg/g	0.024
Standard deviation, pg/g	0.011
Relative standard deviation, %	47
No. of values reported	78
No. of values removed	18
No. of reported non-detects	22

1,2,3,4,6,7,8 HpCDF



Z-score: 1,2,3,4,6,7,8 HpCDF



Trout

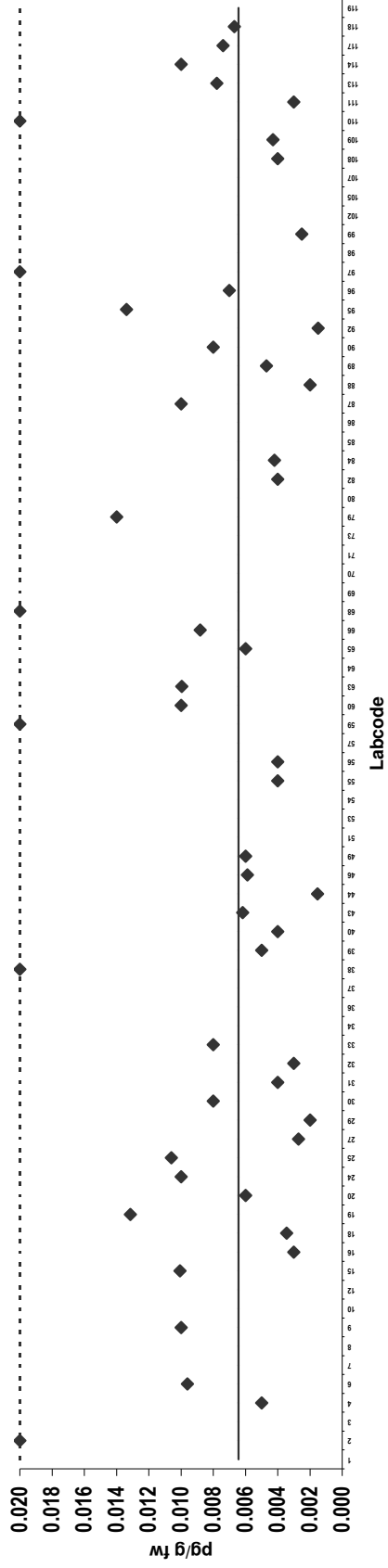
Congener: 1,2,3,4,7,8,9 HpCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.15	Outlier,ND	68	0.020	Outlier,ND
2	0.020	ND	69	0.022	Outlier,ND
3	0.040	Outlier	70	0.038	Outlier,ND
4	0.0050	ND	71	0.20	Outlier,ND
6	0.0096	ND	73	0.021	Outlier
7	0.088	Outlier,ND	79	0.014	ND
8	0.15	Outlier,ND	80	0.043	Outlier,ND
9	0.010	ND	82	0.0040	
10	0.027	Outlier	84	0.0042	
12	0.063	Outlier,ND	85	0.040	Outlier,ND
15	0.010	ND	86	1.0	Outlier,ND
16	0.0030	ND	87	0.010	
18	0.0034		88	0.0020	
19	0.013		89	0.0047	ND
20	0.0060	ND	90	0.0080	
24	0.010	ND	92	0.0015	
25	0.011		95	0.013	
27	0.0027	ND	96	0.0070	ND
29	0.0020	ND	97	0.020	ND
30	0.0080	ND	98	0.11	Outlier
31	0.0040	ND	99	0.0025	ND
32	0.0030	ND	102	0.35	Outlier
33	0.0080	ND	105	0.088	Outlier
34	0.18	Outlier,ND	107	0.14	Outlier,ND
36	0.11	Outlier	108	0.0040	
37	0.045	Outlier,ND	109	0.0043	ND
38	0.020	ND	110	0.020	ND
39	0.0050	ND	111	0.0030	
40	0.0040		113	0.0078	ND
43	0.0062	ND	114	0.010	ND
44	0.0015		117	0.0074	
46	0.0059		118	0.0067	
49	0.0060		119	0.050	Outlier,ND
51	0.033	Outlier			
53	0.039	Outlier			
54	0.050	Outlier			
55	0.0040	ND			
56	0.0040				
57	0.12	Outlier			
59	0.020	ND			
60	0.010				
63	0.0099				
64	0.038	Outlier			
65	0.0060	ND			
66	0.0088	ND			

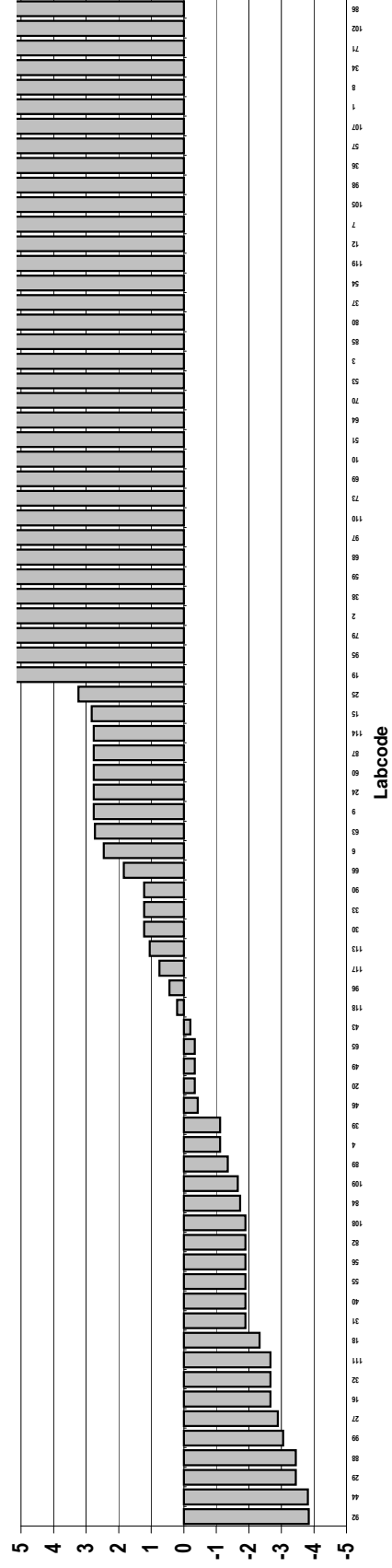
Consensus statistics

Consensus median, pg/g	0.0064
Median all values pg/g	0.010
Consensus mean, pg/g	0.0080
Standard deviation, pg/g	0.0054
Relative standard deviation, %	68
No. of values reported	78
No. of values removed	26
No. of reported non-detects	44

1,2,3,4,7,8,9 HpCDF



Z-score: 1,2,3,4,7,8,9 HpCDF

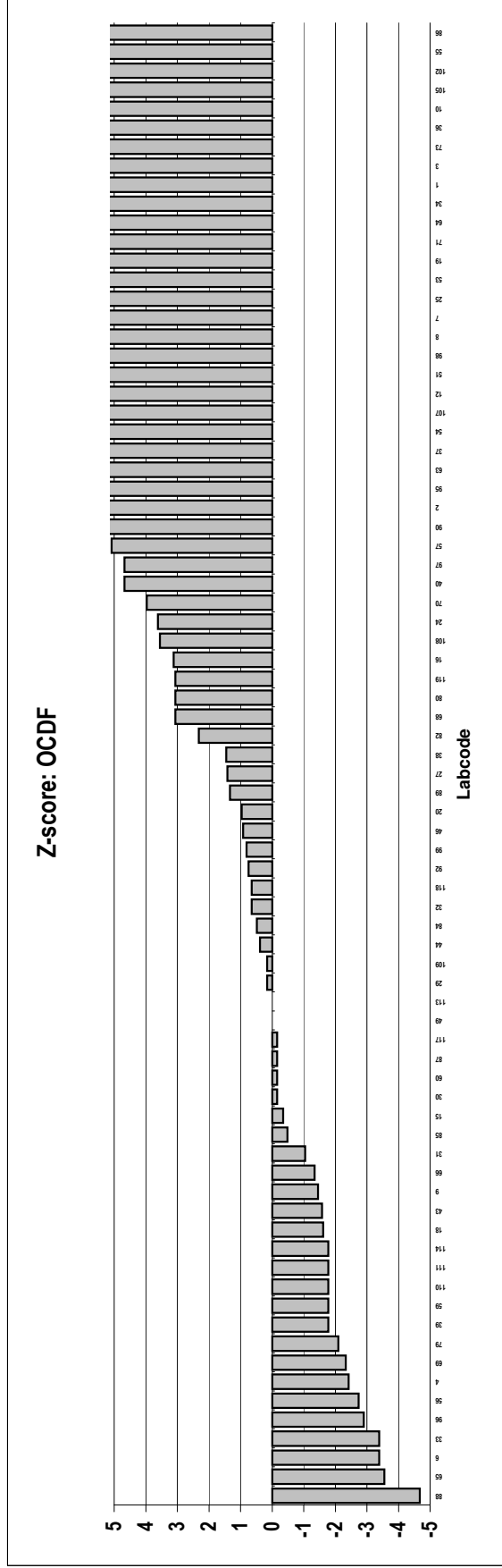
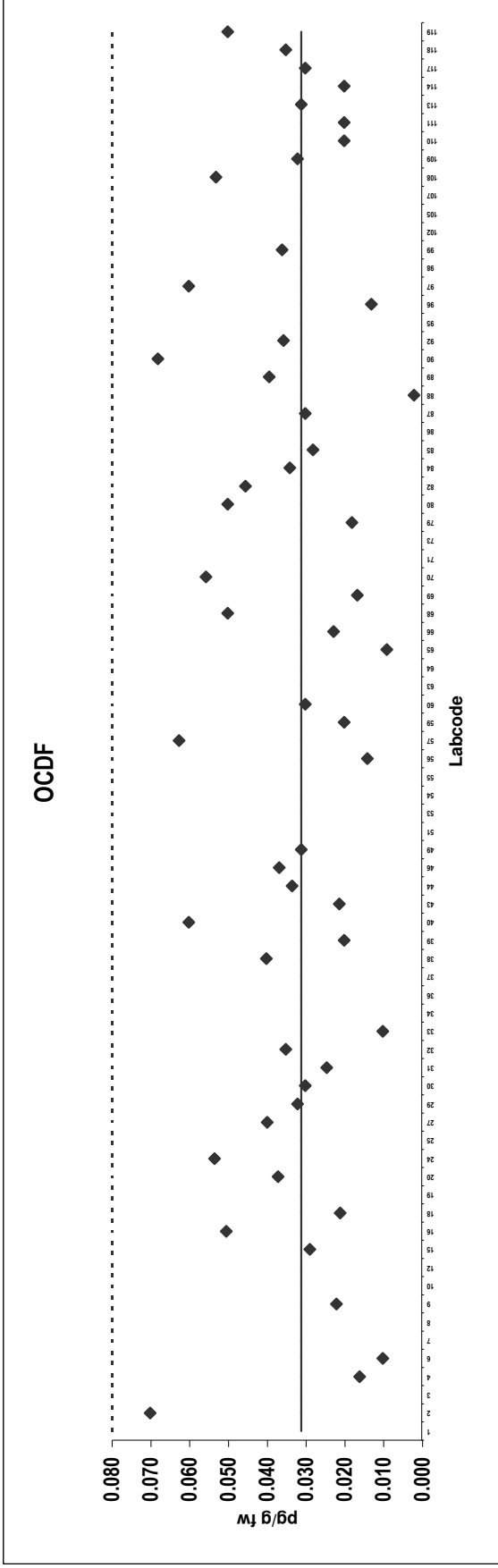


Trout Congener: OCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.27	Outlier,ND	68	0.050	ND
2	0.070		69	0.017	ND
3	0.27		70	0.056	
4	0.016	Outlier	71	0.20	Outlier,ND
6	0.010		73	0.28	Outlier
7	0.14		79	0.018	ND
8	0.14	Outlier,ND	80	0.050	ND
9	0.022	Outlier,ND	82	0.045	
10	0.48	Outlier	84	0.034	
12	0.13	Outlier,ND	85	0.028	
15	0.029		86	2.0	Outlier,ND
16	0.050		87	0.030	ND
18	0.021		88	0.0020	ND
19	0.16	Outlier	89	0.039	
20	0.037		90	0.068	
24	0.053		92	0.036	
25	0.15	Outlier	95	0.080	Outlier
27	0.040		96	0.013	ND
29	0.032		97	0.060	
30	0.030	ND	98	0.13	Outlier
31	0.025		99	0.036	ND
32	0.035		102	0.67	Outlier
33	0.010	ND	105	0.50	Outlier,ND
34	0.24	Outlier,ND	107	0.12	Outlier,ND
36	0.32	Outlier	108	0.053	
37	0.097	Outlier,ND	109	0.032	
38	0.040		110	0.020	ND
39	0.020		111	0.020	
40	0.060	ND	113	0.031	
43	0.021		114	0.020	
44	0.033		117	0.030	
46	0.037		118	0.035	
49	0.031		119	0.050	ND
51	0.13	Outlier			
53	0.15	Outlier			
54	0.10	Outlier			
55	0.69	Outlier			
56	0.014				
57	0.063				
59	0.020				
60	0.030				
63	0.087	Outlier			
64	0.21	Outlier			
65	0.0090	ND			
66	0.023				

Consensus statistics

Consensus median, pg/g	0.031
Median all values pg/g	0.040
Consensus mean, pg/g	0.033
Standard deviation, pg/g	0.016
Relative standard deviation, %	49
No. of values reported	78
No. of values removed	25
No. of reported non-detects	24



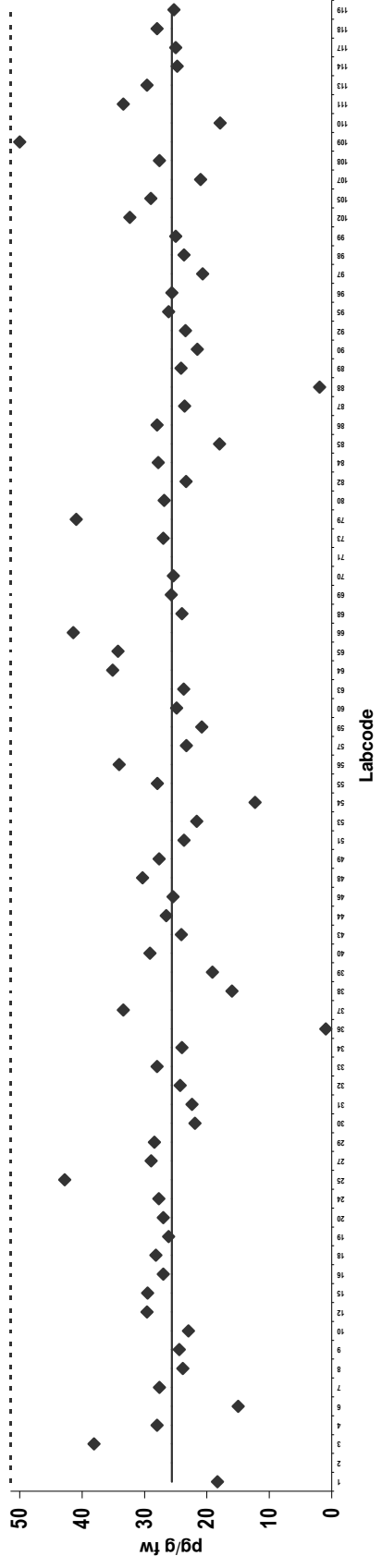
Trout
Congener: PCB 77

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	18		66	41	
2	86		68	24	
3	38	Outlier	69	26	
4	28		70	25	
6	15		71	84	
7	28		73	27	Outlier
8	24		79	41	
9	24		80	27	
10	23		82	23	
12	30		84	28	
15	30		85	18	
16	27		86	28	
18	28		87	24	
19	26		88	2.0	
20	27		89	24	
24	28		90	22	
25	43		92	23	
27	29		95	26	
29	28		96	26	
30	22		97	21	
31	22		98	24	
32	24		99	25	
33	28		102	32	
34	24	ND	105	29	
36	0.94		107	21	
37	33		108	28	
38	16		109	50	
39	19		110	18	
40	29		111	33	
43	24		113	30	
44	26		114	25	
46	25		117	25	
48	30		118	28	
49	28		119	25	
51	24				
53	22				
54	12				
55	28				
56	34				
57	23				
59	21				
60	25				
63	24				
64	35				
65	34				

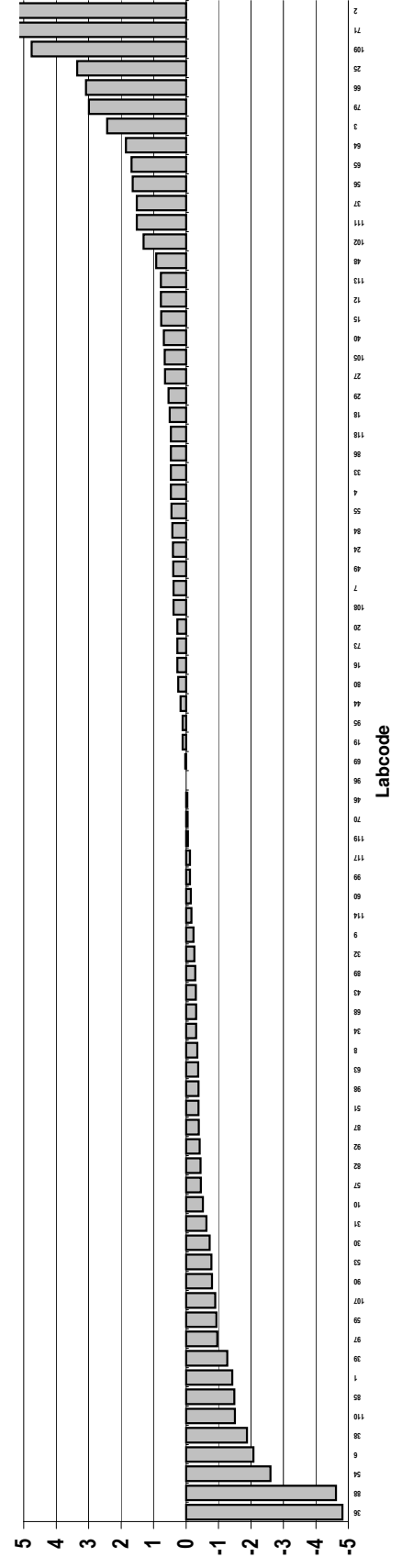
Consensus statistics

Consensus median, pg/g	26
Median all values pg/g	26
Consensus mean, pg/g	26
Standard deviation, pg/g	7.3
Relative standard deviation, %	28
No. of values reported	79
No. of values removed	2
No. of reported non-detects	1

PCB 77



Z-score: PCB 77



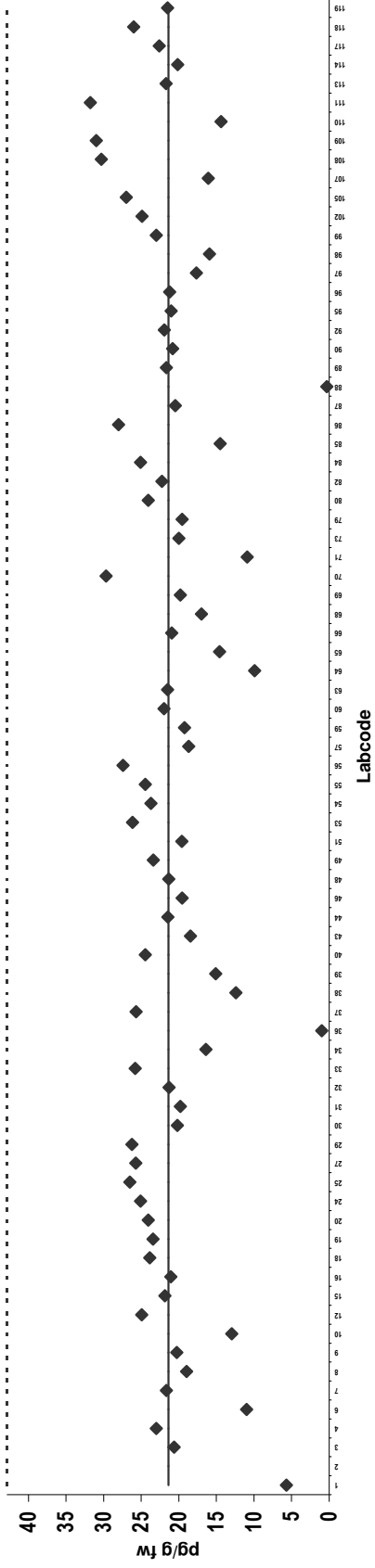
Trout
Congener: PCB 126

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.7		66	21	
2	53		68	17	
3	21	Outlier	69	20	
4	23		70	30	
6	11		71	11	
7	22		73	20	
8	19		79	20	
9	20		80	24	
10	13		82	22	
12	25		84	25	
15	22		85	15	
16	21		86	28	
18	24		87	20	
19	23		88	0.32	
20	24		89	22	
24	25		90	21	
25	27		92	22	
27	26		95	21	
29	26		96	21	
30	20		97	18	
31	20		98	16	
32	21		99	23	
33	26		102	25	
34	16		105	27	
36	1.0		107	16	
37	26		108	30	
38	12		109	31	
39	15		110	14	
40	24		111	32	
43	18		113	22	
44	21		114	20	
46	20		117	23	
48	21		118	26	
49	23		119	22	
51	20				
53	26				
54	24				
55	24				
56	27				
57	19				
59	19				
60	22				
63	21				
64	9.9				
65	15				

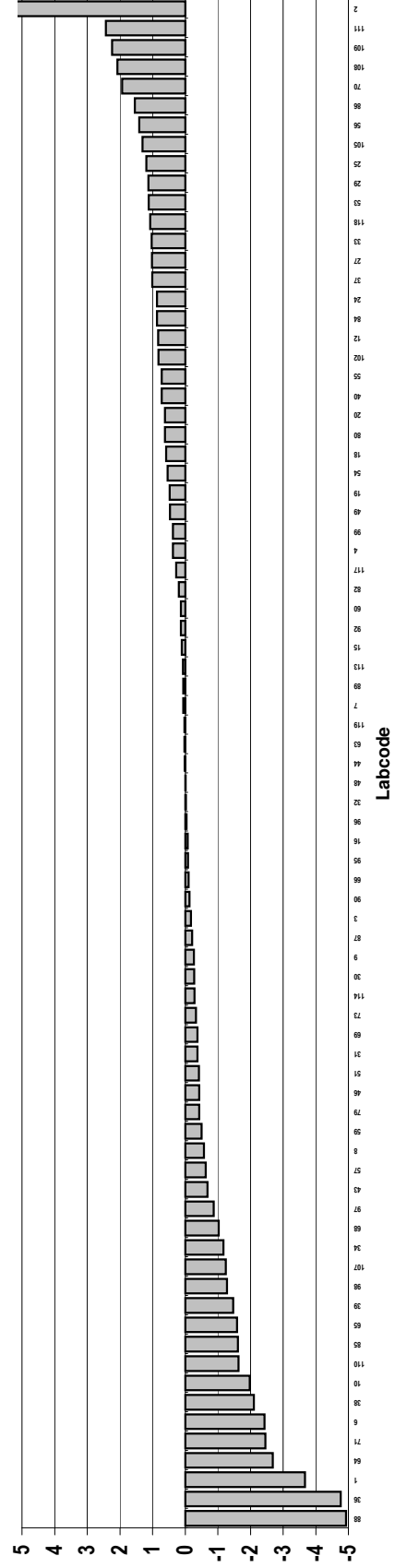
Consensus statistics

Consensus median, pg/g	21
Median all values pg/g	21
Consensus mean, pg/g	21
Standard deviation, pg/g	5.9
Relative standard deviation, %	28
No. of values reported	79
No. of values removed	1
No. of reported non-detects	0

PCB 126



Z-score: PCB 126



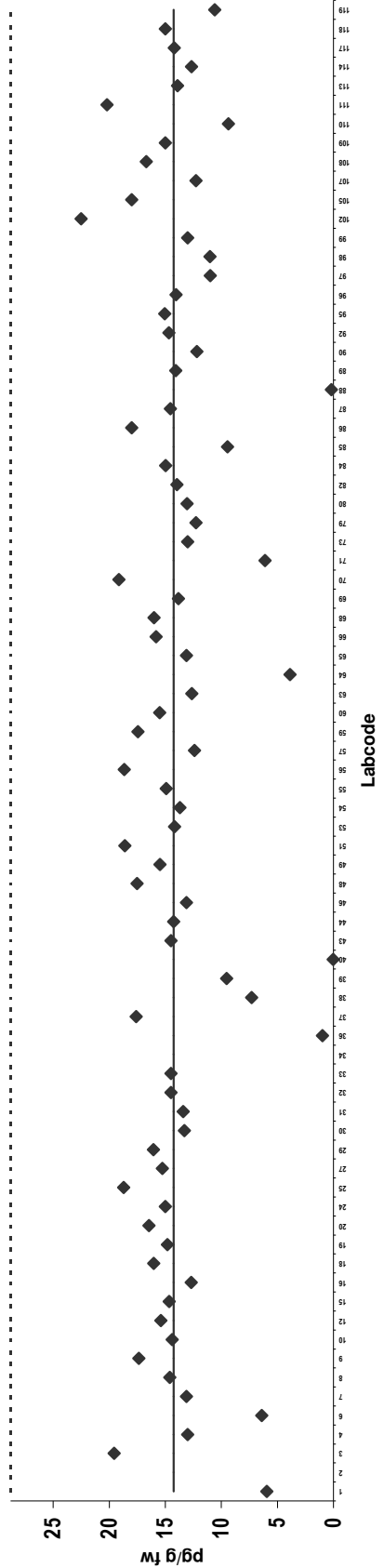
Trout
Congener: PCB 169

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	6.0	ND	66	16	
2	45	Outlier	68	16	
3	20		69	14	
4	13		70	19	
6	6.4		71	6.1	
7	13		73	13	
8	15		79	12	
9	17		80	13	
10	14		82	14	
12	15		84	15	
15	15		85	9.5	
16	13		86	18	
18	16		87	15	
19	15		88	0.19	
20	16		89	14	
24	15		90	12	
25	19		92	15	
27	15		95	15	
29	16		96	14	
30	13		97	11	
31	13		98	11	
32	15		99	13	
33	15		102	23	
34	32	Outlier	105	18	
36	0.98		107	12	
37	18		108	17	
38	7.3		109	15	
39	9.5		110	9.4	
40	0.020	ND	111	20	
43	14		113	14	
44	14		114	13	
46	13		117	14	
48	18		118	15	
49	15		119	11	
51	19				
53	14				
54	14				
55	15				
56	19				
57	12				
59	17				
60	15				
63	13				
64	3.9				
65	13				

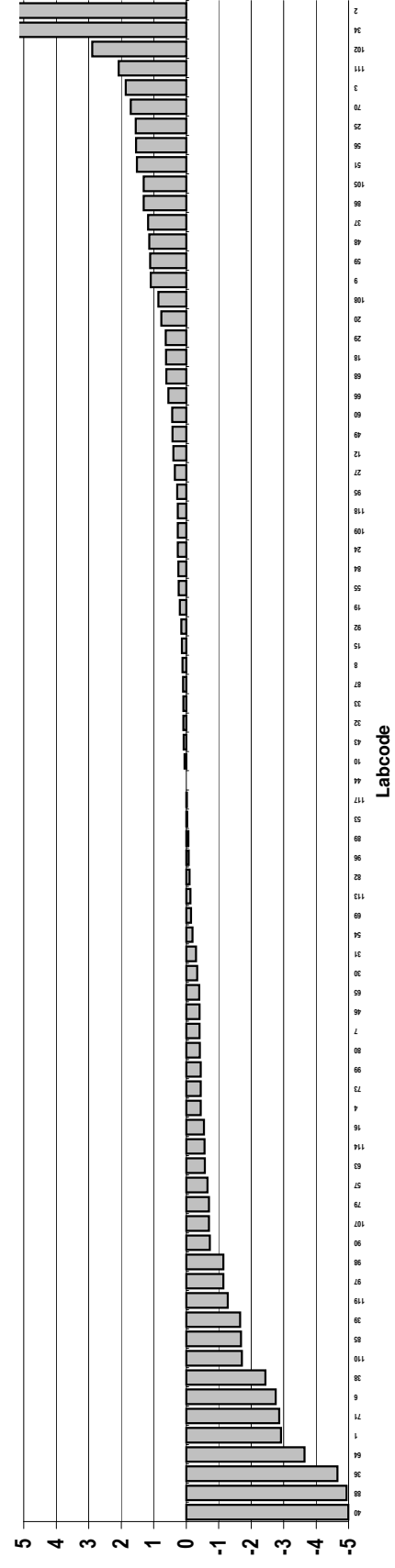
Consensus statistics

Consensus median, pg/g	14
Median all values pg/g	14
Consensus mean, pg/g	14
Standard deviation, pg/g	4.2
Relative standard deviation, %	31
No. of values reported	79
No. of values removed	2
No. of reported non-detects	2

PCB 169



Z-score: PCB 169



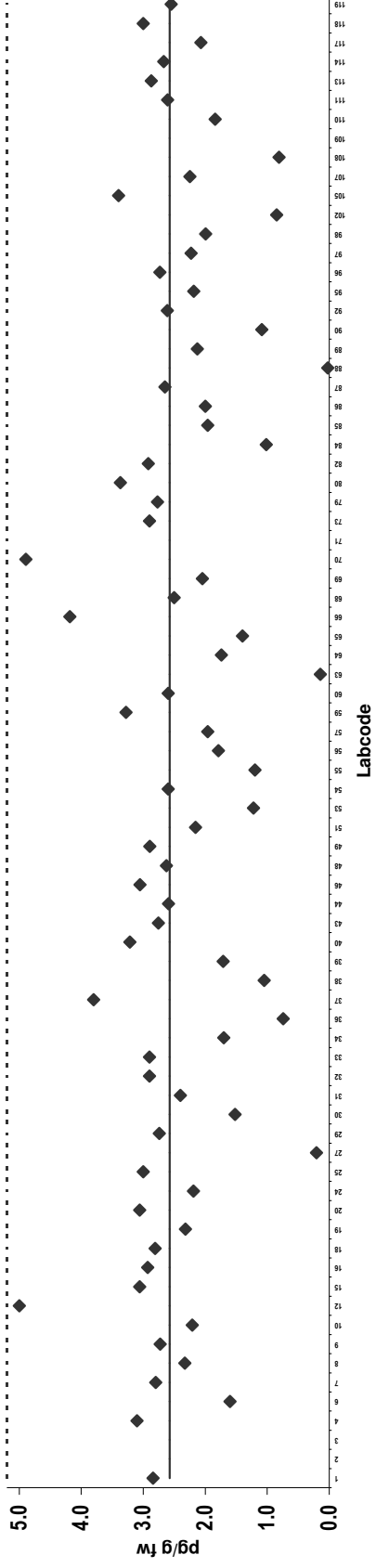
Trout
Congener: PCB 81

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	2.8	ND	66	4.2	
2	9.0	Outlier	68	2.5	
3	3.5	Outlier	69	2.0	
4	3.1		70	4.9	ND
6	1.6		71	11	Outlier
7	2.8		73	2.9	
8	2.3		79	2.8	
9	2.7		80	3.4	
10	2.2		82	2.9	
12	5.0		84	1.0	
15	3.1	ND	85	2.0	
16	2.9		86	2.0	
18	2.8		87	2.7	
19	2.3		88	0.025	
20	3.1		89	2.1	
24	2.2		90	1.1	
25	3.0		92	2.6	
27	0.21		95	2.2	
29	2.7		96	2.7	
30	1.5		97	2.2	
31	2.4		98	2.0	
32	2.9		102	0.85	
33	2.9		105	3.4	
34	1.7	ND	107	2.3	
36	0.74		108	0.81	
37	3.8		109	39	Outlier
38	1.1		110	1.8	
39	1.7		111	2.6	
40	3.2		113	2.9	
43	2.8		114	2.7	
44	2.6		117	2.1	
46	3.1		118	3.0	
48	2.6		119	2.6	
49	2.9				
51	2.2				
53	1.2				
54	2.6				
55	1.2				
56	1.8				
57	2.0				
59	3.3				
60	2.6				
63	0.14	ND			
64	1.7				
65	1.4				

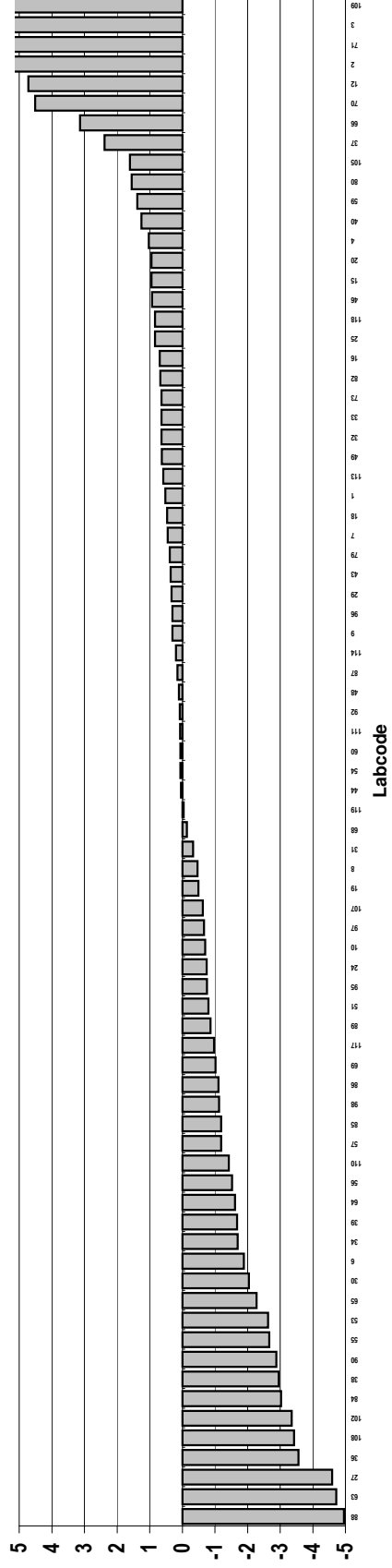
Consensus statistics

Consensus median, pg/g	2.6
Median all values pg/g	2.6
Consensus mean, pg/g	2.4
Standard deviation, pg/g	0.94
Relative standard deviation, %	40
No. of values reported	78
No. of values removed	4
No. of reported non-detects	5

PCB 81



Z-score: PCB 81



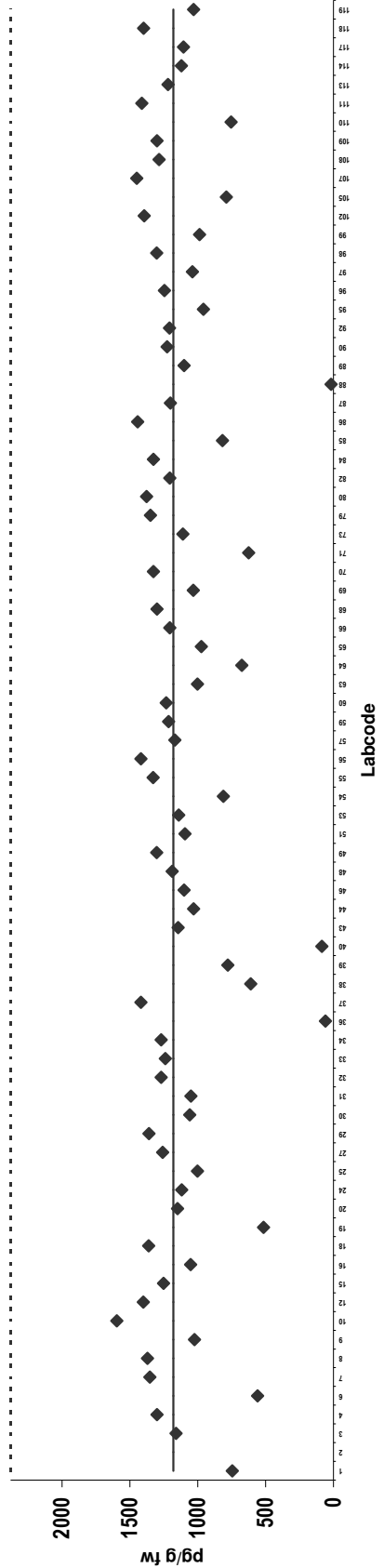
Trout
Congener: PCB 105

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	746		66	1205	
2	4300		68	1300	
3	1161	Outlier	69	1034	
4	1300		70	1328	
6	560		71	626	
7	1353		73	1109	
8	1371		79	1349	
9	1023		80	1376	
10	1597		82	1207	
12	1402		84	1327	
15	1253		85	817	
16	1053		86	1443	
18	1361		87	1201	
19	516		88	17	
20	1148		89	1102	
24	1119		90	1227	
25	1003		92	1208	
27	1258		95	959	
29	1361		96	1245	
30	1060		97	1039	
31	1050		98	1302	
32	1270		99	987	
33	1240		102	1394	
34	1270		105	790	
36	58		107	1449	
37	1420		108	1285	
38	610		109	1300	
39	778		110	754	
40	86		111	1414	
43	1145		113	1220	
44	1031		114	1120	
46	1102		117	1106	
48	1190		118	1400	
49	1302		119	1030	
51	1094				
53	1142				
54	812				
55	1328				
56	1419				
57	1170				
59	1215				
60	1233				
63	1002				
64	676				
65	975				

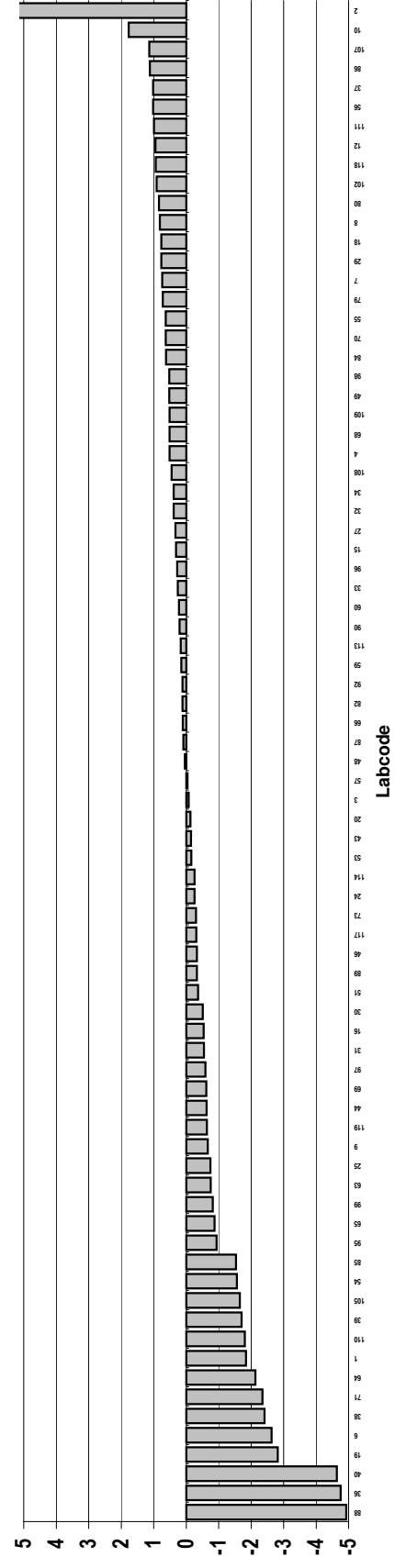
Consensus statistics

Consensus median, pg/g	1180
Median all values pg/g	1190
Consensus mean, pg/g	1102
Standard deviation, pg/g	310
Relative standard deviation, %	28
No. of values reported	79
No. of values removed	1
No. of reported non-detects	0

PCB 105



Z-score: PCB 105



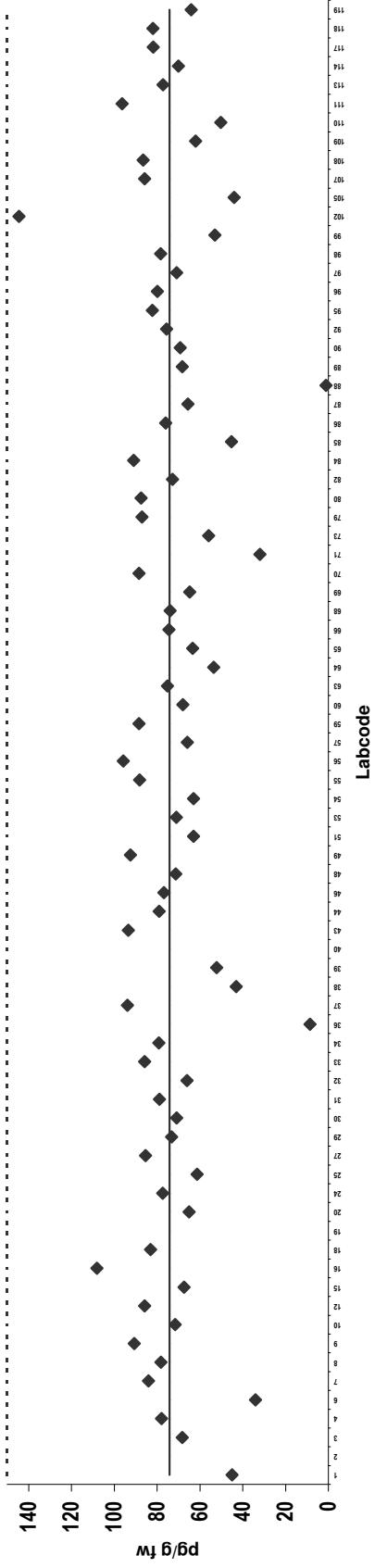
Trout
Congener: PCB 114

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	45		66	74	
2	185	Outlier	68	74	
3	68		69	65	
4	78		70	88	
6	34		71	32	
7	84		73	56	
8	78		79	87	
9	91		80	87	
10	72		82	73	
12	86		84	91	
15	67		85	45	
16	108		86	76	
18	83		87	66	
19	3493	Outlier	88	1.1	
20	65		89	68	
24	77		90	69	
25	61		92	76	
27	85		95	82	
29	73		96	80	
30	71		97	71	
31	79		98	78	
32	66		99	53	
33	86		102	145	
34	79		105	44	
36	8.6		107	86	
37	94		108	87	
38	43		109	62	
39	52		110	50	
40	1393	Outlier	111	96	
43	94		113	77	
44	79		114	70	
46	77		117	82	
48	71		118	82	
49	92		119	64	
51	63				
53	71				
54	63				
55	88				
56	96				
57	66				
59	88				
60	68				
63	75				
64	54				
65	63				

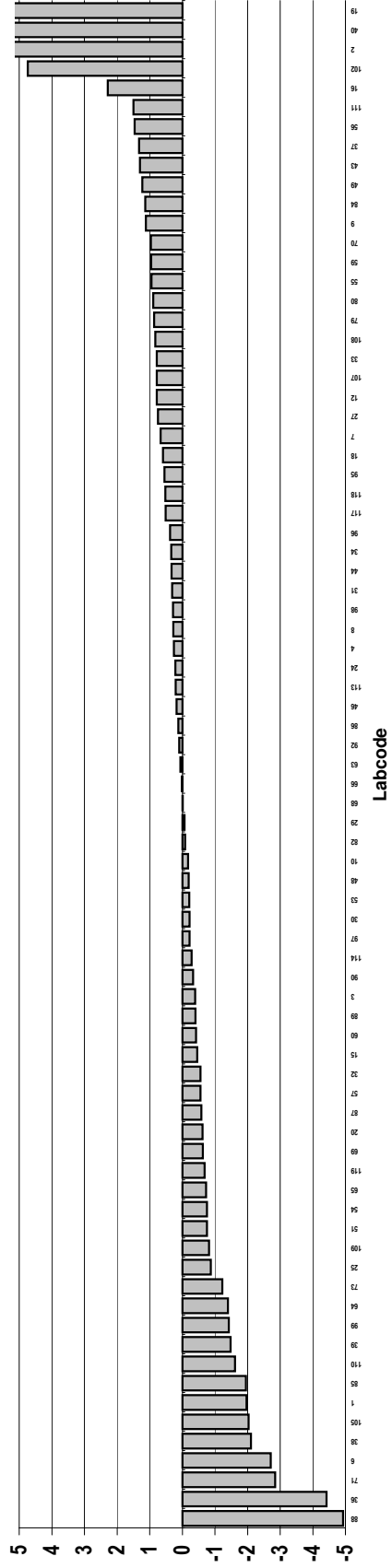
Consensus statistics

Consensus median, pg/g	74
Median all values pg/g	75
Consensus mean, pg/g	72
Standard deviation, pg/g	20
Relative standard deviation, %	28
No. of values reported	79
No. of values removed	3
No. of reported non-detects	0

PCB 114



Z-score: PCB 114



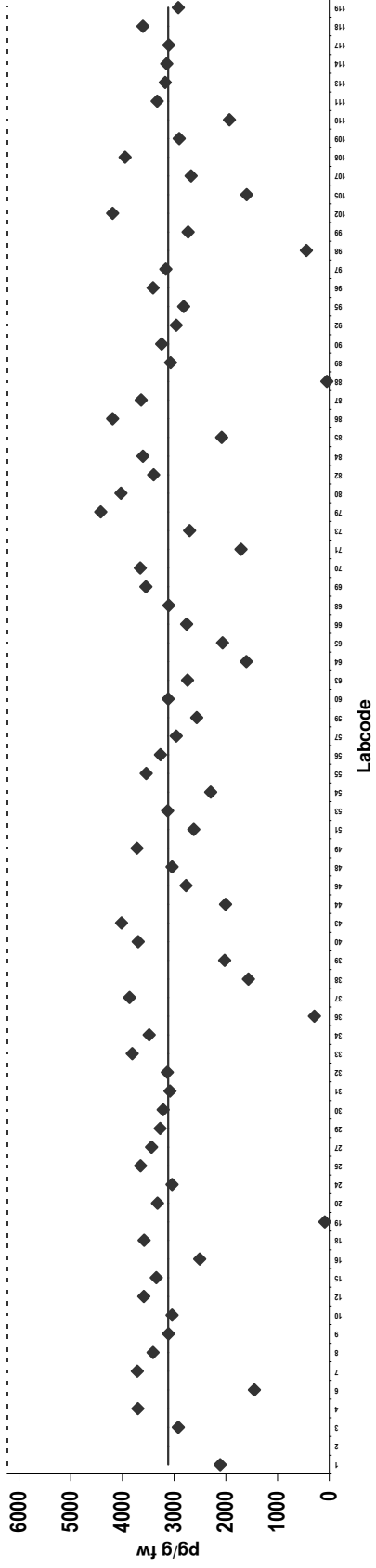
Trout
Congener: PCB 118

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	2110		66	2760	
2	10600		68	3100	
3	2919	Outlier	69	3543	
4	3700		70	3655	
6	1450		71	1707	
7	3712		73	2698	
8	3408		79	4416	
9	3106		80	4026	
10	3037		82	3393	
12	3583		84	3600	
15	3345		85	2080	
16	2505		86	4186	
18	3581		87	3636	
19	85		88	48	
20	3322		89	3066	
24	3037		90	3238	
25	3651		92	2957	
27	3437		95	2817	
29	3271		96	3410	
30	3210		97	3162	
31	3080		98	4444	
32	3130		99	2730	
33	3811		102	4187	
34	3480		105	1600	
36	289		107	2673	
37	3860		108	3950	
38	1560		109	2900	
39	2020		110	1930	
40	3694		111	3329	
43	4015		113	3170	
44	2003		114	3140	
46	2767		117	3103	
48	3038		118	3600	
49	3719		119	2920	
51	2619				
53	3126				
54	2290				
55	3542				
56	3263				
57	2960				
59	2562				
60	3117				
63	2738				
64	1602				
65	2060				

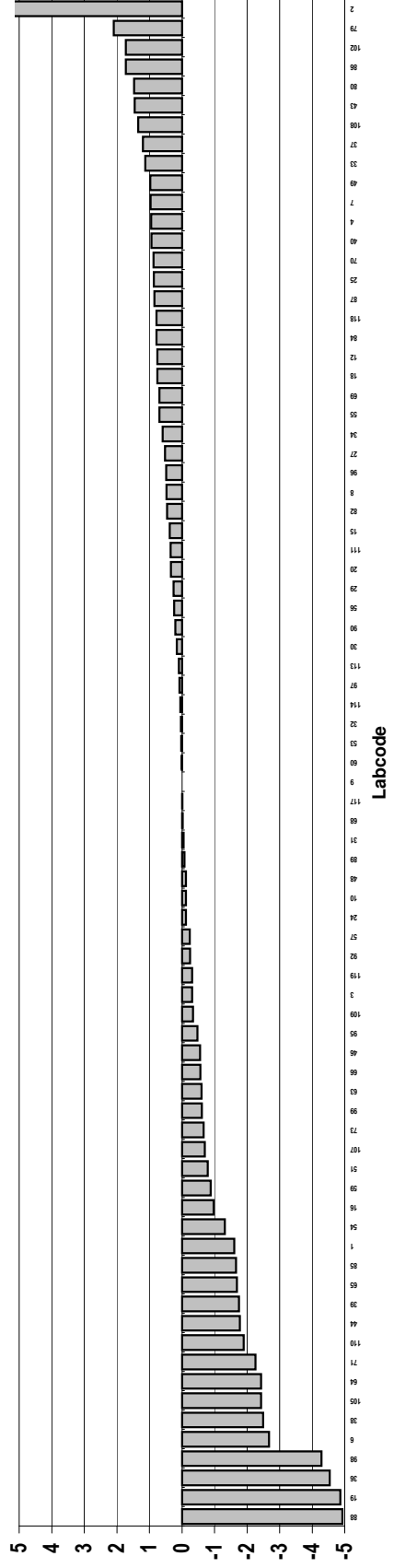
Consensus statistics

Consensus median, pg/g	3112
Median all values pg/g	3117
Consensus mean, pg/g	2923
Standard deviation, pg/g	912
Relative standard deviation, %	31
No. of values reported	79
No. of values removed	1
No. of reported non-detects	0

PCB 118



Z-score: PCB 118



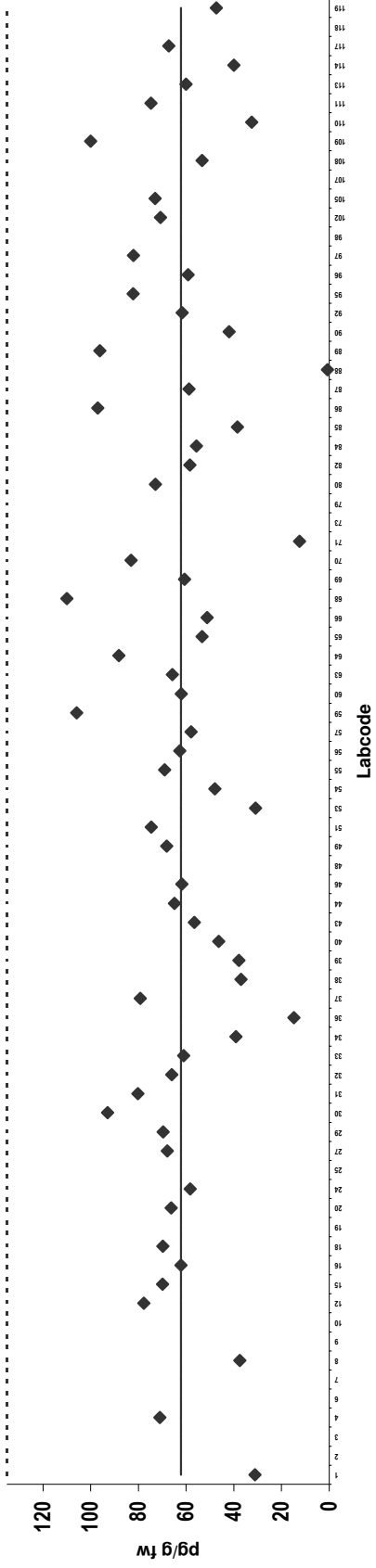
Trout
Congener: PCB 123

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	31		66	51	
2	970	Outlier	68	110	
3	219	Outlier	69	61	
4	71		70	83	
6	247	Outlier	71	12	
7	153	Outlier	73	159	Outlier
8	37		79	148	Outlier
9	140	Outlier	80	73	
10	142	Outlier	82	58	
12	78		84	56	
15	70		85	39	
16	62		86	97	
18	70		87	59	
19	1138	Outlier	88	0.70	
20	66		89	96	
24	58		90	42	
25	289	Outlier	92	62	
27	68		95	82	
29	70		96	59	
30	93		97	82	
31	80		98	491	Outlier
32	66		102	71	
33	61		105	73	
34	39		107	230	Outlier
36	15		108	53	
37	79		109	100	
38	37		110	33	
39	38		111	75	
40	46		113	60	
43	57		114	40	
44	65		117	67	
46	62		118	140	Outlier
48	369		119	47	
49	68				
51	75				
53	31				
54	48				
55	69				
56	63				
57	58				
59	106				
60	62				
63	66				
64	88				
65	53				

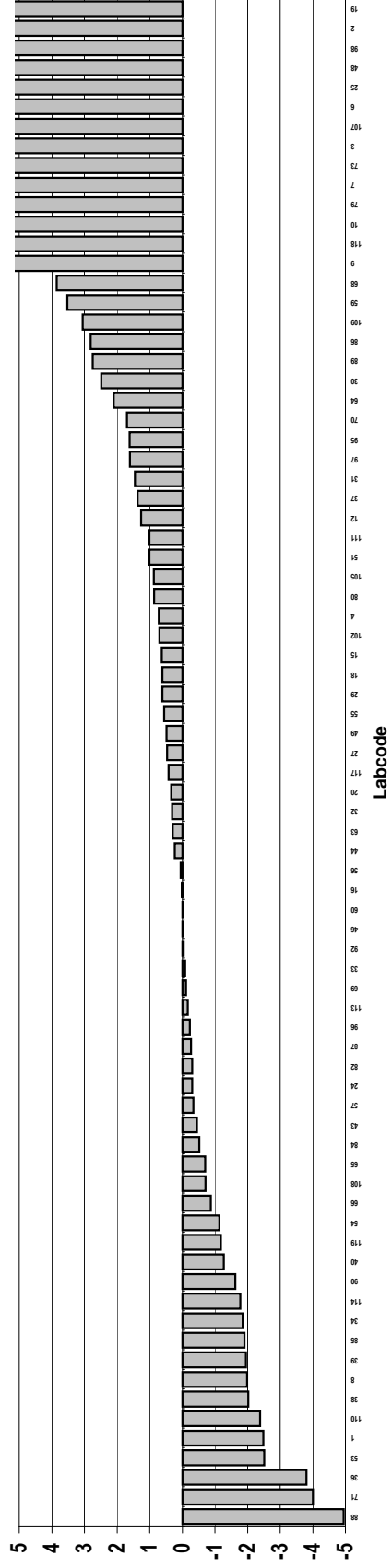
Consensus statistics

Consensus median, pg/g	62
Median all values pg/g	68
Consensus mean, pg/g	62
Standard deviation, pg/g	21
Relative standard deviation, %	35
No. of values reported	78
No. of values removed	14
No. of reported non-detects	0

PCB 123



Z-score: PCB 123



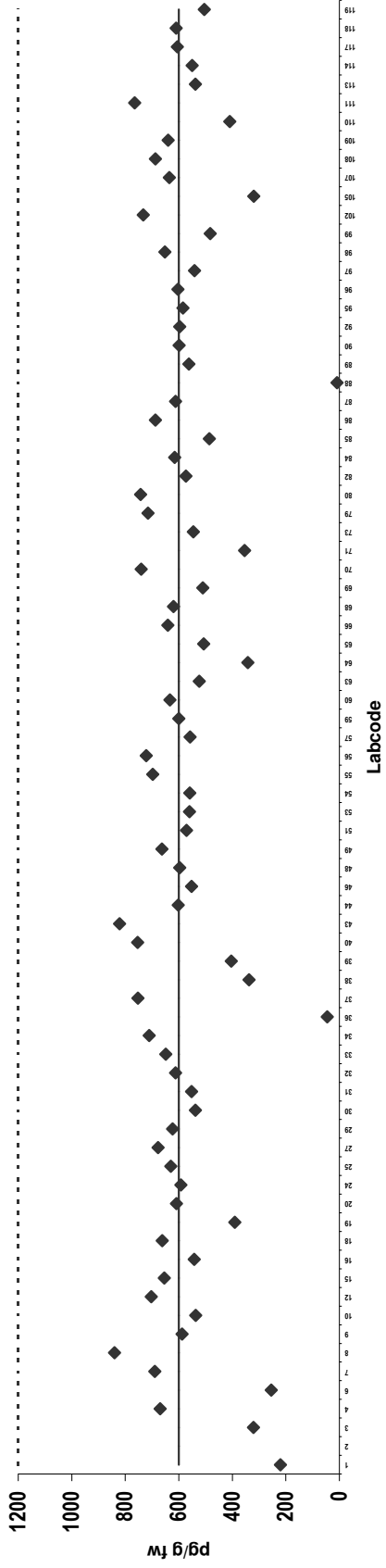
Trout
Congener: PCB 156

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	220		66	641	
2	1960		68	620	
3	321	Outlier	69	510	
4	670		70	741	
6	255		71	354	
7	690		73	546	
8	841		79	715	
9	588		80	742	
10	537		82	574	
12	703		84	615	
15	654		85	486	
16	543		86	688	
18	663		87	613	
19	391		88	8.6	
20	609		89	563	
24	592		90	599	
25	630		92	597	
27	677		95	585	
29	624		96	603	
30	538		97	541	
31	552		98	652	
32	612		99	483	
33	649		102	733	
34	711		105	320	
36	45		107	636	
37	753		108	688	
38	338		109	640	
39	404		110	410	
40	754		111	765	
43	821		113	538	
44	602		114	550	
46	552		117	606	
48	597		118	610	
49	663		119	505	
51	571				
53	561				
54	559				
55	698				
56	722				
57	558				
59	601				
60	633				
63	524				
64	342				
65	507				

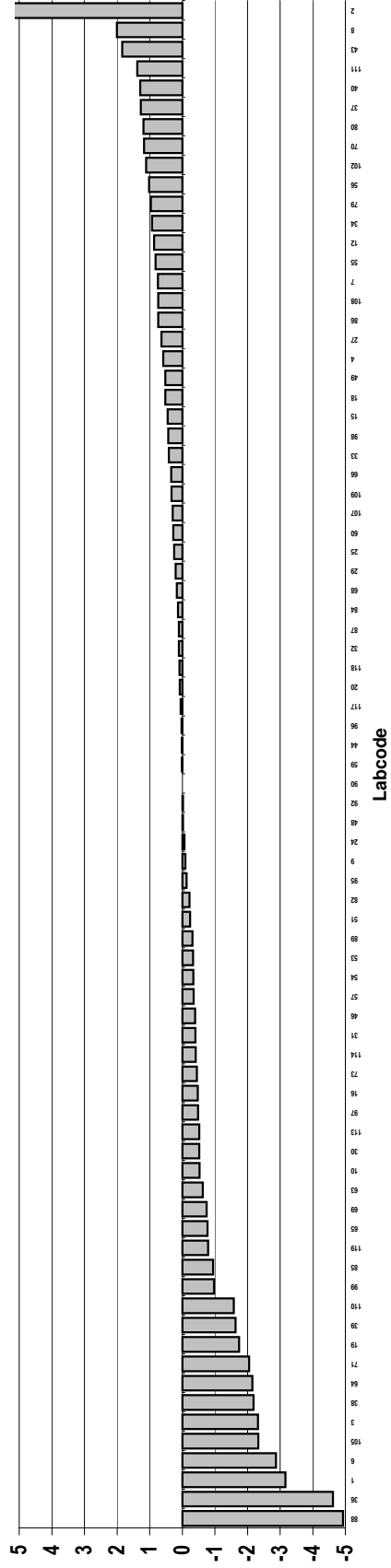
Consensus statistics

Consensus median, pg/g	600
Median all values pg/g	601
Consensus mean, pg/g	571
Standard deviation, pg/g	152
Relative standard deviation, %	27
No. of values reported	79
No. of values removed	1
No. of reported non-detects	0

PCB 156



Z-score: PCB 156



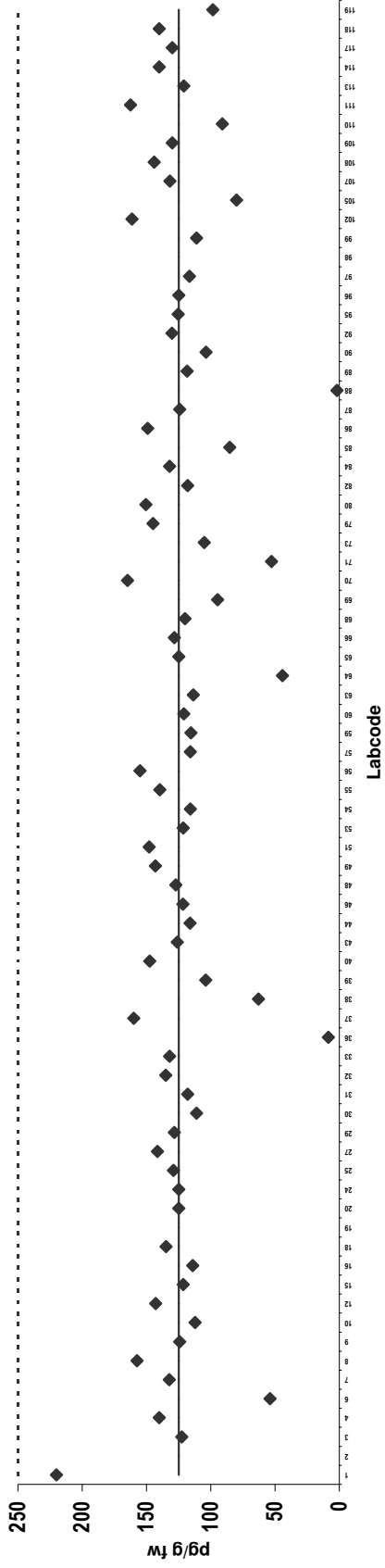
Trout
Congener: PCB 157

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	220		68	120	
2	370		69	95	
3	123		70	165	
4	140		71	53	
6	54		73	105	
7	132		79	145	
8	157		80	150	
9	124		82	118	
10	112		84	132	
12	143		85	85	
15	121		86	149	
16	114		87	124	
18	135		88	1.8	
19	623		89	118	
20	125		90	104	
24	125		92	130	
25	129		95	125	
27	142		96	125	
29	128		97	117	
30	111		98	591	
31	118		99	111	
32	135		102	161	
33	132		105	80	
36	8.5		107	132	
37	160		108	144	
38	63		109	130	
39	104		110	91	
40	148		111	162	
43	126		113	121	
44	116		114	140	
46	122		117	130	
48	127		118	140	
49	143		119	98	
51	148				
53	122				
54	116				
55	140				
56	155				
57	116				
59	116				
60	121				
63	114				
64	44				
65	125				
66	128				

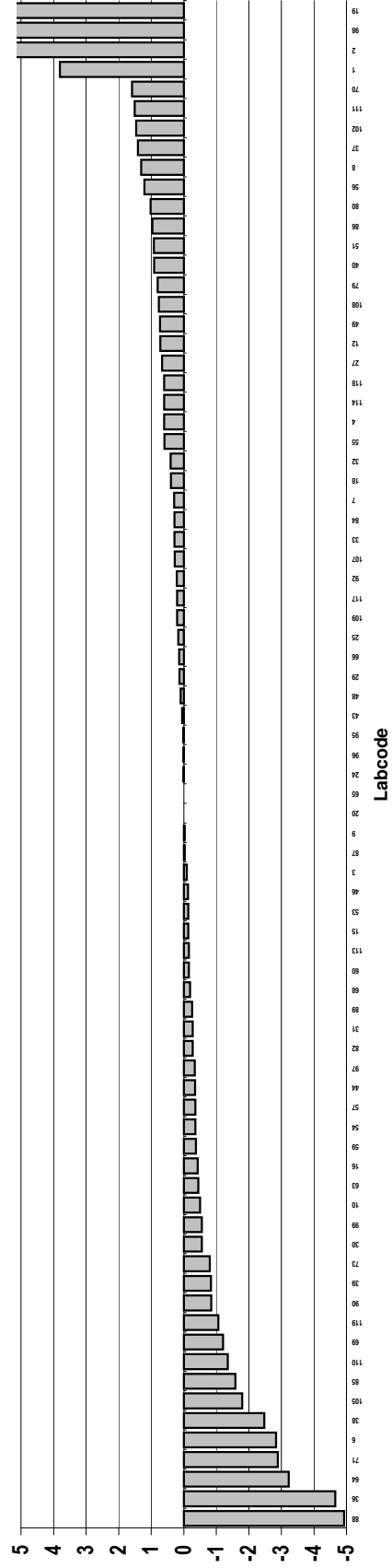
Consensus statistics

Consensus median, pg/g	125
Median all values pg/g	125
Consensus mean, pg/g	121
Standard deviation, pg/g	33
Relative standard deviation, %	27
No. of values reported	78
No. of values removed	3
No. of reported non-detects	0

PCB 157



Z-score: PCB 157



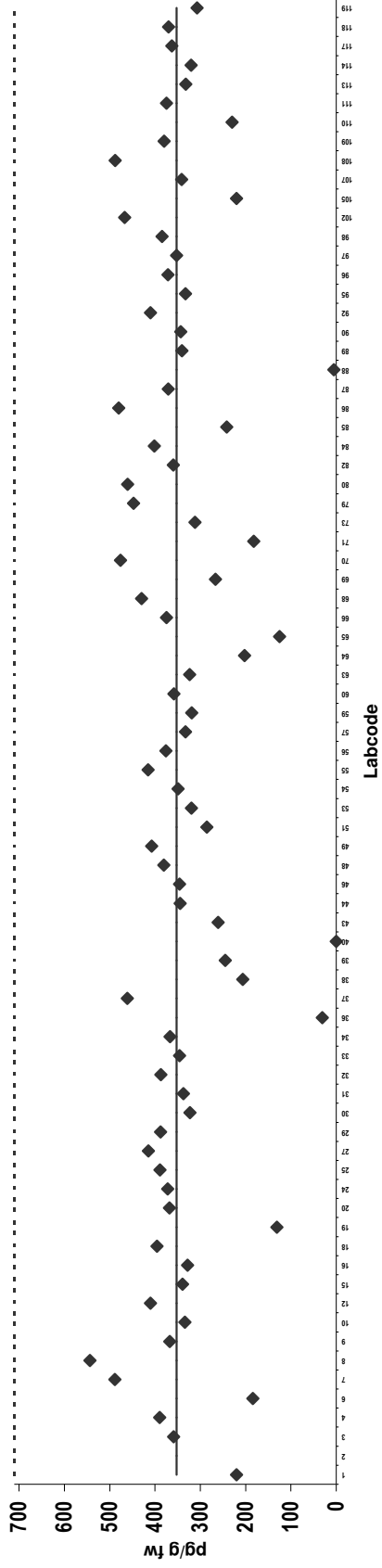
Trout
Congener: PCB 167

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	220		66	375	
2	1120		68	430	
3	359	Outlier	69	267	
4	390		70	476	
6	184		71	182	
7	489		73	312	
8	543		79	447	
9	368		80	461	
10	334		82	360	
12	410		84	401	
15	339		85	242	
16	328		86	480	
18	396		87	371	
19	131		88	5.2	
20	368		89	341	
24	372		90	343	
25	389		92	410	
27	414		95	332	
29	387		96	372	
30	323		97	353	
31	337		98	384	
32	387		102	467	
33	346		105	220	
34	367		107	342	
36	30		108	488	
37	461		109	380	
38	206		110	230	
39	245		111	375	
40	0.016		113	332	
43	261		114	320	
44	345		117	363	
46	346		118	370	
48	381		119	307	
49	407				
51	285				
53	320				
54	349				
55	416				
56	376				
57	333				
59	319				
60	358				
63	323				
64	202				
65	125				

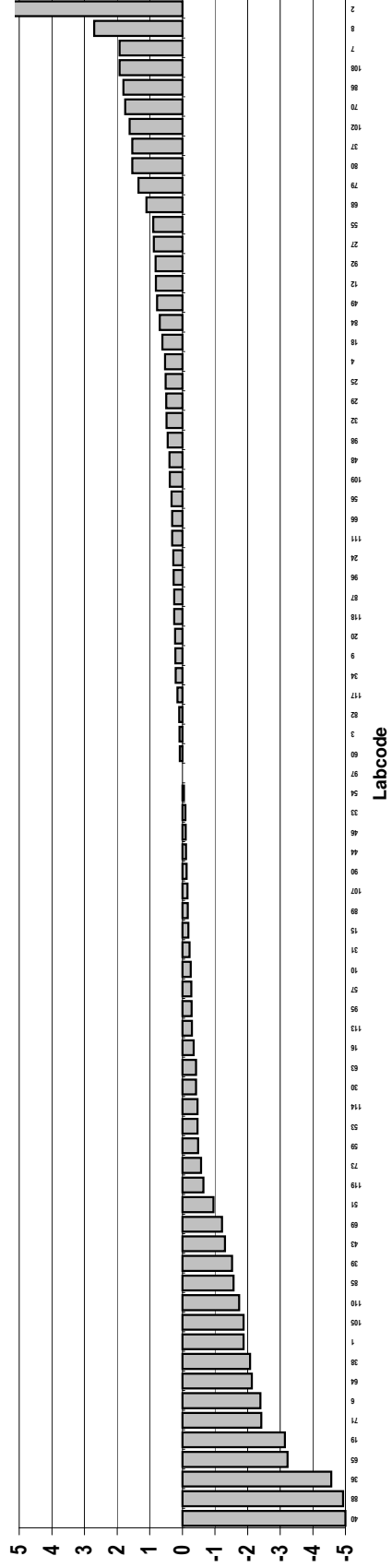
Consensus statistics

Consensus median, pg/g	353
Median all values pg/g	355
Consensus mean, pg/g	335
Standard deviation, pg/g	104
Relative standard deviation, %	31
No. of values reported	78
No. of values removed	1
No. of reported non-detects	1

PCB 167



Z-score: PCB 167



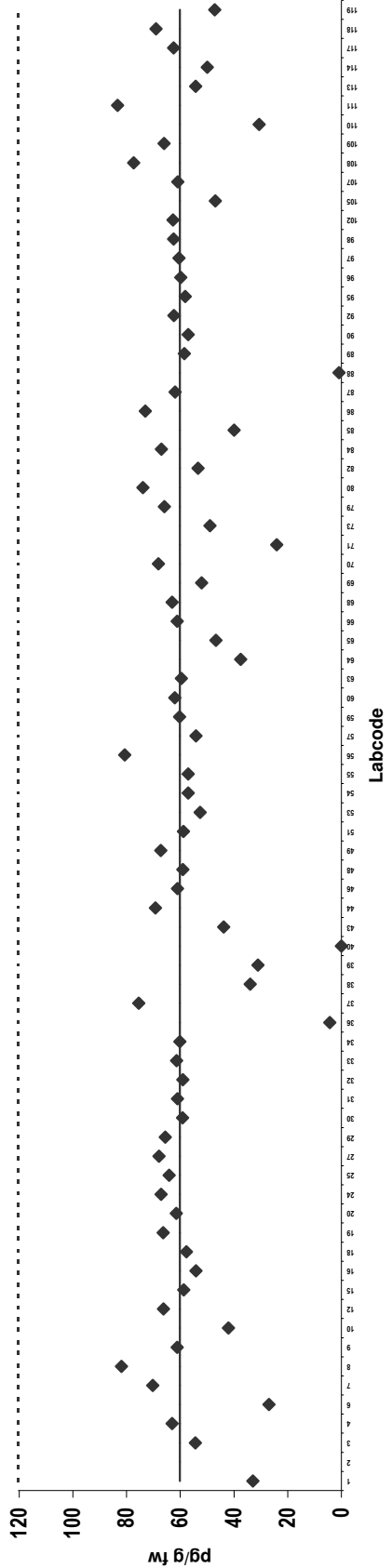
Trout
Congener: PCB 189

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	33		66	61	
2	215		68	63	
3	54	Outlier	69	52	
4	63		70	68	
6	27		71	24	
7	70		73	49	
8	82		79	66	
9	61		80	74	
10	42		82	53	
12	66		84	67	
15	59		85	40	
16	54		86	73	
18	58		87	62	
19	66		88	0.94	
20	62		89	58	
24	67		90	57	
25	64		92	62	
27	68		95	58	
29	66		96	60	
30	59		97	60	
31	61		98	62	
32	59		102	63	
33	61		105	47	
34	60		107	61	
36	4.3		108	77	
37	76		109	66	
38	34		110	31	
39	31		111	83	
40	0.027		113	54	
43	44		114	50	
44	69		117	63	
46	61		118	69	
48	59		119	47	
49	67				
51	59				
53	53				
54	57				
55	57				
56	81				
57	54				
59	60				
60	62				
63	60				
64	38				
65	47				

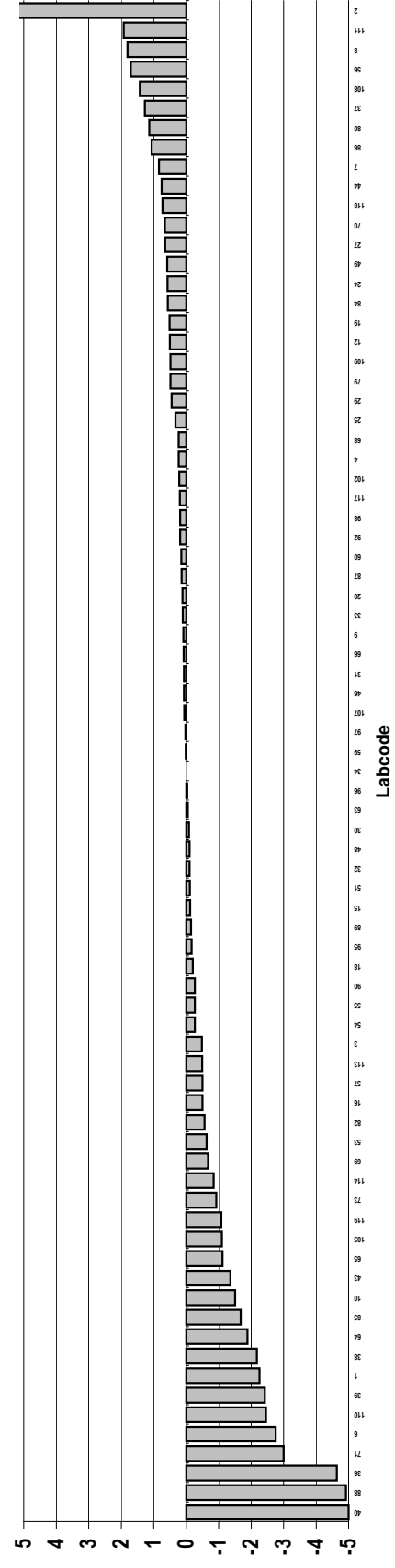
Consensus statistics

Consensus median, pg/g	60
Median all values pg/g	60
Consensus mean, pg/g	56
Standard deviation, pg/g	16
Relative standard deviation, %	29
No. of values reported	78
No. of values removed	1
No. of reported non-detects	1

PCB 189



Z-score: PCB 189



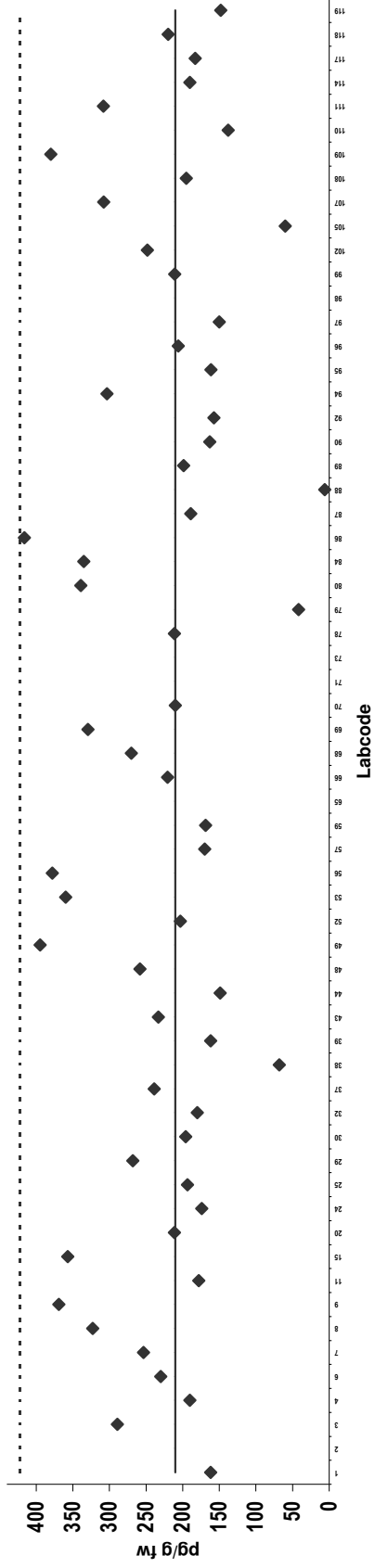
Trout
Congener: CB 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	162		94	303	
2	990	Outlier	95	161	
3	289		96	206	
4	190		97	150	
6	230		98	526	Outlier
7	253		99	211	
8	323		102	248	
9	369		105	60	
11	178		107	308	
15	357		108	195	
20	211		109	380	
24	174		110	138	
25	194		111	308	
29	268		114	190	
30	196		117	183	
32	180		118	220	
37	239		119	148	
38	68				
39	162				
43	233				
44	149				
48	258				
49	395				
52	203				
53	360				
56	378				
57	170				
59	169				
65	474	Outlier			
66	221				
68	270				
69	329				
70	210				
71	1000	Outlier,ND			
73	526	Outlier			
78	211				
79	42				
80	339				
84	335				
86	416				
87	189				
88	6.2				
89	199				
90	163				
92	157				

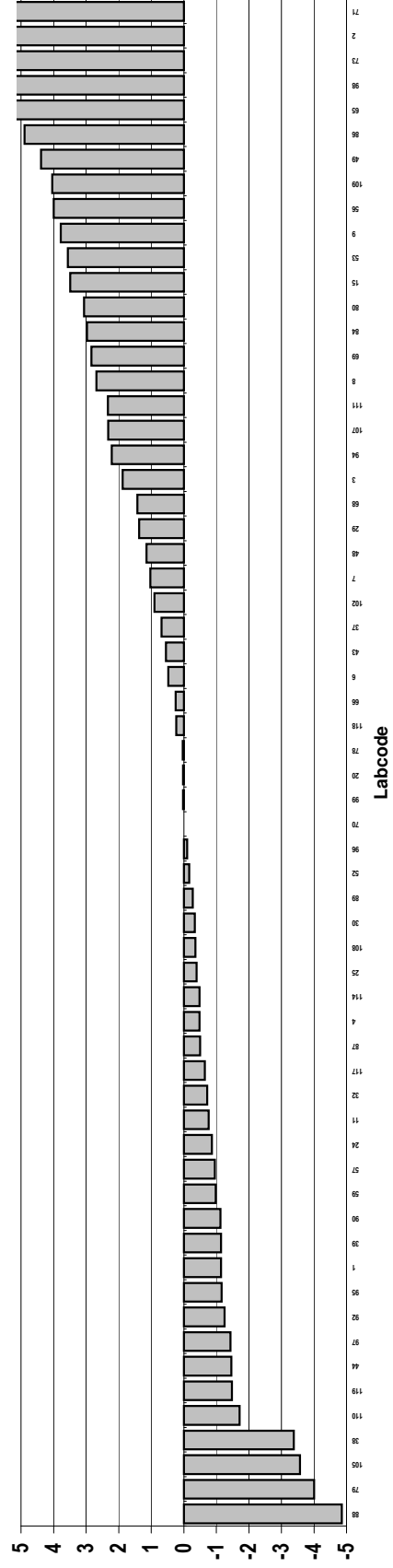
Consensus statistics

Consensus median, pg/g	210
Median all values pg/g	211
Consensus mean, pg/g	226
Standard deviation, pg/g	89
Relative standard deviation, %	40
No. of values reported	62
No. of values removed	5
No. of reported non-detects	1

CB 28



Z-score: CB 28



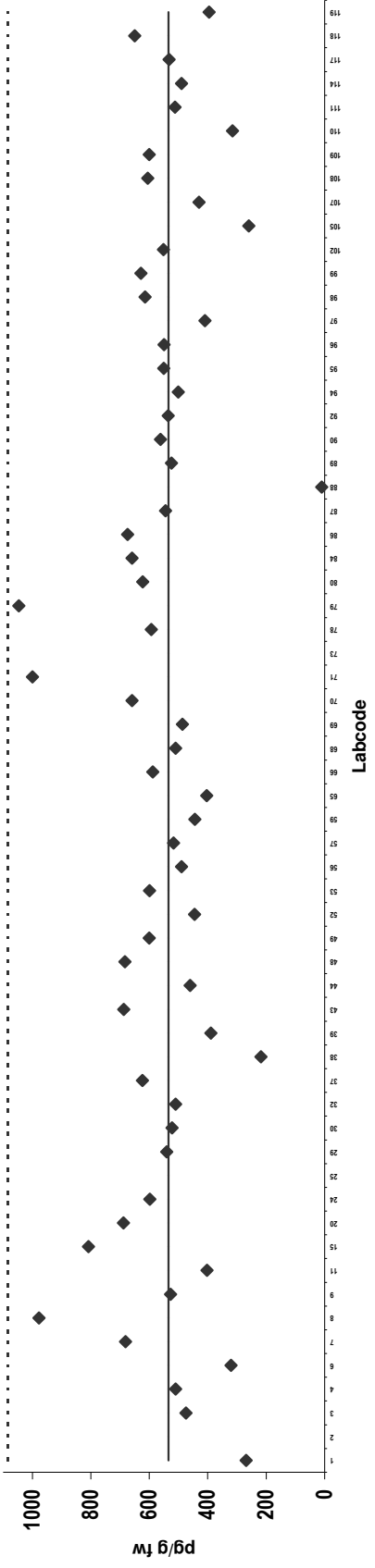
Trout
Congener: CB 52

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	269		94	501	
2	1950		95	551	
3	474	Outlier	96	550	
4	510		97	410	
6	320		98	614	
7	682		99	629	
8	978		102	552	
9	527		105	260	
11	402		107	430	
15	808		108	605	
20	688		109	600	
24	598		110	315	
25	5028	Outlier	111	512	
29	540		114	490	
30	522		117	532	
32	510		118	650	
37	624		119	395	
38	218				
39	389				
43	687				
44	460				
48	683				
49	600				
52	445				
53	600				
56	490				
57	517				
59	444				
65	404				
66	588				
68	510				
69	486				
70	659				
71	1000				
73	1302				
78	593				
79	1046				
80	622				
84	659				
86	674				
87	544				
88	9.7				
89	524				
90	561				
92	536				

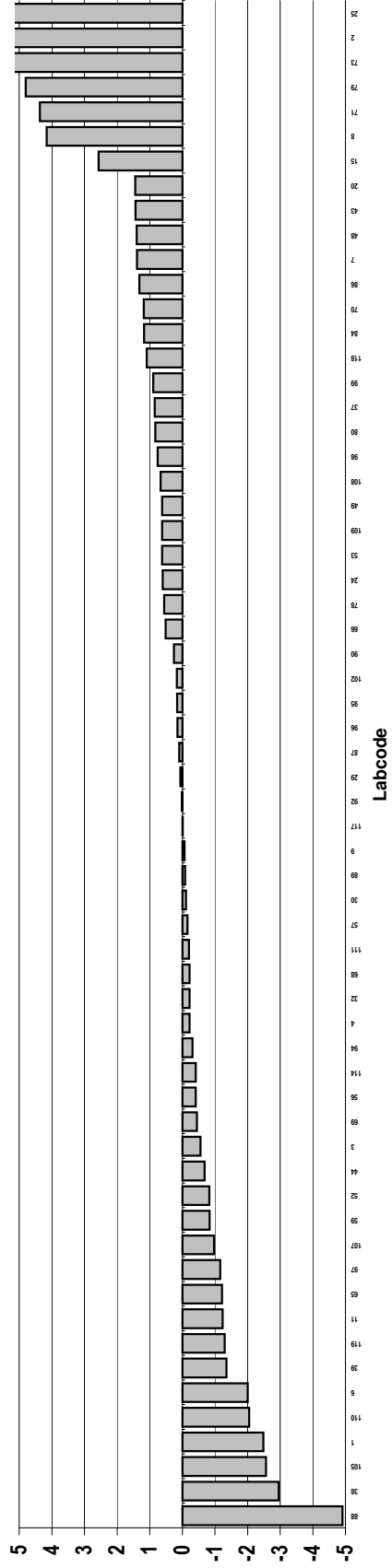
Consensus statistics

Consensus median, pg/g	534
Median all values pg/g	542
Consensus mean, pg/g	542
Standard deviation, pg/g	172
Relative standard deviation, %	32
No. of values reported	62
No. of values removed	3
No. of reported non-detects	1

CB 52



Z-score: CB 52



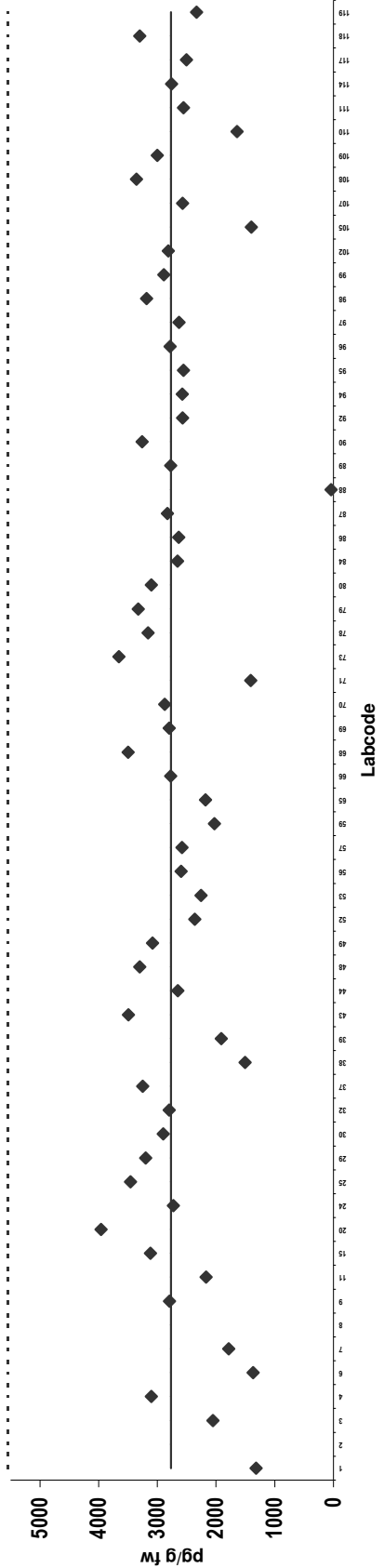
Trout
Congener: CB 101

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1320		94	2577	
2	9800		95	2555	
3	2051	Outlier	96	2785	
4	3100		97	2630	
6	1370		98	3185	
7	1783		99	2891	
8	5703		102	2813	
9	2794	Outlier	105	1400	
11	2170		107	2571	
15	3120		108	3356	
20	3958		109	3000	
24	2725		110	1640	
25	3455		111	2553	
29	3199		114	2760	
30	2900		117	2503	
32	2800		118	3300	
37	3250		119	2330	
38	1508				
39	1910				
43	3491				
44	2649				
48	3299				
49	3083				
52	2363				
53	2255				
56	2597				
57	2580				
59	2027				
65	2180				
66	2775				
68	3500				
69	2801				
70	2875				
71	1410				
73	3654				
78	3156				
79	3325				
80	3100				
84	2658				
86	2638				
87	2830				
88	38				
89	2771				
90	3258				
92	2569				

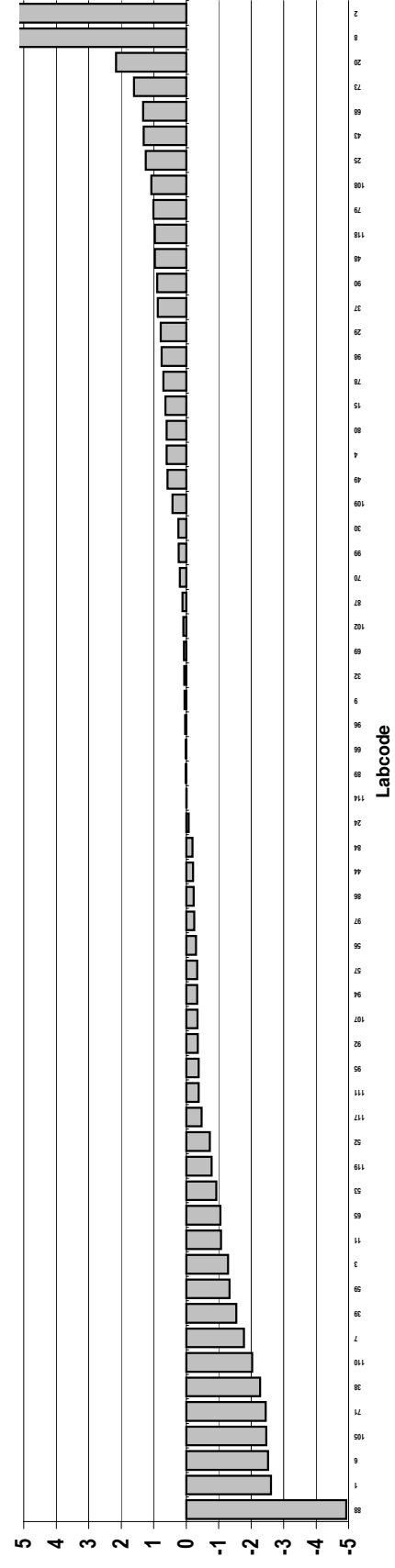
Consensus statistics

Consensus median, pg/g	2765
Median all values pg/g	2773
Consensus mean, pg/g	2636
Standard deviation, pg/g	689
Relative standard deviation, %	26
No. of values reported	62
No. of values removed	2
No. of reported non-detects	0

CB 101



Z-score: CB 101



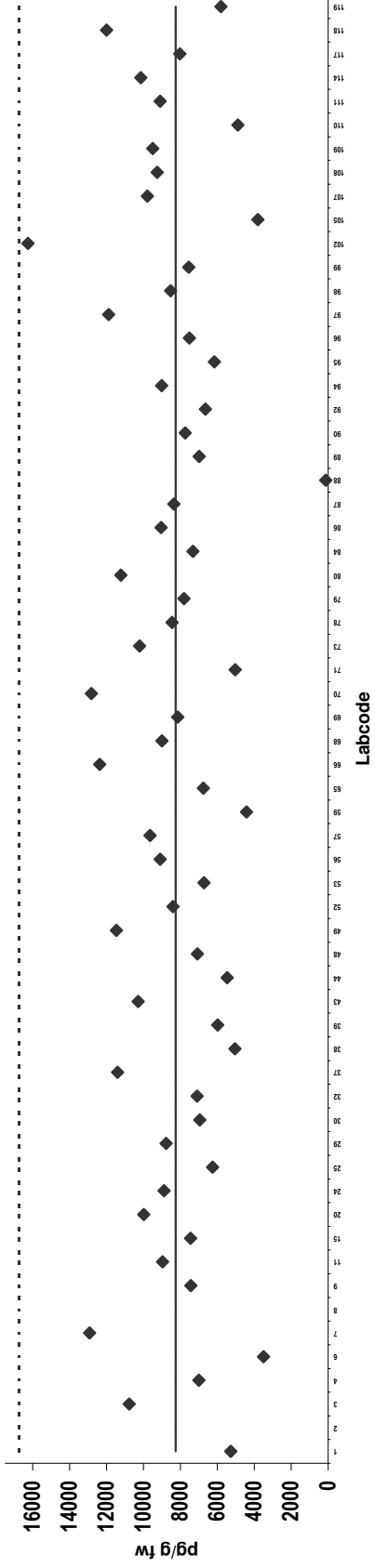
Trout
Congener: CB 138

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5280		94	9008	
2	26000		95	6156	
3	10774	Outlier	96	7515	
4	7000		97	11890	
6	3500		98	8524	
7	12918		99	7553	
8	19984		102	16265	
9	7430	Outlier	105	3800	
11	8974		107	9795	
15	7452		108	9254	
20	9986		109	9500	
24	8890		110	4880	
25	6253		111	9101	
29	8781		114	10150	
30	6950		117	8034	
32	7100		118	12000	
37	11400		119	5810	
38	5049				
39	5990				
43	10295				
44	5465				
48	7089				
49	11465				
52	8398				
53	6726				
56	9095				
57	9650				
59	4412				
65	6760				
66	12379				
68	9000				
69	8153				
70	12826				
71	5030				
73	10209				
78	8456				
79	7808				
80	11220				
84	7321				
86	9046				
87	8350				
88	121				
89	6984				
90	7736				
92	6650				

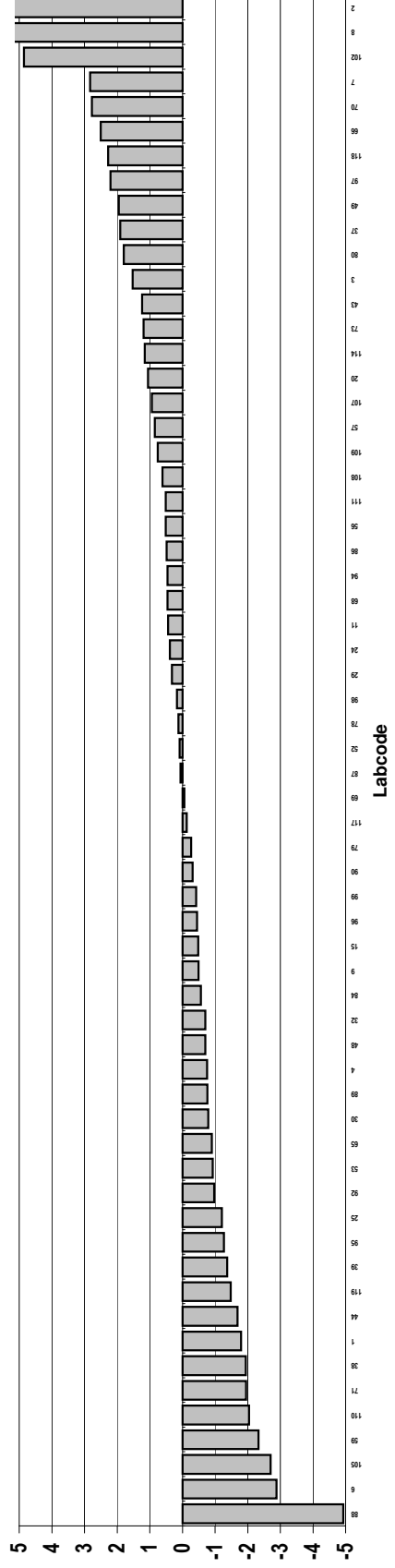
Consensus statistics

Consensus median, pg/g	8251
Median all values pg/g	8374
Consensus mean, pg/g	8227
Standard deviation, pg/g	2676
Relative standard deviation, %	33
No. of values reported	62
No. of values removed	2
No. of reported non-detects	0

CB 138



Z-score: CB 138



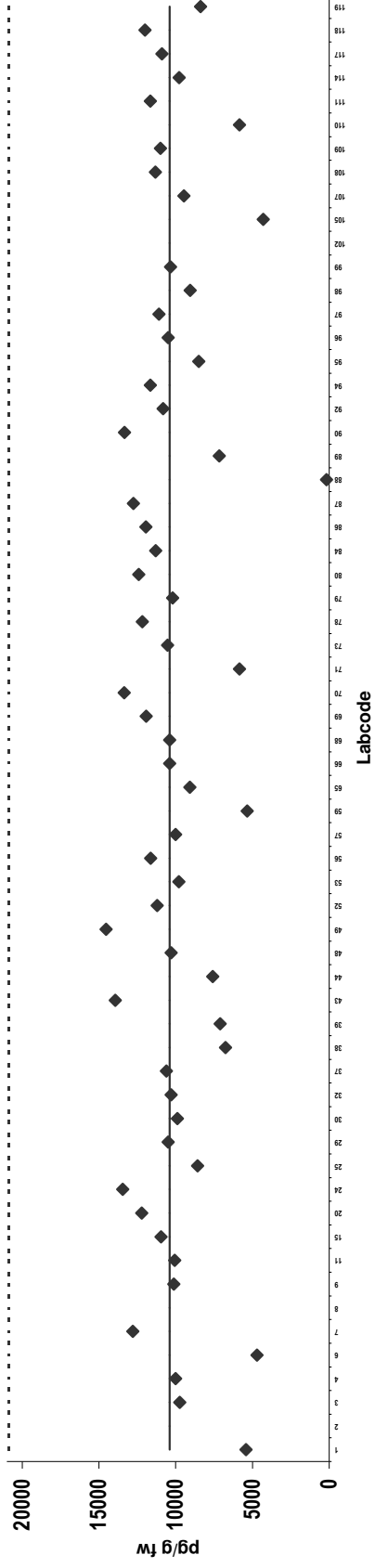
Trout
Congener: CB 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5420		94	11653	
2	32000		95	8488	
3	9734	Outlier	96	10500	
4	10000		97	11090	
6	4700		98	9062	
7	12796		99	10344	
8	21042		102	22795	Outlier
9	10113		105	4300	
11	10062		107	9473	
15	10963		108	11313	
20	12212		109	11000	
24	13445		110	5850	
25	8568		111	11647	
29	10491		114	9770	
30	9890		117	10894	
32	10300		118	12000	
37	10600		119	8380	
38	6763				
39	7100				
43	13927				
44	7582				
48	10290				
49	14537				
52	11203				
53	9787				
56	11640				
57	10000				
59	5347				
65	9080				
66	10394				
68	10400				
69	11922				
70	13348				
71	5840				
73	10533				
78	12180				
79	10201				
80	12410				
84	11299				
86	11934				
87	12750				
88	173				
89	7161				
90	13329				
92	10823				

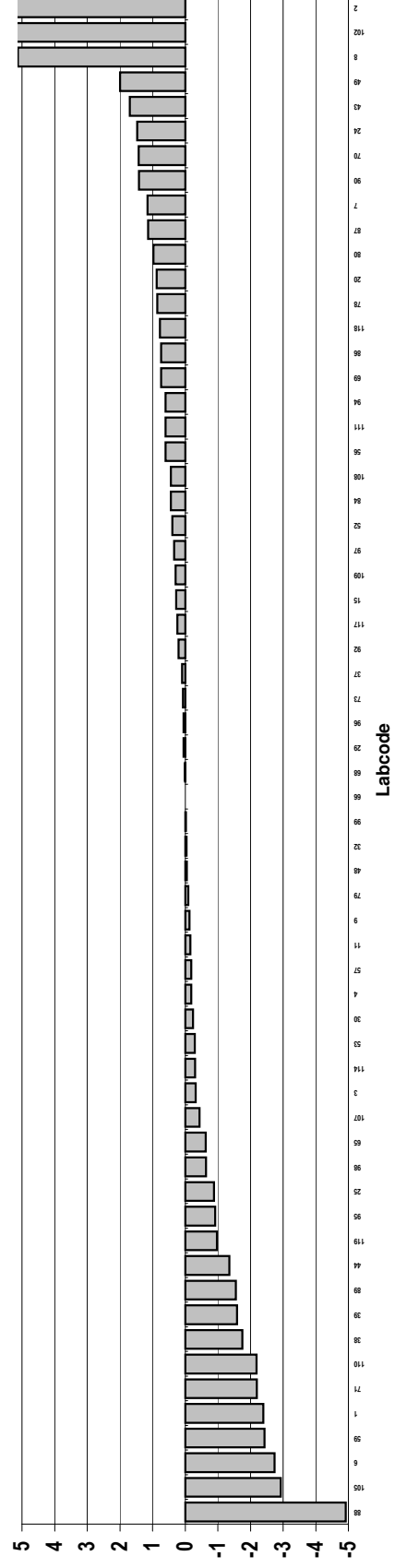
Consensus statistics

Consensus median, pg/g	10394
Median all values pg/g	10446
Consensus mean, pg/g	9949
Standard deviation, pg/g	2652
Relative standard deviation, %	27
No. of values reported	62
No. of values removed	3
No. of reported non-detects	0

CB 153



Z-score: CB 153



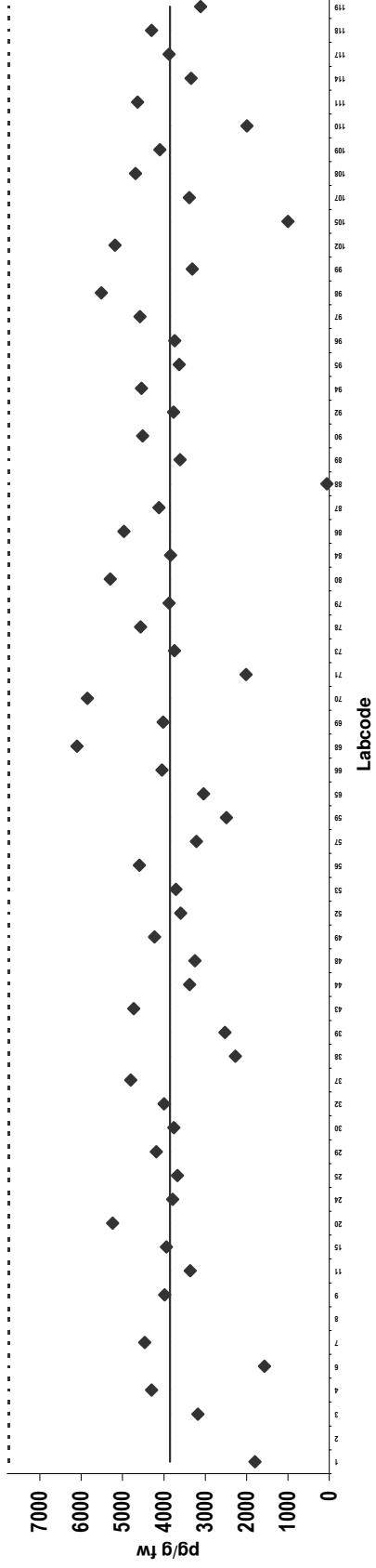
Trout
Congener: CB 180

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1800		94	4547	
2	10500		95	3629	
3	3177	Outlier	96	3740	
4	4300		97	4580	
6	1570		98	5511	
7	4463		99	3314	
8	7963		102	5181	
9	3985	Outlier	105	1000	
11	3362		107	3387	
15	3941		108	4687	
20	5239		109	4100	
24	3785		110	1990	
25	3673		111	4635	
29	4181		114	3340	
30	3760		117	3874	
32	4000		118	4300	
37	4800		119	3110	
38	2273				
39	2520				
43	4729				
44	3378				
48	3247				
49	4226				
52	3596				
53	3708				
56	4592				
57	3210				
59	2484				
65	3040				
66	4048				
68	6100				
69	4016				
70	5849				
71	2010				
73	3747				
78	4565				
79	3873				
80	5300				
84	3838				
86	4965				
87	4120				
88	56				
89	3608				
90	4513				
92	3763				

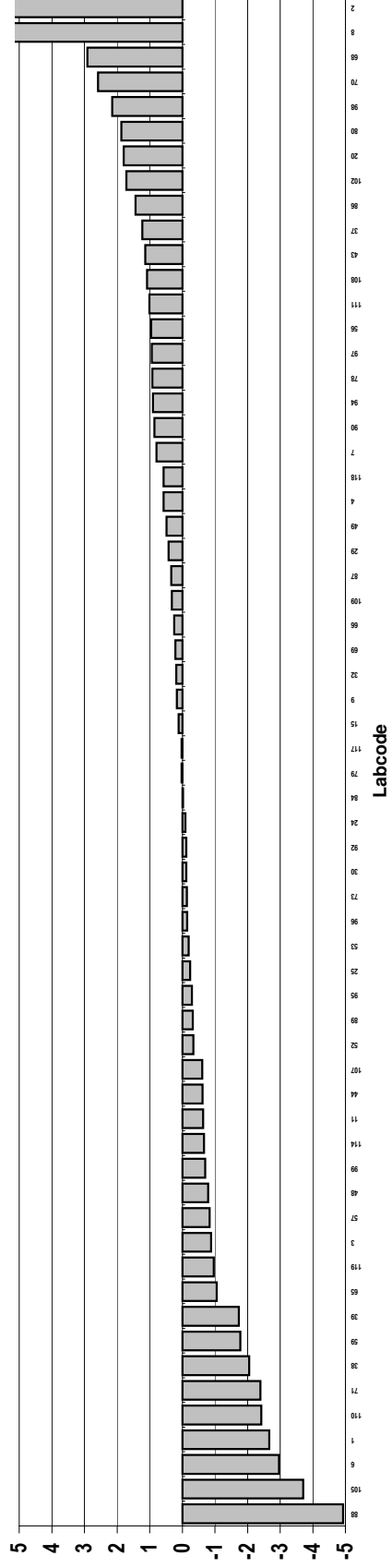
Consensus statistics

Consensus median, pg/g	3856
Median all values pg/g	3874
Consensus mean, pg/g	3772
Standard deviation, pg/g	1121
Relative standard deviation, %	30
No. of values reported	62
No. of values removed	2
No. of reported non-detects	0

CB 180



Z-score: CB 180



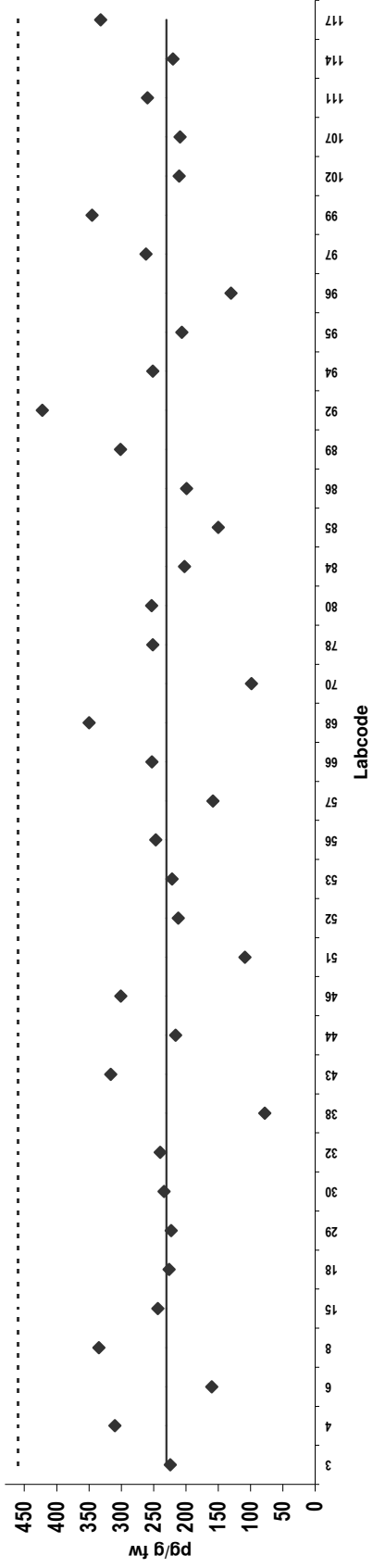
Trout
Congener: BDE 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	224				
4	310				
6	160				
8	335				
15	244				
18	226				
29	223				
30	234				
32	240				
38	78				
43	316				
44	216				
46	301				
51	109				
52	212				
53	221				
56	247				
57	158				
66	252				
68	350				
70	99				
78	251				
80	253				
84	202				
85	150				
86	199				
89	301				
92	422				
94	251				
95	206				
96	130				
97	262				
99	345				
102	211				
107	209				
111	259				
114	220				
117	332				

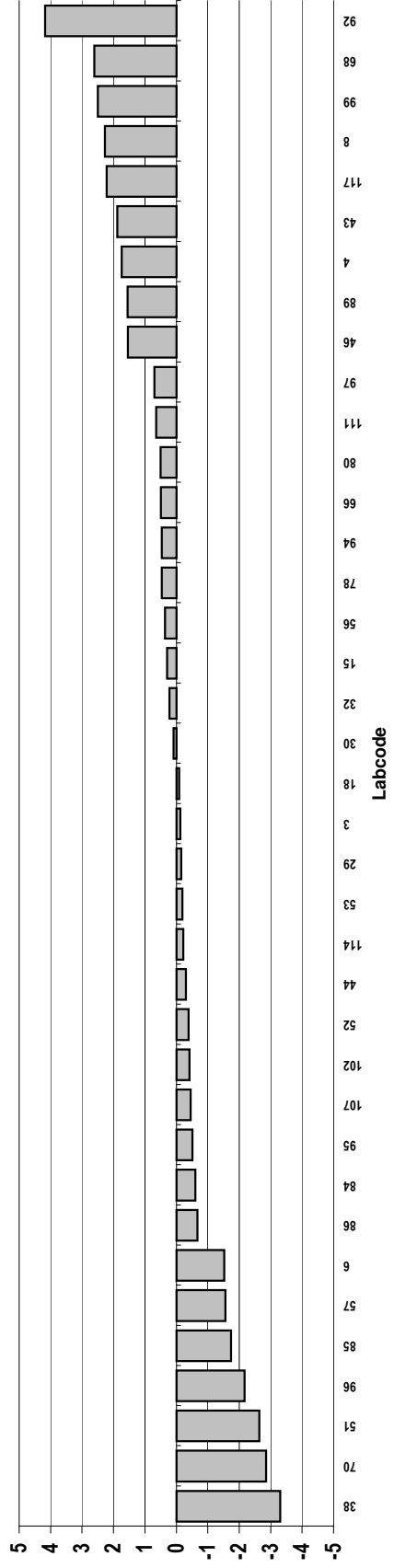
Consensus statistics

Consensus median, pg/g	230
Median all values pg/g	230
Consensus mean, pg/g	236
Standard deviation, pg/g	73
Relative standard deviation, %	31
No. of values reported	38
No. of values removed	0
No. of reported non-detects	0

BDE 28



Z-score: BDE 28



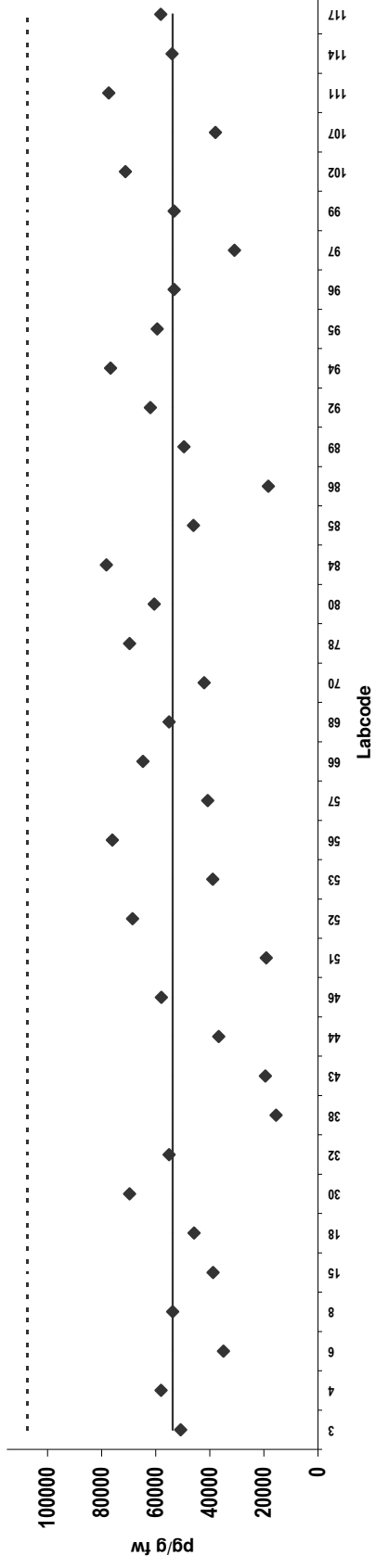
Trout
Congener: BDE 47

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	50702				
4	58000				
6	34900				
8	53670				
15	38740				
18	45805				
30	69600				
32	55000				
38	15500				
43	19418				
44	36702				
46	57895				
51	19060				
52	68535				
53	38934				
56	75969				
57	40700				
66	64653				
68	55000				
70	42100				
78	69597				
80	60570				
84	78171				
85	46000				
86	18381				
89	49506				
92	61995				
94	76649				
95	59372				
96	53200				
97	30897				
99	53148				
102	71170				
107	37943				
111	77328				
114	53920				
117	58111				

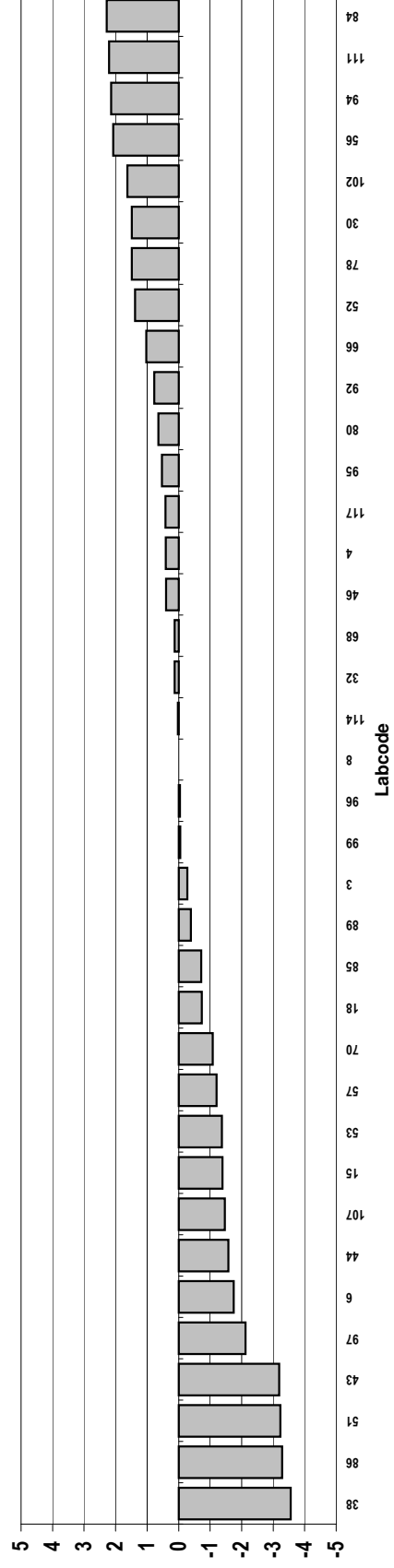
Consensus statistics

Consensus median, pg/g	53670
Median all values pg/g	53670
Consensus mean, pg/g	51266
Standard deviation, pg/g	17244
Relative standard deviation, %	34
No. of values reported	37
No. of values removed	0
No. of reported non-detects	0

BDE 47



Z-score: BDE 47



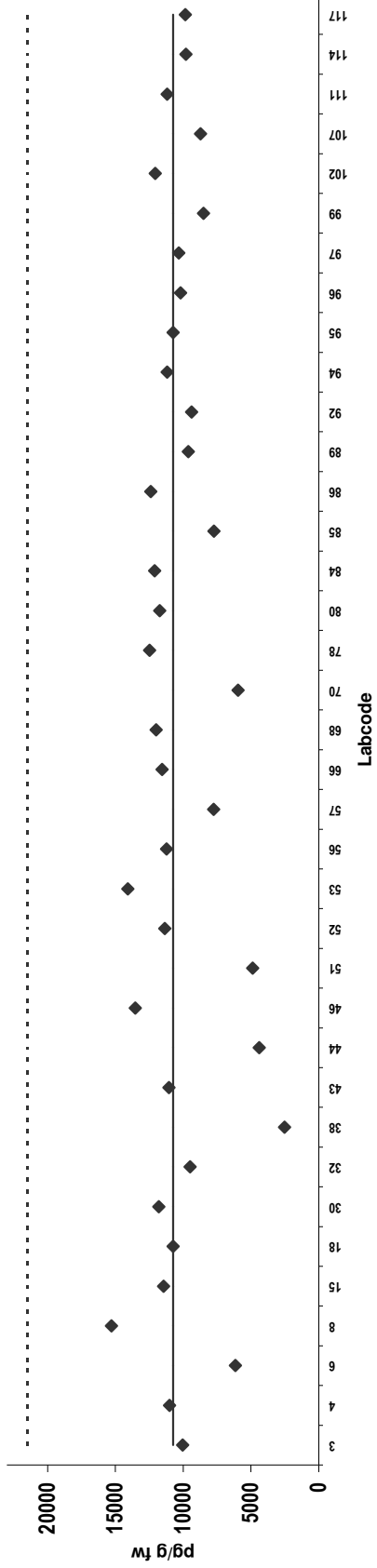
Trout
Congener: BDE 99

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	10040				
4	11000				
6	6150				
8	15289				
15	11448				
18	10732				
30	11800				
32	9500				
38	2530				
43	11049				
44	4385				
46	13523				
51	4868				
52	11355				
53	14077				
56	11220				
57	7760				
66	11549				
68	12000				
70	5950				
78	12487				
80	11740				
84	12106				
85	7730				
86	12389				
89	9611				
92	9372				
94	11173				
95	10744				
96	10200				
97	10333				
99	8491				
102	12066				
107	8732				
111	11182				
114	9790				
117	9844				

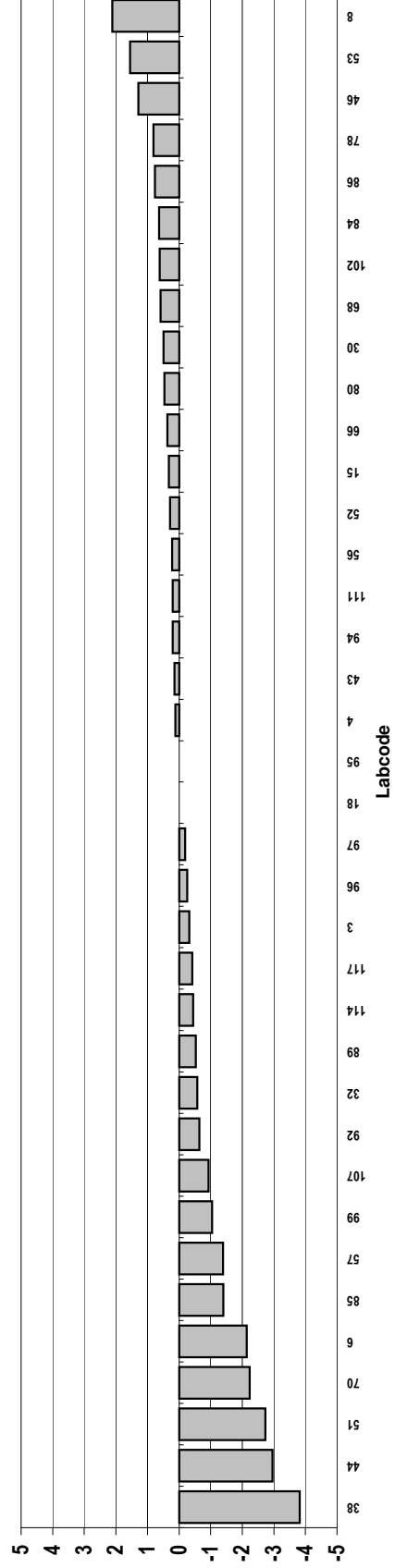
Consensus statistics

Consensus median, pg/g	10744
Median all values pg/g	10744
Consensus mean, pg/g	10114
Standard deviation, pg/g	2693
Relative standard deviation, %	27
No. of values reported	37
No. of values removed	0
No. of reported non-detects	0

BDE 99



Z-score: BDE 99

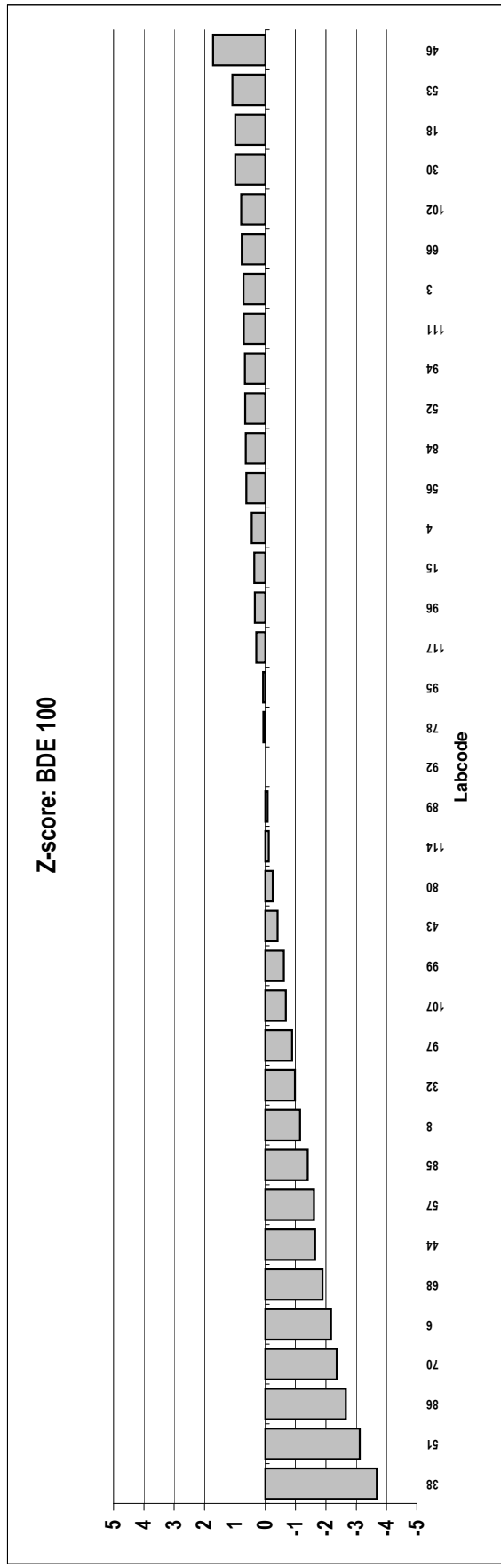
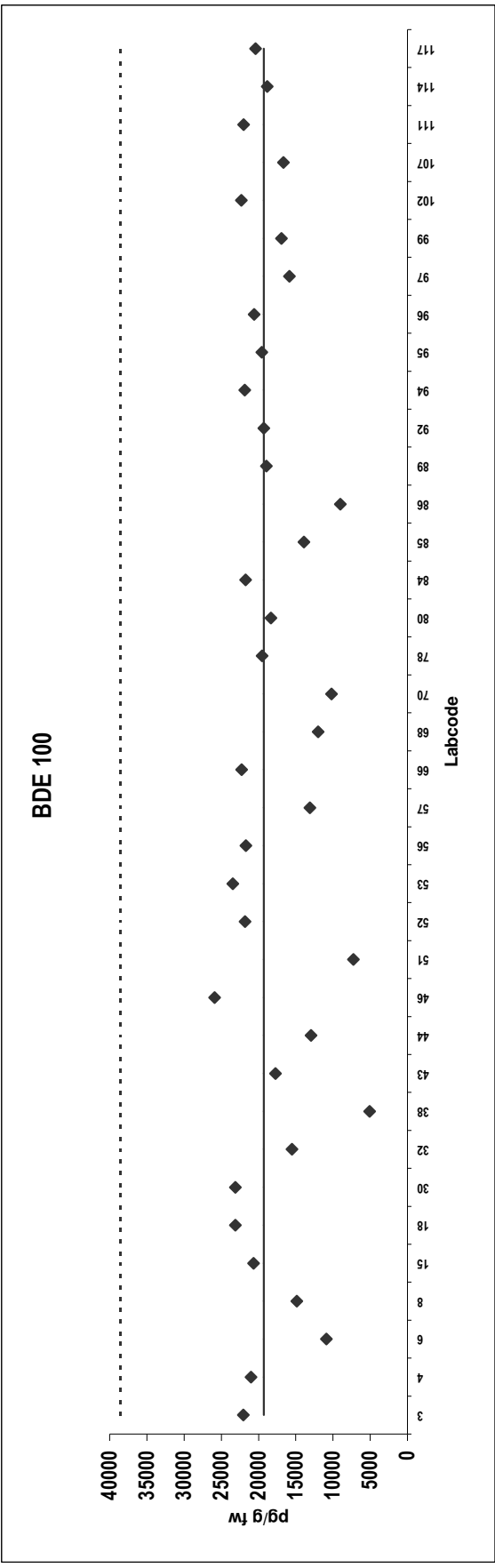


Trout
Congener: BDE 100

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	22050				
4	21000				
6	10900				
8	14846				
15	20679				
18	23102				
30	23100				
32	15500				
38	5100				
43	17724				
44	12948				
46	25906				
51	7267				
52	21830				
53	23446				
56	21699				
57	13100				
66	22267				
68	12000				
70	10200				
78	19505				
80	18320				
84	21747				
85	13900				
86	9032				
89	18964				
92	19287				
94	21870				
95	19567				
96	20600				
97	15857				
99	16906				
102	22330				
107	16662				
111	22000				
114	18820				
117	20408				

Consensus statistics

Consensus median, pg/g	19287
Median all values pg/g	19287
Consensus mean, pg/g	17850
Standard deviation, pg/g	5018
Relative standard deviation, %	28
No. of values reported	37
No. of values removed	0
No. of reported non-detects	0



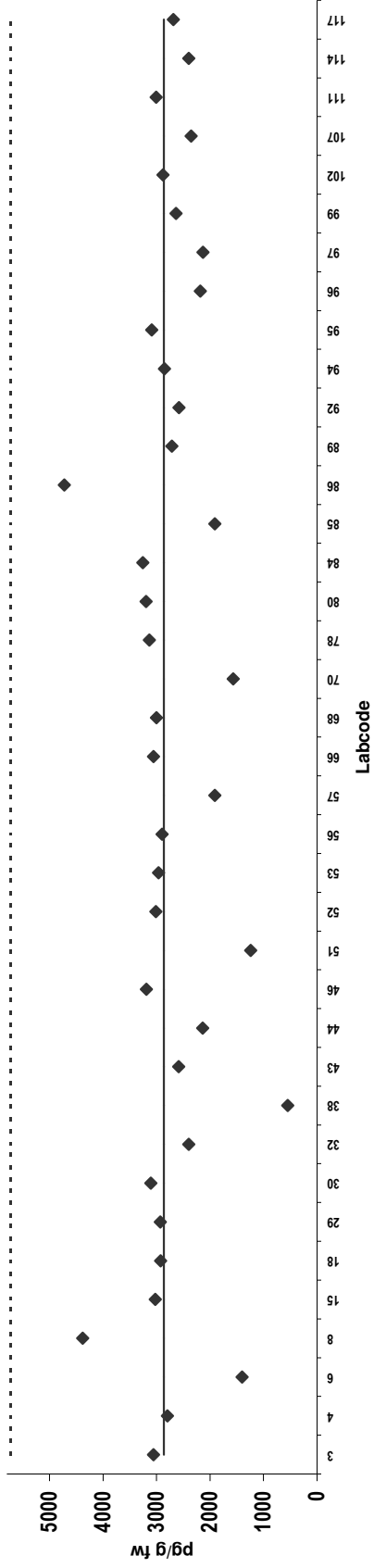
Trout
Congener: BDE 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	3060				
4	2800				
6	1400				
8	4384				
15	3023				
18	2924				
29	2930				
30	3110				
32	2400				
38	550				
43	2586				
44	2138				
46	3190				
51	1241				
52	3016				
53	2966				
56	2896				
57	1910				
66	3057				
68	3000				
70	1570				
78	3136				
80	3194				
84	3259				
85	1910				
86	4727				
89	2713				
92	2583				
94	2852				
95	3089				
96	2180				
97	2130				
99	2635				
102	2878				
107	2354				
111	3006				
114	2400				
117	2684				

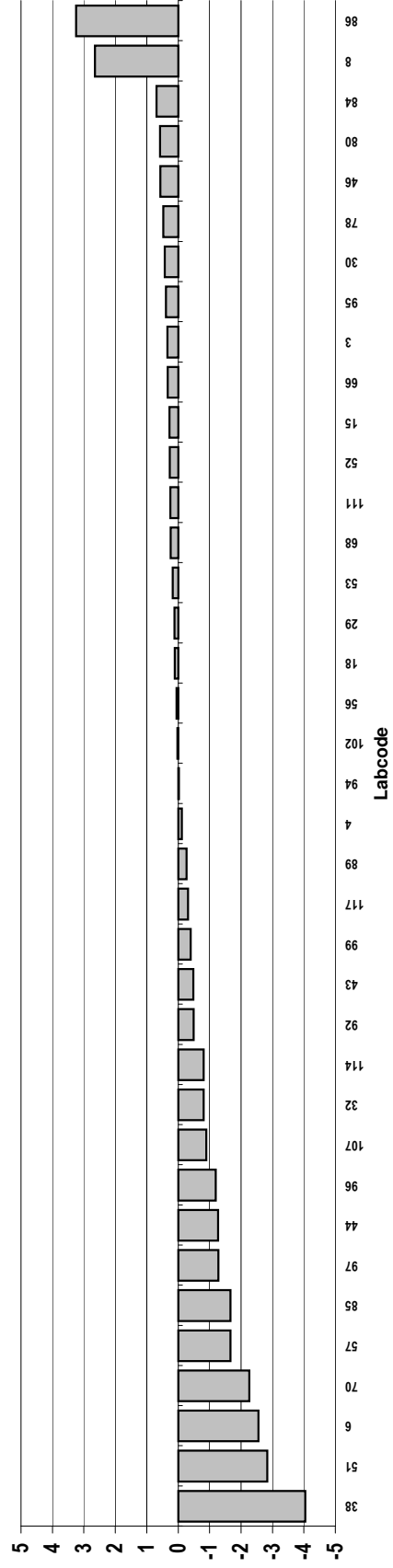
Consensus statistics

Consensus median, pg/g	2865
Median all values pg/g	2865
Consensus mean, pg/g	2681
Standard deviation, pg/g	760
Relative standard deviation, %	28
No. of values reported	38
No. of values removed	0
No. of reported non-detects	0

BDE 153



Z-score: BDE 153



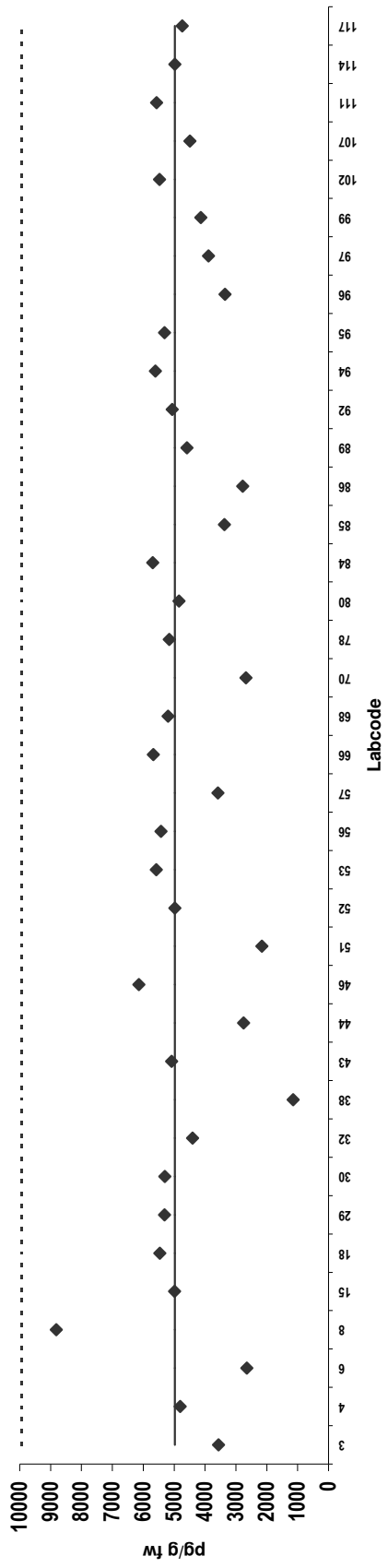
Trout
Congener: BDE 154

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	3565				
4	4800				
6	2650				
8	8819				
15	4982				
18	5462				
29	5306				
30	5300				
32	4400				
38	1150				
43	5078				
44	2754				
46	6144				
51	2158				
52	4975				
53	5574				
56	5426				
57	3580				
66	5676				
68	5200				
70	2670				
78	5157				
80	4839				
84	5692				
85	3370				
86	2780				
89	4584				
92	5058				
94	5608				
95	5310				
96	3350				
97	3883				
99	4140				
102	5471				
107	4488				
111	5566				
114	4980				
117	4742				

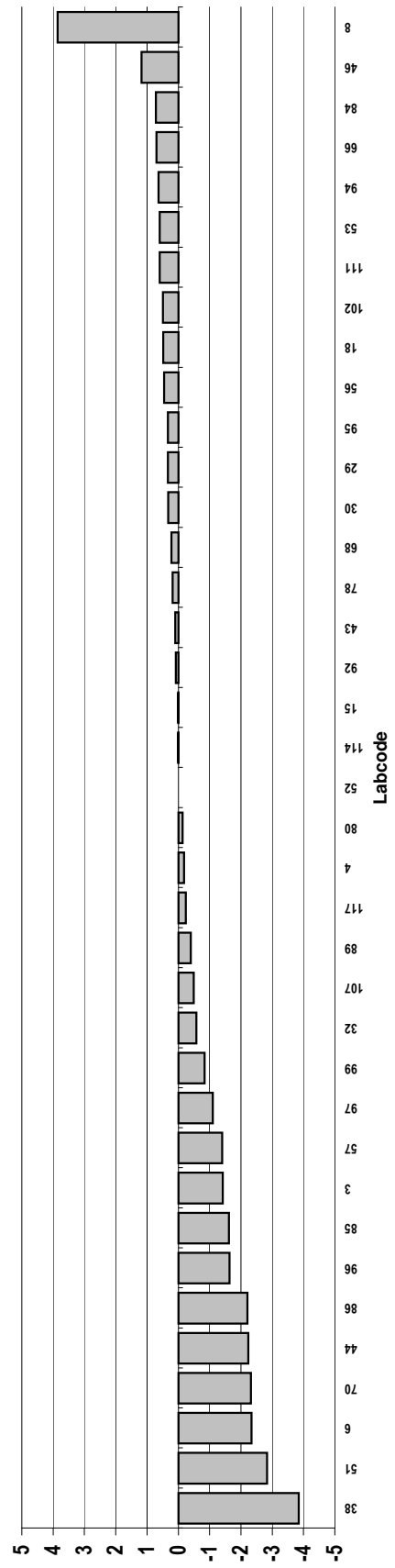
Consensus statistics

Consensus median, pg/g	4978
Median all values pg/g	4978
Consensus mean, pg/g	4597
Standard deviation, pg/g	1364
Relative standard deviation, %	30
No. of values reported	38
No. of values removed	0
No. of reported non-detects	0

BDE 154



Z-score: BDE 154



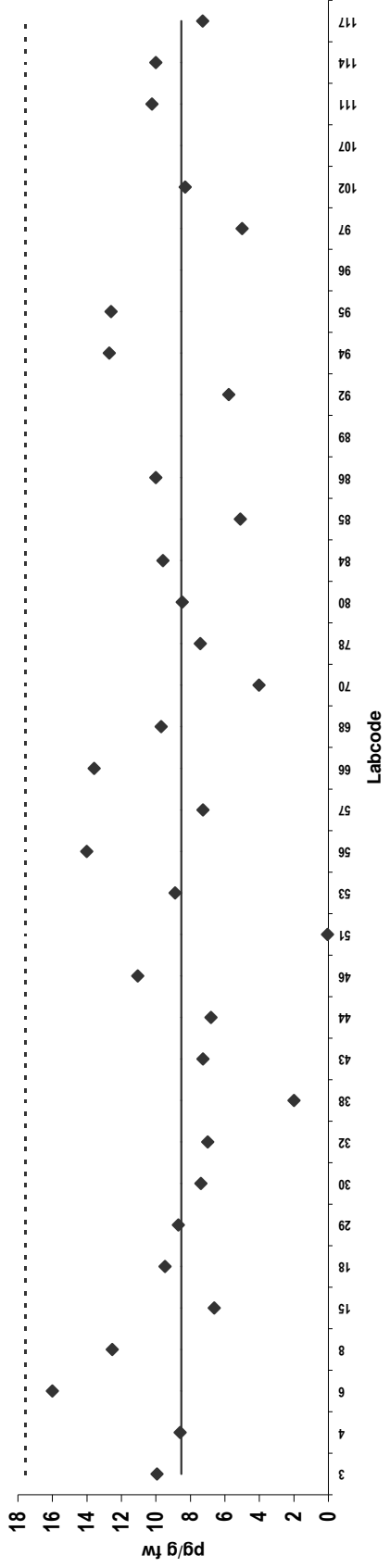
Trout
Congener: BDE 183

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	9.9				
4	8.6				
6	16				
8	13				
15	6.6				
18	9.5				
29	8.7				
30	7.4				
32	7.0				
38	2.0				
43	7.3				
44	6.8				
46	11				
51	0.050	ND			
53	8.9				
56	14				
57	7.3				
66	14	ND			
68	9.7				
70	4.0				
78	7.4				
80	8.5				
84	9.6				
85	5.1				
86	10				
89	40	Outlier			
92	5.8				
94	13				
95	13	ND			
96	21	Outlier			
97	5.0				
102	8.3				
107	20	Outlier			
111	10				
114	10				
117	7.3				

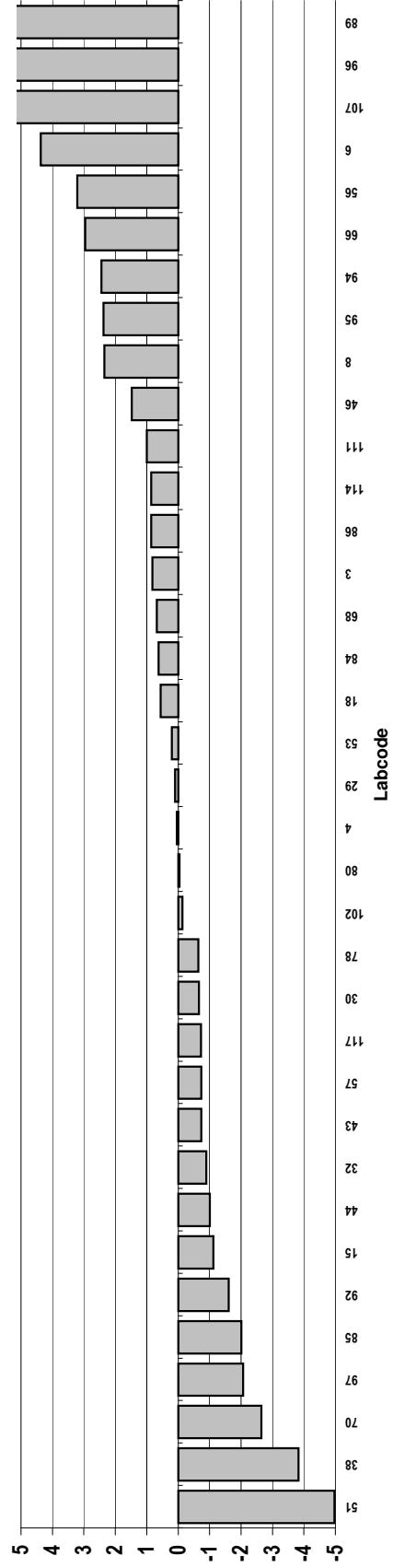
Consensus statistics

Consensus median, pg/g	8.5
Median all values pg/g	8.8
Consensus mean, pg/g	8.6
Standard deviation, pg/g	3.4
Relative standard deviation, %	39
No. of values reported	36
No. of values removed	3
No. of reported non-detects	3

BDE 183



Z-score: BDE 183



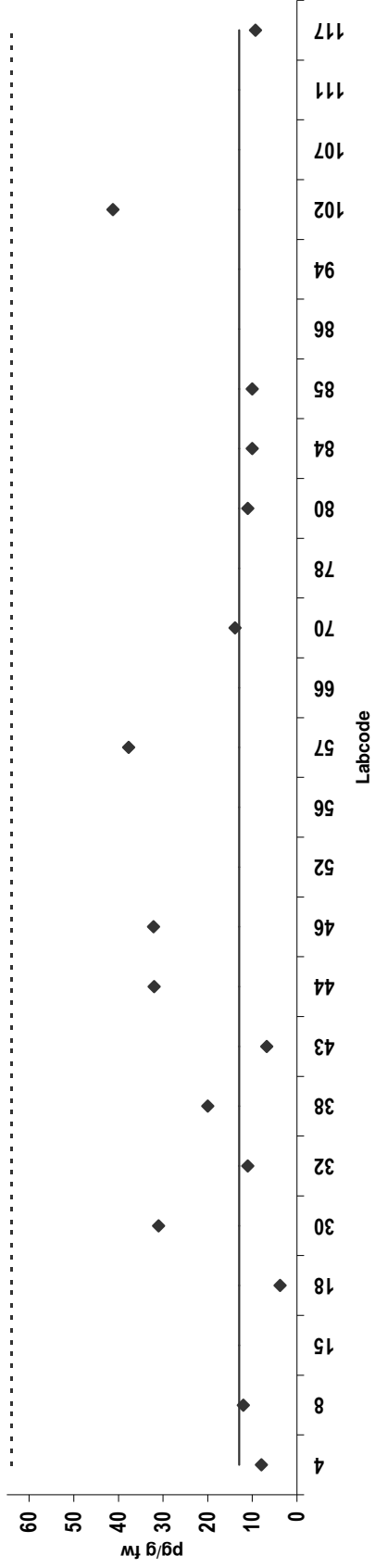
Trout
Congener: BDE 209

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	8.0				
8	12				
15	112	Outlier			
18	3.8				
30	31	ND			
32	11				
38	20				
43	6.8	ND			
44	32				
46	32				
52	92	Outlier			
56	149	Outlier			
57	38				
66	296	Outlier			
70	14				
78	212	Outlier,ND			
80	11	ND			
84	10				
85	10	ND			
86	69	Outlier			
94	156	Outlier			
102	41				
107	237	Outlier,ND			
111	71	Outlier			
117	9.3				

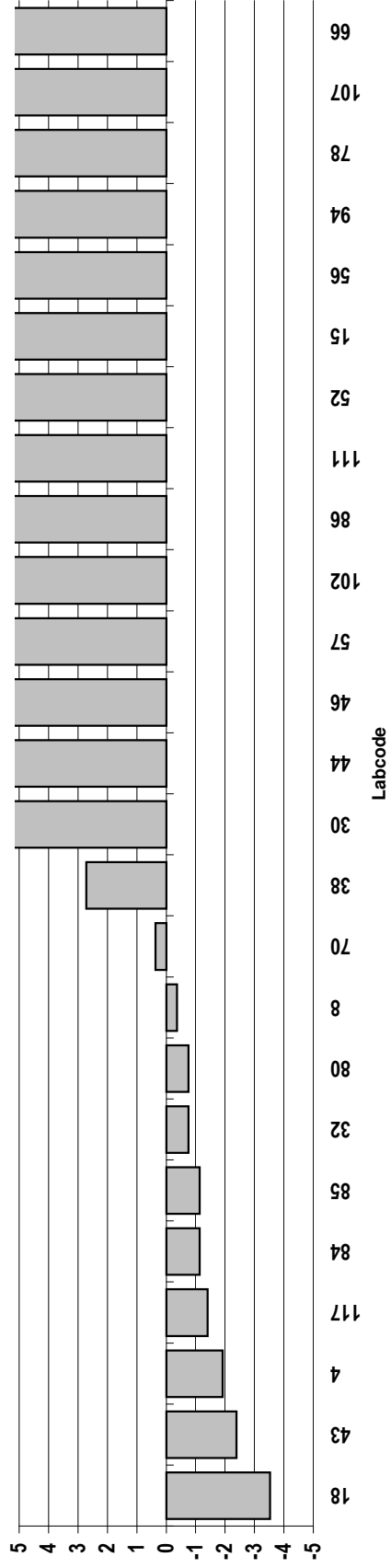
Consensus statistics

Consensus median, pg/g	13
Median all values pg/g	32
Consensus mean, pg/g	18
Standard deviation, pg/g	12
Relative standard deviation, %	68
No. of values reported	25
No. of values removed	9
No. of reported non-detects	6

BDE 209



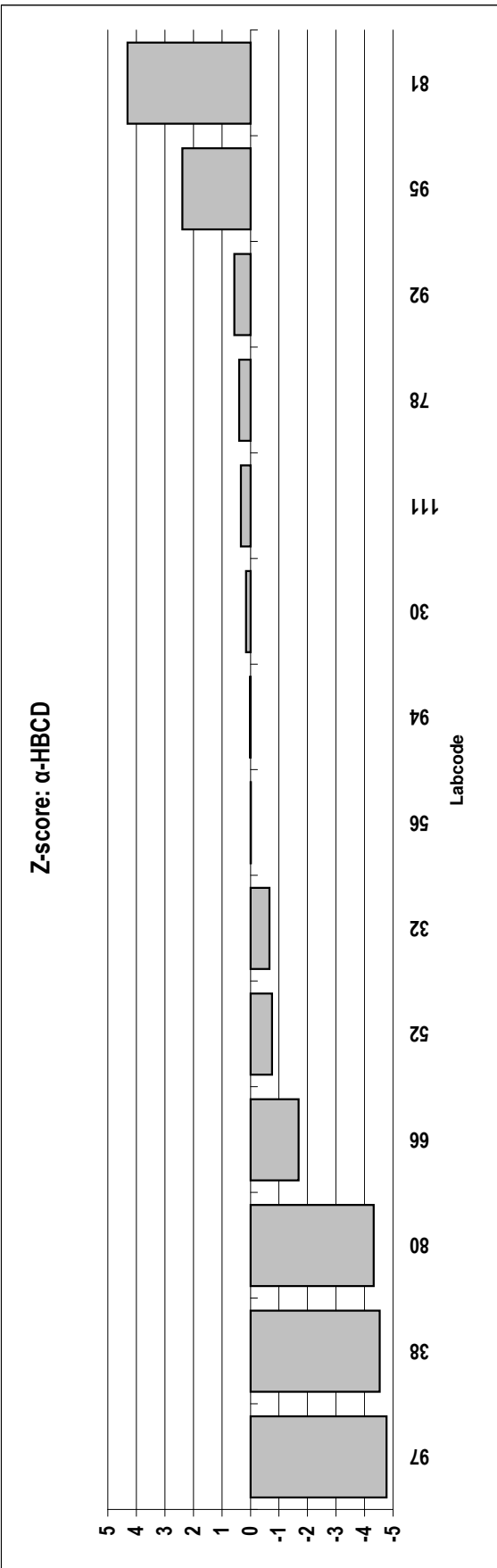
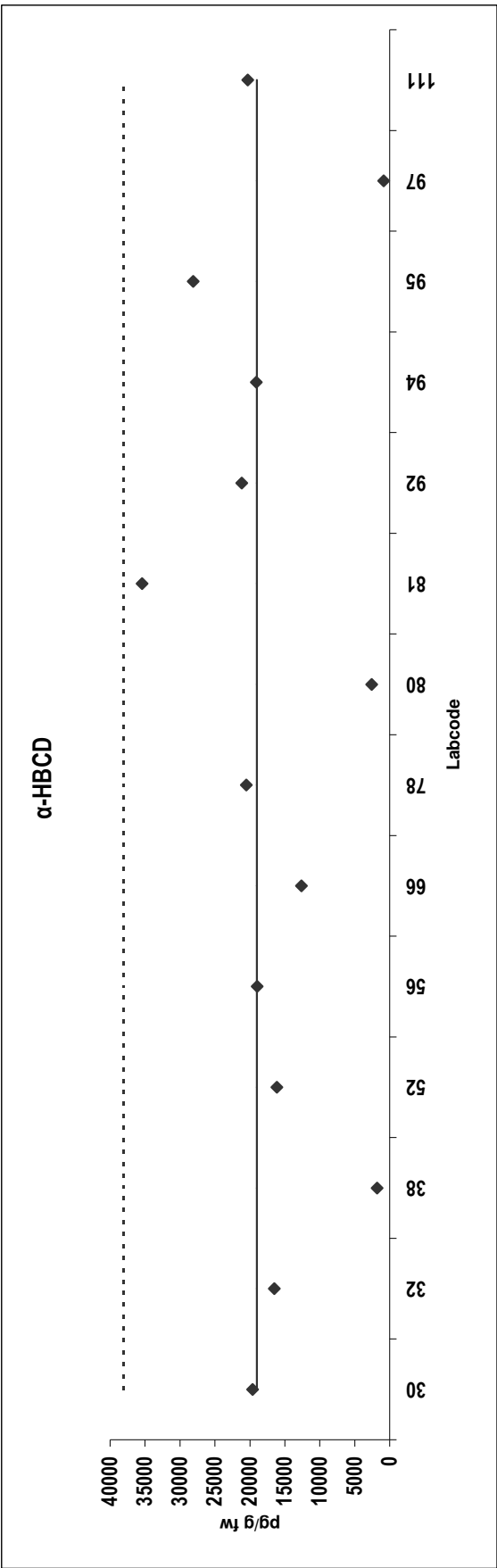
Z-score: BDE 209



Trout
Congener: α -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
30	19600				
32	16500				
38	1800				
52	16125				
56	18940				
66	12605				
78	20530				
80	2570				
81	35409				
92	21168				
94	19088				
95	28093				
97	870				
111	20300				

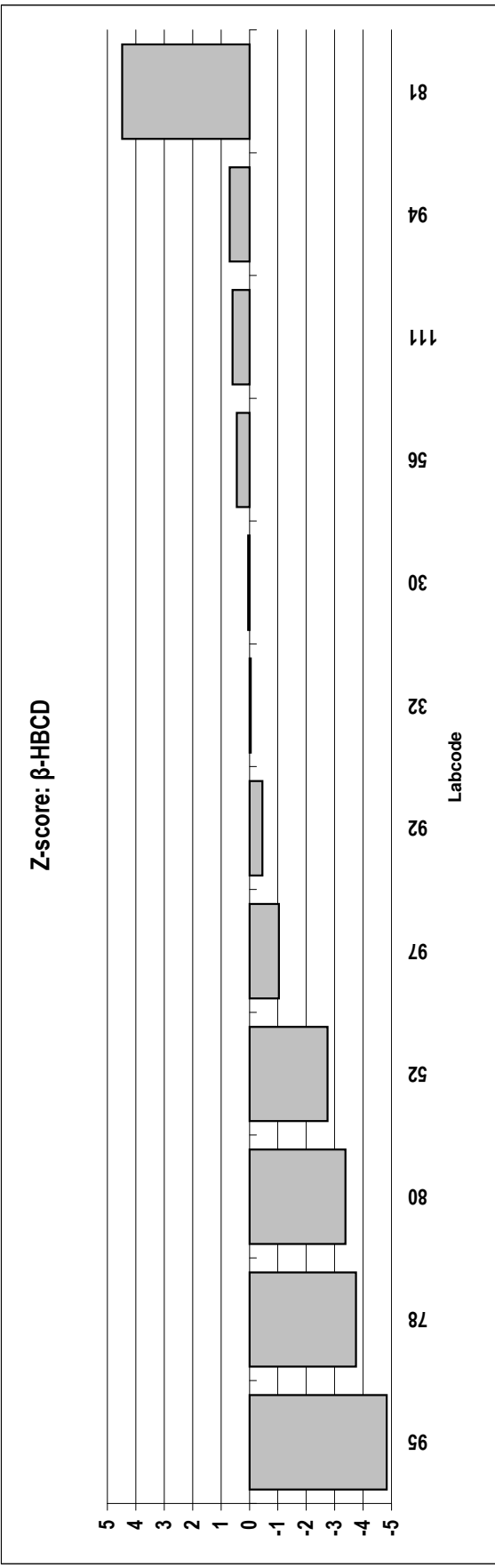
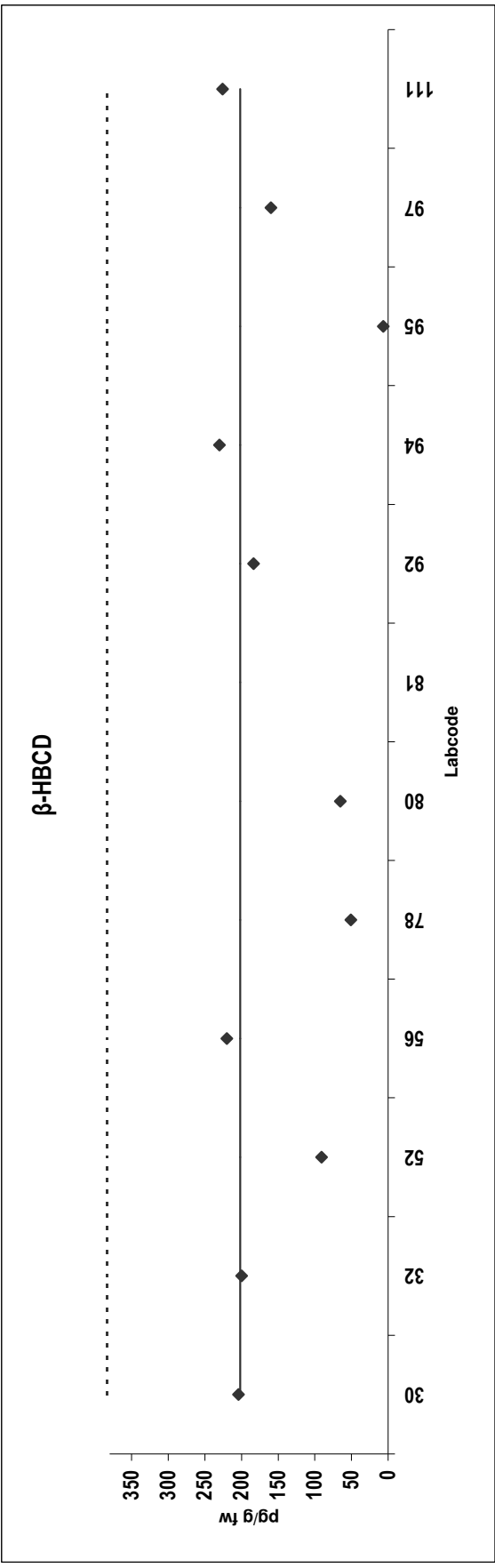
Consensus statistics	
Consensus median, pg/g	19014
Median all values pg/g	19014
Consensus mean, pg/g	16686
Standard deviation, pg/g	9751
Relative standard deviation, %	58
No. of values reported	14
No. of values removed	0
No. of reported non-detects	0



Trout
Congener: β -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
30	204				
32	200				
52	91				
56	220				
78	51	ND			
80	65				
81	383				
92	184				
94	230				
95	6.7	ND			
97	160				
111	226				

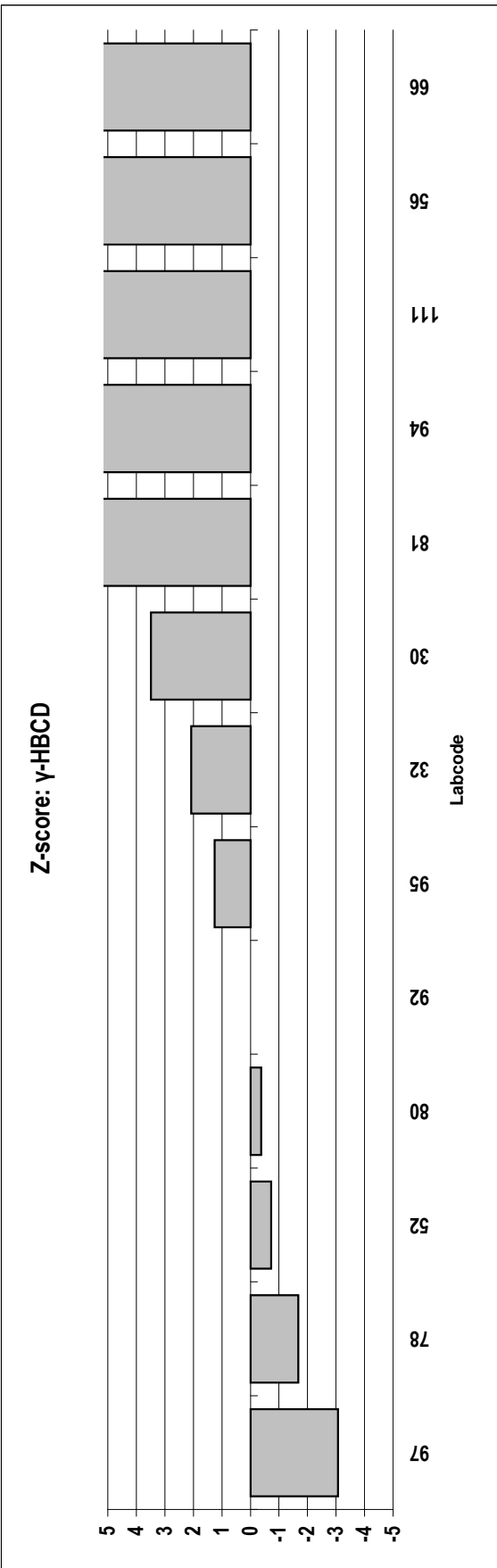
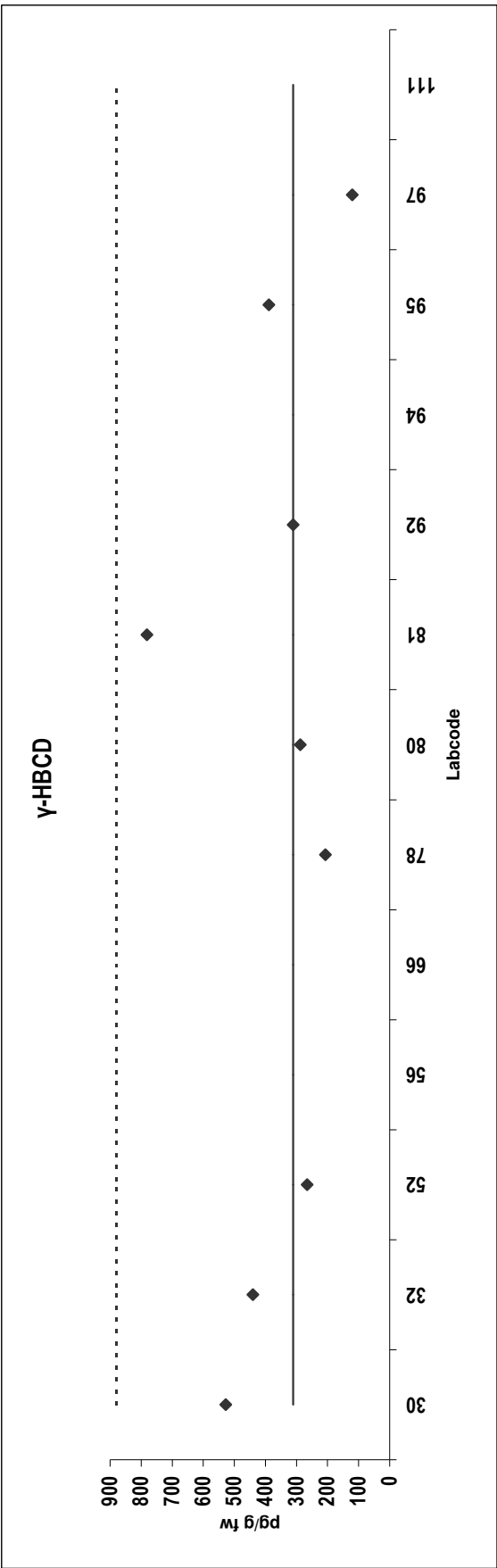
Consensus statistics	
Consensus median, pg/g	202
Median all values pg/g	192
Consensus mean, pg/g	168
Standard deviation, pg/g	102
Relative standard deviation, %	61
No. of values reported	12
No. of values removed	0
No. of reported non-detects	2



Trout
Congener: γ -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
30	528				
32	440				
52	266				
56	1122	Outlier			
66	2361	Outlier			
78	207				
80	288				
81	781				
92	311				
94	932	Outlier			
95	389				
97	120				
111	996	Outlier			

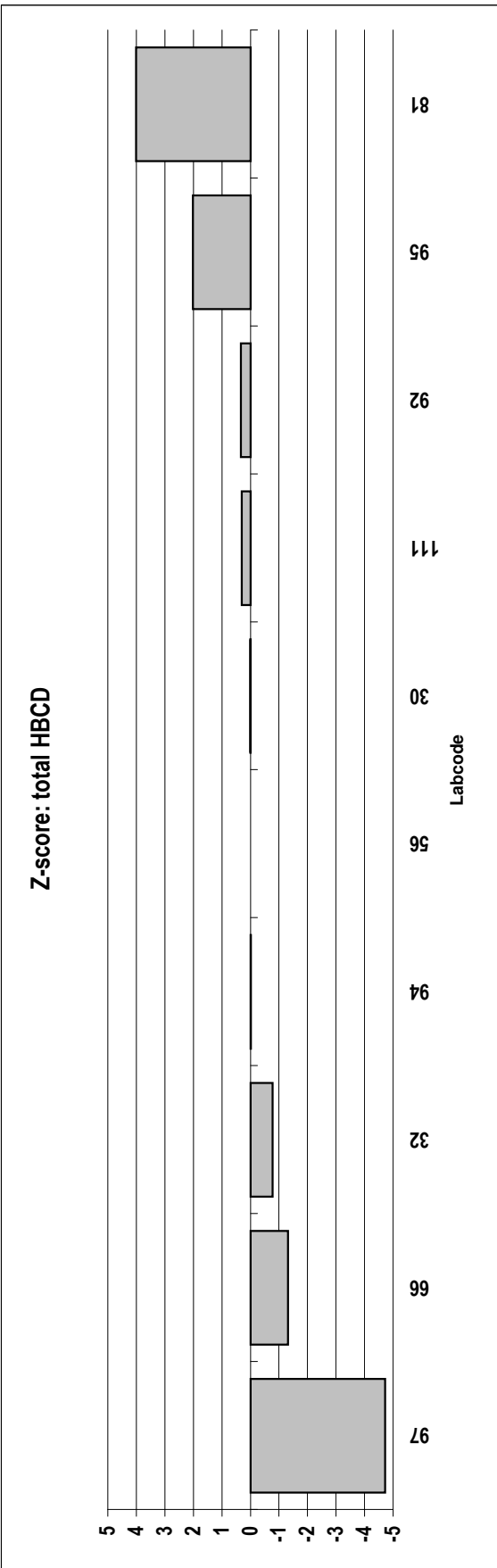
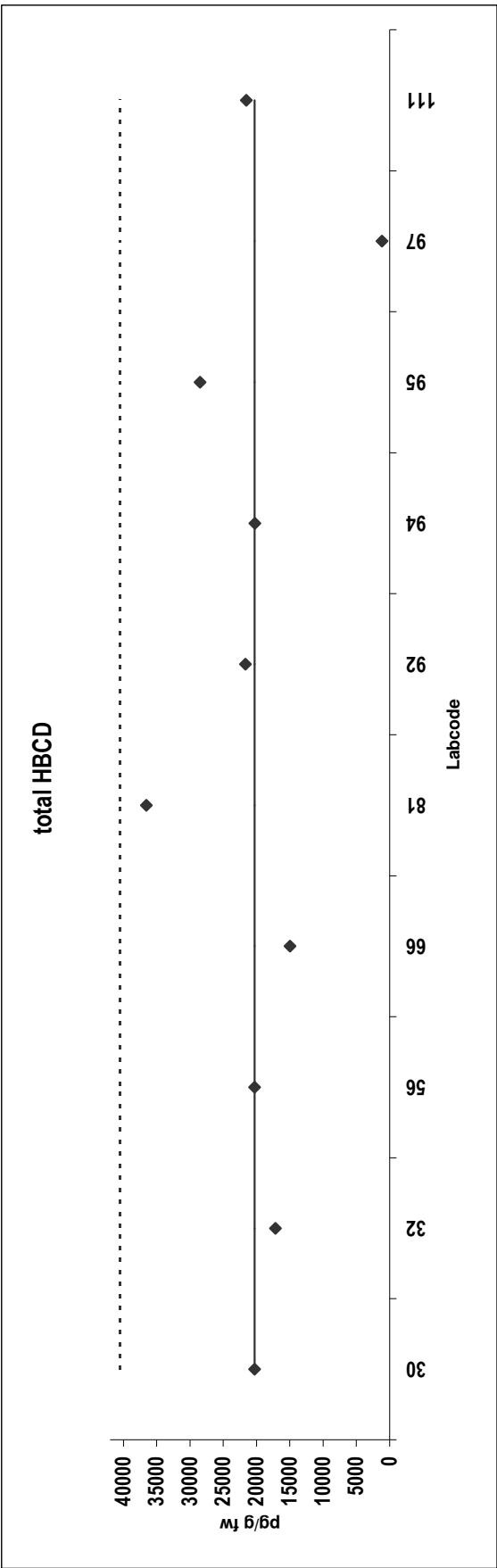
Consensus statistics	
Consensus median, pg/g	311
Median all values pg/g	440
Consensus mean, pg/g	370
Standard deviation, pg/g	197
Relative standard deviation, %	53
No. of values reported	13
No. of values removed	4
No. of reported non-detects	0



Trout
Congener: total HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
30	20300				
32	17140				
56	20282				
66	14966				
81	36573				
92	21663				
94	20250				
95	28482				
97	1150				
111	21522				

Consensus statistics	
Consensus median, pg/g	20291
Median all values pg/g	20291
Consensus mean, pg/g	20233
Standard deviation, pg/g	9069
Relative standard deviation, %	45
No. of values reported	10
No. of values removed	0
No. of reported non-detects	0



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